

List of genes shared by 2 or more conditions

		Genes		
	KO		Q127	
8 week	4 week		4 week	8week
1.3428527	1.0601262	Neat1		1.4284111
2.4652126	1.1489944	Hba-a2		
1.7399819		Prlr		1.0646274
3.111755		Aqp1		1.9575336
1.7956289		Atp6v0c		1.0738758
2.0685086		Car12		1.4035779
1.6790735		Cldn2		1.5474962
1.9205033		Enpp2		1.117159
2.3837333		F5		1.686241
2.7462626		Folr1		1.7731359
2.3995326		Kl		1.6075755
2.3980997		Mfrp		1.5683223
2.3323045		Slc4a5		1.8311877
1.841246		Sostdc1		2.0932417
2.2757316		Tmem72		1.888291
2.991229		Ttr		1.7306032
2.188433		Fos		-1.1277798
	1.1405486	Hba-a1		1.0857738
2.0662901	-1.682463	Serpina3n		
		Pappa	1.2137659	1.4523327
		Hrk	1.1286	1.3608981
		Tph2	2.364149	-2.310985
		Tpm3-rs7	2.9142725	-3.5522106
		Slc6a4	3.024273	-1.7999885
-8.11413		Prl	4.7180734	
-5.324482		Gh	4.0395603	-4.7703366
		Fam107b	-1.586022	-2.375244
		Rgs8	-1.1860577	-1.7970152
		Gng3		-2.5796657
		Gng13	-1.3208373	
		Cep76	-1.1432967	-1.6916614
		Grid2ip	-1.1255116	-1.6129229
		Gm12824	-1.1985961	-2.0349653
		Col18a1	-1.0123405	-1.4858131
-1.1083415		Fgf7	-1.4567494	-2.3024333
		Gpr63	-1.3418	-2.212989
		Car7	-1.0565186	-1.4780756

		Mdf1	-1.736591	-2.3656747
		Stac	-1.1562532	-1.851951
		Opn3	-1.5936227	-1.9498464
		Tmem200b	-1.0901387	-1.7781327
-1.3045175	-1.2721598	Gabra2		-1.2583914
-6.780358	-7.4732094	Atxn2		
-1.8715258	-2.0086167	Ubc		
-1.9141468	-1.602179	Gm10382		
-4.902426		Gm5506		-1.2396859



Number inside colored cell represents fold change

This is a liberal analysis with FDR at 0 and or very low p-value

means up-regulated relative to WT

means down-regulated relative to WT

Common genes upregulated in KO experiments

		Genes		
	KO		Q127	
8 week	4 week		4 week	8week
1.342853	1.060126	Neat1		1.428411
2.465213	1.148994	Hba-a2		

 means up-regulated relative to WT
 means down-regulated relative to WT

Number inside colored cell represents fold change

This is a liberal analysis with FDR at 0 and or very low p-value

Shared genes upregulated in both Tg experiments

NONE

 means up-regulated relative to WT
 means down-regulated relative to WT

Number inside colored cell represents fold change

This is a liberal analysis with FDR at 0 and or very low p-value

Shared genes down-regulated in both KO experiments

		Genes		
	KO		Q127	
8 week	4 week		4 week	8week
-1.30452	-1.27216	Gabra2		-1.25839
-6.78036	-7.47321	Atxn2		
-1.87153	-2.00862	Ubc		
-1.91415	-1.60218	Gm10382		

 means up-regulated relative to WT
 means down-regulated relative to WT

Number inside colored cell represents fold change

This is a liberal analysis with FDR at 0 and or very low p-value

Shared genes down-regulated in both Tg experiments

		Genes		
	KO		Q127	
8 week	4 week		4 week	8week
		Fam107b	-1.586022	-2.375244
		Rgs8	-1.1860577	-1.7970152
		Cep76	-1.1432967	-1.6916614
		Grid2ip	-1.1255116	-1.6129229
		Gm12824	-1.1985961	-2.0349653
		Col18a1	-1.0123405	-1.4858131
-1.1083415		Fgf7	-1.4567494	-2.3024333
		Gpr63	-1.3418	-2.212989
		Car7	-1.0565186	-1.4780756
		Mdfi	-1.736591	-2.3656747
		Stac	-1.1562532	-1.851951
		Opn3	-1.5936227	-1.9498464
		Tmem200b	-1.0901387	-1.7781327



means up-regulated relative to WT

means down-regulated relative to WT

Number inside colored cell represents fold change

This is a liberal analysis with FDR at 0 and or very low p-value

Genes shared by three experiments

		Genes		
	KO		Q127	
8 week	4 week		4 week	8week
2.188433		Fos		-1.12778
2.06629	-1.68246	Serpina3n		
		Tph2	2.364149	-2.31099
		Tpm3-rs7	2.914273	-3.55221
		Slc6a4	3.024273	-1.79999
-8.11413		Prl	4.718073	
-5.32448		Gh	4.03956	-4.77034

 means up-regulated relative to WT
 means down-regulated relative to WT

Number inside colored cell represents fold change

This is a liberal analysis with FDR at 0 and or very low p-value

#DisplayNa Name	Chr	Strand	Start	Stop	TotalRegion
ENSMUSGC ENSMUSG000000042605	chr5	+	122161345	122266502	7062
ENSMUSGC ENSMUSG000000008348	chr5	-	125866334	125870572	2387
ENSMUSGC ENSMUSG000000052305	chr7	-	110975047	110976610	863
ENSMUSGC ENSMUSG000000073940	chr7	-	110961037	110962510	703
ENSMUSGC ENSMUSG000000021091	chr12	+	105644938	105652539	2064
ENSMUSGC ENSMUSG000000000560	chr5	-	71352295	71487088	2392
ENSMUSGC ENSMUSG000000069919	chr11	+	32183510	32184465	812
ENSMUSGC ENSMUSG000000092274	chr19	-	5824707	5845478	20771
ENSMUSGC ENSMUSG000000025270	chrX	+	146981917	147005181	2092
ENSMUSGC ENSMUSG000000069917	chr11	+	32196488	32197301	670
ENSMUSGC ENSMUSG000000024810	chr19	+	29999603	30035194	2872
ENSMUSGC ENSMUSG000000072612	chr5	+	125869691	125870924	727
ENSMUSGC ENSMUSG000000037579	chr15	+	99055291	99073248	3698

NegBinom	BH_FDR_N	Log2((sum	AltSpliceCh	AltSpliceM:	tFPKM	cFPKM	#T1	#C1
856.6655	814.477	-7.473209	0	0	0.067955	13.16553	8	1458
177.0923	137.9141	-2.008617	0	0	12.51521	48.64813	498	1821
70.81023	33.39294	1.098646	0	1.183729	277.6944	125.0254	3995	1692
69.00194	32.83403	1.325187	0	1.382956	78.84564	30.29701	924	334
64.87843	29.67963	-1.682463	0	-2.02924	3.342329	10.41187	115	337
61.83863	27.43164	-1.27216	0	0	8.476501	19.78114	338	742
56.12907	22.39155	1.140549	0	0	76.38808	33.37655	1034	425
52.29129	19.13369	1.060126	0	0	3.494532	1.614868	1210	526
48.11749	15.47141	1.198252	0	1.844039	16.574	6.949951	578	228
47.4221	15.23359	1.148994	0	0	58.10733	25.22201	649	265
43.88784	12.83877	1.182027	0	1.854359	10.42263	4.418524	499	199
42.1752	11.55094	-1.602179	0	0	5.693453	16.84129	69	192
41.97853	11.55094	-1.875152	0	-1.361816	0.665086	2.396936	41	139

varCorrT1 varCorrC1 GenomeVersion=M_musculus_Jul_2007, QueriedTreatObs=16670128, QueriedC

-9.312694	-2.893584	Atxn2
-4.525347	-2.578768	Ubc
-1.597982	-2.68294	Hbb-b1
-3.671171	-4.935489	Hbb-b2
-6.450869	-4.923433	Serpina3n
-5.050366	-3.841214	Gabra2
-3.513957	-4.608866	Hba-a1
-3.293501	-4.317009	Neat1
-4.321183	-5.44504	Alas2
-4.161601	-5.245593	Hba-a2
-4.522606	-5.623947	Il33
-7.074921	-5.670789	Gm10382
-7.678506	-6.088307	Kcnh3

.trlObs=15681638

#DisplayNa Name	Chr	Strand	Start	Stop	TotalRegion
ENSMUSGC ENSMUSG00000086503	chrX	-	100655713	100678556	15434
ENSMUSGC ENSMUSG00000042605	chr5	+	122161345	122266502	7062
ENSMUSGC ENSMUSG00000061808	chr18	+	20823750	20832825	1208
ENSMUSGC ENSMUSG00000021342	chr13	+	27149438	27157073	895
ENSMUSGC ENSMUSG00000083773	chr2	-	28788949	28790200	1251
ENSMUSGC ENSMUSG00000083840	chr5	-	5781529	5783607	81
ENSMUSGC ENSMUSG00000022425	chr15	-	54670452	54751701	3473
ENSMUSGC ENSMUSG00000058488	chr5	+	151755181	151796384	5110
ENSMUSGC ENSMUSG00000091282	chr5	+	5781529	5783636	29
ENSMUSGC ENSMUSG00000021250	chr12	+	86814839	86818223	2352
ENSMUSGC ENSMUSG00000046341	chr4	-	69586234	69587205	971
ENSMUSGC ENSMUSG00000019232	chr3	+	130320365	130338668	3726
ENSMUSGC ENSMUSG00000039672	chr16	+	92292633	92298374	1767
ENSMUSGC ENSMUSG00000020713	chr11	-	106161584	106163179	862
ENSMUSGC ENSMUSG00000039323	chr1	+	72871076	72899048	1847
ENSMUSGC ENSMUSG00000008348	chr5	-	125866334	125870572	2387
ENSMUSGC ENSMUSG00000018451	chr11	-	70845450	70847015	1486
ENSMUSGC ENSMUSG00000026579	chr1	+	166081968	166150408	7168
ENSMUSGC ENSMUSG00000004655	chr6	+	55286425	55298549	2627
ENSMUSGC ENSMUSG00000060989	chr4	+	12159926	12165171	5197
ENSMUSGC ENSMUSG00000015090	chr2	-	25322228	25325566	1649
ENSMUSGC ENSMUSG00000031297	chrX	-	98274548	98281359	3784
ENSMUSGC ENSMUSG00000026051	chr1	+	43787446	43799423	902
ENSMUSGC ENSMUSG00000068323	chr6	+	83169821	83254939	5841
ENSMUSGC ENSMUSG00000024121	chr17	-	24300832	24306647	3384
ENSMUSGC ENSMUSG00000050211	chr2	-	119992147	120071071	6807
ENSMUSGC ENSMUSG00000034739	chr9	+	43909820	43917270	2873
ENSMUSGC ENSMUSG00000022949	chr16	+	92485980	92541488	3914
ENSMUSGC ENSMUSG00000046480	chr9	+	44946519	44962235	4940
ENSMUSGC ENSMUSG00000026826	chr2	-	56959240	56976414	4059
ENSMUSGC ENSMUSG00000028125	chr3	+	121747360	121882979	11813
ENSMUSGC ENSMUSG00000001827	chr7	-	109006844	109019302	2297
ENSMUSGC ENSMUSG00000062353	chr5	+	3236388	3236907	519
ENSMUSGC ENSMUSG00000048583	chr7	-	149836672	149852721	5395
ENSMUSGC ENSMUSG00000023236	chr2	-	113616518	113669278	1569
ENSMUSGC ENSMUSG00000032373	chr9	+	66561492	66614652	4539
ENSMUSGC ENSMUSG00000024299	chr17	+	33661148	33690727	5453
ENSMUSGC ENSMUSG00000024190	chr17	-	26642534	26645464	2697
ENSMUSGC ENSMUSG00000040856	chr12	+	110691032	110701546	5657
ENSMUSGC ENSMUSG00000048149	chr11	-	16534865	16536110	1245
ENSMUSGC ENSMUSG00000023034	chr15	+	101097276	101105223	2474
ENSMUSGC ENSMUSG00000014158	chr5	-	115072160	115108430	4076
ENSMUSGC ENSMUSG00000029135	chr5	+	32438844	32460204	5855
ENSMUSGC ENSMUSG00000031849	chr8	+	72897446	72905964	2425
ENSMUSGC ENSMUSG00000031786	chr8	+	97579002	97602041	2832
ENSMUSGC ENSMUSG00000056174	chr4	+	125964036	125991574	4489

ENSMUSGC ENSMUSG00000055368	chr8	+	95483977	95525566	6176
ENSMUSGC ENSMUSG00000019874	chr10	+	57504686	57508256	1250
ENSMUSGC ENSMUSG00000009216	chr2	-	26965899	26998011	2959
ENSMUSGC ENSMUSG000000092274	chr19	-	5824707	5845478	20771
ENSMUSGC ENSMUSG000000063564	chr11	+	51103421	51397420	5736
ENSMUSGC ENSMUSG000000021091	chr12	+	105644938	105652539	2064
ENSMUSGC ENSMUSG000000080242	chr6	+	37756085	37756553	468
ENSMUSGC ENSMUSG000000053310	chr9	-	37352077	37360330	1293
ENSMUSGC ENSMUSG000000028011	chr3	-	81761011	81780124	3859
ENSMUSGC ENSMUSG000000028341	chr4	+	48058024	48099319	5987
ENSMUSGC ENSMUSG000000021848	chr14	-	49277353	49287319	3397
ENSMUSGC ENSMUSG000000043618	chr5	+	90561253	90561700	447
ENSMUSGC ENSMUSG000000005268	chr15	+	10106992	10303504	15339
ENSMUSGC ENSMUSG000000001506	chr11	+	94797537	94814356	6453
ENSMUSGC ENSMUSG000000000889	chr2	+	27020752	27038720	2692
ENSMUSGC ENSMUSG000000048365	chr6	-	7932357	7933386	1008
ENSMUSGC ENSMUSG000000036169	chr12	+	37040755	37045039	1751
ENSMUSGC ENSMUSG000000073643	chr1	-	79698836	79772718	6182
ENSMUSGC ENSMUSG000000079436	chr1	-	89282937	89291304	647
ENSMUSGC ENSMUSG000000000560	chr5	-	71352295	71487088	2392
ENSMUSGC ENSMUSG000000028393	chr4	-	62170202	62180952	1871
ENSMUSGC ENSMUSG000000048108	chr6	-	116642647	116666931	3610
ENSMUSGC ENSMUSG000000027570	chr2	+	180332494	180356894	3619
ENSMUSGC ENSMUSG000000026879	chr2	+	35111926	35163420	3136
ENSMUSGC ENSMUSG000000043192	chr8	+	5639583	5640996	1413
ENSMUSGC ENSMUSG000000040084	chr2	+	118423946	118467328	4279
ENSMUSGC ENSMUSG000000057969	chr9	-	107500004	107511560	4250
ENSMUSGC ENSMUSG000000069917	chr11	+	32196488	32197301	670
ENSMUSGC ENSMUSG000000067235	chr17	+	35607033	35611508	4348
ENSMUSGC ENSMUSG000000069049	chrY	+	346985	365290	4166
ENSMUSGC ENSMUSG000000027849	chr3	+	103379153	103449490	5262
ENSMUSGC ENSMUSG000000059040	chr18	+	48204988	48208032	1757
ENSMUSGC ENSMUSG000000021390	chr13	+	49703439	49719869	2540
ENSMUSGC ENSMUSG000000068196	chr16	-	57624370	57754850	5108
ENSMUSGC ENSMUSG000000002324	chr14	+	56236873	56244232	2748
ENSMUSGC ENSMUSG000000072612	chr5	+	125869691	125870924	727
ENSMUSGC ENSMUSG000000016024	chr2	+	158132228	158158588	4831
ENSMUSGC ENSMUSG000000035459	chr10	-	86303942	86470770	8616
ENSMUSGC ENSMUSG000000024610	chr18	+	60963501	60972300	1398
ENSMUSGC ENSMUSG000000020681	chr11	+	105829258	105851278	4992
ENSMUSGC ENSMUSG000000053399	chr8	-	116221025	116372641	5960
ENSMUSGC ENSMUSG000000029661	chr6	+	4454813	4491543	12145
ENSMUSGC ENSMUSG000000024042	chr17	-	31981192	31992737	4511
ENSMUSGC ENSMUSG000000032246	chr9	+	62705910	62723725	861
ENSMUSGC ENSMUSG000000020415	chr11	-	43233751	43239753	2000
ENSMUSGC ENSMUSG000000086652	chr2	-	129008217	129009683	1348
ENSMUSGC ENSMUSG000000036322	chr17	-	34478896	34481589	1042

ENSMUSGC ENSMUSG00000055866	chr1	-	93312560	93355907	5841
ENSMUSGC ENSMUSG00000041828	chr11	-	109886947	109957292	6284
ENSMUSGC ENSMUSG00000040125	chr7	+	139158142	139186088	11571
ENSMUSGC ENSMUSG00000046711	chr17	+	27693564	27700619	1890
ENSMUSGC ENSMUSG00000029843	chr6	-	35217956	35258131	4528
ENSMUSGC ENSMUSG00000029718	chr5	-	138046330	138055012	3711
ENSMUSGC ENSMUSG00000031503	chr8	+	11312804	11449287	6554
ENSMUSGC ENSMUSG00000030761	chr7	-	105199569	105268034	8524
ENSMUSGC ENSMUSG00000026043	chr1	+	45368382	45406551	8393
ENSMUSGC ENSMUSG00000027208	chr2	+	125860393	125916921	3248
ENSMUSGC ENSMUSG00000047230	chrX	+	136335366	136345925	3325
ENSMUSGC ENSMUSG00000048376	chr13	-	96371758	96388414	3307
ENSMUSGC ENSMUSG00000044042	chr2	+	113167892	113556924	14965
ENSMUSGC ENSMUSG00000023043	chr15	+	101858646	101862457	1400
ENSMUSGC ENSMUSG00000073403	chr17	-	36278702	36282868	1614
ENSMUSGC ENSMUSG00000041380	chrX	+	143397055	143631820	9328
ENSMUSGC ENSMUSG00000022512	chr16	-	26356727	26371927	3247

NegBinom	BH_FDR_N	Log2((sum	AltSpliceCh	AltSpliceM: t	FPKM	cFPKM	#T1	#C1
1194.025	1151.851	-9.363154	0	0	0.026451	19.39491	7	4408
611.7894	572.6259	-6.780358	0	0	0.115616	13.18361	14	1371
366.4812	329.0786	2.991229	0	0	2697.434	326.4446	55873	5807
356.8141	320.6609	-8.11413	0	0	0.065162	36.42024	1	480
232.3737	197.1896	-6.542622	0	0	0.139856	17.09928	3	315
174.6535	140.2613	-6.91813	0	0	0.719997	175.2209	1	209
167.4832	133.7604	1.920503	0	0	557.7238	141.7809	33213	7251
160.1901	127.0472	2.399533	0	0	19.28775	3.508388	1690	264
148.7337	116.4251	-6.671374	0	0	2.011027	412.1348	1	176
148.5989	116.4251	2.188433	0	0	51.92245	10.94275	2094	379
134.6625	102.9026	-3.183971	0	0	3.363447	29.93292	56	428
128.5236	97.14163	-2.0957	0	-3.0239	5.963455	24.58633	381	1349
122.4918	91.45748	3.047092	0	3.129053	16.76652	1.921578	508	50
120.6433	89.93082	-5.324482	0	0	0.270625	13.23508	4	168
112.3664	81.95357	1.948006	0	0	50.36277	12.53753	1595	341
109.1562	79.02361	-1.871526	0	0	11.58089	40.85325	474	1436
102.7896	72.92028	-1.659646	0	0	36.1457	109.9973	921	2407
101.4193	71.79822	2.383733	0	2.121617	5.329165	0.975807	655	103
100.2577	70.87149	3.111755	0	0	8.080852	0.878908	364	34
99.04582	69.88233	-4.864844	0	0	0.056109	1.907764	5	146
97.82716	68.87557	1.43944	0	1.607643	581.2526	206.2378	16435	5008
96.70541	67.95584	3.684876	0	3.651534	4.037997	0.28714	262	16
90.83535	62.27884	2.127539	0	0	47.06962	10.31427	728	137
90.06135	61.68967	2.332305	0	2.979851	5.641273	1.069609	565	92
87.89302	59.69864	1.795629	0	2.17431	20.38779	5.63898	1183	281
85.86158	57.83752	-2.100855	0	-2.708984	1.319413	5.476981	154	549
85.07996	57.21981	2.3981	0	2.799777	9.804543	1.772761	483	75
82.82781	55.1256	1.694624	0	0	19.17669	5.690857	1287	328
80.47891	52.9291	-1.42255	0	0	13.98966	36.11251	1185	2627
80.27007	52.8675	1.559266	0	1.962792	24.92851	8.13096	1735	486
79.72458	52.46441	2.255535	0	2.22211	2.473394	0.494382	501	86
79.5246	52.40231	2.746263	0	3.29079	8.403937	1.182561	331	40
76.58189	49.59324	-6.475661	0	0	0	10.4676	0	80
74.19058	47.33159	1.305137	0	2.103674	52.11485	20.29075	4821	1612
73.32126	46.58815	-1.271178	0	0	96.86509	225.0635	2606	5200
71.13422	44.52345	2.068509	0	2.274265	6.565632	1.496113	511	100
70.3027	43.81093	1.417318	0	2.783682	20.20283	7.272805	1889	584
70.06362	43.68767	1.455932	0	0	34.92267	12.23714	1615	486
69.59747	43.33432	2.648163	0	2.856417	3.030937	0.456165	294	38
64.16973	38.01654	-3.920742	0	0	0.374746	6.16359	8	113
63.51355	37.4676	1.531656	0	0	23.5495	7.822936	999	285
63.09196	37.22044	2.695603	0	2.558755	3.562714	0.516478	249	31
63.05581	37.22044	1.632379	0	0	7.868936	2.435662	790	210
62.95969	37.22044	-2.45984	0	-3.020928	1.226519	6.608834	51	236
61.83926	36.1976	2.569627	0	2.246993	5.436589	0.863245	264	36
60.64315	35.09695	1.901077	0	2.009527	6.262003	1.603544	482	106

58.57372	33.12091	2.462318	0	0	2.502387	0.428827	265	39
57.30657	31.94519	1.288324	0	0	75.48911	29.71679	1618	547
57.11354	31.84172	-1.73231	0	0	3.192904	10.25858	162	447
56.41328	31.2292	1.342853	0	0	3.546188	1.343721	1263	411
55.33867	30.24059	1.794569	0	1.857241	4.849814	1.337808	477	113
55.05599	30.04224	2.06629	0	2.228822	9.691707	2.204397	343	67
53.39815	28.46712	-1.803414	0	0	15.45225	52.23737	124	360
53.03841	28.18856	-1.866899	0	0	4.871257	17.22661	108	328
52.36789	27.59832	-2.102994	0	-2.895397	1.042774	4.364169	69	248
52.29023	27.59832	1.203719	0	0	16.87153	7.043799	1732	621
51.62352	27.00848	1.678482	0	2.231798	8.618347	2.578807	502	129
51.07392	26.53441	-5.15659	0	0	0.130469	9.267165	1	61
50.00377	25.60404	1.739982	0	1.918494	1.653895	0.473709	435	107
49.99631	25.60404	1.640455	0	2.270048	4.554961	1.399634	504	133
49.83213	25.51165	2.782851	0	1.598998	3.74789	0.504521	173	20
49.5251	25.27523	-3.731208	0	0	0.404998	5.928526	7	88
48.8075	24.62712	1.841246	0	0	12.22351	3.25775	367	84
48.2183	24.11467	-1.352459	0	-1.340669	3.037685	7.480708	322	681
48.15932	24.11467	2.202564	0	0	22.44455	4.618203	249	44
46.73438	22.80032	-1.304518	0	0	8.606555	20.49749	353	722
46.71336	22.80032	-1.234654	0	0	14.3072	32.44803	459	894
46.15929	22.31059	2.275732	0	2.297387	3.570269	0.696016	221	37
44.04254	20.25724	1.133869	0	2.270048	22.01293	9.644932	1366	514
43.49338	19.77057	1.032141	0	1.469193	42.30787	19.9005	2275	919
43.12683	19.46562	-1.756233	0	0	4.003552	13.12034	97	273
42.99755	19.45296	4.902832	0	0	0.926792	0.01587	68	1
42.99351	19.45296	1.812539	0	2.110205	4.29508	1.16643	313	73
42.50796	19.02649	2.465213	0	0	14.97164	2.533902	172	25
42.38881	19.01103	-4.498337	0	0	0.026826	0.890246	2	57
42.37669	19.01103	1.408276	0	1.853038	7.937425	2.868917	567	176
42.13982	18.87433	-1.572351	0	-1.624208	1.529481	4.400765	138	341
42.12717	18.87433	-4.902426	0	0	0.033193	1.971165	1	51
40.80416	17.6709	1.572512	0	0	9.138295	2.940923	398	110
40.44554	17.40989	1.771211	0	1.839174	3.425202	0.957208	300	72
40.28003	17.29702	1.455233	0	2.324601	10.0383	3.509104	473	142
40.19776	17.26676	-1.914147	0	0	5.214285	19.14891	65	205
39.90773	17.02813	1.746472	0	2.202822	3.657812	1.040206	303	74
38.43148	15.65288	-2.963596	0	0	0.087994	0.709351	13	90
38.34727	15.61831	-1.585106	0	0	4.797406	13.94117	115	287
38.12786	15.44797	1.089096	0	2.135532	12.73409	5.754272	1090	423
37.53761	14.90624	1.311071	0	1.682571	5.420999	2.096506	554	184
37.41565	14.83228	1.051031	0	1.862032	5.819973	2.700687	1212	483
37.05802	14.52211	1.35243	0	1.95689	6.41246	2.408639	496	160
36.31229	13.86979	2.37543	0	2.927818	10.0925	1.81405	149	23
36.22353	13.82698	1.576778	0	2.324679	9.535283	3.055886	327	90
35.6594	13.31665	-4.28385	0	0	0.086528	2.468487	2	49
35.60853	13.31665	-5.381904	0	0	0	2.411341	0	37

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35.264	13.17621	1.750912	0	2.301144	7.745113	2.191758	251	61
34.76735	12.77561	1.135678	0	0	9.569697	4.184296	743	279
34.74234	12.77561	1.44954	0	0	5.846121	2.049518	372	112
34.7375	12.77561	1.305291	0	1.641506	4.324597	1.678546	486	162
34.69511	12.77438	1.311223	0	1.641506	3.277237	1.266713	479	159
34.60301	12.72306	1.605014	0	1.710546	2.035946	0.639197	293	79
34.25902	12.47709	-1.108342	0	0	6.428103	13.36009	358	639
34.23695	12.47709	1.679074	0	0	4.595423	1.368383	262	67
33.73225	12.01169	-1.533748	0	0	1.851701	5.195303	105	253
33.54614	11.86453	-1.166373	0	-1.435965	1.079491	2.336981	277	515
32.9076	11.41568	2.750438	0	0	4.332326	0.582074	104	12
32.66069	11.20573	-5.262963	0	0	0	1.43054	0	34
32.31928	10.90096	1.078563	0	1.40221	4.72035	2.147623	755	295
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-4.604197 -6.653506 Slc6a2
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Synaptic damage marker

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Angelman

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	ENSMUSGC ENSMUSG000000064359	chrM	+	9390	9458	68	50.29953
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	ENSMUSGC ENSMUSG000000064361	chrM	+	9807	9875	68	31.56101
	ENSMUSGC ENSMUSG000000038112	chr9	-	39394980	39411988	6110	46.71695
	ENSMUSGC ENSMUSG000000048758	chr9	+	106331784	106333899	796	80.18746
	ENSMUSGC ENSMUSG000000032502	chr9	-	111463940	111592852	2644	37.34574
	ENSMUSGC ENSMUSG000000055368	chr8	+	95483977	95525566	6176	54.29575
	ENSMUSGC ENSMUSG000000031883	chr8	+	107058599	107074243	2459	64.26096
	ENSMUSGC ENSMUSG000000030500	chr7	+	58877199	58926495	4319	77.95024
	ENSMUSGC ENSMUSG000000030043	chr6	+	82352327	82510097	6475	40.34717
	ENSMUSGC ENSMUSG000000062353	chr5	+	3236388	3236907	519	100.3399
	ENSMUSGC ENSMUSG000000046607	chr5	+	118619772	118639487	5366	38.13481
	ENSMUSGC ENSMUSG000000010825	chr5	+	144119016	144153831	4786	103.1905
	ENSMUSGC ENSMUSG000000045345	chr5	-	144158926	144161242	2315	81.9089
	ENSMUSGC ENSMUSG000000040372	chr4	+	24893553	24936380	2370	76.98483
	ENSMUSGC ENSMUSG000000028298	chr4	+	34841027	34854619	649	37.01979
	ENSMUSGC ENSMUSG000000028370	chr4	+	64785207	65018543	11114	46.88462
	ENSMUSGC ENSMUSG000000046341	chr4	-	69586234	69587205	971	36.75738
	ENSMUSGC ENSMUSG000000070867	chr4	+	114079328	114287703	6617	63.00361
	ENSMUSGC ENSMUSG000000083679	chr4	+	121756167	121757313	1146	120.5221
	ENSMUSGC ENSMUSG000000070720	chr4	+	131477685	131478540	855	31.7975
	ENSMUSGC ENSMUSG000000026655	chr2	+	3621284	3699414	3603	204.9966
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	ENSMUSGC ENSMUSG000000085845	chr2	+	77300725	77318995	887	50.41965
	ENSMUSGC ENSMUSG000000027210	chr2	-	115688799	115891575	11872	51.84
	ENSMUSGC ENSMUSG000000046814	chr2	+	118993508	118998126	645	53.43367
	ENSMUSGC ENSMUSG000000027208	chr2	+	125860393	125916921	3248	81.57059
	ENSMUSGC ENSMUSG000000027270	chr2	+	135877974	135895653	2933	126.3944
	ENSMUSGC ENSMUSG000000024960	chr19	-	7028203	7044279	4231	81.02516
	ENSMUSGC ENSMUSG000000024863	chr19	+	30307417	30314175	1101	32.22809
	ENSMUSGC ENSMUSG000000073542	chr18	-	67777050	67800990	3979	118.4519
	ENSMUSGC ENSMUSG000000047507	chr17	-	25379603	25393309	4487	53.81683
	ENSMUSGC ENSMUSG000000025739	chr17	+	25854115	25856351	374	116.9115
	ENSMUSGC ENSMUSG000000032717	chr17	-	47952276	47971640	3092	71.03999
	ENSMUSGC ENSMUSG000000004366	chr16	-	23889666	23890930	599	42.51004
	ENSMUSGC ENSMUSG000000039168	chr15	+	31154139	31204093	1481	48.27807
	ENSMUSGC ENSMUSG000000023064	chr14	-	35183459	35187975	852	44.69648
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	ENSMUSGC ENSMUSG000000021342	chr13	+	27149438	27157073	895	69.98023
	ENSMUSGC ENSMUSG000000021708	chr13	-	92020004	92901611	8810	36.80223
	ENSMUSGC ENSMUSG000000000263	chr11	-	55327739	55421700	2273	69.57433
	ENSMUSGC ENSMUSG000000020838	chr11	+	76812104	76845842	4529	52.75116
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ENSMUSGC ENSMUSG000000042671	chr1	+	155500154	155544797	6984	161.1749
ENSMUSGC ENSMUSG000000038530	chr1	-	171671607	171677773	3098	56.43345
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26.01322	4.738849	0	0	45.18181	0.83629	50	1	
45.73052	4.77468	0	0	13.59609	0.326826	77	2	
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23.08005	2.614067	0	2.6941385	0.975513	0.148917	97	16	
51.59451	3.989914	0	0	8.028286	0.428651	104	6	
15.09187	-1.156253	0	0	3.230397	7.119221	139	331	
29.40946	2.368109	0	2.4048772	1.343164	0.248612	135	27	
38.17857	-1.056519	0	0	11.44483	23.47326	458	1015	
49.71941	1.333437	0	1.9139642	9.688721	3.778893	681	287	
17.58177	4.458555	0	0	0.389087	0.008783	41	1	
68.92145	6.487413	0	0	10.18201	0	86	0	
15.70182	1.1286	0	0	3.847611	1.72744	336	163	
71.39424	-1.125512	0	-1.3343273	13.66065	29.37255	1064	2472	
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49.24617	-1.341803	0	0	6.74105	16.86836	260	703	
14.87619	5.08803	0	0	3.029757	0	32	0	
23.18698	1.213766	0	1.4861087	2.139652	0.905668	387	177	
14.80021	1.317929	0	0	14.61825	5.739483	231	98	
37.02588	-1.198596	0	0	2.572297	5.826859	277	678	
86.76285	-1.505498	0	0	19.83899	55.57754	370	1120	
10.75999	-1.090139	0	0	9.414727	19.82057	131	298	
167.5576	-1.586022	0	-1.6564686	17.89014	52.93766	1049	3354	
36.45467	2.944704	0	0	2.624976	0.316871	115	15	
71.39424	-1.668824	0	0	9.430755	29.6385	192	652	
26.04493	-1.592124	0	0	5.611306	16.79746	81	262	
27.33829	1.720725	0	1.5732143	1.133503	0.335305	219	70	
28.78219	-3.162886	0	-3.2256322	0.857404	8.287701	9	94	
52.37066	-1.456749	0	0	4.048557	10.97785	214	627	
91.96567	2.827383	0	2.9963548	5.991789	0.814335	286	42	
52.19708	-1.122168	0	0	8.379832	17.9837	577	1338	
11.12375	4.901432	0	0	1.562692	0	28	0	
85.27258	-1.143297	0	0	24.0137	52.26572	1555	3657	
29.08848	1.973916	0	1.7718712	2.465012	0.608347	180	48	
84.24369	-1.320837	0	-1.608181	102.3573	252.1035	623	1658	
43.79726	-1.736591	0	0	1.947552	6.437163	98	350	
19.5426	2.003428	0	0	13.43838	3.227885	131	34	
24.39293	-1.222235	0	0	7.094856	16.35763	171	426	
21.35338	1.956409	0	0	10.45757	2.603101	145	39	
14.87619	2.914273	0	0	1.838166	0.216022	63	8	
43.21068	4.718073	0	0	5.080556	0.127079	74	2	
14.80389	1.368393	0	1.3333626	1.499564	0.568032	215	88	
43.07967	2.364149	0	2.6640377	4.94714	0.925696	183	37	
28.17522	3.024273	0	2.8309426	1.234644	0.13812	91	11	
318.6323	4.03956	0	4.1877575	45.1231	2.638874	633	40	

55.68756	-1.012341	0	0	9.942186	19.76318	1136	2440
137.0963	-2.156482	0	-1.980317	1.191004	5.253797	167	796
315.8656	3.70686	0	3.5692139	9.650763	0.716028	711	57
12.06981	1.176866	0	1.5157007	2.518981	1.092198	254	119
43.07967	2.364149	0	2.4626148	3.905818	0.730846	183	37
11.88552	1.045693	0	0	26.53404	12.62038	323	166
125.9544	-1.186058	0	0	93.56982	209.7201	10635	25756
31.38325	1.060629	0	0	14.55852	6.865246	734	374
23.86	-1.593623	0	0	2.409067	7.223659	75	243

GenomeVersion=M_musculus_Jul_2007, QueriedTreatObs=16274118, QueriedCtrlObs=17584664

Zcchc12

Gabrq

mt-Tg

mt-Nd3

mt-Tr

AW551984

Rpl29

Stac

Slc6a2

Car7

Rong

Slc17a6

Tacr1

Gm15772

Hrk

Grid2ip

?Rong

RIKEN cDNA 9530056K15 gene

Gpr63

Cga

Pappa

Gm11223

Gm12824

Gm12892

Tmem200b

Fam107b

Dbh

Gm13394

Gm13944

Meis2

Gchfr

GTP cyclohydrolase feedback regulator

Fgf7

Rong

RIKEN cDNA 6330527O06 gene

Plcb3

Mbl2

Cep76

Baiap3

ventricle

Gng13

Rong

Mdfi

Sst

Dap

Sncg

Tpm3-rs7

Fox1

Prl

Rasgrf2

Gla1

glycine receptor

brainstem contaminati

Slc6a4

Gh

Col18a1

Stab2

Mybpc1

Kcnc2

Tph2

Resp18

Rgs8

Rgs4

Opn3

on?

#DisplayName	Name	Chr	Strand	Start	Stop	TotalRegion
ENSMUSG00000026655	ENSMUSG00000026655	chr2	+	3621284	3699414	3603
ENSMUSG00000042671	ENSMUSG00000042671	chr1	+	1.56E+08	1.56E+08	6984
ENSMUSG00000025739	ENSMUSG00000025739	chr17	+	25854115	25856351	374
ENSMUSG00000061808	ENSMUSG00000061808	chr18	+	20823750	20832825	1208
ENSMUSG00000073542	ENSMUSG00000073542	chr18	-	67777050	67800990	3979
ENSMUSG00000038860	ENSMUSG00000038860	chr2	-	32841885	32987174	12210
ENSMUSG00000020788	ENSMUSG00000020788	chr11	+	72774670	72806546	5281
ENSMUSG00000039662	ENSMUSG00000039662	chr4	+	1.52E+08	1.52E+08	5184
ENSMUSG00000020848	ENSMUSG00000020848	chr11	-	75582467	75609551	4120
ENSMUSG00000026094	ENSMUSG00000026094	chr1	-	53812349	53842068	3293
ENSMUSG00000028222	ENSMUSG00000028222	chr4	+	15808410	15835211	4846
ENSMUSG00000030102	ENSMUSG00000030102	chr6	+	1.08E+08	1.09E+08	10434
ENSMUSG00000010825	ENSMUSG00000010825	chr5	+	1.44E+08	1.44E+08	4786
ENSMUSG00000027716	ENSMUSG00000027716	chr3	-	36519403	36589089	5419
ENSMUSG00000004630	ENSMUSG00000004630	chr8	-	3623370	3625545	971
ENSMUSG00000041261	ENSMUSG00000041261	chr4	-	8070513	8166188	3848
ENSMUSG00000037754	ENSMUSG00000037754	chr2	+	1.58E+08	1.59E+08	8844
ENSMUSG00000054901	ENSMUSG00000054901	chr17	+	80706746	80788028	2936
ENSMUSG00000018965	ENSMUSG00000018965	chr5	+	33361464	33370615	3700
ENSMUSG00000006764	ENSMUSG00000006764	chr10	-	1.15E+08	1.15E+08	2879
ENSMUSG00000070867	ENSMUSG00000070867	chr4	+	1.14E+08	1.14E+08	6617
ENSMUSG00000001435	ENSMUSG00000001435	chr10	-	76514922	76629293	7021
ENSMUSG00000022425	ENSMUSG00000022425	chr15	-	54670452	54751701	3473
ENSMUSG00000027208	ENSMUSG00000027208	chr2	+	1.26E+08	1.26E+08	3248
ENSMUSG00000020866	ENSMUSG00000020866	chr11	-	94269704	94335414	10040
ENSMUSG00000040372	ENSMUSG00000040372	chr4	+	24893553	24936380	2370
ENSMUSG00000063524	ENSMUSG00000063524	chr4	+	1.5E+08	1.5E+08	5379
ENSMUSG00000082286	ENSMUSG00000082286	chr11	+	3025906	3031007	1757
ENSMUSG00000003573	ENSMUSG00000003573	chr8	+	72806725	72818260	2566
ENSMUSG00000053965	ENSMUSG00000053965	chr3	+	1.22E+08	1.23E+08	8859
ENSMUSG00000023764	ENSMUSG00000023764	chr11	-	3031852	3093466	7327
ENSMUSG00000071379	ENSMUSG00000071379	chr12	+	17697619	17798732	1561
ENSMUSG00000045345	ENSMUSG00000045345	chr5	-	1.44E+08	1.44E+08	2315
ENSMUSG00000058488	ENSMUSG00000058488	chr5	+	1.52E+08	1.52E+08	5110
ENSMUSG00000024104	ENSMUSG00000024104	chr6	+	1.16E+08	1.16E+08	4300
ENSMUSG00000042425	ENSMUSG00000042425	chrX	+	1.37E+08	1.37E+08	3453
ENSMUSG00000090223	ENSMUSG00000090223	chr16	+	96689212	96747400	398
ENSMUSG00000042978	ENSMUSG00000042978	chr7	+	1.33E+08	1.33E+08	4092
ENSMUSG00000027296	ENSMUSG00000027296	chr2	+	1.2E+08	1.2E+08	1818
ENSMUSG00000025477	ENSMUSG00000025477	chr7	+	1.47E+08	1.47E+08	3284
ENSMUSG00000059811	ENSMUSG00000059811	chr17	-	80247731	80295463	4146
ENSMUSG00000021097	ENSMUSG00000021097	chr12	-	1.06E+08	1.06E+08	11997
ENSMUSG00000002930	ENSMUSG00000002930	chr6	+	55967508	55982682	1738
ENSMUSG00000035735	ENSMUSG00000035735	chr19	-	10319754	10379367	5747
ENSMUSG00000020644	ENSMUSG00000020644	chr12	-	25778665	25780957	1270
ENSMUSG00000005357	ENSMUSG00000005357	chr10	+	78243240	78277570	2089

ENSMUSG00000031883	ENSMUSG00000031883	chr8	+	1.07E+08	1.07E+08	2459
ENSMUSG00000000560	ENSMUSG00000000560	chr5	-	71352295	71487088	2392
ENSMUSG00000046341	ENSMUSG00000046341	chr4	-	69586234	69587205	971
ENSMUSG00000090461	ENSMUSG00000090461	chr10	-	1.18E+08	1.18E+08	1111
ENSMUSG00000032845	ENSMUSG00000032845	chr18	-	65425182	65553542	6338
ENSMUSG00000083879	ENSMUSG00000083879	chr2	-	1.35E+08	1.35E+08	1581
ENSMUSG00000030905	ENSMUSG00000030905	chr7	-	1.27E+08	1.27E+08	3391
ENSMUSG00000092993	ENSMUSG00000092993	chr4	+	8162728	8162829	101
ENSMUSG00000021250	ENSMUSG00000021250	chr12	+	86814839	86818223	2352
ENSMUSG00000017417	ENSMUSG00000017417	chr11	-	97784551	97847758	4836
ENSMUSG00000028370	ENSMUSG00000028370	chr4	+	64785207	65018543	11114
ENSMUSG00000078670	ENSMUSG00000078670	chr7	+	80885192	80921805	2156
ENSMUSG00000038893	ENSMUSG00000038893	chr11	+	95198331	95243186	3001
ENSMUSG00000032717	ENSMUSG00000032717	chr17	-	47952276	47971640	3092
ENSMUSG00000092274	ENSMUSG00000092274	chr19	-	5824707	5845478	20771
ENSMUSG00000067028	ENSMUSG00000067028	chr1	+	1.02E+08	1.02E+08	5124
ENSMUSG00000014198	ENSMUSG00000014198	chr11	-	1E+08	1.01E+08	3046
ENSMUSG00000058126	ENSMUSG00000058126	chr14	+	1.14E+08	1.14E+08	2106
ENSMUSG00000089815	ENSMUSG00000089815	chr13	+	44216535	44220548	1222
ENSMUSG00000036169	ENSMUSG00000036169	chr12	+	37040755	37045039	1751
ENSMUSG00000005220	ENSMUSG00000005220	chr5	-	72691263	72895779	5033
ENSMUSG00000032502	ENSMUSG00000032502	chr9	-	1.11E+08	1.12E+08	2644
ENSMUSG00000055409	ENSMUSG00000055409	chr7	+	57230233	58120625	5918
ENSMUSG00000064372	ENSMUSG00000064372	chrM	-	15355	15422	67
ENSMUSG00000087040	ENSMUSG00000087040	chr2	+	55264200	55285846	2290
ENSMUSG00000070348	ENSMUSG00000070348	chr7	-	1.52E+08	1.52E+08	3017
ENSMUSG00000026525	ENSMUSG00000026525	chr1	-	1.78E+08	1.78E+08	1913
ENSMUSG00000028364	ENSMUSG00000028364	chr4	-	63620818	63681760	7333
ENSMUSG00000068323	ENSMUSG00000068323	chr6	+	83169821	83254939	5841
ENSMUSG00000020838	ENSMUSG00000020838	chr11	+	76812104	76845842	4529
ENSMUSG00000030351	ENSMUSG00000030351	chr6	+	1.28E+08	1.28E+08	4380
ENSMUSG00000021572	ENSMUSG00000021572	chr13	-	74173942	74199733	3632
ENSMUSG00000074280	ENSMUSG00000074280	chr9	+	57331719	57332392	671
ENSMUSG00000047675	ENSMUSG00000047675	chr4	-	1.17E+08	1.17E+08	1551
ENSMUSG00000079993	ENSMUSG00000079993	chr4	-	8094040	8094500	460
ENSMUSG00000032532	ENSMUSG00000032532	chr9	-	1.21E+08	1.21E+08	848
ENSMUSG00000070720	ENSMUSG00000070720	chr4	+	1.31E+08	1.31E+08	855
ENSMUSG00000046805	ENSMUSG00000046805	chr19	+	12535268	12539774	4335
ENSMUSG00000030303	ENSMUSG00000030303	chr6	+	1.48E+08	1.48E+08	4335
ENSMUSG00000024827	ENSMUSG00000024827	chr19	-	30172938	30249908	3754
ENSMUSG00000022519	ENSMUSG00000022519	chr16	-	4480215	4541816	5325
ENSMUSG00000026579	ENSMUSG00000026579	chr1	+	1.66E+08	1.66E+08	7168
ENSMUSG00000064496	ENSMUSG00000064496	chr12	+	1.11E+08	1.11E+08	73
ENSMUSG00000028927	ENSMUSG00000028927	chr4	+	1.4E+08	1.41E+08	4864
ENSMUSG00000024121	ENSMUSG00000024121	chr17	-	24300832	24306647	3384
ENSMUSG00000046607	ENSMUSG00000046607	chr5	+	1.19E+08	1.19E+08	5366
ENSMUSG00000002055	ENSMUSG00000002055	chr11	+	78115030	78135959	5624

ENSMUSG00000015852	ENSMUSG00000015852	chr3	-	87054679	87067660	2334
ENSMUSG00000025202	ENSMUSG00000025202	chr19	+	44277758	44318506	3552
ENSMUSG00000065037	ENSMUSG00000065037	chr9	-	78023109	78023440	331
ENSMUSG00000026051	ENSMUSG00000026051	chr1	+	43787446	43799423	902
ENSMUSG00000036123	ENSMUSG00000036123	chr13	+	74258962	74303512	2490
ENSMUSG00000032373	ENSMUSG00000032373	chr9	+	66561492	66614652	4539
ENSMUSG00000084403	ENSMUSG00000084403	chr4	-	53803941	53804328	387
ENSMUSG00000048108	ENSMUSG00000048108	chr6	-	1.17E+08	1.17E+08	3610
ENSMUSG00000034739	ENSMUSG00000034739	chr9	+	43909820	43917270	2873
ENSMUSG00000019066	ENSMUSG00000019066	chr9	-	21711934	21722636	4196
ENSMUSG00000054065	ENSMUSG00000054065	chr7	+	1.48E+08	1.48E+08	3616
ENSMUSG00000087083	ENSMUSG00000087083	chr6	+	1.14E+08	1.14E+08	1256
ENSMUSG00000022935	ENSMUSG00000022935	chr16	-	87896440	88289947	3332
ENSMUSG00000004655	ENSMUSG00000004655	chr6	+	55286425	55298549	2627
ENSMUSG00000011034	ENSMUSG00000011034	chr5	+	33446867	33505521	4118
ENSMUSG00000025094	ENSMUSG00000025094	chr19	+	59335367	59370502	3803
ENSMUSG00000069919	ENSMUSG00000069919	chr11	+	32183510	32184465	812
ENSMUSG00000047230	ENSMUSG00000047230	chrX	+	1.36E+08	1.36E+08	3325
ENSMUSG00000023795	ENSMUSG00000023795	chr17	-	3076577	3084183	2138
ENSMUSG00000001827	ENSMUSG00000001827	chr7	-	1.09E+08	1.09E+08	2297
ENSMUSG00000038843	ENSMUSG00000038843	chr19	-	17400630	17431157	5583
ENSMUSG00000031628	ENSMUSG00000031628	chr8	+	47702802	47724060	1455
ENSMUSG00000000120	ENSMUSG00000000120	chr11	-	95430131	95449049	3446
ENSMUSG00000060402	ENSMUSG00000060402	chr7	-	35459486	35597730	2787
ENSMUSG00000059040	ENSMUSG00000059040	chr18	+	48204988	48208032	1757
ENSMUSG00000005268	ENSMUSG00000005268	chr15	+	10106992	10303504	15339
ENSMUSG00000000214	ENSMUSG00000000214	chr7	-	1.5E+08	1.5E+08	2364
ENSMUSG00000020713	ENSMUSG00000020713	chr11	-	1.06E+08	1.06E+08	862

NegBinom	BH_FDR_NoVarOutFilt	Log2((sum	AltSpliceCh	AltSpliceM:t	FPKM	cFPKM	#T1
379.2023	337.0647	-2.37524	0	-2.61468	12.79249	64.38466	730
306.7756	267.64838	-1.79702	0	0	64.85653	218.3928	7174
297.5112	260.1448	-2.57967	0	-2.84603	41.86746	243.3939	248
281.6147	245.49773	1.730603	0	0	999.8724	291.8806	19130
206.4205	171.27266	-1.69166	0	0	16.53447	51.78787	1042
203.2351	168.87906	-1.66546	0	-2.15103	5.714039	17.57409	1105
172.6824	139.57574	-1.42697	0	0	25.05946	65.3065	2096
172.953	139.57574	-1.35354	0	0	53.85801	133.3685	4422
165.5081	132.91295	-1.57835	0	0	12.48984	36.17083	815
162.0985	129.96094	-1.61099	0	0	13.11478	38.85664	684
161.3944	129.67079	-1.26778	0	0	119.9977	279.9788	9210
160.1094	128.76369	-1.23511	0	0	223.2188	509.1261	36888
152.6913	121.69313	-1.61292	0	-2.15435	7.717555	22.90059	585
150.4861	119.8098	-1.44926	0	0	12.15239	32.17393	1043
149.3056	118.92898	-1.38401	0	-1.6754	92.00974	232.7824	1415
145.2177	115.121346	-1.19238	0	0	181.8031	402.5763	11080
144.5317	114.69859	-1.26645	0	-1.87115	20.65362	48.15194	2893
140.612	111.02714	-1.36874	0	0	26.3867	66.05966	1227
127.8564	98.50634	-1.15675	0	0	72.81444	157.3172	4267
127.4331	98.30581	-2.31099	0	-2.75623	2.171151	10.53096	99
127.0473	98.13395	-2.03497	0	-2.54978	1.49808	5.979808	157
126.8473	98.13395	-1.48581	0	-2.42136	5.125927	13.92723	570
126.1166	97.5963	1.117159	0	0	310.8402	138.8315	17098
121.6168	93.28136	-2.30243	0	0	1.827294	8.814714	94
120.2728	92.11463	-1.13791	0	0	21.04837	44.8873	3347
118.8859	90.89803	-2.21299	0	0	2.79729	12.66877	105
118.0481	90.22412	1.358383	0	0	23.20608	8.761795	1977
117.7936	90.12756	-1.63544	0	-1.97063	11.53533	34.8043	321
117.1437	89.63011	-1.17617	0	0	48.67054	106.5972	1978
116.8813	89.514946	-1.25849	0	0	8.246036	19.12541	1157
116.2585	89.03456	-1.64931	0	-2.50625	2.611037	7.955252	303
113.5285	86.44246	-1.17149	0	0	71.75419	156.6503	1774
111.7182	84.76575	-1.93307	0	0	4.254712	15.82374	156
110.9441	84.12131	1.607576	0	0	11.91112	3.778283	964
107.2449	80.54802	-1.06247	0	0	55.15104	111.6185	3756
107.0244	80.45164	-2.06889	0	-2.12579	2.102799	8.610295	115
106.9072	80.45164	-1.12307	0	0	310.6177	655.7166	1958
101.192	74.85227	-1.00857	0	0	82.96616	161.7476	5377
99.44758	73.22066	-1.38427	0	0	16.14937	40.90488	465
95.56621	69.44924	-1.00081	0	0	70.67551	137.0528	3676
95.44903	69.4393	-1.04289	0	0	34.32584	68.54148	2254
95.23392	69.39825	-1.04044	0	0	11.99938	23.91953	2280
95.20113	69.39825	-1.03017	0	0	91.51135	181.1193	2519
92.78645	67.083405	-1.13233	0	-1.74701	11.86531	25.21538	1080
90.25382	64.74383	-1.08004	0	0	66.56921	136.4168	1339
87.96171	62.726105	-1.02124	0	0	55.9152	109.9931	1850

86.81735	61.669487	-1.47808	0	0	7.138104	19.31547	278
85.11256	60.135025	-1.25839	0	0	13.43548	31.18115	509
80.67465	55.779842	-1.7891	0	0	8.258118	27.82199	127
78.11668	53.357304	-3.31177	0	0	0.795629	8.193458	14
74.46548	49.96219	-2.13687	0	-2.27608	0.627603	2.710337	63
71.08926	46.94509	-5.23827	0	0	0.039936	3.018152	1
71.18055	46.94509	-4.80107	0	0	0.037239	1.537058	2
71.10278	46.94509	-1.37775	0	0	160.6602	405.5762	257
70.46018	46.451736	-1.12778	0	0	14.71092	31.18084	548
69.57144	45.629314	-1.04384	0	0	9.909507	19.80997	759
68.91074	45.09826	1.452333	0	1.553005	3.23818	1.142708	570
66.0952	42.34612	-1.1365	0	0	13.61761	29.04423	465
65.64121	41.954624	-1.76289	0	-2.39787	2.103926	6.971696	100
65.47871	41.85372	-2.36567	0	-2.80354	0.775962	3.96494	38
64.70478	41.14054	1.428411	0	0	1.63539	0.586692	538
64.54916	41.044823	-1.28795	0	0	3.425565	8.12332	278
63.76256	40.375607	-1.19805	0	-2.08551	7.337869	16.34028	354
63.22076	39.89133	-3.55221	0	0	0.239844	3.067495	8
61.55855	38.285892	-1.78526	0	0	4.546823	15.31894	88
61.33512	38.1185	2.093242	0	0	8.437742	1.886627	234
60.01471	37.015278	-1.96072	0	-1.85736	0.790333	3.019277	63
59.62777	36.68098	-1.85195	0	-1.77306	1.791003	6.330427	75
59.07062	36.22724	-1.04861	0	0	5.48384	11.00293	514
58.463	35.670418	-1.45165	0	0	149.8369	398.8285	159
58.17528	35.53161	-1.58102	0	-2.19162	3.308585	9.649184	120
57.98662	35.39148	1.081759	0	0	19.69296	9.002975	941
57.75186	35.204704	-1.94985	0	0	2.013314	7.636559	61
55.22229	32.877	-1.17872	0	-2.23494	2.514188	5.526078	292
55.19185	32.877	1.831188	0	1.720836	2.799685	0.754091	259
55.1361	32.866253	-1.79999	0	-2.30709	1.031635	3.517362	74
52.88939	30.708176	-1.24304	0	-1.43729	3.272264	7.525439	227
52.34653	30.20896	-1.65407	0	-2.02169	1.564564	4.810505	90
52.27889	30.184536	-3.45368	0	0	0.658676	7.986563	7
51.0624	29.01083	1.986727	11.4051	2.468338	8.263819	1.987912	203
50.17532	28.20808	-1.10572	0	0	42.55008	88.89083	310
49.35135	27.507622	-1.05306	0	0	26.65531	53.67295	358
48.53981	26.816174	-1.77813	0	0	4.800028	16.14178	65
47.98337	26.376589	1.258474	0	0	6.670723	2.692574	458
46.87867	25.385677	-1.01239	0	0	5.476402	10.71949	376
46.72052	25.327724	-1.04038	0	0	5.701669	11.38121	339
46.61625	25.30654	-1.52417	0	-1.52239	1.173849	3.294867	99
46.07569	24.87234	1.686241	0	2.069531	2.096407	0.624729	238
45.42856	24.294699	4.63653	0	0	48.43527	1.005627	56
45.3127	24.247232	1.104287	0	1.643514	7.451006	3.350572	574
45.00691	24.04205	1.073876	0	1.487326	11.38141	5.228129	610
44.90134	23.96951	1.360898	0	0	4.118262	1.545921	350
44.36108	23.462032	-1.04907	0	-1.61307	3.37923	6.787622	301

43.24276	22.503984	1.538257	0	1.74302	7.033461	2.327504	260
43.14484	22.468552	-1.01169	0	0	5.777061	11.30509	325
40.23323	19.739197	-1.03894	0	0	50.35847	100.4685	264
40.15698	19.692589	1.248907	0	0	25.05954	10.17333	358
40.0124	19.635744	-1.95039	0	-2.4343	0.963565	3.685278	38
39.82223	19.474432	1.403578	0	1.326231	3.867062	1.40708	278
39.21975	18.985495	-5.1721	0	0	0	6.070139	0
38.28705	18.244637	1.888291	0	0	2.693457	0.691403	154
37.13628	17.303104	1.568322	0	2.317926	4.505208	1.456461	205
36.56177	16.804665	-1.22937	0	-1.4343	2.031397	4.636283	135
35.98722	16.329386	-1.29908	0	-1.90052	1.955628	4.68968	112
35.26298	15.653942	-2.57336	0	0	0.653507	4.032915	13
34.8919	15.315871	-1.02225	0	-1.75623	4.18778	8.262013	221
34.84771	15.310859	1.957534	0	2.287336	3.100461	0.754507	129
34.37989	14.914044	-1.13703	0	-1.54978	2.391855	5.11629	156
33.35867	13.985718	-1.04766	0	-1.30877	3.171054	6.370114	191
33.20585	13.855817	1.085774	0	0	28.61465	13.01865	368
33.13697	13.8097315	1.547496	0	0	3.437031	1.125999	181
32.89636	13.591803	-1.31213	0	-1.65256	2.835046	6.867235	96
32.26709	13.07418	1.773136	0	1.998319	3.793278	1.05466	138
32.13176	12.982723	1.235037	0	0	3.019536	1.236004	267
32.04397	12.925172	1.064078	0	1.522801	15.83895	7.315847	365
30.94153	11.94263	1.317793	0	1.643514	4.085885	1.576435	223
30.80615	11.849216	-1.05665	0	0	3.738036	7.5597	165
30.29748	11.376677	-1.23969	0	0	3.629495	8.356374	101
29.96628	11.092071	1.064627	0	1.145204	1.358356	0.626951	330
29.37177	10.538339	-1.56961	0	-1.84183	1.308715	3.819594	49
29.09006	10.317089	-4.77034	0	0	0	2.043919	0

#C1	varCorrT1	varCorrC1	GenomeVersion=M_musculus_Jul_2007, QueriedTreatObs=15838113, QueriedTreatObs=15838113, QueriedTreatObs=15838113	
3160	-5.59662	-3.29162	Fam107b	
20777	-2.38166	-0.59274	Rgs8	
1240	-7.03448	-4.61186	Gng3	
4803	-0.97389	-2.69471	Ttr	
2807	-5.10736	-3.45997	Cep76	
2923	-5.02608	-3.40245	Garnl3	
4698	-4.1311	-2.72629	Atp2a3	Fox2
9418	-3.07281	-1.73017	Icmt	
2030	-5.44586	-3.91904	Doc2b	
1743	-5.68541	-4.13406	Stk17b	
18482	-2.02376	-0.76118	Calb1	
72363	-0.02872	1.205078	Itpr1	
1493	-5.89773	-4.35177	Grid2ip	
2375	-5.10603	-3.697	Trpc3	
3079	-4.68212	-3.32855	Pcp2	
21102	-1.75859	-0.5704	Car8	
5801	-3.67578	-2.42475	Ppp1r16b	
2642	-4.88071	-3.54596	Arhgef33	
7929	-3.12364	-1.97707	Ywhah	
413	-8.1821	-6.12135	Tph2	
539	-7.61609	-5.76151	Gm12824	
1332	-5.93287	-4.51175	Col18a1	
6568	-1.13538	-2.24697	Enpp2	
390	-8.24429	-6.19822	Fgf7	
6139	-3.46902	-2.34369	Cacan1g	pacemaker cells
409	-8.11114	-6.13442	Gpr63	
642	-4.21338	-5.52297	Eno1	
833	-6.69835	-5.16479	Pisd-ps1	
3726	-4.21267	-3.05704	Homer3	
2308	-4.9623	-3.73752	Pde5a	cGMP-specific 3',5'-cyclic phos
794	-6.77399	-5.23098	Sfi1	
3331	-4.36563	-3.21664	Hpcal1	
499	-7.62408	-5.86616	9530056K15Rik	
263	-5.21486	-6.72062	Kl	
6538	-3.30519	-2.25352	D6Wsu116e	
405	-8.00067	-6.14762	Frmpd3	
3555	-4.22696	-3.12398	Pcp4	
9016	-2.79388	-1.79277	Sbk1	
1013	-6.20683	-4.89369	Itpka	
6131	-3.3358	-2.34556	Inpp5a	
3871	-4.02865	-3.00262	Atl2	
3909	-4.01247	-2.98869	Clmn	
4288	-3.87169	-2.85668	Ppp1r17	
1974	-5.05778	-3.95854	Dagla	
2360	-4.75912	-3.70597	Id2	
3130	-4.30672	-3.30519	Slc1a6	

647	-6.88637	-5.51235	Car7						
1016	-6.08549	-4.88958	Gabra2						
368	-7.87914	-6.27588	???						
124	-10.281	-7.68305	Itifb						
234	-8.71384	-6.87332	Alpk2						
65	-12.1004	-8.46561	Gm14038						
71	-11.7416	-8.36139	Crym						
558	-6.98836	-5.71439	AL772336.1						
999	-5.98603	-4.91302	Fos	MAPK			Cholinergic Dopaminergic		
1305	-5.54337	-4.54041	Plxdc1						
173	-5.93287	-7.26292	Pappa						
853	-6.20683	-5.132	Fam174b						
285	-8.17001	-6.61501	Fam117a						
167	-9.27782	-7.30794	Mdfi						
166	-6.01088	-7.31559	Neat1						
567	-6.88637	-5.6926	Cntnap5b				Cell adhesion molecule in myelin-neuron		
678	-6.56952	-5.44821	Zfp385c						
88	-10.7707	-8.10424	Tpm3-rs7						
255	-8.32299	-6.7611	Gm5083						
45	-7.10943	-8.88943	Sostdc1						
207	-8.71384	-7.0324	Corin						
228	-8.51162	-6.90713	Stac						
887	-6.07234	-5.07793	Nell1						
364	-7.60025	-6.29048	mt-Tp						
301	-7.94868	-6.54293	Gm14033						
370	-5.24816	-6.26864	Ccnd1	cancer	cell cycle	p53	Wnt	focal adhes	
199	-8.75084	-7.08327	Opn3						
552	-6.82232	-5.7291	Tnc				ECM receptor interaction		
60	-6.97832	-8.5593	Slc4a5				bile secretion		
217	-8.52732	-6.97133	Slc6a4				serotonergic		
449	-7.14849	-6.00887	Tspan11						
238	-8.29623	-6.85124	Cep72						
73	-10.8794	-8.32841	Gm6166						
42	-7.29151	-8.96701	Rps8						
557	-6.74409	-5.71683	Gm11799						
620	-6.55469	-5.57067	Cck	pancreatic	neuroactive ligand		calcium signaling		
188	-8.67787	-7.15643	Tmem200b						
159	-6.22713	-7.37036	Mpeg1						
633	-6.4898	-5.54229	Far2				peroxisome		
582	-6.62661	-5.65702	Gldc				metabolic pathways		
239	-8.1821	-6.84577	Srl						
61	-7.08759	-8.54002	F5						
1	-8.84828	-12.0137	SNORD113						
222	-5.92341	-6.94178	Padi2						
241	-5.84104	-6.8349	Atp6v0c	phagosome	oxidative phosphorylation			metabolic p	
113	-6.58452	-7.79834	Hrk						
520	-6.78265	-5.81026	Spag5						

74	-6.97332	-8.31222	Fcrls		
547	-6.68209	-5.74148	Scd3	biosynthesis of unsaturated fatty acids	PPAR signa
453	-6.95352	-5.99691	7sk		
125	-6.55469	-7.67305	1500015O10Rik		
125	-9.27782	-7.67305	Slc9a3	Proximal tubule bicarbonate reclamation	Aldosterone
87	-6.88637	-8.11806	Car12		
32	-13.2093	-9.2665	Rps15a-ps8		
34	-7.64021	-9.20062	Tmem72		
57	-7.27901	-8.61892	Mfrp		
265	-7.80383	-6.71068	Rab3d	pancreatic secretion	
231	-8.03286	-6.89012	Pkp3		
69	-10.3489	-8.39522	Gm15083		
375	-7.18287	-6.2507	Grik1	glutamatergic synapse	neuroactive ligand
27	-7.85991	-9.44831	Aqp1		
287	-7.62408	-6.60579	Slc5a1	Carbohydrate digestion and absorption	Bile secreti
330	-7.36903	-6.42106	Slc18a2	Serotonerg Dopaminerg Synaptic vessicle	
144	-6.51826	-7.49569	Hba-a1	disease	
51	-7.43716	-8.74709	Cldn2	Cell adhesion molecules	Tight junction
200	-8.21906	-7.07681	Pisd-ps2		
33	-7.77664	-9.23313	Folr1	Endocytosis	
94	-6.93886	-8.0242	Gcnt1	Mucin type O-Glycan biosynthesis	Metabolic p
145	-6.52909	-7.48697	Casp3	apoptosis serotonerg MAPK	
74	-7.17131	-8.31222	Ngfr	Neurotrophin signaling pathway	Cytokine-cy
287	-7.5538	-6.60579	Chst8		
200	-8.15802	-7.07681	Gm5506		
131	-6.66202	-7.6145	Prlr	Cytokine-cytokine receptor interaction	
123	-8.99851	-7.69314	Th		
24	-13.2093	-9.57185	Gh	GnRH signa Neuroactiv mTOR sign Calcium signaling path	

edCtrlObs=13621985

phodiesterase

purine metabolism

JakSTAT

gastric secretion

pathways lysosome

ling

α-regulated sodium reabsorption

Protein digestion and absorption

Bile secreti

on Mineral absorption

Leukocyte transendothelial migration

pathway

ytokine receptor interaction

Transcriptional misregulation in cancer

Neuroactive ligand-receptor interaction

Jak-STAT signaling pathway

way

on

Mineral absorptio

Apoptosis

Down

PCCMT

IP3R1

SERCA2 (ATP2A2)

INPP5

TRP3

EAAT4

Up

α 1-antichymotrypsin

Down

5 weeks old

Homer-3
Carbonic anhydrase-like sequence
G-substrate
EAAT4
IP3R1
Purkinje cell protein 1
SERCA3 (ATP2A3)
EST
Homeotic protein Gtx

12 weeks old

Homer-3
Carbonic anhydrase-like sequence
G-substrate
EAAT4
IP3R 1
Purkinje cell protein1
SERCA 3
EST
Homeotic protein Gtx
Calcium channel, T type, Alpha 1G subunit
Procollagen type XV
Purkinje cell protein 2
Calbindin 28K

Up

Tachykinin 1
Neurogranin
EST