

Supplementary Materials for
Mitochondrial proteostasis stress in muscle drives a long-range protective response to alleviate dietary obesity independently of ATF4

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Fig. S1

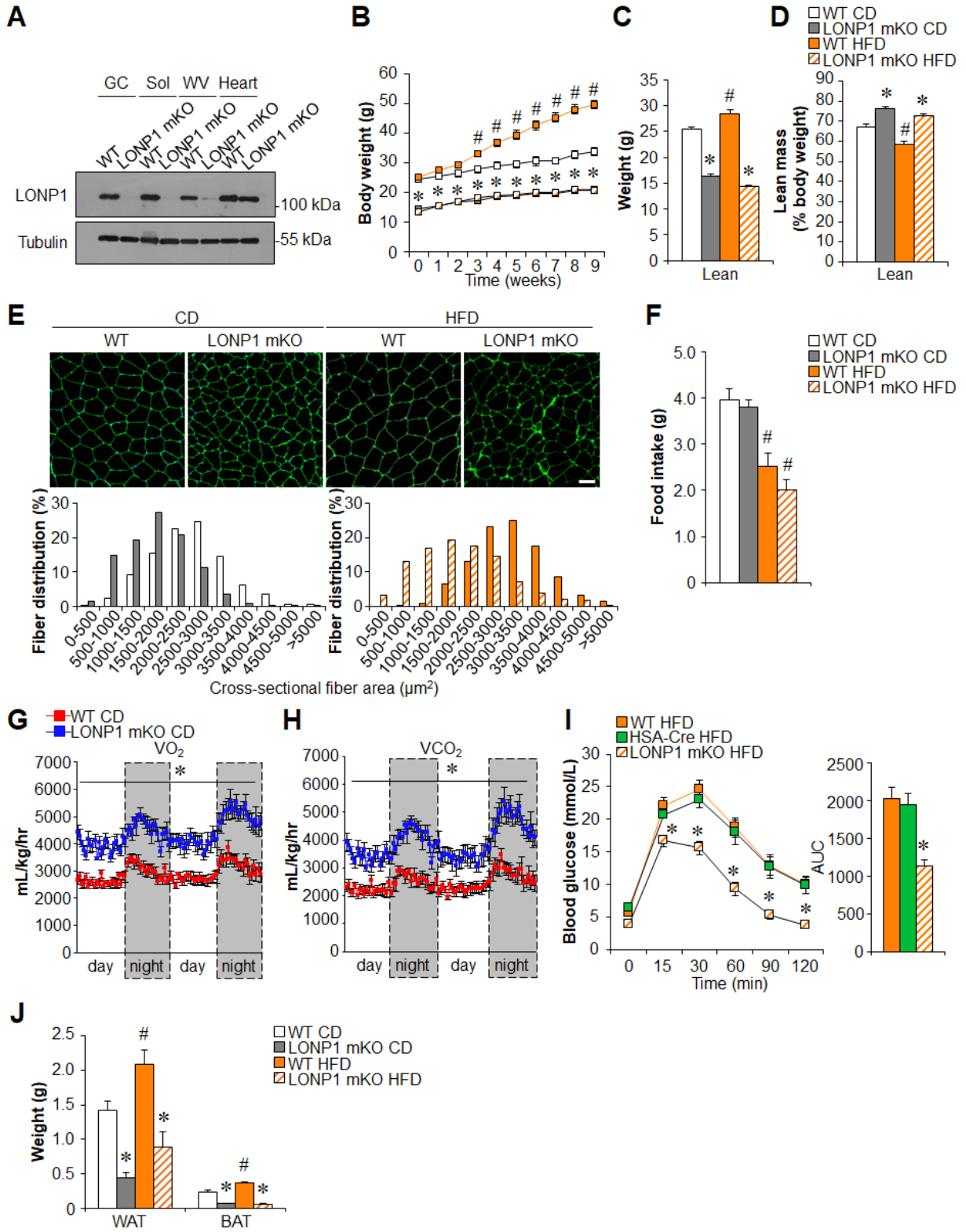


Fig. S1. Metabolic characterization of mice with skeletal muscle-specific ablation of the *Lonp1* gene. (A) Western blot analysis of LONP1 expression in the GC, soleus (Sol), white vastus lateralis (WV) muscles and hearts of WT and LONP1 mKO mice following HFD feeding. (B) Growth curves of indicated mice. n = 8-13 mice per group. (C) Body composition measured to determine lean mass. n = 7-10 mice per group. (D) Lean mass plotted as a percentage of body weight. (E) Top: Representative WGA staining of GC muscle from indicated mice fed either CD or HFD. Scale bar represents 50 μ m. Bottom: Cross-sectional areas of GC myofibers were measured by ImageJ. n = 6-7 mice per group. DAPI, blue; Wheat germ agglutinin (WGA), green. (F) Food consumption. n = 7-8 mice per group. (G and H) Oxygen consumption (G) and carbon dioxide production (H) per hour during the light/dark cycle normalized to body weight. n = 8 mice per group. Color legend for the panel: red, WT CD; blue: LONP1 mKO CD. (I) Left: Glucose tolerance test (GTT). Right: Area under the curve for GTT is shown. n = 4-8 mice per group. (J) Weight of eWAT and BAT from indicated mice. n = 8-10 mice per group. Color legend for the panel: white, WT CD; gray, LONP1 mKO CD; orange, WT HFD; green, HSA-Cre HFD; diagonal hatch, LONP1 mKO HFD. Values represent the mean \pm SEM. * $P < 0.05$ versus corresponding WT controls; # $P < 0.05$ versus corresponding CD controls. The P values were determined using two-tailed unpaired Student's t test (G and H) or one-way ANOVA and Fisher's least-significant difference (LSD) post hoc test (B to D, F, I and J).

Fig. S2

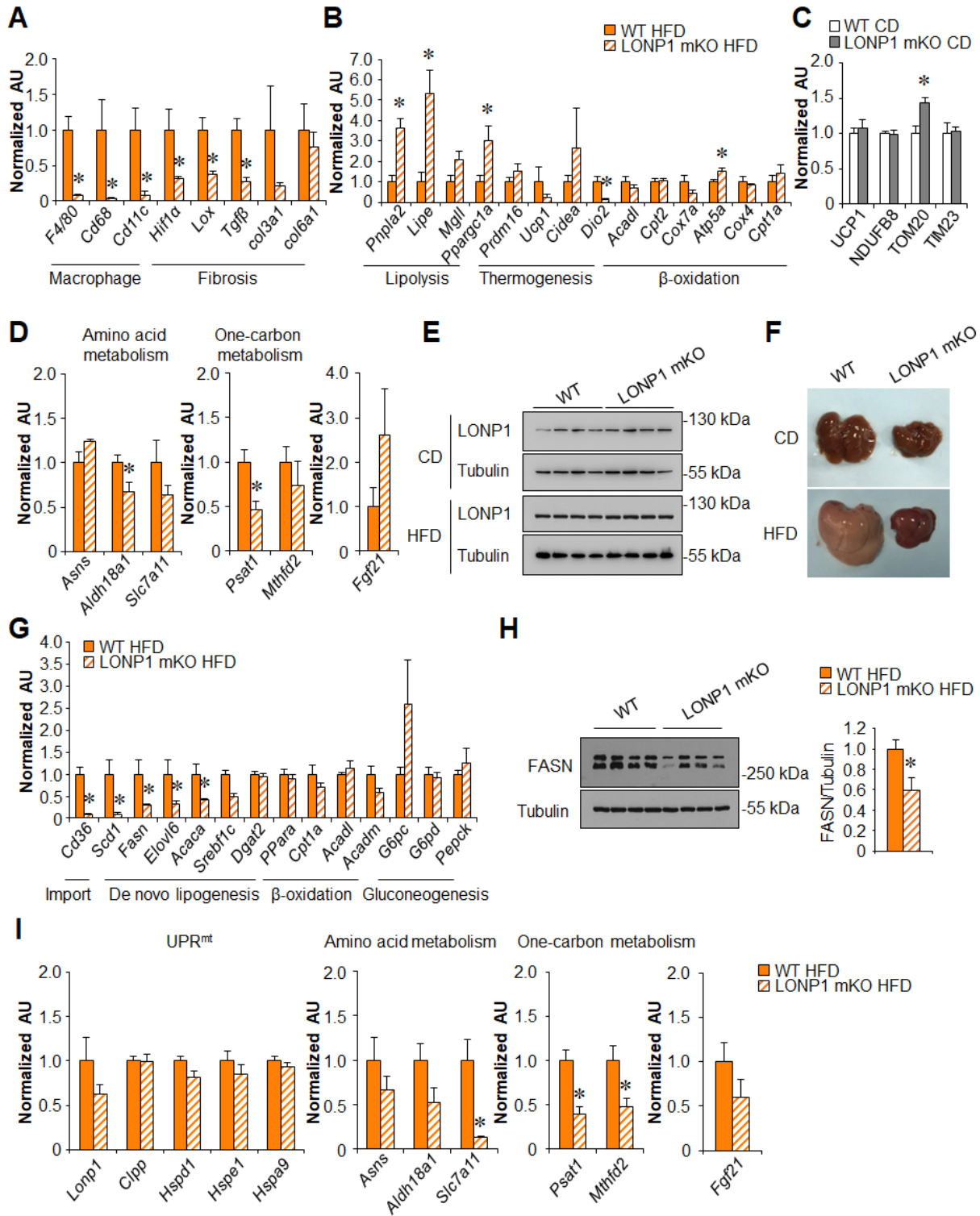


Fig. S2. Muscle LONP1 regulates the response of adipose tissue and liver to HFD. (A and B)

Expression of genes (qRT-PCR) related to macrophages, fibrosis, lipolysis, thermogenesis, and

mitochondrial fatty acid oxidation in the eWAT of the indicated mice following HFD feeding. n = 6 mice per group. (C) Quantification of the UCP1/Tubulin, NDUF88/Tubulin, TOM20/Tubulin and TIM23/Tubulin signal ratios in the BAT from CD-fed LONP1 mKO mice was normalized (= 1.0) to the WT controls fed CD. n = 4 mice per group. (D) Expression of genes (qRT-PCR) related to amino acid metabolism, one-carbon metabolism and *Fgf21* in the BAT from HFD-fed LONP1 mKO mice and WT controls. n = 6 mice per group. (E) Representative western blot analysis of LONP1 protein expression in livers from the indicated mice fed either CD or HFD. n = 4 mice per group. (F) Pictures of livers from the indicated mice fed either CD or HFD. (G) Expression of genes (RT-qPCR) related to fatty acid import, de novo fatty acid lipogenesis, fatty acid oxidation and gluconeogenesis in livers from HFD-fed LONP1 mKO mice and WT controls. n = 6 mice per group. (H) Left: representative western blot analysis of liver lysates for mice of the indicated genotypes using the indicated antibodies. Right: Quantification of the FASN/Tubulin signal ratios normalized (= 1.0) to the WT controls. n = 4 mice per group. (I) Expression of genes (qRT-PCR) related to UPR, amino acid metabolism, one-carbon metabolism and *Fgf21* in the livers from HFD-fed LONP1 mKO mice and WT controls. n = 6 mice per group. Color legend for the panel: white, WT CD; gray, LONP1 mKO CD; orange, WT HFD; diagonal hatch, LONP1 mKO HFD. Values represent mean \pm SEM. * $P < 0.05$ versus WT controls. The P values were determined using a two-tailed unpaired Student's t test.

Fig. S3

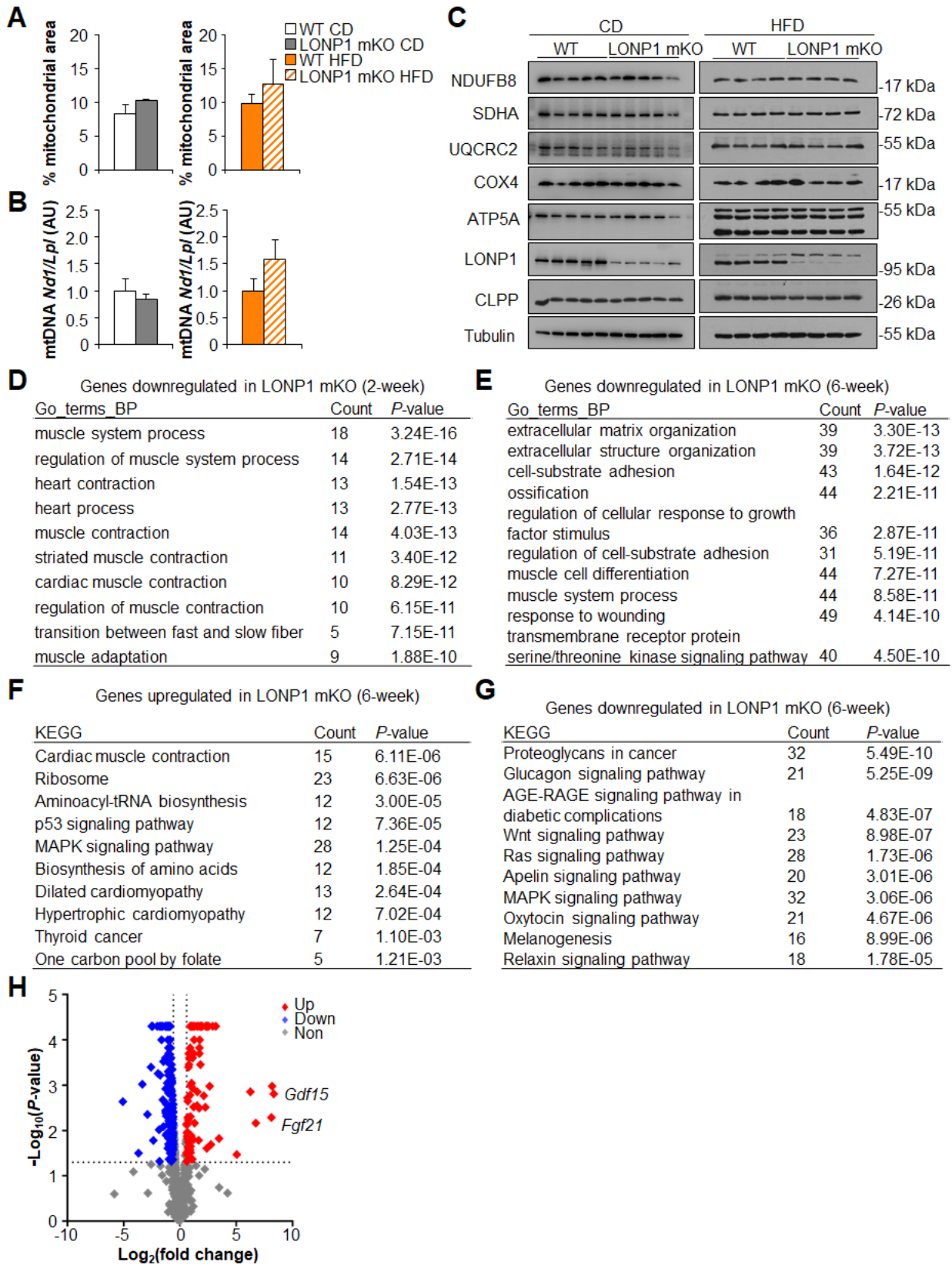


Fig. S3. Analysis of genes regulated in LONP1 mKO muscles. (A) Percentage of mitochondrial area per muscle fiber area in Figure 3A was quantified from the indicated genotypes. (B) Results of quantitative PCR to determine mitochondrial DNA levels in GC muscles from CD or HFD-fed LONP1 mKO mice and WT controls using primers for NADH dehydrogenase (*Ndl*, mitochondria-encoded) and lipoprotein lipase (*Lpl*, nuclear-encoded). *Ndl* levels were normalized to *Lpl* DNA content and expressed relative to WT (=1.0) muscles. n = 6 mice per group. (C) Representative western blot analysis of muscle lysates from the indicated mice fed either CD or HFD. n = 4-5 mice per group. (D and E) GO enrichment analysis of downregulated gene transcripts in LONP1 mKO muscles at the ages of 2 weeks and 6 weeks, with the top ten terms shown. (F and G) KEGG pathway analysis of gene transcripts upregulated (F) or downregulated (G) in LONP1 mKO muscles at the age of 6 weeks. (H) Volcano plot showing fold changes versus *P* values for the regulated myokine genes in GC muscles from 6-week-old male LONP1 mKO mice compared to WT controls. Significantly upregulated genes are represented by red dots, whereas downregulated genes are represented by blue dots. Color legend for the panel: white, WT CD; gray, LONP1 mKO CD; orange, WT HFD; diagonal hatch, LONP1 mKO HFD. Values represent mean \pm SEM.

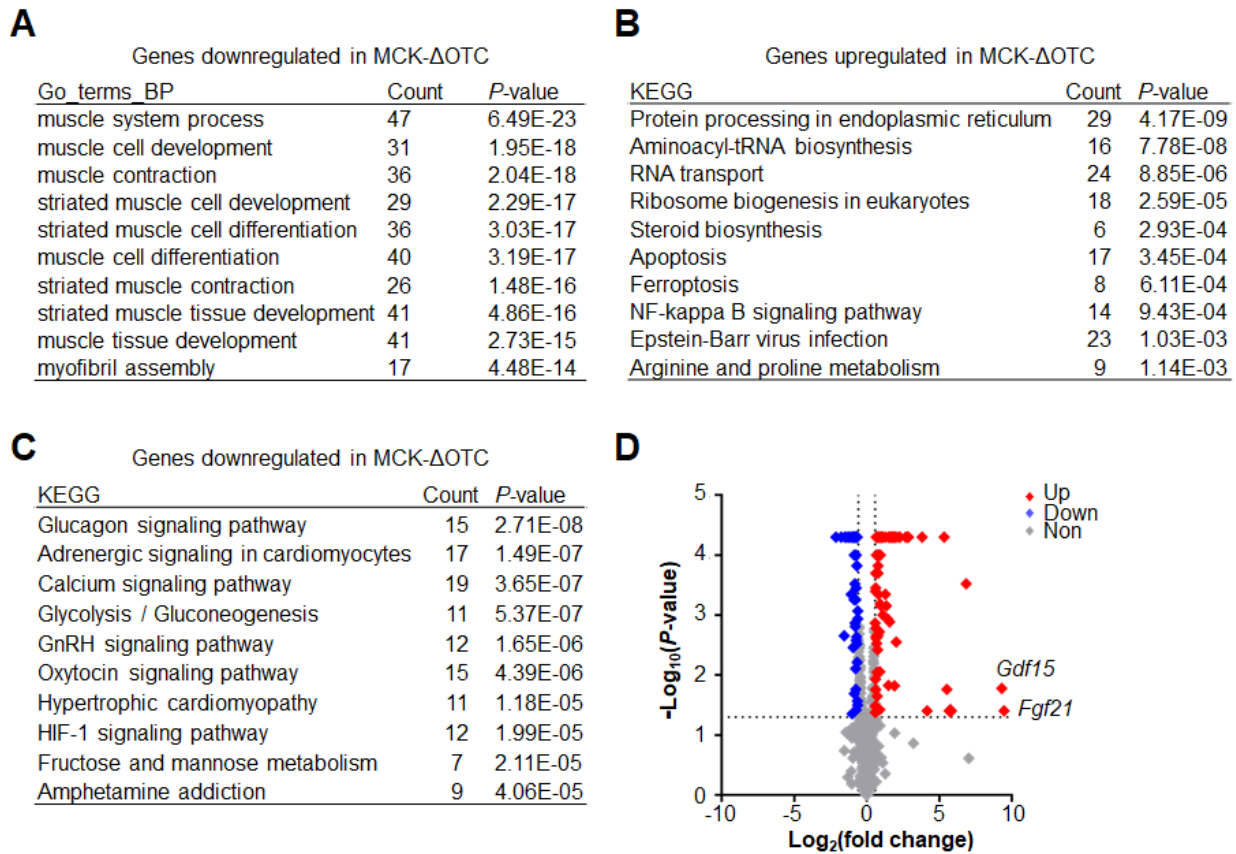
Fig. S4

Fig. S4. Analysis of genes regulated in MCK-ΔOTC muscles. (A) GO enrichment analysis of gene transcripts downregulated in MCK-ΔOTC muscles. (B and C) KEGG pathway analysis of gene transcripts upregulated (B) or downregulated (C) in MCK-ΔOTC muscles. (D) Volcano plot showing fold changes versus P values for the regulated myokine genes in GC muscles from MCK-ΔOTC mice compared to NTG controls. Significantly upregulated genes are represented by red dots, whereas downregulated genes are represented by blue dots.

Fig. S5

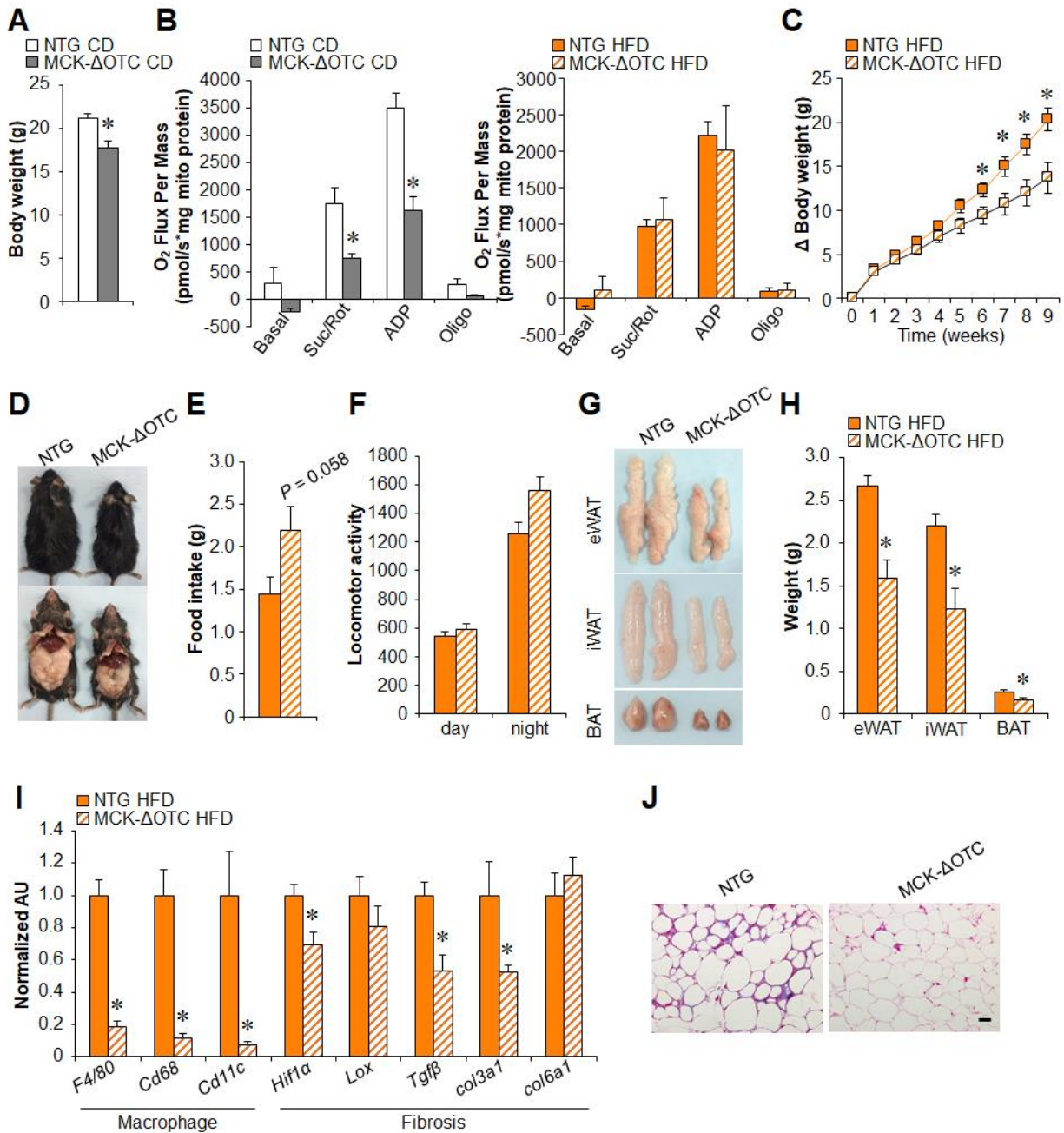


Fig. S5. Muscle-specific overexpression of Δ OTC confers resistance to diet-induced obesity.

(A) Body weight of the indicated 6-week-old mice fed normal chow diet. n = 12-14 mice per group.

(B) Mitochondrial respiration rates were determined on mitochondria isolated from muscles of the indicated mice using succinate as substrate. Succinate/rotenone (Suc/Rot)-stimulated, ADP-dependent respiration, and oligomycin (oligo)-induced respiration are shown. n

= 6 mice for CD and n = 4 mice for HFD. **(C)** Increase in body weight following HFD feeding. n = 12-14 mice per group. **(D)** Representative pictures of the indicated mice fed a HFD for 12 weeks. **(E)** Food consumption. n = 5-6 mice per group. **(F)** Physical activity. n = 5-6 mice per group. **(G)** Representative pictures of eWAT, iWAT and BAT from HFD-fed MCK- Δ OTC mice and NTG controls. **(H)** Weight of eWAT, iWAT and BAT from the indicated mice fed a HFD for 12 weeks. n = 11-14 mice per group. **(I)** Expression of genes (qRT-PCR) related to macrophage and fibrosis in the eWAT from HFD-fed MCK- Δ OTC and WT controls. n = 6 mice per group. **(J)** Masson's trichrome staining in the eWAT of the indicated HFD-fed mice. The scale bar represents 50 μ m. n = 5-6 mice per group. Color legend for the panel: white, NTG CD; gray, MCK- Δ OTC CD; orange, NTG HFD; diagonal hatch, MCK- Δ OTC HFD. Values represent mean \pm SEM. * P < 0.05 versus NTG controls. The P values were determined using a two-tailed unpaired Student's t test.

Fig. S6

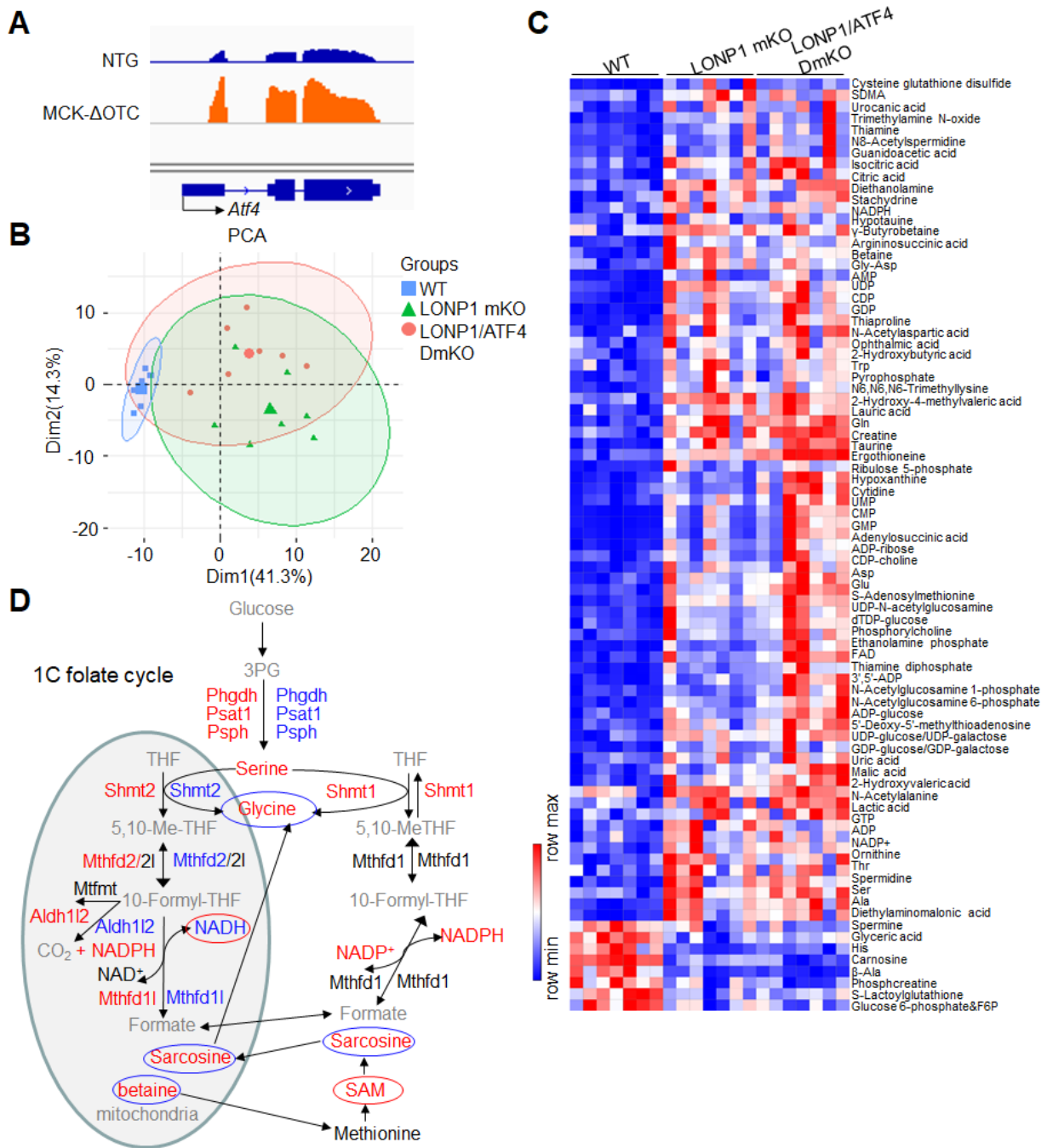


Fig. S6. ATF4-dependent and -independent reprogramming of muscle metabolism by

LONP1. (A) Genome browser tracks of RNA-seq data were visualized in IGV. (B and C)

Principal component analysis (PCA) (B) and Heatmap analysis (C) of muscle metabolites.

Capillary electrophoresis-mass spectrometry (CE-MS) based metabolite analysis were performed

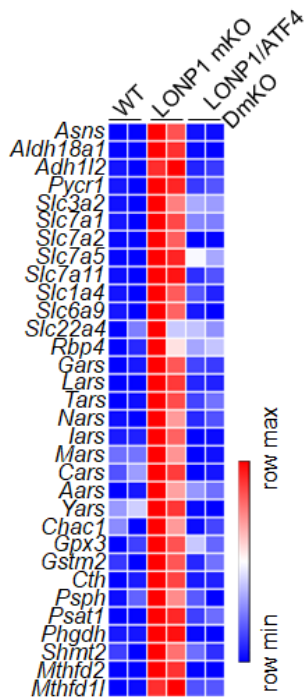
with GC muscles from the indicated mice. n = 7 mice per group. Red represents relative increase in abundance, blue represents relative decrease. **(D)** One-carbon metabolism and associated pathways in WT, LONP1 mKO and LONP1/ATF4 DmKO muscles. Colored text, red, increase in LONP1 mKO muscle; blue, decrease in LONP1/ATF4 DmKO muscle. Circled metabolites changed in LONP1/ATF4 DmKO muscles compared to LONP1 mKO mice; red, increase; blue, decrease.

Fig. S7

A

		Cluster II		Cluster IV	
Go terms BP		Count	P-value	Count	P-value
ATF4-dependent	cellular respiration	20	3.62E-13		
	respiratory electron transport chain	14	1.07E-11		
	antigen processing and presentation of exogenous antigen	10	1.23E-11		
	electron transport chain	14	2.12E-11		
	generation of precursor metabolites and energy	27	2.27E-11		
	antigen processing and presentation of exogenous peptide antigen	9	4.29E-11		
	ATP synthesis coupled electron transport	12	6.65E-11		
	energy derivation by oxidation of organic compounds	21	1.81E-10		
	mitochondrial ATP synthesis coupled electron transport	11	5.23E-10		
	NADH dehydrogenase complex assembly	10	7.41E-10		
ATF4-independent	energy derivation by oxidation of organic compounds	45	1.01E-14		
	ATP metabolic process	44	1.04E-14		
	generation of precursor metabolites and energy	57	1.42E-14		
	muscle cell differentiation	56	1.01E-13		
	striated muscle contraction	32	2.25E-12		
	muscle system process	53	5.06E-12		
	positive regulation of ion transport	46	1.26E-11		
	glucose metabolic process	33	4.22E-11		
	striated muscle cell differentiation	44	8.28E-11		
	extracellular matrix organization	40	1.00E-10		

B



C

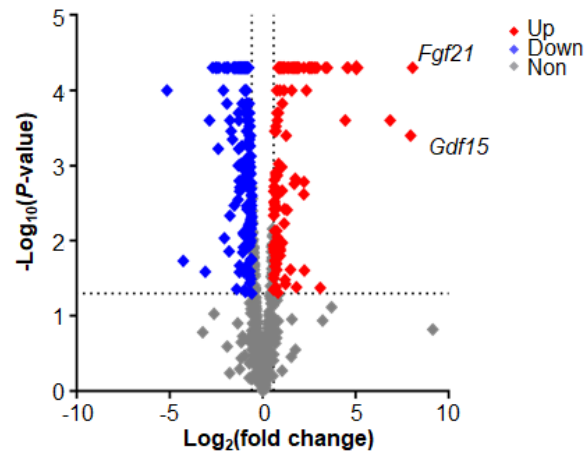


Fig. S7. ATF4-dependent and -independent reprogramming of muscle gene expression by

LONP1. (A) GO enrichment analysis of Cluster II (ATF4-dependent) and IV (ATF4-

independent) genes, with the top ten terms shown. **(B)** Heat-map analysis of ATF4-dependent

genes involved in muscle amino acids and one-carbon metabolism. Red represents relative

increase in abundance, blue represents relative decrease. **(C)** Volcano plot showing fold changes

versus *P* values for the ATF4-independent regulated myokine genes by LONP1 deficiency.

Significantly upregulated genes are represented by red dots, whereas downregulated genes are represented by blue dots.

Fig. S8

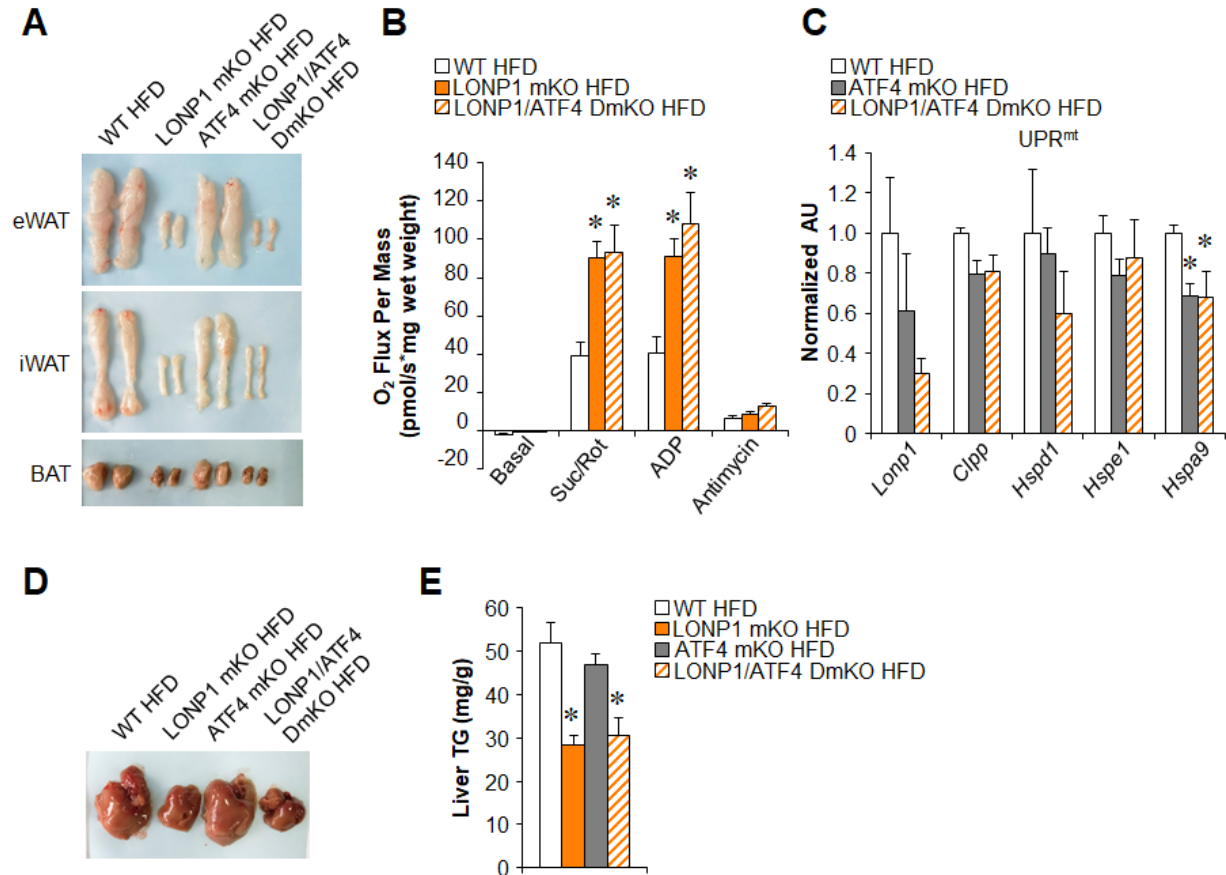


Fig. S8. Mitochondrial proteostasis stress in skeletal muscle directs a long-range metabolic response to alleviate dietary obesity independent of ATF4. (A) Pictures of eWAT, iWAT, and BAT from the indicated mice fed HFD. (B) Mitochondrial respiration rates were determined from the BAT of the indicated genotypes using succinate as substrate. Succinate/rotenone (Suc/Rot)-stimulated, ADP-dependent respiration, and antimycin-induced respiration are shown. n = 5-7 mice per group. (C) Expression of genes (qRT-PCR) related to UPR in the BAT from indicated mice. n = 5-6 mice per group. (D) Pictures of livers from the indicated mice fed HFD. n = 5-6 mice per group. (E) Liver TG (mg/g) for the indicated mice fed HFD. n = 5-6 mice per group.

(E) Liver triglyceride levels from the indicated mice. n = 5-10 mice per group. Color legend for the panel: white, WT HFD; orange, LONP1 mKO HFD; gray, ATF4 mKO HFD; diagonal hatch, LONP1/ATF4 DmKO HFD. Values represent mean \pm SEM. * $P < 0.05$ versus WT controls. The P values were determined using one-way ANOVA and Fisher's least-significant difference (LSD) post hoc test.

Table S1.

Genes commonly upregulated (1.5-fold change and $P < 0.05$) by both LONP1 deficiency and Δ OTC overexpression in skeletal muscle.

Supplemental Table 1 List of muscle UPR^{mt} gene signature			
Gene symbol	Description	Fold change (vs. Control)	
		LONP1 mKO	MCK-ΔOTC
<i>Gdf15</i>	<i>growth differentiation factor 15</i>	320.3	634.2
<i>Cdsn</i>	<i>corneodesmosin</i>	290.9	115.7
<i>Fgf21</i>	<i>fibroblast growth factor 21</i>	276.7	713.8
<i>Soat2</i>	<i>sterol O-acyltransferase 2</i>	234.6	231.9
<i>Trib3</i>	<i>tribbles pseudokinase 3</i>	84.6	172.6
<i>S100a8</i>	<i>S100 calcium binding protein A8</i>	76.1	54.3
<i>Psat1</i>	<i>phosphoserine aminotransferase 1</i>	72.1	21.6
<i>Asns</i>	<i>asparagine synthetase (glutamine-hydrolyzing)</i>	66.4	52.2
<i>Arhgap33</i>	<i>Rho GTPase activating protein 33</i>	64.5	15.5
<i>P2rx3</i>	<i>purinergic receptor P2X 3</i>	63.2	7.9
<i>Dlg2</i>	<i>discs large MAGUK scaffold protein 2</i>	62.6	46.7
<i>Tenm4</i>	<i>teneurin transmembrane protein 4</i>	60.3	16.8
<i>Mthfd2</i>	<i>methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2, methenyltetrahydrofolate cyclohydrolase</i>	54.6	25.1
<i>Slc7a5</i>	<i>solute carrier family 7 member 5</i>	29.5	21.6
<i>Trim66</i>	<i>tripartite motif containing 66</i>	26.5	10.2
<i>Slc7a11</i>	<i>solute carrier family 7 member 11</i>	24.3	71.3
<i>Sox11</i>	<i>SRY-box transcription factor 11</i>	19.7	2.8
<i>Myl4</i>	<i>myosin light chain 4</i>	15.6	4.8
<i>Mt2</i>	<i>metallothionein 1X</i>	15.3	19.6
<i>Slc1a4</i>	<i>solute carrier family 1 member 4</i>	14.9	3.8
<i>Chrng</i>	<i>cholinergic receptor nicotinic gamma subunit</i>	14.8	2.1
<i>Ankrd1</i>	<i>ankyrin repeat domain 1</i>	14.4	12.0
<i>Sesn2</i>	<i>sestrin 2</i>	13.7	18.3
<i>Mthfd11</i>	<i>methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1 like</i>	12.9	6.7
<i>Reep6</i>	<i>receptor accessory protein 6</i>	12.9	11.0
<i>Myh8</i>	<i>myosin heavy chain 8</i>	12.5	2.4
<i>Nrcam</i>	<i>neuronal cell adhesion molecule</i>	12.2	3.6
<i>Cth</i>	<i>cystathionine gamma-lyase</i>	11.8	22.6
<i>Zp2</i>	<i>zona pellucida glycoprotein 2</i>	11.7	6.9
<i>Zfp365</i>	<i>zinc finger protein 365</i>	11.7	2.6
<i>Kcnk2</i>	<i>potassium two pore domain channel subfamily K member 2</i>	10.8	3.0
<i>Aldh18a1</i>	<i>aldehyde dehydrogenase 18 family member A1</i>	10.4	6.2
<i>Slc7a1</i>	<i>solute carrier family 7 member 1</i>	10.3	5.7

<i>Pck2</i>	<i>phosphoenolpyruvate carboxykinase 2, mitochondrial</i>	10.2	6.8
<i>Kcnk3</i>	<i>potassium two pore domain channel subfamily K member 3</i>	9.8	2.2
<i>Gabbr2</i>	<i>gamma-aminobutyric acid type A receptor subunit rho2</i>	9.3	1.8
<i>Smpdl3b</i>	<i>sphingomyelin phosphodiesterase acid like 3B</i>	9.0	7.0
<i>Myog</i>	<i>myogenin</i>	8.4	2.6
<i>Tbc1d31</i>	<i>TBC1 domain family member 31</i>	8.1	8.5
<i>Fam171b</i>	<i>family with sequence similarity 171 member B</i>	7.9	3.6
<i>Lgals3</i>	<i>galectin 3</i>	7.5	40.6
<i>Phgdh</i>	<i>phosphoglycerate dehydrogenase</i>	7.2	6.9
<i>Aldh1l2</i>	<i>aldehyde dehydrogenase 1 family member L2</i>	7.2	4.5
<i>Gadd45a</i>	<i>growth arrest and DNA damage inducible alpha</i>	7.2	4.5
<i>Slc38a1</i>	<i>solute carrier family 38 member 1</i>	7.1	4.9
<i>Uchl1</i>	<i>ubiquitin C-terminal hydrolase L1</i>	7.1	3.1
<i>Pycr1</i>	<i>pyrroline-5-carboxylate reductase 1</i>	7.0	5.3
<i>Arsg</i>	<i>arylsulfatase G</i>	6.7	5.3
<i>Fads3</i>	<i>fatty acid desaturase 3</i>	6.7	6.4
<i>Rassf7</i>	<i>Ras association domain family member 7</i>	6.5	2.8
<i>Slc6a9</i>	<i>solute carrier family 6 member 9</i>	6.4	9.8
<i>Mt1</i>	<i>metallothionein 1A</i>	6.3	10.0
<i>Igfbp2</i>	<i>insulin like growth factor binding protein 2</i>	6.2	3.5
<i>Cpne2</i>	<i>copine 2</i>	6.0	4.5
<i>Arhgdig</i>	<i>Rho GDP dissociation inhibitor gamma</i>	6.0	1.9
<i>Fgf7</i>	<i>fibroblast growth factor 7</i>	5.8	4.6
<i>Arhgef2</i>	<i>Rho/Rac guanine nucleotide exchange factor 2</i>	5.8	2.4
<i>Ttc9</i>	<i>tetratricopeptide repeat domain 9</i>	5.7	1.8
<i>Tubb2b</i>	<i>tubulin beta 2B class IIb</i>	5.6	3.1
<i>Nog</i>	<i>noggin</i>	5.5	14.1
<i>Chrnd</i>	<i>cholinergic receptor nicotinic delta subunit</i>	5.4	4.4
<i>N4bp2l1</i>	<i>NEDD4 binding protein 2 like 1</i>	5.4	5.2
<i>Ostn</i>	<i>osteocrin</i>	5.2	4.9
<i>G0s2</i>	<i>G0/G1 switch 2</i>	5.1	1.9
<i>Gm13889</i>	<i>chromosome 11 open reading frame 96</i>	5.0	4.1
<i>Ncam1</i>	<i>neural cell adhesion molecule 1</i>	5.0	1.7
<i>Atf5</i>	<i>activating transcription factor 5</i>	4.9	5.2
<i>Stc2</i>	<i>stanniocalcin 2</i>	4.9	2.1
<i>Cbx4</i>	<i>chromobox 4</i>	4.8	2.6
<i>Gdf9</i>	<i>growth differentiation factor 9</i>	4.8	2.7
<i>Cdkn1a</i>	<i>cyclin dependent kinase inhibitor 1A</i>	4.7	5.2
<i>Ddit3</i>	<i>DNA damage inducible transcript 3</i>	4.7	5.4
<i>Rin1</i>	<i>Ras and Rab interactor 1</i>	4.6	2.6

<i>Snhg12</i>		4.5	5.8
<i>Zfp52</i>		4.4	1.6
<i>Runx1</i>	<i>RUNX family transcription factor 1</i>	4.4	2.7
<i>Bid</i>	<i>BH3 interacting domain death agonist</i>	4.4	9.4
<i>Dclk1</i>	<i>doublecortin like kinase 1</i>	4.4	2.3
<i>LOC106740</i>	<i>PHD finger protein 10</i>	4.4	4.5
<i>Aldh1b1</i>	<i>aldehyde dehydrogenase 1 family member B1</i>	4.3	1.8
<i>Acot2</i>	<i>acyl-CoA thioesterase 1</i>	4.3	8.1
<i>Cyb5r1</i>	<i>cytochrome b5 reductase 1</i>	4.3	3.5
<i>Slc17a7</i>	<i>solute carrier family 17 member 7</i>	4.2	5.0
<i>Usp11</i>	<i>ubiquitin specific peptidase 11</i>	4.1	3.0
<i>Osbp13</i>	<i>oxysterol binding protein like 3</i>	4.0	2.3
<i>Eif4ebp1</i>	<i>eukaryotic translation initiation factor 4E binding protein 1</i>	4.0	4.0
<i>Ern1</i>	<i>endoplasmic reticulum to nucleus signaling 1</i>	3.9	4.1
<i>Masp1</i>	<i>mannan binding lectin serine peptidase 1</i>	3.8	2.5
<i>Chka</i>	<i>choline kinase alpha</i>	3.8	3.0
<i>Arl14ep</i>	<i>ADP ribosylation factor like GTPase 14 effector protein</i>	3.8	2.1
<i>Ctsl</i>	<i>cathepsin V</i>	3.7	7.3
<i>Tmem82</i>	<i>transmembrane protein 82</i>	3.6	2.0
<i>Rnf185</i>	<i>ring finger protein 185</i>	3.6	4.6
<i>Erdr1</i>		3.6	1.6
<i>Nacad</i>	<i>NAC alpha domain containing</i>	3.6	3.7
<i>Snd1</i>	<i>staphylococcal nuclease and tudor domain containing 1</i>	3.6	3.5
<i>Tmeff1</i>	<i>MSANTD3-TMEFF1 readthrough</i>	3.6	4.8
<i>Ero1l</i>	<i>endoplasmic reticulum oxidoreductase 1 alpha</i>	3.5	3.4
<i>Vat1l</i>	<i>vesicle amine transport 1 like</i>	3.5	4.5
<i>Rrad</i>	<i>RRAD, Ras related glycolysis inhibitor and calcium channel regulator</i>	3.5	5.7
<i>Lgi2</i>	<i>leucine rich repeat LGI family member 2</i>	3.5	2.4
<i>Agpat9</i>	<i>glycerol-3-phosphate acyltransferase 3</i>	3.5	3.3
<i>Eda2r</i>	<i>ectodysplasin A2 receptor</i>	3.4	7.0
<i>Myc</i>	<i>MYC proto-oncogene, bHLH transcription factor</i>	3.4	2.3
<i>Eef1a1</i>	<i>eukaryotic translation elongation factor 1 alpha 1</i>	3.4	2.3
<i>Nol8</i>	<i>nucleolar protein 8</i>	3.4	1.7
<i>Gas5</i>	<i>growth arrest specific 5</i>	3.4	1.7
<i>Tbx6</i>	<i>T-box transcription factor 6</i>	3.4	2.8
<i>Slc3a2</i>	<i>solute carrier family 3 member 2</i>	3.4	5.3
<i>Nupr1</i>	<i>nuclear protein 1, transcriptional regulator</i>	3.4	3.7
<i>Emb</i>	<i>embigin</i>	3.3	7.6
<i>Slc24a3</i>	<i>solute carrier family 24 member 3</i>	3.3	3.6

<i>Phf10</i>	<i>PHD finger protein 10</i>	3.3	4.8
<i>Hhip1l</i>	<i>HHIP like 1</i>	3.3	3.0
<i>Stard5</i>	<i>StAR related lipid transfer domain containing 5</i>	3.3	4.4
<i>Phyhd1</i>	<i>phytanoyl-CoA dioxygenase domain containing 1</i>	3.3	4.0
<i>Napb</i>	<i>NSF attachment protein beta</i>	3.3	2.4
<i>Stbd1</i>	<i>starch binding domain 1</i>	3.3	2.1
<i>Dctd</i>	<i>dCMP deaminase</i>	3.2	1.8
<i>Crym</i>	<i>crystallin mu</i>	3.2	4.7
<i>Cxadr</i>	<i>CXADR Ig-like cell adhesion molecule</i>	3.2	4.1
<i>Glce</i>	<i>glucuronic acid epimerase</i>	3.2	2.4
<i>Aph1c</i>	<i>aph-1 homolog B, gamma-secretase subunit</i>	3.2	5.6
<i>Gars</i>	<i>glycyl-tRNA synthetase 1</i>	3.2	4.8
<i>Ccdc136</i>	<i>coiled-coil domain containing 136</i>	3.2	1.8
<i>Mtbp</i>	<i>MDM2 binding protein</i>	3.2	1.8
<i>Chrna1</i>	<i>cholinergic receptor nicotinic alpha 1 subunit</i>	3.2	1.9
<i>Plekhh1</i>	<i>pleckstrin homology, MyTH4 and FERM domain containing H1</i>	3.1	2.0
<i>Lcn2</i>	<i>lipocalin 2</i>	3.1	46.2
<i>Dennd4a</i>	<i>DENN domain containing 4A</i>	3.1	3.0
<i>Ddit4</i>	<i>DNA damage inducible transcript 4</i>	3.1	1.8
<i>Cbx2</i>	<i>chromobox 2</i>	3.1	2.0
<i>Ciart</i>	<i>circadian associated repressor of transcription</i>	3.1	6.4
<i>Lhfpl2</i>	<i>LHFPL tetraspan subfamily member 2</i>	3.0	2.6
<i>Ghitm</i>	<i>growth hormone inducible transmembrane protein</i>	3.0	2.5
<i>Rundc3a</i>	<i>RUN domain containing 3A</i>	3.0	1.9
<i>Gramd1b</i>	<i>GRAM domain containing 1B</i>	3.0	1.6
<i>Gsto1</i>	<i>glutathione S-transferase omega 1</i>	3.0	9.1
<i>Lars</i>	<i>leucyl-tRNA synthetase 1</i>	2.9	3.8
<i>Map1b</i>	<i>microtubule associated protein 1B</i>	2.9	3.2
<i>Card9</i>	<i>caspase recruitment domain family member 9</i>	2.9	2.4
<i>Lrrc8d</i>	<i>leucine rich repeat containing 8 VRAC subunit D</i>	2.9	3.8
<i>Sncg</i>	<i>synuclein gamma</i>	2.9	2.1
<i>Tubb6</i>	<i>tubulin beta 6 class V</i>	2.9	3.6
<i>Sergef</i>	<i>secretion regulating guanine nucleotide exchange factor</i>	2.9	1.8
<i>Cd68</i>	<i>CD68 molecule</i>	2.8	5.0
<i>Trp53inp1</i>	<i>tumor protein p53 inducible nuclear protein 1</i>	2.8	2.2
<i>Gpnmb</i>	<i>glycoprotein nmb</i>	2.8	6.5
<i>Eif3c</i>	<i>eukaryotic translation initiation factor 3 subunit C like</i>	2.8	4.1
<i>Spag5</i>	<i>sperm associated antigen 5</i>	2.8	2.3
<i>Nlrc3</i>	<i>NLR family CARD domain containing 3</i>	2.7	2.7

<i>Gnmt</i>	<i>glycine N-methyltransferase</i>	2.7	4.6
<i>Atp6v1h</i>	<i>ATPase H⁺ transporting V1 subunit H</i>	2.7	4.5
<i>Tsga10</i>	<i>testis specific 10</i>	2.7	2.0
<i>Sh3bgrl2</i>	<i>SH3 domain binding glutamate rich protein like 2</i>	2.7	2.3
<i>Aif1l</i>	<i>allograft inflammatory factor 1 like</i>	2.7	1.7
<i>Taf15</i>	<i>TATA-box binding protein associated factor 15</i>	2.7	2.7
<i>Pmm1</i>	<i>phosphomannomutase 1</i>	2.6	1.9
<i>Gm11974</i>	<i>small nucleolar RNA host gene 15</i>	2.6	1.9
<i>Htatip2</i>	<i>HIV-1 Tat interactive protein 2</i>	2.6	3.5
<i>Sik1</i>	<i>salt inducible kinase 1B (putative)</i>	2.6	1.7
<i>Igf2bp2</i>	<i>insulin like growth factor 2 mRNA binding protein 2</i>	2.6	1.9
<i>Nradd</i>	<i>neurotrophin receptor associated death domain, pseudogene</i>	2.6	3.3
<i>Prune2</i>	<i>prune homolog 2 with BCH domain</i>	2.6	2.2
<i>Slc19a2</i>	<i>solute carrier family 19 member 2</i>	2.6	2.6
<i>Ubxn11</i>	<i>UBX domain protein 11</i>	2.6	2.3
<i>Osbp18</i>	<i>oxysterol binding protein like 8</i>	2.6	1.6
<i>Flnc</i>	<i>filamin C</i>	2.5	1.9
<i>Clic4</i>	<i>chloride intracellular channel 4</i>	2.5	2.1
<i>Lilrb4a</i>	<i>leukocyte immunoglobulin like receptor B4</i>	2.5	2.6
<i>Xpot</i>	<i>exportin for tRNA</i>	2.5	3.0
<i>Osbp2</i>	<i>oxysterol binding protein 2</i>	2.5	5.2
<i>Dsn1</i>	<i>DSN1 component of MIS12 kinetochore complex</i>	2.5	1.7
<i>Atf6</i>	<i>activating transcription factor 6</i>	2.5	3.2
<i>Slc2a1</i>	<i>solute carrier family 2 member 1</i>	2.5	3.1
<i>Avil</i>	<i>advillin</i>	2.5	6.8
<i>Bbc3</i>	<i>BCL2 binding component 3</i>	2.4	3.2
<i>Snhg1</i>		2.4	2.4
<i>Rnd1</i>	<i>Rho family GTPase 1</i>	2.4	2.0
<i>Cebpg</i>	<i>CCAAT enhancer binding protein gamma</i>	2.4	1.9
<i>Ankrd32</i>	<i>SMC5-SMC6 complex localization factor 1</i>	2.4	1.6
<i>Extl1</i>	<i>exostosin like glycosyltransferase 1</i>	2.4	3.6
<i>Tlr4</i>	<i>toll like receptor 4</i>	2.4	1.6
<i>Trim46</i>	<i>tripartite motif containing 46</i>	2.4	3.3
<i>Sars</i>	<i>seryl-tRNA synthetase 1</i>	2.4	2.7
<i>Adig</i>	<i>adipogenin</i>	2.4	4.5
<i>Trappc6a</i>	<i>trafficking protein particle complex 6A</i>	2.4	1.5
<i>Zfp385b</i>	<i>zinc finger protein 385B</i>	2.4	1.6
<i>Ticam2</i>		2.4	36.3
<i>Wfs1</i>	<i>wolframin ER transmembrane glycoprotein</i>	2.4	3.3
<i>Rcc2</i>	<i>regulator of chromosome condensation 2</i>	2.4	1.9

<i>Lrrc58</i>	<i>leucine rich repeat containing 58</i>	2.4	1.6
<i>Nop58</i>	<i>NOP58 ribonucleoprotein</i>	2.3	1.8
<i>Lcorl</i>	<i>ligand dependent nuclear receptor corepressor like</i>	2.3	2.1
<i>Angptl6</i>	<i>angiopoietin like 6</i>	2.3	4.0
<i>Gtpbp2</i>	<i>GTP binding protein 2</i>	2.3	3.3
<i>Mnd1</i>	<i>meiotic nuclear divisions 1</i>	2.3	2.0
<i>Hmgb2</i>	<i>high mobility group box 2</i>	2.2	2.0
<i>Spg21</i>	<i>SPG21 abhydrolase domain containing, maspardin</i>	2.2	4.5
<i>Slc25a33</i>	<i>solute carrier family 25 member 33</i>	2.2	1.9
<i>Tgif1</i>	<i>TGFB induced factor homeobox 1</i>	2.2	6.1
<i>Leprotl1</i>	<i>leptin receptor overlapping transcript like 1</i>	2.2	3.1
<i>Trmt10a</i>	<i>tRNA methyltransferase 10A</i>	2.2	1.8
<i>Tspyl4</i>	<i>TSPY like 4</i>	2.2	2.6
<i>Slc22a4</i>	<i>solute carrier family 22 member 4</i>	2.2	2.0
<i>Tmed5</i>	<i>transmembrane p24 trafficking protein 5</i>	2.2	1.6
<i>Spg20</i>	<i>spartin</i>	2.2	4.0
<i>Hspb7</i>	<i>heat shock protein family B (small) member 7</i>	2.2	1.6
<i>Mamdc2</i>	<i>MAM domain containing 2</i>	2.2	1.9
<i>Fam175a</i>	<i>abraxas 1, BRCA1 A complex subunit</i>	2.2	2.7
<i>Ifrd1</i>	<i>interferon related developmental regulator 1</i>	2.1	1.8
<i>Atxn2l</i>	<i>ataxin 2 like</i>	2.1	1.8
<i>Bex1</i>	<i>brain expressed X-linked 2</i>	2.1	2.9
<i>Shmt2</i>	<i>serine hydroxymethyltransferase 2</i>	2.1	2.6
<i>Prodh</i>	<i>proline dehydrogenase 1</i>	2.1	1.7
<i>Sclt1</i>	<i>sodium channel and clathrin linker 1</i>	2.1	1.5
<i>Pthr1</i>	<i>peptidyl-tRNA hydrolase 1 homolog</i>	2.1	1.7
<i>Odf2</i>	<i>outer dense fiber of sperm tails 2</i>	2.1	1.6
<i>Zfp945</i>		2.1	2.5
<i>Stap2</i>	<i>signal transducing adaptor family member 2</i>	2.1	3.2
<i>Ddx51</i>	<i>DEAD-box helicase 51</i>	2.1	5.8
<i>Mtm1</i>	<i>myotubularin 1</i>	2.1	2.7
<i>Rhbdd1</i>	<i>rhomboid domain containing 1</i>	2.1	3.3
<i>Dhrs7</i>	<i>dehydrogenase/reductase 7</i>	2.1	1.8
<i>Sfn</i>	<i>stratifin</i>	2.1	1.9
<i>Mid1ip1</i>	<i>MID1 interacting protein 1</i>	2.0	4.5
<i>Dkc1</i>	<i>dyskerin pseudouridine synthase 1</i>	2.0	1.5
<i>Hsp90aa1</i>	<i>heat shock protein 90 alpha family class A member 1</i>	2.0	1.7
<i>Eprs</i>	<i>glutamyl-prolyl-tRNA synthetase 1</i>	2.0	2.6
<i>Scpep1</i>	<i>serine carboxypeptidase 1</i>	2.0	3.4
<i>Adck4</i>	<i>coenzyme Q8B</i>	2.0	1.8

<i>Wbscr27</i>	<i>methyltransferase like 27</i>	2.0	2.9
<i>Parp4</i>	<i>poly(ADP-ribose) polymerase family member 4</i>	2.0	2.6
<i>Pvr</i>	<i>PVR cell adhesion molecule</i>	2.0	1.8
<i>Gyk</i>	<i>glycerol kinase</i>	2.0	2.1
<i>Synj2</i>	<i>synaptojanin 2</i>	2.0	1.7
<i>Agap1</i>	<i>ArfGAP with GTPase domain, ankyrin repeat and PH domain 1</i>	2.0	2.2
<i>Acot6</i>	<i>acyl-CoA thioesterase 6</i>	2.0	1.9
<i>Tfcp2l1</i>	<i>transcription factor CP2 like 1</i>	2.0	8.9
<i>Me2</i>	<i>malic enzyme 2</i>	2.0	2.4
<i>Mks1</i>	<i>MKS transition zone complex subunit 1</i>	2.0	1.5
<i>Ankzf1</i>	<i>ankyrin repeat and zinc finger peptidyl tRNA hydrolase 1</i>	2.0	1.8
<i>Chac1</i>	<i>ChaC glutathione specific gamma-glutamylcyclotransferase 1</i>	2.0	5.0
<i>Baz1a</i>	<i>bromodomain adjacent to zinc finger domain 1A</i>	2.0	1.7
<i>Faap20</i>	<i>FA core complex associated protein 20</i>	2.0	1.7
<i>Shb</i>	<i>SH2 domain containing adaptor protein B</i>	2.0	2.1
<i>Tor3a</i>	<i>torsin family 3 member A</i>	2.0	1.9
<i>Ece2</i>	<i>endothelin converting enzyme 2</i>	2.0	2.7
<i>Cdk20</i>	<i>cyclin dependent kinase 20</i>	2.0	2.5
<i>Hspa9</i>	<i>heat shock protein family A (Hsp70) member 9</i>	2.0	2.2
<i>Maff</i>	<i>MAF bZIP transcription factor F</i>	2.0	1.6
<i>Rpl3</i>	<i>ribosomal protein L3</i>	2.0	2.3
<i>Ncl</i>	<i>nucleolin</i>	1.9	1.9
<i>Gbe1</i>	<i>1,4-alpha-glucan branching enzyme 1</i>	1.9	2.4
<i>Mvd</i>	<i>mevalonate diphosphate decarboxylase</i>	1.9	1.7
<i>Der11</i>	<i>derlin 1</i>	1.9	2.7
<i>Slc39a11</i>	<i>solute carrier family 39 member 11</i>	1.9	2.4
<i>Plk3</i>	<i>polo like kinase 3</i>	1.9	2.1
<i>Arhgap22</i>	<i>Rho GTPase activating protein 22</i>	1.9	5.3
<i>Ak4</i>	<i>adenylate kinase 4</i>	1.9	1.5
<i>Trmt61a</i>	<i>tRNA methyltransferase 61A</i>	1.9	3.0
<i>Tars</i>	<i>threonyl-tRNA synthetase 1</i>	1.9	1.9
<i>Elmsan1</i>	<i>mitotic deacetylase associated SANT domain protein</i>	1.9	1.7
<i>Hebp1</i>	<i>heme binding protein 1</i>	1.9	2.1
<i>Slc25a5</i>	<i>solute carrier family 25 member 5</i>	1.9	1.7
<i>Nars</i>	<i>asparaginyl-tRNA synthetase 1</i>	1.9	2.7
<i>Zfp568</i>	<i>zinc finger protein 568</i>	1.9	1.6
<i>Iars</i>	<i>isoleucyl-tRNA synthetase 1</i>	1.9	2.5
<i>Ciapin1</i>	<i>cytokine induced apoptosis inhibitor 1</i>	1.9	2.7
<i>Tmem205</i>	<i>transmembrane protein 205</i>	1.9	1.7

<i>Tmem62</i>	<i>transmembrane protein 62</i>	1.9	2.1
<i>Cstb</i>	<i>cystatin B</i>	1.9	3.7
<i>Gpc4</i>	<i>glypican 4</i>	1.9	1.5
<i>Mars</i>	<i>methionyl-tRNA synthetase 1</i>	1.9	2.3
<i>Rab27a</i>	<i>RAB27A, member RAS oncogene family</i>	1.9	1.7
<i>Esrrg</i>	<i>estrogen related receptor gamma</i>	1.9	4.3
<i>Mustn1</i>	<i>musculoskeletal, embryonic nuclear protein 1</i>	1.8	2.3
<i>Irak2</i>	<i>interleukin 1 receptor associated kinase 2</i>	1.8	1.9
<i>Dusp14</i>	<i>dual specificity phosphatase 14</i>	1.8	1.8
<i>Llph</i>	<i>LLP homolog, long-term synaptic facilitation factor</i>	1.8	2.0
<i>Garem</i>	<i>GRB2 associated regulator of MAPK1 subtype 1</i>	1.8	1.8
<i>Bri3bp</i>	<i>BRI3 binding protein</i>	1.8	1.8
<i>Arl15</i>	<i>ADP ribosylation factor like GTPase 15</i>	1.8	1.8
<i>Ttc12</i>	<i>tetratricopeptide repeat domain 12</i>	1.8	1.5
<i>Junb</i>	<i>JunB proto-oncogene, AP-1 transcription factor subunit</i>	1.8	2.3
<i>Sh3bp2</i>	<i>SH3 domain binding protein 2</i>	1.8	2.6
<i>Rabggtb</i>	<i>Rab geranylgeranyltransferase subunit beta</i>	1.8	1.5
<i>Eif2s2</i>	<i>eukaryotic translation initiation factor 2 subunit beta</i>	1.8	1.9
<i>Art5</i>	<i>ADP-ribosyltransferase 5</i>	1.8	1.7
<i>Cx3cl1</i>	<i>C-X3-C motif chemokine ligand 1</i>	1.8	1.7
<i>BC048403</i>	<i>chromosome 12 open reading frame 66</i>	1.8	1.8
<i>B4galt6</i>	<i>beta-1,4-galactosyltransferase 6</i>	1.8	1.5
<i>Tubb2a</i>	<i>tubulin beta 2A class IIa</i>	1.8	1.6
<i>Fam83g</i>	<i>family with sequence similarity 83 member G</i>	1.8	8.4
<i>Zw10</i>	<i>zw10 kinetochore protein</i>	1.8	1.9
<i>Timm8a1</i>	<i>translocase of inner mitochondrial membrane 8A</i>	1.8	1.5
<i>Slc15a2</i>	<i>solute carrier family 15 member 2</i>	1.8	1.5
<i>Srm</i>	<i>spermidine synthase</i>	1.8	1.9
<i>Nfkb2</i>	<i>nuclear factor kappa B subunit 2</i>	1.8	3.4
<i>Cars</i>	<i>cysteinyl-tRNA synthetase 1</i>	1.7	2.1
<i>Otulin</i>	<i>OTU deubiquitinase with linear linkage specificity</i>	1.7	1.7
<i>Snrnp48</i>	<i>small nuclear ribonucleoprotein U11/U12 subunit 48</i>	1.7	1.9
<i>Slc16a1</i>	<i>solute carrier family 16 member 1</i>	1.7	2.1
<i>Atf4</i>	<i>activating transcription factor 4</i>	1.7	2.5
<i>Dnajb9</i>	<i>DnaJ heat shock protein family (Hsp40) member B9</i>	1.7	3.0
<i>Fbxo30</i>	<i>F-box protein 30</i>	1.7	2.1
<i>Lrrc2</i>	<i>leucine rich repeat containing 2</i>	1.7	1.5
<i>Bhlhb9</i>	<i>ARMCX5-GPRASP2 readthrough</i>	1.7	1.6

<i>Lrrc51</i>	<i>leucine rich transmembrane and O-methyltransferase domain containing</i>	1.7	2.0
<i>Hax1</i>	<i>HCLS1 associated protein X-1</i>	1.7	2.4
<i>Zfp14</i>	<i>ZFP14 zinc finger protein</i>	1.7	1.5
<i>Eiv5</i>	<i>ETS variant transcription factor 5</i>	1.7	1.5
<i>Tmem176b</i>	<i>transmembrane protein 176B</i>	1.7	3.2
<i>Sorbs1</i>	<i>sorbin and SH3 domain containing 1</i>	1.7	1.7
<i>Rb1</i>	<i>RB transcriptional corepressor 1</i>	1.7	1.9
<i>Ninj1</i>	<i>ninjurin 1</i>	1.7	2.7
<i>Snhg8</i>	<i>small nucleolar RNA host gene 8</i>	1.7	2.1
<i>Ppip5k2</i>	<i>diphosphoinositol pentakisphosphate kinase 2</i>	1.7	1.5
<i>Panx1</i>	<i>pannexin 1</i>	1.7	2.2
<i>Noc4l</i>	<i>nucleolar complex associated 4 homolog</i>	1.7	3.6
<i>Pam</i>	<i>peptidylglycine alpha-amidating monooxygenase</i>	1.7	1.7
<i>Ppfbp1</i>	<i>PPFIA binding protein 1</i>	1.7	1.9
<i>Tnip1</i>	<i>TNFAIP3 interacting protein 1</i>	1.7	3.5
<i>Anxa4</i>	<i>annexin A4</i>	1.7	2.1
<i>Eif3a</i>	<i>eukaryotic translation initiation factor 3 subunit A</i>	1.7	1.5
<i>Thnsl2</i>	<i>threonine synthase like 2</i>	1.7	1.6
<i>Litaf</i>	<i>lipopolysaccharide induced TNF factor</i>	1.7	2.0
<i>Hace1</i>	<i>HECT domain and ankyrin repeat containing E3 ubiquitin protein ligase 1</i>	1.7	1.6
<i>Mknk1</i>	<i>MAPK interacting serine/threonine kinase 1</i>	1.7	2.3
<i>Obfc1</i>	<i>STN1 subunit of CST complex</i>	1.7	1.5
<i>Npm1</i>	<i>nucleophosmin 1</i>	1.7	1.9
<i>Slc19a1</i>	<i>solute carrier family 19 member 1</i>	1.6	1.5
<i>Trmt6</i>	<i>tRNA methyltransferase 6</i>	1.6	2.0
<i>Tmem181a</i>	<i>transmembrane protein 181</i>	1.6	1.8
<i>Nfe2l2</i>	<i>nuclear factor, erythroid 2 like 2</i>	1.6	1.7
<i>Slc25a39</i>	<i>solute carrier family 25 member 39</i>	1.6	2.3
<i>Tuba1c</i>	<i>tubulin alpha 1c</i>	1.6	2.5
<i>Smim15</i>	<i>small integral membrane protein 15</i>	1.6	1.7
<i>Telo2</i>	<i>telomere maintenance 2</i>	1.6	1.6
<i>Sirpa</i>	<i>signal regulatory protein alpha</i>	1.6	1.9
<i>Ddx10</i>	<i>DEAD-box helicase 10</i>	1.6	1.6
<i>Wars</i>	<i>tryptophanyl-tRNA synthetase 1</i>	1.6	3.8
<i>Utp14a</i>	<i>UTP14A small subunit processome component</i>	1.6	1.8
<i>Zbtb8os</i>	<i>zinc finger and BTB domain containing 8 opposite strand</i>	1.6	3.1
<i>Fubp1</i>	<i>far upstream element binding protein 1</i>	1.6	1.6
<i>Kdm4a</i>	<i>lysine demethylase 4A</i>	1.6	1.5
<i>Herpud1</i>	<i>homocysteine inducible ER protein with ubiquitin like domain 1</i>	1.6	2.4

<i>Aars</i>	<i>alanyl-tRNA synthetase 1</i>	1.6	2.1
<i>Gtf2b</i>	<i>general transcription factor IIB</i>	1.6	1.9
<i>Sdf2l1</i>	<i>stromal cell derived factor 2 like 1</i>	1.6	2.6
<i>Krcc1</i>	<i>lysine rich coiled-coil 1</i>	1.6	1.8
<i>Mak16</i>	<i>MAK16 homolog</i>	1.6	1.5
<i>Siah1a</i>	<i>siah E3 ubiquitin protein ligase 1</i>	1.6	1.7
<i>D19Bwg1357e</i>	<i>pumilio RNA binding family member 3</i>	1.6	1.7
<i>Dusp4</i>	<i>dual specificity phosphatase 4</i>	1.6	4.1
<i>Slc16a6</i>	<i>solute carrier family 16 member 6</i>	1.6	1.5
<i>Hgh1</i>	<i>HGH1 homolog</i>	1.6	1.5
<i>Slc38a7</i>	<i>solute carrier family 38 member 7</i>	1.6	1.9
<i>Krtcap2</i>	<i>keratinocyte associated protein 2</i>	1.6	2.0
<i>Canx</i>	<i>calnexin</i>	1.6	1.8
<i>Aen</i>	<i>apoptosis enhancing nuclease</i>	1.6	1.8
<i>Eif1a</i>	<i>eukaryotic translation initiation factor 1A Y-linked</i>	1.6	1.7
<i>Psph</i>	<i>phosphoserine phosphatase</i>	1.6	1.5
<i>Nubpl</i>	<i>nucleotide binding protein like</i>	1.6	1.6
<i>Tcea1</i>	<i>transcription elongation factor A1</i>	1.6	1.9
<i>Msn</i>	<i>moesin</i>	1.5	1.6
<i>Gfod1</i>	<i>glucose-fructose oxidoreductase domain containing 1</i>	1.5	1.7
<i>Slc20a1</i>	<i>solute carrier family 20 member 1</i>	1.5	2.1
<i>Rpl10</i>	<i>ribosomal protein L10</i>	1.5	1.6
<i>Srxn1</i>	<i>sulfiredoxin 1</i>	1.5	4.7
<i>Nfu1</i>	<i>NFU1 iron-sulfur cluster scaffold</i>	1.5	2.1
<i>Cln8</i>	<i>CLN8 transmembrane ER and ERGIC protein</i>	1.5	2.2
<i>Musk</i>	<i>muscle associated receptor tyrosine kinase</i>	1.5	2.9
<i>Hmox1</i>	<i>heme oxygenase 1</i>	1.5	3.8
<i>Manf</i>	<i>mesencephalic astrocyte derived neurotrophic factor</i>	1.5	1.8
<i>Rps18</i>	<i>ribosomal protein S18</i>	1.5	1.6
<i>Erlin1</i>	<i>ER lipid raft associated 1</i>	1.5	2.5
<i>Pacsin2</i>	<i>protein kinase C and casein kinase substrate in neurons 2</i>	1.5	1.5
<i>Wdr46</i>	<i>WD repeat domain 46</i>	1.5	2.0
<i>Bax</i>	<i>BCL2 associated X, apoptosis regulator</i>	1.5	2.2
<i>Yrdc</i>	<i>yrdC N6-threonylcarbamoyltransferase domain containing</i>	1.5	2.1
<i>Ears2</i>	<i>glutamyl-tRNA synthetase 2, mitochondrial</i>	1.5	2.0
<i>Till11</i>	<i>tubulin tyrosine ligase like 11</i>	1.5	2.7
<i>Tmem128</i>	<i>transmembrane protein 128</i>	1.5	1.7
<i>Fam129a</i>	<i>niban apoptosis regulator 1</i>	1.5	2.0

Table S2.
RT-PCR primers.

Supplemental Table 2 RT-PCR primers		
Mouse Gene	Forward	Reverse
<i>36b4</i>	5'-ATCCCTGACGCACCGCCGTGA	5'-TGCATCTGCTTGGAGCCCACGT
<i>F4/80</i>	5'-TTTCCTCGCCTGCTTCTTC	5'-CCCCGTCTCTGTATTCAACC
<i>Cd68</i>	5'-GCAGCACAGTGGACATTCAT	5'-TTGCATTTCCACAGCAGAAG
<i>Cd11c</i>	5'-CAGAACTTCCCAACTGCACA	5'-TCTCTGAAGCTGGCTCATCA
<i>Hif1a</i>	5'-CATGATGGCTCCCTTTTTCA	5'-GTCACCTGGTTGCTGCAATA
<i>Lox</i>	5'-CAGGCTGCACAATTCACC	5'-CAAAACACCAGGTACGGCTTT
<i>Tgfb</i>	5'-TGGAGCAACATGTGGAACCTC	5'-GTCAGCAGCCGGTTACCA
<i>Col3a1</i>	5'-CTCCTGGTGAGCGAGGAC	5'-GACCAGGTTGCCCATCACT
<i>Col6a1</i>	5'-GGGCATCAAGGTCTTTTCTG	5'-ATGTGTGGTCTGTGGCAATG
<i>Pnpla2</i>	5'-CATGATGGTGCCTATACTC	5'-GTGAGAGGTTGTTTCGTACC
<i>Lipe</i>	5'-AGCGCTGGAGGAGTGTTTT	5'-CCGCTCTCCAGTTGAACC
<i>Mgl1</i>	5'-GACGGACAGTACCTCTTTTG	5'-AGAAAAGTAGGTTGGCCTCT
<i>Ppargc1a</i>	5'-GGACATGTGCAGCCAAGACTCT	5'-CACTTCAATCCACCCAGAAAGCT
<i>Prdm16</i>	5'-ACAGGCAGGCTAAGAACCAG	5'-CGTGGAGAGGAGTGCTTTCAG
<i>Ucp1</i>	5'-GGCCTCTACGACTCAGTCCA	5'-TAAGCCGGCTGAGATCTTGT
<i>Cidea</i>	5'-TTCAAGGCCGTGTTAAGGA	5'-CCTTTGGTGCTAGGCTTGG
<i>Ppara</i>	5'-ACTACGGAGTTCACGCATGTG	5'-TTGTCGTACACCAGCTTCAGC
<i>Dio2</i>	5'-CTGCGCTGTGTCTGGAAC	5'-GGAGCATCTTCACCCAGTTT
<i>Cpt2</i>	5'-CCAAAGAAGCAGCGATGG	5'-TAGAGCTCAGGCAGGGTGA
<i>Cox7a</i>	5'-CGAAGAGGGGAGGTGACTC	5'-AGCCTGGGAGACCCGTAG
<i>Atp5a</i>	5'-GCTGAGGAATGTTCAAGCAGA	5'-CCAAGTTCAGGGACATACCC
<i>Cox4</i>	5'-TACTTCGGTGTGCCTTCGA	5'-TGACATGGGCCACATCAG
<i>Cpt1a</i>	5'-CCGATCATGGTTAACAGCAA	5'-TGCAGCAGAGATTTGGCATA
<i>Cd36</i>	5'-TTGAAAAGTCTCGGACATTGAG	5'-TCAGATCCGAACACAGCGTA
<i>Scd1</i>	5'-TGAAATGCCTTTGAGATGG	5'-CCAGCCAGCCTTTGACTAT
<i>Fasn</i>	5'-CTCCGTGGACCTTATCACTA	5'-CTGGGAGAGGTTGTAGTCAG
<i>Elovl6</i>	5'-CAAAGCACCCGAACTAGGTG	5'-GAGCACAGTGATGTGGTGGT
<i>Acaca</i>	5'-CCAGGCCATGTTGAGACGCT	5'-ATCACAGAGCGGACGCCATC
<i>Srebf1c</i>	5'-TGCGGCTGTTGTCTACCATA	5'-TGCTGGAGCTGACAGAGAAA
<i>Dgat2</i>	5'-TCATGGGTGTCTGTGGGTTA	5'-CAGAGTGAAACCAGCCAACA
<i>Acadl</i>	5'-GCTTATGAATGTGTGCAACTCC	5'-CCGAGCATCCACGTAAGC
<i>Acadm</i>	5'-AGGTTTCAAGATCGCAATGG	5'-CATTGTCCAAAAGCCAAACC
<i>G6pc</i>	5'-TCTGTCCCGGATCTACCTTG	5'-GAAAGTTTCAGCCACAGCAA
<i>G6pd</i>	5'-AGGGAAGAGTTGTACCAAAATGA	5'-CTTCTTCTTGGCCAGGTCAC
<i>Pepck</i>	5'-GTGCTGGAGTGGATGTTCCGG	5'-CTGGCTGATTCTCTGTTTCAGG
<i>Atf4</i>	5'-AGCAAAACAAGACAGCAGCC	5'-ACTCTCTTCTTCCCCCTTGC
<i>Atf5</i>	5'-CTGGCTCCCTATGAGGTCCTTG	5'-GAGCTGTGAAATCAACTCGCTCAG
<i>Ddit3</i>	5'-GCGACAGAGCCAGAATAACA	5'-GATGCACTTCCTTCTGGAACA
<i>Lonpl</i>	5'-CATTGCCTTGAACCCTCTC	5'-ATGTCGCTCAGGTAGATGG
<i>Clpp</i>	5'-TGGGCCCGATTGACGACAGTG	5'-TAGATGGCCAGGCCCGCAGT
<i>Hspd1</i>	5'-GATGCTGTGGCCGTTACAATG	5'-GTCAATTGACTTTGCAACAGTCACAC
<i>Hspe1</i>	5'-GGCCCGAGTTCAGAGTCC	5'-TGTCAAAGAGCGGAAGAAACT
<i>Hspa9</i>	5'-CAAGCGACAGGCTGTCACCAAC	5'-CAACCCAGGCATCACCATTGG
<i>Asns</i>	5'-CTGCCTCTGCTCCACCTT	5'-CACATGCTACAGGCGGACT
<i>Aldh112</i>	5'-GCATAACTGGATTCGAGGTCA	5'-TGAGCCGTAGAAAAGTCACCA

<i>Aldh18a1</i>	5'-AGCGGGAAGAGATCCTGTTAG	5'-GTTTGGACGTGGAGAGGCTA
<i>Slc7a11</i>	5'-GATTCATGTCCACAAGCACAC	5'-GAGCATCACCATCGTCAGAG
<i>Slc6a9</i>	5'-CACAGATGGGGACACACTTCT	5'-GGTTGTAGTGGGAGCGTAGC
<i>Psat1</i>	5'-CCGGTGGATGTTTCCAAG	5'-TGATGGGCACTCTCTGAGC
<i>Phgdh</i>	5'-GAGAACCCTGCCAGTCA	5'-AGGCCATTGCTAGAGTCAGG
<i>Shmt2</i>	5'-CCCTGAGATGTGGGAGCTT	5'-CTCGGCTGCAGAAGTTCTCT
<i>Mthfd2</i>	5'-CCTACAGCCCTTCCACCTG	5'-GAGGCCACCCACTCTTCC
<i>Mthfd11</i>	5'-GAGGTGGATATGCTCAGGTCA	5'-ATGTCCCAGTCAGGTGAAG
<i>Fgf21</i>	5'-TACACAGATGACGACCAAGA	5'-GGCTTCAGACTGGTACACAT
<i>Gdf15</i>	5'-GAGCTACGGGGTCGCTTC	5'-GAGTCCTCTCGGCTCTGGT
<i>Angptl6</i>	5'-ATCTTCTCTGCTGCCACA	5'-CGTGAGCCTCTGCACAATC
<i>Igfbp2</i>	5'-GCGGGTACCTGTGAAAAGAG	5'-CCTCAGAGTGGTCGTCATCA
Primers for quantification of mtDNA		
<i>mt-Nd1</i>	5'-CCCATTGCGGTTATCTT	5'-AAGTTGATCGTAACGGAAGC
<i>Lpl</i>	5'-GATGGACGGTAAGAGTGATTC	5'-ATCCAAGGGTAGCAGACAGGT