**Supplemental Table 1** Characteristics of gene-specific primers used for qPCR analysis of gene expression in the liver of 19 mo-old mice

|  |  |  |  |
| --- | --- | --- | --- |
| Gene symbol | Forward primer (3′-5) Reverse primer (5′-3) | Product size (bp) | NCBI Genbank accession no. |
| *Reference genes* |  |  |  |
| *Actb* | AGTGTGACGTTGACATCCGTAGCTCAGTAACAGTCCGCCTA | 296 | NM\_007393 |
| *Atb5b* | GCCAGAGACTATGCGGCGCACCCCCAAATGCTGGGCCACC | 187 | NM\_016774 |
| *Canx* | GTCCCCGGGAGGCTCGAGATAGAACCTCCCCTGTTGGAACTGGAGC | 234 | NM\_007597 |
| *Cyc1* | GCTTCGCCGGACGGTACTGGCGCAATGGAAGCTGCCGGGA | 99 | NM\_025567 |
| *Eif4a2* | ACATGGCGGCCCAGAGGGAATGGTGGGGGCCAATACTAGTGCT | 299 | NM\_013506 |
| *Rpl13a* | GTGGTCGTACGCTGTGAAGGCATCGGCCTCGGGAGGGGTTGGTATT | 109 | NM\_009438 |
| *Target Genes* |  |  |  |
| *Acaca* | ATGTGGCCTGGGTAGATCCTCGGACAAGGTAAGCCCCAAT | 295 | NM\_133360 |
| *Acadm* | AGGTTTCAAGATCGCAATGGCTCCTTGGTGCTCCACTAGC | 152 | NM\_007382 |
| *Aldh9a1* | AGCTGAAGACGGTGTGTGTGCTAATGACCCAAAGCCTGGA | 154 | NM\_019993 |
| *Atf4* | TTCCTCGAATCCAGCAAAGCCCCTCCAACATCCAATCTGTCCGG | 286 | NM\_009716 |
| *Bbox1* | CCTAAAGGCAGAAGCAGTGGTCCGGTCAAATGTCAAATCA | 200 | NM\_130452 |
| *Ddit3* | AGCCAGAATAACAGCCGGAACCGGGACTCAGCTGCCATGACTG | 117 | NM\_007837 |
| *Dnajc3* | CTGCATGGACACAGGTCCCAGAGGCTGGACACCCCTACCTC | 217 | NM\_008929 |
| *Fasn* | AGATGGAAGGCTGGGCTCTAGAAGCGTCTCGGGATCTCTG | 268 | NM\_007988 |
| *Gpam* | AGGAAAGAGCCAGCATCAGGCAAAGGTATCAGCAACAGGGACT | 150 | NM\_008149 |
| *Gpx1* | CTCTTTACCTTCCTGCGGAAGGACAGCAGGGTTTCTATGT | 219 | NM\_008160 |
| *Herpud1* | CGCAGTTGGAGTGTGAGTCGCACCCTTTGTGCTGGTTTCTGGC | 213 | NM\_022331 |
| *Hmox1* | GATTTGTCTGAGGCCTTGAAGCTTAAAGCCTTCTCTGGACAC | 111 | NM\_010442 |
| *Hp* | GCAATGGGTGAACAGAGTCGGAAGAGGTTTTTGGCCGTCG | 213 | NM\_017370 |
| *Hsp90b1* | CCTGCTGACCTTCGGGTTCGCTGTCCTTGAGCCTTCTCGGC | 98 | NM\_011631 |
| *Hspa5* | TCATCGGACGCACTTGGAATGACCGCTGGGCATCATTGAAGTAAGC | 250 | NM\_001163434 |
| *Icam1* | GATGCTCAGGTATCCATCCACCACAGTTCTCAAAGCACAG | 212 | NM\_010493 |
| *Lbp* | TCGTGGGCAGTACGAGTTTCAAGAGATTCAGCAGCCACCC | 327 | NM\_008489 |
| *Nqo1* | ACGTCATTCTCTGGCCGATTCAGAGGTCAAACAGGCTGCTTGGAG | 196 | NM\_008706 |
| *Pdia4* | CCGTTGACTATGATGGCTCCAGGGGTCTGTCTGTTCGGTGGCG | 285 | NM\_009787 |
| *Ppp1r15a* | GCGGCTCAGATTGTTCAAAGCCAGATGGGTTTCTAAGGCGTGCC | 271 | NM\_008654 |
| *Saa1* | CCAGGATGAAGCTACTCACCATGTCTGTTGGCTTCCTGGTC | 313 | NM\_009117 |
| *Scd1* | CGTGGCTTCTTCTTCTCTCACTTCTCGGCTTTCAGGTCAG | 105 | NM\_009127 |
| *Slc22a5/Octn2* | CTTGTCCCTCACACCGTGAACCTAGCTCAGAGAAGTTGGC | 137 | NM\_011396 |
| *Slc25a20/Cact* | GGAGTCACCCCTATGTTCGCATCCGTTCTCCAGGGGTCAT | 161 | NM\_020520 |
| *Slc27a1/Fatp1* | AAGGGCCAGGGATCTCTCTCTCCATGTCGTCGCAGCTCTAGCCGA | 319 | NM\_011977 |
| *Sod1* | GATGACTTGGGCAAAGGTGGCTGCGCAATCCCAATCACTC | 90 | NM\_011434 |
| *Tnf* | CCAAGTGGAGGAGCAGCTGCAAATCGGCTGACGGTGACGGTGT | 189 | NM\_013693 |

**Supplemental Table 2** Characteristics of gene-specific primers used for qPCR validation of microarray data for selected differentially expressed transcripts in skeletal muscle of 19 mo-old mice

|  |  |  |  |
| --- | --- | --- | --- |
| Gene symbol | Forward primer (3′-5) Reverse primer (5′-3) | Product size (bp) | NCBI Genbank accession no. |
| *Reference genes* |  |  |  |
| *Actb* | AGTGTGACGTTGACATCCGTAGCTCAGTAACAGTCCGCCTA | 296 | NM\_007393 |
| *Atb5b* | GCCAGAGACTATGCGGCGCACCCCCAAATGCTGGGCCACC | 187 | NM\_016774 |
| *Canx* | GTCCCCGGGAGGCTCGAGATAGAACCTCCCCTGTTGGAACTGGAGC | 234 | NM\_007597 |
| *Cyc1* | GCTTCGCCGGACGGTACTGGCGCAATGGAAGCTGCCGGGA | 99 | NM\_025567 |
| *Eif4a2* | ACATGGCGGCCCAGAGGGAATGGTGGGGGCCAATACTAGTGCT | 299 | NM\_013506 |
| *Rpl13a* | GTGGTCGTACGCTGTGAAGGCATCGGCCTCGGGAGGGGTTGGTATT | 109 | NM\_009438 |
| *Target genes* |  |  |  |
| *Ankrd2* | CGACACCAACGTGAGAGACAACTGGGCTGGTATAGGCTGA | 365 | XM\_006527234 |
| *B4glant2* | GAGGTGGGGATCATTCCAGGTTGTTCCGTGTGAGCCAAGA | 91 | NM\_008081 |
| *Gamt* | GCTCTCTTCCCATGGTCCTAGTCATCTGAGGGAAGGCATAGT | 275 | XM\_011243370 |
| *Olfr1052* | CACTGGGTCAGTCATAGGTGGTCGTCCAGAAGCTGAGCGTA | 268 | NM\_147010 |
| *Olfr1356* | CGGGCTGCATCACACAGATATGATCCAAGAGCCAGCATCG | 161 | NM\_146308 |
| *Olfr142* | ACCCCTATGCTGAACCCCATCAGCTGTCCTTTTGCTTCCAG | 89 | NM\_146984 |
| *Olfr427* | GGCTCTTATGTACCTGCGCTCAGCTCCCAGAGACAGTGAG | 186 | NM\_207158 |
| *Olfr618* | TTGGTTTCAAGCTGGAGGCAGCAGTATGGCAGACTCGGTT | 92 | NM\_147047 |
| *Ostn* | GCTTCAACTGTGTCAGAAGGCTCACCCCTAGGCTGGTAGAA | 181 | NM\_198112 |
| *Perp* | CTGAGGTTAAGCCGCTGTCATCCGGTCTACGCTGGTTCTA | 141 | NM\_022032 |
| *Pld5* | GGCAGGAAGATCTCATCGCAGCCTTGGAAGAGCGGTAAGT | 239 | NM\_001195816 |
| *Tppp3* | ATCTGCCACCAAGAGCTTCCGGCAAAAGCAGGCAAGAGTC | 171 | XM\_006531324 |

**Supplemental Table 3** Relative mRNA concentrations of genes involved in lipid metabolism in the liver of 19 mo-old mice fed a control diet or a diet supplemented with 1000 mg/kg diet L-carnitine from 3 wk to 19 mo of age

|  |  |  |  |
| --- | --- | --- | --- |
|  | Control | Carnitine |  |
| Gene symbol | Mean | SD | Mean | SD | *P* |
|  | Relative mRNA level (fold of Control = 1.00) |  |
| Lipid catabolism |  |  |  |  |  |
| *Acadm* | 1.00 | 0.30 | 1.18 | 0.48 | 0.36 |
| *Aldh9a1* | 1.00 | 0.56 | 1.73 | 0.81 | 0.04 |
| *Bbox1* | 1.00 | 0.51 | 1.53 | 0.80 | 0.10 |
| *Slc22a5/Octn2* | 1.00 | 0.32 | 1.36 | 0.73 | 0.22 |
| *Slc25a20/Cact* | 1.00 | 0.35 | 1.33 | 0.59 | 0.16 |
| *Slc27a1/Fatp1* | 1.00 | 0.38 | 1.24 | 0.48 | 0.25 |
| Lipid synthesis |  |  |  |  |  |
| *Acaca* | 1.00 | 0.33 | 0.90 | 0.31 | 0.52 |
| *Fasn* | 1.00 | 0.36 | 0.95 | 0.45 | 0.79 |
| *Gpam* | 1.00 | 0.48 | 1.27 | 0.74 | 0.37 |
| *Scd1* | 1.00 | 0.61 | 1.37 | 1.23 | 0.40 |

*n* = 10 mice/group.

Acaca, acetyl-CoA carboxylase alpha; Acadm, acyl-CoA dehydrogenase medium chain; Aldh9a1, aldehyde dehydrogenase 9 family member A1; Bbox1, gamma-butyrobetaine hydroxylase 1; Fasn, fatty acid synthase; Gpam, glycerol-3-phosphate acyltransferase, mitochondrial; Scd1, stearoyl-CoA desaturase; Slc22a5/Octn2, solute carrier family 22 member 5/organic cation transporter 2; Slc25a20/Cact, solute carrier family 25 member 20/carnitine/acylcarnitine translocase; Slc27a1/Fatp1, solute carrier family 27 member 1/fatty acid transporter 1.

**Supplemental Table 4** Relative mRNA concentrations of genes involved in stress signalling and stress adaptation in the liver of 19 mo-old mice fed a control diet or a diet supplemented with 1000 mg/kg diet L-carnitine from 3 wk to 19 mo of age

|  |  |  |  |
| --- | --- | --- | --- |
|  | Control | Carnitine |  |
| Gene symbol | Mean | SD | Mean | SD | *P* |
|  | Relative mRNA level (fold of Control = 1.00) |  |
| ER stress/UPR |  |  |  |  |
| *Atf4* | 1.00 | 0.52 | 1.32 | 0.41 | 0.17 |
| *Ddit3* | 1.00 | 0.43 | 1.08 | 0.37 | 0.71 |
| *Dnajc3* | 1.00 | 0.43 | 1.19 | 0.26 | 0.28 |
| *Herpud1* | 1.00 | 0.41 | 1.13 | 0.30 | 0.47 |
| *Hsp90b1* | 1.00 | 0.41 | 1.13 | 0.20 | 0.44 |
| *Hspa5* | 1.00 | 0.40 | 1.31  | 0.38 | 0.07 |
| *Pdia4* | 1.00 | 0.43 | 1.25 | 0.29 | 0.18 |
| *Ppp1r15a* | 1.00 | 0.25 | 1.04 | 0.29 | 0.81 |
| NF-κB |  |  |  |  |  |
| *Hp* | 1.00 | 0.43 | 0.83 | 0.42 | 0.45 |
| *Icam1* | 1.00 | 0.54 | 0.96 | 0.75 | 0.88 |
| *Lbp* | 1.00 | 0.39 | 0.80 | 0.59 | 0.32 |
| *Saa1* | 1.00 | 0.63 | 0.58 | 0.38 | 0.13 |
| *Tnf* | 1.00 | 0.38 | 1.14 | 0.48 | 0.50 |
| Nrf2 |  |  |  |  |  |
| *Gpx1* | 1.00 | 0.36 | 1.40 | 0.83 | 0.54 |
| *Hmox1* | 1.00 | 0.52 | 1.25 | 1.07 | 0.52 |
| *Nqo1* | 1.00 | 0.56 | 1.08 | 0.66 | 0.76 |
| *Sod1* | 1.00 | 0.33 | 1.18 | 0.41 | 0.34 |

*n* = 10 mice/group.

Atf4, activating transcription factor 4; Ddit3, DNA damage inducible transcript 3; Dnajc3, DnaJ heat shock protein family (Hsp40) member C3; ER stress/UPR, endoplasmic reticulum stress/unfolded protein response; Gpx1, glutathione peroxidase 1; Herpud1, homocysteine inducible ER protein with ubiquitin like domain 1; Hmox1, heme oxygenase 1; Hp, haptoglobin; Hspa5, heat shock protein family A (Hsp70) member 5; Hsp90b1, heat shock protein 90 beta family member 1; Icam1, intercellular adhesion molecule 1; Lbp, lipopolysaccharide binding protein; NF-κB, nuclear factor-kappa B; Nqo1, NAD(P)H quinone dehydrogenase 1; Nrf2, nuclear factor, erythroid 2 like 2; Pdia4, protein disulfide isomerase family A member 4; Ppp1r15a, protein phosphatase 1 regulatory subunit 15A; Saa1, serum amyloid A1; Sod1, superoxide dismutase 1; Tnf, tumor necrosis factor.

**Supplemental Table 5** Up-regulated genes in skeletal muscle of 19 mo-old mice fed a control diet or a diet supplemented with 1000 mg/kg diet carnitine from 3 wk to 19 mo of age\*

|  |  |  |
| --- | --- | --- |
|  |  | Carnitine vs. Control |
| Gene symbol | Gene description | FC | *P*-value |
| *B4galnt2*  | beta-1,4-N-acetyl-galactosaminyl transferase 2  | 3.11 | 0.002 |
| *Perp*  | PERP, TP53 apoptosis effector  | 2.16 | 0.015 |
| *Pld5*  | phospholipase D family, member 5  | 2.16 | 0.040 |
| *Ostn*  | osteocrin  | 2.09 | 0.016 |
| *Gm3594//Gm3269*  | predicted gene 3594 // predicted gene 3269  | 1.69 | 0.016 |
| *Gm3696*  | predicted gene 3696  | 1.65 | 0.026 |
| *Gm14412*  | predicted gene 14412  | 1.64 | 0.015 |
| *Gm17430*  | predicted gene, 17430  | 1.54 | 0.004 |
| *Gamt*  | guanidinoacetate methyltransferase  | 1.53 | 0.020 |
| *Gm4963*  | predicted gene 4963  | 1.52 | 0.003 |
| *Tppp3*  | tubulin polymerization-promoting protein family member 3  | 1.48 | 0.001 |
| *Gm6445*  | predicted gene 6445  | 1.45 | 0.044 |
| *Desi2*  | desumoylating isopeptidase 2  | 1.45 | 0.011 |
| *LOC101056648*  | tubulin alpha-1C chain-like  | 1.44 | 0.013 |
| *Ociad2*  | OCIA domain containing 2  | 1.43 | 0.027 |
| *Gm3173*  | predicted gene 3173  | 1.41 | 0.033 |
| *Cmbl*  | carboxymethylenebutenolidase-like (Pseudomonas)  | 1.41 | 0.031 |
| *Thbs1*  | thrombospondin 1  | 1.40 | 0.038 |
| *Sar1b*  | SAR1 gene homolog B (S. cerevisiae)  | 1.39 | 0.041 |
| *Sar1b*  | SAR1 gene homolog B (S. cerevisiae)  | 1.39 | 0.041 |
| *Pcdh7*  | protocadherin 7  | 1.39 | 0.004 |
| *n-R5s67*  | nuclear encoded rRNA 5S 67  | 1.39 | 0.007 |
| *Cd97*  | CD97 antigen  | 1.38 | 0.019 |
| *Plcd4*  | phospholipase C, delta 4  | 1.38 | 0.023 |
| *Gnai3*  | guanine nucleotide binding protein (G protein), alpha inhibiting 3  | 1.38 | 0.004 |
| *Olfr467*  | olfactory receptor 467  | 1.38 | 0.040 |
| *Klk1*  | kallikrein 1  | 1.38 | 0.003 |
| *Gm3373*  | predicted gene 3373  | 1.37 | 0.031 |
| *3000002C10Rik*  | glyceraldehyde-3-phosphate dehydrogenase pseudogene  | 1.37 | 0.044 |
| *LOC101056658*  | adenosylhomocysteinase-like  | 1.37 | 0.003 |
| *Ephx1*  | epoxide hydrolase 1, microsomal  | 1.36 | 0.016 |
| *Gm5796*  | predicted gene 5796  | 1.36 | 0.026 |
| *Gm15337*  | predicted gene 15337  | 1.36 | 0.024 |
| *Cyp20a1*  | cytochrome P450, family 20, subfamily a, polypeptide 1  | 1.34 | 0.007 |
| *Rexo2*  | REX2, RNA exonuclease 2 homolog (S. cerevisiae)  | 1.34 | 0.015 |
| *Snap29*  | synaptosomal-associated protein 29  | 1.33 | 0.022 |
| *Gm9234*  | predicted pseudogene 9234  | 1.33 | 0.044 |
| *Rfc2*  | replication factor C (activator 1) 2  | 1.33 | 0.008 |
| *Spcs2*  | signal peptidase complex subunit 2 homolog (S. cerevisiae)  | 1.33 | 0.048 |
| *Gm2046*  | predicted gene 2046  | 1.32 | 0.010 |
| *Cst3*  | cystatin C  | 1.32 | 0.017 |
| *Lgals1*  | lectin, galactose binding, soluble 1  | 1.32 | 0.044 |
| *Gm15934*  | predicted gene 15934  | 1.32 | 0.027 |
| *LOC101056547*  | proteasome assembly chaperone 2-like  | 1.32 | 0.017 |
| *Ccnyl1*  | cyclin Y-like 1  | 1.32 | 0.041 |
| *Yae1d1*  | Yae1 domain containing 1  | 1.32 | 0.012 |
| *Gm5481*  | predicted gene 5481  | 1.32 | 0.008 |
| *Mrpl49*  | mitochondrial ribosomal protein L49  | 1.31 | 0.013 |
| *Mrpl16*  | mitochondrial ribosomal protein L16  | 1.30 | 0.020 |
| *Gm21082*  | predicted gene, 21082  | 1.30 | 0.028 |
| *Parm1*  | prostate androgen-regulated mucin-like protein 1  | 1.30 | 0.020 |
| *Slc2a1*  | solute carrier family 2 (facilitated glucose transporter), member 1  | 1.30 | 0.029 |
| *BC031181*  | cDNA sequence BC031181  | 1.30 | 0.038 |
| *Spcs2*  | signal peptidase complex subunit 2 homolog (S. cerevisiae)  | 1.30 | 0.005 |
| *Gm3591*  | predicted gene 3591  | 1.30 | 0.034 |
| *Cuta*  | cutA divalent cation tolerance homolog (E. coli)  | 1.29 | 0.002 |
| *Ccnd1*  | cyclin D1  | 1.29 | 0.001 |
| *Mall*  | mal, T cell differentiation protein-like  | 1.29 | 0.036 |
| *9630033F20Rik*  | RIKEN cDNA 9630033F20 gene  | 1.28 | 0.008 |
| *Olfr221*  | olfactory receptor 221  | 1.28 | 0.005 |
| *Usp37*  | ubiquitin specific peptidase 37  | 1.28 | 0.026 |
| *Erlin1*  | ER lipid raft associated 1  | 1.28 | 0.009 |
| *Vim*  | vimentin  | 1.28 | 0.015 |
| *Tnp2*  | transition protein 2  | 1.28 | 0.044 |
| *Hspe1*  | heat shock protein 1 (chaperonin 10)  | 1.27 | 0.012 |
| *Hdac1*  | histone deacetylase 1  | 1.27 | 0.015 |
| *Gm9855*  | thymine DNA glycosylase pseudogene  | 1.27 | 0.026 |
| *C1qtnf2*  | C1q and tumor necrosis factor related protein 2  | 1.27 | 0.036 |
| *Pcdhb12*  | protocadherin beta 12  | 1.26 | 0.046 |
| *Gm12739*  | predicted gene 12739  | 1.26 | 0.026 |
| *Mfsd1*  | major facilitator superfamily domain containing 1  | 1.26 | 0.049 |
| *Atp8b1*  | ATPase, class I, type 8B, member 1  | 1.26 | 0.035 |
| *Ndufaf5*  | NADH dehydrogenase (ubiquinone) complex I, assembly factor 5  | 1.26 | 0.034 |
| *Angpt2*  | angiopoietin 2  | 1.26 | 0.003 |
| *Gm10228*  | predicted gene 10228  | 1.26 | 0.015 |
| *Prl8a1*  | prolactin family 8, subfamily a, member 1  | 1.26 | 0.002 |
| *Prps1*  | phosphoribosyl pyrophosphate synthetase 1  | 1.26 | 0.005 |
| *Vti1a*  | vesicle transport through interaction with t-SNAREs 1A  | 1.26 | 0.037 |
| *Vmn2r41*  | vomeronasal 2, receptor 41  | 1.26 | 0.035 |
| *Vmn1r79*  | vomeronasal 1 receptor 79  | 1.26 | 0.037 |
| *Mxra8*  | matrix-remodelling associated 8  | 1.26 | 0.014 |
| *Nedd8*  | neural precursor cell expressed, developmentally down-regulated gene 8  | 1.26 | 0.049 |
| *Tmem42*  | transmembrane protein 42  | 1.26 | 0.016 |
| *Rragc*  | Ras-related GTP binding C  | 1.26 | 0.013 |
| *Fads3*  | fatty acid desaturase 3  | 1.26 | 0.004 |
| *Fnta*  | farnesyltransferase, CAAX box, alpha  | 1.26 | 0.020 |
| *Clcn6*  | chloride channel 6  | 1.26 | 0.012 |
| *Tma7-ps*  | translational machinery associated 7 homolog (S. cerevisiae), pseudogene  | 1.26 | 0.035 |
| *Pgap1*  | post-GPI attachment to proteins 1  | 1.26 | 0.030 |
| *Gstm2*  | glutathione S-transferase, mu 2  | 1.26 | 0.034 |
| *Olfr895*  | olfactory receptor 895  | 1.26 | 0.008 |
| *Slc25a33*  | solute carrier family 25, member 33  | 1.26 | 0.013 |
| *Tbx3*  | T-box 3  | 1.26 | 0.026 |
| *Cdan1*  | congenital dyserythropoietic anemia, type I (human)  | 1.25 | 0.011 |
| *Rab30*  | RAB30, member RAS oncogene family  | 1.25 | 0.026 |
| *Nt5c3*  | 5'-nucleotidase, cytosolic III  | 1.25 | 0.037 |
| *Rpl7l1*  | ribosomal protein L7-like 1  | 1.25 | 0.023 |
| *Rpl10*  | ribosomal protein L10  | 1.25 | 0.011 |
| *LOC637657*  | ragulator complex protein LAMTOR3-like  | 1.25 | 0.021 |
| *Vps72*  | vacuolar protein sorting 72 (yeast)  | 1.25 | 0.030 |
| *Smpd4*  | sphingomyelin phosphodiesterase 4  | 1.25 | 0.008 |
| *Gm7634*  | predicted gene 7634  | 1.25 | 0.004 |
| *Hist2h4*  | histone cluster 2, H4  | 1.25 | 0.018 |
| *Anapc4*  | anaphase promoting complex subunit 4  | 1.25 | 0.019 |
| *Npl*  | N-acetylneuraminate pyruvate lyase  | 1.25 | 0.028 |
| *Olfr23*  | olfactory receptor 23  | 1.25 | 0.040 |
| *Ky*  | kyphoscoliosis peptidase  | 1.25 | 0.023 |
| *Pitpna*  | phosphatidylinositol transfer protein, alpha  | 1.24 | 0.016 |
| *Usp14*  | ubiquitin specific peptidase 14  | 1.24 | 0.021 |
| *Lama4*  | laminin, alpha 4  | 1.24 | 0.048 |
| *LOC101056420*  | uncharacterized LOC101056420  | 1.24 | 0.026 |
| *Txndc17*  | thioredoxin domain containing 17  | 1.24 | 0.012 |
| *Naa60*  | N(alpha)-acetyltransferase 60, NatF catalytic subunit  | 1.24 | 0.003 |
| *Map2k1*  | mitogen-activated protein kinase kinase 1  | 1.24 | 0.008 |
| *Necap1*  | NECAP endocytosis associated 1  | 1.24 | 0.025 |
| *Elac2*  | elaC homolog 2 (E. coli)  | 1.24 | 0.032 |
| *Olfr26*  | olfactory receptor 26  | 1.24 | 0.010 |
| *0610031J06Rik*  | RIKEN cDNA 0610031J06 gene  | 1.24 | 0.040 |
| *Casr*  | calcium-sensing receptor  | 1.24 | 0.050 |
| *Rxrg*  | retinoid X receptor gamma  | 1.24 | 0.030 |
| *Sharpin*  | SHANK-associated RH domain interacting protein  | 1.24 | 0.030 |
| *Gm21560*  | predicted gene, 21560  | 1.24 | 0.002 |
| *Smco1*  | single-pass membrane protein with coiled-coil domains 1  | 1.24 | 0.004 |
| *Psmd6*  | proteasome (prosome, macropain) 26S subunit, non-ATPase, 6  | 1.24 | 0.007 |
| *Rab6a*  | RAB6A, member RAS oncogene family  | 1.24 | 0.011 |
| *Mapk9*  | mitogen-activated protein kinase 9  | 1.23 | 0.046 |
| *Gabarapl2*  | gamma-aminobutyric acid (GABA) A receptor-associated protein-like 2  | 1.23 | 0.009 |
| *Cnih*  | cornichon homolog (Drosophila)  | 1.23 | 0.041 |
| *Mmp28*  | matrix metallopeptidase 28 (epilysin)  | 1.23 | 0.016 |
| *Ryr3*  | ryanodine receptor 3  | 1.23 | 0.046 |
| *Alg3*  | asparagine-linked glycosylation 3 (alpha-1,3-mannosyltransferase)  | 1.23 | 0.031 |
| *Mpp1*  | membrane protein, palmitoylated  | 1.23 | 0.044 |
| *Pold2*  | polymerase (DNA directed), delta 2, regulatory subunit  | 1.23 | 0.047 |
| *1700020N15Rik*  | RIKEN cDNA 1700020N15 gene  | 1.23 | 0.048 |
| *n-R5s30*  | nuclear encoded rRNA 5S 30  | 1.23 | 0.012 |
| *Gm5068*  | predicted gene 5068  | 1.23 | 0.009 |
| *Pid1*  | phosphotyrosine interaction domain containing 1  | 1.23 | 0.026 |
| *Ube2cbp*  | ubiquitin-conjugating enzyme E2C binding protein  | 1.23 | 0.041 |
| *Gm2446*  | predicted gene 2446  | 1.23 | 0.001 |
| *Hist1h3f*  | histone cluster 1, H3f  | 1.23 | 0.026 |
| *Crip1*  | cysteine-rich protein 1 (intestinal)  | 1.23 | 0.046 |
| *Slc8a3*  | solute carrier family 8 (sodium/calcium exchanger), member 3  | 1.23 | 0.045 |
| *Gm8526*  | predicted gene 8526  | 1.23 | 0.003 |
| *n-R5s179*  | nuclear encoded rRNA 5S 179  | 1.23 | 0.040 |
| *Rap1gap2*  | RAP1 GTPase activating protein 2  | 1.23 | 0.026 |
| *Flna*  | filamin, alpha  | 1.23 | 0.042 |
| *Aasdhppt*  | aminoadipate-semialdehyde dehydrogenase-phosphopantetheinyl transferase  | 1.22 | 0.018 |
| *Csrp1*  | cysteine and glycine-rich protein 1  | 1.22 | 0.009 |
| *Fam175b*  | family with sequence similarity 175, member B  | 1.22 | 0.042 |
| *Ids*  | iduronate 2-sulfatase  | 1.22 | 0.042 |
| *Hgsnat*  | heparan-alpha-glucosaminide N-acetyltransferase  | 1.22 | 0.030 |
| *Vps25*  | vacuolar protein sorting 25 (yeast)  | 1.22 | 0.017 |
| *Psma1*  | proteasome (prosome, macropain) subunit, alpha type 1  | 1.22 | 0.045 |
| *Pi4k2a*  | phosphatidylinositol 4-kinase type 2 alpha  | 1.22 | 0.034 |
| *Ccdc101*  | coiled-coil domain containing 101  | 1.22 | 0.023 |
| *Rpap2*  | RNA polymerase II associated protein 2  | 1.22 | 0.045 |
| *Qars*  | glutaminyl-tRNA synthetase  | 1.22 | 0.024 |
| *Usp38*  | ubiquitin specific peptidase 38  | 1.22 | 0.021 |
| *Tbc1d7*  | TBC1 domain family, member 7  | 1.22 | 0.044 |
| *Gm5592*  | predicted gene 5592  | 1.22 | 0.010 |
| *Commd9*  | COMM domain containing 9  | 1.22 | 0.018 |
| *BC056474*  | cDNA sequence BC056474  | 1.22 | 0.040 |
| *Eri3*  | exoribonuclease 3  | 1.22 | 0.025 |
| *Fads1*  | fatty acid desaturase 1  | 1.22 | 0.016 |
| *Dhps*  | deoxyhypusine synthase  | 1.22 | 0.028 |
| *Arl8a*  | ADP-ribosylation factor-like 8A  | 1.22 | 0.026 |
| *Cops5*  | COP9 (constitutive photomorphogenic) homolog, subunit 5 (Arabidopsis thaliana)  | 1.22 | 0.003 |
| *Mir5124*  | microRNA 5124  | 1.21 | 0.036 |
| *Zfp60*  | zinc finger protein 60  | 1.21 | 0.040 |
| *Myadm*  | myeloid-associated differentiation marker  | 1.21 | 0.040 |
| *Gm20267*  | predicted gene, 20267  | 1.21 | 0.014 |
| *Mocs2*  | molybdenum cofactor synthesis 2  | 1.21 | 0.046 |
| *Kctd21*  | potassium channel tetramerisation domain containing 21  | 1.21 | 0.005 |
| *Ufsp2*  | UFM1-specific peptidase 2  | 1.21 | 0.035 |
| *Ube2f*  | ubiquitin-conjugating enzyme E2F (putative)  | 1.21 | 0.002 |
| *Gtf3c6*  | general transcription factor IIIC, polypeptide 6, alpha  | 1.21 | 0.045 |
| *Hamp2*  | hepcidin antimicrobial peptide 2  | 1.21 | 0.011 |
| *Metap1*  | methionyl aminopeptidase 1  | 1.21 | 0.049 |
| *Tatdn3*  | TatD DNase domain containing 3  | 1.21 | 0.030 |
| *Hmox2*  | heme oxygenase (decycling) 2  | 1.21 | 0.022 |
| *Gnpda2*  | glucosamine-6-phosphate deaminase 2  | 1.21 | 0.035 |
| *Eif3m*  | eukaryotic translation initiation factor 3, subunit M  | 1.21 | 0.006 |
| *Zfp82*  | zinc finger protein 82  | 1.21 | 0.048 |
| *Gm11368*  | predicted gene 11368  | 1.21 | 0.008 |
| *Ptges3l*  | prostaglandin E synthase 3 (cytosolic)-like  | 1.21 | 0.025 |
| *Gm14989*  | predicted gene 14989  | 1.21 | 0.047 |
| *Mphosph10*  | M-phase phosphoprotein 10 (U3 small nucleolar ribonucleoprotein)  | 1.21 | 0.043 |
| *Cpe*  | carboxypeptidase E  | 1.21 | 0.034 |

\*Filter criteria: FC > 1.2 and *P* < 0.05 between carnitine group vs. control group. FCs were calculated from the signal log ratios, which were calculated from *n* = 5 microarrays per group. FC, fold change.

**Supplemental Table 6** Down-regulated genes in skeletal muscle of 19 mo-old mice fed a control diet or a diet supplemented with 1000 mg/kg diet carnitine from 3 wk to 19 mo of age\*

|  |  |  |
| --- | --- | --- |
|  |  | Carnitine vs. Control |
| Gene symbol | Gene description | FC | *P*-value |
| *Ankrd2*  | ankyrin repeat domain 2 (stretch responsive muscle)  | -2.52 | 0.046 |
| *Gimap1*  | GTPase, IMAP family member 1  | -1.72 | 0.000 |
| *Fggy*  | FGGY carbohydrate kinase domain containing  | -1.60 | 0.046 |
| *Vmn1r20*  | vomeronasal 1 receptor 20  | -1.58 | 0.030 |
| *Olfr142*  | olfactory receptor 142  | -1.53 | 0.008 |
| *Gm13369*  | heterogeneous nuclear ribonucleoprotein A3-like  | -1.52 | 0.007 |
| *Olfr618*  | olfactory receptor 618  | -1.46 | 0.022 |
| *Olfr735*  | olfactory receptor 735  | -1.46 | 0.024 |
| *Olfr437*  | olfactory receptor 437  | -1.46 | 0.024 |
| *Traj25*  | T cell receptor alpha joining 25  | -1.45 | 0.012 |
| *Snhg3*  | small nucleolar RNA host gene (non-protein coding) 3  | -1.45 | 0.037 |
| *Gm11546*  | predicted gene 11546  | -1.44 | 0.005 |
| *Npr3*  | natriuretic peptide receptor 3  | -1.43 | 0.043 |
| *Olfr1052*  | olfactory receptor 1052  | -1.43 | 0.005 |
| *Gm2444*  | predicted gene 2444  | -1.43 | 0.009 |
| *Cyp4a31*  | cytochrome P450, family 4, subfamily a, polypeptide 31  | -1.42 | 0.000 |
| *Gm1078*  | predicted gene 1078  | -1.42 | 0.010 |
| *1700010D01Rik*  | RIKEN cDNA 1700010D01 gene  | -1.42 | 0.012 |
| *Klk1b9*  | kallikrein 1-related peptidase b9  | -1.42 | 0.009 |
| *Gm9705*  | predicted gene 9705  | -1.41 | 0.009 |
| *Gm16105*  | predicted gene 16105  | -1.41 | 0.034 |
| *Obox1*  | oocyte specific homeobox 1  | -1.40 | 0.045 |
| *4921509C19Rik*  | RIKEN cDNA 4921509C19 gene  | -1.40 | 0.005 |
| *Olfr1356*  | olfactory receptor 1356  | -1.40 | 0.023 |
| *Olfr741*  | olfactory receptor 741  | -1.40 | 0.003 |
| *Reg2*  | regenerating islet-derived 2  | -1.40 | 0.000 |
| *Nxpe5*  | neurexophilin and PC-esterase domain family, member 5  | -1.40 | 0.001 |
| *Gm2790*  | predicted gene 2790  | -1.39 | 0.023 |
| *Olfr427*  | olfactory receptor 427  | -1.38 | 0.006 |
| *Vmn2r101*  | vomeronasal 2, receptor 101  | -1.38 | 0.003 |
| *Spink14*  | serine peptidase inhibitor, Kazal type 14  | -1.38 | 0.008 |
| *Lmod2*  | leiomodin 2 (cardiac)  | -1.38 | 0.044 |
| *Cabp7*  | calcium binding protein 7  | -1.38 | 0.005 |
| *Gm8324*  | predicted gene 8324  | -1.38 | 0.006 |
| *Vmn1r26*  | vomeronasal 1 receptor 26  | -1.38 | 0.036 |
| *Vmn1r40*  | vomeronasal 1 receptor 40  | -1.37 | 0.013 |
| *Ctrb1*  | chymotrypsinogen B1  | -1.37 | 0.048 |
| *Olfr449*  | olfactory receptor 449  | -1.37 | 0.014 |
| *Gm5634*  | predicted gene 5634  | -1.37 | 0.024 |
| *Vmn2r26*  | vomeronasal 2, receptor 26  | -1.37 | 0.031 |
| *Hsd3b5*  | hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 5  | -1.36 | 0.018 |
| *Olfr799*  | olfactory receptor 799  | -1.36 | 0.009 |
| *n-R5s45*  | nuclear encoded rRNA 5S 45  | -1.36 | 0.035 |
| *Olfr338*  | olfactory receptor 338  | -1.36 | 0.019 |
| *Olfr630*  | olfactory receptor 630  | -1.36 | 0.038 |
| *Olfr679*  | olfactory receptor 679  | -1.36 | 0.018 |
| *Klk1b8*  | kallikrein 1-related peptidase b8  | -1.36 | 0.001 |
| *Myl6b*  | myosin, light polypeptide 6B  | -1.36 | 0.011 |
| *n-R5s62*  | nuclear encoded rRNA 5S 62  | -1.36 | 0.026 |
| *Gm5218*  | predicted gene 5218  | -1.36 | 0.044 |
| *Olfr418-ps1*  | olfactory receptor 418, pseudogene 1  | -1.36 | 0.037 |
| *Slc28a2*  | solute carrier family 28 (sodium-coupled nucleoside transporter), member 2  | -1.36 | 0.035 |
| *Gm17268*  | predicted gene, 17268  | -1.36 | 0.030 |
| *Vmn2r60*  | vomeronasal 2, receptor 60  | -1.36 | 0.006 |
| *Tcrb-J*  | T cell receptor beta, joining region  | -1.35 | 0.002 |
| *Stfa2l1*  | stefin A2 like 1  | -1.35 | 0.005 |
| *Olfr267*  | olfactory receptor 267  | -1.35 | 0.012 |
| *Gm6976*  | predicted gene 6976  | -1.35 | 0.040 |
| *Traj23*  | T cell receptor alpha joining 23  | -1.35 | 0.002 |
| *7530422B04Rik*  | RIKEN cDNA 7530422B04 gene  | -1.35 | 0.006 |
| *Gm6713*  | predicted gene 6713  | -1.35 | 0.024 |
| *Hps1*  | Hermansky-Pudlak syndrome 1 homolog (human)  | -1.35 | 0.014 |
| *Skint4*  | selection and upkeep of intraepithelial T cells 4  | -1.35 | 0.002 |
| *Cfd*  | complement factor D (adipsin)  | -1.35 | 0.022 |
| *Olfr1298*  | olfactory receptor 1298  | -1.34 | 0.008 |
| *Btbd17*  | BTB (POZ) domain containing 17  | -1.34 | 0.026 |
| *Gm17059*  | predicted gene 17059  | -1.34 | 0.002 |
| *Klk1b3*  | kallikrein 1-related peptidase b3  | -1.34 | 0.010 |
| *Krtap4-9*  | keratin associated protein 4-9  | -1.33 | 0.038 |
| *Gzmd*  | granzyme D  | -1.33 | 0.003 |
| *Vmn1r36*  | vomeronasal 1 receptor 36  | -1.33 | 0.014 |
| *Mafb*  | v-maf musculoaponeurotic fibrosarcoma oncogene family, protein B (avian)  | -1.33 | 0.044 |
| *Gm11415*  | predicted gene 11415  | -1.33 | 0.041 |
| *Gzmf*  | granzyme F  | -1.33 | 0.037 |
| *Taar7a*  | trace amine-associated receptor 7A  | -1.32 | 0.026 |
| *Olfr1501*  | olfactory receptor 1501  | -1.32 | 0.024 |
| *Gm8777*  | predicted gene 8777  | -1.32 | 0.044 |
| *Reg3a*  | regenerating islet-derived 3 alpha  | -1.32 | 0.009 |
| *Speer4f*  | spermatogenesis associated glutamate (E)-rich protein 4f  | -1.32 | 0.035 |
| *Ms4a18*  | membrane-spanning 4-domains, subfamily A, member 18  | -1.32 | 0.033 |
| *Epgn*  | epithelial mitogen  | -1.32 | 0.010 |
| *Olfr495*  | olfactory receptor 495  | -1.32 | 0.040 |
| *Mycs*  | myc-like oncogene, s-myc protein  | -1.32 | 0.001 |
| *Olfr899*  | olfactory receptor 899  | -1.32 | 0.002 |
| *Hoxc8*  | homeobox C8  | -1.31 | 0.030 |
| *Tspan10*  | tetraspanin 10  | -1.31 | 0.000 |
| *Defb33*  | defensin beta 33  | -1.31 | 0.019 |
| *Gm9268*  | predicted gene 9268  | -1.31 | 0.007 |
| *Prg2*  | proteoglycan 2, bone marrow  | -1.31 | 0.003 |
| *Crxos1*  | Crx opposite strand transcript 1  | -1.31 | 0.018 |
| *Gm14199*  | predicted gene 14199  | -1.31 | 0.012 |
| *Gm10914*  | predicted gene 10914  | -1.30 | 0.016 |
| *Igkv1-115*  | immunoglobulin kappa variable 1-115  | -1.30 | 0.029 |
| *Cts7*  | cathepsin 7  | -1.30 | 0.016 |
| *Prss46*  | protease, serine, 46  | -1.30 | 0.039 |
| *Gm13746*  | predicted gene 13746  | -1.30 | 0.012 |
| *Gm17193*  | predicted gene 17193  | -1.30 | 0.034 |
| *Slc22a21*  | solute carrier family 22 (organic cation transporter), member 21  | -1.30 | 0.005 |
| *Ipo4*  | importin 4  | -1.30 | 0.032 |
| *Gm2042*  | predicted gene 2042  | -1.30 | 0.013 |
| *Tubb4a*  | tubulin, beta 4A class IVA  | -1.30 | 0.006 |
| *Tcstv3*  | 2-cell-stage, variable group, member 3  | -1.30 | 0.014 |
| *Gm17677*  | predicted gene, 17677  | -1.30 | 0.036 |
| *Olfr1219*  | olfactory receptor 1219  | -1.29 | 0.037 |
| *Olfr487*  | olfactory receptor 487  | -1.29 | 0.005 |
| *4930430J20Rik*  | RIKEN cDNA 4930430J20 gene  | -1.29 | 0.014 |
| *2410012M07Rik*  | RIKEN cDNA 2410012M07 gene  | -1.29 | 0.006 |
| *Abcb1b*  | ATP-binding cassette, sub-family B (MDR/TAP), member 1B  | -1.29 | 0.050 |
| *Olfr367-ps*  | olfactory receptor 367, pseudogene  | -1.29 | 0.018 |
| *Olfr550*  | olfactory receptor 550  | -1.29 | 0.004 |
| *Trem3*  | triggering receptor expressed on myeloid cells 3  | -1.29 | 0.041 |
| *Vmn1r170*  | vomeronasal 1 receptor 170  | -1.29 | 0.029 |
| *Ctsll3*  | cathepsin L-like 3  | -1.29 | 0.041 |
| *H2-M10.1*  | histocompatibility 2, M region locus 10.1  | -1.29 | 0.014 |
| *Olfr531*  | olfactory receptor 531  | -1.28 | 0.035 |
| *Ces1f*  | carboxylesterase 1F  | -1.28 | 0.003 |
| *Gm11493*  | predicted gene 11493  | -1.28 | 0.043 |
| *Edar*  | ectodysplasin-A receptor  | -1.28 | 0.012 |
| *Zfp503*  | zinc finger protein 503  | -1.28 | 0.043 |
| *Zfp503*  | zinc finger protein 503  | -1.28 | 0.043 |
| *Gm9848*  | predicted gene 9848  | -1.28 | 0.022 |
| *Slc10a4*  | solute carrier family 10 (sodium/bile acid cotransporter family), member 4  | -1.28 | 0.048 |
| *Sult2a1*  | sulfotransferase family 2A, dehydroepiandrosterone (DHEA)-preferring, member 1  | -1.28 | 0.041 |
| *Vmn1r169*  | vomeronasal 1 receptor 169  | -1.28 | 0.006 |
| *Rab15*  | RAB15, member RAS oncogene family  | -1.28 | 0.039 |
| *Olfr281*  | olfactory receptor 281  | -1.28 | 0.010 |
| *Olfr218*  | olfactory receptor 218  | -1.28 | 0.003 |
| *Vmn1r184*  | vomeronasal 1 receptor, 184  | -1.28 | 0.011 |
| *Gyltl1b*  | glycosyltransferase-like 1B  | -1.28 | 0.033 |
| *Vmn1r172*  | vomeronasal 1 receptor 172  | -1.28 | 0.023 |
| *Cldn26*  | claudin 26  | -1.27 | 0.041 |
| *Olfr656*  | olfactory receptor 656  | -1.27 | 0.036 |
| *Zfy2*  | zinc finger protein 2, Y linked  | -1.27 | 0.016 |
| *Gm10024*  | predicted gene 10024  | -1.27 | 0.002 |
| *Klra6*  | killer cell lectin-like receptor, subfamily A, member 6  | -1.27 | 0.005 |
| *Olfr1026*  | olfactory receptor 1026  | -1.27 | 0.037 |
| *Padi2*  | peptidyl arginine deiminase, type II  | -1.27 | 0.040 |
| *mmu-let-7e*  | mmu-let-7e  | -1.27 | 0.019 |
| *Gm12410*  | predicted gene 12410  | -1.27 | 0.014 |
| *Zc3h10*  | zinc finger CCCH type containing 10  | -1.27 | 0.003 |
| *4932431P20Rik*  | RIKEN cDNA 4932431P20 gene  | -1.27 | 0.027 |
| *Cd7*  | CD7 antigen  | -1.27 | 0.016 |
| *Obp1a*  | odorant binding protein IA  | -1.27 | 0.050 |
| *Gm14459*  | predicted gene 14459  | -1.27 | 0.023 |
| *Olfr1106*  | olfactory receptor 1106  | -1.27 | 0.037 |
| *Zfp459*  | zinc finger protein 459  | -1.27 | 0.026 |
| *LOC101056457*  | uncharacterized LOC101056457  | -1.27 | 0.037 |
| *9230009I02Rik*  | RIKEN cDNA 9230009I02 gene  | -1.27 | 0.011 |
| *H2-M1*  | histocompatibility 2, M region locus 1  | -1.27 | 0.044 |
| *Zp3r*  | zona pellucida 3 receptor  | -1.27 | 0.007 |
| *B630019K06Rik*  | novel protein similar to F-box and leucine-rich repeat protein 17 (Fbxl17)  | -1.27 | 0.024 |
| *Fbxw20*  | F-box and WD-40 domain protein 20  | -1.27 | 0.005 |
| *Sox11*  | SRY-box containing gene 11  | -1.27 | 0.016 |
| *Gm5849*  | predicted gene 5849  | -1.26 | 0.023 |
| *Bcl2l10*  | Bcl2-like 10  | -1.26 | 0.003 |
| *Krt36*  | keratin 36  | -1.26 | 0.016 |
| *Snhg11*  | small nucleolar RNA host gene 11  | -1.26 | 0.004 |
| *Gm11011*  | predicted gene 11011  | -1.26 | 0.024 |
| *Mul1*  | mitochondrial ubiquitin ligase activator of NFKB 1  | -1.26 | 0.005 |
| *Olfr1100*  | olfactory receptor 1100  | -1.26 | 0.026 |
| *Krt6a*  | keratin 6A  | -1.26 | 0.041 |
| *Tmem130*  | transmembrane protein 130  | -1.26 | 0.013 |
| *Ropn1l*  | ropporin 1-like  | -1.26 | 0.026 |
| *Olfr131*  | olfactory receptor 131  | -1.26 | 0.036 |
| *Krtap9-3*  | keratin associated protein 9-3  | -1.26 | 0.010 |
| *Olfr108*  | olfactory receptor 108  | -1.26 | 0.043 |
| *Mrgpra3*  | MAS-related GPR, member A3  | -1.26 | 0.048 |
| *Gm10360*  | predicted gene 10360  | -1.26 | 0.000 |
| *Olfr958*  | olfactory receptor 958  | -1.26 | 0.016 |
| *Gm12148*  | predicted gene 12148  | -1.26 | 0.005 |
| *Gm17384*  | predicted gene, 17384  | -1.26 | 0.047 |
| *Gm12248*  | predicted gene 12248  | -1.26 | 0.013 |
| *Gm14179*  | predicted gene 14179  | -1.26 | 0.016 |
| *Mppe1*  | metallophosphoesterase 1  | -1.26 | 0.033 |
| *Gm13782*  | predicted gene 13782  | -1.25 | 0.038 |
| *Olfm3*  | olfactomedin 3  | -1.25 | 0.014 |
| *Olfr481*  | olfactory receptor 481  | -1.25 | 0.040 |
| *Hoxc5*  | homeobox C5  | -1.25 | 0.023 |
| *Vmn1r185*  | vomeronasal 1 receptor 185  | -1.25 | 0.011 |
| *LOC100044625* | disks large homolog 5-like | -1.25 | 0.031 |
| *Olfr628*  | olfactory receptor 628  | -1.25 | 0.010 |
| *BC061194*  | cDNA sequence BC061194  | -1.25 | 0.006 |
| *AF357428*  | snoRNA AF357428  | -1.25 | 0.047 |
| *5730460C07Rik*  | RIKEN cDNA 5730460C07 gene  | -1.25 | 0.039 |
| *Gm10782*  | predicted gene 10782  | -1.25 | 0.016 |
| *Gm12657*  | predicted gene 12657  | -1.25 | 0.028 |
| *Olfr1012*  | olfactory receptor 1012  | -1.25 | 0.014 |
| *Ly6f*  | lymphocyte antigen 6 complex, locus F  | -1.25 | 0.040 |
| *Gm17244*  | predicted gene, 17244  | -1.25 | 0.012 |
| *Kap*  | kidney androgen regulated protein  | -1.25 | 0.027 |
| *Treml4*  | triggering receptor expressed on myeloid cells-like 4  | -1.25 | 0.034 |
| *Olfr448*  | olfactory receptor 448  | -1.25 | 0.020 |
| *Tac2*  | tachykinin 2  | -1.25 | 0.038 |
| *Gm19585*  | predicted gene, 19585  | -1.25 | 0.031 |
| *n-R5s157*  | nuclear encoded rRNA 5S 157  | -1.25 | 0.008 |
| *Vmn2r81*  | vomeronasal 2, receptor 81  | -1.25 | 0.036 |
| *Olfr132*  | olfactory receptor 132  | -1.24 | 0.015 |
| *Hist1h2bm*  | histone cluster 1, H2bm  | -1.24 | 0.019 |
| *Crp*  | C-reactive protein, pentraxin-related  | -1.24 | 0.026 |
| *Fbxw23*  | F-box and WD-40 domain protein 23  | -1.24 | 0.042 |
| *Gm10663*  | predicted gene 10663  | -1.24 | 0.046 |
| *Olfr850*  | olfactory receptor 850  | -1.24 | 0.036 |
| *Acot4*  | acyl-CoA thioesterase 4  | -1.24 | 0.021 |
| *Upk3bl*  | uroplakin 3B-like  | -1.24 | 0.042 |
| *Begain*  | brain-enriched guanylate kinase-associated  | -1.24 | 0.004 |
| *5830411N06Rik*  | RIKEN cDNA 5830411N06 gene  | -1.24 | 0.008 |
| *Calml3*  | calmodulin-like 3  | -1.24 | 0.041 |
| *Vmn1r203*  | vomeronasal 1 receptor 203  | -1.24 | 0.036 |
| *Slc24a5*  | solute carrier family 24, member 5  | -1.24 | 0.048 |
| *Arxes1*  | adipocyte-related X-chromosome expressed sequence 1  | -1.24 | 0.016 |
| *A930002I21Rik*  | RIKEN cDNA A930002I21 gene  | -1.24 | 0.039 |
| *Gm12259*  | predicted gene 12259  | -1.24 | 0.016 |
| *Klra5*  | killer cell lectin-like receptor, subfamily A, member 5  | -1.24 | 0.025 |
| *Olfr576*  | olfactory receptor 576  | -1.24 | 0.033 |
| *Gm5901*  | predicted gene 5901  | -1.24 | 0.037 |
| *Gm15458*  | predicted gene 15458  | -1.24 | 0.044 |
| *Gm2036* | predicted gene 2036 | -1.24 | 0.039 |
| *Tcl1b1*  | T cell leukemia/lymphoma 1B, 1  | -1.24 | 0.043 |
| *Gm12714*  | predicted gene 12714  | -1.24 | 0.001 |
| *Gm5144*  | predicted gene 5144  | -1.24 | 0.017 |
| *Gm10685*  | predicted gene 10685  | -1.24 | 0.025 |
| *Olfr898*  | olfactory receptor 898  | -1.24 | 0.012 |
| *Atp5j2*  | ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F2  | -1.24 | 0.045 |
| *Gm10860*  | predicted gene 10860  | -1.23 | 0.008 |
| *Olfr31*  | olfactory receptor 31  | -1.23 | 0.048 |
| *Rs1*  | retinoschisis (X-linked, juvenile) 1 (human)  | -1.23 | 0.015 |
| *Ceacam2*  | carcinoembryonic antigen-related cell adhesion molecule 2  | -1.23 | 0.009 |
| *Zbtbd6*  | kelch repeat and BTB (POZ) domain containing 6  | -1.23 | 0.011 |
| *Odam*  | odontogenic, ameloblast asssociated  | -1.23 | 0.006 |
| *9530002B09Rik*  | RIKEN cDNA 9530002B09 gene  | -1.23 | 0.002 |
| *Fancg*  | Fanconi anemia, complementation group G  | -1.23 | 0.041 |
| *Gm7367*  | 1110014K08Rik pseudogene  | -1.23 | 0.047 |
| *Ly6k*  | lymphocyte antigen 6 complex, locus K  | -1.23 | 0.006 |
| *Arl13a*  | ADP-ribosylation factor-like 13A  | -1.23 | 0.020 |
| *Gm2240*  | predicted gene 2240  | -1.23 | 0.022 |
| *Gm16191*  | predicted gene 16191  | -1.23 | 0.045 |
| *Prop1*  | paired like homeodomain factor 1  | -1.23 | 0.016 |
| *Sprr3*  | small proline-rich protein 3  | -1.23 | 0.035 |
| *Fabp1*  | fatty acid binding protein 1, liver  | -1.23 | 0.048 |
| *Gm11937* | predicted gene 11937 // keratin associated protein 2-4  | -1.23 | 0.013 |
| *Mip*  | major intrinsic protein of eye lens fiber  | -1.23 | 0.016 |
| *Olfr169*  | olfactory receptor 169  | -1.23 | 0.030 |
| *Asic3*  | acid-sensing (proton-gated) ion channel 3  | -1.23 | 0.011 |
| *Gm14920*  | predicted pseudogene 14920  | -1.23 | 0.010 |
| *Iapp*  | islet amyloid polypeptide  | -1.23 | 0.005 |
| *Gm11656*  | predicted gene 11656  | -1.23 | 0.013 |
| *Kcnh5*  | potassium voltage-gated channel, subfamily H (eag-related), member 5  | -1.23 | 0.031 |
| *Pnliprp1*  | pancreatic lipase related protein 1  | -1.23 | 0.000 |
| *2300002M23Rik*  | RIKEN cDNA 2300002M23 gene  | -1.23 | 0.039 |
| *Igsf10*  | immunoglobulin superfamily, member 10  | -1.23 | 0.029 |
| *Keg1*  | kidney expressed gene 1  | -1.23 | 0.014 |
| *Gm14329*  | predicted gene 14329  | -1.23 | 0.030 |
| *Lyg2*  | lysozyme G-like 2  | -1.23 | 0.007 |
| *Gm16336*  | predicted gene 16336  | -1.22 | 0.018 |
| *Rp1l1*  | retinitis pigmentosa 1 homolog (human)-like 1  | -1.22 | 0.044 |
| *Ifna1*  | interferon alpha 1  | -1.22 | 0.034 |
| *mmu-mir-9-1*  | mmu-mir-9-1  | -1.22 | 0.022 |
| *Olfr466*  | olfactory receptor 466  | -1.22 | 0.049 |
| *Gm15341*  | predicted gene 15341  | -1.22 | 0.009 |
| *Igkv4-55*  | immunoglobulin kappa variable 4-55  | -1.22 | 0.033 |
| *Xkr9*  | X Kell blood group precursor related family member 9 homolog  | -1.22 | 0.000 |
| *Gm19281*  | predicted gene, 19281  | -1.22 | 0.001 |
| *Vpreb3*  | pre-B lymphocyte gene 3  | -1.22 | 0.022 |
| *Mroh5*  | maestro heat-like repeat family member 5  | -1.22 | 0.042 |
| *Gm11567*  | predicted gene 11567  | -1.22 | 0.016 |
| *Ncapg2*  | non-SMC condensin II complex, subunit G2  | -1.22 | 0.017 |
| *Gm14286*  | predicted gene 14286  | -1.22 | 0.027 |
| *Prlr*  | prolactin receptor  | -1.22 | 0.030 |
| *Gm14097*  | predicted gene 14097  | -1.22 | 0.018 |
| *Kif11*  | kinesin family member 11  | -1.22 | 0.002 |
| *Olfr516*  | olfactory receptor 516  | -1.22 | 0.033 |
| *Ctla4*  | cytotoxic T-lymphocyte-associated protein 4  | -1.22 | 0.007 |
| *Selenbp1*  | selenium binding protein 1  | -1.22 | 0.040 |
| *Rnf212*  | ring finger protein 212  | -1.22 | 0.004 |
| *Gm15872*  | predicted gene 15872  | -1.22 | 0.043 |
| *Olfr1002*  | olfactory receptor 1002  | -1.22 | 0.037 |
| *Gm15561*  | predicted gene 15561  | -1.22 | 0.018 |
| *Nutm1*  | NUT midline carcinoma, family member 1  | -1.21 | 0.006 |
| *Syt5*  | synaptotagmin V  | -1.21 | 0.049 |
| *Syk*  | spleen tyrosine kinase  | -1.21 | 0.045 |
| *Gm5538*  | predicted gene 5538  | -1.21 | 0.035 |
| *Wnt8b*  | wingless related MMTV integration site 8b  | -1.21 | 0.028 |
| *Traj59*  | T cell receptor alpha joining 59  | -1.21 | 0.006 |
| *Slc5a8*  | solute carrier family 5 (iodide transporter), member 8  | -1.21 | 0.040 |
| *Zfp947*  | zinc finger protein 947  | -1.21 | 0.032 |
| *Chaf1b*  | chromatin assembly factor 1, subunit B (p60)  | -1.21 | 0.013 |
| *Rgs17*  | regulator of G-protein signaling 17  | -1.21 | 0.045 |
| *Gm13708*  | predicted gene 13708  | -1.21 | 0.016 |
| *Gm17359*  | predicted gene, 17359  | -1.21 | 0.012 |
| *Spink8*  | serine peptidase inhibitor, Kazal type 8  | -1.21 | 0.030 |
| *Prrxl1*  | paired related homeobox protein-like 1  | -1.21 | 0.041 |
| *Defb1*  | defensin beta 1  | -1.21 | 0.027 |
| *Gm16275*  | predicted gene 16275  | -1.21 | 0.032 |
| *Krtap31-2*  | keratin associated protein 31-2  | -1.21 | 0.043 |
| *Kif2b*  | kinesin family member 2B  | -1.21 | 0.035 |
| *Fam72a*  | family with sequence similarity 72, member A  | -1.21 | 0.010 |
| *Pxt1*  | peroxisomal, testis specific 1  | -1.21 | 0.043 |
| *Tmem81*  | transmembrane protein 81  | -1.21 | 0.018 |
| *Rps8*  | ribosomal protein S8  | -1.21 | 0.044 |
| *Gm4988*  | predicted gene 4988  | -1.21 | 0.005 |
| *Gm5097*  | predicted gene 5097  | -1.21 | 0.014 |
| *Sh3tc1*  | SH3 domain and tetratricopeptide repeats 1  | -1.21 | 0.038 |
| *Shank1*  | SH3/ankyrin domain gene 1  | -1.21 | 0.039 |
| *Flrt2*  | fibronectin leucine rich transmembrane protein 2  | -1.21 | 0.046 |
| *Flrt2*  | fibronectin leucine rich transmembrane protein 2  | -1.21 | 0.046 |
| *Olfr461*  | olfactory receptor 461  | -1.21 | 0.006 |
| *Gm7972*  | predicted gene 7972  | -1.21 | 0.014 |
| *Satl1*  | spermidine/spermine N1-acetyl transferase-like 1  | -1.21 | 0.019 |
| *D17Ertd648e*  | DNA segment, Chr 17, ERATO Doi 648, expressed  | -1.21 | 0.037 |
| *Krtap19-5*  | keratin associated protein 19-5  | -1.21 | 0.048 |
| *Sowaha*  | sosondowah ankyrin repeat domain family member A  | -1.21 | 0.006 |
| *Fli1*  | Friend leukemia integration 1  | -1.21 | 0.010 |
| *Tmem120a*  | transmembrane protein 120A  | -1.21 | 0.020 |
| *Gm16567*  | predicted gene 16567  | -1.21 | 0.034 |
| *A230083G16Rik*  | RIKEN cDNA A230083G16 gene  | -1.21 | 0.014 |
| *Vip*  | vasoactive intestinal polypeptide  | -1.21 | 0.042 |
| *Serpinf2*  | serine (or cysteine) peptidase inhibitor, clade F, member 2  | -1.21 | 0.044 |
| *Gm10436*  | predicted gene 10436  | -1.21 | 0.001 |

\*Filter criteria: FC < -1.2 and *P* < 0.05 between carnitine group vs. control group. FCs were calculated from the signal log ratios, which were calculated from *n* = 5 microarrays per group. FC, fold change.

**Supplemental Table 7** The most enriched GO biological process and molecular function terms assigned to the up-regulated genes in skeletal muscle of 19 mo-old mice fed a control diet or a diet supplemented with 1000 mg/kg diet L-carnitine from 3 wk to 19 mo of age

|  |  |
| --- | --- |
| GO category | GO term\* |
| *Biological process* |
|  | macromolecular complex assembly |
|  | homotypic cell-cell adhesion |
|  | cellular component biogenesis |
|  | proteolysis |
|  | protein complex assembly |
|  | protein complex biogenesis |
|  | protein oligomerisation |
|  | response to organic cyclic compound |
|  | protein complex subunit organisation |
|  | organonitrogen compound biosynthetic process |
|  | protein deubiquitination |
|  | peptide metabolic process |
|  | response to magnesium ion |
| *Molecular function* |
|  | peptidase activity |
|  | ubiquitin-like protein-specific protease activity |
|  | enzyme binding |

\*GO terms are sorted by their enrichment *P*-value in increasing order. Only GO terms with enrichment *P*-value < 0.01 are shown.

GO, gene ontology.

**Supplemental Table 8** The most enriched GO biological process and molecular function terms assigned to the down-regulated genes in skeletal muscle of 19 mo-old mice fed a control diet or a diet supplemented with 1000 mg/kg diet L-carnitine from 3 wk to 19 mo of age

|  |  |
| --- | --- |
| GO category | GO term\* |
| *Biological process* |
|  | sensory perception of smell |
|  | sensory perception of chemical stimulus |
|  | sensory perception |
|  | G-protein coupled receptor signalling pathway |
|  | neurological system process |
|  | system process |
|  | detection of chemical stimulus |
|  | detection of chemical stimulus involved in sensory perception |
|  | detection of stimulus |
|  | detection of stimulus involved in sensory perception |
|  | response to pheromone |
| *Molecular function* |
|  | G-protein coupled receptor activity |
|  | olfactory receptor activity |
|  | transmembrane receptor activity |
|  | transmembrane signalling receptor activity |
|  | signalling receptor activity |
|  | receptor activity |
|  | molecular transducer activity |
|  | signal transducer activity |
|  | odorant binding |
|  | pheromone receptor activity |
|  | serine-type endopeptidase activity |

\*GO terms are sorted by their enrichment *P*-value in increasing order. Only GO terms with enrichment *P*-value < 0.01 are shown.

GO, gene ontology.

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**Supplemental Fig. 1**

Concentrations triacylglycerols and cholesterol in plasma (A) and liver (B) of mice at 10 and 19 mo of age fed a control diet or a diet supplemented with 1000 mg/kg diet L-carnitine from 3 wk to 19 mo of age. Bars represent means and SD for *n* = 10 mice/group.

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**Supplemental Fig. 2**

A, Relative protein levels of ALDH9A1, BBOX1 and OCTN2 in the liver of 19 mo-old mice fed a control diet or a diet supplemented with 1000 mg/kg diet L-carnitine from 3 wk to 19 mo of age. Bars represent means and SD for *n* = 6 mice/group and are expressed as fold of control group (= 1.0). B, Representative immunoblots of ALDH9A1, BBOX1, OCTN2 and β-ACTIN for normalisation are shown.

ALDH9A1, aldehyde dehydrogenase 9 family member A1; BBOX1, gamma-butyrobetaine hydroxylase 1; OCTN2; organic cation transporter 2.

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**Supplemental Fig. 3**

A, Relative protein levels of GPX and HMOX in the liver of 19 mo-old mice fed a control diet or a diet supplemented with 1000 mg/kg diet L-carnitine from 3 wk to 19 mo of age. Bars represent means and SD for *n* = 6 mice/group and are expressed as fold of control group (= 1.0). B, Representative immunoblots of GPX, HMOX and β-ACTIN for normalisation are shown.

GPX, glutathione peroxidase; HMOX, heme oxygenase.