

Lens ER-stress response during cataract development in *Mip*-mutant mice

Yuefang Zhou, Thomas M. Bennett, and Alan Shiels

Supplemental Data

Supplemental Figure 1. Boxplot analysis of non-normalized raw microarray data for *Lop/+* and wild-type mouse lenses at P1 and P7.

Supplemental Figure 2. Validation of selected gene expression in the *Lop/+* lens (P7). (A) qPCR analysis confirms up-regulation of *Hspa5* and *Ddit3* transcripts. End-point RT-PCR confirms splicing of *Xbp1* transcripts (B) and up-regulation of *Ddit3*, *Chac1*, *Retnla*, and *Cox6a2* transcripts (C). D. Immunoblot analysis confirms up-regulation of p62.

Supplemental Figure 3. Immunofluorescence imaging of *Ddit3* expression in the *Lop/+* mouse lens. Sagittal cryo-sections of wild-type (A and B) and *Lop/+* (C and D) lenses (P7) stained (red) with anti-GADD153/DDIT3/CHOP (A and C) merged with DAPI staining (blue) of cell nuclei (B and D). Note immunostaining is restricted to nuclei of degenerating fiber cells toward the center of the *Lop/+* lens (C and D).

Supplemental Table 1. PCR primers used for end-point RT-PCR amplification

Supplemental Table 2. E14 *Lop/+* lens differentially regulated genes (>1.3-fold) detected by microarray analysis (Mouse-6 BeadChip).

Supplemental Table 3. P7 *Lop/+* lens differentially regulated genes (>2-fold, $p < 0.05$) detected by microarray analysis (Mouse-Ref8 BeadChip).

Supplemental Table 4. P1 *Lop/+* lens differentially regulated genes (>2-fold, $p < 0.05$) detected by microarray analysis (Mouse-Ref8 BeadChip).

Supplemental Table 5. P1 *Lop/+* lens pathway analysis using the KEGG database

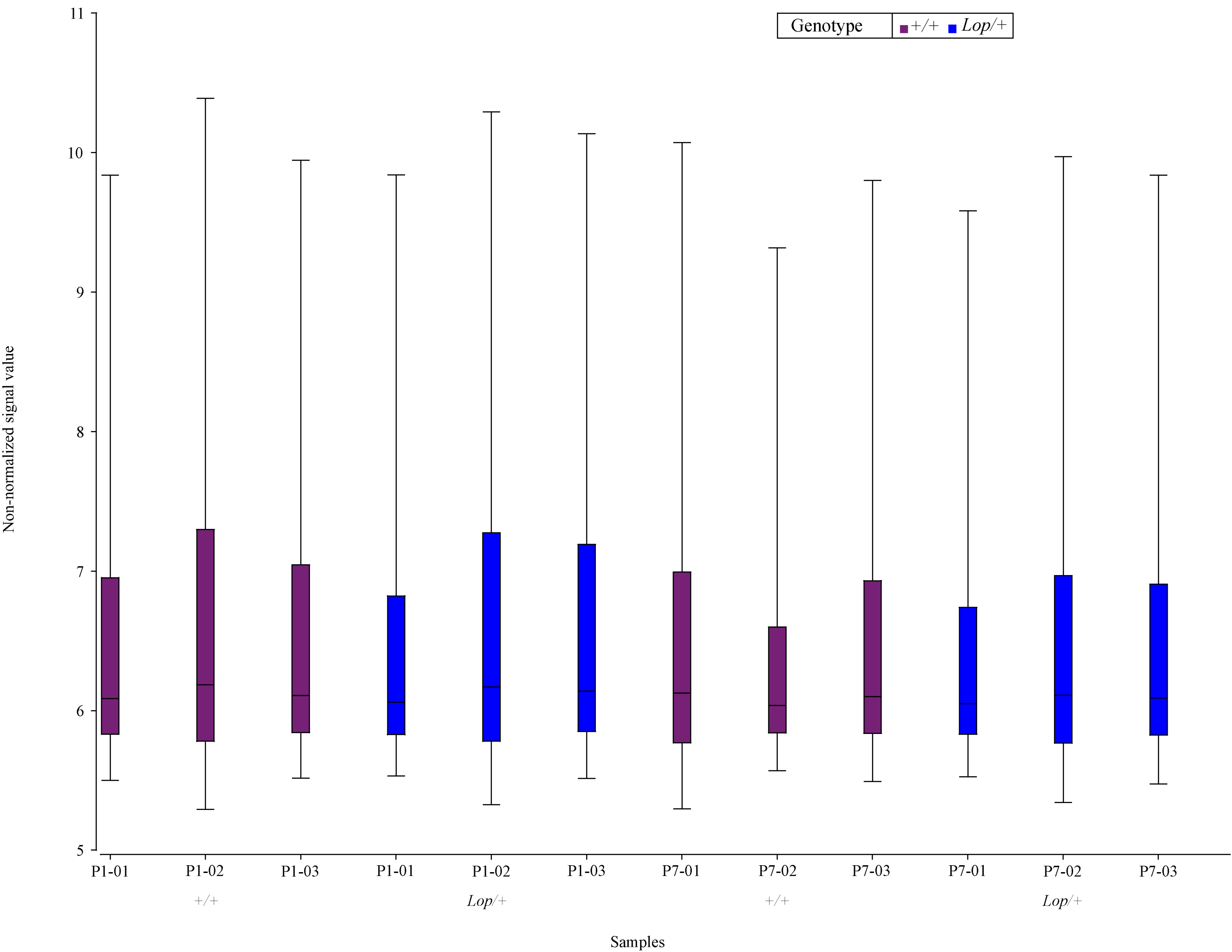
Supplemental Table 6. P7 *Lop/+* lens pathway analysis using the KEGG database

Supplemental Table 7. P7 *Lop/+* lens pathway analysis using the GO database

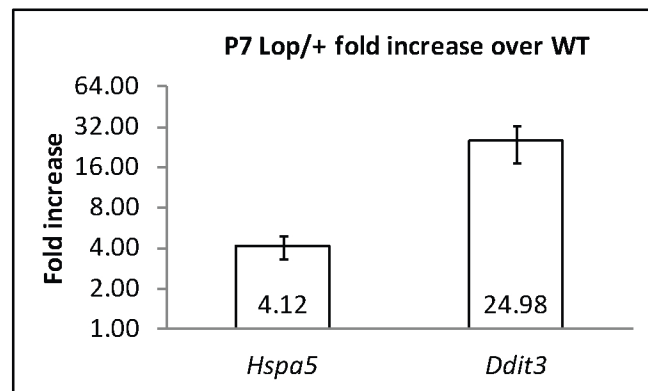
Supplemental Table 8. P7 *Lop/+* lens differentially regulated genes detected by UPR qPCR-array

Supplemental Table 9. P1 *Lop/+* lens differentially regulated genes detected by UPR qPCR-array

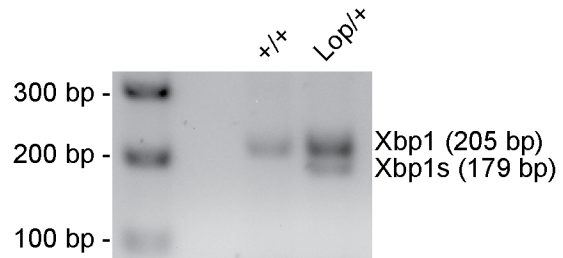
Supplemental Fig 1



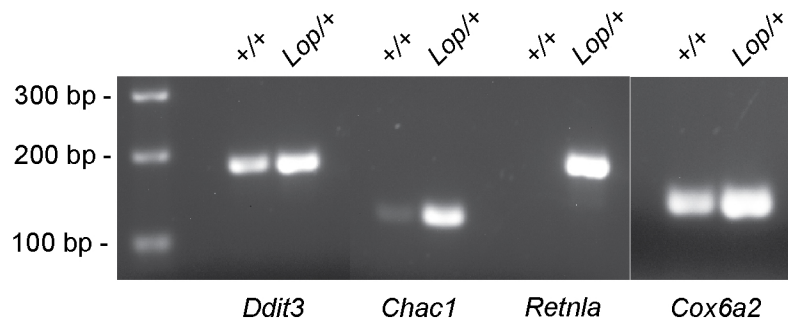
A



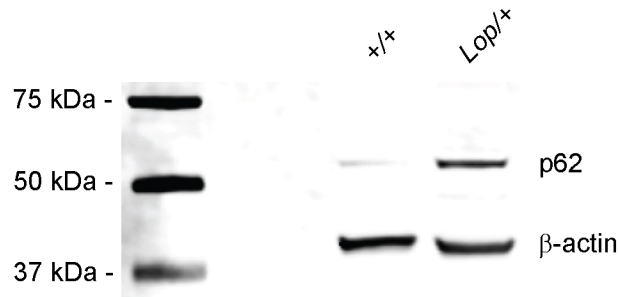
B



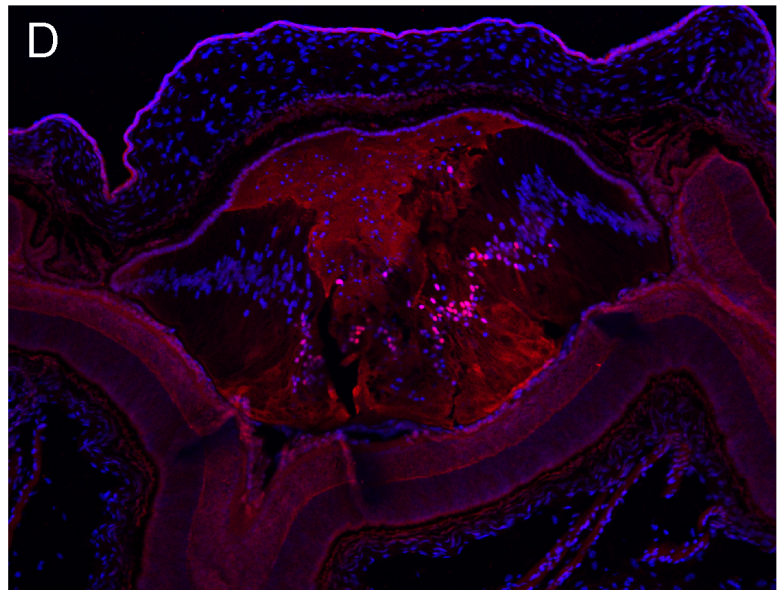
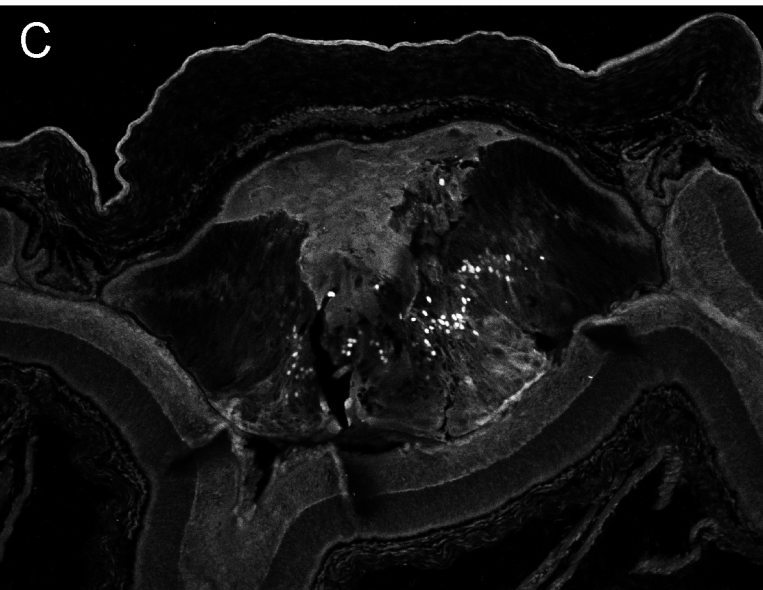
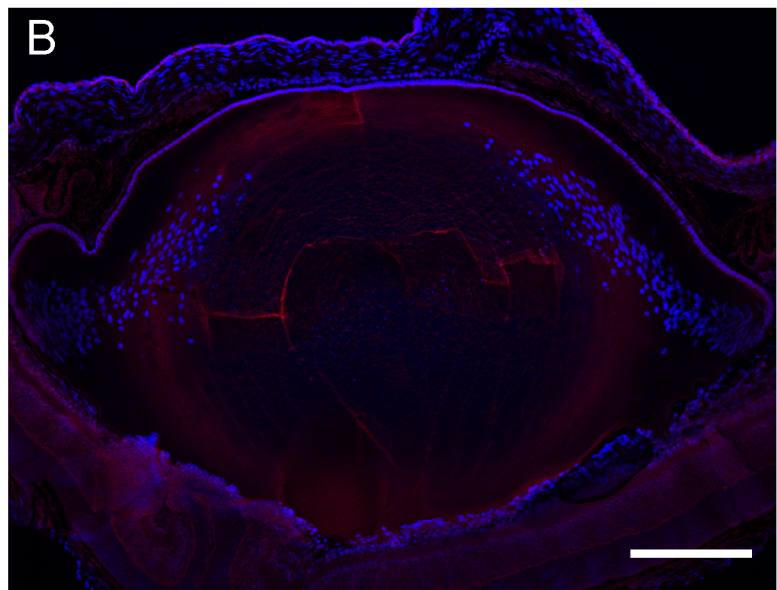
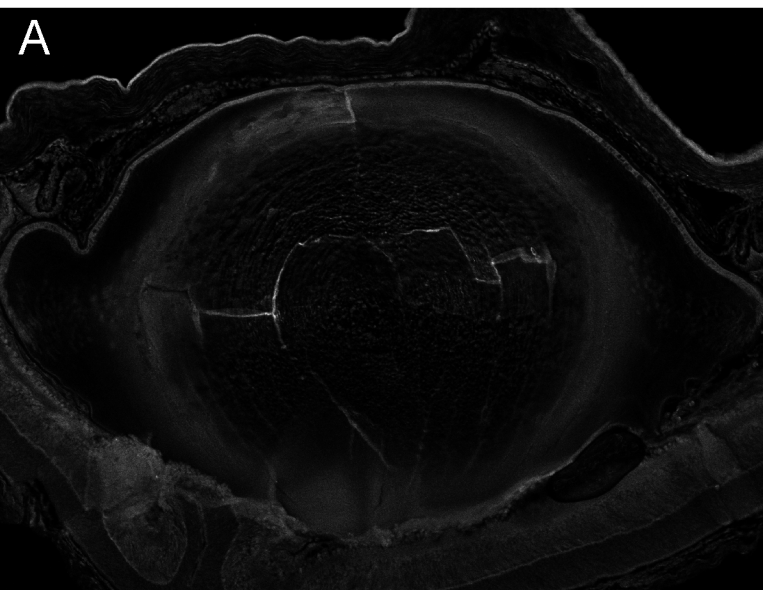
C



D



Supplemental Fig. 3



Supplemental Table 1

Name	Sequence (5' - 3')	Amplicon size (bp)
Chac1 RTF	CTGTGGATTTTCGGGTACGG	122
Chac1 RTR	CCCCTATGGAAGGTGTCTCC	
Cox6A2 RTF	CTGCTCCCTTAAGTCTGGAT	128
Cox6A2 RTR	GATTGTGGAAAAGCGTGTGGT	
Ddit3 RTF	CTGCCTTTCACCTTGGAGAC	178
Ddit3 RTR	CTGTCAGCCAAGCTAGGGAC	
Sqstm1 RTF	ATGTGGAACATGGAGGGAAGA	294
Sqstm1 RTR	GGAGTTCACCTGTAGATGGGT	
Xbp1_RTf	GAACCAGGAGTTAAGAACACG	205/179
Xbp1_RTR	AGGCAACAGTGTCTAGAGTCC	
MipUps-F	AAGGGGTAAAGAGGCAGAGC	307 bp (Ups-F to 151G-R)
Mip151G-R	CTGCACCAATGTAGCCAAGGC	
Mip151C-F	TGGCTTTGGCCTTTGGCCTGC	215 bp (151C-F to 345R)
Mip345R	GTTTCCTCGGACAGCTGGTGG	481 bp (Ups-F to 345R)

Supplemental Table 2

Gene symbol	Fold-Change (E14 * Lop/+ vs. E14 * WT)	p-value (E14 * Lop/+ vs. E14 * WT)
<i>Birc7</i>	1.6945	0.46
<i>mt-Nd4</i>	1.6872	0.37
<i>LOC676420</i>	1.6774	0.34
<i>mtDNA_ND2</i>	1.6322	0.54
<i>Atp6v1b2</i>	1.6261	0.11
<i>Nupr1</i>	1.6128	0.17
<i>Hmox1</i>	1.5977	0.48
<i>mtDNA_ND4</i>	1.5849	0.32
<i>Ank2</i>	1.5777	0.16
<i>LOC381283</i>	1.5701	0.35
<i>mtDNA_ND5</i>	1.5406	0.34
<i>Abi2</i>	1.5106	0.34
<i>mtDNA_COXII</i>	1.4927	0.61
<i>LOC100048638</i>	1.4816	0.65
<i>Stx11</i>	1.4702	0.60
<i>Ndel1</i>	1.4671	0.36
<i>Fat1</i>	1.4604	0.36
<i>LOC385699</i>	1.4527	0.49
<i>Prickle1</i>	1.4498	0.56
<i>Scn11a</i>	1.4444	0.43
<i>Rai14</i>	1.4414	0.34
<i>Iars</i>	1.4410	0.34
<i>LOC100048105</i>	1.4372	0.58
<i>Lama1</i>	1.4367	0.48
<i>mt-Nd1</i>	1.4335	0.69
<i>Sqstm1</i>	1.4316	0.17
<i>Dnase2b</i>	1.4290	0.49
<i>Sema5a</i>	1.4258	0.57
<i>mtDNA_ATP8</i>	1.4237	0.50
<i>Shc1</i>	1.4221	0.46
<i>Mboat1</i>	1.4194	0.40
<i>Prdm16</i>	1.4185	0.24
<i>LOC100043671</i>	1.4183	0.28
<i>Inpp5a</i>	1.4118	0.40
<i>Scd2</i>	1.4085	0.50
<i>Ubg</i>	1.4059	0.53
<i>Ctnna1</i>	1.4046	0.34
<i>Nid1</i>	1.3987	0.68
<i>mt-Cytb</i>	1.3933	0.34
<i>Frag1</i>	1.3929	0.39
<i>Sema5a</i>	1.3893	0.65
<i>Rnf145</i>	1.3874	0.16
<i>Ccdc117</i>	1.3866	0.55
<i>Spnb1</i>	1.3813	0.34

Supplemental Table 2

<i>LOC100044124</i>	1.3807	0.59
<i>Lamc1</i>	1.3721	0.32
<i>Col4a2</i>	1.3701	0.49
<i>Snx18</i>	1.3695	0.71
<i>Hectd1</i>	1.3686	0.32
<i>Nisch</i>	1.3664	0.50
<i>Actn2</i>	1.3648	0.69
<i>Ftl1</i>	1.3629	0.54
<i>Peg3</i>	1.3620	0.58
<i>Tcp1</i>	1.3588	0.51
<i>1110014O20Rik</i>	1.3581	0.46
<i>Spna2</i>	1.3562	0.28
<i>Slc7a11</i>	1.3531	0.42
<i>Ube2o</i>	1.3528	0.71
<i>LOC100048105</i>	1.3520	0.60
<i>B3gnt5</i>	1.3493	0.72
<i>Slc39a7</i>	1.3407	0.34
<i>Synm</i>	1.3394	0.35
<i>Frag1</i>	1.3357	0.52
<i>Gbf1</i>	1.3343	0.57
<i>Csnk1g3</i>	1.3316	0.45
<i>LOC383099</i>	1.3305	0.72
<i>0610010I05Rik</i>	1.3296	0.72
<i>Zmym2</i>	1.3269	0.58
<i>Eif5</i>	1.3253	0.57
<i>0610040O15Rik</i>	1.3252	0.16
<i>App</i>	1.3238	0.76
<i>Herc2</i>	1.3220	0.35
<i>Ccng1</i>	1.3208	0.57
<i>Cnrip1</i>	1.3207	0.53
<i>mtDNA_CytB</i>	1.3206	0.34
<i>LOC100045882</i>	1.3205	0.55
<i>Herpud1</i>	1.3200	0.78
<i>Fads1</i>	1.3195	0.58
<i>Tmbim6</i>	1.3195	0.57
<i>Psmc1</i>	1.3185	0.46
<i>Gadd45a</i>	1.3166	0.56
<i>Igfbp5</i>	1.3162	0.69
<i>Pbrm1</i>	1.3160	0.34
<i>Ubap2</i>	1.3119	0.57
<i>Hspa8</i>	1.3100	0.81
<i>Efna5</i>	1.3095	0.47
<i>Ccnd2</i>	1.3089	0.55
<i>Chordc1</i>	1.3085	0.59
<i>Sept8</i>	1.3079	0.36
<i>Pappa</i>	1.3070	0.47
<i>Kif1b</i>	1.3054	0.43

Supplemental Table 2

<i>Mast4</i>	1.3048	0.34
<i>Sec16a</i>	1.3037	0.46
<i>Spnb3</i>	1.3022	0.45
<i>LOC100048105</i>	1.3018	0.65
<i>LOC100041500</i>	-1.3024	0.40
<i>2310039H08Rik</i>	-1.3114	0.46
<i>1810037I17Rik</i>	-1.3122	0.56
<i>Hist1h1c</i>	-1.3170	0.80
<i>2210013O21Rik</i>	-1.3171	0.36
<i>Hist1h1c</i>	-1.3277	0.75
<i>Esam</i>	-1.3281	0.43
<i>Hbb-bh1</i>	-1.3283	0.35
<i>Npm3</i>	-1.3287	0.36
<i>Fez1</i>	-1.3349	0.58
<i>Hbb-b1</i>	-1.3418	0.81
<i>Hba-x</i>	-1.3470	0.59
<i>Rtn1</i>	-1.3472	0.76
<i>E130112E08Rik</i>	-1.3473	0.80
<i>Sox9</i>	-1.3525	0.46
<i>2410006H16Rik</i>	-1.3572	0.45
<i>0610007P14Rik</i>	-1.3585	0.34
<i>Tcfap2b</i>	-1.3627	0.67
<i>Mgp</i>	-1.3727	0.46
<i>Acta2</i>	-1.3761	0.69
<i>0610006I08Rik</i>	-1.3775	0.39
<i>Stfa1</i>	-1.3804	0.94
<i>Mt1</i>	-1.3905	0.83
<i>Stfa1</i>	-1.3922	0.95
<i>Npm3-ps1</i>	-1.4129	0.17
<i>Ttr</i>	-1.4179	0.77
<i>Cdk5r1</i>	-1.4338	0.65
<i>Slc4a1</i>	-1.4395	0.40
<i>EG434402</i>	-1.4461	0.44
<i>Sox11</i>	-1.4570	0.57
<i>Eraf</i>	-1.4763	0.36
<i>S100a8</i>	-1.5387	0.66
<i>Hbb-b1</i>	-1.6495	0.34
<i>LOC100045403</i>	-1.6523	0.72
<i>Hbb-y</i>	-1.6677	0.74
<i>Hbb-y</i>	-1.9486	0.57

Supplemental Table 3

ILMN_Gene	log2FC (Het vs WT)	Fold Change (Het vs WT)	CI.L	CI.R	AveExpr	t	P.Value	adj.P.Val	B	DEFINITION	ENTREZ_GEN E_ID	CYTOBAND
CHAC1	6.3956	84.1904	5.8633	6.9278	8.9723	26.0267	2.20E-12	6.73E-09	18.0984	Mus musculus ChaC, cation transport regulator-like 1 (E. coli) (Chac1), mRNA.	69065	2qE5
COX6A2	4.9092	30.0486	4.5625	5.2559	11.4451	30.6720	2.83E-13	1.30E-09	19.6262	Mus musculus cytochrome c oxidase, subunit VI a, polypeptide 2 (Cox6a2), nuclear gene encoding mitochondrial protein, mRNA.	12862	7qF3
RETNLA	4.0537	16.6070	3.4747	4.6327	7.8015	15.1643	1.68E-09	9.09E-07	12.2947	Mus musculus resistin like alpha (Retnla), mRNA.	57262	16qB5
DDIT3	3.5623	11.8131	2.8715	4.2532	8.7083	11.1690	6.30E-08	1.38E-05	8.7656	Mus musculus DNA-damage inducible transcript 3 (Ddit3), mRNA.	13198	10qD3
EMP1	3.4874	11.2155	2.5184	4.4564	9.0782	7.7955	3.48E-06	1.97E-04	4.7089	Mus musculus epithelial membrane protein 1 (Emp1), mRNA.	13730	6qG1
FOS	3.4287	10.7685	2.9345	3.9230	7.2473	15.0261	1.88E-09	9.58E-07	12.1899	Mus musculus FBJ osteosarcoma oncogene (Fos), mRNA.	14281	12qD2
IL4	3.0930	8.5327	2.4329	3.7531	9.7319	10.1483	1.89E-07	2.79E-05	7.6635	Mus musculus interleukin 4 (Il4), mRNA.	16189	11qB1.3
HYAL1	3.0694	8.3944	2.7829	3.3559	8.3377	23.2039	9.17E-12	1.68E-08	16.9505	Mus musculus hyaluronoglucosaminidase 1 (Hyal1), mRNA.	15586	9qF1
PLK3	3.0636	8.3606	2.8505	3.2768	8.8272	31.1298	2.35E-13	1.30E-09	19.7567	Mus musculus polo-like kinase 3 (Plk3), mRNA	12795	4 D1
ACTG2	3.0576	8.3259	2.1268	3.9884	6.1892	7.1150	9.05E-06	3.97E-04	3.7290	Mus musculus actin, gamma 2, smooth muscle, enteric (Actg2), mRNA.	11468	6qC3
FAM115C	3.0097	8.0541	2.7514	3.2681	7.8521	25.2358	3.23E-12	7.41E-09	17.7958	Mus musculus family with sequence similarity 115, member C (Fam115c), mRNA.	232748	6qB2.1
EAR11	2.9368	7.6568	2.3975	3.4760	6.7401	11.7968	3.33E-08	8.26E-06	9.3976	Mus musculus eosinophil-associated, ribonuclease A family, member 11 (Ear11), mRNA.	93726	14qC1
TNFRSF12A	2.9116	7.5247	2.5043	3.3190	8.7249	15.4821	1.31E-09	8.59E-07	12.5316	Mus musculus tumor necrosis factor receptor superfamily, member 12a (Tnfrsf12a), mRNA.	27279	17qA3.3
CCK	2.7843	6.8889	2.1763	3.3922	6.9235	9.9196	2.45E-07	3.31E-05	7.4028	Mus musculus cholecystokinin (Cck), mRNA.	12424	9qF4
ARG1	2.6286	6.1843	1.9731	3.2842	6.2751	8.6851	1.08E-06	9.53E-05	5.9007	Mus musculus arginase 1, liver (Arg1), mRNA.	11846	10qA4
ADRB2	2.5858	6.0033	2.2066	2.9650	7.1593	14.7699	2.31E-09	1.01E-06	11.9928	Mus musculus adrenergic receptor, beta 2 (Adrb2), mRNA.	11555	18qE1
CCL7	2.5779	5.9705	2.1876	2.9681	6.8993	14.3088	3.39E-09	1.41E-06	11.6285	Mus musculus chemokine (C-C motif) ligand 7 (Ccl7), mRNA.	20306	11qC
1700029G01RIK	2.4831	5.5908	2.0835	2.8826	7.4774	13.4607	7.03E-09	2.80E-06	10.9242	Mus musculus RIKEN cDNA 1700029G01 gene (1700029G01Rik), mRNA.	66938	4qD2.2
SQSTM1	2.3882	5.2352	2.1249	2.6515	11.8187	19.6456	7.18E-11	7.31E-08	15.1906	Mus musculus sequestosome 1 (Sqstm1), mRNA.	18412	11qB1.3
ATF3	2.3716	5.1752	1.7337	3.0095	6.6251	8.0525	2.46E-06	1.59E-04	5.0632	Mus musculus activating transcription factor 3 (Atf3), mRNA.	11910	1qH6
TNFAIP8	2.2823	4.8647	2.0655	2.4992	8.5861	22.8002	1.14E-11	1.74E-08	16.7699	Mus musculus tumor necrosis factor, alpha-induced protein 8 (Tnfaip8), mRNA.	106869	18qD1
GPNMB	2.2727	4.8322	1.6274	2.9180	6.9411	7.6286	4.37E-06	2.28E-04	4.4742	Mus musculus glycoprotein (transmembrane) nmb (Gpnmb), mRNA.	93695	6qB2.3
LGALS3	2.2499	4.7565	1.6347	2.8651	10.2989	7.9213	2.93E-06	1.82E-04	4.8834	Mus musculus lectin, galactose binding, soluble 3 (Lgals3), mRNA.	16854	14qC1
TRIB3	2.2324	4.6993	1.6538	2.8110	6.6051	8.3573	1.65E-06	1.23E-04	5.4728	Mus musculus tribbles homolog 3 (Drosophila) (Trib3), mRNA.	228775	2qG3
TSPAN10	2.1938	4.5751	1.7957	2.5919	7.2805	11.9357	2.91E-08	7.62E-06	9.5331	Mus musculus tetraspanin 10 (Tspan10), mRNA.	208634	11qE2
EGR1	2.1331	4.3867	1.5315	2.7348	7.7093	7.6796	4.07E-06	2.19E-04	4.5463	Mus musculus early growth response 1 (Egr1), mRNA.	13653	18qB1
XBP1	2.0525	4.1483	1.7623	2.3427	10.8416	15.3187	1.49E-09	9.09E-07	12.4105	Mus musculus X-box binding protein 1 (Xbp1), mRNA.	22433	11qA1
LOC100046232	2.0065	4.0180	1.6739	2.3390	8.7354	13.0680	9.99E-09	3.27E-06	10.5820	PREDICTED: Mus musculus similar to NFIL3/E4BP4 transcription factor (LOC100046232), mRNA (NB: Withdrawn by NCBI - not predicted in a later annotation).	100046232	
C1QB	2.0010	4.0029	1.6034	2.3987	6.7814	10.8993	8.36E-08	1.61E-05	8.4837	Mus musculus complement component 1, q subcomponent, beta polypeptide (C1qb), mRNA.	12260	4qD3
PAQR7	1.9833	3.9540	1.7396	2.2271	9.3063	17.6239	2.72E-10	2.26E-07	13.9945	Mus musculus progesterin and adipoQ receptor family member VII (Paqr7), mRNA.	71904	4qD3
CD74	1.9057	3.7468	1.4238	2.3875	6.5739	8.5661	1.26E-06	1.03E-04	5.7468	Mus musculus CD74 antigen (invariant polypeptide of major histocompatibility complex, class II antigen-associated) (Cd74), transcript variant 1, mRNA.	16149	18qE1
AXUD1	1.9032	3.7403	1.5228	2.2835	6.7958	10.8379	8.92E-08	1.67E-05	8.4186	Mus musculus AXIN1 up-regulated 1 (Axud1), mRNA.	215418	9qF4
NAT6	1.8873	3.6993	1.6386	2.1359	7.5829	16.4408	6.33E-10	4.84E-07	13.2139	Mus musculus N-acetyltransferase 6 (Nat6), mRNA.	56441	9qF1
SRXN1	1.8781	3.6759	1.6246	2.1317	7.1891	16.0448	8.51E-10	6.01E-07	12.9378	Mus musculus sulfiredoxin 1 homolog (S. cerevisiae) (Srxn1), mRNA.	76650	2qG3
CHKB	1.8723	3.6612	1.5300	2.2146	7.8379	11.8485	3.17E-08	8.07E-06	9.4482	Mus musculus choline kinase beta (Chkb), mRNA.	12651	15qE3
ST8SIA5	1.8556	3.6190	1.2633	2.4478	6.1794	6.7863	1.47E-05	5.58E-04	3.2333	Mus musculus ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 5 (St8sia5), transcript variant 2, mRNA.	225742	18qE3
MMD	1.8408	3.5820	1.6496	2.0319	10.2355	20.8553	3.44E-11	4.50E-08	15.8338	Mus musculus monocyte to macrophage differentiation-associated (Mmd), mRNA.	67468	11qC
TGFB1	1.7841	3.4441	1.4639	2.1043	6.4364	12.0701	2.55E-08	7.12E-06	9.6627	Mus musculus transforming growth factor, beta induced (Tgfb1), mRNA.	21810	13qB1
SERPINA3G	1.7387	3.3373	1.1872	2.2901	6.2133	6.8294	1.38E-05	5.33E-04	3.2991	Mus musculus serine (or cysteine) peptidase inhibitor, clade A, member 3G (Serpina3g), mRNA.	20715	12qE
EAR2	1.7384	3.3366	1.1983	2.2784	6.7931	6.9723	1.11E-05	4.54E-04	3.5156	Mus musculus eosinophil-associated, ribonuclease A family, member 2 (Ear2), mRNA.	13587	14qC1
TFRC	1.6740	3.1910	1.3140	2.0340	9.0168	10.0715	2.07E-07	2.91E-05	7.5765	Mus musculus transferrin receptor (Tfrc), mRNA.	22042	16qB3
EAR4	1.6542	3.1475	1.1140	2.1944	5.7854	6.6325	1.85E-05	6.80E-04	2.9962	Mus musculus eosinophil-associated, ribonuclease A family, member 4 (Ear4), mRNA.	53877	
SERPINA3N	1.6494	3.1370	1.0588	2.2400	6.9368	6.0492	4.57E-05	1.36E-03	2.0666	Mus musculus serine (or cysteine) peptidase inhibitor, clade A, member 3N (Serpina3n), mRNA.	20716	12qE
GCH1	1.6073	3.0468	1.1929	2.0217	6.9510	8.4008	1.55E-06	1.18E-04	5.5304	Mus musculus GTP cyclohydrolase 1 (Gch1), mRNA	NA	
1700003F12RIK	1.5979	3.0269	1.3171	1.8786	8.3389	12.3275	1.99E-08	5.89E-06	9.9069	Mus musculus RIKEN cDNA 1700003F12 gene (1700003F12Rik), mRNA. XM_976207	75480	2qH1
LOC641240	1.5939	3.0187	1.1737	2.0141	6.6760	8.2165	1.98E-06	1.37E-04	5.2850	PREDICTED: Mus musculus similar to MHC class II antigen beta chain (LOC641240), mRNA.	641240	
DNAJB9	1.5933	3.0174	1.1448	2.0418	7.0648	7.6942	3.99E-06	2.17E-04	4.5669	Mus musculus DnaJ (Hsp40) homolog, subfamily B, member 9 (Dnajb9), mRNA.	27362	12qB3
LMNA	1.5294	2.8867	1.1950	1.8638	8.5253	9.9074	2.49E-07	3.31E-05	7.3887	Mus musculus lamin A (Lmna), transcript variant 1, mRNA.	16905	3qF1
SLC7A3	1.5279	2.8837	1.1143	1.9416	6.4247	8.0007	2.63E-06	1.69E-04	4.9925	Mus musculus solute carrier family 7 (cationic amino acid transporter, y+ system), member 3 (Slc7a3), mRNA.	11989	XqC3
DHX32	1.4946	2.8179	1.2059	1.7834	13.2014	11.2113	6.03E-08	1.35E-05	8.8093	Mus musculus DEAH (Asp-Glu-Ala-His) box polypeptide 32 (Dhx32), mRNA.	101437	7qF3
ASNS	1.4920	2.8127	1.1823	1.8017	8.0548	10.4343	1.38E-07	2.22E-05	7.9821	Mus musculus asparagine synthetase (Asns), mRNA.	27053	6qA1
DDIT4	1.4844	2.7981	1.1253	1.8436	8.8568	8.9520	7.74E-07	7.48E-05	6.2397	Mus musculus DNA-damage-inducible transcript 4 (Ddit4), mRNA.	74747	10qB4
JUNB	1.4783	2.7861	1.1307	1.8258	6.9352	9.2123	5.63E-07	5.74E-05	6.5626	Mus musculus Jun-B oncogene (Junb), mRNA.	16477	8qC3
ENO2	1.4513	2.7346	1.2005	1.7021	8.6981	12.5336	1.64E-08	5.00E-06	10.0988	Mus musculus enolase 2, gamma neuronal (Eno2), mRNA.	13807	6qF2
C1QC	1.4280	2.6908	0.9756	1.8804	6.6932	6.8365	1.36E-05	5.31E-04	3.3100	Mus musculus complement component 1, q subcomponent, C chain (C1qc), mRNA.	12262	4qD3
H2-AB1	1.4279	2.6905	0.9393	1.9164	6.3753	6.3306	2.93E-05	9.65E-04	2.5212	Mus musculus histocompatibility 2, class II antigen A, beta 1 (H2-Ab1), mRNA.	14961	17qB1
ALDOA	1.4051	2.6484	1.0999	1.7103	11.6439	9.9725	2.31E-07	3.16E-05	7.4636	Mus musculus aldolase A, fructose-bisphosphate (Aldoa), mRNA.	11674	7qF3
FHL2	1.3934	2.6269	1.1213	1.6654	5.7420	11.0942	6.81E-08	1.45E-05	8.6881	Mus musculus four and a half LIM domains 2 (Fhl2), mRNA.	14200	1qB
LYZ	1.3869	2.6152	1.0184	1.7554	7.5281	8.1526	2.15E-06	1.47E-04	5.1990	Mus musculus lysozyme (Lyz), mRNA.	17110	10qD2
I830077J02RIK	1.3849	2.6116	0.9279	1.8420	6.2606	6.5633	2.05E-05	7.38E-04	2.8884	Mus musculus RIKEN cDNA I830077J02 gene (I830077J02Rik), mRNA.	433638	3qF2.2
CD52	1.3831	2.6082	0.9506	1.8156	6.5935	6.9269	1.19E-05	4.77E-04	3.4472	Mus musculus CD52 antigen (Cd52), mRNA.	23833	4qD3
KLF4	1.3431	2.5370	0.9535	1.7327	6.2308	7.4673	5.47E-06	2.70E-04	4.2439	Mus musculus Kruppel-like factor 4 (gut) (Klf4), mRNA.	16600	4qB3
SYN2	1.3357	2.5240	0.9690	1.7024	8.0689	7.8896	3.06E-06	1.87E-04	4.8396	Mus musculus synapsin II (Syn2), mRNA.	20965	6qE3
PDK1	1.3222	2.5004	0.9952	1.6492	7.6288	8.7572	9.87E-07	8.87E-05	5.9931	Mus musculus pyruvate dehydrogenase kinase, isoenzyme 1 (Pdk1), nuclear gene encoding mitochondrial protein, mRNA.	228026	2qC3
CEBPB	1.3209	2.4982	0.6968	1.9450	6.9835	4.5844	5.46E-04	8.75E-03	-0.4747	Mus musculus CCAAT/enhancer binding protein (C/EBP), beta (Cebpb), mRNA.	12608	2qH3
UAP1L1	1.3035	2.4683	1.0127	1.5943	7.3072	9.7087	3.13E-07	3.93E-05	7.1578	Mus musculus UDP-N-acetylglucosamine pyrophosphorylase 1-like 1 (Uap1l1), mRNA. XM_918982	227620	2qA3

Supplemental Table 3

ZFP36	1.3008	2.4637	0.8882	1.7135	9.0024	6.8282	1.38E-05	5.33E-04	3.2973	Mus musculus zinc finger protein 36 (Zfp36), mRNA.	22695	7qA3
RGS16	1.2938	2.4517	0.9349	1.6527	6.9475	7.8087	3.41E-06	1.95E-04	4.7273	Mus musculus regulator of G-protein signaling 16 (Rgs16), mRNA.	19734	1qG3
TMEM39A	1.2567	2.3894	0.9481	1.5652	8.1366	8.8220	9.10E-07	8.42E-05	6.0756	Mus musculus transmembrane protein 39a (Tmem39a), mRNA.	67846	16qB4
HSD17B12	1.2277	2.3419	0.8901	1.5653	8.5929	7.8777	3.11E-06	1.87E-04	4.8231	Mus musculus hydroxysteroid (17-beta) dehydrogenase 12 (Hsd17b12), mRNA.	56348	2qE1
CLIC4	1.2229	2.3341	0.8617	1.5841	7.9386	7.3340	6.61E-06	3.11E-04	4.0510	Mus musculus chloride intracellular channel 4 (mitochondrial) (Clic4), nuclear gene encoding mitochondrial protein, mRNA.	29876	4qD3
GAL	1.2061	2.3071	0.8109	1.6013	5.7952	6.6100	1.91E-05	6.96E-04	2.9612	Mus musculus galanin (Gal), mRNA.	14419	19qA
LYZ2	1.1850	2.2736	0.6255	1.7445	5.5796	4.5878	5.42E-04	8.73E-03	-0.4685	Mus musculus lysozyme 2 (Lyz2), mRNA.	17105	10qD2
CD68	1.1631	2.2394	0.7601	1.5661	6.2394	6.2520	3.32E-05	1.07E-03	2.3953	Mus musculus CD68 antigen (Cd68), mRNA.	12514	11qB3
LAPTM5	1.1623	2.2382	0.8047	1.4361	7.7617	7.0398	1.01E-05	4.23E-04	3.6170	Mus musculus lysosomal-associated protein transmembrane 5 (Laptm5), mRNA.	16792	4qD2.3
VWF	1.1448	2.2111	0.7512	1.5383	6.7804	6.3006	3.07E-05	9.96E-04	2.4733	Mus musculus Von Willebrand factor homolog (Vwf), mRNA.	22371	6qF3
RNF145	1.1377	2.2002	0.8946	1.3807	8.5742	10.1390	1.91E-07	2.79E-05	7.6529	Mus musculus ring finger protein 145 (Rnf145), mRNA.	74315	11qB1.1
LITAF	1.1333	2.1936	0.8981	1.3685	10.0450	10.4359	1.38E-07	2.22E-05	7.9839	Mus musculus LPS-induced TN factor (Litaf), mRNA.	56722	16qA1
FAM129B	1.1273	2.1844	0.8784	1.3762	8.9763	9.8092	2.79E-07	3.60E-05	7.2751	Mus musculus family with sequence similarity 129, member B (Fam129b), mRNA.	227737	2qB
CAR9	1.1184	2.1711	0.8007	1.4361	6.1784	7.6253	4.39E-06	2.28E-04	4.4695	Mus musculus carbonic anhydrase 9 (Car9), mRNA.	230099	4qB1
CD9	1.0977	2.1401	0.7936	1.4018	7.2358	7.8195	3.36E-06	1.95E-04	4.7424	Mus musculus CD9 antigen (Cd9), mRNA	NA	
CDS1	1.0965	2.1384	0.8157	1.3774	6.8561	8.4568	1.45E-06	1.12E-04	5.6040	Mus musculus CDP-diacylglycerol synthase 1 (Cds1), mRNA.	74596	5qE4
P4HB	1.0849	2.1212	0.7953	1.3745	11.2015	8.1149	2.26E-06	1.50E-04	5.1480	Mus musculus prolyl 4-hydroxylase, beta polypeptide (P4hb), mRNA.	18453	11qE2
FHL1	1.0822	2.1173	0.8814	1.2830	10.3575	11.6748	3.76E-08	9.08E-06	9.2774	Mus musculus four and a half LIM domains 1 (Fhl1), transcript variant 2, mRNA.	14199	XqA5
FBXL13	1.0798	2.1137	0.8167	1.3428	6.9865	8.8915	8.35E-07	7.89E-05	6.1636	Mus musculus F-box and leucine-rich repeat protein 13 (Fbxl13), mRNA.	320118	5qA3
SLC6A17	1.0752	2.1069	0.6820	1.4683	8.2845	5.9230	5.59E-05	1.59E-03	1.8592	Mus musculus solute carrier family 6 (neurotransmitter transporter), member 17 (Slc6a17), mRNA.	229706	3qF2.3
FAM102A	1.0626	2.0887	0.8479	1.2774	8.2218	10.7180	1.01E-07	1.76E-05	8.2905	Mus musculus family with sequence similarity 102, member A (Fam102a), mRNA.	98952	2qB
PRNP	1.0603	2.0854	0.7923	1.3283	10.5656	8.5689	1.25E-06	1.03E-04	5.7504	Mus musculus prion protein (Prnp), mRNA.	19122	2qF2
HERPUD1	1.0548	2.0775	0.7226	1.3871	10.7879	6.8763	1.28E-05	5.05E-04	3.3705	Mus musculus homocysteine-inducible, endoplasmic reticulum stress-inducible, ubiquitin-like domain member 1 (Herpud1), mRNA.	64209	8qC5
CPEB1	1.0548	2.0774	0.8423	1.2674	7.0079	10.7486	9.81E-08	1.76E-05	8.3234	Mus musculus cytoplasmic polyadenylation element binding protein 1 (Cpeb1), mRNA.	12877	7qD3
MSI2	1.0547	2.0773	0.8734	1.2360	8.4632	12.6038	1.53E-08	4.85E-06	10.1635	Mus musculus Musashi homolog 2 (Drosophila) (Msi2), mRNA.	76626	11qC
CKMT2	1.0458	2.0645	0.7499	1.3417	7.4612	7.6559	4.21E-06	2.23E-04	4.5129	Mus musculus creatine kinase, mitochondrial 2 (Ckmt2), nuclear gene encoding mitochondrial protein, mRNA.	76722	13qC3
SF3B3	1.0381	2.0535	0.7540	1.3222	9.1452	7.9136	2.96E-06	1.82E-04	4.8727	Mus musculus splicing factor 3b, subunit 3 (Sf3b3), mRNA.	101943	8qE1
D3UCLA1	1.0367	2.0515	0.7761	1.2973	10.2775	8.6169	1.18E-06	1.02E-04	5.8127	Mus musculus DNA segment, Chr 3, University of California at Los Angeles 1 (D3Ucla1), mRNA.	28146	3qD
VAC14	1.0342	2.0479	0.6715	1.3968	8.6590	6.1767	3.73E-05	1.15E-03	2.2740	Mus musculus Vac14 homolog (S. cerevisiae) (Vac14), mRNA.	234729	8qE1
KLF9	1.0248	2.0347	0.7201	1.3295	8.4776	7.2854	7.08E-06	3.30E-04	3.9801	Mus musculus Kruppel-like factor 9 (Klf9), mRNA.	16601	19qB
CCL9	1.0241	2.0337	0.5941	1.4542	6.1733	5.1580	2.00E-04	4.18E-03	0.5541	Mus musculus chemokine (C-C motif) ligand 9 (Ccl9), mRNA.	20308	11qC
LDHA	1.0217	2.0303	0.7632	1.2802	11.6451	8.5603	1.27E-06	1.03E-04	5.7392	Mus musculus lactate dehydrogenase A (Ldha), mRNA.	16828	7qB4
RNF222	1.0196	2.0273	0.7859	1.2532	5.9210	9.4521	4.23E-07	4.73E-05	6.8534	Mus musculus ring finger protein 222 (Rnf222), mRNA.	320040	11qB3
MTHFD2	1.0117	2.0163	0.5199	1.5035	7.2530	4.4561	6.87E-04	1.04E-02	-0.7099	Mus musculus methylenetetrahydrofolate dehydrogenase (NAD+ dependent), methenyltetrahydrofolate cyclohydrolase (Mthfd2), mRNA.	17768	6qC3
TEX9	-1.0008	-2.0011	-1.2841	-0.7174	8.0903	-7.6493	4.25E-06	2.24E-04	4.5036	Mus musculus testis expressed gene 9 (Tex9), mRNA.	21778	9qD
SPRYD4	-1.0056	-2.0078	-1.2881	-0.7231	7.3718	-7.7111	3.90E-06	2.17E-04	4.5907	Mus musculus SPRY domain containing 4 (Spryd4), mRNA.	66701	10qD3
MRPS26	-1.0103	-2.0144	-1.3537	-0.6670	9.6341	-6.3737	2.75E-05	9.12E-04	2.5896	Mus musculus mitochondrial ribosomal protein S26 (Mrps26), nuclear gene encoding mitochondrial protein, mRNA.	99045	2qF1
C030030A07RIK	-1.0535	-2.0755	-1.2967	-0.8103	9.0262	-9.3812	4.60E-07	4.90E-05	6.7680	Mus musculus RIKEN cDNA C030030A07 gene (C030030A07Rik), mRNA.	654818	6qG1
RBM38	-1.0574	-2.0812	-1.3452	-0.7696	8.3239	-7.9590	2.79E-06	1.76E-04	4.9353	Mus musculus RNA binding motif protein 38 (Rbm38), mRNA.	56190	2qH3
TMEM177	-1.0584	-2.0826	-1.3589	-0.7579	7.7882	-7.6295	4.37E-06	2.28E-04	4.4755	Mus musculus transmembrane protein 177 (Tmem177), mRNA.	66343	1qE2.3
CYP7B1	-1.0602	-2.0852	-1.3387	-0.7817	7.8492	-8.2458	1.90E-06	1.33E-04	5.3243	Mus musculus cytochrome P450, family 7, subfamily b, polypeptide 1 (Cyp7b1), mRNA.	13123	3qA1
NASP	-1.0712	-2.1011	-1.3924	-0.7499	7.5692	-7.2216	7.76E-06	3.54E-04	3.8866	Mus musculus nuclear autoantigenic sperm protein (histone-binding) (Nasp), transcript variant 2, mRNA.	50927	4qD1
ORAOV1	-1.0730	-2.1039	-1.4003	-0.7458	8.2491	-7.1022	9.22E-06	4.01E-04	3.7100	Mus musculus oral cancer overexpressed 1 (Oraov1), mRNA.	72284	7qF5
OTTMUSG00000005065	-1.0784	-2.1116	-1.3747	-0.7820	9.0323	-7.8813	3.09E-06	1.87E-04	4.8281	Mus musculus predicted gene, OTTMUSG00000005065 (OTTMUSG00000005065), mRNA.	327860	11qA1
ZFP365	-1.0787	-2.1121	-1.4029	-0.7545	9.7490	-7.2076	7.92E-06	3.59E-04	3.8660	Mus musculus zinc finger protein 365 (Zfp365), mRNA.	216049	10qB5.1
MDK	-1.0905	-2.1295	-1.3691	-0.8119	8.4523	-8.4781	1.41E-06	1.11E-04	5.6320	Mus musculus midkine (Mdk), transcript variant 2, mRNA.	17242	2qE1
ANKRD46	-1.1062	-2.1528	-1.4903	-0.7220	6.5946	-6.2372	3.40E-05	1.08E-03	2.3715	Mus musculus ankyrin repeat domain 46 (Ankrd46), mRNA.	68839	15qB3.1
GADD45B	-1.1226	-2.1775	-1.3600	-0.8853	10.3821	-10.2449	1.70E-07	2.60E-05	7.7720	Mus musculus growth arrest and DNA-damage-inducible 45 beta (Gadd45b), mRNA.	17873	10qC1
HBA-A1	-1.1410	-2.2053	-1.7378	-0.5442	11.0077	-4.1410	1.22E-03	1.62E-02	-1.2944	Mus musculus hemoglobin alpha, adult chain 1 (Hba-a1), mRNA.	15122	11qA4
MXD1	-1.1477	-2.2156	-1.5200	-0.7754	6.3366	-6.6774	1.73E-05	6.44E-04	3.0657	Mus musculus MAX dimerization protein 1 (Mxd1), mRNA.	17119	6qD1
732482	-1.1491	-2.2177	-1.4101	-0.8880	7.9028	-9.5353	3.83E-07	4.45E-05	6.9528	Mus musculus predicted gene, 732482 (732482), non-coding RNA.	732482	8qA2
MTNR1A	-1.1509	-2.2206	-1.4164	-0.8855	6.1658	-9.3915	4.54E-07	4.90E-05	6.7805	Mus musculus melatonin receptor 1A (Mtnr1a), mRNA.	17773	8qB1.1
PPP2R5E	-1.1523	-2.2227	-1.4394	-0.8652	8.9135	-8.6942	1.07E-06	9.52E-05	5.9123	Mus musculus protein phosphatase 2, regulatory subunit B (B56), epsilon isoform (Ppp2r5e), mRNA.	26932	12qC3
SESN1	-1.1548	-2.2266	-1.4556	-0.8541	7.6849	-8.3167	1.73E-06	1.27E-04	5.4190	Mus musculus sestrin 1 (Sesn1), mRNA.	140742	10qB2
SORBS1	-1.1634	-2.2398	-1.4909	-0.8358	7.8965	-7.6930	4.00E-06	2.17E-04	4.5651	Mus musculus sorbin and SH3 domain containing 1 (Sorbs1), transcript variant 3, mRNA.	20411	19qC3
EDNRB	-1.1900	-2.2816	-1.4928	-0.8872	8.6041	-8.5126	1.35E-06	1.08E-04	5.6772	Mus musculus endothelin receptor type B (Ednrb), mRNA.	13618	14qE2.3
PELL1	-1.1958	-2.2908	-1.5140	-0.8776	7.5108	-8.1401	2.19E-06	1.47E-04	5.1821	Mus musculus pellino 1 (Peli1), mRNA.	67245	11qA3.1
CHFR	-1.2035	-2.3030	-1.3999	-1.0071	7.4683	-13.2706	8.32E-09	2.94E-06	10.7598	Mus musculus checkpoint with forkhead and ring finger domains (Chfr), mRNA.	231600	5qF
MYD116	-1.2066	-2.3079	-1.4843	-0.9289	9.4542	-9.4105	4.44E-07	4.85E-05	6.8034	Mus musculus myeloid differentiation primary response gene 116 (Myd116), mRNA.	17872	7qB4
TRIM26	-1.2093	-2.3122	-1.4873	-0.9313	9.2529	-9.4209	4.39E-07	4.85E-05	6.8160	Mus musculus tripartite motif-containing 26 (Trim26), transcript variant 1, mRNA.	22670	17qB1
E330034G19RIK	-1.2159	-2.3229	-1.5597	-0.8721	9.2249	-7.6600	4.19E-06	2.23E-04	4.5187	Mus musculus RIKEN cDNA E330034G19 gene (E330034G19Rik), mRNA.	105418	14qA3
PPP1R3C	-1.2270	-2.3407	-1.5126	-0.9414	9.2598	-9.3049	5.04E-07	5.25E-05	6.6757	Mus musculus protein phosphatase 1, regulatory (inhibitor) subunit 3C (Ppp1r3c), mRNA.	53412	19qC2
1810009O10RIK	-1.2277	-2.3419	-1.5153	-0.9400	8.8451	-9.2446	5.42E-07	5.58E-05	6.6022	Mus musculus RIKEN cDNA 1810009O10 gene (1810009O10Rik), mRNA.	69109	11qB5
HN1L	-1.2303	-2.3461	-1.5516	-0.9089	8.7502	-8.2917	1.79E-06	1.29E-04	5.3856	Mus musculus hematological and neurological expressed 1-like (Hn1l), mRNA.	52009	17qA3.3
ANO4	-1.2374	-2.3577	-1.5130	-0.9617	6.3349	-9.7235	3.07E-07	3.92E-05	7.1752	Mus musculus anoctamin 4 (Ano4), mRNA.	320091	10qC1
CCKBR	-1.2522	-2.3821	-1.5061	-0.9983	9.1480	-10.6822	1.05E-07	1.76E-05	8.2520	Mus musculus cholecystokinin B receptor (Cckbr), mRNA.	12426	7qE3
INTS3	-1.2647	-2.4029	-1.5534	-0.9761	8.7978	-9.4898	4.04E-07	4.58E-05	6.8986	Mus musculus integrator complex subunit 3 (Ints3), transcript variant 1, mRNA.	229543	3qF1
UBR5	-1.2764	-2.4223	-1.5077	-1.0450	9.7484	-11.9491	2.87E-08	7.62E-06	9.5461	Mus musculus ubiquitin protein ligase E3 component n-recognin 5 (Ubr5), mRNA.	70790	15qB3.1
SLC46A3	-1.2802	-2.4287	-1.6238	-0.9365	10.1475	-8.0691	2.40E-06	1.56E-04	5.0859	Mus musculus solute carrier family 46, member 3 (Slc46a3), mRNA.	71706	5qG3

Supplemental Table 3

SKAP2	-1.3007	-2.4636	-1.7525	-0.8490	9.1192	-6.2367	3.40E-05	1.08E-03	2.3707	Mus musculus src family associated phosphoprotein 2 (Skap2), mRNA.	54353	6qB3
BCDO2	-1.3394	-2.5305	-1.6105	-1.0683	6.6189	-10.7020	1.03E-07	1.76E-05	8.2733	Mus musculus beta-carotene 9', 10'-dioxygenase 2 (Bcdo2), mRNA.	170752	9qA5.3
FAS	-1.3633	-2.5727	-1.6344	-1.0921	6.8104	-10.8905	8.44E-08	1.61E-05	8.4744	Mus musculus Fas (TNF receptor superfamily member 6) (Fas), mRNA.	14102	19qC1
2310021H06RIK	-1.3698	-2.5844	-1.6476	-1.0920	6.5562	-10.6799	1.06E-07	1.76E-05	8.2495	Mus musculus RIKEN cDNA 2310021H06 gene (2310021H06Rik), mRNA.	67135	2qH1
GSC	-1.3822	-2.6067	-1.6551	-1.1094	6.1705	-10.9733	7.73E-08	1.57E-05	8.5618	Mus musculus goosecoid homeobox (Gsc), mRNA.	14836	12qE
PBLD	-1.3866	-2.6147	-1.7362	-1.0370	6.8146	-8.5908	1.22E-06	1.03E-04	5.7789	Mus musculus phenazine biosynthesis-like protein domain containing (Pbld), mRNA.	68371	10qB4
DBF4	-1.3881	-2.6173	-1.7520	-1.0241	6.7778	-8.2617	1.86E-06	1.31E-04	5.3455	Mus musculus DBF4 homolog (S. cerevisiae) (Dbf4), mRNA.	27214	5qA1
CCDC53	-1.3988	-2.6368	-1.6038	-1.1938	10.1163	-14.7776	2.30E-09	1.01E-06	11.9988	Mus musculus coiled-coil domain containing 53 (Ccdc53), mRNA.	67282	10qC1
SUSD3	-1.4103	-2.6580	-1.7664	-1.0543	6.2378	-8.5796	1.24E-06	1.03E-04	5.7644	Mus musculus sushi domain containing 3 (Susd3), mRNA.	66329	13qA5
1500012F01RIK	-1.4150	-2.6666	-1.7817	-1.0483	9.6214	-8.3576	1.64E-06	1.23E-04	5.4732	Mus musculus RIKEN cDNA 1500012F01 gene (1500012F01Rik), mRNA.	68949	2qH3
FRMD6	-1.4158	-2.6681	-1.6823	-1.1493	7.6058	-11.5080	4.45E-08	1.05E-05	9.1110	Mus musculus FERM domain containing 6 (Frmd6), mRNA.	319710	12qC2-qC3
STAMBPL1	-1.4176	-2.6714	-1.7736	-1.0615	8.9992	-8.6235	1.17E-06	1.02E-04	5.8212	Mus musculus Stam binding protein like 1 (Stambpl1), mRNA.	76630	19qC1
PLEKHA4	-1.4632	-2.7573	-1.7043	-1.2221	6.1563	-13.1448	9.32E-09	3.16E-06	10.6497	Mus musculus pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 4 (Plekha4), mRNA.	69217	7qB4
H2-Eb1	-1.4686	-2.7675	-1.9279	-1.0093	7.6470	-6.9261	1.19E-05	4.77E-04	3.4459	Mus musculus histocompatibility 2, class II antigen E beta (H2-Eb1), mRNA.	14969	17qB1
SFRS14	-1.4735	-2.7769	-1.7697	-1.1773	9.0454	-10.7751	9.54E-08	1.75E-05	8.3517	Mus musculus splicing factor, arginine/serine-rich 14 (Sfrs14), mRNA.	234373	8qB3.3
PAX4	-1.5010	-2.8303	-1.8162	-1.1858	6.2925	-10.3139	1.58E-07	2.45E-05	7.8489	Mus musculus paired box gene 4 (Pax4), mRNA.	18506	6qA3.3
SCNN1B	-1.5137	-2.8555	-1.8390	-1.1885	7.5718	-10.0801	2.05E-07	2.91E-05	7.5863	Mus musculus sodium channel, nonvoltage-gated 1 beta (Scnn1b), mRNA.	20277	7qF2
PPM1E	-1.5775	-2.9845	-1.8877	-1.2672	6.9521	-11.0122	7.42E-08	1.55E-05	8.6025	Mus musculus protein phosphatase 1E (PP2C domain containing) (Ppm1e), mRNA.	320472	11qC
LENEP	-1.5835	-2.9970	-1.9885	-1.1785	8.5881	-8.4681	1.43E-06	1.12E-04	5.6188	Mus musculus lens epithelial protein (Lenep), mRNA.	NA	
USP45	-1.6638	-3.1686	-1.9325	-1.3952	6.3068	-13.4142	7.32E-09	2.80E-06	10.8842	Mus musculus ubiquitin specific petidase 45 (Usp45), mRNA. XM_920449 XM_920458	77593	4qA3
RAB32	-1.6736	-3.1901	-1.9741	-1.3732	7.2167	-12.0652	2.56E-08	7.12E-06	9.6580	Mus musculus RAB32, member RAS oncogene family (Rab32), mRNA.	67844	10qA1
6330503C03RIK	-1.6838	-3.2128	-2.0638	-1.3039	7.9895	-9.5986	3.56E-07	4.35E-05	7.0280	Mus musculus RIKEN cDNA 6330503C03 gene (6330503C03Rik), mRNA.	76156	6qB2.1
OXT	-1.7209	-3.2963	-2.1691	-1.2726	7.6068	-8.3161	1.74E-06	1.27E-04	5.4181	Mus musculus oxytocin (Oxt), mRNA.	18429	2qF1
SLC6A13	-1.7281	-3.3128	-2.4592	-0.9969	7.1987	-5.1193	2.13E-04	4.39E-03	0.4859	Mus musculus solute carrier family 6 (neurotransmitter transporter, GABA), member 13 (Slc6a13), mRNA.	14412	6qF1
1700021K19RIK	-1.7817	-3.4383	-2.0406	-1.5228	7.9937	-14.9046	2.07E-09	1.00E-06	12.0970	Mus musculus RIKEN cDNA 1700021K19 gene (1700021K19Rik), mRNA.	224118	16qB3
SLC13A4	-1.8382	-3.5756	-2.7997	-0.8767	8.1811	-4.1409	1.22E-03	1.62E-02	-1.2946	Mus musculus solute carrier family 13 (sodium/sulfate symporters), member 4 (Slc13a4), mRNA.	243755	6qB1
TRAFD1	-1.8750	-3.6681	-2.2796	-1.4705	9.1719	-10.0391	2.14E-07	2.98E-05	7.5397	Mus musculus TRAF type zinc finger domain containing 1 (Traf1), mRNA.	231712	5qF
DGAT2	-1.8892	-3.7044	-2.1964	-1.5821	7.7230	-13.3218	7.95E-09	2.92E-06	10.8043	Mus musculus diacylglycerol O-acyltransferase 2 (Dgat2), mRNA.	67800	7qE2
IGF2	-1.9230	-3.7920	-2.6416	-1.2044	10.6363	-5.7963	6.86E-05	1.87E-03	1.6486	Mus musculus insulin-like growth factor 2 (Igf2), mRNA.	16002	7qF5
GADD45G	-1.9941	-3.9838	-2.2780	-1.7103	9.9701	-15.2146	1.62E-09	9.09E-07	12.3325	Mus musculus growth arrest and DNA-damage-inducible 45 gamma (Gadd45g), mRNA.	23882	13qA5
SNX22	-2.0256	-4.0715	-2.4841	-1.5670	9.3734	-9.5675	3.69E-07	4.39E-05	6.9912	Mus musculus sorting nexin 22 (Snx22), mRNA.	382083	9qC
TCP11	-2.1301	-4.3774	-2.6965	-1.5636	9.0544	-8.1447	2.17E-06	1.47E-04	5.1884	Mus musculus t-complex protein 11 (Tcp11), mRNA.	21463	17qA3.3
GJB6	-2.1346	-4.3910	-2.5877	-1.6815	5.9756	-10.2040	1.78E-07	2.68E-05	7.7262	Mus musculus gap junction protein, beta 6 (Gjb6), transcript variant 2, mRNA.	14623	14qC3
KLHL22	-2.4230	-5.3628	-2.7074	-2.1386	8.0373	-18.4513	1.55E-10	1.42E-07	14.5037	Mus musculus kelch-like 22 (Drosophila) (Klhl22), mRNA.	224023	16qA3
HMOX1	-2.4233	-5.3640	-3.0423	-1.8043	11.7014	-8.4798	1.40E-06	1.11E-04	5.6342	Mus musculus heme oxygenase (decycling) 1 (Hmox1), mRNA.	15368	8qC1
RSAD2	-2.4449	-5.4447	-2.9281	-1.9616	7.9109	-10.9576	7.86E-08	1.57E-05	8.5452	Mus musculus radical S-adenosyl methionine domain containing 2 (Rsad2), mRNA.	58185	12qA2
TREX1	-2.5871	-6.0090	-3.1708	-2.0034	9.7744	-9.6002	3.55E-07	4.35E-05	7.0300	Mus musculus three prime repair exonuclease 1 (Trex1), transcript variant 2, mRNA.	22040	9qF2
1190002N15RIK	-2.6266	-6.1757	-3.2726	-1.9806	8.4727	-8.8070	9.27E-07	8.42E-05	6.0565	Mus musculus RIKEN cDNA 1190002N15 gene (1190002N15Rik), mRNA.	68861	9qE3.3
RGS4	-3.0628	-8.3560	-3.3850	-2.7406	8.2222	-20.5902	4.02E-11	4.61E-08	15.6971	Mus musculus regulator of G-protein signaling 4 (Rgs4), mRNA.	19736	1qH3
HSPB1	-3.7833	-13.7687	-5.2072	-2.3594	11.0213	-5.7550	7.34E-05	1.96E-03	1.5796	Mus musculus heat shock protein 1 (Hspb1), mRNA.	15507	5qG2

Supplemental Table 4

ILMN_Gene	log2FC (Het vs WT)	Fold Change (Het vs WT)	CI.L	CI.R	AveExpr	t	P.Value	adj.P.Val	B	DEFINITION	ENTREZ_GENE_ ID	CYTOBAND
ARG1	3.4152	10.6682	2.4406	4.3899	6.3901	7.5124	2.75E-06	1.48E-03	4.952656728	Mus musculus arginase 1, liver (Arg1), mRNA.	11846	10qA4
RETNLA	2.8281	7.1014	2.1440	3.5122	6.6829	8.8632	3.93E-07	3.63E-04	6.71119699	Mus musculus resistin like alpha (Retnla), mRNA.	57262	16qB5
IL4	2.7753	6.8463	2.4617	3.0889	8.6068	18.9735	2.03E-11	1.97E-07	14.21227704	Mus musculus interleukin 4 (Il4), mRNA.	16189	11qB1.3
PLK3	2.2894	4.8885	1.9662	2.6125	8.3382	15.1879	4.04E-10	1.96E-06	12.25439988	Mus musculus polo-like kinase 3 (Plk3), mRNA	NA	
TNFRSF12A	2.1252	4.3627	1.4727	2.7777	8.1059	6.9822	6.26E-06	2.77E-03	4.189179512	Mus musculus tumor necrosis factor receptor superfamily, member 12a (Tnfrsf12a), mRNA.	27279	17qA3.3
FOS	2.0562	4.1588	1.1789	2.9335	6.3049	5.0246	1.83E-04	2.44E-02	0.992403885	Mus musculus FBJ osteosarcoma oncogene (Fos), mRNA.	14281	12qD2
COX6A2	2.0075	4.0210	1.6705	2.3446	9.7204	12.7698	3.97E-09	9.64E-06	10.5573367	Mus musculus cytochrome c oxidase, subunit VI a, polypeptide 2 (Cox6a2), nuclear gene encoding mitochondrial protein, mRNA.	12862	7qF3
TNFAIP8	1.8948	3.7186	1.6135	2.1760	8.6240	14.4420	7.89E-10	2.55E-06	11.7749161	Mus musculus tumor necrosis factor, alpha-induced protein 8 (Tnfaip8), mRNA.	106869	18qD1
EAR11	1.8505	3.6062	1.1876	2.5133	5.9809	5.9850	3.27E-05	9.36E-03	2.634747548	Mus musculus eosinophil-associated, ribonuclease A family, member 11 (Ear11), mRNA.	93726	14qC1
CCL7	1.6071	3.0464	1.2020	2.0122	6.1551	8.5054	6.44E-07	5.21E-04	6.270270428	Mus musculus chemokine (C-C motif) ligand 7 (Ccl7), mRNA.	20306	11qC
ATF3	1.5376	2.9031	0.9015	2.1737	6.1201	5.1823	1.37E-04	2.09E-02	1.27144958	Mus musculus activating transcription factor 3 (Atf3), mRNA.	11910	1qH6
SQSTM1	1.3751	2.5938	1.0412	1.7089	10.9061	8.8293	4.12E-07	3.63E-04	6.670199137	Mus musculus sequestosome 1 (Sqstm1), mRNA.	18412	11qB1.3
OLFM1	1.2554	2.3873	0.9608	1.5500	8.0529	9.1345	2.73E-07	2.94E-04	7.034121708	Mus musculus olfactomedin 1 (Olfm1), transcript variant 1, mRNA. XM_923993 XM_923996 XM_924001	56177	2qA3
TSPAN10	1.2550	2.3867	1.0220	1.4881	7.4148	11.5457	1.46E-08	2.83E-05	9.52104388	Mus musculus tetraspanin 10 (Tspan10), mRNA.	208634	11qE2
PAQR7	1.2301	2.3458	0.9696	1.4906	9.1017	10.1241	7.68E-08	1.07E-04	8.134153257	Mus musculus progesterone and adipoQ receptor family member VII (Paqr7), mRNA.	71904	4qD3
HYAL1	1.1625	2.2384	0.6484	1.6765	8.4138	4.8481	2.55E-04	2.78E-02	0.676352954	Mus musculus hyaluronoglucosaminidase 1 (Hyal1), mRNA.	15586	9qF1
RASGRP1	1.1233	2.1784	0.7986	1.4479	6.4852	7.4181	3.17E-06	1.56E-03	4.820015713	Mus musculus RAS guanyl releasing protein 1 (Rasgrp1), mRNA.	19419	2qE5
TFRC	1.0937	2.1342	0.8016	1.3859	8.6606	8.0259	1.28E-06	8.58E-04	5.651793337	Mus musculus transferrin receptor (Tfrc), mRNA.	22042	16qB3
KLF9	1.0841	2.1201	0.6482	1.5200	7.7912	5.3319	1.04E-04	1.77E-02	1.532828503	Mus musculus Kruppel-like factor 9 (Klf9), mRNA.	16601	19qB
CHST7	1.0789	2.1125	0.6975	1.4604	6.6128	6.0636	2.86E-05	8.94E-03	2.762955183	Mus musculus carbohydrate (N-acetylglucosamino) sulfotransferase 7 (Chst7), mRNA.	60322	XqA1.3
FAM115C	1.0539	2.0761	0.8459	1.2619	6.5474	10.8624	3.17E-08	5.13E-05	8.880943894	Mus musculus family with sequence similarity 115, member C (Fam115c), mRNA.	232748	6qB2.1
PROK2	1.0262	2.0367	0.5782	1.4743	6.4670	4.9106	2.27E-04	2.66E-02	0.788794386	Mus musculus prokineticin 2 (Prok2), transcript variant 1, mRNA.	50501	6qD3
LOC100046232	1.0176	2.0246	0.5526	1.4826	8.2279	4.6919	3.42E-04	3.54E-02	0.393081147	PREDICTED: Mus musculus similar to NFIL3/E4BP4 transcription factor (LOC100046232), mRNA (NB: Withdrawn by NCBI).	100046232	
LGALS3	1.0159	2.0222	0.6202	1.4117	9.0185	5.5037	7.64E-05	1.43E-02	1.828899616	Mus musculus lectin, galactose binding, soluble 3 (Lgals3), mRNA.	16854	14qC1
C1QA	1.0058	2.0081	0.5344	1.4772	6.2390	4.5741	4.28E-04	4.24E-02	0.177780297	Mus musculus complement component 1, q subcomponent, alpha polypeptide (C1qa), mRNA.	12259	4qD3
4921528I01RIK	-1.0844	-2.1206	-1.5498	-0.6190	6.9205	-4.9954	1.93E-04	2.54E-02	0.94048029	Mus musculus RIKEN cDNA 4921528I01 gene (4921528I01Rik), mRNA.	70950	18qA2
DDX3Y	-1.2524	-2.3824	-1.7751	-0.7296	6.6299	-5.1361	1.49E-04	2.16E-02	1.189985213	Mus musculus DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, Y-linked (Ddx3y), mRNA.	26900	YqA1
TREX1	-1.3560	-2.5597	-1.7483	-0.9637	9.0890	-7.4105	3.21E-06	1.56E-03	4.809167734	Mus musculus three prime repair exonuclease 1 (Trex1), transcript variant 2, mRNA.	22040	9qF2
GJB6	-1.3822	-2.6066	-1.7554	-1.0090	5.8098	-7.9407	1.45E-06	8.79E-04	5.538415841	Mus musculus gap junction protein, beta 6 (Gjb6), transcript variant 2, mRNA.	14623	14qC3
GADD45G	-1.4770	-2.7836	-2.0285	-0.9254	10.2744	-5.7413	5.01E-05	1.20E-02	2.231276335	Mus musculus growth arrest and DNA-damage-inducible 45 gamma (Gadd45g), mRNA.	23882	13qA5
1190002N15RIK	-1.8510	-3.6074	-2.3271	-1.3748	8.3065	-8.3332	8.21E-07	6.14E-04	6.05187757	Mus musculus RIKEN cDNA 1190002N15 gene (1190002N15Rik), mRNA.	68861	9qE3.3
HMOX1	-2.0259	-4.0726	-2.5957	-1.4562	11.1805	-7.6234	2.32E-06	1.33E-03	5.106994897	Mus musculus heme oxygenase (decycling) 1 (Hmox1), mRNA.	15368	8qC1
HSPB1	-2.4508	-5.4672	-3.0059	-1.8958	8.9774	-9.4659	1.76E-07	2.14E-04	7.415916082	Mus musculus heat shock protein 1 (Hspb1), mRNA.	15507	5qG2

Supplemental Table 5

	greater.p.geo	greater.st	greater.p.	greater.q.	greater.se	greater.ex	less.p.geo	less.stat.			less.set.siz	stats.stat.		
KEGG_ID	mean	at.mean	val	val	t.size	p1	mean	mean	less.p.val	less.q.val	e	less.exp1	mean	stats.exp1
mmu04142 Lysosome	0.000265601	3.533608	0.000266	0.043293	84	0.000266	0.999734	3.533608	0.999734	0.999734	84	0.999734	3.533608	3.533608
mmu04610 Complement and coagulation cascades	0.006199425	2.626298	0.006199	0.368759	24	0.006199	0.993801	2.626298	0.993801	0.999734	24	0.993801	2.626298	2.626298
mmu00010 Glycolysis / Gluconeogenesis	0.007428368	2.518847	0.007428	0.368759	29	0.007428	0.992572	2.518847	0.992572	0.999734	29	0.992572	2.518847	2.518847
mmu04380 Osteoclast differentiation	0.009556264	2.382646	0.009556	0.368759	62	0.009556	0.990444	2.382646	0.990444	0.999734	62	0.990444	2.382646	2.382646
mmu04060 Cytokine-cytokine receptor interaction	0.011311612	2.314864	0.011312	0.368759	76	0.011312	0.988688	2.314864	0.988688	0.999734	76	0.988688	2.314864	2.314864
mmu00531 Glycosaminoglycan degradation	0.016749761	2.262588	0.01675	0.424087	14	0.01675	0.98325	2.262588	0.98325	0.999734	14	0.98325	2.262588	2.262588
mmu01040 Biosynthesis of unsaturated fatty acids	0.018212333	2.199988	0.018212	0.424087	15	0.018212	0.981788	2.199988	0.981788	0.999734	15	0.981788	2.199988	2.199988
mmu00600 Sphingolipid metabolism	0.022085489	2.080135	0.022085	0.449992	21	0.022085	0.977915	2.080135	0.977915	0.999734	21	0.977915	2.080135	2.080135
mmu00520 Amino sugar and nucleotide sugar metabolism	0.035672244	1.83917	0.035672	0.589158	29	0.035672	0.964328	1.83917	0.964328	0.999734	29	0.964328	1.83917	1.83917
mmu04915 Estrogen signaling pathway	0.036275485	1.820498	0.036275	0.589158	47	0.036275	0.963725	1.820498	0.963725	0.999734	47	0.963725	1.820498	1.820498
mmu04721 Synaptic vesicle cycle	0.04900835	1.67868	0.049008	0.589158	36	0.049008	0.950992	1.67868	0.950992	0.999734	36	0.950992	1.67868	1.67868
mmu04062 Chemokine signaling pathway	0.050116611	1.656004	0.050117	0.589158	71	0.050117	0.949883	1.656004	0.949883	0.999734	71	0.949883	1.656004	1.656004
mmu04670 Leukocyte transendothelial migration	0.051970746	1.639374	0.051971	0.589158	57	0.051971	0.948029	1.639374	0.948029	0.999734	57	0.948029	1.639374	1.639374
mmu00052 Galactose metabolism	0.054737382	1.652539	0.054737	0.589158	16	0.054737	0.945263	1.652539	0.945263	0.999734	16	0.945263	1.652539	1.652539
mmu04668 TNF signaling pathway	0.058339408	1.586541	0.058339	0.589158	49	0.058339	0.941661	1.586541	0.941661	0.999734	49	0.941661	1.586541	1.586541
mmu00511 Other glycan degradation	0.060518646	1.644827	0.060519	0.589158	11	0.060519	0.939481	1.644827	0.939481	0.999734	11	0.939481	1.644827	1.644827
mmu00330 Arginine and proline metabolism	0.061445942	1.592204	0.061446	0.589158	24	0.061446	0.938554	1.592204	0.938554	0.999734	24	0.938554	1.592204	1.592204
mmu04660 T cell receptor signaling pathway	0.069319822	1.498065	0.06932	0.627729	53	0.06932	0.93068	1.498065	0.93068	0.999734	53	0.93068	1.498065	1.498065
mmu00350 Tyrosine metabolism	0.080747409	1.444036	0.080747	0.679239	14	0.080747	0.919253	1.444036	0.919253	0.999734	14	0.919253	1.444036	1.444036
mmu04621 NOD-like receptor signaling pathway	0.089585159	1.370261	0.089585	0.679239	19	0.089585	0.910415	1.370261	0.910415	0.999734	19	0.910415	1.370261	1.370261
mmu00062 Fatty acid elongation	0.09257174	1.365124	0.092572	0.679239	13	0.092572	0.907428	1.365124	0.907428	0.999734	13	0.907428	1.365124	1.365124
mmu04662 B cell receptor signaling pathway	0.100514244	1.294033	0.100514	0.679239	36	0.100514	0.899486	1.294033	0.899486	0.999734	36	0.899486	1.294033	1.294033
mmu04141 Protein processing in endoplasmic reticulum	0.110718688	1.226947	0.110719	0.679239	95	0.110719	0.889281	1.226947	0.889281	0.999734	95	0.889281	1.226947	1.226947
mmu04145 Phagosome	0.112375923	1.218407	0.112376	0.679239	87	0.112376	0.887624	1.218407	0.887624	0.999734	87	0.887624	1.218407	1.218407
mmu02010 ABC transporters	0.112708176	1.245661	0.112708	0.679239	16	0.112708	0.887292	1.245661	0.887292	0.999734	16	0.887292	1.245661	1.245661
mmu03320 PPAR signaling pathway	0.115671792	1.207403	0.115672	0.679239	36	0.115672	0.884328	1.207403	0.884328	0.999734	36	0.884328	1.207403	1.207403
mmu04066 HIF-1 signaling pathway	0.121211934	1.176896	0.121212	0.679239	59	0.121212	0.878788	1.176896	0.878788	0.999734	59	0.878788	1.176896	1.176896
mmu04730 Long-term depression	0.121352536	1.179695	0.121353	0.679239	33	0.121353	0.878647	1.179695	0.878647	0.999734	33	0.878647	1.179695	1.179695
mmu00260 Glycine, serine and threonine metabolism	0.13255882	1.132212	0.132559	0.679239	19	0.132559	0.867441	1.132212	0.867441	0.999734	19	0.867441	1.132212	1.132212
mmu00051 Fructose and mannose metabolism	0.145028981	1.074977	0.145029	0.679239	18	0.145029	0.854971	1.074977	0.854971	0.999734	18	0.854971	1.074977	1.074977
mmu04666 Fc gamma R-mediated phagocytosis	0.151140975	1.037371	0.151141	0.679239	47	0.151141	0.848859	1.037371	0.848859	0.999734	47	0.848859	1.037371	1.037371
mmu04130 SNARE interactions in vesicular transport	0.153139211	1.036544	0.153139	0.679239	25	0.153139	0.846861	1.036544	0.846861	0.999734	25	0.846861	1.036544	1.036544
mmu03410 Base excision repair	0.155064524	1.030461	0.155065	0.679239	20	0.155065	0.844935	1.030461	0.844935	0.999734	20	0.844935	1.030461	1.030461
mmu04620 Toll-like receptor signaling pathway	0.155141491	1.021715	0.155141	0.679239	45	0.155141	0.844859	1.021715	0.844859	0.999734	45	0.844859	1.021715	1.021715
mmu04270 Vascular smooth muscle contraction	0.158566232	1.005513	0.158566	0.679239	51	0.158566	0.841434	1.005513	0.841434	0.999734	51	0.841434	1.005513	1.005513
mmu04964 Proximal tubule bicarbonate reclamation	0.17009559	0.981533	0.170096	0.679239	10	0.170096	0.829904	0.981533	0.829904	0.999734	10	0.829904	0.981533	0.981533
mmu04664 Fc epsilon RI signaling pathway	0.170878821	0.961015	0.170879	0.679239	34	0.170879	0.829121	0.961015	0.829121	0.999734	34	0.829121	0.961015	0.961015
mmu00500 Starch and sucrose metabolism	0.175267492	0.956398	0.175267	0.679239	11	0.175267	0.824733	0.956398	0.824733	0.999734	11	0.824733	0.956398	0.956398
mmu00620 Pyruvate metabolism	0.176252458	0.94148	0.176252	0.679239	20	0.176252	0.823748	0.94148	0.823748	0.999734	20	0.823748	0.94148	0.94148
mmu04966 Collecting duct acid secretion	0.183450733	0.919164	0.183451	0.679239	15	0.183451	0.816549	0.919164	0.816549	0.999734	15	0.816549	0.919164	0.919164
mmu03060 Protein export	0.188788311	0.898639	0.188788	0.679239	16	0.188788	0.811212	0.898639	0.811212	0.999734	16	0.811212	0.898639	0.898639
mmu04530 Tight junction	0.192912558	0.870295	0.192913	0.679239	64	0.192913	0.807087	0.870295	0.807087	0.999734	64	0.807087	0.870295	0.870295
mmu04260 Cardiac muscle contraction	0.207197555	0.822167	0.207198	0.679239	36	0.207198	0.792802	0.822167	0.792802	0.999734	36	0.792802	0.822167	0.822167
mmu00565 Ether lipid metabolism	0.20842096	0.824509	0.208421	0.679239	15	0.208421	0.791579	0.824509	0.791579	0.999734	15	0.791579	0.824509	0.824509
mmu04917 Prolactin signaling pathway	0.213039574	0.801986	0.21304	0.679239	35	0.21304	0.78696	0.801986	0.78696	0.999734	35	0.78696	0.801986	0.801986
mmu00640 Propanoate metabolism	0.21482957	0.803062	0.21483	0.679239	14	0.21483	0.78517	0.803062	0.78517	0.999734	14	0.78517	0.803062	0.803062
mmu04920 Adipocytokine signaling pathway	0.215075603	0.793331	0.215076	0.679239	43	0.215076	0.784924	0.793331	0.784924	0.999734	43	0.784924	0.793331	0.793331
mmu04672 Intestinal immune network for IgA production	0.218324491	0.79748	0.218324	0.679239	15	0.218324	0.781676	0.79748	0.781676	0.999734	15	0.781676	0.79748	0.79748

Supplemental Table 5

mmu04640 Hematopoietic cell lineage	0.226369768	0.758957	0.22637	0.679239	30	0.22637	0.77363	0.758957	0.77363	0.999734	30	0.77363	0.758957	0.758957
mmu03030 DNA replication	0.231621102	0.739661	0.231621	0.679239	25	0.231621	0.768379	0.739661	0.768379	0.999734	25	0.768379	0.739661	0.739661
mmu00900 Terpenoid backbone biosynthesis	0.236230431	0.732876	0.23623	0.679239	14	0.23623	0.76377	0.732876	0.76377	0.999734	14	0.76377	0.732876	0.732876
mmu04010 MAPK signaling pathway	0.239104967	0.710595	0.239105	0.679239	121	0.239105	0.760895	0.710595	0.760895	0.999734	121	0.760895	0.710595	0.710595
mmu00040 Pentose and glucuronate interconversions	0.245142908	0.707921	0.245143	0.679239	10	0.245143	0.754857	0.707921	0.754857	0.999734	10	0.754857	0.707921	0.707921
mmu04713 Circadian entrainment	0.254407499	0.664407	0.254407	0.679239	41	0.254407	0.745593	0.664407	0.745593	0.999734	41	0.745593	0.664407	0.664407
mmu04970 Salivary secretion	0.255201669	0.661256	0.255202	0.679239	40	0.255202	0.744798	0.661256	0.744798	0.999734	40	0.744798	0.661256	0.661256
mmu04150 mTOR signaling pathway	0.257596157	0.654393	0.257596	0.679239	34	0.257596	0.742404	0.654393	0.742404	0.999734	34	0.742404	0.654393	0.654393
mmu04623 Cytosolic DNA-sensing pathway	0.259791366	0.648536	0.259791	0.679239	27	0.259791	0.740209	0.648536	0.740209	0.999734	27	0.740209	0.648536	0.648536
mmu04650 Natural killer cell mediated cytotoxicity	0.261830009	0.640343	0.26183	0.679239	44	0.26183	0.73817	0.640343	0.73817	0.999734	44	0.73817	0.640343	0.640343
mmu04390 Hippo signaling pathway	0.265645717	0.627602	0.265646	0.679239	72	0.265646	0.734354	0.627602	0.734354	0.999734	72	0.734354	0.627602	0.627602
mmu04144 Endocytosis	0.273667988	0.602666	0.273668	0.679239	114	0.273668	0.726332	0.602666	0.726332	0.999734	114	0.726332	0.602666	0.602666
mmu03050 Proteasome	0.276137128	0.598351	0.276137	0.679239	34	0.276137	0.723863	0.598351	0.723863	0.999734	34	0.723863	0.598351	0.598351
mmu00250 Alanine, aspartate and glutamate metabolism	0.27655165	0.600198	0.276552	0.679239	16	0.276552	0.723448	0.600198	0.723448	0.999734	16	0.723448	0.600198	0.600198
mmu04630 Jak-STAT signaling pathway	0.282899094	0.57645	0.282899	0.679239	58	0.282899	0.717101	0.57645	0.717101	0.999734	58	0.717101	0.57645	0.57645
mmu04146 Peroxisome	0.301301769	0.522705	0.301302	0.679239	49	0.301302	0.698698	0.522705	0.698698	0.999734	49	0.698698	0.522705	0.522705
mmu04973 Carbohydrate digestion and absorption	0.304510944	0.519498	0.304511	0.679239	13	0.304511	0.695489	0.519498	0.695489	0.999734	13	0.695489	0.519498	0.519498
mmu04916 Melanogenesis	0.307341251	0.505392	0.307341	0.679239	42	0.307341	0.692659	0.505392	0.692659	0.999734	42	0.692659	0.505392	0.505392
mmu00270 Cysteine and methionine metabolism	0.310173357	0.502229	0.310173	0.679239	14	0.310173	0.689827	0.502229	0.689827	0.999734	14	0.689827	0.502229	0.502229
mmu04726 Serotonergic synapse	0.313521713	0.48789	0.313522	0.679239	41	0.313522	0.686478	0.48789	0.686478	0.999734	41	0.686478	0.48789	0.48789
mmu04725 Cholinergic synapse	0.315897214	0.481025	0.315897	0.679239	49	0.315897	0.684103	0.481025	0.684103	0.999734	49	0.684103	0.481025	0.481025
mmu00590 Arachidonic acid metabolism	0.324857522	0.458245	0.324858	0.679239	18	0.324858	0.675142	0.458245	0.675142	0.999734	18	0.675142	0.458245	0.458245
mmu04975 Fat digestion and absorption	0.325889383	0.45656	0.325889	0.679239	14	0.325889	0.674111	0.45656	0.674111	0.999734	14	0.674111	0.45656	0.45656
mmu00020 Citrate cycle (TCA cycle)	0.336354886	0.427099	0.336355	0.679239	18	0.336355	0.663645	0.427099	0.663645	0.999734	18	0.663645	0.427099	0.427099
mmu00562 Inositol phosphate metabolism	0.336865197	0.423107	0.336865	0.679239	31	0.336865	0.663135	0.423107	0.663135	0.999734	31	0.663135	0.423107	0.423107
mmu04612 Antigen processing and presentation	0.338538076	0.418472	0.338538	0.679239	32	0.338538	0.661462	0.418472	0.661462	0.999734	32	0.661462	0.418472	0.418472
mmu04080 Neuroactive ligand-receptor interaction	0.338810562	0.416556	0.338811	0.679239	74	0.338811	0.661189	0.416556	0.661189	0.999734	74	0.661189	0.416556	0.416556
mmu00510 N-Glycan biosynthesis	0.339434733	0.416607	0.339435	0.679239	28	0.339435	0.660565	0.416607	0.660565	0.999734	28	0.660565	0.416607	0.416607
mmu04912 GnRH signaling pathway	0.342260472	0.407573	0.34226	0.679239	49	0.34226	0.65774	0.407573	0.65774	0.999734	49	0.65774	0.407573	0.407573
mmu04744 Phototransduction	0.34470346	0.410336	0.344703	0.679239	10	0.344703	0.655297	0.410336	0.655297	0.999734	10	0.655297	0.410336	0.410336
mmu00630 Glyoxylate and dicarboxylate metabolism	0.346476973	0.399411	0.346477	0.679239	15	0.346477	0.653523	0.399411	0.653523	0.999734	15	0.653523	0.399411	0.399411
mmu00380 Tryptophan metabolism	0.349349391	0.393931	0.349349	0.679239	10	0.349349	0.650651	0.393931	0.650651	0.999734	10	0.650651	0.393931	0.393931
mmu04350 TGF-beta signaling pathway	0.352055627	0.381186	0.352056	0.679239	40	0.352056	0.647944	0.381186	0.647944	0.999734	40	0.647944	0.381186	0.381186
mmu04320 Dorso-ventral axis formation	0.355694497	0.374125	0.355694	0.679239	16	0.355694	0.644306	0.374125	0.644306	0.999734	16	0.644306	0.374125	0.374125
mmu00561 Glycerolipid metabolism	0.357388564	0.367245	0.357389	0.679239	30	0.357389	0.642611	0.367245	0.642611	0.999734	30	0.642611	0.367245	0.367245
mmu00980 Metabolism of xenobiotics by cytochrome P450	0.35814719	0.366008	0.358147	0.679239	21	0.358147	0.641853	0.366008	0.641853	0.999734	21	0.641853	0.366008	0.366008
mmu00071 Fatty acid degradation	0.358261856	0.365776	0.358262	0.679239	22	0.358262	0.641738	0.365776	0.641738	0.999734	22	0.641738	0.365776	0.365776
mmu04976 Bile secretion	0.361174429	0.357135	0.361174	0.679239	30	0.361174	0.638826	0.357135	0.638826	0.999734	30	0.638826	0.357135	0.357135
mmu00480 Glutathione metabolism	0.364868295	0.347094	0.364868	0.679239	31	0.364868	0.635132	0.347094	0.635132	0.999734	31	0.635132	0.347094	0.347094
mmu04723 Retrograde endocannabinoid signaling	0.366932546	0.341305	0.366933	0.679239	42	0.366933	0.633067	0.341305	0.633067	0.999734	42	0.633067	0.341305	0.341305
mmu00532 Glycosaminoglycan biosynthesis - chondroitin sulfate	0.38131003	0.308116	0.38131	0.679239	10	0.38131	0.61869	0.308116	0.61869	0.999734	10	0.61869	0.308116	0.308116
mmu04918 Thyroid hormone synthesis	0.381777939	0.30211	0.381778	0.679239	33	0.381778	0.618222	0.30211	0.618222	0.999734	33	0.618222	0.30211	0.30211
mmu04961 Endocrine and other factor-regulated calcium reabsorption	0.382933075	0.299374	0.382933	0.679239	28	0.382933	0.617067	0.299374	0.617067	0.999734	28	0.617067	0.299374	0.299374
mmu00830 Retinol metabolism	0.383374257	0.300331	0.383374	0.679239	13	0.383374	0.616626	0.300331	0.616626	0.999734	13	0.616626	0.300331	0.300331
mmu04514 Cell adhesion molecules (CAMs)	0.39842447	0.258001	0.398424	0.690147	65	0.398424	0.601576	0.258001	0.601576	0.999734	65	0.601576	0.258001	0.258001
mmu00280 Valine, leucine and isoleucine degradation	0.401277929	0.251419	0.401278	0.690147	29	0.401278	0.598722	0.251419	0.598722	0.999734	29	0.598722	0.251419	0.251419
mmu04728 Dopaminergic synapse	0.40537309	0.24004	0.405373	0.690147	63	0.405373	0.594627	0.24004	0.594627	0.999734	63	0.594627	0.24004	0.24004
mmu00564 Glycerophospholipid metabolism	0.406466948	0.237382	0.406467	0.690147	44	0.406467	0.593533	0.237382	0.593533	0.999734	44	0.593533	0.237382	0.237382
mmu00650 Butanoate metabolism	0.422262111	0.198945	0.422262	0.707087	11	0.422262	0.577738	0.198945	0.577738	0.999734	11	0.577738	0.198945	0.198945
mmu04070 Phosphatidylinositol signaling system	0.4279736	0.182142	0.427974	0.707087	40	0.427974	0.572026	0.182142	0.572026	0.999734	40	0.572026	0.182142	0.182142

Supplemental Table 5

mmu04722 Neurotrophin signaling pathway	0.432867111	0.169428	0.432867	0.707087	66	0.432867	0.567133	0.169428	0.567133	0.999734	66	0.567133	0.169428	0.169428
mmu00030 Pentose phosphate pathway	0.438324531	0.156555	0.438325	0.707087	16	0.438325	0.561675	0.156555	0.561675	0.999734	16	0.561675	0.156555	0.156555
mmu00970 Aminoacyl-tRNA biosynthesis	0.442663512	0.145003	0.442664	0.707087	29	0.442664	0.557336	0.145003	0.557336	0.999734	29	0.557336	0.145003	0.145003
mmu04151 PI3K-Akt signaling pathway	0.447698154	0.1316	0.447698	0.707087	152	0.447698	0.552302	0.1316	0.552302	0.999734	152	0.552302	0.1316	0.1316
mmu00140 Steroid hormone biosynthesis	0.450165255	0.126677	0.450165	0.707087	13	0.450165	0.549835	0.126677	0.549835	0.999734	13	0.549835	0.126677	0.126677
mmu00190 Oxidative phosphorylation	0.451982783	0.120858	0.451983	0.707087	79	0.451983	0.548017	0.120858	0.548017	0.999734	79	0.548017	0.120858	0.120858
mmu00230 Purine metabolism	0.455773191	0.111285	0.455773	0.707087	75	0.455773	0.544227	0.111285	0.544227	0.999734	75	0.544227	0.111285	0.111285
mmu04622 RIG-I-like receptor signaling pathway	0.463346669	0.092414	0.463347	0.707087	32	0.463347	0.536653	0.092414	0.536653	0.999734	32	0.536653	0.092414	0.092414
mmu04974 Protein digestion and absorption	0.469983969	0.075586	0.469984	0.707087	38	0.469984	0.530016	0.075586	0.530016	0.999734	38	0.530016	0.075586	0.075586
mmu04064 NF-kappa B signaling pathway	0.471202137	0.072472	0.471202	0.707087	42	0.471202	0.528798	0.072472	0.528798	0.999734	42	0.528798	0.072472	0.072472
mmu04972 Pancreatic secretion	0.474518189	0.064144	0.474518	0.707087	37	0.474518	0.525482	0.064144	0.525482	0.999734	37	0.525482	0.064144	0.064144
mmu04978 Mineral absorption	0.482591937	0.043941	0.482592	0.707087	28	0.482592	0.517408	0.043941	0.517408	0.999734	28	0.517408	0.043941	0.043941
mmu00982 Drug metabolism - cytochrome P450	0.488099539	0.030032	0.4881	0.707087	20	0.4881	0.5119	0.030032	0.5119	0.999734	20	0.5119	0.030032	0.030032
mmu00100 Steroid biosynthesis	0.490324553	0.024541	0.490325	0.707087	12	0.490325	0.509675	0.024541	0.509675	0.999734	12	0.509675	0.024541	0.024541
mmu04540 Gap junction	0.497952958	0.005147	0.497953	0.707087	45	0.497953	0.502047	0.005147	0.502047	0.999734	45	0.502047	0.005147	0.005147
mmu04913 Ovarian steroidogenesis	0.499587216	0.001042	0.499587	0.707087	18	0.499587	0.500413	0.001042	0.500413	0.999734	18	0.500413	0.001042	0.001042
mmu00410 beta-Alanine metabolism	0.502352303	-0.00597	0.502352	0.707087	13	0.502352	0.497648	-0.00597	0.497648	0.999734	13	0.497648	-0.00597	-0.00597
mmu00534 Glycosaminoglycan biosynthesis - heparan sulfate / he	0.503202757	-0.00812	0.503203	0.707087	15	0.503203	0.496797	-0.00812	0.496797	0.999734	15	0.496797	-0.00812	-0.00812
mmu04914 Progesterone-mediated oocyte maturation	0.510992526	-0.02765	0.510993	0.711896	41	0.510993	0.489007	-0.02765	0.489007	0.999734	41	0.489007	-0.02765	-0.02765
mmu00670 One carbon pool by folate	0.537665035	-0.0957	0.537665	0.742707	12	0.537665	0.462335	-0.0957	0.462335	0.999734	12	0.462335	-0.0957	-0.0957
mmu04727 GABAergic synapse	0.553900101	-0.13614	0.5539	0.758284	33	0.5539	0.4461	-0.13614	0.4461	0.999734	33	0.4461	-0.13614	-0.13614
mmu04971 Gastric acid secretion	0.558245599	-0.14708	0.558246	0.758284	35	0.558246	0.441754	-0.14708	0.441754	0.999734	35	0.441754	-0.14708	-0.14708
mmu04962 Vasopressin-regulated water reabsorption	0.576491341	-0.19378	0.576491	0.775394	31	0.576491	0.423509	-0.19378	0.423509	0.999734	31	0.423509	-0.19378	-0.19378
mmu04724 Glutamatergic synapse	0.580356526	-0.20346	0.580357	0.775394	45	0.580357	0.419643	-0.20346	0.419643	0.999734	45	0.419643	-0.20346	-0.20346
mmu04720 Long-term potentiation	0.586947393	-0.22054	0.586947	0.777825	37	0.586947	0.413053	-0.22054	0.413053	0.999734	37	0.413053	-0.22054	-0.22054
mmu00240 Pyrimidine metabolism	0.597906518	-0.2486	0.597907	0.778604	54	0.597907	0.402093	-0.2486	0.402093	0.999734	54	0.402093	-0.2486	-0.2486
mmu04114 Oocyte meiosis	0.598416239	-0.24982	0.598416	0.778604	62	0.598416	0.401584	-0.24982	0.401584	0.999734	62	0.401584	-0.24982	-0.24982
mmu00514 Other types of O-glycan biosynthesis	0.601865671	-0.26169	0.601866	0.778604	14	0.601866	0.398134	-0.26169	0.398134	0.999734	14	0.398134	-0.26169	-0.26169
mmu04210 Apoptosis	0.613908578	-0.29052	0.613909	0.782187	42	0.613909	0.386091	-0.29052	0.386091	0.999734	42	0.386091	-0.29052	-0.29052
mmu04340 Hedgehog signaling pathway	0.614232472	-0.29269	0.614232	0.782187	19	0.614232	0.385768	-0.29269	0.385768	0.999734	19	0.385768	-0.29269	-0.29269
mmu04911 Insulin secretion	0.638267167	-0.355	0.638267	0.805095	45	0.638267	0.361733	-0.355	0.361733	0.999734	45	0.361733	-0.355	-0.355
mmu00310 Lysine degradation	0.642100246	-0.36672	0.6421	0.805095	23	0.6421	0.3579	-0.36672	0.3579	0.999734	23	0.3579	-0.36672	-0.36672
mmu04960 Aldosterone-regulated sodium reabsorption	0.652878896	-0.39582	0.652879	0.812361	22	0.652879	0.347121	-0.39582	0.347121	0.999734	22	0.347121	-0.39582	-0.39582
mmu04012 ErbB signaling pathway	0.666294448	-0.43162	0.666294	0.822773	37	0.666294	0.333706	-0.43162	0.333706	0.999734	37	0.333706	-0.43162	-0.43162
mmu04370 VEGF signaling pathway	0.697087279	-0.51971	0.697087	0.854325	33	0.697087	0.302913	-0.51971	0.302913	0.999734	33	0.302913	-0.51971	-0.51971
mmu04310 Wnt signaling pathway	0.72920444	-0.61198	0.729204	0.873959	68	0.729204	0.270796	-0.61198	0.270796	0.999734	68	0.270796	-0.61198	-0.61198
mmu00563 Glycosylphosphatidylinositol(GPI)-anchor biosynthesis	0.735450838	-0.64018	0.735451	0.873959	13	0.735451	0.264549	-0.64018	0.264549	0.999734	13	0.264549	-0.64018	-0.64018
mmu04140 Regulation of autophagy	0.740502215	-0.65278	0.740502	0.873959	18	0.740502	0.259498	-0.65278	0.259498	0.999734	18	0.259498	-0.65278	-0.65278
mmu04742 Taste transduction	0.747400963	-0.67896	0.747401	0.873959	11	0.747401	0.252599	-0.67896	0.252599	0.999734	11	0.252599	-0.67896	-0.67896
mmu03430 Mismatch repair	0.753084919	-0.69463	0.753085	0.873959	15	0.753085	0.246915	-0.69463	0.246915	0.999734	15	0.246915	-0.69463	-0.69463
mmu04520 Adherens junction	0.75667361	-0.69877	0.756674	0.873959	43	0.756674	0.243326	-0.69877	0.243326	0.999734	43	0.243326	-0.69877	-0.69877
mmu04020 Calcium signaling pathway	0.760475014	-0.70956	0.760475	0.873959	78	0.760475	0.239525	-0.70956	0.239525	0.999734	78	0.239525	-0.70956	-0.70956
mmu04910 Insulin signaling pathway	0.762927212	-0.71755	0.762927	0.873959	78	0.762927	0.237073	-0.71755	0.237073	0.999734	78	0.237073	-0.71755	-0.71755
mmu04115 p53 signaling pathway	0.763432921	-0.72221	0.763433	0.873959	34	0.763433	0.236567	-0.72221	0.236567	0.999734	34	0.236567	-0.72221	-0.72221
mmu04810 Regulation of actin cytoskeleton	0.773139912	-0.75059	0.77314	0.873959	110	0.77314	0.22686	-0.75059	0.22686	0.999734	110	0.22686	-0.75059	-0.75059
mmu03040 Spliceosome	0.779687831	-0.77401	0.779688	0.873959	65	0.779688	0.220312	-0.77401	0.220312	0.999734	65	0.220312	-0.77401	-0.77401
mmu04512 ECM-receptor interaction	0.788555614	-0.80599	0.788556	0.873959	41	0.788556	0.211444	-0.80599	0.211444	0.999734	41	0.211444	-0.80599	-0.80599
mmu04330 Notch signaling pathway	0.789325323	-0.81127	0.789325	0.873959	26	0.789325	0.210675	-0.81127	0.210675	0.999734	26	0.210675	-0.81127	-0.81127
mmu03420 Nucleotide excision repair	0.790157031	-0.81369	0.790157	0.873959	30	0.790157	0.209843	-0.81369	0.209843	0.999734	30	0.209843	-0.81369	-0.81369
mmu04510 Focal adhesion	0.793533163	-0.82063	0.793533	0.873959	98	0.793533	0.206467	-0.82063	0.206467	0.999734	98	0.206467	-0.82063	-0.82063

Supplemental Table 5

mmu00860 Porphyrin and chlorophyll metabolism	0.800781652	-0.86313	0.800782	0.876023	16	0.800782	0.199218	-0.86313	0.199218	0.999734	16	0.199218	-0.86313	-0.86313
mmu03018 RNA degradation	0.808399162	-0.8765	0.808399	0.87846	44	0.808399	0.191601	-0.8765	0.191601	0.999734	44	0.191601	-0.8765	-0.8765
mmu04110 Cell cycle	0.822038647	-0.92663	0.822039	0.887366	64	0.822039	0.177961	-0.92663	0.177961	0.999734	64	0.177961	-0.92663	-0.92663
mmu03010 Ribosome	0.828048026	-0.95015	0.828048	0.887973	78	0.828048	0.171952	-0.95015	0.171952	0.999734	78	0.171952	-0.95015	-0.95015
mmu03020 RNA polymerase	0.866774829	-1.1345	0.866775	0.912406	16	0.866775	0.133225	-1.1345	0.133225	0.999734	16	0.133225	-1.1345	-1.1345
mmu04710 Circadian rhythm	0.867504159	-1.13648	0.867504	0.912406	17	0.867504	0.132496	-1.13648	0.132496	0.999734	17	0.132496	-1.13648	-1.13648
mmu03440 Homologous recombination	0.867625146	-1.1357	0.867625	0.912406	18	0.867625	0.132375	-1.1357	0.132375	0.999734	18	0.132375	-1.1357	-1.1357
mmu04740 Olfactory transduction	0.884065967	-1.19827	0.884066	0.923736	161	0.884066	0.115934	-1.19827	0.115934	0.999734	161	0.115934	-1.19827	-1.19827
mmu03008 Ribosome biogenesis in eukaryotes	0.914551454	-1.38598	0.914551	0.945848	39	0.914551	0.085449	-1.38598	0.085449	0.999734	39	0.085449	-1.38598	-1.38598
mmu04360 Axon guidance	0.916833898	-1.39347	0.916834	0.945848	61	0.916834	0.083166	-1.39347	0.083166	0.999734	61	0.083166	-1.39347	-1.39347
mmu03460 Fanconi anemia pathway	0.926567177	-1.48347	0.926567	0.949877	23	0.926567	0.073433	-1.48347	0.073433	0.999734	23	0.073433	-1.48347	-1.48347
mmu03022 Basal transcription factors	0.964471225	-1.86462	0.964471	0.977515	18	0.964471	0.035529	-1.86462	0.035529	0.999734	18	0.035529	-1.86462	-1.86462
mmu03015 mRNA surveillance pathway	0.965520615	-1.8382	0.965521	0.977515	52	0.965521	0.034479	-1.8382	0.034479	0.999734	52	0.034479	-1.8382	-1.8382
mmu04120 Ubiquitin mediated proteolysis	0.976242804	-1.99902	0.976243	0.982269	78	0.976243	0.023757	-1.99902	0.023757	0.999734	78	0.023757	-1.99902	-1.99902
mmu03013 RNA transport	0.992794018	-2.47271	0.992794	0.992794	93	0.992794	0.007206	-2.47271	0.007206	0.999734	93	0.007206	-2.47271	-2.47271

Supplemental Table 6

KEGG_ID	greater.p.geo	greater.st	greater.p.	greater.q.	greater.se	greater.ex	less.p.geo	less.stat.			less.set.siz	stats.stat.			
	mean	at.mean	val	val	t.size	p1	mean	mean	less.p.val	less.q.val	e	less.exp1	mean	stats.exp1	
mmu04141 Protein processing in endoplasmic reticulum	0.000410681	3.40784	0.000411	0.064477	95	0.000411	0.999589	3.40784	0.999589	0.999589		95	0.999589	3.40784	3.40784
mmu04142 Lysosome	0.00256712	2.837921	0.002567	0.201519	82	0.002567	0.997433	2.837921	0.997433	0.999589		82	0.997433	2.837921	2.837921
mmu04145 Phagosome	0.005421831	2.578284	0.005422	0.283742	81	0.005422	0.994578	2.578284	0.994578	0.999589		81	0.994578	2.578284	2.578284
mmu03060 Protein export	0.0072676	2.585855	0.007268	0.285253	17	0.007268	0.992732	2.585855	0.992732	0.999589		17	0.992732	2.585855	2.585855
mmu04130 SNARE interactions in vesicular transport	0.012816358	2.311015	0.012816	0.399603	24	0.012816	0.987184	2.311015	0.987184	0.999589		24	0.987184	2.311015	2.311015
mmu00330 Arginine and proline metabolism	0.016290906	2.226078	0.016291	0.399603	22	0.016291	0.983709	2.226078	0.983709	0.999589		22	0.983709	2.226078	2.226078
mmu04380 Osteoclast differentiation	0.021882925	2.043864	0.021883	0.399603	59	0.021883	0.978117	2.043864	0.978117	0.999589		59	0.978117	2.043864	2.043864
mmu04610 Complement and coagulation cascades	0.02262682	2.086324	0.022627	0.399603	20	0.022627	0.977373	2.086324	0.977373	0.999589		20	0.977373	2.086324	2.086324
mmu04066 HIF-1 signaling pathway	0.022907167	2.021484	0.022907	0.399603	60	0.022907	0.977093	2.021484	0.977093	0.999589		60	0.977093	2.021484	2.021484
mmu04151 PI3K-Akt signaling pathway	0.028479655	1.910993	0.02848	0.447131	152	0.02848	0.97152	1.910993	0.97152	0.999589		152	0.97152	1.910993	1.910993
mmu00531 Glycosaminoglycan degradation	0.047773239	1.76589	0.047773	0.601667	13	0.047773	0.952227	1.76589	0.952227	0.999589		13	0.952227	1.76589	1.76589
mmu04660 T cell receptor signaling pathway	0.049580282	1.671445	0.04958	0.601667	46	0.04958	0.95042	1.671445	0.95042	0.999589		46	0.95042	1.671445	1.671445
mmu04721 Synaptic vesicle cycle	0.056532934	1.606178	0.056533	0.601667	36	0.056533	0.943467	1.606178	0.943467	0.999589		36	0.943467	1.606178	1.606178
mmu04668 TNF signaling pathway	0.063580618	1.539694	0.063581	0.601667	55	0.063581	0.936419	1.539694	0.936419	0.999589		55	0.936419	1.539694	1.539694
mmu04144 Endocytosis	0.068911549	1.489342	0.068912	0.601667	112	0.068912	0.931088	1.489342	0.931088	0.999589		112	0.931088	1.489342	1.489342
mmu00520 Amino sugar and nucleotide sugar metabolism	0.07018986	1.496376	0.07019	0.601667	28	0.07019	0.92981	1.496376	0.92981	0.999589		28	0.92981	1.496376	1.496376
mmu00010 Glycolysis / Gluconeogenesis	0.070506721	1.497907	0.070507	0.601667	26	0.070507	0.929493	1.497907	0.929493	0.999589		26	0.929493	1.497907	1.497907
mmu04060 Cytokine-cytokine receptor interaction	0.072753691	1.464812	0.072754	0.601667	77	0.072754	0.927246	1.464812	0.927246	0.999589		77	0.927246	1.464812	1.464812
mmu04670 Leukocyte transendothelial migration	0.072813171	1.46715	0.072813	0.601667	52	0.072813	0.927187	1.46715	0.927187	0.999589		52	0.927187	1.46715	1.46715
mmu00510 N-Glycan biosynthesis	0.08869987	1.373637	0.0887	0.687069	25	0.0887	0.9113	1.373637	0.9113	0.999589		25	0.9113	1.373637	1.373637
mmu04662 B cell receptor signaling pathway	0.097223618	1.314282	0.097224	0.687069	33	0.097224	0.902776	1.314282	0.902776	0.999589		33	0.902776	1.314282	1.314282
mmu04620 Toll-like receptor signaling pathway	0.101907706	1.281579	0.101908	0.687069	45	0.101908	0.898092	1.281579	0.898092	0.999589		45	0.898092	1.281579	1.281579
mmu00600 Sphingolipid metabolism	0.103341056	1.28633	0.103341	0.687069	20	0.103341	0.896659	1.28633	0.896659	0.999589		20	0.896659	1.28633	1.28633
mmu04530 Tight junction	0.105029704	1.261249	0.10503	0.687069	59	0.10503	0.89497	1.261249	0.89497	0.999589		59	0.89497	1.261249	1.261249
mmu04970 Salivary secretion	0.137949921	1.098335	0.13795	0.726789	38	0.13795	0.86205	1.098335	0.86205	0.999589		38	0.86205	1.098335	1.098335
mmu04150 mTOR signaling pathway	0.147180746	1.056527	0.147181	0.726789	36	0.147181	0.852819	1.056527	0.852819	0.999589		36	0.852819	1.056527	1.056527
mmu04728 Dopaminergic synapse	0.148175845	1.049083	0.148176	0.726789	64	0.148176	0.851824	1.049083	0.851824	0.999589		64	0.851824	1.049083	1.049083
mmu04062 Chemokine signaling pathway	0.149672508	1.042138	0.149673	0.726789	64	0.149673	0.850327	1.042138	0.850327	0.999589		64	0.850327	1.042138	1.042138
mmu04810 Regulation of actin cytoskeleton	0.150480739	1.037346	0.150481	0.726789	102	0.150481	0.849519	1.037346	0.849519	0.999589		102	0.849519	1.037346	1.037346
mmu00511 Other glycan degradation	0.155592363	1.041598	0.155592	0.726789	11	0.155592	0.844408	1.041598	0.844408	0.999589		11	0.844408	1.041598	1.041598
mmu04915 Estrogen signaling pathway	0.166969638	0.972487	0.16697	0.726789	46	0.16697	0.83303	0.972487	0.83303	0.999589		46	0.83303	0.972487	0.972487
mmu04725 Cholinergic synapse	0.167010813	0.971296	0.167011	0.726789	51	0.167011	0.832989	0.971296	0.832989	0.999589		51	0.832989	0.971296	0.971296
mmu04640 Hematopoietic cell lineage	0.171095573	0.960995	0.171096	0.726789	29	0.171096	0.828904	0.960995	0.828904	0.999589		29	0.828904	0.960995	0.960995
mmu04672 Intestinal immune network for IgA production	0.17254049	0.967597	0.17254	0.726789	16	0.17254	0.82746	0.967597	0.82746	0.999589		16	0.82746	0.967597	0.967597
mmu04510 Focal adhesion	0.173330634	0.943532	0.173331	0.726789	99	0.173331	0.826669	0.943532	0.826669	0.999589		99	0.826669	0.943532	0.943532
mmu04270 Vascular smooth muscle contraction	0.179922089	0.920005	0.179922	0.726789	52	0.179922	0.820078	0.920005	0.820078	0.999589		52	0.820078	0.920005	0.920005
mmu04920 Adipocytokine signaling pathway	0.184887989	0.902699	0.184888	0.726789	41	0.184888	0.815112	0.902699	0.815112	0.999589		41	0.815112	0.902699	0.902699
mmu00051 Fructose and mannose metabolism	0.186068469	0.904496	0.186068	0.726789	18	0.186068	0.813932	0.904496	0.813932	0.999589		18	0.813932	0.904496	0.904496
mmu04612 Antigen processing and presentation	0.191192234	0.881331	0.191192	0.726789	31	0.191192	0.808808	0.881331	0.808808	0.999589		31	0.808808	0.881331	0.881331
mmu04320 Dorso-ventral axis formation	0.194565221	0.876124	0.194565	0.726789	14	0.194565	0.805435	0.876124	0.805435	0.999589		14	0.805435	0.876124	0.876124
mmu00562 Inositol phosphate metabolism	0.196100906	0.861786	0.196101	0.726789	33	0.196101	0.803899	0.861786	0.803899	0.999589		33	0.803899	0.861786	0.861786
mmu04664 Fc epsilon RI signaling pathway	0.196574212	0.861079	0.196574	0.726789	32	0.196574	0.803426	0.861079	0.803426	0.999589		32	0.803426	0.861079	0.861079
mmu04722 Neurotrophin signaling pathway	0.208669508	0.814275	0.20867	0.726789	63	0.20867	0.79133	0.814275	0.79133	0.999589		63	0.79133	0.814275	0.814275
mmu04976 Bile secretion	0.214490861	0.798052	0.214491	0.726789	25	0.214491	0.785509	0.798052	0.785509	0.999589		25	0.785509	0.798052	0.798052
mmu04070 Phosphatidylinositol signaling system	0.215208537	0.79247	0.215209	0.726789	42	0.215209	0.784791	0.79247	0.784791	0.999589		42	0.784791	0.79247	0.79247
mmu04621 NOD-like receptor signaling pathway	0.218522603	0.786649	0.218523	0.726789	19	0.218523	0.781477	0.786649	0.781477	0.999589		19	0.781477	0.786649	0.786649
mmu00260 Glycine, serine and threonine metabolism	0.220532982	0.780779	0.220533	0.726789	16	0.220533	0.779467	0.780779	0.779467	0.999589		16	0.779467	0.780779	0.780779
mmu04622 RIG-I-like receptor signaling pathway	0.229145122	0.747621	0.229145	0.726789	32	0.229145	0.770855	0.747621	0.770855	0.999589		32	0.770855	0.747621	0.747621

Supplemental Table 6

mmu00564 Glycerophospholipid metabolism	0.233098535	0.732025	0.233099	0.726789	44	0.233099	0.766901	0.732025	0.766901	0.999589	44	0.766901	0.732025	0.732025
mmu04020 Calcium signaling pathway	0.234958518	0.724495	0.234959	0.726789	75	0.234959	0.765041	0.724495	0.765041	0.999589	75	0.765041	0.724495	0.724495
mmu03050 Proteasome	0.236865942	0.722566	0.236866	0.726789	33	0.236866	0.763134	0.722566	0.763134	0.999589	33	0.763134	0.722566	0.722566
mmu03018 RNA degradation	0.240720025	0.707148	0.24072	0.726789	43	0.24072	0.75928	0.707148	0.75928	0.999589	43	0.75928	0.707148	0.707148
mmu04966 Collecting duct acid secretion	0.260230849	0.65042	0.260231	0.770873	16	0.260231	0.739769	0.65042	0.739769	0.999589	16	0.739769	0.65042	0.65042
mmu00970 Aminoacyl-tRNA biosynthesis	0.269913417	0.617824	0.269913	0.776718	26	0.269913	0.730087	0.617824	0.730087	0.999589	26	0.730087	0.617824	0.617824
mmu00052 Galactose metabolism	0.272098632	0.615357	0.272099	0.776718	14	0.272099	0.727901	0.615357	0.727901	0.999589	14	0.727901	0.615357	0.615357
mmu04514 Cell adhesion molecules (CAMs)	0.278665	0.588644	0.278665	0.778254	55	0.278665	0.721335	0.588644	0.721335	0.999589	55	0.721335	0.588644	0.588644
mmu04010 MAPK signaling pathway	0.283407398	0.573783	0.283407	0.778254	120	0.283407	0.716593	0.573783	0.716593	0.999589	120	0.716593	0.573783	0.573783
mmu00563 Glycosylphosphatidylinositol(GPI)-anchor biosynthe	0.291086339	0.559921	0.291086	0.778254	13	0.291086	0.708914	0.559921	0.708914	0.999589	13	0.708914	0.559921	0.559921
mmu01040 Biosynthesis of unsaturated fatty acids	0.29277543	0.55393	0.292775	0.778254	12	0.292775	0.707225	0.55393	0.707225	0.999589	12	0.707225	0.55393	0.55393
mmu04914 Progesterone-mediated oocyte maturation	0.297421842	0.53432	0.297422	0.778254	39	0.297422	0.702578	0.53432	0.702578	0.999589	39	0.702578	0.53432	0.53432
mmu00620 Pyruvate metabolism	0.315040684	0.486325	0.315041	0.780942	17	0.315041	0.684959	0.486325	0.684959	0.999589	17	0.684959	0.486325	0.486325
mmu04912 GnRH signaling pathway	0.319408718	0.471096	0.319409	0.780942	48	0.319409	0.680591	0.471096	0.680591	0.999589	48	0.680591	0.471096	0.471096
mmu00270 Cysteine and methionine metabolism	0.320476872	0.471943	0.320477	0.780942	14	0.320477	0.679523	0.471943	0.679523	0.999589	14	0.679523	0.471943	0.471943
mmu04260 Cardiac muscle contraction	0.32929606	0.444547	0.329296	0.780942	37	0.329296	0.670704	0.444547	0.670704	0.999589	37	0.670704	0.444547	0.444547
mmu00514 Other types of O-glycan biosynthesis	0.331392716	0.444333	0.331393	0.780942	12	0.331393	0.668607	0.444333	0.668607	0.999589	12	0.668607	0.444333	0.444333
mmu04911 Insulin secretion	0.335792962	0.425557	0.335793	0.780942	42	0.335793	0.664207	0.425557	0.664207	0.999589	42	0.664207	0.425557	0.425557
mmu04512 ECM-receptor interaction	0.337865866	0.419898	0.337866	0.780942	41	0.337866	0.662134	0.419898	0.662134	0.999589	41	0.662134	0.419898	0.419898
mmu00350 Tyrosine metabolism	0.338242267	0.422415	0.338242	0.780942	13	0.338242	0.661758	0.422415	0.661758	0.999589	13	0.661758	0.422415	0.422415
mmu04917 Prolactin signaling pathway	0.345075897	0.400737	0.345076	0.781475	36	0.345076	0.654924	0.400737	0.654924	0.999589	36	0.654924	0.400737	0.400737
mmu00410 beta-Alanine metabolism	0.365436902	0.349175	0.365437	0.781475	11	0.365437	0.634563	0.349175	0.634563	0.999589	11	0.634563	0.349175	0.349175
mmu04080 Neuroactive ligand-receptor interaction	0.366892041	0.340761	0.366892	0.781475	74	0.366892	0.633108	0.340761	0.633108	0.999589	74	0.633108	0.340761	0.340761
mmu00670 One carbon pool by folate	0.368238395	0.341382	0.368238	0.781475	11	0.368238	0.631762	0.341382	0.631762	0.999589	11	0.631762	0.341382	0.341382
mmu04666 Fc gamma R-mediated phagocytosis	0.376125296	0.316884	0.376125	0.781475	42	0.376125	0.623875	0.316884	0.623875	0.999589	42	0.623875	0.316884	0.316884
mmu04730 Long-term depression	0.379922246	0.307398	0.379922	0.781475	31	0.379922	0.620078	0.307398	0.620078	0.999589	31	0.620078	0.307398	0.307398
mmu04720 Long-term potentiation	0.391215532	0.277465	0.391216	0.781475	35	0.391216	0.608784	0.277465	0.608784	0.999589	35	0.608784	0.277465	0.277465
mmu04520 Adherens junction	0.391218294	0.277177	0.391218	0.781475	38	0.391218	0.608782	0.277177	0.608782	0.999589	38	0.608782	0.277177	0.277177
mmu04623 Cytosolic DNA-sensing pathway	0.394934757	0.268268	0.394935	0.781475	28	0.394935	0.605065	0.268268	0.605065	0.999589	28	0.605065	0.268268	0.268268
mmu04713 Circadian entrainment	0.395951298	0.265042	0.395951	0.781475	37	0.395951	0.604049	0.265042	0.604049	0.999589	37	0.604049	0.265042	0.265042
mmu00980 Metabolism of xenobiotics by cytochrome P450	0.401314826	0.251612	0.401315	0.781475	21	0.401315	0.598685	0.251612	0.598685	0.999589	21	0.598685	0.251612	0.251612
mmu03320 PPAR signaling pathway	0.403936897	0.244311	0.403937	0.781475	30	0.403937	0.596063	0.244311	0.596063	0.999589	30	0.596063	0.244311	0.244311
mmu00250 Alanine, aspartate and glutamate metabolism	0.407632705	0.235851	0.407633	0.781475	15	0.407633	0.592367	0.235851	0.592367	0.999589	15	0.592367	0.235851	0.235851
mmu04972 Pancreatic secretion	0.408669735	0.232036	0.40867	0.781475	36	0.40867	0.59133	0.232036	0.59133	0.999589	36	0.59133	0.232036	0.232036
mmu04630 Jak-STAT signaling pathway	0.413136467	0.220003	0.413136	0.781475	59	0.413136	0.586864	0.220003	0.586864	0.999589	59	0.586864	0.220003	0.220003
mmu04918 Thyroid hormone synthesis	0.428766682	0.180171	0.428767	0.801385	37	0.428767	0.571233	0.180171	0.571233	0.999589	37	0.571233	0.180171	0.180171
mmu00500 Starch and sucrose metabolism	0.435308546	0.165499	0.435309	0.80404	10	0.435309	0.564691	0.165499	0.564691	0.999589	10	0.564691	0.165499	0.165499
mmu04390 Hippo signaling pathway	0.444101163	0.140857	0.444101	0.809565	66	0.444101	0.555899	0.140857	0.555899	0.999589	66	0.555899	0.140857	0.140857
mmu04114 Oocyte meiosis	0.448612501	0.129477	0.448613	0.809565	56	0.448613	0.551387	0.129477	0.551387	0.999589	56	0.551387	0.129477	0.129477
mmu04012 ErbB signaling pathway	0.460515295	0.099508	0.460515	0.809623	39	0.460515	0.539485	0.099508	0.539485	0.999589	39	0.539485	0.099508	0.099508
mmu03040 Spliceosome	0.462807262	0.093557	0.462807	0.809623	67	0.462807	0.537193	0.093557	0.537193	0.999589	67	0.537193	0.093557	0.093557
mmu00062 Fatty acid elongation	0.472139127	0.070649	0.472139	0.809623	13	0.472139	0.527861	0.070649	0.527861	0.999589	13	0.527861	0.070649	0.070649
mmu04962 Vasopressin-regulated water reabsorption	0.477402774	0.056939	0.477403	0.809623	28	0.477403	0.522597	0.056939	0.522597	0.999589	28	0.522597	0.056939	0.056939
mmu04210 Apoptosis	0.484198769	0.039746	0.484199	0.809623	42	0.484199	0.515801	0.039746	0.515801	0.999589	42	0.515801	0.039746	0.039746
mmu04916 Melanogenesis	0.485233151	0.037165	0.485233	0.809623	40	0.485233	0.514767	0.037165	0.514767	0.999589	40	0.514767	0.037165	0.037165
mmu04978 Mineral absorption	0.485293498	0.037064	0.485293	0.809623	30	0.485293	0.514707	0.037064	0.514707	0.999589	30	0.514707	0.037064	0.037064
mmu00630 Glyoxylate and dicarboxylate metabolism	0.492785904	0.018279	0.492786	0.809623	14	0.492786	0.507214	0.018279	0.507214	0.999589	14	0.507214	0.018279	0.018279
mmu04330 Notch signaling pathway	0.495100303	0.012359	0.4951	0.809623	28	0.4951	0.5049	0.012359	0.5049	0.999589	28	0.5049	0.012359	0.012359
mmu04973 Carbohydrate digestion and absorption	0.50183242	-0.00465	0.501832	0.809623	14	0.501832	0.498168	-0.00465	0.498168	0.999589	14	0.498168	-0.00465	-0.00465
mmu00900 Terpenoid backbone biosynthesis	0.510708781	-0.02717	0.510709	0.809623	14	0.510709	0.489291	-0.02717	0.489291	0.999589	14	0.489291	-0.02717	-0.02717

Supplemental Table 6

mmu00190 Oxidative phosphorylation	0.515532382	-0.03902	0.515532	0.809623	80	0.515532	0.484468	-0.03902	0.484468	0.999589	80	0.484468	-0.03902	-0.03902
mmu04650 Natural killer cell mediated cytotoxicity	0.518767368	-0.04722	0.518767	0.809623	39	0.518767	0.481233	-0.04722	0.481233	0.999589	39	0.481233	-0.04722	-0.04722
mmu02010 ABC transporters	0.525796499	-0.0653	0.525796	0.809623	16	0.525796	0.474204	-0.0653	0.474204	0.999589	16	0.474204	-0.0653	-0.0653
mmu00310 Lysine degradation	0.528066414	-0.07108	0.528066	0.809623	21	0.528066	0.471934	-0.07108	0.471934	0.999589	21	0.471934	-0.07108	-0.07108
mmu00030 Pentose phosphate pathway	0.541693735	-0.10573	0.541694	0.809623	15	0.541694	0.458306	-0.10573	0.458306	0.999589	15	0.458306	-0.10573	-0.10573
mmu03008 Ribosome biogenesis in eukaryotes	0.542520805	-0.10733	0.542521	0.809623	34	0.542521	0.457479	-0.10733	0.457479	0.999589	34	0.457479	-0.10733	-0.10733
mmu04064 NF-kappa B signaling pathway	0.544062455	-0.11112	0.544062	0.809623	35	0.544062	0.455938	-0.11112	0.455938	0.999589	35	0.455938	-0.11112	-0.11112
mmu00565 Ether lipid metabolism	0.546624297	-0.11833	0.546624	0.809623	14	0.546624	0.453376	-0.11833	0.453376	0.999589	14	0.453376	-0.11833	-0.11833
mmu04140 Regulation of autophagy	0.579597548	-0.20382	0.579598	0.83459	16	0.579598	0.420402	-0.20382	0.420402	0.999589	16	0.420402	-0.20382	-0.20382
mmu04961 Endocrine and other factor-regulated calcium reabs	0.585672504	-0.21777	0.585673	0.83459	27	0.585673	0.414327	-0.21777	0.414327	0.999589	27	0.414327	-0.21777	-0.21777
mmu00480 Glutathione metabolism	0.596915812	-0.24651	0.596916	0.83459	30	0.596916	0.403084	-0.24651	0.403084	0.999589	30	0.403084	-0.24651	-0.24651
mmu00071 Fatty acid degradation	0.609282186	-0.27955	0.609282	0.83459	20	0.609282	0.390718	-0.27955	0.390718	0.999589	20	0.390718	-0.27955	-0.27955
mmu00982 Drug metabolism - cytochrome P450	0.611146736	-0.28462	0.611147	0.83459	18	0.611147	0.388853	-0.28462	0.388853	0.999589	18	0.388853	-0.28462	-0.28462
mmu04370 VEGF signaling pathway	0.612927085	-0.28858	0.612927	0.83459	33	0.612927	0.387073	-0.28858	0.387073	0.999589	33	0.387073	-0.28858	-0.28858
mmu00590 Arachidonic acid metabolism	0.621323768	-0.31153	0.621324	0.83459	18	0.621324	0.378676	-0.31153	0.378676	0.999589	18	0.378676	-0.31153	-0.31153
mmu03430 Mismatch repair	0.621690628	-0.31372	0.621691	0.83459	14	0.621691	0.378309	-0.31372	0.378309	0.999589	14	0.378309	-0.31372	-0.31372
mmu03420 Nucleotide excision repair	0.624396576	-0.31905	0.624397	0.83459	30	0.624397	0.375603	-0.31905	0.375603	0.999589	30	0.375603	-0.31905	-0.31905
mmu03410 Base excision repair	0.630547211	-0.33643	0.630547	0.83459	18	0.630547	0.369453	-0.33643	0.369453	0.999589	18	0.369453	-0.33643	-0.33643
mmu04350 TGF-beta signaling pathway	0.636829411	-0.35126	0.636829	0.83459	41	0.636829	0.363171	-0.35126	0.363171	0.999589	41	0.363171	-0.35126	-0.35126
mmu04913 Ovarian steroidogenesis	0.638255896	-0.35721	0.638256	0.83459	17	0.638256	0.361744	-0.35721	0.361744	0.999589	17	0.361744	-0.35721	-0.35721
mmu04540 Gap junction	0.638902874	-0.35709	0.638903	0.83459	41	0.638903	0.361097	-0.35709	0.361097	0.999589	41	0.361097	-0.35709	-0.35709
mmu00561 Glycerolipid metabolism	0.639765076	-0.35982	0.639765	0.83459	28	0.639765	0.360235	-0.35982	0.360235	0.999589	28	0.360235	-0.35982	-0.35982
mmu04710 Circadian rhythm	0.643218928	-0.37079	0.643219	0.83459	17	0.643219	0.356781	-0.37079	0.356781	0.999589	17	0.356781	-0.37079	-0.37079
mmu04146 Peroxisome	0.65778372	-0.40839	0.657784	0.841482	45	0.657784	0.342216	-0.40839	0.342216	0.999589	45	0.342216	-0.40839	-0.40839
mmu04310 Wnt signaling pathway	0.659250468	-0.41158	0.65925	0.841482	65	0.65925	0.34075	-0.41158	0.34075	0.999589	65	0.34075	-0.41158	-0.41158
mmu03440 Homologous recombination	0.676016782	-0.463	0.676017	0.844071	14	0.676017	0.323983	-0.463	0.323983	0.999589	14	0.323983	-0.463	-0.463
mmu00640 Propanoate metabolism	0.679147499	-0.47182	0.679147	0.844071	12	0.679147	0.320853	-0.47182	0.320853	0.999589	12	0.320853	-0.47182	-0.47182
mmu03013 RNA transport	0.682058828	-0.47435	0.682059	0.844071	94	0.682059	0.317941	-0.47435	0.317941	0.999589	94	0.317941	-0.47435	-0.47435
mmu04726 Serotonergic synapse	0.684640312	-0.48297	0.68464	0.844071	38	0.68464	0.31536	-0.48297	0.31536	0.999589	38	0.31536	-0.48297	-0.48297
mmu00534 Glycosaminoglycan biosynthesis - heparan sulfate /	0.688159729	-0.49685	0.68816	0.844071	16	0.68816	0.31184	-0.49685	0.31184	0.999589	16	0.31184	-0.49685	-0.49685
mmu04971 Gastric acid secretion	0.702384775	-0.53405	0.702385	0.85083	33	0.702385	0.297615	-0.53405	0.297615	0.999589	33	0.297615	-0.53405	-0.53405
mmu00140 Steroid hormone biosynthesis	0.707824013	-0.55361	0.707824	0.85083	16	0.707824	0.292176	-0.55361	0.292176	0.999589	16	0.292176	-0.55361	-0.55361
mmu04960 Aldosterone-regulated sodium reabsorption	0.709928041	-0.55754	0.709928	0.85083	22	0.709928	0.290072	-0.55754	0.290072	0.999589	22	0.290072	-0.55754	-0.55754
mmu04340 Hedgehog signaling pathway	0.717712311	-0.58176	0.717712	0.853643	19	0.717712	0.282288	-0.58176	0.282288	0.999589	19	0.282288	-0.58176	-0.58176
mmu03030 DNA replication	0.725652321	-0.60583	0.725652	0.856597	22	0.725652	0.274348	-0.60583	0.274348	0.999589	22	0.274348	-0.60583	-0.60583
mmu04974 Protein digestion and absorption	0.735217911	-0.63206	0.735218	0.860348	36	0.735218	0.264782	-0.63206	0.264782	0.999589	36	0.264782	-0.63206	-0.63206
mmu03022 Basal transcription factors	0.739789555	-0.64927	0.73979	0.860348	20	0.73979	0.26021	-0.64927	0.26021	0.999589	20	0.26021	-0.64927	-0.64927
mmu04975 Fat digestion and absorption	0.76095654	-0.72256	0.760957	0.871003	13	0.760957	0.239043	-0.72256	0.239043	0.999589	13	0.239043	-0.72256	-0.72256
mmu00020 Citrate cycle (TCA cycle)	0.764809063	-0.73375	0.764809	0.871003	17	0.764809	0.235191	-0.73375	0.235191	0.999589	17	0.235191	-0.73375	-0.73375
mmu04723 Retrograde endocannabinoid signaling	0.775519088	-0.76171	0.775519	0.871003	43	0.775519	0.224481	-0.76171	0.224481	0.999589	43	0.224481	-0.76171	-0.76171
mmu03015 mRNA surveillance pathway	0.775842298	-0.76128	0.775842	0.871003	51	0.775842	0.224158	-0.76128	0.224158	0.999589	51	0.224158	-0.76128	-0.76128
mmu04724 Glutamatergic synapse	0.782053864	-0.78422	0.782054	0.871003	42	0.782054	0.217946	-0.78422	0.217946	0.999589	42	0.217946	-0.78422	-0.78422
mmu04910 Insulin signaling pathway	0.782237993	-0.7821	0.782238	0.871003	70	0.782238	0.217762	-0.7821	0.217762	0.999589	70	0.217762	-0.7821	-0.7821
mmu04742 Taste transduction	0.807165855	-0.88798	0.807166	0.891013	11	0.807166	0.192834	-0.88798	0.192834	0.999589	11	0.192834	-0.88798	-0.88798
mmu03460 Fanconi anemia pathway	0.811560011	-0.89652	0.81156	0.891013	19	0.81156	0.18844	-0.89652	0.18844	0.999589	19	0.18844	-0.89652	-0.89652
mmu00860 Porphyrin and chlorophyll metabolism	0.82817369	-0.9678	0.828174	0.902939	15	0.828174	0.171826	-0.9678	0.171826	0.999589	15	0.171826	-0.9678	-0.9678
mmu04727 GABAergic synapse	0.843070935	-1.01475	0.843071	0.912842	35	0.843071	0.156929	-1.01475	0.156929	0.999589	35	0.156929	-1.01475	-1.01475
mmu04120 Ubiquitin mediated proteolysis	0.85048048	-1.04229	0.85048	0.914558	79	0.85048	0.14952	-1.04229	0.14952	0.999589	79	0.14952	-1.04229	-1.04229
mmu00280 Valine, leucine and isoleucine degradation	0.86361229	-1.1098	0.863612	0.918899	27	0.863612	0.136388	-1.1098	0.136388	0.999589	27	0.136388	-1.1098	-1.1098
mmu04360 Axon guidance	0.876469058	-1.16414	0.876469	0.918899	59	0.876469	0.123531	-1.16414	0.123531	0.999589	59	0.123531	-1.16414	-1.16414

Supplemental Table 6

mmu00230 Purine metabolism	0.876985831	-1.16619	0.876986	0.918899	76	0.876986	0.123014	-1.16619	0.123014	0.999589	76	0.123014	-1.16619	-1.16619
mmu00830 Retinol metabolism	0.877928683	-1.19057	0.877929	0.918899	16	0.877929	0.122071	-1.19057	0.122071	0.999589	16	0.122071	-1.19057	-1.19057
mmu04110 Cell cycle	0.887882832	-1.22215	0.887883	0.923163	57	0.887883	0.112117	-1.22215	0.112117	0.999589	57	0.112117	-1.22215	-1.22215
mmu00650 Butanoate metabolism	0.898174699	-1.31658	0.898175	0.92772	11	0.898175	0.101825	-1.31658	0.101825	0.999589	11	0.101825	-1.31658	-1.31658
mmu03020 RNA polymerase	0.904974848	-1.36101	0.904975	0.928634	17	0.904975	0.095025	-1.36101	0.095025	0.999589	17	0.095025	-1.36101	-1.36101
mmu04740 Olfactory transduction	0.921252129	-1.41841	0.921252	0.939199	160	0.921252	0.078748	-1.41841	0.078748	0.999589	160	0.078748	-1.41841	-1.41841
mmu04115 p53 signaling pathway	0.961173752	-1.79258	0.961174	0.973576	37	0.961174	0.038826	-1.79258	0.038826	0.999589	37	0.038826	-1.79258	-1.79258
mmu00240 Pyrimidine metabolism	0.972283062	-1.94476	0.972283	0.978516	55	0.972283	0.027717	-1.94476	0.027717	0.999589	55	0.027717	-1.94476	-1.94476
mmu03010 Ribosome	0.999293182	-3.27075	0.999293	0.999293	77	0.999293	0.000707	-3.27075	0.000707	0.11097	77	0.000707	-3.27075	-3.27075

Supplemental Table 7

GO_Term	greater.p.g eomean	greater.st at.mean	greater.p. val	greater.q. val	greater.se t.size	greater.ex p1	less.p.geo mean	less.stat. mean	less.p.val	less.q.val	less.set.siz e	stats.stat. mean	stats.exp1 stats.exp1
GO:0034976 response to endoplasmic reticulum stress	0.0025237	2.890434	0.002524	0.777781	60	0.002524	0.997476	2.890434	0.997476	0.997476	60	0.997476	2.890434
GO:0016064 immunoglobulin mediated immune response	0.003433	2.802173	0.003433	0.777781	40	0.003433	0.996567	2.802173	0.996567	0.99688	40	0.996567	2.802173
GO:0006090 pyruvate metabolic process	0.0040044	2.756646	0.004004	0.777781	31	0.004004	0.995996	2.756646	0.995996	0.996621	31	0.995996	2.756646
GO:0006096 glycolytic process	0.004516	2.737182	0.004516	0.777781	25	0.004516	0.995484	2.737182	0.995484	0.996423	25	0.995484	2.737182
GO:0006952 defense response	0.0056105	2.544525	0.00561	0.777781	326	0.00561	0.99439	2.544525	0.99439	0.99564	326	0.99439	2.544525
GO:0072376 protein activation cascade	0.0060184	2.6794	0.006018	0.777781	18	0.006018	0.993982	2.6794	0.993982	0.995544	18	0.993982	2.6794
GO:0016192 vesicle-mediated transport	0.0061804	2.506962	0.00618	0.777781	433	0.00618	0.99382	2.506962	0.99382	0.995544	433	0.99382	2.506962
GO:0061025 membrane fusion	0.0091904	2.399508	0.00919	0.777781	49	0.00919	0.99081	2.399508	0.99081	0.992992	49	0.99081	2.399508
GO:0071456 cellular response to hypoxia	0.0092977	2.459059	0.009298	0.777781	28	0.009298	0.990702	2.459059	0.990702	0.992992	28	0.990702	2.459059
GO:0006812 cation transport	0.0096838	2.344132	0.009684	0.777781	358	0.009684	0.990316	2.344132	0.990316	0.992992	358	0.990316	2.344132
GO:0006984 ER-nucleus signaling pathway	0.0097242	2.446881	0.009724	0.777781	27	0.009724	0.990276	2.446881	0.990276	0.992992	27	0.990276	2.446881
GO:0044724 single-organism carbohydrate catabolic process	0.0098164	2.374422	0.009816	0.777781	49	0.009816	0.990184	2.374422	0.990184	0.992992	49	0.990184	2.374422
GO:0006956 complement activation	0.0099052	2.504577	0.009905	0.777781	15	0.009905	0.990095	2.504577	0.990095	0.992992	15	0.990095	2.504577
GO:0019724 B cell mediated immunity	0.0100083	2.391687	0.010008	0.777781	41	0.010008	0.989992	2.391687	0.989992	0.992992	41	0.989992	2.391687
GO:0005975 carbohydrate metabolic process	0.0100128	2.333647	0.010013	0.777781	249	0.010013	0.989987	2.333647	0.989987	0.992992	249	0.989987	2.333647
GO:0010951 negative regulation of endopeptidase activity	0.0101495	2.350027	0.01015	0.777781	68	0.01015	0.98985	2.350027	0.98985	0.992992	68	0.98985	2.350027
GO:0071310 cellular response to organic substance	0.0101576	2.324544	0.010158	0.777781	499	0.010158	0.989842	2.324544	0.989842	0.992992	499	0.989842	2.324544
GO:0001666 response to hypoxia	0.0102401	2.345693	0.01024	0.777781	78	0.01024	0.98976	2.345693	0.98976	0.992992	78	0.98976	2.345693
GO:0036294 cellular response to decreased oxygen levels	0.0104907	2.404125	0.010491	0.777781	29	0.010491	0.989509	2.404125	0.989509	0.992992	29	0.989509	2.404125
GO:0036293 response to decreased oxygen levels	0.0111113	2.313377	0.011111	0.777781	79	0.011111	0.988889	2.313377	0.988889	0.992992	79	0.988889	2.313377
GO:0016052 carbohydrate catabolic process	0.0124922	2.27623	0.012492	0.777781	52	0.012492	0.987508	2.27623	0.987508	0.992992	52	0.987508	2.27623
GO:0051604 protein maturation	0.0126054	2.251962	0.012605	0.777781	163	0.012605	0.987395	2.251962	0.987395	0.992992	163	0.987395	2.251962
GO:0046916 cellular transition metal ion homeostasis	0.0126799	2.287733	0.01268	0.777781	35	0.01268	0.98732	2.287733	0.98732	0.992992	35	0.98732	2.287733
GO:0009607 response to biotic stimulus	0.0127686	2.242955	0.012769	0.777781	199	0.012769	0.987231	2.242955	0.987231	0.992992	199	0.987231	2.242955
GO:0031329 regulation of cellular catabolic process	0.0137214	2.211188	0.013721	0.777781	290	0.013721	0.986279	2.211188	0.986279	0.992992	290	0.986279	2.211188
GO:0002526 acute inflammatory response	0.0150597	2.231297	0.01506	0.777781	33	0.01506	0.98494	2.231297	0.98494	0.992733	33	0.98494	2.231297
GO:0019216 regulation of lipid metabolic process	0.0155835	2.1693	0.015584	0.777781	109	0.015584	0.984416	2.1693	0.984416	0.992519	109	0.984416	2.1693
GO:0006954 inflammatory response	0.0165115	2.142797	0.016511	0.777781	164	0.016511	0.983489	2.142797	0.983489	0.991897	164	0.983489	2.142797
GO:0071216 cellular response to biotic stimulus	0.0167226	2.161325	0.016723	0.777781	51	0.016723	0.983277	2.161325	0.983277	0.991897	51	0.983277	2.161325
GO:0071219 cellular response to molecule of bacterial origin	0.0168571	2.160561	0.016857	0.777781	42	0.016857	0.983143	2.160561	0.983143	0.991897	42	0.983143	2.160561
GO:0016485 protein processing	0.0172863	2.125939	0.017286	0.777781	153	0.017286	0.982714	2.125939	0.982714	0.991897	153	0.982714	2.125939
GO:0043436 oxoacid metabolic process	0.0174438	2.113609	0.017444	0.777781	370	0.017444	0.982556	2.113609	0.982556	0.991897	370	0.982556	2.113609
GO:0071222 cellular response to lipopolysaccharide	0.0175062	2.149496	0.017506	0.777781	37	0.017506	0.982494	2.149496	0.982494	0.991897	37	0.982494	2.149496
GO:0002684 positive regulation of immune system process	0.0176167	2.113481	0.017617	0.777781	204	0.017617	0.982383	2.113481	0.982383	0.991897	204	0.982383	2.113481
GO:0072511 divalent inorganic cation transport	0.0183072	2.100903	0.018307	0.777781	143	0.018307	0.981693	2.100903	0.981693	0.991897	143	0.981693	2.100903
GO:0006909 phagocytosis	0.0194822	2.094026	0.019482	0.777781	48	0.019482	0.980518	2.094026	0.980518	0.991412	48	0.980518	2.094026
GO:0043207 response to external biotic stimulus	0.0199354	2.063128	0.019935	0.777781	186	0.019935	0.980065	2.063128	0.980065	0.991269	186	0.980065	2.063128
GO:0051707 response to other organism	0.0199354	2.063128	0.019935	0.777781	186	0.019935	0.980065	2.063128	0.980065	0.991269	186	0.980065	2.063128
GO:0019752 carboxylic acid metabolic process	0.0202908	2.051662	0.020291	0.777781	350	0.020291	0.979709	2.051662	0.979709	0.991269	350	0.979709	2.051662
GO:0009896 positive regulation of catabolic process	0.0203322	2.061774	0.020332	0.777781	104	0.020332	0.979668	2.061774	0.979668	0.991269	104	0.979668	2.061774
GO:0050778 positive regulation of immune response	0.0203863	2.059642	0.020386	0.777781	111	0.020386	0.979614	2.059642	0.979614	0.991269	111	0.979614	2.059642
GO:0030968 endoplasmic reticulum unfolded protein response	0.020463	2.181132	0.020463	0.777781	17	0.020463	0.979537	2.181132	0.979537	0.991269	17	0.979537	2.181132
GO:0034620 cellular response to unfolded protein	0.020463	2.181132	0.020463	0.777781	17	0.020463	0.979537	2.181132	0.979537	0.991269	17	0.979537	2.181132
GO:0035967 cellular response to topologically incorrect protein	0.0205358	2.153315	0.020536	0.777781	20	0.020536	0.979464	2.153315	0.979464	0.991269	20	0.979464	2.153315
GO:0044723 single-organism carbohydrate metabolic process	0.0207828	2.043909	0.020783	0.777781	221	0.020783	0.979217	2.043909	0.979217	0.991269	221	0.979217	2.043909
GO:0031668 cellular response to extracellular stimulus	0.0208462	2.05718	0.020846	0.777781	73	0.020846	0.979154	2.05718	0.979154	0.991269	73	0.979154	2.05718
GO:0009894 regulation of catabolic process	0.0216345	2.025163	0.021634	0.777781	334	0.021634	0.978366	2.025163	0.978366	0.991269	334	0.978366	2.025163
GO:0006888 ER to Golgi vesicle-mediated transport	0.0218374	2.055278	0.021837	0.777781	36	0.021837	0.978163	2.055278	0.978163	0.991269	36	0.978163	2.055278

Supplemental Table 7

GO:0070838 divalent metal ion transport	0.0221229	2.022185	0.022123	0.777781	136	0.022123	0.977877	2.022185	0.977877	0.991269	136	0.977877	2.022185	2.022185
GO:0015909 long-chain fatty acid transport	0.0222575	2.094948	0.022257	0.777781	17	0.022257	0.977743	2.094948	0.977743	0.991269	17	0.977743	2.094948	2.094948
GO:0050900 leukocyte migration	0.0225852	2.01978	0.022585	0.777781	85	0.022585	0.977415	2.01978	0.977415	0.991269	85	0.977415	2.01978	2.01978
GO:0070482 response to oxygen levels	0.0229675	2.014285	0.022968	0.777781	82	0.022968	0.977032	2.014285	0.977032	0.991269	82	0.977032	2.014285	2.014285
GO:0006897 endocytosis	0.0230251	2.001708	0.023025	0.777781	187	0.023025	0.976975	2.001708	0.976975	0.991269	187	0.976975	2.001708	2.001708
GO:0031331 positive regulation of cellular catabolic process	0.0233622	2.007945	0.023362	0.777781	77	0.023362	0.976638	2.007945	0.976638	0.991269	77	0.976638	2.007945	2.007945
GO:0071496 cellular response to external stimulus	0.0239199	1.995035	0.02392	0.777781	84	0.02392	0.97608	1.995035	0.97608	0.991269	84	0.97608	1.995035	1.995035
GO:0006082 organic acid metabolic process	0.0240038	1.980581	0.024004	0.777781	376	0.024004	0.975996	1.980581	0.975996	0.991269	376	0.975996	1.980581	1.980581
GO:0043266 regulation of potassium ion transport	0.024197	2.018775	0.024197	0.777781	34	0.024197	0.975803	2.018775	0.975803	0.991269	34	0.975803	2.018775	2.018775
GO:0048002 antigen processing and presentation of peptide antigen	0.0247195	2.022233	0.024719	0.777781	27	0.024719	0.975281	2.022233	0.975281	0.991269	27	0.975281	2.022233	2.022233
GO:0007517 muscle organ development	0.0247233	1.976351	0.024723	0.777781	132	0.024723	0.975277	1.976351	0.975277	0.991269	132	0.975277	1.976351	1.976351
GO:0070972 protein localization to endoplasmic reticulum	0.0255664	2.029805	0.025566	0.777781	18	0.025566	0.974434	2.029805	0.974434	0.991269	18	0.974434	2.029805	2.029805
GO:0009991 response to extracellular stimulus	0.0263557	1.951177	0.026356	0.777781	106	0.026356	0.973644	1.951177	0.973644	0.991269	106	0.973644	1.951177	1.951177
GO:0002455 humoral immune response mediated by circulating immu	0.027501	2.012282	0.027501	0.777781	17	0.027501	0.972499	2.012282	0.972499	0.991269	17	0.972499	2.012282	2.012282
GO:0071453 cellular response to oxygen levels	0.0276111	1.972735	0.027611	0.777781	31	0.027611	0.972389	1.972735	0.972389	0.991269	31	0.972389	1.972735	1.972735
GO:0048146 positive regulation of fibroblast proliferation	0.0278097	1.978619	0.02781	0.777781	21	0.02781	0.97219	1.978619	0.97219	0.991269	21	0.97219	1.978619	1.978619
GO:0044801 single-organism membrane fusion	0.0281736	1.939768	0.028174	0.777781	37	0.028174	0.971826	1.939768	0.971826	0.991269	37	0.971826	1.939768	1.939768
GO:0050766 positive regulation of phagocytosis	0.0282496	1.96735	0.02825	0.777781	20	0.02825	0.97175	1.96735	0.97175	0.991269	20	0.97175	1.96735	1.96735
GO:0070613 regulation of protein processing	0.0283981	1.926593	0.028398	0.777781	78	0.028398	0.971602	1.926593	0.971602	0.991269	78	0.971602	1.926593	1.926593
GO:1903317 regulation of protein maturation	0.0283981	1.926593	0.028398	0.777781	78	0.028398	0.971602	1.926593	0.971602	0.991269	78	0.971602	1.926593	1.926593
GO:0006886 intracellular protein transport	0.028801	1.902045	0.028801	0.777781	330	0.028801	0.971199	1.902045	0.971199	0.991269	330	0.971199	1.902045	1.902045
GO:0061061 muscle structure development	0.0289234	1.902563	0.028923	0.777781	217	0.028923	0.971077	1.902563	0.971077	0.991269	217	0.971077	1.902563	1.902563
GO:0060538 skeletal muscle organ development	0.0289789	1.916802	0.028979	0.777781	75	0.028979	0.971021	1.916802	0.971021	0.991269	75	0.971021	1.916802	1.916802
GO:0031589 cell-substrate adhesion	0.0290053	1.906296	0.029005	0.777781	106	0.029005	0.970995	1.906296	0.970995	0.991269	106	0.970995	1.906296	1.906296
GO:0006826 iron ion transport	0.0290971	1.968659	0.029097	0.777781	17	0.029097	0.970903	1.968659	0.970903	0.991269	17	0.970903	1.968659	1.968659
GO:0070661 leukocyte proliferation	0.029784	1.896745	0.029784	0.777781	97	0.029784	0.970216	1.896745	0.970216	0.991269	97	0.970216	1.896745	1.896745
GO:0035914 skeletal muscle cell differentiation	0.0298817	1.939662	0.029882	0.777781	29	0.029882	0.970118	1.939662	0.970118	0.991269	29	0.970118	1.939662	1.939662
GO:0030162 regulation of proteolysis	0.0300868	1.884819	0.030087	0.777781	219	0.030087	0.969913	1.884819	0.969913	0.991269	219	0.969913	1.884819	1.884819
GO:1901216 positive regulation of neuron death	0.0305828	1.910632	0.030583	0.777781	39	0.030583	0.969417	1.910632	0.969417	0.991269	39	0.969417	1.910632	1.910632
GO:0034105 positive regulation of tissue remodeling	0.030658	1.962912	0.030658	0.777781	14	0.030658	0.969342	1.962912	0.969342	0.991269	14	0.969342	1.962912	1.962912
GO:0007519 skeletal muscle tissue development	0.0308965	1.888128	0.030896	0.777781	74	0.030896	0.969104	1.888128	0.969104	0.991269	74	0.969104	1.888128	1.888128
GO:0010498 proteasomal protein catabolic process	0.0311182	1.875014	0.031118	0.777781	119	0.031118	0.968882	1.875014	0.968882	0.991269	119	0.968882	1.875014	1.875014
GO:0007030 Golgi organization	0.031181	1.903631	0.031181	0.777781	32	0.031181	0.968819	1.903631	0.968819	0.991269	32	0.968819	1.903631	1.903631
GO:0002685 regulation of leukocyte migration	0.0315523	1.885203	0.031552	0.777781	50	0.031552	0.968448	1.885203	0.968448	0.991269	50	0.968448	1.885203	1.885203
GO:0006816 calcium ion transport	0.0317132	1.865209	0.031713	0.777781	129	0.031713	0.968287	1.865209	0.968287	0.991269	129	0.968287	1.865209	1.865209
GO:0002687 positive regulation of leukocyte migration	0.0318002	1.887931	0.0318	0.777781	42	0.0318	0.9682	1.887931	0.9682	0.991269	42	0.9682	1.887931	1.887931
GO:0006906 vesicle fusion	0.0322653	1.894294	0.032265	0.777781	24	0.032265	0.967735	1.894294	0.967735	0.991269	24	0.967735	1.894294	1.894294
GO:0002573 myeloid leukocyte differentiation	0.0324288	1.867488	0.032429	0.777781	65	0.032429	0.967571	1.867488	0.967571	0.991269	65	0.967571	1.867488	1.867488
GO:0070059 intrinsic apoptotic signaling pathway in response to endo	0.0326882	1.944523	0.032688	0.777781	20	0.032688	0.967312	1.944523	0.967312	0.991269	20	0.967312	1.944523	1.944523
GO:0010942 positive regulation of cell death	0.033103	1.842837	0.033103	0.777781	204	0.033103	0.966897	1.842837	0.966897	0.991269	204	0.966897	1.842837	1.842837
GO:0045807 positive regulation of endocytosis	0.0333531	1.858419	0.033353	0.777781	42	0.033353	0.966647	1.858419	0.966647	0.991269	42	0.966647	1.858419	1.858419
GO:1903034 regulation of response to wounding	0.0336818	1.838096	0.033682	0.777781	130	0.033682	0.966318	1.838096	0.966318	0.991269	130	0.966318	1.838096	1.838096
GO:0043065 positive regulation of apoptotic process	0.0339614	1.831725	0.033961	0.777781	189	0.033961	0.966039	1.831725	0.966039	0.991269	189	0.966039	1.831725	1.831725
GO:0032943 mononuclear cell proliferation	0.0339775	1.837395	0.033978	0.777781	95	0.033978	0.966022	1.837395	0.966022	0.991269	95	0.966022	1.837395	1.837395
GO:0046651 lymphocyte proliferation	0.0339775	1.837395	0.033978	0.777781	95	0.033978	0.966022	1.837395	0.966022	0.991269	95	0.966022	1.837395	1.837395
GO:1902107 positive regulation of leukocyte differentiation	0.0340523	1.855354	0.034052	0.777781	45	0.034052	0.965948	1.855354	0.965948	0.991269	45	0.965948	1.855354	1.855354
GO:0048145 regulation of fibroblast proliferation	0.034568	1.845113	0.034568	0.777781	38	0.034568	0.965432	1.845113	0.965432	0.991269	38	0.965432	1.845113	1.845113
GO:0071621 granulocyte chemotaxis	0.0346846	1.864605	0.034685	0.777781	30	0.034685	0.965315	1.864605	0.965315	0.991269	30	0.965315	1.864605	1.864605
GO:0006811 ion transport	0.034942	1.814786	0.034942	0.777781	485	0.034942	0.965058	1.814786	0.965058	0.991269	485	0.965058	1.814786	1.814786
GO:0030001 metal ion transport	0.0352191	1.812837	0.035219	0.777781	272	0.035219	0.964781	1.812837	0.964781	0.991269	272	0.964781	1.812837	1.812837

Supplemental Table 7

GO:0097530 granulocyte migration	0.0356199	1.849726	0.03562	0.777781	31	0.03562	0.96438	1.849726	0.96438	0.991269	31	0.96438	1.849726	1.849726
GO:0032642 regulation of chemokine production	0.0358972	1.871404	0.035897	0.777781	21	0.035897	0.964103	1.871404	0.964103	0.991269	21	0.964103	1.871404	1.871404
GO:0006613 cotranslational protein targeting to membrane	0.0362781	1.912404	0.036278	0.777781	10	0.036278	0.963722	1.912404	0.963722	0.991269	10	0.963722	1.912404	1.912404
GO:0006110 regulation of glycolytic process	0.036303	1.889721	0.036303	0.777781	13	0.036303	0.963697	1.889721	0.963697	0.991269	13	0.963697	1.889721	1.889721
GO:0002449 lymphocyte mediated immunity	0.0364211	1.812223	0.036421	0.777781	69	0.036421	0.963579	1.812223	0.963579	0.991269	69	0.963579	1.812223	1.812223
GO:0052548 regulation of endopeptidase activity	0.0366504	1.798441	0.03665	0.777781	133	0.03665	0.96335	1.798441	0.96335	0.991269	133	0.96335	1.798441	1.798441
GO:0006958 complement activation, classical pathway	0.0368044	1.921562	0.036804	0.777781	11	0.036804	0.963196	1.921562	0.963196	0.991269	11	0.963196	1.921562	1.921562
GO:0030316 osteoclast differentiation	0.0376398	1.825222	0.03764	0.777781	32	0.03764	0.96236	1.825222	0.96236	0.991269	32	0.96236	1.825222	1.825222
GO:0009617 response to bacterium	0.0377484	1.785693	0.037748	0.777781	115	0.037748	0.962252	1.785693	0.962252	0.991269	115	0.962252	1.785693	1.785693
GO:1901018 positive regulation of potassium ion transmembrane tran	0.0380256	1.887312	0.038026	0.777781	10	0.038026	0.961974	1.887312	0.961974	0.991269	10	0.961974	1.887312	1.887312
GO:0045047 protein targeting to ER	0.038214	1.884207	0.038214	0.777781	10	0.038214	0.961786	1.884207	0.961786	0.991269	10	0.961786	1.884207	1.884207
GO:0072599 establishment of protein localization to endoplasmic retic	0.038214	1.884207	0.038214	0.777781	10	0.038214	0.961786	1.884207	0.961786	0.991269	10	0.961786	1.884207	1.884207
GO:0032602 chemokine production	0.0382894	1.834956	0.038289	0.777781	22	0.038289	0.961711	1.834956	0.961711	0.991269	22	0.961711	1.834956	1.834956
GO:0040011 locomotion	0.0386524	1.76857	0.038652	0.777781	484	0.038652	0.961348	1.76857	0.961348	0.991269	484	0.961348	1.76857	1.76857
GO:0048144 fibroblast proliferation	0.0387606	1.789404	0.038761	0.777781	40	0.038761	0.961239	1.789404	0.961239	0.991269	40	0.961239	1.789404	1.789404
GO:0016477 cell migration	0.0389856	1.7652	0.038986	0.777781	379	0.038986	0.961014	1.7652	0.961014	0.991269	379	0.961014	1.7652	1.7652
GO:0000041 transition metal ion transport	0.0391606	1.785234	0.039161	0.777781	38	0.039161	0.960839	1.785234	0.960839	0.991269	38	0.960839	1.785234	1.785234
GO:0030433 ER-associated ubiquitin-dependent protein catabolic proc	0.0392261	1.807258	0.039226	0.777781	21	0.039226	0.960774	1.807258	0.960774	0.991269	21	0.960774	1.807258	1.807258
GO:0043068 positive regulation of programmed cell death	0.0392348	1.765231	0.039235	0.777781	191	0.039235	0.960765	1.765231	0.960765	0.991269	191	0.960765	1.765231	1.765231
GO:0043277 apoptotic cell clearance	0.0392418	1.828018	0.039242	0.777781	15	0.039242	0.960758	1.828018	0.960758	0.991269	15	0.960758	1.828018	1.828018
GO:0050764 regulation of phagocytosis	0.0398188	1.789226	0.039819	0.777781	26	0.039819	0.960181	1.789226	0.960181	0.991269	26	0.960181	1.789226	1.789226
GO:0070663 regulation of leukocyte proliferation	0.0400007	1.76672	0.040001	0.777781	70	0.040001	0.959999	1.76672	0.959999	0.991269	70	0.959999	1.76672	1.76672
GO:0002819 regulation of adaptive immune response	0.0400177	1.774665	0.040018	0.777781	50	0.040018	0.959982	1.774665	0.959982	0.991269	50	0.959982	1.774665	1.774665
GO:0002474 antigen processing and presentation of peptide antigen v	0.0401004	1.810784	0.0401	0.777781	16	0.0401	0.9599	1.810784	0.9599	0.991269	16	0.9599	1.810784	1.810784
GO:0002237 response to molecule of bacterial origin	0.0403795	1.758864	0.040379	0.777781	72	0.040379	0.959621	1.758864	0.959621	0.991269	72	0.959621	1.758864	1.758864
GO:0043268 positive regulation of potassium ion transport	0.0405099	1.810317	0.04051	0.777781	19	0.04051	0.95949	1.810317	0.95949	0.991269	19	0.95949	1.810317	1.810317
GO:0051130 positive regulation of cellular component organization	0.0405181	1.747643	0.040518	0.777781	312	0.040518	0.959482	1.747643	0.959482	0.991269	312	0.959482	1.747643	1.747643
GO:1901016 regulation of potassium ion transmembrane transporter a	0.0409684	1.798256	0.040968	0.777781	17	0.040968	0.959032	1.798256	0.959032	0.991269	17	0.959032	1.798256	1.798256
GO:0010256 endomembrane system organization	0.0411241	1.743399	0.041124	0.777781	159	0.041124	0.958876	1.743399	0.958876	0.991269	159	0.958876	1.743399	1.743399
GO:0097529 myeloid leukocyte migration	0.0417222	1.759551	0.041722	0.777781	42	0.041722	0.958278	1.759551	0.958278	0.991269	42	0.958278	1.759551	1.759551
GO:0006900 membrane budding	0.0425073	1.768658	0.042507	0.777781	20	0.042507	0.957493	1.768658	0.957493	0.991269	20	0.957493	1.768658	1.768658
GO:0030198 extracellular matrix organization	0.0428351	1.729585	0.042835	0.777781	81	0.042835	0.957165	1.729585	0.957165	0.991269	81	0.957165	1.729585	1.729585
GO:0043062 extracellular structure organization	0.0428351	1.729585	0.042835	0.777781	81	0.042835	0.957165	1.729585	0.957165	0.991269	81	0.957165	1.729585	1.729585
GO:0002673 regulation of acute inflammatory response	0.042927	1.781413	0.042927	0.777781	20	0.042927	0.957073	1.781413	0.957073	0.991269	20	0.957073	1.781413	1.781413
GO:0008202 steroid metabolic process	0.0431686	1.723078	0.043169	0.777781	109	0.043169	0.956831	1.723078	0.956831	0.991269	109	0.956831	1.723078	1.723078
GO:0046890 regulation of lipid biosynthetic process	0.0431983	1.731289	0.043198	0.777781	54	0.043198	0.956802	1.731289	0.956802	0.991269	54	0.956802	1.731289	1.731289
GO:0030595 leukocyte chemotaxis	0.0433799	1.735471	0.04338	0.777781	49	0.04338	0.95662	1.735471	0.95662	0.991269	49	0.95662	1.735471	1.735471
GO:0048193 Golgi vesicle transport	0.0434183	1.721788	0.043418	0.777781	91	0.043418	0.956582	1.721788	0.956582	0.991269	91	0.956582	1.721788	1.721788
GO:0006643 membrane lipid metabolic process	0.0445033	1.718643	0.044503	0.777781	52	0.044503	0.955497	1.718643	0.955497	0.991269	52	0.955497	1.718643	1.718643
GO:0045944 positive regulation of transcription from RNA polymerase	0.0449958	1.697722	0.044996	0.777781	387	0.044996	0.955004	1.697722	0.955004	0.991269	387	0.955004	1.697722	1.697722
GO:0032944 regulation of mononuclear cell proliferation	0.0454334	1.705819	0.045433	0.777781	69	0.045433	0.954567	1.705819	0.954567	0.991269	69	0.954567	1.705819	1.705819
GO:0050670 regulation of lymphocyte proliferation	0.0454334	1.705819	0.045433	0.777781	69	0.045433	0.954567	1.705819	0.954567	0.991269	69	0.954567	1.705819	1.705819
GO:0051055 negative regulation of lipid biosynthetic process	0.0460375	1.743639	0.046037	0.777781	17	0.046037	0.953963	1.743639	0.953963	0.991269	17	0.953963	1.743639	1.743639
GO:0022408 negative regulation of cell-cell adhesion	0.0462766	1.744781	0.046277	0.777781	18	0.046277	0.953723	1.744781	0.953723	0.991269	18	0.953723	1.744781	1.744781
GO:0006629 lipid metabolic process	0.0469243	1.677297	0.046924	0.777781	432	0.046924	0.953076	1.677297	0.953076	0.991269	432	0.953076	1.677297	1.677297
GO:0060759 regulation of response to cytokine stimulus	0.046956	1.70312	0.046956	0.777781	31	0.046956	0.953044	1.70312	0.953044	0.991269	31	0.953044	1.70312	1.70312
GO:0002250 adaptive immune response	0.0469785	1.686256	0.046979	0.777781	90	0.046979	0.953021	1.686256	0.953021	0.991269	90	0.953021	1.686256	1.686256
GO:0043470 regulation of carbohydrate catabolic process	0.0474601	1.735463	0.04746	0.777781	15	0.04746	0.95254	1.735463	0.95254	0.991269	15	0.95254	1.735463	1.735463
GO:0043471 regulation of cellular carbohydrate catabolic process	0.0474601	1.735463	0.04746	0.777781	15	0.04746	0.95254	1.735463	0.95254	0.991269	15	0.95254	1.735463	1.735463
GO:0006879 cellular iron ion homeostasis	0.048328	1.715973	0.048328	0.777781	17	0.048328	0.951672	1.715973	0.951672	0.991269	17	0.951672	1.715973	1.715973

Supplemental Table 7

GO:0050868 negative regulation of T cell activation	0.0483411	1.69336	0.048341	0.777781	36	0.048341	0.951659	1.69336	0.951659	0.991269	36	0.951659	1.69336	1.69336
GO:0048284 organelle fusion	0.0486815	1.680969	0.048681	0.777781	36	0.048681	0.951319	1.680969	0.951319	0.991269	36	0.951319	1.680969	1.680969
GO:0043161 proteasome-mediated ubiquitin-dependent protein catak	0.0503547	1.649707	0.050355	0.777781	108	0.050355	0.949645	1.649707	0.949645	0.991269	108	0.949645	1.649707	1.649707

Supplemental Table 8

Gene symbol	Fold-regulation	2 [^] (-Avg.(Delta(Ct)))		Average Ct		Quality control
		Control P7	Lop/+ P7	Control P7	Lop/+ P7	
<i>Ddit3</i>	12.25	0.0331	0.4061	29.02	25.50	OKAY
<i>Dnajb9</i>	5.83	0.0575	0.3353	28.23	25.77	OKAY
<i>Cebpb</i>	5.14	0.0140	0.0721	30.26	27.99	A
<i>Xbp1</i>	3.76	0.1047	0.3941	27.36	25.54	OKAY
<i>Hspa5</i>	2.55	0.6177	1.5728	24.80	23.54	OKAY
<i>Insig1</i>	2.26	0.1162	0.2624	27.21	26.13	OKAY
<i>Herpud1</i>	2.03	0.0055	0.0112	31.62	30.68	B
<i>Edem1</i>	1.80	0.0057	0.0103	31.56	30.80	B
<i>Eif2ak3</i>	1.71	0.0042	0.0071	32.02	31.33	B
<i>Ero1l</i>	1.67	0.0385	0.0644	28.81	28.15	OKAY
<i>Serp1</i>	1.66	0.0925	0.1539	27.54	26.90	OKAY
<i>Armet</i>	1.64	0.0024	0.0040	32.80	32.17	B
<i>Creb3</i>	1.62	0.0623	0.1011	28.11	27.50	OKAY
<i>Sil1</i>	1.48	0.0226	0.0334	29.58	29.10	OKAY
<i>Ern1</i>	1.46	0.0084	0.0123	31.00	30.54	B
<i>Canx</i>	1.44	0.8265	1.1865	24.38	23.95	OKAY
<i>Ubxn4</i>	1.42	0.1555	0.2202	26.79	26.38	OKAY
<i>Dnajc3</i>	1.40	0.0890	0.1244	27.60	27.20	OKAY
<i>Sec63</i>	1.27	0.0035	0.0045	32.25	32.00	B
<i>Srebf2</i>	1.19	0.0518	0.0618	28.38	28.21	OKAY
<i>Atf4</i>	1.17	0.1786	0.2097	26.59	26.45	OKAY
<i>Rpn1</i>	1.17	0.1914	0.2243	26.49	26.35	OKAY
<i>Ero1lb</i>	1.14	0.0063	0.0072	31.42	31.32	B
<i>Prkcsh</i>	1.10	0.0822	0.0905	27.71	27.66	OKAY
<i>Usp14</i>	1.10	0.0944	0.1039	27.51	27.46	OKAY
<i>Hspa4l</i>	1.09	0.0546	0.0595	28.30	28.27	OKAY
<i>Sel1l</i>	1.09	0.0418	0.0454	28.69	28.66	OKAY
<i>Edem3</i>	1.07	0.0974	0.1046	27.47	27.45	OKAY
<i>Atf6</i>	1.07	0.0557	0.0598	28.27	28.26	OKAY
<i>Calr</i>	1.07	0.2491	0.2661	26.11	26.11	OKAY
<i>Fbxo6</i>	1.07	0.0005	0.0006	35.00	35.00	C
<i>Erp44</i>	1.06	0.0236	0.0251	29.51	29.51	OKAY
<i>Syvn1</i>	1.03	0.0591	0.0608	28.19	28.24	OKAY
<i>Mapk8</i>	1.02	0.0137	0.0140	30.30	30.36	B
<i>Srebf1</i>	1.01	0.0813	0.0823	27.73	27.80	OKAY
<i>Insig2</i>	1.01	0.1073	0.1081	27.33	27.41	OKAY
<i>Ube2g2</i>	-1.00	0.1696	0.1692	26.67	26.76	OKAY
<i>Pdia3</i>	-1.01	0.0069	0.0068	31.28	31.39	B
<i>Bax</i>	-1.02	0.1066	0.1049	27.34	27.45	OKAY
<i>Ugcgl1</i>	-1.02	0.0472	0.0461	28.51	28.64	OKAY
<i>Ppp1r15b</i>	-1.03	0.1096	0.1068	27.30	27.42	OKAY
<i>Eif2a</i>	-1.05	0.1047	0.0994	27.36	27.53	OKAY
<i>Mbtps2</i>	-1.06	0.0132	0.0125	30.35	30.52	B
<i>Nucb1</i>	-1.08	0.2615	0.2432	26.04	26.24	OKAY
<i>Vcp</i>	-1.08	0.5743	0.5297	24.91	25.11	OKAY
<i>H47</i>	-1.09	0.2517	0.2316	26.10	26.31	OKAY
<i>Atf6b</i>	-1.11	0.0264	0.0238	29.35	29.59	OKAY
<i>Ganab</i>	-1.11	0.2415	0.2171	26.16	26.40	OKAY

Supplemental Table 8

<i>Ganc</i>	-1.12	0.0028	0.0025	32.57	32.83	B
<i>Sec62</i>	-1.15	0.2316	0.2012	26.22	26.51	OKAY
<i>Der1l</i>	-1.16	0.0018	0.0015	33.25	33.56	B
<i>Mapk9</i>	-1.17	0.0137	0.0117	30.30	30.62	B
<i>Scap</i>	-1.19	0.0759	0.0638	27.83	28.17	OKAY
<i>Ugcgl2</i>	-1.20	0.0138	0.0115	30.28	30.64	B
<i>Os9</i>	-1.21	0.0306	0.0253	29.14	29.50	OKAY
<i>Rnf5</i>	-1.23	0.2088	0.1692	26.37	26.76	OKAY
<i>Ufd1l</i>	-1.27	0.0857	0.0676	27.65	28.08	OKAY
<i>Amfr</i>	-1.27	0.5123	0.4033	25.07	25.51	OKAY
<i>Hsph1</i>	-1.27	0.0288	0.0226	29.23	29.67	OKAY
<i>Cct4</i>	-1.29	0.4897	0.3807	25.14	25.59	OKAY
<i>Der12</i>	-1.29	0.0333	0.0257	29.02	29.48	OKAY
<i>Hspa1l</i>	-1.30	0.0052	0.0040	31.70	32.17	B
<i>Hspa2</i>	-1.31	0.0250	0.0191	29.43	29.90	OKAY
<i>Atxn3</i>	-1.31	0.0327	0.0249	29.04	29.52	OKAY
<i>Rnf139</i>	-1.32	0.0440	0.0333	28.61	29.10	OKAY
<i>Mbtps1</i>	-1.34	0.1539	0.1148	26.81	27.32	OKAY
<i>Dnajc4</i>	-1.39	0.0347	0.0249	28.96	29.53	OKAY
<i>Ppia</i>	-1.40	20.2521	14.4868	19.77	20.34	OKAY
<i>Nploc4</i>	-1.41	0.0786	0.0558	27.78	28.36	OKAY
<i>Hspb9</i>	-1.43	0.0011	0.0008	33.94	34.55	B
<i>Pfdn5</i>	-1.46	0.9931	0.6814	24.12	24.75	OKAY
<i>Pfdn2</i>	-1.48	0.2059	0.1387	26.39	27.05	OKAY
<i>Dnajc10</i>	-1.53	0.0938	0.0612	27.52	28.23	OKAY
<i>Cct7</i>	-1.54	1.9931	1.2983	23.11	23.82	OKAY
<i>Tor1a</i>	-1.56	0.0178	0.0114	29.92	30.66	A
<i>Tcp1</i>	-1.59	2.7321	1.7211	22.66	23.41	OKAY
<i>Htra2</i>	-1.60	0.0720	0.0449	27.90	28.67	OKAY
<i>Ube2j2</i>	-1.66	0.0024	0.0015	32.78	33.61	B
<i>Htra4</i>	-1.70	0.0058	0.0034	31.54	32.40	B
<i>Hspa4</i>	-1.88	0.0470	0.0250	28.52	29.52	OKAY
<i>Mapk10</i>	-2.00	0.0018	0.0009	33.23	34.32	B
<i>Creb3l3</i>	-2.08	0.0014	0.0007	33.62	34.77	B
<i>Dnajb2</i>	-2.65	0.6307	0.2376	24.77	26.27	OKAY
<i>Ern2</i>	-5.59	0.0034	0.0006	32.33	34.90	B
<i>Gusb</i>	1.47	0.0355	0.0522	28.92	28.46	OKAY
<i>Hprt1</i>	1.09	0.1487	0.1627	26.86	26.82	OKAY
<i>Hsp90ab1</i>	-1.82	8.0000	4.4076	21.11	22.06	OKAY
<i>Gapdh</i>	1.19	3.2830	3.9086	22.39	22.23	OKAY
<i>Actb</i>	-1.05	7.2100	6.8369	21.26	21.42	OKAY
<i>MGDC</i>	1.07	0.0005	0.0006	35.00	35.00	C
<i>RTC</i>	2.71	0.0489	0.1324	28.46	27.11	OKAY
<i>RTC</i>	-1.38	0.1713	0.1244	26.65	27.20	OKAY
<i>RTC</i>	-1.37	0.2059	0.1500	26.39	26.93	OKAY
<i>PPC</i>	-2.13	20.8938	9.8264	19.72	20.90	OKAY
<i>PPC</i>	-1.89	19.0273	10.0561	19.86	20.87	OKAY
<i>PPC</i>	-2.03	17.7531	8.7341	19.96	21.07	OKAY

Supplemental Table 9

Gene symbol	Fold-regulation	2 [^] (-Avg.(Delta(Ct)))		Average Ct		Quality control
		Control P1	Lop/+ P1	Control P1	Lop/+ P1	
<i>Dnajb9</i>	2.03	0.0829	0.1682	27.52	26.60	OKAY
<i>Ddit3</i>	1.66	0.0361	0.0599	28.72	28.09	OKAY
<i>Cebpb</i>	1.44	0.0180	0.0261	29.72	29.29	OKAY
<i>Htra4</i>	1.38	0.0016	0.0022	33.20	32.84	B
<i>Xbp1</i>	1.37	0.0970	0.1329	27.30	26.94	OKAY
<i>Ppia</i>	1.35	10.8128	14.6010	20.50	20.16	OKAY
<i>Tcp1</i>	1.30	1.6298	2.1184	23.23	22.95	OKAY
<i>Herpud1</i>	1.27	0.0048	0.0061	31.65	31.40	B
<i>Usp14</i>	1.27	0.1019	0.1297	27.23	26.98	OKAY
<i>Insig2</i>	1.24	0.0611	0.0758	27.96	27.75	OKAY
<i>Ero1lb</i>	1.20	0.0088	0.0106	30.75	30.59	B
<i>Pfdn5</i>	1.19	0.6233	0.7438	24.61	24.46	OKAY
<i>Serp1</i>	1.17	0.1189	0.1390	27.00	26.88	OKAY
<i>Rnf5</i>	1.16	0.1598	0.1853	26.58	26.46	OKAY
<i>Dnajc4</i>	1.16	0.0172	0.0200	29.79	29.68	OKAY
<i>Dnajc10</i>	1.15	0.1117	0.1288	27.09	26.99	OKAY
<i>Calr</i>	1.14	0.2423	0.2761	25.98	25.89	OKAY
<i>Atf4</i>	1.14	0.1133	0.1288	27.07	26.99	OKAY
<i>Ubxn4</i>	1.13	0.1857	0.2107	26.36	26.28	OKAY
<i>Ube2g2</i>	1.13	0.1322	0.1495	26.85	26.77	OKAY
<i>Hspa5</i>	1.13	0.7656	0.8633	24.32	24.24	OKAY
<i>Sel1l</i>	1.10	0.0557	0.0616	28.10	28.05	OKAY
<i>Edem3</i>	1.09	0.0859	0.0936	27.47	27.45	OKAY
<i>Creb3</i>	1.08	0.0720	0.0776	27.73	27.72	OKAY
<i>Syvn1</i>	1.07	0.0569	0.0611	28.07	28.06	OKAY
<i>Ern2</i>	1.07	0.0005	0.0005	35.00	35.00	C
<i>Fbxo6</i>	1.07	0.0005	0.0005	35.00	35.00	C
<i>Erp44</i>	1.05	0.0232	0.0243	29.36	29.39	OKAY
<i>Dnajc3</i>	1.05	0.1197	0.1253	26.99	27.03	OKAY
<i>Cct4</i>	1.04	0.5133	0.5333	24.89	24.94	OKAY
<i>Vcp</i>	1.04	0.4563	0.4740	25.06	25.11	OKAY
<i>Hspa2</i>	1.04	0.0209	0.0217	29.51	29.56	OKAY
<i>Sreb1</i>	1.03	0.0827	0.0850	27.53	27.59	OKAY
<i>Amfr</i>	1.03	0.4093	0.4199	25.22	25.28	OKAY
<i>Eif2a</i>	1.02	0.1084	0.1102	27.14	27.21	OKAY
<i>Sec62</i>	1.02	0.2319	0.2354	26.04	26.12	OKAY
<i>Atf6</i>	1.01	0.0509	0.0516	28.23	28.31	OKAY
<i>Nploc4</i>	-1.00	0.0749	0.0747	27.67	27.77	OKAY
<i>Edem1</i>	-1.01	0.0070	0.0069	31.10	31.21	B
<i>Cct7</i>	-1.02	1.5383	1.5084	23.31	23.44	OKAY
<i>H47</i>	-1.02	0.1888	0.1847	26.34	26.47	OKAY
<i>Hspa4l</i>	-1.03	0.0597	0.0580	28.00	28.14	OKAY
<i>Ugcgl2</i>	-1.04	0.0189	0.0182	29.65	29.81	OKAY
<i>Nucb1</i>	-1.04	0.2701	0.2585	25.82	25.98	OKAY
<i>Ufd1l</i>	-1.06	0.0681	0.0644	27.81	27.99	OKAY
<i>Ugcgl1</i>	-1.06	0.0512	0.0483	28.22	28.40	OKAY
<i>Pfdn2</i>	-1.06	0.1257	0.1181	26.92	27.11	OKAY
<i>Sec63</i>	-1.09	0.0063	0.0058	31.23	31.46	B

Supplemental Table 9

<i>Hspb9</i>	-1.10	0.0008	0.0007	34.22	34.45	B
<i>Canx</i>	-1.13	0.8456	0.7516	24.17	24.44	OKAY
<i>Scap</i>	-1.13	0.0660	0.0586	27.85	28.12	OKAY
<i>Bax</i>	-1.14	0.1082	0.0949	27.14	27.43	OKAY
<i>Creb3l3</i>	-1.14	0.0006	0.0005	34.57	34.86	B
<i>Ganab</i>	-1.14	0.2143	0.1879	26.15	26.44	OKAY
<i>Sil1</i>	-1.14	0.0295	0.0258	29.02	29.31	OKAY
<i>Ero1l</i>	-1.17	0.0439	0.0375	28.44	28.77	OKAY
<i>Ganc</i>	-1.18	0.0023	0.0020	32.69	33.03	B
<i>Mbtps1</i>	-1.18	0.1573	0.1329	26.60	26.94	OKAY
<i>Mapk10</i>	-1.19	0.0011	0.0009	33.81	34.16	B
<i>Insig1</i>	-1.19	0.1647	0.1385	26.53	26.88	OKAY
<i>Derl2</i>	-1.19	0.0322	0.0270	28.89	29.24	OKAY
<i>Derl1</i>	-1.20	0.0016	0.0013	33.25	33.62	B
<i>Tor1a</i>	-1.22	0.0152	0.0125	29.97	30.36	A
<i>Mbtps2</i>	-1.22	0.0168	0.0138	29.83	30.21	A
<i>Ube2j2</i>	-1.23	0.0025	0.0020	32.56	32.96	B
<i>Eif2ak3</i>	-1.24	0.0084	0.0068	30.83	31.23	B
<i>Htra2</i>	-1.27	0.0589	0.0463	28.02	28.46	OKAY
<i>Hspa4</i>	-1.29	0.0349	0.0271	28.77	29.24	OKAY
<i>Pdia3</i>	-1.30	0.0078	0.0060	30.94	31.41	B
<i>Mapk8</i>	-1.31	0.0180	0.0137	29.73	30.22	A
<i>Rnf139</i>	-1.33	0.0524	0.0395	28.19	28.69	OKAY
<i>Rpn1</i>	-1.34	0.2158	0.1608	26.14	26.67	OKAY
<i>Prkcsh</i>	-1.35	0.1231	0.0911	26.95	27.49	OKAY
<i>Dnajb2</i>	-1.36	0.2809	0.2063	25.76	26.31	OKAY
<i>Ern1</i>	-1.36	0.0113	0.0083	30.39	30.94	B
<i>Ppp1r15b</i>	-1.40	0.1154	0.0826	27.05	27.63	OKAY
<i>Os9</i>	-1.40	0.0309	0.0221	28.95	29.53	OKAY
<i>Atf6b</i>	-1.42	0.0281	0.0198	29.09	29.69	OKAY
<i>Atxn3</i>	-1.42	0.0350	0.0247	28.77	29.37	OKAY
<i>Srebf2</i>	-1.44	0.0903	0.0626	27.40	28.03	OKAY
<i>Hsph1</i>	-1.45	0.0547	0.0378	28.12	28.76	OKAY
<i>Mapk9</i>	-1.75	0.0154	0.0088	29.95	30.86	A
<i>Armet</i>	-2.04	0.0068	0.0033	31.14	32.27	B
<i>Hspa1l</i>	-2.10	0.0051	0.0024	31.54	32.71	B
<i>Gusb</i>	-1.16	0.0620	0.0532	27.94	28.26	OKAY
<i>Hprt1</i>	1.00	0.1411	0.1414	26.76	26.85	OKAY
<i>Hsp90ab1</i>	-1.03	6.2680	6.0966	21.28	21.42	OKAY
<i>Gapdh</i>	1.31	3.4216	4.4785	22.16	21.87	OKAY
<i>Actb</i>	-1.10	5.3320	4.8669	21.52	21.75	OKAY
<i>MGDC</i>	1.07	0.0005	0.0005	35.00	35.00	C
<i>RTC</i>	-1.08	0.1181	0.1094	27.01	27.22	OKAY
<i>RTC</i>	-1.09	0.1125	0.1035	27.08	27.30	OKAY
<i>RTC</i>	-1.09	0.1254	0.1153	26.93	27.15	OKAY
<i>PPC</i>	1.00	7.5930	7.6105	21.01	21.10	OKAY
<i>PPC</i>	1.02	7.4712	7.6105	21.03	21.10	OKAY
<i>PPC</i>	-1.09	7.0682	6.4890	21.11	21.33	OKAY