**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* | AGTGTGACGTTGACATCCGT  AGCTCAGTAACAGTCCGCCTA | 296 | NM\_007393 |
| *Atb5b* | GCCAGAGACTATGCGGCGCA  CCCCCAAATGCTGGGCCACC | 187 | NM\_016774 |
| *Canx* | GTCCCCGGGAGGCTCGAGATAGA  ACCTCCCCTGTTGGAACTGGAGC | 234 | NM\_007597 |
| *Cyc1* | GCTTCGCCGGACGGTACTGG  CGCAATGGAAGCTGCCGGGA | 99 | NM\_025567 |
| *Eif4a2* | ACATGGCGGCCCAGAGGGAA  TGGTGGGGGCCAATACTAGTGCT | 299 | NM\_013506 |
| *Rpl13a* | GTGGTCGTACGCTGTGAAGGCATC  GGCCTCGGGAGGGGTTGGTATT | 109 | NM\_009438 |
| *Target Genes* |  |  |  |
| *Acaca* | ATGTGGCCTGGGTAGATCCT  CGGACAAGGTAAGCCCCAAT | 295 | NM\_133360 |
| *Acadm* | AGGTTTCAAGATCGCAATGG  CTCCTTGGTGCTCCACTAGC | 152 | NM\_007382 |
| *Aldh9a1* | AGCTGAAGACGGTGTGTGTG  CTAATGACCCAAAGCCTGGA | 154 | NM\_019993 |
| *Atf4* | TTCCTCGAATCCAGCAAAGCCC  CTCCAACATCCAATCTGTCCGG | 286 | NM\_009716 |
| *Bbox1* | CCTAAAGGCAGAAGCAGTGG  TCCGGTCAAATGTCAAATCA | 200 | NM\_130452 |
| *Ddit3* | AGCCAGAATAACAGCCGGAACC  GGGACTCAGCTGCCATGACTG | 117 | NM\_007837 |
| *Dnajc3* | CTGCATGGACACAGGTCCCAG  AGGCTGGACACCCCTACCTC | 217 | NM\_008929 |
| *Fasn* | AGATGGAAGGCTGGGCTCTA  GAAGCGTCTCGGGATCTCTG | 268 | NM\_007988 |
| *Gpam* | AGGAAAGAGCCAGCATCAGG  CAAAGGTATCAGCAACAGGGACT | 150 | NM\_008149 |
| *Gpx1* | CTCTTTACCTTCCTGCGGAA  GGACAGCAGGGTTTCTATGT | 219 | NM\_008160 |
| *Herpud1* | CGCAGTTGGAGTGTGAGTCGC  ACCCTTTGTGCTGGTTTCTGGC | 213 | NM\_022331 |
| *Hmox1* | GATTTGTCTGAGGCCTTGAAG  CTTAAAGCCTTCTCTGGACAC | 111 | NM\_010442 |
| *Hp* | GCAATGGGTGAACAGAGTCG  GAAGAGGTTTTTGGCCGTCG | 213 | NM\_017370 |
| *Hsp90b1* | CCTGCTGACCTTCGGGTTCG  CTGTCCTTGAGCCTTCTCGGC | 98 | NM\_011631 |
| *Hspa5* | TCATCGGACGCACTTGGAATGAC  CGCTGGGCATCATTGAAGTAAGC | 250 | NM\_001163434 |
| *Icam1* | GATGCTCAGGTATCCATCCA  CCACAGTTCTCAAAGCACAG | 212 | NM\_010493 |
| *Lbp* | TCGTGGGCAGTACGAGTTTC  AAGAGATTCAGCAGCCACCC | 327 | NM\_008489 |
| *Nqo1* | ACGTCATTCTCTGGCCGATTCAG  AGGTCAAACAGGCTGCTTGGAG | 196 | NM\_008706 |
| *Pdia4* | CCGTTGACTATGATGGCTCCAGG  GGTCTGTCTGTTCGGTGGCG | 285 | NM\_009787 |
| *Ppp1r15a* | GCGGCTCAGATTGTTCAAAGCC  AGATGGGTTTCTAAGGCGTGCC | 271 | NM\_008654 |
| *Saa1* | CCAGGATGAAGCTACTCACCA  TGTCTGTTGGCTTCCTGGTC | 313 | NM\_009117 |
| *Scd1* | CGTGGCTTCTTCTTCTCTCA  CTTCTCGGCTTTCAGGTCAG | 105 | NM\_009127 |
| *Slc22a5/Octn2* | CTTGTCCCTCACACCGTGAA  CCTAGCTCAGAGAAGTTGGC | 137 | NM\_011396 |
| *Slc25a20/Cact* | GGAGTCACCCCTATGTTCGC  ATCCGTTCTCCAGGGGTCAT | 161 | NM\_020520 |
| *Slc27a1/Fatp1* | AAGGGCCAGGGATCTCTCTCTCCA  TGTCGTCGCAGCTCTAGCCGA | 319 | NM\_011977 |
| *Sod1* | GATGACTTGGGCAAAGGTGG  CTGCGCAATCCCAATCACTC | 90 | NM\_011434 |
| *Tnf* | CCAAGTGGAGGAGCAGCT  GCAAATCGGCTGACGGTGACGGTGT | 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* | AGTGTGACGTTGACATCCGT  AGCTCAGTAACAGTCCGCCTA | 296 | NM\_007393 |
| *Atb5b* | GCCAGAGACTATGCGGCGCA  CCCCCAAATGCTGGGCCACC | 187 | NM\_016774 |
| *Canx* | GTCCCCGGGAGGCTCGAGATAGA  ACCTCCCCTGTTGGAACTGGAGC | 234 | NM\_007597 |
| *Cyc1* | GCTTCGCCGGACGGTACTGG  CGCAATGGAAGCTGCCGGGA | 99 | NM\_025567 |
| *Eif4a2* | ACATGGCGGCCCAGAGGGAA  TGGTGGGGGCCAATACTAGTGCT | 299 | NM\_013506 |
| *Rpl13a* | GTGGTCGTACGCTGTGAAGGCATC  GGCCTCGGGAGGGGTTGGTATT | 109 | NM\_009438 |
| *Target genes* |  |  |  |
| *Ankrd2* | CGACACCAACGTGAGAGACA  ACTGGGCTGGTATAGGCTGA | 365 | XM\_006527234 |
| *B4glant2* | GAGGTGGGGATCATTCCAGG  TTGTTCCGTGTGAGCCAAGA | 91 | NM\_008081 |
| *Gamt* | GCTCTCTTCCCATGGTCCTAG  TCATCTGAGGGAAGGCATAGT | 275 | XM\_011243370 |
| *Olfr1052* | CACTGGGTCAGTCATAGGTGG  TCGTCCAGAAGCTGAGCGTA | 268 | NM\_147010 |
| *Olfr1356* | CGGGCTGCATCACACAGATA  TGATCCAAGAGCCAGCATCG | 161 | NM\_146308 |
| *Olfr142* | ACCCCTATGCTGAACCCCAT  CAGCTGTCCTTTTGCTTCCAG | 89 | NM\_146984 |
| *Olfr427* | GGCTCTTATGTACCTGCGCT  CAGCTCCCAGAGACAGTGAG | 186 | NM\_207158 |
| *Olfr618* | TTGGTTTCAAGCTGGAGGCA  GCAGTATGGCAGACTCGGTT | 92 | NM\_147047 |
| *Ostn* | GCTTCAACTGTGTCAGAAGGC  TCACCCCTAGGCTGGTAGAA | 181 | NM\_198112 |
| *Perp* | CTGAGGTTAAGCCGCTGTCA  TCCGGTCTACGCTGGTTCTA | 141 | NM\_022032 |
| *Pld5* | GGCAGGAAGATCTCATCGCA  GCCTTGGAAGAGCGGTAAGT | 239 | NM\_001195816 |
| *Tppp3* | ATCTGCCACCAAGAGCTTCC  GGCAAAAGCAGGCAAGAGTC | 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.

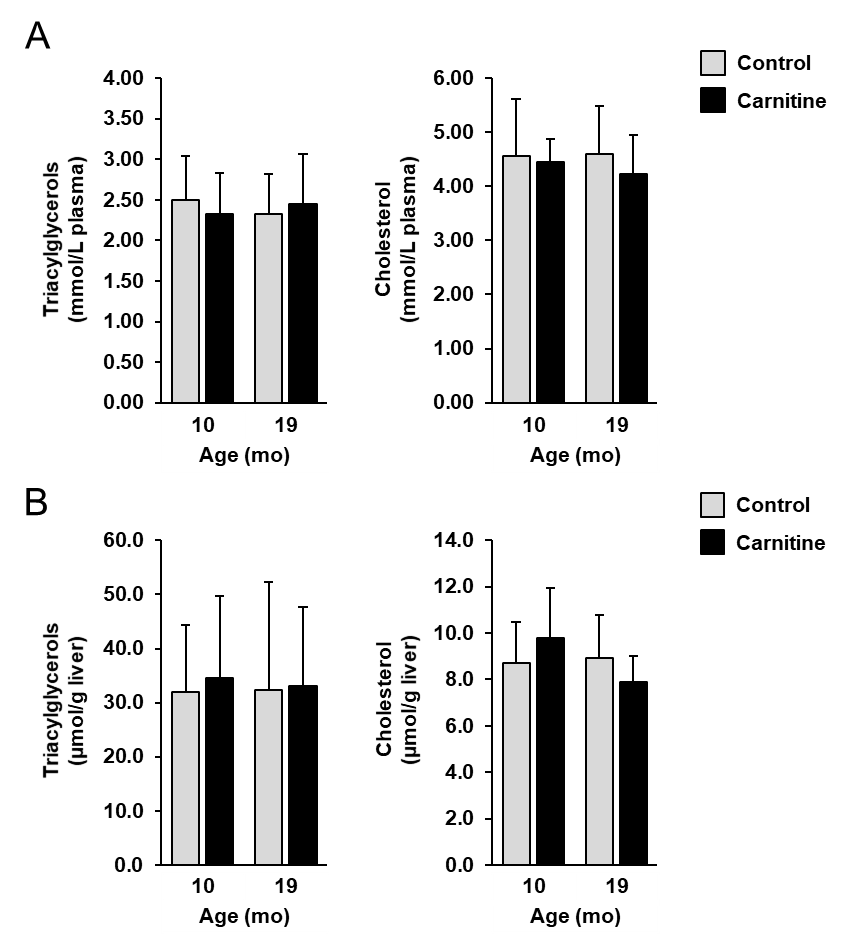
GO, gene ontology.

**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 |

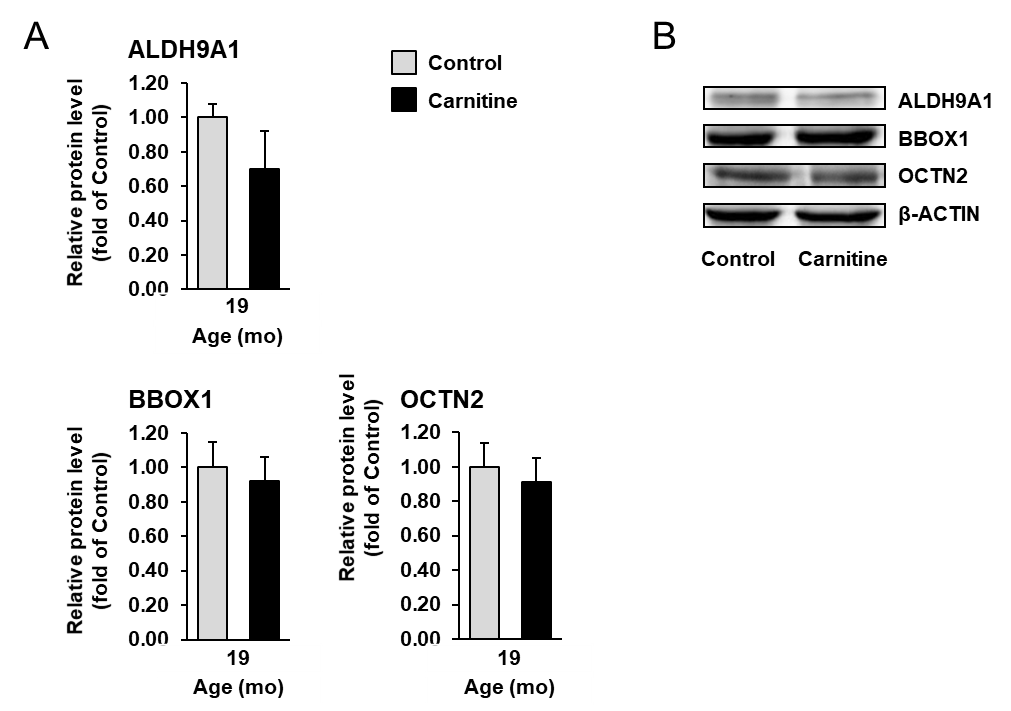
\*GO terms are sorted by their enrichment *P*-value in increasing order. Only GO terms with enrichment *P*-value < 0.01 are shown.

GO, gene ontology.

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**Supplemental Fig. 1**

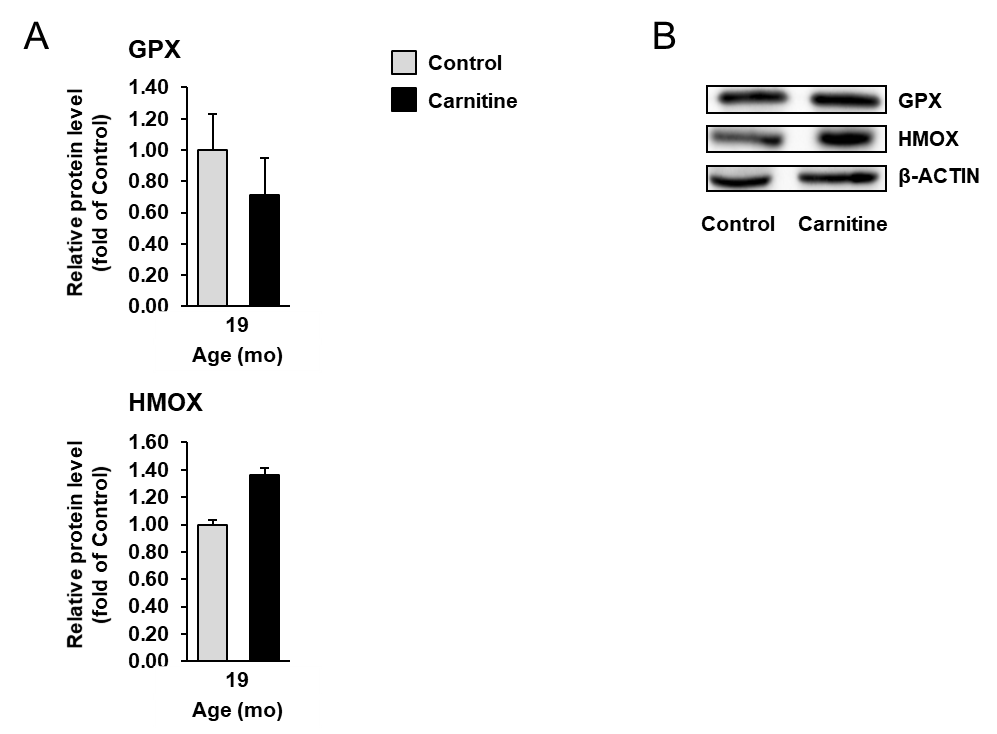
Concentrations triacylglycerols and cholesterol in plasma (A) and liver (B) of mice at 10 and 19 mo of age fed a control diet or a diet supplemented with 1000 mg/kg diet L-carnitine from 3 wk to 19 mo of age. Bars represent means and SD for *n* = 10 mice/group.

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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.