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

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## 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. Saggital 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).

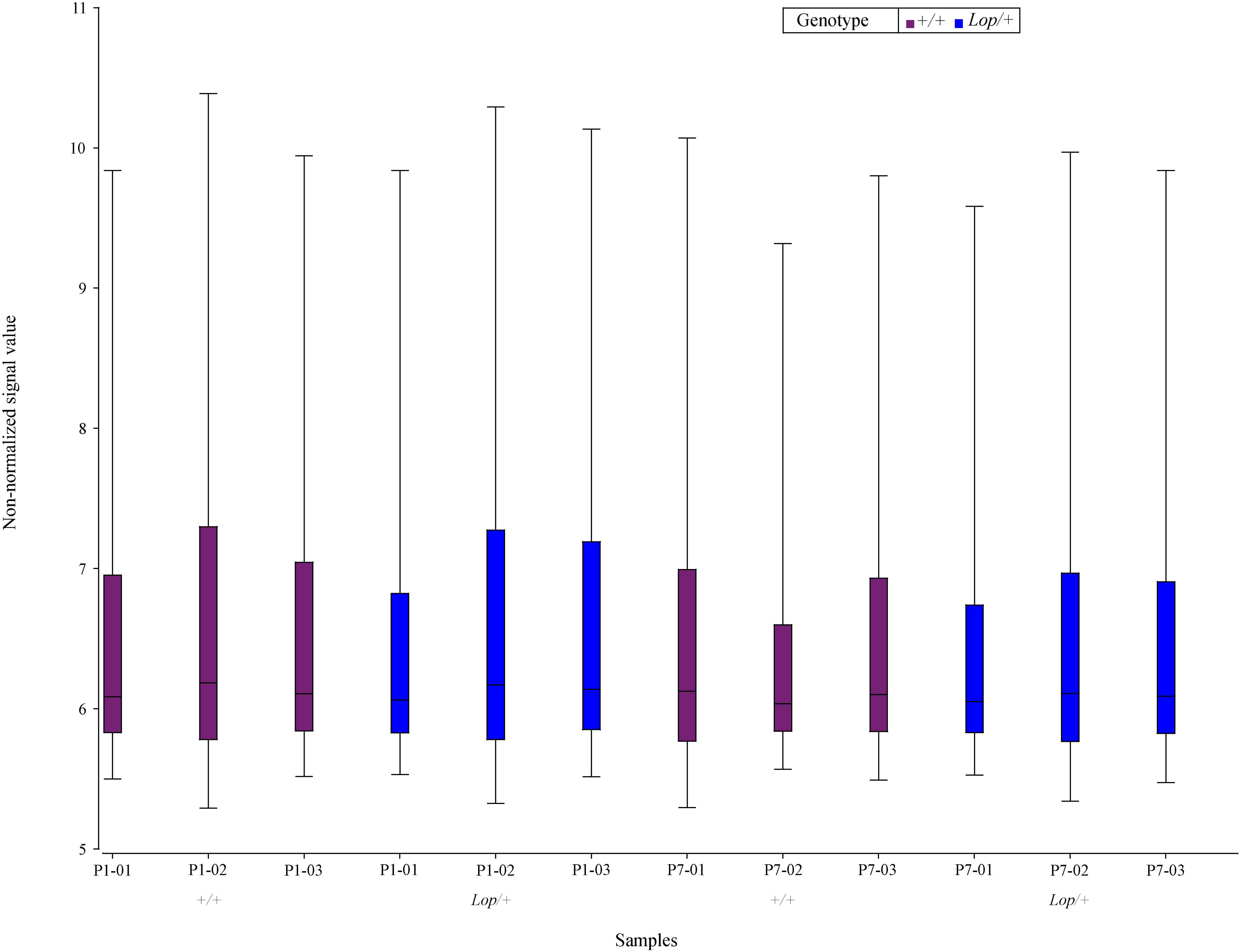
**Supplemental Table 5.** P1 Lop/+ lens pathway analysis using the KEGG database

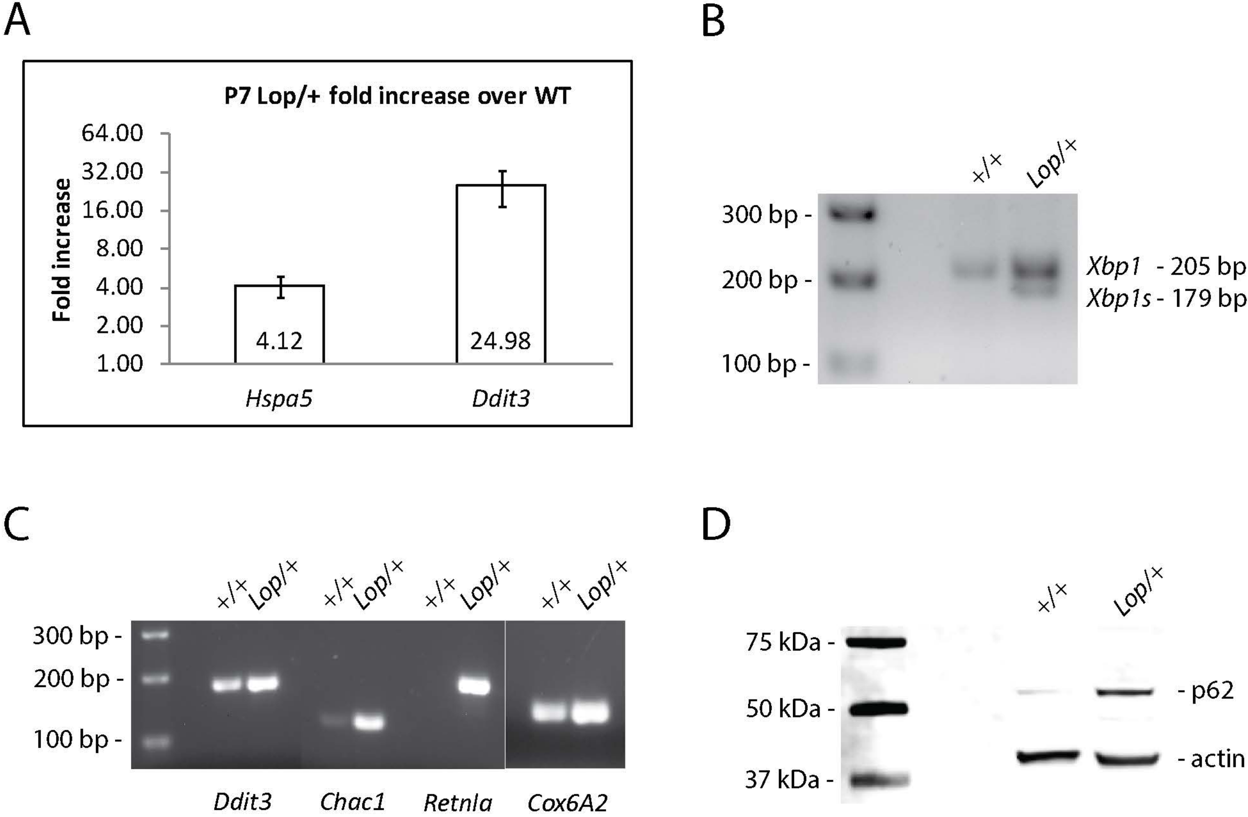
**Supplemental Table 6.** P7 Lop/+ lens pathway analysis using the KEGG database

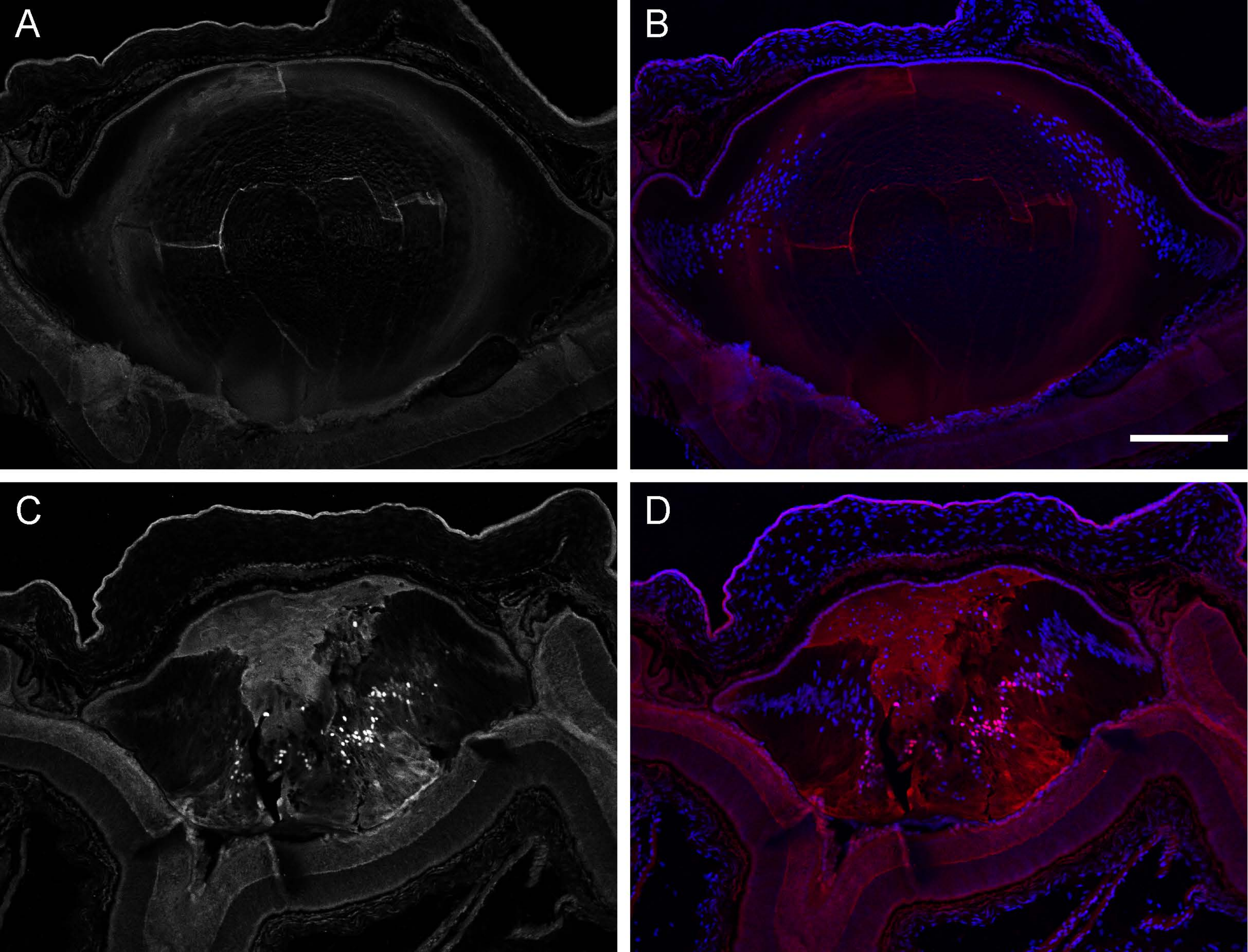
**Supplemental Table 7.** P7 Lop/+ lens pathway analysis using the GO database

**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


Genotype
■ +/+ ■ Lop/+
Non-normalized signal value
11
10
9
8
7
6
5
P1-01
P1-02
P1-03
P1-01
P1-02
P1-03
P7-01
P7-02
P7-03
P7-01
P7-02
P7-03
+/+
Lop/+
+/+
Lop/+
Samples


A
P7 Lop/+ fold increase over WT
Fold increase
64.00
32.00
16.00
8.00
4.00
2.00
1.00
4.12
24.98
Hspa5
Ddit3
B
+/+
Lop/+
300 bp -
200 bp -
100 bp -
Xbp1 - 205 bp
Xbp1s - 179 bp
C
+/+
Lop/+
+/+
Lop/+
+/+
Lop/+
+/+
Lop/+
300 bp -
200 bp -
100 bp -
Ddit3
Chac1
Retnla
Cox6A2
D
+/+
Lop/+
75 kDa -
50 kDa -
37 kDa -
- p62
- actin


A
B
C
D

# Supplemental Table 1

| Name | Sequence (5´ - 3´) | Amplicon size (bp) |
|---|---|---|
| Chac1 RTF | CTGTGGATTTTCGGGTACGG | 122 |
| Chac1 RTR | CCCCTATGGAAGGTGTCTCC | |
| Cox6A2 RTF | CTGCTCCCTTAACTGCTGGAT | 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 | AGGCAACAGTGTCAGAGTCC | |
| MipUps-F | AAGGGGTTAAGAGGCAGAGC | 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) |
|---|---|---|
| *Birc7* | 1.6945 | 0.46 |
| *mt-Nd4* | 1.6872 | 0.37 |
| *LOC676420* | 1.6774 | 0.34 |
| *mtDNA_ND2* | 1.6322 | 0.54 |
| *Atp6v1b2* | 1.6261 | 0.11 |
| *Nupr1* | 1.6128 | 0.17 |
| *Hmox1* | 1.5977 | 0.48 |
| *mtDNA_ND4* | 1.5849 | 0.32 |
| *Ank2* | 1.5777 | 0.16 |
| *LOC381283* | 1.5701 | 0.35 |
| *mtDNA_ND5* | 1.5406 | 0.34 |
| *Abi2* | 1.5106 | 0.34 |
| *mtDNA_COXII* | 1.4927 | 0.61 |
| *LOC100048638* | 1.4816 | 0.65 |
| *Stx11* | 1.4702 | 0.60 |
| *Ndel1* | 1.4671 | 0.36 |
| *Fat1* | 1.4604 | 0.36 |
| *LOC385699* | 1.4527 | 0.49 |
| *Prickle1* | 1.4498 | 0.56 |
| *Scn11a* | 1.4444 | 0.43 |
| *Rai14* | 1.4414 | 0.34 |
| *Iars* | 1.4410 | 0.34 |
| *LOC100048105* | 1.4372 | 0.58 |
| *Lama1* | 1.4367 | 0.48 |
| *mt-Nd1* | 1.4335 | 0.69 |
| *Sqstm1* | 1.4316 | 0.17 |
| *Dnase2b* | 1.4290 | 0.49 |
| *Sema5a* | 1.4258 | 0.57 |
| *mtDNA_ATP8* | 1.4237 | 0.50 |
| *Shc1* | 1.4221 | 0.46 |
| *Mboat1* | 1.4194 | 0.40 |
| *Prdm16* | 1.4185 | 0.24 |
| *LOC100043671* | 1.4183 | 0.28 |
| *Inpp5a* | 1.4118 | 0.40 |
| *Scd2* | 1.4085 | 0.50 |
| *Ubg* | 1.4059 | 0.53 |
| *Ctnna1* | 1.4046 | 0.34 |
| *Nid1* | 1.3987 | 0.68 |
| *mt-Cytb* | 1.3933 | 0.34 |
| *Frag1* | 1.3929 | 0.39 |
| *Sema5a* | 1.3893 | 0.65 |
| *Rnf145* | 1.3874 | 0.16 |
| *Ccdc117* | 1.3866 | 0.55 |
| *Spnb1* | 1.3813 | 0.34 |

| | | |
|---|---|---|
| *LOC100044124* | 1.3807 | 0.59 |
| *Lamc1* | 1.3721 | 0.32 |
| *Col4a2* | 1.3701 | 0.49 |
| *Snx18* | 1.3695 | 0.71 |
| *Hectd1* | 1.3686 | 0.32 |
| *Nisch* | 1.3664 | 0.50 |
| *Actn2* | 1.3648 | 0.69 |
| *Ftl1* | 1.3629 | 0.54 |
| *Peg3* | 1.3620 | 0.58 |
| *Tcp1* | 1.3588 | 0.51 |
| *1110014O20Rik* | 1.3581 | 0.46 |
| *Spna2* | 1.3562 | 0.28 |
| *Slc7a11* | 1.3531 | 0.42 |
| *Ube2o* | 1.3528 | 0.71 |
| *LOC100048105* | 1.3520 | 0.60 |
| *B3gnt5* | 1.3493 | 0.72 |
| *Slc39a7* | 1.3407 | 0.34 |
| *Synm* | 1.3394 | 0.35 |
| *Frag1* | 1.3357 | 0.52 |
| *Gbf1* | 1.3343 | 0.57 |
| *Csnk1g3* | 1.3316 | 0.45 |
| *LOC383099* | 1.3305 | 0.72 |
| *0610010I05Rik* | 1.3296 | 0.72 |
| *Zmym2* | 1.3269 | 0.58 |
| *Eif5* | 1.3253 | 0.57 |
| *0610040O15Rik* | 1.3252 | 0.16 |
| *App* | 1.3238 | 0.76 |
| *Herc2* | 1.3220 | 0.35 |
| *Ccng1* | 1.3208 | 0.57 |
| *Cnrip1* | 1.3207 | 0.53 |
| *mtDNA_CytB* | 1.3206 | 0.34 |
| *LOC100045882* | 1.3205 | 0.55 |
| *Herpud1* | 1.3200 | 0.78 |
| *Fads1* | 1.3195 | 0.58 |
| *Tmbim6* | 1.3195 | 0.57 |
| *Psmd1* | 1.3185 | 0.46 |
| *Gadd45a* | 1.3166 | 0.56 |
| *Igfbp5* | 1.3162 | 0.69 |
| *Pbrm1* | 1.3160 | 0.34 |
| *Ubap2* | 1.3119 | 0.57 |
| *Hspa8* | 1.3100 | 0.81 |
| *Efna5* | 1.3095 | 0.47 |
| *Ccnd2* | 1.3089 | 0.55 |
| *Chordc1* | 1.3085 | 0.59 |
| *Sept8* | 1.3079 | 0.36 |
| *Pappa* | 1.3070 | 0.47 |
| *Kif1b* | 1.3054 | 0.43 |

| | | |
|---|---|---|
| *Mast4* | 1.3048 | 0.34 |
| *Sec16a* | 1.3037 | 0.46 |
| *Spnb3* | 1.3022 | 0.45 |
| *LOC100048105* | 1.3018 | 0.65 |
| *LOC100041500* | -1.3024 | 0.40 |
| *2310039H08Rik* | -1.3114 | 0.46 |
| *1810037I17Rik* | -1.3122 | 0.56 |
| *Hist1h1c* | -1.3170 | 0.80 |
| *2210013O21Rik* | -1.3171 | 0.36 |
| *Hist1h1c* | -1.3277 | 0.75 |
| *Esam* | -1.3281 | 0.43 |
| *Hbb-bh1* | -1.3283 | 0.35 |
| *Npm3* | -1.3287 | 0.36 |
| *Fez1* | -1.3349 | 0.58 |
| *Hbb-b1* | -1.3418 | 0.81 |
| *Hba-x* | -1.3470 | 0.59 |
| *Rtn1* | -1.3472 | 0.76 |
| *E130112E08Rik* | -1.3473 | 0.80 |
| *Sox9* | -1.3525 | 0.46 |
| *2410006H16Rik* | -1.3572 | 0.45 |
| *0610007P14Rik* | -1.3585 | 0.34 |
| *Tcfap2b* | -1.3627 | 0.67 |
| *Mgp* | -1.3727 | 0.46 |
| *Acta2* | -1.3761 | 0.69 |
| *0610006I08Rik* | -1.3775 | 0.39 |
| *Stfa1* | -1.3804 | 0.94 |
| *Mt1* | -1.3905 | 0.83 |
| *Stfa1* | -1.3922 | 0.95 |
| *Npm3-ps1* | -1.4129 | 0.17 |
| *Ttr* | -1.4179 | 0.77 |
| *Cdk5r1* | -1.4338 | 0.65 |
| *Slc4a1* | -1.4395 | 0.40 |
| *EG434402* | -1.4461 | 0.44 |
| *Sox11* | -1.4570 | 0.57 |
| *Eraf* | -1.4763 | 0.36 |
| *S100a8* | -1.5387 | 0.66 |
| *Hbb-b1* | -1.6495 | 0.34 |
| *LOC100045403* | -1.6523 | 0.72 |
| *Hbb-y* | -1.6677 | 0.74 |
| *Hbb-y* | -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_GENE_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 progestin 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 |
| TGFBI | 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 (Tgfbi), 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-acteylglucosamine pyrophosphorylase 1-like 1 (Uap1l1), mRNA. XM_918982 | 227620 | 2qA3 |

| | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 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 | 1.5200 | 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 |
| PELI1 | -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 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 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 (Trafd1), 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 progestin 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

| KEGG_ID | greater.p.geomean | greater.stat.mean | greater.p.val | greater.q.val | greater.set.size | greater.exp1 | less.p.geomean | less.stat.mean | less.p.val | less.q.val | less.set.size | less.exp1 | stats.stat.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

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 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 reabsor | 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 |

| | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 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.geomean | greater.stat.mean | greater.p.val | greater.q.val | greater.set.size | greater.exp1 | less.p.geomean | less.stat.mean | less.p.val | less.q.val | less.set.size | less.exp1 | stats.stat.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 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 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 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 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.geomean | greater.stat.mean | greater.p.val | greater.q.val | greater.set.size | greater.exp1 | less.p.geomean | less.stat.mean | less.p.val | less.q.val | less.set.size | less.exp1 | stats.stat.mean | 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 | 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 | 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 | 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 | 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 | 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 | 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 | 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 | 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 | 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 | 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 | 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 | 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 | 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 | 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 | 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 | 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 | 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 | 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 | 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 | 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 | 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 | 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 | 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 | 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 | 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 | 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 | 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 | 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 | 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 | 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 | 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 | 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 | 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 | 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 | 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 | 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 | 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 | 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 | 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 | 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 | 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 | 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 | 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 | 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 | 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 | 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 | 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 | 2.055278 |

| | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 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 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 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 |

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

Supplemental Table 8

| | | | | | | |
|---|---|---|---|---|---|---|
| *Ganc* | -1.12 | 0.0028 | 0.0025 | 32.57 | 32.83 | B |
| *Sec62* | -1.15 | 0.2316 | 0.2012 | 26.22 | 26.51 | OKAY |
| *Derl1* | -1.16 | 0.0018 | 0.0015 | 33.25 | 33.56 | B |
| *Mapk9* | -1.17 | 0.0137 | 0.0117 | 30.30 | 30.62 | B |
| *Scap* | -1.19 | 0.0759 | 0.0638 | 27.83 | 28.17 | OKAY |
| *Ugcgl2* | -1.20 | 0.0138 | 0.0115 | 30.28 | 30.64 | B |
| *Os9* | -1.21 | 0.0306 | 0.0253 | 29.14 | 29.50 | OKAY |
| *Rnf5* | -1.23 | 0.2088 | 0.1692 | 26.37 | 26.76 | OKAY |
| *Ufd1l* | -1.27 | 0.0857 | 0.0676 | 27.65 | 28.08 | OKAY |
| *Amfr* | -1.27 | 0.5123 | 0.4033 | 25.07 | 25.51 | OKAY |
| *Hsph1* | -1.27 | 0.0288 | 0.0226 | 29.23 | 29.67 | OKAY |
| *Cct4* | -1.29 | 0.4897 | 0.3807 | 25.14 | 25.59 | OKAY |
| *Derl2* | -1.29 | 0.0333 | 0.0257 | 29.02 | 29.48 | OKAY |
| *Hspa1l* | -1.30 | 0.0052 | 0.0040 | 31.70 | 32.17 | B |
| *Hspa2* | -1.31 | 0.0250 | 0.0191 | 29.43 | 29.90 | OKAY |
| *Atxn3* | -1.31 | 0.0327 | 0.0249 | 29.04 | 29.52 | OKAY |
| *Rnf139* | -1.32 | 0.0440 | 0.0333 | 28.61 | 29.10 | OKAY |
| *Mbtps1* | -1.34 | 0.1539 | 0.1148 | 26.81 | 27.32 | OKAY |
| *Dnajc4* | -1.39 | 0.0347 | 0.0249 | 28.96 | 29.53 | OKAY |
| *Ppia* | -1.40 | 20.2521 | 14.4868 | 19.77 | 20.34 | OKAY |
| *Nploc4* | -1.41 | 0.0786 | 0.0558 | 27.78 | 28.36 | OKAY |
| *Hspb9* | -1.43 | 0.0011 | 0.0008 | 33.94 | 34.55 | B |
| *Pfdn5* | -1.46 | 0.9931 | 0.6814 | 24.12 | 24.75 | OKAY |
| *Pfdn2* | -1.48 | 0.2059 | 0.1387 | 26.39 | 27.05 | OKAY |
| *Dnajc10* | -1.53 | 0.0938 | 0.0612 | 27.52 | 28.23 | OKAY |
| *Cct7* | -1.54 | 1.9931 | 1.2983 | 23.11 | 23.82 | OKAY |
| *Tor1a* | -1.56 | 0.0178 | 0.0114 | 29.92 | 30.66 | A |
| *Tcp1* | -1.59 | 2.7321 | 1.7211 | 22.66 | 23.41 | OKAY |
| *Htra2* | -1.60 | 0.0720 | 0.0449 | 27.90 | 28.67 | OKAY |
| *Ube2j2* | -1.66 | 0.0024 | 0.0015 | 32.78 | 33.61 | B |
| *Htra4* | -1.70 | 0.0058 | 0.0034 | 31.54 | 32.40 | B |
| *Hspa4* | -1.88 | 0.0470 | 0.0250 | 28.52 | 29.52 | OKAY |
| *Mapk10* | -2.00 | 0.0018 | 0.0009 | 33.23 | 34.32 | B |
| *Creb3l3* | -2.08 | 0.0014 | 0.0007 | 33.62 | 34.77 | B |
| ***Dnajb2*** | **-2.65** | **0.6307** | **0.2376** | **24.77** | **26.27** | **OKAY** |
| *Ern2* | -5.59 | 0.0034 | 0.0006 | 32.33 | 34.90 | B |
| *Gusb* | 1.47 | 0.0355 | 0.0522 | 28.92 | 28.46 | OKAY |
| *Hprt1* | 1.09 | 0.1487 | 0.1627 | 26.86 | 26.82 | OKAY |
| *Hsp90ab1* | -1.82 | 8.0000 | 4.4076 | 21.11 | 22.06 | OKAY |
| *Gapdh* | 1.19 | 3.2830 | 3.9086 | 22.39 | 22.23 | OKAY |
| *Actb* | -1.05 | 7.2100 | 6.8369 | 21.26 | 21.42 | OKAY |
| *MGDC* | 1.07 | 0.0005 | 0.0006 | 35.00 | 35.00 | C |
| *RTC* | 2.71 | 0.0489 | 0.1324 | 28.46 | 27.11 | OKAY |
| *RTC* | -1.38 | 0.1713 | 0.1244 | 26.65 | 27.20 | OKAY |
| *RTC* | -1.37 | 0.2059 | 0.1500 | 26.39 | 26.93 | OKAY |
| *PPC* | -2.13 | 20.8938 | 9.8264 | 19.72 | 20.90 | OKAY |
| *PPC* | -1.89 | 19.0273 | 10.0561 | 19.86 | 20.87 | OKAY |
| *PPC* | -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** | |
| ***Dnajb9*** | **2.03** | **0.0829** | **0.1682** | **27.52** | **26.60** | **OKAY** |
| ***Ddit3*** | **1.66** | **0.0361** | **0.0599** | **28.72** | **28.09** | **OKAY** |
| ***Cebpb*** | **1.44** | **0.0180** | **0.0261** | **29.72** | **29.29** | **OKAY** |
| *Htra4* | 1.38 | 0.0016 | 0.0022 | 33.20 | 32.84 | B |
| *Xbp1* | 1.37 | 0.0970 | 0.1329 | 27.30 | 26.94 | OKAY |
| *Ppia* | 1.35 | 10.8128 | 14.6010 | 20.50 | 20.16 | OKAY |
| *Tcp1* | 1.30 | 1.6298 | 2.1184 | 23.23 | 22.95 | OKAY |
| *Herpud1* | 1.27 | 0.0048 | 0.0061 | 31.65 | 31.40 | B |
| *Usp14* | 1.27 | 0.1019 | 0.1297 | 27.23 | 26.98 | OKAY |
| *Insig2* | 1.24 | 0.0611 | 0.0758 | 27.96 | 27.75 | OKAY |
| *Ero1lb* | 1.20 | 0.0088 | 0.0106 | 30.75 | 30.59 | B |
| *Pfdn5* | 1.19 | 0.6233 | 0.7438 | 24.61 | 24.46 | OKAY |
| *Serp1* | 1.17 | 0.1189 | 0.1390 | 27.00 | 26.88 | OKAY |
| *Rnf5* | 1.16 | 0.1598 | 0.1853 | 26.58 | 26.46 | OKAY |
| *Dnajc4* | 1.16 | 0.0172 | 0.0200 | 29.79 | 29.68 | OKAY |
| *Dnajc10* | 1.15 | 0.1117 | 0.1288 | 27.09 | 26.99 | OKAY |
| *Calr* | 1.14 | 0.2423 | 0.2761 | 25.98 | 25.89 | OKAY |
| *Atf4* | 1.14 | 0.1133 | 0.1288 | 27.07 | 26.99 | OKAY |
| *Ubxn4* | 1.13 | 0.1857 | 0.2107 | 26.36 | 26.28 | OKAY |
| *Ube2g2* | 1.13 | 0.1322 | 0.1495 | 26.85 | 26.77 | OKAY |
| *Hspa5* | 1.13 | 0.7656 | 0.8633 | 24.32 | 24.24 | OKAY |
| *Sel1l* | 1.10 | 0.0557 | 0.0616 | 28.10 | 28.05 | OKAY |
| *Edem3* | 1.09 | 0.0859 | 0.0936 | 27.47 | 27.45 | OKAY |
| *Creb3* | 1.08 | 0.0720 | 0.0776 | 27.73 | 27.72 | OKAY |
| *Syvn1* | 1.07 | 0.0569 | 0.0611 | 28.07 | 28.06 | OKAY |
| *Ern2* | 1.07 | 0.0005 | 0.0005 | 35.00 | 35.00 | C |
| *Fbxo6* | 1.07 | 0.0005 | 0.0005 | 35.00 | 35.00 | C |
| *Erp44* | 1.05 | 0.0232 | 0.0243 | 29.36 | 29.39 | OKAY |
| *Dnajc3* | 1.05 | 0.1197 | 0.1253 | 26.99 | 27.03 | OKAY |
| *Cct4* | 1.04 | 0.5133 | 0.5333 | 24.89 | 24.94 | OKAY |
| *Vcp* | 1.04 | 0.4563 | 0.4740 | 25.06 | 25.11 | OKAY |
| *Hspa2* | 1.04 | 0.0209 | 0.0217 | 29.51 | 29.56 | OKAY |
| *Srebf1* | 1.03 | 0.0827 | 0.0850 | 27.53 | 27.59 | OKAY |
| *Amfr* | 1.03 | 0.4093 | 0.4199 | 25.22 | 25.28 | OKAY |
| *Eif2a* | 1.02 | 0.1084 | 0.1102 | 27.14 | 27.21 | OKAY |
| *Sec62* | 1.02 | 0.2319 | 0.2354 | 26.04 | 26.12 | OKAY |
| *Atf6* | 1.01 | 0.0509 | 0.0516 | 28.23 | 28.31 | OKAY |
| *Nploc4* | -1.00 | 0.0749 | 0.0747 | 27.67 | 27.77 | OKAY |
| *Edem1* | -1.01 | 0.0070 | 0.0069 | 31.10 | 31.21 | B |
| *Cct7* | -1.02 | 1.5383 | 1.5084 | 23.31 | 23.44 | OKAY |
| *H47* | -1.02 | 0.1888 | 0.1847 | 26.34 | 26.47 | OKAY |
| *Hspa4l* | -1.03 | 0.0597 | 0.0580 | 28.00 | 28.14 | OKAY |
| *Ugcgl2* | -1.04 | 0.0189 | 0.0182 | 29.65 | 29.81 | OKAY |
| *Nucb1* | -1.04 | 0.2701 | 0.2585 | 25.82 | 25.98 | OKAY |
| *Ufd1l* | -1.06 | 0.0681 | 0.0644 | 27.81 | 27.99 | OKAY |
| *Ugcgl1* | -1.06 | 0.0512 | 0.0483 | 28.22 | 28.40 | OKAY |
| *Pfdn2* | -1.06 | 0.1257 | 0.1181 | 26.92 | 27.11 | OKAY |
| *Sec63* | -1.09 | 0.0063 | 0.0058 | 31.23 | 31.46 | B |

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