SUPPLEMENTAL TABLE 1

Changes in gene expression in the medial gastrocnemius of GSL30 mice as compared with wild-type littermates. Genes that passed significance filters consisting of a detection call of 0.5, a *p* -value of 0.05, and an increase or decrease in expression by a magnitude of at least 1.5 fold are listed. A/P, absent/present call; ctl mean, average of wild-type samples; Ctl stdev, standard deviation of wild-type samples; Exp Mean, average of GSL30 samples; Exp stdev, standard deviation of GSL30 samples.

CARBOHYDRATE METABOLISM

GeneSymbol	Genbank	Unigene	A/P	Ctl Mean	Ctl stdev	Exp Mean	Exp stdev	P-value	Fold Change	Gene Description
Fbp2	NM_007994	Mm.289741	1	5190	816	2021	218	0.00039	-2.57	fructose bisphosphatase 2
Slc35a2	BM119992	Mm.214976	0.5	243	53	120	83	0.02748	-2.02	solute carrier family 35 (UDP-galactose transporter), member 2
Pygl	NM_133198	Mm.256926	1	931	218	462	99	0.00474	-2.01	liver glycogen phosphorylase
Ldh2	NM_008492	Mm.9745	1	8141	694	4126	734	0.00002	-1.97	lactate dehydrogenase 2, B chain
G6pdx	NM_008062	Mm.27210	1	1104	264	611	115	0.01238	-1.81	glucose-6-phosphate dehydrogenase X-linked
Slc35a2	CA751962	Mm.214976	0.8	149	50	83	39	0.04999	-1.79	solute carrier family 35 (UDP-galactose transporter), member 2
Idh3b	NM_130884	Mm.29590	1	800	178	452	144	0.00945	-1.77	isocitrate dehydrogenase 3 (NAD+) beta
Ldh2	BY000444	Mm.9745	1	5141	376	2994	931	0.00496	-1.72	lactate dehydrogenase 2, B chain
Idh2	NM_008322	Mm.246432	1	11353	621	6738	1813	0.00299	-1.68	isocitrate dehydrogenase 2 (NADP+), mitochondrial
Pfkfb3	NM_133232	Mm.19669	1	8584	2451	5297	782	0.03555	-1.62	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3
Amy1	NM_007446	Mm.33941	1	1814	463	1129	82	0.03114	-1.61	amylase 1, salivary
Pgam1	BI407347	Mm.16783	1	980	113	613	104	0.00072	-1.6	phosphoglycerate mutase 1
Ugt1a1	D87867	Mm.268456	1	1861	468	1167	135	0.02436	-1.6	UDP-glucuronosyltransferase 1 family, member 1
Ugp2	AV370025	Mm.130747	1	9041	1453	5688	999	0.00379	-1.59	UDP-glucose pyrophosphorylase 2
Aldh9a1	AV028069	Mm.29803	1	1060	263	669	93	0.02606	-1.58	aldehyde dehydrogenase 9, subfamily A1
Pfkl	BE914497	Mm.269649	1	1094	288	695	151	0.03347	-1.57	phosphofructokinase, liver
Aldh9a1	BB703752	Mm.29803	1	1173	268	763	179	0.02503	-1.54	aldehyde dehydrogenase 9, subfamily A1
Ugt1a1	D87867	Mm.268456	1	370	84	245	67	0.03198	-1.51	UDP-glucuronosyltransferase 1 family, member 1
Gpi1	NM_008155	Mm.589	1	25212	1998	38736	2801	0.00005	1.54	glucose phosphate isomerase 1
Pck1	BB225177	Mm.266867	0.7	67	18	107	22	0.01438	1.59	phosphoenolpyruvate carboxykinase 1, cytosolic
Mthfd1	AV215673	Mm.29584	1	69	20	115	36	0.04726	1.66	methylenetetrahydrofolate dehydrogenase
Ppp1r1a	NM_021391	Mm.143788	1	1997	398	3339	481	0.00136	1.67	protein phosphatase 1, regulatory (inhibitor) subunit 1A
Gys1/Gys3	NM_030678	Mm.275654	1	2280	1242	6618	1488	0.00105	2.9	glycogen synthase 1

AMINO ACID METABOLISM

GeneSymbol	Genbank	Unigene	A/P	Ctl Mean	Ctl stdev	Exp Mean	Exp stdev	P-value	Fold Change	Gene Description
Pah	AW106920	Mm.263539	1	192	100	69	45	0.0473	-2.78	phenylalanine hydroxylase
Phgdh	L21027	Mm.16898	1	207	98	74	70	0.0436	-2.78	3-phosphoglycerate dehydrogenase
Mat1a	AW551830	Mm.14064	1	297	127	117	97	0.0408	-2.53	methionine adenosyltransferase I, alpha
B3galt2	BB223909	Mm.285580	1	67	23	32	18	0.02959	-2.1	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 2
Cdo1	NM_033037	Mm.241056	1	3585	1225	1871	484	0.03344	-1.92	cysteine dioxygenase 1, cytosolic
Mat2a	AV260654	Mm.29815.5	1	2124	287	1245	122	0.00149	-1.71	methionine adenosyltransferase II, alpha
Got1	AA792094	Mm.19039	1	21438	4990	12594	1089	0.01797	-1.7	glutamate oxaloacetate transaminase 1, soluble
Gatm	AW108522	Mm.29975	1	463	109	280	109	0.0296	-1.65	glycine amidinotransferase
Asns	BC005552	Mm.2942	1	861	106	528	90	0.00069	-1.63	asparagine synthetase
Fah	NM_010176	Mm.3798	1	1458	117	926	97	0.00005	-1.58	fumarylacetoacetate hydrolase
Eprs	BM238943	Mm.154511	1	1501	390	2267	255	0.00797	1.51	glutamyl-prolyl-tRNA synthetase
Gstm4	AF464943	Mm.31203	1	628	166	961	65	0.00895	1.53	glutathione S-transferase, mu 4
Art1	U31510	Mm.261071	1	12393	792	19251	1098	0.00001	1.55	ADP-ribosyltransferase 1
Ahcy	NM_016661	Mm.2573	1	1964	218	3104	375	0.00109	1.58	S-adenosylhomocysteine hydrolase
Oaz2	AW214584	Mm.116749	1	3945	1620	6364	831	0.02496	1.61	ornithine decarboxylase antizyme 2
Art5	U60881	Mm.2816	1	1709	315	2810	613	0.0118	1.64	ADP-ribosyltransferase 5
Hrmt1l2	AK020120	Mm.27545	1	1416	466	2383	705	0.0377	1.68	HMT1 hnRNP methyltransferase-like 2 (S. cerevisiae)
Slc7a9	NM_021291	Mm.45874	1	159	60	274	39	0.00894	1.72	solute carrier family 7, member 9
Gamt	AF015887	Mm.7329	1	672	147	1202	188	0.00112	1.79	guanidinoacetate methyltransferase, muscle contraction
Art5	AJ297548	Mm.2816	1	846	147	1619	193	0.00019	1.91	ADP-ribosyltransferase 5

LIPID METABOLISM

GeneSymbol	Genbank	Unigene	A/P	Ctl Mean	Ctl stdev	Exp Mean	Exp stdev	P-value	Fold Change	Gene Description
Fads3	NM_021890	Mm.253875	0.6	659	342	112	131	0.02064	-5.87	fatty acid desaturase 3
Cbr2	BC010758	Mm.21454	1	2392	534	785	223	0.00159	-3.05	carbonyl reductase 2

Fabp4	BC002148	Mm.582	1	2700	473	933	164	0.00053	-2.89	fatty acid binding protein 4, adipocyte
Pla2g7	AK005158	Mm.9277	1	2128	983	802	277	0.03368	-2.65	phospholipase A2, group VII
Cte1	NM_012006	Mm.1978	1	554	206	239	28	0.02766	-2.31	cytosolic acyl-CoA thioesterase 1
Pck1	AW106963	Mm.266867	1	4115	1012	2135	837	0.00978	-1.93	phosphoenolpyruvate carboxykinase 1, cytosolic
Bdh	BF322712	Mm.293470	1	2226	793	1153	231	0.03361	-1.93	3-hydroxybutyrate dehydrogenase (heart, mitochondrial)
Cav2	NM_016900	Mm.31915	1	2063	597	1086	197	0.01777	-1.9	caveolin 2
Mgll	BI411560	Mm.272197	1	6233	1384	3282	536	0.00674	-1.9	monoglyceride lipase
Lpl	AK017272	Mm.1514	1	7982	812	4469	710	0.00009	-1.79	lipoprotein lipase
Hmgcs1	BI690696	Mm.61526	1	1577	382	899	259	0.01343	-1.75	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1
Mgll	NM_011844	Mm.272197	1	4759	716	2735	521	0.00139	-1.74	monoglyceride lipase
Mgll	AK006949	Mm.272197	1	3594	770	2188	403	0.01113	-1.64	monoglyceride lipase
Hmgcs2	BC014714	Mm.289131	0.5	548	132	338	85	0.02029	-1.62	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2
Hmgcs1	BI690696	Mm.61526	1	984	212	615	225	0.02891	-1.6	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1
Lipe	NM_010719	Mm.333679	1	3587	903	2270	632	0.03194	-1.58	lipase, hormone sensitive
Scd2	NM_009128	Mm.193096	1	825	98	530	30	0.00135	-1.56	stearoyl-Coenzyme A desaturase 2
Scd2	BB459479	Mm.193096	0.8	740	178	483	130	0.03499	-1.53	stearoyl-Coenzyme A desaturase 2
Ephx2	NM_007940	Mm.15295	1	3592	481	2366	581	0.0067	-1.52	epoxide hydrolase 2, cytoplasmic
Angptl4	NM_020581	Mm.196189	1	4059	883	2663	314	0.02084	-1.52	angiopoietin-like 4
Facl2	BI413218	Mm.210323	1	8595	217	5680	265	0	-1.51	fatty acid Coenzyme A ligase, long chain 2
Pltp	NM_011125	Mm.6105	1	2602	594	1731	371	0.02741	-1.5	phospholipid transfer protein
Siat10	NM_018784	Mm.212742	1	2495	679	3812	871	0.02869	1.53	sialyltransferase 10
Plcg2	AW546508	Mm.192699	1	477	152	752	103	0.01242	1.58	phospholipase C, gamma 2
Hsd17b7	AV235735	Mm.12882	1	785	158	1355	233	0.00275	1.73	hydroxysteroid (17-beta) dehydrogenase 7
Akr1d1	BC018333	Mm.262635	0.8	180	39	321	102	0.03509	1.78	aldo-keto reductase family 1, member D1
Gm2a	NM_010299	Mm.287807	1	521	105	1036	253	0.00848	1.99	GM2 ganglioside activator protein

MISCELLANIOUS METABOLISM

GeneSymbol	Genbank	Unigene	A/P	Ctl Mean	Ctl stdev	Exp Mean	Exp stdev	P-value	Fold Change	Gene Description
Nnmt	AK006371	Mm.8362	1	565	182	243	124	0.01384	-2.32	nicotinamide N-methyltransferase
Aldh1a7	NM_011921	Mm.14609	1	610	231	314	92	0.04552	-1.94	aldehyde dehydrogenase family 1, subfamily A7
Car4	NM_007607	Mm.1641	1	1249	262	661	95	0.00526	-1.89	carbonic anhydrase 4
Papss2	BY038761	Mm.203916	1	1066	206	570	131	0.00269	-1.87	3'-phosphoadenosine 5'-phosphosulfate synthase 2
Pank1	NM_023792	Mm.24742	1	1755	547	946	58	0.03031	-1.86	pantothenate kinase 1
Hmbs	BB000512	Mm.247676	0.6	205	47	110	51	0.01622	-1.86	hydroxymethylbilane synthase
Car14	NM_011797	Mm.224836	1	1502	383	812	93	0.01748	-1.85	carbonic anhydrase 14
Pdlim1	NM_016861	Mm.5567	1	4934	587	2848	465	0.00025	-1.73	PDZ and LIM domain 1 (elfin)
Mte1	NM_134188	Mm.45431	1	1565	513	916	198	0.0461	-1.71	mitochondrial acyl-CoA thioesterase 1
Xdh	AV286265	Mm.11223	1	1750	322	1036	192	0.00378	-1.69	xanthine dehydrogenase
Osbpl11	BM220135	Mm.26564	1	938	172	574	184	0.01234	-1.63	oxysterol binding protein-like 11
Sod3	U38261	Mm.2407	1	2877	513	1783	506	0.00949	-1.61	superoxide dismutase 3, extracellular
Abca1	BB305534	Mm.277376	1	2438	350	1523	145	0.00297	-1.6	ATP-binding cassette, sub-family A (ABC1), member 1
Smox	BC004831	Mm.136586	1	4437	949	2832	402	0.01767	-1.57	spermine oxidase
Pank1	AK017345	Mm.24742	1	851	201	545	130	0.02471	-1.56	pantothenate kinase 1
Vnn1	NM_011704	Mm.27154	1	437	86	288	20	0.01991	-1.52	vanin 1
Car4	NM_007607	Mm.1641	1	988	220	657	92	0.0272	-1.5	carbonic anhydrase 4
Aox1	NM_009676	Mm.26787	1	1432	243	2182	127	0.00088	1.52	aldehyde oxidase 1
Uxs1	AA203925	Mm.201248	1	161	66	310	33	0.00429	1.92	UDP-glucuronate decarboxylase 1

MUSCLE

GeneSymbol	Genbank	Unigene	A/P	Ctl Mean	Ctl stdev	Exp Mean	Exp stdev	P-value	Fold Change	Gene Description
Ppp1r14a	NM_026731	Mm.2343	1	244	86	64	58	0.0061	-3.82	protein phosphatase 1, regulatory (inhibitor) subunit 14A
Myh6	NM_080728	Mm.290003	1	2083	678	670	251	0.00725	-3.11	myosin, heavy polypeptide 6, cardiac muscle, alpha
Tpm3	NM_022314	Mm.240839	1	3938	1024	1586	729	0.00412	-2.48	tropomyosin 3
Tpm3	AV311925	Mm.17306	1	974	313	392	232	0.01251	-2.48	tropomyosin 3
Tnnt1	NM_011618	Mm.711	1	3875	876	1589	556	0.0017	-2.44	troponin T1, skeletal, slow
Myh6	NM_080728	Mm.290003	1	4159	802	1745	509	0.00075	-2.38	myosin, heavy polypeptide 6, cardiac muscle, alpha
Tpm3	NM_022314	Mm.240839	1	3460	945	1555	417	0.0062	-2.22	tropomyosin 3
Myh11	BC026142	Mm.250705	1	1054	184	481	34	0.00243	-2.19	myosin, heavy polypeptide 11, smooth muscle

Myo1b	BI080370	Mm.305823	1	745	112	356	63	0.00052	-2.09	myosin Ib
Tncc	NM_009393	Mm.712	1	5485	1181	2801	1149	0.00658	-1.96	troponin C, cardiac/slow skeletal
Casq2	NM_009814	Mm.15343	1	903	310	463	120	0.03153	-1.95	calsequestrin 2
Tagln	BB114067	Mm.283283	1	3305	280	1724	320	0.00003	-1.92	transgelin
Myl2	NM_010861	Mm.1529	1	16468	1955	8673	2742	0.00129	-1.9	myosin, light polypeptide 2, regulatory, cardiac, slow
Mylk	AI746549	Mm.247544	1	946	129	500	69	0.00049	-1.89	myosin, light polypeptide kinase
Cald1	AV024348	Mm.308134	1	2744	142	1488	374	0.00092	-1.84	caldesmon 1
Myl3	X67685	Mm.7353	1	12179	1439	6740	2019	0.00174	-1.81	myosin, light polypeptide 3, alkali; ventricular, skeletal, slow
Myl3	AK002312	Mm.7353	1	10467	590	5933	1182	0.00026	-1.76	myosin, light polypeptide 3, alkali; ventricular, skeletal, slow
Tnni1	NM_021467	Mm.44379	1	2525	692	1444	261	0.02226	-1.75	troponin I, skeletal, slow 1
Atp2a2	AA245637	Mm.227583	1	6208	952	3638	559	0.00201	-1.71	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2
Mylk	BF451748	Mm.247544	1	2642	463	1562	244	0.00365	-1.69	myosin, light polypeptide kinase
Utrn	AI788797	Mm.331784	1	1654	225	987	165	0.00109	-1.67	utrophin (homologous to dystrophin)
Myl3	X67685	Mm.7353	1	4311	413	2666	762	0.00544	-1.62	myosin, light polypeptide 3, alkali; ventricular, skeletal, slow
Atp2a2	NM_009722	Mm.227583	1	9950	1234	6236	1040	0.00088	-1.6	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2
Myo10	BI079918	Mm.60590	1	1646	212	1027	235	0.00241	-1.6	myosin X
Atp2a2	AA245637	Mm.227583	1	804	72	507	44	0.0001	-1.59	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2
Acta2	NM_007392	Mm.213025	1	7003	915	4468	252	0.00189	-1.57	actin, alpha 2, smooth muscle, aorta
Myl9	AK007972	Mm.271770	1	3671	712	2331	473	0.00997	-1.57	myosin, light polypeptide 9, regulatory
Myo1b	AI255256	Mm.3390	1	630	93	404	40	0.00428	-1.56	myosin IB
Myh2	BC008538	Mm.34425	1	23916	3170	15284	2380	0.00182	-1.56	myosin, heavy polypeptide 2, skeletal muscle, adult
Cnn3	BB724741	Mm.22171	1	3366	555	2161	420	0.00616	-1.56	calponin 3, acidic, tropomyosin binding, troponin C binding
Atp2a2	BI248739	Mm.227583	1	3067	335	1998	345	0.0011	-1.53	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2
Sync	AK004279	Mm.132243	1	691	84	1039	233	0.02568	1.5	syncoilin
Cacna1s	BY366917	Mm.4418	1	5946	933	8951	1558	0.00765	1.51	calcium channel, voltage-dependent, L type, alpha 1S subunit
Ache	NM_009599	Mm.255464	1	566	133	864	130	0.00727	1.53	acetylcholinesterase
Tpm2	NM_009416	Mm.646	1	19336	2162	29850	2148	0.00006	1.54	tropomyosin 2, beta
Lmna	NM_019390	Mm.243014	1	1391	228	2201	312	0.00226	1.58	lamin A
Tpm2	BC024358	Mm.646	1	10655	959	17175	2259	0.00193	1.61	tropomyosin 2, beta
Myh1	AJ002522	Mm.340132	1	1884	533	3084	428	0.00441	1.64	myosin, heavy polypeptide 1, skeletal muscle, adult
Des	AA738859	Mm.6712	1	25559	3323	43093	7218	0.00262	1.69	desmin
Myo5a	NM_010864	Mm.3645	1	189	52	323	104	0.04263	1.71	myosin Va
Sync	NM_023485	Mm.132243	1	475	54	819	198	0.0135	1.72	syncoilin
Tpm2	NM_009416	Mm.646	1	16912	2969	29762	3440	0.00023	1.76	tropomyosin 2, beta
Myoz1	BB216883	Mm.141702	1	1409	321	2632	340	0.00039	1.87	myozenin 1
Sync	AK004279	Mm.132243	1	357	114	746	163	0.00331	2.09	syncoilin
Mybph	NM_016749	Mm.269621	1	4305	1669	9388	1170	0.00084	2.18	myosin binding protein H
Actc1	NM_009608	Mm.686	1	5377	1577	19028	2141	0.00001	3.54	actin, alpha, cardiac

WNT PATHWAY

GeneSymbol	Genbank	Unigene	A/P	Ctl Mean	Ctl stdev	Exp Mean	Exp stdev	P-value	Fold Change	Gene Description
Dkk3	AK004853	Mm.55143	1	576	221	214	55	0.02414	-2.68	dickkopf homolog 3 (Xenopus laevis)
Tcf4	CA567227	Mm.4269	1	196	48	100	48	0.01388	-1.95	transcription factor 4
Smo	AW555326	Mm.29279	1	624	132	346	47	0.00686	-1.8	smoothened homolog (Drosophila)
Tcf7l2	BB175494	Mm.139815	1	341	61	203	46	0.00519	-1.68	transcription factor 7-like 2, T-cell specific, HMG-box
Wnt6	CB273307	Mm.6358	0.8	1030	164	647	118	0.00397	-1.59	wingless-related MMTV integration site 6
Tcf4	U16321	Mm.4269	1	1274	298	804	217	0.02485	-1.58	transcription factor 4
Tcfl1	NM_009336	Mm.133919	1	3577	867	5739	876	0.00443	1.6	transcription factor-like 1
Pkd1	BB759096	Mm.290442	1	1884	243	3491	440	0.00038	1.85	polycystic kidney disease 1 homolog

TRANSCRIPTION FACTOR/REGULATION OF TRANSCRIPTION

GeneSymbol	Genbank	Unigene	A/P	Ctl Mean	Ctl stdev	Exp Mean	Exp stdev	P-value	Fold Change	Gene Description
Peg3	NM_008817	Mm.7952	1	543	225	129	59	0.01059	-4.2	paternally expressed 3
Pparg	NM_011146	Mm.3020	1	388	133	128	108	0.0097	-3.02	peroxisome proliferator activated receptor gamma
Wdr9	BQ031260	Mm.240871	1	323	70	164	24	0.00497	-1.97	WD repeat domain 9
Zfp37	X89264	Mm.5011	1	120	33	61	35	0.02851	-1.95	zinc finger protein 37
Meox2	BC002076	Mm.153716	1	531	148	272	103	0.015	-1.95	mesenchyme homeobox 2
Smarcd2	NM_031878	Mm.21772	1	1121	347	615	286	0.03636	-1.82	SWI/SNF rel, matrix assoc, actin dep reg of chromatin, subfamily d, member 2

Notch4	NM_010929	Mm.173813	1	585	67	333	102	0.00254	-1.75	Notch gene homolog 4 (Drosophila)
Peg3	BM200248	Mm.7952	1	1642	328	954	266	0.00662	-1.72	paternally expressed 3
Plagl1	AF147785	Mm.287857	1	1171	343	687	142	0.03335	-1.7	pleiomorphic adenoma gene-like 1
Nfat5	BM239652	Mm.302083	1	1068	195	638	108	0.00505	-1.67	nuclear factor of activated T-cells 5
Shank3	NM_021423	Mm.146855	1	1307	223	785	245	0.00793	-1.66	SH3/ankyrin domain gene 3
Meox2	BC002076	Mm.153716	1	1144	285	693	276	0.03491	-1.65	mesenchyme homeobox 2
Hoxd10	BC013463	Mm.24420	1	282	46	176	27	0.00446	-1.6	homeo box D10
Sirt1	NM_019812	Mm.150679	1	398	83	252	52	0.01309	-1.58	sirtuin (silent mating type information regulation 2 homolog) 1
Litaf	BG072227	Mm.294753	1	1480	155	974	196	0.00195	-1.52	LPS-induced TN factor
Jun	BC002081	Mm.275071	1	6293	910	4135	830	0.00444	-1.52	Jun oncogene
Ets2	BC005486	Mm.290207	1	2520	374	1669	296	0.00405	-1.51	E26 avian leukemia oncogene 2, 3' domain
Smarcd3	NM_025891	Mm.332257	1	4228	516	6400	560	0.00022	1.51	SWI/SNF rel, matrix assoc, actin dep reg of chromatin, subfamily d, member 3
Dedd	BM121177	Mm.270139	1	286	50	434	82	0.0109	1.52	death effector domain-containing
Dbp	BC018323	Mm.3459	1	641	178	980	202	0.02269	1.53	D site albumin promoter binding protein
Pdlim3	NM_016798	Mm.282900	1	17407	1893	26773	3229	0.00139	1.54	PDZ and LIM domain 3
Rnf14	AF249668	Mm.22086	1	1589	297	2441	543	0.02184	1.54	ring finger protein 14
Phf7	AI427892	Mm.5348	1	513	91	789	97	0.00176	1.54	PHD finger protein 7
Six2	D83147	Mm.5039	1	751	147	1172	212	0.00822	1.56	sine oculis-related homeobox 2 homolog (Drosophila)
Tcfeb	NM_011549	Mm.2305	1	1289	291	2030	411	0.01339	1.57	transcription factor EB
Trp53bp1	AJ414734	Mm.215389	1	539	109	849	157	0.00858	1.57	transformation related protein 53 binding protein 1
Sepr	NM_013759	Mm.28212	1	5383	1168	8483	736	0.00153	1.58	selenoprotein R
Mta1	NM_054081	Mm.212577	1	1056	271	1677	156	0.00441	1.59	metastasis associated 1
Zfp68	BM247506	Mm.27575	1	210	43	334	87	0.02921	1.59	Zinc finger protein 68
Tcea3	BC010807	Mm.112	1	3157	760	5047	489	0.00229	1.6	transcription elongation factor A (SII), 3
Rfx5	BB392192	Mm.24308	1	494	46	802	160	0.00909	1.62	regulatory factor X, 5 (influences HLA class II expression)
Lrrfip1	NM_008515	Mm.45039	1	1439	140	2442	327	0.00149	1.7	leucine rich repeat (in FLII) interacting protein 1
Smarca1	NM_053123	Mm.229151	1	131	12	226	50	0.00942	1.72	SWI/SNF rel, matrix assoc, actin dep reg of chromatin, subfamily a, member 1
Zfp358	BF449729	Mm.299073	1	1272	275	2237	465	0.00722	1.76	hypothetical protein C130036G08
Zfp93	NM_009567	Mm.5066	1	203	21	358	57	0.00243	1.76	zinc finger protein 93
Tbx15	NM_011534	Mm.88761	1	1021	324	1883	523	0.0166	1.84	T-box 15
Mllt3	AK019458	Mm.288898	1	1330	270	2487	502	0.00395	1.87	myeloid/lymphoid or mixed-lineage leukemia trithorax homolog
Relb	NM_009046	Mm.1741	1	441	47	834	165	0.00369	1.89	avian reticuloendotheliosis viral (v-rel) oncogene related B
Nr5a1	BY008174	Mm.31387	1	284	92	542	177	0.02829	1.9	nuclear receptor subfamily 5, group A, member 1
Mef2c	AI595932	Mm.24001	1	1826	1098	3528	923	0.02913	1.93	myocyte enhancer factor 2C
Mllt6	AY050217	Mm.23685	1	152	23	295	78	0.01107	1.94	myeloid/lymphoid or mixed lineage-leukemia translocation to 6 homolog
Hdac11	BC016208	Mm.206218	1	357	54	848	125	0.00049	2.37	histone deacetylase 11

EXTRACELLULAR/MATRIX/CYTOPLASMIC

GeneSymbol	Genbank	Unigene	A/P	Ctl Mean	Ctl stdev	Exp Mean	Exp stdev	P-value	Fold Change	Gene Description
Vegfa	CA748355	Mm.31540	1	1960	260	1019	105	0.00067	-1.92	vascular endothelial growth factor A
Prelp	BC019775	Mm.214514	1	5254	1037	2776	788	0.00379	-1.89	proline arginine-rich end leucine-rich repeat
Vtn	NM_011707	Mm.3667	1	1702	339	899	74	0.00668	-1.89	vitronectin
Nox4	AB041034	Mm.31748	0.8	173	39	94	41	0.01534	-1.83	NADPH oxidase 4
Thbs3	NM_013691	Mm.2114	1	314	49	175	66	0.0073	-1.79	thrombospondin 3
Prg4	NM_021400	Mm.212696	1	2211	631	1233	454	0.02611	-1.79	proteoglycan 4
Bmp6	NM_007556	Mm.254978	1	1320	191	736	97	0.00091	-1.79	bone morphogenetic protein 6
Lama4	U69176	Mm.258065	0.8	1450	266	833	350	0.01647	-1.74	laminin, alpha 4
Fgfbp1	U49641	Mm.46053	1	654	76	378	63	0.00024	-1.73	fibroblast growth factor binding protein 1
Igfbp3	AV175389	Mm.29254	1	727	136	428	137	0.00849	-1.7	insulin-like growth factor binding protein 3
Vwf	BB667216	Mm.22339	1	1225	271	721	112	0.01222	-1.7	Von Willebrand factor homolog
Mmp2	BF147716	Mm.334701	1	3552	679	2152	298	0.00835	-1.65	matrix metalloproteinase 2
Vtn	BB251864	Mm.3667	1	258	41	157	58	0.0173	-1.64	vitronectin
Pcolce2	AF352788	Mm.46016	1	1506	288	923	164	0.00778	-1.63	procollagen C-endopeptidase enhancer 2
Bgn	AI931862	Mm.2608	1	2252	556	1419	566	0.04721	-1.59	biglycan
Dpt	NM_019759	Mm.28935	1	11433	2015	7233	1273	0.00561	-1.58	dermatopontin
Timp4	BB328405	Mm.36851	1	2456	666	1552	470	0.04237	-1.58	tissue inhibitor of metalloproteinase 4
Acrp30	NM_009605	Mm.3969	1	17387	4249	11124	2716	0.02744	-1.56	adipocyte complement related protein, Adiponectin
Col4a5	BM250666	Mm.286892	1	356	66	228	67	0.01712	-1.56	procollagen, type IV, alpha 5
Thbs1	AV026492	Mm.4159	1	686	100	443	129	0.01043	-1.55	thrombospondin 1

Fbln5	NM_011812	Mm.288381	1	2611	535	1709	291	0.01626	-1.53	fibulin 5
Col4a2	CA564668	Mm.181021	1	4709	453	3074	367	0.00024	-1.53	procollagen, type IV, alpha 2
Tnxb	NM_031176	Mm.290527	1	4631	722	3058	597	0.00562	-1.51	tenascin XB
Col4a1	BF158638	Mm.738	1	7332	743	4868	338	0.00052	-1.51	procollagen, type IV, alpha 1
Tuba8	NM_017379	Mm.32884	1	6983	1086	10512	604	0.00072	1.51	tubulin, alpha 8
Pdgfc	NM_019971	Mm.40268	1	422	108	650	58	0.00594	1.54	platelet-derived growth factor, C polypeptide
Sgcg	BB519683	Mm.72173	1	1130	246	1799	328	0.00824	1.59	sarcoglycan, gamma (dystrophin-associated glycoprotein)
Ndph	NM_010883	Mm.5014	0.5	112	27	187	52	0.03009	1.67	Norrie disease homolog
Col9a1	AK004383	Mm.154662	1	244	80	423	97	0.01324	1.73	collagen, type IX, alpha 1
Pdgfc	NM_019971	Mm.40268	1	248	50	453	110	0.00928	1.83	platelet-derived growth factor, C polypeptide
Nodal	X70514	Mm.57195	1	292	52	573	179	0.02032	1.96	nodal
Krt2-6a	NM_008476	Mm.22629	0.6	203	69	435	144	0.0177	2.14	keratin complex 2, basic, gene 6a
Tekt1	AK005801	Mm.42257	1	127	29	347	102	0.00576	2.73	tektin 1

RECEPTORS

GeneSymbol	Genbank	Unigene	A/P	Ctl Mean	Ctl stdev	Exp Mean	Exp stdev	P-value	Fold Change	Gene Description
Ceacam1	BC024320	Mm.14114	0.7	572	110	258	184	0.01373	-2.22	carcinoembryonic antigen-related cell adhesion molecule 1
Trpm7	AF376052	Mm.244705	1	985	150	490	85	0.0007	-2.01	transient receptor potential cation channel, subfamily M, member 7
Tie1	NM_011587	Mm.4345	1	870	195	437	103	0.0046	-1.99	tyrosine kinase receptor 1
F11r	BC021876	Mm.294882	1	764	91	394	61	0.00014	-1.94	F11 receptor
Fmod	BB532202	Mm.41573	1	4580	874	2479	546	0.00262	-1.85	fibromodulin
Pdgfrb	CA563430	Mm.4146	1	1023	170	576	191	0.00453	-1.78	platelet derived growth factor receptor, beta polypeptide
Cd36	AK004192	Mm.18628	1	16485	1312	9272	1091	0.00001	-1.78	CD36 antigen
Mmd	BC021914	Mm.277518	1	3521	930	1974	544	0.01845	-1.78	monocyte to macrophage differentiation-associated
Adrb2	AV083350	Mm.5598	1	1071	254	602	177	0.0118	-1.78	adrenergic receptor, beta 2
Cd36	BE307351	Mm.18628	1	13255	1549	7961	1523	0.00061	-1.66	CD36 antigen
Acvr2	BB818297	Mm.247684	0.9	499	80	304	153	0.04586	-1.64	activin receptor IIA
Procr	NM_011171	Mm.3243	1	890	184	553	152	0.01368	-1.61	protein C receptor, endothelial
Cd36	BB534670	Mm.18628	1	2923	517	1818	237	0.00488	-1.61	CD36 antigen
Fmod	BB483571	Mm.287146	1	3766	407	2335	240	0.00051	-1.61	fibromodulin
Fmod	BB504826	Mm.41573	1	1991	417	1260	160	0.0146	-1.58	fibromodulin
C1qr1	NM_010740	Mm.681	1	2335	401	1475	250	0.00479	-1.58	complement component 1, q subcomponent, receptor 1
Msr1	AA183642	Mm.239291	0.5	277	77	175	45	0.04384	-1.58	macrophage scavenger receptor 1
Fmod	NM_021355	Mm.287146	1	9866	1293	6407	1509	0.0046	-1.54	fibromodulin
Nrp	AK002673	Mm.300641	1	2534	532	1661	240	0.01557	-1.53	Cystatin related protein 1 precursor (CRP-1)
Itga6	BM935811	Mm.225096	1	1603	414	1051	201	0.03675	-1.52	integrin alpha 6
Acvr2	BY014959	Mm.247684	1	1768	259	1171	162	0.0033	-1.51	activin receptor IIA
Tek	NM_013690	Mm.14313	1	1535	258	1022	219	0.00965	-1.5	endothelial-specific receptor tyrosine kinase
Sdfr1	BB464493	Mm.157560	1	2487	359	4022	599	0.00173	1.62	stromal cell derived factor receptor 1
Tnfrsf12a	NM_013749	Mm.28518	1	3024	1228	4950	1109	0.03148	1.64	tumor necrosis factor receptor superfamily, member 12a
Tnfrsf19	AF167552	Mm.281356	1	427	134	724	162	0.01382	1.69	tumor necrosis factor receptor superfamily, member 19
Tnfrsf23	NM_024290	Mm.290780	0.8	288	120	501	109	0.01898	1.74	tumor necrosis factor receptor superfamily, member 23
Tirap	BY017242	Mm.23987	0.6	790	172	1390	272	0.00425	1.76	toll-interleukin 1 receptor (TIR) domain-containing adaptor protein
Itgb6	AK019511	Mm.98193	1	145	26	282	98	0.02972	1.94	integrin, beta 6
Ogfr	NM_031373	Mm.250418	1	1645	226	3250	326	0.00004	1.98	opioid growth factor receptor
Tnfrsf19	NM_013869	Mm.281356	1	741	68	1629	259	0.00071	2.2	tumor necrosis factor receptor superfamily, member 19
Crhr2	NM_009953	Mm.4546	1	130	25	302	55	0.00076	2.31	corticotropin releasing hormone receptor 2
Ogfr	AW476433	Mm.250418	1	560	280	1301	373	0.00943	2.32	opioid growth factor receptor
Crhr2	U21729	Mm.4546	1	252	74	655	139	0.00125	2.6	corticotropin releasing hormone receptor 2

SIGNAL TRANSDUCTION

GeneSymbol	Genbank	Unigene	A/P	Ctl Mean	Ctl stdev	Exp Mean	Exp stdev	P-value	Fold Change	Gene Description
Erbb2ip	BM240030	Mm.277354	0.5	145	29	69	53	0.03295	-2.09	Erbb2 interacting protein
Cidea	NM_007702	Mm.449	1	1485	548	716	290	0.03238	-2.07	cell death-inducing DNA fragmentation factor, alpha subunit-like effector A
Cdc42ep3	BB012489	Mm.275926	1	1165	200	581	86	0.00186	-2	CDC42 effector protein (Rho GTPase binding) 3
Plcb4	AF332072	Mm.38009	0.8	329	57	165	39	0.0012	-1.99	phospholipase C, beta 4
Gdf10	L42114	Mm.40323	1	427	87	240	37	0.00724	-1.78	growth differentiation factor 10
Pecam	NM_008816	Mm.276652	1	3287	264	1882	419	0.00039	-1.75	platelet/endothelial cell adhesion molecule

Pde2a	BG069616	Mm.247564	1	1375	363	798	134	0.02078	-1.72	phosphodiesterase 2A, cGMP-stimulated
Dbi	AV007315	Mm.2785	1	4353	1084	2544	553	0.01595	-1.71	diazepam binding inhibitor
Ywhaq	BB422130	Mm.313073	1	1664	341	1010	263	0.00944	-1.65	Y 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta
Ywhab	NM_018753	Mm.34319	1	1216	137	751	157	0.00107	-1.62	Y 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta
Nedd9	NM_017464	Mm.8315	1	398	83	250	85	0.02399	-1.59	neural precursor cell expressed, developmentally down-regulated gene 9
Dbi	NM_007830	Mm.2785	1	6633	1458	4226	848	0.01885	-1.57	diazepam binding inhibitor
Pdzx	NM_018832	Mm.67912	1	663	144	424	139	0.02882	-1.56	PDZ domain containing, X chromosome
Adcy4	NM_080435	Mm.287010	0.8	411	95	269	87	0.03936	-1.53	adenylate cyclase 4
Erbb2ip	BC028256	Mm.277354	1	932	247	618	115	0.04204	-1.51	erbb2 interacting protein
Cd47	BQ256022	Mm.31752	1	1798	182	1193	233	0.00186	-1.51	CD47 antigen (Rh-related antigen, integrin-associated signal transducer)
Mapkapk5	NM_010765	Mm.272206	1	1565	213	2354	352	0.00367	1.5	MAP kinase-activated protein kinase 5
Sh2bpsm1	NM_011363	Mm.8538	1	1016	128	1556	151	0.0003	1.53	SH2-B PH domain containing signaling mediator 1
Rtkn	BC013820	Mm.4139	0.8	325	93	501	50	0.00994	1.54	rhotekin
Cap2	AV261931	Mm.44529	1	5171	462	7969	596	0.00003	1.54	CAP, adenylate cyclase-associated protein, 2 (yeast)
Scye1	NM_007926	Mm.10507	1	3046	218	4737	376	0.00013	1.56	small inducible cytokine subfamily E, member 1
Lgals1	AI642438	Mm.43831	1	13692	2632	22136	4234	0.00683	1.62	lectin, galactose binding, soluble 1
Lgals1	NM_008495	Mm.43831	1	13703	1954	22344	3128	0.0012	1.63	lectin, galactose binding, soluble 1
Dusp10	NM_022019	Mm.266191	1	1351	258	2255	586	0.01977	1.67	dual specificity phosphatase 10
Lims1	BM213930	Mm.57734	1	2195	453	3721	836	0.01156	1.69	LIM and senescent cell antigen-like domains 1
Lims1	BC005621	Mm.57734	1	543	169	924	294	0.04584	1.7	LIM and senescent cell antigen-like domains 1
Lbcl1	AF177032	Mm.239329	0.7	440	163	762	95	0.00901	1.73	lymphoid blast crisis-like 1
Cap2	AK014979	Mm.44529	1	3347	505	6135	1012	0.0015	1.83	CAP, adenylate cyclase-associated protein, 2 (yeast)
Asb15	NM_080847	Mm.160150	1	756	410	1760	232	0.00313	2.33	ankyrin repeat and SOCS box-containing protein 15
Opn1mw	NM_008106	Mm.284825	0.8	335	217	1369	589	0.01431	4.08	opsin 1, medium-wave-sensitive

POST-TRANSLATIONAL MODIFICATION

GeneSymbol	Genbank	Unigene	A/P	Ctl Mean	Ctl stdev	Exp Mean	Exp stdev	P-value	Fold Change	Gene Description
Sgk	NM_011361	Mm.28405	1	6132	1446	3063	1368	0.00874	-2	serum/glucocorticoid regulated kinase
Temt	NM_009349	Mm.299	1	7871	2082	3937	1082	0.00955	-2	thioether S-methyltransferase
Chuk	BC018243	Mm.3996	1	353	75	206	53	0.00944	-1.71	conserved helix-loop-helix ubiquitous kinase
Vrk1	BC016676	Mm.2981	1	195	35	115	49	0.02182	-1.69	vaccinia related kinase 1
Ptplb	NM_023587	Mm.27286	1	2498	634	1565	293	0.02452	-1.6	protein tyrosine phosphatase-like, member b
Pftk1	NM_011074	Mm.6456	1	369	57	233	83	0.01966	-1.58	PFTAIRE protein kinase 1
Lox	NM_010728	Mm.172	1	2372	484	1533	109	0.01956	-1.55	lysyl oxidase
Snrk	NM_133741	Mm.257989	1	3837	390	2485	496	0.00137	-1.54	SNF-1 related kinase
Stk23	NM_019684	Mm.111904	1	759	87	1143	140	0.00124	1.51	serine/threonine kinase 23
Ppp5c	BC003744	Mm.3294	1	1084	386	1635	131	0.02945	1.51	protein phosphatase 5, catalytic subunit
Tnk2	NM_016788	Mm.256734	1	1459	442	2225	359	0.01701	1.52	tyrosine kinase, non-receptor, 2
Pstpip2	AV229693	Mm.57174	1	2158	133	3284	611	0.01586	1.52	proline-serine-threonine phosphatase-interacting protein 2
Dm15	AW108486	Mm.301960	1	4489	989	6862	1667	0.02907	1.53	dystrophia myotonica-protein kinase
Ppp1r11	AW494322	Mm.105324	1	234	71	362	73	0.02359	1.55	protein phosphatase 1, regulatory (inhibitor) subunit 11
Fastk	NM_023229	Mm.28123	1	2378	745	3702	130	0.01734	1.56	Fas-activated serine/threonine kinase
Dapk3	AI642212	Mm.10294	1	616	197	962	65	0.01392	1.56	death-associated kinase 3
Thop1	NM_022653	Mm.26995	1	485	169	761	114	0.01963	1.57	thimet oligopeptidase 1
Map3k7	AW547374	Mm.258589	1	1024	149	1613	117	0.00012	1.58	mitogen activated protein kinase kinase kinase 7
Srpk2	BG805074	Mm.8709	1	266	117	430	106	0.04906	1.62	serine/arginine-rich protein specific kinase 2
Map3k12	BB370469	Mm.172897	1	146	41	242	68	0.03174	1.65	mitogen activated protein kinase kinase kinase 12
Dyrk1b	NM_010092	Mm.57249	1	1247	369	2185	396	0.00475	1.75	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1b
Mknk2	NM_021462	Mm.42126	1	4683	2804	8587	1964	0.0381	1.83	MAP kinase-interacting serine/threonine kinase 2
Camk2g	BM227770	Mm.235182	1	3187	885	5867	737	0.00082	1.84	calcium/calmodulin-dependent protein kinase (CaM kinase) II gamma
Map3k7	C87327	Mm.258589	1	165	56	305	96	0.03088	1.85	mitogen activated protein kinase kinase kinase 7
Art1	NM_009710	Mm.261071	1	7403	1352	13798	1796	0.00038	1.86	ADP-ribosyltransferase 1
Srpk2	BG805074	Mm.8709	1	148	50	282	91	0.02911	1.9	serine/arginine-rich protein specific kinase 2
Ppp2r5b	BB080065	Mm.118076	1	410	98	825	96	0.00015	2.01	protein phosphatase 2, regulatory subunit B (B56), beta isoform
Apeg1	AF215896	Mm.275397	1	658	254	1344	424	0.01735	2.04	aortic preferentially expressed gene 1

SMALL GTPase MEDIATED SIGNAL TRANSDUCTION

GeneSymbol	Genbank	Unigene	A/P	Ctl Mean	Ctl stdev	Exp Mean	Exp stdev	P-value	Fold Change	Gene Description

Rasd1	BB217136	Mm.3903	0.6	767	258	386	81	0.0256	-1.99	RAS, dexamethasone-induced 1
Ranbp2	BM507707	Mm.142730	1	1857	340	1062	144	0.00485	-1.75	RAN binding protein 2
Gnai1	BQ174580	Mm.297304	1	1734	550	1019	241	0.04491	-1.7	guanine nucleotide binding protein, alpha inhibiting 1
Cxcl12	NM_013655	Mm.465	1	3294	512	2056	132	0.00338	-1.6	chemokine (C-X-C motif) ligand 12
Cdc42ep1	BC016250	Mm.30075	1	992	169	624	194	0.01292	-1.59	CDC42 effector protein (Rho GTPase binding) 1
Arhj	AF309564	Mm.27467	1	3043	722	1945	559	0.02767	-1.56	ras homolog gene family, member J
Rab34	AF327929	Mm.275864	1	778	177	511	64	0.02494	-1.52	RAB34, member of RAS oncogene family
Gnb1	NM_008142	Mm.2344	1	1132	149	746	119	0.00197	-1.52	guanine nucleotide binding protein (G protein), beta polypeptide 1
Ywhaq	AV124281	Mm.289630	1	2154	316	1422	361	0.00926	-1.51	Y 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta
Nras	BB018528	Mm.256975	1	617	50	926	220	0.03801	1.5	neuroblastoma RAS viral (v-ras) oncogene homolog
Arfgap3	BG067878	Mm.258910	0.8	355	54	553	74	0.00197	1.55	ADP-ribosylation factor GTPase activating protein 3
Rab13	BC027214	Mm.29355	1	968	62	1556	325	0.01654	1.61	RAB13, member RAS oncogene family
Tbc1d1	BC004675	Mm.286353	1	909	337	1481	139	0.01717	1.63	TBC1 domain family, member 1
Rgs1	NM_015811	Mm.103701	0.6	152	31	252	32	0.00112	1.66	regulator of G-protein signaling 1
Siah2	BY008407	Mm.2847	0.5	658	94	1138	185	0.00211	1.73	seven in absentia 2
Rab40b	AV364488	Mm.281639	1	249	39	609	120	0.00141	2.45	Rab40b, member RAS oncogene family

MITOCHONDRIAL

GeneSymbol	Genbank	Unigene	A/P	Ctl Mean	Ctl stdev	Exp Mean	Exp stdev	P-value	Fold Change	Gene Description
Nnt	BB205930	Mm.3842	1	908	314	513	126	0.04788	-1.77	nicotinamide nucleotide transhydrogenase
Clpx	BF020441	Mm.30088	1	2481	438	1445	551	0.01108	-1.72	caseinolytic protease X (E.coli)
Acaa2	BB718075	Mm.142498	1	3394	644	1981	475	0.00557	-1.71	acetyl-Coenzyme A acyltransferase 2
Ndufs1	AV256780	Mm.265209	1	716	150	419	153	0.01479	-1.71	NADH dehydrogenase (ubiquinone) Fe-S protein 1
Cox8a	NM_007750	Mm.14022	1	6139	1044	4085	1055	0.01482	-1.5	cytochrome c oxidase, subunit VIIIa

MEMBRANE

GeneSymbol	Genbank	Unigene	A/P	Ctl Mean	Ctl stdev	Exp Mean	Exp stdev	P-value	Fold Change	Gene Description
Cyp4a14	AI327006	Mm.250901	1	350	206	59	40	0.03669	-5.89	cytochrome P450, family 4, subfamily a, polypeptide 14
Slc15a2	NM_021301	Mm.281804	1	1320	489	324	144	0.00731	-4.07	solute carrier family 15 (H+/peptide transporter), member 2
Eva	BC015076	Mm.33240	1	68	15	17	15	0.00101	-3.83	epithelial V-like antigen
Atp1a1	BC025618	Mm.280103	1	2507	819	1123	575	0.01753	-2.23	ATPase, Na+/K+ transporting, alpha 1 polypeptide
Slc1a3	BB365275	Mm.204834	1	292	78	144	71	0.01419	-2.03	solute carrier family 1 (glial high affinity glutamate transporter), member 3
Sec61a1	BC003707	Mm.28375	1	747	242	378	221	0.03635	-1.98	Sec61 alpha 1 subunit (S. cerevisiae)
Sdc2	AI266824	Mm.234266	1	696	265	355	148	0.04652	-1.96	syndecan 2
Slco2a1	NM_033314	Mm.207106	1	238	79	124	52	0.0314	-1.92	solute carrier organic anion transporter family, member 2a1
G0s2	NM_008059	Mm.3283	1	1347	229	715	160	0.00148	-1.88	G0/G1 switch gene 2
Cldn5	NM_013805	Mm.22768	1	2967	783	1628	146	0.01989	-1.82	claudin 5
Atp1a1	BC025618	Mm.280103	1	2089	703	1152	422	0.03776	-1.81	ATPase, Na+/K+ transporting, alpha 1 polypeptide
Mal	NM_010762	Mm.39040	1	403	95	224	133	0.04496	-1.79	myelin and lymphocyte protein, T-cell differentiation protein
Art3	AJ311773	Mm.263514	1	4146	1305	2335	604	0.03056	-1.78	ADP-ribosyltransferase 3
Eltd1	BC017134	Mm.27242	1	1408	142	798	28	0.00071	-1.77	EGF, latrophilin seven transmembrane domain containing 1
Cyp2d22	BF683039	Mm.157435	1	1254	138	708	74	0.00024	-1.77	cytochrome P450, family 2, subfamily d, polypeptide 22
Sdpr	BE197945	Mm.255909	1	2645	370	1520	301	0.00076	-1.74	serum deprivation response
Slc12a4	NM_009195	Mm.292447	1	606	131	349	109	0.00972	-1.74	solute carrier family 12, member 4
Mpp5	AW258373	Mm.30561	1	1738	515	1000	283	0.03095	-1.74	membrane protein, palmitoylated 5
Abcb1b	NM_011075	Mm.146649	1	192	42	111	51	0.02683	-1.72	ATP-binding cassette, sub-family B (MDR/TAP), member 1B
Efnb2	BB453355	Mm.209813	1	435	143	253	66	0.04138	-1.72	ephrin B2
Arl6ip6	BC019550	Mm.37623	1	309	59	179	61	0.00933	-1.72	ADP-ribosylation factor-like 6 interacting protein 6
Mpz	BY229830	Mm.9986	1	3331	1115	1951	545	0.04749	-1.71	myelin protein zero
Cdh5	AW543698	Mm.21767	1	3119	346	1833	172	0.0003	-1.7	cadherin 5
Abcb1a	M30697	Mm.16086	1	351	96	208	54	0.02797	-1.69	ATP-binding cassette, sub-family B (MDR/TAP), member 1A
Fxyd6	AB032010	Mm.208287	1	1635	247	975	84	0.00241	-1.68	FXYD domain-containing ion transport regulator 6
Eltd1	NM_133222	Mm.27242	1	2112	395	1275	152	0.0069	-1.66	EGF, latrophilin seven transmembrane domain containing 1
Kcnj8	NM_008428	Mm.1482	1	1226	272	749	74	0.013	-1.63	potassium inwardly-rectifying channel, subfamily J, member 8
Elovl5	NM_134255	Mm.19130	1	2482	425	1540	648	0.0299	-1.61	ELOVL family member 5, elongation of long chain fatty acids (yeast)
Icam2	NM_010494	Mm.394	1	687	168	427	130	0.0263	-1.61	intercellular adhesion molecule 2
Abcb1a	BB819674	Mm.16086	1	816	84	507	118	0.00208	-1.61	ATP-binding cassette, sub-family B (MDR/TAP), member 1A
Tm4sf3	BC025461	Mm.22270	1	3656	568	2291	538	0.00455	-1.6	transmembrane 4 superfamily member 3

Kitl	NM_013598	Mm.45124	1	1566	390	990	277	0.0312	-1.58	kit ligand
Cyp2f2	NM_007817	Mm.4515	1	942	238	595	85	0.02791	-1.58	cytochrome P450, family 2, subfamily f, polypeptide 2
Tjp1	NM_009386	Mm.4342	1	2251	430	1441	204	0.00899	-1.56	tight junction protein 1
Esam1	AF361882	Mm.41751	1	3415	142	2185	264	0.0001	-1.56	endothelial cell-specific adhesion molecule
Lamp2	NM_010685	Mm.486	1	902	197	587	122	0.019	-1.54	lysosomal membrane glycoprotein 2
Chodl	AF311699	Mm.77895	1	354	100	230	60	0.04959	-1.54	chondrolectin
Sdpr	NM_138741	Mm.255909	1	6017	1008	3962	768	0.00846	-1.52	serum deprivation response
Gpm6a	BB348674	Mm.241700	1	295	63	195	59	0.03285	-1.52	glycoprotein m6a
Trdn	AF223416	Mm.216837	1	618	50	945	167	0.00867	1.53	triadin
Sgcg	NM_011892	Mm.72173	1	4202	580	6582	692	0.00036	1.57	sarcoglycan, gamma (dystrophin-associated glycoprotein)
Ttyh2	BF585303	Mm.271934	1	1065	146	1677	234	0.00166	1.57	tweety homolog 2 (Drosophila)
Bat5	BG071718	Mm.43745	1	4749	1199	7513	808	0.0037	1.58	HLA-B associated transcript 5
Vapb	BB308907	Mm.260456	1	689	138	1087	222	0.01162	1.58	VAMP (vesicle-associated membrane protein)-associated protein B and C
Cdh15	NM_007662	Mm.1976	1	735	48	1171	166	0.00248	1.59	cadherin 15
Scn1b	BC009652	Mm.1418	1	6936	1319	11058	1326	0.00116	1.59	sodium channel, voltage-gated, type I, beta polypeptide
Bak1	NM_007523	Mm.2443	1	442	105	703	59	0.00287	1.59	BCL2-antagonist/killer 1
Stx18	AK007700	Mm.18959	1	436	103	692	148	0.01568	1.59	syntaxin 18
Mg29	NM_008596	Mm.20942	1	2688	680	4298	487	0.00356	1.6	mitsugumin 29
Rfng	NM_009053	Mm.871	1	692	150	1106	298	0.03215	1.6	radical fringe gene homolog (Drosophila)
Slc15a1	NM_053079	Mm.155618	1	72	21	120	28	0.01971	1.65	solute carrier family 15 (oligopeptide transporter), member 1
Napa	NM_025898	Mm.104540	1	524	91	869	136	0.00224	1.66	N-ethylmaleimide sensitive fusion protein attachment protein alpha
Kcnn1	NM_032397	Mm.32074	1	500	59	836	48	0.00001	1.67	K intermediate/small conductance ca-activated channel, subfamily N, member 1
Popdc3	AA116404	Mm.5290	1	2483	304	4242	491	0.00025	1.71	popeye domain containing 3
Amigo	BC022907	Mm.275752	1	331	98	571	82	0.00304	1.72	amphoterin induced gene and ORF
Bat5	BG071718	Mm.43745	1	1272	559	2305	406	0.01243	1.81	HLA-B associated transcript 5
Kcna7	NM_010596	Mm.12955	1	2422	273	4499	431	0.00004	1.86	potassium voltage-gated channel, shaker-related subfamily, member 7
Extl3	NM_018788	Mm.103748	1	133	81	258	66	0.03013	1.93	exostoses (multiple)-like 3
Jph2	NM_021566	Mm.34459	1	1381	563	2879	1162	0.04106	2.08	junctophilin 2
Cacnb1	BF165383	Mm.41252	1	668	184	1415	136	0.00017	2.12	calcium channel, voltage-dependent, beta 1 subunit
Cacng6	AF361348	Mm.219963	1	1185	598	3088	587	0.00096	2.61	calcium channel, voltage-dependent, gamma subunit 6
Itmap1	NM_008411	Mm.142717	1	226	23	738	278	0.01475	3.27	integral membrane-associated protein 1

NUCLEIC ACID BINDING

GeneSymbol	Genbank	Unigene	A/P	Ctl Mean	Ctl stdev	Exp Mean	Exp stdev	P-value	Fold Change	Gene Description
Prpf4b	BB344827	Mm.10027	1	411	92	191	86	0.00453	-2.15	PRP4 pre-mRNA processing factor 4 homolog B (yeast)
Hnrpu	BB667237	Mm.2115	1	629	189	301	69	0.01484	-2.09	heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A)
Eif4el3	BM120823	Mm.227183	1	560	137	269	81	0.0047	-2.08	eukaryotic translation initiation factor 4E like 3
Hnrpa1	BE685966	Mm.237064	1	143	12	70	41	0.01265	-2.04	heterogeneous nuclear ribonucleoprotein A1
Hnrph1	NM_021510	Mm.21740	1	3994	760	2174	379	0.00303	-1.84	heterogeneous nuclear ribonucleoprotein H1
Prpf4b	BB344827	Mm.10027	1	375	93	207	62	0.01226	-1.81	PRP4 pre-mRNA processing factor 4 homolog B (yeast)
Sfrs1	BG071935	Mm.45645	1	1146	287	658	95	0.01562	-1.74	splicing factor, arginine/serine-rich 1 (ASF/SF2)
Sfrs1	BF147037	Mm.45645	1	1023	303	611	83	0.03287	-1.67	splicing factor, arginine/serine-rich 1 (ASF/SF2)
Sfrs1	BM125059	Mm.45645	1	823	128	505	153	0.00756	-1.63	splicing factor, arginine/serine-rich 1 (ASF/SF2)
Rbpms	BG069460	Mm.12436	1	749	89	466	56	0.00054	-1.61	RNA binding protein gene with multiple splicing
Carhsp1	NM_025821	Mm.142095	1	971	158	611	97	0.00348	-1.59	calcium regulated heat stable protein 1
Sfrs1	X66091	Mm.45645	1	1471	346	931	64	0.02665	-1.58	splicing factor, arginine/serine-rich 1 (ASF/SF2)
Prpf8	NM_138659	Mm.3757	1	4111	618	2616	541	0.00361	-1.57	pre-mRNA processing factor 8
Hnrpa2b1	C88150	Mm.155896	1	1241	294	788	113	0.02386	-1.57	heterogeneous nuclear ribonucleoprotein A2/B1
Sfrs1	BF682801	Mm.45645	1	1378	120	888	101	0.00012	-1.55	splicing factor, arginine/serine-rich 1 (ASF/SF2)
Akap1	BG067335	Mm.2969	1	1868	251	1218	107	0.00316	-1.53	A kinase (PRKA) anchor protein 1
Sf3b1	NM_031179	Mm.279736	1	480	107	316	66	0.02283	-1.52	splicing factor 3b, subunit 1
Son	BM244966	Mm.46401	1	700	102	460	35	0.00424	-1.52	Son cell proliferation protein
Rev3l	AB031049	Mm.2167	1	1061	188	705	70	0.01081	-1.5	REV3-like, catalytic subunit of DNA polymerase zeta RAD54 like
Pdcd2	BI526195	Mm.323	1	647	114	979	152	0.00594	1.51	programmed cell death 2
Stau2	AJ244015	Mm.314307	1	1313	141	1988	136	0.00006	1.51	staufen, RNA binding protein, homolog 2
Stau2	BC025118	Mm.216257	1	1618	327	2463	367	0.005	1.52	staufen, RNA binding protein, homolog 2
Fbl	NM_007991	Mm.4595	1	1423	277	2185	165	0.00116	1.54	fibrillarin
Hist2h2aa1	BC010564	Mm.261670	1	1970	341	3065	518	0.00554	1.56	histone 2, H2aa1
Trim27	NM_009054	Mm.135689	1	1094	134	1766	219	0.00065	1.61	tripartite motif protein 27

Trex1	NM_011637	Mm.262117	1	974	127	1567	243	0.00291	1.61	three prime repair exonuclease 1
Xrcc5	AF166486	Mm.246952	1	216	37	347	62	0.00504	1.61	X-ray repair complementing defective repair in Chinese hamster cells 5
Rnpc1	NM_019547	Mm.3865	1	3662	724	5981	791	0.0013	1.63	RNA-binding region (RNP1, RRM) containing 1
Hist1h4i	BC019757	Mm.14775	1	839	236	1402	324	0.01652	1.67	histone 1, H4i
Ddx18	NM_025860	Mm.44219	1	631	135	1072	285	0.02063	1.7	DEAD (Asp-Glu-Ala-Asp) box polypeptide 18
Hist1h4h	BC028550	Mm.158272	1	840	196	1437	243	0.00273	1.71	histone 1, H4h
Gadd45a	NM_007836	Mm.1236	1	905	448	1584	392	0.03428	1.75	growth arrest and DNA-damage-inducible 45 alpha
Mettl3	BB827491	Mm.271759	1	501	148	879	180	0.00674	1.75	methyltransferase-like 3
Vars2	AF087680	Mm.28420	1	1106	258	1953	181	0.00054	1.77	valyl-tRNA synthetase 2
Apobec2	NM_009694	Mm.281793	1	12704	1398	23345	2928	0.00033	1.84	apolipoprotein B editing complex 2
Hist1h3a	NM_013550	Mm.221301	1	3125	1146	5784	1195	0.00709	1.85	histone 1, H3a
Apex1	CA568142	Mm.203	1	1357	359	2522	579	0.00655	1.86	apurinic/apyrimidinic endonuclease 1
Ttll1	BB251824	Mm.235007	1	92	44	181	55	0.02347	1.97	tubulin tyrosine ligase-like family, member 1
Hist2h2be	NM_019469	Mm.219680	1	1007	346	2056	362	0.00157	2.04	histone 2, H2be
Hist2h2aa1	BC015270	Mm.261670	1	238	57	792	143	0.0005	3.32	histone 2, H2ac
Dnase1	BC014718	Mm.239992	1	114	20	874	474	0.02324	7.64	deoxyribonuclease I

PROTEIN CATABOLISM

GeneSymbol	Genbank	Unigene	A/P	Ctl Mean	Ctl stdev	Exp Mean	Exp stdev	P-value	Fold Change	Gene Description
Hp	NM_017370	Mm.26730	1	1925	805	844	272	0.03618	-2.28	haptoglobin
Prss11	NM_019564	Mm.30156	1	3004	352	1407	348	0.00009	-2.13	protease, serine, 11 (Igf binding)
Prss11	BB559067	Mm.30156.2	1	1090	179	567	163	0.00132	-1.92	protease, serine, 11 (Igf binding)
Fgl2	NM_008013	Mm.292100	1	429	50	228	20	0.00042	-1.88	fibrinogen-like protein 2
Psma1	AV101011	Mm.30097.2	1	131	40	72	16	0.03067	-1.81	proteasome (prosome, macropain) subunit, alpha type, 1
Fbxo3	CA567607	Mm.143768	0.8	265	76	148	63	0.03003	-1.78	F-box only protein 3
Enpep	NM_007934	Mm.1193	1	795	197	492	81	0.02452	-1.62	glutamyl aminopeptidase
Casp6	NM_009811	Mm.281379	0.6	383	35	242	87	0.0207	-1.58	caspase 6
Adam15	BB392633	Mm.274049	1	2370	308	1506	178	0.00163	-1.57	a disintegrin and metalloproteinase domain 15 (metargidin)
Naalad2	NM_028279	Mm.7060	1	552	113	362	89	0.0189	-1.52	N-acetylated alpha-linked acidic dipeptidase 2
C1s	BC022123	Mm.24128	1	2520	690	1674	254	0.04988	-1.51	complement component 1, s subcomponent
Psmd4	AB029146	Mm.2261	1	3669	391	5576	347	0.00004	1.52	proteasome (prosome, macropain) 26S subunit, non-ATPase, 4
Agtpbp1	NM_023328	Mm.153008	1	339	135	534	81	0.02846	1.57	ATP/GTP binding protein 1
Serpinb6a	NM_009254	Mm.252210	1	8424	1226	13942	1905	0.00096	1.66	serine (or cysteine) proteinase inhibitor, clade B, member 6a
Usp20	BC019735	Mm.209761	1	555	168	960	260	0.02239	1.73	ubiquitin specific protease 20
Agtpbp1	AK015394	Mm.153008	0.8	197	66	402	84	0.00275	2.04	ATP/GTP binding protein 1
Fbxo17	NM_015796	Mm.88535	0.8	204	81	450	94	0.00226	2.2	F-box only protein 17

MISCELLANIOUS

GeneSymbol	Genbank	Unigene	A/P	Ctl Mean	Ctl stdev	Exp Mean	Exp stdev	P-value	Fold Change	Gene Description
Mup1	NM_031188	Mm.237772	1	24715	12561	4266	4943	0.01952	-5.79	major urinary protein 1
Cp	NM_007752	Mm.13787	1	482	184	193	89	0.02002	-2.49	ceruloplasmin
Lox	M65143	Mm.172	1	2110	498	859	161	0.0031	-2.45	lysyl oxidase
Egfl7	BC024610	Mm.268933	1	2027	260	841	191	0.00008	-2.41	EGF-like-domain, multiple 7
Sncg	NM_011430	Mm.282800	1	1906	695	807	268	0.02155	-2.36	synuclein, gamma
Rbp4	U63146	Mm.2605	1	2393	785	1081	321	0.01814	-2.21	retinol binding protein 4, plasma
Fsp27	BB221402	Mm.10026	1	4113	850	1904	730	0.00227	-2.16	fat specific gene 27
Ptgs1	AA833146	Mm.290010	0.8	166	33	79	50	0.01458	-2.1	prostaglandin-endoperoxide synthase 1
Gja1	BC006894	Mm.4504	1	533	101	258	99	0.00257	-2.06	gap junction membrane channel protein alpha 1
Mbp	BB761376	Mm.252063	1	2044	274	991	274	0.0003	-2.06	myelin basic protein
Tna	NM_011606	Mm.34588	1	1775	674	881	229	0.03766	-2.01	tetranectin (plasminogen binding protein)
Cda08-pending	AW554709	Mm.300723	1	517	111	257	73	0.0033	-2.01	T-cell immunomodulatory protein
Trf	AF440692	Mm.37214	1	4943	1243	2493	911	0.00931	-1.98	transferrin
Sema3b	NM_009153	Mm.4083	0.6	513	136	267	74	0.01228	-1.92	sema domain, immunoglobulin domain, short basic domain, secreted, 3B
Palmd	NM_023245	Mm.331326	1	1197	206	627	80	0.00221	-1.91	palmdelphin
Gas1	CA772806	Mm.22701	1	2265	160	1245	273	0.00036	-1.82	growth arrest specific 1
Sdccag33	AV291373	Mm.102136	1	659	44	362	63	0.00006	-1.82	serologically defined colon cancer antigen 33
Utx	AJ002730	Mm.257498	1	517	116	283	97	0.00889	-1.82	ubiquitously transcribed tetratricopeptide repeat gene, Y chromosome
Ppil4	BC004652	Mm.38927	1	449	74	248	141	0.03099	-1.81	peptidylprolyl isomerase (cyclophilin)-like 4

Mbp	AV328388	Mm.2992	1	1991	290	1100	408	0.00536	-1.81	myelin basic protein
Ccnl2	AK008585	Mm.23492	1	710	72	395	130	0.00326	-1.8	cyclin L2
Idb4	W77144	Mm.283273	1	266	70	149	42	0.01572	-1.78	inhibitor of DNA binding 4
Mbp	AI323506	Mm.252063	1	4450	781	2501	570	0.00279	-1.78	myelin basic protein
Dstn	NM_019771	Mm.28919	1	3061	201	1771	440	0.001	-1.73	destrin
Hrb	AF057287	Mm.6461	1	970	106	564	92	0.0002	-1.72	HIV-1 Rev binding protein
Htf9c	NM_008307	Mm.271798	1	858	235	501	224	0.03971	-1.71	HpaII tiny fragments locus 9c
Thbs4	NM_011582	Mm.20865	1	4121	391	2404	305	0.00006	-1.71	thrombospondin 4
Amot	BG067039	Mm.100068	1	1781	487	1049	223	0.02245	-1.7	angiomotin
CRG-L1	AF282864	Mm.45019	1	1163	76	687	70	0.00001	-1.69	cancer related gene-liver 1
Gas1	NM_008086	Mm.22701	1	2401	530	1431	428	0.01302	-1.68	growth arrest specific 1
Atp1b1	NM_009721	Mm.4550	1	4583	792	2748	453	0.00414	-1.67	ATPase, Na+/K+ transporting, beta 1 polypeptide
Ss18	NM_009280	Mm.31761	1	2504	524	1502	435	0.01112	-1.67	synovial sarcoma translocation, chromosome 18
Fmo5	NM_010232	Mm.281718	1	264	47	158	19	0.00544	-1.67	flavin containing monooxygenase 5
Psg28	AF113598	Mm.298482	1	339	57	203	53	0.0048	-1.67	pregnancy-specific glycoprotein 28
Thoc1	BC024951	Mm.219648	1	177	51	107	39	0.04642	-1.65	THO complex 1
Cp	NM_007752	Mm.13787	1	883	80	537	97	0.00029	-1.64	ceruloplasmin
Pkp4	AV286396	Mm.260938	1	1549	120	945	185	0.00049	-1.64	plakophilin 4
Hrb	CA748278	Mm.6461	1	671	108	412	135	0.01026	-1.63	HIV-1 Rev binding protein
Atp1b1	AV152334	Mm.4550.6	1	5462	827	3342	344	0.00322	-1.63	ATPase, Na+/K+ transporting, beta 1 polypeptide
Topors	BF018714	Mm.251548	1	322	63	201	19	0.01002	-1.6	topoisomerase I binding, arginine/serine-rich
Stag1	BQ174473	Mm.42135	1	570	102	357	84	0.00693	-1.6	stromal antigen 1
Cp	BY013791	Mm.13787	1	477	115	301	71	0.02303	-1.58	ceruloplasmin
Ccnl2	AK008585	Mm.23492	1	2855	395	1824	193	0.00195	-1.57	cyclin L2
Cxcl14	AF252873	Mm.30211	1	1229	243	784	156	0.01081	-1.57	chemokine (C-X-C motif) ligand 14
Ndr1	AV309418	Mm.4063	1	1370	352	877	218	0.03251	-1.56	N-myc downstream regulated 1
Gopc	BI659593	Mm.155704	1	534	89	345	26	0.00618	-1.55	golgi associated PDZ and coiled-coil motif containing, syntaxin-6 binding
Fign	NM_021716	Mm.130769	0.5	203	15	131	41	0.01476	-1.55	fidgetin
Atp1b1	CA578185	Mm.4550	1	6986	767	4528	418	0.00076	-1.54	ATPase, Na+/K+ transporting, beta 1 polypeptide
Ctla2a	NM_007796	Mm.30144	1	2091	392	1359	162	0.012	-1.54	cytotoxic T lymphocyte-associated protein 2 alpha
Ndr1	AI790290	Mm.30837	1	1975	315	1290	263	0.00584	-1.53	N-myc downstream regulated 1
Rgl1	NM_016846	Mm.245270	1	324	65	212	43	0.01577	-1.52	ral guanine nucleotide dissociation stimulator-like 1
Ian6	BB667753	Mm.24781	1	884	226	585	153	0.04494	-1.51	immune associated nucleotide 6
Catnd2	NM_008729	Mm.6680	0.8	81	10	123	23	0.0117	1.51	catenin delta 2
Jtv1	BC026972	Mm.200499	1	5794	649	8724	1619	0.01322	1.51	JTV1 gene
Eif2b4	NM_010122	Mm.29394	1	2710	344	4130	439	0.00046	1.52	eukaryotic translation initiation factor 2B, subunit 4 delta
Hcfc1r1	BF580567	Mm.270281	1	4066	647	6240	1062	0.00585	1.53	host cell factor C1 regulator 1 (XPO1-dependent)
Unc119	BC001990	Mm.284811	0.8	463	66	711	138	0.01103	1.54	unc-119 homolog (C. elegans)
Tpd52l1	NM_009413	Mm.7821	1	556	131	856	173	0.01802	1.54	tumor protein D52-like 1
Tcof1	AW209012	Mm.2215	1	666	70	1024	268	0.03413	1.54	Treacher Collins Franceschetti syndrome 1, homolog
Hgs	BC003239	Mm.7919	1	2921	219	4519	810	0.00805	1.55	HGF-regulated tyrosine kinase substrate
Tgm2	BC016492	Mm.330731	1	6308	934	9881	852	0.00023	1.57	transglutaminase 2
Gas5	NM_013525	Mm.270065	1	4429	1120	7043	867	0.00332	1.59	growth arrest specific 5
Nup62	AV295214	Mm.22687	0.9	692	117	1100	304	0.03798	1.59	nucleoporin 62
Fbxw5	NM_013908	Mm.29170	1	946	205	1517	290	0.00886	1.6	F-box and WD-40 domain protein 5
Anxa6	NM_013472	Mm.265347	1	3729	463	6016	945	0.00284	1.61	annexin A6
Nope	NM_020043	Mm.209041	1	509	33	821	144	0.00929	1.61	neighbor of Punc E11
Tgm2	AW321975	Mm.18843	1	3258	576	5236	893	0.00425	1.61	transglutaminase 2, C polypeptide
Lynx1	NM_011838	Mm.257067	1	1845	386	2981	381	0.00158	1.62	y6/neurotoxin 1
Plac1	AF250838	Mm.274842	0.8	268	79	436	125	0.04005	1.62	placental specific protein 1
Eif4ebp1	AK013033	Mm.6700	1	816	304	1329	230	0.01974	1.63	eukaryotic translation initiation factor 4E binding protein 1
Hspb7	BM124741	Mm.46181	1	10716	3668	17433	3401	0.017	1.63	heat shock protein family, member 7 (cardiovascular)
Cyhr1	NM_019396	Mm.18561	1	907	236	1507	149	0.00199	1.66	cysteine and histidine rich 1
H19	NM_023123	Mm.14802	1	5627	738	9422	1351	0.0015	1.67	H19 fetal liver mRNA
Mlf1	AF100171	Mm.10414	1	5716	1389	9518	721	0.00162	1.67	myeloid leukemia factor 1
Lrba	NM_030695	Mm.239927	1	2478	472	4169	628	0.00195	1.68	LPS-responsive beige-like anchor
Hspb7	BY000290	Mm.46181	1	9232	5091	15599	3067	0.0478	1.69	heat shock protein family, member 7 (cardiovascular)
Tcof1	AW209012	Mm.2215	1	223	51	384	93	0.01471	1.72	Treacher Collins Franceschetti syndrome 1, homolog
Ldb3	AF114378	Mm.29733	1	4127	1041	7113	2189	0.03311	1.72	LIM domain binding 3
Bklhd2	NM_026167	Mm.26546	1	112	18	194	35	0.0037	1.73	kelch-like 13

Bin1	U60884	Mm.4383	1	9359	1192	16399	2273	0.00086	1.75	bridging integrator 1
Ccng1	BG065754	Mm.2103	1	6821	517	12292	1959	0.00179	1.8	cyclin G1
Serf1	AA709993	Mm.286177	1	81	19	146	24	0.00165	1.81	small EDRK-rich factor 1
Defb10	AJ437645	Mm.220170	1	172	59	315	78	0.01429	1.83	defensin beta 10
Neurl	AF401228	Mm.329899	1	3652	362	6768	1110	0.00189	1.85	neuralized-like homolog
Ptov1	BG073526	Mm.42855	1	2775	1485	5240	1794	0.04548	1.89	prostate tumor over expressed gene 1
Mllt1	BG063049	Mm.148748	0.6	498	217	948	123	0.00702	1.9	myeloid/lymphoid or mixed lineage-leukemia translocation to 1 homolog
Spag5	BM208112	Mm.24250	1	169	29	332	61	0.00179	1.96	sperm associated antigen 5
Lgals2	NM_025622	Mm.26934	0.9	210	53	422	124	0.01721	2.01	lectin, galactose-binding, soluble 2
Rex3	NM_009052	Mm.14768	1	1686	506	3451	1179	0.02759	2.05	reduced expression 3
Neurl	AF400063	Mm.329899	1	512	190	1080	349	0.01879	2.11	neuralized-like homolog
Wdr10	AV319292	Mm.333335	1	350	56	745	118	0.00052	2.12	WD repeat domain 10
Exo70	BB749620	Mm.22530	1	968	237	2166	321	0.00028	2.24	exocyst component protein homolog (S. cerevisiae)
Ubc	D50527	Mm.331	1	1211	746	3113	1014	0.01183	2.57	ubiquitin C
Cpne2	BC023348	Mm.291815	1	345	85	1423	788	0.03844	4.12	copine II
Crip3	AF367970	Mm.25168	0.7	127	68	857	187	0.00045	6.74	cysteine-rich protein 3

UNKNOWN

GeneSymbol	Genbank	Unigene	A/P	Ctl Mean	Ctl stdev	Exp Mean	Exp stdev	P-value	Fold Change	Gene Description
A930025J12Ri	BC027354	Mm.260712	0.8	1262	655	319	468	0.03457	-3.95	null
BC018222	BC026654	Mm.31552	1	1104	468	379	161	0.02207	-2.91	cDNA sequence BC018222
0710001E19Ri	NM_029716	Mm.257073	0.5	229	69	78	68	0.0089	-2.9	RIKEN cDNA 0710001E19 gene
AB023957	NM_133237	Mm.276268	1	555	166	228	85	0.00795	-2.43	cDNA sequence AB023957
AI255170	BE134496	Mm.214973	0.8	603	209	251	130	0.01544	-2.4	expressed sequence AI255170
1810057C19Ri	NM_026433	Mm.212428	1	1330	454	581	95	0.02266	-2.29	RIKEN cDNA 1810057C19 gene
A230046K03Ri	BB387783	Mm.278577	0.5	92	32	40	26	0.02448	-2.29	null
1100001G20R	AV006463	Mm.902	1	638	157	295	67	0.00655	-2.16	RIKEN cDNA 1100001G20 gene
2610001E17Ri	BG074158	Mm.181074	0.6	1171	346	545	244	0.01312	-2.15	RIKEN cDNA 2610001E17 gene
A830037N07R	BB752393	Mm.259072	1	395	116	188	39	0.01312	-2.1	RIKEN cDNA A830037N07 gene
NULL	AK002700	Mm.17339.2	1	5168	1028	2500	872	0.00222	-2.07	null
AB023957	NM_133237	Mm.276268	0.8	464	186	225	83	0.03975	-2.06	cDNA sequence AB023957
NULL	AA223007	NULL	1	420	85	205	83	0.0038	-2.05	null
NULL	BI415208	Mm.255066	0.8	497	84	243	99	0.0024	-2.05	null
B430320C24Ri	BG066982	Mm.25259	1	917	354	454	152	0.04356	-2.02	Mus musculus 0 day neonate lung cDNA, clone:E030020K21
A830037N07R	BB752393	Mm.259072	1	426	125	215	103	0.02024	-1.98	RIKEN cDNA A830037N07 gene
2210418I02Ril	AV370981	Mm.73682	1	610	109	310	139	0.00541	-1.97	RIKEN cDNA 2210418I02 gene
2310076L09Ri	BC024138	Mm.254985	1	2389	565	1212	230	0.00764	-1.97	RIKEN cDNA 2310076L09 gene
0610007L05Ri	BI328146	Mm.28231	1	2312	537	1191	193	0.00714	-1.94	RIKEN cDNA 0610007L05 gene
2610510D13R	BG518769	Mm.268185	1	2459	560	1314	318	0.00736	-1.87	null
0610007L05Ri	AV012073	Mm.28231	1	1849	431	1000	260	0.00702	-1.85	null
C330016O16R	BC025434	Mm.156227	1	298	97	163	37	0.03412	-1.83	null
5033405D03R	BB559878	Mm.19352	1	3290	474	1801	422	0.00078	-1.83	RIKEN cDNA 5033405D03 gene
AI595338	BM241485	Mm.275893	1	914	222	499	228	0.01955	-1.83	expressed sequence AI595338
2310075G12R	BC026740	Mm.24635	0.7	1008	188	555	282	0.02054	-1.81	RIKEN cDNA 2310075G12 gene
NULL	AV213552	Mm.12001	0.8	623	214	346	111	0.04284	-1.8	null
BC013720	BG066686	Mm.301521	0.6	390	69	216	45	0.00219	-1.8	Mus musculus transcribed sequences
3300001P08Ri	BC009092	Mm.30927	1	1736	337	972	152	0.00365	-1.79	RIKEN cDNA 3300001P08 gene
6720480D16R	BB329288	Mm.296036	1	312	78	174	81	0.02541	-1.79	null
A230075M04R	AV246615	Mm.24003	1	2316	355	1301	394	0.00268	-1.78	Mus musculus 13 days embryo heart cDNA, clone:D330042I16
2310039E09Ri	NM_026509	Mm.133444	1	6461	1185	3641	299	0.0036	-1.77	RIKEN cDNA 2310039E09 gene
2310043N10Ri	AK018202	Mm.281895	1	19465	3364	11122	2704	0.00254	-1.75	Mus musculus adult male cecum cDNA, clone:9130009H04
E030006K04Ri	AI851258	Mm.247642	1	741	181	424	111	0.01269	-1.75	RIKEN cDNA E030006K04 gene
1810044O22R	BM934224	Mm.20242	1	1691	233	973	295	0.00276	-1.74	RIKEN cDNA 1810044O22 gene
1110001A05Ri	NM_019808	Mm.117709	1	231	66	133	41	0.02627	-1.74	RIKEN cDNA 1110001A05 gene
R75183	BC004774	Mm.295397	1	1170	325	677	200	0.02358	-1.73	expressed sequence R75183
2210404N08Ri	BC026453	Mm.34874	1	707	83	409	73	0.00033	-1.73	RIKEN cDNA 2210404N08 gene
2610001E17Ri	AB075019	Mm.181074	1	4819	1190	2803	61	0.01938	-1.72	RIKEN cDNA 2610001E17 gene
2410018G23R	CA574035	Mm.28626	1	1020	189	598	139	0.00516	-1.7	RIKEN cDNA 2410018G23 gene
6330415F13Ri	BC007185	Mm.27469	1	786	233	464	64	0.03116	-1.69	RIKEN cDNA 6330415F13 gene

NULL	BC023373	Mm.50809	1	1542	297	914	188	0.00528	-1.69	Mus musculus 13 days embryo male testis, clone:6030482D04 product:CDT6
1110048B16Ri	BB364488	Mm.4948	1	2487	650	1470	700	0.0446	-1.69	forkhead box O3
6330415F13Ri	AV234585	Mm.27469	1	361	83	215	63	0.01674	-1.68	RIKEN cDNA 6330415F13 gene
3222402P14Ri	BB376997	Mm.129981	1	1211	226	728	115	0.00538	-1.66	null
AA959601	AA410148	Mm.24477	1	880	197	529	51	0.01212	-1.66	DNA segment, Chr 14, Wayne State University 89, expressed
4632428N05R	NM_028732	Mm.273584	1	791	158	478	142	0.01094	-1.65	RIKEN cDNA 4632428N05 gene
D4Wsu53e	NM_023665	Mm.331964	1	4214	827	2559	883	0.01568	-1.65	Mus musculus transcribed sequence
NULL	AV036158	Mm.2917	0.6	141	26	86	37	0.03045	-1.65	null
2610102K23Ri	BI965039	Mm.294783	1	430	86	262	52	0.00756	-1.64	null
4921515A04Ri	BM119297	Mm.3036	1	513	122	313	101	0.02263	-1.64	RIKEN cDNA 4921515A04 gene
0610013D04R	BG075321	Mm.196330	1	744	139	452	89	0.00562	-1.64	RIKEN cDNA 0610013D04 gene
NULL	AV013785	Mm.208618	0.6	253	29	155	60	0.01704	-1.63	Mus musculus, clone IMAGE:5028242, mRNA
A230106A15R	BG071079	Mm.200220	1	677	97	414	72	0.00193	-1.63	Mus musculus adult male hypothalamus cDNA, clone:A230106A15
MGC18894	BC013479	Mm.29110	1	727	182	447	141	0.02641	-1.63	hypothetical protein MGC18894
2700084L22Ri	NM_026024	Mm.284587	1	195	45	120	36	0.02095	-1.62	RIKEN cDNA 2700084L22 gene
1200002N14R	BC021433	Mm.35450	0.8	1074	309	662	128	0.04064	-1.62	RIKEN cDNA 1200002N14 gene
C330005L02Ri	BB503267	Mm.228067	1	1292	186	802	125	0.0018	-1.61	null
AA959601	BB795072	Mm.24477	1	259	66	161	25	0.02665	-1.61	DNA segment, Chr 14, Wayne State University 89, expressed
1300013C10Ri	BM120233	Mm.10281	1	683	158	428	134	0.02488	-1.6	RIKEN cDNA 1300013C10 gene
4930563P03Ri	AK016213	Mm.10223	1	997	223	624	156	0.01834	-1.6	RIKEN cDNA 4930563P03 gene
2610510E10Ri	BG228848	Mm.324474	1	1251	288	780	143	0.0169	-1.6	Mus musculus transcribed sequence
3110006P09Ri	AW536850	Mm.3035	1	1249	155	788	220	0.00648	-1.59	RIKEN cDNA 3110006P09 gene
2810429C13Ri	BC007170	Mm.259893	1	283	50	178	51	0.01136	-1.59	RIKEN cDNA 2810429C13 gene
9130005N23R	AA201054	Mm.22541	0.8	181	46	114	20	0.02624	-1.59	RIKEN cDNA 9130005N23 gene
AW111922	NM_021792	Mm.261140	1	367	105	231	62	0.0467	-1.59	null
C330007P06Ri	BC021479	Mm.290704	1	986	195	622	97	0.00974	-1.59	RIKEN cDNA C330007P06 gene
A530016L24Ri	BC026527	Mm.185209	0.5	279	70	175	51	0.03154	-1.59	RIKEN cDNA A530016L24 gene
BC013529	BC013529	Mm.33716	1	2296	661	1449	249	0.0439	-1.58	cDNA sequence BC013529
2810055F11Ri	BC004753	Mm.286120	1	248	40	157	30	0.00509	-1.58	RIKEN cDNA 2810055F11 gene
2310001A20Ri	AJ310638	Mm.26599	1	1829	249	1160	240	0.00254	-1.58	RIKEN cDNA 2310001A20 gene
1300006L01Ri	AK018760	Mm.33729	1	3986	787	2527	488	0.00972	-1.58	RIKEN cDNA 1300006L01 gene
1700017I17Ril	BC016606	Mm.150701	1	1270	258	807	211	0.01465	-1.57	null
BC022623	BB008324	Mm.28244	1	501	74	319	121	0.02422	-1.57	cDNA sequence BC022623
AU040950	AF353717	Mm.275054	1	4055	917	2582	238	0.01777	-1.57	expressed sequence AU040950
2610529H08R	AV227727	Mm.258985	1	6505	1046	4160	279	0.00472	-1.56	RIKEN cDNA 2610529H08 gene
3100002M17R	BQ175470	Mm.26017	1	304	72	195	74	0.04702	-1.56	RIKEN cDNA 3100002M17 gene
2310016C16Ri	BC019664	Mm.12715	1	462	61	295	30	0.00161	-1.56	RIKEN cDNA 2310016C16 gene
4933425F03Ri	BC016096	Mm.83840	1	5662	1271	3652	695	0.02111	-1.55	RIKEN cDNA 4933425F03 gene
BC013667	BC013667	Mm.220901	1	507	115	327	85	0.02645	-1.55	null
NULL	AU018141	NULL	1	3624	910	2357	371	0.03449	-1.54	null
D730040F13Ri	AF031164	Mm.296632	1	644	95	419	107	0.00816	-1.54	Mus musculus 12 days embryo spinal ganglion cDNA, clone:D130071L21
AA959601	BB795072	Mm.24477	1	1253	179	816	41	0.00608	-1.54	DNA segment, Chr 14, Wayne State University 89, expressed
AI316828	D50523	Mm.229654	1	1716	201	1118	133	0.00087	-1.54	null
AI450757	AV364671	Mm.33908	1	742	135	486	76	0.01015	-1.53	expressed sequence AI450757
AF424697	AF424697	Mm.281732	1	603	59	397	98	0.00509	-1.52	DNA sequence AF424697
1200003E16Ri	AK004560	Mm.27917	0.8	745	124	489	66	0.00655	-1.52	RIKEN cDNA 1200003E16 gene
9130017A15Ri	AI881989	Mm.251661	1	6490	731	4266	270	0.0014	-1.52	Moderately similar to melanoma antigen, family D, 2; mage-d2 protein
1500005K14Ri	BG070087	Mm.34131	0.7	1253	204	824	202	0.01033	-1.52	RIKEN cDNA 1500005K14 gene
7420700H20R	AK008756	Mm.7381	1	558	98	368	82	0.01084	-1.52	RIKEN cDNA 7420700H20 gene
1110021N07R	AV310010	Mm.289387	0.8	733	131	487	108	0.01219	-1.51	null
NULL	BE335796	Mm.259200	1	714	106	475	94	0.00559	-1.5	null
BC016423	NM_134063	Mm.221609	1	267	39	178	60	0.02925	-1.5	null
1300002A08Ri	NM_025827	Mm.30092	1	1727	332	2597	386	0.00514	1.5	RIKEN cDNA 1300002A08 gene
2310050L06Ri	BC021619	Mm.27166	1	608	130	913	130	0.00607	1.5	RIKEN cDNA 2310050L06 gene
NULL	AK009153	Mm.220982.	1	87	9	132	21	0.00776	1.51	null
5730592L21Ri	AK017880	Mm.292567	0.9	403	76	608	115	0.01315	1.51	RIKEN cDNA 5730592L21 gene
BC029157	BY008172	Mm.221271	0.7	672	278	1017	135	0.04767	1.51	cDNA sequence BC029157
1110027L01Ri	BC027303	Mm.34088	1	304	57	461	83	0.01064	1.51	RIKEN cDNA 1110027L01 gene
NULL	AK016616	Mm.24222.2	1	279	69	423	66	0.01006	1.52	null
8030445B08Ri	BI102531	Mm.78312	1	286	52	433	87	0.01439	1.52	RIKEN cDNA 8030445B08 gene

1300019N10R	AK005069	Mm.71514	1	734	153	1114	99	0.00235	1.52	RIKEN cDNA 1300019N10 gene
NULL	BG067018	Mm.42588	1	171	36	261	33	0.00357	1.52	Mus musculus transcribed sequences
D11Ertd707e	NM_025918	Mm.277638	1	161	19	245	52	0.0204	1.52	DNA segment, Chr 11, ERATO Doi 707, expressed
4933407E01Ri	BC026793	Mm.276043	1	468	73	713	97	0.00289	1.52	RIKEN cDNA 4933407E01 gene
2610034E13Ri	NM_029365	Mm.157778	1	2130	621	3250	578	0.01843	1.53	RIKEN cDNA 2610034E13 gene
2310007F12Ri	BQ177187	Mm.8142	1	194	45	297	40	0.00494	1.53	RIKEN cDNA 2310007F12 gene
1810037C22Ri	BE952060	Mm.294534	1	904	125	1386	256	0.00931	1.53	null
NULL	AK018785	Mm.4009.2	1	640	83	980	62	0.00017	1.53	null
C330013D05R	BG070774	Mm.29914	1	1064	174	1628	284	0.00696	1.53	RIKEN cDNA C330013D05 gene
D19Ertd703e	AK015925	Mm.284686	1	385	83	593	150	0.03573	1.54	null
D230016N13R	BB107552	Mm.111627	1	748	122	1151	164	0.00321	1.54	RIKEN cDNA D230016N13 gene
1110020K19Ri	BM119523	Mm.291291	1	841	42	1298	304	0.02927	1.54	similar to Ras GTPase-activating protein SynGAP
C730048E16Ri	BC014743	Mm.24262	1	546	105	843	95	0.00156	1.54	RIKEN cDNA C730048E16 gene
2900073H19R	AK012124	Mm.20273	1	941	239	1445	232	0.00963	1.54	null
1110003B01Ri	NM_026131	Mm.275648	1	12163	768	18707	1097	0.00001	1.54	RIKEN cDNA 1110003B01 gene
1810004B07Ri	BM210680	Mm.10174	1	821	164	1273	166	0.00254	1.55	RIKEN cDNA 1810004B07 gene
BC014795	BC019442	Mm.185518	0.8	790	182	1223	286	0.02471	1.55	cDNA sequence BC014795
NULL	AK013026	Mm.22619.2	1	1406	248	2177	288	0.00192	1.55	null
2700087H15R	BC005748	Mm.40721	1	1306	463	2033	307	0.02228	1.56	RIKEN cDNA 2700087H15 gene
1810034B16Ri	AK007688	Mm.41925	1	991	183	1549	314	0.01414	1.56	RIKEN cDNA 1810034B16 gene
3010020C06	AV026910	Mm.249594	1	298	75	466	89	0.01254	1.56	hypothetical protein 3010020C06
BC023239	BG076209	Mm.295629	1	6179	287	9712	440	0	1.57	cDNA sequence BC023239
NULL	BM239632	Mm.259678	0.8	117	51	183	25	0.04165	1.57	EST
1110012E06Ri	AK003623	Mm.205625	1	832	142	1306	254	0.01093	1.57	RIKEN cDNA 1110012E06 gene
D16Ertd502e	BC020153	Mm.21473	1	760	73	1192	117	0.00022	1.57	DNA segment, Chr 16, ERATO Doi 502, expressed
ORF63	AY033899	Mm.194466	1	503	227	789	143	0.04902	1.57	open reading frame 63
1300013J15Ri	NM_026183	Mm.100741	1	1063	91	1674	378	0.02472	1.58	RIKEN cDNA 1300013J15 gene
BC002059	BC002059	Mm.255974	0.9	220	26	347	74	0.01523	1.58	cDNA sequence BC002059
B	AK015111	Mm.39082.2	1	406	38	648	107	0.00525	1.59	null
D2Bwg0891e	BC019947	Mm.195525	1	1340	169	2136	183	0.0001	1.59	DNA segment, Chr 2, Brigham & Women's Genetics 0891 expressed
2410005O16R	BB397174	Mm.257603	1	2938	369	4668	387	0.00009	1.59	RIKEN cDNA 2410005O16 gene
3110038K10Ri	AK014142	Mm.44871	0.9	461	123	734	168	0.02213	1.59	null
LOC234776	BQ266886	Mm.259736	0.8	310	74	494	69	0.00379	1.59	null
NULL	NM_028402	NULL	0.8	143	38	229	65	0.04521	1.59	null
4930542G03R	BC005547	Mm.227260	1	9783	887	15643	1590	0.00036	1.6	RIKEN cDNA 4930542G03 gene
1600014E20Ri	AK005451	Mm.22	1	137	25	218	53	0.02097	1.6	RIKEN cDNA 1600014E20 gene
NULL	AK009453	Mm.1417.2	1	183	55	293	46	0.00921	1.6	null
2400004E04Ri	AK010278	Mm.7124	1	1544	145	2487	354	0.0027	1.61	RIKEN cDNA 2400004E04 gene
2900042B11Ri	AK013636	Mm.21787	1	336	49	541	60	0.00039	1.61	RIKEN cDNA 2900042B11 gene
1500005G05R	BC024618	Mm.280230	1	2854	282	4604	676	0.0031	1.61	RIKEN cDNA 1500005G05 gene
0610037P05Ri	BC011300	Mm.42072	1	3609	230	5846	907	0.00308	1.62	RIKEN cDNA 0610037P05 gene
2310001N14R	AF422244	Mm.283493	1	6096	1125	9863	1884	0.0064	1.62	RIKEN cDNA 2310001N14 gene
0610041D19R	AK002882	Mm.284594	1	1468	163	2394	248	0.00022	1.63	RIKEN cDNA 0610041D19 gene
NULL	AV285295	Mm.239583	1	1412	192	2300	208	0.00011	1.63	null
D7Wsu87e	AJ250693	Mm.246240	1	1903	544	3116	317	0.00507	1.64	TRAF-binding protein
NULL	AV034993	NULL	1	456	74	747	193	0.02566	1.64	null
D7Ertd458e	BB049138	Mm.227506	0.5	364	131	601	107	0.01441	1.65	null
D8Ertd812e	BG069220	Mm.275720	1	755	245	1248	56	0.01192	1.65	null
1300010A20Ri	BI440178	Mm.225289	0.8	121	15	202	29	0.00155	1.66	RIKEN cDNA 1300010A20 gene
NULL	AB056443	NULL	1	183	68	305	83	0.03454	1.67	null
4930544L10Ri	BG067288	Mm.235366	1	552	176	923	233	0.02528	1.67	RIKEN cDNA 4930544L10 gene
NULL	AK005822	Mm.322736	0.6	274	80	459	130	0.03097	1.67	null
BC037674	BB479063	Mm.301179	1	9300	832	15522	4696	0.04339	1.67	Mus musculus similar to RIKEN cDNA 4930449I24 (LOC385302), mRNA
2310004N11R	AV091811	Mm.260802	1	1823	158	3071	283	0.00014	1.68	null
1700037B15Ri	AV251625	Mm.250841	1	4716	1023	7915	679	0.00065	1.68	RIKEN cDNA 1700037B15 gene
2410018C20Ri	NM_026423	Mm.278085	1	740	87	1243	121	0.00014	1.68	RIKEN cDNA 4930527D15 gene
D830019K17R	BC016136	Mm.257236	1	1301	486	2200	460	0.01704	1.69	RIKEN cDNA D830019K17 gene
AI839562	NM_019914	Mm.331208	1	1983	304	3361	478	0.00097	1.69	RIKEN cDNA 5730493B19 [Mus musculus]
NULL	AK013560	Mm.100510.	0.8	79	33	134	13	0.02003	1.69	null
2210021J22Ri	BC025858	Mm.33706	1	1174	357	1997	353	0.00638	1.7	RIKEN cDNA 2210021J22 gene

NULL	AK018829	Mm.41682.2	0.6	302	107	513	93	0.01065	1.7	null
BC025872	BC025872	Mm.265552	1	4045	293	6919	685	0.00035	1.71	null
NULL	BB794641	Mm.320036	1	917	152	1571	535	0.04666	1.71	Mus musculus transcribed sequences
2210418O10R	CA566463	Mm.229100	0.6	63	11	109	27	0.01902	1.72	hypothetical protein C230069C04
1190005L06Ri	BB030180	Mm.259223	1	309	90	534	36	0.00361	1.73	RIKEN cDNA 1190005L06 gene
2700071E21Ri	BM946248	Mm.33121	1	1960	733	3388	1101	0.04657	1.73	RIKEN cDNA 2700071E21 gene
2310008N12Ri	BI649826	Mm.30060	0.7	523	48	907	111	0.0009	1.73	RIKEN cDNA 2310008N12 gene
BC003331	BC003331	Mm.222093	1	983	236	1725	188	0.00058	1.75	cDNA sequence BC003331
4930544L10Ri	BI871826	Mm.101141	1	617	154	1086	159	0.0015	1.76	RIKEN cDNA 4930544L10 gene
1810073P09Ri	AK007980	Mm.202157	1	1807	114	3227	183	0	1.79	RIKEN cDNA 1810073P09 gene
NULL	AI627121	Mm.340526	0.5	87	8	159	36	0.0123	1.83	ESTs
3110038L01Ri	NM_026524	Mm.29429	1	2581	574	4762	548	0.00028	1.84	RIKEN cDNA 3110038L01 gene
5830411E10Ri	AK015312	Mm.196290	1	204	67	376	102	0.01639	1.84	null
2210021G21R	BC010346	Mm.32883	0.5	528	136	990	174	0.00162	1.88	RIKEN cDNA 2210021G21 gene
2610005B21Ri	AK011311	Mm.291583	0.7	148	40	278	78	0.01625	1.88	RIKEN cDNA 2610005B21 gene
1110028E10Ri	BB145101	Mm.148425	1	4049	750	7626	249	0.00016	1.88	RIKEN cDNA 1110028E10 gene
NULL	BC021349	Mm.176845.	0.9	433	105	817	162	0.00307	1.89	null
2310047C17Ri	BC028439	Mm.35669	1	370	59	698	90	0.00025	1.89	RIKEN cDNA 2310047C17 gene
BC024683	BI106637	Mm.233067	1	854	94	1618	180	0.00016	1.89	null
NULL	AK006149	NULL	1	944	59	1821	387	0.00749	1.93	null
1110035L05Ri	AV048291	Mm.29140	1	358	235	696	131	0.03117	1.94	RIKEN cDNA 1110035L05 gene
2310047C17Ri	AK009866	Mm.35669	1	583	182	1129	169	0.00119	1.94	null
2700082D03R	AI195545	Mm.259121	1	1691	293	3308	444	0.00026	1.96	RIKEN cDNA 2700082D03 gene
A930031D07R	AI426503	Mm.208445	0.8	224	40	439	165	0.04791	1.96	RIKEN cDNA A930031D07 gene
LOC228785	BC019408	Mm.250604	1	11875	3621	23218	5797	0.00755	1.96	hypothetical protein LOC228785
1110038D17R	AK004153	Mm.29382	1	4432	1061	8807	404	0.00035	1.99	RIKEN cDNA 1110038D17 gene
C030022K24Ri	BC019151	Mm.159924	0.8	193	34	393	87	0.00498	2.03	RIKEN cDNA C030022K24 gene
NULL	BB533448	Mm.34042	1	2809	854	5832	866	0.00054	2.08	null
NULL	NM_133914	NULL	0.8	416	168	871	201	0.00472	2.09	null
NULL	W45978	Mm.178550	1	2062	396	4570	1432	0.01295	2.22	Mus musculus, clone IMAGE:4206343, mRNA
2700055K07Ri	NM_026481	Mm.29358	1	1695	326	3880	400	0.00001	2.29	RIKEN cDNA 2700055K07 gene
1110028E10Ri	BB478892	Mm.148425	1	475	293	1137	440	0.02655	2.39	RIKEN cDNA 1110028E10 gene
1110028G01R	AJ277212	Mm.220895	1	2812	325	6898	1704	0.00623	2.45	RIKEN cDNA 1110028G01 gene
B130052G07R	BC024141	Mm.22856	1	130	67	337	79	0.00217	2.6	RIKEN cDNA B130052G07 gene
1110030K22Ri	NM_024230	Mm.33452	1	1337	149	3495	1348	0.02363	2.61	RIKEN cDNA 1110030K22 gene
3010020C06	NM_021883	Mm.249594	1	3354	782	9051	2066	0.00221	2.7	hypothetical protein 3010020C06
4930586I02Ril	NM_026580	Mm.127378	1	375	73	1031	144	0.0001	2.75	RIKEN cDNA 4930586I02 gene
4930586I02Ril	AK006346	Mm.127378	1	280	132	779	165	0.00076	2.78	RIKEN cDNA 4930586I02 gene

SUPPLEMENTAL TABLE 2
Changes in gene expression in the medial gastrocnemius of MGSKO mice as compared with wild-type littermates. See legend to Supplemental Table 1. Exp, MGSKO samples.

CARBOHYDRATE METABOLISM

GeneSymbol	Genbank	Unigene	A/P	Ctl Mean	Ctl stdev	Exp Mean	Exp stdev	P-value	Fold Change	Gene Description
Gys1/Gys3	NM_008195	Mm.275654	1	5033	947	96	59	0.00031	-52.03	glycogen synthase 1
Gys1/Gys3	NM_030678	Mm.275654	1	2507	464	64	83	0.00033	-38.86	glycogen synthase 1
Ppp1r1a	NM_021391	Mm.143788	1	1561	419	441	64	0.00424	-3.54	protein phosphatase 1, regulatory (inhibitor) subunit 1A
Gyk	NM_008194	Mm.246682	1	358	204	113	46	0.04978	-3.16	glycerol kinase
Pfkfb3	AV282911	Mm.19669	1	2514	942	951	581	0.02728	-2.64	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3
Uap1	AI467637	Mm.27969	0.5	132	48	58	24	0.02913	-2.26	UDP-N-acetylglucosamine pyrophosphorylase 1
Aldo3	BC008184	Mm.7729	0.9	254	77	112	49	0.01987	-2.26	aldolase 3, C isoform
Slc2a3	BB414515	Mm.269857	1	1346	225	658	78	0.00158	-2.04	solute carrier family 2 (facilitated glucose transporter), member 3
Lgals4	BC021632	Mm.210336	1	729	152	385	80	0.00582	-1.89	lectin, galactose binding, soluble 4
Slc2a3	BB414515	Mm.269857	1	884	112	481	92	0.0027	-1.84	solute carrier family 2 (facilitated glucose transporter), member 3
Bdh	BF322712	Mm.293470	1	4060	548	2285	564	0.01214	-1.78	3-hydroxybutyrate dehydrogenase (heart, mitochondrial)
Lman1	AI787074	Mm.290857	1	950	299	543	159	0.0465	-1.75	lectin, mannose-binding, 1
Glo1	AK005055	Mm.261984	1	7725	1825	4628	535	0.01643	-1.67	glyoxalase 1
Glo1	BC024663	Mm.261984	1	3796	1013	2317	273	0.02739	-1.64	glyoxalase 1
Glo1	BC024663	Mm.261984	1	1627	329	1006	132	0.00961	-1.62	glyoxalase 1
Por	NM_008898	Mm.3863	1	2622	731	1641	201	0.03682	-1.6	P450 (cytochrome) oxidoreductase
Pfkfb3	NM_133232	Mm.19669	1	7667	2169	4825	249	0.04421	-1.59	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3
Lman1	AK011495	Mm.290857	1	1084	150	688	175	0.03123	-1.57	lectin, mannose-binding, 1
Glul	AI391218	Mm.210745	1	8415	1091	5601	1273	0.03323	-1.5	glutamate-ammonia ligase (glutamine synthase)
Ugp2	AV370025	Mm.130747	1	7005	1442	11098	613	0.00143	1.58	UDP-glucose pyrophosphorylase 2
Ugp2	AV370025	Mm.130747	1	6808	1737	10947	1320	0.01262	1.61	UDP-glucose pyrophosphorylase 2
Gck	L38990	Mm.220358	1	536	199	902	146	0.02485	1.68	glucokinase
Neu2	AK009828	Mm.45670	0.8	421	77	739	118	0.02562	1.75	neuraminidase 2
Mgat4b	BC026638	Mm.86759	1	1418	461	2554	237	0.00375	1.8	mannoside acetylglucosaminyltransferase 4, isoenzyme B
Gbe1	NM_028803	Mm.29201	1	672	132	1272	106	0.00091	1.89	glucan (1,4-alpha-), branching enzyme 1
Nudt14	BC025444	Mm.7070	0.8	193	105	427	66	0.00839	2.21	nudix (nucleoside diphosphate linked moiety X)-type motif 14

AMINO ACID METABOLISM

GeneSymbol	Genbank	Unigene	A/P	Ctl Mean	Ctl stdev	Exp Mean	Exp stdev	P-value	Fold Change	Gene Description
Odc	C81193	Mm.319739	1	12346	1116	2965	465	0	-4.16	ornithine decarboxylase
Amd1	BM114293	Mm.253533	1	19279	2775	5890	1609	0.00013	-3.27	S-adenosylmethionine decarboxylase 1
Odc	BB519474	Mm.311147	1	5068	592	1601	184	0	-3.16	ornithine decarboxylase
Odc	S64539	Mm.34102	1	2268	148	799	72	0	-2.84	ornithine decarboxylase
Amd1	NM_009665	Mm.253533	1	14888	1915	7630	919	0.00036	-1.95	S-adenosylmethionine decarboxylase 1
Oplah	BC025120	Mm.322738	1	1817	426	1001	148	0.01135	-1.82	Oplah: 5-oxoprolinase
Gstz1	AB041613	Mm.29652	1	2225	709	1262	369	0.04542	-1.76	glutathione transferase zeta 1
Sps2	NM_009266	Mm.20294	1	2249	579	1296	277	0.02043	-1.73	selenophosphate synthetase 2
Mtap	AB056100	Mm.28500	1	477	79	276	67	0.01241	-1.73	methylthioadenosine phosphorylase
Oat	BC008119	Mm.13694	1	10732	2642	6899	1042	0.0277	-1.56	ornithine aminotransferase
Bckdhb	AW047304	Mm.12819	1	1592	219	1021	242	0.02888	-1.56	branched chain ketoacid dehydrogenase E1, beta polypeptide
Dbt	NM_010022	Mm.3636	1	905	143	594	79	0.00755	-1.52	dihydrolipoamide branched chain transacylase E2
Aacs	AI987654	Mm.296918	1	242	87	623	177	0.04052	2.57	acetoacetyl-CoA synthetase
Aacs	BC026817	Mm.296918	1	348	70	920	193	0.03878	2.64	acetoacetyl-CoA synthetase

LIPID METABOLISM

GeneSymbol	Genbank	Unigene	A/P	Ctl Mean	Ctl stdev	Exp Mean	Exp stdev	P-value	Fold Change	Gene Description
Cpt1a	CA564810	Mm.18522	1	105	37	49	21	0.03481	-2.15	carnitine palmitoyltransferase 1a, liver
Sc5d	AB016248	Mm.32700	1	1438	397	686	137	0.01191	-2.1	sterol-C5-desaturase (fungal ERG3, delta-5-desaturase) homolog
Pank1	NM_023792	Mm.24742	1	2325	498	1148	448	0.01835	-2.02	pantothenate kinase 1
Pank1	AK017345	Mm.24742	1	1268	227	634	33	0.00358	-2	pantothenate kinase 1
Acadsb	BF228057	Mm.270388	1	2059	142	1168	222	0.00841	-1.76	acyl-Coenzyme A dehydrogenase, short/branched chain
Oxct	NM_024188	Mm.13445	1	7590	2155	4416	207	0.03087	-1.72	3-oxoacid CoA transferase
Adhfe1	BC026584	Mm.28514	1	1697	286	996	252	0.01524	-1.7	alcohol dehydrogenase, iron containing, 1
Facl2	NM_007981	Mm.210323	1	8434	1745	5076	1259	0.01987	-1.66	fatty acid Coenzyme A ligase
Acads	NM_007383	Mm.18759	1	3318	687	2041	198	0.01148	-1.63	acyl-Coenzyme A dehydrogenase, short chain
Ggps1	C79210	Mm.148039	1	384	59	240	47	0.01311	-1.6	geranylgeranyl diphosphate synthase 1
Nudt7	AK011172	Mm.27889	1	2114	425	1391	294	0.02983	-1.52	nudix (nucleoside diphosphate linked moiety X)-type motif 7
Ppap2a	NM_008903	Mm.317186	1	2234	591	3558	683	0.0495	1.59	phosphatidic acid phosphatase 2a
Facl6	BC022959	Mm.267478	1	1608	378	2788	60	0.00241	1.73	fatty acid Coenzyme A ligase, long chain 6

MISCELLANIOUS METABOLISM

GeneSymbol	Genbank	Unigene	A/P	Ctl Mean	Ctl stdev	Exp Mean	Exp stdev	P-value	Fold Change	Gene Description
Dcxr	BC012247	Mm.231091	1	1609	761	573	237	0.03696	-2.81	dicarbonyl L-xylulose reductase
Hsd17b7	NM_010476	Mm.12882	0.6	338	58	144	79	0.03527	-2.35	hydroxysteroid (17-beta) dehydrogenase 7
Dgat2	NM_026384	Mm.180189	1	3347	1228	1637	188	0.03793	-2.04	diacylglycerol O-acyltransferase 2
Gch	BB698398	Mm.10651	1	367	141	184	63	0.04664	-1.99	GTP cyclohydrolase 1
Entpd5	NM_007647	Mm.10211	1	1106	328	611	189	0.03522	-1.81	ectonucleoside triphosphate diphosphohydrolase 5
Dhrs4	NM_030686	Mm.27427	1	1884	556	1116	220	0.03361	-1.69	dehydrogenase/reductase (SDR family) member 4
Cyp51	BB004104	Mm.140158	0.9	114	35	69	9	0.04557	-1.63	cytochrome P450, 51
Hyal1	NM_008317	Mm.10305	0.7	291	38	183	49	0.04886	-1.59	hyaluronidase 1
Cat	NM_009804	Mm.4215	1	8762	2204	5537	1366	0.04329	-1.58	catalase, response to oxidative stress
Pnp	AK008143	Mm.17932	1	953	252	616	51	0.03434	-1.55	purine-nucleoside phosphorylase
Alad	BC018236	Mm.6988	1	1262	238	834	170	0.02561	-1.51	aminolevulinate, delta-, dehydratase
Dutp	AF091101	Mm.282499	1	194	38	293	16	0.00235	1.51	deoxyuridine triphosphatase
Drpla	NM_007881	Mm.3172	1	338	97	544	84	0.02558	1.61	dentatorubral pallidoluysian atrophy
Adprtl3	BC014870	Mm.273659	1	795	135	1402	78	0.0002	1.76	ADP-ribosyltransferase (NAD+; poly (ADP-ribose polymerase)-like 3
Adprtl3	BC014870	Mm.273659	1	2589	1115	4803	262	0.00813	1.86	ADP-ribosyltransferase (NAD+; poly (ADP-ribose polymerase)-like 3
Car14	NM_011797	Mm.224836	1	1674	80	3150	185	0.00582	1.88	carbonic anhydrase 14

MUSCLE

GeneSymbol	Genbank	Unigene	A/P	Ctl Mean	Ctl stdev	Exp Mean	Exp stdev	P-value	Fold Change	Gene Description
Rsn	NM_019765	Mm.241109	1	5662	1084	3286	270	0.00551	-1.72	restin (Reed-Steinberg cell-expressed intermediate filament-associated protein)
Utrn	AI788797	Mm.331784	1	1068	140	1667	207	0.02151	1.56	utrophin
Myom2	BB474208	Mm.272115	1	14769	1252	23360	3120	0.04499	1.58	myomesin 2
Atp2a2	NM_009722	Mm.227583	1	8051	2025	13383	1666	0.00996	1.66	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2
Myl2	NM_010861	Mm.1529	1	13584	2825	23750	3344	0.01164	1.75	myosin, light polypeptide 2, regulatory, cardiac, slow
Myoz2	NM_021503	Mm.141157	1	5765	663	10290	1372	0.01278	1.78	myozenin 2
Tpm3	NM_022314	Mm.240839	1	3159	1071	5616	1257	0.04759	1.78	tropomyosin 3
Mybph	NM_016749	Mm.269621	1	2337	1078	4262	872	0.03982	1.82	myosin binding protein H
Tpm3	NM_022314	Mm.240839	1	2694	845	5120	815	0.01588	1.9	tropomyosin 3
Myh11	BC026142	Mm.250705	1	661	52	1312	224	0.03849	1.98	myosin, heavy polypeptide 11, smooth muscle
Myh6	NM_080728	Mm.290003	1	3087	1273	6140	1076	0.01521	1.99	myosin, heavy polypeptide 6, cardiac muscle, alpha
Myl3	AK002312	Mm.7353	1	9571	1431	19173	2567	0.00951	2	myosin, light polypeptide 3, alkali; ventricular, skeletal, slow
Tncc	NM_009393	Mm.712	1	4435	1382	9019	1716	0.01719	2.03	troponin C, cardiac/slow skeletal
Tnnt1	NM_011618	Mm.711	1	3091	1119	6599	1397	0.02092	2.13	troponin T1, skeletal, slow
Myl3	X67685	Mm.7353	1	3128	607	6722	1180	0.01628	2.15	myosin, light polypeptide 3, alkali; ventricular, skeletal, slow
Myl3	X67685	Mm.7353	1	10033	1227	21665	3030	0.02397	2.16	myosin, light polypeptide 3, alkali; ventricular, skeletal, slow
Actc1	NM_009608	Mm.686	1	4975	1667	12207	2226	0.01658	2.45	actin, alpha, cardiac
Myh6	NM_080728	Mm.290003	1	1299	458	3392	723	0.02053	2.61	myosin, heavy polypeptide 6, cardiac muscle, alpha

WNT PATHWAY

GeneSymbol	Genbank	Unigene	A/P	Ctl Mean	Ctl stdev	Exp Mean	Exp stdev	P-value	Fold Change	Gene Description
Dkk3	NM_015814	Mm.55143	0.8	1001	199	208	20	0.00092	-4.82	dickkopf homolog 3
Dkk3	AK004853	Mm.55143	1	1062	298	297	25	0.00467	-3.57	dickkopf homolog 3 (Xenopus laevis)
Wnt4	NM_009523	Mm.20355	0.8	938	123	508	78	0.00095	-1.84	wingless-related MMTV integration site 4
Herpud1	AI835088	Mm.29151	1	8083	1631	5327	440	0.01609	-1.52	homocysteine-inducible, ER stress-inducible, ubiquitin-like domain member 1
Herpud1	NM_022331	Mm.29151	1	6599	1213	4359	620	0.01373	-1.51	homocysteine-inducible, ER stress-inducible, ubiquitin-like domain member 1
Catnbip1	NM_023465	Mm.263330	1	549	168	913	145	0.02316	1.66	catenin beta interacting protein 1
Cdh5	AW543698	Mm.21767	1	1376	368	3163	703	0.02663	2.3	cadherin 5
Dkk2	NM_020265	Mm.103593	1	348	104	803	33	0.00029	2.31	dickkopf homolog 2 (Xenopus laevis)

TRANSCRIPTION FACTORS/REGULATION OF TRANSCRIPTION

GeneSymbol	Genbank	Unigene	A/P	Ctl Mean	Ctl stdev	Exp Mean	Exp stdev	P-value	Fold Change	Gene Description
Musk	U37709	Mm.16148	0.8	872	279	375	107	0.01183	-2.33	muscle, skeletal, receptor tyrosine kinase
Creg	NM_011804	Mm.459	1	5136	1840	2295	236	0.02714	-2.24	cellular repressor of E1A-stimulated genes
Creg	BC027426	Mm.294885	1	5011	1589	2500	443	0.02093	-2	cellular repressor of E1A-stimulated genes
Mdm4	BC003750	Mm.326936	1	211	58	120	28	0.02511	-1.75	mouse double minute 4
Hmgb2	C85885	Mm.279998	1	191	49	114	27	0.03087	-1.66	high mobility group box 2
Klf9	AV354744	Mm.19788	1	9905	1835	5981	1543	0.02298	-1.66	Kruppel-like factor 9
Myog	NM_031189	Mm.16528	0.8	485	68	303	48	0.0048	-1.6	myogenin
Sox17	AK004781	Mm.279103	1	832	244	1263	140	0.01954	1.52	SRY-box containing gene 17

Lass4	BB006809	Mm.35511	1	60	22	93	14	0.04608	1.54	longevity assurance homolog 4 (S. cerevisiae)
Mkrn1	AA717142	Mm.270484	1	625	102	968	91	0.00443	1.55	makorin, ring finger protein, 1
Notch4	NM_010929	Mm.173813	1	473	123	738	76	0.00942	1.56	Notch gene homolog 4 (Drosophila)
Zfp100	NM_009541	Mm.4340	1	482	82	756	31	0.00055	1.57	zinc finger protein 100
Nrarp	NM_025980	Mm.46539	1	671	251	1061	170	0.04022	1.58	Notch-regulated ankyrin repeat protein
Per1	AF022992	Mm.7373	1	1575	611	2551	446	0.04094	1.62	period homolog 1 (Drosophila)
Ets1	BB151715	Mm.292415	1	937	375	1540	48	0.02397	1.64	E26 avian leukemia oncogene 1, 5' domain
Fhl2	NM_010212	Mm.6799	0.7	297	65	496	43	0.0021	1.67	four and a half LIM domains 2
Dbp	BY061007	Mm.3459	0.7	238	127	402	50	0.04351	1.69	D site albumin promoter binding protein
Zfp292	BI686420	Mm.38193	1	370	111	641	81	0.00761	1.73	zinc finger protein 292, Zn-15, Zn-16
Ets1	BB151715	Mm.292415	1	486	114	842	89	0.00445	1.73	E26 avian leukemia oncogene 1, 5' domain
Hlx	NM_008250	Mm.1347	0.7	410	137	713	40	0.00577	1.74	H2.0-like homeo box gene
Foxo1	AJ252157	Mm.29891	1	1561	490	2899	325	0.00358	1.86	forkhead box O1
Klf5	BG069607	Mm.308750	1	428	148	797	60	0.00265	1.86	Kruppel-like factor 5 (intestinal)
Relb	NM_009046	Mm.1741	0.7	231	56	473	84	0.02138	2.05	avian reticuloendotheliosis viral (v-rel) oncogene related B
Smarca1	NM_053123	Mm.229151	1	138	48	368	51	0.00328	2.67	SWI/SNF rel, matrix assoc, actin dep reg of chromatin, subfamily a, mem 1

EXTRACELLULAR/MATRIX/CYTOPLASMIC

GeneSymbol	Genbank	Unigene	A/P	Ctl Mean	Ctl stdev	Exp Mean	Exp stdev	P-value	Fold Change	Gene Description
Fgfbp1	U49641	Mm.46053	1	709	213	152	22	0.00443	-4.66	fibroblast growth factor binding protein 1
Umod	BB747266	Mm.10826	0.6	255	155	56	17	0.04742	-4.49	uromodulin
Inhbe	BC010404	Mm.3510	1	409	157	207	35	0.03997	-1.98	inhibin beta E
Btc	NM_007568	Mm.2024	0.6	67	6	40	8	0.02067	-1.66	betacellulin, epidermal growth factor family member
Bmp1	L24755	Mm.27757	0.8	943	248	574	91	0.03031	-1.64	bone morphogenetic protein 1
Igf1	BC012409	Mm.268521	1	899	213	556	116	0.02584	-1.62	insulin-like growth factor 1
Bmp6	NM_007556	Mm.254978	1	1097	188	1782	271	0.03097	1.62	bone morphogenetic protein 6
Cxcl14	AF144754	Mm.30211	1	1923	399	3142	278	0.00228	1.63	chemokine (C-X-C motif) ligand 14
Kitl	NM_013598	Mm.45124	1	1561	480	2769	416	0.01339	1.77	kit ligand
Ptx3	NM_008987	Mm.276776	1	227	105	421	51	0.0131	1.85	pentaxin related gene
Spock2	BM117672	Mm.153429	1	771	139	1711	359	0.04935	2.22	sparc/osteonectin, cwcv and kazal-like domains proteoglycan 2

RECEPTORS

GeneSymbol	Genbank	Unigene	A/P	Ctl Mean	Ctl stdev	Exp Mean	Exp stdev	P-value	Fold Change	Gene Description
Oprs1	AF226605	Mm.22745	1	943	333	409	161	0.02287	-2.3	opioid receptor, sigma 1
Tnfrsf19	AF167554	Mm.281356	0.8	364	87	172	88	0.04086	-2.11	tumor necrosis factor receptor superfamily, member 19
Trfr	NM_011638	Mm.28683	0.8	454	119	230	106	0.03977	-1.98	transferrin receptor
Tnfrsf19	NM_013869	Mm.281356	1	791	239	415	155	0.03602	-1.9	tumor necrosis factor receptor superfamily, member 19
Ptprd	BC025145	Mm.184021	1	522	118	321	18	0.02047	-1.62	protein tyrosine phosphatase, receptor type, D
Trfr	BB810450	Mm.28683	0.7	163	14	101	21	0.02079	-1.61	transferrin receptor
Ghr	BC024375	Mm.3986	1	3469	729	2256	320	0.01781	-1.54	GH RECEPTOR
Chrna1	NM_007389	Mm.4583	1	708	84	1066	157	0.03625	1.5	cholinergic receptor, nicotinic, alpha polypeptide 1 (muscle)
Adrb2	AV083350	Mm.5598	1	924	185	1400	78	0.00236	1.52	adrenergic receptor, beta 2
Itpr1	NM_008789	Mm.2726	1	1524	166	2341	80	0.00009	1.54	inositol 1,4,5-triphosphate receptor 1
C1qr1	NM_010740	Mm.681	1	1655	395	2555	448	0.04556	1.54	complement component 1, q subcomponent, receptor 1
Robo4	BC020129	Mm.293315	1	811	218	1246	100	0.00863	1.54	roundabout homolog 4 (Drosophila)
Gucy1b3	BF472806	Mm.9445	1	375	96	589	110	0.04999	1.57	guanylate cyclase 1, soluble, beta 3, nitric oxide mediated signal transduction
Acvr1	NM_007394	Mm.689	1	643	294	1031	131	0.04335	1.6	activin A receptor, type 1
Trpm7	AF376052	Mm.244705	1	755	266	1212	115	0.0154	1.61	transient receptor potential cation channel, subfamily M, member 7
Trip10	NM_134125	Mm.37368	1	3924	1006	6387	1276	0.04634	1.63	thyroid hormone receptor interactor 10
Tie1	NM_011587	Mm.4345	1	540	137	886	90	0.00517	1.64	tyrosine kinase receptor 1
Ptger4	NM_008965	Mm.18509	1	52	14	88	8	0.0043	1.67	prostaglandin E receptor 4 (subtype EP4)
Flt1	NM_010228	Mm.3464	1	1321	334	2330	287	0.00635	1.76	FMS-like tyrosine kinase 1
Obrgrp	AV156961	Mm.4756	1	266	81	483	7	0.0041	1.82	leptin receptor gene-related protein
Ntsr2	NM_008747	Mm.281715	1	328	90	611	52	0.00138	1.86	neurotensin receptor 2
Tnfrsf21	BG972377	Mm.200792	1	940	163	1789	235	0.01185	1.9	tumor necrosis factor receptor superfamily, member 21
Chrne	NM_009603	Mm.4980	1	362	172	785	98	0.00454	2.17	cholinergic receptor, nicotinic, epsilon polypeptide

SIGNAL TRANSDUCTION

GeneSymbol	Genbank	Unigene	A/P	Ctl Mean	Ctl stdev	Exp Mean	Exp stdev	P-value	Fold Change	Gene Description
Gadd45g	AK007410	Mm.281298	1	5994	742	2427	1029	0.01352	-2.47	growth arrest and DNA-damage-inducible, gamma
Irak1	BY141014	Mm.38241	1	350	88	167	79	0.02971	-2.09	interleukin-1 receptor-associated kinase 1
Ccl9	AF128196	Mm.2271	1	948	200	513	117	0.00827	-1.85	chemokine (C-C motif) ligand 9
Jun	BC002081	Mm.275071	1	8412	1594	4708	1507	0.02166	-1.79	Jun oncogene

Ptk9l	AK002699	Mm.274346	1	5320	1138	3322	595	0.01745	-1.6	Ptk9l: protein tyrosine kinase 9-like (A6-related protein)
Mapk1	NM_011949	Mm.196581	1	745	146	472	139	0.04675	-1.58	mitogen activated protein kinase 1
Map3k7	BF019409	Mm.258589	1	159	23	103	25	0.03534	-1.55	mitogen-activated protein kinase kinase kinase 7
Pxn	BC025493	Mm.18714	1	1000	179	1509	193	0.02097	1.51	paxillin
Stk2	BI111765	Mm.281011	1	748	111	1130	94	0.00359	1.51	serine/threonine kinase 2
Stmn2	BM946869	Mm.29580	0.8	387	174	604	52	0.04873	1.56	stathmin-like 2
Lcp2	BC006948	Mm.265350	0.8	100	34	158	12	0.02026	1.57	lymphocyte cytosolic protein 2
Slc9a3r2	BY079474	Mm.21587	1	1866	293	2987	72	0.00045	1.6	solute carrier family 9 (sodium/hydrogen exchanger), isoform 3 regulator 2
Prkcq	AB062122	Mm.329993	1	1911	304	3099	570	0.04461	1.62	protein kinase C, theta
Traf2	BC003801	Mm.3399	1	397	106	644	66	0.00664	1.62	Tnf receptor-associated factor 2
Grb2	NM_008163	Mm.6900	0.6	819	266	1333	155	0.01365	1.63	growth factor receptor bound protein 2
Prkch	NM_008856	Mm.8040	1	591	174	967	108	0.00957	1.63	protein kinase C, eta
Lyn	M57697	Mm.1834	0.7	583	184	997	107	0.00692	1.71	Yamaguchi sarcoma viral (v-yes-1) oncogene homolog
Dusp6	NM_026268	Mm.1791	1	486	101	857	129	0.01318	1.76	dual specificity phosphatase 6
Camk2b	NM_007595	Mm.4857	1	783	129	1396	234	0.02524	1.78	calcium/calmodulin-dependent protein kinase II, beta
Dusp7	BC025048	Mm.275584	1	590	181	1058	137	0.00925	1.79	dual specificity phosphatase 7
Evl	AW553781	Mm.238841	1	171	98	321	42	0.02478	1.88	Ena-vasodilator stimulated phosphoprotein

POST TRANSLATIONAL MODIFICATION

GeneSymbol	Genbank	Unigene	A/P	Ctl Mean	Ctl stdev	Exp Mean	Exp stdev	P-value	Fold Change	Gene Description
Rps6ka3	BY079468	Mm.24436	1	445	96	243	81	0.02471	-1.83	ribosomal protein S6 kinase polypeptide 3
Adk	NM_007411	Mm.30346	0.6	292	89	160	19	0.02484	-1.82	adenosine kinase
Styx	AK006627	Mm.202561	1	624	142	375	24	0.0188	-1.67	phosphoserine/threonine/tyrosine interaction protein
Prkx	BB367549	Mm.290338	1	295	82	179	36	0.0346	-1.64	putative serine/threonine kinase
Mylk	BF451748	Mm.247544	1	1844	234	2800	208	0.00186	1.52	myosin, light polypeptide kinase
Padi2	NM_008812	Mm.2296	1	2984	680	4559	328	0.0046	1.53	peptidyl arginine deiminase, type II
Ptpla	BB014781	Mm.241205	1	3626	720	5636	462	0.00299	1.55	protein tyrosine phosphatase-like, member a
Snrk	NM_133741	Mm.257989	1	2395	303	3729	410	0.01643	1.56	SNF related kinase
Hipk1	AF071070	Mm.20827	1	2680	413	4327	358	0.00195	1.61	homeodomain interacting protein kinase 1
Apeg1	AF215896	Mm.275397	1	7068	709	11628	1319	0.01168	1.64	aortic preferentially expressed gene 1
Mapkapk5	NM_010765	Mm.272206	1	1328	252	2611	352	0.01175	1.97	MAP kinase-activated protein kinase 5
Prkcl1	AI463328	Mm.213000	0.8	203	57	407	35	0.00083	2	protein kinase C-like 1
Map2k6	BB261602	Mm.14487	1	839	178	1717	183	0.0027	2.05	mitogen activated protein kinase kinase 6
Dm15	AW108486	Mm.301960	1	2844	1024	6285	561	0.00086	2.21	dystrophia myotonica-protein kinase
Apeg1	AF215896	Mm.275397	1	501	94	1161	6	0.0001	2.32	aortic preferentially expressed gene 1

SMALL GTPase MEDIATED SIGNAL TRANSDUCTION

GeneSymbol	Genbank	Unigene	A/P	Ctl Mean	Ctl stdev	Exp Mean	Exp stdev	P-value	Fold Change	Gene Description
Rab32	NM_026405	Mm.31486	0.8	263	104	110	16	0.03332	-2.38	RAB32, member RAS oncogene family
Rab2	C80220	Mm.331473	0.9	129	54	61	15	0.04516	-2.12	RAB2, member RAS oncogene family
Arhgap5	BY014451	Mm.35059	1	361	75	225	70	0.04845	-1.61	Rho GTPase activating protein 5
Arf6	BC003478	Mm.27308	1	1168	226	1784	253	0.02588	1.53	ADP-ribosylation factor 6
Rab40b	AV364488	Mm.281639	1	360	145	573	83	0.03899	1.59	Rab40b, member RAS oncogene family
Hras1	NM_008284	Mm.334313	1	2716	161	4538	601	0.03587	1.67	Harvey rat sarcoma virus oncogene 1
Rras	NM_009101	Mm.257	1	2247	185	3795	362	0.00629	1.69	Harvey rat sarcoma oncogene, subgroup R
Map4k3	BF165548	Mm.251706	1	1111	124	1921	182	0.00651	1.73	mitogen-activated protein kinase kinase kinase kinase 3
Abr	AV325116	Mm.258939	0.8	137	31	237	15	0.001	1.73	active BCR-related gene
Rab5c	BC023027	Mm.29829	1	1212	527	2118	251	0.01706	1.75	RAB5C, member RAS oncogene family
Rpgrip1	NM_023879	Mm.21662	1	736	397	1370	76	0.0259	1.86	retinitis pigmentosa GTPase regulator interacting protein 1

MITOCHONDRIAL

GeneSymbol	Genbank	Unigene	A/P	Ctl Mean	Ctl stdev	Exp Mean	Exp stdev	P-value	Fold Change	Gene Description
Slc25a10	BC003222	Mm.3991	0.6	505	354	55	43	0.04861	-9.06	solute carrier family 25, member 10
Cyp27a1	NM_024264	Mm.85083	1	6925	1800	2650	559	0.00437	-2.61	cytochrome P450, family 27, subfamily a, polypeptide 1
Mte1	NM_134188	Mm.45431	1	2831	1037	1253	364	0.02689	-2.26	mitochondrial acyl-CoA thioesterase 1
Mte1	NM_134188	Mm.45431	1	1051	223	532	187	0.017	-1.97	mitochondrial acyl-CoA thioesterase 1
Gstk1	AK002661	Mm.267014	1	3302	623	1785	411	0.00608	-1.85	glutathione S-transferase kappa 1
Tfb1m	AI429207	Mm.226554	1	409	53	231	35	0.00126	-1.77	transcription factor B1, mitochondrial
Slc40a1	BC003438	Mm.28756	1	3257	552	1864	175	0.00342	-1.75	solute carrier family 40 (iron-regulated transporter), member 1
Slc25a20	AV008091	Mm.29666	1	4007	663	2485	287	0.00423	-1.61	solute carrier family 25, member 20
Kif1b	AF090190	Mm.252497	1	2647	380	4273	674	0.03146	1.61	kinesin family member 1B
Bcl2l	BM228788	Mm.238213	1	959	348	1730	272	0.01766	1.8	Bcl2-like

MEMBRANE

GeneSymbol	Genbank	Unigene	A/P	Ctl Mean	Ctl stdev	Exp Mean	Exp stdev	P-value	Fold Change	Gene Description
Gjb1	BC026833	Mm.21198	0.6	1393	908	206	90	0.04425	-6.76	gap junction membrane channel protein beta 1
Slc6a6	AA589629	Mm.247352	0.6	231	125	43	48	0.02419	-5.31	solute carrier family 6 (neurotransmitter transporter, taurine), member 6
Kcnab1	AK015412	Mm.1438	0.6	660	299	227	63	0.02642	-2.9	potassium channel regulator activity
Ocil	NM_053109	Mm.197536	0.8	1372	522	535	129	0.019	-2.56	osteoclast inhibitory lectin
Ceacam1	NM_011926	Mm.292910	1	1285	469	526	151	0.02069	-2.44	CEA-related cell adhesion molecule 1
Slc12a2	BG069726	Mm.4168	1	1018	348	437	71	0.01562	-2.32	solute carrier family 12, member 2
Ceacam1	NM_011926	Mm.292910	1	1492	553	649	284	0.02974	-2.3	CEA-related cell adhesion molecule 1
Mr1	BB210729	Mm.7580	1	1111	371	518	39	0.02424	-2.14	major histocompatibility complex, class I-related
Slc16a2	NM_009197	Mm.5045	1	408	162	193	30	0.04526	-2.11	solute carrier family 16 (monocarboxylic acid transporters), member 2
Insig2	AV257512	Mm.27136	1	3706	1507	1797	389	0.04349	-2.06	insulin induced gene 2
Mr1	U94989	Mm.7580	0.8	769	207	409	33	0.0192	-1.88	major histocompatibility complex, class I-related
Ceacam1	BC016891	Mm.14114	0.5	380	135	208	33	0.0425	-1.83	CEA-related cell adhesion molecule 1
Ceacam1	X67278	Mm.292910	0.6	320	59	174	72	0.04317	-1.83	CEA-related cell adhesion molecule 1
Tgoln1	NM_009443	Mm.246563	1	647	158	372	65	0.0141	-1.74	trans-golgi network protein
Clcn4-2	NM_011334	Mm.297883	1	1311	266	758	230	0.02691	-1.73	chloride channel 4-2
Slc22a5	AF111425	Mm.42253	0.7	558	170	334	69	0.04099	-1.67	solute carrier family 22 (organic cation transporter), member 5
Copb2	AV109541	Mm.18729	1	421	103	254	43	0.01902	-1.66	coatomer protein complex, subunit beta 2 (beta prime)
Gdap1	BB278235	Mm.18218	0.8	235	39	147	30	0.01648	-1.6	ganglioside-induced differentiation-associated-protein 1
Slc19a2	AF326916	Mm.35444	1	569	94	360	90	0.03568	-1.58	solute carrier family 19 (thiamine transproter), member 2
H47	CA565598	Mm.22362	1	642	94	418	91	0.02965	-1.54	histocompatibility 47
Kcnn2	NM_080465	Mm.246319	0.8	255	56	169	31	0.03216	-1.51	K intermediate/small conductance ca-activated channel, subfamily N, mem 2
Ggcx	AV370848	Mm.19937	0.7	309	52	204	16	0.00895	-1.51	gamma-glutamyl carboxylase
Atp1b2	BG261955	Mm.132333	1	4560	831	6871	886	0.02173	1.51	ATPase, Na+/K+ transporting, beta 2 polypeptide
Slc7a10	NM_017394	Mm.35567	1	533	165	813	109	0.02811	1.52	solute carrier family 7 (cationic amino acid transporter, y+ system), member 10
Tm4sf2	NM_019634	Mm.18590	1	3699	730	5655	406	0.00281	1.53	transmembrane 4 superfamily member 2
Mg29	NM_008596	Mm.20942	1	2509	259	3876	479	0.01978	1.54	mitsugumin 29
Daf1	BM208097	Mm.337491	1	1156	143	1780	244	0.02749	1.54	decay accelerating factor 1
Cnp1	NM_009923	Mm.15711	1	573	62	886	117	0.02399	1.54	cyclic nucleotide phosphodiesterase 1
Tpst2	NM_009419	Mm.250631	1	644	45	995	132	0.04724	1.55	tyrosylprotein sulfotransferase 2
Gpsn2	AK020708	Mm.209651	1	20476	1903	31847	1975	0.00133	1.56	glycoprotein, synaptic 2
Esam1	AF361882	Mm.41751	1	2234	242	3486	94	0.00005	1.56	endothelial cell-specific adhesion molecule
Vat1	BC025496	Mm.29210	1	323	15	508	52	0.02762	1.57	vesicle amine transport protein 1 homolog (T californica)
Atp1b1	AV152334	Mm.4550.6	1	4133	1665	6497	771	0.03452	1.57	ATPase, Na+/K+ transporting, beta 1 polypeptide
Vamp3	BB491065	Mm.273930	1	373	53	589	4	0.00086	1.58	vesicle-associated membrane protein 3
Igsf4	BB832194	Mm.234832	1	511	99	811	49	0.0013	1.59	immunoglobulin superfamily, member 4
Kcna7	NM_010596	Mm.12955	1	2611	626	4175	776	0.04156	1.6	potassium voltage-gated channel, shaker-related subfamily, member 7
Atp1b4	NM_133690	Mm.60134	1	226	81	362	25	0.01852	1.6	ATPase, (Na+)/K+ transporting, beta 4 polypeptide
Golga4	NM_018748	Mm.10409	1	2105	614	3455	393	0.00911	1.64	golgi autoantigen, golgin subfamily a, 4
Gja4	AF216832	Mm.24615	0.5	359	71	592	43	0.00124	1.65	gap junction membrane channel protein alpha 4
Adam15	BB392633	Mm.274049	1	1474	525	2473	245	0.01082	1.68	a disintegrin and metalloproteinase domain 15 (metargidin)
Tmem2	BB667229	Mm.258163	1	369	19	625	39	0.00182	1.69	transmembrane protein 2
Mcl1	CA577851	Mm.1639	1	4059	1244	6928	894	0.0092	1.71	myeloid cell leukemia sequence 1
Cacng1	NM_007582	Mm.57093	1	5826	843	10072	1810	0.03157	1.73	calcium channel, voltage-dependent, gamma subunit 1
Mal	NM_010762	Mm.39040	1	283	91	500	38	0.00336	1.77	myelin and lymphocyte protein, T-cell differentiation protein
Trdn	AF223416	Mm.216837	1	603	232	1072	33	0.0114	1.78	triadin
Slc16a3	NM_030696	Mm.28632	1	6043	2204	10954	2043	0.02417	1.81	solute carrier family 16 (monocarboxylic acid transporters), member 3
Gpsn2	NM_134118	Mm.209651	1	8778	399	16045	1287	0.01089	1.83	glycoprotein, synaptic 2
Mcl1	CA577851	Mm.1639	1	4613	2122	8425	1044	0.01467	1.83	myeloid cell leukemia sequence 1
Tm7sf1	AW546472	Mm.11780	1	55	21	101	14	0.01052	1.83	transmembrane 7 superfamily member 1
Aqp4	BB193413	Mm.298599	1	290	107	906	188	0.01397	3.12	Mus musculus similar to putative pheromone receptor (LOC224572), mRNA
Mpz	BY229830	Mm.9986	1	808	424	2827	565	0.01276	3.5	myelin protein zero

NUCLEIC ACID ASSOCIATED PROTEINS

GeneSymbol	Genbank	Unigene	A/P	Ctl Mean	Ctl stdev	Exp Mean	Exp stdev	P-value	Fold Change	Gene Description
Dnase1	BC014718	Mm.239992	0.6	477	287	85	64	0.03288	-5.6	deoxyribonuclease I
Cova1	BC025915	Mm.24550	1	552	147	162	76	0.00267	-3.39	cytosolic ovarian carcinoma antigen 1
Cova1	BC026450	Mm.24550	1	1070	285	434	18	0.00768	-2.46	cytosolic ovarian carcinoma antigen 1
Nol5	BB729616	Mm.220367	1	376	113	197	56	0.02516	-1.9	nucleolar protein 5
Ssa2	BG069917	Mm.40370	0.8	275	61	155	19	0.01015	-1.77	Sjogren syndrome antigen A2
Gadd45a	NM_007836	Mm.1236	1	879	174	505	122	0.01211	-1.74	growth arrest and DNA-damage-inducible 45 alpha
Rbbp4	BF011461	Mm.12145	1	1289	207	832	232	0.04892	-1.55	retinoblastoma binding protein 4
U2af1	NM_024187	Mm.259570	1	1937	409	1250	185	0.01776	-1.55	U2(RNU2) small nuclear RNA auxiliary factor 1

Dhx16	BB379386	Mm.5624	1	1754	307	2656	212	0.00273	1.51	DEAH (Asp-Glu-Ala-His) box polypeptide 16
Rad23b	BF138887	Mm.196846	1	3248	845	5109	586	0.0105	1.57	RAD23b homolog (S. cerevisiae)
Lrrfip1	NM_008515	Mm.45039	1	1403	204	2210	390	0.0452	1.57	leucine rich repeat (in FLII) interacting protein 1
Eif4el3	BM120823	Mm.227183	1	393	100	615	55	0.00701	1.57	eukaryotic translation initiation factor 4E like 3
Hist1h4h	BC028550	Mm.158272	1	761	369	1238	64	0.04799	1.63	histone 1, H4h
Cpeb3	BB249892	Mm.206779	1	767	222	1255	184	0.02045	1.63	cytoplasmic polyadenylation element binding protein
Polr2a	U37500	Mm.16533	1	1359	295	2663	510	0.02741	1.96	polymerase (RNA) II (DNA directed) polypeptide A

PROTEIN CATABOLISM

GeneSymbol	Genbank	Unigene	A/P	Ctl Mean	Ctl stdev	Exp Mean	Exp stdev	P-value	Fold Change	Gene Description
Serpina3k	BF234005	Mm.196242	0.6	392	226	100	49	0.0389	-3.91	serine (or cysteine) proteinase inhibitor, clade A, member 3K
Birc4	NM_009688	Mm.259879	1	135	29	46	10	0.00171	-2.9	baculoviral IAP repeat-containing 4
Serpinf1	AK012411	Mm.2044.2	1	3812	1167	1607	349	0.01096	-2.37	serine or cysteine proteinase inhibitor, clade F, member 1
Bace	CA563079	Mm.24044	1	459	91	246	76	0.01644	-1.86	beta-site APP cleaving enzyme
Mib1	BC011287	Mm.21500	1	651	148	359	16	0.01222	-1.81	mindbomb homolog 1 (Drosophila)
Ctse	NM_007799	Mm.230249	1	741	224	434	12	0.03809	-1.7	cathepsin E
Psmd8	AK003436	Mm.273152	1	11518	1033	7089	1243	0.00657	-1.62	proteasome (prosome, macropain) 26S subunit, non-ATPase, 8
Fbxo21	BC021871	Mm.21912	1	989	74	611	156	0.02947	-1.62	F-box only protein 21
Pace4	BI157485	Mm.294007	1	1228	205	773	190	0.02488	-1.59	paired basic amino acid cleaving system 4
Ube4a	BC006649	Mm.215069	1	774	86	491	51	0.00117	-1.58	ubiquitination factor E4A, UFD2 homolog (S. cerevisiae)
Skp1a	BI079132	Mm.42944	1	9063	506	5998	432	0.00027	-1.51	S-phase kinase-associated protein 1A
Siah1a	AV008871	Mm.6765	1	727	148	1100	183	0.04031	1.51	seven in absentia 1A
Timp4	BI788452	Mm.255607	1	2372	247	3668	231	0.00067	1.55	tissue inhibitor of metalloproteinase 4
Lcn7	BC005738	Mm.15801	1	2030	347	3232	369	0.01038	1.59	lipocalin 7
Serpine1	NM_008871	Mm.250422	1	586	137	976	106	0.00652	1.66	serine (or cysteine) proteinase inhibitor, clade E, member 1
Herc2	AW701798	Mm.20929	1	772	214	1359	199	0.01117	1.76	hect domain and RCC1 (CHC1)-like domain (RLD) 2

MISCELLANIOUS

GeneSymbol	Genbank	Unigene	A/P	Ctl Mean	Ctl stdev	Exp Mean	Exp stdev	P-value	Fold Change	Gene Description
Cp	BY013791	Mm.13787	1	1368	758	307	140	0.03823	-4.45	ceruloplasmin
Brap	NM_028227	Mm.153372	0.8	356	119	107	90	0.02067	-3.33	BRCA1 associated protein
Sh3d19	NM_012059	Mm.2454	1	174	75	54	42	0.02855	-3.21	SH3 domain protein D19
Lor	AI036317	Mm.1121	0.7	540	177	178	139	0.02406	-3.03	loricrin
Idi1	BC004801	Mm.29847	1	143	60	57	7	0.03434	-2.5	isopentenyl-diphosphate delta isomerase
Gnpnat1	AK008566	Mm.233534	1	688	314	282	38	0.04612	-2.44	glucosamine-phosphate N-acetyltransferase 1
Gclc	BC019374	Mm.89888	1	1297	571	533	77	0.0423	-2.43	glutamate-cysteine ligase, catalytic subunit
Cfh	AI987976	Mm.8655	1	270	88	131	30	0.0234	-2.06	complement component factor h
Asb4	AV113827	Mm.306134	1	718	172	352	40	0.00613	-2.04	ankyrin repeat and SOCS box-containing protein
Tekt1	AK005801	Mm.42257	0.8	245	65	121	49	0.02969	-2.02	tektin 1
Qscn6	NM_023268	Mm.27035	1	1453	477	735	323	0.04453	-1.98	quiescin Q6
Sh3d1B	AI326108	Mm.139128	0.8	185	47	94	42	0.03861	-1.95	SH3 domain protein 1B
Asb4	AV302111	Mm.306134	1	1145	288	625	70	0.01202	-1.83	ankyrin repeat and SOCS box-containing protein
Hspca	C77384	Mm.1843	1	1680	310	928	278	0.01657	-1.81	heat shock protein 1, alpha
Sh3d19	NM_012059	Mm.2454	1	844	237	477	130	0.03044	-1.77	SH3 domain protein D19
Gclc	AW825835	Mm.305531	1	1321	411	784	120	0.04136	-1.68	glutamate-cysteine ligase, catalytic subunit
Gltscr2	BC017637	Mm.277634	1	1350	343	838	182	0.03343	-1.61	glioma tumor suppressor candidate region gene 2
Hspa5	AJ002387	Mm.330160	1	3226	884	2035	122	0.04134	-1.59	heat shock 70kDa protein 5
Tes3	AV048122	Mm.30127	1	550	57	358	42	0.00163	-1.54	testis derived transcript 3
Sepr	NM_013759	Mm.28212	1	7339	1446	4812	175	0.01816	-1.53	selenoprotein R
Cdadc1	BB222482	Mm.2046	1	853	87	559	67	0.00311	-1.53	cytidine and dCMP deaminase domain containing 1
Epc1	NM_007935	Mm.20828	1	1756	352	2642	140	0.00244	1.5	enhancer of polycomb homolog 1 (Drosophila)
Hn1	BI453712	Mm.1775	1	1286	79	1949	102	0.00238	1.52	hematological and neurological expressed sequence 1
Sec14l1	BI652727	Mm.272312	1	2674	473	4054	202	0.00126	1.52	SEC14-like 1 (S. cerevisiae)
Fkbp5	BC015260	Mm.276405	1	4752	589	7276	630	0.00494	1.53	FK506 binding protein 5
Mln51	NM_138660	Mm.40120	1	1081	353	1661	233	0.03152	1.54	MLN51 protein
Epb4.1	BC017137	Mm.30038	1	1242	96	1916	32	0.00003	1.54	erythrocyte protein band 4.1
Sav1	NM_022028	Mm.27514	1	1591	428	2474	338	0.0233	1.55	salvador homolog 1 (Drosophila)
Rapsn	NM_009023	Mm.1272	1	659	81	1025	132	0.02304	1.55	receptor-associated protein of the synapse
Tubgcp3	BC025647	Mm.246402	1	243	74	382	70	0.04603	1.57	tubulin, gamma complex associated protein 3
Cryab	AV016515	Mm.178	1	12417	1905	19650	2515	0.0232	1.58	crystallin, alpha B
Nical	NM_138315	Mm.290431	0.7	154	62	246	6	0.03257	1.59	NEDD9 interacting protein with calponin homology and LIM domains
Ndr4	AI837704	Mm.29846	0.7	200	90	321	41	0.04169	1.6	N-myc downstream regulated 4
Wdr6	NM_031392	Mm.335454	1	375	109	604	85	0.02119	1.61	WD repeat domain 6
Macf1	BM248206	Mm.3350	0.5	907	206	1473	199	0.01849	1.62	microtubule-actin crosslinking factor 1

Catns	NM_007615	Mm.35738	1	818	259	1380	105	0.00516	1.69	catenin (cadherin associated protein), delta 1
Mt1	NM_013602	Mm.192991	1	8942	2821	15322	469	0.0078	1.71	metallothionein 1, nitric oxide mediated signal transduction
Timp3	BI111620	Mm.4871	1	5152	1027	9030	243	0.00047	1.75	tissue inhibitor of metalloproteinase 3
Ccrn4l	AF199491	Mm.86541	1	1294	391	2297	160	0.00231	1.77	CCR4 carbon catabolite repression 4-like (S. cerevisiae)
S100a8	NM_013650	Mm.21567	0.8	99	54	210	34	0.01241	2.12	S100 calcium binding protein A8 (calgranulin A)
Hba-a1	NM_008218	Mm.196110	1	1535	262	3693	641	0.03093	2.41	hemoglobin alpha, adult chain 1

UNKNOWN

GeneSymbol	Genbank	Unigene	A/P	Ctl Mean	Ctl stdev	Exp Mean	Exp stdev	P-value	Fold Change	Gene Description
1810057C19	NM_026433	Mm.212428	1	1509	384	351	205	0.00146	-4.29	RIKEN cDNA 1810057C19 gene
1200015N20	CA772992	Mm.19825	0.8	39	22	9	6	0.03658	-4.21	RIKEN cDNA 1200015N20 gene
2310043K02	BC018204	Mm.23916	1	1282	573	407	72	0.02807	-3.15	RIKEN cDNA 2310043K02 gene
5730454B08	BI107105	Mm.245357	1	703	229	239	206	0.03197	-2.94	RIKEN cDNA G630041M05 gene
1110012D08	AV375008	Mm.24630	0.6	85	27	30	25	0.03566	-2.77	RIKEN cDNA 1110012D08 gene
NULL	NULL	NULL	1	913	250	331	284	0.04291	-2.76	null
4930572L20I	BC025069	Mm.109183	0.7	591	279	220	14	0.04123	-2.68	RIKEN cDNA 4930572L20 gene
1700037B15	AF335325	Mm.250841	1	7758	1751	2924	263	0.00375	-2.65	RIKEN cDNA 1700037B15 gene
NULL	NULL	NULL	1	966	197	370	159	0.00546	-2.61	null
NULL	AK020672	NULL	0.8	470	76	189	30	0.00033	-2.48	null
2610507B11	BI437883	Mm.237103	1	836	333	341	214	0.04355	-2.45	null
9430063L05I	AI639670	Mm.129840	1	2056	650	861	593	0.0449	-2.39	null
1700037B15	AV251625	Mm.250841	1	6135	2138	2561	323	0.02143	-2.39	RIKEN cDNA 1700037B15 gene
B230354B21	BG076162	Mm.87487	0.8	163	25	69	43	0.04058	-2.37	RIKEN cDNA B230354B21 gene
0610007P08I	BI151889	Mm.186610	0.5	349	158	156	39	0.04904	-2.23	RIKEN cDNA 0610007P08 gene
A630053O10	BE631962	Mm.38878	0.5	349	134	158	45	0.03387	-2.2	hypothetical protein A630053O10
NULL	AK007618	Mm.27450.2	1	1355	371	625	238	0.01485	-2.17	null
AI850305	BB534069	Mm.203921	1	511	91	236	126	0.04603	-2.16	OTU domain, ubiquitin aldehyde binding 1
1700027M01	NM_023544	Mm.17880	1	2410	239	1183	79	0.00013	-2.04	RIKEN cDNA 1700027M01 gene
BC016495	BC016495	Mm.211595	1	198	77	98	36	0.04916	-2.01	cDNA sequence BC016495
2310001H12	BC012405	Mm.45217	1	529	120	270	128	0.04753	-1.96	RIKEN cDNA 2310001H12 gene
2010011I20F	AK008190	Mm.30013	0.8	896	261	460	137	0.0214	-1.95	RIKEN cDNA 2010011I20 gene
C80913	AV094811	Mm.23997	1	1093	307	570	67	0.01459	-1.92	expressed sequence C80913
A030012M09	BB549335	Mm.21539	1	840	222	437	167	0.03378	-1.92	RIKEN cDNA A030012M09 gene
NULL	BG297038	NULL	1	2663	899	1394	534	0.04634	-1.91	null
D11Ertd603e	BC005646	Mm.276504	1	242	49	127	48	0.03166	-1.9	DNA segment, Chr 11, ERATO Doi 603, expressed
4933411K20	BB825968	Mm.133623	0.6	200	56	105	38	0.03081	-1.9	RIKEN cDNA 4933411K20 gene
9330160A12	BB051441	Mm.38851	0.8	232	49	124	44	0.02412	-1.88	null
NULL	AW556821	Mm.254283	1	483	139	259	72	0.0249	-1.86	(M.musculus) I58401 protein-tyrosine kinase (EC 2.7.1.112) JAK3 - mouse
1700016A15	AV230748	Mm.5364	0.5	115	12	63	19	0.02449	-1.84	product:hypothetical G-protein beta WD-40 repeats containing protein
LOC213233	BC017613	Mm.296902	0.6	256	56	141	10	0.01123	-1.81	similar to hypothetical protein FLJ10143
NULL	AK004608	Mm.197551.	0.8	250	83	140	26	0.04149	-1.79	null
1300010A20	BI440178	Mm.225289	1	180	29	100	3	0.00387	-1.79	RIKEN cDNA 1300010A20 gene
8430423A01	AW048468	Mm.116767	0.8	292	44	163	32	0.00343	-1.79	RIKEN cDNA 8430423A01 gene
C330021A05	BB303415	Mm.271656	1	625	127	350	89	0.01205	-1.78	null
5730438N18	BC011293	Mm.41877	1	1311	94	741	97	0.00126	-1.77	RIKEN cDNA 5730438N18 gene
2210418I02F	NM_022995	Mm.73682	1	817	231	469	88	0.02339	-1.74	RIKEN cDNA 2210418I02 gene
2510005D08	NM_026526	Mm.45225	1	745	111	428	98	0.00839	-1.74	RIKEN cDNA 2510005D08 gene
BC005682	NM_033562	Mm.28131	1	1290	264	747	80	0.00789	-1.73	cDNA sequence BC005682
NULL	AK006072	Mm.3990.2	1	436	83	251	49	0.00789	-1.73	null
4930504E06I	AI639566	Mm.290947	1	2967	665	1724	167	0.01061	-1.72	null
0610010K06	AK002489	Mm.294813	1	410	98	242	17	0.02037	-1.7	null
BC027342	BC027342	Mm.29046	1	1755	197	1045	219	0.01007	-1.68	cDNA sequence BC027342
2700075B01	BC026452	Mm.108596	1	434	83	259	62	0.01963	-1.68	RIKEN cDNA 2700075B01 gene
1110018M03	BC027250	Mm.291809	1	1964	599	1175	122	0.0362	-1.67	RIKEN cDNA 1110018M03 gene
1810008K03	BC025169	Mm.35083	1	6719	1135	4013	1119	0.03015	-1.67	RIKEN cDNA 1810008K03 gene
NULL	BI454991	Mm.335678	1	755	163	453	35	0.01072	-1.66	null
AW742319	BG075943	Mm.21092	1	2379	710	1439	254	0.04354	-1.65	null
9530098M12	AI875447	Mm.207367	0.6	416	106	251	50	0.02615	-1.65	null
NULL	AA223007	NULL	1	170	36	104	31	0.0437	-1.63	null
AI643885	BB409881	Mm.46749	1	563	120	345	57	0.01371	-1.63	expressed sequence AI643885
2310008M20	NM_025512	Mm.25674	1	216	51	133	35	0.03624	-1.62	RIKEN cDNA 2310008M20 gene
1110001A05	NM_019808	Mm.117709	1	322	69	198	61	0.04715	-1.62	RIKEN cDNA 1110001A05 gene
1110018O08	AK010881	Mm.29432	1	372	67	232	61	0.03008	-1.6	RIKEN cDNA 1110018O08 gene
5830411E10I	AK015312	Mm.196290	1	229	25	143	35	0.03375	-1.6	null
2310044D20	BB667295	Mm.272705	1	116	31	73	11	0.04154	-1.59	RIKEN cDNA 2310044D20 gene

AI415282	NM_134021	Mm.254704	1	1425	395	901	100	0.03713	-1.58	expressed sequence AI415282
NULL	AK009814	Mm.28566.2	1	895	127	566	136	0.02756	-1.58	null
2610507L03	BY239594	Mm.133263	1	348	68	220	42	0.01726	-1.58	RIKEN cDNA 2610507L03 gene
0610009D07	NM_025323	Mm.29712	1	1302	314	830	50	0.03026	-1.57	RIKEN cDNA 0610009D07 gene
A530057M15	AV307219	Mm.29098	1	2100	452	1344	107	0.01601	-1.56	RIKEN cDNA A530057M15 gene
G630024C07	BB823641	Mm.41038	1	663	63	424	73	0.00952	-1.56	null
NULL	AK004647	Mm.27697.2	1	382	64	245	19	0.00676	-1.56	null
1110023P21	NM_025390	Mm.22284	1	537	76	347	57	0.01046	-1.55	RIKEN cDNA 1110023P21 gene
BC013667	BC013667	Mm.220901	1	652	85	424	44	0.00265	-1.54	null
4631422C05	BI648645	Mm.200423	1	3137	573	2057	271	0.01139	-1.53	RIKEN cDNA 4631422C05 gene
4432406C05	AK009236	Mm.10068	0.8	325	20	213	32	0.01275	-1.52	RIKEN cDNA 4432406C05 gene
2610034N03	BC016576	Mm.182574	1	580	73	385	24	0.00282	-1.51	RIKEN cDNA 2610034N03 gene
4930504E06	BM118729	Mm.290947	1	745	129	492	49	0.00773	-1.51	null
NULL	BB010153	Mm.46412	1	2448	403	1618	62	0.01074	-1.51	null
6430628I05	CA576920	Mm.196533	1	2404	313	3617	128	0.00026	1.5	RIKEN cDNA 6430628I05 gene
1190005B03	BC016073	Mm.212227	1	1273	70	1921	233	0.04273	1.51	RIKEN cDNA 1190005B03 gene
2810405K02	AI836168	Mm.41868	1	5748	435	8652	990	0.04063	1.51	RIKEN cDNA 2810405K02 gene
4933408N02	BC005737	Mm.294082	1	318	21	480	20	0.00012	1.51	RIKEN cDNA 4933408N02 gene
1700085D07	AW123286	Mm.234912	1	7319	1418	11027	688	0.00258	1.51	Mus musculus similar to plectin (LOC381012), mRNA
NULL	AA419994	Mm.34106	1	1723	563	2608	85	0.02607	1.51	ESTs, Highly similar to 2118318A promyelocyte leukemia Zn finger protein
BC003332	BB278670	Mm.100116	1	1456	458	2214	256	0.0242	1.52	cDNA sequence BC003332
2210010N04	BB759101	Mm.196541	0.7	1167	204	1774	51	0.00147	1.52	RIKEN cDNA 2210010N04 gene
2310066E14	BC006820	Mm.41261	1	651	149	987	57	0.00413	1.52	RIKEN cDNA 2310066E14 gene
2310047C17	BC028439	Mm.35669	1	275	62	418	56	0.02138	1.52	RIKEN cDNA 2310047C17 gene
1110035L05	NM_026125	Mm.29140	1	1434	330	2214	258	0.01379	1.54	RIKEN cDNA 1110035L05 gene
6330581L23	BG068796	Mm.224766	1	228	79	355	26	0.02228	1.55	RIKEN cDNA 6330581L23 gene
4121402D02	AK014463	Mm.258352	1	576	172	892	77	0.01206	1.55	RIKEN cDNA 4121402D02 gene
NULL	AI467657	Mm.34106	1	3268	969	5076	153	0.01506	1.55	ESTs, Highly similar to 2118318A promyelocyte leukemia Zn finger protein
4933424M23	AK016901	Mm.28864	1	513	109	799	37	0.00305	1.56	null
AW547365	BC025941	Mm.270088	1	1266	330	1974	195	0.00889	1.56	expressed sequence AW547365
2510048K03	AK011112	Mm.39856	0.7	336	86	528	77	0.02239	1.57	RIKEN cDNA 2510048K03 gene
NULL	AV326938	Mm.258250	1	614	107	968	59	0.00097	1.57	RIKEN cDNA 2810425F24 gene
6-Sep	BG920446	Mm.260036	1	58	18	92	17	0.04641	1.57	null, Mam6 Mus musculus cDNA clone IMAGE:4953849 5', MRNA sequence
2310045A20	BC026655	Mm.235020	1	1082	287	1711	117	0.00495	1.58	RIKEN cDNA 2310045A20 gene
1110035O14	AW989410	Mm.202727	1	561	204	890	138	0.03492	1.59	null
1110020B03	AK003844	Mm.253151	0.8	129	35	205	33	0.02794	1.59	null
NULL	BM117074	Mm.259655	1	1031	106	1649	161	0.00972	1.6	null
2600017P15	BM200255	Mm.260997	1	384	130	617	66	0.01551	1.61	RIKEN cDNA 2600017P15 gene
NULL	BE686667	Mm.336431	1	518	224	835	74	0.03356	1.61	ESTs
NULL	BG868949	Mm.259260	1	480	173	780	94	0.01942	1.62	Mus musculus 10, 11 days embryo whole body cDNA, clone:2810410A03
NULL	W45978	Mm.178550	1	3521	832	5720	155	0.00456	1.62	Mus musculus, clone IMAGE:4206343, mRNA
2310022A10	AK009941	Mm.29831	1	966	153	1575	296	0.04575	1.63	null
NULL	AI845177	Mm.181435	1	4515	1759	7351	1132	0.03235	1.63	ESTs
1110006I15	NM_134142	Mm.251890	1	5674	2313	9447	1138	0.02172	1.66	RIKEN cDNA 1110006I15 gene
LOC227619	BM120583	Mm.139243	1	198	78	328	36	0.01932	1.66	hypothetical protein LOC227619
D14Ertd226e	BC025568	Mm.28876	0.5	622	205	1039	120	0.01114	1.67	DNA segment, Chr 14, ERATO Doi 226, expressed
1810058I24	BE627374	Mm.302622	1	2742	537	4582	256	0.00062	1.67	Mus musculus transcribed sequence
MGC25248	NM_008419	Mm.1241	1	808	47	1365	143	0.02269	1.69	hypothetical protein MGC25248
NULL	BM207314	Mm.322432	1	534	107	910	79	0.00132	1.7	null
B930093C12	AI507196	Mm.39296	1	1927	786	3282	505	0.02515	1.7	RIKEN cDNA B930093C12 gene
1110061L23	AK016797	Mm.181689	1	594	112	1028	134	0.00935	1.73	null
0610013D04	NM_030697	Mm.196330	1	814	193	1433	292	0.04708	1.76	RIKEN cDNA 0610013D04 gene
NULL	AK017541	NULL	1	466	125	826	77	0.0024	1.77	null
NULL	AV013785	Mm.208618	0.7	188	101	337	16	0.03242	1.79	Mus musculus, clone IMAGE:5028242, mRNA
2310047C17	BC028439	Mm.35669	1	369	83	660	40	0.00056	1.79	RIKEN cDNA 2310047C17 gene
1810013P09	BC002120	Mm.30886	1	1888	201	3390	117	0.00001	1.8	RIKEN cDNA 1810013P09 gene
1500005K14	BG070087	Mm.34131	1	697	331	1253	246	0.04273	1.8	RIKEN cDNA 1500005K14 gene
1190002H23	NM_025427	Mm.29811	1	3351	852	6100	729	0.00472	1.82	RIKEN cDNA 1190002H23 gene
2700038N03	NM_027356	Mm.124666	1	638	184	1168	88	0.00157	1.83	RIKEN cDNA 2700038N03 gene
2410003C09	BC017528	Mm.251199	1	336	76	616	11	0.00129	1.83	RIKEN cDNA 2410003C09 gene
2310047C17	AK009866	Mm.35669	1	461	90	843	20	0.00027	1.83	null
1110033A15	AW556696	Mm.332097	1	3663	1128	6705	670	0.00306	1.83	Mus musculus transcribed sequences
C730024G01	BE653749	Mm.209730	1	312	86	583	67	0.00439	1.86	RIKEN cDNA C730024G01 gene
1810073P09	BB278286	Mm.202157	0.5	141	20	264	6	0.00006	1.87	RIKEN cDNA 1810073P09 gene
2610042L04	BM195235	Mm.326705	1	185	62	356	41	0.00346	1.93	Mus musculus transcribed seq with sim to protein enhancer of polycomb 1
1190002H23	BY008248	Mm.29811	1	3638	1023	7107	278	0.00083	1.95	RIKEN cDNA 1190002H23 gene
D5Ertd593e	BB667844	Mm.21965	1	873	65	1722	315	0.04419	1.97	DNA segment, Chr 5, ERATO Doi 593, expressed

2810432L12	BC013800	Mm.24564	1	917	232	1815	224	0.00562	1.98	RIKEN cDNA 2810432L12 gene
BC043118	AV276428	Mm.246424	1	565	109	1123	144	0.01035	1.99	cDNA sequence BC043118
AI255170	BE134496	Mm.214973	1	404	212	810	187	0.03735	2	expressed sequence AI255170
NULL	AA266723	Mm.29940	0.5	178	41	366	81	0.03417	2.05	Mus musculus transcribed sequences
C430015I23	BC021326	Mm.186994	1	105	31	227	26	0.00207	2.16	RIKEN cDNA C430015I23 gene
NULL	BG063148	Mm.27585	1	236	108	511	103	0.01571	2.17	ESTs, Weakly similar to tuftelin 1 [Mus musculus]
6530401D17	AK013740	Mm.27579	1	219	129	505	138	0.04469	2.3	RIKEN cDNA 6530401D17 gene
NULL	BE865094	Mm.31961	0.7	92	50	216	28	0.00446	2.34	Mus musculus, Similar to RIKEN cDNA 1200004E24 gene
NULL	NM_133914	NULL	1	317	85	761	81	0.00074	2.39	null
3110038L01	NM_026524	Mm.29429	1	2049	423	5194	50	0.00008	2.53	RIKEN cDNA 3110038L01 gene
NULL	AI467657	Mm.34106	1	1149	456	2973	310	0.00053	2.59	ESTs, similar to 2118318A promyelocyte leukemia Zn finger protein

SUPPLEMENTAL TABLE 3

Changes in gene expression in the anterior tibialis of MGSKO mice as compared with wild-type littermates. See legend to Supplemental Table 1. Exp, MGSKO samples.

CARBOHYDRATE METABOLISM

GeneSymbol	Genbank	Unigene	A/P	Ctl Mean	Ctl stdev	Exp Mean	Exp stdev	P-value	Fold Change	Gene Description
Gys1/Gys3	Mm.35662	NM_008195	1	9271	772	50	18	0.00016	-185.43	glycogen synthase 1
Gys1/Gys3	Mm.18524	NM_030678	1	2404	1062	23	10	0.02072	-102.65	glycogen synthase 1
Ppp1r1a	Mm.14378	NM_021391	1	1805	122	181	70	0	-9.98	protein phosphatase 1, regulatory (inhibitor) subunit 1A
Slc2a3	Mm.3726	BB414515	1	582	134	172	84	0.00357	-3.38	solute carrier family 2 (facilitated glucose transporter), member 3
Slc2a3	Mm.3726	BB414515	1	765	76	248	20	0.00095	-3.08	solute carrier family 2 (facilitated glucose transporter), member 3
Slc2a1	Mm.21002	BM207588	1	722	150	379	75	0.01516	-1.91	solute carrier family 2 (facilitated glucose transporter), member 1
Mod1	Mm.14815	NM_008615	1	5627	1202	3026	303	0.02468	-1.86	malic enzyme
Aldh6a1	Mm.18270	NM_134042	1	3207	724	1901	50	0.03681	-1.69	aldehyde dehydrogenase family 6, subfamily A1
Sdh1	Mm.10492	BI143942	1	3219	508	1926	236	0.00997	-1.67	sorbitol dehydrogenase 1
Sdh1	Mm.10492	AV253518	1	951	164	615	114	0.02021	-1.55	sorbitol dehydrogenase 1
Ids	Mm.23308	BB493523	1	164	41	248	49	0.04063	1.51	iduronate 2-sulfatase
Pdhb	Mm.22676	BC019512	1	14776	650	22562	1264	0.00039	1.53	pyruvate dehydrogenase (lipoamide) beta
Dbr1	Mm.31324	BC006661	1	206	34	324	67	0.03617	1.57	debranching enzyme (S. Cerevisae) homolog 1
Ugp2	Mm.28877	AV370025	1	9724	1862	16403	354	0.00588	1.69	UDP-glucose pyrophosphorylase 2
Ugp2	Mm.28877	AV370025	1	6733	1398	12568	536	0.00147	1.87	UDP-glucose pyrophosphorylase 2
Man2b1	Mm.4219	BC005430	1	916	451	1743	462	0.04291	1.9	mannosidase 2, alpha B1
Gbe1	Mm.29201	NM_028803	1	1399	69	3163	149	0.00003	2.26	glucan (1,4-alpha-), branching enzyme 1

AMINO ACID METABOLISM

GeneSymbol	Genbank	Unigene	A/P	Ctl Mean	Ctl stdev	Exp Mean	Exp stdev	P-value	Fold Change	Gene Description
Odc	Mm.34102	BB519474	1	3399	323	1519	95	0.00037	-2.24	ornithine decarboxylase, structural
Bckdhb	Mm.12819	AW047304	1	1638	197	730	115	0.00051	-2.24	branched chain ketoacid dehydrogenase E1, beta polypeptide
Odc	Mm.34102	C81193	1	4209	894	2023	375	0.01075	-2.08	ornithine decarboxylase, structural
Odc	Mm.34102.	S64539	1	1693	325	845	185	0.00627	-2	ornithine decarboxylase, structural
Gpx3	Mm.7156	NM_008161	1	11129	1177	5715	381	0.00094	-1.95	glutathione peroxidase 3
Mgst1	Mm.14796	BC009155	1	8500	1040	4575	611	0.00128	-1.86	microsomal glutathione S-transferase 1
Gstm2	Mm.14601	NM_008183	1	2364	156	1301	102	0.00009	-1.82	glutathione S-transferase, mu 2
Ivd	Mm.6635	AV221988	1	1491	221	828	167	0.00307	-1.8	isovaleryl coenzyme A dehydrogenase
Amd1	Mm.7880	NM_009665	1	18456	3073	10325	1237	0.008	-1.79	S-adenosylmethionine decarboxylase 1
Glul	Mm.2338	AI391218	1	3916	776	2242	72	0.02323	-1.75	glutamate-ammonia ligase (glutamine synthase)
Pcca	Mm.23876	AY046947	1	3591	249	2187	161	0.00022	-1.64	propionyl-Coenzyme A carboxylase, alpha polypeptide
Sms	Mm.18652	NM_009214	1	2792	351	1776	434	0.01087	-1.57	spermine synthase
Ddt	Mm.5731	NM_010027	1	1330	130	870	98	0.00132	-1.53	D-dopachrome tautomerase
Glul	Mm.2338	U09114	1	2077	152	1384	244	0.00483	-1.5	glutamate-ammonia ligase (glutamine synthase)
Gstm1	Mm.2011	NM_010358	1	7010	1043	4660	199	0.02148	-1.5	glutathione S-transferase, mu 1
Dbt	Mm.3636	NM_010022	1	788	139	524	49	0.02359	-1.5	dihydrolipoamide branched chain transacylase E2
Aox1	Mm.26787	NM_009676	1	889	138	1396	101	0.00105	1.57	aldehyde oxidase 1

LIPID METABOLISM

GeneSymbol	Genbank	Unigene	A/P	Ctl Mean	Ctl stdev	Exp Mean	Exp stdev	P-value	Fold Change	Gene Description
Acadsb	Mm.28430	BF228057	1	1849	159	767	50	0.00021	-2.41	acyl-Coenzyme A dehydrogenase, short/branched chain
Siat9	Mm.38248	BB829192	1	2361	377	1113	700	0.02576	-2.12	CMP-NeuAc:lactosylceramide alpha-2,3-sialyltransferase
Pla2g7	Mm.9277.2	AK005158	1	2081	241	1049	130	0.00066	-1.98	phospholipase A2, group VII
Pla2g7	Mm.9277.2	AK005158	1	2081	241	1049	130	0.00066	-1.98	phospholipase A2, group VII
Cbr2	Mm.21454	BC010758	1	1795	371	953	258	0.01371	-1.88	carbonyl reductase 2
Pip5k1b	Mm.87521	BB822856	1	960	139	548	143	0.00621	-1.75	phosphatidylinositol-4-phosphate 5-kinase, type 1 beta
Siat9	Mm.38248	NM_011375	1	2188	124	1287	206	0.00068	-1.7	CMP-NeuAc:lactosylceramide alpha-2,3-sialyltransferase
Cyp27a1	Mm.26793	NM_024264	1	3973	212	2337	260	0.00007	-1.7	cytochrome P450, family 27, subfamily a, polypeptide 1
Acads	Mm.18759	NM_007383	1	2566	83	1617	357	0.01402	-1.59	acyl-Coenzyme A dehydrogenase, short chain
Acly	Mm.25316	AF332052	1	474	116	744	139	0.02521	1.57	ATP citrate lyase
Siat8d	Mm.10701	NM_009183	1	511	144	865	211	0.03962	1.69	sialyltransferase 8 (alpha-2, 8-sialyltransferase) D
Ppap2a	Mm.2598	NM_008903	1	2772	63	4695	448	0.00343	1.69	phosphatidic acid phosphatase 2a (Ppap2a), mRNA
Ppap2a	Mm.2598	NM_008903	1	3845	612	6657	965	0.0044	1.73	phosphatidic acid phosphatase 2a (Ppap2a), mRNA
Synj2	Mm.30717	AF041858	1	753	55	1356	172	0.00263	1.8	synaptojanin 2
Synj2	Mm.30717	BE944213	1	505	30	1001	208	0.01812	1.98	synaptojanin 2
Ache	Mm.3142	NM_009599	1	909	219	2202	167	0.00008	2.42	acetylcholinesterase
Plcb4	Mm.13209	AF332072	1	88	61	302	122	0.03542	3.41	phospholipase C, beta 4

MISCELLANIOUS METABOLISM

GeneSymbol	Genbank	Unigene	A/P	Ctl Mean	Ctl stdev	Exp Mean	Exp stdev	P-value	Fold Change	Gene Description
Dcxr	Mm.29180	BC012247	1	549	123	144	45	0.00358	-3.81	dicarbonyl L-xylulose reductase
Ces3	Mm.120807	AI315015	1	701	179	372	136	0.02683	-1.88	carboxylesterase 3
Ces3	Mm.120807	NM_053200	1	1341	324	820	129	0.04068	-1.63	carboxylesterase 3
Suox	Mm.23352	BC027197	1	1755	308	1107	134	0.01823	-1.59	sulfite oxidase
Impdh2	Mm.6065	M33934	1	2678	508	1774	90	0.0395	-1.51	inosine 5'-phosphate dehydrogenase 2
Car14	Mm.224836	NM_011797	1	1637	453	2524	417	0.02815	1.54	carbonic anhydrase 14
Gch	Mm.10651	BB698398	1	181	26	289	67	0.04012	1.6	GTP cyclohydrolase 1
Pde7a	Mm.5034	NM_008802	1	2029	569	3388	561	0.01454	1.67	phosphodiesterase 7A
Chuk	Mm.3996.2	BC018243	1	273	60	468	52	0.00291	1.71	conserved helix-loop-helix ubiquitous kinase
Pde7a	Mm.5034	NM_008802	1	1079	180	1914	435	0.02391	1.77	phosphodiesterase 7A
Pctk3	Mm.28130	NM_008795	1	319	109	579	130	0.023	1.81	PCTAIRE-motif protein kinase 3
Egln3	Mm.33484	NM_028133	1	1005	429	2213	145	0.00598	2.2	EGL nine homolog 3 (C. elegans)
Fabp4	Mm.582.2	BC002148	1	634	152	1467	110	0.00031	2.31	fatty acid binding protein 4
Egln3	Mm.33484	BB284358	1	1160	96	2693	209	0.00019	2.32	EGL nine homolog 3 (C. elegans)

MUSCLE

GeneSymbol	Genbank	Unigene	A/P	Ctl Mean	Ctl stdev	Exp Mean	Exp stdev	P-value	Fold Change	Gene Description
Midori-pendin	Mm.25139	NM_054085	1	7360	1300	3499	725	0.00351	-2.1	Midori-pending myocyte induction differentiation originator
Edil3	Mm.41716	BB377340	1	93	10	56	13	0.00557	-1.65	EGF-like repeats and discordin I-like domains 3, integrin ligand
Myla	Mm.43	NM_010858	1	805	108	509	48	0.00752	-1.58	myosin light chain, alkali, cardiac atria
Dmd	Mm.742	BB085328	1	1130	335	1737	292	0.03424	1.54	dystrophin, muscular dystrophy
Itga7	Mm.179747	NM_008398	1	1259	249	1968	98	0.00613	1.56	integrin alpha 7
Synpo2	Mm.212349	NM_080451	1	8363	2806	13151	1817	0.03527	1.57	synaptopodin 2
Pln	Mm.34145	AV005660	1	427	113	740	63	0.00482	1.73	phospholamban
Myo1b	Mm.3390	AI255256	1	370	106	644	135	0.01896	1.74	myosin IB
Myo1b	Mm.3390	BI080370	1	426	104	812	147	0.00786	1.91	myosin IB
Actc1	Mm.686	NM_009608	1	6406	1508	14183	4200	0.02524	2.21	actin, alpha, cardiac
Mybph	Mm.200230	NM_016749	1	1099	758	2908	988	0.02722	2.65	myosin binding protein H, structural constituent of muscle
Mylc	Mm.197678	X67685	1	8536	2982	32994	2670	0.00002	3.87	ventricular alkali myosin light chain, skeletal, slow
Mylc	Mm.7353.2	AK002312	1	5757	2108	27155	2292	0.00001	4.72	myosin light chain, alkali, cardiac ventricles
Mylc	Mm.197678	X67685	1	2745	1082	14813	2549	0.00096	5.4	ventricular alkali myosin light chain

WNT PATHWAY

GeneSymbol	Genbank	Unigene	A/P	Ctl Mean	Ctl stdev	Exp Mean	Exp stdev	P-value	Fold Change	Gene Description
Wnt4	Mm.20355	NM_009523	1	1030	133	182	99	0.00005	-5.64	wingless-related MMTV integration site 4
Wif1	Mm.32831.	BC004048	1	109	41	24	14	0.019	-4.42	Wnt inhibitory factor 1
Dkk3	Mm.55143	AK004853	1	721	184	164	38	0.00971	-4.38	dickkopf homolog 3 (Xenopus laevis)
Tnfrsf19	Mm.21526	NM_013869	1	1317	263	503	85	0.00418	-2.62	tumor necrosis factor receptor superfamily, member 19
Frzb	Mm.3246	NM_011356	1	681	79	378	71	0.00129	-1.8	frizzled-related protein wnt inhibitor
Tcfl1	Mm.133919	NM_009336	1	2999	610	1850	203	0.02338	-1.62	transcription factor-like 1
Ccnd2	Mm.3141	BM118679	1	299	55	187	41	0.01813	-1.6	cyclin D2 (target of wnt pathway)
Smo	Mm.29279	AW555326	1	319	96	536	77	0.0128	1.68	smoothened homolog (Drosophila)
Lrp5	Mm.20876	BC011374	1	115	52	197	31	0.04353	1.71	low density lipoprotein receptor-related protein 5

TRANSCRIPTION FACTORS/REGULATION OF TRANSCRIPTION

GeneSymbol	Genbank	Unigene	A/P	Ctl Mean	Ctl stdev	Exp Mean	Exp stdev	P-value	Fold Change	Gene Description
Ebfaz	Mm.23452	NM_033327	1	458	122	182	68	0.01102	-2.51	early B-cell factor associated zinc finger protein
Klf15	Mm.41389	BC013486	1	1583	480	749	243	0.03641	-2.11	Kruppel-like factor 15
Creg	Mm.459	BC027426	1	3440	141	1724	148	0	-2	cellular repressor of E1A-stimulated genes
Creg	Mm.459	NM_011804	1	3372	213	1891	210	0.00006	-1.78	cellular repressor of E1A-stimulated genes
Lbx1h	Mm.116815	BB248430	1	3336	690	1959	283	0.02105	-1.7	lady bird-like homeobox 1 homolog (Drosophila)
Asb4	Mm.51340	AV113827	1	553	68	327	77	0.00483	-1.69	ankyrin repeat and SOCS box-containing protein 4
Hoxd9	Mm.26544	BC019150	1	391	44	233	57	0.00484	-1.68	homeo box D9
Pdcd7	Mm.29193	NM_016688	1	761	96	488	37	0.00624	-1.56	programmed cell death protein 7
Edr1	Mm.6822	BE650359	1	965	166	632	179	0.03482	-1.53	early development regulator 1 (homolog of polyhomeotic 1)
Csda	Mm.193526	AV216648	1	19266	3037	12740	2391	0.01492	-1.51	cold shock domain protein A
Zfp352	Mm.214642	AF290196	1	59	17	90	10	0.02795	1.52	zinc finger protein 352
Ppargc1	Mm.10707.	BM120569	1	950	189	1462	184	0.00828	1.54	peroxisome proliferative activated receptor, gamma, coactivator 1
Gcn5l2	Mm.218837	NM_020004	1	403	55	627	52	0.0011	1.56	general control of amino acid synthesis-like 2 (yeast)
Zfx	Mm.919.3	BC028506	1	104	30	163	17	0.02098	1.56	zinc finger protein X-linked
Zfp36l1	Mm.18571	BB036959	1	323	32	508	97	0.02274	1.57	zinc finger protein 36, C3H type-like 1

Nr2c1	Mm.3398	NM_011629	1	198	53	315	37	0.01584	1.59	nuclear receptor subfamily 2, group C, member 1
Zfp292	Mm.38193	BI686420	1	199	59	321	69	0.03715	1.61	zinc finger protein 292, Zn-15, Zn-16
hr	Mm.7598	NM_021877	1	439	150	734	110	0.01967	1.67	hairless
Irf5	Mm.6479	NM_012057	1	677	90	1136	108	0.00063	1.68	interferon regulatory factor 5
Zfp62	Mm.16650	BC022935	1	393	113	663	151	0.02864	1.69	zinc finger protein 62
Trpc3	Mm.74363	NM_019510	1	313	53	539	31	0.00074	1.72	transient receptor potential cation channel, subfamily C, member 3
Ankrd2	Mm.14373	NM_020033	1	7149	1877	12795	623	0.00465	1.79	ankyrin repeat domain 2 (stretch responsive muscle)
Wbscr14	Mm.34213	AF245479	1	2420	151	4924	542	0.003	2.03	Williams-Beuren syndrome chromosome region 14 homolog
Csrp3 (MLP)	Mm.17235	NM_013808	1	4576	1782	10328	1636	0.00315	2.26	cysteine-rich protein 3
Crap	Mm.10279	NM_013468	1	575	158	1460	492	0.0268	2.54	cardiac responsive adriamycin protein
Smarca1	Mm.82922	NM_053123	1	177	78	488	181	0.03445	2.76	SWI/SNF rel, matrix assoc, actin dep reg chromatin, subfamily a, member 1
Irf6	Mm.4179	NM_016851	1	108	15	316	118	0.04003	2.9	interferon regulatory factor 6

EXTRACELLULAR/MATRIX/CYTOPLASMIC

GeneSymbol	Genbank	Unigene	A/P	Ctl Mean	Ctl stdev	Exp Mean	Exp stdev	P-value	Fold Change	Gene Description
Fgfbp1	Mm.46053	U49641	1	286	93	143	54	0.04647	-1.99	fibroblast growth factor binding protein 1
Tgfbi	Mm.14455.	BB533460	1	2352	634	1291	186	0.03262	-1.82	transforming growth factor, beta induced
Chad	Mm.8033	NM_007689	1	1171	334	667	136	0.04955	-1.75	chondroadherin
Tgfbi	Mm.14455	NM_009369	1	1720	379	1050	153	0.03063	-1.64	transforming growth factor, beta induced
Fgl2	Mm.3040	NM_008013	1	258	42	157	28	0.01108	-1.64	fibrinogen-like protein 2
Myoc	Mm.10694	AB013592	1	4240	774	2583	361	0.01784	-1.64	myocilin
Ltbp3	Mm.21370	BB324823	1	2201	403	1340	171	0.0171	-1.64	latent transforming growth factor beta binding protein 3
Nov	Mm.5167	X96585	1	671	119	413	122	0.02394	-1.62	nephroblastoma overexpressed gene
Nov	Mm.5167	X96585	1	444	85	284	90	0.04188	-1.56	nephroblastoma overexpressed gene
Art5	Mm.2816	U60881	1	1323	192	867	67	0.01114	-1.53	ADP-ribosyltransferase 5
Thbs4	Mm.20865	NM_011582	1	6115	798	4070	341	0.00925	-1.5	thrombospondin 4
Apel-pending	Mm.29262	BB819942	1	809	129	1232	112	0.0026	1.52	apelin
Bmp5	Mm.11958	NM_007555	1	451	113	707	163	0.04966	1.57	bone morphogenetic protein 5
Vtn	Mm.3667	BB251864	1	297	56	475	24	0.00446	1.6	vitronectin
Inha	Mm.1100	NM_010564	1	866	89	1526	225	0.00557	1.76	inhibin alpha
Ptx3	Mm.4663	NM_008987	1	698	141	1243	195	0.0063	1.78	pentaxin related gene
Angptl2	Mm.19081	NM_011923	1	537	244	1032	299	0.04284	1.92	angiopoietin-like 2
Gsn	Mm.21109	AV025588	1	206	122	477	85	0.01507	2.31	gelsolin
Bdnf	Mm.1442	NM_007540	1	87	44	229	25	0.00269	2.62	brain derived neurotrophic factor
Pdcd1lg1	Mm.16868	NM_021893	1	154	80	481	204	0.04094	3.11	programmed cell death 1 ligand 1
Ifi30	Mm.30241	NM_023065	1	464	80	4647	770	0.0017	10	interferon gamma inducible protein 30

RECEPTORS

GeneSymbol	Genbank	Unigene	A/P	Ctl Mean	Ctl stdev	Exp Mean	Exp stdev	P-value	Fold Change	Gene Description
Ccrl2	Mm.7336	AJ318863	1	864	87	286	147	0.00109	-3.02	chemokine (C-C motif) receptor-like 2
Fmod	Mm.41573	BB532202	1	6651	1663	3187	319	0.02641	-2.09	fibromodulin
Fmod	Mm.41573	BB504826	1	2587	715	1345	173	0.0433	-1.92	fibromodulin
Fmod	Mm.41573	BB235530	1	4500	895	2339	101	0.01727	-1.92	fibromodulin
Fmod	Mm.41573	BB483571	1	4407	1211	2297	143	0.04068	-1.92	fibromodulin
Fmod	Mm.41573	NM_021355	1	9283	1907	4851	469	0.02033	-1.91	fibromodulin
Xpr1	Mm.89968	BB667480	1	3014	288	1877	73	0.00466	-1.61	xenotropic and polytropic retrovirus receptor 1
Kdr	Mm.285	NM_010612	1	2021	427	3154	334	0.00581	1.56	kinase insert domain protein receptor
Tem8-pendin	Mm.29636.	AK013005	1	269	30	430	93	0.03088	1.59	anthrax toxin receptor 1
Nrp	Mm.27448	AK011144	1	1200	192	1912	197	0.00208	1.59	neuropilin
Itgb1	Mm.4712	U37029	1	2801	681	4646	1059	0.03273	1.66	integrin beta 1 (fibronectin receptor beta)
Ednrb	Mm.22953	BB770914	1	487	136	811	160	0.02205	1.66	endothelin receptor type B
Chrna1	Mm.4583	NM_007389	1	707	147	1195	66	0.00385	1.69	cholinergic receptor, nicotinic, alpha polypeptide 1 (muscle)
Klra3	Mm.19605	U49865	1	494	165	852	220	0.04058	1.72	killer cell lectin-like receptor, subfamily A, member 3
Pdgfrb	Mm.4146	NM_008809	1	384	79	675	101	0.00405	1.75	platelet derived growth factor receptor, beta polypeptide
Tpra40-pend	Mm.22067	NM_011906	1	1013	94	1892	266	0.00342	1.87	transmembrane domain protein regulated in adipocytes
Ntsr2	Mm.5153	NM_008747	1	278	89	974	293	0.01058	3.5	neurotensin receptor 2

SIGNAL TRANSDUCTION

GeneSymbol	Genbank	Unigene	A/P	Ctl Mean	Ctl stdev	Exp Mean	Exp stdev	P-value	Fold Change	Gene Description
Gdap1	Mm.18218	AU017649	1	400	71	109	71	0.00115	-3.66	ganglioside-induced differentiation-associated-protein 1
Gdap1	NULL	AK020672	1	1024	147	358	96	0.00065	-2.86	ganglioside-induced differentiation-associated-protein 1
Txnl	Mm.19169	BG063276	1	105	26	41	37	0.03925	-2.52	thioredoxin-like
DBC2	Mm.22932	AF420001	1	633	87	313	39	0.00258	-2.02	Rho-related BTB domain containing 2

Plekhb1	Mm.26633	NM_013746	1	2945	477	1595	167	0.00594	-1.85	pleckstrin homology domain containing, family B member 1
Ramp1	Mm.3272	NM_016894	1	4458	893	2456	429	0.01561	-1.82	receptor (calcitonin) activity modifying protein 1
Hdgf	Mm.1141	C80147	1	7884	1482	4758	725	0.01931	-1.66	hepatoma-derived growth factor
Park7	Mm.2507	BC002187	1	18919	2412	11915	1810	0.00352	-1.59	Parkinson disease (autosomal recessive, early onset) 7
Park7	Mm.2507	BB255468	1	14208	1614	9109	775	0.0047	-1.56	Parkinson disease (autosomal recessive, early onset) 7
Mapkapk5	Mm.22612	NM_010765	1	1691	229	2610	301	0.00286	1.54	MAP kinase-activated protein kinase 5
Mpdz	Mm.3140	NM_010820	1	929	319	1448	274	0.04868	1.56	multiple PDZ domain protein
Imap38	Mm.19747	NM_008376	1	291	78	457	38	0.01889	1.57	immunity-associated protein
Rasgrp2	Mm.20884	NM_011242	1	244	63	386	33	0.01102	1.58	guanyl releasing protein 2
Rab22	Mm.87650	AK014407	1	1008	188	1609	160	0.00285	1.6	RAB22, member RAS oncogene family
Il15	Mm.4392	NM_008357	1	905	169	1480	163	0.00275	1.63	interleukin 15
Iqgap1	Mm.56685	NM_016721	1	704	47	1154	46	0.00001	1.64	IQ motif containing GTPase activating protein 1
Tbc1d1	Mm.56905	BC004675	1	1626	305	2667	341	0.00392	1.64	TBC1 domain family, member 1
Erbb2 IP	Mm.42478	BM240030	1	146	39	244	54	0.03354	1.67	vascular endothelial growth factor
Rgs5	Mm.20954	BF585144	1	3718	916	6210	1542	0.03899	1.67	regulator of G-protein signaling 5
Eps8	Mm.2012	NM_007945	1	344	100	578	61	0.01071	1.68	epidermal growth factor receptor pathway substrate 8
Dapp1	Mm.33987	AF163255	1	231	10	411	26	0.00023	1.77	dual adaptor for phosphotyrosine and 3-phosphoinositides 1
Map3k5	Mm.6595	NM_008580	1	238	41	443	49	0.0007	1.86	mitogen activated protein kinase kinase kinase 5
Gucy1a3	NULL	AK004815	1	309	53	642	185	0.04063	2.08	guanylate cyclase 1, soluble, alpha 3
Tbc1d1	Mm.56905	NM_019636	1	435	231	1199	497	0.04963	2.75	TBC1 domain family, member 1

POST-TRANSLATIONAL MODIFICATION

GeneSymbol	Genbank	Unigene	A/P	Ctl Mean	Ctl stdev	Exp Mean	Exp stdev	P-value	Fold Change	Gene Description
Dusp10	Mm.34912	BC025066	1	1038	162	557	120	0.00316	-1.86	dual specificity phosphatase 1
Pkig	Mm.10091.	BC026550	1	2171	231	1323	483	0.03415	-1.64	protein kinase inhibitor, gamma
Ptk9l	Mm.21852	BB397672	1	5475	794	3378	158	0.01398	-1.62	protein typrotein tyrosine kinase 9-like (A6-related protein)
Styx	Mm.15806	NM_019637	1	3451	577	2176	289	0.01688	-1.59	Styx phosphoserine/threonine/tyrosine interaction protein
Rock1	Mm.6710	BB667679	1	439	76	659	97	0.01195	1.5	Rho-associated coiled-coil forming kinase 1
Mtmr7	Mm.22271	AV094609	1	151	25	242	43	0.01636	1.6	myotubularin related protein 7
Dnaja4	Mm.52319.	BQ176119	1	2940	642	4788	510	0.00407	1.63	DnaJ (Hsp40) homolog, subfamily A, member 4
Akap1	Mm.2969	NM_009648	1	999	109	1633	318	0.01956	1.64	A kinase (PRKA) anchor protein 1
Dnaja4	Mm.52319	BC022948	1	2673	595	4706	688	0.00426	1.76	DnaJ (Hsp40) homolog, subfamily A, member 4
Dusp6	Mm.1791	NM_026268	1	669	126	1187	235	0.01166	1.78	dual specificity phosphatase 6
SMAK	Mm.7693	AF112855	1	545	201	1125	350	0.03478	2.06	serine/threonine kinase 2
Ubl4	Mm.3979	BC010817	1	1480	455	3176	628	0.00723	2.15	ubiquitin-like 4

MITOCHONDRIAL

GeneSymbol	Genbank	Unigene	A/P	Ctl Mean	Ctl stdev	Exp Mean	Exp stdev	P-value	Fold Change	Gene Description
Oxct	Mm.13445.	AK010029	1	8678	796	3299	740	0.00006	-2.63	3-oxoacid CoA transferase
Tst	Mm.15312	BC005644	1	1178	77	519	57	0.00001	-2.27	thiosulfate sulfurtransferase, mitochondrial
Oxct	Mm.13445	NM_024188	1	13492	757	6697	593	0.00001	-2.01	3-oxoacid CoA transferase
Slc40a1	Mm.28756	BC003438	1	2459	381	1278	135	0.00432	-1.92	solute carrier family 39 (iron-regulated transporter), member 1
Slc25a20	Mm.29666	AV008091	1	2937	519	1552	247	0.00855	-1.89	solute carrier family 25, member 20
Oxct	Mm.13445	AV213379	1	4318	980	2395	228	0.03155	-1.8	3-oxoacid CoA transferase
Gpd2	Mm.15595	BC015270	1	394	44	257	46	0.00526	-1.53	glycerol phosphate dehydrogenase 2, mitochondrial
Slc25a5	Mm.658	AA823938	1	2924	302	4426	471	0.00302	1.51	solute carrier family 25, member5
Slc25a5	Mm.658	AV026569	1	3465	381	5295	763	0.01279	1.53	solute carrier family 25, member5
KIF1B	Mm.42027	AF090190	1	2223	175	3413	519	0.01228	1.53	kinesin family member 1B
Aspn	Mm.25755	AF316825	1	695	205	1062	212	0.04755	1.53	asporin
Slc25a5	Mm.658	U27316	1	2468	491	3905	286	0.00392	1.58	solute carrier family 25, member5
Got2	Mm.18916	U82470	1	6975	1601	11614	2209	0.01925	1.67	glutamate oxaloacetate transaminase 2, mitochondrial

MEMBRANE ASSOCIATED

GeneSymbol	Genbank	Unigene	A/P	Ctl Mean	Ctl stdev	Exp Mean	Exp stdev	P-value	Fold Change	Gene Description
Cntnap2	Mm.45210	NM_025771	1	392	42	111	44	0.0001	-3.51	contactin associated protein-like 2
H47	Mm.22362	BB285733	1	632	198	297	49	0.04669	-2.12	histocompatibility 47
Npc1	Mm.3484	BB769209	1	750	125	371	74	0.0035	-2.02	Niemann Pick type C1, autosomal recessive lipid storage disorder
Sdc4	Mm.3815	NM_011521	1	1015	176	579	76	0.01066	-1.75	syndecan 4
H47	Mm.22362	NM_024439	1	2400	311	1391	90	0.00836	-1.72	histocompatibility 47
Pcolce2	Mm.46016	AF352788	1	1311	319	786	134	0.03872	-1.67	procollagen C-endopeptidase enhancer 2
Slc38a4	Mm.22260	AK003626	1	1524	183	943	216	0.00641	-1.62	solute carrier family 38, member 4, amino acid transporter
C4st-pendin	Mm.41887	AV259240	1	88	20	56	12	0.04981	-1.55	chondroitin 4-sulfotransferase
Calm3	Mm.1147	BB396904	1	5997	1121	3928	423	0.02603	-1.53	calmodulin 3

Bnip3l	Mm.29820	NM_009761	1	5083	862	3342	236	0.03008	-1.52	BCL2/adenovirus E1B 19kDa-interacting protein 3-like
Semcap3-pe	Mm.9944	NM_018884	1	5038	1009	3340	433	0.0366	-1.51	semaF cytoplasmic domain associated protein 3
Fkbp8	Mm.6565	NM_010223	1	1910	402	1271	311	0.04591	-1.5	FK506 binding protein 8
Abcc5	Mm.20845	NM_013790	1	1398	111	2111	138	0.0002	1.51	ATP-binding cassette, sub-family C (CFTR/MRP), member 5
Kcnj8	Mm.1482	NM_008428	1	1439	118	2175	246	0.00573	1.51	potassium inwardly-rectifying channel, subfamily J, member 8
Cav2	Mm.31915	NM_016900	1	2161	489	3277	169	0.0126	1.52	caveolin 2
Pecam	Mm.2822	NM_008816	1	1699	252	2575	487	0.02418	1.52	platelet/endothelial cell adhesion molecule
Gpsn2	Mm.14251	AK020708	1	21441	2272	32710	467	0.00232	1.53	glycoprotein, synaptic 2
Pnn	Mm.22347	AV135835	1	393	80	601	102	0.01871	1.53	pinin
Abcg2	Mm.19672	NM_011920	1	1475	200	2266	153	0.00076	1.54	ATP-binding cassette, sub-family G (WHITE), member 2
Daf1	Mm.10159	BM208097	1	742	129	1166	225	0.02247	1.57	decay accelerating factor 1
Jcam2	Mm.41758	NM_023844	1	1392	272	2323	266	0.00274	1.67	junction cell adhesion molecule 2
Kcnb1	Mm.54162	BB324482	1	588	101	988	179	0.01165	1.68	potassium voltage gated channel, Shab-related subfamily, member 1
Bri3	Mm.38011	NM_018772	1	3863	533	6539	1017	0.00555	1.69	brain protein I3
Atp1b2	Mm.23520	NM_013415	1	1755	707	3006	530	0.03	1.71	ATPase, Na+/K+ transporting, beta 2 polypeptide
Slc28a2	Mm.29510	NM_021520	1	592	230	1066	190	0.01922	1.8	solute carrier family 28, member 2
Msn	Mm.28687	NM_010833	1	556	233	1026	296	0.04706	1.84	moesin
Gpsn2	Mm.14251	NM_134118	1	7752	1003	14338	1062	0.0001	1.85	glycoprotein, synaptic 2
Prostein-pen	Mm.20030	BC024519	1	418	23	772	101	0.00645	1.85	prostein protein
Aqp4	Mm.18435	BB193413	1	1445	455	2816	329	0.00457	1.95	aquaporin 4
Scn3b	Mm.45097	BE951842	1	137	60	295	58	0.00936	2.15	sodium channel, voltage-gated, type III, beta
Atp1b4	Mm.60134	NM_133690	1	383	143	1310	436	0.0156	3.42	ATPase, (Na+)/K+ transporting, beta 4 polypeptide
Cacnb4	Mm.28404.	BB768064	1	32	35	173	84	0.03734	5.3	calcium channel, voltage-dependent, beta 4 subunit

NUCLEIC ACID ASSOCIATED PROTEINS

GeneSymbol	Genbank	Unigene	A/P	Ctl Mean	Ctl stdev	Exp Mean	Exp stdev	P-value	Fold Change	Gene Description
Hist2h2aa1	Mm.10024	BC010564	1	4830	834	2390	174	0.01057	-2.02	histone 2, H2aa1
Sfpq	Mm.140	BE986849	1	4596	641	2532	197	0.00356	-1.82	splicing factor proline/glutamine rich
Snrpn	Mm.43721	NM_013670	1	7460	879	4373	1177	0.00568	-1.71	small nuclear ribonucleoprotein N
A2bp1-pendi	Mm.14380	NM_021477	1	8715	1604	5340	468	0.01564	-1.63	ataxin 2 binding protein 1
Orc2l	Mm.3411	AW539841	1	470	140	750	131	0.02716	1.6	origin recognition complex, subunit 2-like (S. cerevisiae)

PROTEIN CATABOLISM

GeneSymbol	Genbank	Unigene	A/P	Ctl Mean	Ctl stdev	Exp Mean	Exp stdev	P-value	Fold Change	Gene Description
Pace4	Mm.32906	BI157485	1	1139	253	648	244	0.03171	-1.76	paired basic amino acid cleaving system 4, convertase
Prss11	Mm.30156.	BB559067	1	1090	153	702	151	0.01138	-1.55	protease, serine, 11
Adamts8	Mm.10058	NM_013906	1	227	68	353	67	0.03961	1.55	disintegrin-like and metalloprotease with thrombospondin type 1 motif, 8
Mest	Mm.1089	AW555393	1	457	63	720	50	0.00063	1.58	mesoderm specific transcript
Casp7	Mm.35687	BB752393	1	947	208	1524	175	0.0055	1.61	caspase 7

MISCELLANIOUS

GeneSymbol	Genbank	Unigene	A/P	Ctl Mean	Ctl stdev	Exp Mean	Exp stdev	P-value	Fold Change	Gene Description
Fin15	Mm.3421	BB388301	1	100	9	46	19	0.00726	-2.17	fibroblast growth factor inducible 15
Kip2	Mm.42192	NM_019686	1	4082	455	2193	242	0.00075	-1.86	kinase interacting protein 2
Nudc	Mm.69	BB772682	1	628	70	357	73	0.00178	-1.76	nuclear distribution gene C homolog (Aspergillus)
Sepr	Mm.28212	NM_013759	1	7857	407	4569	426	0.00003	-1.72	selenoprotein R
Snx10	Mm.29101.	AK010399	1	476	102	278	57	0.01994	-1.71	sorting nexin 10
Cyt19-pendi	Mm.28566.	AK009814	1	1137	247	674	84	0.02383	-1.69	methyltransferase Cyt19
Rrs1	Mm.29061	NM_021511	1	1296	170	766	158	0.00388	-1.69	RRS1 ribosome biogenesis regulator homolog (S. cerevisiae)
Anapc5	Mm.45312	BF720337	1	20876	968	13062	936	0.00002	-1.6	anaphase-promoting complex subunit 5
Myd116	Mm.4048	NM_008654	1	1287	159	810	106	0.00425	-1.59	myeloid differentiation primary response gene 116
Anapc5	Mm.45312	AI842295	1	20395	1205	13058	1099	0.00011	-1.56	anaphase-promoting complex subunit 5
Anapc5	Mm.45312	BF019960	1	8318	752	5404	363	0.00222	-1.54	anaphase-promoting complex subunit 5
Anapc5	Mm.45312	NM_021505	1	14940	1529	9792	723	0.00369	-1.53	anaphase-promoting complex subunit 5
Rbl2	Mm.28027	U47333	1	1387	150	911	17	0.00807	-1.52	retinoblastoma-like 2
Narg1	Mm.28256	NM_053089	1	1280	57	1929	251	0.01521	1.51	NMDA receptor-regulated gene 1
Mcpr	Mm.3989	BE306910	1	404	106	620	95	0.02304	1.54	meiotic check point regulator
Cryab	Mm.178	NM_009964	1	15376	2116	24324	1311	0.00081	1.58	crystallin, alpha B
Macf1	Mm.3350	BM248206	1	838	54	1404	294	0.03258	1.67	microtubule-actin crosslinking factor 1
Catnal1	Mm.21889	BQ031240	1	252	35	429	61	0.00413	1.7	catenin alpha-like 1
Pdgfb	Mm.14408	NM_011057	1	388	59	665	105	0.00595	1.72	platelet derived growth factor, B polypeptide
Frap1	Mm.21158	NM_020009	1	1370	195	2358	202	0.00042	1.72	FK506 binding protein 12-rapamycin associated protein 1
Ccnt2	Mm.24621	BM216130	1	266	25	464	76	0.00805	1.74	cyclin T2

Ifit2	Mm.2036	NM_008332	1	88	9	160	27	0.00831	1.8	interferon-induced protein with tetratricopeptide repeats 2
Nupl1	Mm.18583.	AK006062	1	96	45	179	44	0.03914	1.86	nucleoporin like 1
Mttp	Mm.2941	AW553649	1	89	38	190	42	0.01194	2.13	microsomal triglyceride transfer protein
Cegf1	Mm.40447	BI133839	1	133	47	373	79	0.00349	2.8	CUB domain and EGF-like repeat containing 1
Smoc1	Mm.27643	NM_022316	1	302	134	994	144	0.00042	3.28	SPARC related modular calcium binding 1
G0s2	Mm.3283	NM_008059	1	1417	466	5453	1695	0.01941	3.85	G0/G1 switch gene 2

UNKNOWN

GeneSymbol	Genbank	Unigene	A/P	Ctl Mean	Ctl stdev	Exp Mean	Exp stdev	P-value	Fold Change	Gene Description
6330565B14	Mm.28514	BC026584	1	1190	151	334	38	0.00163	-3.56	6330565B14Rik RIKEN cDNA 6330565B14 gene
1810057C19	Mm.10339	NM_026433	1	691	244	221	62	0.03374	-3.12	1810057C19Rik RIKEN cDNA 1810057C19 gene
A930031D07	Mm.20844	AI426503	1	246	83	79	39	0.02236	-3.09	A930031D07Rik RIKEN cDNA A930031D07 gene
E330010H22	Mm.19669	NM_133232	1	5938	986	2198	385	0.00212	-2.7	E330010H22Rik RIKEN cDNA E330010H22 gene
1810008K03	Mm.35083	BC025169	1	5386	1845	2048	919	0.03173	-2.63	1810008K03Rik RIKEN cDNA 1810008K03 gene
A930031D07	Mm.20844	BQ266468	1	440	142	172	53	0.02426	-2.56	A930031D07Rik RIKEN cDNA A930031D07 gene
1700037B15	Mm.19580	AV251625	1	9045	446	3739	381	0	-2.42	1700037B15Rik RIKEN cDNA 1700037B15 gene
0610040J01	Mm.38143	BC004797	1	605	33	252	173	0.02819	-2.4	0610040J01Rik RIKEN cDNA 0610040J01 gene
2610002J02	Mm.10374	AV218922	1	113	24	47	31	0.01582	-2.39	2610002J02Rik RIKEN cDNA 2610002J02 gene
1700064K09	Mm.20095	BC024415	1	638	67	273	69	0.00029	-2.33	1700064K09Rik RIKEN cDNA 1700064K09 gene
6330565B14	Mm.28514	BC026584	1	1065	195	477	39	0.00981	-2.23	6330565B14Rik RIKEN cDNA 6330565B14 gene
Selenbp1	Mm.19655	NM_009150	1	841	166	378	36	0.01237	-2.22	Selenbp1 selenium binding protein 1
NULL	Mm.27612	BC026208	1	1594	177	725	171	0.00041	-2.2	Mus musculus expressed sequence AW742413
0710001E10	Mm.41630	NM_026161	1	314	43	143	59	0.00558	-2.19	0710001E10Rik RIKEN cDNA 0710001E10 gene
1700037B15	Mm.19580	AF335325	1	9411	761	4422	569	0.00004	-2.13	1700037B15Rik RIKEN cDNA 1700037B15 gene
1200009H11	Mm.30950.	AK004672	1	1335	431	644	133	0.03788	-2.07	1200009H11Rik RIKEN cDNA 1200009H11 gene
4631422C05	Mm.20042	BI648645	1	3863	536	1886	565	0.00229	-2.05	4631422C05Rik RIKEN cDNA 4631422C05 gene
3300001H21	Mm.22097	AV171622	1	1207	252	587	108	0.01075	-2.05	3300001H21Rik RIKEN cDNA 3300001H21 gene
0610025I19	Mm.27395	AK002661	1	3124	452	1535	283	0.00191	-2.03	0610025I19Rik RIKEN cDNA 0610025I19 gene
4631422C05	Mm.20042	BB068040	1	3291	423	1645	185	0.00207	-2	4631422C05Rik RIKEN cDNA 4631422C05 gene
Rex3	Mm.14768	NM_009052	1	3756	1093	1901	220	0.04488	-1.97	Rex3 reduced expression 3
2310043K02	Mm.23916	BC018204	1	2796	209	1442	178	0.00006	-1.94	2310043K02Rik RIKEN cDNA 2310043K02 gene
1810006G21	Mm.28397	BG063931	1	695	175	364	109	0.02402	-1.91	1810006G21Rik RIKEN cDNA 1810006G21 gene
1300010A20	Mm.22528	BI440178	1	159	26	83	17	0.00502	-1.9	1300010A20Rik RIKEN cDNA 1300010A20 gene
4930553M18	Mm.21831	AK016109	1	102	23	54	31	0.04685	-1.9	4930553M18Rik RIKEN cDNA 4930553M18 gene
EIG180	Mm.24631	NM_133237	1	159	38	87	16	0.02591	-1.83	EIG180 ethanol induced gene product EIG180
1110018E21	Mm.38238	BC003284	1	700	71	397	139	0.01804	-1.76	1110018E21Rik RIKEN cDNA 1110018E21 gene
1700027M01	Mm.17880	NM_023544	1	882	133	503	105	0.00428	-1.75	1700027M01Rik RIKEN cDNA 1700027M01 gene
4631422C05	Mm.20042	BI648645	1	1853	459	1058	150	0.03025	-1.75	4631422C05Rik RIKEN cDNA 4631422C05 gene
NULL	Mm.15038	AW556821	1	358	73	206	78	0.02997	-1.74	Mus musculus adult male olfactory brain cDNA, clone:6430524C05
C330021A05	Mm.22004	BQ175552	1	2741	465	1596	300	0.00906	-1.72	C330021A05Rik RIKEN cDNA C330021A05 gene
1110032A03	Mm.17137	NM_023483	1	1024	71	599	96	0.0004	-1.71	1110032A03Rik RIKEN cDNA 1110032A03 gene
AL024210	Mm.19006	AU046270	1	5420	1127	3167	139	0.02867	-1.71	AL024210 expressed sequence AL024210
BC021921	Mm.15578	BC021921	1	58	9	34	11	0.01698	-1.7	BC021921 cDNA sequence BC021921
1110023P21	Mm.22284	NM_025390	1	516	94	306	53	0.01173	-1.69	1110023P21Rik RIKEN cDNA 1110023P21
NULL	Mm.21884	BC024118	1	2269	495	1343	239	0.02816	-1.69	LOC219134 hypothetical protein BC024118
2310007H09	Mm.18775	AK009207	1	479	40	284	75	0.00622	-1.68	2310007H09Rik RIKEN cDNA 2310007H09 gene
Bach-pendin	Mm.19752	NM_133348	1	1435	146	855	193	0.00309	-1.68	Bach-pending brain acyl-CoA hydrolase
1110006I15	Mm.30020	NM_134142	1	7362	1651	4421	1592	0.04267	-1.67	1110006I15Rik RIKEN cDNA 1110006I15 gene
Pm5-pendin	Mm.22121	BC024503	1	729	64	438	92	0.00359	-1.66	Pm5-pending pM5 protein
1810006G21	Mm.28397	BG063931	1	361	40	219	37	0.00221	-1.65	1810006G21Rik RIKEN cDNA 1810006G21 gene
MGC28663	Mm.41308	BC025120	1	1080	243	653	89	0.02991	-1.65	MGC28663 hypothetical protein MGC28663
2310005P05	Mm.6825	NM_026189	1	2247	150	1370	232	0.00145	-1.64	2310005P05Rik RIKEN cDNA 2310005P05 gene
NULL	Mm.21597	BB323985	1	1931	280	1177	190	0.0067	-1.64	AI115348 expressed sequence AI115348
C430041M20	Mm.18654	BG094881	1	854	128	520	111	0.00768	-1.64	C430041M20 hypothetical protein C430041M20
NULL	Mm.11928	AV127170	1	2002	241	1223	31	0.00773	-1.64	EST
C130069N12	Mm.28506	NM_133895	1	822	146	506	88	0.01417	-1.62	C130069N12Rik RIKEN cDNA C130069N12 gene
AI115348	Mm.21597	BC022157	1	4641	616	2888	201	0.00568	-1.61	AI115348 expressed sequence AI115348
0610007P06	Mm.28679	BC003916	1	1656	180	1034	53	0.00272	-1.6	0610007P06Rik RIKEN cDNA 0610007P06 gene
9230117N10	Mm.18235	NM_133775	1	489	91	304	24	0.03022	-1.6	9230117N10Rik RIKEN cDNA 9230117N10 gene
2310032D16	Mm.28697	AV291259	1	10155	2400	6406	1433	0.04377	-1.59	2310032D16Rik RIKEN cDNA 2310032D16 gene
2510005D08	Mm.45225	NM_026526	1	1330	76	843	50	0.00013	-1.58	2510005D08Rik RIKEN cDNA 2510005D08 gene
D0H4S114	Mm.4919	BB369191	1	4468	590	2828	638	0.00931	-1.58	D0H4S114 DNA segment, human D4S114
AI842353	Mm.24417	AI842353	1	401	65	253	69	0.02151	-1.58	AI842353 expressed sequence AI842353
Pm5-pendin	Mm.22121	BC024503	1	3225	218	2053	61	0.00195	-1.57	Pm5-pending pM5 protein
NULL	Mm.10024	BC010564	1	2062	258	1327	125	0.00697	-1.55	Mus musculus, similar to histone H2A, clone IMAGE:3582122

AV229935 R	Mm.29877	AV229935	1	1439	154	930	35	0.00766	-1.55	Mus musculus cDNA clone 4631422K22 3'
D0H4S114	Mm.4919	D45203	1	5330	607	3473	307	0.00548	-1.53	D0H4S114 DNA segment, human D4S114
2310007F12	Mm.8142	BQ177187	1	267	36	175	30	0.00833	-1.53	2310007F12Rik RIKEN cDNA 2310007F12 gene
2900046G09	Mm.19651	BC003957	1	1187	45	780	35	0.00001	-1.52	2900046G09Rik RIKEN cDNA 2900046G09 gene
E130307M08	Mm.34488	BC017625	1	2349	219	1544	134	0.00153	-1.52	E130307M08Rik RIKEN cDNA E130307M08 gene
4933427L07	Mm.17382	BB549381	1	889	55	587	90	0.00231	-1.52	4933427L07Rik RIKEN cDNA 4933427L07 gene
AI595338	Mm.20027	BM241485	1	296	48	195	22	0.01906	-1.52	AI595338 expressed sequence AI595338
LOC228785	Mm.20289	BC019408	1	8569	1286	5649	1373	0.021	-1.52	LOC228785 hypothetical protein LOC228785
9430059P22	Mm.21884	BC024118	1	2529	280	1674	246	0.00376	-1.51	9430059P22Rik RIKEN cDNA 9430059P22 gene
NULL	Mm.42027	BI109632	1	1636	354	2457	209	0.01041	1.5	NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:5027280 5'
1700062C23	Mm.8540	AK005819	1	289	66	437	44	0.01413	1.51	1700062C23Rik RIKEN cDNA 1700062C23 gene
BB737680 R	Mm.29030	BB737680	1	2762	607	4167	775	0.0291	1.51	6 days neonate spleen Mus musculus cDNA clone F430014N09 3'
C820004H04	Mm.21147	AV253284	1	384	108	579	86	0.03057	1.51	C820004H04Rik RIKEN cDNA C820004H04 gene
NULL	Mm.46025	AV299914	1	351	97	533	34	0.02428	1.52	8 days embryo Mus musculus cDNA clone 5730472D08 3'
2510005D08	Mm.45225	BF730076	1	1157	398	1754	238	0.04999	1.52	2510005D08Rik RIKEN cDNA 2510005D08 gene
2210404N08	Mm.34874	BC026453	1	614	41	938	51	0.00007	1.53	2210404N08Rik RIKEN cDNA 2210404N08 gene
NULL	Mm.25864	BI697630	1	347	76	532	20	0.01818	1.53	EST
NULL	Mm.25312	BB500104	1	273	44	418	79	0.02398	1.53	ESTs
NULL	Mm.23491	AI505784	1	302	59	461	88	0.03033	1.53	mouse embryonic region Mus musculus cDNA clone IMAGE:906296 3'
6330505F04	Mm.32498	BB460424	1	543	148	834	81	0.01852	1.54	6330505F04Rik RIKEN cDNA 6330505F04 gene
5033428E16	Mm.64201	NM_024435	1	322	37	494	99	0.03116	1.54	5033428E16Rik RIKEN cDNA 5033428E16 gene
1810073P09	Mm.20215	BB278286	1	204	62	315	16	0.04094	1.54	1810073P09Rik RIKEN cDNA 1810073P09 gene
NULL	Mm.29616	AV375176	1	248	75	382	76	0.04752	1.54	LOC212285 hypothetical protein LOC212285
NULL	Mm.13768	AV377356	1	296	57	458	75	0.01418	1.55	Similar to bromodomain adjacent to zinc finger domain, 2A, clone MGC:38682
AV369255 R	Mm.16122	AV369255	1	656	152	1017	207	0.03126	1.55	AV369255 RIKEN full-length enriched similar to M55637 Mus musculus HAM1
2600011C06	Mm.46005	BG228787	1	239	61	372	55	0.01772	1.56	2600011C06Rik RIKEN cDNA 2600011C06 gene
EST	Mm.25247	AI154956	1	878	195	1376	131	0.00822	1.57	ESTs
AA407930	Mm.24521	NM_133349	1	749	73	1183	98	0.00041	1.58	AA407930 expressed sequence AA407930
C330016H24	Mm.21406	BF319466	1	777	129	1230	139	0.0031	1.58	C330016H24Rik RIKEN cDNA C330016H24 gene
EST	Mm.28337	AK014605	1	771	53	1221	180	0.00881	1.58	hypothetical ABC1 family containing protein
EST	Mm.33838	NM_133901	1	671	164	1060	181	0.01941	1.58	AI481500 expressed sequence AI481500
NGP-1	Mm.90760.	BI666155	1	154	38	244	29	0.00917	1.59	similar to Autoantigen NGP-1, mmr1/hsr1 family of gtp-binding proteins.
Flana-pendin	Mm.28131	BB389641	1	444	78	704	127	0.01744	1.59	Flana-pending carcinoma related gene
9130022A11	Mm.23834	BE981916	1	1077	237	1720	260	0.01073	1.6	9130022A11Rik RIKEN cDNA 9130022A11 gene
EST	Mm.27585	BG063148	1	199	52	318	46	0.01459	1.6	ESTs, Weakly similar to tuftelin 1 [Mus musculus]
EST	Mm.27132	BC026425	1	658	190	1058	99	0.01365	1.61	Mus musculus RIKEN cDNA 2410013I23 gene
NULL	Mm.25739	BC021408	1	416	139	670	71	0.03184	1.61	EST
1100001I23	Mm.29386	BB807707	1	2476	337	4023	397	0.00103	1.62	1100001I23Rik RIKEN cDNA 1100001I23 gene
E230009N18	Mm.20085	BG067039	1	2758	461	4460	204	0.00253	1.62	E230009N18Rik RIKEN cDNA E230009N18 gene
Hn1	Mm.1775	NM_008258	1	1043	291	1692	148	0.01652	1.62	Hn1 hematological and neurological expressed sequence 1
2310035K24	Mm.2937.2	AK009634	1	811	260	1315	165	0.02233	1.62	2310035K24Rik RIKEN cDNA 2310035K24 gene
NULL	Mm.24481	BE686667	1	1413	252	2309	343	0.00565	1.63	ESTs
1810007M14	Mm.347	NM_026110	1	429	139	703	98	0.02355	1.64	1810007M14Rik RIKEN cDNA 1810007M14 gene
LOC217517	Mm.22029	BC024598	1	185	74	303	39	0.03771	1.64	LOC217517 amisyn
EST RAS	Mm.77017	BE688720	1	429	52	710	75	0.0017	1.65	Similar to RAS, guanyl releasing protein 2, clone IMAGE:4481738
EST	Mm.17873	BG071991	1	504	71	838	92	0.00125	1.66	Mus musculus adult male corpora quadrigemina cDNA, clone:B230364F10
Niban	Mm.15770	NM_022018	1	386	77	641	86	0.00458	1.66	Niban niban protein
BB410567 R	Mm.26219	BB410567	1	217	53	359	73	0.02579	1.66	7 days embryo Mus musculus cDNA clone C430018P22 3'
2310047I15	Mm.21967	AW744519	1	438	71	728	186	0.04401	1.66	2310047I15Rik RIKEN cDNA 2310047I15 gene
NULL	Mm.27785	BB834097	1	272	66	453	117	0.04414	1.66	AU018638 expressed sequence AU018638
NULL	Mm.22242	BG071867	1	778	109	1306	71	0.00048	1.68	AW112037 expressed sequence AW112037
6430548M08	Mm.10195	BB282696	1	272	45	456	49	0.00159	1.68	6430548M08Rik RIKEN cDNA 6430548M08 gene
Meg3	Mm.20050	Y13832	1	612	119	1030	145	0.00431	1.68	Meg3 maternally expressed gene 3
NULL	Mm.22034	BF682801	1	366	83	616	83	0.00554	1.68	Mus musculus cDNA clone IMAGE:3468213 5'
NULL	Mm.15389	BB436856	1	298	84	499	79	0.01311	1.68	C79248 expressed sequence C79248
NULL	Mm.41268.	BB252740	1	201	46	338	75	0.02688	1.68	7 days neonate cerebellum Mus musculus cDNA clone A730053E12 3'
D930015E06	Mm.28838	BM234701	1	429	181	722	87	0.04363	1.68	D930015E06Rik RIKEN cDNA D930015E06 gene
2810432L12	Mm.24564	BC013800	1	1767	43	2996	124	0.00005	1.7	2810432L12Rik RIKEN cDNA 2810432L12 gene
2310020L09	Mm.29293	AK009425	1	728	101	1241	211	0.01198	1.7	2310020L09Rik RIKEN cDNA 2310020L09 gene
EST RAS	Mm.77017	BE688720	1	350	89	598	21	0.01243	1.71	Similar to RAS, guanyl releasing protein 2, clone IMAGE:4481738
NULL	Mm.3386	BM117918	1	388	80	668	47	0.00184	1.72	NIA Mouse Newborn Brain cDNA Library Mus musculus cDNA L0858A06 3'
F730027O18	Mm.21300	AI463328	1	210	26	366	54	0.00664	1.74	F730027O18Rik RIKEN cDNA F730027O18 gene
C030022K24	Mm.15992	BC019151	1	198	67	347	72	0.02326	1.75	C030022K24Rik RIKEN cDNA C030022K24 gene
D13Wsu123	Mm.20585	BC013625	1	1374	130	2422	80	0.00004	1.76	D13Wsu123e DNA segment, Chr 13, Wayne State University 123, expressed
C730024G01	Mm.34198	BE653749	1	323	51	568	123	0.02155	1.76	C730024G01Rik RIKEN cDNA C730024G01 gene
2700038N03	Mm.21836	NM_027356	1	1018	37	1818	264	0.00929	1.79	2700038N03Rik RIKEN cDNA 2700038N03 gene
Yap	Mm.4885	BG070675	1	440	188	787	147	0.02721	1.79	Yap yes-associated protein

Doc2g	Mm.40194	NM_021791	1	230	32	413	38	0.00035	1.79	Mus musculus 16 days neonate heart cDNA, clone:D830013O18
1300013J15	Mm.10074	NM_026183	1	2836	363	5123	504	0.00073	1.81	1300013J15Rik RIKEN cDNA 1300013J15 gene
NULL	Mm.21464	BC018558	1	397	141	729	103	0.00907	1.83	fatty acid binding protein 4, adipocyte, clone MGC:18548 IMAGE:3670866
NULL	Mm.24936	BE957307	1	296	90	541	127	0.02555	1.83	ESTs
Meg3	Mm.20050	BM119226	1	117	49	216	37	0.01898	1.85	Meg3 maternally expressed gene 3
2310047C17	Mm.35669	BC028439	1	227	59	422	74	0.00642	1.86	2310047C17Rik RIKEN cDNA 2310047C17 gene
NULL	Mm.35523	BE952347	1	92	11	174	20	0.00098	1.89	ESTs, Weakly similar to RIKEN cDNA 5730493B19
2610042L04	Mm.204	BM195235	1	304	99	574	63	0.00599	1.89	2610042L04Rik RIKEN cDNA 2610042L04 gene
NULL	Mm.4025	BI664122	1	426	76	806	193	0.02175	1.89	NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:5323376 5'
NULL	Mm.44883	BM118398	1	775	104	1472	124	0.00014	1.9	Mus musculus 0 day neonate thymus cDNA, clone:A430017F18
6330437E22	Mm.20845	BB278628	1	117	20	223	40	0.00938	1.9	6330437E22Rik RIKEN cDNA 6330437E22 gene
0610013D04	Mm.19633	BG075321	1	432	45	825	78	0.00033	1.91	0610013D04Rik RIKEN cDNA 0610013D04 gene
D5Ertd593e	Mm.21965	BB667844	1	1354	345	2601	456	0.00479	1.92	D5Ertd593e DNA segment, Chr 5, ERATO Doi 593, expressed
NULL	Mm.30245.	BI454991	1	338	102	651	21	0.00941	1.92	phosphatidylserine decarboxylase, clone MGC:7133 IMAGE:3158145
NULL	Mm.25427	BB794641	1	2627	623	5061	329	0.00098	1.93	ESTs
3110038L01	Mm.29429	NM_026524	1	2247	412	4334	719	0.00399	1.93	3110038L01Rik RIKEN cDNA 3110038L01 gene
2810485I05	Mm.24617	BM215139	1	107	32	207	44	0.01079	1.93	2810485I05Rik RIKEN cDNA 2810485I05 gene
6330437E22	Mm.20845	BB278628	1	149	61	289	81	0.03334	1.94	6330437E22Rik RIKEN cDNA 6330437E22 gene
6720485C15	Mm.18163	NM_026551	1	852	36	1695	54	0	1.99	Mus musculus RIKEN cDNA 6720485C15 gene (6720485C15Rik), mRNA
3100002B05	Mm.46397	BM934830	1	79	37	161	49	0.03976	2.02	3100002B05Rik RIKEN cDNA 3100002B05 gene
D3Ertd330e	Mm.25703.	BG070740	1	86	31	173	55	0.04116	2.02	D3Ertd330e DNA segment, Chr 3, ERATO Doi 330, expressed
2610042L04	Mm.204	BM195235	1	488	183	1007	110	0.00473	2.06	2610042L04Rik RIKEN cDNA 2610042L04 gene
1300012C15	Mm.10497	BC011116	1	1809	345	3806	342	0.00018	2.1	1300012C15Rik RIKEN cDNA 1300012C15 gene
Hn1	Mm.1775	BI453712	1	1432	114	3055	146	0	2.13	Hn1 hematological and neurological expressed sequence 1
1810007I17	Mm.25754	BB475271	1	1013	506	2161	249	0.01528	2.13	1810007I17Rik RIKEN cDNA 1810007I17 gene
NULL	NULL	BG066923	1	193	63	416	126	0.03385	2.16	NIA Mouse 15K cDNA Clone Set Mus musculus cDNA clone H3048E11 3'
EST	Mm.7202	AA717264	1	114	70	248	40	0.02085	2.18	ESTs
2310030G06	Mm.15454	NM_025865	1	542	189	1194	197	0.00309	2.2	2310030G06Rik RIKEN cDNA 2310030G06 gene
6330404E11	Mm.15369	AV274554	1	147	72	325	82	0.01762	2.2	RIKEN cDNA 6330404E11 gene
BB315716 R	Mm.19309	BB315716	1	3355	394	7915	627	0.00006	2.36	RIKEN full-length enriched, male corpora quadrigemina clone B230359J01 3'
4930586I02	Mm.46150	NM_026580	1	589	39	1420	211	0.0045	2.41	4930586I02Rik RIKEN cDNA 4930586I02 gene
2310047C17	Mm.35669	BC028439	1	125	39	316	93	0.0196	2.52	2310047C17Rik RIKEN cDNA 2310047C17 gene
6330417L24	Mm.21020	BC024724	1	58	23	148	50	0.03238	2.53	6330417L24Rik RIKEN cDNA 6330417L24 gene
2410027J01	Mm.26928	AI195046	1	288	50	793	175	0.01161	2.75	2410027J01Rik RIKEN cDNA 2410027J01 gene
NULL	Mm.20911	BC024836	1	52	31	146	21	0.00464	2.79	Mus musculus 12 days embryo male wolffian duct cDNA, clone:6720471E05
BB406585 R	Mm.19309	BB406585	1	1583	87	4487	322	0.00042	2.83	RIKEN full-length enriched, ES cells Mus musculus cDNA clone C330046M01 3'
B130052G07	Mm.22856	BC024141	1	152	29	459	56	0.00021	3.01	B130052G07Rik RIKEN cDNA B130052G07 gene
BB406585 R	Mm.19309	BB406585	1	2007	345	6163	215	0.00001	3.07	RIKEN full-length enriched, ES cells Mus musculus clone C330046M01 3'
4930586I02	Mm.46150	AK006346	1	247	145	761	176	0.0041	3.08	4930586I02Rik RIKEN cDNA 4930586I02 gene
2210408B16	Mm.41565	AI987654	1	221	44	839	102	0.00038	3.79	2210408B16Rik RIKEN cDNA 2210408B16 gene
2210408B16	Mm.41565	BC026817	1	292	74	1129	98	0.00001	3.86	2210408B16Rik RIKEN cDNA 2210408B16 gene
1500011J06	Mm.27799	BB560177	1	188	56	772	192	0.00431	4.1	500011J06Rik RIKEN cDNA 1500011J06 gene

SUPPLEMENTAL TABLE 4
Changes in gene expression in the liver of MGSKO mice as compared with wild-type littermates. See legend to Supplemental Table 1. Exp, MGSKO samples.

CARBOHYDRATE METABOLISM

GeneSymbol	Genbank	Unigene	A/P	Ctl Mean	Ctl stdev	Exp Mean	Exp stdev	P-value	Fold Change	Gene Description
Glcci1	AF374476	Mm.274415	0.8	48	27	110	19	0.0138	-2.26	glucocorticoid induced transcript 1
Gyk	BF683028	Mm.246682	1	2957	732	4701	571	0.00945	-1.59	glycerol kinase
Gpd2	NM_010274	Mm.3711	1	1035	264	1634	211	0.01225	-1.58	glycerol phosphate dehydrogenase 2, mitochondrial
Tktl1	NM_031379	Mm.25057	1	176	31	117	35	0.04624	1.5	transketolase-like 1
Slc3a1	NM_009205	Mm.227176	1	2145	579	1215	345	0.03995	1.77	solute carrier family 3, member 1
Pfkfb3	NM_133232	Mm.19669	0.8	151	41	73	3	0.03315	2.06	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3

AMINO ACID METABOLISM

GeneSymbol	Genbank	Unigene	A/P	Ctl Mean	Ctl stdev	Exp Mean	Exp stdev	P-value	Fold Change	Gene Description
Loxl4	NM_053083	Mm.178767	1	554	69	336	107	0.01894	1.65	lysyl oxidase-like 4
Bcat2	AF031467	Mm.24210	1	657	147	338	100	0.01592	1.94	branched chain aminotransferase 2, mitochondrial

LIPID METABOLISM

GeneSymbol	Genbank	Unigene	A/P	Ctl Mean	Ctl stdev	Exp Mean	Exp stdev	P-value	Fold Change	Gene Description
Apoa4	BC010769	Mm.4533	1	6614		21708	7732	0.02366	-3.28	apolipoprotein A-IV
Apoa4	BY036839	Mm.4533	1	8593	3589	24849	7272	0.01601	-2.89	apolipoprotein A-IV
Pte2a	NM_134246	Mm.202331	1	746	418	1834	302	0.00839	-2.46	peroxisomal acyl-CoA thioesterase 2A
Acacb	BC022940	Mm.81793	0.8	299	169	688	159	0.01565	-2.3	acetyl-Coenzyme A carboxylase beta
1300002P22Rik	NM_023737	Mm.28100	1	9559	3651	19489	3157	0.00626	-2.04	enoyl-Coenzyme A, hydratase/3-hydroxyacyl Coenzyme A dehydrogenase
Mgll	BI411560	Mm.272197	1	5298	1285	10484	267	0.00423	-1.98	monoglyceride lipase
Pte1	NM_133240	Mm.277878	1	1241	196	2114	111	0.00058	-1.7	peroxisomal acyl-CoA thioesterase 1
Mgll	AK006949	Mm.272197	1	3518	582	5920	330	0.00082	-1.68	monoglyceride lipase
Mgll	NM_011844	Mm.272197	1	4111	698	6852	347	0.00215	-1.67	monoglyceride lipase
Pctp	AF114437	Mm.5062	1	3987	386	6638	567	0.00058	-1.66	phosphatidylcholine transfer protein
Pctp	NM_008796	Mm.5062	1	3221	790	5166	427	0.00752	-1.6	phosphatidylcholine transfer protein
Acaa1	NM_130864	Mm.205266	1	18558	3723	29024	1935	0.00415	-1.56	acetyl-Coenzyme A acyltransferase 1
Lip1	AI596237	Mm.157545	1	5526	518	8494	1274	0.0125	-1.54	lysosomal acid lipase 1
Fads2	NM_019699	Mm.38901	1	5332	387	8141	945	0.00534	-1.53	fatty acid desaturase 2
Fads2	BB430611	Mm.301490	1	4271	185	6486	663	0.00764	-1.52	fatty acid desaturase 2
Acox1	AB034914	Mm.259054	1	23973	5373	36158	5728	0.02105	-1.51	acyl-Coenzyme A oxidase 1, palmitoyl

MISCELLANIOUS METABOLISM

GeneSymbol	Genbank	Unigene	A/P	Ctl Mean	Ctl stdev	Exp Mean	Exp stdev	P-value	Fold Change	Gene Description
Vnn1	NM_011704	Mm.27154	1	6508	2799	13618	2020	0.00918	-2.09	vanin 1
Entpd5	NM_007647	Mm.10211	1	6114	1258	9664	937	0.00401	-1.58	ectonucleoside triphosphate diphosphohydrolase 5
Dgat2l1	NM_026713	Mm.41325	1	355	71	557	119	0.03386	-1.57	diacylglycerol O-acyltransferase 2-like 1
Rdh6	NM_009040	Mm.100276	1	2357	816	3574	471	0.04915	-1.52	retinol dehydrogenase 6
Sultn	AI647561	Mm.6824	1	2902	653	1618	148	0.03125	1.79	N-sulfotransferase

WNT PATHWAY

GeneSymbol	Genbank	Unigene	A/P	Ctl Mean	Ctl stdev	Exp Mean	Exp stdev	P-value	Fold Change	Gene Description
Pkd2	AF014010	Mm.6442	1	627	35	406	100	0.0144	1.54	polycystic kidney disease 2

TRANSCRIPTION FACTORS/REGULATION OF TRANSCRIPTION

GeneSymbol	Genbank	Unigene	A/P	Ctl Mean	Ctl stdev	Exp Mean	Exp stdev	P-value	Fold Change	Gene Description
Trim30	AF220015	Mm.295578	0.9	151	40	247	26	0.01055	-1.63	tripartite motif protein 30
Hoxa13	NM_008264	Mm.333065	0.9	203	36	132	15	0.02345	1.54	homeo box A13
Tle4	AU045006	Mm.103638	0.5	594	62	360	57	0.0015	1.65	transducin-like enhancer of split 4, E(spl) homolog (Drosophila)
Zfp207	BB633247	Mm.102253	0.5	101	16	61	24	0.04264	1.65	zinc finger protein 207
Zic3	BB732077	Mm.255890	1	77	20	40	19	0.03432	1.94	zinc finger protein of the cerebellum 3
Hoxb1	AK017686	Mm.890	0.5	130	23	66	8	0.00626	1.97	homeo box B1
Etv1	NM_007960	Mm.4866	0.5	62	20	26	12	0.02678	2.41	ets variant gene 1

EXTRACELLULAR/MATRIX/CYTOPLASM

GeneSymbol	Genbank	Unigene	A/P	Ctl Mean	Ctl stdev	Exp Mean	Exp stdev	P-value	Fold Change	Gene Description

Inhbe	BC010404	Mm.3510	1	1415	434	3290	1030	0.02848	-2.33	inhibin beta E
Tor3a	NM_023141	Mm.206737	1	284	38	450	91	0.02814	-1.59	torsin family 3, member A
Tor3a	AV290846	Mm.206737	1	214	48	339	53	0.01324	-1.59	torsin family 3, member A
Fgf16	NM_030614	Mm.154768	0.8	229	33	129	44	0.01138	1.78	fibroblast growth factor 16
Pspn	NM_008954	Mm.86487	1	334	29	184	24	0.00024	1.81	persephin

RECEPTOR

GeneSymbol	Genbank	Unigene	A/P	Ctl Mean	Ctl stdev	Exp Mean	Exp stdev	P-value	Fold Change	Gene Description
Chrna2	BC011490	Mm.57350	0.5	331	200	768	134	0.01529	-2.32	cholinergic receptor, nicotinic, alpha polypeptide 2 (neuronal)
Cd36	AK004192	Mm.18628	1	1440	345	2985	758	0.02071	-2.07	CD36 antigen
Cd36	BE307351	Mm.18628	1	1553	453	3119	646	0.01069	-2.01	CD36 antigen
Cd36	BB534670	Mm.18628	1	248	101	418	58	0.03486	-1.68	CD36 antigen
Ifngr2	BB283936	Mm.249364	1	569	82	911	26	0.00141	-1.6	interferon gamma receptor 2
Mtnr1a	NM_008639	Mm.5133	1	393	28	599	63	0.0041	-1.52	melatonin receptor 1A
Htr3a	NM_013561	Mm.4831	0.6	1006	182	647	42	0.03143	1.55	5-hydroxytryptamine (serotonin) receptor 3A
Drd2	NM_010077	Mm.41970	0.5	150	13	90	22	0.00647	1.65	dopamine receptor 2
Ors18	NM_020290	Mm.89146	1	191	43	110	40	0.03378	1.74	olfactory receptor 690
V1rb7	NM_053228	Mm.321507	0.5	94	29	48	18	0.047	1.95	vomeronasal 1 receptor, B7

SIGNAL TRANSDUCTION

GeneSymbol	Genbank	Unigene	A/P	Ctl Mean	Ctl stdev	Exp Mean	Exp stdev	P-value	Fold Change	Gene Description
Pex11a	AV377516	Mm.20615	1	2447	912	4367	585	0.01649	-1.78	adaptor-related protein complex 3, sigma 2 subunit
Pex11a	NM_011068	Mm.20615	1	5587	1281	8407	1684	0.03729	-1.5	adaptor-related protein complex 3, sigma 2 subunit
Rgs17	NM_019958	Mm.44606	1	150	23	96	23	0.01805	1.56	regulator of G-protein signaling 17

POST-TRANSLATIONAL MODIFICATION

GeneSymbol	Genbank	Unigene	A/P	Ctl Mean	Ctl stdev	Exp Mean	Exp stdev	P-value	Fold Change	Gene Description
Sphk2	AF245448	Mm.24222	1	722	224	1268	205	0.01159	-1.76	sphingosine kinase 2
Prkcn	NM_029239	Mm.252776	1	2342	370	3684	740	0.03169	-1.57	protein kinase C, nu
Gmfb	BG066438	Mm.87312	1	206	15	318	52	0.01494	-1.54	glia maturation factor, beta
Cask	NM_009806	Mm.253779	0.5	178	43	110	28	0.04668	1.62	calcium/calmodulin-dependent serine, Y protein kinase
Mark1	AF453686	Mm.7445	0.5	173	44	106	22	0.04328	1.63	ELKL motif serine-threonine protein kinase 3

MITOCHODRION

GeneSymbol	Genbank	Unigene	A/P	Ctl Mean	Ctl stdev	Exp Mean	Exp stdev	P-value	Fold Change	Gene Description
Mte1	NM_134188	Mm.45431	1	8317	3469	14482	2850	0.03347	-1.74	mitochondrial acyl-CoA thioesterase 1
Decr1	NM_026172	Mm.24395	1	1724	344	2746	416	0.00914	-1.59	2,4-dienoyl CoA reductase 1, mitochondrial
Bcl2l	BM228788	Mm.238213	1	1468	189	883	88	0.00501	1.66	Bcl2-like

MEMBRANE

GeneSymbol	Genbank	Unigene	A/P	Ctl Mean	Ctl stdev	Exp Mean	Exp stdev	P-value	Fold Change	Gene Description
Abcc6	NM_018795	Mm.63514	1	996	180	2500	521	0.00552	-2.51	ATP-binding cassette, sub-family C (CFTR/MRP), member 6
Gca	BC021450	Mm.219877	0.5	23	17	50	10	0.04339	-2.14	grancalcin, EF-hand calcium binding protein
Ttgn1	BB775176	Mm.4142	1	8342	4154	17415	3471	0.01539	-2.09	trans-golgi network protein 1
H2-D1	X00246	Mm.299320	0.5	103	53	190	33	0.03947	-1.84	olfactory receptor MOR218-1
Clstn3	AV341395	Mm.193701	1	1700	837	3079	115	0.04698	-1.81	calsyntenin 3
Slc22a5	NM_011396	Mm.42253	1	2108	667	3662	925	0.04158	-1.74	solute carrier family 22 (organic cation transporter), member 5
Elovl5	NM_134255	Mm.19130	1	13303	1978	22698	2067	0.0006	-1.71	ELOVL family member 5, elongation of long chain fatty acids (yeast)
Tgoln1	BF228156	Mm.246563	1	2831	634	4631	955	0.02566	-1.64	trans-golgi network protein
Slc22a5	AF111425	Mm.42253	1	1203	400	1938	169	0.02789	-1.61	solute carrier family 22 (organic cation transporter), member 5
Slc4a4	NM_018760	Mm.41044	1	610	208	932	114	0.04264	-1.53	solute carrier family 4 (anion exchanger), member 4
Tde1	NM_012032	Mm.4962	1	4419	743	2888	779	0.02945	1.53	tumor differentially expressed 1
Tde1	BE691746	Mm.4962	1	7812	1624	5025	1156	0.03826	1.55	tumor differentially expressed 1
Vps11	AK004695	Mm.295013	1	847	39	493	171	0.02772	1.72	vacuolar protein sorting 11 (yeast)
Vcam1	NM_011693	Mm.76649	1	426	41	246	73	0.00792	1.73	vascular cell adhesion molecule 1
Efna3	AA388313	Mm.8547	0.5	261	47	146	29	0.00955	1.78	ephrin A3
Cav2	NM_016900	Mm.31915	1	316	98	163	32	0.04172	1.94	caveolin 2
Lect1	NM_010701	Mm.46561	0.8	329	95	158	61	0.03007	2.08	leukocyte cell derived chemotaxin 1

NUCLEIC ACID ASSOCIATED PROTEINS

GeneSymbol	Genbank	Unigene	A/P	Ctl Mean	Ctl stdev	Exp Mean	Exp stdev	P-value	Fold Change	Gene Description
Sfrs3	AV135383	Mm.6787	1	413	29	650	97	0.0097	-1.57	splicing factor, arginine/serine-rich 3 (SRp20)
Hrb	CA748278	Mm.6461	1	176	19	267	47	0.02407	-1.52	HIV-1 Rev binding protein
Hnrph1	BB164501	Mm.21740	0.6	294	53	191	50	0.03093	1.54	heterogeneous nuclear ribonucleoprotein H1
Snrpa1	BC013777	Mm.821	1	335	11	208	30	0.00136	1.61	small nuclear ribonucleoprotein polypeptide A'
Gmnn	NM_020567	Mm.12239	1	386	83	234	49	0.02607	1.65	geminin

PROTEIN CATABOLISM

GeneSymbol	Genbank	Unigene	A/P	Ctl Mean	Ctl stdev	Exp Mean	Exp stdev	P-value	Fold Change	Gene Description
Pace4	BI157485	Mm.294007	1	1364	279	2636	602	0.01855	-1.93	paired basic amino acid cleaving system 4
Pcsk5	D17583	Mm.3401	0.5	337	51	224	20	0.01483	1.5	proprotein convertase subtilisin/kexin type 5
Siah1a	AA982064	Mm.6765	1	526	71	344	63	0.00901	1.53	seven in absentia 1A

MISCELLANIOUS

GeneSymbol	Genbank	Unigene	A/P	Ctl Mean	Ctl stdev	Exp Mean	Exp stdev	P-value	Fold Change	Gene Description
Fsp27	BB221402	Mm.10026	1	223	124	1040	403	0.01795	-4.65	fat specific gene 27
Lamb3	NM_008484	Mm.287014	1	206	87	565	42	0.00176	-2.73	laminin, beta 3
Unc119	BC001990	Mm.284811	0.5	265	103	469	85	0.02249	-1.77	unc-119 homolog (C. elegans)
Olfm3	BB667895	Mm.54183	1	57	8	94	15	0.00916	-1.65	Mus musculus similar to olfactomedin 3 (LOC381467)
Stxbp2	AI314898	Mm.7247	0.6	435	99	716	145	0.02419	-1.64	syntaxin binding protein 2
Ysg2	BM248160	Mm.196345	1	371	114	586	106	0.03404	-1.58	yolk sac gene 2
PRUNEM1	BQ176370	Mm.322809	1	672	107	1058	124	0.00335	-1.58	PIHUSD salivary proline-rich glycoprotein precursor PRB4
Tor1b	BC018456	Mm.249164	1	504	82	782	108	0.00651	-1.55	torsin family 1, member B
Rtn4	AK003859	Mm.192580	1	3970	574	6010	817	0.00953	-1.51	reticulon 4
S100a8	NM_013650	Mm.21567	1	228	40	151	25	0.02239	1.51	S100 calcium binding protein A8 (calgranulin A)
Sec61a1	AF145253	Mm.28375	1	1949	274	1266	201	0.01024	1.54	Sec61 alpha 1 subunit (S. cerevisiae)
Magea3	NM_020018	Mm.196413	0.5	82	7	53	16	0.03221	1.55	melanoma antigen, family A, 3
Stxbp3	AI528529	Mm.12155	0.5	59	8	38	6	0.00861	1.55	syntaxin binding protein 3
Nedd9	BB458177	Mm.8315	0.8	247	55	158	20	0.03958	1.56	neural precursor cell expressed, developmentally down-regulated gene 9
Slitl2	BB530515	Mm.23090	1	121	23	67	16	0.01354	1.78	SLITL2: slit-like 2 (Drosophila)
Trim10	NM_011280	Mm.20159	0.8	272	39	150	54	0.01476	1.81	tripartite motif protein 10
Wdfy1	BM233251	Mm.293273	1	762	123	421	169	0.0225	1.81	WD repeat and FYVE domain containing 1

UNKNOWN

GeneSymbol	Genbank	Unigene	A/P	Ctl Mean	Ctl stdev	Exp Mean	Exp stdev	P-value	Fold Change	Gene Description
D11Lgp2e	NM_030150	Mm.271830	0.8	33	29	123	35	0.00812	-3.65	DNA segment, Chr 11, Lothar Hennighausen 2, expressed
C80913	AV094811	Mm.23997	1	418	214	1377	331	0.00467	-3.29	expressed sequence C80913
2310021M12Rik	BC022922	Mm.142343	1	806	299	2044	428	0.00518	-2.54	RIKEN cDNA 2310021M12 gene
6330406P08Rik	AV059397	Mm.35817	1	371	132	846	144	0.00288	-2.27	RIKEN cDNA 6330406P08 gene
5430439H10Rik	AI607291	Mm.27372	0.9	92	41	184	30	0.01246	-2	RIKEN cDNA 5430439H10 gene
6330406P08Rik	AV059397	Mm.35817	1	451	203	892	261	0.03736	-1.98	RIKEN cDNA 6330406P08 gene
0610041D24Rik	NM_025341	Mm.181473	1	1528	365	2763	340	0.00258	-1.81	abhydrolase domain containing 6
0710001P09Rik	BY005192	Mm.20313	1	94	24	170	40	0.02416	-1.8	RIKEN cDNA 0710001P09 gene
BC016495	BC016495	Mm.211595	1	201	47	342	56	0.00855	-1.7	cDNA sequence BC016495
C230093N12Rik	BC023470	Mm.4065	0.5	106	38	180	39	0.03629	-1.69	RIKEN cDNA C230093N12 gene
1700127B04Rik	BI731645	Mm.218639	1	584	178	953	170	0.0243	-1.63	RIKEN cDNA 1700127B04 gene
D1Ertd396e	AV330655	Mm.289914	0.9	142	52	227	25	0.0435	-1.6	null
1110023P21Rik	NM_025390	Mm.22284	1	384	56	616	56	0.0011	-1.6	RIKEN cDNA 1110023P21 gene
0610039N19Rik	AI325050	Mm.146873	1	2435	502	3817	145	0.01326	-1.57	RIKEN cDNA 0610039N19 gene
1300006M19Rik	AK008203	Mm.18814	1	1688	532	2657	436	0.03052	-1.57	RIKEN cDNA 1300006M19 gene
4932416F07Rik	BC019143	Mm.98366	1	1700	205	2650	472	0.02103	-1.56	RIKEN cDNA 4932416F07 gene
D7Ertd156e	BC024503	Mm.274811	1	277	30	425	43	0.00264	-1.53	DNA segment, Chr 7, ERATO Doi 156, expressed
2610207I16Rik	AJ293845	Mm.272905	1	983	286	1501	207	0.0326	-1.53	RIKEN cDNA 2610207I16 gene
AB041661	NM_021403	Mm.271230	1	353	54	234	43	0.01386	1.51	null
2310016N21Rik	NM_023784	Mm.154776	1	581	126	383	82	0.04739	1.51	RIKEN cDNA 2310016N21 gene
NULL	BB549997	Mm.26817	1	281	49	186	41	0.02532	1.51	null
2610207I16Rik	BM200015	Mm.272905	1	3880	681	5864	914	0.01317	1.51	RIKEN cDNA 2610207I16 gene
2610036L13Rik	NM_026410	Mm.23526	0.8	378	29	249	80	0.03997	1.52	RIKEN cDNA 2610036L13 gene
2810439M05Rik	NM_026046	Mm.288316	0.5	124	26	81	18	0.04615	1.52	RIKEN cDNA 2810439M05 gene
BC025872	BC025872	Mm.265552	1	532	90	349	29	0.0183	1.53	null
5830413E08Rik	AK017926	Mm.21697	1	983	211	633	187	0.04783	1.55	RIKEN cDNA 5830413E08 gene
D2Ertd217e	AW551717	Mm.271147	1	379	26	244	38	0.00225	1.55	Mus musculus 18-day embryo whole body cDNA clone:1110065P14
4833442J19Rik	AV002340	Mm.274099	1	3150	519	1953	454	0.01336	1.61	RIKEN cDNA 4833442J19 gene

4833442J19Rik	AV002340	Mm.274099	1	3150	519	1953	454	0.01336	1.61	RIKEN cDNA 4833442J19 gene
4933416E05Rik	AV226931	Mm.139010	1	154	36	94	23	0.04037	1.63	RIKEN cDNA 4933416E05 gene
2400003B06Rik	CA566638	Mm.45233	1	1457	199	892	145	0.0059	1.63	RIKEN cDNA 2400003B06 gene
D430033M16Rik	BB826950	Mm.307020	0.5	226	42	138	56	0.04785	1.64	Mus musculus transcribed sequences
4732471D19Rik	BB750674	Mm.215784	1	160	33	97	15	0.02749	1.65	null
4632408A20Rik	BC002159	Mm.311831	1	177	34	105	40	0.03577	1.68	Mus musculus adult male hippocampus cDNA clone:C630031O06
1110051N18Rik	BC026506	Mm.287329	1	221	39	130	57	0.04833	1.7	RIKEN cDNA 1110051N18 gene
2900097C17Rik	AK013851	Mm.29909	1	320	28	187	84	0.04024	1.71	null
BC010304	BB324206	Mm.315118	0.8	484	101	282	72	0.0231	1.71	null
4930571B16Rik	AK016268	Mm.264649	1	365	51	204	64	0.00773	1.79	null
2010004A03Rik	AK008082	Mm.77697	0.8	384	104	213	16	0.04862	1.8	null
2010004A03Rik	AK008082	Mm.77697	0.8	384	104	213	16	0.04862	1.8	null
2510027J23Rik	AF439556	Mm.263163	1	119	14	65	22	0.0094	1.82	RWD domain containing 3
NULL	C79122	Mm.5791	0.5	141	18	76	31	0.01672	1.84	Mus musculus transcribed sequences
2900001A12Rik	NM_025971	Mm.275052	0.8	89	11	47	6	0.00145	1.88	RIKEN cDNA 2900001A12 gene
NULL	AK018829	Mm.41682.2	1	639	88	338	87	0.00286	1.89	null
1200020A08Rik	BB775592	Mm.109329	1	93	16	47	20	0.01219	1.96	RIKEN cDNA 1200020A08 gene
NULL	AK013540	Mm.33954.2	0.5	132	36	63	35	0.03417	2.1	null
1600014C10Rik	BI246839	Mm.57075	1	834	126	390	154	0.00434	2.14	RIKEN cDNA 1600014C10 gene
2310067E08Rik	BF168366	Mm.41423	0.5	36	6	16	11	0.02942	2.15	RIKEN cDNA 2310067E08 gene
NULL	BB507994	Mm.2797	0.8	151	35	59	35	0.01079	2.54	Mus musculus 0 day neonate thymus cDNA clone:A430079C03
0610005C13Rik	AI182092	Mm.200459	1	968	153	4724	11	0.00002	4.88	RIKEN cDNA 0610005C13 gene

Supplemental Table 5. Genes whose expression is altered in both gastrocnemius and anterior tibialis muscle in MGSKO mice.

GeneSymbol	Gene Description	Unigene	MGSKO Anterior Tibialis	MGSKO Gastrocnemius
Metabolism				
Gys1	Glycogen synthase 1	Mm.275654	-144.04[a]	-45.44[a]
Ppp1r1a	Protein phosphatase 1, regulatory inhibitor 1	Mm.143788	-9.98	-3.54
Dcxr	Dicarbonyl L-xylulose reductase	Mm.231091	-3.81	-2.81
Slc2a3	Glut3	Mm.269857	-3.23[a]	-1.94[a]
Adhfe1	Alcohol dehydrogenase, iron containing, 1	Mm.28514	-2.90[a]	-1.7
Pfkfb3	Fructose-2,6-biphosphatase 3	Mm.19669	-2.7	-2.11[a]
Acadsb	Acyl-Coenzyme A dehydrogenase	Mm.334274	-2.41	-1.76
Bckdhb	Branched chain ketoacid dehydrogenase E1	Mm.12819	-2.24	-1.56
Oxct	3-oxoacid CoA transferase	Mm.13445	-2.15[b]	-1.72
Odc	Ornithine decarboxylase, structural	Mm.34102	-2.10[b]	-3.39[b]
Gpt2	Glutamic pyruvate transaminase 2	Mm.200423	-1.93[b]	-1.53
Amd1	S-adenosylmethionine decarboxylase 1	Mm.253533	-1.79	-2.61[a]
RS1	Regulatory solute carrier protein	Mm.17880	-1.75	-2.04
Cyp27a1	Cytochrome P450	Mm.85083	-1.7	-2.61
Glul	Glutamate-ammonia ligase (glutamine synthase)	Mm.210745	-1.63[a]	-1.5
Acads	Acyl-Coenzyme A dehydrogenase, short chain	Mm.18759	-1.59	-1.63
Dbt	Dihydrolipoamide branched chain transacylase E2	Mm.3636	-1.5	-1.52
Car14	Carbonic anhydrase 14	Mm.306954	1.54	1.88
Gpsn2	Steroid 5 alpha-reductase 2	Mm.352239	1.72[a]	1.70[a]
Ugp2	UDP-glucose pyrophosphorylase 2	Mm.28877	1.78[a]	1.60[a]
Gbe1	Glucan (1,4-alpha-), branching enzyme 1	Mm.29201	2.26	1.89
Aacs	Acetoacetyl-CoA synthetase	Mm.296918	3.83[a]	2.61[a]
Muscle/Contractile Proteins				
Ddit4l	Ddit4l DNA-damage-inducible transcript 4-like	Mm.250841	-2.28[a]	-2.52[a]
Ptk9l	PTK9 protein typrotein tyrosine kinase 9-like	Mm.274346	-1.62	-1.6
Kif1b	Kinesin family member 1B	Mm.252497	1.52[a]	1.61
Cryab	Crystallin, alpha B	Mm.178	1.58	1.58
Macf1	Microtubule-actin crosslinking factor 1	Mm.3350	1.67	1.62
Mid1ip1	Mid1 interacting protein 1	Mm.29429	1.93	2.53
Aqp4	Aquaporin 4, skeletal muscle water channel	Mm.298599	1.95	3.12
Actc1	Actin, alpha, cardiac	Mm.686	2.21	2.45
Mybph	Myosin binding protein H, Adenosine A1 receptor	Mm.373556	2.65	1.82
Myl3	Myosin, light polypeptide 3	Mm.7353	4.66[b]	2.15[b]
Receptors and Signaling				
Wnt4	Wingless-related MMTV integration site 4	Mm.20355	-5.64	-1.84
Dkk3	Dickkopf homolog 3 (Xenopus laevis)	Mm.55143	-4.38	-4.2[a]
Tnfrsf19	Tumor necrosis factor receptor, member 19	Mm.281356	-2.62	-2.01[a]
Fgfbp1	Fibroblast growth factor binding protein 1	Mm.46053	-1.99	-4.66
2310043K02Rik	Phosphoprotein phosphatase activity	Mm.23916	-1.94	-3.15
C330021A05Rik	Rab-related GTP-binding protein	Mm.271656	-1.72	-1.78
Styx	Phosphoserine/threonine/tyrosine interaction	Mm.202561	-1.59	-1.67
Mapkapk5	MAP kinase-activated protein kinase 5	Mm.272206	1.54	1.97
1810073P09Rik	Kinase activity	Mm.342723	1.54	1.87
Chrna1	Cholinergic receptor, nicotinic, alpha polypeptide 1	Mm.4583	1.69	1.5
Ppap2a	Phosphatidic acid phosphatase 2a	Mm.317186	1.71[a]	1.59
Pkn1	Protein kinase N1	Mm.213000	1.74	2
Dusp6	Dual specificity phosphatase 6	Mm.1791	1.78	1.76
Stk2	STE20-like kinase	Mm.281011	2.06	1.51
2310047C17Rik	Intracellular signaling cascade	Mm.203866	2.19[a]	1.71[b]
Ntsr2	Neurotensin receptor 2	Mm.281715	3.5	1.86
Nucleic Acid Associated Proteins				
Creg	Cellular repressor of E1A-stimulated genes	Mm.294885	-1.89[a]	-2.12[a]
Asb4	Ankyrin repeat, SOCS box-containing protein 4	Mm.51340	-1.69	-1.94[a]
Pop4	Processing of precursor 4	Mm.22284	-1.69	-1.55
2510005D08Rik	N-methyltransferase	Mm.45225	-1.58	-1.74[a]
Tfip11	Tuftelin interacting protein 11, AA407270	Mm.27585	1.6	2.17
Zfp292/Zn16	Zinc finger protein 292	Mm.38193	1.61	1.73
Ankrd32	Ankyrin repeat domain 32	Mm.209730	1.76	1.86
Smarca1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin	Mm.229151	2.76	2.67

Integral to Membrane

Gdap1	Ganglioside-induced differentiation-associated-1	Mm.18218	-3.66	-1.6
1810057C19Rik	Integral to membrane	Mm.212428	-3.12	-4.29
Slc40a1	Solute carrier family 40, member 1	Mm.28756	-1.92	-1.75
H47	Histocompatibility 47	Mm.22362	-1.92[a]	-1.54
1300010A20Rik	Integral to membrane	Mm.225289	-1.9	-1.79
Slc25a20	Solute carrier family 25, member 20	Mm.29666	-1.89	-1.61
Daf1	Decay accelerating factor 1	Mm.101591	1.57	1.54
Atp1b2	ATPase, Na+/K+ transporting, beta	Mm.235204	1.71	1.51
Atp1b4	ATPase, Na+/K+ transporting, beta 4 polypeptide	Mm.60134	3.42	1.6

Other

1810008K03Rik	RIKEN cDNA 1810008K03 gene	Mm.35083	-2.63	-1.67
Gstk1	Glutathione S-transferase kappa 1	Mm.267014	-2.03	-1.85
Pace4	Paired basic amino acid cleaving system 4	Mm.294007	-1.76	-1.59
L0273G12 3'	AW556821	Mm.254283	-1.74	-1.86
Sepx1	Selenoprotein X 1, cellular protein metabolism	Mm.28212	-1.72	-1.53
As3mt	Arsenic (+3 oxidation state) methyltransferase	Mm.28566	-1.69	-1.58
Oplah	5-oxoprolinase (ATP-hydrolysing)	Mm.322738	-1.65	-1.82
2810432L12Rik	RIKEN cDNA 2810432L12 gene	Mm.24564	1.7	1.98
Ptx3	Pentaxin related gene	Mm.276776	1.78	1.85
2700038N03Rik	RIKEN cDNA 2700038N03 gene	Mm.124666	1.79	1.83
Hn1	Hematological/neurological expressed seq 1	Mm.1775	1.88[a]	1.52
0610013D04Rik	RIKEN cDNA 0610013D04 gene, D17Ertd288e	Mm.196330	1.91	1.76
D5Ertd593e	DNA segment, Chr 5, ERATO Doi 593, expressed	Mm.21965	1.92	1.97
2610042L04Rik	RIKEN cDNA 2610042L04 gene	Mm.321089	1.98[a]	1.93

a: Average of 2 probe sets detected in this experiment
b: Average of 3 probe sets detected in this experiment