BioConductor Gene Listing

PM vs. PE

rank	affyId	accNum	geneId	geneName	geneSym	foldChng	tStat	rawPV	fdrPV
1	10463476	NM_178929	107250	Kazal-type serine peptidase in	Kazald1	11.611	10.303	1.42815e-05	0.00075605
2	10514185					8.287	11.102	8.57404e-06	0.000556103
3	10502552	NM_009899	12722	chloride channel calcium activ	Clca1	7.847	8.187	6.66544e-05	0.00209723
4	10576049	ENSMUST00000098351	15227	forkhead box F1a	Foxf1a	7.705	17.768	3.22203e-07	6.88149e-05
5	10485643	AK165089	329480	expressed sequence AI314831	AI314831	7.479	10.984	9.22679e-06	0.000580629
6	10480090	NM_001001309	241226	integrin alpha 8	Itga8	7.381	14.732	1.20442e-06	0.000156235
7	10519717	NM_009152	20346	sema domain, immunoglobulin do	Sema3a	6.575	14.611	1.27649e-06	0.000161613
8	10358581	NM_001024720	545370	hemicentin 1	Hmcn1	6.533	10.45	1.29681e-05	0.000715918
9	10385770	BC055827	257871	olfactory receptor 1372, pseud	Olfr1372-ps1	6.426	10.608	1.17051e-05	0.000668901
10	10591118	NM_001080814	270120	FAT tumor suppressor homolog 3	Fat3	6.327	7.053	0.000175445	0.00405422
11	10422244	NM_175499	239250	SLIT and NTRK-like family, mem	Slitrk6	6.27	11.316	7.51985e-06	0.000510979
12	10474295	NM_144783	22431	Wilms tumor homolog	Wt1	6.262	12.664	3.45893e-06	0.000296938
13	10368240	NM_011545	21412	transcription factor 21	Tcf21	6.142	13.111	2.71823e-06	0.000250979
14	10358577	NM_001024720	545370	hemicentin 1	Hmcn1	5.737	5.333	0.000983682	0.0129492
15	10591169	ENSMUST00000034653	73732	mucin 16	Muc16	5.645	7.396	0.000129292	0.00328181
16	10354374	NM_016917	53945	solute carrier family 40 (iron	Slc40a1	5.383	13.299	2.46182e-06	0.000239929
17	10422728	NM_023118	13132	disabled homolog 2 (Drosophila	Dab2	5.377	29.612	8.47867e-09	1.28491e-05
18	10591123	NM_001080814	270120	FAT tumor suppressor homolog 3	Fat3	5.136	8.168	6.76662e-05	0.00211667
19	10493820	NM_011313	20200	S100 calcium binding protein A	S100a6	5.008	16.887	4.61353e-07	8.78816e-05
20	10344952	NM_133832	98711	retinol dehydrogenase 10 (all-	Rdh10	4.995	13.922	1.78918e-06	0.000195002
21	10440344	NM_175549	268902	roundabout homolog 2 (Drosophi	Robo2	4.957	13.3	2.4602e-06	0.000239929
22	10601519	NM_172781	237010	kelch-like 4 (Drosophila)	Klhl4	4.915	9.987	1.76466e-05	0.000863701
23	10362968	NM_024285	23828	blood vessel epicardial substa	Bves	4.776	9.152	3.17788e-05	0.00128231
24	10358272	NM_001042577	16876	LIM homeobox protein 9	Lhx9	4.716	18.127	2.79692e-07	6.49869e-05
25	10536499	NM_007616	12389	caveolin, caveolae protein 1	Cav1	4.67	10.8	1.03535e-05	0.000623688
26	10439500	NM_178924	22268	uroplakin 1B	Upk1b	4.649	10.439	1.30631e-05	0.00071742
27	10358535	NM_001024720	545370	hemicentin 1	Hmcn1	4.623	4.66	0.00213813	0.0228537
28	10358668	NM_001024720	545370	hemicentin 1	Hmcn1	4.607	7.348	0.000134849	0.00336488
29	10344897	NM_172294	240725	sulfatase 1	Sulf1	4.57	7.96	8.01862e-05	0.00238126
30	10511363	NM_001002927	18619	preproenkephalin 1	Penk1	4.51	6.989	0.000185989	0.00421753
31	10586865	NM_009022	19378	aldehyde dehydrogenase family	Aldh1a2	4.497	8.615	4.75829e-05	0.00169376
32	10368495	NM_028351	72780	R-spondin 3 homolog (Xenopus l	Rspo3	4.474	12.112	4.70694e-06	0.000367274
33	10358670	NM_001024720	545370	hemicentin 1	Hmcn1	4.463	8.209	6.54706e-05	0.00206613
34	10363224	NM_021272	12140	fatty acid binding protein 7,	Fabp7	4.461	11.663	6.10797e-06	0.000437786
35	10547657	NM_009779	12267	complement component 3a recept	C3ar1	4.355	11.766	5.7518e-06	0.00041971
36	10498018	NM_130448	73173	protocadherin 18	Pcdh18	4.33	20.529	1.15728e-07	4.04969e-05
37	10502565	NM_030601	80797	chloride channel calcium activ	Clca2	4.318	5.422	0.000891863	0.0120849
38	10514088	NM_177863	329872	Fras1 related extracellular ma	Frem1	4.235	15.431	8.70113e-07	0.000129704
39	10476628	NM_020595	57329	otoraplin	Otor	4.23	6.038	0.000465284	0.00767799
40	10548892	NM_007486	11857	Rho, GDP dissociation inhibito	Arhgdib	4.229	6.987	0.000186445	0.00422076
41	10565204	NM_007562	12173	basonuclin 1	Bnc1	4.219	25.056	2.79921e-08	2.27641e-05
42	10499870	NM_008508	16939	loricrin	Lor	4.185	9.441	2.57852e-05	0.00111493
43	10592420	NM_178737	244810	expressed sequence AW551984	AW551984	4.108	11.976	5.08952e-06	0.000382321
44	10492355	NM_008604	17380	membrane metallo endopeptidase	Mme	4.073	5.056	0.00134319	0.0162056
45	10358575	NM_001024720	545370	hemicentin 1	Hmcn1	4.065	5.654	0.000693981	0.01019
46	10591978	NM_172290	235106	neurotrimin	Hnt	4.041	6.785	0.000224543	0.00476405

47	10490775	ENSMUST00000099256	100038710	predicted gene, ENSMUSG0000007	ENSMUSG00000074728	4.036	6.99	0.000185856	0.00421753
48	10358664	NM_001024720	545370	hemicentin 1	Hmcn1	4.032	6.382	0.000330277	0.00606651
49	10410931	NM_001081249	13003	versican	Vcan	3.983	17.078	4.26138e-07	8.37046e-05
50	10359504					3.954	11.296	7.61202e-06	0.000510979
51	10601942	NM_013724	27206	Nik related kinase	Nrk	3.938	13.241	2.53778e-06	0.000243904
52	10595211	NM_007730	12816	collagen, type XII, alpha 1	Col12a1	3.901	13.096	2.74019e-06	0.000251907
53	10358533	NM_001024720	545370	hemicentin 1	Hmcn1	3.879	4.373	0.00303972	0.0290298
54	10405587	NM_009369	21810	transforming growth factor, be	Tgfbi	3.853	23.519	4.39788e-08	2.3519e-05
55	10358583	NM_001024720	545370	hemicentin 1	Hmcn1	3.837	13.706	1.99532e-06	0.000210945
56	10494445	ENSMUST00000062058	280411	Lix1-like	Lix1l	3.791	15.646	7.89652e-07	0.000124642
57	10440340					3.781	5.665	0.000686063	0.0101158
58	10484283	NM_016744	18573	phosphodiesterase 1A, calmodul	Pde1a	3.772	14.221	1.54219e-06	0.000182167
59	10599348	NM_016886	53623	glutamate receptor, ionotropic	Gria3	3.76	18.321	2.59412e-07	6.09446e-05
60	10423917					3.755	19.15	1.89554e-07	5.27358e-05
61	10358561	NM_001024720	545370	hemicentin 1	Hmcn1	3.751	5.597	0.000737507	0.0106515
62	10410766	NM_010151	13865	nuclear receptor subfamily 2,	Nr2f1	3.748	13.879	1.82847e-06	0.000197251
63	10469358	NM_008625	17533	mannose receptor, C type 1	Mrc1	3.727	8.985	3.59408e-05	0.00138421
64	10385477					3.675	5.299	0.00102113	0.0133358
65	10358434	NM_008869	18783	phospholipase A2, group IVA (c	Pla2g4a	3.659	16.686	5.02044e-07	9.31159e-05
66	10438445	NM_183390	239743	kelch-like 6 (Drosophila)	Klhl6	3.659	10.618	1.16276e-05	0.000668083
67	10358633	NM_001024720	545370	hemicentin 1	Hmcn1	3.645	8.266	6.25345e-05	0.00203008
68	10433431					3.636	10.411	1.33013e-05	0.000725768
69	10358656	NM_001024720	545370	hemicentin 1	Hmcn1	3.622	6.592	0.000269644	0.00533798
70	10487040	NM_007993	14118	fibrillin 1	Fbn1	3.609	12.424	3.94848e-06	0.000323592
71	10514177	NM_172870	242509	basonuclin 2	Bnc2	3.607	17.97	2.97402e-07	6.61923e-05
72	10422760	NM_011815	23880	FYN binding protein	Fyb	3.602	10.277	1.4523e-05	0.000761775
73	10466374	NM_011600	21888	transducin-like enhancer of sp	Tle4	3.566	18.624	2.30948e-07	5.88333e-05
74	10415651	NM_013518	14180	fibroblast growth factor 9	Fgf9	3.56	12.913	3.02027e-06	0.000268322
75	10358658	NM_001024720	545370	hemicentin 1	Hmcn1	3.557	3.65	0.00776434	0.0567966
76	10565193	NM_013886	29877	hepatoma-derived growth factor	Hdgfrp3	3.557	23.732	4.12364e-08	2.29448e-05
77	10466800	NM_175013	226041	phosphoglucomutase 5	Pgm5	3.541	15.398	8.83342e-07	0.000129704
78	10599581	NM_133729	70415	RIKEN cDNA 2610018G03 gene	2610018G03Rik	3.522	7.447	0.000123756	0.00318334
79	10528207	NM_007643	12491	CD36 antigen	Cd36	3.497	5.024	0.00139405	0.0166332
80	10482448	NM_015753	24136	zinc finger E-box binding home	Zeb2	3.416	8.373	5.74442e-05	0.00190078
81	10358660	NM_001024720	545370	hemicentin 1	Hmcn1	3.4	9.49	2.49002e-05	0.00108779
82	10358662	NM_001024720	545370	hemicentin 1	Hmcn1	3.383	6.607	0.000265775	0.00529601
83	10358650	NM_001024720	545370	hemicentin 1	Hmcn1	3.381	3.654	0.00771823	0.0566647
84	10549102	NM_008428	16523	potassium inwardly-rectifying	Kcnj8	3.358	6.815	0.000218466	0.00469436
85	10484371	NM_018782	54598	calcitonin receptor-like	Calcrl	3.346	10.903	9.70528e-06	0.000594807
86	10554129	ENSMUST00000080024	434198	RIKEN cDNA B130024G19 gene	B130024G19Rik	3.34	11.532	6.60506e-06	0.000464589
87	10358666	NM_001024720	545370	hemicentin 1	Hmcn1	3.322	6.702	0.000242855	0.00502386
88	10550388	NM_010320	14709	guanine nucleotide binding pro	Gng8	3.321	8.175	6.7303e-05	0.00211136
89	10544768	NM_010453	15402	homeo box A5	Hoxa5	3.313	13.322	2.43248e-06	0.000239929
90	10358567	NM_001024720	545370	hemicentin 1	Hmcn1	3.306	4.381	0.00300758	0.0288009
91	10380629	NM_010461	15416	homeo box B8	Hoxb8	3.289	5.497	0.000821611	0.0114592
92	10498935	NM_017469	54195	guanylate cyclase 1, soluble,	Gucy1b3	3.288	8.715	4.40571e-05	0.00159785
93	10573924	NM_008610	17390	matrix metallopeptidase 2	Mmp2	3.261	20.3	1.25361e-07	4.07789e-05
94	10584561	NM_133733	71566	RIKEN cDNA 9030425E11 gene	9030425E11Rik	3.261	11.484	6.79735e-06	0.000471224
95	10473312	BC113787	241520	RIKEN cDNA D430039N05 gene	D430039N05Rik	3.239	6.698	0.000243643	0.00502386
96	10461622	NM_027209	69774	membrane-spanning 4-domains, s	Ms4a6b	3.239	6.104	0.000435053	0.00734139
97	10358579	NM_001024720	545370	hemicentin 1	Hmcn1	3.234	5.705	0.000657478	0.00982453
98	10604175	BC062956	245386	RIKEN cDNA 6430550H21 gene	6430550H21Rik	3.232	12.658	3.46878e-06	0.000296938

99	10358569	NM_001024720	545370	hemicentin 1	Hmcn1	3.231	4.118	0.00419204	0.0360605
100	10473444	NM_011784	23796	angiotensin receptor-like 1	Agtrl1	3.226	12.812	3.19085e-06	0.000281114
101	10576911	NM_010111	13642	ephrin B2	Efnb2	3.221	7.423	0.000126283	0.0032287
102	10435948	NM_026439	67896	coiled-coil domain containing	Ccdc80	3.212	10.915	9.63008e-06	0.00059364
103	10358585	NM_001024720	545370	hemicentin 1	Hmcn1	3.21	9.556	2.3768e-05	0.00105048
104	10452419	NM_207654	13640	ephrin A5	Efna5	3.206	7.215	0.000151792	0.00364301
105	10365974	NM_007833	13179	decorin	Dcn	3.2	6.181	0.000402761	0.00696888
106	10458999	NM_010181	14119	fibrillin 2	Fbn2	3.199	13.859	1.84641e-06	0.000198175
107	10601412	NM_175271	78134	lysophosphatidic acid receptor	Lpar4	3.192	14.765	1.18587e-06	0.00015574
108	10358652	NM_001024720	545370	hemicentin 1	Hmcn1	3.191	3.765	0.00665764	0.0506729
109	10358654	NM_001024720	545370	hemicentin 1	Hmcn1	3.174	3.647	0.00779973	0.0570057
110	10493108	NM_007759	12904	cellular retinoic acid binding	Crabp2	3.171	15.645	7.90117e-07	0.000124642
111	10358565	NM_001024720	545370	hemicentin 1	Hmcn1	3.152	3.286	0.0128175	0.0806105
112	10461856	NM_008137	14675	guanine nucleotide binding pro	Gna14	3.148	5.51	0.000810187	0.0113281
113	10358623	NM_001024720	545370	hemicentin 1	Hmcn1	3.144	8.025	7.59999e-05	0.00229892
114	10521759	NM_178804	20563	slit homolog 2 (Drosophila)	Slit2	3.135	9.13	3.22895e-05	0.00129318
115	10498653	NM_133675	66183	RIKEN cDNA 1110032A04 gene	1110032A04Rik	3.123	10.566	1.20292e-05	0.00068007
116	10505954	NM_013690	21687	endothelial-specific receptor	Tek	3.114	7.714	9.83957e-05	0.00274832
117	10403584	NM_010917	18073	nidogen 1	Nid1	3.11	14.059	1.67047e-06	0.000188879
118	10365559	NM_010512	16000	insulin-like growth factor 1	Igf1	3.102	6.74	0.000234321	0.00490372
119	10380641	NM_008268	15413	homeo box B5	Hoxb5	3.101	8.239	6.39212e-05	0.00205715
120	10581013	NM_009866	12552	cadherin 11	Cdh11	3.089	20.36	1.22747e-07	4.05525e-05
121	10571815	NM_153581	234267	glycoprotein m6a	Gpm6a	3.089	6.806	0.000220268	0.00469964
122	10591135	NM_001080814	270120	FAT tumor suppressor homolog 3	Fat3	3.088	4.863	0.00167989	0.0188834
123	10413416	NM_134437	171463	interleukin 17 receptor D	Il17rd	3.054	14.536	1.32318e-06	0.000163727
124	10529875	NM_001077398	16826	LIM domain binding 2	Ldb2	3.054	17.081	4.25604e-07	8.37046e-05
125	10500808	NM_133859	99543	olfactomedin-like 3	Olfml3	3.051	10.55	1.21521e-05	0.00068336
126	10380648	NM_010459	15412	homeo box B4	Hoxb4	3.049	14.447	1.38084e-06	0.000168766
127	10431697	NM_011994	26874	ATP-binding cassette, sub-fami	Abcd2	3.039	12.441	3.91021e-06	0.000322959
128	10358637	NM_001024720	545370	hemicentin 1	Hmcn1	3.025	5.666	0.000685183	0.0101099
129	10358619	NM_001024720	545370	hemicentin 1	Hmcn1	3.017	4.635	0.00220471	0.0233315
130	10394593	BC052465	76820	DNA segment, Chr 12, ERATO Doi	D12Ertd553e	3.017	8.363	5.79172e-05	0.00191344
131	10453747	NM_130449	140792	collectin sub-family member 12	Colec12	3.016	10.877	9.86515e-06	0.00060112
132	10522749	NM_198702	319387	latrophilin 3	Lphn3	3.014	6.91	0.000200054	0.0044062
133	10513739	NM_011607	21923	tenascin C	Tnc	3.009	5.765	0.000617256	0.00940292
134	10503448	NM_019724	17389	matrix metallopeptidase 16	Mmp16	2.995	14.835	1.1474e-06	0.000154526
135	10358527	NM_001024720	545370	hemicentin 1	Hmcn1	2.989	3.174	0.0150075	0.0904044
136	10498952	NM_021896	60596	guanylate cyclase 1, soluble,	Gucy1a3	2.987	13.053	2.80312e-06	0.000254374
137	10435765					2.984	5.434	0.000880626	0.0119742
138	10358615	NM_001024720	545370	hemicentin 1	Hmcn1	2.977	5.681	0.000674847	0.00997927
139	10506050	NM_001122952	18027	nuclear factor I/A	Nfia	2.973	7.722	9.77537e-05	0.00274125
140	10607403	NM_175429	207474	potassium channel tetramerisat	Kctd12b	2.965	7.103	0.000167709	0.00393132
141	10606016	NM_013563	16186	interleukin 2 receptor, gamma	Il2rg	2.964	6.366	0.000335229	0.00611645
142	10358617	NM_001024720	545370	hemicentin 1	Hmcn1	2.944	11.236	7.89559e-06	0.000524982
143	10435767					2.937	2.758	0.0273788	0.135099
144	10380637	NM_008269	15414	homeo box B6	Hoxb6	2.932	7.596	0.000108818	0.00295358
145	10358587	NM_001024720	545370	hemicentin 1	Hmcn1	2.927	6.743	0.000233519	0.00489349
146	10596812	BC115538	68176	RIKEN cDNA 6230427J02 gene	6230427J02Rik	2.923	13.561	2.14887e-06	0.000221637
147	10427297	NM_175730	15424	homeo box C5	Hoxc5	2.918	5.7	0.000660858	0.00984721
148	10356880	NM_009183	20452	ST8 alpha-N-acetyl-neuraminide	St8sia4	2.917	7.099	0.000168392	0.00394294
149	10358531	NM_001024720	545370	hemicentin 1	Hmcn1	2.913	5.031	0.00138225	0.0165588
150	10503835	NM_027491	52187	Ras-related GTP binding D	Rragd	2.91	7.403	0.000128586	0.00327174
151	10522503	NM_011058	18595	platelet derived growth factor	Pdgfra	2.9	13.071	2.77604e-06	0.000253344
152	10497451	NM_007753	12873	carboxypeptidase A3, mast cell	Cpa3	2.899	4.387	0.00298597	0.0286589

153	10372177	NM_177368	278279	transmembrane and tetratricope	Tmtc2	2.892	10.275	1.45445e-05	0.000761775
154	10513957	NM_011211	19266	protein tyrosine phosphatase,	Ptprd	2.883	10.3	1.43029e-05	0.00075605
155	10542355	NM_010128	13730	epithelial membrane protein 1	Emp1	2.872	8.102	7.1374e-05	0.00220573
156	10564527	NM_009697	11819	nuclear receptor subfamily 2,	Nr2f2	2.867	11.74	5.84039e-06	0.000424361
157	10358529	NM_001024720	545370	hemicentin 1	Hmcn1	2.836	3.512	0.00937401	0.0648149
158	10358515	NM_001024720	545370	hemicentin 1	Hmcn1	2.833	3.297	0.0126198	0.0796516
159	10397645	NM_008152	14744	G-protein coupled receptor 65	Gpr65	2.825	8.417	5.55234e-05	0.00186897
160	10358553	NM_001024720	545370	hemicentin 1	Hmcn1	2.822	5.788	0.000602346	0.00923256
161	10353192	NM_010164	14048	eyes absent 1 homolog (Drosoph	Eya1	2.812	6.941	0.000194467	0.00432822
162	10538802	BC047154	68169	RIKEN cDNA A930038C07 gene	A930038C07Rik	2.804	11.764	5.75652e-06	0.00041971
163	10358559	NM_001024720	545370	hemicentin 1	Hmcn1	2.804	4.414	0.00288818	0.0281158
164	10542575	NM_018779	54611	phosphodiesterase 3A, cGMP inh	Pde3a	2.803	8.499	5.20459e-05	0.0017952
165	10358648	NM_001024720	545370	hemicentin 1	Hmcn1	2.797	3.556	0.0088223	0.0620968
166	10530692	NM_010612	16542	kinase insert domain protein r	Kdr	2.797	7.043	0.000177044	0.00407992
167	10574438	NM_009868	12562	cadherin 5	Cdh5	2.793	9.815	1.98396e-05	0.000940559
168	10495186	BC127040	229694	expressed sequence AI504432	AI504432	2.792	9.423	2.61317e-05	0.0011234
169	10584600					2.786	12.071	4.8193e-06	0.0003692
170	10358525	NM_001024720	545370	hemicentin 1	Hmcn1	2.779	3.415	0.0107152	0.0712233
171	10510129	NM_011303	20148	dehydrogenase/reductase (SDR f	Dhrs3	2.778	8.742	4.31652e-05	0.00157631
172	10521796					2.776	3.936	0.00536766	0.0430807
173	10552469	NM_001039042	626834	kallikrein related-peptidase 1	Klk13	2.776	15.947	6.90551e-07	0.000113186
174	10435745	AY512926	791390	predicted gene, ENSMUSG0000006	ENSMUSG00000068293	2.776	4.689	0.00206493	0.0222419
175	10490777	NM_030708	80892	zinc finger homeodomain 4	Zfhx4	2.776	11.001	9.1286e-06	0.000580043
176	10607484	NM_001093750	211612	patched domain containing 1	Ptchd1	2.773	4.225	0.00365844	0.0328606
177	10556076	NM_172907	244198	olfactomedin-like 1	Olfml1	2.773	12.396	4.0108e-06	0.00032617
178	10497689	NM_013531	14696	guanine nucleotide binding pro	Gnb4	2.772	12.922	3.0069e-06	0.000268322
179	10345777	NM_133193	107527	interleukin 1 receptor-like 2	Il1rl2	2.758	4.135	0.00410171	0.0355728
180	10358573	NM_001024720	545370	hemicentin 1	Hmcn1	2.758	2.717	0.0290334	0.140156
181	10606333	DQ192038	333564	gene model 784, (NCBI)	Gm784	2.753	8.401	5.62148e-05	0.00187182
182	10484307	NM_011356	20378	frizzled-related protein	Frzb	2.749	5.296	0.0010247	0.0133742
183	10566268	NM_008219	15132	hemoglobin Z, beta-like embryo	Hbb-bh1	2.739	4.646	0.00217597	0.0231432
184	10358611	NM_001024720	545370	hemicentin 1	Hmcn1	2.738	7.453	0.000123083	0.00317762
185	10521972	NM_018764	54216	protocadherin 7	Pcdh7	2.733	7.846	8.80681e-05	0.00257553
186	10601980	NM_175541	245631	melanoma associated antigen (m	Mum1l1	2.726	14.395	1.41639e-06	0.000172115
187	10585438	NM_013496	12903	cellular retinoic acid binding	Crabp1	2.709	6.473	0.000302239	0.00575488
188	10438753	NM_173379	210530	leprecan-like 1	Leprel1	2.699	10.44	1.30497e-05	0.00071742
189	10358571	NM_001024720	545370	hemicentin 1	Hmcn1	2.694	3.796	0.00638423	0.0490382
190	10502050	ENSMUST00000029662	71481	alpha-kinase 1	Alpk1	2.689	3.863	0.00584213	0.0461779
191	10523451	NM_013470	11745	annexin A3	Anxa3	2.685	16.504	5.42268e-07	9.74342e-05
192	10563441	NM_010129	13732	epithelial membrane protein 3	Emp3	2.666	12.632	3.5198e-06	0.000297691
193	10374366	NM_207655	13649	epidermal growth factor recept	Egfr	2.663	5.698	0.000662356	0.0098615
194	10403727	NM_008130	14634	GLI-Kruppel family member GLI3	Gli3	2.659	8.901	3.82774e-05	0.001435
195	10543791	NM_013723	27205	podocalyxin-like	Podxl	2.651	10.253	1.4764e-05	0.000767004
196	10526441	NM_175309	100647	uroplakin 3B	Upk3b	2.631	8.341	5.89316e-05	0.00194089
197	10601993	BC113128	102871	RIKEN cDNA D330045A20 gene	D330045A20Rik	2.63	13.31	2.44783e-06	0.000239929
198	10549162	NM_011374	20449	ST8 alpha-N-acetyl-neuraminide	St8sia1	2.62	10.511	1.24634e-05	0.000695317
199	10358549	NM_001024720	545370	hemicentin 1	Hmcn1	2.618	5.733	0.000638126	0.00962378
200	10475544	NM_172537	214968	sema domain, transmembrane dom	Sema6d	2.61	8.457	5.38086e-05	0.00184099
201	10545974	NM_054041	69538	anthrax toxin receptor 1	Antxr1	2.603	9.156	3.16914e-05	0.00128123
202	10401673	NM_009368	21809	transforming growth factor, be	Tgfb3	2.593	11.923	5.24807e-06	0.000390723
203	10567297	NM_001033380	319622	RIKEN cDNA E030018N11 gene	E030018N11Rik	2.587	7.572	0.0001111	0.00299999

204	10416437	NM_008879	18826	lymphocyte cytosolic protein 1	Lcp1	2.583	10.737	1.07786e-05	0.000636968
205	10358517	NM_001024720	545370	hemicentin 1	Hmcn1	2.58	4.223	0.00366883	0.0328981
206	10542592	AK143453	100093700	predicted gene, ENSMUSG0000007	ENSMUSG00000072690	2.577	8.305	6.06441e-05	0.00199108
207	10531724	NM_139198	231507	placenta-specific 8	Plac8	2.574	9.72	2.11939e-05	0.000984889
208	10375261	NM_008070	14401	gamma-aminobutyric acid (GABA-	Gabrb2	2.572	6.664	0.000251597	0.00512009
209	10358521	NM_001024720	545370	hemicentin 1	Hmcn1	2.571	4.544	0.00246254	0.0252023
210	10358613	NM_001024720	545370	hemicentin 1	Hmcn1	2.548	4.854	0.00169816	0.0190584
211	10356020	ENSMUST00000077946	210293	dedicator of cytokinesis 10	Dock10	2.548	10.132	1.59947e-05	0.000816888
212	10445071	NM_001013745	22715	zinc finger protein 57	Zfp57	2.544	15.568	8.17825e-07	0.000125305
213	10368556	NM_013904	15214	hairy/enhancer-of-split relate	Hey2	2.541	5.977	0.000495397	0.00805744
214	10538640	NM_011920	26357	ATP-binding cassette, sub-fami	Abcg2	2.54	12.248	4.35868e-06	0.000348901
215	10488382	NM_010740	17064	CD93 antigen	Cd93	2.532	8.252	6.32582e-05	0.00204829
216	10538126	NM_174990	107526	GTPase, IMAP family member 4	Gimap4	2.531	9.595	2.31235e-05	0.00102993
217	10404606	NM_010745	17084	lymphocyte antigen 86	Ly86	2.527	6.272	0.000367932	0.00651009
218	10407841	NM_001081348	94253	HECT, C2 and WW domain contain	Hecw1	2.525	9.702	2.14602e-05	0.000992896
219	10591120	NM_001080814	270120	FAT tumor suppressor homolog 3	Fat3	2.524	4.438	0.00280104	0.0275466
220	10435271	NM_175256	77446	HEG homolog 1 (zebrafish)	Heg1	2.521	9.065	3.38878e-05	0.0013393
221	10471945	ENSMUST00000064026	433424	predicted gene, OTTMUSG0000001	OTTMUSG00000012358	2.521	5.35	0.000965002	0.0128005
222	10433776	NM_011415	20583	snail homolog 2 (Drosophila)	Snai2	2.521	12.416	3.96699e-06	0.000323854
223	10506031	NM_010905	18027	nuclear factor I/A	Nfia	2.519	13.52	2.19483e-06	0.00022508
224	10440091	NM_007739	12837	collagen, type VIII, alpha 1	Col8a1	2.514	9.699	2.15107e-05	0.000993061
225	10568668	NM_007400	11489	a disintegrin and metallopepti	Adam12	2.51	8.598	4.82182e-05	0.00170608
226	10453678	NM_011546	21417	zinc finger E-box binding home	Zeb1	2.51	14.774	1.18058e-06	0.00015574
227	10579958	NM_008357	16168	interleukin 15	Il15	2.509	5.931	0.000519504	0.00829872
228	10476321	NM_023043	26434	prion protein dublet	Prnd	2.502	7.306	0.000139912	0.00344063
229	10358519	NM_001024720	545370	hemicentin 1	Hmcn1	2.495	3.196	0.0145523	0.0884179
230	10536216	NM_025331	66066	guanine nucleotide binding pro	Gng11	2.492	14.598	1.2841e-06	0.000161613
231	10591127	NM_001080814	270120	FAT tumor suppressor homolog 3	Fat3	2.492	3.669	0.00756551	0.0558733
232	10519857	NM_010427	15234	hepatocyte growth factor	Hgf	2.491	6.295	0.000359687	0.00641108
233	10358563	NM_001024720	545370	hemicentin 1	Hmcn1	2.489	3.42	0.0106335	0.070881
234	10549108	NM_021041	20928	ATP-binding cassette, sub-fami	Abcc9	2.488	5.636	0.000707793	0.0103353
235	10584142	NM_011808	23871	E26 avian leukemia oncogene 1,	Ets1	2.488	9.146	3.19105e-05	0.00128517
236	10484207	ENSMUST00000049544	545428	RIKEN cDNA 2610301F02 gene	2610301F02Rik	2.487	10.484	1.26843e-05	0.000705782
237	10523359	NM_018866	55985	chemokine (C-X-C motif) ligand	Cxcl13	2.481	14.26	1.51266e-06	0.000179684
238	10367634	NM_031185	83397	A kinase (PRKA) anchor protein	Akap12	2.479	9.601	2.30252e-05	0.00102927
239	10502890	NM_011372	20447	ST6 (alpha-N-acetyl-neuraminyl	St6galnac3	2.479	10.536	1.22648e-05	0.000687871
240	10579812	NM_010332	13617	endothelin receptor type A	Ednra	2.475	7.752	9.52953e-05	0.00271553
241	10463070	NM_009848	12495	ectonucleoside triphosphate di	Entpd1	2.472	8.291	6.13239e-05	0.00200098
242	10570957	NM_013834	20377	secreted frizzled-related prot	Sfrp1	2.47	10.603	1.17443e-05	0.000669332
243	10590031	NM_133721	104099	integrin alpha 9	Itga9	2.466	6.615	0.000263589	0.00527277
244	10559207	NM_019391	16985	lymphocyte specific 1	Lsp1	2.465	5.944	0.000512375	0.00821976
245	10514049	NM_001113209	18028	nuclear factor I/B	Nfib	2.453	10.773	1.05329e-05	0.000632693
246	10591131	NM_001080814	270120	FAT tumor suppressor homolog 3	Fat3	2.45	3.996	0.00491048	0.0407485
247	10366052	NM_013598	17311	kit ligand	Kitl	2.448	8.467	5.33794e-05	0.00183223
248	10358557	NM_001024720	545370	hemicentin 1	Hmcn1	2.447	2.979	0.0198394	0.109298
249	10536444	NM_053242	114142	forkhead box P2	Foxp2	2.436	10.091	1.64442e-05	0.000829823
250	10425161	NM_008495	16852	lectin, galactose binding, sol	Lgals1	2.43	9.23	3.00229e-05	0.00123263
251	10384223	NM_008343	16009	insulin-like growth factor bin	Igfbp3	2.427	12.672	3.44226e-06	0.000296938
252	10531931	NM_010097	13602	SPARC-like 1 (mast9, hevin)	Sparcl1	2.418	4.69	0.00206283	0.0222307
253	10406434	NM_025282	17260	myocyte enhancer factor 2C	Mef2c	2.412	18.553	2.37263e-07	5.97226e-05
254	10351867	NM_001013779	383619	absent in melanoma 2	Aim2	2.412	5.985	0.000491163	0.00799473
255	10500559	NM_013821	15497	hydroxy-delta-5-steroid dehydr	Hsd3b6	2.409	3.437	0.0103912	0.0698131

256	10446763	NM_029999	77889	limb-bud and heart	Lbh	2.404	11.305	7.57148e-06	0.000510979
257	10364593	NM_007725	12798	calponin 2	Cnn2	2.4	4.101	0.00428669	0.0366806
258	10483865	NM_010222	14231	FK506 binding protein 7	Fkbp7	2.398	8.769	4.22733e-05	0.00154909
259	10578950	ENSMUST00000098718	100038489	predicted gene, ENSMUSG0000007	ENSMUSG00000074303	2.394	5.027	0.00138903	0.0166024
260	10434291	NM_054052	108105	UDP-GlcNAc:betaGal beta-1,3-N-	B3gnt5	2.392	9.535	2.41236e-05	0.00106264
261	10464425	NM_018869	14773	G protein-coupled receptor kin	Grk5	2.392	6.327	0.000348485	0.00626742
262	10534906	BC028660	100134986	hypothetical LOC100134986	LOC100134986	2.389	9.13	3.22927e-05	0.00129318
263	10421100	NM_008691	18040	neurofilament, medium polypept	Nefm	2.385	5.633	0.00070973	0.0103493
264	10506254	NM_183024	242570	ribonucleoprotein, PTB-binding	Raver2	2.381	6.929	0.000196563	0.00435315
265	10362959	NM_024286	78977	popeye domain containing 3	Popdc3	2.381	4.599	0.00230218	0.0240437
266	10360391	NM_001045481	15950	interferon activated gene 203	Ifi203	2.379	4.591	0.0023258	0.02416
267	10584595	ENSMUST00000098868	70455	RIKEN cDNA 2610203C20 gene	2610203C20Rik	2.379	15.622	7.98261e-07	0.000124642
268	10496359	NM_016885	59308	endomucin	Emcn	2.37	4.531	0.00250042	0.0254055
269	10369023	ENSMUST00000020064	77296	RIKEN cDNA 9430073N08 gene	9430073N08Rik	2.365	4.314	0.00327018	0.0303666
270	10351111	NR_002870	474332	dynamin 3, opposite strand	Dnm3os	2.364	8.244	6.36533e-05	0.0020557
271	10586744	NM_007585	12306	annexin A2	Anxa2	2.364	9.739	2.09202e-05	0.000976462
272	10358631	NM_001024720	545370	hemicentin 1	Hmcn1	2.361	3.506	0.00945295	0.065254
273	10514054	NM_001113209	18028	nuclear factor I/B	Nfib	2.353	8.434	5.47862e-05	0.00186146
274	10453759					2.35	4.015	0.0047852	0.0398968
275	10358593	NM_001024720	545370	hemicentin 1	Hmcn1	2.347	3.845	0.00598342	0.0468915
276	10602840	NM_021389	58194	SH3-domain kinase binding prot	Sh3kbp1	2.345	8.409	5.58636e-05	0.00186897
277	10358591	NM_001024720	545370	hemicentin 1	Hmcn1	2.344	5.905	0.00053349	0.00847492
278	10551883	NM_011662	22177	TYRO protein tyrosine kinase b	Tyrobp	2.339	13.499	2.21823e-06	0.000225492
279	10366746	NM_177152	320398	leucine-rich repeats and immun	Lrig3	2.338	9.294	2.86656e-05	0.00119931
280	10409876	NM_007796	13024	cytotoxic T lymphocyte-associa	Ctla2a	2.338	6.923	0.000197696	0.0043708
281	10492689	NM_019971	54635	platelet-derived growth factor	Pdgfc	2.338	20.168	1.31299e-07	4.16289e-05
282	10456046	NM_008809	18596	platelet derived growth factor	Pdgfrb	2.336	8.211	6.5352e-05	0.00206613
283	10347792	AY169784	16367	insulin receptor substrate 1	Irs1	2.336	14.816	1.15747e-06	0.000154896
284	10423971	NM_138674	192190	polycystic kidney and hepatic	Pkhd1l1	2.335	4.296	0.00334293	0.0308275
285	10469457	NM_026162	67448	plexin domain containing 2	Plxdc2	2.331	10.986	9.21353e-06	0.000580629
286	10424140	NM_181277	12818	collagen, type XIV, alpha 1	Col14a1	2.331	4.356	0.0031016	0.0293686
287	10593293	NM_001081445	17967	neural cell adhesion molecule	Ncam1	2.324	8.059	7.39051e-05	0.00226017
288	10375259	NM_008070	14401	gamma-aminobutyric acid (GABA-	Gabrb2	2.323	4.224	0.00366401	0.0328828
289	10346843	NM_001077403	18187	neuropilin 2	Nrp2	2.32	8.953	3.68298e-05	0.00140819
290	10376778	NM_029568	76293	microfibrillar-associated prot	Mfap4	2.319	6.808	0.000219923	0.00469892
291	10407350	NM_008002	14165	fibroblast growth factor 10	Fgf10	2.318	4.826	0.00175479	0.0195692
292	10502780	NM_001081298	99633	latrophilin 2	Lphn2	2.317	15.421	8.7422e-07	0.000129704
293	10512279	NM_016673	12804	ciliary neurotrophic factor re	Cntfr	2.314	6.871	0.000207388	0.00453465
294	10358555	NM_001024720	545370	hemicentin 1	Hmcn1	2.308	4.131	0.00412397	0.0357073
295	10478928	NM_080455	228911	teashirt zinc finger family me	Tshz2	2.305	17.82	3.15534e-07	6.80781e-05
296	10418171	NM_001101433	71918	RIKEN cDNA 2310047A01 gene	2310047A01Rik	2.305	10.633	1.15206e-05	0.000665549
297	10551736	NM_026731	68458	protein phosphatase 1, regulat	Ppp1r14a	2.304	9.629	2.25837e-05	0.00101814
298	10403796	NM_175007	218038	amphiphysin	Amph	2.295	4.781	0.00185104	0.020374
299	10368243	NM_010167	14051	eyes absent 4 homolog (Drosoph	Eya4	2.293	9.641	2.23927e-05	0.00101169
300	10403579	NM_181852	107849	prolactin family 2, subfamily	Prl2c5	2.291	6.134	0.000422131	0.00720964
301	10505073	NM_172867	242466	zinc finger protein 462	Zfp462	2.289	17.07	4.27549e-07	8.37046e-05
302	10467013	NM_001013833	19091	protein kinase, cGMP-dependent	Prkg1	2.284	4.403	0.00292542	0.028306
303	10604608					2.279	4.268	0.00346515	0.0315806
304	10346321	ENSMUST00000097736	628004	predicted gene, EG628004	EG628004	2.279	3.277	0.0129818	0.0814258
305	10571788	NM_009506	22341	vascular endothelial growth fa	Vegfc	2.279	6.497	0.000295329	0.00566646
306	10473384	NM_021398	58207	solute carrier family 43, memb	Slc43a3	2.278	11.331	7.45404e-06	0.000508433

307	10461614	NM_028595	73656	membrane-spanning 4-domains, s	Ms4a6c	2.275	8.772	4.21808e-05	0.00154839
308	10502778	NM_001081298	99633	latrophilin 2	Lphn2	2.27	7.719	9.79701e-05	0.00274155
309	10358625	NM_001024720	545370	hemicentin 1	Hmcn1	2.268	4.132	0.00411839	0.0356882
310	10368373	NM_029881	77220	RIKEN cDNA C030003D03 gene	C030003D03Rik	2.262	8.679	4.52956e-05	0.00163435
311	10600836	NM_010833	17698	moesin	Msn	2.259	16.739	4.90908e-07	9.18563e-05
312	10358605	NM_001024720	545370	hemicentin 1	Hmcn1	2.251	6.437	0.000313017	0.00586221
313	10497265	NM_024406	11770	fatty acid binding protein 4,	Fabp4	2.247	4.158	0.00398259	0.0348832
314	10513004	ENSMUST00000098069	100038677	predicted gene, ENSMUSG0000007	ENSMUSG00000073850	2.244	3.456	0.010115	0.0685504
315	10482866	AK156640	100038415	predicted gene, ENSMUSG0000007	ENSMUSG00000075328	2.232	12.112	4.70731e-06	0.000367274
316	10358597	NM_001024720	545370	hemicentin 1	Hmcn1	2.231	3.358	0.0115922	0.0750934
317	10360920	NM_009367	21808	transforming growth factor, be	Tgfb2	2.225	8.913	3.79244e-05	0.00142498
318	10502772	NM_001081298	99633	latrophilin 2	Lphn2	2.223	11.196	8.08938e-06	0.000528933
319	10544583	NM_153175	231931	GTPase, IMAP family member 6	Gimap6	2.221	10.095	1.64061e-05	0.000829823
320	10353460	NM_023872	226922	potassium voltage-gated channe	Kcnq5	2.22	6.646	0.000255947	0.00516956
321	10452427					2.219	6.827	0.000215976	0.00466946
322	10374406	NM_029861	380686	cannabinoid receptor interacti	Cnrip1	2.217	11.225	7.94899e-06	0.000526876
323	10554863	NM_001040085	83671	synaptotagmin-like 2	Sytl2	2.216	7.474	0.000120867	0.00314805
324	10472965	NM_008276	15437	homeo box D8	Hoxd8	2.212	4.029	0.00470392	0.0394838
325	10484201	ENSMUST00000049544	545428	RIKEN cDNA 2610301F02 gene	2610301F02Rik	2.212	3.891	0.00563161	0.0450359
326	10412921	NM_008695	18074	nidogen 2	Nid2	2.211	7.506	0.000117544	0.00309835
327	10458731	NM_001085373	328949	mutated in colorectal cancers	Mcc	2.211	11.331	7.45432e-06	0.000508433
328	10392221	NM_008816	18613	platelet/endothelial cell adhe	Pecam1	2.209	11.733	5.86393e-06	0.000424613
329	10358609	NM_001024720	545370	hemicentin 1	Hmcn1	2.207	5.346	0.000970158	0.0128528
330	10536845	NM_001081185	68794	filamin C, gamma (actin bindin	Flnc	2.191	9.294	2.86572e-05	0.00119931
331	10436519	NM_019413	19876	roundabout homolog 1 (Drosophi	Robo1	2.189	9.852	1.93426e-05	0.0009295
332	10458906	NM_008908	19038	peptidylprolyl isomerase C	Ppic	2.187	10.743	1.07356e-05	0.000636968
333	10358733	NM_016846	19731	ral guanine nucleotide dissoci	Rgl1	2.186	5.492	0.000826641	0.011499
334	10517513	NM_007574	12262	complement component 1, q subc	C1qc	2.186	6.974	0.000188534	0.00422741
335	10483081	NM_007986	14089	fibroblast activation protein	Fap	2.175	2.987	0.0196193	0.108456
336	10492021	NM_015784	50706	periostin, osteoblast specific	Postn	2.175	4.97	0.00148425	0.0172257
337	10400607	AK163637	320772	MAM domain containing glycosyl	Mdga2	2.168	8.99	3.58157e-05	0.00138235
338	10484197	ENSMUST00000049544	545428	RIKEN cDNA 2610301F02 gene	2610301F02Rik	2.167	7.007	0.000182975	0.00417349
339	10531195	NM_001081401	330119	a disintegrin-like and metallo	Adamts3	2.163	3.388	0.0111166	0.0729285
340	10500276	BC028528	229600	cDNA sequence BC028528	BC028528	2.162	7.07	0.000172829	0.00401571
341	10504203	AK006581	75952	RIKEN cDNA 4930578G10 gene	4930578G10Rik	2.161	2.464	0.0422278	0.179868
342	10592067	NM_008026	14247	Friend leukemia integration 1	Fli1	2.158	7.301	0.00014058	0.00344552
343	10412345	NM_001081009	52552	poly (ADP-ribose) polymerase f	Parp8	2.153	6.46	0.000306109	0.00579961
344	10380699	NM_019877	56358	coatomer protein complex, subu	Copz2	2.152	9.266	2.9249e-05	0.00120789
345	10591116	NM_001080814	270120	FAT tumor suppressor homolog 3	Fat3	2.148	3.691	0.00735124	0.0545959
346	10472398	NM_001099298	110876	sodium channel, voltage-gated,	Scn2a1	2.147	3.975	0.00504666	0.0415985
347	10388042	NM_134022	103712	RIKEN cDNA 6330403K07 gene	6330403K07Rik	2.146	9.101	3.29831e-05	0.00131336
348	10492682	NM_133187	68659	RIKEN cDNA 1110032E23 gene	1110032E23Rik	2.146	11.193	8.10511e-06	0.000528933
349	10423243	NM_009865	320873	cadherin 10	Cdh10	2.145	7.089	0.000169839	0.0039593
350	10368647	NM_172508	212898	dermatan sulfate epimerase	Dse	2.145	9.918	1.84963e-05	0.00089827
351	10549282	NM_019923	16439	inositol 1,4,5-triphosphate re	Itpr2	2.145	15.731	7.60122e-07	0.000123015
352	10364444	NM_013591	17123	mucosal vascular addressin cel	Madcam1	2.144	7.974	7.92579e-05	0.00236365
353	10464400	ENSMUST00000065383	107376	RIKEN cDNA E330013P04 gene	E330013P04Rik	2.144	9.034	3.46557e-05	0.00135547
354	10381298	NM_019444	54409	receptor (calcitonin) activity	Ramp2	2.14	7.905	8.39102e-05	0.00246416
355	10501586	NM_007901	13609	sphingosine-1-phosphate recept	S1pr1	2.14	6.152	0.000414604	0.00713294

356	10521700	ENSMUST00000087486	100126871	predicted gene, ENSMUSG0000006	ENSMUSG00000067356	2.137	4.685	0.00207531	0.0223423
357	10417713	NM_011243	218772	retinoic acid receptor, beta	Rarb	2.137	4.852	0.00170208	0.0190821
358	10469167	NM_177386	353282	Scm-like with four mbt domains	Sfmbt2	2.133	6.294	0.000359911	0.00641108
359	10422598	NM_009155	20363	selenoprotein P, plasma, 1	Sepp1	2.129	5.842	0.000569347	0.00888721
360	10599927	NM_008032	14266	AF4/FMR2 family, member 2	Aff2	2.129	4.937	0.00154254	0.0177547
361	10536635	NM_001081351	214642	RIKEN cDNA A430107O13 gene	A430107O13Rik	2.129	5.535	0.000788645	0.0111316
362	10494548	NM_008121	14613	gap junction membrane channel	Gja5	2.126	8.15	6.86437e-05	0.00213441
363	10497149	NM_026582	68151	G protein-coupled receptor 177	Gpr177	2.126	16.278	5.97737e-07	0.000102722
364	10558769	NM_026820	68713	interferon induced transmembra	Ifitm1	2.124	4.535	0.00248921	0.0253525
365	10362097	BC132022	19369	retinoic acid early transcript	Raet1b	2.121	5.487	0.000830654	0.0115242
366	10384233	NM_001083587	319939	tensin 3	Tns3	2.12	5.889	0.000542213	0.00858125
367	10492402	NM_010597	16497	potassium voltage-gated channe	Kcnab1	2.119	14.896	1.11475e-06	0.000151092
368	10428376	NM_009640	11600	angiopoietin 1	Angpt1	2.119	4.318	0.003252	0.0302376
369	10582958	NM_001033322	234889	guanylate cyclase 1, soluble,	Gucy1a2	2.119	6.134	0.000422093	0.00720964
370	10477920	BC049974	98932	myosin, light polypeptide 9, r	Myl9	2.118	2.667	0.0312606	0.147777
371	10415766	NM_172809	50720	sacsin	Sacs	2.118	9.644	2.23404e-05	0.00101169
372	10385297	NM_010250	14394	gamma-aminobutyric acid (GABA-	Gabra1	2.113	4.341	0.00316111	0.0297721
373	10495794	NM_153422	242202	phosphodiesterase 5A, cGMP-spe	Pde5a	2.112	7.173	0.000157581	0.00375213
374	10377841	NM_029360	75604	transmembrane 4 superfamily me	Tm4sf5	2.111	6.047	0.000461128	0.00764028
375	10580473	NM_033327	94187	zinc finger protein 423	Zfp423	2.109	7.84	8.85291e-05	0.00258544
376	10498972	XM_907666	633285	predicted gene, EG633285	EG633285	2.109	9.906	1.86448e-05	0.000902119
377	10373073	NM_028027	52666	DNA segment, Chr 10, ERATO Doi	D10Ertd610e	2.107	11.01	9.07914e-06	0.000579968
378	10462922	NM_019588	74055	phospholipase C, epsilon 1	Plce1	2.104	6.828	0.000215825	0.00466946
379	10358490	NM_001024720	545370	hemicentin 1	Hmcn1	2.103	5.484	0.000834	0.0115341
380	10553477	NM_177694	233246	transmembrane protein 16E	Tmem16e	2.099	10.919	9.60563e-06	0.00059364
381	10485711	BC027250	67606	RIKEN cDNA 1110018M03 gene	1110018M03Rik	2.094	7.26	0.000145721	0.00353339
382	10353309	AK081751	57339	junctophilin 1	Jph1	2.094	7.694	0.000100057	0.00277806
383	10358629	NM_001024720	545370	hemicentin 1	Hmcn1	2.091	2.482	0.041124	0.176733
384	10358599	NM_001024720	545370	hemicentin 1	Hmcn1	2.088	3.456	0.0101195	0.0685569
385	10358627	NM_001024720	545370	hemicentin 1	Hmcn1	2.083	5.152	0.00120514	0.0150599
386	10358589	NM_001024720	545370	hemicentin 1	Hmcn1	2.083	5.303	0.00101737	0.0133115
387	10451679	NM_001008231	76441	dishevelled associated activat	Daam2	2.081	6.594	0.000268893	0.00533347
388	10587231	NM_007555	12160	bone morphogenetic protein 5	Bmp5	2.08	4.981	0.00146444	0.017079
389	10405179	NM_010101	13610	endothelial differentiation, s	Edg3	2.079	9.283	2.88963e-05	0.00120036
390	10358607	NM_001024720	545370	hemicentin 1	Hmcn1	2.077	3.153	0.015477	0.0923988
391	10464251	NM_181415	226255	attractin like 1	Atrnl1	2.074	9.714	2.12841e-05	0.00098691
392	10604799	NM_001037863	320940	Atpase, class VI, type 11C	Atp11c	2.068	7.373	0.000131971	0.003318
393	10395466	NM_172803	238130	dedicator of cytokinesis 4	Dock4	2.067	9.328	2.79631e-05	0.00118321
394	10348451	NM_007722	12778	chemokine (C-X-C motif) recept	Cxcr7	2.067	7.403	0.000128494	0.00327174
395	10427303	NM_013553	15423	homeo box C4	Hoxc4	2.066	4.757	0.00190459	0.0208549
396	10352905	NM_001111059	12490	CD34 antigen	Cd34	2.064	6.521	0.00028845	0.00558005
397	10523134	NM_019932	56744	platelet factor 4	Pf4	2.063	3.155	0.0154351	0.09227
398	10570963	NM_177086	320158	zinc finger, matrin type 4	Zmat4	2.059	5.024	0.00139475	0.0166332
399	10435641	NM_008047	14314	follistatin-like 1	Fstl1	2.059	7.665	0.000102632	0.00282558
400	10365482	NM_011595	21859	tissue inhibitor of metallopro	Timp3	2.057	7.825	8.9643e-05	0.00260359
401	10547686					2.056	7.489	0.00011926	0.00312471
402	10519998	NM_028977	74511	leucine rich repeat containing	Lrrc17	2.052	7.205	0.000153132	0.00366269
403	10487987	NM_177303	320974	RIKEN cDNA B430119L13 gene	B430119L13Rik	2.051	12.026	4.9443e-06	0.000373365
404	10559177	AK044960	436015	predicted gene, ENSMUSG0000003	ENSMUSG00000038442	2.049	8.561	4.95847e-05	0.00172721
405	10549097	NM_008492	16832	lactate dehydrogenase B	Ldhb	2.048	12.429	3.93795e-06	0.000323592
406	10357833	NM_213616	381290	ATPase, Ca++ transporting, pla	Atp2b4	2.045	8.434	5.47659e-05	0.00186146

407	10529741	NM_027295	100972	RAB28, member RAS oncogene fam	Rab28	2.045	5.519	0.000802341	0.0112424
408	10531203	NM_001081401	330119	a disintegrin-like and metallo	Adamts3	2.043	8.464	5.34848e-05	0.00183287
409	10501063	NM_007651	12508	CD53 antigen	Cd53	2.043	6.619	0.000262793	0.00526683
410	10554938	NM_029494	75985	RAB30, member RAS oncogene fam	Rab30	2.039	7.732	9.69523e-05	0.0027299
411	10570855	NM_008872	18791	plasminogen activator, tissue	Plat	2.036	10.717	1.09186e-05	0.000637742
412	10400515	NM_009147	20334	SEC23A (S. cerevisiae)	Sec23a	2.036	9.268	2.92154e-05	0.00120789
413	10502451	NM_007560	12167	bone morphogenetic protein rec	Bmpr1b	2.034	3.866	0.00581578	0.0460213
414	10475218	ENSMUST00000028734	668880	START domain containing 9	Stard9	2.033	5.441	0.000873631	0.0119021
415	10446282	NM_010130	13733	EGF-like module containing, mu	Emr1	2.033	5.744	0.000631205	0.00954664
416	10521243	NM_019497	14772	G protein-coupled receptor kin	Grk4	2.031	6.388	0.000328282	0.00605161
417	10468879					2.024	3.576	0.00857967	0.0608753
418	10579776	NM_030113	78514	Rho GTPase activating protein	Arhgap10	2.023	5.803	0.000592894	0.00916385
419	10502770	NM_001081298	99633	latrophilin 2	Lphn2	2.023	5.392	0.000921435	0.0124015
420	10400170	NM_008858	18760	protein kinase D1	Prkd1	2.019	6.709	0.000241164	0.00500409
421	10547100	NM_026376	67784	plexin D1	Plxnd1	2.015	10.141	1.59028e-05	0.00081416
422	10436456	NM_011173	19128	protein S (alpha)	Pros1	2.014	10.841	1.00878e-05	0.000612923
423	10362091	NM_020030	56554	retinoic acid early transcript	Raet1d	2.013	3.543	0.00897547	0.0628593
424	10514070	BC066147	76455	RIKEN cDNA 2310067E19 gene	2310067E19Rik	2.008	11.209	8.02839e-06	0.000528824
425	10591125	NM_001080814	270120	FAT tumor suppressor homolog 3	Fat3	2.007	4.351	0.00312346	0.0294964
426	10468309	AK009333	69633	RIKEN cDNA 2310014D11 gene	2310014D11Rik	2.007	9.589	2.3228e-05	0.00103179
427	10440258	NM_010140	13837	Eph receptor A3	Epha3	2.006	4.841	0.00172468	0.0192843
428	10427336	NM_153505	105855	NCK associated protein 1 like	Nckap1l	2.006	6.499	0.000294716	0.00565984
429	10416215	NM_033325	94352	lysyl oxidase-like 2	Loxl2	2.004	8.568	4.93241e-05	0.00172382
430	10445268	NM_001081178	224792	G protein-coupled receptor 116	Gpr116	2.004	7.591	0.000109283	0.00296023
431	10435752	NM_175548	268890	limbic system-associated membr	Lsamp	2.003	4.996	0.00143977	0.016875
432	10604713	NM_152801	73341	Rac/Cdc42 guanine nucleotide e	Arhgef6	2.001	4.592	0.00232077	0.0241314
433	10369102	ENSMUST00000095691	100038725	predicted gene, ENSMUSG0000003	ENSMUSG00000038594	2.001	6.033	0.000467848	0.00769511
434	10544573	NM_027852	71660	retinoic acid receptor respond	Rarres2	2	6.277	0.000366222	0.00649646
435	10427904	BC050864	448987	F-box and leucine-rich repeat	Fbxl7	1.998	4.28	0.00341415	0.0312912
436	10368585	NM_001013411	432450	Na+/K+ transporting ATPase int	Nkain2	1.997	4.02	0.00475625	0.0397482
437	10358635	NM_001024720	545370	hemicentin 1	Hmcn1	1.996	7.699	9.97027e-05	0.00277383
438	10356084	NM_010570	16367	insulin receptor substrate 1	Irs1	1.996	10.887	9.79936e-06	0.000598837
439	10489759	NM_028072	72043	sulfatase 2	Sulf2	1.994	5.506	0.000813682	0.0113636
440	10580033	NM_011925	26364	CD97 antigen	Cd97	1.993	5.754	0.000624192	0.00948808
441	10395733	NM_013780	27386	neuronal PAS domain protein 3	Npas3	1.992	6.719	0.000238936	0.00496762
442	10484203	ENSMUST00000049544	545428	RIKEN cDNA 2610301F02 gene	2610301F02Rik	1.99	6.063	0.000453497	0.00756735
443	10500295	NM_023320	67220	pleckstrin homology domain con	Plekho1	1.99	10.27	1.45896e-05	0.000761775
444	10584024	NM_177906	330908	opioid binding protein/cell ad	Opcml	1.987	6.728	0.000237016	0.00494227
445	10594044	NM_012043	26968	immunoglobulin superfamily con	Islr	1.984	5.42	0.00089408	0.0121027
446	10600597	NM_175771	192216	transmembrane protein 47	Tmem47	1.983	11.389	7.1973e-06	0.000495699
447	10394534	NM_011859	23967	odd-skipped related 1 (Drosoph	Osr1	1.981	3.102	0.0166397	0.0970498
448	10532085	NM_011578	21814	transforming growth factor, be	Tgfbr3	1.98	11.024	8.99978e-06	0.000578393
449	10358595	NM_001024720	545370	hemicentin 1	Hmcn1	1.98	3.552	0.00887451	0.0623605
450	10455721	NM_026408	67847	synuclein, alpha interacting p	Sncaip	1.979	4.336	0.00318131	0.0298651
451	10503382	NM_001111027	12395	runt-related transcription fac	Runx1t1	1.978	10.092	1.64382e-05	0.000829823
452	10603003					1.976	4.325	0.00322538	0.0301093
453	10346098					1.974	4.904	0.0016022	0.0183009
454	10555027	NM_010248	14389	growth factor receptor bound p	Gab2	1.97	7.747	9.57394e-05	0.00271766
455	10371959	NM_013508	13713	ELK3, member of ETS oncogene f	Elk3	1.969	10.369	1.36751e-05	0.000738749
456	10521995	ENSMUST00000101196	319807	RIKEN cDNA 3110047P20 gene	3110047P20Rik	1.969	5.96	0.000504019	0.0081351
457	10481592	NM_010065	13429	dynamin 1	Dnm1	1.969	6.896	0.000202546	0.00445181
458	10358621	NM_001024720	545370	hemicentin 1	Hmcn1	1.963	6.827	0.000216063	0.00466946

459	10604542	NM_001077202	50786	heparan sulfate 6-O-sulfotrans	Hs6st2	1.963	7.701	9.95296e-05	0.00277267
460	10362538	NM_010681	16775	laminin, alpha 4	Lama4	1.961	6.381	0.000330623	0.00606651
461	10538305	ENSMUST00000070587	77580	RIKEN cDNA 5730596B20 gene	5730596B20Rik	1.956	6.315	0.000352751	0.00632617
462	10521622	AK076499	399596	RIKEN cDNA 4833430A08 gene	4833430A08Rik	1.954	13.683	2.01893e-06	0.00021238
463	10523468	NM_080708	140780	BMP2 inducible kinase	Bmp2k	1.954	5.152	0.00120418	0.0150569
464	10358547	NM_001024720	545370	hemicentin 1	Hmcn1	1.953	4.628	0.00222257	0.0234785
465	10543239	NM_031198	21426	transcription factor EC	Tcfec	1.953	6.501	0.000294234	0.00565571
466	10477986	NM_010923	18111	neuronatin	Nnat	1.953	11.454	6.91743e-06	0.000477981
467	10514000	NM_010820	17475	multiple PDZ domain protein	Mpdz	1.952	10.355	1.37974e-05	0.000740439
468	10561104	NM_009465	26362	AXL receptor tyrosine kinase	Axl	1.951	6.598	0.000268055	0.00532453
469	10460968	NM_011242	19395	RAS, guanyl releasing protein	Rasgrp2	1.95	10.435	1.30972e-05	0.000717426
470	10513256	NM_010336	14745	lysophosphatidic acid receptor	Lpar1	1.95	10.319	1.41296e-05	0.000751899
471	10346000	NM_028450	70676	GULP, engulfment adaptor PTB d	Gulp1	1.948	8.595	4.83077e-05	0.00170608
472	10458314	BC046640	72512	transmembrane protein 173	Tmem173	1.947	7.556	0.000112617	0.00301032
473	10502776	NM_001081298	99633	latrophilin 2	Lphn2	1.946	9.013	3.51998e-05	0.0013674
474	10460541	NM_054042	70445	CD248 antigen, endosialin	Cd248	1.945	7.145	0.000161556	0.00382954
475	10358551	NM_001024720	545370	hemicentin 1	Hmcn1	1.943	3.33	0.0120514	0.077029
476	10606369	NM_008409	16431	integral membrane protein 2A	Itm2a	1.942	6.858	0.000209801	0.00456851
477	10495976	NM_011098	18741	paired-like homeodomain transc	Pitx2	1.941	6.254	0.000374566	0.00659985
478	10459335	ENSMUST00000047480	225617	RIKEN cDNA 9430028L06 gene	9430028L06Rik	1.936	9.825	1.97074e-05	0.000938499
479	10395978	BC099503	217648	gene model 527, (NCBI)	Gm527	1.936	10.675	1.12091e-05	0.000649329
480	10551852	NM_001081114	76686	CAP-GLY domain containing link	Clip3	1.933	10.568	1.20099e-05	0.00068007
481	10484463	NM_009776	12258	serine (or cysteine) peptidase	Serping1	1.927	5.807	0.000590394	0.00913189
482	10360504					1.924	6.419	0.000318297	0.00592342
483	10506225	NM_198037	320508	cache domain containing 1	Cachd1	1.921	10.121	1.61133e-05	0.000820961
484	10501468	NM_030699	80883	netrin G1	Ntng1	1.92	5.165	0.0011878	0.0148785
485	10512499	NM_009416	22004	tropomyosin 2, beta	Tpm2	1.92	3.185	0.014786	0.0892989
486	10556491	NM_026143	67420	male sterility domain containi	Mlstd2	1.92	10.104	1.63022e-05	0.00082859
487	10355500	NM_010518	16011	insulin-like growth factor bin	Igfbp5	1.918	5.798	0.000595966	0.00918447
488	10601492	NM_177747	245595	zinc finger protein 711	Zfp711	1.918	7.39	0.000129999	0.00329581
489	10531197	NM_001081401	330119	a disintegrin-like and metallo	Adamts3	1.917	6.453	0.000308065	0.00580546
490	10502748	NM_001081298	99633	latrophilin 2	Lphn2	1.917	10.723	1.08752e-05	0.000636968
491	10433428					1.917	7.034	0.000178577	0.00410086
492	10462442	NM_133775	77125	interleukin 33	Il33	1.913	3.322	0.0121956	0.0776701
493	10367945	NM_001033257	215789	phosphatase and actin regulato	Phactr2	1.912	12.99	2.89903e-06	0.000261954
494	10564237	ENSMUST00000054860	330552	predicted gene, EG330552	EG330552	1.912	6.868	0.000207855	0.00454016
495	10436658	AK148667	100038676	predicted gene, ENSMUSG0000007	ENSMUSG00000074937	1.91	3.753	0.0067615	0.051242
496	10351455	NM_009063	19737	regulator of G-protein signali	Rgs5	1.906	4.131	0.00412184	0.0357035
497	10502774	NM_001081298	99633	latrophilin 2	Lphn2	1.906	9.476	2.51502e-05	0.00108971
498	10566358	NM_009099	20128	tripartite motif-containing 30	Trim30	1.903	11.494	6.7564e-06	0.000470224
499	10419223	NM_146054	218952	fermitin family homolog 2 (Dro	Fermt2	1.9	6.655	0.000253829	0.00515463
500	10536220	NM_007743	12843	collagen, type I, alpha 2	Col1a2	1.897	7.448	0.000123609	0.00318334
501	10537296					1.897	2.722	0.0288242	0.139559
502	10441902	NM_022315	64074	SPARC related modular calcium	Smoc2	1.896	4.744	0.00193435	0.0210607
503	10377534	ENSMUST00000052108	80515	RIKEN cDNA A030009H04 gene	A030009H04Rik	1.896	9.81	1.99097e-05	0.000941769
504	10559179	AK054458	100038419	predicted gene, ENSMUSG0000007	ENSMUSG00000073783	1.894	4.838	0.00173	0.0193234
505	10450484	NM_019467	11629	allograft inflammatory factor	Aif1	1.893	8.026	7.59259e-05	0.00229892
506	10496519	NM_009472	22253	unc-5 homolog C (C. elegans)	Unc5c	1.89	4.027	0.00471563	0.039535
507	10535807	NM_010228	14254	FMS-like tyrosine kinase 1	Flt1	1.89	7.59	0.000109343	0.00296023
508	10421774	NM_001081336	380921	diacylglycerol kinase, eta	Dgkh	1.889	5.835	0.000573421	0.00892814
509	10583203	BC107288	18689	per-hexamer repeat gene 4	Phxr4	1.887	3.588	0.00844675	0.0602131

510	10590844	ENSMUST00000093893	71544	RIKEN cDNA 9030420J04 gene	9030420J04Rik	1.887	8.242	6.37491e-05	0.0020557
511	10351463	ENSMUST00000027997	19737	regulator of G-protein signali	Rgs5	1.887	3.607	0.00822797	0.0590738
512	10344837	NM_029525	109294	DEP domain containing 2	Depdc2	1.883	7.27	0.000144472	0.00351926
513	10363157	NM_023129	18821	phospholamban	Pln	1.882	5.333	0.000984174	0.0129492
514	10358539	NM_001024720	545370	hemicentin 1	Hmcn1	1.881	5.099	0.00127939	0.0157367
515	10568553	NM_029935	77590	RIKEN cDNA 4631426J05 gene	4631426J05Rik	1.881	6.688	0.000245984	0.0050424
516	10588819	NM_001122635	69398	RIKEN cDNA 1700021K14 gene	1700021K14Rik	1.877	4.006	0.00484695	0.0403004
517	10355893	NM_007936	13838	Eph receptor A4	Epha4	1.877	7.51	0.000117102	0.00309113
518	10601360	NM_001109757	11977	ATPase, Cu++ transporting, alp	Atp7a	1.877	9.083	3.34414e-05	0.00132661
519	10441093	NM_133659	13876	avian erythroblastosis virus E	Erg	1.876	6.701	0.000243129	0.00502386
520	10494271	NM_021281	13040	cathepsin S	Ctss	1.875	7.672	0.000101977	0.00281122
521	10554655	ENSMUST00000082237	108797	mex3 homolog B (C. elegans)	Mex3b	1.874	7.632	0.000105503	0.00288585
522	10384458	NM_019549	56193	pleckstrin	Plek	1.871	7.095	0.000168912	0.00394638
523	10605370	NM_008621	17524	membrane protein, palmitoylate	Mpp1	1.87	7.279	0.000143364	0.00349631
524	10436945	NM_017391	53881	solute carrier family 5 (inosi	Slc5a3	1.87	8.425	5.51548e-05	0.0018689
525	10468668	NM_146102	226250	actin filament associated prot	Afap1l2	1.869	7.251	0.000146895	0.00355371
526	10373223	NM_008512	16971	low density lipoprotein recept	Lrp1	1.869	6.705	0.000242049	0.00501753
527	10435961	ENSMUST00000099728	100038470	predicted gene, ENSMUSG0000007	ENSMUSG00000075047	1.869	6.315	0.000352543	0.00632617
528	10603583	NM_016911	51795	sushi-repeat-containing protei	Srpx	1.868	6.378	0.000331386	0.00606651
529	10405063	NM_008760	18295	osteoglycin	Ogn	1.862	1.575	0.158087	0.405065
530	10572960	XM_001472504	100039235	hypothetical protein LOC100039	LOC100039235	1.862	6.979	0.000187759	0.00422741
531	10451763	NM_009122	20230	special AT-rich sequence bindi	Satb1	1.861	9.567	2.3586e-05	0.0010455
532	10492428	NM_178892	99929	TCDD-inducible poly(ADP-ribose	Tiparp	1.859	5.719	0.000647669	0.0097054
533	10367118					1.858	2.28	0.0555388	0.215154
534	10504424	NM_016678	53614	reversion-inducing-cysteine-ri	Reck	1.857	10.512	1.24498e-05	0.000695317
535	10548038	NM_008742	18205	neurotrophin 3	Ntf3	1.856	3.859	0.00587086	0.0462693
536	10354309	NM_007737	12832	collagen, type V, alpha 2	Col5a2	1.855	7.945	8.11319e-05	0.00240259
537	10495967	NM_145133	211550	TRAF-interacting protein with	Tifa	1.855	6.435	0.000313638	0.00586864
538	10571142	NM_054044	78560	G protein-coupled receptor 124	Gpr124	1.854	11.524	6.63573e-06	0.000464589
539	10514668	NM_146145	16451	Janus kinase 1	Jak1	1.85	8.405	5.60116e-05	0.00187095
540	10461369	NM_009643	66395	AHNAK nucleoprotein (desmoyoki	Ahnak	1.849	7.532	0.00011491	0.00304918
541	10590860	ENSMUST00000034333	71544	RIKEN cDNA 9030420J04 gene	9030420J04Rik	1.845	4.3	0.00332881	0.0307221
542	10358601	NM_001024720	545370	hemicentin 1	Hmcn1	1.845	3.15	0.0155313	0.0925314
543	10345212	NM_133235	170771	KH domain containing, RNA bind	Khdrbs2	1.845	4.746	0.00192987	0.0210292
544	10425852	NM_133167	170736	parvin, beta	Parvb	1.843	7.346	0.000135089	0.00336488
545	10531191	NM_001081401	330119	a disintegrin-like and metallo	Adamts3	1.842	7.911	8.34702e-05	0.00245807
546	10473244	NM_175513	241514	zinc finger protein 804A	Zfp804a	1.842	4.267	0.00346982	0.031596
547	10352152	NM_177757	269152	kinesin family member 26B	Kif26b	1.839	10.954	9.39637e-06	0.000586067
548	10459353					1.839	8.813	4.08971e-05	0.00151707
549	10536494	NM_016900	12390	caveolin 2	Cav2	1.838	8.156	6.83486e-05	0.00213151
550	10439895	NM_009655	11658	activated leukocyte cell adhes	Alcam	1.838	3.998	0.00489535	0.0406389
551	10416175	NM_010910	18039	neurofilament, light polypepti	Nefl	1.837	3.642	0.00785011	0.0572157
552	10372028	NM_018797	54712	plexin C1	Plxnc1	1.835	3.633	0.0079504	0.057744
553	10408861	BC027755	109254	RIKEN cDNA 9530008L14 gene	9530008L14Rik	1.834	5.466	0.000849889	0.0116764
554	10483023	AK169352	56878	RNA binding motif, single stra	Rbms1	1.833	7.306	0.000139942	0.00344063
555	10475890	NM_008587	17289	c-mer proto-oncogene tyrosine	Mertk	1.832	4.601	0.00229737	0.0240288
556	10508663	NM_010686	16792	lysosomal-associated protein t	Laptm5	1.832	9.78	2.03305e-05	0.000959525
557	10391444	NM_026865	73635	RIKEN cDNA 1700113I22 gene	1700113I22Rik	1.831	2.75	0.0276732	0.13614
558	10607865	NM_021278	19241	thymosin, beta 4, X chromosome	Tmsb4x	1.83	9.422	2.61404e-05	0.0011234
559	10440513	NM_144853	224405	cysteine and tyrosine-rich pro	Cyyr1	1.829	6.822	0.000216996	0.00467702
560	10376950	NM_008885	18858	peripheral myelin protein	Pmp22	1.827	3.539	0.00903376	0.0631438
561	10399470	NM_144551	217410	tribbles homolog 2 (Drosophila	Trib2	1.823	6.365	0.000335849	0.00611645
562	10397975	BC128276	52668	DNA segment, Chr 12, ERATO	D12Ertd647e	1.822	6.651	0.000254705	0.00515851

562	10597975	BC128276	52668	Doi	D12Ertd647e	1.822	6.651	0.000254705	0.00515851
563	10544751	NM_010451	15399	homeo box A2	Hoxa2	1.821	4.411	0.00289784	0.0281591
564	10577641	NM_026931	69068	RIKEN cDNA 1810011O10 gene	1810011O10Rik	1.819	5.476	0.000840398	0.0115837
565	10354111	NM_010678	16764	AF4/FMR2 family, member 3	Aff3	1.817	12.827	3.16411e-06	0.000279924
566	10354741	NM_028713	74013	raftlin family member 2	Rftn2	1.815	6.309	0.000354609	0.00634586
567	10605503					1.813	2.51	0.0394274	0.172278
568	10568392	NM_026418	67865	regulator of G-protein signall	Rgs10	1.813	6.76	0.000229978	0.00483366
569	10362113	ENSMUST00000100029	100038582	predicted gene, ENSMUSG0000007	ENSMUSG00000075292	1.813	6.347	0.000341764	0.00618755
570	10431051	NM_022723	64706	signal peptide, CUB domain, EG	Scube1	1.812	10.181	1.54824e-05	0.000800389
571	10484389	NM_011576	21788	tissue factor pathway inhibito	Tfpi	1.808	6.59	0.000269915	0.00533798
572	10428707	NM_008216	15117	hyaluronan synthase 2	Has2	1.808	5.488	0.00083031	0.0115242
573	10607225	NM_001081173	210297	leucine-rich repeats and calpo	Lrch2	1.807	7.466	0.000121663	0.00314865
574	10523128	NM_023785	57349	pro-platelet basic protein	Ppbp	1.806	3.131	0.0159505	0.0942326
575	10554574	NM_145375	107769	transmembrane 6 superfamily me	Tm6sf1	1.805	9.384	2.68734e-05	0.0011479
576	10599530	NM_011228	19337	RAB33A, member of RAS oncogene	Rab33a	1.802	4.735	0.00195555	0.0212259
577	10467840	AK081501	100038488	predicted gene, ENSMUSG0000007	ENSMUSG00000071549	1.801	1.45	0.189146	0.44755
578	10513101					1.799	1.902	0.0976359	0.304531
579	10483025	NM_020296	56878	RNA binding motif, single stra	Rbms1	1.799	8.925	3.76029e-05	0.00142276
580	10413398	NM_134437	171463	interleukin 17 receptor D	Il17rd	1.798	8.831	4.03467e-05	0.0015016
581	10358543	NM_001024720	545370	hemicentin 1	Hmcn1	1.798	3.438	0.0103791	0.0698014
582	10527233	NM_011182	19159	pleckstrin homology, Sec7 and	Pscd3	1.797	4.739	0.00194534	0.0211368
583	10482920	NM_025422	66205	CD302 antigen	Cd302	1.797	5.951	0.00050864	0.00819592
584	10530421	NM_010251	14397	gamma-aminobutyric acid (GABA-	Gabra4	1.796	7.503	0.000117815	0.00309835
585	10498885	NM_013540	14800	glutamate receptor, ionotropic	Gria2	1.795	6.973	0.000188744	0.00422741
586	10406452	AY344585	100126879	predicted gene, ENSMUSG0000007	ENSMUSG00000074792	1.793	3.886	0.00567016	0.0452244
587	10518835	NM_001081557	100072	calmodulin binding transcripti	Camta1	1.792	2.734	0.0283286	0.138077
588	10422164	NM_007904	13618	endothelin receptor type B	Ednrb	1.791	3.241	0.0136601	0.0843789
589	10586118	NM_138304	75600	calmodulin-like 4	Calml4	1.791	2.994	0.0194112	0.107499
590	10462957	NM_145952	209478	TBC1D12: TBC1 domain family, m	Tbc1d12	1.79	4.74	0.00194468	0.0211368
591	10377319	NM_175260	77579	myosin, heavy polypeptide 10,	Myh10	1.788	12.375	4.05842e-06	0.000328779
592	10385036	NM_008005	14172	fibroblast growth factor 18	Fgf18	1.784	7.349	0.00013473	0.00336488
593	10505132	NM_001035533	11641	A kinase (PRKA) anchor protein	Akap2	1.784	2.815	0.0251561	0.127922
594	10538842	NM_025278	14701	guanine nucleotide binding pro	Gng12	1.782	12.718	3.35709e-06	0.000292108
595	10380660	NM_134032	103889	homeo box B2	Hoxb2	1.78	6.063	0.000453863	0.00756735
596	10486041	NM_010825	17536	Meis homeobox 2	Meis2	1.779	7.532	0.000114936	0.00304918
597	10566543	ENSMUST00000078482	233651	dachsous 1 (Drosophila)	Dchs1	1.778	9.287	2.87998e-05	0.00120006
598	10578241	NM_178735	244425	RIKEN cDNA A730069N07 gene	A730069N07Rik	1.777	5.73	0.000640675	0.00963473
599	10422608	NM_024188	67041	3-oxoacid CoA transferase 1	Oxct1	1.775	11.586	6.39403e-06	0.000453676
600	10357137	NM_001081125	14633	GLI-Kruppel family member GLI2	Gli2	1.774	7.519	0.000116195	0.00307489
601	10401238	NM_007564	12192	zinc finger protein 36, C3H ty	Zfp36l1	1.773	5.521	0.000801057	0.0112318
602	10562192	NM_008761	18301	FXYD domain-containing ion tra	Fxyd5	1.773	7.472	0.000121038	0.00314805
603	10423287	NM_001081299	320865	cadherin 18	Cdh18	1.772	3.083	0.0170844	0.0986976
604	10459071	NM_134133	106878	RIKEN cDNA 2010002N04 gene	2010002N04Rik	1.771	8.591	4.84807e-05	0.00170608
605	10358339	NM_009888	12628	complement component factor h	Cfh	1.771	5.732	0.000638779	0.00962676
606	10461721	NM_010821	17476	macrophage expressed gene 1	Mpeg1	1.77	9.434	2.59194e-05	0.00111845
607	10467826	NM_001081257	545291	similar to Heparanase-2 (Hpa2)	LOC545291	1.77	1.693	0.132977	0.366629
608	10578649	NM_011857	23965	odd Oz/ten-m homolog 3 (Drosop	Odz3	1.768	5.885	0.00054477	0.00859115
609	10572130	NM_008509	16956	lipoprotein lipase	Lpl	1.766	9.186	3.10028e-05	0.00126305
				RIKEN cDNA 4930589M24					

610	10369132	NM_001081428	75906	RIKEN cDNA 4930589M24 gene	4930589M24Rik	1.765	8.18	6.70208e-05	0.00210563
611	10421948					1.764	3.843	0.00599458	0.0469175
612	10544732	NM_018773	54353	src family associated phosphop	Skap2	1.764	8.166	6.77726e-05	0.00211667
613	10436304	NM_001014423	320712	ABI gene family, member 3 (NES	Abi3bp	1.764	2.399	0.0465044	0.191643
614	10407211	NM_008247	19012	phosphatidic acid phosphatase	Ppap2a	1.763	3.196	0.014558	0.0884268
615	10574471	NM_024217	68119	CKLF-like MARVEL transmembrane	Cmtm3	1.762	8.969	3.63711e-05	0.0013957
616	10353102	NM_177834	329093	carboxypeptidase A6	Cpa6	1.761	4.238	0.00359804	0.0324929
617	10569714	NM_133189	81904	calcium channel, voltage-depen	Cacng7	1.76	6.273	0.000367457	0.00650713
618	10375402	NM_009616	11492	a disintegrin and metallopepti	Adam19	1.759	4.441	0.00279119	0.0274753
619	10420413	NM_015771	50523	large tumor suppressor 2	Lats2	1.757	8.853	3.96731e-05	0.00147945
620	10578222	NM_015802	50768	deleted in liver cancer 1	Dlc1	1.755	4.9	0.00160998	0.0183611
621	10542594	AY512955	100093699	predicted gene, ENSMUSG0000006	ENSMUSG00000067389	1.754	2.149	0.067558	0.242768
622	10455054	NM_053128	93874	protocadherin beta 3	Pcdhb3	1.749	5.016	0.00140651	0.0166794
623	10369615	NM_011157	19073	serglycin	Srgn	1.747	4.999	0.00143416	0.0168502
624	10387316	NM_146019	216848	chromodomain helicase DNA bind	Chd3	1.742	6.416	0.000319303	0.00592742
625	10537146	NM_008012	14187	aldo-keto reductase family 1,	Akr1b8	1.741	6.246	0.000377415	0.00663347
626	10365749	NM_008517	16993	leukotriene A4 hydrolase	Lta4h	1.741	7.398	0.000129124	0.0032815
627	10447946	BC089489	74917	RIKEN cDNA 4930474M22 gene	4930474M22Rik	1.74	5.1	0.00127785	0.015736
628	10459643	BC057927	269033	RIKEN cDNA 4930503L19 gene	4930503L19Rik	1.737	10.693	1.1085e-05	0.000643904
629	10538354	AK039090	100049166	hypothetical protein LOC100049	LOC100049166	1.737	5.148	0.00121033	0.0150891
630	10564624	NM_009181	20450	ST8 alpha-N-acetyl-neuraminide	St8sia2	1.736	5.716	0.000650115	0.00973514
631	10443949	NM_172619	224697	a disintegrin-like and metallo	Adamts10	1.735	9.67	2.19382e-05	0.00100524
632	10590487	XR_031805	623911	zinc finger protein 660	Zfp660	1.734	6.989	0.000186103	0.00421753
633	10523281	NM_001009818	52398	septin 11	Sept11	1.734	11.617	6.27763e-06	0.000448427
634	10358389	NM_009061	19735	regulator of G-protein signali	Rgs2	1.731	6.361	0.000336973	0.00613164
635	10412298	NM_001033228	109700	integrin alpha 1	Itga1	1.731	2.903	0.0221419	0.117189
636	10497862	NM_019510	22065	transient receptor potential c	Trpc3	1.731	10.36	1.3757e-05	0.000740146
637	10389929	NM_009783	12291	calcium channel, voltage-depen	Cacna1g	1.73	4.976	0.00147435	0.0171413
638	10530100	ENSMUST00000076623	212285	centaurin, delta 1	Centd1	1.73	2.797	0.0258458	0.130239
639	10578521	NM_207213	102141	sorting nexin 25	Snx25	1.728	6.245	0.000378059	0.00663376
640	10350848	BC055845	69953	RIKEN cDNA 2810025M15 gene	2810025M15Rik	1.728	6.168	0.000408233	0.00704626
641	10495869	NM_146140	229801	translocation associated membr	Tram1l1	1.726	8.571	4.92301e-05	0.00172338
642	10436550					1.726	4.937	0.00154196	0.0177547
643	10435305	NM_010580	16419	integrin beta 5	Itgb5	1.723	6.796	0.000222376	0.00473031
644	10529656	NM_010942	18196	neuron specific gene family me	Nsg1	1.722	7.821	8.99834e-05	0.00260646
645	10490856	NM_178631	76897	RALY RNA binding protein-like	Ralyl	1.719	3.75	0.00678643	0.0513389
646	10393559	NM_011594	21858	tissue inhibitor of metallopro	Timp2	1.718	4.946	0.00152529	0.0176188
647	10570982	NM_010206	14182	fibroblast growth factor recep	Fgfr1	1.718	9.479	2.51077e-05	0.00108971
648	10413482	NM_009524	22418	wingless-related MMTV integrat	Wnt5a	1.717	2.553	0.0370138	0.16504
649	10606355	NM_021476	58861	cysteinyl leukotriene receptor	Cysltr1	1.716	9.002	3.54866e-05	0.00137423
650	10544837	BC043099	66873	RIKEN cDNA 1200009O22 gene	1200009O22Rik	1.715	4.933	0.00154932	0.0178231
651	10367734	NM_177387	338362	uronyl-2-sulfotransferase	Ust	1.713	5.316	0.00100275	0.0131609
652	10497817	NM_009673	11747	annexin A5	Anxa5	1.713	7.255	0.00014645	0.00354701
653	10447317	NM_010137	13819	endothelial PAS domain protein	Epas1	1.713	9.731	2.10377e-05	0.00097978
654	10592251	NM_001029838	208076	Pbx/knotted 1 homeobox 2	Pknox2	1.713	6.67	0.000250347	0.00510341
655	10369252	NM_001024911	103080	septin 10	Sept10	1.711	8.646	4.64484e-05	0.00165971
656	10592533					1.711	6.653	0.000254269	0.00515463
657	10472958	NM_013554	15430	homeo box D10	Hoxd10	1.708	1.504	0.175057	0.428228
658	10547404	NM_053204	111173	ELKS/RAB6-interacting/CAST fam	Erc1	1.708	6.692	0.000245085	0.00503604
659	10472240	NM_198294	66860	tetratricopeptide repeat, anky	Tanc1	1.707	10.732	1.08117e-05	0.000636968

660	10601270	ENSMUST00000101339	100038406	predicted gene, ENSMUSG0000007	ENSMUSG00000073037	1.704	2.976	0.0199333	0.109672
661	10412207	BC019664	69590	RIKEN cDNA 2310016C16 gene	2310016C16Rik	1.702	8.328	5.95469e-05	0.0019581
662	10584259	NM_183171	235180	fasciculation and elongation p	Fez1	1.702	4.697	0.00204667	0.022079
663	10513208	NM_022814	64817	sushi, von Willebrand factor t	Svep1	1.701	5.894	0.000539531	0.0085452
664	10544383	NM_032540	23925	Kell blood group	Kel	1.701	1.693	0.132952	0.366605
665	10438769	NM_016674	12737	claudin 1	Cldn1	1.701	3.128	0.0160326	0.0945852
666	10353438	NM_177409	170829	translocating chain-associatin	Tram2	1.701	7.433	0.000125208	0.00321287
667	10352143	BC120791	240945	RIKEN cDNA D230039L06 gene	D230039L06Rik	1.7	5.087	0.00129657	0.0158374
668	10495685	NM_172525	214137	Rho GTPase activating protein	Arhgap29	1.699	6.599	0.000267721	0.00532453
669	10582337	BC039210	234839	cDNA sequence BC039210	BC039210	1.698	7.782	9.29706e-05	0.00266726
670	10493812	NM_011311	20198	S100 calcium binding protein A	S100a4	1.697	4.262	0.00348931	0.0317052
671	10491732	NM_183221	329628	FAT tumor suppressor homolog 4	Fat4	1.696	3.199	0.0145011	0.0882145
672	10500804	BC027582	269472	cDNA sequence BC027582	BC027582	1.696	5.405	0.000908851	0.0122556
673	10596200	NM_178638	81907	transmembrane protein 108	Tmem108	1.696	5.587	0.000745537	0.0107236
674	10400510	NM_025809	66864	C-type lectin domain family 14	Clec14a	1.695	5.446	0.000868579	0.0118638
675	10543802	NM_175750	243743	plexin A4	Plxna4	1.695	7.835	8.89497e-05	0.00259414
676	10604751	NM_010200	14168	fibroblast growth factor 13	Fgf13	1.694	6.506	0.000292766	0.00564804
677	10540509	NM_177328	108073	glutamate receptor, metabotrop	Grm7	1.693	3.223	0.014004	0.0858692
678	10605256	NM_010227	192176	filamin, alpha	Flna	1.693	4.492	0.00262259	0.0262931
679	10363265	NM_026148	110829	LIM and senescent cell antigen	Lims1	1.693	9.479	2.51065e-05	0.00108971
680	10545401	NM_016872	53620	vesicle-associated membrane pr	Vamp5	1.693	5.752	0.000625845	0.00949734
681	10350438	NM_001081027	240776	potassium channel, subfamily T	Kcnt2	1.691	2.524	0.0386141	0.16991
682	10475314	NM_032393	17754	microtubule-associated protein	Mtap1a	1.689	7.358	0.000133766	0.00334716
683	10602739	NM_019736	56360	acyl-CoA thioesterase 9	Acot9	1.686	4.129	0.00413451	0.0357546
684	10455901	NM_001081072	225579	solute carrier family 27 (fatt	Slc27a6	1.685	4.809	0.00179077	0.0198551
685	10607283	NM_030700	80884	melanoma antigen, family D, 2	Maged2	1.685	5.752	0.000625609	0.00949734
686	10455483	ENSMUST00000037763	240255	YTH domain containing 2	Ythdc2	1.685	5.265	0.00106145	0.0136932
687	10405605	NM_008541	17129	MAD homolog 5 (Drosophila)	Smad5	1.683	6.669	0.000250537	0.00510341
688	10502881	NM_012028	26938	ST6 (alpha-N-acetyl-neuraminyl	St6galnac5	1.682	7.416	0.000127069	0.00324487
689	10607189	NM_153319	27494	angiomotin	Amot	1.682	6.145	0.000417736	0.00716699
690	10371379	NM_001004363	77976	NUAK family, SNF1-like kinase,	Nuak1	1.681	5.302	0.00101829	0.0133153
691	10493604	NM_172530	214547	src homology 2 domain-containi	She	1.681	5.048	0.00135708	0.0163206
692	10408693	NM_028784	74145	coagulation factor XIII, A1 su	F13a1	1.681	8.418	5.54712e-05	0.00186897
693	10416974	NM_001079844	23888	glypican 6	Gpc6	1.681	5.208	0.00113136	0.0143157
694	10604832					1.681	2.175	0.0650398	0.237842
695	10467124	NM_007392	11475	actin, alpha 2, smooth muscle,	Acta2	1.68	1.149	0.287226	0.562985
696	10552245	NM_172298	243931	teashirt zinc finger family me	Tshz3	1.68	6.334	0.000346188	0.00625014
697	10411229	NM_010169	14062	coagulation factor II (thrombi	F2r	1.679	7.123	0.00016481	0.00387193
698	10557960	NM_009365	21804	transforming growth factor bet	Tgfb1i1	1.677	3.326	0.0121292	0.0774338
699	10554808	NM_008055	14366	frizzled homolog 4 (Drosophila	Fzd4	1.677	4.614	0.00226116	0.0237861
700	10538706	ENSMUST00000114267	70945	multimerin 1	Mmrn1	1.677	4.533	0.002493	0.0253776
701	10355536	ENSMUST00000050681	21961	tensin 1	Tns1	1.676	6.112	0.000431699	0.00729643
702	10416700	NM_001013753	219228	protocadherin 17	Pcdh17	1.675	6.332	0.000346737	0.00625014
703	10547641	NM_011401	20527	solute carrier family 2 (facil	Slc2a3	1.672	5.134	0.00122962	0.0152577
704	10428534	NM_032000	83925	trichorhinophalangeal syndrome	Trps1	1.671	8.788	4.16924e-05	0.00153847
705	10513320	NM_025968	67103	leukotriene B4 12-hydroxydehyd	Ltb4dh	1.671	6.565	0.00027646	0.00540246
706	10517165	NM_013706	23833	CD52 antigen	Cd52	1.669	4.097	0.0043046	0.0367744
707	10367024	NM_009312	21334	tachykinin 2	Tac2	1.667	2.701	0.0297571	0.142831
708	10604743	NR_002903	353374	small nucleolar RNA, C/D box 6	Snord61	1.666	0.807	0.445255	0.70357
709	10358603	NM_001024720	545370	hemicentin 1	Hmcn1	1.666	5.797	0.000596971	0.00919327
710	10380654	NM_001079869	15410	homeo box B3	Hoxb3	1.665	8.058	7.39709e-05	0.00226017
711	10458894	NM_010728	16948	lysyl oxidase	Lox	1.665	2.407	0.0459437	0.19003
712	10496872	NM_133222	170757	EGF, latrophilin seven transme	Eltd1	1.665	5.885	0.000544278	0.00859115

713	10433075	ENSMUST00000053475	77096	RIKEN cDNA 5730585A16 gene	5730585A16Rik	1.662	1.993	0.0852992	0.280405
714	10499168	NM_130867	170643	kin of IRRE like (Drosophila)	Kirrel	1.662	8.229	6.44151e-05	0.00205963
715	10573115	NM_177378	330812	ring finger protein 150	Rnf150	1.661	5.084	0.0013013	0.0158638
716	10531177	NM_001081401	330119	a disintegrin-like and metallo	Adamts3	1.66	5.112	0.00126079	0.0155532
717	10456071	NM_001037859	12978	colony stimulating factor 1 re	Csf1r	1.66	5.727	0.00064248	0.00965501
718	10519913	NM_015823	50791	membrane associated guanylate	Magi2	1.659	6.646	0.000255984	0.00516956
719	10586718	NM_177159	320440	RIKEN cDNA 9530091C08 gene	9530091C08Rik	1.659	4.643	0.00218263	0.0231857
720	10471721	NM_008969	19224	prostaglandin-endoperoxide syn	Ptgs1	1.659	11.857	5.45444e-06	0.000404662
721	10546421	NM_001081146	243548	prickle-like 2 (Drosophila)	Prickle2	1.659	3.171	0.0150877	0.0907579
722	10363379	NM_144822	216001	calcium binding atopy-related	Cbara1	1.659	4.332	0.00319741	0.0299672
723	10544875	NM_027268	69938	secernin 1	Scrn1	1.658	2.418	0.0452136	0.188022
724	10405633	NM_001025074	18212	neurotrophic tyrosine kinase,	Ntrk2	1.657	2.878	0.0229542	0.120303
725	10585180	ENSMUST00000068730	100036537	predicted gene, ENSMUSG0000006	ENSMUSG00000060603	1.656	4.311	0.00328399	0.0304569
726	10463799	ENSMUST00000104904	329070	predicted gene, EG329070	EG329070	1.656	5.469	0.000847132	0.0116537
727	10528038	NM_001007220	11496	a disintegrin and metallopepti	Adam22	1.655	5.487	0.000831233	0.0115242
728	10606600	NM_001105245	279653	protocadherin 19	Pcdh19	1.655	3.467	0.00997224	0.0679951
729	10436372	NM_028523	73379	discoidin, CUB and LCCL domain	Dcbld2	1.654	6.816	0.000218118	0.00469165
730	10413047	NM_008873	18792	plasminogen activator, urokina	Plau	1.654	4.044	0.00461375	0.0388503
731	10464370	NM_172523	214084	solute carrier family 18 (vesi	Slc18a2	1.654	5.72	0.000647199	0.00970523
732	10429160	NM_009177	20442	ST3 beta-galactoside alpha-2,3	St3gal1	1.654	4.56	0.00241313	0.0248266
733	10455080	NM_053134	93880	protocadherin beta 9	Pcdhb9	1.653	5.124	0.00124324	0.0154086
734	10594066	NM_010729	16949	lysyl oxidase-like 1	Loxl1	1.653	6.534	0.00028503	0.00552972
735	10482030	NM_013515	13830	stomatin	Stom	1.652	3.337	0.0119442	0.0765762
736	10367673	NM_001033253	213783	pleckstrin homology domain con	Plekhg1	1.651	4.81	0.0017891	0.0198551
737	10587107	NM_010864	17918	myosin Va	Myo5a	1.651	7.437	0.000124763	0.00320532
738	10603708	NM_009806	12361	calcium/calmodulin-dependent s	Cask	1.65	4.181	0.00387002	0.0341512
739	10354588	NM_133810	98267	serine/threonine kinase 17b (a	Stk17b	1.648	3.372	0.0113657	0.0739888
740	10571233	NM_134161	171167	fucosyltransferase 10	Fut10	1.648	4.551	0.00243894	0.024997
741	10599680	NM_027510	70691	RIKEN cDNA 3830403N18 gene	3830403N18Rik	1.647	2.458	0.0425963	0.180844
742	10601343	NM_053201	107528	melanoma antigen, family E, 1	Magee1	1.647	6.97	0.000189221	0.00422927
743	10546631	NM_145148	232288	FERM domain containing 4B	Frmd4b	1.646	6.145	0.000417745	0.00716699
744	10428536	NM_032000	83925	trichorhinophalangeal syndrome	Trps1	1.646	4.458	0.00273411	0.0271154
745	10362440					1.646	1.83	0.108672	0.325457
746	10565315	NM_010176	14085	fumarylacetoacetate hydrolase	Fah	1.643	3.73	0.00696872	0.052362
747	10375360	NM_007897	13591	early B-cell factor 1	Ebf1	1.643	2.268	0.0565266	0.217348
748	10439612	NM_172506	117606	biregional cell adhesion molec	Boc	1.643	5.415	0.000898449	0.0121374
749	10600857	NM_010417	15203	hephaestin	Heph	1.642	4.715	0.00200193	0.0216405
750	10585976					1.642	2.425	0.0447447	0.187121
751	10466200	NM_027836	109225	membrane-spanning 4-domains, s	Ms4a7	1.64	6.461	0.00030584	0.00579961
752	10503098	NM_001111096	17096	Yamaguchi sarcoma viral (v-yes	Lyn	1.639	4.87	0.00166729	0.0188053
753	10352234	NM_001081175	320404	inositol 1,4,5-trisphosphate 3	Itpkb	1.638	6.776	0.000226496	0.0047976
754	10548043	NM_145983	16493	potassium voltage-gated channe	Kcna5	1.638	6.512	0.000290936	0.00562298
755	10374842	NM_176841	108686	coiled coil domain containing	Ccdc88a	1.637	9.686	2.17056e-05	0.000999095
756	10497481	ENSMUST00000057404	100040353	RIKEN cDNA 2810416G20 gene	2810416G20Rik	1.637	2.945	0.0208284	0.113009
757	10351491	NM_177068	320078	olfactomedin-like 2B	Olfml2b	1.635	4.495	0.00261382	0.0262175
758	10603551	NM_007807	13058	cytochrome b-245, beta polypep	Cybb	1.635	2.511	0.0394084	0.172266
759	10398240	NM_001043335	68519	echinoderm microtubule associa	Eml1	1.635	9.012	3.52457e-05	0.0013674
760	10447141	NM_001114361	78798	echinoderm microtubule associa	Eml4	1.635	7.659	0.000103105	0.00283493
761	10493798	NM_026416	67860	S100 calcium binding protein A	S100a16	1.635	4.52	0.00253534	0.0256417
762	10571241	NM_001098233	75029	purine-rich element binding pr	Purg	1.635	6.856	0.000210204	0.00457259
763	10497079	NM_011196	19218	prostaglandin E receptor 3 (su	Ptger3	1.634	5.896	0.000538231	0.008531

764	10561212	NM_175641	108075	latent transforming growth fac	Ltbp4	1.633	6.109	0.00043295	0.00731173
765	10544133	NM_172893	243771	poly (ADP-ribose) polymerase f	Parp12	1.632	3.211	0.014259	0.0870861
766	10423548	NM_008304	15529	syndecan 2	Sdc2	1.632	6.402	0.000323767	0.00598926
767	10346015	NM_009930	12825	collagen, type III, alpha 1	Col3a1	1.63	5.292	0.00102983	0.013395
768	10545101	NM_019455	54486	prostaglandin D2 synthase 2, h	Ptgds2	1.629	3.583	0.00850013	0.0604478
769	10521616	NM_175425	109323	C1q and tumor necrosis factor	C1qtnf7	1.628	3.772	0.00658924	0.0502789
770	10429128	NM_001029841	20491	src-like adaptor	Sla	1.627	6.068	0.000451168	0.0075411
771	10371740	NM_178773	320091	transmembrane protein 16D (eig	Tmem16d	1.626	6.185	0.000401394	0.00695093
772	10361807	NM_010437	15273	human immunodeficiency virus t	Hivep2	1.625	2.838	0.0243315	0.125082
773	10416897					1.625	1.63	0.145882	0.387407
774	10545001	NM_175523	243382	protein phosphatase 1K (PP2C d	Ppm1k	1.624	8.223	6.47401e-05	0.00206013
775	10490818	NM_025285	20257	stathmin-like 2	Stmn2	1.621	2.489	0.0406768	0.175848
776	10360479	NM_001099637	545389	centrosomal protein 170	Cep170	1.621	8.794	4.14917e-05	0.00153643
777	10585988					1.62	3.302	0.0125296	0.0792008
778	10347583	NM_010043	13346	desmin	Des	1.62	10.054	1.68593e-05	0.000840941
779	10375046	NM_010405	15126	hemoglobin X, alpha-like embry	Hba-x	1.618	4.482	0.00265484	0.0265502
780	10442069	NM_025681	66643	limb expression 1 homolog (chi	Lix1	1.617	2.916	0.0217241	0.115825
781	10503023	NM_145953	107869	cystathionase (cystathionine g	Cth	1.617	4.821	0.00176565	0.0196489
782	10363696	AK038706	320379	RIKEN cDNA D630028G08 gene	D630028G08Rik	1.615	3.969	0.00508567	0.0417922
783	10590663	NM_019691	14802	glutamate receptor, ionotropic	Gria4	1.615	3.225	0.0139787	0.0858203
784	10495054	NM_007484	11853	ras homolog gene family, membe	Rhoc	1.614	6.563	0.00027701	0.00540322
785	10504375	NM_173788	230103	natriuretic peptide receptor 2	Npr2	1.613	9.609	2.28955e-05	0.00102782
786	10456522	NM_013685	21413	transcription factor 4	Tcf4	1.61	6.879	0.00020588	0.0045157
787	10384504	NM_010789	17268	Meis homeobox 1	Meis1	1.61	10.293	1.43699e-05	0.000757701
788	10455135	NM_053146	93892	protocadherin beta 21	Pcdhb21	1.609	3.753	0.00675918	0.051242
789	10396476	NM_023275	80837	ras homolog gene family, membe	Rhoj	1.609	3.66	0.00766087	0.0563022
790	10393272	ENSMUST00000100202	217340	ring finger protein 157	Rnf157	1.608	6.941	0.000194363	0.00432822
791	10458028	NM_001048207	71683	glycophorin C	Gypc	1.606	5.802	0.000593953	0.00916676
792	10527713	NM_080468	140498	relaxin/insulin-like family pe	Rxfp2	1.605	2.309	0.0532213	0.209282
793	10457644	NM_007664	12558	cadherin 2	Cdh2	1.605	5.017	0.00140531	0.0166745
794	10362245	NM_013511	13822	erythrocyte protein band 4.1-l	Epb4.1l2	1.605	6.433	0.000314019	0.00587058
795	10474671	NM_033524	114715	sprouty protein with EVH-1 dom	Spred1	1.605	7.163	0.00015899	0.00378143
796	10491414	NM_001013024	72607	ubiquitin specific peptidase 1	Usp13	1.605	5.404	0.000909701	0.0122592
797	10395409	NM_008584	17286	mesenchyme homeobox 2	Meox2	1.604	3.975	0.00504666	0.0415985
798	10467038	BC096400	625995	ubiquitin-like 5 pseudogene	LOC625995	1.603	1.863	0.103574	0.316379
799	10380289	NM_026178	67468	monocyte to macrophage differe	Mmd	1.602	3.531	0.00912455	0.0635892
800	10423109	NM_175501	239337	a disintegrin-like and metallo	Adamts12	1.602	9.844	1.94483e-05	0.00093035
801	10448836	NM_001001183	407831	transmembrane protein 204	Tmem204	1.601	7.514	0.00011672	0.00308492
802	10566846	NM_021494	19347	Rab6 interacting protein 1	Rab6ip1	1.601	7.052	0.000175657	0.00405467
803	10603206	ENSMUST00000052299	237246	cDNA sequence BC022960	BC022960	1.601	3.662	0.00763893	0.0562191
804	10608001	NM_012011	26908	eukaryotic translation initiat	Eif2s3y	1.6	0.974	0.361747	0.633386
805	10368999	NM_010349	14806	glutamate receptor, ionotropic	Grik2	1.6	3.717	0.00709944	0.0532079
806	10452613	NM_172964	268970	Rho GTPase activating protein	Arhgap28	1.599	3.92	0.00541852	0.0437454
807	10441787	BC009123	72704	RIKEN cDNA 2810051F02 gene	2810051F02Rik	1.599	4.742	0.00193934	0.0210933
808	10600308					1.598	4.791	0.00182919	0.020186
809	10600169	NM_007542	12111	biglycan	Bgn	1.598	4.274	0.00343746	0.0314073
810	10537712	NM_029555	76263	glutathione S-transferase kapp	Gstk1	1.594	5.262	0.00106405	0.0137094
811	10474229	NM_001111060	12509	CD59a antigen	Cd59a	1.594	1.647	0.142246	0.382232
812	10492798	NM_009144	20319	secreted frizzled-related prot	Sfrp2	1.594	4.073	0.00444018	0.0376095
813	10452485	NM_133685	106572	RAB31, member RAS oncogene fam	Rab31	1.592	4.526	0.00251542	0.0255211
814	10379615	NM_183201	327978	schlafen 5	Slfn5	1.59	4.878	0.00165203	0.0187295
815	10482500	NM_028810	74194	Rho family GTPase 3	Rnd3	1.59	7.245	0.000147753	0.0035704
816	10375245	NM_008070	14401	gamma-aminobutyric acid (GABA-	Gabrb2	1.589	3.617	0.00812287	0.0585578
817	10358513	NM_001024720	545370	hemicentin 1	Hmcn1	1.587	1.678	0.136068	0.372141
818	10361356					1.587	2.933	0.0211995	0.114027

819	10453049	NM_026514	260409	CDC42 effector protein (Rho GT	Cdc42ep3	1.586	2.957	0.0204768	0.111886
820	10579012	NM_172753	234356	chondroitin sulfate N-acetylga	Csgalnact1	1.586	6.417	0.000319167	0.00592742
821	10511180	NM_024263	74761	matrix-remodelling associated	Mxra8	1.586	6.922	0.000197836	0.0043708
822	10366476	NM_029928	19263	protein tyrosine phosphatase,	Ptprb	1.585	8.655	4.61431e-05	0.00165645
823	10474201	NM_008505	16909	LIM domain only 2	Lmo2	1.585	4.354	0.00311078	0.0294293
824	10353252	NM_001033288	226866	gene model 106, (NCBI)	Gm106	1.584	5.228	0.00110599	0.0140789
825	10472378	NM_001099298	110876	sodium channel, voltage-gated,	Scn2a1	1.584	2.848	0.0239873	0.123827
826	10516481	NM_008120	14612	gap junction protein, alpha 4	Gja4	1.584	6.643	0.000256824	0.00517663
827	10604853	NM_178740	245446	SLIT and NTRK-like family, mem	Slitrk4	1.583	5.826	0.000579252	0.00898584
828	10588495	NM_153459	235584	dual specificity phosphatase 7	Dusp7	1.581	4.263	0.00348642	0.0316926
829	10517508	NM_009777	12260	complement component 1, q subc	C1qb	1.581	3.426	0.0105445	0.0705216
830	10370510	ENSMUST00000040580	71709	synapse defective 1, Rho GTPas	Syde1	1.581	6.387	0.000328601	0.00605222
831	10604694	NM_177293	320923	MAP7 domain containing 3	Mtap7d3	1.58	3.639	0.0078783	0.0573618
832	10492169	NM_010750	17116	mab-21-like 1 (C. elegans)	Mab21l1	1.579	5.841	0.00057021	0.00889123
833	10571252	NM_031374	104271	testis expressed gene 15	Tex15	1.579	3.841	0.00601711	0.0469988
834	10507040	NM_026470	67946	spermatogenesis associated 6	Spata6	1.579	7.339	0.000135921	0.0033771
835	10491601	ENSMUST00000057272	229227	RIKEN cDNA 4932438A13 gene	4932438A13Rik	1.579	3.146	0.0156174	0.0928214
836	10503952	NM_199157	387510	interferon kappa	Ifnk	1.579	3.95	0.00520904	0.0424541
837	10604610					1.578	7.261	0.00014566	0.00353339
838	10542857	NM_178797	330450	male sterility domain containi	Mlstd1	1.577	7.975	7.9204e-05	0.00236365
839	10447190	NM_177606	213556	pleckstrin homology domain con	Plekhh2	1.577	4.138	0.00408741	0.0355216
840	10586491	NM_010019	13143	death-associated kinase 2	Dapk2	1.576	7.02	0.000180874	0.00413449
841	10590842	ENSMUST00000098988	100126546	predicted gene, ENSMUSG0000007	ENSMUSG00000074512	1.576	1.621	0.147887	0.390122
842	10608107	NM_009484	22290	ubiquitously transcribed tetra	Uty	1.575	1.335	0.222328	0.492087
843	10414747	BC038136	236118	predicted gene, OTTMUSG0000001	OTTMUSG00000015204	1.575	3.595	0.00836299	0.0597187
844	10578829	NM_001081390	72333	palladin, cytoskeletal associa	Palld	1.575	5.366	0.000948231	0.0126388
845	10498386	ENSMUST00000097075	242050	immunoglobulin superfamily, me	Igsf10	1.575	5.439	0.000875398	0.0119185
846	10458569	NM_008173	14815	nuclear receptor subfamily 3,	Nr3c1	1.574	5.95	0.000509382	0.00819663
847	10506488	NM_080555	67916	phosphatidic acid phosphatase	Ppap2b	1.574	5.09	0.00129218	0.0158118
848	10380571	NM_023121	14710	guanine nucleotide binding pro	Gngt2	1.573	3.65	0.00776574	0.0567966
849	10361771	NM_009538	22634	pleiomorphic adenoma gene-like	Plagl1	1.573	6.192	0.000398484	0.00691185
850	10502240	NM_033525	114249	nephronectin	Npnt	1.573	5.293	0.00102797	0.0133936
851	10344966	NM_016923	17087	lymphocyte antigen 96	Ly96	1.572	2.708	0.0294365	0.141691
852	10492448	NM_008987	19288	pentraxin related gene	Ptx3	1.572	3.716	0.00710143	0.0532079
853	10436830	NM_010509	15976	interferon (alpha and beta) re	Ifnar2	1.572	2.683	0.0305309	0.14545
854	10534862	NM_008788	18542	procollagen C-endopeptidase en	Pcolce	1.572	4.669	0.00211465	0.022662
855	10416931	NM_198865	75409	SLIT and NTRK-like family, mem	Slitrk5	1.571	5.314	0.00100434	0.0131653
856	10425726	NM_011889	24050	septin 3	Sept3	1.568	5.094	0.00128719	0.0158051
857	10358978	NM_010500	15939	immediate early response 5	Ier5	1.568	7.988	7.83339e-05	0.00234935
858	10493555	NM_080466	140493	potassium intermediate/small c	Kcnn3	1.567	7.741	9.61923e-05	0.00272092
859	10554140	BC116191	22774	zinc finger protein of the cer	Zic4	1.566	6.76	0.000229891	0.00483366
860	10496338	NM_008913	19055	protein phosphatase 3, catalyt	Ppp3ca	1.566	4.635	0.00220398	0.0233315
861	10387505	NM_013415	11932	ATPase, Na+/K+ transporting, b	Atp1b2	1.565	3.567	0.00868689	0.0613817
862	10427402	NM_010284	14600	growth hormone receptor	Ghr	1.565	6.393	0.000326555	0.0060276
863	10593856	NM_172924	244895	RIKEN cDNA C230081A13 gene	C230081A13Rik	1.564	5.844	0.000568089	0.00888438
864	10400126	NM_010733	16981	leucine rich repeat protein 3,	Lrrn3	1.564	4.293	0.00335597	0.0309053
865	10505143	ENSMUST00000098066	11641	A kinase (PRKA) anchor protein	Akap2	1.563	1.33	0.224007	0.494176
866	10584598					1.562	1.788	0.115672	0.338219
867	10578989	NM_177698	234353	pleckstrin and Sec7 domain con	Psd3	1.56	5.381	0.000932512	0.0125187
868	10455761	NM_001033281	225518	PR domain containing 6	Prdm6	1.559	3.764	0.00666418	0.0507044
869	10419261	NM_007554	12159	bone morphogenetic protein 4	Bmp4	1.559	3.769	0.00661932	0.0504721

870	10368981	NM_001031772	380669	lin-28 homolog B (C. elegans)	Lin28b	1.559	6.062	0.00045417	0.00756735
871	10398996	NM_024223	68337	cysteine rich protein 2	Crip2	1.559	5.238	0.00109318	0.0139472
872	10413100	NM_017479	54169	MYST histone acetyltransferase	Myst4	1.559	6.764	0.000229087	0.00482451
873	10453231	NM_011406	20541	solute carrier family 8 (sodiu	Slc8a1	1.558	6.73	0.000236565	0.00493774
874	10483800					1.556	3.615	0.00813652	0.0586362
875	10392560	NM_147220	217262	ATP-binding cassette, sub-fami	Abca9	1.556	4.87	0.0016679	0.0188053
876	10607848	NM_019397	54156	EGF-like-domain, multiple 6	Egfl6	1.556	2.189	0.0636781	0.234321
877	10355514	BC055076	21961	tensin 1	Tns1	1.555	8.502	5.19378e-05	0.0017944
878	10491885	NM_001098171	18526	protocadherin 10	Pcdh10	1.555	6.807	0.000220012	0.00469892
879	10544002	NM_178661	208647	cAMP responsive element bindin	Creb3l2	1.553	4.37	0.00304845	0.0290606
880	10382890	NM_028777	74136	SEC14-like 1 (S. cerevisiae)	Sec14l1	1.553	5.547	0.000778638	0.0110271
881	10391332	NM_008986	19285	polymerase I and transcript re	Ptrf	1.553	4.482	0.00265577	0.0265502
882	10577190	NM_009025	19414	RAS p21 protein activator 3	Rasa3	1.553	8.517	5.13102e-05	0.00177562
883	10606694	NM_013482	12229	Bruton agammaglobulinemia tyro	Btk	1.551	7.13	0.000163785	0.00385642
884	10359762	NM_178593	226594	RCSD domain containing 1	Rcsd1	1.55	5.921	0.00052481	0.00836215
885	10403604	NM_010748	17101	lysosomal trafficking regulato	Lyst	1.549	8.046	7.4726e-05	0.00227339
886	10544774	NM_010454	15403	homeo box A6	Hoxa6	1.549	3.966	0.00510552	0.041888
887	10453394	NM_011380	20472	sine oculis-related homeobox 2	Six2	1.549	1.018	0.341518	0.616178
888	10558481	NM_011993	26757	dihydropyrimidinase-like 4	Dpysl4	1.549	4.916	0.00157907	0.0180964
889	10593449	BC139816	244864	layilin	Layn	1.549	6.437	0.000312919	0.00586221
890	10397428	BC048169	70373	RIKEN cDNA 1700020O03 gene	1700020O03Rik	1.548	3.388	0.0111263	0.0729652
891	10491599					1.548	1.618	0.148515	0.390852
892	10349634					1.548	3.129	0.0160137	0.0945266
893	10598757	NM_175669	319200	G protein-coupled receptor 82	Gpr82	1.547	3.341	0.0118664	0.0762622
894	10566454	NM_028444	109042	protein kinase C, delta bindin	Prkcdbp	1.547	5.607	0.000729929	0.010573
895	10553833	NM_010882	17984	necdin	Ndn	1.547	7.643	0.000104506	0.00286229
896	10595392	NM_148941	83603	elongation of very long chain	Elovl4	1.546	2.568	0.0361851	0.162407
897	10452907	NM_199448	225020	fasciculation and elongation p	Fez2	1.546	6.352	0.000340015	0.00617891
898	10366645	ENSMUST00000041178	321010	RIKEN cDNA 1700006J14 gene	1700006J14Rik	1.546	6.304	0.000356516	0.00637209
899	10523766	NM_133897	100604	leucine rich repeat containing	Lrrc8c	1.544	6.365	0.000335624	0.00611645
900	10532753	NM_011779	23790	coronin, actin binding protein	Coro1c	1.544	4.404	0.00292474	0.028306
901	10407709	NM_001081128	238505	5-methyltetrahydrofolate-homoc	Mtr	1.543	4.756	0.0019065	0.0208649
902	10455942	BC075669	225583	RIKEN cDNA A730017C20 gene	A730017C20Rik	1.543	2.048	0.0786376	0.266888
903	10487011	NM_025961	67092	glycine amidinotransferase (L-	Gatm	1.543	3.389	0.011097	0.0728453
904	10563077	NM_026555	52377	reticulocalbin 3, EF-hand calc	Rcn3	1.542	4.731	0.00196494	0.0212971
905	10527799	AK041221	100093622	predicted gene, ENSMUSG0000007	ENSMUSG00000075527	1.542	3.513	0.00936054	0.0647854
906	10392388	NM_011101	18750	protein kinase C, alpha	Prkca	1.541	4.275	0.00343244	0.0314044
907	10452571	NM_008984	19274	protein tyrosine phosphatase,	Ptprm	1.541	4.218	0.00368901	0.033051
908	10358672	NM_001024720	545370	hemicentin 1	Hmcn1	1.54	4	0.00488138	0.0405548
909	10447341	NM_145491	104215	ras homolog gene family, membe	Rhoq	1.538	4.783	0.0018468	0.0203462
910	10562500	NM_178704	233115	dpy-19-like 3 (C. elegans)	Dpy19l3	1.537	6.143	0.000418617	0.00716699
911	10387368	NM_025915	67020	transmembrane protein 88	Tmem88	1.537	7.43	0.000125579	0.00321848
912	10457587	NM_145492	225207	zinc finger protein 521	Zfp521	1.536	6.744	0.000233382	0.00489349
913	10560190	NM_153068	259300	EH-domain containing 2	Ehd2	1.535	5.295	0.00102643	0.0133885
914	10592515	NM_176860	72828	ubiquitin associated and SH3 d	Ubash3b	1.535	5.569	0.000760019	0.0108507
915	10427898	NM_176959	448987	F-box and leucine-rich repeat	Fbxl7	1.534	3.219	0.014099	0.0862835
916	10362717	NM_031877	83767	WASP family 1	Wasf1	1.534	5.178	0.00116934	0.0147079
917	10395320	NM_011658	22160	twist gene homolog 1 (Drosophi	Twist1	1.534	3.344	0.0118273	0.0761033
918	10541075	NM_001012477	20315	chemokine (C-X-C motif) ligand	Cxcl12	1.534	5.242	0.00108922	0.0139352
919	10427918	BC052328	223433	cDNA sequence BC052328	BC052328	1.533	6.905	0.00020098	0.00442197
920	10385635	NM_013922	30944	zinc finger protein 354C	Zfp354c	1.533	7.975	7.91907e-05	0.00236365
921	10515986	NM_001005788	381549	zinc finger protein 69	Zfp69	1.533	7.127	0.000164124	0.00386011
922	10497994	NM_001101479	241989	poly(A) binding protein, cytop	Pabpc4l	1.532	6.054	0.000458028	0.00760508

923	10605616	BC119580	331461	interleukin 1 receptor accesso	Il1rapl1	1.53	1.481	0.180841	0.436777
924	10417787	NM_010315	14702	guanine nucleotide binding pro	Gng2	1.53	7.858	8.72398e-05	0.00255485
925	10358713	BC022177	100038553	predicted gene, ENSMUSG0000007	ENSMUSG00000073540	1.529	3.986	0.00496862	0.0411019
926	10447461	NM_029858	77057	stonin 1	Ston1	1.529	5.791	0.000600526	0.00921618
927	10548105	NM_009829	12444	cyclin D2	Ccnd2	1.529	6.281	0.000364552	0.00647739
928	10591129	NM_001080814	270120	FAT tumor suppressor homolog 3	Fat3	1.528	2.602	0.0344008	0.157065
929	10357115	NM_001081316	319901	dermatan sulfate epimerase-lik	Dsel	1.527	6.625	0.00026113	0.0052421
930	10594645	NM_173413	235442	RAB8B, member RAS oncogene fam	Rab8b	1.527	9.554	2.37979e-05	0.00105048
931	10582388					1.526	1.247	0.251312	0.525436
932	10555510	NM_001008548	207728	phosphodiesterase 2A, cGMP-sti	Pde2a	1.525	8.928	3.75017e-05	0.00142276
933	10518069	NM_025994	27984	EF hand domain containing 2	Efhd2	1.524	5.371	0.000943127	0.0126089
934	10601701	NM_026239	67564	transmembrane protein 35	Tmem35	1.524	5.91	0.000530729	0.00844374
935	10522060	NM_026667	68303	RIKEN cDNA 9130005N14 gene	9130005N14Rik	1.524	3.895	0.00560381	0.0448814
936	10475990	NM_015747	20515	solute carrier family 20, memb	Slc20a1	1.522	5.489	0.000828985	0.011524
937	10559766	NM_001033249	213011	zinc finger protein 583	Zfp583	1.521	6.688	0.00024611	0.0050424
938	10441680	NM_011866	23984	phosphodiesterase 10A	Pde10a	1.521	6.153	0.000414281	0.00713294
939	10455084	NM_053135	93881	protocadherin beta 10	Pcdhb10	1.521	3.234	0.0138037	0.0851165
940	10576046	NM_010426	15227	forkhead box F1a	Foxf1a	1.521	5.885	0.000544804	0.00859115
941	10493831	NM_013650	20201	S100 calcium binding protein A	S100a8	1.519	2.528	0.0384301	0.169439
942	10541564	NM_153197	73149	C-type lectin domain family 4,	Clec4a3	1.519	3.885	0.00567504	0.0452369
943	10426315	NM_025730	66725	leucine-rich repeat kinase 2	Lrrk2	1.518	6.929	0.000196616	0.00435315
944	10439651	NM_010818	17470	Cd200 antigen	Cd200	1.518	4.396	0.00295367	0.0284299
945	10455123	NM_053144	93890	protocadherin beta 19	Pcdhb19	1.518	2.224	0.0603756	0.226645
946	10372648	NM_017372	17105	lysozyme 2	Lyz2	1.517	4.466	0.00270918	0.0269567
947	10351347	NM_011804	433375	cellular repressor of E1A-stim	Creg1	1.517	4.075	0.00443225	0.0375764
948	10606259					1.517	3.517	0.00930495	0.0645485
949	10443980	NM_053214	17916	myosin IF	Myo1f	1.517	4.364	0.00307262	0.0291595
950	10495416	NM_020505	57257	vav 3 oncogene	Vav3	1.516	4.627	0.00222436	0.0234807
951	10423258	NM_001008420	215654	cadherin 12	Cdh12	1.515	3.167	0.0151691	0.0910404
952	10471486	NM_007932	13805	endoglin	Eng	1.514	6.875	0.000206571	0.00452616
953	10427816	NM_001081064	68070	PDZ domain containing 2	Pdzd2	1.514	5.493	0.000825542	0.0114989
954	10521678	NM_007646	12494	CD38 antigen	Cd38	1.514	4.023	0.00473905	0.0396916
955	10499189	NM_030707	80891	Fc receptor-like S, scavenger	Fcrls	1.513	2.453	0.042914	0.181802
956	10466210	NM_026835	68774	membrane-spanning 4-domains, s	Ms4a6d	1.512	3.367	0.0114475	0.074384
957	10605493	BC032926	546336	proline rich Gla (G-carboxyglu	Prrg1	1.512	4.041	0.00463105	0.0389494
958	10546725	NM_018884	55983	PDZ domain containing RING fin	Pdzrn3	1.512	5.467	0.000849013	0.011672
959	10605792	NM_178753	270624	spindlin family, member 4	Spin4	1.511	6.072	0.000449571	0.00752035
960	10404982	NM_007526	12022	BarH-like homeobox 1	Barx1	1.511	3.172	0.0150583	0.0906069
961	10600852					1.51	5.903	0.000534329	0.00848188
962	10498284	NM_133784	97064	WW domain containing transcrip	Wwtr1	1.509	3.83	0.00609919	0.0474981
963	10475414	NM_009735	12010	beta-2 microglobulin	B2m	1.509	5.429	0.000885562	0.0120182
964	10531187	NM_001081401	330119	a disintegrin-like and metallo	Adamts3	1.508	6.097	0.00043841	0.00738884
965	10472408	NM_153409	77771	cysteine-serine-rich nuclear p	Csnrp3	1.507	8.291	6.1302e-05	0.00200098
966	10367591	NM_026793	68632	myc target 1	Myct1	1.507	4.069	0.00446707	0.037811
967	10351905	NM_011465	20739	spectrin alpha 1	Spna1	1.506	1.756	0.121254	0.347823
968	10605181	NM_023132	19703	renin binding protein	Renbp	1.505	3.39	0.0110937	0.0728453
969	10492310	NM_020007	56758	muscleblind-like 1 (Drosophila	Mbnl1	1.504	8.78	4.19352e-05	0.00154473
970	10568298	NM_024414	56216	syntaxin 1B	Stx1b	1.504	6.774	0.000226827	0.0047976
971	10372385	NM_172554	320150	zinc finger, DHHC domain conta	Zdhhc17	1.503	5.95	0.00050895	0.00819592
972	10430555	NM_010059	13404	DMC1 dosage suppressor of mck1	Dmc1	1.503	6.61	0.000264885	0.00528661
973	10349081	BC059254	98432	PH domain and leucine rich rep	Phlpp	1.503	4.107	0.00425399	0.0365189
				MARVEL (membrane-					

974	10463224	BC054384	277010	associating)	Marveld1	1.502	7.496	0.000118613	0.00311159
975	10361509	NM_001079686	64009	synaptic nuclear envelope 1	Syne1	1.502	4.027	0.0047112	0.0395292
976	10505120	NM_172868	242481	paralemmin 2	Palm2	1.502	1.573	0.158389	0.405262
977	10485633	ENSMUST00000099651	100038694	predicted gene, ENSMUSG0000007	ENSMUSG00000074989	1.5	2.155	0.0669341	0.241635
978	10436561	NM_013918	30940	ubiquitin specific peptidase 2	Usp25	1.498	7.302	0.000140405	0.00344552
979	10579744	NM_010687	16795	like-glycosyltransferase	Large	1.498	8.292	6.12758e-05	0.00200098
980	10601354					1.497	0.954	0.37118	0.641982
981	10569618	NM_178642	101772	transmembrane protein 16A	Tmem16a	1.497	2.946	0.0207968	0.112896
982	10472364	NM_001099298	110876	sodium channel, voltage-gated,	Scn2a1	1.496	2.534	0.0380843	0.168569
983	10472436	NM_020283	26877	UDP-Gal:betaGlcNAc beta 1,3-ga	B3galt1	1.496	4.552	0.00243641	0.0249954
984	10523802	NM_009863	12545	cell division cycle 7 (S. cere	Cdc7	1.495	7.363	0.000133117	0.00333883
985	10406598	NM_172588	218442	serine incorporator 5	Serinc5	1.494	4.406	0.00291424	0.0282784
986	10554074	NM_001033877	233332	a disintegrin-like and metallo	Adamts17	1.493	2.866	0.0233848	0.121516
987	10480324	NM_028317	72668	RIKEN cDNA 2810030E01 gene	2810030E01Rik	1.492	6.89	0.000203662	0.00447168
988	10421293	NM_008915	19057	protein phosphatase 3, catalyt	Ppp3cc	1.492	4.952	0.00151487	0.0175413
989	10384579	NM_139297	216558	UDP-glucose pyrophosphorylase	Ugp2	1.492	5.524	0.000797979	0.0112109
990	10431711	NM_001033633	239606	solute carrier family 2 (facil	Slc2a13	1.49	4.336	0.00318228	0.0298651
991	10474096	NM_178725	241568	leucine rich repeat containing	Lrrc4c	1.49	3.561	0.00876053	0.061806
992	10537184	NM_145575	109624	caldesmon 1	Cald1	1.49	3.163	0.0152507	0.0914142
993	10601616	NM_017398	54004	diaphanous homolog 2 (Drosophi	Diap2	1.489	4.41	0.0029004	0.02817
994	10361246	NM_008059	14373	G0/G1 switch gene 2	G0s2	1.489	7.774	9.35501e-05	0.00267301
995	10508012	NM_138683	192199	R-spondin homolog (Xenopus lae	Rspo1	1.489	3.378	0.0112808	0.0735307
996	10376144	NM_173753	216742	folliculin interacting protein	Fnip1	1.488	4.463	0.00271928	0.0270061
997	10485840	NM_177652	20192	ryanodine receptor 3	Ryr3	1.488	4.839	0.00172869	0.0193189
998	10514275	NM_025760	66775	protein tyrosine phosphatase-l	Ptplad2	1.487	2.809	0.0253774	0.128707
999	10404774	NM_007772	110521	human immunodeficiency virus t	Hivep1	1.487	6.597	0.000268191	0.00532453
1000	10439138	ENSMUST00000076810	545156	kalirin, RhoGEF kinase	Kalrn	1.487	5.487	0.000830994	0.0115242
1001	10530633	NM_011890	24051	sarcoglycan, beta (dystrophin-	Sgcb	1.486	2.74	0.0281044	0.137533
1002	10400155	ENSMUST00000066043	664883	neuro-oncological ventral anti	Nova1	1.486	4.941	0.00153396	0.0177042
1003	10499811	NM_008727	18160	natriuretic peptide receptor 1	Npr1	1.486	3.71	0.00715772	0.0535159
1004	10349947	NM_021355	14264	fibromodulin	Fmod	1.486	4.445	0.00277964	0.0273999
1005	10366983	NM_001113211	210035	transmembrane protein 194	Tmem194	1.485	5.164	0.00118875	0.0148816
1006	10491960					1.484	2.909	0.0219604	0.11652
1007	10380174	NM_010824	17523	myeloperoxidase	Mpo	1.484	7.317	0.000138672	0.00342132
1008	10385966	NM_013472	11749	annexin A6	Anxa6	1.484	3.831	0.00609576	0.0474904
1009	10575213	NM_007496	11906	zinc finger homeobox 3	Zfhx3	1.484	6.809	0.000219708	0.00469892
1010	10572786	NM_007456	11767	adaptor-related protein comple	Ap1m1	1.483	6.455	0.000307627	0.00580546
1011	10512022	ENSMUST00000098156	214944	MOB1, Mps One Binder kinase ac	Mobkl2b	1.483	3.335	0.0119798	0.0767115
1012	10346072					1.483	4.513	0.00255626	0.0257993
1013	10506201	NM_013845	26563	receptor tyrosine kinase-like	Ror1	1.483	4.215	0.00370467	0.0331492
1014	10583326	NM_172289	234967	solute carrier family 36 (prot	Slc36a4	1.482	2.957	0.0204924	0.111933
1015	10440019	NM_019631	56277	transmembrane protein 45a	Tmem45a	1.482	3.224	0.0139914	0.0858692
1016	10442087	ENSMUST00000052338	75202	RIKEN cDNA 4930546H06 gene	4930546H06Rik	1.482	5.791	0.000600638	0.00921618
1017	10527936	NM_021457	14362	frizzled homolog 1 (Drosophila	Fzd1	1.481	4.999	0.00143448	0.0168502
1018	10569707	NM_001093765	50918	myeloid-associated differentia	Myadm	1.48	5.854	0.000562107	0.0088169
1019	10554059	ENSMUST00000098385	100038588	predicted gene, ENSMUSG0000007	ENSMUSG00000074077	1.48	2.536	0.0379469	0.168193
1020	10412267	NM_008396	16398	integrin alpha 2	Itga2	1.479	6.078	0.000446997	0.00748914
1021	10455139	NM_053147	93893	protocadherin beta 22	Pcdhb22	1.479	4.995	0.00144093	0.0168793
1022	10445944	NM_172829	240119	beta galactoside alpha 2,6 sia	St6gal2	1.479	2.862	0.0235199	0.122008
1023	10492136	NM_019978	13175	doublecortin-like kinase 1	Dclk1	1.477	5.344	0.000972049	0.0128559
1024	10543145	ENSMUST00000046121	330267	thrombospondin, type I, domain	Thsd7a	1.477	3.915	0.0054562	0.043998
1025	10402268	NM_011175	19141	legumain	Lgmn	1.476	3.513	0.00935667	0.0647798

1026	10568568	NM_016978	18242	ornithine aminotransferase	Oat	1.476	4.752	0.00191656	0.0209391
1027	10440186	BC043118	224273	cDNA sequence BC043118	BC043118	1.476	4.621	0.00224266	0.0236267
1028	10432439	NM_011711	22379	formin-like 3	Fmnl3	1.475	5.568	0.000761308	0.0108617
1029	10436865	NM_008338	15980	interferon gamma receptor 2	Ifngr2	1.475	3.751	0.00678297	0.0513311
1030	10556082	NM_008905	19024	protein tyrosine phosphatase,	Ppfibp2	1.475	4.384	0.00299716	0.028736
1031	10436636	NM_001113208	17968	neural cell adhesion molecule	Ncam2	1.475	3.528	0.00916343	0.063776
1032	10548047	NM_010595	16485	potassium voltage-gated channe	Kcna1	1.475	4.404	0.00292388	0.028306
1033	10457118	NM_175542	246102	rotatin	Rttn	1.474	7.952	8.06976e-05	0.00239308
1034	10474860	NM_028117	72136	carbohydrate (N-acetylgalactos	Chst14	1.473	6.722	0.000238278	0.0049588
1035	10371400	NM_007771	12952	cryptochrome 1 (photolyase-lik	Cry1	1.472	4.506	0.00257865	0.0259757
1036	10500555	NM_001012306	15494	hydroxy-delta-5-steroid dehydr	Hsd3b3	1.471	4.151	0.00401752	0.0350874
1037	10601848	NR_003641	76219	RIKEN cDNA 6530401D17 gene	6530401D17Rik	1.47	4.539	0.00247646	0.0252835
1038	10480035	NM_133232	170768	6-phosphofructo-2-kinase/fruct	Pfkfb3	1.47	2.909	0.0219699	0.116541
1039	10530319	NM_001038999	11980	ATPase, aminophospholipid tran	Atp8a1	1.47	4.463	0.00271672	0.0270061
1040	10418506	NM_138672	192187	stabilin 1	Stab1	1.47	8.353	5.83811e-05	0.00192576
1041	10417068					1.47	1.778	0.117347	0.341384
1042	10578264	NM_031195	20288	macrophage scavenger receptor	Msr1	1.469	4.572	0.00237725	0.0246033
1043	10462363	NM_008413	16452	Janus kinase 2	Jak2	1.468	5.071	0.00132168	0.016024
1044	10607259	NM_001002272	56191	trophinin	Tro	1.468	5.057	0.00134176	0.0162022
1045	10598240	NM_001040459	208431	shroom family member 4	Shroom4	1.467	6.785	0.000224639	0.00476405
1046	10536611	NM_019697	16508	potassium voltage-gated channe	Kcnd2	1.467	6.302	0.000357183	0.00637862
1047	10525016	NM_011535	21386	T-box 3	Tbx3	1.466	5.828	0.000577687	0.00896919
1048	10548879	NM_008597	17313	matrix Gla protein	Mgp	1.466	1.113	0.301503	0.577839
1049	10403255	XM_001472410	100039182	similar to cyclin-dependent ki	LOC100039182	1.466	2.554	0.036925	0.164748
1050	10437205	NM_008791	18546	Purkinje cell protein 4	Pcp4	1.465	2.92	0.0216037	0.11535
1051	10422942					1.464	0.81	0.443698	0.702422
1052	10554752	NM_015760	50490	NADPH oxidase 4	Nox4	1.463	2.159	0.0665838	0.241111
1053	10475229	ENSMUST00000094652	668880	START domain containing 9	Stard9	1.463	5.99	0.000488664	0.00796631
1054	10511333	NM_019969	56711	pleiomorphic adenoma gene 1	Plag1	1.463	3.958	0.00515782	0.0421883
1055	10502830	NM_199465	68810	nexilin	Nexn	1.463	1.159	0.283207	0.55849
1056	10423902	NM_011766	22762	zinc finger protein, multitype	Zfpm2	1.462	5.663	0.00068791	0.010129
1057	10453233	NM_011406	20541	solute carrier family 8 (sodiu	Slc8a1	1.462	3.565	0.00872017	0.0615624
1058	10438980	NM_030138	78618	centaurin, beta 2	Centb2	1.461	5.66	0.000689844	0.0101478
1059	10485198	NM_183180	241556	tetraspanin 18	Tspan18	1.461	6.211	0.00039104	0.00681628
1060	10472050	NM_009398	21930	tumor necrosis factor alpha in	Tnfaip6	1.46	2.625	0.0332466	0.153788
1061	10427049	ENSMUST00000071328	77717	RIKEN cDNA 6030408B16 gene	6030408B16Rik	1.459	3.467	0.00996174	0.0679455
1062	10427471	NM_011019	18414	oncostatin M receptor	Osmr	1.459	5.991	0.000487986	0.0079614
1063	10498383	ENSMUST00000097075	242050	immunoglobulin superfamily, me	Igsf10	1.459	5.975	0.00049639	0.00806739
1064	10377537					1.458	6.113	0.000431303	0.00729643
1065	10433197					1.458	1.096	0.308301	0.585058
1066	10400609	NM_207010	320772	MAM domain containing glycosyl	Mdga2	1.458	3.448	0.0102273	0.0690444
1067	10409737	NM_023328	67269	ATP/GTP binding protein 1	Agtpbp1	1.457	3.651	0.00775212	0.0567952
1068	10394389	ENSMUST00000037953	72669	RIKEN cDNA 2810032G03 gene	2810032G03Rik	1.456	3.151	0.0155056	0.0924565
1069	10488147	NM_178382	71436	fibronectin leucine rich trans	Flrt3	1.456	2.312	0.0529454	0.208508
1070	10544089	NM_028864	78781	zinc finger CCCH type, antivir	Zc3hav1	1.456	5.002	0.00142969	0.0168502
1071	10594301	NM_175484	235431	coronin, actin binding protein	Coro2b	1.456	7.062	0.000174036	0.00403815
1072	10565759	NM_178635	78610	UV radiation resistance associ	Uvrag	1.455	5.768	0.000615065	0.00938306
1073	10502863	NM_001081277	229949	adenylate kinase 5	Ak5	1.455	4.537	0.00248288	0.0253246
1074	10552494	NM_028660	101533	kallikrein related-peptidase 9	Klk9	1.455	5.573	0.00075701	0.0108175
1075	10406456	AY512938	791388	predicted gene, ENSMUSG0000006	ENSMUSG00000069163	1.454	4.725	0.00197854	0.0214206
1076	10517967	NM_133754	74202	filamin binding LIM protein 1	Fblim1	1.454	4.386	0.00299014	0.0286858
1077	10387536	NM_009853	12514	CD68 antigen	Cd68	1.454	3.699	0.0072677	0.0541657

1078	10568024	NM_009898	12721	coronin, actin binding protein	Coro1a	1.454	4.427	0.00284266	0.0278522
1079	10490923	NM_009801	12349	carbonic anhydrase 2	Car2	1.454	1.235	0.255457	0.529807
1080	10493114	NM_016701	18008	nestin	Nes	1.452	6.161	0.000410772	0.00707853
1081	10495925					1.452	1.261	0.246571	0.519739
1082	10544763	NM_008265	15401	homeo box A4	Hoxa4	1.452	6.052	0.000458593	0.00760508
1083	10459671	NM_007831	13176	deleted in colorectal carcinom	Dcc	1.45	2.983	0.0197249	0.108809
1084	10368970	NM_007548	12142	PR domain containing 1, with Z	Prdm1	1.45	4.767	0.00188217	0.0206629
1085	10447294	NM_011104	18754	protein kinase C, epsilon	Prkce	1.45	3.383	0.011203	0.0733139
1086	10537179	NM_007563	12183	2,3-bisphosphoglycerate mutase	Bpgm	1.45	5.422	0.000892193	0.0120849
1087	10461723	BC038020	107373	RIKEN cDNA 4632417K18 gene	4632417K18Rik	1.45	4.398	0.0029447	0.028407
1088	10490304	NM_177191	320558	synaptonemal complex protein 2	Sycp2	1.449	2.351	0.0499946	0.201094
1089	10423274	NM_001081299	320865	cadherin 18	Cdh18	1.449	2.435	0.0441016	0.185146
1090	10363706	BC068318	108829	jumonji domain containing 1C	Jmjd1c	1.448	5.359	0.00095552	0.0127026
1091	10410408	NM_153534	210044	adenylate cyclase 2	Adcy2	1.447	4.56	0.00241409	0.0248266
1092	10542738	ENSMUST00000111704	71323	Ras association (RalGDS/AF-6)	Rassf8	1.447	4.119	0.00418731	0.0360344
1093	10533050	NM_030704	80888	heat shock protein 8	Hspb8	1.447	3.205	0.0143698	0.0876111
1094	10503709	AK051661	100038651	predicted gene, ENSMUSG0000007	ENSMUSG00000073981	1.447	7.383	0.000130843	0.00330137
1095	10504450	NM_027450	384009	GLI pathogenesis-related 2	Glipr2	1.447	5.238	0.00109366	0.0139472
1096	10523297	NM_007635	12452	cyclin G2	Ccng2	1.446	7.292	0.000141648	0.00346644
1097	10455112	NM_053142	93888	protocadherin beta 17	Pcdhb17	1.446	3.058	0.0177161	0.100883
1098	10379489	NM_029537	103743	transmembrane protein 98	Tmem98	1.446	4.913	0.00158458	0.0181497
1099	10498379	XM_913941	242050	immunoglobulin superfamily, me	Igsf10	1.446	5.738	0.000635261	0.00959427
1100	10491136	AK122306	665113	TRAF2 and NCK interacting kina	Tnik	1.446	2.848	0.0239912	0.123827
1101	10366446	NM_146010	216350	tetraspanin 8	Tspan8	1.446	1.246	0.251671	0.525573
1102	10527940	NM_011074	18647	PFTAIRE protein kinase 1	Pftk1	1.446	4.204	0.00375425	0.0333809
1103	10443091	XM_985548	240057	synaptic Ras GTPase activating	Syngap1	1.445	4.184	0.00385353	0.0340489
1104	10570483	NM_172751	234094	Rho guanine nucleotide exchang	Arhgef10	1.444	4.841	0.00172406	0.0192843
1105	10534493	NM_019577	56221	chemokine (C-C motif) ligand 24	Ccl24	1.444	5.323	0.000995181	0.0130696
1106	10537062	NM_008590	17294	mesoderm specific transcript	Mest	1.444	7.055	0.000175255	0.00405422
1107	10567299	NM_001033380	319622	RIKEN cDNA E030018N11 gene	E030018N11Rik	1.443	6.935	0.00019553	0.00434274
1108	10409599					1.443	3.462	0.0100357	0.0682302
1109	10431812	NM_016743	54003	NEL-like 2 (chicken)	Nell2	1.443	3.767	0.00663637	0.0505655
1110	10547282	NM_011763	22750	zinc finger protein 9	Zfp9	1.443	2.843	0.024163	0.124489
1111	10597239	NM_011199	19228	parathyroid hormone receptor 1	Pthr1	1.442	5.948	0.000510146	0.00820268
1112	10484622	NM_146590	258583	olfactory receptor 1085	Olfr1085	1.442	2.347	0.0502544	0.201609
1113	10478219	NM_021280	18803	phospholipase C, gamma 1	Plcg1	1.442	6.411	0.000321069	0.00594977
1114	10575693	BC056927	270097	expressed sequence AI427515	AI427515	1.442	2.458	0.0426389	0.18089
1115	10604630	NM_027409	70380	motile sperm domain containing	Mospd1	1.441	5.688	0.000669361	0.00993888
1116	10444135	NM_001013793	433100	expressed sequence AA388235	AA388235	1.441	4.304	0.0033125	0.0306385
1117	10427095	NM_153533	209039	tensin like C1 domain-containi	Tenc1	1.44	5.842	0.000569531	0.00888721
1118	10374777	NM_146015	216616	epidermal growth factor-contai	Efemp1	1.44	2.453	0.0429384	0.181833
1119	10435748	AK086454	320874	RIKEN cDNA D930030D11 gene	D930030D11Rik	1.44	3.384	0.0111883	0.0732403
1120	10538811	NM_027547	70779	PR domain containing 5	Prdm5	1.44	6.921	0.000198034	0.0043708
1121	10497051	NM_001039094	320840	neuronal growth regulator 1	Negr1	1.44	3.7	0.00726077	0.0541332
1122	10422227	NM_011897	24064	sprouty homolog 2 (Drosophila)	Spry2	1.44	2.875	0.0230578	0.120706
1123	10594540	NM_153119	102595	pleckstrin homology domain con	Plekho2	1.439	3.348	0.0117587	0.0757083
1124	10524983	NM_172424	76199	mediator complex subunit 13-li	Med13l	1.439	8.066	7.35168e-05	0.00225281
1125	10600326	NM_031379	83553	transketolase-like 1	Tktl1	1.439	3.067	0.0174921	0.0999956
1126	10586441	NM_010952	18247	ornithine decarboxylase antizy	Oaz2	1.437	4.464	0.00271552	0.0270061
1127	10407420	NM_019671	56349	neuroepithelial cell transform	Net1	1.437	3.826	0.0061388	0.0476151
1128	10358537	NM_001024720	545370	hemicentin 1	Hmcn1	1.436	4.868	0.00167101	0.0188071
1129	10454632	NM_009793	12326	calcium/calmodulin-dependent p	Camk4	1.436	4.423	0.00285459	0.0279433
1130	10480347	NM_008845	18718	phosphatidylinositol-5-phospha	Pip4k2a	1.435	3.975	0.00504501	0.0415985

1131	10481540	NM_001038700	14269	formin binding protein 1	Fnbp1	1.435	4.763	0.00189177	0.0207467
1132	10370037	NM_008606	17385	matrix metallopeptidase 11	Mmp11	1.435	4.505	0.00258186	0.0259957
1133	10467838					1.434	1.034	0.334746	0.610372
1134	10463482	NM_021901	21908	T-cell leukemia, homeobox 1	Tlx1	1.434	6.441	0.000311557	0.00584812
1135	10540085	NM_007992	14115	fibulin 2	Fbln2	1.434	4.913	0.0015857	0.0181527
1136	10387797	NM_007528	12029	B-cell CLL/lymphoma 6, member	Bcl6b	1.434	3.314	0.012324	0.0782223
1137	10398907	NM_178911	104759	phospholipase D family, member	Pld4	1.434	4.167	0.00393567	0.034558
1138	10439299	NM_025288	20863	stefin A3	Stfa3	1.434	1.347	0.218741	0.486928
1139	10501164	NM_007778	12977	colony stimulating factor 1 (m	Csf1	1.433	3.603	0.00827884	0.0593583
1140	10368175	NM_013875	29863	phosphodiesterase 7B	Pde7b	1.433	2.496	0.0402851	0.17469
1141	10522288	NM_001033415	330096	shisa homolog 3 (Xenopus laevi	Shisa3	1.433	2.44	0.0437798	0.1843
1142	10355050	NM_001045513	77300	Ras association (RalGDS/AF-6)	Raph1	1.432	4.772	0.0018709	0.0205498
1143	10499861	NM_009114	20202	S100 calcium binding protein A	S100a9	1.431	1.482	0.180537	0.43631
1144	10372383	BC051527	320150	zinc finger, DHHC domain conta	Zdhhc17	1.431	6.333	0.000346449	0.00625014
1145	10359480	NM_001038619	103967	dynamin 3	Dnm3	1.431	8.011	7.68696e-05	0.00231859
1146	10544885	NM_153573	231997	FK506 binding protein 14	Fkbp14	1.431	2.495	0.0403569	0.174894
1147	10391762	NM_008122	14615	gap junction protein, gamma 1	Gjc1	1.43	5.842	0.000569428	0.00888721
1148	10344990	NM_031402	83691	cysteine-rich secretory protei	Crispld1	1.43	3.408	0.0108089	0.0715825
1149	10368045	NM_028440	73112	RIKEN cDNA 3110003A17 gene	3110003A17Rik	1.43	3.715	0.00711305	0.0532572
1150	10595979	NM_008624	17532	muscle and microspikes RAS	Mras	1.43	3.403	0.010891	0.0718818
1151	10428157	NM_013923	30945	ring finger protein 19A	Rnf19a	1.43	8.101	7.14587e-05	0.00220573
1152	10469577	ENSMUST00000105000	791278	predicted gene, ENSMUSG0000006	ENSMUSG00000063691	1.429	2.311	0.0530218	0.208731
1153	10569890	BC086763	108909	RIKEN cDNA 2610208M17 gene	2610208M17Rik	1.429	5.044	0.00136288	0.0163592
1154	10549506	NM_177192	320560	RIKEN cDNA D030011O10 gene	D030011O10Rik	1.429	2.872	0.0231838	0.120967
1155	10496605	NM_173763	229905	cysteine conjugate-beta lyase	Ccbl2	1.429	2.837	0.0243776	0.125168
1156	10368409	NM_008481	16773	laminin, alpha 2	Lama2	1.429	2.027	0.0810286	0.271716
1157	10560139	NM_001039146	627280	RIKEN cDNA B430211C08 gene	B430211C08Rik	1.429	5.824	0.000580175	0.00899357
1158	10529206	NM_022424	64339	fibronectin type III domain co	Fndc4	1.429	5.483	0.000834535	0.0115341
1159	10536667	NM_001081306	19283	protein tyrosine phosphatase,	Ptprz1	1.429	3.78	0.00651948	0.0498366
1160	10531175	NM_001081401	330119	a disintegrin-like and metallo	Adamts3	1.428	1.852	0.105192	0.319429
1161	10443095	ENSMUST00000081285	240057	synaptic Ras GTPase activating	Syngap1	1.427	5.201	0.0011406	0.0144068
1162	10371506	NM_138673	192188	stabilin 2	Stab2	1.426	4.635	0.00220433	0.0233315
1163	10491970	NM_175386	108927	lipoma HMGIC fusion partner	Lhfp	1.426	3.464	0.0100072	0.0680857
1164	10490551	NM_021426	58237	Na+/K+ transporting ATPase int	Nkain4	1.426	4.583	0.00234783	0.0243585
1165	10489878	NM_008968	19223	prostaglandin I2 (prostacyclin	Ptgis	1.426	5.166	0.00118591	0.0148636
1166	10584317	NM_027102	69524	endothelial cell-specific adhe	Esam1	1.426	4.099	0.00429693	0.0367385
1167	10441791	ENSMUST00000105044	52042	DNA segment, Chr 17, ERATO Doi	D17Ertd663e	1.425	5.004	0.00142689	0.0168385
1168	10346348	BC021879	67198	RIKEN cDNA 2810022L02 gene	2810022L02Rik	1.425	3.23	0.0138719	0.0854128
1169	10586433	NM_028030	71973	RNA binding protein with multi	Rbpms2	1.425	3.018	0.0187515	0.105112
1170	10489391	NM_007398	11486	adenosine deaminase	Ada	1.424	4.561	0.00241034	0.0248122
1171	10521498	NM_007765	12933	collapsin response mediator pr	Crmp1	1.424	3.867	0.00581009	0.0459935
1172	10605820	NM_001003916	245522	cDNA sequence AK129302	AK129302	1.424	3.981	0.00500338	0.041341
1173	10506134	NM_175029	242557	autophagy-related 4C (yeast)	Atg4c	1.423	2.155	0.0669754	0.241723
1174	10436487	ENSMUST00000116587	73569	vestigial like 3 (Drosophila)	Vgll3	1.422	3.894	0.00560601	0.044882
1175	10587299	NM_019987	56542	intestinal cell kinase	Ick	1.422	4.034	0.00467027	0.0392325
1176	10452793	NM_027864	71685	UDP-N-acetyl-alpha-D-galactosa	Galnt14	1.422	3.043	0.0180949	0.102354
1177	10423520	NM_009154	20356	sema domain, seven thrombospon	Sema5a	1.422	2.649	0.0320895	0.150244
1178	10407416	NM_027416	70405	calmodulin-like 3	Calml3	1.422	4.303	0.00331613	0.0306428
1179	10430145	NM_053104	93686	RNA binding motif protein 9	Rbm9	1.421	6.208	0.000392234	0.00682585
1180	10367822	NM_026405	67844	RAB32, member RAS oncogene fam	Rab32	1.42	2.801	0.0256994	0.129873

1181	10424543	NM_018865	22402	WNT1 inducible signaling pathw	Wisp1	1.42	4.869	0.0016685	0.0188053
1182	10369752	NM_178678	216028	leucine rich repeat transmembr	Lrrtm3	1.42	1.858	0.104302	0.31773
1183	10416958					1.419	2.399	0.046498	0.191643
1184	10391649	NM_011403	20533	solute carrier family 4 (anion	Slc4a1	1.419	1.276	0.241406	0.514329
1185	10358224	NM_001111316	19264	protein tyrosine phosphatase,	Ptprc	1.418	3.884	0.00568061	0.0452369
1186	10566366	NM_199146	209387	expressed sequence AI451617	AI451617	1.418	2.655	0.031847	0.14934
1187	10567589	ENSMUST00000025327	76179	ubiquitin specific peptidase 3	Usp31	1.418	6.372	0.000333275	0.00609055
1188	10446986	NM_015800	50766	cysteine rich transmembrane BM	Crim1	1.418	5.659	0.000690376	0.0101478
1189	10540359	NM_001109749	269784	contactin 4	Cntn4	1.417	2.65	0.032078	0.150244
1190	10360506	NM_011785	23797	thymoma viral proto-oncogene 3	Akt3	1.416	6.147	0.000416678	0.0071628
1191	10593591	NM_144784	110446	acetyl-Coenzyme A acetyltransf	Acat1	1.416	3.146	0.0156345	0.0928584
1192	10454235	ENSMUST00000062608	211961	additional sex combs like 3 (D	Asxl3	1.416	3.829	0.00610766	0.0474981
1193	10515090	NM_007671	12580	cyclin-dependent kinase inhibi	Cdkn2c	1.416	6.972	0.000188875	0.00422741
1194	10480145	NM_009105	20163	Ras suppressor protein 1	Rsu1	1.414	3.99	0.00494519	0.0409882
1195	10578017	AK035883	100101427	predicted gene, ENSMUSG0000005	ENSMUSG00000053570	1.414	0.712	0.498776	0.742429
1196	10468992	NM_172475	209630	FERM domain containing 4A	Frmd4a	1.414	4.215	0.00370303	0.0331485
1197	10385903	NM_019417	30794	PDZ and LIM domain 4	Pdlim4	1.413	5.971	0.000498461	0.00808259
1198	10470283	NM_198724	353156	EGF-like domain 7	Egfl7	1.413	6.043	0.000463226	0.00765191
1199	10597268	NM_011562	21667	teratocarcinoma-derived growth	Tdgf1	1.412	1.544	0.165131	0.415214
1200	10472235	NM_029723	76747	death associated protein-like	Dapl1	1.411	4.18	0.00387208	0.0341512
1201	10511939	NM_026293	67652	sperm acrosome associated 1	Spaca1	1.411	2.818	0.0250776	0.127646
1202	10434094	NM_145479	224023	kelch-like 22 (Drosophila)	Klhl22	1.41	6.119	0.000428824	0.00727109
1203	10386058	NM_009242	20692	secreted acidic cysteine rich	Sparc	1.409	7.47	0.000121232	0.00314805
1204	10400304	NM_028133	112407	EGL nine homolog 3 (C. elegans	Egln3	1.409	1.47	0.183757	0.440966
1205	10466932	NM_013754	27356	insulin-like 6	Insl6	1.408	4.428	0.00283694	0.0278091
1206	10555235	NM_177231	109689	arrestin, beta 1	Arrb1	1.408	7.34	0.000135843	0.0033771
1207	10482772	NM_013613	18227	nuclear receptor subfamily 4,	Nr4a2	1.408	4.615	0.00225855	0.0237704
1208	10531560	NM_133738	71914	anthrax toxin receptor 2	Antxr2	1.408	4.991	0.00144796	0.0169429
1209	10424582					1.407	1.446	0.190286	0.449292
1210	10584208	NM_021339	57810	cell adhesion molecule-related	Cdon	1.406	3.546	0.00894726	0.0627466
1211	10490731	NM_009236	20672	SRY-box containing gene 18	Sox18	1.406	4.305	0.00330819	0.0306119
1212	10439483	NM_020260	12549	Cdc42 GTPase-activating protei	Cdgap	1.404	5.62	0.000720198	0.0104659
1213	10466938	BC024953	67759	RIKEN cDNA 5033414D02 gene	5033414D02Rik	1.404	4.507	0.00257351	0.0259383
1214	10582916					1.404	1.256	0.248124	0.521503
1215	10554586	AK080712	73907	RIKEN cDNA 4833418N17 gene	4833418N17Rik	1.404	1.969	0.0883638	0.286515
1216	10503376	DQ351292	208820	predicted gene, OTTMUSG0000000	OTTMUSG00000004461	1.403	2.627	0.0331554	0.153534
1217	10353258	XM_001475855	75799	RIKEN cDNA 4930444P10 gene	4930444P10Rik	1.403	3.568	0.00867673	0.0613582
1218	10542791	NM_026221	67533	PTPRF interacting protein, bin	Ppfibp1	1.402	4.926	0.00156195	0.0179488
1219	10465424	ENSMUST00000063955	100008567	predicted gene, OTTMUSG0000001	OTTMUSG00000018617	1.401	5.538	0.000785825	0.0110992
1220	10403352	NM_011803	23849	Kruppel-like factor 6	Klf6	1.401	4.315	0.00326731	0.0303532
1221	10602372	NM_009653	11656	aminolevulinic acid synthase 2	Alas2	1.4	2.185	0.0640042	0.23503
1222	10439881	ENSMUST00000089395	68190	RIKEN cDNA 5330426P16 gene	5330426P16Rik	1.4	2.516	0.0390746	0.171271
1223	10585974					1.4	2.123	0.0702355	0.248316
1224	10605437	NM_145629	102866	plastin 3 (T-isoform)	Pls3	1.399	3.68	0.00745279	0.0552143
1225	10434229	NM_013805	12741	claudin 5	Cldn5	1.399	4.396	0.00295212	0.0284299
1226	10372796	NM_010441	15364	high mobility group AT-hook 2	Hmga2	1.399	5.792	0.000599671	0.00921471
1227	10599001	NM_007429	11609	angiotensin II receptor, type	Agtr2	1.398	2.791	0.0260658	0.130787
1228	10578623	NM_133791	52357	WW, C2 and coiled-coil domain	Wwc2	1.398	4.618	0.00224964	0.0236884
1229	10481772	NM_178888	99326	GTPase activating RANGAP domai	Garnl3	1.398	5.29	0.00103185	0.0134013
1230	10471655	NM_146120	227753	gelsolin	Gsn	1.398	3.482	0.00976894	0.0669544
1231	10567626	NM_028758	74105	golgi associated, gamma adapti	Gga2	1.397	6.984	0.000186876	0.00422236
1232	10381849	BC050801	70894	RIKEN cDNA 4921510J17 gene	4921510J17Rik	1.397	3.147	0.0156128	0.0928214

1233	10467110	BC052506	381236	expressed sequence AI747699	AI747699	1.397	2.328	0.0517183	0.205551
1234	10426611	NM_007581	12297	calcium channel, voltage-depen	Cacnb3	1.396	6.415	0.000319799	0.00593143
1235	10505717	NM_029967	77739	ADAMTS-like 1	Adamtsl1	1.396	2.291	0.054623	0.212894
1236	10559649	NM_183406	333182	cytochrome c oxidase subunit V	Cox6b2	1.396	3.163	0.015253	0.0914142
1237	10422496	NM_183031	321019	Epstein-Barr virus induced gen	Ebi2	1.395	5.581	0.000750684	0.0107829
1238	10549760	BC066001	68992	zinc finger protein 580	Zfp580	1.395	4.355	0.00310833	0.0294192
1239	10559964	NM_009577	22775	zinc finger protein interactin	Zik1	1.395	3.797	0.00637747	0.0490168
1240	10393569	NM_021440	58251	differential display clone 8	RP23-394O9.3	1.394	4.448	0.0027689	0.0273322
1241	10572897	NM_010442	15368	heme oxygenase (decycling) 1	Hmox1	1.394	1.92	0.0951115	0.299747
1242	10448094	NM_172827	240028	leucyl/cystinyl aminopeptidase	Lnpep	1.393	4.563	0.00240488	0.024768
1243	10380419	NM_007742	12842	collagen, type I, alpha 1	Col1a1	1.393	4.571	0.00238116	0.0246076
1244	10539517	NM_021469	26903	dysferlin	Dysf	1.392	7.036	0.000178313	0.00410086
1245	10407291	NM_172595	218639	ADP-ribosylation factor-like 1	Arl15	1.392	4.192	0.00381529	0.0337914
1246	10420596	NM_013869	29820	tumor necrosis factor receptor	Tnfrsf19	1.392	2.637	0.0326997	0.152023
1247	10447799	NM_010515	16004	insulin-like growth factor 2 r	Igf2r	1.392	5.172	0.00117758	0.0147767
1248	10366310	NM_175489	237542	oxysterol binding protein-like	Osbpl8	1.391	4.286	0.00338491	0.0310771
1249	10496091	NM_010703	16842	lymphoid enhancer binding fact	Lef1	1.391	4.31	0.00328751	0.0304606
1250	10549504	NM_177192	320560	RIKEN cDNA D030011O10 gene	D030011O10Rik	1.391	2.488	0.0407772	0.176044
1251	10430931	NM_028728	74039	Nfat activating molecule with	Nfam1	1.39	6.93	0.000196407	0.00435315
1252	10526693	NM_001005426	381678	zinc finger, CW type with PWWP	Zcwpw1	1.389	3.66	0.00765924	0.0563022
1253	10388938	NM_019653	78889	WD repeat and SOCS box-contain	Wsb1	1.388	4.823	0.00176209	0.0196302
1254	10474045	NM_023850	76969	carbohydrate (keratan sulfate	Chst1	1.388	7.504	0.000117747	0.00309835
1255	10580324	NM_001037745	244556	zinc finger protein 791	Zfp791	1.386	1.556	0.162427	0.411033
1256	10459225					1.386	2.151	0.0673391	0.242464
1257	10408656	NM_011868	23986	peroxisomal delta3, delta2-eno	Peci	1.386	4.939	0.00153771	0.0177378
1258	10519815	NM_001110843	12293	calcium channel, voltage-depen	Cacna2d1	1.385	2.641	0.0324955	0.151507
1259	10381934	NM_181071	77097	tetratricopeptide repeat, anky	Tanc2	1.384	3.163	0.0152499	0.0914142
1260	10493889	NM_028622	73719	late cornified envelope 1C	Lce1c	1.384	2.819	0.0250087	0.127548
1261	10460603	NM_021474	58859	epidermal growth factor-contai	Efemp2	1.384	5.75	0.000626746	0.00949958
1262	10538247	NM_023456	109648	neuropeptide Y	Npy	1.383	4.983	0.00146109	0.0170587
1263	10597743	NM_009987	13051	chemokine (C-X3-C) receptor 1	Cx3cr1	1.383	4.45	0.00276184	0.0273085
1264	10416785	ENSMUST00000067431	75075	RIKEN cDNA 4930517O19 gene	4930517O19Rik	1.382	2.503	0.0398649	0.173611
1265	10370242	NM_021568	59093	poly(rC) binding protein 3	Pcbp3	1.382	3.877	0.0057321	0.0455152
1266	10515242	NM_028142	72181	NOL1/NOP2/Sun domain family, m	Nsun4	1.382	3.677	0.00748982	0.0554304
1267	10469066	NM_028804	74186	coiled-coil domain containing	Ccdc3	1.381	2.736	0.0282709	0.137931
1268	10419704	NM_015772	50524	sal-like 2 (Drosophila)	Sall2	1.381	2.619	0.0335624	0.154498
1269	10590452	NM_026179	67469	abhydrolase domain containing	Abhd5	1.381	5.638	0.000706229	0.0103196
1270	10591614	NM_177030	319899	dedicator of cytokinesis 6	Dock6	1.38	2.833	0.0245339	0.125878
1271	10363350	NM_011030	18451	procollagen-proline, 2-oxoglut	P4ha1	1.38	4.516	0.00254749	0.0257354
1272	10388465	NM_007873	13447	double C2, beta	Doc2b	1.38	3.369	0.0114175	0.0742122
1273	10431749	NM_177431	223838	a disintegrin-like and metallo	Adamts20	1.38	6.484	0.000298851	0.00571329
1274	10491611	ENSMUST00000057272	229227	RIKEN cDNA 4932438A13 gene	4932438A13Rik	1.38	3.22	0.0140659	0.0861304
1275	10404913	NM_026056	67252	CAP, adenylate cyclase-associa	Cap2	1.379	2.658	0.031678	0.149043
1276	10360377	ENSMUST00000042610	226691	expressed sequence AI607873	AI607873	1.379	2.578	0.035654	0.160842
1277	10360863	NM_145515	226778	MAP/microtubule affinity-regul	Mark1	1.379	4.814	0.001781	0.0197989
1278	10515771	NM_011587	21846	tyrosine kinase receptor 1	Tie1	1.379	6.443	0.000310997	0.00584508
1279	10568735	NM_001113415	13593	early B-cell factor 3	Ebf3	1.378	2.169	0.065578	0.2387
1280	10449284	NM_013642	19252	dual specificity phosphatase 1	Dusp1	1.378	4.397	0.00294941	0.0284299
1281	10406504	NM_001037987	13612	EGF-like repeats and discoidin	Edil3	1.378	2.112	0.0714098	0.250979
1282	10462132	BC087877	226040	RIKEN cDNA E030010A14 gene	E030010A14Rik	1.378	4.031	0.00468908	0.0393749

1283	10415413	BC057379	277154	cDNA sequence BC030046	BC030046	1.378	2.658	0.0326589	0.151867
1284	10359161	NM_009230	20652	sterol O-acyltransferase 1	Soat1	1.378	5.779	0.000608161	0.00929788
1285	10606088	NM_027382	70315	histone deacetylase 8	Hdac8	1.377	5.038	0.00137144	0.0164386
1286	10483439	NM_001081088	14725	low density lipoprotein recept	Lrp2	1.377	5.226	0.00110802	0.0140963
1287	10535034	NM_013844	24135	zinc finger protein 68	Zfp68	1.377	5.216	0.0011213	0.0142129
1288	10371844					1.377	3.827	0.006126	0.0475856
1289	10375055	NM_001033981	544763	RIKEN cDNA F830116E18 gene	F830116E18Rik	1.377	2.041	0.0794613	0.268434
1290	10390117	NM_013565	16400	integrin alpha 3	Itga3	1.377	3.599	0.0083186	0.0595022
1291	10422013	NM_010636	16597	Kruppel-like factor 12	Klf12	1.377	2.871	0.0231991	0.120967
1292	10373407	NM_011843	23943	membrane bound C2 domain conta	Mbc2	1.377	6.177	0.000404553	0.00699418
1293	10604528	NM_134163	171170	muscleblind-like 3 (Drosophila	Mbnl3	1.376	2.206	0.0620841	0.23034
1294	10458555	NM_011898	24066	sprouty homolog 4 (Drosophila)	Spry4	1.376	3.53	0.00914348	0.0636925
1295	10604523	NM_172413	72065	RAP2C, member of RAS oncogene	Rap2c	1.376	4.864	0.00167857	0.0188786
1296	10531173	NM_001081401	330119	a disintegrin-like and metallo	Adamts3	1.376	1.99	0.0856231	0.280865
1297	10457888	BC080777	66648	RIKEN cDNA 5730494M16 gene	5730494M16Rik	1.376	5.492	0.000826532	0.011499
1298	10467979	NM_009127	20249	stearoyl-Coenzyme A desaturase	Scd1	1.376	3.143	0.0156916	0.0930667
1299	10507612	NM_019783	56401	leprecan 1	Lepre1	1.375	3.956	0.00517212	0.0422494
1300	10387100	NM_001034874	380702	gene model 879, (NCBI)	Gm879	1.375	6.502	0.000293707	0.00565571
1301	10403842	NM_080288	140580	engulfment and cell motility 1	Elmo1	1.375	2.62	0.0335219	0.154383
1302	10606366	NM_199468	213436	zinc finger, CCHC domain conta	Zcchc5	1.375	2.59	0.0350549	0.159056
1303	10530145	NM_030682	21897	toll-like receptor 1	Tlr1	1.375	3.133	0.0159157	0.0941049
1304	10543494	NM_008174	14823	glutamate receptor, metabotrop	Grm8	1.374	3.51	0.00939155	0.0648938
1305	10500938	NM_009520	22414	wingless related MMTV integrat	Wnt2b	1.374	3.808	0.00627962	0.0485116
1306	10430510	NM_172608	223693	transmembrane protein 184b	Tmem184b	1.374	3.731	0.00695942	0.0523107
1307	10502766	NM_001081298	99633	latrophilin 2	Lphn2	1.374	1.938	0.0926014	0.294729
1308	10412260	NM_008046	14313	follistatin	Fst	1.374	1.03	0.336202	0.611869
1309	10402117	NM_153587	73086	ribosomal protein S6 kinase, p	Rps6ka5	1.374	4.555	0.002427	0.0249473
1310	10368317	NM_134005	209558	ectonucleotide pyrophosphatase	Enpp3	1.374	1.603	0.151783	0.395645
1311	10436209	NM_001033238	208650	Casitas B-lineage lymphoma b	Cblb	1.373	3.287	0.0128076	0.0805725
1312	10552500	NM_008940	259277	kallikrein related-peptidase 8	Klk8	1.372	2.449	0.0432127	0.182644
1313	10599686	NM_030139	78619	zinc finger protein 449	Zfp449	1.372	6.227	0.000384606	0.00674304
1314	10519486					1.372	2.595	0.0347915	0.158375
1315	10519607	NM_001081029	652925	RIKEN cDNA 4930420K17 gene	4930420K17Rik	1.372	3.724	0.00702919	0.0527601
1316	10532711	NM_008153	14747	chemokine-like receptor 1	Cmklr1	1.372	5.576	0.000754967	0.0108152
1317	10462281	NM_013703	22359	very low density lipoprotein r	Vldlr	1.372	4.146	0.00404716	0.0353025
1318	10432236	NM_172612	223881	Rho family GTPase 1	Rnd1	1.371	3.965	0.00511037	0.0418975
1319	10592140	NM_013932	30959	DEAD (Asp-Glu-Ala-Asp) box pol	Ddx25	1.369	3.244	0.0136043	0.0841821
1320	10412328	NM_134058	105083	pelota homolog (Drosophila)	Pelo	1.369	4.286	0.00338816	0.0310934
1321	10392177	NM_010494	15896	intercellular adhesion molecul	Icam2	1.369	3.21	0.0142731	0.0871222
1322	10574488	NM_001024606	382051	RIKEN cDNA 4833426J09 gene	4833426J09Rik	1.369	4.164	0.00395283	0.0346513
1323	10350247	NM_001039472	16565	kinesin family member 21B	Kif21b	1.369	4.648	0.0021706	0.0231093
1324	10491331	NM_008839	18706	phosphatidylinositol 3-kinase,	Pik3ca	1.369	5.592	0.000741768	0.0106912
1325	10547621	NM_031159	11810	apolipoprotein B editing compl	Apobec1	1.369	3.095	0.0168006	0.0975911
1326	10476237	NM_028306	72630	heat shock protein 12B	Hspa12b	1.368	4.843	0.00172084	0.0192617
1327	10467206	NM_016854	53412	protein phosphatase 1, regulat	Ppp1r3c	1.368	2.437	0.0439879	0.184833
1328	10474700	NM_011580	21825	thrombospondin 1	Thbs1	1.368	2.273	0.0561555	0.216623
1329	10381096	NM_010517	16010	insulin-like growth factor bin	Igfbp4	1.368	5.02	0.00140011	0.016658
1330	10509901	NM_008546	17150	microfibrillar-associated prot	Mfap2	1.368	5.056	0.00134434	0.0162056
1331	10605465	NM_016979	19108	protein kinase, X-linked	Prkx	1.367	1.992	0.0854322	0.280581
1332	10399337	BC145748	208439	kelch-like 29 (Drosophila)	Klhl29	1.366	5.262	0.00106464	0.0137094
1333	10502535					1.366	3.188	0.0147262	0.0890395
1334	10348299	ENSMUST00000097661	76104	RIKEN cDNA 5830472F04 gene	5830472F04Rik	1.366	1.555	0.162693	0.411384
				predicted gene					

1335	10446470	ENSMUST00000069605	791265	ENSMUSG0000005	ENSMUSG00000055855	1.366	1.776	0.117793	0.3424
1336	10456756	NM_145356	207259	zinc finger and BTB domain con	Zbtb7c	1.366	4.542	0.00246728	0.0252264
1337	10607587	NM_008810	18597	pyruvate dehydrogenase E1 alph	Pdha1	1.366	4.566	0.00239479	0.0246761
1338	10548146	NM_011567	21679	TEA domain family member 4	Tead4	1.366	4.488	0.00263406	0.0263956
1339	10373340	NM_001039080	56516	RNA binding motif, single stra	Rbms2	1.365	4.379	0.00301486	0.0288575
1340	10435266	NM_172934	77446	HEG homolog 1 (zebrafish)	Heg1	1.365	4.666	0.00212324	0.022731
1341	10413280					1.365	1.7	0.131579	0.364342
1342	10374464	BC040462	114716	sprouty-related, EVH1 domain c	Spred2	1.364	3.189	0.0147032	0.0889767
1343	10372082	NM_027722	71207	nudix (nucleoside diphosphate	Nudt4	1.364	3.014	0.0188658	0.105433
1344	10489377	NM_012032	26943	serine incorporator 3	Serinc3	1.363	3.749	0.00679628	0.0513767
1345	10455128	NM_053145	93891	protocadherin beta 20	Pcdhb20	1.363	2.193	0.0632656	0.233168
1346	10601846	NR_003642	76976	RIKEN cDNA 2900062L11 gene	2900062L11Rik	1.363	3.296	0.0126385	0.0796771
1347	10422348	NM_001081252	66435	UDP-glucose ceramide glucosylt	Ugcgl2	1.363	3.319	0.0122475	0.0778362
1348	10538299	BC094279	66640	RIKEN cDNA 5730446D14 gene	5730446D14Rik	1.363	3.794	0.00639892	0.0491
1349	10463739	NM_177342	226182	TAF5 RNA polymerase II, TATA b	Taf5	1.363	3.955	0.00517378	0.0422494
1350	10357488	NM_010016	13136	CD55 antigen	Cd55	1.363	2.022	0.0816819	0.272831
1351	10433709	BC022741	67254	RIKEN cDNA 2900011O08 gene	2900011O08Rik	1.362	2.747	0.027809	0.136658
1352	10400795	NM_022028	64010	salvador homolog 1 (Drosophila	Sav1	1.362	4.892	0.00162488	0.0184613
1353	10585214	NM_009964	12955	crystallin, alpha B	Cryab	1.362	3.097	0.0167476	0.0974437
1354	10527963					1.361	3.798	0.00636712	0.0490085
1355	10502823	NM_025926	67035	DnaJ (Hsp40) homolog, subfamil	Dnajb4	1.361	4.598	0.00230434	0.0240488
1356	10459363	ENSMUST00000046860	667742	RIKEN cDNA 9030411M15 gene	9030411M15Rik	1.36	4.091	0.00433796	0.0370043
1357	10414333	NM_001037221	74480	sterile alpha motif domain con	Samd4	1.36	3.617	0.00811667	0.0585528
1358	10495405	NM_172685	229731	solute carrier family 25 (mito	Slc25a24	1.36	3.826	0.00613101	0.0476028
1359	10362676	NM_198164	78334	cell division cycle 2-like 6 (	Cdc2l6	1.359	6.819	0.000217696	0.00468735
1360	10580056	ENSMUST00000098595	100126034	predicted gene, ENSMUSG0000007	ENSMUSG00000074219	1.359	5.465	0.000851368	0.0116881
1361	10584674	NM_023061	84004	melanoma cell adhesion molecul	Mcam	1.358	7.32	0.000138309	0.00342078
1362	10412667	NM_008981	19270	protein tyrosine phosphatase,	Ptprg	1.358	2.663	0.0314534	0.14825
1363	10473349	NM_001005342	241525	yippee-like 4 (Drosophila)	Ypel4	1.358	3.157	0.0153844	0.0920839
1364	10366043	NM_026268	67603	dual specificity phosphatase 6	Dusp6	1.358	2.746	0.0278324	0.136699
1365	10446771	NM_001081071	225010	lysocardiolipin acyltransferas	Lycat	1.358	4.287	0.00338439	0.0310771
1366	10360370	NM_001024721	545384	cDNA sequence BC094916	BC094916	1.358	1.707	0.13032	0.362088
1367	10363703					1.358	5.83	0.000576732	0.00896649
1368	10523490	NM_010203	14176	fibroblast growth factor 5	Fgf5	1.357	6.064	0.000453237	0.00756735
1369	10436666	NM_023844	67374	junction adhesion molecule 2	Jam2	1.357	3.972	0.00506514	0.0416883
1370	10492499	NM_025813	66868	major facilitator superfamily	Mfsd1	1.357	6.826	0.000216203	0.00466946
1371	10459905	NM_053099	240427	SET binding protein 1	Setbp1	1.356	5.044	0.00136326	0.0163592
1372	10348739	NM_172463	208777	sushi, nidogen and EGF-like do	Sned1	1.356	4.569	0.00238822	0.024654
1373	10545255	NM_009075	19895	ribose 5-phosphate isomerase A	Rpia	1.356	2.561	0.0365517	0.163532
1374	10598251	NM_177914	331374	diacylglycerol kinase kappa	Dgkk	1.356	3.692	0.00733603	0.0545596
1375	10412414	ENSMUST00000048965	791300	predicted gene, ENSMUSG0000002	ENSMUSG00000025450	1.355	2.282	0.0554057	0.214717
1376	10472097	NM_172409	71409	formin-like 2	Fmnl2	1.355	4.209	0.00373118	0.0332773
1377	10608138	NM_012008	26900	DEAD (Asp-Glu-Ala-Asp) box pol	Ddx3y	1.355	0.601	0.566164	0.792202
1378	10345981	NM_011729	22592	excision repair cross-compleme	Ercc5	1.355	5.218	0.00111832	0.0141847
1379	10454601	NM_021367	53603	thymic stromal lymphopoietin	Tslp	1.355	1.574	0.158323	0.405255
1380	10426425	ENSMUST00000035399	239618	PDZ domain containing RING fin	Pdzrn4	1.355	3.65	0.00776176	0.0567966
1381	10455253	NM_001033789	545253	predicted gene, EG545253	EG545253	1.355	5.783	0.000605562	0.00926484
1382	10462406	BC125448	226089	RIKEN cDNA C030046E11 gene	C030046E11Rik	1.354	3.795	0.00639256	0.0490793
1383	10501903	ENSMUST00000051443	118449	synaptopodin 2	Synpo2	1.354	2.269	0.0564657	0.217193
				ELAV (embryonic lethal					

1384	10514352	NM_207685	15569	abnorm	Elavl2	1.354	4.223	0.00366883	0.0328981
1385	10402302	NM_172806	238386	BTB (POZ) domain containing 7	Btbd7	1.353	5.59	0.000743176	0.0107042
1386	10494372	NM_022030	64051	synaptic vesicle glycoprotein	Sv2a	1.353	3.597	0.00834739	0.0596476
1387	10544452	BC011487	232748	cDNA sequence BC011487	BC011487	1.353	2.869	0.0232702	0.121189
1388	10519516	NM_178766	319653	solute carrier family 25, memb	Slc25a40	1.353	2.578	0.0356699	0.16088
1389	10585874	NM_010421	15211	hexosaminidase A	Hexa	1.353	3.078	0.0172111	0.0991856
1390	10404836	NM_183204	328234	ring finger protein 182	Rnf182	1.353	2.722	0.028847	0.139575
1391	10545200	ENSMUST00000101325	100046894	similar to Igk-C protein	LOC100046894	1.353	2.391	0.047077	0.192832
1392	10407173	NM_010560	16195	interleukin 6 signal transduce	Il6st	1.353	4.403	0.00292642	0.028306
1393	10400157	ENSMUST00000021438	664883	neuro-oncological ventral anti	Nova1	1.352	4.261	0.00349606	0.0317517
1394	10488623	NM_011438	20667	SRY-box containing gene 12	Sox12	1.351	4.836	0.00173452	0.0193636
1395	10420009					1.35	1.493	0.17772	0.43217
1396	10422028	NM_001081278	210789	TBC1 domain family, member 4	Tbc1d4	1.35	2.826	0.0247788	0.12668
1397	10427895	NM_027395	70350	brain abundant, membrane attac	Basp1	1.349	6.35	0.000340515	0.00618013
1398	10459288	NM_007420	11555	adrenergic receptor, beta 2	Adrb2	1.349	3.626	0.00802247	0.0581313
1399	10501699	NM_001081326	77559	amylo-1,6-glucosidase, 4-alpha	Agl	1.349	4.45	0.00276056	0.0273085
1400	10482509	NM_030243	71684	RNA binding motif protein 43	Rbm43	1.349	2.777	0.0266026	0.132599
1401	10483803	ENSMUST00000100000	399588	RIKEN cDNA 6720416L17 gene	6720416L17Rik	1.348	2.391	0.0470429	0.192831
1402	10368050	ENSMUST00000095817	100039660	hypothetical protein LOC100039	LOC100039660	1.348	1.43	0.194451	0.454557
1403	10400805	NM_008697	18080	ninein	Nin	1.348	3.856	0.00589363	0.0464288
1404	10582376					1.348	1.341	0.220694	0.489689
1405	10498576	NM_016753	17035	latexin	Lxn	1.348	2.532	0.0381714	0.168848
1406	10542164	NM_177686	232413	C-type lectin domain family 12	Clec12a	1.348	4.006	0.0048448	0.0403004
1407	10461794	NM_146302	258299	olfactory receptor 1461	Olfr1461	1.347	1.897	0.0984752	0.30638
1408	10490826	ENSMUST00000091353	229055	zinc finger and BTB domain con	Zbtb10	1.347	2.027	0.0810588	0.271716
1409	10445428					1.347	1.027	0.337587	0.613173
1410	10458498	NM_139206	106952	centaurin, delta 3	Centd3	1.347	6.699	0.000243416	0.00502386
1411	10600093	NM_009549	22673	zinc finger protein 185	Zfp185	1.347	3.908	0.00550367	0.0442639
1412	10373768	NM_053267	114679	selenoprotein M	Selm	1.347	3.35	0.0117205	0.0755777
1413	10607972	NM_011419	20592	jumonji, AT rich interactive d	Jarid1d	1.347	0.629	0.548937	0.77934
1414	10585970					1.347	3.208	0.0143183	0.0873729
1415	10372342	NM_001081035	260315	neuron navigator 3	Nav3	1.347	4.368	0.00305675	0.0290664
1416	10531193	NM_001081401	330119	a disintegrin-like and metallo	Adamts3	1.347	4.54	0.00247388	0.0252694
1417	10366026	NM_027740	382406	WD repeat domain 51B	Wdr51b	1.346	2.541	0.0376747	0.167387
1418	10445293	NM_013737	27226	phospholipase A2, group VII (p	Pla2g7	1.345	3.634	0.00793778	0.0577154
1419	10407591	NM_033269	12671	cholinergic receptor, muscarin	Chrm3	1.345	1.548	0.164201	0.413859
1420	10543204	NM_028990	101118	transmembrane protein 168	Tmem168	1.345	2.86	0.0235594	0.122123
1421	10434302	NM_029436	75785	kelch-like 24 (Drosophila)	Klhl24	1.344	3.946	0.00523657	0.0426339
1422	10389894	NM_029600	76408	ATP-binding cassette, sub-fami	Abcc3	1.344	4.447	0.00277237	0.0273478
1423	10349943					1.344	0.62	0.554066	0.783409
1424	10570516	BC080858	74901	kelch repeat and BTB (POZ) dom	Kbtbd11	1.343	3.04	0.0181875	0.102607
1425	10505674	NM_175275	338349	centlein, centrosomal protein	Cntln	1.343	4.075	0.00443043	0.037576
1426	10428998	NM_010026	13196	development and differentiatio	Ddef1	1.343	5.383	0.000930473	0.0124993
1427	10561351	ENSMUST00000099111	233026	RIKEN cDNA C130069I09 gene	C130069I09Rik	1.343	2.789	0.0261387	0.130964
1428	10401063	NM_028356	109929	zinc finger and BTB domain con	Zbtb25	1.343	3.398	0.0109674	0.0722269
1429	10374485	NM_023324	67245	pellino 1	Peli1	1.342	2.94	0.0209965	0.113397
1430	10455148	NM_033595	93724	protocadherin gamma subfamily	Pcdhga12	1.342	5.007	0.00142103	0.0167856
1431	10577973	NM_013462	11556	adrenergic receptor, beta 3	Adrb3	1.342	2.734	0.028359	0.138162
1432	10596113					1.342	3.108	0.0164817	0.0962943
1433	10416945	AK053349	75957	RIKEN cDNA 5033413D16 gene	5033413D16Rik	1.342	4.416	0.00287852	0.0280477
1434	10369236	NM_010100	13608	ectodysplasin-A receptor	Edar	1.341	3.434	0.0104364	0.0699861
1435	10534041	NM_007941	13852	syntaxin 2	Stx2	1.341	3.102	0.016631	0.0970498
1436	10571601	NM_016798	53318	PDZ and LIM domain 3	Pdlim3	1.341	3.94	0.00528165	0.0429355
1437	10435565	NM_008225	15163	hematopoietic cell specific Ly	Hcls1	1.341	3.183	0.0148159	0.0893521
				predicted gene,					

1438	10502783	ENSMUST00000066092	791262	predicted gene, ENSMUSG0000005	ENSMUSG00000053583	1.341	1.803	0.11313	0.333337
1439	10461423	NM_021890	60527	fatty acid desaturase 3	Fads3	1.34	4.547	0.00245328	0.0251197
1440	10482059	NM_010283	14594	glycoprotein galactosyltransfe	Ggta1	1.34	2.805	0.0255266	0.129273
1441	10587383	NM_153098	235505	CD109 antigen	Cd109	1.339	3.472	0.00989544	0.0675805
1442	10444258	NM_010724	16913	proteasome (prosome, macropain	Psmb8	1.339	3.323	0.0121744	0.0775627
1443	10547009	NM_177683	232334	vestigial like 4 (Drosophila)	Vgll4	1.339	3.13	0.0159849	0.0944005
1444	10400254	NM_177171	320487	HEAT repeat containing 5A	Heatr5a	1.339	4.746	0.00193046	0.0210292
1445	10468980	BC021353	66540	RIKEN cDNA 3110001A13 gene	3110001A13Rik	1.339	4.459	0.0027303	0.0270903
1446	10543959	NM_008973	19242	pleiotrophin	Ptn	1.338	5.919	0.000525754	0.00837089
1447	10522009	NM_025700	66681	phosphoglucomutase 1	Pgm1	1.338	3.477	0.00983344	0.0672657
1448	10436602					1.338	0.795	0.452243	0.708922
1449	10569972	NM_026058	67260	LAG1 homolog, ceramide synthas	Lass4	1.338	3.869	0.00579799	0.0459321
1450	10446756	NM_027166	383295	yippee-like 5 (Drosophila)	Ypel5	1.337	3.052	0.0178773	0.101492
1451	10372807	NM_177092	320183	methionine sulfoxide reductase	Msrb3	1.337	1.936	0.0928523	0.295184
1452	10567725	NM_001081329	210162	zinc finger with KRAB and SCAN	Zkscan2	1.337	2.714	0.0291615	0.140646
1453	10385776	NM_009331	21414	transcription factor 7, T-cell	Tcf7	1.337	5.126	0.00124081	0.0153875
1454	10497622	NM_027941	71827	leucine rich repeat containing	Lrrc34	1.337	1.584	0.156011	0.401839
1455	10391119	NM_176830	66180	RIKEN cDNA 1110036O03 gene	1110036O03Rik	1.337	3.398	0.0109679	0.0722269
1456	10425945	NM_010180	14114	fibulin 1	Fbln1	1.336	3.862	0.00584924	0.0462086
1457	10504564	NM_153167	242418	WD repeat domain 32	Wdr32	1.336	1.9	0.0979397	0.30515
1458	10360040	NM_010188	14131	Fc receptor, IgG, low affinity	Fcgr3	1.336	2.045	0.0788977	0.267427
1459	10468311	NM_008018	14218	SH3 and PX domains 2A	Sh3pxd2a	1.335	3.426	0.0105535	0.0705216
1460	10434778	NM_023386	67775	receptor transporter protein 4	Rtp4	1.335	2.629	0.0330521	0.153299
1461	10367728	NM_138667	68652	mitogen-activated protein kina	Map3k7ip2	1.334	5.343	0.000973136	0.0128576
1462	10365242	NM_001081218	67933	host cell factor C2	Hcfc2	1.334	4.231	0.00363072	0.0326632
1463	10402347	NM_029803	76933	interferon, alpha-inducible pr	Ifi27	1.333	2.294	0.0544132	0.212311
1464	10440246	NM_026577	68146	ADP-ribosylation factor-like 1	Arl13b	1.333	3.79	0.00643926	0.0493482
1465	10401244	NM_134156	109711	actinin, alpha 1	Actn1	1.333	3.366	0.0114626	0.0744592
1466	10588154	NM_009282	20842	stromal antigen 1	Stag1	1.332	5.02	0.00140027	0.016658
1467	10575534	NM_009179	20444	ST3 beta-galactoside alpha-2,3	St3gal2	1.332	4.595	0.00231342	0.024108
1468	10554800	NM_028238	72433	Rab38, member of RAS oncogene	Rab38	1.332	2.722	0.0288346	0.139559
1469	10466530	BC013068	18552	proprotein convertase subtilis	Pcsk5	1.332	4.981	0.00146424	0.017079
1470	10354389	NM_172653	227059	solute carrier family 39 (zinc	Slc39a10	1.331	3.925	0.00538367	0.0435667
1471	10378697	NM_008659	17913	myosin IC	Myo1c	1.331	3.786	0.00647048	0.0494978
1472	10606473	ENSMUST00000113422	245596	highly divergent homeobox	Hdx	1.33	1.615	0.1491	0.391477
1473	10587495	NM_022986	65099	interleukin-1 receptor-associa	Irak1bp1	1.33	2.697	0.0299345	0.143448
1474	10397351	NM_030887	81703	Jun dimerization protein 2	Jdp2	1.329	5.141	0.00122023	0.0151947
1475	10597413	NM_019922	56693	cartilage associated protein	Crtap	1.329	3.631	0.00796566	0.0578187
1476	10518805	NM_009498	22319	vesicle-associated membrane pr	Vamp3	1.329	4.889	0.00162959	0.0185049
1477	10442224	BC076634	381066	cDNA sequence BC049807	BC049807	1.328	3.021	0.0186788	0.104788
1478	10408629	NM_025831	66895	RIKEN cDNA 1300014I06 gene	1300014I06Rik	1.328	3.139	0.0157916	0.0934764
1479	10358541	NM_001024720	545370	hemicentin 1	Hmcn1	1.328	1.757	0.121076	0.347578
1480	10485597	NM_144804	211896	DEP domain containing 7	Depdc7	1.328	3.432	0.010462	0.0701137
1481	10538138	NM_008376	16205	GTPase, IMAP family member 1	Gimap1	1.328	5.241	0.00108943	0.0139352
1482	10422944	AK153592	106074	expressed sequence AW557046	AW557046	1.327	1.93	0.0936365	0.296785
1483	10583207	AK129448	270118	mastermind like 2 (Drosophila)	Maml2	1.327	2.548	0.0372675	0.165996
1484	10477528	BC047134	71425	RIKEN cDNA 4833413D08 gene	4833413D08Rik	1.327	1.507	0.174217	0.427189
1485	10498210	NM_030595	26422	neurobeachin	Nbea	1.327	3.876	0.00574339	0.0455547
1486	10538338	NM_172728	231991	cAMP responsive element bindin	Creb5	1.327	3.71	0.0071611	0.0535222
1487	10502510	NM_010723	16911	LIM domain only 4	Lmo4	1.326	2.411	0.0456634	0.189129
1488	10353632	NM_175642	210933	brain-specific angiogenesis in	Bai3	1.326	2.739	0.0281284	0.137577
1489	10426284	NM_013455	11434	preproacrosin	Acr	1.326	5.239	0.00109188	0.0139472

1490	10546685	NM_025829	66892	eukaryotic translation initiat	Eif4e3	1.326	3.071	0.0173937	0.0997203
1491	10591816	NM_172920	244745	dpy-19-like 1 (C. elegans)	Dpy19l1	1.326	5.379	0.000934875	0.0125346
1492	10475532	NM_021507	59010	sulfide quinone reductase-like	Sqrdl	1.326	2.714	0.0291899	0.140687
1493	10469255	NM_008859	18761	protein kinase C, theta	Prkcq	1.326	3.035	0.0183147	0.103265
1494	10546567	BC048939	101351	RIKEN cDNA A130022J15 gene	A130022J15Rik	1.326	2.635	0.0327646	0.152258
1495	10571657	NM_007981	14081	acyl-CoA synthetase long-chain	Acsl1	1.325	3.43	0.0104897	0.0702104
1496	10566205	NM_001001559	384701	deubiquitinating enzyme 2a	Dub2a	1.325	2.358	0.0494728	0.199857
1497	10600825	NM_001034907	547176	zinc finger CCCH-type containi	Zc3h12b	1.324	2.421	0.0450053	0.187728
1498	10562576	NM_024413	72287	pleckstrin homology domain con	Plekhf1	1.324	2.498	0.0401279	0.174258
1499	10381898	NM_008626	17534	mannose receptor, C type 2	Mrc2	1.324	6.345	0.000342207	0.00618959
1500	10363762	NM_177794	327766	transmembrane protein 26	Tmem26	1.323	5.767	0.000615729	0.00938643
1501	10516103	NM_009600	11426	microtubule-actin crosslinking	Macf1	1.323	4.705	0.00202523	0.02187
1502	10498802	NM_001099624	76089	Rap guanine nucleotide exchang	Rapgef2	1.323	6.091	0.000441069	0.00740801
1503	10544756	NM_010452	15400	homeo box A3	Hoxa3	1.323	3.212	0.0142345	0.0869614
1504	10459084	NM_001109975	104027	synaptopodin	Synpo	1.323	5.089	0.00129368	0.0158118
1505	10562578	NM_025390	66161	processing of precursor 4, rib	Pop4	1.323	1.744	0.123489	0.351591
1506	10388389	NM_010430	15248	hypermethylated in cancer 1	Hic1	1.322	2.184	0.0641529	0.235454
1507	10528799	NM_029376	75657	spermatogenesis associated glu	Speer4a	1.322	1.673	0.136988	0.373595
1508	10496130	BC060502	271981	RIKEN cDNA A630047E20 gene	A630047E20Rik	1.322	4.328	0.00321167	0.0300343
1509	10487645	NM_019696	56264	carboxypeptidase X 1 (M14 fami	Cpxm1	1.322	3.665	0.00761216	0.0560806
1510	10443080	XM_985548	240057	synaptic Ras GTPase activating	Syngap1	1.321	5.371	0.000943055	0.0126089
1511	10493345					1.321	3.937	0.00529991	0.0430343
1512	10518837	NM_001081557	100072	calmodulin binding transcripti	Camta1	1.321	3.548	0.00892419	0.0626471
1513	10582939					1.321	2.841	0.0242488	0.12487
1514	10548139					1.32	3.979	0.0050165	0.0414332
1515	10531183	NM_001081401	330119	a disintegrin-like and metallo	Adamts3	1.32	2.59	0.0350281	0.159003
1516	10399973	NM_024124	79221	histone deacetylase 9	Hdac9	1.32	3.625	0.00803519	0.0581636
1517	10349102	ENSMUST00000066789	320761	RIKEN cDNA D630008O14 gene	D630008O14Rik	1.32	2.498	0.0401772	0.174401
1518	10362674	NR_002842	19850	U3A small nuclear RNA	Rnu3a	1.319	1.006	0.346985	0.621224
1519	10511975	NM_011895	24060	solute carrier family 35 (CMP-	Slc35a1	1.319	4.311	0.00328423	0.0304569
1520	10601878	NM_146236	237052	transcription elongation facto	Tceal1	1.319	3.526	0.00918698	0.0638978
1521	10452047	NM_011218	19280	protein tyrosine phosphatase,	Ptprs	1.318	4.349	0.00313106	0.029555
1522	10445078	NM_019439	54393	gamma-aminobutyric acid (GABA-	Gabbr1	1.318	4.02	0.00475798	0.0397482
1523	10533386	NM_008507	16923	SH2B adaptor protein 3	Sh2b3	1.318	6.027	0.000470822	0.00772908
1524	10394611	ENSMUST00000101609	71169	RIKEN cDNA 4933425L03 gene	4933425L03Rik	1.318	2.535	0.0380215	0.168377
1525	10551614	NM_016772	51798	enoyl coenzyme A hydratase 1,	Ech1	1.316	2.807	0.0254548	0.129038
1526	10596115	AK082061	270190	Eph receptor B1	Ephb1	1.316	2.08	0.0749313	0.25894
1527	10549534					1.316	3.242	0.0136405	0.084307
1528	10374455	NM_033523	114716	sprouty-related, EVH1 domain c	Spred2	1.316	3.382	0.0112206	0.0733781
1529	10491597					1.315	4.086	0.00436602	0.0371789
1530	10600886	NM_029536	76206	G protein-coupled receptor 165	Gpr165	1.315	1.642	0.143324	0.384029
1531	10365344	NM_146008	216198	t-complex 11 (mouse) like 2	Tcp11l2	1.315	2.787	0.0262162	0.131199
1532	10374727	NM_016707	14025	B-cell CLL/lymphoma 11A (zinc	Bcl11a	1.314	4.232	0.00362587	0.0326556
1533	10441497	NM_054040	68842	tubby like protein 4	Tulp4	1.314	2.588	0.0351527	0.159397
1534	10587284	NM_134255	68801	ELOVL family member 5, elongat	Elovl5	1.314	2.738	0.0281828	0.137705
1535	10418251	NM_145221	72993	adaptor protein, phosphotyrosi	Appl1	1.313	3.969	0.00508449	0.0417922
1536	10357043	NM_009741	12043	B-cell leukemia/lymphoma 2	Bcl2	1.313	3.275	0.0130283	0.0816451
1537	10502419	NM_001040690	229877	RAP1, GTP-GDP dissociation sti	Rap1gds1	1.313	3.691	0.00734331	0.0545945
1538	10585803	NM_009291	20897	stimulated by retinoic acid ge	Stra6	1.312	3.075	0.0172775	0.0993516
1539	10475957	NM_027192	69737	tubulin tyrosine ligase	Ttl	1.312	3.35	0.0117181	0.0755777
1540	10493789	NM_009113	20196	S100 calcium binding protein A	S100a13	1.311	3.967	0.00509767	0.041842
1541	10594199	NM_001040426	207596	thrombospondin, type I, domain	Thsd4	1.31	2.938	0.0210597	0.113586
1542	10538408	BC042507	68235	RIKEN cDNA 2410066E13 gene	2410066E13Rik	1.31	4.265	0.00347668	0.0316448

1543	10428522	NM_001081391	239420	CUB and Sushi multiple domains	Csmd3	1.31	1.709	0.129848	0.361535
1544	10472953	NM_008273	15431	homeo box D11	Hoxd11	1.31	1.081	0.31449	0.591308
1545	10456988	NM_053117	93737	par-6 partitioning defective 6	Pard6g	1.31	3.378	0.0112691	0.0735307
1546	10406551	NM_024272	66970	single-stranded DNA binding pr	Ssbp2	1.31	3.48	0.00978831	0.067022
1547	10461439	NM_146094	76267	fatty acid desaturase 1	Fads1	1.309	4.207	0.00374305	0.0333325
1548	10458764	XM_001476513	100046618	similar to ribosomal protein	LOC100046618	1.309	2.954	0.0205596	0.112129
1549	10382028	NM_011947	26406	mitogen-activated protein kina	Map3k3	1.309	2.948	0.0207508	0.112733
1550	10556426	NM_020606	57342	parvin, alpha	Parva	1.309	3.868	0.0058004	0.0459339
1551	10506603	NM_023672	72475	single-stranded DNA binding pr	Ssbp3	1.309	5.417	0.000896741	0.0121232
1552	10584309	BC066002	235184	cDNA sequence BC024479	BC024479	1.309	2.819	0.0250222	0.127548
1553	10420171	NM_080435	104110	adenylate cyclase 4	Adcy4	1.308	5.267	0.00105876	0.0136846
1554	10385883	NM_019723	56517	solute carrier family 22 (orga	Slc22a21	1.308	2.51	0.0394198	0.172278
1555	10485580	AK136931	100038443	predicted gene, ENSMUSG0000007	ENSMUSG00000074998	1.308	3.419	0.0106469	0.0709477
1556	10494889	NM_177857	329727	DENN/MADD domain containing 2C	Dennd2c	1.308	3.758	0.00671894	0.0510108
1557	10596454	NM_020559	11655	aminolevulinic acid synthase 1	Alas1	1.307	2.926	0.0214274	0.114576
1558	10503054	NM_001081358	242274	leucine rich repeat containing	Lrrc7	1.307	1.866	0.10302	0.315188
1559	10405938	NM_198322	212569	zinc finger protein 273	Zfp273	1.307	1.236	0.255045	0.529369
1560	10424607	NM_008975	19245	protein tyrosine phosphatase 4	Ptp4a3	1.307	4.537	0.00248107	0.0253184
1561	10481678	ENSMUST00000009695	70730	RIKEN cDNA 6330409D20 gene	6330409D20Rik	1.307	4.085	0.00437256	0.0372046
1562	10362115	NM_183116	76306	RIKEN cDNA 1110021L09 gene	1110021L09Rik	1.307	2.05	0.0783792	0.266396
1563	10358545	NM_001024720	545370	hemicentin 1	Hmcn1	1.307	2.086	0.074254	0.257711
1564	10356995					1.306	2.556	0.0368175	0.164303
1565	10456486					1.306	3.352	0.0116976	0.0755041
1566	10455118	NM_053143	93889	protocadherin beta 18	Pcdhb18	1.306	1.877	0.101421	0.312055
1567	10445767	NM_001033405	328833	triggering receptor expressed	Treml2	1.305	2.62	0.0335285	0.154383
1568	10532819	NM_026145	330171	potassium channel tetramerisat	Kctd10	1.305	4.823	0.00176211	0.0196302
1569	10423836	NM_026778	68588	collagen triple helix repeat c	Cthrc1	1.305	1.938	0.0925539	0.294729
1570	10565612	BC026557	66273	RIKEN cDNA 1810020D17 gene	1810020D17Rik	1.305	2.727	0.0286216	0.138865
1571	10392413					1.305	0.911	0.391917	0.660136
1572	10410973					1.305	4.074	0.00443771	0.0376076
1573	10357345	NM_172484	210356	RIKEN cDNA E030049G20 gene	E030049G20Rik	1.304	3.95	0.00521038	0.0424541
1574	10519693	NM_028882	108151	sema domain, immunoglobulin do	Sema3d	1.304	1.095	0.30868	0.585251
1575	10397853	NM_177620	217835	Ras and Rab interactor 3	Rin3	1.304	4.086	0.00436985	0.0371965
1576	10415885	NM_011446	20680	SRY-box containing gene 7	Sox7	1.304	2.561	0.0365818	0.163532
1577	10591161	ENSMUST00000034647	72230	zinc finger protein 558	Zfp558	1.304	2.333	0.0513415	0.204669
1578	10491623	ENSMUST00000057272	229227	RIKEN cDNA 4932438A13 gene	4932438A13Rik	1.304	2.848	0.0239935	0.123827
1579	10576051	NM_013519	14234	forkhead box C2	Foxc2	1.304	2.524	0.0386448	0.169947
1580	10352554					1.304	4.375	0.00302937	0.0289701
1581	10468452	NM_021377	58178	VPS10 domain receptor protein	Sorcs1	1.303	1.399	0.203328	0.466186
1582	10392642	NM_147219	217265	ATP-binding cassette, sub-fami	Abca5	1.303	4.212	0.00372101	0.0332532
1583	10458663	NM_009468	22240	dihydropyrimidinase-like 3	Dpysl3	1.303	1.975	0.0875635	0.284794
1584	10366277	NM_178609	52679	E2F transcription factor 7	E2f7	1.303	2.608	0.0341381	0.156271
1585	10471555	NM_011923	26360	angiopoietin-like 2	Angptl2	1.302	3.854	0.0059091	0.046516
1586	10471067	NM_009116	20204	paired related homeobox 2	Prrx2	1.302	3.381	0.0112249	0.0733781
1587	10491609	ENSMUST00000057272	229227	RIKEN cDNA 4932438A13 gene	4932438A13Rik	1.302	2.536	0.0379217	0.168193
1588	10457546	NM_207530	64291	oxysterol binding protein-like	Osbpl1a	1.301	4.231	0.00363182	0.0326632
1589	10360070	NM_010185	14127	Fc receptor, IgE, high affinit	Fcer1g	1.301	4.472	0.00268696	0.0267733
1590	10585834	BC096614	319477	RIKEN cDNA 6030419C18 gene	6030419C18Rik	1.301	3.798	0.00636329	0.0489968
1591	10501778	NM_019550	56195	polypyrimidine tract binding p	Ptbp2	1.301	5.202	0.00113922	0.0143979

1592	10396419					1.301	1.461	0.186287	0.444466
1593	10598771	NM_173740	17161	monoamine oxidase A	Maoa	1.3	4.2	0.00377417	0.0335227
1594	10421361	NM_009755	12153	bone morphogenetic protein 1	Bmp1	1.3	2.757	0.0273872	0.135108
1595	10583905	NM_009859	235072	septin 7	Sept7	1.3	4.752	0.00191714	0.0209391
1596	10581222	NM_177699	234686	formin homology 2 domain conta	Fhod1	1.3	4.165	0.00394657	0.0346394
1597	10486564	NM_026891	68968	congenital dyserythropoietic a	Cdan1	1.3	4.399	0.002941	0.028407
1598	10527959					1.299	1.803	0.113178	0.333338
1599	10354598	NM_001001883	329152	HECT, C2 and WW domain contain	Hecw2	1.299	1.805	0.112854	0.332847
1600	10369750	ENSMUST00000079279	791346	predicted gene, ENSMUSG0000006	ENSMUSG00000062561	1.299	1.771	0.118597	0.343885
1601	10379176	NM_011676	22248	unc-119 homolog (C. elegans)	Unc119	1.299	2.952	0.0206307	0.112253
1602	10358259	NM_021605	59125	NIMA (never in mitosis gene a)	Nek7	1.299	3.075	0.0172941	0.0993717
1603	10354868	NM_172513	213056	DNA segment, Chr 1, ERATO Doi	D1Ertd53e	1.299	4.567	0.00239431	0.0246761
1604	10493519	NM_001113331	20416	src homology 2 domain-containi	Shc1	1.299	1.947	0.0913807	0.292662
1605	10560832	NM_009561	22719	zinc finger protein 61	Zfp61	1.298	4.543	0.00246429	0.025208
1606	10421932	NM_001081377	211712	protocadherin 9	Pcdh9	1.298	1.452	0.188509	0.446593
1607	10365420	BC086492	103266	expressed sequence AI597468	AI597468	1.298	4.455	0.00274472	0.0272078
1608	10488482	NM_080575	68738	acyl-CoA synthetase short-chai	Acss1	1.298	6.034	0.00046703	0.00769071
1609	10462853	NM_007811	13082	cytochrome P450, family 26, su	Cyp26a1	1.297	3.043	0.0180925	0.102354
1610	10522388	NM_173403	231290	solute carrier family 10 (sodi	Slc10a4	1.297	0.78	0.460057	0.714885
1611	10489355	ENSMUST00000017961	59091	junctophilin 2	Jph2	1.297	2.325	0.0519793	0.206172
1612	10594661	NM_024427	22003	tropomyosin 1, alpha	Tpm1	1.297	2.421	0.0450172	0.18774
1613	10394625					1.296	2.261	0.0571415	0.218639
1614	10604292	NM_011855	23963	odd Oz/ten-m homolog 1 (Drosop	Odz1	1.296	1.756	0.121225	0.347818
1615	10606235	NM_175358	108672	zinc finger, DHHC domain conta	Zdhhc15	1.296	3.83	0.00610469	0.0474981
1616	10571325	NM_001081279	52065	malignant fibrous histiocytoma	Mfhas1	1.296	4.013	0.00479766	0.0399849
1617	10402211	NM_011812	23876	fibulin 5	Fbln5	1.296	3.537	0.00905587	0.0632356
1618	10350392	NM_009791	12316	asp (abnormal spindle)-like, m	Aspm	1.296	5.25	0.00107956	0.0138593
1619	10507699	NM_013883	29871	sex comb on midleg homolog 1	Scmh1	1.296	4.133	0.00411223	0.0356495
1620	10376534	NM_201245	26936	expressed sequence AA536749	AA536749	1.296	3.757	0.0067269	0.0510347
1621	10381122	NM_010221	14230	FK506 binding protein 10	Fkbp10	1.296	3.457	0.0101118	0.0685504
1622	10527638	NM_009663	11690	arachidonate 5-lipoxygenase ac	Alox5ap	1.296	1.864	0.103376	0.315955
1623	10457106	NM_172633	12405	cerebellin 2 precursor protein	Cbln2	1.295	3.234	0.0137862	0.0850347
1624	10424082	NM_175503	239435	alanine and arginine rich doma	Aard	1.295	1.155	0.284969	0.560293
1625	10552758	ENSMUST00000107882	67605	AKT1 substrate 1 (proline-rich	Akt1s1	1.295	2.264	0.0568681	0.218146
1626	10577838	ENSMUST00000098860	72108	DDHD domain containing 2	Ddhd2	1.295	5.529	0.000793846	0.0111752
1627	10498192	NM_007628	12427	cyclin A1	Ccna1	1.295	5.366	0.000948627	0.0126388
1628	10552433	NM_001008549	210104	cDNA sequence BC043301	BC043301	1.294	2.87	0.0232429	0.121136
1629	10476395	NM_007553	12156	bone morphogenetic protein 2	Bmp2	1.294	1.758	0.120815	0.347267
1630	10435787					1.294	0.717	0.496028	0.740712
1631	10545252					1.294	3.625	0.0080351	0.0581636
1632	10523161	NM_026788	665563	RIKEN cDNA 1110019K23 gene	1110019K23Rik	1.294	1.694	0.13286	0.366501
1633	10411171	NM_172263	218461	phosphodiesterase 8B	Pde8b	1.294	2.9	0.0222347	0.117415
1634	10472757	NM_028593	73649	cytochrome b reductase 1	Cybrd1	1.294	2.063	0.0768681	0.262866
1635	10385361	NM_024475	79560	ubiquitin-like domain containi	Ublcp1	1.293	1.871	0.102305	0.313633
1636	10386921	NM_133208	170740	zinc finger protein 287	Zfp287	1.293	2.801	0.0256933	0.129873
1637	10387201	NM_177566	442801	Rho guanine nucleotide exchang	Arhgef15	1.293	4.573	0.0023751	0.0245931
1638	10602261	NM_008312	15560	5-hydroxytryptamine (serotonin	Htr2c	1.293	2.938	0.0210637	0.113586
1639	10595382	NM_027448	75782	Leber congenital amaurosis 5 (	Lca5	1.293	3.606	0.0082421	0.0591551
1640	10424485	NM_001081409	239510	PHD finger protein 20-like 1	Phf20l1	1.293	3.572	0.00862861	0.0610776
1641	10499950					1.293	2.735	0.0282794	0.137931
1642	10351107	NM_026078	67292	phosphatidylinositol glycan an	Pigc	1.293	3.438	0.0103756	0.0698
1643	10552480	NM_019974	56538	kallikrein related-peptidase 1	Klk11	1.292	3.802	0.00633528	0.0488424

1644	10421924	NM_001081377	211712	protocadherin 9	Pcdh9	1.292	1.653	0.14096	0.37982
1645	10455108	NM_053141	93887	protocadherin beta 16	Pcdhb16	1.292	2.437	0.0439694	0.184792
1646	10450723	ENSMUST00000074201	15024	histocompatibility 2, T region	H2-T10	1.292	2.147	0.0677591	0.243242
1647	10359929	NM_022563	18214	discoidin domain receptor fami	Ddr2	1.292	1.577	0.157432	0.404021
1648	10516982	NM_133887	100226	syntaxin 12	Stx12	1.292	3.943	0.00525641	0.0427467
1649	10513805	NM_019967	56710	deleted in bladder cancer 1 (h	Dbc1	1.292	1.35	0.217924	0.485848
1650	10428837					1.292	1.96	0.0896054	0.28899
1651	10555873	NM_147048	259050	olfactory receptor 652	Olfr652	1.292	2.642	0.0324282	0.151275
1652	10569344	NM_001122737	16002	insulin-like growth factor 2	Igf2	1.292	4.6	0.00229788	0.0240288
1653	10407707	AK046516	328186	predicted gene, ENSMUSG0000007	ENSMUSG00000071543	1.292	2.321	0.0522742	0.20675
1654	10368052	ENSMUST00000095817	100039660	hypothetical protein LOC100039	LOC100039660	1.291	1.365	0.213186	0.479125
1655	10572747	NM_001001491	326618	tropomyosin 4	Tpm4	1.291	5.745	0.000630432	0.00954177
1656	10582466	NM_020564	57429	sulfotransferase family 5A, me	Sult5a1	1.291	3.016	0.0188025	0.105258
1657	10598750	NM_011823	23890	G protein-coupled receptor 34	Gpr34	1.291	2.418	0.045208	0.188022
1658	10512915	BC013800	67063	RIKEN cDNA 2810432L12 gene	2810432L12Rik	1.291	2.79	0.026125	0.130964
1659	10462237	NM_011416	67155	SWI/SNF related, matrix associ	Smarca2	1.29	4.624	0.00223241	0.0235421
1660	10588192	ENSMUST00000085177	77853	male-specific lethal 2-like 1	Msl2l1	1.29	2.222	0.0605706	0.226995
1661	10520604	NM_133918	100952	elastin microfibril interfacer	Emilin1	1.29	3.834	0.00607253	0.0473442
1662	10573427	ENSMUST00000098571	619292	RIKEN cDNA G430095P16 gene	G430095P16Rik	1.29	4.422	0.00285913	0.0279701
1663	10545086	NM_001042451	20617	synuclein, alpha	Snca	1.29	1.195	0.269778	0.544449
1664	10493995	NM_009112	20194	S100 calcium binding protein A	S100a10	1.29	2.461	0.0424473	0.180512
1665	10360349	NM_053199	94332	cell adhesion molecule 3	Cadm3	1.29	5.555	0.000772048	0.0109705
1666	10544199	NM_172477	209773	DENN/MADD domain containing 2A	Dennd2a	1.29	2.318	0.0524604	0.207138
1667	10472366	NM_001099298	110876	sodium channel, voltage-gated,	Scn2a1	1.289	1.641	0.143539	0.384139
1668	10542880	BC048711	320204	RIKEN cDNA 4833442J19 gene	4833442J19Rik	1.289	1.217	0.261891	0.536313
1669	10367768					1.289	1.479	0.181408	0.437465
1670	10444028	NM_030697	80880	KN motif and ankyrin repeat do	Kank3	1.289	3.446	0.0102664	0.069264
1671	10399801	NM_172951	268534	syntrophin, gamma 2	Sntg2	1.289	1.896	0.0985992	0.30667
1672	10511258	NM_026125	67389	C1q domain containing 2	C1qdc2	1.289	3.427	0.0105406	0.0705216
1673	10512030	BC076612	73205	RIKEN cDNA 3110043O21 gene	3110043O21Rik	1.289	3.369	0.0114173	0.0742122
1674	10345580	NM_030266	269180	inositol polyphosphate-4-phosp	Inpp4a	1.289	3.064	0.0175715	0.100279
1675	10496971	NM_025758	66772	ankyrin repeat and SOCS box-co	Asb17	1.288	1.33	0.224135	0.494224
1676	10454067	BC116990	73677	proteasome (prosome, macropain	Psma8	1.288	2.138	0.0686577	0.245219
1677	10583669	AB124611	382062	cDNA sequence AB124611	AB124611	1.288	3.969	0.00508233	0.0417922
1678	10347948	NM_013673	20684	nuclear antigen Sp100	Sp100	1.287	1.388	0.206527	0.470917
1679	10535329	NM_019943	56522	poly (A) polymerase beta (test	Papolb	1.287	1.998	0.0846768	0.279368
1680	10496438	NM_007409	11522	alcohol dehydrogenase 1 (class	Adh1	1.287	2.205	0.0621486	0.230498
1681	10494114	NM_009150	20341	selenium binding protein 1	Selenbp1	1.287	3.013	0.0188905	0.105499
1682	10450369	NM_010479	193740	heat shock protein 1A	Hspa1a	1.287	2.42	0.0450665	0.187761
1683	10455071	NM_053132	93878	protocadherin beta 7	Pcdhb7	1.287	3.037	0.018259	0.102979
1684	10492006	NM_016984	22066	transient receptor potential c	Trpc4	1.287	1.6	0.152395	0.396241
1685	10531185	NM_001081401	330119	a disintegrin-like and metallo	Adamts3	1.287	2.814	0.0252187	0.128086
1686	10440097					1.286	6.132	0.000423017	0.00721493
1687	10448676	NM_023055	65962	solute carrier family 9 (sodiu	Slc9a3r2	1.286	3.378	0.011278	0.0735307
1688	10417759	NM_144839	218793	ubiquitin-conjugating enzyme E	Ube2e2	1.286	2.93	0.0212837	0.114219
1689	10369541	NM_010438	15275	hexokinase 1	Hk1	1.286	3.219	0.014087	0.0862348
1690	10468746	NM_175199	73442	heat shock protein 12A	Hspa12a	1.286	3.842	0.00600588	0.0469458
1691	10596704	NM_008138	14678	guanine nucleotide binding pro	Gnai2	1.285	5	0.00143361	0.0168502
1692	10418879	NM_016700	26419	mitogen-activated protein kina	Mapk8	1.285	3.314	0.0123337	0.0782223
1693	10486255	NM_001042653	70645	Opa interacting protein 5	Oip5	1.285	2.953	0.0206149	0.112225
1694	10573054	NM_010369	14934	glycophorin A	Gypa	1.285	0.636	0.544422	0.776582
1695	10560174	NM_009156	20364	selenoprotein W, muscle 1	Sepw1	1.284	3.437	0.010394	0.0698131
1696	10500204	NM_007899	13601	extracellular matrix protein 1	Ecm1	1.284	2.419	0.0451472	0.187967
1697	10534927	NM_153510	231805	paired immunoglobin-like type	Pilra	1.284	2.533	0.0381165	0.168676

1698	10411519	NM_008634	17755	microtubule-associated protein	Mtap1b	1.284	2.765	0.0270986	0.134054
1699	10604961	NM_008067	14396	gamma-aminobutyric acid (GABA-	Gabra3	1.284	2.034	0.0802833	0.270212
1700	10419416	BC023359	67419	RIKEN cDNA 3632451O06 gene	3632451O06Rik	1.284	1.459	0.186635	0.444956
1701	10453057	NM_009994	13078	cytochrome P450, family 1, sub	Cyp1b1	1.284	1.033	0.334996	0.610563
1702	10561431	NM_138752	101497	pleckstrin homology domain con	Plekhg2	1.283	4.657	0.00214689	0.0229147
1703	10601569	NM_001081385	245578	protocadherin 11 X-linked	Pcdh11x	1.283	1.974	0.087749	0.285265
1704	10407598	NM_023868	20191	ryanodine receptor 2, cardiac	Ryr2	1.283	2.511	0.0393733	0.172148
1705	10586722	AK045567	320055	RIKEN cDNA F830001A07 gene	F830001A07Rik	1.283	3.014	0.0188785	0.10546
1706	10399725	NM_009234	20666	SRY-box containing gene 11	Sox11	1.283	4.153	0.00400728	0.0350414
1707	10599174	NM_133990	16164	interleukin 13 receptor, alpha	Il13ra1	1.283	1.554	0.162982	0.411818
1708	10605986	NM_007515	11989	solute carrier family 7 (catio	Slc7a3	1.283	1.625	0.146888	0.38876
1709	10497329					1.283	1.528	0.169228	0.42056
1710	10479902	NM_001081131	209692	dehydrogenase E1 and transketo	Dhtkd1	1.283	3.319	0.0122391	0.0778362
1711	10445531	NM_207671	57908	zinc finger protein 318	Zfp318	1.283	4.731	0.00196513	0.0212971
1712	10438907	NM_008148	14729	glycoprotein 5 (platelet)	Gp5	1.282	3.095	0.0167999	0.0975911
1713	10546736	NM_008779	18488	contactin 3	Cntn3	1.282	2.306	0.0534779	0.209823
1714	10573234	NM_181039	330814	latrophilin 1	Lphn1	1.282	5.265	0.0010606	0.0136928
1715	10405263	NM_176987	319719	RIKEN cDNA 4732471D19 gene	4732471D19Rik	1.282	3.11	0.0164506	0.0962721
1716	10528036					1.282	1.976	0.0874618	0.284638
1717	10604347	NM_053123	93761	SWI/SNF related, matrix associ	Smarca1	1.282	3.687	0.00738882	0.0548365
1718	10363070	NM_008147	14727	glycoprotein 49 A	Gp49a	1.282	5.431	0.000882773	0.011988
1719	10385466	NM_011891	24052	sarcoglycan, delta (dystrophin	Sgcd	1.281	2.812	0.0252854	0.128363
1720	10427420	NM_134099	106052	F-box protein 4	Fbxo4	1.281	2.776	0.0266306	0.132645
1721	10458983	NM_177115	320253	membrane-associated ring finge	March3	1.281	4.232	0.00362634	0.0326556
1722	10497773	NM_023644	72039	methylcrotonoyl-Coenzyme A car	Mccc1	1.281	3.608	0.00821782	0.059041
1723	10415642	NM_009119	20220	Sin3-associated polypeptide 18	Sap18	1.281	3.143	0.0156829	0.0930667
1724	10546024	NM_021381	58182	prokineticin receptor 1	Prokr1	1.281	3.339	0.0119034	0.0763612
1725	10435487	NM_027113	69544	WD repeat domain 5B	Wdr5b	1.28	1.978	0.0872245	0.284259
1726	10547410	NM_053204	111173	ELKS/RAB6-interacting/CAST fam	Erc1	1.28	4.597	0.00230873	0.0240828
1727	10502299	NM_008689	18033	nuclear factor of kappa light	Nfkb1	1.28	3.071	0.0173982	0.0997203
1728	10356172	BC080290	98496	RIKEN cDNA 5033414K04 gene	5033414K04Rik	1.28	3.945	0.00524283	0.0426527
1729	10448208	BC120908	210853	predicted gene, EG210853	EG210853	1.28	2.565	0.0363794	0.162967
1730	10439514	NM_008083	14432	growth associated protein 43	Gap43	1.28	3.449	0.0102122	0.0689861
1731	10506301	NM_001122899	16847	leptin receptor	Lepr	1.28	2.083	0.0745703	0.258248
1732	10502537	NM_019464	54673	SH3-domain GRB2-like B1 (endop	Sh3glb1	1.279	4.52	0.00253553	0.0256417
1733	10607924	NM_001081978	11704	amelogenin X chromosome	Amelx	1.279	2.474	0.0415842	0.177907
1734	10578690	NM_146208	234258	nei like 3 (E. coli)	Neil3	1.279	3.862	0.00585257	0.0462086
1735	10390186	NM_025659	66610	ABI gene family, member 3	Abi3	1.278	3.898	0.00558083	0.0447652
1736	10389047	NM_001034013	11418	amiloride-sensitive cation cha	Accn1	1.278	4.875	0.00165672	0.0187471
1737	10554650	XM_912445	619808	hypothetical LOC619808	LOC619808	1.278	2.11	0.0716276	0.251535
1738	10392808	NM_145437	217305	RIKEN cDNA 4732429D16 gene	4732429D16Rik	1.278	3.149	0.0155589	0.0926698
1739	10450876	NM_001011721	258218	olfactory receptor 102	Olfr102	1.278	2.13	0.0695219	0.247137
1740	10524312	ENSMUST00000100894	209683	tetratricopeptide repeat domai	Ttc28	1.278	3.424	0.0105854	0.0706269
1741	10458130	NM_177773	271508	RIKEN cDNA 4933408B17 gene	4933408B17Rik	1.278	1.687	0.134225	0.369304
1742	10578986	NM_030263	234353	pleckstrin and Sec7 domain con	Psd3	1.277	1.811	0.111808	0.331009
1743	10471505	NM_013781	27387	SH2 domain containing 3C	Sh2d3c	1.277	3.848	0.00595845	0.0467952
1744	10529091	ENSMUST00000101411	17527	Mpv17 transgene, kidney diseas	Mpv17	1.277	2.075	0.0754873	0.25974
1745	10491962	NM_019739	56458	forkhead box O1	Foxo1	1.277	2.779	0.0265271	0.132276
1746	10501456	ENSMUST00000046924	329739	RIKEN cDNA B430201A12	B430201A12Rik	1.276	2.526	0.0384945	0.169639

				gene					
1747	10598178	NM_026866	68897	dispatched homolog 1 (Drosophi	Disp1	1.276	1.895	0.0987631	0.306809
1748	10573082	NM_001024617	234515	inositol polyphosphate-4-phosp	Inpp4b	1.276	3.711	0.0071487	0.0534688
1749	10537770	NM_011777	22793	zyxin	Zyx	1.276	4.303	0.00331732	0.0306428
1750	10395252	BC028641	72123	RIKEN cDNA 2010109K11 gene	2010109K11Rik	1.276	2.863	0.0234859	0.121892
1751	10581992	NM_001025577	17132	avian musculoaponeurotic fibro	Maf	1.276	2.301	0.0538333	0.210683
1752	10574166	NM_153507	234577	copine II	Cpne2	1.276	3.341	0.0118761	0.0762783
1753	10388241	NM_031251	83429	cystinosis, nephropathic	Ctns	1.276	1.617	0.148605	0.390955
1754	10384486	NM_026576	68145	Ewing's tumor-associated antig	Etaa1	1.275	4.662	0.0021345	0.02284
1755	10458303	NM_001033141	68545	RIKEN cDNA 1110006O17 gene	1110006O17Rik	1.275	4.399	0.00294003	0.028407
1756	10465820	NM_010316	14704	guanine nucleotide binding pro	Gng3	1.275	1.61	0.150177	0.39328
1757	10585956					1.275	3.468	0.0099532	0.0679092
1758	10494821	NM_027533	70747	tetraspanin 2	Tspan2	1.275	2.232	0.059724	0.225162
1759	10558515	NM_183144	212111	inositol polyphosphate-5-phosp	Inpp5a	1.274	2.339	0.0509018	0.203376
1760	10497441	NM_013755	27357	glycogenin	Gyg	1.274	3.411	0.0107728	0.0715167
1761	10442172	NM_145483	224585	zinc finger protein 160	Zfp160	1.274	3.105	0.0165531	0.0966314
1762	10483604	NM_172436	78830	solute carrier family 25 (mito	Slc25a12	1.274	2.761	0.0272504	0.134591
1763	10548940	NM_207222	109593	LIM domain only 3	Lmo3	1.274	3.707	0.00718615	0.0536715
1764	10391025	NM_008469	16665	keratin 15	Krt15	1.274	4.86	0.00168607	0.0189428
1765	10530201	NM_009466	22235	UDP-glucose dehydrogenase	Ugdh	1.273	3.074	0.0173186	0.0994394
1766	10455873	NM_009194	20496	solute carrier family 12, memb	Slc12a2	1.273	2.395	0.046772	0.192103
1767	10600024	NM_010340	14765	G-protein-coupled receptor 50	Gpr50	1.273	1.305	0.232114	0.502819
1768	10474073	BC096456	399569	RIKEN cDNA C230071H18 gene	C230071H18Rik	1.273	2.162	0.0662852	0.240359
1769	10542172	NM_019985	56760	C-type lectin domain family 1,	Clec1b	1.273	1.733	0.125486	0.354754
1770	10386937	NM_138949	192651	zinc finger protein 286	Zfp286	1.272	2.282	0.0553521	0.214629
1771	10545045	NM_153574	58909	RIKEN cDNA D430015B01 gene	D430015B01Rik	1.272	2.038	0.0797713	0.269041
1772	10388591	NM_007754	12874	carboxypeptidase D	Cpd	1.272	2.673	0.0309926	0.146897
1773	10439455	NM_007414	11544	ADP-ribosylarginine hydrolase	Adprh	1.272	4.468	0.00270133	0.0269039
1774	10380477	NM_172261	217124	protein phosphatase 1, regulat	Ppp1r9b	1.271	4.127	0.00414256	0.0357925
1775	10346551	NM_207653	12633	CASP8 and FADD-like apoptosis	Cflar	1.271	3.141	0.0157282	0.0932316
1776	10436892	NM_010587	16443	intersectin 1 (SH3 domain prot	Itsn1	1.271	4.357	0.00309909	0.029358
1777	10370544	BC082302	72128	RIKEN cDNA 2610008E11 gene	2610008E11Rik	1.271	3.002	0.0191974	0.106734
1778	10346562	NM_207653	12633	CASP8 and FADD-like apoptosis	Cflar	1.27	2.95	0.0206875	0.112504
1779	10588786	NM_177090	320169	RIKEN cDNA D330022A01 gene	D330022A01Rik	1.27	4.54	0.00247285	0.0252694
1780	10488522	NM_207204	78177	RIKEN cDNA 4930519N13 gene	4930519N13Rik	1.27	3.866	0.00582082	0.046044
1781	10407122					1.27	1.369	0.212132	0.477618
1782	10532586	XM_912851	74376	myosin XVIIIb	Myo18b	1.27	1.772	0.118344	0.343378
1783	10469322	NM_011701	22352	vimentin	Vim	1.27	5.086	0.00129834	0.01585
1784	10388996	NM_018776	54394	cytokine receptor-like factor	Crlf3	1.269	2.595	0.0347771	0.158373
1785	10554013	NM_001081163	269941	carbohydrate (chondroitin) syn	Chsy1	1.269	4.668	0.00211884	0.0226955
1786	10440469	XR_031351	547311	similar to Scr3	LOC547311	1.269	4.418	0.00287324	0.0280221
1787	10497731	NM_026222	51938	coiled-coil domain containing	Ccdc39	1.269	3.076	0.0172736	0.0993516
1788	10396877	NM_001081421	108760	UDP-N-acetyl-alpha-D-galactosa	Galntl1	1.269	3.676	0.0074987	0.0554767
1789	10495830	NM_027135	69608	SEC24 related gene family, mem	Sec24d	1.269	3.261	0.0132814	0.0828141
1790	10415411	BC057379	277154	cDNA sequence BC030046	BC030046	1.268	3.323	0.0121747	0.0775627
1791	10527832	NM_175310	100710	PDS5, regulator of cohesion ma	Pds5b	1.268	3.884	0.00568001	0.0452369
1792	10406622	BC134387	218444	predicted gene, EG218444	EG218444	1.268	3.726	0.0070114	0.0526453
1793	10561008	NM_001039185	26365	CEA-related cell adhesion mole	Ceacam1	1.268	2.609	0.0340777	0.156165
1794	10565712	NM_025408	66190	phytoceramidase, alkaline	Phca	1.268	2.088	0.074072	0.257223
1795	10454198	NM_026301	67664	ring finger protein 125	Rnf125	1.268	1.088	0.311529	0.588123

1796	10567564	NM_007672	12585	cerebellar degeneration-relate	Cdr2	1.268	2.939	0.0210192	0.113467
1797	10496494	NM_019571	56224	tetraspanin 5	Tspan5	1.268	2.229	0.0599856	0.225803
1798	10512024	NM_178061	214944	MOB1, Mps One Binder kinase ac	Mobkl2b	1.268	3.822	0.00617145	0.0478157
1799	10522075	NM_175174	71778	kelch-like 5 (Drosophila)	Klhl5	1.267	4.717	0.00199861	0.0216156
1800	10376899	NM_053169	94092	tripartite motif-containing 16	Trim16	1.267	3.93	0.00535078	0.0433807
1801	10500304	NM_013841	22365	vacuolar protein sorting 45 (y	Vps45	1.267	2.61	0.034007	0.156
1802	10435162	NM_001081255	70144	leucine-rich repeats and calpo	Lrch3	1.266	5.802	0.000593709	0.00916676
1803	10591114	NM_001080814	270120	FAT tumor suppressor homolog 3	Fat3	1.266	2.431	0.0443521	0.185883
1804	10515803	BC062805	68625	RIKEN cDNA 1110020C03 gene	1110020C03Rik	1.266	2.301	0.0538813	0.210688
1805	10578021	XM_892922	628189	predicted gene, EG628189	EG628189	1.266	1.221	0.260572	0.535075
1806	10502696	NM_027617	70951	spermatogenesis associated 1	Spata1	1.266	1.513	0.172799	0.425141
1807	10526797	NM_016964	50878	stromal antigen 3	Stag3	1.266	1.493	0.177791	0.432292
1808	10529752	NM_007524	12020	NK3 homeobox 2	Nkx3-2	1.266	4.749	0.0019229	0.0209827
1809	10591164					1.265	2.706	0.029521	0.141958
1810	10585467	NM_177351	235386	RIKEN cDNA C630028N24 gene	C630028N24Rik	1.265	3.524	0.00921158	0.0640058
1811	10479297	NM_177727	241846	LSM14 homolog B (SCD6, S. cere	Lsm14b	1.265	3.435	0.0104257	0.0699422
1812	10358717	BC034723	69399	RIKEN cDNA 1700025G04 gene	1700025G04Rik	1.265	2.83	0.0246266	0.126168
1813	10471994	NM_008449	16574	kinesin family member 5C	Kif5c	1.265	2.583	0.0354101	0.1603
1814	10476969	NM_153781	110078	brain glycogen phosphorylase	Pygb	1.265	1.878	0.101194	0.311538
1815	10375578	NM_008029	14257	FMS-like tyrosine kinase 4	Flt4	1.265	3.276	0.0130069	0.0815434
1816	10532888	ENSMUST00000064959	67642	RIKEN cDNA 4930515G01 gene	4930515G01Rik	1.264	2.663	0.0314339	0.148244
1817	10372652	NM_013590	17110	lysozyme 1	Lyz1	1.264	2.413	0.0455796	0.188847
1818	10470314					1.264	1.064	0.321647	0.598461
1819	10558227	NM_025826	66885	acyl-Coenzyme A dehydrogenase,	Acadsb	1.264	1.518	0.171558	0.423765
1820	10531544	NM_198422	231474	progestin and adipoQ receptor	Paqr3	1.264	3.416	0.0106917	0.0711345
1821	10564209					1.263	2.197	0.0628569	0.232269
1822	10478718	NM_008679	17979	nuclear receptor coactivator 3	Ncoa3	1.263	3.625	0.00803303	0.0581636
1823	10478698	NM_010165	14049	eyes absent 2 homolog (Drosoph	Eya2	1.263	3.769	0.00661578	0.0504632
1824	10600044	NM_001081135	208748	proline rich Gla (G-carboxyglu	Prrg3	1.263	1.624	0.147231	0.389278
1825	10397172	NM_172580	217700	acyl-CoA thioesterase 6	Acot6	1.263	2.951	0.0206693	0.112434
1826	10406419	NM_030257	80289	LysM, putative peptidoglycan-b	Lysmd3	1.263	2.646	0.0322642	0.150768
1827	10354777	NM_139146	212712	special AT-rich sequence bindi	Satb2	1.263	4.206	0.00374679	0.0333426
1828	10413932	NM_178791	320736	RIKEN cDNA E130203B14 gene	E130203B14Rik	1.262	3.196	0.0145503	0.0884179
1829	10570786	NM_019576	56229	thrombospondin, type I, domain	Thsd1	1.262	5.151	0.00120609	0.0150621
1830	10453423	ENSMUST00000095186	100038711	predicted gene, ENSMUSG0000007	ENSMUSG00000071036	1.262	3.152	0.0154828	0.0923988
1831	10369792	NM_023598	71371	AT rich interactive domain 5B	Arid5b	1.262	2.238	0.0591502	0.223974
1832	10479981	NM_008091	14462	GATA binding protein 3	Gata3	1.262	0.764	0.469343	0.721467
1833	10487154	NM_177608	70354	RIKEN cDNA 3110001I20 gene	3110001I20Rik	1.262	3.893	0.00561242	0.0449164
1834	10533529	NM_145358	207565	calcium/calmodulin-dependent p	Camkk2	1.261	4.421	0.00286216	0.0279701
1835	10461844	NM_008139	14682	guanine nucleotide binding pro	Gnaq	1.261	2.929	0.0213377	0.114364
1836	10400057	NM_001039515	11861	ADP-ribosylation factor-like 4	Arl4a	1.261	2.915	0.0217611	0.115928
1837	10449652	ENSMUST00000066999	791320	predicted gene, ENSMUSG0000005	ENSMUSG00000054148	1.261	1.706	0.130462	0.362435
1838	10585703	NM_133982	102614	ribonuclease P 25 subunit (hum	Rpp25	1.261	1.875	0.101683	0.312363
1839	10522217	NM_001001980	77569	LIM and calponin homology doma	Limch1	1.261	4.025	0.00472535	0.0396008
1840	10586591	NM_178396	76459	carbonic anyhydrase 12	Car12	1.26	3.765	0.00665757	0.0506729
1841	10497237	NM_053182	94212	phosphoprotein associated with	Pag1	1.26	3.89	0.00563638	0.0450399
1842	10351140	NM_010629	16579	kinesin-associated protein 3	Kifap3	1.26	3.738	0.00689977	0.0519471
1843	10602977	NM_133194	107815	sex comb on midleg-like 2 (Dro	Scml2	1.26	3.231	0.0138534	0.0853484

1844	10344879	NM_177173	320492	RIKEN cDNA A830018L16 gene	A830018L16Rik	1.26	0.92	0.387513	0.656379
1845	10601449	NM_019989	56726	SH3-binding domain glutamic ac	Sh3bgrl	1.259	5.072	0.00131991	0.0160208
1846	10518147	NM_010329	14726	podoplanin	Pdpn	1.259	1.047	0.329081	0.605314
1847	10514576	NM_172872	242553	KN motif and ankyrin repeat do	Kank4	1.259	2.642	0.0324478	0.151318
1848	10422059	NM_177715	239217	potassium channel tetramerisat	Kctd12	1.259	3.36	0.0115608	0.074982
1849	10524310	BC002262	209683	tetratricopeptide repeat domai	Ttc28	1.259	3.222	0.014025	0.0859548
1850	10375079	NM_173784	327900	ubiquitin domain containing 2	Ubtd2	1.259	3.454	0.0101495	0.0686937
1851	10404404	NM_010225	14238	forkhead box F2	Foxf2	1.258	2.955	0.0205324	0.112035
1852	10495896	NM_001025439	108058	calcium/calmodulin-dependent p	Camk2d	1.258	1.357	0.215813	0.482925
1853	10413574	NM_019460	54650	Scm-like with four mbt domains	Sfmbt1	1.258	2.77	0.0268932	0.133446
1854	10563085	NM_010189	14132	Fc receptor, IgG, alpha chain	Fcgrt	1.258	5	0.001433	0.0168502
1855	10351380	XM_001473525	100039795	similar to C1orf32 putative pr	LOC100039795	1.258	3.032	0.018379	0.103545
1856	10606725	XR_032258	665936	hypothetical LOC665936	LOC665936	1.258	4.466	0.00270899	0.0269567
1857	10394942	NM_020614	21340	TATA box binding protein (Tbp)	Taf1b	1.258	4.097	0.00430681	0.0367784
1858	10544523	NR_004419	19872	RNA, Y1 small cytoplasmic, Ro-	Rny1	1.258	1.926	0.0942964	0.298038
1859	10500434	NM_029933	77578	B-cell CLL/lymphoma 9	Bcl9	1.257	5.551	0.000775302	0.011002
1860	10452430	ENSMUST00000024761	50758	F-box and leucine-rich repeat	Fbxl17	1.257	3.69	0.00736081	0.0546478
1861	10415396	NM_023699	73181	nuclear factor of activated T-	Nfatc4	1.257	3.477	0.00983277	0.0672657
1862	10406536					1.257	1.906	0.0971039	0.303498
1863	10514939	NM_172874	242608	podocan	Podn	1.257	4.091	0.00434256	0.0370182
1864	10584593					1.257	2.264	0.0569366	0.218211
1865	10357122					1.256	4.259	0.00350576	0.0317727
1866	10557992	NM_013863	29810	Bcl2-associated athanogene 3	Bag3	1.256	3.523	0.00922708	0.0640924
1867	10431894	NM_175121	67760	solute carrier family 38, memb	Slc38a2	1.256	4.447	0.00277307	0.0273478
1868	10492004	XR_001873	666444	predicted gene, EG666444	EG666444	1.256	2.765	0.0270986	0.134054
1869	10420198	NM_019955	56532	receptor-interacting serine-th	Ripk3	1.256	4.263	0.00348448	0.0316885
1870	10537157	NM_172398	67861	RIKEN cDNA 2310005E10 gene	2310005E10Rik	1.256	3.379	0.0112592	0.0735223
1871	10508651	NM_011520	20970	syndecan 3	Sdc3	1.256	4.274	0.0034387	0.0314073
1872	10363676	NM_177612	216033	catenin (cadherin associated p	Ctnna3	1.256	3.179	0.0148995	0.0898046
1873	10510090	NM_177571	194225	predicted gene, OTTMUSG0000001	OTTMUSG00000010433	1.256	2.374	0.0482507	0.196195
1874	10486396	NM_133838	98878	EH-domain containing 4	Ehd4	1.256	2.257	0.0574816	0.219583
1875	10475800	NM_009633	11552	adrenergic receptor, alpha 2b	Adra2b	1.255	3.418	0.0106649	0.0710231
1876	10582378					1.255	4.421	0.00286134	0.0279701
1877	10556790	NM_028129	434234	RIKEN cDNA 2610020H08 gene	2610020H08Rik	1.255	3.587	0.00845344	0.0602222
1878	10444665	NM_016765	51793	dimethylarginine dimethylamino	Ddah2	1.255	3.408	0.0108173	0.071604
1879	10361748	NM_027968	71865	F-box protein 30	Fbxo30	1.254	5.459	0.000856874	0.0117343
1880	10428171	NM_175134	68839	ankyrin repeat domain 46	Ankrd46	1.254	2.788	0.0261703	0.131
1881	10348244	NM_010566	16331	inositol polyphosphate-5-phosp	Inpp5d	1.254	4.348	0.00313262	0.0295565
1882	10382228	NM_015732	12006	axin2	Axin2	1.254	2.299	0.0540112	0.211054
1883	10538715	BC107398	232035	RIKEN cDNA C130092O11 gene	C130092O11Rik	1.254	2.581	0.0355142	0.16052
1884	10531189	NM_001081401	330119	a disintegrin-like and metallo	Adamts3	1.254	3.183	0.0148231	0.0893698
1885	10416709	NM_172605	219249	tudor domain containing 3	Tdrd3	1.253	2.926	0.0214369	0.114576
1886	10357158	NM_022327	64143	v-ral simian leukemia viral on	Ralb	1.253	4.421	0.00286263	0.0279701
1887	10565218	NM_010551	16170	interleukin 16	Il16	1.253	2.853	0.0238282	0.123212
1888	10601768	ENSMUST00000055842	102910	armadillo repeat containing, X	Armcx4	1.253	3.525	0.00920186	0.0639593
1889	10458589	NM_029942	77619	PRELI domain containing 2	Prelid2	1.253	1.153	0.285524	0.560861
1890	10452516	NM_001025572	106585	ankyrin repeat domain 12	Ankrd12	1.253	3.653	0.00773036	0.0566947
1891	10382106	ENSMUST00000106794	380732	gene model 885, (NCBI)	Gm885	1.253	1.203	0.266815	0.541465
1892	10522712	NM_011263	19712	RE1-silencing transcription fa	Rest	1.252	3.314	0.0123291	0.0782223
1893	10557058	ENSMUST00000098072	26939	polymerase (RNA) III (DNA dire	Polr3e	1.252	1.828	0.108964	0.325894
1894	10410366	NM_001001187	408068	RIKEN cDNA 3830402I07 gene	3830402I07Rik	1.252	3.503	0.00948127	0.0653855
1895	10423355	NM_177597	211147	membrane-associated ring finge	March11	1.252	3.251	0.0134772	0.0836153
1896	10433403	NM_021477	268859	ataxin 2 binding protein 1	A2bp1	1.252	4.078	0.00441356	0.0375122

1897	10424467	NM_001081409	239510	PHD finger protein 20-like 1	Phf20l1	1.251	3.17	0.0150972	0.0907637
1898	10587350	ENSMUST00000113367	100042356	similar to DEAD (Asp-Glu-Ala-A	LOC100042356	1.251	1.477	0.182023	0.438497
1899	10599612	NM_027642	70998	PHD finger protein 6	Phf6	1.251	3.304	0.0124956	0.0790871
1900	10538394	NM_001001335	231999	pleckstrin homology domain con	Plekha8	1.251	2.725	0.0286977	0.139107
1901	10566585	ENSMUST00000098144	434223	gene model 1966, (NCBI)	Gm1966	1.251	2.731	0.0284448	0.138452
1902	10516966	NM_001033308	230787	cDNA sequence BC013712	BC013712	1.251	3.059	0.0176828	0.100778
1903	10412466	NM_145942	208715	3-hydroxy-3-methylglutaryl-Coe	Hmgcs1	1.251	3.454	0.0101527	0.0686937
1904	10386633	BC031537	24082	gene trap locus F3a	Gtlf3a	1.251	2.064	0.0766996	0.262629
1905	10451287	NM_015783	53606	ISG15 ubiquitin-like modifier	Isg15	1.251	2.284	0.0552489	0.214463
1906	10346651	NM_007561	12168	bone morphogenic protein recep	Bmpr2	1.25	4.106	0.00425571	0.0365189
1907	10527961					1.25	1.467	0.184478	0.442045
1908	10531181	NM_001081401	330119	a disintegrin-like and metallo	Adamts3	1.25	5.142	0.00121827	0.0151792
1909	10366881	NM_007837	13198	DNA-damage inducible transcrip	Ddit3	1.25	4.198	0.00378368	0.0335861
1910	10352150					1.25	2.624	0.0333399	0.154018
1911	10471201	NM_001112703	11350	c-abl oncogene 1, receptor tyr	Abl1	1.25	4.305	0.00330605	0.0306055
1912	10455514	NM_080465	140492	potassium intermediate/small c	Kcnn2	1.25	2.386	0.0474294	0.193793
1913	10373325	NM_007412	11536	G protein-coupled receptor 182	Gpr182	1.25	2.146	0.0678653	0.243316
1914	10350136	NM_007791	13007	cysteine and glycine-rich prot	Csrp1	1.25	2.644	0.0323298	0.151017
1915	10566132	NM_019566	56212	ras homolog gene family, membe	Rhog	1.25	2.597	0.0346913	0.158108
1916	10427906	AK051399	100038662	predicted gene, ENSMUSG0000007	ENSMUSG00000072635	1.25	1.63	0.145864	0.387406
1917	10526014	NM_172276	231769	splicing factor, arginine/seri	Sfrs8	1.25	4.173	0.00390803	0.0343867
1918	10391404	AK052868	319412	RIKEN cDNA D830013H23 gene	D830013H23Rik	1.249	4.237	0.00360059	0.0324929
1919	10591094	NM_001080814	270120	FAT tumor suppressor homolog 3	Fat3	1.249	3.088	0.0169619	0.0981528
1920	10374333	NM_001025597	22778	IKAROS family zinc finger 1	Ikzf1	1.249	3.04	0.0181882	0.102607
1921	10571162	NM_007918	13685	eukaryotic translation initiat	Eif4ebp1	1.249	2.597	0.0346593	0.158007
1922	10428353	NM_172814	239393	low density lipoprotein-relate	Lrp12	1.249	2.384	0.0475677	0.194239
1923	10490047	AY702102	446211	cDNA sequence AY702102	AY702102	1.249	3.234	0.0137864	0.0850347
1924	10349184	NM_172853	241201	cadherin 7, type 2	Cdh7	1.249	3.431	0.0104794	0.0702
1925	10591612	NM_177030	319899	dedicator of cytokinesis 6	Dock6	1.249	5.751	0.000626149	0.00949734
1926	10526211					1.249	2.625	0.0332799	0.153865
1927	10420988	NM_009955	12934	dihydropyrimidinase-like 2	Dpysl2	1.249	2.889	0.022594	0.118837
1928	10539244	NM_009313	21336	tachykinin receptor 1	Tacr1	1.249	1.662	0.139224	0.377453
1929	10596095	NM_173447	270190	Eph receptor B1	Ephb1	1.248	2.984	0.0197068	0.108737
1930	10584435	NM_172767	67776	loss of heterozygosity, 11, ch	Loh11cr2a	1.248	1.568	0.159542	0.40691
1931	10486595	NM_001024856	140810	tau tubulin kinase 2	Ttbk2	1.248	2.839	0.0242968	0.124965
1932	10431424	BC007481	140570	plexin B2	Plxnb2	1.248	3.119	0.0162345	0.0954036
1933	10387659	NM_198862	216856	neuroligin 2	Nlgn2	1.248	2.666	0.0313399	0.148045
1934	10585484	NM_176844	110835	cholinergic receptor, nicotini	Chrna5	1.248	2.229	0.0599643	0.225763
1935	10495449	NM_007729	12814	collagen, type XI, alpha 1	Col11a1	1.248	2.93	0.0212907	0.114228
1936	10359948	NM_133806	107652	UDP-N-acetylglucosamine pyroph	Uap1	1.248	3.663	0.00762562	0.0561407
1937	10412011	NM_008442	16563	kinesin family member 2A	Kif2a	1.247	4.896	0.00161659	0.0184067
1938	10388532	NM_008750	18230	nucleoredoxin	Nxn	1.247	3.333	0.0120082	0.0768465
1939	10457385	NM_026484	67974	cyclin Y	Ccny	1.247	4.628	0.00222259	0.0234785
1940	10468853	NM_053198	94281	sideroflexin 4	Sfxn4	1.247	1.791	0.115196	0.337402
1941	10448235	NM_001110254	240041	RIKEN cDNA A630033E08 gene	A630033E08Rik	1.246	2.4	0.0464533	0.191627
1942	10437695	ENSMUST00000063399	100040872	similar to CG2839-PA	LOC100040872	1.246	2.732	0.0284422	0.138452
1943	10406928	NM_008533	17079	CD180 antigen	Cd180	1.246	3.048	0.0179776	0.101919
1944	10442231	BC064464	73229	RIKEN cDNA 3110052M02 gene	3110052M02Rik	1.246	2.027	0.0811139	0.271716
1945	10358064	NM_153774	226432	importin 9	Ipo9	1.246	4.368	0.0030573	0.0290664
1946	10352916	BC058715	320977	RIKEN cDNA C030002C11 gene	C030002C11Rik	1.246	1.263	0.245897	0.51897

1947	10503085	NM_054089	116940	trimethylguanosine synthase ho	Tgs1	1.246	3.645	0.00781686	0.0570915
1948	10372145	NM_172553	216285	ALX homeobox 1	Alx1	1.246	2.315	0.0527457	0.207909
1949	10392739	NM_172800	237979	sidekick homolog 2 (chicken)	Sdk2	1.245	3.473	0.00988534	0.0675551
1950	10399696	NM_001081977	108089	ring finger protein 144A	Rnf144a	1.245	2.953	0.0206071	0.112225
1951	10476989	BC027537	69270	GINS complex subunit 1 (Psf1 h	Gins1	1.245	2.1	0.0727167	0.254178
1952	10589438	NM_008633	17758	microtubule-associated protein	Mtap4	1.245	3.094	0.0168304	0.0977107
1953	10597575	NM_019676	18799	phospholipase C, delta 1	Plcd1	1.245	2.739	0.0281497	0.137618
1954	10492180	NM_001113413	24017	ring finger protein 13	Rnf13	1.245	1.965	0.0889533	0.28772
1955	10459391	NM_007998	14151	ferrochelatase	Fech	1.245	2.495	0.0403363	0.17484
1956	10379727	NM_001081957	100034251	predicted gene, OTTMUSG0000000	OTTMUSG00000000971	1.244	3.123	0.0161408	0.0950643
1957	10577996	AK220417	210801	unc-5 homolog D (C. elegans)	Unc5d	1.244	2.619	0.0335681	0.154498
1958	10408915	NM_025772	94245	dystrobrevin binding protein 1	Dtnbp1	1.244	4.45	0.00276262	0.0273085
1959	10584288	NM_028783	74144	roundabout homolog 4 (Drosophi	Robo4	1.244	3.684	0.00741915	0.0549844
1960	10422022	ENSMUST00000100344	100038742	predicted gene, ENSMUSG0000007	ENSMUSG00000075488	1.244	1.964	0.0891223	0.287844
1961	10559547	NM_011618	21955	troponin T1, skeletal, slow	Tnnt1	1.243	1.517	0.171693	0.423956
1962	10554127	NR_003648	384639	predicted gene, EG384639	EG384639	1.243	2.974	0.0199984	0.109859
1963	10346576	NM_172656	227154	amyotrophic lateral sclerosis	Als2cr2	1.243	2.217	0.0610127	0.227923
1964	10358982	NM_008209	15064	major histocompatibility compl	Mr1	1.243	2.356	0.0495935	0.200156
1965	10383309					1.243	4.104	0.00427022	0.0365593
1966	10454039	NM_008378	16210	imprinted and ancient	Impact	1.242	2.878	0.022959	0.120303
1967	10397719	NM_028354	104884	tyrosyl-DNA phosphodiesterase	Tdp1	1.242	2.233	0.0596348	0.225083
1968	10580795	NM_001033533	234582	coiled-coil domain containing	Ccdc102a	1.242	3.123	0.0161505	0.0950948
1969	10577963	NM_029674	76615	glutamic-oxaloacetic transamin	Got1l1	1.242	2.478	0.0413753	0.177544
1970	10514779	NM_178143	108079	protein kinase, AMP-activated,	Prkaa2	1.242	2.08	0.0749365	0.25894
1971	10411059	NM_173392	218441	zinc finger, FYVE domain conta	Zfyve16	1.242	2.935	0.0211463	0.113886
1972	10432636	NM_174992	207818	cDNA sequence BC004728	BC004728	1.242	3.223	0.0140051	0.0858692
1973	10519324	NM_009873	12571	cyclin-dependent kinase 6	Cdk6	1.241	2.91	0.0219181	0.116412
1974	10508479	NM_008974	19244	protein tyrosine phosphatase 4	Ptp4a2	1.241	4.514	0.00255276	0.0257763
1975	10421172	NM_026331	67712	solute carrier family 25, memb	Slc25a37	1.241	0.767	0.467196	0.72007
1976	10503303	NM_001081183	66185	RIKEN cDNA 1110037F02 gene	1110037F02Rik	1.241	2.628	0.0331431	0.153511
1977	10540275	NM_198612	232313	glycosyltransferase 8 domain c	Glt8d4	1.241	2.267	0.0566183	0.217582
1978	10586244	XM_001476259	102442	DENN/MADD domain containing 4A	Dennd4a	1.241	1.859	0.104088	0.31726
1979	10474006	NM_001109691	192285	PHD finger protein 21A	Phf21a	1.241	4.13	0.00412832	0.0357303
1980	10451225	NM_030715	80905	polymerase (DNA directed), eta	Polh	1.241	2.903	0.0221365	0.117189
1981	10426669	ENSMUST00000039665	78733	trophinin associated protein	Troap	1.241	3.323	0.012175	0.0775627
1982	10443817	NM_016670	18771	Pbx/knotted 1 homeobox	Pknox1	1.241	3.323	0.0121751	0.0775627
1983	10480714	NM_001033293	227620	UDP-N-acteylglucosamine pyroph	Uap1l1	1.241	3.047	0.0179868	0.101919
1984	10469571	ENSMUST00000052168	71198	OTU domain containing 1	Otud1	1.24	2.954	0.0205718	0.112161
1985	10588899	NM_008160	14775	glutathione peroxidase 1	Gpx1	1.24	1.554	0.162789	0.411428
1986	10532538	NM_028386	72898	aspartate beta-hydroxylase dom	Asphd2	1.24	1.892	0.0990916	0.307348
1987	10520388	NM_028234	381626	proline rich 8	Prr8	1.24	2.174	0.065113	0.237986
1988	10519484	AK141701	74051	six transmembrane epithelial a	Steap2	1.24	1.83	0.108656	0.325457
1989	10504775	NM_009928	12819	collagen, type XV, alpha 1	Col15a1	1.24	3.29	0.012745	0.0802505
1990	10591620	NM_177030	319899	dedicator of cytokinesis 6	Dock6	1.239	2.334	0.0512243	0.204433
1991	10352194	ENSMUST00000097450	226751	Cdc42 binding protein kinase a	Cdc42bpa	1.239	3.832	0.00608935	0.0474579
1992	10515994	NM_133716	69780	stromal membrane-associated GT	Smap2	1.239	2.066	0.0765522	0.262295
1993	10381445	NM_144830	217203	transmembrane protein 106A	Tmem106a	1.239	2.132	0.0692697	0.246644
1994	10524417	NM_025526	66383	IscU iron-sulfur cluster scaff	Iscu	1.239	2.063	0.0767962	0.262747
1995	10533569	NM_001003953	30841	F-box and leucine-rich repeat	Fbxl10	1.239	3.751	0.00678146	0.0513311
1996	10479884	ENSMUST00000071016	791411	predicted gene, OTTMUSG0000001	OTTMUSG00000010878	1.239	2.03	0.0807606	0.271306
1997	10404069	NM_030609	80838	histone cluster 1, H1a	Hist1h1a	1.238	1.33	0.224087	0.49422
1998	10458164	NM_178347	52563	CDC23 (cell division cycle 23	Cdc23	1.238	3.818	0.00620192	0.0480166

1999	10365716	NM_026166	67454	RIKEN cDNA 1200009F10 gene	1200009F10Rik	1.238	2.006	0.0836233	0.27705
2000	10405216	NM_011518	20963	spleen tyrosine kinase	Syk	1.238	2.158	0.0666629	0.241191
2001	10592186	ENSMUST00000065197	791291	predicted gene, ENSMUSG0000005	ENSMUSG00000053016	1.238	2.661	0.0315533	0.148594
2002	10574780	NM_008289	15484	hydroxysteroid 11-beta dehydro	Hsd11b2	1.237	4.23	0.00363712	0.032683
2003	10487906	NM_018824	54338	solute carrier family 23 (nucl	Slc23a2	1.237	4.412	0.00289399	0.0281478
2004	10372528	NM_021452	58802	potassium large conductance ca	Kcnmb4	1.237	2.031	0.0805441	0.27085
2005	10371616	NM_144807	212862	choline phosphotransferase 1	Chpt1	1.237	1.845	0.106306	0.321598
2006	10404783	NM_010104	13614	endothelin 1	Edn1	1.236	3.008	0.0190312	0.106061
2007	10536898	NM_012057	27056	interferon regulatory factor 5	Irf5	1.236	4.343	0.00315505	0.0297283
2008	10508135	NM_013718	27096	trafficking protein particle c	Trappc3	1.236	2.017	0.0823273	0.274433
2009	10555011	NM_153591	244141	asparaginyl-tRNA synthetase 2	Nars2	1.236	1.536	0.167116	0.418117
2010	10557069	NM_021554	59052	methyltransferase like 9	Mettl9	1.236	3.464	0.0100076	0.0680857
2011	10385500	NM_008326	15944	immunity-related GTPase family	Irgm	1.236	1.827	0.109205	0.326457
2012	10501629	NM_001080818	229776	CDC14 cell division cycle 14 h	Cdc14a	1.236	1.552	0.163428	0.412528
2013	10410959	NM_025770	66795	autophagy-related 10 (yeast)	Atg10	1.235	3.076	0.0172605	0.0993347
2014	10387821	NM_007440	11684	arachidonate 12-lipoxygenase	Alox12	1.235	1.567	0.15989	0.407256
2015	10422892	ENSMUST00000110617	73692	RIKEN cDNA 2410089E03 gene	2410089E03Rik	1.235	4.197	0.00379116	0.0336384
2016	10426397	NM_007727	12805	contactin 1	Cntn1	1.235	3.424	0.0105725	0.0705858
2017	10568135	NM_001102563	69017	proline-rich transmembrane pro	Prrt2	1.235	4.473	0.00268441	0.0267606
2018	10404885	NM_025508	66355	guanosine monophosphate reduct	Gmpr	1.234	1.807	0.112448	0.332128
2019	10511366	ENSMUST00000116040	622019	similar to protein-tyrosine ph	LOC622019	1.234	2.396	0.04672	0.192001
2020	10607888	NM_001033330	333605	FERM and PDZ domain containing	Frmpd4	1.234	2.051	0.0782418	0.266143
2021	10482968	NM_008867	18779	phospholipase A2 receptor 1	Pla2r1	1.234	3.987	0.00496521	0.0410898
2022	10551822	NM_001081007	233060	zinc finger protein 382	Zfp382	1.234	2.932	0.0212244	0.114033
2023	10472400	NM_001099298	110876	sodium channel, voltage-gated,	Scn2a1	1.234	0.522	0.617186	0.823029
2024	10409059					1.234	2.378	0.0479858	0.195456
2025	10476594	NM_001013802	72899	MACRO domain containing 2	Macrod2	1.234	0.573	0.584056	0.801849
2026	10571860	NM_010402	15111	heart and neural crest derivat	Hand2	1.234	3.934	0.00532238	0.0431836
2027	10426507	NM_175251	77044	AT rich interactive domain 2 (	Arid2	1.234	3.46	0.0100689	0.0683894
2028	10415052	NM_008608	17387	matrix metallopeptidase 14 (me	Mmp14	1.233	2.703	0.0296549	0.142408
2029	10355984	NM_009255	20720	serine (or cysteine) peptidase	Serpine2	1.233	2.647	0.0322221	0.150731
2030	10466353					1.233	3.89	0.00563508	0.0450399
2031	10606146	ENSMUST00000048061	73300	RIKEN cDNA 1700031F05 gene	1700031F05Rik	1.233	1.777	0.117624	0.342098
2032	10404578	NM_009881	12593	chromodomain protein, Y chromo	Cdyl	1.233	2.777	0.0266246	0.132645
2033	10539710	NM_011585	21841	cytotoxic granule-associated R	Tia1	1.233	3.425	0.0105596	0.0705216
2034	10491629	BC079623	229227	RIKEN cDNA 4932438A13 gene	4932438A13Rik	1.233	2.458	0.0425845	0.180844
2035	10550039	NM_153802	243833	zinc finger protein 128	Zfp128	1.233	3.641	0.00785772	0.0572514
2036	10565794	NM_009825	12406	serine (or cysteine) peptidase	Serpinh1	1.233	4.209	0.00373332	0.0332773
2037	10408525	AK006076	71307	RIKEN cDNA 1700018A04 gene	1700018A04Rik	1.233	1.175	0.277174	0.552231
2038	10349648	NM_007799	13034	cathepsin E	Ctse	1.233	0.644	0.539223	0.772081
2039	10469110	NM_181399	98910	USP6 N-terminal like	Usp6nl	1.232	2.009	0.0832603	0.27641
2040	10375065	NM_177364	268396	SH3 and PX domains 2B	Sh3pxd2b	1.232	2.933	0.021194	0.114027
2041	10468513	ENSMUST00000056757	69319	RIKEN cDNA 1700001K23 gene	1700001K23Rik	1.232	3.242	0.0136348	0.084307
2042	10547217	NM_030165	78752	chondroitin sulfate N-acetylga	Csgalnact2	1.232	2.592	0.0349074	0.158693
2043	10446351	NM_001037997	14158	fer (fms/fps related) protein	Fert2	1.232	1.944	0.0918141	0.293561
2044	10586505	BC004027	235439	hect (homologous to the E6-AP	Herc1	1.232	3.527	0.00918554	0.0638978
2045	10369761	NM_178606	28193	receptor accessory protein 3	Reep3	1.231	2.795	0.0259087	0.130401
2046	10478022	DQ372939	70470	RIKEN cDNA 2610304G08 gene	2610304G08Rik	1.231	3.646	0.00781183	0.0570744
2047	10512514	NM_011602	21894	talin 1	Tln1	1.231	4.448	0.00276729	0.0273322
2048	10578796	BC111102	270049	RIKEN cDNA 4930431L04 gene	4930431L04Rik	1.231	3.024	0.0185971	0.10444
2049	10583450	NM_172919	244721	RIKEN cDNA 2210010B09	2210010B09Rik	1.231	1.595	0.153408	0.397723

				gene					
2050	10551185	NM_011577	21803	transforming growth factor, be	Tgfb1	1.231	2.948	0.0207645	0.112772
2051	10375145	NM_010696	16822	lymphocyte cytosolic protein 2	Lcp2	1.231	2.934	0.0211774	0.113996
2052	10457054	NM_146090	225791	zinc binding alcohol dehydroge	Zadh2	1.231	2.133	0.0691737	0.246514
2053	10580550	NM_173431	244585	Rpgrip1-like	Rpgrip1l	1.231	3.253	0.0134223	0.0833783
2054	10520734	NM_147201	192292	nuclear receptor binding prote	Nrbp1	1.23	3.99	0.00494428	0.0409882
2055	10444890	NM_133662	15937	immediate early response 3	Ier3	1.23	2.816	0.0251172	0.127817
2056	10593316					1.23	2.57	0.0360668	0.162044
2057	10395719	NM_013780	27386	neuronal PAS domain protein 3	Npas3	1.23	2.6	0.0345109	0.157534
2058	10474141	NM_001077514	20511	solute carrier family 1 (glial	Slc1a2	1.23	3.059	0.0176994	0.100845
2059	10458875	NM_026854	68857	DTW domain containing 2	Dtwd2	1.23	4.22	0.00368172	0.0329997
2060	10356367	NM_001081082	76768	alkaline phosphatase, intestin	Alpi	1.23	2.477	0.041401	0.177544
2061	10409666	NM_175214	75050	kinesin family member 27	Kif27	1.229	2.097	0.0730099	0.254739
2062	10551347	NM_144923	233016	biliverdin reductase B (flavin	Blvrb	1.229	2.003	0.0840774	0.278075
2063	10495945	BC030185	71643	RIKEN cDNA 4930422G04 gene	4930422G04Rik	1.229	2.669	0.0311675	0.147467
2064	10413928	AK007434	69069	RIKEN cDNA 1810011H11 gene	1810011H11Rik	1.229	1.91	0.096478	0.302302
2065	10411709	NM_009874	12572	cyclin-dependent kinase 7 (hom	Cdk7	1.229	3.111	0.0164336	0.0962129
2066	10537298	NM_203491	243764	cholinergic receptor, muscarin	Chrm2	1.229	1.393	0.204948	0.468376
2067	10513869	NM_172694	230316	multiple EGF-like-domains 9	Megf9	1.229	2.133	0.069177	0.246514
2068	10482109	NM_026434	67889	RNA binding motif protein 18	Rbm18	1.229	2.142	0.0682626	0.24418
2069	10604564	NM_008150	14735	glypican 4	Gpc4	1.229	1.115	0.300716	0.576877
2070	10451363	NM_020493	20807	serum response factor	Srf	1.228	2.75	0.0276831	0.13614
2071	10504047	NM_026275	67615	ubiquitin-conjugating enzyme E	Ube2r2	1.228	3.417	0.010684	0.0711265
2072	10491564	ENSMUST00000108145	229227	RIKEN cDNA 4932438A13 gene	4932438A13Rik	1.228	3.113	0.0163831	0.0961431
2073	10411774	XR_033506	638361	similar to 60S ribosomal prote	LOC638361	1.228	0.966	0.36514	0.636272
2074	10561128	NM_028775	74134	cytochrome P450, family 2, sub	Cyp2s1	1.228	2.158	0.0666944	0.241223
2075	10350146	NM_013750	27280	pleckstrin homology-like domai	Phlda3	1.228	4.339	0.00316812	0.0298116
2076	10366163	NM_175328	103098	solute carrier family 6 (neuro	Slc6a15	1.228	1.324	0.22607	0.496626
2077	10591090	NM_001080814	270120	FAT tumor suppressor homolog 3	Fat3	1.228	1.989	0.0858729	0.281198
2078	10472962	NM_013555	15438	homeo box D9	Hoxd9	1.228	1.311	0.23014	0.501074
2079	10601729	NM_010078	13497	dystrophin related protein 2	Drp2	1.228	3.041	0.0181588	0.102596
2080	10459723	NM_053255	114615	elaC homolog 1 (E. coli)	Elac1	1.228	3.501	0.00950762	0.0655458
2081	10595793	NM_007502	11933	ATPase, Na+/K+ transporting, b	Atp1b3	1.227	2.169	0.0656193	0.238764
2082	10402096	ENSMUST00000062957	104718	tetratricopeptide repeat domai	Ttc7b	1.227	2.796	0.0258842	0.130308
2083	10552824	NM_009101	20130	Harvey rat sarcoma oncogene, s	Rras	1.227	2.075	0.0754209	0.259639
2084	10500876	NM_001025067	269473	leucine-rich repeats and immun	Lrig2	1.227	2.175	0.0650198	0.237821
2085	10485117	NM_011957	26427	cAMP responsive element bindin	Creb3l1	1.227	3.289	0.0127715	0.0803763
2086	10527732	ENSMUST00000087204	320365	furry homolog (Drosophila)	Fry	1.227	3.778	0.00653679	0.0499508
2087	10471464	NM_016973	50935	ST6 (alpha-N-acetyl-neuraminyl	St6galnac6	1.227	2.305	0.0535231	0.209868
2088	10412830	NM_021504	59007	N-glycanase 1	Ngly1	1.226	1.879	0.101008	0.311148
2089	10560329	NM_016868	53417	hypoxia inducible factor 3, al	Hif3a	1.226	3.594	0.00838058	0.0598039
2090	10444658	NM_033444	114584	chloride intracellular channel	Clic1	1.226	2.926	0.0214266	0.114576
2091	10603700					1.226	1.667	0.138238	0.376165
2092	10484791	NM_001011860	258177	olfactory receptor 1222	Olfr1222	1.226	3.498	0.00954588	0.0657453
2093	10576391	NM_009003	19341	RAB4A, member RAS oncogene fam	Rab4a	1.226	2.603	0.0343438	0.157
2094	10448117	NM_008215	15116	hyaluronan synthase1	Has1	1.226	4.473	0.00268321	0.0267606
2095	10519855	NM_001110843	12293	calcium channel, voltage-depen	Cacna2d1	1.226	1.575	0.158077	0.405065
2096	10417950	NM_010811	17423	N-deacetylase/N-sulfotransfera	Ndst2	1.226	2.66	0.031605	0.148733
2097	10491613	ENSMUST00000057272	229227	RIKEN cDNA 4932438A13 gene	4932438A13Rik	1.226	2.033	0.080307	0.270212
2098	10577164	NM_019521	14456	growth arrest specific 6	Gas6	1.225	2.512	0.0393027	0.171999
2099	10347767	NM_021342	57814	potassium voltage-gated channe	Kcne4	1.225	1.467	0.184581	0.442145
2100	10533345	NM_009656	11669	aldehyde dehydrogenase 2, mito	Aldh2	1.225	3.379	0.0112658	0.0735307

2101	10391052	NM_016958	16664	keratin 14	Krt14	1.225	1.951	0.0907642	0.291305
2102	10554945	NM_028243	72461	prolylcarboxypeptidase (angiot	Prcp	1.225	1.957	0.0899925	0.289452
2103	10428940	XM_139402	239502	predicted gene, EG239502	EG239502	1.225	2.21	0.0616465	0.22936
2104	10546803	ENSMUST00000101091	100038404	predicted gene, ENSMUSG0000007	ENSMUSG00000072853	1.224	2.195	0.0631044	0.232827
2105	10390269					1.224	1.703	0.130996	0.363346
2106	10488709	BC075648	329540	RIKEN cDNA 8430427H17 gene	8430427H17Rik	1.223	3.057	0.0177465	0.100977
2107	10434105	NM_153790	224024	scavenger receptor class F, me	Scarf2	1.223	3.054	0.0178191	0.101281
2108	10453629	NM_001081963	240185	RIKEN cDNA 9430020K01 gene	9430020K01Rik	1.223	4.809	0.00179169	0.0198551
2109	10408882	NM_019930	56705	RAN binding protein 9	Ranbp9	1.223	2.282	0.0553525	0.214629
2110	10359377	NM_173424	240869	zinc finger and BTB domain con	Zbtb37	1.223	2.797	0.0258264	0.130204
2111	10346764	NM_198127	329165	abl-interactor 2	Abi2	1.223	3.547	0.00893163	0.0626785
2112	10377372	NM_028048	71998	solute carrier family 25, memb	Slc25a35	1.223	2.156	0.066907	0.241599
2113	10407049	ENSMUST00000095459	70690	RIKEN cDNA 3830408C21 gene	3830408C21Rik	1.223	1.819	0.11047	0.328752
2114	10438064	NM_016982	22362	pre-B lymphocyte gene 1	Vpreb1	1.223	1.065	0.321301	0.598079
2115	10491627	ENSMUST00000057272	229227	RIKEN cDNA 4932438A13 gene	4932438A13Rik	1.223	3.389	0.0111021	0.0728565
2116	10431738	NM_001033217	106042	prickle like 1 (Drosophila)	Prickle1	1.223	3.546	0.00893943	0.0627124
2117	10449741	NM_010831	17691	SNF1-like kinase	Snf1lk	1.223	3.837	0.00604903	0.0472133
2118	10472794	NM_025633	66559	methionine aminopeptidase-like	Metapl1	1.222	2.203	0.0623491	0.23108
2119	10427428	NM_145930	106064	expressed sequence AW549877	AW549877	1.222	3.672	0.00754216	0.0557411
2120	10522335	NR_003966	231287	ATPase, class V, type 10D	Atp10d	1.222	2.464	0.0422215	0.179868
2121	10542822	NM_025620	66532	RIKEN cDNA 2210417D09 gene	2210417D09Rik	1.222	4.852	0.00170173	0.0190821
2122	10571922	NM_175089	18004	NIMA (never in mitosis gene a)	Nek1	1.222	1.662	0.139219	0.377453
2123	10498907	NM_010298	14658	glycine receptor, beta subunit	Glrb	1.222	2.424	0.0447863	0.187184
2124	10459576	NM_001081073	225659	centrosomal protein 76	Cep76	1.222	2.804	0.0255883	0.129436
2125	10418355	NM_028981	12289	calcium channel, voltage-depen	Cacna1d	1.222	2.117	0.0708458	0.249827
2126	10476314	NM_011170	19122	prion protein	Prnp	1.222	1.628	0.146363	0.3881
2127	10515295	NM_001042743	17776	microtubule associated serine/	Mast2	1.222	2.869	0.02328	0.12121
2128	10457872	NM_139143	106957	solute carrier family 39 (meta	Slc39a6	1.222	4.195	0.00380156	0.0337024
2129	10514221	NM_007408	11520	adipose differentiation relate	Adfp	1.221	1.661	0.139341	0.377524
2130	10386723	NM_011841	23939	mitogen-activated protein kina	Mapk7	1.221	4.488	0.00263607	0.0264031
2131	10503107	AK018133	70720	RIKEN cDNA 6330407A03 gene	6330407A03Rik	1.221	2.937	0.0210892	0.113637
2132	10446473	NM_008480	16772	laminin, alpha 1	Lama1	1.221	2.365	0.0489374	0.198301
2133	10528679	NM_001081441	269633	WD repeat domain 86	Wdr86	1.221	3.443	0.0103027	0.0694203
2134	10354521	NM_008384	16329	inositol polyphosphate-1-phosp	Inpp1	1.221	2.562	0.0365279	0.163494
2135	10494238	NM_001037737	11863	aryl hydrocarbon receptor nucl	Arnt	1.221	2.829	0.0246556	0.126244
2136	10573696	BC117078	330820	RIKEN cDNA 4933402J07 gene	4933402J07Rik	1.221	2.811	0.0253038	0.128426
2137	10408359	NM_009513	22360	neurensin 1	Nrsn1	1.221	2.266	0.0567142	0.217832
2138	10410332	NM_001007575	238693	zinc finger protein 58	Zfp58	1.221	1.639	0.143956	0.384952
2139	10482880	NM_001001182	407823	bromodomain adjacent to zinc f	Baz2b	1.221	4.128	0.00413835	0.0357732
2140	10419779	BC011095	219072	DNA segment, Chr 14, ERATO Doi	D14Ertd500e	1.221	2.362	0.0491427	0.19896
2141	10476592	NM_001013802	72899	MACRO domain containing 2	Macrod2	1.22	1.234	0.256	0.530431
2142	10425410	NM_010815	17444	GRB2-related adaptor protein 2	Grap2	1.22	2.397	0.046639	0.19193
2143	10584315					1.22	0.903	0.395464	0.663311
2144	10473356	NM_019949	56791	ubiquitin-conjugating enzyme E	Ube2l6	1.219	3.028	0.0184959	0.104021
2145	10533304	NM_172275	231712	TRAF type zinc finger domain c	Trafd1	1.219	2.759	0.0273201	0.13484
2146	10473118	NM_009454	22193	ubiquitin-conjugating enzyme E	Ube2e3	1.219	2.674	0.0309585	0.146834
2147	10530163	NM_011258	19687	replication factor C (activato	Rfc1	1.219	2.306	0.0534257	0.209696
2148	10577144	NM_001024504	102323	DCN1, defective in cullin nedd	Dcun1d2	1.219	2.608	0.0341202	0.156257
2149	10495206	NM_146136	229699	solute carrier family 16 (mono	Slc16a4	1.219	1.699	0.131947	0.364978
2150	10538547	NM_012056	27055	FK506 binding protein 9	Fkbp9	1.219	2.902	0.0221812	0.11725
2151	10424383					1.218	2.819	0.025032	0.127567

2152	10494351	NM_181409	194126	myotubularin related protein 1	Mtmr11	1.218	1.911	0.0963662	0.30213
2153	10389214	NM_011338	20308	chemokine (C-C motif) ligand 9	Ccl9	1.218	3.409	0.0108016	0.0715825
2154	10492165					1.218	0.678	0.519056	0.757413
2155	10596072	BC031532	235542	RIKEN cDNA 3222402P14 gene	3222402P14Rik	1.218	2.165	0.0660153	0.239751
2156	10398267	NM_007965	14026	Ena-vasodilator stimulated pho	Evl	1.218	4.61	0.00227262	0.0238828
2157	10437055	NM_011377	20465	single-minded homolog 2 (Droso	Sim2	1.218	3.082	0.017119	0.0987437
2158	10381462	NM_025654	66599	RAD52 motif 1	Rdm1	1.217	3.093	0.0168558	0.0977778
2159	10490802	NM_173181	67306	RIKEN cDNA 3110050N22 gene	3110050N22Rik	1.217	2.404	0.0461437	0.190746
2160	10542740	NM_010656	16651	sarcospan	Sspn	1.217	2.774	0.0267088	0.132919
2161	10411235	NM_027711	544963	IQ motif containing GTPase act	Iqgap2	1.217	1.642	0.143349	0.384029
2162	10494527	NM_026406	67845	zinc finger protein 364	Zfp364	1.217	2.248	0.0582811	0.221755
2163	10425866	NM_022321	64099	parvin, gamma	Parvg	1.217	3.712	0.00714399	0.0534688
2164	10373594	NM_015740	14533	biogenesis of lysosome-related	Bloc1s1	1.217	2.985	0.0196606	0.108567
2165	10463875	NM_025696	66673	sortilin-related VPS10 domain	Sorcs3	1.217	2.161	0.0663891	0.240653
2166	10415572	ENSMUST00000095785	69755	RIKEN cDNA 2410022M11 gene	2410022M11Rik	1.217	1.99	0.085625	0.280865
2167	10428579	NM_010162	14042	exostoses (multiple) 1	Ext1	1.216	2.93	0.0213108	0.114277
2168	10431266	NM_145475	223753	ceramide kinase	Cerk	1.216	2.942	0.0209286	0.113291
2169	10516823	NM_183428	269587	erythrocyte protein band 4.1	Epb4.1	1.216	2.927	0.0213928	0.114514
2170	10392464	BC029169	208659	cDNA sequence BC029169	BC029169	1.216	2.673	0.0309778	0.146884
2171	10577948	NM_025686	66653	BRF2, subunit of RNA polymeras	Brf2	1.216	2.814	0.0252072	0.128059
2172	10462102	ENSMUST00000099560	72351	protein prenyltransferase alph	Ptar1	1.216	1.819	0.110434	0.328752
2173	10371846	NM_001042558	11783	apoptotic peptidase activating	Apaf1	1.216	3.361	0.0115469	0.0749149
2174	10444589					1.216	2.01	0.083202	0.27639
2175	10532741	NM_146162	231633	transmembrane protein 119	Tmem119	1.216	2.268	0.0565711	0.21744
2176	10422240	NM_199065	76965	SLIT and NTRK-like family, mem	Slitrk1	1.216	2.303	0.0536515	0.210153
2177	10424559	NM_010158	13992	KH domain containing, RNA bind	Khdrbs3	1.216	1.419	0.197768	0.458459
2178	10461051	AK134852	70494	RIKEN cDNA 5730409K12 gene	5730409K12Rik	1.216	2.487	0.0407952	0.176072
2179	10596207	NM_025692	66663	ubiquitin-like modifier activa	Uba5	1.215	2.234	0.0594713	0.224707
2180	10555009					1.215	1.584	0.155874	0.40178
2181	10538590	ENSMUST00000031817	67138	hect domain and RLD 5	Herc5	1.215	1.772	0.118389	0.343378
2182	10424905	NM_198885	20289	scleraxis	Scx	1.215	1.269	0.243748	0.516777
2183	10452854	NM_053188	94224	steroid 5 alpha-reductase 2	Srd5a2	1.215	1.976	0.0875481	0.284787
2184	10407766	NM_018886	56048	lectin, galactose binding, sol	Lgals8	1.215	3.464	0.0100115	0.0680872
2185	10490903	NM_024495	71934	carbonic anhydrase 13	Car13	1.215	1.484	0.180265	0.435801
2186	10588454	NM_029896	77305	WD repeat domain containing 82	Wdr82	1.215	2.059	0.0773164	0.263972
2187	10559221	NM_011620	21957	troponin T3, skeletal, fast	Tnnt3	1.214	3.533	0.00911051	0.0635122
2188	10565727	NM_001024619	244152	tsukushin	Tsku	1.214	2.669	0.0311755	0.147467
2189	10593937	NM_025837	110119	mannose phosphate isomerase	Mpi	1.214	3.897	0.00558476	0.044769
2190	10495035	NM_009196	20501	solute carrier family 16 (mono	Slc16a1	1.214	2.594	0.0348228	0.158377
2191	10553080	NM_009800	12348	carbonic anhydrase 11	Car11	1.214	2.142	0.0682451	0.244165
2192	10435329	NM_172824	239839	coiled-coil domain containing	Ccdc14	1.214	3.02	0.0187122	0.104947
2193	10403929	NM_001039115	544922	predicted gene, OTTMUSG0000000	OTTMUSG00000000421	1.214	2.075	0.075445	0.259643
2194	10379936	NM_009324	21385	T-box 2	Tbx2	1.214	2.731	0.0284637	0.13848
2195	10551169	NM_146184	232984	UDP-GlcNAc:betaGal beta-1,3-N-	B3gnt8	1.213	1.486	0.17963	0.434993
2196	10546104	NM_023060	65967	eukaryotic elongation factor,	Eefsec	1.213	3.408	0.0108093	0.0715825
2197	10422912	BC058107	73692	RIKEN cDNA 2410089E03 gene	2410089E03Rik	1.213	3.584	0.00848876	0.0604128
2198	10455098	NM_053139	93885	protocadherin beta 14	Pcdhb14	1.213	1.333	0.223172	0.493026
2199	10363773	NM_001081347	69288	Rho-related BTB domain contain	Rhobtb1	1.213	1.715	0.128882	0.360128
2200	10356271	NM_213615	381287	RIKEN cDNA A530032D15Rik gene	A530032D15Rik	1.213	2.399	0.0464864	0.191643

2201	10369276	NM_001033259	215999	coiled-coil domain containing	Ccdc109a	1.212	1.852	0.105183	0.319429
2202	10546056	NM_001039394	69834	RAB43, member RAS oncogene fam	Rab43	1.212	3.067	0.0174754	0.0999956
2203	10426089	NM_027306	70073	zinc finger, DHHC domain conta	Zdhhc25	1.212	1.396	0.204243	0.467434
2204	10409866	ENSMUST00000021884	13025	cytotoxic T lymphocyte-associa	Ctla2b	1.212	1.973	0.0878545	0.285438
2205	10426955	NM_001077499	20273	sodium channel, voltage-gated,	Scn8a	1.212	2.535	0.0380199	0.168377
2206	10384032	NM_008894	18972	polymerase (DNA directed), del	Pold2	1.212	2.206	0.0620483	0.230288
2207	10577219	ENSMUST00000071308	100044283	hypothetical protein LOC100044	LOC100044283	1.212	2.382	0.047744	0.194809
2208	10478949	NM_029761	76829	docking protein 5	Dok5	1.212	1.586	0.155462	0.400991
2209	10498519	NM_026155	67437	signal sequence receptor, gamm	Ssr3	1.211	3.489	0.00967209	0.0664414
2210	10543273	NM_080285	30785	cortactin binding protein 2	Cttnbp2	1.211	1.227	0.258212	0.532284
2211	10544538					1.211	1.634	0.144921	0.386407
2212	10546807					1.211	2.957	0.0204786	0.111886
2213	10373313	NM_008668	17937	Ngfi-A binding protein 2	Nab2	1.211	2.729	0.0285676	0.138731
2214	10430519	NM_013767	27373	casein kinase 1, epsilon	Csnk1e	1.211	2.278	0.0557439	0.215593
2215	10358523	NM_001024720	545370	hemicentin 1	Hmcn1	1.211	2.666	0.0312985	0.147889
2216	10573779	NM_027280	93960	naked cuticle 1 homolog (Droso	Nkd1	1.211	2.419	0.0451694	0.187967
2217	10586993	NM_028116	72135	pygopus 1	Pygo1	1.211	3.359	0.0115855	0.0750731
2218	10354031	NM_207228	211484	testis specific 10	Tsga10	1.211	1.972	0.0879711	0.28568
2219	10476740	NM_053195	94249	solute carrier family 24 (sodi	Slc24a3	1.21	2.413	0.0455343	0.18878
2220	10441064	NM_007834	13185	Down syndrome critical region	Dscr3	1.21	0.96	0.368181	0.639095
2221	10602068	NM_011845	23947	midline 2	Mid2	1.21	1.292	0.236318	0.508399
2222	10582445	NM_001081379	77087	ankyrin repeat domain 11	Ankrd11	1.21	3.565	0.00870985	0.0615101
2223	10437210	NM_019517	56175	beta-site APP-cleaving enzyme	Bace2	1.21	2.789	0.026151	0.130966
2224	10425138	NM_009164	20401	SH3-domain binding protein 1	Sh3bp1	1.21	3.148	0.0155899	0.0928023
2225	10410590	NM_177333	211446	exocyst complex component 3	Exoc3	1.21	2.902	0.0221906	0.11727
2226	10426557	NM_021514	18642	phosphofructokinase, muscle	Pfkm	1.21	2.334	0.0512906	0.204543
2227	10604944	NM_017369	14404	gamma-aminobutyric acid (GABA-	Gabre	1.21	2.034	0.0802974	0.270212
2228	10348632	NM_007855	13345	twist homolog 2 (Drosophila)	Twist2	1.21	2.339	0.0508656	0.203346
2229	10465619	NM_201411	396184	fibronectin leucine rich trans	Flrt1	1.209	3.185	0.0147904	0.0892997
2230	10394560	NM_025695	67241	structural maintenance of chro	Smc6	1.209	3.504	0.00947477	0.065362
2231	10391685	NM_199200	217219	cDNA sequence BC025575	BC025575	1.209	4.112	0.00422354	0.0362724
2232	10589790					1.209	0.968	0.364399	0.635557
2233	10415875	NM_028228	72400	RIKEN cDNA 2610028A01 gene	2610028A01Rik	1.209	2.376	0.0481443	0.195916
2234	10441422	NM_146073	224454	zinc finger, DHHC domain conta	Zdhhc14	1.208	2.956	0.0205055	0.111975
2235	10446063	NM_025566	66443	tumor necrosis factor, alpha-i	Tnfaip8l1	1.208	3.536	0.00906268	0.0632413
2236	10593713	NM_019686	56506	calcium and integrin binding f	Cib2	1.208	2.53	0.0383069	0.169165
2237	10430794	NM_013872	29858	phosphomannomutase 1	Pmm1	1.208	3.612	0.00817847	0.0588182
2238	10425623	NM_145473	105859	cold shock domain containing C	Csdc2	1.208	1.92	0.0950697	0.299747
2239	10560655	NM_020486	57278	basal cell adhesion molecule	Bcam	1.208	2.567	0.0362281	0.162503
2240	10578880	NM_009390	21892	tolloid-like	Tll1	1.208	2.526	0.038521	0.16972
2241	10509568	NM_025451	66259	calcium/calmodulin-dependent p	Camk2n1	1.208	3.458	0.0100959	0.0685504
2242	10471129	NM_019681	14299	frequenin homolog (Drosophila)	Freq	1.208	2.485	0.0409261	0.176312
2243	10606248	NM_053206	272790	melanoma antigen, family E, 2	Magee2	1.208	2.536	0.0379308	0.168193
2244	10546402	NM_030081	78287	zinc finger, FYVE domain conta	Zfyve20	1.208	1.65	0.141744	0.381301
2245	10568601	BC002195	791302	predicted gene, ENSMUSG0000005	ENSMUSG00000057032	1.208	0.994	0.35233	0.625287
2246	10348653	NM_016696	14733	glypican 1	Gpc1	1.208	2.773	0.0267814	0.133145
2247	10347417	NM_025784	66821	BCS1-like (yeast)	Bcs1l	1.207	1.996	0.0849587	0.279982
2248	10396778	NM_019579	56217	membrane protein, palmitoylate	Mpp5	1.207	3.65	0.00776364	0.0567966
2249	10571297	ENSMUST00000067768	791287	predicted gene, ENSMUSG0000005	ENSMUSG00000054618	1.207	1.619	0.148292	0.390488
2250	10563858	NM_008074	14407	gamma-aminobutyric acid (GABA-	Gabrg3	1.207	2.131	0.0693731	0.246733
2251	10598547					1.207	2.719	0.0289841	0.140013
2252	10491625	ENSMUST00000057272	229227	RIKEN cDNA 4932438A13 gene	4932438A13Rik	1.207	2.65	0.0320858	0.150244

				gene					
2253	10599120	NM_001009947	75974	dedicator of cytokinesis 11	Dock11	1.207	2.213	0.0613754	0.228633
2254	10361098	NM_025424	66208	neuron derived neurotrophic fa	Nenf	1.207	1.24	0.253941	0.528218
2255	10473367	NM_001081349	72401	solute carrier family 43, memb	Slc43a1	1.206	3.442	0.01032	0.0695148
2256	10487675	ENSMUST00000079964	321014	RIKEN cDNA 4930473A02 gene	4930473A02Rik	1.206	3.55	0.00889197	0.0624416
2257	10449419	NM_011566	21678	TEA domain family member 3	Tead3	1.206	1.849	0.105644	0.320213
2258	10491056	NM_030732	81004	transducin (beta)-like 1X-link	Tbl1xr1	1.206	2.691	0.0301925	0.144432
2259	10545629	NM_019752	64704	HtrA serine peptidase 2	Htra2	1.206	2.22	0.0608115	0.227575
2260	10574378	NM_030198	78833	GINS complex subunit 3 (Psf3 h	Gins3	1.205	3.247	0.0135494	0.0839157
2261	10554521	NM_008803	18584	phosphodiesterase 8A	Pde8a	1.205	1.609	0.150429	0.393664
2262	10556658	BC054720	71517	RIKEN cDNA 9030624J02 gene	9030624J02Rik	1.205	1.939	0.0924301	0.294684
2263	10542120	NM_020257	93675	C-type lectin domain family 2,	Clec2i	1.205	3.018	0.0187695	0.105129
2264	10550956	NM_023154	66071	ethylmalonic encephalopathy 1	Ethe1	1.205	1.317	0.22824	0.499214
2265	10599719	NM_172780	236794	solute carrier family 9 (sodiu	Slc9a6	1.205	1.539	0.166398	0.417266
2266	10594221	NM_145616	102747	leucine rich repeat containing	Lrrc49	1.205	1.957	0.090009	0.289452
2267	10358057	NM_175259	77552	shisa homolog 4 (Xenopus laevi	Shisa4	1.205	2.102	0.0724769	0.253591
2268	10474223	NM_181858	333883	CD59b antigen	Cd59b	1.205	1.921	0.0949897	0.299665
2269	10558450	ENSMUST00000097978	100038555	predicted gene, ENSMUSG0000007	ENSMUSG00000073800	1.205	3.098	0.0167412	0.0974333
2270	10450519	NM_025674	106795	transcription factor 19	Tcf19	1.205	2.755	0.0274599	0.135341
2271	10591576	NM_177030	319899	dedicator of cytokinesis 6	Dock6	1.205	3.184	0.0148126	0.0893521
2272	10603135	NM_175027	237211	Fanconi anemia, complementatio	Fancb	1.204	1.633	0.145235	0.386933
2273	10357856					1.204	1.592	0.154152	0.398898
2274	10452860	NM_133771	76890	mediator of cell motility 1	Memo1	1.204	1.796	0.114252	0.335566
2275	10381744	NM_007477	11841	ADP-ribosylation factor 2	Arf2	1.204	2.904	0.0221052	0.117082
2276	10491699	NM_008006	14173	fibroblast growth factor 2	Fgf2	1.204	1.665	0.13865	0.376676
2277	10504849	NM_026343	67727	syntaxin 17	Stx17	1.204	3.511	0.00938616	0.0648777
2278	10566512					1.204	1.436	0.192821	0.452269
2279	10386789	NM_013881	29869	Unc-51 like kinase 2 (C. elega	Ulk2	1.204	2.621	0.033448	0.154315
2280	10402665	NM_183016	217866	Cdc42 binding protein kinase b	Cdc42bpb	1.203	2.484	0.0410192	0.176569
2281	10544788	NM_010456	15405	homeo box A9	Hoxa9	1.203	2.337	0.051036	0.203797
2282	10426999	NM_009612	11482	activin A receptor, type II-li	Acvrl1	1.203	3.512	0.00937129	0.0648149
2283	10418092	ENSMUST00000096098	268723	RIKEN cDNA A830039N20 gene	A830039N20Rik	1.203	1.135	0.292539	0.568731
2284	10583242	NM_030261	75747	sestrin 3	Sesn3	1.203	3.726	0.0070061	0.0526242
2285	10417065	NM_029519	76108	RAS related protein 2a	Rap2a	1.203	2.041	0.0794198	0.26838
2286	10447517	NR_003519	328734	RIKEN cDNA D030013I16 gene	D030013I16Rik	1.203	1.468	0.184423	0.442014
2287	10414802	ENSMUST00000103606	547329	T cell receptor alpha variable	Trav16d/dv11	1.203	0.906	0.394032	0.661801
2288	10505894	NM_024433	66902	methylthioadenosine phosphoryl	Mtap	1.203	2.431	0.0443358	0.185852
2289	10581434	NM_176913	319446	dipeptidase 2	Dpep2	1.203	3.147	0.0156126	0.0928214
2290	10574727	NM_001081332	277973	solute carrier family 9 (sodiu	Slc9a5	1.203	1.523	0.170293	0.421871
2291	10482824	NM_001110204	11477	activin A receptor, type 1	Acvr1	1.202	3.012	0.0189199	0.105608
2292	10445192	NM_011269	19743	Rhesus blood group-associated	Rhag	1.202	0.581	0.578804	0.798528
2293	10517169	NM_080559	73723	SH3 domain binding glutamic ac	Sh3bgrl3	1.202	2.531	0.0382192	0.168945
2294	10367746	NM_175155	70097	SAM and SH3 domain containing	Sash1	1.202	1.976	0.0875214	0.284744
2295	10483215	NM_018732	20269	sodium channel, voltage-gated,	Scn3a	1.202	1.961	0.0895225	0.28881
2296	10352548	NM_001033286	226781	solute carrier family 30, memb	Slc30a10	1.202	3.652	0.00773911	0.0567392
2297	10347921	BC100303	621875	RIKEN cDNA A530040E14 gene	A530040E14Rik	1.202	2.502	0.0399245	0.173732
2298	10596269	ENSMUST00000060084	235567	DnaJ (Hsp40) homolog, subfamil	Dnajc13	1.202	1.14	0.290758	0.567035
2299	10498273	NM_008536	17112	transmembrane 4 superfamily me	Tm4sf1	1.202	2.576	0.0357506	0.161141
2300	10438220	NM_030558	80733	carbonic anhydrase 15	Car15	1.202	3.247	0.013539	0.0838762
2301	10380303	NM_028296	72605	carbonic anhydrase 10	Car10	1.202	1.699	0.131798	0.364709
2302	10534456	NM_146001	215114	huntingtin interacting protein	Hip1	1.202	3.354	0.0116608	0.075402
2303	10555881	NM_146312	258309	olfactory receptor 657	Olfr657	1.202	2.444	0.0434997	0.183402
2304	10450496	NM_010734	16988	leukocyte specific transcript	Lst1	1.201	2.254	0.0577638	0.220422

2305	10434845	NM_008364	16180	interleukin 1 receptor accesso	Il1rap	1.201	2.031	0.0806091	0.270969
2306	10402063	BC029185	71375	forkhead box N3	Foxn3	1.201	3.665	0.00760919	0.0560791
2307	10541426	NM_008646	17837	murinoglobulin 2	Mug2	1.201	3.022	0.0186628	0.104726
2308	10379044	NM_033475	19376	RAB34, member of RAS oncogene	Rab34	1.201	1.731	0.125728	0.355019
2309	10458323	ENSMUST00000115704	381149	neuregulin 2	Nrg2	1.201	3.572	0.00862883	0.0610776
2310	10577757	NM_007404	11502	a disintegrin and metallopepti	Adam9	1.201	2.049	0.0785112	0.266673
2311	10373452	BC132471	229599	gene model 129, (NCBI)	Gm129	1.201	1.879	0.101141	0.311419
2312	10554693	NM_023377	170460	StAR-related lipid transfer (S	Stard5	1.201	2.913	0.0218203	0.116126
2313	10408870	NM_025935	67046	TBC1 domain family, member 7	Tbc1d7	1.2	1.838	0.107464	0.32308
2314	10382300	NM_011943	26399	mitogen-activated protein kina	Map2k6	1.2	2.109	0.0716985	0.251634
2315	10571214	NM_175136	68867	ring finger protein 122	Rnf122	1.2	2.967	0.0201993	0.11056
2316	10453692	NM_025783	66700	vacuolar protein sorting 24 (y	Vps24	1.2	1.011	0.344755	0.618903
2317	10594879	NM_011544	21406	transcription factor 12	Tcf12	1.2	1.864	0.103421	0.316047
2318	10372891	NM_001081037	117600	SLIT-ROBO Rho GTPase activatin	Srgap1	1.2	2.933	0.0212124	0.114027
2319	10461176	NM_019829	56389	syntaxin 5A	Stx5a	1.2	2.975	0.0199469	0.109719
2320	10419370	NM_207214	105504	exocyst complex component 5	Exoc5	1.2	2.463	0.0422908	0.179955
2321	10506431	ENSMUST00000094945	100038724	predicted gene, ENSMUSG0000007	ENSMUSG00000070886	1.199	1.368	0.212411	0.477963
2322	10458641	NM_181543	240239	G protein-coupled receptor 151	Gpr151	1.199	2.008	0.0833883	0.276517
2323	10577623	NM_024240	109145	GINS complex subunit 4 (Sld5 h	Gins4	1.199	2.733	0.0283796	0.13823
2324	10399265	NM_010881	17977	nuclear receptor coactivator 1	Ncoa1	1.199	2.273	0.0561491	0.216623
2325	10437332	NM_001025432	12914	CREB binding protein	Crebbp	1.199	3.424	0.010584	0.0706269
2326	10541071	BC058515	213393	RIKEN cDNA 8430408G22 gene	8430408G22Rik	1.199	2.91	0.0219107	0.116412
2327	10382243	NM_010303	14674	guanine nucleotide binding pro	Gna13	1.199	2.209	0.0617995	0.229738
2328	10485562	NM_010434	15259	homeodomain interacting protei	Hipk3	1.199	2.909	0.0219582	0.11652
2329	10604735	NM_011252	19655	RNA binding motif protein, X c	Rbmx	1.199	2.26	0.0572287	0.218894
2330	10395457	NM_007960	14009	ets variant gene 1	Etv1	1.199	2.3	0.0538876	0.210688
2331	10507500	NM_008135	14664	solute carrier family 6 (neuro	Slc6a9	1.199	2.32	0.0523653	0.207033
2332	10517070	NM_001017968	503610	zinc finger, DHHC domain conta	Zdhhc18	1.198	1.876	0.101604	0.312332
2333	10501222	NM_008183	14863	glutathione S-transferase, mu	Gstm2	1.198	1.564	0.160485	0.407897
2334	10553042	NM_028544	69903	Ras interacting protein 1	Rasip1	1.198	2.524	0.0386283	0.16991
2335	10568529	NM_175115	67143	IKAROS family zinc finger 5	Ikzf5	1.198	1.12	0.298796	0.574899
2336	10517336	NM_013885	29876	chloride intracellular channel	Clic4	1.198	3.826	0.00613861	0.0476151
2337	10588283	NM_173781	270192	RAB6B, member RAS oncogene fam	Rab6b	1.198	1.617	0.148647	0.390994
2338	10362428					1.198	0.47	0.651912	0.844083
2339	10529732	NM_010474	15476	heparan sulfate (glucosamine)	Hs3st1	1.198	1.499	0.176325	0.430163
2340	10549968	XR_034260	628737	similar to aurora kinase C	LOC628737	1.198	3.994	0.00492269	0.0408338
2341	10364888	ENSMUST00000099469	208266	DOT1-like, histone H3 methyltr	Dot1l	1.198	2.225	0.0602985	0.226497
2342	10518226	BC038488	230895	vacuolar protein sorting 13 D	Vps13d	1.198	2.574	0.0358833	0.161438
2343	10590060	NM_133710	69274	CTD (carboxy-terminal domain,	Ctdspl	1.198	2.437	0.0439632	0.184792
2344	10534324	NM_010717	16885	LIM-domain containing, protein	Limk1	1.198	2.153	0.0671356	0.241908
2345	10415021	NM_134076	105501	abhydrolase domain containing	Abhd4	1.198	2.022	0.0816905	0.272831
2346	10573615	NM_019716	56452	origin recognition complex, su	Orc6l	1.197	1.509	0.173878	0.426653
2347	10604620	BC066167	78755	RIKEN cDNA 4632404H22 gene	4632404H22Rik	1.197	1.725	0.126919	0.356905
2348	10531796	NM_172882	72145	WD repeat and FYVE domain cont	Wdfy3	1.197	2.698	0.0298662	0.143184
2349	10511136	NM_178699	230991	RIKEN cDNA B930041F14 gene	B930041F14Rik	1.197	1.838	0.107435	0.323077
2350	10344705					1.197	1.91	0.0965169	0.302379
2351	10536818	NM_184053	12321	calumenin	Calu	1.197	3.253	0.0134232	0.0833783
2352	10589982	NM_013727	27215	5-azacytidine induced gene 2	Azi2	1.196	2.541	0.0376592	0.167353
2353	10595189	NM_172773	235504	solute carrier family 17 (anio	Slc17a5	1.196	2.132	0.0693626	0.246733
2354	10456492	BC096371	52662	DNA segment, Chr 18, ERATO Doi	D18Ertd653e	1.196	1.555	0.162542	0.411049

2355	10500335	NM_010186	14129	Fc receptor, IgG, high affinit	Fcgr1	1.196	1.495	0.17741	0.431801
2356	10547469	NM_001037155	406236	hereditary sensory neuropathy,	Hsn2	1.196	2.127	0.0698307	0.24761
2357	10361139	NM_011633	22033	Tnf receptor-associated factor	Traf5	1.196	1.647	0.14227	0.382232
2358	10575129	NM_126165	116733	vacuolar protein sorting 4a (y	Vps4a	1.196	2.027	0.0810745	0.271716
2359	10529613	NM_021292	59056	Ellis van Creveld gene homolog	Evc	1.196	2.83	0.0246206	0.126168
2360	10580782	NM_053246	114255	docking protein 4	Dok4	1.196	2.17	0.0654586	0.238533
2361	10379630	NM_011408	20556	schlafen 2	Slfn2	1.196	2.89	0.0225746	0.118824
2362	10547140	ENSMUST00000088896	330401	transmembrane and coiled coil	Tmcc1	1.196	2.392	0.0469816	0.192664
2363	10399463					1.195	3.111	0.0164263	0.0962129
2364	10491354	NM_144519	67778	zinc finger protein 639	Zfp639	1.195	1.89	0.0994991	0.30816
2365	10399426					1.195	2.069	0.0761532	0.261436
2366	10463826	NM_026377	67788	RIKEN cDNA 6330577E15 gene	6330577E15Rik	1.195	3.398	0.0109699	0.0722269
2367	10429341	NM_007982	14083	PTK2 protein tyrosine kinase 2	Ptk2	1.195	2.764	0.0271037	0.134054
2368	10376324	DQ508487	631323	interferon-gamma-inducible p47	Irgb10	1.195	2.029	0.0808083	0.271356
2369	10396143	BC027570	73991	spastic paraplegia 3A homolog	Spg3a	1.195	3.295	0.0126528	0.0797173
2370	10375062	NM_175000	216635	hemoglobin, theta 1	Hbq1	1.195	0.791	0.454232	0.710744
2371	10501608	NM_011693	22329	vascular cell adhesion molecul	Vcam1	1.195	2.173	0.0651922	0.238029
2372	10414553	NM_001017422	53877	eosinophil-associated, ribonuc	Ear4	1.195	2.879	0.0229328	0.120261
2373	10372069	NM_007706	216233	suppressor of cytokine signali	Socs2	1.195	2.734	0.0283223	0.138077
2374	10352354	ENSMUST00000066988	329307	RIKEN cDNA A430110L20 gene	A430110L20Rik	1.195	2.119	0.070643	0.249403
2375	10491619	ENSMUST00000057272	229227	RIKEN cDNA 4932438A13 gene	4932438A13Rik	1.195	1.552	0.163343	0.412384
2376	10365899	NM_029852	77048	coiled-coil domain containing	Ccdc41	1.194	2.372	0.0484403	0.196802
2377	10595787	BC053441	73410	RIKEN cDNA 1700065D16 gene	1700065D16Rik	1.194	1.883	0.100412	0.310087
2378	10593589					1.194	1.013	0.343735	0.617864
2379	10471967	NM_029924	109241	methyl-CpG binding domain prot	Mbd5	1.194	2.37	0.0485436	0.196931
2380	10489190	NM_016916	53619	bladder cancer associated prot	Blcap	1.194	2.432	0.0443055	0.185761
2381	10471608	BC038386	26920	centrosomal protein 110	Cep110	1.194	2.528	0.0384198	0.169439
2382	10373610	NM_146318	258315	olfactory receptor 767	Olfr767	1.194	1.528	0.169127	0.42056
2383	10495136	NM_023186	81600	chitinase, acidic	Chia	1.194	3.458	0.0100995	0.0685504
2384	10529156	NM_026298	67661	intraflagellar transport 172 h	Ift172	1.194	2.114	0.0712411	0.250761
2385	10488459	BC023805	668923	zinc finger protein 442	Zfp442	1.194	1.171	0.278999	0.554016
2386	10445291					1.193	0.566	0.588672	0.805172
2387	10409994	ENSMUST00000099446	435366	predicted gene, EG435366	EG435366	1.193	2.572	0.0359887	0.1618
2388	10379646	NM_011409	20557	schlafen 3	Slfn3	1.193	2.789	0.0261445	0.130964
2389	10353311	NM_020604	57339	junctophilin 1	Jph1	1.193	1.657	0.140244	0.378815
2390	10418053	NM_010610	16531	potassium large conductance ca	Kcnma1	1.193	1.124	0.297091	0.573626
2391	10413530	NM_133761	75901	DCP1 decapping enzyme homolog	Dcp1a	1.193	1.721	0.127704	0.358351
2392	10419744	NM_011405	20540	solute carrier family 7 (catio	Slc7a7	1.193	2.149	0.0675554	0.242768
2393	10514300	NM_177361	242519	interferon alpha 12	Ifna12	1.193	1.985	0.0862967	0.282193
2394	10416090	NM_019675	56471	stathmin-like 4	Stmn4	1.193	3.215	0.0141679	0.0866048
2395	10410375	NM_001001130	22746	zinc finger protein 85, relate	Zfp85-rs1	1.193	1.148	0.287781	0.563515
2396	10458424	NM_175770	24074	TAF7 RNA polymerase II, TATA b	Taf7	1.193	1.986	0.086208	0.282077
2397	10493309	NM_009069	19769	Ras-like without CAAX 1	Rit1	1.193	3.091	0.0168898	0.0978674
2398	10381809	NM_016780	16416	integrin beta 3	Itgb3	1.192	2.583	0.03542	0.1603
2399	10516393	NM_153177	76850	eukaryotic translation initiat	Eif2c4	1.192	1.998	0.0847316	0.279408
2400	10486026	NM_175466	228491	zinc finger protein 770	Zfp770	1.192	3.056	0.0177583	0.101017
2401	10567580	NM_030691	80719	immunoglobulin superfamily, me	Igsf6	1.192	1.625	0.147012	0.388942
2402	10374478	NM_021372	58172	SERTA domain containing 2	Sertad2	1.192	2.93	0.0213042	0.114271
2403	10460259	ENSMUST00000100032	621603	aldehyde dehydrogenase 3 famil	Aldh3b2	1.192	2.766	0.02705	0.13393
2404	10359235	NM_177644	226525	RAS protein activator like 2	Rasal2	1.192	1.999	0.0845258	0.279078
2405	10368675	NM_008538	17118	myristoylated alanine rich pro	Marcks	1.192	4.174	0.00390485	0.0343773
2406	10468217	NM_016860	54130	ARP1 actin-related protein 1 h	Actr1a	1.191	1.959	0.0897475	0.289139
2407	10377725	NM_007864	13385	discs, large homolog 4 (Drosop	Dlg4	1.191	2.673	0.030983	0.146884

2408	10463557	NM_178930	107338	golgi-specific brefeldin A-res	Gbf1	1.191	2.322	0.0521603	0.206609
2409	10470529	NM_019498	56177	olfactomedin 1	Olfm1	1.191	3.464	0.0100081	0.0680857
2410	10506388	NM_026100	67344	Tctex1 domain containing 1	Tctex1d1	1.191	1.516	0.171964	0.424079
2411	10491721	NM_011896	24063	sprouty homolog 1 (Drosophila)	Spry1	1.191	2.624	0.0333129	0.153927
2412	10593499	NM_178906	330941	expressed sequence AI593442	AI593442	1.191	2.798	0.0257969	0.130148
2413	10416112	NM_175498	239157	paraneoplastic antigen MA2	Pnma2	1.191	2.146	0.0678893	0.243338
2414	10468294	BC019197	72691	RIKEN cDNA 2810048G17 gene	2810048G17Rik	1.191	2.027	0.0810414	0.271716
2415	10582162	NM_028071	72042	coactosin-like 1 (Dictyosteliu	Cotl1	1.191	1.113	0.301621	0.577839
2416	10549222	NM_007532	12035	branched chain aminotransferas	Bcat1	1.191	3.293	0.0127031	0.0800101
2417	10422009					1.191	1.826	0.109351	0.326755
2418	10503241	NM_013526	242316	growth differentiation factor	Gdf6	1.191	1.893	0.0989785	0.307265
2419	10447490	NM_001025309	224938	praja 2, RING-H2 motif contain	Pja2	1.191	2.171	0.0654142	0.238533
2420	10406482	NM_023243	66671	cyclin H	Ccnh	1.19	3.225	0.0139783	0.0858203
2421	10466712	NM_174857	71738	MAM domain containing 2	Mamdc2	1.19	1.409	0.200582	0.462553
2422	10602401	NM_008001	14163	FYVE, RhoGEF and PH domain con	Fgd1	1.19	3.195	0.0145818	0.0885208
2423	10503134	NM_001098227	53378	syndecan binding protein	Sdcbp	1.19	2.819	0.0250091	0.127548
2424	10584628	NM_009382	21838	thymus cell antigen 1, theta	Thy1	1.19	2.792	0.0260334	0.130751
2425	10505172	BC119039	72429	RIKEN cDNA 2010203O07 gene	2010203O07Rik	1.19	2.933	0.0211935	0.114027
2426	10418848	ENSMUST00000061753	545030	WD repeat and FYVE domain cont	Wdfy4	1.19	2.701	0.0297633	0.142831
2427	10412657					1.19	1.092	0.309914	0.586734
2428	10398459	ENSMUST00000065483	26931	protein phosphatase 2, regulat	Ppp2r5c	1.19	0.713	0.498377	0.742426
2429	10475420	NM_080510	70928	tripartite motif-containing 69	Trim69	1.189	3.898	0.00558011	0.0447652
2430	10590489	NM_009544	22646	zinc finger protein 105	Zfp105	1.189	1.552	0.163243	0.412279
2431	10427538	NM_201232	71175	Nipped-B homolog (Drosophila)	Nipbl	1.189	2.804	0.0255608	0.129389
2432	10369413	NM_009163	20397	sphingosine phosphate lyase 1	Sgpl1	1.189	1.956	0.0901982	0.289885
2433	10477717	NM_011171	19124	protein C receptor, endothelia	Procr	1.189	2.319	0.0523894	0.207062
2434	10479247	NM_001081289	71532	RIKEN cDNA 9030418K01 gene	9030418K01Rik	1.189	2.283	0.0553031	0.214615
2435	10374983	NM_023906	65257	ankyrin repeat and SOCS box-co	Asb3	1.189	1.376	0.210173	0.475495
2436	10590808	NM_009534	22601	yes-associated protein 1	Yap1	1.189	2.886	0.0227115	0.119337
2437	10575733	NM_028131	72155	centromere protein N	Cenpn	1.189	2.086	0.0742639	0.257711
2438	10466355	NM_001011841	258121	olfactory receptor 1465	Olfr1465	1.189	2.076	0.0753142	0.259567
2439	10534640	NM_024474	140709	EMI domain containing 2	Emid2	1.189	3.412	0.010754	0.0714364
2440	10357698	NM_178874	68875	transmembrane and coiled-coil	Tmcc2	1.189	1.88	0.100868	0.310852
2441	10543471	NM_133931	101185	protection of telomeres 1A	Pot1a	1.189	2.61	0.0340112	0.156
2442	10407307	NM_013826	17434	molybdenum cofactor synthesis	Mocs2	1.189	1.953	0.0905717	0.290908
2443	10436692					1.189	1.176	0.277075	0.552231
2444	10464443	XR_031496	100045278	similar to ribosomal protein S	LOC100045278	1.189	1.24	0.253779	0.528036
2445	10578352	NM_145594	234199	fibrinogen-like protein 1	Fgl1	1.189	0.975	0.361112	0.632903
2446	10548899	NM_181988	232441	RAS-like, estrogen-regulated,	Rerg	1.188	1.723	0.127234	0.357506
2447	10578709	NM_028220	244484	WD repeat domain 17	Wdr17	1.188	2.126	0.0698937	0.247709
2448	10455472	ENSMUST00000025350	70640	DCP2 decapping enzyme homolog	Dcp2	1.188	1.907	0.0969761	0.30331
2449	10529937	NM_030265	80334	Kv channel interacting protein	Kcnip4	1.188	2.981	0.0197969	0.109149
2450	10435226	NM_080557	69150	sorting nexin 4	Snx4	1.188	2.746	0.0278489	0.136748
2451	10468885	ENSMUST00000099260	414758	RIKEN cDNA 5830428H23 gene	5830428H23Rik	1.188	1.833	0.108158	0.32441
2452	10488378	NM_009378	21824	thrombomodulin	Thbd	1.188	2.486	0.040886	0.176284
2453	10434552					1.188	2.818	0.0250646	0.127643
2454	10465916	ENSMUST00000096230	225908	gene model 98, (NCBI)	Gm98	1.188	1.589	0.154906	0.400115
2455	10409061					1.187	0.947	0.374089	0.64426
2456	10487277	NM_021450	58800	transient receptor potential c	Trpm7	1.187	3.586	0.00846698	0.0602983
2457	10420348	NM_144842	219105	zinc finger, MYM-type 5	Zmym5	1.187	1.311	0.230069	0.501055
2458	10479026	NM_175112	66679	RAE1 RNA export 1 homolog (S	Rae1	1.187	2.705	0.0295628	0.142063

2459	10507273	NM_181585	18710	phosphatidylinositol 3 kinase,	Pik3r3	1.187	1.435	0.193125	0.452493
2460	10416181	NM_009285	20855	stanniocalcin 1	Stc1	1.187	3.297	0.0126252	0.0796618
2461	10536917	NM_176996	319757	smoothened homolog (Drosophila	Smo	1.187	3.353	0.0116799	0.0754765
2462	10506298	NM_175036	230514	leptin receptor overlapping tr	Leprot	1.187	1.842	0.10686	0.322408
2463	10520043	NM_001081231	269629	lipoma HMGIC fusion partner-li	Lhfpl3	1.187	1.594	0.153759	0.398309
2464	10451039	NM_028711	74011	solute carrier family 25, memb	Slc25a27	1.187	2.271	0.056269	0.216807
2465	10549377	BC052362	73344	RIKEN cDNA 1700034J05 gene	1700034J05Rik	1.187	1.42	0.197368	0.457905
2466	10407209	ENSMUST00000091218	108861	RIKEN cDNA 4833412L08 gene	4833412L08Rik	1.186	1.842	0.10679	0.322336
2467	10350733	NM_011267	19734	regulator of G-protein signali	Rgs16	1.186	2.698	0.0298705	0.143184
2468	10462111	ENSMUST00000067077	791290	predicted gene, ENSMUSG0000005	ENSMUSG00000054178	1.186	2.091	0.0736844	0.256552
2469	10496975	NM_001081263	242259	solute carrier family 44, memb	Slc44a5	1.186	1.648	0.142034	0.381888
2470	10543870	ENSMUST00000075773	18153	neoplastic progression 2	Npn2	1.186	1.244	0.252447	0.526583
2471	10506822	NM_011015	18392	origin recognition complex, su	Orc1l	1.186	2.106	0.07201	0.252375
2472	10398224	NM_010010	13116	cytochrome P450, family 46, su	Cyp46a1	1.186	2.498	0.0401467	0.174304
2473	10351832	ENSMUST00000111226	71870	coiled-coil domain containing	Ccdc19	1.186	2.621	0.0334866	0.154358
2474	10556573	ENSMUST00000032900	68469	RIKEN cDNA 1110006G14 gene	1110006G14Rik	1.186	1.749	0.122428	0.349859
2475	10463410	BC060679	226151	RIKEN cDNA 6030443O07 gene	6030443O07Rik	1.186	2.797	0.025834	0.130211
2476	10491038	NM_030732	81004	transducin (beta)-like 1X-link	Tbl1xr1	1.186	2.094	0.0733497	0.255698
2477	10458940	NM_175751	269023	zinc finger protein 608	Zfp608	1.186	1.717	0.128484	0.359524
2478	10518228	ENSMUST00000036579	230895	vacuolar protein sorting 13 D	Vps13d	1.186	3.456	0.0101153	0.0685504
2479	10477167	NM_025543	66405	malignant T cell amplified seq	Mcts2	1.186	2.575	0.0358317	0.161363
2480	10351603	NM_001005508	226652	Rho GTPase activating protein	Arhgap30	1.186	1.707	0.130276	0.362012
2481	10359405	NM_001039482	226541	kelch-like 20 (Drosophila)	Klhl20	1.185	3	0.019243	0.106903
2482	10529792	ENSMUST00000050556	665775	RIKEN cDNA A230054D04 gene	A230054D04Rik	1.185	2.465	0.0421786	0.179731
2483	10502052	ENSMUST00000029662	71481	alpha-kinase 1	Alpk1	1.185	1.572	0.158644	0.405496
2484	10381113	NM_001025244	432602	predicted gene, OTTMUSG0000000	OTTMUSG00000002177	1.185	3.592	0.00839602	0.0598736
2485	10597758	NM_153287	215418	AXIN1 up-regulated 1	Axud1	1.185	2.369	0.048682	0.197379
2486	10359890	NM_023284	66977	NUF2, NDC80 kinetochore comple	Nuf2	1.185	2.144	0.0680826	0.243829
2487	10503695	NM_007521	12014	BTB and CNC homology 2	Bach2	1.185	3.624	0.00803852	0.0581679
2488	10564451	NM_001033713	17258	myocyte enhancer factor 2A	Mef2a	1.185	1.994	0.085202	0.280273
2489	10407392	NM_134063	105203	cDNA sequence BC016423	BC016423	1.185	3.069	0.0174396	0.0998764
2490	10427253					1.185	1.26	0.246941	0.52026
2491	10489357	NM_021566	59091	junctophilin 2	Jph2	1.185	2.863	0.0234701	0.121869
2492	10450957	NM_031863	83815	centromere protein Q	Cenpq	1.185	2.327	0.0517675	0.20563
2493	10390103	NM_133667	18604	pyruvate dehydrogenase kinase,	Pdk2	1.185	2.496	0.0402468	0.174559
2494	10396640	NM_001101471	238276	A kinase (PRKA) anchor protein	Akap5	1.185	2.305	0.0535489	0.209868
2495	10563611	NM_009117	20208	serum amyloid A 1	Saa1	1.184	1.347	0.218741	0.486928
2496	10517401	NM_001013756	230824	grainyhead-like 3 (Drosophila)	Grhl3	1.184	2.661	0.0315545	0.148594
2497	10425092	NM_028195	72318	pleckstrin homology, Sec7 and	Pscd4	1.184	1.853	0.105067	0.319364
2498	10573210	NM_013641	19216	prostaglandin E receptor 1 (su	Ptger1	1.184	2.326	0.0518944	0.206057
2499	10457183	NM_198295	67988	thioredoxin domain containing	Txndc10	1.184	1.815	0.111164	0.329929
2500	10529457	NM_153107	242939	carboxypeptidase Z	Cpz	1.184	3.581	0.00852594	0.0605551
2501	10597883	NM_133979	102566	transmembrane protein 16K	Tmem16k	1.184	0.903	0.395782	0.663394
2502	10563583	BC087944	78935	serum amyloid A-like 1	Saal1	1.184	2.282	0.0553508	0.214629
2503	10548030	NM_007657	12527	CD9 antigen	Cd9	1.184	2.038	0.0797604	0.269041
2504	10474977	NM_019769	56398	RIKEN cDNA 1500003O03 gene	1500003O03Rik	1.184	1.987	0.0860711	0.2817
2505	10365933	NM_001001932	216238	early endosome antigen 1	Eea1	1.183	2.2	0.0625872	0.23162
2506	10520232					1.183	2.26	0.057269	0.218979
2507	10476163	NM_008980	19262	protein tyrosine phosphatase,	Ptpra	1.183	2.689	0.0302907	0.144706
2508	10426584	BC048654	73302	RIKEN cDNA 1700031M16	1700031M16Rik	1.183	2.947	0.0207687	0.112772

				gene					
2509	10575598	NM_133206	170737	zinc and ring finger 1	Znrf1	1.183	2.476	0.0414842	0.177631
2510	10412773	NM_001033270	218756	solute carrier family 4, sodiu	Slc4a7	1.183	1.316	0.228409	0.49943
2511	10606315	NM_001001176	407786	TAF9B RNA polymerase II, TATA	Taf9b	1.183	1.048	0.328435	0.60481
2512	10457243	ENSMUST00000074702	791318	predicted gene, ENSMUSG0000006	ENSMUSG00000063087	1.183	2.658	0.0316963	0.149063
2513	10545895	XM_485799	434057	N-acetyltransferase 8B	Nat8b	1.183	1.673	0.13697	0.373595
2514	10433057	NM_026192	67488	calcium binding and coiled coi	Calcoco1	1.183	2.146	0.0679146	0.243363
2515	10448380	NM_026305	67673	transcription elongation facto	Tceb2	1.183	1.862	0.10371	0.316611
2516	10385665	NM_013744	27274	zinc finger protein 354B	Zfp354b	1.183	2.654	0.031892	0.149485
2517	10413220	ENSMUST00000100823	100038401	predicted gene, ENSMUSG0000007	ENSMUSG00000072684	1.182	2.914	0.0217885	0.116015
2518	10467400	NM_206537	404195	cytochrome P450, family 2, sub	Cyp2c54	1.182	2.691	0.0301849	0.144428
2519	10380285	NM_026433	67888	transmembrane protein 100	Tmem100	1.182	1.2	0.268048	0.542786
2520	10521337	NM_173402	71729	regulator of G-protein signali	Rgs12	1.182	2.937	0.0210693	0.113587
2521	10366514	ENSMUST00000020371	67342	RIKEN cDNA 1700058G18 gene	1700058G18Rik	1.182	1.807	0.112535	0.33223
2522	10482868	NM_028118	72137	WD repeat, SAM and U-box domai	Wdsub1	1.182	1.705	0.13073	0.362906
2523	10446785	NM_016962	50850	spastin	Spast	1.182	3.109	0.0164794	0.0962943
2524	10551791	BC055817	233058	zinc finger protein 420	Zfp420	1.182	1.334	0.222917	0.492857
2525	10371627	NM_175418	109272	RIKEN cDNA 8030451F13 gene	8030451F13Rik	1.182	1.81	0.112011	0.331272
2526	10351119	NM_016796	53330	vesicle-associated membrane pr	Vamp4	1.182	2.118	0.0707451	0.249639
2527	10509002	NM_011270	19746	Rh blood group, D antigen	Rhd	1.182	0.85	0.42262	0.684899
2528	10421186	ENSMUST00000070887	791405	predicted gene, ENSMUSG0000005	ENSMUSG00000056640	1.182	0.894	0.399933	0.665979
2529	10407533					1.182	2.141	0.0683649	0.244408
2530	10406614	AK090249	238771	similar to Metaxin 1	LOC238771	1.182	1.152	0.286158	0.561637
2531	10505182	NM_025277	14700	guanine nucleotide binding pro	Gng10	1.182	2.627	0.0331742	0.153573
2532	10433929	NM_176833	68606	protein phosphatase 1F (PP2C d	Ppm1f	1.182	2.904	0.0221241	0.117153
2533	10392990	NM_008163	14784	growth factor receptor bound p	Grb2	1.182	1.846	0.106075	0.321233
2534	10543697	NM_172735	232679	zinc finger, C3HC type 1	Zc3hc1	1.181	2.245	0.0585402	0.222381
2535	10374529	AF424701	216560	expressed sequence AV249152	AV249152	1.181	1.403	0.202281	0.465097
2536	10381939	NM_181071	77097	tetratricopeptide repeat, anky	Tanc2	1.181	3.652	0.00774617	0.0567713
2537	10475226	ENSMUST00000094652	668880	START domain containing 9	Stard9	1.181	2.588	0.0351527	0.159397
2538	10395103	NM_181395	69675	peroxidasin homolog (Drosophil	Pxdn	1.181	2.274	0.0560519	0.216314
2539	10429843	BC024074	18810	plectin 1	Plec1	1.181	2.398	0.046601	0.191881
2540	10393544	NM_011180	19157	pleckstrin homology, Sec7 and	Pscd1	1.181	2.878	0.0229732	0.120323
2541	10348493	NM_008515	16978	leucine rich repeat (in FLII)	Lrrfip1	1.181	2.968	0.0201752	0.110487
2542	10608136					1.181	1.893	0.0990187	0.307265
2543	10581289	NM_013477	11972	ATPase, H+ transporting, lysos	Atp6v0d1	1.181	2.217	0.0610706	0.22806
2544	10541895	NM_011609	21937	tumor necrosis factor receptor	Tnfrsf1a	1.181	1.983	0.08653	0.282737
2545	10597518	NM_009371	21813	transforming growth factor, be	Tgfbr2	1.181	2.57	0.0361121	0.162182
2546	10350113	NM_026823	68724	ADP-ribosylation factor-like 8	Arl8a	1.181	2.052	0.0781338	0.265936
2547	10513608	NM_008525	17025	aminolevulinate, delta-, dehyd	Alad	1.181	1.738	0.12458	0.35351
2548	10374442	NM_020558	57316	nuclear DNA binding protein	C1d	1.181	1.517	0.171928	0.424079
2549	10413185	NM_183208	328365	zinc finger, MIZ-type containi	Zmiz1	1.18	2.603	0.034386	0.157065
2550	10490682	BC058179	72147	zinc finger and BTB domain con	Zbtb46	1.18	3.385	0.0111667	0.0731438
2551	10387743	NM_009204	20528	solute carrier family 2 (facil	Slc2a4	1.18	1.914	0.0959276	0.301291
2552	10528527	NM_053090	84652	expressed sequence AB030242	AB030242	1.18	2.002	0.0841879	0.278397
2553	10394627	BC057020	71169	RIKEN cDNA 4933425L03 gene	4933425L03Rik	1.18	2.27	0.0563942	0.217076
2554	10601503	NM_033605	93837	dachshund 2 (Drosophila)	Dach2	1.18	1.053	0.326225	0.602683
2555	10556640	NM_182995	101565	RIKEN cDNA 6330503K22 gene	6330503K22Rik	1.18	1.433	0.193819	0.453387
2556	10459193	NM_133249	170826	peroxisome proliferative activ	Ppargc1b	1.18	3.193	0.0146121	0.0885774
2557	10413059	NM_009502	22330	vinculin	Vcl	1.18	1.52	0.171105	0.422843
2558	10457669	NM_007882	13507	desmocollin 3	Dsc3	1.18	1.842	0.106733	0.32221

2559	10540523	NM_144799	30937	LIM and cysteine-rich domains	Lmcd1	1.18	2.119	0.0706274	0.24939
2560	10578193	NM_026067	67276	three prime histone mRNA exonu	Thex1	1.179	1.803	0.113157	0.333338
2561	10364402	NM_009200	20513	solute carrier family 1 (high	Slc1a6	1.179	2.613	0.0338861	0.155555
2562	10442112	NM_001104542	627132	vomeronasal 2, receptor 93	Vmn2r93	1.179	1.729	0.126159	0.355658
2563	10595560	NM_023814	76365	T-box18	Tbx18	1.179	3.303	0.0125175	0.079148
2564	10499536	NM_010107	13636	ephrin A1	Efna1	1.179	1.725	0.126966	0.356991
2565	10546812	ENSMUST00000053559	319831	RIKEN cDNA 5031434C07 gene	5031434C07Rik	1.179	2.474	0.0415991	0.177907
2566	10599463	NM_133213	170745	X-prolyl aminopeptidase (amino	Xpnpep2	1.179	2.706	0.0295368	0.142003
2567	10522430	NM_178896	100737	DCN1, defective in cullin nedd	Dcun1d4	1.179	2.512	0.0393388	0.172069
2568	10473809	NM_011355	20375	SFFV proviral integration 1	Sfpi1	1.179	2.879	0.0229278	0.120261
2569	10601235	NM_139144	108155	O-linked N-acetylglucosamine (	Ogt	1.179	2.382	0.0477342	0.194806
2570	10434942	NM_007862	13383	discs, large homolog 1 (Drosop	Dlg1	1.179	2.261	0.0571273	0.218625
2571	10472970	NM_010469	15436	homeo box D4	Hoxd4	1.179	1.84	0.107134	0.322599
2572	10607467	NM_009121	20229	spermidine/spermine N1-acetyl	Sat1	1.179	1.401	0.202685	0.465349
2573	10556350	NM_133758	74996	ubiquitin specific peptidase 4	Usp47	1.179	2.805	0.0255317	0.129273
2574	10360806	NM_009794	12334	calpain 2	Capn2	1.179	2.213	0.0613664	0.228633
2575	10360415	NM_011825	23893	gremlin 2 homolog, cysteine kn	Grem2	1.179	0.749	0.477642	0.728348
2576	10551181	NM_172148	232987	B9 protein domain 2	B9d2	1.179	2.305	0.053537	0.209868
2577	10584762	NM_030256	80288	B-cell CLL/lymphoma 9-like	Bcl9l	1.179	3.268	0.0131458	0.0822352
2578	10388377	NM_013761	27364	serine racemase	Srr	1.179	1.989	0.0857593	0.281088
2579	10581605	NM_017370	15439	haptoglobin	Hp	1.179	2.076	0.0754091	0.259639
2580	10378523	NM_001002764	103677	Smg-6 homolog, nonsense mediat	Smg6	1.179	2.477	0.0414051	0.177544
2581	10361381	NM_001079686	64009	synaptic nuclear envelope 1	Syne1	1.179	2.499	0.0401183	0.174258
2582	10474064	NM_001025246	277414	transformation related protein	Trp53i11	1.179	2.248	0.0582536	0.221691
2583	10427606	NM_145468	27401	S-phase kinase-associated prot	Skp2	1.179	2.196	0.0630152	0.232692
2584	10604585					1.178	1.632	0.145522	0.387083
2585	10494945	NM_018800	54524	synaptotagmin VI	Syt6	1.178	2.413	0.0455528	0.18882
2586	10440427	NM_025967	67102	DNA segment, Chr 16, ERATO Doi	D16Ertd472e	1.178	2.463	0.0422884	0.179955
2587	10408490	NM_025588	66482	exocyst complex component 2	Exoc2	1.178	1.641	0.143543	0.384139
2588	10471550	ENSMUST00000043703	269261	ribosomal protein L12	Rpl12	1.178	2.456	0.0427038	0.181093
2589	10598491	ENSMUST00000086274	100038473	predicted gene, ENSMUSG0000007	ENSMUSG00000073290	1.178	0.309	0.766109	0.902642
2590	10524621	NM_011854	23962	2'-5' oligoadenylate synthetas	Oasl2	1.178	2.312	0.0529749	0.208585
2591	10356423	NM_001033291	227334	ubiquitin specific peptidase 4	Usp40	1.178	3.229	0.0138985	0.0854991
2592	10383867	NM_028860	74302	myotubularin related protein 3	Mtmr3	1.178	1.86	0.103897	0.316907
2593	10468159	NM_010697	16825	LIM domain binding 1	Ldb1	1.178	2.316	0.0526202	0.207614
2594	10545233	BC094049	100101480	predicted gene, ENSMUSG0000007	ENSMUSG00000076577	1.178	1.598	0.15292	0.396925
2595	10528484	NM_009274	20817	serine/arginine-rich protein s	Srpk2	1.178	2.972	0.0200366	0.109926
2596	10399032					1.178	0.982	0.358077	0.630354
2597	10388545	NM_198895	109934	active BCR-related gene	Abr	1.178	2.196	0.0629702	0.232607
2598	10477140	NM_009047	19700	rad and gem related GTP bindin	Rem1	1.177	3.308	0.0124236	0.0786715
2599	10407387	BC021422	633640	predicted gene, EG633640	EG633640	1.177	2.1	0.0727534	0.254264
2600	10482200	NM_146122	227801	DENN/MADD domain containing 1A	Dennd1a	1.177	3.369	0.0114163	0.0742122
2601	10498647	NM_020026	26879	UDP-GalNAc:betaGlcNAc beta 1,3	B3galnt1	1.177	1.466	0.184724	0.442299
2602	10346109	ENSMUST00000069293	227058	dynein, axonemal, heavy chain	Dnahc7b	1.177	2.146	0.0678461	0.243316
2603	10468653	NM_170757	213993	RIKEN cDNA A630007B06 gene	A630007B06Rik	1.177	2.243	0.0587444	0.222957
2604	10464529	NM_016921	27060	T-cell, immune regulator 1, AT	Tcirg1	1.177	2.919	0.0216448	0.115512
2605	10603099	NM_010216	14205	c-fos induced growth factor	Figf	1.177	1.242	0.253012	0.52727
2606	10558410	NM_011212	19267	protein tyrosine phosphatase,	Ptpre	1.177	1.895	0.098774	0.306809
2607	10513381	NM_144904	230257	ROD1 regulator of differentiat	Rod1	1.177	2.062	0.0770074	0.263172
2608	10496262	NM_178877	97086	Na+/H+ exchanger domain contai	Nhedc2	1.177	2.321	0.0522423	0.206719

2609	10507032	NM_026279	67621	RIKEN cDNA 2310026E23 gene	2310026E23Rik	1.177	2.253	0.0578741	0.220644
2610	10471929	NM_153820	76117	Rho GTPase activating protein	Arhgap15	1.176	2.602	0.0343959	0.157065
2611	10436471	NM_178647	106143	CGG triplet repeat binding pro	Cggbp1	1.176	3.046	0.0180306	0.102072
2612	10591618	NM_177030	319899	dedicator of cytokinesis 6	Dock6	1.176	2.211	0.0616296	0.22935
2613	10513774					1.176	1.59	0.154578	0.399756
2614	10551770	NM_013705	22693	zinc finger protein 30	Zfp30	1.176	2.432	0.0442979	0.185761
2615	10425749	BC116256	338368	RIKEN cDNA C920005C14 gene	C920005C14Rik	1.176	2.514	0.0392247	0.171818
2616	10602925	NM_172783	110094	phosphorylase kinase alpha 2	Phka2	1.176	2.834	0.024501	0.12574
2617	10407370	NM_001113550	67392	RIKEN cDNA 4833420G17 gene	4833420G17Rik	1.176	2.18	0.0645034	0.23633
2618	10437160	NM_011809	23872	E26 avian leukemia oncogene 2,	Ets2	1.176	1.209	0.264717	0.539955
2619	10534596	NM_009986	13047	cut-like homeobox 1	Cux1	1.176	2.949	0.0207242	0.112646
2620	10605797	NM_001033329	236915	Cdc42 guanine nucleotide excha	Arhgef9	1.176	2.372	0.0484552	0.196802
2621	10438572	BC072629	72190	RIKEN cDNA 2510009E07 gene	2510009E07Rik	1.176	2.131	0.0693729	0.246733
2622	10599773	ENSMUST00000066533	236798	G protein-coupled receptor 112	Gpr112	1.175	3.41	0.0107787	0.071533
2623	10405163	NM_011462	20729	spindlin 1	Spin1	1.175	3.558	0.0087987	0.0620132
2624	10533659	NM_019765	56430	CAP-GLY domain containing link	Clip1	1.175	2.386	0.0474175	0.193793
2625	10386086	NM_153079	216749	neuromedin U receptor 2	Nmur2	1.175	1.476	0.182346	0.438828
2626	10451838	NM_022025	63993	solute carrier family 5 (choli	Slc5a7	1.175	1.368	0.212356	0.477959
2627	10406859	NM_001004149	238803	zinc finger protein 366	Zfp366	1.175	2.279	0.0556662	0.215398
2628	10598976	NM_001044384	21857	tissue inhibitor of metallopro	Timp1	1.175	2.146	0.067867	0.243316
2629	10428763	NM_027435	70472	ATPase family, AAA domain cont	Atad2	1.175	2.979	0.0198487	0.109321
2630	10496656	NM_027770	71355	collagen, type XXIV, alpha 1	Col24a1	1.175	4.037	0.00465506	0.0391358
2631	10503654					1.175	1.737	0.124746	0.353522
2632	10391828	NM_011795	23829	complement component 1, q subc	C1ql1	1.175	1.629	0.146178	0.387985
2633	10605828	ENSMUST00000096366	76386	RIKEN cDNA 1700010D01 gene	1700010D01Rik	1.175	1.16	0.28302	0.55833
2634	10353475	NM_145380	98221	eukaryotic translation initiat	Eif3m	1.174	2.657	0.0317277	0.149088
2635	10508805	NM_153423	242687	WAS protein family, member 2	Wasf2	1.174	2.511	0.0393582	0.172118
2636	10552303	NM_001033782	434172	predicted gene, EG434172	EG434172	1.174	2.22	0.0607887	0.22757
2637	10477991					1.174	1.894	0.0987873	0.306809
2638	10536407	NM_029404	75725	PHD finger protein 14	Phf14	1.174	3.087	0.017	0.098344
2639	10388954	NM_019409	18377	oligodendrocyte myelin glycopr	Omg	1.174	1.576	0.157669	0.404484
2640	10606609	NM_019656	56496	tetraspanin 6	Tspan6	1.174	1.946	0.0914425	0.292815
2641	10495083	NM_001039347	56543	potassium voltage-gated channe	Kcnd3	1.174	0.795	0.451994	0.708815
2642	10558333	NM_025850	66930	fibronectin type 3 and ankyrin	Fank1	1.174	1.919	0.0952348	0.299917
2643	10362941	NM_011156	19072	prolyl endopeptidase	Prep	1.174	2.025	0.0812884	0.272042
2644	10412624	NM_178279	218699	PX domain containing serine/th	Pxk	1.174	1.444	0.190718	0.449693
2645	10429083	NM_152923	110862	potassium voltage-gated channe	Kcnq3	1.174	2.973	0.0200215	0.109926
2646	10544746	NM_010449	15394	homeo box A1	Hoxa1	1.174	2.414	0.0455119	0.18878
2647	10456400	NM_026473	67951	tubulin, beta 6	Tubb6	1.173	1.682	0.135273	0.370739
2648	10407481	NM_019703	56421	phosphofructokinase, platelet	Pfkp	1.173	2.17	0.0654531	0.238533
2649	10542677	AK031560	75320	ethanolamine kinase 1	Etnk1	1.173	2.731	0.0284567	0.138479
2650	10499091	NM_001040461	654362	dual endothelin 1/angiotensin	Dear1	1.173	2.91	0.0219326	0.11646
2651	10600707	NM_007430	11614	nuclear receptor subfamily 0,	Nr0b1	1.173	1.516	0.171993	0.424096
2652	10586306	NM_020043	56741	neighbor of Punc E11	Nope	1.173	3.047	0.0179892	0.101919
2653	10443479					1.173	2.912	0.0218757	0.116333
2654	10417167	NM_029556	69634	citrate lyase beta like	Clybl	1.173	1.246	0.251648	0.525573
2655	10488652	NM_001039122	654459	defensin beta 25	Defb25	1.173	1.62	0.147901	0.390122
2656	10397575	NM_172544	18191	neurexin III	Nrxn3	1.173	3.018	0.0187688	0.105129
2657	10393594	NM_001039167	52897	DNA segment, Chr 11, Brigham &	D11Bwg0517e	1.173	3.775	0.00656415	0.0501236
2658	10553644					1.173	2.408	0.0458957	0.189906
2659	10600235	NM_007435	11666	ATP-binding cassette, sub-fami	Abcd1	1.172	3.336	0.0119487	0.0765816

2660	10471571	NM_177345	227743	mitogen-activated protein kina	Mapkap1	1.172	2.66	0.0315968	0.148727
2661	10515943	NM_016748	51797	cytidine 5'-triphosphate synth	Ctps	1.172	1.969	0.088404	0.286601
2662	10394245	NM_153082	217378	rab and DnaJ domain containing	Rbj	1.172	2.94	0.0209843	0.113389
2663	10472034	NM_177139	320343	LY6/PLAUR domain containing 6	Lypd6	1.172	1.116	0.300043	0.576161
2664	10485674	NM_173750	212772	RIKEN cDNA 2700007P21 gene	2700007P21Rik	1.172	1.994	0.0851259	0.280271
2665	10424700	NM_011759	22701	zinc finger protein 41	Zfp41	1.172	3.066	0.0175202	0.100079
2666	10539263	NM_013586	16950	lysyl oxidase-like 3	Loxl3	1.172	1.661	0.139375	0.377524
2667	10527051	NM_177879	330222	sidekick homolog 1 (chicken)	Sdk1	1.171	1.715	0.128816	0.360038
2668	10538482	NM_007407	11517	adenylate cyclase activating p	Adcyap1r1	1.171	2.735	0.0282785	0.137931
2669	10573731	ENSMUST00000074808	77265	RIKEN cDNA 9430002A10 gene	9430002A10Rik	1.171	2.73	0.0285181	0.138554
2670	10561055	NM_001113368	26367	CEA-related cell adhesion mole	Ceacam2	1.171	0.96	0.368321	0.639181
2671	10550263	NM_148946	110891	solute carrier family 8 (sodiu	Slc8a2	1.171	1.726	0.126799	0.356711
2672	10533781	NM_001081323	269702	M-phase phosphoprotein 9	Mphosph9	1.171	2.922	0.0215321	0.114997
2673	10457489	BC094382	338363	RIKEN cDNA 6030446N20 gene	6030446N20Rik	1.171	1.804	0.112926	0.332876
2674	10532767	NM_198109	231637	slingshot homolog 1 (Drosophil	Ssh1	1.171	2.272	0.0561961	0.216668
2675	10565519	NM_026734	68472	transmembrane protein 126B	Tmem126b	1.171	1.649	0.141974	0.381774
2676	10434313	NM_001033237	208146	YEATS domain containing 2	Yeats2	1.171	2.566	0.036302	0.162739
2677	10558441	NM_008598	17314	O-6-methylguanine-DNA methyltr	Mgmt	1.17	1.926	0.09429	0.298038
2678	10363528	NM_001039194	71361	apoptosis-inducing factor, mit	Aifm2	1.17	2.667	0.0312622	0.147777
2679	10515735	ENSMUST00000075406	230676	cDNA sequence BC059842	BC059842	1.17	1.513	0.172702	0.425051
2680	10583586	NM_152808	68682	solute carrier family 44, memb	Slc44a2	1.17	1.083	0.313853	0.590663
2681	10566296	NM_146329	258326	olfactory receptor 642	Olfr642	1.17	2.333	0.0513627	0.204715
2682	10359624	NM_175686	18933	paired related homeobox 1	Prrx1	1.17	0.414	0.690955	0.864447
2683	10398727	NM_001025360	16593	kinesin light chain 1	Klc1	1.17	2.255	0.0576836	0.220155
2684	10544687	NM_007808	13063	cytochrome c, somatic	Cycs	1.17	0.812	0.44268	0.701385
2685	10483264	NM_001047604	73668	tetratricopeptide repeat domai	Ttc21b	1.17	2.46	0.0425076	0.180696
2686	10430851	NM_019823	56448	cytochrome P450, family 2, sub	Cyp2d22	1.17	1.791	0.115122	0.337402
2687	10570621	NM_013756	27358	defensin beta 3	Defb3	1.169	3.392	0.0110522	0.0726868
2688	10567851	NM_010900	18020	nuclear factor of activated T-	Nfatc2ip	1.169	1.526	0.16971	0.421019
2689	10566346	NM_175677	319236	RIKEN cDNA 9230105E10 gene	9230105E10Rik	1.169	0.782	0.459329	0.714207
2690	10378013	NM_027186	69723	RPA interacting protein	Rpain	1.169	2.002	0.0842041	0.278407
2691	10502284	NM_001040400	214133	tet oncogene family member 2	Tet2	1.169	2.237	0.0592488	0.224067
2692	10565958	NM_183168	233571	pyrimidinergic receptor P2Y, G	P2ry6	1.169	1.134	0.293264	0.569401
2693	10530536	NM_001113460	21682	cytoplasmic tyrosine kinase, D	Tec	1.169	0.671	0.523026	0.759642
2694	10346747	NM_030013	77951	cytochrome P450, family 20, su	Cyp20a1	1.169	1.831	0.108588	0.325441
2695	10390560	NM_146028	217154	SH3 and cysteine rich domain 2	Stac2	1.169	3.099	0.0167083	0.0972956
2696	10439955	ENSMUST00000099705	385658	gene model 1752, (NCBI)	Gm1752	1.169	2.501	0.0399565	0.173817
2697	10561052					1.169	1.754	0.121577	0.34818
2698	10521863	NM_024213	52206	anaphase promoting complex sub	Anapc4	1.169	1.645	0.142757	0.382897
2699	10516305	NM_144941	245877	microtubule-associated protein	Mtap7d1	1.169	2.872	0.0231544	0.120967
2700	10457168	NM_178687	225825	CD226 antigen	Cd226	1.169	2.269	0.0564617	0.217193
2701	10556067	NM_021889	60510	synaptotagmin IX	Syt9	1.169	2.617	0.0336809	0.154849
2702	10352957	NM_021374	58175	regulator of G-protein signali	Rgs20	1.168	2.232	0.0596883	0.225162
2703	10389222	NM_009139	20305	chemokine (C-C motif) ligand 6	Ccl6	1.168	2.253	0.057816	0.220581
2704	10560818	NM_019940	56707	zinc finger protein 111	Zfp111	1.168	1.977	0.0873142	0.284457
2705	10355147	BC026952	67099	RIKEN cDNA 2310038H17 gene	2310038H17Rik	1.168	2.202	0.0624393	0.231292
2706	10367960	NM_019961	56535	peroxisomal biogenesis factor	Pex3	1.168	1.127	0.295701	0.572101
2707	10443449	NM_025888	66989	potassium channel tetramerisat	Kctd20	1.168	2.805	0.0255274	0.129273
2708	10532150	BC116683	67266	RIKEN cDNA 2900024C23 gene	2900024C23Rik	1.168	2.293	0.0544671	0.212482
2709	10560292					1.168	1.347	0.218622	0.486788
2710	10346365	NM_199007	68549	shugoshin-like 2 (S. pombe)	Sgol2	1.168	3.261	0.0132716	0.0827874

2711	10508500	NM_173071	230775	brain-specific angiogenesis in	Bai2	1.168	2.664	0.0314266	0.148244
2712	10558001	NM_178641	101490	inositol polyphosphate-5-phosp	Inpp5f	1.168	1.951	0.0908825	0.291551
2713	10502081	NM_007934	13809	glutamyl aminopeptidase	Enpep	1.168	1.215	0.262518	0.536954
2714	10593832					1.167	0.252	0.807735	0.922567
2715	10554063	NM_001033877	233332	a disintegrin-like and metallo	Adamts17	1.167	2.429	0.0445101	0.186509
2716	10396146	ENSMUST00000070468	791312	predicted gene, ENSMUSG0000005	ENSMUSG00000056391	1.167	2.582	0.0354343	0.16033
2717	10389606	NM_175563	270906	proline rich 11	Prr11	1.167	1.333	0.223104	0.49298
2718	10436727	AY033899	224419	open reading frame 63	ORF63	1.167	1.961	0.0894189	0.288564
2719	10367775	NM_001081344	78808	syntaxin binding protein 5 (to	Stxbp5	1.167	1.424	0.196288	0.45671
2720	10464688	NM_026720	68423	ankyrin repeat domain 13 famil	Ankrd13d	1.167	2.995	0.0194007	0.107469
2721	10455912	NM_025478	66307	isochorismatase domain contain	Isoc1	1.167	1.676	0.136465	0.372893
2722	10446928	NM_019919	268977	latent transforming growth fac	Ltbp1	1.167	1.003	0.348197	0.622132
2723	10539111	NM_144916	232086	transmembrane protein 150	Tmem150	1.167	1.962	0.0893679	0.288444
2724	10564467	NM_175124	67867	leucine rich repeat containing	Lrrc28	1.167	1.163	0.281925	0.557053
2725	10526098	NM_183088	71970	RIKEN cDNA 2410018M08 gene	2410018M08Rik	1.167	1.287	0.237698	0.510106
2726	10561787	NM_001037707	22689	zinc finger protein 27	Zfp27	1.167	1.298	0.2341	0.50534
2727	10509777	NM_183148	212632	expressed sequence C79267	C79267	1.167	2.331	0.051468	0.204942
2728	10365682	BC098373	77531	ankyrin repeat and sterile alp	Anks1b	1.166	1.817	0.110757	0.329467
2729	10403455	NM_001081426	208440	DIP2 disco-interacting protein	Dip2c	1.166	1.279	0.240517	0.513583
2730	10391577	NM_001077696	15184	histone deacetylase 5	Hdac5	1.166	3.2	0.0144775	0.0881404
2731	10517328	NM_027935	71817	transmembrane protein 50A	Tmem50a	1.166	1.763	0.120099	0.346527
2732	10473965	NM_146124	228359	Rho GTPase activating protein	Arhgap1	1.166	2.349	0.0501407	0.201363
2733	10367224	NM_019963	20847	signal transducer and activato	Stat2	1.166	2.083	0.0746066	0.258307
2734	10382115	NM_177088	320162	coiled-coil domain containing	Ccdc45	1.166	2.458	0.0426196	0.180844
2735	10401637	NM_145138	217718	NIMA (never in mitosis gene a)	Nek9	1.166	1.964	0.0891226	0.287844
2736	10443598	NM_013811	13417	dynein, axonemal, heavy chain	Dnahc8	1.165	2.926	0.0214124	0.114576
2737	10402708	NM_021273	12709	creatine kinase, brain	Ckb	1.165	0.584	0.577208	0.797771
2738	10488626	NM_175126	67917	zinc finger, CCHC domain conta	Zcchc3	1.165	1.531	0.168495	0.419875
2739	10350751	NM_178244	240819	transmembrane epididymal prote	Teddm1	1.165	2.614	0.0337881	0.155173
2740	10437073	NM_133229	170765	ripply3 homolog (zebrafish)	Ripply3	1.165	1.812	0.111666	0.330683
2741	10491603	ENSMUST00000057272	229227	RIKEN cDNA 4932438A13 gene	4932438A13Rik	1.165	1.396	0.204152	0.467365
2742	10355530	BC052740	21961	tensin 1	Tns1	1.165	3.112	0.0163988	0.0962086
2743	10600150	NM_031494	27081	zinc finger protein 275	Zfp275	1.165	3.573	0.00861933	0.0610748
2744	10547177	NM_178045	213391	Ras association (RalGDS/AF-6)	Rassf4	1.165	2.127	0.0698722	0.247709
2745	10578746	BC088983	382010	cDNA sequence BC088983	BC088983	1.165	2.5	0.0400107	0.174
2746	10443089	XM_985548	240057	synaptic Ras GTPase activating	Syngap1	1.165	1.962	0.0892758	0.28819
2747	10387111	NM_025510	66358	RIKEN cDNA 2310004I24 gene	2310004I24Rik	1.165	2.941	0.020948	0.113309
2748	10453026	NM_029239	75292	protein kinase D3	Prkd3	1.165	2.049	0.0784351	0.266489
2749	10496387	BC117717	70604	DnaJ (Hsp40) homolog, subfamil	Dnajb14	1.165	1.275	0.241705	0.514457
2750	10550200					1.164	1.133	0.293645	0.56967
2751	10388263					1.164	3.147	0.0156019	0.0928214
2752	10490794	NM_008862	18767	protein kinase inhibitor, alph	Pkia	1.164	2.347	0.0502657	0.201609
2753	10458534	NM_029357	75599	protocadherin 1	Pcdh1	1.164	1.294	0.235634	0.507379
2754	10361234	NM_008288	15483	hydroxysteroid 11-beta dehydro	Hsd11b1	1.164	1.742	0.123779	0.352065
2755	10434577	NM_001081366	209018	vacuolar protein sorting 8 hom	Vps8	1.164	3.342	0.0118598	0.0762431
2756	10475199	NM_009222	20619	synaptosomal-associated protei	Snap23	1.164	2.174	0.0651123	0.237986
2757	10564343	NM_009386	21872	tight junction protein 1	Tjp1	1.164	2.494	0.0403909	0.174969
2758	10391949	NM_019650	56494	golgi SNAP receptor complex me	Gosr2	1.164	1.566	0.159963	0.407305
2759	10455227	NM_020012	56736	ring finger protein 14	Rnf14	1.164	3.28	0.0129363	0.0811915
2760	10575993	BC027126	234797	RIKEN cDNA 6430548M08 gene	6430548M08Rik	1.163	2.735	0.0282854	0.137931
2761	10558150	NM_019564	56213	HtrA serine peptidase 1	Htra1	1.163	1.881	0.100845	0.310827
2762	10456357	NM_021451	58801	phorbol-12-myristate-13-acetat	Pmaip1	1.163	1.694	0.132753	0.36644
2763	10409486	NM_001114088	67399	PDZ and LIM domain 7	Pdlim7	1.163	1.575	0.158016	0.405065

2764	10408127	XR_031997	665703	similar to ETAA16 protein	LOC665703	1.163	1.386	0.206965	0.471406
2765	10508151	NM_175554	269582	claspin homolog (Xenopus laevi	Clspn	1.163	2.622	0.0334263	0.154248
2766	10401841	NM_010050	13371	deiodinase, iodothyronine, typ	Dio2	1.163	2.129	0.0695849	0.247236
2767	10563116	NM_013520	14256	FMS-like tyrosine kinase 3 lig	Flt3l	1.163	2.654	0.0318629	0.149381
2768	10566161	NM_198012	101700	tripartite motif-containing 68	Trim68	1.162	1.311	0.229994	0.501029
2769	10406141	NM_001024508	105246	bromodomain containing 9	Brd9	1.162	2.158	0.0666931	0.241223
2770	10420787	NM_177594	210376	myotubularin related protein 9	Mtmr9	1.162	2.186	0.0639349	0.234857
2771	10372618	NM_177798	327826	fibroblast growth factor recep	Frs2	1.162	1.723	0.127342	0.357621
2772	10374325	ENSMUST00000053570	432534	predicted gene, EG432534	EG432534	1.162	1.998	0.0846577	0.279368
2773	10507606	NM_024462	69216	coiled-coil domain containing	Ccdc23	1.162	1.856	0.104528	0.318143
2774	10604897					1.162	1.084	0.313184	0.589668
2775	10496737	NM_009740	12042	B-cell leukemia/lymphoma 10	Bcl10	1.162	1.701	0.13141	0.364065
2776	10578786	AK006215	66331	RIKEN cDNA 1700021K10 gene	1700021K10Rik	1.162	3.002	0.0192051	0.106749
2777	10369932	NM_027890	71733	sushi domain containing 2	Susd2	1.162	2.59	0.0350428	0.159035
2778	10584537	NM_146615	258608	olfactory receptor 986	Olfr986	1.162	1.69	0.133631	0.368143
2779	10500371	NR_003619	229613	RIKEN cDNA 6330549D23 gene	6330549D23Rik	1.162	2.263	0.0569756	0.218321
2780	10379262	NM_010897	18015	neurofibromatosis 1	Nf1	1.162	2.823	0.0248786	0.127092
2781	10503283	BC033309	66185	RIKEN cDNA 1110037F02 gene	1110037F02Rik	1.162	2.388	0.0472692	0.193319
2782	10574415	ENSMUST00000065508	73323	RIKEN cDNA 1700047G07 gene	1700047G07Rik	1.162	0.585	0.57612	0.797166
2783	10442240	NM_001008501	240034	zinc finger protein 760	Zfp760	1.162	2.982	0.019753	0.108935
2784	10513666	NM_001045514	100182	AT-hook transcription factor	Akna	1.162	2.381	0.0477936	0.194851
2785	10500911	NM_008619	17454	Moloney leukemia virus 10	Mov10	1.162	1.655	0.140626	0.379406
2786	10362630					1.162	1.334	0.222772	0.492656
2787	10453573	NM_146937	258939	olfactory receptor 63	Olfr63	1.162	2.928	0.0213554	0.114429
2788	10413018	NM_027996	268721	RIKEN cDNA 2310021P13 gene	2310021P13Rik	1.162	2.629	0.0330955	0.153434
2789	10585318	NM_001104617	19684	radixin	Rdx	1.162	1.818	0.110593	0.329025
2790	10350102	NM_177081	320139	protein tyrosine phosphatase,	Ptpn7	1.162	3.066	0.0175022	0.100018
2791	10535477	NM_029749	76800	ubiquitin specific peptidase 4	Usp42	1.162	2.009	0.0833205	0.276517
2792	10403466	NM_001081426	208440	DIP2 disco-interacting protein	Dip2c	1.162	1.804	0.112926	0.332876
2793	10386095	BC019518	67726	RIKEN cDNA 1810073G14 gene	1810073G14Rik	1.161	2.391	0.0470594	0.192831
2794	10352936	NM_011441	20671	SRY-box containing gene 17	Sox17	1.161	2.32	0.052334	0.206948
2795	10496036	NM_029838	77018	collagen, type XXV, alpha 1	Col25a1	1.161	2.373	0.0483475	0.196543
2796	10555681	NM_009287	20866	stromal interaction molecule 1	Stim1	1.161	1.331	0.223835	0.493923
2797	10455974	NM_026302	67665	dynactin 4	Dctn4	1.161	2.171	0.0654185	0.238533
2798	10498599	NM_026641	68259	intraflagellar transport 80 ho	Ift80	1.161	1.445	0.190397	0.449354
2799	10551777	NM_146185	233056	zinc finger protein 790	Zfp790	1.161	1.226	0.258723	0.532869
2800	10350077	NM_009307	20980	synaptotagmin II	Syt2	1.161	2.799	0.0257535	0.129991
2801	10511617	NM_026558	68099	RIKEN cDNA 6720467C03 gene	6720467C03Rik	1.161	1.917	0.0955042	0.300408
2802	10402705	BC145736	212539	gene model 266, (NCBI)	Gm266	1.161	1.309	0.230719	0.501597
2803	10475782	NM_010090	13537	dual specificity phosphatase 2	Dusp2	1.161	2.398	0.0465571	0.191742
2804	10479833	NM_181848	71648	optineurin	Optn	1.161	2.415	0.0454224	0.188649
2805	10564266	NM_013788	27412	paternally expressed 12	Peg12	1.161	2.972	0.0200418	0.109926
2806	10478678	NM_170701	21939	CD40 antigen	Cd40	1.161	2.609	0.0340411	0.156063
2807	10409833	NM_008086	14451	growth arrest specific 1	Gas1	1.161	2.733	0.0283915	0.138257
2808	10422725					1.161	1.332	0.223278	0.493208
2809	10531980	NM_172777	236573	cDNA sequence BC057170	BC057170	1.161	2.047	0.0786536	0.2669
2810	10484249	BC003993	80744	cDNA sequence BC003993	BC003993	1.161	0.402	0.699023	0.868099
2811	10440953	NM_021720	60364	downstream neighbor of SON	Donson	1.161	2.62	0.0335004	0.154383
2812	10402787	ENSMUST00000101009	382643	AHNAK nucleoprotein 2	Ahnak2	1.161	1.8	0.113605	0.334131
2813	10407081	NM_178683	218581	DEP domain containing 1B	Depdc1b	1.161	1.545	0.164987	0.415127
2814	10496862					1.16	2.59	0.0350203	0.159001
2815	10499914	NM_026822	68720	late cornified envelope 1B	Lce1b	1.16	0.859	0.418024	0.680624
2816	10603116	NM_026853	68854	ankyrin repeat and SOCS box-co	Asb11	1.16	2.878	0.0229636	0.120303
2817	10443926	NM_001024950	240068	zinc finger protein 563	Zfp563	1.16	1.699	0.150333	0.393494

2817	10443926	NM_001024950	240068	zinc finger protein 563	Zfp563	1.16	1.609	0.150333	0.393494
2818	10600034	ENSMUST00000101495	382221	gene model 1141, (NCBI)	Gm1141	1.16	3.065	0.0175464	0.100162
2819	10536472	NM_175088	16543	MyoD family inhibitor domain c	Mdfic	1.16	2.359	0.0493496	0.199512
2820	10396862	AF031663	20904	striamin	Strm	1.16	1.616	0.148952	0.391187
2821	10600936	NM_010110	13641	ephrin B1	Efnb1	1.16	3.086	0.0170133	0.0983942
2822	10473224	NM_024438	68082	dual specificity phosphatase 1	Dusp19	1.16	1.729	0.126122	0.355658
2823	10573281	NM_183097	73453	RIKEN cDNA 1700067K01 gene	1700067K01Rik	1.16	1.854	0.104861	0.318836
2824	10489891	NM_019835	56336	UDP-Gal:betaGlcNAc beta 1,4-ga	B4galt5	1.16	1.459	0.186674	0.444956
2825	10517463	ENSMUST00000105848	269593	leucine zipper protein 1	Luzp1	1.159	2.84	0.0242852	0.124965
2826	10415408	ENSMUST00000100529	277154	cDNA sequence BC030046	BC030046	1.159	1.752	0.121939	0.348793
2827	10559782	NM_146914	18349	olfactory receptor 5	Olfr5	1.159	1.365	0.213354	0.479304
2828	10374934	NM_134013	103554	proteasome (prosome, macropain	Psme4	1.159	2.681	0.030616	0.14567
2829	10394258	NM_138305	104111	adenylate cyclase 3	Adcy3	1.159	2.579	0.0356072	0.1607
2830	10562592	NM_177890	330513	predicted gene, EG330513	EG330513	1.159	1.967	0.0886754	0.286953
2831	10454286	NM_153058	212307	microtubule-associated protein	Mapre2	1.159	2.231	0.0597407	0.225162
2832	10406852	ENSMUST00000029773	71994	calponin 3, acidic	Cnn3	1.159	0.461	0.658075	0.847091
2833	10483770	NM_001110209	69605	limb and neural patterns	Lnp	1.159	1.154	0.285201	0.560488
2834	10514193					1.159	1.199	0.268366	0.542786
2835	10348917	NM_026321	67698	transmembrane protein 157	Tmem157	1.159	1.544	0.1652	0.415326
2836	10407792	NR_003568	664862	G protein-coupled receptor 137	Gpr137b-ps	1.159	1.663	0.138934	0.377005
2837	10405125	NM_175401	109082	F-box and WD-40 domain protein	Fbxw17	1.159	1.625	0.146833	0.388752
2838	10503711	NM_011997	26885	caspase 8 associated protein 2	Casp8ap2	1.159	3.111	0.0164129	0.0962129
2839	10482918	ENSMUST00000115987	667103	similar to brain protein 44-li	LOC667103	1.159	0.791	0.453978	0.710504
2840	10554969	NM_011858	23966	odd Oz/ten-m homolog 4 (Drosop	Odz4	1.159	2.066	0.0764872	0.262157
2841	10350742	NM_011882	24014	ribonuclease L (2', 5'-oligois	Rnasel	1.158	1.183	0.274237	0.548935
2842	10449551	NM_153166	240058	copine V	Cpne5	1.158	1.944	0.091834	0.293563
2843	10492102	NM_144895	229285	spastic paraplegia 20, spartin	Spg20	1.158	1.919	0.0952832	0.300009
2844	10473125	NM_010576	16401	integrin alpha 4	Itga4	1.158	1.276	0.241499	0.514365
2845	10351443	NM_033652	110648	LIM homeobox transcription fac	Lmx1a	1.158	1.823	0.109854	0.327703
2846	10494972	BC117780	229672	Bcl2-like 15	Bcl2l15	1.158	1.09	0.310804	0.58733
2847	10493666	ENSMUST00000029548	77595	nucleoporin 210-like	Nup210l	1.158	1.721	0.127639	0.358265
2848	10431845	AK037810	791370	predicted gene, ENSMUSG0000005	ENSMUSG00000053098	1.158	1.541	0.165923	0.416511
2849	10388749	NM_009423	22032	Tnf receptor associated factor	Traf4	1.158	2.039	0.0796147	0.268824
2850	10520234	NM_133913	100910	RIKEN cDNA 2010209O12 gene	2010209O12Rik	1.158	2.519	0.0389205	0.17084
2851	10360834	NM_008250	15284	H2.0-like homeobox	Hlx	1.158	2.224	0.0603803	0.226645
2852	10551462					1.158	1.942	0.0920437	0.293984
2853	10480950	BC031595	52838	DNA segment, Chr 2, Brigham &	D2Bwg1335e	1.157	1.273	0.242602	0.515498
2854	10426451	NM_029926	266632	interleukin-1 receptor-associa	Irak4	1.157	1.482	0.180785	0.436709
2855	10602180	NM_177592	209497	transmembrane protein 164	Tmem164	1.157	2.931	0.0212701	0.114175
2856	10461071	BC096638	108899	RIKEN cDNA 2700081O15 gene	2700081O15Rik	1.157	2.049	0.0784444	0.266489
2857	10403743	NM_008380	16323	inhibin beta-A	Inhba	1.157	1.29	0.237028	0.509165
2858	10410644	NM_001081680	238722	zinc finger protein 72	Zfp72	1.157	0.65	0.535639	0.769137
2859	10455738	NM_026386	67804	sorting nexin 2	Snx2	1.157	1.848	0.105806	0.320603
2860	10520111	NM_153092	231042	nucleoporin like 2	Nupl2	1.157	2.231	0.0597516	0.225163
2861	10523168	NM_053087	71920	epithelial mitogen	Epgn	1.157	1.682	0.135195	0.370666
2862	10494460	NM_011069	18632	peroxisomal biogenesis factor	Pex11b	1.157	1.815	0.111194	0.329929
2863	10436598	ENSMUST00000068704	77994	RIKEN cDNA 2810055G20 gene	2810055G20Rik	1.157	0.952	0.371838	0.642152
2864	10522378	NM_153567	75991	SLAIN motif family, member 2	Slain2	1.157	1.639	0.143957	0.384952
2865	10505512	NM_053084	69807	tripartite motif-containing 32	Trim32	1.157	1.79	0.115358	0.337519
2866	10385479					1.157	1.579	0.157054	0.403482

2867	10386628	NM_025294	24083	gene trap locus F3b	Gtlf3b	1.157	2.874	0.0230975	0.120795
2868	10368229	NM_011603	237336	TATA box binding protein-like	Tbpl1	1.156	1.349	0.218081	0.486044
2869	10413657	NM_029626	76485	glycosyltransferase 8 domain c	Glt8d1	1.156	1.903	0.097603	0.304473
2870	10487894	NM_175445	215653	Ras association (RalGDS/AF-6)	Rassf2	1.156	1.932	0.0934785	0.296462
2871	10480321	ENSMUST00000066163	77940	RIKEN cDNA A930004D18 gene	A930004D18Rik	1.156	1.211	0.264258	0.539355
2872	10353213	NM_010827	17681	musculin	Msc	1.156	0.968	0.364233	0.635557
2873	10359446	ENSMUST00000097505	226551	expressed sequence AI848100	AI848100	1.156	2.475	0.0415717	0.177907
2874	10489687	BC067000	381405	gene model 1008, (NCBI)	Gm1008	1.156	2.369	0.0486715	0.197375
2875	10484545	NM_146568	258561	olfactory receptor 1012	Olfr1012	1.156	2.183	0.0642601	0.235643
2876	10504206	BC057092	230085	expressed sequence N28178	N28178	1.156	1.878	0.101228	0.311554
2877	10474159	NM_019735	56369	APAF1 interacting protein	Apip	1.156	1.949	0.0910566	0.291845
2878	10476299					1.156	1.109	0.303171	0.579207
2879	10468113	NM_145703	80906	Kv channel-interacting protein	Kcnip2	1.156	1.828	0.108971	0.325894
2880	10575497	BC060632	244654	cDNA sequence BC060632	BC060632	1.156	1.394	0.204821	0.4682
2881	10418991	NM_027045	72972	granule cell antiserum positiv	Gcap14	1.156	1.923	0.0947001	0.298946
2882	10366951	NM_001098789	407790	NADH dehydrogenase (ubiquinone	Ndufa4l2	1.156	1.139	0.29099	0.567132
2883	10362273	ENSMUST00000041011	100046281	hypothetical protein LOC100046	LOC100046281	1.156	2.389	0.047184	0.19312
2884	10362073	NM_011361	20393	serum/glucocorticoid regulated	Sgk1	1.156	2.286	0.0551008	0.214181
2885	10355582	NM_176972	319651	ubiquitin specific peptidase 3	Usp37	1.156	2.159	0.0665716	0.241108
2886	10530819	NM_175606	74318	HOP homeobox	Hopx	1.156	2.026	0.0812528	0.272009
2887	10545583	NM_025882	66979	polymerase (DNA-directed), eps	Pole4	1.155	1.26	0.246915	0.520256
2888	10491617	ENSMUST00000057272	229227	RIKEN cDNA 4932438A13 gene	4932438A13Rik	1.155	1.397	0.203787	0.466884
2889	10574204	NM_024191	107566	ADP-ribosylation factor-like 2	Arl2bp	1.155	1.29	0.23698	0.509116
2890	10468533	NM_008149	14732	glycerol-3-phosphate acyltrans	Gpam	1.155	1.863	0.103551	0.316379
2891	10590533	NM_177911	331046	transglutaminase 4 (prostate)	Tgm4	1.155	2.204	0.0622637	0.230804
2892	10501492	XM_975707	433643	predicted gene, EG433643	EG433643	1.155	2.486	0.0408567	0.176265
2893	10402266					1.155	1.679	0.135809	0.371624
2894	10381702	NM_027658	71059	hexamthylene bis-acetamide ind	Hexim2	1.155	1.645	0.142737	0.382897
2895	10591241	NM_146221	235028	zinc finger protein 426	Zfp426	1.155	1.333	0.223069	0.49298
2896	10364769	NM_011789	23805	adenomatosis polyposis coli 2	Apc2	1.155	1.427	0.195308	0.455553
2897	10399897	NM_153198	73389	high mobility group box transc	Hbp1	1.155	2.722	0.0288605	0.139608
2898	10577226	BC099613	72148	RIKEN cDNA 2610019F03 gene	2610019F03Rik	1.155	1.162	0.282198	0.557189
2899	10365966	ENSMUST00000074615	432491	predicted gene, EG432491	EG432491	1.155	0.574	0.583444	0.801477
2900	10346970	NM_011086	18711	phosphatidylinositol-3-phospha	Pip5k3	1.155	1.65	0.141673	0.381209
2901	10361186	NM_198247	214791	SERTA domain containing 4	Sertad4	1.155	1.604	0.151594	0.395471
2902	10530783	AK043374	320411	RIKEN cDNA A730089K16 gene	A730089K16Rik	1.155	2.472	0.0417619	0.178314
2903	10398124	NM_178613	66787	RIKEN cDNA 4933433P14 gene	4933433P14Rik	1.155	1.404	0.201913	0.464656
2904	10543362	BC119565	73191	Fez family zinc finger 1	Fezf1	1.155	1.987	0.0860795	0.2817
2905	10392369	NM_019431	54377	calcium channel, voltage-depen	Cacng4	1.155	1.267	0.244703	0.517866
2906	10365983	NM_008524	17022	lumican	Lum	1.155	0.258	0.803372	0.920129
2907	10409711					1.155	1.653	0.14107	0.380022
2908	10542731	NM_027760	71323	Ras association (RalGDS/AF-6)	Rassf8	1.154	1.617	0.148548	0.390854
2909	10420860	NM_028811	74195	elongation protein 3 homolog (	Elp3	1.154	1.822	0.109917	0.327797
2910	10412650	NM_027782	71393	potassium channel tetramerisat	Kctd6	1.154	2.164	0.0660817	0.239852
2911	10538732	NM_008167	14804	glutamate receptor, ionotropic	Grid2	1.154	2.01	0.083155	0.276321
2912	10487021	NM_011774	22785	solute carrier family 30 (zinc	Slc30a4	1.154	1.353	0.216867	0.484361
2913	10460070					1.154	2.449	0.0431645	0.182497
2914	10347873	NM_010472	15463	HIV-1 Rev binding protein	Hrb	1.154	1.92	0.0950881	0.299747
2915	10458583	NM_023311	67180	Yip1 domain family, member 5	Yipf5	1.154	1.319	0.227622	0.498429
2916	10476297					1.154	1.402	0.202442	0.465275
2917	10494151					1.154	1.112	0.301881	0.577905
2918	10384452	NM_024475	79560	ubiquitin-like domain containi	Ublcp1	1.154	1.604	0.151513	0.395407
2919	10443027	BC113191	77128	RIKEN cDNA A930001N09	A930001N09Rik	1.154	2.042	0.0792996	0.268093

				gene					
2920	10578249	AK133068	100038521	predicted gene, ENSMUSG0000007	ENSMUSG00000074383	1.154	1.233	0.25641	0.530714
2921	10536429	NM_027992	71900	transmembrane protein 106B	Tmem106b	1.154	1.436	0.192917	0.452347
2922	10562468	NM_028034	71981	tudor domain containing 12	Tdrd12	1.154	2.485	0.0409248	0.176312
2923	10440314	NM_178721	239857	cell adhesion molecule 2	Cadm2	1.154	2.277	0.0558081	0.215684
2924	10375751	NM_175643	216725	a disintegrin-like and metallo	Adamts2	1.153	3.057	0.0177368	0.10095
2925	10397966	NM_026580	68149	OTU domain, ubiquitin aldehyde	Otub2	1.153	1.925	0.0943502	0.298153
2926	10489694	NM_178411	228876	zinc finger protein 334	Zfp334	1.153	1.162	0.282367	0.557354
2927	10569399	NM_020277	56843	transient receptor potential c	Trpm5	1.153	0.659	0.530482	0.765382
2928	10527694	NM_001081204	381694	beta 1,3-galactosyltransferase	B3galtl	1.153	2.026	0.0812101	0.271995
2929	10532576	XM_912851	74376	myosin XVIIIb	Myo18b	1.153	1.349	0.218078	0.486044
2930	10536827	BC006583	232664	coiled-coil domain containing	Ccdc136	1.153	1.979	0.0871667	0.284169
2931	10531583	ENSMUST00000086912	75500	RIKEN cDNA 1700010H22 gene	1700010H22Rik	1.153	1.485	0.179806	0.43509
2932	10351636	NM_019484	56009	RNA and export factor binding	Refbp2	1.153	2.276	0.0558868	0.21583
2933	10427286	NM_008272	15427	homeo box C9	Hoxc9	1.153	2.252	0.0579612	0.220856
2934	10570875	NM_001081149	244349	MYST histone acetyltransferase	Myst3	1.153	2.031	0.0806373	0.270969
2935	10347351	NM_153088	227292	CTD (carboxy-terminal domain,	Ctdsp1	1.153	1.309	0.230546	0.501476
2936	10485307					1.153	0.726	0.490985	0.737628
2937	10528268	NM_011203	19248	protein tyrosine phosphatase,	Ptpn12	1.153	2.365	0.0489533	0.198327
2938	10571319					1.153	1.111	0.302367	0.578522
2939	10606831	NM_030106	78478	RIKEN cDNA 1700129I15 gene	1700129I15Rik	1.153	0.664	0.527328	0.762963
2940	10524169	NM_011132	18973	polymerase (DNA directed), eps	Pole	1.153	2.284	0.0552403	0.214463
2941	10447742	NM_011948	26407	mitogen-activated protein kina	Map3k4	1.153	1.964	0.0890531	0.287785
2942	10469312	NM_008961	19212	phosphotriesterase related	Pter	1.153	0.967	0.364852	0.635927
2943	10571007	NM_001081269	234135	Wolf-Hirschhorn syndrome candi	Whsc1l1	1.152	1.408	0.200862	0.462789
2944	10456363	NM_010307	14680	guanine nucleotide binding pro	Gnal	1.152	1.631	0.145595	0.387145
2945	10584325	NM_020518	57276	V-set and immunoglobulin domai	Vsig2	1.152	2.599	0.0345897	0.157792
2946	10561337	NM_028538	73430	RIKEN cDNA 1700049G17 gene	1700049G17Rik	1.152	1.232	0.256452	0.530714
2947	10401007	NM_012024	26932	protein phosphatase 2, regulat	Ppp2r5e	1.152	1.911	0.0963563	0.30213
2948	10606730	NM_001007578	278097	armadillo repeat containing, X	Armcx6	1.152	1.537	0.166846	0.417832
2949	10379989	BC117001	66140	RIKEN cDNA 1110001A07 gene	1110001A07Rik	1.152	3.157	0.0153885	0.0920839
2950	10399407	NM_012038	26950	visinin-like 1	Vsnl1	1.152	1.157	0.283972	0.559215
2951	10347521	NM_026846	68818	zinc finger, AN1 type domain 2	Zfand2b	1.152	1.569	0.159287	0.406366
2952	10449631	NM_172618	224671	BTB (POZ) domain containing 9	Btbd9	1.152	1.677	0.136134	0.372273
2953	10551365	NM_019412	19153	periaxin	Prx	1.152	2.591	0.0350061	0.159
2954	10449999	NM_009542	22643	zinc finger protein 101	Zfp101	1.152	2.331	0.0514999	0.205
2955	10416848					1.152	1.237	0.254908	0.529239
2956	10527896	NM_001003909	70797	ankyrin repeat and IBR domain	Ankib1	1.151	1.531	0.168373	0.419736
2957	10436253	NM_025483	66315	SUMO1/sentrin specific peptida	Senp7	1.151	1.568	0.159699	0.407016
2958	10533991	XR_033706	665760	similar to Coiled-coil domain	LOC665760	1.151	0.723	0.492599	0.738532
2959	10389738	NM_019505	56077	diacylglycerol kinase, epsilon	Dgke	1.151	0.784	0.4579	0.713313
2960	10477831	BC027204	70873	RIKEN cDNA 4921517L17 gene	4921517L17Rik	1.151	2.99	0.0195368	0.108081
2961	10360270	NM_178405	98660	ATPase, Na+/K+ transporting, a	Atp1a2	1.151	2.052	0.0781431	0.265936
2962	10369647	NM_053183	94213	DEAD (Asp-Glu-Ala-Asp) box pol	Ddx50	1.151	2.321	0.052228	0.206719
2963	10422781	NM_030168	78757	RIKEN cDNA 4921505C17 gene	4921505C17Rik	1.151	3.062	0.0176125	0.100459
2964	10438708	NM_008555	17174	mannan-binding lectin serine p	Masp1	1.151	1.631	0.145695	0.38722
2965	10589059					1.151	1.89	0.0994987	0.30816
2966	10424392	BC099672	320469	RIKEN cDNA 9930014A18 gene	9930014A18Rik	1.151	1.776	0.117746	0.342357
2967	10406334	NM_030174	78771	multiple C2 domains, transmemb	Mctp1	1.151	1.685	0.134571	0.369832
2968	10531479	ENSMUST00000101028	619319	RIKEN cDNA 4932430I15 gene	4932430I15Rik	1.151	1.336	0.222175	0.491955

2969	10545672	NM_008638	17768	methylenetetrahydrofolate dehy	Mthfd2	1.15	0.935	0.380179	0.649784
2970	10376021	NM_033144	20362	septin 8	Sept8	1.15	3.221	0.0140441	0.0860473
2971	10385872	NM_011396	20520	solute carrier family 22 (orga	Slc22a5	1.15	0.82	0.438315	0.697399
2972	10478936					1.15	2.258	0.0574489	0.219537
2973	10524020	NM_028223	72392	transmembrane protein 175	Tmem175	1.15	2.304	0.0535788	0.209946
2974	10507894	NM_017475	54170	Ras-related GTP binding C	Rragc	1.15	2.413	0.0455623	0.188822
2975	10586384	NM_016688	50996	programmed cell death protein	Pdcd7	1.15	1.624	0.147045	0.388979
2976	10404294	NM_008865	18776	prolactin family 3, subfamily	Prl3b1	1.15	1.356	0.216076	0.483104
2977	10362422					1.15	0.283	0.785369	0.912507
2978	10528120	NM_011806	23857	cyclin D binding myb-like tran	Dmtf1	1.15	1.765	0.11959	0.345865
2979	10458293	NM_029669	76594	DnaJ (Hsp40) homolog, subfamil	Dnajc18	1.15	1.386	0.207123	0.471587
2980	10440993	NM_001081549	54720	regulator of calcineurin 1	Rcan1	1.15	0.963	0.366556	0.637472
2981	10480939	NM_177841	329366	RIKEN cDNA 4932418E24 gene	4932418E24Rik	1.15	3.054	0.0178142	0.101281
2982	10499902	NM_173070	229562	small proline-rich protein 4	Sprr4	1.15	2.275	0.0559824	0.21612
2983	10592719	NM_178644	102644	OAF homolog (Drosophila)	Oaf	1.15	2.687	0.0303708	0.144892
2984	10594750	ENSMUST00000054500	244911	predicted gene, EG244911	EG244911	1.15	1.6	0.152385	0.396241
2985	10525831					1.149	0.686	0.514354	0.754563
2986	10428513	NM_001081391	239420	CUB and Sushi multiple domains	Csmd3	1.149	1.255	0.248741	0.522335
2987	10599893	NM_008031	14265	fragile X mental retardation s	Fmr1	1.149	2.73	0.0285036	0.138515
2988	10371319	AK149870	100038465	predicted gene, ENSMUSG0000007	ENSMUSG00000074845	1.149	1.601	0.152117	0.395855
2989	10350377	NM_172643	226470	zinc finger and BTB domain con	Zbtb41	1.149	1.342	0.220376	0.489097
2990	10500837	NM_133865	140917	DNA cross-link repair 1B, PSO2	Dclre1b	1.149	1.967	0.0886724	0.286953
2991	10417887	BC119816	74843	zinc finger, MYND domain conta	Zmynd17	1.149	1.887	0.0999113	0.308984
2992	10519140	NM_011985	26561	matrix metallopeptidase 23	Mmp23	1.149	2.665	0.0313506	0.148063
2993	10479550	BC058516	66496	RIKEN cDNA 2700038C09 gene	2700038C09Rik	1.149	2.592	0.0349514	0.158825
2994	10565738	NM_172280	233545	RIKEN cDNA 2210018M11 gene	2210018M11Rik	1.149	2.314	0.0527729	0.207945
2995	10503551	NM_152825	77593	ubiquitin specific petidase 45	Usp45	1.149	1.898	0.0982085	0.30582
2996	10593213	NM_144948	67010	RNA binding motif protein 7	Rbm7	1.149	2.243	0.0586986	0.222894
2997	10438169					1.149	1.278	0.240899	0.513879
2998	10376408	NM_001011818	258064	olfactory receptor 316	Olfr316	1.149	0.716	0.496572	0.74102
2999	10360227	NM_011063	18611	phosphoprotein enriched in ast	Pea15a	1.149	1.807	0.112429	0.332128
3000	10561810	NM_011748	243906	zinc finger protein 14	Zfp14	1.148	2.135	0.0689911	0.246119
3001	10455813	NM_010721	16906	lamin B1	Lmnb1	1.148	2.35	0.0500117	0.201094
3002	10434089	ENSMUST00000056962	72315	RIKEN cDNA 2310015A05 gene	2310015A05Rik	1.148	1.837	0.107579	0.323293
3003	10392261	NM_025481	66313	SMAD specific E3 ubiquitin pro	Smurf2	1.148	2.2	0.0625936	0.23162
3004	10381477	NM_144831	217207	DEAH (Asp-Glu-Ala-His) box pol	Dhx8	1.148	2.112	0.0713673	0.250953
3005	10515536	NM_146152	230673	importin 13	Ipo13	1.148	2.297	0.0541604	0.21152
3006	10529819	NM_008009	14181	fibroblast growth factor bindi	Fgfbp1	1.148	0.578	0.580804	0.799773
3007	10498584	ENSMUST00000054825	109222	retinoic acid receptor respond	Rarres1	1.148	0.987	0.355523	0.628098
3008	10354897	NM_172406	70827	trafficking protein, kinesin b	Trak2	1.148	1.534	0.167771	0.419086
3009	10479294					1.148	1.437	0.192551	0.452065
3010	10477012	NM_008019	14225	FK506 binding protein 1a	Fkbp1a	1.148	2.285	0.0551619	0.214244
3011	10578253	NM_145841	244431	sarcoglycan zeta	Sgcz	1.148	1.733	0.125449	0.354707
3012	10491615	ENSMUST00000057272	229227	RIKEN cDNA 4932438A13 gene	4932438A13Rik	1.148	1.619	0.148185	0.390374
3013	10513884	NM_011599	21885	transducin-like enhancer of sp	Tle1	1.148	1.308	0.231105	0.501886
3014	10346943	NM_133828	12912	cAMP responsive element bindin	Creb1	1.148	2.014	0.0826487	0.275157
3015	10358091	NM_173437	215690	neuron navigator 1	Nav1	1.148	1.558	0.161993	0.410397
3016	10511901	NM_001012450	140577	ankyrin repeat domain 6	Ankrd6	1.148	2.503	0.0398804	0.173611
3017	10522467	NM_026878	68939	RAS-like, family 11, member B	Rasl11b	1.148	1.718	0.1283	0.359233
3018	10569429	NM_009876	12577	cyclin-dependent kinase inhibi	Cdkn1c	1.147	1.37	0.211857	0.477389

3019	10521391	NM_030721	80911	acyl-Coenzyme A oxidase 3, pri	Acox3	1.147	2.448	0.0432315	0.182671
3020	10376998	NM_178656	193003	RIKEN cDNA A530088H08 gene	A530088H08Rik	1.147	2.479	0.0413224	0.177398
3021	10456437					1.147	1.385	0.207423	0.47189
3022	10362628	XR_033147	667964	similar to C130022K22Rik prote	LOC667964	1.147	0.529	0.61266	0.820438
3023	10557738	NM_007795	13019	cardiotrophin 1	Ctf1	1.147	1.418	0.197984	0.458849
3024	10546891	NM_133926	52163	calcium/calmodulin-dependent p	Camk1	1.147	1.791	0.11515	0.337402
3025	10535273	NM_010302	14673	guanine nucleotide binding pro	Gna12	1.147	2.123	0.0702528	0.248316
3026	10543879	NM_001013366	101240	WD repeat domain 91	Wdr91	1.147	1.417	0.198088	0.458849
3027	10485687	NM_029790	76894	methyltransferase 5 domain con	Mett5d1	1.147	1.849	0.105647	0.320213
3028	10491825	BC092533	269423	RIKEN cDNA 3110057O12 gene	3110057O12Rik	1.147	2.063	0.076785	0.262747
3029	10527158	NM_007984	14086	fascin homolog 1, actin bundli	Fscn1	1.147	1.622	0.147609	0.389693
3030	10591622	NM_177030	319899	dedicator of cytokinesis 6	Dock6	1.147	1.663	0.139028	0.377126
3031	10522596	NM_011626	21982	transmembrane protein 165	Tmem165	1.147	2.195	0.0631289	0.232827
3032	10362534	ENSMUST00000062667	320504	RIKEN cDNA 5930403N24 gene	5930403N24Rik	1.147	1.531	0.168317	0.419736
3033	10584229					1.147	0.78	0.460335	0.71495
3034	10605884	NM_052976	94190	oligophrenin 1	Ophn1	1.146	1.333	0.223124	0.49298
3035	10539104	BC066053	68364	RIKEN cDNA 0610030E20 gene	0610030E20Rik	1.146	1.911	0.0964193	0.302252
3036	10470954	NM_177725	241296	leucine rich repeat containing	Lrrc8a	1.146	2.116	0.0709782	0.250137
3037	10431722	NM_001033275	223827	glycosyltransferase 8 domain c	Glt8d3	1.146	1.614	0.149234	0.391598
3038	10587315	NM_010357	14860	glutathione S-transferase, alp	Gsta4	1.146	0.694	0.509218	0.750516
3039	10512251	NM_001085515	329828	expressed sequence AI464131	AI464131	1.146	1.992	0.0854278	0.280581
3040	10419790	NM_010590	16475	ajuba	Jub	1.146	2.774	0.0267233	0.132919
3041	10595981	NM_008624	17532	muscle and microspikes RAS	Mras	1.146	1.452	0.188687	0.446774
3042	10477637	NM_025735	66734	microtubule-associated protein	Map1lc3a	1.146	1.46	0.186519	0.444867
3043	10480064	NM_015792	50755	F-box protein 18	Fbxo18	1.146	2.218	0.0609547	0.227869
3044	10394791	ENSMUST00000050990	236260	hypothetical protein LOC236260	LOC236260	1.146	1.115	0.300576	0.576795
3045	10515848	NM_013848	27028	erythroblast membrane-associat	Ermap	1.146	0.958	0.368951	0.639697
3046	10349872					1.146	1.708	0.130115	0.36185
3047	10535381	NM_007393	11461	actin, beta, cytoplasmic	Actb	1.146	2.574	0.0358675	0.161427
3048	10566203	NM_001011847	258139	olfactory receptor 591	Olfr591	1.146	1.62	0.148055	0.390187
3049	10529497	NM_194344	231147	SH3 domain and tetratricopepti	Sh3tc1	1.146	2.576	0.0357723	0.16117
3050	10547993					1.146	1.933	0.0932191	0.295866
3051	10450059	NM_019420	54218	UDP-Gal:betaGlcNAc beta 1,3-ga	B3galt4	1.145	1.866	0.103122	0.315361
3052	10449971	BC056193	73451	RIKEN cDNA 1700065O13 gene	1700065O13Rik	1.145	2.081	0.0747586	0.258738
3053	10465132	NM_011379	20469	signal-induced proliferation a	Sipa1	1.145	2.226	0.0602689	0.226426
3054	10515700	ENSMUST00000075406	230676	cDNA sequence BC059842	BC059842	1.145	1.665	0.138688	0.376676
3055	10566488	NM_018880	55992	tripartite motif-containing 3	Trim3	1.145	1.866	0.103007	0.315188
3056	10370946	NM_172457	208228	MOB1, Mps One Binder kinase ac	Mobkl2a	1.145	2.273	0.0561638	0.216623
3057	10403750	NM_025479	66308	RIKEN cDNA 2810021B07 gene	2810021B07Rik	1.145	2.589	0.0350686	0.159084
3058	10489909	NM_023230	66589	ubiquitin-conjugating enzyme E	Ube2v1	1.145	0.124	0.904451	0.962829
3059	10358476	NM_021400	96875	proteoglycan 4 (megakaryocyte	Prg4	1.145	1.183	0.274455	0.54916
3060	10432471					1.145	1.902	0.348771	0.622419
3061	10390170	NM_130858	104079	neurexophilin 3	Nxph3	1.145	2.224	0.0604069	0.226689
3062	10396402	NM_008856	18755	protein kinase C, eta	Prkch	1.145	1.778	0.117338	0.341384
3063	10543695					1.145	2.06	0.0772161	0.263757
3064	10511541	NM_001081201	381510	dpy-19-like 4 (C. elegans)	Dpy19l4	1.144	0.889	0.402854	0.668022
3065	10399314	NM_001033488	432628	gene model 1964, (NCBI)	Gm1964	1.144	2.079	0.0750099	0.258984
3066	10557831	NM_026370	67773	MYST histone acetyltransferase	Myst1	1.144	2.243	0.0587008	0.222894
3067	10354807	NM_030211	51960	potassium channel tetramerisat	Kctd18	1.144	1.098	0.30762	0.584192
3068	10568131	NM_030240	67278	RIKEN cDNA 2900092E17 gene	2900092E17Rik	1.144	1.954	0.0903843	0.290394
3069	10600031	AK138582	67048	RIKEN cDNA 2610030H06 gene	2610030H06Rik	1.144	1.034	0.334379	0.60995

3070	10582241	NM_080855	142682	zinc finger, CCHC domain conta	Zcchc14	1.144	2.042	0.079327	0.268109
3071	10431726	NM_024189	67057	YY1 associated factor 2	Yaf2	1.144	2.52	0.0388827	0.170745
3072	10585610	NM_019651	56294	protein tyrosine phosphatase,	Ptpn9	1.144	1.381	0.208641	0.47344
3073	10474687					1.144	3.485	0.00972123	0.0667356
3074	10502058	NM_145964	211556	cDNA sequence BC002199	BC002199	1.144	2.326	0.0518595	0.205957
3075	10535759	NM_080795	140887	ligand of numb-protein X 2	Lnx2	1.144	1.667	0.138251	0.376165
3076	10388902	NM_010708	16859	lectin, galactose binding, sol	Lgals9	1.144	2.093	0.0734607	0.255968
3077	10347460	NM_001014974	67534	tubulin tyrosine ligase-like f	Ttll4	1.144	1.62	0.148026	0.390187
3078	10351961	NM_207137	258238	olfactory receptor 417	Olfr417	1.144	1.326	0.225158	0.495241
3079	10544462	NM_029930	77574	RIKEN cDNA 3321401G04 gene	3321401G04Rik	1.144	2.796	0.0258793	0.130308
3080	10352722	ENSMUST00000097438	78721	RIKEN cDNA D730003I15 gene	D730003I15Rik	1.144	2.145	0.0679314	0.243365
3081	10553646	NM_010418	15204	hect (homologous to the E6-AP	Herc2	1.144	2.557	0.0367908	0.164254
3082	10552632	ENSMUST00000107938	243961	SH3/ankyrin domain gene 1	Shank1	1.143	2.027	0.0810937	0.271716
3083	10447708	NM_021881	19317	quaking	Qk	1.143	2.566	0.0363208	0.162774
3084	10496457	ENSMUST00000090166	229871	alcohol dehydrogenase 6B (clas	Adh6b	1.143	1.172	0.278528	0.553444
3085	10555438	NM_199012	207278	FCH and double SH3 domains 2	Fchsd2	1.143	2.681	0.0306544	0.145769
3086	10606186	NM_009197	20502	solute carrier family 16 (mono	Slc16a2	1.143	1.511	0.173182	0.425638
3087	10523255	NM_175096	52331	starch binding domain 1	Stbd1	1.143	1.225	0.259214	0.533466
3088	10401852	NM_181815	75216	RIKEN cDNA 4930534B04 gene	4930534B04Rik	1.143	1.428	0.195188	0.455424
3089	10505734	NM_029967	77739	ADAMTS-like 1	Adamtsl1	1.143	1.716	0.128547	0.359524
3090	10599884					1.143	1.265	0.245372	0.518491
3091	10540923	NM_023290	67027	makorin, ring finger protein,	Mkrn2	1.143	1.78	0.116955	0.340665
3092	10399376	ENSMUST00000062469	319503	RIKEN cDNA 9930038B18 gene	9930038B18Rik	1.143	2.347	0.0502876	0.201609
3093	10572800	NM_008452	16598	Kruppel-like factor 2 (lung)	Klf2	1.143	2.691	0.0302042	0.144448
3094	10547436	NM_198703	232341	WNK lysine deficient protein k	Wnk1	1.143	2.762	0.0272018	0.134413
3095	10388969					1.143	3.177	0.0149525	0.0900988
3096	10350331	NM_177643	226442	zinc finger protein 281	Zfp281	1.143	1.563	0.160839	0.408621
3097	10359266	NM_001085376	23850	pappalysin 2	Pappa2	1.143	2.355	0.0496747	0.200281
3098	10359870	NM_183355	18514	pre B-cell leukemia transcript	Pbx1	1.143	2.051	0.0782205	0.266113
3099	10501183	BC060136	329735	RIKEN cDNA 4933431E20 gene	4933431E20Rik	1.142	1.229	0.257589	0.531672
3100	10534253	NM_001081462	57080	general transcription factor I	Gtf2ird1	1.142	1.534	0.167577	0.418725
3101	10492556	ENSMUST00000054551	68725	RIKEN cDNA 1110032F04 gene	1110032F04Rik	1.142	1.241	0.253605	0.527883
3102	10581996	NM_029441	75796	chromodomain protein, Y chromo	Cdyl2	1.142	1.66	0.139681	0.378012
3103	10511631	NM_145947	208890	solute carrier family 26, memb	Slc26a7	1.142	0.953	0.371285	0.64202
3104	10438778	AK142524	224058	transmembrane protein 207	Tmem207	1.142	1.575	0.158039	0.405065
3105	10349527					1.142	2.318	0.0524997	0.207254
3106	10405174	NM_029173	75124	nucleoredoxin-like 2	Nxnl2	1.142	1.958	0.0898946	0.289349
3107	10389717					1.142	1.122	0.297728	0.5738
3108	10398615	ENSMUST00000084967	791310	predicted gene, ENSMUSG0000006	ENSMUSG00000066331	1.142	1.544	0.165215	0.415326
3109	10416777	NM_009769	12224	Kruppel-like factor 5	Klf5	1.142	2.682	0.0305786	0.145587
3110	10357696					1.141	2.136	0.0688603	0.245818
3111	10588007	NM_178667	211586	transcription factor Dp 2	Tfdp2	1.141	1.226	0.258664	0.532799
3112	10375570	NM_207574	404337	olfactory receptor 1383	Olfr1383	1.141	2.166	0.0659217	0.239534
3113	10380566	NM_153104	237928	phosphatase, orphan 1	Phospho1	1.141	2.2	0.0625698	0.231614
3114	10445688	NM_001081636	12445	cyclin D3	Ccnd3	1.141	2.277	0.055782	0.215622
3115	10414545	NM_203508	219026	gene model 75, (NCBI)	Gm75	1.141	1.084	0.313184	0.589668
3116	10500813	NM_010432	15257	homeodomain interacting protei	Hipk1	1.141	2.516	0.0390754	0.171271
3117	10458755					1.141	1.015	0.342985	0.617132
3118	10592655	NM_027144	69632	Rho guanine nucleotide exchang	Arhgef12	1.141	1.815	0.111073	0.329804
3119	10566213	NM_001011854	258156	olfactory receptor 605	Olfr605	1.141	1.036	0.333866	0.609556
3120	10354286	NM_023645	72050	KDEL (Lys-Asp-Glu-Leu) contain	Kdelc1	1.141	1.658	0.13992	0.378322

3121	10562657	BC068175	434179	predicted gene, EG434179	EG434179	1.141	0.812	0.443012	0.701704
3122	10377508	NM_001024206	245828	trafficking protein particle c	Trappc1	1.141	1.699	0.131871	0.364815
3123	10575976	NM_030209	78892	cysteine-rich secretory protei	Crispld2	1.141	0.782	0.459018	0.7139
3124	10558345	NM_001033420	330662	dedicator of cytokinesis 1	Dock1	1.141	1.587	0.155306	0.400794
3125	10473281	NM_008402	16410	integrin alpha V	Itgav	1.141	1.603	0.151695	0.395641
3126	10404792	NM_198419	218194	phosphatase and actin regulato	Phactr1	1.141	2.916	0.0217444	0.115868
3127	10461400					1.141	2.548	0.0372614	0.165996
3128	10379652	AJ007734	103729	expressed sequence AI450353	AI450353	1.141	1.293	0.235813	0.507639
3129	10421581	NM_001033439	380916	leucine-rich repeats and calpo	Lrch1	1.14	1.321	0.2269	0.497571
3130	10515385	NM_009478	22275	uroporphyrinogen decarboxylase	Urod	1.14	2.262	0.0570439	0.218414
3131	10349249	NM_001081276	76707	CLIP associating protein 1	Clasp1	1.14	2.013	0.0827849	0.275524
3132	10561453	NM_011756	22695	zinc finger protein 36	Zfp36	1.14	1.115	0.300591	0.576795
3133	10606735	NM_026139	67416	armadillo repeat containing, X	Armcx2	1.14	1.609	0.150312	0.393487
3134	10561702	NM_001033525	52150	potassium inwardly-rectifying	Kcnk6	1.14	2.081	0.0748512	0.258816
3135	10468329	NM_175360	108689	oligonucleotide/oligosaccharid	Obfc1	1.14	1.874	0.101826	0.312711
3136	10607832	NM_019773	56382	RAB9, member RAS oncogene fami	Rab9	1.14	2.236	0.0593417	0.224338
3137	10395831	NM_001037756	52592	breast cancer metastasis-suppr	Brms1l	1.14	1.683	0.134959	0.370305
3138	10556456	ENSMUST00000069256	269987	RIKEN cDNA 2610024B07 gene	2610024B07Rik	1.14	2.47	0.0418581	0.178653
3139	10351703	NM_009938	12847	coatomer protein complex subun	Copa	1.14	2.277	0.0557673	0.215622
3140	10593318					1.14	2.044	0.0790583	0.267794
3141	10531675	ENSMUST00000094578	69162	SEC31 homolog A (S. cerevisiae	Sec31a	1.14	1.939	0.0924818	0.294729
3142	10415662	NM_027764	71330	regulator of chromosome conden	Rcbtb1	1.14	1.82	0.110266	0.328467
3143	10459799	DQ284430	75632	RIKEN cDNA 1700003O11 gene	1700003O11Rik	1.14	1.601	0.152085	0.395831
3144	10364324					1.14	2.015	0.08253	0.274805
3145	10601266	ENSMUST00000050654	382231	RIKEN cDNA 8030474K03 gene	8030474K03Rik	1.14	2.456	0.0427614	0.181264
3146	10355534					1.14	3.101	0.0166654	0.0970991
3147	10473432	NM_001081260	228140	tankyrase 1 binding protein 1	Tnks1bp1	1.14	2.279	0.0555994	0.215288
3148	10358191	NM_001081360	67886	calmodulin regulated spectrin-	Camsap1l1	1.14	2.109	0.0717349	0.251634
3149	10427293	NM_010465	15425	homeo box C6	Hoxc6	1.139	1.306	0.231518	0.502383
3150	10372421	NM_146241	237553	TRH-degrading enzyme	Trhde	1.139	3.678	0.00747264	0.0553226
3151	10409709					1.139	2.23	0.0598787	0.225521
3152	10435415	NM_013661	20357	sema domain, seven thrombospon	Sema5b	1.139	3.359	0.0115793	0.0750561
3153	10485582	NM_177190	320554	t-complex 11 like 1	Tcp11l1	1.139	1.963	0.0891667	0.287902
3154	10594103	ENSMUST00000098674	73673	RIKEN cDNA 2410076I21 gene	2410076I21Rik	1.139	1.557	0.162061	0.410473
3155	10466573	NM_017375	20409	osteoclast stimulating factor	Ostf1	1.139	1.675	0.1365	0.372937
3156	10355134	ENSMUST00000027102	74426	RIKEN cDNA 4933402D24 gene	4933402D24Rik	1.139	2.053	0.0779877	0.265568
3157	10402383	NM_026687	68348	serine (or cysteine) peptidase	Serpina1f	1.139	2.477	0.0414406	0.177622
3158	10433578	NM_009223	20621	stannin	Snn	1.139	2.038	0.079781	0.269041
3159	10525833	BC112905	21871	ATPase, H+ transporting, lysos	Atp6v0a2	1.139	1.503	0.175272	0.428483
3160	10540168	NM_172731	232237	FYVE, RhoGEF and PH domain con	Fgd5	1.139	2.803	0.0256288	0.129609
3161	10478560	NM_133763	76233	deoxynucleotidyltransferase, t	Dnttip1	1.139	1.924	0.0944747	0.298436
3162	10407042	NM_025447	66254	DIM1 dimethyladenosine transfe	Dimt1	1.139	1.017	0.341974	0.616342
3163	10603887	NM_183185	245368	zinc finger protein 300	Zfp300	1.139	2.063	0.0768861	0.262885
3164	10479490	NM_145760	228998	ADP-ribosylation factor GTPase	Arfgap1	1.139	1.788	0.115729	0.338307
3165	10516520	NM_001081098	230761	zinc finger protein 362	Zfp362	1.139	2.223	0.0604605	0.226805
3166	10517587	NM_007431	11647	alkaline phosphatase, liver/bo	Alpl	1.139	1.68	0.135646	0.371434
3167	10545014	BC024822	232023	expressed sequence AW146242	AW146242	1.138	1.204	0.266562	0.541262
3168	10345224					1.138	1.335	0.222356	0.492097
3169	10477815	NM_172674	228829	PHD finger protein 20	Phf20	1.138	1.49	0.178615	0.433598
3170	10444780	NM_010380	14964	histocompatibility 2, D region	H2-D1	1.138	1.066	0.320833	0.597681
3171	10521440	NM_027373	70292	actin filament associated prot	Afap1	1.138	2.022	0.0816919	0.272831
				DNA segment, Chr 6, Wayne					

3172	10541002	BC056942	28006	DNA segment, Chr 6, Wayne Stat	D6Wsu116e	1.138	2.771	0.0268266	0.1333
3173	10606989	NM_001077364	14605	TSC22 domain family 3	Tsc22d3	1.138	1.917	0.0955956	0.300606
3174	10432799	NM_019956	56735	keratin 71	Krt71	1.138	2.958	0.0204521	0.111799
3175	10479074	ENSMUST00000073081	75485	RIKEN cDNA 1700010B08 gene	1700010B08Rik	1.138	1.498	0.176441	0.430345
3176	10345230	NM_008999	19335	RAB23, member RAS oncogene fam	Rab23	1.138	1.199	0.268412	0.542786
3177	10542006	BC016429	28040	DNA segment, Chr 6, Wayne Stat	D6Wsu163e	1.138	1.609	0.15029	0.393478
3178	10487879	NM_178607	51902	ring finger protein 24	Rnf24	1.138	2.436	0.0440061	0.184853
3179	10558398	AK019946	78548	RIKEN cDNA 5430417C01 gene	5430417C01Rik	1.138	1.297	0.234483	0.50565
3180	10368683	NM_183254	66337	RIKEN cDNA 1700025K23 gene	1700025K23Rik	1.138	1.182	0.274835	0.549538
3181	10548051	NM_013568	16494	potassium voltage-gated channe	Kcna6	1.138	1.634	0.144945	0.386416
3182	10501860	NM_001114665	214459	formin binding protein 1-like	Fnbp1l	1.138	2.586	0.0352212	0.159639
3183	10385941	NM_021327	57783	TNFAIP3 interacting protein 1	Tnip1	1.138	3.233	0.0138089	0.0851239
3184	10350502					1.138	2.532	0.0381921	0.168893
3185	10485191	ENSMUST00000111274	100042784	PR domain containing 11	Prdm11	1.138	2.634	0.0328215	0.152417
3186	10431137					1.138	2.083	0.0745774	0.258248
3187	10445046	NM_011280	19824	tripartite motif-containing 10	Trim10	1.137	0.552	0.59756	0.81066
3188	10362446					1.137	3.851	0.00593303	0.046687
3189	10451213	BC019423	75564	RIKEN cDNA 1700027N10 gene	1700027N10Rik	1.137	0.965	0.365859	0.636894
3190	10512680	ENSMUST00000086248	20871	aurora kinase C	Aurkc	1.137	1.647	0.142347	0.382389
3191	10465226	NM_023912	78891	SCY1-like 1 (S. cerevisiae)	Scyl1	1.137	2.425	0.0447803	0.187184
3192	10508709					1.137	1.971	0.0881195	0.286074
3193	10442194	NM_172486	210503	zinc finger protein 677	Zfp677	1.137	0.538	0.606848	0.817013
3194	10528790	NM_020570	57434	X-ray repair complementing def	Xrcc2	1.137	0.952	0.372016	0.642325
3195	10410341	NM_133228	170763	zinc finger protein 87	Zfp87	1.137	1.335	0.222627	0.492542
3196	10457663					1.137	1.944	0.0917656	0.293524
3197	10344658	NM_009826	12421	RB1-inducible coiled-coil 1	Rb1cc1	1.137	1.259	0.247298	0.520648
3198	10412394	NR_003544	18115	nicotinamide nucleotide transh	Nnt	1.137	2.116	0.07102	0.250191
3199	10409259					1.137	0.738	0.48369	0.732303
3200	10606441					1.137	2.735	0.0282803	0.137931
3201	10447891	NM_009338	110460	acetyl-Coenzyme A acetyltransf	Acat2	1.137	1.656	0.140404	0.378951
3202	10474269	ENSMUST00000079069	622282	predicted gene, EG622282	EG622282	1.137	1.772	0.118366	0.343378
3203	10510254	NM_010244	14349	Friend virus susceptibility 1	Fv1	1.137	0.534	0.609598	0.818311
3204	10382136	BC124997	69066	RIKEN cDNA 1810010H24 gene	1810010H24Rik	1.137	1.457	0.187347	0.445668
3205	10372781	NM_028679	73914	interleukin-1 receptor-associa	Irak3	1.137	1.851	0.105423	0.319992
3206	10408173					1.137	2.448	0.0432664	0.182768
3207	10376988	NM_026107	52712	zinc finger with KRAB and SCAN	Zkscan6	1.137	0.819	0.439161	0.69843
3208	10565840	NM_016720	50877	neuraminidase 3	Neu3	1.136	1.413	0.199207	0.460684
3209	10500748	NM_009432	22094	thyroid stimulating hormone, b	Tshb	1.136	1.073	0.317955	0.595147
3210	10545771	NM_175475	232174	cytochrome P450, family 26, su	Cyp26b1	1.136	1.84	0.10703	0.322599
3211	10552475	ENSMUST00000107970	69511	kallikrein related-peptidase 1	Klk12	1.136	1.747	0.122902	0.350775
3212	10399034					1.136	2.657	0.0317367	0.149088
3213	10458088	ENSMUST00000097631	633395	predicted gene, ENSMUSG0000007	ENSMUSG00000073607	1.136	0.905	0.394732	0.662293
3214	10433096	NM_008685	18022	nuclear factor, erythroid deri	Nfe2	1.136	0.832	0.431933	0.692351
3215	10407946	NM_024270	76205	STARD3 N-terminal like	Stard3nl	1.136	0.875	0.409975	0.674344
3216	10543004	NM_183308	330260	paraoxonase 2	Pon2	1.136	1.906	0.0971188	0.3035
3217	10578207	NM_001081150	244421	LON peptidase N-terminal domai	Lonrf1	1.136	1.092	0.31002	0.586741
3218	10593878	NM_175483	235406	sorting nexin 33	Snx33	1.136	1.213	0.263529	0.53828
3219	10588942	NM_008483	16779	laminin, beta 2	Lamb2	1.136	1.567	0.159813	0.407118
3220	10516529	NM_172875	242669	arginine decarboxylase	Adc	1.136	1.845	0.106327	0.321598

3221	10569656	NM_146206	233979	two pore segment channel 2	Tpcn2	1.136	1.889	0.0995326	0.308219
3222	10372139	NM_024435	67405	neurotensin	Nts	1.136	0.351	0.735916	0.886874
3223	10489440	NM_183271	68221	WAP four-disulfide core domain	Wfdc15a	1.136	1.991	0.0855428	0.280682
3224	10584494	NM_146505	258498	olfactory receptor 148	Olfr148	1.136	2.152	0.0672942	0.242397
3225	10582925	NM_026303	67667	alkB, alkylation repair homolo	Alkbh8	1.136	1.481	0.180875	0.436777
3226	10431974	NM_144850	223864	Rap guanine nucleotide exchang	Rapgef3	1.135	2.483	0.0410551	0.176652
3227	10452918	NM_011500	268980	striatin, calmodulin binding p	Strn	1.135	1.764	0.119772	0.346027
3228	10373530	NM_183417	12566	cyclin-dependent kinase 2	Cdk2	1.135	1.952	0.0906269	0.290953
3229	10444016	NM_001002842	378460	PML-RAR alpha-regulated adapto	Pram1	1.135	2.453	0.0429374	0.181833
3230	10596442	NM_198931	67905	protein phosphatase 1M	Ppm1m	1.135	1.673	0.137067	0.373617
3231	10493496	AK132440	100048897	predicted gene, ENSMUSG0000007	ENSMUSG00000074468	1.135	1.79	0.115319	0.337519
3232	10364728	NM_023431	68114	melanoma associated antigen (m	Mum1	1.135	1.839	0.10729	0.322741
3233	10491621	ENSMUST00000057272	229227	RIKEN cDNA 4932438A13 gene	4932438A13Rik	1.135	2.078	0.0751658	0.259229
3234	10491526	NM_172678	229211	acyl-Coenzyme A dehydrogenase	Acad9	1.135	1.912	0.0963047	0.302072
3235	10393877	AK047224	17134	v-maf musculoaponeurotic fibro	Mafg	1.135	0.571	0.585272	0.802789
3236	10374746	NM_025923	67030	Fanconi anemia, complementatio	Fancl	1.135	2.518	0.0389713	0.171027
3237	10450529	NM_001033366	268949	diffuse panbronchiolitis criti	Dpcr1	1.135	1.622	0.147497	0.389587
3238	10516576	NM_009030	19646	retinoblastoma binding protein	Rbbp4	1.135	2.4	0.0464658	0.191627
3239	10366767	NM_146012	52468	CTD (carboxy-terminal domain,	Ctdsp2	1.135	1.944	0.0917231	0.293492
3240	10468988					1.135	2.107	0.071975	0.252294
3241	10407568					1.135	2.499	0.040072	0.17423
3242	10515939	NM_194060	329934	forkhead box O6	Foxo6	1.135	1.262	0.246107	0.51906
3243	10451434	NM_009358	21770	protein phosphatase 2, regulat	Ppp2r5d	1.135	1.536	0.167179	0.418175
3244	10568188	NM_144522	68449	TBC1 domain family, member 10b	Tbc1d10b	1.135	1.801	0.113503	0.333876
3245	10406941	NM_144838	218544	small glutamine-rich tetratric	Sgtb	1.135	0.881	0.406857	0.671343
3246	10607244	BC083100	546387	predicted gene, EG546387	EG546387	1.135	3.37	0.0114042	0.0742122
3247	10380634	NM_010460	15415	homeo box B7	Hoxb7	1.135	1.56	0.161448	0.409623
3248	10386205	NM_146376	258373	olfactory receptor 323	Olfr323	1.135	1.913	0.0960612	0.301621
3249	10499160	NM_007639	12479	CD1d1 antigen	Cd1d1	1.134	0.785	0.457632	0.713266
3250	10518218	XR_032523	666194	similar to Integrator complex	LOC666194	1.134	1.726	0.126781	0.356707
3251	10458661					1.134	2.62	0.0335223	0.154383
3252	10542662	NM_177314	321015	RIKEN cDNA 5330439B14 gene	5330439B14Rik	1.134	1.493	0.177841	0.432364
3253	10386909	BC038868	73139	proline-rich polypeptide 6	Prr6	1.134	1.101	0.306313	0.582854
3254	10383731	NM_013870	29856	smoothelin	Smtn	1.134	1.685	0.134593	0.369832
3255	10598833	NM_021715	60322	carbohydrate (N-acetylglucosam	Chst7	1.134	1.601	0.152219	0.39598
3256	10416734					1.134	2.623	0.033384	0.154129
3257	10359339	NM_013862	29809	RAB GTPase activating protein	Rabgap1l	1.134	1.605	0.151342	0.395197
3258	10474915	NM_177157	320415	GTP cyclohydrolase I feedback	Gchfr	1.134	1.717	0.128336	0.359238
3259	10451646	NM_178796	328830	RIKEN cDNA A530064D06 gene	A530064D06Rik	1.134	1.262	0.246357	0.519442
3260	10437945	NM_008565	17217	minichromosome maintenance def	Mcm4	1.134	1.595	0.153416	0.397723
3261	10401317	NM_001038995	214321	predicted gene, EG214321	EG214321	1.134	0.543	0.603657	0.814811
3262	10466622	AK149560	100038579	predicted gene, ENSMUSG0000007	ENSMUSG00000074936	1.134	0.54	0.605148	0.815765
3263	10349316	NM_146103	226351	transmembrane protein 185B	Tmem185b	1.134	2.531	0.0382437	0.168959
3264	10604187	NM_001017959	16784	lysosomal-associated membrane	Lamp2	1.134	1.186	0.273159	0.547717
3265	10479950	NM_001110231	14007	CUG triplet repeat, RNA bindin	Cugbp2	1.134	0.917	0.388689	0.657212
3266	10436623	NM_139134	246048	chondrolectin	Chodl	1.134	0.628	0.5492	0.779541
3267	10552945	NM_030678	14936	glycogen synthase 1, muscle	Gys1	1.134	1.47	0.183783	0.440979
3268	10401607	NM_008827	18654	placental growth factor	Pgf	1.134	1.158	0.283705	0.559004
3269	10546010	NM_001037727	232201	Rho GTPase activating protein	Arhgap25	1.134	2.042	0.0792558	0.26804

3270	10454478	NM_027002	69241	polymerase (RNA) II (DNA direc	Polr2d	1.134	0.893	0.40051	0.666382
3271	10408450	NM_009238	20677	SRY-box containing gene 4	Sox4	1.134	1.392	0.205402	0.469103
3272	10556005	NM_010562	16202	integrin linked kinase	Ilk	1.134	1.4	0.203075	0.465808
3273	10586759	NM_016787	12175	BCL2/adenovirus E1B interactin	Bnip2	1.134	2.319	0.0524118	0.207062
3274	10408647	BC014724	69123	RIKEN cDNA 1810022C23 gene	1810022C23Rik	1.134	2.156	0.0668579	0.241483
3275	10587810	NM_001033184	78459	RIKEN cDNA 1700057G04 gene	1700057G04Rik	1.133	2.976	0.0199226	0.109657
3276	10422585	NM_207667	14169	fibroblast growth factor 14	Fgf14	1.133	1.598	0.152845	0.396925
3277	10422699					1.133	1.594	0.153714	0.398251
3278	10356379	NM_021306	13599	endothelin converting enzyme-l	Ecel1	1.133	2.343	0.0506037	0.202683
3279	10415960	NM_153414	210925	integrator complex subunit 9	Ints9	1.133	1.595	0.153582	0.398104
3280	10571371	NM_030254	80286	tumor suppressor candidate 3	Tusc3	1.133	2.228	0.0600774	0.22593
3281	10414981	ENSMUST00000103674	547428	predicted gene, OTTMUSG0000001	OTTMUSG00000015025	1.133	2.023	0.0815798	0.272821
3282	10510687	NM_133348	70025	acyl-CoA thioesterase 7	Acot7	1.133	2.272	0.0562378	0.21679
3283	10410656	NM_009817	12380	calpastatin	Cast	1.133	1.69	0.133531	0.367916
3284	10562331	NM_016682	50995	ubiquitin-like modifier activa	Uba2	1.133	2.126	0.0699831	0.24786
3285	10401702	NM_001080943	238331	zinc finger, DHHC-type contain	Zdhhc22	1.133	1.557	0.16212	0.410473
3286	10375358	ENSMUST00000109268	13591	early B-cell factor 1	Ebf1	1.133	1.416	0.198514	0.459534
3287	10350758	AK080751	791276	predicted gene, ENSMUSG0000006	ENSMUSG00000066798	1.133	1.153	0.285661	0.561079
3288	10460833	NM_010119	13660	EH-domain containing 1	Ehd1	1.133	2.385	0.0475096	0.194077
3289	10591412	NM_010333	14739	endothelial differentiation, s	Edg5	1.133	1.602	0.151933	0.395759
3290	10537787	NM_199159	387512	taste receptor, type 2, member	Tas2r135	1.133	1.646	0.142431	0.382469
3291	10409065	NM_207232	218232	protein tyrosine phosphatase d	Ptpdc1	1.133	1.144	0.289114	0.565029
3292	10602599	NM_019710	24061	structural maintenance of chro	Smc1a	1.133	2.204	0.0622312	0.230724
3293	10505451	NM_011016	18406	orosomucoid 2	Orm2	1.133	1.704	0.130814	0.362937
3294	10607202					1.133	0.991	0.353814	0.6265
3295	10356997					1.133	2.819	0.025017	0.127548
3296	10475718	NM_177214	320632	activating signal cointegrator	Ascc3l1	1.133	1.753	0.121717	0.348347
3297	10493668	ENSMUST00000029548	77595	nucleoporin 210-like	Nup210l	1.133	2.106	0.0721028	0.252659
3298	10394429	BC046986	68832	RIKEN cDNA 1110057K04 gene	1110057K04Rik	1.133	2.034	0.0802995	0.270212
3299	10538979	NM_009858	12526	CD8 antigen, beta chain 1	Cd8b1	1.133	1.622	0.147513	0.389587
3300	10518841	NM_175152	69876	THAP domain containing, apopto	Thap3	1.132	2.227	0.0601047	0.225949
3301	10436203	XM_001480094	100043404	similar to ribosomal protein	LOC100043404	1.132	2.538	0.0378254	0.16795
3302	10579508	ENSMUST00000093450	382014	transmembrane protein 16H	Tmem16h	1.132	2.037	0.0798916	0.269372
3303	10510019	AK046532	320456	RIKEN cDNA B330016D10 gene	B330016D10Rik	1.132	0.744	0.480587	0.730205
3304	10543846	NM_021435	58246	solute carrier family 35, memb	Slc35b4	1.132	1.853	0.105095	0.319364
3305	10543591	NM_007538	12057	opsin 1 (cone pigments), short	Opn1sw	1.132	1.453	0.188328	0.446362
3306	10477107	NM_177656	228778	RIKEN cDNA 6820408C15 gene	6820408C15Rik	1.132	1.782	0.116761	0.340277
3307	10576840	AK019856	78899	RIKEN cDNA 4932443L11 gene	4932443L11Rik	1.132	1.189	0.271941	0.546343
3308	10401320	NM_009620	11498	a disintegrin and metallopepti	Adam4	1.132	1.112	0.301781	0.577905
3309	10542691	NM_008511	16970	lymphoid-restricted membrane p	Lrmp	1.132	2.794	0.02596	0.130535
3310	10594110	NM_008684	18007	neogenin	Neo1	1.132	1.318	0.227947	0.49895
3311	10510305	NM_020009	56717	FK506 binding protein 12-rapam	Frap1	1.132	1.89	0.0993862	0.308036
3312	10367770	ENSMUST00000066742	791352	predicted gene, ENSMUSG0000005	ENSMUSG00000053980	1.132	1.198	0.268957	0.543518
3313	10385239	NM_134017	108645	methionine adenosyltransferase	Mat2b	1.132	1.223	0.259615	0.533979
3314	10424662	NM_028216	72373	prostate stem cell antigen	Psca	1.132	1.705	0.130632	0.362763
3315	10490872	NM_028915	71710	leucine rich repeat and coiled	Lrrcc1	1.132	0.887	0.403554	0.668494
3316	10446777	NM_020578	57440	EH-domain containing 3	Ehd3	1.132	1.441	0.191529	0.450866
3317	10484425	NM_001033166	72657	RIKEN cDNA 2700094K13 gene	2700094K13Rik	1.132	1.47	0.183738	0.440966
3318	10430302	NM_007781	12984	colony stimulating factor 2 re	Csf2rb2	1.131	1.562	0.160978	0.408854

3319	10354258	NM_026430	67883	UDP-glucuronate decarboxylase	Uxs1	1.131	2.073	0.0757311	0.260282
3320	10540472	NM_011498	20893	basic helix-loop-helix domain	Bhlhb2	1.131	1.509	0.173674	0.426449
3321	10406193	NM_024201	67433	coiled-coil domain containing	Ccdc127	1.131	1.401	0.202801	0.465349
3322	10414417	NM_033602	93834	pellino 2	Peli2	1.131	1.728	0.126355	0.356023
3323	10530360	NM_175519	243043	potassium channel tetramerisat	Kctd8	1.131	1.671	0.137314	0.374193
3324	10436849	NM_010508	15975	interferon (alpha and beta) re	Ifnar1	1.131	2.397	0.046686	0.191982
3325	10455088	NM_053136	93882	protocadherin beta 11	Pcdhb11	1.131	1.246	0.251602	0.525573
3326	10551080	NM_027882	71722	capicua homolog (Drosophila)	Cic	1.131	2.113	0.0713406	0.250903
3327	10582229	ENSMUST00000059018	76291	RIKEN cDNA 1110003O08 gene	1110003O08Rik	1.131	2.172	0.0652787	0.238303
3328	10514520	NM_028979	74519	cytochrome P450, family 2, sub	Cyp2j9	1.131	1.07	0.31899	0.596119
3329	10588669	NM_019713	56289	Ras association (RalGDS/AF-6)	Rassf1	1.131	1.637	0.144387	0.385687
3330	10596543	NM_030730	81000	Rad54 like 2 (S. cerevisiae)	Rad54l2	1.131	0.506	0.627776	0.830715
3331	10448247	NM_009555	22700	zinc finger protein 40	Zfp40	1.131	0.784	0.458091	0.71335
3332	10377215	NM_008088	14457	growth arrest specific 7	Gas7	1.131	2.461	0.0424301	0.180475
3333	10455656	NM_008292	15488	hydroxysteroid (17-beta) dehyd	Hsd17b4	1.131	1.764	0.119826	0.346027
3334	10551393	NM_007434	11652	thymoma viral proto-oncogene 2	Akt2	1.131	1.348	0.218558	0.486749
3335	10485836	NM_205783	213788	cholinergic receptor, muscarin	Chrm5	1.131	1.202	0.267197	0.541834
3336	10390153	NM_177619	217127	MYST histone acetyltransferase	Myst2	1.131	1.055	0.325304	0.601664
3337	10508772	NM_010208	14191	Gardner-Rasheed feline sarcoma	Fgr	1.131	1.83	0.108706	0.325457
3338	10481186	NM_138665	192166	sarcosine dehydrogenase	Sardh	1.131	1.625	0.146863	0.388752
3339	10390252	ENSMUST00000100525	544810	predicted gene, OTTMUSG0000000	OTTMUSG00000001969	1.131	1.457	0.18736	0.445668
3340	10530627	BC031901	231296	cDNA sequence BC031901	BC031901	1.13	2.064	0.076712	0.262629
3341	10528521					1.13	0.817	0.440214	0.699184
3342	10362487	NM_009433	22110	testis-specific protein, Y-enc	Tspyl1	1.13	1.307	0.231244	0.501993
3343	10465673	BC125249	68229	expressed sequence AI846148	AI846148	1.13	2.308	0.053319	0.209428
3344	10391837	NM_152813	72469	phospholipase C, delta 3	Plcd3	1.13	2.339	0.0508604	0.203346
3345	10551815	NM_011981	26466	zinc finger protein 260	Zfp260	1.13	1.83	0.108705	0.325457
3346	10379127	NM_017407	54141	sperm associated antigen 5	Spag5	1.13	1.767	0.119249	0.345349
3347	10531794	ENSMUST00000104987	72145	WD repeat and FYVE domain cont	Wdfy3	1.13	1.996	0.0849442	0.279978
3348	10549986	NM_134207	171241	vomeronasal 1 receptor, G6	V1rg6	1.13	1.401	0.202677	0.465349
3349	10599841	AK082088	331424	RIKEN cDNA C230004F18 gene	C230004F18Rik	1.13	0.33	0.750423	0.894477
3350	10411119	NM_133905	100715	PAP associated domain containi	Papd4	1.13	2.004	0.0839404	0.277752
3351	10528385	NM_011261	19699	reelin	Reln	1.13	1.58	0.156815	0.403187
3352	10461402	NM_010239	14319	ferritin heavy chain 1	Fth1	1.13	1.833	0.108251	0.324616
3353	10586933	NM_010890	17999	neural precursor cell expresse	Nedd4	1.13	2.769	0.0269154	0.133497
3354	10428370	NM_175456	223513	actin-binding Rho activating p	Abra	1.13	1.709	0.129881	0.361535
3355	10504884	BC052696	66665	RIKEN cDNA 5730528L13 gene	5730528L13Rik	1.13	1.463	0.18563	0.443587
3356	10503647	NM_030733	81006	G protein-coupled receptor 63	Gpr63	1.13	2.338	0.0509602	0.203571
3357	10384885	NM_175836	20742	spectrin beta 2	Spnb2	1.13	1.688	0.13396	0.368904
3358	10411804	ENSMUST00000099202	328329	microtubule associated serine/	Mast4	1.129	1.47	0.183659	0.440916
3359	10406736	NM_010170	14064	coagulation factor II (thrombi	F2rl2	1.129	1.219	0.261078	0.535632
3360	10496324	NM_026228	67547	solute carrier family 39 (meta	Slc39a8	1.129	0.868	0.413543	0.677091
3361	10495120	NM_007696	12659	oviductal glycoprotein 1	Ovgp1	1.129	1.083	0.313623	0.59037
3362	10578941	NM_153110	260296	tripartite motif-containing 61	Trim61	1.129	2.886	0.0227005	0.119309
3363	10354203					1.129	0.869	0.412894	0.676379
3364	10462480	NM_031249	83410	cleavage stimulation factor, 3	Cstf2t	1.129	1.567	0.159775	0.407118
3365	10579736	BC055692	66818	RIKEN cDNA 9130011J15 gene	9130011J15Rik	1.129	0.962	0.367101	0.638059
3366	10597648	NM_010851	17874	myeloid differentiation primar	Myd88	1.129	1.05	0.327571	0.603902
3367	10425066	NM_007780	12983	colony stimulating factor 2 re	Csf2rb	1.129	1.565	0.16024	0.407591
3368	10546510	NM_008377	16206	leucine-rich repeats and immun	Lrig1	1.129	0.911	0.391616	0.659944
3369	10497475	NM_175086	11608	angiotensin II receptor, type	Agtr1b	1.129	1.573	0.158466	0.405348
3370	10361705	AK010852	70097	SAM and SH3 domain containing	Sash1	1.129	1.586	0.155486	0.400991
3371	10442143	ENSMUST00000095633	381065	predicted gene, EG381065	EG381065	1.129	1.871	0.102231	0.313502

3372	10372324	NM_009306	20979	synaptotagmin I	Syt1	1.129	1.545	0.164893	0.414961
3373	10579841					1.129	2.076	0.0753798	0.259624
3374	10480813	BC085507	227624	RIKEN cDNA B230208H17 gene	B230208H17Rik	1.129	1.773	0.118182	0.343153
3375	10429926	NM_010046	13350	diacylglycerol O-acyltransfera	Dgat1	1.129	2.092	0.0736273	0.256428
3376	10456383	NM_053261	114663	inositol (myo)-1(or 4)-monopho	Impa2	1.129	1.379	0.209246	0.474354
3377	10583215	NM_023858	77116	myotubularin related protein 2	Mtmr2	1.128	1.567	0.159905	0.407256
3378	10375343	NM_028862	74315	ring finger protein 145	Rnf145	1.128	2.301	0.0538735	0.210688
3379	10532517	NM_021351	12959	crystallin, beta A4	Cryba4	1.128	1.881	0.100798	0.310816
3380	10527252	NM_013557	15467	eukaryotic translation initiat	Eif2ak1	1.128	1.068	0.319848	0.596635
3381	10511156	NM_207678	56036	cyclin L2	Ccnl2	1.128	1.479	0.181326	0.43738
3382	10448064	BC012016	213389	PR domain containing 9	Prdm9	1.128	1.861	0.103855	0.316823
3383	10453461	NM_001081034	225055	F-box protein 11	Fbxo11	1.128	2.73	0.0284901	0.138514
3384	10499560	NM_001037722	11490	a disintegrin and metallopepti	Adam15	1.128	2.719	0.0289767	0.14001
3385	10489253	NM_177263	320799	zinc fingers and homeoboxes 3	Zhx3	1.128	2.079	0.0750735	0.259103
3386	10451372	NM_175168	71461	PTK7 protein tyrosine kinase 7	Ptk7	1.128	2.151	0.0673797	0.242464
3387	10362003	AK155606	619323	RIKEN cDNA F730021E23 gene	F730021E23Rik	1.128	1.721	0.127619	0.358255
3388	10374998	NM_175490	237716	G protein-coupled receptor 75	Gpr75	1.128	2.541	0.0376511	0.167352
3389	10560035	BC094341	232875	zinc finger and SCAN domain co	Zscan18	1.128	1.636	0.144615	0.385933
3390	10498707	NM_198864	386750	SLIT and NTRK-like family, mem	Slitrk3	1.128	1.785	0.11615	0.33888
3391	10446027	NM_013733	27221	chromatin assembly factor 1, s	Chaf1a	1.128	1.906	0.0971598	0.303538
3392	10521182	BC099925	231128	cDNA sequence BC037112	BC037112	1.128	2.332	0.0513764	0.204731
3393	10397052	ENSMUST00000071028	791340	predicted gene, ENSMUSG0000005	ENSMUSG00000056729	1.128	1.599	0.152546	0.396392
3394	10354845	NM_008765	18393	origin recognition complex, su	Orc2l	1.128	1.41	0.200206	0.462134
3395	10360848	NM_133684	67247	MOCO sulphurase C-terminal dom	Mosc2	1.128	1.477	0.182071	0.438564
3396	10536353	NM_010057	13396	distal-less homeobox 6	Dlx6	1.128	1.942	0.092035	0.293984
3397	10424833	NM_026859	68877	MAF1 homolog (S. cerevisiae)	Maf1	1.128	1.985	0.0862969	0.282193
3398	10487513	NM_008569	17222	anaphase promoting complex sub	Anapc1	1.128	2.837	0.0243663	0.125168
3399	10459590	NM_008977	19255	protein tyrosine phosphatase,	Ptpn2	1.127	1.368	0.212374	0.477959
3400	10602385	NM_008824	18639	6-phosphofructo-2-kinase/fruct	Pfkfb1	1.127	1.85	0.105474	0.3201
3401	10441987	NM_007690	12648	chromodomain helicase DNA bind	Chd1	1.127	2.048	0.0786304	0.266888
3402	10489051	AK133873	632764	predicted gene, ENSMUSG0000007	ENSMUSG00000074630	1.127	1.003	0.348323	0.622132
3403	10428374	XR_030860	432947	similar to GC-rich promoter bi	LOC432947	1.127	0.94	0.37766	0.647469
3404	10523905	NM_013827	17765	metal response element binding	Mtf2	1.127	2.482	0.0410893	0.176721
3405	10557106	NM_001081327	195646	heparan sulfate (glucosamine)	Hs3st2	1.127	1.163	0.281841	0.557053
3406	10474545	NM_133649	107723	solute carrier family 12, memb	Slc12a6	1.127	1.614	0.149212	0.391598
3407	10489850	NM_001033196	98999	zinc finger, NFX1-type contain	Znfx1	1.127	2.1	0.072691	0.254172
3408	10439409	AK169533	414072	cDNA sequence BC031361	BC031361	1.127	1.11	0.302805	0.578887
3409	10388958	NM_001033711	14017	ecotropic viral integration si	Evi2a	1.127	1.655	0.140724	0.379507
3410	10362363	NM_026138	67412	RIKEN cDNA 6330407J23 gene	6330407J23Rik	1.127	0.751	0.476468	0.727606
3411	10501372					1.127	1.958	0.0898359	0.289248
3412	10363868	NM_024244	71721	RIKEN cDNA 1200015N20 gene	1200015N20Rik	1.127	1.37	0.211843	0.477389
3413	10418038	NM_145459	218820	zinc finger protein 503	Zfp503	1.127	2.127	0.0698221	0.24761
3414	10521371	NM_172708	231134	docking protein 7	Dok7	1.127	2.608	0.0341002	0.156233
3415	10366707	NM_016847	54140	arginine vasopressin receptor	Avpr1a	1.127	0.905	0.394486	0.662113
3416	10601771	NM_030066	78248	armadillo repeat containing, X	Armcx1	1.127	1.91	0.0965667	0.302436
3417	10453256	NM_153512	225030	potassium voltage-gated channe	Kcng3	1.127	1.735	0.125047	0.354043
3418	10463428					1.127	0.939	0.377883	0.647641
3419	10553635	AK140288	320845	RIKEN cDNA A230056P14 gene	A230056P14Rik	1.126	1.587	0.155238	0.400794
3420	10563114	NR_000002	27209	small nucleolar RNA, C/D box 3	Snord32a	1.126	0.864	0.415611	0.678743
3421	10599032	NM_175180	72404	WD repeat domain 44	Wdr44	1.126	1.686	0.134468	0.369727

3422	10444587					1.126	0.259	0.802613	0.919965
3423	10535586	NM_001038627	75788	SMAD specific E3 ubiquitin pro	Smurf1	1.126	1.417	0.198341	0.459233
3424	10386219	NM_011758	22698	zinc finger protein 39	Zfp39	1.126	1.622	0.147549	0.389587
3425	10402440	NM_010351	14836	goosecoid homeobox	Gsc	1.126	1.419	0.197584	0.458132
3426	10436449					1.126	1.205	0.26628	0.541183
3427	10575619	NM_020584	57321	telomeric repeat binding facto	Terf2ip	1.126	2.146	0.0678715	0.243316
3428	10580953					1.126	1.043	0.330726	0.60702
3429	10573867	NM_011250	19651	retinoblastoma-like 2	Rbl2	1.126	1.829	0.108807	0.325589
3430	10464218	NM_145505	226252	expressed sequence AI450540	AI450540	1.126	1.765	0.119577	0.345865
3431	10544563	NM_020589	68910	zinc finger protein 467	Zfp467	1.126	2.173	0.0651749	0.238029
3432	10376733	NM_008928	26397	mitogen-activated protein kina	Map2k3	1.126	1.887	0.0998372	0.308845
3433	10432540	NM_001113545	65970	LIM domain and actin binding 1	Lima1	1.126	1.506	0.174657	0.427722
3434	10532965	NM_016698	50849	ring finger protein 10	Rnf10	1.125	1.533	0.167841	0.419086
3435	10597973	NM_033322	93730	leucine zipper transcription f	Lztfl1	1.125	1.462	0.185999	0.44418
3436	10431948	NM_028003	71919	RNA polymerase II associated p	Rpap3	1.125	0.898	0.398306	0.664598
3437	10492113	BC089522	320604	RIKEN cDNA A730037C10 gene	A730037C10Rik	1.125	1.513	0.17274	0.425061
3438	10396358	NM_008910	19042	protein phosphatase 1A, magnes	Ppm1a	1.125	2.096	0.0731756	0.255191
3439	10408185	NM_175938	238555	butyrophilin, subfamily 2, mem	Btn2a2	1.125	1.724	0.127036	0.357139
3440	10477032	ENSMUST00000060196	108832	RIKEN cDNA 5430405G05 gene	5430405G05Rik	1.125	1.442	0.191213	0.450375
3441	10345704					1.125	1.24	0.253907	0.528198
3442	10534281	NM_009990	269713	CAP-GLY domain containing link	Clip2	1.125	2.418	0.0451926	0.188022
3443	10397790					1.125	2.768	0.0269729	0.133688
3444	10529273	NM_013502	13016	C-terminal binding protein 1	Ctbp1	1.125	1.782	0.116648	0.340054
3445	10565002	NM_173863	70461	CREB regulated transcription c	Crtc3	1.125	2.902	0.0221733	0.117237
3446	10389795	ENSMUST00000053420	20913	syntaxin binding protein 4	Stxbp4	1.125	0.962	0.367138	0.63807
3447	10414173	XR_033408	382871	similar to Non-SMC element 2 h	LOC382871	1.125	0.887	0.403734	0.6686
3448	10415608	NM_009376	21821	intraflagellar transport 88 ho	Ift88	1.125	1.028	0.337048	0.612719
3449	10500272	BC132471	229599	gene model 129, (NCBI)	Gm129	1.125	0.621	0.553652	0.78319
3450	10589848	NM_001083319	22221	upstream binding protein 1	Ubp1	1.125	2.794	0.0259386	0.130458
3451	10486664	NM_013513	13828	erythrocyte protein band 4.2	Epb4.2	1.125	0.331	0.749943	0.894399
3452	10405745					1.125	1.398	0.203481	0.466435
3453	10508759	NM_011284	19891	replication protein A2	Rpa2	1.125	1.724	0.12718	0.35745
3454	10466606	NM_010730	16952	annexin A1	Anxa1	1.125	1.254	0.249069	0.522866
3455	10484805	NM_001011761	257921	olfactory receptor 1229	Olfr1229	1.124	2.323	0.0520697	0.206366
3456	10495316	NM_019976	56742	proline/serine-rich coiled-coi	Psrc1	1.124	1.423	0.196498	0.457018
3457	10493640	ENSMUST00000029548	77595	nucleoporin 210-like	Nup210l	1.124	1.275	0.241698	0.514457
3458	10475000	BC117848	76246	Rtf1, Paf1/RNA polymerase II c	Rtf1	1.124	1.436	0.192928	0.452347
3459	10460196	BC019471	72056	RIKEN cDNA 1810055G02 gene	1810055G02Rik	1.124	1.491	0.178276	0.433019
3460	10426261	NM_021423	58234	SH3/ankyrin domain gene 3	Shank3	1.124	2.202	0.062428	0.231292
3461	10430825	NM_025639	66570	centromere protein M	Cenpm	1.124	1.325	0.225757	0.496144
3462	10555108	NM_023671	12729	chloride channel, nucleotide-s	Clns1a	1.124	1.379	0.209067	0.474049
3463	10590957	NM_010242	14345	fucosyltransferase 4	Fut4	1.124	1.386	0.207227	0.471647
3464	10590445	NM_133741	20623	SNF related kinase	Snrk	1.124	1.16	0.283113	0.55841
3465	10410892	NM_145452	218397	RAS p21 protein activator 1	Rasa1	1.124	1.517	0.171704	0.423956
3466	10547396	NM_009525	22419	wingless-related MMTV integrat	Wnt5b	1.124	2.049	0.0784258	0.266489
3467	10541532	NM_021899	60611	forkhead box J2	Foxj2	1.124	2.16	0.0664776	0.240889
3468	10501924	NM_031186	83398	N-deacetylase/N-sulfotransfera	Ndst3	1.124	0.735	0.485446	0.733791
3469	10459962	NM_015805	50771	ATPase, class II, type 9B	Atp9b	1.124	1.44	0.191885	0.451201
3470	10478772	NM_001085495	99371	ADP-ribosylation factor guanin	Arfgef2	1.124	1.536	0.167091	0.418103
3471	10571849	NM_015791	50753	F-box protein 8	Fbxo8	1.124	1.85	0.105569	0.320207
3472	10410393	NM_172480	210009	5-methyltetrahydrofolate-homoc	Mtrr	1.124	0.892	0.401079	0.666661
3473	10376245	NM_001113325	14799	glutamate receptor, ionotropic	Gria1	1.123	0.736	0.485116	0.733502
3474	10413012	AK034234	73068	fucosyltransferase 11	Fut11	1.123	-0.37	0.722003	0.879076

3475	10605999					1.123	1.902	0.0976731	0.304546
3476	10481931	NM_028716	74016	PHD finger protein 19	Phf19	1.123	1.762	0.120211	0.346569
3477	10447065	BC024059	381110	expressed sequence AW061290	AW061290	1.123	0.906	0.394193	0.661914
3478	10487480	NM_001113179	12235	budding uninhibited by benzimi	Bub1	1.123	1.507	0.174399	0.427379
3479	10461909	BC016495	225994	cDNA sequence BC016495	BC016495	1.123	0.742	0.481553	0.730886
3480	10390473	NM_054051	108083	phosphatidylinositol-5-phospha	Pip4k2b	1.123	1.114	0.301102	0.5773
3481	10588826	NM_013785	27399	inositol hexaphosphate kinase	Ihpk1	1.123	2.163	0.0661869	0.240085
3482	10543600	NM_001029985	333088	cysteine rich BMP regulator 2	Crim2	1.123	2.459	0.0425191	0.180698
3483	10460666	NM_008520	16998	latent transforming growth fac	Ltbp3	1.123	2.357	0.0494971	0.199917
3484	10564667	NM_008746	18213	neurotrophic tyrosine kinase,	Ntrk3	1.123	1.357	0.215692	0.482806
3485	10458419	BC125010	83885	solute carrier family 25 (mito	Slc25a2	1.123	2.16	0.0664219	0.240731
3486	10418275	NM_177111	320234	coiled-coil domain containing	Ccdc66	1.123	1.682	0.13517	0.370646
3487	10570144	NM_001113518	54126	Rho guanine nucleotide exchang	Arhgef7	1.122	2.339	0.0508659	0.203346
3488	10437712	NM_145931	106205	zinc finger CCCH type containi	Zc3h7a	1.122	1.938	0.0925762	0.294729
3489	10531707	NM_001115010	231506	lin-54 homolog (C. elegans)	Lin54	1.122	1.448	0.189524	0.448035
3490	10389627	NM_053269	114714	Rad51 homolog c (S. cerevisiae	Rad51c	1.122	1.465	0.185013	0.442624
3491	10459618					1.122	2.499	0.0401144	0.174258
3492	10499593	NM_029974	77772	DC-STAMP domain containing 1	Dcst1	1.122	2.157	0.0667943	0.24144
3493	10364361	NM_015790	50723	icos ligand	Icosl	1.122	2.168	0.0656517	0.238799
3494	10598594					1.122	0.635	0.544801	0.776964
3495	10488892	NM_019828	56407	transient receptor potential c	Trpc4ap	1.122	1.038	0.332834	0.608828
3496	10404965	NM_146042	218215	ring finger protein 144B	Rnf144b	1.122	1.062	0.322409	0.599241
3497	10379677	NM_001013386	276952	RAS-like, family 10, member B	Rasl10b	1.122	1.088	0.311807	0.58828
3498	10531645	NM_016690	50926	heterogeneous nuclear ribonucl	Hnrpdl	1.122	2.301	0.0538464	0.210683
3499	10390542	NM_031173	12295	calcium channel, voltage-depen	Cacnb1	1.122	1.834	0.108028	0.324223
3500	10389797	NM_011505	20913	syntaxin binding protein 4	Stxbp4	1.122	1.75	0.122287	0.3496
3501	10415019					1.122	1.601	0.152182	0.395933
3502	10547274	NM_028335	72720	zinc finger protein 248	Zfp248	1.122	1.124	0.297159	0.573644
3503	10567797	NM_028816	74204	exportin 6	Xpo6	1.122	1.368	0.212278	0.477897
3504	10524327	NM_001081235	433938	meningioma 1	Mn1	1.121	2.053	0.0779973	0.265568
3505	10561166					1.121	1.007	0.346548	0.620651
3506	10378341	NM_029031	74637	sedoheptulokinase	Shpk	1.121	1.556	0.162419	0.411033
3507	10367045	NM_009040	19683	retinol dehydrogenase 16	Rdh16	1.121	1.739	0.124385	0.353305
3508	10380341	NM_027569	70834	sperm associated antigen 9	Spag9	1.121	2.615	0.0337616	0.155118
3509	10478424	NM_018753	54401	tyrosine 3-monooxygenase/trypt	Ywhab	1.121	2.151	0.0674009	0.242492
3510	10432178					1.121	1.071	0.318874	0.596082
3511	10536376	BC020002	252875	cDNA sequence BC020002	BC020002	1.121	0.942	0.376581	0.646774
3512	10526459	NM_133914	54153	RAS p21 protein activator 4	Rasa4	1.121	1.825	0.109426	0.326934
3513	10557780					1.121	1.461	0.186087	0.44434
3514	10407192	NM_178746	268706	solute carrier family 38, memb	Slc38a9	1.121	1.921	0.0949973	0.299665
3515	10505224	NM_172468	209131	sorting nexin family member 30	Snx30	1.121	1.47	0.183915	0.441198
3516	10407513	NM_172445	207615	WD repeat domain 37	Wdr37	1.121	1.929	0.0937962	0.297157
3517	10433597	NM_028964	74478	sorting nexin 29	Snx29	1.121	1.506	0.174425	0.427379
3518	10565900	ENSMUST00000064334	402747	RIKEN cDNA D630004N19 gene	D630004N19Rik	1.121	1.729	0.12624	0.355752
3519	10542959	NM_009748	12068	blocked early in transport 1 h	Bet1	1.121	0.543	0.603709	0.814811
3520	10441601	NM_145968	72536	T-cell activation Rho GTPase-a	Tagap	1.121	1.247	0.251441	0.525513
3521	10434133	NM_010047	13353	DiGeorge syndrome critical reg	Dgcr6	1.121	2.115	0.071132	0.250544
3522	10540408	NM_010585	16438	inositol 1,4,5-triphosphate re	Itpr1	1.121	1.122	0.297992	0.573995
3523	10374083	NM_009636	11568	AE binding protein 1	Aebp1	1.12	1.728	0.126432	0.356138
3524	10492438	NM_001037923	624866	predicted gene, EG624866	EG624866	1.12	1.626	0.146806	0.388752
3525	10569898	NM_001039578	213027	ecotropic viral integration si	Evi5l	1.12	1.447	0.19003	0.448738
3526	10504926	NM_182999	109331	ring finger protein 20	Rnf20	1.12	2.035	0.0800775	0.269869
3527	10550383	NM_001081655	629378	dapper homolog 3, antagonist o	Dact3	1.12	2	0.0843826	0.278735
3528	10545417	NM_145569	232087	methionine adenosyltransferase	Mat2a	1.12	1.512	0.173007	0.425494
3529	10565935	NM_001081116	207212	Rho guanine nucleotide exchang	Arhgef17	1.12	2.279	0.0556729	0.215398

3530	10507015	NM_001048189	78933	RIKEN cDNA 4931433A01 gene	4931433A01Rik	1.12	1.204	0.266555	0.541262
3531	10399892	NM_175191	73010	G protein-coupled receptor 22	Gpr22	1.12	0.986	0.355827	0.628276
3532	10542885	NM_026054	67246	RIKEN cDNA 2810474O19 gene	2810474O19Rik	1.12	1.148	0.287712	0.563484
3533	10550394	NM_008967	19222	prostaglandin I receptor (IP)	Ptgir	1.12	1.411	0.200027	0.461823
3534	10415013					1.12	1.778	0.117339	0.341384
3535	10406733	NM_028106	72114	zinc finger, BED domain contai	Zbed3	1.12	1.398	0.203631	0.46673
3536	10566595	NM_146599	258592	olfactory receptor 697	Olfr697	1.12	1.871	0.102228	0.313502
3537	10397000					1.12	1.484	0.180254	0.435801
3538	10358459	NM_145511	226499	cDNA sequence BC003331	BC003331	1.12	1.523	0.170427	0.422073
3539	10471597	XM_887818	623370	predicted gene, EG623370	EG623370	1.12	2.148	0.067675	0.243106
3540	10353048					1.12	1.258	0.247657	0.520853
3541	10493770	NM_026374	67781	interleukin enhancer binding f	Ilf2	1.12	1.558	0.161902	0.410216
3542	10554471	NM_009553	22691	zinc finger and SCAN domain co	Zscan2	1.12	1.392	0.205466	0.469103
3543	10603308					1.12	1.994	0.0852117	0.280273
3544	10511311	NM_028097	72098	transmembrane protein 68	Tmem68	1.12	1.112	0.301627	0.577839
3545	10600474					1.12	1.533	0.167867	0.419104
3546	10603182	NM_009707	11856	Rho GTPase activating protein	Arhgap6	1.12	1.375	0.210402	0.475953
3547	10515870	ENSMUST00000046260	230696	expressed sequence AU022252	AU022252	1.12	1.367	0.212605	0.478213
3548	10410370	BC016248	235907	zinc finger protein 71, releat	Zfp71-rs1	1.119	1.039	0.332529	0.608585
3549	10423358	AK162044	211147	membrane-associated ring finge	March11	1.119	0.003	0.99779	0.999208
3550	10507059	NM_177818	328505	RIKEN cDNA C130057D23 gene	C130057D23Rik	1.119	0.627	0.549707	0.779911
3551	10569011	NM_053088	73835	interferon induced transmembra	Ifitm5	1.119	1.619	0.14819	0.390374
3552	10415363	NM_177992	105446	guanosine monophosphate reduct	Gmpr2	1.119	1.329	0.224198	0.494263
3553	10376796	NM_027817	71520	GRB2-related adaptor protein	Grap	1.119	2.07	0.0760583	0.261237
3554	10478169	NM_145742	71715	DEAH (Asp-Glu-Ala-His) box pol	Dhx35	1.119	1.309	0.230826	0.501612
3555	10352294	BC031781	208768	cDNA sequence BC031781	BC031781	1.119	1.228	0.257962	0.531958
3556	10512129	NM_022305	14595	UDP-Gal:betaGlcNAc beta 1,4- g	B4galt1	1.119	1.664	0.138754	0.376759
3557	10562989	NM_153679	78070	carnitine palmitoyltransferase	Cpt1c	1.119	2.277	0.0558403	0.215766
3558	10605357	NM_181584	210710	growth factor receptor bound p	Gab3	1.119	1.492	0.177995	0.432602
3559	10349314					1.119	1.332	0.223459	0.493403
3560	10537292	ENSMUST00000101536	67705	RIKEN cDNA 1810058I24 gene	1810058I24Rik	1.119	1.401	0.202678	0.465349
3561	10430873	NM_145474	223706	cytochrome P450, family 2, sub	Cyp2d34	1.119	1.992	0.0853957	0.280548
3562	10376941	NM_027660	71062	tektin 3	Tekt3	1.119	2.251	0.0579957	0.220908
3563	10474088	ENSMUST00000028621	70852	RIKEN cDNA 4921507L20 gene	4921507L20Rik	1.119	1.419	0.197691	0.458331
3564	10452188	NM_022328	64144	myeloid/lymphoid or mixed-line	Mllt1	1.118	2.301	0.0538404	0.210683
3565	10599654	NM_028375	72865	CAAX box 1 homolog C (human)	Cxx1c	1.118	1.056	0.324861	0.601266
3566	10414102	NM_153127	105450	multimerin 2	Mmrn2	1.118	1.119	0.29906	0.575096
3567	10464949	NM_153129	107975	phosphofurin acidic cluster so	Pacs1	1.118	1.123	0.297431	0.573687
3568	10384672	NM_172391	268390	AHA1, activator of heat shock	Ahsa2	1.118	1.429	0.19484	0.454963
3569	10476620	NM_021335	20639	U2 small nuclear ribonucleopro	Snrpb2	1.118	1.786	0.116036	0.338784
3570	10423941	NM_025736	66736	tetratricopeptide repeat domai	Ttc35	1.118	1.02	0.340849	0.615921
3571	10508909					1.118	1.318	0.227975	0.49895
3572	10409376	NM_001033245	212032	hexokinase 3	Hk3	1.118	1.687	0.134236	0.369304
3573	10432122	NM_030121	78541	ankyrin repeat and SOCS box-co	Asb8	1.118	1.496	0.177047	0.431359
3574	10584803	BC080764	76568	RIKEN cDNA 1500035H01 gene	1500035H01Rik	1.118	1.164	0.281519	0.556926
3575	10453166	NM_001033443	381113	cyclin-dependent kinase-like 4	Cdkl4	1.118	1.318	0.22792	0.49895
3576	10485081	NM_138306	104418	diacylglycerol kinase zeta	Dgkz	1.118	1.249	0.250541	0.524406
3577	10585093					1.118	1.602	0.151827	0.395645
3578	10389526	NM_001003908	67300	clathrin, heavy polypeptide (H	Cltc	1.118	1.466	0.184801	0.442367
3579	10570397	NM_027276	69957	CDC16 cell division cycle 16 h	Cdc16	1.118	1.908	0.0968139	0.303049
3580	10371387	NM_175451	216197	cytoskeleton-associated protei	Ckap4	1.118	2.727	0.0286157	0.138865
3581	10425037	NM_177744	245282	apolipoprotein L 10a	Apol10a	1.118	1.834	0.107986	0.324143

3582	10419532	NM_133676	66246	O-sialoglycoprotein endopeptid	Osgep	1.118	1.226	0.258615	0.532776
3583	10438570	XR_005142	76222	melanoma antigen family F, 1	Magef1	1.118	1.11	0.302471	0.578616
3584	10489503	NM_001033240	209351	WAP four-disulfide core domain	Wfdc6a	1.118	1.243	0.252657	0.526766
3585	10591628	NM_177030	319899	dedicator of cytokinesis 6	Dock6	1.117	2.253	0.0578324	0.220604
3586	10528476					1.117	0.469	0.653205	0.844576
3587	10410756	NM_134071	105377	ankyrin repeat domain 32	Ankrd32	1.117	1.329	0.224279	0.494263
3588	10385271	NM_009831	12450	cyclin G1	Ccng1	1.117	1.528	0.169153	0.42056
3589	10431601	NM_009713	11883	arylsulfatase A	Arsa	1.117	1.947	0.0913121	0.292531
3590	10541034	NM_001081317	67492	AN1, ubiquitin-like, homolog (	Anubl1	1.117	0.783	0.458495	0.713665
3591	10492826	NM_080428	50754	F-box and WD-40 domain protein	Fbxw7	1.117	1.306	0.231728	0.502487
3592	10600604	NM_007868	13405	dystrophin, muscular dystrophy	Dmd	1.117	0.834	0.431178	0.69177
3593	10580349	NM_175441	213435	myosin light chain kinase 3	Mylk3	1.117	1.636	0.144654	0.38594
3594	10562419	NM_001024707	435965	low density lipoprotein recept	Lrp3	1.117	1.556	0.162513	0.411049
3595	10469579					1.117	1.056	0.324849	0.601266
3596	10368030	NM_028440	73112	RIKEN cDNA 3110003A17 gene	3110003A17Rik	1.117	1.736	0.124882	0.353808
3597	10549592					1.117	0.796	0.451451	0.708527
3598	10544779	NM_010455	15404	homeo box A7	Hoxa7	1.117	1.75	0.122405	0.349842
3599	10368534	NM_172495	211329	nuclear receptor coactivator 7	Ncoa7	1.117	1.208	0.265305	0.540466
3600	10439018	BC021536	106264	RIKEN cDNA 0610012G03 gene	0610012G03Rik	1.117	0.474	0.649704	0.842782
3601	10570573	NM_026792	52123	1-acylglycerol-3-phosphate O-a	Agpat5	1.117	0.866	0.41412	0.677439
3602	10518366	NM_198619	242747	RIKEN cDNA 2810408P10 gene	2810408P10Rik	1.117	0.947	0.374055	0.64426
3603	10447688	AK043779	75060	RIKEN cDNA 4930506C21 gene	4930506C21Rik	1.117	0.977	0.360224	0.632213
3604	10424221	NM_001081396	210544	WD repeat domain 67	Wdr67	1.117	1.842	0.106805	0.322336
3605	10502335	NM_001033350	242248	B-cell scaffold protein with a	Bank1	1.117	1.442	0.191351	0.450599
3606	10564777	BC034093	16576	kinesin family member 7	Kif7	1.117	1.992	0.0854721	0.280625
3607	10601011	NM_008446	16571	kinesin family member 4	Kif4	1.117	1.373	0.210873	0.476393
3608	10425053	NM_008677	17972	neutrophil cytosolic factor 4	Ncf4	1.117	2.604	0.0343368	0.157
3609	10483768					1.117	1.399	0.203183	0.466005
3610	10478401	NM_029512	76080	RIKEN cDNA 5830472M02 gene	5830472M02Rik	1.116	0.737	0.484638	0.733146
3611	10549341	NM_138757	71177	RIKEN cDNA 4933424B01 gene	4933424B01Rik	1.116	1.55	0.163872	0.413228
3612	10404301	NM_025896	67000	prolactin family 3, subfamily	Prl3a1	1.116	1.238	0.254573	0.528857
3613	10483797	ENSMUST00000064205	73429	RIKEN cDNA 1700109F18 gene	1700109F18Rik	1.116	1.246	0.251753	0.525631
3614	10367440	NM_008398	16404	integrin alpha 7	Itga7	1.116	1.908	0.0968203	0.303049
3615	10548367	NM_175526	243653	C-type lectin domain family 1,	Clec1a	1.116	2.088	0.0740571	0.257223
3616	10454809	NM_010771	17184	matrin 3	Matr3	1.116	2.51	0.0394499	0.172341
3617	10494369	NM_153053	107701	splicing factor 3b, subunit 4	Sf3b4	1.116	0.663	0.527913	0.763369
3618	10424731	NM_026960	69146	gasdermin D	Gsdmd	1.116	2.351	0.0499333	0.20095
3619	10374773					1.116	1.36	0.214856	0.481846
3620	10424555					1.116	0.758	0.472753	0.724458
3621	10527441	NM_023142	11867	actin related protein 2/3 comp	Arpc1b	1.116	1.355	0.216427	0.483657
3622	10449236	NM_019731	56520	non-metastatic cells 4, protei	Nme4	1.116	0.805	0.446306	0.704033
3623	10360563	NM_027188	69726	SET and MYND domain containing	Smyd3	1.116	0.549	0.599696	0.812038
3624	10505779	NM_139306	230379	N-acylsphingosine amidohydrola	Asah3l	1.116	1.79	0.115301	0.337519
3625	10471978	NM_172663	227867	enhancer of polycomb homolog 2	Epc2	1.116	1.351	0.217523	0.485293
3626	10411782	NM_001077495	18708	phosphatidylinositol 3-kinase,	Pik3r1	1.116	1.356	0.215879	0.482969
3627	10425923	BC066174	73225	RIKEN cDNA 3110048E14 gene	3110048E14Rik	1.116	1.575	0.158039	0.405065
3628	10576899					1.116	1.104	0.305029	0.581459
3629	10460947	NM_011224	19309	muscle glycogen phosphorylase	Pygm	1.116	1.29	0.23673	0.508837
3630	10585545	NM_011992	26611	reticulocalbin 2	Rcn2	1.116	1.697	0.132201	0.365389

3631	10562368	BC060233	233103	RIKEN cDNA 4931406P16 gene	4931406P16Rik	1.116	1.205	0.266226	0.541183
3632	10590918	NM_001081395	75723	angiomotin-like 1	Amotl1	1.116	1.745	0.123268	0.351406
3633	10503882	NM_011884	24018	RNA guanylyltransferase and 5'	Rngtt	1.116	0.963	0.366876	0.637877
3634	10364650	NM_027521	70719	histocompatibility (minor) HA-	Hmha1	1.116	1.846	0.106139	0.32138
3635	10516666	NM_001005506	109658	taxilin alpha	Txlna	1.116	1.782	0.116675	0.340086
3636	10424796	AK005822	100041269	predicted gene, ENSMUSG0000007	ENSMUSG00000071724	1.116	1.679	0.135704	0.371434
3637	10423505	NM_181588	69574	carboxymethylenebutenolidase-l	Cmbl	1.116	1.028	0.337182	0.612796
3638	10492195	NM_001081229	72033	TSC22 domain family 2	Tsc22d2	1.116	2.133	0.0692101	0.246526
3639	10493498					1.116	2.427	0.0445906	0.186809
3640	10383313	NM_198423	268515	BAH domain and coiled-coil con	Bahcc1	1.116	2.174	0.0650861	0.23797
3641	10479411	NM_031373	72075	opioid growth factor receptor	Ogfr	1.116	1.098	0.307623	0.584192
3642	10376577					1.116	0.683	0.515994	0.755582
3643	10455782					1.116	1.04	0.331776	0.608173
3644	10391914	NM_183288	70559	RIKEN cDNA 5730442P18 gene	5730442P18Rik	1.116	1.927	0.0941677	0.297861
3645	10382200	NM_029606	76380	coiled-coil domain containing	Ccdc46	1.115	1.2	0.268236	0.542786
3646	10574139					1.115	1.5	0.175944	0.429653
3647	10353899	NM_001126047	20353	sema domain, immunoglobulin do	Sema4c	1.115	1.707	0.130246	0.362012
3648	10441115	NM_145125	93871	bromodomain and WD repeat doma	Brwd1	1.115	1.744	0.123336	0.351451
3649	10430433	AK131739	69996	RIKEN cDNA 1700027A07 gene	1700027A07Rik	1.115	1.054	0.325704	0.601982
3650	10529515	NM_030889	81840	sortilin-related VPS10 domain	Sorcs2	1.115	0.978	0.359563	0.63155
3651	10408898					1.115	1.572	0.158699	0.405501
3652	10394477	NM_008640	17775	lysosomal-associated protein t	Laptm4a	1.115	2.324	0.0520032	0.206218
3653	10465844	NM_025610	66514	asparaginase like 1	Asrgl1	1.115	1.202	0.267462	0.542206
3654	10410465	BC026613	218333	cDNA sequence BC018507	BC018507	1.115	1.912	0.0962968	0.302072
3655	10576829	NM_130903	170776	CD209c antigen	Cd209c	1.115	0.747	0.478984	0.729132
3656	10451860	NM_028370	72836	protection of telomeres 1B	Pot1b	1.115	1.319	0.227571	0.49837
3657	10395129	NM_172049	211986	transmembrane protein 18	Tmem18	1.115	1.445	0.190549	0.449454
3658	10345715	NM_008696	26921	mitogen-activated protein kina	Map4k4	1.115	2.129	0.0695739	0.247236
3659	10515731	ENSMUST00000075406	230676	cDNA sequence BC059842	BC059842	1.115	0.781	0.459705	0.714602
3660	10527229	NM_026050	67238	RIKEN cDNA 2810453I06 gene	2810453I06Rik	1.115	0.901	0.396459	0.663863
3661	10503570	ENSMUST00000098238	66625	splicing factor, arginine/seri	Sfrs18	1.114	2.063	0.076849	0.262843
3662	10531166	NM_001081401	330119	a disintegrin-like and metallo	Adamts3	1.114	1.25	0.250298	0.524354
3663	10547943	NM_146171	68298	non-SMC condensin I complex, s	Ncapd2	1.114	0.773	0.464245	0.718069
3664	10450872	NM_146515	258508	olfactory receptor 99	Olfr99	1.114	0.862	0.416376	0.67936
3665	10541910	NM_011708	22371	Von Willebrand factor homolog	Vwf	1.114	1.935	0.0930415	0.295652
3666	10427214	NM_013672	20683	trans-acting transcription fac	Sp1	1.114	1.142	0.290082	0.566261
3667	10362767	NM_138315	171580	microtubule associated monoxyg	Mical1	1.114	1.741	0.123996	0.352437
3668	10420668					1.114	1.056	0.324978	0.601325
3669	10412699					1.114	1.825	0.109572	0.327185
3670	10360105	NM_013919	30941	ubiquitin specific peptidase 2	Usp21	1.114	0.843	0.426433	0.687967
3671	10540935	NM_025958	67088	cullin-associated and neddylat	Cand2	1.114	1.762	0.120263	0.346577
3672	10515429					1.114	1.563	0.160848	0.408621
3673	10588755	NM_145621	235604	CaM kinase-like vesicle-associ	Camkv	1.114	0.921	0.386599	0.655658
3674	10578320	XR_030685	667019	similar to High mobility group	LOC667019	1.114	2.356	0.0496218	0.200156
3675	10427461	NM_008965	19219	prostaglandin E receptor 4 (su	Ptger4	1.114	1.51	0.173667	0.426449
3676	10395324	NM_029294	75456	phosphoribosyl pyrophosphate s	Prps1l1	1.114	1.117	0.299651	0.575741
3677	10554895	NM_145151	233490	CREB/ATF bZIP transcription fa	Crebzf	1.114	1.938	0.0925851	0.294729
3678	10583163	NM_013838	22068	transient receptor potential c	Trpc6	1.114	1.386	0.206996	0.471406
3679	10459703					1.113	2.288	0.0549093	0.213655
3680	10495657	ENSMUST00000093985	66789	asparagine-linked glycosylatio	Alg14	1.113	1.443	0.190984	0.450035
3681	10373054	BC089587	216441	solute carrier family 26, memb	Slc26a10	1.113	1.907	0.0969864	0.30331
3682	10374413					1.113	1.96	0.0896593	0.289031
3683	10486166	NM_199310	269336	coiled-coil domain containing	Ccdc32	1.113	1.514	0.172671	0.425024
3684	10560709	NM_027514	52118	poliovirus receptor	Pvr	1.113	0.915	0.389953	0.658612

3685	10416169	NM_008145	14714	gonadotropin releasing hormone	Gnrh1	1.113	1.528	0.169007	0.420416
3686	10542965	NM_011360	20392	sarcoglycan, epsilon	Sgce	1.113	1.457	0.18728	0.445668
3687	10487577	NM_181589	70466	cytoskeleton associated protei	Ckap2l	1.113	1.427	0.195481	0.455756
3688	10590467	BC080690	382117	DNA segment, Chr 9, ERATO Doi	D9Ertd402e	1.113	1.612	0.149755	0.392417
3689	10533849	NM_021430	75695	Rab interacting lysosomal prot	Rilpl1	1.113	2.171	0.0653447	0.238462
3690	10552932	NM_010596	16495	potassium voltage-gated channe	Kcna7	1.113	1.918	0.0953376	0.300062
3691	10410264	NM_025547	66410	MTERF domain containing 1	Mterfd1	1.113	1.299	0.233894	0.505206
3692	10584013					1.113	2.072	0.0757672	0.260364
3693	10464659	NM_011237	19367	RAD9 homolog (S. pombe)	Rad9	1.113	1.201	0.267711	0.542452
3694	10469811	NM_153077	215274	interleukin 1 family, member 1	Il1f10	1.112	1.988	0.0859164	0.281297
3695	10524331	BC094571	330164	RIKEN cDNA C130026L21 gene	C130026L21Rik	1.112	1.298	0.234232	0.505464
3696	10458098	BC031465	225358	RIKEN cDNA 2610024E20 gene	2610024E20Rik	1.112	1.523	0.170243	0.421869
3697	10404941	NM_172262	218214	amine oxidase, flavin containi	Aof1	1.112	1.598	0.152884	0.396925
3698	10465910					1.112	1.437	0.192578	0.452078
3699	10372928	NM_153395	67074	MON2 homolog (yeast)	Mon2	1.112	1.551	0.163611	0.412815
3700	10595298	NM_001081243	70598	filamin A interacting protein	Filip1	1.112	0.872	0.411329	0.675346
3701	10482695	NM_001037099	12298	calcium channel, voltage-depen	Cacnb4	1.112	1.077	0.316254	0.593179
3702	10376033	NM_008443	16568	kinesin family member 3A	Kif3a	1.112	1.559	0.161794	0.410091
3703	10478590	NM_028028	71971	zinc finger, SWIM domain conta	Zswim1	1.112	0.976	0.360768	0.632458
3704	10586166					1.112	0.446	0.668754	0.852586
3705	10380819	ENSMUST00000060568	72785	RIKEN cDNA 2810474C18 gene	2810474C18Rik	1.112	1.565	0.160249	0.407591
3706	10557862	NM_001082960	16409	integrin alpha M	Itgam	1.112	1.942	0.092043	0.293984
3707	10425755					1.112	1.238	0.254533	0.528824
3708	10470584	NM_022887	64930	tuberous sclerosis 1	Tsc1	1.112	1.18	0.27533	0.550191
3709	10607486	NM_001093750	211612	patched domain containing 1	Ptchd1	1.112	0.44	0.672898	0.854651
3710	10413492	NM_176920	319476	leucine-rich repeats and trans	Lrtm1	1.112	1.316	0.228444	0.499454
3711	10460461	NM_025717	66704	RNA binding motif protein 4B	Rbm4b	1.112	1.263	0.245844	0.51897
3712	10550847	NM_019941	56525	zinc finger protein 235	Zfp235	1.112	1.454	0.187992	0.446224
3713	10413695	NM_001081251	66923	polybromo 1	Pbrm1	1.112	1.342	0.220305	0.488992
3714	10377010	NM_001040026	52892	SCO cytochrome oxidase deficie	Sco1	1.112	0.943	0.376129	0.646208
3715	10509584	NM_001082531	18780	phospholipase A2, group IIA (p	Pla2g2a	1.112	1.336	0.222265	0.492042
3716	10560242	NM_007577	12273	complement component 5a recept	C5ar1	1.112	1.544	0.16534	0.415485
3717	10586448	NM_026515	68026	RIKEN cDNA 2810417H13 gene	2810417H13Rik	1.112	0.676	0.520065	0.757683
3718	10573893	NM_011936	26383	fat mass and obesity associate	Fto	1.112	1.673	0.136978	0.373595
3719	10420080	NM_023397	67881	RIKEN cDNA 1810034K20 gene	1810034K20Rik	1.111	1.307	0.231444	0.502324
3720	10436967	NM_007620	12408	carbonyl reductase 1	Cbr1	1.111	1.044	0.330322	0.606542
3721	10478364	NM_001098799	269389	TOX high mobility group box fa	Tox2	1.111	1.597	0.15296	0.396978
3722	10547613	NM_027664	108653	RIKEN cDNA 4933426K21 gene	4933426K21Rik	1.111	0.657	0.531282	0.765579
3723	10381603	NM_020510	57265	frizzled homolog 2 (Drosophila	Fzd2	1.111	1.232	0.256459	0.530714
3724	10601044	NM_023608	71584	glycerophosphodiester phosphod	Gdpd2	1.111	1.697	0.132201	0.365389
3725	10363445	NM_028732	74048	RIKEN cDNA 4632428N05 gene	4632428N05Rik	1.111	2.152	0.067235	0.242225
3726	10541762	NM_175557	269800	zinc finger protein 384	Zfp384	1.111	1.481	0.18095	0.436858
3727	10398824	BC096642	319942	RIKEN cDNA A530016L24 gene	A530016L24Rik	1.111	2.595	0.0347987	0.158375
3728	10553835	BC054763	27385	melanoma antigen, family L, 2	Magel2	1.111	1.471	0.18357	0.440767
3729	10410975	NM_145453	69085	zinc finger, CCHC domain conta	Zcchc9	1.111	1.526	0.169519	0.420889
3730	10362520	NM_008229	15182	histone deacetylase 2	Hdac2	1.111	2.138	0.0686912	0.245297
3731	10545588	NM_013820	15277	hexokinase 2	Hk2	1.111	1.348	0.218595	0.486779
3732	10590298	NM_026892	68969	eukaryotic translation initiat	Eif1b	1.111	1.387	0.206879	0.471397
3733	10352178	NM_178653	109232	saccharopine dehydrogenase (pu	Sccpdh	1.111	0.999	0.350203	0.623711
3734	10432176					1.111	0.348	0.737962	0.888273

3735	10356657	NM_024197	67273	NADH dehydrogenase (ubiquinone	Ndufa10	1.111	1.53	0.168514	0.419875
3736	10566922	ENSMUST00000098108	619306	RIKEN cDNA B430319F04 gene	B430319F04Rik	1.111	1.106	0.30409	0.580401
3737	10508128	BC029204	230752	RIKEN cDNA 2610027C15 gene	2610027C15Rik	1.111	1.899	0.0980976	0.30552
3738	10469965	NM_175300	99152	anaphase promoting complex sub	Anapc2	1.111	1.272	0.24296	0.51587
3739	10553319	ENSMUST00000070660	629141	predicted gene, ENSMUSG0000005	ENSMUSG00000056509	1.111	1.306	0.231743	0.502487
3740	10438245	NM_022408	27886	expressed sequence 2 embryonic	Es2el	1.111	1.44	0.191906	0.451201
3741	10365769	NM_010401	15109	histidine ammonia lyase	Hal	1.111	1.424	0.1963	0.45671
3742	10510061	BC056931	242736	RIKEN cDNA 4732496O08 gene	4732496O08Rik	1.111	0.563	0.590522	0.806276
3743	10469695	NM_019456	54519	amyloid beta (A4) precursor pr	Apbb1ip	1.111	1.074	0.317468	0.594727
3744	10409804	NM_153538	214290	zinc finger, CCHC domain conta	Zcchc6	1.11	1.374	0.210707	0.476211
3745	10384766					1.11	1.65	0.141632	0.381146
3746	10455959					1.11	2.068	0.076292	0.261682
3747	10600403	NM_138607	108160	DNA segment, human DXS9928E	D0HXS9928E	1.11	1.205	0.266096	0.541183
3748	10453830	NM_144860	225164	mindbomb homolog 1 (Drosophila	Mib1	1.11	1.813	0.111536	0.330459
3749	10514713	NM_146254	242584	WD repeat domain 78	Wdr78	1.11	1.811	0.111847	0.331046
3750	10445033	NM_001025599	22670	tripartite motif-containing 26	Trim26	1.11	1.932	0.0934104	0.296335
3751	10550326	NM_198613	232910	adaptor-related protein comple	Ap2s1	1.11	1.603	0.151764	0.395645
3752	10574451	ENSMUST00000093245	65115	brain expressed, associated wi	Bean	1.11	1.587	0.155322	0.400794
3753	10361250	NM_144817	215303	calcium/calmodulin-dependent p	Camk1g	1.11	1.644	0.142835	0.382955
3754	10390336	NM_198100	73174	TBK1 binding protein 1	Tbkbp1	1.11	2.199	0.062697	0.2318
3755	10357630	NM_001081011	14270	SLIT-ROBO Rho GTPase activatin	Srgap2	1.11	1.271	0.243292	0.516291
3756	10419874	NM_021551	59049	solute carrier family 22 (orga	Slc22a17	1.11	1.626	0.146773	0.388752
3757	10488926	ENSMUST00000099160	613262	cDNA sequence BC029722	BC029722	1.11	1.708	0.130113	0.36185
3758	10544501	NM_007971	14056	enhancer of zeste homolog 2 (D	Ezh2	1.11	2.102	0.0725345	0.253709
3759	10563872	NM_176942	110886	gamma-aminobutyric acid (GABA-	Gabra5	1.11	1.436	0.193025	0.452475
3760	10494832	NM_025679	66641	RIKEN cDNA 5730470L24 gene	5730470L24Rik	1.11	1.238	0.254347	0.528633
3761	10598389	NM_172372	54636	WD repeat domain 45	Wdr45	1.11	2.083	0.0745347	0.258241
3762	10548128	NM_175414	109246	tetraspanin 9	Tspan9	1.11	1.459	0.186694	0.444956
3763	10394381	NM_001099628	320817	ATPase family, AAA domain cont	Atad2b	1.109	1.433	0.193624	0.453103
3764	10424331	NM_026642	68260	tRNA methyltranferase 12 homol	Trmt12	1.109	0.892	0.401398	0.666762
3765	10503359	NM_198957	77604	RIKEN cDNA C430048L16 gene	C430048L16Rik	1.109	1.913	0.0960544	0.301621
3766	10515712	ENSMUST00000075406	230676	cDNA sequence BC059842	BC059842	1.109	1.164	0.28161	0.556928
3767	10522090	NM_153391	213081	WD repeat domain 19	Wdr19	1.109	0.765	0.468336	0.720616
3768	10577315	NM_007426	11601	angiopoietin 2	Angpt2	1.109	1.59	0.154618	0.399809
3769	10596492	NM_145619	235587	poly (ADP-ribose) polymerase f	Parp3	1.109	2.257	0.0574807	0.219583
3770	10427796	NM_008728	18162	natriuretic peptide receptor 3	Npr3	1.109	0.443	0.670867	0.85389
3771	10491595					1.109	0.771	0.465228	0.718906
3772	10381082	NM_009024	19401	retinoic acid receptor, alpha	Rara	1.109	1.57	0.159225	0.406366
3773	10397364	NM_145447	217721	feline leukemia virus subgroup	Flvcr2	1.109	2.216	0.0610995	0.228128
3774	10453918	NM_029623	76482	RIKEN cDNA 3110002H16 gene	3110002H16Rik	1.109	0.893	0.400592	0.666392
3775	10487447	NM_145532	228576	mal, T-cell differentiation pr	Mall	1.109	2.221	0.0606869	0.227229
3776	10416655	NM_001034882	432879	predicted gene, EG432879	EG432879	1.109	1.486	0.179656	0.434993
3777	10498403					1.109	2.386	0.0474308	0.193793
3778	10428877	BC067035	223593	RIKEN cDNA E430025E21 gene	E430025E21Rik	1.109	0.973	0.362202	0.633711
3779	10588903	NM_011678	22258	ubiquitin specific peptidase 4	Usp4	1.109	1.292	0.236334	0.508399
3780	10520696	ENSMUST00000066505	791336	predicted gene, ENSMUSG0000005	ENSMUSG00000053839	1.109	1.22	0.260865	0.535507

3781	10587942	NM_011916	24127	5'-3' exoribonuclease 1	Xrn1	1.109	1.172	0.278429	0.553444
3782	10429385					1.109	0.786	0.457129	0.712903
3783	10504534	NM_001081172	666060	FERM and PDZ domain containing	Frmpd1	1.109	1.809	0.112158	0.331562
3784	10467852	NM_145156	246696	solute carrier family 25, memb	Slc25a28	1.109	2.193	0.0632484	0.233146
3785	10410650	NM_146231	235956	zinc finger protein 825	Zfp825	1.109	1.275	0.241696	0.514457
3786	10377560	NM_026991	69215	spermidine/spermine N1-acetyl	Sat2	1.109	1.057	0.324725	0.60112
3787	10535231	NM_175274	78339	tweety homolog 3 (Drosophila)	Ttyh3	1.109	2.038	0.0797693	0.269041
3788	10354418	NM_028696	109019	oligonucleotide/oligosaccharid	Obfc2a	1.109	0.339	0.744068	0.891263
3789	10410547	NM_028186	72293	naked cuticle 2 homolog (Droso	Nkd2	1.109	2.376	0.0481451	0.195916
3790	10394158	NM_008445	16570	kinesin family member 3C	Kif3c	1.109	1.714	0.129034	0.360251
3791	10578042	XM_282816	330731	predicted gene, EG330731	EG330731	1.109	1.192	0.271075	0.545712
3792	10450379	NM_023893	78376	Ng23 protein	Ng23	1.108	1.278	0.240865	0.513859
3793	10516950	NM_201368	381560	X Kell blood group precursor r	Xkr8	1.108	1.704	0.130926	0.363197
3794	10511755	NM_177327	107568	WW domain containing E3 ubiqui	Wwp1	1.108	1.025	0.338336	0.6139
3795	10455687	NM_001081224	71373	proline rich 16	Prr16	1.108	1.143	0.289505	0.56553
3796	10456206	BC125573	104082	WD repeat domain 7	Wdr7	1.108	1.412	0.199699	0.461464
3797	10441494	NM_001103181	68842	tubby like protein 4	Tulp4	1.108	1.903	0.0975381	0.304315
3798	10514421	NM_175305	100061	leucine rich repeat containing	Lrrc19	1.108	1.358	0.215456	0.482533
3799	10507933	NM_008385	16330	inositol polyphosphate-5-phosp	Inpp5b	1.108	1.713	0.129244	0.360472
3800	10362294	NM_176837	73910	Rho GTPase activating protein	Arhgap18	1.108	0.927	0.3838	0.653229
3801	10452556	NM_024448	19328	RAB12, member RAS oncogene fam	Rab12	1.108	0.458	0.660724	0.848802
3802	10479887	NM_021305	57743	Sec61, alpha subunit 2 (S. cer	Sec61a2	1.108	0.958	0.369008	0.639743
3803	10453627	AK043736	433157	hypothetical gene supported by	LOC433157	1.108	1.302	0.232882	0.503895
3804	10547869	NM_013534	14789	leprecan-like 2	Leprel2	1.108	1.686	0.134367	0.36953
3805	10596231	ENSMUST00000035170	235567	DnaJ (Hsp40) homolog, subfamil	Dnajc13	1.108	2.058	0.0774084	0.264201
3806	10591563	NM_145611	235041	KN motif and ankyrin repeat do	Kank2	1.108	2.178	0.0646823	0.236862
3807	10544982	NM_026004	107569	5'-nucleotidase, cytosolic III	Nt5c3	1.108	0.885	0.404882	0.669594
3808	10565852	ENSMUST00000080817	108937	ring finger protein 169	Rnf169	1.107	1.323	0.226356	0.496985
3809	10493900	NM_033175	94060	late cornified envelope 3C	Lce3c	1.107	0.972	0.362458	0.633904
3810	10399421	NM_008709	18109	v-myc myelocytomatosis viral r	Mycn	1.107	1.13	0.29472	0.570991
3811	10412235	ENSMUST00000057096	319803	RIKEN cDNA A430090L17 gene	A430090L17Rik	1.107	2.167	0.0658192	0.239203
3812	10420891	NM_172604	219151	scavenger receptor class A, me	Scara3	1.107	1.301	0.233439	0.504686
3813	10508797	AY512921	791321	predicted gene, ENSMUSG0000006	ENSMUSG00000066041	1.107	1.729	0.126159	0.355658
3814	10360664	ENSMUST00000070201	791296	predicted gene, ENSMUSG0000005	ENSMUSG00000056615	1.107	1.082	0.313958	0.590809
3815	10578138	NM_011722	22428	dynactin 6	Dctn6	1.107	1.06	0.32321	0.599838
3816	10449815	NM_020508	57261	bromodomain containing 4	Brd4	1.107	1.911	0.0964548	0.302302
3817	10505528					1.107	1.328	0.224641	0.494757
3818	10427199	NM_027044	56612	prefoldin 5	Pfdn5	1.107	1.387	0.206784	0.471259
3819	10412335	NM_021459	16392	ISL1 transcription factor, LIM	Isl1	1.107	0.144	0.889463	0.956457
3820	10404051	NM_175654	319156	histone cluster 1, H4d	Hist1h4d	1.107	0.655	0.533092	0.767147
3821	10363860	NM_025807	66859	solute carrier family 16 (mono	Slc16a9	1.107	1.251	0.2501	0.524217
3822	10356520	AF064749	12835	collagen, type VI, alpha 3	Col6a3	1.107	1.087	0.31219	0.58853
3823	10368041	NM_028440	73112	RIKEN cDNA 3110003A17 gene	3110003A17Rik	1.107	1.092	0.309837	0.586709
3824	10500122	NM_134253	171388	BCL2/adenovirus E1B 19kD inter	Bnipl	1.107	1.694	0.132862	0.366501
3825	10581197	NM_177788	277978	exocyst complex component 3-li	Exoc3l	1.107	1.994	0.0852325	0.280273
3826	10537026	NM_027926	71791	carboxypeptidase A4	Cpa4	1.107	1.193	0.27076	0.545372
3827	10572533	NM_015742	17925	myosin IXb	Myo9b	1.107	2.079	0.0750097	0.258984
3828	10440393	NM_023380	67742	SAM domain, SH3 domain and nuc	Samsn1	1.107	1.742	0.123799	0.352065
3829	10573703	NM_029074	382030	transmembrane protein 188	Tmem188	1.107	1.749	0.122544	0.350144

3830	10568988	NM_018742	54399	blocked early in transport 1 h	Bet1l	1.107	1.036	0.333769	0.609432
3831	10550146	NM_013877	29865	calcium binding protein 5	Cabp5	1.107	1.791	0.115128	0.337402
3832	10483633	NM_001018042	20687	trans-acting transcription fac	Sp3	1.106	1.539	0.166508	0.417287
3833	10381018	NM_028722	74026	RIKEN cDNA 4121402D02 gene	4121402D02Rik	1.106	1.82	0.110262	0.328467
3834	10479988	NM_027748	209361	TAF3 RNA polymerase II, TATA b	Taf3	1.106	1.003	0.348515	0.622153
3835	10456317	NM_207255	328977	zinc finger protein 532	Zfp532	1.106	1.834	0.108129	0.32441
3836	10520698	NM_177677	231098	DnaJ (Hsp40) homolog, subfamil	Dnajc5g	1.106	1.484	0.180179	0.435693
3837	10551359	NM_018820	55942	SERTA domain containing 1	Sertad1	1.106	1.229	0.257557	0.531659
3838	10523865	NM_182745	76421	RIKEN cDNA 1700028K03 gene	1700028K03Rik	1.106	2.264	0.0569029	0.218163
3839	10376897					1.106	0.833	0.431353	0.691897
3840	10505489	NM_021362	18491	pregnancy-associated plasma pr	Pappa	1.106	1.679	0.135691	0.371434
3841	10525387	NM_024216	68080	ATP binding domain 1 family, m	Atpbd1c	1.106	0.753	0.475538	0.72707
3842	10590433					1.106	0.869	0.412598	0.676183
3843	10428827	NM_175212	74868	transmembrane protein 65	Tmem65	1.106	1.25	0.250408	0.524406
3844	10519942	ENSMUST00000088514	50791	membrane associated guanylate	Magi2	1.106	1.658	0.140087	0.378724
3845	10402598	ENSMUST00000073156	380785	brain-enriched guanylate kinas	Begain	1.106	1.927	0.094139	0.297861
3846	10562204	NM_022007	57780	FXYD domain-containing ion tra	Fxyd7	1.106	2.127	0.0697876	0.247552
3847	10494174	NM_011351	20360	sema domain, transmembrane dom	Sema6c	1.106	1.859	0.104103	0.31726
3848	10472538	NM_175512	241452	dehydrogenase/reductase (SDR f	Dhrs9	1.106	1.502	0.175594	0.429072
3849	10402294	NM_022323	64113	modulator of apoptosis 1	Moap1	1.106	1.317	0.228156	0.499185
3850	10554045	NM_001033877	233332	a disintegrin-like and metallo	Adamts17	1.106	1.258	0.247648	0.520853
3851	10380558					1.106	1.263	0.245937	0.51897
3852	10523856					1.106	0.53	0.612305	0.820234
3853	10433219	NM_029090	74763	RIKEN cDNA 1200013P24 gene	1200013P24Rik	1.106	1.185	0.273638	0.548314
3854	10529034	BC023116	68567	cell growth regulator with EF	Cgref1	1.106	1.424	0.196281	0.45671
3855	10445373	ENSMUST00000097319	320063	RIKEN cDNA B230354K17 gene	B230354K17Rik	1.106	0.427	0.681731	0.859336
3856	10573908					1.106	1.309	0.230769	0.501612
3857	10465366	NM_024231	81909	zinc finger like protein 1	Zfpl1	1.106	1.153	0.285519	0.560861
3858	10584407	NM_001011806	258028	olfactory receptor 901	Olfr901	1.106	1.149	0.287329	0.562985
3859	10463404	NM_001081225	226151	RIKEN cDNA 6030443O07 gene	6030443O07Rik	1.106	1.184	0.273866	0.548502
3860	10520521	NM_007681	12615	centromere protein A	Cenpa	1.106	1.725	0.12689	0.356872
3861	10596093	XM_356179	382099	predicted gene, EG382099	EG382099	1.106	1.775	0.117919	0.342718
3862	10604094	NM_001033785	434756	A kinase (PRKA) anchor protein	Akap14	1.106	1.566	0.160055	0.407342
3863	10585572	NM_025812	66867	high mobility group 20A	Hmg20a	1.105	1.275	0.241778	0.514522
3864	10356577	NM_023343	67444	integrin-linked kinase-associa	Ilkap	1.105	1.213	0.263358	0.538069
3865	10468489	NM_133216	170750	X-prolyl aminopeptidase (amino	Xpnpep1	1.105	1.002	0.348705	0.622353
3866	10608509					1.105	0.836	0.429826	0.690652
3867	10513188	ENSMUST00000098063	100038668	predicted gene, OTTMUSG0000000	OTTMUSG00000007322	1.105	0.977	0.360247	0.632213
3868	10510725	NM_001081376	269610	chromodomain helicase DNA bind	Chd5	1.105	2.156	0.0668324	0.241483
3869	10527448	NM_001008705	231889	BUD31 homolog (yeast)	Bud31	1.105	0.693	0.510052	0.751325
3870	10395273	BC052902	14546	ganglioside-induced differenti	Gdap10	1.105	0.663	0.527939	0.763369
3871	10493394	NM_007712	12748	CDC-like kinase 2	Clk2	1.105	1.953	0.0904801	0.290658
3872	10544406	NM_029528	76156	RIKEN cDNA 6330503C03 gene	6330503C03Rik	1.105	1.798	0.113992	0.334988
3873	10519346	BC099581	77036	RIKEN cDNA 1700109H08 gene	1700109H08Rik	1.105	0.764	0.469293	0.721467
3874	10596041	NM_001033543	213208	interleukin 20 receptor beta	Il20rb	1.105	2.195	0.063077	0.232827
3875	10484457	NM_133840	98985	CLP1, cleavage and polyadenyla	Clp1	1.105	0.772	0.464593	0.718344
3876	10518812	NM_001081557	100072	calmodulin binding transcripti	Camta1	1.105	1.509	0.173736	0.426449
3877	10469151	NM_172471	209378	inter-alpha (globulin) inhibit	Itih5	1.105	1.303	0.232678	0.503682
3878	10591224	NM_001004190	434377	zinc finger protein 560	Zfp560	1.105	0.569	0.58637	0.803667
3879	10482144	NM_001100591	319817	ring finger and CCCH-type zinc	Rc3h2	1.105	1.805	0.112732	0.33261

3880	10456501	NM_026440	67897	RNA (guanine-7-) methyltransfe	Rnmt	1.105	0.911	0.391908	0.660136
3881	10531259	ENSMUST00000101038	100038686	predicted gene, ENSMUSG0000007	ENSMUSG00000072833	1.105	1.529	0.168959	0.420416
3882	10514865	NM_025590	329910	acyl-CoA thioesterase 11	Acot11	1.105	1.826	0.109297	0.326638
3883	10507473					1.105	1.422	0.196836	0.457653
3884	10426479	NM_175344	105722	transmembrane protein 16F	Tmem16f	1.105	0.662	0.528744	0.764097
3885	10350749	NM_001008426	433365	predicted gene, EG433365	EG433365	1.105	1.334	0.222765	0.492656
3886	10450101					1.105	1.434	0.193341	0.452663
3887	10349427					1.105	1.937	0.0926986	0.294873
3888	10436369	BC062166	78749	RIKEN cDNA 4631422O05 gene	4631422O05Rik	1.105	1.003	0.348312	0.622132
3889	10369485	NM_007731	12817	collagen, type XIII, alpha 1	Col13a1	1.105	2.124	0.0701371	0.248239
3890	10605711	NM_145630	236900	pyruvate dehydrogenase kinase,	Pdk3	1.105	0.818	0.439609	0.698931
3891	10399555	NM_201531	382571	potassium voltage-gated channe	Kcnf1	1.105	1.016	0.342647	0.616958
3892	10488722	NM_133850	99311	COMM domain containing 7	Commd7	1.105	1.092	0.310104	0.586794
3893	10351277	NM_138314	171567	non-metastatic cells 7, protei	Nme7	1.105	0.561	0.591715	0.806879
3894	10445442	NM_019581	56055	GTP binding protein 2	Gtpbp2	1.105	1.989	0.0857681	0.281088
3895	10410716	NM_175495	238725	G protein-coupled receptor 150	Gpr150	1.105	2.202	0.062467	0.231354
3896	10524525	NM_054093	117146	ubiquitin protein ligase E3B	Ube3b	1.105	1.21	0.26427	0.539355
3897	10468881	BC086681	414758	RIKEN cDNA 5830428H23 gene	5830428H23Rik	1.105	0.317	0.760107	0.89957
3898	10470462	NM_015734	12831	collagen, type V, alpha 1	Col5a1	1.104	1.599	0.152536	0.396392
3899	10588592	NM_020263	56808	calcium channel, voltage-depen	Cacna2d2	1.104	1.847	0.106009	0.321126
3900	10519270	NM_021604	11603	agrin	Agrn	1.104	1.527	0.169261	0.42056
3901	10349661	NM_145509	226421	RIKEN cDNA 5430435G22 gene	5430435G22Rik	1.104	1.705	0.130753	0.362909
3902	10410362	ENSMUST00000071628	78251	zinc finger protein 712	Zfp712	1.104	0.171	0.869164	0.947675
3903	10570644	NM_001025353	574083	predicted gene, EG574083	EG574083	1.104	1.148	0.287425	0.563027
3904	10493688	ENSMUST00000029548	77595	nucleoporin 210-like	Nup210l	1.104	1.871	0.102232	0.313502
3905	10527571					1.104	0.47	0.65202	0.844083
3906	10579525	NM_032398	84094	plasmalemma vesicle associated	Plvap	1.104	1.852	0.105163	0.319429
3907	10410168	ENSMUST00000116396	218304	gene model 274, (NCBI)	Gm274	1.104	2.085	0.074336	0.257888
3908	10525489	ENSMUST00000100731	208043	SET domain containing 1B	Setd1b	1.104	1.175	0.277206	0.552231
3909	10349876	NM_182930	240753	pleckstrin homology domain con	Plekha6	1.104	1.359	0.215207	0.482283
3910	10515558	NM_009711	11876	artemin	Artn	1.104	1.712	0.129332	0.360575
3911	10393373	NM_011371	20445	ST6 (alpha-N-acetyl-neuraminyl	St6galnac1	1.104	1.204	0.26664	0.541268
3912	10408225	NM_178208	319155	histone cluster 1, H4c	Hist1h4c	1.104	0.24	0.817129	0.927197
3913	10591739	NM_001102404	11433	acid phosphatase 5, tartrate r	Acp5	1.104	0.865	0.415005	0.678382
3914	10430920	NM_001114140	21411	transcription factor 20	Tcf20	1.104	1.898	0.0982249	0.305827
3915	10529480	ENSMUST00000068438	74364	RIKEN cDNA 4931431C16 gene	4931431C16Rik	1.104	1.781	0.116926	0.340629
3916	10578757					1.104	0.92	0.387501	0.656379
3917	10512088	NM_134097	106021	topoisomerase I binding, argin	Topors	1.104	0.94	0.377755	0.64758
3918	10601150					1.104	0.704	0.5038	0.746156
3919	10379060	NM_001045516	216974	RIKEN cDNA 4933404M19 gene	4933404M19Rik	1.104	0.466	0.654693	0.845294
3920	10377924	NM_010326	14723	glycoprotein 1b, alpha polypep	Gp1ba	1.104	1.565	0.160415	0.407767
3921	10410273	NM_001012325	432769	zinc finger protein 708	Zfp708	1.104	1.695	0.132732	0.366429
3922	10531274	NM_007568	12223	betacellulin, epidermal growth	Btc	1.103	1.342	0.22016	0.488992
3923	10414025	NM_145741	14560	growth differentiation factor	Gdf10	1.103	0.591	0.572373	0.796254
3924	10400395	NM_021529	59032	protein phosphatase 2, regulat	Ppp2r3c	1.103	0.765	0.468685	0.720927
3925	10598765	NM_025738	66742	cysteine-rich perinuclear thec	Cypt6	1.103	1.523	0.170211	0.421869
3926	10554588	NM_017400	20408	SH3-domain GRB2-like 3	Sh3gl3	1.103	1.594	0.153816	0.398321
3927	10527538	NM_026864	68895	RAS-like, family 11, member A	Rasl11a	1.103	2.185	0.0640796	0.235266
3928	10553967	ENSMUST00000055576	18553	proprotein convertase subtilis	Pcsk6	1.103	1.239	0.254172	0.528502
3929	10382888	AK171830	76972	RIKEN cDNA 2810008D09 gene	2810008D09Rik	1.103	0.836	0.429869	0.690652
3930	10497199	NM_145538	407243	transmembrane protein 189	Tmem189	1.103	0.965	0.365801	0.636847

3931	10463061	ENSMUST00000068094	107141	cytochrome P450, family 2, sub	Cyp2c50	1.103	2.247	0.0583368	0.221848
3932	10395428	NM_178681	217480	diacylglycerol kinase, beta	Dgkb	1.103	0.566	0.588806	0.805202
3933	10525397	NM_019824	56378	actin related protein 2/3 comp	Arpc3	1.103	0.752	0.475683	0.727129
3934	10411853	NM_001005868	59079	Erbb2 interacting protein	Erbb2ip	1.103	1.585	0.155661	0.401373
3935	10353923	NM_201365	381337	cDNA sequence BC050210	BC050210	1.103	1.895	0.0987595	0.306809
3936	10518408	NM_011122	18822	procollagen-lysine, 2-oxogluta	Plod1	1.103	1.433	0.193617	0.453103
3937	10492668	ENSMUST00000091023	75879	RIKEN cDNA 4930589L23 gene	4930589L23Rik	1.103	1.299	0.234044	0.50534
3938	10582941	NM_027545	244672	CWF19-like 2, cell cycle contr	Cwf19l2	1.103	1.074	0.317488	0.594727
3939	10459530	ENSMUST00000054227	338360	RIKEN cDNA B430212C06 gene	B430212C06Rik	1.103	0.922	0.386121	0.655109
3940	10598933	NM_145628	236733	ubiquitin specific peptidase 1	Usp11	1.103	1.167	0.280277	0.555618
3941	10535471	NM_009007	19353	RAS-related C3 botulinum subst	Rac1	1.103	1.674	0.136809	0.373443
3942	10493758	NM_139304	229542	GATA zinc finger domain contai	Gatad2b	1.103	2.053	0.0779575	0.26556
3943	10446044	NM_008233	15193	hepatoma-derived growth factor	Hdgfrp2	1.103	1.95	0.0909397	0.291551
3944	10542079	NM_008021	14235	forkhead box M1	Foxm1	1.103	1.174	0.277646	0.552783
3945	10515983	BC023360	73172	RIKEN cDNA 3110037I16 gene	3110037I16Rik	1.103	1.537	0.1669	0.417872
3946	10354247	NM_010212	14200	four and a half LIM domains 2	Fhl2	1.103	0.958	0.369164	0.639859
3947	10386636	NM_001004143	216825	ubiquitin specific peptidase 2	Usp22	1.103	1.43	0.194565	0.454622
3948	10519179	ENSMUST00000097743	68946	RIKEN cDNA 1500002C15 gene	1500002C15Rik	1.103	1.274	0.242234	0.515115
3949	10550860	NM_018791	54678	zinc finger protein 108	Zfp108	1.103	1.041	0.331457	0.60794
3950	10533285	NM_011202	19247	protein tyrosine phosphatase,	Ptpn11	1.102	0.986	0.356222	0.628749
3951	10509965	NM_010139	13836	Eph receptor A2	Epha2	1.102	1.983	0.0865785	0.282817
3952	10513715	BC048618	75524	RIKEN cDNA 1700018C11 gene	1700018C11Rik	1.102	1.133	0.293455	0.569562
3953	10490138	NM_001081387	664799	CCCTC-binding factor (zinc fin	Ctcfl	1.102	1.885	0.10014	0.309465
3954	10390458	NM_009545	22658	polycomb group ring finger 2	Pcgf2	1.102	1.839	0.107224	0.322736
3955	10424439	NM_133766	76740	EFR3 homolog A (S. cerevisiae)	Efr3a	1.102	1.598	0.152901	0.396925
3956	10558742	NM_001081389	101613	NLR family, pyrin domain conta	Nlrp6	1.102	1.407	0.201078	0.463237
3957	10540105	NM_028766	74122	transmembrane protein 43	Tmem43	1.102	1.529	0.168777	0.420183
3958	10555586	BC092062	66508	RIKEN cDNA 2400001E08 gene	2400001E08Rik	1.102	0.495	0.63512	0.834242
3959	10402080	BC025577	217827	cDNA sequence BC002230	BC002230	1.102	1.505	0.174884	0.427987
3960	10424695	NM_026730	68453	GPI-anchored HDL-binding prote	Gpihbp1	1.102	2.003	0.0840299	0.278005
3961	10435897	BC027231	212547	cDNA sequence BC027231	BC027231	1.102	0.603	0.565202	0.791223
3962	10400896	NM_026038	67217	RIKEN cDNA 2810055F11 gene	2810055F11Rik	1.102	0.846	0.424511	0.686543
3963	10603175					1.102	1.421	0.196974	0.457727
3964	10598073					1.102	0.478	0.646989	0.840859
3965	10359859					1.102	0.89	0.402314	0.667397
3966	10560282	NM_172739	232906	glucocorticoid receptor DNA bi	Grlf1	1.102	1.37	0.211825	0.477389
3967	10538617	NM_133737	71835	LanC (bacterial lantibiotic sy	Lancl2	1.102	1.225	0.259067	0.533309
3968	10569331	ENSMUST00000054910	677289	predicted gene, OTTMUSG0000001	OTTMUSG00000016823	1.101	1.744	0.12347	0.351591
3969	10604057	NM_019942	56526	septin 6	Sept6	1.101	1.37	0.211887	0.477389
3970	10502042	ENSMUST00000029662	71481	alpha-kinase 1	Alpk1	1.101	0.822	0.437356	0.696704
3971	10529689	NM_011715	22388	WD repeat domain 1	Wdr1	1.101	1.563	0.160866	0.408621
3972	10600317	NM_008106	14539	opsin 1 (cone pigments), mediu	Opn1mw	1.101	1.364	0.21374	0.479961
3973	10380489	NM_146025	217125	sterile alpha motif domain con	Samd14	1.101	1.938	0.0925253	0.294729
3974	10521481	NM_178394	76071	janus kinase and microtubule i	Jakmip1	1.101	1.841	0.106973	0.322599
3975	10496125	NM_020265	56811	dickkopf homolog 2 (Xenopus la	Dkk2	1.101	0.749	0.477499	0.728235
3976	10431612	NM_026817	68708	RAB, member of RAS oncogene fa	Rabl2a	1.101	1.804	0.112904	0.332876
3977	10543219	NM_145066	64450	G protein-coupled receptor 85	Gpr85	1.101	1.429	0.194873	0.45499
3978	10586967	NM_001039251	639396	predicted gene, EG639396	EG639396	1.101	0.96	0.368106	0.639027
3979	10345046	EU520262	71877	EF-hand domain (C-terminal) co	Efhc1	1.101	1.623	0.147402	0.389587
3980	10367919	BC118516	74732	syntaxin 11	Stx11	1.101	0.857	0.418937	0.681438
3981	10504294	NM_001037709	100213	RUN and SH3 domain	Rusc2	1.101	1.556	0.162452	0.411033

				containing					
3982	10508788	NM_146155	230793	AT hook, DNA binding motif, co	Ahdc1	1.101	1.545	0.165109	0.415207
3983	10368405	XR_004815	675684	similar to Aldose reductase-re	LOC675684	1.101	0.908	0.393231	0.66124
3984	10587508	NM_009445	22137	Ttk protein kinase	Ttk	1.101	1.444	0.190754	0.449693
3985	10550795	NM_011860	23968	NLR family, pyrin domain conta	Nlrp5	1.101	1.124	0.297111	0.573626
3986	10412771					1.101	1.32	0.227237	0.498001
3987	10452643	NM_026064	67268	RIKEN cDNA 2900073G15 gene	2900073G15Rik	1.101	1.278	0.240768	0.513737
3988	10380665	NM_008266	15407	homeo box B1	Hoxb1	1.101	1.496	0.177081	0.431359
3989	10588403	NM_053159	94062	mitochondrial ribosomal protei	Mrpl3	1.101	0.482	0.643945	0.838914
3990	10400405	NM_010907	18035	nuclear factor of kappa light	Nfkbia	1.101	1.586	0.155492	0.400991
3991	10526319	NM_011714	22385	bromodomain adjacent to zinc f	Baz1b	1.1	1.804	0.113025	0.333083
3992	10517517	NM_007572	12259	complement component 1, q subc	C1qa	1.1	1.466	0.184764	0.442328
3993	10407222	NM_172594	218629	DEAH (Asp-Glu-Ala-His) box pol	Dhx29	1.1	1.037	0.333232	0.609187
3994	10592790	NM_172162	102423	MBD2-interacting zinc finger	Mizf	1.1	1.455	0.187871	0.446188
3995	10485344	NM_007466	11800	apoptosis inhibitor 5	Api5	1.1	0.804	0.447029	0.704723
3996	10436708	NM_024258	74112	ubiquitin specific peptidase 1	Usp16	1.1	1.19	0.271618	0.546245
3997	10516020					1.1	1.101	0.306386	0.582911
3998	10541496	NM_015776	50530	microfibrillar associated prot	Mfap5	1.1	3.101	0.0166523	0.0970498
3999	10373606	NM_001085477	544748	olfactory receptor 765	Olfr765	1.1	0.894	0.399972	0.665979
4000	10549388	NM_008970	19227	parathyroid hormone-like pepti	Pthlh	1.1	1.792	0.114996	0.337282
4001	10594774	NM_007630	12442	cyclin B2	Ccnb2	1.1	1.844	0.106426	0.321744
4002	10442495	NM_013630	18763	polycystic kidney disease 1 ho	Pkd1	1.1	1.62	0.147922	0.390128
4003	10572679	NM_146211	234407	glycosyltransferase 25 domain	Glt25d1	1.1	1.185	0.273483	0.54821
4004	10453553	ENSMUST00000084298	100038746	hypothetical LOC100038746	LOC100038746	1.1	1.216	0.262284	0.536754
4005	10510056	NM_031377	83491	preferentially expressed antig	Pramel1	1.1	2.055	0.0778193	0.265345
4006	10430593	NM_028792	74158	Josephin domain containing 1	Josd1	1.1	0.652	0.534683	0.768432
4007	10437655	BC068110	383103	cDNA sequence BC068110	BC068110	1.1	0.772	0.464592	0.718344
4008	10396712	NM_016893	53618	fucosyltransferase 8	Fut8	1.1	0.888	0.403414	0.668494
4009	10589565	NM_001081340	235626	SET domain containing 2	Setd2	1.1	1.927	0.0940931	0.297785
4010	10514195	NM_001081096	75811	RIKEN cDNA 4930500O09 gene	4930500O09Rik	1.1	1.817	0.110807	0.329565
4011	10584710	NM_010436	15270	H2A histone family, member X	H2afx	1.1	1.152	0.286048	0.561602
4012	10534303	NM_020044	56743	linker for activation of T cel	Lat2	1.1	1.938	0.0925892	0.294729
4013	10503109	NM_181391	66433	coiled-coil-helix-coiled-coil-	Chchd7	1.1	0.685	0.514638	0.754767
4014	10420155	NM_026819	52585	dehydrogenase/reductase (SDR f	Dhrs1	1.1	0.535	0.608493	0.817718
4015	10516259	NM_175223	75563	dynein, axonemal, light interm	Dnali1	1.1	1.36	0.21492	0.481846
4016	10355138					1.1	0.737	0.484584	0.733146
4017	10501433	NM_177091	320181	fibronectin type III domain co	Fndc7	1.099	1.685	0.134672	0.369832
4018	10585099	NM_175482	235323	ubiquitin specific peptidase 2	Usp28	1.099	1.373	0.210889	0.476393
4019	10579296	BC028495	66462	RIKEN cDNA 2810428I15 gene	2810428I15Rik	1.099	0.604	0.564619	0.790721
4020	10461553	ENSMUST00000087947	403202	RIKEN cDNA A430093F15 gene	A430093F15Rik	1.099	1.642	0.14343	0.384029
4021	10401181	NM_021557	17252	retinol dehydrogenase 11	Rdh11	1.099	0.579	0.580152	0.799396
4022	10473919	NM_029437	75786	cytoskeleton associated protei	Ckap5	1.099	1.552	0.163309	0.412349
4023	10377416	NM_028005	71923	RIKEN cDNA 2310047M10 gene	2310047M10Rik	1.099	1.892	0.0992081	0.307631
4024	10361065	NM_001081259	226844	feline leukemia virus subgroup	Flvcr1	1.099	1.317	0.228191	0.499211
4025	10436678	NM_008065	14390	GA repeat binding protein, alp	Gabpa	1.099	1.049	0.327981	0.604237
4026	10557793	NM_009294	20909	syntaxin 4A (placental)	Stx4a	1.099	1.035	0.334284	0.609879
4027	10477475	NM_011126	18843	palate, lung, and nasal epithe	Plunc	1.099	1.537	0.166926	0.417889
4028	10424909	NM_008296	15499	heat shock factor 1	Hsf1	1.099	0.711	0.499714	0.742878
4029	10482486	BC002253	109129	RIKEN cDNA 2010311D03 gene	2010311D03Rik	1.099	0.995	0.352034	0.625181
4030	10556442	NM_009346	21676	TEA domain family member 1	Tead1	1.099	1.087	0.312136	0.58848
4031	10604333	NM_178739	245404	WD repeat domain 40B	Wdr40b	1.099	1.104	0.305231	0.581633

4032	10381619	NM_001110778	11488	a disintegrin and metallopepti	Adam11	1.099	1.028	0.337082	0.612729
4033	10497842	NM_027810	71492	Bardet-Biedl syndrome 7	Bbs7	1.099	1.232	0.256613	0.530799
4034	10528664	NM_025891	66993	SWI/SNF related, matrix associ	Smarcd3	1.099	1.28	0.240031	0.513113
4035	10369620	NM_028197	72320	RIKEN cDNA 2510003E04 gene	2510003E04Rik	1.099	0.998	0.350546	0.624042
4036	10537638	NM_001038996	436522	trypsin 10	Try10	1.099	1.175	0.277403	0.552507
4037	10574939	NM_173432	244631	protein serine kinase H1	Pskh1	1.099	1.298	0.234303	0.50547
4038	10530287	NM_009686	11787	amyloid beta (A4) precursor pr	Apbb2	1.099	0.288	0.78109	0.911042
4039	10486956	NM_177610	214593	dual oxidase 2	Duox2	1.099	1.886	0.100002	0.309109
4040	10423090	NM_008537	17117	alpha-methylacyl-CoA racemase	Amacr	1.099	1.372	0.21107	0.476598
4041	10357946	NM_001081307	329251	protein phosphatase 1, regulat	Ppp1r12b	1.099	1.287	0.237911	0.510297
4042	10474207	NM_212433	57443	F-box protein 3	Fbxo3	1.099	0.804	0.447003	0.704723
4043	10535898	NM_011937	26384	glucosamine-6-phosphate deamin	Gnpda1	1.099	0.895	0.39979	0.66597
4044	10505884	NM_206871	15969	interferon alpha 6	Ifna6	1.099	1.737	0.124608	0.35351
4045	10473754	NM_025991	67136	kelch repeat and BTB (POZ) dom	Kbtbd4	1.099	0.824	0.436168	0.696174
4046	10365574	NM_029971	110312	pro-melanin-concentrating horm	Pmch	1.099	1.017	0.341942	0.616342
4047	10406385	ENSMUST00000091459	68675	RIKEN cDNA 1110033M05 gene	1110033M05Rik	1.099	0.618	0.555559	0.784214
4048	10563434					1.098	1.123	0.297479	0.573687
4049	10539741	NM_001040106	269774	AP2 associated kinase 1	Aak1	1.098	1.791	0.115187	0.337402
4050	10551570	NM_022432	64383	sirtuin 2 (silent mating type	Sirt2	1.098	1.214	0.26309	0.537778
4051	10529252	AY372183	215476	RIKEN cDNA C330019G07 gene	C330019G07Rik	1.098	1.129	0.295007	0.571264
4052	10456579	NM_001039214	240396	mex3 homolog C (C. elegans)	Mex3c	1.098	1.124	0.297096	0.573626
4053	10433008	NM_009582	26404	mitogen-activated protein kina	Map3k12	1.098	1.687	0.134245	0.369304
4054	10437330	ENSMUST00000100216	12914	CREB binding protein	Crebbp	1.098	0.824	0.436371	0.696296
4055	10584057	NM_001115130	235132	zinc finger and BTB domain con	Zbtb44	1.098	1.391	0.205544	0.46918
4056	10348864					1.098	1.149	0.287053	0.562871
4057	10428511	NM_001081391	239420	CUB and Sushi multiple domains	Csmd3	1.098	0.78	0.460423	0.715034
4058	10491064					1.098	1.431	0.194337	0.454391
4059	10360248	ENSMUST00000111243	27222	ATPase, Na+/K+ transporting, a	Atp1a4	1.098	1.746	0.123095	0.351101
4060	10433292	NM_010443	15369	heme oxygenase (decycling) 2	Hmox2	1.098	1.713	0.129172	0.360384
4061	10436588	AK048031	77994	RIKEN cDNA 2810055G20 gene	2810055G20Rik	1.098	1.815	0.11118	0.329929
4062	10501121	NM_153563	229707	RIKEN cDNA 6330569M22 gene	6330569M22Rik	1.098	1.594	0.153603	0.398105
4063	10547597	NM_007905	13619	polyhomeotic-like 1 (Drosophil	Phc1	1.098	0.668	0.525036	0.761313
4064	10481474	NM_007760	12908	carnitine acetyltransferase	Crat	1.098	1.426	0.195688	0.456039
4065	10451104	NM_001013749	210573	transmembrane protein 151B	Tmem151b	1.098	0.709	0.500726	0.743808
4066	10548745	NM_008157	14760	G protein-coupled receptor 19	Gpr19	1.098	1.86	0.104026	0.317208
4067	10596277	ENSMUST00000060084	235567	DnaJ (Hsp40) homolog, subfamil	Dnajc13	1.098	1.309	0.230548	0.501476
4068	10493530	NM_026869	68911	pygopus 2	Pygo2	1.098	1.28	0.240287	0.513351
4069	10554463	NM_026812	68695	HD domain containing 3	Hddc3	1.098	0.727	0.490284	0.737262
4070	10369388	NM_029770	107449	unc-5 homolog B (C. elegans)	Unc5b	1.098	1.56	0.161511	0.409658
4071	10497920	NM_001033198	99696	ankrin repeat domain 50	Ankrd50	1.098	1.266	0.244848	0.518017
4072	10518642	NM_022022	63958	ubiquitination factor E4B, UFD	Ube4b	1.097	1.315	0.228921	0.499975
4073	10508697	NM_020587	57317	splicing factor, arginine/seri	Sfrs4	1.097	1.425	0.196099	0.45647
4074	10565596					1.097	1.607	0.150904	0.394549
4075	10545827	NM_001003955	52055	RAB11 family interacting prote	Rab11fip5	1.097	1.896	0.0984993	0.30641
4076	10456120	NM_146087	93687	casein kinase 1, alpha 1	Csnk1a1	1.097	1.747	0.12294	0.350793
4077	10476545	NM_175467	228677	serine palmitoyltransferase, l	Sptlc3	1.097	1.616	0.148862	0.391099
4078	10484728	NM_146294	258291	olfactory receptor 1167	Olfr1167	1.097	0.384	0.712027	0.873823
4079	10579079	NM_001039967	66869	RIKEN cDNA 1200003I07 gene	1200003I07Rik	1.097	0.984	0.356859	0.629197
4080	10542834					1.097	0.173	0.867769	0.947048
4081	10468802	BC061459	76539	DNA segment, Chr 19, ERATO Doi	D19Ertd737e	1.097	2.006	0.0836697	0.277117
4082	10443527	NM_008842	18712	proviral integration site 1	Pim1	1.097	1.882	0.100664	0.310496

4083	10555425	BC079886	319604	RIKEN cDNA B930006L02 gene	B930006L02Rik	1.097	1.068	0.319791	0.596635
4084	10378668	NM_008850	18738	phosphatidylinositol transfer	Pitpna	1.097	0.912	0.391032	0.659412
4085	10369911	BC024851	68778	RIKEN cDNA 1110038D17 gene	1110038D17Rik	1.097	0.827	0.434963	0.695306
4086	10372417	NM_001033474	382423	RIKEN cDNA 4921506J03 gene	4921506J03Rik	1.097	1.363	0.213966	0.480314
4087	10435057	NM_009981	13026	phosphate cytidylyltransferase	Pcyt1a	1.097	0.232	0.823254	0.929358
4088	10541636	NM_019917	56552	vomeronasal 2, receptor 26	Vmn2r26	1.097	1.468	0.184352	0.441942
4089	10415844	NM_007798	13030	cathepsin B	Ctsb	1.097	1.314	0.228966	0.499975
4090	10472916	NM_025866	66953	cell division cycle associated	Cdca7	1.097	1.2	0.268145	0.542786
4091	10368907	NM_152229	21907	nuclear receptor subfamily 2,	Nr2e1	1.097	1.1	0.306569	0.58301
4092	10557233	NM_144925	233833	trinucleotide repeat containin	Tnrc6a	1.097	1.992	0.0853819	0.280546
4093	10448004	NM_024250	72057	PHD finger protein 10	Phf10	1.096	1.021	0.340254	0.61558
4094	10476569	NM_027093	69487	RIKEN cDNA 2310003L22 gene	2310003L22Rik	1.096	0.979	0.359102	0.631213
4095	10544062	ENSMUST00000078942	330286	RIKEN cDNA D630045J12 gene	D630045J12Rik	1.096	1.51	0.173655	0.426449
4096	10577508	NM_001004140	80986	cytoskeleton associated protei	Ckap2	1.096	1.113	0.301607	0.577839
4097	10577067					1.096	1.54	0.16624	0.41711
4098	10496813	NM_028836	74245	chitobiase, di-N-acetyl-	Ctbs	1.096	0.837	0.429698	0.690652
4099	10396699	NM_145927	110606	farnesyltransferase, CAAX box,	Fntb	1.096	0.983	0.357238	0.62961
4100	10455259	NM_175164	71302	Rho GTPase activating protein	Arhgap26	1.096	0.987	0.355369	0.628032
4101	10510602	ENSMUST00000094445	100041960	RIKEN cDNA 9230110K08 gene	9230110K08Rik	1.096	1.384	0.207663	0.472138
4102	10424686	BC025446	223631	cDNA sequence BC025446	BC025446	1.096	1.36	0.214886	0.481846
4103	10518674	NM_022020	63954	retinol binding protein 7, cel	Rbp7	1.096	1.529	0.168975	0.420416
4104	10356293	BC052931	319997	RIKEN cDNA A630001G21 gene	A630001G21Rik	1.096	1.568	0.159682	0.407016
4105	10391043	NM_201255	107656	keratin 9	Krt9	1.096	1.361	0.214638	0.481467
4106	10533095	NM_172721	231672	F-box and WD-40 domain protein	Fbxw8	1.096	0.651	0.535506	0.769059
4107	10507461					1.096	0.649	0.536512	0.769659
4108	10455092	NM_053137	93883	protocadherin beta 12	Pcdhb12	1.096	0.115	0.911554	0.964659
4109	10517287	NM_207237	230815	mannosidase, alpha, class 1C,	Man1c1	1.096	1.269	0.244006	0.517064
4110	10591630	NM_177030	319899	dedicator of cytokinesis 6	Dock6	1.096	0.809	0.444566	0.70306
4111	10416269	ENSMUST00000078149	66440	cell division cycle 26	Cdc26	1.096	0.241	0.816562	0.926829
4112	10497381	NM_007825	13123	cytochrome P450, family 7, sub	Cyp7b1	1.096	0.397	0.703168	0.869747
4113	10413943	NM_026253	67580	leucine rich repeat containing	Lrrc18	1.096	1.657	0.140142	0.378727
4114	10606880	NM_010297	14657	glycine receptor, alpha 4 subu	Glra4	1.096	1.125	0.2968	0.573371
4115	10361375	NM_025995	67141	F-box protein 5	Fbxo5	1.096	1.072	0.31831	0.595501
4116	10372716	NM_024457	215449	RAS related protein 1b	Rap1b	1.096	1.583	0.156241	0.402137
4117	10367931	NM_181470	353258	LTV1 homolog (S. cerevisiae)	Ltv1	1.096	1.515	0.172183	0.424316
4118	10580202	NM_201227	23863	DAN domain family, member 5	Dand5	1.096	0.769	0.466316	0.719571
4119	10375083	NM_009288	20868	serine/threonine kinase 10	Stk10	1.096	1.555	0.162751	0.411428
4120	10519052	BC030453	66469	RIKEN cDNA 2810405K02 gene	2810405K02Rik	1.096	0.535	0.608536	0.817724
4121	10516867	NM_001122992	56809	glucocorticoid modulatory elem	Gmeb1	1.096	1.373	0.210884	0.476393
4122	10512574	NM_172692	230101	glucosidase beta 2	Gba2	1.095	1.041	0.33135	0.607848
4123	10565570	DQ400346	74041	RIKEN cDNA 4632434I11 gene	4632434I11Rik	1.095	0.319	0.7585	0.898805
4124	10596988	ENSMUST00000084990	665413	predicted gene, EG665413	EG665413	1.095	1.481	0.181019	0.436926
4125	10481128	NM_011513	20933	mediator complex subunit 22	Med22	1.095	0.842	0.426854	0.688211
4126	10573483	NM_011563	21672	peroxiredoxin 2	Prdx2	1.095	0.632	0.546906	0.778024
4127	10465209	NM_181452	17826	mammary tumor virus receptor 2	Mtvr2	1.095	1.343	0.219857	0.488612
4128	10503876	NM_177774	272009	serine-arginine repressor prot	RP23-12I24.6	1.095	2.01	0.0832281	0.27639
4129	10580365	BC040087	66714	RIKEN cDNA 4921524J17 gene	4921524J17Rik	1.095	0.58	0.579618	0.799025
4130	10434804					1.095	0.468	0.653422	0.844695
4131	10606513	NM_018818	12662	choroidermia	Chm	1.095	0.843	0.426329	0.687967
4132	10566272	NM_008221	15135	hemoglobin Y, beta-like embryo	Hbb-y	1.095	2.051	0.0782167	0.266113
4133	10607933	NM_008222	15159	holocytochrome c synthetase	Hccs	1.095	1.311	0.230065	0.501055

4134	10368356	NM_018747	432442	A kinase (PRKA) anchor protein	Akap7	1.095	1.264	0.245507	0.518491
4135	10438478	NM_013790	27416	ATP-binding cassette, sub-fami	Abcc5	1.095	1.628	0.146312	0.38806
4136	10458540	NM_017378	53601	protocadherin 12	Pcdh12	1.095	1.96	0.0896511	0.289031
4137	10399924	NM_020272	30955	phosphoinositide-3-kinase, cat	Pik3cg	1.095	1.663	0.138932	0.377005
4138	10559248	NM_020286	27027	tetraspanin 32	Tspan32	1.095	1.218	0.261513	0.536057
4139	10355706	NM_010544	16147	Indian hedgehog	Ihh	1.095	1.574	0.158222	0.405115
4140	10425936	BC112373	67747	RIB43A domain with coiled-coil	Ribc2	1.095	2.103	0.0723622	0.253324
4141	10437673	NM_013694	21959	transition protein 2	Tnp2	1.095	0.94	0.377485	0.647352
4142	10430686	ENSMUST00000096347	383075	ENTH domain containing 1	Enthd1	1.095	1.159	0.283406	0.558717
4143	10602964					1.095	1.273	0.242455	0.515377
4144	10491605	ENSMUST00000057272	229227	RIKEN cDNA 4932438A13 gene	4932438A13Rik	1.095	0.512	0.624234	0.828379
4145	10489092	ENSMUST00000069098	320706	RIKEN cDNA 9830001H06 gene	9830001H06Rik	1.095	1.583	0.156144	0.401989
4146	10593430	NM_178710	235344	SNF1-like kinase 2	Snf1lk2	1.095	1.807	0.112453	0.332128
4147	10409767	NM_027307	105348	golgi membrane protein 1	Golm1	1.095	0.983	0.357534	0.629926
4148	10570008	AK081065	791373	predicted gene, ENSMUSG0000005	ENSMUSG00000053412	1.095	1.025	0.33858	0.614159
4149	10521731	NM_019438	54392	on-SMC condensin I complex, su	Ncapg	1.095	1.521	0.170831	0.42256
4150	10346838	NM_001081050	72823	par-3 partitioning defective 3	Pard3b	1.095	1.332	0.223428	0.493384
4151	10539179	NM_011036	18489	regenerating islet-derived 3 b	Reg3b	1.095	1.61	0.150241	0.393399
4152	10444927	NM_134122	106582	nurim (nuclear envelope membra	Nrm	1.095	0.917	0.388882	0.657381
4153	10536996	BC060132	76788	RIKEN cDNA 2410127E18 gene	2410127E18Rik	1.095	0.763	0.469688	0.721788
4154	10410016	NM_007985	14088	Fanconi anemia, complementatio	Fancc	1.094	1.37	0.211939	0.477389
4155	10418702	NM_011894	24056	SH3-domain binding protein 5 (	Sh3bp5	1.094	1.494	0.177638	0.43207
4156	10437552	NM_001033220	239691	expressed sequence AU021092	AU021092	1.094	2.027	0.0810913	0.271716
4157	10442691	NM_011930	26373	chloride channel 7	Clcn7	1.094	1.219	0.261252	0.535766
4158	10586011	NM_026235	67557	La ribonucleoprotein domain fa	Larp6	1.094	1.516	0.172049	0.424165
4159	10493307					1.094	0.758	0.472572	0.724273
4160	10589587	NM_001081340	235626	SET domain containing 2	Setd2	1.094	1.401	0.202629	0.465349
4161	10568294					1.094	0.926	0.384298	0.653499
4162	10432263	NM_175232	76061	RIKEN cDNA 5830427D03 gene	5830427D03Rik	1.094	1.298	0.234296	0.50547
4163	10479335	NM_144500	228983	oxysterol binding protein-like	Osbpl2	1.094	1.632	0.145441	0.387083
4164	10457071	NM_025797	109672	cytochrome b-5	Cyb5	1.094	0.816	0.440365	0.699292
4165	10488804	XR_035020	435692	similar to ribosomal protein L	LOC435692	1.094	0.572	0.584752	0.802388
4166	10433589					1.094	2.371	0.0485103	0.196834
4167	10491522	AK138522	654424	RIKEN cDNA A330050B17 gene	A330050B17Rik	1.094	1.4	0.202992	0.465669
4168	10578539	NM_007450	11739	solute carrier family 25 (mito	Slc25a4	1.094	1.893	0.0990356	0.307265
4169	10499666	NM_001081182	54667	Atpase, class I, type 8B, memb	Atp8b2	1.094	1.455	0.187669	0.44605
4170	10485405	NM_009851	12505	CD44 antigen	Cd44	1.094	2.375	0.0482227	0.196119
4171	10574151					1.094	1.31	0.230323	0.501285
4172	10529577	NM_133724	117197	cappuccino	Cno	1.094	1.417	0.198197	0.45902
4173	10494509	NM_146135	229615	protein inhibitor of activated	Pias3	1.094	0.913	0.390731	0.659209
4174	10365729	NM_146239	237459	PCTAIRE-motif protein kinase 2	Pctk2	1.094	1.744	0.123365	0.351451
4175	10439239	NM_153550	224132	disrupted in renal carcinoma 2	Dirc2	1.094	0.678	0.519195	0.757488
4176	10571048	NM_026032	67207	LSM1 homolog, U6 small nuclear	Lsm1	1.094	1.277	0.241053	0.513985
4177	10480672	NM_023464	68475	Sjogren's syndrome nuclear aut	Ssna1	1.094	0.473	0.650355	0.84316
4178	10458560	NM_010197	14164	fibroblast growth factor 1	Fgf1	1.094	1.991	0.0855124	0.280626
4179	10597949	NM_011731	22599	solute carrier family 6 (neuro	Slc6a20b	1.094	1.291	0.236427	0.508546
4180	10599880	NM_198863	245450	SLIT and NTRK-like family, mem	Slitrk2	1.094	0.864	0.415246	0.678399
4181	10355532	BC052740	21961	tensin 1	Tns1	1.094	1.51	0.173659	0.426449
4182	10363970	NM_029781	76877	RAB36, member RAS oncogene fam	Rab36	1.094	1.069	0.319519	0.596487
4183	10589087	NM_008924	19087	protein kinase, cAMP dependent	Prkar2a	1.094	1.47	0.183749	0.440966
4184	10565499	XM_357814	384719	predicted gene, EG384719	EG384719	1.094	0.891	0.401812	0.667094

4185	10567049	NM_033370	70349	coatomer protein complex, subu	Copb1	1.093	0.775	0.463051	0.71752
4186	10578955					1.093	1.005	0.347306	0.621483
4187	10607658	NM_178256	194590	RALBP1 associated Eps domain c	Reps2	1.093	0.889	0.402667	0.667764
4188	10364030	NM_009630	11540	adenosine A2a receptor	Adora2a	1.093	1.716	0.128594	0.359531
4189	10488507	NM_024465	76192	abhydrolase domain containing	Abhd12	1.093	0.817	0.44011	0.69915
4190	10409992					1.093	0.766	0.468256	0.720616
4191	10380534	NM_025287	20747	speckle-type POZ protein	Spop	1.093	1.623	0.147347	0.389535
4192	10512867	NM_172304	269536	testis expressed gene 10	Tex10	1.093	0.851	0.422105	0.684326
4193	10561085	NM_144922	232989	heterogeneous nuclear ribonucl	Hnrpul1	1.093	1.278	0.240767	0.513737
4194	10567412	NM_027698	71151	exonuclease domain containing	Exod1	1.093	0.798	0.45055	0.707814
4195	10356305	NM_008311	15559	5-hydroxytryptamine (serotonin	Htr2b	1.093	0.818	0.439737	0.699031
4196	10373365	AK042023	100126225	predicted gene, ENSMUSG0000005	ENSMUSG00000055902	1.093	0.74	0.482555	0.731356
4197	10549762	NM_146178	232821	coiled-coil domain containing	Ccdc106	1.093	0.894	0.400199	0.666098
4198	10416938	XM_139243	223186	predicted gene, EG223186	EG223186	1.093	1.884	0.100262	0.30975
4199	10466268	NM_001011524	258227	olfactory receptor 1418	Olfr1418	1.093	1.102	0.306047	0.582506
4200	10466423	NM_198019	208518	centrosomal protein 78	Cep78	1.093	0.491	0.638021	0.835923
4201	10449926	NM_177359	240064	RIKEN cDNA 6030490I01 gene	6030490I01Rik	1.093	1.271	0.243255	0.516291
4202	10425287	NM_134090	105785	KDEL (Lys-Asp-Glu-Leu) endopla	Kdelr3	1.093	1.209	0.264923	0.540102
4203	10373000	NM_026858	68876	XRCC6 binding protein 1	Xrcc6bp1	1.093	1.124	0.296856	0.573427
4204	10492330	NM_008772	18441	purinergic receptor P2Y, G-pro	P2ry1	1.093	0.396	0.703727	0.870071
4205	10438358	NM_213614	18951	septin 5	Sept5	1.093	1.06	0.323301	0.599849
4206	10388234	NM_010353	14841	germ cell-specific gene 2	Gsg2	1.093	0.968	0.364392	0.635557
4207	10548086	NM_009013	19362	RAD51 associated protein 1	Rad51ap1	1.093	1.375	0.210452	0.475962
4208	10577792	NM_031257	83436	pleckstrin homology domain-con	Plekha2	1.093	0.616	0.556626	0.785091
4209	10582664	BC058626	69551	RIKEN cDNA 2310022B05 gene	2310022B05Rik	1.093	1.193	0.270564	0.545253
4210	10434289					1.093	0.763	0.46988	0.721925
4211	10378833	NM_177710	237860	slingshot homolog 2 (Drosophil	Ssh2	1.093	0.594	0.570774	0.795023
4212	10583021	NM_027924	71785	platelet-derived growth factor	Pdgfd	1.093	0.548	0.600209	0.812161
4213	10402249	NM_029705	110616	ataxin 3	Atxn3	1.092	1.231	0.25701	0.531359
4214	10488785	NM_007891	13555	E2F transcription factor 1	E2f1	1.092	1.533	0.167943	0.419243
4215	10496455					1.092	1.028	0.337177	0.612796
4216	10355785	BC021773	74577	galactosidase, beta 1-like	Glb1l	1.092	1.151	0.286636	0.562228
4217	10502973	NM_172474	209584	tRNA-yW synthesizing protein 3	Tyw3	1.092	1.077	0.316189	0.59316
4218	10606058	NM_009910	12766	chemokine (C-X-C motif) recept	Cxcr3	1.092	1.342	0.220208	0.488992
4219	10355259	NM_021285	17901	myosin, light polypeptide 1	Myl1	1.092	0.569	0.586353	0.803667
4220	10504957	NM_008017	14211	structural maintenance of chro	Smc2	1.092	1.135	0.292599	0.568731
4221	10391075	NM_212483	68239	keratin 42	Krt42	1.092	1.466	0.184961	0.44255
4222	10478077	NM_177658	228850	RIKEN cDNA B230339M05 gene	B230339M05Rik	1.092	0.938	0.378476	0.648238
4223	10601705	NM_145924	102920	centromere protein I	Cenpi	1.092	1.298	0.234253	0.505464
4224	10551377	NM_001033315	233020	homeodomain interacting protei	Hipk4	1.092	1.556	0.162388	0.411033
4225	10404612	NM_001013392	68750	ras responsive element binding	Rreb1	1.092	0.904	0.395301	0.66309
4226	10533993	NM_133895	100561	solute carrier family 15, memb	Slc15a4	1.092	1.602	0.151847	0.395645
4227	10476207	NM_009730	11990	attractin	Atrn	1.092	1.867	0.102972	0.315176
4228	10581650	NM_011998	26887	carbohydrate (chondroitin 6/ke	Chst4	1.092	1.087	0.312011	0.588349
4229	10350024	NM_153128	240756	kelch-like 12 (Drosophila)	Klhl12	1.092	1.42	0.197428	0.457935
4230	10600744					1.092	1.186	0.273046	0.547665
4231	10427881	XR_001935	666875	predicted gene, EG666875	EG666875	1.092	0.901	0.396768	0.664039
4232	10560548	NM_027189	69731	gem (nuclear organelle) associ	Gemin7	1.092	0.898	0.398095	0.664555
4233	10510809	BC052148	97159	RIKEN cDNA A430005L14 gene	A430005L14Rik	1.092	0.526	0.614458	0.82153
4234	10483698	NM_153138	215280	WAS/WASL interacting protein f	Wipf1	1.092	0.906	0.394257	0.661945
4235	10441923	NM_001039552	381062	RIKEN cDNA 2210404J11 gene	2210404J11Rik	1.092	1.098	0.307618	0.584192

4236	10410321	BC080824	238692	RIKEN cDNA C330011K17 gene	C330011K17Rik	1.092	1.348	0.218393	0.486434
4237	10426722	NM_018786	54614	PRP40 pre-mRNA processing fact	Prpf40b	1.092	1.411	0.199855	0.461578
4238	10549361	NM_026281	67623	transmembrane 7 superfamily me	Tm7sf3	1.092	0.666	0.525985	0.762002
4239	10454129	NM_181682	225256	desmoglein 1 beta	Dsg1b	1.092	1.096	0.308189	0.584951
4240	10591216	NM_146904	57251	olfactory receptor 870	Olfr870	1.092	1.047	0.32905	0.605314
4241	10435654	NM_177093	320184	leucine rich repeat containing	Lrrc58	1.092	1.68	0.135648	0.371434
4242	10594840	NM_001033208	102371	expressed sequence AA407270	AA407270	1.092	1.698	0.131985	0.365036
4243	10362823	NM_017472	54198	sorting nexin 3	Snx3	1.092	0.789	0.455103	0.711341
4244	10595327	NM_001081216	83946	pleckstrin homology domain int	Phip	1.092	1.456	0.187466	0.44575
4245	10436941	NM_017391	53881	solute carrier family 5 (inosi	Slc5a3	1.092	1.419	0.197544	0.45809
4246	10482172	NM_199025	320633	zinc finger and BTB domain con	Zbtb26	1.092	0.993	0.35307	0.625939
4247	10478962	BC016210	67017	RIKEN cDNA 2010011I20 gene	2010011I20Rik	1.091	1.322	0.226612	0.497248
4248	10406548					1.091	0.604	0.564564	0.790721
4249	10412844	NM_009409	21974	topoisomerase (DNA) II beta	Top2b	1.091	1.439	0.192175	0.451484
4250	10515028	NM_183300	230597	zinc finger, FYVE domain conta	Zfyve9	1.091	1.006	0.346837	0.621091
4251	10400866	NM_053167	94090	tripartite motif-containing 9	Trim9	1.091	0.95	0.372735	0.643093
4252	10424842	XM_890873	626280	predicted gene, EG626280	EG626280	1.091	1.718	0.128139	0.358993
4253	10538684	NM_001081145	68140	tigger transposable element de	Tigd2	1.091	0.883	0.405873	0.670443
4254	10605055	NM_028633	73738	UCHL5 interacting protein	Uchl5ip	1.091	0.846	0.424827	0.686739
4255	10355266	NM_021295	14768	LanC (bacterial lantibiotic sy	Lancl1	1.091	1.117	0.299715	0.575741
4256	10445640	NM_001097623	224829	transcriptional regulating fac	Trerf1	1.091	1.306	0.231772	0.502487
4257	10504054					1.091	0.729	0.489167	0.736349
4258	10493692	NM_026677	68328	RAB13, member RAS oncogene fam	Rab13	1.091	1.998	0.0846797	0.279368
4259	10461824	NM_146345	258342	olfactory receptor 1491	Olfr1491	1.091	0.845	0.425145	0.687043
4260	10541065	NM_001011801	258020	olfactory receptor 213	Olfr213	1.091	1.367	0.212659	0.478245
4261	10412038	BC021311	67263	zinc finger, SWIM domain conta	Zswim6	1.091	0.682	0.516239	0.755582
4262	10485378	NM_001083810	72446	RIKEN cDNA 2600010E01 gene	2600010E01Rik	1.091	1.783	0.116596	0.339947
4263	10351551	NM_172845	240913	a disintegrin-like and metallo	Adamts4	1.091	1.744	0.123499	0.351591
4264	10361834	NM_138628	378431	taxilin beta	Txlnb	1.091	1.297	0.23473	0.505978
4265	10541191	NM_011236	19365	RAD52 homolog (S. cerevisiae)	Rad52	1.091	1.732	0.12553	0.354782
4266	10385486	NM_145377	211007	tripartite motif-containing 41	Trim41	1.091	1.6	0.152388	0.396241
4267	10482301	NM_178778	320271	RIKEN cDNA A930041I02 gene	A930041I02Rik	1.091	0.862	0.416251	0.67936
4268	10361799	NM_025748	66757	adenosine deaminase, tRNA-spec	Adat2	1.091	0.582	0.578208	0.79826
4269	10345032	NM_010552	16171	interleukin 17A	Il17a	1.091	1.141	0.290376	0.566551
4270	10605811	NM_175179	72345	RIKEN cDNA 2810002O09 gene	2810002O09Rik	1.091	1.337	0.221858	0.491462
4271	10505282	NM_027297	70052	PRP4 pre-mRNA processing facto	Prpf4	1.091	0.909	0.392686	0.660631
4272	10457886	ENSMUST00000068352	791345	predicted gene, ENSMUSG0000005	ENSMUSG00000054990	1.091	1.11	0.30273	0.578798
4273	10599598	ENSMUST00000068507	319912	RIKEN cDNA A630012P03 gene	A630012P03Rik	1.09	1.762	0.120218	0.346569
4274	10359701	NM_032005	83993	T-box 19	Tbx19	1.09	1.147	0.288136	0.563996
4275	10558754	NM_145387	212974	ATH1, acid trehalase-like 1 (y	Athl1	1.09	1.97	0.0882894	0.286405
4276	10509244	ENSMUST00000084593	320133	RIKEN cDNA 6030445D17 gene	6030445D17Rik	1.09	2.045	0.0789367	0.267474
4277	10404840	NM_009856	12522	CD83 antigen	Cd83	1.09	0.912	0.39146	0.659734
4278	10360003	NM_023173	80915	dual specificity phosphatase 1	Dusp12	1.09	1.092	0.309793	0.586696
4279	10510464	NM_026963	69151	leucine zipper and CTNNBIP1 do	Lzic	1.09	0.736	0.484711	0.733195
4280	10404400	NM_001013788	432743	predicted gene, EG432743	EG432743	1.09	1.298	0.234196	0.505444
4281	10368279	NM_001010828	215855	trace amine-associated recepto	Taar6	1.09	1.312	0.229731	0.500845
4282	10571266	NM_017374	19053	protein phosphatase 2 (formerl	Ppp2cb	1.09	1.001	0.349173	0.622762
4283	10449177	NM_001039038	621239	RIKEN cDNA F430201B04 gene	F430201B04Rik	1.09	1.678	0.135933	0.371867

4284	10523547	NM_172715	231510	1-acylglycerol-3-phosphate O-a	Agpat9	1.09	1.299	0.233794	0.505106
4285	10403464	NM_001081426	208440	DIP2 disco-interacting protein	Dip2c	1.09	1.052	0.326711	0.602834
4286	10389625					1.09	0.384	0.711871	0.873734
4287	10397559	XR_032624	674986	similar to small nuclear ribon	LOC674986	1.09	0.259	0.802881	0.920071
4288	10524647	NM_029012	74585	signal peptide peptidase 3	Sppl3	1.09	1.727	0.126509	0.356138
4289	10408848					1.09	1.167	0.280425	0.555802
4290	10571382	BC069898	80286	tumor suppressor candidate 3	Tusc3	1.09	0.766	0.468037	0.720506
4291	10491805	NM_011495	20873	polo-like kinase 4 (Drosophila	Plk4	1.09	0.829	0.433917	0.694402
4292	10378555	NM_001102611	319822	SET and MYND domain containing	Smyd4	1.09	1.943	0.0919194	0.293764
4293	10462039	NM_001035244	226025	transient receptor potential c	Trpm3	1.09	1.944	0.0917683	0.293524
4294	10359506	BC014872	71449	RIKEN cDNA 5630401D24 gene	5630401D24Rik	1.09	1.372	0.211283	0.476813
4295	10580608	ENSMUST00000098499	75704	RIKEN cDNA 2310039D24 gene	2310039D24Rik	1.09	1.198	0.268901	0.543464
4296	10387807	BC055357	104457	RIKEN cDNA 0610010K14 gene	0610010K14Rik	1.09	0.981	0.358516	0.630584
4297	10588079	NM_001033983	546157	RIKEN cDNA 7420426K07 gene	7420426K07Rik	1.09	1.505	0.174887	0.427987
4298	10532504	NM_153571	100900	HscB iron-sulfur cluster co-ch	Hscb	1.09	0.043	0.967083	0.986963
4299	10506583	NM_177667	230576	tetratricopeptide repeat domai	Ttc22	1.09	1.175	0.277402	0.552507
4300	10608087					1.09	0.781	0.459747	0.71461
4301	10368616	NM_028287	72580	zinc finger with UFM1-specific	Zufsp	1.09	1.336	0.222285	0.492042
4302	10437136	NM_007890	13548	dual-specificity tyrosine-(Y)-	Dyrk1a	1.09	1.664	0.138783	0.376788
4303	10602196	AK220382	209540	retrotransposon gag domain con	Rgag1	1.09	0.845	0.425019	0.686944
4304	10430372	NM_009008	19354	RAS-related C3 botulinum subst	Rac2	1.09	1.3	0.233662	0.505065
4305	10603323	NM_138605	54646	protein phosphatase 1, regulat	Ppp1r3f	1.09	1.628	0.146255	0.388006
4306	10511510	NM_178112	72656	integrator complex subunit 8	Ints8	1.09	1.062	0.322697	0.599359
4307	10455342					1.089	1.628	0.146348	0.3881
4308	10362454					1.089	0.159	0.878032	0.951715
4309	10579331	NM_011819	23886	growth differentiation factor	Gdf15	1.089	1.742	0.12376	0.352065
4310	10500103	NM_029885	213054	GA repeat binding protein, bet	Gabpb2	1.089	0.581	0.578618	0.798427
4311	10405464	NM_001038018	26385	G protein-coupled receptor kin	Grk6	1.089	1.104	0.30496	0.581378
4312	10519504	NM_025618	109552	sorcin	Sri	1.089	1.529	0.168887	0.420407
4313	10509228	NM_028871	74326	heterogeneous nuclear ribonucl	Hnrnpr	1.089	1.027	0.337442	0.613121
4314	10444229	NM_010386	14998	histocompatibility 2, class II	H2-DMa	1.089	1.427	0.195333	0.455561
4315	10494335	NM_001025613	229603	OTU domain containing 7B	Otud7b	1.089	1.443	0.19096	0.450028
4316	10566723	NM_057173	109594	LIM domain only 1	Lmo1	1.089	0.348	0.737779	0.888255
4317	10421250	NM_001004155	268759	RIKEN cDNA 9930012K11 gene	9930012K11Rik	1.089	0.786	0.456731	0.712642
4318	10584034	NM_028874	102607	sorting nexin 19	Snx19	1.089	1.121	0.298361	0.574601
4319	10475625	NM_025613	58521	EP300 interacting inhibitor of	Eid1	1.089	1.355	0.216399	0.483657
4320	10521163	ENSMUST00000094869	381633	gene model 1673, (NCBI)	Gm1673	1.089	1.092	0.309914	0.586734
4321	10564698	NM_029585	76375	de-etiolated homolog 1 (Arabid	Det1	1.089	0.509	0.625839	0.829508
4322	10385542	NM_172793	237754	butyrophilin-like 9	Btnl9	1.089	1.535	0.167425	0.418443
4323	10384502					1.089	0.289	0.780945	0.91101
4324	10589057					1.089	0.896	0.399383	0.665621
4325	10509218	NM_009557	22704	zinc finger protein 46	Zfp46	1.089	1.57	0.159224	0.406366
4326	10534389	NM_020504	57255	claudin 13	Cldn13	1.089	0.21	0.839347	0.935017
4327	10387014	NM_009157	26398	mitogen-activated protein kina	Map2k4	1.089	0.829	0.433529	0.694014
4328	10521068	NM_001081101	71101	RIKEN cDNA 4933407H18 gene	4933407H18Rik	1.089	1.218	0.26159	0.536103
4329	10415806	ENSMUST00000039064	629059	predicted gene, EG629059	EG629059	1.089	1.488	0.179068	0.434349
4330	10352690	NM_021421	52477	angel homolog 2 (Drosophila)	Angel2	1.089	1.297	0.234479	0.50565
4331	10575291	NM_029468	75871	zinc finger protein 821	Zfp821	1.089	0.921	0.386623	0.655658
4332	10359814					1.089	1.408	0.200626	0.462553
4333	10391036	NM_008471	16669	keratin 19	Krt19	1.089	0.195	0.851054	0.94011
4334	10532267	NM_001104621	435864	vomeronasal 2, receptor 9	Vmn2r9	1.089	0.228	0.825973	0.929952
4335	10439788					1.089	1.72	0.12786	0.358645

4335	10459788					1.089	1.72	0.12786	0.358645
4336	10498998	BC062940	229473	RIKEN cDNA D930015E06 gene	D930015E06Rik	1.089	0.924	0.385325	0.654508
4337	10534935	NM_133209	170741	paired immunoglobin-like type	Pilrb1	1.089	1.004	0.347654	0.621632
4338	10522873	NR_003652	654494	predicted gene, EG654494	EG654494	1.089	1.676	0.136421	0.372866
4339	10369702	ENSMUST00000099674	52463	tet oncogene 1	Tet1	1.089	1.228	0.258181	0.532272
4340	10405820	ENSMUST00000099440	66503	RIKEN cDNA 1810034E14 gene	1810034E14Rik	1.089	1.105	0.304633	0.581126
4341	10402715	NM_027404	70369	BCL2-associated athanogene 5	Bag5	1.089	0.634	0.545463	0.777437
4342	10351197	NM_011346	20343	selectin, lymphocyte	Sell	1.089	0.588	0.574507	0.797076
4343	10539766	NM_001040106	269774	AP2 associated kinase 1	Aak1	1.088	0.98	0.358912	0.630983
4344	10516211	NM_001030274	595136	NADH dehydrogenase (ubiquinone	Ndufs5	1.088	0.244	0.814165	0.925212
4345	10370708	NM_025554	66420	polymerase (RNA) II (DNA direc	Polr2e	1.088	0.896	0.399353	0.665621
4346	10460591	NM_021438	58249	fibroblast growth factor (acid	Fibp	1.088	0.931	0.38177	0.651436
4347	10549721					1.088	1.315	0.228627	0.499699
4348	10373330	NM_017473	54150	retinol dehydrogenase 7	Rdh7	1.088	1.632	0.145462	0.387083
4349	10579548	ENSMUST00000098643	234407	glycosyltransferase 25 domain	Glt25d1	1.088	0.966	0.365181	0.636291
4350	10471457	NM_011373	20448	ST6 (alpha-N-acetyl-neuraminyl	St6galnac4	1.088	1.241	0.253549	0.527818
4351	10491920	AK016297	67746	RIKEN cDNA 4930577N17 gene	4930577N17Rik	1.088	0.8	0.449495	0.706889
4352	10472724	NM_027352	70231	golgi reassembly stacking prot	Gorasp2	1.088	1.236	0.255178	0.529489
4353	10530870	NM_007937	13839	Eph receptor A5	Epha5	1.088	0.588	0.574742	0.797076
4354	10579852	NM_133823	109136	methylmalonic aciduria (cobala	Mmaa	1.088	1.014	0.343597	0.617668
4355	10469138					1.088	0.32	0.758366	0.898716
4356	10481857	NM_016768	18516	pre B-cell leukemia transcript	Pbx3	1.088	0.393	0.705805	0.871814
4357	10509463	NM_172703	230861	eukaryotic translation initiat	Eif4g3	1.088	1.522	0.170647	0.422304
4358	10449608	NM_001081160	74762	MAM domain containing glycosyl	Mdga1	1.088	1.891	0.0993161	0.307864
4359	10515733	ENSMUST00000075406	230676	cDNA sequence BC059842	BC059842	1.088	0.993	0.352868	0.625927
4360	10539805	ENSMUST00000095740	320001	RIKEN cDNA E230015B07 gene	E230015B07Rik	1.088	1.492	0.178082	0.432735
4361	10383502	NM_001038653	80879	solute carrier family 16 (mono	Slc16a3	1.088	1.598	0.152908	0.396925
4362	10578071	NM_011721	22427	Werner syndrome homolog (human	Wrn	1.088	1.711	0.129575	0.361014
4363	10590597	NM_030692	83493	SAC1 (suppressor of actin muta	Sacm1l	1.088	1.198	0.268905	0.543464
4364	10464328	NM_011128	18947	pancreatic lipase-related prot	Pnliprp2	1.088	1.56	0.161488	0.409658
4365	10409990	ENSMUST00000091563	211378	RIKEN cDNA 6720489N17 gene	6720489N17Rik	1.088	0.262	0.800846	0.919467
4366	10453734					1.088	0.91	0.392103	0.660239
4367	10350790	ENSMUST00000065673	240832	torsin A interacting protein 2	Tor1aip2	1.088	0.625	0.551091	0.781221
4368	10430778	NM_026737	68479	PHD finger protein 5A	Phf5a	1.088	0.522	0.617362	0.823029
4369	10580169	NM_026350	67736	coiled-coil domain containing	Ccdc130	1.087	1.303	0.232553	0.503492
4370	10599736	NM_001077361	14199	four and a half LIM domains 1	Fhl1	1.087	0.691	0.510998	0.752038
4371	10362271					1.087	0.958	0.369196	0.639859
4372	10529923	NM_172153	209707	ligand dependent nuclear recep	Lcorl	1.087	0.87	0.412167	0.676028
4373	10584067	NM_001115130	235132	zinc finger and BTB domain con	Zbtb44	1.087	0.921	0.38678	0.65582
4374	10472764	NM_010064	13427	dynein cytoplasmic 1 intermedi	Dync1i2	1.087	1.229	0.257739	0.531852
4375	10601583					1.087	0.284	0.784206	0.912068
4376	10551724	NM_029887	77254	Yip1 interacting factor homolo	Yif1b	1.087	1.296	0.234977	0.506303
4377	10568705	ENSMUST00000097984	627214	RIKEN cDNA B830028B13 gene	B830028B13Rik	1.087	1.389	0.206098	0.470186
4378	10594144	NM_175325	102774	Bardet-Biedl syndrome 4 homolo	Bbs4	1.087	1.351	0.217517	0.485293
4379	10459227					1.087	0.887	0.403826	0.668689
4380	10566587	NM_146453	258445	olfactory receptor 693	Olfr693	1.087	1.358	0.215305	0.482386
4381	10534061	NM_172462	22648	zinc finger protein 11	Zfp11	1.087	1.908	0.0968312	0.303049
4382	10513406	NM_021053	30936	solute carrier family 46, memb	Slc46a2	1.087	1.432	0.193925	0.453579
4383	10395227	ENSMUST00000036862	238123	component of oligomeric golgi	Cog5	1.087	0.866	0.414585	0.677853
4384	10344939	NM_009352	21749	telomeric repeat binding facto	Terf1	1.087	1.065	0.321135	0.598048

4385	10516101	NM_022033	64059	3-oxoacid CoA transferase 2A	Oxct2a	1.087	0.955	0.370511	0.641245
4386	10585823	XM_001479935	665268	similar to Rpl17 protein	LOC665268	1.087	0.57	0.585788	0.80308
4387	10579356	NM_008841	18709	phosphatidylinositol 3-kinase,	Pik3r2	1.087	1.779	0.117223	0.341258
4388	10431017	NM_178869	319953	tubulin tyrosine ligase-like 1	Ttll1	1.087	0.242	0.815168	0.925866
4389	10423921	NM_130885	170719	oxidation resistance 1	Oxr1	1.087	1.06	0.323297	0.599849
4390	10477512	BC018465	228802	cDNA sequence BC018465	BC018465	1.087	1.452	0.188458	0.446521
4391	10511330	NM_020021	17451	Moloney sarcoma oncogene	Mos	1.087	1.195	0.269757	0.544449
4392	10375557	NM_146467	258459	olfactory receptor 1388	Olfr1388	1.087	1.312	0.229736	0.500845
4393	10380622	NM_008270	15417	homeo box B9	Hoxb9	1.087	1.087	0.312038	0.588349
4394	10363522	BC119320	71767	trypsin domain containing 1	Tysnd1	1.087	1.009	0.345558	0.619665
4395	10528832					1.087	1.518	0.17148	0.42362
4396	10561376	NM_007866	13389	delta-like 3 (Drosophila)	Dll3	1.087	0.852	0.421673	0.683993
4397	10564791	ENSMUST00000032763	16576	kinesin family member 7	Kif7	1.087	0.462	0.657808	0.846971
4398	10442651	NM_134126	106633	intraflagellar transport 140 h	Ift140	1.087	1.018	0.341691	0.616255
4399	10589616	NM_148940	73336	RIKEN cDNA 1700036D21 gene	1700036D21Rik	1.087	1.905	0.0972185	0.303677
4400	10488303	NM_025820	66877	Crn, crooked neck-like 1 (Dros	Crnkl1	1.086	1.023	0.339347	0.614732
4401	10399965	ENSMUST00000063828	320046	RIKEN cDNA F730043M19 gene	F730043M19Rik	1.086	1.279	0.240603	0.513659
4402	10407803	NM_031999	83924	G protein-coupled receptor 137	Gpr137b	1.086	0.625	0.551293	0.781322
4403	10596796	NM_029169	19654	RNA binding motif protein 6	Rbm6	1.086	1.503	0.17523	0.428429
4404	10568432	ENSMUST00000057557	210711	RIKEN cDNA 1110007A13 gene	1110007A13Rik	1.086	1.309	0.230827	0.501612
4405	10375002	NM_026252	67579	cytoplasmic polyadenylation el	Cpeb4	1.086	0.479	0.646112	0.840365
4406	10365891	NM_172051	319880	transmembrane and coiled coil	Tmcc3	1.086	1.798	0.114032	0.335061
4407	10361270	NM_010778	17221	CD46 antigen, complement regul	Cd46	1.086	0.446	0.668925	0.852739
4408	10362918					1.086	1.52	0.17109	0.422843
4409	10558454	NM_023140	30926	glutaredoxin 3	Glrx3	1.086	0.568	0.587293	0.804205
4410	10347254	NM_018817	54380	Swi/SNF related matrix associa	Smarcal1	1.086	0.992	0.353268	0.626005
4411	10447477	ENSMUST00000097270	623954	hypothetical protein LOC623954	LOC623954	1.086	1.761	0.120386	0.346744
4412	10570429	NM_181854	101994	zinc finger protein 828	Zfp828	1.086	1.103	0.305498	0.581774
4413	10476900	NM_177655	228756	cystatin-like 1	Cstl1	1.086	0.751	0.476198	0.727414
4414	10429295	NM_001033876	223604	potassium channel, subfamily K	Kcnk9	1.086	0.946	0.374945	0.644967
4415	10414366	NM_030236	78938	F-box protein 34	Fbxo34	1.086	1.376	0.21012	0.475469
4416	10573903	ENSMUST00000062522	319388	RIKEN cDNA D230002A01 gene	D230002A01Rik	1.086	1.536	0.167276	0.41822
4417	10477361	ENSMUST00000055893	329541	predicted gene, EG329541	EG329541	1.086	0.842	0.426972	0.688312
4418	10356194	NM_133975	14897	thyroid hormone receptor inter	Trip12	1.086	1.192	0.270854	0.545372
4419	10555840	NM_147120	259124	olfactory receptor 638	Olfr638	1.086	1.664	0.138809	0.37681
4420	10592459					1.086	0.622	0.552925	0.782578
4421	10542200	NM_020590	57436	gamma-aminobutyric acid (GABA(	Gabarapl1	1.086	0.821	0.437931	0.697051
4422	10537076					1.086	1.024	0.33906	0.614614
4423	10588642	NM_018879	56032	tumor suppressor candidate 4	Tusc4	1.086	0.769	0.466068	0.719571
4424	10442300	XR_001815	666030	predicted gene, EG666030	EG666030	1.086	0.713	0.498076	0.742207
4425	10470446	NM_011305	20181	retinoid X receptor alpha	Rxra	1.086	0.965	0.365688	0.636847
4426	10568288	NM_198858	244218	cardiotrophin 2	Ctf2	1.086	1.231	0.256911	0.53126
4427	10485042	NM_001033451	381410	zinc finger protein 408	Zfp408	1.086	1.045	0.329792	0.606148
4428	10404422	NM_011454	20708	serine (or cysteine) peptidase	Serpinb6b	1.086	0.487	0.640604	0.837232
4429	10535497	BC052346	66729	RIKEN cDNA 4921520G13 gene	4921520G13Rik	1.085	1.179	0.275687	0.550593
4430	10541513					1.085	1.251	0.250029	0.524217
4431	10503680	NM_172688	26409	mitogen-activated protein kina	Map3k7	1.085	0.796	0.451339	0.708496
4432	10566217	NM_147082	259086	olfactory receptor 609	Olfr609	1.085	1.574	0.158169	0.405072
4433	10392063	NM_172397	67803	LIM domain containing 2	Limd2	1.085	1.422	0.196699	0.457385
4434	10476596	NM_001013802	72899	MACRO domain containing 2	Macrod2	1.085	1.056	0.325233	0.601585
4435	10603417	NM_008089	14460	GATA binding protein 1	Gata1	1.085	0.644	0.539394	0.77217
4436	10460580	ENSMUST00000093445	414115	RIKEN cDNA D330050I16 gene	D330050I16Rik	1.085	0.555	0.595553	0.809538

4437	10475350	NM_011354	378702	small EDRK-rich factor 2	Serf2	1.085	1.42	0.197316	0.457905
4438	10559261	NM_133655	12520	CD 81 antigen	Cd81	1.085	0.899	0.397668	0.664302
4439	10598238					1.085	0.503	0.629675	0.831325
4440	10545283	NM_009762	12180	SET and MYND domain containing	Smyd1	1.085	1.196	0.269658	0.544449
4441	10471844	NM_021606	59126	NIMA (never in mitosis gene a)	Nek6	1.085	0.876	0.409121	0.673396
4442	10460582	NM_134149	107242	expressed sequence AI837181	AI837181	1.085	0.994	0.352297	0.625281
4443	10393944	NM_009053	19719	RFNG O-fucosylpeptide 3-beta-N	Rfng	1.085	1.166	0.280889	0.556357
4444	10411456	NM_026685	68344	transmembrane protein 174	Tmem174	1.085	0.613	0.558567	0.786256
4445	10397715					1.085	1.063	0.322049	0.598804
4446	10455948	NM_001081328	78923	chondroitin sulfate synthase 3	Chsy3	1.085	2.208	0.0619122	0.229974
4447	10430311	BC107197	73376	RIKEN cDNA 1700061J05 gene	1700061J05Rik	1.085	1.764	0.119815	0.346027
4448	10380689	NM_007622	12412	chromobox homolog 1 (Drosophil	Cbx1	1.085	1.645	0.142693	0.382882
4449	10395596	NM_008241	15228	forkhead box G1	Foxg1	1.085	1.642	0.143427	0.384029
4450	10408037	NM_025719	66707	NFKB activating protein-like	Nkapl	1.085	0.545	0.601921	0.813436
4451	10345791	NM_010743	17082	interleukin 1 receptor-like 1	Il1rl1	1.085	1.474	0.18279	0.439545
4452	10378114	NM_025985	67128	ubiquitin-conjugating enzyme E	Ube2g1	1.085	1.396	0.204249	0.467434
4453	10430032	NM_183091	72749	nuclear factor of kappa light	Nfkbil2	1.085	0.507	0.626955	0.83039
4454	10550365	NM_178900	101540	protein kinase D2	Prkd2	1.085	0.952	0.372122	0.642455
4455	10410435	NM_198600	210106	polymerase (DNA directed) sigm	Pols	1.085	1.232	0.256474	0.530714
4456	10441231	AK148233	100038490	predicted gene, ENSMUSG0000007	ENSMUSG00000074891	1.085	1.06	0.32316	0.59983
4457	10596481	NM_001110271	68644	abhydrolase domain containing	Abhd14a	1.084	1.76	0.120558	0.346982
4458	10350297	NM_001081258	381293	kinesin family member 14	Kif14	1.084	1.486	0.17953	0.434921
4459	10556246	NM_009281	20841	zinc finger protein 143	Zfp143	1.084	0.954	0.371125	0.641955
4460	10518833	NM_001081557	100072	calmodulin binding transcripti	Camta1	1.084	1.411	0.199933	0.461707
4461	10434224	BC029862	13972	guanine nucleotide binding pro	Gnb1l	1.084	0.792	0.453672	0.710123
4462	10457205	NM_001110856	12916	cAMP responsive element modula	Crem	1.084	1.582	0.156453	0.402488
4463	10469425	NM_029466	75869	ADP-ribosylation factor-like 5	Arl5b	1.084	0.923	0.385636	0.654706
4464	10472313	NM_009322	21375	T-box brain gene 1	Tbr1	1.084	1.41	0.200256	0.462199
4465	10515500	NM_017377	53418	UDP-Gal:betaGlcNAc beta 1,4- g	B4galt2	1.084	1.563	0.160694	0.408331
4466	10502522	NM_011828	23908	heparan sulfate 2-O-sulfotrans	Hs2st1	1.084	0.584	0.577026	0.797771
4467	10533323	NM_172126	280668	a disintegrin and metallopepti	Adam1a	1.084	1.157	0.283967	0.559215
4468	10445187	NM_001038500	619517	predicted gene, EG619517	EG619517	1.084	1.603	0.151817	0.395645
4469	10379740	NM_145432	217026	HEAT repeat containing 6	Heatr6	1.084	1.223	0.259738	0.534127
4470	10565255	NM_030728	80982	RIKEN cDNA 9930013L23 gene	9930013L23Rik	1.084	1.869	0.10253	0.314141
4471	10522653	ENSMUST00000086909	320411	RIKEN cDNA A730089K16 gene	A730089K16Rik	1.084	0.829	0.433935	0.694402
4472	10368598	NM_175448	215890	retinaldehyde binding protein	Rlbp1l2	1.084	0.178	0.863662	0.945728
4473	10580191	NM_001081981	18032	nuclear factor I/X	Nfix	1.084	0.768	0.466989	0.719977
4474	10419892	NM_010112	13644	embryonal Fyn-associated subst	Efs	1.084	0.796	0.451304	0.708496
4475	10413808					1.084	0.325	0.754757	0.896801
4476	10557758	NM_178029	233904	SET domain containing 1A	Setd1a	1.084	0.979	0.3592	0.63128
4477	10425880	NM_146061	109270	Rho GTPase activating protein	Arhgap8	1.084	2.163	0.0662142	0.240143
4478	10598575	NM_173414	236285	LanC lantibiotic synthetase co	Lancl3	1.084	0.991	0.353794	0.6265
4479	10404874	NM_153789	218203	myosin regulatory light chain	Mylip	1.084	1.807	0.112445	0.332128
4480	10447120	NM_026516	68027	transmembrane protein 178	Tmem178	1.084	1.349	0.218207	0.486274
4481	10484318	NM_016965	50884	NCK-associated protein 1	Nckap1	1.084	0.95	0.372674	0.643093
4482	10404506	NM_009068	19766	receptor (TNFRSF)-interacting	Ripk1	1.084	1.2	0.268195	0.542786
4483	10361828	NM_010828	17684	Cbp/p300-interacting transacti	Cited2	1.084	0.721	0.493618	0.739168
4484	10381006	NM_178060	21833	thyroid hormone receptor alpha	Thra	1.084	0.587	0.575118	0.797076
4485	10537169	NM_009731	11997	aldo-keto reductase family 1,	Akr1b7	1.084	1.82	0.11024	0.328467
4486	10421817	NM_025832	66897	NMDA receptor regulated 1-like	Narg1l	1.084	0.719	0.494587	0.739625
4487	10392815	NM_134158	140497	cDNA sequence AF251705	AF251705	1.084	1.492	0.178096	0.432735
				RIKEN cDNA 1700019N12					

4488	10465494	BC061075	67077	gene	1700019N12Rik	1.084	2.047	0.0787019	0.267021
4489	10483737	NM_001025093	11909	activating transcription facto	Atf2	1.084	1.537	0.166991	0.417902
4490	10375290	NM_148673	193116	SLU7 splicing factor homolog (	Slu7	1.084	0.608	0.561578	0.788656
4491	10407563					1.084	1.093	0.309665	0.586555
4492	10542335	NM_181444	232431	G protein-coupled receptor, fa	Gprc5a	1.084	1.476	0.182307	0.438828
4493	10362974	NM_172473	209462	HECT domain and ankyrin repeat	Hace1	1.084	1.116	0.300303	0.576441
4494	10578123	NM_019733	19663	RNA binding protein gene with	Rbpms	1.084	0.916	0.38918	0.65778
4495	10573261	NM_024184	66929	ASF1 anti-silencing function 1	Asf1b	1.084	0.793	0.452842	0.709514
4496	10470149	NM_007947	13863	lipocalin 5	Lcn5	1.084	1.268	0.244315	0.51746
4497	10412435	BC117955	245269	RIKEN cDNA E130304F04 gene	E130304F04Rik	1.084	1.256	0.248305	0.521677
4498	10468213	ENSMUST00000065266	75579	RIKEN cDNA 2310034G01 gene	2310034G01Rik	1.083	1.465	0.18507	0.442657
4499	10357391	NM_027678	226409	zinc finger, RAN-binding domai	Zranb3	1.083	1.335	0.222615	0.492542
4500	10365104	BC119790	73822	RIKEN cDNA F630110N24 gene	F630110N24Rik	1.083	1.411	0.199772	0.461487
4501	10418766	NM_001024604	105522	ankyrin repeat domain 28	Ankrd28	1.083	0.599	0.567248	0.792635
4502	10511703	NM_138952	192656	receptor (TNFRSF)-interacting	Ripk2	1.083	1.001	0.349314	0.622835
4503	10449207	BC037132	215445	RAB11 family interacting prote	Rab11fip3	1.083	1.098	0.307524	0.584192
4504	10565786	NM_177448	233549	monoacylglycerol O-acyltransfe	Mogat2	1.083	1.021	0.340426	0.61558
4505	10495763	NM_008129	14630	glutamate-cysteine ligase , mo	Gclm	1.083	0.406	0.696803	0.867016
4506	10434441	NM_025462	107522	endothelin converting enzyme 2	Ece2	1.083	0.381	0.714073	0.874842
4507	10458195	NM_009860	12532	cell division cycle 25 homolog	Cdc25c	1.083	1.086	0.31251	0.588871
4508	10576034	NM_008320	15900	interferon regulatory factor 8	Irf8	1.083	1.494	0.177548	0.432048
4509	10359754	NM_001083897	68481	myelin protein zero-like 1	Mpzl1	1.083	1.763	0.120006	0.34645
4510	10571444	NM_007514	11988	solute carrier family 7 (catio	Slc7a2	1.083	0.152	0.8833	0.95405
4511	10588731	NM_009074	19882	macrophage stimulating 1 recep	Mst1r	1.083	1.598	0.152712	0.396774
4512	10397054	NM_030246	73828	WD repeat domain 21	Wdr21	1.083	0.84	0.42791	0.689167
4513	10375634	NM_016961	26420	mitogen-activated protein kina	Mapk9	1.083	0.462	0.65781	0.846971
4514	10516706	NM_011317	20218	KH domain containing, RNA bind	Khdrbs1	1.083	1.62	0.148047	0.390187
4515	10361055	NM_144879	226841	vasohibin 2	Vash2	1.083	0.573	0.583767	0.801609
4516	10494227	NM_029789	76893	LAG1 homolog, ceramide synthas	Lass2	1.083	0.389	0.708368	0.872343
4517	10351298	NM_001081126	240888	G protein-coupled receptor 161	Gpr161	1.083	1.655	0.14056	0.379276
4518	10581363	NM_177150	320394	centromere protein T	Cenpt	1.083	0.892	0.401151	0.666661
4519	10489038	NM_020255	19018	SCAN domain-containing 1	Scand1	1.083	0.567	0.588216	0.804948
4520	10379957	NM_029788	76892	ring finger protein, transmemb	Rnft1	1.083	1.015	0.342987	0.617132
4521	10589535	NM_008694	18054	neutrophilic granule protein	Ngp	1.083	0.964	0.366101	0.637106
4522	10441313	BC043688	207781	RIKEN cDNA 5830404H04 gene	5830404H04Rik	1.083	1.037	0.333111	0.609187
4523	10474093	BC022909	66457	RIKEN cDNA 2810002D19 gene	2810002D19Rik	1.083	0.915	0.389682	0.658311
4524	10405047	NM_025711	66695	asporin	Aspn	1.083	0.08	0.938032	0.975903
4525	10595856	NM_138756	192287	solute carrier family 25, memb	Slc25a36	1.083	0.935	0.379854	0.64965
4526	10371591	NM_029249	75317	RIKEN cDNA 4930547N16 gene	4930547N16Rik	1.083	0.673	0.521979	0.759008
4527	10375019	NM_008741	18197	neuron specific gene family me	Nsg2	1.083	0.976	0.360867	0.632578
4528	10606475	NM_001080549	245596	highly divergent homeobox	Hdx	1.083	0.729	0.489126	0.736349
4529	10556111	NM_001005488	257919	olfactory receptor 467	Olfr467	1.083	1.435	0.193243	0.452533
4530	10454447	NM_172965	269003	Sin3A associated protein	Sap130	1.083	1.199	0.268445	0.542795
4531	10429859	NM_153122	75475	5-oxoprolinase (ATP-hydrolysin	Oplah	1.083	1.761	0.120342	0.34671
4532	10510127	NM_001081248	435815	similar to arylacetamide deace	RP23-139B20.1	1.083	1.156	0.28438	0.559618
4533	10387699	NM_153788	216859	centaurin, beta 1	Centb1	1.083	2	0.0843567	0.278694
4534	10350516	NM_011198	19225	prostaglandin-endoperoxide syn	Ptgs2	1.083	0.806	0.445851	0.703765
4535	10351525	NM_008623	17528	myelin protein zero	Mpz	1.083	1.14	0.290885	0.567072
4536	10573823	NM_177224	109151	chromodomain helicase DNA bind	Chd9	1.083	1.315	0.228825	0.499925

4537	10422185	NM_026047	72486	ring finger protein 219	Rnf219	1.083	1.48	0.181193	0.437195
4538	10535021	NM_172412	71951	glypican 2 (cerebroglycan)	Gpc2	1.082	1.666	0.138426	0.376399
4539	10574632	NM_022309	12400	core binding factor beta	Cbfb	1.082	1.239	0.254077	0.528397
4540	10557560	NM_138754	52858	CDP-diacylglycerol--inositol 3	Cdipt	1.082	0.79	0.454818	0.711187
4541	10515694	ENSMUST00000075406	230676	cDNA sequence BC059842	BC059842	1.082	0.502	0.630558	0.831653
4542	10485594	NM_001033768	241593	predicted gene, OTTMUSG0000001	OTTMUSG00000014964	1.082	1.501	0.175887	0.429588
4543	10380823	NM_010688	16796	LIM and SH3 protein 1	Lasp1	1.082	1.171	0.278704	0.553637
4544	10574899	NM_026532	68051	nuclear transport factor 2	Nutf2	1.082	0.758	0.472284	0.72404
4545	10463645	NM_015752	24069	suppressor of fused homolog (D	Sufu	1.082	1.052	0.32667	0.602834
4546	10501593	NM_023214	66500	solute carrier family 30 (zinc	Slc30a7	1.082	0.727	0.49001	0.737262
4547	10359917	NM_010476	15490	hydroxysteroid (17-beta) dehyd	Hsd17b7	1.082	0.34	0.743529	0.89082
4548	10443421	NM_001081315	268936	bromodomain and PHD finger con	Brpf3	1.082	1.396	0.204143	0.467365
4549	10485309	ENSMUST00000099688	414123	RIKEN cDNA E530001K10 gene	E530001K10Rik	1.082	1.063	0.321892	0.598705
4550	10494085	NM_019414	20342	selenium binding protein 2	Selenbp2	1.082	1.567	0.159798	0.407118
4551	10435067	NM_199309	245308	zinc finger, DHHC domain conta	Zdhhc19	1.082	1.061	0.323092	0.59983
4552	10421877	NM_019670	56419	diaphanous homolog 3 (Drosophi	Diap3	1.082	1.258	0.247603	0.520853
4553	10345387	NM_009355	21755	testicular serine protease 1	Tesp1	1.082	1.014	0.343394	0.617488
4554	10545135	NM_008354	16162	interleukin 12 receptor, beta	Il12rb2	1.082	1.394	0.204822	0.4682
4555	10591844	AK029497	320752	dpy-19-like 2 (C. elegans)	Dpy19l2	1.082	1.022	0.339783	0.615188
4556	10446376	NM_008549	17158	mannosidase 2, alpha 1	Man2a1	1.082	0.712	0.498947	0.742429
4557	10509992	NM_013868	29818	heat shock protein family, mem	Hspb7	1.082	1.371	0.211441	0.476926
4558	10500100	NM_027206	69769	tumor necrosis factor, alpha-i	Tnfaip8l2	1.082	1.309	0.230613	0.501552
4559	10550047	NM_001001447	232878	zinc finger and SCAN domain co	Zscan22	1.082	0.821	0.438108	0.697167
4560	10581507	NM_139229	97484	component of oligomeric golgi	Cog8	1.082	1.018	0.341505	0.616178
4561	10553568	NM_146190	233276	tubulin, gamma complex associa	Tubgcp5	1.082	0.514	0.622561	0.827273
4562	10433179	NM_009268	20771	salivary protein 2	Spt2	1.082	1.445	0.190525	0.449454
4563	10520109					1.082	0.273	0.79262	0.91549
4564	10434869	NM_026202	67501	coiled-coil domain containing	Ccdc50	1.082	1.479	0.181361	0.437401
4565	10421227	BC021475	219158	RIKEN cDNA 2610301G19 gene	2610301G19Rik	1.082	1.188	0.272609	0.547117
4566	10360858	NM_178692	226777	RIKEN cDNA C130074G19 gene	C130074G19Rik	1.082	1.04	0.33197	0.608173
4567	10459705	NM_008540	17128	MAD homolog 4 (Drosophila)	Smad4	1.082	0.958	0.369154	0.639859
4568	10574242	NM_009090	20021	polymerase (RNA) II (DNA direc	Polr2c	1.082	1.636	0.144683	0.385967
4569	10401114	NM_134050	104886	RAB15, member RAS oncogene fam	Rab15	1.082	1.213	0.26336	0.538069
4570	10434003	NM_007764	12929	v-crk sarcoma virus CT10 oncog	Crkl	1.081	1.142	0.290121	0.566261
4571	10423919	AK016133	620121	RIKEN cDNA 4930555K19 gene	4930555K19Rik	1.081	0.725	0.491286	0.737713
4572	10473217					1.081	0.774	0.463367	0.717662
4573	10495562	NM_175413	109245	leucine rich repeat containing	Lrrc39	1.081	1.326	0.225291	0.495384
4574	10544499	AK080300	320946	RIKEN cDNA A930035D04 gene	A930035D04Rik	1.081	1.074	0.317579	0.594733
4575	10443063	NM_009343	21652	PHD finger protein 1	Phf1	1.081	1.28	0.240333	0.513397
4576	10481827	NM_001085507	241311	zinc finger and BTB domain con	Zbtb34	1.081	1.56	0.161433	0.409623
4577	10597493	NM_024222	68292	STT3, subunit of the oligosacc	Stt3b	1.081	1.449	0.189295	0.447652
4578	10393936	NM_007621	12409	carbonyl reductase 2	Cbr2	1.081	1.189	0.272286	0.546899
4579	10508368	NM_001009819	215493	alpha 1,3-galactosyltransferas	A3galt2	1.081	1.433	0.193636	0.453103
4580	10568897	NM_133755	74237	tubulin, gamma complex associa	Tubgcp2	1.081	0.85	0.422538	0.684818
4581	10347335	NM_013612	18173	solute carrier family 11 (prot	Slc11a1	1.081	1.561	0.161238	0.409319
4582	10427675	NM_177123	320277	sperm flagellar 2	Spef2	1.081	0.892	0.4014	0.666762
4583	10503251	NM_026005	67157	RIKEN cDNA 2610301B20 gene	2610301B20Rik	1.081	1.632	0.145475	0.387083
4584	10425686	NM_172428	76457	coiled-coil domain containing	Ccdc134	1.081	1.168	0.280073	0.55551
4585	10378068	NM_001037713	327959	XIAP associated factor 1	Xaf1	1.081	0.622	0.552954	0.782578

4585	10578008	NM_001037713	327959	XIAP associated factor 1	Xaf1	1.081	0.622	0.552954	0.782578
4586	10466682	NM_153808	226026	structural maintenance of chro	Smc5	1.081	1.096	0.30833	0.585061
4587	10445412	NM_008690	18037	nuclear factor of kappa light	Nfkbie	1.081	1.726	0.126818	0.356718
4588	10588849	NM_177275	320844	adhesion molecule with Ig like	Amigo3	1.081	1.028	0.337333	0.612974
4589	10444821	NM_023124	15019	histocompatibility 2, Q region	H2-Q8	1.081	2.012	0.0828858	0.275729
4590	10355611	NM_029888	77264	zinc finger protein 142	Zfp142	1.081	1.664	0.138881	0.376958
4591	10460616	NM_007687	12631	cofilin 1, non-muscle	Cfl1	1.081	1.172	0.278598	0.553531
4592	10392070	NM_028126	72149	RIKEN cDNA 2610019A05 gene	2610019A05Rik	1.081	0.923	0.385659	0.654706
4593	10591228	NM_011753	22688	zinc finger protein 26	Zfp26	1.081	0.744	0.480379	0.729941
4594	10480541	NM_001012518	77683	euchromatic histone methyltran	Ehmt1	1.081	0.927	0.383912	0.653352
4595	10347970	NM_133781	12283	calcium binding protein 39	Cab39	1.081	0.723	0.492593	0.738532
4596	10382336	ENSMUST00000020950	71203	RIKEN cDNA 4933434M16 gene	4933434M16Rik	1.081	0.617	0.556131	0.784723
4597	10523674	NM_028794	74167	nudix (nucleoside diphosphate	Nudt9	1.081	0.81	0.443948	0.702635
4598	10366667	NM_029364	75612	glucosamine (N-acetyl)-6-sulfa	Gns	1.081	1.039	0.332317	0.608356
4599	10490986	BC023403	70808	RIKEN cDNA 4632415L05 gene	4632415L05Rik	1.081	0.511	0.624844	0.828987
4600	10370303	NR_004429	110532	adenosine deaminase, RNA-speci	Adarb1	1.08	1.218	0.261637	0.536103
4601	10598138	NM_001030293	236576	sprouty homolog 3 (Drosophila)	Spry3	1.08	1.7	0.131751	0.364648
4602	10367803					1.08	0.367	0.724413	0.880611
4603	10408529					1.08	1.112	0.30186	0.577905
4604	10575799	NM_172285	234779	phospholipase C, gamma 2	Plcg2	1.08	1.614	0.1493	0.391663
4605	10496251	NM_027208	69772	3-hydroxybutyrate dehydrogenas	Bdh2	1.08	0.322	0.756662	0.897871
4606	10345913	NM_010879	17974	non-catalytic region of tyrosi	Nck2	1.08	0.856	0.419766	0.682051
4607	10432957	NM_013566	16421	integrin beta 7	Itgb7	1.08	1.457	0.187192	0.445619
4608	10584604	NM_023655	72169	tripartite motif-containing 29	Trim29	1.08	1.276	0.241581	0.5144
4609	10384717	NM_023651	72129	peroxisomal biogenesis factor	Pex13	1.08	1.002	0.348869	0.622541
4610	10359867	NM_001013382	240899	leucine rich repeat containing	Lrrc52	1.08	1.32	0.22731	0.498027
4611	10508992	NM_027995	71904	progestin and adipoQ receptor	Paqr7	1.08	0.794	0.452352	0.708922
4612	10550593	NM_011383	20475	sine oculis-related homeobox 5	Six5	1.08	0.498	0.633268	0.833255
4613	10404531	NM_001101430	69666	proteasome (prosome, macropain	Psmg4	1.08	0.115	0.911513	0.964659
4614	10369264	NM_010959	18302	oncoprotein induced transcript	Oit3	1.08	1.93	0.0937263	0.29698
4615	10388847	NM_172795	237868	sterile alpha and HEAT/Armadil	Sarm1	1.08	1.475	0.182368	0.438828
4616	10562523	BC050041	668501	zinc finger protein 507	zfp507	1.08	1.001	0.349043	0.622715
4617	10520126	NM_008713	18127	nitric oxide synthase 3, endot	Nos3	1.08	1.019	0.340993	0.615921
4618	10384780	AK135532	100038580	predicted gene, ENSMUSG0000007	ENSMUSG00000073100	1.08	0.989	0.354555	0.627182
4619	10499906	NM_008574	17235	sperm mitochondria-associated	Smcp	1.08	1.149	0.2873	0.562985
4620	10546533					1.08	1.22	0.260941	0.535507
4621	10574985	NM_178798	330836	solute carrier family 7 (catio	Slc7a6	1.08	1.193	0.270813	0.545372
4622	10469622	NM_001004761	241263	G protein-coupled receptor 158	Gpr158	1.08	1.052	0.326632	0.602834
4623	10441003	NM_001111023	12394	runt related transcription fac	Runx1	1.08	0.826	0.435138	0.695306
4624	10542112	NM_053165	94071	C-type lectin domain family 2,	Clec2h	1.08	2.114	0.0711772	0.250619
4625	10366848	NM_008080	14421	beta-1,4-N-acetyl-galactosamin	B4galnt1	1.08	1.388	0.206501	0.470907
4626	10510876	ENSMUST00000071251	230971	multiple EGF-like-domains 6	Megf6	1.08	1.069	0.319509	0.596487
4627	10363082	NM_013532	14728	leukocyte immunoglobulin-like	Lilrb4	1.08	1.702	0.131364	0.364031
4628	10490611	NM_009184	20459	PTK6 protein tyrosine kinase 6	Ptk6	1.08	0.974	0.361523	0.633294
4629	10455531	ENSMUST00000037090	100047191	hypothetical protein LOC100047	LOC100047191	1.08	0.769	0.466522	0.719642
4630	10594631	NM_177583	208117	anterior pharynx defective 1b	Aph1b	1.08	1.306	0.231621	0.502487
4631	10441660	NM_013682	21331	brachyury 2	T2	1.08	1.23	0.257132	0.531457
4632	10448912	NM_011665	22196	ubiquitin-conjugating enzyme E	Ube2i	1.08	1.219	0.261104	0.535634
4633	10490159	NM_022995	65112	prostate transmembrane protein	Pmepa1	1.08	1.412	0.199634	0.461419
4634	10412421	NM_028245	72465	zinc finger protein 131	Zfp131	1.08	0.972	0.362297	0.633772
4635	10347310	NM_001039509	56695	paroxysmal nonkinesiogenic dys	Pnkd	1.079	1.265	0.245063	0.518209
4636	10416419	ENSMUST00000100386	100038618	predicted gene, ENSMUSG0000007	ENSMUSG00000075519	1.079	0.433	0.677929	0.856898
4637	10462454	NM_144873	109113	ubiquitin-like, containing PHD	Uhrf2	1.079	0.973	0.362061	0.633596
4638	10345190	NM_153601	266744	glutamate-ammonia ligase (glut	Gluld1	1.079	0.5	0.631755	0.832719

4639	10600973	NM_008784	18518	immunoglobulin (CD79A) binding	Igbp1	1.079	0.534	0.60947	0.818311
4640	10403911	NM_145451	75512	glutathione peroxidase 6	Gpx6	1.079	1.607	0.150738	0.394308
4641	10597592	NM_146230	235674	acetyl-Coenzyme A acyltransfer	Acaa1b	1.079	0.623	0.552633	0.782382
4642	10360666	BC120654	381310	RIKEN cDNA 6330403A02 gene	6330403A02Rik	1.079	1.417	0.198299	0.459186
4643	10368930	BC013506	67851	RIKEN cDNA 1700021F05 gene	1700021F05Rik	1.079	0.948	0.373629	0.643742
4644	10438378	NM_009862	12544	cell division cycle 45 homolog	Cdc45l	1.079	0.898	0.398159	0.664555
4645	10442932	NM_021793	60455	transmembrane protein 8 (five	Tmem8	1.079	1.299	0.2338	0.505106
4646	10508734	NM_001081211	19204	platelet-activating factor rec	Ptafr	1.079	1.531	0.168418	0.419736
4647	10572345	NM_011984	26558	homer homolog 3 (Drosophila)	Homer3	1.079	1.568	0.159715	0.407016
4648	10480286	ENSMUST00000095134	74103	nebulette	Nebl	1.079	0.524	0.615851	0.822286
4649	10532103	NM_133248	170823	glomulin, FKBP associated prot	Glmn	1.079	1.414	0.198932	0.460238
4650	10498095	NM_026225	67542	component of oligomeric golgi	Cog6	1.079	1.014	0.343341	0.617471
4651	10527427	NM_027069	69396	RIKEN cDNA 1700018F24 gene	1700018F24Rik	1.079	0.479	0.646132	0.840365
4652	10526743	NM_012002	26893	COP9 (constitutive photomorpho	Cops6	1.079	0.78	0.460315	0.71495
4653	10419160					1.079	0.604	0.564248	0.79062
4654	10377547	AK006879	74273	hypothetical LOC74273	1700064E03Rik	1.079	1.218	0.261459	0.53605
4655	10580622	NM_001081372	382044	liver carboxylesterase N-like	LOC382044	1.079	1.255	0.248501	0.521986
4656	10529485	NM_030127	78558	HtrA serine peptidase 3	Htra3	1.079	0.908	0.393182	0.661213
4657	10580160	BC025049	67873	RIKEN cDNA 2410018C20 gene	2410018C20Rik	1.079	1.254	0.248905	0.522627
4658	10590182	NM_172456	208194	endonuclease G-like 1	Endogl1	1.079	0.342	0.741836	0.889893
4659	10582171	NM_133967	102193	zinc finger, DHHC domain conta	Zdhhc7	1.079	1.123	0.297235	0.573687
4660	10421730	BC120488	219170	expressed sequence AU021034	AU021034	1.078	1.791	0.11513	0.337402
4661	10591781	NM_028390	68743	anillin, actin binding protein	Anln	1.078	1.031	0.335852	0.611439
4662	10536541	NM_022332	64213	Suppression of tumorigenicity	St7	1.078	1.04	0.332153	0.608213
4663	10448631	NM_011647	22084	tuberous sclerosis 2	Tsc2	1.078	1.443	0.190877	0.449884
4664	10545707	NM_009610	11468	actin, gamma 2, smooth muscle,	Actg2	1.078	0.082	0.93722	0.975526
4665	10404848	NM_021878	16468	jumonji, AT rich interactive d	Jarid2	1.078	1.203	0.267096	0.541725
4666	10457302	NM_007935	13831	enhancer of polycomb homolog 1	Epc1	1.078	1.253	0.249446	0.523503
4667	10582708	NM_198103	102058	exocyst complex component 8	Exoc8	1.078	0.957	0.369714	0.640267
4668	10373588	NM_134006	19682	retinol dehydrogenase 5	Rdh5	1.078	0.796	0.451355	0.708496
4669	10524150	NM_027922	71782	ankyrin repeat and LEM domain	Ankle2	1.078	0.881	0.406609	0.671195
4670	10574276	NM_173036	54672	G protein-coupled receptor 97	Gpr97	1.078	1.377	0.209616	0.474684
4671	10588876	NM_025449	66257	nicolin 1	Nicn1	1.078	0.932	0.381494	0.651192
4672	10515026	AK139207	100038491	predicted gene, ENSMUSG0000007	ENSMUSG00000073776	1.078	0.691	0.511252	0.752255
4673	10465395	NM_198168	225849	protein phosphatase 2, regulat	Ppp2r5b	1.078	0.409	0.694067	0.865705
4674	10458808	NM_173423	240263	fem-1 homolog c (C.elegans)	Fem1c	1.078	0.442	0.671662	0.854336
4675	10416340	NM_008115	14586	glial cell line derived neurot	Gfra2	1.078	1.06	0.323163	0.59983
4676	10430020	NM_025842	66914	vacuolar protein sorting 28 (y	Vps28	1.078	0.561	0.592069	0.807034
4677	10374236	NM_009477	22271	uridine phosphorylase 1	Upp1	1.078	0.744	0.480322	0.729941
4678	10503305	BC028830	66185	RIKEN cDNA 1110037F02 gene	1110037F02Rik	1.078	1.252	0.249551	0.523619
4679	10393751	ENSMUST00000062283	76835	RIKEN cDNA 2900052L18 gene	2900052L18Rik	1.078	0.777	0.461812	0.716402
4680	10441361	NM_001122998	24001	T-cell lymphoma invasion and m	Tiam2	1.078	1.325	0.225461	0.495648
4681	10529082	NM_008622	17527	Mpv17 transgene, kidney diseas	Mpv17	1.078	0.74	0.48293	0.731557
4682	10550212	NM_145709	252829	oocyte specific homeobox 5	Obox5	1.077	1.071	0.318681	0.595932
4683	10346448	NM_023631	71872	aldehyde oxidase 4	Aox4	1.077	1.277	0.241213	0.514029
4684	10387483	NM_007911	13643	ephrin B3	Efnb3	1.077	0.984	0.35679	0.629197
4685	10551696	NM_145149	233046	RAS guanyl releasing protein 4	Rasgrp4	1.077	1.188	0.272599	0.547117
4686	10509620	NM_001037761	12345	capping protein (actin filamen	Capzb	1.077	1.435	0.19317	0.452493
4687	10384529	NM_172260	216543	centrosomal protein 68	Cep68	1.077	1.432	0.19408	0.45384
4688	10402795	NM_028023	71963	cell division cycle associated	Cdca4	1.077	1.024	0.339049	0.614614
4689	10599192	NM_028894	74365	LON peptidase N-terminal domai	Lonrf3	1.077	0.724	0.49165	0.73812
4690	10563344	NM_020013	56636	fibroblast growth factor 21	Fgf21	1.077	0.797	0.450961	0.708142

4691	10405835	XR_033589	238678	similar to Methylmalonic acidu	LOC238678	1.077	1.662	0.139286	0.377524
4692	10425016	NM_025536	66398	COMM domain containing 5	Commd5	1.077	0.508	0.626809	0.83034
4693	10432527	NM_028015	71949	LAG1 homolog, ceramide synthas	Lass5	1.077	0.897	0.398747	0.664967
4694	10561461	NM_175021	233033	sterile alpha motif domain con	Samd4b	1.077	1.57	0.159262	0.406366
4695	10510982	NM_001042407	668173	peroxisome biogenesis factor 1	Pex10	1.077	1.202	0.267323	0.541978
4696	10371141	NM_010440	15353	high mobility group 20 B	Hmg20b	1.077	1.8	0.113654	0.334228
4697	10446425					1.077	0.545	0.602138	0.813626
4698	10596545	NM_030730	81000	Rad54 like 2 (S. cerevisiae)	Rad54l2	1.077	0.577	0.581676	0.800424
4699	10396831	NM_009705	11847	arginase type II	Arg2	1.077	0.832	0.432185	0.692545
4700	10412978	AK007938	75602	RIKEN cDNA 1810062O18 gene	1810062O18Rik	1.077	0.679	0.518476	0.757012
4701	10468869	NM_007452	11757	peroxiredoxin 3	Prdx3	1.077	0.442	0.671464	0.854195
4702	10348354	NM_201644	394434	UDP glucuronosyltransferase 1	Ugt1a9	1.077	1.745	0.12318	0.351285
4703	10453616	NM_026157	67440	PAP associated domain containi	Papd1	1.077	0.604	0.56446	0.790721
4704	10392735	NM_020006	56699	CDC42 effector protein (Rho GT	Cdc42ep4	1.077	0.703	0.504256	0.746511
4705	10513952	BC022621	66928	RIKEN cDNA 3110001D03 gene	3110001D03Rik	1.077	0.758	0.472444	0.724129
4706	10437443	BC004063	66626	RIKEN cDNA 5730403B10 gene	5730403B10Rik	1.077	1.21	0.264441	0.539533
4707	10508492	ENSMUST00000084263	622480	similar to SPOC domain contain	LOC622480	1.077	1.174	0.277575	0.552692
4708	10450908	NM_146327	258324	olfactory receptor 129	Olfr129	1.077	0.992	0.353079	0.625939
4709	10454525	NM_173441	73473	IWS1 homolog (S. cerevisiae)	Iws1	1.077	1.572	0.15868	0.405501
4710	10414973	ENSMUST00000103671	219060	RIKEN cDNA B230359F08 gene	B230359F08Rik	1.077	1.574	0.158119	0.405072
4711	10499904	NM_008412	16447	involucrin	Ivl	1.077	1.607	0.150845	0.394493
4712	10439058	NM_146069	224109	leucine rich repeat containing	Lrrc33	1.077	1.355	0.216316	0.483538
4713	10417095	NM_134082	223254	FERM, RhoGEF (Arhgef) and plec	Farp1	1.077	0.192	0.85328	0.940713
4714	10352703	AK038499	100125339	predicted gene, ENSMUSG0000006	ENSMUSG00000066596	1.076	1.645	0.142786	0.382897
4715	10593799	NM_001081341	244891	S phase cyclin A-associated pr	Scaper	1.076	0.687	0.513695	0.754119
4716	10584541	NM_030713	80902	zinc finger protein 202	Zfp202	1.076	1.185	0.273685	0.548356
4717	10555063	NM_027256	101861	integrator complex subunit 4	Ints4	1.076	0.507	0.627016	0.830395
4718	10419604	NM_207576	404341	olfactory receptor 1514	Olfr1514	1.076	1.409	0.200485	0.462476
4719	10562927	NM_133949	84113	prostate tumor over expressed	Ptov1	1.076	0.889	0.402514	0.667563
4720	10484610	AF178753	100037254	predicted gene, OTTMUSG0000001	OTTMUSG00000013632	1.076	1.003	0.348387	0.622153
4721	10431170	NM_001033273	223739	RIKEN cDNA 5031439G07 gene	5031439G07Rik	1.076	0.756	0.473558	0.7251
4722	10567229	NM_001031814	233789	RIKEN cDNA 2610207I05 gene	2610207I05Rik	1.076	1.536	0.167262	0.41822
4723	10565607					1.076	0.948	0.373808	0.643998
4724	10503145					1.076	1.287	0.237917	0.510297
4725	10506360	NM_144906	73094	SH3-domain GRB2-like (endophil	Sgip1	1.076	0.762	0.470414	0.722494
4726	10543944	NM_008098	14489	myotrophin	Mtpn	1.076	1.195	0.269832	0.544485
4727	10404538	NM_013830	19134	PRP4 pre-mRNA processing facto	Prpf4b	1.076	1.668	0.137911	0.375481
4728	10515481	NM_023178	66233	DNA methyltransferase 1-associ	Dmap1	1.076	0.785	0.457329	0.713005
4729	10589640	NM_183103	74306	RIKEN cDNA 1700112C13 gene	1700112C13Rik	1.076	1.556	0.162457	0.411033
4730	10465011	NM_016882	20227	squamous cell carcinoma antige	Sart1	1.076	1.056	0.324904	0.601293
4731	10515051	NM_173350	100273	oxysterol binding protein-like	Osbpl9	1.076	1.203	0.266981	0.541627
4732	10595680	NM_194334	67016	TBC1 domain family, member 2B	Tbc1d2b	1.076	0.786	0.456696	0.712642
4733	10437852	NM_001081154	223989	RIKEN cDNA 4921513D23 gene	4921513D23Rik	1.076	1.623	0.147422	0.389587
4734	10440491	NM_007471	11820	amyloid beta (A4) precursor pr	App	1.076	0.44	0.672804	0.854651

4735	10546031	BC002179	72103	RIKEN cDNA 2010301N04 gene	2010301N04Rik	1.076	0.95	0.372919	0.643306
4736	10471819	ENSMUST00000050372	241324	crumbs homolog 2 (Drosophila)	Crb2	1.076	1.676	0.136416	0.372866
4737	10596027	NM_001033543	213208	interleukin 20 receptor beta	Il20rb	1.076	1.67	0.137571	0.374653
4738	10514985	NM_001033634	414872	zyg-ll homolog B (C. elegans)	Zyg11b	1.076	0.901	0.396484	0.663863
4739	10469475	NM_010804	17354	myeloid/lymphoid or mixed-line	Mllt10	1.076	1.113	0.301304	0.577534
4740	10552942	NM_008497	16866	luteinizing hormone beta	Lhb	1.076	0.977	0.360304	0.632213
4741	10594561	NM_019797	56404	thyroid hormone receptor inter	Trip4	1.076	0.928	0.38325	0.65267
4742	10433672	NM_001039521	106298	RRN3 RNA polymerase I transcri	Rrn3	1.076	0.526	0.614477	0.82153
4743	10461568	NM_134129	28000	PRP19/PSO4 pre-mRNA processing	Prpf19	1.076	0.645	0.539126	0.772047
4744	10588767	NM_011634	22036	TRAF-interacting protein	Traip	1.076	1.221	0.260358	0.534882
4745	10417732					1.076	0.929	0.383011	0.652511
4746	10583402	NM_172918	244713	zinc finger protein 75	Zfp75	1.076	0.125	0.904067	0.962759
4747	10394093	BC017643	217370	cDNA sequence BC017643	BC017643	1.076	1.099	0.307185	0.583826
4748	10404376	NM_177322	11607	angiotensin II receptor, type	Agtr1a	1.076	1.191	0.271416	0.546126
4749	10517744	NM_172415	72754	Rho guanine nucleotide exchang	Arhgef10l	1.076	1.213	0.263233	0.538018
4750	10462670	NM_019428	54364	ribonuclease P/MRP 30 subunit	Rpp30	1.076	0.926	0.384183	0.653466
4751	10488797	NM_021534	59038	peroxisomal membrane protein 4	Pxmp4	1.076	0.367	0.724098	0.88046
4752	10349834	BC132141	240752	phosphoinositide-3-kinase, cla	Pik3c2b	1.076	0.786	0.456705	0.712642
4753	10378732	NM_133656	12928	v-crk sarcoma virus CT10 oncog	Crk	1.076	0.807	0.445604	0.703754
4754	10378857	NM_139128	216961	coronin, actin binding protein	Coro6	1.076	1.406	0.201352	0.463716
4755	10444932	ENSMUST00000113814	76448	RIKEN cDNA 2310014H01 gene	2310014H01Rik	1.075	1.125	0.296698	0.573278
4756	10493882	NR_003185	20764	small proline-rich protein 2J	Sprr2j	1.075	0.977	0.360177	0.632213
4757	10523260	NM_015756	27428	shroom family member 3	Shroom3	1.075	1.016	0.342517	0.616824
4758	10451710	NM_181397	76438	raftlin lipid raft linker 1	Rftn1	1.075	0.743	0.480943	0.730572
4759	10574184	NM_026274	67610	ring finger and SPRY domain co	Rspry1	1.075	1.199	0.268334	0.542786
4760	10354079	NM_172054	98258	thioredoxin domain containing	Txndc9	1.075	0.659	0.530443	0.765382
4761	10439854	NM_027444	70508	bobby sox homolog (Drosophila)	Bbx	1.075	0.418	0.688283	0.86292
4762	10604745	NM_001033360	245424	G protein-coupled receptor 101	Gpr101	1.075	1.23	0.257192	0.531529
4763	10359849	ENSMUST00000053686	80914	uridine-cytidine kinase 2	Uck2	1.075	0.693	0.510186	0.751325
4764	10601561	NM_053114	93728	poly A binding protein, cytopl	Pabpc5	1.075	0.783	0.458416	0.713646
4765	10408666	NM_145938	208366	ribonuclease P 40 subunit (hum	Rpp40	1.075	0.231	0.823661	0.929493
4766	10525858	AK147443	56087	dynein, axonemal, heavy chain	Dnahc10	1.075	1.012	0.344411	0.618711
4767	10595159	NM_026480	67968	oocyte expressed protein homol	Ooep	1.075	1.618	0.148383	0.390615
4768	10564713	NM_008594	17304	milk fat globule-EGF factor 8	Mfge8	1.075	1.075	0.316826	0.594045
4769	10464409	NM_178421	332397	nanos homolog 1 (Drosophila)	Nanos1	1.075	0.738	0.48408	0.732715
4770	10557928	NM_001029872	381924	integrin, alpha D	Itgad	1.075	1.191	0.271391	0.546126
4771	10600947	NM_001081283	620592	transmembrane protein 28	Tmem28	1.075	1.286	0.238227	0.510705
4772	10458767	NM_178872	28105	tripartite motif-containing 36	Trim36	1.075	0.893	0.400887	0.666612
4773	10518909	NM_001033489	433809	ring finger protein 207	Rnf207	1.075	1.274	0.242341	0.515188
4774	10432601	NM_033476	21422	transcription factor CP2	Tcfcp2	1.075	0.936	0.379361	0.649122
4775	10448399	NM_001077421	638345	spermine binding protein-like	Sbpl	1.075	0.823	0.436876	0.696333
4776	10441436	NM_025664	66616	sorting nexin 9	Snx9	1.075	0.524	0.61583	0.822286
4777	10379389	NM_172133	216991	centaurin, alpha 2	Centa2	1.075	0.577	0.58147	0.800326
4778	10431035	NM_183017	223723	tubulin tyrosine ligase-like f	Ttll12	1.075	0.537	0.607247	0.817135
4779	10377310	NM_177779	276920	coiled-coil domain containing	Ccdc42	1.075	1.234	0.255757	0.530117
4780	10505163	NM_001099323	100041581	zinc finger with KRAB and SCAN	Zkscan16	1.075	0.035	0.972903	0.98829
4781	10477250	NM_010407	15162	hemopoietic cell kinase	Hck	1.075	1.582	0.156423	0.402458
4782	10459633	ENSMUST00000025390	75577	RIKEN cDNA 2310002L13 gene	2310002L13Rik	1.075	1.413	0.199243	0.460717
4783	10537397	NM_138680	192196	LUC7-like 2 (S. cerevisiae)	Luc7l2	1.075	1.573	0.158401	0.405262
4784	10490544	NM_173761	228994	YTH domain family 1	Ythdf1	1.075	1.095	0.308762	0.585303
4785	10525464	NM_175423	109305	ORAI calcium release-activated	Orai1	1.075	1.654	0.140897	0.379749
4786	10563176	ENSMUST00000098463	100038379	predicted gene, ENSMUSG0000007	ENSMUSG00000074126	1.075	1.678	0.135979	0.371946
4787	10407145	NM_172593	218613	mesoderm induction early respo	Mier3	1.075	0.53	0.612007	0.820094

4788	10406564	NM_028790	74156	acyl-CoA thioesterase 12	Acot12	1.075	1.585	0.155747	0.401501
4789	10431635					1.075	0.999	0.350046	0.623549
4790	10461898	NM_019437	54391	riboflavin kinase	Rfk	1.075	0.207	0.841813	0.936059
4791	10494153	NM_009336	21427	vacuolar protein sorting 72 (y	Vps72	1.075	0.647	0.537654	0.770722
4792	10436402	NM_171826	224250	claudin domain containing 1	Cldnd1	1.075	0.59	0.573397	0.796682
4793	10487711	BC115616	77006	RIKEN cDNA 2600009E05 gene	2600009E05Rik	1.075	0.733	0.48663	0.734425
4794	10487937	NM_144944	246313	prokineticin receptor 2	Prokr2	1.075	1.216	0.262436	0.536908
4795	10580582	XM_891082	626493	hypothetical protein LOC626493	LOC626493	1.075	1.115	0.300654	0.576863
4796	10598152	NM_001037925	625360	similar to 2-cell-stage, varia	LOC625360	1.075	0.999	0.350335	0.623841
4797	10373709	NM_023743	74203	eukaryotic translation initiat	Eif4enif1	1.075	1.168	0.280014	0.555458
4798	10394209	NM_007872	13435	DNA methyltransferase 3A	Dnmt3a	1.074	1.073	0.317842	0.595046
4799	10585286	NM_175535	244867	Rho GTPase activating protein	Arhgap20	1.074	0.928	0.38347	0.652869
4800	10589466	NM_009211	20588	SWI/SNF related, matrix associ	Smarcc1	1.074	1.046	0.329453	0.60584
4801	10588466	NM_011876	23999	twinfilin, actin-binding prote	Twf2	1.074	1.2	0.268089	0.542786
4802	10555179	NM_028410	72981	protein-kinase, interferon-ind	Prkrir	1.074	0.713	0.498381	0.742426
4803	10438262	NM_153150	13358	solute carrier family 25 (mito	Slc25a1	1.074	0.544	0.602848	0.814324
4804	10552613	NM_010915	18048	kallikrein 1-related pepidase	Klk1b4	1.074	0.662	0.528803	0.764097
4805	10583870	NM_028472	73230	BMP-binding endothelial regula	Bmper	1.074	0.959	0.368491	0.639236
4806	10404407	NM_008592	17300	forkhead box C1	Foxc1	1.074	1.497	0.176895	0.431106
4807	10427883	NM_022816	64833	acyl-CoA thioesterase 10	Acot10	1.074	0.424	0.683955	0.860099
4808	10350766	NM_021433	58244	syntaxin 6	Stx6	1.074	0.624	0.55166	0.781685
4809	10564573	NM_001081345	244059	chromodomain helicase DNA bind	Chd2	1.074	1.722	0.127441	0.357851
4810	10566943	NM_010826	17540	MRV integration site 1	Mrvi1	1.074	0.882	0.406329	0.670995
4811	10489545	NM_009394	21925	troponin C2, fast	Tnnc2	1.074	0.826	0.435394	0.695578
4812	10591110	NM_001080814	270120	FAT tumor suppressor homolog 3	Fat3	1.074	0.631	0.547741	0.778543
4813	10573266	NM_008854	18747	protein kinase, cAMP dependent	Prkaca	1.074	0.496	0.634613	0.83389
4814	10437432	NM_026393	67824	NmrA-like family domain contai	Nmral1	1.074	0.596	0.569486	0.794081
4815	10351502					1.074	0.343	0.741101	0.889595
4816	10447860	ENSMUST00000097408	240023	poly(A)-specific ribonuclease	Pnldc1	1.074	0.698	0.507241	0.749169
4817	10379184	NM_026740	52466	solute carrier family 46, memb	Slc46a1	1.074	0.434	0.677203	0.856571
4818	10465388	NM_019722	56327	ADP-ribosylation factor-like 2	Arl2	1.074	0.615	0.557259	0.785582
4819	10428388	NM_172815	239405	R-spondin 2 homolog (Xenopus l	Rspo2	1.074	0.455	0.662594	0.849733
4820	10598912	NM_011049	18555	PCTAIRE-motif protein kinase 1	Pctk1	1.074	1.187	0.272705	0.547117
4821	10497248					1.074	1.16	0.283169	0.558466
4822	10554893	ENSMUST00000061391	70054	coiled-coil domain containing	Ccdc89	1.074	0.62	0.554138	0.783409
4823	10477994	NM_025680	66642	catenin, beta like 1	Ctnnbl1	1.074	0.412	0.692322	0.865004
4824	10375614	NM_013529	14584	glutamine fructose-6-phosphate	Gfpt2	1.074	0.533	0.61013	0.818617
4825	10552574	NM_010644	16618	kallikrein 1-related petidase	Klk1b26	1.074	1.421	0.196989	0.457727
4826	10445119	NM_013819	14991	histocompatibility 2, M region	H2-M3	1.074	0.876	0.4091	0.673396
4827	10502165	NM_207209	99683	SEC24 related gene family, mem	Sec24b	1.074	0.666	0.52622	0.762249
4828	10544976	NM_145958	210973	kelch repeat and BTB (POZ) dom	Kbtbd2	1.074	1	0.349695	0.623229
4829	10551336	NM_010950	18223	numb-like	Numbl	1.074	0.329	0.751476	0.895256
4830	10390789	NM_029393	75706	keratin 24	Krt24	1.074	0.743	0.481206	0.730704
4831	10571745	NM_029383	75677	claudin 22	Cldn22	1.074	0.69	0.512033	0.75265
4832	10457598	NM_009280	268996	synovial sarcoma translocation	Ss18	1.074	1.47	0.183916	0.441198
4833	10469300	NM_177268	320816	ankyrin repeat domain 16	Ankrd16	1.074	0.945	0.375159	0.64517
4834	10413304	NM_007479	11843	ADP-ribosylation factor 4	Arf4	1.074	1.273	0.242573	0.515498
4835	10552294	NM_207248	243944	RIKEN cDNA 4930433I11 gene	4930433I11Rik	1.074	1.058	0.324292	0.600792
4836	10393814	NM_001033231	192173	cDNA sequence BC003940	BC003940	1.074	0.262	0.80055	0.91941
4837	10450819	NM_023162	66136	zinc ribbon domain containing,	Znrd1	1.074	0.705	0.503159	0.745637
4838	10374400	BC125589	319701	RIKEN cDNA A630050E13 gene	A630050E13Rik	1.074	0.836	0.429842	0.690652
4839	10376404	NM_207230	216783	olfactory receptor 320	Olfr320	1.074	1.041	0.331556	0.607971
4840	10484440	NM_144887	228136	zinc finger, DHHC domain conta	Zdhhc5	1.074	0.575	0.582918	0.801046

4841	10592201	NM_007691	12649	checkpoint kinase 1 homolog (S	Chek1	1.074	0.869	0.412719	0.676213
4842	10434559	NM_010143	13845	Eph receptor B3	Ephb3	1.074	0.844	0.42584	0.68764
4843	10371888	NM_001080129	21917	thymopoietin	Tmpo	1.073	1.38	0.208964	0.473969
4844	10478884	NM_011427	20613	snail homolog 1 (Drosophila)	Snai1	1.073	1.032	0.33562	0.611175
4845	10353010	NM_008651	17864	myeloblastosis oncogene-like 1	Mybl1	1.073	0.972	0.362291	0.633772
4846	10600249	NM_019587	140571	plexin B3	Plxnb3	1.073	1.329	0.224254	0.494263
4847	10510878	ENSMUST00000071251	230971	multiple EGF-like-domains 6	Megf6	1.073	0.8	0.448993	0.706541
4848	10588243	NM_013649	20187	receptor-like tyrosine kinase	Ryk	1.073	1.005	0.347432	0.62155
4849	10598505	ENSMUST00000068623	70226	RIKEN cDNA 2900002K06 gene	2900002K06Rik	1.073	1.287	0.237734	0.510106
4850	10508376	NM_178110	67525	tripartite motif-containing 62	Trim62	1.073	1.534	0.167693	0.418965
4851	10413216	NM_175264	77592	RIKEN cDNA 4931406H21 gene	4931406H21Rik	1.073	1.185	0.273442	0.54818
4852	10539465	NM_029245	75305	ankyrin repeat domain 53	Ankrd53	1.073	0.665	0.526887	0.762787
4853	10599781	NM_028242	72459	HIV TAT specific factor 1	Htatsf1	1.073	0.587	0.575408	0.797076
4854	10380859	BC057057	69131	Cdc2-related kinase, arginine/	Crkrs	1.073	0.168	0.871428	0.948625
4855	10356764	BC089525	71874	RIKEN cDNA 2310007B03 gene	2310007B03Rik	1.073	1.732	0.125597	0.35484
4856	10426383	NM_207243	239611	mucin 19	Muc19	1.073	2.245	0.0585054	0.222329
4857	10546977	NM_009723	11941	ATPase, Ca++ transporting, pla	Atp2b2	1.073	1.435	0.193273	0.452555
4858	10535017	NM_001033416	330217	galactose-3-O-sulfotransferase	Gal3st4	1.073	0.716	0.496296	0.740946
4859	10455441	NM_001013797	433180	serine peptidase inhibitor, Ka	Spink6	1.073	0.539	0.606041	0.81629
4860	10571696	NM_009810	12367	caspase 3	Casp3	1.073	0.931	0.38198	0.651575
4861	10506146	ENSMUST00000094956	100038722	predicted gene, ENSMUSG0000007	ENSMUSG00000070892	1.073	1.289	0.237308	0.509565
4862	10426535	BC038822	239647	cDNA sequence BC038822	BC038822	1.073	0.892	0.400964	0.666612
4863	10380761	NM_138657	192157	suppressor of cytokine signali	Socs7	1.073	1.404	0.202022	0.464803
4864	10368490	NM_001110197	68031	ring finger protein 146	Rnf146	1.073	1.159	0.283287	0.558595
4865	10564938	NM_010194	14159	feline sarcoma oncogene	Fes	1.073	1.937	0.0927817	0.295048
4866	10524882	NM_021539	59043	WD repeat and SOCS box-contain	Wsb2	1.073	0.909	0.392863	0.660783
4867	10557165	NM_027363	70261	RIKEN cDNA 2010110P09 gene	2010110P09Rik	1.073	1.759	0.120703	0.347135
4868	10348277	NM_029846	77040	autophagy-related 16-like 1 (y	Atg16l1	1.073	0.741	0.482255	0.730954
4869	10488965	ENSMUST00000109611	74562	fer-1-like 4 (C. elegans)	Fer1l4	1.073	1.296	0.23483	0.506141
4870	10471891	NM_029687	76646	WD repeat domain 38	Wdr38	1.073	1.585	0.155678	0.401373
4871	10488642	NM_145157	246700	defensin beta 19	Defb19	1.073	1.673	0.136977	0.373595
4872	10436788	NM_015755	26559	hormonally upregulated Neu-ass	Hunk	1.073	0.259	0.803148	0.920071
4873	10539279	NM_007517	11993	ancient ubiquitous protein	Aup1	1.073	1.566	0.160037	0.407342
4874	10425177	NM_001039156	110253	TRIO and F-actin binding prote	Triobp	1.073	1.573	0.158516	0.40535
4875	10537318	NM_145076	21848	tripartite motif-containing 24	Trim24	1.073	1.251	0.250103	0.524217
4876	10358991	ENSMUST00000035914	207792	cDNA sequence BC034090	BC034090	1.073	1.486	0.179657	0.434993
4877	10593130	NM_172257	214597	SID1 transmembrane family, mem	Sidt2	1.073	0.893	0.400905	0.666612
4878	10415472	NM_001033043	30054	ring finger protein 17	Rnf17	1.073	1.239	0.254197	0.528502
4879	10421515	XR_034294	668487	similar to Rnf26 protein	LOC668487	1.073	0.861	0.416859	0.679627
4880	10362432					1.073	0.849	0.422976	0.685287
4881	10433658					1.073	0.992	0.353082	0.625939
4882	10521709	NM_024434	66988	leucine aminopeptidase 3	Lap3	1.073	0.499	0.632529	0.832839
4883	10517419	BC089372	230824	grainyhead-like 3 (Drosophila)	Grhl3	1.072	0.91	0.392257	0.660367
4884	10430929	BC095996	21378	transforming growth factor bet	Tbrg3	1.072	0.654	0.533283	0.767318
4885	10532720	NM_016926	53890	squamous cell carcinoma antige	Sart3	1.072	0.753	0.475207	0.726714
4886	10415888	ENSMUST00000100481	100038729	predicted gene, ENSMUSG0000007	ENSMUSG00000075568	1.072	1.081	0.314403	0.591225
4887	10521832	NM_028744	67073	phosphatidylinositol 4-kinase	Pi4k2b	1.072	0.815	0.441235	0.700253
4888	10422436	NM_001081039	105445	dedicator of cytokinesis 9	Dock9	1.072	0.633	0.546181	0.777655
4889	10572525	ENSMUST00000098653	665828	predicted gene, EG665828	EG665828	1.072	1.362	0.214352	0.480978
4890	10477147	NM_010376	14950	histocompatibility 13	H13	1.072	1.035	0.333967	0.609581
4891	10489266	NM_173368	71389	chromodomain helicase DNA	Chd6	1.072	0.579	0.579918	0.799181

				bind					
4892	10521848	NM_030185	78796	zinc finger, CCHC domain conta	Zcchc4	1.072	0.929	0.382776	0.652221
4893	10459827	ENSMUST00000026494	225743	ring finger protein 165	Rnf165	1.072	1.289	0.237234	0.509506
4894	10529344	NM_181857	272158	DNA polymerase N	Poln	1.072	1.559	0.161653	0.409879
4895	10459109	NM_011552	21453	Treacher Collins Franceschetti	Tcof1	1.072	0.569	0.586846	0.803852
4896	10579532	NM_198095	69550	bone marrow stromal cell antig	Bst2	1.072	0.361	0.728674	0.882456
4897	10568065	NM_153580	233875	coiled-coil domain containing	Ccdc95	1.072	0.32	0.758343	0.898716
4898	10535027	NM_029693	76658	RIKEN cDNA 1700123K08 gene	1700123K08Rik	1.072	1.066	0.320607	0.597527
4899	10347497	NM_009518	22409	wingless related MMTV integrat	Wnt10a	1.072	1.821	0.110238	0.328467
4900	10493711	NM_028881	74343	CREB regulated transcription c	Crtc2	1.072	1.215	0.262505	0.536954
4901	10588219					1.072	0.822	0.437562	0.696831
4902	10477187	NM_028109	72119	TPX2, microtubule-associated p	Tpx2	1.072	0.831	0.432497	0.692938
4903	10440881	BC027145	67367	RIKEN cDNA 1810007M14 gene	1810007M14Rik	1.072	1.176	0.276943	0.552111
4904	10581450	NM_028038	71986	DEAD (Asp-Glu-Ala-Asp) box pol	Ddx28	1.072	0.078	0.939596	0.976496
4905	10473981	NM_172669	228361	autophagy/beclin 1 regulator 1	Ambra1	1.072	0.943	0.375984	0.646063
4906	10403361	NM_145131	69617	pitrilysin metallepetidase 1	Pitrm1	1.072	0.457	0.661108	0.849033
4907	10384737	NM_172555	216578	poly(A) polymerase gamma	Papolg	1.072	0.713	0.498467	0.742429
4908	10402066	NM_183186	71375	forkhead box N3	Foxn3	1.072	0.486	0.641323	0.837465
4909	10480699	NM_031843	83768	dipeptidylpeptidase 7	Dpp7	1.072	1.149	0.287169	0.562971
4910	10454298	NM_027007	69256	zinc finger protein 397	Zfp397	1.072	0.973	0.362134	0.633645
4911	10495933	ENSMUST00000106383	71643	RIKEN cDNA 4930422G04 gene	4930422G04Rik	1.072	1.509	0.173742	0.426449
4912	10491399	NM_029017	74600	mitochondrial ribosomal protei	Mrpl47	1.072	0.372	0.720467	0.878318
4913	10444747					1.072	1.024	0.339071	0.614614
4914	10607395	NM_023788	75625	melanoma antigen, family H, 1	Mageh1	1.072	1.192	0.270902	0.545416
4915	10377622	NM_001013414	216860	RIKEN cDNA 0610025P10 gene	0610025P10Rik	1.072	1.338	0.221391	0.490784
4916	10401068	NM_013675	20741	spectrin beta 1	Spnb1	1.072	1.511	0.17318	0.425638
4917	10525406	NM_019805	56317	anaphase promoting complex sub	Anapc7	1.072	0.335	0.747406	0.892632
4918	10358879	NM_028749	74091	N-acetylneuraminate pyruvate l	Npl	1.072	0.593	0.571526	0.795651
4919	10535841	NM_027872	71706	solute carrier family 46, memb	Slc46a3	1.072	1.244	0.252399	0.526583
4920	10483561	AK041069	100038655	predicted gene, ENSMUSG0000007	ENSMUSG00000075299	1.072	0.769	0.466211	0.719571
4921	10450605	NM_011655	22154	tubulin, beta 5	Tubb5	1.072	0.807	0.445423	0.703573
4922	10542650	NM_025872	66964	golgi transport 1 homolog B (S	Golt1b	1.072	0.902	0.39634	0.663741
4923	10580872	NM_024467	79233	zinc finger protein 319	Zfp319	1.072	0.114	0.912516	0.965146
4924	10466676	BC023385	66206	RIKEN cDNA 1110059E24 gene	1110059E24Rik	1.072	1.084	0.313118	0.589668
4925	10561047	NM_153576	232983	chemokine (C-X-C motif) ligand	Cxcl17	1.072	1.893	0.0990262	0.307265
4926	10465106	NM_019935	18426	OVO homolog-like 1 (Drosophila	Ovol1	1.071	1.019	0.341089	0.615941
4927	10413991	XM_985917	268729	gene model 626, (NCBI)	Gm626	1.071	1.532	0.168203	0.419669
4928	10560530	NM_177692	232946	biogenesis of lysosome-related	Bloc1s3	1.071	0.625	0.55093	0.781103
4929	10521415	NM_177678	231148	actin-binding LIM protein 2	Ablim2	1.071	1.304	0.232166	0.502859
4930	10440643	NM_181490	239931	claudin 17	Cldn17	1.071	0.762	0.47041	0.722494
4931	10576774	NM_029465	75863	C-type lectin domain family 4,	Clec4g	1.071	2.061	0.0770855	0.263396
4932	10606060	XM_136015	212753	predicted gene, EG212753	EG212753	1.071	1.448	0.189563	0.448035
4933	10453216	BC065413	72167	THUMP domain containing 2	Thumpd2	1.071	0.93	0.382431	0.651896
4934	10554397	NM_177765	269954	tubulin tyrosine ligase-like f	Ttll13	1.071	0.871	0.411697	0.675585
4935	10546791	NM_145937	58911	sulfatase modifying factor 1	Sumf1	1.071	0.662	0.52845	0.763794
4936	10362104	NM_178934	353169	solute carrier family 2 (facil	Slc2a12	1.071	1.181	0.275239	0.550143
4937	10518847	NM_172705	230936	PHD finger protein 13	Phf13	1.071	1.357	0.215754	0.482894
4938	10397267	BC022589	74316	iron-sulfur cluster assembly 2	Isca2	1.071	1.387	0.206916	0.471397
4939	10455852	NM_028447	73137	proline-rich coiled-coil 1	Prrc1	1.071	1.267	0.244549	0.517644
4940	10413853	NM_011960	26430	poly (ADP-ribose) glycohydrola	Parg	1.071	1.295	0.235116	0.506551
4941	10487622	NM_009225	20638	small nuclear ribonucleoprotei	Snrpb	1.071	0.658	0.531005	0.765411
4942	10582458	NM_001081379	77087	ankyrin repeat domain 11	Ankrd11	1.071	0.974	0.361383	0.633168

4943	10526508	NM_025562	66437	fission 1 (mitochondrial outer	Fis1	1.071	0.585	0.576333	0.797356
4944	10461078	BC017138	109168	RIKEN cDNA 5730596K20 gene	5730596K20Rik	1.071	0.406	0.696245	0.866577
4945	10502199					1.071	0.397	0.703015	0.869729
4946	10599232	NM_025937	67050	NFKB activating protein	Nkap	1.071	0.774	0.463765	0.717865
4947	10405427	NM_025596	66494	PRELI domain containing 1	Prelid1	1.071	0.638	0.54334	0.775718
4948	10576973	NM_009931	12826	collagen, type IV, alpha 1	Col4a1	1.071	1.601	0.152134	0.395855
4949	10573675	NM_025827	66887	lon peptidase 2, peroxisomal	Lonp2	1.071	0.968	0.364515	0.635653
4950	10601978	ENSMUST00000113046	71248	RIKEN cDNA 4933428M09 gene	4933428M09Rik	1.071	1.506	0.174505	0.427497
4951	10505927					1.071	0.176	0.865204	0.946153
4952	10397895	NM_022323	64113	modulator of apoptosis 1	Moap1	1.071	0.844	0.425696	0.687513
4953	10431528	NM_178919	105847	lipase maturation factor 2	Lmf2	1.071	1.242	0.252989	0.52727
4954	10397835	NM_172152	238384	solute carrier family 24 (sodi	Slc24a4	1.071	1.206	0.266024	0.54117
4955	10348096	NM_153530	208718	DIS3 mitotic control homolog (	Dis3l2	1.07	1.28	0.240236	0.513302
4956	10430945	NM_178627	73826	polymerase (DNA-directed), del	Poldip3	1.07	0.738	0.483659	0.732303
4957	10504817	NM_009370	21812	transforming growth factor, be	Tgfbr1	1.07	1.008	0.346091	0.620193
4958	10463112	NM_172839	240665	cyclin J	Ccnj	1.07	0.59	0.572929	0.796481
4959	10604576	NM_016697	14734	glypican 3	Gpc3	1.07	1	0.349783	0.62328
4960	10517677	NM_008675	17965	neuroblastoma, suppression of	Nbl1	1.07	0.821	0.437691	0.696922
4961	10406361					1.07	0.857	0.419056	0.681474
4962	10499716	NM_028475	74383	ubiquitin associated protein 2	Ubap2l	1.07	0.775	0.463181	0.717525
4963	10397717	ENSMUST00000101134	100046427	hypothetical protein LOC100046	LOC100046427	1.07	0.392	0.706321	0.871814
4964	10562399	NM_146188	233107	potassium channel tetramerisat	Kctd15	1.07	0.626	0.550731	0.780996
4965	10448563	NM_007893	13560	E4F transcription factor 1	E4f1	1.07	1.799	0.113798	0.334466
4966	10587818	NM_178711	235527	phospholipid scramblase 4	Plscr4	1.07	0.887	0.403461	0.668494
4967	10421768	ENSMUST00000022593	219181	A kinase (PRKA) anchor protein	Akap11	1.07	0.633	0.545982	0.777637
4968	10598403	NM_138602	54637	PRA1 domain family 2	Praf2	1.07	0.593	0.571052	0.795252
4969	10377516	NM_010599	16499	potassium voltage-gated channe	Kcnab3	1.07	1.116	0.300325	0.576441
4970	10369176	NM_001033385	544696	RIKEN cDNA D630037F22 gene	D630037F22Rik	1.07	0.645	0.539039	0.772027
4971	10361104	NM_144880	226849	protein phosphatase 2, regulat	Ppp2r5a	1.07	0.632	0.546852	0.778024
4972	10388132	BC043106	74477	RIKEN cDNA 4933427D14 gene	4933427D14Rik	1.07	1.17	0.279315	0.554538
4973	10595000	NM_016963	50875	tropomodulin 3	Tmod3	1.07	0.642	0.540819	0.773267
4974	10573190	NM_146270	258267	olfactory receptor 370	Olfr370	1.07	1.303	0.232712	0.503682
4975	10347862	BC059229	75734	RIKEN cDNA 5230400G24 gene	5230400G24Rik	1.07	0.846	0.424912	0.686823
4976	10460057	NM_001081300	110796	teashirt zinc finger family me	Tshz1	1.07	0.261	0.801157	0.919484
4977	10346762					1.07	1.037	0.333293	0.609193
4978	10562260	NM_027898	52857	GRAM domain containing 1A	Gramd1a	1.07	1.508	0.174045	0.427013
4979	10481304	NM_008114	14582	growth factor independent 1B	Gfi1b	1.07	1.655	0.140732	0.379507
4980	10466274	ENSMUST00000087857	257938	olfactory receptor 1419	Olfr1419	1.07	1.205	0.266338	0.541183
4981	10583676	NM_021531	59035	coactivator-associated arginin	Carm1	1.07	1.123	0.297553	0.573709
4982	10503401	NM_028264	72519	transmembrane protein 55A	Tmem55a	1.07	1.344	0.219715	0.488604
4983	10459138	NM_201353	240332	solute carrier family 6 (neuro	Slc6a7	1.07	1.068	0.319785	0.596635
4984	10511789	NM_172987	269513	Na+/K+ transporting ATPase int	Nkain3	1.07	1.06	0.32335	0.599886
4985	10515930	BC076608	433752	expressed sequence AA415398	AA415398	1.07	1.615	0.149184	0.391598
4986	10532956	NM_013879	29867	calcium binding protein 1	Cabp1	1.07	0.699	0.506221	0.74808
4987	10359375	XM_885170	620246	G protein-coupled receptor 52	Gpr52	1.07	0.982	0.358008	0.630288
4988	10461191	NM_016813	53319	nuclear RNA export factor 1 ho	Nxf1	1.07	1.135	0.292624	0.568731
4989	10502076					1.07	0.56	0.592316	0.807145
4990	10571321	NM_177741	244416	protein phosphatase 1, regulat	Ppp1r3b	1.07	1.754	0.121702	0.348347
4991	10583759	BC120702	67119	RIKEN cDNA 2510048L02 gene	2510048L02Rik	1.07	0.817	0.439888	0.699113
4992	10478692	NM_130451	170441	solute carrier family 2 (facil	Slc2a10	1.069	1.283	0.239032	0.511774
4993	10596769	NM_148930	83486	RNA binding motif protein 5	Rbm5	1.069	1.401	0.202673	0.465349
4994	10438690	NM_145480	106344	replication factor C (activato	Rfc4	1.069	0.771	0.465358	0.719001
4995	10388716	ENSMUST00000092883	791303	predicted gene,	ENSMUSG00000069804	1.069	1.119	0.299137	0.575152

				ENSMUSG0000006					
4996	10381474	NM_025404	80981	ADP-ribosylation factor-like 4	Arl4d	1.069	1.065	0.321078	0.598048
4997	10491945	NM_016858	19338	RAB33B, member of RAS oncogene	Rab33b	1.069	0.785	0.457361	0.713005
4998	10535213	NM_172277	231834	sorting nexin 8	Snx8	1.069	0.722	0.492791	0.738715
4999	10541246	NM_008359	16172	interleukin 17 receptor A	Il17ra	1.069	1.18	0.275591	0.550454
5000	10464825	NM_016892	12460	copper chaperone for superoxid	Ccs	1.069	0.732	0.487291	0.734951
5001	10524325	ENSMUST00000100889	100038366	predicted gene, ENSMUSG0000007	ENSMUSG00000072730	1.069	1.337	0.221973	0.49161
5002	10346533	NM_022988	65102	Ngg1 interacting factor 3-like	Nif3l1	1.069	0.776	0.462404	0.716899
5003	10517664					1.069	1.016	0.342416	0.616776
5004	10601192	NM_001081008	270627	TAF1 RNA polymerase II, TATA b	Taf1	1.069	0.87	0.412497	0.676163
5005	10538975	ENSMUST00000101310	381785	gene model 1070, (NCBI)	Gm1070	1.069	1.523	0.170255	0.421869
5006	10461709	XR_033950	667078	predicted gene, EG667078	EG667078	1.069	0.343	0.741685	0.88982
5007	10500957	ENSMUST00000098762	78635	RIKEN cDNA 1700095B22 gene	1700095B22Rik	1.069	1.077	0.316255	0.593179
5008	10443561	BC024691	74157	RIKEN cDNA 1300018I05 gene	1300018I05Rik	1.069	0.701	0.505428	0.747535
5009	10599562	AB073967	75404	RIKEN cDNA 1100001E04 gene	1100001E04Rik	1.069	1.095	0.308832	0.585384
5010	10404895	ENSMUST00000038032	76000	RIKEN cDNA 5033430I15 gene	5033430I15Rik	1.069	0.267	0.796806	0.917479
5011	10567591					1.069	1.321	0.226891	0.497571
5012	10466288	NM_146678	258673	olfactory receptor 1428	Olfr1428	1.069	1.531	0.168273	0.419719
5013	10354085	NM_019570	56210	REV1 homolog (S. cerevisiae)	Rev1	1.069	1.112	0.301843	0.577905
5014	10377689	NM_019749	56486	gamma-aminobutyric acid recept	Gabarap	1.069	0.956	0.370086	0.640667
5015	10492757	NM_016784	53317	pleiotropic regulator 1, PRL1	Plrg1	1.069	0.561	0.591599	0.806879
5016	10549633	AK006430	58804	CDC42 effector protein (Rho GT	Cdc42ep5	1.069	0.876	0.409405	0.673759
5017	10354555	NM_133728	70396	asparagine synthetase domain c	Asnsd1	1.069	0.822	0.437286	0.696704
5018	10477583	NM_023130	19383	hnRNP-associated with lethal y	Raly	1.069	0.868	0.413237	0.676799
5019	10384145	BC028539	77605	H2A histone family, member V	H2afv	1.069	1.378	0.2093	0.474426
5020	10391811	BC057614	70218	RIKEN cDNA 3000004C01 gene	3000004C01Rik	1.069	1.471	0.183496	0.440641
5021	10542270					1.068	1.313	0.229299	0.500317
5022	10381311	NM_175638	69847	WNK lysine deficient protein k	Wnk4	1.068	1.192	0.270842	0.545372
5023	10425808	NM_009775	12257	translocator protein	Tspo	1.068	0.946	0.374607	0.644557
5024	10566630	ENSMUST00000060348	76679	RIKEN cDNA 5330417H12 gene	5330417H12Rik	1.068	1.08	0.31497	0.591924
5025	10542378	NM_019426	54343	activating transcription facto	Atf7ip	1.068	0.692	0.510782	0.751982
5026	10584977	NM_027498	70661	cDNA sequence BC033915	BC033915	1.068	1.318	0.227777	0.498719
5027	10475567	NM_175034	317750	solute carrier family 24, memb	Slc24a5	1.068	1.537	0.166864	0.417832
5028	10430186	NM_175391	108956	apolipoprotein L 7c	Apol7c	1.068	0.724	0.492025	0.738272
5029	10384539	NM_018861	55963	solute carrier family 1 (gluta	Slc1a4	1.068	1.136	0.292404	0.568618
5030	10574153					1.068	1.141	0.290469	0.566681
5031	10575763	NM_001081151	209239	giant axonal neuropathy	Gan	1.068	0.437	0.674918	0.855557
5032	10454414	NM_181414	225326	phosphoinositide-3-kinase, cla	Pik3c3	1.068	1.13	0.294731	0.570991
5033	10395365	NM_011783	23795	anterior gradient 2 (Xenopus l	Agr2	1.068	0.822	0.437554	0.696831
5034	10493658					1.068	0.701	0.505109	0.747176
5035	10583610	NM_010561	16201	interleukin enhancer binding f	Ilf3	1.068	0.857	0.41923	0.681547
5036	10390974	NM_027563	16672	keratin 34	Krt34	1.068	1.343	0.220038	0.488911
5037	10595324	NM_010482	15551	5-hydroxytryptamine (serotonin	Htr1b	1.068	0.416	0.689348	0.863636
5038	10420616	NM_011892	24053	sarcoglycan, gamma (dystrophin	Sgcg	1.068	0.932	0.3817	0.651394
5039	10525726	BC046909	72650	RIKEN cDNA 2810006K23 gene	2810006K23Rik	1.068	0.725	0.491537	0.738038
5040	10423577	NM_026002	67154	Metadherin	Mtdh	1.068	0.688	0.512749	0.753201
5041	10589462	U08819	17758	microtubule-associated protein	Mtap4	1.068	0.99	0.35427	0.626867
5042	10488291	NM_015754	26450	retinoblastoma binding protein	Rbbp9	1.068	0.605	0.563651	0.790247
5043	10413152	ENSMUST00000075639	76633	RIKEN cDNA 1700112E06 gene	1700112E06Rik	1.068	0.869	0.41271	0.676213
5044	10516695	NM_199305	230770	transmembrane protein 39b	Tmem39b	1.068	0.949	0.373309	0.643602
5045	10606592	XR_032090	245600	similar to transforming acidic	LOC245600	1.068	1.311	0.229917	0.500912

5046	10391610					1.068	0.897	0.398865	0.665058
5047	10442250					1.068	0.041	0.968177	0.987184
5048	10433027	NM_018787	54615	neuropeptide FF-amide peptide	Npff	1.068	1.507	0.174356	0.427379
5049	10424667	NM_198607	223626	RIKEN cDNA 4930572J05 gene	4930572J05Rik	1.068	1.16	0.283098	0.55841
5050	10349378	AK140652	637749	hypothetical protein LOC637749	LOC637749	1.067	1.628	0.146218	0.388006
5051	10407742	NM_033268	11472	actinin alpha 2	Actn2	1.067	1.348	0.218389	0.486434
5052	10378909	XR_034867	100048535	similar to ribosomal protein L	LOC100048535	1.067	1.13	0.294614	0.570921
5053	10596271	ENSMUST00000060084	235567	DnaJ (Hsp40) homolog, subfamil	Dnajc13	1.067	0.316	0.76115	0.900379
5054	10432511	NM_012025	26934	Rac GTPase-activating protein	Racgap1	1.067	0.496	0.634376	0.833748
5055	10580885	NM_009974	13000	casein kinase 2, alpha prime p	Csnk2a2	1.067	0.863	0.416111	0.679215
5056	10557148	NM_021608	59288	dynactin 5	Dctn5	1.067	0.945	0.375062	0.645055
5057	10383833	NM_177616	216516	RIKEN cDNA 4930562D19 gene	4930562D19Rik	1.067	0.928	0.383525	0.652869
5058	10432939	NM_144942	246277	cysteine sulfinic acid decarbo	Csad	1.067	1.601	0.152087	0.395831
5059	10426180	NM_026813	71474	SAPS domain family, member 2	Saps2	1.067	0.752	0.47569	0.727129
5060	10519555	NM_011075	18669	ATP-binding cassette, sub-fami	Abcb1b	1.067	-0.137	0.894551	0.958419
5061	10566155					1.067	1.259	0.247273	0.520646
5062	10435212	NM_176840	106326	oxysterol binding protein-like	Osbpl11	1.067	1.125	0.296597	0.57323
5063	10481023	NM_153125	227648	SEC16 homolog A (S. cerevisiae	Sec16a	1.067	0.942	0.376553	0.646774
5064	10562731	AK131849	638411	predicted gene, EG638411	EG638411	1.067	1.589	0.154775	0.400004
5065	10495193	NM_008417	16490	potassium voltage-gated channe	Kcna2	1.067	1.267	0.244369	0.517487
5066	10436363	ENSMUST00000099667	78749	RIKEN cDNA 4631422O05 gene	4631422O05Rik	1.067	0.618	0.555439	0.784149
5067	10490169	ENSMUST00000069669	77310	RIKEN cDNA C030010B13 gene	C030010B13Rik	1.067	0.362	0.727462	0.881863
5068	10409857	NM_178098	214639	RIKEN cDNA 4930486L24 gene	4930486L24Rik	1.067	1.66	0.139629	0.37797
5069	10579049	AK129029	378466	predicted gene, ENSMUSG0000005	ENSMUSG00000057924	1.067	0.194	0.851748	0.940193
5070	10592988	NM_145400	140630	ubiquitination factor E4A, UFD	Ube4a	1.067	0.826	0.435464	0.695585
5071	10403919	NM_016684	22758	zinc finger and SCAN domain co	Zscan12	1.067	0.741	0.482206	0.730954
5072	10488646	NM_001037752	433490	predicted gene, OTTMUSG0000001	OTTMUSG00000015859	1.067	1.358	0.215451	0.482533
5073	10571005	ENSMUST00000059474	670853	RIKEN cDNA D830025C05 gene	D830025C05Rik	1.067	0.901	0.396688	0.664034
5074	10557009	NM_007908	13631	eukaryotic elongation factor-2	Eef2k	1.067	0.553	0.597154	0.810309
5075	10497222	NM_133218	170753	zinc finger protein 704	Zfp704	1.067	0.931	0.382087	0.651596
5076	10369738	NM_019812	93759	sirtuin 1 (silent mating type	Sirt1	1.067	0.583	0.577358	0.797771
5077	10354704	NM_031179	81898	splicing factor 3b, subunit 1	Sf3b1	1.067	1.305	0.232105	0.502819
5078	10469954	NM_177344	227615	RIKEN cDNA C730025P13 gene	C730025P13Rik	1.067	0.453	0.66399	0.850267
5079	10504751					1.067	0.583	0.577945	0.798124
5080	10406287	NM_001081352	218343	cDNA sequence AK129128	AK129128	1.067	0.907	0.393735	0.661649
5081	10398211	NM_001044380	214305	hedgehog interacting protein-l	Hhipl1	1.067	1.036	0.333548	0.609432
5082	10379944	NM_011536	21387	T-box 4	Tbx4	1.067	1.385	0.207379	0.471841
5083	10421188	ENSMUST00000050569	71843	R3H domain and coiled-coil con	R3hcc1	1.067	0.415	0.690453	0.864251
5084	10409396	NM_011307	20184	ubiquitin interaction motif co	Uimc1	1.067	0.7	0.506073	0.747966
5085	10434366	NM_007889	13544	dishevelled 3, dsh homolog (Dr	Dvl3	1.067	0.853	0.420836	0.683211
5086	10568714	NM_001081117	17345	antigen identified by monoclon	Mki67	1.067	1.075	0.31683	0.594045
5087	10483626	NM_010054	13392	distal-less homeobox 2	Dlx2	1.067	1.107	0.303672	0.579864
5088	10522655	XM_916109	320827	RIKEN cDNA C530008M17 gene	C530008M17Rik	1.067	0.269	0.795317	0.916955
5089	10535103	NM_174850	231830	MICAL-like 2	Micall2	1.066	1.084	0.313098	0.589668
5090	10551421	ENSMUST00000108336	22718	zinc finger protein 60	Zfp60	1.066	0.238	0.818698	0.92793
5091	10480734	NM_008963	19215	prostaglandin D2 synthase (bra	Ptgds	1.066	1.305	0.231948	0.502664
5092	10431339	ENSMUST00000109353	328580	tubulin, gamma complex associa	Tubgcp6	1.066	0.618	0.555746	0.784373
5093	10398695	NM_021516	17169	MAP/microtubule affinity-regul	Mark3	1.066	1.2	0.268146	0.542786
5094	10565819	NM_175316	101488	solute carrier organic anion t	Slco2b1	1.066	1.204	0.266713	0.541363
5095	10460085	NM_023149	66054	CNDP dipeptidase 2 (metallopep	Cndp2	1.066	0.767	0.467228	0.72007
5096	10349376					1.066	0.582	0.578357	0.798316

5097	10356457	NM_008299	15504	DnaJ (Hsp40) homolog, subfamil	Dnajb3	1.066	0.575	0.582729	0.800924
5098	10396068	NM_001081406	69706	peptidylprolyl isomerase (cycl	Ppil5	1.066	0.817	0.440047	0.699124
5099	10431935	NM_178114	105827	adhesion molecule with Ig like	Amigo2	1.066	0.337	0.745853	0.891987
5100	10578768					1.066	0.625	0.551144	0.781221
5101	10373093	NM_030714	80904	deltex 3 homolog (Drosophila)	Dtx3	1.066	1.279	0.240626	0.513659
5102	10467730	NM_198108	226123	cDNA sequence BC023055	BC023055	1.066	0.568	0.587164	0.80408
5103	10384797	NM_181577	216613	coiled-coil domain containing	Ccdc85a	1.066	0.744	0.480163	0.729941
5104	10545339	NM_025430	66223	mitochondrial ribosomal protei	Mrpl35	1.066	0.241	0.816306	0.92666
5105	10519105	NM_011385	20481	ski sarcoma viral oncogene hom	Ski	1.066	0.998	0.350566	0.624042
5106	10571221	NM_001112729	234138	cDNA sequence BC019943	BC019943	1.066	-0.131	0.899144	0.960129
5107	10536425					1.066	1.132	0.293736	0.569741
5108	10568638	NM_009479	22276	uroporphyrinogen III synthase	Uros	1.066	0.469	0.652661	0.844494
5109	10468519	NM_172429	76479	survival motor neuron domain c	Smndc1	1.066	0.156	0.880299	0.952471
5110	10477595	NM_015770	50518	nonagouti	a	1.066	1.44	0.191768	0.451028
5111	10409282	NM_013846	26564	receptor tyrosine kinase-like	Ror2	1.066	1.545	0.165009	0.415127
5112	10390175	NM_033217	18053	nerve growth factor receptor (	Ngfr	1.066	1.149	0.287261	0.562985
5113	10433691	NM_010946	18203	N-terminal Asn amidase	Ntan1	1.066	0.65	0.53594	0.769309
5114	10354141	NM_001029878	381338	LON peptidase N-terminal domai	Lonrf2	1.066	0.449	0.66649	0.851355
5115	10525419	NM_011027	18439	purinergic receptor P2X, ligan	P2rx7	1.066	1.547	0.164453	0.414282
5116	10369927					1.066	1.311	0.23014	0.501074
5117	10397179	NM_028821	105000	dynein, axonemal, light chain	Dnalc1	1.066	0.747	0.478717	0.729103
5118	10577446	NM_139222	246082	defensin beta 15	Defb15	1.066	0.796	0.45156	0.708606
5119	10496204	NM_173762	229841	centromere protein E	Cenpe	1.066	1.092	0.310009	0.586741
5120	10563112	NR_001277	27208	small nucleolar RNA, C/D box 3	Snord33	1.066	0.417	0.688606	0.863114
5121	10367173	NM_008600	17339	major intrinsic protein of eye	Mip	1.066	0.894	0.399974	0.665979
5122	10521537	NM_001081106	231162	cytokine like 1	Cytl1	1.066	1.179	0.275989	0.550828
5123	10400572	NM_025707	66689	kelch-like 28 (Drosophila)	Klhl28	1.066	0.908	0.39337	0.661285
5124	10406742	BC016527	67463	RIKEN cDNA 1200014M14 gene	1200014M14Rik	1.066	1.145	0.288738	0.564814
5125	10483584	NM_145524	228019	methyltransferase like 8	Mettl8	1.066	0.688	0.513185	0.753594
5126	10445855	NM_177052	319991	kinesin family member 6	Kif6	1.066	1.514	0.172621	0.424951
5127	10540911	NM_199033	381802	tRNA splicing endonuclease 2 h	Tsen2	1.066	0.713	0.498541	0.742429
5128	10421184	ENSMUST00000084187	100038740	predicted gene, ENSMUSG0000007	ENSMUSG00000071316	1.066	0.861	0.41686	0.679627
5129	10500362	NM_027241	69870	polymerase (RNA) III (DNA dire	Polr3gl	1.066	1.114	0.301004	0.577272
5130	10489831	NM_001109906	20853	staufen (RNA binding protein)	Stau1	1.066	0.861	0.416756	0.679627
5131	10473570	NM_001011519	258220	olfactory receptor 1148	Olfr1148	1.065	0.793	0.453026	0.709661
5132	10377550	NM_011640	22059	transformation related protein	Trp53	1.065	0.871	0.41185	0.67572
5133	10499552	NM_007910	13639	ephrin A4	Efna4	1.065	0.74	0.482926	0.731557
5134	10603180	XM_913285	637566	predicted gene, EG637566	EG637566	1.065	1.482	0.180773	0.436709
5135	10457536	ENSMUST00000080906	225187	ankyrin repeat domain 29	Ankrd29	1.065	1.271	0.243299	0.516291
5136	10534718	NM_011639	22051	thyroid hormone receptor inter	Trip6	1.065	0.582	0.578232	0.79826
5137	10427280	NM_010462	209448	homeo box C10	Hoxc10	1.065	0.493	0.636471	0.834887
5138	10508829	NM_016693	53608	mitogen-activated protein kina	Map3k6	1.065	1.067	0.320544	0.597513
5139	10399021	NM_153776	69195	transmembrane protein 121	Tmem121	1.065	0.784	0.457932	0.713313
5140	10588538	BC049769	74267	IQ motif containing F1	Iqcf1	1.065	0.51	0.625211	0.829015
5141	10466282	NM_146809	258805	olfactory receptor 1426	Olfr1426	1.065	0.749	0.477705	0.728391
5142	10493876	NM_011474	20762	small proline-rich protein 2H	Sprr2h	1.065	1.232	0.256431	0.530714
5143	10461408	NM_144538	74760	RAB3A interacting protein (rab	Rab3il1	1.065	1.866	0.103101	0.315343
5144	10591967	NM_023277	83964	junction adhesion molecule 3	Jam3	1.065	0.597	0.568799	0.793578
5145	10478192	AK016829	71081	RIKEN cDNA 4933416E03 gene	4933416E03Rik	1.065	0.835	0.430572	0.691322
5146	10517883	NM_025383	66147	NECAP endocytosis associated 2	Necap2	1.065	0.809	0.444192	0.702635
5147	10384365					1.065	1.064	0.321785	0.598601
5148	10512947					1.065	0.564	0.589873	0.805977
5149	10443589	NM_148926	21769	zinc finger, AN1-type domain 3	Zfand3	1.065	0.482	0.643825	0.838809

5150	10491607	ENSMUST00000057272	229227	RIKEN cDNA 4932438A13 gene	4932438A13Rik	1.065	0.549	0.599682	0.812038
5151	10401586	NM_175198	73422	prospero homeobox 2	Prox2	1.065	0.98	0.358596	0.630638
5152	10449225	NM_011933	26378	2-4-dienoyl-Coenzyme A reducta	Decr2	1.065	1.003	0.348346	0.622132
5153	10521222	NM_001102444	11518	adducin 1 (alpha)	Add1	1.065	0.546	0.601313	0.812925
5154	10456184	NM_133237	494504	adenomatosis polyposis coli do	Apcdd1	1.065	1.315	0.228925	0.499975
5155	10430297	NM_013645	19293	parvalbumin	Pvalb	1.065	0.412	0.69255	0.865136
5156	10534854	NM_030037	68929	motile sperm domain containing	Mospd3	1.065	0.712	0.498676	0.742429
5157	10380956	NM_001007461	450219	gasdermin A3	Gsdma3	1.065	1.601	0.152042	0.395822
5158	10401160	BC066067	268567	RIKEN cDNA 6330442E10 gene	6330442E10Rik	1.065	0.474	0.649245	0.842415
5159	10404061	NM_175664	319178	histone cluster 1, H2bb	Hist1h2bb	1.065	0.449	0.666945	0.851389
5160	10390963	NM_027983	71888	keratin 33A	Krt33a	1.065	0.5	0.63219	0.832782
5161	10348301	NM_009118	20215	retinal S-antigen	Sag	1.065	1.489	0.178798	0.433892
5162	10517274	NM_029100	74777	selenoprotein N, 1	Sepn1	1.065	0.768	0.466982	0.719977
5163	10522661	ENSMUST00000048811	320827	RIKEN cDNA C530008M17 gene	C530008M17Rik	1.065	0.518	0.620053	0.825229
5164	10595871	NM_022319	64085	calsyntenin 2	Clstn2	1.065	1.125	0.296619	0.57323
5165	10436841	NM_008349	16155	interleukin 10 receptor, beta	Il10rb	1.065	0.484	0.642486	0.838098
5166	10466087	NM_134142	68539	transmembrane protein 109	Tmem109	1.065	0.943	0.376425	0.64661
5167	10603651	XM_001474571	100045823	hypothetical protein LOC100045	LOC100045823	1.065	0.604	0.564561	0.790721
5168	10500406	NM_018767	54215	CD160 antigen	Cd160	1.065	0.494	0.636085	0.834743
5169	10350896	NM_007495	11899	astrotactin 1	Astn1	1.065	0.464	0.656132	0.846043
5170	10398874	NM_013929	30954	SIVA1, apoptosis-inducing fact	Siva1	1.064	0.285	0.783353	0.911971
5171	10463515	NM_176785	20170	Hermansky-Pudlak syndrome 6	Hps6	1.064	0.751	0.47641	0.72757
5172	10397359	NM_016767	53314	basic leucine zipper transcrip	Batf	1.064	1.551	0.16367	0.412879
5173	10552938	NM_198190	78405	neurotrophin 5	Ntf5	1.064	0.909	0.392913	0.660814
5174	10575021	NM_011764	22751	zinc finger protein 90	Zfp90	1.064	1.084	0.313135	0.589668
5175	10478897	NM_011201	19246	protein tyrosine phosphatase,	Ptpn1	1.064	0.395	0.704491	0.870894
5176	10383575	NM_029878	108903	tubulin-specific chaperone d	Tbcd	1.064	1.325	0.225575	0.495847
5177	10500117	BC092540	229588	gene model 128, (NCBI)	Gm128	1.064	1.257	0.248044	0.521388
5178	10491060	XR_004805	675593	similar to spindlin	LOC675593	1.064	0.532	0.610985	0.819348
5179	10479945	ENSMUST00000056627	72248	RIKEN cDNA 1700014B07 gene	1700014B07Rik	1.064	0.67	0.523932	0.760561
5180	10515714	ENSMUST00000075406	230676	cDNA sequence BC059842	BC059842	1.064	1.42	0.197224	0.457905
5181	10435832	NM_001029889	207806	gene model 608, (NCBI)	Gm608	1.064	1.266	0.244961	0.518204
5182	10416126	NM_010095	13592	early B-cell factor 2	Ebf2	1.064	1.299	0.233841	0.505143
5183	10356461	BC057309	381280	RIKEN cDNA 6430706D22 gene	6430706D22Rik	1.064	1.007	0.346384	0.62041
5184	10476952	NM_172117	12497	ectonucleoside triphosphate di	Entpd6	1.064	1.205	0.266268	0.541183
5185	10482139	NM_026176	67466	phosducin-like	Pdcl	1.064	0.801	0.448646	0.706217
5186	10375941	NM_011694	22333	voltage-dependent anion channe	Vdac1	1.064	0.321	0.757241	0.898087
5187	10408879	NM_001033399	328232	glucose-fructose oxidoreductas	Gfod1	1.064	1.301	0.233227	0.504383
5188	10594519	NM_178933	330962	organic solute transporter bet	Ostb	1.064	1.184	0.274006	0.548672
5189	10401882	NM_175335	83602	general transcription factor I	Gtf2a1	1.064	0.931	0.382138	0.651607
5190	10544444	NM_203396	403088	experimental autoimmune prosta	Eapa2	1.064	1.094	0.30917	0.585866
5191	10593123	NM_011526	21345	transgelin	Tagln	1.064	0.27	0.79489	0.916821
5192	10463209	BC049703	66765	RIKEN cDNA 4933411K16 gene	4933411K16Rik	1.064	1.21	0.264389	0.539495
5193	10401968	NM_008079	14420	galactosylceramidase	Galc	1.064	0.563	0.590714	0.806356
5194	10574659	NM_011939	26386	heat shock transcription facto	Hsf4	1.064	1.372	0.211346	0.476813
5195	10554081	NM_025905	67009	tetratricopeptide repeat domai	Ttc23	1.064	0.231	0.823458	0.929428
5196	10500982	NM_001033780	433638	RIKEN cDNA I830077J02 gene	I830077J02Rik	1.064	1.338	0.221556	0.491045
5197	10451736	NM_028162	72238	TBC1 domain family, member 5	Tbc1d5	1.064	0.92	0.387394	0.656334
5198	10365723	XM_001476977	100041769	similar to protein translation	LOC100041769	1.064	0.902	0.396148	0.663738
5199	10599792	NM_133251	170828	vestigial like 1 homolog (Dros	Vgll1	1.064	1.402	0.202447	0.465275
5200	10542745	NM_026218	67529	FGFR1 oncogene partner 2	Fgfr1op2	1.064	0.885	0.404825	0.669594
5201	10389421	NM_027421	70422	integrator complex subunit 2	Ints2	1.064	1.022	0.33972	0.615145
5202	10555953	NM_019502	14356	fractured callus expressed tra	Fxc1	1.064	0.541	0.605044	0.815765

5202	10553955	NM_019502	14356	fractured callus expressed tra	Fxc1	1.064	0.541	0.605044	0.815765
5203	10486324	AK016792	100036539	predicted gene, OTTMUSG0000001	OTTMUSG00000015282	1.064	1.241	0.253354	0.527654
5204	10477004	XR_030619	100044416	similar to alpha-tubulin isoty	LOC100044416	1.064	1.099	0.30705	0.583646
5205	10498978	NM_023624	79235	lecithin-retinol acyltransfera	Lrat	1.064	0.24	0.81708	0.92719
5206	10413697	NM_001081251	66923	polybromo 1	Pbrm1	1.064	1.191	0.271264	0.545988
5207	10442363	NM_020487	57256	protease, serine, 21	Prss21	1.064	1.118	0.299271	0.575358
5208	10526675	NM_023910	78829	TSC22 domain family 4	Tsc22d4	1.064	1.025	0.338661	0.614222
5209	10376490	NM_139298	216795	wingless-type MMTV integration	Wnt9a	1.064	0.711	0.499558	0.742751
5210	10562304					1.064	1.006	0.346892	0.621109
5211	10599537	NM_011398	20523	solute carrier family 25 (mito	Slc25a14	1.064	0.688	0.513002	0.753467
5212	10581151	NM_019662	56437	Ras-related associated with di	Rrad	1.064	1.476	0.182301	0.438828
5213	10413951	NM_153800	239027	Rho GTPase activating protein	Arhgap22	1.064	1.092	0.310059	0.586761
5214	10394488	NM_010770	17182	matrilin 3	Matn3	1.063	0.783	0.458595	0.713672
5215	10511803	ENSMUST00000029915	77032	RIKEN cDNA 2610029I01 gene	2610029I01Rik	1.063	0.158	0.878432	0.95179
5216	10446402	NM_146081	70351	protein phosphatase 4, regulat	Ppp4r1	1.063	1.718	0.128146	0.358993
5217	10563893	ENSMUST00000098404	100038650	predicted gene, ENSMUSG0000007	ENSMUSG00000074087	1.063	0.072	0.944231	0.977948
5218	10557742	NM_172748	233902	F-box and leucine-rich repeat	Fbxl19	1.063	1.473	0.18299	0.439824
5219	10587558	BC043710	320615	dopey family member 1	Dopey1	1.063	0.663	0.528193	0.763579
5220	10573578	BC089623	414077	cDNA sequence BC056474	BC056474	1.063	0.079	0.938988	0.976218
5221	10417725					1.063	0.049	0.961937	0.985362
5222	10477237	BC020535	228788	cDNA sequence BC020535	BC020535	1.063	0.807	0.445422	0.703573
5223	10352562	NM_026367	67769	G patch domain containing 2	Gpatch2	1.063	0.383	0.71255	0.874059
5224	10494092	NM_172683	229584	pogo transposable element with	Pogz	1.063	0.919	0.387564	0.656413
5225	10401443	BC062132	217705	RIKEN cDNA 9830169C18 gene	9830169C18Rik	1.063	1.544	0.165313	0.415472
5226	10549420	NM_198967	387314	transmembrane and tetratricope	Tmtc1	1.063	0.509	0.625856	0.829508
5227	10385699	NM_025346	66089	required for meiotic nuclear d	Rmnd5b	1.063	0.822	0.437617	0.696866
5228	10361682	NM_026141	67418	peptidylprolyl isomerase (cycl	Ppil4	1.063	1.048	0.328667	0.605027
5229	10572743	NM_146539	258532	olfactory receptor 373	Olfr373	1.063	0.875	0.409689	0.674122
5230	10581395	NM_009195	20498	solute carrier family 12, memb	Slc12a4	1.063	1.016	0.34243	0.616776
5231	10564795	NM_175640	103968	perilipin	Plin	1.063	1.37	0.211842	0.477389
5232	10408975	NM_010617	16553	kinesin family member 13A	Kif13a	1.063	0.567	0.588107	0.804902
5233	10402512					1.063	1.659	0.139856	0.378196
5234	10380739	NM_001081434	71240	oxysterol binding protein-like	Osbpl7	1.063	1.102	0.30594	0.582459
5235	10574789	NM_001081241	75687	RIKEN cDNA 2310066E14 gene	2310066E14Rik	1.063	1.003	0.34823	0.622132
5236	10544596	NM_023056	65963	transmembrane protein 176B	Tmem176b	1.063	0.562	0.590855	0.806403
5237	10547795	NM_007881	13498	atrophin 1	Atn1	1.063	0.774	0.46341	0.717662
5238	10409547	ENSMUST00000091588	78111	RIKEN cDNA 4930451E10 gene	4930451E10Rik	1.063	0.807	0.445483	0.703614
5239	10478890	NM_009883	12608	CCAAT/enhancer binding protein	Cebpb	1.063	0.791	0.45436	0.710796
5240	10367349	NM_001114097	68094	SWI/SNF related, matrix associ	Smarcc2	1.063	0.781	0.459883	0.714719
5241	10426042	NM_172611	223752	GRAM domain containing 4	Gramd4	1.063	0.899	0.397507	0.664302
5242	10547789	NM_013535	14790	gene rich cluster, C10 gene	Grcc10	1.063	0.503	0.629794	0.831325
5243	10580139	NM_172503	212168	zinc finger, SWIM domain conta	Zswim4	1.063	0.773	0.464029	0.717953
5244	10537909					1.063	0.788	0.455987	0.712382
5245	10601091	NM_018789	54601	forkhead box O4	Foxo4	1.063	1.273	0.242635	0.515498
5246	10356512	ENSMUST00000113094	74918	IQ motif containing with AAA d	Iqca	1.063	1.287	0.237878	0.510297
5247	10402783	NM_001033476	382643	AHNAK nucleoprotein 2	Ahnak2	1.063	0.566	0.588685	0.805172
5248	10603109	NM_011081	18700	phosphatidylinositol glycan an	Piga	1.063	0.801	0.448522	0.706139
5249	10409790	NM_177711	238663	RIKEN cDNA 4932411G14 gene	4932411G14Rik	1.063	1.503	0.175224	0.428429
5250	10407570	NM_144516	66505	zinc finger, MYND domain conta	Zmynd11	1.063	1.017	0.341985	0.616342
5251	10379436	NM_139228	246104	rhomboid, veinlet-like 3 (Dros	Rhbdl3	1.063	0.965	0.365772	0.636847
5252	10562685					1.063	0.37	0.721714	0.878906
5253	10491279	NM_008857	18759	protein kinase C, iota	Prkci	1.063	0.586	0.575547	0.797076

5254	10468789	NM_001033222	107368	PDZ domain containing 8	Pdzd8	1.063	0.477	0.647606	0.841402
5255	10597900	NM_173364	235682	zinc finger protein 445	Zfp445	1.063	1.179	0.276013	0.550828
5256	10537353	NM_153600	264134	tetratricopeptide repeat domai	Ttc26	1.063	0.506	0.628038	0.830847
5257	10354883	NM_175370	108812	amyotrophic lateral sclerosis	Als2cr12	1.063	0.851	0.422284	0.684511
5258	10592355	NM_172454	208098	pannexin 3	Panx3	1.062	0.433	0.677386	0.856571
5259	10447569	NM_001111017	321007	serine active site containing	Serac1	1.062	0.568	0.587545	0.804342
5260	10606263	NM_009530	22589	alpha thalassemia/mental retar	Atrx	1.062	1.164	0.281647	0.556928
5261	10561478	NM_001081115	233038	RIKEN cDNA 1190020J12 gene	1190020J12Rik	1.062	1.19	0.271721	0.546284
5262	10603598	NM_011285	19893	retinitis pigmentosa GTPase re	Rpgr	1.062	-0.026	0.979615	0.991919
5263	10473272	NM_026934	69082	zinc finger CCCH-type containi	Zc3h15	1.062	1.126	0.296165	0.572668
5264	10388971	NM_144826	216987	UTP6, small subunit (SSU) proc	Utp6	1.062	0.503	0.629676	0.831325
5265	10478959	NM_008561	17201	melanocortin 3 receptor	Mc3r	1.062	0.814	0.441731	0.70062
5266	10501485	NM_178891	99890	protein arginine N-methyltrans	Prmt6	1.062	0.837	0.429488	0.690525
5267	10490972	NM_001081281	381485	tripartite motif-containing 55	Trim55	1.062	1.488	0.179182	0.434575
5268	10345904	BC006931	98404	expressed sequence AI597479	AI597479	1.062	1.244	0.252427	0.526583
5269	10411169	ENSMUST00000059598	328309	predicted gene, ENSMUSG0000004	ENSMUSG00000042857	1.062	0.455	0.662325	0.849718
5270	10370127	NM_008787	18541	pericentrin (kendrin)	Pcnt	1.062	1.017	0.342072	0.61636
5271	10489261	NM_182840	280635	elastin microfibril interfacer	Emilin3	1.062	1.134	0.292992	0.569029
5272	10483521	NM_177244	320720	FAST kinase domains 1	Fastkd1	1.062	0.42	0.686537	0.861594
5273	10599296	NM_008955	19202	reproductive homeobox 6	Rhox6	1.062	0.833	0.431464	0.692018
5274	10569485	NM_175649	244237	tumor necrosis factor receptor	Tnfrsf26	1.062	1.605	0.151289	0.395197
5275	10447885	NM_153151	224530	acetyl-Coenzyme A acetyltransf	Acat3	1.062	1.102	0.306042	0.582506
5276	10368575	NM_011509	100041294	suppressor of Ty 4 homolog 2 (	Supt4h2	1.062	0.466	0.65511	0.845541
5277	10577999	NM_153135	210801	unc-5 homolog D (C. elegans)	Unc5d	1.062	1.265	0.245084	0.518209
5278	10533549	NM_021505	59008	anaphase-promoting complex sub	Anapc5	1.062	0.963	0.366696	0.637617
5279	10436802					1.062	0.449	0.666923	0.851389
5280	10373873	NM_026175	67465	splicing factor 3a, subunit 1	Sf3a1	1.062	0.317	0.759876	0.899364
5281	10560043	NM_026046	67230	zinc finger protein 329	Zfp329	1.062	1.243	0.252695	0.526766
5282	10371080	ENSMUST00000056086	74894	RIKEN cDNA 4930442H23 gene	4930442H23Rik	1.062	0.609	0.561327	0.788461
5283	10415955					1.062	1.095	0.308568	0.585197
5284	10474984	NM_133851	108907	nucleolar and spindle associat	Nusap1	1.062	0.423	0.684758	0.860588
5285	10603698	ENSMUST00000050846	260300	gene model 1549, (NCBI)	Gm1549	1.062	1.205	0.26643	0.541205
5286	10487252	NM_207669	14391	GA repeat binding protein, bet	Gabpb1	1.062	1.074	0.317503	0.594727
5287	10481920	NM_080554	66998	proteasome (prosome, macropain	Psmd5	1.062	0.084	0.935028	0.974191
5288	10462504	NM_010799	17330	multiple inositol polyphosphat	Minpp1	1.062	0.591	0.572349	0.796254
5289	10389451	NM_001080931	327987	mediator complex subunit 13	Med13	1.062	1.062	0.322625	0.599294
5290	10598482	NM_011591	21855	translocase of inner mitochond	Timm17b	1.062	0.079	0.939005	0.976218
5291	10367611	ENSMUST00000019901	237250	gene model 221, (NCBI)	Gm221	1.062	1.387	0.206912	0.471397
5292	10444394	NM_017463	18515	pre B-cell leukemia transcript	Pbx2	1.061	0.755	0.473932	0.725516
5293	10596533	NM_011573	21767	testis expressed gene 264	Tex264	1.061	0.862	0.416372	0.67936
5294	10596671	ENSMUST00000066239	100038755	predicted gene, ENSMUSG0000005	ENSMUSG00000053666	1.061	0.435	0.67626	0.855911
5295	10553015	NM_009737	12036	branched chain aminotransferas	Bcat2	1.061	0.913	0.390528	0.659056
5296	10603440	NM_009515	22376	Wiskott-Aldrich syndrome homol	Was	1.061	1.459	0.186719	0.444956
5297	10579703	NM_138585	27967	calcium homeostasis endoplasmi	Cherp	1.061	0.764	0.469166	0.721405
5298	10554076	NM_175215	75099	LysM, putative peptidoglycan-b	Lysmd4	1.061	0.914	0.390334	0.658911
5299	10420811	NM_026322	110265	methionine sulfoxide reductase	Msra	1.061	0.771	0.46505	0.718788
5300	10419557	NM_001011877	497113	ribonuclease, RNase A family,	Rnase11	1.061	1.316	0.228316	0.499328
5301	10547769	NM_013545	15170	protein tyrosine phosphatase,	Ptpn6	1.061	0.987	0.355662	0.628248
5302	10385118	NM_033374	94176	dedicator of cyto-kinesis 2	Dock2	1.061	0.669	0.524384	0.760916
5303	10376832	NM_007413	11541	adenosine A2b receptor	Adora2b	1.061	0.724	0.49197	0.738272
5304	10416266	AK046652	73289	RIKEN cDNA 1700031C06 gene	1700031C06Rik	1.061	0.67	0.523603	0.76025

5305	10374578	BC024460	73873	RIKEN cDNA 4930430E16 gene	4930430E16Rik	1.061	0.396	0.703307	0.869836
5306	10486522	NM_011743	20402	zinc finger protein 106	Zfp106	1.061	1.018	0.341703	0.616255
5307	10453887	NM_022021	63955	Cdk5 and Abl enzyme substrate	Cables1	1.061	0.393	0.706027	0.871814
5308	10360720	NM_145514	226757	WD repeat domain 26	Wdr26	1.061	0.829	0.433509	0.694014
5309	10414315	BC049694	72391	cyclin-dependent kinase inhibi	Cdkn3	1.061	0.727	0.490259	0.737262
5310	10545515	ENSMUST00000114040	330355	dynein, axonemal, heavy chain	Dnahc6	1.061	0.678	0.518911	0.757293
5311	10390798	NM_133730	70810	keratin 25	Krt25	1.061	0.539	0.605958	0.81624
5312	10572989	NM_029736	76775	solute carrier family 10 (sodi	Slc10a7	1.061	0.203	0.84489	0.937
5313	10493794	NM_025393	66166	S100 calcium binding protein A	S100a14	1.061	0.887	0.403436	0.668494
5314	10607085	NM_021487	66240	potassium voltage-gated channe	Kcne1l	1.061	0.397	0.703056	0.86973
5315	10518428	NM_011929	26372	chloride channel 6	Clcn6	1.061	0.939	0.37787	0.647641
5316	10604508	ENSMUST00000060650	385354	FERM domain containing 7	Frmd7	1.061	0.995	0.351909	0.62505
5317	10560964	NM_011138	18987	POU domain, class 2, transcrip	Pou2f2	1.061	1.024	0.338857	0.614476
5318	10475019	NM_146125	228550	inositol 1,4,5-trisphosphate 3	Itpka	1.061	0.494	0.635961	0.834683
5319	10460118	NM_018821	54607	suppressor of cytokine signali	Socs6	1.061	0.245	0.813545	0.925035
5320	10373113	NM_008447	16572	kinesin family member 5A	Kif5a	1.061	1.274	0.242066	0.514861
5321	10599696	NM_172779	236790	DEAD/H (Asp-Glu-Ala-Asp/His) b	Ddx26b	1.061	0.495	0.635234	0.834289
5322	10573419	NM_008535	17095	lymphoblastomic leukemia	Lyl1	1.061	1.631	0.145748	0.38722
5323	10416653	NM_001024135	211255	kelch repeat and BTB (POZ) dom	Kbtbd7	1.061	0.1	0.922844	0.969148
5324	10545077					1.061	1.412	0.199719	0.461464
5325	10413752	NM_027088	104416	Brca1 associated protein 1	Bap1	1.061	0.594	0.570359	0.794811
5326	10587748	NM_001003911	108153	a disintegrin-like and metallo	Adamts7	1.061	1.411	0.19985	0.461578
5327	10480284	ENSMUST00000095134	74103	nebulette	Nebl	1.061	0.918	0.388364	0.65703
5328	10498415	NM_028136	72162	DEAH (Asp-Glu-Ala-His) box pol	Dhx36	1.061	0.911	0.391803	0.660136
5329	10377704	NM_007888	13543	dishevelled 2, dsh homolog (Dr	Dvl2	1.061	0.938	0.378573	0.648305
5330	10372121	NM_001033332	237500	transmembrane and tetratricope	Tmtc3	1.061	0.614	0.558191	0.786038
5331	10417070	NM_023579	70572	importin 5	Ipo5	1.061	0.579	0.58035	0.799512
5332	10460285	NM_025529	66387	nudix (nucleoside diphosphate	Nudt8	1.061	0.607	0.562717	0.789779
5333	10599837	XM_993146	279618	gene model 715, (NCBI)	Gm715	1.061	1.39	0.205977	0.470017
5334	10577528	BC048089	102032	expressed sequence AI316807	AI316807	1.061	0.498	0.633451	0.833323
5335	10346876					1.061	0.824	0.436228	0.696174
5336	10356712	NM_008440	16560	kinesin family member 1A	Kif1a	1.061	1.15	0.286797	0.562475
5337	10575548					1.06	1.285	0.238432	0.511045
5338	10591369	NM_010066	13433	DNA methyltransferase (cytosin	Dnmt1	1.06	1.018	0.341573	0.616178
5339	10605303	NM_027109	69537	deoxyribonuclease 1-like 1	Dnase1l1	1.06	0.434	0.676871	0.856377
5340	10363512	NM_009120	20224	SAR1 gene homolog A (S. cerevi	Sar1a	1.06	0.702	0.504731	0.747027
5341	10369481	NM_207000	404634	H2A histone family, member Y2	H2afy2	1.06	0.663	0.528077	0.763475
5342	10485314	NM_183106	74569	tetratricopeptide repeat domai	Ttc17	1.06	1.09	0.310639	0.587176
5343	10349174	NM_011459	20725	serine (or cysteine) peptdiase	Serpinb8	1.06	0.925	0.384825	0.65414
5344	10572870	NM_178017	70823	high mobility group box 2-like	Hmgb2l1	1.06	0.771	0.464944	0.718729
5345	10497463	NM_029706	76703	carboxypeptidase B1 (tissue)	Cpb1	1.06	0.833	0.431724	0.692222
5346	10449280	ENSMUST00000116632	383229	predicted gene, EG383229	EG383229	1.06	0.662	0.528316	0.763705
5347	10374415	NM_024459	19058	protein phosphatase 3, regulat	Ppp3r1	1.06	0.669	0.524314	0.760916
5348	10406399	AK076753	75507	POU domain class 5, transcript	Pou5f2	1.06	1.283	0.239041	0.511774
5349	10399540	NM_172574	217430	PQ loop repeat containing	Pqlc3	1.06	0.386	0.710377	0.873031
5350	10464819	NM_019869	56275	RNA binding motif protein 14	Rbm14	1.06	0.808	0.4447	0.703166
5351	10510239	ENSMUST00000104964	100038537	predicted gene, ENSMUSG0000007	ENSMUSG00000070585	1.06	1.805	0.112846	0.332847
5352	10433352	NM_026666	170644	ubinuclein 1	Ubn1	1.06	0.426	0.682435	0.859763
5353	10443438	NM_001034885	433091	patatin-like phospholipase dom	Pnpla1	1.06	1.065	0.321179	0.598048
5354	10512011	NM_013889	30046	zinc finger protein 292	Zfp292	1.06	0.857	0.418841	0.681435
5355	10455989	NM_025776	66810	RNA binding motif protein 22	Rbm22	1.06	0.529	0.612817	0.820505
5356	10511661	NM_152812	72201	OTU domain containing 6B	Otud6b	1.06	0.39	0.708014	0.872288
5357	10378154	NM_001045536	195018	zinc finger, ZZ-type with EF h	Zzef1	1.06	0.805	0.446379	0.704083
				RIKEN cDNA A030003K02					

5358	10388732	AK053376	109224	RIKEN cDNA A030003K02 gene	A030003K02Rik	1.06	0.886	0.404157	0.668818
5359	10520782	NM_172993	269639	zinc finger protein 512	Zfp512	1.06	0.333	0.748747	0.893678
5360	10598093	NM_177363	245126	RIKEN cDNA 9930022N03 gene	9930022N03Rik	1.06	1.368	0.212466	0.477963
5361	10560903	NM_182785	232973	Ly6/Plaur domain containing 4	Lypd4	1.06	1.156	0.28454	0.559679
5362	10434124	NM_009436	22115	testis-specific serine kinase	Tssk2	1.06	0.51	0.625561	0.829323
5363	10398117	NM_009747	12062	bradykinin receptor, beta 2	Bdkrb2	1.06	0.988	0.354956	0.627681
5364	10406590	NM_175455	218440	ankyrin repeat domain 34B	Ankrd34b	1.06	1.178	0.276164	0.551025
5365	10570373	NM_009361	21781	transcription factor Dp 1	Tfdp1	1.06	0.647	0.537607	0.770707
5366	10408950					1.06	0.445	0.669279	0.852817
5367	10598101	BC053388	270118	mastermind like 2 (Drosophila)	Maml2	1.06	1.086	0.312282	0.588598
5368	10408200	NM_175655	319157	histone cluster 1, H4f	Hist1h4f	1.06	0.124	0.905009	0.963132
5369	10378214					1.06	0.481	0.644591	0.839238
5370	10516658	NM_025455	66264	coiled coil domain containing	Ccdc28b	1.06	0.322	0.756282	0.897871
5371	10475245	AK006022	99260	expressed sequence AV039307	AV039307	1.06	0.488	0.640142	0.836894
5372	10508711	NM_025579	66464	TAF12 RNA polymerase II, TATA	Taf12	1.06	0.105	0.918886	0.967815
5373	10555186	NM_009519	22411	wingless-related MMTV integrat	Wnt11	1.06	1.665	0.138578	0.376638
5374	10352048	NM_012012	26909	exonuclease 1	Exo1	1.06	0.508	0.626839	0.83034
5375	10526049	NM_025450	66258	mitochondrial ribosomal protei	Mrps17	1.06	0.398	0.702078	0.869258
5376	10539156	ENSMUST00000101278	100038714	predicted gene, OTTMUSG0000002	OTTMUSG00000021199	1.06	1.19	0.27165	0.546245
5377	10384770	ENSMUST00000109511	70626	RIKEN cDNA 5730522E02 gene	5730522E02Rik	1.06	0.734	0.485963	0.734018
5378	10560880	BC037749	210155	predicted gene, EG210155	EG210155	1.059	0.579	0.580461	0.799564
5379	10361031	NM_178775	320119	ribosomal protein S6 kinase po	Rps6kc1	1.059	0.474	0.649614	0.842717
5380	10582008	NM_026844	66531	RIKEN cDNA 2310061C15 gene	2310061C15Rik	1.059	0.435	0.676134	0.855911
5381	10406407	NM_001042591	105171	arrestin domain containing 3	Arrdc3	1.059	0.345	0.740249	0.889357
5382	10518714	NM_177672	230917	transmembrane protein 201	Tmem201	1.059	1.546	0.164703	0.414577
5383	10515832	NM_001011870	258214	olfactory receptor 1329	Olfr1329	1.059	0.379	0.715638	0.875402
5384	10511113	NM_007661	12537	cell division cycle 2-like 1	Cdc2l1	1.059	0.935	0.380004	0.6497
5385	10458081					1.059	0.276	0.790237	0.914539
5386	10410774					1.059	1.209	0.264757	0.539986
5387	10431410	NM_011161	19094	mitogen-activated protein kina	Mapk11	1.059	0.993	0.353065	0.625939
5388	10350099	ENSMUST00000097567	100038590	predicted gene, ENSMUSG0000007	ENSMUSG00000073556	1.059	1.29	0.236876	0.508993
5389	10582330	NM_001033142	68718	ring finger protein 166	Rnf166	1.059	1.016	0.34241	0.616776
5390	10479041	NM_019547	56190	RNA binding motif protein 38	Rbm38	1.059	0.537	0.607371	0.817197
5391	10539931	ENSMUST00000101176	434065	gene model 1965, (NCBI)	Gm1965	1.059	0.964	0.366457	0.637434
5392	10555570	NM_008887	11859	paired-like homeobox 2a	Phox2a	1.059	0.214	0.836691	0.934075
5393	10529285	ENSMUST00000030994	20232	NK1 transcription factor relat	Nkx1-1	1.059	1.055	0.325622	0.601936
5394	10484813	NM_146972	258974	olfactory receptor 1233	Olfr1233	1.059	1.112	0.301715	0.577901
5395	10513776	NM_207109	56079	astrotactin 2	Astn2	1.059	0.523	0.616983	0.823029
5396	10499454	NM_022994	65111	death associated protein 3	Dap3	1.059	0.287	0.78207	0.911385
5397	10506594	BC024426	230579	cDNA sequence BC026682	BC026682	1.059	0.88	0.407234	0.671681
5398	10356489	NM_139152	208372	ankyrin repeat and SOCS box-co	Asb18	1.059	0.898	0.398193	0.664555
5399	10407337	NM_010408	15165	hyperpolarization-activated, c	Hcn1	1.059	-0.393	0.705551	0.871592
5400	10507692	NM_007902	13615	endothelin 2	Edn2	1.059	0.5	0.632256	0.832782
5401	10436451	NM_026588	68159	syntaxin 19	Stx19	1.059	1.068	0.32005	0.596822
5402	10421981	NM_028315	72662	DIS3 mitotic control homolog (	Dis3	1.059	0.461	0.658153	0.847091
5403	10430536	NM_199080	67040	DEAD (Asp-Glu-Ala-Asp) box pol	Ddx17	1.059	0.823	0.436647	0.696302
5404	10408519	NM_153072	210554	Hus1 homolog b (S. pombe)	Hus1b	1.059	1.071	0.318874	0.596082
5405	10607169	NM_009428	22067	transient receptor potential c	Trpc5	1.059	0.453	0.663662	0.850267
5406	10561868	BC054747	233064	WD repeat domain 62	Wdr62	1.059	1.129	0.294868	0.571152
5407	10553131	NM_133950	68137	KDEL (Lys-Asp-Glu-Leu) endopla	Kdelr1	1.059	0.233	0.821896	0.92863
5408	10507484	NM_080469	140546	prion protein interacting prot	Prnpip1	1.059	0.567	0.587709	0.804514

5409	10607724	NM_178794	22184	zinc finger (CCCH type), RNA b	Zrsr2	1.059	0.514	0.622458	0.827231
5410	10406364	BC089469	72371	RIKEN cDNA 2210408I21 gene	2210408I21Rik	1.059	0.135	0.896121	0.95935
5411	10550638	NM_013648	20167	reticulon 2 (Z-band associated	Rtn2	1.059	0.665	0.52681	0.76278
5412	10491547	ENSMUST00000029268	72282	RIKEN cDNA 1810062G17 gene	1810062G17Rik	1.059	0.859	0.41809	0.680624
5413	10580457	BC004022	80750	NEDD4 binding protein 1	N4bp1	1.059	0.342	0.74229	0.890171
5414	10389308	NM_153144	217039	gametogenetin binding protein	Ggnbp2	1.059	1.005	0.347419	0.62155
5415	10360802					1.059	0.909	0.392526	0.660531
5416	10478145	NM_153089	228852	protein phosphatase 1, regulat	Ppp1r16b	1.059	0.667	0.525307	0.76149
5417	10397555	XM_990056	667350	predicted gene, EG667350	EG667350	1.059	0.259	0.80313	0.920071
5418	10529708	NM_001081144	100515	zinc finger protein 518B	Zfp518b	1.059	0.526	0.614796	0.821749
5419	10382788	NM_010254	14428	galanin receptor 2	Galr2	1.059	1.031	0.335684	0.611239
5420	10566877	BC067204	319934	SET binding factor 2	Sbf2	1.059	0.969	0.363961	0.635368
5421	10375031	BC028766	78372	RIKEN cDNA 3300001G02 gene	3300001G02Rik	1.059	0.329	0.751566	0.895256
5422	10566157	NM_146755	258750	olfactory receptor 551	Olfr551	1.058	0.809	0.444454	0.702934
5423	10367252	NM_133992	103135	ubiquitin specific peptidase 5	Usp52	1.058	0.694	0.509216	0.750516
5424	10367179	NM_011589	21853	timeless homolog (Drosophila)	Timeless	1.058	0.622	0.552814	0.782578
5425	10551282	XR_033870	100047728	similar to Cytochrome P450 2A5	LOC100047728	1.058	0.202	0.84561	0.937284
5426	10553788	NM_009728	11982	ATPase, class V, type 10A	Atp10a	1.058	0.119	0.908447	0.963723
5427	10534056					1.058	0.4	0.700604	0.86896
5428	10563178	NM_007645	12493	CD37 antigen	Cd37	1.058	1.158	0.283623	0.558905
5429	10427148	NM_153194	68744	zinc finger protein 740	Zfp740	1.058	0.63	0.548198	0.778657
5430	10428690	NM_026759	68537	mitochondrial ribosomal protei	Mrpl13	1.058	0.099	0.924041	0.969768
5431	10607280	XR_031183	100039716	similar to ribosomal protein L	LOC100039716	1.058	0.809	0.444345	0.702815
5432	10421526	NM_009029	19645	retinoblastoma 1	Rb1	1.058	0.264	0.799418	0.919009
5433	10581073	NM_001013380	234663	dynein, cytoplasmic 1 light in	Dync1li2	1.058	0.585	0.576536	0.79748
5434	10347481	NM_024264	104086	cytochrome P450, family 27, su	Cyp27a1	1.058	1.243	0.252786	0.526904
5435	10437668	NM_009896	12703	suppressor of cytokine signali	Socs1	1.058	0.815	0.441051	0.700013
5436	10381708	NM_019679	57778	formin-like 1	Fmnl1	1.058	1.04	0.331951	0.608173
5437	10420631	NM_026598	68177	emopamil binding protein-like	Ebpl	1.058	0.712	0.498902	0.742429
5438	10482814	NM_001111030	269275	activin A receptor, type IC	Acvr1c	1.058	0.457	0.66135	0.849188
5439	10457487					1.058	0.912	0.391324	0.659653
5440	10551638	NM_008496	16858	lectin, galactose binding, sol	Lgals7	1.058	0.735	0.485766	0.734004
5441	10538169	ENSMUST00000031837	69761	RIKEN cDNA 1600015I10 gene	1600015I10Rik	1.058	0.705	0.502945	0.745637
5442	10547701	NM_008995	19305	peroxisome biogenesis factor 5	Pex5	1.058	0.67	0.523495	0.760167
5443	10584231	NM_023292	67049	pseudouridine synthase 3	Pus3	1.058	0.58	0.579444	0.798942
5444	10469335	NM_011484	20844	signal transducing adaptor mol	Stam	1.058	0.902	0.39619	0.663738
5445	10419638	NM_201637	67772	chromodomain helicase DNA bind	Chd8	1.058	1.406	0.201184	0.463431
5446	10487629	NM_130884	170718	isocitrate dehydrogenase 3 (NA	Idh3b	1.058	0.845	0.425323	0.687277
5447	10495243	NM_010360	14866	glutathione S-transferase, mu	Gstm5	1.058	-0.025	0.980874	0.991919
5448	10384522	NM_146243	66713	ARP2 actin-related protein 2 h	Actr2	1.058	0.985	0.356656	0.629161
5449	10548875	NM_026639	109978	ADP-ribosyltransferase 4	Art4	1.058	0.611	0.560105	0.787428
5450	10470936	NM_146252	70296	TBC1 domain family, member 13	Tbc1d13	1.058	0.691	0.510925	0.752036
5451	10417920	NM_030180	78787	ubiquitin specific peptidase 5	Usp54	1.058	0.512	0.623944	0.828269
5452	10430596	NM_194342	223697	unc-84 homolog B (C. elegans)	Unc84b	1.058	1.668	0.138087	0.375863
5453	10487945	NM_028802	74182	preimplantation protein 4	Prei4	1.058	0.362	0.728079	0.882032
5454	10450784	NM_008205	14997	histocompatibility 2, M region	H2-M9	1.058	0.261	0.801098	0.919467
5455	10390685	NM_025661	66612	ORM1-like 3 (S. cerevisiae)	Ormdl3	1.058	0.936	0.379637	0.649438
5456	10347888	NM_016960	20297	chemokine (C-C motif) ligand 2	Ccl20	1.058	0.8	0.449081	0.706553
5457	10464647	NM_178650	108995	TBC1 domain family, member 10c	Tbc1d10c	1.058	1.801	0.113431	0.333803
5458	10356137	NM_025453	66261	transmembrane 4 L six family m	Tm4sf20	1.058	0.866	0.41414	0.677439
5459	10425511	NM_177310	321003	X-prolyl aminopeptidase (amino	Xpnpep3	1.058	0.582	0.578068	0.798189
5460	10476945	NM_009977	13011	cystatin F (leukocystatin)	Cst7	1.058	0.838	0.428735	0.689638

5461	10562709	NM_001111058	12489	CD33 antigen	Cd33	1.058	0.977	0.360389	0.632213
5462	10511694	NM_145950	209212	oxidative stress induced growt	Osgin2	1.057	0.892	0.401397	0.666762
5463	10561837	NM_011980	26465	zinc finger protein 146	Zfp146	1.057	0.183	0.860059	0.943699
5464	10458262	NM_011397	20522	solute carrier family 23 (nucl	Slc23a1	1.057	0.878	0.408292	0.672667
5465	10531453	NM_177230	320696	RIKEN cDNA 4932413O14 gene	4932413O14Rik	1.057	0.741	0.481994	0.730954
5466	10353135	NM_008678	17978	nuclear receptor coactivator 2	Ncoa2	1.057	0.515	0.621678	0.826662
5467	10408755	NM_139063	17828	muted	Muted	1.057	1.001	0.349058	0.622715
5468	10606969	NM_153586	237073	RNA binding motif protein 41	Rbm41	1.057	1.061	0.323029	0.59983
5469	10483246					1.057	0.854	0.420456	0.682753
5470	10518585	NM_207682	16561	kinesin family member 1B	Kif1b	1.057	0.738	0.483753	0.732322
5471	10504458	NM_001080385	12757	clathrin, light polypeptide (L	Clta	1.057	1.089	0.311107	0.587683
5472	10433077	NM_027885	71726	single-strand selective monofu	Smug1	1.057	1.014	0.343409	0.617488
5473	10389231	NM_011337	20302	chemokine (C-C motif) ligand 3	Ccl3	1.057	1.44	0.19171	0.451028
5474	10408616	NM_001033167	73102	solute carrier family 22, memb	Slc22a23	1.057	0.729	0.489072	0.736349
5475	10391454	NM_012037	26949	vesicle amine transport protei	Vat1	1.057	0.094	0.927396	0.971409
5476	10421012	NM_028032	71978	protein phosphatase 2 (formerl	Ppp2r2a	1.057	1.105	0.304749	0.581187
5477	10550076	NM_011588	21849	tripartite motif-containing 28	Trim28	1.057	0.884	0.405243	0.669725
5478	10467697	NM_028152	72199	MMS19 (MET18 S. cerevisiae)	Mms19	1.057	0.903	0.395572	0.663394
5479	10558159	NM_007769	12945	deleted in malignant brain tum	Dmbt1	1.057	0.712	0.499127	0.742475
5480	10377751	NM_009714	11889	asialoglycoprotein receptor 1	Asgr1	1.057	0.72	0.493936	0.739382
5481	10605421	NM_001039373	17763	mature T-cell proliferation 1	Mtcp1	1.057	0.364	0.726427	0.881516
5482	10607366	NM_172441	110380	shroom family member 2	Shroom2	1.057	1.28	0.240215	0.513302
5483	10503584	NM_172687	230027	coenzyme Q3 homolog, methyltra	Coq3	1.057	0.574	0.583277	0.801352
5484	10408032	NM_001013786	432731	zinc finger protein 187	Zfp187	1.057	0.296	0.775721	0.908358
5485	10543895	BC075651	243753	RIKEN cDNA 2010107G12 gene	2010107G12Rik	1.057	1.454	0.188101	0.446224
5486	10348829	NM_145519	227377	FERM, RhoGEF and pleckstrin do	Farp2	1.057	0.541	0.605053	0.815765
5487	10353733	NM_008922	19076	DNA primase, p58 subunit	Prim2	1.057	0.086	0.93363	0.973502
5488	10549546	NM_025348	66091	NADH dehydrogenase (ubiquinone	Ndufa3	1.057	0.226	0.827444	0.930659
5489	10444841	NM_010391	15007	histocompatibility 2, Q region	H2-Q10	1.057	0.275	0.790707	0.914692
5490	10445407	NM_013688	21645	t-complex-associated testis ex	Tcte1	1.057	1.401	0.202755	0.465349
5491	10445214	NM_008650	17850	methylmalonyl-Coenzyme A mutas	Mut	1.057	0.867	0.41404	0.677432
5492	10594609	NM_175206	74165	F-box and leucine-rich repeat	Fbxl22	1.057	0.857	0.419096	0.681475
5493	10359050	AK172956	74081	centrosomal protein 350	Cep350	1.057	0.933	0.380839	0.650316
5494	10507880					1.057	1.039	0.332199	0.608245
5495	10383282	NM_001085498	208092	chromatin modifying protein 6	Chmp6	1.057	0.805	0.4463	0.704033
5496	10473847	NM_007387	11432	acid phosphatase 2, lysosomal	Acp2	1.057	0.45	0.665657	0.850998
5497	10561777	BC027344	233057	cDNA sequence BC027344	BC027344	1.057	0.354	0.733667	0.886032
5498	10450611	AK017439	71377	RIKEN cDNA 5530401N12 gene	5530401N12Rik	1.057	0.493	0.636655	0.834887
5499	10585301	NM_009041	19684	radixin	Rdx	1.057	0.695	0.50901	0.750516
5500	10558961	NM_053082	64540	tetraspanin 4	Tspan4	1.057	0.651	0.53506	0.768753
5501	10431393	NM_013871	29857	mitogen-activated protein kina	Mapk12	1.057	0.689	0.51209	0.75265
5502	10607862					1.057	0.56	0.59213	0.807064
5503	10587075					1.057	0.996	0.351578	0.624753
5504	10445156	NM_146630	258623	olfactory receptor 123	Olfr123	1.057	1.523	0.170272	0.421869
5505	10483719	NM_001113246	108699	chimerin (chimaerin) 1	Chn1	1.057	0.677	0.519632	0.757547
5506	10544436	NM_146444	258436	olfactory receptor 458	Olfr458	1.057	0.866	0.414368	0.67755
5507	10496490	ENSMUST00000116120	13684	eukaryotic translation initiat	Eif4e	1.057	1.238	0.254388	0.528633
5508	10366344	BC054110	382421	predicted gene, EG382421	EG382421	1.057	0.677	0.519612	0.757547
5509	10461334	NM_011842	23942	metastasis-associated gene fam	Mta2	1.056	0.533	0.610324	0.81867
5510	10510700	NM_178406	100129	G protein-coupled receptor 153	Gpr153	1.056	1.173	0.278113	0.55314
5511	10593478	ENSMUST00000098777	408028	RIKEN cDNA 9230115E21 gene	9230115E21Rik	1.056	1.065	0.321165	0.598048
5512	10591472	NM_016742	12539	cell division cycle 37 homolog	Cdc37	1.056	0.313	0.762972	0.901446

5513	10530560	ENSMUST00000043711	75991	SLAIN motif family, member 2	Slain2	1.056	0.552	0.597566	0.81066
5514	10353479	NM_053270	116837	regulating synaptic membrane e	Rims1	1.056	0.284	0.784302	0.912071
5515	10488404	NM_030059	78240	cystatin 11	Cst11	1.056	1.616	0.148809	0.391099
5516	10461497	NM_015735	13194	damage specific DNA binding pr	Ddb1	1.056	0.484	0.642956	0.838239
5517	10436664					1.056	1.212	0.263662	0.538479
5518	10493009	NM_001003912	213498	Rho guanine nucleotide exchang	Arhgef11	1.056	0.866	0.414208	0.677446
5519	10461158	AK051045	83673	small nucleolar RNA host gene	Snhg1	1.056	1.771	0.118687	0.344006
5520	10403462	NM_001081426	208440	DIP2 disco-interacting protein	Dip2c	1.056	0.481	0.644853	0.83943
5521	10402542	NM_029654	76559	ATG2 autophagy related 2 homol	Atg2b	1.056	0.464	0.656283	0.846043
5522	10538373	NM_030024	78004	proline rich 15	Prr15	1.056	0.74	0.482745	0.731475
5523	10377117	NM_010855	17884	myosin, heavy polypeptide 4, s	Myh4	1.056	0.758	0.472398	0.724111
5524	10555879	NM_147075	259078	olfactory receptor 656	Olfr656	1.056	1.481	0.180861	0.436777
5525	10515716	ENSMUST00000075406	230676	cDNA sequence BC059842	BC059842	1.056	0.305	0.768892	0.904046
5526	10536273	NM_145398	213819	CAS1 domain containing 1	Casd1	1.056	0.844	0.425909	0.687657
5527	10419062	NM_177816	328381	SH2 domain containing 4B	Sh2d4b	1.056	1.121	0.298095	0.574141
5528	10345571	NM_009918	12790	cyclic nucleotide gated channe	Cnga3	1.056	1.328	0.224775	0.494893
5529	10404630	NM_024242	71340	RIO kinase 1 (yeast)	Riok1	1.056	0.22	0.832065	0.932638
5530	10440558	NM_001081068	78913	zinc finger protein 294	Zfp294	1.056	0.332	0.749251	0.893972
5531	10550345	NM_133789	97387	striatin, calmodulin binding p	Strn4	1.056	0.586	0.575655	0.797076
5532	10581538	NM_008706	18104	NAD(P)H dehydrogenase, quinone	Nqo1	1.056	0.399	0.701515	0.869143
5533	10568765	NM_183289	70571	transcription elongation regul	Tcerg1l	1.056	0.39	0.707789	0.872268
5534	10578703	NM_029701	76687	signal peptidase complex subun	Spcs3	1.056	1.087	0.31184	0.58829
5535	10535091	BC016220	78792	RIKEN cDNA 4930432F04 gene	4930432F04Rik	1.056	0.752	0.476001	0.727266
5536	10433721	NM_023317	67203	nuclear distribution gene E ho	Nde1	1.056	0.668	0.524696	0.761127
5537	10430745	ENSMUST00000072910	214685	RIKEN cDNA D930017K21 gene	D930017K21Rik	1.056	0.899	0.397878	0.664302
5538	10472598	NM_177784	277396	kelch-like 23 (Drosophila)	Klhl23	1.056	0.6	0.566762	0.792465
5539	10410776					1.056	0.98	0.358856	0.630937
5540	10391963	NM_008740	18195	N-ethylmaleimide sensitive fus	Nsf	1.056	0.869	0.412916	0.676379
5541	10438942	NM_172614	224090	transmembrane protein 44	Tmem44	1.056	1.249	0.25056	0.524406
5542	10445774	AY522648	320148	RIKEN cDNA B430306N03 gene	B430306N03Rik	1.056	1.044	0.330426	0.606628
5543	10581772	NM_009149	20340	golgi apparatus protein 1	Glg1	1.056	0.514	0.622882	0.827402
5544	10514815	AK028711	329909	transmembrane protein 61	Tmem61	1.056	0.895	0.399569	0.665716
5545	10350975	ENSMUST00000097514	100038672	predicted gene, ENSMUSG0000007	ENSMUSG00000073528	1.056	1.321	0.226748	0.497443
5546	10480891	NM_133835	98766	ubiquitin associated domain co	Ubac1	1.056	0.522	0.617082	0.823029
5547	10418921	NM_011430	20618	synuclein, gamma	Sncg	1.056	0.593	0.571293	0.795379
5548	10432473	BC072572	380969	Riken cDNA C230021P08 gene	C230021P08Rik	1.056	1.357	0.215802	0.482925
5549	10476383	NM_001024385	66586	cardiolipin synthase 1	Crls1	1.056	0.447	0.667994	0.851925
5550	10401926					1.056	0.684	0.515111	0.754817
5551	10348618	NM_001039126	65247	ankyrin repeat and SOCS box-co	Asb1	1.055	1.023	0.339465	0.614887
5552	10494016	NM_025416	66198	thioesterase superfamily membe	Them5	1.055	0.67	0.523953	0.760561
5553	10555470	NM_001040111	69710	centaurin, delta 2	Centd2	1.055	1.334	0.22272	0.492656
5554	10439404	XM_001478262	100047488	similar to hCG1657343	LOC100047488	1.055	1.001	0.349114	0.622715
5555	10366956	NM_009284	20852	signal transducer and activato	Stat6	1.055	0.204	0.844246	0.936764
5556	10477372	NM_025631	66557	bactericidal/permeability-incr	Bpil1	1.055	1.811	0.111725	0.33081
5557	10468131	NM_198296	71617	RIKEN cDNA 9130011E15 gene	9130011E15Rik	1.055	0.679	0.518142	0.756879
5558	10435024	NM_027355	70238	ring fnger protein 168	Rnf168	1.055	0.848	0.42391	0.686151
5559	10380887	NM_011540	21393	titin-cap	Tcap	1.055	0.741	0.482039	0.730954
5560	10467538	NM_011904	24087	tolloid-like 2	Tll2	1.055	1.226	0.258769	0.532905
5561	10370210	NM_009933	12833	collagen, type VI, alpha 1	Col6a1	1.055	0.653	0.534045	0.767997
5562	10393320	NM_173755	217342	ubiquitin-conjugating enzyme E	Ube2o	1.055	1.377	0.209701	0.474741
5563	10429444	ENSMUST00000110021	268816	gene model 628, (NCBI)	Gm628	1.055	0.672	0.522363	0.75928
5564	10355511	NM_009407	21958	transition protein 1	Tnp1	1.055	0.857	0.418871	0.681435
5565	10606936	XR_031468	622432	similar to Glyceraldehyde-3-ph	LOC622432	1.055	0.494	0.635799	0.834627

5566	10400762	NM_201519	399510	mitogen-activated protein kina	Map4k5	1.055	0.733	0.486453	0.734369
5567	10536595	NM_133939	76522	LSM8 homolog, U6 small nuclear	Lsm8	1.055	0.889	0.4025	0.667563
5568	10452269	NM_153551	70785	DENN/MADD domain containing 1C	Dennd1c	1.055	0.752	0.475855	0.727249
5569	10554094	NM_010513	16001	insulin-like growth factor I r	Igf1r	1.055	0.51	0.625513	0.829311
5570	10431352	ENSMUST00000109353	328580	tubulin, gamma complex associa	Tubgcp6	1.055	1.186	0.273219	0.547785
5571	10402766	NM_009652	11651	thymoma viral proto-oncogene 1	Akt1	1.055	0.396	0.703439	0.869898
5572	10492709	NM_021370	58170	amiloride-sensitive cation cha	Accn5	1.055	0.55	0.599102	0.811784
5573	10430574	BC118956	75729	RIKEN cDNA 4933432B09 gene	4933432B09Rik	1.055	0.976	0.36056	0.632355
5574	10402378	ENSMUST00000095451	194604	gene model 46, (NCBI)	Gm46	1.055	0.75	0.476889	0.727649
5575	10352267	NM_001103182	72568	lin-9 homolog (C. elegans)	Lin9	1.055	0.394	0.704782	0.871013
5576	10565591	ENSMUST00000065257	791381	predicted gene, OTTMUSG0000002	OTTMUSG00000021246	1.055	0.29	0.780326	0.910803
5577	10420594	NM_183175	239126	C1q and tumor necrosis factor	C1qtnf9	1.055	0.707	0.501618	0.744504
5578	10347324	NM_001033345	241112	gene model 216, (NCBI)	Gm216	1.055	1.241	0.253327	0.527654
5579	10475623	ENSMUST00000066157	100036535	predicted gene, ENSMUSG0000005	ENSMUSG00000053615	1.055	1.11	0.302645	0.578712
5580	10393241	NM_016857	53413	exocyst complex component 7	Exoc7	1.055	0.841	0.427508	0.688756
5581	10541524	NM_028016	71950	Nanog homeobox	Nanog	1.055	0.774	0.463775	0.717865
5582	10603431	NM_011514	20937	suppressor of variegation 3-9	Suv39h1	1.055	0.302	0.771412	0.905701
5583	10437292	NM_177472	52864	BTB (POZ) domain containing 12	Btbd12	1.055	1.119	0.299051	0.575096
5584	10392683	ENSMUST00000100258	100038364	predicted gene, ENSMUSG0000007	ENSMUSG00000075442	1.055	0.685	0.514544	0.754736
5585	10605740	NM_012010	26905	eukaryotic translation initiat	Eif2s3x	1.055	0.77	0.465796	0.719391
5586	10536324	NM_023048	65255	ankyrin repeat and SOCS box-co	Asb4	1.055	0.046	0.964814	0.986033
5587	10411199	NM_025630	66549	angiogenic factor with G patch	Aggf1	1.055	0.247	0.81155	0.923946
5588	10450744	XR_034279	677333	similar to histone H3	LOC677333	1.055	0.525	0.615568	0.822286
5589	10390780	BC079890	268481	keratin 222	Krt222	1.055	0.55	0.599103	0.811784
5590	10522784	ENSMUST00000100472	100039489	similar to Hmgn2 protein	LOC100039489	1.055	0.375	0.718167	0.87698
5591	10436734	NM_007520	12013	BTB and CNC homology 1	Bach1	1.055	1.08	0.315057	0.591982
5592	10572050	NM_175188	72925	membrane-associated ring finge	March1	1.055	1.351	0.217654	0.4854
5593	10569494	NM_023680	79202	tumor necrosis factor receptor	Tnfrsf22	1.054	0.658	0.530857	0.76539
5594	10421418	NM_013514	13829	erythrocyte protein band 4.9	Epb4.9	1.054	0.921	0.386822	0.655838
5595	10348456	NM_133805	108679	COP9 (constitutive photomorpho	Cops8	1.054	0.491	0.637972	0.835923
5596	10541491	ENSMUST00000043553	74269	RIKEN cDNA 1700063H04 gene	1700063H04Rik	1.054	0.682	0.516457	0.75576
5597	10372917	NM_153059	216395	transmembrane protein 5	Tmem5	1.054	0.903	0.395691	0.663394
5598	10453399	BC100359	78586	S1 RNA binding domain 1	Srbd1	1.054	0.108	0.917222	0.967414
5599	10539220	NM_177884	330361	expressed sequence AW146020	AW146020	1.054	0.599	0.567238	0.792635
5600	10515337	NM_016777	50927	nuclear autoantigenic sperm pr	Nasp	1.054	1.157	0.28418	0.559417
5601	10514930	ENSMUST00000030352	78109	RIKEN cDNA 4930430J20 gene	4930430J20Rik	1.054	1.119	0.29896	0.575074
5602	10561073	NM_177102	320208	transmembrane protein 91	Tmem91	1.054	0.857	0.418994	0.681474
5603	10526311	NM_009745	12054	B-cell CLL/lymphoma 7B	Bcl7b	1.054	0.26	0.802453	0.919965
5604	10576115	NM_145834	234836	interleukin 17C	Il17c	1.054	1.287	0.237755	0.510106
5605	10395628	NM_029825	76983	sec1 family domain containing	Scfd1	1.054	0.223	0.830015	0.931618
5606	10550972	NM_001102613	232970	pleckstrin homology-like domai	Phldb3	1.054	1.432	0.194027	0.453766
5607	10371188	ENSMUST00000063065	319586	bruno-like 5, RNA binding prot	Brunol5	1.054	0.997	0.351206	0.624551
5608	10525741	NM_029532	76167	RIKEN cDNA 6330548G22 gene	6330548G22Rik	1.054	0.919	0.387857	0.656721
5609	10550865	NM_009567	22755	zinc finger protein 93	Zfp93	1.054	0.938	0.378799	0.648423
5610	10377982	NM_153103	16562	kinesin family member 1C	Kif1c	1.054	0.343	0.74116	0.889595
5611	10377802					1.054	0.658	0.530771	0.76539
5612	10401382	NM_010949	18222	numb gene homolog (Drosophila)	Numb	1.054	0.959	0.368504	0.639236
5613	10508228	NM_177462	100177	zinc finger, MYM-type 6	Zmym6	1.054	0.379	0.715762	0.875402

5614	10433719					1.054	0.544	0.603103	0.814471
5615	10401235					1.054	0.979	0.35925	0.631315
5616	10507238	NM_153521	230654	leucine rich repeat containing	Lrrc41	1.054	0	0.999815	0.99988
5617	10547906	NM_008479	16768	lymphocyte-activation gene 3	Lag3	1.054	1.024	0.33913	0.614614
5618	10587534	NM_199195	12040	branched chain ketoacid dehydr	Bckdhb	1.054	0.541	0.605066	0.815765
5619	10485312					1.054	0.604	0.564063	0.790466
5620	10573332	BC075658	74666	RIKEN cDNA 4930432K21 gene	4930432K21Rik	1.054	0.392	0.706362	0.871814
5621	10467041	NM_018830	54447	N-acylsphingosine amidohydrola	Asah2	1.054	0.977	0.360074	0.632184
5622	10602625	NM_001005475	245666	IQ motif and Sec7 domain 2	Iqsec2	1.054	1.164	0.281593	0.556928
5623	10350046	NM_152895	75605	jumonji, AT rich interactive d	Jarid1b	1.054	1.009	0.345498	0.619663
5624	10516490	NM_010291	14622	gap junction protein, beta 5	Gjb5	1.054	0.49	0.638888	0.835923
5625	10495134	XM_001479553	100043129	similar to hCG2040565	LOC100043129	1.054	0.784	0.457833	0.713313
5626	10378482	NM_026197	67493	methyltransferase 10 domain co	Mett10d	1.054	0.468	0.653765	0.844785
5627	10519392	NM_030675	79264	KRIT1, ankyrin repeat containi	Krit1	1.054	0.473	0.649988	0.842995
5628	10588226	NM_019764	56332	angiomotin like 2	Amotl2	1.054	1.005	0.34759	0.621575
5629	10433620	NM_015769	50505	excision repair cross-compleme	Ercc4	1.054	0.524	0.616317	0.822742
5630	10404870					1.054	0.609	0.561277	0.788442
5631	10546152	NM_176973	319655	podocalyxin-like 2	Podxl2	1.054	0.378	0.716118	0.875591
5632	10410355	NM_183146	212281	RIKEN cDNA A530054K11 gene	A530054K11Rik	1.054	0.455	0.662437	0.849733
5633	10541785	NM_016845	54137	proacrosin binding protein	Acrbp	1.054	0.826	0.435455	0.695585
5634	10449979	NM_177719	240069	microrchidia 2B	Morc2b	1.054	0.847	0.424078	0.686315
5635	10509500	NM_010470	15441	heterochromatin protein 1, bin	Hp1bp3	1.054	0.992	0.353187	0.625979
5636	10392012	NM_145436	217232	cell division cycle 27 homolog	Cdc27	1.054	0.672	0.522228	0.75916
5637	10558285	NM_207302	360216	zinc finger, RAN-binding domai	Zranb1	1.054	0.576	0.582267	0.800796
5638	10487371	NM_025296	26371	cytosolic iron-sulfur protein	Ciao1	1.054	0.448	0.66761	0.851783
5639	10394912					1.054	0.39	0.707772	0.872268
5640	10346810	NM_001081050	72823	par-3 partitioning defective 3	Pard3b	1.054	0.374	0.719146	0.877614
5641	10519333	NM_001042501	68152	RIKEN cDNA 5830415L20 gene	5830415L20Rik	1.054	0.432	0.67829	0.857067
5642	10476287	NM_153501	74450	pantothenate kinase 2 (Hallerv	Pank2	1.054	0.719	0.494774	0.739747
5643	10524284	BC046779	209683	tetratricopeptide repeat domai	Ttc28	1.053	1.235	0.255649	0.529946
5644	10409076	NM_011078	18676	PHD finger protein 2	Phf2	1.053	0.806	0.445993	0.703841
5645	10440903	BC032975	74387	RIKEN cDNA 4932438H23 gene	4932438H23Rik	1.053	0.611	0.560045	0.787428
5646	10364321	NM_010670	16694	keratin associated protein 12-	Krtap12-1	1.053	0.823	0.43681	0.696333
5647	10589800	NM_001114347	76499	CLIP associating protein 2	Clasp2	1.053	0.915	0.389546	0.658209
5648	10354400					1.053	1.052	0.326656	0.602834
5649	10546834	NM_021385	58186	RAD18 homolog (S. cerevisiae)	Rad18	1.053	0.806	0.445868	0.703765
5650	10468970	BC119609	18686	per-hexamer repeat gene 1	Phxr1	1.053	1.042	0.331212	0.60765
5651	10451907	NM_013664	20405	SH3-domain GRB2-like 1	Sh3gl1	1.053	0.415	0.690239	0.864076
5652	10443110	XM_985548	240057	synaptic Ras GTPase activating	Syngap1	1.053	0.886	0.404006	0.668777
5653	10600504	NM_026126	67391	FUN14 domain containing 2	Fundc2	1.053	0.249	0.810522	0.923665
5654	10439932					1.053	0.323	0.755987	0.897759
5655	10550723	BC118925	69547	NTPase, KAP family P-loop doma	Nkpd1	1.053	0.673	0.521748	0.75888
5656	10580233	NM_008097	270076	glutaryl-Coenzyme A dehydrogen	Gcdh	1.053	0.373	0.720156	0.878163
5657	10405785	NM_023507	76251	RIKEN cDNA 0610007P08 gene	0610007P08Rik	1.053	0.388	0.709136	0.872707
5658	10557626	XM_001480376	100043590	similar to SMT3B protein	LOC100043590	1.053	0.744	0.480168	0.729941
5659	10491438	NM_025978	67120	tetratricopeptide repeat domai	Ttc14	1.053	0.83	0.433109	0.693552
5660	10500948	NM_030249	80281	CTTNBP2 N-terminal like	Cttnbp2nl	1.053	0.81	0.443985	0.702635
5661	10408010	NM_023685	72739	zinc finger with KRAB and SCAN	Zkscan3	1.053	0.676	0.519865	0.757566
5662	10604337					1.053	0.639	0.5424	0.774847
5663	10565837	ENSMUST00000065741	442845	RIKEN cDNA F730035P03 gene	F730035P03Rik	1.053	1.37	0.211867	0.477389
5664	10395538	NM_026164	67452	patatin-like phospholipase dom	Pnpla8	1.053	0.029	0.97765	0.990817
5665	10559516	NM_175372	108841	retinol dehydrogenase 13 (all-	Rdh13	1.053	0.736	0.48474	0.733195

5666	10501754	NM_177664	229791	DNA segment, Chr 3, Brigham &	D3Bwg0562e	1.053	1.261	0.246643	0.519839
5667	10444114	NM_172620	224705	vacuolar protein sorting 52 (y	Vps52	1.053	0.17	0.869799	0.947894
5668	10591616	NM_177030	319899	dedicator of cytokinesis 6	Dock6	1.053	1.022	0.340002	0.615381
5669	10567576	ENSMUST00000065740	791343	predicted gene, ENSMUSG0000005	ENSMUSG00000053358	1.053	0.679	0.518622	0.757094
5670	10429754	NM_144847	223649	nuclear receptor binding prote	Nrbp2	1.053	0.711	0.499346	0.742592
5671	10452445	ENSMUST00000024896	78057	RIKEN cDNA 4930583I09 gene	4930583I09Rik	1.053	0.456	0.661522	0.849255
5672	10553559	NM_178706	233274	sialic acid binding Ig-like le	Siglech	1.053	1.157	0.28403	0.559277
5673	10398972	NM_054081	116870	metastasis associated 1	Mta1	1.053	0.278	0.788448	0.913849
5674	10511416	NM_145711	252838	thymocyte selection-associated	Tox	1.053	-0.384	0.712362	0.874031
5675	10592342	NM_025289	21376	transforming growth factor bet	Tbrg1	1.053	-0.029	0.977283	0.990677
5676	10537102	NM_009148	20336	exocyst complex component 4	Exoc4	1.053	0.813	0.442206	0.700945
5677	10423768	AK144597	100038592	predicted gene, ENSMUSG0000007	ENSMUSG00000072619	1.053	1.157	0.284325	0.559599
5678	10496629	NM_053102	93684	selenoprotein	Sep15	1.053	0.41	0.693697	0.865705
5679	10456439	BC064462	70799	centrosomal protein 192	Cep192	1.053	0.888	0.403377	0.668494
5680	10530225	NM_001081321	71521	PDS5, regulator of cohesion ma	Pds5a	1.053	0.892	0.401058	0.666661
5681	10386824	NM_019921	56697	A kinase (PRKA) anchor protein	Akap10	1.053	1.44	0.19175	0.451028
5682	10509246	NM_024452	269593	leucine zipper protein 1	Luzp1	1.053	0.525	0.61516	0.822023
5683	10606876	NM_019768	56397	mortality factor 4 like 2	Morf4l2	1.053	0.996	0.351343	0.624637
5684	10381187	NM_016920	11975	ATPase, H+ transporting, lysos	Atp6v0a1	1.053	0.43	0.679956	0.857866
5685	10572727	ENSMUST00000053105	382019	predicted gene, OTTMUSG0000002	OTTMUSG00000022410	1.053	-0.124	0.904416	0.962829
5686	10382912	NM_001113486	53860	septin 9	Sept9	1.053	0.655	0.532715	0.766762
5687	10556169	NM_025344	66085	eukaryotic translation initiat	Eif3f	1.052	0.427	0.681991	0.85946
5688	10488090	NM_175225	75812	taspase, threonine aspartase 1	Tasp1	1.052	0.852	0.42164	0.683993
5689	10561561	NM_009109	20190	ryanodine receptor 1, skeletal	Ryr1	1.052	1.269	0.243864	0.516956
5690	10560886	NM_026862	68891	CD177 antigen	Cd177	1.052	0.906	0.394187	0.661914
5691	10377804	NM_145429	216869	arrestin, beta 2	Arrb2	1.052	0.273	0.792688	0.91549
5692	10380773	NM_021493	58996	RIKEN cDNA 4933428G20 gene	4933428G20Rik	1.052	0.713	0.498291	0.742426
5693	10580219	NM_007591	12317	calreticulin	Calr	1.052	0.355	0.732511	0.885041
5694	10381664					1.052	1.317	0.228139	0.499185
5695	10388045					1.052	-0.178	0.863389	0.945538
5696	10497944	NM_028140	72175	major facilitator superfamily	Mfsd8	1.052	0.664	0.527088	0.762858
5697	10513544	NM_009554	22696	zinc finger protein 37	Zfp37	1.052	0.879	0.40749	0.671862
5698	10421806	NM_001033215	105590	expressed sequence AU017455	AU017455	1.052	0.281	0.786529	0.912916
5699	10491363	NM_024200	67414	mitofusin 1	Mfn1	1.052	0.436	0.675642	0.855911
5700	10428453	NM_001081391	239420	CUB and Sushi multiple domains	Csmd3	1.052	0.673	0.521769	0.75888
5701	10561799	NM_178384	72723	zinc finger protein 74	Zfp74	1.052	0.727	0.490367	0.737313
5702	10408455	NM_144536	68916	CDK5 regulatory subunit associ	Cdkal1	1.052	0.6	0.567063	0.792621
5703	10384179					1.052	0.855	0.420065	0.68238
5704	10538352					1.052	2.076	0.0754063	0.259639
5705	10366399	AK143218	544737	hypothetical LOC544737	LOC544737	1.052	0.526	0.614945	0.821845
5706	10379075	NM_001002004	72503	RIKEN cDNA 2610507B11 gene	2610507B11Rik	1.052	0.576	0.581837	0.800451
5707	10488387	NM_019632	17957	N-ethylmaleimide sensitive fus	Napb	1.052	0.877	0.408854	0.673168
5708	10471784	NM_146121	227800	RAB GTPase activating protein	Rabgap1	1.052	0.49	0.638939	0.835923
5709	10603302					1.052	0.944	0.37571	0.645773
5710	10426645	AK080921	320551	RIKEN cDNA B430209F14 gene	B430209F14Rik	1.052	0.55	0.599025	0.811784
5711	10577824	NM_173012	270035	leucine zipper-EF-hand contain	Letm2	1.052	0.752	0.475743	0.727129
5712	10425987	NM_011144	19013	peroxisome proliferator activa	Ppara	1.052	0.907	0.393917	0.661714
5713	10506754	NM_146255	242607	solute carrier family 1 (gluta	Slc1a7	1.052	1.085	0.312827	0.589257
5714	10551483	NM_198425	386655	EP300 interacting inhibitor of	Eid2	1.052	0.5	0.632146	0.832782
5715	10584405	NM_146869	258869	olfactory receptor 147	Olfr147	1.052	0.705	0.503165	0.745637
5716	10551061	NM_175477	232976	zinc finger protein 574	Zfp574	1.052	0.482	0.644368	0.839103

5717	10585588	NM_139001	121021	chondroitin sulfate proteoglyc	Cspg4	1.052	0.809	0.444183	0.702635
5718	10460400	NM_008797	18563	pyruvate carboxylase	Pcx	1.052	0.827	0.434887	0.695306
5719	10453900	NM_024182	66878	RIO kinase 3 (yeast)	Riok3	1.052	0.451	0.665012	0.850739
5720	10381049	NM_001080925	268480	Rap guanine nucleotide exchang	Rapgefl1	1.052	0.58	0.579818	0.799181
5721	10380871	NM_021547	59045	START domain containing 3	Stard3	1.052	0.761	0.470626	0.722494
5722	10477206	NM_001081044	228785	myosin, light polypeptide kina	Mylk2	1.052	1.012	0.344178	0.618503
5723	10516303					1.051	0.414	0.691203	0.864526
5724	10411019	NM_010829	17686	mutS homolog 3 (E. coli)	Msh3	1.051	0.479	0.646384	0.840589
5725	10558239	NM_008257	15373	H6 homeo box 3	Hmx3	1.051	0.988	0.355087	0.627756
5726	10581612	NM_020046	56749	dihydroorotate dehydrogenase	Dhodh	1.051	0.574	0.583175	0.801264
5727	10359793	NM_001033344	240892	dual specificity phosphatase 2	Dusp27	1.051	1.468	0.184375	0.441948
5728	10481147	NM_011512	20932	surfeit gene 4	Surf4	1.051	0.197	0.849209	0.939006
5729	10404152	NM_029679	193385	RIKEN cDNA 6330500D04 gene	6330500D04Rik	1.051	1.051	0.327019	0.6032
5730	10584862	NM_001013390	399548	sodium channel, type IV, beta	Scn4b	1.051	1.174	0.27787	0.553005
5731	10578763	NM_021788	60406	sin3 associated polypeptide	Sap30	1.051	0.542	0.604174	0.815116
5732	10472277	NM_020575	57438	membrane-associated ring finge	March7	1.051	0.379	0.715955	0.875442
5733	10362922	NM_053069	11793	autophagy-related 5 (yeast)	Atg5	1.051	0.58	0.579397	0.798942
5734	10605510					1.051	0.717	0.49583	0.740541
5735	10492469	NM_001039543	17349	myeloid leukemia factor 1	Mlf1	1.051	0.35	0.736661	0.887367
5736	10386916	BC053455	192976	cDNA sequence BC046404	BC046404	1.051	0.835	0.430726	0.691411
5737	10564805	NM_011068	18631	peroxisomal biogenesis factor	Pex11a	1.051	0.371	0.721097	0.878601
5738	10565735	ENSMUST00000069035	233544	RIKEN cDNA A630091E08 gene	A630091E08Rik	1.051	1.198	0.268789	0.543335
5739	10493809	XM_910611	628324	predicted gene, EG628324	EG628324	1.051	1.01	0.345048	0.619061
5740	10487000	NM_001013829	435684	Src homology 2 domain containi	Shf	1.051	0.931	0.382019	0.651575
5741	10420426	BC117501	219114	RIKEN cDNA F630043A04 gene	F630043A04Rik	1.051	0.085	0.934764	0.974011
5742	10454212	NM_008586	17288	meprin 1 beta	Mep1b	1.051	1.467	0.184702	0.442299
5743	10526195	NM_053266	114674	GTF2I repeat domain containing	Gtf2ird2	1.051	0.689	0.51229	0.752788
5744	10366886	NM_146011	216445	Rho GTPase activating protein	Arhgap9	1.051	0.557	0.594147	0.808459
5745	10419854	NM_016972	50934	solute carrier family 7 (catio	Slc7a8	1.051	0.432	0.678377	0.857067
5746	10438815	NM_177718	239796	RIKEN cDNA 1600021P15 gene	1600021P15Rik	1.051	0.546	0.601534	0.813172
5747	10463277	NM_008699	18089	NK2 transcription factor relat	Nkx2-3	1.051	0.534	0.609135	0.818061
5748	10458997	AK029420	73137	proline-rich coiled-coil 1	Prrc1	1.051	0.883	0.405573	0.670072
5749	10395225	ENSMUST00000101498	100038387	predicted gene, ENSMUSG0000007	ENSMUSG00000073133	1.051	0.36	0.729191	0.882693
5750	10404187	NM_019551	56196	Traf and Tnf receptor associat	Ttrap	1.051	0.425	0.682915	0.859827
5751	10594161	NM_019927	23806	ariadne ubiquitin-conjugating	Arih1	1.051	0.897	0.398726	0.664967
5752	10473690	NM_018828	55935	formin binding protein 4	Fnbp4	1.051	0.87	0.412123	0.676023
5753	10360418	NM_011880	24012	regulator of G protein signali	Rgs7	1.051	0.506	0.627639	0.830619
5754	10479971	ENSMUST00000100426	100038708	predicted gene, ENSMUSG0000007	ENSMUSG00000075538	1.051	0.322	0.75663	0.897871
5755	10490378	NM_133849	99296	histamine receptor H3	Hrh3	1.051	1.003	0.348523	0.622153
5756	10515737	ENSMUST00000075406	230676	cDNA sequence BC059842	BC059842	1.051	0.69	0.511971	0.75265
5757	10601901	BC117076	69389	RIKEN cDNA 1700014N06 gene	1700014N06Rik	1.051	0.765	0.468308	0.720616
5758	10492774	ENSMUST00000116329	229459	dachsous 2 (Drosophila)	Dchs2	1.051	0.974	0.361718	0.633386
5759	10510580	NM_011612	21942	tumor necrosis factor receptor	Tnfrsf9	1.051	0.47	0.652024	0.844083
5760	10385832	NM_021283	16189	interleukin 4	Il4	1.051	0.61	0.56067	0.78784
5761	10505044	NM_139309	246179	fukutin	Fktn	1.051	0.378	0.716586	0.875798
5762	10433114	NM_010577	16402	integrin alpha 5 (fibronectin	Itga5	1.051	0.41	0.693736	0.865705
5763	10513020	NM_026079	230233	inhibitor of kappa light polyp	Ikbkap	1.051	0.74	0.482701	0.731472
5764	10512637	NM_019475	100040268	olfactory receptor 157	Olfr157	1.051	1.046	0.329212	0.605502
5765	10450564	NM_010364	14885	general transcription factor I	Gtf2h4	1.051	0.595	0.569723	0.794081
5766	10476538	NM_145534	228662	BTB (POZ) domain containing 3	Btbd3	1.051	0.453	0.66408	0.850267
5767	10466771	NM_008044	14297	frataxin	Fxn	1.051	-0.02	0.984944	0.993638
5768	10405139	NM_001033400	328250	gene model 806, (NCBI)	Gm806	1.051	0.69	0.511736	0.752549

5769	10451650	NM_001110832	18044	nuclear transcription factor-Y	Nfya	1.051	1.018	0.341685	0.616255
5770	10525313	NM_009125	20239	ataxin 2	Atxn2	1.05	0.598	0.568173	0.793228
5771	10395520	NM_053122	93757	IMP2 inner mitochondrial membr	Immp2l	1.05	0.157	0.879664	0.952313
5772	10468893	NM_009970	12982	colony stimulating factor 2 re	Csf2ra	1.05	0.978	0.359636	0.631626
5773	10475080	NM_011941	26390	mitogen-activated protein kina	Mapkbp1	1.05	0.792	0.453379	0.709874
5774	10585268	NM_019493	56057	B-cell translocation gene 4	Btg4	1.05	0.748	0.47833	0.728924
5775	10375439	NM_025426	66213	mediator complex subunit 7	Med7	1.05	0.426	0.682773	0.859827
5776	10575142	ENSMUST00000093178	100049570	predicted gene, ENSMUSG0000007	ENSMUSG00000074106	1.05	0.248	0.810989	0.923749
5777	10383758	NR_002321	544752	taurine upregulated gene 1	Tug1	1.05	1.083	0.313641	0.59037
5778	10548176	BC027368	72440	RIKEN cDNA 5930416I19 gene	5930416I19Rik	1.05	0.484	0.64284	0.838239
5779	10408613	NM_023716	73710	tubulin, beta 2b	Tubb2b	1.05	0.209	0.840473	0.935549
5780	10418720	NM_025907	67011	methyltransferase like 6	Mettl6	1.05	0.483	0.643142	0.838317
5781	10419736	NM_010015	13135	defender against cell death 1	Dad1	1.05	0.445	0.669342	0.852821
5782	10389752	NM_008711	18121	noggin	Nog	1.05	0.497	0.633825	0.833492
5783	10480725	BC029214	227622	cDNA sequence BC029214	BC029214	1.05	0.713	0.498391	0.742426
5784	10594447	NM_008927	26395	mitogen-activated protein kina	Map2k1	1.05	-0.073	0.94353	0.977948
5785	10497343	XM_001477158	100041785	similar to cytochrome c oxidas	LOC100041785	1.05	0.732	0.487174	0.734936
5786	10416505	NM_026214	67516	potassium channel tetramerisat	Kctd4	1.05	0.741	0.482134	0.730954
5787	10433274	NM_139307	246154	vasorin	Vasn	1.05	0.413	0.691694	0.864682
5788	10413596	ENSMUST00000054230	54650	Scm-like with four mbt domains	Sfmbt1	1.05	0.78	0.460126	0.714915
5789	10406676	NM_172589	218454	lipoma HMGIC fusion partner-li	Lhfpl2	1.05	0.281	0.786785	0.91293
5790	10534343	NM_007925	13717	elastin	Eln	1.05	1.228	0.257925	0.531958
5791	10400628					1.05	0.881	0.40685	0.671343
5792	10598409	NM_172472	209446	transcription factor E3	Tcfe3	1.05	0.537	0.607292	0.817143
5793	10490350	NM_001085501	228966	protein phosphatase 1, regulat	Ppp1r3d	1.05	1.964	0.0890145	0.287785
5794	10404898	BC064117	380842	gene model 1574, (NCBI)	Gm1574	1.05	0.816	0.440423	0.699331
5795	10425999	NM_001033337	239570	expressed sequence AW124722	AW124722	1.05	0.965	0.365791	0.636847
5796	10594590	NM_019727	56440	sorting nexin 1	Snx1	1.05	-0.131	0.899389	0.960245
5797	10591632	NM_177030	319899	dedicator of cytokinesis 6	Dock6	1.05	0.741	0.482236	0.730954
5798	10543725	NM_031998	83922	testis specific gene A14	Tsga14	1.05	0.124	0.904635	0.96288
5799	10605552					1.05	0.635	0.545004	0.77708
5800	10449697	ENSMUST00000065610	791325	predicted gene, ENSMUSG0000005	ENSMUSG00000053280	1.05	0.173	0.867365	0.946934
5801	10357788	AK084736	108954	protein phosphatase 1, regulat	Ppp1r15b	1.05	1.263	0.245723	0.518859
5802	10504654					1.05	1.507	0.174248	0.427214
5803	10416923					1.05	0.448	0.667322	0.851505
5804	10429426	AK132992	268816	gene model 628, (NCBI)	Gm628	1.05	1.682	0.135171	0.370646
5805	10480406					1.05	1.268	0.2443	0.51746
5806	10552339	NM_001105057	637898	vomeronasal 2, receptor 60	Vmn2r60	1.05	1.231	0.257099	0.531457
5807	10411105	ENSMUST00000099317	100038731	predicted gene, ENSMUSG0000007	ENSMUSG00000074772	1.05	1.32	0.227092	0.497889
5808	10471770	NM_146623	258616	olfactory receptor 357	Olfr357	1.05	0.771	0.464998	0.71876
5809	10551487	ENSMUST00000094651	434156	similar to EID-2-like inhibito	LOC434156	1.05	0.469	0.653107	0.844553
5810	10465379	NM_026912	69024	sorting nexin 15	Snx15	1.05	0.881	0.40655	0.671151
5811	10503118	BC055683	242297	RIKEN cDNA 1700012H17 gene	1700012H17Rik	1.05	0.633	0.546045	0.777637
5812	10524781	NM_198163	77407	RAB35, member RAS oncogene fam	Rab35	1.05	1.015	0.342899	0.617132
5813	10574137					1.05	1.101	0.306397	0.582911
5814	10447025	NM_181649	53951	RIKEN cDNA 2310002B06 gene	2310002B06Rik	1.05	0.345	0.739648	0.889275
5815	10561983	BC053749	333193	cDNA sequence BC053749	BC053749	1.05	0.506	0.628126	0.830847
5816	10485622	NM_001123327	99003	glutamine and serine rich 1	Qser1	1.05	0.527	0.613727	0.821135
5817	10453139	ENSMUST00000086549	791338	predicted gene, ENSMUSG0000006	ENSMUSG00000066938	1.05	0.996	0.351298	0.624608
5818	10525374	NM_177242	320717	PTC7 protein phosphatase homol	Pptc7	1.049	0.674	0.521509	0.758794

5819	10457860					1.049	0.646	0.538333	0.771226
5820	10381668	NM_008707	18107	N-myristoyltransferase 1	Nmt1	1.049	0.042	0.967716	0.987137
5821	10421029	NM_175384	108912	cell division cycle associated	Cdca2	1.049	0.474	0.649798	0.842852
5822	10359027	NM_010712	16872	LIM homeobox protein 4	Lhx4	1.049	0.769	0.466407	0.719571
5823	10576274	NM_020497	57247	zinc finger protein (C2H2 type	Zfp276	1.049	1.248	0.250936	0.524807
5824	10460492	NM_025553	66419	mitochondrial ribosomal protei	Mrpl11	1.049	-0.038	0.970643	0.988127
5825	10437171	ENSMUST00000023632	74296	RIKEN cDNA 1700093J21 gene	1700093J21Rik	1.049	0.528	0.613513	0.82095
5826	10382779	NR_004853	69681	cyclin-dependent kinase 3	Cdk3	1.049	0.901	0.396855	0.664116
5827	10364249					1.049	0.465	0.655314	0.845667
5828	10381032	NM_138660	192160	cancer susceptibility candidat	Casc3	1.049	0.339	0.744583	0.891476
5829	10407892	NM_001081058	69562	cell division cycle 2-like 5 (	Cdc2l5	1.049	0.457	0.660965	0.84894
5830	10531290	NM_026557	68098	ring finger and CHY zinc finge	Rchy1	1.049	0.112	0.914059	0.966102
5831	10384483					1.049	1.111	0.302266	0.578434
5832	10390595	NM_013634	19014	mediator complex subunit 1	Med1	1.049	1.09	0.310611	0.587176
5833	10586254	ENSMUST00000038890	102442	DENN/MADD domain containing 4A	Dennd4a	1.049	-0.12	0.908127	0.963723
5834	10450814	NM_029632	76497	protein phosphatase 1, regulat	Ppp1r11	1.049	-0.29	0.780071	0.910713
5835	10558192	NM_175166	71395	RIKEN cDNA 5430419D17 gene	5430419D17Rik	1.049	1.435	0.193235	0.452533
5836	10497904	NM_153561	229228	nudix (nucleoside diphosphate	Nudt6	1.049	1.047	0.329018	0.605314
5837	10489463	NM_011414	20568	secretory leukocyte peptidase	Slpi	1.049	0.978	0.359517	0.63155
5838	10448495	BC072612	72016	RIKEN cDNA 1600002H07 gene	1600002H07Rik	1.049	0.781	0.45992	0.714726
5839	10499216	NM_028460	73182	platelet endothelial aggregati	Pear1	1.049	0.715	0.497097	0.741437
5840	10375838	NM_153393	237759	collagen, type XXIII, alpha 1	Col23a1	1.049	0.538	0.606531	0.816743
5841	10579125	NM_145596	234366	GATA zinc finger domain contai	Gatad2a	1.049	0.142	0.891112	0.957456
5842	10489429	NM_145369	209232	WAP four-disulfide core domain	Wfdc5	1.049	1.009	0.345669	0.619811
5843	10432372	NM_007857	13363	desert hedgehog	Dhh	1.049	0.873	0.410726	0.675052
5844	10557315					1.049	0.451	0.66556	0.850977
5845	10348697	NM_177587	208760	aquaporin 12	Aqp12	1.049	0.862	0.41641	0.67936
5846	10466972	NM_177721	240614	RAN binding protein 6	Ranbp6	1.049	0.181	0.861485	0.944333
5847	10391990	BC054752	76719	RIKEN cDNA 1700081L11 gene	1700081L11Rik	1.049	0.918	0.38829	0.657011
5848	10487660	NM_001114541	319513	RIKEN cDNA A930025D01 gene	A930025D01Rik	1.049	0.63	0.548316	0.77872
5849	10604248	NM_001033422	331401	THO complex 2	Thoc2	1.049	0.705	0.502995	0.745637
5850	10416124					1.049	0.864	0.415273	0.678399
5851	10353947	NM_018872	56030	transmembrane protein 131	Tmem131	1.049	0.36	0.72919	0.882693
5852	10524676	NM_025573	108014	splicing factor, arginine/seri	Sfrs9	1.049	0.623	0.552249	0.782016
5853	10588294	NM_176979	235559	topoisomerase (DNA) II beta bi	Topbp1	1.049	0.561	0.591527	0.806868
5854	10569273	NM_028308	101513	RIKEN cDNA 2700078K21 gene	2700078K21Rik	1.049	0.027	0.979258	0.991782
5855	10589647	NM_146227	235631	testes-specific protease 50	Tsp50	1.049	0.867	0.413905	0.677396
5856	10363701					1.049	0.892	0.400932	0.666612
5857	10416375	NM_026119	67381	mediator of RNA polymerase II	Med4	1.049	0.515	0.622265	0.827079
5858	10537227	NM_197986	68487	transmembrane protein 140	Tmem140	1.049	0.804	0.446891	0.70468
5859	10380896	NM_001003817	13866	v-erb-b2 erythroblastic leukem	Erbb2	1.049	0.928	0.383214	0.65267
5860	10545379	NM_138592	28035	ubiquitin specific peptidase 3	Usp39	1.049	0.194	0.851433	0.940193
5861	10462333	NM_025950	67072	cell division cycle 37 homolog	Cdc37l1	1.049	0.351	0.735296	0.886784
5862	10559406	NM_023524	69714	TCF3 (E2A) fusion partner	Tfpt	1.049	0.186	0.857391	0.942484
5863	10394936	ENSMUST00000101540	100042641	similar to development and dif	LOC100042641	1.049	0.178	0.863975	0.945829
5864	10405853	NM_178364	170936	zinc finger protein 369	Zfp369	1.049	0.105	0.919481	0.967948
5865	10494583	NM_011342	20333	SEC22 vesicle trafficking prot	Sec22b	1.048	0.773	0.464068	0.717953
5866	10524124	NM_008146	269682	golgi autoantigen, golgin subf	Golga3	1.048	0.722	0.493004	0.738773
5867	10560023	NM_001033820	619331	zinc fingr protein 551	Zfp551	1.048	0.36	0.72917	0.882693
5868	10374762	ENSMUST00000089614	628586	predicted gene, EG628586	EG628586	1.048	0.747	0.478438	0.729035
5869	10439874	NM_027046	69339	coiled-coil domain containing	Ccdc54	1.048	0.347	0.738348	0.888438
5870	10603328	NM_138603	54638	coiled-coil domain containing	Ccdc22	1.048	1.063	0.321957	0.598721
5871	10408444	NM_026206	67505	prolactin family 7, subfamily	Prl7c1	1.048	0.519	0.619283	0.82476

5872	10508217	NM_023603	71514	splicing factor proline/glutam	Sfpq	1.048	1.035	0.334123	0.609656
5873	10597103	NM_133347	72831	DEAH (Asp-Glu-Ala-His) box pol	Dhx30	1.048	0.93	0.382662	0.652088
5874	10569227	NM_181729	353328	mucin 6, gastric	Muc6	1.048	0.971	0.362912	0.63431
5875	10408060	NM_146540	258533	olfactory receptor 1364	Olfr1364	1.048	0.483	0.643301	0.838436
5876	10411215	NM_198408	12919	corticotropin releasing hormon	Crhbp	1.048	0.701	0.50515	0.747176
5877	10391863	BC117072	328019	RIKEN cDNA 4933400C05 gene	4933400C05Rik	1.048	0.556	0.595326	0.809385
5878	10458784	NM_172627	225467	protein geranylgeranyltransfer	Pggt1b	1.048	0.347	0.738664	0.88853
5879	10388648	NM_172945	268445	ankyrin repeat domain 13b	Ankrd13b	1.048	1.01	0.345012	0.619054
5880	10434029	NM_025808	66863	leucine-zipper-like transcript	Lztr1	1.048	0.655	0.532922	0.766954
5881	10604380	NM_172465	208884	zinc finger, DHHC domain conta	Zdhhc9	1.048	0.281	0.786368	0.912868
5882	10390535	NM_207231	217151	ADP-ribosylation factor-like 5	Arl5c	1.048	1.323	0.226318	0.496985
5883	10391431	NM_144829	69684	alanyl-tRNA synthetase domain	Aarsd1	1.048	0.473	0.650451	0.843233
5884	10520862	NM_008037	14284	fos-like antigen 2	Fosl2	1.048	0.51	0.625053	0.829015
5885	10380321	NM_134012	103537	mbt domain containing 1	Mbtd1	1.048	0.713	0.498533	0.742429
5886	10591947	NM_025862	66948	acyl-Coenzyme A dehydrogenase	Acad8	1.048	0.304	0.769855	0.904792
5887	10507903	ENSMUST00000097893	108809	RIKEN cDNA 4933407E24 gene	4933407E24Rik	1.048	1.095	0.308718	0.585272
5888	10580752	ENSMUST00000098492	320377	RIKEN cDNA 9330175E14 gene	9330175E14Rik	1.048	0.858	0.418717	0.68129
5889	10373640	NM_146929	258931	olfactory receptor 807	Olfr807	1.048	0.808	0.444926	0.703375
5890	10351884	NM_146717	258712	olfactory receptor 433	Olfr433	1.048	0.734	0.485987	0.734018
5891	10560644	NM_008990	19294	poliovirus receptor-related 2	Pvrl2	1.048	0.277	0.78956	0.914414
5892	10416334	NM_010071	13449	docking protein 2	Dok2	1.048	0.536	0.608052	0.817489
5893	10534883	NM_010571	16369	insulin receptor substrate 3	Irs3	1.048	0.851	0.421877	0.68422
5894	10398398					1.048	0.451	0.665476	0.850921
5895	10535080	NM_197980	68033	COX19 cytochrome c oxidase ass	Cox19	1.048	-0.091	0.929913	0.972408
5896	10547288	NM_001081112	232339	ankyrin repeat domain 26	Ankrd26	1.048	0.753	0.47523	0.726714
5897	10348234	NM_015750	23956	neuraminidase 2	Neu2	1.048	1.14	0.290916	0.567082
5898	10396849	NM_009014	19363	RAD51-like 1 (S. cerevisiae)	Rad51l1	1.048	0.371	0.721239	0.878601
5899	10561679	NM_026545	57296	proteasome (prosome, macropain	Psmd8	1.048	0.088	0.931922	0.97291
5900	10487927	BC033429	70612	RIKEN cDNA 5730494N06 gene	5730494N06Rik	1.048	0.412	0.692481	0.865136
5901	10402283	NM_172584	217837	inositol 1,3,4-triphosphate 5/	Itpk1	1.048	0.838	0.428718	0.689638
5902	10429201	NM_020045	56748	NFU1 iron-sulfur cluster scaff	Nfu1	1.048	0.615	0.557353	0.785582
5903	10556178	NM_021885	22141	tubby candidate gene	Tub	1.048	0.712	0.4988	0.742429
5904	10414278	ENSMUST00000100682	70713	G protein-coupled receptor 137	Gpr137c	1.048	0.6	0.566836	0.792482
5905	10349752	NM_007923	13714	ELK4, member of ETS oncogene f	Elk4	1.048	0.72	0.494061	0.739456
5906	10559590	NM_207270	545902	protein tyrosine phosphatase,	Ptprh	1.048	0.969	0.364042	0.635449
5907	10443918	NM_001045559	240067	RIKEN cDNA C920016K16 gene	C920016K16Rik	1.048	0.264	0.799439	0.919009
5908	10418718					1.048	1.215	0.262585	0.536954
5909	10399689					1.048	0.926	0.384193	0.653466
5910	10488362	NM_023504	228731	NK2 transcription factor relat	Nkx2-4	1.048	0.873	0.410857	0.675081
5911	10352735	NM_178632	77065	integrator complex subunit 7	Ints7	1.048	0.583	0.57769	0.797824
5912	10526038	NM_011846	23948	matrix metallopeptidase 17	Mmp17	1.048	1.088	0.311736	0.58828
5913	10381776	NM_001038609	17762	microtubule-associated protein	Mapt	1.048	0.831	0.432648	0.693129
5914	10366409	NM_001033261	216345	coiled-coil domain containing	Ccdc131	1.048	0.816	0.440763	0.699766
5915	10367772	NM_177271	320825	sterile alpha motif domain con	Samd5	1.048	0.418	0.688408	0.862969
5916	10471761	NM_146940	258942	olfactory receptor 352	Olfr352	1.047	0.823	0.436701	0.696302
5917	10607646	NM_001081052	195727	Nance-Horan syndrome (human)	Nhs	1.047	1.495	0.177309	0.431715
5918	10460072	NM_177450	338403	carnosine dipeptidase 1 (metal	Cndp1	1.047	1.12	0.298815	0.574899
5919	10514830	NM_028209	72354	tetratricopeptide repeat domai	Ttc4	1.047	1.04	0.332071	0.608173
5920	10447649	NM_001081416	68655	fibronectin type III domain co	Fndc1	1.047	0.967	0.364635	0.635759
5921	10444312	NM_079835	547431	butyrophilin-like 2	Btnl2	1.047	1.439	0.191992	0.451351
5922	10456346	NM_025468	66286	SEC11 homolog C (S. cerevisiae	Sec11c	1.047	0.298	0.773973	0.906993

5923	10539574	NR_002702	108176	nucleoplasmin 3, pseudogene 1	Npm3-ps1	1.047	0.542	0.604205	0.815116
5924	10397244	NM_025525	66381	ring finger protein 113A2	Rnf113a2	1.047	0.719	0.494519	0.7396
5925	10518568	XR_034527	666774	similar to ribosomal protein S	LOC666774	1.047	0.536	0.608115	0.817507
5926	10384808	BC059020	320757	RIKEN cDNA A630052C17 gene	A630052C17Rik	1.047	0.403	0.698608	0.867883
5927	10488771	NM_021546	56846	N-terminal EF-hand calcium bin	Necab3	1.047	0.921	0.386927	0.655964
5928	10494288	NM_146133	229593	golgi phosphoprotein 3-like	Golph3l	1.047	-0.182	0.86092	0.944057
5929	10385365	NM_028185	72290	U7 snRNP-specific Sm-like prot	Lsm11	1.047	0.244	0.813693	0.925035
5930	10412205	ENSMUST00000099162	100038414	predicted gene, ENSMUSG0000007	ENSMUSG00000074650	1.047	0.439	0.673268	0.854824
5931	10581175	NM_178879	97440	expressed sequence C76566	C76566	1.047	0.082	0.936718	0.975231
5932	10546586	NM_001081111	232286	TATA element modulatory factor	Tmf1	1.047	0.382	0.713371	0.874578
5933	10549237	NM_177222	320662	cancer susceptibility candidat	Casc1	1.047	0.766	0.467775	0.720367
5934	10464551	NM_144870	225887	NADH dehydrogenase (ubiquinone	Ndufs8	1.047	0.057	0.956093	0.983285
5935	10450835	NM_029747	76797	RIKEN cDNA 2410137M14 gene	2410137M14Rik	1.047	1.093	0.309672	0.586555
5936	10539669	NM_013458	11519	adducin 2 (beta)	Add2	1.047	0.52	0.618963	0.824608
5937	10556734	NM_054094	117147	acyl-CoA synthetase medium-cha	Acsm1	1.047	0.581	0.578935	0.798552
5938	10561525	ENSMUST00000098619	100038382	predicted gene, ENSMUSG0000007	ENSMUSG00000074233	1.047	0.7	0.505806	0.747682
5939	10599187	NM_028325	72693	zinc finger, CCHC domain conta	Zcchc12	1.047	0.71	0.499974	0.743107
5940	10596403	AM748257	665033	predicted gene, EG665033	EG665033	1.047	0.284	0.784177	0.912068
5941	10505908	XM_890156	625574	similar to TGFB-induced factor	LOC625574	1.047	0.906	0.39402	0.661801
5942	10403680	NM_194262	94246	AT rich interactive domain 4B	Arid4b	1.047	0.768	0.466876	0.719927
5943	10600953	NM_010099	13607	ectodysplasin-A	Eda	1.047	0.853	0.421	0.683426
5944	10546967	NM_024206	110379	SEC13 homolog (S. cerevisiae)	Sec13	1.047	0.277	0.789816	0.914502
5945	10539873	NM_008090	14461	GATA binding protein 2	Gata2	1.047	1.297	0.234508	0.505653
5946	10388869	NM_009395	21927	tumor necrosis factor, alpha-i	Tnfaip1	1.047	0.236	0.819901	0.928345
5947	10381383					1.047	0.813	0.442332	0.700945
5948	10560045	NM_009512	26459	solute carrier family 27 (fatt	Slc27a5	1.047	0.95	0.372656	0.643093
5949	10552488	NM_133712	69540	kallikrein related-peptidase 1	Klk10	1.047	0.777	0.462038	0.716594
5950	10509000					1.047	0.432	0.678103	0.856961
5951	10552418	NM_026695	110826	electron transferring flavopro	Etfb	1.047	0.157	0.879543	0.952231
5952	10450412	NM_001033221	106722	expressed sequence AU023871	AU023871	1.047	0.262	0.800889	0.919467
5953	10468909	NM_026866	68897	dispatched homolog 1 (Drosophi	Disp1	1.047	0.675	0.520971	0.758585
5954	10458834	NM_026217	67526	autophagy-related 12 (yeast)	Atg12	1.047	0.384	0.711983	0.87382
5955	10347210	ENSMUST00000097699	100038510	predicted gene, OTTMUSG0000002	OTTMUSG00000022136	1.047	1.071	0.318841	0.596082
5956	10423963	NM_175009	223527	enhancer of yellow 2 homolog (	Eny2	1.046	0.795	0.451852	0.708709
5957	10528622	NM_080444	117590	ankyrin repeat and SOCS box-co	Asb10	1.046	1.017	0.342077	0.61636
5958	10567498	XM_355934	381917	dynein, axonemal, heavy chain	Dnahc3	1.046	0.873	0.410861	0.675081
5959	10398461	NM_012023	26931	protein phosphatase 2, regulat	Ppp2r5c	1.046	0.523	0.616823	0.823029
5960	10471677	NM_001114124	69601	disabled homolog 2 (Drosophila	Dab2ip	1.046	0.763	0.469449	0.721578
5961	10477090	NM_024196	67231	TBC1 domain family, member 20	Tbc1d20	1.046	0.953	0.371411	0.64202
5962	10570356	NM_172282	234076	transmembrane and coiled-coil	Tmco3	1.046	0.442	0.671507	0.854195
5963	10556280	NM_009302	20947	SWA-70 protein	Swap70	1.046	0.524	0.616214	0.822657
5964	10555089	NM_001081267	233532	remodeling and spacing factor	Rsf1	1.046	0.419	0.687443	0.862174
5965	10495183	NM_008418	16491	potassium voltage-gated channe	Kcna3	1.046	1.137	0.291732	0.567783
5966	10403081	NM_146039	217935	WD repeat domain 60	Wdr60	1.046	0.301	0.771889	0.905856
5967	10452701	NM_028887	74355	SMC hinge domain containing 1	Smchd1	1.046	0.214	0.836416	0.933945
5968	10564646	NM_001109753	64176	synaptic vesicle glycoprotein	Sv2b	1.046	0.259	0.803094	0.920071
5969	10367600	NM_007956	13982	estrogen receptor 1 (alpha)	Esr1	1.046	0.979	0.359431	0.631475
5970	10409905	NM_020284	56835	cathepsin R	Ctsr	1.046	1.181	0.275003	0.549798
5971	10362495	NM_009925	12813	collagen, type X, alpha 1	Col10a1	1.046	0.964	0.366226	0.637219
5972	10566432	NM_147069	259072	olfactory receptor 686	Olfr686	1.046	1.087	0.311926	0.588349

5973	10512057					1.046	0.45	0.666115	0.851266
5974	10473874	NM_023854	77038	ADP-ribosylation factor GTPase	Arfgap2	1.046	0.54	0.605321	0.815893
5975	10576924	NM_176849	234023	arginine and glutamate rich 1	Arglu1	1.046	0.745	0.48008	0.729941
5976	10476874	NM_008780	18503	paired box gene 1	Pax1	1.046	0.852	0.421667	0.683993
5977	10454993	NM_080636	70791	histidyl-tRNA synthetase 2, mi	Hars2	1.046	0.276	0.790155	0.914502
5978	10375679	NM_029745	76795	TBC1 domain family, member 9B	Tbc1d9b	1.046	0.378	0.716618	0.875798
5979	10604551	NM_031388	83563	ubiquitin specific peptidase 2	Usp26	1.046	0.003	0.99735	0.999003
5980	10592886	ENSMUST00000071166	100126035	predicted gene, ENSMUSG0000005	ENSMUSG00000057559	1.046	0.268	0.795999	0.917149
5981	10354542	NM_153556	227099	postmeiotic segregation increa	Pms1	1.046	0.981	0.358379	0.630567
5982	10544084	NM_172467	209032	zinc finger CCCH-type, antivir	Zc3hav1l	1.046	0.914	0.390348	0.658911
5983	10496892	NM_057172	51886	far upstream element (FUSE) bi	Fubp1	1.046	1.197	0.269114	0.543784
5984	10487690	NM_080562	140629	U box domain containing 5	Ubox5	1.046	0.684	0.515472	0.754997
5985	10389601	BC020005	74133	RIKEN cDNA 1200011M11 gene	1200011M11Rik	1.046	0.137	0.894535	0.958419
5986	10346323	NM_175439	212679	methionine-tRNA synthetase 2 (	Mars2	1.046	0.657	0.53162	0.765811
5987	10400350	NM_007688	12632	cofilin 2, muscle	Cfl2	1.046	0.389	0.708396	0.872343
5988	10411082	NM_011582	21828	thrombospondin 4	Thbs4	1.046	1.322	0.226471	0.497144
5989	10357944	NM_001081307	329251	protein phosphatase 1, regulat	Ppp1r12b	1.046	0.819	0.439118	0.698413
5990	10539119	NM_019802	56316	gamma-glutamyl carboxylase	Ggcx	1.046	0.518	0.620183	0.825285
5991	10515257	NM_009015	19366	RAD54 like (S. cerevisiae)	Rad54l	1.046	0.371	0.721189	0.878601
5992	10574087	NM_022331	64209	homocysteine-inducible, endopl	Herpud1	1.046	0.376	0.717848	0.876794
5993	10486119	NM_177568	18796	phospholipase C, beta 2	Plcb2	1.046	1.264	0.245425	0.518491
5994	10455769	NM_152809	70425	casein kinase 1, gamma 3	Csnk1g3	1.046	0.314	0.762233	0.901088
5995	10375817	ENSMUST00000074198	622699	hypothetical LOC622699	LOC622699	1.046	1.025	0.338595	0.614159
5996	10489660	NM_207706	140579	engulfment and cell motility 2	Elmo2	1.046	0.48	0.645744	0.840161
5997	10552208	AK045908	110959	nudix (nucleoside diphosphate	Nudt19	1.045	0.606	0.563099	0.789853
5998	10606026	NM_019831	56364	zinc finger, MYM-type 3	Zmym3	1.045	0.604	0.564591	0.790721
5999	10569771	NM_053177	94178	mucolipin 1	Mcoln1	1.045	0.421	0.686317	0.861515
6000	10452658	NM_028887	74355	SMC hinge domain containing 1	Smchd1	1.045	0.944	0.375724	0.645773
6001	10561323	NM_001081292	269881	mitogen-activated protein kina	Map3k10	1.045	0.4	0.700528	0.86896
6002	10379901	NM_138681	192197	breast carcinoma amplified seq	Bcas3	1.045	1.158	0.283871	0.559215
6003	10573048	NM_026904	68999	anaphase promoting complex sub	Anapc10	1.045	0.168	0.870995	0.948568
6004	10405539	NM_175150	69672	thioredoxin domain containing	Txndc15	1.045	0.155	0.880765	0.952675
6005	10412897	XR_033982	632287	similar to pleckstrin homology	LOC632287	1.045	0.688	0.513216	0.753594
6006	10504640					1.045	0.311	0.764321	0.90173
6007	10529218	NM_028150	72195	suppressor of Ty 7 (S. cerevis	Supt7l	1.045	1.445	0.190567	0.449454
6008	10378637	NM_001004157	380713	scavenger receptor class F, me	Scarf1	1.045	1.133	0.293365	0.569485
6009	10534504	NM_172541	215210	transmembrane protein 120A	Tmem120a	1.045	0.026	0.979721	0.991919
6010	10520048	ENSMUST00000094962	69188	myeloid/lymphoid or mixed-line	Mll5	1.045	0.742	0.481703	0.730954
6011	10375650	NM_029004	74563	RasGEF domain family, member 1	Rasgef1c	1.045	0.782	0.45885	0.713797
6012	10541862	BC057601	320678	RIKEN cDNA A930037G23 gene	A930037G23Rik	1.045	0.561	0.591614	0.806879
6013	10446071	NM_010192	14154	feminization 1 homolog a (C. e	Fem1a	1.045	0.451	0.66536	0.850877
6014	10417778	NM_026528	68045	RIKEN cDNA 2700060E02 gene	2700060E02Rik	1.045	0.276	0.79	0.914502
6015	10498591	ENSMUST00000054825	109222	retinoic acid receptor respond	Rarres1	1.045	1.169	0.27963	0.554852
6016	10356780	NM_080850	269224	PAS domain containing serine/t	Pask	1.045	0.519	0.619294	0.82476
6017	10501483	ENSMUST00000051253	100043181	hypothetical protein LOC100043	LOC100043181	1.045	1.228	0.25786	0.531958
6018	10513551	ENSMUST00000084527	338355	FK506 binding protein 15	Fkbp15	1.045	1.24	0.253677	0.527927
6019	10445574	NM_025611	66515	cullin 7	Cul7	1.045	0.834	0.43127	0.691864
6020	10491897					1.045	1.033	0.334807	0.610375
6021	10439249	NM_001039530	547253	poly (ADP-ribose) polymerase f	Parp14	1.045	0.987	0.355548	0.628098
6022	10509163	NM_008321	15903	inhibitor of DNA binding 3	Id3	1.045	0.121	0.906887	0.963531
6023	10488954	NM_008109	14563	growth differentiation factor	Gdf5	1.045	0.424	0.68408	0.860099
6024	10547251	NM_194339	213895	BMS1 homolog, ribosome assembl	Bms1	1.045	0.208	0.840716	0.935634

6025	10577685	NM_009619	11497	a disintegrin and metallopepti	Adam3	1.045	0.454	0.663158	0.849961
6026	10410530	NM_028878	74338	solute carrier family 6 (neuro	Slc6a19	1.045	0.933	0.380847	0.650316
6027	10419676	NM_172601	76338	RAB2B, member RAS oncogene fam	Rab2b	1.045	0.169	0.870157	0.948137
6028	10357952	NM_001081307	329251	protein phosphatase 1, regulat	Ppp1r12b	1.045	0.59	0.572899	0.796481
6029	10571749					1.045	0.221	0.831026	0.932182
6030	10492091	NM_019483	55994	MAD homolog 9 (Drosophila)	Smad9	1.045	0.402	0.699041	0.868099
6031	10479560	NM_001001882	269400	regulator of telomere elongati	Rtel1	1.045	0.953	0.371642	0.64202
6032	10364478	NM_008226	15166	hyperpolarization-activated, c	Hcn2	1.045	0.39	0.708047	0.872288
6033	10594549	XM_001476757	100041121	similar to Sec61-complex gamma	LOC100041121	1.045	0.172	0.868397	0.947244
6034	10464914	NM_001001885	381199	transmembrane protein 151A	Tmem151a	1.045	0.545	0.601997	0.813486
6035	10347277	NM_008342	16008	insulin-like growth factor bin	Igfbp2	1.045	0.061	0.953247	0.981996
6036	10391242	NM_024456	19345	RAB5C, member RAS oncogene fam	Rab5c	1.045	0.155	0.88139	0.953061
6037	10482517	NM_019401	64685	N-myc (and STAT) interactor	Nmi	1.045	0.137	0.894768	0.958505
6038	10550632	NM_207525	403187	optic atrophy 3 (human)	Opa3	1.045	0.459	0.659548	0.848316
6039	10401289	NM_011387	20493	solute carrier family 10 (sodi	Slc10a1	1.045	0.929	0.382976	0.652509
6040	10416230	NM_020275	21933	tumor necrosis factor receptor	Tnfrsf10b	1.045	0.152	0.883488	0.954108
6041	10578120	ENSMUST00000079376	78636	RIKEN cDNA 1700104B16 gene	1700104B16Rik	1.045	0.994	0.352183	0.625281
6042	10579969	NM_145600	30932	zinc finger protein 330	Zfp330	1.045	0.191	0.85392	0.940913
6043	10359677	NM_025505	66352	basic leucine zipper nuclear f	Blzf1	1.045	0.486	0.641058	0.837375
6044	10478196	NM_009408	21969	topoisomerase (DNA) I	Top1	1.045	0.68	0.517498	0.756706
6045	10574464	NM_028524	75502	CKLF-like MARVEL transmembrane	Cmtm2b	1.045	0.306	0.767908	0.903579
6046	10439005	NM_025800	66849	protein phosphatase 1, regulat	Ppp1r2	1.045	0.257	0.804504	0.920877
6047	10511808	ENSMUST00000062777	67735	RIKEN cDNA 4930528A17 gene	4930528A17Rik	1.045	0.522	0.61736	0.823029
6048	10413803	NM_025295	26363	biotinidase	Btd	1.045	0.299	0.773081	0.906652
6049	10494407	NM_175666	319189	histone cluster 2, H2bb	Hist2h2bb	1.045	-0.407	0.695475	0.866211
6050	10493494	AK140090	100038411	predicted gene, ENSMUSG0000007	ENSMUSG00000074470	1.044	0.668	0.525041	0.761313
6051	10495781	NM_013867	29815	breast cancer anti-estrogen re	Bcar3	1.044	0.387	0.709822	0.872992
6052	10398751	NM_026752	68520	zinc finger, FYVE domain conta	Zfyve21	1.044	0.633	0.546298	0.777695
6053	10366653	NM_011915	24117	Wnt inhibitory factor 1	Wif1	1.044	1.151	0.286497	0.562199
6054	10410721	NM_029847	77041	arylsulfatase K	Arsk	1.044	0.389	0.708668	0.872486
6055	10434835					1.044	0.765	0.468749	0.720973
6056	10414427	NR_003630	624367	predicted gene, EG624367	EG624367	1.044	0.81	0.443643	0.702388
6057	10420383	AK139567	105611	expressed sequence AU040096	AU040096	1.044	0.504	0.629298	0.831256
6058	10529567	NM_001081232	320661	DNA segment, Chr 5, ERATO Doi	D5Ertd579e	1.044	0.2	0.847366	0.938194
6059	10560528					1.044	0.577	0.581536	0.800365
6060	10549849	NM_001025163	330463	zinc finger protein 78	Zfp78	1.044	0.935	0.380036	0.6497
6061	10430818	NM_028075	72049	tumor necrosis factor receptor	Tnfrsf13c	1.044	0.309	0.765844	0.902563
6062	10374197	NM_019511	56089	receptor (calcitonin) activity	Ramp3	1.044	0.074	0.943307	0.977948
6063	10532133	NM_007964	14020	ecotropic viral integration si	Evi5	1.044	0.447	0.667919	0.851904
6064	10526848	NM_183025	243308	RIKEN cDNA A430033K04 gene	A430033K04Rik	1.044	0.106	0.918696	0.967805
6065	10481670	NM_130860	107951	cyclin-dependent kinase 9 (CDC	Cdk9	1.044	0.155	0.881302	0.953061
6066	10360046	NM_025321	66052	succinate dehydrogenase comple	Sdhc	1.044	0.522	0.617192	0.823029
6067	10512653					1.044	1.399	0.203402	0.466305
6068	10374769					1.044	0.201	0.846047	0.937284
6069	10430997	NM_011862	23970	protein kinase C and casein ki	Pacsin2	1.044	0.302	0.771186	0.905685
6070	10468292	AK086428	100049155	predicted gene, ENSMUSG0000007	ENSMUSG00000071525	1.044	-0.153	0.882642	0.953681
6071	10600419	NM_008883	18846	plexin A3	Plxna3	1.044	0.641	0.541525	0.773858
6072	10435094	NM_016788	51789	tyrosine kinase, non-receptor,	Tnk2	1.044	0.982	0.357971	0.630288

6073	10583613	NM_144797	210029	meteorin, glial cell different	Metrn	1.044	0.838	0.418443	0.681004
6074	10508465	NM_010807	17357	MARCKS-like 1	Marcksl1	1.044	0.7	0.505794	0.747682
6075	10543551	NM_133925	68272	RNA binding motif protein 28	Rbm28	1.044	0.787	0.45613	0.712448
6076	10415248	NM_028994	74551	phosphoenolpyruvate carboxykin	Pck2	1.044	0.703	0.504276	0.746511
6077	10376496	NM_178659	194952	jumonji domain containing 4	Jmjd4	1.044	0.41	0.693578	0.865705
6078	10381738	NM_009521	22415	wingless-related MMTV integrat	Wnt3	1.044	0.9	0.397326	0.664272
6079	10426225	NM_001115132	52683	non-SMC condensin II complex,	Ncaph2	1.044	0.631	0.547667	0.778543
6080	10587940					1.044	0.556	0.594806	0.808991
6081	10359816	NM_175170	71592	pogo transposable element with	Pogk	1.044	0.614	0.557882	0.785788
6082	10584047	NM_013906	30806	a disintegrin-like and metallo	Adamts8	1.044	0.564	0.590163	0.806047
6083	10592919	NM_145985	213827	archain 1	Arcn1	1.044	0.906	0.394274	0.661945
6084	10540241	NM_022992	65106	ADP-ribosylation factor-like 6	Arl6ip5	1.044	0.269	0.795588	0.916955
6085	10416566	NM_029495	108670	epithelial stromal interaction	Epsti1	1.044	0.914	0.390311	0.658911
6086	10602592	NM_016763	15108	hydroxysteroid (17-beta) dehyd	Hsd17b10	1.044	0.096	0.926128	0.970758
6087	10434975	NM_013900	30060	antigen p97 (melanoma associat	Mfi2	1.044	1.043	0.33055	0.606749
6088	10422509					1.044	1.125	0.296739	0.573306
6089	10539218					1.044	0.669	0.524407	0.760916
6090	10501663	NM_030016	229780	coiled-coil domain containing	Ccdc76	1.044	0.601	0.566474	0.79227
6091	10517364	ENSMUST00000105860	230822	RIKEN cDNA A330049M08 gene	A330049M08Rik	1.044	0.751	0.476673	0.727638
6092	10477134	NM_001037247	266620	defensin beta 36	Defb36	1.044	1.065	0.32128	0.598079
6093	10494262	NM_007802	13038	cathepsin K	Ctsk	1.044	1.223	0.259648	0.533994
6094	10432408	NM_001024702	239659	complement component 1, q subc	C1ql4	1.044	0.902	0.396174	0.663738
6095	10416355	NM_134083	105670	regulator of chromosome conden	Rcbtb2	1.044	0.449	0.666569	0.851355
6096	10510265	NM_008725	230899	natriuretic peptide precursor	Nppa	1.044	0.371	0.7214	0.878683
6097	10537246	ENSMUST00000043815	70699	nucleoporin 205	Nup205	1.044	0.351	0.735367	0.886785
6098	10554057	NM_001033877	233332	a disintegrin-like and metallo	Adamts17	1.044	1.233	0.256392	0.530714
6099	10541112	BC018185	98758	heterogeneous nuclear ribonucl	Hnrpf	1.044	0.277	0.789678	0.914492
6100	10471814	NM_177383	338346	G protein-coupled receptor 21	Gpr21	1.044	0.354	0.733666	0.886032
6101	10524515	ENSMUST00000031566	231646	myosin 1H	Myo1h	1.043	0.195	0.850936	0.94008
6102	10526968	NM_175522	243312	leucine rich repeat and fibron	Elfn1	1.043	1.147	0.288026	0.563886
6103	10496159	NM_027927	71793	integrator complex subunit 12	Ints12	1.043	0.231	0.823373	0.929428
6104	10567838	NM_023712	73658	spinster homolog 1 (Drosophila	Spns1	1.043	0.952	0.371855	0.642152
6105	10358379	NM_013835	20822	TROVE domain family, member 2	Trove2	1.043	0.159	0.877952	0.951715
6106	10491520	AK140083	100049565	predicted gene, ENSMUSG0000007	ENSMUSG00000074633	1.043	0.414	0.69071	0.864369
6107	10596034	NM_001033543	213208	interleukin 20 receptor beta	Il20rb	1.043	1.193	0.270815	0.545372
6108	10580990	NM_001039154	12564	cadherin 8	Cdh8	1.043	0.194	0.851185	0.94011
6109	10581188	BC043046	74356	RIKEN cDNA 4931428F04 gene	4931428F04Rik	1.043	0.911	0.391773	0.660136
6110	10453855					1.043	0.773	0.46434	0.718115
6111	10391752					1.043	0.477	0.647182	0.841007
6112	10535637	NM_133735	71799	pentatricopeptide repeat domai	Ptcd1	1.043	0.505	0.628637	0.830964
6113	10351047	NM_027429	70454	centromere protein L	Cenpl	1.043	0.022	0.982969	0.99264
6114	10566583	XR_035350	668139	predicted gene, EG668139	EG668139	1.043	0.023	0.982379	0.9924
6115	10522696	NM_206935	384185	ADP-ribosylation factor-like 9	Arl9	1.043	0.58	0.579755	0.799162
6116	10438109	NM_009456	22195	ubiquitin-conjugating enzyme E	Ube2l3	1.043	0.301	0.771583	0.905749
6117	10427521	NM_001081402	545085	WD repeat domain 70	Wdr70	1.043	0.089	0.931444	0.972759
6118	10527423	NM_001081362	100683	transformation/transcription d	Trrap	1.043	0.534	0.609075	0.818045
6119	10477739	NM_008383	16328	centrosomal protein 250	Cep250	1.043	1.519	0.171271	0.423203
6120	10534441	NM_148932	107939	nuclear pore membrane protein	Pom121	1.043	0.284	0.784197	0.912068
6121	10530434	NM_178599	27784	COMM domain containing 8	Commd8	1.043	0.269	0.79548	0.916955
6122	10513404	ENSMUST00000098053	100038512	predicted gene, OTTMUSG0000000	OTTMUSG00000007406	1.043	0.535	0.608836	0.817918
6123	10400649	NM_011133	18974	polymerase (DNA directed), eps	Pole2	1.043	0.807	0.445347	0.703573
6124	10571302	NM_026432	67887	transmembrane protein 66	Tmem66	1.043	0.759	0.471976	0.723883
6125	10511099	NM_177186	320541	RIKEN cDNA A530082C11 gene	A530082C11Rik	1.043	0.204	0.843846	0.936634

6126	10374564	NM_009837	12464	chaperonin subunit 4 (delta)	Cct4	1.043	0.603	0.564826	0.790905
6127	10383518	NM_001001333	238023	hexosaminidase (glycosyl hydro	Hexdc	1.043	0.715	0.496871	0.741257
6128	10520379	NM_028234	381626	proline rich 8	Prr8	1.043	0.642	0.540926	0.773315
6129	10600372	ENSMUST00000056152	320703	RIKEN cDNA B230340J04 gene	B230340J04Rik	1.043	0.314	0.76268	0.901202
6130	10531484	NM_175270	78088	ankyrin repeat domain 56	Ankrd56	1.043	0.973	0.361983	0.633538
6131	10400321	NM_134054	104725	RIKEN cDNA 1110002B05 gene	1110002B05Rik	1.043	0.548	0.599958	0.812084
6132	10573346					1.043	1.246	0.251676	0.525573
6133	10407782	NM_133643	171211	EDAR (ectodysplasin-A receptor	Edaradd	1.043	0.945	0.375269	0.645306
6134	10576328	NM_008559	17199	melanocortin 1 receptor	Mc1r	1.043	0.705	0.503062	0.745637
6135	10447130	BC086639	106522	expressed sequence AW548124	AW548124	1.043	0.363	0.727025	0.881688
6136	10597420	NM_009916	12773	chemokine (C-C motif) receptor	Ccr4	1.043	0.723	0.492741	0.738692
6137	10378774	NM_019818	56322	translocase of inner mitochond	Timm22	1.043	-0.687	0.513337	0.753698
6138	10484503	NM_001033346	241528	leucine rich repeat containing	Lrrc55	1.043	0.239	0.817864	0.927532
6139	10600763	XM_894481	629581	predicted gene, EG629581	EG629581	1.043	0.989	0.354667	0.627276
6140	10570418	NM_025924	67031	UPF3 regulator of nonsense tra	Upf3a	1.043	0.373	0.719771	0.878026
6141	10465521	NM_008874	18797	phospholipase C, beta 3	Plcb3	1.043	0.691	0.51144	0.752366
6142	10570599	NM_153115	78128	sperm associated antigen 11	Spag11	1.043	1.3	0.233649	0.505065
6143	10486562					1.043	0.267	0.797019	0.917479
6144	10510270	NM_010840	17769	5,10-methylenetetrahydrofolate	Mthfr	1.043	0.477	0.647738	0.841423
6145	10502071	BC116791	70617	RIKEN cDNA 5730508B09 gene	5730508B09Rik	1.043	0.424	0.683779	0.860022
6146	10460879	NM_008583	17283	multiple endocrine neoplasia 1	Men1	1.043	0.087	0.933003	0.97328
6147	10535508	BC048077	231874	expressed sequence AU022870	AU022870	1.043	0.492	0.637519	0.83564
6148	10519209					1.043	0.718	0.495296	0.740179
6149	10374354					1.043	0.935	0.380099	0.649755
6150	10468722	NM_010279	14585	glial cell line derived neurot	Gfra1	1.043	0.248	0.810922	0.923749
6151	10400546	NM_001033156	70611	F-box protein 33	Fbxo33	1.043	0.444	0.66978	0.853123
6152	10363962	NM_010311	14687	guanine nucleotide binding pro	Gnaz	1.043	0.504	0.629055	0.831244
6153	10604046	NM_029951	77644	RIKEN cDNA C330007P06 gene	C330007P06Rik	1.043	0.306	0.768612	0.903817
6154	10552462	NM_174866	317653	kallikrein related-peptidase 1	Klk14	1.043	1.052	0.326877	0.602991
6155	10528925	AK132123	433868	predicted gene, ENSMUSG0000007	ENSMUSG00000073106	1.043	0.862	0.41662	0.679566
6156	10416531					1.043	1.478	0.181669	0.437894
6157	10407053	BC004049	75616	RIKEN cDNA 2810008M24 gene	2810008M24Rik	1.042	0.251	0.808556	0.922966
6158	10426065	NM_145476	223754	TBC1 domain family, member 22a	Tbc1d22a	1.042	0.289	0.780839	0.911
6159	10599498	NM_028276	72554	UTP14, U3 small nucleolar ribo	Utp14a	1.042	0.458	0.660169	0.848652
6160	10482929	NM_013825	17076	lymphocyte antigen 75	Ly75	1.042	0.014	0.989216	0.995336
6161	10442584	NM_025425	66211	ribosomal protein L3-like	Rpl3l	1.042	0.83	0.433372	0.693905
6162	10561204	NM_181593	233011	inositol 1,4,5-trisphosphate 3	Itpkc	1.042	0.453	0.66414	0.850267
6163	10555753	NM_146360	258357	olfactory receptor 574	Olfr574	1.042	1.378	0.209437	0.474615
6164	10380280	NM_001033266	217071	gene model 525, (NCBI)	Gm525	1.042	0.475	0.649148	0.842371
6165	10576659					1.042	0.488	0.639872	0.836701
6166	10550915	NM_153112	260299	cell adhesion molecule 4	Cadm4	1.042	0.659	0.530613	0.765382
6167	10540233	NM_182808	320265	RIKEN cDNA C630007B19 gene	C630007B19Rik	1.042	0.617	0.555932	0.784531
6168	10352920	NM_001011874	497097	X Kell blood group precursor r	Xkr4	1.042	0.376	0.717928	0.876841
6169	10521385	NM_010445	15371	H6 homeo box 1	Hmx1	1.042	0.987	0.355755	0.628276
6170	10372338	NM_203660	368203	predicted gene, EG368203	EG368203	1.042	0.758	0.472234	0.724017
6171	10350760					1.042	0.935	0.379918	0.6497
6172	10571889					1.042	2.1	0.0727145	0.254178
6173	10491484					1.042	0.554	0.596078	0.80968
6174	10555590	NM_133947	101706	nuclear mitotic apparatus prot	Numa1	1.042	0.244	0.814295	0.925272
6175	10430071	NM_058214	79456	RecQ protein-like 4	Recql4	1.042	0.643	0.539862	0.772463
6176	10407057	NM_028042	71991	excision repaiross-complementi	Ercc8	1.042	0.089	0.9316	0.972759

6177	10509256	BC028950	242707	cDNA sequence BC029684	BC029684	1.042	0.357	0.73157	0.884308
6178	10379344	ENSMUST00000100735	100038730	predicted gene, ENSMUSG0000007	ENSMUSG00000072632	1.042	0.8	0.44904	0.706541
6179	10592942	NM_001081049	214162	myeloid/lymphoid or mixed-line	Mll1	1.042	0.767	0.46733	0.720101
6180	10536176	NM_024260	73288	coiled-coil domain containing	Ccdc132	1.042	0.073	0.943773	0.977948
6181	10383023	ENSMUST00000080727	791367	predicted gene, ENSMUSG0000006	ENSMUSG00000061395	1.042	0.729	0.488954	0.736349
6182	10577065	XR_032000	665373	similar to ribosomal protein L	LOC665373	1.042	0.205	0.842912	0.936352
6183	10503992	BC148227	320500	RIKEN cDNA A930001M12 gene	A930001M12Rik	1.042	0.767	0.46723	0.72007
6184	10441280	BC046433	114604	PR domain containing 15	Prdm15	1.042	0.476	0.648065	0.84174
6185	10509930	NM_172518	213499	F-box protein 42	Fbxo42	1.042	0.145	0.888384	0.956025
6186	10361215	NM_153137	215243	TRAF3 interacting protein 3	Traf3ip3	1.042	0.563	0.590771	0.806356
6187	10382523	NM_001033775	432613	RIKEN cDNA 4933422H20 gene	4933422H20Rik	1.042	0.29	0.780202	0.910759
6188	10454353	NM_026779	68591	molybdenum cofactor sulfurase	Mocos	1.042	0.405	0.697134	0.867224
6189	10596912	NM_030075	78267	kelch domain containing 8B	Klhdc8b	1.042	0.815	0.441355	0.700287
6190	10541216	BC010717	214899	jumonji, AT rich interactive d	Jarid1a	1.042	0.31	0.765661	0.902563
6191	10459262	NM_198649	319713	actin binding LIM protein fami	Ablim3	1.042	0.532	0.610389	0.818705
6192	10477924	NM_173396	228839	TGFB-induced factor 2	Tgif2	1.042	0.382	0.713757	0.874677
6193	10444459	NM_031176	81877	tenascin XB	Tnxb	1.042	0.981	0.358536	0.630584
6194	10377927	NM_027445	70510	ring finger protein 167	Rnf167	1.042	0.62	0.554174	0.783409
6195	10495059	NM_153091	229681	suppression of tumorigenicity	St7l	1.042	0.511	0.624877	0.828987
6196	10554223	NM_026498	67994	mitochondrial ribosomal protei	Mrps11	1.042	0.297	0.77485	0.907674
6197	10552832	NM_025533	66394	nitric oxide synthase interact	Nosip	1.042	0.449	0.666416	0.851355
6198	10451083	NM_152810	71702	cell division cycle 5-like (S.	Cdc5l	1.042	0.397	0.702706	0.869626
6199	10367076	NM_008921	19075	DNA primase, p49 subunit	Prim1	1.042	0.364	0.726263	0.881516
6200	10510260	NM_008726	18158	natriuretic peptide precursor	Nppb	1.041	0.711	0.499237	0.742535
6201	10585555	NM_011193	19200	proline-serine-threonine phosp	Pstpip1	1.041	0.878	0.408207	0.672667
6202	10487847	BC071212	67326	RIKEN cDNA 1700037H04 gene	1700037H04Rik	1.041	0.242	0.815485	0.926126
6203	10535883	NM_153572	231912	katanin p60 subunit A-like 1	Katnal1	1.041	0.586	0.575491	0.797076
6204	10504918	NM_145547	230162	zinc finger protein 189	Zfp189	1.041	0.08	0.938194	0.975903
6205	10496771	NM_026656	68279	mucolipin 2	Mcoln2	1.041	0.816	0.44087	0.699832
6206	10563659	NM_175318	101685	SPT2, Suppressor of Ty, domain	Spty2d1	1.041	0.923	0.386029	0.655019
6207	10453939	ENSMUST00000092070	16774	laminin, alpha 3	Lama3	1.041	0.996	0.351525	0.624753
6208	10412741	NM_139227	246103	ataxin 7	Atxn7	1.041	0.707	0.501522	0.744504
6209	10491231	NM_030557	80732	myoneurin	Mynn	1.041	0.608	0.561909	0.788974
6210	10554967	ENSMUST00000068485	791297	predicted gene, ENSMUSG0000005	ENSMUSG00000055099	1.041	0.773	0.463922	0.717953
6211	10583228	BC043120	72826	RIKEN cDNA 2810485I05 gene	2810485I05Rik	1.041	0.765	0.468666	0.720927
6212	10369877	NM_145420	216080	ubiquitin-conjugating enzyme E	Ube2d1	1.041	0.94	0.377638	0.647469
6213	10515590	NM_172382	230674	jumonji domain containing 2A	Jmjd2a	1.041	0.518	0.620188	0.825285
6214	10569504	NM_024290	79201	tumor necrosis factor receptor	Tnfrsf23	1.041	0.183	0.859946	0.943624
6215	10369704	NM_001079824	432467	heterogeneous nuclear ribonucl	Hnrph3	1.041	0.973	0.36195	0.633538
6216	10517715	NM_011039	18509	paired box gene 7	Pax7	1.041	1.034	0.334411	0.60995
6217	10357954	NM_001081307	329251	protein phosphatase 1, regulat	Ppp1r12b	1.041	0.435	0.676237	0.855911
6218	10567524	AK016186	75838	RIKEN cDNA 4930560O18 gene	4930560O18Rik	1.041	0.397	0.702993	0.869729
6219	10555671	NM_145583	233575	FGF receptor activating protei	Frag1	1.041	1.342	0.220236	0.488992
6220	10489915	BC130272	69553	RIKEN cDNA 2310033K02 gene	2310033K02Rik	1.041	0.817	0.440231	0.699184
6221	10570556	NM_173189	244329	microcephaly, primary autosoma	Mcph1	1.041	0.208	0.84105	0.935759
6222	10566702	NM_001011846	258136	olfactory receptor 517	Olfr517	1.041	0.512	0.624164	0.828379
6223	10373861	NM_027859	71673	ring finger protein 215	Rnf215	1.041	0.478	0.64662	0.840625
6224	10373021	NM_001033262	216438	membrane-associated ring finge	March9	1.041	1.091	0.310372	0.587004
6225	10408064	NM_146542	218066	olfactory receptor 11	Olfr11	1.041	0.38	0.714605	0.875126
6226	10504912					1.041	1.05	0.327455	0.603741

6227	10347297	NM_029711	76709	actin related protein 2/3 comp	Arpc2	1.041	0.868	0.413188	0.676771
6228	10544108	NM_001033171	74253	killer cell lectin-like recept	Klrg2	1.041	0.8	0.449407	0.706889
6229	10539727	BC026926	232196	expressed sequence C87436	C87436	1.041	0.334	0.74806	0.893211
6230	10459604	NM_153794	108654	RIKEN cDNA 4933403F05 gene	4933403F05Rik	1.041	0.526	0.614357	0.821474
6231	10347188	BC094541	320460	RIKEN cDNA A830006F12 gene	A830006F12Rik	1.041	0.892	0.401147	0.666661
6232	10532563	AK077135	74376	myosin XVIIIb	Myo18b	1.041	0.612	0.559232	0.786667
6233	10385837	NM_008355	16163	interleukin 13	Il13	1.041	1.386	0.207133	0.471587
6234	10366825	NM_001033263	216439	centaurin, gamma 1	Centg1	1.041	0.624	0.551839	0.781834
6235	10476136	NM_030559	80743	vacuolar protein sorting 16 (y	Vps16	1.041	0.847	0.424235	0.686411
6236	10571106	NM_199042	73754	THAP domain containing, apopto	Thap1	1.041	-0.026	0.98009	0.991919
6237	10579181	NM_011266	19727	regulatory factor X-associated	Rfxank	1.041	0.797	0.450728	0.708038
6238	10444752	NM_008518	16994	lymphotoxin B	Ltb	1.041	0.226	0.827487	0.930659
6239	10353754	NM_133817	98403	zinc finger protein 451	Zfp451	1.041	0.42	0.686434	0.861515
6240	10577179	NM_025601	66501	RIKEN cDNA 1700029H14 gene	1700029H14Rik	1.041	1.077	0.316108	0.59306
6241	10439049	NM_024464	72084	phosphatidylinositol glycan an	Pigx	1.041	0.226	0.827445	0.930659
6242	10465838					1.041	0.586	0.575679	0.797076
6243	10562280	NM_020563	57426	androgen-binding protein eta	Apbh	1.04	1.26	0.247021	0.520325
6244	10448269	NM_011747	22654	zinc finger protein 13	Zfp13	1.04	0.89	0.40225	0.667397
6245	10545425	BC100525	71130	SH2 domain containing 6	Sh2d6	1.04	0.736	0.485257	0.733662
6246	10435697	NM_001081984	64082	popeye domain containing 2	Popdc2	1.04	1.323	0.226172	0.496799
6247	10386110	NM_008213	15110	heart and neural crest derivat	Hand1	1.04	0.461	0.658275	0.847092
6248	10547793					1.04	0.04	0.969236	0.987586
6249	10444591	NM_013558	15482	heat shock protein 1-like	Hspa1l	1.04	-0.389	0.708469	0.872343
6250	10390707	NM_011623	21973	topoisomerase (DNA) II alpha	Top2a	1.04	0.707	0.501587	0.744504
6251	10424437					1.04	1.069	0.319543	0.596487
6252	10492558	NM_133786	70099	structural maintenance of chro	Smc4	1.04	0.684	0.515135	0.754817
6253	10539486	NM_008717	18139	zinc finger, matrin-like	Zfml	1.04	0.399	0.701101	0.86904
6254	10520815	NM_009206	20534	solute carrier family 4 (anion	Slc4a1ap	1.04	0.404	0.698151	0.867722
6255	10496890	AK052598	100036544	predicted gene, ENSMUSG0000005	ENSMUSG00000054747	1.04	0.667	0.525772	0.761851
6256	10419368					1.04	1.06	0.323527	0.600004
6257	10353786	NM_009356	21756	testicular serine protease 2	Tesp2	1.04	0.927	0.384094	0.653466
6258	10576073	NM_001110100	53325	Btg3 associated nuclear protei	Banp	1.04	0.872	0.411143	0.675147
6259	10378570					1.04	0.188	0.855875	0.941748
6260	10399575					1.04	0.308	0.766748	0.902924
6261	10474361	ENSMUST00000016530	77015	metallophosphoesterase domain	Mpped2	1.04	0.042	0.968011	0.987153
6262	10560614	NM_007385	11425	apolipoprotein C-IV	Apoc4	1.04	0.821	0.437719	0.696922
6263	10467211	NM_028263	72514	fibroblast growth factor bindi	Fgfbp3	1.04	0.976	0.360747	0.632458
6264	10486845	NM_001025371	574418	serine incorporator 4	RP23-433P19.11	1.04	0.571	0.585587	0.80308
6265	10373918	NM_008501	16878	leukemia inhibitory factor	Lif	1.04	0.653	0.533721	0.767706
6266	10479625	BC050777	241850	cDNA sequence BC050777	BC050777	1.04	0.537	0.60767	0.817428
6267	10554789	NM_009982	13032	cathepsin C	Ctsc	1.04	-0.212	0.838185	0.934421
6268	10371676	AB052760	70683	UTP20, small subunit (SSU) pro	Utp20	1.04	0.117	0.909901	0.964056
6269	10510365	NM_016699	50912	exosome component 10	Exosc10	1.04	0.236	0.820117	0.928345
6270	10381238	NM_011550	21428	MAX-like protein X	Mlx	1.04	0.437	0.675224	0.855723
6271	10503947	NM_009889	12640	glycoprotein hormones, alpha s	Cga	1.04	0.566	0.588412	0.805111
6272	10585015	NM_080434	66113	apolipoprotein A-V	Apoa5	1.04	1.05	0.327606	0.603915
6273	10604199	NM_001110142	72584	cullin 4B	Cul4b	1.04	-0.261	0.801498	0.919489
6274	10476497	NM_175667	319196	ankyrin repeat domain 5	Ankrd5	1.04	0.877	0.408947	0.673268
6275	10452709	NM_023294	67052	NDC80 homolog, kinetochore com	Ndc80	1.04	0.408	0.695004	0.866071
6276	10348817	NM_010891	18000	septin 2	Sept2	1.04	0.336	0.746118	0.892253
6277	10529330	NM_011914	24116	Wolf-Hirschhorn syndrome candi	Whsc2	1.04	0.619	0.555117	0.783898
6278	10402428	NM_026535	68054	serine (or cysteine) peptidase	Serpina12	1.04	0.473	0.650209	0.843126

6279	10531610	NM_145839	320292	RasGEF domain family, member 1	Rasgef1b	1.04	0.153	0.882386	0.953551
6280	10357579	NM_008551	17164	MAP kinase-activated protein k	Mapkapk2	1.04	0.007	0.994261	0.997705
6281	10572580	NM_025917	67023	unconventional SNARE in the ER	Use1	1.04	0.308	0.76661	0.902924
6282	10459518	NM_172630	225651	metallophosphoesterase 1	Mppe1	1.04	0.621	0.553685	0.78319
6283	10547807	NM_013509	13807	enolase 2, gamma neuronal	Eno2	1.04	0.659	0.530587	0.765382
6284	10567466	XM_355934	381917	dynein, axonemal, heavy chain	Dnahc3	1.04	0.997	0.351195	0.624551
6285	10409414	NM_009000	19336	RAB24, member RAS oncogene fam	Rab24	1.04	0.684	0.51534	0.754909
6286	10586242	XM_001476259	102442	DENN/MADD domain containing 4A	Dennd4a	1.04	0.763	0.469609	0.721727
6287	10436239	ENSMUST00000050248	271377	zinc finger and BTB domain con	Zbtb11	1.04	0.894	0.400034	0.665979
6288	10485681	NM_008045	14308	follicle stimulating hormone b	Fshb	1.04	0.964	0.366471	0.637434
6289	10528723	NM_001081383	231051	myeloid/lymphoid or mixed-line	Mll3	1.04	0.356	0.732184	0.884722
6290	10417972	NM_178597	12325	calcium/calmodulin-dependent p	Camk2g	1.04	0.633	0.546476	0.777695
6291	10485982	NM_009608	11464	actin, alpha, cardiac	Actc1	1.04	0.45	0.665905	0.851154
6292	10596281	ENSMUST00000060084	235567	DnaJ (Hsp40) homolog, subfamil	Dnajc13	1.04	0.148	0.886734	0.955515
6293	10466794	BC028637	68034	RIKEN cDNA 2900009I07 gene	2900009I07Rik	1.04	0.071	0.945013	0.978279
6294	10362005	NM_026203	52906	Abelson helper integration sit	Ahi1	1.04	0.41	0.693886	0.865705
6295	10454059					1.04	0.173	0.867127	0.946934
6296	10372682	NM_029875	215436	solute carrier family 35, memb	Slc35e3	1.04	0.14	0.892449	0.957747
6297	10423951					1.04	0.034	0.974164	0.988991
6298	10472989	NM_010467	15429	homeo box D1	Hoxd1	1.04	0.482	0.644311	0.839081
6299	10533256	NM_145211	246730	2'-5' oligoadenylate synthetas	Oas1a	1.039	0.386	0.710303	0.873031
6300	10364583	NM_130455	170483	glutamate receptor, ionotropic	Grin3b	1.039	0.565	0.58931	0.80561
6301	10540599	NM_170673	211232	copine family member IX	Cpne9	1.039	0.827	0.434632	0.695096
6302	10559181	NM_015809	50775	keratin associated protein 5-4	Krtap5-4	1.039	1.252	0.24955	0.523619
6303	10412078	BC118005	238875	RIKEN cDNA 9830130M13 gene	9830130M13Rik	1.039	0.953	0.371211	0.641982
6304	10469276	ENSMUST00000100409	100038528	predicted gene, ENSMUSG0000007	ENSMUSG00000075530	1.039	1.225	0.25908	0.533309
6305	10538174	NM_001029987	243376	diamine oxidase-like protein 2	Doxl2	1.039	1.125	0.296592	0.57323
6306	10441620	NM_201230	75296	Fgfr1 oncogene partner	Fgfr1op	1.039	0.436	0.675336	0.855766
6307	10588073	XM_887600	623166	predicted gene, EG623166	EG623166	1.039	0.134	0.897232	0.95959
6308	10527465	NM_016683	22757	zinc finger with KRAB and SCAN	Zkscan5	1.039	0.016	0.987837	0.994998
6309	10560551	NM_016680	53609	splicing factor, arginine/seri	Sfrs16	1.039	0.553	0.596915	0.810212
6310	10392449	NM_145940	52639	WD repeat domain, phosphoinosi	Wipi1	1.039	0.488	0.64002	0.836826
6311	10583809	NM_009922	12797	calponin 1	Cnn1	1.039	0.05	0.961449	0.985172
6312	10528840	NM_018878	55982	PAX interacting (with transcri	Paxip1	1.039	0.638	0.543196	0.775617
6313	10561345	NM_001081021	338354	zinc finger protein 780B	Zfp780b	1.039	0.321	0.757174	0.898087
6314	10368508	NM_001109747	66311	RIKEN cDNA 2610036L11 gene	2610036L11Rik	1.039	0.208	0.841332	0.935777
6315	10409044	ENSMUST00000061899	70971	RIKEN cDNA 4931429P17 gene	4931429P17Rik	1.039	0.785	0.457465	0.713059
6316	10600736	XM_908024	236891	predicted gene, EG236891	EG236891	1.039	0.493	0.636823	0.834986
6317	10485828	ENSMUST00000099590	100038351	predicted gene, ENSMUSG0000007	ENSMUSG00000074940	1.039	0.591	0.572508	0.796254
6318	10464445	XR_034247	433261	similar to Sid393p	LOC433261	1.039	0.226	0.827685	0.93066
6319	10454912	NM_175375	108857	ankyrin repeat and KH domain c	Ankhd1	1.039	0.829	0.433793	0.694279
6320	10479172					1.039	0.722	0.493146	0.738933
6321	10477176					1.039	0.577	0.581307	0.80031
6322	10397201	NM_144833	52708	zinc finger protein 410	Zfp410	1.039	0.594	0.570705	0.795023
6323	10532921					1.039	0.755	0.47406	0.725639
6324	10533182	NM_008052	14357	deltex 1 homolog (Drosophila)	Dtx1	1.039	0.459	0.659459	0.848254
6325	10405833					1.039	0.668	0.524775	0.761136
6326	10589190					1.039	0.644	0.539206	0.772081
6327	10441919	NM_001083881	67912	RIKEN cDNA 1600012H06 gene	1600012H06Rik	1.039	0.518	0.620287	0.825285

6328	10381416	NM_009708	11858	Rho family GTPase 2	Rnd2	1.039	0.075	0.942157	0.977764
6329	10507576	NM_001011856	258159	olfactory receptor 1331	Olfr1331	1.039	0.823	0.43694	0.696363
6330	10356498	ENSMUST00000092611	74918	IQ motif containing with AAA d	Iqca	1.039	0.447	0.667937	0.851904
6331	10558919					1.039	0.249	0.81016	0.923433
6332	10357965	NM_001033409	329252	leucine-rich repeat-containing	Lgr6	1.039	1.062	0.322503	0.599294
6333	10366938	NM_177707	237611	SH3 and cysteine rich domain 3	Stac3	1.039	0.73	0.488169	0.735812
6334	10550931	NM_153134	210146	immunity-related GTPase family	Irgq	1.039	1.005	0.347268	0.621483
6335	10415818	NM_175546	268752	WD repeat and FYVE domain cont	Wdfy2	1.039	0.105	0.918884	0.967815
6336	10527340	NM_001081362	100683	transformation/transcription d	Trrap	1.039	0.503	0.629675	0.831325
6337	10548681					1.039	0.697	0.5074	0.749352
6338	10590191	NM_026236	67561	WD repeat domain 48	Wdr48	1.039	0.556	0.594889	0.809052
6339	10380999	NM_009971	12985	colony stimulating factor 3 (g	Csf3	1.039	0.467	0.65443	0.845176
6340	10515574	NM_009176	20441	ST3 beta-galactoside alpha-2,3	St3gal3	1.039	0.462	0.657999	0.847091
6341	10540391	NM_027296	70047	tRNA nucleotidyl transferase,	Trnt1	1.039	-0.279	0.788311	0.913849
6342	10464618	NM_021485	58988	ribosomal protein S6 kinase, p	Rps6kb2	1.039	0.329	0.751468	0.895256
6343	10587621	NM_001037907	382089	ripply2 homolog (zebrafish)	Ripply2	1.039	0.939	0.378017	0.647713
6344	10592772	NM_138955	192663	ATP-binding cassette, sub-fami	Abcg4	1.039	0.859	0.417938	0.680624
6345	10445629	NM_178385	72726	tubulin-specific chaperone c	Tbcc	1.039	-0.296	0.77578	0.908358
6346	10351390	NM_030245	27878	transcriptional adaptor 1 (HFI	Tada1l	1.039	0.479	0.645816	0.840161
6347	10393881	NM_010756	17134	v-maf musculoaponeurotic fibro	Mafg	1.039	0.721	0.493372	0.739056
6348	10376060	NM_008390	16362	interferon regulatory factor 1	Irf1	1.039	1.057	0.324671	0.601113
6349	10481011	NM_033134	64436	inositol polyphosphate-5-phosp	Inpp5e	1.039	0.596	0.569448	0.794081
6350	10588577	NM_009895	12700	cytokine inducible SH2-contain	Cish	1.039	0.594	0.570492	0.794944
6351	10367215	NM_133996	28194	apolipoprotein N	Apon	1.039	0.479	0.645891	0.840161
6352	10488617	NM_001009948	228777	neurensin 2	Nrsn2	1.039	0.949	0.373518	0.643657
6353	10555793	NM_146756	258751	olfactory receptor 608	Olfr608	1.039	0.95	0.372979	0.643356
6354	10395553	NM_176930	319504	neuron-glia-CAM-related cell a	Nrcam	1.039	0.307	0.76722	0.903106
6355	10510884	ENSMUST00000071251	230971	multiple EGF-like-domains 6	Megf6	1.039	0.275	0.790694	0.914692
6356	10577858	NM_026121	67384	BCL2-associated athanogene 4	Bag4	1.039	0.064	0.951027	0.981095
6357	10516637	NM_182783	230766	cDNA sequence BC030183	BC030183	1.039	1.154	0.285237	0.560506
6358	10504402	NM_001085508	242409	RIKEN cDNA 4930500O05 gene	4930500O05Rik	1.039	0.402	0.699623	0.868422
6359	10597309	NM_016853	20840	src homology three (SH3) and c	Stac	1.039	1.286	0.238042	0.51041
6360	10454741	NM_001081256	277250	jumonji domain containing 1B	Jmjd1b	1.039	0.815	0.4413	0.700287
6361	10480971	NM_172339	227644	small nuclear RNA activating c	Snapc4	1.039	0.78	0.460144	0.714915
6362	10597173	NM_026012	67169	neurotrophin receptor associat	Nradd	1.039	0.842	0.426712	0.68818
6363	10463462	NM_053197	94280	sideroflexin 3	Sfxn3	1.039	0.486	0.641367	0.837465
6364	10385428	NM_010583	16428	IL2-inducible T-cell kinase	Itk	1.039	0.337	0.74585	0.891987
6365	10511952	NM_015824	50793	origin recognition complex, su	Orc3l	1.039	0.286	0.783248	0.911971
6366	10584870	NM_001013373	214531	transmembrane protease, serine	Tmprss13	1.039	0.817	0.439923	0.699115
6367	10458247	NM_178005	107065	leucine rich repeat transmembr	Lrrtm2	1.039	0.426	0.682855	0.859827
6368	10572906	NM_008566	17218	minichromosome maintenance def	Mcm5	1.039	0.051	0.960974	0.985069
6369	10537797					1.039	0.606	0.563024	0.789853
6370	10455863	ENSMUST00000091892	629147	cortexin 3	Ctxn3	1.038	0.583	0.577495	0.797771
6371	10566620	NM_147035	259037	olfactory receptor 711	Olfr711	1.038	0.456	0.661665	0.84929
6372	10431839	NM_207533	223843	developing brain homeobox 2	Dbx2	1.038	0.712	0.498888	0.742429
6373	10383345	NM_172802	238021	fascin homolog 2, actin-bundli	Fscn2	1.038	0.168	0.871179	0.948575
6374	10436873	NM_178880	20658	Son cell proliferation protein	Son	1.038	0.619	0.55507	0.783898
6375	10368380	NM_172787	237339	l(3)mbt-like 3 (Drosophila)	L3mbtl3	1.038	0.49	0.638532	0.835923
6376	10544829	NM_173406	231986	JAZF zinc finger 1	Jazf1	1.038	0.913	0.390895	0.659256
6377	10477423	NM_001034875	381399	gene model 1006, (NCBI)	Gm1006	1.038	0.642	0.540496	0.772962
6378	10380732	NM_026154	107732	mitochondrial ribosomal protei	Mrpl10	1.038	0.508	0.626335	0.82988
6379	10475525	NM_019788	18457	pallidin	Pldn	1.038	0.327	0.753031	0.895959
6380	10569456					1.038	1.258	0.247698	0.520853
6381	10533034	NM_177759	269693	coiled-coil domain containing	Ccdc60	1.038	0.218	0.833653	0.932929

6382	10413282	BC025603	211922	RIKEN cDNA A630054L15 gene	A630054L15Rik	1.038	0.404	0.697589	0.86736
6383	10544801	NM_010450	15396	homeo box A11	Hoxa11	1.038	0.034	0.973994	0.988867
6384	10350343	NM_177397	338375	ATPase, H+ transporting, lysos	Atp6v1g3	1.038	0.382	0.713295	0.874568
6385	10523974	ENSMUST00000100944	100038441	predicted gene, ENSMUSG0000007	ENSMUSG00000072769	1.038	0.903	0.395726	0.663394
6386	10489904	NM_170756	263876	spermatogenesis associated 2	Spata2	1.038	0.366	0.724989	0.880785
6387	10545210	ENSMUST00000103359	385253	gene model 1524, (NCBI)	Gm1524	1.038	1.052	0.326715	0.602834
6388	10505109	BC026590	230234	cDNA sequence BC026590	BC026590	1.038	0.265	0.798508	0.918438
6389	10526520	NM_011962	26433	procollagen-lysine, 2-oxogluta	Plod3	1.038	0.115	0.911357	0.964566
6390	10377018	NM_001099635	17883	myosin, heavy polypeptide 3, s	Myh3	1.038	1.353	0.21708	0.484682
6391	10429442	ENSMUST00000110021	268816	gene model 628, (NCBI)	Gm628	1.038	1.039	0.33243	0.608511
6392	10552262					1.038	0.338	0.744936	0.891598
6393	10399087	NM_133762	76044	non-SMC condensin II complex,	Ncapg2	1.038	0.619	0.554797	0.783816
6394	10377286	NM_001081566	104709	phosphoinositide-3-kinase, reg	Pik3r6	1.038	0.894	0.400213	0.666098
6395	10467001					1.038	0.614	0.557806	0.785788
6396	10394144	ENSMUST00000035629	74173	RIKEN cDNA 1700012B15 gene	1700012B15Rik	1.038	1.004	0.348041	0.622132
6397	10373778	NM_198162	74522	microrchidia 2A	Morc2a	1.038	0.154	0.882005	0.953432
6398	10380524	NM_016752	110172	solute carrier family 35, memb	Slc35b1	1.038	0.293	0.777695	0.909562
6399	10366238	NM_027892	17931	protein phosphatase 1, regulat	Ppp1r12a	1.038	0.55	0.598685	0.811605
6400	10515819					1.038	0.638	0.543031	0.775486
6401	10589610	NM_153099	235628	testis serine protease 2	Tessp2	1.038	0.318	0.759277	0.899156
6402	10371578	NM_008553	17172	achaete-scute complex homolog	Ascl1	1.038	0.247	0.811579	0.923946
6403	10577808	NM_177089	320165	transforming, acidic coiled-co	Tacc1	1.038	0.499	0.632591	0.832846
6404	10534014					1.038	0.306	0.768311	0.903712
6405	10443244	NM_181413	224650	ankyrin repeat and SAM domain	Anks1	1.038	0.777	0.46167	0.716287
6406	10384092	NM_173748	209586	NudC domain containing 3	Nudcd3	1.038	1.02	0.340838	0.615921
6407	10391061	NM_008470	16666	keratin 16	Krt16	1.038	0.433	0.677614	0.856701
6408	10490203					1.038	0.353	0.73448	0.886559
6409	10493347	NM_138679	192195	ash1 (absent, small, or homeot	Ash1l	1.038	0.437	0.674966	0.855557
6410	10370914	BC005632	216169	DNA segment, Chr 10, Brigham &	D10Bwg1364e	1.038	0.402	0.699583	0.868422
6411	10603896	NM_026167	67455	kelch-like 13 (Drosophila)	Klhl13	1.038	-0.144	0.889067	0.95642
6412	10579219	NM_001024922	234374	DEAD (Asp-Glu-Ala-Asp) box pol	Ddx49	1.038	-0.156	0.880662	0.952661
6413	10472044					1.038	1.053	0.326333	0.602796
6414	10421325	NM_021308	57746	piwi-like homolog 2 (Drosophil	Piwil2	1.038	1.128	0.295354	0.571726
6415	10541114	BC145752	70727	RasGEF domain family, member 1	Rasgef1a	1.038	1.048	0.328311	0.604687
6416	10440302	NM_008310	15557	5-hydroxytryptamine (serotonin	Htr1f	1.038	1.009	0.345541	0.619665
6417	10528880	NM_020295	56873	limb region 1	Lmbr1	1.038	0.469	0.652897	0.844541
6418	10426292	NM_001033441	380959	asparagine-linked glycosylatio	Alg10b	1.038	-0.037	0.971473	0.988148
6419	10361089	NM_001109759	619288	RIKEN cDNA 4933417M04 gene	4933417M04Rik	1.038	0.404	0.697862	0.867567
6420	10521261	NM_010414	15194	huntingtin	Htt	1.038	0.841	0.427276	0.688539
6421	10345037	NM_028829	74229	progestin and adipoQ receptor	Paqr8	1.038	0.562	0.591016	0.806534
6422	10568252	NM_175163	71131	zinc finger protein 689	Zfp689	1.038	0.502	0.630741	0.831809
6423	10413598	NM_028839	69179	transmembrane protein 110	Tmem110	1.038	-0.179	0.862774	0.945192
6424	10511739	NM_027769	70568	copine III	Cpne3	1.037	-0.007	0.994586	0.997747
6425	10376555	AK144909	100038754	predicted gene, ENSMUSG0000007	ENSMUSG00000072890	1.037	0.48	0.645371	0.839892
6426	10395684	NM_029760	76826	nucleotide binding protein-lik	Nubpl	1.037	-0.383	0.712825	0.874143
6427	10404178	NM_024473	79555	cDNA sequence BC005537	BC005537	1.037	0.4	0.700626	0.86896
6428	10383799	NM_015749	21452	transcobalamin 2	Tcn2	1.037	0.037	0.971561	0.988148
6429	10591430	NM_027911	71766	ribonucleoprotein, PTB-binding	Raver1	1.037	0.957	0.369644	0.640215
6430	10391742	ENSMUST00000069673	100038535	predicted gene, ENSMUSG0000007	ENSMUSG00000075516	1.037	0.069	0.946672	0.978837
6431	10504690					1.037	0.409	0.694147	0.865705

6432	10561369	NM_175033	280621	cDNA sequence BC089491	BC089491	1.037	0.398	0.702255	0.869368
6433	10501622	NM_022427	64378	G-protein coupled receptor 88	Gpr88	1.037	0.624	0.551718	0.781715
6434	10481349	NM_133501	171171	netrin G2	Ntng2	1.037	0.753	0.475566	0.72707
6435	10408162	NM_001111107	218100	zinc finger protein 322a	Zfp322a	1.037	0.054	0.958682	0.984334
6436	10398195	NM_009832	12454	cyclin K	Ccnk	1.037	0.12	0.907817	0.963723
6437	10382470	NM_001033393	320534	transmembrane protein 104	Tmem104	1.037	0.331	0.750124	0.894442
6438	10407356	NM_008710	18115	nicotinamide nucleotide transh	Nnt	1.037	0.483	0.643656	0.838716
6439	10362210	NM_027347	70208	mediator complex subunit 23	Med23	1.037	0.274	0.791577	0.915198
6440	10461214	BC066781	66836	RIKEN cDNA 0610006I08 gene	0610006I08Rik	1.037	0.162	0.875461	0.950704
6441	10588464					1.037	0.412	0.692287	0.865004
6442	10386402	NM_172941	268417	zinc finger with KRAB and SCAN	Zkscan17	1.037	1.345	0.219356	0.488013
6443	10400989	NM_172805	238271	potassium voltage-gated channe	Kcnh5	1.037	0.488	0.640284	0.836929
6444	10426782	NM_009597	11419	amiloride-sensitive cation cha	Accn2	1.037	0.587	0.575113	0.797076
6445	10565890	NM_153527	69387	DnaJ (Hsp40) related, subfamil	Dnajb13	1.037	0.884	0.405186	0.669695
6446	10372687	NM_134010	103468	nucleoporin 107	Nup107	1.037	0.261	0.801693	0.919646
6447	10528901	AK147752	97236	expressed sequence C79130	C79130	1.037	0.756	0.473407	0.725045
6448	10456435					1.037	0.288	0.781479	0.911143
6449	10474642	BC052040	399568	cDNA sequence BC052040	BC052040	1.037	0.905	0.394505	0.662113
6450	10473097	NM_031256	83435	pleckstrin homology domain-con	Plekha3	1.037	-0.06	0.953571	0.982042
6451	10364744	NM_029272	75406	NADH dehydrogenase (ubiquinone	Ndufs7	1.037	-0.013	0.990123	0.995679
6452	10543904	NM_016877	53621	CCR4-NOT transcription complex	Cnot4	1.037	0.439	0.673802	0.855069
6453	10483631	XM_911155	383712	similar to putative translatio	LOC383712	1.037	0.2	0.846932	0.938058
6454	10380506	NM_053093	93670	tachykinin 4	Tac4	1.037	0.785	0.457368	0.713005
6455	10573939	NM_173014	270084	lysophosphatidylcholine acyltr	Lpcat2	1.037	0.764	0.469255	0.721467
6456	10515706	ENSMUST00000075406	230676	cDNA sequence BC059842	BC059842	1.037	1.277	0.241046	0.513985
6457	10451093	NM_027649	71020	spermatogenesis associated, se	Spats1	1.037	0.558	0.594027	0.808348
6458	10435237	NM_011749	22661	zinc finger protein 148	Zfp148	1.037	0.166	0.87277	0.949165
6459	10409848	NM_027344	70202	RIKEN cDNA 2310051M13 gene	2310051M13Rik	1.037	0.772	0.464844	0.718627
6460	10535653	NM_023322	67235	zinc finger with KRAB and SCAN	Zkscan14	1.037	0.407	0.695499	0.866211
6461	10360090	NM_008911	19044	protoporphyrinogen oxidase	Ppox	1.037	0.323	0.756215	0.897871
6462	10514335	NM_177348	230405	interferon epsilon 1	Ifne1	1.037	0.588	0.574454	0.797076
6463	10479458	BC059022	76425	RIKEN cDNA 2310003C23 gene	2310003C23Rik	1.037	0.505	0.62876	0.83101
6464	10512895	NM_007519	12012	bile acid-Coenzyme A: amino ac	Baat	1.037	0.903	0.395634	0.663394
6465	10455078	NM_053133	93879	protocadherin beta 8	Pcdhb8	1.037	0.527	0.614224	0.821474
6466	10442032	BC002059	213811	cDNA sequence BC002059	BC002059	1.037	-0.046	0.964542	0.985942
6467	10387985	NM_001045526	327957	RIKEN cDNA A430084P05 gene	A430084P05Rik	1.037	0.706	0.502549	0.745467
6468	10498477	BC125500	329659	RIKEN cDNA E130311K13 gene	E130311K13Rik	1.037	0.235	0.82045	0.928587
6469	10493245	NM_001029890	72640	mex3 homolog A (C. elegans)	Mex3a	1.037	0.399	0.701584	0.869143
6470	10345824	NM_010553	16174	interleukin 18 receptor access	Il18rap	1.037	0.832	0.431852	0.692274
6471	10450344	NM_013484	12263	complement component 2 (within	C2	1.037	0.593	0.571244	0.795362
6472	10476102					1.037	0.432	0.67837	0.857067
6473	10547022	NM_080639	110595	tissue inhibitor of metallopro	Timp4	1.037	1.278	0.2407	0.513714
6474	10522606	NM_027270	69940	exocyst complex component 1	Exoc1	1.036	0.131	0.899708	0.960245
6475	10455069	NM_053131	93877	protocadherin beta 6	Pcdhb6	1.036	0.895	0.399444	0.665621
6476	10498158	ENSMUST00000099099	100038482	predicted gene, ENSMUSG0000007	ENSMUSG00000074598	1.036	-0.328	0.752456	0.895764
6477	10544858	ENSMUST00000046683	378878	RIKEN cDNA 9130019P16 gene	9130019P16Rik	1.036	0.878	0.408214	0.672667
6478	10357660	NM_001114662	213006	major facilitator superfamily	Mfsd4	1.036	0.864	0.415492	0.678653
6479	10466620	XM_891145	626549	predicted gene, EG626549	EG626549	1.036	0.471	0.651352	0.843859
6480	10514219					1.036	0.231	0.823491	0.929428

6481	10525460	ENSMUST00000071046	109202	RIKEN cDNA A930024E05 gene	A930024E05Rik	1.036	0.769	0.466196	0.719571
6482	10485989	NM_009702	11834	aquarius	Aqr	1.036	0.164	0.874384	0.949978
6483	10506332	NM_001085516	332923	novel protein similar to Prame	RP23-149D11.5	1.036	0.867	0.413723	0.677229
6484	10375175	NM_011412	20564	slit homolog 3 (Drosophila)	Slit3	1.036	0.569	0.58667	0.803716
6485	10379518	NM_013654	20306	chemokine (C-C motif) ligand 7	Ccl7	1.036	0.251	0.808576	0.922966
6486	10423593	NM_033521	114128	lysosomal-associated protein t	Laptm4b	1.036	-0.022	0.98314	0.992718
6487	10465185	NM_001114597	114601	EH domain binding protein 1-li	Ehbp1l1	1.036	0.828	0.434358	0.694762
6488	10487033	NM_010852	17876	myelin basic protein expressio	Myef2	1.036	0.605	0.563573	0.790198
6489	10384154	NM_178440	246177	myosin IG	Myo1g	1.036	0.885	0.404858	0.669594
6490	10433953	NM_023249	106369	yippee-like 1 (Drosophila)	Ypel1	1.036	0.674	0.52116	0.758676
6491	10598164	NM_027861	71678	RIKEN cDNA 0610010K06 gene	0610010K06Rik	1.036	0.185	0.858086	0.943002
6492	10477604	NM_008395	16396	itchy, E3 ubiquitin protein li	Itch	1.036	0.863	0.416014	0.67919
6493	10387180	NM_023668	83431	nuclear distribution gene E-li	Ndel1	1.036	0.55	0.599061	0.811784
6494	10607738	NM_181315	56078	carbonic anhydrase 5b, mitocho	Car5b	1.036	0.773	0.464039	0.717953
6495	10573232					1.036	0.468	0.653636	0.844772
6496	10516974	NM_146154	100336	protein phosphatase 1, regulat	Ppp1r8	1.036	0.101	0.92267	0.969147
6497	10573110					1.036	0.471	0.651709	0.844083
6498	10563362	NM_020011	56632	sphingosine kinase 2	Sphk2	1.036	0.686	0.514296	0.754529
6499	10497960	BC117739	73297	RIKEN cDNA 1700034I23 gene	1700034I23Rik	1.036	0.091	0.929672	0.972207
6500	10427744	NM_030690	75646	retinoic acid induced 14	Rai14	1.036	0.219	0.83282	0.932703
6501	10476882	ENSMUST00000063608	381384	RIKEN cDNA A530006G24 gene	A530006G24Rik	1.036	1.269	0.243958	0.517035
6502	10412646					1.036	0.379	0.715262	0.875355
6503	10525555	NM_133917	208104	MLX interacting protein	Mlxip	1.036	0.507	0.627485	0.83052
6504	10496569	NM_001083312	229900	guanylate binding protein 6	Gbp6	1.036	0.971	0.363093	0.634368
6505	10373502	NM_011772	22781	IKAROS family zinc finger 4	Ikzf4	1.036	0.336	0.746766	0.892467
6506	10361184	ENSMUST00000057543	320952	RIKEN cDNA A730013G03 gene	A730013G03Rik	1.036	0.886	0.404391	0.668997
6507	10363195	NM_008297	15500	heat shock factor 2	Hsf2	1.036	0.634	0.545772	0.777543
6508	10590494	NM_010620	209737	kinesin family member 15	Kif15	1.036	0.444	0.670325	0.853559
6509	10446109	ENSMUST00000095224	224903	scaffold attachment factor B	Safb	1.036	0.358	0.730449	0.883456
6510	10573916	NM_022428	64379	Iroquois related homeobox 6 (D	Irx6	1.036	0.783	0.458622	0.713672
6511	10607317	NM_175146	69499	TSR2, 20S rRNA accumulation, h	Tsr2	1.036	0.059	0.954711	0.982671
6512	10464298	NM_026925	69060	pancreatic lipase	Pnlip	1.036	0.582	0.578462	0.798316
6513	10598126	BC034362	78772	hedgehog interacting protein-l	Hhipl2	1.036	0.862	0.416439	0.67936
6514	10539813	ENSMUST00000089503	100043118	similar to coiled-coil domain	LOC100043118	1.036	0.846	0.424726	0.686726
6515	10378568					1.036	0.18	0.862413	0.944945
6516	10423078	ENSMUST00000100773	100038608	predicted gene, ENSMUSG0000007	ENSMUSG00000072658	1.036	0.703	0.504083	0.746397
6517	10480432	NM_025979	67121	microtubule associated serine/	Mastl	1.036	0.166	0.872887	0.949165
6518	10472949	NM_008274	15432	homeo box D12	Hoxd12	1.036	1.04	0.33203	0.608173
6519	10358698	NM_011277	19821	ring finger protein 2	Rnf2	1.036	-0.132	0.898239	0.960023
6520	10405779					1.036	0.578	0.580647	0.79961
6521	10385747	NM_199299	76901	PHD finger protein 15	Phf15	1.036	0.799	0.44998	0.707284
6522	10364824	NM_134002	103236	casein kinase 1, gamma 2	Csnk1g2	1.036	0.371	0.720958	0.878601
6523	10424188	NM_134092	105837	Mdm2, transformed 3T3 cell dou	Mtbp	1.036	0.254	0.806376	0.921832
6524	10545458	NM_001079822	21415	transcription factor 3	Tcf3	1.036	0.398	0.702356	0.869396
6525	10479463	NM_183161	228993	RIKEN cDNA 1700019H03 gene	1700019H03Rik	1.036	0.839	0.428183	0.689212
6526	10457665	AK076609	664619	Riken cDNA 4921533I20 gene	4921533I20Rik	1.035	0.72	0.494223	0.739551
6527	10497337	NM_009799	12346	carbonic anhydrase 1	Car1	1.035	0.151	0.883914	0.954252
6528	10474972	NM_026929	69065	ChaC, cation transport regulat	Chac1	1.035	0.635	0.54504	0.77708
6529	10596509	NM_026645	68265	IQ motif containing F3	Iqcf3	1.035	0.716	0.496483	0.741014
6530	10370497	NM_172134	216134	pyridoxal (pyridoxine, vitamin	Pdxk	1.035	0.855	0.420258	0.682515
6531	10401422	NM_027438	70481	paraneoplastic antigen MA1	Pnma1	1.035	1.103	0.305453	0.581741

6532	10559357	ENSMUST00000097928	100038412	predicted gene, ENSMUSG0000007	ENSMUSG00000073778	1.035	0.68	0.51768	0.756816
6533	10421128	NM_021475	58860	ADAM-like, decysin 1	Adamdec1	1.035	0.462	0.657711	0.846971
6534	10555568	BC092139	114641	ribosomal protein L31	Rpl31	1.035	0.141	0.891999	0.95769
6535	10425983					1.035	1.512	0.173043	0.425494
6536	10434233	NM_011672	22230	ubiquitin fusion degradation 1	Ufd1l	1.035	0.272	0.792926	0.915604
6537	10478289					1.035	0.522	0.617373	0.823029
6538	10367041	NM_153133	103142	retinol dehydrogenase 9	Rdh9	1.035	0.138	0.894392	0.958345
6539	10385325	NM_013917	30939	pituitary tumor-transforming 1	Pttg1	1.035	0.436	0.675885	0.855911
6540	10554321	ENSMUST00000098356	100038478	predicted gene, ENSMUSG0000007	ENSMUSG00000074057	1.035	0.994	0.352246	0.625281
6541	10364722	NM_007909	13637	ephrin A2	Efna2	1.035	0.058	0.955631	0.983063
6542	10560270	NM_008718	18142	neuronal PAS domain protein 1	Npas1	1.035	0.564	0.589585	0.805725
6543	10576608					1.035	0.8	0.44946	0.706889
6544	10465772	NM_008577	17254	solute carrier family 3 (activ	Slc3a2	1.035	-0.264	0.799077	0.918893
6545	10443221	NM_001080769	224648	UHRF1 (ICBP90) binding protein	Uhrf1bp1	1.035	0.583	0.577371	0.797771
6546	10566934	NM_053247	114332	lymphatic vessel endothelial h	Lyve1	1.035	0.652	0.534501	0.768432
6547	10424860	ENSMUST00000096385	223658	RIKEN cDNA D330001F17 gene	D330001F17Rik	1.035	0.649	0.536713	0.76984
6548	10350003	NM_028057	72017	cytochrome b5 reductase 1	Cyb5r1	1.035	0.572	0.584488	0.802234
6549	10490950	NM_021560	59058	basic helix-loop-helix domain	Bhlhb5	1.035	1.19	0.271839	0.546343
6550	10602062	NM_021463	19139	phosphoribosyl pyrophosphate s	Prps1	1.035	-0.221	0.831489	0.932333
6551	10494137	NM_175356	107650	phosphatidylinositol 4-kinase,	Pi4kb	1.035	0.335	0.747084	0.892497
6552	10530283					1.035	0.59	0.573343	0.796661
6553	10476928	AB017157	13013	cystatin 9	Cst9	1.035	0.267	0.796951	0.917479
6554	10419814	NM_199470	239096	cadherin-like 24	Cdh24	1.035	0.526	0.61454	0.821562
6555	10409053	NM_026450	67911	zinc finger protein 169	Zfp169	1.035	0.484	0.64296	0.838239
6556	10419542	NM_001033271	219024	transmembrane protein 55b	Tmem55b	1.035	0.27	0.794711	0.916664
6557	10354730					1.035	0.693	0.510184	0.751325
6558	10585037	NM_146000	215051	BUD13 homolog (yeast)	Bud13	1.035	0.287	0.782049	0.911385
6559	10361818	NM_008703	18101	neuromedin B receptor	Nmbr	1.035	0.749	0.477322	0.728069
6560	10576493					1.035	0.502	0.630376	0.831586
6561	10388304					1.035	0.327	0.753269	0.896091
6562	10464240	NM_028115	72133	TruB pseudouridine (psi) synth	Trub1	1.035	0.644	0.539632	0.772302
6563	10551021	NM_023133	20085	ribosomal protein S19	Rps19	1.035	0.6	0.567059	0.792621
6564	10459637					1.035	0.837	0.429195	0.690212
6565	10519211	NM_031872	83771	taste receptor, type 1, member	Tas1r3	1.035	0.575	0.583015	0.801097
6566	10396008	NM_177806	328110	PRP39 pre-mRNA processing fact	Prpf39	1.035	0.722	0.493243	0.739026
6567	10572591	NM_029865	77090	occludin/ELL domain containing	Ocel1	1.035	0.941	0.376913	0.647069
6568	10496727	NM_026993	69219	dimethylarginine dimethylamino	Ddah1	1.035	0.31	0.765337	0.902421
6569	10487433	NM_028141	72180	zinc finger protein 661	Zfp661	1.035	0.313	0.763353	0.901493
6570	10368877	NM_001034858	213402	armadillo repeat containing 2	Armc2	1.035	0.308	0.766566	0.902924
6571	10518492	NM_001083342	242748	patched domain containing 2	Ptchd2	1.035	0.555	0.595417	0.809458
6572	10399823					1.035	0.485	0.642048	0.837836
6573	10408952	NM_175749	218210	nucleoporin 153	Nup153	1.035	0.228	0.825701	0.929887
6574	10356628	NM_207225	208727	histone deacetylase 4	Hdac4	1.035	0.392	0.706327	0.871814
6575	10545372	NM_153778	71093	atonal homolog 8 (Drosophila)	Atoh8	1.035	0.71	0.499901	0.743052
6576	10449191	NM_015830	50817	small optic lobes homolog (Dro	Solh	1.035	0.089	0.931453	0.972759
6577	10517614	NM_001081672	625638	Likely orthologue of human fam	RP23-25C1.8	1.035	0.298	0.774425	0.907422
6578	10421934	NM_053105	93688	kelch-like 1 (Drosophila)	Klhl1	1.035	0.359	0.729839	0.883264
6579	10524572	NM_029992	77832	trichoplein, keratin filament	Tchp	1.034	0.581	0.578841	0.798528
6580	10445061	NM_001099632	386454	ring finger protein 39	Rnf39	1.034	0.83	0.433395	0.693905
6581	10502904	NM_031870	55993	mutS homolog 4 (E. coli)	Msh4	1.034	0.897	0.398808	0.665015
6582	10440050	NM_026254	67581	TBC1 domain family, member 23	Tbc1d23	1.034	0.325	0.754501	0.896702
6583	10560695	NM_001033419	330483	CEA-related cell adhesion mole	Ceacam16	1.034	0.467	0.654424	0.845176

6584	10369688	ENSMUST00000050826	52463	tet oncogene 1	Tet1	1.034	-0.179	0.863196	0.945375
6585	10380384	NM_027799	71452	ankyrin repeat domain 40	Ankrd40	1.034	0.966	0.365127	0.636272
6586	10464560	NM_026316	67689	aldehyde dehydrogenase 3 famil	Aldh3b1	1.034	0.87	0.412559	0.676183
6587	10352281	NM_133225	170760	acyl-Coenzyme A binding domain	Acbd3	1.034	0.629	0.548694	0.779152
6588	10383545	NM_001080932	68837	forkhead box K2	Foxk2	1.034	0.493	0.636543	0.834887
6589	10562251	NM_011322	20266	sodium channel, voltage-gated,	Scn1b	1.034	0.767	0.467527	0.720274
6590	10540639	NM_010957	18294	8-oxoguanine DNA-glycosylase 1	Ogg1	1.034	0.591	0.572499	0.796254
6591	10597833	NM_178677	215474	SEC22 vesicle trafficking prot	Sec22c	1.034	0.092	0.92896	0.972036
6592	10479063	NM_024436	19334	RAB22A, member RAS oncogene fa	Rab22a	1.034	0.044	0.966358	0.986657
6593	10475514	ENSMUST00000099458	214616	spermatogenesis associated 5-l	Spata5l1	1.034	-0.234	0.821324	0.92863
6594	10569569	NM_007803	13043	cortactin	Cttn	1.034	0.471	0.651412	0.843859
6595	10396094	NM_027117	69554	kelch domain containing 2	Klhdc2	1.034	0.057	0.956265	0.983332
6596	10409508	NM_134059	72935	DEAD (Asp-Glu-Ala-Asp) box pol	Ddx41	1.034	0.24	0.817249	0.927212
6597	10510874	ENSMUST00000071251	230971	multiple EGF-like-domains 6	Megf6	1.034	0.683	0.51618	0.755582
6598	10468059	NM_013907	30838	F-box and WD-40 domain protein	Fbxw4	1.034	0.712	0.499053	0.742429
6599	10557951	NM_146205	233912	armadillo repeat containing 5	Armc5	1.034	0.392	0.706459	0.871814
6600	10491182	NM_177586	208691	eukaryotic translation initiat	Eif5a2	1.034	0.68	0.517793	0.756834
6601	10480775	NM_001081199	381352	MAM domain containing 4	Mamdc4	1.034	0.864	0.415412	0.678575
6602	10450025	NM_145486	224703	membrane-associated ring finge	March2	1.034	0.322	0.756857	0.898026
6603	10481291	NM_148928	70239	general transcription factor I	Gtf3c5	1.034	0.12	0.907662	0.963723
6604	10383005	NM_001085535	546519	hypothetical LOC546519	RP23-268N22.9	1.034	0.969	0.363921	0.635352
6605	10536976	NM_010938	18181	nuclear respiratory factor 1	Nrf1	1.034	0.696	0.508347	0.750226
6606	10527920	NM_020010	13121	cytochrome P450, family 51	Cyp51	1.034	0.283	0.785168	0.912507
6607	10426767	NM_009701	11830	aquaporin 5	Aqp5	1.034	0.458	0.660299	0.848652
6608	10458794	BC119623	240261	coiled-coil domain containing	Ccdc112	1.034	-0.376	0.717599	0.876692
6609	10368695	ENSMUST00000045526	72045	RIKEN cDNA 2010001E11 gene	2010001E11Rik	1.034	0.434	0.676653	0.856305
6610	10504611	ENSMUST00000043958	381522	RIKEN cDNA E230008N13 gene	E230008N13Rik	1.034	-0.054	0.95838	0.984334
6611	10425723	ENSMUST00000089154	76505	RIKEN cDNA 1500009C09 gene	1500009C09Rik	1.034	0.543	0.603544	0.814811
6612	10459158	NM_178277	106894	RIKEN cDNA A630042L21 gene	A630042L21Rik	1.034	0.59	0.573034	0.796544
6613	10378319	NM_033321	94045	purinergic receptor P2X, ligan	P2rx5	1.034	0.31	0.765025	0.902309
6614	10361131					1.034	0.313	0.763311	0.901493
6615	10481320	NM_172977	269252	general transcription factor I	Gtf3c4	1.034	0.286	0.783284	0.911971
6616	10416189	NM_010920	18092	NK2 transcription factor relat	Nkx2-6	1.034	0.547	0.600848	0.812558
6617	10355162	NM_001039493	241075	pleckstrin homology domain con	Plekhm3	1.034	0.853	0.421306	0.683765
6618	10534420	NM_177574	194309	vacuolar protein sorting 37D (	Vps37d	1.034	0.751	0.476311	0.727471
6619	10452648	NM_145158	246707	elastin microfibril interfacer	Emilin2	1.034	0.604	0.564474	0.790721
6620	10434993	NM_172822	239827	phosphatidylinositol glycan an	Pigz	1.034	0.588	0.574195	0.797076
6621	10389300	BC022224	192970	cDNA sequence BC022224	BC022224	1.034	0.648	0.536807	0.769874
6622	10526656	NM_146164	231798	leucine-rich repeats and calpo	Lrch4	1.034	0.792	0.453701	0.710123
6623	10511414					1.034	0.252	0.808246	0.922808
6624	10357220	NM_175106	66343	transmembrane protein 177	Tmem177	1.034	0.313	0.762957	0.901446
6625	10471108	NM_178760	277463	G protein-coupled receptor 107	Gpr107	1.034	0.291	0.779485	0.910475
6626	10442801	NM_012034	26945	tryptase gamma 1	Tpsg1	1.034	0.762	0.470517	0.722494
6627	10370950	NM_007460	11776	adaptor-related protein comple	Ap3d1	1.034	0.621	0.553645	0.78319
6628	10510125	ENSMUST00000030328	381572	RIKEN cDNA 9430007A20 gene	9430007A20Rik	1.034	0.186	0.857211	0.942404
6629	10403664	NM_178640	97884	UDP-GalNAc:betaGlcNAc beta 1,3	B3galnt2	1.034	0.253	0.807	0.922086
6630	10562767	ENSMUST00000008172	69349	RIKEN cDNA 1700008O03 gene	1700008O03Rik	1.034	-0.151	0.883938	0.954252
6631	10526943	NM_001038703	80290	G protein-coupled receptor 146	Gpr146	1.034	0.672	0.522626	0.759322

6632	10461867	AK015803	271564	vacuolar protein sorting 13A (	Vps13a	1.034	-0.127	0.90277	0.962008
6633	10486616	NM_009461	22222	ubiquitin protein ligase E3 co	Ubr1	1.034	0.611	0.559725	0.7871
6634	10399478	NM_172950	14245	lipin 1	Lpin1	1.034	0.692	0.510839	0.751986
6635	10572432	NM_023627	71780	myo-inositol 1-phosphate synth	Isyna1	1.034	-0.047	0.963427	0.985684
6636	10538187	NM_053110	93695	glycoprotein (transmembrane) n	Gpnmb	1.034	0.941	0.377206	0.647268
6637	10344622	ENSMUST00000097833	100038431	predicted gene, ENSMUSG0000007	ENSMUSG00000073742	1.033	0.416	0.689671	0.863782
6638	10426542	ENSMUST00000100247	100038643	predicted gene, ENSMUSG0000007	ENSMUSG00000075433	1.033	0.763	0.469614	0.721727
6639	10481870	NM_025709	66691	GTPase activating protein and	Gapvd1	1.033	0.328	0.751941	0.895376
6640	10353522	ENSMUST00000097807	623356	predicted gene, EG623356	EG623356	1.033	0.287	0.782456	0.911672
6641	10404597	NM_024274	69955	phenylalanine-tRNA synthetase	Fars2	1.033	-0.134	0.89703	0.95959
6642	10489305	NM_021464	19281	protein tyrosine phosphatase,	Ptprt	1.033	1.123	0.29751	0.573693
6643	10403244					1.033	0.515	0.621932	0.826948
6644	10394978	NM_009104	20135	ribonucleotide reductase M2	Rrm2	1.033	0.096	0.926364	0.970777
6645	10460237	NM_019449	54445	unc-93 homolog B1 (C. elegans)	Unc93b1	1.033	0.923	0.385878	0.654817
6646	10483646	ENSMUST00000102689	20687	trans-acting transcription fac	Sp3	1.033	0.43	0.679542	0.857705
6647	10376839	NM_028360	72795	tetratricopeptide repeat domai	Ttc19	1.033	0.232	0.822829	0.929127
6648	10580870	ENSMUST00000098479	79233	zinc finger protein 319	Zfp319	1.033	0.061	0.953051	0.981889
6649	10401737	NM_001033475	382620	transmembrane emp24 domain con	Tmed8	1.033	0.491	0.638338	0.835923
6650	10377148	NM_177369	17885	myosin, heavy polypeptide 8, s	Myh8	1.033	0.498	0.633232	0.833255
6651	10523529	NM_012001	26891	COP9 (constitutive photomorpho	Cops4	1.033	-0.567	0.588054	0.804881
6652	10525495	BC038367	208043	SET domain containing 1B	Setd1b	1.033	0.432	0.67865	0.857345
6653	10465411	NM_009203	20521	solute carrier family 22 (orga	Slc22a12	1.033	0.535	0.60844	0.817698
6654	10560070	NM_145578	22192	ubiquitin-conjugating enzyme E	Ube2m	1.033	-0.108	0.916944	0.967219
6655	10484547	NM_001011758	257915	olfactory receptor 1016	Olfr1016	1.033	0.503	0.629834	0.831325
6656	10382438	NM_170758	217303	CD300A antigen	Cd300a	1.033	0.786	0.457079	0.712878
6657	10462005	NM_031997	83921	transmembrane protein 2	Tmem2	1.033	0.194	0.851775	0.940193
6658	10418002	XM_907340	620119	predicted gene, EG620119	EG620119	1.033	0.221	0.831346	0.932333
6659	10566182	NM_001011536	258168	olfactory receptor 566	Olfr566	1.033	0.053	0.959546	0.984837
6660	10464974	NM_030109	319322	splicing factor 3b, subunit 2	Sf3b2	1.033	0.149	0.885801	0.955239
6661	10449672	NM_080727	140765	transmembrane protease, serine	Tmprss3	1.033	0.633	0.546444	0.777695
6662	10557806					1.033	0.939	0.378006	0.647713
6663	10435841	NM_144550	212514	coiled-coil domain containing	Ccdc52	1.033	0.286	0.782708	0.911672
6664	10348999	NM_011800	23836	cadherin 20	Cdh20	1.033	1.011	0.344913	0.61898
6665	10397281	NM_178363	56531	YLP motif containing 1	Ylpm1	1.033	0.534	0.609195	0.818089
6666	10512594	NM_001099314	100039672	hypothetical protein LOC100039	RP23-191F22.4	1.033	0.811	0.443559	0.702308
6667	10557644	BC027193	14123	fibrosin	Fbrs	1.033	0.16	0.87691	0.951412
6668	10479249	NM_198656	381409	cadherin-like 26	Cdh26	1.033	1.01	0.34532	0.61945
6669	10461452	ENSMUST00000081739	100038753	predicted gene, ENSMUSG0000006	ENSMUSG00000064032	1.033	0.575	0.582702	0.800924
6670	10486154	NM_001001982	214239	RIKEN cDNA A430105I19 gene	A430105I19Rik	1.033	0.747	0.478939	0.729132
6671	10488806	NM_026030	67204	eukaryotic translation initiat	Eif2s2	1.033	0.588	0.574296	0.797076
6672	10532040	NM_026856	52397	zinc finger protein 644	Zfp644	1.033	0.529	0.61269	0.820438
6673	10521090	NM_001040435	21335	transforming, acidic coiled-co	Tacc3	1.033	0.579	0.579964	0.799189
6674	10519151	NM_145124	76580	mindbomb homolog 2 (Drosophila	Mib2	1.033	0.681	0.51737	0.756572
6675	10593219	NM_010924	18113	nicotinamide N-methyltransfera	Nnmt	1.033	0.362	0.727865	0.881998
6676	10451123	NM_022880	63959	solute carrier family 29 (nucl	Slc29a1	1.033	0.505	0.628537	0.830964
6677	10513583	NM_139291	66440	cell division cycle 26	Cdc26	1.033	-0.256	0.805459	0.921471
6678	10389786	NM_172563	217082	hepatic leukemia factor	Hlf	1.033	0.579	0.579914	0.799181
6679	10425354	NM_010795	17309	mannoside acetylglucosaminyltr	Mgat3	1.033	0.487	0.640635	0.837232
6680	10502655	NM_010516	16007	cysteine rich protein 61	Cyr61	1.033	0.75	0.477155	0.727867
6681	10558612	NM_146518	258511	olfactory receptor 523	Olfr523	1.033	0.835	0.430334	0.691097
6682	10519007	NM_026388	67808	transformation related protein	Tprgl	1.033	-0.118	0.909306	0.963879
6683	10550501	NM_153761	243864	MHC I like leukocyte 2	Mill2	1.033	0.831	0.432831	0.693264
6684	10443344					1.033	0.973	0.361874	0.633538

6685	10494873	NM_001033303	229665	adenosine monophosphate deamin	Ampd1	1.033	0.714	0.497636	0.741949
6686	10540141	NM_172730	232236	RIKEN cDNA C130022K22 gene	C130022K22Rik	1.033	-0.109	0.915937	0.966745
6687	10595840	NM_153420	235534	acid phosphatase-like 2	Acpl2	1.033	0.479	0.646225	0.840435
6688	10378802	NM_178645	104184	bleomycin hydrolase	Blmh	1.033	-0.092	0.92955	0.972207
6689	10606102	NM_008832	18679	phosphorylase kinase alpha 1	Phka1	1.033	0.277	0.789502	0.914397
6690	10470665	NM_198033	269254	senataxin	Setx	1.033	-0.066	0.94919	0.980395
6691	10421624	NM_177381	338337	component of oligomeric golgi	Cog3	1.033	0.451	0.665147	0.850823
6692	10396030	NM_178912	104806	Fanconi anemia, complementatio	Fancm	1.033	0.532	0.610607	0.818945
6693	10452307	NM_019418	50930	tumor necrosis factor (ligand)	Tnfsf14	1.033	0.69	0.512053	0.75265
6694	10395259	NM_021524	59027	nicotinamide phosphoribosyltra	Nampt	1.033	-0.242	0.81568	0.926149
6695	10484865					1.033	0.456	0.66167	0.84929
6696	10475843	ENSMUST00000099399	100038529	predicted gene, ENSMUSG0000007	ENSMUSG00000074816	1.033	0.596	0.569712	0.794081
6697	10494592	NM_001033779	433632	predicted gene, EG433632	EG433632	1.033	1.037	0.333188	0.609187
6698	10532582	XM_912851	74376	myosin XVIIIb	Myo18b	1.033	0.568	0.587059	0.804041
6699	10589413	NM_018757	54369	non-metastatic cells 6, protei	Nme6	1.033	0.193	0.85235	0.940463
6700	10521755	AK015432	73955	RIKEN cDNA 4930449I04 gene	4930449I04Rik	1.032	0.197	0.849387	0.939132
6701	10421258	NM_145978	213019	PDZ and LIM domain 2	Pdlim2	1.032	1.256	0.24815	0.521506
6702	10494536	NM_021517	59020	PDZ domain containing 1	Pdzk1	1.032	0.443	0.671068	0.853953
6703	10375127	AK006938	73493	RIKEN cDNA 1700072H12 gene	1700072H12Rik	1.032	0.753	0.47534	0.726829
6704	10485429	NM_175094	27402	pyruvate dehydrogenase complex	Pdhx	1.032	0.06	0.953499	0.982042
6705	10440911					1.032	-0.122	0.906005	0.963405
6706	10462791	NM_027314	69104	membrane-associated ring finge	March5	1.032	-0.066	0.949322	0.980484
6707	10424622					1.032	0.971	0.363067	0.634368
6708	10398052	NM_001034870	546546	serine (or cysteine) peptidase	Serpina3h	1.032	1.051	0.327122	0.603338
6709	10441642	NM_018819	55951	brain protein 44-like	Brp44l	1.032	0.553	0.59679	0.810126
6710	10510923	NM_013783	27390	membrane metallo-endopeptidase	Mmel1	1.032	0.426	0.682729	0.859827
6711	10437023	NM_001045529	338467	microrchidia 3	Morc3	1.032	0.232	0.822868	0.929127
6712	10469987	NM_001029983	227619	mannosidase, alpha, class 1B,	Man1b1	1.032	0.386	0.710604	0.873091
6713	10510886	BC031402	230971	multiple EGF-like-domains 6	Megf6	1.032	0.718	0.495139	0.740032
6714	10399751	NM_027866	71693	collectin sub-family member 11	Colec11	1.032	0.729	0.489024	0.736349
6715	10368027					1.032	0.913	0.390774	0.659209
6716	10559243	ENSMUST00000097935	624121	predicted gene, EG624121	EG624121	1.032	0.187	0.85712	0.942404
6717	10442834	NM_028009	106707	RNA pseudouridylate synthase d	Rpusd1	1.032	0.189	0.855441	0.941478
6718	10460631	NM_009045	19697	v-rel reticuloendotheliosis vi	Rela	1.032	0.036	0.972459	0.988158
6719	10580415					1.032	0.607	0.56271	0.789779
6720	10485645	NM_009037	19672	reticulocalbin 1	Rcn1	1.032	0.232	0.822727	0.929111
6721	10377822	NM_025397	66172	mediator of RNA polymerase II	Med11	1.032	0.077	0.940679	0.977
6722	10503431	NM_013752	27354	nibrin	Nbn	1.032	-0.038	0.971088	0.988148
6723	10541206	NM_016718	29862	ninjurin 2	Ninj2	1.032	1.239	0.253989	0.528265
6724	10550274	NM_008627	17537	Meis homeobox 3	Meis3	1.032	0.156	0.880589	0.952631
6725	10537728	NM_007610	12366	caspase 2	Casp2	1.032	0.641	0.54108	0.773484
6726	10555297	NM_020574	57442	potassium voltage-gated channe	Kcne3	1.032	0.212	0.837898	0.934421
6727	10550574	NM_032418	13400	dystrophia myotonica-protein k	Dmpk	1.032	0.631	0.547538	0.778461
6728	10469867	NM_146251	241274	patatin-like phospholipase dom	Pnpla7	1.032	0.962	0.366983	0.638
6729	10567303	NM_009940	12850	demethyl-Q 7	Coq7	1.032	0.174	0.867014	0.946934
6730	10361200	NM_145415	215193	expressed sequence AA408296	AA408296	1.032	0.289	0.780977	0.91101
6731	10572466	NM_201607	110385	phosphodiesterase 4C, cAMP spe	Pde4c	1.032	0.837	0.42927	0.69028
6732	10568225	NM_146202	233890	zinc finger protein 768	Zfp768	1.032	0.509	0.626128	0.82971
6733	10421911	NM_178685	219257	protocadherin 20	Pcdh20	1.032	0.467	0.654468	0.845176
6734	10493824	NM_199422	381493	S100 calcium binding protein A	S100a7a	1.032	1.02	0.34061	0.615753
6735	10580061	NM_016671	50931	interleukin 27 receptor, alpha	Il27ra	1.032	0.471	0.651827	0.844083

6736	10561958	NM_178252	233071	sorting nexin 26	Snx26	1.032	0.796	0.451398	0.708512
6737	10504218	NM_019874	56323	DnaJ (Hsp40) homolog, subfamil	Dnajb5	1.032	0.416	0.689621	0.863782
6738	10579313	NM_133772	76900	single stranded DNA binding pr	Ssbp4	1.032	0.37	0.722256	0.879223
6739	10579277	NM_178771	234378	kelch-like 26 (Drosophila)	Klhl26	1.032	0.329	0.751757	0.895263
6740	10571907	NM_027756	71306	microfibrillar-associated prot	Mfap3l	1.032	0.285	0.783904	0.912068
6741	10402841	NM_028193	72308	BRF1 homolog, subunit of RNA p	Brf1	1.032	0.664	0.527299	0.762963
6742	10467921	NM_007700	12675	conserved helix-loop-helix ubi	Chuk	1.032	0.212	0.838238	0.934421
6743	10503617	NM_199467	212377	RIKEN cDNA F730047E07 gene	F730047E07Rik	1.032	0.388	0.709531	0.872938
6744	10409557	NM_012015	26914	H2A histone family, member Y	H2afy	1.032	0.599	0.567529	0.792875
6745	10474355	ENSMUST00000037284	329482	doublecortin domain containing	Dcdc5	1.032	1.017	0.341852	0.616313
6746	10442840	BC052484	328783	cDNA sequence BC052484	BC052484	1.032	0.493	0.636519	0.834887
6747	10558596	NM_153783	212503	polyamine oxidase (exo-N4-amin	Paox	1.032	0.311	0.764543	0.901841
6748	10555836					1.032	0.335	0.747206	0.892524
6749	10502105	NM_010113	13645	epidermal growth factor	Egf	1.032	0.422	0.685484	0.861073
6750	10528172					1.032	0.538	0.606587	0.816766
6751	10513362	ENSMUST00000107544	634731	similar to sushi domain contai	LOC634731	1.032	0.212	0.838254	0.934421
6752	10607356	NM_027543	70771	G-protein coupled receptor 173	Gpr173	1.031	0.253	0.80738	0.922371
6753	10428825					1.031	0.531	0.611697	0.819835
6754	10604148	NM_001004193	434768	reproductive homeobox 8	Rhox8	1.031	0.726	0.490542	0.737328
6755	10366038	NM_015737	14426	UDP-N-acetyl-alpha-D-galactosa	Galnt4	1.031	0.099	0.924011	0.969768
6756	10572962	NM_001081240	102182	expressed sequence AI931714	AI931714	1.031	0.221	0.83107	0.932182
6757	10532187	NM_153569	231580	cyclin G associated kinase	Gak	1.031	0.096	0.926266	0.970777
6758	10576749	NM_008790	18545	Purkinje cell protein 2 (L7)	Pcp2	1.031	0.569	0.586625	0.803706
6759	10433199	NM_148924	74120	zinc finger protein 263	Zfp263	1.031	0.151	0.884421	0.95453
6760	10583898	ENSMUST00000098926	100038418	predicted gene, ENSMUSG0000007	ENSMUSG00000074465	1.031	1.1	0.306527	0.582999
6761	10382956	NM_181856	217356	transmembrane channel-like 8	Tmc8	1.031	0.646	0.538054	0.771077
6762	10454873	BC100467	74966	RIKEN cDNA 4930471G03 gene	4930471G03Rik	1.031	1.073	0.317662	0.594815
6763	10391625	NM_011551	21429	upstream binding transcription	Ubtf	1.031	-0.037	0.971514	0.988148
6764	10529887					1.031	0.165	0.873344	0.949372
6765	10538150	NM_025326	66058	transmembrane protein 176A	Tmem176a	1.031	0.51	0.624992	0.829015
6766	10481508	NM_133346	72323	ankyrin repeat and SOCS box-co	Asb6	1.031	0.438	0.674281	0.855309
6767	10538310	NM_007966	14028	even skipped homeotic gene 1 h	Evx1	1.031	0.537	0.607552	0.817336
6768	10455007	NM_025594	66492	zinc finger, matrin type 2	Zmat2	1.031	0.341	0.74295	0.89053
6769	10504905	NM_178756	272031	RIKEN cDNA E130309F12 gene	E130309F12Rik	1.031	0.869	0.412672	0.676213
6770	10517173	NM_144527	70012	coiled-coil domain containing	Ccdc21	1.031	0.419	0.687239	0.862117
6771	10529801	NM_178729	242960	F-box and leucine-rich repeat	Fbxl5	1.031	0.32	0.758182	0.898649
6772	10587778					1.031	0.04	0.969277	0.987586
6773	10590137	NM_130864	113868	acetyl-Coenzyme A acyltransfer	Acaa1a	1.031	0.158	0.878607	0.951851
6774	10446537	NM_177278	320858	l(3)mbt-like 4 (Drosophila)	L3mbtl4	1.031	0.505	0.628523	0.830964
6775	10516225	AK015982	75220	RIKEN cDNA 4930535I16 gene	4930535I16Rik	1.031	0.549	0.599787	0.812076
6776	10504955	XR_031565	100045339	similar to ribosomal protein L	LOC100045339	1.031	-0.302	0.771437	0.905701
6777	10500183	NM_144899	229595	ADAMTS-like 4	Adamtsl4	1.031	1.068	0.319922	0.59668
6778	10497390	NM_028840	74252	armadillo repeat containing 1	Armc1	1.031	-0.143	0.890125	0.956731
6779	10496715	NM_001081094	229937	RIKEN cDNA 2410019A14 gene	2410019A14Rik	1.031	-0.053	0.95903	0.98454
6780	10511017	NM_177674	544678	RIKEN cDNA 2010015L04 gene	2010015L04Rik	1.031	0.455	0.662504	0.849733
6781	10434934	NM_175177	71911	3-hydroxybutyrate dehydrogenas	Bdh1	1.031	0.67	0.523625	0.76025
6782	10397736	NM_146037	217826	potassium channel, subfamily K	Kcnk13	1.031	0.966	0.365258	0.636343
6783	10574384	NM_145602	234593	N-myc downstream regulated gen	Ndrg4	1.031	0.371	0.720998	0.878601
6784	10375774	BC041684	108072	glutamate receptor, metabotrop	Grm6	1.031	0.504	0.629292	0.831256
6785	10578262					1.031	0.367	0.724423	0.880611

6786	10512739	NM_011728	22590	xeroderma pigmentosum, complem	Xpa	1.031	-0.227	0.826729	0.930499
6787	10516348	NM_153402	214150	eukaryotic translation initiat	Eif2c3	1.031	0.348	0.737905	0.88827
6788	10348643	NM_206896	257890	olfactory receptor 12	Olfr12	1.031	1.076	0.316704	0.593914
6789	10450034	NM_008997	19326	RAB11B, member RAS oncogene fa	Rab11b	1.031	-0.221	0.831401	0.932333
6790	10350977	ENSMUST00000060298	67647	RIKEN cDNA 4930523C07 gene	4930523C07Rik	1.031	0.174	0.866652	0.946757
6791	10603011	NM_009031	245688	retinoblastoma binding protein	Rbbp7	1.031	0.338	0.744938	0.891598
6792	10481700	BC118617	227736	RIKEN cDNA 1700019L03 gene	1700019L03Rik	1.031	0.391	0.707372	0.872175
6793	10379410	NM_021536	59040	ras homolog gene family, membe	Rhot1	1.031	0.161	0.876201	0.950949
6794	10549871	NM_146916	258918	olfactory receptor 1346	Olfr1346	1.031	0.181	0.8613	0.944277
6795	10345206					1.031	0.312	0.764214	0.90173
6796	10490164	ENSMUST00000029022	70065	ankyrin repeat domain 60	Ankrd60	1.031	0.947	0.374354	0.644466
6797	10546370	BC099701	243547	glutamate receptor interacting	Grip2	1.031	0.148	0.886484	0.955393
6798	10592126	NM_194257	109229	protein phosphatase 4, regulat	Ppp4r1l	1.031	0.118	0.909612	0.964056
6799	10345370	NM_011206	19253	protein tyrosine phosphatase,	Ptpn18	1.031	0.625	0.551222	0.781273
6800	10527172	NM_177681	231866	zinc finger protein 12	Zfp12	1.031	0.747	0.478917	0.729132
6801	10430289	NM_025931	67042	RAB, member of RAS oncogene fa	Rabl4	1.031	0.129	0.900797	0.960826
6802	10371277	BC040349	237411	RIKEN cDNA B230315N10 gene	B230315N10Rik	1.031	-0.034	0.973682	0.988697
6803	10509379	NM_130879	170707	ubiquitin specific peptidase 4	Usp48	1.031	0.469	0.652777	0.844541
6804	10493726	NM_201407	229541	DENN/MADD domain containing 4B	Dennd4b	1.031	0.877	0.408519	0.672914
6805	10536787					1.031	0.247	0.81186	0.924032
6806	10482089	NM_026703	68375	NADH dehydrogenase (ubiquinone	Ndufa8	1.031	0.431	0.679002	0.857533
6807	10581340	NM_145824	74334	RAN binding protein 10	Ranbp10	1.031	0.374	0.719085	0.877614
6808	10365492	ENSMUST00000116047	382395	predicted gene, EG382395	EG382395	1.031	0.677	0.519576	0.757547
6809	10413670	NM_001081251	66923	polybromo 1	Pbrm1	1.031	0.124	0.904906	0.963071
6810	10367036	NM_080436	107605	retinol dehydrogenase 1 (all t	Rdh1	1.031	0.244	0.814025	0.925212
6811	10582299	NM_133202	170732	thyrotropin releasing hormone	Trhr2	1.031	0.368	0.723259	0.879946
6812	10428604	NM_008764	18383	tumor necrosis factor receptor	Tnfrsf11b	1.031	0.454	0.663104	0.849961
6813	10464359	XR_031213	674623	similar to Elongation factor 1	LOC674623	1.03	0.362	0.727751	0.88191
6814	10420572	NM_170591	71844	nucleoporin like 1	Nupl1	1.03	0.386	0.710333	0.873031
6815	10519060	NM_178931	230979	tumor necrosis factor receptor	Tnfrsf14	1.03	0.328	0.752487	0.895764
6816	10442331	NM_023058	268930	protein kinase, membrane assoc	Pkmyt1	1.03	0.631	0.547261	0.778305
6817	10345445	NM_145996	214855	AT rich interactive domain 5A	Arid5a	1.03	0.84	0.428097	0.689167
6818	10439701	NM_172511	213012	abhydrolase domain containing	Abhd10	1.03	0.037	0.971311	0.988148
6819	10585358	NM_001081152	244879	nuclear protein in the AT regi	Npat	1.03	0.008	0.993837	0.997702
6820	10384936	NM_029344	75572	acylphosphatase 2, muscle type	Acyp2	1.03	0.352	0.735227	0.886784
6821	10442986	NM_028190	66978	Luc7 homolog (S. cerevisiae)-l	Luc7l	1.03	0.378	0.716218	0.875663
6822	10359770	NM_011137	18986	POU domain, class 2, transcrip	Pou2f1	1.03	0.141	0.891541	0.957571
6823	10433032	ENSMUST00000096143	223922	activating transcription facto	Atf7	1.03	0.747	0.47896	0.729132
6824	10590821	BC115525	234912	RIKEN cDNA 9230110C19 gene	9230110C19Rik	1.03	0.238	0.818174	0.927633
6825	10381502	ENSMUST00000078285	73887	RIKEN cDNA 4930417O22 gene	4930417O22Rik	1.03	1.109	0.303191	0.579207
6826	10410380					1.03	0.818	0.439705	0.699031
6827	10532590	XM_912851	74376	myosin XVIIIb	Myo18b	1.03	0.29	0.780049	0.910713
6828	10544219	NM_139294	109880	Braf transforming gene	Braf	1.03	0.431	0.678912	0.857533
6829	10399391	NM_177331	209334	Gen homolog 1, endonuclease (D	Gen1	1.03	-0.048	0.963299	0.985684
6830	10512465	NM_177377	329831	RIKEN cDNA 4833436C18 gene	4833436C18Rik	1.03	0.548	0.600531	0.812284
6831	10379880	BC048674	73634	RIKEN cDNA 1700125H20 gene	1700125H20Rik	1.03	0.565	0.588898	0.805202
6832	10549733	NM_173008	269855	RIKEN cDNA A430110N23 gene	A430110N23Rik	1.03	0.607	0.562764	0.789779
				GDP-mannose					

6833	10588836	NM_177910	331026	pyrophosphorylase	Gmppb	1.03	1.03	0.33649	0.61218
6834	10481259	AK158259	100038452	predicted gene, OTTMUSG0000001	OTTMUSG00000011627	1.03	0.24	0.817336	0.927212
6835	10471337	NM_145145	99011	protein-O-mannosyltransferase	Pomt1	1.03	0.548	0.600108	0.812128
6836	10608204					1.03	0.417	0.688932	0.863319
6837	10365098	NM_009325	21390	thromboxane A2 receptor	Tbxa2r	1.03	0.925	0.384668	0.654022
6838	10570029	NM_001081397	244281	myosin XVI	Myo16	1.03	0.914	0.390329	0.658911
6839	10527934					1.03	0.229	0.824932	0.929565
6840	10418129					1.03	0.805	0.446299	0.704033
6841	10364489	NM_023304	67112	fibroblast growth factor 22	Fgf22	1.03	1.038	0.332803	0.608825
6842	10371025	NM_001038655	14708	guanine nucleotide binding pro	Gng7	1.03	0.443	0.671079	0.853953
6843	10471387	NM_028412	68379	CDKN1A interacting zinc finger	Ciz1	1.03	0.484	0.642998	0.838239
6844	10540579	NM_026849	97287	myotubularin related protein 1	Mtmr14	1.03	0.657	0.531377	0.765618
6845	10508737	NM_010166	14050	eyes absent 3 homolog (Drosoph	Eya3	1.03	0.258	0.803419	0.920133
6846	10544798	NM_008263	15395	homeo box A10	Hoxa10	1.03	-0.082	0.936664	0.975223
6847	10526514	NM_021719	60363	claudin 15	Cldn15	1.03	0.787	0.456223	0.712479
6848	10446346	XR_034674	433129	similar to Obox6 protein	LOC433129	1.03	1.142	0.289839	0.566077
6849	10350341					1.03	0.115	0.91164	0.964691
6850	10570894	NM_001110783	11733	ankyrin 1, erythroid	Ank1	1.03	0.34	0.74375	0.891034
6851	10541741	NM_145385	30853	myeloid leukemia factor 2	Mlf2	1.03	0.12	0.908125	0.963723
6852	10586880	NM_146224	235469	suppressor of hairy wing homol	Suhw4	1.03	0.637	0.544018	0.776161
6853	10404697	ENSMUST00000069457	791406	predicted gene, ENSMUSG0000005	ENSMUSG00000055732	1.03	0.508	0.626835	0.83034
6854	10526363	NM_008898	18984	P450 (cytochrome) oxidoreducta	Por	1.03	-0.508	0.6269	0.830369
6855	10546184	NM_008881	18844	plexin A1	Plxna1	1.03	0.223	0.829388	0.93131
6856	10603310					1.03	0.342	0.74227	0.890171
6857	10488584	AK016149	75283	RIKEN cDNA 4930556L07 gene	4930556L07Rik	1.03	0.454	0.663087	0.849961
6858	10377368	NM_009080	19941	ribosomal protein L26	Rpl26	1.029	-0.192	0.852926	0.940713
6859	10573691	ENSMUST00000098532	666945	predicted gene, ENSMUSG0000007	ENSMUSG00000074178	1.029	0.723	0.492244	0.738375
6860	10386551	NM_022009	14248	flightless I homolog (Drosophi	Flii	1.029	-0.15	0.885062	0.954881
6861	10483789	NM_007967	14029	even skipped homeotic gene 2 h	Evx2	1.029	0.224	0.828959	0.931175
6862	10559399	NM_175632	232790	osteoclast associated receptor	Oscar	1.029	0.959	0.368431	0.639213
6863	10568865	BC145730	381933	RIKEN cDNA 6430531B16 gene	6430531B16Rik	1.029	0.507	0.627346	0.83052
6864	10430783	NM_030229	78929	polymerase (RNA) III (DNA dire	Polr3h	1.029	0.053	0.959034	0.98454
6865	10467599	NM_015748	20562	slit homolog 1 (Drosophila)	Slit1	1.029	0.549	0.599801	0.812076
6866	10540659	NM_133923	101100	tubulin tyrosine ligase-like f	Ttll3	1.029	0.65	0.535626	0.769137
6867	10592160	XM_892150	627480	predicted gene, EG627480	EG627480	1.029	0.588	0.574235	0.797076
6868	10515253	NM_025641	66576	ubiquinol-cytochrome c reducta	Uqcrh	1.029	0.282	0.785936	0.912636
6869	10534921	NM_144913	231803	methylphosphate capping enzyme	Mepce	1.029	-0.587	0.574924	0.797076
6870	10603525	NM_001081565	631002	synovial sarcoma, X member B,	Ssxb8	1.029	0.63	0.548023	0.778543
6871	10562629					1.029	1.111	0.302394	0.578522
6872	10439009	NM_007470	11815	apolipoprotein D	Apod	1.029	0.437	0.674885	0.855557
6873	10546944	NM_175101	66087	transmembrane protein 111	Tmem111	1.029	-0.041	0.968288	0.987245
6874	10511490					1.029	0.493	0.636708	0.834887
6875	10475280	NM_029475	75894	adenosine deaminase-like	Adal	1.029	0.025	0.980772	0.991919
6876	10601314	NM_009440	22127	testis specific X-linked gene	Tsx	1.029	0.543	0.603267	0.814526
6877	10534990	NM_009315	21343	TAF6 RNA polymerase II, TATA b	Taf6	1.029	0.111	0.914776	0.966446
6878	10452440	ENSMUST00000050753	320004	RIKEN cDNA A930002H24 gene	A930002H24Rik	1.029	0.295	0.776042	0.908612
6879	10414799	ENSMUST00000103605	100046023	similar to TRAV8D-2	LOC100046023	1.029	0.269	0.795592	0.916955
6880	10486029	NM_025675	66632	ATP binding domain 4	Atpbd4	1.029	-0.49	0.638946	0.835923
6881	10488762	NM_009228	20648	syntrophin, acidic 1	Snta1	1.029	0.548	0.59996	0.812084
6882	10570199	ENSMUST00000068194	70966	RIKEN cDNA 4931415C17	4931415C17Rik	1.029	0.372	0.720668	0.878411

				gene					
6883	10371041	NM_024499	52551	small glutamine-rich tetratric	Sgta	1.029	0.392	0.706246	0.871814
6884	10414271	NM_008964	19217	prostaglandin E receptor 2 (su	Ptger2	1.029	0.373	0.719654	0.877935
6885	10522411	BC016523	231293	RIKEN cDNA C130090K23 gene	C130090K23Rik	1.029	0.398	0.701889	0.869258
6886	10353519	NM_025746	66755	RIKEN cDNA 4933415F23 gene	4933415F23Rik	1.029	0.498	0.63352	0.833323
6887	10351788	NM_026234	67556	phosphatidylinositol glycan an	Pigm	1.029	0.109	0.916223	0.966842
6888	10495306	NM_026831	68753	myosin binding protein H-like	Mybphl	1.029	0.528	0.613106	0.820787
6889	10418218	NM_032008	83997	sarcolemma associated protein	Slmap	1.029	0.17	0.869471	0.947682
6890	10561819	NM_177889	330502	zinc finger protein 82	Zfp82	1.029	-0.158	0.878506	0.95179
6891	10435724	NM_019804	56375	UDP-Gal:betaGlcNAc beta 1,4-ga	B4galt4	1.029	0.168	0.871518	0.948642
6892	10573401	NM_198020	212528	TRM1 tRNA methyltransferase 1	Trmt1	1.029	0.135	0.896205	0.95935
6893	10562408	NM_175140	68947	carbohydrate (N-acetylgalactos	Chst8	1.029	0.405	0.696972	0.867134
6894	10520718	NM_153680	266781	sorting nexin 17	Snx17	1.029	0.605	0.563801	0.790309
6895	10476560	ENSMUST00000099307	319909	RIKEN cDNA 5430433G21 gene	5430433G21Rik	1.029	0.291	0.778903	0.910097
6896	10564262	NM_011746	22652	makorin, ring finger protein,	Mkrn3	1.029	0.251	0.808734	0.92302
6897	10428119	NM_053071	12864	cytochrome c oxidase, subunit	Cox6c	1.029	0.317	0.759891	0.899364
6898	10475394	NM_212450	329506	CTD (carboxy-terminal domain,	Ctdspl2	1.029	0.44	0.672583	0.854651
6899	10444218					1.029	0.823	0.436673	0.696302
6900	10529237	ENSMUST00000101373	100038480	predicted gene, ENSMUSG0000007	ENSMUSG00000073053	1.029	0.626	0.550871	0.781094
6901	10404024	NM_153173	69386	histone cluster 1, H4h	Hist1h4h	1.029	0.122	0.905965	0.963405
6902	10425293	NM_028634	73739	chibby homolog 1 (Drosophila)	Cby1	1.029	-0.033	0.97458	0.989224
6903	10350840	NM_028333	72713	angiopoietin-like 1	Angptl1	1.029	0.109	0.916185	0.966842
6904	10555574					1.029	0.011	0.991298	0.99653
6905	10508253	NM_198618	242667	discs, large (Drosophila) homo	Dlgap3	1.029	0.401	0.699753	0.868438
6906	10562687	ENSMUST00000107974	210094	RIKEN cDNA A230106M20 gene	A230106M20Rik	1.029	0.258	0.803329	0.920129
6907	10473880	NM_172668	228357	low density lipoprotein recept	Lrp4	1.029	0.93	0.382316	0.651795
6908	10361063					1.029	0.125	0.90415	0.962767
6909	10592926	NM_027865	71687	transmembrane protein 25	Tmem25	1.029	0.565	0.589498	0.805725
6910	10529133	NM_175311	101023	zinc finger protein 513	Zfp513	1.029	0.783	0.458298	0.713568
6911	10346116					1.028	0.362	0.72762	0.881903
6912	10397342	BC049940	72350	RIKEN cDNA 2810002I04 gene	2810002I04Rik	1.028	0.175	0.865571	0.946261
6913	10533628	BC117082	76399	interleukin 31	Il31	1.028	0.86	0.417406	0.680204
6914	10455065	NM_053130	93876	protocadherin beta 5	Pcdhb5	1.028	0.864	0.415264	0.678399
6915	10472058	NM_175238	51869	Rap1 interacting factor 1 homo	Rif1	1.028	0.118	0.90906	0.963765
6916	10520247	NR_003953	72252	RIKEN cDNA 1700022A21 gene	1700022A21Rik	1.028	1.087	0.311971	0.588349
6917	10416110	NM_001034881	432870	predicted gene, EG432870	EG432870	1.028	0.144	0.889321	0.956449
6918	10415095	BC011283	58248	RIKEN cDNA 1700123O20 gene	1700123O20Rik	1.028	0.398	0.702043	0.869258
6919	10400109	NM_172575	246196	zinc finger protein 277	Zfp277	1.028	0.293	0.777732	0.909562
6920	10571797	NM_029569	76294	ankyrin repeat and SOCs box-co	Asb5	1.028	0.512	0.623647	0.828031
6921	10481240	NM_001113574	67382	bromodomain containing 3	Brd3	1.028	-0.06	0.953416	0.982042
6922	10537921	NM_146175	101095	zinc finger protein 282	Zfp282	1.028	0.283	0.78513	0.912507
6923	10582477	NM_030176	78779	spermatogenesis associated 2-l	Spata2L	1.028	0.859	0.417832	0.680583
6924	10382104					1.028	0.258	0.80394	0.92048
6925	10590933	NM_177905	330890	piwi-like homolog 4 (Drosophil	Piwil4	1.028	0.993	0.353005	0.625939
6926	10498871	NM_027495	70652	transmembrane protein 144	Tmem144	1.028	0.422	0.685203	0.860862
6927	10379564	NM_010716	16882	ligase III, DNA, ATP-dependent	Lig3	1.028	0.023	0.982604	0.992413
6928	10520499	NM_001033460	381738	gene model 1060, (NCBI)	Gm1060	1.028	0.184	0.859106	0.943452
6929	10578423	XM_001473828	100045396	hypothetical protein LOC100045	LOC100045396	1.028	-0.351	0.735438	0.886804
6930	10360983	BC048476	56330	programmed cell death 5	Pdcd5	1.028	0.053	0.959236	0.984606
6931	10482167	NM_146253	241322	zinc finger and BTB domain con	Zbtb6	1.028	-0.258	0.80364	0.920237
6932	10495935	BC085187	71643	RIKEN cDNA 4930422G04 gene	4930422G04Rik	1.028	0.299	0.773598	0.9067

6933	10467182	NM_008315	15566	5-hydroxytryptamine (serotonin	Htr7	1.028	0.364	0.726051	0.88142
6934	10458882	XR_033028	674866	similar to glyceraldehyde-3-ph	LOC674866	1.028	0.235	0.820507	0.928587
6935	10597432	NM_153585	78893	CCR4-NOT transcription complex	Cnot10	1.028	0.344	0.740744	0.889595
6936	10510668	NM_033042	85030	tumor necrosis factor receptor	Tnfrsf25	1.028	0.727	0.490142	0.737262
6937	10455647	NM_134131	106869	tumor necrosis factor, alpha-i	Tnfaip8	1.028	-0.476	0.64824	0.841813
6938	10431848	NR_003627	402773	RIKEN cDNA D030018L15 gene	D030018L15Rik	1.028	0.564	0.589973	0.805977
6939	10456727	NM_027727	69190	dymeclin	Dym	1.028	0.48	0.645472	0.839972
6940	10404975	NM_031166	15904	inhibitor of DNA binding 4	Id4	1.028	0.063	0.951404	0.981144
6941	10405535	BC051430	78521	RIKEN cDNA B230219D22 gene	B230219D22Rik	1.028	0.17	0.869374	0.947675
6942	10407316	ENSMUST00000099155	670198	predicted gene, ENSMUSG0000007	ENSMUSG00000074642	1.028	0.307	0.767226	0.903106
6943	10544648	NM_018769	54722	deafness, autosomal dominant 5	Dfna5h	1.028	0.393	0.70544	0.871557
6944	10509137	NM_008254	15356	3-hydroxy-3-methylglutaryl-Coe	Hmgcl	1.028	0.191	0.853836	0.940875
6945	10542522	NM_144920	109135	pleckstrin homology domain con	Plekha5	1.028	0.23	0.824798	0.929565
6946	10516859	NM_145393	213541	YTH domain family 2	Ythdf2	1.028	0.28	0.787317	0.913152
6947	10455801	NM_019996	56698	RNA U, small nuclear RNA expor	Rnuxa	1.028	0.038	0.970696	0.988127
6948	10439798	NM_001110017	224170	DAZ interacting protein 3, zin	Dzip3	1.028	0.548	0.600388	0.812266
6949	10418817	NM_009891	12647	choline acetyltransferase	Chat	1.028	0.409	0.694112	0.865705
6950	10362450					1.028	0.535	0.608693	0.817883
6951	10597773					1.028	1.342	0.220302	0.488992
6952	10597279	NM_017466	54199	chemokine (C-C motif) receptor	Ccrl2	1.028	0.422	0.685261	0.860862
6953	10452609	NM_001033340	240131	leucine rich repeat containing	Lrrc30	1.028	1.265	0.24505	0.518209
6954	10531288					1.028	0.549	0.599339	0.811907
6955	10353794	BC040511	214469	cDNA sequence BC043098	BC043098	1.028	-0.05	0.961097	0.985069
6956	10405211	NM_011817	23882	growth arrest and DNA-damage-i	Gadd45g	1.028	0.981	0.358407	0.630567
6957	10514896	NM_025617	66526	RIKEN cDNA 2210012G02 gene	2210012G02Rik	1.028	0.547	0.601044	0.812694
6958	10416423	NM_198642	271221	RIKEN cDNA 5031414D18 gene	5031414D18Rik	1.028	0.232	0.822623	0.929111
6959	10493317	BC016616	76022	RIKEN cDNA 5830417I10 gene	5830417I10Rik	1.028	0.349	0.737303	0.887888
6960	10486722	NM_013735	27223	transformation related protein	Trp53bp1	1.028	0.162	0.875698	0.950842
6961	10583459	NM_175110	66662	RIKEN cDNA 5730577I03 gene	5730577I03Rik	1.028	0.352	0.734957	0.886784
6962	10524229	ENSMUST00000059200	231603	RIKEN cDNA A630023P12 gene	A630023P12Rik	1.028	0.316	0.761255	0.900424
6963	10440483	NM_016755	11957	ATP synthase, H+ transporting,	Atp5j	1.028	0.062	0.952351	0.981503
6964	10586971	NM_175485	235472	protogenin homolog (Gallus gal	Prtg	1.028	0.224	0.829334	0.93131
6965	10604958	NM_001085506	236852	melanoma antigen family A, 10	Magea10	1.028	0.501	0.631026	0.832075
6966	10434067	NM_029945	77626	sphingomyelin phosphodiesteras	Smpd4	1.027	0.074	0.942677	0.977825
6967	10396231	ENSMUST00000021482	75266	RIKEN cDNA 4930553D19 gene	4930553D19Rik	1.027	0.637	0.543698	0.775862
6968	10507905	NM_011141	18991	POU domain, class 3, transcrip	Pou3f1	1.027	0.154	0.881529	0.953086
6969	10581523	NM_009353	21750	telomeric repeat binding facto	Terf2	1.027	0.203	0.845002	0.937001
6970	10498168	NM_027148	69639	exosome component 8	Exosc8	1.027	0.215	0.835462	0.933323
6971	10538459	NM_007472	11826	aquaporin 1	Aqp1	1.027	0.381	0.714244	0.874919
6972	10445544	NM_053250	114570	cysteine-rich protein 3	Crip3	1.027	0.543	0.603692	0.814811
6973	10465912	NM_007999	14156	flap structure specific endonu	Fen1	1.027	0.036	0.972145	0.98815
6974	10481155	NM_207234	227656	REX4, RNA exonuclease 4 homolo	Rexo4	1.027	-0.036	0.971986	0.98815
6975	10346150	NM_019790	56363	transmembrane protein with EGF	Tmeff2	1.027	-0.04	0.969558	0.987616
6976	10560862	BC145686	641361	RIKEN cDNA 2310033E01 gene	2310033E01Rik	1.027	0.702	0.504878	0.747036
6977	10490541	ENSMUST00000098982	676369	predicted gene, OTTMUSG0000001	OTTMUSG00000016394	1.027	0.424	0.684183	0.86012
6978	10527012	NM_008494	16848	LFNG O-fucosylpeptide 3-beta-N	Lfng	1.027	0.15	0.884562	0.954633
				RIKEN cDNA C230078M08					

6979	10443007	NM_176995	319749	gene	C230078M08Rik	1.027	0.54	0.605149	0.815765
6980	10530096					1.027	0.148	0.886704	0.955515
6981	10401774	ENSMUST00000051601	217738	thrombospondin, type I, domain	Thsd3	1.027	0.244	0.814199	0.925212
6982	10599222	NM_019668	22209	ubiquitin-conjugating enzyme E	Ube2a	1.027	-0.208	0.841134	0.935777
6983	10447315					1.027	0.302	0.771294	0.905701
6984	10461547	NM_181403	107305	vacuolar protein sorting 37C (	Vps37c	1.027	0.199	0.847616	0.938277
6985	10379445	NM_011751	22680	zinc finger protein 207	Zfp207	1.027	0.761	0.470915	0.722763
6986	10457942	NM_009308	20983	synaptotagmin IV	Syt4	1.027	0.387	0.709993	0.873031
6987	10449955	NM_130882	170716	cytochrome P450, family 4, sub	Cyp4f13	1.027	0.533	0.610221	0.818642
6988	10585905	NM_029922	67287	poly (ADP-ribose) polymerase f	Parp6	1.027	0.765	0.468374	0.720616
6989	10425695	NM_033218	20788	sterol regulatory element bind	Srebf2	1.027	0.133	0.897828	0.959787
6990	10401035	NM_207707	13983	estrogen receptor 2 (beta)	Esr2	1.027	0.686	0.51421	0.754507
6991	10377431	NM_009497	22318	vesicle-associated membrane pr	Vamp2	1.027	0.091	0.930041	0.972493
6992	10464128	NM_007611	12369	caspase 7	Casp7	1.027	0.234	0.821563	0.92863
6993	10470125	ENSMUST00000064242	545410	predicted gene, OTTMUSG0000001	OTTMUSG00000012511	1.027	1.487	0.179347	0.434671
6994	10588542	BC125546	75470	IQ motif containing F5	Iqcf5	1.027	0.715	0.497385	0.741763
6995	10512489	BC080700	230098	RIKEN cDNA E130306D19 gene	E130306D19Rik	1.027	0.481	0.644857	0.83943
6996	10522472	NM_024183	66899	FIP1 like 1 (S. cerevisiae)	Fip1l1	1.027	0.295	0.776365	0.908709
6997	10478647	NM_020333	57138	solute carrier family 12, memb	Slc12a5	1.027	0.4	0.700606	0.86896
6998	10532407	NM_029337	75560	E1A binding protein p400	Ep400	1.027	0.312	0.763592	0.901503
6999	10535389	NM_080561	108086	ring finger protein 216	Rnf216	1.027	0.254	0.806722	0.921832
7000	10555116	ENSMUST00000070021	791341	predicted gene, ENSMUSG0000005	ENSMUSG00000056106	1.027	0.052	0.960067	0.985
7001	10405566	BC107250	328258	expressed sequence AU042651	AU042651	1.027	0.806	0.445833	0.703765
7002	10600065	NM_020280	17140	melanoma antigen, family A, 4	Magea4	1.027	0.356	0.731979	0.88455
7003	10463517	NM_001081214	226169	peroxisome proliferative activ	Pprc1	1.027	0.219	0.832702	0.932699
7004	10586700	NM_013646	19883	RAR-related orphan receptor al	Rora	1.027	0.133	0.897733	0.959787
7005	10391518	NM_007863	13384	membrane protein, palmitoylate	Mpp3	1.027	0.718	0.495311	0.740179
7006	10405686	BC134405	328264	predicted gene, EG328264	EG328264	1.027	0.351	0.735269	0.886784
7007	10371012	NM_010722	16907	lamin B2	Lmnb2	1.027	0.637	0.543628	0.775859
7008	10506893	NM_146150	230598	nardilysin, N-arginine dibasic	Nrd1	1.027	0.41	0.693808	0.865705
7009	10449394	NM_026836	68776	TAF11 RNA polymerase II, TATA	Taf11	1.027	-0.207	0.841511	0.935878
7010	10410136	XR_004644	674402	similar to Peptidyl-prolyl cis	LOC674402	1.026	-0.228	0.826111	0.929952
7011	10552966	NM_008807	56734	tubby-like protein 2	Tulp2	1.026	0.382	0.713517	0.874653
7012	10386850	NM_011308	20185	nuclear receptor co-repressor	Ncor1	1.026	0.779	0.460652	0.715179
7013	10572724	NM_145624	236193	zinc finger protein 709	Zfp709	1.026	0.008	0.994193	0.997702
7014	10600082	NM_010941	18194	NAD(P) dependent steroid dehyd	Nsdhl	1.026	-0.586	0.57552	0.797076
7015	10371830	NM_025914	67019	ARP6 actin-related protein 6 h	Actr6	1.026	-0.056	0.956944	0.983559
7016	10551752	ENSMUST00000098602	114675	RIKEN cDNA 4932431P20 gene	4932431P20Rik	1.026	0.704	0.503669	0.746064
7017	10410351	BC047145	380856	expressed sequence AA987161	AA987161	1.026	-0.164	0.874587	0.949978
7018	10598837					1.026	0.627	0.550034	0.78027
7019	10584252	XM_994373	676959	similar to Urinary protein 1 p	LOC676959	1.026	0.57	0.585784	0.80308
7020	10474477	XR_034254	623301	similar to LaXp180 protein	LOC623301	1.026	0.085	0.934229	0.97382
7021	10490706	ENSMUST00000108789	269401	zinc finger protein 512B	Znf512b	1.026	-0.005	0.995993	0.998402
7022	10390484	NM_026186	67480	coiled-coil domain containing	Ccdc49	1.026	0.358	0.730281	0.883456
7023	10493235	NM_198410	68957	progestin and adipoQ receptor	Paqr6	1.026	0.886	0.404005	0.668777
7024	10375926	NM_019411	19052	protein phosphatase 2 (formerl	Ppp2ca	1.026	0.077	0.940864	0.977046
7025	10519138	ENSMUST00000088499	100038426	predicted gene, ENSMUSG0000007	ENSMUSG00000073682	1.026	0.158	0.878935	0.952091
7026	10442258	NM_001025373	74670	RIKEN cDNA 4930432O21 gene	4930432O21Rik	1.026	-0.142	0.891189	0.957485
7027	10376507	ENSMUST00000096104	74476	RIKEN cDNA 4933439C10 gene	4933439C10Rik	1.026	0.095	0.926836	0.971063
7028	10437134	NM_007890	13548	dual-specificity tyrosine-(Y)-	Dyrk1a	1.026	0.4	0.700929	0.868962
7029	10384456					1.026	0.177	0.864022	0.945829
7030	10423388	NM_133365	110082	dynein, axonemal, heavy chain	Dnahc5	1.026	0.475	0.648573	0.841922

7030	10423388	NM_133365	110082	dynein, axonemal, heavy chain	Dnahc5	1.026	0.475	0.648573	0.841922
7031	10592870	NM_001033469	382074	forkhead box R1	Foxr1	1.026	0.247	0.811908	0.924032
7032	10409369	NM_033610	104069	synuclein, beta	Sncb	1.026	0.427	0.681648	0.859335
7033	10474333	AK140480	18508	paired box gene 6	Pax6	1.026	-0.363	0.726866	0.881629
7034	10559853	NM_011334	12727	chloride channel 4-2	Clcn4-2	1.026	0.449	0.666727	0.851355
7035	10501277	NM_175470	229714	G protein-coupled receptor 61	Gpr61	1.026	-0.149	0.885702	0.95523
7036	10386193	ENSMUST00000081743	258179	olfactory receptor 331	Olfr331	1.026	0.685	0.514983	0.754817
7037	10512301	NM_001017362	550619	AT rich interactive domain 3C	Arid3c	1.026	-0.273	0.792498	0.91549
7038	10582390	NM_009698	11821	adenine phosphoribosyl transfe	Aprt	1.026	0.18	0.86218	0.944751
7039	10435581	NM_029977	77782	polymerase (DNA directed), the	Polq	1.026	0.605	0.563934	0.79039
7040	10408610	NM_009450	22151	tubulin, beta 2a	Tubb2a	1.026	0.436	0.675853	0.855911
7041	10552570	NM_010640	16613	kallikrein 1-related peptidase	Klk1b11	1.026	0.448	0.666983	0.851389
7042	10567335	NM_019580	56209	glycerophosphodiester phosphod	Gde1	1.026	-0.285	0.783939	0.912068
7043	10369210	NM_019760	56442	serine incorporator 1	Serinc1	1.026	0.28	0.787345	0.913152
7044	10376603	NM_021354	13495	developmentally regulated GTP	Drg2	1.026	-0.429	0.680621	0.85838
7045	10409464	NM_019813	56320	drebrin 1	Dbn1	1.026	0.377	0.71729	0.876366
7046	10505356	ENSMUST00000107415	72701	zinc fingerprotein 618	Zfp618	1.026	0.25	0.809451	0.923176
7047	10450038	NM_020581	57875	angiopoietin-like 4	Angptl4	1.026	1.187	0.272958	0.547572
7048	10550424	NM_054064	114872	pregnancy-specific glycoprotei	Psg29	1.026	0.592	0.571878	0.795983
7049	10437180	NM_015825	50795	SH3-binding domain glutamic ac	Sh3bgr	1.026	0.68	0.517865	0.756834
7050	10479270	ENSMUST00000041998	68175	RIKEN cDNA 4930591A17 gene	4930591A17Rik	1.026	0.504	0.629296	0.831256
7051	10387295	NM_172560	216846	centrobin, centrosomal BRCA2 i	Cntrob	1.026	0.613	0.558849	0.786425
7052	10423654	NM_054049	107587	odd-skipped related 2 (Drosoph	Osr2	1.026	0.554	0.596437	0.809856
7053	10394448	NM_030723	80913	pumilio 2 (Drosophila)	Pum2	1.026	0.455	0.662739	0.849837
7054	10381514	NM_027987	52685	CD300 antigen like family memb	Cd300lg	1.026	0.753	0.475141	0.726714
7055	10539295	NM_033606	93838	DEAQ RNA-dependent ATPase	Dqx1	1.026	0.836	0.430046	0.690844
7056	10453276	EF222207	240174	thyroid adenoma associated	Thada	1.026	0.185	0.858482	0.943242
7057	10523923	NM_028481	73254	coiled-coil domain containing	Ccdc18	1.026	0.075	0.941936	0.977644
7058	10459785	NM_201354	269037	gene model 672, (NCBI)	Gm672	1.026	0.653	0.533873	0.767853
7059	10439915					1.026	0.281	0.786811	0.91293
7060	10421026	ENSMUST00000100447	100038671	predicted gene, ENSMUSG0000007	ENSMUSG00000075548	1.026	0.493	0.636437	0.834887
7061	10570448	ENSMUST00000098916	100038645	predicted gene, ENSMUSG0000007	ENSMUSG00000074461	1.025	0.016	0.98784	0.994998
7062	10603208	NM_010797	17318	midline 1	Mid1	1.025	0.744	0.480328	0.729941
7063	10417689	NM_025550	66413	proteasome (prosome, macropain	Psmd6	1.025	0.02	0.984392	0.993413
7064	10552270	NM_001004139	70227	zinc finger protein 619	Zfp619	1.025	-0.232	0.823214	0.929358
7065	10433034	NM_146065	223922	activating transcription facto	Atf7	1.025	0.822	0.43739	0.696704
7066	10601922					1.025	0.515	0.621981	0.826961
7067	10346592	AK144579	100038354	predicted gene, ENSMUSG0000007	ENSMUSG00000073665	1.025	0.66	0.529524	0.764772
7068	10347807	NM_007734	12828	collagen, type IV, alpha 3	Col4a3	1.025	0.748	0.478043	0.728592
7069	10537441	NM_178873	57869	aarF domain containing kinase	Adck2	1.025	0.272	0.793417	0.915898
7070	10596070					1.025	0.106	0.91873	0.967805
7071	10411949	NM_029879	52882	regulator of G-protein signall	Rgs7bp	1.025	1.032	0.335246	0.610757
7072	10412913	XR_033495	667344	similar to Speer4e protein	LOC667344	1.025	0.745	0.480115	0.729941
7073	10400326	NM_025456	66266	E2F-associated phosphoprotein	Eapp	1.025	-0.184	0.858943	0.943374
7074	10444386	NM_134116	106512	G-protein signalling modulator	Gpsm3	1.025	0.446	0.66846	0.852263
7075	10416488	ENSMUST00000022579	75272	RIKEN cDNA 4930564B18 gene	4930564B18Rik	1.025	0.338	0.7451	0.891615
7076	10467006	NM_010051	13380	dickkopf homolog 1 (Xenopus la	Dkk1	1.025	0.327	0.752855	0.89585
7077	10529758	NM_001081422	665775	RIKEN cDNA A230054D04 gene	A230054D04Rik	1.025	0.25	0.809495	0.923176
7078	10463695	BC027506	66439	RIKEN cDNA 2010012O05 gene	2010012O05Rik	1.025	0.173	0.867699	0.947039
7079	10404055	NM_010377	107970	histone cluster 1, H1t	Hist1h1t	1.025	0.679	0.518306	0.756954
7080	10461671	NM_172635	225929	protein associated with topois	Patl1	1.025	0.168	0.871217	0.948575

7081	10498053	NM_026358	67749	RIKEN cDNA 4930583H14 gene	4930583H14Rik	1.025	0.414	0.690683	0.864369
7082	10554839	NM_146194	233489	phosphatidylinositol binding c	Picalm	1.025	0.322	0.756417	0.897871
7083	10512165	NM_139236	230082	nucleolar protein family 6 (RN	Nol6	1.025	0.672	0.522424	0.759283
7084	10392699	ENSMUST00000100254	100038732	predicted gene, OTTMUSG0000000	OTTMUSG00000003311	1.025	0.886	0.404348	0.668978
7085	10541188					1.025	0.661	0.528862	0.764129
7086	10605571	NM_212444	14933	glycerol kinase	Gyk	1.025	0.582	0.578211	0.79826
7087	10549820	NM_178028	232836	galanin-like peptide	Galp	1.025	0.662	0.528804	0.764097
7088	10572461	ENSMUST00000116458	637079	RIKEN cDNA 2410018E23 gene	2410018E23Rik	1.025	0.613	0.558668	0.786292
7089	10457862	NM_144861	225283	cDNA sequence BC021395	BC021395	1.025	0.177	0.864628	0.946153
7090	10555414	NM_024287	19346	RAB6, member RAS oncogene fami	Rab6	1.025	0.503	0.629885	0.831325
7091	10424119	NM_010930	18133	nephroblastoma overexpressed g	Nov	1.025	0.46	0.659373	0.848209
7092	10571784					1.025	0.574	0.583517	0.801489
7093	10539364	NM_007835	13191	dynactin 1	Dctn1	1.025	-0.078	0.940161	0.9767
7094	10499265	NM_033573	94315	papillary renal cell carcinoma	Prcc	1.025	0.138	0.89378	0.958124
7095	10481909	NM_013890	30050	F-box and WD-40 domain protein	Fbxw2	1.025	0.426	0.682203	0.859614
7096	10507112	NM_009185	20460	Scl/Tal1 interrupting locus	Stil	1.025	-0.22	0.831595	0.932402
7097	10586194	NM_172522	214058	multiple EGF-like-domains 11	Megf11	1.025	0.787	0.456087	0.712435
7098	10385616	NM_172557	216724	RUN and FYVE domain containing	Rufy1	1.025	0.38	0.715217	0.875355
7099	10432573	NM_008732	18174	solute carrier family 11 (prot	Slc11a2	1.025	0.394	0.705297	0.871482
7100	10574641	NM_145604	234678	RIKEN cDNA D230025D16 gene	D230025D16Rik	1.025	-0.288	0.781335	0.911076
7101	10463661	NM_053100	93679	tripartite motif protein 8	Trim8	1.025	0.049	0.962568	0.985405
7102	10462140	NM_028785	76088	dedicator of cytokinesis 8	Dock8	1.025	0.166	0.872832	0.949165
7103	10535608	NM_001013774	381686	expressed sequence AW146299	AW146299	1.025	0.379	0.715459	0.875402
7104	10380830	NM_001080935	68127	RIKEN cDNA B230217C12 gene	B230217C12Rik	1.025	0.386	0.710876	0.873183
7105	10420503	NM_001081024	239122	SET domain, bifurcated 2	Setdb2	1.025	-0.164	0.874364	0.949978
7106	10383409	NM_008101	14527	glucagon receptor	Gcgr	1.025	0.39	0.707642	0.872268
7107	10568243	NM_146203	233893	zinc finger protein 764	Zfp764	1.025	0.299	0.773623	0.9067
7108	10370025	NM_011418	20587	SWI/SNF related, matrix associ	Smarcb1	1.025	-0.162	0.875979	0.95093
7109	10493409	NM_011886	24045	secretory carrier membrane pro	Scamp3	1.025	-0.014	0.98944	0.995361
7110	10481518	NM_022415	64292	prostaglandin E synthase	Ptges	1.025	0.486	0.64133	0.837465
7111	10469828	NM_177611	215632	pleckstrin and Sec7 domain con	Psd4	1.025	0.831	0.432782	0.693239
7112	10361787					1.025	0.497	0.633967	0.833567
7113	10430066	NM_007989	14106	forkhead box H1	Foxh1	1.025	0.661	0.529126	0.76441
7114	10457407					1.025	0.838	0.428741	0.689638
7115	10449386	NM_001033279	224647	DNA segment, Chr 17, Wayne Sta	D17Wsu92e	1.025	-0.11	0.915507	0.966659
7116	10465072	NM_027877	71711	MUS81 endonuclease homolog (ye	Mus81	1.025	0.272	0.792916	0.915604
7117	10603659	NM_001048208	26896	mediator complex subunit 14	Med14	1.025	0.458	0.660728	0.848802
7118	10397346	NM_010234	14281	FBJ osteosarcoma oncogene	Fos	1.025	0.494	0.636001	0.834684
7119	10379968	NM_019756	56427	tubulin, delta 1	Tubd1	1.025	0.373	0.720164	0.878163
7120	10375735	NM_021510	59013	heterogeneous nuclear ribonucl	Hnrph1	1.025	0.386	0.710523	0.873041
7121	10379840	BC007156	66196	myosin XIX	Myo19	1.025	0.643	0.540334	0.772836
7122	10362394	NM_027168	69692	HD domain containing 2	Hddc2	1.025	-0.322	0.756612	0.897871
7123	10566743	NM_181853	330627	tripartite motif-containing 66	Trim66	1.025	0.914	0.390463	0.659
7124	10429524	BC055822	78725	RIKEN cDNA D730001G18 gene	D730001G18Rik	1.025	0.729	0.488999	0.736349
7125	10509014	BC043057	27981	DNA segment, Chr 4, Wayne Stat	D4Wsu53e	1.024	0.646	0.538084	0.771077
7126	10488472	ENSMUST00000046399	71881	RIKEN cDNA 2310001A20 gene	2310001A20Rik	1.024	0.215	0.835831	0.933525
7127	10514556	AK132939	100038661	predicted gene,	ENSMUSG00000066990	1.024	0.666	0.526291	0.762289

				ENSMUSG0000006					
7128	10547034	NM_029780	110157	v-raf-leukemia viral oncogene	Raf1	1.024	0.659	0.530346	0.765382
7129	10394699	NM_009072	19878	Rho-associated coiled-coil con	Rock2	1.024	0.056	0.957012	0.983559
7130	10516466	NM_026670	68310	zinc finger, MYM domain contai	Zmym1	1.024	0.213	0.837392	0.934421
7131	10496956	NM_178016	329777	phosphatidylinositol glycan an	Pigk	1.024	-0.253	0.807231	0.922301
7132	10362186	NM_021509	59012	monooxygenase, DBH-like 1	Moxd1	1.024	-0.482	0.644029	0.838972
7133	10432429					1.024	0.388	0.709126	0.872707
7134	10562911	NM_001042655	233204	TBC1 domain family, member 17	Tbc1d17	1.024	0.146	0.888089	0.955903
7135	10519203	NM_001033394	320587	RIKEN cDNA A230069A22 gene	A230069A22Rik	1.024	0.301	0.771798	0.90585
7136	10532999	ENSMUST00000112066	75387	sirtuin 4 (silent mating type	Sirt4	1.024	0.077	0.941039	0.97709
7137	10483665					1.024	0.45	0.665642	0.850998
7138	10421694					1.024	0.457	0.661421	0.849228
7139	10564857	NM_173011	269951	isocitrate dehydrogenase 2 (NA	Idh2	1.024	0.264	0.799387	0.919009
7140	10589938	ENSMUST00000098321	100038368	predicted gene, ENSMUSG0000007	ENSMUSG00000074035	1.024	0.219	0.832592	0.932679
7141	10504562	AK016397	66362	exosome component 3	Exosc3	1.024	0.191	0.853959	0.940913
7142	10566302	NM_207144	258247	olfactory receptor 645	Olfr645	1.024	0.456	0.661943	0.84942
7143	10572693	NM_013564	16336	insulin-like 3	Insl3	1.024	0.41	0.693855	0.865705
7144	10476880	XR_034866	381384	RIKEN cDNA A530006G24 gene	A530006G24Rik	1.024	0.333	0.748846	0.893695
7145	10434932	BC099947	224093	cDNA sequence BC022623	BC022623	1.024	0.276	0.790144	0.914502
7146	10572745	NM_146338	258335	olfactory receptor 374	Olfr374	1.024	0.578	0.58056	0.799564
7147	10420359	NM_016975	14611	gap junction protein, alpha 3	Gja3	1.024	0.871	0.41173	0.675587
7148	10406248					1.024	0.995	0.352087	0.625224
7149	10533644	NM_029929	77573	vacuolar protein sorting 33A (	Vps33a	1.024	0.425	0.683252	0.859827
7150	10426544	BC022913	67739	RIKEN cDNA 4930570C03 gene	4930570C03Rik	1.024	-0.156	0.880045	0.952396
7151	10375499					1.024	0.072	0.944369	0.977948
7152	10441400	NM_001085355	239985	AT rich interactive domain 1B	Arid1b	1.024	0.252	0.80812	0.922738
7153	10403258	NM_008112	14569	guanosine diphosphate (GDP) di	Gdi2	1.024	0.135	0.896237	0.95935
7154	10463043	NM_010001	13096	cytochrome P450, family 2, sub	Cyp2c37	1.024	0.098	0.924758	0.970324
7155	10569393	ENSMUST00000072468	97423	expressed sequence R74862	R74862	1.024	0.089	0.931635	0.972759
7156	10551741	NM_013874	29861	D4, zinc and double PHD finger	Dpf1	1.024	-0.031	0.976329	0.990137
7157	10365518	NM_175331	103466	5'-nucleotidase domain contain	Nt5dc3	1.024	0.054	0.958522	0.984334
7158	10451198	NM_001025250	22339	vascular endothelial growth fa	Vegfa	1.024	0.183	0.859925	0.943624
7159	10493633	NM_022314	59069	tropomyosin 3, gamma	Tpm3	1.024	0.234	0.821761	0.92863
7160	10349453	NM_178690	226407	RAB3 GTPase activating protein	Rab3gap1	1.024	0.32	0.758348	0.898716
7161	10599243	NM_153503	69942	ring finger protein 113A1	Rnf113a1	1.024	-0.172	0.868192	0.947187
7162	10442762	NM_178372	328780	protease, serine, 34	Prss34	1.024	0.266	0.797689	0.917953
7163	10436828	NM_016968	50914	oligodendrocyte transcription	Olig1	1.024	0.136	0.895443	0.958936
7164	10474807	ENSMUST00000099551	100043272	similar to F32B6.11	LOC100043272	1.024	0.252	0.808103	0.922738
7165	10364810	NM_139226	246086	one cut domain, family member	Onecut3	1.024	0.476	0.64812	0.84176
7166	10560908	ENSMUST00000116343	232974	predicted gene, EG232974	EG232974	1.024	0.321	0.757083	0.898052
7167	10442311	NM_153784	212733	coiled-coil domain containing	Ccdc64b	1.024	0.63	0.548316	0.77872
7168	10605324	NM_145406	214601	solute carrier family 10 (sodi	Slc10a3	1.024	0.619	0.554857	0.783816
7169	10539321	NM_001081266	243510	coiled-coil domain containing	Ccdc142	1.024	-0.014	0.988937	0.995308
7170	10605659					1.024	0.087	0.932688	0.973153
7171	10466441	NM_173028	271564	vacuolar protein sorting 13A (	Vps13a	1.024	0.504	0.629618	0.831325
7172	10448262	NM_001033496	449521	zinc finger protein 213	Zfp213	1.024	0.695	0.508861	0.750513
7173	10540480	NM_026011	67166	ADP-ribosylation factor-like 8	Arl8b	1.024	0.03	0.976955	0.990541
7174	10543522	XR_032572	384360	hypothetical gene supported by	LOC384360	1.024	0.238	0.818593	0.927912
7175	10568202	NM_017461	54204	septin 1	Sept1	1.023	0.621	0.553543	0.783151
7176	10400460	NM_145442	217588	MAP3K12 binding inhibitory pro	Mbip	1.023	0.138	0.89383	0.958124
7177	10504703	NM_001033201	433702	expressed sequence AU014645	AU014645	1.023	0.335	0.747469	0.892656
7178	10362389					1.023	-0.002	0.998828	0.999589
				UDP-GlcNAc:betaGal beta-1,3-					

7179	10579607	BC026418	72297	N-	B3gnt3	1.023	-0.016	0.987456	0.994834
7180	10369779	NM_001005419	211488	2-aminoethanethiol (cysteamine	Ado	1.023	0.056	0.956575	0.983555
7181	10592079	ENSMUST00000066604	442804	RIKEN cDNA A130066N16 gene	A130066N16Rik	1.023	0.521	0.618292	0.823818
7182	10584165	NM_026324	67703	kin of IRRE like 3 (Drosophila	Kirrel3	1.023	0.724	0.491787	0.738245
7183	10553450	NM_001037906	338352	NEL-like 1 (chicken)	Nell1	1.023	0.304	0.769907	0.904792
7184	10558057	NM_172255	207425	bromodomain and WD repeat doma	Brwd2	1.023	0.189	0.855458	0.941478
7185	10397741	NM_008947	19179	protease (prosome, macropain)	Psmc1	1.023	-0.147	0.887138	0.955613
7186	10372096					1.023	0.856	0.419731	0.682047
7187	10504692	NM_021883	21916	tropomodulin 1	Tmod1	1.023	-0.037	0.971677	0.988148
7188	10582146	NM_025734	66733	potassium voltage-gated channe	Kcng4	1.023	0.212	0.838131	0.934421
7189	10377588	NM_009235	20670	SRY-box containing gene 15	Sox15	1.023	0.259	0.80262	0.919965
7190	10389561	NM_026191	67487	DEAH (Asp-Glu-Ala-His) box pol	Dhx40	1.023	-0.525	0.615616	0.822286
7191	10591517	NM_009878	12581	cyclin-dependent kinase inhibi	Cdkn2d	1.023	-0.046	0.96428	0.9859
7192	10508074	NM_007782	12986	colony stimulating factor 3 re	Csf3r	1.023	0.727	0.490017	0.737262
7193	10421853	NM_010701	16840	leukocyte cell derived chemota	Lect1	1.023	-0.106	0.918239	0.967805
7194	10516046					1.023	1.15	0.286961	0.562743
7195	10450622	BC028847	73242	RIKEN cDNA 2610110G12 gene	2610110G12Rik	1.023	0.216	0.835179	0.933323
7196	10374551					1.023	-0.182	0.860271	0.943883
7197	10379539					1.023	0.425	0.68309	0.859827
7198	10347117	NM_001080809	227231	carbamoyl-phosphate synthetase	Cps1	1.023	0.57	0.585714	0.80308
7199	10492335	NM_028712	74012	RAP2B, member of RAS oncogene	Rap2b	1.023	0.149	0.885506	0.955213
7200	10349051	NM_009399	21934	tumor necrosis factor receptor	Tnfrsf11a	1.023	0.261	0.801095	0.919467
7201	10365991	NM_007884	13516	epiphycan	Epyc	1.023	0.353	0.734475	0.886559
7202	10489705	NM_054055	114644	solute carrier family 13 (sodi	Slc13a3	1.023	0.262	0.800614	0.91941
7203	10400191	NM_052973	94186	striatin, calmodulin binding p	Strn3	1.023	0.353	0.734217	0.886455
7204	10435251	NM_134251	171286	solute carrier family 12 (pota	Slc12a8	1.023	0.873	0.410992	0.675081
7205	10487858	NM_027641	70997	sperm flagellar 1	Spef1	1.023	0.534	0.609631	0.818311
7206	10479627	NM_025482	66314	tumor protein D52-like 2	Tpd52l2	1.023	-0.002	0.998173	0.99936
7207	10354191	NM_001033135	67702	ring finger protein 149	Rnf149	1.023	0.101	0.922156	0.968977
7208	10370798	NM_001113548	66548	ADAMTS-like 5	Adamtsl5	1.023	0.646	0.538154	0.771126
7209	10601659	NM_026838	68792	sushi-repeat-containing protei	Srpx2	1.023	0.658	0.530935	0.765398
7210	10456329					1.023	0.111	0.914719	0.966446
7211	10472418	AK039017	100038743	predicted gene, OTTMUSG0000001	OTTMUSG00000013098	1.023	0.157	0.87971	0.952314
7212	10393309	BC029621	67763	phosphoribosyl pyrophosphate s	Prpsap1	1.023	-0.122	0.906275	0.963405
7213	10526630	NM_015799	50765	transferrin receptor 2	Trfr2	1.023	0.963	0.366583	0.637472
7214	10473363	NM_013899	30059	translocase of inner mitochond	Timm10	1.023	-0.119	0.908492	0.963723
7215	10501649	NM_025517	66368	RNA terminal phosphate cyclase	Rtcd1	1.023	-0.025	0.980836	0.991919
7216	10604612					1.023	0.755	0.474148	0.725639
7217	10446309	NM_001081653	620292	contactin associated protein-l	Cntnap5c	1.023	0.626	0.550874	0.781094
7218	10534654	NM_027318	70103	zinc finger, HIT domain contai	Znhit1	1.023	-0.204	0.843875	0.936634
7219	10377490	NM_009659	11686	arachidonate 12-lipoxygenase,	Alox12b	1.023	-0.115	0.911243	0.964566
7220	10371176	NM_008688	18029	nuclear factor I/C	Nfic	1.023	0.168	0.871274	0.948575
7221	10557587	NM_177362	244216	zinc finger protein 771	Zfp771	1.023	0.49	0.638362	0.835923
7222	10475708	NM_026678	109778	biliverdin reductase A	Blvra	1.023	0.198	0.848198	0.938472
7223	10458478	NM_175684	319262	FCH and double SH3 domains 1	Fchsd1	1.023	0.631	0.547688	0.778543
7224	10422718	NM_026213	67515	tetratricopeptide repeat domai	Ttc33	1.023	0.432	0.67839	0.857067
7225	10431371	NM_199198	170787	histone deacetylase 10	Hdac10	1.023	0.712	0.498876	0.742429
7226	10352947	NM_025300	27395	mitochondrial ribosomal protei	Mrpl15	1.023	-0.123	0.90538	0.963333
7227	10531208	NM_001033310	231430	COX18 cytochrome c oxidase ass	Cox18	1.023	0.313	0.763352	0.901493
7228	10594322	NM_019663	56469	protein inhibitor of activated	Pias1	1.023	0.039	0.970055	0.987783
7229	10581643					1.023	0.856	0.419481	0.681847

7230	10346374	NM_009676	11761	aldehyde oxidase 1	Aox1	1.023	0.787	0.456571	0.712611
7231	10595911	NR_003248	768252	forkhead box L2 opposite stran	Foxl2os	1.023	0.804	0.447197	0.704901
7232	10458355	NM_146085	225372	amyloid beta (A4) precursor pr	Apbb3	1.023	0.119	0.908344	0.963723
7233	10529041	NM_016703	50907	prolactin regulatory element b	Preb	1.023	0.008	0.994045	0.997702
7234	10470349	NM_001001322	279028	a disintegrin-like and metallo	Adamts13	1.023	0.533	0.610099	0.818617
7235	10551626	NM_010706	16855	lectin, galactose binding, sol	Lgals4	1.023	0.31	0.765122	0.90235
7236	10400054					1.023	0.9	0.397139	0.664239
7237	10462231	NM_145831	226049	doublesex and mab-3 related tr	Dmrt2	1.023	0.12	0.908092	0.963723
7238	10356833	NM_021537	59041	serine/threonine kinase 25 (ye	Stk25	1.023	0.357	0.731631	0.884308
7239	10445542					1.023	0.48	0.64529	0.839839
7240	10486697	ENSMUST00000110675	640543	transglutaminase 7	Tgm7	1.023	0.38	0.715225	0.875355
7241	10512728	NM_173033	272027	cDNA sequence BC057893	BC057893	1.023	-0.237	0.819394	0.928264
7242	10562382	NM_025948	67070	LSM14 homolog A (SCD6, S. cere	Lsm14a	1.022	0.402	0.699031	0.868099
7243	10576661	NM_010578	16412	integrin beta 1 (fibronectin r	Itgb1	1.022	0.283	0.784917	0.912507
7244	10518494	NM_001083342	242748	patched domain containing 2	Ptchd2	1.022	0.213	0.837074	0.934383
7245	10381548	NM_153544	217216	cDNA sequence BC030867	BC030867	1.022	-0.167	0.871824	0.94878
7246	10599487	NM_028773	74131	SAM and SH3 domain containing	Sash3	1.022	0.951	0.372506	0.642907
7247	10427418					1.022	-0.142	0.891117	0.957456
7248	10480605	NM_021393	58202	cofactor of BRCA1	Cobra1	1.022	0.343	0.741338	0.889595
7249	10585825	NM_026942	69106	stomatin-like 1	Stoml1	1.022	0.332	0.749374	0.893972
7250	10465881	NM_011913	24115	bestrophin 1	Best1	1.022	0.436	0.675382	0.855772
7251	10550980	NM_133743	72434	Ly6/Plaur domain containing 3	Lypd3	1.022	0.314	0.762304	0.901088
7252	10569341	NR_001592	14955	H19 fetal liver mRNA	H19	1.022	0.098	0.924862	0.970324
7253	10530892	NM_007683	12617	centromere protein C1	Cenpc1	1.022	-0.26	0.801983	0.919813
7254	10432593	NM_153407	207785	cysteine-serine-rich nuclear p	Csnrp2	1.022	0.542	0.604015	0.815116
7255	10521515	NM_145920	68525	Ellis van Creveld syndrome 2 h	Evc2	1.022	0.745	0.479708	0.729728
7256	10371970	BC121826	71761	amidohydrolase domain containi	Amdhd1	1.022	0.113	0.913235	0.96552
7257	10433536	NM_177562	74374	C-type lectin domain family 16	Clec16a	1.022	0.664	0.527095	0.762858
7258	10483401	NM_025565	66442	SPC25, NDC80 kinetochore compl	Spc25	1.022	0.093	0.928358	0.971746
7259	10593767	NM_148944	108015	cholinergic receptor, nicotini	Chrnb4	1.022	0.314	0.762574	0.901202
7260	10597875	NM_010012	13124	cytochrome P450, family 8, sub	Cyp8b1	1.022	0.521	0.618059	0.82356
7261	10497309	NM_029068	74718	sorting nexin 16	Snx16	1.022	0.116	0.911071	0.964566
7262	10438801	NM_183064	14167	fibroblast growth factor 12	Fgf12	1.022	0.235	0.820732	0.92863
7263	10537406	NM_001101507	665180	C-type lectin domain family, m	Clec2l	1.022	0.23	0.824156	0.929508
7264	10558118	NM_001081038	330660	BTB (POZ) domain containing 16	Btbd16	1.022	0.247	0.812062	0.924124
7265	10401944					1.022	0.292	0.778836	0.910097
7266	10577048	NM_133971	102334	ankyrin repeat domain 10	Ankrd10	1.022	0.154	0.882143	0.953469
7267	10590558	NM_011606	21922	C-type lectin domain family 3,	Clec3b	1.022	-0.03	0.977116	0.990609
7268	10571647	BC049135	66756	RIKEN cDNA 4933411K20 gene	4933411K20Rik	1.022	0.387	0.70993	0.873031
7269	10568434					1.022	0.212	0.837625	0.934421
7270	10403975	ENSMUST00000055536	193453	predicted gene, OTTMUSG0000000	OTTMUSG00000000469	1.022	0.15	0.884894	0.954845
7271	10546066	NM_133934	57905	ISY1 splicing factor homolog (	Isy1	1.022	-0.111	0.91502	0.966585
7272	10605614					1.022	0.523	0.616554	0.822954
7273	10562486	NM_145840	243923	regulator of G-protein signall	Rgs9bp	1.022	0.535	0.60894	0.817955
7274	10515690	ENSMUST00000075406	230676	cDNA sequence BC059842	BC059842	1.022	0.199	0.848075	0.938472
7275	10576401					1.022	0.383	0.713017	0.874277
7276	10363735	NM_010118	13654	early growth response 2	Egr2	1.022	0.132	0.898704	0.960077
7277	10490894	NM_007892	13559	E2F transcription factor 5	E2f5	1.022	0.13	0.899817	0.960314
7278	10515878	NM_011732	22608	Y box protein 1	Ybx1	1.022	-0.315	0.761539	0.900659
7279	10463457	NM_145503	226154	leucine zipper, putative tumor	Lzts2	1.022	0.188	0.856427	0.941981
7280	10559385	NM_145379	211577	MAS-related GPR, member F	Mrgprf	1.022	1.12	0.298736	0.574899
7281	10584200	NM_028040	71989	RNA pseudouridylate synthase d	Rpusd4	1.022	-0.039	0.970035	0.987783

7282	10520622	NR_003522	57742	abhydrolase domain containing	Abhd1	1.022	0.102	0.921414	0.968656
7283	10416464	NM_026083	67302	zinc finger CCCH type containi	Zc3h13	1.022	0.038	0.970995	0.988148
7284	10363312	BC119028	76138	coiled-coil domain containing	Ccdc138	1.022	0.44	0.67291	0.854651
7285	10595156	NM_025274	434423	developmental pluripotency ass	Dppa5a	1.022	-0.331	0.749998	0.894414
7286	10457273	NM_008448	16573	kinesin family member 5B	Kif5b	1.022	0.25	0.80931	0.923176
7287	10401192	NM_001008550	211978	zinc finger, FYVE domain conta	Zfyve26	1.022	0.72	0.49409	0.739456
7288	10495891	NM_173451	271970	arylsulfatase J	Arsj	1.022	0.472	0.650886	0.843602
7289	10592830	NM_027889	71732	vacuolar protein sorting 11 (y	Vps11	1.022	0.047	0.964079	0.985864
7290	10432006	NM_019572	56233	histone deacetylase 7	Hdac7	1.022	0.716	0.496497	0.741014
7291	10497808	NM_198192	229214	G protein-coupled receptor 103	Gpr103	1.022	0.87	0.412403	0.676163
7292	10564813	NM_008588	17292	mesoderm posterior 1	Mesp1	1.022	-0.449	0.666699	0.851355
7293	10565813	NR_002172	449630	predicted gene, EG449630	EG449630	1.022	0.558	0.593597	0.808175
7294	10494160	NM_016712	50874	tropomodulin 4	Tmod4	1.022	0.402	0.699298	0.868281
7295	10387588	NM_009089	20020	polymerase (RNA) II (DNA direc	Polr2a	1.022	0.159	0.877766	0.951715
7296	10391697	NM_010575	16399	integrin alpha 2b	Itga2b	1.022	0.621	0.553547	0.783151
7297	10565292	NM_007488	11864	aryl hydrocarbon receptor nucl	Arnt2	1.022	0.341	0.742824	0.89053
7298	10463981	ENSMUST00000095969	73713	RNA binding motif protein 20	Rbm20	1.022	0.696	0.508028	0.749912
7299	10557655	ENSMUST00000084563	546001	Snf2-related CREBBP activator	Srcap	1.022	0.61	0.560279	0.787564
7300	10532594	XM_912851	74376	myosin XVIIIb	Myo18b	1.022	0.321	0.757594	0.898154
7301	10454252					1.022	-0.43	0.679428	0.857705
7302	10529305	NM_026698	68366	transmembrane protein 129	Tmem129	1.022	0.332	0.749687	0.894292
7303	10373439	NM_134003	103284	zinc finger CCCH type containi	Zc3h10	1.022	0.659	0.5306	0.765382
7304	10414623	BC059018	268739	RIKEN cDNA E130112L23 gene	E130112L23Rik	1.022	0.554	0.596053	0.80968
7305	10443276	NM_001004366	268935	signal peptide, CUB domain, EG	Scube3	1.022	-0.025	0.980632	0.991919
7306	10464169	ENSMUST00000099297	75628	RIKEN cDNA 1700010L13 gene	1700010L13Rik	1.022	-0.056	0.956986	0.983559
7307	10525185	XM_001473338	100039686	hypothetical protein LOC100039	LOC100039686	1.022	0.224	0.828943	0.931175
7308	10546163	NM_008564	17216	minichromosome maintenance def	Mcm2	1.022	-0.212	0.838229	0.934421
7309	10361712	NM_172937	268281	SNF2 histone linker PHD RING h	Shprh	1.022	0.063	0.95142	0.981144
7310	10402519	NM_029654	76559	ATG2 autophagy related 2 homol	Atg2b	1.021	0.198	0.84815	0.938472
7311	10408739	ENSMUST00000078232	669420	predicted gene, ENSMUSG0000006	ENSMUSG00000063303	1.021	0.403	0.698541	0.867855
7312	10583920	NM_026189	67484	endonuclease/exonuclease/phosp	Eepd1	1.021	0.183	0.859616	0.943578
7313	10407511					1.021	0.403	0.698544	0.867855
7314	10408741	NM_145367	105245	thioredoxin domain containing	Txndc5	1.021	-0.269	0.795298	0.916955
7315	10579089	NM_177899	330788	RIKEN cDNA D330038O06 gene	D330038O06Rik	1.021	0.166	0.872698	0.949165
7316	10360321	NM_026725	68440	dual specificity phosphatase 2	Dusp23	1.021	-0.011	0.991721	0.996671
7317	10357878	NM_001008533	11539	adenosine A1 receptor	Adora1	1.021	0.565	0.588942	0.805212
7318	10562130	NM_194057	233081	free fatty acid receptor 1	Ffar1	1.021	0.116	0.910629	0.96426
7319	10448186	NM_029281	75424	zinc finger protein 820	Zfp820	1.021	0.223	0.829945	0.93159
7320	10478967	NM_024199	67337	cleavage stimulation factor, 3	Cstf1	1.021	0.054	0.958471	0.984334
7321	10583122	NM_013903	30800	matrix metallopeptidase 20 (en	Mmp20	1.021	0.381	0.714527	0.875126
7322	10572419	NM_007924	13716	elongation factor RNA polymera	Ell	1.021	0.411	0.693261	0.865563
7323	10593032	ENSMUST00000098827	100038468	predicted gene, ENSMUSG0000007	ENSMUSG00000074385	1.021	0.478	0.646917	0.840859
7324	10429520	NM_010742	17068	lymphocyte antigen 6 complex,	Ly6d	1.021	0.336	0.74619	0.892285
7325	10460735	NM_001111317	433215	cDNA sequence BC048609	BC048609	1.021	0.313	0.763304	0.901493
7326	10384615	NM_011023	18423	orthodenticle homolog 1 (Droso	Otx1	1.021	0.794	0.452364	0.708922
7327	10351640					1.021	0.252	0.808286	0.922808
7328	10553813	NM_011668	22215	ubiquitin protein ligase E3A	Ube3a	1.021	0.465	0.655911	0.846006
7329	10556820	NM_145586	233806	transmembrane protein 159	Tmem159	1.021	0.416	0.689683	0.863782
7330	10535410					1.021	0.798	0.450141	0.707431
7331	10568282	NM_009746	12055	B-cell CLL/lymphoma 7C	Bcl7c	1.021	0.042	0.967871	0.987137
7332	10421557	NM_008410	16432	integral membrane protein 2B	Itm2b	1.021	-0.104	0.919709	0.967952

7332	10421557	NM_008410	16432	integral membrane protein 2B	Itm2b	1.021	-0.104	0.919709	0.967952
7333	10580210	NM_009010	19358	RAD23a homolog (S. cerevisiae)	Rad23a	1.021	0.04	0.96952	0.987616
7334	10419096	NM_009160	20390	surfactant associated protein	Sftpd	1.021	0.611	0.560107	0.787428
7335	10485607	NM_001123327	99003	glutamine and serine rich 1	Qser1	1.021	0.1	0.922886	0.969148
7336	10460696	NM_134154	107375	solute carrier family 25, memb	Slc25a45	1.021	0.577	0.581427	0.800326
7337	10380891	NM_008890	18948	phenylethanolamine-N-methyltra	Pnmt	1.021	0.121	0.906723	0.963405
7338	10414703	ENSMUST00000103568	100042372	T cell receptor alpha variable	Trav2	1.021	1.138	0.291606	0.567641
7339	10562601					1.021	1.045	0.329743	0.606148
7340	10383453	NM_153545	217366	leucine rich repeat containing	Lrrc45	1.021	0.014	0.988856	0.995308
7341	10407159	NM_029898	77318	ankyrin repeat domain 55	Ankrd55	1.021	0.39	0.707787	0.872268
7342	10546903	NM_133932	101206	transcriptional adaptor 3 (NGG	Tada3l	1.021	-0.017	0.987265	0.994746
7343	10532216	NM_199011	110524	diacylglycerol kinase, theta	Dgkq	1.021	0.202	0.845709	0.937284
7344	10442893	NM_173741	268933	WD repeat domain 24	Wdr24	1.021	-0.061	0.952895	0.981871
7345	10440576	NM_001081068	78913	zinc finger protein 294	Zfp294	1.021	-0.561	0.591969	0.807001
7346	10433445	NM_172961	268860	4-aminobutyrate aminotransfera	Abat	1.021	-0.272	0.793164	0.915729
7347	10445816	NM_027452	70530	leucine rich repeat and fibron	Lrfn2	1.021	0.428	0.68136	0.859075
7348	10376283					1.021	0.531	0.611614	0.819829
7349	10378579	NM_138659	192159	pre-mRNA processing factor 8	Prpf8	1.021	-0.097	0.925322	0.970455
7350	10500656	NM_001099332	630146	immunoglobulin superfamily, me	Igsf2	1.021	0.898	0.398228	0.664555
7351	10388306	NM_146707	258702	olfactory receptor 410	Olfr410	1.021	1.079	0.315527	0.59239
7352	10385870					1.021	1.037	0.333269	0.609193
7353	10413810	ENSMUST00000061517	320621	RIKEN cDNA D830044D21 gene	D830044D21Rik	1.021	0.676	0.520129	0.757722
7354	10472570	NM_001081086	228005	peptidyl-prolyl isomerase G (c	Ppig	1.021	0.164	0.874569	0.949978
7355	10549171	NM_029081	74741	RIKEN cDNA 5730419I09 gene	5730419I09Rik	1.021	0.441	0.672047	0.854437
7356	10547408	NM_053204	111173	ELKS/RAB6-interacting/CAST fam	Erc1	1.021	0.601	0.56622	0.792228
7357	10369894	NR_003644	108950	RIKEN cDNA 1700049L16 gene	1700049L16Rik	1.021	0.667	0.525607	0.761716
7358	10372235	NM_001081432	237523	protein tyrosine phosphatase,	Ptprq	1.021	0.318	0.759513	0.899247
7359	10542596	NM_021471	58807	solute carrier organic anion t	Slco1c1	1.021	0.521	0.618031	0.82356
7360	10557211	NM_011247	19647	retinoblastoma binding protein	Rbbp6	1.021	0.503	0.629863	0.831325
7361	10554156	BC034069	100038347	cDNA sequence BC034069	BC034069	1.021	-0.242	0.815258	0.925918
7362	10437454	NM_028301	72615	ankyrin repeat and sterile alp	Anks3	1.021	0.007	0.994505	0.997747
7363	10478973	NM_001033538	320664	Cas scaffolding protein family	Cass4	1.021	0.71	0.500116	0.743152
7364	10585732	ENSMUST00000053230	71742	unc-51-like kinase 3 (C. elega	Ulk3	1.021	0.279	0.788138	0.913843
7365	10427166	NM_001014976	105988	extra spindle poles-like 1 (S.	Espl1	1.021	0.192	0.853362	0.940713
7366	10441669	NM_009309	20997	brachyury	T	1.021	0.54	0.605443	0.815953
7367	10558811	NM_013782	27388	phosphatidylserine synthase 2	Ptdss2	1.021	0.339	0.744166	0.89128
7368	10376427	BC058081	69944	RIKEN cDNA 2810021J22 gene	2810021J22Rik	1.021	-0.188	0.856312	0.941981
7369	10532289	NM_016715	57914	cytokine receptor-like factor	Crlf2	1.021	0.383	0.712806	0.874143
7370	10572378	NM_016685	12845	cartilage oligomeric matrix pr	Comp	1.021	0.544	0.602769	0.81427
7371	10503995	NM_008298	15502	DnaJ (Hsp40) homolog, subfamil	Dnaja1	1.021	0.265	0.798347	0.918353
7372	10505105					1.021	-0.011	0.991479	0.996624
7373	10410743	NM_134071	105377	ankyrin repeat domain 32	Ankrd32	1.021	0.117	0.910343	0.96415
7374	10394331	NM_028376	382562	profilin family, member 4	Pfn4	1.021	0.422	0.685252	0.860862
7375	10430127	NM_001007568	71591	zinc finger protein 251	Zfp251	1.021	-0.055	0.957324	0.983751
7376	10478778	NM_001085495	99371	ADP-ribosylation factor guanin	Arfgef2	1.021	0.289	0.780892	0.91101
7377	10498827	ENSMUST00000076136	329679	folliculin interacting protein	Fnip2	1.021	0.013	0.989721	0.995512
7378	10456846					1.021	0.128	0.901682	0.961371
7379	10364856	NM_199322	208266	DOT1-like, histone H3 methyltr	Dot1l	1.021	0.208	0.84103	0.935759
7380	10535435	NM_017467	54201	zinc finger protein 316	Zfp316	1.021	0.202	0.845634	0.937284
7381	10538438	BC118940	330323	RIKEN cDNA C330043M08 gene	C330043M08Rik	1.021	0.084	0.935554	0.974509
7382	10503966	NM_007386	11428	aconitase 1	Aco1	1.021	-0.287	0.782105	0.911385
7383	10527009	NM_021528	59031	carbohydrate sulfotransferase	Chst12	1.021	0.158	0.878899	0.952091
7384	10472782	NM_026115	107435	histone aminotransferase 1	Hat1	1.021	0.184	0.85896	0.943374
7385	10381588	NM_008175	14824	granulin	Grn	1.021	-0.47	0.652329	0.844168
7386	10401365	NM_183154	217695	zinc finger, FYVE domain conta	Zfyve1	1.021	0.257	0.804579	0.920913

7387	10360412	NM_146715	258710	olfactory receptor 419	Olfr419	1.021	0.202	0.845472	0.937284
7388	10443786	NM_008804	18585	phosphodiesterase 9A	Pde9a	1.021	-0.017	0.986918	0.994585
7389	10590623	NM_030712	80901	chemokine (C-X-C motif) recept	Cxcr6	1.02	0.398	0.701979	0.869258
7390	10424979	NM_182805	76282	glutamic pyruvic transaminase,	Gpt	1.02	0.764	0.469331	0.721467
7391	10587419	NM_146003	215351	SUMO/sentrin specific peptidas	Senp6	1.02	-0.073	0.944137	0.977948
7392	10507848					1.02	0.279	0.787766	0.913537
7393	10382866	NM_172948	268510	mannoside acetylglucosaminyltr	Mgat5b	1.02	0.726	0.490611	0.737328
7394	10385647	NM_172794	237758	zinc finger protein 454	Zfp454	1.02	0.279	0.788348	0.913849
7395	10404535	BC049659	108161	DNA segment, human D6S2654E	D0H6S2654E	1.02	0.648	0.537058	0.770181
7396	10346485	NM_001008419	213043	aldehyde oxidase 3-like 1	Aox3l1	1.02	0.452	0.664207	0.850267
7397	10515704	ENSMUST00000075406	230676	cDNA sequence BC059842	BC059842	1.02	-0.248	0.810903	0.923749
7398	10364011	NM_153406	74392	SPECC1-like	Specc1l	1.02	0.234	0.821688	0.92863
7399	10444788	NM_010390	15006	histocompatibility 2, Q region	H2-Q1	1.02	1.06	0.323177	0.59983
7400	10543524	NM_028900	74375	golgi coiled coil 1	Gcc1	1.02	0.28	0.786996	0.912989
7401	10530652	NM_001114660	212986	sec1 family domain containing	Scfd2	1.02	0.484	0.643031	0.838239
7402	10386236	NM_206882	382522	histone cluster 3, H2bb	Hist3h2bb	1.02	0.274	0.791767	0.915215
7403	10467203	AK165489	676676	predicted gene, ENSMUSG0000007	ENSMUSG00000074893	1.02	0.525	0.615108	0.82201
7404	10354955	NM_145143	227157	membrane protein, palmitoylate	Mpp4	1.02	0.488	0.640047	0.836826
7405	10589327	AF331517	171530	urocortin 2	Ucn2	1.02	1.306	0.231761	0.502487
7406	10400981	ENSMUST00000070425	380765	RIKEN cDNA D830013O20 gene	D830013O20Rik	1.02	0.707	0.501898	0.744769
7407	10517559	NM_009861	12540	cell division cycle 42 homolog	Cdc42	1.02	0.338	0.744814	0.891598
7408	10388734	NM_022313	57837	Era (G-protein)-like 1 (E. col	Eral1	1.02	0.72	0.494193	0.739551
7409	10361897	NM_010511	15979	interferon gamma receptor 1	Ifngr1	1.02	-0.148	0.886463	0.955393
7410	10374929	NM_176829	216622	RIKEN cDNA 4931440F15 gene	4931440F15Rik	1.02	0.373	0.720182	0.878163
7411	10602690	ENSMUST00000096265	436240	predicted gene, EG436240	EG436240	1.02	0.435	0.676065	0.855911
7412	10552715	ENSMUST00000094460	69578	RIKEN cDNA 2310016G11 gene	2310016G11Rik	1.02	0.556	0.594998	0.809148
7413	10443009	NM_026170	67458	endoplasmic reticulum-golgi in	Ergic1	1.02	-0.301	0.771847	0.905856
7414	10543226	BC070405	66520	RIKEN cDNA 2610001J05 gene	2610001J05Rik	1.02	0.366	0.725103	0.880804
7415	10583324					1.02	-0.131	0.89945	0.960245
7416	10583697	NM_011417	20586	SWI/SNF related, matrix associ	Smarca4	1.02	0.225	0.827909	0.930688
7417	10417130	NM_026861	68889	ubiquitin associated domain co	Ubac2	1.02	-0.069	0.947013	0.978959
7418	10415377	NM_026403	67842	RIKEN cDNA 2610027L16 gene	2610027L16Rik	1.02	-0.186	0.857378	0.942484
7419	10571054	NM_011485	20845	steroidogenic acute regulatory	Star	1.02	0.346	0.738984	0.888726
7420	10529858	NM_173764	231225	transmembrane anterior posteri	Tapt1	1.02	0.103	0.921041	0.968443
7421	10444041	NM_023202	66416	NADH dehydrogenase (ubiquinone	Ndufa7	1.02	-0.344	0.740458	0.889372
7422	10503643	BC028764	68493	RIKEN cDNA 1110007M04 gene	1110007M04Rik	1.02	-0.25	0.809525	0.923176
7423	10447951	NM_011581	21826	thrombospondin 2	Thbs2	1.02	0.895	0.399891	0.665979
7424	10561401	NM_013676	20924	suppressor of Ty 5 homolog (S.	Supt5h	1.02	-0.133	0.898103	0.959986
7425	10569265	NM_023764	54473	toll interacting protein	Tollip	1.02	0.343	0.74104	0.889595
7426	10369307	NM_023370	22295	cadherin 23 (otocadherin)	Cdh23	1.02	0.176	0.864769	0.946153
7427	10559389	NM_203490	211578	MAS-related GPR, member D	Mrgprd	1.02	0.351	0.735381	0.886785
7428	10371396	NM_028832	74238	MTERF domain containing 3	Mterfd3	1.02	0.344	0.740374	0.889357
7429	10564500					1.02	0.239	0.817511	0.927282
7430	10592330	NM_022029	64011	neurogranin	Nrgn	1.02	0.728	0.489295	0.736434
7431	10497644	AK016981	71280	RIKEN cDNA 4933429H19 gene	4933429H19Rik	1.02	0.338	0.744835	0.891598
7432	10574410	ENSMUST00000098472	319960	RIKEN cDNA 4930513N10 gene	4930513N10Rik	1.02	0.219	0.832894	0.932703
7433	10566822	NM_020052	56788	signal peptide, CUB domain, EG	Scube2	1.02	0.728	0.489428	0.736546
7434	10374315	NM_177033	319922	von Willebrand factor C domain	Vwc2	1.02	0.485	0.641971	0.837836
7435	10375820	NM_007714	12750	CDC like kinase 4	Clk4	1.02	0.464	0.656577	0.846246
7436	10491091	NM_009425	22035	tumor necrosis factor (ligand)	Tnfsf10	1.02	-0.045	0.965347	0.986124

7437	10351465	NM_001033185	78465	RIKEN cDNA 1700084C01 gene	1700084C01Rik	1.02	0.531	0.611287	0.819546
7438	10410173	NM_133680	66631	hippocampus abundant transcrip	Hiatl1	1.02	0.159	0.878193	0.951744
7439	10376074	NM_011031	18452	procollagen-proline, 2-oxoglut	P4ha2	1.02	0.091	0.930328	0.97262
7440	10605766	NM_019791	94275	melanoma antigen, family D, 1	Maged1	1.02	0.18	0.861809	0.94442
7441	10500069	NM_008847	18720	phosphatidylinositol-4-phospha	Pip5k1a	1.02	-0.002	0.998478	0.999521
7442	10384654	XR_032901	666078	similar to Rps16 protein	LOC666078	1.02	-0.04	0.96939	0.987616
7443	10516784					1.02	0.506	0.628229	0.830922
7444	10594248	NM_018853	56040	ribosomal protein, large, P1	Rplp1	1.02	0.042	0.967834	0.987137
7445	10593205	NM_024233	104444	REX2, RNA exonuclease 2 homolo	Rexo2	1.02	-0.397	0.70294	0.869729
7446	10512612	BC119804	242408	RIKEN cDNA 4930412F15 gene	4930412F15Rik	1.02	0.144	0.889791	0.956712
7447	10532596	XM_912851	74376	myosin XVIIIb	Myo18b	1.02	0.281	0.786346	0.912868
7448	10382047	ENSMUST00000100326	100038448	predicted gene, ENSMUSG0000007	ENSMUSG00000075480	1.02	0.776	0.462261	0.716783
7449	10532524	NM_027323	70118	SRR1 domain containing	Srrd	1.02	-0.114	0.912032	0.96491
7450	10391744	AK135410	100038535	predicted gene, ENSMUSG0000007	ENSMUSG00000075516	1.02	0.287	0.782165	0.911391
7451	10536620	NM_023626	71777	inhibitor of growth family, me	Ing3	1.02	-0.21	0.839366	0.935017
7452	10419284	ENSMUST00000074862	328388	predicted gene, ENSMUSG0000006	ENSMUSG00000061510	1.019	0.787	0.456237	0.712479
7453	10350173	NM_011619	21956	troponin T2, cardiac	Tnnt2	1.019	0.301	0.771643	0.905769
7454	10544248					1.019	0.354	0.733185	0.885653
7455	10469503					1.019	0.339	0.744487	0.891461
7456	10534889	NM_178162	231801	HIV-1 Rev binding protein-like	Hrbl	1.019	0.59	0.573248	0.796645
7457	10500378	BC115559	78373	nudix (nucleoside diphosphate	Nudt17	1.019	0.176	0.864795	0.946153
7458	10444911	NM_001010833	240087	mediator of DNA damage checkpo	Mdc1	1.019	-0.147	0.887337	0.955613
7459	10377255	NM_018768	55943	syntaxin 8	Stx8	1.019	-0.617	0.556386	0.784857
7460	10567825	NM_010689	16797	linker for activation of T cel	Lat	1.019	0.691	0.511093	0.752126
7461	10353844	NM_153408	214854	lung-inducible neuralized-rela	Lincr	1.019	0.141	0.891425	0.957571
7462	10430358	NM_028331	72709	C1q and tumor necrosis factor	C1qtnf6	1.019	0.122	0.905979	0.963405
7463	10348376	AK144378	381280	RIKEN cDNA 6430706D22 gene	6430706D22Rik	1.019	0.509	0.625706	0.829462
7464	10555875	NM_147074	57250	olfactory receptor 653	Olfr653	1.019	0.454	0.663103	0.849961
7465	10524909	NM_008712	18125	nitric oxide synthase 1, neuro	Nos1	1.019	0.271	0.794169	0.916289
7466	10437132					1.019	0.809	0.444186	0.702635
7467	10373626	NM_146931	258933	olfactory receptor 796	Olfr796	1.019	0.665	0.526985	0.762858
7468	10479274	NM_009867	12561	cadherin 4	Cdh4	1.019	0.557	0.594661	0.808846
7469	10533444	ENSMUST00000100746	75325	RIKEN cDNA 4930565B19 gene	4930565B19Rik	1.019	0.191	0.853528	0.940713
7470	10456488					1.019	-0.302	0.771457	0.905701
7471	10454398	NM_001033532	225289	expressed sequence AW554918	AW554918	1.019	0.2	0.846981	0.938064
7472	10485635	NM_145380	98221	eukaryotic translation initiat	Eif3m	1.019	-0.004	0.996918	0.99884
7473	10568038	AK035633	100038751	predicted gene, ENSMUSG0000005	ENSMUSG00000055323	1.019	0.499	0.632964	0.833181
7474	10421456	NM_023045	65246	exportin 7	Xpo7	1.019	0.089	0.931318	0.972759
7475	10529311	AK144327	100048901	predicted gene, ENSMUSG0000007	ENSMUSG00000073039	1.019	0.322	0.756494	0.897871
7476	10471533					1.019	0.727	0.49023	0.737262
7477	10345091	NM_172124	280645	beta-1,3-glucuronyltransferase	B3gat2	1.019	0.381	0.714139	0.874842
7478	10550222	NM_001099277	666528	zinc finger protein 541	Zfp541	1.019	0.485	0.642308	0.838072
7479	10574018	NM_013603	17751	metallothionein 3	Mt3	1.019	0.506	0.628261	0.830922
7480	10394054	NM_009854	12516	CD7 antigen	Cd7	1.019	0.357	0.731121	0.883967
7481	10465861	NM_016692	16319	inner centromere protein	Incenp	1.019	0.273	0.792308	0.915409
7482	10475932	NM_024237	70370	fibulin 7	Fbln7	1.019	0.175	0.866173	0.946491
7483	10450874	NM_146834	258831	olfactory receptor 101	Olfr101	1.019	0.089	0.931675	0.972759
7484	10523693	NM_016779	13406	dentin matrix protein 1	Dmp1	1.019	0.345	0.739745	0.889275

7485	10491704	NM_021343	57815	spermatogenesis associated 5	Spata5	1.019	0.067	0.948502	0.980098
7486	10362837	NM_153055	140740	SEC63-like (S. cerevisiae)	Sec63	1.019	0.202	0.8455	0.937284
7487	10552668	NM_198250	272381	leucine rich repeat containing	Lrrc4b	1.019	0.219	0.832574	0.932679
7488	10382321	NM_008425	16518	potassium inwardly-rectifying	Kcnj2	1.019	0.176	0.864878	0.946153
7489	10448925	NM_021415	58226	calcium channel, voltage-depen	Cacna1h	1.019	-0.109	0.916393	0.966925
7490	10494500	NM_001081139	213121	ankyrin repeat domain 35	Ankrd35	1.019	0.451	0.665239	0.850823
7491	10363281	NM_011240	19386	RAN binding protein 2	Ranbp2	1.019	0.254	0.806517	0.921832
7492	10425801	NM_007546	12124	Bcl2-interacting killer	Bik	1.019	0.104	0.920062	0.968088
7493	10507580	NM_133892	100470	L-amino acid oxidase 1	Lao1	1.019	0.513	0.623422	0.827888
7494	10593966	NM_007783	12988	c-src tyrosine kinase	Csk	1.019	-0.424	0.683607	0.859974
7495	10563338	NM_008654	17872	myeloid differentiation primar	Myd116	1.019	0.037	0.971593	0.988148
7496	10425430	NM_144812	213988	trinucleotide repeat containin	Tnrc6b	1.019	0.49	0.638823	0.835923
7497	10410309					1.019	0.91	0.392328	0.660367
7498	10509273	ENSMUST00000097840	22417	wingless-related MMTV integrat	Wnt4	1.019	0.448	0.667131	0.851389
7499	10420837	NM_018788	54616	exostoses (multiple)-like 3	Extl3	1.019	-0.036	0.972615	0.988226
7500	10389025	NM_177390	338367	myosin ID	Myo1d	1.019	-0.536	0.607917	0.817473
7501	10495255					1.019	0.368	0.723745	0.880392
7502	10363137	NM_030250	52014	nuclear undecaprenyl pyrophosp	Nus1	1.019	-0.004	0.996592	0.998765
7503	10369690	ENSMUST00000099674	52463	tet oncogene 1	Tet1	1.019	-0.118	0.909068	0.963765
7504	10429222	BC125645	70363	RIKEN cDNA 1700010C24 gene	1700010C24Rik	1.019	0.786	0.45678	0.712642
7505	10523182	NM_009704	11839	amphiregulin	Areg	1.019	0.373	0.719854	0.878078
7506	10546884	NM_177763	269788	lipoma HMGIC fusion partner-li	Lhfpl4	1.019	1.062	0.322531	0.599294
7507	10480421	AK015028	319264	RIKEN cDNA A130006I12 gene	A130006I12Rik	1.019	0.392	0.706701	0.871943
7508	10360761	ENSMUST00000070987	433384	predicted gene, EG433384	EG433384	1.019	0.295	0.776089	0.908617
7509	10537410	NM_011539	21391	thromboxane A synthase 1, plat	Tbxas1	1.019	-0.036	0.972362	0.98815
7510	10598882	NM_009457	22201	ubiquitin-like modifier activa	Uba1	1.019	0.006	0.995402	0.998188
7511	10591626	NM_177030	319899	dedicator of cytokinesis 6	Dock6	1.019	0.477	0.647277	0.841078
7512	10390969	ENSMUST00000073890	16671	keratin 33B	Krt33b	1.019	0.703	0.503824	0.746156
7513	10387029	NM_001099633	237806	dynein, axonemal, heavy chain	Dnahc9	1.019	0.584	0.576826	0.797672
7514	10396205	NM_001081195	238247	AT rich interactive domain 4A	Arid4a	1.019	-0.039	0.970287	0.987901
7515	10584518	NM_147107	259111	olfactory receptor 974	Olfr974	1.019	0.044	0.965805	0.98633
7516	10397450	NM_177354	238328	vasohibin 1	Vash1	1.019	0.36	0.729304	0.88278
7517	10369586	NM_181423	338359	suppressor of var1, 3-like 1 (	Supv3l1	1.019	-0.19	0.854547	0.94107
7518	10450006	NM_029804	76936	heterogeneous nuclear ribonucl	Hnrpm	1.019	0.257	0.804006	0.920506
7519	10439695	NM_019754	56370	transgelin 3	Tagln3	1.019	0.047	0.963433	0.985684
7520	10462091	NM_010638	16601	Kruppel-like factor 9	Klf9	1.019	0.279	0.788241	0.913849
7521	10463486	NM_001037758	12234	beta-transducin repeat contain	Btrc	1.019	-0.183	0.859465	0.943578
7522	10388298	NM_147003	259005	olfactory receptor 139	Olfr139	1.019	0.478	0.646815	0.840789
7523	10573451	NM_027954	71846	synaptonemal complex central e	Syce2	1.019	-0.471	0.651677	0.844083
7524	10385814	NM_153069	259301	liver-expressed antimicrobial	Leap2	1.019	0.216	0.834905	0.933323
7525	10546960					1.018	-0.2	0.847238	0.938167
7526	10580382	NM_001081324	74513	neuropilin (NRP) and tolloid (	Neto2	1.018	-0.067	0.948578	0.980098
7527	10421351	NM_025945	67065	polymerase (RNA) III (DNA dire	Polr3d	1.018	0.152	0.883688	0.954177
7528	10528630	NM_177676	231045	RIKEN cDNA 4931409K22 gene	4931409K22Rik	1.018	0.706	0.50253	0.745467
7529	10576971	NM_001081212	384783	insulin receptor substrate 2	Irs2	1.018	-0.239	0.817772	0.927527
7530	10603811	BC049702	278255	cDNA sequence BC049702	BC049702	1.018	0.127	0.902556	0.961829
7531	10574059	NM_019415	20497	solute carrier family 12, memb	Slc12a3	1.018	0.529	0.612754	0.820472
7532	10462501	ENSMUST00000025824	67188	RIKEN cDNA 2700046G09 gene	2700046G09Rik	1.018	0.062	0.952033	0.981385
7533	10394366	NM_001099628	320817	ATPase family, AAA domain cont	Atad2b	1.018	0.292	0.778191	0.909741
7534	10513008	NM_010637	16600	Kruppel-like factor 4 (gut)	Klf4	1.018	0.467	0.654334	0.845158
7535	10580957	NM_172758	234595	solute carrier family 38, memb	Slc38a7	1.018	0.345	0.739851	0.889275
7536	10541771	NM_133345	28019	inhibitor of growth family, me	Ing4	1.018	0.247	0.811705	0.923946
7537	10566159	NM_207621	233578	olfactory receptor 553	Olfr553	1.018	0.333	0.748536	0.893578

7538	10418901	ENSMUST00000063372	432839	G protein regulated inducer of	Gprin2	1.018	0.847	0.4244	0.686521
7539	10450895	NM_146287	258284	olfactory receptor 114	Olfr114	1.018	-0.045	0.965121	0.986124
7540	10404593					1.018	0.597	0.568514	0.793239
7541	10596222	NM_145700	252837	chemokine (C-C motif) receptor	Ccrl1	1.018	0.693	0.510043	0.751325
7542	10509441	NM_199307	230857	endothelin converting enzyme 1	Ece1	1.018	-0.31	0.765419	0.902421
7543	10380976	NM_021347	57911	gasdermin A1	Gsdma1	1.018	0.088	0.932274	0.973077
7544	10508142	NM_199473	329941	collagen, type VIII, alpha 2	Col8a2	1.018	0.113	0.912775	0.965173
7545	10426656	NM_013639	19132	peripherin	Prph	1.018	-0.143	0.889979	0.956731
7546	10539449	NM_134157	110935	ATPase, H+ transporting, lysos	Atp6v1b1	1.018	0.323	0.755572	0.897366
7547	10414548	NM_030098	78416	ribonuclease, RNase A family,	Rnase6	1.018	-0.051	0.960786	0.985069
7548	10600786	NM_001039060	236904	kelch-like 15 (Drosophila)	Klhl15	1.018	0.515	0.622109	0.827029
7549	10572485	NM_009001	19339	RAB3A, member RAS oncogene fam	Rab3a	1.018	0.361	0.728702	0.882456
7550	10506569	BC030081	329908	ubiquitin specific peptidase 2	Usp24	1.018	-0.342	0.741981	0.889973
7551	10534667	NM_008871	18787	serine (or cysteine) peptidase	Serpine1	1.018	0.399	0.701678	0.869143
7552	10391339	NM_008949	19183	proteasome (prosome, macropain	Psmc3ip	1.018	0.098	0.924937	0.970324
7553	10588893	NM_016802	11848	ras homolog gene family, membe	Rhoa	1.018	0.302	0.771323	0.905701
7554	10533003	BC061108	66123	RIKEN cDNA 1110006O24 gene	1110006O24Rik	1.018	0.609	0.561422	0.788542
7555	10409311					1.018	0.474	0.649453	0.84256
7556	10508115	NM_028800	74178	serine/threonine kinase 40	Stk40	1.018	-0.096	0.925982	0.970758
7557	10348201	NM_146112	227331	GRB10 interacting GYF protein	Gigyf2	1.018	0.031	0.976281	0.990137
7558	10468421	NM_001001738	414801	cDNA sequence BC063749	BC063749	1.018	0.226	0.827574	0.93066
7559	10479077	NM_019806	56491	vesicle-associated membrane pr	Vapb	1.018	0.131	0.899057	0.960129
7560	10371464	AK038758	791330	predicted gene, ENSMUSG0000005	ENSMUSG00000055288	1.018	-0.042	0.967425	0.987082
7561	10580085	BC057552	212123	cDNA sequence BC057552	BC057552	1.018	0.157	0.879913	0.952396
7562	10414003	XM_985917	268729	gene model 626, (NCBI)	Gm626	1.018	0.625	0.550954	0.781103
7563	10427063	BC048463	66322	RIKEN cDNA 1700011A15 gene	1700011A15Rik	1.018	0.359	0.730033	0.883264
7564	10361635	NM_001033466	381990	zinc finger and BTB domain con	Zbtb2	1.018	0.05	0.961665	0.985234
7565	10603796	BC118515	75905	RIKEN cDNA 4930578C19 gene	4930578C19Rik	1.018	-0.122	0.906583	0.963405
7566	10574375					1.018	0.293	0.777568	0.909562
7567	10581036	NM_021028	57813	thymidine kinase 2, mitochondr	Tk2	1.018	0.623	0.552216	0.782016
7568	10497711					1.018	-0.219	0.832906	0.932703
7569	10377245	NM_001013013	68460	dehydrogenase/reductase (SDR f	Dhrs7c	1.018	1.036	0.333636	0.609432
7570	10353533	NM_028534	98366	stromal membrane-associated pr	Smap1	1.018	0.011	0.991608	0.99665
7571	10535881					1.018	0.769	0.466296	0.719571
7572	10552622	BC059896	66976	RIKEN cDNA 2410002F23 gene	2410002F23Rik	1.018	0.235	0.820577	0.928617
7573	10602733					1.018	0.02	0.984745	0.993532
7574	10509280	NM_008305	15530	perlecan (heparan sulfate prot	Hspg2	1.018	0.42	0.686419	0.861515
7575	10409424	NM_016662	17121	Max dimerization protein 3	Mxd3	1.018	0.343	0.74108	0.889595
7576	10486988	NM_145395	213696	dual oxidase maturation factor	Duoxa1	1.018	0.62	0.554211	0.783409
7577	10514405	NM_172695	18786	phospholipase A2, activating p	Plaa	1.018	0.09	0.931116	0.972759
7578	10461840	NM_001011850	258151	olfactory receptor 1505	Olfr1505	1.018	0.385	0.711437	0.873563
7579	10591253	AK081787	77519	RIKEN cDNA 5730601F06 gene	5730601F06Rik	1.018	0.059	0.954179	0.982421
7580	10549569	NM_146176	232791	CCR4-NOT transcription complex	Cnot3	1.017	-0.076	0.941123	0.977122
7581	10386951	NM_018805	54710	heparan sulfate (glucosamine)	Hs3st3b1	1.017	0.026	0.980126	0.991919
7582	10347860					1.017	0.332	0.749199	0.893965
7583	10419872	ENSMUST00000100563	105651	protein phosphatase 1, regulat	Ppp1r3e	1.017	0.256	0.804799	0.921015
7584	10566430	NM_001011857	258160	olfactory receptor 685	Olfr685	1.017	0.29	0.779859	0.910713
7585	10583508	NM_023167	66163	mitochondrial ribosomal protei	Mrpl4	1.017	0.269	0.795794	0.917013
7586	10377439	NM_011065	18626	period homolog 1 (Drosophila)	Per1	1.017	0.538	0.607074	0.817118
7587	10499045	NM_030706	80890	tripartite motif-containing 2	Trim2	1.017	0.073	0.943667	0.977948
7588	10377605	BC117077	69186	RIKEN cDNA 1810027O10 gene	1810027O10Rik	1.017	-0.193	0.852515	0.940498
7589	10527646	AK030804	70717	RIKEN cDNA 6330406I15 gene	6330406I15Rik	1.017	0.345	0.73993	0.889278

7590	10596014	NM_019815	56492	claudin 18	Cldn18	1.017	0.264	0.799377	0.919009
7591	10479154	NM_001080971	545486	tubulin, beta 1	Tubb1	1.017	0.159	0.877785	0.951715
7592	10510708	NM_133788	57295	isoprenylcysteine carboxyl met	Icmt	1.017	0.303	0.770398	0.905061
7593	10415721					1.017	0.47	0.651986	0.844083
7594	10481525	NM_144884	30931	torsin family 1, member A (tor	Tor1a	1.017	0.069	0.946623	0.978837
7595	10562073	NM_133693	68035	RNA binding motif protein 42	Rbm42	1.017	-0.233	0.82195	0.92863
7596	10555256	ENSMUST00000098265	100038557	predicted gene, ENSMUSG0000007	ENSMUSG00000073999	1.017	0.085	0.934707	0.974001
7597	10513016	NM_025271	11471	actin-like 7b	Actl7b	1.017	-0.278	0.788818	0.914061
7598	10546417	NM_009426	22044	thyrotropin releasing hormone	Trh	1.017	0.516	0.621239	0.826183
7599	10581547	NM_026277	67619	NIN1/RPN12 binding protein 1 h	Nob1	1.017	0.115	0.911225	0.964566
7600	10469058	EF529510	68527	RIKEN cDNA 1110017I16 gene	1110017I16Rik	1.017	0.65	0.536082	0.769315
7601	10480804	NM_029293	75454	phosphohistidine phosphatase 1	Phpt1	1.017	-0.102	0.921718	0.968773
7602	10495223	NM_133867	99662	ESP8-like 3	Eps8l3	1.017	0.479	0.645895	0.840161
7603	10464905	NM_153553	225872	neuronal PAS domain protein 4	Npas4	1.017	0.368	0.72375	0.880392
7604	10370522	NM_009809	12365	caspase 14	Casp14	1.017	0.204	0.844339	0.936805
7605	10386007	NM_172258	215332	solute carrier family 36 (prot	Slc36a3	1.017	0.633	0.546205	0.777655
7606	10530847	BC132661	231332	phosphoprotein enriched in ast	Pea15b	1.017	0.751	0.476695	0.727638
7607	10513006					1.017	-0.234	0.821565	0.92863
7608	10587226	NM_027309	70082	LysM, putative peptidoglycan-b	Lysmd2	1.017	0.097	0.925605	0.970543
7609	10581961	NM_172466	208936	a disintegrin-like and metallo	Adamts18	1.017	-0.088	0.932646	0.973153
7610	10572332	NM_172755	234373	splicing factor, arginine/seri	Sfrs14	1.017	0.106	0.918171	0.967805
7611	10417212	NM_145467	223272	integrin, beta-like 1	Itgbl1	1.017	0.749	0.477485	0.728235
7612	10541061	NM_146912	258914	olfactory receptor 211	Olfr211	1.017	0.415	0.690038	0.863987
7613	10453721	NM_153085	225131	WW domain containing adaptor w	Wac	1.017	0.218	0.8334	0.932893
7614	10345626	NM_198303	226982	eukaryotic translation initiat	Eif5b	1.017	-0.072	0.944894	0.978204
7615	10556611					1.017	0.214	0.836328	0.933896
7616	10563766	XM_001474703	639116	predicted gene, EG639116	EG639116	1.017	0.312	0.763984	0.90173
7617	10404815	NM_178848	68346	sirtuin 5 (silent mating type	Sirt5	1.017	-0.047	0.963436	0.985684
7618	10469957	BC089508	97031	RIKEN cDNA C430004E15 gene	C430004E15Rik	1.017	0.164	0.874033	0.949893
7619	10552252	NM_001085385	72244	RIKEN cDNA 1600014C10 gene	1600014C10Rik	1.017	-0.483	0.64317	0.838317
7620	10596960	NM_001012236	22040	three prime repair exonuclease	Trex1	1.017	0.2	0.84714	0.938142
7621	10556165	NM_146723	258718	olfactory receptor 513	Olfr513	1.017	1.034	0.334482	0.60995
7622	10459241	NM_178928	106877	actin filament associated prot	Afap1l1	1.017	0.411	0.693027	0.865443
7623	10371092	NM_178662	16467	ataxia, cerebellar, Cayman typ	Atcay	1.017	0.206	0.84281	0.936326
7624	10457040	NM_183033	329003	zinc finger protein 516	Zfp516	1.017	0.473	0.649929	0.84297
7625	10562670	NM_027264	69930	zinc finger protein 715	Zfp715	1.017	-0.209	0.840195	0.93535
7626	10554349					1.017	0.391	0.707376	0.872175
7627	10548884	NM_026983	69187	endoplasmic reticulum protein	Erp27	1.017	0.818	0.43945	0.698732
7628	10551077	BC022632	77124	RIKEN cDNA 9130221H12 gene	9130221H12Rik	1.017	0.051	0.9605	0.985069
7629	10406203	XR_033696	434490	similar to stomatin-like prote	LOC434490	1.017	-0.179	0.862959	0.945293
7630	10490653	NM_198169	229004	glucocorticoid modulatory elem	Gmeb2	1.017	0.18	0.861827	0.94442
7631	10569611	NM_010175	14082	Fas (TNFRSF6)-associated via d	Fadd	1.017	0.209	0.840112	0.935328
7632	10390923	NM_026807	68673	RIKEN cDNA 1110033F04 gene	1110033F04Rik	1.017	0.394	0.705186	0.871395
7633	10574417	XR_032458	333331	similar to medium-chain acyl-C	LOC333331	1.017	0.386	0.710348	0.873031
7634	10495929					1.017	-0.001	0.998951	0.999589
7635	10474998					1.017	0.367	0.724096	0.88046
7636	10460891	NM_009006	26412	mitogen-activated protein kina	Map4k2	1.017	0.411	0.692933	0.865409
7637	10515974	NM_008692	18046	nuclear transcription factor-Y	Nfyc	1.017	0.543	0.603198	0.814484
7638	10398936	NM_001081170	217893	phosphofurin acidic cluster so	Pacs2	1.017	0.035	0.972704	0.988268
7639	10448350	NM_023824	76498	progestin and adipoQ receptor	Paqr4	1.017	-0.004	0.996971	0.99884
7640	10538755	NM_007958	13990	SWI/SNF-related, matrix-associ	Smarcad1	1.017	-0.03	0.97653	0.990253
7641	10375549	NM_146468	258460	olfactory receptor 1391	Olfr1391	1.017	0.433	0.677364	0.856571

7642	10354630	NM_001033194	98488	general transcription factor I	Gtf3c3	1.017	-0.003	0.997945	0.999268
7643	10423568	ENSMUST00000069422	70515	RIKEN cDNA 5730407I07 gene	5730407I07Rik	1.017	0.589	0.573824	0.797007
7644	10431585	NR_004843	100134861	choline kinase beta, carnitine	Chkb-cpt1b	1.017	0.378	0.716451	0.875796
7645	10504419	NM_027789	71406	RIKEN cDNA 5430416O09 gene	5430416O09Rik	1.017	0.463	0.657232	0.846702
7646	10445117	NM_146514	258507	olfactory receptor 96	Olfr96	1.017	0.126	0.90353	0.962464
7647	10541678	NM_023143	50909	complement component 1, r subc	C1r	1.016	0.915	0.389803	0.658464
7648	10558274	NM_198017	109359	RIKEN cDNA C430003P19 gene	C430003P19Rik	1.016	-0.116	0.911144	0.964566
7649	10518372	NM_001025365	28010	DNA segment, Chr 4, Wayne Stat	D4Wsu114e	1.016	0.476	0.648281	0.841814
7650	10538159	ENSMUST00000101425	666105	predicted gene, EG666105	EG666105	1.016	0.652	0.534677	0.768432
7651	10516678	NM_008468	16650	karyopherin (importin) alpha 6	Kpna6	1.016	0.35	0.736236	0.887109
7652	10473606					1.016	0.683	0.51607	0.755582
7653	10493449	NM_013691	21827	thrombospondin 3	Thbs3	1.016	0.228	0.825668	0.929887
7654	10456601	NM_028868	74322	CXXC finger 1 (PHD domain)	Cxxc1	1.016	-0.265	0.798192	0.918238
7655	10594551	NM_172536	214812	zinc finger protein 609	Zfp609	1.016	-0.06	0.953542	0.982042
7656	10470705	NM_001039087	107746	Rap guanine nucleotide exchang	Rapgef1	1.016	-0.23	0.824201	0.929508
7657	10505187	NM_011673	22234	UDP-glucose ceramide glucosylt	Ugcg	1.016	0.676	0.519913	0.757566
7658	10570388	ENSMUST00000044736	272465	gene model 687, (NCBI)	Gm687	1.016	0.68	0.517568	0.756753
7659	10407358	NM_145457	218693	polyadenylate binding protein-	Paip1	1.016	-0.345	0.74004	0.889339
7660	10581865	NM_027570	52815	lactate dehydrogenase D	Ldhd	1.016	0.935	0.380208	0.649784
7661	10433389	NM_145362	208211	asparagine-linked glycosylatio	Alg1	1.016	0.56	0.592477	0.807174
7662	10484553	NM_001005230	257900	olfactory receptor 1024	Olfr1024	1.016	0.398	0.701933	0.869258
7663	10589960	ENSMUST00000084841	73748	glutamate decarboxylase-like 1	Gadl1	1.016	0.241	0.816527	0.926829
7664	10504056	NM_023305	67123	ubiquitin-associated protein 1	Ubap1	1.016	0.153	0.882836	0.953745
7665	10356335	NM_010341	14767	neuromedin U receptor 1	Nmur1	1.016	0.475	0.649086	0.842359
7666	10559373	NM_008003	14170	fibroblast growth factor 15	Fgf15	1.016	0.292	0.77838	0.909839
7667	10381617					1.016	0.997	0.351129	0.624551
7668	10559831	BC023179	232855	cDNA sequence BC023179	BC023179	1.016	-0.443	0.671	0.853953
7669	10542636	NM_183165	232491	pyridine nucleotide-disulphide	Pyroxd1	1.016	0.022	0.982739	0.992455
7670	10593225	NM_001033324	235320	zinc finger and BTB domain con	Zbtb16	1.016	0.456	0.661973	0.84942
7671	10442739	NM_028789	74154	unkempt-like (Drosophila)	Unkl	1.016	0.295	0.776369	0.908709
7672	10457378	ENSMUST00000070164	791280	predicted gene, ENSMUSG0000005	ENSMUSG00000056177	1.016	0.028	0.978296	0.991282
7673	10381115	NM_011508	20918	eukaryotic translation initiat	Eif1	1.016	-0.2	0.847302	0.938173
7674	10366774	NM_009635	11567	advillin	Avil	1.016	0.312	0.763617	0.901503
7675	10429547	NM_009991	13072	cytochrome P450, family 11, su	Cyp11b2	1.016	0.324	0.754816	0.896821
7676	10544547	NM_001081382	72306	zinc finger protein 777	Zfp777	1.016	-0.046	0.964205	0.985887
7677	10373846	NM_001029937	380683	SEC14-like 3 (S. cerevisiae)	Sec14l3	1.016	0.409	0.694385	0.86574
7678	10524588	NM_026718	68420	ankyrin repeat domain 13a	Ankrd13a	1.016	-0.405	0.697509	0.867333
7679	10488451	BC132262	69277	RIKEN cDNA 3300002I08 gene	3300002I08Rik	1.016	-0.022	0.983206	0.992738
7680	10393294	NM_001033267	217341	glutamine rich 2	Qrich2	1.016	0.273	0.792324	0.915409
7681	10589958	XR_032777	675823	similar to Glyceraldehyde-3-ph	LOC675823	1.016	0.667	0.525441	0.76158
7682	10425522	NM_019712	56438	ring-box 1	Rbx1	1.016	-0.175	0.866023	0.946491
7683	10557076	NM_139310	246190	otoancorin	Otoa	1.016	0.762	0.470509	0.722494
7684	10420823	NM_177338	219150	homeobox containing 1	Hmbox1	1.016	-0.025	0.980675	0.991919
7685	10589913	NM_146229	235661	dynein cytoplasmic 1 light int	Dync1li1	1.016	-0.079	0.939204	0.976281
7686	10348791	NM_207031	404545	transmembrane protein 16g	Tmem16g	1.016	0.047	0.964014	0.985864
7687	10433564	ENSMUST00000037913	223970	RIKEN cDNA A630055G03 gene	A630055G03Rik	1.016	0.213	0.837598	0.934421
7688	10457948	NM_026165	67453	solute carrier family 25, memb	Slc25a46	1.016	0.11	0.915133	0.966602
7689	10365015	ENSMUST00000092282	103406	RIKEN cDNA 9130206N08 gene	9130206N08Rik	1.016	0.476	0.648191	0.8418
7690	10392251	NM_007840	13207	DEAD (Asp-Glu-Ala-Asp) box pol	Ddx5	1.016	0.292	0.778249	0.909741
7691	10398306	AK147993	212198	WD repeat domain 25	Wdr25	1.016	0.447	0.668181	0.851959
7692	10541721	NM_013539	14794	splA/ryanodine receptor domain	Spsb2	1.016	0.519	0.619434	0.824819

7693	10573613	NM_146859	258858	olfactory receptor 371	Olfr371	1.016	0.582	0.578607	0.798427
7694	10565904	NM_198831	52443	mitochondrial ribosomal protei	Mrpl48	1.016	-0.464	0.656183	0.846043
7695	10466735	NM_001114174	381217	gene model 967, (NCBI)	Gm967	1.016	1.074	0.31759	0.594733
7696	10605104	NM_001029868	245469	PDZ domain containing 4	Pdzd4	1.016	-0.137	0.894995	0.958652
7697	10566097	NM_022979	269966	nucleoporin 98	Nup98	1.016	-0.049	0.962154	0.985362
7698	10565996	NM_010567	16332	inositol polyphosphate phospha	Inppl1	1.016	0.251	0.809098	0.923112
7699	10481175	BC062145	66139	RIKEN cDNA 1110002H13 gene	1110002H13Rik	1.016	0.44	0.672579	0.854651
7700	10515046	NM_027453	70533	basic transcription factor 3-l	Btf3l4	1.016	-0.027	0.979188	0.991758
7701	10466976	NM_138595	104174	glycine decarboxylase	Gldc	1.016	0.216	0.834896	0.933323
7702	10467739	NM_027106	69534	arginine vasopressin-induced 1	Avpi1	1.016	-0.007	0.994578	0.997747
7703	10439566	NM_007508	11964	ATPase, H+ transporting, lysos	Atp6v1a	1.016	0.016	0.988033	0.995045
7704	10493834	NM_207263	384997	peptidoglycan recognition prot	Pglyrp4	1.016	1.038	0.332804	0.608825
7705	10487871	NM_007682	12616	centromere protein B	Cenpb	1.016	0.046	0.964528	0.985942
7706	10542066	NM_026743	68498	tetraspanin 11	Tspan11	1.016	0.25	0.80961	0.923191
7707	10514319	NM_172871	242521	kelch-like 9 (Drosophila)	Klhl9	1.016	0.426	0.682668	0.859827
7708	10592303	AF060570	19649	roundabout homolog 3 (Drosophi	Robo3	1.016	0.669	0.524258	0.760908
7709	10392135	NM_008117	14599	growth hormone	Gh	1.016	0.191	0.853589	0.940713
7710	10484999	NM_028119	107986	damage specific DNA binding pr	Ddb2	1.016	0.267	0.796995	0.917479
7711	10572318	NM_145597	234371	transmembrane protein 161A	Tmem161a	1.016	0.413	0.69186	0.864682
7712	10532865	NM_019834	26431	G protein-coupled receptor kin	Git2	1.016	-0.078	0.940291	0.976739
7713	10583992	NM_001033323	235086	immunoglobulin superfamily, me	Igsf9b	1.015	-0.058	0.955297	0.98291
7714	10592734	NM_007619	12402	Casitas B-lineage lymphoma	Cbl	1.015	-0.714	0.49769	0.741949
7715	10555862	NM_030684	94094	tripartite motif-containing 34	Trim34	1.015	0.485	0.642043	0.837836
7716	10526418	NM_011776	22788	zona pellucida glycoprotein 3	Zp3	1.015	1.057	0.324612	0.601113
7717	10586446					1.015	0.518	0.619749	0.825031
7718	10527327	NM_018772	55950	brain protein I3	Bri3	1.015	-0.558	0.593461	0.808046
7719	10464728	NM_001001984	225876	F-box and leucine-rich repeat	Fbxl11	1.015	-0.081	0.937833	0.975815
7720	10440560	NM_001081068	78913	zinc finger protein 294	Zfp294	1.015	0.159	0.877759	0.951715
7721	10435525	NM_177128	320299	IQ calmodulin-binding motif co	Iqcb1	1.015	-0.013	0.990276	0.995786
7722	10413270	ENSMUST00000059648	71106	RIKEN cDNA 4933413J09 gene	4933413J09Rik	1.015	0.106	0.918367	0.967805
7723	10405343	NM_028841	74257	tetraspanin 17	Tspan17	1.015	-0.147	0.886931	0.955613
7724	10450525	AB242596	672682	mucin 21	Muc21	1.015	0.69	0.512019	0.75265
7725	10367598	ENSMUST00000073478	791342	predicted gene, ENSMUSG0000006	ENSMUSG00000061261	1.015	0.908	0.39326	0.66124
7726	10344929	ENSMUST00000067599	791392	predicted gene, ENSMUSG0000005	ENSMUSG00000054493	1.015	0.41	0.69376	0.865705
7727	10449699	NM_021322	57773	WD repeat domain 4	Wdr4	1.015	0.087	0.933338	0.973406
7728	10547173	NM_026057	67255	zinc finger protein 422	Zfp422	1.015	0.122	0.906577	0.963405
7729	10383212	ENSMUST00000093902	672511	hypothetical LOC672511	LOC672511	1.015	0.366	0.724823	0.880713
7730	10572170	NM_172491	211135	RIKEN cDNA D130040H23 gene	D130040H23Rik	1.015	-0.318	0.759153	0.89915
7731	10486284	NM_027175	69702	NADH dehydrogenase (ubiquinone	Ndufaf1	1.015	-0.088	0.932394	0.973077
7732	10464569	AK079024	73788	RIKEN cDNA 4833408A19 gene	4833408A19Rik	1.015	-0.275	0.791287	0.915061
7733	10477725	NM_010808	17391	matrix metallopeptidase 24	Mmp24	1.015	0.016	0.987863	0.994998
7734	10492699	NM_177662	229445	cathepsin O	Ctso	1.015	0.069	0.947213	0.979071
7735	10490813					1.015	0.389	0.708184	0.872296
7736	10386743	NM_010148	13855	epsin 2	Epn2	1.015	0.263	0.799738	0.919181
7737	10481368	NM_145520	227682	TruB pseudouridine (psi) synth	Trub2	1.015	-0.096	0.926334	0.970777
7738	10459930	NM_026295	67655	CTD (carboxy-terminal domain,	Ctdp1	1.015	0.118	0.90926	0.963879
7739	10518526	NM_001039554	654812	angiopoietin-like 7	Angptl7	1.015	0.404	0.698078	0.867716
7740	10451932	NM_020568	57435	plasma membrane associated pro	S3-12	1.015	0.249	0.810344	0.923512
7741	10391567	NM_029649	76547	transmembrane protein 101	Tmem101	1.015	0.454	0.6634	0.850117
7742	10453792	XR_031453	435554	similar to RAE1 RNA export 1 h	LOC435554	1.015	-0.159	0.877983	0.951715
7743	10511069	NM_008142	14688	guanine nucleotide binding pro	Gnb1	1.015	0.224	0.829329	0.93131
7744	10535732	NM_001010941	14738	G-protein coupled receptor 12	Gpr12	1.015	-0.193	0.852513	0.940498

7745	10454885	NM_172830	240215	solute carrier family 4, sodiu	Slc4a9	1.015	0.226	0.827432	0.930659
7746	10521136	NM_001081102	107823	Wolf-Hirschhorn syndrome candi	Whsc1	1.015	-0.294	0.777164	0.909278
7747	10372060	NM_009950	12905	CASP2 and RIPK1 domain contain	Cradd	1.015	0.181	0.861067	0.94412
7748	10348858	NM_016778	51800	Bcl-2-related ovarian killer p	Bok	1.015	-0.041	0.968069	0.987165
7749	10469849	NM_026021	67187	zinc finger, MYND domain conta	Zmynd19	1.015	0.3	0.77295	0.906599
7750	10474958	NM_019454	54485	delta-like 4 (Drosophila)	Dll4	1.015	0.179	0.862805	0.945192
7751	10558029	NM_001029982	207352	Sec23 interacting protein	Sec23ip	1.015	-0.121	0.906948	0.963547
7752	10370911	NM_078477	118445	Kruppel-like factor 16	Klf16	1.015	-0.063	0.951398	0.981144
7753	10393341	NM_172572	217344	rhomboid 5 homolog 2 (Drosophi	Rhbdf2	1.015	0.219	0.832516	0.932679
7754	10354979	NM_028717	74018	amyotrophic lateral sclerosis	Als2	1.015	-0.054	0.958225	0.984334
7755	10476005	ENSMUST00000071053	329513	RIKEN cDNA A730036I17 gene	A730036I17Rik	1.015	0.287	0.781897	0.911385
7756	10585778	NM_011352	20361	sema domain, immunoglobulin do	Sema7a	1.015	0.348	0.738061	0.888294
7757	10526427	NM_023742	74198	deltex 2 homolog (Drosophila)	Dtx2	1.015	0.074	0.942813	0.977825
7758	10393197	NM_025276	14027	envoplakin	Evpl	1.015	0.194	0.851563	0.940193
7759	10573956	NM_009209	20538	solute carrier family 6 (neuro	Slc6a2	1.015	0.013	0.9901	0.995679
7760	10507334	BC022733	68394	RIKEN cDNA 0610037D15 gene	0610037D15Rik	1.015	0.437	0.67465	0.855467
7761	10442948	NM_024227	68611	mitochondrial ribosomal protei	Mrpl28	1.015	-0.427	0.681592	0.859316
7762	10391254	NM_001081194	380728	potassium voltage-gated channe	Kcnh4	1.015	0.17	0.869521	0.947688
7763	10520648					1.015	0.288	0.781198	0.911067
7764	10401428	ENSMUST00000110294	238317	RIKEN cDNA C130039O16 gene	C130039O16Rik	1.015	0.285	0.783902	0.912068
7765	10385926	NM_178626	72729	CDC42 small effector 2	Cdc42se2	1.015	-0.307	0.767273	0.903106
7766	10502469	NM_019808	56376	PDZ and LIM domain 5	Pdlim5	1.015	-0.154	0.882117	0.953469
7767	10468525	ENSMUST00000099340	100038642	predicted gene, ENSMUSG0000007	ENSMUSG00000074788	1.015	0.773	0.464133	0.717962
7768	10372534	NM_001037846	72068	CCR4-NOT transcription complex	Cnot2	1.015	0.189	0.855411	0.941478
7769	10581271	NM_175160	70796	zinc finger, DHHC domain conta	Zdhhc1	1.015	0.221	0.831089	0.932182
7770	10551828	NM_001033540	330503	predicted gene, EG330503	EG330503	1.015	0.44	0.672708	0.854651
7771	10487797	NM_033615	110751	a disintegrin and metallopepti	Adam33	1.015	0.248	0.811186	0.923829
7772	10450856	NM_146456	258448	olfactory receptor 92	Olfr92	1.015	0.125	0.903786	0.962655
7773	10379204	NM_026389	67811	polymerase (DNA-directed), del	Poldip2	1.015	-0.327	0.752804	0.89584
7774	10369748	ENSMUST00000054760	631906	predicted gene, EG631906	EG631906	1.014	0.205	0.843529	0.936586
7775	10471062	BC027220	66617	RIKEN cDNA 2610205E22 gene	2610205E22Rik	1.014	0.251	0.80885	0.923103
7776	10372853	NM_019786	56480	TANK-binding kinase 1	Tbk1	1.014	0.229	0.825293	0.929712
7777	10601178	NM_013712	26549	integrin beta 1 binding protei	Itgb1bp2	1.014	0.321	0.757084	0.898052
7778	10564522					1.014	-0.101	0.922457	0.969068
7779	10481574	NM_175511	241303	RIKEN cDNA A130092J06 gene	A130092J06Rik	1.014	0.383	0.712813	0.874143
7780	10352166	BC054802	226744	RIKEN cDNA 9630058J23 gene	9630058J23Rik	1.014	0.26	0.802408	0.919965
7781	10577544	NM_011130	18970	polymerase (DNA directed), bet	Polb	1.014	-0.132	0.898778	0.960077
7782	10528598	NM_023229	66587	Fas-activated serine/threonine	Fastk	1.014	0.009	0.992909	0.997248
7783	10383887	NM_197979	66152	RIKEN cDNA 1110020P15 gene	1110020P15Rik	1.014	-0.357	0.731653	0.884308
7784	10572514	ENSMUST00000050921	442796	RIKEN cDNA A230052G05 gene	A230052G05Rik	1.014	0.615	0.557192	0.785575
7785	10359097	NM_144791	208263	torsin A interacting protein 1	Tor1aip1	1.014	-0.015	0.98873	0.995308
7786	10352945					1.014	0.134	0.897013	0.95959
7787	10436498	ENSMUST00000050665	71135	RIKEN cDNA 4933411O13 gene	4933411O13Rik	1.014	0.433	0.677839	0.856898
7788	10525236	BC051044	269700	expressed sequence AU042671	AU042671	1.014	0.302	0.770889	0.905387
7789	10437561	BC051078	70511	RIKEN cDNA 5730409G15 gene	5730409G15Rik	1.014	0.074	0.942996	0.977825
7790	10600921	NM_199018	236920	START domain containing 8	Stard8	1.014	0.224	0.828819	0.931167
7791	10461110					1.014	0.505	0.628438	0.830964
				RIKEN cDNA E130201H02					

7792	10556938	ENSMUST00000053151	78552	gene	E130201H02Rik	1.014	0.793	0.453181	0.70973
7793	10348471	NM_053015	171531	melanophilin	Mlph	1.014	0.598	0.568358	0.793239
7794	10344715					1.014	0.416	0.689407	0.863658
7795	10503036	NM_001093752	69207	splicing factor, arginine/seri	Sfrs11	1.014	0.401	0.699973	0.868609
7796	10396905	AK028383	217682	RIKEN cDNA 3830431G21 gene	3830431G21Rik	1.014	0.587	0.575334	0.797076
7797	10603807					1.014	0.272	0.793065	0.9157
7798	10587000	NM_026314	67685	dyslexia susceptibility 1 cand	Dyx1c1	1.014	0.274	0.79208	0.915332
7799	10477649	NM_019811	60525	acyl-CoA synthetase short-chai	Acss2	1.014	0.208	0.84126	0.935777
7800	10605195	NM_008224	15161	host cell factor C1	Hcfc1	1.014	-0.194	0.851497	0.940193
7801	10378126	NM_009671	11736	ankyrin repeat and FYVE domain	Ankfy1	1.014	0.137	0.894814	0.958505
7802	10430438	NM_144849	223690	ankyrin repeat domain 54	Ankrd54	1.014	0.289	0.780633	0.910911
7803	10435626	NM_013547	15233	homogentisate 1, 2-dioxygenase	Hgd	1.014	0.765	0.468837	0.721057
7804	10557853	ENSMUST00000079045	319527	RIKEN cDNA B230325K18 gene	B230325K18Rik	1.014	0.34	0.743185	0.890598
7805	10448811	NM_020608	57354	Crm, cramped-like (Drosophila)	Cramp1l	1.014	0.458	0.660292	0.848652
7806	10516325	NM_133883	100206	ADP-ribosylhydrolase like 2	Adprhl2	1.014	0.224	0.828928	0.931175
7807	10495518	NM_153157	229759	olfactomedin 3	Olfm3	1.014	0.592	0.572072	0.796172
7808	10461012	NM_026306	67674	RIKEN cDNA 0610038D11 gene	0610038D11Rik	1.014	-0.044	0.965961	0.986394
7809	10596951	NM_011790	23807	ariadne homolog 2 (Drosophila)	Arih2	1.014	-0.392	0.706043	0.871814
7810	10383055	NM_007623	12416	chromobox homolog 2 (Drosophil	Cbx2	1.014	-0.152	0.883173	0.954001
7811	10468562	NM_001081076	73707	guanylate cyclase 2g	Gucy2g	1.014	0.198	0.848339	0.938486
7812	10518331					1.014	0.614	0.558301	0.786038
7813	10415415	BC116260	219094	RIKEN cDNA 9130227C08Rik gene	9130227C08Rik	1.014	0.12	0.908014	0.963723
7814	10516323	ENSMUST00000097890	667193	predicted gene, EG667193	EG667193	1.014	-0.014	0.989119	0.995308
7815	10595169	AK016017	67648	RIKEN cDNA 4930542C12 gene	4930542C12Rik	1.014	0.422	0.684975	0.860758
7816	10360344	NM_010045	13349	Duffy blood group, chemokine r	Darc	1.014	0.289	0.780682	0.910917
7817	10593947	NM_146223	235415	complexin 3	Cplx3	1.014	1.109	0.303075	0.579092
7818	10537501	NM_020502	57253	taste receptor, type 2, member	Tas2r108	1.014	0.143	0.890368	0.956943
7819	10371446	NM_177772	270757	bactericidal/permeability-incr	Bpil2	1.014	0.618	0.555525	0.784214
7820	10584787	NM_021481	58866	trehalase (brush-border membra	Treh	1.014	0.591	0.572292	0.796254
7821	10422657	ENSMUST00000045736	223825	RIKEN cDNA 4930455B06 gene	4930455B06Rik	1.014	0.394	0.704794	0.871013
7822	10435714	NM_026407	67846	transmembrane protein 39a	Tmem39a	1.014	-0.184	0.858801	0.943374
7823	10363475	NM_011073	18646	perforin 1 (pore forming prote	Prf1	1.014	0.61	0.560647	0.78784
7824	10574903	NM_181594	234699	enhancer of mRNA decapping 4	Edc4	1.014	-0.042	0.967634	0.987137
7825	10402140	ENSMUST00000101128	100038679	predicted gene, ENSMUSG0000007	ENSMUSG00000072880	1.014	0.138	0.894196	0.958327
7826	10574427	NM_011830	23918	inosine 5'-phosphate dehydroge	Impdh2	1.014	-0.505	0.628326	0.830956
7827	10403052	XR_033970	638798	similar to transcription elong	LOC638798	1.014	-1.251	0.250123	0.524217
7828	10569100					1.014	0.722	0.492899	0.73872
7829	10584624	ENSMUST00000116604	100042548	similar to HVEC cell-cell adhe	LOC100042548	1.014	0.419	0.687448	0.862174
7830	10392010	AK153679	76719	RIKEN cDNA 1700081L11 gene	1700081L11Rik	1.014	0.359	0.72993	0.883264
7831	10449914	NM_172458	208292	RIKEN cDNA 9030612M13 gene	9030612M13Rik	1.014	0.678	0.518675	0.757118
7832	10435470	NM_008465	16646	karyopherin (importin) alpha 1	Kpna1	1.014	0.342	0.742357	0.890171
7833	10430533	NM_008427	16520	potassium inwardly-rectifying	Kcnj4	1.014	0.176	0.865076	0.946153
7834	10592593	NM_009347	21683	tectorin alpha	Tecta	1.014	0.296	0.775782	0.908358
7835	10525516	ENSMUST00000069311	269701	WD repeat domain 66	Wdr66	1.014	0.302	0.770858	0.905387
7836	10547508	NM_033567	94047	cat eye syndrome chromosome re	Cecr6	1.014	0.217	0.834314	0.933071
7837	10585851	NM_001081192	330953	hyperpolarization-activated, c	Hcn4	1.013	0.11	0.915181	0.966602
7838	10581890	NM_009954	12927	breast cancer anti-estrogen re	Bcar1	1.013	0.021	0.984166	0.993232
7839	10492480	NM_138591	28030	G elongation factor, mitochond	Gfm1	1.013	-0.318	0.759312	0.899156

7840	10430693	NM_001082536	223701	MKL (megakaryoblastic leukemia	Mkl1	1.013	0.189	0.854938	0.941302
7841	10563891	AF043260	17974	non-catalytic region of tyrosi	Nck2	1.013	0.89	0.402272	0.667397
7842	10455395	NM_001081180	72432	serine peptidase inhibitor, Ka	Spink5	1.013	0.524	0.615821	0.822286
7843	10409445	NM_029303	75477	profilin 3	Pfn3	1.013	0.308	0.766864	0.902924
7844	10511282	NM_011659	22163	tumor necrosis factor receptor	Tnfrsf4	1.013	0.045	0.965333	0.986124
7845	10365125	AK080664	102115	deoxyhypusine hydroxylase/mono	Dohh	1.013	0.139	0.892996	0.957774
7846	10450237	ENSMUST00000047263	632302	cytochrome P450, family 21, su	Cyp21a2-ps	1.013	-0.055	0.957831	0.984129
7847	10545127	ENSMUST00000065878	75373	RIKEN cDNA 4930597O21 gene	4930597O21Rik	1.013	-0.277	0.789465	0.914397
7848	10352705	ENSMUST00000077889	75558	RIKEN cDNA 1700022P22 gene	1700022P22Rik	1.013	1.236	0.255349	0.529739
7849	10402808	NM_010588	16450	jagged 2	Jag2	1.013	0.276	0.790044	0.914502
7850	10397536	XM_001476146	100045836	hypothetical protein LOC100045	LOC100045836	1.013	-0.202	0.845745	0.937284
7851	10527516	NM_145155	245880	WAS protein family, member 3	Wasf3	1.013	-0.459	0.659762	0.848541
7852	10503190	NM_001081417	320790	chromodomain helicase DNA bind	Chd7	1.013	0.774	0.463612	0.717772
7853	10582482	AY751521	72325	RIKEN cDNA 1300018I17 gene	1300018I17Rik	1.013	0.078	0.940027	0.976656
7854	10501402	NM_029522	76123	G-protein signalling modulator	Gpsm2	1.013	0.17	0.869792	0.947894
7855	10434754	ENSMUST00000089895	100037399	RIKEN cDNA B630019A10 gene	B630019A10Rik	1.013	0.331	0.750218	0.894442
7856	10440977	NM_138597	28080	ATP synthase, H+ transporting,	Atp5o	1.013	-0.365	0.725582	0.88115
7857	10524369	NM_138646	192232	Hermansky-Pudlak syndrome 4 ho	Hps4	1.013	0.118	0.908949	0.963765
7858	10504728	NM_183298	110805	forkhead box E1 (thyroid trans	Foxe1	1.013	-0.069	0.947182	0.979071
7859	10489591	NM_199027	329559	zinc finger protein 335	Zfp335	1.013	0.222	0.830677	0.932075
7860	10399559	NM_133699	68775	ATPase, H+ transporting, lysos	Atp6v1c2	1.013	0.438	0.673973	0.855115
7861	10484237	NM_178723	241494	zinc finger protein 385B	Zfp385b	1.013	0.235	0.821069	0.92863
7862	10581664	BC016254	76527	RIKEN cDNA 2010004A03 gene	2010004A03Rik	1.013	0.269	0.795359	0.916955
7863	10586390	NM_001033158	70784	RAS-like, family 12	Rasl12	1.013	0.399	0.701534	0.869143
7864	10543118	XR_031071	100044855	similar to F-box protein 5	LOC100044855	1.013	0.222	0.830164	0.931737
7865	10520574	NM_001048192	231093	ATP/GTP binding protein-like 5	Agbl5	1.013	0.232	0.823249	0.929358
7866	10575861	NM_024219	68196	heat shock factor binding prot	Hsbp1	1.013	-0.404	0.697613	0.86736
7867	10559708	NM_011813	23877	Flt3 interacting zinc finger p	Fiz1	1.013	-0.247	0.811697	0.923946
7868	10543213	NM_175312	101148	RIKEN cDNA B630005N14 gene	B630005N14Rik	1.013	-0.268	0.795983	0.917149
7869	10401473	NM_134042	104776	aldehyde dehydrogenase family	Aldh6a1	1.013	0.037	0.971515	0.988148
7870	10355763	NM_001003917	245860	autophagy-related 9A (yeast)	Atg9a	1.013	0.348	0.737677	0.888186
7871	10459153	NM_009880	12590	caudal type homeo box 1	Cdx1	1.013	0.285	0.783572	0.912068
7872	10368224					1.013	0.283	0.784866	0.912507
7873	10462603	NM_007987	14102	Fas (TNF receptor superfamily	Fas	1.013	0.237	0.819206	0.928258
7874	10544555	ENSMUST00000073124	69228	zinc finger protein 746	Zfp746	1.013	-0.219	0.832922	0.932703
7875	10385671	ENSMUST00000109123	74408	RIKEN cDNA 4933414I15 gene	4933414I15Rik	1.013	0.335	0.747367	0.892632
7876	10494632	NM_027665	71078	a disintegrin and metallopepti	Adam30	1.013	0.495	0.635305	0.834289
7877	10448424	NM_011062	18607	3-phosphoinositide dependent p	Pdpk1	1.013	-0.071	0.945248	0.978427
7878	10592763	NM_178420	270151	NLR family member X1	Nlrx1	1.013	0.297	0.774597	0.907574
7879	10409314	NM_013601	17702	homeobox, msh-like 2	Msx2	1.013	0.213	0.837536	0.934421
7880	10491695	NM_001008502	241950	Bardet-Biedl syndrome 12 (huma	Bbs12	1.013	-0.049	0.962535	0.985405
7881	10519747	NM_011348	20349	sema domain, immunoglobulin do	Sema3e	1.013	0.336	0.746229	0.892285
7882	10562439	NM_026181	67471	G patch domain containing 1	Gpatch1	1.013	-0.269	0.795682	0.916955
7883	10567460	XM_355934	381917	dynein, axonemal, heavy chain	Dnahc3	1.013	0.379	0.715596	0.875402
7884	10499080	NM_001081093	99889	ADP-ribosylation factor intera	Arfip1	1.013	0.061	0.95338	0.982042
7885	10590389	NM_010918	18087	natural killer tumor recogniti	Nktr	1.013	0.412	0.692636	0.865144
7886	10463296	NM_001113562	66388	cutC copper transporter homolo	Cutc	1.013	-0.099	0.923941	0.96976
7887	10384595	BC109353	237694	RIKEN cDNA 4932414J04 gene	4932414J04Rik	1.013	-0.013	0.990053	0.995679
7888	10418729	NM_009937	382864	collagen-like tail subunit (si	Colq	1.013	0.359	0.73016	0.883361
7889	10575745	NM_177700	234776	ATM interactor	Atmin	1.013	0.24	0.817297	0.927212

7890	10562705	BC100510	434181	predicted gene, EG434181	EG434181	1.013	0.188	0.856207	0.941981
7891	10364984	NM_010731	16969	zinc finger and BTB domain con	Zbtb7a	1.013	0.212	0.838197	0.934421
7892	10551519	NM_030562	80749	leucine rich repeat and fibron	Lrfn1	1.013	0.014	0.989097	0.995308
7893	10356345	NM_010933	18159	natriuretic peptide precursor	Nppc	1.013	0.665	0.526851	0.762787
7894	10499891	NM_009265	20754	small proline-rich protein 1B	Sprr1b	1.013	0.402	0.699069	0.868099
7895	10445758	NM_001033922	224840	triggering receptor expressed	Treml4	1.013	0.485	0.64224	0.838036
7896	10445695	NM_020048	56771	mediator complex subunit 20	Med20	1.013	0.817	0.44006	0.699124
7897	10440926	NM_001099738	246738	open reading frame 28	ORF28	1.013	-0.017	0.987118	0.994703
7898	10399232	ENSMUST00000101635	100038522	predicted gene, ENSMUSG0000007	ENSMUSG00000073242	1.013	0.552	0.597363	0.810488
7899	10517028	NM_025667	52174	DNA segment, Chr 4, ERATO Doi	D4Ertd196e	1.013	-0.591	0.572521	0.796254
7900	10552288	NM_021387	58188	V-set and transmembrane domain	Vstm2b	1.013	0.377	0.717284	0.876366
7901	10520362	NM_153526	231070	insulin induced gene 1	Insig1	1.013	-0.327	0.753125	0.895971
7902	10361133					1.013	-0.162	0.875641	0.950829
7903	10564294	BC116270	330554	myotubularin related protein 1	Mtmr15	1.013	-0.06	0.953684	0.982088
7904	10586614	BC039571	75697	RIKEN cDNA 3300001A09 gene	3300001A09Rik	1.013	0.255	0.806129	0.921832
7905	10564909	NM_172903	140481	mannosidase 2, alpha 2	Man2a2	1.013	0.275	0.791341	0.915073
7906	10379006	NM_183286	70451	dehydrogenase/reductase (SDR f	Dhrs13	1.012	-0.12	0.907553	0.963723
7907	10508036	NM_175246	76793	Smad nuclear interacting prote	Snip1	1.012	0.124	0.904752	0.962956
7908	10373009	NM_025537	66399	Ts translation elongation fact	Tsfm	1.012	0.015	0.988164	0.995129
7909	10472814	NM_201366	381371	gene model 1631, (NCBI)	Gm1631	1.012	0.836	0.429836	0.690652
7910	10437773					1.012	0.434	0.677247	0.856571
7911	10465103	NM_023781	75555	RIKEN cDNA 1700020D05 gene	1700020D05Rik	1.012	0.363	0.726841	0.881629
7912	10605938	NM_020621	57385	pyrimidinergic receptor P2Y, G	P2ry4	1.012	0.436	0.675622	0.855911
7913	10438171	NM_026909	69009	THAP domain containing 7	Thap7	1.012	-0.359	0.730038	0.883264
7914	10414360	NM_010705	16854	lectin, galactose binding, sol	Lgals3	1.012	-0.001	0.999238	0.999589
7915	10515378	NM_146256	242642	4-hydroxyphenylpyruvate dioxyg	Hpdl	1.012	0.319	0.758959	0.899117
7916	10510836	NM_201226	72946	leucine rich repeat containing	Lrrc47	1.012	-0.112	0.913824	0.96595
7917	10476893	NM_028986	74533	GDNF-inducible zinc finger pro	Gzf1	1.012	-0.365	0.725442	0.881081
7918	10427679	NM_177123	320277	sperm flagellar 2	Spef2	1.012	-0.343	0.741044	0.889595
7919	10460645	NM_022012	26403	mitogen-activated protein kina	Map3k11	1.012	-0.423	0.684759	0.860588
7920	10374590	NM_134014	103573	exportin 1, CRM1 homolog (yeas	Xpo1	1.012	0.23	0.824441	0.929508
7921	10425814	NM_172610	223726	metallophosphoesterase domain	Mpped1	1.012	0.206	0.842532	0.936185
7922	10376358	NM_024480	79566	SH3 binding domain protein 5 l	Sh3bp5l	1.012	0.363	0.726699	0.881595
7923	10415576	NM_029498	76007	zinc finger, MYM-type 2	Zmym2	1.012	-0.049	0.96254	0.985405
7924	10579144	BC125568	74549	RIKEN cDNA 9130404D08 gene	9130404D08Rik	1.012	0.285	0.783484	0.912068
7925	10430282	NM_007583	12300	calcium channel, voltage-depen	Cacng2	1.012	0.302	0.770876	0.905387
7926	10414154					1.012	0.849	0.423	0.685287
7927	10518364	XM_204069	277692	similar to Rps19 protein	LOC277692	1.012	-0.368	0.723164	0.879931
7928	10348639	NM_146490	258483	olfactory receptor 1411	Olfr1411	1.012	0.719	0.495018	0.739955
7929	10507635	NM_153105	242653	claudin 19	Cldn19	1.012	0.206	0.842295	0.936059
7930	10458340	NM_010415	15200	heparin-binding EGF-like growt	Hbegf	1.012	0.139	0.893237	0.957788
7931	10394735	NM_027959	71853	protein disulfide isomerase as	Pdia6	1.012	-0.056	0.956906	0.983559
7932	10589030	NM_001114119	69232	glutamine-rich 1	Qrich1	1.012	0.122	0.906094	0.963405
7933	10595668	NM_207260	330998	ankyrin repeat domain 34C	Ankrd34c	1.012	0.219	0.832742	0.932699
7934	10477495	NM_001012392	228801	cDNA sequence U46068	U46068	1.012	0.337	0.745512	0.891679
7935	10587266	NM_010295	14629	glutamate-cysteine ligase, cat	Gclc	1.012	-0.568	0.587461	0.804278
7936	10446549	XM_001480132	622645	predicted gene, EG622645	EG622645	1.012	-0.054	0.958363	0.984334
7937	10561994	NM_029377	75660	lin-37 homolog (C. elegans)	Lin37	1.012	-0.387	0.710153	0.873031
7938	10396367	NM_011384	20476	sine oculis-related homeobox 6	Six6	1.012	-0.165	0.873626	0.949568
7939	10571878	BC030500	234290	cDNA sequence BC030500	BC030500	1.012	0.597	0.569025	0.793724
7940	10451077					1.012	0.174	0.866609	0.946757
7941	10559713	NM_001039532	654801	zinc finger protein 784	Zfp784	1.012	0.507	0.627455	0.83052

7942	10601473	NM_026565	68117	apolipoprotein O-like	Apool	1.012	-0.264	0.799391	0.919009
7943	10558248	NM_009774	12237	budding uninhibited by benzimi	Bub3	1.012	0.002	0.998616	0.999521
7944	10350689	NM_010877	17970	neutrophil cytosolic factor 2	Ncf2	1.012	0.006	0.995758	0.998271
7945	10410311	NM_001001186	408065	zinc finger protein 456	Zfp456	1.012	0.153	0.882813	0.953745
7946	10546817	BC116438	243612	RIKEN cDNA D630042P16 gene	D630042P16Rik	1.012	0.274	0.791695	0.915198
7947	10448483	NM_010947	18209	netrin 2-like (chicken)	Ntn2l	1.012	0.129	0.900587	0.960747
7948	10454306	NM_011755	22694	zinc finger protein 35	Zfp35	1.012	0.009	0.992707	0.99722
7949	10396346	NM_026327	67708	RIKEN cDNA 1810048J11 gene	1810048J11Rik	1.012	0.125	0.904165	0.962767
7950	10497682	XM_001475546	435726	potassium large conductance ca	Kcnmb3	1.012	0.036	0.972366	0.98815
7951	10444407	NM_007425	11596	advanced glycosylation end pro	Ager	1.012	0.38	0.71462	0.875126
7952	10555722	NM_147104	259108	olfactory receptor 550	Olfr550	1.012	0.525	0.615381	0.822218
7953	10521085	ENSMUST00000065707	433873	predicted gene, EG433873	EG433873	1.012	-0.031	0.976362	0.990137
7954	10391359	NM_146030	217198	pleckstrin homology domain con	Plekhh3	1.012	0.148	0.886407	0.955393
7955	10543058	NM_198854	13395	distal-less homeobox 5	Dlx5	1.012	-0.018	0.986143	0.994146
7956	10559702	NM_026741	68490	zinc finger protein 579	Zfp579	1.012	0.217	0.834324	0.933071
7957	10448127	ENSMUST00000061516	14293	formyl peptide receptor 1	Fpr1	1.012	0.151	0.884375	0.95453
7958	10426169	NM_027905	223776	RIKEN cDNA 1300018J18 gene	1300018J18Rik	1.012	0.342	0.741872	0.889893
7959	10516051	NM_007598	12331	CAP, adenylate cyclase-associa	Cap1	1.012	-0.407	0.695924	0.866433
7960	10409567	NM_145976	212937	TRAF-interacting protein with	Tifab	1.012	0.43	0.679625	0.857705
7961	10481491	NM_030244	72500	immediate early response 5-lik	Ier5l	1.012	0.146	0.887921	0.955819
7962	10392033					1.012	-0.134	0.897185	0.95959
7963	10394929	AK132630	668662	predicted gene, EG668662	EG668662	1.012	0.042	0.967428	0.987082
7964	10400570					1.012	0.472	0.651119	0.843737
7965	10424676	NM_008529	17069	lymphocyte antigen 6 complex,	Ly6e	1.012	-0.072	0.944284	0.977948
7966	10465485	NM_007953	26379	estrogen related receptor, alp	Esrra	1.012	0.078	0.939997	0.976656
7967	10446397	XR_035029	100043871	hypothetical protein LOC100043	LOC100043871	1.012	-0.018	0.986496	0.994397
7968	10411448	NM_145455	218490	basic transcription factor 3	Btf3	1.012	-0.04	0.9695	0.987616
7969	10447557	NM_175349	106557	lactate dehydrogenase A-like 6	Ldhal6b	1.012	0.634	0.545879	0.777611
7970	10520706	NM_021447	58522	tripartite motif-containing 54	Trim54	1.012	0.198	0.848472	0.938584
7971	10384572	NM_173752	216551	RIKEN cDNA 1110067D22 gene	1110067D22Rik	1.012	0.286	0.782895	0.911739
7972	10542665	NM_009908	12764	cytidine monophospho-N-acetyln	Cmas	1.012	0.037	0.971772	0.988148
7973	10566400	NM_147060	259062	olfactory receptor 667	Olfr667	1.012	0.154	0.881531	0.953086
7974	10389387					1.012	0.175	0.866184	0.946491
7975	10581577	NM_178380	64340	DEAH (Asp-Glu-Ala-His) box pol	Dhx38	1.012	-0.274	0.792084	0.915332
7976	10420614	AK081218	791379	predicted gene, ENSMUSG0000005	ENSMUSG00000052400	1.012	0.279	0.788076	0.913843
7977	10356771	NM_178051	69821	MTERF domain containing 2	Mterfd2	1.012	-0.262	0.800497	0.91941
7978	10394102	NM_025793	66840	Wdr45 like	Wdr45l	1.012	-0.279	0.788341	0.913849
7979	10398759	BC115831	74691	tudor domain containing 9	Tdrd9	1.012	0.527	0.613754	0.821135
7980	10478285	ENSMUST00000067526	77288	RIKEN cDNA 9430021M05 gene	9430021M05Rik	1.012	0.097	0.925681	0.970574
7981	10579199	NM_001007570	73095	solute carrier family 25, memb	Slc25a42	1.012	-0.144	0.889279	0.956449
7982	10359084					1.012	0.351	0.735531	0.886814
7983	10455824	ENSMUST00000097569	100038410	predicted gene, ENSMUSG0000007	ENSMUSG00000073558	1.011	-0.276	0.790481	0.914692
7984	10504362	NM_172866	242406	RGP1 retrograde golgi transpor	Rgp1	1.011	0.016	0.987892	0.994998
7985	10357814	NM_144530	70579	zinc finger CCCH type containi	Zc3h11a	1.011	0.133	0.897844	0.959787
7986	10384622	NM_153078	216565	EH domain binding protein 1	Ehbp1	1.011	0.101	0.922187	0.968977
7987	10453766	NM_153552	225160	THO complex 1	Thoc1	1.011	-0.004	0.997288	0.998988
7988	10479311	NM_178750	269397	synovial sarcoma translocation	Ss18l1	1.011	0.162	0.87548	0.950704
7989	10588936	NM_133744	72454	coiled-coil domain containing	Ccdc71	1.011	-0.01	0.992125	0.996887
7990	10495201	NM_026774	68576	hepatitis B virus x interactin	Hbxip	1.011	-0.16	0.877238	0.951586
7991	10456891	NM_007505	11946	ATP synthase, H+ transporting,	Atp5a1	1.011	-0.518	0.619947	0.825151
7992	10414970	AK043253	211027	RIKEN cDNA A730076H11 gene	A730076H11Rik	1.011	0.512	0.624142	0.828379

7993	10385719	NM_175255	77371	SEC24 related gene family, mem	Sec24a	1.011	0.166	0.872375	0.949019
7994	10369825	XM_356468	382371	predicted gene, EG382371	EG382371	1.011	0.218	0.833551	0.932911
7995	10569717					1.011	1.005	0.347305	0.621483
7996	10573461	NM_010062	13423	deoxyribonuclease II alpha	Dnase2a	1.011	0.338	0.745113	0.891615
7997	10514588	ENSMUST00000097964	545660	RIKEN cDNA I0C0044D17 gene	I0C0044D17Rik	1.011	0.002	0.998561	0.999521
7998	10563026	NM_029410	75736	BCL2-like 12 (proline rich)	Bcl2l12	1.011	-0.215	0.835928	0.933525
7999	10484927	NM_026721	68427	solute carrier family 39 (meta	Slc39a13	1.011	0.452	0.664337	0.850284
8000	10344743	BC066997	76982	RIKEN cDNA 3110035E14 gene	3110035E14Rik	1.011	0.269	0.795433	0.916955
8001	10540650	NM_026552	68089	actin related protein 2/3 comp	Arpc4	1.011	-0.391	0.707166	0.872175
8002	10370651	NM_181681	216152	cDNA sequence BC005764	BC005764	1.011	0.336	0.746611	0.892388
8003	10496485	NM_007917	13684	eukaryotic translation initiat	Eif4e	1.011	0.191	0.853453	0.940713
8004	10357773	NM_008575	17248	transformed mouse 3T3 cell dou	Mdm4	1.011	0.105	0.919004	0.967837
8005	10526274	NM_025362	66114	Williams-Beuren syndrome chrom	Wbscr18	1.011	-0.354	0.733454	0.885927
8006	10551102	NM_001081294	623131	proline rich 19	Prr19	1.011	0.425	0.683018	0.859827
8007	10499200	ENSMUST00000023846	74485	RIKEN cDNA 4933430H15 gene	4933430H15Rik	1.011	0.355	0.732762	0.885293
8008	10552845	NM_029406	68845	PIH1 domain containing 1	Pih1d1	1.011	-0.505	0.628404	0.830964
8009	10548097	NM_177003	319801	RIKEN cDNA 9630033F20 gene	9630033F20Rik	1.011	0.375	0.718142	0.87698
8010	10547553	NM_153396	194401	microtubule associated monoxyg	Mical3	1.011	0.106	0.918566	0.967805
8011	10517689	NM_145384	212555	PQ loop repeat containing 2	Pqlc2	1.011	0.145	0.888481	0.956033
8012	10383767	NM_152818	74309	oxysterol binding protein 2	Osbp2	1.011	0.443	0.670828	0.85389
8013	10369901	ENSMUST00000009214	71236	rhabdoid tumor deletion region	Rtdr1	1.011	0.397	0.702709	0.869626
8014	10405918	NM_001013769	380855	regulator of sex limited prote	Rsl1	1.011	-0.034	0.973803	0.98872
8015	10588137	NM_028258	72507	DAZ interacting protein 1-like	Dzip1l	1.011	0.118	0.909058	0.963765
8016	10546723					1.011	0.686	0.51403	0.754437
8017	10390147	NM_007867	13394	distal-less homeobox 4	Dlx4	1.011	-0.302	0.771541	0.905749
8018	10400710	NM_001033236	207965	gene model 71, (NCBI)	Gm71	1.011	-0.586	0.575828	0.797128
8019	10448441	NM_172935	245847	amidohydrolase domain containi	Amdhd2	1.011	0.159	0.877705	0.951715
8020	10576140	NM_026014	67177	chromatin licensing and DNA re	Cdt1	1.011	-0.232	0.822619	0.929111
8021	10489422	NM_008435	16538	K+ voltage-gated channel, subf	Kcns1	1.011	-0.192	0.852676	0.940561
8022	10483828	NM_001081033	241489	phosphodiesterase 11A	Pde11a	1.011	0.198	0.848718	0.938708
8023	10589166	NM_134420	171429	solute carrier family 26, memb	Slc26a6	1.011	0.318	0.759332	0.899156
8024	10567464	XM_355934	381917	dynein, axonemal, heavy chain	Dnahc3	1.011	0.451	0.665217	0.850823
8025	10492205	NM_001005509	229317	eukaryotic translation initiat	Eif2a	1.011	-0.017	0.9868	0.994561
8026	10502201	AK040169	319637	RIKEN cDNA A430072C10 gene	A430072C10Rik	1.011	0.379	0.715702	0.875402
8027	10391732	BC019948	237943	G patch domain containing 8	Gpatch8	1.011	-0.064	0.950571	0.980959
8028	10408168	NM_013924	30946	activator of basal transcripti	Abt1	1.011	-0.08	0.938487	0.976028
8029	10509147	NM_178389	74246	galactose-4-epimerase, UDP	Gale	1.011	0.194	0.851171	0.94011
8030	10365469	ENSMUST00000116049	67341	achaete-scute complex homolog	Ascl4	1.011	-0.096	0.9258	0.970651
8031	10493664	ENSMUST00000029548	77595	nucleoporin 210-like	Nup210l	1.011	0.773	0.464034	0.717953
8032	10477406	NM_194357	378700	antimicrobial peptide RYA3	RP23-244H7.9	1.011	0.199	0.848035	0.938472
8033	10530017					1.011	0.3	0.772457	0.906272
8034	10423742	NM_001039368	17749	polymerase (RNA) II (DNA direc	Polr2k	1.011	-0.448	0.667059	0.851389
8035	10461979	NM_013467	11668	aldehyde dehydrogenase family	Aldh1a1	1.011	0.264	0.799133	0.918907
8036	10607250	NM_029943	77622	apurinic/apyrimidinic endonucl	Apex2	1.011	0.409	0.694366	0.86574
8037	10427590	NM_148938	20512	solute carrier family 1 (glial	Slc1a3	1.011	0.061	0.953013	0.981889
8038	10523955	NM_026106	13486	down-regulator of transcriptio	Dr1	1.011	-0.01	0.992292	0.99696
8039	10583343	XR_032517	244710	similar to eukaryotic translat	LOC244710	1.011	-0.577	0.581795	0.800451
8040	10545812	NM_178639	94282	sideroflexin 5	Sfxn5	1.011	0.431	0.679277	0.857678
8041	10429495	NM_008415	16469	jerky	Jrk	1.011	-0.348	0.738001	0.888273
8042	10479112	NM_022000	14683	GNAS (guanine nucleotide bindi	Gnas	1.011	0.031	0.976183	0.990137
8043	10405628	NM_028904	74386	RMI1, RecQ mediated genome ins	Rmi1	1.011	-0.374	0.719427	0.877797
8044	10360695	NM_026171	67459	nuclear VCP-like	Nvl	1.011	0.089	0.931449	0.972759

8044	10360695	NM_026171	67459	nuclear VCP-like	Nvl	1.011	0.089	0.931449	0.972739
8045	10477103	ENSMUST00000089083	791417	predicted gene, OTTMUSG0000001	OTTMUSG00000015846	1.011	0.252	0.80809	0.922738
8046	10508860	NM_016981	20544	solute carrier family 9 (sodiu	Slc9a1	1.011	0.31	0.765393	0.902421
8047	10357097	XR_033060	675394	similar to Elongation factor 2	LOC675394	1.011	0.506	0.628075	0.830847
8048	10529636	NM_022416	64293	serine/threonine kinase 32B	Stk32b	1.011	0.06	0.953709	0.982088
8049	10486681	NM_028799	74176	transglutaminase 5	Tgm5	1.011	0.441	0.67197	0.854437
8050	10493912	NM_001081200	381457	cornulin	Crnn	1.011	0.775	0.462774	0.71721
8051	10522134	NM_024471	79464	lipoic acid synthetase	Lias	1.011	-0.426	0.682725	0.859827
8052	10377790	NM_001114971	216867	solute carrier family 16 (mono	Slc16a11	1.011	0.211	0.838846	0.934783
8053	10349733	NM_175294	98415	nuclear casein kinase and cycl	Nucks1	1.011	0.167	0.872003	0.948845
8054	10427659					1.011	0.114	0.912323	0.965068
8055	10362062	ENSMUST00000042671	76924	RIKEN cDNA 1700021A07 gene	1700021A07Rik	1.011	0.463	0.656955	0.846475
8056	10374323	AK012991	100038540	predicted gene, ENSMUSG0000007	ENSMUSG00000070560	1.01	-0.102	0.921424	0.968656
8057	10560181	NM_133831	68077	glioma tumor suppressor candid	Gltscr2	1.01	-0.064	0.950965	0.981078
8058	10415649					1.01	-0.024	0.981603	0.992092
8059	10448842	NM_027880	71718	TEL2, telomere maintenance 2,	Telo2	1.01	0.451	0.664988	0.850739
8060	10542321	NM_026360	67755	DEAD (Asp-Glu-Ala-Asp) box pol	Ddx47	1.01	-0.152	0.883471	0.954108
8061	10415742	NM_027436	70478	mitochondrial intermediate pep	Mipep	1.01	-0.324	0.754893	0.896835
8062	10476889	NM_001110159	56488	NTF2-related export protein 1	Nxt1	1.01	-0.481	0.644722	0.839358
8063	10576062	NM_020605	57340	junctophilin 3	Jph3	1.01	0.222	0.830693	0.932075
8064	10557206	NM_175023	19647	retinoblastoma binding protein	Rbbp6	1.01	-0.021	0.983452	0.992843
8065	10568921	NM_026769	68566	calcyon neuron-specific vesicu	Caly	1.01	0.59	0.573124	0.796617
8066	10408677	NM_201358	380840	LYR motif containing 4	Lyrm4	1.01	-0.289	0.780762	0.910961
8067	10599335	NM_026902	68995	malignant T cell amplified seq	Mcts1	1.01	0.402	0.699389	0.868342
8068	10580135					1.01	0.591	0.572482	0.796254
8069	10440288	NM_028059	72020	zinc finger protein 654	Zfp654	1.01	-0.042	0.967944	0.987137
8070	10549447	NM_001081113	320727	importin 8	Ipo8	1.01	-0.255	0.80604	0.921787
8071	10557498	BC093505	68952	RIKEN cDNA 1500016O10 gene	1500016O10Rik	1.01	0.67	0.523975	0.760561
8072	10485241	NM_183220	329470	1-aminocyclopropane-1-carboxyl	Accs	1.01	0.225	0.828069	0.930769
8073	10390196	NM_008081	14422	beta-1,4-N-acetyl-galactosamin	B4galnt2	1.01	0.252	0.807722	0.922567
8074	10428753					1.01	0.219	0.832545	0.932679
8075	10431284	NM_001033274	223770	bromodomain containing 1	Brd1	1.01	-0.095	0.927202	0.971253
8076	10489018	NM_133242	170791	RNA binding motif protein 39	Rbm39	1.01	0.109	0.916202	0.966842
8077	10548375	NM_020008	56644	C-type lectin domain family 7,	Clec7a	1.01	0.144	0.889062	0.95642
8078	10604106	NM_001033234	194854	gene model 9, (NCBI)	Gm9	1.01	0.276	0.790602	0.914692
8079	10522627	NM_199032	381644	centrosomal protein 135	Cep135	1.01	-0.39	0.707935	0.872288
8080	10474825	NM_026412	51944	DNA segment, Chr 2, ERATO Doi	D2Ertd750e	1.01	-0.351	0.735794	0.886874
8081	10495001	NM_172684	229675	rosbin, round spermatid basic	Rsbn1	1.01	-0.135	0.896449	0.959489
8082	10604424	NM_153532	208968	zinc finger protein 280c	Zfp280c	1.01	0.066	0.948915	0.980236
8083	10445514	NM_207666	106565	delta-like 2 homolog (Drosophi	Dlk2	1.01	0.28	0.787554	0.913342
8084	10427772	NM_033074	110960	threonyl-tRNA synthetase	Tars	1.01	-0.634	0.545748	0.777543
8085	10486789	NM_080459	140476	stereocilin	Strc	1.01	-0.015	0.988364	0.995236
8086	10347662	NM_177056	319998	transmembrane protein 198	Tmem198	1.01	0.043	0.966549	0.986746
8087	10391957	NM_011719	22412	wingless-type MMTV integration	Wnt9b	1.01	0.061	0.953124	0.981917
8088	10406031	NM_145376	210992	lysophosphatidylcholine acyltr	Lpcat1	1.01	0.171	0.86855	0.947362
8089	10361979	NM_001025392	72567	BCL2-associated transcription	Bclaf1	1.01	-0.226	0.827289	0.930659
8090	10478291	NM_026499	67996	splicing factor, arginine/seri	Sfrs6	1.01	0.353	0.734437	0.886559
8091	10402752	NM_027360	70257	RIKEN cDNA 2010107E04 gene	2010107E04Rik	1.01	-0.128	0.901828	0.961392
8092	10424781	NM_023168	66168	glutamate receptor, ionotropic	Grina	1.01	-0.241	0.815906	0.926256
8093	10364548					1.01	0.327	0.752994	0.895959
8094	10472621	NM_001081548	68795	zinc finger protein 650	Zfp650	1.01	-0.053	0.959274	0.984606
8095	10529995	NM_007839	13204	DEAH (Asp-Glu-Ala-His) box	Dhx15	1.01	-0.046	0.964311	0.9859

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8096	10433241	NM_010061	13419	deoxyribonuclease I	Dnase1	1.01	0.604	0.564506	0.790721
8097	10602223	NM_026247	67574	asparagine-linked glycosylatio	Alg13	1.01	-0.215	0.835878	0.933525
8098	10501084	NM_001044382	246691	prokineticin 1	Prok1	1.01	0.452	0.664281	0.850267
8099	10428682	ENSMUST00000066358	791337	predicted gene, ENSMUSG0000005	ENSMUSG00000053749	1.01	0.092	0.929357	0.972164
8100	10489985	NM_015731	11981	ATPase, class II, type 9A	Atp9a	1.01	-0.159	0.877987	0.951715
8101	10531944	ENSMUST00000069263	791327	predicted gene, ENSMUSG0000005	ENSMUSG00000058736	1.01	0.462	0.657473	0.84686
8102	10430058	NM_019396	54151	cysteine and histidine rich 1	Cyhr1	1.01	-0.228	0.826105	0.929952
8103	10598369	NM_175097	54630	prickle homolog 3 (Drosophila)	Prickle3	1.01	0.266	0.797535	0.917931
8104	10504763	NM_172693	230145	UDP-N-acetyl-alpha-D-galactosa	Galnt12	1.01	0.021	0.98394	0.993077
8105	10477325	NM_001003961	13436	DNA methyltransferase 3B	Dnmt3b	1.01	-0.014	0.989141	0.995308
8106	10498076	NM_001004176	433586	mastermind like 3 (Drosophila)	Maml3	1.01	0.453	0.664006	0.850267
8107	10532248	XM_001476621	671564	ring finger protein 212	Rnf212	1.01	0.8	0.449385	0.706889
8108	10386821	ENSMUST00000101077	103880	RIKEN cDNA A530017D24 gene	A530017D24Rik	1.01	0.326	0.753738	0.896244
8109	10456136	NM_019508	56069	interleukin 17B	Il17b	1.01	0.262	0.80089	0.919467
8110	10510552	NM_001085492	68703	arginine glutamic acid dipepti	Rere	1.01	0.126	0.902909	0.962108
8111	10584582	ENSMUST00000098870	100038567	predicted gene, ENSMUSG0000007	ENSMUSG00000074421	1.01	0.22	0.831714	0.932437
8112	10397377	NM_001081423	320244	tubulin tyrosine ligase-like f	Ttll5	1.01	-0.161	0.876514	0.951096
8113	10500253	NM_027541	70767	PRP3 pre-mRNA processing facto	Prpf3	1.01	0.152	0.883471	0.954108
8114	10569896	BC118542	70192	CD209g antigen	Cd209g	1.01	0.233	0.82194	0.92863
8115	10517579	NM_001033979	435811	low density lipoprotein recept	Ldlrad2	1.01	0.382	0.713739	0.874677
8116	10550059	NM_029809	381845	RIKEN cDNA 2310014L17 gene	2310014L17Rik	1.01	0.177	0.86451	0.946153
8117	10550833	NM_001045486	210135	zinc finger protein 180	Zfp180	1.01	-0.093	0.928324	0.971746
8118	10372668	NM_010786	17246	transformed mouse 3T3 cell dou	Mdm2	1.01	0.026	0.980004	0.991919
8119	10435543	ENSMUST00000039855	224139	golgi autoantigen, golgin subf	Golgb1	1.01	-0.522	0.617278	0.823029
8120	10375537	NM_001110148	17308	mannoside acetylglucosaminyltr	Mgat1	1.01	0.099	0.923897	0.96976
8121	10474875	NM_029617	76464	cancer susceptibility candidat	Casc5	1.01	-0.01	0.992018	0.996827
8122	10593988	NM_007713	102414	CDC-like kinase 3	Clk3	1.009	-0.208	0.840992	0.935759
8123	10603312	ENSMUST00000066557	54651	ubiquitin specific peptidase 2	Usp27x	1.009	0.17	0.86942	0.947676
8124	10356482	XR_031409	383542	hypothetical gene supported by	LOC383542	1.009	0.165	0.873335	0.949372
8125	10489936	NM_009628	11538	activity-dependent neuroprotec	Adnp	1.009	0.239	0.817818	0.92753
8126	10406050	NM_010020	13162	solute carrier family 6 (neuro	Slc6a3	1.009	0.117	0.909822	0.964056
8127	10373052					1.009	0.334	0.74765	0.892822
8128	10424674	AJ011022	15202	hematopoietic cell transcript	Hemt1	1.009	0.407	0.695494	0.866211
8129	10416371	NM_175116	67168	purinergic receptor P2Y, G-pro	P2ry5	1.009	-0.343	0.74157	0.889732
8130	10526564	NM_027356	70240	UFM1-specific peptidase 1	Ufsp1	1.009	-0.312	0.764023	0.90173
8131	10512640	NM_015828	50798	glucosamine	Gne	1.009	-0.305	0.76881	0.904
8132	10514240	NM_172426	76376	solute carrier family 24 (sodi	Slc24a2	1.009	0.628	0.549225	0.779541
8133	10597598	NM_001037749	382113	solute carrier family 22 (orga	Slc22a14	1.009	0.386	0.710655	0.873102
8134	10461251	NM_001013019	68852	RIKEN cDNA 1110067I12 gene	1110067I12Rik	1.009	-0.157	0.879925	0.952396
8135	10464030	NM_007417	11551	adrenergic receptor, alpha 2a	Adra2a	1.009	0.305	0.76915	0.904298
8136	10531488	NM_017367	12453	cyclin I	Ccni	1.009	-0.559	0.59329	0.807893
8137	10596489	ENSMUST00000116026	436090	G protein-coupled receptor 62	Gpr62	1.009	-0.05	0.961454	0.985172
8138	10573747	NM_007406	11513	adenylate cyclase 7	Adcy7	1.009	0.237	0.819346	0.928264
8139	10350149	NM_021467	21952	troponin I, skeletal, slow 1	Tnni1	1.009	0.385	0.711426	0.873563
8140	10509998	NM_009541	22642	zinc finger and BTB domain con	Zbtb17	1.009	0.437	0.674655	0.855467
8141	10420780	NM_021480	58865	L-threonine dehydrogenase	Tdh	1.009	0.289	0.780389	0.910806
8142	10410690					1.009	0.661	0.529237	0.76441
8143	10400002	ENSMUST00000061679	70844	RIKEN cDNA 4921508M14 gene	4921508M14Rik	1.009	-0.081	0.937371	0.975526
8144	10406714	NM_011021	18420	orthopedia homolog (Drosophila	Otp	1.009	0.492	0.637565	0.835648
8145	10510720	NM_009079	19934	ribosomal protein L22	Rpl22	1.009	-0.081	0.937633	0.975655
8146	10514697					1.009	0.685	0.514998	0.754817

8147	10474004					1.009	0.803	0.447559	0.705227
8148	10455682	AY692449	225497	gene model 93, (NCBI)	Gm93	1.009	0.362	0.727933	0.88203
8149	10387255	AK033665	100038433	predicted gene, ENSMUSG0000007	ENSMUSG00000072807	1.009	0.028	0.978582	0.991413
8150	10456516					1.009	-0.18	0.861763	0.94442
8151	10533720	NM_030701	80885	G protein-coupled receptor 109	Gpr109a	1.009	0.54	0.605607	0.816017
8152	10405950	NM_027123	69577	FAST kinase domains 3	Fastkd3	1.009	-0.07	0.945954	0.978614
8153	10577782	NM_001081187	330723	HtrA serine peptidase 4	Htra4	1.009	0.169	0.87074	0.948568
8154	10581448	AK089165	319446	dipeptidase 2	Dpep2	1.009	-0.018	0.986153	0.994146
8155	10507394	NM_175244	76608	HECT domain containing 3	Hectd3	1.009	0.004	0.996746	0.998777
8156	10456922	ENSMUST00000044622	71423	RIKEN cDNA 5430411K18 gene	5430411K18Rik	1.009	0.602	0.565686	0.791744
8157	10489872	NM_008420	16500	potassium voltage gated channe	Kcnb1	1.009	0.473	0.650503	0.843249
8158	10438975	BC031419	268880	expressed sequence AI480653	AI480653	1.009	-0.017	0.986714	0.994522
8159	10393364	NM_030206	114886	cytoglobin	Cygb	1.009	0.747	0.478939	0.729132
8160	10596967	NM_172774	235610	RIKEN cDNA 6620401K05 gene	6620401K05Rik	1.009	-0.367	0.724093	0.88046
8161	10559513					1.009	0.489	0.639395	0.836375
8162	10425364	NM_009716	11911	activating transcription facto	Atf4	1.009	-0.079	0.939002	0.976218
8163	10477450	NM_008953	19194	parotid secretory protein	Psp	1.009	0.519	0.61925	0.82476
8164	10413919	NM_001001796	107751	paired related homeobox protei	Prrxl1	1.009	0.586	0.575602	0.797076
8165	10582719	NM_001081337	244668	signal-induced proliferation-a	Sipa1l2	1.009	-0.013	0.990122	0.995679
8166	10413381	NM_080856	142687	ankyrin repeat and SOCS box-co	Asb14	1.009	0.306	0.768549	0.903793
8167	10367033	NM_198035	320080	zinc finger and BTB domain con	Zbtb39	1.009	0.244	0.813665	0.925035
8168	10551758	ENSMUST00000063585	442797	RIKEN cDNA 6330444E15 gene	6330444E15Rik	1.009	0.236	0.819641	0.928312
8169	10412960	BC069846	105428	expressed sequence AA536717	AA536717	1.009	-0.498	0.633532	0.833323
8170	10450145	NM_013585	16912	proteasome (prosome, macropain	Psmb9	1.009	0.04	0.969243	0.987586
8171	10580577	NM_008393	16373	Iroquois related homeobox 3 (D	Irx3	1.009	0.444	0.670298	0.853559
8172	10494281	NM_026489	67981	HORMA domain containing 1	Hormad1	1.009	0.215	0.835352	0.933323
8173	10419850	NM_207131	110794	CCAAT/enhancer binding protein	Cebpe	1.009	0.383	0.712526	0.874059
8174	10580082	ENSMUST00000071067	442802	RIKEN cDNA C330011M18 gene	C330011M18Rik	1.009	0.416	0.689294	0.863619
8175	10360410	NM_001005520	404222	olfactory receptor 244	Olfr244	1.009	0.383	0.712904	0.874189
8176	10353165					1.009	-0.045	0.965463	0.986124
8177	10374185	NM_146014	216527	cerebral cavernous malformatio	Ccm2	1.009	-0.579	0.57992	0.799181
8178	10504865	NM_010569	16348	inversin	Invs	1.009	0.309	0.765793	0.902563
8179	10346668	NM_001037725	72750	amyotrophic lateral sclerosis	Als2cr13	1.009	-0.063	0.951551	0.981156
8180	10586284	NM_028906	74388	dipeptidylpeptidase 8	Dpp8	1.009	-0.048	0.963359	0.985684
8181	10505107	NM_009611	11470	actin-like 7a	Actl7a	1.009	0.405	0.69743	0.867333
8182	10442123					1.009	0.668	0.524733	0.761127
8183	10363331					1.009	0.045	0.965602	0.986218
8184	10420457	NM_028643	68514	EF hand domain family A1	Efha1	1.009	-0.293	0.777805	0.909568
8185	10495077	ENSMUST00000070584	75269	RIKEN cDNA 4930564D02 gene	4930564D02Rik	1.009	0.233	0.82192	0.92863
8186	10583952	NM_178113	78658	non-SMC condensin II complex,	Ncapd3	1.009	0.052	0.959751	0.984908
8187	10525804	NM_011596	21871	ATPase, H+ transporting, lysos	Atp6v0a2	1.009	0.047	0.963447	0.985684
8188	10450675	NM_008207	15042	histocompatibility 2, T region	H2-T24	1.009	0.402	0.699564	0.868422
8189	10450126	NM_001025387	14312	bromodomain containing 2	Brd2	1.008	0.105	0.919574	0.967948
8190	10597714	NM_011887	24046	sodium channel, voltage-gated,	Scn11a	1.008	-0.044	0.965924	0.986394
8191	10562942	NM_029365	75613	mediator of RNA polymerase II	Med25	1.008	0.151	0.884378	0.95453
8192	10357986	NM_007955	13924	protein tyrosine phosphatase,	Ptprv	1.008	0.25	0.809327	0.923176
8193	10442393	AK017296	100036538	predicted gene, ENSMUSG0000005	ENSMUSG00000054651	1.008	-0.072	0.944345	0.977948
8194	10388337	NM_013625	18472	platelet-activating factor ace	Pafah1b1	1.008	0.049	0.962062	0.985362
8195	10487787	NM_020014	14588	glial cell line derived neurot	Gfra4	1.008	0.225	0.828055	0.930769
8196	10458958					1.008	-0.129	0.900526	0.960731
8197	10511819	NM_001033531	212390	kelch-like 32 (Drosophila)	Klhl32	1.008	0.07	0.945921	0.978614
8198	10560028	NM_001081449	666085	vomeronasal 2, receptor 54	Vmn2r54	1.008	0.3	0.772407	0.906263

8199	10461156	AK051045	83673	small nucleolar RNA host gene	Snhg1	1.008	0.212	0.838347	0.934421
8200	10456246	XR_034153	638407	similar to 40S ribosomal prote	LOC638407	1.008	-0.132	0.898676	0.960077
8201	10506118	NM_146144	230484	ubiquitin specific peptdiase 1	Usp1	1.008	-0.077	0.940773	0.977
8202	10511290	NM_009400	21936	tumor necrosis factor receptor	Tnfrsf18	1.008	0.216	0.834901	0.933323
8203	10351658	NM_007649	12506	CD48 antigen	Cd48	1.008	0.318	0.759274	0.899156
8204	10550167					1.008	0.098	0.9246	0.970306
8205	10566632	NM_177216	320635	cytochrome b5 reductase 2	Cyb5r2	1.008	0.152	0.883209	0.954001
8206	10539211	NM_178731	243499	leucine rich repeat transmembr	Lrrtm4	1.008	-0.117	0.91015	0.964056
8207	10392787	ENSMUST00000063993	319819	RIKEN cDNA 4932435O22 gene	4932435O22Rik	1.008	0.256	0.804875	0.921052
8208	10380087	NM_133215	170749	myotubularin related protein 4	Mtmr4	1.008	-0.373	0.719925	0.878109
8209	10462303	NM_183179	240595	potassium channel, subfamily V	Kcnv2	1.008	0.28	0.787302	0.913152
8210	10353288	NM_025773	66799	ubiquitin-conjugating enzyme E	Ube2w	1.008	-0.478	0.646514	0.840625
8211	10515528	NM_026344	67728	DPH2 homolog (S. cerevisiae)	Dph2	1.008	0.09	0.930941	0.972759
8212	10368845	NM_029132	103268	RIKEN cDNA 2410017P07 gene	2410017P07Rik	1.008	-0.23	0.824834	0.929565
8213	10418747	NM_019975	56794	2-hydroxyacyl-CoA lyase 1	Hacl1	1.008	-0.155	0.881384	0.953061
8214	10450870					1.008	0.282	0.785623	0.912507
8215	10542028	NM_022657	64654	fibroblast growth factor 23	Fgf23	1.008	0.214	0.836472	0.933958
8216	10437963	BC027550	72083	RIKEN cDNA 2410018G20 gene	2410018G20Rik	1.008	-0.893	0.400426	0.666294
8217	10359635	NM_178883	98376	SCY1-like 1 binding protein 1	Scyl1bp1	1.008	0.148	0.886444	0.955393
8218	10450858	NM_001011813	258051	olfactory receptor 93	Olfr93	1.008	0.352	0.735177	0.886784
8219	10599229	NM_173779	245381	ankyrin repeat domain 58	Ankrd58	1.008	0.32	0.757966	0.898457
8220	10390701	ENSMUST00000100494	100037262	predicted gene, OTTMUSG0000000	OTTMUSG00000006457	1.008	0.291	0.779149	0.910184
8221	10510844	NM_021499	59002	WD repeat domain 8	Wdr8	1.008	-0.031	0.976074	0.990137
8222	10428052	NM_007637	12465	chaperonin subunit 5 (epsilon)	Cct5	1.008	-0.465	0.65566	0.845958
8223	10409551	NM_011097	18740	paired-like homeodomain transc	Pitx1	1.008	-0.046	0.964626	0.985942
8224	10446001	NM_183178	240121	fibronectin type 3 and SPRY do	Fsd1	1.008	0.097	0.92553	0.970539
8225	10507418	NM_001111277	108067	eukaryotic translation initiat	Eif2b3	1.008	-0.391	0.707096	0.872175
8226	10469816	NM_031167	16181	interleukin 1 receptor antagon	Il1rn	1.008	0.105	0.91925	0.967863
8227	10572251	NM_032004	83984	testis-specific serine kinase	Tssk6	1.008	0.165	0.873307	0.949372
8228	10593628	NM_175562	270160	RAB39, member RAS oncogene fam	Rab39	1.008	0.198	0.84817	0.938472
8229	10533844	NM_030259	80291	Rab interacting lysosomal prot	Rilpl2	1.008	-0.316	0.761058	0.900342
8230	10416989	NM_021434	58245	G protein-coupled receptor 180	Gpr180	1.008	-0.079	0.939164	0.976281
8231	10603005	XR_033102	676160	similar to thyroid hormone rec	LOC676160	1.008	0.69	0.512007	0.75265
8232	10582287	NM_007608	12352	carbonic anhydrase 5a, mitocho	Car5a	1.008	0.178	0.863838	0.945829
8233	10534585	NM_018825	23921	SH2B adaptor protein 2	Sh2b2	1.008	0.55	0.59868	0.811605
8234	10568078	ENSMUST00000071268	381921	TAO kinase 2	Taok2	1.008	0.037	0.971212	0.988148
8235	10393836	NM_133796	192662	Rho GDP dissociation inhibitor	Arhgdia	1.008	-0.16	0.877059	0.95149
8236	10389245	NM_172562	217031	transcriptional adaptor 2 (ADA	Tada2l	1.008	-0.589	0.573604	0.796812
8237	10427205	NM_021713	60315	melanocyte proliferating gene	Myg1	1.008	-0.221	0.831466	0.932333
8238	10349744	NM_145977	212980	solute carrier family 45, memb	Slc45a3	1.008	0.59	0.573512	0.79679
8239	10391196	NM_177790	278304	zinc finger protein 385C	Zfp385c	1.008	0.438	0.674028	0.855133
8240	10535095	NM_133349	100494	zinc finger, AN1-type domain 2	Zfand2a	1.008	0.266	0.797739	0.917953
8241	10427671					1.008	0.297	0.774991	0.907674
8242	10566804	NM_020050	56786	TMEM9 domain family, member B	Tmem9b	1.008	-0.486	0.64135	0.837465
8243	10521543	NM_026959	71116	syntaxin 18	Stx18	1.008	-0.062	0.952155	0.981389
8244	10524973	BC104372	76792	RIKEN cDNA 2410131K14 gene	2410131K14Rik	1.008	0.105	0.919605	0.967948
8245	10508351	NM_018774	54383	polyhomeotic-like 2 (Drosophil	Phc2	1.008	-0.106	0.918252	0.967805
8246	10547995	NM_009446	22144	tubulin, alpha 3A	Tuba3a	1.008	-0.201	0.846042	0.937284
8247	10593060	NM_001081373	214552	centrosomal protein 164	Cep164	1.008	0.324	0.755316	0.897145
8248	10511139	NM_026899	68991	Ssu72 RNA polymerase II CTD ph	Ssu72	1.008	-0.631	0.547423	0.778445
8249	10404928	NM_001033192	97863	expressed sequence C78339	C78339	1.008	0.308	0.766532	0.902924

8249	10404928	NM_001033192	97863	expressed sequence C78339	C78339	1.008	0.308	0.766332	0.902924
8250	10346224	ENSMUST00000087708	227094	RIKEN cDNA 5330401P04 gene	5330401P04Rik	1.008	0.132	0.898418	0.960023
8251	10585759	NM_153799	353190	enhancer of mRNA decapping 3 h	Edc3	1.008	-0.106	0.918261	0.967805
8252	10378024	NM_025993	67139	MIS12 homolog (yeast)	Mis12	1.008	-0.463	0.656942	0.846475
8253	10465263	NM_011262	19708	D4, zinc and double PHD finger	Dpf2	1.008	-0.183	0.859565	0.943578
8254	10419049	NM_008734	18183	neuregulin 3	Nrg3	1.008	0.11	0.91531	0.966602
8255	10423172	NM_025673	66629	golgi phosphoprotein 3	Golph3	1.008	-0.184	0.858929	0.943374
8256	10399549	XM_126830	73667	RIKEN cDNA 2410004P03 gene	2410004P03Rik	1.008	1.09	0.310712	0.587208
8257	10412258					1.008	-0.571	0.58553	0.80308
8258	10443940	BC094586	77652	zinc finger protein 422, relat	Zfp422-rs1	1.008	0.078	0.940125	0.9767
8259	10605790	XM_141955	236914	gene model 371, (NCBI)	Gm371	1.008	0.378	0.71629	0.875701
8260	10418989					1.008	0.658	0.531017	0.765411
8261	10397818	NM_016856	51786	cleavage and polyadenylation s	Cpsf2	1.008	-0.304	0.769912	0.904792
8262	10566140	BC106830	257926	olfactory receptor 544	Olfr544	1.008	0.149	0.885776	0.955239
8263	10522786					1.008	0.521	0.617841	0.823459
8264	10417561	NM_183187	268709	cDNA sequence BC055107	BC055107	1.008	0.149	0.885672	0.95523
8265	10455572	NM_001033446	381142	gene model 949, (NCBI)	Gm949	1.008	0.151	0.883846	0.954252
8266	10569583	ENSMUST00000093967	233977	protein tyrosine phosphatase,	Ppfia1	1.008	-0.322	0.756486	0.897871
8267	10498446	BC119599	229357	G protein-coupled receptor 149	Gpr149	1.008	-0.26	0.802391	0.919965
8268	10350992	NM_001024952	381305	RING CCCH (C3H) domains 1	Rc3h1	1.008	-0.142	0.890943	0.957416
8269	10444431	NM_030890	260297	proline-rich transmembrane pro	Prrt1	1.008	-0.05	0.961679	0.985234
8270	10470318					1.008	0.088	0.93256	0.973153
8271	10444685	NM_178592	193742	HLA-B associated transcript 5	Bat5	1.008	0.146	0.887917	0.955819
8272	10408555					1.008	-0.243	0.814659	0.925586
8273	10366517	AK016591	71013	RIKEN cDNA 4933400F03 gene	4933400F03Rik	1.007	0.24	0.816756	0.926972
8274	10515164	NM_025647	66588	cytidine monophosphate (UMP-CM	Cmpk1	1.007	-0.362	0.727404	0.881863
8275	10597098	NM_009921	12796	cathelicidin antimicrobial pep	Camp	1.007	0.168	0.870979	0.948568
8276	10606789	NM_025355	66104	transcription elongation facto	Tceal6	1.007	-0.215	0.835647	0.933431
8277	10377695	NM_030064	78246	PHD finger protein 23	Phf23	1.007	-0.518	0.619956	0.825151
8278	10532828	NM_029956	77697	methylmalonic aciduria (cobala	Mmab	1.007	0.167	0.872293	0.948998
8279	10374908	NM_194054	68585	reticulon 4	Rtn4	1.007	0.09	0.930954	0.972759
8280	10425109	ENSMUST00000018150	78623	RIKEN cDNA 1700041B01 gene	1700041B01Rik	1.007	0.361	0.728588	0.882433
8281	10361767	NM_175102	66125	splicing factor 3b, subunit 5	Sf3b5	1.007	-0.352	0.73504	0.886784
8282	10469070	NM_016918	53893	nudix (nucleoside diphosphate	Nudt5	1.007	-0.099	0.923625	0.969694
8283	10410919	XR_034009	435373	similar to high mobility group	LOC435373	1.007	0.063	0.951413	0.981144
8284	10552843					1.007	0.483	0.643485	0.838573
8285	10473107					1.007	0.083	0.935726	0.974582
8286	10562059	NM_025628	110323	cytochrome c oxidase, subunit	Cox6b1	1.007	-0.268	0.796425	0.917464
8287	10370422	NM_029546	110816	PWP2 periodic tryptophan prote	Pwp2	1.007	-0.159	0.877992	0.951715
8288	10466528	AK041805	100036532	predicted gene, ENSMUSG0000005	ENSMUSG00000055458	1.007	0.224	0.828763	0.931153
8289	10363210	NM_008863	18768	protein kinase inhibitor beta,	Pkib	1.007	0.29	0.780059	0.910713
8290	10555233					1.007	-0.323	0.755743	0.89752
8291	10592114	NM_172291	235169	FAD-dependent oxidoreductase d	Foxred1	1.007	-0.072	0.944302	0.977948
8292	10386996	NM_145136	214384	myocardin	Myocd	1.007	-0.016	0.988001	0.995045
8293	10428755	NM_009572	22770	zinc fingers and homeoboxes 1	Zhx1	1.007	-0.158	0.878493	0.95179
8294	10555401					1.007	0.173	0.86732	0.946934
8295	10571530	NM_001081286	14107	FAT tumor suppressor homolog 1	Fat1	1.007	-0.558	0.593657	0.808175
8296	10351482	BC099563	76925	RIKEN cDNA 1700015E13 gene	1700015E13Rik	1.007	0.087	0.933374	0.973406
8297	10465446	NM_001081291	78317	coiled-coil domain containing	Ccdc88b	1.007	0.139	0.893135	0.957774
8298	10365116	NM_133964	102115	deoxyhypusine hydroxylase/mono	Dohh	1.007	0.232	0.823217	0.929358
8299	10420372	NM_030004	68631	crystallin, lambda 1	Cryl1	1.007	0.4	0.700977	0.868962
8300	10356677	ENSMUST00000097642	66915	myeloma overexpressed 2	Myeov2	1.007	-0.238	0.818169	0.927633

8301	10481210	NM_009500	22325	vav 2 oncogene	Vav2	1.007	-0.125	0.903562	0.962464
8302	10392142	NM_008339	15985	CD79B antigen	Cd79b	1.007	0.449	0.666902	0.851389
8303	10440550	NM_001081068	78913	zinc finger protein 294	Zfp294	1.007	-0.654	0.533636	0.767668
8304	10481654	NM_010236	14287	folylpolyglutamyl synthetase	Fpgs	1.007	0.218	0.833145	0.932804
8305	10362581	NM_028006	71924	epsilon-tubulin 1	Tube1	1.007	0.336	0.74628	0.892295
8306	10446553	NM_013813	13823	erythrocyte protein band 4.1-l	Epb4.1l3	1.007	-0.435	0.676132	0.855911
8307	10470200	NM_001100455	227630	lipocalin 11	Lcn11	1.007	0.227	0.826809	0.93054
8308	10484648	NM_146767	258763	olfactory receptor 1104	Olfr1104	1.007	0.23	0.824499	0.929523
8309	10518113	NM_144531	71529	RIKEN cDNA 9030409G11 gene	9030409G11Rik	1.007	-0.211	0.838623	0.934583
8310	10478487	NM_025575	66460	SYS1 Golgi-localized integral	Sys1	1.007	0.075	0.942563	0.977825
8311	10365384	NM_001024918	71137	regulatory factor X, 4 (influe	Rfx4	1.007	0.642	0.540796	0.773267
8312	10415156	ENSMUST00000085837	545052	predicted gene, EG545052	EG545052	1.007	-0.103	0.920614	0.968204
8313	10554710					1.007	-0.174	0.866782	0.946802
8314	10594460	NM_001001295	213550	DIS3 mitotic control homolog (	Dis3l	1.007	-0.039	0.969586	0.987616
8315	10573295	NM_009055	19724	regulatory factor X, 1 (influe	Rfx1	1.007	0.14	0.892347	0.957747
8316	10377569	NM_011814	23879	fragile X mental retardation,	Fxr2	1.007	-0.262	0.800303	0.919317
8317	10456764	NM_010754	17126	MAD homolog 2 (Drosophila)	Smad2	1.007	-0.209	0.840132	0.935328
8318	10403964	NM_183014	193452	zinc finger protein 184 (Krupp	Zfp184	1.007	-0.487	0.640922	0.837375
8319	10508001	NM_177573	194268	RIKEN cDNA 9930104L06 gene	9930104L06Rik	1.007	0.286	0.782593	0.911672
8320	10474836	NM_019826	56357	isovaleryl coenzyme A dehydrog	Ivd	1.007	0.103	0.921083	0.968443
8321	10533007	NM_001080808	75665	coiled-coil domain containing	Ccdc64	1.007	0.003	0.997621	0.999133
8322	10451918	NM_024432	66530	UBX domain containing 1	Ubxd1	1.007	-0.11	0.915238	0.966602
8323	10495012	NM_013629	18685	putative homeodomain transcrip	Phtf1	1.007	-0.141	0.892014	0.95769
8324	10501313	XR_032348	668686	similar to Siva1 protein	LOC668686	1.007	-0.208	0.840971	0.935759
8325	10562665					1.007	0.192	0.853259	0.940713
8326	10404339	ENSMUST00000095920	100041036	novel protein similar to dynei	RP23-374O23.1	1.007	0.588	0.574332	0.797076
8327	10481401	NM_178694	227693	zer-1 homolog (C. elegans)	Zer1	1.007	0.071	0.945656	0.978514
8328	10606770	NM_175446	215693	zinc finger, matrin type 1	Zmat1	1.007	-0.285	0.783879	0.912068
8329	10457400					1.007	0.255	0.805671	0.921565
8330	10345930	NM_009418	22019	tripeptidyl peptidase II	Tpp2	1.007	-0.122	0.9066	0.963405
8331	10552143	NM_017394	53896	solute carrier family 7 (catio	Slc7a10	1.007	0.248	0.810967	0.923749
8332	10542686	ENSMUST00000100817	52285	DNA segment, Chr 6, ERATO Doi	D6Ertd474e	1.007	0.261	0.801036	0.919467
8333	10607116	NM_019496	56068	Alport syndrome, mental retard	Ammecr1	1.007	-0.218	0.83378	0.932972
8334	10385591	NM_175334	103806	mastermind like 1 (Drosophila)	Maml1	1.007	0.231	0.823862	0.929508
8335	10417895	NM_008914	19056	protein phosphatase 3, catalyt	Ppp3cb	1.007	-0.209	0.840589	0.93555
8336	10415700	NM_144843	219135	myotubularin related protein 6	Mtmr6	1.007	0.106	0.918783	0.967805
8337	10375038	NM_010822	268395	N-methylpurine-DNA glycosylase	Mpg	1.007	-0.243	0.814893	0.925752
8338	10447897	NM_001113533	60532	Wilms' tumour 1-associating pr	Wtap	1.007	-0.001	0.999197	0.999589
8339	10582310	NM_138656	192156	mevalonate (diphospho) decarbo	Mvd	1.007	0.002	0.998179	0.99936
8340	10590245	NM_144793	208638	solute carrier family 25, memb	Slc25a38	1.006	0.081	0.937293	0.975526
8341	10514296	NM_010507	15972	interferon alpha 9	Ifna9	1.006	0.394	0.704746	0.871013
8342	10370330	ENSMUST00000092369	544710	predicted gene, EG544710	EG544710	1.006	-0.238	0.818133	0.927633
8343	10470158	NM_177840	620709	lipocalin 6	Lcn6	1.006	0.105	0.919465	0.967948
8344	10461365	NM_026007	67160	eukaryotic translation elongat	Eef1g	1.006	-0.326	0.753779	0.896244
8345	10402608	BC048462	66323	RIKEN cDNA 1700001K19 gene	1700001K19Rik	1.006	-0.623	0.552301	0.782016
8346	10571111	NM_001101502	353310	zinc finger protein 703	Zfp703	1.006	0.39	0.707984	0.872288
8347	10360235	NM_009813	12372	calsequestrin 1	Casq1	1.006	0.629	0.548801	0.779201
8348	10469712	NM_019501	56075	prenyl (solanesyl) diphosphate	Pdss1	1.006	0.031	0.97636	0.990137
8349	10394931					1.006	0.386	0.710422	0.873031
8350	10574013	NM_008631	17752	metallothionein 4	Mt4	1.006	0.188	0.856359	0.941981
8351	10518050	NM_007919	13706	elastase 2A	RP23-395H4.4	1.006	0.024	0.981629	0.992092
8352	10578066					1.006	0.251	0.809043	0.923112
8353	10546929	NM_178373	14311	cell death-inducing DFFA-like	Cidec	1.006	0.105	0.919503	0.967948
8354	10516994	BC008163	230789	cDNA sequence BC008163	BC008163	1.006	-0.338	0.745121	0.891615

8355	10524965					1.006	0.09	0.930693	0.972759
8356	10392410	ENSMUST00000100300	100038581	predicted gene, ENSMUSG0000007	ENSMUSG00000075466	1.006	0.473	0.650342	0.84316
8357	10372230	NM_008657	17878	myogenic factor 6	Myf6	1.006	0.398	0.7021	0.869258
8358	10437270	AK018837	78377	RIKEN cDNA 1700016D08 gene	1700016D08Rik	1.006	0.215	0.835384	0.933323
8359	10595183	NM_010106	13627	eukaryotic translation elongat	Eef1a1	1.006	-0.015	0.988814	0.995308
8360	10574330	NM_199455	73407	RIKEN cDNA 1700055M20 gene	1700055M20Rik	1.006	-0.066	0.948989	0.980236
8361	10448559					1.006	0.209	0.840058	0.935328
8362	10587049					1.006	0.6	0.566851	0.792482
8363	10540148	NM_198668	381798	RIKEN cDNA 4930590J08 gene	4930590J08Rik	1.006	0.259	0.802611	0.919965
8364	10487380	ENSMUST00000099407	545459	predicted gene, ENSMUSG0000007	ENSMUSG00000074822	1.006	-0.226	0.827463	0.930659
8365	10529797					1.006	-0.146	0.887558	0.955671
8366	10533026	NM_031869	19079	protein kinase, AMP-activated,	Prkab1	1.006	-0.431	0.679316	0.857678
8367	10346544	NM_025597	66495	NADH dehydrogenase (ubiquinone	Ndufb3	1.006	-0.074	0.943261	0.977948
8368	10506591	NM_172272	230577	prolyl-tRNA synthetase (mitoch	Pars2	1.006	-0.194	0.851832	0.940193
8369	10415353	NM_027673	71099	testis-specific serine kinase	Tssk4	1.006	0.299	0.773567	0.9067
8370	10471080	NM_028846	74270	ubiquitin specific peptidase 2	Usp20	1.006	0.138	0.894147	0.958326
8371	10452903	XM_001481192	100043886	L antigen family, member 3 pse	LOC100043886	1.006	-0.094	0.928039	0.971746
8372	10389973	NM_144827	217116	spermatogenesis associated 20	Spata20	1.006	0.77	0.465848	0.719391
8373	10526842	NM_028130	72154	zinc finger protein 157	Zfp157	1.006	-0.233	0.821902	0.92863
8374	10591418	NM_001103168	100009600	GATA-like 1	Glp1	1.006	0.319	0.758774	0.898998
8375	10506397	NM_027696	71148	mesoderm induction early respo	Mier1	1.006	-0.318	0.759668	0.899311
8376	10480652	NM_001082476	78797	NADPH dependent diflavin oxido	Ndor1	1.006	-0.419	0.68732	0.862149
8377	10596166	BC021390	71775	RIKEN cDNA 1300017J02 gene	1300017J02Rik	1.006	-0.098	0.924812	0.970324
8378	10581214	NM_177449	234684	leucine rich repeat containing	Lrrc29	1.006	0.201	0.846612	0.937778
8379	10462473	NM_010776	17195	mannose binding lectin (C)	Mbl2	1.006	0.051	0.960799	0.985069
8380	10373902	BC039988	71962	RIKEN cDNA 2410008K03 gene	2410008K03Rik	1.006	-0.138	0.894371	0.958345
8381	10578425	ENSMUST00000084536	434310	cDNA sequence AY512931	AY512931	1.006	0.466	0.655084	0.845541
8382	10511843	NM_026194	67490	RIKEN cDNA 1810074P20 gene	1810074P20Rik	1.006	-0.064	0.950917	0.981077
8383	10556576	NM_019772	56372	RIKEN cDNA 1110004F10 gene	1110004F10Rik	1.006	-0.554	0.59603	0.80968
8384	10575120	NM_009229	20650	syntrophin, basic 2	Sntb2	1.006	0.143	0.889877	0.956717
8385	10557816	NM_009739	12041	branched chain ketoacid dehydr	Bckdk	1.006	-0.371	0.721031	0.878601
8386	10472422	NM_001033477	383709	gene model 1322, (NCBI)	Gm1322	1.006	-0.087	0.932866	0.973233
8387	10487508					1.006	-0.062	0.952098	0.981385
8388	10566286					1.006	0.628	0.549673	0.779911
8389	10430431	ENSMUST00000100469	100038696	predicted gene, ENSMUSG0000007	ENSMUSG00000075561	1.006	0.628	0.549172	0.779541
8390	10349821	NM_029025	74626	transmembrane protein 81	Tmem81	1.006	0.087	0.9334	0.973406
8391	10503845	NM_019586	56228	ubiquitin-conjugating enzyme E	Ube2j1	1.006	-0.75	0.477117	0.727862
8392	10521383	NM_007418	11553	adrenergic receptor, alpha 2c	Adra2c	1.006	0.203	0.844778	0.936998
8393	10382152	NM_198298	78455	helicase with zinc finger doma	Helz	1.006	-0.181	0.861542	0.944347
8394	10534142	NM_023248	66711	Shwachman-Bodian-Diamond syndr	Sbds	1.006	0.065	0.950035	0.980663
8395	10442827					1.006	0.135	0.896549	0.959489
8396	10593842	NM_019793	56434	tetraspanin 3	Tspan3	1.006	-0.425	0.683423	0.859874
8397	10539850	BC024401	232210	RIKEN cDNA 8430410A17 gene	8430410A17Rik	1.006	0.051	0.960752	0.985069
8398	10391286	NM_001113563	20851	signal transducer and activato	Stat5b	1.006	-0.285	0.78395	0.912068
8399	10606195	NM_011276	19820	ring finger protein 12	Rnf12	1.006	-0.113	0.913463	0.965665
8400	10591357	NM_016876	53356	eukaryotic translation initiat	Eif3g	1.006	-0.477	0.647445	0.841245
8401	10588752	BC115773	67722	RIKEN cDNA 4921517D21 gene	4921517D21Rik	1.006	0.463	0.657274	0.846702

8402	10434645	NM_029457	75826	SUMO/sentrin specific peptidas	Senp2	1.006	0.101	0.922623	0.969146
8403	10563608					1.006	-0.17	0.869341	0.947675
8404	10390430	NM_018873	56013	P140 gene	RP23-157O10.7	1.006	0.151	0.883866	0.954252
8405	10535979	NM_027009	69263	replication factor C (activato	Rfc3	1.006	-0.358	0.730649	0.883548
8406	10534679	NM_201373	384309	tripartite motif-containing 56	Trim56	1.006	0.074	0.943002	0.977825
8407	10597554	BC104378	74638	zinc finger, CW type with PWWP	Zcwpw2	1.006	0.39	0.708054	0.872288
8408	10470973	NM_198304	227699	nucleoporin 188	Nup188	1.005	-0.173	0.867465	0.946957
8409	10553256	NM_010866	17927	myogenic differentiation 1	Myod1	1.005	0.68	0.517894	0.756834
8410	10403984	NM_001080972	626299	predicted gene, OTTMUSG0000000	OTTMUSG00000000480	1.005	0.538	0.607032	0.817118
8411	10393431	NM_009387	21877	thymidine kinase 1	Tk1	1.005	0.128	0.901929	0.961403
8412	10577240	NM_053171	94109	CUB and Sushi multiple domains	Csmd1	1.005	0.11	0.915298	0.966602
8413	10534202	NM_010876	17969	neutrophil cytosolic factor 1	Ncf1	1.005	0.363	0.726993	0.881688
8414	10422238	XM_001003482	668761	predicted gene, EG668761	EG668761	1.005	-0.074	0.943333	0.977948
8415	10460061	ENSMUST00000049917	240476	zinc finger protein 407	Zfp407	1.005	-0.219	0.832712	0.932699
8416	10576586	NM_175434	210027	solute carrier family 35, memb	Slc35f3	1.005	0.195	0.850497	0.939883
8417	10418004	NM_018829	55946	adaptor-related protein comple	Ap3m1	1.005	-0.192	0.852706	0.940561
8418	10542656	ENSMUST00000088263	319552	RIKEN cDNA B230216G23 gene	B230216G23Rik	1.005	0.617	0.556264	0.784737
8419	10552857	NM_182993	72961	solute carrier family 17 (sodi	Slc17a7	1.005	0.131	0.899115	0.960129
8420	10579500	NM_022419	64296	abhydrolase domain containing	Abhd8	1.005	-0.387	0.709679	0.872992
8421	10539008	NM_025783	66700	vacuolar protein sorting 24 (y	Vps24	1.005	0.653	0.534023	0.767997
8422	10548118	NM_201371	381813	protein arginine N-methyltrans	Prmt8	1.005	0.167	0.872145	0.948885
8423	10399290	NM_029107	74855	RIKEN cDNA 4930417G10 gene	4930417G10Rik	1.005	0	0.999635	0.999777
8424	10445702	NM_198421	224836	ubiquitin specific peptidase 4	Usp49	1.005	-0.3	0.772709	0.906416
8425	10466091	NM_009580	22786	zona pellucida glycoprotein 1	Zp1	1.005	0.622	0.553105	0.782691
8426	10460257	ENSMUST00000025794	73458	RIKEN cDNA 1700055N04 gene	1700055N04Rik	1.005	-0.008	0.993801	0.997702
8427	10420019	ENSMUST00000100552	100038376	predicted gene, ENSMUSG0000007	ENSMUSG00000075607	1.005	0.499	0.632377	0.832782
8428	10537204	NM_178630	76223	ATP/GTP binding protein-like 3	Agbl3	1.005	0.408	0.69515	0.866183
8429	10496638	NM_025714	52184	outer dense fiber of sperm tai	Odf2l	1.005	0.33	0.75107	0.895037
8430	10550052	NM_009095	20103	ribosomal protein S5	Rps5	1.005	-0.184	0.859342	0.94355
8431	10583034	NM_029775	76863	DCN1, defective in cullin nedd	Dcun1d5	1.005	-0.034	0.973753	0.988716
8432	10532472	NM_009469	22241	Unc-51 like kinase 1 (C. elega	Ulk1	1.005	0.108	0.917147	0.967383
8433	10456021	NM_177407	12322	calcium/calmodulin-dependent p	Camk2a	1.005	0.084	0.935563	0.974509
8434	10589420	NM_007658	12530	cell division cycle 25 homolog	Cdc25a	1.005	-0.21	0.839284	0.935017
8435	10574545	NM_172759	234673	carboxylesterase 5	Ces5	1.005	0.08	0.938512	0.976028
8436	10368935	NM_001081054	76563	glutaminyl-tRNA synthase (glut	Qrsl1	1.005	-0.063	0.951355	0.981144
8437	10525134	NM_013832	19415	RAS protein activator like 1 (	Rasal1	1.005	0.132	0.898323	0.960023
8438	10543134	NM_010886	17992	NADH dehydrogenase (ubiquinone	Ndufa4	1.005	-0.506	0.628125	0.830847
8439	10500412	NM_026229	67549	G protein-coupled receptor 89	Gpr89	1.005	-0.242	0.815659	0.926149
8440	10579767					1.005	0.259	0.803104	0.920071
8441	10448081	NM_178615	68799	RGM domain family, member B	Rgmb	1.005	-0.001	0.999024	0.999589
8442	10582586	BC036300	73420	RIKEN cDNA 1700054N08 gene	1700054N08Rik	1.005	0.079	0.939312	0.976298
8443	10540822	NM_172890	243616	solute carrier family 6 (neuro	Slc6a11	1.005	0.048	0.963078	0.985611
8444	10455249	ENSMUST00000097595	381155	RIKEN cDNA 9630014M24 gene	9630014M24Rik	1.005	0.023	0.982262	0.9924
8445	10349319	NM_001012322	319229	secretin receptor	Sctr	1.005	0.35	0.736579	0.887367
8446	10378870	NM_001004144	216963	G protein-coupled receptor kin	Git1	1.005	-0.55	0.599125	0.811784
8447	10604665					1.005	0.613	0.558911	0.786425
8448	10374771					1.005	0.263	0.800063	0.919271
8449	10365056	NM_018758	57267	amyloid beta (A4) precursor pr	Apba3	1.005	-0.04	0.969078	0.987586
8450	10545760	NM_146169	232164	poly(A) binding protein intera	Paip2b	1.005	0.02	0.984624	0.993504

8451	10465963	NM_001111140	278795	gene model 705, (NCBI)	Gm705	1.005	-0.597	0.568518	0.793239
8452	10379560	NM_025884	66983	zinc finger protein 830	Zfp830	1.005	-0.201	0.845911	0.937284
8453	10592266	NM_020258	56857	solute carrier family 37 (glyc	Slc37a2	1.005	0.171	0.869009	0.947569
8454	10556244	AF357383	233726	importin 7	Ipo7	1.005	-0.344	0.74077	0.889595
8455	10384396					1.005	0.326	0.754036	0.896425
8456	10541083	AK162833	330403	predicted gene, EG330403	EG330403	1.005	0.147	0.887424	0.955613
8457	10555055	NM_024220	68197	NADH dehydrogenase (ubiquinone	Ndufc2	1.005	-0.32	0.757755	0.898294
8458	10401708	NM_022414	64242	neuroglobin	Ngb	1.005	0.05	0.961603	0.985234
8459	10352306	NM_133705	69051	pyrroline-5-carboxylate reduct	Pycr2	1.005	-0.253	0.807371	0.922371
8460	10442542	NM_008743	18207	nth (endonuclease III)-like 1	Nthl1	1.005	-0.117	0.910208	0.964056
8461	10539588	NM_001007472	384452	notochord homolog (Xenopus lae	Noto	1.005	0.001	0.999316	0.999589
8462	10589196	NM_025407	22273	ubiquinol-cytochrome c reducta	Uqcrc1	1.005	-0.676	0.520004	0.757647
8463	10348468	ENSMUST00000070048	433332	predicted gene, EG433332	EG433332	1.005	0.322	0.756273	0.897871
8464	10438456	NM_198599	208158	MAP6 domain containing 1	Map6d1	1.005	0.11	0.915764	0.966695
8465	10424416					1.005	0.842	0.426728	0.68818
8466	10510643	NM_001004156	269608	pleckstrin homology domain con	Plekhg5	1.005	0.336	0.7464	0.892337
8467	10573910	NM_018826	54352	Iroquois related homeobox 5 (D	Irx5	1.005	0.029	0.977509	0.990738
8468	10350197					1.005	0.123	0.90555	0.963405
8469	10471766					1.005	0.132	0.898965	0.960129
8470	10553280	NM_008186	14884	general transcription factor I	Gtf2h1	1.005	-0.215	0.835373	0.933323
8471	10604327	NM_175539	245403	WD repeat domain 40C	Wdr40c	1.005	-0.03	0.976786	0.990463
8472	10565216	ENSMUST00000098325	100038384	predicted gene, ENSMUSG0000007	ENSMUSG00000074038	1.005	0.56	0.592683	0.807299
8473	10347593	NM_007463	11790	SPEG complex locus	Speg	1.005	0.204	0.843985	0.936644
8474	10572815	NM_176940	319555	NACHT and WD repeat domain con	Nwd1	1.005	-0.145	0.888887	0.956324
8475	10493137	NM_001033484	404710	IQ motif containing GTPase act	Iqgap3	1.005	-0.087	0.933347	0.973406
8476	10569389					1.005	0.453	0.663943	0.850267
8477	10370690	NM_001003949	216157	open reading frame 61	ORF61	1.005	-0.007	0.994977	0.998046
8478	10377851	NM_008946	19175	proteasome (prosome, macropain	Psmb6	1.005	-0.346	0.739053	0.88873
8479	10363185	ENSMUST00000067972	791298	predicted gene, ENSMUSG0000005	ENSMUSG00000054758	1.005	0.566	0.588871	0.805202
8480	10514708	NM_011831	23919	insulin-like 5	Insl5	1.005	0.455	0.662556	0.849733
8481	10392983	NM_026071	67283	solute carrier family 25 (mito	Slc25a19	1.005	-0.399	0.701582	0.869143
8482	10531894	BC049644	74218	RIKEN cDNA 1700016H13 gene	1700016H13Rik	1.005	0.389	0.70884	0.872545
8483	10427807	NM_011294	20024	SUB1 homolog (S. cerevisiae)	Sub1	1.005	0.101	0.921999	0.968972
8484	10437151	NM_019664	16516	potassium inwardly-rectifying	Kcnj15	1.005	0.149	0.885583	0.95523
8485	10512156	NM_016689	11828	aquaporin 3	Aqp3	1.005	0.338	0.745199	0.891643
8486	10438232	NM_010048	13356	DiGeorge syndrome critical reg	Dgcr2	1.005	-0.297	0.774976	0.907674
8487	10554370	NM_175433	209225	zinc finger protein 710	Zfp710	1.005	-0.439	0.673739	0.855069
8488	10563390	NM_011181	19158	pleckstrin homology, Sec7 and	Pscd2	1.005	-0.176	0.865177	0.946153
8489	10506433	NM_177259	13131	disabled homolog 1 (Drosophila	Dab1	1.005	-0.411	0.693203	0.865542
8490	10355109	NM_146250	241070	G protein-coupled receptor 1	Gpr1	1.005	0.112	0.914182	0.966149
8491	10525473	NM_001039723	330189	transmembrane protein 120B	Tmem120b	1.005	0.313	0.763108	0.901493
8492	10561247	NM_138676	192192	Sh3kbp1 binding protein 1	Shkbp1	1.005	-0.173	0.867132	0.946934
8493	10588429	NM_001081309	75669	phosphatidylinositol 3 kinase,	Pik3r4	1.005	-0.413	0.69186	0.864682
8494	10514158	NM_133948	101739	PC4 and SFRS1 interacting prot	Psip1	1.005	-0.169	0.870427	0.948285
8495	10504988	NM_146858	258857	olfactory receptor 275	Olfr275	1.005	0.139	0.893094	0.957774
8496	10519612	BC132290	231014	RIKEN cDNA 9330182L06 gene	9330182L06Rik	1.005	-0.236	0.819863	0.928345
8497	10359255	NM_207583	240843	RIKEN cDNA 6430517E21 gene	6430517E21Rik	1.005	0.522	0.617294	0.823029
8498	10416917	NM_198601	212085	tripartite motif-containing 52	Trim52	1.005	0.102	0.921562	0.968694
8499	10499945	NM_028628	73730	late cornified envelope 1L	Lce1l	1.005	-0.369	0.723053	0.879847
8500	10580504	NM_027840	71607	sorting nexin 20	Snx20	1.004	0.176	0.865184	0.946153
8501	10497077					1.004	-0.175	0.865897	0.94648
8502	10401322	NM_025292	24071	synaptojanin 2 binding protein	Synj2bp	1.004	-0.318	0.759676	0.899311
8503	10381649	NM_080846	75689	HIG1 domain family, member 1B	Higd1b	1.004	0.273	0.792266	0.915409

8504	10559509	NM_021454	58804	CDC42 effector protein (Rho GT	Cdc42ep5	1.004	-0.458	0.660097	0.848652
8505	10405842	NM_001083890	238683	RIKEN cDNA 4932441B19 gene	4932441B19Rik	1.004	0.303	0.770806	0.905387
8506	10578037					1.004	0.141	0.891689	0.957629
8507	10524718	NM_007475	11837	acidic ribosomal phosphoprotei	Arbp	1.004	-0.282	0.785599	0.912507
8508	10418341	NM_019583	50905	interleukin 17 receptor B	Il17rb	1.004	-0.373	0.719963	0.878109
8509	10604840	ENSMUST00000116143	631922	predicted gene, EG631922	EG631922	1.004	0.088	0.932285	0.973077
8510	10390653	NM_011869	23989	mediator complex subunit 24	Med24	1.004	-0.44	0.673148	0.854824
8511	10494839	NM_144901	229663	cold shock domain containing E	Csde1	1.004	0.051	0.960682	0.985069
8512	10575909	ENSMUST00000098361	75773	adenosine deaminase domain con	Adad2	1.004	0.028	0.978155	0.991187
8513	10520405	NM_001033457	433864	gene model 1040, (NCBI)	Gm1040	1.004	-0.226	0.827764	0.93066
8514	10437573					1.004	0.206	0.842667	0.936227
8515	10398455	ENSMUST00000065483	26931	protein phosphatase 2, regulat	Ppp2r5c	1.004	-0.148	0.886097	0.955393
8516	10391504	NM_010791	17285	mesenchyme homeobox 1	Meox1	1.004	-0.004	0.997205	0.998953
8517	10596815	NM_032543	84585	ring finger protein 123	Rnf123	1.004	-0.014	0.98906	0.995308
8518	10349724	NM_144875	226422	RAB7, member RAS oncogene fami	Rab7l1	1.004	-0.141	0.892059	0.95769
8519	10497615	AK005488	73249	RIKEN cDNA 1600017P15 gene	1600017P15Rik	1.004	0.321	0.757593	0.898154
8520	10364319					1.004	0.228	0.825746	0.929888
8521	10468030	NM_177605	212684	PDZ domain containing 7	Pdzd7	1.004	0.401	0.699699	0.868422
8522	10464932	NM_008451	16594	kinesin light chain 2	Klc2	1.004	-0.012	0.990839	0.996163
8523	10556957	BC030336	233812	cDNA sequence BC030336	BC030336	1.004	-0.115	0.9113	0.964566
8524	10577096	NM_178708	234069	PCI domain containing 2	Pcid2	1.004	0.08	0.938398	0.976019
8525	10545731	NM_016751	51811	C-type lectin domain family 4,	Clec4f	1.004	0.244	0.814015	0.925212
8526	10383365	NM_008244	15239	HGF-regulated tyrosine kinase	Hgs	1.004	0.026	0.980074	0.991919
8527	10560510	NM_172279	232944	MAP/microtubule affinity-regul	Mark4	1.004	0.385	0.711235	0.873556
8528	10529410	NM_026660	68294	major facilitator superfamily	Mfsd10	1.004	0.233	0.822591	0.929111
8529	10589976					1.004	0.171	0.868785	0.947491
8530	10581421	NM_027960	71854	dipeptidase 3	Dpep3	1.004	0.217	0.833993	0.933071
8531	10580010	NM_177262	320795	protein kinase N1	Pkn1	1.004	0.21	0.839112	0.934917
8532	10514340	NM_001040654	12578	cyclin-dependent kinase inhibi	Cdkn2a	1.004	0.297	0.774694	0.907637
8533	10345457	AK132955	211430	fer-1-like 5 (C. elegans)	Fer1l5	1.004	0.385	0.71156	0.873605
8534	10471715	NM_026422	67871	mitochondrial ribosome recycli	Mrrf	1.004	-0.185	0.858612	0.943286
8535	10597913	BC034133	66202	RIKEN cDNA 1110059G10 gene	1110059G10Rik	1.004	-0.554	0.596416	0.809856
8536	10497831	NM_009828	12428	cyclin A2	Ccna2	1.004	-0.157	0.879362	0.952124
8537	10390901	NM_001039502	629873	predicted gene, OTTMUSG0000000	OTTMUSG00000004966	1.004	0.311	0.764382	0.901752
8538	10524098	BC007165	320875	RIKEN cDNA A830023I12 gene	A830023I12Rik	1.004	-0.235	0.820794	0.92863
8539	10574429					1.004	0.525	0.615195	0.822023
8540	10429329	NM_153178	239528	eukaryotic translation initiat	Eif2c2	1.004	-0.015	0.988552	0.995308
8541	10585860	NM_028121	72141	ADP-dependent glucokinase	Adpgk	1.004	-0.675	0.520717	0.758319
8542	10383953	NM_080595	140703	EMI domain containing 1	Emid1	1.004	-0.015	0.988249	0.995168
8543	10435043	ENSMUST00000115149	277203	transmembrane 4 L six family m	Tm4sf19	1.004	-0.06	0.953457	0.982042
8544	10402981	ENSMUST00000103414	380792	gene model 900, (NCBI)	Gm900	1.004	0.379	0.715923	0.875442
8545	10345840	NM_177084	110895	solute carrier family 9 (sodiu	Slc9a4	1.004	0.059	0.954384	0.982496
8546	10509557	ENSMUST00000062902	58213	hypothetical protein, MNCb-245	AB041806	1.004	0.557	0.594425	0.808629
8547	10467102	BC052355	67795	RIKEN cDNA 6530404N21 gene	6530404N21Rik	1.004	-0.308	0.767151	0.903106
8548	10574246	NM_001033468	382045	G protein-coupled receptor 114	Gpr114	1.004	-0.088	0.932345	0.973077
8549	10441392	NM_001101560	621628	claudin 20	Cldn20	1.004	0.251	0.809002	0.923112
8550	10420589	ENSMUST00000089421	100038409	predicted gene, ENSMUSG0000006	ENSMUSG00000068233	1.004	0.329	0.751636	0.895256
8551	10589723	NM_027742	71268	leucine rich repeat (in FLII)	Lrrfip2	1.004	-0.228	0.826006	0.929952
8552	10555844	NM_147056	259058	olfactory receptor 646	Olfr646	1.004	-0.023	0.982249	0.9924
8553	10440918	NM_030018	77975	transmembrane protein 50B	Tmem50b	1.004	-0.84	0.427847	0.689144
8554	10428103	NM_019635	56274	serine/threonine kinase 3 (Ste	Stk3	1.004	-0.086	0.93409	0.97379

8555	10594353	NM_011840	23938	mitogen-activated protein kina	Map2k5	1.004	-0.365	0.725676	0.881163
8556	10394914	NM_026347	67732	isoamyl acetate-hydrolyzing es	Iah1	1.004	-0.805	0.446313	0.704033
8557	10595439					1.004	0.726	0.490464	0.737328
8558	10447417	NM_010830	17688	mutS homolog 6 (E. coli)	Msh6	1.004	-0.2	0.847252	0.938167
8559	10498064	NM_080793	73251	SET domain containing (lysine	Setd7	1.004	-0.322	0.756615	0.897871
8560	10520371	NM_028234	381626	proline rich 8	Prr8	1.004	0.123	0.905836	0.963405
8561	10456812	ENSMUST00000097522	76987	haloacid dehalogenase-like hyd	Hdhd2	1.004	0.342	0.742332	0.890171
8562	10564417	NM_053080	56847	aldehyde dehydrogenase family	Aldh1a3	1.003	0.114	0.912064	0.96491
8563	10506743	BC019215	74098	RIKEN cDNA 0610037L13 gene	0610037L13Rik	1.003	-0.051	0.960987	0.985069
8564	10578681					1.003	0.433	0.677389	0.856571
8565	10429776	NM_144848	223650	epiplakin 1	Eppk1	1.003	0.503	0.63015	0.831393
8566	10391066	NM_010663	16667	keratin 17	Krt17	1.003	0.423	0.684476	0.860387
8567	10477460					1.003	0.392	0.706659	0.871942
8568	10526869					1.003	0.621	0.553952	0.783357
8569	10542140	NM_153094	232408	killer cell lectin-like recept	Klrb1f	1.003	-0.147	0.88696	0.955613
8570	10451611					1.003	0.039	0.969986	0.987783
8571	10354267	NM_001013799	433294	RIKEN cDNA A530098C11 gene	A530098C11Rik	1.003	-0.065	0.950052	0.980663
8572	10603742					1.003	0.795	0.452215	0.708922
8573	10408049	NM_139141	93681	zinc finger protein 192	Zfp192	1.003	0.023	0.982332	0.9924
8574	10351792	NM_029612	98365	SLAM family member 9	Slamf9	1.003	0.129	0.900663	0.96078
8575	10523245					1.003	0.399	0.701194	0.869046
8576	10600310	NM_019404	12000	arginine vasopressin receptor	Avpr2	1.003	0.153	0.882222	0.953469
8577	10606064	NM_183318	331474	retrotransposon gag domain con	Rgag4	1.003	-0.035	0.972912	0.98829
8578	10481711	NM_001113569	20910	syntaxin binding protein 1	Stxbp1	1.003	-0.769	0.466263	0.719571
8579	10588874	AK154501	100048896	predicted gene, ENSMUSG0000007	ENSMUSG00000074081	1.003	0.265	0.798459	0.918432
8580	10379215	NM_018854	55978	intraflagellar transport 20 ho	Ift20	1.003	-0.391	0.707017	0.872175
8581	10371082	NM_027120	69564	integrin beta 1 binding protei	Itgb1bp3	1.003	0.263	0.800249	0.919317
8582	10439744	NM_032465	84544	CD96 antigen	Cd96	1.003	-0.1	0.922752	0.969148
8583	10524436	NM_001033202	100756	ubiquitin specific peptidase 3	Usp30	1.003	-0.361	0.728567	0.882433
8584	10361091	NM_007498	11910	activating transcription facto	Atf3	1.003	0.049	0.962153	0.985362
8585	10520800	NM_133756	74254	GPN-loop GTPase 1	Gpn1	1.003	-0.207	0.842108	0.936059
8586	10405511	NM_145975	212880	DEAD (Asp-Glu-Ala-Asp) box pol	Ddx46	1.003	-0.158	0.87844	0.95179
8587	10528029					1.003	-0.308	0.766745	0.902924
8588	10417933	NM_021508	59011	myozenin 1	Myoz1	1.003	0.057	0.955787	0.98316
8589	10447356	NM_019654	56468	suppressor of cytokine signali	Socs5	1.003	-0.029	0.977371	0.990677
8590	10578557	NM_001001184	408022	coiled-coil domain containing	Ccdc111	1.003	-0.38	0.714587	0.875126
8591	10349993	NM_031189	17928	myogenin	Myog	1.003	0.229	0.825326	0.929712
8592	10584777	NM_001110826	13209	DEAD (Asp-Glu-Ala-Asp) box pol	Ddx6	1.003	-0.255	0.806174	0.921832
8593	10579724	NM_177766	270066	solute carrier family 35, memb	Slc35e1	1.003	-0.008	0.994151	0.997702
8594	10480878	NM_001115076	227634	calmodulin regulated spectrin-	Camsap1	1.003	-0.209	0.840597	0.93555
8595	10450431	NM_148939	266614	lymphocyte antigen 6 complex,	Ly6g5b	1.003	-0.146	0.888168	0.955939
8596	10459075	NM_133363	170947	myozenin 3	Myoz3	1.003	0.128	0.901717	0.961371
8597	10383708	NM_145355	193670	ring finger protein 185	Rnf185	1.003	0.608	0.561562	0.788656
8598	10356339	NM_008801	18582	phosphodiesterase 6D, cGMP-spe	Pde6d	1.003	-0.237	0.819619	0.928312
8599	10586246	XM_001476259	102442	DENN/MADD domain containing 4A	Dennd4a	1.003	0.717	0.49605	0.740712
8600	10472382	NM_001099298	110876	sodium channel, voltage-gated,	Scn2a1	1.003	0.397	0.703133	0.869747
8601	10397786	ENSMUST00000116071	74947	RIKEN cDNA 4930463M05 gene	4930463M05Rik	1.003	-0.074	0.943402	0.977948
8602	10550296	NM_198631	330474	zinc finger CCCH-type containi	Zc3h4	1.003	-0.047	0.963677	0.985728
8603	10550706	ENSMUST00000011407	74463	exocyst complex component 3-li	Exoc3l2	1.003	0.268	0.796475	0.917464
8604	10523518	NM_026421	67870	enolase-phosphatase 1	Enoph1	1.003	-0.003	0.997922	0.999268
8605	10545099					1.003	0.273	0.792463	0.91549

8606	10533428	NM_183307	330188	coiled-coil domain containing	Ccdc63	1.003	0.221	0.830968	0.932182
8607	10366703	ENSMUST00000116001	216394	predicted gene, EG216394	EG216394	1.003	0.226	0.827234	0.930659
8608	10500720	BC094925	242126	solute carrier family 22 (orga	Slc22a15	1.003	0.051	0.960845	0.985069
8609	10438069					1.003	0.117	0.909938	0.964056
8610	10443112	NM_001005916	474156	zinc finger and BTB domain con	Zbtb9	1.003	-0.136	0.895236	0.958812
8611	10462451	NM_025741	66745	tumor protein D52-like 3	Trpd52l3	1.003	0.119	0.908354	0.963723
8612	10416302	NM_021877	15460	hairless	Hr	1.003	0.389	0.708434	0.872343
8613	10420225	NM_010780	17228	chymase 1, mast cell	Cma1	1.003	0.433	0.677492	0.85665
8614	10433717					1.003	0.417	0.6889	0.863319
8615	10420516	NM_027986	71891	cytidine and dCMP deaminase do	Cdadc1	1.003	-0.189	0.855273	0.941477
8616	10538939	NM_010121	13666	eukaryotic translation initiat	Eif2ak3	1.003	-0.367	0.724222	0.88056
8617	10390869	NM_213730	237934	keratin 39	Krt39	1.003	-0.083	0.936058	0.974832
8618	10369885	NM_134007	52637	CDGSH iron sulfur domain 1	Cisd1	1.003	-0.284	0.784228	0.912068
8619	10507719	NM_177570	194219	schlafen like 1	Slfnl1	1.003	0.143	0.890086	0.956731
8620	10464603	NM_016666	11632	aryl-hydrocarbon receptor-inte	Aip	1.003	-0.735	0.48571	0.73398
8621	10378681	NM_008916	19062	putative phosphatase	RP23-136K12.4	1.003	-0.452	0.664791	0.85061
8622	10360058	NM_001037170	641376	translocase of outer mitochond	Tomm40l	1.003	-0.313	0.763429	0.901503
8623	10553148	NM_001033243	211535	coiled-coil domain containing	Ccdc114	1.003	-0.132	0.898768	0.960077
8624	10456622	NM_013594	17190	methyl-CpG binding domain prot	Mbd1	1.003	-0.183	0.859636	0.943578
8625	10577922	NM_207659	320191	hook homolog 3 (Drosophila)	Hook3	1.003	-0.098	0.924826	0.970324
8626	10479058	BC050790	72221	RIKEN cDNA 1700021F07 gene	1700021F07Rik	1.003	-0.159	0.877709	0.951715
8627	10432767	NR_003960	432987	predicted gene, EG432987	EG432987	1.003	0.128	0.901805	0.961392
8628	10467859	NM_144874	226139	COX15 homolog, cytochrome c ox	Cox15	1.003	-0.345	0.739885	0.889275
8629	10344950	XM_001473720	675046	similar to 60S ribosomal prote	LOC675046	1.003	0.142	0.890871	0.957386
8630	10388098	NM_053245	114230	aryl hydrocarbon receptor-inte	Aipl1	1.003	0.058	0.955425	0.982946
8631	10515844	NM_183140	195522	zinc finger protein 691	Zfp691	1.003	0.228	0.826054	0.929952
8632	10539017	NM_178608	52250	receptor accessory protein 1	Reep1	1.003	0.407	0.695617	0.866211
8633	10597136	NM_001081043	104831	protein tyrosine phosphatase,	Ptpn23	1.003	-0.182	0.86048	0.943954
8634	10461991	NM_009551	22682	zinc finger, AN1-type domain 5	Zfand5	1.003	0.026	0.979583	0.991919
8635	10426030	NM_028063	72026	tRNA 5-methylaminomethyl-2-thi	Trmu	1.003	-0.664	0.527561	0.763239
8636	10349442	NM_028399	72949	cyclin T2	Ccnt2	1.003	0.025	0.980895	0.991919
8637	10411306	NM_012048	27015	polymerase (DNA directed), kap	Polk	1.003	-0.182	0.860892	0.944057
8638	10348537	NM_016894	51801	receptor (calcitonin) activity	Ramp1	1.003	-0.036	0.972366	0.98815
8639	10456814	NM_008602	17344	protein inhibitor of activated	Pias2	1.002	0.069	0.946598	0.978837
8640	10480121	NM_024185	66960	RIKEN cDNA 2310047O13 gene	2310047O13Rik	1.002	-0.103	0.920505	0.968204
8641	10606362					1.002	0.074	0.942852	0.977825
8642	10474606	NM_029232	75275	RIKEN cDNA 4930563P21 gene	4930563P21Rik	1.002	0.176	0.865304	0.946164
8643	10351903	NM_146305	258302	olfactory receptor 420	Olfr420	1.002	0.18	0.862452	0.944945
8644	10538993	NM_001081110	12525	CD8 antigen, alpha chain	Cd8a	1.002	0.286	0.782672	0.911672
8645	10461934	NM_153417	225997	transient receptor potential c	Trpm6	1.002	-0.071	0.945172	0.978396
8646	10399675	XM_911478	629364	similar to actin related prote	LOC629364	1.002	-0.246	0.812783	0.924689
8647	10443369	BC049559	67645	RIKEN cDNA 4930511I11 gene	4930511I11Rik	1.002	0.161	0.876193	0.950949
8648	10435019	BC125555	69576	RIKEN cDNA 2310010M20 gene	2310010M20Rik	1.002	0.442	0.671511	0.854195
8649	10494804	NM_009814	12373	calsequestrin 2	Casq2	1.002	0.498	0.633411	0.833323
8650	10605952					1.002	0.26	0.802064	0.919826
8651	10540554	NM_028385	72895	SET domain containing 5	Setd5	1.002	-0.078	0.940011	0.976656
8652	10378038	NM_177618	216881	WSC domain containing 1	Wscd1	1.002	0.157	0.879399	0.952124
8653	10499470	NM_028188	72296	RUN and SH3 domain containing	Rusc1	1.002	-0.205	0.843441	0.936586
8654	10481457	NM_139302	227700	SH3-domain GRB2-like endophili	Sh3glb2	1.002	0.22	0.831703	0.932437
8655	10405811	NM_019986	56541	hyaluronic acid binding protei	Habp4	1.002	-1.035	0.33412	0.609656
8656	10510991	NM_001081100	76866	MORN repeat containing 1	Morn1	1.002	0.167	0.872084	0.948867
8657	10577604	NM_018743	102247	1-acylglycerol-3-phosphate O-a	Agpat6	1.002	-0.236	0.81996	0.928345

8658	10402551					1.002	0.109	0.915906	0.966745
8659	10572212	NM_198101	78816	Gem-interacting protein	Gmip	1.002	0.226	0.827117	0.930659
8660	10552006	ENSMUST00000085702	233075	predicted gene, EG233075	EG233075	1.002	-0.034	0.973555	0.988697
8661	10426439	NM_146062	223828	periphilin 1	Pphln1	1.002	-0.596	0.569693	0.794081
8662	10555280	NM_133709	69121	chordin-like 2	Chrdl2	1.002	-0.016	0.987457	0.994834
8663	10364109	NM_009514	22364	pre-B lymphocyte gene 3	Vpreb3	1.002	0.295	0.776383	0.908709
8664	10346928					1.002	0.96	0.368247	0.639105
8665	10583254	NM_023153	66070	CWC15 homolog (S. cerevisiae)	Cwc15	1.002	-0.406	0.696429	0.866754
8666	10551382	NM_175107	66367	RIKEN cDNA 2310022A10 gene	2310022A10Rik	1.002	-0.094	0.927913	0.971746
8667	10490502	NM_178254	277353	transcription factor-like 5 (b	Tcfl5	1.002	0.278	0.789033	0.914104
8668	10571737	ENSMUST00000098781	546058	hypothetical protein LOC546058	LOC546058	1.002	-0.01	0.992467	0.997088
8669	10360909	ENSMUST00000053934	319562	RIKEN cDNA 9630028B13 gene	9630028B13Rik	1.002	0.217	0.834305	0.933071
8670	10476759	NM_028724	74030	Ras and Rab interactor 2	Rin2	1.002	-0.461	0.658248	0.847092
8671	10470320					1.002	-0.132	0.898271	0.960023
8672	10481111					1.002	0.226	0.827819	0.93066
8673	10387620	NM_019871	56293	acyl-malonyl condensing enzyme	Amac1	1.002	-0.117	0.910135	0.964056
8674	10394060	NM_026907	58210	secreted and transmembrane 1B	Sectm1b	1.002	0.347	0.738615	0.88853
8675	10397476	BC026384	217732	RIKEN cDNA 2310044G17 gene	2310044G17Rik	1.002	-0.01	0.991964	0.99682
8676	10504017	NM_023739	74164	nuclear transcription factor,	Nfx1	1.002	-0.065	0.950217	0.980737
8677	10397085	NM_027349	67039	RNA binding motif protein 25	Rbm25	1.002	0.118	0.909543	0.964056
8678	10502949					1.002	-0.039	0.969871	0.987764
8679	10347218					1.002	-0.05	0.961707	0.985234
8680	10461765	NM_134152	107321	leupaxin	Lpxn	1.002	0.118	0.909312	0.963879
8681	10401564	BC060658	68497	RIKEN cDNA 1110018G07 gene	1110018G07Rik	1.002	-0.091	0.929671	0.972207
8682	10430723	AJ006341	20524	solute carrier family 25 (mito	Slc25a17	1.002	0.07	0.946123	0.978614
8683	10439848	XR_035106	224180	predicted gene, EG224180	EG224180	1.002	0.255	0.805624	0.921565
8684	10506939	NM_007943	13858	epidermal growth factor recept	Eps15	1.002	-0.4	0.700812	0.868962
8685	10478615	NM_146129	228866	RIKEN cDNA F730014I05 gene	F730014I05Rik	1.002	-0.085	0.934572	0.973973
8686	10595407	NM_001081282	108837	inhibitor of Bruton agammaglob	Ibtk	1.002	-0.421	0.685755	0.861188
8687	10354157	NM_145142	98388	carbohydrate sulfotransferase	Chst10	1.002	0.086	0.934026	0.973771
8688	10487595					1.002	-0.012	0.99045	0.995913
8689	10375545	NM_146470	258462	olfactory receptor 1392	Olfr1392	1.002	0.047	0.963638	0.985728
8690	10440552	NM_001081068	78913	zinc finger protein 294	Zfp294	1.002	-0.123	0.905427	0.963335
8691	10453055	ENSMUST00000097280	100038718	predicted gene, ENSMUSG0000007	ENSMUSG00000073373	1.002	-0.057	0.956118	0.983285
8692	10493803	NM_011310	20197	S100 calcium binding protein A	S100a3	1.002	0.155	0.881282	0.953061
8693	10519048	NM_028513	73353	actin-related protein T2	Actrt2	1.002	0.27	0.794691	0.916664
8694	10574812	NM_181322	13018	CCCTC-binding factor	Ctcf	1.002	-0.202	0.845346	0.937238
8695	10435982	NM_001037719	208154	B and T lymphocyte associated	Btla	1.002	0.561	0.591765	0.806879
8696	10507840	NM_013905	56198	hairy/enhancer-of-split relate	Heyl	1.002	-0.106	0.918752	0.967805
8697	10434922					1.002	-0.184	0.859145	0.943452
8698	10417128					1.002	0.361	0.7286	0.882433
8699	10541184					1.002	0.341	0.742583	0.890291
8700	10388409	NM_026653	68275	replication protein A1	Rpa1	1.002	-0.401	0.699854	0.868513
8701	10389170	NM_001013759	237891	growth arrest-specific 2 like	Gas2l2	1.002	0.496	0.63496	0.834095
8702	10495712	NM_007378	11304	ATP-binding cassette, sub-fami	Abca4	1.002	0.362	0.727548	0.881884
8703	10442081					1.002	0.364	0.726348	0.881516
8704	10417620	NM_080433	54713	Fez family zinc finger 2	Fezf2	1.002	0.115	0.911207	0.964566
8705	10522303	NM_172711	231279	GUF1 GTPase homolog (S. cerevi	Guf1	1.002	0.181	0.861381	0.944316
8706	10450296	NM_021337	108077	superkiller viralicidic activi	Skiv2l	1.002	0.095	0.927116	0.971253
8707	10591494	NM_053190	94226	endothelial differentiation, s	Edg8	1.002	0.234	0.821636	0.92863

8708	10465508	NM_207220	107173	G protein-coupled receptor 137	Gpr137	1.002	0.587	0.574905	0.797076
8709	10556059	NM_029660	76572	RNA binding motif protein, X-l	Rbmxl2	1.002	-0.136	0.895345	0.958881
8710	10411839	NM_172592	218543	splicing factor, arginine/seri	Sfrs12	1.002	0.191	0.854166	0.941009
8711	10392300	NM_176850	207165	bromodomain PHD finger transcr	Bptf	1.002	-0.401	0.700101	0.868717
8712	10562323	NM_207212	101543	WT1-interacting protein	Wtip	1.002	-0.4	0.700579	0.86896
8713	10516518	NM_205823	384059	toll-like receptor 12	Tlr12	1.002	-0.103	0.920941	0.968408
8714	10571128	NM_054057	114863	proline synthetase co-transcri	Prosc	1.002	-0.613	0.558868	0.786425
8715	10571612	NM_001033246	212392	coiled-coil domain containing	Ccdc110	1.002	0.488	0.639816	0.83668
8716	10564618	AK080460	320262	RIKEN cDNA A830073O21 gene	A830073O21Rik	1.002	0.113	0.912742	0.965173
8717	10561025	NM_001081375	72383	cornifelin	Cnfn	1.002	0.366	0.725197	0.880835
8718	10516435	NM_001114399	67785	zinc finger, MYM-type 4	Zmym4	1.002	0.089	0.931375	0.972759
8719	10467768	NM_053083	67573	lysyl oxidase-like 4	Loxl4	1.002	0.56	0.592663	0.807299
8720	10527475	NM_028298	72611	zinc finger protein 655	Zfp655	1.002	-0.351	0.735899	0.886874
8721	10401309	BC005675	66272	RIKEN cDNA 1810020G14 gene	1810020G14Rik	1.002	-0.329	0.751466	0.895256
8722	10511321	AK034690	442813	RIKEN cDNA 9430025C20 gene	9430025C20Rik	1.002	0.236	0.819649	0.928312
8723	10544640	ENSMUST00000101417	101214	transformer 2 alpha homolog (D	Tra2a	1.002	0.097	0.925384	0.970455
8724	10544610	NM_023670	140488	insulin-like growth factor 2 m	Igf2bp3	1.002	-0.572	0.584415	0.802186
8725	10542395	ENSMUST00000066689	54343	activating transcription facto	Atf7ip	1.002	-0.75	0.476821	0.727649
8726	10464479	NM_029456	52036	SAPS domain family, member 3	Saps3	1.002	-0.107	0.917746	0.967684
8727	10471763	NM_146939	258941	olfactory receptor 354	Olfr354	1.002	0.495	0.635481	0.834416
8728	10550100	NM_134226	171260	vomeronasal 1 receptor, J2	V1rj2	1.001	0.266	0.797716	0.917953
8729	10588855	NM_008243	15235	macrophage stimulating 1 (hepa	Mst1	1.001	0.02	0.984678	0.993512
8730	10572398	NM_018827	12931	cytokine receptor-like factor	Crlf1	1.001	-0.018	0.985884	0.994073
8731	10466935	NM_011272	19773	relaxin 1	Rln1	1.001	0.344	0.740357	0.889357
8732	10402579	NM_181328	214663	solute carrier family 25 (mito	Slc25a29	1.001	0.005	0.996397	0.998711
8733	10529028	NM_024460	67695	RIKEN cDNA 2310016E02 gene	2310016E02Rik	1.001	-0.533	0.610082	0.818617
8734	10572838	NM_009188	20467	transcriptional regulator, SIN	Sin3b	1.001	-0.266	0.79798	0.918148
8735	10572739	AK032580	791365	predicted gene, ENSMUSG0000006	ENSMUSG00000060719	1.001	-0.001	0.999471	0.99966
8736	10458285	NM_029485	71242	RIKEN cDNA 5133400G04 gene	5133400G04Rik	1.001	-0.108	0.916822	0.967184
8737	10551600	NM_177301	15388	heterogeneous nuclear ribonucl	Hnrnpl	1.001	-0.288	0.781301	0.911076
8738	10607246	ENSMUST00000059256	382245	transmembrane protein 29	Tmem29	1.001	-0.172	0.868323	0.947244
8739	10499348	NM_024246	71913	transmembrane protein 79	Tmem79	1.001	0.264	0.798977	0.918828
8740	10348119					1.001	-0.025	0.981105	0.99199
8741	10417829	NM_134081	108671	DnaJ (Hsp40) homolog, subfamil	Dnajc9	1.001	-0.304	0.769423	0.904519
8742	10605914	XR_030913	436219	similar to Glyceraldehyde-3-ph	LOC436219	1.001	0.35	0.736185	0.887097
8743	10598287					1.001	0.23	0.824401	0.929508
8744	10344633	NM_011541	21399	transcription elongation facto	Tcea1	1.001	-0.3	0.77269	0.906416
8745	10436596	ENSMUST00000068704	77994	RIKEN cDNA 2810055G20 gene	2810055G20Rik	1.001	-0.025	0.981069	0.99199
8746	10589940	NM_148958	74486	oxysterol binding protein-like	Osbpl10	1.001	0.171	0.868771	0.947491
8747	10382254	ENSMUST00000055404	320509	RIKEN cDNA 9930022D16 gene	9930022D16Rik	1.001	-0.19	0.85433	0.94105
8748	10404988	BC045201	68128	RIKEN cDNA C030044B11 gene	C030044B11Rik	1.001	0.263	0.799875	0.919211
8749	10577560	NM_010546	16150	inhibitor of kappaB kinase bet	Ikbkb	1.001	-0.088	0.932566	0.973153
8750	10394680	XR_034647	668492	similar to zinc finger CCHC-ty	LOC668492	1.001	-0.333	0.748606	0.89361
8751	10437664	NM_021428	58239	dexamethasone-induced transcri	Dexi	1.001	-0.174	0.866314	0.946535
8752	10479975					1.001	-0.107	0.917917	0.967712
8753	10521205	NM_011893	24055	SH3-domain binding protein 2	Sh3bp2	1.001	-0.156	0.880056	0.952396
8754	10574102					1.001	-0.045	0.965279	0.986124
8755	10517948	NM_019763	56381	SPEN homolog, transcriptional	Spen	1.001	-0.304	0.769589	0.904613
8756	10564978	NM_007550	12144	Bloom syndrome homolog (human)	Blm	1.001	-0.131	0.899197	0.960136

8757	10511898	NM_010289	14610	gap junction protein, alpha 10	Gja10	1.001	0.39	0.708147	0.872296
8758	10578619	NM_172407	70925	CDKN2A interacting protein	Cdkn2aip	1.001	0.207	0.842087	0.936059
8759	10382198					1.001	0.442	0.671457	0.854195
8760	10462435	NM_029993	77836	melan-A	Mlana	1.001	0.674	0.521447	0.758794
8761	10514590	NM_026082	67299	dedicator of cytokinesis 7	Dock7	1.001	-0.065	0.949926	0.980663
8762	10584071	NM_001080817	382066	PR domain containing 10	Prdm10	1.001	0.023	0.982583	0.992413
8763	10554221	BC006942	791275	predicted gene, ENSMUSG0000005	ENSMUSG00000052629	1.001	0.22	0.832125	0.93265
8764	10572290	NM_001025586	75692	nuclear receptor 2C2-associate	Nr2c2ap	1.001	-0.003	0.997587	0.999133
8765	10392364	NM_007582	12299	calcium channel, voltage-depen	Cacng1	1.001	0.47	0.652203	0.844159
8766	10382022	NM_027346	70207	coiled-coil domain containing	Ccdc44	1.001	-0.926	0.384566	0.653901
8767	10358896	ENSMUST00000059036	240816	regulator of G-protein signali	Rgsl1	1.001	-0.036	0.972155	0.98815
8768	10428310	NM_001102458	54375	antizyme inhibitor 1	Azin1	1.001	0.148	0.886201	0.955393
8769	10452480	NM_153519	213272	thioredoxin domain containing	Txndc2	1.001	0.084	0.935403	0.974485
8770	10568417	BC038342	210711	RIKEN cDNA 1110007A13 gene	1110007A13Rik	1.001	-0.137	0.895117	0.958733
8771	10460926	NM_001110791	22668	splicing factor 1	Sf1	1.001	-0.019	0.985468	0.993977
8772	10447551	NM_027457	70544	RIKEN cDNA 5730437N04 gene	5730437N04Rik	1.001	-0.156	0.880214	0.952468
8773	10579860	NM_008539	17125	MAD homolog 1 (Drosophila)	Smad1	1.001	-0.382	0.713531	0.874653
8774	10386388	BC029025	67826	RIKEN cDNA 1110031B06 gene	1110031B06Rik	1.001	-0.683	0.515653	0.755158
8775	10528686	NM_153076	214301	crystallin, gamma N	Crygn	1.001	-0.105	0.919065	0.967837
8776	10438442	ENSMUST00000100083	68162	RIKEN cDNA A930003A15 gene	A930003A15Rik	1.001	0.325	0.754504	0.896702
8777	10439411	NM_010936	18171	nuclear receptor subfamily 1,	Nr1i2	1.001	0.112	0.914218	0.966149
8778	10379636	NM_011410	20558	schlafen 4	Slfn4	1.001	0.165	0.873831	0.949742
8779	10429515	NM_011838	23936	Ly6/neurotoxin 1	Lynx1	1.001	0.162	0.875915	0.95093
8780	10390985	NM_010665	16670	keratin 32	Krt32	1.001	-0.459	0.659998	0.848652
8781	10589934	ENSMUST00000064735	100038631	predicted gene, ENSMUSG0000005	ENSMUSG00000052724	1.001	0.166	0.872896	0.949165
8782	10391143	NM_172565	217194	kelch-like 11 (Drosophila)	Klhl11	1.001	0.195	0.85058	0.939883
8783	10555303	NM_027629	70974	phosphoglucomutase 2-like 1	Pgm2l1	1.001	-0.335	0.746895	0.892495
8784	10414663	NM_023879	77945	retinitis pigmentosa GTPase re	Rpgrip1	1.001	0.106	0.918738	0.967805
8785	10391750	ENSMUST00000069673	100038535	predicted gene, ENSMUSG0000007	ENSMUSG00000075516	1.001	-0.299	0.773065	0.906652
8786	10519207	AK005805	100115	expressed sequence AI428898	AI428898	1.001	-0.267	0.796577	0.917464
8787	10381860	NM_172567	52686	methyltransferase like 2	Mettl2	1.001	-0.299	0.773148	0.906681
8788	10461454	BC024923	69038	RIKEN cDNA 1810006K21 gene	1810006K21Rik	1.001	0.146	0.887706	0.955685
8789	10525343	NM_010861	17906	myosin, light polypeptide 2, r	Myl2	1.001	-0.204	0.843924	0.93664
8790	10505118					1.001	0.216	0.835141	0.933323
8791	10522668	NM_025939	67054	phosphoribosylaminoimidazole c	Paics	1.001	-0.179	0.863065	0.94533
8792	10404772	ENSMUST00000099561	100038577	predicted gene, ENSMUSG0000007	ENSMUSG00000074927	1.001	-0.187	0.856814	0.942193
8793	10586274	NM_175153	69882	RIKEN cDNA 2010321M09 gene	2010321M09Rik	1.001	-0.186	0.857203	0.942404
8794	10561078	NM_028771	52132	coiled-coil domain containing	Ccdc97	1.001	-0.026	0.980292	0.991919
8795	10510957	NM_172990	269614	pantothenate kinase 4	Pank4	1.001	-0.088	0.932354	0.973077
8796	10395974					1.001	0.594	0.570702	0.795023
8797	10445664	NM_146079	107477	guanylate cyclase activator 1B	Guca1b	1	0.167	0.871897	0.948811
8798	10425628	ENSMUST00000072779	545121	predicted gene, EG545121	EG545121	1	-0.05	0.961301	0.985156
8799	10606009	ENSMUST00000101358	245536	gene model 614, (NCBI)	Gm614	1	0.157	0.879374	0.952124
8800	10420470	XR_004746	675187	similar to Glyceraldehyde-3-ph	LOC675187	1	0.419	0.687522	0.862217
8801	10598569	NM_001038697	434729	predicted gene, EG434729	EG434729	1	0.489	0.639635	0.836546
8802	10437080	NM_009441	22129	tetratricopeptide repeat domai	Ttc3	1	-0.283	0.785287	0.912507
8803	10369989	NM_010027	13202	D-dopachrome tautomerase	Ddt	1	-0.392	0.706111	0.871814
8804	10480238	NM_145838	241230	ST8 alpha-N-acetyl-neuraminide	St8sia6	1	0.201	0.8461	0.937284
8805	10384725	NM_009044	19696	reticuloendotheliosis oncogene	Rel	1	-0.229	0.825138	0.929627

8806	10495613	NM_029425	75769	RIKEN cDNA 4833424O15 gene	4833424O15Rik	1		0.051	0.960674	0.985069
8807	10355742	NM_023732	74104	ATP-binding cassette, sub-fami	Abcb6	1		-0.259	0.802663	0.919965
8808	10573472	NM_144929	234542	retbindin	Rtbdn	1		0.048	0.963097	0.985611
8809	10352192					1		-0.251	0.808637	0.922966
8810	10481634	NM_146118	227731	solute carrier family 25 (mito	Slc25a25	1		0.195	0.850864	0.94008
8811	10437846	NM_028968	74482	interferon induced transmembra	Ifitm7	1		0.38	0.715182	0.875355
8812	10447431	NM_180974	14236	forkhead box N2	Foxn2	1		-0.162	0.875442	0.950704
8813	10488687	NM_178939	68559	p53 and DNA damage regulated 1	Pdrg1	1		-0.325	0.754143	0.896425
8814	10549875	NM_146389	258384	olfactory receptor 1350	Olfr1350	1		-0.294	0.777026	0.909262
8815	10353849	BC132293	226976	RIKEN cDNA 4632411B12 gene	4632411B12Rik	1		-0.294	0.777169	0.909278
8816	10449510	BC117930	207819	RIKEN cDNA 4930539E08 gene	4930539E08Rik	1		0.466	0.654756	0.845294
8817	10432756	NM_001003670	406223	predicted gene, EG406223	EG406223	1		-0.057	0.956226	0.983332
8818	10348424	NM_133816	98402	SH3-domain binding protein 4	Sh3bp4	1		0.054	0.958775	0.984381
8819	10545921	NM_010751	17119	MAX dimerization protein 1	Mxd1	1		-0.379	0.715817	0.875402
8820	10431030	NM_001030014	223722	malonyl CoA:ACP acyltransferas	Mcat	1		-0.131	0.899494	0.960245
8821	10421309	NM_144808	213053	solute carrier family 39 (zinc	Slc39a14	1		-0.111	0.914388	0.966207
8822	10582006	XM_001480002	100043053	hypothetical protein LOC100043	LOC100043053	1		-0.155	0.880758	0.952675
8823	10547858	NM_013530	14695	guanine nucleotide binding pro	Gnb3	1		-0.158	0.879065	0.952124
8824	10535413					1		-0.022	0.983393	0.992843
8825	10348600	NM_028718	74019	TNF receptor-associated factor	Traf3ip1	1		0.153	0.882567	0.953648
8826	10425302	NM_013818	14904	GTP binding protein 1	Gtpbp1	1		-0.335	0.746911	0.892495
8827	10397627					1		0.314	0.762282	0.901088
8828	10426240	ENSMUST00000116193	546648	kelch domain containing 7B	Klhdc7b	1		0.198	0.848771	0.938719
8829	10509645	NM_146157	230866	RIKEN cDNA C230096C10 gene	C230096C10Rik	1		-0.166	0.872402	0.949019
8830	10445877	ENSMUST00000105022	628926	predicted gene, ENSMUSG0000005	ENSMUSG00000058380	1		0.09	0.931079	0.972759
8831	10360297	NM_008429	16524	potassium inwardly-rectifying	Kcnj9	1		0.067	0.948746	0.980224
8832	10534842	NM_010312	14693	guanine nucleotide binding pro	Gnb2	1		0.059	0.954737	0.982671
8833	10460194					1		0.002	0.998655	0.999521
8834	10511896	AK144923	414068	cDNA sequence BC024582	BC024582	1		0.235	0.82099	0.92863
8835	10544284	NM_001001451	387513	taste receptor, type 2, member	Tas2r138	1		0.62	0.554642	0.783704
8836	10560856	NM_199013	210145	immunity-related GTPase family	Irgc1	1		0.164	0.87458	0.949978
8837	10355264	ENSMUST00000076473	100043192	similar to ribosomal protein L	LOC100043192	1		-0.437	0.674969	0.855557
8838	10376765	NM_007436	11670	aldehyde dehydrogenase family	Aldh3a1	1		-0.217	0.834334	0.933071
8839	10499927	NM_026394	67828	late cornified envelope 1F	Lce1f	1		0.464	0.656255	0.846043
8840	10465150	NM_144868	104401	pecanex-like 3 (Drosophila)	Pcnxl3	1		-0.104	0.919756	0.967952
8841	10512063					1		0.12	0.907603	0.963723
8842	10391798	NM_010277	14580	glial fibrillary acidic protei	Gfap	1		0.413	0.69185	0.864682
8843	10351400	BC132161	226610	RIKEN cDNA C030014K22 gene	C030014K22Rik	1		-0.154	0.882186	0.953469
8844	10515649	BC059842	230676	cDNA sequence BC059842	BC059842	1		0.397	0.702726	0.869626
8845	10491958	ENSMUST00000099104	100038447	predicted gene, ENSMUSG0000007	ENSMUSG00000074603	1		0.184	0.859209	0.943452
8846	10442458	NM_175682	319259	RIKEN cDNA 9930021D14 gene	9930021D14Rik	1		0.259	0.803202	0.920074
8847	10529093	NM_027901	71752	general transcription factor I	Gtf3c2	1		-0.226	0.827789	0.93066
8848	10440388	NM_030201	110920	stress 70 protein chaperone, m	Stch	1		-0.638	0.543304	0.775718
8849	10552264					1		0.064	0.950892	0.981077
8850	10401420					1		0.252	0.808011	0.922738
8851	10361075	NM_001081259	226844	feline leukemia virus subgroup	Flvcr1	1		-0.191	0.853472	0.940713
8852	10474725	NM_013719	27103	eukaryotic translation initiat	Eif2ak4	1		-0.065	0.949721	0.980608
8853	10548616					1		-0.002	0.998294	0.999428
8854	10418868					1		0.421	0.685765	0.861188
8855	10415890	NM_146246	271209	retinitis pigmentosa 1 homolog	Rp1l1	1		0.184	0.858763	0.943374

8856	10377652	NM_019726	56310	G protein pathway suppressor 2	Gps2	1	-0.147	0.887035	0.955613
8857	10411508	NM_026873	68927	pentatricopeptide repeat domai	Ptcd2	1	-0.38	0.714677	0.875137
8858	10468089	NM_023799	76055	meningioma expressed antigen 5	Mgea5	1	-0.026	0.980144	0.991919
8859	10365069	NM_008844	18717	phosphatidylinositol-4-phospha	Pip5k1c	1	0.182	0.860688	0.943954
8860	10364550	NM_053244	114229	KISS1 receptor	Kiss1r	1	0.001	0.999028	0.999589
8861	10403834	NM_016687	20379	secreted frizzled-related prot	Sfrp4	1	0.209	0.839859	0.935328
8862	10510872					1	0.545	0.602278	0.81371
8863	10430132	NM_172817	239546	zinc finger protein 647	Zfp647	0.999	-0.402	0.699052	0.868099
8864	10411052	ENSMUST00000040106	73942	RIKEN cDNA 4930405M20 gene	4930405M20Rik	0.999	0.139	0.893553	0.957981
8865	10504609					0.999	-0.19	0.854347	0.94105
8866	10587637	AK141776	100038531	predicted gene, ENSMUSG0000007	ENSMUSG00000074152	0.999	-0.043	0.966932	0.986963
8867	10557481	NM_026875	66090	yippee-like 3 (Drosophila)	Ypel3	0.999	-0.449	0.666571	0.851355
8868	10469145	NM_025280	16588	antigenic determinant of rec-A	Kin	0.999	-0.673	0.522063	0.759078
8869	10382927	ENSMUST00000092394	432615	predicted gene, OTTMUSG0000000	OTTMUSG00000003802	0.999	0.29	0.780287	0.910803
8870	10511226	NM_207223	140500	centaurin, beta 5	Centb5	0.999	0.036	0.971876	0.988148
8871	10607111	XM_142195	245651	predicted gene, EG245651	EG245651	0.999	0.196	0.849992	0.939578
8872	10544171	NM_028123	72144	solute carrier family 37 (glyc	Slc37a3	0.999	-0.382	0.713598	0.874653
8873	10538123	NM_174960	317758	GTPase, IMAP family member 9	Gimap9	0.999	-0.457	0.661306	0.849184
8874	10393177	NM_015729	11430	acyl-Coenzyme A oxidase 1, pal	Acox1	0.999	-0.64	0.542233	0.77466
8875	10575550	NM_146217	234734	alanyl-tRNA synthetase	Aars	0.999	-0.34	0.743844	0.89106
8876	10386955	NM_178379	70383	COX10 homolog, cytochrome c ox	Cox10	0.999	0.078	0.939853	0.976619
8877	10592154	BC035953	76832	hydrolethalus syndrome 1	Hyls1	0.999	-0.036	0.972309	0.98815
8878	10440849	ENSMUST00000023696	104015	synaptojanin 1	Synj1	0.999	0.128	0.901465	0.961344
8879	10378816	NM_010484	15567	solute carrier family 6 (neuro	Slc6a4	0.999	-0.465	0.655315	0.845667
8880	10370180	NM_146007	12834	collagen, type VI, alpha 2	Col6a2	0.999	0.227	0.826971	0.930622
8881	10579663	NM_007944	13859	epidermal growth factor recept	Eps15l1	0.999	-0.419	0.687346	0.862149
8882	10557213	NM_011247	19647	retinoblastoma binding protein	Rbbp6	0.999	-0.065	0.949836	0.980663
8883	10567702	NM_144529	70497	Rho GTPase activating protein	Arhgap17	0.999	-0.249	0.810075	0.923405
8884	10578377	NM_013522	14300	FSHD region gene 1	Frg1	0.999	-0.191	0.854153	0.941009
8885	10549827	NM_133204	170734	zinc finger protein 371	Zfp371	0.999	0.274	0.791587	0.915198
8886	10582082	NM_001009950	234788	solute carrier family 38, memb	Slc38a8	0.999	-0.04	0.968857	0.987519
8887	10429064	ENSMUST00000100584	654498	HERV-H LTR-associating 1	Hhla1	0.999	0.456	0.661836	0.8494
8888	10427877	AK157781	100038530	predicted gene, ENSMUSG0000007	ENSMUSG00000072643	0.999	-0.065	0.950144	0.98071
8889	10530223					0.999	0.024	0.98187	0.992194
8890	10539773	NM_013528	14583	glutamine fructose-6-phosphate	Gfpt1	0.999	-0.408	0.695225	0.866195
8891	10367154	NM_001033264	216456	glutaminase 2 (liver, mitochon	Gls2	0.999	0.495	0.635275	0.834289
8892	10572861	NM_007975	14065	coagulation factor II (thrombi	F2rl3	0.999	-0.049	0.96234	0.985405
8893	10515280					0.999	0.594	0.570606	0.795023
8894	10371286					0.999	-0.153	0.882525	0.953648
8895	10447337	ENSMUST00000042172	78469	RIKEN cDNA 1700090G07 gene	1700090G07Rik	0.999	0.108	0.916651	0.967052
8896	10525210	ENSMUST00000055859	269700	expressed sequence AU042671	AU042671	0.999	-0.038	0.970817	0.988148
8897	10595604	NM_019796	56403	synaptotagmin binding, cytopla	Syncrip	0.999	0.005	0.996503	0.998723
8898	10389087	NM_001007465	67338	ring finger and FYVE like doma	Rffl	0.999	0.132	0.898455	0.960023
8899	10517566					0.999	-0.069	0.94682	0.978856
8900	10425601	NM_017376	21685	thyrotroph embryonic factor	Tef	0.999	0.233	0.822303	0.92893
8901	10410576	NM_028959	74470	centrosomal protein 72	Cep72	0.999	-0.467	0.654078	0.845086
8902	10473650	NM_021512	59015	nucleoporin 160	Nup160	0.999	-0.373	0.71954	0.877846
8903	10367413	NM_028873	74330	DnaJ (Hsp40) homolog, subfamil	Dnajc14	0.999	-0.494	0.635928	0.834683
8904	10434998	NM_026554	68092	nuclear cap binding protein su	Ncbp2	0.999	-0.288	0.78118	0.911067
8905	10551716	NM_182694	243897	gametogenetin	Ggn	0.999	0.351	0.735806	0.886874
8906	10450514	NM_010909	18038	nuclear factor of kappa light	Nfkbil1	0.999	0.094	0.927514	0.971484
8907	10600547	NM_020601	21372	transducin (beta)-like 1 X-lin	Tbl1x	0.999	-0.388	0.708974	0.87266

8908	10577356					0.999	-0.147	0.887129	0.955613
8909	10506500	ENSMUST00000094933	329908	ubiquitin specific peptidase 2	Usp24	0.999	-0.135	0.896494	0.959489
8910	10356403	NM_001110227	100040591	potassium inwardly-rectifying	Kcnj13	0.999	0.335	0.747014	0.892497
8911	10468016	NM_026061	67264	NADH dehydrogenase (ubiquinone	Ndufb8	0.999	-0.358	0.730697	0.883556
8912	10451322	NM_001081335	78309	p53-associated parkin-like cyt	Parc	0.999	0.122	0.906603	0.963405
8913	10525923	XM_915709	208151	transmembrane protein 132B	Tmem132b	0.999	-0.025	0.980731	0.991919
8914	10405189					0.999	-0.665	0.526778	0.76278
8915	10435676	NM_019827	56637	glycogen synthase kinase 3 bet	Gsk3b	0.999	-0.326	0.753649	0.896241
8916	10458538	BC002117	66839	RIKEN cDNA 0610009O20 gene	0610009O20Rik	0.999	0.053	0.959103	0.98454
8917	10345411	NM_183019	226970	Rho guanine nucleotide exchang	Arhgef4	0.999	-0.121	0.906698	0.963405
8918	10441344	BC075621	106583	RNA binding motif protein 16	Rbm16	0.999	-0.261	0.801078	0.919467
8919	10383810	ENSMUST00000042344	75342	RIKEN cDNA 4930556J24 gene	4930556J24Rik	0.999	0.063	0.951144	0.981129
8920	10468174	NM_008852	18742	paired-like homeodomain transc	Pitx3	0.999	0.309	0.765923	0.902563
8921	10583133	NM_010810	17393	matrix metallopeptidase 7	Mmp7	0.999	0.073	0.943611	0.977948
8922	10520080	NM_177323	72772	RAD50 interactor 1	Rint1	0.999	-0.008	0.993915	0.997702
8923	10478381	ENSMUST00000065731	69517	RIKEN cDNA 2310001K24 gene	2310001K24Rik	0.999	0.174	0.866481	0.946668
8924	10560459	NM_009499	22323	vasodilator-stimulated phospho	Vasp	0.999	0.408	0.695	0.866071
8925	10578157	NM_175091	21951	tankyrase, TRF1-interacting an	Tnks	0.999	-0.429	0.680581	0.85838
8926	10524631	NM_145209	231655	2'-5' oligoadenylate synthetas	Oasl1	0.999	-0.104	0.919701	0.967952
8927	10375487	NM_008143	14694	guanine nucleotide binding pro	Gnb2l1	0.999	-0.47	0.652112	0.844145
8928	10379557	ENSMUST00000092851	791422	predicted gene, OTTMUSG0000000	OTTMUSG00000000913	0.999	0.017	0.986852	0.994566
8929	10439021	NM_177103	320213	SUMO/sentrin specific peptidas	Senp5	0.999	-0.546	0.601701	0.813257
8930	10414325	NM_026832	68755	cell growth regulator with rin	Cgrrf1	0.999	0.019	0.98544	0.993977
8931	10468229					0.999	0.134	0.897233	0.95959
8932	10526880	ENSMUST00000100518	70744	RIKEN cDNA 6330403L08 gene	6330403L08Rik	0.999	0.181	0.861705	0.94442
8933	10532346	NM_153400	231602	purinergic receptor P2X, ligan	P2rx2	0.999	0.069	0.94676	0.978842
8934	10354414					0.999	0.284	0.784078	0.912068
8935	10599205	XR_032644	621983	similar to Ribosomal protein L	LOC621983	0.999	-0.286	0.782651	0.911672
8936	10350646	NM_001039644	66967	ER degradation enhancer, manno	Edem3	0.999	-0.543	0.603701	0.814811
8937	10580486	NM_012047	26992	bromodomain containing 7	Brd7	0.999	-0.27	0.79443	0.916541
8938	10446713					0.999	-0.206	0.842844	0.936326
8939	10601880	NM_001033001	436230	cDNA sequence BC065397	BC065397	0.999	-0.182	0.860605	0.943954
8940	10507433	NM_008958	19207	patched homolog 2	Ptch2	0.999	0.037	0.971734	0.988148
8941	10511719					0.999	0.241	0.815897	0.926256
8942	10440673	NM_013707	23927	keratin associated protein 14	Krtap14	0.999	-0.036	0.972502	0.988158
8943	10607557					0.999	0.096	0.926165	0.970758
8944	10485342	NM_183106	74569	tetratricopeptide repeat domai	Ttc17	0.999	-0.335	0.747124	0.892497
8945	10405576	NM_178674	213311	F-box and leucine-rich repeat	Fbxl21	0.999	0.073	0.943934	0.977948
8946	10391612	NM_001098836	217218	ataxin 7-like 3	Atxn7l3	0.998	-0.281	0.786707	0.91293
8947	10391540	NM_016695	50997	membrane protein, palmitoylate	Mpp2	0.998	-0.198	0.848238	0.938472
8948	10376332	ENSMUST00000108834	73988	RIKEN cDNA 4930438A08 gene	4930438A08Rik	0.998	0.314	0.762663	0.901202
8949	10598292	NM_054039	20371	forkhead box P3	Foxp3	0.998	0.364	0.726521	0.881528
8950	10539810	NM_021418	58229	hypothetical protein, MNCb-477	AB041550	0.998	0.491	0.638112	0.835923
8951	10497765	NM_033623	114893	DCUN1D1 DCN1, defective in cul	Dcun1d1	0.998	-0.106	0.918697	0.967805
8952	10586184	NM_025372	66131	timeless interacting protein	Tipin	0.998	-0.633	0.546086	0.777643
8953	10479639	NM_016775	13002	DnaJ (Hsp40) homolog, subfamil	Dnajc5	0.998	-0.131	0.899664	0.960245
8954	10589870					0.998	0.648	0.537249	0.770298
8955	10393687	NM_009734	12009	5-azacytidine induced gene 1	Azi1	0.998	0.173	0.867219	0.946934
8956	10415293	NM_194346	268749	ring finger protein 31	Rnf31	0.998	-0.1	0.92291	0.969148
8957	10512791	NM_198664	381605	TBC1 domain family, member 2	Tbc1d2	0.998	0.13	0.899902	0.960355
8958	10454674	NM_025527	66384	signal recognition particle 19	Srp19	0.998	-0.25	0.809632	0.923191
8959	10420295	NM_010374	14943	granzyme F	Gzmf	0.998	0.596	0.56941	0.794081

8960	10465059	NM_009985	13041	cathepsin W	Ctsw	0.998	0.097	0.92504	0.970374
8961	10425341	NM_025609	66513	mitogen-activated protein kina	Map3k7ip1	0.998	0.182	0.860658	0.943954
8962	10504278	NM_177195	320571	RIKEN cDNA 4930417M19 gene	4930417M19Rik	0.998	0.13	0.90041	0.960656
8963	10438198	NM_033609	94112	mediator complex subunit 15	Med15	0.998	-0.178	0.863984	0.945829
8964	10565924	NM_177073	320100	RELT tumor necrosis factor rec	Relt	0.998	0.029	0.977358	0.990677
8965	10398147	NM_011112	18789	poly (A) polymerase alpha	Papola	0.998	-0.252	0.80777	0.922567
8966	10597920	NM_026917	69035	zinc finger, DHHC domain conta	Zdhhc3	0.998	-0.139	0.893322	0.957829
8967	10504902	NM_026509	68016	RIKEN cDNA 2310039E09 gene	2310039E09Rik	0.998	-0.365	0.725851	0.881326
8968	10428554	NM_080635	68135	eukaryotic translation initiat	Eif3h	0.998	-0.538	0.606913	0.817049
8969	10508619	NM_030722	80912	pumilio 1 (Drosophila)	Pum1	0.998	-0.226	0.827841	0.93066
8970	10535189	NM_010752	17120	mitotic arrest deficient 1-lik	Mad1l1	0.998	-0.206	0.842152	0.936059
8971	10415897	BC048657	74215	RIKEN cDNA 1700007N14 gene	1700007N14Rik	0.998	-0.098	0.924876	0.970324
8972	10549544	ENSMUST00000100766	100038707	predicted gene, ENSMUSG0000007	ENSMUSG00000072655	0.998	0	0.999942	0.999942
8973	10545212	ENSMUST00000103364	434037	predicted gene, ENSMUSG0000007	ENSMUSG00000076563	0.998	0.27	0.794521	0.916545
8974	10448459	NM_173186	224617	TBC1 domain family, member 24	Tbc1d24	0.998	0.087	0.933055	0.973286
8975	10489239	AK079109	68108	RIKEN cDNA 9430008C03 gene	9430008C03Rik	0.998	-0.046	0.964489	0.985942
8976	10526087	NM_026445	67902	sulfatase modifying factor 2	Sumf2	0.998	-0.396	0.703392	0.86989
8977	10427667					0.998	0.112	0.913984	0.966071
8978	10528872	NM_009170	20423	sonic hedgehog	Shh	0.998	-0.093	0.928403	0.971746
8979	10356800	NM_133808	110611	high density lipoprotein (HDL)	Hdlbp	0.998	-0.648	0.537186	0.770298
8980	10580903					0.998	0.027	0.979102	0.991719
8981	10467749	NM_145123	72832	cartilage acidic protein 1	Crtac1	0.998	-0.119	0.908419	0.963723
8982	10345401	BC070435	211383	RIKEN cDNA 9430069J07 gene	9430069J07Rik	0.998	0.478	0.646505	0.840625
8983	10481734	NM_199302	227738	leucine rich repeat and steril	Lrsam1	0.998	0.283	0.785021	0.912507
8984	10470298	NM_019833	56279	RIKEN cDNA B230317C12 gene	B230317C12Rik	0.998	-0.096	0.925995	0.970758
8985	10401698	AF525300	238330	RIKEN cDNA 6430527G18 gene	6430527G18Rik	0.998	0.068	0.947472	0.979243
8986	10474077	ENSMUST00000099693	100038525	predicted gene, ENSMUSG0000007	ENSMUSG00000075025	0.998	0.071	0.945481	0.97847
8987	10558992	BC034197	17831	mucin 2	Muc2	0.998	0.229	0.825163	0.929627
8988	10566309	NM_198624	244179	ubiquilin-like	Ubqlnl	0.998	0.144	0.889422	0.956457
8989	10570749	NM_010030	13215	defensin beta 2	Defb2	0.998	0.375	0.718514	0.877128
8990	10545910	NM_025823	66881	prenylcysteine oxidase 1	Pcyox1	0.998	-0.166	0.872842	0.949165
8991	10376956	NM_178870	15478	heparan sulfate (glucosamine)	Hs3st3a1	0.998	-0.278	0.788446	0.913849
8992	10381172	NM_011488	20850	signal transducer and activato	Stat5a	0.998	0.056	0.957044	0.983559
8993	10389389	ENSMUST00000100674	100038438	predicted gene, ENSMUSG0000007	ENSMUSG00000072590	0.998	0.085	0.934635	0.973973
8994	10388352	NM_197943	97761	small G protein signaling modu	Sgsm2	0.998	0.145	0.8883	0.956025
8995	10553071	NM_001033356	243967	gene model 484, (NCBI)	Gm484	0.998	0.574	0.583639	0.801548
8996	10573733	BC145737	214627	PAP associated domain containi	Papd5	0.998	-0.139	0.893079	0.957774
8997	10379524	NM_011330	20292	small chemokine (C-C motif) li	Ccl11	0.998	0.117	0.910177	0.964056
8998	10384782	NM_027260	69922	vaccinia related kinase 2	Vrk2	0.998	-0.452	0.664784	0.85061
8999	10563355	NM_019934	56546	secretory blood group 1	Sec1	0.998	0.051	0.96036	0.985069
9000	10519181					0.998	0.119	0.908186	0.963723
9001	10401753	BC023716	104799	expressed sequence AI413782	AI413782	0.998	-0.932	0.381705	0.651394
9002	10511817	ENSMUST00000098232	212390	kelch-like 32 (Drosophila)	Klhl32	0.998	0.042	0.967693	0.987137
9003	10361110	NM_029766	76843	denticleless homolog (Drosophi	Dtl	0.998	-0.519	0.61935	0.82476
9004	10403453	NM_001081426	208440	DIP2 disco-interacting protein	Dip2c	0.998	-0.048	0.962876	0.985577
9005	10512254	NM_001048005	73721	RIKEN cDNA 1110017D15 gene	1110017D15Rik	0.998	0.05	0.961116	0.985069
9006	10597095	BC061210	378954	RIKEN cDNA 3000002C10 gene	3000002C10Rik	0.998	-0.318	0.759537	0.899247
				RIKEN cDNA 6720463M24					

9007	10416736	BC052183	77744	RIKEN cDNA 6720463M24 gene	6720463M24Rik	0.998	-0.007	0.994952	0.998046
9008	10520633	NM_053085	69852	transcription factor 23	Tcf23	0.998	0.225	0.82826	0.930848
9009	10400589	BC052175	217653	expressed sequence C79407	C79407	0.998	0.105	0.919088	0.967837
9010	10345620	NM_027098	107734	mitochondrial ribosomal protei	Mrpl30	0.998	-1.216	0.262204	0.53666
9011	10580516	XR_031896	625801	predicted gene, EG625801	EG625801	0.998	0.046	0.964377	0.985919
9012	10350853					0.998	-0.058	0.955073	0.982833
9013	10463173	NM_023740	74168	zinc finger, DHHC domain conta	Zdhhc16	0.998	-0.937	0.379031	0.648769
9014	10345556	XR_032810	100046859	hypothetical protein LOC100046	LOC100046859	0.998	0.358	0.730489	0.883456
9015	10537911	NM_027477	272347	zinc finger protein 398	Zfp398	0.998	0.337	0.745374	0.891675
9016	10402073	BC049109	78767	RIKEN cDNA 2610021K21 gene	2610021K21Rik	0.998	-0.407	0.696116	0.866518
9017	10401267	NM_177267	320808	WD repeat domain 22	Wdr22	0.998	0.047	0.964116	0.985864
9018	10481627	NM_008491	16819	lipocalin 2	Lcn2	0.998	0.367	0.723941	0.88046
9019	10509868	NM_029097	74772	ATPase type 13A2	Atp13a2	0.998	0.016	0.987864	0.994998
9020	10405400	NM_008739	18193	nuclear receptor-binding SET-d	Nsd1	0.998	-0.189	0.855193	0.941477
9021	10492536					0.998	0.033	0.974449	0.989186
9022	10482017	NM_026697	68365	RAB14, member RAS oncogene fam	Rab14	0.998	-0.193	0.851943	0.940258
9023	10533446	NM_001039153	654470	tectonic 1	Tect1	0.998	0.161	0.87637	0.951084
9024	10376339	NM_182996	103836	zinc finger protein 692	Zfp692	0.998	0.145	0.888379	0.956025
9025	10550906	NM_011113	18793	plasminogen activator, urokina	Plaur	0.997	-0.171	0.868911	0.947512
9026	10566379	NM_147049	259051	olfactory receptor 658	Olfr658	0.997	0.072	0.944469	0.978004
9027	10573790	NM_145857	257632	nucleotide-binding oligomeriza	Nod2	0.997	0.029	0.977817	0.99094
9028	10544036	NM_080467	140494	ATPase, H+ transporting, lysos	Atp6v0a4	0.997	0.248	0.811234	0.923829
9029	10594638	NM_026674	68318	anterior pharynx defective 1c	Aph1c	0.997	0.031	0.976353	0.990137
9030	10461017	NM_007522	12015	Bcl-associated death promoter	Bad	0.997	-0.107	0.917691	0.967684
9031	10378053	BC029115	109212	RIKEN cDNA 6720460F02 gene	6720460F02Rik	0.997	0.054	0.958683	0.984334
9032	10353689	NM_001081080	213109	PHD finger protein 3	Phf3	0.997	-0.363	0.726804	0.881629
9033	10406757	NM_023420	68018	collagen, type IV, alpha 3 (Go	Col4a3bp	0.997	-0.314	0.762371	0.901088
9034	10590801	NM_007464	11796	baculoviral IAP repeat-contain	Birc3	0.997	-0.259	0.802921	0.920071
9035	10361669	NM_011835	23924	katanin p60 (ATPase-containing	Katna1	0.997	-0.611	0.559865	0.787244
9036	10421717	NM_001033440	380920	gene model 1587, (NCBI)	Gm1587	0.997	0.026	0.98032	0.991919
9037	10481164	NM_172659	227659	solute carrier family 2 (facil	Slc2a6	0.997	0.157	0.879829	0.952394
9038	10586842	ENSMUST00000098589	235461	RIKEN cDNA B230380D07 gene	B230380D07Rik	0.997	-0.126	0.903453	0.962464
9039	10375014	BC114574	67592	RIKEN cDNA 4930524B15 gene	4930524B15Rik	0.997	0.194	0.851668	0.940193
9040	10472289	NM_011529	21353	TRAF family member-associated	Tank	0.997	-0.366	0.72475	0.880713
9041	10514892	NM_025617	66526	RIKEN cDNA 2210012G02 gene	2210012G02Rik	0.997	-0.464	0.656217	0.846043
9042	10417048	NM_015820	50787	heparan sulfate 6-O-sulfotrans	Hs6st3	0.997	0.006	0.995754	0.998271
9043	10461842					0.997	0.092	0.929305	0.972164
9044	10401441	ENSMUST00000046266	238317	RIKEN cDNA C130039O16 gene	C130039O16Rik	0.997	-0.485	0.642353	0.83808
9045	10351414	NM_019993	56752	aldehyde dehydrogenase 9, subf	Aldh9a1	0.997	-0.239	0.81799	0.927626
9046	10545940	NM_011818	23885	germ cell-less homolog 1 (Dros	Gmcl1	0.997	-0.021	0.983625	0.992971
9047	10542302	NM_177687	232430	cAMP responsive element bindin	Crebl2	0.997	0.226	0.827591	0.93066
9048	10576784	NM_133238	170786	CD209a antigen	Cd209a	0.997	-0.122	0.906046	0.963405
9049	10500333	NM_033596	97122	histone cluster 2, H4	Hist2h4	0.997	-0.45	0.666229	0.851266
9050	10552796	NM_001077591	22116	serine/threonine kinase 22 sub	Stk22s1	0.997	-0.208	0.841277	0.935777
9051	10373542	NM_016811	13139	diacylglycerol kinase, alpha	Dgka	0.997	0.073	0.943832	0.977948
9052	10532124	NM_010278	14581	growth factor independent 1	Gfi1	0.997	0.063	0.951777	0.981246
9053	10462228	NM_177360	240590	doublesex and mab-3 related tr	Dmrt3	0.997	-0.077	0.940958	0.97709
9054	10451458	NM_028065	72029	canopy 3 homolog (zebrafish)	Cnpy3	0.997	-0.721	0.493552	0.739168
9055	10531627	AK044414	319818	RIKEN cDNA A930011G23 gene	A930011G23Rik	0.997	-0.117	0.910189	0.964056
9056	10551410	NM_009560	22718	zinc finger protein 60	Zfp60	0.997	-0.331	0.749778	0.894303
9057	10540993	NM_138311	171506	H1 histone family, member O, o	H1foo	0.997	0.192	0.853133	0.940713

9058	10475027	NM_019392	22174	TYRO3 protein tyrosine kinase	Tyro3	0.997	-0.351	0.735901	0.886874
9059	10508272	ENSMUST00000074081	329942	CUB and Sushi multiple domains	Csmd2	0.997	0.021	0.983819	0.993071
9060	10377953	NM_153103	16562	kinesin family member 1C	Kif1c	0.997	-0.345	0.740072	0.889339
9061	10523683	NM_010080	666279	dentin sialophosphoprotein	Dspp	0.997	0.037	0.971597	0.988148
9062	10525839					0.997	0.277	0.789483	0.914397
9063	10366586	NM_008337	15978	interferon gamma	Ifng	0.997	-0.276	0.790072	0.914502
9064	10496946	NM_198416	108946	zinc finger, ZZ domain contain	Zzz3	0.997	-0.527	0.613863	0.821228
9065	10521698					0.997	0.074	0.942871	0.977825
9066	10383897	NM_010898	18016	neurofibromatosis 2	Nf2	0.997	-0.418	0.687947	0.862647
9067	10373642	NM_146550	258543	olfactory receptor 810	Olfr810	0.997	0.13	0.900091	0.960389
9068	10539617	NM_145223	236266	Alstrom syndrome 1 homolog (hu	Alms1	0.997	-0.17	0.869322	0.947675
9069	10431856	NM_028148	72193	splicing factor, arginine/seri	Sfrs2ip	0.997	-0.609	0.561193	0.788377
9070	10477791	NM_139151	245865	sperm associated antigen 4	Spag4	0.997	0.706	0.502619	0.745467
9071	10489784	NM_177782	277360	cDNA sequence BC067047	BC067047	0.997	-0.009	0.993162	0.997422
9072	10347781	BC082310	241134	RIKEN cDNA 9430031J16 gene	9430031J16Rik	0.997	0.347	0.738392	0.88844
9073	10358140	EU429481	226438	immunoglobulin-like and fibron	Igfn1	0.997	0.466	0.655086	0.845541
9074	10512274	BC021944	69638	RIKEN cDNA 2310040A07 gene	2310040A07Rik	0.997	-0.13	0.900115	0.960389
9075	10604403					0.997	-0.025	0.980759	0.991919
9076	10557895	NM_021334	16411	integrin alpha X	Itgax	0.997	-0.024	0.981385	0.992092
9077	10527624	NM_001115153	231915	ubiquitin specific peptidase l	Uspl1	0.997	-0.641	0.541457	0.773858
9078	10465559	NM_011697	22340	vascular endothelial growth fa	Vegfb	0.997	-0.091	0.930288	0.97262
9079	10501104	NM_172271	229706	solute carrier family 6 (neuro	Slc6a17	0.997	0.018	0.985828	0.994073
9080	10398193	ENSMUST00000082269	73160	RIKEN cDNA 3110018I06 gene	3110018I06Rik	0.997	0.162	0.875784	0.950887
9081	10432154	NM_147036	259038	olfactory receptor 283	Olfr283	0.997	0.04	0.968884	0.987519
9082	10489065	NM_013865	29812	N-myc downstream regulated gen	Ndrg3	0.997	-0.478	0.646649	0.840625
9083	10419825	NM_023190	56215	apoptotic chromatin condensati	Acin1	0.997	-0.321	0.756977	0.898026
9084	10411958	NM_027934	71816	ring finger protein 180	Rnf180	0.997	-0.189	0.855418	0.941478
9085	10439068	NM_145932	106407	organic solute transporter alp	Osta	0.997	0.262	0.800584	0.91941
9086	10516081	NM_019489	56031	peptidylprolyl isomerase E (cy	Ppie	0.997	-0.069	0.946578	0.978837
9087	10454786	NM_009818	12385	catenin (cadherin associated p	Ctnna1	0.997	-0.587	0.575014	0.797076
9088	10482528	NM_010889	17996	nebulin	Neb	0.997	0.193	0.852008	0.940258
9089	10395984	BC062107	328108	RIKEN cDNA A430041B07 gene	A430041B07Rik	0.997	-0.631	0.547544	0.778461
9090	10527285	ENSMUST00000031618	75136	RIKEN cDNA 4930526H21 gene	4930526H21Rik	0.997	-0.12	0.907951	0.963723
9091	10428008	NM_027496	67434	RIKEN cDNA 5730557B15 gene	5730557B15Rik	0.997	-0.082	0.93694	0.975366
9092	10569539	NM_203492	381974	MAS-related GPR, member G	Mrgprg	0.997	0.217	0.834353	0.933071
9093	10380614	NM_008267	15408	homeo box B13	Hoxb13	0.997	-0.08	0.938364	0.976019
9094	10568228	BC058799	269997	RIKEN cDNA 6430604K15 gene	6430604K15Rik	0.997	0.282	0.785545	0.912507
9095	10569513	NM_024289	79196	oxysterol binding protein-like	Osbpl5	0.997	-0.006	0.995633	0.998271
9096	10434446	NM_139293	107522	endothelin converting enzyme 2	Ece2	0.997	-0.212	0.837781	0.934421
9097	10421810	NM_025427	66214	RIKEN cDNA 1190002H23 gene	1190002H23Rik	0.997	0.153	0.882266	0.953469
9098	10474335	NM_028260	66541	IMP1 inner mitochondrial membr	Immp1l	0.997	-0.469	0.652854	0.844541
9099	10575578	NM_198308	319518	RIKEN cDNA 4930402E16 gene	4930402E16Rik	0.997	-0.457	0.660996	0.84894
9100	10532802	NM_175016	231642	alkB, alkylation repair homolo	Alkbh2	0.997	-0.795	0.451779	0.708709
9101	10348641	NM_146491	258484	olfactory receptor 1410	Olfr1410	0.996	0.42	0.686374	0.861515
9102	10365174	NM_027480	70615	ankyrin repeat domain 24	Ankrd24	0.996	-0.069	0.946528	0.978837
9103	10368596	ENSMUST00000092602	432450	Na+/K+ transporting ATPase int	Nkain2	0.996	0.141	0.891455	0.957571
9104	10585249	NM_001034085	73699	protein phosphatase 2 (formerl	Ppp2r1b	0.996	-0.031	0.975794	0.989981
9105	10558297	BC072596	214764	RIKEN cDNA 2700050L05 gene	2700050L05Rik	0.996	-0.256	0.805289	0.921326
9106	10489235					0.996	-0.036	0.971931	0.988148

9107	10531383	NM_172713	231452	SDA1 domain containing 1	Sdad1	0.996	-0.432	0.67833	0.857067
9108	10450280	NM_011413	625018	complement component 4A (Rodge	C4a	0.996	-0.096	0.926178	0.970758
9109	10396121	ENSMUST00000021378	74724	RIKEN cDNA 4930512B01 gene	4930512B01Rik	0.996	0.248	0.810709	0.923749
9110	10601865	XR_032046	666196	similar to Btf3 protein	LOC666196	0.996	-0.133	0.897674	0.959787
9111	10364217	NM_029661	76573	RIKEN cDNA 1700027D21 gene	1700027D21Rik	0.996	0.147	0.887458	0.955613
9112	10572456	NM_010592	16478	Jun proto-oncogene related gen	Jund	0.996	-0.12	0.907558	0.963723
9113	10453254	NM_009187	20463	cytochrome c oxidase subunit V	Cox7a2l	0.996	-0.312	0.764139	0.90173
9114	10401488	NM_008992	19300	ATP-binding cassette, sub-fami	Abcd4	0.996	-0.001	0.999352	0.999589
9115	10523151	NM_008176	14825	chemokine (C-X-C motif) ligand	Cxcl1	0.996	-0.234	0.821377	0.92863
9116	10561513	NM_011885	24030	mitochondrial ribosomal protei	Mrps12	0.996	-0.297	0.774888	0.907674
9117	10391301	NM_213659	20848	signal transducer and activato	Stat3	0.996	-0.233	0.822191	0.928853
9118	10391831	NM_026551	68087	dephospho-CoA kinase domain co	Dcakd	0.996	-0.656	0.532337	0.766374
9119	10458398	NM_008214	15115	histidyl-tRNA synthetase	Hars	0.996	-0.464	0.656014	0.846043
9120	10393917	NM_016665	20892	stimulated by retinoic acid 13	Stra13	0.996	-0.392	0.706312	0.871814
9121	10451195	ENSMUST00000039106	72240	RIKEN cDNA 1600014C23 gene	1600014C23Rik	0.996	-0.231	0.823681	0.929493
9122	10393021	NM_130454	170472	RecQ protein-like 5	Recql5	0.996	0.006	0.995165	0.998139
9123	10472443	ENSMUST00000116497	383710	gene model 1323, (NCBI)	Gm1323	0.996	-0.101	0.922554	0.969122
9124	10524555	NM_023556	17855	mevalonate kinase	Mvk	0.996	-0.065	0.949686	0.980608
9125	10535954	BC037393	381695	NEDD4 binding protein 2-like 2	N4bp2l2	0.996	0.22	0.83207	0.932638
9126	10488844	NM_019825	56406	nuclear receptor coactivator 6	Ncoa6	0.996	-0.195	0.850482	0.939883
9127	10492615	NM_001018031	229389	gene model 414, (NCBI)	Gm414	0.996	-0.22	0.832008	0.932638
9128	10460392	NM_027196	69745	polymerase (DNA-directed), del	Pold4	0.996	-0.073	0.943975	0.977948
9129	10384985	NM_010117	13650	rhomboid family 1 (Drosophila)	Rhbdf1	0.996	-0.447	0.667777	0.851815
9130	10533088	ENSMUST00000100834	100039359	hypothetical protein LOC100039	LOC100039359	0.996	0.152	0.883116	0.953998
9131	10541268	NM_001081048	71803	solute carrier family 25 (mito	Slc25a18	0.996	0.119	0.908527	0.963723
9132	10489620	NM_144892	228869	nuclear receptor coactivator 5	Ncoa5	0.996	-0.366	0.724561	0.880619
9133	10348144	ENSMUST00000044533	69453	RIKEN cDNA 1700027L20 gene	1700027L20Rik	0.996	0	0.999833	0.99988
9134	10444637	NM_138582	27762	DNA segment, Chr 17, human D6S	D17H6S56E-3	0.996	-0.308	0.766986	0.90301
9135	10558458	NM_026391	52432	protein phosphatase 2, regulat	Ppp2r2d	0.996	-0.493	0.636449	0.834887
9136	10390831	NM_010660	16661	keratin 10	Krt10	0.996	-0.402	0.699583	0.868422
9137	10450191	NR_004051	81497	butyrophilin-like 5	Btnl5	0.996	-0.351	0.73526	0.886784
9138	10559367	NM_010202	14175	fibroblast growth factor 4	Fgf4	0.996	-0.374	0.71936	0.877778
9139	10424746	NM_030199	78834	zinc finger protein 623	Zfp623	0.996	-0.554	0.596507	0.809898
9140	10401795	NM_001102565	211064	alkB, alkylation repair homolo	Alkbh1	0.996	-0.289	0.780629	0.910911
9141	10603373	NM_019478	54633	polyglutamine binding protein	Pqbp1	0.996	-0.334	0.748187	0.893262
9142	10421737	NM_011613	21943	tumor necrosis factor (ligand)	Tnfsf11	0.996	-0.057	0.956127	0.983285
9143	10572083					0.996	0.36	0.728934	0.882586
9144	10364455	NM_177613	216150	cell division cycle 34 homolog	Cdc34	0.996	-0.419	0.687222	0.862117
9145	10363333	NM_172788	237353	SH3 multiple domains 4	Sh3md4	0.996	0.211	0.838903	0.934797
9146	10557397	ENSMUST00000042859	233865	RIKEN cDNA D430042O09 gene	D430042O09Rik	0.996	0.19	0.854539	0.94107
9147	10572669	ENSMUST00000073799	100037278	BCNP1 homolog	Bcnp1	0.996	-0.521	0.617881	0.823459
9148	10593174					0.996	0.278	0.788977	0.914104
9149	10484854	NM_010990	18347	olfactory receptor 48	Olfr48	0.996	0.073	0.943541	0.977948
9150	10469243					0.996	0.221	0.831366	0.932333
9151	10446441	NM_001003919	320209	DEAD/H (Asp-Glu-Ala-Asp/His) b	Ddx11	0.996	-0.396	0.703505	0.869929
9152	10558698	NM_027019	69287	outer dense fiber of sperm tai	Odf3	0.996	-0.194	0.851546	0.940193
9153	10419691	NM_019721	56335	methyltransferase-like 3	Mettl3	0.996	-0.103	0.92057	0.968204
9154	10514763	NM_146148	230558	complement component 8, alpha	C8a	0.996	0.159	0.877734	0.951715
9155	10541885	NM_011324	20276	sodium channel, nonvoltage-gat	Scnn1a	0.996	-0.317	0.76058	0.900078
9156	10539818	NM_018762	54368	glycoprotein 9 (platelet)	Gp9	0.996	-0.321	0.757231	0.898087

9157	10602499					0.996	0.397	0.703193	0.869747
9158	10471171	NM_001033389	320267	far upstream element (FUSE) bi	Fubp3	0.996	-0.186	0.857619	0.94267
9159	10380474	NM_018792	54388	histone H1-like protein in spe	Hils1	0.996	-0.201	0.845881	0.937284
9160	10601753	XR_030778	674122	hypothetical LOC674122	LOC674122	0.996	-0.424	0.684084	0.860099
9161	10537078	NM_013791	27418	muskelin 1, intracellular medi	Mkln1	0.996	-0.485	0.641843	0.837827
9162	10514292	NM_206975	404549	interferon, alpha 14	Ifna14	0.996	0.383	0.712753	0.874143
9163	10414137	NM_008166	14803	glutamate receptor, ionotropic	Grid1	0.996	0.259	0.803111	0.920071
9164	10533703	NM_025438	208606	arginine/serine-rich coiled-co	Rsrc2	0.996	-0.275	0.79124	0.915056
9165	10416753	NM_029320	52023	progesterone immunomodulatory	Pibf1	0.996	-0.255	0.805672	0.921565
9166	10449315	BC030629	67267	RIKEN cDNA 2900010M23 gene	2900010M23Rik	0.996	-0.682	0.516793	0.756112
9167	10498990	ENSMUST00000047876	100038599	predicted gene, ENSMUSG0000007	ENSMUSG00000074517	0.996	0.045	0.965416	0.986124
9168	10405495	NM_146045	218271	xylosylprotein beta1,4-galacto	B4galt7	0.996	-0.366	0.724889	0.880713
9169	10567450	BC051401	381917	dynein, axonemal, heavy chain	Dnahc3	0.996	-0.142	0.891077	0.957456
9170	10385022	BC087911	69306	RIKEN cDNA 1700007I06 gene	1700007I06Rik	0.996	-0.222	0.83033	0.931873
9171	10437928	BC011300	66086	RIKEN cDNA 0610037P05 gene	0610037P05Rik	0.996	-0.319	0.759093	0.89915
9172	10361078	ENSMUST00000085633	68972	TatD DNase domain containing 3	Tatdn3	0.996	0.111	0.914842	0.966446
9173	10557631	NM_145589	233895	proline rich 14	Prr14	0.996	-0.423	0.684687	0.860588
9174	10571516	XR_030892	622082	similar to bromodomain adjacen	LOC622082	0.996	-0.031	0.976016	0.990137
9175	10373690					0.996	-0.159	0.878078	0.951717
9176	10463229	NM_177319	319740	zinc finger, FYVE domain conta	Zfyve27	0.996	-0.025	0.980698	0.991919
9177	10379736	NM_183249	66107	RIKEN cDNA 1100001G20 gene	1100001G20Rik	0.996	0.489	0.639425	0.836375
9178	10539472	NM_019542	56174	N-acetylglucosamine kinase	Nagk	0.996	-0.329	0.751585	0.895256
9179	10602827	NM_001033472	382252	RIKEN cDNA A830080D01 gene	A830080D01Rik	0.996	-0.344	0.740815	0.889595
9180	10547837	NM_013700	22225	ubiquitin specific peptidase 5	Usp5	0.996	-0.452	0.664553	0.850409
9181	10433462	NM_016881	54128	phosphomannomutase 2	Pmm2	0.996	-0.453	0.664207	0.850267
9182	10433331	NM_025839	66911	nudix (nucleoside diphosphate	Nudt16l1	0.996	-0.425	0.683134	0.859827
9183	10497421	NM_080634	12807	Hermansky-Pudlak syndrome 3 ho	Hps3	0.996	-0.008	0.994004	0.997702
9184	10545154	NM_144548	209590	interleukin 23 receptor	Il23r	0.996	0.06	0.953873	0.982209
9185	10516296	NM_146153	230753	thyroid hormone receptor assoc	Thrap3	0.996	-0.439	0.673853	0.855069
9186	10415086	NM_175204	73902	proteasome (prosome, macropain	Psmb11	0.996	-0.038	0.971039	0.988148
9187	10580452	NM_009172	20437	seven in absentia 1A	Siah1a	0.996	-0.148	0.886478	0.955393
9188	10388488	ENSMUST00000021207	76566	RIKEN cDNA 1500005K14 gene	1500005K14Rik	0.996	-0.338	0.745229	0.891643
9189	10383233	AK173199	629974	ring finger protein 213	Rnf213	0.996	0.048	0.96299	0.985606
9190	10592618	NM_173038	272589	tubulin folding cofactor E-lik	Tbcel	0.996	-0.794	0.452362	0.708922
9191	10400967	NM_009189	20471	sine oculis-related homeobox 1	Six1	0.995	-0.324	0.754913	0.896835
9192	10434670	XR_035704	666421	predicted gene, EG666421	EG666421	0.995	-0.071	0.945534	0.97847
9193	10574934	NM_175024	234700	neuritin 1-like	Nrn1l	0.995	0.33	0.750432	0.894477
9194	10358921	NM_178243	240817	RIKEN cDNA 5830403L16 gene	5830403L16Rik	0.995	0.14	0.89268	0.957773
9195	10446833	NM_007566	12211	baculoviral IAP repeat-contain	Birc6	0.995	-0.104	0.919792	0.967952
9196	10453451	NM_007589	12314	calmodulin 2	Calm2	0.995	-0.02	0.984546	0.993473
9197	10458956					0.995	-0.033	0.974243	0.989025
9198	10421749	ENSMUST00000022593	219181	A kinase (PRKA) anchor protein	Akap11	0.995	-0.106	0.918648	0.967805
9199	10447691	AK043779	75060	RIKEN cDNA 4930506C21 gene	4930506C21Rik	0.995	-0.215	0.835951	0.933525
9200	10359282	NM_001085376	23850	pappalysin 2	Pappa2	0.995	0.045	0.96531	0.986124
9201	10444223	NM_008206	15001	histocompatibility 2, O region	H2-Oa	0.995	-0.388	0.709074	0.872707
9202	10569335	NR_001592	14955	H19 fetal liver mRNA	H19	0.995	-0.1	0.922887	0.969148
9203	10366337	NM_015781	53605	nucleosome assembly protein 1-	Nap1l1	0.995	-0.205	0.843014	0.936367
9204	10462127	ENSMUST00000025731	75521	RIKEN cDNA 1700021P04 gene	1700021P04Rik	0.995	0.745	0.480081	0.729941
9205	10488185	NM_009751	12075	beaded filament structural pro	Bfsp1	0.995	0.215	0.835437	0.933323
9206	10454483	NM_028866	74320	WD repeat domain 33	Wdr33	0.995	-0.213	0.837461	0.934421
9207	10425653	AK132940	328573	RIKEN cDNA 4930407I10 gene	4930407I10Rik	0.995	0.006	0.995728	0.998271

9208	10472707	NM_008077	14415	glutamic acid decarboxylase 1	Gad1	0.995	0.101	0.922156	0.968977
9209	10455602	NM_001081371	240283	Dmx-like 1	Dmxl1	0.995	-0.275	0.790868	0.914727
9210	10380238	NM_024174	64656	mitochondrial ribosomal protei	Mrps23	0.995	-0.384	0.712194	0.873926
9211	10525506	NM_026000	67151	proteasome (prosome, macropain	Psmd9	0.995	-0.058	0.955004	0.982833
9212	10496789	NM_022983	65086	lysophosphatidic acid receptor	Lpar3	0.995	-0.085	0.934212	0.97382
9213	10382998	NM_001012273	11799	baculoviral IAP repeat-contain	Birc5	0.995	-0.183	0.859687	0.943585
9214	10404439	NM_011452	20706	serine (or cysteine) peptidase	Serpinb9b	0.995	0.365	0.725577	0.88115
9215	10477557	NM_199304	228807	zinc finger protein 341	Zfp341	0.995	-0.327	0.75261	0.895764
9216	10558661	NM_146964	18362	olfactory receptor 61	Olfr61	0.995	0.269	0.795701	0.916955
9217	10408066	NM_146541	258534	olfactory receptor 1361	Olfr1361	0.995	0.259	0.802624	0.919965
9218	10404686	NM_007556	12161	bone morphogenetic protein 6	Bmp6	0.995	-0.134	0.897051	0.95959
9219	10594835	NM_178602	28015	glutamate receptor, ionotropic	Grinl1a	0.995	-0.676	0.52023	0.757767
9220	10396175	ENSMUST00000101349	100038476	predicted gene, ENSMUSG0000007	ENSMUSG00000073041	0.995	0.004	0.996998	0.99884
9221	10569767	NM_080461	140482	zinc finger protein 358	Zfp358	0.995	-0.245	0.813008	0.924803
9222	10382846	NR_003364	193217	cDNA sequence BC018473	BC018473	0.995	0.197	0.849411	0.939132
9223	10413981	XM_985917	268729	gene model 626, (NCBI)	Gm626	0.995	-0.141	0.891354	0.957565
9224	10373515	NM_173733	211389	sulfite oxidase	Suox	0.995	-0.384	0.711847	0.873734
9225	10463361	NM_183216	329065	stearoyl-coenzyme A desaturase	Scd4	0.995	0.15	0.88495	0.954857
9226	10479510	ENSMUST00000094214	320800	RIKEN cDNA 9230112E08 gene	9230112E08Rik	0.995	0.072	0.944816	0.978171
9227	10420483	NM_172603	219131	PHD finger protein 11	Phf11	0.995	0.561	0.59165	0.806879
9228	10459089	NM_008306	15531	N-deacetylase/N-sulfotransfera	Ndst1	0.995	-0.407	0.696002	0.866441
9229	10354432	NM_010863	17912	myosin IB	Myo1b	0.995	-0.066	0.949469	0.98056
9230	10408227	NM_010424	15216	hemochromatosis	Hfe	0.995	0.092	0.929119	0.972108
9231	10389190	NM_001045543	629303	predicted gene, OTTMUSG0000000	OTTMUSG00000000990	0.995	0.194	0.851667	0.940193
9232	10445909	NM_020005	18519	p300/CBP-associated factor	Pcaf	0.995	-0.25	0.809819	0.923213
9233	10575512	NM_133973	102339	component of oligomeric golgi	Cog4	0.995	-0.887	0.403741	0.6686
9234	10516241	BC065047	215090	gene model 50, (NCBI)	Gm50	0.995	-0.389	0.708644	0.872486
9235	10453082	NM_144802	72692	heterogeneous nuclear ribonucl	Hnrpll	0.995	-0.16	0.877167	0.951558
9236	10518520	NM_027873	71707	UbiA prenyltransferase domain	Ubiad1	0.995	-0.399	0.701673	0.869143
9237	10462699					0.995	-0.155	0.881392	0.953061
9238	10364072	NM_011820	23887	gamma-glutamyltransferase 5	Ggt5	0.995	0.328	0.75259	0.895764
9239	10451261	NM_145140	224814	ATP-binding cassette, sub-fami	Abcc10	0.995	-0.182	0.860747	0.943965
9240	10422504	NM_022987	65100	zinc finger protein of the cer	Zic5	0.995	-0.085	0.934947	0.974155
9241	10462846	NM_001105201	546726	cytochrome P450, family 26, su	Cyp26c1	0.995	0.169	0.870368	0.948269
9242	10580897	NM_027640	70993	RIKEN cDNA 4931432M23 gene	4931432M23Rik	0.995	0.12	0.907542	0.963723
9243	10577602					0.995	0.042	0.967949	0.987137
9244	10363575	NM_177372	327762	DNA replication helicase 2 hom	Dna2	0.995	-0.466	0.654647	0.845294
9245	10452356	NM_030084	78308	G protein-coupled receptor 108	Gpr108	0.995	-0.455	0.66217	0.84957
9246	10383235	BC056486	338371	RIKEN cDNA A730011L01 gene	A730011L01Rik	0.995	-0.236	0.819896	0.928345
9247	10525575	NM_001033461	381741	leucine rich repeat containing	Lrrc43	0.995	0.515	0.62211	0.827029
9248	10485514	NM_016739	53872	cell cycle associated protein	Caprin1	0.995	-0.237	0.819575	0.928312
9249	10595126	NM_023605	71538	f-box protein 9	Fbxo9	0.995	-0.033	0.974653	0.989251
9250	10533176	BC021365	100764	RIKEN cDNA 1110008J03 gene	1110008J03Rik	0.995	-0.23	0.824716	0.929565
9251	10360147	AK047216	100048917	RIKEN cDNA B930036N10 gene	B930036N10Rik	0.995	-0.016	0.987495	0.994834
9252	10538848	XR_033973	100042837	similar to protein (peptidyl-p	LOC100042837	0.995	0.11	0.915596	0.966659
9253	10529264	NM_133903	100689	spondin 2, extracellular matri	Spon2	0.995	0.502	0.630295	0.831532
9254	10410460	ENSMUST00000065118	76980	RIKEN cDNA 3110006E14 gene	3110006E14Rik	0.995	-0.029	0.977354	0.990677
9255	10602501	NM_021523	59026	HECT, UBA and WWE domain conta	Huwe1	0.995	-0.325	0.754114	0.896425
9256	10595863	NM_030219	78911	tripartite motif-containing 42	Trim42	0.995	0.209	0.840312	0.93543
9257	10580331	NM_022997	65114	vacuolar protein sorting 35	Vps35	0.995	-0.444	0.670205	0.85351
9258	10574232	NM_026452	67914	coenzyme Q9 homolog (yeast)	Coq9	0.995	-0.362	0.727562	0.881884
9259	10420775					0.995	0.283	0.785348	0.912507

9260	10595805	NM_053268	114713	RAS p21 protein activator 2	Rasa2	0.995	-0.07	0.945942	0.978614
9261	10598198	NM_177389	338366	melanoma inhibitory activity 3	Mia3	0.995	-0.341	0.742869	0.89053
9262	10487175	NM_009939	12848	COP9 (constitutive photomorpho	Cops2	0.995	-0.162	0.876035	0.95093
9263	10420209	NM_019820	56410	cerebellin 3 precursor protein	Cbln3	0.995	0.373	0.720172	0.878163
9264	10598079					0.995	-0.161	0.876141	0.950949
9265	10498058	NM_025523	66377	NADH dehydrogenase (ubiquinone	Ndufc1	0.995	-0.933	0.380887	0.650316
9266	10493103	NM_177663	229504	interferon stimulated exonucle	Isg20l2	0.995	-0.488	0.640178	0.836894
9267	10425283	NM_010755	17133	v-maf musculoaponeurotic fibro	Maff	0.995	-0.577	0.581446	0.800326
9268	10448755	ENSMUST00000097372	193838	essential meiotic endonuclease	Eme2	0.995	-0.212	0.838333	0.934421
9269	10532954	ENSMUST00000112121	109154	RIKEN cDNA 2410014A08 gene	2410014A08Rik	0.995	-0.375	0.718232	0.876988
9270	10438854	NM_172613	224079	ATPase type 13A4	Atp13a4	0.995	0.307	0.767371	0.903161
9271	10601324	NM_029158	75064	cellular nucleic acid binding	Cnbp2	0.995	-0.045	0.96512	0.986124
9272	10581246	NM_177791	279499	potassium channel tetramerisat	Kctd19	0.995	-0.235	0.820883	0.92863
9273	10446084	NM_172132	193796	jumonji domain containing 2B	Jmjd2b	0.995	0.299	0.773627	0.9067
9274	10582592	NM_009606	11459	actin, alpha 1, skeletal muscl	Acta1	0.995	-0.707	0.50157	0.744504
9275	10348910	NM_173772	241159	sialidase 4	Neu4	0.995	0.291	0.77907	0.910184
9276	10517250	NM_019578	56219	exostoses (multiple)-like 1	Extl1	0.995	-0.281	0.786589	0.912923
9277	10345172	ENSMUST00000064487	791399	predicted gene, ENSMUSG0000005	ENSMUSG00000052558	0.995	-0.258	0.80351	0.920138
9278	10436972	XM_487442	435489	predicted gene, EG435489	EG435489	0.995	-0.008	0.993555	0.997612
9279	10364251	NM_030262	80294	protein O-fucosyltransferase 2	Pofut2	0.995	-0.598	0.568221	0.793239
9280	10416522	NM_207652	21807	TSC22 domain family, member 1	Tsc22d1	0.995	-0.621	0.553846	0.783297
9281	10375326	ENSMUST00000061070	70802	PWWP domain containing 2A	Pwwp2a	0.994	-0.436	0.675889	0.855911
9282	10533687	NM_027494	70650	zinc finger, CCHC domain conta	Zcchc8	0.994	-0.009	0.993177	0.997422
9283	10466075	NM_133804	98170	transmembrane protein 132A	Tmem132a	0.994	-0.228	0.825876	0.929952
9284	10432677	XM_001479184	668225	predicted gene, EG668225	EG668225	0.994	-0.172	0.867946	0.947144
9285	10559504	NM_175529	243813	leukocyte receptor cluster (LR	Leng9	0.994	0.025	0.980467	0.991919
9286	10456798	NM_029826	76987	haloacid dehalogenase-like hyd	Hdhd2	0.994	-0.353	0.73453	0.886568
9287	10350128	ENSMUST00000067468	215714	predicted gene, EG215714	EG215714	0.994	0.288	0.781807	0.911385
9288	10406626	NM_147176	26556	homer homolog 1 (Drosophila)	Homer1	0.994	-0.206	0.842244	0.936059
9289	10512226	NM_026893	68970	WD repeat domain 40A	Wdr40a	0.994	-0.268	0.796095	0.91721
9290	10538545	ENSMUST00000087544	100038736	predicted gene, ENSMUSG0000006	ENSMUSG00000067371	0.994	0.247	0.811729	0.923946
9291	10450735	NM_008208	15043	histocompatibility 2, T region	H2-T3	0.994	-0.262	0.800774	0.919467
9292	10517009	NM_031393	269589	synaptotagmin-like 1	Sytl1	0.994	-0.024	0.981533	0.992092
9293	10386352	NM_080454	118454	gap junction protein, gamma 2	Gjc2	0.994	0.227	0.826954	0.930622
9294	10382096	ENSMUST00000009354	75573	RIKEN cDNA 2310007L24 gene	2310007L24Rik	0.994	-0.014	0.989477	0.995361
9295	10413502	NM_027493	56249	ARP8 actin-related protein 8 h	Actr8	0.994	-0.742	0.481298	0.730704
9296	10527801	NM_001081001	12190	breast cancer 2	Brca2	0.994	-0.274	0.792008	0.915332
9297	10576538	NM_174854	244667	disrupted in schizophrenia 1	Disc1	0.994	0.109	0.915948	0.966745
9298	10345706	BC049091	52846	DNA segment, Chr 1, Brigham &	D1Bwg0212e	0.994	-0.449	0.666574	0.851355
9299	10409526	BC025483	212483	cDNA sequence BC021381	BC021381	0.994	0.077	0.94077	0.977
9300	10560993	NM_001031667	606496	glycogen synthase kinase 3 alp	Gsk3a	0.994	-0.225	0.828244	0.930848
9301	10581902	NM_011801	23837	craniofacial development prote	Cfdp1	0.994	-0.205	0.843167	0.93639
9302	10477042	NM_009641	11602	angiopoietin 4	Angpt4	0.994	0.04	0.968878	0.987519
9303	10558090	NM_001004468	57752	transforming, acidic coiled-co	Tacc2	0.994	-0.474	0.649262	0.842415
9304	10497169	XR_030720	620283	similar to mCBP	LOC620283	0.994	-0.116	0.910501	0.964214
9305	10596568	ENSMUST00000098424	109095	RNA binding motif protein 15B	Rbm15b	0.994	-0.383	0.712421	0.874053
9306	10427083	NM_145625	75705	eukaryotic translation initiat	Eif4b	0.994	-0.413	0.691309	0.864541
9307	10389617	NM_177167	320472	protein phosphatase 1E (PP2C d	Ppm1e	0.994	-0.176	0.864924	0.946153
9308	10425905	NM_016714	18141	nucleoporin 50	Nup50	0.994	-0.514	0.622834	0.827402
9309	10586616	NM_177184	320528	vacuolar protein sorting 13C (	Vps13c	0.994	-0.271	0.79382	0.91617
9310	10570189	NM_009233	20664	SRY-box containing gene 1	Sox1	0.994	-0.871	0.411974	0.67583
9311	10430647					0.994	-0.14	0.892241	0.957739

9312	10505630	NM_029949	77634	small nuclear RNA activating c	Snapc3	0.994	-0.547	0.60059	0.812284
9313	10453485					0.994	0.409	0.694441	0.865758
9314	10398929	NM_201646	399566	BTB (POZ) domain containing 6	Btbd6	0.994	0.019	0.985563	0.993996
9315	10448376	NM_029798	76917	FLYWCH family member 2	Flywch2	0.994	-1.272	0.242979	0.51587
9316	10466970	ENSMUST00000061906	553138	predicted gene, ENSMUSG0000004	ENSMUSG00000048936	0.994	-0.179	0.862987	0.945293
9317	10552725	NM_133945	101568	vaccinia related kinase 3	Vrk3	0.994	-0.542	0.604322	0.815222
9318	10567578					0.994	0.61	0.560319	0.787568
9319	10566698	NM_146726	258721	olfactory receptor 514	Olfr514	0.994	0.073	0.94345	0.977948
9320	10365145	NM_019725	21886	transducin-like enhancer of sp	Tle2	0.994	0.325	0.754716	0.896801
9321	10561017	NM_008776	18476	platelet-activating factor ace	Pafah1b3	0.994	-0.918	0.388189	0.656892
9322	10565609	NM_009381	21835	thyroid hormone responsive SPO	Thrsp	0.994	-0.11	0.915079	0.9666
9323	10387559	NM_030702	80886	SUMO/sentrin specific peptidas	Senp3	0.994	-0.448	0.667185	0.851407
9324	10399254	NM_134046	52504	centromere protein O	Cenpo	0.994	-0.503	0.62967	0.831325
9325	10528567	NM_001002897	213948	ATG9 autophagy related 9 homol	Atg9b	0.994	-0.045	0.965182	0.986124
9326	10471833	NM_010710	16870	LIM homeobox protein 2	Lhx2	0.994	-0.093	0.928402	0.971746
9327	10425527	NM_177821	328572	E1A binding protein p300	Ep300	0.994	-0.405	0.697503	0.867333
9328	10508112	NM_138721	116748	U7 snRNP-specific Sm-like prot	Lsm10	0.994	-0.316	0.760897	0.900252
9329	10554325	NM_029835	77011	RIKEN cDNA 5730590G19 gene	5730590G19Rik	0.994	-0.598	0.568423	0.793239
9330	10408062	NM_146744	258739	olfactory receptor 1362	Olfr1362	0.994	-0.104	0.920291	0.968139
9331	10607124	NM_001114385	83453	chordin-like 1	Chrdl1	0.994	-0.53	0.611932	0.820046
9332	10507826	NM_174998	170638	hippocalcin-like 4	Hpcal4	0.994	-0.164	0.874323	0.949978
9333	10482229	NM_011187	19177	proteasome (prosome, macropain	Psmb7	0.994	-0.424	0.684048	0.860099
9334	10570738					0.994	0.112	0.914259	0.966149
9335	10430711	NM_011399	20524	solute carrier family 25 (mito	Slc25a17	0.994	-0.933	0.380871	0.650316
9336	10581132	NM_007663	12556	cadherin 16	Cdh16	0.994	-0.381	0.713985	0.874805
9337	10410641	ENSMUST00000022064	432779	expressed sequence AI595366	AI595366	0.994	0.218	0.833593	0.932911
9338	10368762	BC061220	71713	cell division cycle 40 homolog	Cdc40	0.994	-0.349	0.737226	0.887888
9339	10547322	NM_009781	12288	calcium channel, voltage-depen	Cacna1c	0.994	-0.074	0.942825	0.977825
9340	10563615	NM_001005247	246694	Hermansky-Pudlak syndrome 5 ho	Hps5	0.994	0.018	0.986315	0.994262
9341	10507908	NM_010213	14201	four and a half LIM domains 3	Fhl3	0.994	0.065	0.950292	0.980767
9342	10580137					0.994	0.074	0.942886	0.977825
9343	10569441	NM_008672	17955	nucleosome assembly protein 1-	Nap1l4	0.994	-0.559	0.592871	0.807502
9344	10591263	NM_001002846	30843	F-box and leucine-rich repeat	Fbxl12	0.994	-0.129	0.901212	0.961171
9345	10427222	NM_144547	110542	anti-Mullerian hormone type 2	Amhr2	0.994	0.267	0.796901	0.917479
9346	10455199	NM_153793	225392	RELT-like 2	Rell2	0.994	-0.041	0.968504	0.987362
9347	10544660	NM_027881	71720	oxysterol binding protein-like	Osbpl3	0.994	-0.039	0.969793	0.987731
9348	10425757	BC092006	69029	RIKEN cDNA 1500032L24 gene	1500032L24Rik	0.994	-0.271	0.793749	0.916154
9349	10558707	NM_053194	101489	resistance to inhibitors of ch	Ric8	0.994	-0.728	0.489319	0.736434
9350	10438904	NM_028973	74488	leucine rich repeat containing	Lrrc15	0.994	0.245	0.813251	0.9249
9351	10418812	BC107222	67085	RIKEN cDNA 1700024G13 gene	1700024G13Rik	0.994	0.387	0.70999	0.873031
9352	10455019	NM_007766	12936	protocadherin alpha 4	Pcdha4	0.994	-0.304	0.769471	0.904525
9353	10596810	AK029954	19654	RNA binding motif protein 6	Rbm6	0.994	-0.143	0.890124	0.956731
9354	10550316	NM_026938	69094	transmembrane protein 160	Tmem160	0.993	-0.378	0.71657	0.875798
9355	10379820	NM_133360	107476	acetyl-Coenzyme A carboxylase	Acaca	0.993	-0.044	0.965747	0.986319
9356	10372407					0.993	-0.179	0.863155	0.945375
9357	10471036	NM_020329	57170	dolichyl pyrophosphate phospha	Dolpp1	0.993	-0.131	0.899047	0.960129
9358	10409970	NM_178875	71508	RIKEN cDNA 8430426H19 gene	8430426H19Rik	0.993	-0.404	0.698059	0.867716
9359	10528583	NM_007668	12568	cyclin-dependent kinase 5	Cdk5	0.993	-0.633	0.546448	0.777695
9360	10349345	NM_010133	13798	engrailed 1	En1	0.993	-0.077	0.940486	0.976893
9361	10382848	BC026936	74319	RIKEN cDNA 1110005A03 gene	1110005A03Rik	0.993	-0.075	0.942274	0.977825
9362	10529799	AK041797	791401	predicted gene,	ENSMUSG00000054483	0.993	0.126	0.903147	0.962265

9362	10529799	AK041797	791401	ENSMUSG0000005	ENSMUSG00000054483	0.993	0.126	0.903147	0.962265
9363	10376263	NM_145426	216760	microfibrillar-associated prot	Mfap3	0.993	-0.63	0.547875	0.778543
9364	10371230	NM_010301	14672	guanine nucleotide binding pro	Gna11	0.993	-1.138	0.291517	0.567624
9365	10380417					0.993	0.028	0.978115	0.991187
9366	10352393	NM_012058	27058	signal recognition particle 9	Srp9	0.993	0.133	0.897831	0.959787
9367	10498775	NM_175193	73124	golgi integral membrane protei	Golim4	0.993	-0.293	0.777895	0.909621
9368	10512411	NM_053081	60534	Fanconi anemia, complementatio	Fancg	0.993	-0.104	0.920044	0.968088
9369	10448694	NM_011522	20974	synaptogyrin 3	Syngr3	0.993	0.309	0.765834	0.902563
9370	10459999	NM_178280	20689	sal-like 3 (Drosophila)	Sall3	0.993	0.208	0.841171	0.935777
9371	10561004	NM_010155	13875	Ets2 repressor factor	Erf	0.993	-0.672	0.522749	0.759448
9372	10435963	NM_026402	67841	autophagy-related 3 (yeast)	Atg3	0.993	-0.515	0.622162	0.827046
9373	10451451	NM_010321	14711	glycine N-methyltransferase	Gnmt	0.993	0.325	0.754565	0.896724
9374	10407141	NM_175497	238880	actin, beta-like 2	Actbl2	0.993	0.407	0.695585	0.866211
9375	10463242	BC049116	71146	RIKEN cDNA 4933417O08 gene	4933417O08Rik	0.993	-0.036	0.9724	0.98815
9376	10516229	NM_026031	67205	UTP11-like, U3 small nucleolar	Utp11l	0.993	-0.253	0.807697	0.922567
9377	10393453	ENSMUST00000084803	69926	dynein, axonemal, heavy chain	Dnahc17	0.993	0.001	0.999326	0.999589
9378	10528864	NM_175651	269637	canopy 1 homolog (zebrafish)	Cnpy1	0.993	0.175	0.86553	0.946261
9379	10593418	NM_024441	69253	heat shock protein 2	Hspb2	0.993	-0.065	0.949953	0.980663
9380	10502686	NM_019957	56629	deoxyribonuclease II beta	Dnase2b	0.993	-0.072	0.944243	0.977948
9381	10518857	NM_133879	100090	zinc finger and BTB domain con	Zbtb48	0.993	-0.234	0.821574	0.92863
9382	10345879	NM_008900	18993	POU domain, class 3, transcrip	Pou3f3	0.993	0.026	0.97996	0.991919
9383	10533401	ENSMUST00000111752	13048	cut-like homeobox 2	Cux2	0.993	-0.381	0.713902	0.874754
9384	10485225	NM_010163	14043	exostoses (multiple) 2	Ext2	0.993	-0.507	0.627143	0.830395
9385	10587211	NM_001039522	235497	Leo1, Paf1/RNA polymerase II c	Leo1	0.993	-0.54	0.605408	0.815953
9386	10474123	NM_029635	76501	COMM domain containing 9	Commd9	0.993	-0.498	0.633544	0.833323
9387	10574141					0.993	0.289	0.780554	0.910911
9388	10478926	ENSMUST00000077067	619302	RIKEN cDNA 1700101G07 gene	1700101G07Rik	0.993	-0.087	0.933149	0.973336
9389	10572779	NM_026455	67922	RIKEN cDNA 2510049I19 gene	2510049I19Rik	0.993	-0.183	0.859885	0.943624
9390	10534537	ENSMUST00000111153	109267	scavenger receptor cysteine ri	Srcrb4d	0.993	-0.089	0.931191	0.972759
9391	10584615	NM_021424	58235	poliovirus receptor-related 1	Pvrl1	0.993	-0.278	0.788676	0.91399
9392	10523516	ENSMUST00000046721	75129	RIKEN cDNA 4930524J08 gene	4930524J08Rik	0.993	-0.47	0.652275	0.844168
9393	10360028	NM_001077189	14130	Fc receptor, IgG, low affinity	Fcgr2b	0.993	-0.027	0.979305	0.991782
9394	10434808	NM_175165	71338	transformation related protein	Tprg	0.993	-0.02	0.984483	0.993457
9395	10604599					0.993	-0.095	0.927108	0.971253
9396	10577125	NM_172750	234072	ADP-ribosylhydrolase like 1	Adprhl1	0.993	0.285	0.783312	0.911971
9397	10352066	NM_029756	76816	serologically defined colon ca	Sdccag8	0.993	-0.131	0.899651	0.960245
9398	10480477	NM_011040	18510	paired box gene 8	Pax8	0.993	-0.235	0.820845	0.92863
9399	10581378	NM_013640	19171	proteasome (prosome, macropain	Psmb10	0.993	-0.888	0.40316	0.668374
9400	10584524	XR_001606	72224	RIKEN cDNA 1700001J11 gene	1700001J11Rik	0.993	0.598	0.568316	0.793239
9401	10438527	NM_028420	73047	calcium/calmodulin-dependent p	Camk2n2	0.993	-0.515	0.622239	0.827079
9402	10407467	NM_018859	56043	aldo-keto reductase family 1,	Akr1e1	0.993	-0.038	0.970687	0.988127
9403	10570741	NM_007843	13214	defensin beta 1	Defb1	0.993	0.329	0.751769	0.895263
9404	10375307	NM_026979	69183	C1q and tumor necrosis factor	C1qtnf2	0.993	-0.204	0.844016	0.936644
9405	10359078					0.993	-0.085	0.934304	0.97382
9406	10589464	ENSMUST00000098355	100038739	predicted gene, ENSMUSG0000007	ENSMUSG00000074056	0.993	-0.023	0.982423	0.9924
9407	10348321	BC048957	227333	diacylglycerol kinase, delta	Dgkd	0.993	-0.587	0.575071	0.797076
9408	10474381	NM_139303	228421	kinesin family member 18A	Kif18a	0.993	-1.24	0.253717	0.527959
9409	10594015	NM_029212	382077	coiled-coil domain containing	Ccdc33	0.993	0.189	0.855269	0.941477
9410	10488195	NM_024281	81910	ribosome binding protein 1	Rrbp1	0.993	-0.206	0.84254	0.936185
9411	10561854	NM_025548	66411	tubulin folding cofactor B	Tbcb	0.993	-0.893	0.400588	0.666392
9412	10534966	NM_019747	56314	zinc finger protein 113	Zfp113	0.993	-0.489	0.639691	0.836568
9413	10579600	ENSMUST00000066837	791308	predicted gene, ENSMUSG0000005	ENSMUSG00000054044	0.993	0.353	0.734227	0.886455
9414	10471840					0.993	-0.103	0.920534	0.968204
9415	10377662	NM_016875	53422	Y box protein 2	Ybx2	0.993	-0.32	0.757978	0.898457

9416	10501098	NM_145922	99738	potassium voltage gated channe	Kcnc4	0.993	0.139	0.892926	0.957774
9417	10407907	NM_019491	56044	v-ral simian leukemia viral on	Rala	0.993	-0.563	0.590312	0.806156
9418	10606544					0.993	0.136	0.895551	0.959003
9419	10356689	NM_172850	241158	ankyrin repeat and MYND domain	Ankmy1	0.993	-0.233	0.821873	0.92863
9420	10454030	NM_027687	71132	calcium-binding tyrosine-(Y)-p	Cabyr	0.993	-0.168	0.871199	0.948575
9421	10570131	NM_011919	26356	inhibitor of growth family, me	Ing1	0.993	-0.56	0.592312	0.807145
9422	10512598	NM_001007463	433700	sperm associated antigen 8	Spag8	0.993	-0.44	0.672885	0.854651
9423	10468916	NM_001081161	269233	RIKEN cDNA 9630050M13 gene	9630050M13Rik	0.993	-0.181	0.861448	0.944333
9424	10471586	NM_022310	14828	heat shock protein 5	Hspa5	0.993	-0.513	0.623177	0.827667
9425	10345895	NM_053107	93690	G protein-coupled receptor 45	Gpr45	0.993	-0.049	0.962082	0.985362
9426	10383943	NM_007968	14030	Ewing sarcoma breakpoint regio	Ewsr1	0.993	-0.254	0.806386	0.921832
9427	10383754					0.993	-0.328	0.751976	0.895376
9428	10379685	NM_025492	66330	RIKEN cDNA 1700020L24 gene	1700020L24Rik	0.993	0.229	0.825042	0.92959
9429	10547985	NM_001033126	21940	CD27 antigen	Cd27	0.993	0.357	0.731014	0.883888
9430	10403511	NM_144835	217995	HEAT repeat containing 1	Heatr1	0.993	-0.405	0.697419	0.867333
9431	10534405	NM_025375	66138	Williams Beuren syndrome chrom	Wbscr22	0.993	-0.347	0.738539	0.88853
9432	10560873	NM_019981	56746	testis expressed gene 101	Tex101	0.993	0.154	0.881888	0.953353
9433	10477630	NM_025947	67068	dynein light chain roadblock-t	Dynlrb1	0.993	-0.367	0.723992	0.88046
9434	10399189	NM_177082	320145	trans-acting transcription fac	Sp8	0.993	0.168	0.871457	0.948625
9435	10570068	NM_009932	12827	collagen, type IV, alpha 2	Col4a2	0.993	0.294	0.776712	0.908994
9436	10567919	NM_183020	233871	ataxin 2-like	Atxn2l	0.993	-0.144	0.889788	0.956712
9437	10454966	NM_011879	24010	IK cytokine	Ik	0.993	-0.415	0.68992	0.863942
9438	10426773	NM_175087	11831	aquaporin 6	Aqp6	0.993	0.073	0.943985	0.977948
9439	10490053	NM_001033299	228913	zinc finger protein 217	Zfp217	0.992	-0.275	0.791168	0.915023
9440	10419999	NM_177049	319984	junctophilin 4	Jph4	0.992	0.032	0.975374	0.989745
9441	10562761	NM_009131	20256	C-type lectin domain family 11	Clec11a	0.992	-0.134	0.89693	0.95959
9442	10447617					0.992	-0.564	0.590016	0.805977
9443	10382367	ENSMUST00000100243	100038601	predicted gene, OTTMUSG0000000	OTTMUSG00000003387	0.992	0.21	0.83967	0.935306
9444	10417208					0.992	-0.312	0.764153	0.90173
9445	10442719	ENSMUST00000073277	207209	gene model 317, (NCBI)	Gm317	0.992	0.123	0.905333	0.963331
9446	10527213	NM_144915	231871	diacylglycerol lipase, beta	Daglb	0.992	0.209	0.840038	0.935328
9447	10563101	NM_009438	22121	ribosomal protein L13a	Rpl13a	0.992	-0.291	0.77928	0.910287
9448	10581388	NM_008490	16816	lecithin cholesterol acyltrans	Lcat	0.992	-0.186	0.857229	0.942404
9449	10348087	NM_172974	26895	COP9 (constitutive photomorpho	Cops7b	0.992	-0.371	0.721305	0.878631
9450	10560919	NM_144921	232975	ATPase, Na+/K+ transporting, a	Atp1a3	0.992	0.008	0.994061	0.997702
9451	10539665	NM_012013	26910	folliculogenesis specific basi	Figla	0.992	-0.315	0.761622	0.900675
9452	10387568	NM_001034097	619441	tumor necrosis factor (ligand)	Tnfsf12-tnfsf13	0.992	0.085	0.934605	0.973973
9453	10460018	ENSMUST00000097504	329002	zinc finger protein 236	Zfp236	0.992	-0.496	0.634761	0.833935
9454	10531420	NM_019494	56066	chemokine (C-X-C motif) ligand	Cxcl11	0.992	-0.102	0.921321	0.968644
9455	10458581	ENSMUST00000071086	791268	predicted gene, ENSMUSG0000005	ENSMUSG00000056742	0.992	-0.222	0.830774	0.932075
9456	10445434	NM_026768	68565	mitochondrial ribosomal protei	Mrps18a	0.992	-0.665	0.526726	0.762763
9457	10461758	BC010803	64697	kidney expressed gene 1	Keg1	0.992	0.089	0.931409	0.972759
9458	10591634	NM_177030	319899	dedicator of cytokinesis 6	Dock6	0.992	-0.072	0.94429	0.977948
9459	10407251	NM_001081062	218630	cyclin O	Ccno	0.992	-0.104	0.920235	0.968133
9460	10395250					0.992	0.024	0.981712	0.992129
9461	10580850					0.992	0.068	0.94732	0.979133
9462	10538318	NM_025816	52440	Tax1 (human T-cell leukemia vi	Tax1bp1	0.992	-0.681	0.517255	0.756501
9463	10505791	NM_001081184	230393	cDNA sequence BC057079	BC057079	0.992	-0.453	0.66388	0.850267
9464	10498371	NM_027571	70839	purinergic receptor P2Y, G-pro	P2ry12	0.992	-0.129	0.900779	0.960826
9465	10488879	NM_008180	14854	glutathione synthetase	Gss	0.992	-0.257	0.804679	0.920977
9466	10510914	BC068299	242800	RIKEN cDNA B230396O12 gene	B230396O12Rik	0.992	-0.108	0.916946	0.967219

9467	10507131	NM_011527	21349	T-cell acute lymphocytic leuke	Tal1	0.992	0.07	0.946073	0.978614
9468	10476401	NM_019677	18795	phospholipase C, beta 1	Plcb1	0.992	0.052	0.959819	0.984926
9469	10375547	NM_206822	18307	olfactory receptor 10	Olfr10	0.992	0.212	0.838096	0.934421
9470	10465740	XR_031281	620946	similar to hCG2043493	LOC620946	0.992	0.193	0.852459	0.940498
9471	10414932					0.992	0.381	0.713829	0.874714
9472	10417940	NM_175132	68760	synaptopodin 2-like	Synpo2l	0.992	-0.037	0.971257	0.988148
9473	10352097	NM_027077	69428	RIKEN cDNA 1700016C15 gene	1700016C15Rik	0.992	-0.103	0.920562	0.968204
9474	10425370	NM_001044308	239556	calcium channel, voltage-depen	Cacna1i	0.992	-0.109	0.916215	0.966842
9475	10535065	NM_172723	231821	centaurin, alpha 1	Centa1	0.992	0.052	0.960185	0.985016
9476	10415030	NM_026936	69089	oxidase assembly 1-like	Oxa1l	0.992	-0.968	0.364398	0.635557
9477	10478495	NM_001048227	52840	dysbindin (dystrobrevin bindin	Dbndd2	0.992	0.008	0.99386	0.997702
9478	10416256	NM_021328	57784	bridging integrator 3	Bin3	0.992	-0.368	0.723576	0.880282
9479	10504652					0.992	-0.113	0.913062	0.965385
9480	10387871	NM_029231	75273	proline, glutamic acid and leu	Pelp1	0.992	-0.566	0.588483	0.805157
9481	10449765	AK138248	623548	predicted gene, ENSMUSG0000000	ENSMUSG00000002791	0.992	-0.243	0.815045	0.925775
9482	10577326	NM_176951	319581	X Kell blood group precursor-r	Xkr5	0.992	-0.022	0.98268	0.992443
9483	10487597	NM_008361	16176	interleukin 1 beta	Il1b	0.992	-0.122	0.906319	0.963405
9484	10492971	NM_178165	229499	Fc receptor-like 1	Fcrl1	0.992	1.038	0.332718	0.608795
9485	10490510	NM_175551	23856	death inducer-obliterator 1	Dido1	0.992	-0.213	0.837194	0.934421
9486	10412616	NM_025938	67053	ribonuclease P 14 subunit (hum	Rpp14	0.992	-1.095	0.30865	0.585248
9487	10376986	AK046601	791305	predicted gene, ENSMUSG0000005	ENSMUSG00000052860	0.992	0.286	0.783246	0.911971
9488	10442302	NM_001033425	332221	zinc finger and SCAN domain co	Zscan10	0.992	-0.14	0.892121	0.957703
9489	10454564	NM_133658	13872	excision repair cross-compleme	Ercc3	0.992	-1.034	0.334428	0.60995
9490	10529068	NM_011773	22784	solute carrier family 30 (zinc	Slc30a3	0.992	-0.037	0.971357	0.988148
9491	10596263					0.992	-0.06	0.954136	0.982421
9492	10431564	NM_009948	12895	carnitine palmitoyltransferase	Cpt1b	0.992	-0.164	0.874059	0.949893
9493	10392259	ENSMUST00000100311	66313	SMAD specific E3 ubiquitin pro	Smurf2	0.992	-0.37	0.721948	0.879059
9494	10433088	NM_007626	12419	chromobox homolog 5 (Drosophil	Cbx5	0.992	-0.024	0.981624	0.992092
9495	10569733	NM_133962	102098	rho/rac guanine nucleotide exc	Arhgef18	0.992	-0.264	0.798833	0.918762
9496	10516880	NM_001081651	242681	RIKEN cDNA 9530096D07 gene	9530096D07Rik	0.992	-0.004	0.996707	0.998777
9497	10408810					0.992	0.141	0.892021	0.95769
9498	10449873	NM_212438	22404	widely-interspaced zinc finger	Wiz	0.992	-0.472	0.650895	0.843602
9499	10371159	NM_019757	56371	fizzy/cell division cycle 20 r	Fzr1	0.992	-0.263	0.799821	0.919199
9500	10398814	NM_001097621	668303	kinesin family member 26A	Kif26a	0.992	0.086	0.933446	0.973406
9501	10479933	XR_031822	634939	similar to TRAF-interacting pr	LOC634939	0.992	-0.19	0.854526	0.94107
9502	10477737					0.992	0.33	0.750774	0.894733
9503	10480849	NM_007995	14133	ficolin A	Fcna	0.992	0.466	0.654759	0.845294
9504	10438702	BC106179	320099	cDNA sequence BC106179	BC106179	0.992	-0.209	0.840507	0.935549
9505	10357570	NM_001009940	329244	interleukin 19	Il19	0.992	0.063	0.951153	0.981129
9506	10540191	NM_011630	22026	nuclear receptor subfamily 2,	Nr2c2	0.992	-0.457	0.660975	0.84894
9507	10550870	NM_029806	76942	Ly6/Plaur domain containing 5	Lypd5	0.992	0.062	0.952194	0.981389
9508	10522208	NM_011670	22223	ubiquitin carboxy-terminal hyd	Uchl1	0.992	-0.776	0.462369	0.716898
9509	10430140	NM_013593	17189	myoglobin	Mb	0.992	0.431	0.679255	0.857678
9510	10379627					0.992	-0.44	0.672961	0.854651
9511	10357292	NM_025860	66942	DEAD (Asp-Glu-Ala-Asp) box pol	Ddx18	0.992	-0.786	0.456793	0.712642
9512	10602772	NM_148945	110651	ribosomal protein S6 kinase po	Rps6ka3	0.992	-0.458	0.66033	0.848652
9513	10479649	NM_133701	68879	PRP6 pre-mRNA splicing factor	Prpf6	0.992	-0.683	0.516106	0.755582
9514	10528077	NM_013726	27214	DBF4 homolog (S. cerevisiae)	Dbf4	0.992	0.055	0.957638	0.983978
9515	10532984	NM_019682	56455	dynein light chain LC8-type 1	Dynll1	0.992	-0.502	0.630494	0.831639
9516	10546217	NM_025351	66098	coiled-coil-helix-coiled-coil-	Chchd6	0.992	-0.403	0.698845	0.868075
9517	10380137	NM_172449	207777	benzodiazapine receptor associ	Bzrap1	0.992	-0.139	0.89318	0.957774
9518	10397068	NM_027349	67039	RNA binding motif protein 25	Rbm25	0.992	-0.049	0.962035	0.985362

9518	10597068	NM_027349	67039	RNA binding motif protein 25	Rbm25	0.992	-0.049	0.962055	0.983362
9519	10571634	NM_026278	67620	Lrp2 binding protein	Lrp2bp	0.992	-0.034	0.973524	0.988697
9520	10392318	NM_176850	207165	bromodomain PHD finger transcr	Bptf	0.991	-0.49	0.638638	0.835923
9521	10399825	NM_007861	13382	dihydrolipoamide dehydrogenase	Dld	0.991	-0.599	0.567788	0.792987
9522	10474698					0.991	0.15	0.884708	0.954694
9523	10568968	ENSMUST00000026553	74075	synaptonemal complex central e	Syce1	0.991	0.002	0.998523	0.999521
9524	10397416	BC038915	76411	RIKEN cDNA 1700019E19 gene	1700019E19Rik	0.991	-0.524	0.615672	0.822286
9525	10350864	NM_033354	89867	SEC16 homolog B (S. cerevisiae	Sec16b	0.991	-0.39	0.707661	0.872268
9526	10395604	ENSMUST00000056234	620583	predicted gene, ENSMUSG0000004	ENSMUSG00000045946	0.991	-0.408	0.694806	0.866071
9527	10579731	NM_027485	70625	mediator complex subunit 26	Med26	0.991	-0.606	0.56284	0.789799
9528	10425985					0.991	0.726	0.490743	0.737369
9529	10577645	NM_145949	209176	indoleamine-pyrrole 2,3 dioxyg	Indol1	0.991	0.244	0.814155	0.925212
9530	10487109	NM_001081091	99100	centrosomal protein 152	Cep152	0.991	0.213	0.837073	0.934383
9531	10509858	NM_023374	67680	succinate dehydrogenase comple	Sdhb	0.991	-0.622	0.552926	0.782578
9532	10470907	AK031561	56086	SET translocation	Set	0.991	0.433	0.677937	0.856898
9533	10563050	NM_175022	233210	proline rich 12	Prr12	0.991	-0.299	0.773637	0.9067
9534	10526956	NM_013702	22255	UNC homeobox	Uncx	0.991	0.237	0.819028	0.928106
9535	10527186	NM_133355	170935	glutamate receptor, ionotropic	Grid2ip	0.991	-0.038	0.970762	0.988147
9536	10427125	NM_008344	16012	insulin-like growth factor bin	Igfbp6	0.991	0.105	0.919168	0.967863
9537	10446592	ENSMUST00000003366	224997	discs, large (Drosophila) homo	Dlgap1	0.991	-0.061	0.952665	0.981683
9538	10585749	NM_009992	13076	cytochrome P450, family 1, sub	Cyp1a1	0.991	0.025	0.9806	0.991919
9539	10505627	XM_001477111	100046944	hypothetical protein LOC100046	LOC100046944	0.991	-0.075	0.941949	0.977644
9540	10437775	ENSMUST00000100177	70100	RIKEN cDNA 2310015D24 gene	2310015D24Rik	0.991	0.052	0.960123	0.985
9541	10469786	NM_153511	215257	interleukin 1 family, member 9	Il1f9	0.991	0.287	0.782117	0.911385
9542	10468593	NM_008733	18175	nebulin-related anchoring prot	Nrap	0.991	-0.129	0.901257	0.961171
9543	10591869	NM_020586	80517	HERPUD family member 2	Herpud2	0.991	-0.186	0.857649	0.94267
9544	10431912					0.991	-0.089	0.931629	0.972759
9545	10472562	NM_001081087	228003	kelch repeat and BTB (POZ) dom	Kbtbd10	0.991	-0.051	0.960671	0.985069
9546	10465474	NM_012021	54683	peroxiredoxin 5	Prdx5	0.991	-0.812	0.442532	0.701207
9547	10476872					0.991	0.239	0.818046	0.927633
9548	10512628	NM_019476	29849	olfactory receptor 159	Olfr159	0.991	-0.022	0.98311	0.992718
9549	10608024					0.991	0.025	0.98072	0.991919
9550	10554475	NM_178707	233410	zinc finger protein 592	Zfp592	0.991	-0.07	0.946108	0.978614
9551	10425031	ENSMUST00000048285	71939	apolipoprotein L 6	Apol6	0.991	-0.281	0.786634	0.912925
9552	10470027	NM_008721	18146	neural proliferation, differen	Npdc1	0.991	-0.071	0.945568	0.97847
9553	10559568	NM_001033548	436022	RIKEN cDNA 6030429G01 gene	6030429G01Rik	0.991	-0.604	0.564199	0.790603
9554	10367582	NM_011702	22353	vasoactive intestinal polypept	Vip	0.991	0.028	0.978564	0.991413
9555	10454580	NM_009668	30948	bridging integrator 1	Bin1	0.991	-0.784	0.45815	0.71339
9556	10413795	NM_028932	74427	ELL associated factor 1	Eaf1	0.991	-0.517	0.620811	0.825734
9557	10592503	NM_019465	54698	cytotoxic and regulatory T cel	Crtam	0.991	-0.01	0.992218	0.996933
9558	10510286	NM_027985	71890	MAD2 mitotic arrest deficient-	Mad2l2	0.991	-0.488	0.640229	0.836909
9559	10578045	NM_178591	211323	neuregulin 1	Nrg1	0.991	-0.217	0.834253	0.933071
9560	10448748	NM_011956	26426	nucleotide binding protein 2	Nubp2	0.991	0.052	0.960097	0.985
9561	10462752	NM_001080706	107182	BTAF1 RNA polymerase II, B-TFI	Btaf1	0.991	-0.357	0.731396	0.884161
9562	10347362					0.991	-0.114	0.912581	0.965167
9563	10430201	NM_022410	17886	myosin, heavy polypeptide 9, n	Myh9	0.991	-0.586	0.575641	0.797076
9564	10597764	NM_001081339	22437	xin actin-binding repeat conta	Xirp1	0.991	0.51	0.625177	0.829015
9565	10388109	NM_001024927	327958	PITPNM family member 3	Pitpnm3	0.991	-0.043	0.967125	0.986963
9566	10549780	NM_010147	13854	epsin 1	Epn1	0.991	-0.1	0.923109	0.969271
9567	10579070	NM_172754	234362	expressed sequence AI449175	AI449175	0.991	-0.761	0.470937	0.722763
9568	10556962	NM_177697	233813	von Willebrand factor A domain	Vwa3a	0.991	0.146	0.887624	0.955679
9569	10542229					0.991	0.182	0.86067	0.943954
9570	10576191	NM_153176	234847	spastic paraplegia 7 homolog (	Spg7	0.991	-0.802	0.448241	0.70581

9571	10367546	NM_001039652	18390	opioid receptor, mu 1	Oprm1	0.991	-0.128	0.901647	0.961371
9572	10600529					0.991	-0.301	0.772168	0.906083
9573	10579406	NM_027560	70807	arrestin domain containing 2	Arrdc2	0.991	-0.146	0.887655	0.955679
9574	10556135					0.991	0.343	0.741244	0.889595
9575	10558242	NM_145998	15372	H6 homeo box 2	Hmx2	0.991	-0.363	0.727159	0.881698
9576	10523275	XR_004671	674636	similar to ribosomal protein L	LOC674636	0.991	-0.234	0.821265	0.92863
9577	10461663	NM_025606	94063	mitochondrial ribosomal protei	Mrpl16	0.991	-0.751	0.476204	0.727414
9578	10494957	NM_026193	67489	adaptor-related protein comple	Ap4b1	0.991	-0.795	0.451873	0.708709
9579	10345228	ENSMUST00000051203	67503	RIKEN cDNA 1700001G17 gene	1700001G17Rik	0.991	-0.389	0.708742	0.872527
9580	10364301	ENSMUST00000092368	252974	RIKEN cDNA C330046G03 gene	C330046G03Rik	0.991	-0.135	0.896073	0.95935
9581	10448278	NM_001033339	240047	matrix metallopeptidase 25	Mmp25	0.991	-0.451	0.665363	0.850877
9582	10458843	NM_018744	20358	sema domain, transmembrane dom	Sema6a	0.991	-0.26	0.802164	0.919892
9583	10405355	NM_153131	107448	unc-5 homolog A (C. elegans)	Unc5a	0.991	0.07	0.946415	0.978837
9584	10499363	NM_001037939	12096	bone gamma carboxyglutamate pr	Bglap1	0.991	0.196	0.850137	0.939689
9585	10448582	NM_019988	56716	G protein beta subunit-like	Gbl	0.991	-0.45	0.66594	0.851154
9586	10431486	NM_001081030	77980	SET binding factor 1	Sbf1	0.991	-0.299	0.773467	0.9067
9587	10445992	NM_009168	20420	src homology 2 domain-containi	Shd	0.991	0.036	0.972334	0.98815
9588	10562044	NM_021397	58206	zinc finger and BTB domain con	Zbtb32	0.991	0.08	0.938545	0.976028
9589	10582429	NM_009824	12398	core-binding factor, runt doma	Cbfa2t3	0.991	0.049	0.962534	0.985405
9590	10357870	NM_054077	116847	proline arginine-rich end leuc	Prelp	0.991	0.199	0.84741	0.938194
9591	10407274					0.991	0.206	0.842338	0.936059
9592	10520982	NM_001025426	277854	DEP domain containing 5	Depdc5	0.991	-0.265	0.798204	0.918238
9593	10347988	ENSMUST00000027426	71141	RIKEN cDNA 4933407L21 gene	4933407L21Rik	0.991	0.026	0.979902	0.991919
9594	10458685	ENSMUST00000097589	76217	janus kinase and microtubule i	Jakmip2	0.991	-0.139	0.893179	0.957774
9595	10377405	NM_011496	20877	aurora kinase B	Aurkb	0.991	-0.538	0.606639	0.816784
9596	10451413	BC011248	224823	cDNA sequence BC011248	BC011248	0.991	0.09	0.930768	0.972759
9597	10380793	NM_139311	246198	myeloid/lymphoid or mixed-line	Mllt6	0.991	-0.176	0.865276	0.946164
9598	10516495	ENSMUST00000030614	635169	hypothetical LOC635169	LOC635169	0.991	-0.114	0.912149	0.964951
9599	10405994	NM_138596	28077	mediator of RNA polymerase II	Med10	0.991	-0.653	0.534306	0.768319
9600	10434528	NM_009893	12667	chordin	Chrd	0.991	-0.006	0.995214	0.998141
9601	10481101					0.991	-0.165	0.873356	0.949372
9602	10389064	NM_011329	20290	chemokine (C-C motif) ligand 1	Ccl1	0.991	-0.222	0.830757	0.932075
9603	10503856	NM_008076	14409	gamma-aminobutyric acid (GABA-	Gabrr2	0.991	-0.246	0.812719	0.924689
9604	10534660	NM_007457	11769	adaptor protein complex AP-1,	Ap1s1	0.99	-0.224	0.829161	0.931303
9605	10374106	NM_019661	56418	YKT6 homolog (S. Cerevisiae)	Ykt6	0.99	-0.673	0.522127	0.759088
9606	10413559	NM_177815	328370	RFT1 homolog (S. cerevisiae)	Rft1	0.99	0.055	0.957916	0.984168
9607	10426603	AK140384	100048895	predicted gene, ENSMUSG0000007	ENSMUSG00000075426	0.99	-0.414	0.690911	0.864447
9608	10490672	NM_029702	76688	ADP-ribosylation factor relate	Arfrp1	0.99	-0.891	0.40187	0.667094
9609	10525983	NM_009391	19384	RAN, member RAS oncogene famil	Ran	0.99	-0.272	0.793096	0.9157
9610	10375234	NM_026023	52653	NudC domain containing 2	Nudcd2	0.99	-0.155	0.880978	0.952856
9611	10606619	NM_013757	27359	synaptotagmin-like 4	Sytl4	0.99	0.055	0.958013	0.98422
9612	10364262	NM_008404	16414	integrin beta 2	Itgb2	0.99	-0.017	0.986593	0.994448
9613	10348180	NM_001039169	26987	eukaryotic translation initiat	Eif4e2	0.99	-0.544	0.602963	0.814375
9614	10368630	NM_025614	66521	RWD domain containing 1	Rwdd1	0.99	-0.285	0.783304	0.911971
9615	10384004	NM_178623	72046	RIKEN cDNA 2010005J08 gene	2010005J08Rik	0.99	-0.509	0.625901	0.829513
9616	10570472	NM_012000	26889	ceroid-lipofuscinosis, neurona	Cln8	0.99	-0.351	0.735504	0.886814
9617	10393387	NM_033398	107817	jumonji domain containing 6	Jmjd6	0.99	-0.356	0.732205	0.884722
9618	10485294	NM_019657	56348	hydroxysteroid (17-beta) dehyd	Hsd17b12	0.99	-0.695	0.509049	0.750516
9619	10406838	ENSMUST00000095522	667718	predicted gene, EG667718	EG667718	0.99	-0.099	0.923775	0.96976
9620	10511832	ENSMUST00000052917	319564	RIKEN cDNA C230012O17 gene	C230012O17Rik	0.99	-0.052	0.959754	0.984908

9621	10493490	NM_026767	68563	dolichyl-phosphate mannosyltra	Dpm3	0.99	-0.395	0.704608	0.870986
9622	10404575					0.99	0.207	0.841968	0.936059
9623	10429593	NM_011837	23934	lymphocyte antigen 6 complex,	Ly6h	0.99	0.166	0.872704	0.949165
9624	10430006	NM_028064	72027	solute carrier family 39 (zinc	Slc39a4	0.99	-0.14	0.892162	0.957703
9625	10472984	NM_010468	15434	homeo box D3	Hoxd3	0.99	-0.104	0.920033	0.968088
9626	10404063	NM_175660	319172	histone cluster 1, H2ab	Hist1h2ab	0.99	-0.641	0.541201	0.773605
9627	10593095	NM_001081373	214552	centrosomal protein 164	Cep164	0.99	0.062	0.952004	0.981385
9628	10552752	NM_026270	67605	AKT1 substrate 1 (proline-rich	Akt1s1	0.99	-0.197	0.849537	0.939222
9629	10523880	NM_144911	231571	RNA polymerase II associated p	Rpap2	0.99	-0.547	0.600571	0.812284
9630	10458816	NM_173394	225471	toll-like receptor adaptor mol	Ticam2	0.99	0.231	0.823557	0.929452
9631	10456414	NM_134138	107047	proteasome (prosome, macropain	Psmg2	0.99	-0.337	0.745382	0.891675
9632	10349510					0.99	-0.192	0.853134	0.940713
9633	10550003	NM_026112	67370	zinc finger protein 606	Zfp606	0.99	-0.477	0.647164	0.841007
9634	10468891					0.99	-0.122	0.906582	0.963405
9635	10458806	ENSMUST00000061488	72076	motile sperm domain containing	Mospd4	0.99	-0.02	0.98486	0.9936
9636	10390426					0.99	0.089	0.931584	0.972759
9637	10568376	BC017158	233913	cDNA sequence BC017158	BC017158	0.99	-0.098	0.924892	0.970324
9638	10355550	NM_178241	227288	interleukin 8 receptor, alpha	Il8ra	0.99	0.39	0.708116	0.872296
9639	10604169	NM_001025083	382282	reproductive homeobox 12	Rhox12	0.99	-0.209	0.840025	0.935328
9640	10455146	ENSMUST00000097608	320513	RIKEN cDNA 3222401L13 gene	3222401L13Rik	0.99	-0.407	0.695624	0.866211
9641	10541968	NM_153589	243634	transmembrane protein 16B	Tmem16b	0.99	0.014	0.988835	0.995308
9642	10486469	NM_147153	269338	vacuolar protein sorting 39 (y	Vps39	0.99	-0.778	0.46128	0.715891
9643	10554198	NM_182782	207952	kelch-like 25 (Drosophila)	Klhl25	0.99	-0.092	0.929396	0.972164
9644	10344725	NM_175236	76187	alcohol dehydrogenase, iron co	Adhfe1	0.99	0.043	0.967068	0.986963
9645	10589212	NM_007738	12836	collagen, type VII, alpha 1	Col7a1	0.99	0.004	0.997047	0.998842
9646	10591624	NM_177030	319899	dedicator of cytokinesis 6	Dock6	0.99	-0.387	0.709763	0.872992
9647	10530142					0.99	-0.438	0.673957	0.855115
9648	10583647	NM_001039520	13430	dynamin 2	Dnm2	0.99	-0.51	0.6252	0.829015
9649	10391103	NM_010593	16480	junction plakoglobin	Jup	0.99	-0.362	0.727677	0.88191
9650	10374931	ENSMUST00000101403	666427	predicted gene, EG666427	EG666427	0.99	0.083	0.936113	0.974841
9651	10568355	NM_023258	66824	PYD and CARD domain containing	Pycard	0.99	-0.397	0.702875	0.869709
9652	10517114					0.99	0.476	0.648364	0.841814
9653	10595614	BC032970	72655	RIKEN cDNA 2810026P18 gene	2810026P18Rik	0.99	-0.518	0.620291	0.825285
9654	10545932	NM_025665	66618	RIKEN cDNA 2610209M04 gene	2610209M04Rik	0.99	-0.613	0.559001	0.7865
9655	10582419	NM_001007462	382035	poly(A)binding protein nuclear	Pabpnl1	0.99	-0.072	0.944693	0.978132
9656	10463951	NM_007790	13006	structural maintenace of chrom	Smc3	0.99	-0.545	0.601891	0.813436
9657	10458382	NM_009841	12475	CD14 antigen	Cd14	0.99	-0.409	0.694108	0.865705
9658	10540984	NM_145383	212541	rhodopsin	Rho	0.99	0.121	0.906617	0.963405
9659	10348906	NM_001039219	619597	predicted gene, EG619597	EG619597	0.99	0.076	0.941754	0.977585
9660	10477966	NM_026968	69161	mannosidase, beta A, lysosomal	Manbal	0.99	-0.052	0.96007	0.985
9661	10517996	ENSMUST00000084203	69582	pleckstrin homology domain con	Plekhm2	0.99	-0.04	0.969099	0.987586
9662	10471438	NM_010073	13481	dolichol-phosphate (beta-D) ma	Dpm2	0.99	-0.558	0.593717	0.808186
9663	10403748					0.99	0.192	0.853232	0.940713
9664	10395064	NM_201357	380752	tumor suppressing subtransfera	Tssc1	0.99	-0.349	0.737277	0.887888
9665	10583496	NM_145610	235036	peter pan homolog (Drosophila)	Ppan	0.99	-0.476	0.648342	0.841814
9666	10529375	NM_010753	17122	Max dimerization protein 4	Mxd4	0.99	-0.232	0.822654	0.929111
9667	10347427	NM_175031	269209	serine/threonine kinase 36 (fu	Stk36	0.99	-0.075	0.942635	0.977825
9668	10464572	NM_133666	17995	NADH dehydrogenase (ubiquinone	Ndufv1	0.99	-0.553	0.596696	0.81005
9669	10401136	XR_032827	230765	similar to histone deacetylase	LOC230765	0.99	-0.563	0.590463	0.806248
9670	10429462	BC111897	69439	RIKEN cDNA 1700016M24 gene	1700016M24Rik	0.99	0.001	0.999089	0.999589
9671	10446715	NM_177087	320159	RIKEN cDNA 4632412N22 gene	4632412N22Rik	0.99	-0.127	0.902335	0.961642
9672	10573198	NM_018808	81489	DnaJ (Hsp40) homolog, subfamil	Dnajb1	0.99	-0.424	0.684158	0.86012

9673	10376721	NM_001085440	237782	Smith-Magenis syndrome chromos	Smcr8	0.99	-0.644	0.539449	0.772177
9674	10537880					0.99	0.93	0.382525	0.65196
9675	10594418	NM_008542	17130	MAD homolog 6 (Drosophila)	Smad6	0.99	-0.418	0.688373	0.862969
9676	10471703	BC036965	75495	RIKEN cDNA 1700010A17 gene	1700010A17Rik	0.99	0.144	0.889432	0.956457
9677	10426298					0.99	-0.217	0.834005	0.933071
9678	10471535	BC027843	227737	RIKEN cDNA 9130404D14 gene	9130404D14Rik	0.99	-0.425	0.683028	0.859827
9679	10579486	NM_181418	234395	Usher syndrome 1C binding prot	Ushbp1	0.989	0.177	0.864158	0.94589
9680	10419267	NM_009919	12793	cornichon homolog (Drosophila)	Cnih	0.989	-0.784	0.458017	0.713341
9681	10469611	XR_035323	442817	RIKEN cDNA C130046B21 gene	C130046B21Rik	0.989	0.115	0.911353	0.964566
9682	10505145	NM_001037127	18198	muscle, skeletal, receptor tyr	Musk	0.989	-0.212	0.837932	0.934421
9683	10477264	NM_133847	99237	transmembrane 9 superfamily pr	Tm9sf4	0.989	-0.53	0.612288	0.820234
9684	10479794	NM_026045	67229	PRP18 pre-mRNA processing fact	Prpf18	0.989	-0.453	0.663785	0.850267
9685	10532618	XM_912851	74376	myosin XVIIIb	Myo18b	0.989	-0.3	0.772615	0.906407
9686	10579165	NM_007789	13004	neurocan	Ncan	0.989	-0.314	0.762263	0.901088
9687	10528922	XR_001540	242914	predicted gene, EG242914	EG242914	0.989	-0.175	0.86587	0.94648
9688	10383991					0.989	-0.203	0.844637	0.93694
9689	10525296	NM_028227	72399	BRCA1 associated protein	Brap	0.989	-0.385	0.711443	0.873563
9690	10524227					0.989	-0.614	0.558347	0.78605
9691	10382571					0.989	0.309	0.765899	0.902563
9692	10580534					0.989	-0.711	0.499175	0.742494
9693	10433228	NM_029738	76779	clusterin associated protein 1	Cluap1	0.989	-0.627	0.55023	0.780495
9694	10514919	ENSMUST00000069271	56296	DMRT-like family B with prolin	Dmrtb1	0.989	-0.349	0.737244	0.887888
9695	10607473	XM_911239	270667	gene model 650, (NCBI)	Gm650	0.989	0.053	0.959116	0.98454
9696	10361698	NM_172785	237256	zinc finger CCCH type containi	Zc3h12d	0.989	-0.078	0.93981	0.976619
9697	10576118	ENSMUST00000059529	319574	RIKEN cDNA 9330133O14 gene	9330133O14Rik	0.989	-0.502	0.630583	0.831653
9698	10551273	NM_013809	13108	cytochrome P450, family 2, sub	Cyp2g1	0.989	-0.162	0.875828	0.950887
9699	10569152	NM_172116	213350	Parkinson disease 7 domain con	Pddc1	0.989	-0.263	0.799762	0.919181
9700	10607950					0.989	-0.244	0.814113	0.925212
9701	10424624	NM_174991	107831	brain-specific angiogenesis in	Bai1	0.989	-0.025	0.980436	0.991919
9702	10562634	XR_031546	637913	predicted gene, EG637913	EG637913	0.989	0.19	0.854396	0.94105
9703	10489566	NM_001082974	415115	neuralized-like 2 (Drosophila)	Neurl2	0.989	0.043	0.967018	0.986963
9704	10482434	NM_172662	227835	glycosyltransferase-like domai	Gtdc1	0.989	-0.877	0.408747	0.673095
9705	10593903	NM_025417	66199	COMM domain containing 4	Commd4	0.989	-0.439	0.673779	0.855069
9706	10378271	NM_025818	66874	RIKEN cDNA 1200014J11 gene	1200014J11Rik	0.989	-0.513	0.623251	0.827713
9707	10509590	NM_012044	26970	phospholipase A2, group IIE	Pla2g2e	0.989	0.168	0.871046	0.948568
9708	10424577	NM_053068	93696	chromatin accessibility comple	Chrac1	0.989	-1.005	0.347506	0.621575
9709	10558847	BC145719	101471	expressed sequence AA673488	AA673488	0.989	-0.54	0.605669	0.81605
9710	10465054	NM_198616	240514	coiled-coil domain containing	Ccdc85b	0.989	-0.355	0.733059	0.88559
9711	10595798	BC035950	270185	cDNA sequence BC043934	BC043934	0.989	0.318	0.759437	0.899229
9712	10491252	NM_029489	75953	sterile alpha motif domain con	Samd7	0.989	-0.31	0.765247	0.90237
9713	10497636	XR_002334	320352	leucine rich repeat containing	Lrrc31	0.989	-0.101	0.92218	0.968977
9714	10364950	NM_008655	17873	growth arrest and DNA-damage-i	Gadd45b	0.989	-0.555	0.595816	0.809631
9715	10365971	NM_007569	12226	B-cell translocation gene 1, a	Btg1	0.989	-0.217	0.833948	0.933071
9716	10370603	NM_001033473	382384	gene model 1157, (NCBI)	Gm1157	0.989	-0.51	0.625125	0.829015
9717	10474234	BC048438	68243	RIKEN cDNA A930018P22 gene	A930018P22Rik	0.989	-0.453	0.663739	0.850267
9718	10581033	ENSMUST00000087562	100038620	predicted gene, ENSMUSG0000007	ENSMUSG00000074128	0.989	-0.274	0.791708	0.915198
9719	10352292	ENSMUST00000097448	666457	predicted gene, EG666457	EG666457	0.989	-0.427	0.681991	0.85946
9720	10438091	BC039993	70458	RIKEN cDNA 2610318N02 gene	2610318N02Rik	0.989	0.194	0.851811	0.940193
9721	10513622	NM_021498	59001	polymerase (DNA directed), eps	Pole3	0.989	-0.34	0.743379	0.89069
9722	10566050	NM_010531	16068	interleukin 18 binding protein	Il18bp	0.989	0.408	0.694891	0.866071

9723	10432488	NM_029236	75284	BCDIN3 domain containing	Bcdin3d	0.989	-0.469	0.653099	0.844553
9724	10517988	NM_001013780	384071	solute carrier family 25, memb	Slc25a34	0.989	-0.035	0.972912	0.98829
9725	10387516	NM_011367	20415	sex hormone binding globulin	Shbg	0.989	0.152	0.88361	0.954141
9726	10577471	NM_177898	330721	NIMA (never in mitosis gene a)	Nek5	0.989	-0.216	0.834836	0.933323
9727	10373179	NM_010296	14632	GLI-Kruppel family member GLI1	Gli1	0.989	-0.224	0.828721	0.931153
9728	10346260	NM_028091	72085	O-sialoglycoprotein endopeptid	Osgepl1	0.989	-0.216	0.834725	0.933323
9729	10589685	NM_028838	74249	leucine rich repeat containing	Lrrc2	0.989	-0.138	0.894284	0.958327
9730	10551526	NM_177396	338374	interleukin 28B	Il28b	0.989	-0.148	0.886487	0.955393
9731	10605943	NM_028303	72621	PDZ domain containing 11	Pdzd11	0.989	-0.709	0.50084	0.743872
9732	10600539	BC127031	17143	melanoma antigen, family A, 7	Magea7	0.989	0.058	0.955418	0.982946
9733	10526654	XR_001865	640050	predicted gene, EG640050	EG640050	0.989	-0.245	0.81291	0.924742
9734	10550029	NM_022981	65020	zinc finger protein 110	Zfp110	0.989	-0.702	0.504483	0.746712
9735	10415392	NM_008519	16995	leukotriene B4 receptor 1	Ltb4r1	0.989	-0.194	0.851839	0.940193
9736	10432267	NM_011718	22410	wingless related MMTV integrat	Wnt10b	0.989	-0.126	0.902986	0.962141
9737	10401359	NM_058212	70127	D4, zinc and double PHD finger	Dpf3	0.989	-0.674	0.521213	0.758676
9738	10447695					0.989	0.217	0.834177	0.933071
9739	10444879	NM_020576	57390	psoriasis susceptibility 1 can	Psors1c2	0.989	0.324	0.755343	0.897145
9740	10419759	NM_013768	27374	protein arginine N-methyltrans	Prmt5	0.989	-0.465	0.655328	0.845667
9741	10567522	XM_355934	381917	dynein, axonemal, heavy chain	Dnahc3	0.989	0.206	0.842585	0.936186
9742	10501117	NM_026261	67591	ubiquitin-like 4B	Ubl4b	0.989	-0.199	0.847618	0.938277
9743	10508089	NM_025544	66407	mitochondrial ribosomal protei	Mrps15	0.989	-0.975	0.360906	0.632595
9744	10501286	NM_175183	72522	ataxin 7-like 2	Atxn7l2	0.989	-0.45	0.66579	0.851116
9745	10578547	NM_173789	234219	Hey-like transcription factor	Helt	0.989	-0.362	0.728066	0.882032
9746	10491455	NM_001113188	14359	fragile X mental retardation g	Fxr1	0.989	-0.434	0.676805	0.856344
9747	10500404					0.989	0.019	0.985639	0.994007
9748	10521088	ENSMUST00000101353	100038624	predicted gene, ENSMUSG0000007	ENSMUSG00000073044	0.989	-0.384	0.711749	0.873734
9749	10476689	ENSMUST00000099289	668917	similar to Zinc finger protein	LOC668917	0.989	-0.347	0.738572	0.88853
9750	10409063					0.989	0.404	0.697779	0.867515
9751	10468200	NM_024192	67116	CUE domain containing 2	Cuedc2	0.989	-0.492	0.637399	0.835535
9752	10518955	ENSMUST00000097768	407834	cDNA sequence BC049688	BC049688	0.989	-0.011	0.991533	0.996624
9753	10539592	NM_144918	232187	SET and MYND domain containing	Smyd5	0.989	-0.738	0.483699	0.732303
9754	10509985	NM_001085513	277743	gene model 693, (NCBI)	Gm693	0.989	-0.173	0.867506	0.946957
9755	10474057	BC100298	433456	RIKEN cDNA 4631405J19 gene	4631405J19Rik	0.989	-0.037	0.971327	0.988148
9756	10357436	NM_008567	17219	minichromosome maintenance def	Mcm6	0.989	-0.971	0.362944	0.63431
9757	10591497	NM_145416	215194	KRI1 homolog (S. cerevisiae)	Kri1	0.989	-0.328	0.752114	0.895422
9758	10557394	BC042743	233865	RIKEN cDNA D430042O09 gene	D430042O09Rik	0.989	-0.254	0.806313	0.921832
9759	10381133	NM_025727	66720	kelch-like 10 (Drosophila)	Klhl10	0.989	-0.009	0.992777	0.99722
9760	10441161	NM_008251	15312	high mobility group nucleosoma	Hmgn1	0.989	-0.192	0.85338	0.940713
9761	10481759	NM_019488	56017	solute carrier family 2, (faci	Slc2a8	0.989	-0.658	0.530819	0.76539
9762	10498623	NM_008467	16649	karyopherin (importin) alpha 4	Kpna4	0.989	-0.675	0.520457	0.757993
9763	10477887	BC020112	68295	RIKEN cDNA 0610011L14 gene	0610011L14Rik	0.989	-0.49	0.638854	0.835923
9764	10512098	NM_025545	66408	aprataxin	Aptx	0.989	-0.43	0.679781	0.85785
9765	10428209	ENSMUST00000100713	100038735	predicted gene, ENSMUSG0000007	ENSMUSG00000072618	0.989	0.093	0.928706	0.971962
9766	10397002	NM_172579	217692	signal-induced proliferation-a	Sipa1l1	0.988	-0.256	0.805069	0.921124
9767	10350710	BC113157	71836	RIKEN cDNA 1700012A16 gene	1700012A16Rik	0.988	-0.249	0.810284	0.923493
9768	10575074	NM_173037	272538	transmembrane and coiled-coil	Tmco7	0.988	-0.248	0.810801	0.923749
9769	10592752	NM_133226	170761	PDZ domain containing 3	Pdzd3	0.988	0.058	0.955485	0.98296
9770	10588482	NM_027354	70235	WD repeat domain 51A	Wdr51a	0.988	-0.64	0.542067	0.774475
9771	10449547					0.988	-0.176	0.864773	0.946153
9772	10370931	NM_021462	17347	MAP kinase-interacting serine/	Mknk2	0.988	-0.234	0.821136	0.92863
9773	10394075	NM_027622	70956	RIKEN cDNA 4921530G04 gene	4921530G04Rik	0.988	0.283	0.784989	0.912507

				gene					
9774	10571958	NM_021506	59009	SH3 domain containing ring fin	Sh3rf1	0.988	-0.445	0.669299	0.852817
9775	10519239	ENSMUST00000097733	100038526	predicted gene, ENSMUSG0000007	ENSMUSG00000073673	0.988	0.199	0.847976	0.938472
9776	10476834	NM_011917	24128	5'-3' exoribonuclease 2	Xrn2	0.988	-0.632	0.546758	0.777971
9777	10566350	NM_175648	244183	RIKEN cDNA A530023O14 gene	A530023O14Rik	0.988	0.141	0.891731	0.957629
9778	10518967	ENSMUST00000097764	68859	RIKEN cDNA 1190007F08 gene	1190007F08Rik	0.988	-0.37	0.721739	0.878906
9779	10407346					0.988	-0.405	0.696984	0.867134
9780	10386455	NM_009026	19416	RAS, dexamethasone-induced 1	Rasd1	0.988	-0.293	0.777979	0.909621
9781	10466302					0.988	0.186	0.857874	0.942819
9782	10555378	NM_009464	22229	uncoupling protein 3 (mitochon	Ucp3	0.988	-0.237	0.819407	0.928264
9783	10492951					0.988	0.188	0.856268	0.941981
9784	10356353	NM_007433	11650	alkaline phosphatase 5	Akp5	0.988	0.009	0.993446	0.997551
9785	10512688	BC094565	269529	F-box protein 10	Fbxo10	0.988	-0.219	0.832557	0.932679
9786	10496742	NM_025555	66421	RIKEN cDNA 2410004B18 gene	2410004B18Rik	0.988	-0.449	0.666612	0.851355
9787	10349348	NM_001025156	70829	coiled-coil domain containing	Ccdc93	0.988	-0.168	0.870896	0.948568
9788	10408787					0.988	-0.129	0.901133	0.961136
9789	10478580	NM_133924	101113	sorting nexin family member 21	Snx21	0.988	-0.109	0.916369	0.966925
9790	10583478	NM_001030290	235033	retinol dehydrogenase 8	Rdh8	0.988	0.235	0.820466	0.928587
9791	10386394	BC050078	237775	cDNA sequence BC050078	BC050078	0.988	-0.395	0.704114	0.870478
9792	10560247	NM_172297	243846	coiled-coil domain containing	Ccdc9	0.988	0.159	0.877906	0.951715
9793	10574617	BC026374	234677	cDNA sequence BC026374	BC026374	0.988	0.002	0.998135	0.99936
9794	10399234	NM_001082483	668212	EFR3 homolog B (S. cerevisiae)	Efr3b	0.988	-0.504	0.629355	0.831277
9795	10568017	NM_029420	75764	GIY-YIG domain containing 2	Giyd2	0.988	-0.011	0.991654	0.99665
9796	10406777	AK157788	218476	gene model 73, (NCBI)	Gm73	0.988	0.066	0.949488	0.98056
9797	10470564	NM_009058	19730	ral guanine nucleotide dissoci	Ralgds	0.988	-0.236	0.819699	0.928319
9798	10394776					0.988	-0.392	0.706403	0.871814
9799	10387838	NM_145684	11685	arachidonate lipoxygenase, epi	Alox12e	0.988	0.312	0.763967	0.90173
9800	10497754	NM_026332	67713	DnaJ (Hsp40) homolog, subfamil	Dnajc19	0.988	-0.814	0.44163	0.700534
9801	10581311	NM_001012638	497652	adrenocortical dysplasia	Acd	0.988	-0.47	0.652181	0.844159
9802	10347732					0.988	-0.522	0.617065	0.823029
9803	10555870	NM_146813	258809	olfactory receptor 651	Olfr651	0.988	-0.335	0.746804	0.892467
9804	10556458	NM_175279	78748	Ras association (RalGDS/AF-6)	Rassf10	0.988	-0.036	0.971922	0.988148
9805	10469923	NM_028093	72090	ectonucleoside triphosphate di	Entpd8	0.988	0.215	0.835368	0.933323
9806	10490467	NM_145851	252966	Cdk5 and Abl enzyme substrate	Cables2	0.988	-0.776	0.462684	0.717151
9807	10579874	NM_015751	24015	ATP-binding cassette, sub-fami	Abce1	0.988	-0.537	0.607736	0.817428
9808	10447773	NM_011395	20519	solute carrier family 22 (orga	Slc22a3	0.988	-0.224	0.828598	0.931115
9809	10598422	NM_207670	54645	GRIP1 associated protein 1	Gripap1	0.988	-0.514	0.622642	0.827306
9810	10543967	NM_001081206	320127	diacylglycerol kinase, iota	Dgki	0.988	-0.358	0.730618	0.883548
9811	10543231					0.988	-0.623	0.552188	0.782016
9812	10450482					0.988	0.141	0.891659	0.957629
9813	10482237	NM_139051	26423	nuclear receptor subfamily 5,	Nr5a1	0.988	0.275	0.790755	0.914692
9814	10370665	NM_198107	216154	mediator complex subunit 16	Med16	0.988	-0.465	0.655573	0.845931
9815	10463737	AK144917	226180	internexin neuronal intermedia	Ina	0.988	0.058	0.955229	0.982897
9816	10595803	NM_011279	19823	ring finger protein 7	Rnf7	0.988	-0.089	0.931468	0.972759
9817	10535900					0.988	0.133	0.897836	0.959787
9818	10382516	NM_183285	70382	potassium channel tetramerisat	Kctd2	0.988	-0.635	0.545299	0.777255
9819	10526566	NM_010144	13846	Eph receptor B4	Ephb4	0.988	-0.434	0.677123	0.856541
9820	10499924	NM_026811	68694	late cornified envelope 1E	Lce1e	0.988	0.193	0.852129	0.940318
9821	10507475					0.988	-0.193	0.852286	0.940441
9822	10405504	NM_007596	12328	calcium modulating ligand	Caml	0.988	-0.329	0.751476	0.895256
9823	10412177	NM_028151	72198	superkiller viralicidic activi	Skiv2l2	0.988	-0.588	0.574381	0.797076
9824	10537882	NM_012042	26965	cullin 1	Cul1	0.988	-0.438	0.674367	0.855358
9825	10459866	NM_028122	108052	solute carrier family 14 (urea	Slc14a1	0.988	-0.056	0.956994	0.983559
9826	10442381	NM_175440	213171	protease, serine 27	Prss27	0.988	-0.08	0.938129	0.975903

9827	10379721	NM_013652	20303	chemokine (C-C motif) ligand 4	Ccl4	0.988	-0.139	0.892991	0.957774
9828	10606071	NM_146235	236930	excision repair cross-compleme	Ercc6l	0.988	-0.184	0.859198	0.943452
9829	10449289	ENSMUST00000011196	73365	RIKEN cDNA 1700049J03 gene	1700049J03Rik	0.988	-0.123	0.905777	0.963405
9830	10371037	NM_134135	106947	solute carrier family 39 (zinc	Slc39a3	0.988	0.092	0.928932	0.972036
9831	10359334	NM_009786	12301	calcyclin binding protein	Cacybp	0.988	-0.771	0.465193	0.718903
9832	10486172	NM_001033136	67809	RIKEN cDNA 1200015F23 gene	1200015F23Rik	0.988	-0.423	0.684377	0.860314
9833	10494423	NM_027126	69585	hemochromatosis type 2 (juveni	Hfe2	0.988	-0.209	0.84003	0.935328
9834	10493247	NM_033526	94232	ubiquilin 4	Ubqln4	0.988	-0.081	0.937442	0.975553
9835	10399841	NM_134048	104836	Casitas B-lineage lymphoma-lik	Cbll1	0.988	-0.573	0.583832	0.801645
9836	10455050	NM_053127	93873	protocadherin beta 2	Pcdhb2	0.988	-0.282	0.785762	0.912565
9837	10534148	ENSMUST00000063656	381673	RIKEN cDNA A330070K13 gene	A330070K13Rik	0.988	0.081	0.937574	0.975641
9838	10512827	ENSMUST00000060283	230143	gene model 568, (NCBI)	Gm568	0.988	0.084	0.935609	0.974509
9839	10416942					0.988	-0.484	0.642795	0.838239
9840	10548180	NM_133927	101142	integrin alpha FG-GAP repeat c	Itfg2	0.988	0.014	0.988951	0.995308
9841	10409021	NM_016785	22017	thiopurine methyltransferase	Tpmt	0.988	-0.702	0.504821	0.747036
9842	10428204	NM_011740	22631	tyrosine 3-monooxygenase/trypt	Ywhaz	0.988	-0.278	0.788584	0.913935
9843	10535524	NM_033039	18261	oncomodulin	Ocm	0.988	0.197	0.849137	0.939006
9844	10507572	NM_146304	258301	olfactory receptor 1340	Olfr1340	0.988	0.05	0.961456	0.985172
9845	10436783	NM_011434	20655	superoxide dismutase 1, solubl	Sod1	0.988	-0.411	0.693135	0.865508
9846	10581625	BC039052	71955	RIKEN cDNA 2400003C14 gene	2400003C14Rik	0.988	-0.299	0.773271	0.9067
9847	10552210	NM_145633	245886	ankyrin repeat domain 27 (VPS9	Ankrd27	0.988	-0.261	0.80132	0.919489
9848	10429538	NM_001033229	110115	cytochrome P450, family 11, su	Cyp11b1	0.988	0.08	0.938735	0.976177
9849	10559524	NM_029834	232807	protein phosphatase 1, regulat	Ppp1r12c	0.988	-0.005	0.995769	0.998271
9850	10528102	NM_023733	74114	carnitine O-octanoyltransferas	Crot	0.988	-0.766	0.468014	0.720506
9851	10495173	NM_001039488	321000	RIKEN cDNA 4933421E11 gene	4933421E11Rik	0.987	-0.717	0.495767	0.740536
9852	10502333	ENSMUST00000116270	100039350	similar to Scoc protein	LOC100039350	0.987	-0.059	0.954218	0.982421
9853	10574159					0.987	-0.19	0.854729	0.941172
9854	10563764	NM_207537	404238	MAS-related GPR, member B3	Mrgprb3	0.987	-0.411	0.693042	0.865443
9855	10345404	AK082264	241052	RIKEN cDNA C230030N03 gene	C230030N03Rik	0.987	-0.042	0.967492	0.987099
9856	10371054	NM_145365	208677	cAMP responsive element bindin	Creb3l3	0.987	-0.145	0.88854	0.956048
9857	10388784	AF357367	268449	ribosomal protein L23a	Rpl23a	0.987	0.231	0.823848	0.929508
9858	10467842	NM_010324	14718	glutamate oxaloacetate transam	Got1	0.987	-0.874	0.410226	0.674586
9859	10378787	NM_177709	237858	tumor suppressor candidate 5	Tusc5	0.987	-0.134	0.897192	0.95959
9860	10408056	NM_146283	258280	olfactory receptor 1366	Olfr1366	0.987	-0.096	0.926379	0.970777
9861	10385557	NM_212484	104625	CCR4-NOT transcription complex	Cnot6	0.987	-0.445	0.669236	0.852817
9862	10554392	NM_178752	269952	RIKEN cDNA D330012F22 gene	D330012F22Rik	0.987	-0.191	0.853676	0.940747
9863	10350506	NM_153539	215378	RIKEN cDNA B830045N13 gene	B830045N13Rik	0.987	-0.086	0.93402	0.973771
9864	10589074	ENSMUST00000098384	100038635	predicted gene, ENSMUSG0000007	ENSMUSG00000074075	0.987	-0.247	0.81173	0.923946
9865	10547171	NM_146446	258438	olfactory receptor 215	Olfr215	0.987	0.212	0.837705	0.934421
9866	10360745	NM_133815	98386	lamin B receptor	Lbr	0.987	-0.208	0.841301	0.935777
9867	10416155	NM_001111028	105440	potassium channel tetramerisat	Kctd9	0.987	-0.408	0.69502	0.866071
9868	10568296					0.987	-0.168	0.870835	0.948568
9869	10345368	ENSMUST00000097783	52318	DNA segment, Chr 1, ERATO Doi	D1Ertd448e	0.987	0.327	0.752771	0.89584
9870	10478109	NM_145635	246747	cDNA sequence BC054059	BC054059	0.987	-0.261	0.801482	0.919489
9871	10469732	NM_013771	27377	YME1-like 1 (S. cerevisiae)	Yme1l1	0.987	-0.849	0.423021	0.685287
9872	10519354	NM_027777	71382	peroxisome biogenesis factor 1	Pex1	0.987	-0.282	0.785734	0.912565
9873	10451061	NM_009820	12393	runt related transcription fac	Runx2	0.987	0.341	0.743155	0.890598
9874	10475941	NM_178404	78751	zinc finger CCCH type containi	Zc3h6	0.987	0.005	0.995833	0.998288
9875	10512093	NM_001033305	230075	NADH dehydrogenase (ubiquinone	Ndufb6	0.987	-0.629	0.54902	0.779406
9876	10401296	NM_080440	110893	solute carrier family 8 (sodiu	Slc8a3	0.987	-0.081	0.93729	0.975526

9877	10588655	NM_053253	114602	zinc finger, MYND domain conta	Zmynd10	0.987	-0.049	0.962633	0.985423
9878	10528145	NM_181850	108069	glutamate receptor, metabotrop	Grm3	0.987	-0.171	0.868855	0.947499
9879	10539990	NM_144940	243537	urocanase domain containing 1	Uroc1	0.987	-0.011	0.991502	0.996624
9880	10452768					0.987	0.023	0.982455	0.9924
9881	10526541					0.987	-0.234	0.821201	0.92863
9882	10426598					0.987	0.134	0.897213	0.95959
9883	10511146	ENSMUST00000067628	70448	RIKEN cDNA 2610204G22 gene	2610204G22Rik	0.987	-0.394	0.704752	0.871013
9884	10355639	NM_153744	241113	protein kinase, AMP-activated,	Prkag3	0.987	-0.069	0.946502	0.978837
9885	10350039	NM_145510	98710	RAB interacting factor	Rabif	0.987	-0.727	0.490269	0.737262
9886	10348062	NM_145222	227327	UDP-GlcNAc:betaGal beta-1,3-N-	B3gnt7	0.987	-0.131	0.899386	0.960245
9887	10437687	NM_019980	56722	LPS-induced TN factor	Litaf	0.987	-0.301	0.772213	0.906086
9888	10413609	NM_181390	66175	musculoskeletal, embryonic nuc	Mustn1	0.987	0.219	0.833065	0.932765
9889	10524703	NM_011223	19303	paxillin	Pxn	0.987	-0.522	0.617434	0.823037
9890	10546349	NM_009531	22591	xeroderma pigmentosum, complem	Xpc	0.987	-0.23	0.824262	0.929508
9891	10468049	NM_020032	56626	polymerase (DNA directed), lam	Poll	0.987	-0.251	0.808617	0.922966
9892	10542040	NM_181402	101187	poly (ADP-ribose) polymerase f	Parp11	0.987	-0.974	0.361544	0.633294
9893	10576413					0.987	-0.264	0.799482	0.919009
9894	10517116	NM_009097	20111	ribosomal protein S6 kinase po	Rps6ka1	0.987	-0.108	0.916589	0.967047
9895	10553956	NM_178056	68634	TM2 domain containing 3	Tm2d3	0.987	-0.412	0.692017	0.864827
9896	10377612	NM_023564	70310	phospholipid scramblase 3	Plscr3	0.987	-0.203	0.844856	0.937
9897	10391130	NM_026561	68106	5'-nucleotidase, cytosolic III	Nt5c3l	0.987	-0.691	0.511381	0.752366
9898	10592816	NM_013551	15288	hydroxymethylbilane synthase	Hmbs	0.987	-0.356	0.731734	0.884354
9899	10536527	NM_007604	12343	capping protein (actin filamen	Capza2	0.987	-0.759	0.471833	0.72372
9900	10428192	NM_008774	18458	poly A binding protein, cytopl	Pabpc1	0.987	-0.328	0.75209	0.895422
9901	10494910	NM_026602	68183	breast carcinoma amplified seq	Bcas2	0.987	-0.605	0.563887	0.790376
9902	10536805	NM_207258	330277	cDNA sequence BC048651	BC048651	0.987	0.007	0.99431	0.997705
9903	10531495	ENSMUST00000064781	330129	predicted gene, EG330129	EG330129	0.987	0.211	0.838508	0.934504
9904	10481122	NM_009298	20935	surfeit gene 6	Surf6	0.987	-0.158	0.87917	0.952124
9905	10464452	NM_009212	20589	immunoglobulin mu binding prot	Ighmbp2	0.987	-0.071	0.945306	0.978439
9906	10534301	NM_001013751	214292	gene model 52, (NCBI)	Gm52	0.987	0.114	0.912643	0.965173
9907	10507742	NM_007741	12840	collagen, type IX, alpha 2	Col9a2	0.987	0.113	0.912748	0.965173
9908	10522666	ENSMUST00000101090	70284	RIKEN cDNA 2310040G07 gene	2310040G07Rik	0.987	0.241	0.816586	0.926829
9909	10504662					0.987	-0.008	0.994183	0.997702
9910	10526687	BC052497	69871	RIKEN cDNA 2010007H12 gene	2010007H12Rik	0.987	-0.088	0.931958	0.97291
9911	10423894	NM_029422	75766	transmembrane 7 superfamily me	Tm7sf4	0.987	-0.138	0.894242	0.958327
9912	10499996	NM_029721	76742	sorting nexin family member 27	Snx27	0.987	-0.971	0.362918	0.63431
9913	10449327	NM_146075	224640	LEM domain containing 2	Lemd2	0.987	-0.231	0.82346	0.929428
9914	10522868	BC103787	73779	RIKEN cDNA 4930432K09 gene	4930432K09Rik	0.987	-0.113	0.91341	0.965657
9915	10380403	NM_133807	98238	leucine rich repeat containing	Lrrc59	0.987	-0.676	0.519897	0.757566
9916	10476042	NM_009374	21818	transglutaminase 3, E polypept	Tgm3	0.987	-0.151	0.884385	0.95453
9917	10586416	NM_172453	208084	PIF1 5'-to-3' DNA helicase hom	Pif1	0.987	0.037	0.971604	0.988148
9918	10354307	ENSMUST00000030051	22166	thioredoxin 1	Txn1	0.986	-0.336	0.746364	0.892337
9919	10559436	NM_029934	77582	membrane bound O-acyltransfera	Mboat7	0.986	-0.247	0.8117	0.923946
9920	10376938	NM_025496	66338	CMT1A duplicated region transc	Cdrt4	0.986	0.236	0.820353	0.928562
9921	10494007	NM_029431	75778	thioesterase superfamily membe	Them4	0.986	-0.119	0.908424	0.963723
9922	10504914					0.986	-0.326	0.753578	0.896207
9923	10429327	ENSMUST00000100562	100038495	predicted gene, ENSMUSG0000007	ENSMUSG00000072493	0.986	-0.259	0.802817	0.920071
9924	10545897	NM_028099	72102	dual specificity phosphatase 1	Dusp11	0.986	-0.212	0.838331	0.934421
9925	10383360	NM_152807	67291	coiled-coil domain containing	Ccdc137	0.986	-0.348	0.737569	0.888107
9926	10375713	NM_145926	103534	mannoside acetylglucosaminyltr	Mgat4b	0.986	-0.743	0.481164	0.730704

9927	10398483	NM_030238	13424	dynein cytoplasmic 1 heavy cha	Dync1h1	0.986	-0.78	0.460473	0.715038
9928	10578794					0.986	-0.329	0.751486	0.895256
9929	10391746	ENSMUST00000069673	100038535	predicted gene, ENSMUSG0000007	ENSMUSG00000075516	0.986	-0.2	0.846635	0.937778
9930	10490104	NM_011497	20878	aurora kinase A	Aurka	0.986	-0.639	0.542769	0.775164
9931	10428020	NM_172606	223455	membrane-associated ring finge	March6	0.986	-0.38	0.714753	0.875137
9932	10351500					0.986	0.262	0.800384	0.919346
9933	10532616	XM_912851	74376	myosin XVIIIb	Myo18b	0.986	-0.165	0.873344	0.949372
9934	10406017	NM_018885	50916	Iroquois related homeobox 4 (D	Irx4	0.986	0.267	0.796769	0.917479
9935	10414978	ENSMUST00000103673	547427	predicted gene, OTTMUSG0000001	OTTMUSG00000015026	0.986	-0.144	0.889306	0.956449
9936	10443332	NM_011145	19015	peroxisome proliferator activa	Ppard	0.986	-0.09	0.930795	0.972759
9937	10386427	NM_146018	216805	folliculin	Flcn	0.986	-0.372	0.720339	0.878213
9938	10520211	NM_139153	213990	centaurin, gamma 3	Centg3	0.986	-0.535	0.608914	0.817955
9939	10565627	NM_175105	66333	aquaporin 11	Aqp11	0.986	0.051	0.960939	0.985069
9940	10573319	NM_001013384	244550	podocan-like 1	Podnl1	0.986	-0.075	0.942451	0.977825
9941	10449940	NM_022434	64385	cytochrome P450, family 4, sub	Cyp4f14	0.986	-0.212	0.8377	0.934421
9942	10375811					0.986	0.095	0.927156	0.971253
9943	10538850					0.986	-0.064	0.950833	0.981077
9944	10406718	NM_172590	218460	WD repeat domain 41	Wdr41	0.986	-0.447	0.66811	0.851935
9945	10478748	NM_023815	76367	transformation related protein	Trp53rk	0.986	-0.119	0.908784	0.963765
9946	10418971	NM_013887	30044	opsin 4 (melanopsin)	Opn4	0.986	-0.499	0.63268	0.832911
9947	10583529	NM_023892	78369	intercellular adhesion molecul	Icam4	0.986	-0.097	0.925077	0.970374
9948	10542093	NM_021717	60345	nuclear receptor interacting p	Nrip2	0.986	-0.444	0.669984	0.853279
9949	10567518	XM_355934	381917	dynein, axonemal, heavy chain	Dnahc3	0.986	-0.257	0.80441	0.920819
9950	10473750	NM_026161	67445	C1q and tumor necrosis factor	C1qtnf4	0.986	-0.116	0.910957	0.964559
9951	10488594	NM_019705	24105	RanBP-type and C3HC4-type zinc	Rbck1	0.986	-0.417	0.688524	0.863063
9952	10554233	NM_026531	68048	interferon stimulated exonucle	Isg20l1	0.986	-0.391	0.707384	0.872175
9953	10389293	NM_145433	217038	mitochondrial rRNA methyltrans	Mrm1	0.986	-0.278	0.788905	0.914104
9954	10487886	NM_013460	11550	adrenergic receptor, alpha 1d	Adra1d	0.986	-0.679	0.518599	0.757094
9955	10455094	NM_053138	93884	protocadherin beta 13	Pcdhb13	0.986	0.073	0.943875	0.977948
9956	10534984					0.986	-0.413	0.691271	0.864541
9957	10550131	NM_001004762	232889	phospholipase A2, group IVC (c	Pla2g4c	0.986	0.242	0.815585	0.926149
9958	10563253	NM_011698	22342	lin-7 homolog B (C. elegans)	Lin7b	0.986	-0.639	0.542461	0.774881
9959	10421670					0.986	0.178	0.863697	0.945728
9960	10513920	XR_032741	623115	similar to heterogeneous nucle	LOC623115	0.986	-0.024	0.981295	0.992092
9961	10457961	ENSMUST00000054984	67158	SFT2 domain containing 3	Sft2d3	0.986	-0.045	0.965274	0.986124
9962	10346340	BC071241	68115	RIKEN cDNA 9430016H08 gene	9430016H08Rik	0.986	-0.616	0.556957	0.785453
9963	10557488	NM_011538	21389	T-box 6	Tbx6	0.986	-0.376	0.717697	0.876761
9964	10444895	NM_008027	14251	flotillin 1	Flot1	0.986	-0.217	0.834057	0.933071
9965	10490491	NM_008093	14464	GATA binding protein 5	Gata5	0.986	-0.271	0.794035	0.91622
9966	10437942	NM_023585	70620	ubiquitin-conjugating enzyme E	Ube2v2	0.986	-0.362	0.727389	0.881863
9967	10595673	NM_001039147	21761	mortality factor 4 like 1	Morf4l1	0.986	-0.277	0.789727	0.914492
9968	10569545	NM_030221	78914	NAD synthetase 1	Nadsyn1	0.986	-0.357	0.731166	0.883971
9969	10457745	NM_029491	75964	RIKEN cDNA D030074E01 gene	D030074E01Rik	0.986	-0.634	0.54577	0.777543
9970	10511298	BC004010	230996	RIKEN cDNA 9430015G10 gene	9430015G10Rik	0.986	-0.03	0.976832	0.990463
9971	10385353	NM_007416	11548	adrenergic receptor, alpha 1b	Adra1b	0.986	0.05	0.961097	0.985069
9972	10363894	NM_027184	69718	inositol polyphosphate multiki	Ipmk	0.986	-0.372	0.72059	0.878367
9973	10384824	BC033930	67939	RIKEN cDNA 2010316F05 gene	2010316F05Rik	0.986	-1.013	0.343925	0.618153
9974	10414993	BC038285	219065	RIKEN cDNA A630038E17 gene	A630038E17Rik	0.986	0.049	0.962417	0.985405
9975	10461999	NM_146096	226016	RIKEN cDNA 5730446C15 gene	5730446C15Rik	0.986	-0.366	0.724866	0.880713
9976	10585697	ENSMUST00000085711	330948	predicted gene, EG330948	EG330948	0.986	-0.339	0.74434	0.891431

9977	10567510	XM_355934	381917	dynein, axonemal, heavy chain	Dnahc3	0.986	0.121	0.907213	0.963723
9978	10452147	NM_008738	18188	neurturin	Nrtn	0.986	-0.054	0.958619	0.984334
9979	10463599	NM_019408	18034	nuclear factor of kappa light	Nfkb2	0.986	-0.089	0.931372	0.972759
9980	10451291	NM_144856	108114	solute carrier family 22 (orga	Slc22a7	0.986	-0.256	0.805005	0.921108
9981	10464924	NM_029576	76308	RAB1B, member RAS oncogene fam	Rab1b	0.986	-0.523	0.616944	0.823029
9982	10495574	NM_028349	72776	spindle assembly 6 homolog (C.	Sass6	0.986	-0.403	0.698387	0.867855
9983	10581355	NM_023182	109660	chymotrypsin-like	Ctrl	0.986	-0.238	0.818467	0.927818
9984	10558263	ENSMUST00000098000	100038673	predicted gene, ENSMUSG0000007	ENSMUSG00000073814	0.986	0.215	0.835438	0.933323
9985	10370681	NM_177994	109284	RIKEN cDNA C030046I01 gene	C030046I01Rik	0.986	-0.581	0.578725	0.798523
9986	10572516	NM_173013	270058	microtubule-associated protein	Mtap1s	0.986	-0.14	0.892377	0.957747
9987	10353915	NM_027957	381337	cDNA sequence BC050210	BC050210	0.986	-0.154	0.881731	0.953233
9988	10460771	ENSMUST00000025699	76663	RIKEN cDNA 1700123I01 gene	1700123I01Rik	0.986	-0.107	0.917363	0.967481
9989	10514658	ENSMUST00000097960	67733	integrin beta 3 binding protei	Itgb3bp	0.986	-0.516	0.621317	0.826234
9990	10483706	NM_007389	11435	cholinergic receptor, nicotini	Chrna1	0.986	-0.083	0.935936	0.974753
9991	10590563	NM_153168	102436	leucyl-tRNA synthetase, mitoch	Lars2	0.986	-0.25	0.809766	0.923201
9992	10431792	NM_172437	78895	pseudouridylate synthase 7 hom	Pus7l	0.986	-0.399	0.701534	0.869143
9993	10350777	NM_028250	72482	acyl-Coenzyme A binding domain	Acbd6	0.986	-0.659	0.530608	0.765382
9994	10390691	NM_145434	217166	nuclear receptor subfamily 1,	Nr1d1	0.986	-0.17	0.869847	0.947897
9995	10478383	NM_001099331	100043899	novel SCP-like extracellular p	RP23-36P22.5	0.986	0.266	0.797995	0.918148
9996	10491977	NM_173382	212127	RIKEN cDNA 2810046L04 gene	2810046L04Rik	0.986	-0.876	0.409182	0.673445
9997	10478774	NM_001085495	99371	ADP-ribosylation factor guanin	Arfgef2	0.986	-0.439	0.67328	0.854824
9998	10456745	NM_001042660	17131	MAD homolog 7 (Drosophila)	Smad7	0.986	-0.284	0.784236	0.912068
9999	10548295	ENSMUST00000032517	667622	predicted gene, EG667622	EG667622	0.986	0.234	0.821276	0.92863
10000	10535972	ENSMUST00000067770	77867	RIKEN cDNA D730045B01 gene	D730045B01Rik	0.986	-0.678	0.518803	0.757221
10001	10500580					0.986	-0.277	0.789757	0.914492
10002	10385004	NM_181569	17168	alpha globin regulatory elemen	Mare	0.986	-0.284	0.784102	0.912068
10003	10345438					0.986	-0.409	0.69425	0.865724
10004	10381109	NM_001126323	670550	novel member of the keratin as	RP23-212C14.10	0.986	-0.306	0.768205	0.90369
10005	10597854	NM_001033784	434446	coiled-coil domain containing	Ccdc13	0.986	-0.168	0.871419	0.948625
10006	10530128	BC079612	791323	predicted gene, ENSMUSG0000005	ENSMUSG00000054714	0.986	-0.062	0.952448	0.981554
10007	10470014	NM_009849	12496	ectonucleoside triphosphate di	Entpd2	0.986	0.028	0.978613	0.991413
10008	10564434					0.986	-0.186	0.857808	0.942795
10009	10543921	NM_172892	243755	solute carrier family 13 (sodi	Slc13a4	0.985	0.012	0.990524	0.995941
10010	10498566					0.985	-0.147	0.886991	0.955613
10011	10545651	NM_023547	70020	zinc finger, HIT type 4	Znhit4	0.985	-0.336	0.746598	0.892388
10012	10385893	NM_019687	30805	solute carrier family 22 (orga	Slc22a4	0.985	-0.032	0.975366	0.989745
10013	10590690	NM_029851	110350	dynein cytoplasmic 2 heavy cha	Dync2h1	0.985	-0.268	0.796535	0.917464
10014	10438313	NM_033324	94223	DiGeorge syndrome critical reg	Dgcr8	0.985	-0.331	0.750377	0.894477
10015	10378401					0.985	-0.07	0.94605	0.978614
10016	10351644	NM_018729	18106	CD244 natural killer cell rece	Cd244	0.985	-0.08	0.938162	0.975903
10017	10378367	NM_145099	246788	transient receptor potential c	Trpv3	0.985	-0.079	0.939076	0.976244
10018	10547206	NM_033648	108017	FXYD domain-containing ion tra	Fxyd4	0.985	0.028	0.978425	0.991366
10019	10370519	NM_001011737	257883	olfactory receptor 1357	Olfr1357	0.985	-0.044	0.966344	0.986657
10020	10536172	XR_030507	667375	similar to COX11 homolog, cyto	LOC667375	0.985	0.203	0.844494	0.936859
10021	10372410	NM_028608	73690	GLI pathogenesis-related 1 (gl	Glipr1	0.985	-0.23	0.824437	0.929508
10022	10483536	BC125570	75051	RIKEN cDNA 4930578N16 gene	4930578N16Rik	0.985	-0.887	0.403553	0.668494
10023	10571474	NM_023662	18536	pericentriolar material 1	Pcm1	0.985	-0.534	0.609531	0.818311
10024	10549998					0.985	-0.375	0.71874	0.877276
10025	10558496	NM_027164	76612	leucine rich repeat containing	Lrrc27	0.985	-0.448	0.667105	0.851389
10026	10607943					0.985	-0.133	0.897698	0.959787
10027	10394124	NM_178664	210004	UDP-GlcNAc:betaGal beta-1,3-N-	B3gntl1	0.985	-0.737	0.484227	0.732769
				predicted gene					

10028	10487575	ENSMUST00000099385	100043736	predicted gene, ENSMUSG0000007	ENSMUSG00000074807	0.985	-0.297	0.774834	0.907674
10029	10398831	NM_198411	70435	RIKEN cDNA 2610204M08 gene	2610204M08Rik	0.985	0.088	0.932171	0.973077
10030	10409278	NM_017373	18030	nuclear factor, interleukin 3,	Nfil3	0.985	-1.035	0.334096	0.609656
10031	10359723	NM_145513	226591	TIP41, TOR signalling pathway	Tiprl	0.985	-0.533	0.610226	0.818642
10032	10509238	NM_008309	15552	5-hydroxytryptamine (serotonin	Htr1d	0.985	-0.408	0.694893	0.866071
10033	10543173	BC076621	232585	gene model 467, (NCBI)	Gm467	0.985	-0.223	0.829762	0.931483
10034	10418835	NM_021712	20508	solute carrier family 18 (vesi	Slc18a3	0.985	0.209	0.839863	0.935328
10035	10441398	ENSMUST00000097433	100038678	predicted gene, ENSMUSG0000007	ENSMUSG00000073473	0.985	0.425	0.68315	0.859827
10036	10500990	NM_009725	11950	ATP synthase, H+ transporting,	Atp5f1	0.985	-1.078	0.315605	0.592484
10037	10583519	NM_010493	15894	intercellular adhesion molecul	Icam1	0.985	0.012	0.991136	0.996414
10038	10517540	NM_198248	230848	zinc finger and BTB domain con	Zbtb40	0.985	-0.176	0.864981	0.946153
10039	10538214	BC055818	231946	RIKEN cDNA D330028D13 gene	D330028D13Rik	0.985	-0.052	0.960123	0.985
10040	10464153	NM_025811	66866	NHL repeat containing 2	Nhlrc2	0.985	-0.224	0.828755	0.931153
10041	10504743	NM_053179	94181	N-acetylneuraminic acid syntha	Nans	0.985	-0.73	0.488165	0.735812
10042	10466130	NM_022430	64381	membrane-spanning 4-domains, s	Ms4a8a	0.985	0.475	0.648623	0.841922
10043	10461028	NM_153597	107328	tRNA phosphotransferase 1	Trpt1	0.985	-0.063	0.951621	0.98118
10044	10408006	XM_905894	625752	ribosomal protein L29 pseudoge	RP23-54E4.8	0.985	-0.227	0.826409	0.930238
10045	10544629	NM_198102	101214	transformer 2 alpha homolog (D	Tra2a	0.985	-0.001	0.99924	0.999589
10046	10581181	NM_001033161	71609	TNFRSF1A-associated via death	Tradd	0.985	-0.672	0.522492	0.759283
10047	10364502	NM_023128	18483	paralemmin	Palm	0.985	-0.205	0.843091	0.93639
10048	10444524	NM_145830	110147	euchromatic histone lysine N-m	Ehmt2	0.985	-0.499	0.632547	0.832839
10049	10393761	NM_027980	71885	RIKEN cDNA 2310003H01 gene	2310003H01Rik	0.985	-0.246	0.812597	0.924634
10050	10406254	NM_138953	192657	elongation factor RNA polymera	Ell2	0.985	0.054	0.958542	0.984334
10051	10440292	XM_001480385	433036	similar to zinc finger protein	LOC433036	0.985	-0.49	0.638767	0.835923
10052	10387397	NM_001081330	327954	dynein, axonemal, heavy chain	Dnahc2	0.985	0.097	0.925372	0.970455
10053	10355329	NM_007525	12021	BRCA1 associated RING domain 1	Bard1	0.985	-0.293	0.777747	0.909562
10054	10511665	NM_178617	69352	N-terminal EF-hand calcium bin	Necab1	0.985	-0.733	0.486472	0.734369
10055	10557357	NM_001081022	233865	RIKEN cDNA D430042O09 gene	D430042O09Rik	0.985	-0.255	0.806009	0.921787
10056	10547204	ENSMUST00000035534	74471	RIKEN cDNA 4933440N22 gene	4933440N22Rik	0.985	-0.084	0.935148	0.974268
10057	10375472	NM_178759	276891	T-cell immunoglobulin and muci	Timd4	0.985	0.578	0.580565	0.799564
10058	10422234					0.985	-0.332	0.749333	0.893972
10059	10448062	XR_032603	636398	similar to zinc finger protein	LOC636398	0.985	-0.455	0.662446	0.849733
10060	10528648	NM_013853	27407	ATP-binding cassette, sub-fami	Abcf2	0.985	-0.487	0.64057	0.837232
10061	10438293	NM_172151	27801	zinc finger, DHHC domain conta	Zdhhc8	0.985	-0.892	0.401115	0.666661
10062	10568139	NM_010772	17188	MYC-associated zinc finger pro	Maz	0.985	-0.174	0.866987	0.946934
10063	10381683	NM_025988	67131	acyl-Coenzyme A binding domain	Acbd4	0.985	-0.346	0.739302	0.888979
10064	10548815	ENSMUST00000058713	243676	RIKEN cDNA E330021D16 gene	E330021D16Rik	0.985	-0.014	0.989329	0.995355
10065	10588479	NM_031178	81897	toll-like receptor 9	Tlr9	0.985	0.681	0.516863	0.756112
10066	10573008	NM_178267	622675	zinc finger protein 827	Zfp827	0.985	-0.441	0.671989	0.854437
10067	10449152	NM_139154	224624	Rab40c, member RAS oncogene fa	Rab40c	0.985	-0.385	0.711687	0.87371
10068	10507731	NM_182929	242662	regulating synaptic membrane e	Rims3	0.985	-0.3	0.772899	0.906589
10069	10357590	NM_145508	226419	dual-specificity tyrosine-(Y)-	Dyrk3	0.985	-1.297	0.234436	0.50565
10070	10418578	NM_022656	64652	nischarin	Nisch	0.985	-0.839	0.428562	0.689543
10071	10471256	NM_172268	227720	nucleoporin 214	Nup214	0.985	-0.62	0.554367	0.783473
10072	10448593	NM_153792	224619	Tnf receptor-associated factor	Traf7	0.985	-0.63	0.547995	0.778543
10073	10452468	BC096657	64657	mitochondrial ribosomal protei	Mrps10	0.985	-0.758	0.472767	0.724458
10074	10557508	NM_010069	13446	double C2, alpha	Doc2a	0.985	-0.501	0.631488	0.832534
				RIKEN cDNA 4732444A12					

10075	10383434	ENSMUST00000066154	100015211	gene	4732444A12Rik	0.985	-0.532	0.610906	0.819294
10076	10397866	NM_013747	27277	golgi autoantigen, golgin subf	Golga5	0.985	-0.453	0.66409	0.850267
10077	10398446	NM_172119	107585	deiodinase, iodothyronine type	Dio3	0.985	0.003	0.997727	0.999192
10078	10355202	NM_007774	12964	crystallin, gamma A	Cryga	0.985	-0.493	0.636966	0.835122
10079	10596261					0.985	-0.935	0.380132	0.649758
10080	10582221	NM_029597	76405	RIKEN cDNA 1700018B08 gene	1700018B08Rik	0.985	-0.198	0.848307	0.938486
10081	10596664	NM_019720	56368	cytochrome b-561 domain contai	Cyb561d2	0.985	-0.55	0.598612	0.811605
10082	10397530	NM_026958	380773	RIKEN cDNA 1810035L17 gene	1810035L17Rik	0.985	-0.783	0.458669	0.713672
10083	10575844	NM_019707	12554	cadherin 13	Cdh13	0.985	-0.536	0.607924	0.817473
10084	10520796	NM_026296	67656	RIKEN cDNA 4930548H24 gene	4930548H24Rik	0.985	-0.017	0.987128	0.994703
10085	10446427	NM_001037757	68767	open reading frame 19	ORF19	0.985	-0.413	0.691357	0.864541
10086	10433373	ENSMUST00000116667	239690	similar to SEC14-like 1	LOC239690	0.984	-0.09	0.930877	0.972759
10087	10375103	NM_134015	103583	F-box and WD-40 domain protein	Fbxw11	0.984	-0.737	0.484197	0.732769
10088	10350792	NM_022329	64164	interferon alpha responsive ge	Ifrg15	0.984	-0.682	0.516264	0.755582
10089	10476886	NM_009219	20608	somatostatin receptor 4	Sstr4	0.984	0.241	0.8159	0.926256
10090	10545298	NM_024288	68477	required for meiotic nuclear d	Rmnd5a	0.984	-0.503	0.630125	0.831393
10091	10555205	NM_201352	233552	glycerophosphodiester phosphod	Gdpd5	0.984	-0.103	0.920627	0.968204
10092	10560168	NM_007770	12951	cone-rod homeobox containing g	Crx	0.984	-0.124	0.904542	0.962829
10093	10556546	NM_054084	116903	calcitonin-related polypeptide	Calcb	0.984	-0.215	0.835552	0.933375
10094	10347564	NM_178055	56812	DnaJ (Hsp40) homolog, subfamil	Dnajb10	0.984	-0.42	0.68687	0.861858
10095	10555007					0.984	-0.338	0.745283	0.891658
10096	10345921	NM_024283	78896	RIKEN cDNA 1500015O10 gene	1500015O10Rik	0.984	0.001	0.999181	0.999589
10097	10447023					0.984	-0.448	0.667057	0.851389
10098	10370983	NM_023900	78670	pleckstrin homology domain con	Plekhj1	0.984	-0.229	0.824908	0.929565
10099	10540790	NM_009507	22346	von Hippel-Lindau syndrome hom	Vhlh	0.984	-0.551	0.598245	0.811268
10100	10556998	ENSMUST00000116276	436008	predicted gene, EG436008	EG436008	0.984	-0.017	0.987265	0.994746
10101	10570975	NM_027194	69742	TM2 domain containing 2	Tm2d2	0.984	-0.95	0.37303	0.643392
10102	10476482	NM_029530	76161	RIKEN cDNA 6330527O06 gene	6330527O06Rik	0.984	-0.035	0.973252	0.988537
10103	10550967	NM_001102613	232970	pleckstrin homology-like domai	Phldb3	0.984	0.018	0.986125	0.994146
10104	10508974	NM_133880	100163	platelet-activating factor ace	Pafah2	0.984	-0.159	0.878156	0.951744
10105	10490734					0.984	0.331	0.750276	0.894442
10106	10604375	NM_013912	30878	apelin	Apln	0.984	-0.326	0.753359	0.8961
10107	10567423	NM_173408	233805	DCN1, defective in cullin nedd	Dcun1d3	0.984	-0.045	0.965266	0.986124
10108	10535532	BC046968	70381	RIKEN cDNA 2210010N04 gene	2210010N04Rik	0.984	-0.292	0.77868	0.909988
10109	10477069	NM_009328	21407	transcription factor 15	Tcf15	0.984	-0.064	0.950679	0.981023
10110	10495199	NM_001081140	242151	potassium voltage-gated channe	Kcna10	0.984	-0.064	0.950907	0.981077
10111	10565888	ENSMUST00000098254	100038497	predicted gene, ENSMUSG0000007	ENSMUSG00000073994	0.984	-0.007	0.994429	0.997732
10112	10532330					0.984	-0.196	0.849803	0.939466
10113	10562741	XM_621786	546967	acid phosphatase, testicular	Acpt	0.984	-0.111	0.91454	0.96632
10114	10557374	NM_001081022	233865	RIKEN cDNA D430042O09 gene	D430042O09Rik	0.984	-0.384	0.712075	0.873832
10115	10519495	BC049718	70920	RIKEN cDNA 4921511H03 gene	4921511H03Rik	0.984	0.058	0.955238	0.982897
10116	10430725	NM_133726	70356	suppression of tumorigenicity	St13	0.984	-0.744	0.480362	0.729941
10117	10568629	NM_152944	214766	matrix metallopeptidase 21	Mmp21	0.984	-0.224	0.82902	0.931194
10118	10531776	NM_172405	70681	coiled-coil domain containing	Ccdc98	0.984	-0.324	0.755172	0.897043
10119	10532716	ENSMUST00000047891	73476	RIKEN cDNA 1700069L16 gene	1700069L16Rik	0.984	-0.023	0.982011	0.992289
10120	10385248	NM_013552	15366	hyaluronan mediated motility r	Hmmr	0.984	-0.878	0.408296	0.672667
10121	10542297	NM_026371	67774	loss of heterozygosity, 12, ch	Loh12cr1	0.984	-0.283	0.785246	0.912507
10122	10432139	NM_173769	239652	zinc finger protein 641	Zfp641	0.984	0.128	0.901574	0.961364
				RIKEN cDNA 4921511H13					

10123	10440800	ENSMUST00000037810	207932	gene	4921511H13Rik	0.984	-0.261	0.801435	0.919489
10124	10375975	NM_026479	67966	zinc finger, CCHC domain conta	Zcchc10	0.984	-0.261	0.801732	0.919646
10125	10420216	NM_001082975	654795	RIKEN cDNA 2310014G06 gene	2310014G06Rik	0.984	-0.973	0.361954	0.633538
10126	10363641	NM_026101	67345	hect domain and RLD 4	Herc4	0.984	-0.257	0.804191	0.920618
10127	10348432	NM_178119	347722	centaurin, gamma 2	Centg2	0.984	-0.645	0.538961	0.772021
10128	10451395	NM_029091	74764	kinesin light chain 4	Klc4	0.984	-0.338	0.744995	0.891615
10129	10424929	NM_172960	268822	aarF domain containing kinase	Adck5	0.984	-0.556	0.595101	0.809184
10130	10478160	BC068129	71878	RIKEN cDNA 2310007D09 gene	2310007D09Rik	0.984	-0.366	0.7248	0.880713
10131	10431154	NM_001081166	271305	PHD finger protein 21B	Phf21b	0.984	-0.176	0.865435	0.94621
10132	10532660	NM_021352	12962	crystallin, beta B3	Crybb3	0.984	-0.254	0.806509	0.921832
10133	10486320	XM_917516	70715	RIKEN cDNA 6330405D24 gene	6330405D24Rik	0.984	-0.124	0.904427	0.962829
10134	10591960	NM_178027	69091	vacuolar protein sorting 26 ho	Vps26b	0.984	-0.601	0.566459	0.79227
10135	10524004	NM_172716	69587	polycomb group ring finger 3	Pcgf3	0.984	-0.44	0.672942	0.854651
10136	10437594	NM_001003918	252870	ubiquitin specific peptidase 7	Usp7	0.984	-0.437	0.67459	0.855467
10137	10388669	NM_001024920	216964	transformation related protein	Trp53i13	0.984	-0.136	0.895665	0.959029
10138	10560726					0.984	0.149	0.885634	0.95523
10139	10494817	NM_013609	18049	nerve growth factor	Ngf	0.984	-0.458	0.660358	0.848652
10140	10432831	NM_212485	223915	keratin 73	Krt73	0.984	0.25	0.809691	0.923191
10141	10458870	XR_034277	628477	similar to ribosomal protein L	LOC628477	0.984	-0.645	0.538715	0.771721
10142	10565547	NM_029078	74737	cleavage and polyadenylation f	Pcf11	0.984	-0.124	0.904517	0.962829
10143	10565514	NM_025460	66271	transmembrane protein 126A	Tmem126a	0.984	-1.162	0.28215	0.557189
10144	10376461	NM_053168	94091	tripartite motif-containing 11	Trim11	0.984	-0.133	0.897871	0.959787
10145	10366725	NM_182807	268354	expressed sequence AI851790	AI851790	0.984	-0.263	0.800088	0.919271
10146	10596273	ENSMUST00000060084	235567	DnaJ (Hsp40) homolog, subfamil	Dnajc13	0.984	-0.425	0.683222	0.859827
10147	10405741	XR_030564	100044367	similar to high mobility group	LOC100044367	0.984	-0.312	0.764032	0.90173
10148	10522802	NM_177680	231386	YTH domain containing 1	Ythdc1	0.984	-0.386	0.710877	0.873183
10149	10389672	NM_146412	258407	olfactory receptor 464	Olfr464	0.984	-0.043	0.966516	0.986746
10150	10445627	NM_025966	67101	RIKEN cDNA 2310039H08 gene	2310039H08Rik	0.984	-0.962	0.367007	0.638
10151	10443830	NM_013501	12954	crystallin, alpha A	Cryaa	0.984	-0.177	0.864234	0.945925
10152	10546339	NM_009527	22421	wingless-related MMTV integrat	Wnt7a	0.984	-0.273	0.792741	0.91549
10153	10580058	ENSMUST00000056686	70134	RIKEN cDNA 2210011C24 gene	2210011C24Rik	0.984	-0.265	0.798188	0.918238
10154	10386624	NM_173453	216821	transmembrane protein 11	Tmem11	0.984	-0.606	0.563096	0.789853
10155	10428441	XM_001473255	432950	predicted gene, EG432950	EG432950	0.984	-0.741	0.48203	0.730954
10156	10382257	NM_025275	13929	archaelysin family metallopept	Amz2	0.984	-0.712	0.498866	0.742429
10157	10385203	NM_011856	23964	odd Oz/ten-m homolog 2 (Drosop	Odz2	0.984	-0.085	0.934387	0.973859
10158	10519949	BC020055	320770	RIKEN cDNA A630072M18 gene	A630072M18Rik	0.984	-0.273	0.792666	0.91549
10159	10453260	NM_025325	107766	3-hydroxyanthranilate 3,4-diox	Haao	0.984	-0.254	0.806601	0.921832
10160	10555695	NM_009103	20133	ribonucleotide reductase M1	Rrm1	0.984	-0.941	0.376988	0.647069
10161	10390996	NM_016880	53617	keratin 35	Krt35	0.983	-0.25	0.809488	0.923176
10162	10437817	NM_053181	94184	pyridoxal-dependent decarboxyl	Pdxdc1	0.983	-0.763	0.469739	0.721815
10163	10601610	XR_030551	100044428	similar to transformed mouse 3	LOC100044428	0.983	-0.353	0.734147	0.886455
10164	10520459	BC113782	242915	gene model 444, (NCBI)	Gm444	0.983	0.276	0.790033	0.914502
10165	10518927	NM_010598	16498	potassium voltage-gated channe	Kcnab2	0.983	0.026	0.980016	0.991919
10166	10491272	BC116649	71862	G protein-coupled receptor 160	Gpr160	0.983	0.077	0.941045	0.97709
10167	10380710					0.983	-0.343	0.741371	0.889595
10168	10449435	NM_021478	22157	tubby like protein 1	Tulp1	0.983	-0.261	0.80141	0.919489
10169	10417181	ENSMUST00000100294	100038380	predicted gene, ENSMUSG0000007	ENSMUSG00000075465	0.983	-0.498	0.633188	0.833255
10170	10525591	NM_001042421	208628	kinetochore associated 1	Kntc1	0.983	-0.84	0.42807	0.689167
10171	10444521	NM_198886	193736	zinc finger and BTB domain con	Zbtb12	0.983	-0.633	0.546029	0.777637
10172	10366335	ENSMUST00000040454	71769	Bardet-Biedl syndrome 10 (huma	Bbs10	0.983	-0.535	0.608804	0.817918
10173	10576772	AK016282	75863	C-type lectin domain family 4	Clec4g	0.983	-0.309	0.766042	0.902642

10173	10576772	AK016282	73805	C-type lectin domain family 4,	Clec4g	0.983	-0.309	0.766042	0.902042
10174	10431326	NM_133241	170790	megalencephalic leukoencephalo	Mlc1	0.983	0.134	0.897139	0.95959
10175	10450854	NM_182714	258470	olfactory receptor 91	Olfr91	0.983	0.094	0.927693	0.971576
10176	10551734					0.983	0.168	0.87095	0.948568
10177	10576561	BC025168	66566	RIKEN cDNA 2310079N02 gene	2310079N02Rik	0.983	-0.472	0.651076	0.843733
10178	10422055	ENSMUST00000066461	791326	predicted gene, ENSMUSG0000005	ENSMUSG00000053821	0.983	-0.059	0.95474	0.982671
10179	10496405	XM_001473061	100039528	similar to hCG2038359	LOC100039528	0.983	-0.16	0.87754	0.951715
10180	10376004	NM_008110	14566	growth differentiation factor	Gdf9	0.983	0.054	0.95829	0.984334
10181	10479607	NM_023684	72699	Lck interacting transmembrane	Lime1	0.983	-0.757	0.473151	0.724844
10182	10525932	ENSMUST00000051260	208213	transmembrane protein 132C	Tmem132c	0.983	0.204	0.84367	0.936632
10183	10430280					0.983	-0.251	0.80912	0.923112
10184	10566966	NM_013507	13690	eukaryotic translation initiat	Eif4g2	0.983	-0.463	0.657292	0.846702
10185	10434396	NM_013852	27406	ATP-binding cassette, sub-fami	Abcf3	0.983	-0.617	0.556189	0.784737
10186	10447704	NR_003636	67543	poly(A) binding protein, cytop	Pabpc3	0.983	-0.243	0.814508	0.925464
10187	10428839	ENSMUST00000075109	546638	predicted gene, EG546638	EG546638	0.983	-0.418	0.688129	0.862825
10188	10357858	NM_054076	269120	opticin	Optc	0.983	0.564	0.589582	0.805725
10189	10450212	NM_152922	81701	EGF-like domain 8	Egfl8	0.983	-0.11	0.915761	0.966695
10190	10392998	NM_080643	140721	cask-interacting protein 2	Caskin2	0.983	-0.581	0.578997	0.798586
10191	10467134					0.983	-0.364	0.726467	0.881516
10192	10379511	NM_011333	20296	chemokine (C-C motif) ligand 2	Ccl2	0.983	-0.032	0.975588	0.989867
10193	10372191	BC067068	216292	cDNA sequence BC067068	BC067068	0.983	-0.35	0.73664	0.887367
10194	10411593	BC001981	100049162	predicted gene, ENSMUSG0000005	ENSMUSG00000050599	0.983	-0.147	0.887301	0.955613
10195	10393804	NM_197995	70317	ADP-ribosylation factor-like 1	Arl16	0.983	-0.565	0.589259	0.805593
10196	10565381					0.983	-0.159	0.877977	0.951715
10197	10553004	NM_025330	66065	hydroxysteroid (17-beta) dehyd	Hsd17b14	0.983	0.093	0.928222	0.971746
10198	10603125	NM_027027	69299	ankyrin repeat and SOCS box-co	Asb9	0.983	-0.099	0.923582	0.969694
10199	10603623					0.983	0.289	0.780414	0.910806
10200	10568115	NM_080638	78388	major vault protein	Mvp	0.983	0.076	0.941397	0.977311
10201	10507653					0.983	0.207	0.841994	0.936059
10202	10388834	NM_022411	20500	solute carrier family 13 (sodi	Slc13a2	0.983	0.218	0.833729	0.932964
10203	10481560	NM_183424	227717	pyroglutamylated RFamide pepti	Qrfp	0.983	-0.529	0.612426	0.820343
10204	10602770	XR_002032	667483	predicted gene, EG667483	EG667483	0.983	-0.15	0.884667	0.954694
10205	10569319	NM_009983	13033	cathepsin D	Ctsd	0.983	-1.213	0.263511	0.53828
10206	10565067	NM_026523	68039	neuromedin B	Nmb	0.983	-0.458	0.660189	0.848652
10207	10433910	NM_011624	21976	topoisomerase (DNA) III beta	Top3b	0.983	-0.837	0.429585	0.690576
10208	10564736	NM_017462	18975	polymerase (DNA directed), gam	Polg	0.983	-0.446	0.668955	0.852739
10209	10454709	NM_009004	19348	kinesin family member 20A	Kif20a	0.983	-0.715	0.497251	0.741615
10210	10588109	ENSMUST00000056103	69797	RIKEN cDNA 1600029I14 gene	1600029I14Rik	0.983	-0.056	0.956479	0.983504
10211	10415092	ENSMUST00000038631	75913	RIKEN cDNA 4930579G18 gene	4930579G18Rik	0.983	-0.141	0.89191	0.95769
10212	10429428	AK132992	268816	gene model 628, (NCBI)	Gm628	0.983	0.152	0.883573	0.954141
10213	10392721	NM_026682	52670	cleavage and polyadenylation s	Cpsf4l	0.983	0.05	0.961122	0.985069
10214	10421870					0.983	0.04	0.969432	0.987616
10215	10553057	DQ534901	74490	RIKEN cDNA 5430432N15 gene	5430432N15Rik	0.983	-0.162	0.875469	0.950704
10216	10559681	NM_172737	232813	RIKEN cDNA D430041B17 gene	D430041B17Rik	0.983	-0.083	0.936311	0.974999
10217	10497066	NM_017381	53861	zinc finger, RAN-binding domai	Zranb2	0.983	-0.307	0.767687	0.903483
10218	10348570	NM_001033292	227357	espin-like	Espnl	0.983	-0.081	0.937353	0.975526
10219	10517568	NM_001126318	242711	novel protein similar to elast	RP23-246F18.6	0.983	-0.048	0.962795	0.985542
10220	10544150	NM_001033430	338523	jumonji C domain-containing hi	Jhdm1d	0.983	-0.372	0.720254	0.878163
10221	10358928	NM_009782	12290	calcium channel, voltage-depen	Cacna1e	0.983	-0.211	0.838389	0.934421
10222	10393774	NM_199469	217365	nuclear protein localization 4	Nploc4	0.983	-0.61	0.560736	0.78784
10223	10564726	NM_020599	19771	retinaldehyde binding protein	Rlbp1	0.983	-0.044	0.966166	0.986556
10224	10369898	ENSMUST00000049520	108950	RIKEN cDNA 1700049L16 gene	1700049L16Rik	0.983	-0.724	0.492038	0.738272
10225	10415228	NM_009947	12891	copine VI	Cpne6	0.983	0.043	0.966585	0.986746

10225	10415228	NM_009947	12891	copine VI	Cpne6	0.983	0.043	0.966583	0.986746
10226	10455346	NM_001039474	56070	transcription elongation regul	Tcerg1	0.983	-0.486	0.641587	0.837649
10227	10348879	NM_025454	66262	inhibitor of growth family, me	Ing5	0.983	-0.426	0.682551	0.859827
10228	10573549	NM_026791	68628	F-box and WD-40 domain protein	Fbxw9	0.983	-0.66	0.530007	0.76526
10229	10532578	XM_912851	74376	myosin XVIIIb	Myo18b	0.983	-0.068	0.94785	0.97949
10230	10489946	NM_010072	13480	dolichol-phosphate (beta-D) ma	Dpm1	0.983	-0.536	0.608397	0.817693
10231	10552000	NM_026961	69147	RIKEN cDNA 2200002J24 gene	2200002J24Rik	0.983	-0.121	0.907011	0.963565
10232	10398649	NM_028807	74190	RIKEN cDNA 1200009I06 gene	1200009I06Rik	0.983	-0.173	0.867174	0.946934
10233	10440617					0.983	-0.164	0.874581	0.949978
10234	10424573	XR_032206	383051	similar to PRUNEM1	LOC383051	0.983	-0.507	0.627609	0.830619
10235	10455312	AY461716	225432	RNA binding motif protein 27	Rbm27	0.983	-0.459	0.660071	0.848652
10236	10576816	NM_026972	69165	CD209b antigen	Cd209b	0.982	0.126	0.903484	0.962464
10237	10474492	NM_146381	258379	olfactory receptor 1284	Olfr1284	0.982	0.234	0.821745	0.92863
10238	10550627	NM_175668	319197	G protein-coupled receptor 4	Gpr4	0.982	-0.431	0.679335	0.857678
10239	10605674	NM_008892	18968	polymerase (DNA directed), alp	Pola1	0.982	-0.621	0.553872	0.783297
10240	10393749					0.982	-0.282	0.785626	0.912507
10241	10424557	ENSMUST00000075602	633752	predicted gene, EG633752	EG633752	0.982	-0.353	0.734408	0.886559
10242	10512288	BC047068	69961	RIKEN cDNA 2810432D09 gene	2810432D09Rik	0.982	-0.679	0.51805	0.756834
10243	10604930	XM_001474636	100040409	similar to syndecan-1	LOC100040409	0.982	-0.1	0.922945	0.969148
10244	10530516	NM_001122754	22165	TXK tyrosine kinase	Txk	0.982	-0.068	0.94761	0.979302
10245	10427241	NM_001103165	18521	poly(rC) binding protein 2	Pcbp2	0.982	-0.561	0.59174	0.806879
10246	10490221	NM_025983	67126	ATP synthase, H+ transporting,	Atp5e	0.982	-1.112	0.301742	0.577902
10247	10511692					0.982	-0.652	0.534712	0.768432
10248	10476270	BC048399	69596	RIKEN cDNA 2310035K24 gene	2310035K24Rik	0.982	-0.19	0.854704	0.941172
10249	10499839	NM_133854	20615	SNAP-associated protein	Snapin	0.982	-0.651	0.535442	0.769059
10250	10418164	ENSMUST00000062438	75163	RIKEN cDNA 4930542C16 gene	4930542C16Rik	0.982	-0.157	0.879309	0.952124
10251	10517240	NM_001099296	72690	glycine/arginine rich protein	Grrp1	0.982	0.034	0.973614	0.988697
10252	10385027	ENSMUST00000020508	69351	RIKEN cDNA 1700008A04 gene	1700008A04Rik	0.982	-0.476	0.648413	0.841814
10253	10381111	XR_001819	630936	similar to nuclease sensitive	LOC630936	0.982	-0.468	0.653526	0.844695
10254	10439527	ENSMUST00000096065	100043314	similar to poliovirus receptor	LOC100043314	0.982	-0.004	0.9967	0.998777
10255	10519124	NM_008072	14403	gamma-aminobutyric acid (GABA-	Gabrd	0.982	0.107	0.917753	0.967684
10256	10456599	ENSMUST00000066583	433202	predicted gene, ENSMUSG0000005	ENSMUSG00000053861	0.982	-0.173	0.867594	0.947004
10257	10535647	NM_020582	57423	ATP synthase, H+ transporting,	Atp5j2	0.982	-1.058	0.324358	0.600843
10258	10535458	NM_028379	72881	zinc finger, DHHC domain conta	Zdhhc4	0.982	-0.285	0.783602	0.912068
10259	10382284	NM_021880	19084	protein kinase, cAMP dependent	Prkar1a	0.982	-0.523	0.61672	0.82302
10260	10433977	ENSMUST00000069420	224019	transmembrane protein 191C	Tmem191c	0.982	-0.497	0.634279	0.833748
10261	10454735	BC057111	66306	RIKEN cDNA 2810012G03 gene	2810012G03Rik	0.982	-0.967	0.364673	0.635773
10262	10509267	NM_009523	22417	wingless-related MMTV integrat	Wnt4	0.982	-0.232	0.822873	0.929127
10263	10601673	NM_133196	108062	cleavage stimulation factor, 3	Cstf2	0.982	-0.659	0.530382	0.765382
10264	10454326	BC084681	68046	RIKEN cDNA 2700062C07 gene	2700062C07Rik	0.982	-0.5	0.632172	0.832782
10265	10505919					0.982	-0.033	0.974823	0.989376
10266	10357658					0.982	0.214	0.83668	0.934075
10267	10554061	NM_001033877	233332	a disintegrin-like and metallo	Adamts17	0.982	0.271	0.793849	0.91617
10268	10512999	NM_001033454	381524	expressed sequence AI427809	AI427809	0.982	-0.421	0.685998	0.861365
10269	10551435	NM_001122603	215384	Fc fragment of IgG binding pro	Fcgbp	0.982	-0.328	0.751991	0.895376
10270	10451493	ENSMUST00000086675	442840	RIKEN cDNA A330017A19 gene	A330017A19Rik	0.982	-0.079	0.939421	0.976362
10271	10561194	NM_015782	53607	small nuclear ribonucleoprotei	Snrpa	0.982	-0.35	0.736562	0.887367
10272	10359908	NM_009062	19736	regulator of G-protein signali	Rgs4	0.982	-0.156	0.880446	0.952526
10273	10370837	NM_011548	21423	transcription factor E2a	Tcfe2a	0.982	-0.695	0.508845	0.750513

10274	10381567	NM_028076	72053	transmembrane and ubiquitin-li	Tmub2	0.982	-0.412	0.692255	0.865004
10275	10492590	NM_178726	242083	protein phosphatase 1 (formerl	Ppm1l	0.982	-0.804	0.446924	0.70468
10276	10355864	NM_001001566	74241	chondroitin polymerizing facto	Chpf	0.982	-0.306	0.768482	0.903765
10277	10505888	NM_010505	15968	interferon alpha 5	Ifna5	0.982	0.189	0.855497	0.941478
10278	10555254					0.982	0.051	0.960862	0.985069
10279	10474683					0.982	0.212	0.838075	0.934421
10280	10429584					0.982	-0.361	0.728102	0.882032
10281	10557624					0.982	-0.342	0.74232	0.890171
10282	10590909	NM_028013	71946	endonuclease domain containing	Endod1	0.982	-0.955	0.370405	0.641116
10283	10383532	NM_026272	67608	nuclear prelamin A recognition	Narf	0.982	-0.54	0.605493	0.815969
10284	10462343	ENSMUST00000065159	433237	predicted gene, ENSMUSG0000005	ENSMUSG00000052976	0.982	-0.093	0.928073	0.971746
10285	10374880	NM_133767	76784	mitochondrial translational in	Mtif2	0.982	-0.983	0.357536	0.629926
10286	10577946					0.982	-0.366	0.725053	0.880804
10287	10480999	NM_026563	68112	serologically defined colon ca	Sdccag3	0.982	-0.576	0.582385	0.800864
10288	10424945	NM_010630	16581	kinesin family member C2	Kifc2	0.982	0.066	0.948917	0.980236
10289	10387890	NM_023158	66102	chemokine (C-X-C motif) ligand	Cxcl16	0.982	-0.203	0.844439	0.936859
10290	10516721	XR_032427	100040532	similar to ribosomal protein L	LOC100040532	0.982	0.093	0.928407	0.971746
10291	10362711	NM_177793	327747	RIKEN cDNA 9030224M15 gene	9030224M15Rik	0.982	0.218	0.833298	0.932877
10292	10399782	NM_009417	22018	thyroid peroxidase	Tpo	0.982	-0.217	0.834475	0.933157
10293	10429957	NM_013909	30840	F-box and leucine-rich repeat	Fbxl6	0.982	0.086	0.933893	0.973728
10294	10535780	NM_010229	14255	FMS-like tyrosine kinase 3	Flt3	0.982	-0.018	0.985892	0.994073
10295	10511207	NM_028020	71957	cleavage and polyadenylation s	Cpsf3l	0.982	-0.58	0.579314	0.798918
10296	10369290	NM_029083	74747	DNA-damage-inducible transcrip	Ddit4	0.982	-0.467	0.654283	0.845158
10297	10465005	NM_001038231	23825	barrier to autointegration fac	Banf1	0.982	-0.961	0.367431	0.638358
10298	10449061	NM_144816	214951	rhomboid, veinlet-like 1 (Dros	Rhbdl1	0.982	-0.171	0.869198	0.947675
10299	10436804	NM_029844	77037	melanocortin 2 receptor access	Mrap	0.982	-0.231	0.82398	0.929508
10300	10401128	NM_008558	17187	Max protein	Max	0.982	-0.749	0.47778	0.7284
10301	10517600	NM_026880	68943	PTEN induced putative kinase 1	Pink1	0.982	-0.281	0.786907	0.912989
10302	10606554	NM_138742	54561	nucleosome assembly protein 1-	Nap1l3	0.982	-1.521	0.170919	0.422729
10303	10531428	NM_183392	269113	nucleoporin 54	Nup54	0.982	-0.558	0.593764	0.808198
10304	10578938	NM_001033429	333307	tripartite motif-containing 75	Trim75	0.982	-0.344	0.74047	0.889372
10305	10567173	NM_011083	18704	phosphatidylinositol 3-kinase,	Pik3c2a	0.982	-0.587	0.574916	0.797076
10306	10522149	NM_016786	53323	ubiquitin-conjugating enzyme E	Ube2k	0.982	-0.651	0.535259	0.768906
10307	10586039	NM_001083927	21887	transducin-like enhancer of sp	Tle3	0.982	-0.694	0.509484	0.750804
10308	10556242					0.982	0.125	0.903973	0.962757
10309	10466404					0.982	-0.553	0.596997	0.810251
10310	10376366	NM_001083884	70163	RIKEN cDNA 2210415F13 gene	2210415F13Rik	0.982	0.11	0.915449	0.966659
10311	10414168	NM_173418	239038	leucine-rich repeat, immunoglo	Lrit2	0.982	0.002	0.99867	0.999521
10312	10379342					0.982	-0.161	0.876766	0.951319
10313	10436196					0.982	-0.306	0.768394	0.903712
10314	10427301					0.982	-0.222	0.830714	0.932075
10315	10428070	AK020480	77358	RIKEN cDNA 9430069I07 gene	9430069I07Rik	0.982	-0.005	0.996462	0.998723
10316	10460513	NM_175383	108902	UDP-GlcNAc:betaGal beta-1,3-N-	B3gnt1	0.982	-0.663	0.527867	0.763369
10317	10576799	NM_130905	170780	CD209e antigen	Cd209e	0.982	-0.086	0.933508	0.973422
10318	10501143	NM_145542	229709	S-adenosylhomocysteine hydrola	Ahcyl1	0.982	-0.607	0.562517	0.789713
10319	10552425	BC112410	75690	RIKEN cDNA 2210412E05 gene	2210412E05Rik	0.982	-0.619	0.554976	0.783898
10320	10440463	XR_031142	383172	predicted gene, EG383172	EG383172	0.982	-0.707	0.501487	0.744504
10321	10521031	NM_011738	22629	tyrosine 3-monooxygenase/trypt	Ywhah	0.982	-0.563	0.590592	0.80632
10322	10403765	NM_172120	218035	vacuolar protein sorting 41 (y	Vps41	0.982	-0.947	0.374347	0.644466
10323	10377681	NM_026017	67181	Dullard homolog (Xenopus laevi	Dullard	0.982	-0.905	0.394531	0.662113
10324	10588931	BC048562	434439	cDNA sequence BC048562	BC048562	0.981	0.371	0.721057	0.878601
10325	10442954	NM_009733	12005	axin 1	Axin1	0.981	-0.587	0.574889	0.797076
10326	10543676	ENSMUST00000059487	73533	RIKEN cDNA 1700080G18 gene	1700080G18Rik	0.981	-0.658	0.531167	0.765576
10327	10485361	BC025075	68170	RIKEN cDNA B230118H07	B230118H07Rik	0.981	1.099	0.30706	0.583646

				gene					
10328	10380751	NM_025927	67036	mitochondrial ribosomal protei	Mrpl45	0.981	-0.678	0.518937	0.757293
10329	10586176	NM_183316	330959	small nuclear RNA activating c	Snapc5	0.981	-0.576	0.581864	0.800451
10330	10461475	NM_172302	269061	RIKEN cDNA 5730453I16 gene	5730453I16Rik	0.981	-0.652	0.534572	0.768432
10331	10540405	BC045208	74729	SET domain and mariner transpo	Setmar	0.981	-0.347	0.738333	0.888438
10332	10394690	NM_033270	50496	E2F transcription factor 6	E2f6	0.981	-1.019	0.341311	0.616096
10333	10460397	AK137104	619307	RIKEN cDNA 9430078G10 gene	9430078G10Rik	0.981	-0.414	0.691012	0.864447
10334	10478997	NM_009335	21420	transcription factor AP-2, gam	Tcfap2c	0.981	0.042	0.967717	0.987137
10335	10561266	NM_032610	80297	spectrin beta 4	Spnb4	0.981	-0.018	0.98608	0.994146
10336	10348070	NM_010880	17975	nucleolin	Ncl	0.981	-0.453	0.664062	0.850267
10337	10439276	NM_027342	70186	RIKEN cDNA 2310056P07 gene	2310056P07Rik	0.981	-1.015	0.343087	0.617171
10338	10352717	NM_030060	381319	basic leucine zipper transcrip	Batf3	0.981	-0.254	0.806554	0.921832
10339	10517243	NM_146156	230809	PDLIM1 interacting kinase 1 li	Pdik1l	0.981	-0.617	0.556142	0.784723
10340	10568215					0.981	-0.056	0.956983	0.983559
10341	10584352	NM_146882	258882	olfactory receptor 874	Olfr874	0.981	-0.419	0.687572	0.862228
10342	10437272	NM_001081280	268857	NLR family, CARD domain contai	Nlrc3	0.981	0.066	0.948966	0.980236
10343	10379117	NM_001045522	216976	cDNA sequence BC030499	BC030499	0.981	0.453	0.664088	0.850267
10344	10454984	NM_026464	67936	WD repeat domain 55	Wdr55	0.981	-0.436	0.675731	0.855911
10345	10513912	EF662061	353204	aldolase 1, A isoform, retroge	Aldoart1	0.981	-0.202	0.845823	0.937284
10346	10426891	NM_027334	70152	methyltransferase like 7A1	Mettl7a1	0.981	-0.708	0.501193	0.744202
10347	10445458	NM_028198	72322	exportin 5	Xpo5	0.981	-0.849	0.423071	0.685314
10348	10604245					0.981	0.001	0.999275	0.999589
10349	10399214	NM_016676	19325	RAB10, member RAS oncogene fam	Rab10	0.981	-0.765	0.46838	0.720616
10350	10524338	NM_023695	12960	crystallin, beta B1	Crybb1	0.981	-0.057	0.955819	0.98316
10351	10348521	NM_001033408	329207	RNA binding motif protein 44	Rbm44	0.981	-0.114	0.91241	0.965082
10352	10458461	NM_010411	15183	histone deacetylase 3	Hdac3	0.981	-0.619	0.555135	0.783898
10353	10545859	NM_020596	13656	early growth response 4	Egr4	0.981	-0.166	0.872606	0.949165
10354	10368780	NM_199058	140741	G protein-coupled receptor 6	Gpr6	0.981	0.433	0.677585	0.856701
10355	10515924	BC057371	194237	cDNA sequence BC057371	BC057371	0.981	-0.091	0.929617	0.972207
10356	10418244	AK076950	791355	predicted gene, ENSMUSG0000005	ENSMUSG00000053165	0.981	-0.757	0.472844	0.724458
10357	10382935	NM_198022	217351	trinucleotide repeat containin	Tnrc6c	0.981	-0.424	0.68374	0.860022
10358	10460767	NM_028967	74481	basic leucine zipper transcrip	Batf2	0.981	0.014	0.988921	0.995308
10359	10575672	NM_029139	668110	RIKEN cDNA 4930481F22 gene	4930481F22Rik	0.981	0.272	0.793492	0.915908
10360	10419674					0.981	0.191	0.8536	0.940713
10361	10564482	NM_201639	233335	desmuslin	Dmn	0.981	-0.736	0.485013	0.733398
10362	10397651	NM_178914	104871	spermatogenesis associated 7	Spata7	0.981	-0.243	0.814846	0.925748
10363	10511881	NM_172865	242362	mannosidase, endo-alpha	Manea	0.981	-0.657	0.5318	0.766019
10364	10503484	BC096046	66302	RIKEN cDNA 2410005O16 gene	2410005O16Rik	0.981	-0.439	0.673339	0.854824
10365	10378549	NM_177708	237847	reticulon 4 receptor-like 1	Rtn4rl1	0.981	-0.069	0.946709	0.978837
10366	10425741	NM_029066	74716	WBP2 N-terminal like	Wbp2nl	0.981	-0.577	0.581605	0.800408
10367	10370007	NM_029472	75886	glutathione S-transferase, the	Gstt4	0.981	0.12	0.907438	0.963723
10368	10464772	BC021951	69861	RIKEN cDNA 2010003K11 gene	2010003K11Rik	0.981	-0.066	0.948976	0.980236
10369	10478299	NM_001081338	241764	l(3)mbt-like (Drosophila)	L3mbtl	0.981	-0.518	0.619702	0.825021
10370	10406681	NM_009680	11774	adaptor-related protein comple	Ap3b1	0.981	-0.631	0.547756	0.778543
10371	10601547					0.981	0.025	0.980568	0.991919
10372	10574962	NM_010901	18021	nuclear factor of activated T-	Nfatc3	0.981	-0.802	0.448351	0.705929
10373	10357790	NM_011439	20668	SRY-box containing gene 13	Sox13	0.981	-0.643	0.53989	0.772463
10374	10354816	NM_001042634	12747	CDC-like kinase 1	Clk1	0.981	-0.246	0.81282	0.924689
10375	10509820	NM_173867	108911	regulator of chromosome conden	Rcc2	0.981	-0.594	0.570747	0.795023
10376	10364792	NM_183152	216166	RIKEN cDNA 6330514A18 gene	6330514A18Rik	0.981	0.047	0.963852	0.985834
10377	10441195	NM_031174	13508	Down syndrome cell adhesion mo	Dscam	0.981	0.319	0.758861	0.899051

10378	10525893	NM_030210	78894	acetoacetyl-CoA synthetase	Aacs	0.981	-0.338	0.744656	0.891513
10379	10547492	NM_026028	67200	coiled-coil domain containing	Ccdc77	0.981	-0.943	0.376203	0.646281
10380	10389882	NM_026313	67684	RIKEN cDNA 3300001P08 gene	3300001P08Rik	0.981	-0.345	0.739702	0.889275
10381	10569134	NM_016874	54006	deformed epidermal autoregulat	Deaf1	0.981	-0.205	0.843565	0.936586
10382	10456619					0.981	-0.382	0.713387	0.874578
10383	10372003					0.981	-0.294	0.776994	0.909262
10384	10384219	XR_033922	665339	similar to RBBP5 protein	LOC665339	0.981	-0.364	0.726405	0.881516
10385	10507726	NM_019563	56222	Cbp/p300-interacting transacti	Cited4	0.981	-0.761	0.470844	0.722723
10386	10563558	NM_013789	27414	secretion regulating guanine n	Sergef	0.981	-0.176	0.864869	0.946153
10387	10575476	NM_146216	234729	Vac14 homolog (S. cerevisiae)	Vac14	0.981	-0.767	0.467683	0.720331
10388	10452087	NM_001029979	224902	scaffold attachment factor B2	Safb2	0.981	-0.568	0.587161	0.80408
10389	10502805	NM_008966	19220	prostaglandin F receptor	Ptgfr	0.981	-0.159	0.878259	0.951767
10390	10500237	BC067054	75137	RIKEN cDNA 4930535B03 gene	4930535B03Rik	0.981	-0.776	0.462591	0.717093
10391	10574421	ENSMUST00000098469	100038583	predicted gene, ENSMUSG0000007	ENSMUSG00000074134	0.981	-0.274	0.791487	0.915192
10392	10439357	NM_001037321	207215	F-box protein 40	Fbxo40	0.981	-0.528	0.61329	0.820877
10393	10518570	NM_001081274	110208	phosphogluconate dehydrogenase	Pgd	0.981	-0.901	0.396586	0.663981
10394	10584698					0.981	0.121	0.906693	0.963405
10395	10453518	NM_020252	18189	neurexin I	Nrxn1	0.981	-0.391	0.707041	0.872175
10396	10561031	NM_010719	16890	lipase, hormone sensitive	Lipe	0.981	-0.176	0.864963	0.946153
10397	10540248	NM_001113198	17342	microphthalmia-associated tran	Mitf	0.981	-0.43	0.679833	0.857865
10398	10372457	NM_025706	66687	TBC1 domain family, member 15	Tbc1d15	0.981	-0.46	0.659106	0.848007
10399	10527268	NM_008886	18861	postmeiotic segregation increa	Pms2	0.981	-0.879	0.407776	0.672177
10400	10410092	NM_175494	238673	zinc finger protein 367	Zfp367	0.981	-0.364	0.726292	0.881516
10401	10576524	NM_001111141	244666	gene model 505, (NCBI)	Gm505	0.981	-0.806	0.445811	0.703765
10402	10572497	NM_008353	16161	interleukin 12 receptor, beta	Il12rb1	0.98	0.325	0.754124	0.896425
10403	10360315	EF032497	677296	Fc receptor-like 6	Fcrl6	0.98	0.195	0.850899	0.94008
10404	10436024	NM_008099	14525	germinal center expressed tran	Gcet2	0.98	-0.335	0.747053	0.892497
10405	10383993	NM_134033	104479	coiled-coil domain containing	Ccdc117	0.98	-1.003	0.348344	0.622132
10406	10388994	ENSMUST00000100734	100038598	predicted gene, ENSMUSG0000007	ENSMUSG00000072631	0.98	-0.303	0.77036	0.905061
10407	10451081	XM_910980	635812	similar to CG8435-PA	LOC635812	0.98	-0.469	0.65275	0.844541
10408	10424810	NM_010331	14731	GPI anchor attachment protein	Gpaa1	0.98	-0.661	0.529203	0.76441
10409	10365170	ENSMUST00000099442	268319	cDNA sequence BC025920	BC025920	0.98	-0.442	0.671749	0.854369
10410	10607346	NM_029836	52808	TSPY-like 2	Tspyl2	0.98	-0.744	0.480239	0.729941
10411	10474307	BC057916	74088	RIKEN cDNA 0610012H03 gene	0610012H03Rik	0.98	-0.189	0.85498	0.941302
10412	10532588	XM_912851	74376	myosin XVIIIb	Myo18b	0.98	-0.119	0.908889	0.963765
10413	10493421	BC088990	68521	RIKEN cDNA 1110013L07 gene	1110013L07Rik	0.98	-0.421	0.686309	0.861515
10414	10390258	NM_028965	74479	sorting nexin 11	Snx11	0.98	-0.24	0.817296	0.927212
10415	10382542	NM_001002929	445007	nucleoporin 85	Nup85	0.98	-0.156	0.880207	0.952468
10416	10431558	BC087962	70113	RIKEN cDNA 2010001J22 gene	2010001J22Rik	0.98	-0.172	0.868361	0.947244
10417	10365428	NM_028709	74007	BTB (POZ) domain containing 11	Btbd11	0.98	-0.331	0.750233	0.894442
10418	10371154	NM_001014836	432479	RIKEN cDNA 4930404N11 gene	4930404N11Rik	0.98	-0.445	0.669545	0.852924
10419	10433161	XR_033297	668321	similar to MARCKS-like protein	LOC668321	0.98	-0.027	0.978902	0.991611
10420	10358155	XR_033650	76422	RIKEN cDNA 2310006M14 gene	2310006M14Rik	0.98	-0.172	0.86805	0.947171
10421	10596265					0.98	-0.577	0.581271	0.80031
10422	10400210	ENSMUST00000042052	207304	HECT domain containing 1	Hectd1	0.98	-0.548	0.60045	0.812278
10423	10345352					0.98	0.314	0.76226	0.901088
10424	10547088	NM_010774	17193	methyl-CpG binding domain prot	Mbd4	0.98	-1.083	0.313607	0.59037
10425	10454782	NM_007913	13653	early growth response 1	Egr1	0.98	-0.288	0.781693	0.911343
10426	10589503	NM_001081381	72341	transmembrane protein 103	Tmem103	0.98	-0.311	0.764314	0.90173

10427	10574288	NM_001042715	330830	coiled-coil domain containing	Ccdc135	0.98	-0.415	0.690272	0.864076
10428	10571036	NM_028000	71910	phosphatidic acid phosphatase	Ppapdc1	0.98	-0.644	0.539472	0.772177
10429	10435821	NM_028108	72117	N-acetyltransferase 13	Nat13	0.98	-0.637	0.544092	0.776215
10430	10569953	NM_133968	102209	small nuclear RNA activating c	Snapc2	0.98	-0.435	0.676134	0.855911
10431	10427687	NM_177123	320277	sperm flagellar 2	Spef2	0.98	0.438	0.674288	0.855309
10432	10376615	NM_010862	17910	myosin XV	Myo15	0.98	-0.116	0.910541	0.964214
10433	10533751	NM_011256	19679	phosphatidylinositol transfer	Pitpnm2	0.98	-0.387	0.709646	0.872992
10434	10588975	NM_027804	71472	ubiquitin specific peptidase 1	Usp19	0.98	-0.262	0.800316	0.919317
10435	10380514	BC055690	215512	RIKEN cDNA 5730593F17 gene	5730593F17Rik	0.98	0.006	0.995053	0.998075
10436	10428931					0.98	-0.126	0.903283	0.962361
10437	10372766	NM_080446	117599	helicase (DNA) B	Helb	0.98	-0.665	0.527011	0.762858
10438	10380109	NM_001045527	327992	heat shock transcription facto	Hsf5	0.98	-0.23	0.824251	0.929508
10439	10562152	NM_010758	17136	myelin-associated glycoprotein	Mag	0.98	-0.316	0.760643	0.900103
10440	10402659	NM_175207	74251	ankyrin repeat domain 9	Ankrd9	0.98	-0.169	0.870319	0.948265
10441	10570955	ENSMUST00000061860	71655	RIKEN cDNA 4930518F22 gene	4930518F22Rik	0.98	-0.099	0.9239	0.96976
10442	10539238	NM_145570	232146	transmembrane protein 166	Tmem166	0.98	-0.249	0.810188	0.923433
10443	10413640	NM_011849	23955	NIMA (never in mitosis gene a)	Nek4	0.98	-0.439	0.67329	0.854824
10444	10567316	NM_172476	209760	transmembrane channel-like gen	Tmc7	0.98	-0.367	0.723964	0.88046
10445	10563816	NM_001115087	100040608	Fanconi anemia, complementatio	Fancf	0.98	-0.589	0.57407	0.797076
10446	10469140					0.98	0.033	0.974506	0.989196
10447	10428561	NM_009009	19357	RAD21 homolog (S. pombe)	Rad21	0.98	-0.742	0.481479	0.730878
10448	10520250	NM_016736	53312	negative regulator of ubiquiti	Nub1	0.98	-0.645	0.539107	0.772047
10449	10518686	NM_008840	18707	phosphatidylinositol 3-kinase	Pik3cd	0.98	-0.306	0.768025	0.903579
10450	10512682	NM_173399	230119	zinc finger and BTB domain con	Zbtb5	0.98	-0.496	0.634799	0.833935
10451	10552110	XM_001481136	435962	similar to hCG16001	LOC435962	0.98	0.199	0.848132	0.938472
10452	10533403	NM_007804	13048	cut-like homeobox 2	Cux2	0.98	-0.441	0.672466	0.854651
10453	10534873	ENSMUST00000031732	71176	F-box protein 24	Fbxo24	0.98	-0.299	0.77345	0.9067
10454	10485277					0.98	-0.154	0.881551	0.953086
10455	10431546	NM_138302	72962	thymidine phosphorylase	Tymp	0.98	-0.666	0.525906	0.76194
10456	10447042	NM_028611	73694	RIKEN cDNA 2410091C18 gene	2410091C18Rik	0.98	-0.176	0.865046	0.946153
10457	10365297	BC094241	28109	DNA segment, Chr 10, Wayne Sta	D10Wsu102e	0.98	-0.807	0.445364	0.703573
10458	10421758	AK129178	219181	A kinase (PRKA) anchor protein	Akap11	0.98	-0.437	0.675071	0.855635
10459	10598020					0.98	-0.516	0.621079	0.826022
10460	10552888	XM_914689	381884	solute carrier family 6, membe	Slc6a16	0.98	-0.171	0.868802	0.947491
10461	10464415	BC013514	67894	RIKEN cDNA 1810055E12 gene	1810055E12Rik	0.98	-0.439	0.673631	0.855069
10462	10348590	NM_173395	227358	cDNA sequence BC056923	BC056923	0.98	-0.237	0.818922	0.928035
10463	10426110	NM_145478	223775	proviral integration site 3	Pim3	0.98	-0.442	0.671769	0.854369
10464	10555777					0.98	0.006	0.995337	0.99817
10465	10372204					0.98	-0.177	0.864568	0.946153
10466	10453114	NM_198942	106794	DEAH (Asp-Glu-Ala-Asp/His) box	Dhx57	0.98	-0.319	0.758526	0.898805
10467	10527573					0.98	-0.194	0.851732	0.940193
10468	10531581					0.98	-0.161	0.876484	0.951096
10469	10521705	ENSMUST00000053250	624224	clarin 2	Clrn2	0.98	-0.493	0.636569	0.834887
10470	10396867	NM_133798	97827	exonuclease 3"-5" domain-lik	Exdl2	0.98	-0.44	0.672936	0.854651
10471	10591715	NM_177318	319601	zinc finger protein 653	Zfp653	0.98	-0.047	0.963619	0.985728
10472	10595202					0.98	0.07	0.945868	0.978614
10473	10510399	NM_001003893	17175	mannan-binding lectin serine p	Masp2	0.98	-0.117	0.909818	0.964056
10474	10478374	NM_144891	228858	ganglioside-induced differenti	Gdap1l1	0.98	-0.44	0.67288	0.854651
10475	10469943	BC061039	68222	cDNA sequence BC061039	BC061039	0.98	-0.045	0.965436	0.986124
10476	10545692					0.98	-0.49	0.638961	0.835923
10477	10410287	NM_001001152	238690	zinc finger protein 458	Zfp458	0.98	-0.56	0.592279	0.807145
10478	10480842	NM_001109993	51875	transmembrane protein 141	Tmem141	0.98	-0.539	0.606172	0.816415
10479	10437680	NM_008933	19119	protamine 2	Prm2	0.98	-0.619	0.555116	0.783898
10480	10434211	NM_023120	13972	guanine nucleotide binding pro	Gnb1l	0.98	-0.345	0.740168	0.889339

10481	10535467					0.98	-0.038	0.970517	0.988088
10482	10444306	NM_001033978	381091	histocompatibility 2, class II	H2-Eb2	0.98	-0.321	0.757457	0.898154
10483	10370413	NM_138601	28295	DNA segment, Chr 10, Johns Hop	D10Jhu81e	0.98	-0.55	0.599062	0.811784
10484	10479483	ENSMUST00000108875	329581	baculoviral IAP repeat-contain	Birc7	0.98	-0.172	0.867837	0.947073
10485	10459823	NM_001039252	639653	predicted gene, EG639653	EG639653	0.98	-0.438	0.674458	0.855422
10486	10463751	NM_011053	18572	programmed cell death protein	Pdcd11	0.98	-0.571	0.585194	0.802735
10487	10606252					0.98	-0.494	0.636196	0.834785
10488	10568810	BC116882	212124	RIKEN cDNA E030019B06 gene	E030019B06Rik	0.98	0.054	0.958623	0.984334
10489	10400413	NM_001112714	56784	GTPase activating RANGAP domai	Garnl1	0.98	-0.541	0.604711	0.815591
10490	10526754	NM_021392	11781	adaptor-related protein comple	Ap4m1	0.98	-0.301	0.772149	0.906083
10491	10352792	XR_033810	100042611	similar to Cks1 protein homolo	LOC100042611	0.98	-0.228	0.825671	0.929887
10492	10454514	NM_144862	225341	LIM and senescent cell antigen	Lims2	0.98	0.091	0.929675	0.972207
10493	10444761	NM_019693	53817	HLA-B-associated transcript 1A	Bat1a	0.979	-0.682	0.516581	0.755888
10494	10408828	NM_008104	107889	glial cells missing homolog 2	Gcm2	0.979	-0.224	0.829258	0.93131
10495	10567022	NM_133700	68815	BTB (POZ) domain containing 10	Btbd10	0.979	-0.4	0.700429	0.86896
10496	10550650	NM_007948	13870	excision repair cross-compleme	Ercc1	0.979	-0.684	0.515091	0.754817
10497	10388896					0.979	-0.425	0.683458	0.859874
10498	10479402	NM_028479	73247	RIKEN cDNA 1600027N09 gene	1600027N09Rik	0.979	-0.346	0.739008	0.888726
10499	10539444	NM_011912	24113	ventral anterior homeobox cont	Vax2	0.979	-0.225	0.828576	0.931115
10500	10490931	NM_172677	229096	YTH domain family 3	Ythdf3	0.979	-0.478	0.646562	0.840625
10501	10568233	BC031466	78921	RIKEN cDNA 9130019O22 gene	9130019O22Rik	0.979	-1.657	0.140256	0.378815
10502	10394346					0.979	-0.517	0.620626	0.825679
10503	10596267					0.979	-0.259	0.802641	0.919965
10504	10372877	NM_001081056	73192	exportin, tRNA (nuclear export	Xpot	0.979	-0.712	0.498924	0.742429
10505	10535418	NM_021326	57782	RB-associated KRAB repressor	Rbak	0.979	-0.389	0.708431	0.872343
10506	10508178	ENSMUST00000097886	230757	RIKEN cDNA 5730409E04Rik gene	5730409E04Rik	0.979	0.156	0.880306	0.952471
10507	10467962	NM_181422	329064	polycystic kidney disease 2-li	Pkd2l1	0.979	0.351	0.735864	0.886874
10508	10384930	NM_001100394	75087	RIKEN cDNA 4930505A04 gene	4930505A04Rik	0.979	0.032	0.975718	0.989951
10509	10397216	NM_172582	217707	coenzyme Q6 homolog (yeast)	Coq6	0.979	-0.741	0.482007	0.730954
10510	10566091	NM_001081424	504186	cholinergic receptor, nicotini	Chrna10	0.979	0.117	0.90985	0.964056
10511	10370584	BC089008	237397	RIKEN cDNA 4932409I22 gene	4932409I22Rik	0.979	0.036	0.971917	0.988148
10512	10426798	NM_031842	83797	SWI/SNF related, matrix associ	Smarcd1	0.979	-0.723	0.492194	0.738375
10513	10548701	NM_008514	16974	low density lipoprotein recept	Lrp6	0.979	-0.456	0.662074	0.849499
10514	10362201	NM_010217	14219	connective tissue growth facto	Ctgf	0.979	-0.339	0.744425	0.891438
10515	10383684	NM_010718	16886	LIM motif-containing protein k	Limk2	0.979	-0.464	0.656298	0.846043
10516	10562754					0.979	0.151	0.884167	0.954451
10517	10442857	NM_026238	67563	nuclear prelamin A recognition	Narfl	0.979	-0.387	0.709782	0.872992
10518	10437885	NM_013607	17880	myosin, heavy polypeptide 11,	Myh11	0.979	0.12	0.907965	0.963723
10519	10433494	NM_011955	26425	nucleotide binding protein 1	Nubp1	0.979	-0.331	0.749727	0.894292
10520	10443378	NM_001034871	328788	gene model 749, (NCBI)	Gm749	0.979	0.027	0.979036	0.991699
10521	10598029	ENSMUST00000082392	17716	NADH dehydrogenase subunit 1	ND1	0.979	-0.553	0.597132	0.810309
10522	10415127	NM_080729	140806	interleukin 25	Il25	0.979	-0.137	0.894709	0.958505
10523	10412082	NM_028487	73274	GC-rich promoter binding prote	Gpbp1	0.979	-0.705	0.503192	0.745637
10524	10360542					0.979	-0.306	0.768009	0.903579
10525	10576951	ENSMUST00000098943	100038550	predicted gene, ENSMUSG0000007	ENSMUSG00000074477	0.979	0.117	0.91016	0.964056
10526	10363486	NM_153542	216011	leucine rich repeat containing	Lrrc20	0.979	-0.088	0.931917	0.97291
10527	10516884	NM_027925	71787	tRNA selenocysteine associated	Trspap1	0.979	-1.03	0.336228	0.611869
10528	10476347	ENSMUST00000099333	767814	expressed sequence AU019990	AU019990	0.979	0.074	0.943001	0.977825
10529	10427035	NM_010444	15370	nuclear receptor subfamily 4,	Nr4a1	0.979	-0.046	0.964695	0.985959
10530	10465303	NM_198650	381203	solute carrier family 22 (orga	Slc22a20	0.979	-0.432	0.678053	0.856948

10531	10501051	NM_133869	99712	choline/ethanolaminephosphotra	Cept1	0.979	-0.399	0.701658	0.869143	
10532	10451465	NM_011195	19208	pre T-cell antigen receptor al	Ptcra	0.979	-0.122	0.906013	0.963405	
10533	10433575	ENSMUST00000100182	100038543	predicted gene, ENSMUSG0000007	ENSMUSG00000075403	0.979	-0.585	0.576479	0.797453	
10534	10574342	BC016418	101985	expressed sequence AA960436	AA960436	0.979	-0.924	0.385426	0.654626	
10535	10368484	ENSMUST00000070359	791368	predicted gene, ENSMUSG0000005	ENSMUSG00000056316	0.979	-0.125	0.903948	0.962757	
10536	10500429	NM_008123	14616	gap junction protein, alpha 8	Gja8	0.979	-0.375	0.718297	0.876988	
10537	10353574	NM_007733	12823	collagen, type XIX, alpha 1	Col19a1	0.979	-0.079	0.93887	0.976218	
10538	10568328	NM_178600	27973	vitamin K epoxide reductase co	Vkorc1	0.979	-0.656	0.532108	0.766201	
10539	10398082	ENSMUST00000021520	73928	RIKEN cDNA 4930408O17 gene	4930408O17Rik	0.979	0.054	0.958256	0.984334	
10540	10518679	NM_133435	66454	nicotinamide nucleotide adenyl	Nmnat1	0.979	-0.429	0.680645	0.85838	
10541	10358177	BC053100	67313	RIKEN cDNA 5730559C18 gene	5730559C18Rik	0.979	-0.131	0.899596	0.960245	
10542	10374466	NM_008996	19324	RAB1, member RAS oncogene fami	Rab1	0.979	-0.683	0.516117	0.755582	
10543	10568586	NM_175268	77938	RIKEN cDNA A930008G19 gene	A930008G19Rik	0.979	-1.065	0.321292	0.598079	
10544	10524640	BC031162	72357	RIKEN cDNA 2210016L21 gene	2210016L21Rik	0.979	-0.572	0.584596	0.802272	
10545	10599648					0.979	0.156	0.880414	0.952526	
10546	10513195	NM_011660	22166	thioredoxin 1	Txn1	0.979	-0.433	0.677972	0.856898	
10547	10530380	NM_001038015	67980	glucosamine-6-phosphate deamin	Gnpda2	0.979	-0.601	0.566059	0.792149	
10548	10362899	ENSMUST00000099888	414125	RIKEN cDNA F830002L21 gene	F830002L21Rik	0.979	0.015	0.988714	0.995308	
10549	10453047	XR_034816	668812	similar to ribosomal protein	LOC668812	0.979	-0.236	0.820107	0.928345	
10550	10512265	NM_027993	71901	RIKEN cDNA 2310028H24 gene	2310028H24Rik	0.979	-0.283	0.785351	0.912507	
10551	10542724	NR_003625	381827	RIKEN cDNA 1700073E17 gene	1700073E17Rik	0.979	-0.45	0.666193	0.851266	
10552	10533462	NM_144912	231724	RAD9 homolog B (S. cerevisiae)	Rad9b	0.979	-0.497	0.633842	0.833492	
10553	10581299	NM_007427	11604	agouti related protein	Agrp	0.979	-0.102	0.921597	0.968694	
10554	10476252	NM_023117	12531	cell division cycle 25 homolog	Cdc25b	0.979	-0.075	0.942318	0.977825	
10555	10393045	AK140207	100038636	predicted gene, ENSMUSG0000007	ENSMUSG00000075418	0.979	0.184	0.858877	0.943374	
10556	10374706	NM_028304	74467	pseudouridylate synthase 10	Pus10	0.979	-1.151	0.286532	0.562214	
10557	10360443	NM_010209	14194	fumarate hydratase 1	Fh1	0.979	-0.743	0.480807	0.730487	
10558	10472994	NM_016804	53375	metaxin 2	Mtx2	0.979	-0.594	0.570957	0.795189	
10559	10573713	NM_172757	234549	HEAT repeat containing 3	Heatr3	0.979	-0.657	0.531277	0.765579	
10560	10446013	NM_026530	68047	MPN domain containing	Mpnd	0.979	-1.082	0.314141	0.590943	
10561	10560505					0.979	-0.292	0.77886	0.910097	
10562	10477600					0.979	-0.072	0.944732	0.978132	
10563	10454469	NM_153515	225339	AMME chromosomal region gene 1	Ammecr1l	0.979	-0.94	0.377649	0.647469	
10564	10390407	NM_001081220	217143	G protein-coupled receptor 179	Gpr179	0.979	-0.116	0.910491	0.964214	
10565	10503902	NM_007726	12801	cannabinoid receptor 1 (brain)	Cnr1	0.979	-0.248	0.810901	0.923749	
10566	10592701	NM_001034863	235300	transmembrane protein 136	Tmem136	0.978	-0.9	0.39715	0.664239	
10567	10551423	BC024577	71163	RIKEN cDNA 4933426I21 gene	4933426I21Rik	0.978	-0.594	0.570968	0.795189	
10568	10527880	BC029549	269623	RIKEN cDNA C030048B08 gene	C030048B08Rik	0.978	-0.385	0.711423	0.873563	
10569	10425655	AY270177	74369	meiosis defective 1	Mei1	0.978	-0.207	0.841768	0.936059	
10570	10391348	BC016089	67998	RIKEN cDNA 1300010M03 gene	1300010M03Rik	0.978	-0.44	0.672793	0.854651	
10571	10539822	NM_017477	54161	coatomer protein complex, subu	Copg	0.978	-0.469	0.652588	0.844451	
10572	10529052	NM_177870	330064	solute carrier family 5 (sodiu	Slc5a6	0.978	-0.431	0.679267	0.857678	
10573	10381260	NM_134028	103768	tubulin, gamma 2	Tubg2	0.978	0.036	0.972317	0.98815	
10574	10579772					0.978	-0.207	0.841886	0.936059	
10575	10552689	BC049752	75538	RIKEN cDNA 1700021P22 gene	1700021P22Rik	0.978	-0.208	0.84105	0.935759	
10576	10602105	NM_007736	12830	collagen, type IV, alpha 5	Col4a5	0.978	-0.384	0.711816	0.873734	

10577	10458386	NM_010885	17991	NADH dehydrogenase (ubiquinone	Ndufa2	0.978	-1.172	0.278362	0.553374
10578	10423745	NM_012031	26942	sperm associated antigen 1	Spag1	0.978	-0.371	0.720998	0.878601
10579	10439084	ENSMUST00000099984	675921	predicted gene, ENSMUSG0000007	ENSMUSG00000075265	0.978	-0.122	0.906517	0.963405
10580	10438726	XR_032916	625969	predicted gene, EG625969	EG625969	0.978	-0.533	0.609745	0.818413
10581	10404356	XM_909282	626683	similar to ribosomal protein L	LOC626683	0.978	-0.175	0.865905	0.94648
10582	10597377	NM_178624	72179	F-box and leucine-rich repeat	Fbxl2	0.978	-0.427	0.681691	0.859336
10583	10364990	NM_007907	13629	eukaryotic translation elongat	Eef2	0.978	-0.872	0.411372	0.675346
10584	10380210	NM_173374	110809	splicing factor, arginine/seri	Sfrs1	0.978	-0.866	0.414259	0.677477
10585	10477970	NM_009271	20779	Rous sarcoma oncogene	Src	0.978	-0.619	0.554762	0.783816
10586	10479807	XR_031780	666973	similar to Protein regulator o	LOC666973	0.978	-0.307	0.767748	0.903505
10587	10571329	XM_146277	244417	gene model 501, (NCBI)	Gm501	0.978	-0.074	0.943356	0.977948
10588	10435288	NM_010739	17063	mucin 13, epithelial transmemb	Muc13	0.978	-0.318	0.759158	0.89915
10589	10506335	NM_019840	18578	phosphodiesterase 4B, cAMP spe	Pde4b	0.978	-0.548	0.59993	0.812084
10590	10541803	NM_145979	107932	chromodomain helicase DNA bind	Chd4	0.978	-0.729	0.489114	0.736349
10591	10537437	AB106871	621427	predicted gene, ENSMUSG0000006	ENSMUSG00000068601	0.978	-0.16	0.876942	0.951412
10592	10559200	NM_009405	21953	troponin I, skeletal, fast 2	Tnni2	0.978	0.049	0.962542	0.985405
10593	10516419	NM_198960	332937	transcription factor AP-2, eps	Tcfap2e	0.978	-0.39	0.707642	0.872268
10594	10574492	ENSMUST00000067136	21893	T lymphoma oncogene	Tlm	0.978	-0.136	0.895723	0.959042
10595	10424772	ENSMUST00000100531	432964	RIKEN cDNA K230010J24 gene	K230010J24Rik	0.978	-0.096	0.926076	0.970758
10596	10460658	NM_010609	16530	potassium channel, subfamily K	Kcnk7	0.978	0.007	0.994353	0.997705
10597	10583942	NM_144543	77862	thymocyte nuclear protein 1	Thyn1	0.978	-0.86	0.417215	0.680154
10598	10420320	NM_001014996	219103	centromere protein J	Cenpj	0.978	-0.599	0.567197	0.792635
10599	10577866	NM_011791	23808	ash2 (absent, small, or homeot	Ash2l	0.978	-0.612	0.559383	0.786775
10600	10460621	ENSMUST00000058632	76513	RIKEN cDNA 1810058N15 gene	1810058N15Rik	0.978	-0.269	0.795633	0.916955
10601	10499847	BC120651	66511	RIKEN cDNA 2500003M10 gene	2500003M10Rik	0.978	-0.717	0.495728	0.740536
10602	10444883	NM_001008424	386463	corneodesmosin	Cdsn	0.978	-0.327	0.75263	0.895764
10603	10579987	NM_001039137	56367	short coiled-coil protein	Scoc	0.978	0.38	0.714736	0.875137
10604	10362479	BC099502	692132	BET3 like (S. cerevisiae)	Bet3l	0.978	-0.025	0.980726	0.991919
10605	10379891	NM_016910	53892	protein phosphatase 1D magnesi	Ppm1d	0.978	-0.714	0.497624	0.741949
10606	10515162	NM_015758	30923	forkhead box E3	Foxe3	0.978	-0.487	0.640761	0.837345
10607	10424105	NM_173422	239447	collectin sub-family member 10	Colec10	0.978	-0.469	0.653077	0.844553
10608	10500736	NM_177545	229658	vang-like 1 (van gogh, Drosoph	Vangl1	0.978	-0.727	0.490287	0.737262
10609	10440794	NM_025642	66578	RIKEN cDNA 2610039C10 gene	2610039C10Rik	0.978	-0.555	0.595748	0.809631
10610	10413733	NM_001025379	218877	sema domain, immunoglobulin do	Sema3g	0.978	-0.173	0.867191	0.946934
10611	10551953	BC065044	381868	gene model 1082, (NCBI)	Gm1082	0.978	0.118	0.909066	0.963765
10612	10464110	ENSMUST00000099314	269094	RIKEN cDNA D730002M21 gene	D730002M21Rik	0.978	0.093	0.928073	0.971746
10613	10412064					0.978	-0.014	0.988965	0.995308
10614	10387757	NM_018740	54351	retinoic acid induced 12	Rai12	0.978	-0.656	0.531915	0.766132
10615	10466027	NM_021453	58803	pepsinogen 5, group I	Pga5	0.978	0.052	0.959606	0.984851
10616	10409643	ENSMUST00000007980	77134	heterogeneous nuclear ribonucl	Hnrnpa0	0.978	0.087	0.932697	0.973153
10617	10432378	NM_029098	74775	limb region 1 like	Lmbr1l	0.978	-0.256	0.804793	0.921015
10618	10351781	NM_001039484	16513	potassium inwardly-rectifying	Kcnj10	0.978	0.056	0.957026	0.983559
10619	10465965	NM_133689	67752	RIKEN cDNA 4930579J09 gene	4930579J09Rik	0.978	0.111	0.914842	0.966446
10620	10566597	NM_146602	258595	olfactory receptor 698	Olfr698	0.978	-0.275	0.790795	0.914692
10621	10366192					0.978	0.106	0.91874	0.967805
10622	10585599	NM_133976	102462	IMP3, U3 small nucleolar ribon	Imp3	0.978	-0.392	0.706172	0.871814
10623	10355567	NM_027154	69660	transmembrane BAX inhibitor mo	Tmbim1	0.978	-0.388	0.709219	0.872758
10624	10528523	NM_025394	66169	translocase of outer mitochond	Tomm7	0.978	-0.684	0.515189	0.754845

10625	10478913	BC115985	69372	molybdenum cofactor synthesis	Mocs3	0.978	-0.425	0.683	0.859827
10626	10504650					0.978	-0.065	0.949649	0.980608
10627	10430384	NM_183141	207393	leucine rich repeat and fibron	Elfn2	0.978	0.05	0.96124	0.985142
10628	10463789	NM_021360	18011	neuralized-like homolog (Droso	Neurl	0.978	-0.101	0.922286	0.969033
10629	10392035	BC099431	73431	RIKEN cDNA 1700052K11 gene	1700052K11Rik	0.978	-0.506	0.627841	0.83073
10630	10558535	NM_177469	52389	G protein-coupled receptor 123	Gpr123	0.978	-0.144	0.889128	0.956437
10631	10542414	NM_011216	19277	protein tyrosine phosphatase,	Ptpro	0.978	-0.915	0.389666	0.658311
10632	10376557	NM_134029	103850	5',3'-nucleotidase, mitochondr	Nt5m	0.978	-0.435	0.676039	0.855911
10633	10370327					0.978	0.023	0.982496	0.9924
10634	10475845	NM_028765	74121	acyl-Coenzyme A oxidase-like	Acoxl	0.978	-0.422	0.685161	0.860862
10635	10466040	NM_007650	12507	CD5 antigen	Cd5	0.977	-0.267	0.797234	0.917672
10636	10584819					0.977	0.11	0.915638	0.966659
10637	10522500	NM_133256	14843	GS homeobox 2	Gsx2	0.977	-0.267	0.796696	0.917464
10638	10541354	NM_175628	232345	alpha-2-macroglobulin	A2m	0.977	-0.271	0.793925	0.916207
10639	10427162	BC009140	106073	DNA Segment, Chr 15, Mouse Gen	D15Mgi27	0.977	-1.185	0.273631	0.548314
10640	10488929	NM_010579	16418	eukaryotic translation initiat	Eif6	0.977	-0.793	0.453037	0.709661
10641	10579287	NM_182991	67937	transmembrane protein 59-like	Tmem59l	0.977	-0.127	0.902237	0.9616
10642	10415784	NM_023233	66597	tripartite motif-containing 13	Trim13	0.977	-0.469	0.652946	0.844541
10643	10499963	NM_148949	207213	TD and POZ domain containing 1	Tdpoz1	0.977	0.037	0.971309	0.988148
10644	10390328	NM_019507	57765	T-box 21	Tbx21	0.977	-0.327	0.753087	0.895971
10645	10439063	NM_173439	268882	F-box protein 45	Fbxo45	0.977	-0.583	0.577637	0.797824
10646	10476033	NM_183262	67333	serine/threonine kinase 35	Stk35	0.977	-0.652	0.534541	0.768432
10647	10535124	NM_026748	68510	integrator complex subunit 1	Ints1	0.977	-0.443	0.67082	0.85389
10648	10386705	NM_009548	22671	zinc finger protein 179	Zfp179	0.977	-0.399	0.701397	0.869143
10649	10474081	NM_007442	11695	aristaless 4	Alx4	0.977	-0.133	0.897789	0.959787
10650	10568805	NM_183248	14912	NK6 transcription factor relat	Nkx6-2	0.977	-0.204	0.844258	0.936764
10651	10565330	NM_022985	65098	zinc finger, AN1-type domain 6	Zfand6	0.977	-0.374	0.719145	0.877614
10652	10363845	NM_001111121	76551	coiled-coil domain containing	Ccdc6	0.977	-0.721	0.493721	0.739216
10653	10600247					0.977	-0.199	0.848098	0.938472
10654	10582014	BC100501	69528	RIKEN cDNA 1700030J22 gene	1700030J22Rik	0.977	-0.524	0.616215	0.822657
10655	10373367	NM_001081040	210582	coenzyme Q10 homolog A (yeast)	Coq10a	0.977	-0.741	0.482197	0.730954
10656	10582626	NM_019552	56199	ATP-binding cassette, sub-fami	Abcb10	0.977	-0.555	0.595889	0.809631
10657	10565250	NM_030705	80889	mesoderm development candidate	Mesdc1	0.977	-0.732	0.487491	0.735095
10658	10375216	NM_145962	211347	pantothenate kinase 3	Pank3	0.977	-0.435	0.676193	0.855911
10659	10417730					0.977	-0.185	0.858268	0.943104
10660	10470696	NM_026896	68975	mediator complex subunit 27	Med27	0.977	-0.844	0.425812	0.68764
10661	10551011	NM_027732	71241	doublesex and mab-3 related tr	Dmrtc2	0.977	-0.043	0.967054	0.986963
10662	10383289	NM_130862	108100	brain-specific angiogenesis in	Baiap2	0.977	-0.585	0.576453	0.797453
10663	10503602	NM_172988	269514	F-box and leucine-rich repeat	Fbxl4	0.977	-0.454	0.663134	0.849961
10664	10579691	NM_029782	73316	calreticulin 3	Calr3	0.977	0.24	0.817014	0.927166
10665	10505326	NM_019492	50780	regulator of G-protein signali	Rgs3	0.977	-0.206	0.842217	0.936059
10666	10593652	NM_007810	13075	cytochrome P450, family 19, su	Cyp19a1	0.977	0.196	0.849859	0.939479
10667	10395039	NM_020557	22169	cytidine monophosphate (UMP-CM	Cmpk2	0.977	-0.158	0.878493	0.95179
10668	10506415	NM_025909	67013	OMA1 homolog, zinc metallopept	Oma1	0.977	-0.86	0.417445	0.680214
10669	10476349	BC100475	73747	RIKEN cDNA 1110034G24 gene	1110034G24Rik	0.977	-0.714	0.497695	0.741949
10670	10418982	NM_001033766	239036	RIKEN cDNA 4930596D02 gene	4930596D02Rik	0.977	-0.222	0.830516	0.932033
10671	10525365	NM_001042489	74096	hydrogen voltage-gated channel	Hvcn1	0.977	-0.566	0.588855	0.805202
10672	10525487	ENSMUST00000081006	74366	RIKEN cDNA 4932422M17 gene	4932422M17Rik	0.977	-0.059	0.95443	0.982496
10673	10590427	NM_021609	59289	chemokine binding protein 2	Ccbp2	0.977	0.095	0.926691	0.970959

10674	10373372	NM_001081040	210582	coenzyme Q10 homolog A (yeast)	Coq10a	0.977	-0.574	0.583685	0.801548
10675	10360544	NM_016805	51810	heterogeneous nuclear ribonucl	Hnrnpu	0.977	-0.575	0.58294	0.801046
10676	10362692	NM_027572	70840	solute carrier family 22 (orga	Slc22a16	0.977	0.093	0.92821	0.971746
10677	10565437	NM_028343	72759	transmembrane protein 135	Tmem135	0.977	-0.333	0.748801	0.893692
10678	10528257	NM_001080977	242860	round spermatid basic protein	Rsbn1l	0.977	-1.027	0.337845	0.613423
10679	10537558	ENSMUST00000103262	621968	T cell receptor beta variable	Trbv1	0.977	0.029	0.977525	0.990738
10680	10517056					0.977	-0.205	0.843139	0.93639
10681	10543939	BC064033	208164	cDNA sequence BC064033	BC064033	0.977	-0.041	0.968367	0.987277
10682	10594582	NM_001025612	382083	sorting nexin 22	Snx22	0.977	-0.433	0.677886	0.856898
10683	10472040	AF390105	227885	similar to Hsp90ab1 protein	LOC227885	0.977	-0.385	0.711272	0.873556
10684	10465833	NM_009073	19881	rod outer segment membrane pro	Rom1	0.977	-0.851	0.421995	0.684306
10685	10607330	BC025887	331547	RIKEN cDNA A230072E10 gene	A230072E10Rik	0.977	-0.308	0.766787	0.902924
10686	10438256	BC125356	195333	goosecoid homebox 2	Gsc2	0.977	-0.39	0.707747	0.872268
10687	10422194	NM_134077	74213	RNA binding motif protein 26	Rbm26	0.977	-0.666	0.525846	0.761906
10688	10501676	NM_008246	15247	hippocampus abundant gene tran	Hiat1	0.977	-0.243	0.814993	0.925775
10689	10520942	NM_001081407	665270	phospholipase B1	Plb1	0.977	0.238	0.81827	0.927645
10690	10403110	ENSMUST00000100985	100038689	predicted gene, ENSMUSG0000007	ENSMUSG00000072792	0.977	-0.313	0.763499	0.901503
10691	10505515					0.977	-0.13	0.90005	0.960389
10692	10501091	NM_001045807	229700	RNA binding motif protein 15	Rbm15	0.977	-0.514	0.622671	0.827306
10693	10386683	NM_026183	67473	solute carrier family 47, memb	Slc47a1	0.977	-0.187	0.856488	0.941981
10694	10592237	NM_007915	13663	etoposide induced 2.4 mRNA	Ei24	0.977	-0.442	0.671284	0.854164
10695	10513880	ENSMUST00000084489	791420	predicted gene, OTTMUSG0000000	OTTMUSG00000000276	0.977	-0.263	0.799973	0.919271
10696	10540785	BC010582	101314	RIKEN cDNA 6720456B07 gene	6720456B07Rik	0.977	-0.987	0.355532	0.628098
10697	10371217	NM_010102	13611	endothelial differentiation, G	Edg6	0.977	-0.273	0.792275	0.915409
10698	10491300	NM_011386	20482	SKI-like	Skil	0.977	-0.325	0.754625	0.896745
10699	10355024	NM_027407	70375	islet cell autoantigen 1-like	Ica1l	0.977	-0.216	0.835172	0.933323
10700	10556266	NM_009516	22390	wee 1 homolog (S. pombe)	Wee1	0.977	-0.36	0.729468	0.882928
10701	10564290	NM_021366	50794	Kruppel-like factor 13	Klf13	0.977	-0.092	0.928834	0.972036
10702	10417798	NM_021542	16529	potassium channel, subfamily K	Kcnk5	0.977	-0.461	0.658138	0.847091
10703	10566870	NM_153525	233724	transmembrane protein 41B	Tmem41b	0.977	-0.946	0.37462	0.644557
10704	10426467	NM_178789	320709	transmembrane protein 117	Tmem117	0.977	-0.196	0.850366	0.939843
10705	10537642	NM_001038997	436523	predicted gene, EG436523	EG436523	0.977	-0.283	0.785222	0.912507
10706	10545835	BC115452	73327	RIKEN cDNA 1700040I03 gene	1700040I03Rik	0.977	-0.562	0.591196	0.806572
10707	10468974	NM_177647	227526	arginine-rich, mutated in earl	Armet1l	0.977	-0.65	0.536011	0.769315
10708	10601099	NM_021521	59024	mediator of RNA polymerase II	Med12	0.977	-0.537	0.607736	0.817428
10709	10368918	NM_175407	109205	sine oculis-binding protein ho	Sobp	0.977	-0.092	0.929404	0.972164
10710	10389238	NM_019819	56405	dual specificity phosphatase 1	Dusp14	0.977	-0.456	0.661657	0.84929
10711	10365727					0.977	-0.62	0.554075	0.783409
10712	10594965	NM_001081153	208898	unc-13 homolog C (C. elegans)	Unc13c	0.977	-0.033	0.974904	0.98939
10713	10528090	NM_198620	242819	RUN domain containing 3B	Rundc3b	0.977	-0.921	0.386995	0.655973
10714	10576532	NM_016909	53424	translin-associated factor X	Tsnax	0.977	-0.586	0.57544	0.797076
10715	10549382	NM_001034903	545893	predicted gene, EG545893	EG545893	0.977	-0.248	0.811193	0.923829
10716	10516640	NM_018799	54709	eukaryotic translation initiat	Eif3i	0.977	-1.337	0.22186	0.491462
10717	10597162	NM_177771	270201	kelch-like 18 (Drosophila)	Klhl18	0.977	-0.337	0.745479	0.891679
10718	10510452	NM_001025296	13347	DNA fragmentation factor, alph	Dffa	0.977	-0.21	0.839144	0.934917
10719	10389373	NM_025825	66884	amyloid beta precursor protein	Appbp2	0.977	-0.481	0.64459	0.839238
10720	10433507	NM_007575	12265	class II transactivator	Ciita	0.977	-0.261	0.801311	0.919489
10721	10370397	NM_009646	11634	autoimmune regulator (autoimmu	Aire	0.977	-0.509	0.625953	0.82953
10722	10377380	NM_026889	68964	RIKEN cDNA 1500010J02 gene	1500010J02Rik	0.977	-0.663	0.527746	0.763341
10723	10578771	NM_144731	108150	UDP-N-acetyl-alpha-D-galactosa	Galnt7	0.976	-0.964	0.366199	0.637219
10724	10376402	NM_207693	404346	olfactory receptor 216	Olfr216	0.976	-0.115	0.911675	0.964691
10725	10460529	NM_145495	225870	Ras and Rab interactor 1	Rin1	0.976	-0.14	0.892635	0.957773

10726	10568239	BC010442	101604	RIKEN cDNA E430018J23 gene	E430018J23Rik	0.976	-0.207	0.841751	0.936059
10727	10508533	NM_028266	107581	collagen, type XVI, alpha 1	Col16a1	0.976	-0.28	0.787019	0.912989
10728	10586920	NM_001033536	319758	regulatory factor X domain con	Rfxdc2	0.976	-0.733	0.486956	0.73476
10729	10573203	NM_018771	67903	GIPC PDZ domain containing fam	Gipc1	0.976	-0.824	0.436149	0.696174
10730	10587988	NM_177352	235533	glycerol kinase 5 (putative)	Gk5	0.976	-0.414	0.690664	0.864369
10731	10490942					0.976	-0.599	0.567545	0.792875
10732	10559095	NM_028801	74180	mucin 5, subtype B, tracheobro	Muc5b	0.976	-0.34	0.743857	0.89106
10733	10349828	NM_010732	16980	leucine rich repeat protein 2,	Lrrn2	0.976	-0.47	0.651928	0.844083
10734	10397683	NM_198311	76260	tetratricopeptide repeat domai	Ttc8	0.976	-0.847	0.424396	0.686521
10735	10369661	NM_026201	67500	cell division cycle and apopto	Ccar1	0.976	-0.717	0.496032	0.740712
10736	10585509	NM_028049	71999	F-box protein 22	Fbxo22	0.976	-0.529	0.612571	0.820435
10737	10385583	NM_008521	17001	leukotriene C4 synthase	Ltc4s	0.976	-0.4	0.70047	0.86896
10738	10475866	NM_207680	12125	BCL2-like 11 (apoptosis facili	Bcl2l11	0.976	-0.698	0.506839	0.748732
10739	10390877	NM_001039666	406221	keratin 40	Krt40	0.976	-0.314	0.762667	0.901202
10740	10456001	NM_020600	20044	ribosomal protein S14	Rps14	0.976	-0.796	0.451592	0.708606
10741	10592416	NM_146508	258501	olfactory receptor 959	Olfr959	0.976	-0.178	0.863907	0.945829
10742	10557229	BC016578	100134980	hypothetical LOC100134980	LOC100134980	0.976	-0.278	0.788822	0.914061
10743	10437748	NM_146066	14852	G1 to S phase transition 1	Gspt1	0.976	-0.899	0.397798	0.664302
10744	10518869	NM_031867	110326	taste receptor, type 1, member	Tas1r1	0.976	-0.504	0.629598	0.831325
10745	10477555					0.976	-0.132	0.898611	0.960077
10746	10372815	NM_001081193	380664	LEM domain containing 3	Lemd3	0.976	-0.18	0.861832	0.94442
10747	10521168	NM_001001985	269642	N-acetyltransferase 8-like	Nat8l	0.976	-0.273	0.792725	0.91549
10748	10393222	NM_146032	217337	signal recognition particle 68	Srp68	0.976	-0.821	0.437886	0.697031
10749	10450694	NM_010397	15039	histocompatibility 2, T region	H2-T22	0.976	0.403	0.698373	0.867855
10750	10345882	NM_023514	69527	mitochondrial ribosomal protei	Mrps9	0.976	-0.498	0.633296	0.833255
10751	10532997	ENSMUST00000078701	78154	RIKEN cDNA 4930430O22 gene	4930430O22Rik	0.976	0.082	0.936986	0.975366
10752	10406108	ENSMUST00000022049	71390	RIKEN cDNA 5430425J12 gene	5430425J12Rik	0.976	-0.331	0.750242	0.894442
10753	10601764					0.976	-0.127	0.902123	0.961561
10754	10573434	NM_025648	66590	phenylalanyl-tRNA synthetase,	Farsa	0.976	-1.012	0.344217	0.618521
10755	10344707	NM_183028	319263	protein-L-isoaspartate (D-aspa	Pcmtd1	0.976	-0.656	0.532242	0.766334
10756	10362387					0.976	-0.336	0.746582	0.892388
10757	10386470	ENSMUST00000057382	320201	RIKEN cDNA 4930412M03 gene	4930412M03Rik	0.976	-0.712	0.499017	0.742429
10758	10389391	ENSMUST00000092818	327986	predicted gene, OTTMUSG0000000	OTTMUSG00000001044	0.976	-0.128	0.901907	0.961403
10759	10374553	NM_153596	103765	transmembrane protein 17	Tmem17	0.976	-0.72	0.494296	0.739556
10760	10577025	NM_011227	19332	RAB20, member RAS oncogene fam	Rab20	0.976	-0.375	0.718578	0.877128
10761	10441633	NM_009835	12458	chemokine (C-C motif) receptor	Ccr6	0.976	0.025	0.981039	0.99199
10762	10449666	NM_009362	21784	trefoil factor 1	Tff1	0.976	-0.237	0.819326	0.928264
10763	10516266	NM_153159	230738	zinc finger CCCH type containi	Zc3h12a	0.976	-0.372	0.720256	0.878163
10764	10588927	BC061048	112418	RIKEN cDNA 1700102P08 gene	1700102P08Rik	0.976	-0.172	0.868089	0.947171
10765	10429856	ENSMUST00000100512	100038659	predicted gene, ENSMUSG0000007	ENSMUSG00000075583	0.976	0.325	0.754049	0.896425
10766	10477897	NM_146128	228836	discs, large homolog-associate	Dlgap4	0.976	-0.495	0.635603	0.834519
10767	10600971	BC153817	408193	OTU domain containing 6A	Otud6a	0.976	-0.336	0.746528	0.892388
10768	10481830	NM_027947	71834	zinc finger and BTB domain con	Zbtb43	0.976	-0.655	0.532684	0.766762
10769	10431282	AK012625	72146	RIKEN cDNA 2810001A02 gene	2810001A02Rik	0.976	-0.379	0.71544	0.875402
10770	10597960	NM_139142	102680	solute carrier family 6 (neuro	Slc6a20a	0.976	0.009	0.992898	0.997248
10771	10371466	NM_013722	27204	synapsin III	Syn3	0.976	-0.284	0.784348	0.912074
10772	10380620					0.976	0.143	0.889886	0.956717
10773	10425651	AK132940	328573	RIKEN cDNA 4930407I10 gene	4930407I10Rik	0.976	-0.424	0.683842	0.86005
10774	10543872	BC029235	78412	RIKEN cDNA 3110062M04 gene	3110062M04Rik	0.976	-0.89	0.402159	0.667342
10775	10598562	BC055780	102941	RIKEN cDNA B630019K06 gene	B630019K06Rik	0.976	-0.656	0.532052	0.766201

10776	10506652	NM_001081272	546840	similar to low density lipopro	LOC546840	0.976	-0.39	0.707871	0.872288
10777	10497752	AF414101	52502	calcium regulated heat stable	Carhsp1	0.976	-0.955	0.370407	0.641116
10778	10541753	BC065170	319352	RIKEN cDNA C530028O21 gene	C530028O21Rik	0.976	-0.173	0.867396	0.946934
10779	10605729	NM_001044386	22764	zinc finger protein X-linked	Zfx	0.976	-0.997	0.351061	0.624551
10780	10582129	NM_021441	21341	TATA box binding protein (Tbp)	Taf1c	0.976	-0.238	0.818651	0.927928
10781	10432785	NM_027011	110308	keratin 5	Krt5	0.976	0.324	0.755146	0.897043
10782	10447564	XM_001476448	100046577	hypothetical protein LOC100046	LOC100046577	0.976	-0.572	0.58497	0.802565
10783	10556035	NM_147034	259036	olfactory receptor 713	Olfr713	0.976	-0.42	0.686974	0.861886
10784	10434629	NM_172821	71751	mitogen-activated protein kina	Map3k13	0.976	-0.292	0.778254	0.909741
10785	10387492	NM_144824	216853	WD repeat domain 79	Wdr79	0.976	-0.916	0.389503	0.658209
10786	10404939	AK008011	69829	RIKEN cDNA 2010001K21 gene	2010001K21Rik	0.976	-0.176	0.8651	0.946153
10787	10546659					0.976	0.104	0.920105	0.968088
10788	10595990	NM_028768	74125	armadillo repeat containing 8	Armc8	0.976	-1.114	0.30111	0.5773
10789	10356177	NM_152915	227325	delta/notch-like EGF-related r	Dner	0.976	-0.106	0.918217	0.967805
10790	10505931	NM_026319	67694	intraflagellar transport 74 ho	Ift74	0.976	-0.892	0.401273	0.666759
10791	10371420	NM_181650	72843	PR domain containing 4	Prdm4	0.976	-0.773	0.464343	0.718115
10792	10559635	NM_024172	66245	RIKEN cDNA 1500019G21 gene	1500019G21Rik	0.976	-0.551	0.598036	0.811052
10793	10524790	NM_007708	12704	citron	Cit	0.976	-0.562	0.591158	0.806572
10794	10489237	AK040893	68108	RIKEN cDNA 9430008C03 gene	9430008C03Rik	0.976	0.149	0.885905	0.955303
10795	10423185	NM_026799	14000	ribonuclease III, nuclear	Rnasen	0.976	-1.379	0.20912	0.474118
10796	10577222	BC029192	66423	RIKEN cDNA 2410022L05 gene	2410022L05Rik	0.976	-0.386	0.710853	0.873183
10797	10454647	ENSMUST00000097634	433171	predicted gene, ENSMUSG0000007	ENSMUSG00000073610	0.976	-0.523	0.616638	0.822962
10798	10589494	NM_013884	29873	chondroitin sulfate proteoglyc	Cspg5	0.976	-0.204	0.844249	0.936764
10799	10444068	NM_001025313	21356	TAP binding protein	Tapbp	0.976	-0.497	0.63416	0.833715
10800	10507675	AY454346	16656	human immunodeficiency virus t	Hivep3	0.976	-0.105	0.919223	0.967863
10801	10458283	ENSMUST00000097619	381148	gene model 1614, (NCBI)	Gm1614	0.976	0.055	0.957518	0.983902
10802	10539921	NM_175017	232217	RIKEN cDNA 4933427D06 gene	4933427D06Rik	0.976	0.132	0.898849	0.960104
10803	10360828	NM_001033547	433386	RIKEN cDNA 4922505E12 gene	4922505E12Rik	0.975	-0.094	0.927648	0.971576
10804	10410449	ENSMUST00000070942	210373	RIKEN cDNA A530095I07 gene	A530095I07Rik	0.975	-0.006	0.995279	0.998159
10805	10563447	NM_018795	27421	ATP-binding cassette, sub-fami	Abcc6	0.975	-0.393	0.70539	0.871546
10806	10405001	NM_001039179	76895	bicaudal D homolog 2 (Drosophi	Bicd2	0.975	-0.175	0.86608	0.946491
10807	10361265					0.975	-0.426	0.682797	0.859827
10808	10504373	ENSMUST00000105153	100038450	predicted gene, OTTMUSG0000000	OTTMUSG00000007018	0.975	0.229	0.825575	0.929887
10809	10376715	NM_001009927	237781	Smith-Magenis syndrome chromos	Smcr7	0.975	-0.49	0.638459	0.835923
10810	10393955	NM_026824	68730	dihydrouridine synthase 1-like	Dus1l	0.975	-0.884	0.405191	0.669695
10811	10370892	NM_025852	66932	REX1, RNA exonuclease 1 homolo	Rexo1	0.975	-0.738	0.48411	0.732715
10812	10437992	NM_152816	74006	dynamin 1-like	Dnm1l	0.975	-0.644	0.539524	0.7722
10813	10417544	NM_053115	93732	acyl-Coenzyme A oxidase 2, bra	Acox2	0.975	0.157	0.879196	0.952124
10814	10500157	NM_018877	84505	SET domain, bifurcated 1	Setdb1	0.975	-0.732	0.487219	0.734947
10815	10566199	NM_147111	259115	olfactory receptor 586	Olfr586	0.975	-0.24	0.816953	0.927145
10816	10573515	BC029622	68544	RIKEN cDNA 2310036O22 gene	2310036O22Rik	0.975	-0.708	0.501219	0.744202
10817	10537098	BC087908	76382	RIKEN cDNA 1700012A03 gene	1700012A03Rik	0.975	-0.13	0.900075	0.960389
10818	10588419	NM_025651	66595	asteroid homolog 1 (Drosophila	Aste1	0.975	-0.635	0.545088	0.77708
10819	10465033	ENSMUST00000044527	78306	testis specific 10 interacting	Tsga10ip	0.975	-0.25	0.809204	0.923158
10820	10408348	NM_001013389	380836	MRS2 magnesium homeostasis fac	Mrs2	0.975	-0.561	0.591956	0.807001
10821	10445558	NM_207161	381101	cDNA sequence BC048355	BC048355	0.975	-1.254	0.249033	0.522842
10822	10434148	NM_008307	15547	HpaII tiny fragments locus 9c	Htf9c	0.975	-0.965	0.365645	0.636847

10823	10451943	NM_001077348	66968	RIKEN cDNA 2310076L09 gene	2310076L09Rik	0.975	-0.183	0.859826	0.943624
10824	10552030	AK049951	791088	predicted gene, ENSMUSG0000005	ENSMUSG00000052691	0.975	0.168	0.871009	0.948568
10825	10361616					0.975	-0.204	0.843695	0.936632
10826	10470816	NM_028923	74412	GLE1 RNA export mediator (yeas	Gle1	0.975	-0.296	0.775407	0.90807
10827	10362372	AK034141	212448	RIKEN cDNA 9330159F19 gene	9330159F19Rik	0.975	-0.315	0.761991	0.900992
10828	10519183	NM_179203	108888	ATPase family, AAA domain cont	Atad3a	0.975	-0.584	0.577271	0.797771
10829	10545471	NM_019715	74287	potassium channel modulatory f	Kcmf1	0.975	-0.894	0.400395	0.666294
10830	10474921	NM_028054	72008	zinc finger, FYVE domain conta	Zfyve19	0.975	-0.622	0.552956	0.782578
10831	10413967	ENSMUST00000096028	268729	gene model 626, (NCBI)	Gm626	0.975	-0.117	0.909672	0.964056
10832	10361869	NM_173390	215819	NHS-like 1	Nhsl1	0.975	-0.742	0.481282	0.730704
10833	10537955					0.975	-0.071	0.945482	0.97847
10834	10529957	ENSMUST00000030971	70693	G protein-coupled receptor 125	Gpr125	0.975	-0.903	0.395811	0.663394
10835	10385995	NM_177471	52570	coiled-coil domain containing	Ccdc69	0.975	-0.254	0.806734	0.921832
10836	10365088	AY934504	70312	RIKEN cDNA 2510012J08 gene	2510012J08Rik	0.975	-0.986	0.356252	0.628749
10837	10511723					0.975	-0.382	0.713633	0.874653
10838	10594652	NM_030717	80907	lactamase, beta	Lactb	0.975	-0.489	0.639301	0.836316
10839	10496295	NM_025356	66105	ubiquitin-conjugating enzyme E	Ube2d3	0.975	-0.487	0.640987	0.837375
10840	10432157	NM_010679	16770	lactalbumin, alpha	Lalba	0.975	-0.495	0.635638	0.834519
10841	10388160	NM_001004148	237831	solute carrier family 13 (sodi	Slc13a5	0.975	-0.021	0.983965	0.993077
10842	10574976	NM_133792	192654	lysophospholipase 3	Lypla3	0.975	-0.496	0.6344	0.833748
10843	10361156	NM_144814	214742	REST corepressor 3	Rcor3	0.975	-0.7	0.505592	0.747576
10844	10398069	NM_009253	20717	serine (or cysteine) peptidase	Serpina3m	0.975	-0.024	0.981528	0.992092
10845	10590654	NM_026276	67618	aminoadipate-semialdehyde dehy	Aasdhppt	0.975	-1.182	0.274548	0.54916
10846	10475264	NM_010761	17151	cyclin D-type binding-protein	Ccndbp1	0.975	-0.649	0.536187	0.76935
10847	10491058	NR_004439	19784	ribonuclease P RNA-like 2	Rprl2	0.975	-0.182	0.860693	0.943954
10848	10348032	NM_030184	78795	armadillo repeat containing 9	Armc9	0.975	-0.596	0.569546	0.794081
10849	10505308	BC116650	214106	RIKEN cDNA 4933430I17 gene	4933430I17Rik	0.975	-0.23	0.824235	0.929508
10850	10557342	NM_021887	60504	interleukin 21 receptor	Il21r	0.975	-0.28	0.787347	0.913152
10851	10355628	NM_021313	57751	ring finger protein 25	Rnf25	0.975	-0.787	0.456605	0.712611
10852	10600284	NM_019684	56504	serine/arginine-rich protein s	Srpk3	0.975	-0.423	0.684889	0.860701
10853	10604932	NM_138309	171486	Cd99 antigen-like 2	Cd99l2	0.975	-0.986	0.356211	0.628749
10854	10363377					0.975	-0.123	0.905646	0.963405
10855	10515960	NM_001081142	60613	potassium voltage-gated channe	Kcnq4	0.975	0.216	0.835293	0.933323
10856	10510950	NM_010419	15208	hairy and enhancer of split 5	Hes5	0.975	-0.248	0.811401	0.923946
10857	10574676	NM_030152	78688	nucleolar protein 3 (apoptosis	Nol3	0.975	0.187	0.856588	0.942035
10858	10534190	NM_033572	94254	Williams-Beuren syndrome chrom	Wbscr16	0.975	-0.496	0.634646	0.83389
10859	10545576	NM_026490	56284	mitochondrial ribosomal protei	Mrpl19	0.975	-0.825	0.435543	0.695606
10860	10372750	ENSMUST00000020315	71902	cullin associated and neddylat	Cand1	0.975	-0.994	0.352272	0.625281
10861	10572622	NM_032544	70359	GTP binding protein 3	Gtpbp3	0.975	-0.332	0.749086	0.893932
10862	10420254	NM_008572	17231	mast cell protease 8	Mcpt8	0.975	-0.357	0.731406	0.884161
10863	10459292	ENSMUST00000064248	791322	predicted gene, ENSMUSG0000005	ENSMUSG00000052390	0.975	-0.447	0.667681	0.851783
10864	10474919	NM_001039223	623781	predicted gene, OTTMUSG0000001	OTTMUSG00000015762	0.975	0.164	0.874423	0.949978
10865	10384974	NM_008374	16199	interleukin 9 receptor	Il9r	0.975	-0.041	0.968543	0.987362
10866	10416689	NM_001030294	380924	olfactomedin 4	Olfm4	0.975	0.067	0.948566	0.980098
10867	10394018	NM_027745	71276	coiled-coil domain containing	Ccdc57	0.975	-0.636	0.544532	0.776685
10868	10469289	NM_008358	16169	interleukin 15 receptor, alpha	Il15ra	0.975	-0.413	0.691417	0.864541
10869	10345666	NM_026850	68833	phosducin-like 3	Pdcl3	0.975	-0.759	0.471802	0.72372
10870	10394498	NM_172470	74682	WD repeat domain 35	Wdr35	0.975	-1.302	0.232859	0.503895
10871	10369604	NM_133672	30930	vacuolar protein sorting 26 ho	Vps26a	0.975	-0.815	0.440975	0.699945
10872	10542050	NM_001033464	381812	EF-hand calcium binding domain	Efcab4b	0.975	-0.107	0.917378	0.967481
10873	10360957	NM_172650	226823	potassium channel tetramerisat	Kctd3	0.975	-0.463	0.656719	0.846325
10874	10525961	NM_021311	57749	piwi-like homolog 1 (Drosophil	Piwil1	0.975	-0.382	0.713655	0.874653
10875	10445380	NM_198608	224805	alanyl-tRNA synthetase 2, mito	Aars2	0.975	-0.491	0.638206	0.835923

10876	10370054	NM_023219	64454	solute carrier family 5 (neutr	Slc5a4b	0.975	-0.132	0.898767	0.960077
10877	10409190	NM_025495	66336	centromere protein P	Cenpp	0.975	-1.07	0.319272	0.596377
10878	10444284	NM_010389	15002	histocompatibility 2, O region	H2-Ob	0.975	-0.018	0.985744	0.994065
10879	10515708	ENSMUST00000075406	230676	cDNA sequence BC059842	BC059842	0.975	-0.056	0.956906	0.983559
10880	10510681	NM_008236	15206	hairy and enhancer of split 2	Hes2	0.975	-0.417	0.688931	0.863319
10881	10383920	NM_010904	380684	neurofilament, heavy polypepti	Nefh	0.974	-0.434	0.677055	0.856509
10882	10449756	ENSMUST00000002145	74377	heat shock transcription facto	Hsf2bp	0.974	-0.542	0.604142	0.815116
10883	10529671	NM_001102414	117591	solute carrier family 2 (facil	Slc2a9	0.974	-0.343	0.741296	0.889595
10884	10555885					0.974	0.064	0.950548	0.980959
10885	10565858	BC145760	330602	predicted gene, EG330602	EG330602	0.974	-0.133	0.897833	0.959787
10886	10360985	NM_001081363	108000	centromere protein F	Cenpf	0.974	-0.677	0.519469	0.757547
10887	10427657					0.974	0.03	0.977006	0.990545
10888	10545208	ENSMUST00000103357	235952	gene model 189, (NCBI)	Gm189	0.974	-0.188	0.855875	0.941748
10889	10556613	ENSMUST00000068576	67745	RIKEN cDNA 4930583K01 gene	4930583K01Rik	0.974	-0.242	0.815617	0.926149
10890	10505925					0.974	-0.456	0.661944	0.84942
10891	10532169	NM_172883	243197	major facilitator superfamily	Mfsd7	0.974	-0.223	0.829358	0.93131
10892	10349922	NM_031193	19702	renin 2 tandem duplication of	Ren2	0.974	-0.475	0.648778	0.842046
10893	10394286	BC067010	69709	RIKEN cDNA 2410017P09 gene	2410017P09Rik	0.974	-0.014	0.989446	0.995361
10894	10584691	NM_001081369	270150	cDNA sequence BC038167	BC038167	0.974	-0.387	0.710252	0.873031
10895	10396383	BC048389	625098	solute carrier family 38, memb	Slc38a6	0.974	-0.319	0.758603	0.898845
10896	10517263	BC026808	76824	RIKEN cDNA 2410166I05 gene	2410166I05Rik	0.974	-0.495	0.635151	0.834242
10897	10551469	NM_001037957	13549	dual-specificity tyrosine-(Y)-	Dyrk1b	0.974	-0.71	0.500145	0.743152
10898	10390502	NM_022891	65019	ribosomal protein L23	Rpl23	0.974	-0.736	0.484865	0.733332
10899	10402721	NM_028875	74335	X-ray repair complementing def	Xrcc3	0.974	-0.192	0.853289	0.940713
10900	10529468	BC152332	78890	RIKEN cDNA 2310079F23 gene	2310079F23Rik	0.974	-0.614	0.558291	0.786038
10901	10600901	NM_013476	11835	androgen receptor	Ar	0.974	0.05	0.96175	0.985234
10902	10539421	NM_145571	232157	MOB1, Mps One Binder kinase ac	Mobkl1b	0.974	-0.712	0.49867	0.742429
10903	10548788					0.974	0.146	0.888068	0.955903
10904	10437541	NM_013796	27426	N-acetylglucosamine-1-phosphod	Nagpa	0.974	-0.496	0.634753	0.833935
10905	10428672	NM_183089	72107	defective in sister chromatid	Dscc1	0.974	-0.84	0.427771	0.689074
10906	10413997	XM_985917	268729	gene model 626, (NCBI)	Gm626	0.974	-0.09	0.930604	0.972759
10907	10450829					0.974	0.177	0.864057	0.945829
10908	10464896	NM_172835	240518	pellino 3	Peli3	0.974	-0.28	0.787034	0.912989
10909	10594246	ENSMUST00000098658	100038496	predicted gene, ENSMUSG0000007	ENSMUSG00000074256	0.974	-0.577	0.581351	0.800318
10910	10582647					0.974	0.225	0.828272	0.930848
10911	10534519	NM_029659	76571	serine/threonine/tyrosine inte	Styxl1	0.974	-0.69	0.511508	0.752366
10912	10524345	NM_009419	22022	protein-tyrosine sulfotransfer	Tpst2	0.974	-0.697	0.507587	0.749509
10913	10556127	NM_001011742	257891	olfactory receptor 479	Olfr479	0.974	-0.723	0.492489	0.738472
10914	10522676	NM_025691	66661	signal recognition particle 72	Srp72	0.974	-0.959	0.36877	0.639488
10915	10413008	NM_028428	73068	fucosyltransferase 11	Fut11	0.974	-0.441	0.671827	0.854391
10916	10548041	ENSMUST00000100934	100038574	predicted gene, ENSMUSG0000007	ENSMUSG00000072759	0.974	0.062	0.952061	0.981385
10917	10429048	NM_010953	18256	otoconin 90	Oc90	0.974	-0.135	0.896164	0.95935
10918	10552369	NM_145581	233186	sialic acid binding Ig-like le	Siglec5	0.974	-0.406	0.696572	0.86683
10919	10468877					0.974	-0.631	0.547287	0.778305
10920	10602893					0.974	-0.307	0.767281	0.903106
10921	10424340	NM_023172	66218	NADH dehydrogenase (ubiquinone	Ndufb9	0.974	-1.048	0.328614	0.604982
10922	10383133	NM_178743	268512	solute carrier family 26, memb	Slc26a11	0.974	-0.427	0.681795	0.859366
10923	10499372	NM_178696	229517	solute carrier family 25, memb	Slc25a44	0.974	-0.961	0.367725	0.638723
10924	10590529	NM_025339	66079	transmembrane protein 42	Tmem42	0.974	-0.635	0.545103	0.77708
10925	10371589	ENSMUST00000099388	100038372	predicted gene, ENSMUSG0000007	ENSMUSG00000074809	0.974	-0.716	0.496537	0.74102

10926	10476058	NM_177726	241636	transglutaminase 6	Tgm6	0.974	-0.282	0.785954	0.912636
10927	10410687					0.974	-0.414	0.691009	0.864447
10928	10366541	NM_146242	237560	leucine rich repeat containing	Lrrc10	0.974	-0.051	0.960588	0.985069
10929	10505064	NM_028053	52076	transmembrane protein 38B	Tmem38b	0.974	-0.505	0.628646	0.830964
10930	10444595	NM_030597	27756	LSM2 homolog, U6 small nuclear	Lsm2	0.974	-0.734	0.486013	0.734018
10931	10378445	NM_001013784	432582	RIKEN cDNA E130309D14 gene	E130309D14Rik	0.974	-0.075	0.941937	0.977644
10932	10419296	NM_172598	218973	WD repeat and HMG-box DNA bind	Wdhd1	0.974	-0.558	0.593671	0.808175
10933	10482791	XM_001477205	271788	similar to Charged multivesicu	LOC271788	0.974	-0.459	0.659996	0.848652
10934	10552532	NM_019928	56640	kallikrein related-peptidase 4	Klk4	0.974	-0.103	0.920915	0.968408
10935	10419471	NM_009351	21745	telomerase associated protein	Tep1	0.974	-0.203	0.84452	0.936859
10936	10356143	XR_030656	100044526	similar to mitochondrial ribos	LOC100044526	0.974	-1.04	0.331943	0.608173
10937	10517465	NM_133872	99982	amine oxidase (flavin containi	Aof2	0.974	-0.849	0.423265	0.685524
10938	10525733	NM_030241	67956	SET domain containing (lysine	Setd8	0.974	-0.818	0.439327	0.698588
10939	10497582	BC119391	208613	RIKEN cDNA E030011K20 gene	E030011K20Rik	0.974	-0.247	0.811538	0.923946
10940	10478799	NM_023565	110750	chromosome segregation 1-like	Cse1l	0.974	-0.859	0.417773	0.680539
10941	10453318	NM_031884	27409	ATP-binding cassette, sub-fami	Abcg5	0.974	0.2	0.847117	0.938142
10942	10450424					0.974	-0.269	0.795373	0.916955
10943	10370508	ENSMUST00000069431	791283	predicted gene, ENSMUSG0000005	ENSMUSG00000055704	0.974	-0.215	0.835757	0.933505
10944	10362633	NM_011264	19714	REV3-like, catalytic subunit o	Rev3l	0.974	-0.554	0.596231	0.809783
10945	10370559	NM_027422	70427	mesoderm induction early respo	Mier2	0.974	-0.475	0.648643	0.841922
10946	10493343					0.974	-0.331	0.749927	0.894399
10947	10441899	BC107382	635895	predicted gene, EG635895	EG635895	0.974	0.079	0.938933	0.976218
10948	10488266	NM_172859	241688	RIKEN cDNA 6330439K17 gene	6330439K17Rik	0.974	-0.449	0.666711	0.851355
10949	10516943	NM_007512	11983	ATPase inhibitory factor 1	Atpif1	0.973	-0.953	0.371473	0.64202
10950	10498204	ENSMUST00000062651	791319	predicted gene, ENSMUSG0000004	ENSMUSG00000048888	0.973	-0.385	0.711547	0.873605
10951	10453544	NM_176917	76781	methyltransferase like 4	Mettl4	0.973	-1.16	0.282913	0.55817
10952	10597477	NM_175380	333433	glycerol-3-phosphate dehydroge	Gpd1l	0.973	-0.66	0.529657	0.764911
10953	10360674	NM_013729	27217	Mix1 homeobox-like 1 (Xenopus	Mixl1	0.973	-0.213	0.837419	0.934421
10954	10350985	NM_025474	64659	mitochondrial ribosomal protei	Mrps14	0.973	-1.095	0.308612	0.585228
10955	10462587	NM_029682	76630	Stam binding protein like 1	Stambpl1	0.973	-0.504	0.628968	0.831181
10956	10428338	NM_022722	64705	dihydropyrimidinase	Dpys	0.973	-0.415	0.690141	0.864031
10957	10557591	NM_008400	16408	integrin alpha L	Itgal	0.973	-0.097	0.925556	0.970539
10958	10433073	ENSMUST00000100166	100038459	predicted gene, ENSMUSG0000007	ENSMUSG00000075396	0.973	-0.172	0.86821	0.947187
10959	10500091	NM_027013	69269	sodium channel modifier 1	Scnm1	0.973	-0.484	0.642642	0.838146
10960	10532944	BC035300	109154	RIKEN cDNA 2410014A08 gene	2410014A08Rik	0.973	-0.572	0.584615	0.802272
10961	10526487	NM_028070	72041	alkB, alkylation repair homolo	Alkbh4	0.973	-0.549	0.599369	0.811907
10962	10601152	NM_172932	245537	neuroligin 3	Nlgn3	0.973	-0.533	0.609812	0.81845
10963	10419611	NM_033618	114741	suppressor of Ty 16 homolog (S	Supt16h	0.973	-0.78	0.460254	0.71495
10964	10560983	NM_207677	67379	death effector domain-containi	Dedd2	0.973	-0.511	0.62473	0.828896
10965	10365870	NM_011629	22025	nuclear receptor subfamily 2,	Nr2c1	0.973	-0.262	0.800999	0.919467
10966	10383850					0.973	-0.457	0.660816	0.848863
10967	10379543	NM_023438	270893	transmembrane protein 132E	Tmem132e	0.973	-0.458	0.660411	0.848652
10968	10530910	NM_172712	231380	ubiquitin-like modifier activa	Uba6	0.973	-1.194	0.270195	0.545029
10969	10440704	NM_183296	71369	keratin associated protein 16-	Krtap16-10	0.973	-0.527	0.614158	0.821467
10970	10392152	NM_133199	110880	sodium channel, voltage-gated,	Scn4a	0.973	-0.673	0.521784	0.75888
10971	10420338	NM_025682	66645	paraspeckle protein 1	Pspc1	0.973	-1.033	0.335054	0.610618
10972	10552708	NM_008422	16504	potassium voltage gated channe	Kcnc3	0.973	-0.494	0.636185	0.834785
10973	10405248	NM_001010973	15466	histamine receptor H2	Hrh2	0.973	-0.194	0.851507	0.940193
10974	10576235	NM_007876	13479	dipeptidase 1 (renal)	Dpep1	0.973	-0.375	0.718576	0.877128
10975	10537742	NM_013491	12723	chloride channel 1	Clcn1	0.973	-0.035	0.973193	0.988528

10975	10557742	NM_013491	12725	chloride channel 1	Clcn1	0.973	-0.055	0.975195	0.988528
10976	10593260	NM_172922	244859	ankyrin repeat and kinase doma	Ankk1	0.973	-0.219	0.83256	0.932679
10977	10366597	NM_028736	74053	glutamate receptor interacting	Grip1	0.973	-0.991	0.353595	0.626322
10978	10396055	NM_027614	70948	WD repeat domain 20b	Wdr20b	0.973	-0.401	0.699687	0.868422
10979	10488020	NM_029148	52837	thioredoxin domain containing	Txndc13	0.973	-0.592	0.57216	0.796219
10980	10451597	ENSMUST00000113300	381104	gene model 939, (NCBI)	Gm939	0.973	-0.49	0.638582	0.835923
10981	10499427	NM_181817	242093	relaxin family peptide recepto	Rxfp4	0.973	-0.738	0.483781	0.732322
10982	10372023	BC092352	215472	predicted gene, EG215472	EG215472	0.973	-0.137	0.894778	0.958505
10983	10518855					0.973	-0.907	0.393819	0.661654
10984	10570758	NM_139223	246083	defensin beta 13	Defb13	0.973	0.037	0.971312	0.988148
10985	10455104	NM_053140	93886	protocadherin beta 15	Pcdhb15	0.973	0.198	0.848571	0.938624
10986	10493864	NM_011470	20758	small proline-rich protein 2D	Sprr2d	0.973	-0.063	0.951492	0.981144
10987	10555818					0.973	-0.341	0.743072	0.890574
10988	10568399	NM_009383	21843	Tia1 cytotoxic granule-associa	Tial1	0.973	-0.41	0.693486	0.865698
10989	10491385	NM_019673	56456	actin-like 6A	Actl6a	0.973	-0.677	0.519248	0.757488
10990	10520867					0.973	0.039	0.970127	0.987786
10991	10576175	NM_007662	12555	cadherin 15	Cdh15	0.973	0.032	0.975433	0.989757
10992	10478594	NM_008906	19025	cathepsin A	Ctsa	0.973	-1.264	0.245453	0.518491
10993	10604671					0.973	-0.661	0.529133	0.76441
10994	10589756	NM_175266	77781	EPM2A (laforin) interacting pr	Epm2aip1	0.973	-1.204	0.266603	0.541262
10995	10446172	NM_144858	224907	dihydrouridine synthase 3-like	Dus3l	0.973	-0.729	0.488847	0.736349
10996	10393879	AK047224	17134	v-maf musculoaponeurotic fibro	Mafg	0.973	-0.092	0.929205	0.972148
10997	10567010	NM_015814	50781	dickkopf homolog 3 (Xenopus la	Dkk3	0.973	-0.329	0.75169	0.895263
10998	10586079	NM_176922	319480	integrin, alpha 11	Itga11	0.973	-0.187	0.856471	0.941981
10999	10384715	NR_004857	100134990	selenoprotein K pseudogene	LOC100134990	0.973	-0.288	0.78131	0.911076
11000	10394685	NM_008747	18217	neurotensin receptor 2	Ntsr2	0.973	-0.426	0.682414	0.859763
11001	10603860	NM_008823	18636	complement factor properdin	Cfp	0.973	-0.4	0.700919	0.868962
11002	10440406	NM_173440	268903	nuclear receptor interacting p	Nrip1	0.973	-0.597	0.569053	0.793724
11003	10375503	NM_053166	94089	tripartite motif-containing 7	Trim7	0.973	-0.218	0.833536	0.932911
11004	10463904	XR_034741	668536	similar to ribosomal protein L	LOC668536	0.973	-0.725	0.491092	0.737687
11005	10381408	NM_027320	70110	interferon-induced protein 35	Ifi35	0.973	-0.587	0.575036	0.797076
11006	10480139	NM_153155	227580	C1q-like 3	C1ql3	0.973	-0.282	0.786159	0.912775
11007	10594754	NM_022378	64290	forkhead box B1	Foxb1	0.973	-1.088	0.311743	0.58828
11008	10567863	NM_009844	12478	CD19 antigen	Cd19	0.973	-0.498	0.633625	0.833377
11009	10509168	NM_177733	242705	E2F transcription factor 2	E2f2	0.973	-0.795	0.452134	0.708922
11010	10505839					0.973	-0.815	0.441341	0.700287
11011	10493984	ENSMUST00000064257	99681	trichohyalin	Tchh	0.973	-0.212	0.837721	0.934421
11012	10549899	NM_146179	232854	zinc finger protein 418	Zfp418	0.973	-0.46	0.659384	0.848209
11013	10447602	NM_009510	22350	ezrin	Ezr	0.973	-0.61	0.560654	0.78784
11014	10424287	XM_977315	631797	fer-1-like 6 (C. elegans)	Fer1l6	0.973	-0.589	0.573988	0.797076
11015	10390622	NM_001033537	320655	per1-like domain containing 1	Perld1	0.973	-0.288	0.78108	0.911042
11016	10546396	NM_025578	64658	mitochondrial ribosomal protei	Mrps25	0.973	-0.614	0.557948	0.785803
11017	10565530					0.973	-0.201	0.84604	0.937284
11018	10393106	NM_172570	217333	tripartite motif-containing 47	Trim47	0.973	-0.424	0.683705	0.860022
11019	10395293	NM_001033436	380753	ataxin 7-like 1	Atxn7l1	0.973	0.019	0.985581	0.993996
11020	10585767	NM_001122873	69459	ubiquitin-like 7 (bone marrow	Ubl7	0.973	-0.932	0.381651	0.651394
11021	10450845	NM_010814	17441	myelin oligodendrocyte glycopr	Mog	0.973	-0.193	0.85259	0.940531
11022	10600821	XM_994723	631319	predicted gene, EG631319	EG631319	0.973	-0.033	0.974931	0.98939
11023	10353792	ENSMUST00000062557	73589	RIKEN cDNA 1700101I19 gene	1700101I19Rik	0.973	-0.299	0.773733	0.906763
11024	10462346	NM_021525	59028	RNA terminal phosphate cyclase	Rcl1	0.973	-0.536	0.60837	0.817693
11025	10372656	NM_001013391	432508	cleavage and polyadenylation s	Cpsf6	0.973	-0.274	0.791817	0.915223
11026	10419607	NM_016884	15381	heterogeneous nuclear ribonucl	Hnrnpc	0.973	-0.943	0.376072	0.646162
11027	10415606					0.973	-0.677	0.519631	0.757547
11028	10383061	NM_175430	207607	coiled-coil domain containing	Ccdc40	0.973	-0.43	0.679876	0.857866
11029	10423733	AK122302	666173	vacuolar protein sorting 13B (	Vps13b	0.972	-0.218	0.833195	0.932811
11030	10432278	NM_001013741	13199	dendrin	Ddn	0.972	0.262	0.8003	0.919317
11031	10367515					0.972	-0.841	0.427372	0.688641

11032	10387274	NM_008192	14919	guanylate cyclase 2e	Gucy2e	0.972	-0.181	0.861029	0.94412
11033	10428613	ENSMUST00000054380	383032	predicted gene, EG383032	EG383032	0.972	-0.981	0.358349	0.630567
11034	10562563	NM_007633	12447	cyclin E1	Ccne1	0.972	-0.451	0.665012	0.850739
11035	10554323					0.972	0.047	0.963874	0.985834
11036	10588722	NM_028369	72825	MON1 homolog A (yeast)	Mon1a	0.972	-0.925	0.384884	0.654157
11037	10441917	XR_033311	664856	similar to ribosomal protein	LOC664856	0.972	-1.573	0.158395	0.405262
11038	10565587					0.972	-0.309	0.765832	0.902563
11039	10429199					0.972	-0.442	0.671359	0.854195
11040	10378793	NM_025655	66601	transmembrane and immunoglobul	Tmigd1	0.972	-0.4	0.700997	0.868962
11041	10593103	NM_178709	235315	ring finger protein 214	Rnf214	0.972	-0.808	0.444932	0.703375
11042	10458938	XR_033768	667360	similar to High mobility group	LOC667360	0.972	-0.9	0.397158	0.664239
11043	10451604	NM_010783	17240	MyoD family inhibitor	Mdfi	0.972	-0.558	0.593865	0.808283
11044	10454332	NM_021448	58523	elongation protein 2 homolog (	Elp2	0.972	-0.44	0.672602	0.854651
11045	10428068	NM_001085421	239364	testis-specific protein, Y-enc	Tspyl5	0.972	0.187	0.857065	0.942404
11046	10361135	ENSMUST00000069573	74265	RIKEN cDNA 1700034H15 gene	1700034H15Rik	0.972	-0.766	0.46807	0.720506
11047	10428426	NM_176998	319613	RIKEN cDNA 5730410E15 gene	5730410E15Rik	0.972	-0.73	0.488478	0.736112
11048	10543952	ENSMUST00000101535	319472	RIKEN cDNA 9330158H04 gene	9330158H04Rik	0.972	-0.308	0.76664	0.902924
11049	10567361	NM_001024138	209776	G protein-coupled receptor 139	Gpr139	0.972	-0.363	0.727081	0.881698
11050	10560826	NM_020262	56869	zinc finger protein 109	Zfp109	0.972	-0.674	0.521417	0.758794
11051	10552406	NM_024253	72310	natural killer cell group 7 se	Nkg7	0.972	-0.468	0.6535	0.844695
11052	10437590	NM_025821	52502	calcium regulated heat stable	Carhsp1	0.972	-0.603	0.564892	0.790912
11053	10476935	NM_001085521	433485	predicted gene, OTTMUSG0000001	OTTMUSG00000015750	0.972	-0.204	0.843873	0.936634
11054	10522944	XR_004645	674405	similar to semaphorin 3A	LOC674405	0.972	-0.307	0.767845	0.903568
11055	10458645	NM_028392	72930	protein phosphatase 2 (formerl	Ppp2r2b	0.972	-0.205	0.843545	0.936586
11056	10591988	NM_001024139	235130	a disintegrin-like and metallo	Adamts15	0.972	-0.316	0.761175	0.900379
11057	10521057	NM_021500	59003	macrophage erythroblast attach	Maea	0.972	-0.858	0.418649	0.681283
11058	10582599	NM_172288	234865	nucleoporin 133	Nup133	0.972	-0.826	0.435158	0.695306
11059	10559324	XM_146165	244239	gene model 498, (NCBI)	Gm498	0.972	-0.049	0.962462	0.985405
11060	10589698	AK086953	791282	predicted gene, ENSMUSG0000005	ENSMUSG00000057802	0.972	-0.074	0.943233	0.977948
11061	10526345	NM_145414	100609	NOL1/NOP2/Sun domain family, m	Nsun5	0.972	-0.455	0.662821	0.84989
11062	10550877	NM_008433	16534	potassium intermediate/small c	Kcnn4	0.972	-0.377	0.717095	0.876228
11063	10385114	NM_023907	14233	forkhead box I1	Foxi1	0.972	-0.388	0.709278	0.87278
11064	10531338					0.972	0.118	0.908905	0.963765
11065	10428366	ENSMUST00000100702	100038501	predicted gene, ENSMUSG0000007	ENSMUSG00000072614	0.972	-0.494	0.635849	0.83464
11066	10592061	NM_010605	16521	potassium inwardly-rectifying	Kcnj5	0.972	-0.705	0.502718	0.745562
11067	10353891	NM_026241	109346	ankyrin repeat domain 39	Ankrd39	0.972	-0.158	0.879086	0.952124
11068	10465831	BC027679	67531	RIKEN cDNA 5730408K05 gene	5730408K05Rik	0.972	-0.537	0.607158	0.817118
11069	10424245	NM_173862	239463	cDNA sequence BC030396	BC030396	0.972	-0.071	0.945523	0.97847
11070	10575609	NM_001037665	22640	zinc finger protein 1	Zfp1	0.972	-0.787	0.456395	0.712554
11071	10598872	NM_145627	236732	RNA binding motif protein 10	Rbm10	0.972	-0.586	0.575601	0.797076
11072	10386416	NM_001011789	257962	olfactory receptor 222	Olfr222	0.972	-0.501	0.631556	0.832548
11073	10495625	NM_170778	99586	dihydropyrimidine dehydrogenas	Dpyd	0.972	-0.176	0.865376	0.946195
11074	10346799	NM_017480	54167	inducible T-cell co-stimulator	Icos	0.972	-0.201	0.846034	0.937284
11075	10522716	NM_153798	231329	polymerase (RNA) II (DNA direc	Polr2b	0.972	-0.951	0.372215	0.642563
11076	10376690	NM_008502	16897	lethal giant larvae homolog 1	Llgl1	0.972	-0.536	0.60826	0.817612
11077	10449839	NM_019774	56399	A kinase (PRKA) anchor protein	Akap8	0.972	-0.896	0.399069	0.665345
11078	10472321	NM_033552	94229	solute carrier family 4, sodiu	Slc4a10	0.972	-0.192	0.853386	0.940713
11079	10459912	NM_175028	240442	ADNP homeobox 2	Adnp2	0.972	-0.899	0.397609	0.664302
11080	10462217	NM_015826	50796	doublesex and mab-3 related tr	Dmrt1	0.972	-0.267	0.796706	0.917464
11081	10461217	NM_001098237	75291	zinc finger and BTB domain con	Zbtb3	0.972	-0.581	0.578918	0.798552

11082	10468816	BC026363	78832	RIKEN cDNA 2700078E11 gene	2700078E11Rik	0.972	-1.158	0.283943	0.559215
11083	10351487					0.972	-0.199	0.847527	0.938274
11084	10393801	NM_025560	66431	RIKEN cDNA 1810049H13 gene	1810049H13Rik	0.972	-0.79	0.454487	0.710892
11085	10602644	NM_013668	20591	jumonji, AT rich interactive d	Jarid1c	0.972	-0.314	0.76253	0.901202
11086	10579437	NM_026964	234388	coiled-coil domain containing	Ccdc124	0.972	-1.512	0.173145	0.425638
11087	10497617	NM_029690	76652	actin related protein M1	Arpm1	0.972	-0.11	0.915618	0.966659
11088	10553115	NM_001005511	381983	lemur tyrosine kinase 3	Lmtk3	0.972	-0.526	0.614762	0.821749
11089	10398920	BC090976	217887	cDNA sequence BC022687	BC022687	0.972	-0.673	0.522142	0.759088
11090	10416950					0.972	-0.588	0.574163	0.797076
11091	10394988					0.972	0.131	0.899698	0.960245
11092	10547758	NM_013536	14791	EMG1 nucleolar protein homolog	Emg1	0.972	-1.015	0.342768	0.617098
11093	10568792	NM_021302	57740	serine/threonine kinase 32C	Stk32c	0.972	0.127	0.90225	0.9616
11094	10449320	NM_173027	271424	inositol hexaphosphate kinase	Ihpk3	0.972	-0.471	0.651392	0.843859
11095	10588049	NM_015827	50797	coatomer protein complex, subu	Copb2	0.972	-0.974	0.361513	0.633294
11096	10473760	NM_017368	13046	CUG triplet repeat, RNA bindin	Cugbp1	0.972	-0.592	0.571772	0.795942
11097	10369929					0.972	-0.406	0.696649	0.866876
11098	10572064					0.972	-0.213	0.837433	0.934421
11099	10470248	NM_153410	67839	G-protein signalling modulator	Gpsm1	0.972	-1.044	0.330091	0.606486
11100	10452937	NM_001081179	320473	HEAT repeat containing 5B	Heatr5b	0.972	-0.985	0.356537	0.629004
11101	10519219	NM_024472	79554	glycolipid transfer protein do	Gltpd1	0.972	-1.047	0.328831	0.605213
11102	10590974	NM_176807	64931	folate receptor 4 (delta)	Folr4	0.972	0.41	0.693492	0.865698
11103	10497998					0.972	-0.576	0.582405	0.800864
11104	10552566	NM_010116	13648	kallikrein 1-related peptidase	Klk1b9	0.972	0.231	0.823922	0.929508
11105	10588326	NM_028721	74025	nephronophthisis 3 (adolescent	Nphp3	0.972	-0.455	0.662557	0.849733
11106	10461274	NM_176843	109077	integrator complex subunit 5	Ints5	0.972	-1.144	0.288996	0.565029
11107	10423629	NM_152894	67724	processing of precursor 1, rib	Pop1	0.972	-0.53	0.611875	0.820022
11108	10364338	NM_026431	67884	RIKEN cDNA 1810043G02 gene	1810043G02Rik	0.972	-0.981	0.358503	0.630584
11109	10448527	NM_001031621	381072	ATP-binding cassette, sub-fami	Abca17	0.972	0.115	0.911375	0.964566
11110	10456194	NM_028017	108123	N-ethylmaleimide sensitive fus	Napg	0.972	-0.907	0.3939	0.661714
11111	10507110					0.972	-0.271	0.794066	0.91622
11112	10578279	ENSMUST00000098818	100038612	predicted gene, ENSMUSG0000007	ENSMUSG00000074381	0.972	0.23	0.824845	0.929565
11113	10454944	NM_201256	108112	eukaryotic translation initiat	Eif4ebp3	0.971	-0.692	0.510742	0.751976
11114	10402353	NM_145449	217845	RIKEN cDNA 1810023F06 gene	1810023F06Rik	0.971	-0.123	0.905702	0.963405
11115	10357339	NM_145100	72585	Ly6/Plaur domain containing 1	Lypd1	0.971	-0.642	0.540855	0.773267
11116	10386934	NM_021539	59043	WD repeat and SOCS box-contain	Wsb2	0.971	-0.203	0.844997	0.937001
11117	10486552	NM_025657	66606	leucine rich repeat containing	Lrrc57	0.971	-1.079	0.315435	0.592323
11118	10511309	AK137636	435821	RIKEN cDNA 9930005F22 gene	9930005F22Rik	0.971	-0.237	0.819431	0.928264
11119	10442649	AK005803	100038762	predicted gene, ENSMUSG0000005	ENSMUSG00000054119	0.971	-0.312	0.763579	0.901503
11120	10416494	ENSMUST00000066181	791335	predicted gene, ENSMUSG0000005	ENSMUSG00000053632	0.971	-0.148	0.886301	0.955393
11121	10561356	NM_011874	23996	proteasome (prosome, macropain	Psmc4	0.971	-0.981	0.358319	0.630567
11122	10449527	NM_134115	106504	serine/threonine kinase 38	Stk38	0.971	-0.431	0.678984	0.857533
11123	10575833	NM_008290	15486	hydroxysteroid (17-beta) dehyd	Hsd17b2	0.971	-0.463	0.656848	0.84644
11124	10348547	NM_026454	67921	ubiquitin-conjugating enzyme E	Ube2f	0.971	-0.85	0.422461	0.684746
11125	10395312	NM_172253	28071	TWIST neighbor	Twistnb	0.971	-2.096	0.0731167	0.255028
11126	10509161					0.971	-0.255	0.805771	0.921628
11127	10459837	BC120889	212163	RIKEN cDNA 8030462N17 gene	8030462N17Rik	0.971	-0.936	0.379757	0.649537
11128	10455297	ENSMUST00000091925	225416	predicted gene, EG225416	EG225416	0.971	-0.522	0.617299	0.823029
11129	10553769	ENSMUST00000085241	791383	predicted gene, ENSMUSG0000005	ENSMUSG00000055048	0.971	0.023	0.982277	0.9924
11130	10405783					0.971	0.454	0.663355	0.850117

11131	10545623	NM_010070	13448	docking protein 1	Dok1	0.971	-0.371	0.721199	0.878601
11132	10398601	NM_198023	217864	REST corepressor 1	Rcor1	0.971	-0.88	0.407188	0.67168
11133	10458782	ENSMUST00000084260	225467	protein geranylgeranyltransfer	Pggt1b	0.971	-0.533	0.610005	0.818605
11134	10364841	NM_027829	71564	RIKEN cDNA 9030607L17 gene	9030607L17Rik	0.971	-0.277	0.789253	0.914259
11135	10391207	NM_030150	80861	DEXH (Asp-Glu-X-His) box polyp	Dhx58	0.971	-0.043	0.967174	0.986966
11136	10564762	NM_019799	56315	Rhesus blood group-associated	Rhcg	0.971	-0.219	0.832424	0.932679
11137	10387557					0.971	-0.391	0.707139	0.872175
11138	10575917	NM_023395	67866	WAP four-disulfide core domain	Wfdc1	0.971	-0.264	0.798934	0.918828
11139	10476130	BC049710	75656	RIKEN cDNA 1700020A23 gene	1700020A23Rik	0.971	-0.34	0.743218	0.890598
11140	10379200	NM_008759	18292	SEBOX homeobox	Sebox	0.971	-0.107	0.91788	0.967712
11141	10395672	NM_021710	11782	adaptor-related protein comple	Ap4s1	0.971	-0.949	0.373202	0.64348
11142	10548871	NM_001039558	654818	RIKEN cDNA C030030A07 gene	C030030A07Rik	0.971	0.23	0.824111	0.929508
11143	10540812	NM_001033463	381801	TatD DNase domain containing 2	Tatdn2	0.971	-0.534	0.609603	0.818311
11144	10378065	ENSMUST00000066087	75304	RIKEN cDNA 4930563E22 gene	4930563E22Rik	0.971	-0.107	0.917435	0.967494
11145	10551030	NM_008488	16801	Rho guanine nucleotide exchang	Arhgef1	0.971	-1.137	0.291819	0.567841
11146	10581674	NM_133953	101943	splicing factor 3b, subunit 3	Sf3b3	0.971	-0.86	0.417395	0.680204
11147	10449523	NM_153390	69307	peroxisomal, testis specific 1	Pxt1	0.971	0.093	0.9282	0.971746
11148	10605252	ENSMUST00000114328	385380	testis expressed 28	Tex28	0.971	0.48	0.64522	0.839798
11149	10463189	NM_020033	56642	ankyrin repeat domain 2 (stret	Ankrd2	0.971	-0.5	0.631867	0.832719
11150	10586602	ENSMUST00000098612	100038381	predicted gene, ENSMUSG0000007	ENSMUSG00000074232	0.971	-0.29	0.780119	0.910713
11151	10607841	NM_001007577	245695	RIKEN cDNA A630018P17 gene	A630018P17Rik	0.971	-0.337	0.745507	0.891679
11152	10371296	NM_029102	74782	glycosyltransferase 8 domain c	Glt8d2	0.971	0.12	0.908045	0.963723
11153	10459236	NM_021296	17714	GrpE-like 2, mitochondrial	Grpel2	0.971	-0.688	0.513168	0.753594
11154	10596583	NM_153413	208869	dedicator of cyto-kinesis 3	Dock3	0.971	-0.841	0.427131	0.688411
11155	10475643	NM_008008	14178	fibroblast growth factor 7	Fgf7	0.971	-0.226	0.827678	0.93066
11156	10508892	NM_172876	242691	G patch domain containing 3	Gpatch3	0.971	-0.562	0.590882	0.806403
11157	10420035	NM_024267	75751	importin 4	Ipo4	0.971	-0.753	0.475156	0.726714
11158	10462632	NM_183046	240641	kinesin family member 20B	Kif20b	0.971	-0.58	0.579525	0.798949
11159	10380954	ENSMUST00000116117	192852	gene model 12, (NCBI)	Gm12	0.971	-0.168	0.871276	0.948575
11160	10492341	NM_001081295	622434	RIKEN cDNA 4631416L12 gene	4631416L12Rik	0.971	-0.392	0.706473	0.871814
11161	10549386					0.971	-0.389	0.708835	0.872545
11162	10581111	NM_144931	234664	NEDD8 activating enzyme E1 sub	Nae1	0.971	-1.08	0.314887	0.59182
11163	10583548	AK006986	76618	RIKEN cDNA 1700084C06 gene	1700084C06Rik	0.971	-0.4	0.700981	0.868962
11164	10420785	ENSMUST00000089320	210376	myotubularin related protein 9	Mtmr9	0.971	-0.736	0.48499	0.733398
11165	10593605	NM_027807	75717	cullin 5	Cul5	0.971	-1.075	0.31697	0.594204
11166	10449581	NM_019880	56462	mitochondrial carrier homolog	Mtch1	0.971	-0.832	0.432148	0.692537
11167	10465246	NM_026169	67457	FERM domain containing 8	Frmd8	0.971	-0.441	0.672012	0.854437
11168	10502230					0.971	-0.627	0.549697	0.779911
11169	10448737	NM_026684	68342	NADH dehydrogenase (ubiquinone	Ndufb10	0.971	-1.129	0.295179	0.571492
11170	10537007	BC049755	75647	RIKEN cDNA 1700025E21 gene	1700025E21Rik	0.971	-0.484	0.642963	0.838239
11171	10405948	NM_001001185	408058	cDNA sequence BC048507	BC048507	0.971	-0.659	0.530067	0.765294
11172	10450224					0.971	-0.281	0.786727	0.91293
11173	10382701	NM_020483	57230	SAP30 binding protein	Sap30bp	0.971	-0.684	0.51546	0.754997
11174	10477894	ENSMUST00000069111	791421	predicted gene, OTTMUSG0000001	OTTMUSG00000015868	0.971	-0.287	0.782045	0.911385
11175	10590915	NM_173433	244694	jumonji domain containing 2D	Jmjd2d	0.971	-0.557	0.594198	0.808477
11176	10356510	ENSMUST00000113094	74918	IQ motif containing with AAA d	Iqca	0.971	-0.633	0.546205	0.777655
11177	10463200	BC016430	67432	RIKEN cDNA 0610010D20 gene	0610010D20Rik	0.971	-0.316	0.761046	0.900342
11178	10371796	NM_182959	216227	solute carrier family 17 (sodi	Slc17a8	0.971	-0.074	0.942643	0.977825

11179	10577154	NM_009724	11945	ATPase, H+/K+ exchanging, beta	Atp4b	0.971	-0.238	0.818854	0.928008
11180	10382376	NM_053273	117160	tweety homolog 2 (Drosophila)	Ttyh2	0.971	-0.518	0.61982	0.825074
11181	10580852					0.971	-0.583	0.577353	0.797771
11182	10452633	NM_009372	21815	TG interacting factor 1	Tgif1	0.971	-0.679	0.518495	0.757012
11183	10374119	NM_010956	18293	oxoglutarate dehydrogenase (li	Ogdh	0.971	-1.202	0.267249	0.54188
11184	10583286	NM_010287	14608	G protein-coupled receptor 83	Gpr83	0.971	0.103	0.920959	0.968408
11185	10557311	ENSMUST00000104912	791408	predicted gene, ENSMUSG0000006	ENSMUSG00000066185	0.971	-0.573	0.58424	0.80205
11186	10468300	NM_001081271	546729	predicted gene, EG546729	EG546729	0.971	-0.378	0.716344	0.875716
11187	10411491	NM_178716	238799	transportin 1	Tnpo1	0.971	-0.718	0.495076	0.73999
11188	10454831	NM_026420	67869	polyadenylate-binding protein-	Paip2	0.971	-0.723	0.492373	0.738402
11189	10598107	NM_021466	21339	TATA box binding protein (Tbp)	Taf1a	0.971	-0.275	0.790725	0.914692
11190	10345656	NM_001011684	433292	neuromedin S	Nms	0.971	-0.445	0.669171	0.852809
11191	10558643	NM_001011776	257939	olfactory receptor 527	Olfr527	0.971	-0.112	0.913699	0.965865
11192	10511935	NM_001033225	108767	proline-rich nuclear receptor	Pnrc1	0.971	-1.322	0.226504	0.497153
11193	10484987	NM_013839	22259	nuclear receptor subfamily 1,	Nr1h3	0.971	-0.434	0.677057	0.856509
11194	10409236					0.971	-0.537	0.607196	0.817118
11195	10397761	ENSMUST00000101129	100038713	predicted gene, ENSMUSG0000007	ENSMUSG00000072882	0.971	-0.238	0.818811	0.928008
11196	10505980	NM_001113412	75578	FGGY carbohydrate kinase domai	Fggy	0.971	-0.046	0.964632	0.985942
11197	10500345	NR_001579	21748	telomerase RNA component	Terc	0.971	-0.009	0.992787	0.99722
11198	10548769	NM_010352	14840	germ cell-specific gene 1	Gsg1	0.971	-0.643	0.540054	0.772571
11199	10411464	NM_172591	218503	FCH domain only 2	Fcho2	0.971	-0.49	0.638567	0.835923
11200	10503008					0.971	-0.119	0.908647	0.963765
11201	10504948	ENSMUST00000041392	74914	cylicin, basic protein of sper	Cylc2	0.971	-0.347	0.738215	0.88841
11202	10505102	ENSMUST00000084590	791419	predicted gene, OTTMUSG0000000	OTTMUSG00000007234	0.971	0.162	0.876048	0.95093
11203	10503723	NM_001081392	100019	midasin homolog (yeast)	Mdn1	0.97	-0.719	0.494849	0.739807
11204	10453761					0.97	0.205	0.84336	0.936555
11205	10356470	NM_008132	14659	glutamine repeat protein 1	Glrp1	0.97	-0.139	0.893494	0.957966
11206	10525195	AK137099	269700	expressed sequence AU042671	AU042671	0.97	-0.694	0.509282	0.750558
11207	10541301	NM_017379	53857	tubulin, alpha 8	Tuba8	0.97	-0.021	0.983708	0.993007
11208	10600899	BC111868	245526	G protein-coupled receptor 15-	Pgr15l	0.97	-0.128	0.901572	0.961364
11209	10424493	NM_009375	21819	thyroglobulin	Tg	0.97	-0.367	0.72395	0.88046
11210	10553598	NM_011370	20430	cytoplasmic FMR1 interacting p	Cyfip1	0.97	-1.053	0.326465	0.602834
11211	10475144	NM_007601	12335	calpain 3	Capn3	0.97	-0.79	0.454495	0.710892
11212	10394954	NM_145890	195733	grainyhead-like 1 (Drosophila)	Grhl1	0.97	-0.282	0.785996	0.912636
11213	10593913	NM_028820	74211	septin 14	Sept14	0.97	-0.794	0.452341	0.708922
11214	10550564	NM_010058	13401	dystrophia myotonica-containin	Dmwd	0.97	-0.552	0.597315	0.810475
11215	10606654	NM_183319	331524	X Kell blood group precursor r	Xkrx	0.97	-0.142	0.890677	0.957227
11216	10595013	NM_016711	50876	tropomodulin 2	Tmod2	0.97	-1.17	0.279085	0.554134
11217	10415778	NM_177337	219144	ADP-ribosylation factor-like 1	Arl11	0.97	-0.41	0.693398	0.865683
11218	10582201	NM_010926	18117	COX4 neighbor	Cox4nb	0.97	-0.926	0.384186	0.653466
11219	10557035	NM_025298	26939	polymerase (RNA) III (DNA dire	Polr3e	0.97	-0.885	0.40491	0.669594
11220	10383208	ENSMUST00000093902	672511	hypothetical LOC672511	LOC672511	0.97	0.009	0.993446	0.997551
11221	10550625					0.97	0.167	0.871657	0.948704
11222	10360187	NM_033509	93840	vang-like 2 (van gogh, Drosoph	Vangl2	0.97	-1.092	0.310009	0.586741
11223	10349610	NM_010709	16865	ligatin	Lgtn	0.97	-0.857	0.419154	0.681475
11224	10350753	NM_008131	14645	glutamate-ammonia ligase (glut	Glul	0.97	-0.695	0.509087	0.750516
11225	10448975	NM_145409	214901	CTF18, chromosome transmission	Chtf18	0.97	-0.663	0.528084	0.763475
11226	10480087	XR_032234	675534	similar to Importin alpha-2 su	LOC675534	0.97	-0.569	0.586509	0.803673
11227	10477543	NM_172860	12396	core-binding factor, runt doma	Cbfa2t2	0.97	-0.684	0.515232	0.754854
11228	10476276	NM_144888	228607	RIKEN cDNA D430028G21 gene	D430028G21Rik	0.97	-0.43	0.679583	0.857705
11229	10460544	NM_026553	68090	Yip1 interacting factor homolo	Yif1a	0.97	-1.452	0.188699	0.446774

11230	10438060	ENSMUST00000100136	16136	immunoglobulin lambda-like pol	Igll1	0.97	-0.286	0.782698	0.911672
11231	10542836	NM_001081237	232539	kelch domain containing 5	Klhdc5	0.97	-0.825	0.435901	0.695863
11232	10529651	NM_010835	17701	homeobox, msh-like 1	Msx1	0.97	-0.34	0.74336	0.89069
11233	10585889	NM_175235	76183	bruno-like 6, RNA binding prot	Brunol6	0.97	-0.7	0.505633	0.747578
11234	10345141	NM_026719	68421	LMBR1 domain containing 1	Lmbrd1	0.97	-0.587	0.575255	0.797076
11235	10353679	XR_004787	675497	hypothetical protein LOC675497	LOC675497	0.97	-0.757	0.47283	0.724458
11236	10522895	NM_007786	12994	casein kappa	Csn3	0.97	-0.364	0.726054	0.88142
11237	10479765	NM_022724	64707	suppressor of variegation 3-9	Suv39h2	0.97	-0.917	0.38861	0.657212
11238	10463630					0.97	-0.229	0.824921	0.929565
11239	10534638	AK014627	74576	RIKEN cDNA 4731417B20 gene	4731417B20Rik	0.97	-0.272	0.79344	0.915898
11240	10487238	NM_008230	15186	histidine decarboxylase	Hdc	0.97	-0.654	0.533506	0.767534
11241	10574350	NM_008609	17388	matrix metallopeptidase 15	Mmp15	0.97	-0.586	0.57559	0.797076
11242	10510047	ENSMUST00000097804	100038693	predicted gene, ENSMUSG0000007	ENSMUSG00000073728	0.97	-0.035	0.973296	0.988537
11243	10459602	AK171711	19255	protein tyrosine phosphatase,	Ptpn2	0.97	-0.462	0.657542	0.846871
11244	10470381	NM_029862	381356	RIKEN cDNA 5930434B04 gene	5930434B04Rik	0.97	-0.437	0.675188	0.855723
11245	10494122	NM_017395	53970	regulatory factor X, 5 (influe	Rfx5	0.97	-0.414	0.691018	0.864447
11246	10529903	AB257856	58227	RIKEN cDNA 9630031F12 gene	9630031F12Rik	0.97	-0.273	0.792608	0.91549
11247	10519497	NM_054098	117167	STEAP family member 4	Steap4	0.97	-0.408	0.695242	0.866195
11248	10528202					0.97	-0.096	0.926473	0.97081
11249	10402757	ENSMUST00000050754	319590	RIKEN cDNA A730018C14 gene	A730018C14Rik	0.97	-0.077	0.940728	0.977
11250	10501775					0.97	-0.499	0.632808	0.833028
11251	10365408	NM_183172	237422	resistance to inhibitors of ch	Ric8b	0.97	-0.674	0.521197	0.758676
11252	10480869	NM_001001714	227631	spermatogenesis and oogenesis	Sohlh1	0.97	-0.221	0.831319	0.932333
11253	10571384	ENSMUST00000068999	78506	RIKEN cDNA 2900075B16 gene	2900075B16Rik	0.97	-0.487	0.640987	0.837375
11254	10484920	NM_025576	66461	protein tyrosine phosphatase,	Ptpmt1	0.97	-0.387	0.710102	0.873031
11255	10504316	NM_011571	21754	testis specific protein kinase	Tesk1	0.97	-0.822	0.437337	0.696704
11256	10433660	NM_025976	67118	bifunctional apoptosis regulat	Bfar	0.97	-0.835	0.430707	0.691411
11257	10518473	NM_015797	50762	F-box protein 6	Fbxo6	0.97	-0.33	0.750772	0.894733
11258	10539091	NM_147779	20388	surfactant associated protein	Sftpb	0.97	-0.339	0.744129	0.89128
11259	10370999	BC072620	237403	cDNA sequence BC072620	BC072620	0.97	-0.43	0.679614	0.857705
11260	10550935	NM_009532	22594	X-ray repair complementing def	Xrcc1	0.97	-1.155	0.284843	0.56015
11261	10506638	NM_172873	242603	CUB domain containing protein	Cdcp2	0.97	-0.11	0.915526	0.966659
11262	10518902	NM_008237	15207	hairy and enhancer of split 3	Hes3	0.97	-0.633	0.546552	0.77773
11263	10414163	NM_146245	239037	leucine-rich repeat, immunoglo	Lrit1	0.97	0.014	0.98955	0.995388
11264	10566395	NM_201409	381944	deubiquitinating enzyme 1a	Dub1a	0.97	-0.212	0.838113	0.934421
11265	10516956	NM_133888	100340	sphingomyelin phosphodiesteras	Smpdl3b	0.97	-0.343	0.74134	0.889595
11266	10549057	NM_023042	19691	RecQ protein-like	Recql	0.97	-0.529	0.612882	0.820539
11267	10580875	NM_008187	14894	gene trap locus 3	Gtl3	0.97	-0.581	0.578842	0.798528
11268	10606914	NM_007957	13984	extraembryonic, spermatogenesi	Esx1	0.97	0.096	0.926503	0.97081
11269	10491691					0.97	-0.014	0.989082	0.995308
11270	10438289	ENSMUST00000100100	66779	RIKEN cDNA 4933432I09 gene	4933432I09Rik	0.97	-0.185	0.858604	0.943286
11271	10559172	ENSMUST00000084414	77215	keratin associated protein 5-3	Krtap5-3	0.97	0.163	0.875331	0.950704
11272	10426760	NM_009699	11827	aquaporin 2	Aqp2	0.97	-0.285	0.783806	0.912068
11273	10495964	NM_009718	11924	neurogenin 2	Neurog2	0.97	-0.348	0.737459	0.888025
11274	10454655	NM_007462	11789	adenomatosis polyposis coli	Apc	0.97	-0.613	0.558497	0.786209
11275	10563323	NM_008749	18220	nucleobindin 1	Nucb1	0.97	-0.88	0.407124	0.671626
11276	10395136					0.97	-0.721	0.493338	0.739056
11277	10452000	NM_172624	224897	dipeptidylpeptidase 9	Dpp9	0.97	-0.84	0.427946	0.689167
11278	10576797	XM_001472875	664870	Wilms' tumour 1-associating pr	LOC664870	0.97	-0.467	0.654573	0.84526
11279	10487269	NM_029163	75083	ubiquitin specific peptidase 5	Usp50	0.97	-0.716	0.496653	0.741089
11280	10555720	NM_147101	259105	olfactory receptor 549	Olfr549	0.97	-0.219	0.833008	0.932751
11281	10395692	NM_009706	11855	Rho GTPase activating protein	Arhgap5	0.97	-0.566	0.588883	0.805202

11282	10499309	NM_144897	246703	apolipoprotein A-I binding pro	Apoa1bp	0.97	-1.25	0.250333	0.524575
11283	10577237	NM_001007591	434285	expressed sequence BB014433	BB014433	0.97	-0.234	0.821531	0.92863
11284	10515696	ENSMUST00000075406	230676	cDNA sequence BC059842	BC059842	0.97	-0.53	0.612118	0.820192
11285	10562064	NM_007959	14008	ets variant gene 2	Etv2	0.97	0.04	0.969201	0.987586
11286	10445789	NM_027763	71326	triggering receptor expressed	Treml1	0.97	-0.235	0.821053	0.92863
11287	10546624	NM_001081157	320502	leiomodin 3 (fetal)	Lmod3	0.97	-0.165	0.873506	0.949487
11288	10369453	NM_013753	27355	cDNA sequence X99384	X99384	0.97	-0.809	0.444193	0.702635
11289	10566434	NM_020290	56860	olfactory receptor 690	Olfr690	0.97	-0.528	0.613429	0.820926
11290	10528507	NM_178403	78697	pseudouridylate synthase 7 hom	Pus7	0.97	-0.557	0.594596	0.80881
11291	10414497	NM_009632	11546	poly (ADP-ribose) polymerase f	Parp2	0.97	-0.939	0.378305	0.648156
11292	10539880	NM_019964	56691	DnaJ (Hsp40) homolog, subfamil	Dnajb8	0.97	-0.23	0.824149	0.929508
11293	10495279	NM_011967	26442	proteasome (prosome, macropain	Psma5	0.97	-0.843	0.426387	0.687967
11294	10380501	NM_010055	13393	distal-less homeobox 3	Dlx3	0.97	-0.484	0.642554	0.838134
11295	10603425	NM_027227	69824	glyoxalase domain containing 5	Glod5	0.97	-0.206	0.842157	0.936059
11296	10357288	NM_010483	15564	5-hydroxytryptamine (serotonin	Htr5b	0.97	-0.643	0.540405	0.772885
11297	10442454	BC083113	67078	RIKEN cDNA 1700012G19 gene	1700012G19Rik	0.969	-0.706	0.502162	0.745102
11298	10349559	NM_178691	226418	YOD1 OTU deubiquitinating enzy	Yod1	0.969	-1.111	0.302247	0.578434
11299	10461100	NM_025731	66727	HRAS-like suppressor family, m	Hrasls5	0.969	-0.628	0.549503	0.779882
11300	10599579	NM_207240	236784	olfactory receptor 1320	Olfr1320	0.969	0.092	0.928938	0.972036
11301	10417912	NM_030180	78787	ubiquitin specific peptidase 5	Usp54	0.969	-1.078	0.315844	0.592774
11302	10359970	NM_001109985	70729	nitric oxide synthase 1 (neuro	Nos1ap	0.969	-0.6	0.567045	0.792621
11303	10532308	XR_033031	675756	hypothetical protein LOC675756	LOC675756	0.969	-1.152	0.286092	0.561612
11304	10363983	NM_001081412	110279	breakpoint cluster region homo	Bcr	0.969	-0.919	0.387867	0.656721
11305	10444436	NM_019873	56299	FK506 binding protein-like	Fkbpl	0.969	-0.647	0.537711	0.770752
11306	10378497	NM_010813	17428	max binding protein	Mnt	0.969	-0.589	0.573893	0.797007
11307	10400894	NM_181752	238252	G protein-coupled receptor 135	Gpr135	0.969	-0.375	0.718281	0.876988
11308	10389114	NM_145431	217011	notchless homolog 1 (Drosophil	Nle1	0.969	-0.522	0.61735	0.823029
11309	10473160	NM_080558	70599	sperm specific antigen 2	Ssfa2	0.969	-1.13	0.294581	0.570921
11310	10496621	NM_145546	229906	general transcription factor I	Gtf2b	0.969	-0.834	0.43086	0.691522
11311	10453499	NM_013523	14309	follicle stimulating hormone r	Fshr	0.969	-0.043	0.966896	0.986963
11312	10382756	NM_172569	217331	unkempt homolog (Drosophila)	Unk	0.969	-0.808	0.44475	0.703193
11313	10527026	BC068301	231841	EST AA881470	AA881470	0.969	-0.537	0.607186	0.817118
11314	10597918					0.969	-1.393	0.205179	0.468786
11315	10424363	NM_026746	68501	non-SMC element 2 homolog (MMS	Nsmce2	0.969	-0.476	0.648004	0.841712
11316	10568982	NM_001001180	407812	cDNA sequence BC066028	BC066028	0.969	-0.421	0.686028	0.861365
11317	10607334					0.969	-0.776	0.462702	0.717151
11318	10450800	NM_001024134	69097	tripartite motif-containing 15	Trim15	0.969	-0.802	0.448221	0.70581
11319	10443550	NM_021419	58230	ring finger protein 8	Rnf8	0.969	-0.829	0.433623	0.694075
11320	10397482	NM_172583	217733	transmembrane protein 63c	Tmem63c	0.969	-0.367	0.724472	0.880611
11321	10354233	NM_001013025	73122	transforming growth factor, be	Tgfbrap1	0.969	-0.564	0.590035	0.805977
11322	10468303	XM_001472011	240669	predicted gene, EG240669	EG240669	0.969	-0.182	0.860692	0.943954
11323	10499493	NM_008227	15168	hyperpolarization-activated, c	Hcn3	0.969	-0.131	0.899026	0.960129
11324	10598723	NM_010028	13205	DEAD/H (Asp-Glu-Ala-Asp/His) b	Ddx3x	0.969	-0.677	0.519388	0.757547
11325	10387251					0.969	-0.284	0.784607	0.912276
11326	10570850	NM_145592	234130	dickkopf homolog 4 (Xenopus la	Dkk4	0.969	-0.833	0.431695	0.692222
11327	10387372	NM_001017426	216850	jumonji domain containing 3	Jmjd3	0.969	-0.693	0.510278	0.751397
11328	10461237	NM_008144	14705	Bernardinelli-Seip congenital	Bscl2	0.969	-0.437	0.674776	0.855557
11329	10354938	NM_001033449	381259	amyotrophic lateral sclerosis	Als2cr4	0.969	-0.278	0.789006	0.914104
11330	10463371	NM_011720	22423	wingless related MMTV integrat	Wnt8b	0.969	-0.254	0.806715	0.921832
11331	10356484	NM_010262	14472	gastrulation brain homeobox 2	Gbx2	0.969	-0.714	0.497599	0.741949
11332	10417998					0.969	-0.258	0.803469	0.920138
11333	10582078					0.969	-0.959	0.368619	0.639331
11334	10576883	NM_011369	20419	Shc SH2-domain binding protein	Shcbp1	0.969	-0.795	0.452118	0.708922
11335	10537657	NM_007680	13848	Eph receptor B6	Ephb6	0.969	-0.248	0.810943	0.923749

11336	10353993	NM_198006	76178	RIKEN cDNA 6330578E17 gene	6330578E17Rik	0.969	-0.637	0.543597	0.775859
11337	10384102	NM_207242	237636	NPC1-like 1	Npc1l1	0.969	-0.439	0.673538	0.855025
11338	10601861					0.969	0.251	0.808643	0.922966
11339	10370446	NM_001081055	216131	transmembrane protein 1	Tmem1	0.969	-0.833	0.431755	0.692222
11340	10349997	BC116694	240755	RIKEN cDNA 4933406M09 gene	4933406M09Rik	0.969	-0.266	0.797546	0.917931
11341	10516093	NM_007558	12163	bone morphogenetic protein 8a	Bmp8a	0.969	-0.727	0.490391	0.737313
11342	10405851					0.969	-0.285	0.78389	0.912068
11343	10462313	NM_009199	20510	solute carrier family 1 (neuro	Slc1a1	0.969	-0.462	0.657494	0.84686
11344	10547697	BC120816	76921	RIKEN cDNA 1700013D24 gene	1700013D24Rik	0.969	-0.361	0.728358	0.882292
11345	10464783	NM_023131	19671	RCE1 homolog, prenyl protein p	Rce1	0.969	-0.056	0.957177	0.983648
11346	10555901	NM_147043	259045	olfactory receptor 669	Olfr669	0.969	-0.519	0.619111	0.824741
11347	10537494	NM_028358	381760	single-stranded DNA binding pr	Ssbp1	0.969	-0.461	0.65841	0.847214
11348	10431625	NM_018803	54526	synaptotagmin X	Syt10	0.969	-0.269	0.795479	0.916955
11349	10453705	NM_181070	19330	RAB18, member RAS oncogene fam	Rab18	0.969	-0.595	0.569818	0.794162
11350	10456353	NM_175012	225642	gastrin releasing peptide	Grp	0.969	-0.704	0.503677	0.746064
11351	10474596	NM_028844	74268	apoptosis, caspase activation	Aven	0.969	-0.657	0.531451	0.765672
11352	10557109	ENSMUST00000065310	76613	RIKEN cDNA 1700069B07 gene	1700069B07Rik	0.969	-0.142	0.891312	0.957565
11353	10386189	NM_146879	258879	olfactory receptor 330	Olfr330	0.969	-0.031	0.976369	0.990137
11354	10415513	NM_023773	75339	M-phase phosphoprotein 8	Mphosph8	0.969	-0.88	0.407253	0.671681
11355	10589361	NM_025689	66658	coiled-coil domain containing	Ccdc51	0.969	-0.445	0.669457	0.852871
11356	10446613	ENSMUST00000092011	546695	similar to ribosomal protein L	LOC546695	0.969	-0.498	0.633082	0.833233
11357	10457409	NM_021522	59025	ubiquitin specific peptidase 1	Usp14	0.969	-0.996	0.351502	0.624753
11358	10564507	NM_001042592	66412	arrestin domain containing 4	Arrdc4	0.969	-0.66	0.529964	0.765251
11359	10534694	NM_031405	83701	arsenate resistance protein 2	Ars2	0.969	-0.705	0.502883	0.745637
11360	10360840	NM_001081361	66112	MOCO sulphurase C-terminal dom	Mosc1	0.969	-0.334	0.748116	0.893228
11361	10442085					0.969	0.024	0.981834	0.992194
11362	10378988	NM_174852	268448	PHD finger protein 12	Phf12	0.969	-0.842	0.426638	0.68818
11363	10436053	NM_028615	73703	developmental pluripotency ass	Dppa2	0.969	-0.119	0.908142	0.963723
11364	10360158	NM_008534	17085	lymphocyte antigen 9	Ly9	0.969	-0.614	0.558047	0.78589
11365	10592493	NM_001081121	70989	RIKEN cDNA 4931429I11 gene	4931429I11Rik	0.969	-0.634	0.545514	0.777457
11366	10605651					0.969	-0.435	0.676018	0.855911
11367	10349480	NM_181750	226412	R3H domain 1 (binds single-str	R3hdm1	0.969	-0.734	0.486361	0.734369
11368	10414920	ENSMUST00000103637	100042410	T-cell receptor alpha variable	Trav7d-2	0.969	0.269	0.795432	0.916955
11369	10404347	NM_023746	28078	prolactin family 5, subfamily	Prl5a1	0.969	-0.528	0.613538	0.82095
11370	10432840	NM_010668	16681	keratin 2	Krt2	0.969	-0.113	0.912815	0.965173
11371	10347650	NM_183022	241118	amiloride-sensitive cation cha	Accn4	0.969	-0.569	0.586451	0.803673
11372	10380591	NM_033568	27681	SNF8, ESCRT-II complex subunit	Snf8	0.968	-1.357	0.215636	0.482783
11373	10393395	NM_011358	20382	splicing factor, arginine/seri	Sfrs2	0.968	-0.452	0.664375	0.850284
11374	10379654	NM_001035854	71770	adaptor-related protein comple	Ap2b1	0.968	-1.132	0.293875	0.56996
11375	10454015	BC020021	72747	RIKEN cDNA 2810439F02 gene	2810439F02Rik	0.968	-0.697	0.507841	0.749793
11376	10459918	BC064066	68731	RIKEN cDNA 1110032A13 gene	1110032A13Rik	0.968	-0.299	0.773214	0.9067
11377	10433003	NM_130458	170574	trans-acting transcription fac	Sp7	0.968	-0.233	0.821909	0.92863
11378	10364051	NM_026095	67332	small nuclear ribonucleoprotei	Snrpd3	0.968	-0.493	0.636472	0.834887
11379	10508961	NM_001039677	230810	solute carrier family 30 (zinc	Slc30a2	0.968	-0.497	0.63387	0.833492
11380	10533869	NM_144819	215707	coiled-coil domain containing	Ccdc92	0.968	-0.63	0.547932	0.778543
11381	10481393	NM_025428	66220	zinc finger, DHHC domain conta	Zdhhc12	0.968	-0.556	0.595238	0.809319
11382	10585417	NM_029573	67834	isocitrate dehydrogenase 3 (NA	Idh3a	0.968	-0.751	0.476652	0.727638
11383	10429972	NM_053193	94230	cleavage and polyadenylation s	Cpsf1	0.968	-0.827	0.434963	0.695306
11384	10390227	NM_172300	268470	ubiquitin-conjugating enzyme E	Ube2z	0.968	-0.805	0.446442	0.70413
11385	10414040					0.968	-0.226	0.827236	0.930659
11386	10584954	NM_008794	18554	proprotein convertase subtilis	Pcsk7	0.968	-0.801	0.448735	0.706272

11387	10557156	NM_011121	18817	polo-like kinase 1 (Drosophila	Plk1	0.968	-1.052	0.326705	0.602834
11388	10351769	NM_080419	140559	immunoglobulin superfamily, me	Igsf8	0.968	-0.61	0.560624	0.78784
11389	10382482	NM_172801	237987	otopetrin 2	Otop2	0.968	-0.695	0.508727	0.750513
11390	10453825	NM_009226	20641	small nuclear ribonucleoprotei	Snrpd1	0.968	-0.743	0.481192	0.730704
11391	10405013	NM_199056	75678	inositol 1,3,4,5,6-pentakispho	Ippk	0.968	-0.259	0.803237	0.920074
11392	10560532	BC070402	232947	cDNA sequence BC024868	BC024868	0.968	-0.641	0.541494	0.773858
11393	10481182	NM_175427	109349	RIKEN cDNA C630035N08 gene	C630035N08Rik	0.968	-0.581	0.579114	0.798694
11394	10447467	NM_023630	71828	general transcription factor I	Gtf2a1l	0.968	-0.322	0.756668	0.897871
11395	10444066	NM_020625	81630	zinc finger and BTB domain con	Zbtb22	0.968	-1.356	0.216047	0.48309
11396	10424711	NM_008164	14787	rhophilin, Rho GTPase binding	Rhpn1	0.968	-0.268	0.796371	0.917464
11397	10532542	NM_019982	56747	seizure related 6 homolog like	Sez6l	0.968	-0.512	0.623751	0.828064
11398	10509555					0.968	-0.235	0.820761	0.92863
11399	10391572	NM_172947	268490	LSM12 homolog (S. cerevisiae)	Lsm12	0.968	-0.762	0.470453	0.722494
11400	10360018	NM_145141	98752	Fc receptor-like A	Fcrla	0.968	-0.482	0.64423	0.839078
11401	10526133	NM_019983	56715	RAB guanine nucleotide exchang	Rabgef1	0.968	-0.501	0.631578	0.832548
11402	10421863	NM_001042726	18530	protocadherin 8	Pcdh8	0.968	-0.388	0.709527	0.872938
11403	10585444	NM_022655	64602	iron responsive element bindin	Ireb2	0.968	-0.468	0.653864	0.844861
11404	10432923	NM_001033277	223918	SPRY domain containing 3	Spryd3	0.968	-0.552	0.597829	0.81086
11405	10428910	ENSMUST00000096421	71088	RIKEN cDNA 4933412E24 gene	4933412E24Rik	0.968	-0.041	0.968181	0.987184
11406	10357124	NM_011650	22099	translin	Tsn	0.968	-0.824	0.436215	0.696174
11407	10550521	NM_145579	232934	Myb protein P42POP	P42pop	0.968	-0.302	0.770841	0.905387
11408	10566601	NM_146600	258593	olfactory receptor 700	Olfr700	0.968	-0.206	0.842294	0.936059
11409	10393685					0.968	-0.074	0.942898	0.977825
11410	10605831	NM_152822	76130	LAS1-like (S. cerevisiae)	Las1l	0.968	-1.341	0.220712	0.489689
11411	10452142	NM_178926	106639	expressed sequence AI662250	AI662250	0.968	-0.813	0.442074	0.7009
11412	10465089	NM_001024560	225861	sorting nexin 32	Snx32	0.968	-0.138	0.893695	0.958083
11413	10478133	NM_175419	109275	ARP5 actin-related protein 5 h	Actr5	0.968	-0.517	0.620804	0.825734
11414	10552907	NM_001033176	76713	RIKEN cDNA 1700039E15 gene	1700039E15Rik	0.968	-0.226	0.8273	0.930659
11415	10544271	NM_146382	258380	olfactory receptor 461	Olfr461	0.968	-0.115	0.911765	0.964738
11416	10566609	NM_146353	258350	olfactory receptor 706	Olfr706	0.968	-0.164	0.874207	0.949962
11417	10601648	NM_022322	64103	tenomodulin	Tnmd	0.968	-0.073	0.944026	0.977948
11418	10378627	NM_001029938	280408	Rab interacting lysosomal prot	Rilp	0.968	-0.583	0.577534	0.797771
11419	10567108	NM_011445	20679	SRY-box containing gene 6	Sox6	0.968	-0.447	0.667787	0.851815
11420	10450648	NM_013854	224742	ATP-binding cassette, sub-fami	Abcf1	0.968	-0.726	0.490605	0.737328
11421	10513186	XM_884359	619973	similar to LRRGT00183	LOC619973	0.968	-0.311	0.764276	0.90173
11422	10444717	NM_033477	114585	DNA segment, Chr 17, human D6S	D17H6S53E	0.968	-0.996	0.351658	0.624753
11423	10428326					0.968	-0.123	0.905846	0.963405
11424	10378572	BC021945	380712	RIKEN cDNA 2010305C02 gene	2010305C02Rik	0.968	-0.416	0.689751	0.863782
11425	10594538	ENSMUST00000098627	102595	pleckstrin homology domain con	Plekho2	0.968	-0.19	0.854373	0.94105
11426	10508727	NM_172400	68598	DnaJ (Hsp40) homolog, subfamil	Dnajc8	0.968	-0.852	0.42184	0.684212
11427	10463803	NM_009289	20874	STE20-like kinase (yeast)	Slk	0.968	-0.527	0.613963	0.821282
11428	10535739	NM_011669	22217	ubiquitin specific peptidase 1	Usp12	0.968	-0.817	0.439852	0.699109
11429	10480423	NM_001077190	11308	abl-interactor 1	Abi1	0.968	-0.805	0.44649	0.704154
11430	10552672	BC019451	68352	RIKEN cDNA 0610012D14 gene	0610012D14Rik	0.968	-0.117	0.909898	0.964056
11431	10347726	XR_030615	383531	similar to Rpl7a protein	LOC383531	0.968	-0.12	0.908015	0.963723
11432	10527101	NM_199068	17425	forkhead box K1	Foxk1	0.968	-0.62	0.554412	0.783484
11433	10518989	NM_011642	22062	transformation related protein	Trp73	0.968	-0.576	0.582097	0.800654
11434	10524681	NM_026933	69076	TP53 regulated inhibitor of ap	Triap1	0.968	-0.491	0.637687	0.835756
11435	10563130	NM_145954	69748	aldehyde dehydrogenase 16 fami	Aldh16a1	0.968	-0.563	0.590319	0.806156
11436	10557716	NM_172281	233900	ring finger protein 40	Rnf40	0.968	-0.678	0.518817	0.757221
11437	10568150	NM_145588	110033	kinesin family member 22	Kif22	0.968	-1.186	0.273055	0.547665
11438	10506150	NM_010425	15221	forkhead box D3	Foxd3	0.968	-0.76	0.471104	0.722944
11439	10443039	NM_172149	224630	BCL2/adenovirus E1B interactin	Bnip1	0.968	-0.766	0.467949	0.720483

11440	10425207	NM_008197	14958	H1 histone family, member 0	H1f0	0.968	-0.885	0.404629	0.669338
11441	10545538	NM_009819	12386	catenin (cadherin associated p	Ctnna2	0.968	-0.182	0.860417	0.943954
11442	10385842	NM_009012	19360	RAD50 homolog (S. cerevisiae)	Rad50	0.968	-1.022	0.339856	0.615232
11443	10476691	NM_029763	70408	polymerase (RNA) III (DNA dire	Polr3f	0.968	-1.036	0.333616	0.609432
11444	10576124	BC036332	66965	RIKEN cDNA 2310061F22 gene	2310061F22Rik	0.968	-0.886	0.4041	0.668818
11445	10558265	NM_029609	76429	RIKEN cDNA 2310007H09 gene	2310007H09Rik	0.968	-0.195	0.851001	0.940103
11446	10494467	NM_001081053	213119	integrin, alpha 10	Itga10	0.968	0.087	0.932953	0.973276
11447	10347282	NM_001034060	435626	RUN and FYVE domain containing	Rufy4	0.968	-0.14	0.892403	0.957747
11448	10518735	NM_029035	74646	splA/ryanodine receptor domain	Spsb1	0.968	-0.68	0.517981	0.756834
11449	10449775	NM_008716	18131	Notch gene homolog 3 (Drosophi	Notch3	0.968	-0.587	0.57512	0.797076
11450	10518132	NM_001081355	110593	PR domain containing 2, with Z	Prdm2	0.967	-1.153	0.285516	0.560861
11451	10522248	XR_033663	624662	similar to MGC69457 protein	LOC624662	0.967	-1.159	0.283428	0.558717
11452	10386209	NM_001011769	257931	olfactory receptor 317	Olfr317	0.967	-0.31	0.765145	0.90235
11453	10591423	ENSMUST00000115494	100009600	GATA-like 1	Glp1	0.967	-0.791	0.45436	0.710796
11454	10396956	NM_018814	54604	pecanex homolog (Drosophila)	Pcnx	0.967	-0.681	0.516877	0.756112
11455	10516507	NM_177758	269585	zinc finger and SCAN domains 2	Zscan20	0.967	-0.726	0.490541	0.737328
11456	10400324					0.967	-0.293	0.778075	0.909683
11457	10476915	NM_009978	13012	cystatin 8 (cystatin-related e	Cst8	0.967	-0.148	0.886531	0.955393
11458	10379588	NM_030224	78919	fibronectin type III domain co	Fndc8	0.967	-0.706	0.502474	0.745462
11459	10376285	NM_001081168	50724	SAP30-like	Sap30l	0.967	-0.59	0.573344	0.796661
11460	10580484	AK044128	234549	HEAT repeat containing 3	Heatr3	0.967	-0.26	0.801937	0.919813
11461	10398095	NM_013773	27379	T-cell leukemia/lymphoma 1B, 1	Tcl1b1	0.967	0.072	0.944731	0.978132
11462	10565962	NM_008773	18442	purinergic receptor P2Y, G-pro	P2ry2	0.967	-0.391	0.707255	0.872175
11463	10580100	NM_145970	212139	coiled-coil and C2 domain cont	Cc2d1a	0.967	-0.69	0.512072	0.75265
11464	10424252	BC051524	76773	RIKEN cDNA 2410187C16 gene	2410187C16Rik	0.967	-0.711	0.499497	0.742712
11465	10392863	NM_010350	14813	glutamate receptor, ionotropic	Grin2c	0.967	-0.35	0.736324	0.887164
11466	10567444	BC051401	381917	dynein, axonemal, heavy chain	Dnahc3	0.967	-0.369	0.722486	0.87936
11467	10357888	ENSMUST00000027729	68507	protein tyrosine phosphatase,	Ppfia4	0.967	-0.115	0.911878	0.964809
11468	10569181	NM_022654	57913	leucine-rich and death domain	Lrdd	0.967	-0.522	0.617353	0.823029
11469	10397538	XM_001476146	100045836	hypothetical protein LOC100045	LOC100045836	0.967	-0.352	0.735178	0.886784
11470	10510767	NM_153424	260305	nephronophthisis 4 (juvenile)	Nphp4	0.967	-0.315	0.761637	0.900675
11471	10414081	NM_181529	319508	synaptotagmin XV	Syt15	0.967	-0.261	0.801415	0.919489
11472	10471411	NM_133783	96979	prostaglandin E synthase 2	Ptges2	0.967	-0.417	0.68901	0.863366
11473	10514347	NM_007670	12579	cyclin-dependent kinase inhibi	Cdkn2b	0.967	-0.199	0.847891	0.938472
11474	10451238	NM_009085	20016	RNA polymerase 1-1	Rpo1-1	0.967	-0.988	0.35515	0.627794
11475	10451193	AK143033	100038605	predicted gene, ENSMUSG0000007	ENSMUSG00000073391	0.967	0.057	0.956045	0.983285
11476	10482496	ENSMUST00000102769	109129	RIKEN cDNA 2010311D03 gene	2010311D03Rik	0.967	-0.292	0.778669	0.909988
11477	10434481	NM_145941	208643	eukaryotic translation initiat	Eif4g1	0.967	-1.011	0.344834	0.618925
11478	10415187	NM_001024645	268747	leucine rich repeat containing	Lrrc16b	0.967	-0.813	0.44223	0.700945
11479	10567879	NM_007504	11937	ATPase, Ca++ transporting, car	Atp2a1	0.967	-0.408	0.695418	0.866211
11480	10459534	NM_027130	69597	AFG3(ATPase family gene 3)-lik	Afg3l2	0.967	-0.606	0.562789	0.789779
11481	10526931	ENSMUST00000031521	545817	cytochrome P450, family 2, sub	Cyp2w1	0.967	-0.449	0.666742	0.851355
11482	10560685	NM_033601	12051	B-cell leukemia/lymphoma 3	Bcl3	0.967	-0.886	0.404099	0.668818
11483	10570201	NM_015804	50770	ATPase, class VI, type 11A	Atp11a	0.967	-0.487	0.640945	0.837375
11484	10490745	BC087873	277496	RIKEN cDNA 4930526D03 gene	4930526D03Rik	0.967	-0.62	0.55429	0.783468
11485	10605726	XM_994312	668103	predicted gene, EG668103	EG668103	0.967	-0.504	0.629286	0.831256
11486	10388018	NM_178367	216877	DEAH (Asp-Glu-Ala-His) box pol	Dhx33	0.967	-0.689	0.512509	0.752977
11487	10481649	ENSMUST00000100190	319245	RIKEN cDNA 9430097D07 gene	9430097D07Rik	0.967	0.089	0.931372	0.972759

11488	10563852	NM_153578	233280	non imprinted in Prader-Willi/	Nipa1	0.967	-0.136	0.895653	0.959029
11489	10405662	NM_030153	78689	MAK10 homolog, amino-acid N-ac	Mak10	0.967	-1.247	0.251498	0.525513
11490	10388300	NM_147004	259006	olfactory receptor 399	Olfr399	0.967	-0.122	0.90656	0.963405
11491	10548244					0.967	-0.994	0.352565	0.625599
11492	10377847	NM_146020	216871	glycolipid transfer protein do	Gltpd2	0.967	-0.598	0.56843	0.793239
11493	10389177	NM_080453	118453	matrix metallopeptidase 28 (ep	Mmp28	0.967	-0.447	0.667678	0.851783
11494	10557843	NM_139149	233908	fusion, derived from t(12;16)	Fus	0.967	-0.806	0.445911	0.703765
11495	10493856	ENSMUST00000090872	20755	small proline-rich protein 2A	Sprr2a	0.967	-0.223	0.829481	0.931316
11496	10493858	ENSMUST00000090872	20755	small proline-rich protein 2A	Sprr2a	0.967	-0.223	0.829481	0.931316
11497	10480275	NM_028757	74103	nebulette	Nebl	0.967	-0.899	0.397762	0.664302
11498	10400975	NM_029580	76357	TRM5 tRNA methyltransferase 5	Trmt5	0.967	-0.936	0.379533	0.649311
11499	10440465					0.967	0.124	0.904466	0.962829
11500	10360589	NM_026375	226747	AT hook containing transcripti	Ahctf1	0.967	-0.767	0.467631	0.720331
11501	10490225	NM_025531	66390	slowmo homolog 2 (Drosophila)	Slmo2	0.967	-0.559	0.593106	0.80777
11502	10512487	NR_001460	19782	RNA component of mitochondrial	Rmrp	0.967	-0.063	0.951457	0.981144
11503	10499512					0.967	-0.524	0.615831	0.822286
11504	10370089	NM_001081419	64451	DIP2 disco-interacting protein	Dip2a	0.967	-0.599	0.56762	0.792928
11505	10551496	NM_019458	54624	Paf1, RNA polymerase II associ	Paf1	0.967	-1.098	0.307624	0.584192
11506	10550172	BC060121	228829	PHD finger protein 20	Phf20	0.967	-0.844	0.425628	0.687513
11507	10383109	NM_130886	170720	caspase recruitment domain fam	Card14	0.967	-0.725	0.491128	0.737687
11508	10553743	NM_021879	18431	oculocutaneous albinism II	Oca2	0.967	-0.145	0.888448	0.956033
11509	10586724	NM_145618	93697	NMDA receptor-regulated gene 2	Narg2	0.967	-0.84	0.428081	0.689167
11510	10415017					0.967	-0.01	0.992568	0.997143
11511	10466165	XM_355147	381213	membrane-spanning 4-domains, s	Ms4a12	0.967	-0.123	0.905112	0.963148
11512	10511190	NM_010091	13542	dishevelled, dsh homolog 1 (Dr	Dvl1	0.967	-0.586	0.575896	0.797128
11513	10448030	XR_004875	676111	similar to Ubiquitin-conjugati	LOC676111	0.967	-0.637	0.543659	0.775859
11514	10551104	NM_183311	330485	transmembrane protein 145	Tmem145	0.967	-0.946	0.374803	0.64482
11515	10560414	NM_001033314	232933	coiled-coil domain containing	Ccdc61	0.967	-0.612	0.559212	0.786667
11516	10524698	NM_011107	18778	phospholipase A2, group IB, pa	Pla2g1b	0.967	-0.197	0.849181	0.939006
11517	10349968	NM_007695	12654	chitinase 3-like 1	Chi3l1	0.967	-0.426	0.682235	0.859614
11518	10520173	NM_183000	171209	amiloride-sensitive cation cha	Accn3	0.967	-0.286	0.782753	0.911674
11519	10431124	NM_029427	75772	patatin-like phospholipase dom	Pnpla5	0.967	0.025	0.980611	0.991919
11520	10448355	NM_028416	73016	kringle containing transmembra	Kremen2	0.967	-0.147	0.887281	0.955613
11521	10468828	NM_010123	13669	eukaryotic translation initiat	Eif3s10	0.967	-1.123	0.297382	0.573687
11522	10441973	NM_013684	21374	TATA box binding protein	Tbp	0.967	-0.923	0.385722	0.654755
11523	10607419					0.967	-1.57	0.159234	0.406366
11524	10379228	NM_010927	18126	nitric oxide synthase 2, induc	Nos2	0.967	-0.769	0.466358	0.719571
11525	10548684	XR_034780	622962	similar to actin	LOC622962	0.967	-0.41	0.693647	0.865705
11526	10510880	ENSMUST00000071251	230971	multiple EGF-like-domains 6	Megf6	0.967	-0.202	0.845122	0.937084
11527	10493585	NM_027315	70093	ubiquitin-conjugating enzyme E	Ube2q1	0.967	-1.21	0.264536	0.539638
11528	10507931					0.967	-0.245	0.813626	0.925035
11529	10403577					0.967	-0.191	0.853585	0.940713
11530	10571739					0.967	-0.505	0.628809	0.831023
11531	10514491	NM_001100182	242546	cytochrome P450, family 2, sub	Cyp2j12	0.967	-0.119	0.908193	0.963723
11532	10597656	NM_021544	20271	sodium channel, voltage-gated,	Scn5a	0.967	-0.394	0.70491	0.871105
11533	10375901					0.966	-0.378	0.716575	0.875798
11534	10476108	NM_001110513	228598	early B-cell factor 4	Ebf4	0.966	-0.548	0.600289	0.812216
11535	10461526	BC043473	71768	von Willebrand factor C and EG	Vwce	0.966	-0.414	0.691109	0.86451
11536	10367624					0.966	-0.078	0.940234	0.976727
11537	10393714	NM_183137	78777	RIKEN cDNA 2410002I01 gene	2410002I01Rik	0.966	-0.269	0.795432	0.916955
11538	10420165	NM_009894	12684	cell death-inducing DNA fragme	Cideb	0.966	-0.245	0.813297	0.9249
11539	10462096					0.966	0.047	0.964136	0.985864
11540	10505436					0.966	0.065	0.950009	0.980663

11541	10604653	NM_001009549	333473	zinc finger protein 36, C3H ty	Zfp36l3	0.966	-0.503	0.630039	0.831349
11542	10408081	NM_020034	56702	histone cluster 1, H1b	Hist1h1b	0.966	-1.173	0.27809	0.55314
11543	10566306	NM_198623	244178	ubiquilin 3	Ubqln3	0.966	-0.29	0.779632	0.910547
11544	10381361	NM_178932	237940	amine oxidase, copper containi	Aoc2	0.966	-0.496	0.634419	0.833748
11545	10478355	NM_008652	17865	myeloblastosis oncogene-like 2	Mybl2	0.966	-0.662	0.528747	0.764097
11546	10596023	ENSMUST00000054819	20669	SRY-box containing gene 14	Sox14	0.966	-0.117	0.910001	0.964056
11547	10523206	NM_019490	56041	USO1 homolog, vesicle docking	Uso1	0.966	-1.065	0.321164	0.598048
11548	10540012	NM_173002	80292	ZXD family zinc finger C	Zxdc	0.966	-0.658	0.530851	0.76539
11549	10449932	XR_034756	631266	similar to ribosomal protein L	LOC631266	0.966	-0.615	0.557446	0.785582
11550	10578962	ENSMUST00000098707	100038435	predicted gene, ENSMUSG0000007	ENSMUSG00000074294	0.966	-0.471	0.651364	0.843859
11551	10487685	NM_009732	11998	arginine vasopressin	Avp	0.966	-0.178	0.863536	0.94565
11552	10607718	NR_003640	74264	RIKEN cDNA 1700045I19 gene	1700045I19Rik	0.966	-0.335	0.747231	0.892524
11553	10552604	NM_010643	16617	kallikrein 1-related peptidase	Klk1b24	0.966	-0.252	0.808138	0.922738
11554	10547386	NM_197985	68465	adiponectin receptor 2	Adipor2	0.966	-0.77	0.465527	0.719157
11555	10410560	NM_027182	69716	thyroid hormone receptor inter	Trip13	0.966	-0.928	0.383437	0.652869
11556	10451033	NM_198418	210510	tudor domain containing 6	Tdrd6	0.966	-0.371	0.721433	0.878683
11557	10576158					0.966	-0.422	0.685511	0.861073
11558	10569069	XR_034790	546015	similar to ribosomal protein S	LOC546015	0.966	-0.899	0.397555	0.664302
11559	10589113	NM_030729	80987	NCK interacting protein with S	Nckipsd	0.966	-0.348	0.737818	0.888255
11560	10606001	NM_001110310	55988	sorting nexin 12	Snx12	0.966	-1.175	0.277212	0.552231
11561	10579939	NM_027554	74841	ubiquitin specific peptidase 3	Usp38	0.966	-0.956	0.369964	0.640508
11562	10433207					0.966	-0.12	0.908138	0.963723
11563	10586773	NM_001039519	235459	general transcription factor I	Gtf2a2	0.966	-0.836	0.429745	0.690652
11564	10532839	NM_022017	63873	transient receptor potential c	Trpv4	0.966	-0.318	0.759774	0.899364
11565	10447082	ENSMUST00000066194	73265	RIKEN cDNA 1700038P13 gene	1700038P13Rik	0.966	-0.606	0.563163	0.789853
11566	10562050	NM_026815	109637	uroplakin 1A	Upk1a	0.966	-0.23	0.824369	0.929508
11567	10557372	AK052528	233865	RIKEN cDNA D430042O09 gene	D430042O09Rik	0.966	-0.218	0.83347	0.932911
11568	10381140	NM_028918	74407	tetratricopeptide repeat domai	Ttc25	0.966	-0.531	0.611555	0.819829
11569	10384662	NM_144514	17846	COMM domain containing 1	Commd1	0.966	-0.999	0.350059	0.623549
11570	10598154	AF067063	380878	cDNA sequence AF067063	AF067063	0.966	-0.218	0.83338	0.932893
11571	10348556	XR_032669	665783	similar to Zinc finger protein	LOC665783	0.966	-0.149	0.885423	0.955173
11572	10349773	NM_144810	213417	kelch domain containing 8A	Klhdc8a	0.966	-0.306	0.768179	0.90369
11573	10363346	NM_172939	268301	ankyrin repeat domain 57	Ankrd57	0.966	-0.507	0.627056	0.830395
11574	10562818	NM_011131	18971	polymerase (DNA directed), del	Pold1	0.966	-0.732	0.487346	0.734981
11575	10345099	AK005585	68002	RIKEN cDNA 1110058L19 gene	1110058L19Rik	0.966	-0.548	0.600196	0.812161
11576	10551841	NM_027259	69920	polymerase (RNA) II (DNA direc	Polr2i	0.966	-0.977	0.360145	0.632213
11577	10545993	NM_025466	66283	gastrokine 1	Gkn1	0.966	-0.339	0.744556	0.891476
11578	10387257	NM_009661	11688	arachidonate 8-lipoxygenase	Alox8	0.966	-0.57	0.585694	0.80308
11579	10576029	NM_009941	12857	cytochrome c oxidase subunit I	Cox4i1	0.966	-0.953	0.371657	0.64202
11580	10497045					0.966	-0.673	0.521879	0.758967
11581	10423293	NM_019472	17909	myosin X	Myo10	0.966	-0.694	0.509123	0.750516
11582	10521583	NM_013503	13492	dopamine receptor 5	Drd5	0.966	-0.123	0.905115	0.963148
11583	10387638	NM_010198	14166	fibroblast growth factor 11	Fgf11	0.966	-0.5	0.631904	0.832719
11584	10465587	NM_153795	108101	fermitin family homolog 3 (Dro	Fermt3	0.966	-0.811	0.443559	0.702308
11585	10453600	XR_030739	621501	predicted gene, EG621501	EG621501	0.966	-0.705	0.502762	0.745575
11586	10370013	NM_010361	14872	glutathione S-transferase, the	Gstt2	0.966	-0.47	0.652328	0.844168
11587	10397081	NM_027349	67039	RNA binding motif protein 25	Rbm25	0.966	-0.791	0.454366	0.710796
11588	10374032					0.966	-0.203	0.844775	0.936998
11589	10575702	NM_001007223	403395	C-type lectin domain family 3,	Clec3a	0.966	-0.365	0.725897	0.88133
11590	10570119	BC019538	69225	RIKEN cDNA 0710008K08 gene	0710008K08Rik	0.966	-0.445	0.669162	0.852809
11591	10415911	NM_001081177	16554	kinesin family member 13B	Kif13b	0.966	-0.681	0.516944	0.756158
11592	10445378					0.966	-0.453	0.664115	0.850267
11593	10469035	NM_175400	109079	selenophosphate synthetase 1	Sephs1	0.966	-0.984	0.356895	0.629197
11594	10434888	NM_133752	74143	optic atrophy 1 homolog (human	Opa1	0.966	-0.946	0.374583	0.644557

11595	10524411	NM_001010825	231630	FIC domain containing	Ficd	0.966	-0.817	0.439971	0.699124
11596	10565241	BC061016	75556	RIKEN cDNA 1700026D08 gene	1700026D08Rik	0.966	-0.093	0.928593	0.971893
11597	10507914	NM_029157	75062	splicing factor 3a, subunit 3	Sf3a3	0.966	-0.944	0.375682	0.645773
11598	10370780	NM_008793	18551	proprotein convertase subtilis	Pcsk4	0.966	-0.379	0.715839	0.875402
11599	10467941	NM_001081077	72502	CWF19-like 1, cell cycle contr	Cwf19l1	0.966	-1.064	0.321808	0.598601
11600	10578149	NM_026609	68192	leptin receptor overlapping tr	Leprotl1	0.966	-0.726	0.490679	0.737369
11601	10572109	NM_027590	70885	integrator complex subunit 10	Ints10	0.966	-0.922	0.386399	0.655384
11602	10405545	NM_028281	72562	pterin 4 alpha carbinolamine d	Pcbd2	0.966	-0.437	0.674952	0.855557
11603	10414487	NM_001011738	257884	olfactory receptor 744	Olfr744	0.966	0.172	0.868106	0.947171
11604	10348072	ENSMUST00000097665	319336	RIKEN cDNA C130036L24 gene	C130036L24Rik	0.966	-0.105	0.919537	0.967948
11605	10417836	NM_025440	66242	mitochondrial ribosomal protei	Mrps16	0.966	-0.825	0.435708	0.695606
11606	10598069	ENSMUST00000082421	17711	cytochrome b	CYTB	0.966	-0.783	0.458802	0.713797
11607	10563745	NM_207538	404239	MAS-related GPR, member B5	Mrgprb5	0.966	-0.322	0.756323	0.897871
11608	10515012	NM_172697	230596	PRP38 pre-mRNA processing fact	Prpf38a	0.966	-1.281	0.239912	0.512931
11609	10516723	NM_198959	230777	hypocretin (orexin) receptor 1	Hcrtr1	0.966	-0.445	0.669055	0.852809
11610	10366350	NM_178610	52705	KRR1, small subunit (SSU) proc	Krr1	0.966	-1.221	0.26032	0.534856
11611	10365127	BC117023	72273	RIKEN cDNA 2210404O07 gene	2210404O07Rik	0.966	-0.754	0.474851	0.726501
11612	10401713	NM_153415	217734	protein-O-mannosyltransferase	Pomt2	0.966	-0.693	0.510193	0.751325
11613	10401335	NM_027213	69792	mediator of RNA polymerase II	Med6	0.966	-0.769	0.466079	0.719571
11614	10557361	BC042743	233865	RIKEN cDNA D430042O09 gene	D430042O09Rik	0.966	-0.713	0.498043	0.742207
11615	10516238					0.965	-0.858	0.418445	0.681004
11616	10561664	BC023421	73833	RIKEN cDNA 1110006G06 gene	1110006G06Rik	0.965	-0.352	0.735007	0.886784
11617	10362171	NM_016797	53331	syntaxin 7	Stx7	0.965	-0.691	0.510992	0.752038
11618	10354207	NM_170597	263764	cellular repressor of E1A-stim	Creg2	0.965	-0.254	0.806689	0.921832
11619	10574423	ENSMUST00000064349	234624	RIKEN cDNA A330008L17 gene	A330008L17Rik	0.965	-0.17	0.869906	0.947912
11620	10407255	NM_001037914	622408	predicted gene, EG622408	EG622408	0.965	-0.769	0.46639	0.719571
11621	10507101	NM_001085549	666048	predicted gene, OTTMUSG0000000	OTTMUSG00000008561	0.965	-0.228	0.825932	0.929952
11622	10383632	NM_030207	78887	Sfi1 homolog, spindle assembly	Sfi1	0.965	-0.175	0.8661	0.946491
11623	10447725	U44941	19317	quaking	Qk	0.965	-0.737	0.48432	0.732823
11624	10413771	NM_009796	12339	calpain 7	Capn7	0.965	-0.712	0.499061	0.742429
11625	10445983	NM_028381	72886	coiled-coil domain containing	Ccdc94	0.965	-0.659	0.53054	0.765382
11626	10385048	NM_019916	27140	T-cell leukemia, homeobox 3	Tlx3	0.965	-0.593	0.571193	0.795344
11627	10552982	NM_148927	69217	pleckstrin homology domain con	Plekha4	0.965	-0.274	0.791705	0.915198
11628	10423291	NM_001013791	432939	predicted gene, EG432939	EG432939	0.965	-0.159	0.877732	0.951715
11629	10453575	NM_029402	71745	cullin 2	Cul2	0.965	-1.056	0.324941	0.601308
11630	10503534	NM_016746	51813	cyclin C	Ccnc	0.965	-0.61	0.560731	0.78784
11631	10556812	NM_029610	73919	LYR motif containing 1	Lyrm1	0.965	-0.527	0.614288	0.821474
11632	10503828	NM_175364	108755	LYR motif containing 2	Lyrm2	0.965	-1.04	0.332149	0.608213
11633	10583199					0.965	-0.286	0.782847	0.911733
11634	10579974					0.965	-0.769	0.466304	0.719571
11635	10545182	ENSMUST00000103337	243451	gene model 459, (NCBI)	Gm459	0.965	-0.119	0.908479	0.963723
11636	10376568	NM_009021	19377	retinoic acid induced 1	Rai1	0.965	-0.603	0.565075	0.791097
11637	10363415	NM_052994	94214	sparc/osteonectin, cwcv and ka	Spock2	0.965	-0.725	0.491109	0.737687
11638	10586368	NM_011802	270166	caseinolytic peptidase X (E.co	Clpx	0.965	-0.971	0.362938	0.63431
11639	10346146	XM_001487804	666962	predicted gene, EG666962	EG666962	0.965	-0.526	0.614657	0.821667
11640	10517312	NM_025382	66146	transmembrane protein 57	Tmem57	0.965	-0.875	0.409904	0.674344
11641	10594289	NM_033320	93683	glucuronyl C5-epimerase	Glce	0.965	-0.773	0.464025	0.717953
11642	10537506	NM_146383	258381	olfactory receptor 460	Olfr460	0.965	-0.94	0.377499	0.647352
11643	10360460	NM_021350	12663	choroideremia-like	Chml	0.965	-0.86	0.417601	0.680363
11644	10571045	AK090261	100038760	predicted gene, ENSMUSG0000005	ENSMUSG00000054427	0.965	-1.438	0.192327	0.451739

11645	10552871	NM_053256	114640	parathyroid hormone 2	Pth2	0.965	-0.517	0.620703	0.82573
11646	10574143					0.965	-0.421	0.686092	0.861394
11647	10567458	XM_355934	381917	dynein, axonemal, heavy chain	Dnahc3	0.965	-0.663	0.527737	0.763341
11648	10543492	XR_032094	626912	predicted gene, EG626912	EG626912	0.965	-0.573	0.584339	0.802134
11649	10532592	XM_912851	74376	myosin XVIIIb	Myo18b	0.965	-0.377	0.717002	0.876165
11650	10392040	NM_001039242	632687	membrane-associated ring finge	March10	0.965	-0.005	0.996064	0.998425
11651	10549402	NM_026168	67456	ERGIC and golgi 2	Ergic2	0.965	-1.032	0.335511	0.611134
11652	10558580	NM_009482	22286	undifferentiated embryonic cel	Utf1	0.965	-0.742	0.481553	0.730886
11653	10371067	NM_021501	59004	protein inhibitor of activated	Pias4	0.965	-0.464	0.656312	0.846043
11654	10373890	NM_134023	103724	TBC1 domain family, member 10a	Tbc1d10a	0.965	-0.507	0.62727	0.830494
11655	10421906	BC085191	56419	diaphanous homolog 3 (Drosophi	Diap3	0.965	-0.193	0.852031	0.940258
11656	10513867	ENSMUST00000098013	214444	CDK5 regulatory subunit associ	Cdk5rap2	0.965	-1.082	0.314013	0.590842
11657	10458913	NM_178686	225523	coiled-coil domain containing	Ccdc100	0.965	-1.154	0.285187	0.560488
11658	10574872	BC125412	71046	RIKEN cDNA 4933405L10 gene	4933405L10Rik	0.965	0.167	0.871665	0.948704
11659	10361680					0.965	-0.403	0.698477	0.867855
11660	10567556	NM_001040136	67983	RIKEN cDNA 4930408O21 gene	4930408O21Rik	0.965	-0.908	0.393381	0.661285
11661	10477935	ENSMUST00000099140	383766	gene model 1332, (NCBI)	Gm1332	0.965	-0.042	0.967269	0.987015
11662	10354220	NM_172499	211798	major facilitator superfamily	Mfsd9	0.965	-0.584	0.576779	0.797659
11663	10581835	NM_176923	319481	WD repeat domain 59	Wdr59	0.965	-0.5	0.631944	0.83272
11664	10480956	NM_001037747	332579	caspase recruitment domain fam	Card9	0.965	-0.082	0.936542	0.975144
11665	10418247	NM_178668	211948	RIKEN cDNA E430028B21 gene	E430028B21Rik	0.965	-0.643	0.539891	0.772463
11666	10432404	NM_011653	22142	tubulin, alpha 1A	Tuba1a	0.965	-0.964	0.366035	0.63705
11667	10363163	NM_025541	66403	ASF1 anti-silencing function 1	Asf1a	0.965	-0.91	0.392366	0.660367
11668	10391178	NM_019795	56354	DnaJ (Hsp40) homolog, subfamil	Dnajc7	0.965	-1.032	0.335592	0.611175
11669	10514732	NM_177732	242585	solute carrier family 35 (UDP-	Slc35d1	0.965	-0.387	0.709739	0.872992
11670	10364164	NM_019434	54387	minichromosome maintenance def	Mcm3ap	0.965	-0.748	0.478023	0.728592
11671	10541186	ENSMUST00000062454	67289	RIKEN cDNA 3110021A11 gene	3110021A11Rik	0.965	-0.388	0.709327	0.87279
11672	10378424					0.965	-0.234	0.821305	0.92863
11673	10448390	NM_027644	71003	RIKEN cDNA 4931440B09 gene	4931440B09Rik	0.965	-0.67	0.523983	0.760561
11674	10442127					0.965	-0.833	0.431818	0.69227
11675	10479556	BC051628	332713	cDNA sequence BC051628	BC051628	0.965	-0.147	0.887238	0.955613
11676	10532624					0.965	-0.15	0.885189	0.954969
11677	10535369	XR_034208	677204	hypothetical protein LOC677204	LOC677204	0.965	-0.846	0.424624	0.686672
11678	10386370	NM_007476	11840	ADP-ribosylation factor 1	Arf1	0.965	-0.617	0.556437	0.784877
11679	10561907	NM_001033140	68332	RIKEN cDNA 0610010E21 gene	0610010E21Rik	0.965	-1.234	0.255843	0.530243
11680	10400357	ENSMUST00000038926	217578	bromodomain adjacent to zinc f	Baz1a	0.965	-1.283	0.239257	0.512081
11681	10526302	NM_013763	27368	transducin (beta)-like 2	Tbl2	0.965	-0.868	0.41354	0.677091
11682	10593776	NM_032002	83961	neuregulin 4	Nrg4	0.965	-0.368	0.723252	0.879946
11683	10520154	NM_029020	74610	ATP-binding cassette, sub-fami	Abcb8	0.965	-0.686	0.514055	0.754437
11684	10553430	NM_148931	104245	solute carrier family 6 (neuro	Slc6a5	0.965	-0.537	0.607462	0.817267
11685	10539433	ENSMUST00000055261	232157	MOB1, Mps One Binder kinase ac	Mobkl1b	0.965	-0.917	0.388679	0.657212
11686	10522530	NM_001122733	16590	kit oncogene	Kit	0.965	-0.427	0.681892	0.859437
11687	10442155	NM_016891	51792	protein phosphatase 2 (formerl	Ppp2r1a	0.965	-1.306	0.231518	0.502383
11688	10555789	NM_010089	13532	deubiquitinating enzyme 2	Dub2	0.965	0.216	0.834977	0.933323
11689	10439891	XR_035012	627543	similar to eukaryotic translat	LOC627543	0.965	-1.022	0.339889	0.61524
11690	10595402	ENSMUST00000098501	212943	cDNA sequence BC023892	BC023892	0.965	0.041	0.968781	0.987519
11691	10449356	NM_001002895	106672	expressed sequence AI413582	AI413582	0.965	-0.282	0.785835	0.912599
11692	10589192	BC111913	69384	transmembrane protein 89	Tmem89	0.965	-0.778	0.461497	0.716124
11693	10511812	NM_008899	18992	POU domain, class 3, transcrip	Pou3f2	0.965	-0.597	0.568845	0.79359
11694	10564337	NM_023239	66647	necdin-like 2	Ndnl2	0.964	-0.968	0.364258	0.635557
11695	10414460	NM_001081430	70646	N-acetyltransferase 12	Nat12	0.964	-0.726	0.490513	0.737328

11696	10348131	NM_007432	11648	alkaline phosphatase 3, intest	Akp3	0.964	-0.284	0.784128	0.912068
11697	10577882	NM_029884	52120	heparan-alpha-glucosaminide N-	Hgsnat	0.964	-1.471	0.183469	0.440626
11698	10499961	NM_001007222	399673	TD and POZ domain containing 2	Tdpoz2	0.964	0.316	0.760821	0.900213
11699	10534912	NM_175521	243300	RIKEN cDNA 6430598A04 gene	6430598A04Rik	0.964	-0.079	0.939299	0.976298
11700	10394749	NM_001008421	217431	nucleolar protein 10	Nol10	0.964	-0.677	0.519585	0.757547
11701	10437399	NM_030205	78885	coronin 7	Coro7	0.964	-1.039	0.332469	0.608528
11702	10429898	NM_183099	73542	testis-specific serine kinase	Tssk5	0.964	-0.341	0.743005	0.890544
11703	10366554	NM_148922	17245	transformed mouse 3T3 cell dou	Mdm1	0.964	-0.493	0.636619	0.834887
11704	10518557	NM_007745	12854	cortistatin	Cort	0.964	-0.321	0.757545	0.898154
11705	10439392	NM_028812	74197	general transcription factor I	Gtf2e1	0.964	-0.942	0.376886	0.647069
11706	10446149	NM_027933	71810	RAN binding protein 3	Ranbp3	0.964	-0.768	0.467021	0.719977
11707	10389010	BC055024	70591	RIKEN cDNA 5730455P16 gene	5730455P16Rik	0.964	-0.655	0.532685	0.766762
11708	10550889	BC034211	71997	RIKEN cDNA 1500002O20 gene	1500002O20Rik	0.964	-0.387	0.710126	0.873031
11709	10506125	NM_013913	30924	angiopoietin-like 3	Angptl3	0.964	-0.542	0.604116	0.815116
11710	10373157	NM_001003913	216443	methionine-tRNA synthetase	Mars	0.964	-0.865	0.415118	0.678399
11711	10374560	NM_011663	22183	zinc finger (CCCH type), RNA b	Zrsr1	0.964	-0.544	0.602937	0.814375
11712	10602255	NM_001033795	619287	zinc finger, CCHC domain conta	Zcchc16	0.964	-0.201	0.846077	0.937284
11713	10569163	NM_021316	57754	cell cycle exit and neuronal d	Cend1	0.964	-0.087	0.932806	0.973219
11714	10595909					0.964	-0.501	0.6311	0.832075
11715	10477353	NM_007896	13589	microtubule-associated protein	Mapre1	0.964	-1.126	0.296059	0.572513
11716	10510861	ENSMUST00000030897	230971	multiple EGF-like-domains 6	Megf6	0.964	-0.601	0.566399	0.79227
11717	10357064	NM_009190	20479	vacuolar protein sorting 4b (y	Vps4b	0.964	-1.223	0.2599	0.53415
11718	10461305	NM_024256	72727	beta-1,3-glucuronyltransferase	B3gat3	0.964	-1.036	0.333746	0.609432
11719	10437257	NM_001033159	71063	zinc finger protein 597	Zfp597	0.964	-0.996	0.351638	0.624753
11720	10419274	NM_022023	63985	glia maturation factor, beta	Gmfb	0.964	-0.922	0.386256	0.655195
11721	10497167					0.964	-1.022	0.340026	0.615381
11722	10467315	ENSMUST00000092265	619304	RIKEN cDNA I830134H01 gene	I830134H01Rik	0.964	-0.444	0.669908	0.853234
11723	10386495	NM_153080	216810	target of myb1-like 2 (chicken	Tom1l2	0.964	-0.827	0.434478	0.694903
11724	10516566	NM_001033189	97130	expressed sequence C77080	C77080	0.964	-0.341	0.742926	0.89053
11725	10351026	NR_002840	14455	growth arrest specific 5	Gas5	0.964	-0.742	0.481616	0.730928
11726	10525103	NM_029408	75732	IQ motif containing D	Iqcd	0.964	-0.842	0.426837	0.688211
11727	10568502	NM_008411	16433	CUB and zona pellucida-like do	Cuzd1	0.964	-0.352	0.734896	0.886784
11728	10555834	NM_146354	258351	olfactory receptor 633	Olfr633	0.964	0.203	0.844913	0.937
11729	10472386	NM_001099298	110876	sodium channel, voltage-gated,	Scn2a1	0.964	-0.668	0.524732	0.761127
11730	10434117	ENSMUST00000090145	433004	RIKEN cDNA B830017H08 gene	B830017H08Rik	0.964	-0.583	0.577418	0.797771
11731	10515739	ENSMUST00000075406	230676	cDNA sequence BC059842	BC059842	0.964	-1.001	0.349109	0.622715
11732	10509023	NM_026780	68592	SYF2 homolog, RNA splicing fac	Syf2	0.964	-1.258	0.247537	0.520853
11733	10509030	NM_019732	12399	runt related transcription fac	Runx3	0.964	-0.607	0.562717	0.789779
11734	10552553	NM_029831	76999	RIKEN cDNA 1700127D06 gene	1700127D06Rik	0.964	-0.452	0.664523	0.850409
11735	10364460	NM_008504	16904	granzyme M (lymphocyte met-ase	Gzmm	0.964	-0.549	0.599671	0.812038
11736	10416485	XM_914736	380918	gene model 912, (NCBI)	Gm912	0.964	-0.091	0.930346	0.97262
11737	10462879					0.964	-0.392	0.706151	0.871814
11738	10355554	NM_146110	227290	angio-associated migratory pro	Aamp	0.964	-1.026	0.337969	0.613519
11739	10501199	NM_026672	68312	glutathione S-transferase, mu	Gstm7	0.964	-0.704	0.503417	0.745918
11740	10400668	NM_025441	66244	serologically defined colon ca	Sdccag1	0.964	-1.108	0.303393	0.579489
11741	10353420	NM_008563	17215	minichromosome maintenance def	Mcm3	0.964	-1.041	0.33156	0.607971
11742	10587503	NM_172507	212531	SH3 domain binding glutamic ac	Sh3bgrl2	0.964	-0.721	0.49333	0.739056
11743	10567788	NM_001101488	269994	GSG1-like	Gsg1l	0.964	-0.332	0.749353	0.893972
11744	10568826	ENSMUST00000074388	664857	RIKEN cDNA 9330101J02 gene	9330101J02Rik	0.964	-0.663	0.527703	0.763341
11745	10422075	NM_207215	105689	MYC binding protein 2	Mycbp2	0.964	-0.784	0.457893	0.713313

11746	10557470	NM_024228	68616	glycerophosphodiester phosphod	Gdpd3	0.964	-0.436	0.675794	0.855911
11747	10386963	AK086503	654805	RIKEN cDNA F930015N05 gene	F930015N05Rik	0.964	-0.346	0.738992	0.888726
11748	10570614	NM_054074	116746	defensin beta 6	Defb6	0.964	-0.582	0.578297	0.798297
11749	10533106	NM_172998	269695	ring finger protein, transmemb	Rnft2	0.964	-0.229	0.824886	0.929565
11750	10604761					0.964	-0.504	0.629263	0.831256
11751	10486448	NM_001024145	271844	phospholipase A2, group IVF	Pla2g4f	0.964	-0.403	0.698519	0.867855
11752	10478421	NM_001030292	241769	potassium channel, subfamily K	Kcnk15	0.964	-1.082	0.314271	0.591082
11753	10401805	NM_025507	66354	SNW domain containing 1	Snw1	0.964	-0.976	0.36066	0.632426
11754	10413212	NM_183208	328365	zinc finger, MIZ-type containi	Zmiz1	0.964	-0.475	0.649099	0.842359
11755	10493484	NM_025327	66059	keratinocyte associated protei	Krtcap2	0.964	-0.331	0.750165	0.894442
11756	10517573	NM_026419	67868	elastase 3, pancreatic	Ela3	0.964	-0.204	0.843761	0.936634
11757	10522658					0.964	-0.782	0.459259	0.714171
11758	10592705	NM_011139	18988	POU domain, class 2, transcrip	Pou2f3	0.964	-0.534	0.609084	0.818045
11759	10439523	ENSMUST00000068934	791329	predicted gene, ENSMUSG0000005	ENSMUSG00000055370	0.964	-1.062	0.322556	0.599294
11760	10586157	NM_024212	67891	ribosomal protein L4	Rpl4	0.964	-1.05	0.327727	0.604012
11761	10356681	NM_153114	260301	otospiralin	Otos	0.964	-0.682	0.516828	0.756112
11762	10517090	NM_001080819	93760	AT rich interactive domain 1A	Arid1a	0.964	-0.856	0.419447	0.681847
11763	10388211	NM_029932	77577	spinster homolog 3 (Drosophila	Spns3	0.964	-0.175	0.866057	0.946491
11764	10535184	NM_025604	66506	proteasome (prosome, macropain	Psmg3	0.963	-1.994	0.0851986	0.280273
11765	10455017	ENSMUST00000077710	627427	predicted gene, EG627427	EG627427	0.963	-0.524	0.615821	0.822286
11766	10478994	ENSMUST00000029007	76426	RIKEN cDNA 1700029J11 gene	1700029J11Rik	0.963	0.229	0.825409	0.929756
11767	10376269	NM_134189	171212	UDP-N-acetyl-alpha-D-galactosa	Galnt10	0.963	-1.605	0.151266	0.395197
11768	10391378	NM_007970	14055	enhancer of zeste homolog 1 (D	Ezh1	0.963	-0.326	0.753578	0.896207
11769	10416122					0.963	-0.245	0.813576	0.925035
11770	10453811	NM_001083628	381157	cDNA sequence AK220484	AK220484	0.963	-0.019	0.985249	0.993851
11771	10568180	NM_027353	70233	CD2 antigen (cytoplasmic tail)	Cd2bp2	0.963	-0.799	0.449593	0.70698
11772	10570005	ENSMUST00000048606	66719	RIKEN cDNA 4921522P10 gene	4921522P10Rik	0.963	-0.714	0.497843	0.741974
11773	10587368	NM_026658	68291	mitochondrial translation opti	Mto1	0.963	-0.643	0.539878	0.772463
11774	10402564	NM_028262	52690	SET domain containing 3	Setd3	0.963	-1.072	0.318372	0.595538
11775	10538109	BC145740	243373	expressed sequence AI854703	AI854703	0.963	-0.299	0.773566	0.9067
11776	10432695	NM_001003668	406219	keratin 83	Krt83	0.963	-0.226	0.827414	0.930659
11777	10489629	NM_174988	104010	cadherin 22	Cdh22	0.963	-0.601	0.56636	0.79227
11778	10388914	NM_013571	16706	kinase suppressor of ras 1	Ksr1	0.963	-0.613	0.55891	0.786425
11779	10479811	NM_027290	70024	minichromosome maintenance def	Mcm10	0.963	-0.854	0.420597	0.68293
11780	10440564	NM_001081068	78913	zinc finger protein 294	Zfp294	0.963	-0.157	0.879336	0.952124
11781	10375903	NM_029976	52626	CDKN2A interacting protein N-t	Cdkn2aipnl	0.963	-1.162	0.282102	0.557189
11782	10543442	NM_026614	68202	NADH dehydrogenase (ubiquinone	Ndufa5	0.963	-1.082	0.31406	0.590842
11783	10564888	NM_133952	101869	unc-45 homolog A (C. elegans)	Unc45a	0.963	-0.702	0.504405	0.74665
11784	10597686	NM_009134	20264	sodium channel, voltage-gated,	Scn10a	0.963	-0.699	0.506617	0.748509
11785	10486898	BC019404	214585	spastic paraplegia 11	Spg11	0.963	-0.579	0.580339	0.799512
11786	10443470	NM_001002786	442827	RIKEN cDNA 9830134C10 gene	9830134C10Rik	0.963	-0.147	0.887222	0.955613
11787	10495623	ENSMUST00000066215	791377	predicted gene, ENSMUSG0000005	ENSMUSG00000053651	0.963	-0.202	0.84535	0.937238
11788	10351857	NM_008763	18313	olfactory receptor 16	Olfr16	0.963	0.068	0.947622	0.979302
11789	10596521	BC115866	108068	glutamate receptor, metabotrop	Grm2	0.963	-0.698	0.506936	0.74877
11790	10529544	AK043305	76710	RIKEN cDNA 2210406O10 gene	2210406O10Rik	0.963	-0.462	0.657682	0.846971
11791	10547381	NM_172492	211187	leucine-rich repeats and trans	Lrtm2	0.963	-0.299	0.773553	0.9067
11792	10596925	NM_023247	66706	RIKEN cDNA 4733401H18 gene	4733401H18Rik	0.963	-0.684	0.515606	0.755142
11793	10419323	NM_144553	218977	discs, large homolog 7 (Drosop	Dlg7	0.963	-1.096	0.308426	0.585137
11794	10372104	XR_002021	667407	predicted gene, EG667407	EG667407	0.963	-0.98	0.3587	0.630757
11795	10532807	NM_148935	116810	forkhead box N4	Foxn4	0.963	-0.076	0.94134	0.9773
11796	10567516	XM_355934	381917	dynein, axonemal, heavy chain	Dnahc3	0.963	-0.428	0.680849	0.858584

11797	10399357	NM_013527	238057	growth differentiation factor	Gdf7	0.963	-0.132	0.898454	0.960023
11798	10429176	AK143207	20442	ST3 beta-galactoside alpha-2,3	St3gal1	0.963	-0.236	0.820087	0.928345
11799	10470392	NM_029981	77794	ADAMTS-like 2	Adamtsl2	0.963	-0.679	0.518471	0.757012
11800	10545308	NM_173001	104263	jumonji domain containing 1A	Jmjd1a	0.963	-1	0.349676	0.623229
11801	10449266	NM_207217	106581	integrin alpha FG-GAP repeat c	Itfg3	0.963	-0.733	0.486523	0.734369
11802	10606389	ENSMUST00000116167	236954	gene model 379, (NCBI)	Gm379	0.963	-0.31	0.7656	0.902563
11803	10434556	XR_034101	676915	similar to nuclear domain 10 p	LOC676915	0.963	0.012	0.990823	0.996163
11804	10463066	ENSMUST00000112231	12495	ectonucleoside triphosphate di	Entpd1	0.963	-0.421	0.686218	0.8615
11805	10464365	NM_207261	332396	potassium channel, subfamily K	Kcnk18	0.963	-0.236	0.819811	0.928345
11806	10474199					0.963	-1.021	0.340288	0.61558
11807	10568536	NM_018867	55987	carboxypeptidase X 2 (M14 fami	Cpxm2	0.963	-0.602	0.565464	0.791538
11808	10600357	NM_181516	66826	tafazzin	Taz	0.963	-0.582	0.578065	0.798189
11809	10563377	NM_017465	54200	sulfotransferase family, cytos	Sult2b1	0.963	-0.326	0.753736	0.896244
11810	10398424					0.963	-0.49	0.638666	0.835923
11811	10443854	NM_177307	320997	cytochrome P450, family 4, sub	Cyp4f39	0.963	-0.777	0.461918	0.716461
11812	10581702	NM_172283	234730	fucokinase	Fuk	0.963	-0.667	0.52537	0.761529
11813	10482467	NM_011958	26428	origin recognition complex, su	Orc4l	0.963	-0.92	0.387366	0.656334
11814	10386741	ENSMUST00000074908	73216	RIKEN cDNA 3110043A19 gene	3110043A19Rik	0.963	-0.371	0.721168	0.878601
11815	10555620	NM_011644	22064	transient receptor potential c	Trpc2	0.963	-0.716	0.496354	0.740946
11816	10591853	NM_194263	57246	T-box 20	Tbx20	0.963	-0.124	0.904439	0.962829
11817	10499366	NM_025928	67037	polyamine-modulated factor 1	Pmf1	0.963	-1.527	0.169239	0.42056
11818	10593233	NM_013561	15561	5-hydroxytryptamine (serotonin	Htr3a	0.963	-0.343	0.741553	0.889732
11819	10594053	NM_178087	18854	promyelocytic leukemia	Pml	0.963	-0.615	0.557592	0.785718
11820	10545436	NM_144917	232089	RNA binding motif and ELMO dom	Rbed1	0.963	-1.184	0.273796	0.548502
11821	10545891	NM_023160	66116	camello-like 1	Cml1	0.963	-0.435	0.676311	0.855923
11822	10366866	NM_027151	69654	dynactin 2	Dctn2	0.963	-0.873	0.410934	0.675081
11823	10395816	NM_011968	26443	proteasome (prosome, macropain	Psma6	0.963	-1.119	0.298998	0.575095
11824	10551355	NM_133210	170742	SERTA domain containing 3	Sertad3	0.963	-1.05	0.327675	0.60399
11825	10439463	BC002243	76916	RIKEN cDNA 4930455C21 gene	4930455C21Rik	0.963	-0.863	0.415694	0.678825
11826	10473541	ENSMUST00000062494	259030	olfactory receptor 1125	Olfr1125	0.963	-0.185	0.858313	0.943105
11827	10465990	BC052053	68642	RIKEN cDNA 2810441K11 gene	2810441K11Rik	0.963	-0.413	0.691787	0.864682
11828	10534168	NM_177047	319974	autism susceptibility candidat	Auts2	0.963	-0.802	0.447926	0.705628
11829	10480646	NM_001033410	329360	gene model 757, (NCBI)	Gm757	0.963	-0.263	0.800102	0.919271
11830	10534728	NM_031406	83704	solute carrier family 12 (pota	Slc12a9	0.963	-0.261	0.801509	0.919489
11831	10472688	NM_022435	64406	trans-acting transcription fac	Sp5	0.963	-0.77	0.465653	0.7193
11832	10597898					0.963	-0.165	0.873305	0.949372
11833	10442870	ENSMUST00000095500	381077	coiled-coil domain containing	Ccdc78	0.963	-0.523	0.616594	0.822955
11834	10553107	NM_001033170	73813	RIKEN cDNA 4930403C10 gene	4930403C10Rik	0.963	-0.615	0.557628	0.785718
11835	10549473	NM_181541	232560	caprin family member 2	Caprin2	0.963	-0.452	0.664257	0.850267
11836	10390454	BC055770	103551	RIKEN cDNA E130012A19 gene	E130012A19Rik	0.963	-0.211	0.838956	0.934806
11837	10515841	ENSMUST00000084312	433751	predicted gene, OTTMUSG0000000	OTTMUSG00000008833	0.963	-0.138	0.893868	0.958124
11838	10519951	NM_175437	212167	RIKEN cDNA A530088I07 gene	A530088I07Rik	0.963	-0.216	0.83502	0.933323
11839	10496756	NM_134160	171166	mucolipin 3	Mcoln3	0.963	-1.058	0.324082	0.600613
11840	10463308	NM_013806	12780	ATP-binding cassette, sub-fami	Abcc2	0.963	-0.161	0.876516	0.951096
11841	10529026					0.963	-0.156	0.87997	0.952396
11842	10354832	NM_027351	70225	peptidylprolyl isomerase (cycl	Ppil3	0.963	-1.401	0.202789	0.465349
11843	10410929	NM_023538	69923	acylglycerol kinase	Agk	0.963	-0.982	0.357774	0.630135
11844	10596570	BC052180	109095	RNA binding motif protein 15B	Rbm15b	0.963	-0.358	0.730456	0.883456
11845	10550557	NM_031255	83434	radial spokehead-like 1	Rshl1	0.963	-0.367	0.724339	0.880611
11846	10435443	NM_175111	66667	Hspb associated protein 1	Hspbap1	0.963	-0.53	0.612161	0.820198
11847	10445232	ENSMUST00000074428	73235	RIKEN cDNA 3110082D06	3110082D06Rik	0.963	-0.528	0.613145	0.820788

				gene					
11848	10400642	BC062898	109065	RIKEN cDNA 1110034A24 gene	1110034A24Rik	0.963	-0.52	0.618593	0.824167
11849	10603478	NM_172478	209815	TBC1 domain family, member 25	Tbc1d25	0.963	-0.287	0.781926	0.911385
11850	10372844	NM_138956	192678	Ras association (RalGDS/AF-6)	Rassf3	0.963	-0.693	0.510168	0.751325
11851	10379594	NM_178680	217012	unc-45 homolog B (C. elegans)	Unc45b	0.963	-0.039	0.970077	0.987783
11852	10359648	BC052855	381306	cDNA sequence BC055324	BC055324	0.963	-0.899	0.397694	0.664302
11853	10434052	NM_011028	18440	purinergic receptor P2X, ligan	P2rx6	0.962	-0.919	0.387952	0.656721
11854	10504891	NM_021436	230157	transmembrane protein with EGF	Tmeff1	0.962	-0.491	0.638346	0.835923
11855	10440574	NM_001081068	78913	zinc finger protein 294	Zfp294	0.962	-0.979	0.359292	0.631337
11856	10519046	AK141913	320939	RIKEN cDNA 5930403L14 gene	5930403L14Rik	0.962	-0.591	0.572612	0.796254
11857	10604837	NM_009237	20675	SRY-box containing gene 3	Sox3	0.962	-1.126	0.296218	0.572717
11858	10591022	BC016078	70984	RIKEN cDNA 4931406C07 gene	4931406C07Rik	0.962	-0.947	0.374224	0.644376
11859	10403903	NM_009054	19720	tripartite motif-containing 27	Trim27	0.962	-0.97	0.363421	0.634688
11860	10540622	NM_030178	78783	bromodomain and PHD finger con	Brpf1	0.962	-0.703	0.504094	0.746397
11861	10463513	ENSMUST00000096033	75056	RIKEN cDNA 4930505N22 gene	4930505N22Rik	0.962	-0.612	0.559272	0.786672
11862	10400706	ENSMUST00000053451	100036526	predicted gene, ENSMUSG0000005	ENSMUSG00000052673	0.962	-0.425	0.682933	0.859827
11863	10576506	NM_010322	14712	glyceronephosphate O-acyltrans	Gnpat	0.962	-0.968	0.36451	0.635653
11864	10415570	ENSMUST00000072032	100125977	predicted gene, ENSMUSG0000005	ENSMUSG00000058045	0.962	-0.75	0.476809	0.727649
11865	10389207	NM_013653	20304	chemokine (C-C motif) ligand 5	Ccl5	0.962	-0.275	0.790726	0.914692
11866	10521596					0.962	-0.756	0.473341	0.725045
11867	10578916	NM_025436	66234	sterol-C4-methyl oxidase-like	Sc4mol	0.962	-1.186	0.273159	0.547717
11868	10568174	NM_009259	20737	sialophorin	Spn	0.962	-0.148	0.886484	0.955393
11869	10432723	NM_053249	114566	keratin 82	Krt82	0.962	-0.606	0.563126	0.789853
11870	10352969	ENSMUST00000044180	226304	neuropeptides B/W receptor 1	Npbwr1	0.962	-0.379	0.715568	0.875402
11871	10566615	NM_146601	258594	olfactory receptor 710	Olfr710	0.962	-0.774	0.463438	0.717662
11872	10481420	BC078441	227695	DNA segment, Chr 2, Wayne Stat	D2Wsu81e	0.962	-0.942	0.376741	0.646995
11873	10581327	BC052498	102124	RIKEN cDNA E130303B06 gene	E130303B06Rik	0.962	-1.415	0.19876	0.459902
11874	10437684	NM_013637	19118	protamine 1	Prm1	0.962	-0.141	0.89153	0.957571
11875	10419596	NM_027248	69890	zinc finger protein 219	Zfp219	0.962	-1.183	0.27426	0.548935
11876	10503204	NM_001081417	320790	chromodomain helicase DNA bind	Chd7	0.962	-0.864	0.415218	0.678399
11877	10574656	NM_015821	50788	F-box and leucine-rich repeat	Fbxl8	0.962	-0.481	0.645084	0.839674
11878	10549854	NM_175247	22690	zinc finger protein 28	Zfp28	0.962	-0.92	0.387323	0.65632
11879	10345482	NM_033570	94220	cyclin M4	Cnnm4	0.962	-1.184	0.27405	0.548672
11880	10477813	AY061882	170791	RNA binding motif protein 39	Rbm39	0.962	-0.723	0.492433	0.73844
11881	10575380	NM_172916	244653	hydrocephalus inducing	Hydin	0.962	-0.659	0.530408	0.765382
11882	10590267	NR_002902	104433	small nucleolar RNA, H/ACA box	Snora62	0.962	-0.989	0.354706	0.627293
11883	10438405	M94350	16142	immunoglobulin lambda chain, v	Igl-V1	0.962	-0.105	0.91893	0.967815
11884	10395659	NM_007728	12810	coagulation factor C homolog (	Coch	0.962	-1.285	0.238434	0.511045
11885	10561706	NM_028179	72275	RIKEN cDNA 2200002D01 gene	2200002D01Rik	0.962	-0.853	0.420833	0.683211
11886	10549751	NM_001033383	319748	RIKEN cDNA 6430526N21 gene	6430526N21Rik	0.962	-1.344	0.219838	0.488612
11887	10583847	NM_181316	319845	Bardet-Biedl syndrome 9	Bbs9	0.962	-0.953	0.371558	0.64202
11888	10405999	ENSMUST00000022091	77166	RIKEN cDNA 8030423J24 gene	8030423J24Rik	0.962	-0.554	0.596358	0.809852
11889	10486327	ENSMUST00000110756	640524	spectrin beta 5	Spnb5	0.962	-0.901	0.396665	0.664034
11890	10535247	NM_028833	74239	IQ motif containing E	Iqce	0.962	-0.478	0.64665	0.840625
11891	10430866	NM_010005	13101	cytochrome P450, family 2, sub	Cyp2d10	0.962	-0.732	0.487141	0.734936
11892	10517371					0.962	-0.476	0.64844	0.841814
11893	10593384	NM_178118	330938	DIX domain containing 1	Dixdc1	0.962	-1.648	0.142101	0.38202

11894	10601882	BC065397	436230	cDNA sequence BC065397	BC065397	0.962	-1.25	0.250493	0.524406
11895	10457038					0.962	-0.724	0.492008	0.738272
11896	10406280	NM_029343	75571	spermatogenesis associated 9	Spata9	0.962	-0.333	0.748344	0.893398
11897	10440562	NM_001081068	78913	zinc finger protein 294	Zfp294	0.962	-0.269	0.795407	0.916955
11898	10596043	NM_010878	17973	non-catalytic region of tyrosi	Nck1	0.962	-1.063	0.322204	0.598969
11899	10421685	BC100483	72661	stress-associated endoplasmic	Serp2	0.962	-0.512	0.624088	0.828379
11900	10463185	NM_145500	226122	ubiquitin domain containing 1	Ubtd1	0.962	-0.727	0.489905	0.737211
11901	10472402	NM_001099298	110876	sodium channel, voltage-gated,	Scn2a1	0.962	-0.339	0.744377	0.891431
11902	10591777	BC011413	625603	predicted gene, EG625603	EG625603	0.962	-0.782	0.458918	0.713797
11903	10375322	ENSMUST00000056256	75727	RIKEN cDNA 4933415A04 gene	4933415A04Rik	0.962	-0.655	0.532845	0.766896
11904	10588582	BC116708	235599	RIKEN cDNA 6430571L13 gene	6430571L13Rik	0.962	-0.413	0.691678	0.864682
11905	10569356					0.962	0.101	0.921995	0.968972
11906	10475804	AB257502	215456	RIKEN cDNA A530057A03 gene	A530057A03Rik	0.962	-0.558	0.593941	0.808302
11907	10557855	NM_001079932	434246	tripartite motif-containing 72	Trim72	0.962	-0.626	0.550445	0.780695
11908	10424965	NM_033371	73062	protein phosphatase 1, regulat	Ppp1r16a	0.962	-0.345	0.740191	0.889339
11909	10431113	NM_013873	29859	sulfotransferase family 4A, me	Sult4a1	0.962	-0.542	0.604048	0.815116
11910	10593169	NM_023114	11814	apolipoprotein C-III	Apoc3	0.962	-0.566	0.588576	0.805172
11911	10451547	XM_001480078	100043385	similar to high mobility group	LOC100043385	0.962	-0.989	0.354462	0.627071
11912	10351517	BC061017	75472	RIKEN cDNA 1700009P17 gene	1700009P17Rik	0.962	-0.099	0.923929	0.96976
11913	10511084	NM_138671	192185	NAD kinase	Nadk	0.962	-0.987	0.355768	0.628276
11914	10408638	ENSMUST00000021851	71864	RIKEN cDNA 1700026J04 gene	1700026J04Rik	0.962	-0.817	0.440217	0.699184
11915	10460052					0.962	-0.583	0.577363	0.797771
11916	10557308	ENSMUST00000106437	628779	predicted gene, EG628779	EG628779	0.962	-1.457	0.187244	0.445643
11917	10419575	NM_177544	219033	angiogenin, ribonuclease A fam	Ang4	0.962	-0.271	0.793973	0.916212
11918	10470911					0.962	-1.164	0.281452	0.55689
11919	10605644	XR_031824	633246	similar to splicing factor, ar	LOC633246	0.962	-0.742	0.481309	0.730704
11920	10374500	NM_139061	245944	vacuolar protein sorting 54 (y	Vps54	0.962	-1.156	0.284441	0.559618
11921	10417526	NM_007870	13421	deoxyribonuclease 1-like 3	Dnase1l3	0.962	-0.901	0.396712	0.664034
11922	10430660	NM_011057	18591	platelet derived growth factor	Pdgfb	0.962	-0.359	0.729776	0.883251
11923	10439889					0.962	-0.111	0.914287	0.966149
11924	10493267	NM_008487	16800	rho/rac guanine nucleotide exc	Arhgef2	0.962	-0.751	0.476525	0.72763
11925	10606488	ENSMUST00000026601	73809	spermidine/spermine N1-acetyl	Satl1	0.962	-0.429	0.680647	0.85838
11926	10402444	NM_148948	192119	Dicer1, Dcr-1 homolog (Drosoph	Dicer1	0.962	-1.011	0.344658	0.61884
11927	10378765	NM_021294	13168	diazepam binding inhibitor-lik	Dbil5	0.962	-0.474	0.649348	0.842476
11928	10479726	NM_153594	245867	protein-L-isoaspartate (D-aspa	Pcmtd2	0.962	-1.403	0.202057	0.464803
11929	10488693	NM_198617	241732	TSPY-like 3	Tspyl3	0.962	-0.56	0.592433	0.807166
11930	10533198	NM_145227	246728	2'-5' oligoadenylate synthetas	Oas2	0.962	-0.668	0.524675	0.761127
11931	10509941	ENSMUST00000097813	76166	RIKEN cDNA 6330545A04 gene	6330545A04Rik	0.962	-0.047	0.964134	0.985864
11932	10479615	AK082896	329584	hypothetical protein C430010C0	C430010C01	0.962	-0.754	0.474947	0.726596
11933	10398578	NM_001081057	104859	RIKEN cDNA 4930573I19 gene	4930573I19Rik	0.962	-1.014	0.343194	0.617311
11934	10439887					0.962	-0.101	0.922417	0.969068
11935	10442629	NM_027141	79043	splA/ryanodine receptor domain	Spsb3	0.962	-0.586	0.576018	0.797128
11936	10530310	XM_001477289	666938	predicted gene, EG666938	EG666938	0.961	-0.69	0.511514	0.752366
11937	10534316	NM_033561	22384	eukaryotic translation initiat	Eif4h	0.961	-0.797	0.450883	0.708135
11938	10493382	NM_013631	18770	pyruvate kinase liver and red	Pklr	0.961	-1.08	0.315008	0.591942
11939	10510473	NM_023465	67087	catenin beta interacting prote	Ctnnbip1	0.961	-1.406	0.20133	0.463716
11940	10474002	NM_007699	12672	cholinergic receptor, muscarin	Chrm4	0.961	-0.132	0.898376	0.960023
11941	10404195	BC115940	210108	RIKEN cDNA D130043K22 gene	D130043K22Rik	0.961	-0.685	0.514807	0.754817
11942	10607012	NM_053185	94216	collagen, type IV, alpha 6	Col4a6	0.961	-0.661	0.529209	0.76441
11943	10464917	NM_009920	12794	cornichon homolog 2 (Drosophil	Cnih2	0.961	-1.073	0.317693	0.594819
11944	10428443	NM_026200	67498	potassium channel, subfamily V	Kcnv1	0.961	-0.443	0.670728	0.85389
11945	10416503	AF357400	22070	tumor protein, translationally	Tpt1	0.961	-0.393	0.705879	0.871814
11946	10564877	NM_173445	269955	RCC1 domain containing 1	Rccd1	0.961	-0.707	0.501776	0.744686
11947	10557033	ENSMUST00000098074	13631	eukaryotic elongation factor-2	Eef2k	0.961	-0.219	0.832564	0.932679

11948	10501265	NM_010306	14679	guanine nucleotide binding pro	Gnai3	0.961	-1.316	0.228488	0.499498
11949	10485115	ENSMUST00000099709	104418	diacylglycerol kinase zeta	Dgkz	0.961	-0.514	0.622712	0.827309
11950	10576881	ENSMUST00000058918	665044	predicted gene, EG665044	EG665044	0.961	-0.591	0.572552	0.796254
11951	10461257	NM_146093	225896	DNA segment, Chr 19, ERATO Doi	D19Ertd721e	0.961	-1.288	0.237407	0.509669
11952	10549869	NM_146915	258917	olfactory receptor 1336	Olfr1336	0.961	-0.164	0.874213	0.949962
11953	10429607	NM_028404	72960	DNA topoisomerase 1, mitochond	Top1mt	0.961	-0.771	0.465307	0.718975
11954	10431080	NM_029946	77627	EF-hand calcium binding domain	Efcab3	0.961	-0.034	0.973687	0.988697
11955	10460317	NM_008851	18739	phosphatidylinositol membrane-	Pitpnm1	0.961	-0.518	0.619636	0.824984
11956	10580756	BC027060	102122	RIKEN cDNA 2310065K24 gene	2310065K24Rik	0.961	-1.096	0.308362	0.585068
11957	10464034	NM_009348	21684	tectorin beta	Tectb	0.961	-0.884	0.405152	0.669695
11958	10404380	NM_001037955	105352	dual specificity phosphatase 2	Dusp22	0.961	-0.729	0.489005	0.736349
11959	10535904	NM_013559	15505	heat shock 105kDa/110kDa prote	Hsph1	0.961	-0.99	0.354259	0.626867
11960	10371201	NM_134009	103425	nicalin homolog (zebrafish)	Ncln	0.961	-0.738	0.483551	0.732287
11961	10603870	NM_007922	13712	ELK1, member of ETS oncogene f	Elk1	0.961	-1.047	0.329027	0.605314
11962	10513397	NM_001013577	66209	RIKEN cDNA 1110054O05 gene	1110054O05Rik	0.961	-1.029	0.3367	0.612455
11963	10511252	NM_021402	140499	ubiquitin-conjugating enzyme E	Ube2j2	0.961	-0.638	0.543397	0.775747
11964	10567608	NM_001033318	233824	component of oligomeric golgi	Cog7	0.961	-0.51	0.625413	0.829231
11965	10420637	NM_008466	16648	karyopherin (importin) alpha 3	Kpna3	0.961	-1.732	0.12567	0.354951
11966	10585146	NM_030709	80893	transmembrane protease, serine	Tmprss5	0.961	-0.462	0.657954	0.847091
11967	10493210	NM_178246	229512	Smg-5 homolog, nonsense mediat	Smg5	0.961	-0.961	0.367648	0.638641
11968	10559241	NR_002855	111975	insulin-like growth factor 2,	Igf2as	0.961	-0.536	0.607967	0.817473
11969	10474689	NM_026620	68215	RIKEN cDNA 2610510H03 gene	2610510H03Rik	0.961	-1.302	0.233059	0.504071
11970	10419810	NM_011186	19173	proteasome (prosome, macropain	Psmb5	0.961	-1.84	0.107136	0.322599
11971	10563718	XM_001474409	677457	similar to MAS-related GPR, me	LOC677457	0.961	-0.347	0.738676	0.88853
11972	10462130	AK033223	68034	RIKEN cDNA 2900009I07 gene	2900009I07Rik	0.961	-0.668	0.524831	0.761165
11973	10607747	NM_009173	20438	seven in absentia 1B	Siah1b	0.961	-0.343	0.741198	0.889595
11974	10495042	NM_027982	71887	protein phosphatase 1J	Ppm1j	0.961	-0.138	0.893937	0.958149
11975	10538307	ENSMUST00000068976	791364	predicted gene, OTTMUSG0000001	OTTMUSG00000018874	0.961	-0.379	0.715439	0.875402
11976	10591035	NM_176976	319675	RIKEN cDNA 5830418K08 gene	5830418K08Rik	0.961	-0.825	0.435655	0.695606
11977	10537627	NM_009430	22072	protease, serine, 2	Prss2	0.961	-0.497	0.634088	0.833675
11978	10459296	NM_134136	107035	F-box protein 38	Fbxo38	0.961	-1.378	0.209451	0.474615
11979	10383791	NM_153142	103710	solute carrier family 35, memb	Slc35e4	0.961	-0.407	0.695785	0.866361
11980	10521964	ENSMUST00000101200	330086	predicted gene, ENSMUSG0000007	ENSMUSG00000072936	0.961	-0.586	0.575955	0.797128
11981	10423080	NM_030888	81799	C1q and tumor necrosis factor	C1qtnf3	0.961	-0.947	0.374105	0.64426
11982	10573996					0.961	-1.001	0.349422	0.622897
11983	10478114	ENSMUST00000099133	545481	chromosome 20 open reading fra	RP23-392P11.3	0.961	-0.035	0.972907	0.98829
11984	10398288	NM_009537	22632	YY1 transcription factor	Yy1	0.961	-1.123	0.297397	0.573687
11985	10427928	NM_001081302	223435	triple functional domain (PTPR	Trio	0.961	-0.992	0.353424	0.626177
11986	10516219	ENSMUST00000097894	100038647	predicted gene, ENSMUSG0000007	ENSMUSG00000073760	0.961	-0.188	0.856305	0.941981
11987	10395827	NM_020287	56856	insulinoma-associated 2	Insm2	0.961	-0.939	0.378343	0.648167
11988	10584653	NM_145613	235312	C1q and tumor necrosis factor	C1qtnf5	0.961	-0.449	0.666473	0.851355
11989	10468037	ENSMUST00000076452	435601	predicted gene, EG435601	EG435601	0.961	-0.575	0.582731	0.800924
11990	10428398	NM_008388	16341	eukaryotic translation initiat	Eif3e	0.961	-0.78	0.460325	0.71495
11991	10529425	NM_029278	75416	nucleolar protein 14	Nol14	0.961	-1.19	0.271636	0.546245
11992	10353127	NM_001081209	383491	PR domain containing 14	Prdm14	0.961	-0.391	0.706912	0.872152
11993	10541642	XM_917643	623374	similar to putative glialblast	LOC623374	0.961	-0.31	0.765201	0.902365
11994	10402703	ENSMUST00000101035	100038720	predicted gene, ENSMUSG0000007	ENSMUSG00000072830	0.961	-0.489	0.639546	0.836482

11995	10451565	NM_022015	63856	TAF8 RNA polymerase II, TATA b	Taf8	0.961	-0.774	0.463808	0.717865
11996	10426016	NM_013882	29870	G two S phase expressed protei	Gtse1	0.961	-0.652	0.534628	0.768432
11997	10460706	NM_028769	74126	synovial apoptosis inhibitor 1	Syvn1	0.961	-0.895	0.399662	0.665809
11998	10430245					0.961	-0.351	0.735978	0.886898
11999	10408600	NM_009254	20719	serine (or cysteine) peptidase	Serpinb6a	0.961	-1.123	0.297288	0.573687
12000	10517842	NM_172122	230872	ciliary rootlet coiled-coil, r	Crocc	0.961	-0.806	0.445892	0.703765
12001	10364766	NM_009091	20054	ribosomal protein S15	Rps15	0.961	-1.286	0.238025	0.51041
12002	10555917	NM_146750	258745	olfactory receptor 689	Olfr689	0.961	-0.221	0.830924	0.932182
12003	10490982	BC002189	620316	predicted gene, ENSMUSG0000007	ENSMUSG00000074670	0.961	-0.42	0.686953	0.861886
12004	10463625	NM_133694	68431	F-box and leucine-rich repeat	Fbxl15	0.961	-1.015	0.343036	0.617132
12005	10545658	NM_023790	75659	WD repeat domain 54	Wdr54	0.961	-1.036	0.333561	0.609432
12006	10383970	NM_032396	84035	kringle containing transmembra	Kremen1	0.961	-0.826	0.435102	0.695306
12007	10558405	NM_183193	270004	forkhead box I2	Foxi2	0.961	-0.793	0.453168	0.70973
12008	10401398					0.961	-0.522	0.617593	0.823197
12009	10523579	NM_029270	231532	Rho GTPase activating protein	Arhgap24	0.961	-1.213	0.263312	0.538069
12010	10351015	NM_080844	11905	serine (or cysteine) peptidase	Serpinc1	0.961	-0.559	0.593302	0.807893
12011	10598203	NM_020279	56838	chemokine (C-C motif) ligand 2	Ccl28	0.961	-0.229	0.824988	0.929578
12012	10372597	XR_033859	544741	similar to ribosomal protein S	LOC544741	0.961	-0.847	0.42446	0.686543
12013	10423518	NM_020503	57254	taste receptor, type 2, member	Tas2r119	0.961	-0.403	0.69876	0.868021
12014	10430096	NM_198119	378937	leucine rich repeat containing	Lrrc24	0.961	-0.671	0.523023	0.759642
12015	10482273	NM_029793	76899	golgi autoantigen, golgin subf	Golga1	0.96	-0.903	0.395828	0.663394
12016	10380275	ENSMUST00000107892	414094	RIKEN cDNA A930013B10 gene	A930013B10Rik	0.96	-0.407	0.696013	0.866441
12017	10370334	NM_145152	237387	leucine rich repeat containing	Lrrc3	0.96	-0.468	0.653527	0.844695
12018	10447006	NM_028813	74199	vitrin	Vit	0.96	-0.393	0.705906	0.871814
12019	10368193					0.96	-0.25	0.809489	0.923176
12020	10413989	XM_985917	268729	gene model 626, (NCBI)	Gm626	0.96	-0.596	0.569612	0.794081
12021	10394682	XR_032386	633944	similar to Glyceraldehyde-3-ph	LOC633944	0.96	-0.297	0.774973	0.907674
12022	10524460	NM_133904	100705	acetyl-Coenzyme A carboxylase	Acacb	0.96	-0.656	0.532273	0.766334
12023	10529077	NM_021290	22226	urocortin	Ucn	0.96	-0.343	0.741026	0.889595
12024	10391918	NM_183034	353047	pleckstrin homology domain con	Plekhm1	0.96	-0.69	0.512018	0.75265
12025	10350335	ENSMUST00000097558	623818	predicted gene, EG623818	EG623818	0.96	-0.319	0.759013	0.899129
12026	10366457	NM_011217	19279	protein tyrosine phosphatase,	Ptprr	0.96	-0.751	0.476552	0.72763
12027	10476353					0.96	-0.549	0.599649	0.812038
12028	10344797	AK032310	211660	centrosome and spindle pole as	Cspp1	0.96	-1.291	0.236612	0.508732
12029	10510629	NM_028727	74035	nucleolar protein 9	Nol9	0.96	-1.332	0.223416	0.493384
12030	10540738	NM_001033244	211651	Fanconi anemia, complementatio	Fancd2	0.96	-1.022	0.339802	0.615188
12031	10412054	AB183434	75597	NADH dehydrogenase (ubiquinone	Ndufaf2	0.96	-0.823	0.436663	0.696302
12032	10569542	NM_175534	244238	MAS-related GPR, member E	Mrgpre	0.96	-0.141	0.891928	0.95769
12033	10509410	NM_001081155	110351	Rap1 GTPase-activating protein	Rap1gap	0.96	-0.752	0.475998	0.727266
12034	10567216	NM_170669	267019	ribosomal protein S15a	Rps15a	0.96	-0.547	0.60097	0.81267
12035	10593867	NM_181074	235402	leucine rich repeat and Ig dom	Lingo1	0.96	-0.257	0.804144	0.920614
12036	10455919	NM_175506	240322	a disintegrin-like and metallo	Adamts19	0.96	-0.278	0.788467	0.913849
12037	10413014	NM_025366	66121	coiled-coil-helix-coiled-coil-	Chchd1	0.96	-1.348	0.21834	0.486434
12038	10381162	NM_028024	71966	NFKB inhibitor interacting Ras	Nkiras2	0.96	-0.957	0.369379	0.639995
12039	10494322	NM_023210	66471	acidic (leucine-rich) nuclear	Anp32e	0.96	-0.863	0.416113	0.679215
12040	10456293					0.96	-0.246	0.812748	0.924689
12041	10490602	NM_007906	13628	eukaryotic translation elongat	Eef1a2	0.96	-0.686	0.514198	0.754507
12042	10420021	ENSMUST00000066106	320942	RIKEN cDNA A730061H03 gene	A730061H03Rik	0.96	-1.019	0.340984	0.615921
12043	10448506	NM_007634	12449	cyclin F	Ccnf	0.96	-0.552	0.59765	0.810721
12044	10521696	ENSMUST00000072800	100041413	hypothetical protein LOC100041	LOC100041413	0.96	-0.548	0.600045	0.812117
12045	10418167	AK019686	68173	peptidylprolyl isomerase F, op	Ppifos	0.96	-0.013	0.989899	0.995644
12046	10537978	ENSMUST00000043676	243369	SCO-spondin	Sspo	0.96	-0.364	0.72656	0.881528
12047	10580771	NM_134141	109006	cytokine induced apoptosis inh	Ciapin1	0.96	-1.011	0.344852	0.618925

12047	[illegible]	[illegible]	[illegible]	cytokine induced apoptosis inh	Ciapin1	0.96	-1.011	[illegible]	[illegible]
12048	10592449	NM_207138	235256	olfactory receptor 149	Olfr149	0.96	-0.504	0.6293	0.831256
12049	10470741	NM_178693	227683	coenzyme Q4 homolog (yeast)	Coq4	0.96	-0.374	0.719458	0.877797
12050	10438328	BC005445	27883	DNA segment, Chr 16, human D22	D16H22S680E	0.96	-0.851	0.422072	0.684326
12051	10596275	ENSMUST00000060084	235567	DnaJ (Hsp40) homolog, subfamil	Dnajc13	0.96	-0.67	0.523467	0.760167
12052	10538885					0.96	-0.925	0.384715	0.654049
12053	10440600	NM_009840	12469	chaperonin subunit 8 (theta)	Cct8	0.96	-1.015	0.342783	0.617098
12054	10398453	ENSMUST00000065483	26931	protein phosphatase 2, regulat	Ppp2r5c	0.96	-0.836	0.429894	0.690652
12055	10418927	NM_009758	12166	bone morphogenetic protein rec	Bmpr1a	0.96	-0.72	0.494374	0.739567
12056	10398569	ENSMUST00000021699	72805	RIKEN cDNA 2810455K09 gene	2810455K09Rik	0.96	-0.834	0.430976	0.691603
12057	10562358					0.96	-0.741	0.481838	0.730954
12058	10362243					0.96	-0.703	0.504045	0.746397
12059	10471139	NM_177649	665700	hemicentin 2	Hmcn2	0.96	-0.27	0.794481	0.916545
12060	10352971	ENSMUST00000097832	654788	RIKEN cDNA 4732440D04 gene	4732440D04Rik	0.96	-0.431	0.678922	0.857533
12061	10518947	NM_001099299	230959	adherens junction associated p	Ajap1	0.96	-0.315	0.761426	0.900576
12062	10572089	NM_010874	17961	N-acetyltransferase 2 (arylami	Nat2	0.96	-0.309	0.766119	0.902642
12063	10487366	BC117065	329509	RIKEN cDNA 1810024B03 gene	1810024B03Rik	0.96	-0.689	0.512583	0.753008
12064	10547888	NM_013533	14788	G protein-coupled receptor 162	Gpr162	0.96	-1.097	0.307893	0.584494
12065	10434144	NM_022982	65079	reticulon 4 receptor	Rtn4r	0.96	-0.832	0.432016	0.692431
12066	10450167	NM_030746	632126	butyrophilin-like 4	Btnl4	0.96	-0.547	0.600607	0.812284
12067	10442638	NM_023260	79044	mitochondrial ribosomal protei	Mrps34	0.96	-1.565	0.160204	0.407576
12068	10598678	NM_009481	22284	ubiquitin specific peptidase 9	Usp9x	0.96	-1.209	0.264927	0.540102
12069	10399430	NM_134040	104721	DEAD (Asp-Glu-Ala-Asp) box pol	Ddx1	0.96	-0.846	0.424697	0.686726
12070	10577030	ENSMUST00000049461	71941	cysteinyl-tRNA synthetase 2 (m	Cars2	0.96	-0.664	0.527334	0.762963
12071	10368859	NM_001034858	213402	armadillo repeat containing 2	Armc2	0.96	-0.893	0.400724	0.666476
12072	10508936	NM_026257	67586	UBX domain containing 5	Ubxd5	0.96	-0.988	0.355168	0.627794
12073	10420724	NM_001039566	73670	defensin beta 30	Defb30	0.96	-0.696	0.508443	0.750263
12074	10411532	NM_030026	78038	methylcrotonoyl-Coenzyme A car	Mccc2	0.96	-0.49	0.638838	0.835923
12075	10401956					0.96	-0.96	0.368112	0.639027
12076	10497673	NM_009517	22401	zinc finger matrin type 3	Zmat3	0.96	-0.416	0.689712	0.863782
12077	10460485	NM_027476	70605	zinc finger, DHHC domain conta	Zdhhc24	0.96	-0.65	0.536064	0.769315
12078	10411711	NM_009874	12572	cyclin-dependent kinase 7 (hom	Cdk7	0.96	-1.426	0.195689	0.456039
12079	10488982	NM_170588	266692	copine I	Cpne1	0.96	-1.097	0.307848	0.58446
12080	10445839	NM_177052	319991	kinesin family member 6	Kif6	0.96	-0.118	0.909054	0.963765
12081	10373355	NM_025716	66701	SPRY domain containing 4	Spryd4	0.96	-1.414	0.19907	0.460469
12082	10381960	ENSMUST00000066077	791371	predicted gene, ENSMUSG0000005	ENSMUSG00000053568	0.96	-0.682	0.516247	0.755582
12083	10366275					0.959	-0.543	0.603657	0.814811
12084	10528163	XR_002130	668059	predicted gene, EG668059	EG668059	0.959	-0.889	0.402928	0.668092
12085	10517343					0.959	-0.383	0.712693	0.874143
12086	10383436	NM_026877	68938	alveolar soft part sarcoma chr	Aspscr1	0.959	-1.039	0.332246	0.608279
12087	10574365	NM_172914	244608	coiled-coil domain containing	Ccdc113	0.959	-0.499	0.632448	0.832813
12088	10412385	NM_021556	59054	mitochondrial ribosomal protei	Mrps30	0.959	-1.205	0.266427	0.541205
12089	10558631	NM_175533	244234	RIKEN cDNA 5830411N06 gene	5830411N06Rik	0.959	-0.868	0.413435	0.677072
12090	10375886	BC095931	97775	RIKEN cDNA D930048N14 gene	D930048N14Rik	0.959	-0.835	0.430465	0.691254
12091	10502370	NM_177860	329763	predicted gene, EG329763	EG329763	0.959	0.236	0.820034	0.928345
12092	10573519	NM_145390	212999	transportin 2 (importin 3, kar	Tnpo2	0.959	-0.9	0.397142	0.664239
12093	10460371	NM_016933	19265	protein tyrosine phosphatase,	Ptprcap	0.959	-0.991	0.353951	0.626638
12094	10538201	ENSMUST00000031839	75593	RIKEN cDNA 2410003K15 gene	2410003K15Rik	0.959	-0.666	0.526227	0.762249
12095	10371256	NM_181586	50721	sirtuin 6 (silent mating type	Sirt6	0.959	-1.183	0.274197	0.548913

12096	10435031	ENSMUST00000115151	224111	UBX domain containing 7	Ubxd7	0.959	-0.735	0.485434	0.733791
12097	10444778					0.959	-0.266	0.797668	0.917953
12098	10409502	NM_013739	27261	docking protein 3	Dok3	0.959	-0.306	0.767972	0.903579
12099	10604100	NM_019443	54405	NADH dehydrogenase (ubiquinone	Ndufa1	0.959	-0.824	0.436499	0.696302
12100	10521667	NM_009763	12182	bone marrow stromal cell antig	Bst1	0.959	-0.174	0.866304	0.946535
12101	10479008	AK082914	100036524	predicted gene, ENSMUSG0000005	ENSMUSG00000053526	0.959	-0.589	0.573895	0.797007
12102	10601404	NM_001033541	331493	predicted gene, EG331493	EG331493	0.959	-0.277	0.789863	0.914502
12103	10599514	NM_178782	320376	BCL6 co-repressor-like 1	Bcorl1	0.959	-0.801	0.448861	0.706418
12104	10552193	NM_021291	30962	solute carrier family 7 (catio	Slc7a9	0.959	-0.473	0.650248	0.843126
12105	10369295	BC025117	52717	DNA segment, Chr 10, ERATO Doi	D10Ertd641e	0.959	-1.262	0.246223	0.519211
12106	10410513	NM_001040692	22598	solute carrier family 6 (neuro	Slc6a18	0.959	-0.505	0.628624	0.830964
12107	10388747					0.959	-0.618	0.555599	0.784217
12108	10471018	BC051404	108958	RIKEN cDNA 5730472N09 gene	5730472N09Rik	0.959	-0.293	0.777739	0.909562
12109	10373751					0.959	-0.519	0.619338	0.82476
12110	10439583	NM_198034	320007	SID1 transmembrane family, mem	Sidt1	0.959	0.092	0.929121	0.972108
12111	10476653	NM_207275	403171	barrier to autointegration fac	Banf2	0.959	0.022	0.983422	0.992843
12112	10496322					0.959	-0.529	0.612464	0.820343
12113	10405191	NM_029279	75420	SECIS binding protein 2	Secisbp2	0.959	-0.899	0.397451	0.664302
12114	10375551	NM_147065	259068	olfactory receptor 1390	Olfr1390	0.959	0.122	0.906514	0.963405
12115	10471045	NM_138748	110854	protein phosphatase 2A, regula	Ppp2r4	0.959	-0.962	0.36737	0.638316
12116	10410134	XR_033575	665612	similar to glucocorticoid rece	LOC665612	0.959	-0.009	0.993232	0.997431
12117	10546936	NM_172487	210673	proline-rich transmembrane pro	Prrt3	0.959	-0.431	0.67896	0.857533
12118	10465374	NM_133678	66406	SAC3 domain containing 1	Sac3d1	0.959	-0.749	0.477559	0.728273
12119	10350478	NM_001038592	69367	glutaredoxin 2 (thioltransfera	Glrx2	0.959	-1.009	0.34583	0.619997
12120	10580765	NM_026385	67801	plasma membrane proteolipid	Pllp	0.959	-0.674	0.521126	0.758676
12121	10560311					0.959	-1.323	0.226375	0.496985
12122	10414449	BC023094	74385	RIKEN cDNA 4932432K03 gene	4932432K03Rik	0.959	-0.822	0.43715	0.696541
12123	10504658					0.959	-0.908	0.393376	0.661285
12124	10451220	NM_025649	66591	MAD2L1 binding protein	Mad2l1bp	0.959	-1.215	0.262781	0.537303
12125	10551989	NM_145580	101883	transmembrane protein 149	Tmem149	0.959	-0.922	0.386174	0.655109
12126	10463265	NM_031396	83674	cyclin M1	Cnnm1	0.959	-0.598	0.568014	0.793164
12127	10493986	NM_027762	71325	trichohyalin-like 1	Tchhl1	0.959	-0.187	0.856626	0.942035
12128	10569702	NM_133190	81905	calcium channel, voltage-depen	Cacng8	0.959	-0.192	0.85311	0.940713
12129	10473517					0.959	-0.786	0.457013	0.712826
12130	10550320					0.959	-1.021	0.340135	0.615475
12131	10440593	NM_016924	53858	RWD domain containing 2B	Rwdd2b	0.959	-0.749	0.477758	0.7284
12132	10552440					0.959	-0.799	0.449899	0.707208
12133	10554204	NM_172902	244071	ATP/GTP binding protein-like 1	Agbl1	0.959	-0.531	0.611687	0.819835
12134	10521798	BC018481	66768	RIKEN cDNA 4933428G09 gene	4933428G09Rik	0.959	-1.023	0.339196	0.614614
12135	10379838					0.959	-0.784	0.458053	0.713343
12136	10347018	NM_139270	213527	parathyroid hormone 2 receptor	Pth2r	0.959	0.026	0.980328	0.991919
12137	10525452	NM_030564	80751	ring finger protein 34	Rnf34	0.959	-0.774	0.463492	0.717691
12138	10475352	NM_026318	67693	RIKEN cDNA 2310003F16 gene	2310003F16Rik	0.959	-1.067	0.320356	0.597215
12139	10581636	NM_001080930	52335	ataxin 1-like	Atxn1l	0.959	-1.328	0.224611	0.494757
12140	10435004	BC023715	66994	RIKEN cDNA 1500031L02 gene	1500031L02Rik	0.959	-1.12	0.298798	0.574899
12141	10540269	NM_008158	14761	G protein-coupled receptor 27	Gpr27	0.959	-0.439	0.673328	0.854824
12142	10527430	NM_019767	56443	actin related protein 2/3 comp	Arpc1a	0.959	-1.306	0.231767	0.502487
12143	10573288	NM_028877	74337	RIKEN cDNA 4432412L15 gene	4432412L15Rik	0.959	-0.895	0.399575	0.665716
12144	10360454	NM_010098	13603	opsin 3	Opn3	0.959	-0.573	0.583997	0.80182
12145	10472153					0.959	-0.196	0.850337	0.939843
12146	10471298	BC055116	227723	RIKEN cDNA 5830434P21 gene	5830434P21Rik	0.959	-0.765	0.468482	0.720721
12147	10531899	NM_178741	246293	kelch-like 8 (Drosophila)	Klhl8	0.959	-0.514	0.622347	0.827136

12148	10426835	NM_172819	239667	DIP2 disco-interacting protein	Dip2b	0.959	-0.759	0.471835	0.72372
12149	10402179	NM_211355	68734	SMEK homolog 1, suppressor of	Smek1	0.959	-1.165	0.281146	0.556689
12150	10520952	NM_172707	19046	protein phosphatase 1, catalyt	Ppp1cb	0.959	-1.265	0.245049	0.518209
12151	10601430	XM_908498	71011	RIKEN cDNA 4933401B06 gene	4933401B06Rik	0.959	-0.821	0.43788	0.697031
12152	10518300	NM_011610	21938	tumor necrosis factor receptor	Tnfrsf1b	0.959	-0.856	0.419555	0.681865
12153	10597461	NM_133978	102545	CKLF-like MARVEL transmembrane	Cmtm7	0.959	-0.81	0.443942	0.702635
12154	10437646	NM_001099275	70426	tektin 5	Tekt5	0.958	-0.245	0.813312	0.9249
12155	10446596	NM_177639	224997	discs, large (Drosophila) homo	Dlgap1	0.958	-0.313	0.763171	0.901493
12156	10535629	NM_001033313	231887	PDGFA associated protein 1	Pdap1	0.958	-1.246	0.251554	0.525573
12157	10465244	NR_002847	72289	metastasis associated lung ade	Malat1	0.958	-0.405	0.697454	0.867333
12158	10421840	NM_018765	22380	WW domain binding protein 4	Wbp4	0.958	-1.37	0.21181	0.477389
12159	10425240	NM_177461	27008	microtubule associated monoxyg	Micall1	0.958	-0.711	0.49971	0.742878
12160	10400137	NM_013760	27362	DnaJ (Hsp40) homolog, subfamil	Dnajb9	0.958	-0.685	0.514708	0.754767
12161	10540679	NM_145826	57890	interleukin 17 receptor E	Il17re	0.958	-0.81	0.444104	0.702635
12162	10413710	NM_027289	70021	5'-nucleotidase domain contain	Nt5dc2	0.958	-1.144	0.289115	0.565029
12163	10585010	NM_007468	11808	apolipoprotein A-IV	Apoa4	0.958	-0.347	0.738241	0.88841
12164	10438681	NM_201375	385643	kininogen 2	Kng2	0.958	-0.811	0.443207	0.70194
12165	10575473	AK006604	672398	predicted gene, ENSMUSG0000006	ENSMUSG00000067794	0.958	-0.492	0.637356	0.83553
12166	10469129	ENSMUST00000026889	381347	RIKEN cDNA 4930412O13 gene	4930412O13Rik	0.958	-0.49	0.638371	0.835923
12167	10389484	NM_001114334	72508	ribosomal protein S6 kinase, p	Rps6kb1	0.958	-1.086	0.312234	0.58856
12168	10572445	NM_153074	211228	leucine rich repeat containing	Lrrc25	0.958	-1.092	0.309802	0.586696
12169	10532901	XR_033041	676123	hypothetical protein LOC676123	LOC676123	0.958	-0.996	0.35146	0.624753
12170	10514350					0.958	-0.772	0.464585	0.718344
12171	10385572	NM_011018	18412	sequestosome 1	Sqstm1	0.958	-1.23	0.257349	0.531592
12172	10384762	ENSMUST00000068360	268391	RIKEN cDNA A830031A19 gene	A830031A19Rik	0.958	-0.565	0.589483	0.805725
12173	10475448	NM_025777	66811	dual oxidase maturation factor	Duoxa2	0.958	-1.096	0.308277	0.585058
12174	10557317	NM_029842	77035	jumonji domain containing 5	Jmjd5	0.958	-0.596	0.569552	0.794081
12175	10524969	NM_007545	12123	harakiri, BCL2 interacting pro	Hrk	0.958	-0.555	0.595735	0.809631
12176	10350286	NM_026500	67997	DEAD (Asp-Glu-Ala-Asp) box pol	Ddx59	0.958	-1.06	0.323488	0.599986
12177	10373334	NM_013786	27400	hydroxysteroid (17-beta) dehyd	Hsd17b6	0.958	-0.364	0.726432	0.881516
12178	10607774	NM_029730	76763	motile sperm domain containing	Mospd2	0.958	-0.604	0.564429	0.790721
12179	10536799	NM_001101486	245884	expressed sequence AI507611	AI507611	0.958	-0.767	0.46749	0.720274
12180	10483322					0.958	-0.625	0.551148	0.781221
12181	10489492	ENSMUST00000017864	73603	RIKEN cDNA 1700126L10 gene	1700126L10Rik	0.958	-0.599	0.567812	0.792987
12182	10445826	NM_020042	56738	molybdenum cofactor synthesis	Mocs1	0.958	-1.052	0.326765	0.602837
12183	10415119	NM_019402	54196	poly(A) binding protein, nucle	Pabpn1	0.958	-1.063	0.322058	0.598804
12184	10368077	ENSMUST00000095817	100039660	hypothetical protein LOC100039	LOC100039660	0.958	-0.311	0.764957	0.902279
12185	10569886	NM_025701	66682	trafficking protein particle c	Trappc5	0.958	-0.741	0.482084	0.730954
12186	10435793	NM_007877	13490	dopamine receptor 3	Drd3	0.958	-0.693	0.509939	0.751318
12187	10477311	NM_001039939	228790	additional sex combs like 1 (D	Asxl1	0.958	-1.142	0.290112	0.566261
12188	10448690	NM_001099664	381073	neuropeptide W	Npw	0.958	-0.622	0.553151	0.782697
12189	10450878	NM_146833	258830	olfactory receptor 103	Olfr103	0.958	0.059	0.95481	0.982696
12190	10419469					0.958	-0.454	0.663115	0.849961
12191	10348645	NM_022320	64095	G protein-coupled receptor 35	Gpr35	0.958	-0.564	0.590036	0.805977
12192	10348635	NM_147037	259039	olfactory receptor 1413	Olfr1413	0.958	-0.304	0.769718	0.904715
12193	10365302	NM_001033375	319277	RIKEN cDNA A230046K03 gene	A230046K03Rik	0.958	-0.875	0.409968	0.674344
12194	10517159	NM_145833	83557	lin-28 homolog (C. elegans)	Lin28	0.958	-0.537	0.607108	0.817118
12195	10566079	NM_007491	11875	ADP-ribosyltransferase 5	Art5	0.958	-0.398	0.702376	0.869396
12196	10490119	NM_001039560	654821	glucosaminyl (N-acetyl) transf	Gcnt7	0.958	-0.294	0.777156	0.909278
12197	10522186	NM_001081104	231252	cholinergic receptor, nicotini	Chrna9	0.958	-0.386	0.710886	0.873183
12198	10526735	NM_011757	22697	zinc finger and SCAN domain co	Zscan21	0.958	-0.906	0.394341	0.662004

12199	10418131	NM_001081247	218832	polymerase (RNA) III (DNA dire	Polr3a	0.958	-1.152	0.286198	0.561664
12200	10389151	NM_181542	237887	schlafen 10	Slfn10	0.958	-0.719	0.494625	0.739629
12201	10515352	NM_021473	58810	aldo-keto reductase family 1,	Akr1a4	0.958	-1.166	0.280822	0.556319
12202	10379762					0.958	0.062	0.952544	0.981606
12203	10509039	NM_030189	78806	RIKEN cDNA 4930555I21 gene	4930555I21Rik	0.958	-0.759	0.471648	0.72359
12204	10515839	ENSMUST00000097910	100038571	predicted gene, OTTMUSG0000000	OTTMUSG00000008822	0.958	-0.308	0.766871	0.902924
12205	10381218	NM_010475	15485	hydroxysteroid (17-beta) dehyd	Hsd17b1	0.958	-0.143	0.890125	0.956731
12206	10391424	XM_894901	629949	similar to ribosomal protein L	LOC629949	0.958	-0.7	0.505583	0.747576
12207	10348664					0.958	-0.633	0.546372	0.777695
12208	10372965	NM_027604	14479	ubiquitin specific peptidase 1	Usp15	0.958	-1.005	0.347519	0.621575
12209	10420097	NM_145705	28113	Terf1 (TRF1)-interacting nucle	Tinf2	0.958	-0.957	0.369526	0.640116
12210	10352767	NM_010892	18005	NIMA (never in mitosis gene a)	Nek2	0.958	-0.436	0.675876	0.855911
12211	10572772	NM_197944	209488	hematopoietic SH2 domain conta	Hsh2d	0.958	-0.746	0.479187	0.729179
12212	10376813	NM_001029936	432572	sperm antigen with calponin ho	Specc1	0.958	-0.869	0.412605	0.676183
12213	10502934	NM_011231	19352	RAB geranylgeranyl transferase	Rabggtb	0.958	-1.302	0.233025	0.50405
12214	10579262	NM_001004062	382056	CREB regulated transcription c	Crtc1	0.958	-1.053	0.326344	0.602796
12215	10596931	NM_031392	83669	WD repeat domain 6	Wdr6	0.958	-0.855	0.420144	0.682455
12216	10460273	NM_001001320	109575	T-box 10	Tbx10	0.958	-0.614	0.557901	0.785788
12217	10411690	NM_011233	19356	RAD17 homolog (S. pombe)	Rad17	0.958	-0.781	0.45963	0.714537
12218	10369379	NM_023596	71279	solute carrier family 29 (nucl	Slc29a3	0.958	-0.248	0.810876	0.923749
12219	10408523					0.958	-0.658	0.530778	0.76539
12220	10601471	XM_887733	385407	predicted gene, EG385407	EG385407	0.958	-1.193	0.270645	0.545314
12221	10362939	XM_894477	215974	predicted gene, EG215974	EG215974	0.958	-0.369	0.722789	0.87962
12222	10523231	NM_181728	109979	ADP-ribosyltransferase 3	Art3	0.958	-0.027	0.979439	0.99187
12223	10525877	NM_001081750	269704	zinc finger protein 664	Zfp664	0.958	-1.44	0.191715	0.451028
12224	10521892	NM_011402	20531	solute carrier family 34 (sodi	Slc34a2	0.958	-0.185	0.858202	0.943082
12225	10557300	NM_007474	11833	aquaporin 8	Aqp8	0.958	-0.153	0.882779	0.953745
12226	10382565	NM_025305	50529	mitchondrial ribosomal protein	Mrps7	0.958	-2.091	0.0737361	0.256638
12227	10468239	NM_007809	13074	cytochrome P450, family 17, su	Cyp17a1	0.957	-0.672	0.522488	0.759283
12228	10374450	XR_033115	635455	hypothetical LOC635455	LOC635455	0.957	-0.903	0.395799	0.663394
12229	10391854	BC100507	69441	RIKEN cDNA 1700023F06 gene	1700023F06Rik	0.957	-1.114	0.301205	0.577397
12230	10373027	NM_025982	67125	tetraspanin 31	Tspan31	0.957	-0.964	0.366344	0.637372
12231	10514392	NM_026954	69136	tumor suppressor candidate 1	Tusc1	0.957	-1.146	0.288586	0.564651
12232	10450669	NM_145487	75210	proline-rich polypeptide 3	Prr3	0.957	-1.142	0.289946	0.566234
12233	10569102	NM_016850	54123	interferon regulatory factor 7	Irf7	0.957	-0.008	0.99421	0.997702
12234	10531415	NM_021274	15945	chemokine (C-X-C motif) ligand	Cxcl10	0.957	-0.4	0.700755	0.868962
12235	10473779	ENSMUST00000111449	13046	CUG triplet repeat, RNA bindin	Cugbp1	0.957	-1.099	0.306999	0.583635
12236	10591706	NM_010487	15571	ELAV (embryonic lethal, abnorm	Elavl3	0.957	-0.4	0.700705	0.868962
12237	10407348					0.957	-0.957	0.369396	0.639995
12238	10495987	DQ851564	435755	POU domain, class 5, transcrip	LOC435755	0.957	-0.765	0.46831	0.720616
12239	10382573	NM_028014	71947	RIKEN cDNA 2310067B10 gene	2310067B10Rik	0.957	-0.839	0.428582	0.689543
12240	10470412	NM_138942	13166	dopamine beta hydroxylase	Dbh	0.957	-0.912	0.39138	0.659653
12241	10436037					0.957	-1.086	0.31241	0.588786
12242	10527575	NM_028291	72587	PAN3 polyA specific ribonuclea	Pan3	0.957	-0.783	0.458667	0.713672
12243	10480381	NM_001081364	71435	Rho GTPase activating protein	Arhgap21	0.957	-0.84	0.428018	0.689167
12244	10408113	NM_175656	319158	histone cluster 1, H4i	Hist1h4i	0.957	-1.046	0.32954	0.60586
12245	10455695	NM_026040	67222	serum response factor binding	Srfbp1	0.957	-1.023	0.339181	0.614614
12246	10475665	NM_019729	84092	ubiquitin specific peptidase 8	Usp8	0.957	-1.575	0.158079	0.405065
12247	10532032	NM_001005477	104382	BarH-like 2 (Drosophila)	Barhl2	0.957	-0.687	0.513602	0.754034
12248	10439532	NM_029128	106248	queuine tRNA-ribosyltransferas	Qtrtd1	0.957	-0.955	0.370688	0.641417
12249	10562965	NM_007458	11771	adaptor protein complex AP-2,	Ap2a1	0.957	-0.747	0.478715	0.729103
12250	10595671					0.957	0.069	0.946945	0.978938
12251	10488233	ENSMUST00000099292	433481	predicted gene, EG433481	EG433481	0.957	-0.379	0.715829	0.875402

12252	10590983	NM_019482	55991	pannexin 1	Panx1	0.957	-1.234	0.256054	0.530431
12253	10591270	NM_173777	244723	olfactomedin 2	Olfm2	0.957	-0.45	0.666213	0.851266
12254	10449893	NM_178785	320484	RIKEN cDNA A430107D22 gene	A430107D22Rik	0.957	-0.967	0.36479	0.635871
12255	10518464	BC060239	70433	RIKEN cDNA 2610109H07 gene	2610109H07Rik	0.957	-0.329	0.751627	0.895256
12256	10401527	NM_013589	16997	latent transforming growth fac	Ltbp2	0.957	-0.281	0.78654	0.912916
12257	10355341					0.957	-0.911	0.391823	0.660136
12258	10376314	NM_026949	69125	CCR4-NOT transcription complex	Cnot8	0.957	-1.183	0.274518	0.54916
12259	10591087	NM_145712	244701	melatonin receptor 1B	Mtnr1b	0.957	0.059	0.954331	0.98249
12260	10466515	NM_008023	14240	forkhead box B2	Foxb2	0.957	-0.429	0.680356	0.858268
12261	10466104	NM_023731	108673	coiled-coil domain containing	Ccdc86	0.957	-1.228	0.257979	0.531958
12262	10532652	NM_007773	12961	crystallin, beta B2	Crybb2	0.957	-0.334	0.747996	0.893185
12263	10386442	NM_011991	26572	COP9 (constitutive photomorpho	Cops3	0.957	-1.309	0.230729	0.501597
12264	10350725	NM_026380	67792	regulator of G-protein signali	Rgs8	0.957	-0.245	0.813228	0.9249
12265	10497276	BC030910	75497	RIKEN cDNA 1700008G05 gene	1700008G05Rik	0.957	0.024	0.981577	0.992092
12266	10570450	NM_172910	244310	discs, large (Drosophila) homo	Dlgap2	0.957	-0.87	0.41219	0.676028
12267	10457585					0.957	-0.968	0.36433	0.635557
12268	10453456	NM_199251	210741	potassium channel, subfamily K	Kcnk12	0.957	-0.448	0.667342	0.851505
12269	10359181	NM_023141	30935	torsin family 3, member A	Tor3a	0.957	-1.003	0.348534	0.622153
12270	10441489	NM_181392	66467	general transcription factor I	Gtf2h5	0.957	-1.158	0.283629	0.558905
12271	10560851	NR_003638	69301	RIKEN cDNA 1700008P20 gene	1700008P20Rik	0.957	-0.321	0.757462	0.898154
12272	10467344	NM_021315	57753	nucleolar complex associated 3	Noc3l	0.957	-0.992	0.353224	0.625979
12273	10499545	NM_010108	13638	ephrin A3	Efna3	0.957	-0.274	0.791965	0.915332
12274	10449596					0.957	-0.195	0.850575	0.939883
12275	10540271					0.957	-1.04	0.331912	0.608173
12276	10588638	NM_019704	56395	transmembrane protein 115	Tmem115	0.957	-1.143	0.28961	0.565682
12277	10540727	NM_133930	171508	cysteine-rich with EGF-like do	Creld1	0.957	-1.182	0.274554	0.54916
12278	10420302	NM_010371	14940	granzyme C	Gzmc	0.957	0.085	0.934294	0.97382
12279	10407833	NM_010282	14593	geranylgeranyl diphosphate syn	Ggps1	0.957	-0.997	0.35124	0.624559
12280	10444810	ENSMUST00000105041	15013	histocompatibility 2, Q region	H2-Q2	0.957	-0.106	0.918495	0.967805
12281	10529977	ENSMUST00000053488	19017	peroxisome proliferative activ	Ppargc1a	0.957	-0.039	0.969734	0.987719
12282	10448998					0.957	-0.376	0.717768	0.876765
12283	10527133	NM_178398	74781	WD repeat domain, phosphoinosi	Wipi2	0.957	-0.629	0.548744	0.779171
12284	10398966	NM_029381	75671	testis expressed gene 22	Tex22	0.957	-0.874	0.410385	0.67479
12285	10438672	NM_001081368	70573	TBCC domain containing 1	Tbccd1	0.957	-1.482	0.180711	0.436631
12286	10579422	NM_032397	84036	potassium intermediate/small c	Kcnn1	0.957	-0.536	0.607836	0.817473
12287	10362874	ENSMUST00000053792	74530	RIKEN cDNA 9030612E09 gene	9030612E09Rik	0.957	-0.492	0.637099	0.835244
12288	10502440					0.957	-1.04	0.331937	0.608173
12289	10354227					0.957	-0.614	0.558268	0.786038
12290	10454807	NR_002905	436583	small nucleolar RNA, H/ACA box	Snora74a	0.957	-0.367	0.724465	0.880611
12291	10606149	NM_027591	70887	DMRT-like family C1a	Dmrtc1a	0.957	-0.631	0.547219	0.778305
12292	10478409	NM_001039390	18769	protein kinase inhibitor, gamm	Pkig	0.957	-1.044	0.330127	0.606499
12293	10587488	BC096613	75033	RIKEN cDNA 4930486G11 gene	4930486G11Rik	0.957	-0.425	0.683389	0.859874
12294	10527455	NM_178576	54188	cleavage and polyadenylation s	Cpsf4	0.957	-0.815	0.44141	0.700321
12295	10443912	NM_153063	224691	zinc finger protein 472	Zfp472	0.957	-0.59	0.573258	0.796645
12296	10356299	NM_001033290	227326	G protein-coupled receptor 55	Gpr55	0.957	-0.058	0.955083	0.982833
12297	10396076	AK034052	414085	RIKEN cDNA 9330151L19 gene	9330151L19Rik	0.957	-0.932	0.38137	0.651086
12298	10431802	NM_008971	19230	twinfilin, actin-binding prote	Twf1	0.957	-1.079	0.315355	0.592275
12299	10390748	NM_172564	217169	tensin 4	Tns4	0.957	-0.293	0.777941	0.909621
12300	10427159	ENSMUST00000066324	432988	predicted gene, EG432988	EG432988	0.957	-0.646	0.538204	0.771145
12301	10526772	NM_178612	66455	canopy 4 homolog (zebrafish)	Cnpy4	0.957	-0.982	0.357862	0.630237
12302	10524450	NM_001040691	22256	uracil DNA glycosylase	Ung	0.956	-0.528	0.613443	0.820926

12303	10390574	NM_028149	72194	F-box and leucine-rich repeat	Fbxl20	0.956	-0.731	0.487864	0.735554
12304	10515201	NM_007823	13120	cytochrome P450, family 4, sub	Cyp4b1	0.956	-0.435	0.676226	0.855911
12305	10491081					0.956	-0.849	0.423381	0.685554
12306	10447848	NM_008552	17171	MAS1 oncogene	Mas1	0.956	-0.311	0.764243	0.90173
12307	10364379					0.956	-0.456	0.661801	0.8494
12308	10528519	AK030236	330053	RIKEN cDNA 4933427G23 gene	4933427G23Rik	0.956	-0.891	0.401865	0.667094
12309	10414817	U07662	21473	T-cell receptor alpha chain	Tcra	0.956	-0.883	0.405946	0.670467
12310	10537823	NM_146652	18310	olfactory receptor 13	Olfr13	0.956	-1.193	0.270542	0.545253
12311	10456836	NM_153124	225742	ST8 alpha-N-acetyl-neuraminide	St8sia5	0.956	-0.477	0.647741	0.841423
12312	10525885	ENSMUST00000100700	639281	predicted gene, EG639281	EG639281	0.956	-0.523	0.616459	0.82288
12313	10551981	NM_145580	101883	transmembrane protein 149	Tmem149	0.956	-0.912	0.391232	0.659561
12314	10550322	NM_011927	26368	CEA-related cell adhesion mole	Ceacam9	0.956	-0.649	0.536604	0.76974
12315	10601549					0.956	-0.539	0.606316	0.816556
12316	10373016					0.956	-0.281	0.786305	0.912868
12317	10497086	ENSMUST00000029827	69042	RIKEN cDNA 1810013D15 gene	1810013D15Rik	0.956	-0.674	0.521117	0.758676
12318	10493690	ENSMUST00000029548	77595	nucleoporin 210-like	Nup210l	0.956	0.107	0.917835	0.967712
12319	10442807	NM_027951	71840	tektin 4	Tekt4	0.956	-1.078	0.315788	0.592722
12320	10460344	NM_001078649	66990	transmembrane protein 134	Tmem134	0.956	-1.122	0.297931	0.57393
12321	10443946	NM_183282	69481	RIKEN cDNA 1700029I08 gene	1700029I08Rik	0.956	-0.139	0.893134	0.957774
12322	10577093	ENSMUST00000098932	100038554	predicted gene, OTTMUSG0000002	OTTMUSG00000020606	0.956	-0.145	0.888649	0.956116
12323	10502732	NM_011100	18749	protein kinase, cAMP dependent	Prkacb	0.956	-0.709	0.500593	0.743662
12324	10357418	NM_001081078	226413	lactase	Lct	0.956	-0.413	0.691839	0.864682
12325	10413434	NM_001114879	218850	DNA segment, Chr 14, Abbott 1	D14Abb1e	0.956	-0.86	0.417357	0.680204
12326	10587633	ENSMUST00000113149	244958	similar to Chromosome 6 open r	LOC244958	0.956	-0.461	0.658154	0.847091
12327	10411751	NM_022885	69048	solute carrier family 30 (zinc	Slc30a5	0.956	-1.145	0.288725	0.564814
12328	10577492	NM_011848	23954	NIMA (never in mitosis gene a)	Nek3	0.956	-1.18	0.275554	0.550454
12329	10390841	NM_010661	268482	keratin 12	Krt12	0.956	-0.467	0.654304	0.845158
12330	10545697	NM_013764	27369	deoxyguanosine kinase	Dguok	0.956	-1.029	0.336802	0.612536
12331	10542060					0.956	-0.5	0.631874	0.832719
12332	10481621	BC024615	73737	RIKEN cDNA 1110008P14 gene	1110008P14Rik	0.956	-1.129	0.29497	0.571244
12333	10499273	BC023814	229503	cDNA sequence BC023814	BC023814	0.956	-0.887	0.403581	0.668494
12334	10425024	BC038324	117171	RIKEN cDNA 1110038F14 gene	1110038F14Rik	0.956	-0.91	0.392139	0.660248
12335	10448168	ENSMUST00000071189	14290	formyl peptide receptor, relat	Fpr-rs3	0.956	-0.647	0.537805	0.770834
12336	10486292	NM_177294	68925	RNA polymerase II associated p	Rpap1	0.956	-0.631	0.547814	0.778543
12337	10479996	NM_020615	11949	ATP synthase, H+ transporting,	Atp5c1	0.956	-1.055	0.325484	0.60184
12338	10519477					0.956	-0.886	0.404005	0.668777
12339	10497399	NM_001122759	18583	phosphodiesterase 7A	Pde7a	0.956	-1.14	0.290734	0.567035
12340	10434717					0.956	-0.292	0.778641	0.909988
12341	10574825	NM_001033320	234695	RGD motif, leucine rich repeat	Rltpr	0.956	-0.536	0.608143	0.817507
12342	10462796	NM_010615	16551	kinesin family member 11	Kif11	0.956	-1.282	0.239431	0.51235
12343	10388308	NM_146709	258704	olfactory receptor 411	Olfr411	0.956	-0.391	0.707209	0.872175
12344	10560089					0.956	-0.061	0.952942	0.981873
12345	10411353	NM_025585	66479	RIKEN cDNA 1700029F12 gene	1700029F12Rik	0.956	-0.434	0.67677	0.856344
12346	10562166	NM_183257	66438	hepcidin antimicrobial peptide	Hamp2	0.956	0.014	0.989306	0.995355
12347	10438621	NM_009186	20462	splicing factor, arginine/seri	Sfrs10	0.956	-1.25	0.250438	0.524406
12348	10549886	AF365933	116812	zinc finger protein 264	Zfp264	0.956	-0.718	0.495607	0.740468
12349	10551120	ENSMUST00000085962	269878	multiple EGF-like-domains 8	Megf8	0.956	-0.542	0.604164	0.815116
12350	10445729	NM_011549	21425	transcription factor EB	Tcfeb	0.956	-0.935	0.380035	0.6497
12351	10510447	BC035954	69743	castor homolog 1, zinc finger	Casz1	0.956	-0.784	0.457917	0.713313
12352	10547575	NM_001033354	243621	IQ motif and Sec7 domain 3	Iqsec3	0.956	-0.404	0.698105	0.867716
12353	10508420	NM_134151	107271	tyrosyl-tRNA synthetase	Yars	0.956	-1.019	0.341365	0.616096
12354	10364903	NM_007445	11705	anti-Mullerian hormone	Amh	0.956	-0.38	0.714799	0.875142
12355	10365450	NM_133993	103136	PWP1 homolog (S. cerevisiae)	Pwp1	0.956	-0.71	0.499758	0.742891
12356	10558614	NM_172909	244233	CD163 molecule-like 1	Cd163l1	0.956	-0.673	0.521644	0.75888
				RIKEN cDNA 5830433M19					

12357	10514398	BC020067	67770	gene	5830433M19Rik	0.956	-1.145	0.288967	0.565029
12358	10462359	ENSMUST00000064449	791409	predicted gene, ENSMUSG0000005	ENSMUSG00000052521	0.956	-0.701	0.505553	0.747576
12359	10590096	ENSMUST00000055775	320256	deleted in lung and esophageal	Dlec1	0.956	-1.11	0.302562	0.578687
12360	10582551	NM_028146	72185	dysbindin (dystrobrevin bindin	Dbndd1	0.956	-0.892	0.401227	0.666736
12361	10351801	NM_033608	93842	immunoglobulin superfamily, me	Igsf9	0.956	-0.637	0.543652	0.775859
12362	10583535	NM_008319	15898	intercellular adhesion molecul	Icam5	0.956	-0.44	0.672833	0.854651
12363	10349793	NM_172516	213452	receptor interacting protein k	Ripk5	0.956	-0.551	0.598405	0.811434
12364	10369479	ENSMUST00000051330	320949	RIKEN cDNA D830039M14 gene	D830039M14Rik	0.956	-0.512	0.624185	0.828379
12365	10599976	NM_019926	17772	X-linked myotubular myopathy g	Mtm1	0.956	-0.605	0.56344	0.790064
12366	10542557	NM_001005605	11569	AE binding protein 2	Aebp2	0.956	-0.716	0.496382	0.740946
12367	10508149	AK146848	100048926	predicted gene, OTTMUSG0000000	OTTMUSG00000009351	0.956	-0.907	0.39368	0.661649
12368	10584520	NM_147105	259109	olfactory receptor 978	Olfr978	0.956	-1	0.349697	0.623229
12369	10388031					0.955	-0.284	0.784416	0.912103
12370	10582209	NM_172761	234814	methenyltetrahydrofolate synth	Mthfsd	0.955	-0.793	0.452995	0.709661
12371	10380248	NR_003564	217066	predicted gene, OTTMUSG0000000	OTTMUSG00000001305	0.955	-1.216	0.262213	0.53666
12372	10585276	NM_011136	18985	POU domain, class 2, associati	Pou2af1	0.955	-0.556	0.59504	0.809153
12373	10360130	NM_012049	27045	nitrilase 1	Nit1	0.955	-1.281	0.239796	0.512804
12374	10596394	NM_172927	245026	RIKEN cDNA E330026B02 gene	E330026B02Rik	0.955	-0.826	0.435052	0.695306
12375	10447415	XR_034864	668863	similar to ribosomal protein	LOC668863	0.955	-0.623	0.552455	0.782182
12376	10576354	NM_054070	114896	AFG3(ATPase family gene 3)-lik	Afg3l1	0.955	-1.185	0.273613	0.548314
12377	10562397					0.955	-0.689	0.512221	0.752738
12378	10482133	NM_146368	258365	olfactory receptor 361	Olfr361	0.955	-0.887	0.403896	0.668753
12379	10560097	NM_177312	321008	RIKEN cDNA 6330408A02 gene	6330408A02Rik	0.955	-0.387	0.71026	0.873031
12380	10496192	NM_021382	21338	tachykinin receptor 3	Tacr3	0.955	-0.646	0.538308	0.771226
12381	10528482	ENSMUST00000101522	269630	cDNA sequence BC050254	BC050254	0.955	-0.993	0.35278	0.625874
12382	10604344					0.955	-0.746	0.479139	0.729179
12383	10537809	NM_146656	258650	olfactory receptor 444	Olfr444	0.955	-0.106	0.918448	0.967805
12384	10561831	NM_152814	72556	zinc finger protein 566	Zfp566	0.955	-0.778	0.461157	0.715789
12385	10534551	NM_027891	71735	leucine-rich repeats and WD re	Lrwd1	0.955	-0.663	0.527851	0.763369
12386	10499095	NM_172682	229488	RIKEN cDNA 9930021J17 gene	9930021J17Rik	0.955	-0.608	0.561907	0.788974
12387	10395702	NM_198111	238161	A kinase (PRKA) anchor protein	Akap6	0.955	-0.234	0.821464	0.92863
12388	10419566	NM_007449	11731	angiogenin, ribonuclease A fam	Ang2	0.955	-1.309	0.230702	0.501597
12389	10425559	NM_145993	214669	l(3)mbt-like 2 (Drosophila)	L3mbtl2	0.955	-1.017	0.341911	0.616342
12390	10416279	NM_145219	213469	leucine-rich repeat LGI family	Lgi3	0.955	-0.22	0.832248	0.932679
12391	10385343	NM_133795	66827	tetratricopeptide repeat domai	Ttc1	0.955	-1.183	0.274501	0.54916
12392	10582882					0.955	-0.024	0.981317	0.992092
12393	10523672					0.955	-0.469	0.653172	0.844576
12394	10596117	AK137058	28135	centrosomal protein 63	Cep63	0.955	-0.362	0.727984	0.882032
12395	10607886	XM_891970	627311	predicted gene, EG627311	EG627311	0.955	-0.114	0.91235	0.965068
12396	10559788	NM_207136	269862	olfactory receptor 1349	Olfr1349	0.955	-0.167	0.87172	0.948716
12397	10596257					0.955	-0.696	0.508523	0.75032
12398	10435112	NM_080457	140474	mucin 4	Muc4	0.955	-0.311	0.764454	0.901786
12399	10425082	NM_001081367	72844	potassium channel tetramerisat	Kctd17	0.955	-0.51	0.625108	0.829015
12400	10380840	NM_001109626	69131	Cdc2-related kinase, arginine/	Crkrs	0.955	-1.059	0.323638	0.600158
12401	10548141	ENSMUST00000071101	434089	predicted gene, ENSMUSG0000005	ENSMUSG00000056771	0.955	-0.526	0.614903	0.82184
12402	10443319	NM_027185	23853	differentially expressed in FD	Def6	0.955	-0.615	0.557314	0.785582
12403	10436976					0.955	-0.38	0.714932	0.875237
12404	10355844	NM_001110831	13437	aspartyl aminopeptidase	Dnpep	0.955	-1.06	0.323278	0.599849
12405	10445753	NM_021407	58218	triggering receptor expressed	Trem3	0.955	-0.547	0.601092	0.812694
12406	10589632	NM_153172	260408	cDNA sequence BC107230	BC107230	0.955	-0.422	0.685175	0.860862
12407	10452734	NM_007439	11682	anaplastic lymphoma kinase	Alk	0.955	-0.37	0.721872	0.879017

12407	10452734	NM_007439	11682	anaplastic lymphoma kinase	Alk	0.955	-0.37	0.721872	0.879017
12408	10382538	NM_177778	276905	armadillo repeat containing 7	Armc7	0.955	-1.135	0.29264	0.568731
12409	10462113	NM_177034	319924	amyloid beta (A4) precursor pr	Apba1	0.955	-0.621	0.553743	0.783219
12410	10605612	XM_992998	637027	predicted gene, EG637027	EG637027	0.955	-1.025	0.338573	0.614159
12411	10451054	NM_199016	224794	ectonucleotide pyrophosphatase	Enpp4	0.955	-0.905	0.394608	0.66219
12412	10469433					0.955	0.076	0.941582	0.977455
12413	10367335					0.955	-0.239	0.817406	0.927212
12414	10543835	NM_025336	66075	coiled-coil-helix-coiled-coil-	Chchd3	0.955	-1.46	0.186369	0.444561
12415	10349208	NM_001077425	636808	contactin associated protein-l	Cntnap5a	0.955	-0.223	0.829692	0.931455
12416	10533812	NM_001081203	243272	sno, strawberry notch homolog	Sbno1	0.955	-1.211	0.263909	0.538844
12417	10534426	NM_010246	14371	frizzled homolog 9 (Drosophila	Fzd9	0.955	-0.184	0.859408	0.943573
12418	10413125	NM_026283	67630	sterile alpha motif domain con	Samd8	0.955	-0.825	0.435643	0.695606
12419	10530731					0.955	-0.931	0.381925	0.651558
12420	10540991	AK164314	212541	rhodopsin	Rho	0.955	-0.534	0.609488	0.818311
12421	10451953	NM_029796	76905	leucine-rich alpha-2-glycoprot	Lrg1	0.955	-0.37	0.72229	0.879223
12422	10579114	ENSMUST00000059500	234365	cDNA sequence BC028663	BC028663	0.955	-1.053	0.326477	0.602834
12423	10591350	NM_145154	70726	angiopoietin-like 6	Angptl6	0.955	-0.901	0.3969	0.664139
12424	10496919	NM_133247	170822	ubiquitin specific peptidase 3	Usp33	0.955	-1.29	0.236838	0.508973
12425	10409539					0.955	-0.281	0.786439	0.912899
12426	10418455	NM_008406	16424	inter-alpha trypsin inhibitor,	Itih1	0.955	-0.739	0.483457	0.732251
12427	10452085	ENSMUST00000052092	224902	scaffold attachment factor B2	Safb2	0.955	-0.702	0.504925	0.747039
12428	10493565	NM_001038587	56417	adenosine deaminase, RNA-speci	Adar	0.955	-0.554	0.596184	0.809771
12429	10382692	BC065414	66528	RIKEN cDNA 2210020M01 gene	2210020M01Rik	0.955	-0.413	0.691788	0.864682
12430	10468249	ENSMUST00000086963	100049552	predicted gene, ENSMUSG0000006	ENSMUSG00000067124	0.955	-0.71	0.500105	0.743152
12431	10477169	NM_010495	15901	inhibitor of DNA binding 1	Id1	0.955	-1.355	0.216438	0.483657
12432	10493292	ENSMUST00000029696	74200	RIKEN cDNA 2810403A07 gene	2810403A07Rik	0.955	-0.993	0.353011	0.625939
12433	10555887	NM_146748	258743	olfactory receptor 661	Olfr661	0.955	-0.239	0.817405	0.927212
12434	10407814	NM_178337	70430	tubulin-specific chaperone e	Tbce	0.955	-1.126	0.296323	0.572868
12435	10539905	AK133241	100038356	predicted gene, ENSMUSG0000007	ENSMUSG00000072920	0.955	-0.484	0.642431	0.838098
12436	10580282	NM_008416	16477	Jun-B oncogene	Junb	0.955	-0.979	0.359378	0.631436
12437	10420030	NM_011190	19188	proteasome (prosome, macropain	Psme2	0.955	-1.312	0.229655	0.500806
12438	10460102	BC034297	67105	RIKEN cDNA 1700034H14 gene	1700034H14Rik	0.955	-0.835	0.430704	0.691411
12439	10485466	NM_009804	12359	catalase	Cat	0.955	-1.082	0.314208	0.591017
12440	10523577	XM_984344	666515	predicted gene, EG666515	EG666515	0.955	-0.611	0.560211	0.787521
12441	10477286	NM_080463	140484	protein O-fucosyltransferase 1	Pofut1	0.955	-0.582	0.578438	0.798316
12442	10421875					0.955	-0.575	0.582603	0.800924
12443	10355227	NM_001122738	68691	RIKEN cDNA 1110028C15 gene	1110028C15Rik	0.955	-1.227	0.258514	0.532776
12444	10356508					0.955	-0.272	0.793266	0.915797
12445	10518546	NM_019781	56273	peroxisomal biogenesis factor	Pex14	0.955	-0.763	0.469795	0.721848
12446	10590365	NM_011703	22354	vasoactive intestinal peptide	Vipr1	0.954	-1.167	0.280297	0.555618
12447	10585517	BC068128	244886	expressed sequence AI118078	AI118078	0.954	-0.042	0.967892	0.987137
12448	10600453	NM_178590	16151	inhibitor of kappaB kinase gam	Ikbkg	0.954	-0.734	0.486053	0.734026
12449	10575328	NM_001122594	244650	PH domain and leucine rich rep	Phlppl	0.954	-0.786	0.457181	0.712928
12450	10555550	NM_009191	20480	ClpB caseinolytic peptidase B	Clpb	0.954	-1.516	0.172147	0.424279
12451	10504613	ENSMUST00000043958	381522	RIKEN cDNA E230008N13 gene	E230008N13Rik	0.954	-0.587	0.575391	0.797076
12452	10539584	NM_010131	13796	empty spiracles homolog 1 (Dro	Emx1	0.954	-0.554	0.596063	0.80968
12453	10400504	NM_008259	15375	forkhead box A1	Foxa1	0.954	-0.313	0.763216	0.901493
12454	10360972	NM_010607	16526	potassium channel, subfamily K	Kcnk2	0.954	-1.018	0.34157	0.616178
12455	10515159	NM_008593	17301	forkhead box D2	Foxd2	0.954	-0.303	0.770249	0.905037
12456	10596190	NM_001002896	107993	beaded filament structural pro	Bfsp2	0.954	-0.415	0.689975	0.86396
12457	10371415					0.954	-1.136	0.292109	0.568202

12458	10539080	NM_011375	20454	ST3 beta-galactoside alpha-2,3	St3gal5	0.954	-0.778	0.461161	0.715789
12459	10373400	NM_172259	216459	myosin, light polypeptide 6B	Myl6b	0.954	-1.165	0.281238	0.556788
12460	10362861	NM_172938	268297	sex comb on midleg-like 4 (Dro	Scml4	0.954	-0.19	0.85418	0.941009
12461	10585233	NM_133981	102580	asparagine-linked glycosylatio	Alg9	0.954	-0.704	0.503547	0.746058
12462	10358675					0.954	-0.76	0.471365	0.72321
12463	10382502	NM_001080929	237988	cerebellar degeneration-relate	Cdr2l	0.954	-0.201	0.846035	0.937284
12464	10597323	NM_033264	74100	cyclic AMP-regulated phosphopr	Arpp21	0.954	-0.434	0.677283	0.856571
12465	10363915	AK138135	432471	hypothetical gene supported by	LOC432471	0.954	-0.451	0.665402	0.850877
12466	10517521	NM_007939	13842	Eph receptor A8	Epha8	0.954	-0.635	0.545292	0.777255
12467	10408121	XR_032696	665690	similar to ribosomal protein L	LOC665690	0.954	-0.982	0.35776	0.630135
12468	10459512	NM_016977	17202	melanocortin 4 receptor	Mc4r	0.954	-0.575	0.582503	0.800913
12469	10535449	NM_172726	231868	RIKEN cDNA E130309D02 gene	E130309D02Rik	0.954	-1.188	0.272643	0.547117
12470	10375980	NM_033565	93736	AF4/FMR2 family, member 4	Aff4	0.954	-1.195	0.26974	0.544449
12471	10542840	AK054296	402777	RIKEN cDNA E330012B07 gene	E330012B07Rik	0.954	-0.297	0.775026	0.907674
12472	10399299	BC145648	207921	RIKEN cDNA A830093I24 gene	A830093I24Rik	0.954	-0.483	0.643481	0.838573
12473	10515452	NM_001033774	381544	gene model 1661, (NCBI)	Gm1661	0.954	-0.962	0.367091	0.638059
12474	10572741	NM_207555	404315	olfactory receptor 372	Olfr372	0.954	0.326	0.753361	0.8961
12475	10512136	NM_009736	12017	Bcl2-associated athanogene 1	Bag1	0.954	-1.297	0.234433	0.50565
12476	10355474	NM_001045533	381270	membrane-associated ring finge	March4	0.954	-0.964	0.366397	0.637411
12477	10359525	NM_001081290	226562	BAT2 domain containing 1	Bat2d	0.954	-1.408	0.200731	0.462663
12478	10402336	NM_020494	27225	DEAD (Asp-Glu-Ala-Asp) box pol	Ddx24	0.954	-1.019	0.340994	0.615921
12479	10433472	BC116778	69053	RIKEN cDNA 1810013L24 gene	1810013L24Rik	0.954	-1.361	0.214597	0.481427
12480	10593664	ENSMUST00000098759	73567	RIKEN cDNA 1700104A03 gene	1700104A03Rik	0.954	-0.135	0.896563	0.959489
12481	10490473	NM_173031	271887	cDNA sequence BC066135	BC066135	0.954	-0.571	0.585639	0.80308
12482	10468738	BC049561	67507	RIKEN cDNA 1700019N19 gene	1700019N19Rik	0.954	-0.125	0.904031	0.962759
12483	10438959	NM_178069	224092	large subunit GTPase 1 homolog	Lsg1	0.954	-1.459	0.186677	0.444956
12484	10408212	NM_015787	50709	histone cluster 1, H1e	Hist1h1e	0.954	-1.018	0.341411	0.616096
12485	10589004	NM_133794	97541	glutaminyl-tRNA synthetase	Qars	0.954	-1.702	0.131262	0.363844
12486	10392791	BC122876	72014	RIKEN cDNA 1500005I02 gene	1500005I02Rik	0.954	-0.304	0.769379	0.904517
12487	10372926					0.954	-0.533	0.60993	0.818557
12488	10410364	ENSMUST00000087803	319231	RIKEN cDNA 6720487G11 gene	6720487G11Rik	0.954	-0.422	0.685631	0.861122
12489	10420280	NM_010375	14944	granzyme G	Gzmg	0.954	-0.615	0.557457	0.785582
12490	10472499					0.954	-0.685	0.51458	0.754736
12491	10425120	NM_145929	106039	golgi associated, gamma adapti	Gga1	0.954	-0.905	0.394452	0.662113
12492	10527605	BC055016	77521	RIKEN cDNA C130038G02 gene	C130038G02Rik	0.954	-0.634	0.545638	0.777543
12493	10445867	NM_013880	224860	phospholipase C-like 2	Plcl2	0.954	-0.472	0.650553	0.843262
12494	10512431	NM_020035	56703	phosphatidylinositol glycan an	Pigo	0.954	-0.847	0.424213	0.686411
12495	10507539	NM_019422	54325	elongation of very long chain	Elovl1	0.954	-0.886	0.40425	0.668868
12496	10349571	NM_144960	64435	Fc receptor, IgA, IgM, high af	Fcamr	0.954	0.158	0.878964	0.952091
12497	10552451	NM_028236	72431	CEA-related cell adhesion mole	Ceacam18	0.954	-0.814	0.441952	0.700812
12498	10549794	NR_003622	272350	predicted gene, EG272350	EG272350	0.954	0.135	0.896594	0.959489
12499	10386169	ENSMUST00000065533	100038519	predicted gene, ENSMUSG0000005	ENSMUSG00000053218	0.954	-0.346	0.738886	0.888726
12500	10383556	NM_181420	238024	cDNA sequence BC032265	BC032265	0.954	-0.696	0.508088	0.749949
12501	10556297	NM_009627	11535	adrenomedullin	Adm	0.954	-0.862	0.416341	0.67936
12502	10551971	NM_170760	233073	U2 small nuclear RNA auxiliary	U2af1l4	0.954	-1.229	0.257488	0.531656
12503	10469250					0.954	-0.795	0.451892	0.708709
12504	10532626					0.954	-0.46	0.659209	0.848087
12505	10542104	ENSMUST00000082030	791299	predicted gene, ENSMUSG0000005	ENSMUSG00000059659	0.954	-0.399	0.701763	0.869198
12506	10500155	ENSMUST00000098867	100038425	predicted gene, ENSMUSG0000007	ENSMUSG00000074414	0.954	-0.828	0.434335	0.694762

12507	10505532	XR_033213	433716	similar to ribosomal protein L	LOC433716	0.954	-0.585	0.576238	0.797276
12508	10383088	NM_008064	14387	glucosidase, alpha, acid	Gaa	0.954	-1.344	0.219655	0.488523
12509	10582196	BC027666	68918	RIKEN cDNA 1190005I06 gene	1190005I06Rik	0.954	-1.161	0.282511	0.55755
12510	10519266					0.954	-0.7	0.505845	0.747682
12511	10398315					0.954	-1.003	0.34851	0.622153
12512	10500133	NM_173347	229589	prune homolog (Drosophila)	Prune	0.954	-1.075	0.317095	0.594333
12513	10505092	NM_009011	19359	RAD23b homolog (S. cerevisiae)	Rad23b	0.954	-1.758	0.120858	0.347273
12514	10600341	NM_007927	13726	emerin	Emd	0.954	-1.31	0.230468	0.501476
12515	10371907	NM_008682	17997	neural precursor cell expresse	Nedd1	0.954	-0.848	0.42355	0.685776
12516	10486081	NM_027759	71313	fibrous sheath-interacting pro	Fsip1	0.954	-0.852	0.421469	0.683872
12517	10561552	NM_028659	73830	eukaryotic translation initiat	Eif3k	0.954	-1.297	0.234609	0.505768
12518	10436444					0.953	-0.09	0.931038	0.972759
12519	10438733	NM_001008230	224055	receptor transporter protein 2	Rtp2	0.953	-0.207	0.841405	0.935809
12520	10365132	AK076844	100038685	predicted gene, ENSMUSG0000007	ENSMUSG00000071156	0.953	-0.01	0.991928	0.99682
12521	10379779	NM_030096	78394	DEAD (Asp-Glu-Ala-Asp) box pol	Ddx52	0.953	-0.918	0.388151	0.65688
12522	10513722	NM_177371	326623	tumor necrosis factor (ligand)	Tnfsf15	0.953	-0.288	0.781395	0.911096
12523	10470001	AB197927	72080	RIKEN cDNA 2010317E24 gene	2010317E24Rik	0.953	-0.821	0.438125	0.697167
12524	10544720	NM_016806	53379	heterogeneous nuclear ribonucl	Hnrnpa2b1	0.953	-1.026	0.33825	0.613849
12525	10477058	ENSMUST00000064061	545474	scratch homolog 2, zinc finger	Scrt2	0.953	-0.686	0.513954	0.754437
12526	10372441					0.953	-0.267	0.797023	0.917479
12527	10377541	NM_030083	78304	LSM domain containing 1	Lsmd1	0.953	-1.515	0.172319	0.424503
12528	10442357	NM_027220	69814	protease, serine, 32	Prss32	0.953	-0.494	0.635686	0.83453
12529	10413528					0.953	-0.651	0.535018	0.768753
12530	10582231	NM_133765	76454	F-box protein 31	Fbxo31	0.953	-0.856	0.419619	0.681917
12531	10463945	NM_001085390	240672	dual specificity phosphatase 5	Dusp5	0.953	-0.683	0.516197	0.755582
12532	10509811	NM_031873	83770	taste receptor, type 1, member	Tas1r2	0.953	-0.596	0.569542	0.794081
12533	10513824	NM_145990	214444	CDK5 regulatory subunit associ	Cdk5rap2	0.953	-1.175	0.277195	0.552231
12534	10517443	NM_013736	27224	transcription elongation facto	Tceb3	0.953	-1.636	0.144587	0.385907
12535	10600531					0.953	-0.471	0.651536	0.843968
12536	10555174	NM_001113379	434215	leucine rich repeat containing	Lrrc32	0.953	-1.199	0.268415	0.542786
12537	10393591					0.953	-0.245	0.81327	0.9249
12538	10546606	NM_011666	22200	ubiquitin-like modifier activa	Uba3	0.953	-1.008	0.346284	0.620388
12539	10567219	NM_019419	54208	ADP-ribosylation factor-like 6	Arl6ip1	0.953	-1.089	0.311085	0.587683
12540	10383025	NM_019959	56745	C1q and tumor necrosis factor	C1qtnf1	0.953	-0.409	0.694368	0.86574
12541	10469979	ENSMUST00000028340	78217	RIKEN cDNA 4930571C24 gene	4930571C24Rik	0.953	-0.258	0.803854	0.920431
12542	10350590	XM_916146	625534	predicted gene, EG625534	EG625534	0.953	-0.283	0.785331	0.912507
12543	10441751					0.953	-0.746	0.479137	0.729179
12544	10363112	NM_153786	215031	vestigial like 2 homolog (Dros	Vgll2	0.953	-0.563	0.590372	0.806176
12545	10551401	NM_028417	73032	tetratricopeptide repeat domai	Ttc9b	0.953	-0.605	0.563757	0.790299
12546	10539983	BC048671	243535	cDNA sequence BC048671	BC048671	0.953	-0.4	0.700901	0.868962
12547	10570754	NM_139224	246084	defensin beta 35	Defb35	0.953	-0.147	0.887401	0.955613
12548	10385083	NM_146017	216643	gamma-aminobutyric acid (GABA-	Gabrp	0.953	-0.413	0.69142	0.864541
12549	10432972	NM_011244	19411	retinoic acid receptor, gamma	Rarg	0.953	-0.525	0.61561	0.822286
12550	10517742	ENSMUST00000063789	791389	predicted gene, ENSMUSG0000005	ENSMUSG00000052098	0.953	-0.167	0.872019	0.948845
12551	10372116	NM_027945	71832	citrate synthase like	Csl	0.953	-0.709	0.500811	0.743872
12552	10428004	NM_027496	67434	RIKEN cDNA 5730557B15 gene	5730557B15Rik	0.953	-0.23	0.824388	0.929508
12553	10410741	ENSMUST00000099365	634611	predicted gene, ENSMUSG0000007	ENSMUSG00000074798	0.953	-0.684	0.51508	0.754817
12554	10548163	NM_011657	22158	tubby-like protein 3	Tulp3	0.953	-1.226	0.258587	0.532776
12555	10489646	NM_144893	228875	solute carrier family 35, memb	Slc35c2	0.953	-0.681	0.517286	0.756501
12556	10590265					0.953	-0.873	0.410733	0.675052
12557	10439218	NM_028295	72599	protein disulfide isomerase as	Pdia5	0.953	-0.669	0.524522	0.76103

12558	10443535	NM_198647	381085	TBC1 domain family, member 22B	Tbc1d22b	0.953	-1.196	0.269515	0.544449
12559	10521702	ENSMUST00000079389	75783	RIKEN cDNA 4930431F12 gene	4930431F12Rik	0.953	-1.042	0.331195	0.60765
12560	10404127	NM_175658	319163	histone cluster 1, H2aa	Hist1h2aa	0.953	-1.292	0.236056	0.508109
12561	10526120	NM_013837	22021	protein-tyrosine sulfotransfer	Tpst1	0.953	-1.003	0.348236	0.622132
12562	10585713	BC112403	78323	RIKEN cDNA 2310046O06 gene	2310046O06Rik	0.953	-0.712	0.498992	0.742429
12563	10493203	NM_020003	56700	RIKEN cDNA 0610031J06 gene	0610031J06Rik	0.953	-1.605	0.151345	0.395197
12564	10392328	NM_133702	68979	nucleolar protein 11	Nol11	0.953	-0.993	0.352956	0.625939
12565	10539441	AK075695	320775	RIKEN cDNA B230319C09 gene	B230319C09Rik	0.953	-0.429	0.680497	0.85838
12566	10581266	NM_026481	67971	tubulin polymerization-promoti	Tppp3	0.953	-0.918	0.388476	0.657074
12567	10440727	ENSMUST00000072280	16703	keratin associated protein 8-1	Krtap8-1	0.953	-0.618	0.555286	0.783985
12568	10562132	NM_009845	12483	CD22 antigen	Cd22	0.953	-0.826	0.435149	0.695306
12569	10489532					0.953	-0.569	0.586885	0.803854
12570	10571911	BC042740	72612	RIKEN cDNA 2700029M09 gene	2700029M09Rik	0.953	-1.476	0.182301	0.438828
12571	10430265	NM_018749	55944	eukaryotic translation initiat	Eif3d	0.953	-1.278	0.240968	0.513974
12572	10387791	NM_172371	69309	solute carrier family 16 (mono	Slc16a13	0.953	-1.267	0.244421	0.517519
12573	10483766					0.953	-0.812	0.442938	0.701639
12574	10385677	NM_008936	19127	paired like homeodomain factor	Prop1	0.953	-0.44	0.672645	0.854651
12575	10551801	AK138949	625421	RIKEN cDNA C230062I16 gene	C230062I16Rik	0.953	-0.883	0.405517	0.670072
12576	10583573	NM_153583	235040	autophagy-related 4D (yeast)	Atg4d	0.953	-0.721	0.493795	0.739224
12577	10514315	NM_010503	15965	interferon alpha 2	Ifna2	0.953	-0.524	0.615859	0.822286
12578	10522409	XR_033390	667154	similar to ribosomal protein	LOC667154	0.953	-0.562	0.591086	0.80656
12579	10445898	NM_025887	271457	RAB5A, member RAS oncogene fam	Rab5a	0.953	-0.38	0.714959	0.875237
12580	10461311	NM_144872	225898	echinoderm microtubule associa	Eml3	0.953	-0.781	0.459402	0.714235
12581	10574098					0.953	-0.12	0.908024	0.963723
12582	10401330	NM_020330	56622	a disintegrin and metallopepti	Adam21	0.953	-0.801	0.44855	0.706139
12583	10395961	NM_178714	238205	leucine rich repeat and fibron	Lrfn5	0.953	-0.615	0.557449	0.785582
12584	10568651	NM_133941	101437	DEAH (Asp-Glu-Ala-His) box pol	Dhx32	0.953	-1.208	0.265024	0.540178
12585	10478014	NM_198627	277432	V-set and transmembrane domain	Vstm2l	0.953	-0.421	0.685961	0.861365
12586	10449111	BC043315	106618	WD repeat domain 90	Wdr90	0.953	-0.976	0.360722	0.632458
12587	10538832	NM_019499	56150	MAD2 (mitotic arrest deficient	Mad2l1	0.953	-1.22	0.260907	0.535507
12588	10420089	NM_008683	18002	neural precursor cell expresse	Nedd8	0.953	-1.108	0.303241	0.579251
12589	10513200	NM_026132	67402	thioredoxin domain containing	Txndc8	0.953	-0.179	0.86249	0.944945
12590	10527182					0.953	-0.799	0.449707	0.707065
12591	10479230	NM_028806	74189	phosphatase and actin regulato	Phactr3	0.953	-0.79	0.454718	0.711136
12592	10356001	NM_016716	26554	cullin 3	Cul3	0.953	-1.176	0.276901	0.552079
12593	10358038	NM_145417	215615	arginyl aminopeptidase (aminop	Rnpep	0.953	-1.165	0.281162	0.556689
12594	10551760	NM_023750	74352	zinc finger protein 84	Zfp84	0.953	-0.872	0.411142	0.675147
12595	10466120	NM_001034898	545279	membrane-spanning 4-domains, s	Ms4a15	0.953	-0.729	0.489109	0.736349
12596	10499620	NM_020517	57275	lens epithelial protein	Lenep	0.953	-0.953	0.371374	0.64202
12597	10472155	NM_008426	16519	potassium inwardly-rectifying	Kcnj3	0.952	-0.09	0.931112	0.972759
12598	10352127	NM_025511	66359	RIKEN cDNA 2310005N03 gene	2310005N03Rik	0.952	-0.672	0.522382	0.75928
12599	10533961	NM_203319	208144	DEAH (Asp-Glu-Ala-His) box pol	Dhx37	0.952	-0.256	0.805011	0.921108
12600	10514842	ENSMUST00000106770	381538	gene model 1027, (NCBI)	Gm1027	0.952	-0.789	0.455104	0.711341
12601	10507555					0.952	-0.553	0.597081	0.810309
12602	10546272	ENSMUST00000101153	232227	IQ motif and Sec7 domain 1	Iqsec1	0.952	-1.265	0.245086	0.518209
12603	10359307	NM_177839	329278	tenascin N	Tnn	0.952	-0.286	0.782638	0.911672
12604	10516778	NM_153160	619605	zinc finger, CCHC domain conta	Zcchc17	0.952	-1.106	0.30444	0.580964
12605	10478572	NM_026785	68612	ubiquitin-conjugating enzyme E	Ube2c	0.952	-0.963	0.366526	0.637472
12606	10566457	NM_009685	11785	amyloid beta (A4) precursor pr	Apbb1	0.952	-0.926	0.384238	0.653466

12607	10568709	NM_178669	212070	clarin 3	Clrn3	0.952	-0.028	0.978659	0.991413
12608	10426296	ENSMUST00000100308	100038621	predicted gene, ENSMUSG0000007	ENSMUSG00000075469	0.952	-0.183	0.859842	0.943624
12609	10364542	NM_013459	11537	complement factor D (adipsin)	Cfd	0.952	-0.586	0.575981	0.797128
12610	10536359	NM_001077713	71238	ACN9 homolog (S. cerevisiae)	Acn9	0.952	-1.378	0.209499	0.474666
12611	10510592					0.952	-0.498	0.633076	0.833233
12612	10583900	NM_173412	235067	cysteine-rich perinuclear thec	Cypt4	0.952	-1.173	0.278001	0.553138
12613	10516852	NM_013622	18386	opioid receptor, delta 1	Oprd1	0.952	-0.689	0.512526	0.752977
12614	10580532	ENSMUST00000098517	626231	predicted gene, EG626231	EG626231	0.952	-0.616	0.557083	0.785473
12615	10605917	ENSMUST00000101369	100038584	predicted gene, OTTMUSG0000001	OTTMUSG00000018066	0.952	-0.767	0.46726	0.72007
12616	10559784	NM_146385	258383	olfactory receptor 1347	Olfr1347	0.952	-0.414	0.691203	0.864526
12617	10572596	BC005692	68251	RIKEN cDNA 5430437P03 gene	5430437P03Rik	0.952	-0.705	0.503132	0.745637
12618	10495854	NM_008939	19142	protease, serine, 12 neurotryp	Prss12	0.952	-0.003	0.997572	0.999133
12619	10347491	NM_009526	22420	wingless-related MMTV integrat	Wnt6	0.952	-0.867	0.413902	0.677396
12620	10377987	NM_019400	54189	rabaptin, RAB GTPase binding e	Rabep1	0.952	-1.408	0.2008	0.462697
12621	10361169	NM_144881	226861	hedgehog acyltransferase	Hhat	0.952	-0.431	0.67936	0.857678
12622	10376474	NM_026035	67212	mitochondrial ribosomal protei	Mrpl55	0.952	-1.372	0.211231	0.476809
12623	10560429	ENSMUST00000098778	100126357	predicted gene, ENSMUSG0000007	ENSMUSG00000074355	0.952	-0.883	0.405578	0.670072
12624	10522462	AK016772	71184	RIKEN cDNA 1700112M01 gene	1700112M01Rik	0.952	-0.293	0.777552	0.909562
12625	10474518					0.952	-0.246	0.812213	0.924247
12626	10517687	ENSMUST00000097827	100038595	predicted gene, ENSMUSG0000007	ENSMUSG00000073739	0.952	-0.958	0.369167	0.639859
12627	10546249	BC047211	243538	coiled-coil domain containing	Ccdc37	0.952	-0.458	0.660484	0.848669
12628	10349913	NM_178260	280287	KiSS-1 metastasis-suppressor	Kiss1	0.952	-0.414	0.690988	0.864447
12629	10607952	NM_011515	20955	vesicle-associated membrane pr	Vamp7	0.952	-1.327	0.224885	0.494934
12630	10391870	NM_016896	53859	mitogen-activated protein kina	Map3k14	0.952	-0.443	0.67063	0.853845
12631	10499937					0.952	-0.363	0.726894	0.881629
12632	10373647	NM_146795	258791	olfactory receptor 812	Olfr812	0.952	-0.633	0.546399	0.777695
12633	10377055	NM_001039545	17882	myosin, heavy polypeptide 2, s	Myh2	0.952	-1.068	0.319837	0.596635
12634	10361754	NM_010146	13853	epilepsy, progressive myocloni	Epm2a	0.952	-0.33	0.750491	0.894497
12635	10488608	NM_175093	228775	tribbles homolog 3 (Drosophila	Trib3	0.952	-0.312	0.763685	0.901533
12636	10465282	NM_008893	18969	polymerase (DNA directed), alp	Pola2	0.952	-0.725	0.49128	0.737713
12637	10546551	NR_003643	78482	RIKEN cDNA 1700123L14 gene	1700123L14Rik	0.952	-0.405	0.697021	0.867134
12638	10461558	NM_023044	65221	solute carrier family 15, memb	Slc15a3	0.952	-0.248	0.811063	0.923783
12639	10438338					0.952	-0.268	0.796532	0.917464
12640	10507657	NM_172699	230700	forkhead box J3	Foxj3	0.952	-1.117	0.299671	0.575741
12641	10367475					0.952	-0.322	0.756944	0.898026
12642	10364451	NM_148934	110012	gene trap ROSA b-geo 22	Gtrgeo22	0.952	-0.755	0.474104	0.725639
12643	10386665	NM_001033542	380701	solute carrier family 47, memb	Slc47a2	0.952	-0.546	0.60163	0.813251
12644	10588081	NM_012020	26927	forkhead box L2	Foxl2	0.952	-0.866	0.414204	0.677446
12645	10453102	NM_146083	225027	splicing factor, arginine/seri	Sfrs7	0.952	-1.138	0.29157	0.567624
12646	10347307	NM_174985	227289	G protein-coupled bile acid re	Gpbar1	0.952	-0.503	0.629792	0.831325
12647	10579347	NM_023065	65972	interferon gamma inducible pro	Ifi30	0.952	-1.455	0.187874	0.446188
12648	10574104	ENSMUST00000053085	434341	NLR family, CARD domain contai	Nlrc5	0.952	-0.704	0.503692	0.746064
12649	10549723	NM_170759	232816	zinc finger protein 628	Zfp628	0.952	-0.877	0.408669	0.673019
12650	10351843	NM_177723	240916	V-set and immunoglobulin domai	Vsig8	0.952	-0.576	0.582125	0.800654
12651	10419167	NM_008962	19214	prostaglandin D receptor	Ptgdr	0.952	-0.618	0.555807	0.784407
12652	10535902					0.952	0.251	0.808928	0.923112
12653	10350199	NM_001081023	12292	calcium channel, voltage-depen	Cacna1s	0.952	-0.486	0.641429	0.837493
12654	10420628	XR_033691	432864	predicted gene, EG432864	EG432864	0.952	-0.923	0.38575	0.654755
12655	10464013					0.952	-0.702	0.504951	0.747039
12656	10465943	NM_198114	269060	diacylglycerol lipase, alpha	Dagla	0.952	-0.407	0.695909	0.866433
12657	10456887	ENSMUST00000059746	240411	lipoxygenase homology domains	Loxhd1	0.952	-0.047	0.963606	0.985728

12658	10403706	NM_008944	19166	proteasome (prosome, macropain	Psma2	0.952	-1.387	0.206769	0.471259
12659	10476819	NM_001033298	228730	gene model 114, (NCBI)	Gm114	0.952	-1.299	0.23398	0.505288
12660	10531215	NM_030886	81702	ankyrin repeat domain 17	Ankrd17	0.952	-1.422	0.19667	0.457369
12661	10533504	NM_009879	12589	intraflagellar transport 81 ho	Ift81	0.952	-1.427	0.195479	0.455756
12662	10415957	XR_034757	100043657	similar to Nonhistone chromoso	LOC100043657	0.952	-0.344	0.740348	0.889357
12663	10534531	NM_018871	22628	tyrosine 3-monooxygenase/trypt	Ywhag	0.952	-1.231	0.256973	0.531335
12664	10489349	NM_026630	68236	gametocyte specific factor 1-l	Gtsf1l	0.952	-1.105	0.304832	0.581243
12665	10376163	NM_175258	192786	Rap guanine nucleotide exchang	Rapgef6	0.952	-1.148	0.287762	0.563515
12666	10409786	NM_028157	72219	RIKEN cDNA 1700013B16 gene	1700013B16Rik	0.952	-0.14	0.892621	0.957773
12667	10592044	NM_144936	235135	transmembrane protein 45b	Tmem45b	0.952	-0.359	0.730033	0.883264
12668	10390308	NM_030220	78912	Sp2 transcription factor	Sp2	0.952	-0.751	0.476611	0.727638
12669	10579209	NM_133972	76813	armadillo repeat containing 6	Armc6	0.952	-0.969	0.363838	0.63526
12670	10433973	NM_178922	58180	hypermethylated in cancer 2	Hic2	0.952	-1.035	0.333945	0.609581
12671	10550636					0.952	-0.783	0.458468	0.713665
12672	10530441	NM_016869	53419	corin	Corin	0.952	-0.844	0.425915	0.687657
12673	10373814	NM_022889	64934	pescadillo homolog 1, containi	Pes1	0.952	-0.637	0.543893	0.776035
12674	10580829	ENSMUST00000070212	333329	cyclic nucleotide gated channe	Cngb1	0.952	-0.761	0.470563	0.722494
12675	10477233	NM_001011732	228787	X Kell blood group precursor r	Xkr7	0.952	-0.509	0.626228	0.82979
12676	10526055	NM_008095	14467	glioblastoma amplified sequenc	Gbas	0.951	-2.169	0.0655696	0.2387
12677	10393793	NM_012065	18588	phosphodiesterase 6G, cGMP-spe	Pde6g	0.951	-0.447	0.668123	0.851935
12678	10490192					0.951	-0.139	0.893156	0.957774
12679	10402334	ENSMUST00000056140	77225	RIKEN cDNA 9330161L09 gene	9330161L09Rik	0.951	-0.593	0.571141	0.795324
12680	10375543	NM_146471	258463	olfactory receptor 1393	Olfr1393	0.951	0.073	0.944037	0.977948
12681	10397112	NM_130887	170721	papilin, proteoglycan-like sul	Papln	0.951	-0.452	0.664245	0.850267
12682	10387944	NM_178116	216874	calmodulin binding transcripti	Camta2	0.951	-0.675	0.520937	0.758585
12683	10426503	XR_032232	676777	similar to Eukaryotic translat	LOC676777	0.951	0.17	0.869369	0.947675
12684	10456519					0.951	-0.649	0.536747	0.76984
12685	10383010	U72673	12702	suppressor of cytokine signali	Socs3	0.951	-0.877	0.408547	0.672914
12686	10499429	ENSMUST00000090946	791281	predicted gene, ENSMUSG0000006	ENSMUSG00000068924	0.951	-0.352	0.735063	0.886784
12687	10458709	NM_001033280	225443	gene model 94, (NCBI)	Gm94	0.951	-0.173	0.867716	0.947039
12688	10369431	NM_001081127	237360	a disintegrin-like and metallo	Adamts14	0.951	-1.027	0.337514	0.613145
12689	10429430	NM_001033365	268816	gene model 628, (NCBI)	Gm628	0.951	-0.42	0.686795	0.861816
12690	10503917	NM_001007589	433693	RIKEN cDNA 2700059D21 gene	2700059D21Rik	0.951	-1.048	0.328348	0.604702
12691	10465580	NM_026675	68323	nudix (nucleoside diphosphate	Nudt22	0.951	-1.21	0.264302	0.539369
12692	10591999	ENSMUST00000068033	100036527	predicted gene, ENSMUSG0000005	ENSMUSG00000054797	0.951	-0.88	0.40746	0.671862
12693	10442596	NM_013759	27361	selenoprotein X 1	Sepx1	0.951	-0.752	0.475732	0.727129
12694	10453390	NR_015387	100043902	Six3 opposite strand transcrip	Six3os1	0.951	-0.056	0.956917	0.983559
12695	10425166	NM_133800	97961	nucleolar protein 12	Nol12	0.951	-1.281	0.23975	0.512773
12696	10450790	NM_177636	224756	histocompatibility 2, M region	H2-M1	0.951	-0.287	0.781968	0.911385
12697	10446190	BC116283	78625	RIKEN cDNA 1700061G19 gene	1700061G19Rik	0.951	-0.212	0.83802	0.934421
12698	10402570	ENSMUST00000101053	544890	predicted gene, ENSMUSG0000007	ENSMUSG00000072840	0.951	-0.15	0.885055	0.954881
12699	10382852	NM_178620	69900	major facilitator superfamily	Mfsd11	0.951	-0.637	0.543616	0.775859
12700	10443814	ENSMUST00000013706	78104	RIKEN cDNA 4833413E03 gene	4833413E03Rik	0.951	-0.944	0.375819	0.645831
12701	10523960	NM_001081234	433931	phosphatidylinositol glycan an	Pigg	0.951	-0.8	0.449484	0.706889
12702	10527667	NM_029440	381693	RIKEN cDNA 4930434E21 gene	4930434E21Rik	0.951	-0.506	0.62779	0.830715
12703	10550102	NM_001083188	16881	ligase I, DNA, ATP-dependent	Lig1	0.951	-1.543	0.165396	0.415485
12704	10455212	BC002117	66839	RIKEN cDNA 0610009O20 gene	0610009O20Rik	0.951	-1.03	0.33615	0.611869
12705	10476680	AF332089	171588	zinc finger protein 133	Zfp133	0.951	-0.298	0.77408	0.907069
12706	10364222	NM_080845	14317	formiminotransferase cyclodeam	Ftcd	0.951	-0.254	0.806454	0.921832
12707	10440664	BC133700	69661	RIKEN cDNA 2310061N02 gene	2310061N02Rik	0.951	0.075	0.941996	0.977645

12708	10402325	NM_023049	65256	ankyrin repeat and SOCS box-co	Asb2	0.951	-0.276	0.790149	0.914502
12709	10541738	ENSMUST00000069553	442825	RIKEN cDNA A230083G16 gene	A230083G16Rik	0.951	-0.624	0.551973	0.781881
12710	10371770	NM_001033331	237436	growth arrest-specific 2 like	Gas2l3	0.951	-1.005	0.347259	0.621483
12711	10426150	NM_001002005	406218	pannexin 2	Panx2	0.951	-0.412	0.692285	0.865004
12712	10582712	NM_053207	112405	EGL nine homolog 1 (C. elegans	Egln1	0.951	-1.105	0.304654	0.581126
12713	10489542	ENSMUST00000043448	71856	WAP four-disulfide core domain	Wfdc3	0.951	-0.705	0.503149	0.745637
12714	10568605	NM_009980	13017	C-terminal binding protein 2	Ctbp2	0.951	-1.193	0.270547	0.545253
12715	10368277	AF357393	20042	ribosomal protein S12	Rps12	0.951	-0.685	0.514832	0.754817
12716	10556691	NM_001081446	434232	IQ motif containing K	Iqck	0.951	-0.344	0.740848	0.889595
12717	10476725	NM_001033297	228715	gene model 561, (NCBI)	Gm561	0.951	-0.897	0.398474	0.664721
12718	10466054	NM_009852	12511	CD6 antigen	Cd6	0.951	-0.968	0.364588	0.635729
12719	10406710	NM_009321	21371	tubulin cofactor a	Tbca	0.951	-1.188	0.272658	0.547117
12720	10416120	ENSMUST00000052898	75892	RIKEN cDNA 4930578I07 gene	4930578I07Rik	0.951	-0.363	0.727139	0.881698
12721	10372001					0.951	-0.944	0.375537	0.645662
12722	10599554	NM_173376	209003	RNA binding motif protein, X-l	Rbmx2	0.951	-1.127	0.295906	0.572322
12723	10570666	XR_030959	637882	similar to 60S ribosomal prote	LOC637882	0.951	-0.803	0.447433	0.70522
12724	10542750	NM_025315	108098	mediator complex subunit 21	Med21	0.951	-1.408	0.20079	0.462697
12725	10360522	NM_007422	11566	adenylosuccinate synthetase, n	Adss	0.951	-1.275	0.241941	0.514804
12726	10386180					0.951	-0.365	0.725673	0.881163
12727	10429407					0.951	-0.453	0.663958	0.850267
12728	10572357	NM_021538	59042	coatomer protein complex, subu	Cope	0.951	-1.492	0.178208	0.432908
12729	10594785	NM_033604	93836	ring finger 111	Rnf111	0.951	-1.091	0.31045	0.587082
12730	10543054	NM_009169	20422	split hand/foot malformation (	Shfm1	0.951	-1.394	0.204848	0.4682
12731	10497105	NM_024194	67144	leucine rich repeat containing	Lrrc40	0.951	-1.56	0.161527	0.409658
12732	10541545	NM_026267	67602	NECAP endocytosis associated 1	Necap1	0.951	-1.453	0.188245	0.446318
12733	10359593	NM_008030	14262	flavin containing monooxygenas	Fmo3	0.951	-0.498	0.633156	0.833255
12734	10604154	NM_023894	104384	reproductive homeobox 9	Rhox9	0.951	-0.583	0.577658	0.797824
12735	10375380	XR_031806	633082	ferritin light chain 1 pseudog	LOC633082	0.951	-0.333	0.748714	0.893678
12736	10364009	NM_001081412	110279	breakpoint cluster region homo	Bcr	0.951	-0.718	0.495515	0.740384
12737	10526792	NM_001081108	66096	RIKEN cDNA 0910001L09 gene	0910001L09Rik	0.951	-1.171	0.278736	0.553649
12738	10466270					0.951	-0.441	0.672065	0.854437
12739	10381395	NM_172566	217201	RUN domain containing 1	Rundc1	0.951	-1.025	0.338401	0.613965
12740	10590686	NM_027942	71829	DDI1, DNA-damage inducible 1,	Ddi1	0.951	-0.359	0.729945	0.883264
12741	10360012	NM_001029984	435653	Fc receptor-like B	Fcrlb	0.951	-0.465	0.655673	0.845958
12742	10368703	NM_001113385	215928	cDNA sequence BC021785	BC021785	0.951	-0.77	0.465998	0.71957
12743	10429216	ENSMUST00000022953	70363	RIKEN cDNA 1700010C24 gene	1700010C24Rik	0.951	-1.207	0.265367	0.540498
12744	10455591					0.951	-0.846	0.424483	0.686543
12745	10506658	BC021897	72938	RIKEN cDNA 2900042B11 gene	2900042B11Rik	0.95	-0.766	0.467952	0.720483
12746	10370259	NM_009929	12822	collagen, type XVIII, alpha 1	Col18a1	0.95	-0.714	0.497722	0.741949
12747	10414990					0.95	-1.021	0.340393	0.61558
12748	10465633	NM_007750	12868	cytochrome c oxidase, subunit	Cox8a	0.95	-1.548	0.164363	0.414169
12749	10424335	NM_175226	75841	ring finger protein 139	Rnf139	0.95	-0.768	0.466667	0.719708
12750	10591281	NM_016919	53867	collagen, type V, alpha 3	Col5a3	0.95	-0.803	0.447554	0.705227
12751	10440471	NM_017404	27393	mitochondrial ribosomal protei	Mrpl39	0.95	-1.036	0.333679	0.609432
12752	10540059	NM_027868	71699	solute carrier family 41, memb	Slc41a3	0.95	-0.499	0.632348	0.832782
12753	10401705	NM_001080943	238331	zinc finger, DHHC-type contain	Zdhhc22	0.95	-0.243	0.815039	0.925775
12754	10380219	NM_016686	22344	vascular endothelial zinc fing	Vezf1	0.95	-1.369	0.212008	0.47745
12755	10402554	NM_001079883	58208	B-cell leukemia/lymphoma 11B	Bcl11b	0.95	-0.54	0.605207	0.815791
12756	10599425	NM_028514	73360	actin-related protein T1	Actrt1	0.95	-0.471	0.65177	0.844083
12757	10437224	NR_003508	17858	myxovirus (influenza virus) re	Mx2	0.95	-0.941	0.376992	0.647069
12758	10419286	ENSMUST00000100671	100038654	predicted gene, ENSMUSG0000007	ENSMUSG00000072589	0.95	-0.245	0.813618	0.925035
12759	10551405	NM_198417	112415	RIKEN cDNA C030039L03 gene	C030039L03Rik	0.95	-1.196	0.269443	0.544395
12760	10375951	BC034829	213673	RIKEN cDNA 9530068E07 gene	9530068E07Rik	0.95	-0.927	0.383934	0.653352

12761	10409099	NM_001033268	218236	cDNA sequence BC010304	BC010304	0.95	-0.792	0.453608	0.710123
12762	10473861	NM_028733	80708	protein kinase C and casein ki	Pacsin3	0.95	-0.714	0.497765	0.741949
12763	10477100	XR_035000	628060	similar to ribosomal protein l	LOC628060	0.95	-1.042	0.331005	0.607479
12764	10493626	BC048560	73545	RIKEN cDNA 1700094D03 gene	1700094D03Rik	0.95	-0.585	0.576658	0.797596
12765	10393136	NM_172571	217335	Fas (TNFRSF6) binding factor 1	Fbf1	0.95	-1.113	0.30155	0.577839
12766	10562172	NM_011680	22282	upstream transcription factor	Usf2	0.95	-1.074	0.317481	0.594727
12767	10402415	NM_199314	380780	serine (or cysteine) peptidase	Serpina11	0.95	-1.07	0.319292	0.596377
12768	10418950	NM_001039074	24131	LIM domain binding 3	Ldb3	0.95	-0.503	0.629981	0.831325
12769	10591446	NM_018793	54721	tyrosine kinase 2	Tyk2	0.95	-1.011	0.34469	0.618844
12770	10359888	XM_917451	640480	similar to suppressor of initi	LOC640480	0.95	-0.306	0.768395	0.903712
12771	10455653	AK170322	100038430	predicted gene, ENSMUSG0000007	ENSMUSG00000073567	0.95	-0.606	0.563296	0.789914
12772	10369815	NM_007659	12534	cell division cycle 2 homolog	Cdc2a	0.95	-1.269	0.243738	0.516777
12773	10356088	NM_007735	12829	collagen, type IV, alpha 4	Col4a4	0.95	-0.857	0.418934	0.681438
12774	10450435	NM_009975	13001	casein kinase 2, beta polypept	Csnk2b	0.95	-1.426	0.195561	0.455892
12775	10352314	NM_010094	13590	left right determination facto	Lefty1	0.95	-0.699	0.506466	0.748338
12776	10393728	NM_024249	72055	solute carrier family 38, memb	Slc38a10	0.95	-0.82	0.4387	0.697907
12777	10579799	NM_145599	234463	transmembrane protein 34	Tmem34	0.95	-1.261	0.246686	0.519877
12778	10585022	NM_011752	22687	zinc finger protein 259	Zfp259	0.95	-1.273	0.242678	0.515498
12779	10459755	BC019940	66468	RIKEN cDNA 2810433K01 gene	2810433K01Rik	0.95	-1.045	0.32978	0.606148
12780	10458046	NM_053078	27528	DNA segment, human D4S114	D0H4S114	0.95	-1.291	0.236593	0.508732
12781	10552874	NM_011565	21677	TEA domain family member 2	Tead2	0.95	-1.569	0.159469	0.406781
12782	10595404	ENSMUST00000034802	212943	cDNA sequence BC023892	BC023892	0.95	-0.988	0.355034	0.627756
12783	10569719	NM_001033378	319493	RIKEN cDNA A430078G23 gene	A430078G23Rik	0.95	-0.601	0.566088	0.792149
12784	10480912	NM_001039653	16871	LIM homeobox protein 3	Lhx3	0.95	-0.759	0.472134	0.723934
12785	10421214	NM_153514	246710	Rho-related BTB domain contain	Rhobtb2	0.95	-1.284	0.239008	0.511774
12786	10490955	NM_026182	67472	mitochondrial fission regulato	Mtfr1	0.95	-1.219	0.261187	0.535753
12787	10468344	NM_007732	12821	collagen, type XVII, alpha 1	Col17a1	0.95	-0.668	0.525132	0.761393
12788	10517901	NM_024412	12733	chloride channel Ka	Clcnka	0.95	-0.914	0.390302	0.658911
12789	10565567	ENSMUST00000098305	666737	RIKEN cDNA 4632427E13 gene	4632427E13Rik	0.95	-0.857	0.419033	0.681474
12790	10426704	NM_010601	16512	potassium voltage-gated channe	Kcnh3	0.95	-0.586	0.575816	0.797128
12791	10526153	NM_001015876	100929	tRNA-yW synthesizing protein 1	Tyw1	0.95	-1.167	0.280199	0.555564
12792	10505465	BC023748	230279	RIKEN cDNA 6330416G13 gene	6330416G13Rik	0.95	-0.792	0.453652	0.710123
12793	10526452	BC115564	69665	RIKEN cDNA 2310043J07 gene	2310043J07Rik	0.95	-0.891	0.401916	0.667094
12794	10547202					0.95	-0.596	0.569702	0.794081
12795	10542036	ENSMUST00000100929	100038603	predicted gene, ENSMUSG0000007	ENSMUSG00000072756	0.95	-0.531	0.611608	0.819829
12796	10399038	NM_001004066	56220	zinc finger protein 386 (Krupp	Zfp386	0.95	-1.305	0.232035	0.502782
12797	10499751	NM_030080	78284	cAMP responsive element bindin	Creb3l4	0.95	-0.921	0.386961	0.655969
12798	10428728	ENSMUST00000050155	319829	RIKEN cDNA 9330154K18 gene	9330154K18Rik	0.95	-0.692	0.510666	0.751917
12799	10517345	NM_016799	51796	serine/arginine repetitive mat	Srrm1	0.95	-1.374	0.210511	0.475962
12800	10350123	NM_053106	93689	leiomodin 1 (smooth muscle)	Lmod1	0.95	-0.294	0.776677	0.908994
12801	10363007	BC059917	77987	activating signal cointegrator	Ascc3	0.95	-1.233	0.256132	0.53053
12802	10382816	NM_009591	11298	arylalkylamine N-acetyltransfe	Aanat	0.95	-0.097	0.925221	0.970428
12803	10461715	NM_146683	258678	olfactory receptor 1441	Olfr1441	0.95	-0.632	0.546871	0.778024
12804	10490736	NM_026446	56470	regulator of G-protein signali	Rgs19	0.95	-1.199	0.268491	0.542836
12805	10393898	BC091000	68515	RIKEN cDNA 1110012N22 gene	1110012N22Rik	0.95	-0.729	0.488734	0.736349
12806	10399943	NM_001024478	68764	RIKEN cDNA 1110049B09 gene	1110049B09Rik	0.95	-0.354	0.733776	0.886114
12807	10426689	NM_139140	72572	spermatogenesis associated, se	Spats2	0.95	-0.968	0.364332	0.635557
12808	10550062	NM_178732	243834	zinc finger protein 324	Zfp324	0.95	-1.465	0.18509	0.442657
12809	10508707	ENSMUST00000094666	623230	transmembrane protein 200B	Tmem200b	0.95	-0.985	0.356408	0.628882

12810	10392803	NM_199225	387565	CD300C antigen	Cd300c	0.95	-0.37	0.722349	0.879243
12811	10498837	NM_025794	66841	electron transferring flavopro	Etfdh	0.95	-1.344	0.21954	0.48837
12812	10549770	NM_133671	22185	U2 small nuclear ribonucleopro	U2af2	0.95	-0.914	0.390336	0.658911
12813	10482121	NM_206903	18328	olfactory receptor 3	Olfr3	0.95	-0.496	0.634559	0.833879
12814	10470913	NM_153805	263803	protein kinase N3	Pkn3	0.95	-0.716	0.496377	0.740946
12815	10572804	BC008558	72254	RIKEN cDNA 1700030K09 gene	1700030K09Rik	0.95	-0.647	0.537895	0.770912
12816	10499093					0.95	-1.033	0.334914	0.610467
12817	10499655	NM_010559	16194	interleukin 6 receptor, alpha	Il6ra	0.95	-0.842	0.426812	0.688211
12818	10443852					0.949	-0.352	0.735136	0.886784
12819	10457844	NM_021559	59057	zinc finger protein 191	Zfp191	0.949	-1.224	0.259489	0.533772
12820	10507347	NM_146151	230661	testis-specific kinase 2	Tesk2	0.949	-0.589	0.5736	0.796812
12821	10370818	NM_198615	237400	mex3 homolog D (C. elegans)	Mex3d	0.949	-0.811	0.443512	0.702308
12822	10448214	NM_176962	319615	RIKEN cDNA 6330416L07 gene	6330416L07Rik	0.949	-1.601	0.152046	0.395822
12823	10566502	NM_029802	76932	ADP-ribosylation factor intera	Arfip2	0.949	-1.587	0.155325	0.400794
12824	10472942	ENSMUST00000100005	100038532	predicted gene, ENSMUSG0000007	ENSMUSG00000075281	0.949	-0.679	0.518038	0.756834
12825	10593646	NM_001033535	244882	tumor necrosis factor, alpha-i	Tnfaip8l3	0.949	-1.07	0.318967	0.596119
12826	10390022	NM_001013381	237926	radical S-adenosyl methionine	Rsad1	0.949	-0.181	0.861229	0.944248
12827	10434733	NM_013506	13682	eukaryotic translation initiat	Eif4a2	0.949	-0.935	0.380036	0.6497
12828	10441657	NM_178774	320111	proline rich region 18	Prr18	0.949	-0.612	0.559471	0.786846
12829	10586140	NM_145835	235435	lactase-like	Lctl	0.949	-0.082	0.936516	0.975144
12830	10584095	NM_172766	235134	nuclear factor related to kapp	Nfrkb	0.949	-1.007	0.346347	0.620403
12831	10382795	XR_034731	668255	similar to ribosomal protein S	LOC668255	0.949	-1.128	0.295332	0.571726
12832	10586405	NM_138584	27965	spastic paraplegia 21 homolog	Spg21	0.949	-1.394	0.204731	0.468184
12833	10446656	NM_022882	64898	lipin 2	Lpin2	0.949	-1.284	0.238879	0.511686
12834	10600144	NM_007978	14070	factor 8-associated gene A	F8a	0.949	-1.009	0.34578	0.619959
12835	10382393	NM_001034878	432611	dynein, axonemal, intermediate	Dnaic2	0.949	-0.68	0.518009	0.756834
12836	10413148	AK046931	319486	RIKEN cDNA A430057M04 gene	A430057M04Rik	0.949	-0.568	0.587435	0.804278
12837	10454950	NM_026404	67843	solute carrier family 35, memb	Slc35a4	0.949	-1.104	0.305218	0.581633
12838	10506680	NM_028355	72787	transmembrane protein 48	Tmem48	0.949	-0.793	0.453333	0.709863
12839	10600180	NM_177236	320707	ATPase, Ca++ transporting, pla	Atp2b3	0.949	-0.325	0.754412	0.896694
12840	10460139					0.949	-0.891	0.401872	0.667094
12841	10430436	ENSMUST00000100464	100038602	predicted gene, ENSMUSG0000007	ENSMUSG00000075558	0.949	-0.741	0.482159	0.730954
12842	10461906					0.949	-0.894	0.400047	0.665979
12843	10418838	ENSMUST00000051440	320321	RIKEN cDNA 9430077A04 gene	9430077A04Rik	0.949	-0.834	0.431127	0.691741
12844	10489589	BC037706	74886	RIKEN cDNA 4930445K14 gene	4930445K14Rik	0.949	-0.782	0.458892	0.713797
12845	10603805					0.949	-0.456	0.661493	0.849255
12846	10549588	NM_029767	76846	ribosomal protein S9	Rps9	0.949	-1.315	0.228673	0.499748
12847	10364696	NM_025313	66043	ATP synthase, H+ transporting,	Atp5d	0.949	-1.829	0.108827	0.325602
12848	10401781	NM_011479	20773	serine palmitoyltransferase, l	Sptlc2	0.949	-1.205	0.266366	0.541183
12849	10464813	NM_009032	19653	RNA binding motif protein 4	Rbm4	0.949	-1.14	0.290818	0.567038
12850	10397780					0.949	-1.107	0.303966	0.580269
12851	10473180	NM_172420	75276	protein phosphatase 1, regulat	Ppp1r1c	0.949	-0.934	0.380729	0.650316
12852	10447349	NM_019936	56724	cysteine-rich PDZ-binding prot	Cript	0.949	-1.397	0.203752	0.466884
12853	10443690	NM_021332	14652	glucagon-like peptide 1 recept	Glp1r	0.949	-0.751	0.476157	0.727414
12854	10526213					0.949	-0.777	0.461774	0.716395
12855	10446214	NM_025538	66400	alkB, alkylation repair homolo	Alkbh7	0.949	-0.849	0.4233	0.685528
12856	10404402	NM_008239	15220	forkhead box Q1	Foxq1	0.949	-0.458	0.660403	0.848652
12857	10390256	ENSMUST00000100522	100038600	predicted gene, OTTMUSG0000000	OTTMUSG00000001775	0.949	-0.08	0.938116	0.975903
12858	10364971	NM_023138	26396	mitogen-activated protein kina	Map2k2	0.949	-1.711	0.129511	0.360884
12859	10458960	NM_138600	110695	aldehyde dehydrogenase family	Aldh7a1	0.949	-1.421	0.19715	0.457903
12860	10508676	NM_010769	17180	matrilin 1, cartilage matrix p	Matn1	0.949	-0.468	0.653342	0.844695
12861	10580077	NM_173184	212108	relaxin 3	Rln3	0.949	-0.529	0.612641	0.820438

12862	10562005	NM_029274	75410	WW domain binding protein 7	Wbp7	0.949	-1.257	0.248019	0.521387
12863	10557808	NM_172749	233905	zinc finger protein 646	Zfp646	0.949	-1.02	0.340563	0.615722
12864	10429491	NM_018790	11838	activity regulated cytoskeleta	Arc	0.949	-0.77	0.465753	0.719391
12865	10459770					0.949	-1.302	0.232964	0.50397
12866	10472549	NM_028284	72569	Bardet-Biedl syndrome 5 (human	Bbs5	0.949	-0.96	0.368247	0.639105
12867	10588720					0.949	-1.162	0.282205	0.557189
12868	10438347	NM_011532	21380	T-box 1	Tbx1	0.949	-0.541	0.604933	0.815765
12869	10349980	NM_016749	53311	myosin binding protein H	Mybph	0.949	-0.14	0.89252	0.957747
12870	10388758	NM_080849	140859	NIMA (never in mitosis gene a)	Nek8	0.949	-0.689	0.512348	0.75282
12871	10391277	NM_031871	80860	GH3 domain containing	Ghdc	0.949	-0.873	0.41089	0.675081
12872	10529581	NM_026242	67568	Morf4 family associated protei	Mrfap1	0.949	-0.86	0.417304	0.680204
12873	10513103	ENSMUST00000053681	230235	RIKEN cDNA 6430704M03 gene	6430704M03Rik	0.949	-0.729	0.489193	0.736349
12874	10352119	NM_024282	78825	RIKEN cDNA 5830417C01 gene	5830417C01Rik	0.949	-1.294	0.23557	0.50735
12875	10605629					0.949	-0.689	0.512126	0.752651
12876	10508182	NM_011970	26445	proteasome (prosome, macropain	Psmb2	0.949	-1.522	0.170617	0.422304
12877	10573430	NM_183358	102060	growth arrest and DNA-damage-i	Gadd45gip1	0.949	-1.456	0.187407	0.445729
12878	10598025					0.949	-1.274	0.242065	0.514861
12879	10510532	NM_001085529	435818	solute carrier family 2 (facil	Slc2a7	0.949	-0.362	0.727443	0.881863
12880	10564436	NR_003961	117589	ankyrin repeat and SOCS box-co	Asb7	0.949	-1.444	0.190844	0.449855
12881	10346914	NM_172422	75619	FAST kinase domains 2	Fastkd2	0.949	-0.97	0.363416	0.634688
12882	10512451	BC046771	230088	RIKEN cDNA B230312A22 gene	B230312A22Rik	0.949	-0.503	0.629981	0.831325
12883	10472605	NM_009278	20823	Sjogren syndrome antigen B	Ssb	0.949	-1.258	0.247637	0.520853
12884	10502442	XM_001473461	621343	similar to zinc finger, CCHC d	LOC621343	0.949	-0.37	0.722186	0.879197
12885	10355117	NM_001081658	241073	dystrotelin	Dytn	0.949	-0.891	0.401575	0.666842
12886	10541644	NM_053094	93671	CD163 antigen	Cd163	0.949	-0.574	0.58366	0.801548
12887	10362156	NM_001009574	215854	trace amine-associated recepto	Taar5	0.949	-0.484	0.642473	0.838098
12888	10567987	NM_145636	246779	interleukin 27	Il27	0.949	-0.55	0.598791	0.811696
12889	10521111	NM_008010	14184	fibroblast growth factor recep	Fgfr3	0.948	-1.207	0.265598	0.540607
12890	10385681	BC049762	193286	cDNA sequence BC049762	BC049762	0.948	-0.679	0.518378	0.756999
12891	10352396	NM_173378	209456	transformation related protein	Trp53bp2	0.948	-1.709	0.129926	0.361535
12892	10486262	NM_203345	17005	leukocyte tyrosine kinase	Ltk	0.948	-0.65	0.535883	0.769279
12893	10409575	NM_010896	18014	neurogenin 1	Neurog1	0.948	-0.589	0.573831	0.797007
12894	10395849	NM_011041	18511	paired box gene 9	Pax9	0.948	-0.711	0.499273	0.742535
12895	10538356	NM_023543	69993	chimerin (chimaerin) 2	Chn2	0.948	-0.49	0.638578	0.835923
12896	10570837	NM_011394	20516	solute carrier family 20, memb	Slc20a2	0.948	-0.96	0.367932	0.638955
12897	10481366					0.948	-0.588	0.574536	0.797076
12898	10584481	XR_033953	667260	similar to gamma actin-like pr	LOC667260	0.948	-0.72	0.494372	0.739567
12899	10605782					0.948	-1.31	0.230324	0.501285
12900	10581491	ENSMUST00000088866	68163	RIKEN cDNA A930006D01 gene	A930006D01Rik	0.948	-0.824	0.436364	0.696296
12901	10598586	NM_023500	22439	Kell blood group precursor (Mc	Xk	0.948	-1.036	0.333483	0.609432
12902	10470628	NM_001033294	227674	DEAD/H (Asp-Glu-Ala-Asp/His) b	Ddx31	0.948	-0.827	0.434906	0.695306
12903	10524248	NM_027156	69663	DEAD (Asp-Glu-Ala-Asp) box pol	Ddx51	0.948	-0.872	0.411346	0.675346
12904	10514806	NM_080458	140475	Bartter syndrome, infantile, w	Bsnd	0.948	-0.65	0.536095	0.769315
12905	10510025	NM_001081408	75986	agmatine ureohydrolase (agmati	Agmat	0.948	-0.496	0.6344	0.833748
12906	10371321	NM_177388	338365	solute carrier family 41, memb	Slc41a2	0.948	-0.767	0.467276	0.72007
12907	10475113	NM_145378	211429	phospholipase A2, group IVB (c	Pla2g4b	0.948	-1.383	0.2079	0.472478
12908	10437580	ENSMUST00000058298	268860	4-aminobutyrate aminotransfera	Abat	0.948	-0.512	0.623625	0.828031
12909	10473221	XR_032728	624223	similar to ribosomal protein L	LOC624223	0.948	-0.149	0.886	0.955356
12910	10463389	NM_011037	18504	paired box gene 2	Pax2	0.948	-1.036	0.333766	0.609432
12911	10414693	NM_023434	268741	TOX high mobility group box fa	Tox4	0.948	-1.09	0.310617	0.587176
12912	10345393	NM_007685	12627	cripto, FRL-1, cryptic family	Cfc1	0.948	-0.174	0.866754	0.946802

12913	10579845	ENSMUST00000034109	67687	RIKEN cDNA 1700011L22 gene	1700011L22Rik	0.948	0.019	0.985	0.993647
12914	10468307	ENSMUST00000116052	629389	predicted gene, EG629389	EG629389	0.948	-0.89	0.401968	0.667128
12915	10580370	NM_019794	56445	DnaJ (Hsp40) homolog, subfamil	Dnaja2	0.948	-1.329	0.224275	0.494263
12916	10432101	NM_144851	223870	SUMO1/sentrin specific peptida	Senp1	0.948	-1.278	0.240686	0.513714
12917	10360912	XR_033455	677785	similar to CDK105	LOC677785	0.948	-1.163	0.281692	0.556928
12918	10463844	NM_026619	68214	glutathione S-transferase omeg	Gsto2	0.948	-0.72	0.494063	0.739456
12919	10576160	NM_144932	257633	acyl-CoA synthetase family mem	Acsf3	0.948	-1.14	0.290754	0.567035
12920	10456754	ENSMUST00000097524	100038353	predicted gene, ENSMUSG0000007	ENSMUSG00000073534	0.948	-1.062	0.322634	0.599294
12921	10396108	NM_007481	11845	ADP-ribosylation factor 6	Arf6	0.948	-1.279	0.240503	0.513583
12922	10387983					0.948	-1.188	0.272635	0.547117
12923	10360076	NM_153064	226646	NADH dehydrogenase (ubiquinone	Ndufs2	0.948	-1.494	0.177702	0.43217
12924	10454310	NM_013814	14423	UDP-N-acetyl-alpha-D-galactosa	Galnt1	0.948	-1.137	0.291843	0.567841
12925	10503150	NM_021518	59021	RAB2A, member RAS oncogene fam	Rab2a	0.948	-1.066	0.320771	0.597672
12926	10570344	NM_010684	16783	lysosomal-associated membrane	Lamp1	0.948	-1.894	0.0989054	0.307086
12927	10450272	NM_009995	13079	cytochrome P450, family 21, su	Cyp21a1	0.948	-0.183	0.859548	0.943578
12928	10358757	NM_001005507	226517	Smg-7 homolog, nonsense mediat	Smg7	0.948	-1.233	0.256286	0.530714
12929	10555758	NM_147053	259055	olfactory receptor 582	Olfr582	0.948	-0.006	0.995747	0.998271
12930	10439976	BC017620	66391	RIKEN cDNA 2310061J03 gene	2310061J03Rik	0.948	-0.95	0.372891	0.643306
12931	10517825	NM_011059	18599	peptidyl arginine deiminase, t	Padi1	0.948	-0.577	0.581693	0.800424
12932	10521495	ENSMUST00000094840	381634	gene model 1043, (NCBI)	Gm1043	0.948	-0.205	0.842957	0.936353
12933	10580286	NM_145388	212989	bestrophin 2	Best2	0.948	-0.594	0.570655	0.795023
12934	10432045	NM_031163	12824	collagen, type II, alpha 1	Col2a1	0.948	-0.938	0.378638	0.648305
12935	10357705	NM_177129	21367	contactin 2	Cntn2	0.948	-0.808	0.444657	0.703151
12936	10374744					0.948	-0.227	0.826621	0.930428
12937	10590438	BC113767	245050	RIKEN cDNA C730027P07 gene	C730027P07Rik	0.948	-0.173	0.86728	0.946934
12938	10433614	ENSMUST00000068397	791359	predicted gene, ENSMUSG0000005	ENSMUSG00000055015	0.948	-0.021	0.983963	0.993077
12939	10419343	BC090995	218978	DNA segment, Chr 14, ERATO Doi	D14Ertd436e	0.948	-0.887	0.403532	0.668494
12940	10605606	NM_001101541	436212	predicted gene, EG436212	EG436212	0.948	-0.555	0.59586	0.809631
12941	10481329	NM_019446	54422	BarH-like 1 (Drosophila)	Barhl1	0.948	-0.63	0.547843	0.778543
12942	10588028	NM_144533	74080	nicotinamide nucleotide adenyl	Nmnat3	0.948	-0.648	0.537286	0.770299
12943	10561063	NM_007533	12039	branched chain ketoacid dehydr	Bckdha	0.948	-0.58	0.579483	0.798943
12944	10485068					0.947	-0.313	0.763501	0.901503
12945	10580905	BC018281	234594	CCR4-NOT transcription complex	Cnot1	0.947	-1.402	0.202316	0.465127
12946	10455061	NM_053129	93875	protocadherin beta 4	Pcdhb4	0.947	-0.429	0.680319	0.858268
12947	10379363	NM_001029856	237877	ATPase family, AAA domain cont	Atad5	0.947	-1.041	0.331433	0.60794
12948	10396177	NM_019785	56444	ARP10 actin-related protein 10	Actr10	0.947	-1.164	0.281421	0.55689
12949	10384044	NM_022879	17898	myosin, light polypeptide 7, r	Myl7	0.947	-1.287	0.237967	0.510354
12950	10528610	NM_022418	64295	transmembrane and ubiquitin-li	Tmub1	0.947	-0.465	0.655775	0.845986
12951	10474041	ENSMUST00000054316	75641	RIKEN cDNA 1700029I15 gene	1700029I15Rik	0.947	-0.664	0.527325	0.762963
12952	10569291	NM_027844	71623	keratin associated protein 5-2	Krtap5-2	0.947	-0.291	0.779048	0.910184
12953	10521389	AF009367	15371	H6 homeo box 1	Hmx1	0.947	-1.04	0.332073	0.608173
12954	10589625	NM_199471	272643	testis serine protease 3	Tessp3	0.947	-0.322	0.756944	0.898026
12955	10406461	ENSMUST00000052354	320203	RIKEN cDNA C130071C03 gene	C130071C03Rik	0.947	-0.417	0.689155	0.863496
12956	10352358	NM_028408	72978	cornichon homolog 3 (Drosophil	Cnih3	0.947	-0.555	0.595757	0.809631
12957	10444244	NM_013683	21354	transporter 1, ATP-binding cas	Tap1	0.947	-0.633	0.546491	0.777695
12958	10355325	NM_007525	12021	BRCA1 associated RING domain 1	Bard1	0.947	-0.513	0.623554	0.828011
12959	10361846	NM_009048	19707	RalBP1 associated Eps domain c	Reps1	0.947	-1.592	0.154174	0.398904
12960	10453334	NM_028233	72416	leucine-rich PPR-motif contain	Lrpprc	0.947	-1.33	0.223987	0.494176

12961	10467328	NM_001081075	70567	RIKEN cDNA 5730455O13 gene	5730455O13Rik	0.947	-0.853	0.421216	0.683672
12962	10474373	NM_021275	16492	potassium voltage-gated channe	Kcna4	0.947	-0.108	0.9166	0.967047
12963	10555156	ENSMUST00000098274	14918	guanylate cyclase 2d	Gucy2d	0.947	-0.251	0.809043	0.923112
12964	10546101					0.947	-1.001	0.349391	0.622894
12965	10409222	NM_009167	20418	src homology 2 domain-containi	Shc3	0.947	-0.644	0.539346	0.772158
12966	10421269	NM_011366	20410	sorbin and SH3 domain containi	Sorbs3	0.947	-0.843	0.426534	0.688078
12967	10534743	NM_011741	22635	zonadhesin	Zan	0.947	-0.598	0.568379	0.793239
12968	10603785	NM_028058	72018	FUN14 domain containing 1	Fundc1	0.947	-0.614	0.557842	0.785788
12969	10373192	NM_008382	16326	inhibin beta E	Inhbe	0.947	0.051	0.960696	0.985069
12970	10579538					0.947	-0.623	0.552294	0.782016
12971	10440284	BC020029	67609	RIKEN cDNA 4930453N24 gene	4930453N24Rik	0.947	-1.058	0.324069	0.600613
12972	10418011	NM_001013826	435391	dual specificity phosphatase a	Dupd1	0.947	-0.454	0.662869	0.849901
12973	10577586	NM_001122820	64933	adaptor-related protein comple	Ap3m2	0.947	-1.078	0.315872	0.592775
12974	10425018	NM_012053	26961	ribosomal protein L8	Rpl8	0.947	-1.369	0.212012	0.47745
12975	10576386	NM_133955	69581	ras homolog gene family, membe	Rhou	0.947	-0.925	0.38483	0.65414
12976	10369250					0.947	-0.827	0.434734	0.695207
12977	10533483	NM_001110140	11938	ATPase, Ca++ transporting, car	Atp2a2	0.947	-1.263	0.246057	0.51906
12978	10492671	NM_026352	67738	peptidylprolyl isomerase D (cy	Ppid	0.947	-1.36	0.214707	0.48157
12979	10381528	NM_178053	217214	N-acetylglutamate synthase	Nags	0.947	-0.369	0.722824	0.87962
12980	10399208	ENSMUST00000058644	217951	transmembrane protein 196	Tmem196	0.947	-0.548	0.600402	0.812266
12981	10525076	NM_145565	231691	serine dehydratase	Sds	0.947	-0.928	0.383288	0.652674
12982	10499941	NM_028629	433619	keratinocyte expressed, prolin	Kprp	0.947	-0.134	0.896709	0.959515
12983	10351037	NR_002840	14455	growth arrest specific 5	Gas5	0.947	-0.971	0.362995	0.63431
12984	10402730	NM_011625	21981	protein phosphatase 1, regulat	Ppp1r13b	0.947	-0.75	0.476887	0.727649
12985	10583291	BC055786	69137	RIKEN cDNA 2200002K05 gene	2200002K05Rik	0.947	-0.587	0.575415	0.797076
12986	10364752	NM_133188	70248	DAZ associated protein 1	Dazap1	0.947	-1.048	0.328285	0.604687
12987	10444496	NM_033613	112403	DOM-3 homolog Z (C. elegans)	Dom3z	0.947	-1.075	0.316898	0.594121
12988	10574743	NM_001081333	102075	pleckstrin homology domain con	Plekhg4	0.947	-0.12	0.907549	0.963723
12989	10541279	NM_153516	94044	BCL2-like 13 (apoptosis facili	Bcl2l13	0.947	-0.667	0.525518	0.761639
12990	10514789	XR_033866	433742	similar to ubiquitin-conjugati	LOC433742	0.947	-0.912	0.391171	0.65951
12991	10593471					0.947	-0.571	0.585121	0.802686
12992	10576795	ENSMUST00000111031	170786	CD209a antigen	Cd209a	0.947	-0.482	0.644208	0.839078
12993	10448765	NM_013931	30957	mitogen-activated protein kina	Mapk8ip3	0.947	-1.503	0.175361	0.4286
12994	10479136	NM_020580	57314	TH1-like homolog (Drosophila)	Th1l	0.947	-1.246	0.251808	0.525693
12995	10415636	NM_145837	239114	interleukin 17D	Il17d	0.947	-0.789	0.455127	0.711341
12996	10580807	NM_010631	16582	kinesin family member C3	Kifc3	0.947	-0.928	0.383542	0.652869
12997	10427454	ENSMUST00000055038	239319	caspase recruitment domain fam	Card6	0.947	-0.503	0.62998	0.831325
12998	10592727	ENSMUST00000065379	213211	ring finger protein 26	Rnf26	0.947	-1.071	0.318592	0.595817
12999	10390618	NM_010895	18013	neurogenic differentiation 2	Neurod2	0.947	-0.62	0.5542	0.783409
13000	10499354	NM_031368	12095	bone gamma-carboxyglutamate pr	Bglap-rs1	0.947	-0.254	0.80637	0.921832
13001	10449363	NM_019837	56409	nudix (nucleotide diphosphate	Nudt3	0.947	-1.196	0.269639	0.544449
13002	10489127	NM_011249	19650	retinoblastoma-like 1 (p107)	Rbl1	0.947	-0.933	0.38082	0.650316
13003	10498531	NM_019937	56706	cyclin L1	Ccnl1	0.947	-1.135	0.292669	0.568731
13004	10522946	NM_009664	11698	ameloblastin	Ambn	0.947	-1.288	0.23738	0.509664
13005	10479481					0.947	-0.244	0.813995	0.925212
13006	10494332					0.947	-0.499	0.632385	0.832782
13007	10571367					0.947	-1.448	0.189557	0.448035
13008	10493548	NM_026784	68603	phosphomevalonate kinase	Pmvk	0.947	-1.226	0.258582	0.532776
13009	10520506	NM_010608	16527	potassium channel, subfamily K	Kcnk3	0.947	-0.998	0.350687	0.624059
13010	10519096	NM_026395	67830	RER1 retention in endoplasmic	Rer1	0.947	-1.027	0.33757	0.613173
13011	10427492	ENSMUST00000082239	791333	predicted gene, ENSMUSG0000005	ENSMUSG00000058898	0.947	-1.228	0.257923	0.531958
13012	10553521	NM_008087	14453	growth arrest specific 2	Gas2	0.947	-1.291	0.236613	0.508732
				RAB, member of RAS oncogene					

13013	10435617	NM_001042499	67657	RAB, member of RAS oncogene fa	Rabl3	0.947	-1.029	0.336746	0.612486
13014	10428449					0.947	-0.705	0.503074	0.745637
13015	10558773	NM_177897	330671	beta-1,4-N-acetyl-galactosamin	B4galnt4	0.946	-1.322	0.226522	0.497153
13016	10492540	NM_008351	16159	interleukin 12a	Il12a	0.946	-0.497	0.634197	0.833715
13017	10370320	AF391115	108707	RIKEN cDNA 1810008A18 gene	1810008A18Rik	0.946	-1.234	0.25603	0.530431
13018	10408058	NM_207572	404335	olfactory receptor 1365	Olfr1365	0.946	-0.641	0.541401	0.773838
13019	10585325	XM_001478980	100042876	similar to Btf3 protein	LOC100042876	0.946	-1.2	0.268165	0.542786
13020	10575151	ENSMUST00000046116	78571	RIKEN cDNA C630050I24 gene	C630050I24Rik	0.946	-1.372	0.211326	0.476813
13021	10378739	NM_009536	22627	tyrosine 3-monooxygenase/trypt	Ywhae	0.946	-1.5	0.175974	0.429653
13022	10527562	NM_008178	14842	GS homeobox 1	Gsx1	0.946	-0.79	0.454885	0.711239
13023	10366814	NM_009870	12567	cyclin-dependent kinase 4	Cdk4	0.946	-1.632	0.145333	0.387047
13024	10385656	NM_001044697	22678	zinc finger protein 2	Zfp2	0.946	-1.454	0.188017	0.446224
13025	10376482	BC002181	67862	RIKEN cDNA 2310033P09 gene	2310033P09Rik	0.946	-1.437	0.192739	0.452222
13026	10440570	NM_001081068	78913	zinc finger protein 294	Zfp294	0.946	-1.259	0.247125	0.520387
13027	10493709	NM_013901	30791	solute carrier family 39 (zinc	Slc39a1	0.946	-0.843	0.426246	0.687967
13028	10537799	NM_146445	258437	olfactory receptor 450	Olfr450	0.946	-0.428	0.681032	0.858763
13029	10586015	ENSMUST00000064351	73298	RIKEN cDNA 1700036A12 gene	1700036A12Rik	0.946	-0.389	0.708455	0.872343
13030	10344772	NM_177722	240697	RIKEN cDNA 6030422M02 gene	6030422M02Rik	0.946	-0.597	0.568516	0.793239
13031	10413183	ENSMUST00000100826	100038485	predicted gene, ENSMUSG0000007	ENSMUSG00000072686	0.946	-0.812	0.442711	0.701385
13032	10428215					0.946	-1.2	0.267929	0.542737
13033	10409261	NM_001024474	68203	DIRAS family, GTP-binding RAS-	Diras2	0.946	-1.012	0.344267	0.618557
13034	10352980	NM_027671	71096	syntrophin, gamma 1	Sntg1	0.946	-0.591	0.572637	0.796254
13035	10584760	ENSMUST00000080911	77381	RIKEN cDNA C030014I23 gene	C030014I23Rik	0.946	-0.998	0.350597	0.624045
13036	10484482	NM_199223	269295	reticulon 4 receptor-like 2	Rtn4rl2	0.946	-1.235	0.255518	0.529847
13037	10512195	NM_026872	68926	ubiquitin-associated protein 2	Ubap2	0.946	-1.35	0.217877	0.485795
13038	10399061	NM_028731	52635	DNA segment, Chr 12, ERATO Doi	D12Ertd551e	0.946	-0.553	0.59693	0.810212
13039	10349016	NM_173187	227446	RIKEN cDNA 2310035C23 gene	2310035C23Rik	0.946	-1.146	0.288335	0.564287
13040	10437970	BC089026	224008	RIKEN cDNA 2310008H04 gene	2310008H04Rik	0.946	-1.182	0.274847	0.549538
13041	10510034	NM_015733	12371	caspase 9	Casp9	0.946	-0.814	0.441494	0.700402
13042	10559667	NM_008350	16156	interleukin 11	Il11	0.946	-0.507	0.627475	0.83052
13043	10512830	NM_001024136	75691	ankyrin repeat and sterile alp	Anks6	0.946	-0.821	0.438136	0.697167
13044	10526997	XM_917042	231836	predicted gene, EG231836	EG231836	0.946	-0.823	0.437048	0.696483
13045	10562532	NM_172385	243937	zinc finger protein 536	Zfp536	0.946	-0.408	0.694789	0.866071
13046	10577910	NM_008033	14272	farnesyltransferase, CAAX box,	Fnta	0.946	-1.468	0.184296	0.44191
13047	10345174					0.946	-0.998	0.35038	0.623869
13048	10400006	NM_013464	11622	aryl-hydrocarbon receptor	Ahr	0.946	-0.798	0.450261	0.707462
13049	10391407	NM_026618	52469	coiled-coil domain containing	Ccdc56	0.946	-1.487	0.179255	0.434671
13050	10397311	NM_030225	78920	dihydrolipoamide S-succinyltra	Dlst	0.946	-1.033	0.335201	0.610757
13051	10470427	NM_080848	140858	WD repeat domain 5	Wdr5	0.946	-1.397	0.203767	0.466884
13052	10515368	NM_026654	68276	target of EGR1, member 1 (nucl	Toe1	0.946	-1.216	0.262114	0.536613
13053	10579234	NM_001122829	19704	UPF1 regulator of nonsense tra	Upf1	0.946	-1.374	0.210718	0.476211
13054	10505213	NM_153158	230259	RIKEN cDNA E130308A19 gene	E130308A19Rik	0.946	-1.176	0.276772	0.551925
13055	10581914	NM_019950	56773	carbohydrate (N-acetylglucosam	Chst5	0.946	-1.249	0.250623	0.52441
13056	10600741	ENSMUST00000096371	546347	predicted gene, EG546347	EG546347	0.946	-0.541	0.604501	0.815411
13057	10494039	NM_177250	320747	leucine rich repeat and Ig dom	Lingo4	0.946	-0.541	0.605019	0.815765
13058	10469083	NM_001081132	326622	UPF2 regulator of nonsense tra	Upf2	0.946	-1.229	0.257676	0.531801
13059	10468251					0.946	-0.865	0.414831	0.67815
13060	10521574	NM_172709	21906	otopetrin 1	Otop1	0.946	-1.59	0.154501	0.399653
13061	10530625	XR_034092	627733	similar to MGC27348 protein	LOC627733	0.946	-0.992	0.353476	0.626216
13062	10414612	NM_001039676	214922	solute carrier family 39 (zinc	Slc39a2	0.946	-0.79	0.454789	0.711187

13063	10502257	NM_026231	67553	glutathione S-transferase, C-t	Gstcd	0.946	-1.351	0.217689	0.485428
13064	10378785	BC048728	320522	RIKEN cDNA A830053O21 gene	A830053O21Rik	0.946	-1.075	0.317017	0.594239
13065	10548817	BC019793	66857	RIKEN cDNA 1100001H23 gene	1100001H23Rik	0.946	-1.027	0.337504	0.613145
13066	10488497	NM_054068	114889	visual system homeobox 1 homol	Vsx1	0.946	-0.321	0.757558	0.898154
13067	10545780	BC145693	75914	exocyst complex component 6B	Exoc6b	0.946	-0.819	0.438866	0.698065
13068	10420758	NM_007549	12143	B lymphoid kinase	Blk	0.946	-0.696	0.508163	0.750006
13069	10369028	NM_153071	210198	G protein-coupled receptor, fa	Gprc6a	0.946	-0.656	0.532104	0.766201
13070	10442341	NM_175229	75956	serine/arginine repetitive mat	Srrm2	0.946	-1.336	0.222212	0.491984
13071	10368654	NM_176968	319638	5'-nucleotidase domain contain	Nt5dc1	0.946	-1.04	0.332017	0.608173
13072	10345616	NM_001037918	623661	lipoyltransferase 1	Lipt1	0.946	-1.629	0.14605	0.387754
13073	10525043	NM_028762	74111	RNA binding motif protein 19	Rbm19	0.946	-1.269	0.243968	0.517035
13074	10431226	NM_011105	18766	polycystic kidney disease (pol	Pkdrej	0.946	-0.471	0.651894	0.844083
13075	10391005	NR_003957	16673	keratin 36	Krt36	0.946	-0.549	0.599367	0.811907
13076	10454856	NM_028707	74002	pleckstrin and Sec7 domain con	Psd2	0.946	-0.309	0.765791	0.902563
13077	10424660					0.946	-1.23	0.257458	0.531656
13078	10553917	NM_007461	11784	amyloid beta (A4) precursor pr	Apba2	0.946	-0.51	0.625207	0.829015
13079	10411780					0.946	-0.662	0.528421	0.763794
13080	10525086	NM_133221	170756	solute carrier family 24 (sodi	Slc24a6	0.946	-0.819	0.4388	0.698014
13081	10445347	NM_172621	224796	chloride intracellular channel	Clic5	0.946	-0.764	0.469038	0.721314
13082	10607705	NM_009789	12309	S100 calcium binding protein G	S100g	0.946	-0.813	0.442213	0.700945
13083	10373358	NM_031252	83430	interleukin 23, alpha subunit	Il23a	0.946	-0.527	0.61398	0.821282
13084	10555225	ENSMUST00000037359	72184	RIKEN cDNA 2810406K13 gene	2810406K13Rik	0.945	-0.747	0.478472	0.729035
13085	10366994	NM_001081219	432516	myosin IA	Myo1a	0.945	-0.722	0.492896	0.73872
13086	10563110	NR_002455	27210	small nucleolar RNA, C/D box 3	Snord34	0.945	-0.402	0.69922	0.868235
13087	10383245	NM_028898	74370	RIKEN cDNA 4932417H02 gene	4932417H02Rik	0.945	-1.064	0.321468	0.598233
13088	10584700	NM_007875	13478	dolichyl-phosphate (UDP-N-acet	Dpagt1	0.945	-1.519	0.17132	0.423276
13089	10534489	NM_001013412	541307	chemokine (C-C motif) ligand 2	Ccl26	0.945	-0.135	0.89668	0.959515
13090	10473045	NM_153405	241490	RNA binding motif protein 45	Rbm45	0.945	-0.899	0.397438	0.664302
13091	10479369	ENSMUST00000069943	100036520	predicted gene, OTTMUSG0000001	OTTMUSG00000016300	0.945	-0.887	0.40354	0.668494
13092	10520096	NM_026448	52323	kelch-like 7 (Drosophila)	Klhl7	0.945	-0.98	0.358944	0.630988
13093	10345855	NM_001033289	226999	solute carrier family 9 (sodiu	Slc9a2	0.945	-0.659	0.530414	0.765382
13094	10587892	ENSMUST00000034980	245000	ataxia telangiectasia and Rad3	Atr	0.945	-1.124	0.297122	0.573626
13095	10542757	NM_172734	232533	serine/threonine kinase 38 lik	Stk38l	0.945	-1.02	0.340677	0.615782
13096	10510814	NM_177673	230967	cDNA sequence BC046331	BC046331	0.945	-0.736	0.484949	0.733398
13097	10481114	NM_030718	80908	ABO blood group (transferase A	Abo	0.945	-0.605	0.564008	0.79044
13098	10412719	NM_028052	72003	synaptoporin	Synpr	0.945	-0.546	0.601711	0.813257
13099	10596255					0.945	-1	0.349785	0.62328
13100	10606858	NM_025703	66684	transcription elongation facto	Tceal8	0.945	-1.133	0.293511	0.569566
13101	10361995	NM_027930	71804	RIKEN cDNA 2610016C23 gene	2610016C23Rik	0.945	-0.518	0.620288	0.825285
13102	10460738	NM_026410	67849	cell division cycle associated	Cdca5	0.945	-1.909	0.0966275	0.302546
13103	10478073					0.945	-0.735	0.485795	0.734004
13104	10490287	XM_994502	675837	similar to ribosomal protein L	LOC675837	0.945	-1.021	0.340166	0.615478
13105	10430974	NM_025445	66251	ADP-ribosylation factor GTPase	Arfgap3	0.945	-1.523	0.170259	0.421869
13106	10563436	NM_021482	58867	synaptogyrin 4	Syngr4	0.945	-0.599	0.567261	0.792635
13107	10425158	NM_020271	57028	pyridoxal (pyridoxine, vitamin	Pdxp	0.945	-0.948	0.373919	0.644137
13108	10534839	NM_028753	74097	processing of precursor 7, rib	Pop7	0.945	-1.66	0.139583	0.37794
13109	10513943	ENSMUST00000102837	242505	RAS and EF hand domain contain	Rasef	0.945	-1.13	0.294542	0.570921
13110	10463632	NM_029186	75146	transmembrane protein 180	Tmem180	0.945	-0.696	0.508393	0.750241
13111	10480288	BC119802	74103	nebulette	Nebl	0.945	-1.205	0.26614	0.541183
13112	10514396					0.945	-0.293	0.777551	0.909562
13113	10597823	NM_026915	69032	lysozyme-like 4	Lyzl4	0.945	-0.912	0.39105	0.659412

13113	10597823	NM_026915	69032	lysozyme-like 4	Lyzl4	0.945	-0.912	0.39103	0.639412
13114	10426081	NM_134096	106014	expressed sequence AW049604	AW049604	0.945	-0.848	0.423912	0.686151
13115	10460829					0.945	-0.651	0.534933	0.768697
13116	10414706	ENSMUST00000103569	100042372	T cell receptor alpha variable	Trav2	0.945	-0.216	0.835258	0.933323
13117	10491993	NM_153156	229277	stomatin (Epb7.2)-like 3	Stoml3	0.945	-1.349	0.218282	0.48639
13118	10538959	ENSMUST00000069634	232077	similar to hCG33270	LOC232077	0.945	-0.695	0.508809	0.750513
13119	10480760	NM_009422	22030	Tnf receptor-associated factor	Traf2	0.945	-0.713	0.498104	0.742207
13120	10454233	XR_031954	546708	similar to Ribosomal protein S	LOC546708	0.945	-0.398	0.701993	0.869258
13121	10480676	NM_008169	14810	glutamate receptor, ionotropic	Grin1	0.945	-0.793	0.453334	0.709863
13122	10551155					0.945	-0.502	0.630863	0.831917
13123	10466814	NM_008022	14237	forkhead box D4	Foxd4	0.945	-0.555	0.595792	0.809631
13124	10374151	NM_028601	52915	zinc finger, MIZ-type containi	Zmiz2	0.945	-0.981	0.358357	0.630567
13125	10441178	NM_008405	16415	integrin beta 2-like	Itgb2l	0.945	-0.23	0.824684	0.929565
13126	10449303	NM_007523	12018	BCL2-antagonist/killer 1	Bak1	0.945	-1.662	0.1392	0.377453
13127	10594998	AK137986	100038597	predicted gene, ENSMUSG0000007	ENSMUSG00000074197	0.945	-0.511	0.624688	0.828892
13128	10489413	NM_025996	67145	translocase of outer mitochond	Tomm34	0.945	-0.841	0.427131	0.688411
13129	10470206	NM_029959	77704	lipocalin 9	Lcn9	0.945	-0.971	0.363117	0.634368
13130	10354792	NR_004860	68736	RIKEN cDNA 1110034B05 gene	1110034B05Rik	0.945	-1.164	0.281545	0.556926
13131	10565532	NM_028665	73845	ankyrin repeat domain 42	Ankrd42	0.945	-0.709	0.500458	0.743513
13132	10428648	NM_001081288	319944	TAF2 RNA polymerase II, TATA b	Taf2	0.945	-1.42	0.197433	0.457935
13133	10498296	NM_175095	52245	COMM domain containing 2	Commd2	0.945	-1.396	0.204214	0.467434
13134	10350684	NM_026369	67771	actin related protein 2/3 comp	Arpc5	0.945	-1.598	0.152784	0.396864
13135	10480057	NM_152824	76938	RNA binding motif protein 17	Rbm17	0.945	-1.489	0.178864	0.43395
13136	10605351					0.945	-0.677	0.519439	0.757547
13137	10543772	DQ534758	619665	Kruppel-like factor 14	Klf14	0.945	-1.156	0.284551	0.559679
13138	10430344	NM_008368	16185	interleukin 2 receptor, beta c	Il2rb	0.945	-0.941	0.377244	0.647281
13139	10506148	ENSMUST00000094955	100137011	predicted gene, OTTMUSG0000000	OTTMUSG00000007987	0.945	-0.276	0.790575	0.914692
13140	10570513	ENSMUST00000058886	67262	RIKEN cDNA 2900016B01 gene	2900016B01Rik	0.945	-0.26	0.802008	0.919813
13141	10453676	BC025933	100038402	predicted gene, ENSMUSG0000007	ENSMUSG00000073645	0.945	-0.5	0.632176	0.832782
13142	10574100					0.945	-0.584	0.57677	0.797659
13143	10377181	NM_001081250	544791	myosin, heavy polypeptide 13,	Myh13	0.945	-0.74	0.482782	0.731475
13144	10568873	NM_007403	11501	a disintegrin and metallopepti	Adam8	0.945	-1.091	0.310197	0.586865
13145	10378754	NM_027773	116972	RIKEN cDNA 2310047D13 gene	2310047D13Rik	0.945	-1.055	0.3256	0.601936
13146	10480492	NM_001042528	12287	calcium channel, voltage-depen	Cacna1b	0.945	-0.473	0.650149	0.843113
13147	10523979	NM_008806	18587	phosphodiesterase 6B, cGMP, ro	Pde6b	0.945	-1.129	0.295072	0.571337
13148	10367393	NM_030100	78428	within bgcn homolog (Drosophil	Wibg	0.945	-1.276	0.241426	0.514329
13149	10478415	NM_016873	22403	WNT1 inducible signaling pathw	Wisp2	0.945	-0.352	0.734924	0.886784
13150	10416195	NM_010921	18095	NK-3 transcription factor, loc	Nkx3-1	0.945	-0.617	0.556245	0.784737
13151	10394527	NM_029321	75516	tetratricopeptide repeat domai	Ttc32	0.945	-1.263	0.245927	0.51897
13152	10472589	NM_028521	73373	phosphatase, orphan 2	Phospho2	0.945	-0.971	0.363171	0.63441
13153	10418895	NM_001013777	382867	zinc finger protein 488	Zfp488	0.945	-1.255	0.248471	0.521974
13154	10520923	NM_001081407	665270	phospholipase B1	Plb1	0.945	-0.595	0.570191	0.794629
13155	10578027	NM_026453	67920	RNA binding motif protein 13	Rbm13	0.945	-1.437	0.192731	0.452222
13156	10572070	NM_010934	18166	neuropeptide Y receptor Y1	Npy1r	0.945	-0.634	0.545924	0.777622
13157	10559238	NR_002855	111975	insulin-like growth factor 2,	Igf2as	0.945	-1.445	0.190362	0.44932
13158	10392715	NM_138598	28081	DNA segment, Chr 11, Wayne Sta	D11Wsu99e	0.945	-1.453	0.188212	0.446289
13159	10398881	ENSMUST00000037962	382639	predicted gene, EG382639	EG382639	0.945	-0.415	0.690154	0.864031
13160	10533261	NM_011286	19894	rabphilin 3A	Rph3a	0.945	-0.864	0.415188	0.678399
13161	10474399	NM_001048139	12064	brain derived neurotrophic fac	Bdnf	0.945	-0.682	0.516311	0.755598
13162	10459927	ENSMUST00000077962	240444	potassium voltage-gated channe	Kcng2	0.945	-1.163	0.281905	0.557053
13163	10470214	NM_175462	227632	potassium channel, subfamily T	Kcnt1	0.945	-0.302	0.771393	0.905701

13164	10420532	NM_015803	50769	ATPase, aminophospholipid tran	Atp8a2	0.945	-0.512	0.624262	0.828379
13165	10567041	ENSMUST00000098100	434228	predicted gene, EG434228	EG434228	0.945	-0.276	0.790274	0.914539
13166	10543650	NM_177296	320938	transportin 3	Tnpo3	0.944	-1.564	0.160649	0.408266
13167	10529711	NM_013748	27278	cytokine-dependent hematopoiet	Clnk	0.944	-0.29	0.779872	0.910713
13168	10531729	NM_027978	71883	coenzyme Q2 homolog, prenyltra	Coq2	0.944	-1.435	0.193115	0.452493
13169	10395376	NM_146033	217473	ankyrin repeat and MYND domain	Ankmy2	0.944	-0.894	0.399954	0.665979
13170	10509113	NM_010178	14105	FUS interacting protein (serin	Fusip1	0.944	-0.747	0.478572	0.729081
13171	10440985	NM_029252	75328	RIKEN cDNA 4930563D23 gene	4930563D23Rik	0.944	-1.155	0.285006	0.560313
13172	10443195	NM_016660	15361	high mobility group AT-hook 1	Hmga1	0.944	-1.002	0.348598	0.622215
13173	10447933					0.944	-0.959	0.368667	0.639361
13174	10491915	NM_009834	12457	CCR4 carbon catabolite repress	Ccrn4l	0.944	-1.164	0.281339	0.556831
13175	10438639	NM_138650	110197	diacylglycerol kinase, gamma	Dgkg	0.944	-0.859	0.418092	0.680624
13176	10576490					0.944	-0.36	0.728972	0.882586
13177	10472930	NM_001005343	381373	trans-acting transcription fac	Sp9	0.944	-0.897	0.398561	0.66476
13178	10584120					0.944	-0.519	0.619141	0.824741
13179	10603738	NM_026128	67395	RIKEN cDNA 4930403L05 gene	4930403L05Rik	0.944	-0.458	0.660337	0.848652
13180	10455578	NM_178377	69456	COMM domain containing 10	Commd10	0.944	-1.497	0.176759	0.430877
13181	10532744	NM_009151	20345	selectin, platelet (p-selectin	Selplg	0.944	-0.348	0.737915	0.88827
13182	10568916	NM_010836	17703	homeobox, msh-like 3	Msx3	0.944	-1.128	0.295524	0.57195
13183	10378768	NM_183263	67390	RNA methyltransferase like 1	Rnmtl1	0.944	-1.208	0.265062	0.540178
13184	10460987	NM_020253	18190	neurexin II	Nrxn2	0.944	-0.602	0.56565	0.791744
13185	10528877	NM_020295	56873	limb region 1	Lmbr1	0.944	-1.776	0.117778	0.3424
13186	10461640					0.944	-1.142	0.290046	0.566261
13187	10576152	NM_021502	59005	trafficking protein particle c	Trappc2l	0.944	-1.02	0.340856	0.615921
13188	10583903					0.944	-0.717	0.495683	0.74053
13189	10481451	BC062268	67350	RIKEN cDNA 1700084E18 gene	1700084E18Rik	0.944	-0.824	0.436459	0.696302
13190	10526882	NM_001081265	433956	HEAT repeat containing 2	Heatr2	0.944	-0.762	0.470047	0.72213
13191	10406968	NM_021790	60411	centromere protein K	Cenpk	0.944	-1.539	0.166426	0.417266
13192	10406843					0.944	-0.823	0.436888	0.696333
13193	10592050	NM_013800	12023	BarH-like homeobox 2	Barx2	0.944	-0.314	0.762366	0.901088
13194	10580309	NM_026399	67836	RIKEN cDNA 1500041N16 gene	1500041N16Rik	0.944	-0.825	0.435555	0.695606
13195	10364702	NM_021565	59090	midnolin	Midn	0.944	-1.098	0.307661	0.584211
13196	10530041	ENSMUST00000064097	211001	RIKEN cDNA 8030423F21 gene	8030423F21Rik	0.944	-0.981	0.358484	0.630584
13197	10490913	NM_007606	12350	carbonic anhydrase 3	Car3	0.944	-0.439	0.673724	0.855069
13198	10453740					0.944	-0.422	0.685623	0.861122
13199	10458033	NM_133774	170459	StAR-related lipid transfer (S	Stard4	0.944	-1.448	0.189669	0.44816
13200	10545075					0.944	-0.397	0.702512	0.869514
13201	10364287	NM_019929	20610	SMT3 suppressor of mif two 3 h	Sumo3	0.944	-1.168	0.28012	0.55551
13202	10374348	XR_032931	432537	similar to Elongation factor 2	LOC432537	0.944	-0.994	0.35228	0.625281
13203	10516487	NM_008127	14621	gap junction protein, beta 4	Gjb4	0.944	-0.188	0.855694	0.941646
13204	10355974	NM_001111279	69368	WD repeat and FYVE domain cont	Wdfy1	0.944	-1.302	0.232798	0.503816
13205	10390072					0.944	-0.544	0.603149	0.814471
13206	10405924					0.944	-0.586	0.575864	0.797128
13207	10346310	NM_025283	19070	MOB1, Mps One Binder kinase ac	Mobkl3	0.944	-1.114	0.301128	0.5773
13208	10484733	XM_621554	546769	olfactory receptor 1174	Olfr1174	0.944	-0.189	0.85495	0.941302
13209	10531664					0.944	-0.259	0.802604	0.919965
13210	10544638	AB052758	101214	transformer 2 alpha homolog (D	Tra2a	0.944	-0.941	0.376991	0.647069
13211	10536658	NM_053116	93735	wingless-related MMTV integrat	Wnt16	0.944	-0.817	0.43982	0.699109
13212	10560315	NM_011155	19060	protein phosphatase 5, catalyt	Ppp5c	0.944	-1.037	0.333057	0.609184
13213	10580131	NM_194059	244551	nanos homolog 3 (Drosophila)	Nanos3	0.944	-1.194	0.270298	0.545133
13214	10372488	NM_133683	67226	transmembrane protein 19	Tmem19	0.944	-1.127	0.29571	0.572101

13215	10544805	NM_008264	15398	homeo box A13	Hoxa13	0.944	-0.833	0.451336	0.691897
13216	10591658					0.944	-1.046	0.329489	0.605855
13217	10489451	NM_017390	53878	seminal vesicle secretory prot	Svs2	0.944	-0.796	0.451335	0.708496
13218	10486241	NM_172857	241624	exonuclease 3'-5' domain-like	Exdl1	0.944	-0.632	0.547025	0.778141
13219	10383472	NM_133223	170758	RAS-related C3 botulinum subst	Rac3	0.944	-0.531	0.611102	0.819454
13220	10557262	NM_146198	233836	solute carrier family 5 (sodiu	Slc5a11	0.944	-0.497	0.633764	0.833492
13221	10385993					0.944	-0.306	0.768261	0.903705
13222	10438555	NM_009379	21832	thrombopoietin	Thpo	0.944	-1.023	0.339196	0.614614
13223	10562774	AY761096	69683	RIKEN cDNA 2310044H10 gene	2310044H10Rik	0.944	-1.422	0.196929	0.457727
13224	10527184	AK144491	67672	RIKEN cDNA 0610040B10 gene	0610040B10Rik	0.944	-1.017	0.342082	0.61636
13225	10558795	NM_019762	56460	plakophilin 3	Pkp3	0.944	-0.676	0.519829	0.757566
13226	10390927	NM_029613	76444	keratin associated protein 4-7	Krtap4-7	0.944	-0.383	0.712516	0.874059
13227	10418016	NM_001007268	27389	dual specificity phosphatase 1	Dusp13	0.943	-0.733	0.486723	0.734514
13228	10462618	NM_010501	15959	interferon-induced protein wit	Ifit3	0.943	-0.29	0.779611	0.910547
13229	10566290					0.943	-0.953	0.371403	0.64202
13230	10532164	ENSMUST00000049628	11958	ATP synthase, H+ transporting,	Atp5k	0.943	-1.504	0.175092	0.428242
13231	10413813	NM_030166	78754	UDP-N-acetyl-alpha-D-galactosa	Galntl2	0.943	-0.43	0.679564	0.857705
13232	10507798	NM_008506	16918	v-myc myelocytomatosis viral o	Mycl1	0.943	-1.646	0.14245	0.38247
13233	10352914	AK171382	320400	RIKEN cDNA A330023F24 gene	A330023F24Rik	0.943	-0.875	0.409831	0.674303
13234	10398665	NM_009396	21928	tumor necrosis factor, alpha-i	Tnfaip2	0.943	-1.223	0.2598	0.53415
13235	10357932	NM_001081307	329251	protein phosphatase 1, regulat	Ppp1r12b	0.943	-0.263	0.799675	0.919181
13236	10477673	NM_001085378	668940	myosin, heavy chain 7B, cardia	Myh7b	0.943	-1.02	0.340684	0.615782
13237	10559694	ENSMUST00000032598	381836	gene model 1079, (NCBI)	Gm1079	0.943	-0.823	0.436704	0.696302
13238	10597513					0.943	-0.59	0.572951	0.796481
13239	10353028	NM_173443	70675	valosin containing protein (p9	Vcpip1	0.943	-1.532	0.168094	0.4195
13240	10443215	NM_011432	20630	U1 small nuclear ribonucleopro	Snrpc	0.943	-1.118	0.299325	0.575408
13241	10569870	NM_022984	57264	resistin	Retn	0.943	-0.463	0.657052	0.846548
13242	10558295	ENSMUST00000106157	360216	zinc finger, RAN-binding domai	Zranb1	0.943	-1.025	0.338688	0.614222
13243	10517436	NM_025411	66193	RIKEN cDNA 1110049F12 gene	1110049F12Rik	0.943	-1.307	0.231222	0.501993
13244	10393851	NM_024229	68671	phosphate cytidylyltransferase	Pcyt2	0.943	-1.441	0.19144	0.450707
13245	10383819	NM_144520	67815	SEC14-like 2 (S. cerevisiae)	Sec14l2	0.943	-0.608	0.561916	0.788974
13246	10571170	NM_173212	108043	cholinergic receptor, nicotini	Chrnb3	0.943	-1.241	0.25338	0.527654
13247	10535771	NM_007673	12591	caudal type homeo box 2	Cdx2	0.943	-0.484	0.64262	0.838146
13248	10399687					0.943	-0.622	0.553111	0.782691
13249	10470547	NM_080452	118451	mitochondrial ribosomal protei	Mrps2	0.943	-1.615	0.149184	0.391598
13250	10572301	NM_008578	17259	myocyte enhancer factor 2B	Mef2b	0.943	-1.793	0.11479	0.336959
13251	10363905	NM_025635	52696	ZW10 interactor	Zwint	0.943	-1.115	0.300681	0.576863
13252	10470788	NM_001113213	18286	outer dense fiber of sperm tai	Odf2	0.943	-1.283	0.239089	0.511826
13253	10414175	XM_001474680	100040439	similar to isolog of yeast sui	LOC100040439	0.943	-1.044	0.330285	0.606542
13254	10410279	ENSMUST00000091526	432769	zinc finger protein 708	Zfp708	0.943	-0.603	0.564675	0.790747
13255	10578191					0.943	-0.95	0.372727	0.643093
13256	10568011	AK153779	68681	RIKEN cDNA 1110030E23 gene	1110030E23Rik	0.943	-0.38	0.71456	0.875126
13257	10566264	ENSMUST00000106866	436003	predicted gene, EG436003	EG436003	0.943	-0.405	0.697487	0.867333
13258	10366519	AK077360	327824	RIKEN cDNA 5330438D12 gene	5330438D12Rik	0.943	-0.659	0.530634	0.765382
13259	10558600	NM_199301	212508	mitochondrial GTPase 1 homolog	Mtg1	0.943	-1.756	0.121226	0.347818
13260	10438575	NM_023737	74147	enoyl-Coenzyme A, hydratase/3-	Ehhadh	0.943	-0.6	0.56658	0.792358
13261	10388296	NM_146710	258705	olfactory receptor 398	Olfr398	0.943	-0.592	0.571838	0.79598
13262	10547513	NM_144815	214932	cat eye syndrome chromosome re	Cecr5	0.943	-0.487	0.640958	0.837375
13263	10493076	NM_021309	27371	SH2 domain protein 2A	Sh2d2a	0.943	-1.156	0.284521	0.559679
13264	10444505	NM_001045864	27632	RD RNA-binding protein	Rdbp	0.943	-1.995	0.0850371	0.280082
13265	10522024	NM_019636	57915	TBC1 domain family, member 1	Tbc1d1	0.943	-0.737	0.484637	0.733146
13266	10389754	NM_172534	214604	RIKEN cDNA 4932411E22 gene	4932411E22Rik	0.943	-0.198	0.848597	0.938624
13267	10511588	NM_177861	329795	transmembrane protein 67	Tmem67	0.943	-1.177	0.276454	0.551448

13268	10552540	NM_174865	317652	kallikrein related-peptidase 1	Klk15	0.943	-0.326	0.753533	0.896207
13269	10390319	NM_027026	69297	leucine rich repeat containing	Lrrc46	0.943	-1.127	0.295815	0.572251
13270	10471569					0.943	-1.276	0.241541	0.514365
13271	10450682	NM_010398	15040	histocompatibility 2, T region	H2-T23	0.943	-0.625	0.55152	0.781591
13272	10491753	NM_175515	380614	inturned planar cell polarity	Intu	0.943	-1.495	0.177283	0.431715
13273	10440708	XM_925382	621595	keratin associated protein 19-	Krtap19-7	0.943	-0.468	0.653761	0.844785
13274	10537826	NM_146653	258647	olfactory receptor 435	Olfr435	0.943	-0.934	0.380542	0.650143
13275	10437243	NM_019453	54483	Mediterranean fever	Mefv	0.943	-0.709	0.500367	0.743431
13276	10598456	NM_138604	54644	OTU domain containing 5	Otud5	0.943	-1.562	0.161089	0.40899
13277	10500218	NM_027931	71807	threonyl-tRNA synthetase 2, mi	Tars2	0.943	-0.697	0.507613	0.749509
13278	10361882	NM_173390	215819	NHS-like 1	Nhsl1	0.943	-1.388	0.206634	0.47111
13279	10348775	NM_023200	66385	protein phosphatase 1, regulat	Ppp1r7	0.943	-1.051	0.327308	0.603524
13280	10471443	NM_198191	227733	phosphatidylinositol-4-phospha	Pip5kl1	0.943	-0.881	0.406781	0.671322
13281	10492662					0.943	-1.047	0.328991	0.605314
13282	10427323	NM_019817	56447	coatomer protein complex, subu	Copz1	0.943	-0.835	0.43028	0.691063
13283	10401283	ENSMUST00000056602	68354	RIKEN cDNA 0610009B14 gene	0610009B14Rik	0.943	-0.741	0.48211	0.730954
13284	10371293	ENSMUST00000079648	544717	RIKEN cDNA 1190007I07 gene	1190007I07Rik	0.943	-0.455	0.662618	0.849733
13285	10576249	NM_177279	320869	RIKEN cDNA 4732415M23 gene	4732415M23Rik	0.943	-1.2	0.268013	0.542786
13286	10457967	NM_032394	17922	myosin VIIb	Myo7b	0.943	-0.524	0.615697	0.822286
13287	10494452	NM_001102407	60365	RNA binding motif protein 8a	Rbm8a	0.943	-1.111	0.30231	0.578465
13288	10450384	NM_013600	17687	mutS homolog 5 (E. coli)	Msh5	0.943	-0.582	0.578397	0.798316
13289	10376755	NM_021349	57916	tumor necrosis factor receptor	Tnfrsf13b	0.943	-0.798	0.450202	0.707462
13290	10607475	NM_016764	53381	peroxiredoxin 4	Prdx4	0.943	-2.068	0.0762992	0.261682
13291	10552740	NM_053074	18226	nucleoporin 62	Nup62	0.943	-1.27	0.243387	0.51639
13292	10393239					0.943	-1.068	0.319847	0.596635
13293	10488558	NM_198214	241727	syntaphilin	Snph	0.943	-0.934	0.380519	0.650143
13294	10369116	NM_027830	71567	minichromosome maintenance com	Mcm9	0.943	-0.87	0.412456	0.676163
13295	10417946	AK018074	76133	RIKEN cDNA 6230400D17 gene	6230400D17Rik	0.943	-1.169	0.279445	0.554692
13296	10442786	NM_010781	17229	tryptase beta 2	Tpsb2	0.943	-0.923	0.385616	0.654706
13297	10452525	NM_028388	72900	NADH dehydrogenase (ubiquinone	Ndufv2	0.943	-1.695	0.132712	0.366423
13298	10406672	NM_009712	11881	arylsulfatase B	Arsb	0.943	-1.179	0.275887	0.550733
13299	10490352	NM_001081092	228980	TAF4A RNA polymerase II, TATA	Taf4a	0.943	-0.491	0.637831	0.835893
13300	10510150	BC085112	433804	predicted gene, OTTMUSG0000001	OTTMUSG00000010673	0.943	-1.035	0.33409	0.609656
13301	10472649	NM_177376	329421	myosin IIIB	Myo3b	0.943	-0.502	0.630481	0.831639
13302	10429298	NM_180662	76510	trafficking protein particle c	Trappc9	0.943	-1.204	0.266603	0.541262
13303	10407097	NM_011056	238871	phosphodiesterase 4D, cAMP spe	Pde4d	0.943	-0.828	0.434277	0.694762
13304	10374821	NM_134034	104570	SMEK homolog 2, suppressor of	Smek2	0.943	-1.315	0.22885	0.499928
13305	10599663	BC115663	75013	RIKEN cDNA 4930502E18 gene	4930502E18Rik	0.943	-0.345	0.740133	0.889339
13306	10461826					0.943	-0.219	0.832373	0.932679
13307	10443087					0.943	-0.541	0.604543	0.815416
13308	10377473	NM_011786	23801	arachidonate lipoxygenase 3	Aloxe3	0.943	-0.424	0.683619	0.859974
13309	10505614	NM_031202	22178	tyrosinase-related protein 1	Tyrp1	0.943	-0.491	0.638208	0.835923
13310	10432281	NM_016781	19082	protein kinase, AMP-activated,	Prkag1	0.943	-0.938	0.378395	0.648204
13311	10553092	NM_016974	13170	D site albumin promoter bindin	Dbp	0.942	-0.927	0.384054	0.653452
13312	10458138	NM_030147	78656	bromodomain containing 8	Brd8	0.942	-1.405	0.201628	0.464202
13313	10436041					0.942	-1.528	0.169009	0.420416
13314	10450948	BC132063	71583	RIKEN cDNA 9130008F23 gene	9130008F23Rik	0.942	-0.993	0.352692	0.625772
13315	10400299	NM_008159	14762	G protein-coupled receptor 33	Gpr33	0.942	-0.366	0.724521	0.880619
13316	10394068	NM_145373	209588	secreted and transmembrane 1A	Sectm1a	0.942	-0.318	0.759833	0.899364
13317	10417124	BC096543	320268	RIKEN cDNA B930095G15	B930095G15Rik	0.942	-0.788	0.456061	0.712435

				gene				
13318	10571680	NM_027973	71876	myeloid leukemia factor 1 inte	Mlf1ip	0.942	-1.216	0.262417	0.536908
13319	10364317					0.942	-0.36	0.728976	0.882586
13320	10532937	NM_175352	106840	unc-119 homolog B (C. elegans)	Unc119b	0.942	-1.196	0.269586	0.544449
13321	10450508	NM_010735	16992	lymphotoxin A	Lta	0.942	-0.139	0.893024	0.957774
13322	10520869	NM_001081407	665270	phospholipase B1	Plb1	0.942	-0.754	0.474787	0.726456
13323	10447786	NM_009202	20517	solute carrier family 22 (orga	Slc22a1	0.942	-0.85	0.422727	0.68502
13324	10489151	NM_001039557	629499	RIKEN cDNA 4922505G16 gene	4922505G16Rik	0.942	-0.947	0.37424	0.644376
13325	10354803					0.942	-0.881	0.40654	0.671151
13326	10369920	BC055322	192734	expressed sequence AI646023	AI646023	0.942	-0.969	0.364067	0.635449
13327	10571763	ENSMUST00000033963	75359	RIKEN cDNA 4930555F03 gene	4930555F03Rik	0.942	-0.631	0.547489	0.778461
13328	10463505	NM_172639	226162	RIKEN cDNA 5330431N19 gene	5330431N19Rik	0.942	-0.829	0.433633	0.694075
13329	10364932	NM_001081688	432478	transmembrane protease, serine	Tmprss9	0.942	-0.974	0.361601	0.633308
13330	10388786	NM_009297	20926	suppressor of Ty 6 homolog (S.	Supt6h	0.942	-1.44	0.191835	0.451135
13331	10472630	NM_001081548	68795	zinc finger protein 650	Zfp650	0.942	-1.568	0.159648	0.407016
13332	10504072	NM_175138	68922	dynein, axonemal, intermediate	Dnaic1	0.942	-1.67	0.137632	0.374771
13333	10399579	ENSMUST00000075542	69513	RIKEN cDNA 1700030C10 gene	1700030C10Rik	0.942	-0.724	0.492042	0.738272
13334	10545271	NM_178413	232078	threonine synthase-like 2 (bac	Thnsl2	0.942	-0.557	0.594331	0.808582
13335	10390050	NM_177752	268465	essential meiotic endonuclease	Eme1	0.942	-1.27	0.243491	0.51649
13336	10428124	XM_891200	626596	regulator of G-protein signall	Rgs22	0.942	-0.734	0.485994	0.734018
13337	10399593	NM_008403	16413	integrin beta 1 binding protei	Itgb1bp1	0.942	-0.751	0.476285	0.727471
13338	10419465	NM_001111119	239083	cyclin B1 interacting protein	Ccnb1ip1	0.942	-0.341	0.742487	0.890277
13339	10568339	NM_001081374	77613	protease, serine, 36	Prss36	0.942	-0.507	0.627083	0.830395
13340	10589955					0.942	-0.66	0.529861	0.765154
13341	10531633	NM_001077265	11991	heterogeneous nuclear ribonucl	Hnrnpd	0.942	-1.457	0.187108	0.445468
13342	10529154	ENSMUST00000068997	621407	predicted gene, ENSMUSG0000005	ENSMUSG00000055424	0.942	-0.821	0.437762	0.696939
13343	10541290	NM_028730	74043	peroxisome biogenesis factor 2	Pex26	0.942	-1.068	0.320169	0.596972
13344	10586240	XM_001476259	102442	DENN/MADD domain containing 4A	Dennd4a	0.942	0.082	0.936901	0.975366
13345	10533213	NM_145226	246727	2'-5' oligoadenylate synthetas	Oas3	0.942	-0.292	0.778628	0.909988
13346	10421661	NM_026816	68705	general transcription factor I	Gtf2f2	0.942	-0.847	0.423949	0.686158
13347	10394358	BC068281	238037	cDNA sequence BC068281	BC068281	0.942	-0.819	0.439206	0.698449
13348	10606941	NM_001037915	622473	ripply1 homolog (zebrafish)	Ripply1	0.942	-0.56	0.592379	0.807145
13349	10524234	NM_198306	231605	UDP-N-acetyl-alpha-D-galactosa	Galnt9	0.942	-0.924	0.385463	0.654637
13350	10478432	NM_001114079	381404	RIKEN cDNA 1810053B01 gene	1810053B01Rik	0.942	-1.106	0.304057	0.58039
13351	10490621	NM_011481	20811	src-related kinase lacking C-t	Srms	0.942	-0.283	0.785485	0.912507
13352	10477852	XM_001481161	632394	similar to Rpl37a protein	LOC632394	0.942	-1.305	0.231909	0.502663
13353	10605355					0.942	-0.358	0.730462	0.883456
13354	10515431	NM_134471	73804	kinesin family member 2C	Kif2c	0.942	-1.123	0.297572	0.573709
13355	10413930	BC117714	105511	RIKEN cDNA 4922501K12 gene	4922501K12Rik	0.942	-0.477	0.647673	0.841423
13356	10444298	NM_010382	14969	histocompatibility 2, class II	H2-Eb1	0.942	-0.303	0.770375	0.905061
13357	10473219					0.942	-0.118	0.908998	0.963765
13358	10389654	NM_007946	13861	eosinophil peroxidase	Epx	0.942	-0.898	0.398247	0.664555
13359	10486203	NM_026574	68142	INO80 complex homolog 1 (S. ce	Inoc1	0.942	-1.454	0.188094	0.446224
13360	10489341					0.942	-0.349	0.737033	0.887765
13361	10465260	NM_198634	332359	tigger transposable element de	Tigd3	0.942	-0.699	0.506215	0.74808
13362	10446679	AY820307	70891	speedy homolog A (Drosophila)	Spdya	0.942	-2.422	0.0449439	0.187583
13363	10505438	NM_008768	18405	orosomucoid 1	Orm1	0.942	-0.29	0.77999	0.910713
13364	10354216	AK133372	619289	RIKEN cDNA 4933400N17 gene	4933400N17Rik	0.942	-0.301	0.771739	0.905831
13365	10518163					0.942	-1.119	0.29908	0.575096
13366	10447437	NM_028658	73825	coiled-coil domain containing	Ccdc128	0.942	-1.526	0.169484	0.420889

13367	10402864	BC018315	16019	immunoglobulin heavy chain 6 (	Igh-6	0.942	-0.843	0.426417	0.687967
13368	10436206	ENSMUST00000023314	78639	RIKEN cDNA 1700116B05 gene	1700116B05Rik	0.942	-0.469	0.652858	0.844541
13369	10360540	AK015919	75164	RIKEN cDNA 4930527J03 gene	4930527J03Rik	0.942	-0.879	0.407531	0.671878
13370	10502961	NM_010713	16875	LIM homeobox protein 8	Lhx8	0.942	-1.119	0.298875	0.574963
13371	10428002	ENSMUST00000075576	67434	RIKEN cDNA 5730557B15 gene	5730557B15Rik	0.942	-0.649	0.536315	0.769429
13372	10568374	NM_177001	100043133	RIKEN cDNA 9130023H24 gene	9130023H24Rik	0.942	-1.311	0.230157	0.501074
13373	10384373	NM_021891	60530	fidgetin-like 1	Fignl1	0.941	-1.231	0.256834	0.531151
13374	10558468	BC119557	74004	RIKEN cDNA 6330417G02 gene	6330417G02Rik	0.941	-0.677	0.519685	0.757547
13375	10411927	NM_026072	67285	serologically defined colon ca	Sdccag10	0.941	-1.631	0.14559	0.387145
13376	10536746	NM_007480	11844	ADP-ribosylation factor 5	Arf5	0.941	-1.082	0.314059	0.590842
13377	10425265	ENSMUST00000100455	100038350	predicted gene, ENSMUSG0000007	ENSMUSG00000075555	0.941	-0.743	0.480967	0.730572
13378	10360306	NM_029084	74748	SLAM family member 8	Slamf8	0.941	-0.56	0.592342	0.807145
13379	10498413					0.941	-0.903	0.39587	0.663413
13380	10552444	NM_028913	74400	zinc finger protein 819	Zfp819	0.941	-0.81	0.444015	0.702635
13381	10495371	ENSMUST00000062935	329738	RIKEN cDNA 4921525H12 gene	4921525H12Rik	0.941	-0.809	0.444198	0.702635
13382	10360324	XR_030924	100045972	similar to high mobility group	LOC100045972	0.941	-0.858	0.41824	0.680775
13383	10426991	NM_144790	208258	ankyrin repeat domain 33	Ankrd33	0.941	-0.953	0.371307	0.64202
13384	10557754	NM_198424	269999	ORAI calcium release-activated	Orai3	0.941	-1.156	0.284663	0.559847
13385	10495592					0.941	-0.776	0.462248	0.716783
13386	10571065	NM_008432	16532	potassium channel, subfamily U	Kcnu1	0.941	-0.845	0.425388	0.68733
13387	10400383	BC056967	72658	RIKEN cDNA 2700097O09 gene	2700097O09Rik	0.941	-1.072	0.318414	0.595538
13388	10357604	NM_019777	56489	inhibitor of kappaB kinase eps	Ikbke	0.941	-0.988	0.355067	0.627756
13389	10397561	NM_028105	72113	aarF domain containing kinase	Adck1	0.941	-1.057	0.324617	0.601113
13390	10392241	NM_015810	50776	polymerase (DNA directed), gam	Polg2	0.941	-0.473	0.650159	0.843113
13391	10512621	NM_019485	56014	olfactory receptor 70	Olfr70	0.941	-0.619	0.554869	0.783816
13392	10515755	NM_001122949	17480	myeloproliferative leukemia vi	Mpl	0.941	-0.406	0.696202	0.866574
13393	10379346	NM_199196	52615	suppressor of zeste 12 homolog	Suz12	0.941	-1.466	0.184944	0.44255
13394	10591726	NM_012029	26940	ECSIT homolog (Drosophila)	Ecsit	0.941	-1.295	0.235246	0.50678
13395	10517081	XM_620107	545683	similar to ribosomal protein	LOC545683	0.941	-0.745	0.480041	0.729941
13396	10432215	NM_001080981	74351	DEAD (Asp-Glu-Ala-Asp) box pol	Ddx23	0.941	-1.932	0.0934656	0.296462
13397	10562729					0.941	-0.9	0.397287	0.664261
13398	10486107	NM_009273	20813	signal recognition particle 14	Srp14	0.941	-1.122	0.297829	0.573889
13399	10544542	NM_177882	330301	zinc finger protein 786	Zfp786	0.941	-0.733	0.486811	0.734594
13400	10378030	ENSMUST00000100923	619299	RIKEN cDNA 9230020A06 gene	9230020A06Rik	0.941	-0.949	0.373174	0.64348
13401	10430400	NM_130859	105844	caspase recruitment domain fam	Card10	0.941	-0.853	0.421088	0.683517
13402	10377240	ENSMUST00000084600	544792	similar to hCG1653800	LOC544792	0.941	-0.45	0.666223	0.851266
13403	10475767	NM_175145	69470	transmembrane protein 127	Tmem127	0.941	-1.216	0.262415	0.536908
13404	10585535	NM_027397	104360	insulin related protein 2 (isl	Isl2	0.941	-0.982	0.35801	0.630288
13405	10470050	NM_007379	11305	ATP-binding cassette, sub-fami	Abca2	0.941	-0.987	0.355378	0.628032
13406	10540705	NM_134159	171095	interleukin 17 receptor C	Il17rc	0.941	-0.708	0.501238	0.744202
13407	10416666	NM_026474	67955	SGT1, suppressor of G2 allele	Sugt1	0.941	-1.845	0.106327	0.321598
13408	10457091	NM_144946	246317	neuropilin (NRP) and tolloid (	Neto1	0.941	-0.601	0.566293	0.79227
13409	10529605	NM_011716	22393	Wolfram syndrome 1 homolog (hu	Wfs1	0.941	-1.439	0.192228	0.451559
13410	10537343	BC104375	77522	RIKEN cDNA D630002J15 gene	D630002J15Rik	0.941	-0.45	0.665937	0.851154
13411	10423740					0.941	-0.591	0.572699	0.796287
13412	10528617	NM_015739	231044	gastrulation brain homeobox 1	Gbx1	0.941	-1.457	0.187325	0.445668
13413	10385642	BC118537	214779	RIKEN cDNA 9630041N07 gene	9630041N07Rik	0.941	-0.828	0.434354	0.694762
13414	10448192	XR_033753	624960	similar to Y box transcription	LOC624960	0.941	-1.205	0.266173	0.541183
13415	10402575	NM_027299	70059	degenerative spermatocyte homo	Degs2	0.941	0.969	0.364099	0.635452

13415	10402575	NM_027299	70059	degenerative spermatocyte homo	Degs2	0.941	-0.969	0.364099	0.655452
13416	10383342	ENSMUST00000050697	66838	RIKEN cDNA 0610009L18 gene	0610009L18Rik	0.941	-0.902	0.396227	0.663741
13417	10597459	XR_034079	665772	similar to ribosomal protein S	LOC665772	0.941	-1.646	0.142395	0.38242
13418	10368370	XR_032337	667519	similar to high mobility group	LOC667519	0.941	-0.881	0.406736	0.671301
13419	10606180	NM_001045541	621818	predicted gene, ENSMUSG0000004	ENSMUSG00000043661	0.941	-0.322	0.756676	0.897871
13420	10396442	NM_178392	75627	small nuclear RNA activating c	Snapc1	0.941	-1.001	0.349329	0.622835
13421	10425223	NM_015738	14429	galanin receptor 3	Galr3	0.941	-1.206	0.265989	0.54117
13422	10601551	ENSMUST00000055309	100039300	similar to enhancer of yellow	LOC100039300	0.941	-0.91	0.392361	0.660367
13423	10538704					0.941	-0.654	0.533454	0.767511
13424	10552121	NM_009596	11354	androgen binding protein alpha	Abpa	0.941	-0.293	0.777757	0.909562
13425	10600781	XM_994395	245516	predicted gene, EG245516	EG245516	0.941	-0.407	0.6956	0.866211
13426	10393844	NM_011568	21681	THO complex 4	Thoc4	0.941	-1.3	0.233715	0.505106
13427	10558533					0.941	-1.171	0.278981	0.554016
13428	10478554	NM_001040055	641368	predicted gene, OTTMUSG0000001	OTTMUSG00000016293	0.941	-0.591	0.572606	0.796254
13429	10551587	BC046530	320435	RIKEN cDNA 5830482F20 gene	5830482F20Rik	0.941	-0.732	0.487177	0.734936
13430	10393580	NM_029502	76025	calcium activated nucleotidase	Cant1	0.941	-0.858	0.418688	0.68129
13431	10421567	NM_172527	214254	nudix (nucleoside diphosphate	Nudt15	0.941	-0.282	0.785541	0.912507
13432	10377984	NM_177565	193043	zinc finger protein 3	Zfp3	0.941	-1.733	0.12544	0.354707
13433	10583310	BC056964	75316	Josephin domain containing 3	Josd3	0.941	-0.483	0.643748	0.838761
13434	10429440	AK132992	268816	gene model 628, (NCBI)	Gm628	0.941	-0.451	0.665206	0.850823
13435	10521984	NM_019468	14380	glucose-6-phosphate dehydrogen	G6pd2	0.941	-1.247	0.251476	0.525513
13436	10478754	NM_001085495	99371	ADP-ribosylation factor guanin	Arfgef2	0.941	-0.7	0.505817	0.747682
13437	10439268	NM_001013371	209200	deltex 3-like (Drosophila)	Dtx3l	0.941	-1.602	0.151846	0.395645
13438	10372478	NM_024454	216344	RAB21, member RAS oncogene fam	Rab21	0.941	-1.435	0.193159	0.452493
13439	10477808	NM_025946	67067	RIKEN cDNA 2010100O12 gene	2010100O12Rik	0.941	-1.771	0.118671	0.344006
13440	10367471	NM_146861	18373	olfactory receptor 9	Olfr9	0.941	-0.445	0.669154	0.852809
13441	10568266	BC066021	233899	gene model 166, (NCBI)	Gm166	0.941	-0.823	0.436678	0.696302
13442	10533612	NM_008277	15445	4-hydroxyphenylpyruvic acid di	Hpd	0.94	-0.065	0.949712	0.980608
13443	10515072	NM_013876	29864	ring finger protein 11	Rnf11	0.94	-1.888	0.0997229	0.308614
13444	10552656	NM_016663	20981	synaptotagmin III	Syt3	0.94	-0.654	0.533198	0.767248
13445	10345423	NM_145516	226971	pleckstrin homology domain con	Plekhb2	0.94	-1.859	0.104067	0.317243
13446	10490150	NM_021394	58203	Z-DNA binding protein 1	Zbp1	0.94	-1.044	0.330351	0.606543
13447	10370991	NM_028001	71912	junctional sarcoplasmic reticu	Jsrp1	0.94	-1.674	0.136698	0.373246
13448	10356568	NM_008998	19329	RAB17, member RAS oncogene fam	Rab17	0.94	-0.735	0.48567	0.733972
13449	10480937	ENSMUST00000115988	77481	RIKEN cDNA C030048H21 gene	C030048H21Rik	0.94	-0.566	0.588563	0.805172
13450	10352829	BC055955	319266	RIKEN cDNA A130010J15 gene	A130010J15Rik	0.94	-1.284	0.238918	0.511718
13451	10529385	NM_001015039	231125	zinc finger, FYVE domain conta	Zfyve28	0.94	-0.747	0.478565	0.729081
13452	10409796	ENSMUST00000055343	74224	RIKEN cDNA 1700014D04 gene	1700014D04Rik	0.94	-0.747	0.478656	0.729103
13453	10390705	NM_178596	353155	gap junction protein, delta 3	Gjd3	0.94	-0.887	0.403708	0.6686
13454	10360139	NM_001033039	68874	kelch domain containing 9	Klhdc9	0.94	-0.92	0.387132	0.656147
13455	10589907	AK046107	12091	galactosidase, beta 1	Glb1	0.94	-0.341	0.74258	0.890291
13456	10386178	NM_146878	18329	olfactory receptor 30	Olfr30	0.94	-0.742	0.48133	0.730704
13457	10419170	NM_172597	70561	thioredoxin domain containing	Txndc16	0.94	-0.861	0.416815	0.679627
13458	10463687	BC058949	226178	DNA segment, Chr 19, Wayne Sta	D19Wsu162e	0.94	-1.621	0.147794	0.389986
13459	10397788	XM_909198	74947	RIKEN cDNA 4930463M05 gene	4930463M05Rik	0.94	-0.833	0.431552	0.692107
13460	10351563	NM_020579	57370	UDP-Gal:betaGlcNAc beta 1,4- ga	B4galt3	0.94	-1.243	0.252677	0.526766
13461	10452118	NM_028782	74142	lon peptidase 1, mitochondrial	Lonp1	0.94	-1.907	0.0969239	0.303204
13462	10570168	BC049746	75528	RIKEN cDNA 1700018L24 gene	1700018L24Rik	0.94	-0.761	0.470712	0.722574
13463	10555846					0.94	-0.775	0.4631	0.71752
13464	10422493	NM_182806	110168	G protein-coupled receptor 18	Gpr18	0.94	-1.008	0.345897	0.620063

13465	10401616	NM_175337	217716	mutL homolog 3 (E coli)	Mlh3	0.94	-0.472	0.651036	0.843733
13466	10554413	NM_031375	83485	neugrin, neurite outgrowth ass	Ngrn	0.94	-1.543	0.165378	0.415485
13467	10591610	NM_177030	319899	dedicator of cytokinesis 6	Dock6	0.94	-0.894	0.400369	0.666294
13468	10350535	NM_133780	108989	translocated promoter region	Tpr	0.94	-1.538	0.166748	0.417738
13469	10465336	NM_026246	18120	mitochondrial ribosomal protei	Mrpl49	0.94	-1.85	0.105567	0.320207
13470	10362886	NM_199028	331623	cDNA sequence AK122525	AK122525	0.94	-1.037	0.3332	0.609187
13471	10405432	NM_016758	51791	regulator of G-protein signali	Rgs14	0.94	-1.021	0.340354	0.61558
13472	10539933	NM_153162	232223	thioredoxin reductase 3	Txnrd3	0.94	-1.067	0.320278	0.597122
13473	10605507	XM_621046	546337	predicted gene, EG546337	EG546337	0.94	-1.971	0.0882016	0.286252
13474	10520483	NM_027652	28042	DNA segment, Chr 5, Wayne Stat	D5Wsu178e	0.94	-1.527	0.169311	0.420571
13475	10415811	AK053602	319433	RIKEN cDNA E130113E03 gene	E130113E03Rik	0.94	-0.871	0.411875	0.67572
13476	10443346	BC016538	72775	Fanconi anemia, complementatio	Fance	0.94	-1.128	0.295402	0.571766
13477	10363741	ENSMUST00000099661	100038508	predicted gene, ENSMUSG0000007	ENSMUSG00000074999	0.94	-0.681	0.51716	0.756421
13478	10487823	NM_011426	20612	sialic acid binding Ig-like le	Siglec1	0.94	-1.088	0.311806	0.58828
13479	10576088	ENSMUST00000055537	195209	gene model 22, (NCBI)	Gm22	0.94	-0.583	0.577356	0.797771
13480	10546227	NM_020521	107798	vomeronasal 1 receptor, B5	V1rb5	0.94	-0.008	0.99402	0.997702
13481	10419390	XR_033116	218997	similar to Ribosomal protein L	LOC218997	0.94	-0.485	0.641894	0.837836
13482	10604834					0.94	-0.379	0.715533	0.875402
13483	10421143	NM_010082	13522	a disintegrin and metallopepti	Adam28	0.94	-0.724	0.492111	0.738324
13484	10416251	NM_018781	13655	early growth response 3	Egr3	0.94	-1.103	0.305448	0.581741
13485	10547015	NM_026894	68971	RIKEN cDNA 1500001M20 gene	1500001M20Rik	0.94	-1.741	0.124053	0.352504
13486	10377265	NM_177320	320207	phosphoinositide-3-kinase, reg	Pik3r5	0.94	-0.308	0.7666	0.902924
13487	10524089	NM_207279	403178	phosphatidylinositol-specific	Plcxd1	0.94	-0.746	0.479263	0.729241
13488	10387222	BC114997	237823	phosphoribosylformylglycinamid	Pfas	0.94	-1.117	0.299762	0.575778
13489	10587550					0.94	-0.626	0.550662	0.780951
13490	10539143	NM_026159	67442	retinol saturase (all trans re	Retsat	0.94	-0.869	0.412814	0.676316
13491	10574226	NM_011332	20295	chemokine (C-C motif) ligand 1	Ccl17	0.94	-1.292	0.236283	0.508392
13492	10397763	BC021385	217830	RIKEN cDNA 9030617O03 gene	9030617O03Rik	0.94	-0.577	0.581733	0.800427
13493	10552812	NM_016849	54131	interferon regulatory factor 3	Irf3	0.94	-1.85	0.1056	0.320213
13494	10529706	XR_032717	195712	RIKEN cDNA 4930421P07 gene	4930421P07Rik	0.94	-0.399	0.701168	0.869046
13495	10460177	NM_001039657	17771	metallothionein-like 5, testis	Mtl5	0.94	-0.86	0.41736	0.680204
13496	10520513	BC019457	74919	RIKEN cDNA 4930471M23 gene	4930471M23Rik	0.94	-1.726	0.126749	0.356666
13497	10500582	NM_175552	269470	WD repeat domain 3	Wdr3	0.94	-1.117	0.299904	0.575946
13498	10408249					0.94	-0.078	0.939813	0.976619
13499	10445638					0.94	-0.279	0.788159	0.913843
13500	10416099	NM_013461	11549	adrenergic receptor, alpha 1a	Adra1a	0.94	-0.771	0.465111	0.71883
13501	10578399					0.94	-1.019	0.340973	0.615921
13502	10607002	XR_032787	632685	similar to ribosomal protein S	LOC632685	0.94	-1.137	0.291723	0.567783
13503	10525711	NM_025671	66627	2-oxoglutarate and iron-depend	Ogfod2	0.94	-1.122	0.297898	0.573918
13504	10584883	NM_022004	59095	FXYD domain-containing ion tra	Fxyd6	0.94	-0.823	0.436806	0.696333
13505	10522604	ENSMUST00000101096	665055	predicted gene, EG665055	EG665055	0.94	-1.666	0.138396	0.376395
13506	10371482	NM_011631	22027	heat shock protein 90, beta (G	Hsp90b1	0.94	-1.582	0.156472	0.402488
13507	10505747	NM_178376	68441	Ras-related GTP binding A	Rraga	0.94	-1.328	0.224658	0.494757
13508	10436951	NM_138743	68936	RIKEN cDNA 1190017O12 gene	1190017O12Rik	0.94	-0.919	0.387896	0.656721
13509	10384015	NM_018870	56012	phosphoglycerate mutase 2	Pgam2	0.94	-0.677	0.51966	0.757547
13510	10446074	NM_010931	18140	ubiquitin-like, containing PHD	Uhrf1	0.939	-0.774	0.463724	0.717865
13511	10542445	NM_011499	20901	serine/threonine kinase recept	Strap	0.939	-1.461	0.186156	0.444356
13512	10385818	NM_025352	22272	ubiquinol-cytochrome c reducta	Uqcrq	0.939	-1.448	0.189761	0.448303
13513	10520612	NM_008439	16548	ketohexokinase	Khk	0.939	-1.154	0.285277	0.560533
13514	10389326	NM_027388	70325	phosphatidylinositol glycan an	Pigw	0.939	-0.827	0.434866	0.695306
13515	10520010	NM_028431	73078	peptidase (mitochondrial proce	Pmpcb	0.939	-1.431	0.194394	0.454475

13516	10447288	NM_011381	20473	sine oculis-related homeobox 3	Six3	0.939	-1.109	0.30302	0.579039
13517	10494757					0.939	-1.157	0.2843	0.559599
13518	10347796	NM_029777	76867	rhomboid domain containing 1	Rhbdd1	0.939	-1.027	0.337622	0.61318
13519	10410654					0.939	-0.514	0.6229	0.827402
13520	10464811					0.939	-1.023	0.339253	0.614614
13521	10372629	NM_026570	64050	YEATS domain containing 4	Yeats4	0.939	-1.573	0.158555	0.40535
13522	10527598	NM_025624	66537	proteasome maturation protein	Pomp	0.939	-1.711	0.12949	0.360872
13523	10594988	NM_015806	50772	mitogen-activated protein kina	Mapk6	0.939	-1.859	0.10406	0.317243
13524	10384838	NM_146016	237711	RIKEN cDNA C230094A16 gene	C230094A16Rik	0.939	-1.359	0.21524	0.482305
13525	10456096	NM_146086	225600	phosphodiesterase 6A, cGMP-spe	Pde6a	0.939	-0.461	0.65827	0.847092
13526	10551293	NM_007817	13107	cytochrome P450, family 2, sub	Cyp2f2	0.939	-0.909	0.392742	0.660631
13527	10483824	NM_030188	78802	tetratricopeptide repeat domai	Ttc30a1	0.939	-0.931	0.381822	0.651436
13528	10525165	NM_145153	243262	2'-5' oligoadenylate synthetas	Oas1f	0.939	-0.878	0.408482	0.672914
13529	10424894	AK170702	223658	RIKEN cDNA D330001F17 gene	D330001F17Rik	0.939	-0.849	0.422942	0.685287
13530	10498597	AK033123	100036536	predicted gene, ENSMUSG0000005	ENSMUSG00000054030	0.939	-1.061	0.323043	0.59983
13531	10491474	XR_032892	435727	similar to Ab1-115	LOC435727	0.939	-0.393	0.705966	0.871814
13532	10427997	NM_027496	67434	RIKEN cDNA 5730557B15 gene	5730557B15Rik	0.939	-0.438	0.674164	0.855254
13533	10594969	NM_001081153	208898	unc-13 homolog C (C. elegans)	Unc13c	0.939	-0.586	0.576009	0.797128
13534	10508953	NM_001039048	433766	tripartite motif-containing 63	Trim63	0.939	-0.231	0.823885	0.929508
13535	10519224	ENSMUST00000097737	433813	pseudouridylate synthase-like	Pusl1	0.939	-1.367	0.212706	0.478299
13536	10555407	NM_183270	68185	coiled-coil-helix-coiled-coil-	Chchd8	0.939	-1.172	0.278309	0.553321
13537	10393266	NM_008240	15223	forkhead box J1	Foxj1	0.939	-1.026	0.338284	0.613858
13538	10576719	NM_026951	69129	peroxisomal biogenesis factor	Pex11c	0.939	-0.928	0.383256	0.65267
13539	10545608	NM_011350	20355	sema domain, immunoglobulin do	Sema4f	0.939	-0.664	0.527117	0.762858
13540	10503010	NM_029330	75540	fucose-1-phosphate guanylyltra	Fpgt	0.939	-1.172	0.278499	0.553444
13541	10500780	NM_198658	381463	nuclear receptor subfamily 1,	Nr1h5	0.939	-0.04	0.969155	0.987586
13542	10571467	NM_026840	68797	platelet-derived growth factor	Pdgfrl	0.939	-0.464	0.656281	0.846043
13543	10552343					0.939	-1.047	0.328727	0.605085
13544	10492049	BC052702	56790	DNA segment, Chr 3, ERATO Doi	D3Ertd300e	0.939	-1.426	0.195603	0.45594
13545	10345902	ENSMUST00000039080	71524	RIKEN cDNA 8430432A02 gene	8430432A02Rik	0.939	-0.956	0.36994	0.640508
13546	10514902	NM_029985	77809	leucine rich repeat containing	Lrrc42	0.939	-1.856	0.104593	0.318248
13547	10417702					0.939	-0.787	0.4564	0.712554
13548	10438340	NM_001111062	12846	catechol-O-methyltransferase	Comt	0.939	-1.283	0.23922	0.512053
13549	10398299	NM_001012310	104910	expressed sequence AI132487	AI132487	0.939	-0.316	0.760729	0.900154
13550	10565057	ENSMUST00000026816	71968	WD repeat domain 73	Wdr73	0.939	-0.944	0.375619	0.64575
13551	10398286					0.939	-0.465	0.655744	0.845986
13552	10507236	ENSMUST00000049266	76237	RIKEN cDNA 6430628N08 gene	6430628N08Rik	0.939	-0.694	0.509187	0.750516
13553	10443836	NM_028244	72462	ribosomal RNA processing 1 hom	Rrp1b	0.939	-1.351	0.21753	0.485293
13554	10480445	NM_029773	76857	speckle-type POZ protein-like	Spopl	0.939	-0.886	0.404207	0.668849
13555	10453141	NM_009231	20662	Son of sevenless homolog 1 (Dr	Sos1	0.939	-1.314	0.229074	0.500108
13556	10510215	BC024323	666532	predicted gene, OTTMUSG0000001	OTTMUSG00000010657	0.939	-1.166	0.280654	0.556047
13557	10559558	NM_009406	21954	troponin I, cardiac	Tnni3	0.939	-0.873	0.411022	0.675081
13558	10598956	NM_009703	11836	v-raf murine sarcoma 3611 vira	Araf	0.939	-1.225	0.259088	0.533309
13559	10397440	NM_011934	26380	estrogen related receptor, bet	Esrrb	0.939	-0.934	0.380464	0.650115
13560	10587085	NM_001113283	235493	cDNA sequence BC031353	BC031353	0.939	-1.802	0.113261	0.333396
13561	10565802	NM_012052	27050	ribosomal protein S3	Rps3	0.939	-1.334	0.2228	0.492667
13562	10364535	NM_015779	50701	elastase 2, neutrophil	Ela2	0.939	-0.672	0.52281	0.759485
13563	10357381	XM_914055	22625	Yeast Sps1/Ste20-related kinas	Ysk4	0.939	-0.902	0.396349	0.663741

13564	10350697	NM_175460	226518	nicotinamide nucleotide adenyl	Nmnat2	0.939	-0.716	0.496371	0.740946
13565	10367830	NM_001114333	14816	glutamate receptor, metabotrop	Grm1	0.939	-0.826	0.435257	0.695412
13566	10602020	NM_001081499	245638	TBC1 domain family, member 8B	Tbc1d8b	0.939	-1.205	0.266222	0.541183
13567	10549615	NM_172736	232798	leukocyte receptor cluster (LR	Leng8	0.939	-1.739	0.124296	0.353099
13568	10424070	XR_033092	671518	similar to RNA-binding protein	LOC671518	0.939	-0.507	0.627156	0.830395
13569	10471882	NM_172854	241327	olfactomedin-like 2A	Olfml2a	0.939	-1.233	0.256326	0.530714
13570	10582743	NM_175561	270109	pecanex-like 2 (Drosophila)	Pcnxl2	0.939	-0.769	0.466447	0.719579
13571	10539342	NM_133641	20166	rhotekin	Rtkn	0.939	-1.042	0.3311	0.607602
13572	10397230	NM_028377	72873	RIKEN cDNA 2900006K08 gene	2900006K08Rik	0.939	-1.079	0.315311	0.592249
13573	10605429	XR_034103	667496	similar to high mobility group	LOC667496	0.939	-1.556	0.162293	0.410862
13574	10569313	BC049666	320802	RIKEN cDNA 6330512M04 gene	6330512M04Rik	0.939	-0.92	0.387159	0.656147
13575	10540855	NM_008285	15465	histamine receptor H1	Hrh1	0.939	-0.917	0.388878	0.657381
13576	10375436	NM_001013783	432552	predicted gene, OTTMUSG0000000	OTTMUSG00000005491	0.939	-0.685	0.514689	0.754767
13577	10596737	NM_008140	14685	guanine nucleotide binding pro	Gnat1	0.939	-0.802	0.448166	0.705796
13578	10576857	NM_011592	21856	translocase of inner mitochond	Timm44	0.939	-1.871	0.102348	0.313722
13579	10380862	NM_144828	19049	protein phosphatase 1, regulat	Ppp1r1b	0.939	-0.697	0.507879	0.749798
13580	10477389	NM_199303	228796	bactericidal/permeability-incr	Bpil3	0.939	-0.967	0.364726	0.635812
13581	10446581	NM_009547	22666	zinc finger protein 161	Zfp161	0.939	-0.899	0.397732	0.664302
13582	10568001	NM_133670	20887	sulfotransferase family 1A, ph	Sult1a1	0.939	-0.839	0.428339	0.689379
13583	10570011					0.939	-1.166	0.280556	0.555959
13584	10440543	NM_001081068	78913	zinc finger protein 294	Zfp294	0.939	-1.5	0.176031	0.429741
13585	10470109	NM_013908	30839	F-box and WD-40 domain protein	Fbxw5	0.939	-1.27	0.243395	0.51639
13586	10600566					0.939	-0.304	0.769961	0.904799
13587	10574155					0.939	-0.313	0.763024	0.901457
13588	10435501	NM_001082543	20861	stefin A1	Stfa1	0.939	-0.223	0.829561	0.931357
13589	10534428	NM_033571	94244	FK506 binding protein 6	Fkbp6	0.939	-1.12	0.29857	0.574742
13590	10367708	NM_008786	18537	protein-L-isoaspartate (D-aspa	Pcmt1	0.938	-1.517	0.171859	0.424012
13591	10441032	NM_019500	56173	claudin 14	Cldn14	0.938	-0.677	0.51925	0.757488
13592	10507804	NM_025873	66966	tRNA isopentenyltransferase 1	Trit1	0.938	-1.421	0.197182	0.457903
13593	10530280					0.938	-1.515	0.172258	0.424438
13594	10446617	XR_033984	240156	similar to ribosomal protein L	LOC240156	0.938	-0.346	0.739363	0.889001
13595	10345016	NM_001025305	21419	transcription factor AP-2 beta	Tcfap2b	0.938	-0.685	0.515029	0.754817
13596	10427766	NM_178717	239336	relaxin family peptide recepto	Rxfp3	0.938	-0.471	0.651334	0.843859
13597	10393509	ENSMUST00000106296	72344	ubiquitin specific peptidase 3	Usp36	0.938	-1.211	0.264072	0.539055
13598	10539653	NM_176842	69786	Tp53rk binding protein	Tprkb	0.938	-0.65	0.535823	0.769253
13599	10510509	NM_177366	269604	G protein-coupled receptor 157	Gpr157	0.938	-0.075	0.942357	0.977825
13600	10353305	ENSMUST00000116144	545306	predicted gene, EG545306	EG545306	0.938	-1.107	0.303879	0.580207
13601	10502622	NM_017474	23844	chloride channel calcium activ	Clca3	0.938	-0.801	0.448667	0.706217
13602	10563350	NM_018876	14344	fucosyltransferase 2	Fut2	0.938	-1.362	0.214202	0.480692
13603	10449343	NM_001013385	268934	glutamate receptor, metabotrop	Grm4	0.938	-1.673	0.136888	0.373561
13604	10418842	XM_484361	432836	RIKEN cDNA 3425401B19 gene	3425401B19Rik	0.938	-0.667	0.52572	0.761828
13605	10540931	ENSMUST00000068960	352968	RIKEN cDNA D830050J10 gene	D830050J10Rik	0.938	-0.999	0.350083	0.623549
13606	10563421	NM_008172	14814	glutamate receptor, ionotropic	Grin2d	0.938	-1.178	0.276051	0.550851
13607	10525989	NM_001081342	243277	G protein-coupled receptor 133	Gpr133	0.938	-0.445	0.669461	0.852871
13608	10552088	ENSMUST00000098547	100038516	predicted gene, EG668322	EG668322	0.938	-0.197	0.848935	0.93885
13609	10432243	NM_024169	66120	FK506 binding protein 11	Fkbp11	0.938	-1.498	0.176527	0.430507
13610	10440414	NM_007990	14109	Finkel-Biskis-Reilly murine sa	Fau	0.938	-1.459	0.186572	0.444895
13611	10554231					0.938	-0.398	0.702271	0.869368
13612	10444152	NM_009926	12815	collagen, type XI, alpha 2	Col11a2	0.938	-1.18	0.275437	0.550302
13613	10382653	ENSMUST00000093911	217328	myosin XVB	Myo15b	0.938	-0.803	0.447626	0.705227
13614	10522182	NM_001081105	74734	ras homolog gene family, membe	Rhoh	0.938	-0.355	0.733092	0.88559
13615	10433104	NM_013866	29813	zinc finger protein 385A	Zfp385a	0.938	-1.454	0.187941	0.446224

13616	10495539	NM_021388	58193	exostoses (multiple)-like 2	Extl2	0.938	-1.958	0.0899252	0.289403
13617	10566209	NM_146314	258311	olfactory receptor 601	Olfr601	0.938	-0.267	0.796679	0.917464
13618	10475051	NM_013720	29808	MAX gene associated	Mga	0.938	-1.586	0.155403	0.400908
13619	10501567	NM_001038696	67225	RNA-binding region (RNP1, RRM)	Rnpc3	0.938	-1.027	0.337649	0.61318
13620	10454229	ENSMUST00000050671	74644	RIKEN cDNA 4930426D05 gene	4930426D05Rik	0.938	-1.189	0.271957	0.546343
13621	10532461					0.938	-0.41	0.693993	0.865705
13622	10472136	NM_173030	271786	UDP-N-acetyl-alpha-D-galactosa	Galnt13	0.938	-0.374	0.719184	0.877614
13623	10349809	NM_172517	213464	retinoblastoma binding protein	Rbbp5	0.938	-1.97	0.0883264	0.286438
13624	10408798	NM_011547	21418	transcription factor AP-2, alp	Tcfap2a	0.938	-0.947	0.374112	0.64426
13625	10548656	BC069935	381818	predicted gene, EG381818	EG381818	0.938	-0.784	0.457846	0.713313
13626	10371006	NM_013895	30055	translocase of inner mitochond	Timm13	0.938	-1.674	0.13687	0.373561
13627	10563170	NM_015789	50722	dickkopf-like 1	Dkkl1	0.938	-0.634	0.545765	0.777543
13628	10348004	NM_027357	70247	proteasome (prosome, macropain	Psmd1	0.938	-1.855	0.104803	0.318752
13629	10505198	AK006094	72245	RIKEN cDNA 1700018M17 gene	1700018M17Rik	0.938	-1.214	0.262959	0.537563
13630	10531972	NM_029509	76074	RIKEN cDNA 5830443L24 gene	5830443L24Rik	0.938	-0.209	0.839912	0.935328
13631	10498921	NM_019911	56720	tryptophan 2,3-dioxygenase	Tdo2	0.938	-0.598	0.568132	0.793223
13632	10464793	ENSMUST00000096325	381196	gene model 960, (NCBI)	Gm960	0.938	-0.386	0.710474	0.873031
13633	10466624	NM_011921	26358	aldehyde dehydrogenase family	Aldh1a7	0.938	0.084	0.935513	0.974509
13634	10540493	NM_138677	192193	ER degradation enhancer, manno	Edem1	0.938	-1.245	0.251905	0.525844
13635	10572271	NM_181540	107770	transmembrane 6 superfamily me	Tm6sf2	0.938	-0.9	0.397199	0.664239
13636	10572241	NM_001024954	80720	pre-B-cell leukemia homeobox 4	Pbx4	0.938	-1.13	0.294547	0.570921
13637	10598381	NM_173747	209416	G patch domain and KOW motifs	Gpkow	0.938	-1.248	0.250891	0.524763
13638	10364153	ENSMUST00000009260	100036541	predicted gene, ENSMUSG0000000	ENSMUSG00000009116	0.938	-1.587	0.155298	0.400794
13639	10530827	NM_183284	69982	serine peptidase inhibitor, Ka	Spink2	0.938	-0.732	0.487462	0.735095
13640	10514201	ENSMUST00000070607	230376	RIKEN cDNA 6230416J20 gene	6230416J20Rik	0.938	-1.04	0.331814	0.608173
13641	10375935	NM_011543	21402	S-phase kinase-associated prot	Skp1a	0.938	-1.219	0.261332	0.535842
13642	10562667					0.938	-1.439	0.192136	0.451484
13643	10465043	XM_886587	622178	predicted gene, EG622178	EG622178	0.938	-1.684	0.134744	0.369956
13644	10520392	NM_021470	56874	ring finger protein 32	Rnf32	0.938	-0.808	0.445118	0.703541
13645	10437499	NM_001079814	74022	RIKEN cDNA 3930401K13 gene	3930401K13Rik	0.938	-1.243	0.252599	0.526721
13646	10575706	NM_019573	80707	WW domain-containing oxidoredu	Wwox	0.938	-1.19	0.271845	0.546343
13647	10369630	NM_019553	56200	DEAD (Asp-Glu-Ala-Asp) box pol	Ddx21	0.938	-1.636	0.144501	0.385726
13648	10534152	NM_145218	212996	Williams-Beuren syndrome chrom	Wbscr17	0.938	-1.003	0.34812	0.622132
13649	10480254					0.938	-0.847	0.424169	0.68641
13650	10550674	NM_007949	13871	excision repair cross-compleme	Ercc2	0.938	-1.252	0.24967	0.52381
13651	10579609	NM_028715	74015	FCH domain only 1	Fcho1	0.938	-0.544	0.602713	0.814246
13652	10384776	ENSMUST00000101447	70626	RIKEN cDNA 5730522E02 gene	5730522E02Rik	0.938	-1.25	0.250236	0.524321
13653	10360120	NM_025388	66155	ubiquitin-fold modifier conjug	Ufc1	0.938	-1.318	0.227977	0.49895
13654	10482095	NM_008500	16874	LIM homeobox protein 6	Lhx6	0.938	-0.486	0.641212	0.837465
13655	10501315	ENSMUST00000098691	100038453	predicted gene, OTTMUSG0000000	OTTMUSG00000007300	0.938	-1.217	0.262004	0.536439
13656	10591997	ENSMUST00000098918	100038748	predicted gene, ENSMUSG0000007	ENSMUSG00000074462	0.938	-0.465	0.655903	0.846006
13657	10459452	ENSMUST00000068927	381174	RIKEN cDNA A330084C13 gene	A330084C13Rik	0.938	-0.605	0.563682	0.790247
13658	10485963	NM_181416	228482	Rho GTPase activating protein	Arhgap11a	0.938	-1.09	0.310921	0.587446
13659	10387855	NM_009660	11687	arachidonate 15-lipoxygenase	Alox15	0.938	-0.295	0.776293	0.908709
13660	10413985	XM_985917	268729	gene model 626, (NCBI)	Gm626	0.938	-0.284	0.784256	0.912068
13661	10429029	NM_009623	11514	adenylate cyclase 8	Adcy8	0.938	-1.904	0.0973657	0.303957
13662	10385824	ENSMUST00000057722	432561	predicted gene, ENSMUSG0000004	ENSMUSG00000049427	0.938	-0.486	0.641678	0.837715

13663	10451481	ENSMUST00000040624	210982	cDNA sequence BC032203	BC032203	0.938	-0.308	0.76667	0.902924
13664	10367337	NM_026259	67588	ring finger protein 41	Rnf41	0.938	-1.179	0.275746	0.550639
13665	10592850	NM_021789	60409	trafficking protein particle c	Trappc4	0.938	-1.935	0.0929707	0.295472
13666	10482323	NM_024209	67857	protein phosphatase 6, catalyt	Ppp6c	0.938	-1.485	0.179795	0.43509
13667	10550067	NM_175558	269870	zinc finger protein 446	Zfp446	0.938	-0.665	0.526592	0.762621
13668	10394437	NM_021429	58240	HCLS1 binding protein 3	Hs1bp3	0.938	-0.535	0.6088	0.817918
13669	10457895	NM_133195	108013	bruno-like 4, RNA binding prot	Brunol4	0.938	-1.581	0.156687	0.402992
13670	10522396	NM_023429	68095	OCIA domain containing 1	Ociad1	0.938	-1.26	0.246976	0.520282
13671	10590325	NM_007614	12387	catenin (cadherin associated p	Ctnnb1	0.938	-1.526	0.169678	0.420989
13672	10550237	NM_025898	108124	N-ethylmaleimide sensitive fus	Napa	0.938	-1.135	0.292749	0.568767
13673	10409779	NM_183290	70900	RIKEN cDNA 4921517D22 gene	4921517D22Rik	0.937	-0.579	0.580245	0.799472
13674	10532989	NM_029645	384281	glutamyl-tRNA(Gln) amidotransf	Gatc	0.937	-1.478	0.181822	0.438179
13675	10408146	NM_134218	171252	vomeronasal 1 receptor, H9	V1rh9	0.937	-0.404	0.698226	0.867766
13676	10503963					0.937	-0.772	0.464708	0.71847
13677	10483756	NM_175015	228033	ATP synthase, H+ transporting,	Atp5g3	0.937	-1.809	0.112167	0.331562
13678	10590407	BC030045	270210	zinc finger protein 651	Zfp651	0.937	-0.938	0.378632	0.648305
13679	10401684	NM_144524	68737	angel homolog 1 (Drosophila)	Angel1	0.937	-0.938	0.378438	0.648225
13680	10565705	NM_011010	18378	olfactory marker protein	Omp	0.937	-0.528	0.613401	0.820926
13681	10395463	ENSMUST00000038121	629820	predicted gene, EG629820	EG629820	0.937	-1.637	0.144481	0.385726
13682	10349644	NM_011924	26361	arginine vasopressin receptor	Avpr1b	0.937	-0.572	0.584937	0.802565
13683	10595900	NM_025485	64655	mitochondrial ribosomal protei	Mrps22	0.937	-1.506	0.174626	0.427694
13684	10392953	NM_173048	260302	golgi associated, gamma adapti	Gga3	0.937	-1.471	0.183424	0.440568
13685	10478847	NM_001081005	68949	RIKEN cDNA 1500012F01 gene	1500012F01Rik	0.937	-1.188	0.272358	0.54694
13686	10408789	AF548110	218165	orofacial cleft 1 candidate 1	Ofcc1	0.937	-0.965	0.365929	0.636964
13687	10446069					0.937	-0.371	0.721472	0.878683
13688	10362745	XR_032514	633979	similar to hCG2030702	LOC633979	0.937	-0.578	0.580558	0.799564
13689	10376685	NM_172943	268420	alkB, alkylation repair homolo	Alkbh5	0.937	-1.006	0.347172	0.621453
13690	10514133	NM_027238	69863	RIKEN cDNA 1810054D07 gene	1810054D07Rik	0.937	-0.716	0.496707	0.741117
13691	10419561	NM_207558	404319	olfactory receptor 750	Olfr750	0.937	-0.733	0.486629	0.734425
13692	10596675	NM_001081244	434436	cDNA sequence BY080835	BY080835	0.937	-0.644	0.539349	0.772158
13693	10465638	BC020020	70999	N-acetyltransferase 11	Nat11	0.937	-1.163	0.281704	0.556928
13694	10397962	XM_619025	544888	predicted gene, EG544888	EG544888	0.937	-0.966	0.365271	0.636343
13695	10426208	NM_182928	223780	adrenomedullin 2	Adm2	0.937	-1.135	0.292677	0.568731
13696	10365812	AK016739	74454	RIKEN cDNA 4933408J17 gene	4933408J17Rik	0.937	-1.056	0.325191	0.601561
13697	10491261	NM_027016	69276	SEC62 homolog (S. cerevisiae)	Sec62	0.937	-1.387	0.206684	0.471173
13698	10397158	NM_134246	171281	acyl-CoA thioesterase 3	Acot3	0.937	-1.758	0.120818	0.347267
13699	10598499	XM_905995	632013	predicted gene, EG632013	EG632013	0.937	-1.449	0.189481	0.448035
13700	10428150	NM_001081253	78803	F-box protein 43	Fbxo43	0.937	-0.562	0.591276	0.806576
13701	10587655	ENSMUST00000034998	71640	RIKEN cDNA 4930422I07 gene	4930422I07Rik	0.937	-1.313	0.229439	0.500438
13702	10440118					0.937	-0.792	0.453407	0.709874
13703	10432298	ENSMUST00000023741	381022	myeloid/lymphoid or mixed-line	Mll2	0.937	-1.58	0.156931	0.403374
13704	10589654	NM_146228	235633	ALS2 C-terminal like	Als2cl	0.937	-0.875	0.409677	0.674122
13705	10426242	AK083297	319362	RIKEN cDNA C730034F03 gene	C730034F03Rik	0.937	-0.914	0.390455	0.659
13706	10387903	NM_001013607	327956	vitelline membrane outer layer	Vmo1	0.937	-0.86	0.417666	0.680417
13707	10515213	NM_130865	140477	diencephalon/mesencephalon hom	Dmbx1	0.937	-0.752	0.476004	0.727266
13708	10355141	NM_033563	93691	Kruppel-like factor 7 (ubiquit	Klf7	0.937	-1.403	0.202187	0.464958
13709	10399383	NM_173417	238076	potassium voltage-gated channe	Kcns3	0.937	-0.562	0.591242	0.806576
13710	10524396	NM_001012726	503692	activator of yeast meiotic pro	Aym1	0.937	-0.648	0.537248	0.770298
13711	10593258	XM_001478811	100042785	similar to hCG1646420	LOC100042785	0.937	-1.205	0.266326	0.541183
13712	10387907	BC047268	18806	phospholipase D2	Pld2	0.937	-0.717	0.495792	0.740536
13713	10441017	NM_145482	224440	SET domain containing 4	Setd4	0.937	-1.718	0.128233	0.35912
13714	10438112	NM_001001983	224020	phosphatidylinositol 4-kinase,	Pi4ka	0.937	-1.568	0.159711	0.407016

13715	10344811	NM_026493	211660	centrosome and spindle pole as	Cspp1	0.937	-0.558	0.593955	0.808302
13716	10409449	NM_021489	58992	coagulation factor XII (Hagema	F12	0.937	-0.83	0.433008	0.693487
13717	10603087	NM_027153	69656	pirin	Pir	0.937	-1.182	0.274696	0.549393
13718	10468070	NM_010205	14179	fibroblast growth factor 8	Fgf8	0.937	-0.667	0.525264	0.76149
13719	10473414	NM_182990	20833	structure specific recognition	Ssrp1	0.937	-1.958	0.0898777	0.289338
13720	10516551	NM_029036	74648	S100P binding protein	S100pbp	0.937	-1.604	0.151507	0.395407
13721	10592467	NM_146608	258601	olfactory receptor 984	Olfr984	0.937	-0.438	0.674509	0.855435
13722	10551644	NM_001110807	60594	calpain 12	Capn12	0.937	-1.169	0.279559	0.554795
13723	10374621	ENSMUST00000101465	17847	ubiquitin specific peptidase 3	Usp34	0.937	-1.342	0.220191	0.488992
13724	10410625	NM_023281	66945	succinate dehydrogenase comple	Sdha	0.937	-1.314	0.228946	0.499975
13725	10548859	NM_021714	60321	WW domain binding protein 11	Wbp11	0.937	-1.419	0.197526	0.45809
13726	10550332	NM_009201	20514	solute carrier family 1 (neutr	Slc1a5	0.937	-1.215	0.262564	0.536954
13727	10534002	NM_172885	243274	transmembrane protein 132D	Tmem132d	0.937	-0.849	0.423342	0.685543
13728	10559606	NM_023440	68255	transmembrane protein 86B	Tmem86b	0.937	-0.412	0.692639	0.865144
13729	10513360	XM_909473	634672	similar to 40S ribosomal prote	LOC634672	0.937	-0.482	0.644302	0.839081
13730	10584584	NM_178245	244813	brain specific homeobox	Bsx	0.937	-0.928	0.383557	0.652869
13731	10433055					0.937	-1.164	0.281474	0.55689
13732	10541307	NM_011909	24110	ubiquitin specific peptidase 1	Usp18	0.937	-0.238	0.818216	0.927633
13733	10389736					0.937	-0.59	0.573228	0.796645
13734	10483761	XR_032757	622659	similar to glyceraldehyde-3-ph	LOC622659	0.937	-0.599	0.567729	0.792975
13735	10558723	NM_011875	23997	proteasome (prosome, macropain	Psmd13	0.937	-1.258	0.247716	0.520853
13736	10429739	NM_028364	67959	poly-U binding splicing factor	Puf60	0.937	-1.609	0.150478	0.393678
13737	10516602	NM_080442	58864	testis-specific serine kinase	Tssk3	0.937	-0.953	0.371429	0.64202
13738	10538106	NM_173429	243372	zinc finger protein 775	Zfp775	0.937	-0.458	0.660504	0.848669
13739	10576373	NM_018855	104346	growth arrest specific 8	Gas8	0.937	-1.814	0.111364	0.330249
13740	10532678	AK157047	100038385	predicted gene, ENSMUSG0000007	ENSMUSG00000072712	0.937	-0.685	0.514572	0.754736
13741	10560058	NM_001024699	232879	zinc finger and BTB domain con	Zbtb45	0.937	-1.32	0.227151	0.497938
13742	10597427	NM_001042503	636931	tripartite motif-containing 71	Trim71	0.937	-0.587	0.575143	0.797076
13743	10455533	NM_010120	13664	eukaryotic translation initiat	Eif1a	0.937	-1.865	0.103214	0.315552
13744	10431300	NM_145477	223774	asparagine-linked glycosylatio	Alg12	0.937	-0.972	0.362599	0.634038
13745	10460623	NM_001033448	381201	gene model 962, (NCBI)	Gm962	0.937	-0.338	0.744902	0.891598
13746	10443704	NM_177465	52020	uromodulin-like 1	Umodl1	0.937	-1.072	0.318402	0.595538
13747	10379482	NM_009871	12569	cyclin-dependent kinase 5, reg	Cdk5r1	0.937	-1.284	0.238691	0.511419
13748	10351616	NM_009480	22278	upstream transcription factor	Usf1	0.937	-1.45	0.189207	0.447572
13749	10366161	XR_033492	382413	similar to hCG1783090	LOC382413	0.937	-1.379	0.209013	0.474029
13750	10348074	BC100497	71863	RIKEN cDNA 1700019O17 gene	1700019O17Rik	0.937	-0.724	0.491661	0.73812
13751	10423805	NM_025494	66335	ATPase, H+ transporting, lysos	Atp6v1c1	0.937	-1.267	0.244441	0.517519
13752	10604473	NM_177591	209268	immunoglobulin superfamily, me	Igsf1	0.937	-1.531	0.168397	0.419736
13753	10449991	NM_207541	224694	zinc finger protein 81	Zfp81	0.937	-1.494	0.177636	0.43207
13754	10415903	AB009660	73382	RIKEN cDNA 1700049K14 gene	1700049K14Rik	0.937	-0.445	0.669584	0.852924
13755	10486059					0.936	-0.693	0.509748	0.75114
13756	10599420	ENSMUST00000105113	236774	gene model 362, (NCBI)	Gm362	0.936	-0.73	0.488175	0.735812
13757	10563685	NM_013643	19259	protein tyrosine phosphatase,	Ptpn5	0.936	-0.953	0.371612	0.64202
13758	10497971	NM_001081411	67161	sodium channel and clathrin li	Sclt1	0.936	-1.003	0.348124	0.622132
13759	10449452	NM_010220	14229	FK506 binding protein 5	Fkbp5	0.936	-1.264	0.245421	0.518491
13760	10452151	NM_009056	19725	regulatory factor X, 2 (influe	Rfx2	0.936	-0.652	0.534458	0.768432
13761	10568492	AB036742	114660	ectopic ossification 1	Etos1	0.936	-0.479	0.64587	0.840161
13762	10354054	NM_026913	69028	MIT, microtubule interacting a	Mitd1	0.936	-1.174	0.277721	0.552827
13763	10573975	NM_001003951	67935	carboxylesterase 7	Ces7	0.936	-1.133	0.293493	0.569566
13764	10391490	NM_008815	18612	ets variant gene 4 (E1A enhanc	Etv4	0.936	-0.747	0.478965	0.729132
13765	10440556	NM_001081068	78913	zinc finger protein 294	Zfp294	0.936	-0.919	0.387961	0.656721
13766	10393449	NM_007707	12702	suppressor of cytokine signali	Socs3	0.936	-1.098	0.307537	0.584192
13767	10493842	NM_207247	242100	peptidoglycan recognition prot	Pglyrp3	0.936	-0.68	0.517962	0.756834
13768	10476093	NM_024193	67134	nucleolar protein 5A	Nol5a	0.936	-1.654	0.140923	0.379771
				RIKEN cDNA E230001N04					

13769	10443367	ENSMUST00000095448	320187	gene	E230001N04Rik	0.936	-0.702	0.504802	0.747036
13770	10553895					0.936	-0.39	0.707622	0.872268
13771	10538526	BC117878	78937	RIKEN cDNA 5830411G16 gene	5830411G16Rik	0.936	-1.383	0.207945	0.472478
13772	10381770	NM_199019	237958	RIKEN cDNA 4933407P14 gene	4933407P14Rik	0.936	-0.888	0.403161	0.668374
13773	10588132	NM_001077424	333424	alpha-1,4-N-acetylglucosaminyl	A4gnt	0.936	-0.588	0.574308	0.797076
13774	10504329	BC027414	622404	hypothetical protein LOC622404	RP23-195K8.6	0.936	-0.668	0.525034	0.761313
13775	10556487	NM_177248	320743	RIKEN cDNA A630005I04 gene	A630005I04Rik	0.936	-0.571	0.585614	0.80308
13776	10554166	ENSMUST00000065516	75547	A kinase (PRKA) anchor protein	Akap13	0.936	-1.416	0.198365	0.459238
13777	10402630	NM_011973	26448	renal tumor antigen	Rage	0.936	-1.445	0.190354	0.44932
13778	10502982	NM_177066	435766	TNNI3 interacting kinase	Tnni3k	0.936	-1.088	0.311572	0.588151
13779	10363392	NM_019965	56709	DnaJ (Hsp40) homolog, subfamil	Dnajb12	0.936	-1.425	0.196022	0.456422
13780	10366909	NM_027900	71750	R3H domain containing 2	R3hdm2	0.936	-1.428	0.195187	0.455424
13781	10398340					0.936	-0.767	0.467544	0.720274
13782	10513692	NM_001008791	73750	whirlin	Whrn	0.936	-1.229	0.257751	0.531852
13783	10475648	NM_026981	69185	DTW domain containing 1	Dtwd1	0.936	-0.482	0.644172	0.839078
13784	10551069	NM_175436	210172	zinc finger protein 526	Zfp526	0.936	-1.101	0.306253	0.582793
13785	10591691	BC057069	77609	RIKEN cDNA C330001K17 gene	C330001K17Rik	0.936	-1.87	0.102408	0.313858
13786	10593177	ENSMUST00000070831	74361	RIKEN cDNA 4931429L15 gene	4931429L15Rik	0.936	-0.567	0.587885	0.804702
13787	10552760	NM_021549	59047	polynucleotide kinase 3'- phos	Pnkp	0.936	-1.093	0.309349	0.586099
13788	10432556	XM_001476618	100046686	similar to ubiquinol-cytochrom	LOC100046686	0.936	-0.484	0.642885	0.838239
13789	10541094	NM_177684	232337	zinc finger protein 637	Zfp637	0.936	-1.538	0.166704	0.417678
13790	10393436	NM_027919	71776	threonine aldolase 1	Tha1	0.936	-0.846	0.424787	0.686726
13791	10510604	NM_172704	230935	DnaJ (Hsp40) homolog, subfamil	Dnajc11	0.936	-1.516	0.171966	0.424079
13792	10590462					0.936	-0.461	0.658603	0.847411
13793	10521356	NM_019447	54426	hepatocyte growth factor activ	Hgfac	0.936	-1.129	0.294948	0.571244
13794	10551159	XR_034166	100047962	similar to ribosomal protein L	LOC100047962	0.936	-0.393	0.705507	0.871589
13795	10397752	NM_009790	12313	calmodulin 1	Calm1	0.936	-1.853	0.105086	0.319364
13796	10512709	NM_001009949	230125	mitochondrial carrier triple r	Mcart1	0.936	-1.396	0.204063	0.467365
13797	10520948	NM_001081407	665270	phospholipase B1	Plb1	0.936	-0.713	0.498488	0.742429
13798	10444991	NM_001034909	547347	predicted gene, EG547347	EG547347	0.936	-0.719	0.494514	0.7396
13799	10444978	NM_008136	14670	guanine nucleotide binding pro	Gna-rs1	0.936	-0.852	0.421419	0.683844
13800	10548057	NM_025358	66108	NADH dehydrogenase (ubiquinone	Ndufa9	0.936	-1.229	0.257529	0.531656
13801	10396645	NM_178744	268564	zinc finger and BTB domain con	Zbtb1	0.936	-0.703	0.504157	0.74644
13802	10444352	NM_010929	18132	Notch gene homolog 4 (Drosophi	Notch4	0.936	-1.011	0.344651	0.61884
13803	10582188	ENSMUST00000054057	74227	RIKEN cDNA 1700016A09 gene	1700016A09Rik	0.936	-1.092	0.310158	0.586843
13804	10557432	AK144875	100038390	predicted gene, ENSMUSG0000007	ENSMUSG00000073831	0.936	-1.652	0.141342	0.38056
13805	10592802	NM_027909	71764	C2 calcium-dependent domain co	C2cd2l	0.936	-0.425	0.683213	0.859827
13806	10383032	NM_172573	217364	RIKEN cDNA D230014K01 gene	D230014K01Rik	0.936	-0.867	0.413608	0.677093
13807	10421021	NM_001037931	628416	predicted gene, EG628416	EG628416	0.936	-1.062	0.322435	0.599241
13808	10488430	ENSMUST00000099266	100038377	predicted gene, ENSMUSG0000007	ENSMUSG00000074739	0.936	-0.756	0.473446	0.725045
13809	10451559	BC028263	75462	RIKEN cDNA 1700001C19 gene	1700001C19Rik	0.936	-0.416	0.689455	0.863666
13810	10531970	XM_909311	545790	predicted gene, EG545790	EG545790	0.936	-1.207	0.265464	0.540577
13811	10394288	NM_011365	20403	intersectin 2	Itsn2	0.936	-1.374	0.210518	0.475962
13812	10376406	NM_146500	258493	olfactory receptor 319	Olfr319	0.936	-0.063	0.951708	0.981222
13813	10560298					0.936	-0.914	0.390063	0.658746
13814	10588121	NM_031403	83703	debranching enzyme homolog 1 (	Dbr1	0.936	-0.968	0.364199	0.635557
13815	10553842	NM_130880	170711	OTU domain containing 7A	Otud7a	0.936	-1.415	0.198651	0.459751
13816	10532534	NM_001039228	625424	predicted gene, EG625424	EG625424	0.936	-0.671	0.523023	0.759642
13817	10429500	NM_020519	57277	secreted Ly6/Plaur domain cont	Slurp1	0.936	-0.747	0.478977	0.729132

13817	10429500	NM_020519	57277	secreted Ly6/Plaur domain cont	Slurp1	0.936	-0.747	0.478977	0.729152
13818	10506154	NM_001081264	320438	asparagine-linked glycosylatio	Alg6	0.936	-0.941	0.377279	0.647289
13819	10351533	NM_009803	12355	nuclear receptor subfamily 1,	Nr1i3	0.936	-0.536	0.608002	0.817473
13820	10406953	NM_030731	81003	tripartite motif-containing 23	Trim23	0.936	-1.531	0.168377	0.419736
13821	10466604					0.936	-0.576	0.582051	0.800654
13822	10459730	NM_145494	107029	malic enzyme 2, NAD(+)-depende	Me2	0.936	-1.932	0.0933732	0.296261
13823	10382830	DQ390337	100038570	predicted gene, OTTMUSG0000000	OTTMUSG00000003947	0.936	-0.684	0.515118	0.754817
13824	10367292	NM_026444	12974	citrate synthase	Cs	0.936	-2.218	0.0609244	0.227796
13825	10573077	ENSMUST00000042585	70793	predicted gene, EG70793	EG70793	0.936	-0.912	0.391104	0.65945
13826	10602590					0.936	-1.642	0.14331	0.384029
13827	10423098	NM_053077	22293	solute carrier family 45, memb	Slc45a2	0.936	-0.504	0.629466	0.831325
13828	10526781	BC038925	330216	cDNA sequence BC038925	BC038925	0.936	-0.592	0.572088	0.796172
13829	10500268	NM_078479	66292	mitochondrial ribosomal protei	Mrps21	0.935	-1.551	0.163589	0.412809
13830	10459614	ENSMUST00000025428	78931	RIKEN cDNA 4930546C10 gene	4930546C10Rik	0.935	-0.651	0.53508	0.768753
13831	10406530	NM_025335	66074	transmembrane protein 167	Tmem167	0.935	-1.069	0.319571	0.596487
13832	10431229	NM_009886	12614	cadherin, EGF LAG seven-pass G	Celsr1	0.935	-1.151	0.286645	0.562228
13833	10476072	NM_138655	192140	transmembrane channel-like gen	Tmc2	0.935	-0.636	0.544716	0.776896
13834	10478744					0.935	-0.097	0.925152	0.970405
13835	10552526	NM_026806	68668	kallikrein related-peptidase 5	Klk5	0.935	-0.408	0.695374	0.866211
13836	10452022	NM_174989	106759	toll-like receptor adaptor mol	Ticam1	0.935	-1.193	0.270706	0.545331
13837	10431220	BC025858	72355	RIKEN cDNA 2210021J22 gene	2210021J22Rik	0.935	-1.239	0.254237	0.528521
13838	10475965	NM_009086	20017	RNA polymerase 1-2	Rpo1-2	0.935	-1.263	0.245923	0.51897
13839	10482731	NM_018785	56194	PRP40 pre-mRNA processing fact	Prpf40a	0.935	-1.454	0.188079	0.446224
13840	10390763	NM_007719	12775	chemokine (C-C motif) receptor	Ccr7	0.935	-1.157	0.284174	0.559417
13841	10458368	NM_172831	240216	Riken cDNA E230025N22 gene	E230025N22Rik	0.935	-1.247	0.251382	0.525502
13842	10384208					0.935	-0.336	0.746663	0.892399
13843	10440333	NM_173069	224318	spermatogenesis associated glu	Speer2	0.935	-0.607	0.562688	0.789779
13844	10460560	NM_139301	225865	cation channel of sperm 1	Catsper1	0.935	-0.399	0.701229	0.869046
13845	10489346	XR_032746	241765	glyceraldehyde-3-phosphate deh	LOC241765	0.935	-1.334	0.222752	0.492656
13846	10559185	NM_018802	55925	synaptotagmin VIII	Syt8	0.935	-0.741	0.481948	0.730954
13847	10449968	ENSMUST00000025144	77875	cytochrome P450, family 4, sub	Cyp4f41-ps	0.935	-1.008	0.345939	0.620086
13848	10510859	ENSMUST00000030897	230971	multiple EGF-like-domains 6	Megf6	0.935	-0.64	0.542024	0.774466
13849	10352661	NM_008976	19250	protein tyrosine phosphatase,	Ptpn14	0.935	-1.774	0.118156	0.343124
13850	10439985	NM_029092	52575	RNA (guanine-9-) methyltransfe	Rg9mtd1	0.935	-2.221	0.0606495	0.22717
13851	10574682	NM_148952	104394	E2F transcription factor 4	E2f4	0.935	-1.229	0.257526	0.531656
13852	10590320	NM_025974	67115	ribosomal protein L14	Rpl14	0.935	-1.539	0.166336	0.417201
13853	10600988	NM_001081136	245533	diacylglycerol O-acyltransfera	Dgat2l3	0.935	-1.011	0.344544	0.61884
13854	10418410	NM_011103	18753	protein kinase C, delta	Prkcd	0.935	-1.433	0.193822	0.453387
13855	10468810	NM_201615	226278	prolactin releasing hormone re	Prlhr	0.935	-1.172	0.278527	0.553444
13856	10387138	NM_173754	216835	ubiquitin specific peptidase 4	Usp43	0.935	-0.624	0.552021	0.781881
13857	10528951	NM_001014394	381628	G protein-coupled receptor 113	Gpr113	0.935	-0.995	0.351931	0.62505
13858	10555662	NM_009710	11870	ADP-ribosyltransferase 1	Art1	0.935	-0.835	0.430525	0.691299
13859	10406067	NM_146047	218335	CLPTM1-like	Clptm1l	0.935	-1.425	0.195831	0.456219
13860	10489782					0.935	-2.112	0.0713786	0.250953
13861	10377418	NM_028336	66910	transmembrane protein 107	Tmem107	0.935	-1.48	0.181083	0.437031
13862	10415388	NM_020490	57260	leukotriene B4 receptor 2	Ltb4r2	0.935	-0.677	0.519784	0.757566
13863	10408266	NM_175663	319177	histone cluster 1, H2ba	Hist1h2ba	0.935	-1.41	0.200078	0.46189
13864	10474577	BC080661	72425	RIKEN cDNA 2410042D21 gene	2410042D21Rik	0.935	-1.417	0.198205	0.45902
13865	10432820	NM_213728	105866	keratin 72	Krt72	0.935	-0.926	0.384248	0.653466
13866	10408487	NM_025710	66694	ubiquinol-cytochrome c reducta	Uqcrfs1	0.935	-2.188	0.0637164	0.234381
13867	10563037	NM_001008422	233208	SR-related CTD-associated fact	Scaf1	0.935	-1.22	0.260797	0.535471
13868	10441055	NM_019543	56176	phosphatidylinositol glycan an	Pigp	0.935	-1.42	0.197377	0.457905

13869	10447977	NM_175173	71682	WD repeat domain 27	Wdr27	0.935	-1.401	0.202809	0.465349
13870	10520833	NM_025796	66845	mitochondrial ribosomal protei	Mrpl33	0.935	-1.382	0.208223	0.472843
13871	10437582					0.935	-0.381	0.714126	0.874842
13872	10515399	NM_013807	12795	polo-like kinase 3 (Drosophila	Plk3	0.935	-0.735	0.485546	0.733891
13873	10536697	NM_080847	78910	ankyrin repeat and SOCS box-co	Asb15	0.935	-0.898	0.398375	0.66466
13874	10446545	NM_177278	320858	l(3)mbt-like 4 (Drosophila)	L3mbtl4	0.935	-0.976	0.360595	0.632365
13875	10496425	NM_009626	11529	alcohol dehydrogenase 7 (class	Adh7	0.935	-0.643	0.540053	0.772571
13876	10440685	NM_130857	77918	keratin associated protein 16-	Krtap16-5	0.935	-0.872	0.41144	0.675374
13877	10569008	NM_007751	12869	cytochrome c oxidase, subunit	Cox8b	0.935	-0.606	0.563188	0.789853
13878	10358849	NM_007842	13211	DEAH (Asp-Glu-Ala-His) box pol	Dhx9	0.935	-1.574	0.158334	0.405255
13879	10372280	ENSMUST00000116233	628870	predicted gene, EG628870	EG628870	0.935	-0.873	0.410656	0.67503
13880	10416837	NM_008392	16365	immunoresponsive gene 1	Irg1	0.935	-0.53	0.612301	0.820234
13881	10571747					0.935	-0.327	0.752656	0.895764
13882	10599670					0.935	-0.68	0.517602	0.756753
13883	10362490	NM_030203	72480	TSPY-like 4	Tspyl4	0.935	-0.927	0.384018	0.653442
13884	10362289					0.935	-0.351	0.735572	0.886814
13885	10580522	NM_172913	244579	TOX high mobility group box fa	Tox3	0.935	-1.274	0.242307	0.515166
13886	10457884	ENSMUST00000067987	78597	predicted gene, ENSMUSG0000005	ENSMUSG00000054745	0.935	-0.841	0.427483	0.688756
13887	10420316	ENSMUST00000100516	100038506	predicted gene, ENSMUSG0000007	ENSMUSG00000075584	0.935	-0.799	0.449758	0.707093
13888	10451805	NM_028232	72415	shugoshin-like 1 (S. pombe)	Sgol1	0.935	-1.294	0.235711	0.507471
13889	10570321	NM_146207	99375	cullin 4A	Cul4a	0.935	-1.748	0.122639	0.350324
13890	10532905	ENSMUST00000066959	791292	predicted gene, ENSMUSG0000005	ENSMUSG00000054123	0.935	-1.401	0.202766	0.465349
13891	10356866	NM_008798	18566	programmed cell death 1	Pdcd1	0.935	-0.469	0.652977	0.844541
13892	10545917	NM_011865	23983	poly(rC) binding protein 1	Pcbp1	0.935	-1.734	0.12527	0.354486
13893	10346607	NM_008057	14369	frizzled homolog 7 (Drosophila	Fzd7	0.935	-1.421	0.19717	0.457903
13894	10377001	BC110628	338369	RIKEN cDNA A730055C05 gene	A730055C05Rik	0.935	-0.721	0.493744	0.739216
13895	10511442					0.935	-1.436	0.19283	0.452269
13896	10512236	NM_024241	109242	kinesin family member 24	Kif24	0.935	-1.282	0.239523	0.512495
13897	10383429	NM_153288	208990	neuropeptide B	Npb	0.935	-0.856	0.419511	0.681847
13898	10386844	BC109343	69747	RIKEN cDNA 2410012H22 gene	2410012H22Rik	0.935	-1.183	0.27433	0.548974
13899	10401743	BC125331	71275	RIKEN cDNA 4933437F05 gene	4933437F05Rik	0.935	-1.245	0.252199	0.526303
13900	10372110	ENSMUST00000060761	18687	per-hexamer repeat gene 2	Phxr2	0.935	-1.1	0.306588	0.58301
13901	10404264	NM_011164	19109	prolactin	Prl	0.934	-0.837	0.429542	0.690559
13902	10381072	NM_011799	23834	cell division cycle 6 homolog	Cdc6	0.934	-0.733	0.486496	0.734369
13903	10395328	NM_001014973	217463	sorting nexin 13	Snx13	0.934	-1.193	0.270699	0.545331
13904	10525880	BC053444	73121	RIKEN cDNA 3110032G18 gene	3110032G18Rik	0.934	-0.921	0.386739	0.655803
13905	10478776	NM_001085495	99371	ADP-ribosylation factor guanin	Arfgef2	0.934	-0.907	0.393772	0.661649
13906	10470834	NM_001076554	20740	spectrin alpha 2	Spna2	0.934	-1.847	0.105938	0.320958
13907	10541349					0.934	-1.18	0.275401	0.550282
13908	10402761	NM_178915	104885	transmembrane protein 179	Tmem179	0.934	-0.436	0.675262	0.855723
13909	10438889	ENSMUST00000070439	320589	RIKEN cDNA 9530020O07 gene	9530020O07Rik	0.934	-1.346	0.219068	0.487473
13910	10348489	NM_001101647	623503	prolactin releasing hormone	Prlh	0.934	-0.443	0.670957	0.853953
13911	10463930	NM_010847	17859	Max interacting protein 1	Mxi1	0.934	-1.333	0.223128	0.49298
13912	10357917	NM_020588	57439	transmembrane protein 183A	Tmem183a	0.934	-1.433	0.193624	0.453103
13913	10388898	BC027022	69109	RIKEN cDNA 1810009O10 gene	1810009O10Rik	0.934	-1.174	0.277526	0.552648
13914	10413897	NM_001081221	319955	excision repair cross-compleme	Ercc6	0.934	-1.72	0.127938	0.358673
13915	10583264	NM_018736	17535	meiotic recombination 11 homol	Mre11a	0.934	-1.321	0.22687	0.497571
13916	10511042	BC113168	381581	RIKEN cDNA C030017K20 gene	C030017K20Rik	0.934	-0.643	0.540211	0.772711
13917	10461690	NM_001033174	76303	oxysterol binding protein	Osbp	0.934	-0.96	0.368359	0.639194

13918	10596185	NM_175565	321022	carnitine deficiency-associate	Cdv3	0.934	-1.711	0.129592	0.361014
13919	10441740	NM_026644	68262	1-acylglycerol-3-phosphate O-a	Agpat4	0.934	-1.824	0.109593	0.327201
13920	10544365	NM_001007572	194352	transient receptor potential c	Trpv5	0.934	-0.29	0.780101	0.910713
13921	10381962	NM_207624	11421	angiotensin I converting enzym	Ace	0.934	-0.807	0.445253	0.70357
13922	10603270	NM_009757	12155	bone morphogenetic protein 15	Bmp15	0.934	-0.755	0.47415	0.725639
13923	10500443	NM_146275	258272	olfactory receptor 1402	Olfr1402	0.934	-0.677	0.519809	0.757566
13924	10573566	NM_001039514	330817	deoxyhypusine synthase	Dhps	0.934	-1.251	0.249947	0.524217
13925	10396079	NM_178253	271005	kelch domain containing 1	Klhdc1	0.934	-1.03	0.336483	0.61218
13926	10535043	NM_008808	18590	platelet derived growth factor	Pdgfa	0.934	-0.879	0.407647	0.672017
13927	10428066	AK006993	73486	RIKEN cDNA 1700084J12 gene	1700084J12Rik	0.934	-0.583	0.577539	0.797771
13928	10416037	NM_023209	52033	PDZ binding kinase	Pbk	0.934	-0.925	0.385041	0.654288
13929	10512807	NM_001081141	242425	gamma-aminobutyric acid (GABA)	Gabbr2	0.934	-1.597	0.153072	0.397119
13930	10583465	NM_025401	66177	ubiquitin-like 5	Ubl5	0.934	-1.68	0.135655	0.371434
13931	10401002	NM_175644	217674	glycoprotein hormone beta 5	Gphb5	0.934	-0.737	0.48425	0.732769
13932	10535312	NM_178702	231858	RIKEN cDNA D930005D10 gene	D930005D10Rik	0.934	-1.273	0.242682	0.515498
13933	10350594	NM_054102	117198	influenza virus NS1A binding p	Ivns1abp	0.934	-1.408	0.200741	0.462663
13934	10501302	NM_008596	17306	synaptophysin-like 2	Sypl2	0.934	-1.008	0.345973	0.620094
13935	10417869	NM_009674	11750	annexin A7	Anxa7	0.934	-1.168	0.280094	0.55551
13936	10471360	NM_133852	99412	golgi autoantigen, golgin subf	Golga2	0.934	-1.514	0.172551	0.424877
13937	10451675					0.934	-1.205	0.266202	0.541183
13938	10457838	BC117067	328918	RIKEN cDNA C230097I24 gene	C230097I24Rik	0.934	-1.04	0.331895	0.608173
13939	10569458	NM_013742	27267	cysteinyl-tRNA synthetase	Cars	0.934	-1.755	0.121451	0.347955
13940	10604982	NM_001100461	385377	paraneoplastic antigen family	Pnma5	0.934	-0.464	0.656628	0.846261
13941	10599693	BC052359	320237	RIKEN cDNA 6330419J24 gene	6330419J24Rik	0.934	-1.208	0.265325	0.540466
13942	10525588	NM_198611	231727	UDP-GlcNAc:betaGal beta-1,3-N-	B3gnt4	0.934	-1.011	0.344782	0.618903
13943	10474079	ENSMUST00000099692	100038360	predicted gene, ENSMUSG0000007	ENSMUSG00000075024	0.934	-0.867	0.4136	0.677093
13944	10364326	NM_001024709	544710	predicted gene, EG544710	EG544710	0.934	-0.212	0.838169	0.934421
13945	10497713	NM_021483	58869	peroxisomal biogenesis factor	Pex5l	0.934	-1.489	0.178883	0.43395
13946	10492997	NM_001083318	27049	ets variant gene 3	Etv3	0.934	-0.587	0.57496	0.797076
13947	10414697	ENSMUST00000103567	627171	predicted gene, OTTMUSG0000001	OTTMUSG00000015242	0.934	-0.508	0.626447	0.829976
13948	10570870	ENSMUST00000068068	73299	RIKEN cDNA 1700041G16 gene	1700041G16Rik	0.934	-0.93	0.382341	0.651795
13949	10447693					0.934	-0.587	0.575407	0.797076
13950	10519945	NM_177601	212090	transmembrane protein 60	Tmem60	0.934	-1.732	0.125626	0.354875
13951	10371987	NM_019648	56307	methionine aminopeptidase 2	Metap2	0.934	-1.928	0.0939275	0.297484
13952	10352794	ENSMUST00000097436	100038712	predicted gene, ENSMUSG0000007	ENSMUSG00000073476	0.934	-1.134	0.293182	0.569293
13953	10362758	NM_153398	268294	zinc finger and BTB domain con	Zbtb24	0.934	-1.086	0.312448	0.588806
13954	10550698	NM_007710	12715	creatine kinase, muscle	Ckm	0.934	-0.861	0.416816	0.679627
13955	10495107	NM_009631	11542	adenosine A3 receptor	Adora3	0.934	-1.157	0.284153	0.559417
13956	10436781	ENSMUST00000099559	100038709	predicted gene, ENSMUSG0000007	ENSMUSG00000074924	0.934	-0.459	0.660026	0.848652
13957	10564326	NM_183087	70638	RIKEN cDNA 5730507A09 gene	5730507A09Rik	0.934	-0.984	0.35685	0.629197
13958	10387768	NM_017366	11370	acyl-Coenzyme A dehydrogenase,	Acadvl	0.934	-1.559	0.161742	0.410008
13959	10513822	XR_032571	242497	similar to eukaryotic translat	LOC242497	0.934	-1.313	0.229312	0.500317
13960	10552240	ENSMUST00000052454	78547	RIKEN cDNA E130304I02 gene	E130304I02Rik	0.934	-0.514	0.622568	0.827273
13961	10568260	NM_177226	320683	zinc finger protein 629	Zfp629	0.934	-1.448	0.189679	0.44816
13962	10414433	NM_172600	218989	RIKEN cDNA 6720456H20 gene	6720456H20Rik	0.934	-1.117	0.299901	0.575946
13963	10489053	ENSMUST00000099141	74704	RIKEN cDNA 4930518I15 gene	4930518I15Rik	0.934	-0.587	0.575132	0.797076
13964	10514304	BC053719	381590	expressed sequence C87499	C87499	0.934	-0.439	0.673856	0.855069
13965	10532317	NM_145147	107999	GTP binding protein 6 (putativ	Gtpbp6	0.934	-1.274	0.24229	0.515166

13966	10498620	NM_025863	66949	tripartite motif-containing 59	Trim59	0.934	-0.936	0.379358	0.649122
13967	10401416					0.934	-1.065	0.321378	0.598118
13968	10408902	NM_001081059	76137	coiled-coil domain containing	Ccdc90a	0.934	-1.277	0.241067	0.513985
13969	10467688	NM_025644	66583	exosome component 1	Exosc1	0.934	-0.984	0.357192	0.629582
13970	10384221	XR_032579	665343	similar to HSP-90	LOC665343	0.934	-0.458	0.660665	0.848802
13971	10430467	NM_020516	57274	solute carrier family 16 (mono	Slc16a8	0.934	-0.685	0.514873	0.754817
13972	10588203	NM_024291	16716	kyphoscoliosis peptidase	Ky	0.934	-0.794	0.452465	0.709029
13973	10397275					0.934	-0.277	0.789221	0.914259
13974	10412713					0.934	-0.855	0.41987	0.682115
13975	10459944	NM_198429	18018	nuclear factor of activated T-	Nfatc1	0.933	-0.855	0.420278	0.682515
13976	10418475	NM_026911	69019	signal peptidase complex subun	Spcs1	0.933	-1.462	0.18598	0.44418
13977	10575255	NM_001039700	244646	polycystic kidney disease 1 li	Pkd1l3	0.933	-1.011	0.344612	0.61884
13978	10605113	NM_008478	16728	L1 cell adhesion molecule	L1cam	0.933	-0.958	0.369247	0.639896
13979	10473024	NM_172666	228061	alkylglycerone phosphate synth	Agps	0.933	-1.817	0.110837	0.329565
13980	10459455	ENSMUST00000035548	225638	alpha-kinase 2	Alpk2	0.933	-0.658	0.530781	0.76539
13981	10379689	NM_027427	70439	TAF15 RNA polymerase II, TATA	Taf15	0.933	-1.191	0.271454	0.546126
13982	10608193	NM_011564	21674	sex determining region of Chr	Sry	0.933	-0.209	0.840035	0.935328
13983	10416006	ENSMUST00000079469	239151	gene model 600, (NCBI)	Gm600	0.933	-0.606	0.563195	0.789853
13984	10414661	XR_032084	667348	similar to Ac2-210	LOC667348	0.933	-1.8	0.113704	0.334282
13985	10526339	NM_178240	215061	tripartite motif-containing 50	Trim50	0.933	-1.195	0.269744	0.544449
13986	10464704	NM_130863	110355	adrenergic receptor kinase, be	Adrbk1	0.933	-1.546	0.164721	0.414577
13987	10497703	NM_029017	74600	mitochondrial ribosomal protei	Mrpl47	0.933	-1.091	0.310346	0.587004
13988	10344620	ENSMUST00000097833	100038431	predicted gene, ENSMUSG0000007	ENSMUSG00000073742	0.933	-0.959	0.368828	0.639536
13989	10437765	BC034347	223978	RIKEN cDNA C530044N13 gene	C530044N13Rik	0.933	-0.845	0.425088	0.687003
13990	10532368	NM_028596	381668	RIKEN cDNA 2410025L10 gene	2410025L10Rik	0.933	-1.32	0.22703	0.497805
13991	10516024	NM_001081312	69469	transmembrane and coiled-coil	Tmco2	0.933	-0.396	0.703744	0.870071
13992	10370587	NM_001024539	216148	src homology 2 domain-containi	Shc2	0.933	-1.189	0.27225	0.546879
13993	10368475					0.933	-1.486	0.179751	0.43509
13994	10586017	NM_028283	72565	uveal autoantigen with coiled-	Uaca	0.933	-1.128	0.295609	0.57201
13995	10606912					0.933	-1.223	0.259867	0.53415
13996	10420877	NM_028039	71988	establishment of cohesion 1 ho	Esco2	0.933	-1.089	0.311404	0.587941
13997	10569877	NM_026985	69189	RIKEN cDNA 1810033B17 gene	1810033B17Rik	0.933	-1.048	0.32827	0.604687
13998	10582694	BC115734	69627	RIKEN cDNA 2310031A18 gene	2310031A18Rik	0.933	-0.746	0.479059	0.729179
13999	10459858	NM_001101038	620235	sialic acid binding Ig-like le	Siglec15	0.933	-0.658	0.530924	0.765398
14000	10550925	NM_146183	232969	zinc finger protein 428	Zfp428	0.933	-0.97	0.363216	0.634435
14001	10502714	NM_027371	70285	brix domain containing 5	Bxdc5	0.933	-1.627	0.14645	0.388184
14002	10583090	NM_019471	17384	matrix metallopeptidase 10	Mmp10	0.933	-0.984	0.356753	0.629197
14003	10432032	NM_009504	22337	vitamin D receptor	Vdr	0.933	-1.055	0.325693	0.601982
14004	10569985	NM_145591	233987	cDNA sequence BC003267	BC003267	0.933	-1.394	0.204758	0.468195
14005	10409629	ENSMUST00000091583	627648	predicted gene, EG627648	EG627648	0.933	-0.672	0.52256	0.759322
14006	10571114	NM_153592	244373	ER lipid raft associated 2	Erlin2	0.933	-1.24	0.253637	0.527897
14007	10452535					0.933	-1.249	0.250662	0.524426
14008	10567084					0.933	-0.467	0.654138	0.845112
14009	10579925	NM_021356	14388	growth factor receptor bound p	Gab1	0.933	-1.159	0.283494	0.558795
14010	10403925					0.933	-0.536	0.607906	0.817473
14011	10456423	NM_001039088	72124	SEH1-like (S. cerevisiae	Seh1l	0.933	-2.223	0.0605263	0.22695
14012	10404675	NM_026382	67797	RIKEN cDNA 6530403A03 gene	6530403A03Rik	0.933	-1.813	0.111494	0.330405
14013	10513918					0.933	-1.319	0.227411	0.498174
14014	10346840	XR_033701	667592	similar to ribosomal protein S	LOC667592	0.933	-1.07	0.319285	0.596377
14015	10390961	NM_001099774	77914	keratin associated protein 17-	Krtap17-1	0.933	-0.608	0.562107	0.78919
14016	10376326	NM_018738	16145	interferon gamma induced GTPas	Igtp	0.933	-1.169	0.279555	0.554795

14017	10487613	NM_018863	18610	prodynorphin	Pdyn	0.933	-1.145	0.288601	0.564651
14018	10447880	NM_026310	67681	mitochondrial ribosomal protei	Mrpl18	0.933	-1.445	0.190567	0.449454
14019	10364293	NM_019803	22213	ubiquitin-conjugating enzyme E	Ube2g2	0.933	-1.04	0.331783	0.608173
14020	10491551	NM_019393	50911	exosome component 9	Exosc9	0.933	-1.619	0.1482	0.390374
14021	10428176	NM_025712	66696	sorting nexin 31	Snx31	0.933	-0.809	0.444161	0.702635
14022	10484884	NM_146980	258982	olfactory receptor 1272	Olfr1272	0.933	-0.931	0.382027	0.651575
14023	10390352	NM_008379	16211	karyopherin (importin) beta 1	Kpnb1	0.933	-1.792	0.11493	0.337218
14024	10495343	NM_181400	99512	WD repeat domain 47	Wdr47	0.933	-0.845	0.42543	0.687346
14025	10540838	NM_178703	232333	solute carrier family 6 (neuro	Slc6a1	0.933	-0.863	0.416125	0.679215
14026	10349340	NM_207233	226359	complement component 1, q subc	C1ql2	0.933	-1.208	0.265082	0.540178
14027	10496475	NM_007410	11532	alcohol dehydrogenase 5 (class	Adh5	0.933	-1.666	0.138449	0.376412
14028	10479869	NM_133837	98828	cell division cycle 123 homolo	Cdc123	0.933	-1.777	0.117584	0.342028
14029	10355658	NM_153111	260298	FEV (ETS oncogene family)	Fev	0.933	-1.103	0.305439	0.581741
14030	10522973	NM_023054	65961	UTP3, small subunit (SSU) proc	Utp3	0.933	-1.959	0.0897133	0.289125
14031	10485282	NM_026944	69113	alkB, alkylation repair homolo	Alkbh3	0.933	-2.029	0.0807941	0.271356
14032	10466317	NM_001039718	664779	zinc finger protein 91, ciliar	Zfp91-cntf	0.933	-1.494	0.177617	0.43207
14033	10425914	NM_023478	22270	uroplakin 3A	Upk3a	0.933	-0.61	0.560895	0.788011
14034	10405822	NM_053180	105278	cell cycle related kinase	Ccrk	0.933	-1.028	0.336979	0.6127
14035	10581031	XM_001476323	100041397	similar to retinitis pigmentos	LOC100041397	0.933	-0.436	0.675556	0.855911
14036	10390950	NM_001100614	670496	similar to 2300006N05Rik prote	LOC670496	0.933	-0.253	0.807485	0.922441
14037	10374430	NM_178909	103784	WD repeat domain 92	Wdr92	0.933	-1.552	0.163281	0.412327
14038	10448292	NM_001008425	386612	THO complex 6 homolog (Drosoph	Thoc6	0.933	-0.93	0.382218	0.651691
14039	10351471					0.933	-0.332	0.749145	0.893951
14040	10376434	NM_138678	192194	butyrophilin related 1	Butr1	0.933	-0.797	0.450892	0.708135
14041	10553773	NM_008071	14402	gamma-aminobutyric acid (GABA-	Gabrb3	0.932	-1.006	0.346852	0.621091
14042	10382508	NM_026729	68572	immature colon carcinoma trans	Ict1	0.932	-1.872	0.10221	0.313502
14043	10591535					0.932	-1.334	0.222932	0.492857
14044	10402572	ENSMUST00000116391	668158	predicted gene, EG668158	EG668158	0.932	-1.212	0.263795	0.538698
14045	10402136	NM_175493	238377	G protein-coupled receptor 68	Gpr68	0.932	-1.454	0.187957	0.446224
14046	10469856	NM_001031808	107733	mitochondrial ribosomal protei	Mrpl41	0.932	-1.633	0.145135	0.386782
14047	10566529	NM_009906	12751	tripeptidyl peptidase I	Tpp1	0.932	-1.241	0.253421	0.527654
14048	10563643	NM_021884	22088	tumor susceptibility gene 101	Tsg101	0.932	-1.272	0.242864	0.515832
14049	10429510	NM_001081961	69462	RIKEN cDNA 2300005B03 gene	2300005B03Rik	0.932	-0.674	0.521384	0.758794
14050	10391373	NM_007721	12777	chemokine (C-C motif) receptor	Ccr10	0.932	-1.193	0.270516	0.545253
14051	10345509	NM_009539	22637	zeta-chain (TCR) associated pr	Zap70	0.932	-0.56	0.592629	0.807299
14052	10585840	ENSMUST00000098676	100038634	predicted gene, ENSMUSG0000007	ENSMUSG00000074273	0.932	-1.029	0.336963	0.6127
14053	10465224	ENSMUST00000099954	100038547	predicted gene, ENSMUSG0000007	ENSMUSG00000075240	0.932	-1.22	0.260872	0.535507
14054	10446166	BC059729	69875	NADH dehydrogenase (ubiquinone	Ndufa11	0.932	-1.694	0.132794	0.366458
14055	10455335	NM_138945	18998	POU domain, class 4, transcrip	Pou4f3	0.932	-0.91	0.392343	0.660367
14056	10445430	NM_026732	68463	mitochondrial ribosomal protei	Mrpl14	0.932	-1.238	0.254646	0.528904
14057	10557405	NM_030566	70314	rabaptin, RAB GTPase binding e	Rabep2	0.932	-0.953	0.371497	0.64202
14058	10587610	AK039418	319556	RIKEN cDNA A330041J22 gene	A330041J22Rik	0.932	-1.402	0.202523	0.465349
14059	10370339	NM_138301	28240	transient receptor potential c	Trpm2	0.932	-0.899	0.397819	0.664302
14060	10385822	ENSMUST00000084653	100038498	predicted gene, ENSMUSG0000007	ENSMUSG00000072963	0.932	-0.735	0.485406	0.733791
14061	10362033	XR_031343	100039870	similar to uracil DNA glycosyl	LOC100039870	0.932	-1.09	0.310912	0.587446
14062	10585377					0.932	-0.802	0.447965	0.705637
14063	10480829	ENSMUST00000028309	77058	RIKEN cDNA 4921530D09 gene	4921530D09Rik	0.932	-0.929	0.383155	0.652657
14064	10493193	NM_009836	12462	chaperonin subunit 3 (gamma)	Cct3	0.932	-1.692	0.133219	0.367198
14065	10589761	ENSMUST00000058533	320429	lupus brain antigen 1	Lba1	0.932	-0.667	0.525283	0.76149
14066	10368713	BC018406	215929	expressed sequence AI317395	AI317395	0.932	-0.615	0.557324	0.785582

14067	10467175	ENSMUST00000069084	329056	RIKEN cDNA A830019P07 gene	A830019P07Rik	0.932	-0.517	0.620823	0.825734
14068	10497964	ENSMUST00000058578	70804	progesterone receptor membrane	Pgrmc2	0.932	-1.661	0.13932	0.377524
14069	10430681	NM_175109	66538	ribosomal protein S19 binding	Rps19bp1	0.932	-2.325	0.0519619	0.206172
14070	10430195	BC129972	239552	apolipoprotein L 8	Apol8	0.932	-0.564	0.590153	0.806047
14071	10518957	NM_007859	13368	DNA fragmentation factor, beta	Dffb	0.932	-0.719	0.494732	0.739736
14072	10390919	NM_001048196	665891	RIKEN cDNA A030010K20 gene	A030010K20Rik	0.932	-0.364	0.726603	0.881529
14073	10603881	NM_001013387	319535	zinc finger protein 182	Zfp182	0.932	-0.684	0.515327	0.754909
14074	10514662	ENSMUST00000097954	100038687	predicted gene, ENSMUSG0000007	ENSMUSG00000073789	0.932	-0.322	0.756569	0.897871
14075	10543466	NM_010338	14763	G protein-coupled receptor 37	Gpr37	0.932	-0.549	0.599477	0.812001
14076	10441862	ENSMUST00000059824	236574	sperm motility kinase 2B	Smok2b	0.932	-0.851	0.422165	0.684371
14077	10539135	NM_007599	12332	capping protein (actin filamen	Capg	0.932	-1.184	0.273888	0.548502
14078	10378545					0.932	-1.339	0.221093	0.490317
14079	10566791	BC051019	57355	cDNA sequence BC051019	BC051019	0.932	-0.742	0.481764	0.730954
14080	10376007	NM_027917	71774	shroom family member 1	Shroom1	0.932	-1.079	0.315381	0.592275
14081	10375242					0.932	-0.364	0.726282	0.881516
14082	10400030	NM_025840	66912	basic leucine zipper and W2 do	Bzw2	0.932	-1.068	0.320061	0.596822
14083	10567743	NM_026330	67711	non-SMC element 1 homolog (S.	Nsmce1	0.932	-1.81	0.111904	0.331062
14084	10460376	NM_031868	19045	protein phosphatase 1, catalyt	Ppp1ca	0.932	-1.997	0.0848126	0.279632
14085	10370824	NM_013595	17192	methyl-CpG binding domain prot	Mbd3	0.932	-1.311	0.229913	0.500912
14086	10444056	NM_007829	13163	Fas death domain-associated pr	Daxx	0.932	-1.959	0.0897293	0.289125
14087	10391013	NM_010662	16663	keratin 13	Krt13	0.932	-0.98	0.358724	0.630757
14088	10523977	AK165889	100038441	predicted gene, ENSMUSG0000007	ENSMUSG00000072769	0.932	-0.48	0.64559	0.840022
14089	10438603	NM_183029	319765	insulin-like growth factor 2 m	Igf2bp2	0.932	-1.797	0.114132	0.335262
14090	10488655	NM_009743	12048	Bcl2-like 1	Bcl2l1	0.932	-1.664	0.138753	0.376759
14091	10588201					0.932	-0.443	0.670517	0.853752
14092	10499896	NM_011478	20766	small proline-rich protein 3	Sprr3	0.932	-0.639	0.542563	0.774975
14093	10424750	NM_001081065	69020	zinc finger protein 707	Zfp707	0.932	-1.138	0.291379	0.56746
14094	10489498	NM_001048227	52840	dysbindin (dystrobrevin bindin	Dbndd2	0.932	-0.393	0.705819	0.871814
14095	10474867	XR_035630	677379	similar to ubiquinol-cytochrom	LOC677379	0.932	-0.94	0.377495	0.647352
14096	10445565	NM_025302	27398	mitochondrial ribosomal protei	Mrpl2	0.932	-1.727	0.126511	0.356138
14097	10439989					0.932	-0.345	0.739764	0.889275
14098	10438530	NM_009900	12724	chloride channel 2	Clcn2	0.932	-1.374	0.210576	0.476042
14099	10572647	NM_011977	26457	solute carrier family 27 (fatt	Slc27a1	0.932	-1.255	0.248591	0.522089
14100	10370072	NM_133182	15468	protein arginine N-methyltrans	Prmt2	0.932	-1.681	0.135452	0.371032
14101	10566875	ENSMUST00000098110	767812	expressed sequence AA474408	AA474408	0.932	-1.744	0.123391	0.351473
14102	10541711	NM_007531	12034	prohibitin 2	Phb2	0.932	-1.755	0.121473	0.347955
14103	10474112	NM_009424	22034	Tnf receptor-associated factor	Traf6	0.931	-1.557	0.162092	0.410473
14104	10523746	AK164034	243171	cDNA sequence BC005561	BC005561	0.931	-0.9	0.397214	0.664239
14105	10539242					0.931	-0.425	0.683299	0.859827
14106	10563373	NM_027055	69363	sperm acrosome associated 4	Spaca4	0.931	-1.152	0.28606	0.561602
14107	10393047	NM_016905	14635	galactokinase 1	Galk1	0.931	-1.642	0.143396	0.384029
14108	10464407	XM_001480761	74445	RIKEN cDNA 4933412A08 gene	4933412A08Rik	0.931	-1.462	0.185817	0.443894
14109	10513002	XM_001476039	435784	similar to Rps15a protein	LOC435784	0.931	-0.941	0.377108	0.647206
14110	10389164	NM_134025	103737	peroxisomal biogenesis factor	Pex12	0.931	-1.059	0.323783	0.600286
14111	10563797	NM_001005232	13172	developing brain homeobox 1	Dbx1	0.931	-0.761	0.47062	0.722494
14112	10586331	NM_008988	19289	putative neuronal cell adhesio	Punc	0.931	-0.828	0.434093	0.694548
14113	10405619	NM_198004	75731	RIKEN cDNA 5133401N09 gene	5133401N09Rik	0.931	-2.083	0.0745385	0.258241
14114	10404996	NM_013610	18081	ninjurin 1	Ninj1	0.931	-2.109	0.0717598	0.251634
14115	10511501	NM_001085493	76947	RIKEN cDNA 2310030N02 gene	2310030N02Rik	0.931	-0.852	0.42164	0.683993
14116	10560260	NM_019748	56459	SUMO1 activating enzyme subuni	Sae1	0.931	-1.186	0.273126	0.547717

14117	10475293	NM_153387	51885	tubulin, gamma complex associa	Tubgcp4	0.931	-1.825	0.109564	0.327185
14118	10444858	NM_146248	240084	coiled-coil alpha-helical rod	Cchcr1	0.931	-1.424	0.196143	0.456495
14119	10405747					0.931	-0.464	0.65634	0.846043
14120	10412981	NM_172596	218811	SEC24 related gene family, mem	Sec24c	0.931	-1.183	0.274331	0.548974
14121	10598309	NM_019582	54652	calcium channel, voltage-depen	Cacna1f	0.931	-0.414	0.690649	0.864369
14122	10436500	NM_028803	74185	glucan (1,4-alpha-), branching	Gbe1	0.931	-2.069	0.0761895	0.261455
14123	10398111	NM_013774	27380	T-cell leukemia/lymphoma 1B, 4	Tcl1b4	0.931	-0.104	0.920239	0.968133
14124	10566714	NM_001038624	320360	resistance to inhibitors of ch	Ric3	0.931	-1.373	0.210776	0.476291
14125	10383311	ENSMUST00000070897	76377	RIKEN cDNA 2810410L24 gene	2810410L24Rik	0.931	-1.12	0.298515	0.574741
14126	10372600	NM_007636	12461	chaperonin subunit 2 (beta)	Cct2	0.931	-1.73	0.125962	0.355325
14127	10386125	NM_172558	216766	gem (nuclear organelle) associ	Gemin5	0.931	-1.788	0.115683	0.338219
14128	10605143	NM_138630	171207	Rho GTPase activating protein	Arhgap4	0.931	-0.78	0.460304	0.71495
14129	10549836	ENSMUST00000072947	627821	predicted gene, EG627821	EG627821	0.931	-1.001	0.349199	0.622762
14130	10504000					0.931	-0.678	0.519124	0.757461
14131	10566993	NM_173739	233733	UDP-N-acetyl-alpha-D-galactosa	Galntl4	0.931	-0.372	0.720533	0.878348
14132	10483563	NM_172664	228012	tousled-like kinase 1	Tlk1	0.931	-1.757	0.121095	0.347578
14133	10493177	NM_133665	17261	myocyte enhancer factor 2D	Mef2d	0.931	-1.539	0.166442	0.417266
14134	10461583	NM_009962	14764	G protein-coupled receptor 44	Gpr44	0.931	-0.744	0.480233	0.729941
14135	10510081	BC080695	329986	cDNA sequence BC080695	BC080695	0.931	-0.506	0.628069	0.830847
14136	10432897	NM_146063	223917	keratin 79	Krt79	0.931	-1.218	0.2616	0.536103
14137	10461143	NM_001112697	12669	cholinergic receptor, muscarin	Chrm1	0.931	-0.725	0.491215	0.737712
14138	10496888					0.931	-0.871	0.411636	0.675585
14139	10410501	NM_010573	16371	Iroquois related homeobox 1 (D	Irx1	0.931	-1.149	0.28735	0.562985
14140	10410164	NM_001081129	238680	contactin associated protein-l	Cntnap3	0.931	-1.042	0.331213	0.60765
14141	10431943	XR_033584	100046892	similar to high mobility group	LOC100046892	0.931	-0.698	0.50689	0.748755
14142	10351865	NM_146651	258645	olfactory receptor 1403	Olfr1403	0.931	-1.355	0.216245	0.48343
14143	10546086	XR_034267	665416	similar to Rps19 protein	LOC665416	0.931	-2.143	0.0681413	0.243952
14144	10485483	NM_153126	98956	N-acetyltransferase 10	Nat10	0.931	-1.461	0.186188	0.44438
14145	10370610	NM_172551	216151	polymerase (RNA) mitochondrial	Polrmt	0.931	-1.627	0.146547	0.388392
14146	10415163	NM_027790	71412	dehydrogenase/reductase member	Dhrs2	0.931	-0.577	0.581286	0.80031
14147	10508486					0.931	-0.63	0.548081	0.778543
14148	10579954					0.93	-1.48	0.181245	0.437271
14149	10436809	AF358257	70967	RIKEN cDNA 4931408A02 gene	4931408A02Rik	0.93	-1.353	0.217009	0.484575
14150	10579047	BC127607	211134	leucine zipper, putative tumor	Lzts1	0.93	-0.844	0.425538	0.687467
14151	10355931	NM_011811	23874	phenylalanyl-tRNA synthetase,	Farsb	0.93	-1.258	0.247587	0.520853
14152	10570178	ENSMUST00000098935	619290	RIKEN cDNA A230072I06 gene	A230072I06Rik	0.93	-1.483	0.180424	0.436136
14153	10420439	NM_029492	75965	zinc finger, DHHC domain conta	Zdhhc20	0.93	-2.201	0.0625176	0.231461
14154	10583444	NM_146825	258822	olfactory receptor 39	Olfr39	0.93	-1.019	0.341285	0.616096
14155	10374202	NM_009622	432530	adenylate cyclase 1	Adcy1	0.93	-1.008	0.346094	0.620193
14156	10493500	XM_283860	329702	DC-STAMP domain containing 2	Dcst2	0.93	-0.8	0.449015	0.706541
14157	10603837	NM_019435	104130	NADH dehydrogenase (ubiquinone	Ndufb11	0.93	-1.841	0.106976	0.322599
14158	10509122	NM_009924	12802	cannabinoid receptor 2 (macrop	Cnr2	0.93	-0.522	0.617389	0.823029
14159	10532281	NM_001104625	231591	vomeronasal 2, receptor 14	Vmn2r14	0.93	-0.41	0.693779	0.865705
14160	10485048	NM_145528	51897	harbinger transposase derived	Harbi1	0.93	-1.368	0.212451	0.477963
14161	10459208					0.93	-0.855	0.41982	0.682087
14162	10478983	BC049072	66404	RIKEN cDNA 2410001C21 gene	2410001C21Rik	0.93	-2.057	0.07755	0.264513
14163	10445237	ENSMUST00000048691	627626	similar to CG11212-PA	LOC627626	0.93	-0.5	0.632084	0.832782
14164	10575369	ENSMUST00000116422	384866	gene model 1467, (NCBI)	Gm1467	0.93	-0.811	0.443228	0.70194
14165	10479165	NM_007903	13616	endothelin 3	Edn3	0.93	-1.03	0.336258	0.611869
14166	10430626	NM_001013362	504193	neuronal pentraxin with chromo	Npcd	0.93	-1.681	0.135355	0.370815
14167	10436698	NM_026366	67768	N-6 adenine-specific DNA methy	N6amt1	0.93	-1.251	0.249945	0.524217

14168	10351117	ENSMUST00000086070	100049562	predicted gene, ENSMUSG0000006	ENSMUSG00000066752	0.93	-0.686	0.514146	0.754507
14169	10363559	AK016975	71229	RIKEN cDNA 4933428P19 gene	4933428P19Rik	0.93	-0.63	0.547964	0.778543
14170	10467650	NM_177603	212398	frequently rearranged in advan	Frat2	0.93	-1.476	0.182306	0.438828
14171	10368689					0.93	-2.081	0.0747473	0.258738
14172	10465701	NM_019516	56072	lectin, galactose binding, sol	Lgals12	0.93	-1.389	0.206118	0.470186
14173	10412251	NM_010887	17993	NADH dehydrogenase (ubiquinone	Ndufs4	0.93	-1.712	0.129396	0.360656
14174	10598448	NM_008423	16506	potassium voltage-gated channe	Kcnd1	0.93	-0.49	0.638672	0.835923
14175	10576218	NM_170684	102278	copine VII	Cpne7	0.93	-0.918	0.388483	0.657074
14176	10359113	BC116972	329274	RIKEN cDNA A230106N23 gene	A230106N23Rik	0.93	-0.679	0.518153	0.756879
14177	10582322	NM_013914	30927	snail homolog 3 (Drosophila)	Snai3	0.93	-0.964	0.366039	0.63705
14178	10604669					0.93	-0.931	0.381814	0.651436
14179	10567663	NM_001081238	233826	partner and localizer of BRCA2	Palb2	0.93	-1.273	0.242634	0.515498
14180	10384577					0.93	-0.443	0.670761	0.85389
14181	10509927	AK132662	100038750	predicted gene, ENSMUSG0000007	ENSMUSG00000073734	0.93	-1.712	0.129376	0.36065
14182	10447429	XM_140116	225058	predicted gene, EG225058	EG225058	0.93	-1.223	0.259882	0.53415
14183	10550451					0.93	-1.005	0.347558	0.621575
14184	10457203					0.93	-0.838	0.428953	0.689875
14185	10493537	NM_146131	229534	pre-B-cell leukemia transcript	Pbxip1	0.93	-0.775	0.463144	0.71752
14186	10396919	BC040401	217684	RIKEN cDNA 4933426M11 gene	4933426M11Rik	0.93	-1.239	0.254265	0.528527
14187	10565846	NM_025668	66624	signal peptidase complex subun	Spcs2	0.93	-1.636	0.144653	0.38594
14188	10455299	NM_172966	269016	SH3 domain containing ring fin	Sh3rf2	0.93	-0.823	0.43687	0.696333
14189	10348866	NM_174874	66615	autophagy-related 4B (yeast)	Atg4b	0.93	-1.244	0.252428	0.526583
14190	10449142	BC024332	68241	RIKEN cDNA 9530058B02 gene	9530058B02Rik	0.93	-1.169	0.279728	0.554993
14191	10501454					0.93	-0.993	0.35286	0.625927
14192	10466073	ENSMUST00000099686	100038352	predicted gene, ENSMUSG0000007	ENSMUSG00000075017	0.93	-0.978	0.359548	0.63155
14193	10464363	ENSMUST00000026083	75800	RIKEN cDNA 4930442E04 gene	4930442E04Rik	0.93	-0.548	0.600062	0.812117
14194	10562963	AK141792	52819	DNA segment, Chr 7, Brigham &	D7Bwg0826e	0.93	-1.547	0.164482	0.414282
14195	10549679	NM_001003920	381979	BR serine/threonine kinase 1	Brsk1	0.93	-1.104	0.305107	0.581502
14196	10457333	NM_001081393	74934	armadillo repeat containing 4	Armc4	0.93	-0.891	0.401487	0.666803
14197	10382010	NM_027946	71833	WD repeat domain 68	Wdr68	0.93	-1.814	0.111251	0.330054
14198	10347730					0.93	-0.409	0.694153	0.865705
14199	10376747	NM_010603	16515	potassium inwardly-rectifying	Kcnj12	0.93	-1.217	0.261881	0.536313
14200	10485536					0.93	-0.859	0.418012	0.680624
14201	10454512	AK160455	100049078	RIKEN cDNA 1810036N14 gene	1810036N14Rik	0.93	-0.9	0.397013	0.664239
14202	10390979	NM_010659	16660	keratin 31	Krt31	0.93	-0.992	0.353319	0.626044
14203	10596652	NM_133984	69536	HemK methyltransferase family	Hemk1	0.929	-1.159	0.283568	0.558889
14204	10409322	NM_028597	73666	THO complex 3	Thoc3	0.929	-1.872	0.102147	0.313496
14205	10533327	NM_010765	17165	MAP kinase-activated protein k	Mapkapk5	0.929	-2.158	0.0666474	0.241189
14206	10359082					0.929	-1.532	0.168249	0.419709
14207	10442565	NM_027988	71893	NADPH oxidase organizer 1	Noxo1	0.929	-1.408	0.200628	0.462553
14208	10489078	NM_025853	66934	DSN1, MIND kinetochore complex	Dsn1	0.929	-1.048	0.328557	0.604982
14209	10460554	ENSMUST00000099983	321016	predicted gene, ENSMUSG0000007	ENSMUSG00000075264	0.929	-0.626	0.550428	0.780695
14210	10410148	NM_001081129	238680	contactin associated protein-l	Cntnap3	0.929	-0.756	0.473808	0.725379
14211	10450864	NM_146513	258506	olfactory receptor 95	Olfr95	0.929	-0.269	0.795535	0.916955
14212	10436947	NM_134110	246133	potassium voltage-gated channe	Kcne2	0.929	-0.55	0.599117	0.811784
14213	10448048	NM_011185	19170	proteasome (prosome, macropain	Psmb1	0.929	-1.455	0.187874	0.446188
14214	10416400					0.929	-0.468	0.653536	0.844695
14215	10560237	NM_176912	319430	G protein-coupled receptor 77	Gpr77	0.929	-1.13	0.294778	0.57103
14216	10591482	NM_016679	50868	kelch-like ECH-associated prot	Keap1	0.929	-1.437	0.19252	0.452044

14216	10591482	NM_010679	50868	kelch-like ECH-associated prot	Keap1	0.929	-1.457	0.19252	0.452044
14217	10426157	NM_026485	67976	TraB domain containing	Trabd	0.929	-1.341	0.220574	0.489486
14218	10474809	BC031454	53906	RIKEN cDNA 1810007E14 gene	1810007E14Rik	0.929	-0.102	0.921474	0.968661
14219	10505978					0.929	-0.835	0.430769	0.691428
14220	10543448	NM_028459	73178	Wiskott-Aldrich syndrome-like	Wasl	0.929	-1.37	0.211938	0.477389
14221	10470186	NM_001099301	383678	novel lipocalin protein	RP23-225D24.3	0.929	-0.762	0.470519	0.722494
14222	10356601	NM_011066	18627	period homolog 2 (Drosophila)	Per2	0.929	-1.5	0.176165	0.429929
14223	10546775	NM_021449	58799	cereblon	Crbn	0.929	-2.062	0.0769492	0.263058
14224	10441359					0.929	-1.202	0.267201	0.541834
14225	10393125	NM_024177	60441	mitochondrial ribosomal protei	Mrpl38	0.929	-1.88	0.100952	0.311019
14226	10394119	NM_178763	319530	zinc finger protein 750	Zfp750	0.929	-1.232	0.256587	0.530797
14227	10473814	NM_008653	17868	myosin binding protein C, card	Mybpc3	0.929	-0.695	0.508786	0.750513
14228	10406538					0.929	-1.054	0.326048	0.602461
14229	10528691	NM_053075	19744	RAS-homolog enriched in brain	Rheb	0.929	-1.515	0.172397	0.42462
14230	10494299	NM_019561	56205	endosulfine alpha	Ensa	0.929	-1.597	0.153108	0.397119
14231	10499652	ENSMUST00000038450	74034	RIKEN cDNA 4632404H12 gene	4632404H12Rik	0.929	-0.651	0.535177	0.768839
14232	10470736	ENSMUST00000113808	433416	predicted gene, OTTMUSG0000001	OTTMUSG00000012686	0.929	-0.564	0.58992	0.805977
14233	10532584	XM_912851	74376	myosin XVIIIb	Myo18b	0.929	-0.616	0.55669	0.78513
14234	10492679	BC052483	75939	RIKEN cDNA 4930579G24 gene	4930579G24Rik	0.929	-1.069	0.319546	0.596487
14235	10399768	NM_178811	217449	tetratricopeptide repeat domai	Ttc15	0.929	-1.442	0.191202	0.450375
14236	10445016					0.929	-1.092	0.309933	0.586734
14237	10427290	NM_010466	15426	homeo box C8	Hoxc8	0.929	-0.586	0.575456	0.797076
14238	10528287	ENSMUST00000116156	626903	predicted gene, EG626903	EG626903	0.929	-1.221	0.260428	0.53495
14239	10474437	NM_026613	68201	coiled-coil domain containing	Ccdc34	0.929	-1.792	0.115035	0.337303
14240	10386652	NM_007437	11671	aldehyde dehydrogenase family	Aldh3a2	0.929	-1.207	0.265599	0.540607
14241	10455809	BC099538	67343	RIKEN cDNA 1700065I17 gene	1700065I17Rik	0.929	-1.923	0.0946526	0.298885
14242	10517147	NM_026144	67422	dehydrodolichyl diphosphate sy	Dhdds	0.929	-1.331	0.223598	0.493567
14243	10367100	NM_019766	56351	prostaglandin E synthase 3 (cy	Ptges3	0.929	-1.32	0.22723	0.498001
14244	10427308	ENSMUST00000100163	100038520	predicted gene, ENSMUSG0000007	ENSMUSG00000075393	0.929	-0.789	0.45507	0.711341
14245	10569303					0.929	-0.255	0.805866	0.921687
14246	10393628	NM_172443	207592	TBC1 domain family, member 16	Tbc1d16	0.929	-1.296	0.234964	0.506303
14247	10480258	NM_028950	74455	NOL1/NOP2/Sun domain family 6	Nsun6	0.929	-1.118	0.299504	0.575641
14248	10515461	BC058415	66743	RIKEN cDNA 4931406I20 gene	4931406I20Rik	0.929	-1.944	0.0917967	0.293549
14249	10533071	NM_178622	71954	suppressor of defective silenc	Suds3	0.929	-1.973	0.0878562	0.285438
14250	10423134	NM_011767	22763	zinc finger RNA binding protei	Zfr	0.929	-1.705	0.130682	0.362855
14251	10511446	NM_023066	65973	aspartate-beta-hydroxylase	Asph	0.929	-1.491	0.178383	0.433134
14252	10550161	XR_033718	666256	predicted gene, EG666256	EG666256	0.929	-1.091	0.310496	0.587103
14253	10511721					0.929	-0.694	0.509134	0.750516
14254	10437263	NM_028484	73261	RIKEN cDNA 1700037C18 gene	1700037C18Rik	0.929	-1.288	0.237625	0.510033
14255	10356848	NM_025920	67026	THAP domain containing 4	Thap4	0.929	-1.428	0.195099	0.455317
14256	10359861	NM_025569	66447	microsomal glutathione S-trans	Mgst3	0.929	-0.747	0.478724	0.729103
14257	10355105	AF362573	100126881	predicted gene, ENSMUSG0000004	ENSMUSG00000040847	0.929	-1.429	0.194731	0.454775
14258	10368806	NM_009213	20598	sphingomyelin phosphodiesteras	Smpd2	0.929	-2.357	0.0495504	0.200094
14259	10355730	BC028815	69171	RIKEN cDNA 1810031K17 gene	1810031K17Rik	0.929	-1.835	0.107897	0.323967
14260	10443869	NM_024442	70101	cytochrome P450, family 4, sub	Cyp4f16	0.929	-0.598	0.568013	0.793164
14261	10593872	NM_198673	382075	outer dense fiber of sperm tai	Odf3l1	0.929	-1.309	0.230555	0.501476
14262	10400630					0.929	-0.962	0.367209	0.638141
14263	10443301	NM_172617	224656	zinc finger protein 523	Zfp523	0.929	-1.307	0.231237	0.501993
14264	10579101	NM_026818	68709	cartilage intermediate layer p	Cilp2	0.929	-1.103	0.305368	0.581741
14265	10379030	NM_145430	216971	cDNA sequence BC017647	BC017647	0.929	-1.683	0.134896	0.370228

14266	10572605	BC145659	234396	ankyrin repeat and LEM domain	Ankle1	0.929	-1.292	0.236162	0.508287
14267	10567903	NM_011363	20399	SH2B adaptor protein 1	Sh2b1	0.929	-1.923	0.0946885	0.298946
14268	10434880	NM_013751	27281	HRAS-like suppressor	Hrasls	0.929	-0.915	0.389933	0.658612
14269	10498485	NM_015728	11416	solute carrier family 33 (acet	Slc33a1	0.929	-1.213	0.263539	0.53828
14270	10442779	NM_053260	114662	protease, serine, 29	Prss29	0.929	-0.776	0.462166	0.71674
14271	10585652	NM_028636	73744	mannosidase, alpha, class 2C,	Man2c1	0.929	-1.562	0.161033	0.408897
14272	10376216	NM_153139	215335	solute carrier family 36 (prot	Slc36a1	0.929	-0.669	0.524376	0.760916
14273	10494769	NM_194343	229644	tripartite motif-containing 45	Trim45	0.929	-1.021	0.340426	0.61558
14274	10486112	NM_138313	171543	Bcl2 modifying factor	Bmf	0.929	-1.839	0.107265	0.322736
14275	10497250					0.928	-0.351	0.735789	0.886874
14276	10391513	NM_028207	72349	dual specificity phosphatase 3	Dusp3	0.928	-0.96	0.367954	0.638955
14277	10476133	BC049728	66766	RIKEN cDNA 4933425O20 gene	4933425O20Rik	0.928	-0.195	0.851125	0.94011
14278	10584401	NM_207552	404312	olfactory receptor 250	Olfr250	0.928	-0.408	0.694986	0.866071
14279	10555725	NM_147102	259106	olfactory receptor 552	Olfr552	0.928	-0.566	0.588397	0.805111
14280	10488959	ENSMUST00000109617	320095	RIKEN cDNA 6430550D23 gene	6430550D23Rik	0.928	-0.638	0.543155	0.775611
14281	10400605	ENSMUST00000081908	238217	predicted gene, EG238217	EG238217	0.928	-0.375	0.718528	0.877128
14282	10393408	NM_145439	217353	transmembrane channel-like gen	Tmc6	0.928	-1.458	0.186913	0.445182
14283	10395910	NM_008891	18949	pinin	Pnn	0.928	-1.556	0.162499	0.411049
14284	10395287	NM_001033436	380753	ataxin 7-like 1	Atxn7l1	0.928	-1.515	0.172272	0.424438
14285	10384778					0.928	-0.369	0.722761	0.87962
14286	10350806	NM_130456	170484	nephrosis 2 homolog, podocin (	Nphs2	0.928	-0.891	0.401569	0.666842
14287	10526966					0.928	-0.64	0.541991	0.774466
14288	10423346	NM_144523	52521	zinc finger protein 622	Zfp622	0.928	-1.938	0.0926395	0.294729
14289	10470768	NM_026615	68205	ubiquitin related modifier 1 h	Urm1	0.928	-1.196	0.269692	0.544449
14290	10603620	ENSMUST00000101687	100038758	predicted gene, ENSMUSG0000007	ENSMUSG00000073288	0.928	-0.909	0.392664	0.660631
14291	10425299	NM_172609	223696	translocase of outer mitochond	Tomm22	0.928	-1.559	0.161734	0.410008
14292	10444291	NM_207105	14961	histocompatibility 2, class II	H2-Ab1	0.928	-0.559	0.593311	0.807893
14293	10408367	NM_008232	15192	hepatoma derived growth factor	Hdgfl1	0.928	-0.797	0.450923	0.708135
14294	10469320	ENSMUST00000064229	791315	predicted gene, ENSMUSG0000005	ENSMUSG00000052389	0.928	-0.843	0.426345	0.687967
14295	10590791	NM_007465	11797	baculoviral IAP repeat-contain	Birc2	0.928	-1.696	0.132392	0.365778
14296	10347672	NM_027886	71728	serine/threonine kinase 11 int	Stk11ip	0.928	-1.032	0.335436	0.61105
14297	10554468					0.928	-0.495	0.63543	0.834401
14298	10390909	NM_029351	75586	RIKEN cDNA 2310040M23 gene	2310040M23Rik	0.928	-0.674	0.52155	0.758801
14299	10485013	BC085239	228356	RIKEN cDNA 1110051M20 gene	1110051M20Rik	0.928	-1.439	0.192172	0.451484
14300	10357249	NM_001085409	68428	STEAP family member 3	Steap3	0.928	-1.019	0.341065	0.615941
14301	10412231	NM_019960	56534	heat shock protein 3	Hspb3	0.928	-0.936	0.379479	0.649272
14302	10591608	NM_177030	319899	dedicator of cytokinesis 6	Dock6	0.928	-1.726	0.126711	0.356607
14303	10528721	ENSMUST00000066954	77870	RIKEN cDNA E130116L18 gene	E130116L18Rik	0.928	-0.87	0.412363	0.676163
14304	10413163	NM_001033214	105418	RIKEN cDNA E330034G19 gene	E330034G19Rik	0.928	-1.382	0.208244	0.472843
14305	10583347	NM_025844	66917	cysteine and histidine-rich do	Chordc1	0.928	-1.487	0.179489	0.434871
14306	10599997	NM_016985	53332	myotubularin related protein 1	Mtmr1	0.928	-1.758	0.120918	0.347273
14307	10433735	NM_008576	17250	ATP-binding cassette, sub-fami	Abcc1	0.928	-0.841	0.427243	0.688539
14308	10393818	NM_026814	68701	dysferlin interacting protein	Dysfip1	0.928	-0.941	0.377351	0.647352
14309	10422396	NM_145465	223255	serine/threonine kinase 24 (ST	Stk24	0.928	-1.421	0.196989	0.457727
14310	10513082	NM_175518	242474	RIKEN cDNA D730040F13 gene	D730040F13Rik	0.928	-1.193	0.270542	0.545253
14311	10504470	NM_010790	17279	maternal embryonic leucine zip	Melk	0.928	-1.486	0.179663	0.434993
14312	10462088	ENSMUST00000058189	68248	RIKEN cDNA 2410080I02 gene	2410080I02Rik	0.928	-0.803	0.447568	0.705227
14313	10364683	NM_011492	20869	serine/threonine kinase 11	Stk11	0.928	-1.51	0.173422	0.426129
14314	10439642	NM_028756	74102	solute carrier family 35, memb	Slc35a5	0.928	-1.059	0.323817	0.600286
14315	10353343	XM_001476278	100046479	similar to Ac2-210	LOC100046479	0.928	-1.196	0.269683	0.544449

14316	10593159	NM_008775	18475	platelet-activating factor ace	Pafah1b2	0.928	-1.694	0.132821	0.366483
14317	10529239	NM_177298	320951	phosphatidylserine decarboxyla	Pisd	0.928	-1.616	0.148819	0.391099
14318	10517639	NM_178671	212190	UBX domain containing 3	Ubxd3	0.928	-0.752	0.475926	0.727266
14319	10605919	NM_001083110	18744	praja1, RING-H2 motif containi	Pja1	0.928	-1.38	0.208922	0.473969
14320	10590323	ENSMUST00000064646	76100	RIKEN cDNA 5830454E08 gene	5830454E08Rik	0.928	-0.746	0.479185	0.729179
14321	10422854	NM_133227	170762	nucleoporin 155	Nup155	0.928	-1.611	0.150038	0.393062
14322	10405483	NM_001030296	432763	proline rich 7 (synaptic)	Prr7	0.928	-0.643	0.540076	0.772571
14323	10602178	XM_001474727	100045676	similar to 40S ribosomal prote	LOC100045676	0.928	-1.508	0.174089	0.427073
14324	10583056	NM_008605	17381	matrix metallopeptidase 12	Mmp12	0.928	-1.149	0.28713	0.562971
14325	10540897	NM_011146	19016	peroxisome proliferator activa	Pparg	0.928	-1.122	0.297766	0.573822
14326	10563657					0.928	-0.781	0.459778	0.71461
14327	10432734	BC118024	239673	RIKEN cDNA 4732456N10 gene	4732456N10Rik	0.928	-0.652	0.534471	0.768432
14328	10402422	NM_027997	71907	serine (or cysteine) peptidase	Serpina9	0.928	-0.409	0.694222	0.865724
14329	10584522	NM_146286	258283	olfactory receptor 981	Olfr981	0.928	-0.87	0.412468	0.676163
14330	10401519	NM_023409	67963	Niemann Pick type C2	Npc2	0.928	-1.344	0.219743	0.488612
14331	10485667	NM_026992	99349	DPH4 homolog (JJJ3, S. cerevis	Dph4	0.928	-1.624	0.147194	0.389229
14332	10367059	NM_145424	216454	cDNA sequence BC089597	BC089597	0.928	-0.691	0.511403	0.752366
14333	10459620	NM_001082553	80718	RAB27b, member RAS oncogene fa	Rab27b	0.928	-0.825	0.435605	0.695606
14334	10585842	NM_009145	20320	neuroplastin	Nptn	0.928	-0.787	0.456395	0.712554
14335	10410345	NM_001035231	212276	zinc finger protein 748	Zfp748	0.928	-0.977	0.360426	0.632225
14336	10535378	ENSMUST00000014133	442800	RIKEN cDNA D430018E03 gene	D430018E03Rik	0.928	-1.187	0.272679	0.547117
14337	10351182	NM_011345	20339	selectin, endothelial cell	Sele	0.928	-1.385	0.20729	0.47169
14338	10348150	NM_021600	11447	cholinergic receptor, nicotini	Chrnd	0.927	-0.358	0.730457	0.883456
14339	10593270	NM_172770	235330	tetratricopeptide repeat domai	Ttc12	0.927	-1.193	0.270599	0.545272
14340	10567442	XM_355934	381917	dynein, axonemal, heavy chain	Dnahc3	0.927	-0.4	0.700595	0.86896
14341	10377593	NM_029348	75580	zinc finger and BTB domain con	Zbtb4	0.927	-0.874	0.410414	0.67479
14342	10400135					0.927	-0.5	0.631815	0.832719
14343	10351013	NM_001024952	381305	RING CCCH (C3H) domains 1	Rc3h1	0.927	-1.665	0.138585	0.376638
14344	10454828	AY223547	448986	cDNA sequence AY223547	AY223547	0.927	-1.242	0.253116	0.527384
14345	10428396					0.927	-0.876	0.409107	0.673396
14346	10515744	NM_023223	107995	cell division cycle 20 homolog	Cdc20	0.927	-1.589	0.154731	0.399955
14347	10538857	NM_025814	66870	Serpine1 mRNA binding protein	Serbp1	0.927	-1.738	0.124475	0.35337
14348	10414355	NM_178684	218975	mitogen-activated protein kina	Mapk1ip1l	0.927	-1.731	0.125786	0.355049
14349	10356873					0.927	-0.725	0.491167	0.737693
14350	10579119	NM_023312	67184	NADH dehydrogenase (ubiquinone	Ndufa13	0.927	-2.051	0.0782684	0.266177
14351	10394344					0.927	-1.021	0.340311	0.61558
14352	10560300	NM_173430	243853	fukutin related protein	Fkrp	0.927	-1.792	0.114978	0.337276
14353	10351056	BC049713	73844	ankyrin repeat domain 45	Ankrd45	0.927	-2.043	0.0791609	0.267948
14354	10376410	NM_146538	258531	olfactory receptor 315	Olfr315	0.927	-0.759	0.47205	0.723892
14355	10499859					0.927	-1.015	0.342905	0.617132
14356	10485656	NM_023876	77766	elongation protein 4 homolog (	Elp4	0.927	-1.84	0.107034	0.322599
14357	10447502	NM_009625	11516	adenylate cyclase activating p	Adcyap1	0.927	-1.244	0.252483	0.526583
14358	10368893	NM_145743	215951	lactation elevated 1	Lace1	0.927	-1.466	0.18473	0.442299
14359	10444439	NM_017406	12915	cAMP responsive element bindin	Crebl1	0.927	-1.812	0.111559	0.330459
14360	10516753	NM_001034872	332942	gene model 853, (NCBI)	Gm853	0.927	-1.18	0.27527	0.550143
14361	10407543	NM_027000	69237	GTP binding protein 4	Gtpbp4	0.927	-1.761	0.120441	0.346759
14362	10357133					0.927	-1.702	0.131322	0.363963
14363	10604497	NM_001011794	257978	olfactory receptor 1322	Olfr1322	0.927	-0.321	0.757545	0.898154
14364	10485170	NM_009963	12953	cryptochrome 2 (photolyase-lik	Cry2	0.927	-1.773	0.118318	0.343378
14365	10383353	NM_145363	208634	tetraspanin 10	Tspan10	0.927	-1.105	0.304681	0.581126
14366	10502395	ENSMUST00000012186	67741	RIKEN cDNA 4930579F01 gene	4930579F01Rik	0.927	-0.427	0.682038	0.859468
14367	10574404	NM_001035123	66083	SET domain containing 6	Setd6	0.927	-1.439	0.192012	0.451351
14368	10529873	AB232585	59021	RAB2A, member RAS oncogene fam	Rab2a	0.927	-1.036	0.333695	0.609432

14369	10397083	NM_027349	67039	RNA binding motif protein 25	Rbm25	0.927	-1.316	0.228386	0.49943
14370	10474243	NM_145529	228410	cleavage stimulation factor, 3	Cstf3	0.927	-1.895	0.0986442	0.306683
14371	10574220	NM_009142	20312	chemokine (C-X3-C motif) ligan	Cx3cl1	0.927	-0.773	0.464142	0.717962
14372	10352838	NM_008484	16780	laminin, beta 3	Lamb3	0.927	-1.397	0.204016	0.467308
14373	10513604	NM_024257	72748	haloacid dehalogenase-like hyd	Hdhd3	0.927	-0.72	0.49429	0.739556
14374	10582427	NM_009824	12398	core-binding factor, runt doma	Cbfa2t3	0.927	-0.743	0.481132	0.730704
14375	10412218	NM_008196	14945	granzyme K	Gzmk	0.927	-0.848	0.423771	0.686081
14376	10437191	NM_033149	93961	UDP-Gal:betaGlcNAc beta 1,3-ga	B3galt5	0.927	-1.351	0.217602	0.485334
14377	10594186	XR_001723	665385	predicted gene, EG665385	EG665385	0.927	-0.563	0.590705	0.806356
14378	10586252	XM_001476259	102442	DENN/MADD domain containing 4A	Dennd4a	0.927	-0.764	0.469162	0.721405
14379	10515702	ENSMUST00000075406	230676	cDNA sequence BC059842	BC059842	0.927	-1.786	0.115998	0.338719
14380	10457583					0.927	-1.235	0.255438	0.529807
14381	10412735					0.927	-0.865	0.414756	0.678079
14382	10576495	BC094596	330863	tripartite motif-containing 67	Trim67	0.927	-1.145	0.288836	0.564954
14383	10476617	XR_034950	677513	similar to RNA binding motif p	LOC677513	0.927	-2.084	0.0744335	0.258046
14384	10439509	BC115688	74663	RIKEN cDNA 4930435E12 gene	4930435E12Rik	0.927	-0.65	0.535728	0.769213
14385	10587241	NM_173731	208982	3-hydroxymethyl-3-methylglutar	Hmgcll1	0.927	-0.454	0.663385	0.850117
14386	10515920	NM_026494	106564	phosphopantothenoylcysteine sy	Ppcs	0.927	-1.421	0.197039	0.457727
14387	10528972	NM_031875	83762	otoferlin	Otof	0.927	-0.619	0.555232	0.783961
14388	10377467	NM_033041	84653	hairy and enhancer of split 7	Hes7	0.927	-1.547	0.164486	0.414282
14389	10550978	NM_001102613	232970	pleckstrin homology-like domai	Phldb3	0.927	-0.62	0.554358	0.783473
14390	10479397	NM_018766	18216	neurotensin receptor 1	Ntsr1	0.927	-0.36	0.728834	0.882565
14391	10492454					0.927	-1.099	0.307238	0.583826
14392	10355916	NM_008781	18505	paired box gene 3	Pax3	0.927	-0.741	0.48219	0.730954
14393	10407262	ENSMUST00000109244	238896	cell division cycle 20 homolog	Cdc20b	0.927	-0.613	0.558633	0.786292
14394	10555087					0.927	-0.441	0.672386	0.854651
14395	10451110	NM_008302	15516	heat shock protein 90kDa alpha	Hsp90ab1	0.927	-1.765	0.11964	0.345914
14396	10394109	NM_139147	217371	Rab40b, member RAS oncogene fa	Rab40b	0.927	-0.923	0.385813	0.654758
14397	10595895	BC092140	75881	RIKEN cDNA 4930579K19 gene	4930579K19Rik	0.927	-0.84	0.427767	0.689074
14398	10415991	NM_199029	380912	zinc finger protein 395	Zfp395	0.927	-1.946	0.0915464	0.293059
14399	10514338					0.927	-0.379	0.71558	0.875402
14400	10358357	ENSMUST00000081144	226472	predicted gene, EG226472	EG226472	0.927	-1.632	0.145362	0.387047
14401	10475879	ENSMUST00000099394	241634	gene model 355, (NCBI)	Gm355	0.927	-1.127	0.296005	0.572462
14402	10598087	ENSMUST00000082419	17722	NADH dehydrogenase subunit 6	ND6	0.927	-1.12	0.298438	0.574644
14403	10546919	BC116825	101122	RNA pseudouridylate synthase d	Rpusd3	0.927	-1.217	0.261941	0.536363
14404	10478892	ENSMUST00000021742	329562	RIKEN cDNA A530013C23 gene	A530013C23Rik	0.927	-1.033	0.334826	0.610375
14405	10488802					0.927	-1.11	0.302658	0.578712
14406	10463211	NM_145501	84095	phosphatidylinositol 4-kinase	Pi4k2a	0.927	-2.142	0.0683171	0.244333
14407	10460787	NM_194348	329015	ATG2 autophagy related 2 homol	Atg2a	0.927	-1.709	0.129895	0.361535
14408	10519636					0.927	-1.499	0.176355	0.430187
14409	10459925	ENSMUST00000037107	791289	predicted gene, ENSMUSG0000005	ENSMUSG00000053474	0.927	-1.015	0.342936	0.617132
14410	10363231	NM_020561	57319	sphingomyelin phosphodiesteras	Smpdl3a	0.927	-1.066	0.32077	0.597672
14411	10436606					0.927	-0.891	0.401489	0.666803
14412	10589128					0.927	-1.026	0.33787	0.613423
14413	10507362	NM_133250	70603	mutY homolog (E. coli)	Mutyh	0.927	-1.383	0.208003	0.472478
14414	10461038	NM_134147	107227	MACRO domain containing 1	Macrod1	0.927	-1.458	0.186924	0.445182
14415	10478075					0.927	-0.702	0.504852	0.747036
14416	10356671	NM_147038	259040	olfactory receptor 1416	Olfr1416	0.927	-0.539	0.605858	0.8162
14417	10518385	NM_133201	170731	mitofusin 2	Mfn2	0.927	-1.762	0.12025	0.346577
14418	10529549	NM_001113362	100855	TBC1 domain family, member 14	Tbc1d14	0.927	-1.589	0.154845	0.400004
14419	10550169	BC060121	228829	PHD finger protein 20	Phf20	0.927	-0.87	0.412375	0.676163

14419	10350169	BC060121	228829	PHD finger protein 20	Phf20	0.927	-0.87	0.412375	0.676165
14420	10474526	NM_207206	99010	1-acylglycerol-3-phosphate O-a	Agpat7	0.926	-2.164	0.0660281	0.239756
14421	10450089	NM_009066	19763	ring finger protein 1	Ring1	0.926	-0.904	0.395278	0.66309
14422	10515396	ENSMUST00000106445	78611	RIKEN cDNA 9530048O09 gene	9530048O09Rik	0.926	-0.947	0.374485	0.644557
14423	10460291	NM_021791	60425	double C2, gamma	Doc2g	0.926	-1.489	0.178878	0.43395
14424	10495675	NM_010171	14066	coagulation factor III	F3	0.926	-0.769	0.466405	0.719571
14425	10524668	NM_026504	52064	coenzyme Q5 homolog, methyltra	Coq5	0.926	-1.455	0.187797	0.446159
14426	10564377	NM_146191	233328	leucine-rich repeat kinase 1	Lrrk1	0.926	-1.453	0.188438	0.446521
14427	10388623					0.926	-1.402	0.202469	0.465275
14428	10466110	NM_023529	69826	membrane-spanning 4-domains, s	Ms4a10	0.926	-0.354	0.733498	0.88593
14429	10416107	ENSMUST00000071522	791407	predicted gene, ENSMUSG0000005	ENSMUSG00000057913	0.926	-0.44	0.672864	0.854651
14430	10512655	NM_001038993	73469	ring finger protein 38	Rnf38	0.926	-1.39	0.205833	0.46974
14431	10351749	NM_153555	98193	WD repeat domain 42A	Wdr42a	0.926	-1.739	0.124407	0.35332
14432	10590135	ENSMUST00000093527	100038738	predicted gene, ENSMUSG0000007	ENSMUSG00000074029	0.926	-0.308	0.766667	0.902924
14433	10405942	ENSMUST00000060609	328280	predicted gene, EG328280	EG328280	0.926	-0.721	0.493403	0.739056
14434	10561861	ENSMUST00000047308	381867	OVO homolog-like 3 (Drosophila	Ovol3	0.926	-0.831	0.432754	0.693239
14435	10467342	ENSMUST00000065022	791286	predicted gene, ENSMUSG0000005	ENSMUSG00000052663	0.926	-0.521	0.617906	0.823459
14436	10465625	NM_134150	107260	OTU domain, ubiquitin aldehyde	Otub1	0.926	-1.898	0.0983371	0.306086
14437	10405303	NM_001033364	268663	protocadherin 24	Pcdh24	0.926	-1.014	0.343476	0.617556
14438	10353296	NM_026456	67923	transcription elongation facto	Tceb1	0.926	-1.622	0.147551	0.389587
14439	10383012	NM_133757	74451	phosphatidylglycerophosphate s	Pgs1	0.926	-1.46	0.186565	0.444895
14440	10368159	NM_029529	76157	solute carrier family 35, memb	Slc35d3	0.926	-0.232	0.822709	0.929111
14441	10471909					0.926	-0.825	0.435685	0.695606
14442	10360741	ENSMUST00000058825	403180	coiled-coil domain containing	Ccdc121	0.926	-1.032	0.335227	0.610757
14443	10347503	NM_009872	12570	cyclin-dependent kinase 5, reg	Cdk5r2	0.926	-1.504	0.175116	0.428251
14444	10565968	NM_001111111	73683	autophagy related 16 like 2 (S	Atg16l2	0.926	-1.435	0.193182	0.452493
14445	10582123	NM_175185	72552	hydroxysteroid dehydrogenase l	Hsdl1	0.926	-1.42	0.197314	0.457905
14446	10558971	NM_007459	11772	adaptor protein complex AP-2,	Ap2a2	0.926	-1.555	0.162734	0.411428
14447	10390816	NM_010666	16675	keratin 27	Krt27	0.926	-0.505	0.628618	0.830964
14448	10575873	NM_027950	71839	oxidative stress induced growt	Osgin1	0.926	-0.96	0.367959	0.638955
14449	10593756	NM_145129	110834	cholinergic receptor, nicotini	Chrna3	0.926	-1.427	0.195427	0.45573
14450	10509635	NM_025337	110198	aldo-keto reductase family 7,	Akr7a5	0.926	-1.835	0.107874	0.323945
14451	10364916	NM_175195	73218	RIKEN cDNA 3110056O03 gene	3110056O03Rik	0.926	-1.328	0.224703	0.494806
14452	10594855	NM_026599	68178	cingulin-like 1	Cgnl1	0.926	-1.01	0.345353	0.619455
14453	10371842	AK087890	791344	predicted gene, ENSMUSG0000005	ENSMUSG00000054515	0.926	-1.291	0.236464	0.508575
14454	10461164	NM_134139	107071	WD repeat domain 74	Wdr74	0.926	-2.126	0.0698916	0.247709
14455	10590381	NM_011703	22354	vasoactive intestinal peptide	Vipr1	0.926	-0.939	0.377978	0.647713
14456	10502845	BC098205	215708	RIKEN cDNA C030011O14 gene	C030011O14Rik	0.926	-1.529	0.168744	0.420183
14457	10405894	NM_008959	19210	phosphatidylserine synthase 1	Ptdss1	0.926	-1.298	0.234099	0.50534
14458	10401900	NM_001039089	20338	sel-1 suppressor of lin-12-lik	Sel1l	0.926	-1.382	0.208326	0.472978
14459	10541069	NM_146759	258754	olfactory receptor 214	Olfr214	0.926	-0.505	0.62871	0.830996
14460	10398075	NM_009252	20716	serine (or cysteine) peptidase	Serpina3n	0.926	-0.513	0.623017	0.827506
14461	10555925	NM_001033317	233649	cyclic nucleotide gated channe	Cnga4	0.926	-1.556	0.162524	0.411049
14462	10400474	NM_009385	21869	NK2 homeobox 1	Nkx2-1	0.926	-0.847	0.424312	0.686483
14463	10345608	NM_026123	67387	unc-50 homolog (C. elegans)	Unc50	0.926	-1.421	0.196963	0.457727
14464	10502214	ENSMUST00000106337	71519	cytochrome P450, family 2, sub	Cyp2u1	0.926	-1.414	0.198949	0.460238
14465	10460263	NM_027857	71670	aspartoacylase (aminoacylase)	Acy3	0.926	-1.22	0.260935	0.535507
14466	10520355	NM_008314	15563	5-hydroxytryptamine (serotonin	Htr5a	0.926	-0.391	0.707374	0.872175
14467	10345406					0.926	-1.485	0.179872	0.435199

14468	10465354	BC118930	68505	RIKEN cDNA 1110014N23 gene	1110014N23Rik	0.926	-1.735	0.125023	0.354024
14469	10479324	NM_181424	52856	GTP binding protein 5	Gtpbp5	0.926	-1.55	0.163848	0.413216
14470	10517488	NM_010142	13844	Eph receptor B2	Ephb2	0.926	-1.376	0.210089	0.475449
14471	10450116	NM_008202	14977	solute carrier family 39 (zinc	Slc39a7	0.926	-1.291	0.236682	0.508784
14472	10470166	NM_178036	332578	lipocalin 10	Lcn10	0.926	-1.354	0.216629	0.483982
14473	10574478	AK158572	100038474	predicted gene, ENSMUSG0000007	ENSMUSG00000074125	0.926	-0.88	0.407419	0.671862
14474	10567645	NM_026140	67417	glutamyl-tRNA synthetase 2 (mi	Ears2	0.926	-1.884	0.100316	0.309873
14475	10442549	NM_183149	213753	zinc finger protein 598	Zfp598	0.926	-1.43	0.194527	0.454622
14476	10576934	NM_173446	270028	expressed sequence AW121567	AW121567	0.926	-0.672	0.522592	0.759322
14477	10416023	NM_028903	71145	scavenger receptor class A, me	Scara5	0.926	-1.137	0.292016	0.568125
14478	10413497	NM_019979	80795	selenoprotein K	Selk	0.926	-0.979	0.359188	0.63128
14479	10570618	NM_001025351	574081	predicted gene, EG574081	EG574081	0.926	-0.091	0.930157	0.972567
14480	10557782	NM_133943	101502	hydroxy-delta-5-steroid dehydr	Hsd3b7	0.926	-1.701	0.131388	0.364051
14481	10580469	NM_019626	12404	cerebellin 1 precursor protein	Cbln1	0.926	-0.434	0.676769	0.856344
14482	10345967	NM_144558	246229	basic, immunoglobulin-like var	Bivm	0.926	-1.48	0.181113	0.437053
14483	10399461	XR_034642	238091	similar to Glyceraldehyde-3-ph	LOC238091	0.926	-0.991	0.353868	0.626543
14484	10500710	BC037703	242125	cDNA sequence BC037703	BC037703	0.926	-1.37	0.211881	0.477389
14485	10584975	AK139379	100101457	predicted gene, ENSMUSG0000007	ENSMUSG00000074379	0.926	-1.149	0.287274	0.562985
14486	10560868	NM_001033205	101544	zinc finger protein 575	Zfp575	0.925	-1.006	0.347022	0.621237
14487	10437174	NM_207301	71446	tryptophan rich basic protein	Wrb	0.925	-0.983	0.357343	0.629743
14488	10386262	BC044882	380698	obscurin, cytoskeletal calmodu	Obscn	0.925	-0.673	0.52169	0.75888
14489	10454606	NM_001110015	225348	WD repeat domain 36	Wdr36	0.925	-1.524	0.170203	0.421869
14490	10450752	NM_024468	79263	tripartite motif-containing 39	Trim39	0.925	-1.179	0.27598	0.550828
14491	10432135	NM_027304	70069	H1 histone family, member N, t	H1fnt	0.925	-1.683	0.134893	0.370228
14492	10449000	NM_018857	56047	mesothelin	Msln	0.925	-0.778	0.461369	0.715977
14493	10412828					0.925	-1.242	0.253227	0.527562
14494	10542319	NM_001109914	381823	apolipoprotein L domain contai	Apold1	0.925	-0.911	0.391895	0.660136
14495	10415873					0.925	-0.715	0.497082	0.741437
14496	10592217	NM_008408	16430	STT3, subunit of the oligosacc	Stt3a	0.925	-2.173	0.0651787	0.238029
14497	10399308	NM_016863	14226	FK506 binding protein 1b	Fkbp1b	0.925	-1.244	0.252569	0.526711
14498	10603618					0.925	-0.734	0.485892	0.734018
14499	10363967					0.925	-0.447	0.668102	0.851935
14500	10363492	ENSMUST00000020287	237362	neuropeptide FF receptor 1	Npffr1	0.925	-0.88	0.407115	0.671626
14501	10506454	NM_133882	110382	complement component 8, beta s	C8b	0.925	-0.6	0.566613	0.792358
14502	10521824	NM_011435	20657	superoxide dismutase 3, extrac	Sod3	0.925	-1.2	0.268058	0.542786
14503	10457780	NM_001033445	381126	gene model 944, (NCBI)	Gm944	0.925	-1.647	0.142371	0.382404
14504	10417794	BC027644	67509	RIKEN cDNA 1810063B07 gene	1810063B07Rik	0.925	-1.757	0.121054	0.347578
14505	10549862	NM_177061	257882	olfactory receptor 1344	Olfr1344	0.925	-0.587	0.575307	0.797076
14506	10468783	NM_009501	22326	ventral anterior homeobox cont	Vax1	0.925	-1.249	0.250596	0.524406
14507	10551891	NM_172142	243910	nuclear factor of kappa light	Nfkbid	0.925	-1.434	0.193581	0.453103
14508	10393113	NM_178802	338364	tripartite motif-containing 65	Trim65	0.925	-1.075	0.317213	0.594448
14509	10556553	NM_173767	233752	inscuteable homolog (Drosophil	Insc	0.925	-0.758	0.472341	0.724076
14510	10464836	NM_013456	11474	actinin alpha 3	Actn3	0.925	-0.986	0.356049	0.628563
14511	10502484	NM_178654	109333	protein kinase N2	Pkn2	0.925	-1.791	0.11518	0.337402
14512	10518075	BC038692	329977	forkhead-associated (FHA) phos	Fhad1	0.925	-0.761	0.470571	0.722494
14513	10399224	ENSMUST00000095903	68571	RIKEN cDNA 1110002L01 gene	1110002L01Rik	0.925	-1.132	0.293974	0.570098
14514	10417749	NM_009455	22194	ubiquitin-conjugating enzyme E	Ube2e1	0.925	-1.484	0.180175	0.435693
14515	10436955	ENSMUST00000054592	76785	RIKEN cDNA 2410124H12 gene	2410124H12Rik	0.925	-0.813	0.44199	0.70082
14516	10553537	NM_178705	233271	leucine zipper protein 2	Luzp2	0.925	-0.412	0.692523	0.865136
14517	10489958	NM_001081134	241794	potassium voltage-gated channe	Kcng1	0.925	-1.597	0.153093	0.397119
14518	10568318	NM_001081268	330657	cDNA sequence BC039632	BC039632	0.925	-1.089	0.311226	0.587812
14519	10362052	NM_178713	237320	aldehyde dehydrogenase 8 famil	Aldh8a1	0.925	-1.402	0.202554	0.465349
14520	10573998	NM_177767	270086	2-oxoglutarate and iron-depend	Ogfod1	0.925	-2.027	0.0810678	0.271716

14521	10602722	NM_001005370	278240	spindlin family, member 2	Spin2	0.925	-1.366	0.213093	0.478965
14522	10473406	NM_016914	53856	proteoglycan 3	Prg3	0.925	-1.114	0.30083	0.57699
14523	10450579	NM_007584	12305	discoidin domain receptor fami	Ddr1	0.925	-1.497	0.176846	0.431034
14524	10418616	BC023155	110084	dynein, axonemal, heavy chain	Dnahc1	0.925	-1.299	0.233791	0.505106
14525	10445741					0.925	-1.23	0.257249	0.53155
14526	10431732	NM_026025	67197	zinc finger CCHC-type and RNA	Zcrb1	0.925	-1.876	0.101543	0.31225
14527	10379260	AK154065	790910	predicted gene, OTTMUSG0000000	OTTMUSG00000000169	0.925	-0.972	0.362679	0.634126
14528	10557975	NM_133254	246787	solute carrier family 5 (sodiu	Slc5a2	0.925	-0.783	0.458836	0.713797
14529	10519713					0.925	-1.25	0.250258	0.524321
14530	10487382	NM_029629	68126	fumarylacetoacetate hydrolase	Fahd2a	0.925	-0.721	0.493451	0.739076
14531	10347386	NM_021383	58184	rcd1 (required for cell differ	Rqcd1	0.925	-1.77	0.118866	0.344334
14532	10415159	NM_153083	105663	thiamine triphosphatase	Thtpa	0.925	-1.574	0.158174	0.405072
14533	10450451	NM_020027	53761	HLA-B associated transcript 2	Bat2	0.925	-1.92	0.0951351	0.299747
14534	10524353	NM_018783	54723	tuftelin interacting protein 1	Tfip11	0.925	-1.665	0.138671	0.376676
14535	10532574	XM_912851	74376	myosin XVIIIb	Myo18b	0.925	-0.727	0.490202	0.737262
14536	10551666	NM_008279	26411	mitogen-activated protein kina	Map4k1	0.925	-0.978	0.359763	0.631744
14537	10459747	NM_172632	225724	mitogen-activated protein kina	Mapk4	0.925	-1.79	0.11528	0.337519
14538	10444802	NM_010392	15013	histocompatibility 2, Q region	H2-Q2	0.924	-0.774	0.463555	0.717736
14539	10589846					0.924	-0.478	0.646977	0.840859
14540	10523138	NM_203320	330122	chemokine (C-X-C motif) ligand	Cxcl3	0.924	-0.411	0.692929	0.865409
14541	10374060	NM_023816	76389	ankyrin repeat domain 36	Ankrd36	0.924	-1.286	0.238101	0.510486
14542	10436750	ENSMUST00000009191	546672	predicted gene, EG546672	EG546672	0.924	-0.896	0.399318	0.665621
14543	10405751					0.924	-1.241	0.253409	0.527654
14544	10488439	XR_034724	279056	similar to XPMC2 prevents mito	LOC279056	0.924	-0.859	0.417959	0.680624
14545	10490984					0.924	-1.36	0.214921	0.481846
14546	10498367	NM_028808	74191	purinergic receptor P2Y, G-pro	P2ry13	0.924	-1.529	0.168967	0.420416
14547	10509526	NM_010623	16559	kinesin family member 17	Kif17	0.924	-1.207	0.265573	0.540607
14548	10432619	NM_010127	19009	POU domain, class 6, transcrip	Pou6f1	0.924	-1.159	0.283366	0.5587
14549	10366004	NM_026482	67972	ATPase, Ca++ transporting, pla	Atp2b1	0.924	-1.232	0.256497	0.530714
14550	10440621	NM_146072	14805	glutamate receptor, ionotropic	Grik1	0.924	-0.417	0.688864	0.863319
14551	10503264	NM_009830	12448	cyclin E2	Ccne2	0.924	-1.626	0.146823	0.388752
14552	10444824	NM_207648	110557	histocompatibility 2, Q region	H2-Q6	0.924	-0.844	0.42565	0.687513
14553	10545804	NM_001034902	545861	predicted gene, EG545861	EG545861	0.924	-1.123	0.297443	0.573687
14554	10598573	ENSMUST00000116161	436193	predicted gene, EG436193	EG436193	0.924	-0.564	0.589544	0.805725
14555	10540860	NM_028835	74244	autophagy-related 7 (yeast)	Atg7	0.924	-1.76	0.120542	0.346982
14556	10457225	NM_007746	26410	mitogen-activated protein kina	Map3k8	0.924	-0.873	0.410594	0.67498
14557	10525336	BC120681	231717	RIKEN cDNA A230106M15 gene	A230106M15Rik	0.924	-1.712	0.129314	0.360573
14558	10388225					0.924	-1.124	0.29704	0.573626
14559	10346191	NM_009283	20846	signal transducer and activato	Stat1	0.924	-2.209	0.061792	0.229738
14560	10544823					0.924	-0.873	0.41098	0.675081
14561	10529215					0.924	-0.826	0.435037	0.695306
14562	10471951					0.924	-1.138	0.291429	0.567505
14563	10450843	NM_001115075	240095	histocompatibility 2, M region	H2-M5	0.924	-0.859	0.418115	0.680624
14564	10515049	AK042682	100049569	predicted gene, ENSMUSG0000005	ENSMUSG00000053880	0.924	-0.73	0.488291	0.735934
14565	10357239	NM_019432	170706	transmembrane protein 37	Tmem37	0.924	-1.079	0.315505	0.59239
14566	10448316	ENSMUST00000062827	320309	RIKEN cDNA 1520401A03 gene	1520401A03Rik	0.924	-1.614	0.149386	0.39179
14567	10576873	NM_010485	15568	ELAV (embryonic lethal, abnorm	Elavl1	0.924	-1.607	0.150756	0.394308
14568	10516221	AK051152	442805	RIKEN cDNA D130007C19 gene	D130007C19Rik	0.924	-0.925	0.384928	0.654157
14569	10561498	BC094908	101744	RIKEN cDNA C330005M16 gene	C330005M16Rik	0.924	-0.599	0.567675	0.792953
14570	10555921	ENSMUST00000106805	545989	predicted gene, EG545989	EG545989	0.924	-1.399	0.203323	0.466186
14571	10426098	NM_029720	76737	cysteine-rich with EGF-like do	Creld2	0.924	-2.022	0.08166	0.272831
14572	10404904	NM_001081425	666794	RNA binding motif protein 24	Rbm24	0.924	-0.838	0.428941	0.689875

14573	10386123	XR_034114	676530	hypothetical protein LOC676530	LOC676530	0.924	-0.676	0.520163	0.757722
14574	10353272	NM_001111271	29819	staufen (RNA binding protein)	Stau2	0.924	-1.538	0.166623	0.417525
14575	10525854	ENSMUST00000037065	56087	dynein, axonemal, heavy chain	Dnahc10	0.924	-0.824	0.436406	0.6963
14576	10459405	NM_027350	70223	asparaginyl-tRNA synthetase	Nars	0.924	-2.118	0.0708258	0.249798
14577	10488437	ENSMUST00000099264	319470	RIKEN cDNA C530025M09 gene	C530025M09Rik	0.924	-0.944	0.375795	0.645831
14578	10564960	NM_011046	18550	furin (paired basic amino acid	Furin	0.924	-1.906	0.0970817	0.303474
14579	10581560	NM_010817	17463	proteasome (prosome, macropain	Psmd7	0.924	-1.531	0.168406	0.419736
14580	10479423	NM_009936	12841	collagen, type IX, alpha 3	Col9a3	0.924	-0.832	0.432254	0.692602
14581	10369409	ENSMUST00000036304	73616	RIKEN cDNA 1700125F08 gene	1700125F08Rik	0.924	-1.06	0.323463	0.599986
14582	10499514	NM_183037	360213	tripartite motif-containing 46	Trim46	0.924	-0.619	0.55515	0.783898
14583	10443459	NM_013663	20383	splicing factor, arginine/seri	Sfrs3	0.924	-2.24	0.0589811	0.22351
14584	10556321	NM_009431	22083	Ctr9, Paf1/RNA polymerase II c	Ctr9	0.924	-1.625	0.146826	0.388752
14585	10576854	NM_183315	330695	cortexin 1	Ctxn1	0.924	-1.073	0.31798	0.595147
14586	10418434	NM_008407	16426	inter-alpha trypsin inhibitor,	Itih3	0.924	-1.637	0.144455	0.385726
14587	10524659	NM_026398	117109	processing of precursor 5, rib	Pop5	0.924	-2.219	0.0608774	0.227701
14588	10563780	NM_001013368	108961	E2F transcription factor 8	E2f8	0.924	-1.506	0.174427	0.427379
14589	10444997	BC092081	637119	RIKEN cDNA 2410017I17 gene	2410017I17Rik	0.924	-0.987	0.355809	0.628276
14590	10364529	NM_011178	19152	proteinase 3	Prtn3	0.924	-1.421	0.197041	0.457727
14591	10463716	NM_033569	94219	cyclin M2	Cnnm2	0.924	-1.184	0.273848	0.548502
14592	10380392	AB045721	217116	spermatogenesis associated 20	Spata20	0.924	-0.794	0.452299	0.708922
14593	10411274	BC132111	75209	synaptic vesicle glycoprotein	Sv2c	0.924	-1.208	0.265242	0.5404
14594	10571741					0.924	-1.45	0.189022	0.447306
14595	10381666	AK013898	68087	dephospho-CoA kinase domain co	Dcakd	0.924	-1.277	0.241211	0.514029
14596	10368092	NM_019487	56016	heme binding protein 2	Hebp2	0.924	-2.023	0.0816115	0.272821
14597	10569222	AK016549	100036523	predicted gene, ENSMUSG0000003	ENSMUSG00000038461	0.924	-0.812	0.442762	0.701414
14598	10409031	NM_025900	110052	DEK oncogene (DNA binding)	Dek	0.924	-1.733	0.125424	0.354707
14599	10581573					0.924	-0.919	0.387968	0.656721
14600	10597627	NM_133985	108737	oxidative-stress responsive 1	Oxsr1	0.924	-2.266	0.0567471	0.217919
14601	10586816	NM_025690	66660	SAFB-like, transcription modul	Sltm	0.924	-2.183	0.0642562	0.235643
14602	10390498	NM_028156	72215	RIKEN cDNA 1700001P01 gene	1700001P01Rik	0.924	-0.101	0.922397	0.969068
14603	10555389	NM_011671	22228	uncoupling protein 2 (mitochon	Ucp2	0.924	-1.458	0.186861	0.445172
14604	10575662	NM_173015	270096	MON1 homolog b (yeast)	Mon1b	0.924	-1.233	0.256404	0.530714
14605	10429699	NM_134089	105782	scribbled homolog (Drosophila)	Scrib	0.924	-1.605	0.151358	0.395197
14606	10460255	AK081788	73458	RIKEN cDNA 1700055N04 gene	1700055N04Rik	0.924	-1.031	0.335775	0.611352
14607	10353002					0.923	-1.048	0.32859	0.604982
14608	10358711					0.923	-0.523	0.616972	0.823029
14609	10374068	NM_013810	13169	drebrin-like	Dbnl	0.923	-1.377	0.209709	0.474741
14610	10381695					0.923	0.081	0.937973	0.975903
14611	10424743	NM_178646	105734	tigger transposable element de	Tigd5	0.923	-1.537	0.16686	0.417832
14612	10413180	ENSMUST00000038250	70955	RIKEN cDNA 4931403M11 gene	4931403M11Rik	0.923	-1.219	0.261226	0.535766
14613	10441706	NM_025851	66931	RIKEN cDNA 1700010I14 gene	1700010I14Rik	0.923	-0.68	0.517869	0.756834
14614	10386756					0.923	-0.657	0.531559	0.765775
14615	10557285	NM_025304	30949	leucine carboxyl methyltransfe	Lcmt1	0.923	-2.2	0.0626287	0.231629
14616	10449654	ENSMUST00000097355	100038436	predicted gene, ENSMUSG0000007	ENSMUSG00000073427	0.923	-0.837	0.429314	0.690297
14617	10581499	NM_145412	214987	RIKEN cDNA 5830457O10 gene	5830457O10Rik	0.923	-1.597	0.153019	0.397035
14618	10352439	NM_144796	96935	sushi domain containing 4	Susd4	0.923	-0.657	0.531297	0.765579
14619	10439830					0.923	-0.353	0.733942	0.886263
14620	10452172	NM_001039114	328845	acyl-CoA synthetase bubblegum	Acsbg2	0.923	-0.844	0.426037	0.687748
14621	10481835	NM_010725	16917	LIM homeobox transcription fac	Lmx1b	0.923	-0.946	0.374949	0.644967
14622	10597352					0.923	-0.465	0.655897	0.846006
14623	10502791	NM_133871	99899	interferon-induced protein 44	Ifi44	0.923	-1.107	0.303648	0.579864

14624	10437639	NM_007929	13731	epithelial membrane protein 2	Emp2	0.923	-0.785	0.457213	0.712928
14625	10567454	XM_355934	381917	dynein, axonemal, heavy chain	Dnahc3	0.923	-1.619	0.148263	0.390488
14626	10546557	NM_177233	320701	RIKEN cDNA C130034I18 gene	C130034I18Rik	0.923	-1.019	0.341254	0.616096
14627	10473505	NM_146406	258401	olfactory receptor 1076	Olfr1076	0.923	-0.22	0.831907	0.932604
14628	10443000	NM_001081656	240055	predicted gene, EG240055	EG240055	0.923	-0.806	0.446175	0.704033
14629	10559377	NM_028184	72284	oral cancer overexpressed 1	Oraov1	0.923	-1.612	0.149737	0.392417
14630	10400052	BC118038	75847	RIKEN cDNA 4930579E17 gene	4930579E17Rik	0.923	-1.473	0.183012	0.439827
14631	10576556					0.923	-0.356	0.731846	0.884439
14632	10471216	NM_011836	23928	laminin gamma 3	Lamc3	0.923	-0.802	0.448067	0.705745
14633	10560702	NM_177036	319930	CEA-related cell adhesion mole	Ceacam19	0.923	-0.541	0.605127	0.815765
14634	10355037	NM_021312	57750	WD repeat domain 12	Wdr12	0.923	-2.476	0.0414641	0.177622
14635	10600823	ENSMUST00000116173	675747	hypothetical protein LOC675747	LOC675747	0.923	-0.835	0.430253	0.691063
14636	10517067	NM_018754	55948	stratifin	Sfn	0.923	-1.029	0.336677	0.612455
14637	10399874	NM_007530	12033	B-cell receptor-associated pro	Bcap29	0.923	-2.396	0.0467314	0.192011
14638	10486102	NM_201367	381413	G protein-coupled receptor 176	Gpr176	0.923	-0.755	0.474287	0.725796
14639	10552258					0.923	-1.56	0.161392	0.409613
14640	10562696	BC132158	74054	RIKEN cDNA 4931406B18 gene	4931406B18Rik	0.923	-0.603	0.564905	0.790912
14641	10585169	NM_010077	13489	dopamine receptor 2	Drd2	0.923	-0.984	0.356998	0.629293
14642	10415693	NM_145463	219134	shisa homolog 2 (Xenopus laevi	Shisa2	0.923	-2.01	0.0832258	0.27639
14643	10376092					0.923	-1.148	0.287621	0.563359
14644	10570308	NM_025834	66901	protein Z, vitamin K-dependent	Proz	0.923	-0.9	0.397175	0.664239
14645	10452210	NM_008954	19197	persephin	Pspn	0.923	-0.69	0.51154	0.752366
14646	10448383	NM_001081399	353130	protease, serine, 33	Prss33	0.923	-0.834	0.430961	0.691603
14647	10526952	NM_029771	76854	G protein-coupled estrogen rec	Gper	0.923	-0.598	0.568077	0.793199
14648	10381170	ENSMUST00000017976	75482	heat shock protein, alpha-crys	Hspb9	0.923	-1.104	0.3051	0.581502
14649	10366803	NM_010009	13115	cytochrome P450, family 27, su	Cyp27b1	0.923	-0.76	0.471124	0.722944
14650	10397750	ENSMUST00000101131	100038378	predicted gene, ENSMUSG0000007	ENSMUSG00000072884	0.923	-0.782	0.459142	0.714041
14651	10529313	NM_019694	56384	leucine zipper-EF-hand contain	Letm1	0.923	-1.283	0.239341	0.51221
14652	10413461	NM_177814	238988	ELKS/RAB6-interacting/CAST fam	Erc2	0.923	-1.265	0.24517	0.518285
14653	10598216					0.923	-0.821	0.438045	0.697167
14654	10448916	NM_031187	17230	tryptase alpha/beta 1	Tpsab1	0.923	-0.987	0.355707	0.628274
14655	10510482	NM_023051	65945	calsyntenin 1	Clstn1	0.923	-1.708	0.13009	0.36185
14656	10504636					0.923	-0.949	0.373445	0.643632
14657	10412555	AK007001	73498	RIKEN cDNA 1700084P21 gene	1700084P21Rik	0.923	-0.791	0.454232	0.710744
14658	10539606	NM_007638	12468	chaperonin subunit 7 (eta)	Cct7	0.923	-2.292	0.0545865	0.21288
14659	10443749	NM_177823	328795	ubiquitin associated and SH3 d	Ubash3a	0.923	-1.136	0.292467	0.568688
14660	10557925	ENSMUST00000106237	381924	integrin, alpha D	Itgad	0.923	-1.065	0.321199	0.598048
14661	10525030	NM_011537	21388	T-box 5	Tbx5	0.923	-1.122	0.297641	0.573736
14662	10492660					0.923	-0.789	0.455457	0.711765
14663	10442683	BC107381	68509	RIKEN cDNA 1110018H23 gene	1110018H23Rik	0.923	-0.49	0.6385	0.835923
14664	10512065	XR_033416	621880	similar to PDZ binding kinase	LOC621880	0.923	-0.567	0.588169	0.804936
14665	10433340	ENSMUST00000090457	74684	RIKEN cDNA 4930451G09 gene	4930451G09Rik	0.923	-1.526	0.169558	0.420889
14666	10432986	NM_153416	223921	achalasia, adrenocortical insu	Aaas	0.922	-1.155	0.285059	0.560366
14667	10449051	NM_019719	56424	STIP1 homology and U-Box conta	Stub1	0.922	-2.237	0.059229	0.224032
14668	10488748	NM_025876	66971	CDK5 regulatory subunit associ	Cdk5rap1	0.922	-0.775	0.462951	0.717432
14669	10395005	NM_001081378	77480	RIKEN cDNA C330002I19 gene	C330002I19Rik	0.922	-1.484	0.180033	0.435501
14670	10442052	AK164331	626854	predicted gene, EG626854	EG626854	0.922	-0.342	0.741835	0.889893
14671	10416332	AK081168	791332	predicted gene, ENSMUSG0000003	ENSMUSG00000030810	0.922	-0.973	0.361921	0.633538
14672	10370777	NM_025521	66374	RIKEN cDNA 2310011J03 gene	2310011J03Rik	0.922	-1.063	0.322172	0.598962
14673	10581940	NM_053092	85305	lysyl-tRNA synthetase	Kars	0.922	-1.852	0.105191	0.319429
14674	10369474	NM_010124	13688	eukaryotic translation initiat	Eif4ebp2	0.922	-0.924	0.385191	0.654386

14675	10531950					0.922	-0.597	0.569033	0.793724
14676	10480579	NM_001031808	107733	mitochondrial ribosomal protei	Mrpl41	0.922	-1.765	0.119713	0.346027
14677	10502029	NM_138593	28036	La ribonucleoprotein domain fa	Larp7	0.922	-2.292	0.0546	0.21288
14678	10542842	NM_025911	67015	coiled-coil domain containing	Ccdc91	0.922	-1.499	0.176189	0.429929
14679	10594315	NM_010193	14155	feminization 1 homolog b (C. e	Fem1b	0.922	-2.222	0.0606078	0.227054
14680	10543572	NM_011829	23917	inosine 5'-phosphate dehydroge	Impdh1	0.922	-1.733	0.1255	0.354754
14681	10453006	NM_001024806	12607	CCAAT/enhancer binding protein	Cebpz	0.922	-1.905	0.0972389	0.303696
14682	10574897	NM_021513	59016	THAP domain containing 11	Thap11	0.922	-1.729	0.126224	0.355752
14683	10421488	NM_207636	319448	fibronectin type III domain co	Fndc3a	0.922	-1.917	0.0954758	0.300369
14684	10604850					0.922	-1.342	0.220304	0.488992
14685	10542875	BC106181	109163	RIKEN cDNA 3010003L21 gene	3010003L21Rik	0.922	-0.611	0.559657	0.787057
14686	10354275	BC119032	75623	RIKEN cDNA 1700029F09 gene	1700029F09Rik	0.922	-2.286	0.0550819	0.214169
14687	10417676	NM_025435	66231	THO complex 7 homolog (Drosoph	Thoc7	0.922	-2.331	0.051502	0.205
14688	10586611					0.922	-0.637	0.543795	0.775948
14689	10524034	NM_008325	15932	iduronidase, alpha-L-	Idua	0.922	-1.413	0.199404	0.461039
14690	10364814	NM_019575	56214	secretory carrier membrane pro	Scamp4	0.922	-0.726	0.490782	0.737375
14691	10577070	NM_198031	259279	tubulin, gamma complex associa	Tubgcp3	0.922	-1.622	0.147542	0.389587
14692	10420071	NM_028780	74140	transmembrane 9 superfamily me	Tm9sf1	0.922	-2.232	0.0596987	0.225162
14693	10454701	NM_009290	20890	wingless-related MMTV integrat	Wnt8a	0.922	-0.884	0.405193	0.669695
14694	10460585	NM_010235	14283	fos-like antigen 1	Fosl1	0.922	-1.133	0.293342	0.569485
14695	10500293					0.922	-0.718	0.495343	0.740179
14696	10494924	NM_053170	94093	tripartite motif-containing 33	Trim33	0.922	-1.682	0.135246	0.370739
14697	10396112	NM_026536	68055	ATP synthase, H+ transporting,	Atp5s	0.922	-1.481	0.180907	0.436804
14698	10471072	NM_133673	30934	torsin family 1, member B	Tor1b	0.922	-1.861	0.103742	0.316662
14699	10487321	NM_023220	66552	RIKEN cDNA 2010106G01 gene	2010106G01Rik	0.922	-1.632	0.145496	0.387083
14700	10473261	ENSMUST00000099963	241516	fibrous sheath-interacting pro	Fsip2	0.922	-1.532	0.168105	0.4195
14701	10484646					0.922	-0.384	0.712235	0.873926
14702	10509049	BC059720	73937	RIKEN cDNA 1700029M20 gene	1700029M20Rik	0.922	-0.774	0.463439	0.717662
14703	10356626					0.922	-0.482	0.644415	0.839112
14704	10386582	NM_009410	21975	topoisomerase (DNA) III alpha	Top3a	0.922	-1.402	0.202468	0.465275
14705	10545192	NR_004434	19783	ribonuclease P RNA-like 1	Rprl1	0.922	-0.884	0.404996	0.669624
14706	10463448	NM_153796	226153	progressive external ophthalmo	Peo1	0.922	-1.621	0.147751	0.389922
14707	10398436					0.922	-1.237	0.254743	0.528967
14708	10599377	NM_021465	20843	stromal antigen 2	Stag2	0.922	-1.762	0.120211	0.346569
14709	10451580	NM_016859	53414	bystin-like	Bysl	0.922	-1.169	0.279418	0.554692
14710	10499639	NM_016904	54124	CDC28 protein kinase 1b	Cks1b	0.922	-1.623	0.147413	0.389587
14711	10394778	NM_016677	53602	hippocalcin-like 1	Hpcal1	0.922	-1.626	0.146762	0.388752
14712	10462276	NM_001033407	329047	gene model 815, (NCBI)	Gm815	0.922	-0.519	0.619588	0.824972
14713	10440770	NM_178923	224432	splicing factor, arginine/seri	Sfrs15	0.922	-1.54	0.166311	0.417188
14714	10390895	ENSMUST00000055502	69473	keratin associated protein 3-1	Krtap3-1	0.922	-1.207	0.265568	0.540607
14715	10516335	NM_011902	24084	tektin 2	Tekt2	0.922	-0.743	0.480915	0.730572
14716	10550527	NM_178757	272359	interferon regulatory factor 2	Irf2bp1	0.922	-1.72	0.127914	0.358671
14717	10447938	NM_172826	240025	dapper homolog 2, antagonist o	Dact2	0.922	-1.191	0.271405	0.546126
14718	10381653	NM_028492	73293	coiled-coil domain containing	Ccdc103	0.922	-1.495	0.177426	0.431801
14719	10378429	NM_146708	258703	olfactory receptor 402	Olfr402	0.922	-0.25	0.809929	0.923287
14720	10399586	AJ005350	22651	zinc finger protein 125	Zfp125	0.922	-1.433	0.19373	0.453274
14721	10405749					0.922	-0.366	0.725131	0.880804
14722	10378216	NM_016745	53313	ATPase, Ca++ transporting, ubi	Atp2a3	0.921	-0.931	0.382101	0.651596
14723	10557455					0.921	-1.351	0.217537	0.485293
14724	10538377	XM_620310	330319	WAS/WASL interacting protein f	Wipf3	0.921	-1.191	0.27125	0.545988
14725	10537567	X00438	21580	T-cell receptor beta, joining	Tcrb-J	0.921	-1.278	0.240784	0.513737
14726	10551848	ENSMUST00000014072	75629	THAP domain containing 8	Thap8	0.921	-0.335	0.746999	0.892497
14727	10474950	NM_172269	228545	vacuolar protein sorting 18 (y	Vps18	0.921	-1.1	0.306508	0.582999

14728	10361267					0.921	-0.714	0.497791	0.741949
14729	10532598	ENSMUST00000086617	74376	myosin XVIIIb	Myo18b	0.921	-0.983	0.357446	0.629873
14730	10447125					0.921	-1.139	0.291307	0.567423
14731	10465045	NM_024176	66556	Dr1 associated protein 1 (nega	Drap1	0.921	-1.915	0.0958239	0.301049
14732	10394858					0.921	-0.861	0.416707	0.679627
14733	10438308	NM_011239	19385	RAN binding protein 1	Ranbp1	0.921	-1.637	0.144483	0.385726
14734	10540298	NM_007697	12661	cell adhesion molecule with ho	Chl1	0.921	-1.166	0.280597	0.555987
14735	10380067	NM_011129	18952	septin 4	Sept4	0.921	-1.238	0.254632	0.528904
14736	10385709	NM_145974	212706	RIKEN cDNA C330016O10 gene	C330016O10Rik	0.921	-1.468	0.184335	0.441942
14737	10411552	NM_001081061	544971	B double prime 1, subunit of R	Bdp1	0.921	-1.732	0.125555	0.354782
14738	10476326	NM_138651	110911	CDP-diacylglycerol synthase (p	Cds2	0.921	-1.634	0.144961	0.386416
14739	10351574	NM_011615	21945	death effector domain-containi	Dedd	0.921	-1.891	0.0992277	0.307635
14740	10588522	NM_145620	27966	RRP9, small subunit (SSU) proc	Rrp9	0.921	-1.453	0.188291	0.446362
14741	10589099	NM_029634	76500	inositol hexaphosphate kinase	Ihpk2	0.921	-1.285	0.238619	0.511336
14742	10465790	NM_146092	225895	TAF6-like RNA polymerase II, p	Taf6l	0.921	-1.522	0.170647	0.422304
14743	10569113	NM_001114322	72040	mucin-like protocadherin	Mupcdh	0.921	-1.604	0.151505	0.395407
14744	10364093	NM_024440	70377	Der1-like domain family, membe	Derl3	0.921	-1.712	0.12929	0.360552
14745	10355454	XR_032730	383528	similar to SLC25A5 protein	LOC383528	0.921	-0.468	0.653714	0.844785
14746	10369655	ENSMUST00000045500	216021	storkhead box 1	Stox1	0.921	-1.542	0.165699	0.416146
14747	10538466	NM_001003685	14602	growth hormone releasing hormo	Ghrhr	0.921	-1.096	0.308185	0.584951
14748	10586126					0.921	-1.86	0.103962	0.317058
14749	10504656					0.921	-0.578	0.580576	0.799564
14750	10512669	NM_008782	18507	paired box gene 5	Pax5	0.921	-1.425	0.196043	0.456422
14751	10505749	NM_001081014	329877	DENN/MADD domain containing 4C	Dennd4c	0.921	-1.069	0.319401	0.596434
14752	10479047	NM_011044	18534	phosphoenolpyruvate carboxykin	Pck1	0.921	-0.867	0.413954	0.677396
14753	10437586	NM_025708	66690	transmembrane protein 186	Tmem186	0.921	-1.898	0.0983277	0.306086
14754	10444420	NM_018862	55979	1-acylglycerol-3-phosphate O-a	Agpat1	0.921	-1.844	0.106486	0.321808
14755	10435345	NM_139300	107589	myosin, light polypeptide kina	Mylk	0.921	-0.188	0.856405	0.941981
14756	10424097	NM_027212	69790	mediator complex subunit 30	Med30	0.921	-2.026	0.0812457	0.272009
14757	10480901	NM_001037098	67991	BTB (POZ) domain containing 14	Btbd14a	0.921	-1.58	0.156974	0.403436
14758	10478407	ENSMUST00000076667	68386	RIKEN cDNA 0610039K10 gene	0610039K10Rik	0.921	-1.091	0.310382	0.587004
14759	10371220	NM_010304	14676	guanine nucleotide binding pro	Gna15	0.921	-0.376	0.717783	0.876765
14760	10527483	NM_001081431	666311	zinc finger protein 498	Zfp498	0.921	-0.733	0.486515	0.734369
14761	10598067	ENSMUST00000082418	17721	NADH dehydrogenase subunit 5	ND5	0.921	-1.522	0.170468	0.422107
14762	10502191	NM_025509	66357	RIKEN cDNA 2310008M10 gene	2310008M10Rik	0.921	-1.686	0.134379	0.36953
14763	10416271					0.921	-0.602	0.56579	0.791837
14764	10385790	NM_008300	15525	heat shock protein 4	Hspa4	0.921	-2.219	0.0608344	0.227598
14765	10425357	NM_178719	239555	Smith-Magenis syndrome chromos	Smcr7l	0.921	-1.521	0.170701	0.422338
14766	10481378					0.921	-0.457	0.661292	0.849184
14767	10601326	NM_001081189	331487	uracil phosphoribosyltransfera	Uprt	0.921	-1.529	0.168775	0.420183
14768	10518882	NM_207687	56226	espin	Espn	0.921	-1.52	0.170993	0.422803
14769	10421577	BC006743	638575	predicted gene, ENSMUSG0000004	ENSMUSG00000043225	0.921	-0.566	0.58866	0.805172
14770	10585625	NM_011378	20466	transcriptional regulator, SIN	Sin3a	0.921	-1.806	0.11268	0.332566
14771	10478825	NM_153065	228889	DEAD (Asp-Glu-Ala-Asp) box pol	Ddx27	0.921	-2.242	0.058766	0.22297
14772	10363146	NM_178675	215085	solute carrier family 35, memb	Slc35f1	0.921	-0.955	0.370702	0.641417
14773	10596377	XR_032330	664981	hypothetical LOC664981	LOC664981	0.921	-1.505	0.174735	0.427817
14774	10576101	NM_001029993	76014	zinc finger CCCH-type containi	Zc3h18	0.921	-1.991	0.0855025	0.280626
14775	10416153	AK148586	100093629	predicted gene, ENSMUSG0000007	ENSMUSG00000075550	0.921	-1.165	0.280984	0.556442
14776	10452417					0.921	-0.972	0.362395	0.633892
14777	10413874	NM_001081130	239017	oxoglutarate dehydrogenase-lik	Ogdhl	0.921	-1.981	0.0868892	0.283516

14778	10493052	NM_011832	23920	insulin receptor-related recep	Insrr	0.921	-1.089	0.311285	0.587855
14779	10566136	NM_001011782	257947	olfactory receptor 543	Olfr543	0.921	-0.483	0.643674	0.838716
14780	10538868	ENSMUST00000103302	16114	immunoglobulin kappa chain var	Igk-V28	0.921	-0.663	0.527775	0.763341
14781	10379710	AK087588	414102	RIKEN cDNA E230016K23 gene	E230016K23Rik	0.921	-0.551	0.598047	0.811052
14782	10499954	NM_025420	66203	late cornified envelope 1M	Lce1m	0.921	-1.016	0.342544	0.616824
14783	10425078	NM_138670	246221	mercaptopyruvate sulfurtransfe	Mpst	0.921	-0.509	0.625858	0.829508
14784	10375732	ENSMUST00000052596	76653	chibby homolog 3 (Drosophila)	Cby3	0.921	-0.848	0.423847	0.686151
14785	10521725	NM_025895	66999	mediator of RNA polymerase II	Med28	0.921	-1.843	0.106641	0.32207
14786	10385686	NM_001048061	15384	heterogeneous nuclear ribonucl	Hnrpab	0.921	-2.058	0.0774718	0.264332
14787	10406111	NM_011390	20499	solute carrier family 12, memb	Slc12a7	0.921	-2.228	0.0600593	0.22593
14788	10351971	NM_019445	54418	formin 2	Fmn2	0.921	-1.12	0.298558	0.574742
14789	10573803	NM_173369	74256	cylindromatosis (turban tumor	Cyld	0.921	-1.876	0.101535	0.31225
14790	10406086	NM_009354	21752	telomerase reverse transcripta	Tert	0.921	-1.504	0.175066	0.428228
14791	10525872	NM_001081750	269704	zinc finger protein 664	Zfp664	0.921	-1.249	0.250555	0.524406
14792	10535225	NM_030022	77998	galectin-related inter-fiber p	Grifin	0.921	-1.66	0.139629	0.37797
14793	10503334	NM_010276	14579	GTP binding protein (gene over	Gem	0.921	-0.561	0.59192	0.807001
14794	10406176	NM_001081060	105243	solute carrier family 9 (sodiu	Slc9a3	0.921	-0.575	0.582743	0.800924
14795	10424370	NM_144549	211770	tribbles homolog 1 (Drosophila	Trib1	0.921	-1.723	0.127325	0.357621
14796	10533603	NM_175092	23912	ras homolog gene family, membe	Rhof	0.921	-1.66	0.139671	0.378012
14797	10385155	NM_001004147	237730	expressed sequence AI595406	AI595406	0.921	-0.706	0.502235	0.745158
14798	10555548					0.921	-1.226	0.258627	0.532776
14799	10381753	NM_007762	12921	corticotropin releasing hormon	Crhr1	0.921	-1.034	0.334486	0.60995
14800	10351891	NM_146722	258717	olfactory receptor 429	Olfr429	0.92	-0.635	0.544951	0.77708
14801	10390519	NM_028199	72324	plexin domain containing 1	Plxdc1	0.92	-1.052	0.326727	0.602834
14802	10429234	XM_981889	69700	collagen, type XXII, alpha 1	Col22a1	0.92	-1.116	0.300111	0.57624
14803	10496492					0.92	-0.534	0.609281	0.818153
14804	10597841	NM_029095	74770	hedgehog acyltransferase-like	Hhatl	0.92	-0.799	0.450032	0.707313
14805	10556463	NM_007489	11865	aryl hydrocarbon receptor nucl	Arntl	0.92	-1.62	0.148027	0.390187
14806	10497648	NM_153421	241915	polyhomeotic-like 3 (Drosophil	Phc3	0.92	-1.302	0.232947	0.50397
14807	10576482	NM_026855	68865	ARV1 homolog (yeast)	Arv1	0.92	-1.51	0.173632	0.426449
14808	10575349	NM_146214	234724	tyrosine aminotransferase	Tat	0.92	-1.633	0.145321	0.387047
14809	10599435	NM_177215	320634	oculocerebrorenal syndrome of	Ocrl	0.92	-1.193	0.270545	0.545253
14810	10560575	NM_009046	19698	avian reticuloendotheliosis vi	Relb	0.92	-0.952	0.37194	0.642247
14811	10546695	NM_015768	50501	prokineticin 2	Prok2	0.92	-1.224	0.25947	0.533772
14812	10376959	NM_023479	68626	elaC homolog 2 (E. coli)	Elac2	0.92	-1.319	0.227514	0.498297
14813	10597748	NM_028976	74498	golgi reassembly stacking prot	Gorasp1	0.92	-1.511	0.173178	0.425638
14814	10426909	NM_134093	68614	LETM1 domain containing 1	Letmd1	0.92	-1.169	0.279575	0.554795
14815	10522902	ENSMUST00000069773	243090	cDNA sequence BC051076	BC051076	0.92	-1.07	0.319007	0.596119
14816	10468180	NM_028627	73728	pleckstrin and Sec7 domain con	Psd	0.92	-0.843	0.426204	0.687965
14817	10396454	NM_172804	238266	synaptotagmin XVI	Syt16	0.92	-1.171	0.278969	0.554016
14818	10361892					0.92	-1.259	0.247105	0.520387
14819	10444680	NM_027366	70274	lymphocyte antigen 6 complex,	Ly6g6e	0.92	-0.366	0.724881	0.880713
14820	10346678	NM_139150	241066	calcium response factor	Carf	0.92	-0.791	0.454098	0.710639
14821	10550597	NM_175530	243867	F-box protein 46	Fbxo46	0.92	-1.058	0.324132	0.600616
14822	10554965					0.92	-1.058	0.32414	0.600616
14823	10399387	NM_019544	56184	mesogenin 1	Msgn1	0.92	-0.759	0.472146	0.723934
14824	10572368	NM_008107	14559	growth differentiation factor	Gdf1	0.92	-0.899	0.397697	0.664302
14825	10348166	NM_009604	11449	cholinergic receptor, nicotini	Chrng	0.92	-1.068	0.319928	0.59668
14826	10421444	NM_181345	328440	nucleophosmin/nucleoplasmin 2	Npm2	0.92	-1.308	0.230881	0.501612
14827	10491068	NM_029150	70862	spermatogenesis associated 16	Spata16	0.92	-1.019	0.341092	0.615941
14828	10559786	NM_146913	258915	olfactory receptor 1348	Olfr1348	0.92	-0.449	0.666843	0.851389
14829	10605090	NM_008323	15929	isocitrate dehydrogenase 3 (NA	Idh3g	0.92	-2.235	0.0594327	0.224601
14830	10410295	NM_177622	218314	zin finger protein 595	Zfp595	0.92	-2.325	0.0519234	0.206134
14831	10574161					0.92	-0.574	0.583529	0.801489
14832	10551207					0.92	-0.992	0.353191	0.625979

14833	10531323	NM_011816	23881	GTPase activating protein (SH3	G3bp2	0.92	-1.938	0.0926314	0.294729
14834	10401138	NM_023721	73834	ATPase, H+ transporting, lysos	Atp6v1d	0.92	-2.094	0.0733571	0.255698
14835	10499299	NM_022031	73940	hyaluronan and proteoglycan li	Hapln2	0.92	-1.378	0.209527	0.474666
14836	10434348	NM_172265	224045	eukaryotic translation initiat	Eif2b5	0.92	-1.466	0.184855	0.44244
14837	10545638	NM_009392	21909	T-cell leukemia, homeobox 2	Tlx2	0.92	-1.782	0.116773	0.340277
14838	10507250	NM_026651	68273	protein O-linked mannose beta1	Pomgnt1	0.92	-2.079	0.0750102	0.258984
14839	10459481	NM_027400	70361	lectin, mannose-binding, 1	Lman1	0.92	-1.602	0.15204	0.395822
14840	10354468					0.92	-1.409	0.200455	0.46246
14841	10439237	ENSMUST00000059080	66481	ribosomal protein S21	Rps21	0.92	-1.274	0.242178	0.515049
14842	10401987	NM_029911	72258	potassium channel, subfamily K	Kcnk10	0.92	-0.549	0.599294	0.811907
14843	10595914	NM_001080776	382097	gene model 1123, (NCBI)	Gm1123	0.92	-0.991	0.353571	0.626322
14844	10466837					0.92	-1.517	0.171758	0.423994
14845	10583753	NM_001080940	624219	predicted gene, EG624219	EG624219	0.92	-0.953	0.371626	0.64202
14846	10388884	NM_008702	18099	nemo like kinase	Nlk	0.92	-2.169	0.065566	0.2387
14847	10349593	NM_026976	69169	Fas apoptotic inhibitory molec	Faim3	0.92	-0.807	0.445712	0.703765
14848	10480224	NM_010067	13434	tRNA aspartic acid methyltrans	Trdmt1	0.92	-0.531	0.611201	0.819483
14849	10600377	NM_018794	54411	ATPase, H+ transporting, lysos	Atp6ap1	0.92	-1.363	0.21398	0.480314
14850	10528027					0.92	-0.864	0.415559	0.678709
14851	10402318	NM_133364	170952	proline rich membrane anchor 1	Prima1	0.92	-0.907	0.393538	0.661497
14852	10442493					0.92	-0.362	0.727744	0.88191
14853	10521585					0.92	-1.505	0.174736	0.427817
14854	10382774	BC027639	69535	RIKEN cDNA 2310004N24 gene	2310004N24Rik	0.92	-1.811	0.111858	0.331046
14855	10518327					0.92	-0.624	0.551989	0.781881
14856	10534940	NM_001024932	545812	paired immunoglobin-like type	Pilrb2	0.92	-0.539	0.605965	0.81624
14857	10572253	NM_027481	70616	splicing factor 4	Sf4	0.92	-1.895	0.0987419	0.306809
14858	10561170	NM_053208	112406	EGL nine homolog 2 (C. elegans	Egln2	0.92	-1.676	0.136316	0.372676
14859	10493380	XR_033961	628070	similar to LOC506492 protein	LOC628070	0.92	-1.447	0.189936	0.448565
14860	10534583	XR_032332	269718	similar to ribosomal protein L	LOC269718	0.92	-2.212	0.0614847	0.22896
14861	10591660	NM_010149	13857	erythropoietin receptor	Epor	0.92	-0.814	0.441921	0.700812
14862	10504617	ENSMUST00000043958	381522	RIKEN cDNA E230008N13 gene	E230008N13Rik	0.92	-0.376	0.718076	0.876971
14863	10447697	ENSMUST00000097416	67791	RIKEN cDNA 6530411M01 gene	6530411M01Rik	0.92	-1.531	0.168381	0.419736
14864	10402800	NM_019925	56696	G protein-coupled receptor 132	Gpr132	0.92	-1.359	0.215014	0.481962
14865	10376418	BC117002	258529	olfactory receptor 313	Olfr313	0.919	-0.806	0.445806	0.703765
14866	10444008	NM_026712	328801	zinc finger protein 414	Zfp414	0.919	-1.734	0.125197	0.354326
14867	10393926	NM_026428	67880	dicarbonyl L-xylulose reductas	Dcxr	0.919	-1.184	0.273822	0.548502
14868	10369228	NM_001034869	245263	predicted gene, EG245263	EG245263	0.919	-0.584	0.576875	0.797689
14869	10460782	NM_130453	170458	glycoprotein hormone alpha 2	Gpha2	0.919	-0.94	0.377396	0.647352
14870	10433996	NM_023348	67474	synaptosomal-associated protei	Snap29	0.919	-1.165	0.280939	0.556405
14871	10468022	NM_053164	94067	mitochondrial ribosomal protei	Mrpl43	0.919	-1.799	0.113724	0.334294
14872	10503613	XR_031966	664911	similar to ribosomal protein S	LOC664911	0.919	-0.898	0.398249	0.664555
14873	10386182	NM_001011770	257932	olfactory receptor 332	Olfr332	0.919	-0.295	0.77621	0.908709
14874	10473793	NM_008948	19182	proteasome (prosome, macropain	Psmc3	0.919	-1.83	0.108761	0.325499
14875	10560397	ENSMUST00000108482	114864	pregnancy-specific glycoprotei	Psg20	0.919	-1.994	0.0851909	0.280273
14876	10439092	BC060601	224118	RIKEN cDNA 1700021K19 gene	1700021K19Rik	0.919	-1.748	0.12272	0.350505
14877	10349295	NM_023755	81879	transcription factor CP2-like	Tcfcp2l1	0.919	-1.706	0.130481	0.362441
14878	10565634	NM_008663	17921	myosin VIIa	Myo7a	0.919	-1.133	0.293603	0.56967
14879	10536973	ENSMUST00000052497	76419	RIKEN cDNA 1700023L04 gene	1700023L04Rik	0.919	-0.653	0.533734	0.767706
14880	10561920	NM_011827	23900	hematopoietic cell signal tran	Hcst	0.919	-0.37	0.722169	0.879197
14881	10561059	ENSMUST00000098663	632778	predicted gene, EG632778	EG632778	0.919	-1.289	0.23731	0.509565
14882	10509071	AK162333	100038432	predicted gene, ENSMUSG0000007	ENSMUSG00000073746	0.919	-0.569	0.586406	0.803667
14883	10433797	NM_011159	19090	protein kinase, DNA activated,	Prkdc	0.919	-2.054	0.0779188	0.265471
14884	10460151	NM_172252	353242	mitochondrial ribosomal protei	Mrpl21	0.919	-1.568	0.159558	0.40691
14885	10489004	NM_010911	18041	nitrogen fixation gene 1 (S. c	Nfs1	0.919	-1.805	0.112742	0.33261

14886	10474769	NM_009773	12236	budding uninhibited by benzimi	Bub1b	0.919	-1.447	0.189926	0.448565
14887	10585224	NM_198675	382137	RIKEN cDNA D630004A14 gene	D630004A14Rik	0.919	-0.144	0.889196	0.956449
14888	10449018	NM_026897	68977	hydroxyacylglutathione hydrola	Haghl	0.919	-1.918	0.0953809	0.300154
14889	10502232	NM_007926	13722	small inducible cytokine subfa	Scye1	0.919	-2.548	0.0373065	0.166124
14890	10380025	NM_031386	83560	testis expressed gene 14	Tex14	0.919	-1.344	0.219652	0.488523
14891	10393620	NM_007625	12418	chromobox homolog 4 (Drosophil	Cbx4	0.919	-1.28	0.240062	0.51313
14892	10444320	BC052925	100038862	butyrophilin-like 1	Btnl1	0.919	-0.55	0.598679	0.811605
14893	10426822	BC059905	66379	RIKEN cDNA 2310016M24 gene	2310016M24Rik	0.919	-1.469	0.184027	0.441415
14894	10529402	NM_139064	231130	TNFAIP3 interacting protein 2	Tnip2	0.919	-1.516	0.172066	0.424165
14895	10576010	NM_198671	382034	genetic suppressor element 1	Gse1	0.919	-1.428	0.194994	0.455123
14896	10547633	NM_008108	14562	growth differentiation factor	Gdf3	0.919	-0.561	0.592028	0.80703
14897	10424922	NM_029643	52710	G protein-coupled receptor 172	Gpr172b	0.919	-1.924	0.094513	0.298489
14898	10559610	NM_172894	243819	SAPS domain family, member 1	Saps1	0.919	-1.425	0.195954	0.456422
14899	10382610	NM_029557	76265	tRNA splicing endonuclease 54	Tsen54	0.919	-1.344	0.219807	0.488612
14900	10539795	NM_025467	66284	gastrokine 2	Gkn2	0.919	-0.634	0.545795	0.777543
14901	10535946	NM_201369	381695	NEDD4 binding protein 2-like 2	N4bp2l2	0.919	-1.975	0.0875779	0.284796
14902	10566525	NM_020024	24075	TAF10 RNA polymerase II, TATA	Taf10	0.919	-2.488	0.0407805	0.176044
14903	10345875					0.919	-0.63	0.548049	0.778543
14904	10362916					0.919	-1.512	0.173007	0.425494
14905	10545394	NM_025607	66510	ring finger protein 181	Rnf181	0.919	-0.975	0.361227	0.633052
14906	10532030	XR_032153	433945	predicted gene, EG433945	EG433945	0.919	-1.073	0.317907	0.595116
14907	10421197	NM_134078	105513	CHMP family, member 7	Chmp7	0.919	-1.149	0.287183	0.562971
14908	10496417	NM_175389	108943	RNA (guanine-9-) methyltransfe	Rg9mtd2	0.919	-2.147	0.0678045	0.243316
14909	10444268	NM_011530	21355	transporter 2, ATP-binding cas	Tap2	0.919	-0.76	0.471327	0.723204
14910	10584901	NM_001081270	114873	Down syndrome cell adhesion mo	Dscaml1	0.919	-1.527	0.169258	0.42056
14911	10348076	ENSMUST00000086964	100040414	similar to ribosomal protein L	LOC100040414	0.919	-1.037	0.333372	0.609285
14912	10546889					0.919	-0.491	0.638351	0.835923
14913	10605247	NM_010788	17257	methyl CpG binding protein 2	Mecp2	0.919	-0.753	0.475193	0.726714
14914	10486935	NM_026251	67578	protein associated with topois	Patl2	0.919	-0.642	0.540729	0.773244
14915	10485213	NM_007656	12521	CD82 antigen	Cd82	0.919	-1.357	0.21585	0.482956
14916	10480808	NM_001005424	381353	gene model 996, (NCBI)	Gm996	0.919	-0.741	0.481849	0.730954
14917	10409330	BC033445	97820	RIKEN cDNA 4833439L19 gene	4833439L19Rik	0.919	-1.582	0.156333	0.402325
14918	10430909	NM_029562	76279	cytochrome P450, family 2, sub	Cyp2d26	0.919	-1.673	0.137062	0.373617
14919	10594092	NM_133983	102657	CD276 antigen	Cd276	0.919	-1.584	0.156062	0.401895
14920	10357371	NM_028135	72160	transmembrane protein 163	Tmem163	0.919	-0.84	0.428122	0.689167
14921	10523483	NM_029947	77630	PR domain containing 8	Prdm8	0.919	-0.864	0.415172	0.678399
14922	10565137	NM_172904	244091	fibronectin type III and SPRY	Fsd2	0.919	-1.134	0.292944	0.569014
14923	10391273	NM_010410	15171	hypocretin	Hcrt	0.919	-0.844	0.426014	0.687748
14924	10476668	NM_181417	228714	cysteine and glycine-rich prot	Csrp2bp	0.919	-2.154	0.0670381	0.241804
14925	10479159	NM_001099328	100043757	likely orthologue of H. sapien	RP23-45P4.1	0.919	-1.822	0.11004	0.328028
14926	10473584					0.919	-1.01	0.345075	0.619061
14927	10544442	NM_001081301	546896	predicted gene, EG546896	EG546896	0.919	-1.102	0.305807	0.582258
14928	10532332	NM_028273	72542	phosphoglycerate mutase family	Pgam5	0.919	-2.919	0.0216248	0.115434
14929	10520638	NM_027855	381629	RIKEN cDNA 0610007C21 gene	0610007C21Rik	0.919	-2.353	0.0498096	0.200566
14930	10439032	NM_177326	224105	p21 (CDKN1A)-activated kinase	Pak2	0.919	-1.583	0.156234	0.402137
14931	10453426	NM_029121	74915	ATPase, H+ transporting, lysos	Atp6v1e2	0.919	-1.429	0.19499	0.455123
14932	10497929					0.919	-0.68	0.517777	0.756834
14933	10526069	NM_009838	12466	chaperonin subunit 6a (zeta)	Cct6a	0.919	-2.632	0.0329244	0.152833
14934	10398297					0.919	-0.734	0.486155	0.734128
14935	10386418	XR_032580	668157	similar to high mobility group	LOC668157	0.919	-0.259	0.803088	0.920071
14936	10499316	NM_172526	214191	tetratricopeptide repeat domai	Ttc24	0.919	-0.583	0.577438	0.797771
14937	10409212					0.919	-1.151	0.28658	0.562228

14938	10549730	NM_201355	269854	N-acetyltransferase 14	Nat14	0.919	-1.021	0.34011	0.615475
14939	10346114					0.919	-0.62	0.554641	0.783704
14940	10380398	NM_007689	12643	chondroadherin	Chad	0.918	-0.793	0.453172	0.70973
14941	10490061	NM_029815	76960	breast carcinoma amplified seq	Bcas1	0.918	-0.971	0.362986	0.63431
14942	10525381	NM_019780	56433	vacuolar protein sorting 29 (S	Vps29	0.918	-1.503	0.175328	0.42857
14943	10359961	NM_010633	16589	U2AF homology motif (UHM) kina	Uhmk1	0.918	-1.529	0.168758	0.420183
14944	10353415	NM_145856	257630	interleukin 17F	Il17f	0.918	-1.105	0.304499	0.581024
14945	10550840	NM_021307	57745	zinc finger protein 112	Zfp112	0.918	-0.951	0.372327	0.642651
14946	10526587	NM_031408	57330	GRB10 interacting GYF protein	Gigyf1	0.918	-1.6	0.152484	0.396375
14947	10460359	NM_011778	23789	coronin, actin binding protein	Coro1b	0.918	-2.329	0.0516378	0.205347
14948	10539026	NM_029673	76614	inner membrane protein, mitoch	Immt	0.918	-1.716	0.128565	0.359526
14949	10352125	ENSMUST00000069568	791357	predicted gene, ENSMUSG0000005	ENSMUSG00000055831	0.918	-1.033	0.334835	0.610375
14950	10397604					0.918	-0.485	0.641998	0.837836
14951	10593751	NM_145229	246735	cDNA sequence AY074887	AY074887	0.918	-0.584	0.577278	0.797771
14952	10568939	NM_053119	93747	enoyl Coenzyme A hydratase, sh	Echs1	0.918	-2.184	0.0641009	0.235304
14953	10367671					0.918	-0.65	0.536126	0.769315
14954	10579915	NM_053124	93762	SWI/SNF related, matrix associ	Smarca5	0.918	-2.231	0.0597391	0.225162
14955	10414258					0.918	-0.962	0.367264	0.638184
14956	10553140	NM_144801	70209	transmembrane protein 143	Tmem143	0.918	-1.583	0.156145	0.401989
14957	10408077	NM_178183	319169	histone cluster 1, H2ak	Hist1h2ak	0.918	-1.004	0.347794	0.621829
14958	10447084	NM_176963	319625	galactose mutarotase	Galm	0.918	-1.737	0.124744	0.353522
14959	10571621	NM_138668	192169	UFM1-specific peptidase 2	Ufsp2	0.918	-2.211	0.061583	0.229285
14960	10363430	NM_011179	19156	prosaposin	Psap	0.918	-1.79	0.115364	0.337519
14961	10447729	U44941	19317	quaking	Qk	0.918	-1.237	0.255	0.529326
14962	10580080	ENSMUST00000098592	100038416	predicted gene, ENSMUSG0000007	ENSMUSG00000074215	0.918	-0.544	0.603126	0.814471
14963	10557326	NM_001008700	16190	interleukin 4 receptor, alpha	Il4ra	0.918	-1.301	0.233334	0.504511
14964	10601277	XR_031632	676150	similar to transcriptional ada	LOC676150	0.918	-1.178	0.27629	0.551172
14965	10541144	NM_001033382	319734	calcium channel, voltage-depen	Cacna2d4	0.918	-1.316	0.228539	0.499559
14966	10535053	NM_008923	19085	protein kinase, cAMP dependent	Prkar1b	0.918	-1.525	0.169858	0.421288
14967	10548857	NM_175652	320332	histone cluster 4, H4	Hist4h4	0.918	-1.87	0.102452	0.313948
14968	10594613	NM_144937	235441	ubiquitin specific peptidase 3	Usp3	0.918	-1.654	0.140753	0.379507
14969	10544570	NM_001024622	76302	PEST proteolytic signal contai	Pcnp	0.918	-1.53	0.168731	0.420183
14970	10571514					0.918	-0.946	0.374588	0.644557
14971	10521626	NM_172274	231214	coiled-coil and C2 domain cont	Cc2d2a	0.918	-1.501	0.17575	0.429353
14972	10575029	ENSMUST00000066875	330837	RIKEN cDNA 6030452D12 gene	6030452D12Rik	0.918	-0.41	0.693955	0.865705
14973	10392845	NM_145634	246746	CD300 antigen like family memb	Cd300lf	0.918	-1.352	0.21732	0.485013
14974	10380297	NM_199008	69802	COX11 homolog, cytochrome c ox	Cox11	0.918	-1.415	0.198722	0.459864
14975	10605222	NM_008363	16179	interleukin-1 receptor-associa	Irak1	0.918	-1.747	0.122954	0.350793
14976	10535006	NM_001115015	231807	cDNA sequence BC037034	BC037034	0.918	-1.313	0.229556	0.500642
14977	10566678	NM_001011810	258041	olfactory receptor 485	Olfr485	0.918	-0.42	0.686681	0.861723
14978	10542310	NM_009875	12576	cyclin-dependent kinase inhibi	Cdkn1b	0.918	-2.036	0.0800143	0.269699
14979	10542674	ENSMUST00000100821	665037	predicted gene, EG665037	EG665037	0.918	-0.804	0.447051	0.704723
14980	10542034	ENSMUST00000009097	243642	predicted gene, EG243642	EG243642	0.918	-1.406	0.201419	0.463821
14981	10605786					0.918	-1.456	0.18751	0.445758
14982	10417813	NM_027475	70601	ecdysoneless homolog (Drosophi	Ecd	0.918	-1.989	0.0858284	0.281187
14983	10520650	NM_023525	69719	carbamoyl-phosphate synthetase	Cad	0.918	-1.764	0.119801	0.346027
14984	10400971	NM_011382	20474	sine oculis-related homeobox 4	Six4	0.918	-1.579	0.157169	0.403641
14985	10542221					0.918	-1.875	0.101626	0.312332
14986	10476342	ENSMUST00000028819	70845	RIKEN cDNA 4921508D12 gene	4921508D12Rik	0.918	-0.784	0.457767	0.713313
14987	10373912	NM_001013365	18413	oncostatin M	Osm	0.918	-0.789	0.455152	0.711341
				Williams Beuren syndrome					

14988	10534399	AY081954	71304	chrom	Wbscr25	0.918	-0.788	0.455938	0.712359
14989	10426875	NM_007497	11908	activating transcription facto	Atf1	0.918	-1.926	0.0942107	0.29789
14990	10585601	NM_178374	66069	snurportin 1	Snupn	0.918	-1.702	0.131219	0.363772
14991	10467989	NM_001033343	240667	Sec31 homolog B (S. cerevisiae	Sec31b	0.918	-0.846	0.424769	0.686726
14992	10593367	NM_145614	235339	dihydrolipoamide S-acetyltrans	Dlat	0.918	-2.44	0.0437952	0.1843
14993	10448878	ENSMUST00000056357	545192	BAI1-associated protein 3	Baiap3	0.918	-1.219	0.261269	0.535766
14994	10346867	NM_018796	55949	eukaryotic translation elongat	Eef1b2	0.918	-2.084	0.0744217	0.258046
14995	10537938	BC119280	101197	expressed sequence AI894139	AI894139	0.918	-1.772	0.118381	0.343378
14996	10560434	NM_026111	67369	glutaminyl-peptide cyclotransf	Qpctl	0.918	-1.044	0.330007	0.606438
14997	10505030	NM_176966	319636	fibronectin type III and SPRY	Fsd1l	0.918	-1.438	0.19243	0.451882
14998	10538751	NM_007500	11921	atonal homolog 1 (Drosophila)	Atoh1	0.918	-0.978	0.359717	0.631715
14999	10530130	NM_145923	100532	RELT-like 1	Rell1	0.918	-2.16	0.0664884	0.240889
15000	10444079	NM_009059	19732	ral guanine nucleotide dissoci	Rgl2	0.917	-1.584	0.155933	0.401839
15001	10551195					0.917	-1.246	0.251657	0.525573
15002	10437364	NM_009624	11515	adenylate cyclase 9	Adcy9	0.917	-0.813	0.442334	0.700945
15003	10575842					0.917	-0.315	0.761934	0.900975
15004	10395612	NM_001015099	217558	RIKEN cDNA 6030408C04 gene	6030408C04Rik	0.917	-1.57	0.159217	0.406366
15005	10533989	ENSMUST00000116112	231736	predicted gene, EG231736	EG231736	0.917	-0.798	0.450257	0.707462
15006	10542255	NM_207018	387345	taste receptor, type 2, member	Tas2r113	0.917	-0.214	0.83671	0.934075
15007	10490199					0.917	-0.739	0.483407	0.732228
15008	10454836	AK006900	73449	RIKEN cDNA 1700066B19 gene	1700066B19Rik	0.917	-0.54	0.605577	0.816017
15009	10428796	NM_026346	67731	F-box protein 32	Fbxo32	0.917	-1.382	0.20818	0.472799
15010	10376912	NM_001033669	213980	F-box and WD-40 domain protein	Fbxw10	0.917	-1.484	0.180153	0.435693
15011	10356401					0.917	-0.867	0.414035	0.677432
15012	10430474	NM_177580	207495	BAI1-associated protein 2-like	Baiap2l2	0.917	-1.429	0.194738	0.454775
15013	10584580					0.917	-0.651	0.535423	0.769059
15014	10544795					0.917	-0.651	0.535512	0.769059
15015	10596465	NM_025371	109652	aminoacylase 1	Acy1	0.917	-1.095	0.308535	0.585197
15016	10352459	BC057872	98732	RAB3 GTPase activating protein	Rab3gap2	0.917	-1.235	0.255629	0.529946
15017	10484720	NM_146650	258644	olfactory receptor 1166	Olfr1166	0.917	-0.657	0.531314	0.765579
15018	10390381	NM_008942	19155	aminopeptidase puromycin sensi	Npepps	0.917	-1.824	0.109664	0.327274
15019	10478258	NM_022883	64899	lipin 3	Lpin3	0.917	-2	0.0844567	0.278893
15020	10357191	NM_019933	19258	protein tyrosine phosphatase,	Ptpn4	0.917	-1.659	0.139798	0.378113
15021	10504660					0.917	-1.097	0.307758	0.584342
15022	10394555	NM_023697	105014	retinol dehydrogenase 14 (all-	Rdh14	0.917	-1.241	0.253508	0.527784
15023	10375525	NM_146877	258877	olfactory receptor 1395	Olfr1395	0.917	-0.996	0.351591	0.624753
15024	10383047	NM_001030291	238011	ectonucleotide pyrophosphatase	Enpp7	0.917	-0.539	0.605815	0.816194
15025	10488673	NM_010226	14239	forkhead box S1	Foxs1	0.917	-1.085	0.312822	0.589257
15026	10590149	NM_001033209	102448	xylulokinase homolog (H. influ	Xylb	0.917	-1.942	0.0920119	0.293984
15027	10353477					0.917	-1.314	0.229164	0.500215
15028	10484559	NM_207561	404323	olfactory receptor 1040	Olfr1040	0.917	-1.008	0.346116	0.620193
15029	10535894	NM_010439	15289	high mobility group box 1	Hmgb1	0.917	-1.409	0.200538	0.462549
15030	10601863	XR_035494	666180	similar to RIKEN cDNA 5730427N	LOC666180	0.917	-0.564	0.589639	0.805747
15031	10363639	NM_016864	53404	atonal homolog 7 (Drosophila)	Atoh7	0.917	-1.041	0.3315	0.607966
15032	10561673	NM_182927	101809	sprouty-related, EVH1 domain c	Spred3	0.917	-1.276	0.241404	0.514329
15033	10546092	ENSMUST00000113596	19349	RAB7, member RAS oncogene fami	Rab7	0.917	-1.206	0.265823	0.540907
15034	10537957	NM_133922	77827	KRAB-A domain containing 1	Krba1	0.917	-0.766	0.468122	0.720533
15035	10567407	NM_145585	233802	THUMP domain containing 1	Thumpd1	0.917	-1.613	0.149494	0.391928
15036	10434281	ENSMUST00000074116	635992	similar to ubiquitin-conjugati	LOC635992	0.917	-0.974	0.361614	0.633308
15037	10428308	AK145170	100038726	predicted gene, ENSMUSG0000007	ENSMUSG00000072615	0.917	-2.393	0.046928	0.192513
15038	10585129	NM_012039	26951	ZW10 homolog (Drosophila), cen	Zw10	0.917	-1.383	0.207924	0.472478

15039	10593953	NM_199222	235416	lectin, mannose-binding 1 like	Lman1l	0.917	-1.207	0.26569	0.540741
15040	10560354	XR_033421	666767	similar to 2410004N11Rik prote	LOC666767	0.917	-2.025	0.0812694	0.272022
15041	10427268	NM_010464	15422	homeo box C13	Hoxc13	0.917	-1.495	0.17729	0.431715
15042	10430382					0.917	-0.695	0.508552	0.75032
15043	10576728	NM_026156	67439	XPA binding protein 2	Xab2	0.917	-1.648	0.142166	0.382143
15044	10421672	NM_026177	67467	RIKEN cDNA 1200011I18 gene	1200011I18Rik	0.917	-2.219	0.0608392	0.227598
15045	10451303	BC059249	106763	tau tubulin kinase 1	Ttbk1	0.917	-0.695	0.508903	0.750516
15046	10521461	NM_024478	17713	GrpE-like 1, mitochondrial	Grpel1	0.917	-1.735	0.125001	0.354008
15047	10523647	NM_001080798	17355	AF4/FMR2 family, member 1	Aff1	0.917	-1.448	0.189521	0.448035
15048	10505276	NM_175090	20529	solute carrier family 31, memb	Slc31a1	0.917	-2.231	0.059766	0.225177
15049	10535282	NM_175362	108723	caspase recruitment domain fam	Card11	0.917	-1.275	0.242007	0.51484
15050	10549552	NM_027328	68988	PRP31 pre-mRNA processing fact	Prpf31	0.917	-1.772	0.11847	0.343564
15051	10530558	AK082524	75991	SLAIN motif family, member 2	Slain2	0.917	-1.259	0.247346	0.520698
15052	10425611	NM_080633	11429	aconitase 2, mitochondrial	Aco2	0.917	-1.731	0.125827	0.355111
15053	10477551	DQ080431	75480	RIKEN cDNA 1700003F12 gene	1700003F12Rik	0.917	-1.816	0.111047	0.329804
15054	10401950	NM_027076	69423	RIKEN cDNA 1700019M22 gene	1700019M22Rik	0.917	-0.14	0.892499	0.957747
15055	10444936	NM_026987	69192	DEAH (Asp-Glu-Ala-His) box pol	Dhx16	0.917	-1.571	0.158956	0.406061
15056	10515115	NM_145551	230612	solute carrier family 5 (sodiu	Slc5a9	0.917	-0.933	0.380787	0.650316
15057	10537789	NM_207028	387353	taste receptor, type 2, member	Tas2r126	0.917	-0.842	0.427084	0.688411
15058	10532784	NM_026805	68666	SV2 related protein	Svop	0.917	-1.101	0.306251	0.582793
15059	10600685	BC049727	71996	RIKEN cDNA 1600014K23 gene	1600014K23Rik	0.917	-0.817	0.440032	0.699124
15060	10559486	NM_001113474	52855	leukocyte-associated Ig-like r	Lair1	0.917	-0.616	0.557008	0.785453
15061	10513268	BC058684	230249	expressed sequence AI314180	AI314180	0.916	-2.342	0.0506562	0.202722
15062	10553897	NM_172742	233315	myotubularin related protein 1	Mtmr10	0.916	-1.685	0.134623	0.369832
15063	10480633	NM_080854	142681	solute carrier family 34 (sodi	Slc34a3	0.916	-1.164	0.281312	0.556831
15064	10477035	NM_001040689	228770	R-spondin family, member 4	Rspo4	0.916	-1.506	0.174436	0.427379
15065	10523785	NM_018759	54367	zinc finger protein 326	Zfp326	0.916	-2.169	0.065605	0.238752
15066	10374223	NM_008341	16006	insulin-like growth factor bin	Igfbp1	0.916	-0.691	0.511249	0.752255
15067	10603354	NM_018832	54634	MAGI family member, X-linked	Magix	0.916	-0.768	0.466647	0.719708
15068	10481453	NM_177648	227697	dolichol kinase	Dolk	0.916	-0.721	0.493592	0.739168
15069	10592878	NM_009476	22269	uroplakin 2	Upk2	0.916	-1.163	0.281672	0.556928
15070	10444719	NM_057171	224727	HLA-B-associated transcript 3	Bat3	0.916	-1.938	0.0926362	0.294729
15071	10344933					0.916	-0.676	0.520398	0.75796
15072	10349529	NM_172485	210417	thrombospondin, type I, domain	Thsd7b	0.916	-0.731	0.487788	0.735492
15073	10593024	NM_007648	12501	CD3 antigen, epsilon polypepti	Cd3e	0.916	-1.124	0.296898	0.573455
15074	10557450	NM_175103	66162	bolA-like 2 (E. coli)	Bola2	0.916	-2.132	0.069325	0.246733
15075	10440578	NM_001081068	78913	zinc finger protein 294	Zfp294	0.916	-1.671	0.13738	0.374325
15076	10416584	XR_034373	219180	similar to ribosomal protein S	LOC219180	0.916	-1.044	0.330309	0.606542
15077	10398678	NM_173363	217869	eukaryotic translation initiat	Eif5	0.916	-1.936	0.0928207	0.295128
15078	10448700	NM_023040	11692	growth factor, erv1 (S. cerevi	Gfer	0.916	-1.668	0.138026	0.375747
15079	10419900	NM_010856	17888	myosin, heavy polypeptide 6, c	Myh6	0.916	-0.878	0.408047	0.672572
15080	10504582	BC111889	74152	RIKEN cDNA 1300002K09 gene	1300002K09Rik	0.916	-0.645	0.539036	0.772027
15081	10587552					0.916	-1.395	0.204398	0.467676
15082	10549758	NM_029849	77043	RIKEN cDNA 4632433K11 gene	4632433K11Rik	0.916	-1.965	0.0888923	0.287567
15083	10413983	XM_985917	268729	gene model 626, (NCBI)	Gm626	0.916	-1.271	0.243164	0.516159
15084	10569786	NM_001122818	50767	patatin-like phospholipase dom	Pnpla6	0.916	-1.835	0.107914	0.323972
15085	10449602	ENSMUST00000114648	68597	RIKEN cDNA 1110021J02 gene	1110021J02Rik	0.916	-1.927	0.094051	0.297697
15086	10387992	NM_172394	19069	nucleoporin 88	Nup88	0.916	-1.717	0.128375	0.35928
15087	10419717	NM_146431	258423	olfactory receptor 1510	Olfr1510	0.916	-0.38	0.715238	0.875355
15088	10375608	NM_170727	68662	secretoglobin, family 3A, memb	Scgb3a1	0.916	-1.379	0.209053	0.474049
15089	10507594	NM_011400	20525	solute carrier family 2 (facil	Slc2a1	0.916	-2.043	0.0792291	0.268035
15090	10367379	NM_021882	20431	silver	Si	0.916	-1.258	0.247601	0.520853

15091	10410452	NM_175283	78925	steroid 5 alpha-reductase 1	Srd5a1	0.916	-0.986	0.356273	0.628749
15092	10606924					0.916	-1.758	0.120931	0.347273
15093	10508608	NM_026441	67898	penta-EF hand domain containin	Pef1	0.916	-2.02	0.0819688	0.273497
15094	10405488	NM_026211	67511	transmembrane emp24 protein tr	Tmed9	0.916	-1.8	0.113683	0.334268
15095	10405119	XM_914954	218241	gene model 270, (NCBI)	Gm270	0.916	-1.005	0.347369	0.621544
15096	10431836	BC106998	100043315	hypothetical LOC100043315	LOC100043315	0.916	-0.585	0.576096	0.797166
15097	10507677	NM_010657	16656	human immunodeficiency virus t	Hivep3	0.916	-1.138	0.291333	0.567423
15098	10375265	NM_176999	319767	ATPase, class V, type 10B	Atp10b	0.916	-0.688	0.513231	0.753594
15099	10507190	BC059213	230648	RIKEN cDNA 4732418C07 gene	4732418C07Rik	0.916	-1.451	0.188721	0.446774
15100	10500034	NM_008945	19172	proteasome (prosome, macropain	Psmb4	0.916	-2.178	0.0647178	0.236951
15101	10374426					0.916	-0.951	0.372279	0.642621
15102	10448195	NR_003549	73233	RIKEN cDNA 3110048L19 gene	3110048L19Rik	0.916	-1.388	0.206365	0.470648
15103	10591806	NM_018739	55934	retinitis pigmentosa 9 (human)	rp9	0.916	-1.045	0.329994	0.606438
15104	10407300	ENSMUST00000063230	75161	RIKEN cDNA 4930544M13 gene	4930544M13Rik	0.916	-0.686	0.51402	0.754437
15105	10482075	NM_028921	74410	tubulin tyrosine ligase-like f	Ttll11	0.916	-1.326	0.225329	0.495409
15106	10429218	ENSMUST00000022953	70363	RIKEN cDNA 1700010C24 gene	1700010C24Rik	0.916	-1.675	0.136582	0.373064
15107	10553274	NM_011314	20209	serum amyloid A 2	Saa2	0.916	-0.485	0.641813	0.837827
15108	10509277	NM_027063	69380	RIKEN cDNA 1700013G24 gene	1700013G24Rik	0.916	-0.048	0.962998	0.985606
15109	10499420	NM_031248	83409	mitogen-activated protein bind	Mapbpip	0.916	-2.186	0.0639731	0.234957
15110	10479775	NM_015765	50497	heat shock protein 14	Hspa14	0.916	-1.97	0.0883196	0.286438
15111	10587010					0.916	-1.451	0.188755	0.446774
15112	10552508	NM_011872	23993	kallikrein related-peptidase 7	Klk7	0.916	-0.533	0.610304	0.81867
15113	10467637	NM_027667	71085	Rho GTPase activating protein	Arhgap19	0.916	-1.757	0.121103	0.347578
15114	10390746					0.916	-1.019	0.340982	0.615921
15115	10584602	ENSMUST00000098865	100038649	predicted gene, ENSMUSG0000007	ENSMUSG00000074413	0.916	-1.093	0.309606	0.586533
15116	10446423	XM_001478639	71331	RIKEN cDNA 5430411C19 gene	5430411C19Rik	0.916	-1.125	0.296525	0.573205
15117	10504417	NM_027511	100039781	RIKEN cDNA 3830408D24 gene	3830408D24Rik	0.916	-0.527	0.61434	0.821474
15118	10449292	NM_008700	18091	NK2 transcription factor relat	Nkx2-5	0.916	-1.054	0.326015	0.602453
15119	10406459	NM_025523	66377	NADH dehydrogenase (ubiquinone	Ndufc1	0.916	-1.123	0.297469	0.573687
15120	10389668	NM_146411	258406	olfactory receptor 462	Olfr462	0.916	-1.144	0.289075	0.565029
15121	10410390					0.916	-0.954	0.371134	0.641955
15122	10374117	XR_033814	665250	similar to RNA polymerase II t	LOC665250	0.916	-0.729	0.488903	0.736349
15123	10351353	NM_001113394	12503	CD247 antigen	Cd247	0.916	-1.787	0.115818	0.338426
15124	10563014	NM_019830	15469	protein arginine N-methyltrans	Prmt1	0.916	-1.444	0.190645	0.449586
15125	10355214	NM_010497	15926	isocitrate dehydrogenase 1 (NA	Idh1	0.915	-3.551	0.00888271	0.0623974
15126	10527870	NM_013823	16591	klotho	Kl	0.915	-0.965	0.36568	0.636847
15127	10433478					0.915	-1.706	0.13052	0.362499
15128	10396170	NM_028127	319710	FERM domain containing 6	Frmd6	0.915	-1.069	0.3194	0.596434
15129	10566300	NM_147121	259125	olfactory receptor 644	Olfr644	0.915	-0.768	0.466818	0.71989
15130	10453732	XR_031272	225134	similar to ribosomal protein S	LOC225134	0.915	-0.673	0.521975	0.759008
15131	10376868	NM_011706	22368	transient receptor potential c	Trpv2	0.915	-0.871	0.411693	0.675585
15132	10406825	NM_023472	68558	ankyrin repeat, family A (RFXA	Ankra2	0.915	-1.755	0.121381	0.347955
15133	10539857	AK020089	434064	predicted gene, EG434064	EG434064	0.915	-1.352	0.217154	0.484774
15134	10391508	NM_024449	74499	sclerostin	Sost	0.915	-1.339	0.221134	0.490317
15135	10366196	NM_177373	327814	protein tyrosine phosphatase,	Ppfia2	0.915	-1.161	0.282634	0.557724
15136	10588324					0.915	-1.081	0.314344	0.591167
15137	10452729	BC046516	225004	cDNA sequence BC027072	BC027072	0.915	-1.015	0.343028	0.617132
15138	10528915	NM_021288	22171	thymidylate synthase	Tyms	0.915	-1.956	0.0901864	0.289885
15139	10448416	NM_027008	69259	potassium channel tetramerisat	Kctd5	0.915	-1.339	0.221278	0.490585
15140	10583694	BC057071	69773	RIKEN cDNA 1810026J23 gene	1810026J23Rik	0.915	-1.358	0.21542	0.482533
15141	10579468	BC003935	76478	RIKEN cDNA 2410004L22 gene	2410004L22Rik	0.915	-2.46	0.042456	0.180513

15142	10550660	NM_001010836	333654	protein phosphatase 1, regulat	Ppp1r13l	0.915	-1.314	0.229192	0.500215
15143	10511007	BC117034	67513	RIKEN cDNA 2610002J02 gene	2610002J02Rik	0.915	-1.174	0.277889	0.553005
15144	10383152	ENSMUST00000093902	672511	hypothetical LOC672511	LOC672511	0.915	-1.339	0.221082	0.490317
15145	10403868	XR_032236	665386	similar to prothymosin, alpha	LOC665386	0.915	-1.886	0.10001	0.309109
15146	10581212					0.915	-0.957	0.369602	0.640195
15147	10576965					0.915	-0.947	0.374446	0.644557
15148	10535776	NM_001039678	231903	parahox cluster neighbor	Prhoxnb	0.915	-0.786	0.456951	0.712826
15149	10525271	BC132172	231713	RIKEN cDNA C330023M02 gene	C330023M02Rik	0.915	-1.552	0.163447	0.412528
15150	10350015	NM_028320	72674	adiponectin receptor 1	Adipor1	0.915	-2.248	0.058305	0.221767
15151	10480621	BC132286	74472	RIKEN cDNA 4933433C11 gene	4933433C11Rik	0.915	-1.204	0.266458	0.541209
15152	10365355	NM_027423	70428	polymerase (RNA) III (DNA dire	Polr3b	0.915	-1.792	0.115026	0.337303
15153	10444605	NM_011690	22321	valyl-tRNA synthetase	Vars	0.915	-1.913	0.0961015	0.301703
15154	10448055	NM_008799	18567	programmed cell death 2	Pdcd2	0.915	-2.37	0.0485999	0.197122
15155	10463282	NM_053103	93685	ectonucleoside triphosphate di	Entpd7	0.915	-1.364	0.213466	0.479498
15156	10582464					0.915	-1.993	0.0853183	0.280424
15157	10444713	NM_032460	81845	HLA-B associated transcript 4	Bat4	0.915	-1.472	0.183361	0.440466
15158	10383763	ENSMUST00000087968	100038445	predicted gene, ENSMUSG0000006	ENSMUSG00000067584	0.915	-1.088	0.311617	0.588183
15159	10489179	NM_010285	14601	growth hormone releasing hormo	Ghrh	0.915	-1.335	0.222597	0.492542
15160	10360662	NR_003623	277333	predicted gene, EG277333	EG277333	0.915	-1.65	0.141594	0.381092
15161	10383194	ENSMUST00000093902	672511	hypothetical LOC672511	LOC672511	0.915	-1.198	0.268739	0.543286
15162	10414202	NM_023134	20387	surfactant associated protein	Sftpa1	0.915	-1.14	0.290661	0.567002
15163	10570587	NM_183035	360211	defensin beta 34	Defb34	0.915	-0.775	0.463127	0.71752
15164	10572146	NM_007509	11966	ATPase, H+ transporting, lysos	Atp6v1b2	0.915	-1.551	0.163675	0.412879
15165	10477179	NM_053091	84682	cytochrome c oxidase subunit I	Cox4i2	0.915	-1.445	0.19051	0.449454
15166	10398334					0.915	-0.715	0.496916	0.741273
15167	10574133					0.915	-0.787	0.456251	0.712479
15168	10387932	NM_011072	18643	profilin 1	Pfn1	0.915	-1.783	0.116468	0.339621
15169	10564448	NM_080443	117589	ankyrin repeat and SOCS box-co	Asb7	0.915	-1.072	0.318089	0.595218
15170	10364237	ENSMUST00000099552	100038479	predicted gene, ENSMUSG0000007	ENSMUSG00000074919	0.915	-0.949	0.373334	0.643602
15171	10594188	NM_013708	23958	nuclear receptor subfamily 2,	Nr2e3	0.915	-1.062	0.322606	0.599294
15172	10552380	NM_172900	243958	sialic acid binding Ig-like le	Siglecg	0.915	-0.807	0.445407	0.703573
15173	10606910	NM_001082412	67062	mitochondrial carrier triple r	Mcart6	0.915	-1.139	0.291108	0.567231
15174	10515698	ENSMUST00000075406	230676	cDNA sequence BC059842	BC059842	0.915	-1.53	0.168673	0.420172
15175	10349580	NM_011082	18703	polymeric immunoglobulin recep	Pigr	0.915	-0.499	0.632381	0.832782
15176	10482712	NM_019667	56324	signal transducing adaptor mol	Stam2	0.915	-2.01	0.0831229	0.276258
15177	10397143	ENSMUST00000053744	71952	RIKEN cDNA 2410016O06 gene	2410016O06Rik	0.915	-1.919	0.0952153	0.2999
15178	10596322	BC048436	73532	RIKEN cDNA 1700080E11 gene	1700080E11Rik	0.915	-0.75	0.477076	0.727851
15179	10488048	NM_021527	59030	McKusick-Kaufman syndrome prot	Mkks	0.915	-1.468	0.18429	0.44191
15180	10368635	NM_001081165	270711	RIKEN cDNA 4732454E20 gene	4732454E20Rik	0.915	-1.454	0.188055	0.446224
15181	10442468	NM_027937	268932	CASK interacting protein 1	Caskin1	0.915	-1.022	0.339673	0.615113
15182	10378964	NM_021286	20370	seizure related gene 6	Sez6	0.915	-1.072	0.318102	0.595218
15183	10403973	ENSMUST00000017126	195236	gene model 24, (NCBI)	Gm24	0.915	-0.859	0.41795	0.680624
15184	10455599					0.915	-0.754	0.474511	0.726086
15185	10359851	NM_030724	80914	uridine-cytidine kinase 2	Uck2	0.915	-1.109	0.302928	0.579019
15186	10518059	NM_001033875	76701	chymotrypsin C (caldecrin)	Ctrc	0.915	-0.904	0.394942	0.662592
15187	10436800	ENSMUST00000060246	68500	RIKEN cDNA 1110008E08 gene	1110008E08Rik	0.915	-0.679	0.51831	0.756954
15188	10571857					0.915	-0.938	0.378705	0.648368
15189	10598474	NM_078484	22232	solute carrier family 35 (UDP-	Slc35a2	0.915	-1.044	0.330171	0.606529
15190	10504992	ENSMUST00000107666	73398	RIKEN cDNA 1700054F22 gene	1700054F22Rik	0.915	-1.298	0.23419	0.505444
15191	10454095					0.914	-0.575	0.582776	0.800924
15192	10365005	NM_007828	13144	death-associated kinase 3	Dapk3	0.914	-0.992	0.353209	0.625979

15193	10363498	NM_026438	67895	pyrophosphatase (inorganic) 1	Ppa1	0.914	-1.342	0.220299	0.488992
15194	10440964	NM_133679	66609	crystallin, zeta (quinone redu	Cryzl1	0.914	-1.977	0.0873523	0.284457
15195	10450055	NM_010385	14976	H2-K region expressed gene 2	H2-Ke2	0.914	-2.288	0.0548634	0.213516
15196	10519314					0.914	-0.738	0.483612	0.732303
15197	10542156	NM_053109	93694	C-type lectin domain family 2,	Clec2d	0.914	-0.004	0.996797	0.998781
15198	10606948	NM_029413	75746	microrchidia 4	Morc4	0.914	-1.075	0.317199	0.594448
15199	10563649	NM_001040695	54122	UEV and lactate/malate dehyrog	Uevld	0.914	-1.141	0.290327	0.566507
15200	10452228	NM_010613	16549	KH-type splicing regulatory pr	Khsrp	0.914	-2.124	0.0701648	0.248254
15201	10575302	NM_009677	11765	adaptor protein complex AP-1,	Ap1g1	0.914	-2.147	0.0677428	0.243242
15202	10405929	AK154519	100038627	predicted gene, ENSMUSG0000007	ENSMUSG00000074823	0.914	-1.289	0.237101	0.509272
15203	10562784	NM_178067	233199	myosin binding protein C, fast	Mybpc2	0.914	-1.687	0.134198	0.369304
15204	10477485	BC115526	67135	RIKEN cDNA 2310021H06 gene	2310021H06Rik	0.914	-0.545	0.602207	0.813667
15205	10574308	NM_028805	74187	katanin p80 (WD40-containing)	Katnb1	0.914	-1.613	0.149423	0.39184
15206	10363599	NM_027425	70432	RUN and FYVE domain-containing	Rufy2	0.914	-1.858	0.104346	0.317818
15207	10352586	NM_021408	22283	Usher syndrome 2A (autosomal r	Ush2a	0.914	-1.25	0.250453	0.524406
15208	10393904	NM_175263	77583	notum pectinacetylesterase hom	Notum	0.914	-0.745	0.479887	0.729876
15209	10548359	BC117712	71183	C-type lectin domain family 12	Clec12b	0.914	-1.574	0.158186	0.405072
15210	10392437	ENSMUST00000070956	100036768	predicted gene, OTTMUSG0000000	OTTMUSG00000003456	0.914	-1.262	0.246126	0.51906
15211	10593740	NM_001025375	66317	WD repeat domain 61	Wdr61	0.914	-2.144	0.0680839	0.243829
15212	10588195	ENSMUST00000078519	442798	RIKEN cDNA 9630041A04 gene	9630041A04Rik	0.914	-0.405	0.697473	0.867333
15213	10393064	NM_001009573	70450	unc-13 homolog D (C. elegans)	Unc13d	0.914	-1.683	0.134933	0.370281
15214	10603453	NM_026137	73447	WD repeat domain 13	Wdr13	0.914	-1.376	0.210177	0.475495
15215	10489522	NM_001012723	277345	WAP four-disulfide core domain	Wfdc16	0.914	-1.094	0.309301	0.586062
15216	10544891	NM_172729	107607	nucleotide-binding oligomeriza	Nod1	0.914	-1.185	0.273578	0.548314
15217	10382462	NM_012030	26941	solute carrier family 9 (sodiu	Slc9a3r1	0.914	-1.418	0.19802	0.458849
15218	10438517	NM_145939	208624	asparagine-linked glycosylatio	Alg3	0.914	-2.067	0.0764094	0.262018
15219	10488106	XM_001005575	269365	similar to ribosomal protein S	LOC269365	0.914	-1.155	0.284934	0.560276
15220	10457007	NM_025861	66943	PQ loop repeat containing 1	Pqlc1	0.914	-1.251	0.250134	0.524217
15221	10436034					0.914	-1.177	0.276725	0.551883
15222	10547191	BC093486	319776	RIKEN cDNA C230095G01 gene	C230095G01Rik	0.914	-0.864	0.415236	0.678399
15223	10419034	AK012157	70045	RIKEN cDNA 2610528A11 gene	2610528A11Rik	0.914	-0.924	0.385508	0.654661
15224	10590029					0.914	-0.563	0.590758	0.806356
15225	10551314	BC024978	414069	cDNA sequence BC024978	BC024978	0.914	-0.88	0.407012	0.671546
15226	10466272	NM_001011775	257938	olfactory receptor 1419	Olfr1419	0.914	-0.539	0.606403	0.816622
15227	10413138	NM_011695	22334	voltage-dependent anion channe	Vdac2	0.914	-2.245	0.0585319	0.222381
15228	10406426	NM_007684	12626	centrin 3	Cetn3	0.914	-1.95	0.0909512	0.291551
15229	10366303					0.914	-1.133	0.293639	0.56967
15230	10545742	NM_144943	246278	CD 207 antigen	Cd207	0.914	-1.037	0.333222	0.609187
15231	10448369	NM_153791	224613	FLYWCH-type zinc finger 1	Flywch1	0.914	-1.57	0.159208	0.406366
15232	10540542	XM_917008	620161	predicted gene, EG620161	EG620161	0.914	-1.141	0.290227	0.566365
15233	10422606					0.914	-0.895	0.399454	0.665621
15234	10593035	NM_145403	214523	transmembrane protease, serine	Tmprss4	0.914	-1.052	0.326579	0.602834
15235	10362064	BC099546	67692	RIKEN cDNA 1700020N01 gene	1700020N01Rik	0.914	-0.925	0.385108	0.654297
15236	10499329	NM_021375	58176	Rhesus blood group-associated	Rhbg	0.914	-0.734	0.485969	0.734018
15237	10517058	AK051860	100036542	predicted gene, ENSMUSG0000005	ENSMUSG00000056524	0.914	-0.949	0.373554	0.643666
15238	10389130	AK005634	76392	RIKEN cDNA 1700003F17 gene	1700003F17Rik	0.914	-1.661	0.13937	0.377524
15239	10359734	ENSMUST00000027856	74106	IQ motif and WD repeats 1	Iqwd1	0.914	-0.842	0.426697	0.68818
15240	10427131	NM_146064	223920	sterol O-acyltransferase 2	Soat2	0.914	-0.868	0.413509	0.677091
15241	10534384	NM_029681	76629	Williams-Beuren syndrome chrom	Wbscr28	0.914	-0.949	0.373096	0.643427

15242	10459066	ENSMUST00000090260	100044195	hypothetical protein LOC100044	LOC100044195	0.914	-0.705	0.502943	0.745637
15243	10364385	NM_173751	216136	ilvB (bacterial acetolactate s	Ilvbl	0.914	-1.616	0.148832	0.391099
15244	10398332					0.914	-1.08	0.314827	0.59176
15245	10586064	NM_009672	11737	acidic (leucine-rich) nuclear	Anp32a	0.914	-1.77	0.118781	0.344229
15246	10382345	NM_013581	16834	component of oligomeric golgi	Cog1	0.914	-1.796	0.114275	0.335588
15247	10571250	BC090989	628431	high mobility group box 1, rel	Hmgb1-rs17	0.914	-0.903	0.395732	0.663394
15248	10368064	ENSMUST00000095817	100039660	hypothetical protein LOC100039	LOC100039660	0.914	-1.403	0.202065	0.464803
15249	10519642	XR_034137	242809	similar to Ribosomal protein L	LOC242809	0.914	-1.657	0.140318	0.378815
15250	10512774	NM_178893	107684	coronin, actin binding protein	Coro2a	0.914	-1.262	0.246122	0.51906
15251	10350090	NM_026024	67196	ubiquitin-conjugating enzyme E	Ube2t	0.913	-2.081	0.07481	0.258759
15252	10571312	NM_176933	319520	dual specificity phosphatase 4	Dusp4	0.913	-1.641	0.143593	0.384223
15253	10568581	NM_009123	20231	NK1 transcription factor relat	Nkx1-2	0.913	-1.339	0.221085	0.490317
15254	10532241	NM_174870	231583	solute carrier family 26 (sulf	Slc26a1	0.913	-1.083	0.313847	0.590663
15255	10565089	NM_007755	12877	cytoplasmic polyadenylation el	Cpeb1	0.913	-1.085	0.312743	0.589203
15256	10389990	NM_027984	71889	epsin 3	Epn3	0.913	-1.879	0.101135	0.311419
15257	10601335	BC035042	67683	RIKEN cDNA 2610029G23 gene	2610029G23Rik	0.913	-1.638	0.14416	0.385253
15258	10489719	NM_001007581	381406	RIKEN cDNA 2810408M09 gene	2810408M09Rik	0.913	-1.524	0.170105	0.421852
15259	10471294	NM_145521	227721	phosphatidic acid phosphatase	Ppapdc3	0.913	-1.549	0.164037	0.413545
15260	10354168	NM_018775	54610	TBC1 domain family, member 8	Tbc1d8	0.913	-2.034	0.0802518	0.270212
15261	10446341	AK132847	75039	RIKEN cDNA 4930505H01 gene	4930505H01Rik	0.913	-1.204	0.266612	0.541262
15262	10605328	NM_025473	66294	RIKEN cDNA 1810037C20 gene	1810037C20Rik	0.913	-1.888	0.0996886	0.308576
15263	10563731					0.913	-1.188	0.272422	0.547018
15264	10353878	NM_153502	78321	ankyrin repeat domain 23	Ankrd23	0.913	-0.715	0.496846	0.741257
15265	10564480					0.913	-1.134	0.292957	0.569014
15266	10419563	NM_011271	19752	ribonuclease, RNase A family,	Rnase1	0.913	-0.75	0.476909	0.727649
15267	10383389	NM_027204	56282	mitochondrial ribosomal protei	Mrpl12	0.913	-2.351	0.049948	0.200971
15268	10514333	ENSMUST00000057837	75246	RIKEN cDNA 4930553M12 gene	4930553M12Rik	0.913	-0.805	0.446276	0.704033
15269	10487564	NM_020594	57432	zinc finger CCCH type containi	Zc3h8	0.913	-1.266	0.244756	0.517875
15270	10606816	ENSMUST00000033786	75829	preferentially expressed antig	Prame	0.913	-1.894	0.0988256	0.306883
15271	10493435	NM_001077411	14466	glucosidase, beta, acid	Gba	0.913	-1.615	0.149055	0.391409
15272	10368947	NM_172393	11630	absent in melanoma 1	Aim1	0.913	-1.613	0.149578	0.392051
15273	10442924	AK052760	240054	RIKEN cDNA gene D630044L22 gen	D630044L22Rik	0.913	-1.562	0.161011	0.40889
15274	10364381	ENSMUST00000095474	258224	olfactory receptor 1358	Olfr1358	0.913	-0.635	0.545069	0.77708
15275	10460202	NM_144871	225888	suppressor of variegation 4-20	Suv420h1	0.913	-1.734	0.12534	0.354588
15276	10567546	NM_016669	12971	crystallin, mu	Crym	0.913	-1.051	0.327174	0.603382
15277	10533367	NM_028037	71985	acyl-Coenzyme A dehydrogenase	Acad10	0.913	-0.814	0.441788	0.700657
15278	10500054	NM_008951	19185	proteasome (prosome, macropain	Psmd4	0.913	-2.402	0.0463189	0.191233
15279	10555039	NM_001039039	622320	potassium channel tetramerisat	Kctd21	0.913	-0.902	0.396107	0.663738
15280	10570972	ENSMUST00000066740	208924	RIKEN cDNA A730045E13 gene	A730045E13Rik	0.913	-0.795	0.451728	0.708709
15281	10448707	NM_145396	213773	transducin (beta)-like 3	Tbl3	0.913	-1.632	0.145431	0.387083
15282	10344624	NM_008866	18777	lysophospholipase 1	Lypla1	0.913	-2.074	0.0756056	0.260007
15283	10507213	NM_175308	100465	MOB1, Mps One Binder kinase ac	Mobkl2c	0.913	-1.392	0.205399	0.469103
15284	10519196	NM_147776	246228	von Willebrand factor A domain	Vwa1	0.913	-0.89	0.402379	0.667444
15285	10541507	NM_009645	11628	activation-induced cytidine de	Aicda	0.913	-1.144	0.2891	0.565029
15286	10395610	XM_001473056	100039525	similar to ribosomal protein S	LOC100039525	0.913	-1.046	0.32955	0.60586
15287	10557519	NM_172746	233876	HIRA interacting protein 3	Hirip3	0.913	-1.494	0.177628	0.43207
15288	10526229	ENSMUST00000100641	100038504	predicted gene, ENSMUSG0000007	ENSMUSG00000072573	0.913	-1.173	0.278197	0.553196
15289	10346074	NM_028599	73674	WD repeat domain 75	Wdr75	0.913	-1.95	0.0909012	0.291551
15290	10409352	NM_134064	105239	ring finger protein 44	Rnf44	0.913	-1.807	0.112527	0.33223

15291	10428918	AK139928	399603	RIKEN cDNA D330050I23 gene	D330050I23Rik	0.913	-1.32	0.227291	0.498027
15292	10509601	NM_029857	77056	transmembrane and coiled-coil	Tmco4	0.913	-1.539	0.16642	0.417266
15293	10607495	XR_031668	640803	similar to ribosomal protein L	LOC640803	0.913	-1.059	0.323812	0.600286
15294	10584187	ENSMUST00000093873	78934	RIKEN cDNA 4930581F22 gene	4930581F22Rik	0.913	-1.703	0.131104	0.36355
15295	10550487	NM_153749	266815	MHC I like leukocyte 1	Mill1	0.913	-0.49	0.63841	0.835923
15296	10390936	NM_026834	68768	RIKEN cDNA 1110054P19 gene	1110054P19Rik	0.913	-0.873	0.411038	0.675081
15297	10608184	NM_009571	22768	zinc finger protein 2, Y linke	Zfy2	0.913	-1.249	0.25068	0.524426
15298	10415144	NM_026890	68966	neuroguidin, EIF4E binding pro	Ngdn	0.913	-2.579	0.0355871	0.160643
15299	10388194	BC025823	216892	spinster homolog 2 (Drosophila	Spns2	0.913	-0.674	0.521463	0.758794
15300	10548116	BC049086	12444	cyclin D2	Ccnd2	0.913	-1.26	0.246841	0.520152
15301	10395869	BC100489	70846	RIKEN cDNA 4921506M07 gene	4921506M07Rik	0.913	-0.462	0.657821	0.846971
15302	10474371	ENSMUST00000104890	791267	predicted gene, ENSMUSG0000005	ENSMUSG00000055181	0.913	-0.807	0.445192	0.70357
15303	10432431	NM_001081254	545136	predicted gene, EG545136	EG545136	0.913	-1.557	0.1621	0.410473
15304	10415678	NM_026908	69008	calcium binding protein 39-lik	Cab39l	0.913	-1.417	0.19807	0.458849
15305	10436779	XR_034815	100048581	similar to myosin regulatory l	LOC100048581	0.913	-1.464	0.185388	0.443222
15306	10499529	NM_009057	19729	recombination activating gene	Rag1ap1	0.913	-1.754	0.121626	0.348228
15307	10591194	NM_146523	258516	olfactory receptor 850	Olfr850	0.913	-0.972	0.362729	0.634161
15308	10371032	NM_145217	208666	DIRAS family, GTP-binding RAS-	Diras1	0.912	-0.756	0.473518	0.725091
15309	10396730					0.912	-0.97	0.363572	0.6349
15310	10574866	NM_001047436	56513	par-6 (partitioning defective	Pard6a	0.912	-1.19	0.271882	0.546343
15311	10505534	XR_033232	636266	similar to 3-hydroxyisobutyrat	LOC636266	0.912	-1.105	0.304833	0.581243
15312	10525766	NM_181410	209357	general transcription factor I	Gtf2h3	0.912	-1.225	0.259132	0.533348
15313	10454877	NM_008989	19290	purine rich element binding pr	Pura	0.912	-1.487	0.17931	0.434671
15314	10559644	BC022651	330460	cDNA sequence BC022651	BC022651	0.912	-1.466	0.184873	0.44244
15315	10442083					0.912	-0.693	0.509977	0.75132
15316	10543333	NM_013930	30956	aminoadipate-semialdehyde synt	Aass	0.912	-1.953	0.090601	0.290914
15317	10527024	ENSMUST00000081114	791272	predicted gene, ENSMUSG0000006	ENSMUSG00000060929	0.912	-1.12	0.29843	0.574644
15318	10453248					0.912	-0.823	0.437086	0.696491
15319	10554005	NM_024439	109815	histocompatibility 47	H47	0.912	-2.741	0.0280323	0.137362
15320	10414065	NM_013473	11752	annexin A8	Anxa8	0.912	-0.782	0.45935	0.714207
15321	10510804	ENSMUST00000097769	100044224	hypothetical protein LOC100044	LOC100044224	0.912	-1.175	0.277489	0.552625
15322	10551319	NM_133770	76889	aarF domain containing kinase	Adck4	0.912	-1.901	0.0978611	0.304963
15323	10352777	NM_009579	22782	solute carrier family 30 (zinc	Slc30a1	0.912	-1.205	0.266322	0.541183
15324	10403943	NM_178200	319186	histone cluster 1, H2bm	Hist1h2bm	0.912	-1.852	0.105186	0.319429
15325	10379953	BC067002	74038	RIKEN cDNA 4632419I22 gene	4632419I22Rik	0.912	-2.008	0.0833713	0.276517
15326	10500388	BC026793	74414	polymerase (RNA) III (DNA dire	Polr3c	0.912	-1.074	0.317552	0.594733
15327	10389339	NM_001029934	237898	ubiquitin specific peptidase 3	Usp32	0.912	-1.635	0.144883	0.38638
15328	10414305	BC085089	56291	phosphoserine/threonine/tyrosi	Styx	0.912	-0.507	0.627431	0.83052
15329	10540122	NM_009320	21366	solute carrier family 6 (neuro	Slc6a6	0.912	-1.773	0.118254	0.343268
15330	10471191	NM_144886	227715	exosome component 2	Exosc2	0.912	-1.395	0.204455	0.467724
15331	10439634	NM_025332	66067	GTP-binding protein 8 (putativ	Gtpbp8	0.912	-1.479	0.181331	0.43738
15332	10565815	ENSMUST00000078533	245190	predicted gene, EG245190	EG245190	0.912	-1.882	0.100609	0.31038
15333	10452815	NM_011723	22436	xanthine dehydrogenase	Xdh	0.912	-1.221	0.260579	0.535075
15334	10449041	NM_133719	70083	meteorin, glial cell different	Metrn	0.912	-1.886	0.100001	0.309109
15335	10447239	NM_026180	67470	ATP-binding cassette, sub-fami	Abcg8	0.912	-0.768	0.467046	0.719977
15336	10538100	NM_001079901	58887	replication initiator 1	Repin1	0.912	-1.526	0.169549	0.420889
15337	10356240	NM_027921	71781	solute carrier family 16 (mono	Slc16a14	0.912	-1.267	0.244514	0.517622
15338	10422176	ENSMUST00000105171	320671	RIKEN cDNA D130079A08 gene	D130079A08Rik	0.912	-1.605	0.151338	0.395197
15339	10391461	NM_009764	12189	breast cancer 1	Brca1	0.912	-1.613	0.14953	0.391974
15340	10529287	NM_178390	74504	RIKEN cDNA 2410018C17 gene	2410018C17Rik	0.912	-1.753	0.121805	0.348456
15341	10480744	NM_029958	77701	lipocalin 12	Lcn12	0.912	-0.776	0.462597	0.717093

15342	10365637	NM_025859	104303	ADP-ribosylation factor-like 1	Arl1	0.912	-1.646	0.14253	0.382589
15343	10509562	NM_026689	68350	mitochondrial ubiquitin ligase	Mul1	0.912	-2.549	0.0372502	0.165989
15344	10389505	ENSMUST00000069425	327988	predicted gene, ENSMUSG0000005	ENSMUSG00000055697	0.912	-1.228	0.257931	0.531958
15345	10507574	NM_146852	258851	olfactory receptor 1339	Olfr1339	0.912	-0.91	0.392004	0.66023
15346	10505374	NM_025685	373864	collagen, type XXVII, alpha 1	Col27a1	0.912	-1.547	0.164536	0.414357
15347	10539393	ENSMUST00000113900	232156	solute carrier family 4, sodiu	Slc4a5	0.912	-1.323	0.226369	0.496985
15348	10606546					0.912	-2.65	0.0320517	0.150167
15349	10550740	NM_027839	71601	CEA-related cell adhesion mole	Ceacam20	0.912	-1.207	0.265392	0.540498
15350	10393662	NM_008730	18164	neuronal pentraxin 1	Nptx1	0.912	-0.882	0.406386	0.671037
15351	10390283	NM_030248	80280	CDK5 regulatory subunit associ	Cdk5rap3	0.912	-1.731	0.125719	0.355019
15352	10472128	NM_022989	65103	ADP-ribosylation factor-like 6	Arl6ip6	0.912	-1.517	0.171898	0.424059
15353	10447188	ENSMUST00000112344	116871	metastasis associated 3	Mta3	0.912	-0.628	0.549596	0.77991
15354	10529739					0.912	-1.064	0.321616	0.598456
15355	10562812	NM_019866	272382	Spi-B transcription factor (Sp	Spib	0.912	-0.863	0.415746	0.678857
15356	10370573	NM_011583	21830	testicular haploid expressed g	Theg	0.912	-0.952	0.371708	0.642056
15357	10471858					0.912	-0.816	0.440484	0.699376
15358	10578582	NM_177240	320714	RIKEN cDNA D030016E14 gene	D030016E14Rik	0.912	-2.008	0.0834347	0.276555
15359	10511950					0.912	-1.035	0.333907	0.609578
15360	10405804	NM_001013608	76251	RIKEN cDNA 0610007P08 gene	0610007P08Rik	0.911	-1.303	0.232491	0.503408
15361	10430324	NM_027902	71753	transmembrane serine protease	Tmprss6	0.911	-0.961	0.367454	0.638358
15362	10409579	NM_019568	57266	chemokine (C-X-C motif) ligand	Cxcl14	0.911	-1.218	0.26167	0.536119
15363	10582843					0.911	-1.81	0.111982	0.331246
15364	10550514	NM_001029877	384569	neuro-oncological ventral anti	Nova2	0.911	-0.982	0.357924	0.630288
15365	10353117	NM_172841	240726	solute carrier organic anion t	Slco5a1	0.911	-0.929	0.383039	0.652511
15366	10572722	XR_033804	100047513	similar to H3 histone, family	LOC100047513	0.911	-1.475	0.182361	0.438828
15367	10500899	NM_183224	329731	RIKEN cDNA 7530404M11 gene	7530404M11Rik	0.911	-1.104	0.304911	0.581338
15368	10400564	EF133693	623046	fibrous sheath CABYR binding p	Fscb	0.911	-0.955	0.370597	0.641341
15369	10541877	NM_001080557	22317	vesicle-associated membrane pr	Vamp1	0.911	-1.265	0.245241	0.518331
15370	10578922	NM_178633	77113	kelch-like 2, Mayven (Drosophi	Klhl2	0.911	-1.987	0.0860559	0.2817
15371	10356999	NM_011563	21672	peroxiredoxin 2	Prdx2	0.911	-1.73	0.125908	0.355243
15372	10499766	NM_011988	26568	solute carrier family 27 (fatt	Slc27a3	0.911	-1.938	0.0925946	0.294729
15373	10402585	NM_011710	22375	tryptophanyl-tRNA synthetase	Wars	0.911	-1.436	0.192968	0.452392
15374	10409616	NM_009262	20745	sparc/osteonectin, cwcv and ka	Spock1	0.911	-0.909	0.392737	0.660631
15375	10552044	NM_172899	73712	dermokine	Dmkn	0.911	-1.219	0.261059	0.535632
15376	10386344	BC094909	216792	RIKEN cDNA A230051G13 gene	A230051G13Rik	0.911	-0.599	0.567328	0.792677
15377	10363557	BC019469	74706	RIKEN cDNA 4930507D05 gene	4930507D05Rik	0.911	-1.003	0.348264	0.622132
15378	10563275	NM_011304	20174	RuvB-like protein 2	Ruvbl2	0.911	-2.484	0.0409873	0.176468
15379	10594244					0.911	-0.895	0.399455	0.665621
15380	10586168					0.911	-0.745	0.479816	0.729821
15381	10388684	NM_144825	216965	TAO kinase 1	Taok1	0.911	-1.747	0.122914	0.350775
15382	10492957	NM_007640	12480	CD1d2 antigen	Cd1d2	0.911	-1.268	0.244281	0.51746
15383	10524105	NM_172717	231600	checkpoint with forkhead and r	Chfr	0.911	-2.065	0.0766266	0.262465
15384	10566034	NM_008034	14275	folate receptor 1 (adult)	Folr1	0.911	-0.949	0.37343	0.643632
15385	10536711	NM_053098	93677	leiomodin 2 (cardiac)	Lmod2	0.911	-0.704	0.503632	0.746064
15386	10512443	NM_023231	66592	stomatin (Epb7.2)-like 2	Stoml2	0.911	-1.194	0.270224	0.545035
15387	10382532	NM_001080934	217316	solute carrier family 16 (mono	Slc16a5	0.911	-1.06	0.323425	0.599973
15388	10598674	XM_141626	245350	similar to Ubiquitin-conjugati	LOC245350	0.911	-0.832	0.432077	0.692476
15389	10427369	NM_008800	18574	phosphodiesterase 1B, Ca2+-cal	Pde1b	0.911	-0.628	0.54954	0.779883
15390	10516926	NM_026039	67219	mediator of RNA polymerase II	Med18	0.911	-1.509	0.173826	0.426575
15391	10363460	NM_001017433	65971	RIKEN cDNA 1700021K02 gene	1700021K02Rik	0.911	-1.741	0.124017	0.352448
15392	10381697	NM_138753	192231	hexamethylene bis-acetamide in	Hexim1	0.911	-1.888	0.0996917	0.308576
				predicted gene,					

15393	10360804	ENSMUST00000097444	669853	predicted gene, ENSMUSG0000007	ENSMUSG00000073482	0.911	-1.164	0.281462	0.55689
15394	10375704	BC028428	68067	RIKEN cDNA 3010026O09 gene	3010026O09Rik	0.911	-2.136	0.0689029	0.245893
15395	10566628					0.911	-0.824	0.436536	0.696302
15396	10442771	NM_053259	114661	protease, serine, 28	Prss28	0.911	-0.99	0.354317	0.626867
15397	10389835	NM_028547	73470	kinesin family member 2B	Kif2b	0.911	-0.834	0.43108	0.691717
15398	10389269	NM_019816	56321	apoptosis antagonizing transcr	Aatf	0.911	-1.312	0.229749	0.500845
15399	10515519	NM_033617	114143	ATPase, H+ transporting, lysos	Atp6v0b	0.911	-1.223	0.25978	0.53415
15400	10440690	NM_130873	170654	keratin associated protein 16-	Krtap16-4	0.911	-1.203	0.26684	0.541465
15401	10426118	NM_031260	83456	Moloney leukemia virus 10-like	Mov10l1	0.911	-0.844	0.425676	0.687513
15402	10415045	NM_026851	68836	mitochondrial ribosomal protei	Mrpl52	0.911	-2.09	0.073842	0.256795
15403	10535720	BC048528	69282	RIKEN cDNA 1700001J03 gene	1700001J03Rik	0.911	-0.686	0.514267	0.754529
15404	10429409	AK132992	268816	gene model 628, (NCBI)	Gm628	0.911	-0.803	0.447638	0.705227
15405	10425263	ENSMUST00000100456	100038573	predicted gene, ENSMUSG0000007	ENSMUSG00000075556	0.911	-1.114	0.301039	0.577287
15406	10512747	BC092543	74753	RIKEN cDNA 5830415F09 gene	5830415F09Rik	0.911	-1.31	0.230516	0.501476
15407	10503244					0.911	-1.454	0.187994	0.446224
15408	10476590	NM_001013802	72899	MACRO domain containing 2	Macrod2	0.911	-1.948	0.0912161	0.292267
15409	10502196	NM_026724	68436	ribosomal protein L34	Rpl34	0.911	-1.46	0.186348	0.44456
15410	10430770	NM_020507	57259	transducer of ERBB2, 2	Tob2	0.911	-1.256	0.248255	0.521623
15411	10462866	NM_028760	74107	centrosomal protein 55	Cep55	0.911	-1.123	0.297444	0.573687
15412	10438272	NM_011172	19125	proline dehydrogenase	Prodh	0.911	-1.598	0.152848	0.396925
15413	10477052	BC016127	69698	RIKEN cDNA 2310046K01 gene	2310046K01Rik	0.911	-0.74	0.482807	0.731475
15414	10434128	NM_016983	22363	pre-B lymphocyte gene 2	Vpreb2	0.911	-1.016	0.342505	0.616824
15415	10499909	AK019072	78382	RIKEN cDNA 2210420J11 gene	2210420J11Rik	0.911	-1.089	0.311405	0.587941
15416	10370721	NM_183426	216161	strawberry notch homolog 2 (Dr	Sbno2	0.911	-2.239	0.0591067	0.22389
15417	10420390	NM_020506	57258	exportin 4	Xpo4	0.911	-1.697	0.132192	0.365389
15418	10490751					0.911	-0.549	0.599677	0.812038
15419	10594758	NM_028087	72077	glucosaminyl (N-acetyl) transf	Gcnt3	0.911	-1.251	0.250048	0.524217
15420	10533729	NM_177876	330192	vacuolar protein sorting 37B (	Vps37b	0.911	-0.808	0.445136	0.703541
15421	10570018	NM_033622	24099	tumor necrosis factor (ligand)	Tnfsf13b	0.911	-1.02	0.340543	0.615722
15422	10459471	NM_013833	19434	retina and anterior neural fol	Rax	0.91	-2.012	0.0828588	0.275685
15423	10427995					0.91	-0.693	0.509913	0.751318
15424	10545751	NM_009357	21766	testis expressed gene 261	Tex261	0.91	-1.454	0.188012	0.446224
15425	10511269	NM_011341	20318	stromal cell derived factor 4	Sdf4	0.91	-1.698	0.132136	0.365356
15426	10496822	NM_010318	14707	guanine nucleotide binding pro	Gng5	0.91	-2.066	0.0764657	0.262126
15427	10384229					0.91	-0.745	0.479697	0.729728
15428	10443199	ENSMUST00000097361	619324	RIKEN cDNA C130040N14 gene	C130040N14Rik	0.91	-1.112	0.30181	0.577905
15429	10439087	NM_146071	224116	mucin 20	Muc20	0.91	-0.624	0.551953	0.781881
15430	10418796	NM_172254	105638	DPH3 homolog (KTI11, S. cerevi	Dph3	0.91	-2.074	0.0756139	0.260007
15431	10368888	NM_019740	56484	forkhead box O3a	Foxo3a	0.91	-1.485	0.1798	0.43509
15432	10508042	BC108404	70088	RIKEN cDNA 2310005N01 gene	2310005N01Rik	0.91	-1.331	0.223605	0.493567
15433	10498526	ENSMUST00000099076	71004	RIKEN cDNA 4931440P22 gene	4931440P22Rik	0.91	-0.972	0.362556	0.634015
15434	10381930					0.91	-0.43	0.679918	0.857866
15435	10375382	NM_001045520	216705	clathrin interactor 1	Clint1	0.91	-2.038	0.0797417	0.269041
15436	10371603	AK132809	626115	predicted gene, EG626115	EG626115	0.91	-1.12	0.298632	0.574809
15437	10504648					0.91	-1.055	0.32534	0.601678
15438	10347531	NM_026187	52231	ankyrin repeat and zinc finger	Ankzf1	0.91	-1.787	0.115813	0.338426
15439	10582501	NM_016925	14087	Fanconi anemia, complementatio	Fanca	0.91	-1.445	0.190348	0.44932
15440	10351489	XR_031469	640532	similar to Rpl17 protein	LOC640532	0.91	-0.805	0.446578	0.704239
15441	10401595	NM_146244	238323	ribosomal protein S6 kinase-li	Rps6kl1	0.91	-0.913	0.390786	0.659209
15442	10532926	NM_007383	11409	acyl-Coenzyme A dehydrogenase,	Acads	0.91	-1.327	0.225026	0.495052
15443	10462973	NM_008234	15201	helicase, lymphoid specific	Hells	0.91	-2.344	0.0504961	0.202329

15444	10604078	NM_026573	68134	UPF3 regulator of nonsense tra	Upf3b	0.91	-2.217	0.0610232	0.227923
15445	10493086	NM_008231	15191	hepatoma-derived growth factor	Hdgf	0.91	-1.458	0.187086	0.445467
15446	10415140	AK052874	791403	predicted gene, ENSMUSG0000005	ENSMUSG00000053118	0.91	-1.178	0.276289	0.551172
15447	10370920	NM_145361	208198	BTB (POZ) domain containing 2	Btbd2	0.91	-1.14	0.290803	0.567038
15448	10398422					0.91	-0.899	0.397572	0.664302
15449	10535849	BC006902	71706	solute carrier family 46, memb	Slc46a3	0.91	-1.395	0.204508	0.467724
15450	10517005	NM_008154	14748	G-protein coupled receptor 3	Gpr3	0.91	-0.572	0.584995	0.802565
15451	10571528					0.91	-0.965	0.365765	0.636847
15452	10371432	BC003288	28088	DNA segment, Chr 10, Wayne Sta	D10Wsu52e	0.91	-2.091	0.0737224	0.256633
15453	10387525	NM_011900	24070	mannose-P-dolichol utilization	Mpdu1	0.91	-1.337	0.222008	0.491636
15454	10575685	NM_024437	67528	nudix (nucleoside diphosphate	Nudt7	0.91	-1.542	0.165763	0.416208
15455	10558641	NM_146956	258958	olfactory receptor 525	Olfr525	0.91	-0.957	0.369337	0.639995
15456	10483856	NM_011871	23992	protein kinase, interferon ind	Prkra	0.91	-1.566	0.160096	0.407397
15457	10411432	NM_178918	105372	UTP15, U3 small nucleolar ribo	Utp15	0.91	-1.545	0.16509	0.415207
15458	10418905	NM_029389	75698	RIKEN cDNA 3110001K24 gene	3110001K24Rik	0.91	-1.113	0.301552	0.577839
15459	10448471	NM_025718	66705	deoxyribonuclease 1-like 2	Dnase1l2	0.91	-0.71	0.500124	0.743152
15460	10520268	ENSMUST00000075081	70258	RIKEN cDNA 1500035N22 gene	1500035N22Rik	0.91	-0.392	0.706616	0.87194
15461	10490970					0.91	-1.044	0.330068	0.606486
15462	10594297	NM_025721	66712	sperm equatorial segment prote	Spesp1	0.91	-1.328	0.224655	0.494757
15463	10594524	XM_917864	384945	ankyrin repeat and death domai	Ankdd1a	0.91	-1.253	0.24937	0.523394
15464	10413542	NM_009388	21881	transketolase	Tkt	0.91	-2.016	0.0824104	0.274537
15465	10491858					0.91	-1.166	0.280843	0.556319
15466	10573344					0.91	-0.917	0.388636	0.657212
15467	10373197	NM_010565	16325	inhibin beta-C	Inhbc	0.91	-1.118	0.299596	0.575721
15468	10604879	XR_031567	627734	similar to checkpoint suppress	LOC627734	0.91	-1.622	0.147545	0.389587
15469	10545720	NM_024239	70527	Stam binding protein	Stambp	0.91	-1.694	0.132781	0.366458
15470	10353773	XM_920965	433287	predicted gene, OTTMUSG0000002	OTTMUSG00000022109	0.91	-1.173	0.278209	0.553196
15471	10485151	NM_011162	19099	mitogen-activated protein kina	Mapk8ip1	0.91	-1.727	0.126492	0.356138
15472	10469522	BC049634	381350	cDNA sequence BC061194	BC061194	0.91	-0.953	0.371555	0.64202
15473	10475830	NM_029963	77721	mitochondrial ribosomal protei	Mrps5	0.909	-1.621	0.147721	0.389891
15474	10500114	NM_019914	56772	myeloid/lymphoid or mixed-line	Mllt11	0.909	-1.552	0.163458	0.412528
15475	10430968	NM_001004150	239559	alpha 1,4-galactosyltransferas	A4galt	0.909	-0.719	0.494536	0.7396
15476	10416510	NM_013745	27275	nuclear fragile X mental retar	Nufip1	0.909	-2.064	0.0767698	0.262742
15477	10360631	NM_023341	67426	chaperone, ABC1 activity of bc	Cabc1	0.909	-1.802	0.113248	0.333396
15478	10363629	NM_026701	68371	phenazine biosynthesis-like pr	Pbld	0.909	-1.61	0.15008	0.393124
15479	10433101	NM_030720	80910	G protein-coupled receptor 84	Gpr84	0.909	-1.352	0.217238	0.484882
15480	10429674	NM_031201	22122	tissue specific transplantatio	Tsta3	0.909	-1.647	0.142266	0.382232
15481	10422067	NM_015822	50789	F-box and leucine-rich repeat	Fbxl3	0.909	-1.816	0.111053	0.329804
15482	10534075	NM_133900	100678	phosphoserine phosphatase	Psph	0.909	-1.774	0.118118	0.343095
15483	10529794	XR_001803	636612	predicted gene, EG636612	EG636612	0.909	-1.276	0.241455	0.514338
15484	10559361	NM_008007	14174	fibroblast growth factor 3	Fgf3	0.909	-1.205	0.266368	0.541183
15485	10362596	NM_001122893	14360	Fyn proto-oncogene	Fyn	0.909	-1.454	0.18816	0.446289
15486	10489562	BC116354	75642	RIKEN cDNA 1700020C07 gene	1700020C07Rik	0.909	-1.089	0.311304	0.587855
15487	10377826	NM_001029929	574428	zinc finger, MYND-type contain	Zmynd15	0.909	-0.924	0.385552	0.654682
15488	10554017	NM_152815	72635	lines homolog 2 (Drosophila)	Lins2	0.909	-1.451	0.188735	0.446774
15489	10580704	NM_011787	23802	autocrine motility factor rece	Amfr	0.909	-2.147	0.0677482	0.243242
15490	10563303	NM_007527	12028	Bcl2-associated X protein	Bax	0.909	-2.028	0.0809791	0.271716
15491	10562349	NM_026549	68079	programmed cell death 2-like	Pdcd2l	0.909	-1.761	0.120409	0.346759
15492	10438899	NM_027904	71756	carboxypeptidase N, polypeptid	Cpn2	0.909	-1.836	0.10779	0.323783
15493	10404129	ENSMUST00000056790	71199	RIKEN cDNA 4933427I18 gene	4933427I18Rik	0.909	-0.916	0.389374	0.658054
15494	10357155	NM_008381	16324	inhibin beta-B	Inhbb	0.909	-1.245	0.252189	0.526303
15495	10530641	NM_177561	69727	ubiquitin specific peptidase 4	Usp46	0.909	-1.816	0.110944	0.329706

15496	10481262	NM_010190	14134	ficolin B	Fcnb	0.909	-0.748	0.47791	0.728494
15497	10579142	XR_032879	665649	similar to Nucleoside diphosph	LOC665649	0.909	-1.814	0.111335	0.33023
15498	10413419	NM_027871	71704	Rho guanine nucleotide exchang	Arhgef3	0.909	-2.242	0.0587691	0.22297
15499	10499703					0.909	-0.902	0.396349	0.663741
15500	10457250	NM_001039692	75415	Rho GTPase activating protein	Arhgap12	0.909	-1.831	0.108508	0.325246
15501	10579976	NM_178736	244548	ELMO domain containing 2	Elmod2	0.909	-1.276	0.24153	0.514365
15502	10501591	AK137339	68161	RIKEN cDNA A930005H10 gene	A930005H10Rik	0.909	-2.102	0.0724742	0.253591
15503	10582580					0.909	-1.602	0.151966	0.395759
15504	10444756	NM_023179	66237	ATPase, H+ transporting, lysos	Atp6v1g2	0.909	-1.491	0.178295	0.433019
15505	10441244	NM_020622	52793	open reading frame 9	ORF9	0.909	-0.806	0.445803	0.703765
15506	10549530					0.909	-1.157	0.28397	0.559215
15507	10368079	ENSMUST00000095817	100039660	hypothetical protein LOC100039	LOC100039660	0.909	-0.99	0.354295	0.626867
15508	10490045					0.909	-1.452	0.188573	0.446595
15509	10345030					0.909	-1.167	0.280305	0.555618
15510	10375129	ENSMUST00000101371	216644	RIKEN cDNA D130052B06 gene	D130052B06Rik	0.909	-0.877	0.40885	0.673168
15511	10568948	NM_183147	212518	shadow of prion protein	Sprn	0.909	-1.312	0.229767	0.500845
15512	10544913	NM_009953	12922	corticotropin releasing hormon	Crhr2	0.909	-1.107	0.303939	0.580269
15513	10538855	XM_921076	545845	similar to Superoxide dismutas	LOC545845	0.909	-1.509	0.173738	0.426449
15514	10534974	NM_008568	17220	minichromosome maintenance def	Mcm7	0.909	-2.173	0.0651774	0.238029
15515	10416406	NM_172812	15558	5-hydroxytryptamine (serotonin	Htr2a	0.909	-1.263	0.246047	0.51906
15516	10579066	XR_032700	100041482	similar to cadherin-11	LOC100041482	0.909	-1.645	0.142646	0.382804
15517	10393887	NM_144795	209027	pyrroline-5-carboxylate reduct	Pycr1	0.909	-1.467	0.18454	0.442142
15518	10534140	ENSMUST00000078925	625540	predicted gene, EG625540	EG625540	0.909	-1.65	0.141737	0.381301
15519	10570647	XR_030580	100039037	similar to CG6004-PB	LOC100039037	0.909	-0.802	0.44811	0.70576
15520	10368511	NM_028604	73681	tRNA methyltransferase 11 homo	Trmt11	0.909	-0.796	0.451475	0.708527
15521	10544717	ENSMUST00000067831	791277	predicted gene, ENSMUSG0000005	ENSMUSG00000054663	0.909	-0.981	0.358286	0.630567
15522	10568258	ENSMUST00000066769	629159	RIKEN cDNA 1700008J07 gene	1700008J07Rik	0.909	-1.23	0.257279	0.531552
15523	10559825	BC117497	76373	RIKEN cDNA 2810409K11 gene	2810409K11Rik	0.909	-1.769	0.118896	0.344375
15524	10558583	BC065404	69752	zinc finger protein 511	Zfp511	0.909	-1.685	0.134655	0.369832
15525	10604451	NM_145951	209224	ecto-NOX disulfide-thiol excha	Enox2	0.909	-2.15	0.0675113	0.242726
15526	10555907	NM_146758	258753	olfactory receptor 678	Olfr678	0.909	-1.014	0.343531	0.617603
15527	10498332	NM_009174	20439	seven in absentia 2	Siah2	0.909	-2.403	0.0462369	0.190954
15528	10433278	NM_023646	83945	DnaJ (Hsp40) homolog, subfamil	Dnaja3	0.909	-1.994	0.0852128	0.280273
15529	10515710	ENSMUST00000075406	230676	cDNA sequence BC059842	BC059842	0.908	-1.101	0.306429	0.582919
15530	10468651	XM_894554	629643	predicted gene, EG629643	EG629643	0.908	-1.365	0.213354	0.479304
15531	10493335	BC059914	76022	RIKEN cDNA 5830417I10 gene	5830417I10Rik	0.908	-0.261	0.801069	0.919467
15532	10543682					0.908	-1.11	0.302558	0.578687
15533	10499138	NM_027539	70762	doublecortin-like kinase 2	Dclk2	0.908	-1.622	0.14752	0.389587
15534	10547767					0.908	-0.25	0.809713	0.923191
15535	10479685	NM_011012	18389	opioid receptor-like 1	Oprl1	0.908	-1.767	0.119275	0.34536
15536	10567941	NM_146200	56347	eukaryotic translation initiat	Eif3c	0.908	-2.592	0.0349438	0.158824
15537	10368144	NM_009397	21929	tumor necrosis factor, alpha-i	Tnfaip3	0.908	-2.232	0.0597165	0.225162
15538	10412760	NM_008369	16188	interleukin 3 receptor, alpha	Il3ra	0.908	-1.071	0.318781	0.596066
15539	10576439	NM_029746	76332	component of oligomeric golgi	Cog2	0.908	-2.247	0.0583638	0.22191
15540	10369735	ENSMUST00000054837	641387	RIKEN cDNA 1700120B22 gene	1700120B22Rik	0.908	-1.234	0.255973	0.530431
15541	10524388	NM_001033428	333048	gene model 854, (NCBI)	Gm854	0.908	-0.659	0.530329	0.765382
15542	10444236	NM_010388	15000	histocompatibility 2, class II	H2-DMb2	0.908	-1.277	0.241095	0.513985
15543	10534216	NM_001080746	14886	general transcription factor I	Gtf2i	0.908	-2.399	0.0465435	0.191723
15544	10387936	NM_172561	216873	sperm associated antigen 7	Spag7	0.908	-1.793	0.114813	0.336981
15545	10460517	NM_134155	107392	breast cancer metastasis-suppr	Brms1	0.908	-1.931	0.0935341	0.296593
15546	10478281	ENSMUST00000088383	100126880	predicted gene,	OTTMUSG00000016070	0.908	-0.984	0.356914	0.629197

15546	10478281	ENSMUST00000088585	100126880	OTTMUSG0000001	OTTMUSG00000016070	0.908	-0.984	0.356914	0.629197
15547	10471525	NM_178595	329384	peptidyl-tRNA hydrolase 1 homo	Ptrh1	0.908	-1.005	0.347593	0.621575
15548	10454543					0.908	-1.188	0.272472	0.547065
15549	10347980	NM_022417	64294	integral membrane protein 2C	Itm2c	0.908	-1.685	0.134622	0.369832
15550	10594517	NM_028974	74492	RIKEN cDNA 5430433E21 gene	5430433E21Rik	0.908	-0.998	0.350723	0.624059
15551	10545842	NM_001001160	330369	F-box protein 41	Fbxo41	0.908	-0.706	0.502615	0.745467
15552	10507990	ENSMUST00000106185	230735	Eph receptor A10	Epha10	0.908	-1.237	0.254752	0.528967
15553	10441813	AF357405	21454	t-complex protein 1	Tcp1	0.908	-1.496	0.177175	0.431538
15554	10568622					0.908	-1.492	0.178	0.432602
15555	10590169	NM_007397	11481	activin receptor IIB	Acvr2b	0.908	-1.479	0.181561	0.437783
15556	10533594	NM_029112	74890	MORN repeat containing 3	Morn3	0.908	-1.695	0.132598	0.36625
15557	10504615	ENSMUST00000043958	381522	RIKEN cDNA E230008N13 gene	E230008N13Rik	0.908	-0.878	0.408231	0.672667
15558	10548697					0.908	-1.308	0.230883	0.501612
15559	10398121	NM_007539	12061	bradykinin receptor, beta 1	Bdkrb1	0.908	-0.554	0.596325	0.809852
15560	10467653	NM_199447	107094	ribosomal RNA processing 12 ho	Rrp12	0.908	-1.967	0.0886669	0.286953
15561	10505612	XR_033396	667922	similar to Ribosomal protein S	LOC667922	0.908	-2.004	0.0839012	0.277666
15562	10596409	AM748257	665033	predicted gene, EG665033	EG665033	0.908	-1.304	0.232463	0.503399
15563	10430113	BC060637	223666	DNA segment, Chr 15, Wayne Sta	D15Wsu169e	0.908	-1.836	0.107813	0.323807
15564	10496182	NM_001004367	319478	CXXC finger 4	Cxxc4	0.908	-1.399	0.203213	0.466024
15565	10458762	XR_033442	100047177	similar to SMT3B protein	LOC100047177	0.908	-0.244	0.813805	0.925112
15566	10455826	NM_001001979	70417	multiple EGF-like-domains 10	Megf10	0.908	-1.614	0.149328	0.391688
15567	10422518	NM_028651	70551	transmembrane and tetratricope	Tmtc4	0.908	-2.195	0.0631027	0.232827
15568	10383999	NM_026080	64660	mitochondrial ribosomal protei	Mrps24	0.908	-1.386	0.207009	0.471406
15569	10364280	NM_145925	108705	pituitary tumor-transforming 1	Pttg1ip	0.908	-2.423	0.0449116	0.187485
15570	10373756	NM_172791	237625	phospholipase A2, group III	Pla2g3	0.908	-1.242	0.253067	0.527333
15571	10507874	NM_183163	230726	rhomboid, veinlet-like 2 (Dros	Rhbdl2	0.908	-1.12	0.29871	0.574899
15572	10599849					0.908	-0.418	0.688287	0.86292
15573	10425461	NM_009634	11564	adenylosuccinate lyase	Adsl	0.908	-2.349	0.0501213	0.201363
15574	10536481	XR_031404	100045223	similar to high-mobility group	LOC100045223	0.908	-0.949	0.373396	0.643632
15575	10450920	AY036118	170798	cDNA sequence AY036118	AY036118	0.908	-2.09	0.0738101	0.256746
15576	10547926	NM_012003	26894	COP9 (constitutive photomorpho	Cops7a	0.908	-1.803	0.113211	0.333342
15577	10425477	NM_134091	105835	small G protein signaling modu	Sgsm3	0.908	-0.949	0.373473	0.643632
15578	10587051	NM_001033500	546144	WD repeat domain 72	Wdr72	0.908	-1.487	0.179321	0.434671
15579	10461220	NM_001081196	68693	heterogeneous nuclear ribonucl	Hnrpul2	0.908	-1.694	0.132908	0.366563
15580	10544017	NM_177200	320590	SV2 related protein homolog (r	Svopl	0.908	-0.377	0.716699	0.875846
15581	10537934	NM_145576	232784	Zinc finger protein 212	Zfp212	0.907	-1.59	0.154669	0.399843
15582	10352709	NM_198654	381318	NSL1, MIND kinetochore complex	Nsl1	0.907	-1.719	0.128032	0.358796
15583	10495359	NM_145543	229725	chloride channel CLIC-like 1	Clcc1	0.907	-1.27	0.243521	0.516501
15584	10425333	ENSMUST00000100423	80287	apolipoprotein B editing compl	Apobec3	0.907	-0.591	0.572282	0.796254
15585	10492442					0.907	-1.33	0.22413	0.494224
15586	10578281	NM_030610	80857	fibroblast growth factor 20	Fgf20	0.907	-1.291	0.236634	0.508732
15587	10362829	NM_172416	14628	osteopetrosis associated trans	Ostm1	0.907	-1.707	0.130259	0.362012
15588	10441565	NM_011299	20112	ribosomal protein S6 kinase, p	Rps6ka2	0.907	-1.882	0.100557	0.310299
15589	10439498					0.907	-0.919	0.38803	0.656728
15590	10500845	AK048683	100125931	RIKEN cDNA A130049A11 gene	A130049A11Rik	0.907	-0.574	0.583364	0.80142
15591	10382421	NM_181749	217302	G protein-coupled receptor 142	Gpr142	0.907	-0.425	0.68327	0.859827
15592	10596259					0.907	-1.875	0.101644	0.312332
15593	10523853	NM_027599	70902	acyltransferase like 1B	Aytl1b	0.907	-1.319	0.227459	0.498227
15594	10485280	XM_885087	620695	hypothetical protein LOC620695	LOC620695	0.907	-1.517	0.171838	0.42401
15595	10367106	NM_016774	11947	ATP synthase, H+ transporting	Atp5b	0.907	-2.489	0.0406885	0.175862
15596	10466920					0.907	-1.049	0.327926	0.604189
15597	10541729	NM_013538	14793	cell division cycle associated	Cdca3	0.907	-1.517	0.171792	0.423994
15598	10537375	NM_177185	320538	RIKEN cDNA D130059P03 gene	D130059P03Rik	0.907	-2.708	0.0294288	0.141691

15599	10538936					0.907	-0.884	0.405024	0.669624
15600	10531752	NM_001081107	191578	helicase, mus308-like (Drosoph	Hel308	0.907	-2.279	0.0556416	0.215355
15601	10452213	NM_133801	98053	general transcription factor I	Gtf2f1	0.907	-1.578	0.157429	0.404021
15602	10368058	ENSMUST00000095817	100039660	hypothetical protein LOC100039	LOC100039660	0.907	-1.412	0.199476	0.461105
15603	10504064	NM_025539	66401	nudix (nucleoside diphosphate	Nudt2	0.907	-2.7	0.0297808	0.142883
15604	10399629	NM_011739	22630	tyrosine 3-monooxygenase/trypt	Ywhaq	0.907	-2.806	0.025489	0.12918
15605	10441053					0.907	-1.761	0.120287	0.3466
15606	10599956	XM_001474469	100040304	similar to syndecan-1	LOC100040304	0.907	-0.894	0.400007	0.665979
15607	10499285	NM_007529	12032	brevican	Bcan	0.907	-1.45	0.189219	0.447572
15608	10578153	XR_035697	619780	similar to Fatty acid binding	LOC619780	0.907	-0.58	0.579436	0.798942
15609	10552412	NM_028849	74276	claudin domain containing 2	Cldnd2	0.907	-1.019	0.341175	0.616038
15610	10362402					0.907	-0.906	0.39412	0.661897
15611	10599747	NM_001110790	236798	G protein-coupled receptor 112	Gpr112	0.907	-1.745	0.123297	0.351408
15612	10566516	BC022923	101867	RIKEN cDNA 1500003O22 gene	1500003O22Rik	0.907	-2.253	0.0578483	0.220625
15613	10441107	NM_019537	56088	proteasome (prosome, macropain	Psmg1	0.907	-1.766	0.119546	0.345831
15614	10466521	NM_173442	14537	glucosaminyl (N-acetyl) transf	Gcnt1	0.907	-1.977	0.0873827	0.284469
15615	10346337	ENSMUST00000042734	73467	RIKEN cDNA 1700066M21 gene	1700066M21Rik	0.907	-1.11	0.302831	0.578887
15616	10445941	XR_034600	100043485	hypothetical protein LOC100043	LOC100043485	0.907	-1.532	0.168018	0.41938
15617	10599812	NM_009575	22773	zinc finger protein of the cer	Zic3	0.907	-1.398	0.203745	0.466884
15618	10520544	NM_133350	100732	microtubule-associated protein	Mapre3	0.907	-1.877	0.101353	0.311893
15619	10466925	NM_021299	56248	adenylate kinase 3	Ak3	0.907	-1.691	0.133347	0.367457
15620	10576460	NM_023709	73647	calpain 9 (nCL-4)	Capn9	0.907	-0.959	0.368397	0.639207
15621	10586227	ENSMUST00000098640	319526	RIKEN cDNA F730015K02 gene	F730015K02Rik	0.907	-0.998	0.350485	0.624003
15622	10533526					0.907	-1.711	0.129634	0.361037
15623	10375167	BC072605	574403	predicted gene, EG574403	EG574403	0.907	-0.999	0.350295	0.623822
15624	10539002	NM_009543	22644	ring finger protein 103	Rnf103	0.907	-1.651	0.141548	0.381018
15625	10411332	NM_008255	15357	3-hydroxy-3-methylglutaryl-Coe	Hmgcr	0.907	-2.874	0.023105	0.120804
15626	10574147					0.907	-1.038	0.332729	0.608795
15627	10492452					0.907	-0.122	0.906242	0.963405
15628	10449242	NM_026506	68011	small nuclear ribonucleoprotei	Snrpg	0.907	-1.372	0.211288	0.476813
15629	10384152	NM_011221	19291	purine rich element binding pr	Purb	0.907	-2.729	0.0285323	0.138591
15630	10502438	ENSMUST00000116118	229879	predicted gene, EG229879	EG229879	0.907	-1.003	0.348234	0.622132
15631	10549813	NM_028316	72667	zinc finger protein 444	Zfp444	0.907	-1.451	0.188806	0.446844
15632	10395074	NM_001093775	17933	myelin transcription factor 1-	Myt1l	0.907	-1.439	0.192092	0.451438
15633	10391221	NM_001038010	14534	GCN5 general control of amino	Gcn5l2	0.906	-2.599	0.03456	0.157724
15634	10429686	BC047213	223648	RIKEN cDNA 2410075B13 gene	2410075B13Rik	0.906	-0.918	0.388437	0.657074
15635	10477022	NM_145535	228765	syndecan binding protein (synt	Sdcbp2	0.906	-1.43	0.194535	0.454622
15636	10437677	NM_013638	19120	protamine 3	Prm3	0.906	-1.719	0.127996	0.358742
15637	10385375	NM_001080969	66628	tRNA-histidine guanylyltransfe	Thg1l	0.906	-2.127	0.0697908	0.247552
15638	10396421	NM_010431	15251	hypoxia inducible factor 1, al	Hif1a	0.906	-1.753	0.121747	0.348385
15639	10591416					0.906	-1.223	0.259867	0.53415
15640	10405372	NM_012017	26919	zinc finger protein 346	Zfp346	0.906	-1.45	0.18919	0.447572
15641	10378443	NM_001011851	258153	olfactory receptor 412	Olfr412	0.906	-0.527	0.614263	0.821474
15642	10585398	NM_177350	235379	gliomedin	Gldn	0.906	-0.649	0.536255	0.769395
15643	10439936	NM_030612	80859	nuclear factor of kappa light	Nfkbiz	0.906	-0.985	0.356403	0.628882
15644	10586484	NM_026635	68250	RIKEN cDNA 5730536A07 gene	5730536A07Rik	0.906	-2.317	0.0525462	0.207399
15645	10575209					0.906	-1.154	0.285119	0.560432
15646	10452876					0.906	-0.96	0.367979	0.638955
15647	10511014					0.906	-0.73	0.488524	0.736128
15648	10526217	NM_020022	19718	replication factor C (activato	Rfc2	0.906	-2.097	0.0730535	0.254849
15649	10575955	BC025816	234796	cDNA sequence BC025816	BC025816	0.906	-1.758	0.120881	0.347273
15650	10603147	NM_146238	237221	gem (nuclear organelle) associ	Gemin8	0.906	-0.862	0.416629	0.679566
15651	10504670					0.906	-0.941	0.37696	0.647069

15652	10389395	NM_178309	237911	BRCA1 interacting protein C-te	Brip1	0.906	-1.311	0.230077	0.501055
15653	10585428	NM_021422	58233	DnaJ (Hsp40) homolog, subfamil	Dnaja4	0.906	-1.445	0.190494	0.449454
15654	10574230					0.906	-1.573	0.158563	0.40535
15655	10412392	ENSMUST00000099152	100038690	predicted gene, ENSMUSG0000007	ENSMUSG00000074638	0.906	-1.714	0.128997	0.360251
15656	10425000	NM_145471	223664	leucine rich repeat containing	Lrrc14	0.906	-1.405	0.201715	0.464266
15657	10499394	NM_001002011	16905	lamin A	Lmna	0.906	-1.449	0.189283	0.447652
15658	10415111	NM_007537	12050	Bcl2-like 2	Bcl2l2	0.906	-1.545	0.165018	0.415127
15659	10474028	NM_145122	18633	peroxisome biogenesis factor 1	Pex16	0.906	-1.055	0.32542	0.601773
15660	10457836	ENSMUST00000097651	100044699	hypothetical protein LOC100044	LOC100044699	0.906	-1.373	0.21103	0.476598
15661	10564272	NM_007390	11441	cholinergic receptor, nicotini	Chrna7	0.906	-0.899	0.397582	0.664302
15662	10546137	NM_030251	80283	ankyrin repeat and BTB (POZ) d	Abtb1	0.906	-1.404	0.202024	0.464803
15663	10498797	XR_035682	383883	similar to Rpl17 protein	LOC383883	0.906	-0.553	0.596659	0.81005
15664	10435015	NM_026898	68980	WD repeat domain 53	Wdr53	0.906	-2.191	0.0634861	0.233737
15665	10590277					0.906	-0.677	0.519416	0.757547
15666	10492381	NM_001033300	229363	guanine monphosphate synthetas	Gmps	0.906	-2.209	0.0618024	0.229738
15667	10453178	NM_001081357	225028	mitogen-activated protein kina	Map4k3	0.906	-1.715	0.128872	0.360128
15668	10471701	ENSMUST00000100156	100038606	predicted gene, ENSMUSG0000007	ENSMUSG00000075388	0.906	-1.195	0.26991	0.54456
15669	10452470	NM_013933	30960	vesicle-associated membrane pr	Vapa	0.906	-2.133	0.0691719	0.246514
15670	10450772	NM_201608	110696	histocompatibility 2, M region	H2-M10.3	0.906	-0.778	0.46118	0.715789
15671	10463227	BC089359	628994	predicted gene, EG628994	EG628994	0.906	-1.57	0.159048	0.406199
15672	10397094	NM_008943	19164	presenilin 1	Psen1	0.906	-2.325	0.0519636	0.206172
15673	10456995	NM_178604	27366	thioredoxin-like 4A	Txnl4a	0.906	-2.397	0.0466671	0.19197
15674	10442270	BC098460	74149	RIKEN cDNA 1300003B13 gene	1300003B13Rik	0.906	-1.007	0.34635	0.620403
15675	10565817					0.906	-0.587	0.575358	0.797076
15676	10452978	NR_003363	625054	predicted gene, EG625054	EG625054	0.906	-1.346	0.21919	0.487694
15677	10514366	ENSMUST00000064404	30926	glutaredoxin 3	Glrx3	0.906	-1.619	0.148145	0.390374
15678	10570379	NM_011881	24013	G protein-coupled receptor kin	Grk1	0.906	-0.851	0.421974	0.684306
15679	10367120					0.906	-0.783	0.458668	0.713672
15680	10491329	ENSMUST00000057768	67576	RIKEN cDNA 4930429B21 gene	4930429B21Rik	0.906	-0.745	0.479721	0.729728
15681	10421486	AK155102	100038369	predicted gene, ENSMUSG0000007	ENSMUSG00000075526	0.906	-1.605	0.151304	0.395197
15682	10510050					0.906	-1.513	0.172844	0.425203
15683	10537821	NM_146296	258293	olfactory receptor 437	Olfr437	0.906	-1.012	0.344356	0.618664
15684	10345492	NM_001039551	94218	cyclin M3	Cnnm3	0.906	-1.787	0.115899	0.338549
15685	10351404	NM_001039483	68944	transmembrane and coiled-coil	Tmco1	0.906	-1.762	0.120144	0.346566
15686	10454445	AK138158	654823	RIKEN cDNA B930094E09 gene	B930094E09Rik	0.906	-1.29	0.236842	0.508973
15687	10351163	NM_028776	240880	SCY1-like 3 (S. cerevisiae)	Scyl3	0.906	-2.215	0.0612327	0.228343
15688	10507328	NM_011034	18477	peroxiredoxin 1	Prdx1	0.906	-2.164	0.0660445	0.239774
15689	10427704	ENSMUST00000080845	78244	DnaJ (Hsp40) homolog, subfamil	Dnajc21	0.906	-2.342	0.0506249	0.202691
15690	10465895	NM_019699	56473	fatty acid desaturase 2	Fads2	0.906	-3.082	0.0171204	0.0987437
15691	10416421					0.906	-1.272	0.242919	0.51587
15692	10539861	NM_133933	103963	ribophorin I	Rpn1	0.906	-1.816	0.110938	0.329706
15693	10378508	NM_177325	104662	TSR1, 20S rRNA accumulation, h	Tsr1	0.906	-1.369	0.212051	0.477488
15694	10503989	ENSMUST00000030114	66434	RIKEN cDNA 2010003O02 gene	2010003O02Rik	0.906	-1.054	0.325935	0.602357
15695	10511062	ENSMUST00000023920	69671	transmembrane protein 52	Tmem52	0.906	-1.144	0.289014	0.565029
15696	10522368	NM_001081205	70701	NIPA-like domain containing 1	Npal1	0.905	-1.305	0.231957	0.502664
15697	10594490	NM_144813	214111	solute carrier family 24 (sodi	Slc24a1	0.905	-1.743	0.123654	0.351843
15698	10592289	NM_001081429	245902	coiled-coil domain containing	Ccdc15	0.905	-2.482	0.0411129	0.176721
15699	10470751	NM_011989	26569	solute carrier family 27 (fatt	Slc27a4	0.905	-1.731	0.125883	0.355221
15700	10523293	ENSMUST00000031330	75610	RIKEN cDNA 2010109A12 gene	2010109A12Rik	0.905	-0.886	0.404128	0.668818

15701	10553309	NM_013580	16833	lactate dehydrogenase C	Ldhc	0.905	-1.888	0.0996754	0.308576
15702	10465812	NM_027412	70387	tetratricopeptide repeat domai	Ttc9c	0.905	-0.959	0.368586	0.639326
15703	10373964	NM_172438	107829	THO complex 5	Thoc5	0.905	-1.867	0.10287	0.314909
15704	10384192	NM_134011	21379	transforming growth factor bet	Tbrg4	0.905	-1.833	0.108167	0.32441
15705	10377763	NM_007493	11890	asialoglycoprotein receptor 2	Asgr2	0.905	-1.065	0.321329	0.598079
15706	10486754	NM_178795	327655	histidine acid phosphatase dom	Hisppd2a	0.905	-2.638	0.0326551	0.151867
15707	10448232	XR_035724	545191	predicted gene, EG545191	EG545191	0.905	-1.641	0.143519	0.384139
15708	10357008	NM_013784	27392	phosphatidylinositol glycan an	Pign	0.905	-1.462	0.185989	0.44418
15709	10387219	NM_021329	57785	RAN guanine nucleotide release	Rangrf	0.905	-0.937	0.37926	0.649054
15710	10469906	NM_001039386	56876	nasal embryonic LHRH factor	Nelf	0.905	-1.774	0.118089	0.343079
15711	10418177	ENSMUST00000064134	100036528	predicted gene, ENSMUSG0000005	ENSMUSG00000052323	0.905	-0.849	0.423215	0.685496
15712	10378649	NM_173388	215113	solute carrier family 43, memb	Slc43a2	0.905	-1.091	0.31024	0.586894
15713	10507231	NM_001039124	654462	kinocilin	Kncn	0.905	-1.522	0.170674	0.422321
15714	10358754	XR_034437	639787	predicted gene, EG639787	EG639787	0.905	-1.031	0.336042	0.611732
15715	10603023					0.905	-0.905	0.394718	0.662293
15716	10522250	NM_028975	67878	transmembrane protein 33	Tmem33	0.905	-2.362	0.0491851	0.199006
15717	10418903	ENSMUST00000096019	432839	G protein regulated inducer of	Gprin2	0.905	-1.161	0.28252	0.55755
15718	10604405	NM_012019	26926	apoptosis-inducing factor, mit	Aifm1	0.905	-2.482	0.0410951	0.176721
15719	10583551	NM_183408	18577	phosphodiesterase 4A, cAMP spe	Pde4a	0.905	-1.248	0.250888	0.524763
15720	10559498					0.905	-1.201	0.267687	0.542452
15721	10447275	NM_028576	73582	RIKEN cDNA 1700106N22 gene	1700106N22Rik	0.905	-1.346	0.219022	0.487441
15722	10496373	NM_030143	73284	DNA-damage-inducible transcrip	Ddit4l	0.905	-1.687	0.134148	0.369279
15723	10525014					0.905	-0.949	0.373111	0.643427
15724	10398717	NM_177374	328162	RIKEN cDNA 6720458F09 gene	6720458F09Rik	0.905	-1.208	0.265046	0.540178
15725	10552458	NM_145582	233189	ATP binding domain 3	Atpbd3	0.905	-1.901	0.0978068	0.304839
15726	10515282	NM_133681	66805	tetraspanin 1	Tspan1	0.905	-0.933	0.380889	0.650316
15727	10434516	BC092532	78408	RIKEN cDNA 2900046G09 gene	2900046G09Rik	0.905	-1.79	0.115292	0.337519
15728	10414736	ENSMUST00000103580	640552	similar to T-cell receptor alp	LOC640552	0.905	-0.528	0.613286	0.820877
15729	10516776	ENSMUST00000097865	100038640	predicted gene, ENSMUSG0000007	ENSMUSG00000073752	0.905	-1.196	0.269616	0.544449
15730	10537428	NM_011226	19331	RAB19, member RAS oncogene fam	Rab19	0.905	-1.624	0.147077	0.388984
15731	10566315	BC058791	244180	RIKEN cDNA E030002O03 gene	E030002O03Rik	0.905	-0.973	0.362076	0.633596
15732	10450762	NM_177923	333715	histocompatibility 2, M region	H2-M10.2	0.905	-0.606	0.563215	0.789853
15733	10558825	NM_153777	70552	leucine rich repeat containing	Lrrc56	0.905	-1.789	0.115524	0.337938
15734	10552037	NM_172205	282619	suprabasin	Sbsn	0.905	-0.787	0.456587	0.712611
15735	10596383	NM_001102607	245026	RIKEN cDNA E330026B02 gene	E330026B02Rik	0.905	-1.191	0.271461	0.546126
15736	10415857	NM_177628	219148	cDNA sequence BC065085	BC065085	0.905	-1.516	0.172081	0.424165
15737	10526356	NM_146002	215160	rhomboid domain containing 2	Rhbdd2	0.905	-2.381	0.0477854	0.194851
15738	10493003	XM_621583	546801	ets variant gene 3-like	Etv3l	0.905	-0.666	0.526403	0.7624
15739	10508723					0.905	-0.917	0.388737	0.657241
15740	10538882	ENSMUST00000103316	434025	predicted gene, EG434025	EG434025	0.905	-0.568	0.587422	0.804278
15741	10569385	NM_008554	17173	achaete-scute complex homolog	Ascl2	0.905	-1.076	0.316608	0.593787
15742	10347214					0.905	-1.425	0.196012	0.456422
15743	10541799	BC117528	381810	lysophosphatidic acid receptor	Lpar5	0.905	-0.724	0.491814	0.738245
15744	10398795	BC126962	104816	RIKEN cDNA A530050D06 gene	A530050D06Rik	0.905	-2.011	0.0830344	0.276137
15745	10476362	NM_025676	66634	minichromosome maintenance def	Mcm8	0.905	-2.183	0.0642238	0.235594
15746	10405094	NM_172015	105148	isoleucine-tRNA synthetase	Iars	0.905	-1.553	0.163143	0.412125
15747	10600688	NM_025729	66724	mitogen-activated protein kina	Map3k7ip3	0.905	-1.338	0.22145	0.490864
15748	10569962	NM_009138	20300	chemokine (C-C motif) ligand 2	Ccl25	0.905	-0.913	0.390805	0.659209
15749	10592455	NM_146828	258825	olfactory receptor 975	Olfr975	0.905	-0.78	0.460493	0.715038

15750	10419867	NM_183174	239099	homeodomain leucine zipper-enc	Homez	0.905	-1.813	0.111461	0.330397
15751	10462214					0.905	-1.42	0.197342	0.457905
15752	10593508	BC080729	77591	DEAD (Asp-Glu-Ala-Asp) box pol	Ddx10	0.905	-1.792	0.114942	0.337218
15753	10596880	NM_007567	12217	bassoon	Bsn	0.904	-1.396	0.20411	0.467365
15754	10528970	ENSMUST00000116150	384325	predicted gene, EG384325	EG384325	0.904	-0.569	0.586727	0.803741
15755	10498160	NM_026435	67890	ubiquitin-fold modifier 1	Ufm1	0.904	-1.845	0.106363	0.321644
15756	10458251	NM_030749	81500	endoplasmic reticulum chaperon	Sil1	0.904	-1.861	0.103798	0.316741
15757	10594251	NM_024245	71819	kinesin family member 23	Kif23	0.904	-2.043	0.0791321	0.267921
15758	10495340	NM_025444	99730	TAF13 RNA polymerase II, TATA	Taf13	0.904	-2.837	0.0243748	0.125168
15759	10434467	NM_134101	21762	proteasome (prosome, macropain	Psmd2	0.904	-1.815	0.111175	0.329929
15760	10375799	NM_009329	21408	zinc finger protein 354A	Zfp354a	0.904	-1.982	0.0867024	0.283082
15761	10556302	NM_009667	11717	AMP deaminase 3	Ampd3	0.904	-1.643	0.143217	0.383898
15762	10360934	NM_026041	67223	ribosomal RNA processing 15 ho	Rrp15	0.904	-1.499	0.176264	0.430064
15763	10460626	NM_026616	68209	ribonuclease H2, subunit C	Rnaseh2c	0.904	-1.679	0.135832	0.371639
15764	10380250	NR_003492	72381	RIKEN cDNA 2210409E12 gene	2210409E12Rik	0.904	-0.897	0.398424	0.664689
15765	10362424					0.904	-0.303	0.770239	0.905037
15766	10398618	NM_011632	22031	Tnf receptor-associated factor	Traf3	0.904	-2.381	0.047819	0.194851
15767	10349512	NM_026390	67812	UBX domain containing 2	Ubxd2	0.904	-2.472	0.0417306	0.178221
15768	10499378	NM_013658	20351	sema domain, immunoglobulin do	Sema4a	0.904	-1.672	0.137219	0.373982
15769	10539692	NM_031199	21802	transforming growth factor alp	Tgfa	0.904	-1.19	0.271895	0.546343
15770	10564375					0.904	-0.708	0.501112	0.744172
15771	10405291	NM_178397	76577	UBX domain containing 8	Ubxd8	0.904	-1.845	0.106332	0.321598
15772	10417841	ENSMUST00000022349	76670	tetratricopeptide repeat domai	Ttc18	0.904	-1.066	0.320827	0.597681
15773	10365578	NM_028334	69736	nucleoporin 37	Nup37	0.904	-2.561	0.036571	0.163532
15774	10448079	XM_891173	626573	predicted gene, EG626573	EG626573	0.904	-1.456	0.187435	0.445746
15775	10541845	NM_138747	110109	nucleolar protein 1	Nol1	0.904	-1.343	0.220106	0.488992
15776	10567380	NM_009470	22242	uromodulin	Umod	0.904	-0.842	0.426877	0.688211
15777	10487969	NM_175113	66926	tRNA methyltransferase 6 homol	Trmt6	0.904	-1.32	0.227162	0.497938
15778	10355871	NM_178884	98733	obscurin-like 1	Obsl1	0.904	-1.883	0.100444	0.31011
15779	10402262	XM_001474563	100040305	hypothetical protein LOC100040	LOC100040305	0.904	-1.927	0.0941733	0.297861
15780	10565461	AK038819	791393	predicted gene, ENSMUSG0000005	ENSMUSG00000052436	0.904	-1.737	0.124741	0.353522
15781	10414374	NM_008477	16709	kinectin 1	Ktn1	0.904	-2.673	0.0310167	0.146945
15782	10607204	XR_001912	666730	predicted gene, EG666730	EG666730	0.904	-0.898	0.3981	0.664555
15783	10544148	NM_001033430	338523	jumonji C domain-containing hi	Jhdm1d	0.904	-1.066	0.320609	0.597527
15784	10380226	NM_198013	103841	CUE domain containing 1	Cuedc1	0.904	-2.109	0.0717407	0.251634
15785	10423471	NM_008729	18163	catenin (cadherin associated p	Ctnnd2	0.904	-1.294	0.235543	0.50735
15786	10457380					0.904	-1.162	0.282084	0.557189
15787	10541318	NM_144512	14412	solute carrier family 6 (neuro	Slc6a13	0.904	-1.037	0.33313	0.609187
15788	10501190					0.904	-1.284	0.238984	0.511774
15789	10383853	NM_029458	75828	HORMA domain containing 2	Hormad2	0.904	-1.509	0.173754	0.426449
15790	10517053	NM_001081156	69539	RIKEN cDNA 2300002D11 gene	2300002D11Rik	0.904	-1.396	0.20427	0.467434
15791	10573194	NM_025843	66916	NADH dehydrogenase (ubiquinone	Ndufb7	0.904	-2.375	0.0482034	0.196078
15792	10512480	NM_019436	54390	suppression inducing transmemb	Sit1	0.904	-0.977	0.360377	0.632213
15793	10414473	NM_146666	258660	olfactory receptor 736	Olfr736	0.904	-0.345	0.739805	0.889275
15794	10566043	BC025128	69358	leucine rich repeat containing	Lrrc51	0.904	-1.838	0.107485	0.323096
15795	10515688	ENSMUST00000075406	230676	cDNA sequence BC059842	BC059842	0.904	-0.671	0.523244	0.759907
15796	10579602	NM_028189	72297	UDP-GlcNAc:betaGal beta-1,3-N-	B3gnt3	0.904	-1.25	0.250426	0.524406
15797	10443201	NM_011861	23969	protein kinase C and casein ki	Pacsin1	0.904	-1.659	0.139793	0.378113
15798	10415319	NM_008394	16391	interferon regulatory factor 9	Irf9	0.904	-1.527	0.169282	0.42056
15799	10449339					0.904	-1.04	0.33178	0.608173
15800	10545226					0.903	-0.692	0.510855	0.751986
15801	10594277	NM_028748	74090	progestin and adipoQ receptor	Paqr5	0.903	-1.282	0.239652	0.512719

15802	10381419	NM_008676	17966	neighbor of Brca1 gene 1	Nbr1	0.903	-2.147	0.067737	0.243242
15803	10349404	NM_145128	107895	mannoside acetylglucosaminyltr	Mgat5	0.903	-2.348	0.0502153	0.201596
15804	10414211	NM_010775	17194	mannose binding lectin (A)	Mbl1	0.903	-1.277	0.241154	0.514009
15805	10347697	NM_009208	20536	solute carrier family 4 (anion	Slc4a3	0.903	-1.613	0.149485	0.391928
15806	10464015	NM_019658	56392	soc-2 (suppressor of clear) ho	Shoc2	0.903	-1.813	0.111483	0.330405
15807	10602765	NM_001081667	245683	kelch-like 34 (Drosophila)	Klhl34	0.903	-1.514	0.172442	0.424658
15808	10397666	NM_029334	75553	zinc finger CCCH type containi	Zc3h14	0.903	-2.597	0.0346498	0.157998
15809	10346523	NM_025824	66882	basic leucine zipper and W2 do	Bzw1	0.903	-2.414	0.0455218	0.18878
15810	10388154	NM_026068	67279	mediator of RNA polymerase II	Med31	0.903	-1.566	0.160002	0.407336
15811	10552681	NM_025368	66124	Josephin domain containing 2	Josd2	0.903	-1.816	0.110962	0.329706
15812	10508770	AK142202	100038703	predicted gene, OTTMUSG0000001	OTTMUSG00000010099	0.903	-2.036	0.080005	0.269699
15813	10540028	NM_023184	66277	Kruppel-like factor 15	Klf15	0.903	-1.098	0.307523	0.584192
15814	10455238	NM_022996	65113	Nedd4 family interacting prote	Ndfip1	0.903	-2.393	0.0469356	0.192513
15815	10489983	ENSMUST00000099065	100038688	predicted gene, ENSMUSG0000007	ENSMUSG00000074574	0.903	-0.8	0.449177	0.706652
15816	10352973					0.903	-1.925	0.0944108	0.2983
15817	10355327	NM_007525	12021	BRCA1 associated RING domain 1	Bard1	0.903	-1.844	0.106459	0.321797
15818	10583785	BC150493	66962	RIKEN cDNA 2310047B19 gene	2310047B19Rik	0.903	-1.255	0.2486	0.522089
15819	10518484	NM_173401	230903	F-box protein 44	Fbxo44	0.903	-2.265	0.0568571	0.218146
15820	10423842	NM_198606	223499	WD repeats and SOF domain cont	Wdsof1	0.903	-2.027	0.08109	0.271716
15821	10433702	NM_033564	93734	Mpv17 transgene, kidney diseas	Mpv17l	0.903	-1.269	0.24371	0.516777
15822	10535372	NM_001033312	231863	F-box and leucine-rich repeat	Fbxl18	0.903	-1.841	0.106991	0.322599
15823	10574033	NM_172410	71805	nucleoporin 93	Nup93	0.903	-2.031	0.0805479	0.27085
15824	10414805	ENSMUST00000103607	639655	T cell receptor alpha variable	Trav13d-4	0.903	-0.466	0.654857	0.845369
15825	10562897	NM_178734	243963	zinc finger protein 473	Zfp473	0.903	-1.211	0.263917	0.538844
15826	10514645					0.903	-2.01	0.0832219	0.27639
15827	10528548	NM_013569	16511	potassium voltage-gated channe	Kcnh2	0.903	-2.071	0.0759458	0.260936
15828	10399212	AK132117	217951	transmembrane protein 196	Tmem196	0.903	-0.99	0.354084	0.62682
15829	10467191	NM_013468	107765	ankyrin repeat domain 1 (cardi	Ankrd1	0.903	-1.539	0.166472	0.417266
15830	10584841	NM_001005421	270152	adhesion molecule, interacts w	Amica1	0.903	-1.182	0.274779	0.549506
15831	10346328	BC132343	212679	methionine-tRNA synthetase 2 (	Mars2	0.903	-1.839	0.107232	0.322736
15832	10532620	XM_912851	74376	myosin XVIIIb	Myo18b	0.903	-1.325	0.22571	0.496094
15833	10536794	NM_023516	69573	RIKEN cDNA 2310016C08 gene	2310016C08Rik	0.903	-2.604	0.0342954	0.156855
15834	10564704	NM_178255	67666	hyaluronan and proteoglycan li	Hapln3	0.903	-1.822	0.110041	0.328028
15835	10557528	NM_172747	233877	potassium channel tetramerisat	Kctd13	0.903	-0.995	0.351769	0.624867
15836	10384423	NM_172496	12808	cordon-bleu	Cobl	0.903	-0.785	0.45772	0.713313
15837	10457853	BC060961	225280	RIKEN cDNA D030070L09 gene	D030070L09Rik	0.903	-1.491	0.178363	0.433134
15838	10369890	XR_032286	216081	similar to phosphoribosylamino	LOC216081	0.903	-0.913	0.39085	0.659231
15839	10489406	NM_183023	241770	regulating synaptic membrane e	Rims4	0.903	-1.762	0.120112	0.346527
15840	10531348	NM_011148	19023	protein phosphatase, EF hand c	Ppef2	0.903	-0.756	0.473453	0.725045
15841	10549536	NM_001113424	232566	antagonist of mitotic exit net	Amn1	0.903	-2.503	0.0398799	0.173611
15842	10526482	NM_011293	20022	polymerase (RNA) II (DNA direc	Polr2j	0.903	-1.659	0.139807	0.378113
15843	10408475	NM_010093	13557	E2F transcription factor 3	E2f3	0.903	-1.743	0.123591	0.351711
15844	10407281	NM_023612	71690	endothelial cell-specific mole	Esm1	0.903	-1.306	0.231754	0.502487
15845	10536297	NM_181595	243725	protein phosphatase 1, regulat	Ppp1r9a	0.903	-1.982	0.0867277	0.283113
15846	10423271	XM_001487793	320865	cadherin 18	Cdh18	0.903	-1.688	0.133989	0.368936
15847	10597266					0.903	-0.615	0.55772	0.785788
15848	10445710	NM_144939	107971	fibroblast growth factor recep	Frs3	0.903	-1.766	0.119485	0.345748
15849	10505457	AK017104	66783	RIKEN cDNA 4933437N03 gene	4933437N03Rik	0.903	-0.828	0.433972	0.694408
15850	10385159	NM_025936	104458	arginyl-tRNA synthetase	Rars	0.903	-2.391	0.0470678	0.192831

15851	10387909	NM_009603	11448	cholinergic receptor, nicotini	Chrne	0.903	-0.701	0.50512	0.747176
15852	10367434	AK086046	100038704	predicted gene, ENSMUSG0000006	ENSMUSG00000065996	0.903	-1.969	0.088469	0.28668
15853	10382985	NM_027827	71562	arylformamidase	Afmid	0.903	-1.673	0.137021	0.373617
15854	10366698	BC065058	270802	cDNA sequence BC048403	BC048403	0.903	-2.348	0.0502274	0.201596
15855	10532857	NM_019821	56356	glycolipid transfer protein	Gltp	0.903	-3.093	0.016853	0.0977778
15856	10524384	ENSMUST00000100882	625464	predicted gene, EG625464	EG625464	0.903	-0.697	0.507554	0.749509
15857	10491406	NM_025316	66046	NADH dehydrogenase (ubiquinone	Ndufb5	0.903	-2.657	0.031744	0.149088
15858	10419038	NM_078478	66092	growth hormone inducible trans	Ghitm	0.903	-2.083	0.0745705	0.258248
15859	10346235	NM_146108	227095	3-hydroxyisobutyryl-Coenzyme A	Hibch	0.903	-1.639	0.143993	0.384952
15860	10375529	NM_001024846	22720	zinc finger protein 62	Zfp62	0.903	-1.902	0.0976985	0.304546
15861	10523778	ENSMUST00000055994	320751	RIKEN cDNA D830014E11 gene	D830014E11Rik	0.903	-2.133	0.0691801	0.246514
15862	10549700	NM_146177	232811	suppressor of variegation 4-20	Suv420h2	0.903	-1.773	0.118223	0.343225
15863	10500347	BC107364	329716	cDNA sequence BC107364	BC107364	0.902	-0.784	0.458016	0.713341
15864	10589329	NM_173019	270198	6-phosphofructo-2-kinase/fruct	Pfkfb4	0.902	-0.866	0.414327	0.677534
15865	10571207	NM_025869	66959	dual specificity phosphatase 2	Dusp26	0.902	-1.452	0.188537	0.446595
15866	10462861	XR_034565	240657	similar to peptidase (prosome,	LOC240657	0.902	-2.006	0.0837227	0.277205
15867	10460693	ENSMUST00000052291	69595	predicted gene, ENSMUSG0000004	ENSMUSG00000043488	0.902	-1.103	0.305277	0.581669
15868	10465571	NM_020566	57431	DnaJ (Hsp40) homolog, subfamil	Dnajc4	0.902	-2.045	0.0788964	0.267427
15869	10429885	NM_025340	106025	SHANK-associated RH domain int	Sharpin	0.902	-1.948	0.0911734	0.292175
15870	10534575	NM_025774	66801	Prkr interacting protein 1 (IL	Prkrip1	0.902	-1.502	0.175668	0.429204
15871	10385153	NM_027411	70385	coiled-coil domain containing	Ccdc99	0.902	-1.548	0.164191	0.413859
15872	10466008	NM_145496	225913	dihydroxyacetone kinase 2 homo	Dak	0.902	-1.239	0.254203	0.528502
15873	10490080	NM_009996	13081	cytochrome P450, family 24, su	Cyp24a1	0.902	-0.94	0.377497	0.647352
15874	10382049	NM_028074	72047	DEAD (Asp-Glu-Ala-Asp) box pol	Ddx42	0.902	-2.028	0.0809331	0.27167
15875	10420385	NM_026526	68043	N-6 adenine-specific DNA methy	N6amt2	0.902	-3.075	0.0172843	0.0993635
15876	10403951	NM_178202	319188	histone cluster 1, H2bp	Hist1h2bp	0.902	-0.977	0.359997	0.632103
15877	10441794	NM_030726	80978	MAS-related GPR, member H	Mrgprh	0.902	-0.989	0.354589	0.62719
15878	10508917	ENSMUST00000040805	230806	absent in melanoma 1-like	Aim1l	0.902	-1.25	0.250239	0.524321
15879	10518532	NM_145556	230908	TAR DNA binding protein	Tardbp	0.902	-1.814	0.111383	0.330259
15880	10373616	NM_146863	258862	olfactory receptor 770	Olfr770	0.902	-0.729	0.488954	0.736349
15881	10450808	NM_001033235	195359	tripartite motif-containing 40	Trim40	0.902	-1.329	0.224364	0.494324
15882	10414522	NM_009687	11792	apurinic/apyrimidinic endonucl	Apex1	0.902	-2.034	0.0802173	0.270211
15883	10551511	NM_022024	63986	glia maturation factor, gamma	Gmfg	0.902	-1.036	0.333715	0.609432
15884	10351966	NM_146761	258756	olfactory receptor 414	Olfr414	0.902	-1.405	0.201722	0.464266
15885	10520501	BC060996	75434	RIKEN cDNA 1700001C02 gene	1700001C02Rik	0.902	-1.199	0.268287	0.542786
15886	10409016	NM_175340	105193	NHL repeat containing 1	Nhlrc1	0.902	-1.167	0.280192	0.555564
15887	10542518					0.902	-0.924	0.38531	0.654508
15888	10481900	NM_145522	227746	Rab9 effector protein with kel	Rabepk	0.902	-2.099	0.0728306	0.254366
15889	10542192	BC120661	330428	RIKEN cDNA D630042F21 gene	D630042F21Rik	0.902	-1.447	0.189908	0.448565
15890	10410291	NM_001003666	431706	zinc finger protein 457	Zfp457	0.902	-0.659	0.530219	0.765382
15891	10438098	NM_022324	64136	stromal cell-derived factor 2-	Sdf2l1	0.902	-1.463	0.185555	0.44347
15892	10468527	ENSMUST00000025996	381232	RIKEN cDNA 5830416P10 gene	5830416P10Rik	0.902	-0.874	0.410168	0.674542
15893	10503315	NM_001039556	623474	RIKEN cDNA E130016E03 gene	E130016E03Rik	0.902	-1.95	0.0909305	0.291551
15894	10443383	NM_026571	328789	tetraspan transmembrane protei	Tmhs	0.902	-1.572	0.158658	0.405496
15895	10403193	NM_009239	20688	trans-acting transcription fac	Sp4	0.902	-2.156	0.0668521	0.241483
15896	10377603	ENSMUST00000100977	74341	RIKEN cDNA G630025P09 gene	G630025P09Rik	0.902	-1.188	0.272355	0.54694
15897	10432746	NM_133357	109052	keratin 75	Krt75	0.902	-2.042	0.0792903	0.268093

15898	10442736	BC094389	214489	cDNA sequence BC003965	BC003965	0.902	-1.284	0.238815	0.511601
15899	10406519	NM_013500	12950	hyaluronan and proteoglycan li	Hapln1	0.902	-0.555	0.595466	0.809472
15900	10389127	AK040863	100038761	predicted gene, ENSMUSG0000005	ENSMUSG00000054421	0.902	-0.938	0.378757	0.648404
15901	10498547	NM_145820	72789	ventricular zone expressed PH	Veph1	0.902	-1.659	0.139755	0.378113
15902	10449295	NM_026307	67675	cutA divalent cation tolerance	Cuta	0.902	-2.141	0.0684179	0.244528
15903	10344835					0.902	-0.877	0.408573	0.672914
15904	10572408	NM_001111066	14232	FK506 binding protein 8	Fkbp8	0.902	-1.506	0.174601	0.427682
15905	10420261	NM_007800	13035	cathepsin G	Ctsg	0.902	-0.722	0.492885	0.73872
15906	10452496	NM_009067	19765	ralA binding protein 1	Ralbp1	0.902	-2.25	0.0581247	0.22132
15907	10347748	NM_028817	74205	acyl-CoA synthetase long-chain	Acsl3	0.902	-2.422	0.0449734	0.187645
15908	10516246	NM_026560	52276	cell division cycle associated	Cdca8	0.902	-1.49	0.178653	0.43364
15909	10395163	NM_008482	16777	laminin B1 subunit 1	Lamb1-1	0.902	-1.527	0.169415	0.420782
15910	10390090	NM_009161	20391	sarcoglycan, alpha (dystrophin	Sgca	0.902	-1.452	0.188565	0.446595
15911	10524568	BC057022	433940	cDNA sequence BC057022	BC057022	0.902	-2.243	0.058718	0.222896
15912	10350823	NM_009595	11352	v-abl Abelson murine leukemia	Abl2	0.902	-1.524	0.170185	0.421869
15913	10505000	NM_025623	66536	nipsnap homolog 3A (C. elegans	Nipsnap3a	0.902	-1.308	0.230902	0.501612
15914	10379496	NM_029367	75622	sperm acrosome associated 3	Spaca3	0.902	-1.16	0.282886	0.55817
15915	10562211	NM_052992	56188	FXYD domain-containing ion tra	Fxyd1	0.902	-1.637	0.144389	0.385687
15916	10502329	NM_025902	67006	CDGSH iron sulfur domain 2	Cisd2	0.901	-2.123	0.0702455	0.248316
15917	10568997	NM_022433	64384	sirtuin 3 (silent mating type	Sirt3	0.901	-1.383	0.208002	0.472478
15918	10504630					0.901	-0.753	0.475209	0.726714
15919	10559818					0.901	-1.304	0.232416	0.50335
15920	10379981	NM_175004	217057	peptidyl-tRNA hydrolase 2	Ptrh2	0.901	-2.707	0.0294754	0.141836
15921	10470444					0.901	-0.464	0.65648	0.846173
15922	10588357	NM_175324	102632	acyl-Coenzyme A dehydrogenase	Acad11	0.901	-1.058	0.324377	0.600843
15923	10495549	NM_010022	13171	dihydrolipoamide branched chai	Dbt	0.901	-2.708	0.0294385	0.141691
15924	10394040	NM_027874	104318	casein kinase 1, delta	Csnk1d	0.901	-2.128	0.0697717	0.247552
15925	10560063	NM_026885	68953	chromatin modifying protein 2A	Chmp2a	0.901	-1.852	0.10523	0.319497
15926	10533633	NM_023232	66593	diablo homolog (Drosophila)	Diablo	0.901	-1.653	0.141098	0.380048
15927	10429621	NM_194350	378435	v-maf musculoaponeurotic fibro	Mafa	0.901	-1.813	0.11141	0.330293
15928	10375864	NM_028398	72947	alanine-glyoxylate aminotransf	Agxt2l2	0.901	-1.966	0.0887924	0.287288
15929	10567213	XR_033846	100047986	similar to eukaryotic translat	LOC100047986	0.901	-1.968	0.0885877	0.286933
15930	10364955	NM_022653	50492	thimet oligopeptidase 1	Thop1	0.901	-2.927	0.0213766	0.114508
15931	10373944	NM_026015	67178	zinc finger, matrin type 5	Zmat5	0.901	-1.596	0.153184	0.397268
15932	10348580	NM_027551	70788	kelch-like 30 (Drosophila)	Klhl30	0.901	-1.168	0.279898	0.555279
15933	10405911	NM_172392	268670	zinc finger protein 759	Zfp759	0.901	-1.163	0.282017	0.557182
15934	10461160					0.901	-0.727	0.490086	0.737262
15935	10414372	ENSMUST00000100667	625730	predicted gene, EG625730	EG625730	0.901	-1.618	0.148529	0.390852
15936	10475772	NM_139308	99138	START domain containing 7	Stard7	0.901	-1.778	0.117309	0.341384
15937	10504466	AK038173	623796	predicted gene, OTTMUSG0000000	OTTMUSG00000007209	0.901	-1.372	0.211342	0.476813
15938	10407982	NM_175688	319293	RIKEN cDNA A530099J19 gene	A530099J19Rik	0.901	-0.467	0.654197	0.845136
15939	10508099	NM_172701	230751	RIKEN cDNA 1810007P19 gene	1810007P19Rik	0.901	-1.779	0.117131	0.3411
15940	10476582	NM_028387	72899	MACRO domain containing 2	Macrod2	0.901	-1.024	0.339011	0.614614
15941	10566398	NM_147096	259100	olfactory receptor 666	Olfr666	0.901	-1.07	0.319148	0.59633
15942	10565620	AK037770	434213	predicted gene, ENSMUSG0000005	ENSMUSG00000056003	0.901	-1.035	0.334303	0.609879
15943	10387971	NM_213729	103844	expressed sequence AI842396	AI842396	0.901	-1.755	0.121447	0.347955
15944	10380672	NM_001033186	78473	src family associated phosphop	Skap1	0.901	-1.575	0.157952	0.405065
15945	10406139					0.901	-1.526	0.169662	0.420989
15946	10469514	NM_007552	12151	Bmi1 polycomb ring finger onco	Bmi1	0.901	-2.05	0.0782935	0.26619
15947	10543082	NM_001037865	213945	collagen, type XXVIII, alpha 1	Col28a1	0.901	-1.382	0.208368	0.473022
15948	10417734	NM_011584	353187	nuclear receptor subfamily 1,	Nr1d2	0.901	-1.574	0.158272	0.405195
15949	10351583	NM_011070	18637	prefoldin 2	Pfdn2	0.901	-2.123	0.0702472	0.248316
15950	10565360					0.901	-1.231	0.256798	0.531129
15951	10463535	NM_053086	70769	nucleolar and coiled-body phos	Nolc1	0.901	-1.903	0.0975031	0.304251

15951	10463535	NM_053086	70769	nucleolar and coiled-body phos	Nolc1	0.901	-1.905	0.0975051	0.304251
15952	10538781	AF037047	667141	predicted gene, EG667141	EG667141	0.901	-1.13	0.294671	0.570978
15953	10461487	NM_201351	225912	cytochrome b, ascorbate depend	Cybasc3	0.901	-2.122	0.0703549	0.24851
15954	10347724	ENSMUST00000097692	20536	solute carrier family 4 (anion	Slc4a3	0.901	-0.586	0.575578	0.797076
15955	10427814					0.901	-1.862	0.103696	0.316611
15956	10410209	NM_019743	56353	RING1 and YY1 binding protein	Rybp	0.901	-2.899	0.0222896	0.117676
15957	10550605	BC055476	72205	echinoderm microtubule associa	Eml2	0.901	-1.808	0.112368	0.332063
15958	10457020					0.901	-0.731	0.488114	0.735812
15959	10434007	NM_175178	72168	apoptosis-inducing factor, mit	Aifm3	0.901	-1.737	0.124723	0.353522
15960	10378059	NM_026559	52700	thioredoxin domain containing	Txndc17	0.901	-2.664	0.0314115	0.148244
15961	10475686	NM_175550	108011	adaptor-related protein comple	Ap4e1	0.901	-1.357	0.215667	0.482802
15962	10559500	AK011493	57776	tweety homolog 1 (Drosophila)	Ttyh1	0.901	-1.209	0.264835	0.540056
15963	10497173	NM_008994	19302	peroxisome biogenesis factor 2	Pex2	0.901	-2.347	0.0502799	0.201609
15964	10477129	NM_207276	403172	defensin beta 21	Defb21	0.901	-1.709	0.129867	0.361535
15965	10529584	NM_008550	17160	mannosidase 2, alpha B2	Man2b2	0.901	-1.654	0.140815	0.379623
15966	10595140					0.9	-1.665	0.13867	0.376676
15967	10449034	BC096050	214917	cDNA sequence BC008155	BC008155	0.9	-1.817	0.110859	0.329583
15968	10568512	NM_027037	69318	RIKEN cDNA 1700007K09 gene	1700007K09Rik	0.9	-0.816	0.440855	0.699832
15969	10376596	BC044901	66771	RIKEN cDNA 4933439F18 gene	4933439F18Rik	0.9	-1.657	0.140306	0.378815
15970	10440731	NM_001113406	16693	keratin associated protein 11-	Krtap11-1	0.9	-1.231	0.257111	0.531457
15971	10353674	NM_025520	66373	LSM5 homolog, U6 small nuclear	Lsm5	0.9	-1.96	0.0895568	0.288877
15972	10492755	NM_001111048	14161	fibrinogen, alpha polypeptide	Fga	0.9	-1.738	0.124562	0.35351
15973	10530215	BC009097	68552	RIKEN cDNA 1110003E01 gene	1110003E01Rik	0.9	-2.353	0.0498258	0.200593
15974	10581473	NM_001007567	66432	solute carrier family 7, membe	Slc7a6os	0.9	-2.403	0.046209	0.190903
15975	10535938	NM_133898	100637	NEDD4 binding protein 2-like 1	N4bp2l1	0.9	-1.063	0.322237	0.598978
15976	10443117	ENSMUST00000025033	75393	RIKEN cDNA 0610031G08 gene	0610031G08Rik	0.9	-1.571	0.158997	0.406117
15977	10360185					0.9	-1.218	0.261726	0.536181
15978	10541288	ENSMUST00000064287	791394	predicted gene, ENSMUSG0000005	ENSMUSG00000052437	0.9	-1.146	0.288393	0.564348
15979	10464858	NM_001033128	52028	Bardet-Biedl syndrome 1 homolo	Bbs1	0.9	-2.125	0.0700342	0.247958
15980	10388392	NM_144491	116905	DPH1 homolog (S. cerevisiae)	Dph1	0.9	-1.982	0.0867488	0.283113
15981	10517199	NM_177866	329954	channel, sperm associated 4	Catsper4	0.9	-1.385	0.207495	0.471907
15982	10573342					0.9	-1.012	0.344105	0.618424
15983	10567171	BC085269	68052	ribosomal protein S13	Rps13	0.9	-0.572	0.58463	0.802272
15984	10404113	NM_009198	20504	solute carrier family 17 (sodi	Slc17a1	0.9	-0.994	0.352449	0.625445
15985	10351507	ENSMUST00000097468	100038407	predicted gene, ENSMUSG0000007	ENSMUSG00000073493	0.9	-0.892	0.400947	0.666612
15986	10527559	NM_009087	20018	RNA polymerase 1-3	Rpo1-3	0.9	-2.949	0.0207228	0.112646
15987	10567211	XR_034261	668485	similar to ribosomal protein L	LOC668485	0.9	-1.881	0.100843	0.310827
15988	10543544	NM_138682	192198	leucine rich repeat containing	Lrrc4	0.9	-1.745	0.123204	0.351285
15989	10507983	NM_177671	230735	Eph receptor A10	Epha10	0.9	-0.72	0.49447	0.7396
15990	10359303	ENSMUST00000028061	75255	RIKEN cDNA 4930562F07 gene	4930562F07Rik	0.9	-0.699	0.506455	0.748338
15991	10526559	NM_009599	11423	acetylcholinesterase	Ache	0.9	-1.54	0.166233	0.41711
15992	10465980	NM_025333	66072	RIKEN cDNA 0610038F07 gene	0610038F07Rik	0.9	-1.548	0.164405	0.414225
15993	10364601	NM_013850	27403	ATP-binding cassette, sub-fami	Abca7	0.9	-1.156	0.284399	0.559618
15994	10355113					0.9	-0.707	0.501902	0.744769
15995	10553261	NM_008421	16502	potassium voltage gated channe	Kcnc1	0.9	-0.956	0.369935	0.640508
15996	10372208	NM_198636	380660	acyl-CoA synthetase short-chai	Acss3	0.9	-1.05	0.327802	0.604012
15997	10515979					0.9	-0.396	0.703586	0.869978
15998	10478544	NM_001012704	408190	WAP four-disulfide core domain	Wfdc13	0.9	-0.766	0.467867	0.720457
15999	10397264	BC103771	432677	RIKEN cDNA 7420416P09 gene	7420416P09Rik	0.9	-1.143	0.289451	0.565477
16000	10372745	NM_001014390	69181	dual-specificity tyrosine-(Y)-	Dyrk2	0.9	-2.531	0.0382534	0.168964
16001	10467802	NM_019424	192236	Hermansky-Pudlak syndrome 1 ho	Hps1	0.9	-2.113	0.0713217	0.250884
16002	10386230	AB030190	108660	ring finger protein 187	Rnf187	0.9	-2.869	0.0232691	0.121189
16003	10409276					0.9	-0.099	0.923649	0.969694

16004	10378078	NM_001099688	628100	F-box protein 39	Fbxo39	0.9	-0.822	0.437417	0.696704
16005	10558872	NM_027797	71448	transmembrane protein 80	Tmem80	0.9	-1.969	0.0884562	0.28668
16006	10364518	NM_001077363	19205	polypyrimidine tract binding p	Ptbp1	0.9	-2.617	0.0336752	0.154849
16007	10439080					0.9	-1.127	0.295899	0.572322
16008	10428736	NM_024207	67819	Der1-like domain family, membe	Derl1	0.9	-1.883	0.100465	0.31011
16009	10431946	ENSMUST00000058494	76076	RIKEN cDNA 5830453K13 gene	5830453K13Rik	0.9	-0.796	0.451666	0.708669
16010	10429657	NM_029663	66656	eukaryotic translation elongat	Eef1d	0.9	-2.503	0.0398697	0.173611
16011	10363786	NM_146005	11735	ankyrin 3, epithelial	Ank3	0.9	-1.137	0.292071	0.568181
16012	10416588	BC019143	219189	RIKEN cDNA 1300010F03 gene	1300010F03Rik	0.9	-1.779	0.117136	0.3411
16013	10441797	NM_013686	21454	t-complex protein 1	Tcp1	0.9	-2.393	0.0469041	0.192492
16014	10420114	NM_019984	21816	transglutaminase 1, K polypept	Tgm1	0.9	-0.974	0.361366	0.633168
16015	10563149	BC050196	384619	cDNA sequence BC050196	BC050196	0.9	-1.085	0.312703	0.589181
16016	10388227	NM_001024926	192986	cytochrome b5 domain containin	Cyb5d2	0.9	-1.42	0.197317	0.457905
16017	10354472	NM_001081081	14660	glutaminase	Gls	0.9	-1.507	0.174182	0.427153
16018	10599853	NM_001018087	434784	leucine zipper, down-regulated	Ldoc1	0.9	-0.629	0.548622	0.779103
16019	10470329	NM_198628	279029	gene model 711, (NCBI)	Gm711	0.9	-1.332	0.223541	0.493531
16020	10352781	BC103778	74023	RIKEN cDNA 3322402L07 gene	3322402L07Rik	0.9	-1.482	0.180595	0.436401
16021	10493377					0.9	-0.768	0.466625	0.719708
16022	10366401					0.899	-0.987	0.35546	0.628098
16023	10380189	NM_001039684	380718	Meckel syndrome, type 1	Mks1	0.899	-1.823	0.109756	0.327457
16024	10527043	NM_173405	231842	archaelysin family metallopept	Amz1	0.899	-1.315	0.228776	0.49987
16025	10433963	NM_026940	69101	YdjC homolog (bacterial)	Ydjc	0.899	-1.849	0.10564	0.320213
16026	10481585	BC021748	72931	RIKEN cDNA 2900010J23 gene	2900010J23Rik	0.899	-1.499	0.176184	0.429929
16027	10466266	NM_146936	258938	olfactory receptor 1417	Olfr1417	0.899	-1.131	0.294317	0.570607
16028	10471842					0.899	-1.063	0.321939	0.598721
16029	10563094	BC003786	14132	Fc receptor, IgG, alpha chain	Fcgrt	0.899	-2.009	0.0832422	0.276393
16030	10442968	NM_001081069	50782	regulator of G-protein signali	Rgs11	0.899	-1.314	0.229194	0.500215
16031	10520288	NM_144908	231050	UDP-N-acetyl-alpha-D-galactosa	Galnt11	0.899	-1.843	0.106563	0.321974
16032	10494655	NM_172863	242109	zinc finger protein 697	Zfp697	0.899	-1.023	0.339192	0.614614
16033	10416640	NM_145960	211253	mitochondrial translational re	Mtrf1	0.899	-1.849	0.105634	0.320213
16034	10484735	XM_621555	546770	olfactory receptor 1175	Olfr1175	0.899	-0.808	0.445084	0.703541
16035	10411107	ENSMUST00000062122	76469	cardiomyopathy associated 5	Cmya5	0.899	-1.718	0.128198	0.359071
16036	10346695	NM_173444	269198	neurobeachin like 1	Nbeal1	0.899	-1.281	0.239921	0.512931
16037	10400581	NM_013902	30795	FK506 binding protein 3	Fkbp3	0.899	-2.377	0.0480966	0.195794
16038	10569923	NM_028175	72267	leucine rich repeat containing	Lrrc8e	0.899	-0.922	0.386169	0.655109
16039	10537805	NM_146988	258990	olfactory receptor 447	Olfr447	0.899	-1.533	0.167793	0.419086
16040	10583773	NM_144935	235044	cDNA sequence BC018242	BC018242	0.899	-1.393	0.205114	0.468705
16041	10367843	NM_011682	22288	utrophin	Utrn	0.899	-2.339	0.0508572	0.203346
16042	10418096	BC021314	71228	discs, large homolog 5 (Drosop	Dlg5	0.899	-2.286	0.0550516	0.21409
16043	10591735	NM_170777	66126	elongation factor 1 homolog (E	Elof1	0.899	-1.308	0.231123	0.501886
16044	10585284	XR_034458	668070	similar to ribosomal protein L	LOC668070	0.899	-1.543	0.165392	0.415485
16045	10464594	BC034269	225884	cDNA sequence BC021614	BC021614	0.899	-0.748	0.477894	0.728494
16046	10604234	XM_976867	636756	predicted gene, EG636756	EG636756	0.899	-1.125	0.29666	0.573257
16047	10486061	NM_011246	19419	RAS guanyl releasing protein 1	Rasgrp1	0.899	-1.193	0.270492	0.545253
16048	10419715	NM_146271	258268	olfactory receptor 1511	Olfr1511	0.899	-0.796	0.45127	0.708496
16049	10412663	XR_033177	667030	similar to hCG28692	LOC667030	0.899	-1.37	0.211748	0.477389
16050	10561842	NM_009795	12336	calpain, small subunit 1	Capns1	0.899	-1.846	0.106211	0.321554
16051	10362811	NM_001013370	140742	sestrin 1	Sesn1	0.899	-1.393	0.205194	0.468786
16052	10458607	NM_134137	107045	leucyl-tRNA synthetase	Lars	0.899	-1.907	0.0970017	0.303313
16053	10473190	NM_024181	66861	DnaJ (Hsp40) homolog, subfamil	Dnajc10	0.899	-1.616	0.148951	0.391187
16054	10387170	NM_008744	18208	netrin 1	Ntn1	0.899	-1.59	0.154545	0.399718
16055	10510624	NM_001033352	242785	kelch-like 21 (Drosophila)	Klhl21	0.899	-1.793	0.114745	0.336905
16056	10376425	ENSMUST00000093768	237769	predicted gene, OTTMUSG0000000	OTTMUSG00000005767	0.899	-1.238	0.254391	0.528633
16057	10457382	NM_153086	225152	gap junction protein, delta 4	Gjd4	0.899	-0.903	0.395686	0.663394
16058	10585940	ENSMUST00000086982	71121	RIKEN cDNA 4933407I18 gene	4933407I18Rik	0.899	-0.721	0.493755	0.739216

16059	10429666	NM_025412	66194	pyrroline-5-carboxylate reduct	Pycrl	0.899	-2.122	0.0703701	0.248523
16060	10448257	ENSMUST00000088673	381070	predicted gene, EG381070	EG381070	0.899	-1.09	0.310707	0.587208
16061	10395317	NM_033522	114712	Fer3-like (Drosophila)	Ferd3l	0.899	-0.998	0.35071	0.624059
16062	10390907	NM_001085526	435273	novel protein similar to kerat	RP23-272C1.7	0.899	-0.732	0.487278	0.734951
16063	10450533	NM_175137	68915	valyl-tRNA synthetase 2, mitoc	Vars2	0.899	-1.995	0.0850204	0.280082
16064	10529454	ENSMUST00000069741	442795	RIKEN cDNA E130018O15 gene	E130018O15Rik	0.899	-1.106	0.304408	0.580956
16065	10435457	NM_030253	80285	poly (ADP-ribose) polymerase f	Parp9	0.899	-1.723	0.127313	0.357621
16066	10499483	NM_134469	110196	farnesyl diphosphate synthetas	Fdps	0.899	-2.048	0.0786303	0.266888
16067	10399591	AK086127	382686	RIKEN cDNA 3110053B16 gene	3110053B16Rik	0.898	-0.883	0.405881	0.670443
16068	10571248					0.898	-1.455	0.187749	0.446159
16069	10461878	BC094224	353211	RIKEN cDNA A230083H22 gene	A230083H22Rik	0.898	-1.329	0.224368	0.494324
16070	10436428	NM_025910	67014	myc induced nuclear antigen	Mina	0.898	-1.476	0.182139	0.438626
16071	10471247	NM_145144	108897	RIKEN cDNA 2810003C17 gene	2810003C17Rik	0.898	-3.066	0.0175229	0.100079
16072	10415132	NM_026066	67272	CKLF-like MARVEL transmembrane	Cmtm5	0.898	-0.583	0.577522	0.797771
16073	10489246	NM_010658	16658	v-maf musculoaponeurotic fibro	Mafb	0.898	-1.365	0.213357	0.479304
16074	10378427	NM_146706	258701	olfactory receptor 401	Olfr401	0.898	-0.986	0.355959	0.628456
16075	10399820	NM_001110239	11431	acid phosphatase 1, soluble	Acp1	0.898	-1.162	0.282185	0.557189
16076	10362158	NM_001010827	209517	trace amine-associated recepto	Taar7b	0.898	-0.343	0.741086	0.889595
16077	10598034					0.898	-2.292	0.0545927	0.21288
16078	10493662	ENSMUST00000029548	77595	nucleoporin 210-like	Nup210l	0.898	-0.88	0.407437	0.671862
16079	10568311	NM_146259	244219	zinc finger protein 668	Zfp668	0.898	-2.446	0.0433886	0.183115
16080	10452138					0.898	-1.439	0.192088	0.451438
16081	10548573	NM_172891	243659	serine/threonine/tyrosine kina	Styk1	0.898	-1.428	0.195221	0.455452
16082	10552398	NM_177693	233187	lens intrinsic membrane protei	Lim2	0.898	-1.487	0.179363	0.434671
16083	10398635	NM_033603	93835	amnionless	Amn	0.898	-1.881	0.100841	0.310827
16084	10362904	NM_130892	170728	reticulon 4 interacting protei	Rtn4ip1	0.898	-2.433	0.0442461	0.185686
16085	10359201	NM_023884	78255	Ral GEF with PH domain and SH3	Ralgps2	0.898	-1.997	0.0848461	0.279698
16086	10468949	NM_146114	227525	DNA cross-link repair 1C, PSO2	Dclre1c	0.898	-2.206	0.0620967	0.230346
16087	10375331	NM_008352	16160	interleukin 12b	Il12b	0.898	-1.252	0.249692	0.52381
16088	10492846	NM_144896	229487	PET112-like (yeast)	Pet112l	0.898	-1.58	0.15682	0.403187
16089	10512470	NM_001110320	12517	CD72 antigen	Cd72	0.898	-1.524	0.170167	0.421869
16090	10548547	AK136154	625558	predicted gene, EG625558	EG625558	0.898	-0.69	0.511631	0.752446
16091	10367626	NM_024261	73419	RIKEN cDNA 1700052N19 gene	1700052N19Rik	0.898	-1.719	0.127954	0.358673
16092	10463836	NM_010362	14873	glutathione S-transferase omeg	Gsto1	0.898	-2.362	0.0491526	0.19896
16093	10578448	NM_133969	102294	cytochrome P450, family 4, sub	Cyp4v3	0.898	-1.906	0.0970499	0.303419
16094	10547820	NM_013588	16977	leucine rich repeat containing	Lrrc23	0.898	-1.405	0.201561	0.464097
16095	10442603	NM_001012402	328779	heparan sulfate (glucosamine)	Hs3st6	0.898	-1.405	0.201701	0.464266
16096	10429424					0.898	-0.612	0.559183	0.786667
16097	10521467	NM_025725	66717	coiled-coil domain containing	Ccdc96	0.898	-0.679	0.518311	0.756954
16098	10440713	NM_130856	68484	keratin associated protein 16-	Krtap16-8	0.898	-0.923	0.385807	0.654758
16099	10410709	NM_178916	218341	Rieske (Fe-S) domain containin	Rfesd	0.898	-1.095	0.308567	0.585197
16100	10592248	XR_033620	627681	similar to nucleolar protein 5	LOC627681	0.898	-0.627	0.549934	0.780181
16101	10542872	NR_003634	66184	ribosomal protein S4, Y-linked	Rps4y2	0.898	-1.969	0.0884431	0.28668
16102	10484762	NM_001005227	257887	olfactory receptor 1200	Olfr1200	0.898	-0.695	0.509103	0.750516
16103	10576054	NM_008024	14241	forkhead box L1	Foxl1	0.898	-1.933	0.0932208	0.295866
16104	10491229					0.898	-1.832	0.108407	0.325036
16105	10568369	NM_009943	12862	cytochrome c oxidase, subunit	Cox6a2	0.898	-1.517	0.171779	0.423994
16106	10581336	NM_027469	70575	glucose-fructose oxidoreductas	Gfod2	0.898	-1.051	0.327246	0.603462
16107	10397784	ENSMUST00000055270	319760	RIKEN cDNA D130020L05 gene	D130020L05Rik	0.898	-1.755	0.121466	0.347955
16108	10421873					0.898	-1.044	0.330214	0.606542

16109	10461268	BC047099	66276	RIKEN cDNA 1810009A15 gene	1810009A15Rik	0.898	-2.991	0.0195131	0.107978
16110	10562847	NM_009473	22260	nuclear receptor subfamily 1,	Nr1h2	0.898	-1.356	0.216025	0.48309
16111	10455446	NM_030061	78242	serine peptidase inhibitor, Ka	Spink12	0.898	-1.945	0.0916321	0.293245
16112	10432180	NM_009833	12455	cyclin T1	Ccnt1	0.898	-0.874	0.410491	0.674864
16113	10413993	XM_985917	268729	gene model 626, (NCBI)	Gm626	0.898	-0.936	0.379685	0.649466
16114	10501489					0.898	-2.146	0.067842	0.243316
16115	10372130	NM_175128	68281	RIKEN cDNA 4930430F08 gene	4930430F08Rik	0.898	-1.653	0.141	0.379882
16116	10395257					0.898	-1.478	0.181614	0.437813
16117	10596318	NM_029385	75686	nudix (nucleoside diphosphate	Nudt16	0.898	-2.081	0.0747678	0.258738
16118	10558220	NM_001039534	214580	phosphoseryl-tRNA kinase	Pstk	0.898	-1.762	0.120181	0.346569
16119	10444137	NM_011306	20182	retinoid X receptor beta	Rxrb	0.898	-2.271	0.0562887	0.216807
16120	10376230	NM_013716	27041	Ras-GTPase-activating protein	G3bp1	0.898	-1.853	0.105085	0.319364
16121	10412655	ENSMUST00000067738	78393	RIKEN cDNA 2610318M16 gene	2610318M16Rik	0.898	-1.218	0.261621	0.536103
16122	10495773	NM_153806	99480	deoxynucleotidyltransferase, t	Dnttip2	0.898	-1.81	0.111883	0.331046
16123	10471904	NM_028809	74192	actin related protein 2/3 comp	Arpc5l	0.898	-2.236	0.0593115	0.224264
16124	10406546					0.898	-2.688	0.0303381	0.144768
16125	10376096	NM_001033598	216739	acyl-CoA synthetase long-chain	Acsl6	0.898	-1.453	0.188191	0.446289
16126	10351968	ENSMUST00000085861	546747	olfactory receptor 220	Olfr220	0.898	-1.485	0.179796	0.43509
16127	10428933	NR_003523	67552	H2A histone family, member Y3	H2afy3	0.898	-1.831	0.108457	0.325142
16128	10557353	NM_001081022	233865	RIKEN cDNA D430042O09 gene	D430042O09Rik	0.897	-1.573	0.158413	0.405262
16129	10605929	NM_177746	245532	diacylglycerol O-acyltransfera	Dgat2l4	0.897	-1.837	0.107638	0.323419
16130	10369948	NM_172549	104248	calcineurin binding protein 1	Cabin1	0.897	-1.974	0.0878072	0.28541
16131	10526493	NM_021611	59310	myosin light chain 2, precurso	Mylc2pl	0.897	-1.708	0.130064	0.36185
16132	10511149	NM_025570	66448	mitochondrial ribosomal protei	Mrpl20	0.897	-1.758	0.120831	0.347267
16133	10507529	NM_020000	80509	mediator of RNA polymerase II	Med8	0.897	-2.302	0.0537428	0.210433
16134	10570604					0.897	-1.703	0.131082	0.363535
16135	10578251					0.897	-1.435	0.193136	0.452493
16136	10348682	NM_011796	23830	calpain 10	Capn10	0.897	-1.43	0.194702	0.454775
16137	10348670	NM_181405	108657	arginyl aminopeptidase (aminop	Rnpepl1	0.897	-1.996	0.0849756	0.279994
16138	10352092	NM_001012330	30928	zinc finger protein 238	Zfp238	0.897	-1.81	0.112022	0.331272
16139	10524221	NM_001033459	381667	gene model 1679, (NCBI)	Gm1679	0.897	-1.311	0.229915	0.500912
16140	10500140	NM_001085383	71790	annexin A9	Anxa9	0.897	-1.287	0.237709	0.510106
16141	10542401	NM_178776	320135	cDNA sequence BC049715	BC049715	0.897	-0.983	0.357656	0.630084
16142	10381798	NM_010858	17896	myosin, light polypeptide 4	Myl4	0.897	-0.925	0.384933	0.654157
16143	10473608	NM_001011517	329460	olfactory receptor 1193	Olfr1193	0.897	-0.247	0.811937	0.924032
16144	10528788	ENSMUST00000072180	100038373	predicted gene, ENSMUSG0000005	ENSMUSG00000059244	0.897	-1.469	0.184058	0.441439
16145	10549748	NM_025324	66056	zinc finger protein 524	Zfp524	0.897	-1.305	0.232123	0.502819
16146	10517655	NM_011110	18784	phospholipase A2, group V	Pla2g5	0.897	-1.329	0.224244	0.494263
16147	10566666	ENSMUST00000084758	626674	olfactory receptor 471	Olfr471	0.897	-0.789	0.455504	0.711786
16148	10605568	AB032764	60600	testis specific gene A8	Tsga8	0.897	-1.163	0.281883	0.557053
16149	10560294	BC125404	101434	CEA-related cell adhesion mole	Ceacam15	0.897	-1.131	0.294305	0.570607
16150	10505270	NM_025286	20530	solute carrier family 31, memb	Slc31a2	0.897	-1.952	0.0906749	0.291063
16151	10525916	ENSMUST00000031446	208151	transmembrane protein 132B	Tmem132b	0.897	-1.281	0.239721	0.512764
16152	10447264	NM_009205	20532	solute carrier family 3, membe	Slc3a1	0.897	-1.573	0.158541	0.40535
16153	10514561	ENSMUST00000107065	319865	RIKEN cDNA E130114P18 gene	E130114P18Rik	0.897	-0.814	0.441644	0.700534
16154	10427991	NM_001081302	223435	triple functional domain (PTPR	Trio	0.897	-1.229	0.25753	0.531656
16155	10516735	NM_023476	94242	tubulointerstitial nephritis a	Tinagl	0.897	-1.602	0.151879	0.39568
16156	10390075	NM_001105561	217122	predicted gene, OTTMUSG0000000	OTTMUSG00000002043	0.897	-1.176	0.277043	0.552231
16157	10359024	XM_994738	433367	predicted gene, EG433367	EG433367	0.897	-1.455	0.18778	0.446159
16158	10470614	NM_001033874	68870	RIKEN cDNA 1190002A17 gene	1190002A17Rik	0.897	-1.327	0.224902	0.494934
16159	10605051	NM_011907	24102	three prime repair exonuclease	Trex2	0.897	-0.723	0.492285	0.738375

16160	10477218	NM_001083618	74711	tubulin tyrosine ligase-like f	Ttll9	0.897	-1.565	0.160384	0.407738
16161	10427045	BC016463	68118	RIKEN cDNA 9430023L20 gene	9430023L20Rik	0.897	-2.506	0.0396946	0.173124
16162	10425981	XM_139514	223745	predicted gene, EG223745	EG223745	0.897	-1.786	0.116082	0.338824
16163	10574572	BC027185	72361	RIKEN cDNA 2210023G05 gene	2210023G05Rik	0.897	-0.888	0.40329	0.668494
16164	10603262	BC100377	102991	expressed sequence AU022751	AU022751	0.897	-1.308	0.230939	0.501641
16165	10488553	BC119071	381393	RIKEN cDNA 4921509C19 gene	4921509C19Rik	0.897	-0.557	0.594352	0.808582
16166	10449163	NM_011822	14755	phosphatidylinositol glycan an	Pigq	0.897	-2.621	0.0334855	0.154358
16167	10607062	XM_001472085	633596	similar to high mobility group	LOC633596	0.897	-1.273	0.242632	0.515498
16168	10592731	ENSMUST00000098854	100038560	predicted gene, ENSMUSG0000007	ENSMUSG00000074408	0.897	-0.934	0.380389	0.65004
16169	10395049	NM_011275	19819	ribonuclease H1	Rnaseh1	0.897	-1.741	0.123965	0.352394
16170	10483157					0.897	-0.711	0.499395	0.742612
16171	10438891	NM_001033403	328657	gene model 1968, (NCBI)	Gm1968	0.897	-1.378	0.209586	0.474666
16172	10428302	NM_013692	21847	Kruppel-like factor 10	Klf10	0.897	-1.657	0.14028	0.378815
16173	10438094					0.897	-0.552	0.597807	0.81086
16174	10355717	NM_194333	22626	solute carrier family 23 (nucl	Slc23a3	0.897	-1.05	0.327783	0.604012
16175	10580854	BC016201	234586	cDNA sequence BC016201	BC016201	0.897	-1.209	0.264942	0.540102
16176	10497012	BC145840	71845	RIKEN cDNA 4922501L14 gene	4922501L14Rik	0.897	-2.19	0.0635422	0.233902
16177	10436046					0.897	-1.934	0.093093	0.295671
16178	10517924	NM_019701	56365	chloride channel Kb	Clcnkb	0.897	-1.871	0.10226	0.313542
16179	10561388	NM_025616	66525	translocase of inner mitochond	Timm50	0.897	-2.288	0.0548602	0.213516
16180	10386359	NM_008193	14923	guanylate kinase 1	Guk1	0.896	-2.581	0.0354843	0.160453
16181	10450603					0.896	-0.91	0.392051	0.660239
16182	10490116					0.896	-0.783	0.458341	0.713583
16183	10495270	NM_146137	229715	adhesion molecule with Ig like	Amigo1	0.896	-1.916	0.0956278	0.300662
16184	10445496	NM_145353	28064	Yip1 domain family, member 3	Yipf3	0.896	-2.005	0.0837875	0.277377
16185	10506498					0.896	-1.109	0.30296	0.579028
16186	10569958	ENSMUST00000098949	20300	chemokine (C-C motif) ligand 2	Ccl25	0.896	-1.152	0.286037	0.561602
16187	10481845	BC059907	72543	RIKEN cDNA 2610528K11 gene	2610528K11Rik	0.896	-2.71	0.0293484	0.141418
16188	10499899	NM_009264	20753	small proline-rich protein 1A	Sprr1a	0.896	-0.726	0.490729	0.737369
16189	10428602					0.896	-0.777	0.461615	0.716254
16190	10406663	NM_009712	11881	arylsulfatase B	Arsb	0.896	-1.94	0.0923057	0.294385
16191	10516213	NM_023423	68050	RIKEN cDNA 6330407G11 gene	6330407G11Rik	0.896	-2.339	0.050875	0.203346
16192	10448402	NM_013921	30943	transmembrane protease, serine	Tmprss8	0.896	-1.102	0.305807	0.582258
16193	10422259	NM_029578	76355	TDP-glucose 4,6-dehydratase	Tgds	0.896	-1.614	0.149284	0.391663
16194	10385043	NM_008722	18148	nucleophosmin 1	Npm1	0.896	-1.827	0.109236	0.326503
16195	10506701	NM_147221	230587	GLIS family zinc finger 1	Glis1	0.896	-1.442	0.191385	0.450628
16196	10365282	ENSMUST00000076984	70003	RIKEN cDNA 1700028I16 gene	1700028I16Rik	0.896	-1.364	0.213597	0.479693
16197	10443047	NM_053173	16580	kinesin family member C1	Kifc1	0.896	-1.301	0.233251	0.504383
16198	10600588					0.896	-1.338	0.221604	0.491101
16199	10389701	NM_009648	11640	A kinase (PRKA) anchor protein	Akap1	0.896	-1.417	0.198079	0.458849
16200	10569927	NM_001042557	26400	mitogen-activated protein kina	Map2k7	0.896	-2.932	0.0212275	0.114033
16201	10445781	NM_031254	83433	triggering receptor expressed	Trem2	0.896	-1.236	0.255111	0.5294
16202	10441811					0.896	-0.883	0.4059	0.670443
16203	10462309	ENSMUST00000035141	107372	RIKEN cDNA C030016D13 gene	C030016D13Rik	0.896	-1.309	0.230704	0.501597
16204	10430255	NM_001017983	239554	FAD-dependent oxidoreductase d	Foxred2	0.896	-1.279	0.240389	0.513465
16205	10419803	BC029624	74359	RIKEN cDNA 4931414P19 gene	4931414P19Rik	0.896	-0.793	0.452826	0.709514
16206	10386159	NM_178761	319475	zinc finger protein 672	Zfp672	0.896	-1.779	0.11716	0.341121
16207	10396795	NM_026114	13665	eukaryotic translation initiat	Eif2s1	0.896	-2.724	0.0287367	0.139246
16208	10429446	ENSMUST00000110021	268816	gene model 628, (NCBI)	Gm628	0.896	-0.569	0.586602	0.803706
16209	10394892	NM_018813	54451	cleavage and polyadenylation s	Cpsf3	0.896	-2.581	0.0355135	0.16052
16210	10507773					0.896	-2.463	0.0422826	0.179955
16211	10481566	NM_178887	98970	fibrinogen C domain containing	Fibcd1	0.896	-1.977	0.087332	0.284457

16212	10583384					0.896	-1.141	0.290226	0.566365
16213	10420957	NM_172498	19229	PTK2 protein tyrosine kinase 2	Ptk2b	0.896	-1.632	0.145353	0.387047
16214	10595953	NM_177775	272636	DNA segment, Chr 9, ERATO Doi	D9Ertd280e	0.896	-1.327	0.224933	0.494952
16215	10408531	NM_146041	218138	GDP-mannose 4, 6-dehydratase	Gmds	0.896	-2.208	0.0618714	0.229873
16216	10469538	ENSMUST00000028069	74629	RIKEN cDNA 4930426L09 gene	4930426L09Rik	0.896	-0.599	0.567249	0.792635
16217	10466406					0.896	-1.321	0.226847	0.497571
16218	10535575	XM_886369	621967	predicted gene, EG621967	EG621967	0.896	-1.162	0.282267	0.55726
16219	10430105	NM_198119	378937	leucine rich repeat containing	Lrrc24	0.896	-1.893	0.0990676	0.307319
16220	10362934					0.896	-1.939	0.0925099	0.294729
16221	10492640	NM_178673	213262	follistatin-like 5	Fstl5	0.896	-1.196	0.269667	0.544449
16222	10458597	NM_001033426	332309	gene model 851, (NCBI)	Gm851	0.896	-1.184	0.274049	0.548672
16223	10508052	NM_001081097	14807	glutamate receptor, ionotropic	Grik3	0.896	-0.887	0.403486	0.668494
16224	10520301	NM_198621	242891	gene model 443, (NCBI)	Gm443	0.896	-0.746	0.479366	0.729345
16225	10411945	NM_029984	77803	RIKEN cDNA A930021C24 gene	A930021C24Rik	0.896	-1.023	0.339496	0.614887
16226	10517191	NM_001080712	665186	predicted gene, EG665186	EG665186	0.896	-1.173	0.278073	0.55314
16227	10466963	BC125582	240613	RIKEN cDNA 9930021J03 gene	9930021J03Rik	0.896	-1.383	0.20795	0.472478
16228	10440425					0.896	-1.971	0.0880853	0.286007
16229	10412062	XR_030949	631589	similar to 60S ribosomal prote	LOC631589	0.896	-1.265	0.245276	0.518352
16230	10353803	NM_198899	320011	UDP-glucose ceramide glucosylt	Ugcgl1	0.896	-1.967	0.0886666	0.286953
16231	10467784	NM_029011	74580	RIKEN cDNA 4833409A17 gene	4833409A17Rik	0.896	-1.947	0.0913432	0.292586
16232	10603249	NM_010850	17870	myc-like oncogene, s-myc prote	Mycs	0.896	-1.577	0.157552	0.404282
16233	10463732	NM_146100	226180	internexin neuronal intermedia	Ina	0.896	-1.534	0.167536	0.418673
16234	10572613	NM_053162	94065	mitochondrial ribosomal protei	Mrpl34	0.896	-2.154	0.067102	0.241886
16235	10460556	NM_001024717	545276	galactose-3-O-sulfotransferase	Gal3st3	0.896	-1.526	0.169669	0.420989
16236	10369301	NM_016803	53374	carbohydrate (chondroitin 6/ke	Chst3	0.895	-0.901	0.396778	0.664039
16237	10442904	BC010800	72106	RIKEN cDNA 2610003J06 gene	2610003J06Rik	0.895	-0.9	0.397243	0.664239
16238	10510505					0.895	-0.813	0.442275	0.700945
16239	10379340					0.895	-1.057	0.324693	0.601113
16240	10527982	BC062906	207686	RIKEN cDNA A330021E22 gene	A330021E22Rik	0.895	-1.603	0.151696	0.395641
16241	10391410	NM_019584	56208	beclin 1, autophagy related	Becn1	0.895	-2.158	0.0667094	0.241235
16242	10551554	NM_023637	71984	seryl-aminoacyl-tRNA synthetas	Sars2	0.895	-1.23	0.257321	0.531588
16243	10470268	NM_173180	66865	peptidase (mitochondrial proce	Pmpca	0.895	-2.132	0.0693509	0.246733
16244	10525657	NM_026603	68184	density-regulated protein	Denr	0.895	-2.895	0.0224134	0.118094
16245	10554445	NM_145150	233406	protein regulator of cytokines	Prc1	0.895	-2.323	0.0521162	0.206473
16246	10555832	NM_147119	259123	olfactory receptor 632	Olfr632	0.895	-0.884	0.405004	0.669624
16247	10529118	NM_010122	13667	eukaryotic translation initiat	Eif2b4	0.895	-1.975	0.0876117	0.284863
16248	10355084	NM_145518	227197	NADH dehydrogenase (ubiquinone	Ndufs1	0.895	-2.094	0.0733533	0.255698
16249	10508719					0.895	-1.361	0.214468	0.481188
16250	10484195	ENSMUST00000099980	22138	titin	Ttn	0.895	-1.046	0.329417	0.605827
16251	10509596	NM_025786	66825	ring finger protein 186	Rnf186	0.895	-0.975	0.36128	0.633093
16252	10559687	NM_026158	67441	isochorismatase domain contain	Isoc2b	0.895	-1.856	0.104548	0.318157
16253	10465427	NM_019924	56613	ribosomal protein S6 kinase, p	Rps6ka4	0.895	-1.342	0.220197	0.488992
16254	10433584	NM_011608	21935	tumor necrosis factor receptor	Tnfrsf17	0.895	-1.523	0.170429	0.422073
16255	10401023	NM_026020	67186	ribosomal protein, large P2	Rplp2	0.895	-1.982	0.0866693	0.283017
16256	10367305	NM_172790	237615	ankyrin repeat domain 52	Ankrd52	0.895	-1.764	0.119813	0.346027
16257	10562905	NM_030693	107503	activating transcription facto	Atf5	0.895	-2.02	0.0819132	0.273441
16258	10554281	NM_145946	208836	Fanconi anemia, complementatio	Fanci	0.895	-1.808	0.112321	0.331971
16259	10567520	XM_355934	381917	dynein, axonemal, heavy chain	Dnahc3	0.895	-2.063	0.0768184	0.262781
16260	10607465	XR_032773	675813	similar to 40S ribosomal prote	LOC675813	0.895	-1.413	0.199193	0.460684
16261	10397891	BC096606	320351	RIKEN cDNA D230037D09 gene	D230037D09Rik	0.895	-1.526	0.16952	0.420889
16262	10431463	NM_027081	69440	RIKEN cDNA 1700027J05 gene	1700027J05Rik	0.895	-2.231	0.0597404	0.225162
16263	10544644	ENSMUST00000101405	14210	hypothetical LOC14210	LOC14210	0.895	-2.512	0.0393149	0.172

16264	10543460	NM_177013	319832	RIKEN cDNA 6332401O19 gene	6332401O19Rik	0.895	-1.176	0.276826	0.551981
16265	10589350	NM_025858	66940	shisa homolog 5 (Xenopus laevi	Shisa5	0.895	-2.29	0.0547008	0.213119
16266	10494857	NM_010937	18176	neuroblastoma ras oncogene	Nras	0.895	-2.683	0.0305233	0.14545
16267	10393648	NM_018822	27029	N-sulfoglucosamine sulfohydrol	Sgsh	0.895	-1.312	0.22988	0.500912
16268	10408156	NM_134239	171273	vomeronasal 1 receptor, H14	V1rh14	0.895	-1.353	0.216974	0.484549
16269	10539337	NM_020619	57377	glucosidase 1	Gcs1	0.895	-2.065	0.0765879	0.262374
16270	10406171	NM_182839	72948	tubulin polymerization promoti	Tppp	0.895	-1.594	0.15362	0.398105
16271	10390931					0.895	-0.406	0.69652	0.866816
16272	10579043	NM_199364	211134	leucine zipper, putative tumor	Lzts1	0.895	-1.145	0.288961	0.565029
16273	10409592	NM_010702	16841	leukocyte cell-derived chemota	Lect2	0.895	-0.576	0.582429	0.800864
16274	10443122	NM_027544	70772	gametogenetin binding protein	Ggnbp1	0.894	-1.51	0.173568	0.426438
16275	10458415	ENSMUST00000097612	100049566	predicted gene, ENSMUSG0000007	ENSMUSG00000073594	0.894	-2.414	0.0454656	0.188717
16276	10497285	NM_018864	55980	inositol (myo)-1(or 4)-monopho	Impa1	0.894	-2.043	0.079221	0.268035
16277	10436106	NM_172616	224171	RIKEN cDNA C330027C09 gene	C330027C09Rik	0.894	-1.511	0.173218	0.425677
16278	10579373	BC024265	546071	microtubule associated serine/	Mast3	0.894	-2.297	0.0541322	0.211449
16279	10528913	ENSMUST00000065372	332993	predicted gene, EG332993	EG332993	0.894	-1.834	0.108082	0.324339
16280	10472300	NM_021526	59029	proteasome (prosome, macropain	Psmd14	0.894	-2.059	0.0773151	0.263972
16281	10460573	NM_027236	69860	eukaryotic translation initiat	Eif1ad	0.894	-2.085	0.0743393	0.257888
16282	10415866	NM_173393	219149	X Kell blood group precursor r	Xkr6	0.894	-1.139	0.291127	0.567231
16283	10535426	NM_029048	74673	speedy homolog B (Drosophila)	Spdyb	0.894	-0.839	0.428451	0.689486
16284	10497335	BC115807	69126	RIKEN cDNA 1810022K09 gene	1810022K09Rik	0.894	-1.628	0.14625	0.388006
16285	10595723	NM_001114977	67958	RIKEN cDNA 2610101N10 gene	2610101N10Rik	0.894	-2.417	0.0452772	0.18819
16286	10535208	NM_026510	68017	FtsJ homolog 2 (E. coli)	Ftsj2	0.894	-1.373	0.211015	0.476598
16287	10469613	NM_177588	208967	threonine synthase-like 1 (bac	Thnsl1	0.894	-2.489	0.0407095	0.175879
16288	10574996	NM_145404	214572	protein arginine N-methyltrans	Prmt7	0.894	-2.452	0.042997	0.182022
16289	10525955	NM_175284	93897	frizzled homolog 10 (Drosophil	Fzd10	0.894	-1.351	0.217591	0.485334
16290	10583485	NM_175687	319278	RIKEN cDNA A230050P20 gene	A230050P20Rik	0.894	-1.874	0.101873	0.31281
16291	10577954	NM_001080813	75767	RAB11 family interacting prote	Rab11fip1	0.894	-1.456	0.187479	0.44575
16292	10607694	NM_025932	67043	synapse associated protein 1	Syap1	0.894	-2.183	0.0642244	0.235594
16293	10598798	NM_009483	22289	ubiquitously transcribed tetra	Utx	0.894	-1.099	0.307225	0.583826
16294	10381250	NM_134024	103733	tubulin, gamma 1	Tubg1	0.894	-1.659	0.139791	0.378113
16295	10439991	NM_019678	21787	Trk-fused gene	Tfg	0.894	-3.045	0.0180498	0.102153
16296	10482135	NM_147051	259053	olfactory receptor 362	Olfr362	0.894	-1.701	0.131474	0.364159
16297	10586458	NM_173185	214897	casein kinase 1, gamma 1	Csnk1g1	0.894	-1.868	0.102699	0.314522
16298	10538269	AK047380	14210	hypothetical LOC14210	LOC14210	0.894	-0.945	0.374998	0.644998
16299	10456161	NM_008313	15562	5 hydroxytryptamine (serotonin	Htr4	0.894	-0.867	0.414092	0.677439
16300	10551431	NM_001024726	545938	zinc finger proten 607	Zfp607	0.894	-1.444	0.190739	0.449693
16301	10388451	ENSMUST00000051512	192652	WD repeat domain 81	Wdr81	0.894	-1.429	0.194909	0.455025
16302	10508972	BC080727	434166	similar to hypothetical protei	LOC434166	0.894	-2.032	0.0804885	0.270736
16303	10464171	NM_001002238	83561	tudor domain containing 1	Tdrd1	0.894	-1.737	0.124642	0.353512
16304	10540283	NM_182939	232314	protein phosphatase 4, regulat	Ppp4r2	0.894	-1.72	0.127795	0.35851
16305	10432294	ENSMUST00000092304	320003	RIKEN cDNA C430014K11 gene	C430014K11Rik	0.894	-1.235	0.255526	0.529847
16306	10463023	NM_001011707	69888	cytochrome P450, family 2, sub	Cyp2c66	0.894	-0.759	0.472023	0.723892
16307	10377364	NM_177060	320040	RIKEN cDNA 9930039A11 gene	9930039A11Rik	0.894	-1.935	0.0929382	0.295413
16308	10443494	NM_023734	74116	peptidase inhibitor 16	Pi16	0.894	-0.771	0.465458	0.719103
16309	10419934	NM_080728	140781	myosin, heavy polypeptide 7, c	Myh7	0.894	-1.265	0.245111	0.518211
16310	10376564	NM_138675	192191	mediator of RNA polymerase II	Med9	0.894	-2.043	0.0791652	0.267948
16311	10439934					0.894	-0.724	0.491946	0.738272
16312	10423289	XR_004732	624863	similar to 23 kD highly basic	LOC624863	0.894	-1.247	0.251308	0.525436
16313	10453797	NM_001083628	381157	cDNA sequence AK220484	AK220484	0.894	-1.011	0.344607	0.61884

16314	10398100	NM_013776	27382	T-cell leukemia/lymphoma 1B, 5	Tcl1b5	0.894	-1.578	0.157356	0.403974
16315	10419015	NM_130878	170677	protocadherin 21	Pcdh21	0.894	-1.737	0.124628	0.353512
16316	10395394	NM_178629	75847	RIKEN cDNA 4930579E17 gene	4930579E17Rik	0.894	-2.831	0.0245778	0.126012
16317	10363563	NM_175194	73132	solute carrier family 25 (mito	Slc25a16	0.894	-0.656	0.531997	0.766197
16318	10414350	NM_080843	67296	suppressor of cytokine signali	Socs4	0.894	-2.065	0.0766583	0.26253
16319	10536390	NM_133236	170772	glucocorticoid induced transcr	Glcci1	0.894	-1.401	0.202714	0.465349
16320	10532511	BC087866	269683	RIKEN cDNA E130006D01 gene	E130006D01Rik	0.894	-1.078	0.315652	0.59252
16321	10446589					0.894	-1.328	0.224813	0.494893
16322	10525718	NM_144509	65105	ADP-ribosylation factor-like 6	Arl6ip4	0.893	-2.613	0.033882	0.155555
16323	10576559	NM_028908	74393	RIKEN cDNA 4933403G14 gene	4933403G14Rik	0.893	-2.873	0.0231223	0.120865
16324	10383681	ENSMUST00000065594	791413	predicted gene, OTTMUSG0000000	OTTMUSG00000007639	0.893	-1.645	0.142645	0.382804
16325	10499911	NM_025984	67127	late cornified envelope 1A1	Lce1a1	0.893	-1.645	0.142785	0.382897
16326	10477929	NM_026124	67388	RIKEN cDNA 1110008F13 gene	1110008F13Rik	0.893	-2.312	0.0529376	0.208508
16327	10409319	NM_010076	13488	dopamine receptor D1A	Drd1a	0.893	-1.135	0.29284	0.568891
16328	10434523	NM_145632	245841	polymerase (RNA) II (DNA direc	Polr2h	0.893	-2.752	0.0276178	0.135992
16329	10350948					0.893	-1.039	0.332577	0.608621
16330	10376196	NM_008248	15254	histidine triad nucleotide bin	Hint1	0.893	-2.567	0.0362222	0.162503
16331	10359520					0.893	-0.878	0.408293	0.672667
16332	10525921	XM_915709	208151	transmembrane protein 132B	Tmem132b	0.893	-0.837	0.429648	0.690624
16333	10349100	XR_033564	626075	similar to high mobility group	LOC626075	0.893	-1.676	0.136466	0.372893
16334	10362420					0.893	-1.122	0.297863	0.573903
16335	10447128	XM_916806	625514	predicted gene, EG625514	EG625514	0.893	-1.463	0.185555	0.44347
16336	10541333	NM_133661	14411	solute carrier family 6 (neuro	Slc6a12	0.893	-0.92	0.387191	0.656149
16337	10544941	NM_011054	18575	phosphodiesterase 1C	Pde1c	0.893	-0.991	0.353773	0.6265
16338	10445422	NM_028662	73836	solute carrier family 35, memb	Slc35b2	0.893	-1.559	0.161615	0.409832
16339	10426550	NM_201359	380967	transmembrane protein 106C	Tmem106c	0.893	-1.605	0.151226	0.395197
16340	10552697	NM_008437	16541	napsin A aspartic peptidase	Napsa	0.893	-0.82	0.438379	0.697449
16341	10466248	NM_001025307	20908	syntaxin 3	Stx3	0.893	-1.055	0.325607	0.601936
16342	10477644	NM_178111	68728	transformation related protein	Trp53inp2	0.893	-2.271	0.0562935	0.216807
16343	10409294	NM_009269	268656	serine palmitoyltransferase, l	Sptlc1	0.893	-2.328	0.0517412	0.205603
16344	10512847	NM_019998	56737	asparagine-linked glycosylatio	Alg2	0.893	-2.221	0.0606657	0.22719
16345	10428412	NM_026149	67429	NudC domain containing 1	Nudcd1	0.893	-1.742	0.123797	0.352065
16346	10510391	NM_009272	20810	spermidine synthase	Srm	0.893	-1.943	0.0918427	0.293563
16347	10488862	NM_144786	207182	gamma-glutamyltransferase 7	Ggt7	0.893	-1.023	0.339235	0.614614
16348	10581926	NM_013925	30947	adenosine deaminase, tRNA-spec	Adat1	0.893	-1.666	0.138407	0.376395
16349	10551173	NM_138586	27998	exosome component 5	Exosc5	0.893	-1.964	0.0890548	0.287785
16350	10595280	NM_009945	12866	cytochrome c oxidase, subunit	Cox7a2	0.893	-2.731	0.0284735	0.138496
16351	10390059	NM_145828	217119	xylosyltransferase II	Xylt2	0.893	-1.666	0.138301	0.376252
16352	10542762	XR_031050	621842	similar to ribosomal protein S	LOC621842	0.893	-1.226	0.258791	0.532905
16353	10441339	ENSMUST00000099483	320586	RIKEN cDNA A630089N07 gene	A630089N07Rik	0.893	-1.575	0.15804	0.405065
16354	10468231	NM_019718	56350	ADP-ribosylation factor-like 3	Arl3	0.893	-2.433	0.044253	0.185686
16355	10435661	NM_153394	239845	G protein-coupled receptor 156	Gpr156	0.893	-1.267	0.244702	0.517866
16356	10432886	NM_008475	16682	keratin 4	Krt4	0.893	-2.161	0.0663356	0.240501
16357	10598827					0.893	-0.386	0.71046	0.873031
16358	10488639	NM_001001444	75400	defensin beta 29	Defb29	0.893	-1.07	0.319273	0.596377
16359	10486185	NM_139139	69408	DnaJ (Hsp40) homolog, subfamil	Dnajc17	0.893	-0.893	0.400615	0.666392
16360	10379866	NM_007607	12351	carbonic anhydrase 4	Car4	0.893	-1.583	0.156071	0.401895
16361	10542317	NM_009875	12576	cyclin-dependent kinase inhibi	Cdkn1b	0.893	-2.993	0.0194375	0.107616
16362	10524398	NM_177292	320916	WSC domain containing 2	Wscd2	0.893	-1.19	0.271576	0.546245
16363	10427026	NM_019518	56149	GRP1 (general receptor for pho	Grasp	0.893	-1.569	0.159281	0.406366
16364	10516022					0.893	-0.997	0.350901	0.624323
16365	10393406	XR_034089	667423	predicted gene, EG667423	EG667423	0.893	-1.322	0.226707	0.497406

16366	10391669	NM_026542	68066	solute carrier family 25, memb	Slc25a39	0.893	-2.853	0.0238196	0.1232
16367	10388728	ENSMUST00000068419	791423	predicted gene, OTTMUSG0000000	OTTMUSG00000000071	0.893	-1.202	0.267491	0.542213
16368	10533055	NM_026886	68955	RIKEN cDNA 1500001A10 gene	1500001A10Rik	0.893	-1.242	0.253267	0.527594
16369	10384968	NM_001024919	69556	RIKEN cDNA 2310022M17 gene	2310022M17Rik	0.893	-1.598	0.152739	0.396795
16370	10489723	NM_027230	228880	protein kinase C binding prote	Prkcbp1	0.893	-2.701	0.0297474	0.14282
16371	10588678	NM_019742	80385	tumor suppressor candidate 2	Tusc2	0.893	-1.435	0.193061	0.452493
16372	10578287	NM_011135	18983	CCR4-NOT transcription complex	Cnot7	0.892	-2.536	0.0379515	0.168193
16373	10383511	AF285590	73679	testis expressed gene 19	Tex19	0.892	-0.562	0.591111	0.80656
16374	10575144	NM_025391	66164	nuclear import 7 homolog (S. c	Nip7	0.892	-2.026	0.0812467	0.272009
16375	10401286	NM_001008423	380768	gene model 1568, (NCBI)	Gm1568	0.892	-0.756	0.473751	0.725344
16376	10357948	NM_001081307	329251	protein phosphatase 1, regulat	Ppp1r12b	0.892	-1.344	0.219844	0.488612
16377	10450501	NM_013693	21926	tumor necrosis factor	Tnf	0.892	-1.292	0.236264	0.508392
16378	10521566	NM_025480	66309	transmembrane protein 128	Tmem128	0.892	-2.158	0.0666261	0.241189
16379	10559043	NM_010844	17833	mucin 5, subtypes A and C, tra	Muc5ac	0.892	-0.919	0.387844	0.656721
16380	10425822	NM_054088	116939	patatin-like phospholipase dom	Pnpla3	0.892	-1.514	0.172581	0.4249
16381	10600485	NM_001030307	245474	dyskeratosis congenita 1, dysk	Dkc1	0.892	-1.776	0.117715	0.342314
16382	10427391	XR_030618	100044414	similar to Ewing sarcoma break	LOC100044414	0.892	-2.309	0.0532361	0.209301
16383	10505922					0.892	-2.709	0.02938	0.141538
16384	10507160					0.892	-2.132	0.0692782	0.246644
16385	10565775	NM_026384	67800	diacylglycerol O-acyltransfera	Dgat2	0.892	-1.7	0.131701	0.364584
16386	10456650					0.892	-1.593	0.1539	0.39844
16387	10502405	NM_175224	75624	methionyl aminopeptidase 1	Metap1	0.892	-1.372	0.211141	0.476707
16388	10533725	NM_175520	243270	G protein-coupled receptor 81	Gpr81	0.892	-1.279	0.24059	0.513659
16389	10529299	NM_009193	20492	stem-loop binding protein	Slbp	0.892	-2.156	0.0668549	0.241483
16390	10510422	NM_027195	69743	castor homolog 1, zinc finger	Casz1	0.892	-2.876	0.0230347	0.120616
16391	10368222	NM_053264	114671	RIKEN cDNA 4930444G20 gene	4930444G20Rik	0.892	-0.937	0.379136	0.648895
16392	10470119	NM_021519	59022	endothelial differentiation-re	Edf1	0.892	-1.956	0.0900751	0.289577
16393	10516027	NM_001081013	109263	rearranged L-myc fusion sequen	Rlf	0.892	-1.459	0.186724	0.444956
16394	10490097	NM_175631	228942	cerebellin 4 precursor protein	Cbln4	0.892	-1.081	0.314512	0.591308
16395	10573112					0.892	-1.671	0.137423	0.374395
16396	10444708	NM_148947	114652	lymphocyte antigen 6 complex,	Ly6g5c	0.892	-1.237	0.254995	0.529326
16397	10384183	NM_001081652	192950	cDNA sequence AB182283	AB182283	0.892	-1.714	0.12904	0.360251
16398	10538115	NM_001077410	243374	GTPase, IMAP family member 8	Gimap8	0.892	-0.875	0.409984	0.674344
16399	10567043	NM_025846	66922	related RAS viral (r-ras) onco	Rras2	0.892	-2.077	0.0752825	0.2595
16400	10416353					0.892	-0.569	0.586525	0.803673
16401	10435453					0.892	-0.92	0.387465	0.656379
16402	10516590	NM_028603	73680	RIKEN cDNA 2410081M15 gene	2410081M15Rik	0.892	-1.699	0.131835	0.364763
16403	10409586	NM_008373	16198	interleukin 9	Il9	0.892	-1.497	0.176734	0.430877
16404	10564313	NM_026483	67973	M-phase phosphoprotein 10 (U3	Mphosph10	0.892	-2.076	0.0753753	0.259624
16405	10457429	NM_009071	19877	Rho-associated coiled-coil con	Rock1	0.892	-2.131	0.0694671	0.246984
16406	10346611	NM_001013771	381260	gene model 973, (NCBI)	Gm973	0.892	-1.268	0.244179	0.517327
16407	10372078	NM_026065	67270	DNA segment, Chr 10, ERATO Doi	D10Ertd322e	0.892	-2.078	0.0751702	0.259229
16408	10582978	BC014729	78100	RIKEN cDNA 8430410K20 gene	8430410K20Rik	0.892	-2.446	0.0434066	0.18312
16409	10456361	ENSMUST00000066628	791372	predicted gene, ENSMUSG0000005	ENSMUSG00000053891	0.892	-1.989	0.0857729	0.281088
16410	10516227	ENSMUST00000053604	70249	RIKEN cDNA 3100002H09 gene	3100002H09Rik	0.892	-0.688	0.512984	0.753467
16411	10586357	NM_173385	214425	cartilage intermediate layer p	Cilp	0.892	-1.322	0.226579	0.497227
16412	10516620	NM_010693	16818	lymphocyte protein tyrosine ki	Lck	0.892	-1.201	0.267824	0.542576
16413	10380560	NM_201609	268469	zinc finger protein 652	Zfp652	0.892	-2.237	0.0592061	0.224025
16414	10391895	NM_133715	544817	Rho GTPase activating protein	Arhgap27	0.892	-1.635	0.144772	0.386155

16415	10545758					0.892	-1.855	0.104752	0.318627
16416	10382932	ENSMUST00000067484	78403	RIKEN cDNA 2900041M22 gene	2900041M22Rik	0.892	-1.634	0.145092	0.386717
16417	10516427	NM_011986	26562	neurochondrin	Ncdn	0.892	-2.715	0.0291353	0.140551
16418	10524314	NM_019640	56305	phosphatidylinositol transfer	Pitpnb	0.892	-2.902	0.0221643	0.117219
16419	10566219	NM_147081	259085	olfactory receptor 610	Olfr610	0.892	-1.517	0.171716	0.423956
16420	10557359	NM_001081022	233865	RIKEN cDNA D430042O09 gene	D430042O09Rik	0.892	-1.938	0.0925948	0.294729
16421	10515729	ENSMUST00000075406	230676	cDNA sequence BC059842	BC059842	0.892	-1.167	0.280495	0.555889
16422	10546244	XM_994764	71797	carbohydrate (chondroitin 4) s	Chst13	0.892	-1.759	0.120649	0.347112
16423	10448743	NM_023480	68636	fumarylacetoacetate hydrolase	Fahd1	0.892	-2.064	0.0767314	0.262653
16424	10394794	BC030401	245297	predicted gene, EG245297	EG245297	0.891	-1.396	0.204143	0.467365
16425	10437311	NM_026508	68015	TNF receptor-associated protei	Trap1	0.891	-3.078	0.0172091	0.0991856
16426	10383202	ENSMUST00000093902	672511	hypothetical LOC672511	LOC672511	0.891	-1.326	0.225294	0.495384
16427	10445607	NM_145488	224824	peroxisomal biogenesis factor	Pex6	0.891	-2.102	0.0725178	0.253692
16428	10594911	NM_009359	21778	testis expressed gene 9	Tex9	0.891	-2.234	0.0595504	0.224825
16429	10449661	NM_009363	21785	trefoil factor 2 (spasmolytic	Tff2	0.891	-1.105	0.30469	0.581126
16430	10587194	NM_138719	14697	guanine nucleotide binding pro	Gnb5	0.891	-1.142	0.290034	0.566261
16431	10560078	NM_145819	109889	myeloid zinc finger 1	Mzf1	0.891	-1.366	0.21302	0.478905
16432	10459879	NM_207651	27411	solute carrier family 14 (urea	Slc14a2	0.891	-1.028	0.337206	0.612796
16433	10440655	ENSMUST00000052337	69699	RIKEN cDNA 2310079G19 gene	2310079G19Rik	0.891	-1.07	0.31893	0.596119
16434	10454202	NM_207623	56515	ring finger protein 138	Rnf138	0.891	-1.484	0.180037	0.435501
16435	10453604	NM_026505	68010	BMP and activin membrane-bound	Bambi	0.891	-1.774	0.11803	0.342994
16436	10371670					0.891	-0.744	0.480277	0.729941
16437	10514558	XR_004941	676606	similar to heterogeneous nucle	LOC676606	0.891	-2.132	0.0693509	0.246733
16438	10525542	NM_029850	77045	B-cell CLL/lymphoma 7A	Bcl7a	0.891	-2.679	0.0307129	0.145866
16439	10367122	NM_054078	116848	bromodomain adjacent to zinc f	Baz2a	0.891	-2.585	0.0352694	0.159823
16440	10470909					0.891	-1.333	0.222957	0.492859
16441	10349637	BC145667	108900	RIKEN cDNA 2700049P18 gene	2700049P18Rik	0.891	-1.893	0.0989944	0.307265
16442	10518313	NM_009401	21941	tumor necrosis factor receptor	Tnfrsf8	0.891	-1.589	0.154839	0.400004
16443	10443191	ENSMUST00000097363	100038429	predicted gene, ENSMUSG0000007	ENSMUSG00000073430	0.891	-1.111	0.302182	0.578377
16444	10519527	NM_011076	18671	ATP-binding cassette, sub-fami	Abcb1a	0.891	-0.945	0.375325	0.64535
16445	10453436	NM_176808	193813	multiple coagulation factor de	Mcfd2	0.891	-2.349	0.0501063	0.201363
16446	10432866	NM_001003667	406220	keratin 77	Krt77	0.891	-0.84	0.42796	0.689167
16447	10364155	NM_029816	76964	RIKEN cDNA 2610028H24 gene	2610028H24Rik	0.891	-1.475	0.182516	0.439034
16448	10555919	NM_146355	258352	olfactory receptor 692	Olfr692	0.891	-1.216	0.26214	0.536615
16449	10552075	NM_144556	243914	leucine-rich repeat LGI family	Lgi4	0.891	-1.294	0.235644	0.507379
16450	10359086	BC089561	74081	centrosomal protein 350	Cep350	0.891	-1.7	0.131633	0.364442
16451	10546129	AK016973	74589	kelch domain containing 6	Klhdc6	0.891	-1.589	0.154823	0.400004
16452	10366544	AF221104	94118	kinesin family member C5C	Kifc5c	0.891	-0.965	0.365567	0.636806
16453	10349711	NM_173865	98396	solute carrier family 41, memb	Slc41a1	0.891	-2.043	0.0792269	0.268035
16454	10382409	NM_001102615	286942	kinesin family member 19A	Kif19a	0.891	-0.976	0.360543	0.632355
16455	10485830	NM_026519	68032	transmembrane protein 85	Tmem85	0.891	-2.663	0.0314466	0.14825
16456	10445803	NM_152823	76589	unc-5 homolog C (C. elegans)-l	Unc5cl	0.891	-1.203	0.266956	0.541627
16457	10352514	NM_029735	107508	glutamyl-prolyl-tRNA synthetas	Eprs	0.891	-2.912	0.021868	0.116321
16458	10380318					0.891	-1.139	0.290996	0.567132
16459	10520025	NM_011188	19181	proteasome (prosome, macropain	Psmc2	0.891	-2.784	0.0263399	0.131631
16460	10381385					0.89	-0.624	0.551655	0.781685
16461	10557139	NM_138589	28018	ubiquitin family domain contai	Ubfd1	0.89	-1.992	0.0854547	0.280611
16462	10585706	NM_007747	12858	cytochrome c oxidase, subunit	Cox5a	0.89	-2.575	0.0357977	0.16125
16463	10477006	NM_198326	386649	NSFL1 (p97) cofactor (p47)	Nsfl1c	0.89	-2.582	0.0354664	0.160407
16464	10554502	NM_001004184	434203	solute carrier family 28 (sodi	Slc28a1	0.89	-0.899	0.39756	0.664302
16465	10549635	NM_001081239	232801	predicted gene, EG232801	EG232801	0.89	-1.324	0.226065	0.496626
16466	10592938	BC026825	192653	cDNA sequence BC021608	BC021608	0.89	-1.343	0.219852	0.488612

16467	10504094	NM_016658	14430	galactose-1-phosphate uridyl t	Galt	0.89	-1.403	0.202131	0.464903
16468	10562416	NM_009884	12611	CCAAT/enhancer binding protein	Cebpg	0.89	-2.861	0.0235503	0.122106
16469	10476106					0.89	-0.575	0.582614	0.800924
16470	10484861	NM_020515	57272	olfactory receptor 140	Olfr140	0.89	-1.139	0.291058	0.567201
16471	10515935	NM_008191	14916	guanylate cyclase activator 2b	Guca2b	0.89	-1.392	0.205404	0.469103
16472	10478943	NM_001110152	109054	prefoldin 4	Pfdn4	0.89	-2.099	0.0727933	0.25432
16473	10452295	NM_009451	22153	tubulin, beta 4	Tubb4	0.89	-2.583	0.0354175	0.1603
16474	10605338	NM_008062	14381	glucose-6-phosphate dehydrogen	G6pdx	0.89	-2.506	0.0396893	0.173124
16475	10525835					0.89	-1.425	0.195831	0.456219
16476	10412227	NM_130796	170625	sorting nexin 18	Snx18	0.89	-2.305	0.0535448	0.209868
16477	10450746	NM_026308	67676	ribonuclease P 21 subunit (hum	Rpp21	0.89	-1.724	0.127197	0.35745
16478	10526145	BC033455	71667	RIKEN cDNA 0610007L01 gene	0610007L01Rik	0.89	-3.26	0.0133018	0.0828894
16479	10436662					0.89	-1.475	0.182589	0.439161
16480	10406423	NM_028372	72852	RIKEN cDNA 2900024O10 gene	2900024O10Rik	0.89	-1.695	0.132663	0.366336
16481	10399882	NM_028002	71916	dihydrouridine synthase 4-like	Dus4l	0.89	-1.442	0.19127	0.450457
16482	10381574	NM_016759	51799	RUN domain containing 3A	Rundc3a	0.89	-1.194	0.270171	0.545029
16483	10504514	ENSMUST00000095105	73405	RIKEN cDNA 1700055D18 gene	1700055D18Rik	0.89	-1.386	0.206974	0.471406
16484	10593101	XR_034358	640094	similar to Glyceraldehyde-3-ph	LOC640094	0.89	-1.026	0.338128	0.613733
16485	10429970	ENSMUST00000100504	100038562	predicted gene, ENSMUSG0000007	ENSMUSG00000075578	0.89	-1.175	0.277187	0.552231
16486	10414265	BC061237	385138	cDNA sequence BC061237	BC061237	0.89	-1.584	0.156003	0.401839
16487	10566593					0.89	-0.867	0.413927	0.677396
16488	10500754	NM_011516	20957	synaptonemal complex protein 1	Sycp1	0.89	-0.779	0.460879	0.715479
16489	10365335					0.89	-0.813	0.44224	0.700945
16490	10497201					0.89	-1.362	0.214106	0.480529
16491	10386173	BC048595	403200	RIKEN cDNA 4930504O13 gene	4930504O13Rik	0.89	-1.237	0.254714	0.528967
16492	10499247	NM_001033124	18211	neurotrophic tyrosine kinase,	Ntrk1	0.89	-1.38	0.208963	0.473969
16493	10559415	NM_027203	69757	leukocyte receptor cluster (LR	Leng1	0.89	-1.324	0.226057	0.496626
16494	10517774	NM_153106	242726	peptidyl arginine deiminase, t	Padi6	0.89	-1.473	0.182973	0.439824
16495	10432780	NM_008476	16687	keratin 6A	Krt6a	0.89	-0.424	0.684045	0.860099
16496	10382271	NM_028710	74008	arylsulfatase G	Arsg	0.89	-1.188	0.272556	0.547117
16497	10344815	NM_026493	211660	centrosome and spindle pole as	Cspp1	0.89	-1.878	0.101211	0.311546
16498	10398721	BC071262	68020	RIKEN cDNA 2810002N01 gene	2810002N01Rik	0.89	-1.617	0.148664	0.390994
16499	10390299	NM_134021	103711	pyridoxine 5'-phosphate oxidas	Pnpo	0.89	-1.718	0.128307	0.359233
16500	10512704	NM_025513	66362	exosome component 3	Exosc3	0.89	-1.804	0.113028	0.333083
16501	10468517					0.89	-0.957	0.369462	0.640058
16502	10365134					0.89	-1.894	0.0987865	0.306809
16503	10584502	NM_001011859	258165	olfactory receptor 965	Olfr965	0.89	-0.91	0.392072	0.660239
16504	10575376	BC025546	234728	cDNA sequence BC025546	BC025546	0.89	-2.206	0.0620343	0.230276
16505	10443808	NM_030087	78330	RIKEN cDNA 1500032D16 gene	1500032D16Rik	0.89	-1.737	0.124727	0.353522
16506	10504504	NM_080289	76238	glyoxylate reductase/hydroxypy	Grhpr	0.89	-3.265	0.0132139	0.0825633
16507	10419005	NM_021340	57811	retinal G protein coupled rece	Rgr	0.89	-1.976	0.0875068	0.284741
16508	10476192	NM_011025	18429	oxytocin	Oxt	0.889	-1.18	0.27528	0.550143
16509	10518019	NM_001017966	68817	DNA-damage inducible protein 2	Ddi2	0.889	-2.262	0.0570824	0.218492
16510	10469135					0.889	-1.67	0.137496	0.374537
16511	10357051	NM_027534	70750	3-ketodihydrosphingosine reduc	Kdsr	0.889	-2.18	0.0644793	0.236295
16512	10517236	NM_024215	68040	zinc finger protein 593	Zfp593	0.889	-2.524	0.0386056	0.16991
16513	10364239	NM_031196	20509	solute carrier family 19 (sodi	Slc19a1	0.889	-2.13	0.0695599	0.24723
16514	10525751	NM_026409	67848	DEAD (Asp-Glu-Ala-Asp) box pol	Ddx55	0.889	-2.78	0.026496	0.132161
16515	10358677	BC060204	66875	RIKEN cDNA 1200016B10 gene	1200016B10Rik	0.889	-2.241	0.0589024	0.223325
16516	10504666					0.889	-1.967	0.0886587	0.286953

16517	10451472	NM_025433	66229	ribosomal protein L7-like 1	Rpl7l1	0.889	-2.734	0.0283465	0.138133
16518	10533875	NM_011424	20602	nuclear receptor co-repressor	Ncor2	0.889	-3.052	0.0178667	0.10147
16519	10461130	NM_008766	18399	solute carrier family 22 (orga	Slc22a6	0.889	-1.174	0.277749	0.552831
16520	10457776					0.889	-0.723	0.492266	0.738375
16521	10355464	NM_023523	111175	peroxisomal trans-2-enoyl-CoA	Pecr	0.889	-1.984	0.0865104	0.282717
16522	10413987	XM_985917	268729	gene model 626, (NCBI)	Gm626	0.889	-0.946	0.374597	0.644557
16523	10530683	NM_028850	74277	cysteine-rich hydrophobic doma	Chic2	0.889	-2.625	0.0332778	0.153865
16524	10433940	NM_011949	26413	mitogen-activated protein kina	Mapk1	0.889	-2.528	0.0384101	0.169439
16525	10400336	NM_026998	72183	sorting nexin 6	Snx6	0.889	-2.291	0.054675	0.213057
16526	10463856	BC057135	381229	coiled-coil domain containing	Ccdc147	0.889	-1.467	0.184582	0.442145
16527	10561516	NM_010908	18036	nuclear factor of kappa light	Nfkbib	0.889	-2.217	0.0610032	0.227923
16528	10493860	NM_011469	20756	small proline-rich protein 2B	Sprr2b	0.889	-0.531	0.61115	0.819466
16529	10554034	DQ646881	545975	LAG1 homolog, ceramide synthas	Lass3	0.889	-1.761	0.120378	0.346744
16530	10507471	XM_903276	630172	similar to DNA-directed RNA po	LOC630172	0.889	-2.169	0.0655611	0.2387
16531	10440729	ENSMUST00000056118	71363	keratin associated protein 7-1	Krtap7-1	0.889	-1.958	0.0898199	0.289247
16532	10394240	NM_008895	18976	pro-opiomelanocortin-alpha	Pomc	0.889	-1.89	0.099486	0.30816
16533	10424825	NM_025567	66445	cytochrome c-1	Cyc1	0.889	-3.643	0.00783892	0.0571538
16534	10388613	NM_001012309	237859	coiled-coil domain containing	Ccdc55	0.889	-2.188	0.0637282	0.234383
16535	10429641	NM_172607	223646	nicotinate phosphoribosyltrans	Naprt1	0.889	-1.618	0.148332	0.390528
16536	10389331	NM_001005223	448850	zinc finger, HIT type 3	Znhit3	0.889	-2.436	0.0440283	0.184892
16537	10466000	NM_028411	72982	transmembrane protein 138	Tmem138	0.889	-1.206	0.266029	0.54117
16538	10404038	NM_178204	319149	histone cluster 1, H3d	Hist1h3d	0.889	-1.627	0.146435	0.388184
16539	10524889	NM_001114545	333050	kinase suppressor of ras 2	Ksr2	0.889	-1.594	0.153797	0.398319
16540	10550998	BC100485	545936	predicted gene, EG545936	EG545936	0.889	-1.381	0.208641	0.47344
16541	10581729	NM_007916	13680	DEAD (Asp-Glu-Ala-Asp) box pol	Ddx19a	0.889	-1.941	0.0921234	0.294194
16542	10582649	NM_171824	209966	piggyBac transposable element	Pgbd5	0.889	-0.882	0.406142	0.670739
16543	10553199	U96411	18419	otogelin	Otog	0.889	-2.024	0.0814359	0.272449
16544	10347639	NM_133708	69080	GDP-mannose pyrophosphorylase	Gmppa	0.889	-2.381	0.0477665	0.194851
16545	10598493	NM_013892	30052	proprotein convertase subtilis	Pcsk1n	0.889	-2.912	0.021866	0.116321
16546	10386033	NM_001029988	245827	FAT tumor suppressor homolog 2	Fat2	0.889	-1.288	0.23758	0.509988
16547	10517646	NM_012045	26971	phospholipase A2, group IIF	Pla2g2f	0.889	-1.883	0.100415	0.310087
16548	10381211	NM_013792	27419	alpha-N-acetylglucosaminidase	Naglu	0.889	-1.258	0.247742	0.520858
16549	10424705	XM_001481291	72665	RIKEN cDNA 2810039B14 gene	2810039B14Rik	0.889	-1.554	0.162887	0.411627
16550	10538887	ENSMUST00000103319	381776	predicted gene, EG381776	EG381776	0.889	-1.263	0.245736	0.518859
16551	10464612	NM_144532	73660	calcium binding protein 4	Cabp4	0.889	-1.028	0.337023	0.612719
16552	10437384	NM_031182	83383	transcription factor AP4	Tcfap4	0.889	-1.82	0.110337	0.328633
16553	10487340	NM_144818	215387	non-SMC condensin I complex, s	Ncaph	0.889	-2.681	0.0306166	0.14567
16554	10531529	NM_178854	231464	CCR4-NOT transcription complex	Cnot6l	0.889	-1.218	0.261492	0.536057
16555	10471058	NM_030137	78617	CSA-conditional, T cell activa	Cstad	0.888	-1.392	0.205448	0.469103
16556	10532580	XM_912851	74376	myosin XVIIIb	Myo18b	0.888	-1.366	0.212933	0.478759
16557	10501244	NM_028779	109674	adenosine monophosphate deamin	Ampd2	0.888	-1.806	0.112699	0.332576
16558	10447254	NM_011151	19043	protein phosphatase 1B, magnes	Ppm1b	0.888	-1.976	0.0874391	0.284608
16559	10544608					0.888	-1.306	0.231558	0.502418
16560	10384123	NM_026538	52513	DEAD (Asp-Glu-Ala-Asp) box pol	Ddx56	0.888	-2.234	0.0595062	0.224759
16561	10561527	NM_021895	60595	actinin alpha 4	Actn4	0.888	-2.978	0.0198667	0.109391
16562	10464775	NM_153388	225875	leucine rich repeat and fibron	Lrfn4	0.888	-1.539	0.16648	0.417266
16563	10545346	NM_027275	69956	pentatricopeptide repeat domai	Ptcd3	0.888	-2.103	0.0723647	0.253324
16564	10515692	ENSMUST00000075406	230676	cDNA sequence BC059842	BC059842	0.888	-1.208	0.265125	0.540213
16565	10359293	ENSMUST00000062159	72025	RIKEN cDNA 1600012P17 gene	1600012P17Rik	0.888	-1.259	0.247417	0.520777
16566	10585162	BC132633	235327	predicted gene, EG235327	EG235327	0.888	-1.266	0.244737	0.517875
				immunoglobin superfamily					

16567	10517731	NM_198610	230868	immunoglobulin superfamily, memb	Igsf21	0.888	-1.642	0.143429	0.384029
16568	10608018					0.888	-1.056	0.325179	0.601561
16569	10412100	NM_011945	26401	mitogen-activated protein kina	Map3k1	0.888	-2.167	0.0657572	0.239101
16570	10383765					0.888	-0.486	0.641061	0.837375
16571	10591092	NM_001080814	270120	FAT tumor suppressor homolog 3	Fat3	0.888	-1.705	0.130735	0.362906
16572	10507817	NM_007559	12164	bone morphogenetic protein 8b	Bmp8b	0.888	-2.391	0.0470578	0.192831
16573	10600210	NM_133987	102857	solute carrier family 6 (neuro	Slc6a8	0.888	-2.178	0.0646721	0.236862
16574	10429555	NM_025929	67038	RIKEN cDNA 2010109I03 gene	2010109I03Rik	0.888	-1.84	0.107136	0.322599
16575	10449071	NM_145999	214952	ras homolog gene family, membe	Rhot2	0.888	-2.856	0.0237117	0.122732
16576	10358999	NM_011273	19775	xenotropic and polytropic retr	Xpr1	0.888	-2.081	0.0748106	0.258759
16577	10420798	NM_026359	67750	RIKEN cDNA 4930578I06 gene	4930578I06Rik	0.888	-1.234	0.256059	0.530431
16578	10386460	NM_008819	18618	phosphatidylethanolamine N-met	Pemt	0.888	-1.142	0.289986	0.566261
16579	10445891	ENSMUST00000039366	211468	potassium voltage-gated channe	Kcnh8	0.888	-1.955	0.0902688	0.290067
16580	10367726	ENSMUST00000065124	76227	RIKEN cDNA 6530403G13 gene	6530403G13Rik	0.888	-1.271	0.243049	0.515966
16581	10411728	NM_021886	26886	centromere protein H	Cenph	0.888	-1.868	0.102679	0.314508
16582	10453738	NM_008058	14370	frizzled homolog 8 (Drosophila	Fzd8	0.888	-1.19	0.271886	0.546343
16583	10473576	NM_001011834	258103	olfactory receptor 1152	Olfr1152	0.888	-0.787	0.456556	0.712611
16584	10539316	NM_010692	16815	ladybird homeobox homolog 2 (D	Lbx2	0.888	-2.486	0.040876	0.176276
16585	10440077	NM_025599	66497	RIKEN cDNA 2610528E23 gene	2610528E23Rik	0.888	-3.058	0.0177181	0.100883
16586	10506989	NM_007983	14084	Fas-associated factor 1	Faf1	0.888	-2.945	0.0208477	0.113084
16587	10460114					0.888	-1.464	0.18525	0.442974
16588	10408709	NM_025965	107513	signal sequence receptor, alph	Ssr1	0.888	-2.746	0.0278581	0.136762
16589	10594426	NM_026507	68014	Zwilch, kinetochore associated	Zwilch	0.888	-1.473	0.182962	0.439824
16590	10508879	NM_175307	100342	RIKEN cDNA 4732473B16 gene	4732473B16Rik	0.888	-1.201	0.267657	0.542452
16591	10572449	NM_015816	50783	LSM4 homolog, U6 small nuclear	Lsm4	0.888	-1.738	0.124604	0.35351
16592	10477122	NM_176950	319579	defensin beta 20	Defb20	0.888	-1.605	0.15132	0.395197
16593	10481682	NM_177384	338348	tetratricopeptide repeat domai	Ttc16	0.888	-1.032	0.335592	0.611175
16594	10578959					0.888	-0.57	0.586193	0.803531
16595	10384212	NM_011709	22373	whey acidic protein	Wap	0.888	-2.112	0.0714291	0.251005
16596	10355954	BC034187	269211	cDNA sequence BC035947	BC035947	0.888	-1.861	0.103839	0.31682
16597	10526101	BC100444	69034	RIKEN cDNA 4930579G22 gene	4930579G22Rik	0.888	-1.844	0.106493	0.321808
16598	10557628	AK041042	654803	RIKEN cDNA B130055M24 gene	B130055M24Rik	0.888	-1.33	0.224057	0.494207
16599	10520419	NM_133907	100763	ubiquitin protein ligase E3C	Ube3c	0.888	-2.492	0.0405314	0.175358
16600	10579442	NM_053248	114479	solute carrier family 5 (sodiu	Slc5a5	0.888	-2.274	0.0560531	0.216314
16601	10430649	NM_144811	52609	chromobox homolog 7	Cbx7	0.888	-1.332	0.223425	0.493384
16602	10553027	NM_008051	14343	fucosyltransferase 1	Fut1	0.888	-1.61	0.150169	0.39328
16603	10385932	NM_029327	75530	LYR motif containing 7	Lyrm7	0.888	-1.657	0.140312	0.378815
16604	10590799	ENSMUST00000054878	77616	RIKEN cDNA C330006D17 gene	C330006D17Rik	0.888	-1.018	0.341394	0.616096
16605	10455374	NM_178749	269019	serine/threonine kinase 32A	Stk32a	0.888	-0.352	0.734628	0.886636
16606	10587616	NM_178738	244954	protease, serine, 35	Prss35	0.887	-1.151	0.286625	0.562228
16607	10568696	NM_001081331	71007	RIKEN cDNA 4933400E14 gene	4933400E14Rik	0.887	-1.941	0.0921791	0.294263
16608	10430447	BC068203	27660	RIKEN cDNA 1700088E04 gene	1700088E04Rik	0.887	-1.629	0.146016	0.387715
16609	10454546	NM_011946	26405	mitogen-activated protein kina	Map3k2	0.887	-0.892	0.401363	0.666762
16610	10434741					0.887	-2.389	0.0472026	0.193141
16611	10351588	NM_027893	71740	poliovirus receptor-related 4	Pvrl4	0.887	-1.803	0.113198	0.333342
16612	10453634	ENSMUST00000097689	100038439	predicted gene, ENSMUSG0000007	ENSMUSG00000073646	0.887	-0.998	0.350707	0.624059
16613	10533145	NM_145853	252972	two pore channel 1	Tpcn1	0.887	-1.44	0.191744	0.451028
16614	10498180	NM_133231	170767	regulatory factor X-associated	Rfxap	0.887	-2.492	0.0405002	0.175263
16615	10406795	NM_177266	320806	G elongation factor, mitochond	Gfm2	0.887	-2.718	0.0290077	0.140095

16616	10398562	NM_027149	69641	WD repeat domain 20a	Wdr20a	0.887	-0.999	0.34999	0.623541
16617	10362426					0.887	-0.722	0.49295	0.738744
16618	10459375	NM_016792	53382	thioredoxin-like 1	Txnl1	0.887	-3.093	0.0168503	0.0977778
16619	10532463	NM_001025561	56361	pseudouridine synthase 1	Pus1	0.887	-2.123	0.0702352	0.248316
16620	10473250	XR_032818	433550	similar to mitochondrial ribos	LOC433550	0.887	-2.342	0.0506612	0.202722
16621	10372102					0.887	-1.631	0.145722	0.38722
16622	10442030	XR_032712	665085	similar to cyclin B	LOC665085	0.887	-2.256	0.057625	0.220051
16623	10606178	NR_001463	213742	inactive X specific transcript	Xist	0.887	-0.223	0.829899	0.931588
16624	10461728	BC089619	240549	predicted gene, EG240549	EG240549	0.887	-1.338	0.221658	0.49117
16625	10490569	NM_010611	16536	potassium voltage-gated channe	Kcnq2	0.887	-1.091	0.310517	0.587103
16626	10587782	NM_009576	22774	zinc finger protein of the cer	Zic4	0.887	-1.827	0.10918	0.326429
16627	10374181	XM_001001271	677190	similar to SMT3 suppressor of	LOC677190	0.887	-2.078	0.0750939	0.259103
16628	10417000					0.887	-2.561	0.036575	0.163532
16629	10368473					0.887	-1.235	0.255589	0.529926
16630	10514706	ENSMUST00000051043	242574	RIKEN cDNA C130073F10 gene	C130073F10Rik	0.887	-2.61	0.0340124	0.156
16631	10448032	ENSMUST00000097391	100038481	predicted gene, ENSMUSG0000007	ENSMUSG00000073453	0.887	-1.816	0.111028	0.329804
16632	10574880	NM_024445	72236	translin-associated factor X (	Tsnaxip1	0.887	-0.917	0.388977	0.657489
16633	10461277	NM_008060	14376	alpha glucosidase 2 alpha neut	Ganab	0.887	-1.99	0.0856752	0.280986
16634	10509073	NM_001085509	242702	myomesin family, member 3	Myom3	0.887	-0.855	0.420188	0.682474
16635	10554375	NM_013659	20352	sema domain, immunoglobulin do	Sema4b	0.887	-2.126	0.0699196	0.247718
16636	10590263					0.887	-1.313	0.229377	0.500403
16637	10353524	NM_001081079	70155	opioid growth factor receptor-	Ogfrl1	0.887	-2.126	0.0699633	0.247831
16638	10514317	NM_008336	15974	interferon alpha B	Ifnab	0.887	-0.874	0.410041	0.674386
16639	10554240	NM_020583	57444	interferon-stimulated protein	Isg20	0.887	-1.628	0.146287	0.388044
16640	10390850	NM_023256	66809	keratin 20	Krt20	0.887	-0.977	0.360366	0.632213
16641	10564692	NM_023331	67308	mitochondrial ribosomal protei	Mrpl46	0.887	-2.264	0.0569157	0.21817
16642	10570280	NM_010172	14068	coagulation factor VII	F7	0.887	-1.026	0.337981	0.613519
16643	10439303	NM_013803	12374	calcium-sensing receptor	Casr	0.887	-1.377	0.209859	0.47503
16644	10452030	NM_025836	66905	mannose-6-phosphate receptor b	M6prbp1	0.887	-2.103	0.0723446	0.253324
16645	10405448	NM_011392	20505	solute carrier family 34 (sodi	Slc34a1	0.887	-1.277	0.241081	0.513985
16646	10593492	ENSMUST00000038822	244871	zinc finger CCCH type containi	Zc3h12c	0.887	-2.014	0.0827112	0.275322
16647	10364571	NM_175450	216156	WD repeat domain 18	Wdr18	0.887	-1.931	0.0936273	0.296785
16648	10397907	NM_001039049	75483	cytochrome c oxidase, subunit	Cox8c	0.887	-0.606	0.563066	0.789853
16649	10345926	BC002254	78896	RIKEN cDNA 1500015O10 gene	1500015O10Rik	0.886	-2.941	0.020967	0.11338
16650	10435712	BC131959	12519	CD80 antigen	Cd80	0.886	-1.014	0.343263	0.617382
16651	10569071	NM_008284	15461	Harvey rat sarcoma virus oncog	Hras1	0.886	-2.271	0.0562922	0.216807
16652	10576657					0.886	-1.2	0.268213	0.542786
16653	10445507	ENSMUST00000095262	224813	gene model 88, (NCBI)	Gm88	0.886	-1.593	0.15393	0.398468
16654	10465215	NM_020491	56390	Sjogren's syndrome/scleroderma	Sssca1	0.886	-2.334	0.0512769	0.204543
16655	10469081	ENSMUST00000100443	100038463	predicted gene, ENSMUSG0000007	ENSMUSG00000075547	0.886	-1.194	0.270428	0.545253
16656	10564565	XR_033989	665570	similar to LOC654472 protein	LOC665570	0.886	-1.504	0.174949	0.42804
16657	10588238	NM_001034892	434510	predicted gene, EG434510	EG434510	0.886	-1.03	0.336262	0.611869
16658	10579341	BC051227	234384	cDNA sequence BC051227	BC051227	0.886	-2.381	0.0477883	0.194851
16659	10481383	NM_001008498	71820	WD repeat domain 34	Wdr34	0.886	-1.75	0.122321	0.349649
16660	10514374	XR_030634	664886	hypothetical LOC664886	LOC664886	0.886	-0.99	0.354248	0.626867
16661	10553811					0.886	-1.941	0.0922145	0.294263
16662	10475456	NM_001099297	99439	dual oxidase 1	Duox1	0.886	-1.08	0.314799	0.59176
16663	10544497					0.886	-1.211	0.264065	0.539055
16664	10433311	NM_029657	17237	mahogunin, ring finger 1	Mgrn1	0.886	-2.091	0.073687	0.256552
16665	10528238	NM_172992	68770	putative homeodomain transcrip	Phtf2	0.886	-2.306	0.0534466	0.209739
16666	10520940	NM_001081407	665270	phospholipase B1	Plb1	0.886	-0.719	0.494978	0.739948
16667	10432571	AK010113	70281	RIKEN cDNA 2310068J16 gene	2310068J16Rik	0.886	-2.208	0.0618535	0.229847
				RIKEN cDNA A730017L22					

16668	10487785	AK166222	613258	RIKEN cDNA A730017L22 gene	A730017L22Rik	0.886	-0.982	0.357761	0.630135
16669	10442816	NM_029624	76483	lipase maturation factor 1	Lmf1	0.886	-2.076	0.0753461	0.259592
16670	10573610	NM_001037922	624855	predicted gene, EG624855	EG624855	0.886	-1.395	0.204485	0.467724
16671	10392856	NM_025400	66176	NAT9	Nat9	0.886	-1.915	0.0958134	0.301049
16672	10450374	L78788	110956	DNA segment, Chr 17, human D6S	D17H6S56E-5	0.886	-2.665	0.0313754	0.148147
16673	10376320	NM_175001	216767	mitochondrial ribosomal protei	Mrpl22	0.886	-1.631	0.145708	0.38722
16674	10561456	NM_026042	67224	mediator complex subunit 29	Med29	0.886	-1.247	0.251393	0.525502
16675	10566138	NM_020289	257926	olfactory receptor 544	Olfr544	0.886	-1.364	0.213573	0.479689
16676	10607910	NM_010832	17692	male-specific lethal-3 homolog	Msl31	0.886	-2.464	0.0422397	0.179883
16677	10456587	NM_027741	71263	Maestro	Mro	0.886	-0.6	0.566764	0.792465
16678	10539581					0.886	-1.851	0.105391	0.319942
16679	10565528					0.886	-1.299	0.234075	0.50534
16680	10358188	ENSMUST00000086395	383563	G protein-coupled receptor 25	Gpr25	0.886	-1.391	0.20549	0.469108
16681	10425630	BC048460	66346	RIKEN cDNA 1700029P11 gene	1700029P11Rik	0.886	-1.55	0.163721	0.412946
16682	10481380	ENSMUST00000047607	70319	RIKEN cDNA 2600006K01 gene	2600006K01Rik	0.886	-1.123	0.297419	0.573687
16683	10507284	XR_032826	631400	similar to H3 histone, family	LOC631400	0.886	-1.095	0.308906	0.58547
16684	10499777	NM_145540	229543	integrator complex subunit 3	Ints3	0.886	-2.717	0.0290749	0.140292
16685	10405757	NM_028079	72061	RIKEN cDNA 2010111I01 gene	2010111I01Rik	0.886	-1.175	0.277212	0.552231
16686	10585390	NM_025540	66402	sarcolipin	Sln	0.886	-1.356	0.21592	0.483011
16687	10580510	NM_021390	58198	sal-like 1 (Drosophila)	Sall1	0.886	-2.003	0.084075	0.278075
16688	10548735	NM_130447	70686	dual specificity phosphatase 1	Dusp16	0.886	-2.228	0.0600206	0.225894
16689	10432711	NM_008474	16680	keratin 84	Krt84	0.886	-1.108	0.303606	0.579844
16690	10479596	NM_001048148	229007	zinc finger, CCCH-type with G	Zgpat	0.886	-2.046	0.0787665	0.267154
16691	10526923	BC019557	67604	RIKEN cDNA 1110007L15 gene	1110007L15Rik	0.886	-1.3	0.233763	0.505106
16692	10389639	NM_080420	76113	lactoperoxidase	Lpo	0.886	-1.056	0.32519	0.601561
16693	10413979	XM_985917	268729	gene model 626, (NCBI)	Gm626	0.886	-0.907	0.393785	0.661649
16694	10504916					0.886	-1.654	0.140743	0.379507
16695	10606595					0.885	-0.57	0.585937	0.803231
16696	10569198	AK149132	100126795	hypothetical LOC100126795	LOC100126795	0.885	-1.84	0.107047	0.322599
16697	10516894	NM_133878	100088	regulator of chromosome conden	Rcc1	0.885	-2.848	0.0239922	0.123827
16698	10459496	NM_178793	320924	collagen and calcium binding E	Ccbe1	0.885	-1.685	0.134589	0.369832
16699	10470950	NM_007931	13804	endonuclease G	Endog	0.885	-3.304	0.0125024	0.0790998
16700	10598289	ENSMUST00000065293	78185	RIKEN cDNA 4930524L23 gene	4930524L23Rik	0.885	-0.785	0.457397	0.713005
16701	10580300	NM_019652	56495	arsA (bacterial) arsenite tran	Asna1	0.885	-2.562	0.0365116	0.163455
16702	10375730					0.885	-0.712	0.498726	0.742429
16703	10584526	NM_146854	258853	olfactory receptor 982	Olfr982	0.885	-1.089	0.31113	0.587683
16704	10412417	ENSMUST00000099148	67304	RIKEN cDNA 3110070M22 gene	3110070M22Rik	0.885	-1.326	0.225214	0.49531
16705	10481312	NM_027283	69987	RIKEN cDNA 1700026L06 gene	1700026L06Rik	0.885	-1.737	0.124769	0.353539
16706	10378088	NM_016776	18432	MYB binding protein (P160) 1a	Mybbp1a	0.885	-1.977	0.0873134	0.284457
16707	10354411					0.885	-1.358	0.215321	0.482386
16708	10356710	ENSMUST00000097638	100037260	RIKEN cDNA 9430060I03 gene	9430060I03Rik	0.885	-1.244	0.252458	0.526583
16709	10380411	NM_053161	94064	mitochondrial ribosomal protei	Mrpl27	0.885	-2.055	0.0777398	0.265118
16710	10364494	NM_031380	83554	follistatin-like 3	Fstl3	0.885	-1.272	0.242972	0.51587
16711	10407431	NM_031250	83428	urocortin 3	Ucn3	0.885	-1.2	0.268027	0.542786
16712	10360538					0.885	-0.77	0.465845	0.719391
16713	10596940	NM_028944	74443	RIKEN cDNA 4933406E20 gene	4933406E20Rik	0.885	-1.297	0.234606	0.505768
16714	10353989					0.885	-1.609	0.150454	0.393664
16715	10554150	NM_177740	244058	RGM domain family, member A	Rgma	0.885	-1.579	0.157191	0.40365
16716	10368886	ENSMUST00000105502	56484	forkhead box O3a	Foxo3a	0.885	-1.409	0.200592	0.462553
16717	10413615	NM_018746	16427	inter alpha-trypsin inhibitor,	Itih4	0.885	-1.28	0.24024	0.513302
16718	10528911					0.885	-2.401	0.0464083	0.191502
16719	10487700	NM_197945	241638	ProSAPiP1 protein	RP23-100C5.8	0.885	-0.984	0.3568	0.629197
16720	10551542	NM_015796	50760	F-box protein 17	Fbxo17	0.885	-2.286	0.0550273	0.214036
16721	10559146	NM_029426	75770	BR serine/threonine kinase 2	Brsk2	0.885	-1.461	0.186236	0.444444
16722	10436169	NM_028680	73916	intraflagellar transport 57 ho	Ift57	0.885	-3.109	0.0164579	0.0962883

16722	10436169	NM_028680	73916	intraflagellar transport 57 ho	Ift57	0.885	-3.109	0.0164379	0.0962885
16723	10582821					0.885	-0.863	0.415923	0.679095
16724	10480649	BC117777	67859	RIKEN cDNA 2310002J15 gene	2310002J15Rik	0.885	-1.219	0.261067	0.535632
16725	10596303	NM_019807	56318	acid phosphatase, prostate	Acpp	0.885	-2.423	0.0448731	0.187435
16726	10451248	NM_028751	74094	tight junction associated prot	Tjap1	0.885	-1.792	0.114927	0.337218
16727	10375027	XR_033651	669207	similar to hCG2016250	LOC669207	0.885	-1.588	0.155098	0.400513
16728	10575249	NM_175646	234723	thioredoxin-like 4B	Txnl4b	0.885	-2.116	0.0709545	0.250127
16729	10558866	NM_007878	13491	dopamine receptor 4	Drd4	0.885	-1.329	0.224293	0.494263
16730	10420935	NM_007940	13850	epoxide hydrolase 2, cytoplasm	Ephx2	0.885	-0.757	0.472865	0.724458
16731	10554960	NM_021427	58238	RIKEN cDNA A830059I20 gene	A830059I20Rik	0.885	-2.628	0.0331394	0.153511
16732	10383932	NM_030228	78926	growth arrest-specific 2 like	Gas2l1	0.885	-2.033	0.0804034	0.270493
16733	10598111	NM_001033326	236082	dehydrogenase/reductase (SDR f	Dhrsx	0.885	-1.504	0.174935	0.42804
16734	10510908					0.885	-0.639	0.542703	0.775122
16735	10500976	NM_145541	109905	RAS-related protein-1a	Rap1a	0.885	-1.957	0.0900033	0.289452
16736	10471778	NM_001005569	236509	olfactory receptor 366	Olfr366	0.885	-1.221	0.260442	0.53495
16737	10560217	NM_027883	71723	DEAH (Asp-Glu-Ala-His) box pol	Dhx34	0.885	-2.671	0.0310916	0.147201
16738	10595657	AF529169	209743	cDNA sequence AF529169	AF529169	0.884	-1.709	0.129933	0.361535
16739	10510053	ENSMUST00000052458	242735	leucine rich repeat containing	Lrrc38	0.884	-1.779	0.11724	0.341261
16740	10373740	NM_178149	216505	phosphoinositide-3-kinase inte	Pik3ip1	0.884	-1.49	0.178489	0.433342
16741	10530733	NM_007715	12753	circadian locomoter output cyc	Clock	0.884	-2.424	0.0448364	0.187319
16742	10581917	BC100402	234740	RIKEN cDNA 4932417I16 gene	4932417I16Rik	0.884	-1.355	0.216474	0.483687
16743	10549708	ENSMUST00000013235	78052	transmembrane protein 190	Tmem190	0.884	-0.897	0.398519	0.664744
16744	10402650	NM_026048	67236	RIKEN cDNA 2810452K22 gene	2810452K22Rik	0.884	-2.415	0.045395	0.188572
16745	10345552	XR_032810	100046859	hypothetical protein LOC100046	LOC100046859	0.884	-1.279	0.240497	0.513583
16746	10515363	NM_025962	67096	methylmalonic aciduria cblC ty	Mmachc	0.884	-2.127	0.0697822	0.247552
16747	10416082	NM_029979	66854	tripartite motif-containing 35	Trim35	0.884	-2.282	0.0554258	0.214756
16748	10417605	NM_010210	14198	fragile histidine triad gene	Fhit	0.884	-1.296	0.234955	0.506303
16749	10365204	ENSMUST00000099432	100038681	predicted gene, ENSMUSG0000007	ENSMUSG00000074855	0.884	-0.493	0.636691	0.834887
16750	10385826	NM_183173	237761	ankyrin repeat domain 43	Ankrd43	0.884	-1.63	0.145821	0.387343
16751	10585097	BC011344	434402	predicted gene, EG434402	EG434402	0.884	-1.838	0.107448	0.323077
16752	10568480	ENSMUST00000035253	67872	non-SMC element 4 homolog A (S	Nsmce4a	0.884	-2.939	0.0210201	0.113467
16753	10437940					0.884	-1.221	0.260558	0.535075
16754	10527115	NM_172725	231855	RIKEN cDNA C330006K01 gene	C330006K01Rik	0.884	-1.906	0.0971476	0.303538
16755	10406898	NM_027592	108143	TAF9 RNA polymerase II, TATA b	Taf9	0.884	-2.99	0.0195444	0.108095
16756	10551905	ENSMUST00000098579	54631	nephrosis 1 homolog, nephrin (	Nphs1	0.884	-2.06	0.0772299	0.263762
16757	10556295	XR_033117	668368	predicted gene, EG668368	EG668368	0.884	-1.317	0.228085	0.499133
16758	10471419	NM_194335	71254	nuclear apoptosis inducing fac	Naif1	0.884	-2.566	0.0362888	0.162734
16759	10447521	NM_146074	224481	transcription factor B1, mitoc	Tfb1m	0.884	-2.608	0.0341167	0.156257
16760	10545177					0.884	-1.135	0.292553	0.568731
16761	10423503	XM_890363	625796	predicted gene, EG625796	EG625796	0.884	-1.061	0.323129	0.59983
16762	10464285	XR_031070	100044901	similar to ribosomal protein L	LOC100044901	0.884	-1.645	0.14279	0.382897
16763	10348240	BC115669	73234	RIKEN cDNA 3110079O15 gene	3110079O15Rik	0.884	-1.152	0.286011	0.561602
16764	10555059	NM_001012434	233529	potassium channel tetramerisat	Kctd14	0.884	-0.767	0.467677	0.720331
16765	10401511	NM_001033334	627191	transmembrane protein 90a	Tmem90a	0.884	-0.748	0.478173	0.728737
16766	10352798	NM_010600	16510	potassium voltage-gated channe	Kcnh1	0.884	-2.165	0.0659354	0.239542
16767	10426643	AK157795	100049164	predicted gene, ENSMUSG0000007	ENSMUSG00000075423	0.884	-1.522	0.170545	0.422248
16768	10353934	NM_146107	226977	ARP1 actin-related protein 1 h	Actr1b	0.884	-2.09	0.0738158	0.256746
16769	10567739	ENSMUST00000061823	71208	RIKEN cDNA 4933440M02 gene	4933440M02Rik	0.884	-1.099	0.306934	0.583565
16770	10395158	ENSMUST00000101508	432645	RIKEN cDNA 6030469F06 gene	6030469F06Rik	0.884	-1.043	0.330467	0.606651
16771	10487453	NM_016902	53885	nephronophthisis 1 (juvenile)	Nphp1	0.884	-2.972	0.0200304	0.109926

16772	10589798					0.884	-1.455	0.187799	0.446159
16773	10535725	NM_028774	74132	ring finger protein (C3H2C3 ty	Rnf6	0.884	-2.039	0.0795946	0.268799
16774	10540118	NM_026309	67678	LSM3 homolog, U6 small nuclear	Lsm3	0.884	-2.691	0.030166	0.144371
16775	10432152	NM_146281	258278	olfactory receptor 284	Olfr284	0.884	-1.147	0.28816	0.563996
16776	10408197	NM_178197	319182	histone cluster 1, H2bh	Hist1h2bh	0.884	-2.507	0.039626	0.172895
16777	10433633	NM_181860	239719	MKL/myocardin-like 2	Mkl2	0.884	-1.819	0.110453	0.328752
16778	10496864	ENSMUST00000092878	381483	predicted gene, EG381483	EG381483	0.884	-1.973	0.0878221	0.285415
16779	10594404	NM_016769	17127	MAD homolog 3 (Drosophila)	Smad3	0.884	-1.76	0.12061	0.347059
16780	10539042	NM_009088	20019	RNA polymerase 1-4	Rpo1-4	0.884	-2.334	0.0512859	0.204543
16781	10426812	NM_010271	14555	glycerol-3-phosphate dehydroge	Gpd1	0.884	-1.134	0.293025	0.56904
16782	10495218	NM_007441	11694	aristaless 3	Alx3	0.883	-1.173	0.27822	0.553196
16783	10528457	NM_011959	26429	origin recognition complex, su	Orc5l	0.883	-2.24	0.0589389	0.223414
16784	10432675	ENSMUST00000089252	619313	RIKEN cDNA I730030J21 gene	I730030J21Rik	0.883	-0.93	0.38253	0.65196
16785	10596433	NM_174846	235582	glycerate kinase	Glyctk	0.883	-2.282	0.055388	0.214688
16786	10596747	NM_011349	20350	sema domain, immunoglobulin do	Sema3f	0.883	-2.943	0.0208953	0.113256
16787	10430846	NM_025987	67130	NADH dehydrogenase (ubiquinone	Ndufa6	0.883	-1.863	0.103562	0.316379
16788	10589076	NM_020520	57279	solute carrier family 25 (mito	Slc25a20	0.883	-1.736	0.124941	0.353886
16789	10574765	NM_001033371	270091	leucine rich repeat containing	Lrrc36	0.883	-1.764	0.119762	0.346027
16790	10392904	NM_176847	16470	Usher syndrome 1G homolog (hum	Ush1g	0.883	-1.513	0.172746	0.425061
16791	10507137	NM_026018	67182	PDZK1 interacting protein 1	Pdzk1ip1	0.883	-0.86	0.417567	0.680361
16792	10576967	ENSMUST00000040608	74027	RIKEN cDNA 3930402G23 gene	3930402G23Rik	0.883	-1.717	0.128343	0.359238
16793	10415832	NM_001039125	654465	predicted gene, EG654465	EG654465	0.883	-0.99	0.354276	0.626867
16794	10593918	NM_176831	66812	phosphopantothenoylcysteine de	Ppcdc	0.883	-2.693	0.0300838	0.144075
16795	10582823	NM_172762	52202	RNA binding motif protein 34	Rbm34	0.883	-3.37	0.0114095	0.0742122
16796	10508454	NM_133889	100383	BSD domain containing 1	Bsdc1	0.883	-1.929	0.0938188	0.297184
16797	10467115	NM_024204	52024	ankyrin repeat domain 22	Ankrd22	0.883	-0.614	0.557855	0.785788
16798	10359697	NM_008510	16963	chemokine (C motif) ligand 1	Xcl1	0.883	-1.692	0.133135	0.367016
16799	10601857	NM_009750	12070	nerve growth factor receptor (	Ngfrap1	0.883	-2.785	0.0262908	0.131448
16800	10405287	NM_025933	67044	HIG1 domain family, member 2A	Higd2a	0.883	-1.977	0.087345	0.284457
16801	10385761	NM_009458	22210	ubiquitin-conjugating enzyme E	Ube2b	0.883	-2.938	0.0210555	0.113586
16802	10455048	NM_053126	93872	protocadherin beta 1	Pcdhb1	0.883	-1.132	0.29369	0.569705
16803	10386115					0.883	-1.913	0.0961698	0.301828
16804	10430834	NM_008669	17939	N-acetyl galactosaminidase, al	Naga	0.883	-1.774	0.11813	0.343095
16805	10528615	ENSMUST00000101490	100038444	predicted gene, ENSMUSG0000007	ENSMUSG00000073129	0.883	-1.133	0.293388	0.569485
16806	10497505	NM_138666	192167	neuroligin 1	Nlgn1	0.883	-0.699	0.506671	0.748536
16807	10517616	BC132477	75718	RIKEN cDNA 4931403E03 gene	4931403E03Rik	0.883	-1.353	0.216846	0.484361
16808	10484925	XM_205095	279067	similar to acidic ribosomal ph	LOC279067	0.883	-1.93	0.0937181	0.29698
16809	10458349	NM_025291	24068	steroid receptor RNA activator	Sra1	0.883	-1.887	0.0999516	0.309064
16810	10510882	ENSMUST00000071251	230971	multiple EGF-like-domains 6	Megf6	0.883	-1.565	0.160268	0.407592
16811	10520040	ENSMUST00000084713	100038682	predicted gene, ENSMUSG0000007	ENSMUSG00000073152	0.883	-1.357	0.21561	0.482777
16812	10472893	NM_023057	65964	RIKEN cDNA B230120H23 gene	B230120H23Rik	0.883	-1.144	0.289328	0.565289
16813	10523750	BC023132	100662	RIKEN cDNA D930016D06 gene	D930016D06Rik	0.883	-2.547	0.0373119	0.166124
16814	10580467	ENSMUST00000098528	100038706	predicted gene, ENSMUSG0000007	ENSMUSG00000074176	0.883	-1.533	0.167809	0.419086
16815	10473737	NM_019758	56428	mitochondrial carrier homolog	Mtch2	0.883	-2.474	0.0415928	0.177907
16816	10547056	NM_144805	94346	transmembrane protein 40	Tmem40	0.883	-1.682	0.135275	0.370739
16817	10415090	AK006648	239096	cadherin-like 24	Cdh24	0.883	-1.118	0.299359	0.575422
16818	10438515	AK149512	100038507	predicted gene, ENSMUSG0000007	ENSMUSG00000075326	0.883	-1.822	0.11002	0.328028

16819	10398025	BC063325	74069	serine (or cysteine) peptidase	Serpina3a	0.883	-0.803	0.447616	0.705227
16820	10574595					0.883	-1.938	0.0926111	0.294729
16821	10466410	NM_177420	107272	phosphoserine aminotransferase	Psat1	0.883	-2.42	0.0450579	0.187761
16822	10396372	NM_008612	17420	menage a trois 1	Mnat1	0.882	-3.083	0.0170964	0.0987125
16823	10387651	NM_175368	108803	RIKEN cDNA 4933402P03 gene	4933402P03Rik	0.882	-1.758	0.120905	0.347273
16824	10429908	NM_013481	12181	block of proliferation 1	Bop1	0.882	-1.787	0.11576	0.338351
16825	10597871	NM_019814	56295	HIG1 domain family, member 1A	Higd1a	0.882	-1.079	0.315222	0.592133
16826	10458760	XR_032774	225457	hypothetical gene supported by	LOC225457	0.882	-1.144	0.289247	0.565183
16827	10442375	NM_001077633	620253	demilune cell and parotid prot	Dcpp3	0.882	-0.428	0.681192	0.858913
16828	10500469	NM_001039376	83679	phosphodiesterase 4D interacti	Pde4dip	0.882	-2.785	0.0263104	0.131515
16829	10547153	NM_009662	11689	arachidonate 5-lipoxygenase	Alox5	0.882	-1.047	0.328854	0.605213
16830	10605784					0.882	-1.843	0.106626	0.32207
16831	10459835					0.882	-1.646	0.142467	0.38247
16832	10377938	NM_007933	13808	enolase 3, beta muscle	Eno3	0.882	-2.104	0.0723067	0.253289
16833	10460312	NM_026373	52004	CDK2-associated protein 2	Cdk2ap2	0.882	-2.814	0.0252049	0.128059
16834	10436182	NM_010581	16423	CD47 antigen (Rh-related antig	Cd47	0.882	-1.626	0.146747	0.388752
16835	10407120	BC084675	20091	ribosomal protein S3a	Rps3a	0.882	-1.92	0.0950633	0.299747
16836	10401166	NM_029988	110417	phosphatidylinositol glycan an	Pigh	0.882	-2.246	0.0584339	0.222137
16837	10553403	NM_016865	53415	HIV-1 tat interactive protein	Htatip2	0.882	-1.174	0.277695	0.552827
16838	10435193	NM_172823	239833	leishmanolysin-like (metallope	Lmln	0.882	-2.008	0.0834176	0.276541
16839	10491066	ENSMUST00000099182	100045726	hypothetical protein LOC100045	LOC100045726	0.882	-1.638	0.14414	0.385253
16840	10578685					0.882	-1.327	0.224961	0.494961
16841	10414288	NM_025959	67089	proteasome (prosome, macropain	Psmc6	0.882	-2.609	0.0340779	0.156165
16842	10462330	NM_028922	74411	phosphatidic acid phosphatase	Ppapdc2	0.882	-2.728	0.028606	0.138854
16843	10554704	NM_023403	67943	mesoderm development candidate	Mesdc2	0.882	-2.872	0.0231831	0.120967
16844	10499939	XM_001478521	631101	hypothetical LOC631101	LOC631101	0.882	-1.535	0.167371	0.418358
16845	10519711					0.882	-1.285	0.238528	0.511194
16846	10584194	NM_026130	67398	signal recognition particle re	Srpr	0.882	-2.157	0.0667975	0.24144
16847	10604111	NM_001025084	385343	reproductive homeobox 1	Rhox1	0.882	-1.228	0.257897	0.531958
16848	10552173	NM_028120	72140	coiled-coil domain containing	Ccdc123	0.882	-2.315	0.0526889	0.207807
16849	10589541	NM_010628	16578	kinesin family member 9	Kif9	0.882	-1.673	0.13704	0.373617
16850	10472501	NM_172856	241447	LAG1 homolog, ceramide synthas	Lass6	0.882	-2.757	0.0274153	0.135184
16851	10592891	NM_153537	102693	pleckstrin homology-like domai	Phldb1	0.882	-2.801	0.0256994	0.129873
16852	10376929	BC115504	67510	RIKEN cDNA 1810036I24 gene	1810036I24Rik	0.882	-2.26	0.0572172	0.218889
16853	10517421	NM_026383	52830	proline-rich nuclear receptor	Pnrc2	0.882	-2.64	0.0325447	0.151569
16854	10407390	NM_001077363	19205	polypyrimidine tract binding p	Ptbp1	0.882	-2.719	0.0289703	0.14001
16855	10439835					0.882	-1.152	0.286157	0.561637
16856	10411915	NM_172807	238831	peptidylprolyl isomerase domai	Ppwd1	0.882	-2.034	0.080189	0.270159
16857	10501827	ENSMUST00000050571	319738	RIKEN cDNA A730020M07 gene	A730020M07Rik	0.882	-1.495	0.17737	0.431765
16858	10593050	NM_008348	16154	interleukin 10 receptor, alpha	Il10ra	0.882	-1.264	0.245472	0.518491
16859	10441718	NM_016694	50873	parkin	Park2	0.882	-1.686	0.134304	0.369418
16860	10587038	NM_025890	66991	RIKEN cDNA 2410004A20 gene	2410004A20Rik	0.882	-2.472	0.0417316	0.178221
16861	10440572	NM_001081068	78913	zinc finger protein 294	Zfp294	0.881	-2.105	0.0721344	0.252727
16862	10487619	ENSMUST00000086387	100038393	predicted gene, ENSMUSG0000006	ENSMUSG00000066864	0.881	-1.058	0.323993	0.600552
16863	10381872	NM_001112705	24086	tousled-like kinase 2 (Arabido	Tlk2	0.881	-2.285	0.0551414	0.214227
16864	10575867	NM_019966	56690	malonyl-CoA decarboxylase	Mlycd	0.881	-1.66	0.139553	0.37791
16865	10429402	NM_173365	239530	G protein-coupled receptor 20	Gpr20	0.881	-0.999	0.349912	0.623456
16866	10438730	NM_009215	20604	somatostatin	Sst	0.881	-1.496	0.177079	0.431359
16867	10419073	NM_145928	52588	tetraspanin 14	Tspan14	0.881	-1.374	0.210613	0.476075
16868	10458391	NM_173383	213236	dead end homolog 1 (zebrafish)	Dnd1	0.881	-2.407	0.0459889	0.19018
16869	10557439	NM_029339	75565	coiled-coil domain containing	Ccdc101	0.881	-2.279	0.0556415	0.215355
16870	10418898	NM_008919	19065	pancreatic polypeptide recepto	Ppyr1	0.881	-0.788	0.455565	0.711828

16871	10405693	NM_029653	69635	death associated protein kinas	Dapk1	0.881	-3.109	0.0164692	0.0962891
16872	10607539	NM_172307	270669	membrane-bound transcription f	Mbtps2	0.881	-2.742	0.0280012	0.137267
16873	10372831	ENSMUST00000064107	74694	TBC1 domain family, member 30	Tbc1d30	0.881	-1.19	0.271712	0.546284
16874	10576946	NM_176953	319583	ligase IV, DNA, ATP-dependent	Lig4	0.881	-2.284	0.0552355	0.214463
16875	10560094					0.881	-0.985	0.356535	0.629004
16876	10394283	BC067010	69709	RIKEN cDNA 2410017P09 gene	2410017P09Rik	0.881	-1.915	0.0958361	0.301049
16877	10433971	NM_001033338	239731	RIMS binding protein 3	Rimbp3	0.881	-1.448	0.189618	0.448114
16878	10546337	XR_034314	665716	similar to ribosomal protein L	LOC665716	0.881	-1.896	0.0986118	0.30667
16879	10385511	NM_011190	19188	proteasome (prosome, macropain	Psme2	0.881	-2.238	0.0591794	0.224005
16880	10451495	NM_146078	224826	ubiquitin protein ligase E3 co	Ubr2	0.881	-1.692	0.133278	0.367315
16881	10536743	ENSMUST00000060288	76224	RIKEN cDNA 6530409C15 gene	6530409C15Rik	0.881	-2.869	0.0232702	0.121189
16882	10576305	NM_001037878	66855	transcription factor 25 (basic	Tcf25	0.881	-2.952	0.0206245	0.112248
16883	10487943	ENSMUST00000099339	100038551	predicted gene, ENSMUSG0000007	ENSMUSG00000074787	0.881	-0.843	0.426375	0.687967
16884	10442625	NM_008340	16005	insulin-like growth factor bin	Igfals	0.881	-1.584	0.155969	0.401839
16885	10552743	NM_010215	14204	interleukin 4 induced 1	Il4i1	0.881	-1.689	0.133907	0.368806
16886	10470543	BC070440	241289	gene model 347, (NCBI)	Gm347	0.881	-1.767	0.11938	0.345588
16887	10382083	NM_029467	75870	testicular cell adhesion molec	Tcam1	0.881	-1.011	0.344632	0.61884
16888	10450265	NM_019442	54402	serine/threonine kinase 19	Stk19	0.881	-2.234	0.0595222	0.224779
16889	10370483	NM_010925	18114	ribosomal RNA processing 1 hom	Rrp1	0.881	-3.736	0.0069139	0.0520241
16890	10527888	NM_026033	67210	GATA zinc finger domain contai	Gatad1	0.881	-2.413	0.0455283	0.18878
16891	10464999	NM_028623	73720	cystatin E/M	Cst6	0.881	-1.7	0.131574	0.364342
16892	10409162	NM_025491	66329	sushi domain containing 3	Susd3	0.881	-1.766	0.11947	0.345748
16893	10508019	NM_145552	230737	guanine nucleotide binding pro	Gnl2	0.881	-2.445	0.0434343	0.183199
16894	10551531	NM_026716	68416	syncollin	Sycn	0.881	-1.748	0.12264	0.350324
16895	10504068	ENSMUST00000038960	76992	RIKEN cDNA 1700066J24 gene	1700066J24Rik	0.881	-2.128	0.0696821	0.247457
16896	10490799	XR_030888	667807	similar to ubiquitin-like doma	LOC667807	0.881	-0.777	0.461884	0.71646
16897	10508686	NM_025297	26922	mitochondrial trans-2-enoyl-Co	Mecr	0.881	-2.791	0.0260592	0.130787
16898	10504646					0.881	-0.881	0.406474	0.67113
16899	10386376	NM_009522	22416	wingless-related MMTV integrat	Wnt3a	0.881	-1.102	0.306009	0.582506
16900	10434121	NM_009435	22114	testis-specific serine kinase	Tssk1	0.881	-2.542	0.0375944	0.167135
16901	10575894	NM_026648	68270	leucine rich repeat containing	Lrrc50	0.881	-1.081	0.314531	0.591308
16902	10459229	NM_172832	240334	prenylcysteine oxidase 1 like	Pcyox1l	0.881	-1.716	0.128533	0.359524
16903	10508996	NM_001081099	69885	RIKEN cDNA 2610002D18 gene	2610002D18Rik	0.881	-1.815	0.111121	0.329899
16904	10378902	NM_001024205	68564	nuclear fragile X mental retar	Nufip2	0.881	-2.393	0.0469121	0.192492
16905	10503341	NM_019753	12557	cadherin 17	Cdh17	0.881	-0.967	0.365014	0.636157
16906	10447361	NM_028639	225049	tetratricopeptide repeat domai	Ttc7	0.881	-2.154	0.0670675	0.241827
16907	10511923	ENSMUST00000067819	242377	peptidase M20 domain containin	Pm20d2	0.881	-1.701	0.131479	0.364159
16908	10403394	XR_031052	382722	similar to hCG2022736	LOC382722	0.881	-2.053	0.0780317	0.265642
16909	10445601	NM_010787	17256	male enhanced antigen 1	Mea1	0.881	-2.536	0.0379393	0.168193
16910	10487392	NM_019789	56461	Kv channel interacting protein	Kcnip3	0.881	-1.1	0.306886	0.583525
16911	10365640	NM_145423	216225	solute carrier family 5 (iodid	Slc5a8	0.881	-1.825	0.109446	0.326945
16912	10518561	NM_027263	69928	apoptosis-inducing, TAF9-like	Apitd1	0.881	-2.159	0.0665617	0.241108
16913	10601819	NM_001009575	494468	armadillo repeat containing, X	Armcx5	0.88	-2.263	0.0570157	0.218378
16914	10393823	NM_011032	18453	prolyl 4-hydroxylase, beta pol	P4hb	0.88	-2.301	0.0538259	0.210683
16915	10473630	NM_146981	258983	olfactory receptor 1260	Olfr1260	0.88	-1.873	0.101948	0.312948
16916	10385096	NM_027398	70357	Kv channel-interacting protein	Kcnip1	0.88	-0.797	0.45092	0.708135
16917	10393642	NM_138669	192170	eukaryotic translation initiat	Eif4a3	0.88	-1.97	0.0882491	0.286363
16918	10410115	NM_025370	66129	RIKEN cDNA 1110018J18 gene	1110018J18Rik	0.88	-1.363	0.213988	0.480314
16919	10408134	NM_134225	171259	vomeronasal 1 receptor, I9	V1ri9	0.88	-0.873	0.410889	0.675081
16920	10452082	NM_011483	20834	zinc and ring finger 4	Znrf4	0.88	-1.408	0.200672	0.462604
16921	10451421	NM_027910	71765	kelch domain containing 3	Klhdc3	0.88	-2.116	0.070981	0.250137
16922	10427742	XR_001896	666579	predicted gene, EG666579	EG666579	0.88	-1.493	0.177938	0.432551
16923	10525439	NM_011026	18438	purinergic receptor P2X, ligan	P2rx4	0.88	-1.652	0.141253	0.380418

16924	10452538	NM_001114098	68617	RIKEN cDNA 1110012J17 gene	1110012J17Rik	0.88	-1.262	0.246395	0.51947
16925	10547540	BC043122	194401	microtubule associated monoxyg	Mical3	0.88	-1.521	0.170943	0.42274
16926	10593526	NM_007499	11920	ataxia telangiectasia mutated	Atm	0.88	-2.135	0.0690215	0.246186
16927	10416199	NM_026174	67464	ectonucleoside triphosphate di	Entpd4	0.88	-1.855	0.104762	0.318672
16928	10570180	BC066076	434280	predicted gene, EG434280	EG434280	0.88	-1.609	0.15044	0.393664
16929	10548679					0.88	-0.852	0.421397	0.683844
16930	10449687	NM_025290	22092	radial spoke head 1 homolog (C	Rsph1	0.88	-2.21	0.0616835	0.229458
16931	10415446	NM_138652	192113	ATPase, H+/K+ transporting, no	Atp12a	0.88	-1.545	0.165105	0.415207
16932	10460385	NM_019952	56708	cardiotrophin-like cytokine fa	Clcf1	0.88	-1.595	0.153406	0.397723
16933	10467871	NM_028029	71972	dynamin binding protein	Dnmbp	0.88	-2.91	0.0219105	0.116412
16934	10403076					0.88	-1.66	0.139544	0.37791
16935	10597978	NM_148925	17281	FYVE and coiled-coil domain co	Fyco1	0.88	-2.215	0.0612162	0.228343
16936	10596637	NM_178907	102626	mitogen-activated protein kina	Mapkapk3	0.88	-2.295	0.0542864	0.211894
16937	10438822	NM_175650	268878	ATPase type 13A5	Atp13a5	0.88	-0.79	0.454605	0.711012
16938	10574213	NM_009137	20299	chemokine (C-C motif) ligand 2	Ccl22	0.88	-1.314	0.229001	0.5
16939	10516908					0.88	-1.017	0.341841	0.616313
16940	10501922					0.88	-1.069	0.319717	0.596635
16941	10555576	BC006736	75430	RIKEN cDNA 3200002M19 gene	3200002M19Rik	0.88	-3.417	0.0106871	0.0711265
16942	10406466	NM_175187	72745	transmembrane protein 161B	Tmem161b	0.88	-2.381	0.0478179	0.194851
16943	10459552	NM_194355	68166	spire homolog 1 (Drosophila)	Spire1	0.88	-2.191	0.0634459	0.233643
16944	10448409	NM_133731	70835	protease, serine, 22	Prss22	0.88	-1.839	0.107221	0.322736
16945	10371877	NM_133668	18674	solute carrier family 25 (mito	Slc25a3	0.88	-3.122	0.0161608	0.0951292
16946	10600524	NM_011692	22327	von Hippel-Lindau binding prot	Vbp1	0.88	-1.713	0.129196	0.360384
16947	10542264	ENSMUST00000100864	381820	RIKEN cDNA 2700089E24 gene	2700089E24Rik	0.88	-2.215	0.0611823	0.228316
16948	10596137	NM_009275	20818	signal recognition particle re	Srprb	0.88	-3.911	0.00548632	0.0441916
16949	10395825	NR_003959	79459	aldolase 1, A isoform, retroge	Aldoart2	0.88	-1.864	0.103357	0.315943
16950	10530257	ENSMUST00000101177	384261	hypothetical LOC384261	LOC384261	0.88	-1.436	0.192918	0.452347
16951	10581640	XR_033068	668089	similar to Larp2 protein	LOC668089	0.879	-1.815	0.111067	0.329804
16952	10542371					0.879	-1.624	0.147083	0.388984
16953	10554667	NM_177695	233424	transmembrane channel-like gen	Tmc3	0.879	-1.657	0.140135	0.378727
16954	10550290	NM_133234	170770	Bcl-2 binding component 3	Bbc3	0.879	-3.028	0.0184979	0.104021
16955	10357242	NM_001037999	13167	diazepam binding inhibitor	Dbi	0.879	-3.218	0.014113	0.0863198
16956	10498146	NM_172501	212114	NHL repeat containing 3	Nhlrc3	0.879	-2.655	0.0318381	0.149331
16957	10404496	NM_020282	18105	NAD(P)H dehydrogenase, quinone	Nqo2	0.879	-1.629	0.146148	0.387967
16958	10552779	NM_027376	70300	fuzzy homolog (Drosophila)	Fuz	0.879	-1.284	0.238706	0.511419
16959	10555339	NM_001017985	277939	C2 calcium-dependent domain co	C2cd3	0.879	-2.49	0.0406012	0.175593
16960	10457508	NM_008720	18145	Niemann Pick type C1	Npc1	0.879	-2.016	0.0824357	0.274578
16961	10566188					0.879	-1.487	0.179366	0.434671
16962	10586110	NM_001033175	76524	ceroid-lipofuscinosis, neurona	Cln6	0.879	-2.228	0.0600451	0.22593
16963	10363481	NM_013611	18119	nodal	Nodal	0.879	-1.356	0.215995	0.483076
16964	10568278	ENSMUST00000094032	68232	RIKEN cDNA 1700120K04 gene	1700120K04Rik	0.879	-1.635	0.144892	0.38638
16965	10545768	ENSMUST00000101229	100038556	predicted gene, ENSMUSG0000007	ENSMUSG00000072956	0.879	-1.785	0.11613	0.338871
16966	10351738	NM_023041	19298	peroxisome biogenesis factor 1	Pex19	0.879	-2.448	0.0432764	0.182768
16967	10565288	NM_133722	70178	RIKEN cDNA 2210412D01 gene	2210412D01Rik	0.879	-2.509	0.0394794	0.172434
16968	10555848	NM_001013616	94088	tripartite motif-containing 6	Trim6	0.879	-2.889	0.0226073	0.118878
16969	10524684	NM_008629	17690	Musashi homolog 1(Drosophila)	Msi1	0.879	-1.967	0.0886611	0.286953
16970	10506668	NM_145550	230584	Yip1 domain family, member 1	Yipf1	0.879	-1.95	0.0909413	0.291551
16971	10351041					0.879	-0.91	0.392406	0.660382
16972	10576696	NM_010568	16337	insulin receptor	Insr	0.879	-2.164	0.0661014	0.239857
16973	10593723	NM_053178	94180	acyl-CoA synthetase bubblegum	Acsbg1	0.879	-1.577	0.157644	0.404469
16974	10356932	BC023951	52392	DNA segment, Chr 1, ERATO Doi	D1Ertd622e	0.879	-1.616	0.148845	0.391099

16975	10589793	XR_034007	636680	similar to Glyceraldehyde-3-ph	LOC636680	0.879	-1.008	0.346226	0.620338
16976	10576090	NM_009569	22761	zinc finger protein, multitype	Zfpm1	0.879	-2.316	0.0526724	0.207781
16977	10473600	NM_146919	258921	olfactory receptor 1188	Olfr1188	0.879	-1.027	0.337725	0.613265
16978	10601356	NM_025379	66142	cytochrome c oxidase subunit V	Cox7b	0.879	-2.117	0.0709104	0.250013
16979	10557313	ENSMUST00000060220	75207	RIKEN cDNA 4930533L02 gene	4930533L02Rik	0.879	-1.428	0.195254	0.455478
16980	10373374	NM_028092	72002	solute carrier family 39 (meta	Slc39a5	0.879	-1.697	0.132234	0.365389
16981	10411595	NM_010872	17948	NLR family, apoptosis inhibito	Naip2	0.879	-1.349	0.218045	0.486044
16982	10441774	NM_013667	20518	solute carrier family 22 (orga	Slc22a2	0.879	-1.631	0.145686	0.38722
16983	10517945	NM_001033374	277744	gene model 694, (NCBI)	Gm694	0.879	-0.938	0.378616	0.648305
16984	10452766					0.879	-1.11	0.30261	0.578712
16985	10591763	NM_145612	235050	zinc finger protein 810	Zfp810	0.879	-1.704	0.130814	0.362937
16986	10437040	NM_028083	110749	chromatin assembly factor 1, s	Chaf1b	0.879	-2.308	0.0532863	0.209343
16987	10523001	NM_026735	68473	MOB1, Mps One Binder kinase ac	Mobkl1a	0.879	-2.672	0.0310419	0.146999
16988	10484486	ENSMUST00000099933	228139	purinergic receptor P2X, ligan	P2rx3	0.879	-1.326	0.225153	0.495241
16989	10411899	NM_025879	66975	RIKEN cDNA 2410002O22 gene	2410002O22Rik	0.879	-2.209	0.0617906	0.229738
16990	10464504	NM_008513	16973	low density lipoprotein recept	Lrp5	0.879	-2.523	0.0386937	0.170092
16991	10399389	ENSMUST00000055358	73304	RIKEN cDNA 1700034J04 gene	1700034J04Rik	0.879	-2.109	0.071763	0.251634
16992	10600390	NM_010273	14567	guanosine diphosphate (GDP) di	Gdi1	0.879	-2.653	0.0319022	0.149499
16993	10593245	NM_020274	57014	5-hydroxytryptamine (serotonin	Htr3b	0.879	-1.026	0.338176	0.613769
16994	10516652	NM_198026	230767	IQ motif containing C	Iqcc	0.879	-2.266	0.0567738	0.217982
16995	10490535	NM_080641	140489	basic helix-loop-helix domain	Bhlhb4	0.879	-1.426	0.195761	0.456157
16996	10480314					0.878	-1.94	0.0923754	0.294554
16997	10358283	NM_133239	170788	crumbs homolog 1 (Drosophila)	Crb1	0.878	-1.666	0.138356	0.376355
16998	10488630	NM_001037933	629114	defensin beta 23	Defb23	0.878	-0.89	0.40216	0.667342
16999	10560487	NM_145822	70333	CD3E antigen, epsilon polypept	Cd3eap	0.878	-3.74	0.00688347	0.0518504
17000	10456291					0.878	-0.836	0.430236	0.691063
17001	10582094	NM_019709	56453	membrane-bound transcription f	Mbtps1	0.878	-2.129	0.0696418	0.247355
17002	10598598	NM_026096	67334	RIKEN cDNA 1700054O13 gene	1700054O13Rik	0.878	-2.126	0.0699124	0.247718
17003	10381334	NM_026562	68107	cyclin N-terminal domain conta	Cntd1	0.878	-1.868	0.102753	0.314642
17004	10486322					0.878	-2.078	0.0751792	0.259229
17005	10545644	NM_016757	22377	WW domain binding protein 1	Wbp1	0.878	-1.933	0.0932933	0.296052
17006	10438911	ENSMUST00000061350	224088	ATPase type 13A3	Atp13a3	0.878	-1.964	0.0890392	0.287785
17007	10504349	NM_013497	12913	cAMP responsive element bindin	Creb3	0.878	-2.041	0.0794428	0.268415
17008	10535750	NM_029581	76366	mitochondrial translational in	Mtif3	0.878	-1.785	0.116183	0.338931
17009	10400844	NM_133198	110095	liver glycogen phosphorylase	Pygl	0.878	-0.915	0.389559	0.658209
17010	10465553	NM_008020	14227	FK506 binding protein 2	Fkbp2	0.878	-2.238	0.0591652	0.223991
17011	10445107	ENSMUST00000080694	224763	predicted gene, EG224763	EG224763	0.878	-1.591	0.154304	0.399194
17012	10428211	NM_026521	68036	zinc finger protein 706	Zfp706	0.878	-2.199	0.0627085	0.231802
17013	10539251	AF084364	110958	DNA segment, Chr 6, Miriam Mei	D6Mm5e	0.878	-1.633	0.145246	0.386933
17014	10549256	NM_021284	16653	v-Ki-ras2 Kirsten rat sarcoma	Kras	0.878	-2.444	0.0435331	0.183506
17015	10553471	BC060958	243996	RIKEN cDNA 4933405O20 gene	4933405O20Rik	0.878	-0.932	0.381476	0.651192
17016	10603508	NM_133991	54632	FtsJ homolog 1 (E. coli)	Ftsj1	0.878	-1.489	0.178769	0.433871
17017	10376412	NM_001011760	257917	olfactory receptor 314	Olfr314	0.878	-1.13	0.294608	0.570921
17018	10401661	NM_026775	68581	transmembrane emp24-like traff	Tmed10	0.878	-2.608	0.0341294	0.156265
17019	10471519	NM_152800	30933	torsin family 2, member A	Tor2a	0.878	-1.867	0.102824	0.314815
17020	10545009	NM_025574	66459	phosphatidylinositol glycan an	Pigy	0.878	-2.664	0.0314266	0.148244
17021	10348666	NM_175118	67446	dual specificity phosphatase 2	Dusp28	0.878	-2.228	0.0600836	0.22593
17022	10522265	NM_178651	109108	solute carrier family 30 (zinc	Slc30a9	0.878	-1.625	0.146958	0.388895
17023	10446594					0.878	-2.169	0.0655794	0.2387
17024	10591009	NM_144933	234959	mediator complex subunit 17	Med17	0.878	-2.503	0.0398642	0.173611
17025	10583887	NM_175678	319239	neuropeptide S receptor 1	Npsr1	0.878	-0.996	0.351675	0.624753
17026	10538970	NM_145568	57896	lysine-rich coiled-coil 1	Krcc1	0.878	-2.675	0.030913	0.146668

17027	10551714	AK004111	68686	RIKEN cDNA 1110035H17 gene	1110035H17Rik	0.878	-1.247	0.251487	0.525513
17028	10376459	XM_905850	382523	similar to histone H3	LOC382523	0.878	-2.367	0.048825	0.197883
17029	10449471	NM_016795	20815	serine/arginine-rich protein s	Srpk1	0.878	-2.953	0.0205872	0.112161
17030	10450852	NM_146477	258469	olfactory receptor 90	Olfr90	0.878	-0.636	0.544408	0.776582
17031	10598407	XM_977398	236622	predicted gene, EG236622	EG236622	0.878	-1.453	0.188174	0.446289
17032	10369835	NM_178621	70911	phytanoyl-CoA hydroxylase inte	Phyhipl	0.878	-1.066	0.32076	0.597672
17033	10532180	NM_007756	12889	complexin 1	Cplx1	0.878	-1.744	0.123468	0.351591
17034	10416379	NM_011506	20916	succinate-Coenzyme A ligase, A	Sucla2	0.878	-2.904	0.0220999	0.117082
17035	10463380	NM_176958	319594	hypoxia-inducible factor 1, al	Hif1an	0.878	-1.459	0.186822	0.445139
17036	10345357	NM_178601	27993	IMP4, U3 small nucleolar ribon	Imp4	0.878	-2.136	0.0689423	0.245987
17037	10369086	NM_053187	94221	golgi associated PDZ and coile	Gopc	0.878	-1.825	0.109518	0.327115
17038	10475630	NM_175154	69976	galactokinase 2	Galk2	0.878	-1.817	0.110836	0.329565
17039	10484563	NM_146577	258570	olfactory receptor 1043	Olfr1043	0.878	-1.173	0.278008	0.553138
17040	10445670	NM_183086	64657	mitochondrial ribosomal protei	Mrps10	0.878	-2.518	0.0389918	0.171081
17041	10582190	NM_178856	272551	GINS complex subunit 2 (Psf2 h	Gins2	0.877	-1.946	0.0914849	0.292907
17042	10404521	NM_026512	68021	biphenyl hydrolase-like (serin	Bphl	0.877	-1.915	0.0957542	0.30097
17043	10365572	NR_000040	22172	thymidylate synthase, pseudoge	Tyms-ps	0.877	-2.328	0.0517104	0.205551
17044	10421180	NM_173420	239167	RIKEN cDNA D930020E02 gene	D930020E02Rik	0.877	-1.657	0.140173	0.378762
17045	10432362	NM_026967	69159	Ras homolog enriched in brain	Rhebl1	0.877	-0.65	0.535828	0.769253
17046	10555197	NM_010837	17760	microtubule-associated protein	Mtap6	0.877	-1.057	0.32451	0.601037
17047	10344935	NM_001098528	98741	potassium voltage gated channe	Kcnb2	0.877	-1.023	0.33952	0.614887
17048	10570236	NM_178076	17207	mcf.2 transforming sequence-li	Mcf2l	0.877	-2.397	0.0466544	0.191956
17049	10537452	NM_026612	68198	NADH dehydrogenase (ubiquinone	Ndufb2	0.877	-1.682	0.13514	0.370646
17050	10361651	NM_145706	69912	nucleoporin 43	Nup43	0.877	-2.399	0.0465234	0.191678
17051	10407955	NM_134065	105298	ependymin related protein 1 (z	Epdr1	0.877	-2.485	0.0409098	0.176312
17052	10430618	NM_017470	54152	dynein, axonemal, light chain	Dnalc4	0.877	-1.995	0.0851085	0.280258
17053	10378349	NM_001001445	193034	transient receptor potential c	Trpv1	0.877	-1.373	0.211064	0.476598
17054	10551996					0.877	-1.649	0.141784	0.381361
17055	10346250	NM_010834	17700	myostatin	Mstn	0.877	-0.952	0.371817	0.642152
17056	10582658	NM_007428	11606	angiotensinogen (serpin peptid	Agt	0.877	-1.934	0.0931686	0.295834
17057	10399722	ENSMUST00000063754	636791	predicted gene, EG636791	EG636791	0.877	-0.918	0.388362	0.65703
17058	10506781	BC012391	69893	RIKEN cDNA 2010305A19 gene	2010305A19Rik	0.877	-1.547	0.164625	0.414483
17059	10416273	NM_145981	105653	phytanoyl-CoA hydroxylase inte	Phyhip	0.877	-1.681	0.135303	0.370761
17060	10414984	ENSMUST00000103675	100046160	predicted gene, OTTMUSG0000001	OTTMUSG00000015007	0.877	-1.162	0.282082	0.557189
17061	10597770	ENSMUST00000068626	546166	predicted gene, EG546166	EG546166	0.877	-1.437	0.192662	0.452175
17062	10570764	NM_183142	207958	asparagine-linked glycosylatio	Alg11	0.877	-2.505	0.039733	0.173255
17063	10351138	XR_031476	665237	similar to hCG31107	LOC665237	0.877	-2.154	0.0670633	0.241827
17064	10445633	NM_008938	19133	peripherin 2	Prph2	0.877	-1.908	0.0968716	0.303131
17065	10491313	NM_008770	18417	claudin 11	Cldn11	0.877	-2.525	0.0385767	0.169907
17066	10465114	NM_178637	81601	HIV-1 tat interactive protein,	Htatip	0.877	-2.233	0.0595558	0.224825
17067	10428328	NM_172402	69906	solute carrier family 25, memb	Slc25a32	0.877	-1.384	0.20763	0.472138
17068	10519234	NM_080445	117592	UDP-Gal:betaGal beta 1,3-galac	B3galt6	0.877	-1.759	0.120755	0.347238
17069	10497203	NM_010423	15213	hairy/enhancer-of-split relate	Hey1	0.877	-2.031	0.0805892	0.270946
17070	10382316	NM_010604	16517	potassium inwardly-rectifying	Kcnj16	0.877	-1.07	0.319314	0.596377
17071	10539739	NM_026414	67855	aspartic peptidase, retroviral	Asprv1	0.877	-1.549	0.163943	0.413358
17072	10467744	NM_018780	54612	secreted frizzled-related sequ	Sfrp5	0.877	-1.875	0.101633	0.312332
17073	10377889	NM_001045959	50932	misshapen-like kinase 1 (zebra	Mink1	0.877	-3.556	0.00881744	0.0620832
17074	10516079	AK081449	100038759	predicted gene, ENSMUSG0000005	ENSMUSG00000055050	0.877	-1.501	0.175879	0.429588
17075	10418846	AK132190	432836	RIKEN cDNA 3425401B19 gene	3425401B19Rik	0.877	-2.487	0.040823	0.176156
17076	10572865	NM_027837	71597	intestine specific homeobox	Isx	0.877	-1.386	0.207175	0.47163
17077	10601062	NM_016747	53310	discs, large homolog 3 (Drosop	Dlg3	0.877	-2.397	0.0466308	0.19193
17078	10560474	BC096372	232941	expressed sequence C79127	C79127	0.877	-1.016	0.342368	0.616776

17079	10569370	NM_009377	21823	tyrosine hydroxylase	Th	0.876	-1.217	0.261793	0.536245
17080	10562084	BC118934	71909	RIKEN cDNA 2310022K01 gene	2310022K01Rik	0.876	-1.224	0.259406	0.533772
17081	10460055					0.876	-1.275	0.241977	0.514828
17082	10561178	NM_029391	19342	RAB4B, member RAS oncogene fam	Rab4b	0.876	-2.222	0.0605645	0.226995
17083	10514956	NM_011327	20280	sterol carrier protein 2, live	Scp2	0.876	-2.171	0.0654275	0.238533
17084	10488372	XR_002266	668919	similar to ribosomal protein L	LOC668919	0.876	-1.352	0.217167	0.484774
17085	10533474	BC019498	68948	RIKEN cDNA 1500011H22 gene	1500011H22Rik	0.876	-2.829	0.0246588	0.126244
17086	10581750	NM_181549	353287	mannose receptor-like precurso	Mrcl	0.876	-1.542	0.165743	0.416207
17087	10495197	ENSMUST00000098749	100038499	predicted gene, ENSMUSG0000007	ENSMUSG00000074335	0.876	-1.689	0.133837	0.368663
17088	10585410	BC116842	244885	RIKEN cDNA 4933412E14 gene	4933412E14Rik	0.876	-1.232	0.256555	0.530783
17089	10380244	ENSMUST00000037268	74297	RIKEN cDNA 1700106J16 gene	1700106J16Rik	0.876	-1.276	0.241673	0.514457
17090	10434252	NM_010435	15260	histone cell cycle regulation	Hira	0.876	-1.989	0.0857625	0.281088
17091	10549200	NM_011444	20678	SRY-box containing gene 5	Sox5	0.876	-1.885	0.100224	0.309678
17092	10421394	ENSMUST00000116455	239170	retinoic acid induced 16	Rai16	0.876	-1.931	0.0936084	0.296784
17093	10380721	NM_146027	217140	secernin 2	Scrn2	0.876	-2.446	0.0433866	0.183115
17094	10569168	NM_026646	68267	solute carrier family 25 (mito	Slc25a22	0.876	-1.85	0.10553	0.320207
17095	10520351	NM_207282	403186	RIKEN cDNA B930011P16 gene	B930011P16Rik	0.876	-1.748	0.122775	0.350597
17096	10351063					0.876	-1.721	0.127586	0.35821
17097	10563407	NM_145963	211480	potassium inwardly-rectifying	Kcnj14	0.876	-1.203	0.267022	0.541627
17098	10437936	ENSMUST00000063394	442816	RIKEN cDNA F830005K03 gene	F830005K03Rik	0.876	-1.087	0.312039	0.588349
17099	10431311	NM_172818	239591	tubulin tyrosine ligase-like f	Ttll8	0.876	-2.112	0.0713976	0.250978
17100	10430389	NM_008595	17305	MFNG O-fucosylpeptide 3-beta-N	Mfng	0.876	-1.584	0.15598	0.401839
17101	10494306	NM_008562	17210	myeloid cell leukemia sequence	Mcl1	0.876	-2.377	0.0480482	0.195635
17102	10560911	NM_010261	14470	Rab acceptor 1 (prenylated)	Rabac1	0.876	-2.058	0.0774319	0.264238
17103	10540880	NM_001111015	20965	synapsin II	Syn2	0.876	-1.915	0.0958318	0.301049
17104	10483648	NM_025942	67059	Obg-like ATPase 1	Ola1	0.876	-2.332	0.0513898	0.204746
17105	10490852					0.876	-1.567	0.159925	0.407256
17106	10400189	XR_030785	636070	similar to hCG1992406	LOC636070	0.876	-2.021	0.0818226	0.273224
17107	10592652	AK035675	442822	RIKEN cDNA 9530085L02 gene	9530085L02Rik	0.876	-1.401	0.20261	0.465349
17108	10425211	NM_013847	26912	glycine C-acetyltransferase (2	Gcat	0.876	-1.656	0.140526	0.379231
17109	10449935	NM_207245	240066	cDNA sequence BC066107	BC066107	0.876	-2.298	0.054111	0.211405
17110	10595443	AK034076	442799	RIKEN cDNA 9330154J02 gene	9330154J02Rik	0.876	-1.522	0.170626	0.422304
17111	10420675	NM_172810	239134	guanylate cyclase 1, soluble,	Gucy1b2	0.876	-2.195	0.0631227	0.232827
17112	10523195	BC089377	381650	THAP domain containing 6	Thap6	0.876	-1.662	0.139285	0.377524
17113	10530787	NM_173765	231326	aminoadipate-semialdehyde dehy	Aasdh	0.876	-2.447	0.0433328	0.182953
17114	10558049	NM_001080963	381925	phosphatidic acid phosphatase	Ppapdc1a	0.876	-1.251	0.250047	0.524217
17115	10527508	NM_153599	264064	cyclin-dependent kinase 8	Cdk8	0.876	-3.113	0.0163804	0.0961431
17116	10381539	NM_175935	68401	glucose 6 phosphatase, catalyt	G6pc3	0.876	-3.477	0.00983051	0.0672657
17117	10446619	NM_010867	17929	myomesin 1	Myom1	0.876	-0.291	0.779117	0.910184
17118	10551464					0.876	-2.666	0.0312997	0.147889
17119	10481337	NM_001085514	329375	RIKEN cDNA 1700101E01 gene	1700101E01Rik	0.876	-1.806	0.112589	0.332345
17120	10464342	NM_178689	226265	RIKEN cDNA 6430537H07 gene	6430537H07Rik	0.875	-2.485	0.0409108	0.176312
17121	10348932	NM_026250	252876	zinc finger, H2C2 domain conta	Zh2c2	0.875	-1.761	0.120429	0.346759
17122	10440734	XM_925173	640684	hypothetical protein LOC640684	LOC640684	0.875	-1.149	0.287393	0.563017
17123	10606728	ENSMUST00000096324	100038691	predicted gene, ENSMUSG0000007	ENSMUSG00000071690	0.875	-1.375	0.210439	0.475962
17124	10457221					0.875	-1.523	0.170434	0.422073
17125	10370644	NM_001042710	73106	protease, serine-like 1	Prssl1	0.875	-2.351	0.0499335	0.20095
17126	10493670	ENSMUST00000029548	77595	nucleoporin 210-like	Nup210l	0.875	-1.357	0.215568	0.482734
17127	10454953	NM_028036	71983	transmembrane and coiled-coil	Tmco6	0.875	-3.047	0.0179838	0.101919
17128	10589911					0.875	-2.603	0.0343492	0.157

17129	10556216	NM_181517	233726	importin 7	Ipo7	0.875	-2.195	0.0631241	0.232827
17130	10414651	NM_001033805	619301	RIKEN cDNA G630016D24 gene	G630016D24Rik	0.875	-2.513	0.0392507	0.171896
17131	10365208	NM_001024626	408062	cDNA sequence BC062115	BC062115	0.875	-2.558	0.0367446	0.164082
17132	10389062	NM_001033765	237880	RIKEN cDNA 1700071K01 gene	1700071K01Rik	0.875	-2.223	0.0605186	0.22695
17133	10426581	BC090621	239650	expressed sequence AI836003	AI836003	0.875	-1.118	0.299527	0.575641
17134	10593473	BC120857	69809	RIKEN cDNA 1810046K07 gene	1810046K07Rik	0.875	-1.181	0.275147	0.550034
17135	10428842	NM_175151	69694	TatD DNase domain containing 1	Tatdn1	0.875	-2.723	0.0288009	0.139479
17136	10526391	NM_021403	58212	RIKEN cDNA 2900083I11 gene	2900083I11Rik	0.875	-1.746	0.123085	0.351101
17137	10379068	NM_009143	20316	stromal cell derived factor 2	Sdf2	0.875	-2.18	0.0644815	0.236295
17138	10605315	NM_025410	66192	L antigen family, member 3	Lage3	0.875	-2.545	0.0374645	0.166652
17139	10554900	NM_011807	23859	discs, large homolog 2 (Drosop	Dlg2	0.875	-0.779	0.460547	0.715069
17140	10410695	NM_028493	73296	Rho-related BTB domain contain	Rhobtb3	0.875	-2.714	0.0291708	0.140658
17141	10476319					0.875	-1.812	0.111603	0.330541
17142	10446739	NM_030179	78785	CAP-GLY domain containing link	Clip4	0.875	-2.023	0.0816106	0.272821
17143	10566186	NM_147085	259089	olfactory receptor 571	Olfr571	0.875	-0.977	0.36019	0.632213
17144	10458804	ENSMUST00000116061	225468	predicted gene, EG225468	EG225468	0.875	-1.842	0.106857	0.322408
17145	10539015	XR_034118	668034	similar to Ribosomal protein L	LOC668034	0.875	-0.925	0.385104	0.654297
17146	10465278	NM_026772	104252	CDC42 effector protein (Rho GT	Cdc42ep2	0.875	-1.565	0.160295	0.40761
17147	10485070	NM_010784	17242	midkine	Mdk	0.875	-2.975	0.0199701	0.109789
17148	10371811	NM_198021	213326	SCY1-like 2 (S. cerevisiae)	Scyl2	0.875	-3.199	0.0144939	0.0882145
17149	10574944	NM_025518	66369	dihydrouridine synthase 2-like	Dus2l	0.875	-1.246	0.251708	0.525589
17150	10587854	NM_177909	331004	solute carrier family 9 (sodiu	Slc9a9	0.875	-1.528	0.169133	0.42056
17151	10371134	NM_148951	209047	GIPC PDZ domain containing fam	Gipc3	0.875	-1.201	0.267812	0.542576
17152	10495257	ENSMUST00000070502	791415	predicted gene, OTTMUSG0000000	OTTMUSG00000007191	0.875	-1.537	0.16698	0.417902
17153	10398350					0.875	-2.246	0.0584926	0.22232
17154	10450325	NM_008198	14962	complement factor B	Cfb	0.875	-1.89	0.0994893	0.30816
17155	10588091	NM_023873	68121	centrosomal protein 70	Cep70	0.875	-2.078	0.0750896	0.259103
17156	10562605	BC099396	233168	expressed sequence AI987944	AI987944	0.875	-2.149	0.0675538	0.242768
17157	10454771	NM_144865	225362	receptor accessory protein 2	Reep2	0.875	-1.135	0.292709	0.568741
17158	10390211	NM_009951	140486	insulin-like growth factor 2 m	Igf2bp1	0.874	-2.05	0.0783765	0.266396
17159	10558325	NM_025392	66165	BRCA2 and CDKN1A interacting p	Bccip	0.874	-2.623	0.0333833	0.154129
17160	10413377					0.874	-1.682	0.135105	0.370617
17161	10371240	NM_053254	114606	transducin-like enhancer of sp	Tle6	0.874	-2.285	0.055116	0.214183
17162	10583929	NM_029792	76898	beta-1,3-glucuronyltransferase	B3gat1	0.874	-1.694	0.132919	0.366563
17163	10469143	AK049866	791351	predicted gene, ENSMUSG0000005	ENSMUSG00000053987	0.874	-1.094	0.309151	0.585866
17164	10503234	NM_028940	74438	retinaldehyde binding protein	Rlbp1l1	0.874	-1.685	0.134657	0.369832
17165	10577994	XR_001871	666422	predicted gene, EG666422	EG666422	0.874	-1.597	0.152993	0.397015
17166	10352242	NM_007415	11545	poly (ADP-ribose) polymerase f	Parp1	0.874	-3.557	0.00881341	0.0620755
17167	10413517	NM_175343	218865	choline dehydrogenase	Chdh	0.874	-2.054	0.0778491	0.265362
17168	10508721					0.874	-1.079	0.315187	0.59212
17169	10429944	NM_130893	170729	scratch homolog 1, zinc finger	Scrt1	0.874	-1.762	0.120114	0.346527
17170	10394971	NM_178357	194655	Kruppel-like factor 11	Klf11	0.874	-2.031	0.0806473	0.270969
17171	10398396					0.874	-1.058	0.324203	0.600678
17172	10359982	NM_001081304	226641	activating transcription facto	Atf6	0.874	-2.663	0.031438	0.148244
17173	10347552	NM_011494	20872	serine/threonine kinase 16	Stk16	0.874	-2.858	0.0236308	0.122403
17174	10598180	BC085271	434632	cDNA sequence BC085271	BC085271	0.874	-2.529	0.0383632	0.169307
17175	10490028	NM_009564	22722	zinc finger protein 64	Zfp64	0.874	-2.891	0.022548	0.118743
17176	10415645	NM_026401	67840	mitochondrial ribosomal protei	Mrp63	0.874	-3.149	0.0155654	0.0926823
17177	10481619					0.874	-2.278	0.0557071	0.215491
17178	10433618	ENSMUST00000023138	72555	RIKEN cDNA 2700045P11 gene	2700045P11Rik	0.874	1.497	0.176761	0.430877

17179	10363551	NM_009314	21337	tachykinin receptor 2	Tacr2	0.874	-1.122	0.297716	0.5738
17180	10376017	ENSMUST00000067523	791266	predicted gene, ENSMUSG0000005	ENSMUSG00000054450	0.874	-1.077	0.315978	0.592922
17181	10560304	NM_007590	12315	calmodulin 3	Calm3	0.874	-2.905	0.0220935	0.117082
17182	10386020	NM_153170	246049	solute carrier family 36 (prot	Slc36a2	0.874	-1.356	0.215949	0.483023
17183	10543737	NM_017478	54160	coatomer protein complex, subu	Copg2	0.874	-2.422	0.0449766	0.187645
17184	10428074	NM_009083	19946	ribosomal protein L30	Rpl30	0.874	-2.143	0.0681359	0.243952
17185	10548011	NM_198604	213522	pleckstrin homology domain con	Plekhg6	0.874	-1.637	0.144429	0.385726
17186	10560719	NM_027308	70080	RIKEN cDNA 2210010C17 gene	2210010C17Rik	0.874	-1.578	0.157428	0.404021
17187	10467216	NM_198300	208922	cytoplasmic polyadenylation el	Cpeb3	0.874	-2.081	0.0748515	0.258816
17188	10515095	NM_010488	15572	ELAV (embryonic lethal, abnorm	Elavl4	0.874	-1.557	0.162108	0.410473
17189	10389865	NM_008704	18102	non-metastatic cells 1, protei	Nme1	0.874	-2.529	0.0383531	0.169298
17190	10554367	NM_008589	17293	mesoderm posterior 2	Mesp2	0.874	-1.789	0.115539	0.337938
17191	10511879					0.874	-2.373	0.048355	0.196543
17192	10386368	AK137066	67862	RIKEN cDNA 2310033P09 gene	2310033P09Rik	0.874	-3.406	0.0108471	0.0716946
17193	10347728	XR_030663	100039137	similar to Ac2-210	LOC100039137	0.874	-2.154	0.0671067	0.241886
17194	10410617	NM_011051	18570	programmed cell death 6	Pdcd6	0.874	-1.887	0.0998289	0.308845
17195	10457235	NM_178722	240186	zinc finger protein 438	Zfp438	0.874	-1.687	0.134239	0.369304
17196	10385384	BC139819	214112	RIKEN cDNA 9530066K23 gene	9530066K23Rik	0.874	-1.453	0.188361	0.446391
17197	10580274	NM_027187	69724	ribonuclease H2, large subunit	Rnaseh2a	0.874	-2.042	0.0793095	0.268093
17198	10470649	NM_009442	22130	transcription termination fact	Ttf1	0.874	-2.301	0.0538603	0.210688
17199	10549655	NM_026146	67425	EPS8-like 1	Eps8l1	0.874	-1.973	0.0879176	0.285594
17200	10358124	NM_019645	18772	plakophilin 1	Pkp1	0.874	-1.941	0.0922007	0.294263
17201	10452248	NM_175333	103775	solute carrier family 25, memb	Slc25a41	0.874	-1.611	0.149999	0.393007
17202	10423821	NM_080640	118452	brain and acute leukemia, cyto	Baalc	0.874	-0.73	0.488406	0.736055
17203	10449657	NM_011575	21786	trefoil factor 3, intestinal	Tff3	0.874	-2.399	0.0465058	0.191643
17204	10553993	NM_021336	68981	small nuclear ribonucleoprotei	Snrpa1	0.874	-2.798	0.0257969	0.130148
17205	10452442					0.873	-1.057	0.324693	0.601113
17206	10536762	NM_019776	56463	staphylococcal nuclease and tu	Snd1	0.873	-3.005	0.0191023	0.106344
17207	10399605	NM_009615	11491	a disintegrin and metallopepti	Adam17	0.873	-2.439	0.0438088	0.1843
17208	10510980					0.873	-1.23	0.257253	0.53155
17209	10348000	ENSMUST00000027429	72792	RIKEN cDNA 2810459M11 gene	2810459M11Rik	0.873	-2.176	0.0649321	0.237571
17210	10398934	AK033757	791402	predicted gene, ENSMUSG0000005	ENSMUSG00000051997	0.873	-2.078	0.075115	0.259134
17211	10450365					0.873	-1.673	0.136914	0.373586
17212	10545682	ENSMUST00000089622	194388	tet oncogene family member 3	Tet3	0.873	-1.766	0.119532	0.345831
17213	10455294	ENSMUST00000091927	383348	potassium channel tetramerisat	Kctd16	0.873	-1.14	0.29084	0.567038
17214	10555718					0.873	-1.515	0.172406	0.42462
17215	10520553	BC029150	68796	RIKEN cDNA 1110039B18 gene	1110039B18Rik	0.873	-2.449	0.0431639	0.182497
17216	10519136					0.873	-2.414	0.045488	0.188773
17217	10430572					0.873	-1.264	0.245513	0.518491
17218	10371307	NM_010914	18045	nuclear transcription factor-Y	Nfyb	0.873	-2.771	0.0268315	0.1333
17219	10347910	NM_025386	66153	F-box protein 36	Fbxo36	0.873	-2.077	0.0752643	0.259479
17220	10513266	NM_146920	258922	olfactory receptor 267	Olfr267	0.873	-1.574	0.158136	0.405072
17221	10366403					0.873	-1.537	0.166983	0.417902
17222	10457707	NM_013504	13505	desmocollin 1	Dsc1	0.873	-1.384	0.207723	0.472217
17223	10393264					0.873	-1.123	0.297601	0.573712
17224	10594967	NM_001081153	208898	unc-13 homolog C (C. elegans)	Unc13c	0.873	-1.872	0.102156	0.313496
17225	10407870	NM_029271	75398	mitochondrial ribosomal protei	Mrpl32	0.873	-2.991	0.0194961	0.107912
17226	10465826	AY941793	107197	expressed sequence AI462493	AI462493	0.873	-2.439	0.0438382	0.184351
17227	10368527	NM_025798	66847	histidine triad nucleotide bin	Hint3	0.873	-1.505	0.174802	0.427927
17228	10567750	NM_207239	233863	general transcription factor I	Gtf3c1	0.873	-3.144	0.0156718	0.0930276
17229	10531887	NM_029415	75750	solute carrier family 10 (sodi	Slc10a6	0.873	-3.319	0.0122439	0.0778362

17229	10551887	NM_029415	75750	solute carrier family 10 (sodi	Slc10a6	0.873	-3.319	0.0122459	0.0778362
17230	10347060	BC116430	241076	RIKEN cDNA C030018G13 gene	C030018G13Rik	0.873	-2.502	0.0398942	0.173636
17231	10574057					0.873	-1.6	0.152432	0.39629
17232	10498319	NM_030685	28146	DNA segment, Chr 3, University	D3Ucla1	0.873	-2.818	0.025071	0.127643
17233	10464070	NM_016862	53611	vesicle transport through inte	Vti1a	0.873	-2.141	0.0683551	0.244408
17234	10518455	NM_009642	11610	angiotensin II, type I recepto	Agtrap	0.873	-1.924	0.0944821	0.298436
17235	10409170	NM_015759	30938	FYVE, RhoGEF and PH domain con	Fgd3	0.872	-1.528	0.169149	0.42056
17236	10556701	NM_178758	272428	acyl-CoA synthetase medium-cha	Acsm5	0.872	-0.997	0.351101	0.624551
17237	10460732	NM_013859	29805	zinc finger, HIT domain contai	Znhit2	0.872	-2.034	0.0802718	0.270212
17238	10507299	NM_029868	77110	GC-rich promoter binding prote	Gpbp1l1	0.872	-2.813	0.0252345	0.128136
17239	10536908	NM_146173	232670	tetraspanin 33	Tspan33	0.872	-1.958	0.089813	0.289247
17240	10429391	NM_001033219	106068	solute carrier family 45, memb	Slc45a4	0.872	-1.061	0.322838	0.599569
17241	10379013	NM_008028	14252	flotillin 2	Flot2	0.872	-2.468	0.0420083	0.17915
17242	10541098	NM_001001792	22685	zinc finger protein 239	Zfp239	0.872	-2.14	0.0684767	0.244681
17243	10503123	NM_026534	68053	RIKEN cDNA 3110003A22 gene	3110003A22Rik	0.872	-1.934	0.0931035	0.295671
17244	10429802	NM_011117	18810	plectin 1	Plec1	0.872	-3.133	0.0159214	0.0941049
17245	10430679					0.872	-0.547	0.601103	0.812694
17246	10478875	NM_030743	81018	zinc finger protein 313	Zfp313	0.872	-2.398	0.046609	0.191881
17247	10364112	NM_198635	333669	predicted gene, EG333669	EG333669	0.872	-2.258	0.057396	0.219375
17248	10375956	NM_177059	320027	follistatin-like 4	Fstl4	0.872	-2.093	0.0734501	0.255968
17249	10434930	ENSMUST00000061675	75531	RIKEN cDNA 1700025H01 gene	1700025H01Rik	0.872	-1.105	0.304562	0.581092
17250	10484820	NM_146970	258972	olfactory receptor 1239	Olfr1239	0.872	-1.72	0.127786	0.35851
17251	10546079	NM_013493	12785	cellular nucleic acid binding	Cnbp	0.872	-1.837	0.107581	0.323293
17252	10383200	ENSMUST00000093902	672511	hypothetical LOC672511	LOC672511	0.872	-0.862	0.416311	0.67936
17253	10439547	NM_153528	207798	GRAM domain containing 1C	Gramd1c	0.872	-1.281	0.239813	0.512804
17254	10363917	XR_032177	544705	similar to HNRPA2B1 protein	LOC544705	0.872	-1.727	0.126471	0.356138
17255	10423386	ENSMUST00000064878	791316	predicted gene, ENSMUSG0000005	ENSMUSG00000052811	0.872	-1.382	0.208392	0.473025
17256	10375443	NM_134250	171285	hepatitis A virus cellular rec	Havcr2	0.872	-1.675	0.136546	0.373015
17257	10472384	NM_001099298	110876	sodium channel, voltage-gated,	Scn2a1	0.872	-1.478	0.181595	0.437813
17258	10465726	BC014805	236149	cDNA sequence BC014805	BC014805	0.872	-1.616	0.1489	0.391148
17259	10569300	NM_001037822	114666	keratin associated protein 5-5	Krtap5-5	0.872	-1.303	0.232691	0.503682
17260	10396952	NM_001033149	69480	tetratricopeptide repeat domai	Ttc9	0.871	-1.64	0.143681	0.384361
17261	10563108	NR_000003	27211	RNA, U35a small nucleolar	Rnu35a	0.871	-2.151	0.0673392	0.242464
17262	10461459	NM_173068	54525	synaptotagmin VII	Syt7	0.871	-1.716	0.12854	0.359524
17263	10463164	NM_008043	14296	frequently rearranged in advan	Frat1	0.871	-2.458	0.0426135	0.180844
17264	10460146					0.871	-0.512	0.623728	0.828064
17265	10464413					0.871	-2.031	0.0806338	0.270969
17266	10487405	NM_178047	192212	prominin 2	Prom2	0.871	-1.331	0.223627	0.493567
17267	10486499	NM_173734	211499	transmembrane protein 87A	Tmem87a	0.871	-3.335	0.0119752	0.0767053
17268	10470042	NM_013524	14347	fucosyltransferase 7	Fut7	0.871	-1.91	0.0965782	0.302436
17269	10562461	NM_178643	101831	RIKEN cDNA C230052I12 gene	C230052I12Rik	0.871	-2.089	0.0738989	0.256909
17270	10514473					0.871	-2.215	0.061266	0.228427
17271	10526977	NM_133916	27979	eukaryotic translation initiat	Eif3b	0.871	-2.708	0.0294344	0.141691
17272	10435149	NM_027226	69823	forty-two-three domain contain	Fyttd1	0.871	-2.769	0.0269257	0.133517
17273	10357454	NM_177445	226414	aspartyl-tRNA synthetase	Dars	0.871	-2.531	0.0382443	0.168959
17274	10520271	ENSMUST00000063159	67261	RIKEN cDNA 2900005J15 gene	2900005J15Rik	0.871	-2.008	0.0833852	0.276517
17275	10570951	ENSMUST00000071588	74561	NK6 transcription factor relat	Nkx6-3	0.871	-1.674	0.136789	0.373436
17276	10470388	BC027257	381356	RIKEN cDNA 5930434B04 gene	5930434B04Rik	0.871	-2.465	0.0421787	0.179731
17277	10557585	NM_146201	233887	zinc finger protein 553	Zfp553	0.871	-1.91	0.0964637	0.302302
17278	10517703	XR_034198	626000	similar to Cyclin D3	LOC626000	0.871	-0.631	0.547222	0.778305
17279	10449377	NM_013891	30051	SAM pointed domain containing	Spdef	0.871	-2.714	0.0291831	0.140686
17280	10444332	BC051142	407788	cDNA sequence BC051142	BC051142	0.871	-2.382	0.0476881	0.194656

17281	10366073	NM_146009	216274	centrosomal protein 290	Cep290	0.871	-1.801	0.1135	0.333876
17282	10556749	NM_178414	233801	acyl-CoA synthetase medium-cha	Acsm4	0.871	-1.497	0.176757	0.430877
17283	10376396	NM_001039047	216781	tripartite motif-containing 58	Trim58	0.871	-2.657	0.0317385	0.149088
17284	10595892	ENSMUST00000061643	70457	RIKEN cDNA 2610303G11 gene	2610303G11Rik	0.871	-1.607	0.150877	0.394527
17285	10479938	NM_024208	67856	enoyl Coenzyme A hydratase dom	Echdc3	0.871	-2.084	0.0744166	0.258046
17286	10603843	NM_013680	20964	synapsin I	Syn1	0.871	-1.695	0.132631	0.366293
17287	10559764	NM_001013012	67109	zinc finger protein 787	Zfp787	0.871	-1.804	0.112904	0.332876
17288	10572757	NM_023126	17274	RAB8A, member RAS oncogene fam	Rab8a	0.871	-1.593	0.15397	0.398476
17289	10459804	NM_027721	71206	katanin p60 subunit A-like 2	Katnal2	0.871	-1.588	0.154979	0.400254
17290	10398173	NM_011705	22367	vaccinia related kinase 1	Vrk1	0.871	-2.696	0.0299461	0.143448
17291	10587554	NM_011627	21983	trophoblast glycoprotein	Tpbg	0.871	-2.146	0.0679193	0.243363
17292	10499128	NR_004417	19870	U73A small nuclear RNA	Rnu73a	0.871	-2.328	0.0516873	0.205505
17293	10567680	NM_012016	26918	endoplasmic reticulum (ER) to	Ern2	0.871	-1.616	0.14876	0.391099
17294	10489055	NM_029983	77799	Src-like-adaptor 2	Sla2	0.871	-1.994	0.0852206	0.280273
17295	10528929	NM_178878	97212	hydroxyacyl-Coenzyme A dehydro	Hadha	0.871	-2.395	0.0467819	0.192107
17296	10584634	NM_198092	53376	ubiquitin specific peptidase 2	Usp2	0.871	-1.95	0.0909364	0.291551
17297	10575725	NM_029297	75465	dynein light chain roadblock-t	Dynlrb2	0.871	-2.188	0.0637111	0.234381
17298	10459467					0.871	-2.35	0.0500263	0.201094
17299	10500630	NM_001013026	74044	transcription termination fact	Ttf2	0.871	-1.695	0.132578	0.366243
17300	10598571	ENSMUST00000059967	75775	RIKEN cDNA 4930402K13 gene	4930402K13Rik	0.871	-1.733	0.125406	0.354707
17301	10595496	NM_013669	20616	synaptosomal-associated protei	Snap91	0.871	-1.666	0.138467	0.376413
17302	10603306					0.871	-1.27	0.243601	0.516619
17303	10440307	NM_026879	68942	chromatin modifying protein 2B	Chmp2b	0.87	-1.437	0.192651	0.452175
17304	10346874					0.87	-0.913	0.390763	0.659209
17305	10563666					0.87	-1.882	0.100704	0.310572
17306	10393970	NM_007988	14104	fatty acid synthase	Fasn	0.87	-2.722	0.0288372	0.139559
17307	10400479	NM_008701	18094	NK2 transcription factor relat	Nkx2-9	0.87	-1.277	0.241152	0.514009
17308	10502131	XM_914534	242235	leucine-rich repeat, immunoglo	Lrit3	0.87	-1.158	0.283813	0.559164
17309	10572928	ENSMUST00000041083	75141	RASD family, member 2	Rasd2	0.87	-1.477	0.181829	0.438179
17310	10529895	NM_024236	110391	quinoid dihydropteridine reduc	Qdpr	0.87	-2.295	0.0543038	0.211923
17311	10512757	NM_053149	93966	hemogen	Hemgn	0.87	-0.48	0.645542	0.840011
17312	10379889	AK014613	66884	amyloid beta precursor protein	Appbp2	0.87	-0.93	0.382667	0.652088
17313	10559359	ENSMUST00000084390	791284	predicted gene, ENSMUSG0000006	ENSMUSG00000066092	0.87	-1.235	0.255448	0.529807
17314	10594377	BC116242	69478	RIKEN cDNA 2300009A05 gene	2300009A05Rik	0.87	-2.17	0.0654555	0.238533
17315	10568060	BC048622	78118	RIKEN cDNA 4930451I11 gene	4930451I11Rik	0.87	-1.226	0.25856	0.532776
17316	10563220	NM_029741	76787	protein tyrosine phosphatase,	Ppfia3	0.87	-1.584	0.155953	0.401839
17317	10491098	NM_177330	208188	growth hormone secretagogue re	Ghsr	0.87	-1.528	0.16917	0.42056
17318	10422249	NM_010024	13190	dopachrome tautomerase	Dct	0.87	-1.907	0.0969	0.303175
17319	10461775	ENSMUST00000081313	383436	predicted gene, EG383436	EG383436	0.87	-1.409	0.200456	0.46246
17320	10352864					0.87	-2.007	0.0835247	0.276766
17321	10485948	NM_011824	23892	gremlin 1	Grem1	0.87	-1.136	0.292237	0.568399
17322	10421212	XR_033481	382919	predicted gene, EG382919	EG382919	0.87	-1.525	0.169732	0.421023
17323	10535747	ENSMUST00000100438	100038524	predicted gene, ENSMUSG0000007	ENSMUSG00000075546	0.87	-1.263	0.245934	0.51897
17324	10561690	BC022688	320225	RIKEN cDNA A230107C01 gene	A230107C01Rik	0.87	-1.064	0.321746	0.598593
17325	10439130	NM_009471	22247	uridine monophosphate syntheta	Umps	0.87	-2.279	0.0556038	0.215288
17326	10601350	NM_030614	80903	fibroblast growth factor 16	Fgf16	0.87	-1.648	0.142183	0.382143
17327	10499438	NM_144898	229524	misato homolog 1 (Drosophila)	Msto1	0.87	-3.183	0.014815	0.0893521
17328	10606893	NM_176971	319642	RAB9B, member RAS oncogene fam	Rab9b	0.87	-1.413	0.199426	0.46104
17329	10397257	NM_007701	12677	visual system homeobox 2	Vsx2	0.87	-2.222	0.0606071	0.227054

17329	10597257	NM_007701	12677	visual system homeobox 2	Vsx2	0.87	-2.222	0.0606071	0.227054
17330	10567095	NM_007587	12310	calcitonin/calcitonin-related	Calca	0.87	-2.362	0.0491867	0.199006
17331	10490194	ENSMUST00000099033	100038374	predicted gene, ENSMUSG0000007	ENSMUSG00000074555	0.87	-0.987	0.355392	0.628032
17332	10442254					0.87	-2.028	0.0809591	0.271714
17333	10504551	NM_027266	69934	RNA (guanine-9-) methyltransfe	Rg9mtd3	0.87	-2.718	0.0290215	0.14013
17334	10419966	NM_001039198	239102	zinc finger homeobox 2	Zfhx2	0.87	-3.265	0.01321	0.0825632
17335	10443120					0.87	-1.21	0.264459	0.539533
17336	10598501	NR_003632	627782	predicted gene, EG627782	EG627782	0.87	-1.275	0.241785	0.514522
17337	10407929	NM_175006	218030	POU domain, class 6, transcrip	Pou6f2	0.87	-3.38	0.0112472	0.0734663
17338	10569311	XR_034827	270015	similar to ribosomal protein L	LOC270015	0.87	-1.418	0.198057	0.458849
17339	10440131	BC119501	71223	G protein-coupled receptor 15	Gpr15	0.87	-1.052	0.326704	0.602834
17340	10584591					0.87	-2.196	0.0630102	0.232692
17341	10534988					0.87	-0.787	0.456546	0.712611
17342	10475335	NM_007952	14827	protein disulfide isomerase as	Pdia3	0.87	-3.273	0.0130658	0.0818315
17343	10489912	NM_145538	407243	transmembrane protein 189	Tmem189	0.87	-1.173	0.278046	0.55314
17344	10540952	NM_031177	81896	intraflagellar transport 122 h	Ift122	0.87	-2.54	0.0377507	0.167689
17345	10546829	NM_001081147	18430	oxytocin receptor	Oxtr	0.87	-1.072	0.318084	0.595218
17346	10521459	NM_175249	76943	prosaposin-like 1	Psapl1	0.87	-0.909	0.392563	0.66054
17347	10488108	NM_001081090	66580	ESF1, nucleolar pre-rRNA proce	Esf1	0.87	-2.786	0.0262575	0.131343
17348	10430804	BC056972	28075	DNA segment, Chr 15, Wayne Sta	D15Wsu75e	0.87	-2.165	0.0660142	0.239751
17349	10352725	NM_025864	66950	transmembrane protein 206	Tmem206	0.87	-2.97	0.0201021	0.110172
17350	10514791	NM_153565	100102	proprotein convertase subtilis	Pcsk9	0.87	-1.5	0.175964	0.429653
17351	10453688					0.87	-0.833	0.431643	0.692201
17352	10597354	NM_011052	18571	programmed cell death 6 intera	Pdcd6ip	0.87	-1.989	0.0857702	0.281088
17353	10580418	NM_172912	244562	ATP-binding cassette, sub-fami	Abcc12	0.869	-1.5	0.176147	0.429929
17354	10572180	NM_133224	170759	ATPase type 13A1	Atp13a1	0.869	-3.058	0.0177204	0.100883
17355	10445360	NM_178652	109115	suppressor of Ty 3 homolog (S.	Supt3h	0.869	-3.582	0.00851197	0.0604965
17356	10350337	ENSMUST00000054333	320138	RIKEN cDNA A130050O07 gene	A130050O07Rik	0.869	-1.579	0.157127	0.403583
17357	10466344					0.869	-1.261	0.246451	0.519536
17358	10409999	NM_007994	14120	fructose bisphosphatase 2	Fbp2	0.869	-1.486	0.179599	0.434993
17359	10426592	NM_146457	258449	olfactory receptor 282	Olfr282	0.869	-1.532	0.168213	0.419669
17360	10465604	NM_016737	20867	stress-induced phosphoprotein	Stip1	0.869	-2.594	0.0348149	0.158375
17361	10595831	NM_175537	245007	zinc finger and BTB domain con	Zbtb38	0.869	-2.967	0.0201755	0.110487
17362	10569014	NM_030694	80876	interferon induced transmembra	Ifitm2	0.869	-2.035	0.0801373	0.270028
17363	10423383					0.869	-2.009	0.0833135	0.276517
17364	10442027	ENSMUST00000067349	100036531	predicted gene, ENSMUSG0000005	ENSMUSG00000054339	0.869	-0.816	0.44035	0.699292
17365	10596900	NM_133986	102791	T-cell leukemia translocation	Tcta	0.869	-2.781	0.0264676	0.132113
17366	10553399					0.869	-1.554	0.162772	0.411428
17367	10579543	NM_145598	234404	nucleoredoxin-like 1	Nxnl1	0.869	-1.926	0.0942997	0.298038
17368	10407034	NM_008308	15550	5-hydroxytryptamine (serotonin	Htr1a	0.869	-1.389	0.206226	0.470383
17369	10495867	ENSMUST00000109540	668809	predicted gene, EG668809	EG668809	0.869	-1.716	0.128534	0.359524
17370	10474619	NM_010230	14260	formin 1	Fmn1	0.869	-1.128	0.295571	0.57199
17371	10585068	BC094249	244853	RIKEN cDNA D930028F11 gene	D930028F11Rik	0.869	-1.536	0.167222	0.418184
17372	10387922	NM_024211	67863	solute carrier family 25 (mito	Slc25a11	0.869	-2.476	0.0414653	0.177622
17373	10448967	NM_011447	20681	SRY-box containing gene 8	Sox8	0.869	-1.756	0.12128	0.347845
17374	10602719	NM_173367	69361	cysteine-rich perinuclear thec	Cypt3	0.869	-1.685	0.134634	0.369832
17375	10542894					0.869	-2.355	0.0496818	0.200281
17376	10456545	NM_201362	381175	coiled-coil domain containing	Ccdc68	0.869	-1.684	0.134874	0.370228
17377	10441330	NM_175428	114565	zinc finger protein 295	Zfp295	0.869	-2.269	0.0565068	0.217312
17378	10352348	NM_030131	98417	cornichon homolog 4 (Drosophil	Cnih4	0.869	-3.407	0.0108244	0.0716116
17379	10499643	NM_009602	11444	cholinergic receptor, nicotini	Chrnb2	0.869	-1.483	0.180445	0.436137
17380	10583472	NM_023371	23988	protein (peptidyl-prolyl cis/t	Pin1	0.869	-1.912	0.0962029	0.301887
				TBC1 domain family, member					

17381	10521927	NM_144517	67249	TBC1 domain family, member 19	Tbc1d19	0.869	-2.73	0.0284968	0.138514
17382	10354019	BC072639	72097	RIKEN cDNA 2010300C02 gene	2010300C02Rik	0.869	-2.26	0.0572718	0.218979
17383	10357736	NM_182716	269116	neurofascin	Nfasc	0.869	-2.253	0.0578652	0.220644
17384	10530029	NM_144945	246316	leucine-rich repeat LGI family	Lgi2	0.869	-1.663	0.139032	0.377126
17385	10552557	NM_008457	16624	kallikrein 1-related peptidase	Klk1b8	0.869	-2.113	0.0712748	0.250796
17386	10604687	NM_146234	236792	transmembrane protein 32	Tmem32	0.869	-2.552	0.0370795	0.165263
17387	10472361					0.869	-1.758	0.120919	0.347273
17388	10590586	NM_013860	29806	LIM domains containing 1	Limd1	0.869	-1.84	0.107104	0.322599
17389	10541049	NM_027920	71779	membrane-associated ring finge	March8	0.868	-1.63	0.145757	0.38722
17390	10384474	NM_025443	66249	partner of NOB1 homolog (S. ce	Pno1	0.868	-2.188	0.0637763	0.234479
17391	10563728	XM_915262	435978	predicted gene, EG435978	EG435978	0.868	-0.766	0.467729	0.720349
17392	10479099	NM_213733	228961	aminopeptidase-like 1	Npepl1	0.868	-2.304	0.0536115	0.210036
17393	10597775	BC109365	209012	unc-51-like kinase 4 (C. elega	Ulk4	0.868	-2.59	0.0350124	0.159
17394	10497968	ENSMUST00000105030	100038440	predicted gene, ENSMUSG0000007	ENSMUSG00000074617	0.868	-1.756	0.121295	0.347845
17395	10380135					0.868	-0.548	0.599925	0.812084
17396	10409338	BC012213	28126	DNA segment, Chr 13, Wayne Sta	D13Wsu177e	0.868	-2.605	0.0342569	0.156747
17397	10437575	BC027071	74720	RIKEN cDNA 4930511J11 gene	4930511J11Rik	0.868	-0.941	0.376998	0.647069
17398	10540075	NM_144919	232232	histone deacetylase 11	Hdac11	0.868	-0.872	0.411391	0.675346
17399	10558088					0.868	-0.839	0.428351	0.689379
17400	10563838	NM_023647	93790	non imprinted in Prader-Willi/	Nipa2	0.868	-1.897	0.0984737	0.30638
17401	10383351	ENSMUST00000069526	791271	predicted gene, ENSMUSG0000005	ENSMUSG00000055790	0.868	-1.203	0.267007	0.541627
17402	10487139	NM_199022	271849	SHC (Src homology 2 domain con	Shc4	0.868	-2.458	0.0426053	0.180844
17403	10536442					0.868	-1.941	0.0922058	0.294263
17404	10417538	NM_024221	68263	pyruvate dehydrogenase (lipoam	Pdhb	0.868	-2.471	0.0418027	0.178453
17405	10531407	NM_008599	17329	chemokine (C-X-C motif) ligand	Cxcl9	0.868	-1.638	0.144143	0.385253
17406	10353050	NM_013715	26754	COP9 (constitutive photomorpho	Cops5	0.868	-2.926	0.0214362	0.114576
17407	10396125	NM_178628	73991	spastic paraplegia 3A homolog	Spg3a	0.868	-2.495	0.0403078	0.174753
17408	10464672	NM_198113	245857	slingshot homolog 3 (Drosophil	Ssh3	0.868	-2.194	0.0631456	0.232848
17409	10452043	NM_029799	76920	arrestin domain containing 5	Arrdc5	0.868	-1.941	0.0922353	0.294284
17410	10524723	NM_172719	231659	GCN1 general control of amino-	Gcn1l1	0.868	-3.452	0.0101815	0.0688008
17411	10373924	NM_029291	75452	activating signal cointegrator	Ascc2	0.868	-2.546	0.0373655	0.166292
17412	10406865	NM_173757	218506	mitochondrial ribosomal protei	Mrps27	0.868	-1.905	0.0973022	0.303848
17413	10578025					0.868	-2.362	0.0491248	0.198945
17414	10489471	NM_013592	17183	matrilin 4	Matn4	0.868	-1.642	0.143308	0.384029
17415	10553336	NM_028031	243983	zinc finger, DHHC domain conta	Zdhhc13	0.868	-2.752	0.0276177	0.135992
17416	10459802	XR_034415	668184	similar to ribosomal protein L	LOC668184	0.868	-2.351	0.0500016	0.201094
17417	10565577	ENSMUST00000098303	100036533	predicted gene, ENSMUSG0000005	ENSMUSG00000054061	0.868	-1.589	0.154832	0.400004
17418	10432150	NM_001011778	257943	olfactory receptor 285	Olfr285	0.868	-0.893	0.400642	0.666392
17419	10398342	NR_002848	76880	RIKEN cDNA 6430411K18 gene	6430411K18Rik	0.868	-1.731	0.125785	0.355049
17420	10565525					0.868	-1.31	0.230217	0.501153
17421	10566564	NM_025301	27397	mitochondrial ribosomal protei	Mrpl17	0.868	-2.419	0.0451655	0.187967
17422	10551966	NM_001012401	243912	heat shock protein, alpha-crys	Hspb6	0.868	-2.35	0.0500175	0.201094
17423	10556125	XR_033898	626732	similar to peptidylprolyl isom	LOC626732	0.868	-1.809	0.112088	0.33142
17424	10415787	NM_206974	328424	potassium channel regulator	Kcnrg	0.868	-2.237	0.059205	0.224025
17425	10410889					0.868	-1.887	0.0998809	0.308935
17426	10345529	ENSMUST00000067178	215413	RIKEN cDNA A230074B11 gene	A230074B11Rik	0.868	-1.797	0.114097	0.335204
17427	10428912	XR_035243	399603	RIKEN cDNA D330050I23 gene	D330050I23Rik	0.868	-1.935	0.0930572	0.295658
17428	10576940	AK149049	270028	expressed sequence AW121567	AW121567	0.868	-1.688	0.134055	0.36907
17429	10408364	XR_033316	214973	similar to peptidylprolyl isom	LOC214973	0.868	-1.79	0.115333	0.337519
17430	10480345	XR_032045	625815	similar to ATP synthase, H+ tr	LOC625815	0.868	-2.618	0.0335944	0.154552
17431	10493094	NM_026591	67707	mitochondrial ribosomal protei	Mrpl24	0.868	-2.672	0.031035	0.146999

17432	10600584					0.868	-1.542	0.165679	0.416146
17433	10476104					0.868	-1.441	0.191553	0.450872
17434	10573457	NM_010635	16596	Kruppel-like factor 1 (erythro	Klf1	0.868	-0.74	0.482598	0.731369
17435	10579052	ENSMUST00000095282	378466	predicted gene, ENSMUSG0000005	ENSMUSG00000057924	0.868	-1.52	0.171041	0.422803
17436	10355528					0.868	-1.139	0.291174	0.56727
17437	10437737	NM_025546	66409	ribosomal L1 domain containing	Rsl1d1	0.867	-2.482	0.0411107	0.176721
17438	10364315					0.867	-1.764	0.119808	0.346027
17439	10386473	NM_011480	20787	sterol regulatory element bind	Srebf1	0.867	-2.774	0.0267221	0.132919
17440	10591537	NM_010744	17083	transmembrane emp24 domain con	Tmed1	0.867	-2.457	0.0426904	0.181072
17441	10518763	NM_173774	242773	solute carrier family 45, memb	Slc45a1	0.867	-1.163	0.281866	0.557053
17442	10569654	AK007416	381935	RIKEN cDNA 1810010D01 gene	1810010D01Rik	0.867	-1.115	0.300819	0.57699
17443	10483559	ENSMUST00000115986	100039766	similar to High mobility group	LOC100039766	0.867	-1.018	0.341793	0.616313
17444	10493894					0.867	-0.851	0.422092	0.684326
17445	10546710	NM_181590	72171	SHQ1 homolog (S. cerevisiae)	Shq1	0.867	-2.935	0.0211416	0.113886
17446	10442829	NM_022422	64337	guanine nucleotide binding pro	Gng13	0.867	-2.321	0.0522417	0.206719
17447	10373101	NM_054097	117150	phosphatidylinositol-5-phospha	Pip4k2c	0.867	-2.039	0.0796989	0.269022
17448	10574511	BC015286	234669	cDNA sequence BC015286	BC015286	0.867	-2.093	0.0734709	0.255968
17449	10541182	NM_133940	101358	F-box and leucine-rich repeat	Fbxl14	0.867	-2.837	0.0243635	0.125168
17450	10449977	NM_001009544	74042	RIKEN cDNA 4921501E09 gene	4921501E09Rik	0.867	-1.707	0.130239	0.362012
17451	10550509	NM_009402	21946	peptidoglycan recognition prot	Pglyrp1	0.867	-2.809	0.0254056	0.128819
17452	10429528	NM_029627	76486	lymphocyte antigen 6 complex,	Ly6k	0.867	-1.58	0.156914	0.403374
17453	10471953	NM_007396	11480	activin receptor IIA	Acvr2a	0.867	-3.812	0.00625328	0.0483612
17454	10353115					0.867	-2.282	0.0553722	0.214666
17455	10559270	NM_020285	56844	tumor-suppressing subchromosom	Tssc4	0.867	-2.201	0.0625091	0.231461
17456	10384883	NM_176829	216622	RIKEN cDNA 4931440F15 gene	4931440F15Rik	0.867	-1.766	0.119462	0.345748
17457	10484807	NM_146789	258785	olfactory receptor 1230	Olfr1230	0.867	-1.763	0.120072	0.346527
17458	10392098	NM_025310	56095	FtsJ homolog 3 (E. coli)	Ftsj3	0.867	-2.584	0.0353281	0.160055
17459	10563825					0.867	-1.579	0.157069	0.403482
17460	10442616	NM_024284	14651	hydroxyacyl glutathione hydrol	Hagh	0.867	-2.23	0.0599066	0.225586
17461	10375527	NM_146276	258273	olfactory receptor 1394	Olfr1394	0.867	-1.238	0.254448	0.5287
17462	10422272	NM_177753	223227	SRY-box containing gene 21	Sox21	0.867	-2.403	0.0462394	0.190954
17463	10588083	NM_001122851	23873	Fas apoptotic inhibitory molec	Faim	0.867	-2.359	0.0494124	0.19969
17464	10537426	ENSMUST00000101511	75379	RIKEN cDNA 4930599N23 gene	4930599N23Rik	0.867	-2.289	0.0548085	0.21346
17465	10532390	NM_153570	100608	nucleolar complex associated 4	Noc4l	0.867	-3.139	0.0157705	0.0934297
17466	10349383	NM_028787	74150	solute carrier family 35, memb	Slc35f5	0.867	-1.754	0.121667	0.348297
17467	10349239	NM_026472	67949	Mki67 (FHA domain) interacting	Mki67ip	0.867	-2.142	0.0682471	0.244165
17468	10472925	ENSMUST00000077161	67686	RIKEN cDNA 1700011J10 gene	1700011J10Rik	0.867	-1.918	0.095326	0.300062
17469	10379836					0.867	-1.059	0.32382	0.600286
17470	10573637	NM_199446	102093	phosphorylase kinase beta	Phkb	0.867	-1.986	0.0862544	0.282185
17471	10542764	NM_172309	272322	aryl hydrocarbon receptor nucl	Arntl2	0.867	-2.19	0.0635778	0.233993
17472	10428744	BC050895	75758	RIKEN cDNA 9130401M01 gene	9130401M01Rik	0.867	-1.934	0.0930989	0.295671
17473	10433639	NM_153588	239719	MKL/myocardin-like 2	Mkl2	0.866	-3.153	0.0154643	0.09237
17474	10416725	ENSMUST00000022596	219249	tudor domain containing 3	Tdrd3	0.866	-0.501	0.631083	0.832075
17475	10482119					0.866	-1.333	0.223014	0.492935
17476	10488944	NM_018888	56046	ubiquinol-cytochrome c reducta	Uqcc	0.866	-2.441	0.0436798	0.184014
17477	10559446	NM_011095	18733	leukocyte immunoglobulin-like	Lilrb3	0.866	-0.991	0.353745	0.6265
17478	10561474	NM_001024673	330496	interleukin 28A	Il28a	0.866	-1.27	0.243449	0.516453
17479	10495094	BC052371	109050	RIKEN cDNA 6530418L21 gene	6530418L21Rik	0.866	-1.347	0.218754	0.486928
17480	10424062	XR_035197	239410	RIKEN cDNA A930017M01 gene	A930017M01Rik	0.866	-1.649	0.141934	0.381716
17481	10568247	NM_026999	69234	zinc finger protein 688	Zfp688	0.866	-2.332	0.0514048	0.204767
17482	10422537	NM_177393	338370	sodium leak channel, non-selec	Nalcn	0.866	-1.343	0.220001	0.48888

17483	10460356	NM_206973	269053	G protein-coupled receptor 152	Gpr152	0.866	-1.839	0.107264	0.322736
17484	10352454					0.866	-1.7	0.131759	0.364648
17485	10350159	NM_133664	16763	ladinin	Lad1	0.866	-2.599	0.0345892	0.157792
17486	10594798					0.866	-0.397	0.702871	0.869709
17487	10381561	NM_148953	217217	ankyrin repeat and SOCS box-co	Asb16	0.866	-1.843	0.106601	0.322042
17488	10474793	NM_001033254	214230	p21 (CDKN1A)-activated kinase	Pak6	0.866	-1.83	0.108745	0.325496
17489	10444674	NM_023463	68468	lymphocyte antigen 6 complex,	Ly6g6c	0.866	-1.224	0.259489	0.533772
17490	10413222	NM_134084	105675	peptidylprolyl isomerase F (cy	Ppif	0.866	-1.819	0.110431	0.328752
17491	10384940	NM_025745	66753	RIKEN cDNA 4933407N01 gene	4933407N01Rik	0.866	-2.087	0.074139	0.257405
17492	10515326	NM_177670	230657	transmembrane protein 69	Tmem69	0.866	-1.703	0.13117	0.363684
17493	10456248	NM_194268	225631	one cut domain, family member	Onecut2	0.866	-3.304	0.0125086	0.0791151
17494	10361323	NM_172546	215748	Cnksr family member 3	Cnksr3	0.866	-3.095	0.0167948	0.0975911
17495	10460157	NM_013495	12894	carnitine palmitoyltransferase	Cpt1a	0.866	-1.927	0.094171	0.297861
17496	10454851	NM_133687	67393	CXXC finger 5	Cxxc5	0.866	-2.099	0.0728658	0.254427
17497	10522160	NM_001024917	333789	NEDD4 binding protein 2	N4bp2	0.866	-3.416	0.0107013	0.0711644
17498	10470182	NM_023326	107771	brain expressed myelocytomatos	Bmyc	0.866	-3.111	0.0164234	0.0962129
17499	10366846	AK014574	216440	amplified in osteosarcoma	Os9	0.866	-2.767	0.0270038	0.133769
17500	10599200	NM_016783	53328	progesterone receptor membrane	Pgrmc1	0.866	-2.995	0.0193798	0.107409
17501	10394831	ENSMUST00000101569	544848	predicted gene, EG544848	EG544848	0.866	-1.307	0.231369	0.502215
17502	10578322					0.866	-2.479	0.0413227	0.177398
17503	10471782	NM_146374	258371	olfactory receptor 368	Olfr368	0.866	-2.641	0.0325115	0.151516
17504	10476301	NM_145533	228608	spermine oxidase	Smox	0.866	-2.2	0.0626098	0.231629
17505	10355670	NM_001039495	241116	coiled-coil domain containing	Ccdc108	0.866	-2.187	0.0638158	0.234583
17506	10486290					0.866	-2.415	0.0454413	0.18869
17507	10500614	NM_010763	17156	mannosidase, alpha, class 1A,	Man1a2	0.866	-2.662	0.031487	0.148343
17508	10382339	ENSMUST00000105048	791285	predicted gene, ENSMUSG0000005	ENSMUSG00000053270	0.865	-0.89	0.40232	0.667397
17509	10464642	BC023699	107239	expressed sequence AI790298	AI790298	0.865	-1.412	0.19975	0.461486
17510	10512111	NM_021535	74255	smu-1 suppressor of mec-8 and	Smu1	0.865	-2.649	0.0321213	0.150359
17511	10517425	NM_011942	26394	lysophospholipase 2	Lypla2	0.865	-3.643	0.00783857	0.0571538
17512	10585328	ENSMUST00000034550	74695	RIKEN cDNA 4930510E17 gene	4930510E17Rik	0.865	-1.731	0.125788	0.355049
17513	10599118					0.865	-1.508	0.174151	0.427126
17514	10499932	NM_026335	67718	late cornified envelope 1H	Lce1h	0.865	-2.356	0.0496224	0.200156
17515	10563260	NM_009224	20637	U1 small nuclear ribonucleopro	Snrp70	0.865	-3.574	0.00860491	0.0610135
17516	10400538	NM_030057	78232	trafficking protein particle c	Trappc6b	0.865	-2.31	0.0531561	0.209143
17517	10395534	XM_001472023	100039062	hypothetical protein LOC100039	LOC100039062	0.865	-1.011	0.344941	0.61898
17518	10480249	NM_013935	30963	protein tyrosine phosphatase-l	Ptpla	0.865	-1.317	0.228219	0.499214
17519	10590269	NM_001039364	17433	myelin-associated oligodendroc	Mobp	0.865	-1.632	0.14549	0.387083
17520	10554658	ENSMUST00000066005	330578	Riken cDNA A530021J07 gene	A530021J07Rik	0.865	-1.652	0.141309	0.38052
17521	10382139	NM_025894	66997	proteasome (prosome, macropain	Psmd12	0.865	-3.075	0.0173005	0.0993755
17522	10430247	NM_019913	56551	thioredoxin 2	Txn2	0.865	-2.615	0.033739	0.155049
17523	10417183	NM_144844	110821	propionyl-Coenzyme A carboxyla	Pcca	0.865	-2.818	0.025049	0.127623
17524	10456793	NM_025409	66191	immediate early response 3 int	Ier3ip1	0.865	-2.64	0.0325186	0.151516
17525	10559310					0.865	-1.842	0.106712	0.32221
17526	10464754	NM_007485	11854	ras homolog gene family, membe	Rhod	0.865	-1.991	0.0854996	0.280626
17527	10523506	NM_173404	110075	bone morphogenetic protein 3	Bmp3	0.865	-1.43	0.19466	0.454744
17528	10568593	NM_028095	72096	methyltransferase like 10	Mettl10	0.865	-2.04	0.079557	0.268715
17529	10383671	NM_007879	13494	developmentally regulated GTP	Drg1	0.865	-3.099	0.0167154	0.09731
17530	10498309	NM_019410	18645	profilin 2	Pfn2	0.865	-3.06	0.0176533	0.100664
17531	10444098	NM_020603	57315	WD repeat domain 46	Wdr46	0.865	-2.845	0.0240974	0.124223
17532	10606301	NM_025952	67075	magnesium transporter 1	Magt1	0.865	-2.123	0.070207	0.248316
17533	10537851	NM_001004357	66797	contactin associated protein-l	Cntnap2	0.865	-2.362	0.0491565	0.19896
17534	10506627	BC043687	230582	RIKEN cDNA 2810410C14 gene	2810410C14Rik	0.865	-2.856	0.0237294	0.122794
17535	10511368	NM_177730	242291	inositol monophosphatase domai	Impad1	0.865	-2.415	0.0454563	0.188715

17536	10584236	ENSMUST00000098906	330921	gene model 846, (NCBI)	Gm846	0.865	-2.617	0.0336755	0.154849
17537	10447093	BC118946	67737	RIKEN cDNA 4930560E09 gene	4930560E09Rik	0.865	-2.688	0.0303349	0.144768
17538	10599960					0.865	-0.957	0.369734	0.640267
17539	10454254	NM_207650	13527	dystrobrevin alpha	Dtna	0.865	-2.17	0.065457	0.238533
17540	10603362	NM_207202	54648	coiled-coil domain containing	Ccdc120	0.865	-1.786	0.116063	0.338816
17541	10457022	NM_010777	17196	myelin basic protein	Mbp	0.865	-2.867	0.0233255	0.121327
17542	10518774	NM_020569	57320	Parkinson disease (autosomal r	Park7	0.865	-2.838	0.0243296	0.125082
17543	10514884	NM_025500	56280	mitochondrial ribosomal protei	Mrpl37	0.865	-2.703	0.0296379	0.142372
17544	10532628					0.865	-1.366	0.213091	0.478965
17545	10584855	NM_001014761	72821	sodium channel, voltage-gated,	Scn2b	0.865	-2.546	0.0373836	0.166338
17546	10363170	NR_003618	73390	RIKEN cDNA 1700060H10 gene	1700060H10Rik	0.865	-1.541	0.165864	0.416412
17547	10526381	NM_008617	17448	malate dehydrogenase 2, NAD (m	Mdh2	0.865	-4.052	0.00456533	0.0385193
17548	10404717	NM_026550	68083	PAK1 interacting protein 1	Pak1ip1	0.865	-2.218	0.0609241	0.227796
17549	10576942					0.865	-1.214	0.26287	0.537432
17550	10453764	ENSMUST00000116082	433161	predicted gene, EG433161	EG433161	0.865	-1.713	0.129112	0.36034
17551	10468450	ENSMUST00000071866	433251	predicted gene, EG433251	EG433251	0.864	-0.902	0.396339	0.663741
17552	10593887	NM_028347	72774	nei endonuclease VIII-like 1 (	Neil1	0.864	-2.396	0.0467607	0.192094
17553	10467173					0.864	-1.384	0.207666	0.472138
17554	10380986	NM_009439	22123	proteasome (prosome, macropain	Psmd3	0.864	-2.68	0.0306941	0.145809
17555	10497372	DQ055451	381484	SIRP beta 1 like 1 protein	LOC381484	0.864	-1.62	0.1479	0.390122
17556	10494761	NM_178594	242122	V-set domain containing T cell	Vtcn1	0.864	-2.45	0.0431436	0.182497
17557	10497646	BC050266	241915	polyhomeotic-like 3 (Drosophil	Phc3	0.864	-1.508	0.174147	0.427126
17558	10479740					0.864	-1.24	0.253854	0.52814
17559	10560202	NM_001081418	243842	glioma tumor suppressor candid	Gltscr1	0.864	-1.466	0.184726	0.442299
17560	10504986	XR_031665	666761	nascent polypeptide-associated	LOC666761	0.864	-1.179	0.275876	0.550733
17561	10405969					0.864	-1.919	0.0952924	0.300009
17562	10515335	AK039789	654318	RIKEN cDNA C530005A16 gene	C530005A16Rik	0.864	-1.248	0.251049	0.524992
17563	10548779	NM_029595	76400	phosphatidylethanolamine bindi	Pbp2	0.864	-2.494	0.0403719	0.174923
17564	10382069	NM_008950	19184	protease (prosome, macropain)	Psmc5	0.864	-2.798	0.0258194	0.130201
17565	10523541	NM_026826	68735	mitochondrial ribosomal protei	Mrps18c	0.864	-2.864	0.0234377	0.121731
17566	10540795	NM_172161	108960	interleukin-1 receptor-associa	Irak2	0.864	-2.327	0.0517556	0.205622
17567	10361191	NM_181546	329324	synaptotagmin XIV	Syt14	0.864	-1.857	0.104411	0.31797
17568	10538206	NM_175098	57895	coiled-coil domain containing	Ccdc126	0.864	-2.039	0.0796864	0.269022
17569	10425890	NM_028455	73167	RIKEN cDNA 3110043J09 gene	3110043J09Rik	0.864	-2.164	0.0660886	0.239852
17570	10568758	ENSMUST00000068996	77252	RIKEN cDNA 9430038I01 gene	9430038I01Rik	0.864	-3.051	0.0178859	0.101498
17571	10462613	NM_008332	15958	interferon-induced protein wit	Ifit2	0.864	-1.52	0.171046	0.422803
17572	10500960	NM_017397	53975	DEAD (Asp-Glu-Ala-Asp) box pol	Ddx20	0.864	-3.117	0.0162832	0.0956368
17573	10542555	BC006653	620031	hypothetical protein LOC620031	MGC7817	0.864	-0.996	0.35155	0.624753
17574	10351345					0.864	-0.786	0.457005	0.712826
17575	10398085	NM_028419	73046	glutaredoxin 5 homolog (S. cer	Glrx5	0.864	-2.098	0.0728862	0.254434
17576	10576288	NM_172287	234857	spire homolog 2 (Drosophila)	Spire2	0.864	-1.457	0.187323	0.445668
17577	10500847	NM_133853	99470	membrane associated guanylate	Magi3	0.864	-1.637	0.144395	0.385687
17578	10541873	NM_025595	66493	mitochondrial ribosomal protei	Mrpl51	0.864	-2.737	0.0281936	0.137705
17579	10365290	NM_021439	58250	carbohydrate sulfotransferase	Chst11	0.864	-1.818	0.110593	0.329025
17580	10587293	NM_008103	14531	glial cells missing homolog 1	Gcm1	0.864	-1.743	0.123517	0.351593
17581	10354494	NM_008667	17936	Ngfi-A binding protein 1	Nab1	0.864	-2.216	0.0611748	0.228316
17582	10393614	NM_013926	30951	chromobox homolog 8 (Drosophil	Cbx8	0.864	-1.754	0.121619	0.348228
17583	10487441	NM_010762	17153	myelin and lymphocyte protein,	Mal	0.864	-1.37	0.211922	0.477389
17584	10559276	NM_008434	16535	potassium voltage-gated channe	Kcnq1	0.864	-2.497	0.0402282	0.174515
17585	10548699	XR_035025	668063	similar to ubiquitin-conjugati	LOC668063	0.864	-2.173	0.0651912	0.238029
17586	10405334	NM_001033269	218268	eukaryotic translation initiat	Eif4e1b	0.864	-1.368	0.212337	0.477959
17587	10404412	NM_030215	78903	Werner helicase interacting pr	Wrnip1	0.864	-2.539	0.0377721	0.167749

17588	10578203	NM_027998	71908	claudin 23	Cldn23	0.864	-1.785	0.116118	0.338871
17589	10362876	NM_027772	71365	prenyl (solanesyl) diphosphate	Pdss2	0.863	-2.099	0.0727829	0.25432
17590	10540296					0.863	-1.527	0.169286	0.42056
17591	10501447	NM_025845	66921	PRP38 pre-mRNA processing fact	Prpf38b	0.863	-3.172	0.0150566	0.0906069
17592	10547719	NM_153508	232370	calsyntenin 3	Clstn3	0.863	-1.917	0.0955197	0.300412
17593	10414031	NM_019506	12165	growth differentiation factor	Gdf2	0.863	-1.109	0.303017	0.579039
17594	10582025	NM_029686	76645	polycystic kidney disease 1 li	Pkd1l2	0.863	-1.842	0.106725	0.32221
17595	10521693					0.863	-1.52	0.171049	0.422803
17596	10570013	NM_001081119	68904	abhydrolase domain containing	Abhd13	0.863	-2.683	0.030535	0.14545
17597	10412823	AK138270	77981	RIKEN cDNA B230110C06 gene	B230110C06Rik	0.863	-0.798	0.450552	0.707814
17598	10396896	BC117754	328133	solute carrier family 39 (zinc	Slc39a9	0.863	-3.386	0.0111488	0.0730722
17599	10434773	NM_001004151	239766	receptor transporter protein 1	Rtp1	0.863	-1.921	0.0949284	0.299577
17600	10463121	NM_028319	72672	zinc finger protein 518	Zfp518	0.863	-2.107	0.0719508	0.252251
17601	10364149	NM_009115	20203	S100 protein, beta polypeptide	S100b	0.863	-2.499	0.0400883	0.174258
17602	10449854	NM_017476	54194	A kinase (PRKA) anchor protein	Akap8l	0.863	-2.439	0.0438271	0.184341
17603	10593497	ENSMUST00000038822	244871	zinc finger CCCH type containi	Zc3h12c	0.863	-1.581	0.156746	0.403094
17604	10347508	NM_170755	227298	cDNA sequence BC038286	BC038286	0.863	-2.646	0.0322585	0.150768
17605	10473158	ENSMUST00000066625	100126874	predicted gene, ENSMUSG0000005	ENSMUSG00000053902	0.863	-1.203	0.266795	0.541465
17606	10451591	NM_025365	66119	prickle homolog 4 (Drosophila)	Prickle4	0.863	-1.921	0.0950106	0.299665
17607	10532993	NM_007748	12861	cytochrome c oxidase, subunit	Cox6a1	0.863	-2.644	0.0323404	0.151017
17608	10430993	ENSMUST00000100370	69291	RIKEN cDNA 1700001L05 gene	1700001L05Rik	0.863	-1.642	0.143396	0.384029
17609	10364890	NM_013651	20222	splicing factor 3a, subunit 2	Sf3a2	0.863	-2.406	0.0460382	0.190346
17610	10424102	ENSMUST00000100666	665097	predicted gene, EG665097	EG665097	0.863	-0.994	0.352209	0.625281
17611	10568040	NM_019674	56420	protein phosphatase 4, catalyt	Ppp4c	0.862	-3.033	0.018371	0.103528
17612	10391768	NM_011431	20624	elongation factor Tu GTP bindi	Eftud2	0.862	-2.524	0.0386277	0.16991
17613	10572235	NM_020028	53978	lysophosphatidic acid receptor	Lpar2	0.862	-2.136	0.0688553	0.245818
17614	10490690	NM_026765	68556	uridine-cytidine kinase 1-like	Uckl1	0.862	-2.142	0.068237	0.244165
17615	10348558	NM_016717	50880	selenocysteine lyase	Scly	0.862	-2	0.0844535	0.278893
17616	10401172	NM_016800	53612	vesicle transport through inte	Vti1b	0.862	-3.938	0.00528998	0.0429867
17617	10375483	XR_031591	628753	similar to hCG2016250	LOC628753	0.862	-2.214	0.0612863	0.228462
17618	10572616	BC093523	66498	DET1 and DDB1 associated 1	Dda1	0.862	-2.167	0.0657812	0.239147
17619	10560491	NM_146182	232943	kinesin light chain 3	Klc3	0.862	-2.323	0.0520689	0.206366
17620	10549445					0.862	-2.537	0.0378738	0.168059
17621	10470322	NM_013678	20931	surfeit gene 2	Surf2	0.862	-2.319	0.0524379	0.207126
17622	10523481					0.862	-1.425	0.196018	0.456422
17623	10381371	NM_009675	11754	amine oxidase, copper containi	Aoc3	0.862	-1.857	0.104487	0.318109
17624	10465500	NM_008431	16528	potassium channel, subfamily K	Kcnk4	0.862	-2.016	0.0823696	0.274487
17625	10446804	NM_144798	210148	solute carrier family 30 (zinc	Slc30a6	0.862	-2.388	0.0473125	0.193459
17626	10493120	NM_025663	66614	G patch domain containing 4	Gpatch4	0.862	-2.644	0.03234	0.151017
17627	10501218	NM_010359	14864	glutathione S-transferase, mu	Gstm3	0.862	-0.997	0.351173	0.624551
17628	10597132					0.862	-1.96	0.0896436	0.289031
17629	10440554	NM_001081068	78913	zinc finger protein 294	Zfp294	0.862	-1.323	0.226237	0.496889
17630	10365206	ENSMUST00000099431	666790	predicted gene, EG666790	EG666790	0.862	-1.137	0.291834	0.567841
17631	10443506	NM_013710	26382	FYVE, RhoGEF and PH domain con	Fgd2	0.862	-1.213	0.263261	0.538023
17632	10426905	NM_001034883	432982	predicted gene, EG432982	EG432982	0.862	-0.87	0.412327	0.676163
17633	10442752	BC027751	68327	RIKEN cDNA 0610007P22 gene	0610007P22Rik	0.862	-3.249	0.0135041	0.0837087
17634	10529547					0.862	-2.538	0.0378589	0.168029
17635	10426924	NM_021530	59033	solute carrier family 4 (anion	Slc4a8	0.862	-2.216	0.0611436	0.228252
17636	10550402	NM_001007569	71691	PNMA-like 1	Pnmal1	0.862	-2.054	0.0779053	0.265468
17637	10367436	NM_001042580	12512	Cd63 antigen	Cd63	0.862	-2.359	0.049386	0.199621
17638	10489219	NM_177657	228846	RIKEN cDNA D630003M21 gene	D630003M21Rik	0.862	-2.816	0.0251449	0.127896
17639	10427459	ENSMUST00000055038	239319	caspase recruitment domain fam	Card6	0.862	-2.241	0.05888	0.223325
17640	10416948					0.862	-1.377	0.209657	0.474726

17641	10510022	ENSMUST00000097812	100163	expressed sequence AI507597	AI507597	0.862	-1.463	0.183661	0.443387
17642	10375553	NM_147066	259069	olfactory receptor 1389	Olfr1389	0.862	-2.519	0.0389103	0.17083
17643	10472809	NM_010053	13390	distal-less homeobox 1	Dlx1	0.862	-1.378	0.209399	0.474598
17644	10498038	NM_023502	69257	E74-like factor 2	Elf2	0.862	-2.321	0.0522468	0.206719
17645	10568861	XR_030607	244229	similar to ribosomal protein S	LOC244229	0.862	-2.356	0.0496078	0.200156
17646	10395893	NM_025656	66603	survivor of motor neuron prote	Sip1	0.862	-2.454	0.0428807	0.181734
17647	10604053	NM_029891	77286	NF-kappaB repressing factor	Nkrf	0.862	-2.118	0.070768	0.249678
17648	10540676	NM_026365	67767	jagunal homolog 1 (Drosophila)	Jagn1	0.862	-2.91	0.0219148	0.116412
17649	10413229	NM_013469	11744	annexin A11	Anxa11	0.861	-2.74	0.0280818	0.137509
17650	10561153	NM_001081148	243881	cytochrome P450, family 2, sub	Cyp2b23	0.861	-1.292	0.236262	0.508392
17651	10397145	NM_134188	171210	acyl-CoA thioesterase 2	Acot2	0.861	-1.179	0.275762	0.550639
17652	10565709	NM_001081167	272411	UDP-GlcNAc:betaGal beta-1,3-N-	B3gnt6	0.861	-1.729	0.126173	0.355658
17653	10550482	NM_001003393	232925	IGF-like family member 3	Igfl3	0.861	-1.865	0.103187	0.315516
17654	10477061	NM_029688	76650	sulfiredoxin 1 homolog (S. cer	Srxn1	0.861	-2.168	0.0657281	0.239036
17655	10471735	NM_001081410	666118	olfactory receptor 335	Olfr335	0.861	-1.456	0.187524	0.445758
17656	10460490					0.861	-2.315	0.0527425	0.207909
17657	10454653					0.861	-1.23	0.257463	0.531656
17658	10517808	NM_011060	18601	peptidyl arginine deiminase, t	Padi3	0.861	-2.157	0.0668003	0.24144
17659	10588035	XR_031771	667298	similar to ribosomal protein S	LOC667298	0.861	-2.926	0.0214313	0.114576
17660	10383717	NM_172439	170835	phosphatidylinositol (4,5) bis	Pib5pa	0.861	-2.489	0.0407174	0.175879
17661	10476941					0.861	-1.892	0.0992119	0.307631
17662	10535084	NM_028469	73212	RIKEN cDNA 3110082I17 gene	3110082I17Rik	0.861	-2.303	0.0536674	0.210176
17663	10416044	NM_145944	67179	coiled-coil domain containing	Ccdc25	0.861	-2.425	0.044743	0.187121
17664	10415737	NM_183175	239126	C1q and tumor necrosis factor	C1qtnf9	0.861	-0.907	0.393696	0.661649
17665	10485550	NM_001033347	241589	RIKEN cDNA D430041D05 gene	D430041D05Rik	0.861	-2.128	0.0697803	0.247552
17666	10560630	NM_001109748	53333	translocase of outer mitochond	Tomm40	0.861	-2.58	0.0355727	0.160632
17667	10434675	NM_026400	67838	DnaJ (Hsp40) homolog, subfamil	Dnajb11	0.861	-2.742	0.0279968	0.137267
17668	10474870	NM_173450	271842	RNA pseudouridylate synthase d	Rpusd2	0.861	-3.071	0.0173916	0.0997203
17669	10430768	XR_031503	667073	similar to ribosomal protein L	LOC667073	0.861	-1.714	0.128932	0.36017
17670	10476660	BC063088	74528	RIKEN cDNA 8430406I07 gene	8430406I07Rik	0.861	-1.928	0.0940224	0.297695
17671	10479514	BC016112	73368	collagen, type XX, alpha 1	Col20a1	0.861	-1.437	0.192746	0.452222
17672	10523843					0.861	-0.954	0.371107	0.641955
17673	10509571	NM_008868	18781	phospholipase A2, group IIC	Pla2g2c	0.861	-1.84	0.107082	0.322599
17674	10400131	XM_001471947	791391	predicted gene, ENSMUSG0000006	ENSMUSG00000066507	0.861	-0.799	0.449852	0.707187
17675	10517980	NM_145987	213989	transmembrane protein 82	Tmem82	0.861	-1.171	0.278645	0.553572
17676	10388010	NM_007573	12261	complement component 1, q subc	C1qbp	0.861	-3.304	0.0124967	0.0790871
17677	10432492	NM_028224	72393	Fas apoptotic inhibitory molec	Faim2	0.861	-1.201	0.267667	0.542452
17678	10512626	NM_019486	56015	olfactory receptor 71	Olfr71	0.861	-1.359	0.215018	0.481962
17679	10364102	NM_175329	103172	Nur77 downstream gene 2	Ndg2	0.861	-1.897	0.098436	0.306348
17680	10365337					0.861	-3.152	0.0155016	0.0924565
17681	10352756	NM_172266	226856	lysophosphatidylglycerol acylt	Lpgat1	0.861	-2.903	0.0221505	0.117205
17682	10526553	NM_001039385	381677	VGF nerve growth factor induci	Vgf	0.861	-1.845	0.106273	0.321598
17683	10542824	NM_145573	232536	mitochondrial ribosomal protei	Mrps35	0.861	-4.078	0.00441403	0.0375122
17684	10417700	XR_033308	667152	enolase 1, alpha non-neuron ps	LOC667152	0.861	-1.751	0.122223	0.349463
17685	10365260	NM_001042523	50493	thioredoxin reductase 1	Txnrd1	0.861	-3.009	0.0190162	0.106006
17686	10533090	NM_028128	72151	replication factor C (activato	Rfc5	0.861	-2.965	0.0202358	0.110703
17687	10362896	NM_009846	12484	CD24a antigen	Cd24a	0.861	-2.871	0.0231914	0.120967
17688	10491922	NM_053089	74838	NMDA receptor-regulated gene 1	Narg1	0.861	-2.58	0.035554	0.160597
17689	10520304	NM_001004365	242894	ARP3 actin-related protein 3 h	Actr3b	0.861	-3.558	0.00880444	0.062033
17690	10525111	NM_028041	71990	DEAD (Asp-Glu-Ala-Asp) box pol	Ddx54	0.861	-3.387	0.0111291	0.0729652
17691	10392839	NM_172050	217306	CD300e antigen	Cd300e	0.861	-1.265	0.245235	0.518331
17692	10552311	XR_031416	100045562	similar to ornithine decarboxy	LOC100045562	0.861	-1.759	0.12078	0.347262

17693	10472946	NM_008275	15433	homeo box D13	Hoxd13	0.861	-1.732	0.12556	0.354782
17694	10399710	NM_021384	58185	radical S-adenosyl methionine	Rsad2	0.86	-1.245	0.252122	0.526247
17695	10400559					0.86	-2.155	0.0669813	0.241723
17696	10421922					0.86	-1.59	0.154656	0.399843
17697	10564849	BC031379	70420	RIKEN cDNA 2610034B18 gene	2610034B18Rik	0.86	-2.98	0.0198131	0.109209
17698	10384322	NM_008316	15574	Hus1 homolog (S. pombe)	Hus1	0.86	-3.915	0.00545813	0.043998
17699	10440206	NM_019665	56297	ADP-ribosylation factor-like 6	Arl6	0.86	-2.533	0.0381441	0.168763
17700	10515132					0.86	-2.668	0.0312261	0.147673
17701	10460303	NM_013878	29866	calcium binding protein 2	Cabp2	0.86	-2.001	0.0843459	0.278694
17702	10474902	NM_011234	19361	RAD51 homolog (S. cerevisiae)	Rad51	0.86	-2.769	0.026934	0.133527
17703	10429506	NM_026671	68311	Ly6/Plaur domain containing 2	Lypd2	0.86	-1.337	0.221728	0.491272
17704	10481531	BC005624	227707	cDNA sequence BC005624	BC005624	0.86	-4.148	0.00403509	0.0352117
17705	10573217	NM_197982	68278	DEAD (Asp-Glu-Ala-Asp) box pol	Ddx39	0.86	-2.742	0.0280006	0.137267
17706	10373218	NM_183297	104080	neurexophilin 4	Nxph4	0.86	-2.29	0.0547713	0.213354
17707	10365123	AK080664	102115	deoxyhypusine hydroxylase/mono	Dohh	0.86	-1.535	0.167368	0.418358
17708	10394471	NM_011519	20969	syndecan 1	Sdc1	0.86	-1.663	0.139029	0.377126
17709	10408321	NM_020567	57441	geminin	Gmnn	0.86	-2.268	0.056561	0.21744
17710	10472514	NM_181547	329416	nitric oxide synthase traffick	Nostrin	0.86	-1.764	0.119872	0.346111
17711	10500360	ENSMUST00000107095	100038464	predicted gene, OTTMUSG0000002	OTTMUSG00000021867	0.86	-1.578	0.157294	0.403864
17712	10421046	NM_177780	68813	dedicator of cytokinesis 5	Dock5	0.86	-2.195	0.0630842	0.232827
17713	10488938	BC113797	71405	RIKEN cDNA 5530400B04 gene	5530400B04Rik	0.86	-1.147	0.288017	0.563886
17714	10562599	XM_973360	434168	predicted gene, EG434168	EG434168	0.86	-2.388	0.0472605	0.193319
17715	10503926	NM_181406	109093	arginyl-tRNA synthetase 2, mit	Rars2	0.86	-2.361	0.0492485	0.199218
17716	10533180					0.86	-1.869	0.102653	0.314472
17717	10398859	NM_007421	11565	adenylosuccinate synthetase li	Adssl1	0.86	-1.763	0.120053	0.346527
17718	10504672	NM_146142	100121	tudor domain containing 7	Tdrd7	0.86	-2.419	0.0451659	0.187967
17719	10585201	NM_013897	30057	translocase of inner mitochond	Timm8b	0.86	-3.631	0.00797125	0.0578394
17720	10423803	XR_032597	382986	ferritin light chain 1 pseudog	LOC382986	0.86	-1.363	0.213857	0.480173
17721	10480317	NM_026627	68231	RIKEN cDNA 1700113O17 gene	1700113O17Rik	0.86	-2.001	0.0843139	0.278691
17722	10589130	NM_080437	107934	cadherin, EGF LAG seven-pass G	Celsr3	0.86	-2.084	0.0744181	0.258046
17723	10420804	BC115562	71037	RIKEN cDNA 4933401F05 gene	4933401F05Rik	0.86	-1.258	0.247433	0.520777
17724	10509053	NM_174851	242700	interleukin 28 receptor alpha	Il28ra	0.86	-1.862	0.103637	0.316489
17725	10390271	NM_008686	18023	nuclear factor, erythroid deri	Nfe2l1	0.859	-2.82	0.0249757	0.127526
17726	10597612	NM_133980	102570	solute carrier family 22 (orga	Slc22a13	0.859	-1.138	0.291565	0.567624
17727	10484402	NM_007615	12388	catenin (cadherin associated p	Ctnnd1	0.859	-3.325	0.0121331	0.0774348
17728	10353686	ENSMUST00000065469	791350	predicted gene, ENSMUSG0000005	ENSMUSG00000053185	0.859	-1.215	0.262558	0.536954
17729	10384603	NM_008618	17449	malate dehydrogenase 1, NAD (s	Mdh1	0.859	-3.33	0.0120562	0.077029
17730	10478124	NM_009508	22348	solute carrier family 32 (GABA	Slc32a1	0.859	-1.866	0.103085	0.31534
17731	10384064	NM_007595	12323	calcium/calmodulin-dependent p	Camk2b	0.859	-2.15	0.067512	0.242726
17732	10506452	AY512949	791274	predicted gene, ENSMUSG0000006	ENSMUSG00000066088	0.859	-1.209	0.264843	0.540056
17733	10550250	NM_133727	70394	kaptin	Kptn	0.859	-1.847	0.106025	0.321127
17734	10361282	NM_013499	12946	complement component (3b/4b) r	Cr1l	0.859	-3.644	0.00783165	0.0571403
17735	10365590	NM_026070	67282	coiled-coil domain containing	Ccdc53	0.859	-3.015	0.0188444	0.105433
17736	10458086	XM_001474242	669999	hypothetical protein LOC669999	LOC669999	0.859	-1.19	0.271602	0.546245
17737	10362669	ENSMUST00000099957	75299	RIKEN cDNA 4930547M16 gene	4930547M16Rik	0.859	-1.391	0.205671	0.469421
17738	10360794	NM_175127	67948	F-box protein 28	Fbxo28	0.859	-3.218	0.0141131	0.0863198
17739	10435048	NM_025329	66061	Tctex1 domain containing 2	Tctex1d2	0.859	-1.857	0.104464	0.318087
17740	10359080					0.859	-2.946	0.0208153	0.112967
17741	10364035	BC082775	544707	predicted gene, EG544707	EG544707	0.859	-2.044	0.0790819	0.267794

17742	10405058	NM_012050	27047	osteomodulin	Omd	0.859	-1.003	0.348231	0.622132
17743	10384150	ENSMUST00000059507	19291	purine rich element binding pr	Purb	0.859	-1.443	0.191138	0.450298
17744	10399228	XR_034503	627245	similar to Odc1 protein	LOC627245	0.859	-3.35	0.0117274	0.0755987
17745	10466361	NM_146741	258736	olfactory receptor 1497	Olfr1497	0.859	-1.505	0.174849	0.427987
17746	10437376	NM_175347	106393	sarcalumenin	Srl	0.859	-2.591	0.0350025	0.159
17747	10444886	BC107265	69542	RIKEN cDNA 2300002M23 gene	2300002M23Rik	0.859	-1.705	0.130779	0.362933
17748	10409684					0.859	-2.354	0.0497697	0.20052
17749	10506736	NM_010760	17149	mago-nashi homolog, proliferat	Magoh	0.859	-3.005	0.0191071	0.106344
17750	10365887	NM_025551	66414	NADH dehydrogenase (ubiquinone	Ndufa12	0.859	-2.605	0.0342702	0.156774
17751	10440300					0.859	-2.345	0.0504255	0.202084
17752	10400803					0.859	-0.974	0.361642	0.633308
17753	10488156	NM_001081133	16558	kinesin family member 16B	Kif16b	0.859	-2.206	0.0620683	0.230322
17754	10552071	NM_175240	76415	transmembrane protein 162	Tmem162	0.858	-2.022	0.0816636	0.272831
17755	10484488	NM_145526	228139	purinergic receptor P2X, ligan	P2rx3	0.858	-1.305	0.231875	0.502642
17756	10376887					0.858	-1.467	0.18446	0.442045
17757	10398444					0.858	-1.38	0.208834	0.473827
17758	10551529					0.858	-2.079	0.0750103	0.258984
17759	10597258	NM_146260	20776	transmembrane inner ear	Tmie	0.858	-1.824	0.109632	0.327224
17760	10433212	NM_008762	18312	olfactory receptor 15	Olfr15	0.858	-1.566	0.160014	0.407336
17761	10603627	NM_175045	71458	Bcl6 interacting corepressor	Bcor	0.858	-2.289	0.0548564	0.213516
17762	10392087	NM_026009	67163	coiled-coil domain containing	Ccdc47	0.858	-3.033	0.0183488	0.10343
17763	10373986	NM_007454	11764	adaptor protein complex AP-1,	Ap1b1	0.858	-3.227	0.0139358	0.0856066
17764	10488237	NM_024225	69178	sorting nexin 5	Snx5	0.858	-3.621	0.00807281	0.058396
17765	10395682	ENSMUST00000077293	544864	predicted gene, EG544864	EG544864	0.858	-2.63	0.0330318	0.153264
17766	10522465	ENSMUST00000066220	70036	RIKEN cDNA 2700023E23 gene	2700023E23Rik	0.858	-2.473	0.0416748	0.178117
17767	10523526	ENSMUST00000066813	791375	predicted gene, ENSMUSG0000005	ENSMUSG00000054032	0.858	-1.517	0.171709	0.423956
17768	10588509	NM_021567	59092	poly(rC) binding protein 4	Pcbp4	0.858	-2.8	0.0257149	0.129873
17769	10547916	NM_026988	69202	parathymosin	Ptms	0.858	-1.62	0.147981	0.390187
17770	10387689	NM_153143	216858	potassium channel tetramerisat	Kctd11	0.858	-2.092	0.0735962	0.256362
17771	10603625					0.858	-1.461	0.186264	0.444461
17772	10457614	NM_009700	11829	aquaporin 4	Aqp4	0.858	-2.706	0.0295445	0.142007
17773	10599369	NM_009688	11798	X-linked inhibitor of apoptosi	Xiap	0.858	-1.747	0.122878	0.350766
17774	10437149					0.858	-2.11	0.0716215	0.251535
17775	10503361					0.858	-1.639	0.143986	0.384952
17776	10388679					0.858	-2.125	0.0700598	0.248007
17777	10538783	BC119578	243407	RIKEN cDNA C130060K24 gene	C130060K24Rik	0.858	-1.394	0.204844	0.4682
17778	10566026	NM_008035	14276	folate receptor 2 (fetal)	Folr2	0.858	-1.365	0.213339	0.479304
17779	10438585	NM_025693	66664	transmembrane protein 41a	Tmem41a	0.858	-2.075	0.0754467	0.259643
17780	10512308	NM_011014	18391	opioid receptor, sigma 1	Oprs1	0.858	-2.199	0.0626775	0.231769
17781	10398370					0.858	-1.017	0.341842	0.616313
17782	10507557	NM_026932	69072	EBNA1 binding protein 2	Ebna1bp2	0.858	-3.461	0.0100525	0.0683224
17783	10416411	NM_016903	13885	esterase D/formylglutathione h	Esd	0.858	-2.967	0.0201916	0.110546
17784	10560624	NM_009696	11816	apolipoprotein E	Apoe	0.858	-2.36	0.0493094	0.199391
17785	10558590	NM_009475	22264	proline-rich acidic protein 1	Prap1	0.857	-2.113	0.0713235	0.250884
17786	10449712	NM_144855	12411	cystathionine beta-synthase	Cbs	0.857	-2.527	0.0384726	0.169578
17787	10450189	NR_004051	81497	butyrophilin-like 5	Btnl5	0.857	-0.729	0.488864	0.736349
17788	10581737	NM_172284	234733	DEAD (Asp-Glu-Ala-Asp) box pol	Ddx19b	0.857	-2.851	0.0239011	0.123501
17789	10562360	NM_008155	14751	glucose phosphate isomerase 1	Gpi1	0.857	-2.942	0.020922	0.113291
17790	10409204	XM_001474265	100040099	similar to immediate early res	LOC100040099	0.857	-1.913	0.0961645	0.301828
17791	10602756	NM_025357	66106	small muscle protein, X-linked	Smpx	0.857	-2.477	0.041395	0.177544
17792	10488456	XR_034978	100048737	similar to protein phosphatase	LOC100048737	0.857	-1.658	0.140111	0.378727
17793	10357535	NM_008825	18640	6-phosphofructo-2-kinase/fruct	Pfkfb2	0.857	-1.227	0.258336	0.532488
17794	10464601					0.857	-0.735	0.485628	0.733962

17795	10489107	NM_018851	56045	SAM domain and HD domain, 1	Samhd1	0.857	-2.628	0.0331147	0.15348
17796	10456566	NM_010773	17191	methyl-CpG binding domain prot	Mbd2	0.857	-2.532	0.0381973	0.168893
17797	10355711	NM_029342	75570	nonhomologous end-joining fact	Nhej1	0.857	-1.487	0.179273	0.434671
17798	10607004	NM_016883	53380	proteasome (prosome, macropain	Psmd10	0.857	-3.596	0.00835228	0.0596624
17799	10510299	NM_176848	230904	F-box protein 2	Fbxo2	0.857	-2.173	0.0651633	0.238029
17800	10484472	NM_024230	68678	smoothelin-like 1	Smtnl1	0.857	-1.552	0.163234	0.412279
17801	10562546					0.857	-2.517	0.0390391	0.171199
17802	10499696					0.857	-2.583	0.0353835	0.160238
17803	10482788	ENSMUST00000067049	227923	RIKEN cDNA A930012O16 gene	A930012O16Rik	0.857	-1.716	0.128618	0.359531
17804	10588223	NM_181394	69010	anaphase promoting complex sub	Anapc13	0.857	-3.407	0.0108338	0.0716516
17805	10607398					0.857	-2.276	0.055856	0.215766
17806	10594825	NM_022026	64008	aquaporin 9	Aqp9	0.857	-1.152	0.286036	0.561602
17807	10394798	XR_034692	668539	similar to neural visinin-like	LOC668539	0.857	-2.33	0.0515974	0.205225
17808	10590212	NM_028735	74052	tetratricopeptide repeat domai	Ttc21a	0.857	-1.927	0.0940494	0.297697
17809	10590968	NM_019683	56503	ankyrin repeat domain 49	Ankrd49	0.857	-2.772	0.0267899	0.133156
17810	10511498	NM_175175	71801	pleckstrin homology domain con	Plekhf2	0.857	-2.835	0.0244319	0.125416
17811	10566438	BC063093	74349	RIKEN cDNA 4632419K20 gene	4632419K20Rik	0.857	-2.866	0.0233549	0.12142
17812	10589061	NM_026378	67789	DALR anticodon binding domain	Dalrd3	0.857	-3.692	0.00733313	0.0545572
17813	10604974	NM_019405	26370	centrin 2	Cetn2	0.857	-1.848	0.105806	0.320603
17814	10525942	NM_177005	319804	glycosyltransferase 1 domain c	Glt1d1	0.856	-2.224	0.0604139	0.226689
17815	10607302	NM_198110	237107	guanine nucleotide binding pro	Gnl3l	0.856	-2.819	0.0250185	0.127548
17816	10412900	NM_023526	69721	NFKB inhibitor interacting Ras	Nkiras1	0.856	-2.771	0.0268619	0.133357
17817	10597619	ENSMUST00000010790	109280	RIKEN cDNA 9330176C04 gene	9330176C04Rik	0.856	-2.909	0.0219416	0.116478
17818	10546113	NM_016906	53421	Sec61 alpha 1 subunit (S. cere	Sec61a1	0.856	-2.676	0.0308777	0.146582
17819	10380815	NM_011971	26446	proteasome (prosome, macropain	Psmb3	0.856	-3.163	0.0152453	0.0914142
17820	10352558	NM_033077	110957	DNA segment, Chr 1, Pasteur In	D1Pas1	0.856	-2.353	0.0497958	0.200566
17821	10405927	NM_001048204	218311	zinc finger protein 455	Zfp455	0.856	-1.044	0.330322	0.606542
17822	10557705	NM_026888	68961	phosphorylase kinase, gamma 2	Phkg2	0.856	-3.389	0.011097	0.0728453
17823	10406856	XR_035362	328320	gene model 807, (NCBI)	Gm807	0.856	-1.189	0.271956	0.546343
17824	10422393					0.856	-1.077	0.31609	0.59306
17825	10565210	NM_177894	330577	RIKEN cDNA 1700129I04 gene	1700129I04Rik	0.856	-2.656	0.0317749	0.1492
17826	10430892	BC116321	93882	protocadherin beta 11	Pcdhb11	0.856	-1.714	0.12908	0.3603
17827	10357280	NM_133748	72999	insulin induced gene 2	Insig2	0.856	-3.228	0.0139029	0.0854991
17828	10440657	NM_027105	69533	keratin associated protein 26-	Krtap26-1	0.856	-2.012	0.0829018	0.27574
17829	10599207	NM_001085497	194744	solute carrier family 25, memb	Slc25a43	0.856	-1.823	0.10988	0.327734
17830	10434191	NM_013711	26462	thioredoxin reductase 2	Txnrd2	0.856	-2.371	0.0485037	0.196834
17831	10468448					0.856	-1.052	0.326735	0.602834
17832	10377859	NM_008876	18806	phospholipase D2	Pld2	0.856	-2.871	0.0231968	0.120967
17833	10474851	NM_001045523	228536	bromo adjacent homology domain	Bahd1	0.856	-2.011	0.083068	0.276162
17834	10470101	NM_027085	69454	chloride intracellular channel	Clic3	0.856	-1.72	0.127911	0.358671
17835	10469239					0.856	-1.339	0.221132	0.490317
17836	10433484	AY903215	75329	activating transcription facto	Atf7ip2	0.856	-1.679	0.135692	0.371434
17837	10452639	NM_023402	67938	myosin light chain, regulatory	Mylc2b	0.856	-2.595	0.034774	0.158373
17838	10461150					0.856	-1.561	0.161324	0.409487
17839	10376052	XR_002067	667731	similar to ribosomal protein S	LOC667731	0.856	-1.425	0.196047	0.456422
17840	10518781	NM_011067	18628	period homolog 3 (Drosophila)	Per3	0.856	-2.133	0.0691833	0.246514
17841	10453272	NM_001001806	12193	zinc finger protein 36, C3H ty	Zfp36l2	0.856	-2.321	0.0522728	0.20675
17842	10383813	NM_026443	67900	RIKEN cDNA 1700020C11 gene	1700020C11Rik	0.856	-2.296	0.0542433	0.211765
17843	10435489	NM_198645	381045	coiled-coil domain containing	Ccdc58	0.856	-3.457	0.0101057	0.0685504
17844	10461152	AK051045	83673	small nucleolar RNA host gene	Snhg1	0.856	-1.945	0.0915805	0.293124
17845	10433433	BC024814	239706	cDNA sequence BC024814	BC024814	0.856	-1.819	0.110468	0.328752
17846	10458213	NM_144866	225363	eukaryotic translation termina	Etf1	0.856	-3.055	0.0177996	0.101225

17847	10447480					0.856	-2.595	0.0347736	0.158373
17848	10406226	XM_619124	544954	predicted gene, EG544954	EG544954	0.856	-1.713	0.129159	0.360384
17849	10408900					0.856	-1.47	0.183673	0.440916
17850	10439710	NM_153412	208177	pleckstrin homology-like domai	Phldb2	0.855	-1.989	0.0858297	0.281187
17851	10523277	AK034152	319240	RIKEN cDNA 9330159N05 gene	9330159N05Rik	0.855	-1.546	0.164658	0.414518
17852	10580981	J02622	14719	glutamate oxaloacetate transam	Got2	0.855	-2.114	0.0711639	0.250614
17853	10579996	NM_134118	106529	glycoprotein, synaptic 2	Gpsn2	0.855	-3.2	0.0144667	0.0881005
17854	10606217	NM_009592	11306	ATP-binding cassette, sub-fami	Abcb7	0.855	-2.151	0.0673817	0.242464
17855	10590004	NM_018748	54214	golgi autoantigen, golgin subf	Golga4	0.855	-3.194	0.0145919	0.0885309
17856	10487748	BC052447	228602	RIKEN cDNA 4930402H24 gene	4930402H24Rik	0.855	-2.198	0.0627804	0.232027
17857	10461830	NM_146344	258341	olfactory receptor 1495	Olfr1495	0.855	-1.723	0.127255	0.357519
17858	10420694	NM_008715	18130	integrator complex subunit 6	Ints6	0.855	-3.201	0.0144483	0.0880388
17859	10456018	NM_001038499	545260	arylsulfatase i	Arsi	0.855	-1.385	0.207497	0.471907
17860	10404595	XM_127272	76487	protein phosphatase 1, regulat	Ppp1r3g	0.855	-2.432	0.0442685	0.185686
17861	10366595	ENSMUST00000059966	74415	RIKEN cDNA 4932442E05 gene	4932442E05Rik	0.855	-1.327	0.224838	0.494896
17862	10414594	NM_001029990	52535	methyltransferase 11 domain co	Mett11d1	0.855	-2.528	0.038411	0.169439
17863	10441167	NM_001001492	385668	Leber congenital amaurosis 5-l	Lca5l	0.855	-2.081	0.0747943	0.258759
17864	10408097	NM_019429	54373	protease, serine, 16 (thymus)	Prss16	0.855	-1.911	0.0963649	0.30213
17865	10571300	NM_001126314	234155	membrane bound O-acyltransfera	Mboat4	0.855	-1.477	0.181993	0.438476
17866	10429220	ENSMUST00000022953	70363	RIKEN cDNA 1700010C24 gene	1700010C24Rik	0.855	-1.123	0.297455	0.573687
17867	10425781	NM_023475	68607	serine hydrolase-like	Serhl	0.855	-3.741	0.006873	0.05179
17868	10439980	NM_001024622	76302	PEST proteolytic signal contai	Pcnp	0.855	-1.82	0.110354	0.328637
17869	10490665	NM_009133	20262	stathmin-like 3	Stmn3	0.855	-1.631	0.145619	0.387145
17870	10427849	BC119058	77877	RIKEN cDNA 6030458C11 gene	6030458C11Rik	0.855	-1.594	0.153774	0.398309
17871	10361977	NM_001101561	621697	predicted gene, EG621697	EG621697	0.854	-2.479	0.0413291	0.177398
17872	10397277	NM_028632	73736	FCF1 small subunit (SSU) proce	Fcf1	0.854	-2.878	0.0229617	0.120303
17873	10516371	NM_153403	236511	eukaryotic translation initiat	Eif2c1	0.854	-3.877	0.00573461	0.0455152
17874	10455461	NM_001033621	58916	myotilin	Myot	0.854	-3.339	0.0118976	0.0763471
17875	10489961	NM_010899	18019	nuclear factor of activated T-	Nfatc2	0.854	-3.554	0.00884755	0.0621917
17876	10532339	NM_008993	19301	peroxisomal membrane protein 2	Pxmp2	0.854	-2.986	0.0196363	0.108498
17877	10494781	NM_207205	78908	immunoglobulin superfamily, me	Igsf3	0.854	-3.381	0.0112302	0.0733781
17878	10385599	NM_007597	12330	calnexin	Canx	0.854	-3.515	0.00933597	0.0646788
17879	10451142	DQ190000	653016	predicted gene, EG653016	EG653016	0.854	-1.228	0.258134	0.532228
17880	10404077	NM_144836	218103	solute carrier family 17 (sodi	Slc17a2	0.854	-2.553	0.0369932	0.165018
17881	10468639	NM_018831	55947	DNA cross-link repair 1A, PSO2	Dclre1a	0.854	-3.482	0.00976371	0.0669403
17882	10600810	XR_002150	668156	predicted gene, EG668156	EG668156	0.854	-2.324	0.0520553	0.206366
17883	10371111	NM_013769	27375	tight junction protein 3	Tjp3	0.854	-2.79	0.0260948	0.13087
17884	10415781	BC064093	219144	ADP-ribosylation factor-like 1	Arl11	0.854	-1.983	0.0866395	0.282963
17885	10505643	BC039810	320226	RIKEN cDNA 4930473A06 gene	4930473A06Rik	0.854	-1.876	0.101475	0.312131
17886	10597134	AK134160	100038626	predicted gene, ENSMUSG0000007	ENSMUSG00000074053	0.854	-1.786	0.115976	0.338701
17887	10401418	AK132490	100038552	predicted gene, ENSMUSG0000007	ENSMUSG00000072948	0.854	-2.44	0.0437954	0.1843
17888	10476526	NM_001038641	74243	RIKEN cDNA 2210009G21 gene	2210009G21Rik	0.854	-1.953	0.0905929	0.290914
17889	10576335	NM_054046	23854	differentially expressed in FD	Def8	0.854	-2.747	0.0278176	0.136658
17890	10511175	NM_025338	66077	aurora kinase A interacting pr	Aurkaip1	0.854	-2.66	0.0315941	0.148727
17891	10505587	NM_144787	76804	jumonji domain containing 2C	Jmjd2c	0.854	-2.348	0.0502196	0.201596
17892	10515427					0.854	-0.795	0.451843	0.708709
17893	10411974	NM_029665	76582	importin 11	Ipo11	0.854	-3.708	0.0071786	0.053634
17894	10514441	NM_177239	320713	myb-like, SWIRM and MPN domain	Mysm1	0.854	-2.796	0.0258659	0.130308
17895	10544815	NM_145567	58875	3-hydroxyisobutyrate dehydroge	Hibadh	0.854	-3.04	0.018168	0.102596

17896	10392701	NM_027216	69806	solute carrier family 39 (meta	Slc39a11	0.854	-1.902	0.097686	0.304546
17897	10356312	NM_010880	17975	nucleolin	Ncl	0.854	-3.745	0.00683339	0.0515651
17898	10494200	NM_172395	57912	CDC42 small effector 1	Cdc42se1	0.854	-3.668	0.00758355	0.0559869
17899	10603649					0.854	-2.022	0.0816678	0.272831
17900	10511580	NM_001098230	381511	protein phosphatase 2C, magnes	Ppm2c	0.854	-2.89	0.0225548	0.11875
17901	10456296	NM_172833	240354	mucosa associated lymphoid tis	Malt1	0.854	-2.915	0.0217726	0.11596
17902	10368730	NM_023323	67239	brix domain containing 1	Bxdc1	0.854	-2.728	0.0285833	0.138775
17903	10567072	NM_011965	26440	proteasome (prosome, macropain	Psma1	0.854	-3.124	0.0161133	0.0949818
17904	10562736	ENSMUST00000037220	70004	RIKEN cDNA 1700028J19 gene	1700028J19Rik	0.854	-1.249	0.250595	0.524406
17905	10518726	NM_027460	70556	solute carrier family 25, memb	Slc25a33	0.853	-3.579	0.00855448	0.060717
17906	10529824	NM_008935	19126	prominin 1	Prom1	0.853	-2.493	0.0404488	0.175113
17907	10346298	NM_001039710	67876	coenzyme Q10 homolog B (S. cer	Coq10b	0.853	-1.236	0.255098	0.5294
17908	10466848	NM_177474	52874	DNA segment, Chr 19, Brigham &	D19Bwg1357e	0.853	-2.856	0.0237005	0.122704
17909	10596053	NM_025835	66904	propionyl Coenzyme A carboxyla	Pccb	0.853	-3.34	0.0118823	0.0762953
17910	10484561	NM_001011777	257941	olfactory receptor 1042	Olfr1042	0.853	-1.409	0.200347	0.462359
17911	10566281	ENSMUST00000108195	67713	DnaJ (Hsp40) homolog, subfamil	Dnajc19	0.853	-1.755	0.121482	0.347955
17912	10478326	NM_013731	27219	serum/glucocorticoid regulated	Sgk2	0.853	-3.133	0.0159245	0.0941049
17913	10461652	NM_008118	14603	gastric intrinsic factor	Gif	0.853	-1.015	0.342969	0.617132
17914	10530666	NM_010727	16924	ligand of numb-protein X 1	Lnx1	0.853	-3.693	0.00732792	0.0545377
17915	10513803					0.853	-1.268	0.244046	0.517096
17916	10361129					0.853	-1.232	0.25648	0.530714
17917	10539927	NM_001033491	434065	gene model 1965, (NCBI)	Gm1965	0.853	-1.656	0.140354	0.378864
17918	10425632	NM_010247	14375	X-ray repair complementing def	Xrcc6	0.853	-3.439	0.0103668	0.0698
17919	10435388	NM_001012765	224129	adenylate cyclase 5	Adcy5	0.853	-1.526	0.169589	0.420916
17920	10366293	NM_007792	13008	cysteine and glycine-rich prot	Csrp2	0.853	-3.019	0.0187246	0.104989
17921	10371916	ENSMUST00000067705	380654	RIKEN cDNA 4930485B16 gene	4930485B16Rik	0.853	-1.537	0.166863	0.417832
17922	10363241	NM_027375	70297	GRIP and coiled-coil domain co	Gcc2	0.853	-2.58	0.0355378	0.160558
17923	10434226	ENSMUST00000100090	619305	RIKEN cDNA 4930588K23 gene	4930588K23Rik	0.853	-1.116	0.300143	0.576249
17924	10424804	NM_175399	109075	exosome component 4	Exosc4	0.853	-2.683	0.0305429	0.14545
17925	10498992	NM_011905	24088	toll-like receptor 2	Tlr2	0.853	-2.74	0.0281063	0.137533
17926	10520965	NM_009535	22612	Yamaguchi sarcoma viral (v-yes	Yes1	0.853	-3.09	0.0169163	0.0979671
17927	10605319	NM_145405	27643	ubiquitin-like 4	Ubl4	0.853	-3.786	0.00646728	0.0494912
17928	10487890	BC099428	71995	endogenous retroviral sequence	Erv3	0.853	-1.403	0.202199	0.464958
17929	10596893	NM_010017	13138	dystroglycan 1	Dag1	0.852	-2.224	0.0603808	0.226645
17930	10368197	ENSMUST00000100040	100038717	predicted gene, ENSMUSG0000007	ENSMUSG00000075301	0.852	-1.476	0.182127	0.438626
17931	10376889	NM_175002	216829	cDNA sequence BC025076	BC025076	0.852	-2.626	0.0332203	0.1537
17932	10469984	NM_146117	227618	leucine rich repeat containing	Lrrc26	0.852	-2.024	0.0813929	0.272349
17933	10446136	BC116633	106757	transmembrane protein 146	Tmem146	0.852	-2.001	0.0843163	0.278691
17934	10582074	NM_026758	68533	M phase phosphoprotein 6	Mphosph6	0.852	-3.582	0.00851606	0.0605052
17935	10432129	NM_001011733	545140	olfactory receptor 288	Olfr288	0.852	-1.147	0.28805	0.563886
17936	10360884	NM_198653	381314	isoleucine-tRNA synthetase 2,	Iars2	0.852	-4.23	0.00363696	0.032683
17937	10409152	BC047205	68480	RIKEN cDNA 1110007C09 gene	1110007C09Rik	0.852	-3.426	0.0105509	0.0705216
17938	10571920	ENSMUST00000052189	320383	RIKEN cDNA B230317F23 gene	B230317F23Rik	0.852	-1.368	0.212421	0.477963
17939	10512005	BC027508	66291	RIKEN cDNA 1810030N24 gene	1810030N24Rik	0.852	-2.473	0.0416903	0.178117
17940	10435862	ENSMUST00000085772	212517	WD repeat domain 52	Wdr52	0.852	-2.469	0.0419465	0.178958
17941	10607585	ENSMUST00000112513	245684	connector enhancer of kinase s	Cnksr2	0.852	-2.012	0.0828595	0.275685
17942	10580155	BC024662	101966	DNA segment, Chr 8, ERATO Doi	D8Ertd738e	0.852	-3.255	0.0133949	0.0833003
17943	10420013	NM_008736	18185	neural retina leucine zipper g	Nrl	0.852	-1.383	0.208016	0.472478
17944	10365495	NM_001003910	103220	cDNA sequence BC030307	BC030307	0.852	-3.325	0.0121434	0.0774775

17945	10605505					0.852	-1.337	0.221952	0.49161
17946	10381063	NM_197940	68524	WAS/WASL interacting protein f	Wipf2	0.852	-1.787	0.115908	0.338549
17947	10402490	NM_001042699	212073	RIKEN cDNA 4831426I19 gene	4831426I19Rik	0.852	-1.633	0.145231	0.386933
17948	10508645					0.852	-1.457	0.187216	0.445625
17949	10374793	NM_027869	71701	polyribonucleotide nucleotidyl	Pnpt1	0.852	-3.339	0.0118976	0.0763471
17950	10353783	NM_027159	69668	coiled-coil domain containing	Ccdc115	0.852	-2.862	0.0234919	0.121893
17951	10351825	NM_178598	21346	transgelin 2	Tagln2	0.852	-2.84	0.0242798	0.124965
17952	10403273	NM_080857	142688	ankyrin repeat and SOCS box-co	Asb13	0.852	-2.938	0.021041	0.11355
17953	10432907	NM_212487	332131	keratin 78	Krt78	0.851	-1.677	0.136263	0.372579
17954	10512766	NM_029077	74735	tripartite motif-containing 14	Trim14	0.851	-3.17	0.0151017	0.090765
17955	10398438					0.851	-1.378	0.209583	0.474666
17956	10400089	NM_001033437	380755	gene model 889, (NCBI)	Gm889	0.851	-2.204	0.0621959	0.230633
17957	10601088	XR_031413	668271	similar to high-mobility group	LOC668271	0.851	-1.195	0.269848	0.544485
17958	10355152	NM_022721	14367	frizzled homolog 5 (Drosophila	Fzd5	0.851	-2.249	0.0582219	0.22161
17959	10460841	ENSMUST00000025681	240505	CDC42 binding protein kinase g	Cdc42bpg	0.851	-1.833	0.108142	0.32441
17960	10370174	NM_172550	216119	RIKEN cDNA A130042E20 gene	A130042E20Rik	0.851	-2.005	0.0838434	0.277518
17961	10507885	NM_019660	56309	c-myc binding protein	Mycbp	0.851	-3.378	0.0112729	0.0735307
17962	10595466	NM_028352	109785	phosphoglucomutase 3	Pgm3	0.851	-2.64	0.032519	0.151516
17963	10378453	BC072573	74148	RIKEN cDNA 1300001I01 gene	1300001I01Rik	0.851	-2.347	0.0502659	0.201609
17964	10456723	BC016084	407819	cDNA sequence BC031181	BC031181	0.851	-3.251	0.0134719	0.0836071
17965	10516277	BC053421	66938	RIKEN cDNA 1700029G01 gene	1700029G01Rik	0.851	-1.866	0.102992	0.315188
17966	10589602	NM_010859	17897	myosin, light polypeptide 3	Myl3	0.851	-1.917	0.0954776	0.300369
17967	10400740					0.851	-1.08	0.315137	0.592079
17968	10517301	NM_145554	100017	low density lipoprotein recept	Ldlrap1	0.851	-2.486	0.040876	0.176276
17969	10356018	ENSMUST00000116132	620899	predicted gene, EG620899	EG620899	0.851	-1.72	0.12792	0.358671
17970	10357553	NM_053095	93672	interleukin 24	Il24	0.851	-1.772	0.118351	0.343378
17971	10542953	NM_009364	21789	tissue factor pathway inhibito	Tfpi2	0.851	-2.109	0.0717515	0.251634
17972	10347968					0.851	-0.799	0.44962	0.70698
17973	10362036	NM_019702	56422	Hbs1-like (S. cerevisiae)	Hbs1l	0.851	-3.416	0.0107029	0.0711644
17974	10601867	NM_177749	245616	killer cell immunoglobulin-lik	Kir3dl1	0.851	-2.111	0.0715763	0.251439
17975	10600720	XR_002105	547215	predicted gene, EG547215	EG547215	0.851	-2.738	0.0281898	0.137705
17976	10359837	NM_172844	240894	flavin containing monooxygenas	Fmo9	0.851	-0.674	0.521509	0.758794
17977	10399011	NM_134041	104732	RIKEN cDNA 4930427A07 gene	4930427A07Rik	0.85	-1.883	0.100476	0.31011
17978	10379998	NM_197987	68729	tripartite motif-containing 37	Trim37	0.85	-2.954	0.0205854	0.112161
17979	10574598	BC057188	382053	esterase 31	Es31	0.85	-1.313	0.229399	0.500403
17980	10424077	BC046791	78581	RIKEN cDNA D530033C11 gene	D530033C11Rik	0.85	-2.488	0.0407328	0.17591
17981	10573954	ENSMUST00000104947	69543	calpain, small subunit 2	Capns2	0.85	-1.43	0.194592	0.454635
17982	10495528	ENSMUST00000064809	791369	predicted gene, ENSMUSG0000005	ENSMUSG00000052769	0.85	-0.96	0.36811	0.639027
17983	10550519	NM_194064	378430	nanos homolog 2 (Drosophila)	Nanos2	0.85	-1.682	0.135108	0.370617
17984	10362434					0.85	-1.331	0.223752	0.493792
17985	10502146	NM_026578	68147	nucleolar protein family A, me	Nola1	0.85	-2.423	0.0448932	0.187445
17986	10507456	NM_175030	242646	Tctex1 domain containing 4	Tctex1d4	0.85	-1.385	0.207259	0.47167
17987	10419977	NM_007455	11766	adaptor protein complex AP-1,	Ap1g2	0.85	-2.761	0.0272213	0.134478
17988	10500321	NM_026975	69168	bolA-like 1 (E. coli)	Bola1	0.85	-2.424	0.0447962	0.187188
17989	10368739	NM_026113	67371	general transcription factor I	Gtf3c6	0.85	-2.628	0.0330975	0.153434
17990	10544525	NM_009787	12304	protein disulfide isomerase as	Pdia4	0.85	-3.876	0.0057439	0.0455547
17991	10502079	BC039568	70617	RIKEN cDNA 5730508B09 gene	5730508B09Rik	0.85	-0.839	0.428584	0.689543
17992	10516484	NM_008126	14620	gap junction protein, beta 3	Gjb3	0.85	-1.639	0.143962	0.384952
17993	10525887	NM_029752	76809	Bri3 binding protein	Bri3bp	0.85	-3.011	0.0189576	0.105763
17994	10509910	NM_177867	329972	spermatogenesis associated 21	Spata21	0.85	-2.124	0.0701539	0.248254
17995	10556598	NM_175645	233781	xylosyltransferase 1	Xylt1	0.85	-2.644	0.0323656	0.151101

17996	10438071	NM_144954	66053	peptidylprolyl isomerase (cycl	Ppil2	0.85	-3.296	0.0126418	0.0796771
17997	10382360	BC048942	276852	DNA segment, Chr 11, Wayne Sta	D11Wsu47e	0.85	-2.155	0.0670051	0.241742
17998	10403348	ENSMUST00000065956	432723	predicted gene, EG432723	EG432723	0.85	-2.087	0.0741862	0.257526
17999	10546661	NM_053202	108655	forkhead box P1	Foxp1	0.85	-2.31	0.0531209	0.209043
18000	10392970	NM_027162	69674	MIF4G domain containing	Mif4gd	0.85	-2.224	0.0603631	0.226645
18001	10499504	NM_013604	17827	metaxin 1	Mtx1	0.85	-1.735	0.12508	0.35409
18002	10388520	NM_026029	67201	glyoxalase domain containing 4	Glod4	0.85	-2.394	0.0468624	0.192371
18003	10597878	NM_153540	215494	expressed sequence C85492	C85492	0.85	-2.97	0.020099	0.110172
18004	10348378	NM_134252	171382	transient receptor potential c	Trpm8	0.85	-1.069	0.319629	0.596543
18005	10430458	BC023356	20665	SRY-box containing gene 10	Sox10	0.85	-2.147	0.0678141	0.243316
18006	10597511	ENSMUST00000075898	546164	predicted gene, EG546164	EG546164	0.85	-2.17	0.0654771	0.238533
18007	10593356	NM_025848	66925	succinate dehydrogenase comple	Sdhd	0.85	-3.337	0.0119338	0.0765328
18008	10408850	NM_001111324	18003	neural precursor cell expresse	Nedd9	0.85	-1.957	0.0900625	0.289577
18009	10442219	NM_144515	22710	zinc finger protein 52	Zfp52	0.85	-2.845	0.0240993	0.124223
18010	10524077					0.85	-1.162	0.282363	0.557354
18011	10446235	NM_134125	106628	thyroid hormone receptor inter	Trip10	0.849	-3.111	0.0164288	0.0962129
18012	10514323	AK144774	100037413	predicted gene, ENSMUSG0000007	ENSMUSG00000073810	0.849	-1.163	0.281905	0.557053
18013	10604242	XR_032497	385344	similar to 3-phosphoglycerate	LOC385344	0.849	-1.657	0.140211	0.378815
18014	10565132	ENSMUST00000073406	210321	cDNA sequence BC048679	BC048679	0.849	-2.436	0.0440101	0.184853
18015	10568785	NM_009760	12176	BCL2/adenovirus E1B interactin	Bnip3	0.849	-2.408	0.0459101	0.189928
18016	10477001	XM_983502	675602	similar to Glyceraldehyde-3-ph	LOC675602	0.849	-0.883	0.40558	0.670072
18017	10363622	NM_026085	67307	RIKEN cDNA 3110049J23 gene	3110049J23Rik	0.849	-1.963	0.0891729	0.287902
18018	10348889	NM_178882	98314	D-2-hydroxyglutarate dehydroge	D2hgdh	0.849	-3.028	0.018488	0.104021
18019	10558914	AK012402	67186	ribosomal protein, large P2	Rplp2	0.849	-2.513	0.0392748	0.171931
18020	10489701	BC020160	74614	RIKEN cDNA 4833422F24 gene	4833422F24Rik	0.849	-1.861	0.103788	0.316741
18021	10583806	XR_001828	625409	predicted gene, EG625409	EG625409	0.849	-2.559	0.0367009	0.163921
18022	10604290	XM_987385	333830	predicted gene, EG333830	EG333830	0.849	-2.347	0.0502995	0.201617
18023	10533131	NM_023625	71772	RIKEN cDNA 1300012G16 gene	1300012G16Rik	0.849	-2.866	0.0233718	0.121478
18024	10580519					0.849	-1.579	0.157013	0.403436
18025	10481496	ENSMUST00000100212	100038700	predicted gene, OTTMUSG0000001	OTTMUSG00000016805	0.849	-1.443	0.191133	0.450298
18026	10373143	NM_033072	110962	methyl-CpG binding domain prot	Mbd6	0.849	-2.421	0.0450324	0.187748
18027	10398400					0.849	-1.472	0.183244	0.440236
18028	10539907	NM_011906	24100	G protein-coupled receptor 175	Gpr175	0.849	-2.044	0.0790184	0.267708
18029	10384691	NM_027860	71675	RIKEN cDNA 0610010F05 gene	0610010F05Rik	0.849	-1.922	0.0948569	0.299396
18030	10589909	AK048065	791362	predicted gene, ENSMUSG0000005	ENSMUSG00000052207	0.849	-0.723	0.492323	0.738379
18031	10479379	NM_148933	108115	solute carrier organic anion t	Slco4a1	0.849	-2.088	0.0740038	0.257104
18032	10483150	NM_021716	60344	fidgetin	Fign	0.849	-1.985	0.0862797	0.282193
18033	10594381	ENSMUST00000042322	78250	IQ motif containing H	Iqch	0.849	-1.736	0.124897	0.353808
18034	10366796	NM_010792	17299	methyltransferase-like 1	Mettl1	0.849	-2.63	0.033023	0.153257
18035	10355668					0.849	-1.42	0.197356	0.457905
18036	10576027	ENSMUST00000098354	100038388	predicted gene, ENSMUSG0000007	ENSMUSG00000074055	0.849	-1.54	0.166264	0.417121
18037	10478048	NM_008489	16803	lipopolysaccharide binding pro	Lbp	0.849	-1.628	0.146192	0.387985
18038	10533120					0.849	-1.566	0.16015	0.407486
18039	10360648	NM_011183	19165	presenilin 2	Psen2	0.848	-2.356	0.0495993	0.200156
18040	10595288	NM_133718	69981	transmembrane protein 30A	Tmem30a	0.848	-4.021	0.00474894	0.0397482
18041	10523012	NM_007832	13178	deoxycytidine kinase	Dck	0.848	-3.04	0.0181723	0.102596
18042	10382838	BC055707	66293	RIKEN cDNA 1810032O08 gene	1810032O08Rik	0.848	-1.663	0.139051	0.377128
18043	10408346	ENSMUST00000069594	100036543	predicted gene, ENSMUSG0000005	ENSMUSG00000055849	0.848	-3.803	0.00632923	0.0488235
18044	10480751	NM_027062	69379	complement component 8, gamma	C8g	0.848	-1.88	0.100921	0.310968
18045	10450242	NM_009780	12268	complement component 4B	C4b	0.848	-1.324	0.226038	0.496626

				(Child					
18046	10547830	NM_009415	21991	triosephosphate isomerase 1	Tpi1	0.848	-2.292	0.0546093	0.21288
18047	10541063	NM_001011800	258019	olfactory receptor 212	Olfr212	0.848	-1.371	0.21141	0.476907
18048	10578219	ENSMUST00000065297	244421	LON peptidase N-terminal domai	Lonrf1	0.848	-1.951	0.090828	0.291466
18049	10551881					0.848	-3.146	0.0156342	0.0928584
18050	10368090	XR_032028	667036	predicted gene, EG667036	EG667036	0.848	-1.269	0.243882	0.516956
18051	10515007	NM_024198	67305	glutathione peroxidase 7	Gpx7	0.848	-3.686	0.00739657	0.0548555
18052	10583788	NM_008925	19089	protein kinase C substrate 80K	Prkcsh	0.848	-3.117	0.0162802	0.0956368
18053	10587639	NM_011851	23959	5' nucleotidase, ecto	Nt5e	0.848	-2.448	0.0432165	0.182644
18054	10586454	AK050877	319910	RIKEN cDNA D030028M11 gene	D030028M11Rik	0.848	-0.857	0.419143	0.681475
18055	10415835	NM_001039121	654458	defensin beta 43	Defb43	0.848	-1.774	0.118092	0.343079
18056	10368486	NM_001110197	68031	ring finger protein 146	Rnf146	0.848	-2.241	0.0589022	0.223325
18057	10512145	NM_007473	11832	aquaporin 7	Aqp7	0.848	-1.759	0.12067	0.347112
18058	10417704	NM_146052	218763	leucine rich repeat containing	Lrrc3b	0.848	-2.473	0.0416885	0.178117
18059	10355312	NM_011770	22779	IKAROS family zinc finger 2	Ikzf2	0.848	-2.565	0.0363411	0.16283
18060	10348420					0.848	-1.376	0.209885	0.475038
18061	10568521	BC044749	68277	RIKEN cDNA 2310057M21 gene	2310057M21Rik	0.848	-1.84	0.107062	0.322599
18062	10470775	NM_207298	99151	cerebral endothelial cell adhe	Cercam	0.848	-2.553	0.0370122	0.16504
18063	10382973	ENSMUST00000106331	77727	RIKEN cDNA 6030468B19 gene	6030468B19Rik	0.848	-1.575	0.158044	0.405065
18064	10376208	NM_010299	14667	GM2 ganglioside activator prot	Gm2a	0.847	-2.743	0.027967	0.1372
18065	10384961	NM_011491	20856	stanniocalcin 2	Stc2	0.847	-1.83	0.108663	0.325457
18066	10401667	BC004591	58520	RIKEN cDNA 0610007P14 gene	0610007P14Rik	0.847	-3.302	0.0125354	0.0792136
18067	10463254	NM_177464	52013	DNA segment, Chr 19, ERATO Doi	D19Ertd386e	0.847	-3.191	0.0146593	0.0887615
18068	10508436	NM_023485	68828	syncoilin	Sync	0.847	-2.044	0.0790727	0.267794
18069	10386758	NM_001033227	109342	solute carrier family 5 (sodiu	Slc5a10	0.847	-1.793	0.114755	0.336905
18070	10375893	NM_025535	66397	SAR1 gene homolog B (S. cerevi	Sar1b	0.847	-3.946	0.0052385	0.0426339
18071	10447224	NM_172256	213575	dynein cytoplasmic 2 light int	Dync2li1	0.847	-3.153	0.0154649	0.09237
18072	10464167	NM_007419	11554	adrenergic receptor, beta 1	Adrb1	0.847	-1.599	0.152517	0.396392
18073	10349826	ENSMUST00000097577	100038653	predicted gene, ENSMUSG0000007	ENSMUSG00000073566	0.847	-1.18	0.275586	0.550454
18074	10408042	ENSMUST00000076238	791358	predicted gene, ENSMUSG0000005	ENSMUSG00000059459	0.847	-1.697	0.132229	0.365389
18075	10583432					0.847	-1.441	0.191686	0.451028
18076	10504499	NM_138590	319885	zinc finger, CCHC domain conta	Zcchc7	0.847	-2.418	0.0452323	0.188044
18077	10552348					0.847	-1.698	0.132084	0.365262
18078	10361887	NM_022032	64058	PERP, TP53 apoptosis effector	Perp	0.847	-2.42	0.0450549	0.187761
18079	10507011	NM_172296	242620	doublesex and mab-3 related tr	Dmrta2	0.847	-2.678	0.0307523	0.14602
18080	10421615	NM_026457	67926	spermatid associated	Spert	0.847	-1.926	0.0942087	0.29789
18081	10523513	ENSMUST00000031274	75094	RIKEN cDNA 4930522N08 gene	4930522N08Rik	0.847	-1.765	0.119736	0.346027
18082	10508819	NM_027152	69655	CD164 sialomucin-like 2	Cd164l2	0.847	-1.437	0.192773	0.452235
18083	10553913	NM_028626	73724	methylmalonyl CoA epimerase	Mcee	0.847	-2.402	0.0463348	0.191236
18084	10598027					0.847	-2.485	0.0409404	0.176338
18085	10373692	NM_001103366	625131	vomeronasal 2, receptor 87	Vmn2r87	0.847	-0.99	0.35424	0.626867
18086	10507099	NM_001085549	666048	predicted gene, OTTMUSG0000000	OTTMUSG00000008561	0.847	-1.626	0.146672	0.388673
18087	10350489	NM_019562	56207	ubiquitin carboxyl-terminal es	Uchl5	0.847	-3.263	0.0132456	0.082664
18088	10453867	NM_001081223	225182	retinoblastoma binding protein	Rbbp8	0.847	-3.666	0.00759509	0.056033
18089	10348713	XM_001474855	381284	RIKEN cDNA E030010N08 gene	E030010N08Rik	0.847	-2.098	0.0728722	0.254427
18090	10487359	BC130218	73338	RIKEN cDNA 1700041B20 gene	1700041B20Rik	0.847	-3.102	0.0166457	0.0970498
18091	10569203	NM_026522	68038	chitinase domain containing 1	Chid1	0.847	-3.221	0.0140535	0.0860798
18092	10446693	ENSMUST00000047086	72515	WD repeat domain 43	Wdr43	0.847	-3.844	0.00599366	0.0469175
18093	10508190	NM_001035526	100317	expressed sequence AU040320	AU040320	0.847	2.475	0.0415608	0.177907

18093	10508190	NM_001033320	100517	expressed sequence AU040320	AU040320	0.847	-2.475	0.0415008	0.177967
18094	10526726	NM_133906	74570	zinc finger with KRAB and SCAN	Zkscan1	0.847	-2.827	0.0247177	0.126484
18095	10599427					0.847	-1.384	0.207746	0.472219
18096	10582152	BC030874	74347	RIKEN cDNA 4632415K11 gene	4632415K11Rik	0.847	-1.995	0.085042	0.280082
18097	10540533	NM_007617	12391	caveolin 3	Cav3	0.847	-2.089	0.0738982	0.256909
18098	10545513					0.847	-0.972	0.362462	0.633904
18099	10572038	NM_028427	73067	transmembrane protein 192	Tmem192	0.847	-2.682	0.0305951	0.145633
18100	10491319	NM_028231	72413	potassium large conductance ca	Kcnmb2	0.847	-3.152	0.015492	0.0924277
18101	10400315					0.847	-1.904	0.0974432	0.304154
18102	10510256	BC012878	77034	RIKEN cDNA 2510039O18 gene	2510039O18Rik	0.847	-2.77	0.02689	0.133446
18103	10429772	NM_144848	223650	epiplakin 1	Eppk1	0.846	-2.167	0.0657932	0.239149
18104	10473641	NM_146343	258340	olfactory receptor 1265	Olfr1265	0.846	-1.346	0.21903	0.487441
18105	10545930					0.846	-2.3	0.0539111	0.210728
18106	10370632	NM_144528	70294	ring finger protein 126	Rnf126	0.846	-2.459	0.0425435	0.18074
18107	10582262	NM_145605	234825	kelch domain containing 4	Klhdc4	0.846	-3.032	0.0183927	0.103567
18108	10557060	ENSMUST00000033166	74466	RIKEN cDNA 4933427G17 gene	4933427G17Rik	0.846	-1.481	0.181014	0.436926
18109	10395855	BC110357	328099	expressed sequence AU021838	AU021838	0.846	-4.391	0.00297034	0.0285477
18110	10500011	NM_011656	22156	tuftelin 1	Tuft1	0.846	-2.628	0.0331368	0.153511
18111	10458823					0.846	-3.691	0.00735041	0.0545959
18112	10404033	NM_145713	14957	histone cluster 1, H1d	Hist1h1d	0.846	-2.776	0.0266586	0.132753
18113	10495530	NM_027193	69740	DPH5 homolog (S. cerevisiae)	Dph5	0.846	-2.561	0.0365828	0.163532
18114	10492291	ENSMUST00000094227	229333	RIKEN cDNA C130079G13 gene	C130079G13Rik	0.846	-1.306	0.23178	0.502487
18115	10388174	NM_011569	21689	tektin 1	Tekt1	0.846	-2.289	0.0548255	0.213486
18116	10595529	NM_199316	382090	RIKEN cDNA 4922501C03 gene	4922501C03Rik	0.846	-2.927	0.0213813	0.114508
18117	10576417	NM_139272	108148	UDP-N-acetyl-alpha-D-galactosa	Galnt2	0.846	-2.262	0.0570515	0.218414
18118	10517682	BC055791	433771	RIKEN cDNA 2310028O11 gene	2310028O11Rik	0.846	-2.285	0.0551052	0.214181
18119	10483548	NM_029280	75422	methyltransferase like 5	Mettl5	0.846	-2.177	0.0647902	0.237175
18120	10508477					0.846	-1.001	0.348996	0.622715
18121	10450444	NM_018816	55938	apolipoprotein M	Apom	0.846	-1.299	0.233961	0.505288
18122	10363403	NM_026937	69090	activating signal cointegrator	Ascc1	0.846	-3.299	0.0125834	0.0794934
18123	10419399	NM_029238	75288	solute carrier family 35, memb	Slc35f4	0.846	-3.014	0.0188586	0.105433
18124	10567504	XM_355934	381917	dynein, axonemal, heavy chain	Dnahc3	0.846	-2.895	0.0224115	0.118094
18125	10516064	NM_029662	76574	major facilitator superfamily	Mfsd2	0.846	-1.386	0.207211	0.471647
18126	10534501					0.846	-3.096	0.0167699	0.0975469
18127	10590892	NM_026665	74360	centrosomal protein 57	Cep57	0.846	-3.859	0.0058712	0.0462693
18128	10371107	NM_025317	66047	mitochondrial ribosomal protei	Mrpl54	0.846	-2.413	0.0455863	0.188847
18129	10548810	BC099944	243676	RIKEN cDNA E330021D16 gene	E330021D16Rik	0.846	-1.54	0.16615	0.417017
18130	10346634	NM_018868	55989	nucleolar protein 5	Nol5	0.846	-3.281	0.0129171	0.0811163
18131	10347741	NM_026713	68393	monoacylglycerol O-acyltransfe	Mogat1	0.846	-1.496	0.176987	0.43128
18132	10381345	NM_011192	19192	proteaseome (prosome, macropai	Psme3	0.846	-3.633	0.00794892	0.057744
18133	10424430	AK016931	74460	RIKEN cDNA 4933426G20 gene	4933426G20Rik	0.846	-2.27	0.0563538	0.217
18134	10461115	NM_031194	19879	solute carrier family 22 (orga	Slc22a8	0.846	-1.674	0.136702	0.373246
18135	10452508	NM_023053	65960	twisted gastrulation homolog 1	Twsg1	0.846	-2.67	0.0311459	0.147425
18136	10416393	XR_034309	629583	similar to Nuclear autoantigen	LOC629583	0.846	-1.463	0.185667	0.443587
18137	10506843	NM_177045	319965	coiled-coil and C2 domain cont	Cc2d1b	0.846	-3.297	0.0126338	0.0796771
18138	10507961	NM_008636	17764	metal response element binding	Mtf1	0.845	-2.897	0.0223291	0.117825
18139	10344973	NM_010267	14545	ganglioside-induced differenti	Gdap1	0.845	-1.734	0.125302	0.354527
18140	10604641					0.845	-1.993	0.0853463	0.280473
18141	10375501					0.845	-2.111	0.0715095	0.251246
18142	10547894	NM_013488	12504	CD4 antigen	Cd4	0.845	-1.603	0.151784	0.395645

18143	10589784	NM_172928	245038	doublecortin-like kinase 3	Dclk3	0.845	-2.83	0.024626	0.126168
18144	10423556	NM_018755	54381	plasma glutamate carboxypeptid	Pgcp	0.845	-2.425	0.0447425	0.187121
18145	10459329	ENSMUST00000048109	78449	RIKEN cDNA 2700046A07 gene	2700046A07Rik	0.845	-1.116	0.300416	0.576564
18146	10483871	NM_011652	22138	titin	Ttn	0.845	-3.272	0.0130801	0.0818967
18147	10474541	NM_025403	66181	nucleolar protein family A, me	Nola3	0.845	-2.305	0.0535443	0.209868
18148	10587255	NM_172925	244923	kelch-like 31 (Drosophila)	Klhl31	0.845	-2.927	0.0213862	0.114508
18149	10557434	NM_138310	171504	apolipoprotein B48 receptor	Apob48r	0.845	-2.364	0.0490096	0.198517
18150	10414590	NM_053111	93719	eosinophil-associated, ribonuc	Ear6	0.845	-2.441	0.0437165	0.184132
18151	10544403	NM_146576	258569	olfactory receptor 459	Olfr459	0.845	-2.038	0.0797183	0.269041
18152	10453555	NM_153780	72139	RIKEN cDNA 2610044O15 gene	2610044O15Rik	0.845	-2.414	0.0455231	0.18878
18153	10593421	CT010205	68721	RIKEN cDNA 1110032A03 gene	1110032A03Rik	0.845	-2.655	0.0318113	0.149238
18154	10568951	NM_146952	258954	olfactory receptor 522	Olfr522	0.845	-1.179	0.275857	0.550733
18155	10565341	XM_884867	620480	predicted gene, EG620480	EG620480	0.845	-2.215	0.0612251	0.228343
18156	10565873	NM_028292	72590	protein phosphatase methyleste	Ppme1	0.845	-3.342	0.0118539	0.0762284
18157	10362129	NM_011979	26464	vanin 3	Vnn3	0.845	-1.877	0.101453	0.312109
18158	10397518	NM_146036	217737	AHA1, activator of heat shock	Ahsa1	0.845	-3.095	0.0167931	0.0975911
18159	10582403	NM_016722	50917	galactosamine (N-acetyl)-6-sul	Galns	0.844	-2.371	0.0485091	0.196834
18160	10344895	XR_032183	665262	similar to adenine nucleotide	LOC665262	0.844	-1.765	0.119633	0.345914
18161	10494060	NM_030116	78523	mitochondrial ribosomal protei	Mrpl9	0.844	-2.404	0.0461566	0.190761
18162	10599658					0.844	-0.881	0.406643	0.6712
18163	10593198	NM_030069	78252	RIKEN cDNA 4432416J03 gene	4432416J03Rik	0.844	-0.894	0.400094	0.666004
18164	10442057	NM_025934	67045	RIO kinase 2 (yeast)	Riok2	0.844	-2.074	0.0756271	0.26001
18165	10419460	NM_177625	219022	tetratricopeptide repeat domai	Ttc5	0.844	-2.191	0.0634497	0.233643
18166	10494441	NM_001024851	545554	ankyrin repeat domain 34A	Ankrd34a	0.844	-2.846	0.0240617	0.124118
18167	10468795	NM_001033172	74998	RAB11 family interacting prote	Rab11fip2	0.844	-2.207	0.0619203	0.229974
18168	10583179	NM_008829	18667	progesterone receptor	Pgr	0.844	-2.717	0.0290742	0.140292
18169	10523901					0.844	-0.739	0.483505	0.73227
18170	10565862	NM_133692	67967	polymerase (DNA-directed), del	Pold3	0.844	-2.054	0.0778819	0.265431
18171	10546229					0.844	-0.789	0.455078	0.711341
18172	10501074	NM_001111143	229697	gene model 131, (NCBI)	Gm131	0.844	-1.473	0.183133	0.440069
18173	10460149	XR_001789	665806	predicted gene, EG665806	EG665806	0.844	-2.068	0.0762907	0.261682
18174	10546088	NM_198622	243529	H1 histone family, member X	H1fx	0.844	-4.152	0.00401441	0.0350747
18175	10471563	ENSMUST00000065087	329385	Riken cDNA C130021I20 gene	C130021I20Rik	0.844	-2.113	0.0712692	0.250796
18176	10560842	NM_009568	22756	zinc finger protein 94	Zfp94	0.844	-1.961	0.0895183	0.28881
18177	10596279	ENSMUST00000060084	235567	DnaJ (Hsp40) homolog, subfamil	Dnajc13	0.844	-1.644	0.142847	0.382955
18178	10484941	NM_145527	228355	MAP-kinase activating death do	Madd	0.844	-2.75	0.0276828	0.13614
18179	10392347	NM_145823	71795	phosphatidylinositol transfer	Pitpnc1	0.844	-3.81	0.00626611	0.048425
18180	10425834	NM_178614	68653	sorting and assembly machinery	Samm50	0.844	-3.122	0.0161698	0.0951294
18181	10572733	BC049349	234413	cDNA sequence BC049349	BC049349	0.844	-2.048	0.0785724	0.266838
18182	10478523					0.844	-1.206	0.265762	0.540834
18183	10497090	NM_001013806	433667	ankyrin repeat domain 13c	Ankrd13c	0.844	-3.482	0.00976346	0.0669403
18184	10489368	NM_173397	228859	RIKEN cDNA D930001I22 gene	D930001I22Rik	0.843	-1.979	0.0871174	0.284086
18185	10349333	BC028767	73103	RIKEN cDNA 3110009E18 gene	3110009E18Rik	0.843	-1.98	0.0869824	0.283733
18186	10470905	AK031561	56086	SET translocation	Set	0.843	-0.954	0.371051	0.641955
18187	10604342	NM_001085510	245405	predicted gene, EG245405	EG245405	0.843	-0.891	0.401904	0.667094
18188	10400718	ENSMUST00000035773	20663	Son of sevenless homolog 2 (Dr	Sos2	0.843	-2.804	0.0255884	0.129436
18189	10550715	NM_025960	67091	trafficking protein particle c	Trappc6a	0.843	-4.366	0.0030662	0.0291248
18190	10450862	NM_001011518	258219	olfactory receptor 94	Olfr94	0.843	-1.548	0.16432	0.414109
18191	10381304	NM_026776	28084	vacuolar protein sorting 25 (y	Vps25	0.843	-4.14	0.00407628	0.0354541
18192	10605081	NM_012060	27061	B-cell receptor-associated pro	Bcap31	0.843	-2.845	0.0240996	0.124223
18193	10593927	NM_020270	56807	secretory carrier membrane pro	Scamp5	0.843	-2.492	0.0405387	0.175358
18194	10428809	BC132483	268807	RIKEN cDNA 8230402K04 gene	8230402K04Rik	0.843	-1.458	0.187027	0.445377
18195	10583071	NM_010809	17392	matrix metallopeptidase 3	Mmp3	0.843	-1.604	0.151567	0.395471
18196	10498011					0.843	-1.529	0.168978	0.420416

18197	10557399	NM_145587	104175	SH3-binding kinase 1	Sbk1	0.843	-2.392	0.0470083	0.192737
18198	10430941	BC012523	74778	RIKEN cDNA 1110014J01 gene	1110014J01Rik	0.843	-2.396	0.0467062	0.191982
18199	10481272	BC099566	69327	RIKEN cDNA 1700007K13 gene	1700007K13Rik	0.843	-1.711	0.129614	0.361026
18200	10560608	NM_009695	11813	apolipoprotein C-II	Apoc2	0.843	-1.616	0.148863	0.391099
18201	10592170					0.843	-3.168	0.0151544	0.0910185
18202	10593789	NM_145615	110842	electron transferring flavopro	Etfa	0.843	-2.8	0.0257297	0.129902
18203	10356936	NM_173760	227399	histidine acid phosphatase dom	Hisppd1	0.843	-3.186	0.0147697	0.0892259
18204	10578515	NM_001039562	654824	ankyrin repeat domain 37	Ankrd37	0.843	-2.479	0.0412805	0.177297
18205	10550400	NM_001099636	434128	PNMA-like 2	Pnmal2	0.843	-2.598	0.0346091	0.157846
18206	10525780	NM_026486	67978	tectonic family member 2	Tctn2	0.843	-3.145	0.0156478	0.0929115
18207	10431147	NM_177630	223732	leucine zipper, down-regulated	Ldoc1l	0.843	-3.928	0.00536269	0.043444
18208	10413314	AK136848	654819	RIKEN cDNA 9930004E17 gene	9930004E17Rik	0.843	-2.524	0.0386225	0.16991
18209	10400742	NM_145443	217666	L-2-hydroxyglutarate dehydroge	L2hgdh	0.843	-2.466	0.0421106	0.17955
18210	10556583	NM_016773	53322	nucleobindin 2	Nucb2	0.843	-2.308	0.0532574	0.209308
18211	10374020	NM_177370	279766	rhomboid domain containing 3	Rhbdd3	0.843	-3.258	0.0133394	0.0830286
18212	10490370	NM_011969	26444	proteasome (prosome, macropain	Psma7	0.843	-4.106	0.00425779	0.036522
18213	10375909	NM_153785	213084	cyclin-dependent kinase-like 3	Cdkl3	0.843	-2.874	0.023088	0.120775
18214	10378082	NM_027819	71522	gamma-glutamyltransferase 6	Ggt6	0.843	-1.738	0.124444	0.35337
18215	10523376	NM_175473	231470	Fraser syndrome 1 homolog (hum	Fras1	0.843	-2.827	0.0247361	0.126547
18216	10465220	NM_020491	56390	Sjogren's syndrome/scleroderma	Sssca1	0.842	-3.66	0.00766033	0.0563022
18217	10511795	NM_001080771	230025	PR domain containing 13	Prdm13	0.842	-1.845	0.10631	0.321598
18218	10584712	NM_021395	12282	hypoxia up-regulated 1	Hyou1	0.842	-4.278	0.00342019	0.0313194
18219	10517892	NM_001025608	213491	DNA segment, Chr 4, ERATO Doi	D4Ertd22e	0.842	-2.248	0.0582994	0.221767
18220	10405074	NM_001081350	70930	nucleolar protein 8	Nol8	0.842	-3.438	0.0103751	0.0698
18221	10489372	BC025862	68314	RIKEN cDNA 0610008F07 gene	0610008F07Rik	0.842	-2.123	0.0703003	0.248442
18222	10387733	NM_181582	276770	eukaryotic translation initiat	Eif5a	0.842	-2.97	0.0201023	0.110172
18223	10508468	BC024696	76799	RIKEN cDNA 2510006D16 gene	2510006D16Rik	0.842	-2.795	0.0259176	0.130415
18224	10544704	NM_021892	60531	neuropeptide VF precursor	Npvf	0.842	-1.461	0.186157	0.444356
18225	10504456	NM_001002787	442829	calicin	Ccin	0.842	-0.912	0.391356	0.659653
18226	10593882	ENSMUST00000098697	100038566	predicted gene, ENSMUSG0000007	ENSMUSG00000074284	0.842	-1.839	0.107273	0.322736
18227	10349868	NM_133819	108954	protein phosphatase 1, regulat	Ppp1r15b	0.842	-3.282	0.0129004	0.0810359
18228	10495252	NM_025946	67067	RIKEN cDNA 2010100O12 gene	2010100O12Rik	0.842	-2.621	0.0334557	0.154317
18229	10554778	NM_001081414	108071	glutamate receptor, metabotrop	Grm5	0.842	-2.171	0.0654361	0.238533
18230	10410039	NM_008957	19206	patched homolog 1	Ptch1	0.842	-3.062	0.0176009	0.100419
18231	10383395	NM_013770	27376	solute carrier family 25 (mito	Slc25a10	0.842	-4.217	0.00369371	0.0330791
18232	10462390	NM_021893	60533	CD274 antigen	Cd274	0.842	-2.349	0.0501274	0.201363
18233	10410508	NM_010888	407785	NADH dehydrogenase (ubiquinone	Ndufs6	0.842	-3.376	0.0113138	0.0736965
18234	10481499	BC023044	73598	RIKEN cDNA 1700001O22 gene	1700001O22Rik	0.842	-1.707	0.130234	0.362012
18235	10419198	NM_015774	50527	ERO1-like (S. cerevisiae)	Ero1l	0.842	-2.237	0.0592201	0.224032
18236	10592162	XM_001477902	100047164	similar to high mobility group	LOC100047164	0.842	-1.31	0.230529	0.501476
18237	10554164	XM_001477681	100042171	similar to 40S ribosomal prote	LOC100042171	0.842	-1.474	0.182782	0.439545
18238	10551162	NM_025504	66349	ATP5S-like	Atp5sl	0.842	-1.814	0.111342	0.33023
18239	10547227	NM_001080780	19713	ret proto-oncogene	Ret	0.842	-3.077	0.0172318	0.0992523
18240	10596857	NM_146226	235606	acylpeptide hydrolase	Apeh	0.842	-2.754	0.0275141	0.135576
18241	10347106	NM_025683	66646	ribulose-5-phosphate-3-epimera	Rpe	0.842	-2.69	0.0302163	0.144448
18242	10488575	NM_212446	228769	proteasome (prosome, macropain	Psmf1	0.842	-3.192	0.0146444	0.0887225
18243	10411506	XR_033231	100047350	similar to Ribosomal protein L	LOC100047350	0.842	-1.028	0.336968	0.6127
18244	10346882	NM_011780	23792	a disintegrin and metallopepti	Adam23	0.842	-1.225	0.258901	0.53308
18245	10353064	NM_001102430	211673	ADP-ribosylation factor guanin	Arfgef1	0.841	-2.476	0.0414818	0.177631
18246	10350951	NM_022312	21960	tenascin R	Tnr	0.841	-2.33	0.0515842	0.205217

18247	10416705	XR_033980	668603	similar to Rpl17 protein	LOC668603	0.841	-3.151	0.0155142	0.0924676
18248	10535852	NM_007513	11987	solute carrier family 7 (catio	Slc7a1	0.841	-2.446	0.0434071	0.18312
18249	10494664	NM_027462	70560	tryptophanyl tRNA synthetase 2	Wars2	0.841	-2.232	0.0597202	0.225162
18250	10590888	XR_031035	665154	similar to MGC27348 protein	LOC665154	0.841	-1.625	0.147002	0.388942
18251	10590890					0.841	-1.464	0.185462	0.443349
18252	10376002					0.841	-1.34	0.220873	0.489996
18253	10503200	NM_001081417	320790	chromodomain helicase DNA bind	Chd7	0.841	-1.903	0.0974795	0.304223
18254	10574157					0.841	-2.917	0.0216905	0.115697
18255	10456158	ENSMUST00000067743	225609	predicted gene, EG225609	EG225609	0.841	-1.199	0.268367	0.542786
18256	10468046	NM_010691	16814	ladybird homeobox homolog 1 (D	Lbx1	0.841	-2.017	0.0822666	0.274404
18257	10455691	NM_026286	67634	ferritin mitochondrial	Ftmt	0.841	-1.222	0.260147	0.534552
18258	10594802	NM_172772	235461	RIKEN cDNA B230380D07 gene	B230380D07Rik	0.841	-1.984	0.0864385	0.282525
18259	10582669	NM_145607	234875	tetratricopeptide repeat domai	Ttc13	0.841	-3.607	0.00822706	0.0590738
18260	10602474	NM_001113354	320595	PHD finger protein 8	Phf8	0.841	-3.39	0.0110911	0.0728453
18261	10501048	AK140363	69206	RIKEN cDNA 2010016I18 gene	2010016I18Rik	0.841	-2.681	0.0306411	0.145754
18262	10376726	NM_145428	216820	dehydrogenase/reductase (SDR f	Dhrs7b	0.841	-3.846	0.00597234	0.0468395
18263	10517083	NM_178698	230801	phosphatidylinositol glycan an	Pigv	0.841	-2.023	0.0816025	0.272821
18264	10352503	NM_011794	23827	bisphosphate 3'-nucleotidase 1	Bpnt1	0.841	-3.41	0.0107906	0.0715675
18265	10372293	XM_893664	628870	predicted gene, EG628870	EG628870	0.841	-1.37	0.21181	0.477389
18266	10569280	NM_008748	18218	dual specificity phosphatase 8	Dusp8	0.841	-2.141	0.0683728	0.244408
18267	10576692	NM_010568	16337	insulin receptor	Insr	0.841	-1.756	0.121236	0.347818
18268	10578109	NM_178648	108159	UBX domain containing 6	Ubxd6	0.841	-2.904	0.0221034	0.117082
18269	10460010	NM_008082	14427	galanin receptor 1	Galr1	0.841	-2.06	0.0771949	0.263727
18270	10524866	NM_001033311	231668	cDNA sequence BC023744	BC023744	0.841	-1.67	0.137511	0.374537
18271	10356593	NM_019479	55927	hairy and enhancer of split 6	Hes6	0.841	-1.544	0.165299	0.415472
18272	10597945	NM_001002267	72309	transmembrane protein 158	Tmem158	0.84	-1.709	0.129925	0.361535
18273	10441091	AK078339	791404	predicted gene, ENSMUSG0000005	ENSMUSG00000055423	0.84	-2.14	0.0684955	0.244681
18274	10569308	NM_015808	50774	keratin associated protein 5-1	Krtap5-1	0.84	-1.145	0.288939	0.565029
18275	10571288	NM_026584	68153	general transcription factor I	Gtf2e2	0.84	-4.392	0.00296668	0.0285255
18276	10490384	NM_001081171	16776	laminin, alpha 5	Lama5	0.84	-3.381	0.0112281	0.0733781
18277	10580984	XR_032470	636859	similar to Glyceraldehyde-3-ph	LOC636859	0.84	-1.787	0.115907	0.338549
18278	10548727					0.84	-0.756	0.473361	0.725045
18279	10580733	NM_026116	67378	Bardet-Biedl syndrome 2 homolo	Bbs2	0.84	-3.042	0.0181289	0.102464
18280	10403945	NM_178210	319159	histone cluster 1, H4j	Hist1h4j	0.84	-2.118	0.0707452	0.249639
18281	10478508	NM_133779	78928	phosphatidylinositol glycan an	Pigt	0.84	-3.787	0.00646332	0.0494788
18282	10542407	NM_023898	78600	phosphodiesterase 6H, cGMP-spe	Pde6h	0.84	-1.845	0.106282	0.321598
18283	10357261	NM_010766	17167	macrophage receptor with colla	Marco	0.84	-2.349	0.0501341	0.201363
18284	10445977	NM_015766	50498	Epstein-Barr virus induced gen	Ebi3	0.84	-2.322	0.0522183	0.206719
18285	10499062	NM_001033301	229474	FH2 domain containing 1	Fhdc1	0.84	-1.136	0.2923	0.568468
18286	10537347					0.84	-2.353	0.0498075	0.200566
18287	10589511	NM_001001144	235623	SREBF chaperone	Scap	0.84	-3.886	0.00566638	0.0452113
18288	10364712	NM_007705	12696	cold inducible RNA binding pro	Cirbp	0.84	-3.107	0.0165144	0.0964322
18289	10436348	NM_138599	28185	translocase of outer mitochond	Tomm70a	0.84	-4.175	0.00389722	0.0343345
18290	10508901	NM_133884	100210	GPN-loop GTPase 2	Gpn2	0.84	-2.789	0.0261634	0.130997
18291	10598105	NM_207175	258251	olfactory receptor 239	Olfr239	0.84	-1.401	0.202873	0.465446
18292	10424349	NM_009270	20775	squalene epoxidase	Sqle	0.839	-4.02	0.00475586	0.0397482
18293	10395889	NM_009216	20605	somatostatin receptor 1	Sstr1	0.839	-1.807	0.112507	0.33223
18294	10506880	NM_029571	100087	KTI12 homolog, chromatin assoc	Kti12	0.839	-4.403	0.00292645	0.028306
18295	10489535	NM_027961	71856	WAP four-disulfide core domain	Wfdc3	0.839	-2.473	0.0416899	0.178117
18296	10569437	NM_009434	22113	pleckstrin homology-like domai	Phlda2	0.839	-2.774	0.0267139	0.132919
18297	10515981					0.839	-1.088	0.311807	0.58828

18298	10374228	NM_001037928	626870	predicted gene, OTTMUSG0000000	OTTMUSG00000005148	0.839	-1.637	0.144319	0.38563
18299	10499876	ENSMUST00000029535	69332	ate cornified envelope-like pr	Lelp1	0.839	-1.487	0.179388	0.434675
18300	10430739	NM_021317	57755	DnaJ (Hsp40) homolog, subfamil	Dnajb7	0.839	-1.117	0.299704	0.575741
18301	10474271	XR_034128	668744	similar to Tardbp protein	LOC668744	0.839	-1.641	0.14345	0.384035
18302	10541670	NM_181344	232371	complement component 1, r subc	C1rl	0.839	-1.6	0.152374	0.396241
18303	10428238	NM_001081359	70790	ubiquitin protein ligase E3 co	Ubr5	0.839	-3.694	0.00731687	0.0544884
18304	10429178	NM_198644	380993	zinc finger and AT hook domain	Zfat	0.839	-2.673	0.0310062	0.146929
18305	10577230	NM_001034862	234086	glutamate-rich 1	Erich1	0.839	-2.417	0.0452966	0.1882
18306	10411373	NM_010422	15212	hexosaminidase B	Hexb	0.839	-2.828	0.0247112	0.126481
18307	10400391	NM_145632	245841	polymerase (RNA) II (DNA direc	Polr2h	0.839	-3.042	0.0181284	0.102464
18308	10451665	NM_009694	11811	apolipoprotein B editing compl	Apobec2	0.839	-2.192	0.0633477	0.23339
18309	10534120	NM_133768	109900	argininosuccinate lyase	Asl	0.839	-4.26	0.00349969	0.0317517
18310	10504518	NM_022811	64424	polymerase (RNA) I polypeptide	Polr1e	0.839	-3.004	0.0191539	0.106576
18311	10358050	NM_011590	21854	translocase of inner mitochond	Timm17a	0.839	-3.355	0.0116423	0.0753259
18312	10376803	NM_178618	69640	RIKEN cDNA 2310040C09 gene	2310040C09Rik	0.839	-1.958	0.089822	0.289247
18313	10565811	NR_002173	449631	RNA, U15b small nucleolar	Rnu15-b	0.839	-1.605	0.15131	0.395197
18314	10471474	NM_021515	11636	adenylate kinase 1	Ak1	0.839	-2.826	0.0247799	0.12668
18315	10507479	NM_026837	68777	transmembrane protein 53	Tmem53	0.839	-2.719	0.0289532	0.13996
18316	10427718	NM_026396	67832	brix domain containing 2	Bxdc2	0.839	-4.448	0.00276821	0.0273322
18317	10577903	BC027296	74653	RIKEN cDNA 4930444A02 gene	4930444A02Rik	0.839	-2.01	0.0831231	0.276258
18318	10440417	AK140789	319723	RIKEN cDNA 9430053O09 gene	9430053O09Rik	0.839	-1.492	0.178161	0.432844
18319	10368566	NM_009413	21987	tumor protein D52-like 1	Tpd52l1	0.839	-2.624	0.0333026	0.153913
18320	10454369	NM_175276	225288	formin homology 2 domain conta	Fhod3	0.839	-1.573	0.158495	0.40535
18321	10388682	NM_144825	216965	TAO kinase 1	Taok1	0.839	-2.896	0.0223713	0.117989
18322	10401820	ENSMUST00000073177	100038992	similar to beacon	LOC100038992	0.839	-2.423	0.0448857	0.187445
18323	10477642					0.838	-0.696	0.507977	0.749889
18324	10384555	NM_181411	216549	aftiphilin	Aftph	0.838	-2.821	0.0249697	0.127526
18325	10516596	NM_153541	215627	zinc finger and BTB domain con	Zbtb8	0.838	-3.085	0.0170422	0.0985074
18326	10423068	NM_011232	19355	RAD1 homolog (S. pombe)	Rad1	0.838	-2.868	0.0232987	0.121277
18327	10529226	NM_153196	71336	ribokinase	Rbks	0.838	-3.538	0.00904422	0.0631751
18328	10519420	NM_194462	100986	A kinase (PRKA) anchor protein	Akap9	0.838	-2.501	0.0399605	0.173817
18329	10566574	NM_029000	74558	GTPase, very large interferon	Gvin1	0.838	-1.744	0.123367	0.351451
18330	10408047	AK132930	100038371	predicted gene, OTTMUSG0000001	OTTMUSG00000018077	0.838	-1.053	0.326487	0.602834
18331	10428594	NM_177225	320679	sterile alpha motif domain con	Samd12	0.838	-1.236	0.255205	0.529492
18332	10432256	NM_007478	11842	ADP-ribosylation factor 3	Arf3	0.838	-3.954	0.00518339	0.0422994
18333	10403071					0.838	-1.144	0.289165	0.565075
18334	10424260	BC070426	210998	DNA segment, Chr 15, ERATO Doi	D15Ertd621e	0.838	-4.369	0.00305185	0.0290634
18335	10442206	NM_009558	22709	zinc finger protein 51	Zfp51	0.838	-2.267	0.0566397	0.217625
18336	10374558					0.838	-1.632	0.14551	0.387083
18337	10460498	NM_007854	13340	solute carrier family 29 (nucl	Slc29a2	0.838	-1.762	0.120227	0.346569
18338	10365471	NM_153195	69754	F-box protein 7	Fbxo7	0.838	-2.297	0.0541969	0.211623
18339	10568954	NM_001011814	258055	olfactory receptor 524	Olfr524	0.838	-1.32	0.22732	0.498027
18340	10550730	NM_022409	63872	zinc finger protein 296	Zfp296	0.838	-2.188	0.0637762	0.234479
18341	10565190					0.838	-1.177	0.276611	0.551708
18342	10575326	AK156953	672735	hypothetical protein LOC672735	LOC672735	0.838	-2.136	0.0689044	0.245893
18343	10601537	XM_910030	635086	similar to ubiquitin-conjugati	LOC635086	0.838	-1.759	0.120678	0.347112
18344	10367697	NM_133485	76142	protein phosphatase 1, regulat	Ppp1r14c	0.838	-1.989	0.0858496	0.28119
18345	10543253	NM_023653	22413	wingless-related MMTV integrat	Wnt2	0.838	-1.985	0.086329	0.282254
18346	10388824	NM_008238	15218	forkhead box N1	Foxn1	0.837	-2.277	0.0557733	0.215622
18347	10565072	NM_019951	56529	SEC11 homolog A (S. cerevisiae	Sec11a	0.837	-3.492	0.00962746	0.0661778
18348	10367055	NM_147222	216453	retinol dehydrogenase 19	Rdh19	0.837	-1.103	0.305382	0.581741

18349	10358787	NM_008485	16782	laminin, gamma 2	Lamc2	0.837	-3.217	0.0141198	0.0863356
18350	10444046	NM_019421	54219	CD320 antigen	Cd320	0.837	-2.333	0.0513104	0.204584
18351	10560672	NM_023224	80794	Casitas B-lineage lymphoma c	Cblc	0.837	-2.531	0.0382251	0.168945
18352	10554269	NM_018811	54608	abhydrolase domain containing	Abhd2	0.837	-1.565	0.160366	0.407738
18353	10550734					0.837	-3.193	0.0146068	0.0885706
18354	10532709					0.837	-1.156	0.284424	0.559618
18355	10351368	NM_021610	59290	glycoprotein A33 (transmembran	Gpa33	0.837	-1.816	0.110962	0.329706
18356	10409645	NM_152234	56085	ubiquilin 1	Ubqln1	0.837	-3.835	0.00605826	0.0472588
18357	10353672					0.837	-1.131	0.294236	0.570555
18358	10584572	NM_031165	15481	heat shock protein 8	Hspa8	0.837	-1.421	0.197014	0.457727
18359	10444995	ENSMUST00000097330	547347	predicted gene, EG547347	EG547347	0.837	-1.74	0.124213	0.35291
18360	10600512	NM_145956	210766	BRCA1/BRCA2-containing complex	Brcc3	0.837	-4.339	0.00317105	0.0298259
18361	10425507	NM_145132	207911	melanin-concentrating hormone	Mchr1	0.837	-1.617	0.148675	0.390994
18362	10481435	NM_172404	70266	cysteine conjugate-beta lyase	Ccbl1	0.837	-2.409	0.045801	0.189588
18363	10439960	NM_028815	74201	centrosomal protein 97	Cep97	0.837	-2.029	0.0808595	0.271466
18364	10504002	NM_011463	20731	serine peptidase inhibitor, Ka	Spink4	0.837	-2.494	0.0404063	0.175
18365	10517383	NM_028995	74552	NIPA-like domain containing 3	Npal3	0.837	-2.504	0.0398167	0.173584
18366	10400004					0.837	-1.9	0.0979499	0.30515
18367	10457916	XR_031062	665916	similar to ribosomal protein L	LOC665916	0.837	-1.998	0.0846091	0.279309
18368	10569085	BC119093	72000	RIKEN cDNA 1600016N20 gene	1600016N20Rik	0.837	-2.767	0.0270041	0.133769
18369	10364130	NM_177475	64453	zinc finger protein 280b	Zfp280b	0.837	-4.631	0.00221442	0.0234225
18370	10461162	NR_004445	100127111	small nucleolar RNA, C/D box 2	Snord22	0.837	-1.604	0.151425	0.395324
18371	10533122	NM_133902	257635	serine dehydratase-like	Sdsl	0.837	-1.994	0.085163	0.280273
18372	10559297	NM_001042760	18400	solute carrier family 22 (orga	Slc22a18	0.837	-2.14	0.0684894	0.244681
18373	10544186	NM_018810	54484	makorin, ring finger protein,	Mkrn1	0.837	-4.129	0.00413288	0.0357546
18374	10358023	NM_134438	171469	G protein-coupled receptor 37-	Gpr37l1	0.837	-1.618	0.148508	0.390852
18375	10384020	NM_017401	54125	polymerase (DNA directed), mu	Polm	0.837	-2.724	0.0287396	0.139246
18376	10359280	NM_001085376	23850	pappalysin 2	Pappa2	0.836	-2.023	0.0815139	0.272667
18377	10599560					0.836	-2.125	0.0700096	0.247912
18378	10383423	NM_025389	66156	anaphase promoting complex sub	Anapc11	0.836	-2.995	0.0193975	0.107469
18379	10506714	NM_053073	16975	low density lipoprotein recept	Lrp8	0.836	-2.535	0.0380108	0.168377
18380	10508382	NM_016895	11637	adenylate kinase 2	Ak2	0.836	-3.614	0.00815734	0.0587204
18381	10490770					0.836	-1.985	0.0863665	0.282334
18382	10478633	NM_013599	17395	matrix metallopeptidase 9	Mmp9	0.836	-4.507	0.00257371	0.0259383
18383	10521822	XR_032388	666265	similar to ribosomal protein L	LOC666265	0.836	-0.195	0.850688	0.939953
18384	10443482	BC058575	80748	cDNA sequence BC004004	BC004004	0.836	-3.896	0.00559432	0.0448224
18385	10498771	NM_019745	56426	programmed cell death 10	Pdcd10	0.836	-2.484	0.0409819	0.176468
18386	10606714	NM_013463	11605	galactosidase, alpha	Gla	0.836	-2.275	0.055959	0.21607
18387	10442391	ENSMUST00000097377	100038386	predicted gene, ENSMUSG0000007	ENSMUSG00000073440	0.836	-1.308	0.230993	0.501708
18388	10418604	NM_027949	71838	PHD finger protein 7	Phf7	0.836	-3.32	0.0122251	0.0778342
18389	10362442					0.836	-0.708	0.50111	0.744172
18390	10559756					0.836	-2.017	0.0823541	0.274479
18391	10369828					0.836	-3.092	0.0168793	0.0978602
18392	10394394	NM_009693	238055	apolipoprotein B	Apob	0.836	-2.325	0.0519563	0.206172
18393	10526961	NM_010757	17135	v-maf musculoaponeurotic fibro	Mafk	0.836	-2.337	0.051013	0.203744
18394	10475610	NM_023595	110074	deoxyuridine triphosphatase	Dut	0.836	-3.974	0.00505249	0.0416166
18395	10514083	NM_009887	12622	cerberus 1 homolog (Xenopus la	Cer1	0.836	-2.465	0.0421523	0.179691
18396	10520187	NM_009207	20535	solute carrier family 4 (anion	Slc4a2	0.836	-3.526	0.00919549	0.063936
18397	10575095	NM_008217	15118	hyaluronan synthase 3	Has3	0.836	-3.637	0.00790144	0.0575105
18398	10446224	NM_177638	224912	crumbs homolog 3 (Drosophila)	Crb3	0.836	-3.886	0.00566572	0.0452113
18399	10398308	ENSMUST00000047115	212198	WD repeat domain 25	Wdr25	0.836	-1.862	0.10364	0.316489
18400	10575926	EF688288	69047	ATPase, Ca++ transporting, typ	Atp2c2	0.836	-2.524	0.0386038	0.16991
18401	10486875	NM_172673	228564	FERM domain containing 5	Frmd5	0.836	-1.902	0.0976841	0.304546
18402	10562105	NM_008085	14447	glyceraldehyde-3-phosphate deh	Gapdhs	0.836	-2.8	0.0257178	0.129873
18403	10463670	NM_053196	94279	sideroflexin 2	Sfxn2	0.836	-3.246	0.0135552	0.0839271

18404	10437813	ENSMUST00000082339	100048925	predicted gene, EG622757	EG622757	0.836	-1.424	0.196111	0.45647
18405	10509838	NM_008812	18600	peptidyl arginine deiminase, t	Padi2	0.836	-2.895	0.0223964	0.118063
18406	10402835	NM_025399	66174	nudix (nucleoside diphosphate	Nudt14	0.835	-2.781	0.0264428	0.132021
18407	10589927					0.835	-1.374	0.2105	0.475962
18408	10561306	NM_011116	18807	phospholipase D family, member	Pld3	0.835	-2.635	0.0327993	0.152386
18409	10467091	NM_026487	67979	ATPase family, AAA domain cont	Atad1	0.835	-2.523	0.038686	0.170092
18410	10434743					0.835	-2.483	0.0410392	0.17662
18411	10504008	NM_029814	76959	chromatin modifying protein 5	Chmp5	0.835	-4.238	0.00359872	0.0324929
18412	10586907	NM_008613	17427	meiosis-specific nuclear struc	Mns1	0.835	-2.664	0.0314074	0.148244
18413	10460831					0.835	-0.7	0.505596	0.747576
18414	10599321	NM_020256	56805	zinc finger and BTB domain con	Zbtb33	0.835	-2.355	0.0496692	0.200281
18415	10465686	NM_001003934	20168	reticulon 3	Rtn3	0.835	-3.877	0.00573389	0.0455152
18416	10551865	NM_198027	233065	alkB, alkylation repair homolo	Alkbh6	0.835	-1.655	0.140691	0.379507
18417	10378763					0.835	-2.941	0.0209772	0.11338
18418	10457938					0.835	-2.006	0.083708	0.2772
18419	10401050	XR_032933	665957	similar to high mobility group	LOC665957	0.835	-2.155	0.0670095	0.241742
18420	10498593	ENSMUST00000116062	208424	gene model 412, (NCBI)	Gm412	0.835	-1.308	0.230872	0.501612
18421	10492598	NM_133787	97112	NMD3 homolog (S. cerevisiae)	Nmd3	0.835	-2.875	0.0230764	0.120761
18422	10345200					0.835	-2.699	0.0298116	0.142998
18423	10463158	BC116837	226118	expressed sequence AI606181	AI606181	0.835	-1.921	0.0950128	0.299665
18424	10552917	BC100502	76713	RIKEN cDNA 1700039E15 gene	1700039E15Rik	0.835	-3.007	0.0190619	0.106204
18425	10442285	XM_001478718	383218	predicted gene, EG383218	EG383218	0.835	-2.779	0.0265316	0.132276
18426	10556940	NM_025899	67003	ubiquinol cytochrome c reducta	Uqcrc2	0.835	-5.091	0.00129121	0.0158118
18427	10372005	NM_172538	215008	vezatin, adherens junctions tr	Vezt	0.835	-2.07	0.0760539	0.261237
18428	10446220					0.835	-2.901	0.0222112	0.117349
18429	10585721	NM_022813	24044	secretory carrier membrane pro	Scamp2	0.835	-3.733	0.00694031	0.0521856
18430	10418917	ENSMUST00000052126	69134	RIKEN cDNA 2200001I15 gene	2200001I15Rik	0.835	-2.054	0.0778314	0.265345
18431	10446587	ENSMUST00000097289	77533	RIKEN cDNA C030034I22 gene	C030034I22Rik	0.835	-1.681	0.135318	0.370761
18432	10360053	NM_025557	66425	Purkinje cell protein 4-like 1	Pcp4l1	0.835	-1.072	0.318289	0.595501
18433	10436590	AK148800	77994	RIKEN cDNA 2810055G20 gene	2810055G20Rik	0.834	-1.395	0.204495	0.467724
18434	10421723	NM_025384	66148	DnaJ (Hsp40) homolog, subfamil	Dnajc15	0.834	-2.643	0.032409	0.151237
18435	10374043	NM_023816	76389	ankyrin repeat domain 36	Ankrd36	0.834	-2.949	0.020733	0.112665
18436	10603567	NM_025975	67117	dynein light chain Tctex-type	Dynlt3	0.834	-3.449	0.01022	0.0690169
18437	10498651	ENSMUST00000091052	19952	ribosomal protein L32, pseudog	Rpl32-ps	0.834	-2.323	0.0520919	0.206415
18438	10408251	NM_177016	319848	solute carrier family 17 (sodi	Slc17a4	0.834	-1.79	0.115293	0.337519
18439	10507589					0.834	-3.765	0.00665398	0.0506729
18440	10537828	NM_146369	258366	olfactory receptor 434	Olfr434	0.834	-1.378	0.209582	0.474666
18441	10349832	XR_033420	638636	similar to ribosomal protein S	LOC638636	0.834	-2.267	0.0566679	0.217694
18442	10385335					0.834	-3.04	0.0181691	0.102596
18443	10431962	NM_008902	19011	placental protein 11 related	Pp11r	0.834	-2.621	0.03348	0.154358
18444	10482073					0.834	-2.08	0.0749325	0.25894
18445	10419158	NM_001011876	630952	angiogenin, ribonuclease A fam	Ang6	0.834	-1.256	0.248237	0.521623
18446	10423512	BC030179	68073	RIKEN cDNA A930016P21 gene	A930016P21Rik	0.834	-3.498	0.00955328	0.0657534
18447	10515220	NM_010173	14073	fatty acid amide hydrolase	Faah	0.834	-2.699	0.0298223	0.143017
18448	10395198	XR_032641	668786	similar to tripartite motif pr	LOC668786	0.834	-2.94	0.0209965	0.113397
18449	10592084	NM_009178	20443	ST3 beta-galactoside alpha-2,3	St3gal4	0.834	-2.516	0.0390861	0.171282
18450	10407012	NM_026075	67288	SFRS12-interacting protein 1	Sfrs12ip1	0.834	-3.422	0.0106051	0.0707361
18451	10364331	BC061019	75188	RIKEN cDNA 1700009J07 gene	1700009J07Rik	0.834	-1.453	0.188307	0.446362
18452	10439208	NM_133704	317717	SEC22 vesicle trafficking prot	Sec22a	0.834	-2.8	0.0257152	0.129873
18453	10389842	NM_001013375	217109	UTP18, small subunit (SSU) pro	Utp18	0.834	-3.499	0.00953352	0.065703
18454	10578393	NM_177742	244448	tripartite motif family-like 1	Triml1	0.834	-1.714	0.129046	0.360251
18455	10392881	NM_007997	14149	ferredoxin reductase	Fdxr	0.834	-2.64	0.0325424	0.151569
18456	10558508	NM_001098636	101631	PWWP domain containing 2B	Pwwp2b	0.834	-2.355	0.0496999	0.200281
18457	10416290	NM_180588	72549	receptor accessory protein 4	Reep4	0.834	-3.239	0.0136899	0.0845385

18457	10416290	NM_180588	72549	receptor accessory protein 4	Reep4	0.834	-3.259	0.0130899	0.0845585
18458	10483110	NM_027835	71586	interferon induced with helica	Ifih1	0.834	-2.378	0.0479826	0.195456
18459	10544348	NM_022413	64177	transient receptor potential c	Trpv6	0.834	-1.593	0.153949	0.398469
18460	10488912	NM_145537	108687	ER degradation enhancer, manno	Edem2	0.834	-4.164	0.00395148	0.0346513
18461	10457963	NM_001025381	574402	G protein-coupled receptor 17	Gpr17	0.834	-1.841	0.106999	0.322599
18462	10462697					0.834	-1.679	0.135749	0.371508
18463	10537123	ENSMUST00000070189	74354	leucine-rich repeats and guany	Lrguk	0.834	-1.767	0.119285	0.34536
18464	10514313	NM_206867	230398	predicted gene, OTTMUSG0000001	OTTMUSG00000011275	0.834	-1.56	0.161455	0.409623
18465	10466779	NM_008846	18719	phosphatidylinositol-4-phospha	Pip5k1b	0.834	-1.738	0.12446	0.35337
18466	10563411	NM_153419	101612	glutamate-rich WD repeat conta	Grwd1	0.833	-3.685	0.0074108	0.0549418
18467	10364371					0.833	-1.875	0.101756	0.312541
18468	10558936	NM_001025103	213573	EF-hand calcium binding domain	Efcab4a	0.833	-2.264	0.0568926	0.218163
18469	10361642	NM_172784	237253	low density lipoprotein recept	Lrp11	0.833	-2.09	0.0738105	0.256746
18470	10453715	BC056351	19330	RAB18, member RAS oncogene fam	Rab18	0.833	-1.989	0.0858572	0.28119
18471	10529661	NM_029162	75079	zinc finger protein 509	Zfp509	0.833	-2.578	0.0356391	0.16081
18472	10571728	NM_203507	192174	RWD domain containing 4A	Rwdd4a	0.833	-3.121	0.0161986	0.0952457
18473	10477854	NM_013510	13821	erythrocyte protein band 4.1-l	Epb4.1l1	0.833	-4.331	0.00319927	0.0299713
18474	10556413	AB359922	70877	MICAL C-terminal like	Micalcl	0.833	-2.017	0.0822985	0.274433
18475	10449575	NM_026845	68816	peptidylprolyl isomerase (cycl	Ppil1	0.833	-3.988	0.00495921	0.0410723
18476	10349771	ENSMUST00000116023	638532	predicted gene, EG638532	EG638532	0.833	-1.998	0.0847186	0.279408
18477	10521331	BC116928	403174	RIKEN cDNA A930005I04 gene	A930005I04Rik	0.833	-1.372	0.211212	0.476809
18478	10582474	NM_145606	234852	chromatin modifying protein 1A	Chmp1a	0.833	-2.158	0.0666509	0.241189
18479	10538275	NM_010903	18025	nuclear factor, erythroid deri	Nfe2l3	0.833	-3.33	0.0120585	0.077029
18480	10521757					0.833	-1.616	0.148796	0.391099
18481	10574163	ENSMUST00000098489	102084	expressed sequence AI451557	AI451557	0.833	-1.39	0.206036	0.4701
18482	10494643	NM_008256	15360	3-hydroxy-3-methylglutaryl-Coe	Hmgcs2	0.833	-2.943	0.0209151	0.113291
18483	10510910	AK140029	100038561	predicted gene, ENSMUSG0000007	ENSMUSG00000073693	0.833	-2.452	0.0430003	0.182022
18484	10525731					0.833	-1.97	0.0882866	0.286405
18485	10599776	NM_009766	12209	bombesin-like receptor 3	Brs3	0.833	-1.281	0.239722	0.512764
18486	10374115	AK080521	791363	predicted gene, ENSMUSG0000005	ENSMUSG00000053792	0.833	-2.27	0.0563693	0.21702
18487	10359713	NM_145512	108735	SFT2 domain containing 2	Sft2d2	0.833	-2.069	0.0761261	0.261385
18488	10389670	NM_146413	258408	olfactory receptor 463	Olfr463	0.833	-2.069	0.0761735	0.261455
18489	10570827	NM_020560	57312	mitochondrial ribosomal protei	Mrps31	0.833	-2.973	0.0200098	0.109893
18490	10469559	NM_029619	76467	methionine sulfoxide reductase	Msrb2	0.833	-2.534	0.0380592	0.168493
18491	10573490	NM_133255	170833	hook homolog 2 (Drosophila)	Hook2	0.833	-3.938	0.00529599	0.043019
18492	10374035	NM_013842	22433	X-box binding protein 1	Xbp1	0.833	-2.68	0.0306641	0.145769
18493	10386518	NM_145427	246782	ATP synthase mitochondrial F1	Atpaf2	0.833	-2.848	0.0240046	0.123854
18494	10497296	NM_001010834	241877	solute carrier family 10 (sodi	Slc10a5	0.833	-1.665	0.13862	0.376676
18495	10356859	NM_001105667	21915	deoxythymidylate kinase	Dtymk	0.832	-3.083	0.0170941	0.0987125
18496	10552125	NM_008820	18624	peptidase D	Pepd	0.832	-1.982	0.0867524	0.283113
18497	10533734	NM_019875	56325	ATP-binding cassette, sub-fami	Abcb9	0.832	-1.89	0.0994885	0.30816
18498	10603151	NM_023122	14758	glycoprotein m6b	Gpm6b	0.832	-3.264	0.0132237	0.0825934
18499	10527886	AK162341	67210	GATA zinc finger domain contai	Gatad1	0.832	-1.9	0.098046	0.305404
18500	10368875	NM_001034858	213402	armadillo repeat containing 2	Armc2	0.832	-1.77	0.118829	0.344323
18501	10599604	NM_001034059	434778	RIKEN cDNA 6330534C20 gene	6330534C20Rik	0.832	-3.251	0.0134677	0.0836057
18502	10478447	NM_021420	58231	serine/threonine kinase 4	Stk4	0.832	-3.23	0.0138764	0.0854159
18503	10352499					0.832	-1.728	0.126369	0.356023
18504	10517060	NM_010948	18221	nuclear distribution gene C ho	Nudc	0.832	-2.384	0.047536	0.194147
18505	10394770	NM_013614	18263	ornithine decarboxylase, struc	Odc1	0.832	-3.018	0.0187645	0.105129
18506	10540213					0.832	-2.227	0.0601572	0.226087
18507	10539159	NM_019879	56451	succinate-CoA ligase, GDP-form	Suclg1	0.832	-5.012	0.00141373	0.0167368
18508	10452867	NM_024428	66310	dpy-30 homolog (C. elegans)	Dpy30	0.832	-2.804	0.0255855	0.129436
18509	10523060	ENSMUST00000068250	791294	predicted gene,	ENSMUSG00000054945	0.832	1.895	0.0987228	0.306809

18509	[illegible]	[illegible]	[illegible]	ENSMUSG0000005	[illegible]	0.832	-1.893	0.0987228	0.306809
18510	10446066	ENSMUST00000070225	320593	RIKEN cDNA A230051N06 gene	A230051N06Rik	0.832	-1.92	0.0951382	0.299747
18511	10565486	NM_021876	13626	embryonic ectoderm development	Eed	0.832	-3.484	0.00974195	0.0668561
18512	10562548	NM_011274	19777	expressed sequence C80913	C80913	0.832	-4.301	0.0033233	0.0306847
18513	10428012	NM_145852	252967	ropporin 1-like	Ropn1l	0.832	-2.629	0.0330537	0.153299
18514	10355278	NM_010154	13869	v-erb-a erythroblastic leukemi	Erbb4	0.832	-2.029	0.080814	0.271356
18515	10518031	NM_172338	214063	DnaJ (Hsp40) homolog, subfamil	Dnajc16	0.832	-2.658	0.0316955	0.149063
18516	10535502	NM_146165	231872	JTV1 gene	Jtv1	0.832	-3.102	0.0166343	0.0970498
18517	10569992	XR_031532	674846	similar to CG5323-PA	LOC674846	0.832	-2.986	0.0196567	0.108567
18518	10558647	NM_146954	258956	olfactory receptor 535	Olfr535	0.832	-2.051	0.0782771	0.266177
18519	10499981	NM_016901	53814	ornithine decarboxylase antizy	Oaz3	0.832	-1.964	0.0890759	0.287809
18520	10398338					0.832	-1.074	0.317451	0.594727
18521	10502613	NM_001033199	99709	expressed sequence AI747448	AI747448	0.832	-1.328	0.224813	0.494893
18522	10488256	NM_026924	107586	ovo-like 2 (Drosophila)	Ovol2	0.832	-4.021	0.00475145	0.0397482
18523	10573027	NM_001081164	73945	OTU domain containing 4	Otud4	0.832	-3.332	0.0120168	0.0768787
18524	10542021	XR_034903	624256	similar to small nuclear ribon	LOC624256	0.832	-2.24	0.0589853	0.22351
18525	10374350					0.832	-1.464	0.185264	0.442974
18526	10434799					0.832	-1.912	0.0962685	0.302048
18527	10598601	ENSMUST00000057113	385317	RIKEN cDNA 4930557A04 gene	4930557A04Rik	0.832	-4.209	0.00373473	0.0332773
18528	10376292	ENSMUST00000071487	73158	La ribonucleoprotein domain fa	Larp1	0.832	-3.298	0.0126118	0.079625
18529	10526113	NM_007761	12909	calcitonin gene-related peptid	Crcp	0.832	-3.167	0.0151611	0.0910185
18530	10362937	XR_033499	635061	similar to ribosomal protein S	LOC635061	0.832	-1.661	0.13934	0.377524
18531	10450418	NM_033478	114654	lymphocyte antigen 6 complex,	Ly6g6d	0.831	-1.594	0.153688	0.398233
18532	10555293	BC115472	67164	RIKEN cDNA 2610209A20 gene	2610209A20Rik	0.831	-2.062	0.0769765	0.263109
18533	10425226	NM_145139	223691	eukaryotic translation initiat	Eif3eip	0.831	-4.137	0.00408973	0.0355272
18534	10566304	ENSMUST00000053743	70980	RIKEN cDNA 4931431F19 gene	4931431F19Rik	0.831	-1.003	0.348486	0.622153
18535	10535866	NM_011908	24109	ubiquitin-like 3	Ubl3	0.831	-3.167	0.0151592	0.0910185
18536	10462724	ENSMUST00000025729	74493	tankyrase, TRF1-interacting an	Tnks2	0.831	-4.321	0.00324276	0.0301848
18537	10448963	NM_011425	20609	somatostatin receptor 5	Sstr5	0.831	-1.83	0.108661	0.325457
18538	10449598	BC116867	71138	RIKEN cDNA 4933413N12 gene	4933413N12Rik	0.831	-1.714	0.129021	0.360251
18539	10512919	NM_001033351	242443	glutamate receptor ionotropic,	Grin3a	0.831	-1.033	0.335199	0.610757
18540	10422628	NM_177355	239318	phosphatidylinositol-specific	Plcxd3	0.831	-3.309	0.0124178	0.0786588
18541	10575630	NM_130457	170571	contactin associated protein-l	Cntnap4	0.831	-2.22	0.0608049	0.227575
18542	10479736	NM_025901	67005	polymerase (RNA) III (DNA dire	Polr3k	0.831	-2.783	0.0263859	0.13183
18543	10588547	NM_001015507	321006	Vpr (HIV-1) binding protein	Vprbp	0.831	-3.335	0.0119637	0.0766545
18544	10514647					0.831	-1.708	0.130188	0.362005
18545	10382449	NM_021411	58222	RAB37, member of RAS oncogene	Rab37	0.831	-1.575	0.158036	0.405065
18546	10598743	NM_173415	236690	nyctalopin	Nyx	0.831	-1.625	0.146867	0.388752
18547	10596575	NM_029103	74840	arginine-rich, mutated in earl	Armet	0.831	-3.718	0.00708525	0.0531431
18548	10465649	NM_007928	13728	MAP/microtubule affinity-regul	Mark2	0.831	-4.14	0.00407373	0.035447
18549	10396161	NM_028339	72736	thioredoxin domain containing	Txndc1	0.831	-3.065	0.017527	0.100079
18550	10381154	NM_009923	12799	2',3'-cyclic nucleotide 3' pho	Cnp	0.831	-2.264	0.0568661	0.218146
18551	10389283	NM_008498	16869	LIM homeobox protein 1	Lhx1	0.831	-1.593	0.153881	0.398439
18552	10413949	AY775400	67580	leucine rich repeat containing	Lrrc18	0.831	-2.914	0.0217978	0.116036
18553	10508269	NM_030252	80284	cDNA sequence BC003266	BC003266	0.831	-3.632	0.00795263	0.057744
18554	10583732	NM_010700	16835	low density lipoprotein recept	Ldlr	0.831	-3.418	0.0106624	0.0710231
18555	10437698	NM_029582	106200	thioredoxin domain containing	Txndc11	0.831	-3.608	0.00821454	0.059041
18556	10374012	NM_145216	75668	RAS-like, family 10, member A	Rasl10a	0.831	-2.437	0.0439299	0.184699
18557	10415714	BC056350	72125	RIKEN cDNA 2600011E07 gene	2600011E07Rik	0.831	-1.553	0.163086	0.412032
18558	10582811	ENSMUST00000054960	270110	interferon regulatory factor 2	Irf2bp2	0.831	-3.092	0.0168856	0.0978674
18559	10481135	NM_013677	20930	surfeit gene 1	Surf1	0.831	-2.255	0.0576741	0.220155
18560	10429691	BC117947	105732	expressed sequence AA409316	AA409316	0.83	-2.537	0.0379146	0.168193

18561	10532907	NM_009327	21405	HNF1 homeobox A	Hnf1a	0.83	-2.757	0.0274066	0.135172
18562	10451167	NM_198167	224807	transmembrane protein 63b	Tmem63b	0.83	-3.706	0.00720462	0.0537715
18563	10434165	NM_033474	11877	armadillo repeat gene deleted	Arvcf	0.83	-2.863	0.0234796	0.121889
18564	10419525	BC119374	328399	RIKEN cDNA A930018M24 gene	A930018M24Rik	0.83	-1.348	0.218394	0.486434
18565	10514128	NM_027238	69863	RIKEN cDNA 1810054D07 gene	1810054D07Rik	0.83	-2.903	0.0221596	0.117219
18566	10526193					0.83	-1.803	0.113167	0.333338
18567	10444554	NM_023557	70129	solute carrier family 44, memb	Slc44a4	0.83	-3.849	0.00594807	0.0467532
18568	10536294	NM_001040611	170676	paternally expressed 10	Peg10	0.83	-2.538	0.0378396	0.167978
18569	10366186	NM_025602	52713	coiled-coil domain containing	Ccdc59	0.83	-2.371	0.0484969	0.196834
18570	10520445	NM_001037941	23950	DnaJ (Hsp40) homolog, subfamil	Dnajb6	0.83	-1.392	0.205458	0.469103
18571	10446207	NM_017393	53895	caseinolytic peptidase, ATP-de	Clpp	0.83	-2.943	0.0208939	0.113256
18572	10464283	ENSMUST00000071072	791347	predicted gene, ENSMUSG0000005	ENSMUSG00000056739	0.83	-1.207	0.265482	0.540577
18573	10485183	NM_211358	228368	solute carrier family 35, memb	Slc35c1	0.83	-4.164	0.00395425	0.0346513
18574	10506883	NM_023537	69908	RAB3B, member RAS oncogene fam	Rab3b	0.83	-2.308	0.0532522	0.209308
18575	10597182	ENSMUST00000093780	235627	neurobeachin-like 2	Nbeal2	0.83	-2.986	0.0196378	0.108498
18576	10466903	NM_198651	381218	RIKEN cDNA 4430402I18 gene	4430402I18Rik	0.83	-2.463	0.042278	0.179955
18577	10540287	ENSMUST00000071059	791269	predicted gene, ENSMUSG0000005	ENSMUSG00000056743	0.83	-1.721	0.1277	0.358351
18578	10447513	ENSMUST00000097269	100038500	predicted gene, ENSMUSG0000007	ENSMUSG00000073366	0.83	-1.614	0.149238	0.391598
18579	10574480	NM_053070	12354	carbonic anhydrase 7	Car7	0.83	-2.473	0.0416671	0.178117
18580	10352918	BC058715	320977	RIKEN cDNA C030002C11 gene	C030002C11Rik	0.83	-1.217	0.261807	0.536245
18581	10438189	NM_144852	224022	solute carrier family 7 (catio	Slc7a4	0.83	-1.94	0.092268	0.294344
18582	10396950					0.83	-1.533	0.167826	0.419086
18583	10373202	NM_028230	108037	serine hydroxymethyltransferas	Shmt2	0.83	-2.754	0.0275233	0.13559
18584	10355456	NM_001005423	381269	melanoregulin	Mreg	0.829	-2.763	0.027161	0.134251
18585	10346137	XR_033155	666909	glyceraldehyde-3-phosphate deh	LOC666909	0.829	-0.984	0.356879	0.629197
18586	10458226	NM_010481	15526	heat shock protein 9	Hspa9	0.829	-4.204	0.00375689	0.0333904
18587	10437804	NM_011987	26565	phospholipase A2, group X	Pla2g10	0.829	-2.075	0.0755182	0.259804
18588	10352556	XR_033497	100042375	glyceraldehyde-3-phosphate deh	LOC100042375	0.829	-1.957	0.0899508	0.289442
18589	10586604	NM_026467	67941	ribosomal protein S27-like	Rps27l	0.829	-2.831	0.0245772	0.126012
18590	10415065	NM_022993	65107	low-density lipoprotein recept	Lrp10	0.829	-2.263	0.0570217	0.218378
18591	10417147	NM_080556	68059	transmembrane 9 superfamily me	Tm9sf2	0.829	-3.534	0.00909707	0.0634394
18592	10583834	BC054761	68283	RIKEN cDNA 9530077C05 gene	9530077C05Rik	0.829	-2.689	0.0302908	0.144706
18593	10531370	NM_025972	67111	Nacylethanolamine acid amidase	Naaa	0.829	-3.796	0.0063849	0.0490382
18594	10473343	NM_025885	381379	mediator of RNA polymerase II	Med19	0.829	-3.922	0.00540855	0.0437317
18595	10503833	BC091747	56040	ribosomal protein, large, P1	Rplp1	0.829	-3.573	0.00861631	0.0610738
18596	10549079	NM_145572	232493	glycogen synthase 2	Gys2	0.829	-4.259	0.00350505	0.0317727
18597	10412607	NM_025341	66082	abhydrolase domain containing	Abhd6	0.829	-3.66	0.00765629	0.0563022
18598	10371390	NM_010214	14202	four and a half LIM domains 4	Fhl4	0.829	-1.354	0.216676	0.484036
18599	10391555	NM_008918	19064	pancreatic polypeptide	Ppy	0.829	-2.074	0.0756403	0.260013
18600	10552516	NM_011177	19144	kallikrein related-peptidase 6	Klk6	0.828	-3.602	0.00828506	0.0593818
18601	10519069	NM_175556	269615	phospholipase C, eta 2	Plch2	0.828	-1.859	0.104136	0.317316
18602	10376787	NM_013717	27078	B9 protein domain 1	B9d1	0.828	-4.779	0.00185473	0.020404
18603	10384398	NM_010345	14783	growth factor receptor bound p	Grb10	0.828	-5.223	0.00111162	0.0141204
18604	10451613	NM_001110824	74123	forkhead box P4	Foxp4	0.828	-3.088	0.0169623	0.0981528
18605	10566452	XR_032323	100046114	similar to HBxAg transactivate	LOC100046114	0.828	-2.223	0.0604664	0.226805
18606	10374313					0.828	-2.36	0.0493103	0.199391
18607	10467493	NM_026260	67590	tectonic family member 3	Tctn3	0.828	-2.497	0.0402274	0.174515
18608	10407124	ENSMUST00000099179	105178	expressed sequence AI452195	AI452195	0.828	-1.752	0.122046	0.349051
18609	10351035	NR_002840	14455	growth arrest specific 5	Gas5	0.828	-2.129	0.0696343	0.247355
18610	10450226	NM_019441	54397	palmitoyl-protein thioesterase	Ppt2	0.828	-1.855	0.104822	0.318763

18611	10547075	BC060267	212516	cDNA sequence BC060267	BC060267	0.828	-2.868	0.0233167	0.121319
18612	10504621	ENSMUST00000043958	381522	RIKEN cDNA E230008N13 gene	E230008N13Rik	0.828	-2.544	0.0374777	0.166652
18613	10584124	NM_177379	330914	Rho GTPase-activating protein	Grit	0.828	-2.134	0.0690807	0.246356
18614	10495332	BC116223	75504	RIKEN cDNA 1700013F07 gene	1700013F07Rik	0.828	-2.33	0.051559	0.205188
18615	10526261	NM_016801	20907	syntaxin 1A (brain)	Stx1a	0.828	-1.727	0.126573	0.356265
18616	10479228	ENSMUST00000108926	100125272	KRAB box and zinc finger, C2H2	RP24-87L14.2	0.828	-2.773	0.0267787	0.133145
18617	10593634	NM_177769	270162	ELMO domain containing 1	Elmod1	0.828	-2.793	0.025976	0.130584
18618	10483679	NM_001080707	68526	G protein-coupled receptor 155	Gpr155	0.828	-2.151	0.0673507	0.242464
18619	10578189	XR_030714	676031	similar to chromodomain helica	LOC676031	0.828	-2.669	0.0311737	0.147467
18620	10456405	NM_144867	225655	slowmo homolog 1 (Drosophila)	Slmo1	0.828	-1.716	0.128611	0.359531
18621	10597273	NM_153100	235636	receptor transporter protein 3	Rtp3	0.827	-3.613	0.00815932	0.0587204
18622	10399908	NM_011158	19088	protein kinase, cAMP dependent	Prkar2b	0.827	-4.104	0.00426752	0.0365593
18623	10402988					0.827	-1.138	0.291317	0.567423
18624	10548000	NM_010736	17000	lymphotoxin B receptor	Ltbr	0.827	-2.418	0.0452182	0.188022
18625	10443730	NM_009593	11307	ATP-binding cassette, sub-fami	Abcg1	0.827	-3.154	0.0154468	0.0923141
18626	10453373	NM_145984	213760	prolyl endopeptidase-like	Prepl	0.827	-3.813	0.00624289	0.0482985
18627	10501909	BC052204	210529	RIKEN cDNA G430022H21 gene	G430022H21Rik	0.827	-3.421	0.0106262	0.0708545
18628	10439471	NM_172380	224143	KTEL (Lys-Tyr-Glu-Leu) contain	Ktelc1	0.827	-2.78	0.026488	0.132152
18629	10424756	NM_177922	332110	mitogen-activated protein kina	Mapk15	0.827	-2.042	0.0792443	0.26804
18630	10450614	NM_001033630	69662	RIKEN cDNA 2310061I04 gene	2310061I04Rik	0.827	-4.027	0.00471514	0.039535
18631	10500181	XR_031134	277589	hypothetical gene supported by	LOC277589	0.827	-2.646	0.0322555	0.150768
18632	10492193					0.827	-2.153	0.0671304	0.241908
18633	10602795	NM_025437	66235	eukaryotic translation initiat	Eif1ay	0.827	-4.601	0.00229511	0.0240237
18634	10382713	NM_001005608	192897	integrin beta 4	Itgb4	0.827	-2.61	0.0340286	0.15604
18635	10475362	NM_030234	241627	WD repeat domain 76	Wdr76	0.827	-2.932	0.0212415	0.11408
18636	10486712	ENSMUST00000110661	99334	zinc finger SCAN domains 29	Zscan29	0.827	-3.974	0.00504833	0.0415985
18637	10431208					0.827	-1.802	0.113298	0.33346
18638	10507309	NM_001037916	622665	coiled-coil domain containing	RP23-233B9.8	0.827	-2.569	0.036132	0.162237
18639	10399352					0.827	-2.693	0.0300996	0.144118
18640	10396074	NM_146035	217664	mannoside acetylglucosaminyltr	Mgat2	0.827	-3.481	0.00977402	0.0669675
18641	10416843	NM_001033242	211286	ceroid-lipofuscinosis, neurona	Cln5	0.826	-3.823	0.00615771	0.0477267
18642	10449148	NM_001100454	215001	WAP, FS, Ig, KU, and NTR-conta	Wfikkn1	0.826	-3.084	0.0170771	0.0986823
18643	10538253	NM_019939	56524	membrane protein, palmitoylate	Mpp6	0.826	-3.12	0.0162183	0.0953351
18644	10427468					0.826	-1.047	0.329061	0.605314
18645	10601347	NM_173436	245566	cysteine-rich perinuclear thec	Cypt2	0.826	-1.001	0.34931	0.622835
18646	10433264	NM_031184	83396	GLIS family zinc finger 2	Glis2	0.826	-3.959	0.00515317	0.0421829
18647	10512291	NM_016890	53598	dynactin 3	Dctn3	0.826	-3.955	0.00517527	0.0422494
18648	10421436	NM_008004	14171	fibroblast growth factor 17	Fgf17	0.826	-2.099	0.0728058	0.254321
18649	10516544	NM_010471	15444	hippocalcin	Hpca	0.826	-2.646	0.0322657	0.150768
18650	10584271	BC034160	66279	RIKEN cDNA 1810021J13 gene	1810021J13Rik	0.826	-5.134	0.00122892	0.0152577
18651	10406823					0.826	-1.824	0.109631	0.327224
18652	10357332	NM_023735	74117	ARP3 actin-related protein 3 h	Actr3	0.826	-3.289	0.0127726	0.0803763
18653	10569358	NM_008387	16334	insulin II	Ins2	0.826	-2.387	0.0473705	0.193658
18654	10383891	NM_138948	192650	calcium binding protein 7	Cabp7	0.826	-2.474	0.0415925	0.177907
18655	10550738	ENSMUST00000094754	243872	predicted gene, EG243872	EG243872	0.826	-2.222	0.0605634	0.226995
18656	10347186					0.826	-1.387	0.206789	0.471259
18657	10389507	NM_029478	75909	transmembrane protein 49	Tmem49	0.826	-4.528	0.00251051	0.0254835
18658	10418480	NM_153547	30877	guanine nucleotide binding pro	Gnl3	0.826	-4.123	0.00416464	0.0359141
18659	10491860	NM_172303	269424	PHD finger protein 17	Phf17	0.826	-3.264	0.0132265	0.0825934
18660	10530496	NM_174877	317755	zygote arrest 1	Zar1	0.826	-2.58	0.035577	0.160632
18661	10560592	NM_019649	56457	cleft lip and palate associate	Clptm1	0.826	-3.334	0.0119926	0.0767701
18662	10414113	NM_001004436	218914	wings apart-like homolog (Dros	Wapal	0.826	-3.394	0.0110343	0.0725916
18663	10440568	NM_001081068	78913	zinc finger protein 294	Zfp294	0.825	-1.641	0.143638	0.384296

18664	10367282	NM_019953	56530	canopy 2 homolog (zebrafish)	Cnpy2	0.825	-4.899	0.00161131	0.0183663
18665	10470390	XR_033627	665315	similar to ribosomal protein L	LOC665315	0.825	-3.089	0.016945	0.0981068
18666	10387723	BC069874	70419	RIKEN cDNA 2810408A11 gene	2810408A11Rik	0.825	-3.437	0.0103827	0.0698033
18667	10477942	U27178	19650	retinoblastoma-like 1 (p107)	Rbl1	0.825	-2.675	0.0309165	0.146668
18668	10575840					0.825	-2.001	0.0843379	0.278694
18669	10466296	NM_146688	258683	olfactory receptor 262	Olfr262	0.825	-1.724	0.127171	0.35745
18670	10371672	BC100581	237433	predicted gene, EG237433	EG237433	0.825	-1.73	0.125987	0.355325
18671	10467470	NM_019698	56454	aldehyde dehydrogenase 18 fami	Aldh18a1	0.825	-4.345	0.00314511	0.0296612
18672	10423663	ENSMUST00000048646	666173	vacuolar protein sorting 13B (	Vps13b	0.825	-3.232	0.0138373	0.0852742
18673	10425046	XR_004836	626711	similar to heterogeneous nucle	LOC626711	0.825	-2.739	0.0281257	0.137577
18674	10503216	NM_001081417	320790	chromodomain helicase DNA bind	Chd7	0.825	-2.09	0.0737831	0.256746
18675	10434782	NM_178665	210126	LIM domain containing preferre	Lpp	0.824	-2.906	0.0220496	0.116905
18676	10465783	NM_026325	67706	transmembrane protein 179B	Tmem179b	0.824	-3.213	0.0142104	0.0868397
18677	10495259	NM_008141	14686	guanine nucleotide binding pro	Gnat2	0.824	-2.75	0.0276721	0.13614
18678	10530140					0.824	-1.582	0.156404	0.402458
18679	10467907	NM_145502	226144	ER lipid raft associated 1	Erlin1	0.824	-2.503	0.0398264	0.173591
18680	10433904	NM_198246	70120	tyrosyl-tRNA synthetase 2 (mit	Yars2	0.824	-2.684	0.0304941	0.145382
18681	10514475	ENSMUST00000049565	319247	RIKEN cDNA 9530080O11 gene	9530080O11Rik	0.824	-3.187	0.014734	0.0890612
18682	10527099					0.824	-2.283	0.0553083	0.214615
18683	10457606	NM_134112	106931	potassium channel tetramerisat	Kctd1	0.824	-3.124	0.0161258	0.0950038
18684	10526972	NM_008637	17766	nudix (nucleoside diphosphate	Nudt1	0.824	-2.627	0.0331784	0.153573
18685	10445137	NM_146835	258832	olfactory receptor 109	Olfr109	0.824	-1.579	0.156997	0.403436
18686	10344817	NM_026493	211660	centrosome and spindle pole as	Cspp1	0.824	-2.942	0.0209409	0.113309
18687	10464202	NM_172840	240675	von Willebrand factor A domain	Vwa2	0.824	-3.986	0.00497311	0.041123
18688	10350894					0.824	-2.656	0.0318018	0.149238
18689	10375432	BC104394	320116	RIKEN cDNA C030019I05 gene	C030019I05Rik	0.824	-2.895	0.0223955	0.118063
18690	10375463	NM_134248	171283	hepatitis A virus cellular rec	Havcr1	0.824	-1.755	0.121361	0.347955
18691	10586074					0.824	-1.474	0.182839	0.439611
18692	10500800					0.824	-1.743	0.123559	0.351666
18693	10509178	NM_001008232	230837	development and differentiatio	Ddefl1	0.824	-3.259	0.0133154	0.082928
18694	10521602	NM_175937	231207	cytoplasmic polyadenylation el	Cpeb2	0.824	-4.599	0.00230271	0.0240437
18695	10603706	XR_032128	668990	similar to vitamin D receptor	LOC668990	0.823	-0.75	0.476823	0.727649
18696	10574456	NM_001037841	75458	chemokine-like factor	Cklf	0.823	-2.969	0.020141	0.110355
18697	10447560					0.823	-3.157	0.0153909	0.0920839
18698	10441038	NM_139145	110948	holocarboxylase synthetase (bi	Hlcs	0.823	-3.235	0.0137839	0.0850347
18699	10466745	NM_011597	21873	tight junction protein 2	Tjp2	0.823	-5.07	0.00132245	0.016024
18700	10503206	NM_001081417	320790	chromodomain helicase DNA bind	Chd7	0.823	-3.846	0.00597598	0.0468506
18701	10370860	NM_026094	67331	ATPase, class I, type 8B, memb	Atp8b3	0.823	-1.29	0.236965	0.509116
18702	10381379					0.823	-1.512	0.173038	0.425494
18703	10605392	NM_007977	14069	coagulation factor VIII	F8	0.823	-4.019	0.00476601	0.0397838
18704	10416325	NM_153136	213484	nudix (nucleoside diphosphate	Nudt18	0.823	-2.212	0.0614606	0.22891
18705	10563770	NM_013808	13009	cysteine and glycine-rich prot	Csrp3	0.823	-2.143	0.0681964	0.244108
18706	10484258					0.823	-2.76	0.0272778	0.134663
18707	10365817	NM_021320	57764	netrin 4	Ntn4	0.823	-3.042	0.0181202	0.102464
18708	10576598	BC038634	67892	RIKEN cDNA 1810063B05 gene	1810063B05Rik	0.823	-2.017	0.0823115	0.274433
18709	10382326	XR_032804	667003	similar to eukaryotic translat	LOC667003	0.823	-1.314	0.229234	0.500249
18710	10521174	NM_011278	19822	ring finger protein 4	Rnf4	0.823	-3.412	0.0107598	0.0714525
18711	10582303	NM_007806	13057	cytochrome b-245, alpha polype	Cyba	0.823	-3.885	0.00567719	0.0452369
18712	10447412					0.823	-2.07	0.0760838	0.261283
18713	10405971	NM_145354	28114	NOL1/NOP2/Sun domain family 2	Nsun2	0.823	-4.191	0.003818	0.0337914
18714	10519514	XR_031102	433840	similar to ribosomal protein L	LOC433840	0.823	-2.265	0.0568361	0.218146

18715	10575034	NM_001037809	12560	cadherin 3	Cdh3	0.823	-2.791	0.0260605	0.130787
18716	10507520	NM_026601	68180	hydroxypyruvate isomerase homo	Hyi	0.823	-2.535	0.038025	0.168377
18717	10383564	NM_001038699	63828	fructosamine 3 kinase	Fn3k	0.823	-1.441	0.191638	0.451022
18718	10543512	NM_001081678	627049	zinc finger protein 800	Zfp800	0.823	-3.604	0.00826102	0.0592507
18719	10520763	NM_144909	231103	glucokinase regulatory protein	Gckr	0.823	-3.316	0.0123002	0.0781006
18720	10377800					0.823	-1.916	0.0956775	0.300774
18721	10483817	AK031731	100038544	predicted gene, ENSMUSG0000007	ENSMUSG00000075275	0.823	-1.94	0.0923085	0.294385
18722	10355310	XR_032645	675609	similar to 60S ribosomal prote	LOC675609	0.823	-2.648	0.0321806	0.150603
18723	10571884					0.822	-2.459	0.0425253	0.180698
18724	10534986					0.822	-1.998	0.0846708	0.279368
18725	10585932	NM_011099	18746	pyruvate kinase, muscle	Pkm2	0.822	-5.497	0.000822211	0.01146
18726	10580188	NM_025788	66830	BTB (POZ) domain containing 14	Btbd14b	0.822	-3.925	0.00538403	0.0435667
18727	10488860					0.822	-2.544	0.0374745	0.166652
18728	10509856					0.822	-1.458	0.186878	0.445172
18729	10402225	ENSMUST00000021605	109181	thyroid hormone receptor inter	Trip11	0.822	-3.401	0.010927	0.0720425
18730	10384266	ENSMUST00000055297	171395	polycystic kidney disease 1 li	Pkd1l1	0.822	-2.857	0.0236611	0.12253
18731	10442580	NM_008503	16898	ribosomal protein S2	Rps2	0.822	-2.158	0.0666475	0.241189
18732	10516906					0.822	-1.411	0.199981	0.461766
18733	10372889	AK135663	270802	cDNA sequence BC048403	BC048403	0.822	-2.767	0.0270081	0.133769
18734	10436890	ENSMUST00000114029	100038392	predicted gene, ENSMUSG0000007	ENSMUSG00000074911	0.822	-1.944	0.0917748	0.293524
18735	10501795	NM_028456	73170	RWD domain containing 3	Rwdd3	0.822	-2.706	0.0295148	0.141958
18736	10560443	NM_001080815	381853	gastric inhibitory polypeptide	Gipr	0.822	-3.014	0.0188621	0.105433
18737	10457475	NM_134130	106861	abhydrolase domain containing	Abhd3	0.822	-2.089	0.0739176	0.256931
18738	10540215	NM_026255	67582	solute carrier family 25 (mito	Slc25a26	0.821	-2.008	0.0834513	0.276567
18739	10562234	NM_001110252	15451	hepsin	Hpn	0.821	-2.207	0.0619593	0.230038
18740	10436600					0.821	-0.486	0.641352	0.837465
18741	10377308	BC024997	215723	cDNA sequence BC024997	BC024997	0.821	-1.836	0.10775	0.323709
18742	10389099	NM_011235	19364	RAD51-like 3 (S. cerevisiae)	Rad51l3	0.821	-2.86	0.0235811	0.122205
18743	10417579	BC064468	74430	RIKEN cDNA 4930452B06 gene	4930452B06Rik	0.821	-3.443	0.010301	0.0694203
18744	10598018					0.821	-1.418	0.197918	0.458756
18745	10446229	NM_009404	21950	tumor necrosis factor (ligand)	Tnfsf9	0.821	-1.73	0.125977	0.355325
18746	10374790					0.821	-0.899	0.397865	0.664302
18747	10594048	NM_177193	320563	immunoglobulin superfamily con	Islr2	0.821	-3.146	0.015615	0.0928214
18748	10585680	ENSMUST00000105102	791384	predicted gene, ENSMUSG0000006	ENSMUSG00000060915	0.821	-3.797	0.00637293	0.0490168
18749	10344723	NM_021511	59014	RRS1 ribosome biogenesis regul	Rrs1	0.821	-4.37	0.00304769	0.0290606
18750	10562096	NM_027215	69804	transmembrane protein 147	Tmem147	0.821	-2.623	0.0333858	0.154129
18751	10542477	NM_011084	18705	phosphatidylinositol 3-kinase,	Pik3c2g	0.821	-2.871	0.023185	0.120967
18752	10553555					0.821	-1.998	0.0846965	0.27938
18753	10606376	BC016070	67028	RIKEN cDNA 2610002M06 gene	2610002M06Rik	0.821	-3.397	0.0109758	0.072229
18754	10512059	ENSMUST00000108122	242384	leucine rich repeat and Ig dom	Lingo2	0.821	-2.308	0.0532835	0.209343
18755	10578361	NM_019734	11886	N-acylsphingosine amidohydrola	Asah1	0.821	-2.444	0.0434904	0.183399
18756	10406005	NM_010574	16372	Iroquois related homeobox 2 (D	Irx2	0.821	-3.265	0.013203	0.0825439
18757	10365037	NM_010768	17179	megakaryocyte-associated tyros	Matk	0.821	-2.622	0.033404	0.154179
18758	10421709	NM_001037935	629678	predicted gene, EG629678	EG629678	0.821	-2.425	0.0447786	0.187184
18759	10409365	NM_012014	26913	G protein-regulated inducer of	Gprin1	0.821	-2.898	0.022316	0.117786
18760	10446907	NM_152817	74196	tetratricopeptide repeat domai	Ttc27	0.821	-3.828	0.00611965	0.0475713
18761	10539960					0.821	-1.92	0.0951163	0.299747
18762	10489506	NM_029325	75526	serine protease inhibitor-like	Spinlw1	0.821	-1.224	0.259487	0.533772
18763	10550531	BC049852	68188	symplekin	Sympk	0.821	-3.702	0.00723919	0.0540104
18764	10596680	NM_001042779	20347	sema domain, immunoglobulin do	Sema3b	0.821	-2.77	0.0268987	0.133446
18765	10393668	NM_007377	11302	apoptosis-associated tyrosine	Aatk	0.82	-1.718	0.128153	0.358993

18766	10480329	NM_007869	13418	DnaJ (Hsp40) homolog, subfamil	Dnajc1	0.82	-3.355	0.011637	0.0753148
18767	10443876	NM_001100187	677156	cytochrome P450, family 4, sub	Cyp4f37	0.82	-2.602	0.0343959	0.157065
18768	10566067	NM_029211	75212	ring finger protein 121	Rnf121	0.82	-3.04	0.0181766	0.102596
18769	10414489	NM_146299	258296	olfactory receptor 745	Olfr745	0.82	-1.536	0.167139	0.418125
18770	10591544	NM_138303	74766	Yip1 domain family, member 2	Yipf2	0.82	-3.006	0.019086	0.106283
18771	10470647					0.82	-0.616	0.557031	0.785453
18772	10430899	NM_023623	71754	cytochrome P450, family 2, sub	Cyp2d40	0.82	-0.977	0.360352	0.632213
18773	10392374	NM_080644	140723	calcium channel, voltage-depen	Cacng5	0.82	-3.125	0.0160876	0.094857
18774	10345409					0.82	-2.119	0.0706656	0.249441
18775	10389674	NM_026556	68097	dynein light chain LC8-type 2	Dynll2	0.82	-3.356	0.0116255	0.0752784
18776	10434689	NM_013465	11625	alpha-2-HS-glycoprotein	Ahsg	0.82	-2.122	0.0703303	0.248465
18777	10512721	NM_018741	75426	insulin-like growth factor bin	Igfbpl1	0.82	-3.205	0.0143803	0.0876498
18778	10364718	BC146018	69770	RIKEN cDNA 1600002K03 gene	1600002K03Rik	0.82	-2.872	0.023174	0.120967
18779	10344960	NM_027415	70397	transmembrane protein 70	Tmem70	0.82	-2.44	0.0437508	0.18424
18780	10368577	ENSMUST00000081989	268291	ring finger protein 217	Rnf217	0.82	-3.249	0.01351	0.0837207
18781	10410124	NM_009984	13039	cathepsin L	Ctsl	0.82	-3.65	0.00776886	0.0567997
18782	10447038	ENSMUST00000063817	68554	RIKEN cDNA 1110001A16 gene	1110001A16Rik	0.82	-3.28	0.0129367	0.0811915
18783	10533929	NM_016741	20778	scavenger receptor class B, me	Scarb1	0.82	-3.794	0.00640297	0.0491057
18784	10569368	ENSMUST00000116041	640264	predicted gene, EG640264	EG640264	0.82	-2.427	0.0446381	0.186934
18785	10376885					0.82	-1.53	0.168565	0.419952
18786	10468584	NM_001033573	66980	zinc finger, DHHC domain conta	Zdhhc6	0.82	-2.885	0.0227416	0.119465
18787	10403716	NM_134067	105351	expressed sequence AW209491	AW209491	0.819	-3.505	0.0094634	0.0653049
18788	10565689	NM_007602	12337	calpain 5	Capn5	0.819	-2.789	0.0261281	0.130964
18789	10452202	NM_175731	171168	N-acylsphingosine amidohydrola	Asah3	0.819	-1.904	0.0973473	0.303944
18790	10501397	BC050932	67495	RIKEN cDNA 2010200O16 gene	2010200O16Rik	0.819	-3.361	0.0115425	0.0749094
18791	10369288	XR_030676	664936	similar to ribosomal protein L	LOC664936	0.819	-1.872	0.102201	0.313502
18792	10437451	BC013706	207740	RIKEN cDNA 1500031H01 gene	1500031H01Rik	0.819	-3.009	0.018997	0.105954
18793	10457465	NM_001081222	77805	establishment of cohesion 1 ho	Esco1	0.819	-2.426	0.044707	0.187121
18794	10406026	NM_053163	94066	mitochondrial ribosomal protei	Mrpl36	0.819	-4.569	0.00238587	0.0246443
18795	10359386	NM_172644	226539	aspartyl-tRNA synthetase 2 (mi	Dars2	0.819	-2.561	0.0365692	0.163532
18796	10586397	NM_027134	69606	mitochondrial methionyl-tRNA f	Mtfmt	0.819	-2.867	0.0233393	0.121369
18797	10472738	BC031546	75763	RIKEN cDNA 4833418A01 gene	4833418A01Rik	0.819	-2.849	0.0239649	0.1238
18798	10414260	NM_001123394	11730	angiogenin, ribonuclease A fam	Ang3	0.819	-3.013	0.0189024	0.105538
18799	10446823	NM_026417	67864	Yip1 domain family, member 4	Yipf4	0.819	-4.59	0.00232641	0.02416
18800	10595924	NM_029094	74769	phosphatidylinositol 3-kinase,	Pik3cb	0.819	-2.75	0.0276864	0.13614
18801	10347226	NM_175564	271711	transmembrane protein 169	Tmem169	0.819	-1.42	0.197237	0.457905
18802	10590304	XR_033018	638068	similar to Interleukin-1 recep	LOC638068	0.819	-1.873	0.101941	0.312948
18803	10405236	NM_027324	14057	sideroflexin 1	Sfxn1	0.819	-4.333	0.00319173	0.0299405
18804	10376854	NM_001039536	327942	phosphatidylinositol glycan an	Pigl	0.819	-3.278	0.0129578	0.0812998
18805	10529890	ENSMUST00000030975	73975	RIKEN cDNA 4930435H24 gene	4930435H24Rik	0.819	-3.62	0.00808861	0.0584536
18806	10465314	NM_007600	12333	calpain 1	Capn1	0.819	-3.988	0.00495577	0.0410599
18807	10554549	NM_001004185	434204	WAS protein homology region 2	Whdc1	0.819	-3.664	0.00762116	0.0561274
18808	10583297	NM_029248	75316	Josephin domain containing 3	Josd3	0.819	-3.862	0.00585188	0.0462086
18809	10444957	NM_175934	52040	protein phosphatase 1, regulat	Ppp1r10	0.819	-4.572	0.00237919	0.0246076
18810	10346330	NM_001114663	227120	phospholipase C-like 1	Plcl1	0.819	-1.251	0.250097	0.524217
18811	10575961	NM_009462	22224	ubiquitin specific peptidase 1	Usp10	0.818	-2.954	0.0205602	0.112129
18812	10586844	NM_007399	11487	a disintegrin and metallopepti	Adam10	0.818	-3.111	0.0164341	0.0962129
18813	10576944	ENSMUST00000075769	100126875	predicted gene, ENSMUSG0000005	ENSMUSG00000059543	0.818	-1.604	0.151584	0.395471
18814	10424991	NM_027122	69572	major facilitator superfamily	Mfsd3	0.818	-2.417	0.0452852	0.18819
18815	10354644	XM_907010	627915	predicted gene, EG627915	EG627915	0.818	-1.675	0.136622	0.373124
18816	10376579	NM_029044	74665	leucine rich repeat containing	Lrrc48	0.818	-3.447	0.0102471	0.0691558

18817	10584835	NM_176993	319742	myelin protein zero-like 3	Mpzl3	0.818	-2.057	0.0774889	0.264348
18818	10366229	NM_001039354	108030	lin-7 homolog A (C. elegans)	Lin7a	0.818	-1.397	0.203945	0.467196
18819	10436200	XR_034572	100048225	hypothetical protein LOC100048	LOC100048225	0.818	-1.018	0.341392	0.616096
18820	10530306	NM_008888	18935	paired-like homeobox 2b	Phox2b	0.818	-1.315	0.228741	0.499844
18821	10373728	NM_019574	56218	POZ (BTB) and AT hook containi	Patz1	0.818	-2.522	0.0387639	0.170294
18822	10485546	NM_001033347	241589	RIKEN cDNA D430041D05 gene	D430041D05Rik	0.818	-2.215	0.061208	0.228343
18823	10379034	NM_026708	68385	TLC domain containing 1	Tlcd1	0.818	-2.966	0.0202179	0.110633
18824	10584741	NM_008063	14385	solute carrier family 37 (gluc	Slc37a4	0.818	-2.688	0.0303142	0.144742
18825	10458334	NM_026027	67199	prefoldin 1	Pfdn1	0.818	-4.519	0.00253633	0.0256417
18826	10425578	NM_001081016	20286	zinc finger CCCH type containi	Zc3h7b	0.818	-3.509	0.00940992	0.0649994
18827	10526250	NM_145215	68758	abhydrolase domain containing	Abhd11	0.818	-2.923	0.0215207	0.114965
18828	10474181	NM_178890	99382	ankyrin repeat and BTB (POZ) d	Abtb2	0.818	-3.245	0.0135859	0.0840927
18829	10465804	NM_026329	67710	polymerase (RNA) II (DNA direc	Polr2g	0.818	-3.724	0.007033	0.0527699
18830	10529142	NM_008014	14208	protein phosphatase 1G (former	Ppm1g	0.818	-3.904	0.00553143	0.0444702
18831	10566705	NM_146306	258303	olfactory receptor 518	Olfr518	0.818	-2.181	0.0644307	0.236227
18832	10501420	NM_011504	20912	syntaxin binding protein 3A	Stxbp3a	0.817	-1.54	0.166164	0.417017
18833	10530045	NM_172490	211006	Sep (O-phosphoserine) tRNA:Sec	Sepsecs	0.817	-2.795	0.0259285	0.130438
18834	10588707	NM_025903	15983	interferon-related development	Ifrd2	0.817	-3.14	0.0157659	0.0934287
18835	10428447	XM_484465	432951	predicted gene, EG432951	EG432951	0.817	-1.424	0.196337	0.456744
18836	10526614	NM_031404	83766	actin-like 6B	Actl6b	0.817	-2.128	0.0697763	0.247552
18837	10372497	NM_025780	66816	THAP domain containing, apopto	Thap2	0.817	-2.259	0.0572941	0.219025
18838	10507671	NM_008190	14915	guanylate cyclase activator 2a	Guca2a	0.817	-3.095	0.0167962	0.0975911
18839	10475247	NM_175285	96957	transmembrane protein 62	Tmem62	0.817	-2.194	0.0632101	0.233045
18840	10469505	NM_147778	12238	COMM domain containing 3	Commd3	0.817	-4.67	0.00211372	0.022662
18841	10387108	ENSMUST00000101039	100038666	predicted gene, OTTMUSG0000000	OTTMUSG00000005912	0.817	-1.888	0.0997332	0.308614
18842	10574718	NM_025486	66320	transmembrane protein 208	Tmem208	0.817	-3.433	0.0104482	0.0700433
18843	10582642	NM_133966	102162	TAF5-like RNA polymerase II, p	Taf5l	0.817	-3.465	0.00999332	0.0680694
18844	10445229					0.817	-2.527	0.0384331	0.169439
18845	10466290	NM_146682	258677	olfactory receptor 76	Olfr76	0.817	-1.895	0.0986449	0.306683
18846	10457834	AK032191	319211	nucleolar protein 4	Nol4	0.817	-2.873	0.023143	0.120943
18847	10415723					0.817	-1.753	0.121773	0.348413
18848	10443391	NM_011951	26416	mitogen-activated protein kina	Mapk14	0.817	-3.274	0.0130406	0.0816981
18849	10545807	NM_011467	20751	sepiapterin reductase	Spr	0.817	-2.985	0.0196807	0.10865
18850	10557571	BC038694	101602	expressed sequence AI467606	AI467606	0.817	-2.507	0.0396063	0.172845
18851	10551750	XR_035432	114675	RIKEN cDNA 4932431P20 gene	4932431P20Rik	0.817	-2.084	0.0744888	0.258195
18852	10349065	NM_001122676	227449	zinc finger, CCHC domain conta	Zcchc2	0.816	-2.574	0.0358853	0.161438
18853	10575102	NM_011574	21771	cirrhosis, autosomal recessive	Cirh1a	0.816	-3.046	0.0180176	0.102026
18854	10583312					0.816	-1.751	0.122155	0.349316
18855	10529815					0.816	-1.968	0.0885841	0.286933
18856	10571415	NM_033560	52348	vacuolar protein sorting 37A (	Vps37a	0.816	-2.814	0.0251909	0.128038
18857	10591072	NM_181816	234964	coiled-coil domain containing	Ccdc67	0.816	-3.903	0.00554313	0.0445473
18858	10528332	NM_178728	242864	N-acyl phosphatidylethanolamin	Napepld	0.816	-2.309	0.0532062	0.209262
18859	10400095	NM_013562	15982	interferon-related development	Ifrd1	0.816	-3.086	0.0170212	0.0984128
18860	10381601	M86736	14824	granulin	Grn	0.816	-4.411	0.00289795	0.0281591
18861	10527323	NM_010800	17341	basic helix-loop-helix domain	Bhlhb8	0.816	-2.825	0.024818	0.126844
18862	10382698	ENSMUST00000100221	68528	RIKEN cDNA 1110017F19 gene	1110017F19Rik	0.816	-2.336	0.0510667	0.203881
18863	10440929	NM_010256	14450	phosphoribosylglycinamide form	Gart	0.816	-4.152	0.0040116	0.0350646
18864	10555736	NM_147093	259097	olfactory receptor 558	Olfr558	0.816	-0.919	0.387994	0.656721
18865	10445678	BC006605	224833	expressed sequence AI661453	AI661453	0.816	-3.173	0.015046	0.0905843
18866	10369783	NM_178679	216049	zinc finger protein 365	Zfp365	0.816	-1.587	0.155334	0.400794
18867	10497520	NM_007900	13605	ect2 oncogene	Ect2	0.816	-3.847	0.00596448	0.0467952

18868	10380252	NM_016706	12812	coilin	Coil	0.816	-3.821	0.00617808	0.0478496
18869	10542929	NM_007588	12311	calcitonin receptor	Calcr	0.816	-2.861	0.0235296	0.122028
18870	10378893	NM_026185	67477	RIKEN cDNA 1300007F04 gene	1300007F04Rik	0.816	-2.344	0.0505219	0.202394
18871	10540537					0.816	-1.62	0.148039	0.390187
18872	10509253	BC048442	67663	RIKEN cDNA 4930549C01 gene	4930549C01Rik	0.816	-2.218	0.0609869	0.227909
18873	10558740	XM_001480612	100043546	similar to DnaJ-like protein	LOC100043546	0.816	-1.569	0.159275	0.406366
18874	10523903					0.816	-1.98	0.0869118	0.283546
18875	10348030					0.816	-3.23	0.0138628	0.0853818
18876	10355069	NM_001114609	227195	RIKEN cDNA A430093A21 gene	A430093A21Rik	0.815	-4.043	0.00461559	0.0388503
18877	10420659	BC037015	66674	RIKEN cDNA 6330409N04 gene	6330409N04Rik	0.815	-2.576	0.0357426	0.161141
18878	10422962	NM_001085410	68646	RIKEN cDNA 1110020G09 gene	1110020G09Rik	0.815	-1.813	0.111547	0.330459
18879	10375497					0.815	-1.968	0.0885137	0.286781
18880	10499958	ENSMUST00000055957	383891	predicted gene, EG383891	EG383891	0.815	-1.571	0.158924	0.406028
18881	10465342	NM_028454	73166	transmembrane 7 superfamily me	Tm7sf2	0.815	-3.319	0.0122459	0.0778362
18882	10510516	NM_019741	56485	solute carrier family 2 (facil	Slc2a5	0.815	-3.029	0.0184576	0.103905
18883	10568780	NM_001045483	69546	mitogen-activated protein kina	Mapk1ip1	0.815	-4.653	0.00215687	0.0229748
18884	10422980	NM_177178	320506	LMBR1 domain containing 2	Lmbrd2	0.815	-2.819	0.0250198	0.127548
18885	10387119	NM_175681	93896	glucagon-like peptide 2 recept	Glp2r	0.815	-2.179	0.064577	0.236559
18886	10490212	NM_022325	64138	cathepsin Z	Ctsz	0.815	-3.892	0.00562487	0.044999
18887	10350614	NM_026876	98685	RIKEN cDNA 1190005F20 gene	1190005F20Rik	0.815	-3.133	0.0159192	0.0941049
18888	10410302	NM_001038651	629016	RIKEN cDNA E130120F12 gene	E130120F12Rik	0.815	-1.875	0.101667	0.312356
18889	10467139	NM_021460	16889	lysosomal acid lipase A	Lipa	0.814	-1.438	0.19238	0.451814
18890	10503650	XM_001000802	384001	peroxiredoxin 6, related seque	Prdx6-rs2	0.814	-2.356	0.0495782	0.200156
18891	10358359	NM_145991	214498	cell division cycle 73, Paf1/R	Cdc73	0.814	-4.603	0.00229069	0.0239893
18892	10412701	NM_146051	218734	RIKEN cDNA 3830406C13 gene	3830406C13Rik	0.814	-3.453	0.0101614	0.0687311
18893	10591200	XM_888877	624341	predicted gene, EG624341	EG624341	0.814	-1.267	0.244377	0.517487
18894	10375485					0.814	-2.508	0.0395718	0.172766
18895	10499948	NM_001039594	545548	late cornified envelope 3A	Lce3a	0.814	-1.503	0.175421	0.4287
18896	10417002	AK043702	320427	RIKEN cDNA A830021K08 gene	A830021K08Rik	0.814	-1.882	0.100612	0.31038
18897	10587653	AK133266	100038370	predicted gene, ENSMUSG0000007	ENSMUSG00000074150	0.814	-2.806	0.0255111	0.129261
18898	10554419	NM_178070	233405	vacuolar protein sorting 33B (	Vps33b	0.814	-3.197	0.0145386	0.0884107
18899	10484190	ENSMUST00000099981	22138	titin	Ttn	0.814	-2.39	0.0471268	0.192955
18900	10593325	NM_011220	19286	6-pyruvoyl-tetrahydropterin sy	Pts	0.814	-4.172	0.00391431	0.0344133
18901	10373571	BC037624	73827	RIKEN cDNA 1110012D08 gene	1110012D08Rik	0.814	-3.402	0.0109016	0.0719199
18902	10606393	NM_001081477	382236	bromodomain and WD repeat doma	Brwd3	0.814	-2.587	0.0352054	0.159602
18903	10420853	NM_010932	18155	prepronociceptin	Pnoc	0.814	-2.573	0.0359018	0.161478
18904	10364559	NM_007880	13496	AT rich interactive domain 3A	Arid3a	0.814	-2.815	0.0251633	0.127928
18905	10571774	NM_001005847	11593	aspartylglucosaminidase	Aga	0.814	-3.347	0.0117711	0.0757648
18906	10600476	XM_141845	245472	predicted gene, EG245472	EG245472	0.814	-2.45	0.0431132	0.182463
18907	10383358					0.814	-2.269	0.0564551	0.217193
18908	10389879	NM_181819	278507	WAP, follistatin/kazal, immuno	Wfikkn2	0.814	-2.663	0.0314781	0.148334
18909	10526947	NM_177000	319772	RIKEN cDNA C130050O18 gene	C130050O18Rik	0.814	-2.186	0.0638943	0.23479
18910	10392207	NM_198292	21763	testis expressed gene 2	Tex2	0.814	-3.311	0.0123716	0.0784363
18911	10600911	NM_207633	77929	Yip1 domain family, member 6	Yipf6	0.814	-4.076	0.00442677	0.0375626
18912	10383930	ENSMUST00000092922	100038587	predicted gene, ENSMUSG0000006	ENSMUSG00000069821	0.813	-2.02	0.0819952	0.273542
18913	10560481	NM_008036	14282	FBJ osteosarcoma oncogene B	Fosb	0.813	-2.571	0.0360195	0.161869
18914	10421975	BC117005	76789	RIKEN cDNA 2410129H14 gene	2410129H14Rik	0.813	-3.404	0.0108711	0.0718087
18915	10585992	ENSMUST00000085569	270163	myosin IXa	Myo9a	0.813	-2.425	0.0447206	0.187121

18915	10585992	ENSMUST00000085569	270163	myosin IXa	Myo9a	0.813	-2.425	0.0447206	0.187121
18916	10354732	NM_010477	15510	heat shock protein 1 (chaperon	Hspd1	0.813	-3.965	0.00510723	0.041888
18917	10391755	NM_025918	52715	coiled-coil domain containing	Ccdc43	0.813	-4.599	0.00230166	0.0240437
18918	10604076	NR_002900	104369	small nucleolar RNA, H/ACA box	Snora69	0.813	-1.76	0.120567	0.346982
18919	10452935	BC019508	320473	HEAT repeat containing 5B	Heatr5b	0.813	-2.287	0.0550015	0.213975
18920	10517673	NM_021358	15565	5-hydroxytryptamine (serotonin	Htr6	0.813	-2.425	0.044728	0.187121
18921	10547200					0.813	-3.437	0.010394	0.0698131
18922	10575019	ENSMUST00000098440	100038487	predicted gene, ENSMUSG0000007	ENSMUSG00000074113	0.813	-1.172	0.278469	0.553444
18923	10539769	NM_020045	56748	NFU1 iron-sulfur cluster scaff	Nfu1	0.813	-5	0.00143249	0.0168502
18924	10435991	XR_034995	385905	similar to proteasome alpha7/C	LOC385905	0.813	-1.856	0.104514	0.318143
18925	10392910	BC024617	217310	RIKEN cDNA C630004H02 gene	C630004H02Rik	0.813	-2.583	0.035376	0.160238
18926	10424050	NM_019480	55960	estrogen receptor-binding frag	Ebag9	0.813	-3.091	0.016908	0.0979462
18927	10578615	NM_023503	69260	inhibitor of growth family, me	Ing2	0.813	-3.007	0.0190699	0.106221
18928	10364194	NM_146006	16987	lanosterol synthase	Lss	0.812	-3.633	0.00794895	0.057744
18929	10579479	NM_010150	13864	nuclear receptor subfamily 2,	Nr2f6	0.812	-3.773	0.00658698	0.0502789
18930	10385052	NM_023146	66011	RAN binding protein 17	Ranbp17	0.812	-2.41	0.0457808	0.189542
18931	10350504					0.812	-3.067	0.0174857	0.0999956
18932	10540231					0.812	-1.745	0.123302	0.351408
18933	10438103	NM_029779	76872	coiled-coil domain containing	Ccdc116	0.812	-3.924	0.00539149	0.0436105
18934	10346255	NM_145517	227102	ORM1-like 1 (S. cerevisiae)	Ormdl1	0.812	-3.398	0.010972	0.0722269
18935	10475211	NM_025475	66296	centrosomal protein 27	Cep27	0.812	-5.138	0.00122449	0.0152338
18936	10388707	NM_009965	12957	crystallin, beta A1	Cryba1	0.812	-2.076	0.0753386	0.259592
18937	10492748	NM_010196	14161	fibrinogen, alpha polypeptide	Fga	0.812	-3.581	0.00852899	0.0605564
18938	10450914	NM_146488	258481	olfactory receptor 137	Olfr137	0.812	-1.087	0.311974	0.588349
18939	10539435	NM_175277	78653	bolA-like 3 (E. coli)	Bola3	0.812	-3.454	0.0101426	0.0686695
18940	10458183	NM_010280	14587	glial cell line derived neurot	Gfra3	0.812	-1.475	0.182449	0.438923
18941	10602704	NM_173780	245671	Kruppel-like factor 8	Klf8	0.811	-3.717	0.00709414	0.053191
18942	10398442	AJ517767	373070	miRNA containing gene	Mirg	0.811	-1.727	0.126485	0.356138
18943	10372988	NM_011391	20503	solute carrier family 16 (mono	Slc16a7	0.811	-1.606	0.15114	0.395116
18944	10503615					0.811	-2.396	0.0466937	0.191982
18945	10363130	BC028546	94221	golgi associated PDZ and coile	Gopc	0.811	-2.08	0.0748944	0.258922
18946	10594480	NM_017382	53869	RAB11a, member RAS oncogene fa	Rab11a	0.811	-3.518	0.0092909	0.0644811
18947	10461354	NM_197993	70044	terminal uridylyl transferase	Tut1	0.811	-3.256	0.013365	0.0831391
18948	10363743	NM_001081346	170799	rhotekin 2	Rtkn2	0.811	-2.937	0.0210747	0.113588
18949	10396278	NM_026102	208846	dishevelled associated activat	Daam1	0.811	-2.727	0.0286445	0.138945
18950	10477777	NM_025516	66366	ERGIC and golgi 3	Ergic3	0.811	-4.655	0.00215123	0.0229481
18951	10427052	NM_033073	110310	keratin 7	Krt7	0.811	-1.536	0.167199	0.418175
18952	10507784	NM_008917	19063	palmitoyl-protein thioesterase	Ppt1	0.811	-3.91	0.005492	0.0441924
18953	10538082	NM_133764	76252	ATPase, H+ transporting, lysos	Atp6v0e2	0.811	-2.859	0.0236194	0.122374
18954	10551939	NM_019546	56189	proline dehydrogenase (oxidase	Prodh2	0.811	-3.108	0.0164956	0.096349
18955	10493612	NM_025762	99650	RIKEN cDNA 4933434E20 gene	4933434E20Rik	0.811	-4.371	0.00304659	0.0290606
18956	10518108	NM_145402	214359	transmembrane protein 51	Tmem51	0.811	-3.807	0.00629427	0.0485716
18957	10456490					0.811	-1.735	0.125131	0.354186
18958	10514926	ENSMUST00000097930	619295	RIKEN cDNA B230314M03 gene	B230314M03Rik	0.811	-2.559	0.0366662	0.163801
18959	10433214	NM_001081217	385674	zinc finger protein 174	Zfp174	0.811	-1.91	0.096546	0.302425
18960	10462521	NM_008960	19211	phosphatase and tensin homolog	Pten	0.811	-2.853	0.0237994	0.123126
18961	10462702	NM_172637	226098	HECT domain containing 2	Hectd2	0.811	-1.619	0.148298	0.390488
18962	10440338	ENSMUST00000072455	73946	RIKEN cDNA 4930423O20 gene	4930423O20Rik	0.811	-2.253	0.0578867	0.220652
18963	10387816	NM_173742	52898	ribonuclease, RNase K	Rnasek	0.811	-3.541	0.00901109	0.063027
18964	10566477	NM_017371	15458	hemopexin	Hpx	0.81	-2.655	0.0318078	0.149238
18965	10592099	NM_027030	69305	decapping enzyme, scavenger	Dcps	0.81	-5.376	0.000937969	0.0125681
18966	10447923	NM_022311	21646	t-complex-associated testis ex	Tcte2	0.81	-4.036	0.00466003	0.039162
18967	10375232					0.81	-1.978	0.0871716	0.284169

18968	10542239	NM_031499	83380	proline rich protein 2	Prp2	0.81	-0.83	0.433036	0.693487
18969	10351998	AK142791	100093628	predicted gene, ENSMUSG0000007	ENSMUSG00000073488	0.81	-1.381	0.208447	0.4731
18970	10590306	NM_178676	215446	ectonucleoside triphosphate di	Entpd3	0.81	-2.594	0.034806	0.158375
18971	10444578	NM_010893	18010	neuraminidase 1	Neu1	0.81	-2.088	0.0740746	0.257223
18972	10350800	NM_172843	240832	torsin A interacting protein 2	Tor1aip2	0.81	-3.436	0.0104099	0.0698973
18973	10495651	NM_024178	66789	asparagine-linked glycosylatio	Alg14	0.81	-2.56	0.0366491	0.163763
18974	10576896	XM_001473319	669393	similar to ribosomal protein L	LOC669393	0.81	-2.771	0.0268473	0.133319
18975	10581479	NM_021491	58994	sphingomyelin phosphodiesteras	Smpd3	0.81	-1.791	0.115147	0.337402
18976	10596428	NM_026763	68553	RIKEN cDNA 1110001D15 gene	1110001D15Rik	0.81	-1.199	0.26831	0.542786
18977	10403428	NM_172585	217980	La ribonucleoprotein domain fa	Larp5	0.81	-4.938	0.00154001	0.0177449
18978	10477946	NM_019642	20014	ribophorin II	Rpn2	0.81	-3.775	0.0065626	0.0501236
18979	10606542					0.81	-1.654	0.14089	0.379749
18980	10418500	ENSMUST00000049732	66487	small nucleolar RNA host gene	Snhg8	0.81	-5.061	0.00133556	0.0161644
18981	10364375	NM_007793	13014	cystatin B	Cstb	0.81	-4.67	0.00211369	0.022662
18982	10528480	ENSMUST00000079716	100042067	similar to Rpl17 protein	LOC100042067	0.81	-4.214	0.003711	0.0331918
18983	10427910	NM_001013792	432940	cDNA sequence BC087945	BC087945	0.81	-3.748	0.00681085	0.0514316
18984	10490632	NM_183162	229003	cDNA sequence BC006779	BC006779	0.81	-3.483	0.00974959	0.0668869
18985	10462535	NM_177096	320193	RIKEN cDNA B430203M17 gene	B430203M17Rik	0.81	-1.416	0.198567	0.459606
18986	10522589	NM_020611	57357	steroid 5 alpha-reductase 3	Srd5a3	0.81	-3.353	0.0116745	0.0754648
18987	10451079	ENSMUST00000052701	75341	RIKEN cDNA 4930564C03 gene	4930564C03Rik	0.809	-3.317	0.0122795	0.0779924
18988	10369531	NM_197996	70423	tetraspanin 15	Tspan15	0.809	-2.283	0.0553186	0.214616
18989	10594340	NM_172446	207667	ladybird homeobox 1 homolog (D	Lbxcor1	0.809	-2.208	0.0618285	0.229795
18990	10399005	NM_007763	12925	cysteine-rich protein 1 (intes	Crip1	0.809	-3.375	0.0113208	0.0737193
18991	10568464	NM_013799	11907	arginine-tRNA-protein transfer	Ate1	0.809	-4.661	0.0021362	0.0228467
18992	10545239					0.809	-1.385	0.207468	0.471907
18993	10478066	NM_175692	319317	RIKEN cDNA A930034L06 gene	A930034L06Rik	0.809	-2.227	0.0601099	0.225949
18994	10517373	NM_022980	53902	regulator of calcineurin 3	Rcan3	0.809	-2.675	0.0308956	0.146635
18995	10590479	BC119591	382118	zinc finger protein 167	Zfp167	0.809	-2.512	0.0393067	0.171999
18996	10506054	ENSMUST00000062256	78687	RIKEN cDNA 0610025J13 gene	0610025J13Rik	0.809	-3.882	0.0056971	0.0453196
18997	10514461	ENSMUST00000064804	791416	predicted gene, OTTMUSG0000000	OTTMUSG00000008033	0.809	-2.045	0.0789215	0.267465
18998	10489204	NM_009373	21817	transglutaminase 2, C polypept	Tgm2	0.809	-1.748	0.122785	0.350597
18999	10440238	NM_178925	106338	NOL1/NOP2/Sun domain family 3	Nsun3	0.809	-3.445	0.0102818	0.0693232
19000	10398336					0.809	-2.202	0.0624392	0.231292
19001	10595447					0.809	-2.449	0.0431532	0.182497
19002	10579554	NM_001029873	382018	unc-13 homolog A (C. elegans)	Unc13a	0.809	-3.109	0.0164675	0.0962891
19003	10457729	ENSMUST00000025187	13505	desmocollin 1	Dsc1	0.809	-2.68	0.0306787	0.145769
19004	10396740	NM_172952	268566	gephyrin	Gphn	0.809	-4.508	0.0025717	0.0259383
19005	10507976	NM_153566	230734	yrdC domain containing (E.coli	Yrdc	0.809	-2.207	0.0619429	0.230018
19006	10570630	XR_031858	244335	similar to la related protein	LOC244335	0.809	-2.852	0.0238335	0.123212
19007	10353667					0.808	-0.896	0.399162	0.665449
19008	10543369	NM_153163	320405	Ca2+-dependent activator prote	Cadps2	0.808	-1.85	0.105545	0.320207
19009	10602166	NM_172782	237082	nuclear transport factor 2-lik	Nxt2	0.808	-3.754	0.0067553	0.0512317
19010	10376094					0.808	-4.607	0.00227946	0.0239191
19011	10359826	NM_025650	66594	ubiquinol-cytochrome c reducta	Uqcr	0.808	-2.953	0.0206132	0.112225
19012	10361366	NM_175374	108853	mitochondrial translational re	Mtrf1l	0.808	-3.711	0.0071489	0.0534688
19013	10600471					0.808	-1.714	0.128923	0.36017
19014	10403396	NM_052977	94191	adenosine deaminase, RNA-speci	Adarb2	0.808	-2.476	0.0414651	0.177622
19015	10556037	NM_147033	259035	olfactory receptor 714	Olfr714	0.808	-3.561	0.00876476	0.0618152
19016	10485395	NM_020267	80985	tripartite motif-containing 44	Trim44	0.808	-3.999	0.00488565	0.0405743

19017	10352827	ENSMUST00000016334	319266	RIKEN cDNA A130010J15 gene	A130010J15Rik	0.808	-2.793	0.0260038	0.130662
19018	10591643	NM_031874	19340	RAB3D, member RAS oncogene fam	Rab3d	0.808	-2.838	0.0243446	0.125119
19019	10415176	NM_030686	28200	dehydrogenase/reductase (SDR f	Dhrs4	0.808	-4.079	0.00440785	0.0374898
19020	10495111	NM_027432	70465	WD repeat domain 77	Wdr77	0.808	-4.605	0.00228507	0.0239423
19021	10482766	NM_023396	67874	reprimo, TP53 dependent G2 arr	Rprm	0.808	-2.791	0.0260724	0.130789
19022	10434815	NM_011641	22061	transformation related protein	Trp63	0.808	-3.199	0.0145022	0.0882145
19023	10602716	NM_018798	54609	ubiquilin 2	Ubqln2	0.808	-5.047	0.00135843	0.0163206
19024	10544333	NM_001003405	435889	RIKEN cDNA 1810049H19 gene	1810049H19Rik	0.808	-2.006	0.0836458	0.277081
19025	10606658	BC056937	215201	RIKEN cDNA 4732479N06 gene	4732479N06Rik	0.808	-2.31	0.0530866	0.208947
19026	10424584	NM_001081066	105841	DENN/MADD domain containing 3	Dennd3	0.807	-3.64	0.00786999	0.057321
19027	10585206	NM_028300	72614	PIH1 domain containing 2	Pih1d2	0.807	-2.931	0.0212565	0.114131
19028	10586347	NM_177460	214424	poly (ADP-ribose) polymerase f	Parp16	0.807	-2.251	0.0579903	0.220908
19029	10579825	NM_138944	18997	POU domain, class 4, transcrip	Pou4f2	0.807	-2.378	0.048019	0.195553
19030	10373036	NM_177614	216440	amplified in osteosarcoma	Os9	0.807	-4.257	0.00351251	0.0318203
19031	10543067	NM_012055	27053	asparagine synthetase	Asns	0.807	-3.398	0.0109648	0.0722269
19032	10553401	AK157552	100038585	predicted gene, ENSMUSG0000007	ENSMUSG00000074104	0.807	-4.706	0.00202403	0.0218682
19033	10475378	NM_177054	319996	cancer susceptibility candidat	Casc4	0.807	-2.508	0.0395667	0.172766
19034	10405280	NM_019968	56795	ADP-ribosylation factor-like 1	Arl10	0.807	-2.958	0.0204418	0.111772
19035	10562643	NM_027702	71162	RIKEN cDNA 4933421I07 gene	4933421I07Rik	0.807	-2.116	0.0710132	0.250191
19036	10518743	NM_173371	100198	hexose-6-phosphate dehydrogena	H6pd	0.807	-3.254	0.0134037	0.0833309
19037	10353032	NM_026632	68240	replication protein A3	Rpa3	0.807	-3.481	0.0097812	0.0669951
19038	10559312	NM_007856	13360	7-dehydrocholesterol reductase	Dhcr7	0.807	-4.076	0.00442514	0.0375626
19039	10598996	NM_198633	331392	predicted gene, EG331392	EG331392	0.806	-1.983	0.0865813	0.282817
19040	10432682	NM_028770	74127	keratin 80	Krt80	0.806	-3.715	0.00711202	0.0532572
19041	10357120					0.806	-2.128	0.0697473	0.247552
19042	10415011					0.806	-1.587	0.15534	0.400794
19043	10404731	NM_025387	66154	transmembrane protein 14C	Tmem14c	0.806	-1.879	0.101091	0.311356
19044	10405462	BC038268	100038756	predicted gene, ENSMUSG0000007	ENSMUSG00000074889	0.806	-3.26	0.0133053	0.0828894
19045	10558687	NM_029821	76974	RIKEN cDNA 1190003J15 gene	1190003J15Rik	0.806	-2.264	0.0569036	0.218163
19046	10450075	NM_001001892	14972	histocompatibility 2, K1, K re	H2-K1	0.806	-4.2	0.00377495	0.0335227
19047	10425116	NM_027219	104445	CDC42 effector protein (Rho GT	Cdc42ep1	0.806	-2.515	0.0391547	0.171547
19048	10505705	NM_019535	20404	SH3-domain GRB2-like 2	Sh3gl2	0.806	-5.526	0.000796019	0.0111983
19049	10378253	NM_018883	55984	calcium/calmodulin-dependent p	Camkk1	0.806	-2.211	0.0616067	0.229333
19050	10558257	NM_173410	233919	G protein-coupled receptor 26	Gpr26	0.806	-2.339	0.0508925	0.203376
19051	10456140	NM_172628	225608	SH3 domain and tetratricopepti	Sh3tc2	0.806	-2.168	0.0656474	0.238799
19052	10530492	AK164247	100978	nuclear transcription factor,	Nfxl1	0.806	-4.42	0.00286469	0.0279774
19053	10523058	ENSMUST00000108609	276770	eukaryotic translation initiat	Eif5a	0.806	-3.401	0.0109243	0.0720425
19054	10353775	BC057378	320705	RIKEN cDNA B230209C24 gene	B230209C24Rik	0.806	-2.997	0.0193341	0.107268
19055	10367400	NM_021412	58223	matrix metallopeptidase 19	Mmp19	0.806	-2.646	0.0322397	0.150768
19056	10491083	NM_178772	320024	arylacetamide deacetylase-like	Aadacl1	0.806	-3.377	0.0112928	0.0735824
19057	10477297	NM_008444	16569	kinesin family member 3B	Kif3b	0.805	-3.496	0.00957801	0.0659022
19058	10468419	XM_129357	70806	DNA segment, Chr 19, ERATO Doi	D19Ertd652e	0.805	-3.173	0.0150272	0.0904973
19059	10548585	NM_139117	56449	cold shock domain protein A	Csda	0.805	-4.642	0.00218621	0.0232055
19060	10601844	NM_198161	70237	basic helix-loop-helix domain	Bhlhb9	0.805	-5.256	0.00107207	0.0137798
19061	10491477	NM_011443	20674	SRY-box containing gene 2	Sox2	0.805	-2.64	0.0325574	0.151595
19062	10380415	BC094502	216150	cell division cycle 34 homolog	Cdc34	0.805	-1.603	0.151736	0.395645
19063	10399330	NM_145441	217379	UBX domain containing 4	Ubxd4	0.805	-3.382	0.0112185	0.0733781
19064	10579307	BC048938	75620	RIKEN cDNA 2810422J05 gene	2810422J05Rik	0.805	-4.33	0.00320372	0.0299943
19065	10483249	NM_015736	14425	UDP-N-acetyl-alpha-D-galactosa	Galnt3	0.805	-2.62	0.0335279	0.154383
19066	10603485	NM_007898	13595	phenylalkylamine Ca2+ antagoni	Ebp	0.805	-3.194	0.0146006	0.0885588
19067	10378914	NM_011586	360013	myosin XVIIIa	Myo18a	0.805	-4.595	0.0023121	0.024106

19068	10542993	NM_173006	269823	paraoxonase 3	Pon3	0.805	-2.079	0.0750337	0.259023
19069	10474171	NM_010125	13711	E74-like factor 5	Elf5	0.805	-2.383	0.0476072	0.194363
19070	10525665	XM_915492	208908	coiled-coil domain containing	Ccdc62	0.805	-2.027	0.0811132	0.271716
19071	10428983	BC011343	223601	RIKEN cDNA 0910001A06 gene	0910001A06Rik	0.804	-5.965	0.000501179	0.00810782
19072	10520003	NM_026034	67211	armadillo repeat containing 10	Armc10	0.804	-2.572	0.03597	0.16175
19073	10434806	ENSMUST00000078988	210126	LIM domain containing preferre	Lpp	0.804	-2.557	0.0367997	0.164259
19074	10509127	NM_024243	71665	fucosidase, alpha-L- 1, tissue	Fuca1	0.804	-4.343	0.00315466	0.0297283
19075	10554629	NM_175317	101592	elongation factor Tu GTP bindi	Eftud1	0.804	-4.14	0.00407379	0.035447
19076	10375880	NM_026631	52530	nucleolar protein family A, me	Nola2	0.804	-5.119	0.00125036	0.0154515
19077	10590279	NM_144557	245049	myosin VIIA and Rab interactin	Myrip	0.804	-2.642	0.0324315	0.151275
19078	10585338	NM_212445	68304	KDEL (Lys-Asp-Glu-Leu) contain	Kdelc2	0.804	-2.241	0.0589049	0.223325
19079	10448615	BC094931	328778	RAB26, member RAS oncogene fam	Rab26	0.804	-3.477	0.00983738	0.0672709
19080	10493189	ENSMUST00000104974	17261	myocyte enhancer factor 2D	Mef2d	0.804	-3.884	0.00568435	0.0452369
19081	10393098	NM_016852	22378	WW domain binding protein 2	Wbp2	0.804	-3.276	0.0130082	0.0815434
19082	10531653	BC055321	231503	cDNA sequence BC062109	BC062109	0.804	-2.118	0.0707898	0.249713
19083	10522301	AY616753	433899	cDNA sequence, AY616753	AY616753	0.804	-2.045	0.0788815	0.267427
19084	10575153	NM_025558	66427	cytochrome b5 type B	Cyb5b	0.804	-4.536	0.00248636	0.025348
19085	10503184	NM_001081417	320790	chromodomain helicase DNA bind	Chd7	0.804	-1.622	0.147664	0.389789
19086	10461154	AK051045	83673	small nucleolar RNA host gene	Snhg1	0.804	-1.965	0.0889881	0.287785
19087	10357875	NM_007570	12227	B-cell translocation gene 2, a	Btg2	0.804	-2.756	0.02745	0.135323
19088	10368979					0.804	-2.745	0.0278898	0.136886
19089	10530806	BC023841	231327	phosphoribosyl pyrophosphate a	Ppat	0.804	-2.576	0.0357648	0.16117
19090	10546508					0.804	-2.529	0.0383243	0.169206
19091	10381226	NM_027896	71743	Coenzyme A synthase	Coasy	0.804	-4.205	0.00375202	0.0333752
19092	10603492	NM_016913	53627	porcupine homolog (Drosophila)	Porcn	0.803	-3.121	0.0161854	0.0951945
19093	10462630	AK019493	75735	pantothenate kinase 1	Pank1	0.803	-2.088	0.0739946	0.257104
19094	10559698	AK138915	381835	gene model 1078, (NCBI)	Gm1078	0.803	-2.34	0.0507961	0.203223
19095	10465651	NM_007928	13728	MAP/microtubule affinity-regul	Mark2	0.803	-4.209	0.00373095	0.0332773
19096	10520318	NM_010075	13483	dipeptidylpeptidase 6	Dpp6	0.803	-3.051	0.0178955	0.101524
19097	10602426					0.803	-2.089	0.0739505	0.257004
19098	10557231	XR_034502	628696	similar to ribosomal protein L	LOC628696	0.803	-1.294	0.235583	0.50735
19099	10565479	NM_026304	67669	lethal, Chr 7, Rinchik 6	l7Rn6	0.803	-3.654	0.00772498	0.0566946
19100	10519578	NM_008830	18670	ATP-binding cassette, sub-fami	Abcb4	0.803	-2.176	0.0649156	0.237571
19101	10426594	NM_146280	258277	olfactory receptor 281	Olfr281	0.803	-1.461	0.186131	0.444356
19102	10494753					0.803	-4.437	0.0028079	0.0275884
19103	10351179	BC050143	69962	RIKEN cDNA 2810422O20 gene	2810422O20Rik	0.803	-2.943	0.0209144	0.113291
19104	10422707	NM_001013367	105787	protein kinase, AMP-activated,	Prkaa1	0.803	-4.26	0.00350044	0.0317517
19105	10394862	NM_001098168	211914	development and differentiatio	Ddef2	0.803	-3.413	0.0107412	0.0713743
19106	10398404					0.803	-2.243	0.0587068	0.222894
19107	10425317					0.802	-1.738	0.124503	0.353403
19108	10524876	NM_001033311	231668	cDNA sequence BC023744	BC023744	0.802	-2.255	0.0576657	0.220155
19109	10566692	NM_146739	258734	olfactory receptor 502	Olfr502	0.802	-2.175	0.0650228	0.237821
19110	10474169					0.802	-3.124	0.016126	0.0950038
19111	10576403	NM_001029876	382038	cDNA sequence AK122209	AK122209	0.802	-2.469	0.0418961	0.178779
19112	10406245					0.802	-2.721	0.0288965	0.13975
19113	10466839	XR_034316	637203	similar to 60S ribosomal prote	LOC637203	0.802	-3.015	0.0188409	0.105433
19114	10384370	ENSMUST00000101517	100038572	predicted gene, OTTMUSG0000000	OTTMUSG00000005162	0.802	-2.347	0.0502877	0.201609
19115	10466818	NM_146097	226043	COBW domain containing 1	Cbwd1	0.802	-4.454	0.00274931	0.0272406
19116	10413086	NM_134079	11534	adenosine kinase	Adk	0.802	-3.568	0.00868421	0.0613817
19117	10607059	NM_010572	16370	insulin receptor substrate 4	Irs4	0.802	-2.016	0.0823929	0.274522
19118	10601915	BC031748	245622	cDNA sequence BC031748	BC031748	0.802	-2.493	0.0404573	0.175113
19119	10436983	NM_027293	70028	dopey family member 2	Dopey2	0.802	-3.17	0.0150964	0.0907637

19120	10506274	NM_198412	72685	DnaJ (Hsp40) homolog, subfamil	Dnajc6	0.802	-3.349	0.0117337	0.0756162
19121	10533085	NM_018858	23980	phosphatidylethanolamine bindi	Pebp1	0.802	-1.741	0.123886	0.352219
19122	10489870	XM_983885	675636	similar to 60S ribosomal prote	LOC675636	0.802	-0.774	0.463422	0.717662
19123	10526502	NM_026073	67286	RAB, member of RAS oncogene fa	Rabl5	0.802	-3.403	0.0108924	0.0718818
19124	10552929	U88401	50994	metastasis associated gene 2	Mtag2	0.802	-2.103	0.072411	0.253444
19125	10395389	NM_025312	66042	sclerostin domain containing 1	Sostdc1	0.802	-1.263	0.246	0.519052
19126	10442211	NM_013843	24132	zinc finger protein 53	Zfp53	0.802	-3.349	0.0117434	0.0756561
19127	10434758	NM_145933	20440	beta galactoside alpha 2,6 sia	St6gal1	0.802	-4.29	0.00337165	0.0310227
19128	10422026	NM_029680	76627	RIKEN cDNA 1700110M21 gene	1700110M21Rik	0.801	-1.838	0.107366	0.322922
19129	10492220	NM_001040396	69227	RIKEN cDNA 2810407C02 gene	2810407C02Rik	0.801	-5.486	0.00083172	0.0115242
19130	10519117	NM_008860	18762	protein kinase C, zeta	Prkcz	0.801	-2.176	0.0649313	0.237571
19131	10473783	NM_009023	19400	receptor-associated protein of	Rapsn	0.801	-2.489	0.0407092	0.175879
19132	10408932	XR_031090	667204	similar to Predicted gene, EG2	LOC667204	0.801	-0.872	0.411496	0.675413
19133	10460097	AK141732	433208	hypothetical LOC433208	LOC433208	0.801	-1.685	0.134682	0.369832
19134	10468691	NM_178688	226251	actin-binding LIM protein 1	Ablim1	0.801	-3.808	0.00628327	0.0485221
19135	10373454	NM_011119	18813	proliferation-associated 2G4	Pa2g4	0.801	-3.621	0.00807629	0.0584012
19136	10456721					0.801	-1.116	0.300182	0.576271
19137	10526232	NM_024479	79565	Williams Beuren syndrome chrom	Wbscr27	0.801	-3.453	0.0101671	0.0687475
19138	10349429					0.801	-2.974	0.0199958	0.109859
19139	10485698	XR_034534	623145	similar to L-lactate dehydroge	LOC623145	0.8	-1.789	0.115563	0.337961
19140	10491518					0.8	-2.493	0.0404267	0.175053
19141	10469568	ENSMUST00000070378	74169	RIKEN cDNA 1810010K12 gene	1810010K12Rik	0.8	-4.673	0.00210562	0.0226111
19142	10588505	NM_029631	76491	abhydrolase domain containing	Abhd14b	0.8	-4.324	0.00322912	0.0301308
19143	10393866	NM_153056	209011	sirtuin 7 (silent mating type	Sirt7	0.8	-4.444	0.00278376	0.0274277
19144	10592023	NM_001102455	11804	amyloid beta (A4) precursor-li	Aplp2	0.8	-3.697	0.00728864	0.0543027
19145	10596051	NM_001101483	245020	transmembrane protein 22	Tmem22	0.8	-3.168	0.0151387	0.0909615
19146	10386423	NM_183139	194908	RIKEN cDNA 4933433K01 gene	4933433K01Rik	0.8	-2.843	0.0241775	0.124534
19147	10404036	NM_178196	319181	histone cluster 1, H2bg	Hist1h2bg	0.8	-2.214	0.0613072	0.2285
19148	10560945	NM_008168	14809	glutamate receptor, ionotropic	Grik5	0.8	-3.41	0.0107847	0.0715509
19149	10598839	NM_133669	19889	retinitis pigmentosa 2 homolog	Rp2h	0.8	-3.734	0.00693466	0.0521617
19150	10459510					0.8	-1.841	0.106904	0.322497
19151	10565170	BC027500	67290	RIKEN cDNA 3110040N11 gene	3110040N11Rik	0.8	-3.296	0.0126427	0.0796771
19152	10441956	NM_024203	67544	RIKEN cDNA 4932442K08 gene	4932442K08Rik	0.8	-5.763	0.000618549	0.00941584
19153	10438738	NM_009744	12053	B-cell leukemia/lymphoma 6	Bcl6	0.8	-2.097	0.0730087	0.254739
19154	10497912	NM_198657	381438	predicted gene, EG381438	EG381438	0.8	-2.626	0.033215	0.1537
19155	10408024	BC089360	319207	piggyBac transposable element	Pgbd1	0.8	-2.342	0.050656	0.202722
19156	10503116	AK052165	100036540	predicted gene, ENSMUSG0000005	ENSMUSG00000054541	0.8	-2.358	0.0494517	0.19981
19157	10442370	NM_019910	13184	demilune cell and parotid prot	Dcpp1	0.8	-2.047	0.0787214	0.267044
19158	10349562	NM_177604	212439	expressed sequence AA986860	AA986860	0.799	-2.015	0.0825087	0.274778
19159	10399584	AK144596	100038502	predicted gene, ENSMUSG0000007	ENSMUSG00000073180	0.799	-2.104	0.0723256	0.253313
19160	10399588	ENSMUST00000079237	22651	zinc finger protein 125	Zfp125	0.799	-2.355	0.0497008	0.200281
19161	10531919	NM_053262	114664	hydroxysteroid (17-beta) dehyd	Hsd17b11	0.799	-2.313	0.0529194	0.208483
19162	10600755	NM_007492	11878	aristaless related homeobox ge	Arx	0.799	-2.053	0.0779701	0.26556
19163	10515423					0.799	-1.547	0.164624	0.414483
19164	10503220	NM_001081417	320790	chromodomain helicase DNA bind	Chd7	0.799	-2.827	0.0247509	0.126592
19165	10575160	NM_133957	54446	nuclear factor of activated T-	Nfat5	0.799	-1.978	0.0871833	0.284169
19166	10494428	NM_001009935	56338	thioredoxin interacting protei	Txnip	0.799	-2.391	0.0470967	0.192875
19167	10456699	NM_177470	52538	acetyl-Coenzyme A acyltransfer	Acaa2	0.799	-4.289	0.00337634	0.0310523

19168	10488415	NM_009976	13010	cystatin C	Cst3	0.799	-3.33	0.0120577	0.077029
19169	10578324	NM_001005863	102103	mitochondrial tumor suppressor	Mtus1	0.799	-3.882	0.00569977	0.0453238
19170	10492078	NM_025442	66248	asparagine-linked glycosylatio	Alg5	0.799	-4.91	0.00159157	0.0182002
19171	10388579	NM_016810	53334	golgi SNAP receptor complex me	Gosr1	0.799	-4.18	0.00387184	0.0341512
19172	10451879	NM_144546	104349	zinc finger protein 119	Zfp119	0.799	-2.098	0.0729553	0.254633
19173	10494595	NM_010928	18129	Notch gene homolog 2 (Drosophi	Notch2	0.799	-2.764	0.0271341	0.134173
19174	10572663	NM_025396	66171	6-phosphogluconolactonase	Pgls	0.799	-4.499	0.00260118	0.0261175
19175	10387514					0.798	-2.192	0.0633447	0.23339
19176	10418297	XR_032191	665370	similar to Small nuclear RNA a	LOC665370	0.798	-0.981	0.35819	0.6305
19177	10563387	NM_001033792	545963	predicted gene, EG545963	EG545963	0.798	-2.567	0.0362296	0.162503
19178	10447395	NM_008628	17685	mutS homolog 2 (E. coli)	Msh2	0.798	-3.122	0.0161654	0.0951294
19179	10607363					0.798	-2.342	0.0506207	0.202691
19180	10586174					0.798	-1.747	0.122873	0.350766
19181	10388476	NM_029548	380714	rabphilin 3A-like (without C2	Rph3al	0.798	-3.759	0.00670759	0.0509613
19182	10586477	NM_011149	19035	peptidylprolyl isomerase B	Ppib	0.798	-5.083	0.00130248	0.0158638
19183	10412943	NM_026341	67725	nudix (nucleoside diphosphate	Nudt13	0.798	-3.554	0.00884616	0.0621917
19184	10392415	NM_011268	19739	regulator of G-protein signali	Rgs9	0.798	-3.488	0.00968526	0.0665103
19185	10601854	NM_011712	22381	WW domain binding protein 5	Wbp5	0.798	-4.852	0.00170348	0.0190876
19186	10350188	NM_025439	66241	transmembrane protein 9	Tmem9	0.798	-4.373	0.00303963	0.0290298
19187	10533237	NM_033541	114643	2'-5' oligoadenylate synthetas	Oas1c	0.798	-2.02	0.081968	0.273497
19188	10429638	XR_033200	672572	similar to glyceraldehyde-3-ph	LOC672572	0.797	-1.259	0.247108	0.520387
19189	10596381					0.797	-1.823	0.109755	0.327457
19190	10579023	NM_153054	110877	solute carrier family 18 (vesi	Slc18a1	0.797	-3.027	0.0185212	0.104097
19191	10499612	NM_009565	22724	zinc finger and BTB domain con	Zbtb7b	0.797	-2.657	0.0317366	0.149088
19192	10503178	NM_001081417	320790	chromodomain helicase DNA bind	Chd7	0.797	-2.279	0.0556	0.215288
19193	10512714	ENSMUST00000061986	230126	src homology 2 domain-containi	Shb	0.797	-3.362	0.011528	0.0748614
19194	10504491	NM_177027	319885	zinc finger, CCHC domain conta	Zcchc7	0.797	-4.019	0.00476208	0.0397667
19195	10356406	NM_001111314	53972	neuronal guanine nucleotide ex	Ngef	0.797	-3.201	0.0144548	0.0880534
19196	10509790	NM_175438	212647	aldehyde dehydrogenase 4 famil	Aldh4a1	0.797	-3.283	0.0128825	0.0809488
19197	10535310					0.797	-2.999	0.0192895	0.107077
19198	10508249	ENSMUST00000094712	100039968	predicted gene, OTTMUSG0000000	OTTMUSG00000009332	0.796	-3.987	0.00496333	0.0410898
19199	10382425	NM_001110337	70355	G protein-coupled receptor, fa	Gprc5c	0.796	-4.871	0.00166523	0.0187985
19200	10388033	NM_033562	116891	Der1-like domain family, membe	Derl2	0.796	-3.465	0.009996	0.0680694
19201	10517213	NM_001081047	194231	connector enhancer of kinase s	Cnksr1	0.796	-4.894	0.00162073	0.018434
19202	10389858	NM_008705	18103	non-metastatic cells 2, protei	Nme2	0.796	-2.811	0.0253115	0.128435
19203	10521950	NM_001081103	116873	stromal interaction molecule 2	Stim2	0.796	-3.701	0.00724594	0.0540417
19204	10448034	NM_007865	13388	delta-like 1 (Drosophila)	Dll1	0.796	-2.824	0.024838	0.126915
19205	10517036	NM_199306	230796	WD and tetratricopeptide repea	Wdtc1	0.796	-3.472	0.00989909	0.0675836
19206	10487722	NM_001081162	269356	solute carrier family 4, sodiu	Slc4a11	0.795	-2.046	0.078842	0.267367
19207	10468413	BC107403	70806	DNA segment, Chr 19, ERATO Doi	D19Ertd652e	0.795	-2.394	0.0468644	0.192371
19208	10379401	NM_028019	71956	ring finger protein 135	Rnf135	0.795	-2.49	0.0406387	0.175719
19209	10493703	NM_206924	23922	jumping translocation breakpoi	Jtb	0.795	-3.958	0.00515566	0.042187
19210	10515111					0.795	-1.409	0.200395	0.462419
19211	10400143	NM_144552	217517	syntaxin binding protein 6 (am	Stxbp6	0.795	-2.657	0.0317148	0.149088
19212	10591653	NM_178577	235043	transmembrane protein 205	Tmem205	0.795	-3.955	0.00517356	0.0422494
19213	10388517	NM_177367	276919	gem (nuclear organelle) associ	Gemin4	0.795	-3.46	0.0100637	0.0683765
19214	10410099	NM_172587	218294	CDC14 cell division cycle 14 h	Cdc14b	0.795	-2.132	0.0692724	0.246644
19215	10373702	NR_003517	236604	phosphatidylserine decarboxyla	LOC236604	0.795	-3.314	0.0123341	0.0782223
19216	10551872	NM_153577	233066	expressed sequence AI428936	AI428936	0.794	-4.209	0.00373379	0.0332773
19217	10578504	BC107256	69479	RIKEN cDNA 1700029J07 gene	1700029J07Rik	0.794	-1.964	0.0890412	0.287785
19218	10396800	ENSMUST00000039928	211945	pleckstrin homology domain con	Plekhh1	0.794	-4.82	0.00176861	0.0196715
19219	10508412	NM_027402	384061	fibronectin type III domain co	Fndc5	0.794	-2.871	0.0232135	0.121012

19220	10469951	NM_176834	68846	ring finger protein 208	Rnf208	0.794	-4.383	0.00300161	0.0287567
19221	10346878	ENSMUST00000114132	73884	zinc finger, DBF-type containi	Zdbf2	0.794	-3.002	0.0191847	0.106692
19222	10575596					0.794	-2.079	0.0749866	0.258984
19223	10414182	BC049632	69496	DPY30 domain containing 1	Dydc1	0.794	-2.574	0.0358615	0.161427
19224	10564502	ENSMUST00000032770	78444	RIKEN cDNA C330024D12 gene	C330024D12Rik	0.794	-4.098	0.00430232	0.0367697
19225	10502375	NM_008642	17777	microsomal triglyceride transf	Mttp	0.794	-2.252	0.0579206	0.220742
19226	10442396	NM_013855	27410	ATP-binding cassette, sub-fami	Abca3	0.794	-3.96	0.00514193	0.0421073
19227	10512606	NM_026871	68917	histidine triad nucleotide bin	Hint2	0.794	-3.614	0.00814945	0.0587093
19228	10494388	NM_178214	319190	histone cluster 2, H2be	Hist2h2be	0.794	-3.612	0.00817198	0.0587915
19229	10418027	NM_026965	69156	catechol-O-methyltransferase d	Comtd1	0.793	-3.797	0.00637317	0.0490168
19230	10383210	ENSMUST00000093902	672511	hypothetical LOC672511	LOC672511	0.793	-3.223	0.0140069	0.0858692
19231	10542714	NM_133688	67636	LYR motif containing 5	Lyrm5	0.793	-5.371	0.000943686	0.0126089
19232	10450103	NM_013543	14979	H2-K region expressed gene 6	H2-Ke6	0.793	-4.416	0.00287842	0.0280477
19233	10420730	NM_010191	14137	farnesyl diphosphate farnesyl	Fdft1	0.793	-4.358	0.00309562	0.0293384
19234	10501235	NM_026764	14865	glutathione S-transferase, mu	Gstm4	0.793	-2.975	0.0199628	0.109777
19235	10498187	BC058995	329641	RIKEN cDNA 6030405A18 gene	6030405A18Rik	0.793	-2.68	0.0306774	0.145769
19236	10364038	NM_133995	103149	ureidopropionase, beta	Upb1	0.793	-3.028	0.0184821	0.104016
19237	10349945	ENSMUST00000097572	100038692	predicted gene, ENSMUSG0000007	ENSMUSG00000073560	0.793	-2.976	0.0199254	0.109657
19238	10467425	NM_178362	20411	sorbin and SH3 domain containi	Sorbs1	0.793	-2.498	0.0401274	0.174258
19239	10407276					0.793	-2.319	0.0524079	0.207062
19240	10578493	NM_126166	142980	toll-like receptor 3	Tlr3	0.793	-4.274	0.00343708	0.0314073
19241	10522004	BC004797	76261	RIKEN cDNA 0610040J01 gene	0610040J01Rik	0.793	-3.07	0.017413	0.0997508
19242	10571978	NM_145595	234309	carbonyl reductase 4	Cbr4	0.793	-6.091	0.000441103	0.00740801
19243	10588696	NM_019750	56441	N-acetyltransferase 6	Nat6	0.793	-3.196	0.0145466	0.0884179
19244	10384811	NM_025740	216618	coiled-coil domain containing	Ccdc104	0.793	-4.654	0.00215307	0.0229481
19245	10478341	NM_172150	245866	intraflagellar transport 52 ho	Ift52	0.792	-5.121	0.00124741	0.0154422
19246	10439766	NM_021496	58998	poliovirus receptor-related 3	Pvrl3	0.792	-5.178	0.00117027	0.0147079
19247	10530841	NM_008048	29817	insulin-like growth factor bin	Igfbp7	0.792	-3.512	0.00936969	0.0648149
19248	10494551	NM_019800	66659	acid phosphatase 6, lysophosph	Acp6	0.792	-3.962	0.00513124	0.0420523
19249	10346164	NM_138741	20324	serum deprivation response	Sdpr	0.792	-2.228	0.0600723	0.22593
19250	10471878					0.792	-3.069	0.0174444	0.0998765
19251	10505200	NM_024255	72479	hydroxysteroid dehydrogenase l	Hsdl2	0.792	-3.299	0.0125941	0.0795368
19252	10405892	ENSMUST00000099412	100038538	predicted gene, ENSMUSG0000007	ENSMUSG00000074826	0.792	-2.435	0.0441061	0.185146
19253	10376446	NM_031172	56631	tripartite motif-containing 17	Trim17	0.792	-4.353	0.00311263	0.0294336
19254	10359118	BC099972	214575	tudor domain containing 5	Tdrd5	0.792	-2.944	0.0208689	0.113171
19255	10463347	NM_024450	30049	stearoyl-coenzyme A desaturase	Scd3	0.792	-4.179	0.00387667	0.0341677
19256	10564567					0.792	-1.651	0.141399	0.380665
19257	10361660	NM_010690	16798	large tumor suppressor	Lats1	0.792	-4.33	0.00320455	0.0299943
19258	10528702	NM_145401	108099	protein kinase, AMP-activated,	Prkag2	0.792	-2.4	0.046459	0.191627
19259	10422052	NM_001033132	66200	COMM domain containing 6	Commd6	0.792	-5.755	0.000623691	0.00948728
19260	10392936	NM_015807	50773	5',3'-nucleotidase, cytosolic	Nt5c	0.792	-3.855	0.00590756	0.046516
19261	10476588	NM_001013802	72899	MACRO domain containing 2	Macrod2	0.792	-1.475	0.182447	0.438923
19262	10396440	XM_204772	277089	predicted gene, EG277089	EG277089	0.792	-2.372	0.0484559	0.196802
19263	10368083	NM_144820	215814	coiled-coil domain containing	Ccdc28a	0.791	-3.644	0.00782829	0.0571354
19264	10412562	NM_134080	286940	filamin, beta	Flnb	0.791	-3.352	0.0116984	0.0755041
19265	10532301					0.791	-1.112	0.301693	0.577901
19266	10563480	NM_010602	16514	potassium inwardly rectifying	Kcnj11	0.791	-3.498	0.00955223	0.0657534
19267	10501282	NM_001081320	72023	cytochrome b-561 domain contai	Cyb561d1	0.791	-3.31	0.0123963	0.0785459
19268	10363173	NM_010288	14609	gap junction protein, alpha 1	Gja1	0.791	-3.746	0.0068208	0.0514884
19269	10420672	NM_173419	239133	deleted in lymphocytic leukemi	Dleu7	0.791	-2.597	0.0346965	0.158108
19270	10592629	NM_175481	110637	glutamate receptor, ionotropic	Grik4	0.791	-3.143	0.0156882	0.0930667
19271	10531304	NM_016912	53886	cyclin-dependent kinase-like 2	Cdkl2	0.791	-2.84	0.0242778	0.124965
19272	10440840	BC019533	68001	RIKEN cDNA 1110004E09 gene	1110004E09Rik	0.791	-3.953	0.00519336	0.042348
19273	10388492	NM_026664	68299	vacuolar protein sorting 53 (y	Vps53	0.791	-4.997	0.00143838	0.0168681

19274	10510594	NM_011910	24111	urotensin 2	Uts2	0.791	-1.367	0.212622	0.478213
19275	10503593	NM_175234	76132	RIKEN cDNA 6230409E13 gene	6230409E13Rik	0.791	-4.322	0.00323555	0.0301509
19276	10567999					0.791	-3.026	0.0185431	0.104192
19277	10365286	NM_025499	66341	EP300 interacting inhibitor of	Eid3	0.791	-3.083	0.0171034	0.0987261
19278	10561911	NM_175478	233067	leucine rich repeat and fibron	Lrfn3	0.79	-2.517	0.0390427	0.171199
19279	10593884	ENSMUST00000098697	100038566	predicted gene, ENSMUSG0000007	ENSMUSG00000074284	0.79	-3.332	0.012023	0.0768949
19280	10607806	NM_177429	237222	oral-facial-digital syndrome 1	Ofd1	0.79	-3.271	0.0131006	0.0819766
19281	10447486					0.79	-2.318	0.052457	0.207138
19282	10558903	NM_011528	21351	transaldolase 1	Taldo1	0.79	-4.096	0.00431443	0.0368285
19283	10529953	AK036806	625026	hypothetical LOC625026	LOC625026	0.79	-2.02	0.0819096	0.273441
19284	10591556	NM_026282	67629	SPC24, NDC80 kinetochore compl	Spc24	0.79	-4.105	0.00426455	0.0365503
19285	10462683	NM_029508	76073	polycomb group ring finger 5	Pcgf5	0.79	-3.206	0.0143566	0.0875561
19286	10575777	ENSMUST00000095172	74440	RIKEN cDNA 4933407C03 gene	4933407C03Rik	0.79	-4.876	0.00165515	0.0187448
19287	10582069	BC038819	74032	RIKEN cDNA 4632417N05 gene	4632417N05Rik	0.79	-3.1	0.0166797	0.0971556
19288	10483819	NM_028235	72421	tetratricopeptide repeat domai	Ttc30b	0.79	-0.941	0.377169	0.647258
19289	10411142	NM_016668	12116	betaine-homocysteine methyltra	Bhmt	0.79	-2.602	0.0343984	0.157065
19290	10454731					0.79	-1.253	0.249362	0.523394
19291	10434802	BC005613	210126	LIM domain containing preferre	Lpp	0.79	-2.507	0.0395961	0.172836
19292	10503161	NM_001081417	320790	chromodomain helicase DNA bind	Chd7	0.79	-5.197	0.0011451	0.0144463
19293	10538413	NM_199143	387524	zinc and ring finger 2	Znrf2	0.79	-3.613	0.00815908	0.0587204
19294	10563099	NR_000004	27212	small nucleolar RNA, C/D box 3	Snord35b	0.79	-1.506	0.174433	0.427379
19295	10535331	NM_175217	75104	monocyte to macrophage differe	Mmd2	0.789	-3.027	0.0185127	0.104077
19296	10587446	NM_001039546	17920	myosin VI	Myo6	0.789	-2.447	0.0432804	0.182768
19297	10587829	NM_011961	26432	procollagen lysine, 2-oxogluta	Plod2	0.789	-3.101	0.0166521	0.0970498
19298	10454077	ENSMUST00000067347	72504	TAF4B RNA polymerase II, TATA	Taf4b	0.789	-3.507	0.00942867	0.0651077
19299	10525041					0.789	-2.15	0.0675021	0.242726
19300	10412066	NM_023852	67295	RAB3C, member RAS oncogene fam	Rab3c	0.789	-3.593	0.00838522	0.0598168
19301	10361640	XM_001472599	100039303	ribosomal protein L35a pseudog	LOC100039303	0.789	-2.576	0.0357461	0.161141
19302	10426244	NM_021921	60597	mitogen-activated protein kina	Mapk8ip2	0.789	-2.375	0.0481901	0.196062
19303	10500042	NM_030074	78266	zinc finger protein 687	Zfp687	0.789	-4.24	0.00358936	0.0324747
19304	10394173	NM_172421	75302	additional sex combs like 2 (D	Asxl2	0.789	-4.207	0.00374407	0.0333325
19305	10556381	NM_177282	320878	microtubule associated monoxyg	Mical2	0.789	-3.156	0.0154096	0.0921438
19306	10401343	NM_177395	338372	mitogen-activated protein kina	Map3k9	0.788	-5.379	0.000934718	0.0125346
19307	10607639	NM_001001496	414089	gap junction protein, alpha 6	Gja6	0.788	-5.223	0.0011118	0.0141204
19308	10368782	NM_133999	103199	FIG4 homolog (S. cerevisiae)	Fig4	0.788	-2.719	0.0289492	0.13996
19309	10568099	NM_026827	68742	RIKEN cDNA 1110032O16 gene	1110032O16Rik	0.788	-4.822	0.0017642	0.0196431
19310	10511382	NM_010945	18201	neutral sphingomyelinase (N-SM	Nsmaf	0.788	-2.999	0.0192732	0.107015
19311	10434418	BC052055	328643	cDNA sequence BC052055	BC052055	0.788	-2.638	0.0326302	0.151834
19312	10492456	NM_025822	66880	arginine/serine-rich coiled-co	Rsrc1	0.788	-4.059	0.00452072	0.0382191
19313	10579550	BC058348	382018	unc-13 homolog A (C. elegans)	Unc13a	0.788	-1.972	0.0879537	0.285667
19314	10474241					0.788	-2.163	0.0661335	0.239933
19315	10497613	ENSMUST00000091270	545510	predicted gene, EG545510	EG545510	0.788	-2.265	0.0568446	0.218146
19316	10385234					0.788	-2.918	0.0216749	0.115643
19317	10573583	NM_010764	17159	mannosidase 2, alpha B1	Man2b1	0.788	-3.791	0.00642741	0.0492752
19318	10512930	NM_001004025	19059	protein phosphatase 3, regulat	Ppp3r2	0.788	-1.755	0.121479	0.347955
19319	10428857	NM_144800	211401	metastasis suppressor 1	Mtss1	0.787	-4.521	0.00253105	0.0256417
19320	10533858	NM_145371	209354	eukaryotic translation initiat	Eif2b1	0.787	-2.736	0.028274	0.137931
19321	10593834	NM_183111	75258	RIKEN cDNA 4930563M21 gene	4930563M21Rik	0.787	-3.515	0.00932601	0.064631
19322	10411147	NM_022884	64918	betaine-homocysteine methyltra	Bhmt2	0.787	-3.188	0.0147206	0.0890307
19323	10509542	NM_007838	13200	dolichyl-di-phosphooligosaccha	Ddost	0.787	-4.868	0.00167133	0.0188071

19324	10383785	BC048445	67430	RIKEN cDNA 4921536K21 gene	4921536K21Rik	0.787	-2.889	0.022588	0.118836
19325	10565081	NM_011590	21854	translocase of inner mitochond	Timm17a	0.787	-3.538	0.00903906	0.0631599
19326	10458278	BC064044	69816	RIKEN cDNA 2010001M09 gene	2010001M09Rik	0.787	-2.218	0.0609696	0.227884
19327	10592106	NM_054096	117149	toll-interleukin 1 receptor (T	Tirap	0.787	-3.627	0.00800568	0.0580494
19328	10345101	NM_007740	12839	collagen, type IX, alpha 1	Col9a1	0.787	-2.442	0.0436392	0.18388
19329	10501690	NM_144902	229782	solute carrier family 35 (UDP-	Slc35a3	0.787	-2.497	0.0401872	0.174409
19330	10384956	NM_026527	68044	ChaC, cation transport regulat	Chac2	0.787	-1.667	0.138227	0.376165
19331	10478907	NM_021409	58220	par-6 (partitioning defective	Pard6b	0.787	-4.499	0.00260138	0.0261175
19332	10454061	XM_001474128	100040129	similar to put. HMG-17 protein	LOC100040129	0.787	-2.234	0.0594969	0.224759
19333	10384652	XR_034248	100042846	similar to initiation factor 2	LOC100042846	0.787	-2.522	0.0387215	0.170143
19334	10442321	NM_181821	353502	host cell factor C1 regulator	Hcfc1r1	0.786	-2.811	0.025321	0.128452
19335	10558548	NM_177261	76484	kinase non-catalytic C-lobe do	Kndc1	0.786	-1.602	0.151954	0.395759
19336	10559673	NM_029384	664968	RIKEN cDNA 2210411K11 gene	2210411K11Rik	0.786	-2.547	0.037351	0.166263
19337	10555946	NM_011421	20597	sphingomyelin phosphodiesteras	Smpd1	0.786	-3.588	0.00844931	0.0602131
19338	10544252	NM_175528	243780	RIKEN cDNA E330009J07 gene	E330009J07Rik	0.786	-3.13	0.0159879	0.0944005
19339	10400124	XR_034872	638487	similar to protein phosphatase	LOC638487	0.786	-2.238	0.0591217	0.223906
19340	10562856	NM_028021	71960	myosin, heavy polypeptide 14	Myh14	0.786	-3.194	0.014586	0.0885208
19341	10516789	NM_001083119	19273	protein tyrosine phosphatase,	Ptpru	0.786	-3.745	0.00683642	0.0515695
19342	10602176	XM_001472450	633736	predicted gene, EG633736	EG633736	0.786	-4.463	0.00271903	0.0270061
19343	10532157	NM_028876	73130	transmembrane emp24 protein tr	Tmed5	0.786	-2.896	0.0223668	0.117989
19344	10577114	NM_025768	66790	GH regulated TBC protein 1	Grtp1	0.786	-4.136	0.0040985	0.0355595
19345	10475981	NM_025395	66170	coiled-coil-helix-coiled-coil-	Chchd5	0.786	-4.316	0.00326121	0.0303099
19346	10569823	BC089480	546049	RIKEN cDNA C330021F23 gene	C330021F23Rik	0.786	-2.998	0.0192951	0.10708
19347	10361007	NM_026796	226830	SET and MYND domain containing	Smyd2	0.785	-5.2	0.00114156	0.0144102
19348	10486710	ENSMUST00000110674	329504	leucine carboxyl methyltransfe	Lcmt2	0.785	-3.128	0.0160273	0.0945805
19349	10376312	BC063078	73158	La ribonucleoprotein domain fa	Larp1	0.785	-2.522	0.0387191	0.170143
19350	10409265	NM_016709	11992	AU RNA binding protein/enoyl-c	Auh	0.785	-3.258	0.0133347	0.0830238
19351	10370754	NM_015761	216164	downstream of Stk11	Dos	0.785	-4.143	0.0040576	0.0353643
19352	10417708	NM_027695	71147	3-oxoacyl-ACP synthase, mitoch	Oxsm	0.785	-3.75	0.0067898	0.051346
19353	10483624	NR_002854	111970	distal-less homeobox 1, antise	Dlx1as	0.785	-1.993	0.0852481	0.280281
19354	10592856	NM_201372	382073	coiled-coil domain containing	Ccdc84	0.785	-2.214	0.0613516	0.228625
19355	10405725					0.785	-2.456	0.0427398	0.181209
19356	10351304	NM_027430	70456	brain protein 44	Brp44	0.784	-3.889	0.00564143	0.0450633
19357	10412376	AK012975	100036525	predicted gene, ENSMUSG0000004	ENSMUSG00000043151	0.784	-2.688	0.0303074	0.144742
19358	10518761	ENSMUST00000116088	384091	similar to Snrpf protein	LOC384091	0.784	-2.008	0.0833723	0.276517
19359	10488697	NM_018807	54711	pleiomorphic adenoma gene-like	Plagl2	0.784	-4.813	0.00178219	0.0198017
19360	10470959	NM_172267	227696	phytanoyl-CoA dioxygenase doma	Phyhd1	0.784	-3.626	0.00801938	0.0581289
19361	10565102	NM_021492	11775	adaptor-related protein comple	Ap3b2	0.784	-2.305	0.0535304	0.209868
19362	10521555	NM_025281	17089	Ly1 antibody reactive clone	Lyar	0.784	-3.694	0.00731872	0.0544884
19363	10506968	BC023883	230603	RIKEN cDNA 4922503N01 gene	4922503N01Rik	0.784	-3.916	0.00545003	0.0439662
19364	10436594					0.784	-1.558	0.161867	0.410176
19365	10498323	NM_001081262	545527	RIKEN cDNA 4932431H17 gene	4932431H17Rik	0.784	-4.273	0.00344386	0.0314408
19366	10535577	NM_177735	243339	transmembrane protein 130	Tmem130	0.784	-2.307	0.053384	0.20961
19367	10502359	NM_011932	26377	dual adaptor for phosphotyrosi	Dapp1	0.784	-3.046	0.0180167	0.102026
19368	10356475	NM_177305	320982	ADP-ribosylation factor-like 4	Arl4c	0.784	-3.19	0.0146687	0.0887935
19369	10509947	NM_172520	213649	Rho guanine nucleotide exchang	Arhgef19	0.784	-4.592	0.00232053	0.0241314
19370	10541131	NM_001033379	319618	DCP1 decapping enzyme homolog	Dcp1b	0.784	-2.916	0.0217254	0.115825

19371	10396306	NM_024205	104771	RIKEN cDNA 1200003C05 gene	1200003C05Rik	0.783	-3.902	0.00554646	0.0445509
19372	10583316	BC056964	75316	Josephin domain containing 3	Josd3	0.783	-2.881	0.0228705	0.120053
19373	10425335	NM_207708	20972	synaptogyrin 1	Syngr1	0.783	-3.073	0.0173304	0.0994394
19374	10463155	AK145489	381224	gene model 340, (NCBI)	Gm340	0.783	-2.575	0.035838	0.161363
19375	10395142	NM_013709	24057	Sh3 domain YSC-like 1	Sh3yl1	0.783	-2.839	0.024296	0.124965
19376	10451004	NM_009847	12488	CD2-associated protein	Cd2ap	0.783	-4.727	0.00197387	0.0213809
19377	10571344	NM_172911	244418	DNA segment, Chr 8, ERATO Doi	D8Ertd82e	0.783	-5.884	0.00054487	0.00859115
19378	10406581	NM_010049	13361	dihydrofolate reductase	Dhfr	0.783	-3.544	0.00896785	0.0628492
19379	10508392	ENSMUST00000030584	75234	ring finger protein 19B	Rnf19b	0.783	-3.542	0.00899183	0.0629339
19380	10360205	NM_021607	59287	nicastrin	Ncstn	0.783	-4.439	0.00279979	0.0275466
19381	10346722	NM_173444	269198	neurobeachin like 1	Nbeal1	0.783	-2.453	0.0429073	0.181802
19382	10496854	ENSMUST00000037942	70892	tubulin tyrosine ligase-like f	Ttll7	0.782	-3.744	0.00684365	0.0516056
19383	10586248	XM_001476259	102442	DENN/MADD domain containing 4A	Dennd4a	0.782	-2.432	0.04427	0.185686
19384	10547521	NM_007510	11973	VATPase, H+ transporting, lyso	Atp6v1e1	0.782	-3.672	0.00754234	0.0557411
19385	10400892	XR_034366	666213	similar to glyceraldehyde-3-ph	LOC666213	0.782	-2.736	0.0282606	0.137931
19386	10503210	NM_001081417	320790	chromodomain helicase DNA bind	Chd7	0.782	-2.594	0.0348079	0.158375
19387	10543709	NM_178625	72649	transmembrane protein 209	Tmem209	0.782	-4.756	0.00190782	0.0208686
19388	10392440	NM_001029842	104681	solute carrier family 16 (mono	Slc16a6	0.782	-2.816	0.0251263	0.127832
19389	10426921	NM_011873	23994	DAZ associated protein 2	Dazap2	0.782	-3.445	0.0102731	0.0692867
19390	10526181	NM_030719	80909	opposite strand transcription	Gats	0.781	-5.418	0.000895607	0.0121156
19391	10446965	NM_207246	240168	RAS, guanyl releasing protein	Rasgrp3	0.781	-1.979	0.0870698	0.283974
19392	10383206	ENSMUST00000093902	672511	hypothetical LOC672511	LOC672511	0.781	-2.942	0.0209284	0.113291
19393	10461668	NM_146410	258405	olfactory receptor 1420	Olfr1420	0.781	-1.845	0.106384	0.321662
19394	10492522	NM_001113421	30953	schwannomin interacting protei	Schip1	0.781	-4.677	0.00209493	0.0225077
19395	10570291	NM_007972	14058	coagulation factor X	F10	0.781	-4.749	0.00192322	0.0209827
19396	10351043					0.781	-3.961	0.00513381	0.0420571
19397	10542397	NM_177688	232440	H2A histone family, member J	H2afj	0.781	-4.231	0.00363154	0.0326632
19398	10594241	ENSMUST00000063858	791387	predicted gene, ENSMUSG0000005	ENSMUSG00000052143	0.781	-2.048	0.0785896	0.266854
19399	10406276					0.781	-3.644	0.00782357	0.0571207
19400	10516910	NM_175306	100169	phosphatase and actin regulato	Phactr4	0.781	-4.93	0.001554	0.0178672
19401	10532630	NM_177078	320129	adrenergic receptor kinase, be	Adrbk2	0.78	-2.211	0.061633	0.22935
19402	10538658	NM_028705	73998	hect domain and RLD 3	Herc3	0.78	-3.073	0.0173267	0.0994394
19403	10438400	NM_010922	18100	mitochondrial ribosomal protei	Mrpl40	0.78	-3.917	0.00544445	0.0439379
19404	10368199	NM_010848	17863	myeloblastosis oncogene	Myb	0.78	-2.875	0.0230797	0.120761
19405	10408008					0.78	-1.33	0.22402	0.494176
19406	10580231	XR_031475	546080	similar to ATP synthase, H+ tr	LOC546080	0.78	-1.858	0.104294	0.31773
19407	10458992	ENSMUST00000025488	77422	RIKEN cDNA C330018D20 gene	C330018D20Rik	0.78	-4.574	0.00237393	0.024593
19408	10531133	NM_178700	231413	G-rich RNA sequence binding fa	Grsf1	0.78	-4.609	0.002275	0.0238935
19409	10461930	BC020125	225995	RIKEN cDNA D030056L22 gene	D030056L22Rik	0.78	-3.023	0.0186256	0.104545
19410	10491014	NM_009210	20585	helicase-like transcription fa	Hltf	0.78	-5.244	0.00108648	0.0139228
19411	10408477	NM_010093	13557	E2F transcription factor 3	E2f3	0.779	-2.458	0.0426098	0.180844
19412	10597564	BC056653	67899	RIKEN cDNA 2010110K16 gene	2010110K16Rik	0.779	-3.672	0.00753423	0.0557201
19413	10437735					0.779	-2.109	0.0717381	0.251634
19414	10489484	NM_011521	20971	syndecan 4	Sdc4	0.779	-3.706	0.00720105	0.0537638
19415	10422024					0.779	-1.755	0.121416	0.347955
19416	10427494					0.779	-2.61	0.0340111	0.156
19417	10497894	NM_145825	207175	centrin 4	Cetn4	0.779	-3.667	0.00759274	0.056033
19418	10469720	NM_001102437	74159	acyl-Coenzyme A binding domain	Acbd5	0.779	-3.081	0.0171315	0.0987807
19419	10523670	NM_001080798	17355	AF4/FMR2 family, member 1	Aff1	0.779	-2.404	0.0462014	0.190903
19420	10451993	NM_080837	28106	DNA segment, Chr 17, Wayne	D17Wsu104e	0.779	-3.474	0.0098725	0.0674892

19420	10431993	NM_080837	28106	Sta	D17Wsu104e	0.779	-3.474	0.0098725	0.0674892
19421	10413826	NM_145460	218885	oxidoreductase NAD-binding dom	Oxnad1	0.779	-3.343	0.0118443	0.0761899
19422	10421697	BC116748	210808	RIKEN cDNA 9030625A04 gene	9030625A04Rik	0.779	-3.597	0.00834351	0.05964
19423	10575184	NM_025830	66894	WW domain containing E3 ubiqui	Wwp2	0.779	-4.394	0.00295982	0.0284724
19424	10489553	NM_133240	170789	acyl-CoA thioesterase 8	Acot8	0.779	-2.872	0.02318	0.120967
19425	10591884	NM_153803	244757	galactosidase, beta 1-like 2	Glb1l2	0.778	-3.921	0.00541475	0.0437454
19426	10530477	NM_133921	100978	nuclear transcription factor,	Nfxl1	0.778	-4.052	0.0045629	0.0385142
19427	10353871	NM_001013374	214895	lectin, mannose-binding 2-like	Lman2l	0.778	-2.186	0.0638938	0.23479
19428	10495993	NM_130450	170439	ELOVL family member 6, elongat	Elovl6	0.778	-4.041	0.00462693	0.0389303
19429	10448803	NM_198937	52009	hematological and neurological	Hn1l	0.778	-3.146	0.0156195	0.0928214
19430	10440566	NM_001081068	78913	zinc finger protein 294	Zfp294	0.778	-0.913	0.390699	0.659209
19431	10536931	NM_021414	74340	S-adenosylhomocysteine hydrola	Ahcyl2	0.778	-4.637	0.00219897	0.0233174
19432	10478854	NM_148929	77031	solute carrier family 9 (sodiu	Slc9a8	0.778	-5.065	0.00133082	0.0161162
19433	10415604	ENSMUST00000100511	100038565	predicted gene, ENSMUSG0000007	ENSMUSG00000075582	0.778	-2.069	0.076196	0.261455
19434	10371607	NM_027878	71712	RIKEN cDNA 1200002N14 gene	1200002N14Rik	0.777	-3.658	0.00767996	0.0564033
19435	10536369	NM_052993	94192	core 1 synthase, glycoprotein-	C1galt1	0.777	-3.651	0.00775497	0.0567964
19436	10592585	NM_172769	235293	sterol-C5-desaturase (fungal E	Sc5d	0.777	-2.411	0.0457	0.189244
19437	10402560	AK079474	319630	RIKEN cDNA A130014H13 gene	A130014H13Rik	0.777	-1.164	0.281329	0.556831
19438	10475912	NM_028248	72477	transmembrane protein 87B	Tmem87b	0.777	-3.495	0.00958712	0.0659434
19439	10468275	NM_027654	71041	polycomb group ring finger 6	Pcgf6	0.777	-3.848	0.0059618	0.0467952
19440	10405964	BC119515	69315	RIKEN cDNA 1700001L19 gene	1700001L19Rik	0.777	-4.295	0.00334853	0.0308637
19441	10416791					0.777	-3.541	0.00900658	0.0630163
19442	10423333	BC019494	66270	RIKEN cDNA 1810015C04 gene	1810015C04Rik	0.777	-3.686	0.00739572	0.0548555
19443	10494735	NM_010269	14547	ganglioside-induced differenti	Gdap2	0.776	-3.352	0.0116901	0.0755041
19444	10399046	NM_009511	22355	vasoactive intestinal peptide	Vipr2	0.776	-2.9	0.0222283	0.117411
19445	10423155	NM_172958	268783	myotubularin related protein 1	Mtmr12	0.776	-3.83	0.00610253	0.0474981
19446	10449401	NM_013687	21463	t-complex protein 11	Tcp11	0.776	-2.742	0.0280065	0.137267
19447	10365926	AK165804	414105	RIKEN cDNA 4732465J04 gene	4732465J04Rik	0.776	-2.693	0.0301158	0.144163
19448	10395807	BC034876	66132	RIKEN cDNA 1110008L16 gene	1110008L16Rik	0.776	-4.353	0.00311592	0.0294515
19449	10500327	NM_054045	97114	histone cluster 2, H3c2	Hist2h3c2	0.776	-0.94	0.377795	0.647597
19450	10594501	NM_021345	57874	protein tyrosine phosphatase-l	Ptplad1	0.776	-4.684	0.00207913	0.0223721
19451	10344813	NM_026493	211660	centrosome and spindle pole as	Cspp1	0.776	-1.941	0.0921654	0.294263
19452	10526897	NM_024451	77053	unc-84 homolog A (C. elegans)	Unc84a	0.776	-5.711	0.00065369	0.00977484
19453	10594183	NM_027838	71599	SUMO/sentrin specific peptidas	Senp8	0.776	-4.251	0.00353917	0.0320343
19454	10407704					0.776	-1.827	0.109147	0.326375
19455	10426751	NM_026669	110213	testis enhanced gene transcrip	Tegt	0.776	-3.91	0.00549103	0.0441924
19456	10461798	NM_001011840	258120	olfactory receptor 1463	Olfr1463	0.775	-3.014	0.0188559	0.105433
19457	10598023					0.775	-2.24	0.0590153	0.223583
19458	10367973	NM_025446	66253	androgen-induced 1	Aig1	0.775	-4.184	0.00385121	0.0340426
19459	10503192	NM_001081417	320790	chromodomain helicase DNA bind	Chd7	0.775	-1.713	0.129187	0.360384
19460	10564839	NM_009682	11778	adaptor-related protein comple	Ap3s2	0.775	-5.578	0.000753039	0.0108021
19461	10411156	NM_029153	107767	secretory carrier membrane pro	Scamp1	0.775	-3.384	0.01118	0.0732086
19462	10498307	XM_887553	623114	predicted gene, EG623114	EG623114	0.775	-2.581	0.0355235	0.160527
19463	10478587	NM_178375	67538	zinc finger, SWIM domain conta	Zswim3	0.775	-4.593	0.00231748	0.024131
19464	10462195	NM_181404	107351	KN motif and ankyrin repeat do	Kank1	0.775	-3.406	0.0108439	0.0716946
19465	10474419	NM_172671	107515	leucine-rich repeat-containing	Lgr4	0.775	-2.634	0.0328276	0.152417
19466	10588683	NM_010489	15587	hyaluronoglucosaminidase 2	Hyal2	0.775	-4.998	0.00143657	0.0168562
19467	10563191	NM_175130	68667	transient receptor potential c	Trpm4	0.775	-4.078	0.00441595	0.0375134
19468	10445494					0.774	-3.761	0.00669272	0.0508666
19469	10583145	NM_133739	71929	transmembrane protein 123	Tmem123	0.774	-4.283	0.00340181	0.0311965

19470	10561485	NM_027470	70584	p21 (CDKN1A)-activated kinase	Pak4	0.774	-3.52	0.00927379	0.0643957
19471	10500283	NM_011797	23831	carbonic anhydrase 14	Car14	0.774	-5.342	0.000973562	0.0128576
19472	10430489	NM_016915	53357	phospholipase A2, group VI	Pla2g6	0.774	-5.022	0.00139808	0.016658
19473	10359422	NM_007453	11758	peroxiredoxin 6	Prdx6	0.774	-4.552	0.00243863	0.024997
19474	10355452					0.773	-2.68	0.0306773	0.145769
19475	10569278	ENSMUST00000051217	71434	RIKEN cDNA 5530400B01 gene	5530400B01Rik	0.773	-1.875	0.101616	0.312332
19476	10547054	XR_034896	100043759	similar to RNA polymerase II T	LOC100043759	0.773	-2.478	0.0413835	0.177544
19477	10455784	NM_026240	107022	GRAM domain containing 3	Gramd3	0.773	-4.091	0.00433852	0.0370043
19478	10523754					0.773	-1.28	0.240129	0.513219
19479	10543249	BC120768	232599	predicted gene, EG232599	EG232599	0.773	-3.43	0.0104848	0.0702
19480	10603266	NM_001031664	102954	nudix (nucleoside diphosphate	Nudt10	0.773	-2.315	0.052754	0.207909
19481	10489241	ENSMUST00000099127	329554	gene model 826, (NCBI)	Gm826	0.773	-3.351	0.011704	0.0755169
19482	10419240	NM_001042719	114874	DDHD domain containing 1	Ddhd1	0.773	-3.109	0.0164717	0.0962891
19483	10409345	NM_028870	74325	clathrin, light polypeptide (L	Cltb	0.773	-5.375	0.00093868	0.0125696
19484	10583634	NM_021888	60507	queuine tRNA-ribosyltransferas	Qtrt1	0.773	-5.1	0.00127867	0.0157367
19485	10499431	NM_018804	229521	synaptotagmin XI	Syt11	0.773	-2.88	0.0229059	0.120209
19486	10448731	NM_026205	67504	ring finger protein 151	Rnf151	0.772	-3.848	0.00595646	0.0467952
19487	10590343	NM_175114	67095	trafficking protein, kinesin b	Trak1	0.772	-6.375	0.00033235	0.00607891
19488	10512901	NM_178603	28028	mitochondrial ribosomal protei	Mrpl50	0.772	-6.25	0.000376009	0.00661426
19489	10434248	NM_001033164	72307	RIKEN cDNA 2510002D24 gene	2510002D24Rik	0.772	-4.275	0.00343564	0.0314073
19490	10593668	BC023075	235380	Dmx-like 2	Dmxl2	0.772	-4.733	0.00195923	0.021255
19491	10349671	NM_177243	320718	solute carrier family 26, memb	Slc26a9	0.772	-5.45	0.00086533	0.0118271
19492	10537499	NM_001025385	574417	taste receptor, type 2, member	Tas2r137	0.772	-1.312	0.229811	0.500888
19493	10363190					0.772	-2.956	0.0205237	0.112026
19494	10402473	NM_053155	94040	calmin	Clmn	0.772	-2.643	0.0324066	0.151237
19495	10415282	NM_011189	19186	proteasome (prosome, macropain	Psme1	0.772	-5.556	0.000771306	0.0109674
19496	10400883	NM_013896	30056	translocase of inner mitochond	Timm9	0.772	-3.911	0.0054856	0.0441916
19497	10366739					0.772	-2.306	0.0534139	0.209689
19498	10438096					0.772	-1.558	0.16183	0.410131
19499	10448312	NM_020293	56863	claudin 9	Cldn9	0.772	-5.049	0.00135439	0.016299
19500	10467162	NM_023792	75735	pantothenate kinase 1	Pank1	0.772	-2.402	0.046325	0.191233
19501	10464877	NM_133803	75221	dipeptidylpeptidase 3	Dpp3	0.772	-4.947	0.00152387	0.0176166
19502	10494565	NM_010232	14263	flavin containing monooxygenas	Fmo5	0.772	-3.493	0.00962172	0.0661599
19503	10602454	NM_198105	207375	open reading frame 34	ORF34	0.772	-4.643	0.00218326	0.0231857
19504	10451670	NM_027292	70026	benzodiazapine receptor, perip	Bzrpl1	0.771	-2.818	0.0250662	0.127643
19505	10404059	NM_015786	50708	histone cluster 1, H1c	Hist1h1c	0.771	-3.076	0.0172665	0.0993421
19506	10412060	XR_032565	668123	similar to ribosomal protein L	LOC668123	0.771	-6.006	0.000480975	0.00785915
19507	10563314	NM_027903	71755	dihydrodiol dehydrogenase (dim	Dhdh	0.771	-4.894	0.00162162	0.0184342
19508	10506170	NM_145549	230500	EF-hand calcium binding domain	Efcab7	0.771	-4.145	0.00404923	0.0353059
19509	10531437	NM_007644	12492	scavenger receptor class B, me	Scarb2	0.771	-3.564	0.00872622	0.0615845
19510	10355813	NM_008985	19275	protein tyrosine phosphatase,	Ptprn	0.771	-4.123	0.00416484	0.0359141
19511	10522051	NM_008453	16599	Kruppel-like factor 3 (basic)	Klf3	0.771	-5.48	0.000837253	0.011563
19512	10469056	ENSMUST00000116105	381346	similar to ribosomal protein L	LOC381346	0.771	-2.572	0.036005	0.161839
19513	10550406	ENSMUST00000094805	434130	hypothetical LOC434130	LOC434130	0.771	-3.97	0.00507721	0.0417714
19514	10383214	AK173199	629974	ring finger protein 213	Rnf213	0.771	-3.07	0.0174121	0.0997508
19515	10605172	NM_019870	56292	N-acetyltransferase ARD1 homol	Ard1	0.771	-4.31	0.00328708	0.0304606
19516	10486191	NM_028104	72112	protein phosphatase 1, regulat	Ppp1r14d	0.771	-3.348	0.0117557	0.0757083
19517	10344789	NM_026493	211660	centrosome and spindle pole as	Cspp1	0.771	-3.285	0.0128317	0.080676
19518	10533320	NM_172125	280667	a disintegrin and metallopepti	Adam1b	0.77	-4.325	0.0032252	0.0301093
19519	10450892	NM_146289	258286	olfactory receptor 113	Olfr113	0.77	-2.819	0.0250178	0.127548
19520	10450206	NM_019403	54197	ring finger protein 5	Rnf5	0.77	-3.077	0.0172321	0.0992523
19521	10400760					0.77	-2.726	0.0286743	0.139025
19522	10559343	NM_001113373	210274	SH3/ankyrin domain gene 2	Shank2	0.77	-3.465	0.00999129	0.0680694
19523	10522976	NM_027530	52822	RUN and FYVE domain containing	Rufy3	0.77	-4.742	0.0019385	0.0210933

				containing					
19524	10606182					0.77	-1.053	0.326214	0.602683
19525	10441530	NM_031395	83672	synaptotagmin-like 3	Sytl3	0.77	-2.156	0.0669126	0.241599
19526	10571752	NM_178788	320685	dCMP deaminase	Dctd	0.77	-3.829	0.00610799	0.0474981
19527	10365219	DQ459435	237412	predicted gene, EG237412	EG237412	0.77	-2.552	0.0370506	0.165169
19528	10564869	NM_011870	23991	calcium and integrin binding 1	Cib1	0.77	-3.6	0.00830995	0.0594604
19529	10370376	NM_008826	18641	phosphofructokinase, liver, B-	Pfkl	0.77	-4.76	0.00189746	0.0207875
19530	10351045					0.77	-2.703	0.0296407	0.142372
19531	10388861	NM_199199	195040	transmembrane protein 199	Tmem199	0.77	-3.976	0.00503863	0.0415985
19532	10500666	NM_011197	19221	prostaglandin F2 receptor nega	Ptgfrn	0.77	-6.046	0.000461752	0.00764028
19533	10401028	NM_030750	81535	sphingosine-1-phosphate phosph	Sgpp1	0.77	-2.17	0.0654687	0.238533
19534	10594679	NM_001081242	70549	talin 2	Tln2	0.77	-5.075	0.00131523	0.0159824
19535	10424126	NM_001037937	97998	DEP domain containing 6	Depdc6	0.77	-4.376	0.00302801	0.0289701
19536	10581824	NM_178086	338521	fatty acid 2-hydroxylase	Fa2h	0.77	-3.186	0.0147638	0.0892159
19537	10552008	NM_018731	11944	ATPase, H+/K+ exchanging, gast	Atp4a	0.769	-5.192	0.00115196	0.0145155
19538	10477572	NM_029362	75608	chromatin modifying protein 4B	Chmp4b	0.769	-5.02	0.00140025	0.016658
19539	10569024	NM_023059	24058	single immunoglobulin and toll	Sigirr	0.769	-3.032	0.0183856	0.103555
19540	10456378	NM_024190	67064	chromatin modifying protein 1B	Chmp1b	0.769	-4.396	0.00295078	0.0284299
19541	10587532	AK085082	546150	predicted gene, EG546150	EG546150	0.769	-3.009	0.0190058	0.105975
19542	10577217	XR_032429	665516	similar to 3-phosphoglycerate	LOC665516	0.769	-1.568	0.159595	0.406955
19543	10580247	NM_019945	56527	microtubule associated serine/	Mast1	0.769	-2.83	0.024632	0.126168
19544	10530013	BC025881	242997	gene model 447, (NCBI)	Gm447	0.769	-3.982	0.00499672	0.041302
19545	10552118	XM_001481141	100043865	similar to SMT3B protein	LOC100043865	0.768	-2.563	0.0364519	0.163223
19546	10587627	NM_024195	266690	cytochrome b5 reductase 4	Cyb5r4	0.768	-3.403	0.0108904	0.0718818
19547	10604505	BC066100	103012	RIKEN cDNA 6720401G13 gene	6720401G13Rik	0.768	-3.827	0.00612515	0.0475856
19548	10362803	NM_016898	53599	CD164 antigen	Cd164	0.768	-4.679	0.00209084	0.0224752
19549	10474369	NM_177110	320230	RIKEN cDNA C130023O10 gene	C130023O10Rik	0.768	-1.477	0.181864	0.438215
19550	10607336	NM_025660	66611	RIB43A domain with coiled-coil	Ribc1	0.768	-2.995	0.0193789	0.107409
19551	10408762	NM_025380	66143	eukaryotic translation elongat	Eef1e1	0.768	-5.566	0.000762432	0.0108704
19552	10605067	NM_012040	93843	pregnancy upregulated non-ubiq	Pnck	0.768	-5.471	0.000845736	0.0116421
19553	10386992	ENSMUST00000108696	74282	RIKEN cDNA 1700086D15 gene	1700086D15Rik	0.768	-3.228	0.0139142	0.0854991
19554	10456289					0.768	-2.322	0.0521929	0.206699
19555	10542275	NM_007961	14011	ets variant gene 6 (TEL oncoge	Etv6	0.768	-5.364	0.000950698	0.0126584
19556	10578477	NM_153535	212326	cDNA sequence BC035537	BC035537	0.768	-5.053	0.00134913	0.0162541
19557	10445067	BC027007	76416	RIKEN cDNA 1700022C21 gene	1700022C21Rik	0.767	-4.09	0.00434469	0.0370182
19558	10456639	NM_028948	74453	coiled-coil domain containing	Ccdc11	0.767	-3.595	0.00837172	0.0597609
19559	10405563	ENSMUST00000099476	100038494	predicted gene, ENSMUSG0000007	ENSMUSG00000074885	0.767	-2.11	0.0716762	0.251634
19560	10515277	ENSMUST00000030469	68075	RIKEN cDNA 1520402A15 gene	1520402A15Rik	0.767	-2.879	0.022925	0.120261
19561	10394353	NM_025323	66055	RIKEN cDNA 0610009D07 gene	0610009D07Rik	0.767	-5.184	0.00116149	0.0146268
19562	10453717	BC056351	19330	RAB18, member RAS oncogene fam	Rab18	0.767	-3.354	0.0116612	0.075402
19563	10578964	BC016246	66282	RIKEN cDNA 1810029B16 gene	1810029B16Rik	0.767	-4.612	0.00226611	0.0238263
19564	10486197	NM_145530	228543	ras homolog gene family, membe	Rhov	0.767	-5.659	0.000690629	0.0101478
19565	10482687	NM_182994	75423	ADP-ribosylation factor-like 5	Arl5a	0.767	-3.887	0.005657	0.0451705
19566	10357676	NM_008795	18557	PCTAIRE-motif protein kinase 3	Pctk3	0.767	-3.082	0.0171155	0.0987437
19567	10357103	NM_001081386	227485	cadherin 19, type 2	Cdh19	0.767	-2.109	0.0717009	0.251634
19568	10356329	AF357416	17975	nucleolin	Ncl	0.767	-1.781	0.116817	0.340359
19569	10585282	ENSMUST00000050829	69849	RIKEN cDNA 2010007H06 gene	2010007H06Rik	0.767	-4.999	0.00143527	0.0168502
19570	10369867	NM_009360	21780	transcription factor A, mitoch	Tfam	0.766	-3.85	0.00593916	0.0467005
19571	10546476	NM_001029850	14924	membrane associated guanylate	Magi1	0.766	-3.801	0.00633861	0.0488424

19572	10555041	NM_199035	381903	asparagine-linked glycosylatio	Alg8	0.766	-3.31	0.0123901	0.07853
19573	10443021	NM_025272	11974	ATPase, H+ transporting, lysos	Atp6v0e	0.766	-2.984	0.0197009	0.108733
19574	10366391	NM_001025581	268345	potassium voltage gated channe	Kcnc2	0.766	-3.514	0.00934878	0.0647463
19575	10463430	NM_011976	26456	sema domain, immunoglobulin do	Sema4g	0.766	-5.082	0.00130522	0.0158881
19576	10395277	NM_198710	19027	synaptophysin-like protein	Sypl	0.766	-5.415	0.000898937	0.0121374
19577	10581159	BC055880	68523	RIKEN cDNA 1110019N10 gene	1110019N10Rik	0.766	-3.254	0.0134168	0.0833783
19578	10584941	NM_011792	23821	beta-site APP cleaving enzyme	Bace1	0.765	-4.26	0.00349874	0.0317517
19579	10479087	NM_172675	228960	syntaxin 16	Stx16	0.765	-4.883	0.00164154	0.0186306
19580	10353167	NM_028173	72265	translocating chain-associatin	Tram1	0.765	-3.825	0.00614481	0.0476442
19581	10604846	XM_892078	627420	predicted gene, EG627420	EG627420	0.765	-2.42	0.0450763	0.187765
19582	10385716	BC024353	66050	RIKEN cDNA 0610009B22 gene	0610009B22Rik	0.765	-3.742	0.00686338	0.051736
19583	10557535	NM_144926	233878	seizure related 6 homolog like	Sez6l2	0.765	-4.126	0.00414842	0.0358163
19584	10362615	NM_134000	103213	Traf3 interacting protein 2	Traf3ip2	0.765	-4.628	0.00222304	0.0234785
19585	10527547	NM_025652	66596	general transcription factor I	Gtf3a	0.765	-6.567	0.000276072	0.00540246
19586	10451784	NM_001031811	211468	potassium voltage-gated channe	Kcnh8	0.764	-2.197	0.0628987	0.232383
19587	10431140	BC062953	72301	RIKEN cDNA 1810041L15 gene	1810041L15Rik	0.764	-4.701	0.00203719	0.0219879
19588	10501358	NM_011319	20226	seryl-aminoacyl-tRNA synthetas	Sars	0.764	-3.788	0.00645247	0.0494315
19589	10588701	NM_178020	109685	hyaluronoglucosaminidase 3	Hyal3	0.764	-5.685	0.000672004	0.00996413
19590	10548565	NM_025564	66441	mago-nashi homolog B (Drosophi	Magohb	0.764	-5.008	0.00142063	0.0167856
19591	10511679	NM_026172	67460	2,4-dienoyl CoA reductase 1, m	Decr1	0.764	-3.884	0.00568457	0.0452369
19592	10372503	NM_010195	14160	leucine rich repeat containing	Lgr5	0.764	-3.534	0.00908755	0.063394
19593	10483809	NM_010902	18024	nuclear factor, erythroid deri	Nfe2l2	0.764	-3.092	0.0168747	0.0978602
19594	10588691	NM_008317	15586	hyaluronoglucosaminidase 1	Hyal1	0.764	-3.137	0.0158316	0.0936872
19595	10463355	NM_009128	20250	stearoyl-Coenzyme A desaturase	Scd2	0.764	-4.977	0.00147226	0.0171324
19596	10362902	XM_001477881	668192	predicted gene, EG668192	EG668192	0.764	-2.33	0.0515857	0.205217
19597	10536405	ENSMUST00000101672	18231	neurexophilin 1	Nxph1	0.764	-2.792	0.0260432	0.130766
19598	10409543					0.764	-1.43	0.194557	0.454622
19599	10506643	NM_029565	56374	transmembrane protein 59	Tmem59	0.764	-5.136	0.00122626	0.0152338
19600	10531049					0.764	-1.928	0.0939823	0.297613
19601	10350473	NM_020025	26878	UDP-Gal:betaGlcNAc beta 1,3-ga	B3galt2	0.763	-2.964	0.0202758	0.110893
19602	10579335	NM_023217	66522	pyroglutamyl-peptidase I	Pgpep1	0.763	-4.362	0.00307908	0.0292078
19603	10593196	ENSMUST00000098800	100038460	predicted gene, ENSMUSG0000007	ENSMUSG00000074363	0.763	-3.014	0.0188686	0.105433
19604	10450363					0.763	-2.172	0.0653045	0.238356
19605	10529445	NM_013587	16976	low density lipoprotein recept	Lrpap1	0.763	-4.99	0.0014492	0.0169479
19606	10353545	BC028981	68002	RIKEN cDNA 1110058L19 gene	1110058L19Rik	0.763	-2.793	0.0259939	0.130643
19607	10392096					0.763	-2.133	0.0692027	0.246526
19608	10463997	NM_011050	18569	programmed cell death 4	Pdcd4	0.763	-4.287	0.00338219	0.0310771
19609	10490768	ENSMUST00000091375	383815	predicted gene, EG383815	EG383815	0.763	-2.775	0.026675	0.132803
19610	10524874	NM_001033311	231668	cDNA sequence BC023744	BC023744	0.763	-2.25	0.0580648	0.221132
19611	10527332	NM_016789	53324	neuronal pentraxin 2	Nptx2	0.763	-2.593	0.0348834	0.158618
19612	10423599	NM_016762	17181	matrilin 2	Matn2	0.763	-2.636	0.0327354	0.152156
19613	10347774	NM_001081210	69163	mitochondrial ribosomal protei	Mrpl44	0.763	-5.124	0.00124406	0.0154098
19614	10594928	NM_018889	55981	phosphatidylinositol glycan an	Pigb	0.763	-6.144	0.000417947	0.00716699
19615	10354504	XR_031113	546736	glyceraldehyde-3-phosphate deh	LOC546736	0.762	-1.465	0.185037	0.442633
19616	10544689	BC055110	70821	RIKEN cDNA 4921507P07 gene	4921507P07Rik	0.762	-2.929	0.0213225	0.114311
19617	10589596	NM_028312	72654	coiled-coil domain containing	Ccdc12	0.762	-4.195	0.00379855	0.0336898
19618	10567289	NM_138649	110058	synaptotagmin XVII	Syt17	0.762	-2.73	0.0284907	0.138514
19619	10553533	XM_904670	620782	predicted gene, EG620782	EG620782	0.762	-2.236	0.0593703	0.224406
19620	10394990	NM_026037	67216	membrane bound O-acyltransfera	Mboat2	0.762	-4.12	0.00417997	0.0359859
19621	10584334	NM_011734	22619	sialic acid acetylesterase	Siae	0.762	-2.792	0.0260339	0.130751
19622	10599951	BC024574	68618	RIKEN cDNA 1110012L19 gene	1110012L19Rik	0.762	-3.62	0.00808906	0.0584536

19622	10399931	BC024574	68618	RIKEN cDNA 1110012L19 gene	1110012L19Rik	0.762	-3.62	0.00808906	0.0384336
19623	10470555	NM_139197	227671	globoside alpha-1,3-N-acetylga	Gbgt1	0.762	-2.69	0.0302147	0.144448
19624	10355246	NM_007381	11363	acyl-Coenzyme A dehydrogenase,	Acadl	0.762	-6.432	0.000314479	0.00587397
19625	10489195	BC053067	75425	RIKEN cDNA 2610036D13 gene	2610036D13Rik	0.762	-4.322	0.00323941	0.0301736
19626	10589889	NM_009752	12091	galactosidase, beta 1	Glb1	0.762	-3.249	0.013497	0.0836895
19627	10375313	NM_001045530	380694	cyclin J-like	Ccnjl	0.762	-2.933	0.0212049	0.114027
19628	10433492	BC018510	75329	activating transcription facto	Atf7ip2	0.761	-1.957	0.0899756	0.289452
19629	10428222	NM_134094	52589	neurocalcin delta	Ncald	0.761	-4.358	0.00309403	0.0293364
19630	10462628					0.761	-1.223	0.259947	0.534194
19631	10558840	NM_025886	66985	Ras association (RalGDS/AF-6)	Rassf7	0.761	-5.435	0.000878966	0.0119594
19632	10472162	NM_010274	14571	glycerol phosphate dehydrogena	Gpd2	0.761	-5.265	0.00106076	0.0136928
19633	10577517	NM_181325	18408	solute carrier family 25 (mito	Slc25a15	0.761	-3.826	0.00613272	0.0476028
19634	10605559					0.761	-1.359	0.215169	0.482248
19635	10537394	BC059710	66117	RIKEN cDNA 1110001J03 gene	1110001J03Rik	0.76	-5.359	0.000955816	0.0127026
19636	10347073	ENSMUST00000050986	329178	cDNA sequence BC042720	BC042720	0.76	-4.328	0.00321346	0.0300378
19637	10506786	NM_175472	230594	zinc finger, CCHC domain conta	Zcchc11	0.76	-5.09	0.00129342	0.0158118
19638	10459844	NM_146089	225745	coiled-coil domain containing	Ccdc5	0.76	-3.529	0.00915692	0.0637517
19639	10494023	NM_011281	19885	RAR-related orphan receptor ga	Rorc	0.76	-3.077	0.0172425	0.0992784
19640	10588043	NM_009034	19660	retinol binding protein 2, cel	Rbp2	0.76	-6.365	0.000335765	0.00611645
19641	10382492	NM_027132	69602	otopetrin 3	Otop3	0.76	-2.74	0.0280897	0.137515
19642	10596347	NM_175025	235574	ATPase, Ca++-sequestering	Atp2c1	0.76	-5.291	0.0010305	0.013395
19643	10415791	NM_026001	67153	ribonuclease H2, subunit B	Rnaseh2b	0.76	-4.237	0.00360472	0.0325163
19644	10496748	ENSMUST00000039517	214804	synapse defective 1, Rho GTPas	Syde2	0.76	-2.906	0.0220389	0.116877
19645	10570771	NM_027338	70160	vacuolar protein sorting 36 (y	Vps36	0.76	-3.618	0.00810579	0.0585345
19646	10556208	NM_020616	57373	RIKEN cDNA D930014E17 gene	D930014E17Rik	0.76	-4.021	0.00475237	0.0397482
19647	10530832	BC017154	56412	RIKEN cDNA 2610024G14 gene	2610024G14Rik	0.76	-5.09	0.00129338	0.0158118
19648	10479672	NM_009326	21400	transcription elongation facto	Tcea2	0.76	-3.574	0.00860438	0.0610135
19649	10420736	NM_201610	382913	nei like 2 (E. coli)	Neil2	0.76	-3	0.0192545	0.106939
19650	10595046	XR_034893	100048639	similar to Glyceraldehyde-3-ph	LOC100048639	0.76	-2.017	0.0823236	0.274433
19651	10430365	NM_009218	20607	somatostatin receptor 3	Sstr3	0.76	-2.942	0.0209452	0.113309
19652	10509514	NM_001099631	230863	SH2 domain containing 5	Sh2d5	0.759	-3.051	0.0178802	0.101492
19653	10567134	NM_172743	233765	pleckstrin homology domain con	Plekha7	0.759	-3.545	0.00895899	0.062808
19654	10587604	NM_027100	69519	RWD domain containing 2A	Rwdd2a	0.759	-3.452	0.0101763	0.0687874
19655	10538290	NM_028035	71982	sorting nexin 10	Snx10	0.759	-3.835	0.00605934	0.0472588
19656	10433988	NM_008223	15160	serine (or cysteine) peptidase	Serpind1	0.759	-2.615	0.0337837	0.155173
19657	10392894	NM_178035	328035	fatty acid desaturase domain f	Fads6	0.758	-3.457	0.010103	0.0685504
19658	10369806	BC087900	73287	RIKEN cDNA 1700040L02 gene	1700040L02Rik	0.758	-3.807	0.00629344	0.0485716
19659	10524052	NM_054071	116701	fibroblast growth factor recep	Fgfrl1	0.758	-5.443	0.000871826	0.0119005
19660	10373834	NM_146013	103655	SEC14-like 4 (S. cerevisiae)	Sec14l4	0.758	-3.897	0.00558553	0.044769
19661	10357950	NM_001081307	329251	protein phosphatase 1, regulat	Ppp1r12b	0.758	-2.396	0.0466987	0.191982
19662	10547531	NM_007544	12122	BH3 interacting domain death a	Bid	0.758	-4.319	0.00324897	0.0302227
19663	10606445	NM_025949	67071	ribosomal protein S6 kinase po	Rps6ka6	0.758	-5.059	0.00133899	0.0161873
19664	10449415	ENSMUST00000056274	319712	RIKEN cDNA C230013L11 gene	C230013L11Rik	0.757	-2.771	0.026848	0.133319
19665	10430861	NM_001104531	545123	cytochrome P450, family 2, sub	Cyp2d11	0.757	-1.821	0.110234	0.328467
19666	10392943	NM_008258	15374	hematological and neurological	Hn1	0.757	-4.121	0.00417656	0.0359859
19667	10582180	NM_001033980	436062	RIKEN cDNA 1700120B06 gene	1700120B06Rik	0.757	-2.639	0.0325906	0.151717
19668	10404737	XM_001472337	637277	similar to 145 kDa nucleolar p	LOC637277	0.757	-5.117	0.00125312	0.0154766
19669	10409434	NM_025828	66890	lectin, mannose-binding 2	Lman2	0.756	-5.031	0.00138331	0.0165621
19670	10366640	BC096681	66225	RIKEN cDNA 1190005P17 gene	1190005P17Rik	0.756	-2.616	0.0337381	0.155049
19671	10476189	NM_207207	99045	mitochondrial ribosomal protei	Mrps26	0.756	-4.519	0.002537	0.0256417
19672	10538087	NM_177736	243371	leucine rich repeat containing	Lrrc61	0.756	-2.686	0.0304291	0.145105
19673	10572097	BC116682	72281	SH2 domain containing 4A	Sh2d4a	0.756	-4.418	0.00287292	0.0280221
19674	10460468	NM_019861	56464	cathepsin F	Ctsf	0.756	-2.263	0.0570194	0.218378

19675	10506870	NM_025334	66073	thioredoxin domain containing	Txndc12	0.756	-3.184	0.0148027	0.0893485
19676	10441954	AK019108	381062	RIKEN cDNA 2210404J11 gene	2210404J11Rik	0.756	-2.276	0.0558601	0.215766
19677	10347364	NM_009509	22349	villin 1	Vil1	0.756	-3.341	0.0118756	0.0762783
19678	10566144	NM_009277	20821	tripartite motif-containing 21	Trim21	0.756	-5.897	0.000537973	0.008531
19679	10567343	NM_023197	66356	RIKEN cDNA 2310008H09 gene	2310008H09Rik	0.756	-4.568	0.00239027	0.024654
19680	10488033	NM_172858	241656	p21 (CDKN1A)-activated kinase	Pak7	0.756	-4.185	0.00384787	0.0340273
19681	10469581	NM_001081006	208618	enhancer trap locus 4	Etl4	0.756	-3.489	0.00966864	0.0664393
19682	10591668	NM_023622	71746	ral guanine nucleotide dissoci	Rgl3	0.756	-5.244	0.00108592	0.0139228
19683	10490833	XM_908050	621504	similar to peptidylprolyl isom	LOC621504	0.756	-1.977	0.0873831	0.284469
19684	10466865	NM_011265	19726	regulatory factor X, 3 (influe	Rfx3	0.755	-4.784	0.00184464	0.0203352
19685	10539310	NM_197992	69837	polycomb group ring finger 1	Pcgf1	0.755	-3.466	0.00998774	0.0680694
19686	10344807	NM_026493	211660	centrosome and spindle pole as	Cspp1	0.755	-3.86	0.00586112	0.0462423
19687	10454881	BC028765	66060	RIKEN cDNA 0610010O12 gene	0610010O12Rik	0.755	-5.643	0.000702026	0.0102795
19688	10498166	AY512944	791313	predicted gene, ENSMUSG0000006	ENSMUSG00000069012	0.755	-3.156	0.0153982	0.092102
19689	10479749	NM_001013376	227522	ribonuclease P/MRP 38 subunit	Rpp38	0.755	-3.319	0.0122418	0.0778362
19690	10551534	NM_207238	233040	F-box protein 27	Fbxo27	0.755	-4.235	0.00361374	0.0325838
19691	10542287	NM_025778	66813	Bcl2-like 14 (apoptosis facili	Bcl2l14	0.755	-3.228	0.0139112	0.0854991
19692	10362314	NM_008983	19272	protein tyrosine phosphatase,	Ptprk	0.755	-5.047	0.00135851	0.0163206
19693	10369993	NM_133994	103140	glutathione S-transferase, the	Gstt3	0.755	-3.074	0.0173255	0.0994394
19694	10533316	NM_026129	67397	endoplasmic reticulum protein	Erp29	0.755	-6.851	0.000211208	0.00458971
19695	10603387	NM_010413	15185	histone deacetylase 6	Hdac6	0.755	-4.337	0.00317829	0.0298542
19696	10578952	AK131860	407795	cDNA sequence BC030870	BC030870	0.755	-2.606	0.0342155	0.156591
19697	10474048	NM_030725	80976	synaptotagmin XIII	Syt13	0.755	-4.875	0.00165743	0.0187471
19698	10411167					0.755	-2.956	0.0205254	0.112026
19699	10445972	NM_145490	224893	cDNA sequence BC011426	BC011426	0.755	-1.77	0.11885	0.344334
19700	10590073	NM_011700	22351	villin-like	Vill	0.755	-3.468	0.00994829	0.0678975
19701	10584549	NM_178227	235281	sodium channel, voltage-gated,	Scn3b	0.755	-2.101	0.0725968	0.253885
19702	10398352					0.754	-1.631	0.145614	0.387145
19703	10601888	NM_011123	18823	proteolipid protein (myelin) 1	Plp1	0.754	-2.782	0.0263978	0.131858
19704	10483326	NM_018852	20274	sodium channel, voltage-gated,	Scn9a	0.754	-2.477	0.0414264	0.177599
19705	10524266	NM_016681	50883	CHK2 checkpoint homolog (S. po	Chek2	0.754	-5.794	0.000599016	0.00921398
19706	10479852	NM_177343	227541	calcium/calmodulin-dependent p	Camk1d	0.754	-3.075	0.0172951	0.0993717
19707	10499854	NM_011309	20193	S100 calcium binding protein A	S100a1	0.754	-2.933	0.0212155	0.114027
19708	10365658	NM_029166	75089	UHRF1 (ICBP90) binding protein	Uhrf1bp1l	0.754	-5.37	0.000944029	0.0126089
19709	10512851	NM_029572	76299	thioredoxin domain containing	Txndc4	0.754	-3.23	0.0138817	0.0854233
19710	10571724	ENSMUST00000074466	676582	predicted gene, ENSMUSG0000006	ENSMUSG00000060559	0.754	-1.959	0.0897231	0.289125
19711	10586180	BC028529	330959	small nuclear RNA activating c	Snapc5	0.754	-3.967	0.00509431	0.0418307
19712	10580183	NM_010499	15936	immediate early response 2	Ier2	0.754	-4.296	0.00334315	0.0308275
19713	10605431	NM_175122	67790	RAB39B, member RAS oncogene fa	Rab39b	0.754	-4.121	0.00417855	0.0359859
19714	10406877	NM_011353	20365	small EDRK-rich factor 1	Serf1	0.754	-5.274	0.00105033	0.0135996
19715	10584535	XR_034073	235279	similar to rRNA-processing pro	LOC235279	0.753	-4.303	0.00331718	0.0306428
19716	10567964	NM_009907	12752	ceroid lipofuscinosis, neurona	Cln3	0.753	-6.143	0.000418465	0.00716699
19717	10442887	BC132383	214931	F-box and leucine-rich repeat	Fbxl16	0.753	-2.786	0.0262477	0.131326
19718	10354649	ENSMUST00000094950	241062	post-GPI attachment to protein	Pgap1	0.753	-5.025	0.0013918	0.0166183
19719	10441456	NM_011523	20975	synaptojanin 2	Synj2	0.753	-3.517	0.00931179	0.0645748
19720	10483381	NM_016866	53416	serine/threonine kinase 39, ST	Stk39	0.752	-4.872	0.00166302	0.0187836
19721	10450640	NM_025878	66973	mitochondrial ribosomal protei	Mrps18b	0.752	-6.864	0.000208726	0.00454979
19722	10376444	NM_030082	78303	histone cluster 3, H2ba	Hist3h2ba	0.752	-4.486	0.00264306	0.0264606
19723	10600765	NM_211138	236899	phosphate cytidylyltransferase	Pcyt1b	0.752	-5.176	0.00117227	0.0147188
19724	10565910	NM_013746	27276	pleckstrin homology domain con	Plekhb1	0.752	-3.243	0.0136265	0.0842945
19725	10365830					0.752	-4.294	0.00335248	0.0308867

19726	10499132	NM_011839	23937	mab-21-like 2 (C. elegans)	Mab21l2	0.752	-4.499	0.00259958	0.0261175
19727	10415952					0.752	-2.059	0.0773388	0.264006
19728	10556581	ENSMUST00000098096	100037281	predicted gene, ENSMUSG0000007	ENSMUSG00000073861	0.752	-2.427	0.0446157	0.186877
19729	10405253	NM_009946	12890	complexin 2	Cplx2	0.751	-3.151	0.0155162	0.0924676
19730	10546346	NM_133928	72170	coiled-coil-helix-coiled-coil-	Chchd4	0.751	-5.029	0.0013855	0.0165789
19731	10407051	XR_031811	100040366	similar to Cytochrome c	LOC100040366	0.751	-5.501	0.000817931	0.0114154
19732	10484584					0.751	-2.008	0.083359	0.276517
19733	10573128	NM_001111304	71310	TBC1 domain family, member 9	Tbc1d9	0.751	-5.69	0.000668142	0.00992775
19734	10528340	NM_009584	22791	DnaJ (Hsp40) homolog, subfamil	Dnajc2	0.751	-5.698	0.00066275	0.0098615
19735	10505982	NM_029347	75578	FGGY carbohydrate kinase domai	Fggy	0.751	-4.123	0.00416801	0.0359268
19736	10452257	NM_025877	66972	solute carrier family 25 (mito	Slc25a23	0.751	-4.451	0.00275684	0.0272896
19737	10441815	NM_013671	20656	superoxide dismutase 2, mitoch	Sod2	0.751	-5.941	0.000514067	0.00824067
19738	10468929	NM_008708	18108	N-myristoyltransferase 2	Nmt2	0.751	-3.426	0.010553	0.0705216
19739	10503186	NM_001081417	320790	chromodomain helicase DNA bind	Chd7	0.75	-3.053	0.0178495	0.101427
19740	10348637	NM_146277	258274	olfactory receptor 1412	Olfr1412	0.75	-1.811	0.11188	0.331046
19741	10366737	XR_031069	674596	similar to 60S ribosomal prote	LOC674596	0.75	-2.638	0.032641	0.151851
19742	10431874	NM_134086	105727	solute carrier family 38, memb	Slc38a1	0.75	-6.624	0.000261312	0.0052421
19743	10398392					0.75	-1.883	0.100481	0.31011
19744	10386070	NM_009720	11927	ATX1 (antioxidant protein 1) h	Atox1	0.75	-6.008	0.00048	0.00785536
19745	10344821	NM_026493	211660	centrosome and spindle pole as	Cspp1	0.75	-3.788	0.00645675	0.0494464
19746	10473494	NM_001011872	258216	olfactory receptor 1034	Olfr1034	0.75	-3.352	0.0116938	0.0755041
19747	10594747	AK147236	100038475	predicted gene, ENSMUSG0000007	ENSMUSG00000074230	0.75	-2.332	0.0514425	0.204879
19748	10412755	XR_033275	667125	similar to Casein kinase 2, al	LOC667125	0.75	-1.964	0.0891277	0.287844
19749	10431210	NM_009528	22422	wingless-related MMTV integrat	Wnt7b	0.75	-4.407	0.00291196	0.0282692
19750	10382189	NM_013475	11818	apolipoprotein H	Apoh	0.75	-2.911	0.0218883	0.116371
19751	10585972					0.75	-2.513	0.0392658	0.171927
19752	10603878	NM_013840	22294	ubiquitously expressed transcr	Uxt	0.75	-2.941	0.0209767	0.11338
19753	10460423	NM_021287	20743	spectrin beta 3	Spnb3	0.749	-4.68	0.00208798	0.0224558
19754	10514650	NM_026348	67733	integrin beta 3 binding protei	Itgb3bp	0.749	-4.153	0.00400706	0.0350414
19755	10383168	ENSMUST00000093902	672511	hypothetical LOC672511	LOC672511	0.749	-3.583	0.00850226	0.0604478
19756	10398420					0.749	-0.584	0.576929	0.79771
19757	10430748	NM_011241	19387	RAN GTPase activating protein	Rangap1	0.749	-4.434	0.00281732	0.0276552
19758	10437778	NM_028761	74108	poly(A)-specific ribonuclease	Parn	0.749	-3.842	0.00600922	0.0469545
19759	10488046					0.749	-2.749	0.0277324	0.136334
19760	10570278					0.749	-3.157	0.0153738	0.09206
19761	10513592	NM_023597	71354	WD repeat domain 31	Wdr31	0.748	-4.09	0.0043454	0.0370182
19762	10433885	NM_007679	12609	CCAAT/enhancer binding protein	Cebpd	0.748	-2.226	0.0602528	0.226406
19763	10397332	NM_145445	217715	eukaryotic translation initiat	Eif2b2	0.748	-6.633	0.000259091	0.00521239
19764	10563068	NM_022999	65116	proline-rich Gla (G-carboxyglu	Prrg2	0.748	-5.163	0.00119037	0.014893
19765	10396694	NM_206534	211151	churchill domain containing 1	Churc1	0.748	-2.317	0.0525618	0.207422
19766	10494574	NM_182997	108097	protein kinase, AMP-activated,	Prkab2	0.748	-5.242	0.00108831	0.0139352
19767	10411646	NM_022011	23894	general transcription factor I	Gtf2h2	0.748	-5.51	0.000810601	0.0113281
19768	10376455	NM_178218	319162	histone cluster 3, H2a	Hist3h2a	0.748	-4.775	0.00186413	0.0204861
19769	10500445	NM_026539	68058	chromodomain helicase DNA bind	Chd11	0.747	-4.581	0.00235214	0.0243912
19770	10452316	NM_009778	12266	complement component 3	C3	0.747	-3.665	0.0076093	0.0560791
19771	10590549	NM_001081188	66446	exosome component 7	Exosc7	0.747	-5.094	0.00128672	0.0158051
19772	10515211	ENSMUST00000106521	75173	RIKEN cDNA 4930544O15 gene	4930544O15Rik	0.747	-2.521	0.0388132	0.170475
19773	10571705	NM_008391	16363	interferon regulatory factor 2	Irf2	0.747	-2.18	0.0644826	0.236295
19774	10415262	NM_133734	28199	WD repeat domain 23	Wdr23	0.747	-2.683	0.0305396	0.14545
19775	10486819	NM_153075	212670	cation channel, sperm associat	Catsper2	0.747	-2.462	0.0423594	0.180211
19776	10357003	NM_178779	320311	ring finger protein 152	Rnf152	0.747	-2.707	0.0294884	0.141867

19777	10575880	NM_054095	117148	N-terminal EF-hand calcium bin	Necab2	0.747	-4.987	0.00145409	0.0169958
19778	10447118	XM_001480757	100043697	hypothetical protein LOC100043	LOC100043697	0.747	-3.767	0.00663596	0.0505655
19779	10360832	ENSMUST00000050306	73363	RIKEN cDNA 1700056E22 gene	1700056E22Rik	0.747	-4.239	0.00359584	0.0324929
19780	10587104	NM_021548	59046	cAMP-regulated phosphoprotein	Arpp19	0.747	-4.912	0.00158756	0.0181641
19781	10518145	ENSMUST00000084200	110593	PR domain containing 2, with Z	Prdm2	0.747	-3.165	0.0152015	0.0912093
19782	10389783	ENSMUST00000092790	791385	predicted gene, ENSMUSG0000006	ENSMUSG00000069765	0.746	-4.279	0.00341701	0.0313038
19783	10403658	NM_010317	14706	guanine nucleotide binding pro	Gng4	0.746	-3.95	0.00521334	0.0424618
19784	10345762	NM_008362	16177	interleukin 1 receptor, type I	Il1r1	0.746	-1.521	0.170798	0.422528
19785	10396608	NM_001005510	319565	synaptic nuclear envelope 2	Syne2	0.746	-2.785	0.026282	0.131435
19786	10385081	AY702092	448829	acidic leucine-rich nuclear ph	Anp32c	0.746	-3.572	0.00863128	0.0610776
19787	10352133	NM_026626	68226	EF-hand calcium binding domain	Efcab2	0.745	-4.878	0.00165104	0.0187283
19788	10397642					0.745	-4.186	0.00384467	0.0340133
19789	10366712	NM_001110218	319468	protein phosphatase 1H (PP2C d	Ppm1h	0.745	-6.495	0.000295831	0.00567095
19790	10510546	NM_023119	13806	enolase 1, alpha non-neuron	Eno1	0.745	-3.748	0.0068107	0.0514316
19791	10399632					0.745	-2.249	0.0582209	0.22161
19792	10598467	NM_138606	18715	proviral integration site 2	Pim2	0.745	-4.525	0.00251782	0.0255333
19793	10403246	XR_030658	667375	similar to COX11 homolog, cyto	LOC667375	0.745	-2.319	0.0524105	0.207062
19794	10458016	NM_008934	19123	protein C	Proc	0.745	-4.571	0.00238069	0.0246076
19795	10376239	AF357392	21454	t-complex protein 1	Tcp1	0.745	-1.472	0.183161	0.440085
19796	10580411					0.744	-4.369	0.00305365	0.0290634
19797	10581910	NM_025781	66817	transmembrane protein 170	Tmem170	0.744	-3.139	0.0157754	0.0934331
19798	10524878	NM_001033311	231668	cDNA sequence BC023744	BC023744	0.744	-4.747	0.00192808	0.0210249
19799	10488060	NM_013822	16449	jagged 1	Jag1	0.744	-2.307	0.0533277	0.209428
19800	10492888					0.744	-3.21	0.0142722	0.0871222
19801	10423825	NM_008056	14368	frizzled homolog 6 (Drosophila	Fzd6	0.744	-3.738	0.00690122	0.0519471
19802	10402606	NM_184109	353326	retrotransposon-like 1	Rtl1	0.744	-5.331	0.000985605	0.01296
19803	10376532	NM_001011740	257886	olfactory receptor 225	Olfr225	0.744	-2.122	0.0703169	0.248459
19804	10599962	NM_001081354	333639	mastermind-like domain contain	Mamld1	0.744	-4.48	0.00266086	0.0265885
19805	10388782					0.743	-1.495	0.177331	0.43172
19806	10532669	NM_172884	243219	RIKEN cDNA 2900026A02 gene	2900026A02Rik	0.743	-3.957	0.00516451	0.0422268
19807	10554487	NM_054085	116904	alpha-kinase 3	Alpk3	0.743	-1.784	0.116276	0.33911
19808	10400293	BC089589	328092	RIKEN cDNA 6530401N04 gene	6530401N04Rik	0.743	-7.188	0.000155416	0.00371308
19809	10448865	NM_172529	214505	N-acetylglucosamine-1-phosphot	Gnptg	0.743	-4.977	0.00147202	0.0171324
19810	10368836					0.743	-4.192	0.00381443	0.0337914
19811	10511444	XM_001472912	100039478	similar to ribosomal protein L	LOC100039478	0.743	-2.498	0.0401229	0.174258
19812	10404218	NM_008156	14756	glycosylphosphatidylinositol s	Gpld1	0.743	-4.503	0.00258759	0.0260286
19813	10424213	NM_199449	387609	zinc fingers and homeoboxes 2	Zhx2	0.743	-6.441	0.000311712	0.00584812
19814	10476702	NM_019787	27054	SEC23B (S. cerevisiae)	Sec23b	0.743	-4.212	0.00371807	0.033241
19815	10545886	BC029200	75541	RIKEN cDNA 1700019G17 gene	1700019G17Rik	0.743	-3.196	0.0145622	0.0884274
19816	10442445	NM_010023	13177	dodecenoyl-Coenzyme A delta is	Dci	0.743	-5.97	0.000498854	0.00808259
19817	10345350					0.742	-3.319	0.0122442	0.0778362
19818	10344799	NM_026493	211660	centrosome and spindle pole as	Cspp1	0.742	-4.271	0.00345126	0.0314812
19819	10527148	NM_146257	243328	solute carrier family 29 (nucl	Slc29a4	0.742	-3.267	0.0131677	0.0823476
19820	10463704	NM_020577	57344	arsenic (+3 oxidation state) m	As3mt	0.742	-2.766	0.0270596	0.13393
19821	10496110	NM_011863	23971	3'-phosphoadenosine 5'-phospho	Papss1	0.742	-4.056	0.00454295	0.0383611
19822	10411882	NM_029447	75805	neurolysin (metallopeptidase M	Nln	0.742	-5.056	0.00134359	0.0162056
19823	10370000	NM_008185	14871	glutathione S-transferase, the	Gstt1	0.742	-2.389	0.0472075	0.193141
19824	10588037	NM_011254	19659	retinol binding protein 1, cel	Rbp1	0.742	-5.396	0.0009181	0.0123645
19825	10383204	ENSMUST00000093902	672511	hypothetical LOC672511	LOC672511	0.742	-1.423	0.19646	0.45698
19826	10381994	NM_001037712	192775	potassium voltage-gated channe	Kcnh6	0.741	-4.307	0.00329957	0.030559
19827	10504668					0.741	-4.579	0.00235792	0.0244392
19828	10568217	BC004623	66422	RIKEN cDNA 2410015N17 gene	2410015N17Rik	0.741	-5.058	0.00134118	0.0162022
19829	10468253	NM_029810	76952	5'-nucleotidase, cytosolic II	Nt5c2	0.741	-3.601	0.00829427	0.0594047

19830	10552156	NM_027897	52428	rhophilin, Rho GTPase binding	Rhpn2	0.741	-4.29	0.00337087	0.0310227
19831	10424853	NM_021555	59053	brain protein 16	Brp16	0.741	-3.191	0.0146558	0.0887615
19832	10438178	BC115678	74685	RIKEN cDNA 4930451C15 gene	4930451C15Rik	0.741	-2.78	0.0264795	0.132141
19833	10404763	ENSMUST00000116419	621976	predicted gene, EG621976	EG621976	0.741	-3.881	0.00570731	0.0453497
19834	10562320	XR_035017	100043866	similar to ribosomal protein L	LOC100043866	0.741	-1.92	0.0951583	0.299766
19835	10538179	NM_172888	243377	seminal vesicle secretory prot	Svs1	0.741	-2.372	0.0484334	0.196802
19836	10501832	NM_008991	19299	ATP-binding cassette, sub-fami	Abcd3	0.741	-5.931	0.000519221	0.00829872
19837	10367641	NM_172308	270685	methylenetetrahydrofolate dehy	Mthfd1l	0.741	-6.347	0.000341802	0.00618755
19838	10426827	NM_001024526	207214	La ribonucleoprotein domain fa	Larp4	0.74	-7.386	0.000130474	0.00329708
19839	10521469					0.74	-2.2	0.0626225	0.231629
19840	10551998					0.74	-3.617	0.00811942	0.0585528
19841	10449312	NM_001122657	100038804	predicted gene, ENSMUSG0000007	ENSMUSG00000073431	0.74	-2.368	0.0487008	0.197418
19842	10448557					0.739	-2.481	0.0411674	0.176883
19843	10563820	ENSMUST00000098414	75744	RIKEN cDNA 6620401M08 gene	6620401M08Rik	0.739	-4.412	0.00289412	0.0281478
19844	10384566					0.739	-4.267	0.00346858	0.031596
19845	10357594	NM_018750	54354	Ras association (RalGDS/AF-6)	Rassf5	0.739	-5.344	0.000971617	0.0128559
19846	10553301	NM_010699	16828	lactate dehydrogenase A	Ldha	0.739	-3.224	0.013999	0.0858692
19847	10366705	XR_034838	668275	similar to glyceraldehyde-3-ph	LOC668275	0.739	-3.111	0.0164294	0.0962129
19848	10397153	NM_134247	171282	acyl-CoA thioesterase 4	Acot4	0.739	-3.53	0.0091454	0.0636925
19849	10364091					0.739	-2.421	0.0450367	0.187748
19850	10500529	NM_016966	236539	3-phosphoglycerate dehydrogena	Phgdh	0.739	-2.269	0.0564515	0.217193
19851	10495163	NM_026013	67171	transmembrane protein 77	Tmem77	0.738	-3.067	0.0174936	0.0999956
19852	10410947	NM_028012	108138	X-ray repair complementing def	Xrcc4	0.738	-2.336	0.0510981	0.203968
19853	10578572	NM_001114311	71069	storkhead box 2	Stox2	0.738	-2.741	0.0280525	0.137429
19854	10474588	BC115477	73024	RIKEN cDNA 2900064A13 gene	2900064A13Rik	0.738	-4.415	0.00288508	0.0280987
19855	10344819	NM_026493	211660	centrosome and spindle pole as	Cspp1	0.738	-4.593	0.00231792	0.024131
19856	10408812	NM_008547	17152	male germ cell-associated kina	Mak	0.738	-3.873	0.00576628	0.045698
19857	10381736	NM_001033212	104582	reprimo-like	Rprml	0.737	-2.419	0.0451684	0.187967
19858	10561721	NM_001081028	74206	signal-induced proliferation-a	Sipa1l3	0.737	-4.796	0.00181873	0.0201231
19859	10568050	NM_007438	11674	aldolase 1, A isoform	Aldoa	0.737	-3.752	0.00677271	0.0513086
19860	10537458	NM_001004182	434008	predicted gene, EG434008	EG434008	0.737	-2.114	0.0712202	0.250729
19861	10347232	NM_009533	22596	X-ray repair complementing def	Xrcc5	0.737	-6.692	0.000245081	0.00503604
19862	10509204	NM_011542	21401	transcription elongation facto	Tcea3	0.737	-6.654	0.000254141	0.00515463
19863	10390001	NM_170671	104601	Mycbp associated protein	Mycbpap	0.737	-3.257	0.013358	0.0831201
19864	10496023	NM_009811	12368	caspase 6	Casp6	0.737	-4.371	0.00304428	0.0290602
19865	10482846	BC062650	227933	coiled-coil domain containing	Ccdc148	0.736	-3.843	0.00599844	0.0469175
19866	10398885	NM_001024602	217882	expressed sequence AW555464	AW555464	0.736	-7.747	9.57557e-05	0.00271766
19867	10370471	NM_053014	28169	1-acylglycerol-3-phosphate O-a	Agpat3	0.736	-4.902	0.00160656	0.0183319
19868	10344637	NM_133826	108664	ATPase, H+ transporting, lysos	Atp6v1h	0.736	-6.053	0.000458097	0.00760508
19869	10572077	ENSMUST00000015051	234344	nuclear assembly factor 1 homo	Naf1	0.736	-2.726	0.0286623	0.138999
19870	10438666					0.735	-2.56	0.0366499	0.163763
19871	10351039	NR_002840	14455	growth arrest specific 5	Gas5	0.735	-2.974	0.0199776	0.109802
19872	10408937	NM_009124	20238	ataxin 1	Atxn1	0.735	-2.426	0.0446947	0.187121
19873	10479973	ENSMUST00000076071	791270	predicted gene, ENSMUSG0000006	ENSMUSG00000062319	0.735	-1.258	0.247667	0.520853
19874	10539358	BC126949	71837	RIKEN cDNA 1700003E16 gene	1700003E16Rik	0.735	-2.027	0.0810244	0.271716
19875	10527306	NM_001081109	231876	lemur tyrosine kinase 2	Lmtk2	0.735	-5.663	0.000687741	0.010129
19876	10415074	NM_080726	140743	rad and gem related GTP bindin	Rem2	0.735	-3.115	0.0163356	0.0959177
19877	10539577	ENSMUST00000095768	20751	sepiapterin reductase	Spr	0.734	-3.762	0.0066788	0.0507973
19878	10577340	NM_181683	353320	defensin beta 37	Defb37	0.734	-1.829	0.108879	0.325713
19879	10580391	NM_028007	71927	integrin alpha FG-GAP repeat c	Itfg1	0.734	-5.722	0.000646162	0.00969655
19880	10373810	NM_173745	75219	dual specificity phosphatase 1	Dusp18	0.734	-5.635	0.000708676	0.0103411
19881	10607143	NM_007603	12338	calpain 6	Capn6	0.733	-3.426	0.0105562	0.0705216
19882	10579649	BC120812	234421	calcium and integrin binding f	Cib3	0.733	-2.916	0.0217353	0.115848

19883	10360789	NM_007853	13244	degenerative spermatocyte homo	Degs1	0.733	-4.352	0.00311773	0.0294554
19884	10499342	NM_029801	76927	RIKEN cDNA 1700021C14 gene	1700021C14Rik	0.733	-4.872	0.00166225	0.0187836
19885	10503170	NM_001081417	320790	chromodomain helicase DNA bind	Chd7	0.733	-5.102	0.00127551	0.0157256
19886	10452110	BC056164	224904	RIKEN cDNA 2410015M20 gene	2410015M20Rik	0.733	-4.114	0.00421274	0.0361943
19887	10428232	NM_199476	382985	ribonucleotide reductase M2 B	Rrm2b	0.733	-4.367	0.00305997	0.0290786
19888	10382625	NM_145438	217325	lethal giant larvae homolog 2	Llgl2	0.733	-4.739	0.00194691	0.021143
19889	10537834	NM_133674	54324	Rho guanine nucleotide exchang	Arhgef5	0.732	-5.607	0.000730066	0.010573
19890	10469536					0.732	-4.809	0.00179029	0.0198551
19891	10457927	XR_031234	433168	similar to ribosomal protein L	LOC433168	0.732	-3.188	0.0147138	0.0890152
19892	10500796					0.732	-0.601	0.566412	0.79227
19893	10596119	NM_001081122	28135	centrosomal protein 63	Cep63	0.732	-7.288	0.000142212	0.00347475
19894	10561918					0.732	-2.008	0.0833973	0.276517
19895	10595371	NM_026122	94353	high mobility group nucleosoma	Hmgn3	0.732	-4.555	0.00242826	0.024948
19896	10571975					0.732	-1.095	0.308555	0.585197
19897	10495820	NM_007980	14079	fatty acid binding protein 2,	Fabp2	0.732	-1.745	0.123209	0.351285
19898	10474411	NM_011699	22343	lin-7 homolog C (C. elegans)	Lin7c	0.732	-6.688	0.000245987	0.0050424
19899	10515822	NM_146713	258708	olfactory receptor 1342	Olfr1342	0.732	-1.937	0.0927529	0.295001
19900	10500677	NM_013486	12481	CD2 antigen	Cd2	0.732	-2.3	0.0539179	0.210728
19901	10572637	BC020119	73711	RIKEN cDNA 1110012M11 gene	1110012M11Rik	0.732	-5.244	0.00108645	0.0139228
19902	10354205	XR_031026	329126	predicted gene, EG329126	EG329126	0.731	-1.801	0.113481	0.333876
19903	10369909					0.731	-1.517	0.171832	0.42401
19904	10413726	NM_009393	21924	troponin C, cardiac/slow skele	Tnnc1	0.731	-3.782	0.00650266	0.0497259
19905	10546452	NM_175314	101401	a disintegrin-like and metallo	Adamts9	0.731	-6.074	0.000448459	0.00750769
19906	10389022	NM_177390	338367	myosin ID	Myo1d	0.731	-4.338	0.00317496	0.0298423
19907	10396652	NM_001002012	15512	heat shock protein 2	Hspa2	0.731	-4.105	0.00426311	0.0365503
19908	10387155	NM_027963	71860	WD repeat domain 16	Wdr16	0.731	-3.93	0.00534818	0.0433763
19909	10544114	NM_010433	15258	homeodomain interacting protei	Hipk2	0.73	-5.64	0.000704823	0.0103062
19910	10464583	NM_013541	14870	glutathione S-transferase, pi	Gstp1	0.73	-4.592	0.00232138	0.0241314
19911	10425966	NM_016843	54138	ataxin 10	Atxn10	0.73	-6.393	0.000326695	0.0060276
19912	10485131	NM_172670	228366	glycosyltransferase-like 1B	Gyltl1b	0.73	-5.015	0.00140906	0.0166908
19913	10349782	NM_028778	74137	NUAK family, SNF1-like kinase,	Nuak2	0.73	-2.987	0.01962	0.108456
19914	10364468	NM_009768	12215	basigin	Bsg	0.73	-6.768	0.000228282	0.00481235
19915	10545065	NM_183183	243385	GPRIN family member 3	Gprin3	0.73	-3.584	0.00849329	0.0604247
19916	10525677	NM_145070	29816	huntingtin interacting protein	Hip1r	0.73	-4.868	0.00167043	0.0188071
19917	10503410	NM_181401	100201	transmembrane protein 64	Tmem64	0.729	-7.498	0.000118351	0.0031086
19918	10547073					0.729	-3.601	0.00829654	0.0594047
19919	10382802	NM_011451	20698	sphingosine kinase 1	Sphk1	0.729	-4.522	0.00252773	0.0256215
19920	10575363	NM_175480	234725	zinc finger protein 612	Zfp612	0.729	-4.533	0.00249542	0.0253791
19921	10573348	NM_007578	12286	calcium channel, voltage-depen	Cacna1a	0.729	-5.596	0.000738423	0.0106575
19922	10461057	NM_054048	104383	REST corepressor 2	Rcor2	0.728	-4.369	0.00305424	0.0290634
19923	10550181					0.728	-1.742	0.123831	0.35211
19924	10541695	NM_145130	14792	membrane bound O-acyltransfera	Mboat5	0.728	-5.116	0.00125567	0.015499
19925	10505996	NM_001113412	75578	FGGY carbohydrate kinase domai	Fggy	0.728	-1.785	0.116227	0.339013
19926	10422219					0.728	-2.57	0.0360736	0.162044
19927	10587792	NM_011636	22038	phospholipid scramblase 1	Plscr1	0.728	-6.011	0.000478322	0.00783396
19928	10445796	BC022574	106821	expressed sequence AI314976	AI314976	0.728	-4.975	0.00147465	0.0171413
19929	10344809	NM_026493	211660	centrosome and spindle pole as	Cspp1	0.728	-2.796	0.0258829	0.130308
19930	10497048					0.728	-5.484	0.000833634	0.0115341
19931	10544106					0.728	-2.371	0.0484905	0.196834
19932	10379163	NM_201406	276846	phosphatidylinositol glycan an	Pigs	0.728	-5.61	0.000727668	0.0105559
19933	10538420	NM_180678	353172	glycyl-tRNA synthetase	Gars	0.727	-5.811	0.000588188	0.00910442

19934	10503222	NM_001081417	320790	chromodomain helicase DNA bind	Chd7	0.727	-4.271	0.00345115	0.0314812
19935	10379153	NM_009657	11676	aldolase 3, C isoform	Aldoc	0.727	-5.878	0.000548788	0.00862719
19936	10352867	NM_008882	18845	plexin A2	Plxna2	0.727	-3.011	0.0189497	0.105746
19937	10402142	NM_026681	68339	coiled-coil domain containing	Ccdc88c	0.727	-4.974	0.00147625	0.0171505
19938	10485027	NM_010168	14061	coagulation factor II	F2	0.727	-4.238	0.00359916	0.0324929
19939	10469941					0.726	-2.02	0.0819438	0.273497
19940	10507286	NM_008389	16351	IAP promoted placental gene	Ipp	0.726	-6.941	0.000194324	0.00432822
19941	10489569	NM_011125	18830	phospholipid transfer protein	Pltp	0.726	-5.563	0.000765217	0.0109028
19942	10351259	NM_054087	116914	solute carrier family 19 (thia	Slc19a2	0.726	-3.048	0.0179641	0.101886
19943	10392120	NM_031878	83796	SWI/SNF related, matrix associ	Smarcd2	0.726	-6.054	0.000457857	0.00760508
19944	10356333	NR_002851	80828	small nucleolar RNA, C/D box 8	Snord82	0.726	-3.134	0.0159001	0.0940661
19945	10582973	NM_026962	69149	kelch repeat and BTB (POZ) dom	Kbtbd3	0.726	-5.019	0.0014018	0.016658
19946	10515797	NM_172383	230678	transmembrane protein 125	Tmem125	0.726	-2.738	0.0281769	0.137705
19947	10572730	NM_133358	170938	zinc finger protein 617	Zfp617	0.726	-4.801	0.00180811	0.0200266
19948	10588263	NM_033314	24059	solute carrier organic anion t	Slco2a1	0.726	-3.665	0.00760457	0.0560791
19949	10401149	NM_013738	27260	pleckstrin 2	Plek2	0.726	-2.468	0.04199	0.179108
19950	10398380					0.726	-1.05	0.327784	0.604012
19951	10580537	NM_010241	14339	thymoma viral proto-oncogene 1	Aktip	0.725	-4.438	0.00280415	0.0275644
19952	10545528	AF216308	56176	phosphatidylinositol glycan an	Pigp	0.725	-3.751	0.00677658	0.0513195
19953	10593671	ENSMUST00000047765	235380	Dmx-like 2	Dmxl2	0.725	-5.695	0.000664335	0.00987813
19954	10416004	NM_199029	380912	zinc finger protein 395	Zfp395	0.725	-4.323	0.00323309	0.0301509
19955	10603026	NM_018737	55936	cytidine 5'-triphosphate synth	Ctps2	0.725	-7.318	0.000138488	0.00342078
19956	10595753	NM_011643	22063	transient receptor potential c	Trpc1	0.725	-2.996	0.019368	0.107409
19957	10360914	NM_146106	226791	lysophospholipase-like 1	Lyplal1	0.725	-4.047	0.00459405	0.0387152
19958	10537722	NM_175408	109218	transmembrane protein 139	Tmem139	0.724	-6.983	0.000187092	0.00422236
19959	10582699	BC023675	66523	RIKEN cDNA 2810004N23 gene	2810004N23Rik	0.724	-5.68	0.000674913	0.00997927
19960	10557459	NM_011952	26417	mitogen-activated protein kina	Mapk3	0.724	-6.501	0.000294136	0.00565571
19961	10440099	NM_018784	54613	ST3 beta-galactoside alpha-2,3	St3gal6	0.724	-4.169	0.00392673	0.0344939
19962	10389680	NM_054043	76626	Musashi homolog 2 (Drosophila)	Msi2	0.724	-4.568	0.00239031	0.024654
19963	10473976	BC094315	241547	RIKEN cDNA D230010M03 gene	D230010M03Rik	0.724	-4.98	0.00146751	0.0171053
19964	10473089	NM_001080711	381375	deafness, autosomal recessive	Dfnb59	0.723	-3.059	0.01768	0.100778
19965	10383982	NM_001080924	407821	zinc and ring finger 3	Znrf3	0.723	-4.946	0.00152573	0.0176188
19966	10559341	ENSMUST00000105902	210274	SH3/ankyrin domain gene 2	Shank2	0.723	-2.696	0.0299457	0.143448
19967	10553163	NM_153057	211548	nodal modulator 1	Nomo1	0.722	-7.266	0.000144958	0.00352702
19968	10386604	NM_009171	20425	serine hydroxymethyltransferas	Shmt1	0.722	-5.362	0.000952517	0.0126746
19969	10353034	NR_004410	266793	RNA, U87 small nucleolar	Rnu87	0.722	-2.271	0.0562891	0.216807
19970	10586172					0.722	-0.969	0.363696	0.635063
19971	10598032					0.722	-2.151	0.0673657	0.242464
19972	10532892	ENSMUST00000112160	66236	RIKEN cDNA 1500011B03 gene	1500011B03Rik	0.721	-4.992	0.00144647	0.0169348
19973	10516765	NM_172702	230779	serine incorporator 2	Serinc2	0.721	-5.704	0.000658154	0.0098277
19974	10462918	NM_175507	240660	transmembrane protein 20	Tmem20	0.721	-3.378	0.0112814	0.0735307
19975	10430370	XM_891575	626952	predicted gene, EG626952	EG626952	0.721	-3.928	0.00536052	0.043443
19976	10551803	NM_001033355	243905	zinc finger protein 568	Zfp568	0.721	-6.044	0.000462327	0.00764304
19977	10503259	NM_021897	60599	transformation related protein	Trp53inp1	0.721	-5.07	0.00132198	0.016024
19978	10419578	NM_013864	29811	N-myc downstream regulated gen	Ndrg2	0.721	-4.66	0.00213902	0.0228537
19979	10376201	NM_001083929	14778	glutathione peroxidase 3	Gpx3	0.72	-5.215	0.00112256	0.0142129
19980	10475324	NM_009897	12716	creatine kinase, mitochondrial	Ckmt1	0.72	-5.544	0.00078116	0.0110457
19981	10489343	ENSMUST00000114755	30963	protein tyrosine phosphatase-l	Ptpla	0.72	-2.647	0.0321949	0.150637
19982	10606436	NM_016710	50887	nucleosome binding protein 1	Nsbp1	0.72	-6.012	0.00047784	0.00783213
19983	10503659	NM_010141	13841	Eph receptor A7	Epha7	0.72	-2.15	0.0674764	0.242722
19984	10495826	NM_024461	67704	RIKEN cDNA 1810037I17 gene	1810037I17Rik	0.72	-4.921	0.00157041	0.0180265
19985	10347193	NM_026195	108147	5-aminoimidazole-4-	Atic	0.719	-6.538	0.000283884	0.00551694

				carboxamide					
19986	10396671	NM_153804	263406	pleckstrin homology domain con	Plekhg3	0.719	-3.91	0.0054927	0.0441924
19987	10531256	ENSMUST00000088076	100798	expressed sequence AU017193	AU017193	0.719	-2.563	0.0364411	0.163209
19988	10512949	NM_013454	11303	ATP-binding cassette, sub-fami	Abca1	0.719	-4.139	0.00407902	0.0354634
19989	10585347	BC115639	75311	RIKEN cDNA 4930550C14 gene	4930550C14Rik	0.719	-3.261	0.0132732	0.0827874
19990	10494751					0.719	-6.166	0.000408793	0.00705019
19991	10423363	NM_020332	11732	progressive ankylosis	Ank	0.719	-2.893	0.0224652	0.118337
19992	10562181	NM_017405	54135	lipolysis stimulated lipoprote	Lsr	0.719	-6.379	0.000331088	0.00606651
19993	10571362	NM_001039220	621080	expressed sequence AI429214	AI429214	0.719	-3.637	0.00790513	0.0575176
19994	10516007	NM_172700	230709	zinc metallopeptidase, STE24 h	Zmpste24	0.719	-5.251	0.00107822	0.0138505
19995	10416657	NM_007920	13709	E74-like factor 1	Elf1	0.718	-6.122	0.000427562	0.00726718
19996	10479698	NM_008665	17932	myelin transcription factor 1	Myt1	0.718	-3.585	0.00848484	0.0604052
19997	10595573	NM_172926	244962	sorting nexin 14	Snx14	0.718	-6.808	0.000219817	0.00469892
19998	10576569	NM_145608	234878	cDNA sequence BC021891	BC021891	0.718	-5.738	0.000635262	0.00959427
19999	10553413	NM_133740	71974	protein arginine N-methyltrans	Prmt3	0.718	-7.472	0.000121074	0.00314805
20000	10565018	NM_016721	29875	IQ motif containing GTPase act	Iqgap1	0.718	-4.857	0.0016918	0.018997
20001	10415332	NM_020062	56739	REC8 homolog (yeast)	Rec8	0.718	-4.812	0.00178552	0.0198283
20002	10519012	NM_001112744	230972	Rho guanine nucleotide exchang	Arhgef16	0.718	-3.844	0.00598702	0.0469024
20003	10604038	NM_001081956	338351	splicing factor, arginine/seri	Sfrs17b	0.718	-3.356	0.0116278	0.0752784
20004	10448307	NM_013749	27279	tumor necrosis factor receptor	Tnfrsf12a	0.718	-3.554	0.00884193	0.0621917
20005	10466304	NM_172442	207521	deltex 4 homolog (Drosophila)	Dtx4	0.717	-4.156	0.00399566	0.0349831
20006	10402994	XM_975252	674110	similar to Ig heavy chain V re	LOC674110	0.717	-1.627	0.146417	0.388184
20007	10524941	NM_145564	231670	F-box protein 21	Fbxo21	0.717	-6.469	0.000303225	0.00576563
20008	10583817	NM_001082532	66268	phosphatidylinositol glycan an	Pigyl	0.717	-5.674	0.000679256	0.0100365
20009	10549877					0.717	-4.337	0.00317562	0.0298423
20010	10504337	NM_139305	230099	carbonic anhydrase 9	Car9	0.717	-2.186	0.0639215	0.234849
20011	10554819	NM_181407	109264	malic enzyme 3, NADP(+)-depend	Me3	0.717	-3.653	0.00772892	0.0566947
20012	10451893	NM_145934	106766	signal transducing adaptor fam	Stap2	0.717	-4.695	0.00205203	0.0221255
20013	10547976	NM_145391	213233	TAP binding protein-like	Tapbpl	0.716	-4.452	0.00275372	0.0272715
20014	10514510	NM_010008	13110	cytochrome P450, family 2, sub	Cyp2j6	0.716	-4.897	0.00161439	0.0183915
20015	10368720	NM_001114332	72472	solute carrier family 16 (mono	Slc16a10	0.716	-6.114	0.000431044	0.00729643
20016	10552140	NM_007678	12606	CCAAT/enhancer binding protein	Cebpa	0.716	-4.501	0.00259359	0.0260765
20017	10378286	NM_008399	16407	integrin, alpha E, epithelial-	Itgae	0.716	-5.094	0.0012862	0.0158051
20018	10515425					0.716	-2.183	0.064194	0.235564
20019	10555323	NM_177161	320452	procollagen-proline, 2-oxoglut	P4ha3	0.715	-1.737	0.124734	0.353522
20020	10433656	ENSMUST00000100178	100038483	predicted gene, ENSMUSG0000007	ENSMUSG00000075401	0.715	-6.466	0.000304113	0.00577733
20021	10587012	NM_001114328	72278	cell cycle progression 1	Ccpg1	0.715	-7.076	0.00017184	0.00400153
20022	10503208	NM_001081417	320790	chromodomain helicase DNA bind	Chd7	0.715	-4.104	0.00427078	0.0365593
20023	10501734	NM_023245	114301	palmdelphin	Palmd	0.715	-2.954	0.0205774	0.112161
20024	10396511	NM_001005510	319565	synaptic nuclear envelope 2	Syne2	0.714	-6.456	0.000307319	0.00580546
20025	10432190	NM_007405	11512	adenylate cyclase 6	Adcy6	0.714	-6.325	0.000349286	0.00627469
20026	10384670					0.714	-2.146	0.0678281	0.243316
20027	10589368	NM_172775	235611	plexin B1	Plxnb1	0.714	-6.096	0.000438913	0.00738884
20028	10364784	NM_139292	70335	receptor accessory protein 6	Reep6	0.714	-7.674	0.000101826	0.00281072
20029	10502951	NM_007382	11364	acyl-Coenzyme A dehydrogenase,	Acadm	0.713	-7.307	0.00013985	0.00344063
20030	10575775	ENSMUST00000039866	74440	RIKEN cDNA 4933407C03 gene	4933407C03Rik	0.713	-4.533	0.00249407	0.0253776
20031	10505008	NM_133891	100434	solute carrier family 44, memb	Slc44a1	0.713	-3.157	0.0153731	0.09206
20032	10452892	NM_133747	72722	RIKEN cDNA 2810405J04 gene	2810405J04Rik	0.713	-5.09	0.00129241	0.0158118
20033	10362672	XM_986164	666342	predicted gene, EG666342	EG666342	0.713	-2.996	0.0193725	0.107409
20034	10590830	BC119072	234915	cDNA sequence AK129341	AK129341	0.713	-4.044	0.00461044	0.0388379
20035	10488589	NM_028666	73847	RIKEN cDNA 5430432M24 gene	5430432M24Rik	0.713	-3.618	0.00810419	0.0585345

20036	10383192	ENSMUST00000093902	672511	hypothetical LOC672511	LOC672511	0.713	-2.449	0.043156	0.182497
20037	10526241	NM_009902	12739	claudin 3	Cldn3	0.712	-5.268	0.00105707	0.0136785
20038	10368011	NM_025418	66201	Vps20-associated 1 homolog (S.	Vta1	0.712	-4.877	0.00165373	0.0187387
20039	10472860	NM_019688	56508	Rap guanine nucleotide exchang	Rapgef4	0.712	-5.442	0.000872555	0.0119016
20040	10443131	NM_080553	16440	inositol 1,4,5-triphosphate re	Itpr3	0.712	-7.232	0.000149509	0.00360048
20041	10403558	NM_026184	67475	ERO1-like beta (S. cerevisiae)	Ero1lb	0.712	-5.631	0.000711736	0.0103714
20042	10513143	ENSMUST00000075637	545622	protein tyrosine phosphatase,	Ptpn3	0.712	-2.798	0.0258198	0.130201
20043	10478924	ENSMUST00000063891	791354	predicted gene, ENSMUSG0000005	ENSMUSG00000052368	0.712	-4.018	0.00476882	0.0397916
20044	10408767	NM_134060	108652	solute carrier family 35, memb	Slc35b3	0.712	-6.174	0.000405665	0.00700767
20045	10396237	ENSMUST00000045907	76967	RIKEN cDNA 2700049A03 gene	2700049A03Rik	0.711	-6.288	0.000362158	0.00644567
20046	10583314	BC056964	75316	Josephin domain containing 3	Josd3	0.711	-6.126	0.000425617	0.00723994
20047	10538638					0.711	-3.001	0.0192177	0.106791
20048	10604922	NM_001033328	236848	cDNA sequence BC023829	BC023829	0.711	-5.93	0.000519651	0.00829872
20049	10366630	NM_026617	68212	transmembrane BAX inhibitor mo	Tmbim4	0.71	-7.565	0.000111747	0.0030099
20050	10398344					0.71	-4.396	0.00295405	0.0284299
20051	10395932	NM_146034	217615	CTAGE family, member 5	Ctage5	0.71	-6.697	0.000244017	0.00502386
20052	10491877	NM_028667	73852	DNA segment, Chr 3, ERATO Doi	D3Ertd751e	0.71	-2.443	0.0435595	0.18358
20053	10403112	NM_010060	13411	dynein, axonemal, heavy chain	Dnahc11	0.71	-5.293	0.00102809	0.0133936
20054	10365845	NM_053072	13998	FYVE, RhoGEF and PH domain con	Fgd6	0.709	-4.073	0.0044415	0.0376095
20055	10360764	NM_010135	13800	enabled homolog (Drosophila)	Enah	0.709	-8.168	6.76749e-05	0.00211667
20056	10438909	XM_001480958	224088	ATPase type 13A3	Atp13a3	0.709	-2.231	0.0597886	0.225222
20057	10482181	NM_009261	20744	spermatid perinuclear RNA bind	Strbp	0.709	-5.722	0.000645828	0.00969655
20058	10420591					0.709	-4.799	0.00181286	0.0200687
20059	10361926	NM_008580	26408	mitogen-activated protein kina	Map3k5	0.709	-4.783	0.00184756	0.0203462
20060	10568930	NM_026928	69064	RIKEN cDNA 1810014F10 gene	1810014F10Rik	0.708	-5.956	0.000506074	0.00816204
20061	10389005	NM_183275	68550	RIKEN cDNA 1110002N22 gene	1110002N22Rik	0.708	-6.684	0.00024695	0.00504981
20062	10476443	NM_013829	18798	phospholipase C, beta 4	Plcb4	0.707	-2.285	0.0551473	0.214227
20063	10437236	BC056174	245305	predicted gene, EG245305	EG245305	0.707	-3.095	0.016813	0.0976362
20064	10497209	NM_025434	66230	mitochondrial ribosomal protei	Mrps28	0.707	-5.945	0.000511642	0.00821424
20065	10570437	NM_025785	66822	F-box protein 25	Fbxo25	0.707	-4.009	0.00482367	0.04017
20066	10416850	NM_022886	64929	sciellin	Scel	0.707	-3.434	0.0104265	0.0699422
20067	10473058	NM_145525	99031	oxysterol binding protein-like	Osbpl6	0.707	-3.39	0.0110898	0.0728453
20068	10442199	NM_011760	22712	zinc finger protein 54	Zfp54	0.707	-3.317	0.0122709	0.0779612
20069	10358027	NM_007921	13710	E74-like factor 3	Elf3	0.707	-4.016	0.00478048	0.0398731
20070	10524955	NM_021344	57816	tescalcin	Tesc	0.707	-3.679	0.00746764	0.055305
20071	10439206					0.707	-1.412	0.199687	0.461464
20072	10553324	NM_026436	67893	transmembrane protein 86A	Tmem86a	0.707	-6.583	0.00027191	0.00536314
20073	10513164	ENSMUST00000075637	545622	protein tyrosine phosphatase,	Ptpn3	0.707	-6.58	0.000272698	0.00536864
20074	10503168	NM_001081417	320790	chromodomain helicase DNA bind	Chd7	0.707	-3.797	0.00637694	0.0490168
20075	10520842	NM_181279	107976	brain and reproductive organ-e	Bre	0.707	-4.977	0.00147195	0.0171324
20076	10400023	NM_025359	66109	tetraspanin 13	Tspan13	0.706	-5.043	0.00136467	0.0163668
20077	10425421	NM_145986	213956	expressed sequence AW544981	AW544981	0.706	-3.068	0.0174536	0.0999022
20078	10439285	AK133264	627962	predicted gene, EG627962	EG627962	0.706	-2.257	0.0575378	0.219758
20079	10600777	ENSMUST00000088107	385493	expressed sequence AU015836	AU015836	0.706	-4.626	0.00222887	0.0235165
20080	10491835	NM_001040399	214048	La ribonucleoprotein domain fa	Larp2	0.706	-3.794	0.00639991	0.0491
20081	10561927	NM_007467	11803	amyloid beta (A4) precursor-li	Aplp1	0.705	-5.019	0.00140208	0.016658
20082	10532680	NM_172718	52850	small G protein signaling modu	Sgsm1	0.705	-7.757	9.4905e-05	0.00270806
20083	10503182	NM_001081417	320790	chromodomain helicase DNA bind	Chd7	0.705	-2.566	0.0363053	0.162739
20084	10363669	NM_013888	30045	DnaJ (Hsp40) homolog, subfamil	Dnajc12	0.705	-7.622	0.000106427	0.00290359
20085	10548598					0.705	-3.748	0.00680307	0.0514096
20086	10464084	NM_009333	21416	transcription factor 7-like 2	Tcf7l2	0.705	-5.342	0.000974311	0.0128594

20087	10603814	NM_177353	236727	solute carrier family 9 (sodiu	Slc9a7	0.705	-2.75	0.0276855	0.13614
20088	10556528	NM_011055	18576	phosphodiesterase 3B, cGMP-inh	Pde3b	0.704	-4.191	0.00381729	0.0337914
20089	10424086	NM_172816	239436	solute carrier family 30 (zinc	Slc30a8	0.704	-3.067	0.0174868	0.0999956
20090	10422844	NM_010275	14573	glial cell line derived neurot	Gdnf	0.704	-5.55	0.00077585	0.0110024
20091	10427496	NM_178748	268780	EGF-like, fibronectin type III	Egflam	0.704	-3.975	0.00504302	0.0415985
20092	10387625	NM_009601	11443	cholinergic receptor, nicotini	Chrnb1	0.704	-4.058	0.00452729	0.0382594
20093	10598091					0.703	-5	0.00143282	0.0168502
20094	10517727	NM_173427	242721	kelch domain containing 7A	Klhdc7a	0.703	-3.811	0.00625985	0.0483943
20095	10364056	NM_008116	14598	gamma-glutamyltransferase 1	Ggt1	0.703	-3.758	0.00671195	0.0509761
20096	10557177	NM_008855	18751	protein kinase C, beta 1	Prkcb1	0.703	-3.26	0.0133041	0.0828894
20097	10532896	NM_181075	330173	RIKEN cDNA 2610524H06 gene	2610524H06Rik	0.703	-5.558	0.000769619	0.0109508
20098	10501555	NM_007446	11722	amylase 1, salivary	Amy1	0.703	-4.939	0.00153863	0.0177387
20099	10427235	NM_025385	66151	proline rich 13	Prr13	0.703	-4.402	0.00292858	0.0283136
20100	10439114	NM_178378	69707	IQ motif containing G	Iqcg	0.702	-2.763	0.0271627	0.134251
20101	10352576	NM_011935	26381	estrogen-related receptor gamm	Esrrg	0.702	-2.789	0.0261439	0.130964
20102	10525829					0.702	-3.242	0.0136451	0.0843112
20103	10454651					0.702	-3.024	0.018603	0.104445
20104	10367221	NM_133997	103161	apolipoprotein F	Apof	0.702	-4.584	0.00234461	0.024337
20105	10472933	NM_029022	74616	secernin 3	Scrn3	0.702	-5.179	0.00116899	0.0147079
20106	10356968	NM_013626	18484	peptidylglycine alpha-amidatin	Pam	0.702	-5.336	0.000981019	0.0129238
20107	10366266	NM_054056	114774	PRKC, apoptosis, WT1, regulato	Pawr	0.701	-3.757	0.0067263	0.0510347
20108	10401630	NM_025421	66204	acylphosphatase 1, erythrocyte	Acyp1	0.701	-4.234	0.00361711	0.0326002
20109	10437483	NM_133185	66049	rogdi homolog (Drosophila)	Rogdi	0.701	-5.616	0.000722568	0.0104931
20110	10344801	NM_026493	211660	centrosome and spindle pole as	Cspp1	0.701	-4.34	0.00316676	0.0298116
20111	10576639	NM_008737	18186	neuropilin 1	Nrp1	0.701	-5.573	0.000757187	0.0108175
20112	10503176	NM_001081417	320790	chromodomain helicase DNA bind	Chd7	0.701	-2.882	0.022843	0.119939
20113	10414093	NM_008133	14661	glutamate dehydrogenase 1	Glud1	0.701	-5.576	0.00075498	0.0108152
20114	10365136	NM_010347	14797	amino-terminal enhancer of spl	Aes	0.701	-7.187	0.00015559	0.00371308
20115	10383198	ENSMUST00000093902	672511	hypothetical LOC672511	LOC672511	0.701	-2.972	0.020038	0.109926
20116	10603316	AF038507	68355	RIKEN cDNA 2010204K13 gene	2010204K13Rik	0.7	-5.681	0.000674646	0.00997927
20117	10604661	XM_001478226	100047705	similar to Atf1 protein	LOC100047705	0.7	-3.435	0.0104197	0.0699412
20118	10394082	BC024349	66179	RIKEN cDNA 1110031I02 gene	1110031I02Rik	0.7	-7.457	0.000122626	0.00316968
20119	10545130	NM_007836	13197	growth arrest and DNA-damage-i	Gadd45a	0.7	-2.066	0.0764439	0.262093
20120	10439732	ENSMUST00000089478	433022	phosphatidylinositol-specific	Plcxd2	0.7	-5.169	0.00118201	0.0148235
20121	10576610	NM_033620	93742	par-3 (partitioning defective	Pard3	0.699	-6.478	0.000300806	0.00574459
20122	10516932	NM_144907	230784	sestrin 2	Sesn2	0.699	-4.389	0.00297884	0.0286164
20123	10530467	NM_133921	100978	nuclear transcription factor,	Nfxl1	0.699	-5.015	0.00140801	0.0166877
20124	10373577	NM_024180	66844	ORM1-like 2 (S. cerevisiae)	Ormdl2	0.698	-5.573	0.0007569	0.0108175
20125	10425257	NM_027231	69833	polymerase (RNA) II (DNA direc	Polr2f	0.698	-4.364	0.00307049	0.0291524
20126	10587262	NM_172925	244923	kelch-like 31 (Drosophila)	Klhl31	0.698	-6.224	0.000385754	0.00675756
20127	10369844	NM_031397	83675	bicaudal C homolog 1 (Drosophi	Bicc1	0.698	-3.518	0.00929218	0.0644811
20128	10447167	NM_054082	116871	metastasis associated 3	Mta3	0.698	-5.561	0.000767278	0.0109248
20129	10490815	XR_031642	545500	similar to ubiquitin specific	LOC545500	0.698	-2.131	0.0694576	0.246984
20130	10547471	NM_198884	330406	beta-1,4-N-acetyl-galactosamin	B4galnt3	0.698	-4.21	0.00372672	0.0332773
20131	10375667	NM_021540	59044	ring finger protein 130	Rnf130	0.698	-6.751	0.000231804	0.00486719
20132	10401891	NM_175367	108800	stonin 2	Ston2	0.697	-6.555	0.000279192	0.00544077
20133	10453636	NM_153153	225115	supervillin	Svil	0.697	-2.568	0.0361689	0.162368
20134	10478540	NM_001039501	629756	WAP four-disulfide core domain	Wfdc10	0.697	-4.521	0.0025326	0.0256417
20135	10476728	NM_025314	66044	D-tyrosyl-tRNA deacylase 1 hom	Dtd1	0.697	-6.713	0.000240296	0.00499098
20136	10389581	NM_001005341	77864	yippee-like 2 (Drosophila)	Ypel2	0.697	-5.548	0.000777546	0.0110191

20137	10409240	NM_013660	20354	sema domain, immunoglobulin do	Sema4d	0.697	-7.386	0.000130517	0.00329708
20138	10558134	NM_133942	101476	pleckstrin homology domain con	Plekha1	0.697	-4.476	0.00267435	0.0266854
20139	10398693	AF357387	217869	eukaryotic translation initiat	Eif5	0.696	-3.207	0.014337	0.0874613
20140	10396270	NM_021532	59036	dapper homolog 1, antagonist o	Dact1	0.695	-3.543	0.00897821	0.0628593
20141	10441753	NM_008877	18815	plasminogen	Plg	0.695	-6.578	0.00027317	0.00537028
20142	10578155					0.695	-3.283	0.0128827	0.0809488
20143	10420131	NM_019519	56187	Rab geranylgeranyl transferase	Rabggta	0.695	-7.043	0.000177136	0.00407992
20144	10389699					0.695	-2.066	0.0765239	0.26224
20145	10371332	NM_153543	216188	aldehyde dehydrogenase 1 famil	Aldh1l2	0.695	-5.01	0.0014168	0.0167544
20146	10373826	NM_016922	53897	galactose-3-O-sulfotransferase	Gal3st1	0.695	-3.602	0.00828772	0.0593818
20147	10601328	NM_001081189	331487	uracil phosphoribosyltransfera	Uprt	0.695	-5.259	0.00106765	0.0137397
20148	10361790	NM_025799	66848	fucosidase, alpha-L- 2, plasma	Fuca2	0.695	-5.413	0.000900322	0.0121483
20149	10490302	ENSMUST00000108923	353208	RIKEN cDNA 2810021G02 gene	2810021G02Rik	0.695	-1.83	0.108717	0.325457
20150	10506571	NM_053272	74754	24-dehydrocholesterol reductas	Dhcr24	0.695	-4.116	0.00420339	0.0361433
20151	10362069	ENSMUST00000071008	432436	predicted gene, EG432436	EG432436	0.694	-4.918	0.00157633	0.0180846
20152	10352815	NM_016851	54139	interferon regulatory factor 6	Irf6	0.694	-7.301	0.00014063	0.00344552
20153	10398358					0.694	-2.011	0.083057	0.276162
20154	10450197	NR_004051	81497	butyrophilin-like 5	Btnl5	0.694	-1.771	0.118633	0.343944
20155	10416793	NM_016723	50933	ubiquitin carboxyl-terminal es	Uchl3	0.694	-6.465	0.000304645	0.00578223
20156	10490724	NM_172676	229011	sterile alpha motif domain con	Samd10	0.694	-5.513	0.000807777	0.0113035
20157	10366376	NM_178278	353025	calcyphosphine 2	Caps2	0.694	-3.761	0.00668904	0.0508569
20158	10546706	NM_019743	56353	RING1 and YY1 binding protein	Rybp	0.694	-2.517	0.0390189	0.171165
20159	10447056	NM_027455	70536	glutaminyl-peptide cyclotransf	Qpct	0.694	-3.617	0.00811458	0.0585528
20160	10508887	NM_011850	23957	nuclear receptor subfamily 0,	Nr0b2	0.693	-6.565	0.000276456	0.00540246
20161	10575616	AK134873	93739	gamma-aminobutyric acid (GABA-	Gabarapl2	0.693	-2.739	0.0281477	0.137618
20162	10359034	NM_001024945	104009	quiescin Q6 sulfhydryl oxidase	Qsox1	0.693	-3.6	0.00830685	0.0594584
20163	10463729					0.693	-3.499	0.00954475	0.0657453
20164	10390640	NM_011771	22780	IKAROS family zinc finger 3	Ikzf3	0.693	-4.621	0.00224212	0.0236267
20165	10569149	NM_177280	320871	RIKEN cDNA B230206H07 gene	B230206H07Rik	0.693	-5.929	0.000520527	0.00830643
20166	10585978					0.693	-3.003	0.0191732	0.106655
20167	10587023	NM_023635	11891	RAB27A, member RAS oncogene fa	Rab27a	0.692	-3.921	0.00541417	0.0437454
20168	10580955					0.692	-4.124	0.00416161	0.0359141
20169	10393166	NM_009180	20446	ST6 (alpha-N-acetyl-neuraminyl	St6galnac2	0.692	-3.802	0.00633688	0.0488424
20170	10505917	XR_033774	664840	similar to hCG1640785	LOC664840	0.692	-1.83	0.108648	0.325457
20171	10406881	NM_011420	20595	survival motor neuron 1	Smn1	0.692	-3.968	0.00508783	0.0417938
20172	10416800	NM_201529	380928	LIM domain only 7	Lmo7	0.691	-2.781	0.0264365	0.13202
20173	10481056	NM_008714	18128	Notch gene homolog 1 (Drosophi	Notch1	0.691	-7.677	0.000101538	0.0028101
20174	10569057	NM_145135	107702	ribonuclease/angiogenin inhibi	Rnh1	0.691	-6.245	0.000378056	0.00663376
20175	10388238	NM_025318	66048	transmembrane protein 93	Tmem93	0.691	-5.887	0.000543678	0.00859115
20176	10511429	NM_007592	12319	carbonic anhydrase 8	Car8	0.691	-7.738	9.64561e-05	0.00272292
20177	10422512	BC006662	223267	cDNA sequence BC006662	BC006662	0.691	-5.177	0.00117071	0.0147079
20178	10390209	NM_009951	140486	insulin-like growth factor 2 m	Igf2bp1	0.691	-4.154	0.00400326	0.0350352
20179	10421648	NM_026232	67554	solute carrier family 25, memb	Slc25a30	0.691	-6.419	0.000318527	0.00592342
20180	10601459	NM_008901	18994	POU domain, class 3, transcrip	Pou3f4	0.69	-6.379	0.000331243	0.00606651
20181	10562117	NM_146187	233079	free fatty acid receptor 2	Ffar2	0.69	-3.263	0.0132339	0.0826153
20182	10357472	NM_009911	12767	chemokine (C-X-C motif) recept	Cxcr4	0.69	-4.959	0.00150353	0.0174291
20183	10602253					0.69	-3.554	0.00884097	0.0621917
20184	10502205	NM_008212	15107	hydroxyacyl-Coenzyme A dehydro	Hadh	0.689	-6.386	0.000328953	0.00605343
20185	10497590	NM_007963	14013	ecotropic viral integration si	Evi1	0.689	-2.686	0.0304183	0.145086
20186	10452980	NM_011163	19106	eukaryotic translation initiat	Eif2ak2	0.689	-3.691	0.00734944	0.0545959
20187	10598664	NM_027439	70495	ATPase, H+ transporting, lysos	Atp6ap2	0.689	-4.239	0.00359449	0.0324929
20188	10513536	XM_001472530	100039345	hypothetical protein LOC100039	LOC100039345	0.688	-2.865	0.0233907	0.121516

20189	10431915	NM_027052	69354	solute carrier family 38, memb	Slc38a4	0.688	-5.093	0.00128884	0.0158118
20190	10467560	NM_133352	107358	transmembrane 9 superfamily me	Tm9sf3	0.688	-6.611	0.000264604	0.00528661
20191	10501879	NM_133857	99526	ubiquitin specific peptidase 5	Usp53	0.688	-3.608	0.0082177	0.059041
20192	10438460	NM_001005767	381038	presenilin associated, rhomboi	Parl	0.687	-6.131	0.000423627	0.00721493
20193	10579894	NM_020259	15245	Hedgehog-interacting protein	Hhip	0.687	-3.25	0.0134889	0.0836635
20194	10479925	BC025867	227545	RIKEN cDNA 5430407P10 gene	5430407P10Rik	0.687	-4.418	0.00287276	0.0280221
20195	10410877	NM_001081176	67486	polymerase (RNA) III (DNA dire	Polr3g	0.687	-4.917	0.00157813	0.0180955
20196	10502273	ENSMUST00000054105	319825	RIKEN cDNA D630013G24 gene	D630013G24Rik	0.686	-6.675	0.000249067	0.00508328
20197	10571353	BC052184	319582	RIKEN cDNA 6430573F11 gene	6430573F11Rik	0.686	-6.194	0.000397545	0.00690123
20198	10520527	NM_023047	65254	dihydropyrimidinase-like 5	Dpysl5	0.686	-5.05	0.00135341	0.0162964
20199	10478474	NM_009036	19668	recombination signal binding p	Rbpjl	0.686	-5.649	0.000698096	0.0102382
20200	10523891	NR_003639	73318	RIKEN cDNA 1700013N18 gene	1700013N18Rik	0.686	-4.777	0.00186065	0.0204585
20201	10555118	NM_011035	18479	p21 (CDKN1A)-activated kinase	Pak1	0.686	-6.543	0.000282581	0.00549668
20202	10585980					0.686	-3.361	0.01154	0.0749094
20203	10500610	BC120717	74645	RIKEN cDNA 4930431B09 gene	4930431B09Rik	0.686	-3.567	0.00868877	0.0613817
20204	10511496	XR_001926	666840	similar to Ldha protein	LOC666840	0.686	-2.409	0.0458627	0.189807
20205	10562125	NM_001033316	233080	free fatty acid receptor 3	Ffar3	0.686	-3.454	0.0101423	0.0686695
20206	10408331	NM_025790	66834	thioesterase superfamily membe	Them2	0.685	-4.531	0.00249941	0.0254055
20207	10606864	NM_177919	331532	transcription elongation facto	Tceal5	0.685	-4.987	0.00145558	0.0170037
20208	10373388	NM_027257	69917	oligonucleotide/oligosaccharid	Obfc2b	0.685	-5.12	0.00124961	0.0154515
20209	10456719					0.685	-2.272	0.0561843	0.216663
20210	10553935	NM_172310	272396	threonyl-tRNA synthetase-like	Tarsl2	0.685	-6.26	0.000372468	0.00657916
20211	10480601	BC013092	227612	RIKEN cDNA A830007P12 gene	A830007P12Rik	0.685	-8.234	6.4165e-05	0.00205873
20212	10471424	NM_153560	98952	RIKEN cDNA C230093N12 gene	C230093N12Rik	0.685	-6.533	0.000285064	0.00552972
20213	10443764	NM_153062	224674	solute carrier family 37 (glyc	Slc37a1	0.685	-5.628	0.000713922	0.0103961
20214	10384656	NM_016888	53625	UDP-GlcNAc:betaGal beta-1,3-N-	B3gnt2	0.685	-5.681	0.00067443	0.00997927
20215	10498345	NM_173398	229323	G protein-coupled receptor 171	Gpr171	0.684	-4.323	0.00323505	0.0301509
20216	10476512	NM_011428	20614	synaptosomal-associated protei	Snap25	0.684	-7.072	0.000172585	0.00401446
20217	10449258	NM_008113	14570	Rho GDP dissociation inhibitor	Arhgdig	0.684	-5.256	0.00107197	0.0137798
20218	10543530	NM_011038	18506	paired box gene 4	Pax4	0.684	-2.74	0.0280725	0.137495
20219	10412380					0.684	-3.875	0.0057493	0.0455805
20220	10345442	NM_015818	50785	heparan sulfate 6-O-sulfotrans	Hs6st1	0.684	-5.479	0.000838407	0.0115713
20221	10447097	NM_026053	67242	gem (nuclear organelle) associ	Gemin6	0.683	-6.091	0.000440935	0.00740801
20222	10406817	NM_007930	13803	ectodermal-neural cortex 1	Enc1	0.683	-5.828	0.000577754	0.00896919
20223	10578136					0.683	-1.112	0.301969	0.578022
20224	10544417	NM_023580	13835	Eph receptor A1	Epha1	0.683	-6.522	0.000288241	0.00558005
20225	10485955	NM_009162	20394	secretogranin V	Scg5	0.683	-4.999	0.0014346	0.0168502
20226	10512892	DQ469311	230161	novel protein similar to bile	RP23-34B24.1	0.683	-4.329	0.00321087	0.0300343
20227	10523727	NM_008861	18764	polycystic kidney disease 2	Pkd2	0.682	-5.483	0.000834615	0.0115341
20228	10594762	BC025646	76886	RIKEN cDNA 6430514L14 gene	6430514L14Rik	0.682	-3.242	0.0136379	0.084307
20229	10510413	NM_001085505	230909	gene model 572, (NCBI)	Gm572	0.682	-6.697	0.00024385	0.00502386
20230	10349904	NM_026680	68338	golgi transport 1 homolog A (S	Golt1a	0.682	-2.525	0.0385793	0.169907
20231	10431637	NM_025815	66871	copine VIII	Cpne8	0.682	-4.142	0.00406354	0.0354015
20232	10556828	NM_028085	72074	ankyrin repeat and sterile alp	Anks4b	0.681	-4.462	0.00272054	0.0270061
20233	10597288	NM_026810	17350	mutL homolog 1 (E. coli)	Mlh1	0.681	-5.58	0.000751781	0.0107913
20234	10525553					0.681	-2.656	0.0318012	0.149238
20235	10572161	NM_001013379	234358	cDNA sequence D10627	D10627	0.681	-5.433	0.000881604	0.0119798
20236	10463402	XR_034011	383450	similar to 3-phosphoglycerate	LOC383450	0.68	-6.703	0.000242651	0.00502386
20237	10482177	AY380798	319517	RIKEN cDNA 6430510M02 gene	6430510M02Rik	0.68	-8.266	6.25516e-05	0.00203008
20238	10586250	XM_001476259	102442	DENN/MADD domain containing 4A	Dennd4a	0.68	2.868	0.0233182	0.121319

20238	10586250	XM_001476259	102442	containing 4A	Dennd4a	0.68	-2.868	0.0235182	0.121319
20239	10503214	NM_001081417	320790	chromodomain helicase DNA bind	Chd7	0.68	-3.604	0.00825892	0.0592507
20240	10589929	NM_026036	67213	CKLF-like MARVEL transmembrane	Cmtm6	0.679	-6.342	0.000343349	0.00620493
20241	10469609	ENSMUST00000100373	100038451	predicted gene, OTTMUSG0000001	OTTMUSG00000011664	0.679	-2.766	0.0270551	0.13393
20242	10603289	NM_016691	12728	chloride channel 5	Clcn5	0.679	-6.574	0.000274196	0.00538052
20243	10399465	NM_029007	105005	expressed sequence AW125753	AW125753	0.679	-1.934	0.0932055	0.295866
20244	10568169	NM_133686	67375	quinolinate phosphoribosyltran	Qprt	0.679	-4.265	0.00347919	0.031654
20245	10467068	NM_144792	208449	sphingomyelin synthase 1	Sgms1	0.678	-5.878	0.000548531	0.00862719
20246	10562612	NM_001033530	101835	expressed sequence AW146154	AW146154	0.678	-4.15	0.00402498	0.035138
20247	10462623	NM_008331	15957	interferon-induced protein wit	Ifit1	0.678	-4.276	0.00343018	0.0313973
20248	10503166	NM_001081417	320790	chromodomain helicase DNA bind	Chd7	0.678	-3.848	0.00596233	0.0467952
20249	10548194	NM_010219	14228	FK506 binding protein 4	Fkbp4	0.677	-7.033	0.000178728	0.00410086
20250	10347669	NM_010564	16322	inhibin alpha	Inha	0.677	-5.908	0.000531552	0.00845048
20251	10569017	NM_025378	66141	interferon induced transmembra	Ifitm3	0.677	-2.582	0.0354663	0.160407
20252	10380712	NM_146026	217138	ATPase family, AAA domain cont	Atad4	0.677	-4.006	0.00484097	0.0402982
20253	10423796					0.676	-4.904	0.00160297	0.0183009
20254	10598638	NM_026524	68041	Mid1 interacting protein 1 (ga	Mid1ip1	0.676	-5.239	0.0010929	0.0139472
20255	10367717	NM_145418	215751	cDNA sequence BC013529	BC013529	0.676	-5.838	0.000571891	0.00891087
20256	10544250	AK122457	243780	RIKEN cDNA E330009J07 gene	E330009J07Rik	0.675	-3.438	0.0103739	0.0698
20257	10419082	BC056635	70564	RIKEN cDNA 5730469M10 gene	5730469M10Rik	0.675	-5.785	0.000604643	0.00925747
20258	10472846	NM_172665	228026	pyruvate dehydrogenase kinase,	Pdk1	0.675	-4.608	0.00227589	0.0238935
20259	10464107	X65588	26930	per-pentamer repeat gene	Ppnr	0.675	-3.54	0.00901822	0.063056
20260	10423379	AF075717	223431	TGF-beta1-induced anti-apoptot	Tiaf2	0.674	-2.325	0.0519818	0.206172
20261	10519241	NM_029264	330010	tubulin tyrosine ligase-like f	Ttll10	0.674	-5.37	0.000944597	0.0126089
20262	10503202	NM_001081417	320790	chromodomain helicase DNA bind	Chd7	0.674	-3.92	0.00541842	0.0437454
20263	10536593	BC145701	66637	RIKEN cDNA 5730449L18 gene	5730449L18Rik	0.674	-4.173	0.00390533	0.0343773
20264	10424347	XM_001475049	665565	similar to Ribosomal protein L	LOC665565	0.673	-2.074	0.075608	0.260007
20265	10598359	NM_009305	20977	synaptophysin	Syp	0.673	-5.077	0.00131253	0.0159678
20266	10568221	NM_009266	20768	selenophosphate synthetase 2	Sephs2	0.673	-4.636	0.00220091	0.0233264
20267	10424404	NR_003368	19296	plasmacytoma variant transloca	Pvt1	0.673	-4.136	0.00409523	0.0355458
20268	10535956	NM_146258	243362	StAR-related lipid transfer (S	Stard13	0.672	-2.48	0.0412336	0.177132
20269	10551065	ENSMUST00000098678	434147	RIKEN cDNA D930028M14 gene	D930028M14Rik	0.672	-6.038	0.000465531	0.00767799
20270	10585186	NM_029639	76509	RIKEN cDNA 1600029D21 gene	1600029D21Rik	0.672	-3.516	0.00931747	0.064593
20271	10363887	ENSMUST00000058942	75189	RIKEN cDNA 4930533K18 gene	4930533K18Rik	0.672	-4.006	0.00484519	0.0403004
20272	10459772	NM_010720	16891	lipase, endothelial	Lipg	0.671	-4.172	0.00391313	0.0344133
20273	10498357	AK170843	320463	RIKEN cDNA F630111L10 gene	F630111L10Rik	0.671	-5.389	0.000924684	0.0124374
20274	10469046	NM_010726	16922	phytanoyl-CoA hydroxylase	Phyh	0.671	-7.62	0.000106601	0.0029046
20275	10353549	BC070446	68187	RIKEN cDNA 4921533L14 gene	4921533L14Rik	0.671	-6.191	0.000398818	0.00691197
20276	10594800	NM_172772	235461	RIKEN cDNA B230380D07 gene	B230380D07Rik	0.67	-4.428	0.00283678	0.0278091
20277	10492231	ENSMUST00000040325	329650	mediator of RNA polymerase II	Med12l	0.67	-5.622	0.000718408	0.0104471
20278	10574694	NM_172760	234683	engulfment and cell motility 3	Elmo3	0.67	-9.073	3.36919e-05	0.00133405
20279	10499113	NM_001001650	368202	gene model 1019, (NCBI)	Gm1019	0.67	-5.23	0.00110381	0.0140596
20280	10566767	NM_001001326	76954	suppression of tumorigenicity	St5	0.67	-5.387	0.000926638	0.0124557
20281	10483178	NM_177025	319876	Cobl-like 1	Cobll1	0.67	-3.228	0.0139071	0.0854991
20282	10598626	NM_019634	21912	tetraspanin 7	Tspan7	0.67	-3.052	0.0178623	0.10147
20283	10420747	NM_008092	14463	GATA binding protein 4	Gata4	0.669	-3.598	0.0083335	0.0595886
20284	10596718	NM_023805	76257	solute carrier family 38, memb	Slc38a3	0.669	-3.86	0.00586169	0.0462423
20285	10501319	NM_017392	53883	cadherin, EGF LAG seven-pass	Celsr2	0.667	-6.569	0.000275425	0.0053972

20285	10501519	NM_017392	53883	G	Celsr2	0.667	-6.309	0.000275425	0.0055972
20286	10399148	NM_175930	217944	Rap guanine nucleotide exchang	Rapgef5	0.667	-7.132	0.000163453	0.00385291
20287	10350349	NM_181347	329260	DENN/MADD domain containing 1B	Dennd1b	0.667	-4.181	0.00387026	0.0341512
20288	10389732	NR_003564	217066	predicted gene, OTTMUSG0000000	OTTMUSG00000001305	0.667	-2.777	0.0266163	0.132636
20289	10606174	NM_008671	17954	nucleosome assembly protein 1-	Nap1l2	0.667	-2.689	0.0302895	0.144706
20290	10388718	NM_008952	19193	pipecolic acid oxidase	Pipox	0.667	-5.119	0.00125002	0.0154515
20291	10503174	NM_001081417	320790	chromodomain helicase DNA bind	Chd7	0.666	-5.474	0.000843114	0.0116136
20292	10545450	NM_009443	22134	trans-golgi network protein	Tgoln1	0.666	-8.724	4.37511e-05	0.00159221
20293	10398386					0.666	-2.832	0.0245495	0.125928
20294	10365601	NM_001004164	432486	N-acetylglucosamine-1-phosphat	Gnptab	0.666	-8.974	3.624e-05	0.0013932
20295	10503194	NM_001081417	320790	chromodomain helicase DNA bind	Chd7	0.666	-4.553	0.00243418	0.0249846
20296	10502816	NM_016867	54120	GIPC PDZ domain containing fam	Gipc2	0.665	-5.626	0.000715228	0.010408
20297	10592535	NM_011436	20660	sortilin-related receptor, LDL	Sorl1	0.665	-8.222	6.47932e-05	0.00206013
20298	10497485	XM_975226	635702	N-acetylated alpha-linked acid	Naaladl2	0.665	-3.537	0.00906035	0.0632413
20299	10408557	NM_025429	66222	serine (or cysteine) peptidase	Serpinb1a	0.665	-3.071	0.0173911	0.0997203
20300	10557575	NM_016754	17907	myosin light chain, phosphoryl	Mylpf	0.665	-3.86	0.00586339	0.0462423
20301	10352320	NM_144794	208795	transmembrane protein 63a	Tmem63a	0.665	-5.137	0.00122514	0.0152338
20302	10396485	NM_001005510	319565	synaptic nuclear envelope 2	Syne2	0.665	-7.107	0.0001671	0.00392137
20303	10542727	NM_009449	22147	tubulin, alpha 3B	Tuba3b	0.664	-1.971	0.0881542	0.286143
20304	10345241	NM_134448	13518	dystonin	Dst	0.664	-8.379	5.7182e-05	0.00189507
20305	10578574	NM_175162	71069	storkhead box 2	Stox2	0.664	-6.002	0.000482931	0.00788501
20306	10499108	NM_177130	320302	glycosyltransferase 28 domain	Glt28d2	0.664	-2.625	0.0332849	0.153865
20307	10398366					0.663	-2.935	0.0211602	0.113932
20308	10587699	NM_011245	19417	RAS protein-specific guanine n	Rasgrf1	0.663	-6.617	0.000263232	0.00527061
20309	10599342	NM_183126	77883	RIKEN cDNA 6030498E09 gene	6030498E09Rik	0.662	-2.482	0.0411081	0.176721
20310	10419551	NM_028312	72654	coiled-coil domain containing	Ccdc12	0.662	-5.713	0.000652206	0.00975955
20311	10452404	NM_026497	67993	nudix (nucleoside diphosphate	Nudt12	0.662	-6.472	0.000302387	0.00575488
20312	10407286	ENSMUST00000078163	408066	cDNA sequence BC067074	BC067074	0.661	-5.239	0.00109184	0.0139472
20313	10481092	NM_026212	67512	1-acylglycerol-3-phosphate O-a	Agpat2	0.661	-5.346	0.00096959	0.0128528
20314	10391084	NM_010404	15114	huntingtin-associated protein	Hap1	0.661	-4.321	0.00324347	0.0301848
20315	10467258	NM_001099634	226101	fer-1-like 3, myoferlin (C. el	Fer1l3	0.661	-2.688	0.0303188	0.144742
20316	10436392	NM_007757	12892	coproporphyrinogen oxidase	Cpox	0.66	-2.845	0.0241073	0.124232
20317	10503218	NM_001081417	320790	chromodomain helicase DNA bind	Chd7	0.66	-3.881	0.00570684	0.0453497
20318	10496837	ENSMUST00000038090	70892	tubulin tyrosine ligase-like f	Ttll7	0.659	-5.018	0.00140328	0.0166598
20319	10514072	NM_026647	68268	zinc finger, DHHC domain conta	Zdhhc21	0.659	-6.408	0.000321953	0.00596092
20320	10388185	NM_177776	276829	smoothelin-like 2	Smtnl2	0.659	-8.301	6.08211e-05	0.0019938
20321	10373583	NM_010272	14561	growth differentiation factor	Gdf11	0.659	-6.457	0.000306984	0.00580546
20322	10453062	NM_019717	56298	ADP-ribosylation factor-like 6	Arl6ip2	0.659	-9.191	3.08847e-05	0.00126067
20323	10519028	NM_027504	70673	PR domain containing 16	Prdm16	0.659	-3.972	0.00506416	0.0416883
20324	10420846	NM_021458	14365	frizzled homolog 3 (Drosophila	Fzd3	0.658	-5.923	0.000523409	0.00834613
20325	10479747					0.658	-2.034	0.0802868	0.270212
20326	10435693	NM_001017429	12856	cytochrome c oxidase, subunit	Cox17	0.658	-4.968	0.00148745	0.0172522
20327	10369232	ENSMUST00000066340	791309	predicted gene, ENSMUSG0000005	ENSMUSG00000053739	0.658	-4.764	0.00188939	0.0207313
20328	10388440	NM_008878	18816	serine (or cysteine) peptidase	Serpinf2	0.658	-4.063	0.00450018	0.0380607
20329	10571274	NM_010344	14782	glutathione reductase	Gsr	0.657	-10.26	1.46883e-05	0.000764951
20330	10542460	NM_172733	232449	2-deoxyribose-5-phosphate aldo	Dera	0.657	-5.749	0.000627606	0.0095058
20331	10439442	NM_134102	85031	phospholipase A1 member A	Pla1a	0.657	-4.478	0.00266655	0.0266202
20332	10600301	NM_009279	20832	signal sequence receptor, delt	Ssr4	0.657	-7.33	0.00013707	0.00340165
20333	10595848	NM_145134	211949	splA/ryanodine receptor domain	Spsb4	0.657	-5.768	0.000615006	0.00938306
20334	10595702	NM_001033145	68861	RIKEN cDNA 1190002N15 gene	1190002N15Rik	0.657	-4.442	0.00278817	0.0274583

20335	10497031					0.656	-4.05	0.00457432	0.0385644
20336	10458090	NM_007874	13476	receptor accessory protein 5	Reep5	0.656	-3.843	0.00599569	0.0469175
20337	10558921	NM_025802	66853	patatin-like phospholipase dom	Pnpla2	0.655	-8.583	4.87496e-05	0.00171223
20338	10398356					0.655	-3.851	0.00593744	0.0467005
20339	10536483	NM_207176	21753	testis derived transcript	Tes	0.655	-6.964	0.000190299	0.00424888
20340	10488830	NM_001004721	228812	phosphatidylinositol glycan an	Pigu	0.655	-8.237	6.4028e-05	0.00205746
20341	10429968					0.655	-4.313	0.00327477	0.0303959
20342	10581069	BC022771	791360	predicted gene, ENSMUSG0000005	ENSMUSG00000051554	0.655	-3.11	0.0164359	0.0962129
20343	10398364					0.655	-4.18	0.00387319	0.0341512
20344	10583820	NM_001033813	619310	RIKEN cDNA 9530015I07 gene	9530015I07Rik	0.654	-4.398	0.00294483	0.028407
20345	10467420	NM_016861	54132	PDZ and LIM domain 1 (elfin)	Pdlim1	0.654	-5.7	0.000660836	0.00984721
20346	10507379	NM_001029912	74464	zinc finger, SWIM domain conta	Zswim5	0.654	-5.53	0.000792773	0.0111675
20347	10586130	BC027311	66939	RIKEN cDNA 2310007F21 gene	2310007F21Rik	0.654	-5.73	0.000640429	0.00963473
20348	10575750	NM_021486	63857	beta-carotene 15,15'-monooxyge	Bcmo1	0.653	-5.34	0.000976531	0.0128727
20349	10401997	NM_011877	24000	protein tyrosine phosphatase,	Ptpn21	0.653	-6.583	0.000271911	0.00536314
20350	10471880					0.653	-3.193	0.0146239	0.0886236
20351	10504234	NM_001081413	22249	unc-13 homolog B (C. elegans)	Unc13b	0.653	-5.464	0.000851845	0.0116881
20352	10604616	NM_019538	56096	placental specific protein 1	Plac1	0.653	-2.98	0.0198217	0.109228
20353	10537849	NM_133674	54324	Rho guanine nucleotide exchang	Arhgef5	0.653	-6.643	0.000256648	0.00517663
20354	10445241	NM_178589	94185	tumor necrosis factor receptor	Tnfrsf21	0.653	-5.025	0.00139193	0.0166183
20355	10432652	NM_033612	109901	elastase 1, pancreatic	Ela1	0.652	-4.37	0.00305019	0.0290634
20356	10492864	NM_001082414	27059	SH3 domain protein D19	Sh3d19	0.652	-7.694	0.000100118	0.00277806
20357	10398368					0.651	-2.889	0.0225863	0.118836
20358	10543120	NM_010492	15893	islet cell autoantigen 1	Ica1	0.651	-3.139	0.0157867	0.0934735
20359	10394802					0.651	-3.634	0.00793121	0.0576875
20360	10386965	NM_175003	216831	expressed sequence AU040829	AU040829	0.651	-8.928	3.75204e-05	0.00142276
20361	10398326	NR_003633	17263	maternally expressed 3	Meg3	0.65	-4.051	0.00456937	0.038538
20362	10558948	NM_009842	12476	CD151 antigen	Cd151	0.65	-5.019	0.00140234	0.016658
20363	10571840	NM_008278	15446	hydroxyprostaglandin dehydroge	Hpgd	0.65	-5.291	0.00103072	0.013395
20364	10563527	NM_153677	72088	Usher syndrome 1C homolog (hum	Ush1c	0.65	-6.444	0.000310856	0.00584508
20365	10468990	NM_001005767	381038	presenilin associated, rhomboi	Parl	0.649	-5.344	0.000972215	0.0128559
20366	10466947	NM_001081213	226090	endoplasmic reticulum metallop	Ermp1	0.649	-4.638	0.00219676	0.0233057
20367	10481278	NM_009885	12613	carboxyl ester lipase	Cel	0.649	-4.224	0.00366342	0.0328828
20368	10366346	NM_009344	21664	pleckstrin homology-like domai	Phlda1	0.649	-3.901	0.0055545	0.0445878
20369	10499988	BC107021	66353	RIKEN cDNA 2310007A19 gene	2310007A19Rik	0.648	-4.835	0.00173777	0.0193896
20370	10482249	NM_010264	14536	nuclear receptor subfamily 6,	Nr6a1	0.648	-4.785	0.00184178	0.0203143
20371	10480585	NM_172204	241275	NADPH oxidase activator 1	Noxa1	0.648	-8.409	5.5864e-05	0.00186897
20372	10549879	NM_021323	57775	ubiquitin specific peptidase 2	Usp29	0.648	-8.21	6.54225e-05	0.00206613
20373	10384051	NM_010292	103988	glucokinase	Gck	0.648	-3.252	0.0134397	0.0834564
20374	10594001	NM_019689	56380	AT rich interactive domain 3B	Arid3b	0.648	-4.012	0.00480534	0.0400332
20375	10389134	NM_172796	237886	schlafen 9	Slfn9	0.648	-5.089	0.00129372	0.0158118
20376	10353750	NM_145392	213539	Bcl2-associated athanogene 2	Bag2	0.647	-5.085	0.00129957	0.0158558
20377	10607562	NM_177751	245684	connector enhancer of kinase s	Cnksr2	0.647	-7.132	0.000163428	0.00385291
20378	10584891	NM_007503	11936	FXYD domain-containing ion tra	Fxyd2	0.647	-8.598	4.81917e-05	0.00170608
20379	10585381	NM_028060	72022	solute carrier family 35, memb	Slc35f2	0.647	-4.056	0.00454088	0.038359
20380	10433163	NM_021391	58200	protein phosphatase 1, regulat	Ppp1r1a	0.647	-9.515	2.44681e-05	0.00107113
20381	10382435	NM_001110337	70355	G protein-coupled receptor, fa	Gprc5c	0.646	-6.772	0.000227356	0.00480242
20382	10409118	NM_029361	75607	WNK lysine deficient protein k	Wnk2	0.645	-4.55	0.00244323	0.0250289
20383	10543306	NM_173007	269831	tetraspanin 12	Tspan12	0.645	-8.231	6.43268e-05	0.00205963
20384	10430425	NM_025622	107753	lectin, galactose-binding, sol	Lgals2	0.645	-3.077	0.017246	0.0992784
20385	10554926	NM_025515	66365	coiled-coil domain containing	Ccdc90b	0.645	-7.468	0.000121491	0.00314805
20386	10400941	NM_025522	66375	dehydrogenase/reductase (SDR f	Dhrs7	0.645	-4.398	0.00294495	0.028407
20387	10488322	NM_001033348	241694	RIKEN cDNA A230067G21 gene	A230067G21Rik	0.645	-4.1	0.0042913	0.0367052
20388	10536401	NM_008751	18231	neurexophilin 1	Nxph1	0.644	-4.076	0.00442707	0.0375626

20389	10357164	NM_145506	226352	erythrocyte protein band 4.1-l	Epb4.1l5	0.644	-7.907	8.37374e-05	0.00246251
20390	10403229	NM_177290	320910	integrin beta 8	Itgb8	0.644	-2.76	0.027277	0.134663
20391	10548729	NM_026345	67729	MANSC domain containing 1	Mansc1	0.644	-6.397	0.000325409	0.00601439
20392	10494069	NM_172434	78784	trinucleotide repeat containin	Tnrc4	0.644	-5.027	0.00138894	0.0166024
20393	10539702	BC103775	66488	RIKEN cDNA 2010309E21 gene	2010309E21Rik	0.644	-8.478	5.28974e-05	0.0018216
20394	10568109	NM_001039645	233879	aspartate beta-hydroxylase dom	Asphd1	0.644	-5.641	0.000703529	0.0102944
20395	10593483	NM_007996	14148	ferredoxin 1	Fdx1	0.644	-7.212	0.000152149	0.00364743
20396	10346564	NM_009812	12370	caspase 8	Casp8	0.644	-5.303	0.00101684	0.0133115
20397	10410477	NM_172053	271127	a disintegrin-like and metallo	Adamts16	0.644	-5.774	0.000611299	0.00933909
20398	10463911	NM_013758	27360	adducin 3 (gamma)	Add3	0.643	-9.104	3.2932e-05	0.00131336
20399	10362379	NM_025855	52665	enoyl Coenzyme A hydratase dom	Echdc1	0.643	-4.761	0.0018954	0.0207757
20400	10375677					0.643	-2.309	0.0531767	0.209185
20401	10408935	ENSMUST00000099550	100038539	predicted gene, ENSMUSG0000007	ENSMUSG00000074917	0.643	-2.315	0.0527317	0.207909
20402	10397148	NM_012006	26897	acyl-CoA thioesterase 1	Acot1	0.642	-9.884	1.89239e-05	0.000913534
20403	10453429	NM_008838	18701	phosphatidylinositol glycan an	Pigf	0.642	-6.656	0.000253565	0.00515463
20404	10503198	NM_001081417	320790	chromodomain helicase DNA bind	Chd7	0.642	-3.628	0.00800293	0.0580494
20405	10602198	NM_008778	18481	p21 (CDKN1A)-activated kinase	Pak3	0.64	-5.461	0.000855048	0.0117245
20406	10398378					0.64	-3.026	0.0185551	0.104232
20407	10364511	BC013508	78906	RIKEN cDNA 9130017N09 gene	9130017N09Rik	0.64	-5.275	0.00104984	0.0135996
20408	10544487	NM_013861	29807	thiamine pyrophosphokinase	Tpk1	0.64	-3.838	0.00603698	0.0471366
20409	10486833	NM_145973	269344	elongation factor RNA polymera	Ell3	0.64	-4.794	0.00182205	0.0201388
20410	10379795	NM_194341	217030	AP1 gamma subunit binding prot	Ap1gbp1	0.639	-8.753	4.28059e-05	0.0015659
20411	10354677	NM_001081433	329154	ankyrin repeat domain 44	Ankrd44	0.639	-6.347	0.000341617	0.00618755
20412	10458122	NM_080637	75533	non-metastatic cells 5, protei	Nme5	0.639	-4.387	0.0029852	0.0286589
20413	10409660	NM_019832	56278	G kinase anchoring protein 1	Gkap1	0.639	-5.584	0.000748324	0.0107563
20414	10410778	NM_054053	110789	G protein-coupled receptor 98	Gpr98	0.638	-7.359	0.000133533	0.0033453
20415	10369525	BC024943	69894	RIKEN cDNA 2010107G23 gene	2010107G23Rik	0.638	-5.881	0.000546902	0.00861677
20416	10540227	NM_001008785	243574	kelch repeat and BTB (POZ) dom	Kbtbd8	0.638	-9.337	2.77946e-05	0.00118247
20417	10396606	NM_001005510	319565	synaptic nuclear envelope 2	Syne2	0.638	-6.866	0.000208361	0.00454653
20418	10598075					0.638	-2.083	0.0745359	0.258241
20419	10490016	NM_175303	99377	sal-like 4 (Drosophila)	Sall4	0.638	-4.127	0.00414396	0.0357925
20420	10530563	NM_028194	72313	furry homolog-like (Drosophila	Fryl	0.637	-9.655	2.21832e-05	0.00101021
20421	10392183	NM_023913	78943	endoplasmic reticulum (ER) to	Ern1	0.637	-5.968	0.000500009	0.00809509
20422	10404827	NM_023554	70078	nucleolar protein 7	Nol7	0.637	-9.623	2.26704e-05	0.00101988
20423	10540544	NM_008188	14911	THUMP domain containing 3	Thumpd3	0.637	-6.425	0.000316675	0.00590456
20424	10543114					0.637	-5.788	0.000602579	0.00923256
20425	10526277	NM_021455	58805	MLX interacting protein-like	Mlxipl	0.637	-4.483	0.00265064	0.026524
20426	10423791	ENSMUST00000022897	74892	RIKEN cDNA 4930447A16 gene	4930447A16Rik	0.637	-8.552	4.996e-05	0.00173457
20427	10354647	ENSMUST00000097739	241062	post-GPI attachment to protein	Pgap1	0.637	-4.405	0.00292071	0.028306
20428	10455752	NM_029394	69226	sorting nexing 24	Snx24	0.636	-4.333	0.00319375	0.0299462
20429	10441254	NM_015775	50528	transmembrane protease, serine	Tmprss2	0.636	-4.067	0.00447599	0.0378713
20430	10499130	NR_004418	19871	U73B small nuclear RNA	Rnu73b	0.636	-2.39	0.0471345	0.192955
20431	10380116	NM_172448	207742	ring finger protein 43	Rnf43	0.636	-7.966	7.97783e-05	0.00237582
20432	10495147	NM_001093754	72121	DENN/MADD domain containing 2D	Dennd2d	0.636	-5.525	0.000797659	0.0112109
20433	10559333	ENSMUST00000105902	210274	SH3/ankyrin domain gene 2	Shank2	0.636	-7.061	0.000174177	0.00403815
20434	10523845	NM_001001804	384214	abhydrolase domain containing	Abhd7	0.635	-6.275	0.000366745	0.00649997
20435	10542911	ENSMUST00000001113	209086	sterile alpha motif domain con	Samd9l	0.635	-2.503	0.0398799	0.173611
20436	10435769	NM_019778	56490	zinc finger and BTB domain con	Zbtb20	0.635	-6.032	0.000468388	0.00769511
20437	10506767	NM_026728	52430	enoyl Coenzyme A hydratase dom	Echdc2	0.635	-4.724	0.00198029	0.0214285
20438	10476021	NM_007547	19261	signal-regulatory protein alph	Sirpa	0.634	-7.013	0.000181927	0.00415407

20439	10404700	NM_145441	217379	UBX domain containing 4	Ubxd4	0.634	-7.536	0.000114575	0.00304727
20440	10595664	NM_025360	66111	transmembrane emp24 domain con	Tmed3	0.634	-6.938	0.000194876	0.00433276
20441	10558880	NM_133191	98845	EPS8-like 2	Eps8l2	0.634	-7.73	9.71144e-05	0.00273057
20442	10606902	NM_207267	399591	RIKEN cDNA 4930488E11 gene	4930488E11Rik	0.633	-4.282	0.00340235	0.0311965
20443	10398426					0.633	-6.33	0.000347577	0.00625994
20444	10561942	NM_172898	243911	kin of IRRE like 2 (Drosophila	Kirrel2	0.633	-7.142	0.000161956	0.00383373
20445	10506110	NM_001081202	381591	LINE-1 type transposase domain	L1td1	0.632	-5.531	0.000792329	0.0111675
20446	10425012	NM_145916	223669	zinc finger protein 7	Zfp7	0.632	-3.126	0.0160837	0.094857
20447	10427908	ENSMUST00000067671	791293	predicted gene, ENSMUSG0000005	ENSMUSG00000054546	0.632	-6.096	0.000438684	0.00738884
20448	10398362	AF357355	75745	RNA imprinted and accumulated	Rian	0.632	-5.301	0.00101912	0.0133179
20449	10498119	NM_172862	242022	Fras1 related extracellular ma	Frem2	0.632	-7.914	8.32927e-05	0.00245807
20450	10472212	NM_026361	227937	plakophilin 4	Pkp4	0.631	-9.125	3.24079e-05	0.00129534
20451	10528227	NM_010305	14677	guanine nucleotide binding pro	Gnai1	0.631	-5.793	0.000599187	0.00921398
20452	10457323	NM_177595	210719	mohawk	Mkx	0.631	-2.634	0.0328157	0.152417
20453	10551907	NM_019459	54631	nephrosis 1 homolog, nephrin (	Nphs1	0.631	-4.374	0.0030346	0.0290071
20454	10367805	NM_172547	215772	RIKEN cDNA 9130014G24 gene	9130014G24Rik	0.631	-4.271	0.00345304	0.0314839
20455	10398432					0.631	-2.192	0.0633664	0.233418
20456	10458828	NM_033037	12583	cysteine dioxygenase 1, cytoso	Cdo1	0.631	-3.405	0.0108533	0.0717133
20457	10457359	NM_001081287	75739	membrane protein, palmitoylate	Mpp7	0.63	-7.98	7.88695e-05	0.00236206
20458	10564631	NM_023908	108116	solute carrier organic anion t	Slco3a1	0.629	-7.14	0.00016222	0.00383373
20459	10425267	NM_008837	18693	protein interacting with C kin	Pick1	0.629	-7.878	8.57624e-05	0.00251506
20460	10595718	NM_018763	54371	carbohydrate sulfotransferase	Chst2	0.629	-6.297	0.000358884	0.00640358
20461	10405380	NM_008011	14186	fibroblast growth factor recep	Fgfr4	0.629	-5.604	0.000731899	0.0105923
20462	10427015	NM_007395	11479	activin A receptor, type 1B	Acvr1b	0.629	-8.419	5.54375e-05	0.00186897
20463	10387668	NM_031880	83813	tyrosine kinase, non-receptor,	Tnk1	0.629	-7.145	0.000161543	0.00382954
20464	10385391	NM_133769	76884	cytoplasmic FMR1 interacting p	Cyfip2	0.628	-7.775	9.34761e-05	0.00267301
20465	10552919	NM_010473	15464	histidine rich calcium binding	Hrc	0.628	-6.683	0.000247212	0.00505029
20466	10460221	NM_013490	12660	choline kinase alpha	Chka	0.628	-9.251	2.95577e-05	0.00121589
20467	10442914	NM_026686	68347	RIKEN cDNA 0610011F06 gene	0610011F06Rik	0.627	-5.852	0.000563529	0.00883266
20468	10404702	NM_023887	14538	glucosaminyl (N-acetyl) transf	Gcnt2	0.627	-7.732	9.69615e-05	0.0027299
20469	10434925	NM_008235	15205	hairy and enhancer of split 1	Hes1	0.627	-6.45	0.000308914	0.00581628
20470	10469020	BC096430	209645	RIKEN cDNA E130319B15 gene	E130319B15Rik	0.627	-9.991	1.75966e-05	0.000863256
20471	10349401	BC085285	71111	G protein-coupled receptor 39	Gpr39	0.626	-4.606	0.00228306	0.0239354
20472	10434436	BC125016	328644	predicted gene, EG328644	EG328644	0.626	-5.701	0.000660443	0.00984721
20473	10368162	NM_008822	18634	peroxisome biogenesis factor 7	Pex7	0.626	-8.003	7.73766e-05	0.00232724
20474	10463906	NM_008386	16333	insulin I	Ins1	0.626	-5.283	0.0010401	0.0134837
20475	10582839	BC025186	628856	predicted gene, ENSMUSG0000005	ENSMUSG00000053531	0.626	-4.406	0.00291741	0.0282962
20476	10459768					0.625	-6.473	0.0003022	0.00575488
20477	10542896	NM_009753	12121	bicaudal D homolog 1 (Drosophi	Bicd1	0.625	-7.227	0.000150078	0.00361008
20478	10420023	AB054001	85308	RIKEN cDNA 1500005A01 gene	1500005A01Rik	0.625	-4.643	0.00218317	0.0231857
20479	10496796	NM_138744	99167	synovial sarcoma, X breakpoint	Ssx2ip	0.625	-5.477	0.000839708	0.0115817
20480	10493259	NM_025448	66256	signal sequence receptor, beta	Ssr2	0.625	-10.014	1.73266e-05	0.000855965
20481	10545409	NM_016794	22320	vesicle-associated membrane pr	Vamp8	0.624	-7.574	0.000110825	0.00299652
20482	10497001	NM_009968	12972	crystallin, zeta	Cryz	0.624	-7.426	0.000125964	0.00322444
20483	10513190	BC095953	242484	RIKEN cDNA D630039A03 gene	D630039A03Rik	0.624	-5.603	0.000733388	0.0106065
20484	10483163	NM_016719	50915	growth factor receptor bound p	Grb14	0.623	-4.97	0.00148435	0.0172257
20485	10589695	NM_153100	235636	receptor transporter protein 3	Rtp3	0.623	-6.871	0.00020732	0.00453465
20486	10503180	NM_001081417	320790	chromodomain helicase DNA bind	Chd7	0.623	-4.654	0.00215329	0.0229481
20487	10459183	NM_007885	13521	solute carrier family 26 (sulf	Slc26a2	0.622	-8.476	5.2991e-05	0.00182186
20488	10595109	NM_172528	214345	leucine rich repeat containing	Lrrc1	0.622	-6.983	0.000187115	0.00422236

20488	10393109	NM_172528	214543	leucine rich repeat containing	Lrrc1	0.622	-6.983	0.000187115	0.00422236
20489	10422822	NM_013584	16880	leukemia inhibitory factor rec	Lifr	0.622	-3.926	0.00537504	0.0435273
20490	10573626	NM_173866	108682	glutamic pyruvate transaminase	Gpt2	0.622	-5.971	0.000498331	0.00808259
20491	10606835	NM_009749	12069	brain expressed X-linked 2	Bex2	0.622	-9.594	2.31374e-05	0.00102993
20492	10345058	NM_029398	75712	transmembrane protein 14A	Tmem14a	0.622	-5.075	0.00131521	0.0159824
20493	10374840					0.621	-2.747	0.0278125	0.136658
20494	10397912	AB257853	217843	RIKEN cDNA 9030205A07 Gene	9030205A07Rik	0.621	-5.543	0.000781517	0.0110457
20495	10534021	NM_001081388	231760	RIMS binding protein 2	Rimbp2	0.62	-6.59	0.00027013	0.00533798
20496	10507218	NM_021461	17346	MAP kinase-interacting serine/	Mknk1	0.62	-8.206	6.56313e-05	0.00206812
20497	10581061	NM_153582	97487	CKLF-like MARVEL transmembrane	Cmtm4	0.619	-4.95	0.00151944	0.017575
20498	10546294	NM_018815	54563	nucleoporin 210	Nup210	0.618	-9.772	2.0439e-05	0.000962498
20499	10466888	NM_175459	226075	GLIS family zinc finger 3	Glis3	0.618	-7.449	0.000123458	0.00318334
20500	10524844	NM_001081308	330177	TAO kinase 3	Taok3	0.618	-5.533	0.000790265	0.011147
20501	10594812	NM_008280	15450	lipase, hepatic	Lipc	0.617	-10.144	1.58699e-05	0.00081416
20502	10480921	NM_153559	227638	quiescin Q6 sulfhydryl oxidase	Qsox2	0.617	-6.647	0.000255708	0.00516956
20503	10505994	NM_001113412	75578	FGGY carbohydrate kinase domai	Fggy	0.617	-2.381	0.047811	0.194851
20504	10519988	NM_177869	330050	expressed sequence AI847670	AI847670	0.617	-6.422	0.000317391	0.0059127
20505	10443898	NM_134127	106648	cytochrome P450, family 4, sub	Cyp4f15	0.616	-4.658	0.00214384	0.0228936
20506	10379321	NM_175543	268451	RAB11 family interacting prote	Rab11fip4	0.616	-4.751	0.00191724	0.0209391
20507	10571399	NM_178395	70546	zinc finger, DHHC domain conta	Zdhhc2	0.616	-7.372	0.00013213	0.003318
20508	10368101	NM_001033258	215821	DNA segment, Chr 10, Brigham &	D10Bwg1379e	0.615	-5.288	0.00103451	0.0134277
20509	10492720	NM_001081230	213582	microtubule-associated protein	Mtap9	0.615	-4.792	0.00182654	0.0201672
20510	10495285	NM_019972	20661	sortilin 1	Sort1	0.615	-9.415	2.62771e-05	0.00112698
20511	10509577	NM_011109	18782	phospholipase A2, group IID	Pla2g2d	0.615	-8.036	7.5303e-05	0.00228437
20512	10514255	NM_027326	70122	myeloid/lymphoid or mixed-line	Mllt3	0.614	-3.57	0.00865041	0.0611925
20513	10440738	NM_009384	21844	T-cell lymphoma invasion and m	Tiam1	0.613	-5.357	0.000957914	0.0127224
20514	10369842	ENSMUST00000099633	75189	RIKEN cDNA 4930533K18 gene	4930533K18Rik	0.613	-3.017	0.0187939	0.105238
20515	10417053	NM_175341	105559	muscleblind-like 2	Mbnl2	0.612	-9.292	2.87008e-05	0.00119931
20516	10395155	BC085288	104943	RIKEN cDNA 9030611O19 gene	9030611O19Rik	0.612	-5.644	0.000701407	0.0102776
20517	10559796	NM_008817	18616	paternally expressed 3	Peg3	0.612	-6.214	0.000389776	0.00679985
20518	10441864	NM_010806	17356	myeloid/lymphoid or mixed-line	Mllt4	0.612	-9.477	2.51471e-05	0.00108971
20519	10541260	ENSMUST00000112686	330409	cat eye syndrome chromosome re	Cecr2	0.612	-8.574	4.91178e-05	0.0017223
20520	10399691	NM_010496	15902	inhibitor of DNA binding 2	Id2	0.612	-7.799	9.16544e-05	0.00263665
20521	10576844	NM_207203	73072	cDNA sequence BC068157	BC068157	0.611	-6.214	0.000389691	0.00679985
20522	10590383	NM_026794	26901	differentially expressed in B1	Deb1	0.61	-8.708	4.42859e-05	0.00160339
20523	10437516	NM_008909	19041	periplakin	Ppl	0.61	-7.475	0.000120708	0.00314805
20524	10598863	NM_009060	19733	regucalcin	Rgn	0.61	-5.004	0.0014271	0.0168385
20525	10498350	NM_133200	140795	purinergic receptor P2Y, G-pro	P2ry14	0.61	-5.327	0.000989951	0.013009
20526	10459655	NM_011972	26447	polymerase (DNA directed), iot	Poli	0.609	-8.674	4.54804e-05	0.00163822
20527	10441270	NM_023663	72388	receptor-interacting serine-th	Ripk4	0.609	-5.221	0.0011145	0.0141447
20528	10452721	AK032413	68789	RIKEN cDNA 1110039F03 gene	1110039F03Rik	0.609	-5.442	0.000873029	0.0119016
20529	10513160	ENSMUST00000075637	545622	protein tyrosine phosphatase,	Ptpn3	0.609	-5.97	0.000498769	0.00808259
20530	10457820	NM_199024	319211	nucleolar protein 4	Nol4	0.608	-4.023	0.00473994	0.0396916
20531	10531869	NM_009158	26414	mitogen-activated protein kina	Mapk10	0.607	-5.352	0.00096385	0.0127933
20532	10469936	NM_025980	67122	Notch-regulated ankyrin repeat	Nrarp	0.607	-2.852	0.0238615	0.123326
20533	10396669	ENSMUST00000101281	100038469	predicted gene, ENSMUSG0000007	ENSMUSG00000073000	0.606	-4.606	0.00228328	0.0239354
20534	10520753	NM_027221	69815	keratinocyte associated protei	Krtcap3	0.606	-5.544	0.00078131	0.0110457
20535	10523365	NM_053158	94061	mitochondrial ribosomal protei	Mrpl1	0.606	-10.069	1.66948e-05	0.00083847
20536	10388880	NM_133706	69071	transmembrane protein 97	Tmem97	0.606	-6.975	0.000188401	0.00422741

20537	10548761	NM_013546	15199	heme binding protein 1	Hebp1	0.605	-8.098	7.1617e-05	0.00220739
20538	10391146	NM_134037	104112	ATP citrate lyase	Acly	0.605	-9.879	1.89852e-05	0.000914403
20539	10494043	NM_028307	72634	tudor and KH domain containing	Tdrkh	0.605	-8.219	6.49278e-05	0.00206063
20540	10581645	NM_028584	73608	MARVEL (membrane-associating)	Marveld3	0.605	-6.487	0.000298235	0.00570669
20541	10501971	NM_178655	109676	ankyrin 2, brain	Ank2	0.605	-7.004	0.000183477	0.00418043
20542	10565456	NM_029614	76453	protease, serine, 23	Prss23	0.604	-5.215	0.00112227	0.0142129
20543	10398416					0.604	-2.638	0.0326219	0.151829
20544	10588883	NM_001013814	434437	aminomethyltransferase	Amt	0.604	-3.954	0.00518573	0.0423021
20545	10472820	NM_008397	16403	integrin alpha 6	Itga6	0.603	-4.895	0.00161897	0.0184239
20546	10410317	NM_177811	328274	zinc finger protein 459	Zfp459	0.603	-3.392	0.0110576	0.0726995
20547	10497663	NM_172861	241919	solute carrier family 7 (catio	Slc7a14	0.603	-5.306	0.00101401	0.0132839
20548	10481804	NM_175211	241308	Ral GEF with PH domain and SH3	Ralgps1	0.603	-5.01	0.00141643	0.0167544
20549	10407435	NM_134066	105349	aldo-keto reductase family 1,	Akr1c18	0.602	-4.503	0.0025876	0.0260286
20550	10496169	NM_146141	74776	pyrophosphatase (inorganic) 2	Ppa2	0.602	-9.94	1.82182e-05	0.000887571
20551	10425321	NM_030255	80287	apolipoprotein B editing compl	Apobec3	0.602	-7.386	0.000130506	0.00329708
20552	10390860	NM_033373	94179	keratin 23	Krt23	0.602	-7.802	9.13772e-05	0.00263226
20553	10355662	NM_021541	12958	crystallin, beta A2	Cryba2	0.602	-5.734	0.000637707	0.00962378
20554	10398360					0.601	-3.671	0.00755021	0.0557797
20555	10475653	NM_011978	26458	solute carrier family 27 (fatt	Slc27a2	0.601	-7.748	9.56617e-05	0.00271766
20556	10597531	NM_178660	207181	RNA binding motif, single stra	Rbms3	0.6	-5.267	0.00105883	0.0136846
20557	10600205	NM_029352	75590	dual specificity phosphatase 9	Dusp9	0.6	-12.113	4.70623e-06	0.000367274
20558	10379223	NM_001076681	66274	RIKEN cDNA 1810012P15 gene	1810012P15Rik	0.598	-6.846	0.000212229	0.00460715
20559	10478389	NM_008261	15378	hepatic nuclear factor 4, alph	Hnf4a	0.598	-6.13	0.000423806	0.00721493
20560	10429140	NM_008681	17988	N-myc downstream regulated gen	Ndrg1	0.597	-6.972	0.000188938	0.00422741
20561	10440037	NM_023175	52633	nitrilase family, member 2	Nit2	0.597	-6.592	0.000269516	0.00533798
20562	10363856	ENSMUST00000020090	69563	RIKEN cDNA 2310015B20 gene	2310015B20Rik	0.597	-3.544	0.00897412	0.0628593
20563	10377253	ENSMUST00000068548	72804	RIKEN cDNA 9130017K11 gene	9130017K11Rik	0.597	-4.001	0.00487504	0.040518
20564	10546855	NM_080448	259302	SLIT-ROBO Rho GTPase activatin	Srgap3	0.597	-7.09	0.000169766	0.0039593
20565	10344803	NM_026493	211660	centrosome and spindle pole as	Cspp1	0.596	-5.522	0.000800251	0.0112279
20566	10501229	NM_010358	14862	glutathione S-transferase, mu	Gstm1	0.596	-4.555	0.00242974	0.0249511
20567	10442643	NM_019730	79059	non-metastatic cells 3, protei	Nme3	0.595	-8.699	4.45954e-05	0.00161184
20568	10351269	BC048086	74895	RIKEN cDNA 4930455F23 gene	4930455F23Rik	0.594	-6.577	0.000273289	0.00537028
20569	10564211	NM_013670	20646	small nuclear ribonucleoprotei	Snrpn	0.593	-10.316	1.41532e-05	0.000751899
20570	10497580					0.593	-3.271	0.0130933	0.0819555
20571	10491780	NM_011020	18415	heat shock protein 4 like	Hspa4l	0.592	-6.032	0.00046803	0.00769511
20572	10435802	ENSMUST00000023385	212153	RIKEN cDNA 2610015P09 gene	2610015P09Rik	0.592	-8.719	4.39297e-05	0.00159596
20573	10371356	NM_145220	216190	adaptor protein, phosphotyrosi	Appl2	0.592	-6.206	0.000392901	0.00683183
20574	10503188	NM_001081417	320790	chromodomain helicase DNA bind	Chd7	0.591	-7.208	0.000152696	0.00365639
20575	10587871	NM_198414	75552	progestin and adipoQ receptor	Paqr9	0.591	-6.384	0.000329636	0.00606072
20576	10505028	AK141895	100434	solute carrier family 44, memb	Slc44a1	0.59	-9.663	2.20513e-05	0.00100703
20577	10350630	NM_022018	63913	niban protein	Niban	0.59	-3.431	0.0104825	0.0702
20578	10416899	NM_029561	76273	Nedd4 family interacting prote	Ndfip2	0.59	-9.327	2.79798e-05	0.00118321
20579	10542340	ENSMUST00000111915	74525	RIKEN cDNA 8430419L09 gene	8430419L09Rik	0.59	-5.084	0.0013021	0.0158638
20580	10604906	NM_010498	15931	iduronate 2-sulfatase	Ids	0.589	-4.67	0.002112	0.022662
20581	10582778					0.588	-6.352	0.000340156	0.00617891
20582	10547030	NM_001101431	70291	RIKEN cDNA 2510049J12 gene	2510049J12Rik	0.588	-5.732	0.000639332	0.00962823
20583	10355403	NM_010233	14268	fibronectin 1	Fn1	0.588	-8.289	6.14329e-05	0.00200144
20584	10601303	NM_009767	12212	cysteine-rich hydrophobic doma	Chic1	0.587	-10.464	1.28494e-05	0.000712974
20585	10387648	NM_001033433	380705	transmembrane protein 102	Tmem102	0.587	-4.436	0.00281078	0.0276039
20586	10528008	NM_001103157	74051	six transmembrane epithelial a	Steap2	0.586	-5.595	0.00073969	0.0106685

20586	10528008	NM_001103157	74051	six transmembrane epithelial a	Steap2	0.586	-5.595	0.00073969	0.0106683
20587	10382980	NM_009304	20973	synaptogyrin 2	Syngr2	0.586	-7.553	0.00011284	0.00301249
20588	10458430	NM_007858	13367	diaphanous homolog 1 (Drosophi	Diap1	0.585	-9.303	2.84686e-05	0.0011967
20589	10390635	NM_025559	103742	RIKEN cDNA 1810046J19 gene	1810046J19Rik	0.585	-7.825	8.96358e-05	0.00260359
20590	10591754	NM_181419	235048	cDNA sequence BC050092	BC050092	0.585	-8.923	3.76643e-05	0.00142276
20591	10515894	NM_029286	73332	RIKEN cDNA 1700041C02 gene	1700041C02Rik	0.585	-7.057	0.000174858	0.00404951
20592	10503196	NM_001081417	320790	chromodomain helicase DNA bind	Chd7	0.584	-5.196	0.00114695	0.014461
20593	10414514	NM_013632	18950	purine-nucleoside phosphorylas	Pnp1	0.582	-5.262	0.00106441	0.0137094
20594	10512067	NM_172689	230073	DEAD (Asp-Glu-Ala-Asp) box pol	Ddx58	0.582	-4.795	0.00182057	0.0201329
20595	10437195	NM_028078	72058	immunoglobulin superfamily, me	Igsf5	0.582	-7.487	0.000119479	0.00312656
20596	10415725	ENSMUST00000022566	219140	spermatogenesis associated 13	Spata13	0.582	-6.254	0.000374513	0.00659985
20597	10406782	ENSMUST00000042517	320557	RIKEN cDNA B230112C05 gene	B230112C05Rik	0.582	-5.15	0.00120707	0.0150621
20598	10380381	NM_009427	22057	transducer of ErbB-2.1	Tob1	0.581	-8.412	5.57418e-05	0.00186897
20599	10492628	NM_009250	20713	serine (or cysteine) peptidase	Serpini1	0.581	-2.334	0.0512444	0.204475
20600	10523190	BC006604	231440	RIKEN cDNA 9130213B05 gene	9130213B05Rik	0.581	-5.203	0.00113711	0.0143799
20601	10483046	NM_010074	13482	dipeptidylpeptidase 4	Dpp4	0.581	-3.617	0.00811849	0.0585528
20602	10476648	NM_019771	56431	destrin	Dstn	0.581	-4.115	0.00420924	0.036179
20603	10401454	NM_001026214	12499	ectonucleoside triphosphate di	Entpd5	0.581	-6.08	0.000445977	0.00747798
20604	10344805	NM_026493	211660	centrosome and spindle pole as	Cspp1	0.581	-5.67	0.000682182	0.0100727
20605	10462507	NM_011864	23972	3'-phosphoadenosine 5'-phospho	Papss2	0.58	-4.646	0.00217446	0.0231388
20606	10373950	NM_008698	18082	4-nitrophenylphosphatase domai	Nipsnap1	0.58	-8.218	6.50039e-05	0.00206063
20607	10521907	ENSMUST00000073903	66278	RIKEN cDNA 1810013D10 gene	1810013D10Rik	0.58	-6.606	0.000266003	0.00529601
20608	10447732	NM_027032	69310	Park2 co-regulated	Pacrg	0.579	-7.146	0.000161406	0.00382954
20609	10408335	NM_172532	214579	aldhehyde dehydrogenase family	Aldh5a1	0.579	-8.242	6.37787e-05	0.0020557
20610	10439542	NM_001007460	332175	zinc finger, DHHC domain conta	Zdhhc23	0.578	-3.386	0.0111553	0.0730917
20611	10396314	NM_030070	78257	leucine rich repeat containing	Lrrc9	0.578	-3.558	0.00879546	0.0620111
20612	10469404	NM_023116	12296	calcium channel, voltage-depen	Cacnb2	0.578	-6.214	0.000389649	0.00679985
20613	10546454	NM_175314	101401	a disintegrin-like and metallo	Adamts9	0.577	-4.794	0.00182336	0.0201427
20614	10346168	NM_011487	20849	signal transducer and activato	Stat4	0.577	-6.112	0.000431529	0.00729643
20615	10506929	NM_001033226	108802	calreticulin 4	Calr4	0.577	-4.498	0.00260369	0.0261283
20616	10344750	NM_133220	170755	serum/glucocorticoid regulated	Sgk3	0.576	-5.523	0.000798827	0.0112154
20617	10569848	NM_011503	20911	syntaxin binding protein 2	Stxbp2	0.576	-9.964	1.79198e-05	0.000875051
20618	10389590	NM_025638	66569	glycerophosphodiester phosphod	Gdpd1	0.575	-3.323	0.0121674	0.0775627
20619	10427862	NM_007666	12563	cadherin 6	Cdh6	0.575	-6.054	0.000457826	0.00760508
20620	10509063	NM_178257	230828	interleukin 22 receptor, alpha	Il22ra1	0.575	-7.325	0.000137617	0.00341122
20621	10388430	NM_011340	20317	serine (or cysteine) peptidase	Serpinf1	0.574	-12.048	4.88317e-06	0.000371402
20622	10543031	NM_015829	50799	solute carrier family 25 (mito	Slc25a13	0.573	-7.237	0.000148829	0.00359228
20623	10578300	NM_001040699	54384	myotubularin related protein 7	Mtmr7	0.573	-7.224	0.000150463	0.00361522
20624	10559580	NM_016908	53420	synaptotagmin V	Syt5	0.573	-7.608	0.000107669	0.00292993
20625	10380260	NM_009546	217069	tripartite motif-containing 25	Trim25	0.573	-9.745	2.08277e-05	0.000974293
20626	10582275	NM_011404	20539	solute carrier family 7 (catio	Slc7a5	0.572	-5.88	0.000547557	0.00862067
20627	10399178	NM_146040	217946	cell division cycle associated	Cdca7l	0.572	-9.044	3.44205e-05	0.00135203
20628	10585331	NM_176846	320051	exophilin 5	Exph5	0.572	-5.284	0.0010389	0.0134764
20629	10372583	NM_001003950	216363	RAB3A interacting protein	Rab3ip	0.57	-14.534	1.32413e-06	0.000163727
20630	10553354	NM_175272	78286	neuron navigator 2	Nav2	0.57	-7.14	0.000162277	0.00383373
20631	10593413	BC027409	66952	RIKEN cDNA 2310030G06 gene	2310030G06Rik	0.57	-6.774	0.000226901	0.0047976
20632	10578810	NM_007711	12725	chloride channel 3	Clcn3	0.57	-10.395	1.34441e-05	0.000728876
20633	10604447	NM_181751	236781	G-protein coupled receptor 119	Gpr119	0.569	-8.935	3.73217e-05	0.00142276
20634	10463140	NM_172154	212391	ligand dependent nuclear recep	Lcor	0.569	-10.611	1.1686e-05	0.000668901

20635	10497608	NM_021442	17251	myelodysplasia syndrome 1 homo	Mds1	0.569	-4.137	0.00409319	0.0355426
20636	10351224	NM_007976	14067	coagulation factor V	F5	0.569	-6.036	0.00046635	0.0076855
20637	10458245					0.568	-2.887	0.0226837	0.11925
20638	10381118	NM_010257	14459	gastrin	Gast	0.568	-7.806	9.10703e-05	0.002627
20639	10592336	NM_011449	20686	sperm autoantigenic protein 17	Spa17	0.568	-7.742	9.61072e-05	0.00272092
20640	10358816	NM_010683	226519	laminin, gamma 1	Lamc1	0.568	-6.046	0.000461799	0.00764028
20641	10553197	ENSMUST00000063311	791374	predicted gene, ENSMUSG0000005	ENSMUSG00000051803	0.568	-5.456	0.000859212	0.0117587
20642	10604393	NM_019680	56501	E74-like factor 4 (ets domain	Elf4	0.567	-7.414	0.000127294	0.00324668
20643	10540207	ENSMUST00000057977	74516	RIKEN cDNA A730049H05 gene	A730049H05Rik	0.566	-6.221	0.00038721	0.00677185
20644	10534102	NM_010368	110006	glucuronidase, beta	Gusb	0.566	-8.739	4.32569e-05	0.00157694
20645	10378749	NM_198637	74230	RIKEN cDNA 1700016K19 gene	1700016K19Rik	0.566	-4.254	0.00352496	0.0319194
20646	10545041	NM_021432	58243	nucleosome assembly protein 1-	Nap1l5	0.566	-6.251	0.000375661	0.00661363
20647	10494208	BC094388	75007	RIKEN cDNA 4930504E06 gene	4930504E06Rik	0.566	-7.525	0.000115657	0.00306446
20648	10457733	NM_019737	56386	UDP-Gal:betaGlcNAc beta 1,4- ga	B4galt6	0.565	-7.184	0.000155954	0.00371759
20649	10393573	NM_011150	19039	lectin, galactoside-binding, s	Lgals3bp	0.565	-4.423	0.00285377	0.0279433
20650	10572024	NM_023689	72902	sparc/osteonectin, cwcv and ka	Spock3	0.565	-6.284	0.000363577	0.0064655
20651	10585005	NM_009692	11806	apolipoprotein A-I	Apoa1	0.565	-5.072	0.00131892	0.016018
20652	10349694	NM_178079	212933	peptidase M20 domain containin	Pm20d1	0.565	-7.556	0.000112553	0.00301032
20653	10447100	NM_194269	378462	MORN repeat containing 2	Morn2	0.563	-6.502	0.000293908	0.00565571
20654	10486201	ENSMUST00000099535	100038511	predicted gene, OTTMUSG0000001	OTTMUSG00000015946	0.561	-6.453	0.000308046	0.00580546
20655	10384138	NM_134020	103694	transmembrane emp24 protein tr	Tmed4	0.561	-8.144	6.89794e-05	0.0021417
20656	10422280	NM_001033336	239273	ATP-binding cassette, sub-fami	Abcc4	0.561	-6.222	0.000386806	0.00677039
20657	10497548	NM_173182	72007	fibronectin type III domain co	Fndc3b	0.56	-5.06	0.00133834	0.0161873
20658	10351430	NM_009107	20183	retinoid X receptor gamma	Rxrg	0.559	-5.589	0.000744339	0.0107136
20659	10483131	NM_133207	170738	potassium voltage-gated channe	Kcnh7	0.559	-4.384	0.00299809	0.028736
20660	10487476	BC116797	67885	RIKEN cDNA 1500011K16 gene	1500011K16Rik	0.558	-5.34	0.000976068	0.0128727
20661	10396610	NM_138745	108156	methylenetetrahydrofolate dehy	Mthfd1	0.558	-7.911	8.34572e-05	0.00245807
20662	10603051	NM_026887	108012	adaptor-related protein comple	Ap1s2	0.558	-6.798	0.000221853	0.00472392
20663	10546434	NM_175314	101401	a disintegrin-like and metallo	Adamts9	0.558	-4.875	0.00165802	0.0187471
20664	10400984	NM_178715	238257	transmembrane protein 30B	Tmem30b	0.558	-6.458	0.000306663	0.00580491
20665	10434745					0.557	-7.821	8.99885e-05	0.00260646
20666	10483851	NM_009989	13067	cytochrome c, testis	Cyct	0.556	-2.924	0.0214771	0.114762
20667	10500685	NM_144900	11928	ATPase, Na+/K+ transporting, a	Atp1a1	0.555	-8.565	4.94509e-05	0.0017254
20668	10556769	NM_016870	20216	acyl-CoA synthetase medium-cha	Acsm3	0.555	-5.985	0.000491147	0.00799473
20669	10503212	NM_001081417	320790	chromodomain helicase DNA bind	Chd7	0.555	-5.1	0.00127734	0.015736
20670	10453857	NM_010258	14465	GATA binding protein 6	Gata6	0.555	-4.164	0.00395449	0.0346513
20671	10402020	NM_001081191	319670	echinoderm microtubule associa	Eml5	0.555	-5.233	0.00109994	0.0140187
20672	10548905	NM_007945	13860	epidermal growth factor recept	Eps8	0.554	-7.57	0.000111237	0.00299999
20673	10359190	BC023737	215015	RIKEN cDNA C530043G21 gene	C530043G21Rik	0.554	-8.005	7.72676e-05	0.00232724
20674	10347734	NM_001004173	433323	sphingosine-1-phosphate phosph	Sgpp2	0.554	-5.137	0.00122572	0.0152338
20675	10436608	NM_009988	13052	coxsackievirus and adenovirus	Cxadr	0.554	-6.199	0.000395678	0.00687445
20676	10598848	NM_199317	382207	PHD finger protein 16	Phf16	0.553	-8.99	3.58272e-05	0.00138235
20677	10577449	NM_007511	11979	ATPase, Cu++ transporting, bet	Atp7b	0.553	-5.459	0.000856838	0.0117343
20678	10491106	NM_008875	18805	phospholipase D1	Pld1	0.553	-12.032	4.92977e-06	0.000373365
20679	10527965	NM_022890	64945	claudin 12	Cldn12	0.552	-13.326	2.42674e-06	0.000239929
20680	10496302	NM_027288	110173	mannosidase, beta A, lysosomal	Manba	0.551	-5.872	0.000552093	0.00866626
				FGGY carbohydrate kinase					

20681	10503998	NM_001113412	73578	domai	Fggy	0.551	-2.744	0.0279419	0.137109
20682	10428698	NM_016667	20649	syntrophin, basic 1	Sntb1	0.551	-8.087	7.22369e-05	0.00222002
20683	10506188	NM_028132	72157	phosphoglucomutase 2	Pgm2	0.551	-7.817	9.0226e-05	0.00260729
20684	10508883	NM_001083916	69073	RIKEN cDNA 1810019J16 gene	1810019J16Rik	0.551	-7.561	0.000112156	0.00301032
20685	10424400	NM_010849	17869	myelocytomatosis oncogene	Myc	0.55	-5.649	0.000698238	0.0102382
20686	10519886	NM_013657	20348	sema domain, immunoglobulin do	Sema3c	0.55	-3.152	0.0154809	0.0923988
20687	10392484	NM_013851	27404	ATP-binding cassette, sub-fami	Abca8b	0.548	-4.95	0.00151839	0.0175724
20688	10438626	NM_023794	104156	ets variant gene 5	Etv5	0.548	-3.816	0.00621754	0.0481199
20689	10587880	NM_029620	76477	procollagen C-endopeptidase en	Pcolce2	0.546	-9.162	3.15479e-05	0.00127787
20690	10505788	BC060063	230379	N-acylsphingosine amidohydrola	Asah3l	0.546	-6.531	0.000285829	0.00553948
20691	10402394	NM_009246	20703	serine (or cysteine) peptidase	Serpina1d	0.544	-6.627	0.000260755	0.00524089
20692	10503172	NM_001081417	320790	chromodomain helicase DNA bind	Chd7	0.544	-5.61	0.00072789	0.0105559
20693	10602009	NM_023270	66889	ring finger protein 128	Rnf128	0.543	-5.292	0.00103012	0.013395
20694	10399121	NM_011215	19276	protein tyrosine phosphatase,	Ptprn2	0.543	-10.911	9.6584e-06	0.000593655
20695	10435383	NM_023587	70757	protein tyrosine phosphatase-l	Ptplb	0.541	-6.99	0.000185902	0.00421753
20696	10389816	NM_028011	71943	target of myb1-like 1 (chicken	Tom1l1	0.541	-11.22	7.9759e-06	0.000527007
20697	10353181	NM_145381	212442	lactamase, beta 2	Lactb2	0.541	-7.318	0.000138452	0.00342078
20698	10416541	NM_172813	239188	ecto-NOX disulfide-thiol excha	Enox1	0.54	-10.994	9.16528e-06	0.000580212
20699	10530592	NM_177136	72313	furry homolog-like (Drosophila	Fryl	0.539	-12.114	4.70332e-06	0.000367274
20700	10443408	NM_011950	26415	mitogen-activated protein kina	Mapk13	0.539	-8.921	3.76999e-05	0.00142276
20701	10514466	NM_010591	16476	Jun oncogene	Jun	0.539	-6.732	0.000236027	0.00493138
20702	10431872	ENSMUST00000100262	105727	solute carrier family 38, memb	Slc38a1	0.539	-7.74	9.62565e-05	0.00272092
20703	10602805	NM_001081124	78283	MAP7 domain containing 2	Mtap7d2	0.539	-8.051	7.43807e-05	0.00226615
20704	10546853	NM_080448	259302	SLIT-ROBO Rho GTPase activatin	Srgap3	0.539	-8.412	5.57103e-05	0.00186897
20705	10392056	NM_007805	13056	cytochrome b-561	Cyb561	0.539	-6.918	0.000198526	0.00437711
20706	10525256	NM_029912	77462	transmembrane protein 116	Tmem116	0.538	-5.315	0.00100399	0.0131653
20707	10428089	NM_145469	223473	NIPA-like domain containing 2	Npal2	0.538	-8.67	4.56041e-05	0.00163988
20708	10603000	NM_198409	24004	retinoic acid induced 2	Rai2	0.537	-4.432	0.00282436	0.0277115
20709	10394186	NM_007886	13528	dystrobrevin, beta	Dtnb	0.537	-14.635	1.26163e-06	0.000161613
20710	10435789	ENSMUST00000033479	56490	zinc finger and BTB domain con	Zbtb20	0.537	-8.59	4.84939e-05	0.00170608
20711	10529979	NM_008904	19017	peroxisome proliferative activ	Ppargc1a	0.536	-6.477	0.000301031	0.00574459
20712	10398354					0.536	-5.801	0.000594382	0.00916676
20713	10506058	NM_172696	12695	InaD-like (Drosophila)	Inadl	0.536	-14.023	1.70052e-06	0.000189817
20714	10430956	NM_029787	109754	cytochrome b5 reductase 3	Cyb5r3	0.536	-12.641	3.50249e-06	0.000297416
20715	10382341	NM_009217	20606	somatostatin receptor 2	Sstr2	0.535	-6.132	0.000423258	0.00721493
20716	10369040	NM_011282	19886	Ros1 proto-oncogene	Ros1	0.535	-10.043	1.69897e-05	0.000841289
20717	10355960	NM_009129	20254	secretogranin II	Scg2	0.534	-5.832	0.000575585	0.00895525
20718	10548207	NM_007376	11287	pregnancy zone protein	Pzp	0.532	-8.652	4.62474e-05	0.00165738
20719	10513162	ENSMUST00000075637	545622	protein tyrosine phosphatase,	Ptpn3	0.531	-4.535	0.00248852	0.0253525
20720	10440534	NM_011782	23794	a disintegrin-like and metallo	Adamts5	0.531	-6.51	0.000291609	0.00563085
20721	10406646	NM_028772	74129	dimethylglycine dehydrogenase	Dmgdh	0.53	-6.49	0.000297369	0.00569526
20722	10513112	NM_019427	54357	erythrocyte protein band 4.1-l	Epb4.1l4b	0.53	-8.93	3.74587e-05	0.00142276
20723	10549594	NM_021324	57776	tweety homolog 1 (Drosophila)	Ttyh1	0.529	-3.472	0.00989335	0.0675805
20724	10450731	XR_034252	630294	MHC class Ib T9	H2-t9	0.529	-2.149	0.0676086	0.242908
20725	10582020	NM_026572	68133	glycine cleavage system protei	Gcsh	0.529	-13.114	2.71317e-06	0.000250979
20726	10474814	NM_170593	214240	dispatched homolog 2 (Drosophi	Disp2	0.529	-13.203	2.58941e-06	0.000245496
20727	10569038	BC049815	71345	transmembrane protein 16J	Tmem16j	0.528	-6.015	0.000476328	0.00781341
20728	10483000	NM_021359	16420	integrin beta 6	Itgb6	0.527	-5.573	0.00075672	0.0108175

20729	10398319	NM_010052	13386	delta-like 1 homolog (Drosophi	Dlk1	0.527	-9.14	3.20692e-05	0.00128911
20730	10479221	BC098094	433520	predicted gene, OTTMUSG0000001	OTTMUSG00000016571	0.526	-5.962	0.000503152	0.00812731
20731	10549842	NM_001024928	384763	zinc finger protein 667	Zfp667	0.526	-8.403	5.61044e-05	0.00187109
20732	10556509	NM_145584	233744	spondin 1, (f-spondin) extrace	Spon1	0.525	-13.115	2.71163e-06	0.000250979
20733	10601903	NM_001035510	66995	zinc finger, CCHC domain conta	Zcchc18	0.524	-4.956	0.00150822	0.0174739
20734	10435514	NM_134109	106347	immunoglobulin-like domain con	Ildr1	0.521	-5.947	0.000510803	0.008207
20735	10406205	NM_030711	80898	endoplasmic reticulum aminopep	Erap1	0.519	-10.347	1.38687e-05	0.000740626
20736	10587733	NM_007801	13036	cathepsin H	Ctsh	0.519	-11.266	7.75294e-06	0.000517123
20737	10523758	NM_001033550	433926	leucine rich repeat containing	Lrrc8b	0.519	-6.687	0.00024637	0.00504284
20738	10385175	NM_170779	211652	WW, C2 and coiled-coil domain	Wwc1	0.519	-8.543	5.02826e-05	0.00174291
20739	10399505	NM_015764	268527	gene regulated by estrogen in	Greb1	0.518	-6.791	0.000223358	0.00474642
20740	10464471	NM_010253	14419	galanin	Gal	0.518	-7.097	0.00016865	0.00394462
20741	10397507	NM_010363	14874	glutathione transferase zeta 1	Gstz1	0.517	-7.784	9.27977e-05	0.00266592
20742	10508907					0.517	-3.328	0.0120882	0.077195
20743	10419089	NM_027717	71200	DPY30 domain containing 2	Dydc2	0.516	-4.529	0.00250532	0.025443
20744	10554160	ENSMUST00000098370	100038684	predicted gene, ENSMUSG0000007	ENSMUSG00000074066	0.516	-3.359	0.0115717	0.0750297
20745	10430319	NM_009437	22117	thiosulfate sulfurtransferase,	Tst	0.515	-12.617	3.54763e-06	0.000298849
20746	10445879	NM_001031811	211468	potassium voltage-gated channe	Kcnh8	0.515	-7.708	9.89087e-05	0.002759
20747	10375137	NM_031169	16533	potassium large conductance ca	Kcnmb1	0.514	-5.425	0.00088862	0.0120519
20748	10397882	NM_007693	12652	chromogranin A	Chga	0.512	-12.23	4.40158e-06	0.000348901
20749	10541751					0.512	-2.883	0.022803	0.119758
20750	10594973	NM_001081153	208898	unc-13 homolog C (C. elegans)	Unc13c	0.512	-4.171	0.00391898	0.0344401
20751	10515613	NM_011213	19268	protein tyrosine phosphatase,	Ptprf	0.512	-11.298	7.60403e-06	0.000510979
20752	10583320	NM_133214	170748	cDNA sequence BC017612	BC017612	0.512	-6.802	0.000221097	0.00471258
20753	10566926	NM_025999	67150	ring finger protein 141	Rnf141	0.51	-12.675	3.4366e-06	0.000296938
20754	10585982					0.509	-3.865	0.00582379	0.0460502
20755	10498981	NM_181849	110135	fibrinogen, B beta polypeptide	Fgb	0.509	-6.641	0.000257184	0.00517895
20756	10601312	AK147435	331484	predicted gene, ENSMUSG0000007	ENSMUSG00000073019	0.509	-6.259	0.000372769	0.00657916
20757	10476814	NM_016889	53626	insulinoma-associated 1	Insm1	0.509	-5.936	0.000516826	0.00827861
20758	10515003	NM_001099303	545667	predicted gene, OTTMUSG0000000	OTTMUSG00000008243	0.508	-9.093	3.31773e-05	0.00131861
20759	10537509	ENSMUST00000071535	232714	maltase-glucoamylase	Mgam	0.508	-6.836	0.000214259	0.00464644
20760	10581518	NM_025458	66269	transmembrane emp24 protein tr	Tmed6	0.507	-9.642	2.23834e-05	0.00101169
20761	10490129	NM_007557	12162	bone morphogenetic protein 7	Bmp7	0.507	-6.973	0.000188808	0.00422741
20762	10439362	NM_172440	207227	syntaxin binding protein 5-lik	Stxbp5l	0.507	-4.14	0.00407379	0.035447
20763	10370552	NM_015817	50784	phosphatidic acid phosphatase	Ppap2c	0.507	-6.277	0.00036624	0.00649646
20764	10530612	NM_028194	72313	furry homolog-like (Drosophila	Fryl	0.507	-7.261	0.000145684	0.00353339
20765	10523595	NM_011204	19249	protein tyrosine phosphatase,	Ptpn13	0.506	-8.592	4.84155e-05	0.00170608
20766	10506269	NM_009647	11639	adenylate kinase 3 alpha-like	Ak3l1	0.506	-5.368	0.000946611	0.0126278
20767	10535174	NM_144914	231832	transmembrane protein 184a	Tmem184a	0.505	-6.134	0.000422093	0.00720964
20768	10592471	NM_172768	235283	GRAM domain containing 1B	Gramd1b	0.504	-13.194	2.6008e-06	0.000245496
20769	10423498	NM_146057	223453	death-associated protein	Dap	0.503	-10.158	1.57242e-05	0.000808937
20770	10488374	NM_010446	15376	forkhead box A2	Foxa2	0.503	-10.724	1.08654e-05	0.000636968
20771	10514933	NM_009949	12896	carnitine palmitoyltransferase	Cpt2	0.503	-12.476	3.83662e-06	0.000319376
20772	10411126	NM_021310	57748	junction-mediating and regulat	Jmy	0.501	-10.27	1.45913e-05	0.000761775
20773	10467230	NM_031156	15925	insulin degrading enzyme	Ide	0.501	-14.743	1.1984e-06	0.000156235

20774	10417807	ENSMUST00000024155	74571	potassium channel, subfamily K	Kcnk16	0.5	-6.822	0.000216971	0.00467702
20775	10445308	NM_018887	56050	cytochrome P450, family 39, su	Cyp39a1	0.5	-7.675	0.000101752	0.00281072
20776	10534395	NM_009903	12740	claudin 4	Cldn4	0.499	-7.689	0.000100565	0.00278682
20777	10411226	NM_007974	14063	coagulation factor II (thrombi	F2rl1	0.498	-8.071	7.32222e-05	0.00224704
20778	10526853	NM_030565	80752	cDNA sequence BC004044	BC004044	0.498	-12.644	3.49666e-06	0.000297416
20779	10384378	NM_016672	13195	dopa decarboxylase	Ddc	0.497	-9.915	1.85228e-05	0.00089827
20780	10546430	NM_175314	101401	a disintegrin-like and metallo	Adamts9	0.496	-5.551	0.000775	0.011002
20781	10496015	NM_183423	66350	phospholipase A2, group XIIA	Pla2g12a	0.495	-8.041	7.50367e-05	0.00227956
20782	10484227	NM_175465	228071	SEC14 and spectrin domains 1	Sestd1	0.495	-6.119	0.000428556	0.00727109
20783	10604226	NM_021550	59048	C1GALT1-specific chaperone 1	C1galt1c1	0.494	-10.047	1.69451e-05	0.000841289
20784	10583825	NM_172763	235047	zinc finger protein 809	Zfp809	0.492	-7.65	0.000103885	0.00284897
20785	10368343	NM_007482	11846	arginase 1, liver	Arg1	0.491	-10.575	1.19576e-05	0.000679657
20786	10408268	NM_145399	214189	secretagogin, EF-hand calcium	Scgn	0.49	-3.658	0.00767724	0.0564029
20787	10607089	NM_207625	50790	acyl-CoA synthetase long-chain	Acsl4	0.489	-6.974	0.000188644	0.00422741
20788	10362499	NM_010237	14302	fyn-related kinase	Frk	0.485	-7.929	8.22263e-05	0.0024316
20789	10599627	NM_013556	15452	hypoxanthine guanine phosphori	Hprt1	0.485	-8.432	5.48473e-05	0.00186146
20790	10370766	NM_010255	14431	guanidinoacetate methyltransfe	Gamt	0.484	-13.349	2.39805e-06	0.000239929
20791	10600814	NM_008179	14853	G1 to S phase transition 2	Gspt2	0.484	-7.346	0.000135111	0.00336488
20792	10467578	NM_031376	83490	phosphoinositide-3-kinase adap	Pik3ap1	0.483	-7.776	9.33772e-05	0.00267301
20793	10399360	NM_007483	11852	ras homolog gene family, membe	Rhob	0.483	-6.208	0.000392086	0.00682585
20794	10393379	NM_026280	67622	matrix-remodelling associated	Mxra7	0.483	-13.574	2.13416e-06	0.000221199
20795	10491846					0.481	-3.843	0.00600004	0.0469175
20796	10523111	ENSMUST00000094615	622307	similar to LOC360919 protein	LOC622307	0.481	-7.998	7.76866e-05	0.00233325
20797	10363132	NM_025684	66650	nephrocan	Nepn	0.48	-3.408	0.0108198	0.071604
20798	10378240	NM_008771	18436	purinergic receptor P2X, ligan	P2rx1	0.479	-13.278	2.48815e-06	0.000241328
20799	10568332	NM_133351	76560	protease, serine, 8 (prostasin	Prss8	0.479	-4.922	0.0015689	0.0180189
20800	10397189	NM_029880	77219	zinc binding alcohol dehydroge	Zadh1	0.479	-9.846	1.94317e-05	0.00093035
20801	10484894	NM_008982	19271	protein tyrosine phosphatase,	Ptprj	0.478	-14.925	1.09953e-06	0.00015001
20802	10595452	NM_027394	70348	ubiquitin-conjugating enzyme E	Ube2cbp	0.478	-8.92	3.77492e-05	0.00142276
20803	10569646	NM_007631	12443	cyclin D1	Ccnd1	0.478	-10.804	1.03281e-05	0.000623688
20804	10462887	NM_033614	110855	phosphodiesterase 6C, cGMP spe	Pde6c	0.478	-8.599	4.81477e-05	0.00170608
20805	10607619	NM_001024624	382253	cyclin-dependent kinase-like 5	Cdkl5	0.477	-9.338	2.77696e-05	0.00118247
20806	10581455	NM_176838	77411	RNA binding motif protein 35b	Rbm35b	0.477	-11.528	6.62141e-06	0.000464589
20807	10513061	NM_018761	54366	catenin (cadherin associated p	Ctnnal1	0.477	-13.745	1.95588e-06	0.000208864
20808	10416887	NM_198014	105439	SLAIN motif family, member 1	Slain1	0.476	-10.746	1.07172e-05	0.000636968
20809	10485979	NM_010290	14617	gap junction protein, delta 2	Gjd2	0.476	-3.902	0.00554779	0.0445509
20810	10461093	NM_139269	225845	HRAS like suppressor 3	Hrasls3	0.476	-10.054	1.68634e-05	0.000840941
20811	10411395	NM_012026	110596	Rho-guanine nucleotide exchang	Rgnef	0.475	-10.943	9.46563e-06	0.000588651
20812	10513141	ENSMUST00000075637	545622	protein tyrosine phosphatase,	Ptpn3	0.475	-7.468	0.000121475	0.00314805
20813	10506820					0.475	-3.409	0.0107973	0.0715825
20814	10399680	NM_138686	12879	cystin 1	Cys1	0.474	-9.652	2.22166e-05	0.00101021
20815	10569830	BC048787	69697	RIKEN cDNA 2310057J16 gene	2310057J16Rik	0.474	-11.194	8.10039e-06	0.000528933
20816	10344679	NM_173868	240690	suppression of tumorigenicity	St18	0.472	-7.725	9.7489e-05	0.00273746
20817	10406270	NM_053108	93692	glutaredoxin	Glrx	0.47	-12.932	2.99061e-06	0.000268322

20818	10369567	NM_145419	216019	hexokinase domain containing 1	Hkdc1	0.47	-10.366	1.36961e-05	0.000738749
20819	10396656	AK133227	210762	gene model 70, (NCBI)	Gm70	0.469	-6.726	0.000237297	0.00494326
20820	10573979	NM_010308	14681	guanine nucleotide binding pro	Gnao1	0.468	-6.564	0.000276843	0.00540322
20821	10496001	NM_007686	12630	complement component factor i	Cfi	0.468	-6.431	0.00031476	0.00587404
20822	10355836	NM_009049	19711	regulated endocrine-specific p	Resp18	0.468	-12.919	3.01173e-06	0.000268322
20823	10505299	NM_138653	192120	B-box and SPRY domain containi	Bspry	0.466	-14.469	1.3665e-06	0.000167985
20824	10563487	NM_011510	20927	ATP-binding cassette, sub-fami	Abcc8	0.466	-13.707	1.99373e-06	0.000210945
20825	10586781	NM_181072	71602	myosin IE	Myo1e	0.466	-8.913	3.79427e-05	0.00142498
20826	10519770	NM_011995	26875	piccolo (presynaptic cytomatri	Pclo	0.465	-12.752	3.29504e-06	0.000287894
20827	10567355	NM_022420	64297	G protein-coupled receptor, fa	Gprc5b	0.464	-10.057	1.68293e-05	0.000840941
20828	10507551	BC022764	66451	RIKEN cDNA 2610528J11 gene	2610528J11Rik	0.464	-6.552	0.000279967	0.00545084
20829	10602428	ENSMUST00000096285	279561	WNK lysine deficient protein k	Wnk3	0.464	-15.383	8.89508e-07	0.000129709
20830	10369171	AK156585	320305	RIKEN cDNA 9530009G21 gene	9530009G21Rik	0.462	-7.374	0.000131796	0.003318
20831	10513641	NM_010616	16552	kinesin family member 12	Kif12	0.462	-11.089	8.64363e-06	0.000558902
20832	10435075	NM_011638	22042	transferrin receptor	Tfrc	0.459	-9.017	3.51171e-05	0.0013674
20833	10359571	NM_010231	14261	flavin containing monooxygenas	Fmo1	0.458	-3.408	0.0108098	0.0715825
20834	10513922	NM_001017427	242505	RAS and EF hand domain contain	Rasef	0.458	-13.419	2.31203e-06	0.000232789
20835	10523772	NM_178701	231549	leucine rich repeat containing	Lrrc8d	0.457	-11.296	7.61249e-06	0.000510979
20836	10498710	NM_009738	12038	butyrylcholinesterase	Bche	0.457	-8.387	5.68349e-05	0.00188652
20837	10597935	NM_133974	109332	CUB domain containing protein	Cdcp1	0.456	-6.007	0.000480534	0.00785801
20838	10606868	NM_009052	19716	brain expressed gene 1	Bex1	0.455	-7.556	0.000112575	0.00301032
20839	10366153	NM_146240	237504	Ras association (RalGDS/AF-6)	Rassf9	0.455	-10.46	1.2881e-05	0.000712974
20840	10559816					0.454	-5.848	0.000565861	0.00885608
20841	10493516					0.454	-5.451	0.000863898	0.0118152
20842	10500021	BC108378	70737	cingulin	Cgn	0.453	-7.026	0.000179887	0.00412082
20843	10402604					0.453	-6.309	0.000354749	0.00634586
20844	10398408					0.452	-3.572	0.00863051	0.0610776
20845	10398388					0.452	-2.619	0.0335882	0.154552
20846	10506108					0.45	-3.142	0.0157127	0.093166
20847	10585048	NM_207675	54725	cell adhesion molecule 1	Cadm1	0.45	-11.562	6.48857e-06	0.000458844
20848	10406229	NM_013628	18548	proprotein convertase subtilis	Pcsk1	0.449	-6.082	0.000444954	0.00746676
20849	10408280	NM_026825	68732	leucine rich repeat containing	Lrrc16a	0.448	-14.188	1.56763e-06	0.000184145
20850	10457357	ENSMUST00000097679	75739	membrane protein, palmitoylate	Mpp7	0.447	-4.48	0.00266263	0.0265936
20851	10568436	NM_010207	14183	fibroblast growth factor recep	Fgfr2	0.447	-5.601	0.000734643	0.0106174
20852	10517609	NM_028176	72269	cytidine deaminase	Cda	0.447	-5.931	0.000519303	0.00829872
20853	10400926	NM_153457	104001	reticulon 1	Rtn1	0.445	-9.255	2.94923e-05	0.00121557
20854	10445338	NM_032003	83965	ectonucleotide pyrophosphatase	Enpp5	0.444	-9.016	3.51323e-05	0.0013674
20855	10554814					0.441	-6.053	0.000458273	0.00760508
20856	10411527	NM_013732	27220	CART prepropeptide	Cartpt	0.44	-9.991	1.75941e-05	0.000863256
20857	10480570	NM_178408	215705	arrestin domain containing 1	Arrdc1	0.44	-13.298	2.46238e-06	0.000239929
20858	10397633	NM_201518	399558	fibronectin leucine rich trans	Flrt2	0.439	-8.869	3.92002e-05	0.0014663
20859	10380581	NM_008119	14607	gastric inhibitory polypeptide	Gip	0.439	-5.849	0.00056529	0.0088537
20860	10389719	NM_029023	74617	serine carboxypeptidase 1	Scpep1	0.438	-14.291	1.49019e-06	0.000178014
20861	10369154	NM_008548	17155	mannosidase 1, alpha	Man1a	0.438	-11.973	5.09907e-06	0.000382321

20862	10596148	NM_133977	22041	transferrin	Trf	0.438	-7.472	0.000121068	0.00314805
20863	10523021	NM_018760	54403	solute carrier family 4 (anion	Slc4a4	0.437	-7.657	0.000103304	0.00283671
20864	10601161	NM_008124	14618	gap junction protein, beta 1	Gjb1	0.436	-13.245	2.53264e-06	0.000243904
20865	10602692	NM_001004154	245670	Ras-related GTP binding B	Rragb	0.436	-15.315	9.17742e-07	0.000132005
20866	10466886					0.436	-7.962	8.00205e-05	0.00237968
20867	10388310	NM_001015046	380711	GTPase activating RANGAP domai	Garnl4	0.435	-7.817	9.02636e-05	0.00260729
20868	10417628	NM_012061	27062	Ca2+-dependent secretion activ	Cadps	0.435	-12.242	4.3732e-06	0.000348901
20869	10602865	ENSMUST00000033665	270672	mitogen-activated protein kina	Map3k15	0.435	-12.272	4.29968e-06	0.000346994
20870	10539200	NM_009042	19692	regenerating islet-derived 1	Reg1	0.435	-9.523	2.43384e-05	0.00106766
20871	10433887	NM_026163	67451	plakophilin 2	Pkp2	0.434	-9.275	2.90533e-05	0.00120452
20872	10565156	NM_011983	26557	homer homolog 2 (Drosophila)	Homer2	0.432	-8.265	6.25998e-05	0.00203008
20873	10607877	NM_026662	110639	phosphoribosyl pyrophosphate s	Prps2	0.432	-18.663	2.2757e-07	5.86798e-05
20874	10415980	NM_015795	50759	F-box protein 16	Fbxo16	0.431	-11.826	5.55169e-06	0.000410437
20875	10462822	NM_175353	107371	exocyst complex component 6	Exoc6	0.429	-9.194	3.08275e-05	0.00126067
20876	10584827	NM_007962	14012	myelin protein zero-like 2	Mpzl2	0.429	-10.169	1.56049e-05	0.000804756
20877	10352448	NM_022019	63953	dual specificity phosphatase 1	Dusp10	0.428	-12.264	4.31926e-06	0.000347249
20878	10406982	NM_001081020	108154	a disintegrin-like and metallo	Adamts6	0.427	-6.31	0.000354297	0.00634586
20879	10607156	NM_001110222	13193	doublecortin	Dcx	0.427	-8.634	4.68831e-05	0.00167166
20880	10543319	NM_138587	27999	DNA segment, Chr 6, Wayne Stat	D6Wsu176e	0.427	-16.582	5.24686e-07	9.57331e-05
20881	10485445	NM_007914	13661	ets homologous factor	Ehf	0.427	-9.331	2.79111e-05	0.00118321
20882	10485388	NM_178886	241576	low density lipoprotein recept	Ldlrad3	0.426	-21.697	7.81034e-08	3.30284e-05
20883	10574259	NM_018882	14766	G protein-coupled receptor 56	Gpr56	0.426	-11.332	7.44913e-06	0.000508433
20884	10380599	NM_172799	237930	tubulin tyrosine ligase-like f	Ttll6	0.426	-3.237	0.0137368	0.0848032
20885	10428081	NM_008287	15473	heat-responsive protein 12	Hrsp12	0.423	-11.966	5.11891e-06	0.000382453
20886	10591522	NM_001110300	11768	adaptor protein complex AP-1,	Ap1m2	0.421	-14.576	1.29817e-06	0.000162417
20887	10597470	NM_027294	70031	CKLF-like MARVEL transmembrane	Cmtm8	0.421	-13.116	2.71056e-06	0.000250979
20888	10491486	NM_029570	76295	ATPase, class VI, type 11B	Atp11b	0.42	-11.724	5.89348e-06	0.000425296
20889	10356154	NM_172430	77629	SPHK1 interactor, AKAP domain	Sphkap	0.42	-8.453	5.39577e-05	0.00184311
20890	10538753					0.419	-9.53	2.42109e-05	0.00106427
20891	10554249	NM_007424	11595	aggrecan	Acan	0.418	-13.451	2.2738e-06	0.000230034
20892	10606083	NM_007709	12705	Cbp/p300-interacting transacti	Cited1	0.418	-9.033	3.46816e-05	0.00135547
20893	10464045	NM_027976	433256	acyl-CoA synthetase long-chain	Acsl5	0.416	-15.399	8.82916e-07	0.000129704
20894	10571599					0.416	-8.116	7.05776e-05	0.00218491
20895	10421950	NM_007826	13134	dachshund 1 (Drosophila)	Dach1	0.415	-6.574	0.000274319	0.00538052
20896	10355225	ENSMUST00000097706	100038569	predicted gene, ENSMUSG0000007	ENSMUSG00000073656	0.414	-4.287	0.00338205	0.0310771
20897	10414192	NM_133653	11720	methionine adenosyltransferase	Mat1a	0.413	-14.094	1.64172e-06	0.000187819
20898	10456254	NM_001114386	83814	neural precursor cell expresse	Nedd4l	0.41	-16.579	5.2521e-07	9.57331e-05
20899	10562223	NM_008557	17178	FXYD domain-containing ion tra	Fxyd3	0.409	-14.984	1.0695e-06	0.000149759
20900	10528015	NM_027399	70358	six transmembrane epithelial a	Steap1	0.407	-7.625	0.000106103	0.00289852

20901	10354506	NM_133829	98682	RIKEN cDNA 2210010L05 gene	2210010L05Rik	0.407	-9.993	1.75696e-05	0.000863256
20902	10576581	NM_008430	16525	potassium channel, subfamily K	Kcnk1	0.405	-9.042	3.44657e-05	0.00135203
20903	10546450	NM_175314	101401	a disintegrin-like and metallo	Adamts9	0.405	-5.875	0.000550114	0.00864162
20904	10502279	BC049886	77669	RIKEN cDNA 9130221D24 gene	9130221D24Rik	0.403	-10.069	1.66882e-05	0.00083847
20905	10401109	NM_030677	14776	glutathione peroxidase 2	Gpx2	0.402	-6.809	0.000219541	0.00469892
20906	10522127	NM_031180	83379	klotho beta	Klb	0.4	-10.8	1.03528e-05	0.000623688
20907	10569129	NM_011328	20287	secretin	Sct	0.4	-10.704	1.10052e-05	0.000641032
20908	10495596	NM_001113478	20321	ferric-chelate reductase 1	Frrs1	0.399	-10.403	1.33678e-05	0.000726604
20909	10595768	NM_001033210	102502	expressed sequence AI427122	AI427122	0.399	-8.447	5.4203e-05	0.0018485
20910	10392522	NM_153145	217258	ATP-binding cassette, sub-fami	Abca8a	0.398	-6.263	0.00037139	0.00656579
20911	10571567	NM_172752	234214	sorbin and SH3 domain containi	Sorbs2	0.397	-7.719	9.80236e-05	0.00274155
20912	10421970					0.396	-5.518	0.000803673	0.0112535
20913	10510574	NM_133753	74155	ERBB receptor feedback inhibit	Errfi1	0.396	-18.009	2.92923e-07	6.61923e-05
20914	10404053	NM_023422	68024	histone cluster 1, H2bc	Hist1h2bc	0.395	-9.163	3.15324e-05	0.00127787
20915	10559790	NM_011769	22776	zinc finger, imprinted 1	Zim1	0.393	-5.687	0.000670329	0.00994627
20916	10398382					0.392	-4.21	0.00372734	0.0332773
20917	10492890	NM_030695	80877	LPS-responsive beige-like anch	Lrba	0.392	-17.549	3.51697e-07	7.43628e-05
20918	10458052	NM_013512	13824	erythrocyte protein band 4.1-l	Epb4.1l4a	0.392	-9.684	2.17359e-05	0.000999095
20919	10397984	NM_028980	74521	RIKEN cDNA 8430415E04 gene	8430415E04Rik	0.391	-12.08	4.79453e-06	0.0003692
20920	10367982	NM_001002268	215798	G protein-coupled receptor 126	Gpr126	0.39	-7.556	0.000112592	0.00301032
20921	10540401	NM_008516	16979	leucine rich repeat protein 1,	Lrrn1	0.39	-6.58	0.000272614	0.00536864
20922	10603746	NM_172778	109731	monoamine oxidase B	Maob	0.39	-9.387	2.6814e-05	0.00114768
20923	10585990					0.389	-8.646	4.64693e-05	0.00165971
20924	10389775	NM_008796	18559	phosphatidylcholine transfer p	Pctp	0.388	-17.028	4.35075e-07	8.43966e-05
20925	10351546	NM_013474	11807	apolipoprotein A-II	Apoa2	0.387	-2.439	0.0438068	0.1843
20926	10578904	NM_013494	12876	carboxypeptidase E	Cpe	0.387	-6.771	0.000227589	0.00480253
20927	10567995	NM_019738	56312	nuclear protein 1	Nupr1	0.386	-7.546	0.00011354	0.00302355
20928	10546432	NM_175314	101401	a disintegrin-like and metallo	Adamts9	0.385	-5.223	0.00111192	0.0141204
20929	10539894	NM_011844	23945	monoglyceride lipase	Mgll	0.385	-6.61	0.000265031	0.00528661
20930	10526191	BC026208	80909	opposite strand transcription	Gats	0.385	-9.762	2.0586e-05	0.000965757
20931	10426685	BC039633	72778	RIKEN cDNA 2810451A06 gene	2810451A06Rik	0.385	-12.055	4.86303e-06	0.000371205
20932	10359561	NM_144878	226564	flavin containing monooxygenas	Fmo4	0.384	-5.811	0.000588162	0.00910442
20933	10504606	NM_028270	72535	aldehyde dehydrogenase 1 famil	Aldh1b1	0.382	-9.286	2.88324e-05	0.00120006
20934	10517666	ENSMUST00000097830	73162	OTU domain containing 3	Otud3	0.382	-17.873	3.0896e-07	6.80484e-05
20935	10389877	ENSMUST00000061469	278507	WAP, follistatin/kazal, immuno	Wfikkn2	0.38	-9.059	3.40409e-05	0.00134033
20936	10366546	BC100404	70574	carboxypeptidase M	Cpm	0.379	-9.172	3.13185e-05	0.00127346
20937	10456653	NM_201600	17919	myosin Vb	Myo5b	0.378	-16.927	4.53733e-07	8.72158e-05
20938	10403303	NM_013778	27384	aldo-keto reductase family 1,	Akr1c13	0.378	-8.15	6.86416e-05	0.00213441
20939	10438017	NM_139232	224014	FYVE, RhoGEF and PH domain con	Fgd4	0.377	-16.772	4.84165e-07	9.14034e-05
20940	10351623	NM_172647	16456	F11 receptor	F11r	0.377	-6.739	0.000234471	0.00490372
20941	10535559	NM_025833	66898	BAI1-associated protein 2-like	Baiap2l1	0.374	-11.796	5.64915e-06	0.000416187
20942	10576332	NM_023279	22152	tubulin, beta 3	Tubb3	0.372	-6.327	0.000348585	0.00626742
20943	10409713	NM_022317	114304	solute carrier family 28 (sodi	Slc28a3	0.369	-7.825	8.96356e-05	0.00260359
20944	10427075	NM_010664	16668	keratin 18	Krt18	0.369	-9.305	2.84435e-05	0.0011967
20945	10585986					0.369	-7.372	0.000132124	0.003318
20946	10598064					0.368	-4.326	0.00322163	0.0301008
20947	10457686	NM_013505	13506	desmocollin 2	Dsc2	0.368	-8.089	7.21194e-05	0.00221964
20948	10435733	NM_170599	207683	immunoglobulin superfamily, me	Igsf11	0.365	-13.069	2.77979e-06	0.000253344

20949	10597817	NM_031161	12424	cholecystokinin	Cck	0.362	-7.599	0.000108531	0.00294958
20950	10411459	NM_001025606	380863	transmembrane protein 171	Tmem171	0.362	-10.727	1.08498e-05	0.000636968
20951	10580635	NM_053200	104158	carboxylesterase 3	Ces3	0.361	-9.669	2.19646e-05	0.00100524
20952	10347036	NM_001039934	17756	microtubule-associated protein	Mtap2	0.36	-7.287	0.000142316	0.00347475
20953	10591749	AK142481	69862	RIKEN cDNA 1810064F22 gene	1810064F22Rik	0.359	-14.613	1.27494e-06	0.000161613
20954	10598236	NM_021431	58242	nudix (nucleoside diphosphate	Nudt11	0.359	-8.416	5.55599e-05	0.00186897
20955	10396472	NM_198866	386753	DNA binding protein with his-t	Dbpht2	0.358	-20.759	1.06925e-07	4.03719e-05
20956	10368477	BC021783	67719	RIKEN cDNA 2310057J18 gene	2310057J18Rik	0.356	-10.916	9.62811e-06	0.00059364
20957	10501762	NM_029655	76561	sorting nexin 7	Snx7	0.354	-11.68	6.04856e-06	0.000435003
20958	10355806	NM_009447	22145	tubulin, alpha 4A	Tuba4a	0.353	-12.077	4.8032e-06	0.0003692
20959	10581882	NM_025583	66473	chymotrypsinogen B1	Ctrb1	0.353	-3.801	0.00634423	0.0488679
20960	10531790	NM_144955	18096	NK6 transcription factor relat	Nkx6-1	0.352	-14.601	1.28223e-06	0.000161613
20961	10564539	NM_001024703	244049	multiple C2 domains, transmemb	Mctp2	0.352	-8.789	4.16406e-05	0.00153847
20962	10363118	NM_025705	66686	discoidin, CUB and LCCL domain	Dcbld1	0.351	-14.017	1.7057e-06	0.000189817
20963	10414537	NM_007447	11727	angiogenin, ribonuclease, RNas	Ang	0.347	-14.081	1.65221e-06	0.000187819
20964	10555460	NM_019990	56018	START domain containing 10	Stard10	0.347	-14.784	1.17539e-06	0.00015574
20965	10497487	XM_975226	635702	N-acetylated alpha-linked acid	Naaladl2	0.345	-8.829	4.0409e-05	0.0015016
20966	10462881	NM_181748	107221	G protein-coupled receptor 120	Gpr120	0.344	-21.86	7.40391e-08	3.19486e-05
20967	10363056	NM_011376	20464	single-minded homolog 1 (Droso	Sim1	0.342	-9.059	3.40213e-05	0.00134033
20968	10361358	NM_019958	56533	regulator of G-protein signali	Rgs17	0.34	-10.229	1.49974e-05	0.000777221
20969	10561712	NM_011464	20733	serine protease inhibitor, Kun	Spint2	0.34	-15.093	1.0165e-06	0.000144248
20970	10365545	NM_008777	18478	phenylalanine hydroxylase	Pah	0.34	-10.409	1.33181e-05	0.000725768
20971	10353036	ENSMUST00000097824	100038398	predicted gene, ENSMUSG0000007	ENSMUSG00000073738	0.34	-6.99	0.000185881	0.00421753
20972	10490845	NM_025519	66371	chromatin modifying protein 4C	Chmp4c	0.338	-13.199	2.59442e-06	0.000245496
20973	10395058	NM_134052	104923	acireductone dioxygenase 1	Adi1	0.337	-19.461	1.69132e-07	4.83261e-05
20974	10595081	NM_012033	26944	tubulointerstitial nephritis a	Tinag	0.334	-5.964	0.000502027	0.00811534
20975	10513156	ENSMUST00000075637	545622	protein tyrosine phosphatase,	Ptpn3	0.334	-14.152	1.59575e-06	0.000185387
20976	10562480	NM_033080	110959	nudix (nucleoside diphosphate	Nudt19	0.334	-11.058	8.81146e-06	0.000568017
20977	10593167	D00925	21399	transcription elongation facto	Tcea1	0.333	-6.12	0.000428354	0.00727109
20978	10406905	NM_183115	76041	coiled-coil domain containing	Ccdc125	0.333	-11.121	8.47577e-06	0.000551421
20979	10544906	BC080818	68252	RIKEN cDNA A030007L17 gene	A030007L17Rik	0.332	-14.925	1.09968e-06	0.00015001
20980	10396936	NM_022316	64075	SPARC related modular calcium	Smoc1	0.332	-8.226	6.45703e-05	0.00205963
20981	10498741	NM_026460	67931	serine (or cysteine) peptidase	Serpini2	0.331	-2.724	0.0287693	0.139358
20982	10404359	NM_153546	218121	membrane bound O-acyltransfera	Mboat1	0.329	-9.83	1.96474e-05	0.000937755
20983	10574027	NM_013602	17748	metallothionein 1	Mt1	0.328	-18.759	2.19448e-07	5.80001e-05
20984	10498448	NM_183191	269437	phospholipase C, eta 1	Plch1	0.328	-14.989	1.06721e-06	0.000149759
20985	10420899	NM_178747	268756	gulonolactone (L-) oxidase	Gulo	0.326	-8.957	3.67095e-05	0.00140613
20986	10354529	BC048645	67080	RIKEN cDNA 1700019D03 gene	1700019D03Rik	0.324	-9.198	3.07194e-05	0.00125878
20987	10469565	NM_018809	19213	pancreas specific transcriptio	Ptf1a	0.324	-	1.47101e-06	0.000176721

							14.317		
20988	10467153	NM_172838	240638	solute carrier family 16 (mono	Slc16a12	0.32	-8.387	5.68151e-05	0.00188652
20989	10361956	NM_008635	17761	microtubule-associated protein	Mtap7	0.319	-13.138	2.67983e-06	0.000250979
20990	10488366	NM_010919	18088	NK2 transcription factor relat	Nkx2-2	0.318	-11.588	6.38572e-06	0.000453676
20991	10416057	NM_013492	12759	clusterin	Clu	0.317	-12.548	3.68524e-06	0.000309209
20992	10485624	NM_178695	228413	proline rich Gla (G-carboxyglu	Prrg4	0.313	-10.553	1.21263e-05	0.00068336
20993	10502224	NM_028943	74442	sphingomyelin synthase 2	Sgms2	0.311	-10.623	1.15936e-05	0.000667944
20994	10420362	NM_008125	14619	gap junction protein, beta 2	Gjb2	0.31	-9.817	1.98108e-05	0.000940559
20995	10456237	NM_009182	20451	ST8 alpha-N-acetyl-neuraminide	St8sia3	0.306	-11.289	7.64707e-06	0.000511676
20996	10480003	NM_010582	16425	inter-alpha trypsin inhibitor,	Itih2	0.306	-6.812	0.000218977	0.00469892
20997	10542917	BC096374	101202	expressed sequence AI987662	AI987662	0.301	-15.45	8.62559e-07	0.000129704
20998	10407126	NM_152804	20620	polo-like kinase 2 (Drosophila	Plk2	0.296	-13.973	1.74347e-06	0.000191999
20999	10423855	NM_053271	116838	regulating synaptic membrane e	Rims2	0.295	-22.293	6.44078e-08	2.96052e-05
21000	10513166	NM_011207	545622	protein tyrosine phosphatase,	Ptpn3	0.295	-18.429	2.48799e-07	6.09446e-05
21001	10505623	BC030404	52829	DNA segment, Chr 4, Brigham &	D4Bwg0951e	0.294	-8.012	7.68287e-05	0.00231859
21002	10559420	NM_181820	353499	transmembrane channel-like gen	Tmc4	0.293	-25.112	2.75539e-08	2.27641e-05
21003	10497214	NM_001025261	21985	tumor protein D52	Tpd52	0.29	-9.603	2.30048e-05	0.00102927
21004	10513152	ENSMUST00000075637	545622	protein tyrosine phosphatase,	Ptpn3	0.29	-9.761	2.05995e-05	0.000965757
21005	10355176	BC051128	70861	RIKEN cDNA 4921521F21 gene	4921521F21Rik	0.289	-11.017	9.03675e-06	0.00057901
21006	10485402	NM_010218	14221	four jointed box 1 (Drosophila	Fjx1	0.289	-22.796	5.49299e-08	2.63963e-05
21007	10382328	NM_011448	20682	SRY-box containing gene 9	Sox9	0.285	-18.72	2.22714e-07	5.81367e-05
21008	10459421	NM_001001488	54670	ATPase, class I, type 8B, memb	Atp8b1	0.283	-18.885	2.09281e-07	5.6013e-05
21009	10348410	NM_029269	75396	secreted phosphoprotein 2	Spp2	0.282	-15.601	8.05891e-07	0.000124642
21010	10476868	ENSMUST00000066038	78068	RIKEN cDNA 6430503K07 gene	6430503K07Rik	0.281	-16.26	6.02419e-07	0.000102722
21011	10407072	NM_029001	74559	ELOVL family member 7, elongat	Elovl7	0.28	-12.784	3.23915e-06	0.000284185
21012	10530059	NM_172710	231238	RIKEN cDNA 2310045A20 gene	2310045A20Rik	0.279	-15.725	7.62152e-07	0.000123015
21013	10408838	NM_019423	54326	elongation of very long chain	Elovl2	0.275	-18.373	2.54238e-07	6.09446e-05
21014	10445325	NM_030598	53901	regulator of calcineurin 2	Rcan2	0.273	-17.468	3.63344e-07	7.55229e-05
21015	10353346	NM_153179	241035	polycystic kidney and hepatic	Pkhd1	0.273	-12.074	4.81242e-06	0.0003692
21016	10499412	NM_016899	53868	RAB25, member RAS oncogene fam	Rab25	0.271	-11.786	5.68336e-06	0.000417253
21017	10565152	ENSMUST00000098326	319890	RIKEN cDNA 9330120H11 gene	9330120H11Rik	0.27	-19.021	1.98871e-07	5.39092e-05
21018	10513154	ENSMUST00000075637	545622	protein tyrosine phosphatase,	Ptpn3	0.269	-11.493	6.7607e-06	0.000470224
21019	10419288	NM_008102	14528	GTP cyclohydrolase 1	Gch1	0.269	-17.972	2.97179e-07	6.61923e-05
21020	10363545	NM_009719	11925	neurogenin 3	Neurog3	0.268	-4.845	0.00171744	0.0192339
21021	10545958	NM_013471	11746	annexin A4	Anxa4	0.267	-12.104	4.72893e-06	0.000367604
21022	10513158	ENSMUST00000075637	545622	protein tyrosine phosphatase,	Ptpn3	0.267	-8.555	4.98436e-05	0.00173338

21023	10433782	NM_025769	66793	EF hand calcium binding domain	Efcab1	0.267	-16.227	6.10892e-07	0.000103334
21024	10431659	NM_001109040	16564	kinesin family member 21A	Kif21a	0.265	-21.307	8.88667e-08	3.61346e-05
21025	10508405	NM_025452	66260	transmembrane protein 54	Tmem54	0.264	-16.009	6.72064e-07	0.000111017
21026	10592001	NM_011176	19143	suppression of tumorigenicity	St14	0.263	-16.196	6.19294e-07	0.000103923
21027	10506004	NM_030014	77963	hook homolog 1 (Drosophila)	Hook1	0.262	-22.872	5.36456e-08	2.63786e-05
21028	10587082	NM_008262	15379	one cut domain, family member	Onecut1	0.261	-24.084	3.71263e-08	2.29448e-05
21029	10564818	NM_008486	16790	alanyl (membrane) aminopeptida	Anpep	0.254	-16.458	5.52975e-07	9.74342e-05
21030	10462818	NM_008245	15242	hematopoietically expressed ho	Hhex	0.254	-8.226	6.45827e-05	0.00205963
21031	10546962	NM_021488	58991	ghrelin	Ghrl	0.25	-16.459	5.52915e-07	9.74342e-05
21032	10474312	NM_013627	18508	paired box gene 6	Pax6	0.25	-24.584	3.20625e-08	2.29448e-05
21033	10432918	NM_031170	16691	keratin 8	Krt8	0.243	-14.97	1.07659e-06	0.000149759
21034	10443463	NM_007669	12575	cyclin-dependent kinase inhibi	Cdkn1a	0.241	-15.596	8.07605e-07	0.000124642
21035	10513145	ENSMUST00000075637	545622	protein tyrosine phosphatase,	Ptpn3	0.239	-18.083	2.84514e-07	6.53889e-05
21036	10404649	BC033467	109620	desmoplakin	Dsp	0.239	-12.229	4.40581e-06	0.000348901
21037	10396466	ENSMUST00000095617	74284	RIKEN cDNA 1700086L19 gene	1700086L19Rik	0.237	-8.054	7.42222e-05	0.00226458
21038	10424113	NM_178920	105853	mal, T-cell differentiation pr	Mal2	0.236	-20.51	1.16496e-07	4.04969e-05
21039	10490559	NM_015730	11438	cholinergic receptor, nicotini	Chrna4	0.236	-13.898	1.81104e-06	0.000196372
21040	10530269	NM_178446	245945	RNA binding motif protein 47	Rbm47	0.235	-17.28	3.92155e-07	7.94047e-05
21041	10379765	NM_009330	21410	HNF1 homeobox B	Hnf1b	0.23	-23.859	3.96996e-08	2.29448e-05
21042	10484276	NM_010894	18012	neurogenic differentiation 1	Neurod1	0.229	-10.046	1.69554e-05	0.000841289
21043	10501963	NM_011674	22239	UDP galactosyltransferase 8A	Ugt8a	0.228	-10.959	9.36993e-06	0.000586067
21044	10472350	NM_145523	227960	grancalcin	Gca	0.226	-13.512	2.20353e-06	0.00022508
21045	10380927	NM_010346	14786	growth factor receptor bound p	Grb7	0.226	-24.064	3.73452e-08	2.29448e-05
21046	10492735	NM_133862	99571	fibrinogen, gamma polypeptide	Fgg	0.224	-22.41	6.20414e-08	2.91512e-05
21047	10360328	NM_011318	20219	serum amyloid P-component	Apcs	0.223	-16.473	5.49468e-07	9.74342e-05
21048	10530615	NM_026950	433904	OCIA domain containing 2	Ociad2	0.221	-16.404	5.66015e-07	9.89076e-05
21049	10402360	NM_144834	217847	serine (or cysteine) peptidase	Serpina10	0.22	-24.354	3.42941e-08	2.29448e-05
21050	10492174	NM_145539	229302	transmembrane 4 superfamily me	Tm4sf4	0.219	-21.365	8.71454e-08	3.61295e-05
21051	10587150	NM_001081322	208943	myosin VC	Myo5c	0.219	-31.702	5.20151e-09	1.14953e-05
21052	10428619	NM_015744	18606	ectonucleotide pyrophosphatase	Enpp2	0.215	-17.267	3.94319e-07	7.94047e-05
21053	10478525	NM_026323	67701	WAP four-disulfide core domain	Wfdc2	0.21	-15.7	7.70784e-07	0.000123466
21054	10491952	NM_174995	211666	microsomal glutathione S-trans	Mgst2	0.205	-13.975	1.74218e-06	0.000191999
21055	10501811	NM_145394	213603	solute carrier family 44, memb	Slc44a3	0.205	-12.491	3.80371e-06	0.000317888
21056	10491171	NM_031197	20526	solute carrier family 2 (facil	Slc2a2	0.202	-20.887	1.02352e-07	4.00763e-05
21057	10468762	NM_001114312	71653	RIKEN cDNA 4930506M07 gene	4930506M07Rik	0.201	-19.918	1.43431e-07	4.26325e-05

21058	10416451	NM_019775	56373	carboxypeptidase B2 (plasma)	Cpb2	0.201	-19.923	1.43174e-07	4.26325e-05
21059	10474936	NM_016907	20732	serine protease inhibitor, Kun	Spint1	0.198	-24.295	3.48876e-08	2.29448e-05
21060	10373467	NM_010153	13867	v-erb-b2 erythroblastic leukem	Erbb3	0.193	-14.046	1.68116e-06	0.000189077
21061	10542632	NM_010491	15874	islet amyloid polypeptide	Iapp	0.193	-7.023	0.000180317	0.00412621
21062	10493474	NM_013605	17829	mucin 1, transmembrane	Muc1	0.19	-22.001	7.07319e-08	3.11574e-05
21063	10377673	NM_016887	53624	claudin 7	Cldn7	0.188	-22.135	6.77343e-08	3.04718e-05
21064	10530089	NM_009827	12425	cholecystokinin A receptor	Cckar	0.183	-18.343	2.57165e-07	6.09446e-05
21065	10362138	NM_011704	22361	vanin 1	Vnn1	0.183	-12.464	3.86249e-06	0.000320269
21066	10354003	NM_173870	269181	mannoside acetylglucosaminyltr	Mgat4a	0.181	-11	9.13518e-06	0.000580043
21067	10536505	NM_008591	17295	met proto-oncogene	Met	0.18	-10.978	9.25767e-06	0.000580843
21068	10440522	NM_009621	11504	a disintegrin-like and metallo	Adamts1	0.179	-14.156	1.59244e-06	0.000185387
21069	10423623	BC030476	239368	cDNA sequence BC030476	BC030476	0.178	-27.345	1.4989e-08	1.7607e-05
21070	10399202	ENSMUST00000048880	238455	RIKEN cDNA 4732474O15 gene	4732474O15Rik	0.177	-20.136	1.32758e-07	4.16289e-05
21071	10386211	BC117741	75429	RIKEN cDNA 3100002J23 gene	3100002J23Rik	0.176	-20.113	1.3388e-07	4.16289e-05
21072	10587077	BC023444	15379	one cut domain, family member	Onecut1	0.174	-28.384	1.14802e-08	1.5171e-05
21073	10523095	NM_145146	280662	afamin	Afm	0.173	-24.196	3.59175e-08	2.29448e-05
21074	10476355	NM_007694	12653	chromogranin B	Chgb	0.173	-10.753	1.06669e-05	0.000636968
21075	10368289	NM_008813	18605	ectonucleotide pyrophosphatase	Enpp1	0.172	-14.116	1.6243e-06	0.000187673
21076	10551836	NM_009944	12865	cytochrome c oxidase, subunit	Cox7a1	0.169	-13.672	2.02982e-06	0.000212468
21077	10467887	NM_030703	93721	carboxypeptidase N, polypeptid	Cpn1	0.169	-23.321	4.67024e-08	2.40848e-05
21078	10407327	NM_010330	13723	embigin	Emb	0.168	-17.461	3.64327e-07	7.55229e-05
21079	10523062	NM_009654	11657	albumin	Alb	0.168	-3.158	0.0153526	0.0919852
21080	10436958	NM_172469	209195	chloride intracellular channel	Clic6	0.168	-30.816	6.37253e-09	1.22492e-05
21081	10454172	NM_007883	13511	desmoglein 2	Dsg2	0.166	-15.158	9.86341e-07	0.000140913
21082	10487994	NM_198029	241639	RIKEN cDNA 5830467P10 gene	5830467P10Rik	0.165	-10.767	1.05765e-05	0.00063351
21083	10404250	NM_177577	195208	doublecortin domain containing	Dcdc2a	0.165	-8.868	3.92512e-05	0.0014663
21084	10442327	NM_018777	54419	claudin 6	Cldn6	0.164	-14.085	1.64962e-06	0.000187819
21085	10407445	NM_013777	622402	aldo-keto reductase family 1,	Akr1c12	0.163	-13.954	1.7604e-06	0.000192859
21086	10542470	NM_019946	56615	microsomal glutathione S-trans	Mgst1	0.163	-33.159	3.769e-09	1.13845e-05
21087	10501374	NM_001033304	229722	RIKEN cDNA 5330417C22 gene	5330417C22Rik	0.161	-29.955	7.80704e-09	1.28491e-05
21088	10560431	NM_008260	15377	forkhead box A3	Foxa3	0.161	-14.32	1.46914e-06	0.000176721
21089	10574023	NM_008630	17750	metallothionein 2	Mt2	0.16	-7.551	0.000113059	0.00301454
21090	10423770	NM_026496	252973	grainyhead-like 2 (Drosophila)	Grhl2	0.157	-24.124	3.66895e-08	2.29448e-05
21091	10476633	NM_008792	18549	proprotein convertase subtilis	Pcsk2	0.157	-18.503	2.41868e-07	6.01655e-05
21092	10483074	NM_008100	14526	glucagon	Gcg	0.156	-5.15	0.00120745	0.0150621
21093	10379190	NM_011707	22370	vitronectin	Vtn	0.15	-20.031	1.37779e-07	4.22202e-05

21094	10527565	NM_008814	18609	pancreatic and duodenal homeob	Pdx1	0.15	-29.44	8.83995e-09	1.28491e-05
21095	10497490	XM_975226	635702	N-acetylated alpha-linked acid	Naaladl2	0.144	-15.53	8.32142e-07	0.000126581
21096	10462484	NM_001081074	69865	APOBEC1 complementation factor	A1cf	0.144	-18.331	2.58414e-07	6.09446e-05
21097	10595033	NM_009130	20255	secretogranin III	Scg3	0.142	-26.827	1.71887e-08	1.81719e-05
21098	10363090	NM_177306	320995	regulatory factor X domain con	Rfxdc1	0.14	-19.884	1.45173e-07	4.26325e-05
21099	10351852	NM_007768	12944	C-reactive protein, pentraxin-	Crp	0.14	-17.836	3.1362e-07	6.80781e-05
21100	10595070	BC120577	208994	RIKEN cDNA C530008M07 gene	C530008M07Rik	0.137	-14.95	1.08702e-06	0.00015001
21101	10411668	NM_008756	18260	occludin	Ocln	0.136	-31.507	5.43665e-09	1.14953e-05
21102	10474129	NM_173749	210622	RIKEN cDNA E430002G05 gene	E430002G05Rik	0.13	-16.046	6.61224e-07	0.000110086
21103	10471567	AK147796	329385	Riken cDNA C130021I20 gene	C130021I20Rik	0.13	-20.804	1.05314e-07	4.03719e-05
21104	10363455	NM_025273	13180	pterin 4 alpha carbinolamine d	Pcbd1	0.122	-20.606	1.12721e-07	4.04969e-05
21105	10464313	NM_018874	18946	pancreatic lipase related prot	Pnliprp1	0.121	-8.132	6.96765e-05	0.00216018
21106	10447383	NM_008532	17075	tumor-associated calcium signa	Tacstd1	0.121	-23.741	4.11228e-08	2.29448e-05
21107	10523078	NM_007423	11576	alpha fetoprotein	Afp	0.121	-4.904	0.00160282	0.0183009
21108	10560618	NM_007469	11812	apolipoprotein C-I	Apoc1	0.119	-28.07	1.24318e-08	1.54622e-05
21109	10391561	NM_145435	217212	peptide YY	Pyy	0.119	-23.808	4.03044e-08	2.29448e-05
21110	10449467	NM_025469	109791	colipase, pancreatic	Clps	0.118	-20.434	1.19625e-07	4.04969e-05
21111	10395925	NM_177321	338320	melanoma inhibitory activity 2	Mia2	0.115	-29.314	9.11545e-09	1.28491e-05
21112	10467319	NM_011255	19662	retinol binding protein 4, pla	Rbp4	0.113	-10.347	1.3871e-05	0.000740626
21113	10359689	NM_009721	11931	ATPase, Na+/K+ transporting, b	Atp1b1	0.109	-20.699	1.09146e-07	4.04873e-05
21114	10603573	NM_177704	236643	synaptotagmin-like 5	Sytl5	0.105	-22.905	5.31096e-08	2.63786e-05
21115	10454192	NM_013697	22139	transthyretin	Ttr	0.103	-8.775	4.20807e-05	0.0015474
21116	10537051	NM_025350	109697	carboxypeptidase A1	Cpa1	0.1	-26.842	1.71167e-08	1.81719e-05
21117	10531034	NM_153598	100727	UDP glucuronosyltransferase 2	Ugt2b34	0.098	-13.613	2.09192e-06	0.00021789
21118	10411680	NM_001038602	218518	MARVEL (membrane-associating)	Marveld2	0.094	-38.169	1.37329e-09	6.19394e-06
21119	10575052	NM_009864	12550	cadherin 1	Cdh1	0.089	-26.334	1.96246e-08	1.88611e-05
21120	10458704	NM_009258	20730	serine peptidase inhibitor, Ka	Spink3	0.086	-7.562	0.00011204	0.00301032
21121	10358210	NM_030676	26424	nuclear receptor subfamily 5,	Nr5a2	0.083	-16.35	5.79451e-07	0.000100426
21122	10345065	NM_001077353	14859	glutathione S-transferase, alp	Gsta3	0.081	-21.135	9.41409e-08	3.75569e-05
21123	10392687	BC038904	217294	cDNA sequence BC006965	BC006965	0.08	-25.455	2.50062e-08	2.27641e-05
21124	10603059	NM_020626	57394	transmembrane protein 27	Tmem27	0.079	-9.312	2.82863e-05	0.00119378
21125	10359582	NM_018881	55990	flavin containing monooxygenas	Fmo2	0.078	-17.279	3.92392e-07	7.94047e-05
21126	10489444	NM_138685	192201	WAP four-disulfide core domain	Wfdc15b	0.077	-41.186	7.95238e-10	6.19394e-06
21127	10561187	NM_019394	12587	melanoma inhibitory activity 1	Mia1	0.075	-19.529	1.64981e-07	4.77857e-05
21128	10598507	NM_172479	209837	solute carrier family 38, memb	Slc38a5	0.073	-23.481	4.44931e-08	2.3519e-05
21129	10511560	NM_194055	207920	RNA binding motif protein 35A	Rbm35a	0.072	-39.093	1.15669e-09	6.19394e-06

21130	10464113	NM_146101	226243	hyaluronic acid binding protei	Habp2	0.066	-37.828	1.4647e-09	6.19394e-06
21131	10523717	NM_009263	20750	secreted phosphoprotein 1	Spp1	0.065	-24.264	3.52101e-08	2.29448e-05
21132	10497501	XM_975226	635702	N-acetylated alpha-linked acid	Naaladl2	0.065	-25.159	2.71855e-08	2.27641e-05
21133	10361023	NM_008937	19130	prospero-related homeobox 1	Prox1	0.062	-33.85	3.25123e-09	1.13845e-05
21134	10402390	NM_009244	20701	serine (or cysteine) preptidas	Serpina1b	0.06	-7.233	0.000149324	0.00360013
21135	10423024	NM_029341	75568	calcyphosine-like	Capsl	0.059	-26.553	1.84954e-08	1.86223e-05
21136	10537014	NM_001024698	232680	carboxypeptidase A2, pancreati	Cpa2	0.057	-15.366	8.96243e-07	0.000129796
21137	10403312	NM_001013785	432720	aldo-keto reductase family 1,	Akr1c19	0.044	-19.167	1.88384e-07	5.27358e-05
21138	10471912	NM_027552	70789	kynureninase (L-kynurenine hyd	Kynu	0.043	-19.1	1.93138e-07	5.30351e-05
21139	10392685	BC038904	217294	cDNA sequence BC006965	BC006965	0.041	-32.32	4.52994e-09	1.14953e-05
21140	10419392	BC026534	67082	RIKEN cDNA 1700011H14 gene	1700011H14Rik	0.04	-20.409	1.20663e-07	4.04969e-05
21141	10402368	NM_007618	12401	serine (or cysteine) peptidase	Serpina6	0.038	-7.032	0.000178821	0.00410086
21142	10513630	NM_007443	11699	alpha 1 microglobulin/bikunin	Ambp	0.032	-20.414	1.20456e-07	4.04969e-05
21143	10531149	NM_008096	14473	group specific component	Gc	0.028	-39.958	9.88268e-10	6.19394e-06
21144	10402406	NM_009245	20702	serine (or cysteine) peptidase	Serpina1c	0.015	-13.226	2.55786e-06	0.000244721