

Appendix

Coupling of mitochondrial function and skeletal muscle fiber type by a miR-499/Fnip1/AMPK circuit

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Appendix Table S1. List of calcium signaling and muscle contraction genes up-regulated in MCK-miR-499 gastrocnemius muscle

Gene	Description	Fold Change
<i>Ablim1</i>	actin-binding LIM protein 1	1.5
<i>Actn2</i>	actinin alpha 2	1.5
<i>Arpc1b</i>	actin related protein 2/3 complex, subunit 1B	1.4
<i>Atp2a2</i>	ATPase, Ca ⁺⁺ transporting, cardiac muscle, slow twitch 2	2.6
<i>Casq2</i>	calsequestrin 2 (cardiac muscle)	1.8
<i>Chrna1</i>	cholinergic receptor, nicotinic, alpha 1 (muscle)	4.6
<i>Chrnd</i>	cholinergic receptor, nicotinic, delta (muscle)	1.3
<i>Csrp3</i>	cysteine and glycine-rich protein 3	2.3
<i>Dmd</i>	dystrophin, muscular dystrophy	1.9
<i>Enah</i>	enabled homolog (Drosophila)	1.6
<i>Gys2</i>	glycogen synthase 2	1.5
<i>Hdac9</i>	histone deacetylase 9	1.8
<i>Micu1</i>	mitochondrial calcium uptake 1	1.4
<i>Murc</i>	muscle-related coiled-coil protein	1.3
<i>Myh1</i>	myosin, heavy polypeptide 2, skeletal muscle, adult; myosin, heavy polypeptide 1, skeletal muscle, adult	1.5
<i>Myh2</i>	myosin, heavy chain 2, skeletal muscle, adult	1.3
<i>Myh6</i>	myosin, heavy polypeptide 6, cardiac muscle, alpha	1.9
<i>Myh7</i>	myosin, heavy polypeptide 7, cardiac muscle, beta	3.2
<i>Myh8</i>	myosin, heavy polypeptide 8, skeletal muscle, perinatal	1.5
<i>Myl2</i>	myosin, light polypeptide 2, regulatory, cardiac, slow	2.9
<i>Myl3</i>	myosin, light polypeptide 3	5.5
<i>Myl6b</i>	myosin, light polypeptide 6B	1.6
<i>Myoz2</i>	myozenin 2	3.1
<i>Pgm5</i>	phosphoglucomutase 5	1.7
<i>Ptpn11</i>	protein tyrosine phosphatase, non-receptor type 11	1.4
<i>Rap1a</i>	RAP1A, member of RAS oncogene family	1.6
<i>Rcan2</i>	regulator of calcineurin 2	2.0
<i>Rhou</i>	ras homolog gene family, member U	1.5
<i>Slc8a1</i>	solute carrier family 8 (sodium/calcium exchanger), member 1	2.2
<i>Slc8a3</i>	solute carrier family 8 (sodium/calcium exchanger), member 3	2.2
<i>Slmap</i>	sarcolemma associated protein	1.9
<i>Smtnl1</i>	smoothelin-like 1	3.2
<i>Tnnc1</i>	troponin C type 1 (slow)	7.9
<i>Tnni1</i>	troponin I type 1 (skeletal, slow)	6.7
<i>Tnnt1</i>	troponin T type 1 (skeletal, slow)	9.0
<i>Tnnt2</i>	troponin T2, cardiac	3.1
<i>Tpm3</i>	predicted gene 7848; predicted gene 7839; predicted gene 4157; similar to tropomyosin 3, gamma; tropomyosin 3, gamma; predicted gene 4903	3.1
<i>Trdn</i>	triadin	4.2

<i>Ush1g</i>	Usher syndrome 1G homolog (human)	1.3
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Genes involved in calcium signaling and muscle contraction (Gene Ontology) were compared between NTG and MCK-miR-499 gastrocnemius. 39 up-regulated genes (fold change greater than 1.3 and a significant p value < 0.05) are shown.

Appendix Table S2. List of mitochondrial related genes up-regulated in MCK-miR-499 gastrocnemius muscle

Gene	Description	Fold Change
<i>Abcd2</i>	ATP-binding cassette, sub-family D (ALD), member 2	1.6
<i>Acad8</i>	acyl-Coenzyme A dehydrogenase family, member 8	1.4
<i>Acadl</i>	acyl-Coenzyme A dehydrogenase, long-chain	1.6
<i>Acot13</i>	acyl-CoA thioesterase 13	1.3
<i>Acs1l</i>	acyl-CoA synthetase long-chain family member 1	1.4
<i>Agpat5</i>	1-acylglycerol-3-phosphate O-acyltransferase 5 (lysophosphatidic acid acyltransferase, epsilon)	1.4
<i>Agxt2l2</i>	alanine-glyoxylate aminotransferase 2-like 2	1.3
<i>Akr1b10</i>	RIKEN cDNA 2310005E10 gene	1.3
<i>Aldh2</i>	aldehyde dehydrogenase 2, mitochondrial	1.4
<i>Armc1</i>	armadillo repeat containing 1	1.5
<i>Atp5e</i>	ATP synthase, H+ transporting, mitochondrial F1 complex, epsilon subunit	1.6
<i>Atp5g1</i>	predicted gene 12337; predicted gene 10039; predicted gene 4479; ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 1	1.3
<i>Atp5l</i>	predicted gene 10221; predicted gene 4602; predicted gene 9391; ATP synthase, H+ transporting, mitochondrial FO complex, subunit G2, pseudogene; predicted gene 11477; predicted gene 9712; ATP synthase, H+ transporting, mitochondrial F0 complex, subunit g; predicted gene 4045	1.5
<i>Bbox1</i>	butyrobetaine (gamma), 2-oxoglutarate dioxygenase 1 (gamma-butyrobetaine hydroxylase)	9.4
<i>Bnip3</i>	predicted gene 14506; BCL2/adenovirus E1B interacting protein 3; predicted gene 6532; similar to E1B 19K/Bcl-2-binding protein homolog	1.4
<i>Brp44</i>	brain protein 44; similar to brain protein 44; predicted gene 3982	1.7
<i>Cabc1</i>	chaperone, ABC1 activity of bc1 complex like (S. pombe)	1.3
<i>Cbaral</i>	calcium binding atopy-related autoantigen 1	1.4
<i>Cox6c</i>	predicted gene 6265; similar to cytochrome c oxidase, subunit VIc; cytochrome c oxidase, subunit VIc	1.8
<i>Cox7a1</i>	cytochrome c oxidase, subunit VIIa 1	1.6
<i>Cox7b</i>	cytochrome c oxidase subunit VIIb	1.5
<i>Crat</i>	carnitine acetyltransferase	1.4
<i>Cycs</i>	predicted gene 10108; cytochrome c, somatic; predicted gene 10053; similar to cytochrome c	1.3
<i>D9Ert402e</i>	DNA segment, Chr 9, ERATO Doi 402, expressed	1.5
<i>Dci</i>	dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenzyme A isomerase)	1.5
<i>Efhal</i>	EF hand domain family A1	1.4
<i>Etfa</i>	predicted gene 2893; electron transferring flavoprotein, alpha polypeptide	1.3
<i>Fam36a</i>	predicted gene 15683; RIKEN cDNA 2310005N03 gene; similar to RIKEN cDNA 2310005N03	1.4
<i>Gate</i>	glutamyl-tRNA(Gln) amidotransferase, subunit C homolog (bacterial)	1.5
<i>Gbas</i>	glioblastoma amplified sequence	1.4
<i>Gimap5</i>	GTPase, IMAP family member 5	1.6
<i>Glx</i>	glutaredoxin	1.4

<i>Gm9108</i>	predicted gene 13910; similar to Hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit; hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit; predicted gene 9108	1.5
<i>Got2</i>	glutamate oxaloacetate transaminase 2, mitochondrial	1.3
<i>Gpx1</i>	glutathione peroxidase 1	1.3
<i>Grsf1</i>	G-rich RNA sequence binding factor 1	1.4
<i>Gtpbp10</i>	GTP-binding protein 10 (putative); predicted gene 6877	1.5
<i>Hccs</i>	holocytochrome c synthetase	1.8
<i>Hint2</i>	histidine triad nucleotide binding protein 2	1.3
<i>Hsdl2</i>	hydroxysteroid dehydrogenase like 2	1.5
<i>Hspb7</i>	heat shock protein family, member 7 (cardiovascular)	1.4
<i>Idh1</i>	isocitrate dehydrogenase 1 (NADP+), soluble	1.3
<i>Idh2</i>	isocitrate dehydrogenase 2 (NADP+), mitochondrial	1.5
<i>Imp11</i>	IMP1 inner mitochondrial membrane peptidase-like (<i>S. cerevisiae</i>)	1.7
<i>Imp21</i>	IMP2 inner mitochondrial membrane peptidase-like (<i>S. cerevisiae</i>)	1.6
<i>Isca1</i>	iron-sulfur cluster assembly 1 homolog (<i>S. cerevisiae</i>)	1.5
<i>Ldhb</i>	lactate dehydrogenase B; predicted gene 5514	3.7
<i>Lym5</i>	LYR motif containing 5	1.7
<i>Lym7</i>	LYR motif containing 7	1.3
<i>Maob</i>	monoamine oxidase B	2.7
<i>Mapk10</i>	mitogen-activated protein kinase 10	1.8
<i>Mavs</i>	mitochondrial antiviral signaling protein	1.3
<i>Mcee</i>	methylmalonyl CoA epimerase	1.5
<i>Mdh1</i>	malate dehydrogenase 1, NAD (soluble)	1.7
<i>Mgst1</i>	microsomal glutathione S-transferase 1	1.7
<i>Mrps15</i>	mitochondrial ribosomal protein S15	1.3
<i>Mrps33</i>	mitochondrial ribosomal protein S33; predicted gene 12540	1.6
<i>Mrps36</i>	predicted gene 10078; predicted gene 3544; similar to mitochondrial ribosomal protein S36; mitochondrial ribosomal protein S36; predicted gene 7258; predicted gene 4676	1.3
<i>Mrrf</i>	mitochondrial ribosome recycling factor; similar to mitochondrial ribosome recycling factor; predicted gene 6374	1.4
<i>MsrB2</i>	methionine sulfoxide reductase B2	1.5
<i>Mtfr1</i>	mitochondrial fission regulator 1	1.3
<i>Ndufa1</i>	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 1	1.7
<i>Ndufa4</i>	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4	1.4
<i>Ndufa5</i>	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5	1.3
<i>Ndufaf4</i>	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, assembly factor 4	1.8
<i>Ndufc1</i>	predicted gene 4237; NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 1	1.6
<i>Ndufc2</i>	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 2; similar to NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 2	1.3
<i>Ndufs4</i>	NADH dehydrogenase (ubiquinone) Fe-S protein 4	1.5
<i>Ndufs6</i>	similar to NADH dehydrogenase (ubiquinone) Fe-S protein 6; NADH dehydrogenase (ubiquinone) Fe-S protein 6; predicted gene 6415	1.5
<i>Nln</i>	neurolysin (metallopeptidase M3 family)	1.3

<i>Nnt</i>	nicotinamide nucleotide transhydrogenase	1.9
<i>Nrd1</i>	nardilysin, N-arginine dibasic convertase, NRD convertase 1	1.6
<i>Nudt19</i>	nudix (nucleoside diphosphate linked moiety X)-type motif 19	1.4
<i>Ociad2</i>	O CIA domain containing 2	2.0
<i>Oma1</i>	OMA1 homolog, zinc metallopeptidase (<i>S. cerevisiae</i>)	1.4
<i>Opa3</i>	optic atrophy 3 (human)	1.4
<i>Pdha1</i>	pyruvate dehydrogenase E1 alpha 1	1.5
<i>Pdk1</i>	pyruvate dehydrogenase kinase, isoenzyme 1	1.6
<i>Pdp1</i>	protein phosphatase 2C, magnesium dependent, catalytic subunit	2.0
<i>Peci</i>	peroxisomal delta3, delta2-enoil-Coenzyme A isomerase	1.7
<i>Perp</i>	PERP, TP53 apoptosis effector	1.4
<i>Phyh</i>	phytanoyl-CoA hydroxylase	1.5
<i>Pink1</i>	PTEN induced putative kinase 1	1.4
<i>Pnkd</i>	paroxysmal nonkinesiogenic dyskinesia	1.4
<i>Ppm1k</i>	protein phosphatase 1K (PP2C domain containing)	1.5
<i>Prdx6</i>	similar to Peroxiredoxin-6 (Antioxidant protein 2) (1-Cys peroxiredoxin) (1-Cys PRX) (Acidic calcium-independent phospholipase A2) (aiPLA2) (Non-selenium glutathione peroxidase) (NSGPx); peroxiredoxin 6	1.7
<i>Sdhaf2</i>	RIKEN cDNA 0610038F07 gene	1.4
<i>Sdhd</i>	succinate dehydrogenase complex, subunit D, integral membrane protein	1.4
<i>Sh3bp5</i>	SH3-domain binding protein 5 (BTK-associated)	1.4
<i>Slc25a30</i>	solute carrier family 25, member 30	1.7
<i>Slc25a34</i>	solute carrier family 25, member 34	1.4
<i>Stard7</i>	START domain containing 7	1.4
<i>Synj2bp</i>	RIKEN cDNA 1810020G14 gene; synaptojanin 2 binding protein; predicted gene 4116	1.4
<i>Tmem65</i>	transmembrane protein 65	1.8
<i>Tmem8b</i>	RIKEN cDNA 4930500O05 gene	1.4
<i>Tmtc1</i>	transmembrane and tetratricopeptide repeat containing 1	1.5
<i>Trmt2b</i>	TRM2 tRNA methyltransferase 2 homolog B (<i>S. cerevisiae</i>)	1.4
<i>Ttc35</i>	tetratricopeptide repeat domain 35; predicted gene 5333	2.0
<i>Uqcr11</i>	ubiquinol-cytochrome c reductase (6.4kD) subunit; similar to ubiquinol-cytochrome c reductase subunit	1.5
<i>Uqcrb</i>	predicted gene 2962; ubiquinol-cytochrome c reductase binding protein	1.3
<i>Uqcrh</i>	predicted gene 14088; ubiquinol-cytochrome c reductase hinge protein	1.3
<i>Vamp8</i>	vesicle-associated membrane protein 8	1.6
<i>Ywhae</i>	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide	1.3
<i>0610009O20Rik</i>	RIKEN cDNA 0610009O20 gene	1.4
<i>1110058L19Rik</i>	RIKEN cDNA 1110058L19 gene	1.4
<i>2010107H07Rik</i>	RIKEN cDNA 2010107H07 gene	1.5
<i>9430016H08Rik</i>	RIKEN cDNA 9430016H08 gene	2.0

Genes relate to mitochondrial (Gene Ontology cellular compartments) were compared between NTG and MCK-miR-499 gastrocnemius. 107 up-regulated genes (fold change greater than 1.3 and a significant p value < 0.05) are shown.

Appendix Table S3. Downregulated miR-499 targets, predicted by TargetScan and MicroCosm, in MCK-miR-499 gastrocnemius muscle.

Gene	Description	Fold Change
<i>Amd1</i>	S-adenosylmethionine decarboxylase 1	0.47
<i>Ankra2</i>	ankyrin repeat, family A (RFXANK-like), 2	0.75
<i>Ankrd27</i>	ankyrin repeat domain 27 (VPS9 domain)	0.75
<i>Arhgap32</i>	Rho GTPase activating protein 32	0.83
<i>Asb7</i>	ankyrin repeat and SOCS box-containing 7	0.70
<i>BC017647</i>	family with sequence similarity 222, member B	0.71
<i>Best3</i>	bestrophin 3	0.74
<i>C130073F10Rik</i>	RIKEN cDNA C130073F10 gene	0.69
<i>C2cd2</i>	C2 calcium-dependent domain containing 2	0.60
<i>Ccrn4l</i>	nocturnin	0.79
<i>Cdc27</i>	cell division cycle 27	0.82
<i>Cdkn1a</i>	cyclin-dependent kinase inhibitor 1A (P21)	0.74
<i>Celf2</i>	CUGBP, Elav-like family member 2	0.79
<i>Cgrrf1</i>	cell growth regulator with ring finger domain 1	0.47
<i>Cntnap2</i>	contactin associated protein-like 2	0.64
<i>Cpd</i>	carboxypeptidase D	0.77
<i>Csnk2a2</i>	casein kinase 2, alpha prime polypeptide	0.80
<i>Cyb5r4</i>	cytochrome b5 reductase 4	0.69
<i>Dcaf12</i>	DDB1 and CUL4 associated factor 12	0.74
<i>Dgcr8</i>	DiGeorge syndrome critical region gene 8	0.81
<i>Dst</i>	dystonin	0.74
<i>Dynlt1a</i>	dynein light chain Tctex-type 1A	0.75
<i>Dynlt1c</i>	dynein light chain Tctex-type 1C	0.75
<i>Eif4a2</i>	eukaryotic translation initiation factor 4A2	0.79
<i>Enpp1</i>	ectonucleotide pyrophosphatase/phosphodiesterase 1	0.82
<i>Fam168a</i>	family with sequence similarity 168, member A	0.81
<i>Fam199x</i>	family with sequence similarity 199, X-linked	0.73
<i>Fnip1</i>	folliculin interacting protein 1	0.82
<i>G6pc3</i>	glucose 6 phosphatase, catalytic, 3	0.77
<i>Gadl1</i>	glutamate decarboxylase-like 1	0.49
<i>Gm5567</i>	transmembrane protein 178B	0.82
<i>Gxylt1</i>	glucoside xylosyltransferase 1	0.78
<i>H2afz</i>	H2A histone family, member Z	0.49
<i>Hax1</i>	HCLS1 associated X-1	0.68
<i>Hgsnat</i>	heparan-alpha-glucosaminide N-acetyltransferase	0.80
<i>Hps5</i>	Hermansky-Pudlak syndrome 5	0.58
<i>Hspa1l</i>	heat shock protein 1-like	0.78

<i>Ide</i>	insulin degrading enzyme	0.66
<i>Ikzf2</i>	IKAROS family zinc finger 2	0.74
<i>Iscu</i>	iron-sulfur cluster assembly enzyme	0.75
<i>Jhdm1d</i>	lysine (K)-specific demethylase 7A	0.81
<i>Kcnn3</i>	potassium intermediate/small conductance calcium-activated channel, subfamily N, member 3	0.83
<i>Kif3c</i>	kinesin family member 3C	0.77
<i>Letmd1</i>	LETM1 domain containing 1	0.80
<i>Lrrc30</i>	leucine rich repeat containing 30	0.73
<i>Lysmd2</i>	LysM, putative peptidoglycan-binding, domain containing 2	0.77
<i>Magea5</i>	melanoma antigen, family A, 5	0.82
<i>Mapk6</i>	mitogen-activated protein kinase 6	0.67
<i>Mast4</i>	microtubule associated serine/threonine kinase family member 4	0.62
<i>Mdm4</i>	transformed mouse 3T3 cell double minute 4	0.83
<i>Mrpl37</i>	mitochondrial ribosomal protein L37	0.69
<i>Mtcl1</i>	microtubule crosslinking factor 1	0.83
<i>Mthfd1</i>	methylenetetrahydrofolate dehydrogenase (NADP+ dependent), methenyltetrahydrofolate cyclohydrolase, formyltetrahydrofolate synthase	0.82
<i>Mtmr2</i>	myotubularin related protein 2	0.61
<i>Nat1</i>	N-acetyl transferase 1	0.74
<i>Ndst2</i>	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 2	0.80
<i>Nop9</i>	NOP9 nucleolar protein	0.76
<i>Nr2c2</i>	nuclear receptor subfamily 2, group C, member 2	0.77
<i>Nup210</i>	nucleoporin 210	0.80
<i>Nup214</i>	nucleoporin 214	0.80
<i>Omg</i>	oligodendrocyte myelin glycoprotein	0.82
<i>Pacs2</i>	phosphofurin acidic cluster sorting protein 2	0.71
<i>Pam</i>	peptidylglycine alpha-amidating monooxygenase	0.82
<i>Pcbp2</i>	poly(rC) binding protein 2	0.79
<i>Pdpr</i>	pyruvate dehydrogenase phosphatase regulatory subunit	0.68
<i>Pfkm</i>	phosphofructokinase, muscle	0.79
<i>Plod3</i>	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 3	0.80
<i>Pogz</i>	pogo transposable element with ZNF domain	0.82
<i>Psm8</i>	proteasome (prosome, macropain) 26S subunit, non-ATPase, 8	0.64
<i>Ptar1</i>	protein prenyltransferase alpha subunit repeat containing 1	0.67
<i>Ptpn14</i>	protein tyrosine phosphatase, non-receptor type 14	0.63
<i>Ptprg</i>	protein tyrosine phosphatase, receptor type, G	0.81
<i>Rab5c</i>	RAB5C, member RAS oncogene family	0.67
<i>Ranbp2</i>	RAN binding protein 2	0.76
<i>Rcn2</i>	reticulocalbin 2	0.64
<i>Reep1</i>	receptor accessory protein 1	0.33
<i>Rhbdl1</i>	rhomboid, veinlet-like 1 (Drosophila)	0.59

<i>Rhobtb3</i>	Rho-related BTB domain containing 3	0.62
<i>Rnf145</i>	ring finger protein 145	0.81
<i>Rnf44</i>	ring finger protein 44	0.83
<i>Rnh1</i>	ribonuclease/angiogenin inhibitor 1	0.69
<i>Rpap2</i>	RNA polymerase II associated protein 2	0.82
<i>Rqcd1</i>	RCD1 required for cell differentiation 1 homolog	0.77
<i>Samd8</i>	sterile alpha motif domain containing 8	0.77
<i>Sdc2</i>	syndecan 2	0.81
<i>Sec11a</i>	SEC11 homolog A, signal peptidase complex subunit	0.79
<i>Sec14l1</i>	SEC14-like lipid binding 1	0.72
<i>Setdb1</i>	SET domain, bifurcated 1	0.70
<i>Sfrs9</i>	serine/arginine-rich splicing factor 9	0.82
<i>Slc24a2</i>	solute carrier family 24 (sodium/potassium/calcium exchanger), member 2	0.75
<i>Slc35a4</i>	solute carrier family 35, member A4	0.73
<i>Slc43a1</i>	solute carrier family 43, member 1	0.53
<i>Sos2</i>	son of sevenless homolog 2 (Drosophila)	0.53
<i>Sox6</i>	SRY (sex determining region Y)-box 6	0.65
<i>Spns2</i>	spinster homolog 2	0.43
<i>Stac3</i>	SH3 and cysteine rich domain 3	0.68
<i>Tbc1d22b</i>	TBC1 domain family, member 22B	0.82
<i>Tbrg1</i>	transforming growth factor beta regulated gene 1	0.82
<i>Tcf12</i>	transcription factor 12	0.81
<i>Tlr7</i>	toll-like receptor 7	0.80
<i>Tmbim6</i>	transmembrane BAX inhibitor motif containing 6	0.64
<i>Tmem39b</i>	transmembrane protein 39b	0.77
<i>Trmt44</i>	tRNA methyltransferase 44	0.78
<i>Trp53bp1</i>	transformation related protein 53 binding protein 1	0.72
<i>Tspan8</i>	tetraspanin 8	0.23
<i>Uap1</i>	UDP-N-acetylglucosamine pyrophosphorylase 1	0.70
<i>Ube2n</i>	ubiquitin-conjugating enzyme E2N	0.82
<i>Ubn1</i>	ubinuclein 1	0.77
<i>Ubn2</i>	ubinuclein 2	0.77
<i>Uevld</i>	UEV and lactate/malate dehydrogenase domains	0.63
<i>Usp12</i>	ubiquitin specific peptidase 12	0.75
<i>Vps53</i>	VPS53 GARP complex subunit	0.79
<i>Wdr35</i>	WD repeat domain 35	0.72
<i>Zbtb22</i>	zinc finger and BTB domain containing 22	0.79
<i>Zc3hav1</i>	zinc finger CCCH type, antiviral 1	0.83
<i>Zdbf2</i>	zinc finger, DBF-type containing 2	0.77
<i>Zfp26</i>	zinc finger protein 26	0.74
<i>Zfp266</i>	zinc finger protein 266	0.78

<i>Zfp42</i>	zinc finger protein 42	0.79
<i>Zscan4c</i>	zinc finger and SCAN domain containing 4C	0.79

mRNA expression was assessed on and analyzed using Partek Genomics Suite. Downregulation was defined as a fold-change <-1.2 .

Appendix Table S4. RT-PCR primers

Mouse Gene	Forward	Reverse
<i>36b4</i>	5'-ATCCCTGACGCACCGCCGTGA	5'-TGCATCTGCTTGGAGCCCACGT
<i>Ndufa1</i>	5'-TGA TGG AAC GCG ATA GAC G	5'-GCC AGG AAA ATG CTT CCT TA
<i>ndufs4</i>	5'-GAT GGG AAA ATC CTT TGA TGG	5'-GAA GGT CAG AAC CAT GTT GGA
<i>Ndufaf4</i>	5'-AAA ATG AGA GCT GAG AGA GCT GTT	5'-ACT TTA CCC AAA CCA CCC ACT
<i>Sdhd</i>	5'-CCT GCT CTG TGG TGG ACT ACT	5'-CCC ATG AAC GTA GTC GGT AAC
<i>Uqcr11</i>	5'-CCACAGGCCTCGATGGTA	5'-GCAGCCCTAGTGTCTGTCAA
<i>Cox7a1</i>	5'-CGA AGA GGG GAG GTG ACT C	5'-AGC CTG GGA GAC CCG TAG
<i>Cox7b</i>	5'-AAC GCA CTA AGC CGT CTC C	5'-CAT GGA AAC TAG GTG CCC TCT
<i>Atp5e</i>	5'-CAA AGC GAA CGC TGA GAA G	5'-TCA GCA CTT CAG GCT TCA GA
<i>Atp5l</i>	5'-AAA ACT GGT AGC TTC AAA CAC CTT	5'-ACA ATG CCA CGT TTG CCT AT
<i>mt-Nd2</i>	5'-CCATCAACTCAATCTCACTTCTATG	5'-GAATCCTGTTAGTGGTGGAAAGG
<i>mt-Co1</i>	5'-ACCATCATTCTCCTTCTCCTA	5'-TAGATTCCGGCTAGAGGTG
<i>mt-Co2</i>	5'-TGAAGACGTCCTCCACTCATG	5'-CCCTGGTCGGTTTGATGTTA
<i>mt-Atp6</i>	5'-CCATAAATCTAAGTATAGCCATTCCAC	5'-AGCTTTTAGTTGTGTCCGGAAG
<i>mt-Cytb</i>	5'-CATTTATTATCGCGGCCCTA	5'-TGGGTTGTTGATCCTGTTTC
<i>Cycs</i>	5'-ACCAAATCTCCACGGTCTGTT	5'-GGATTCTCAAATACTCCATCAG
<i>Lpl</i>	5'-TTTGTGAAATGCCATGACAAG	5'-CAGATGCTTCTTCTCTTGTGTTGT
<i>Ldha</i>	5'-TGCCTACGAGGTGATCAAGCT	5'-GCACCCGCCTAAGGTTCTTC
<i>Ldhb</i>	5'-AGTCTCCCGTGCATCCTCAA	5'-AGGGTGTCCGCACTCTCCT
<i>Ppargc1a</i>	5'-CGGAAATCATATCCAACCAG	5'-TGAGAACCGCTAGCAAGTTTG
<i>Ppargc1b</i>	5'-TCCAGAAGTCAGCGGCCT	5'-CTGAGCCCGCAGTGTGG
<i>Esrra</i>	5'-AGGAGTACGTCTTGCTG	5'-CCTCAGCATCTTCAATG
<i>Esrrb</i>	5'-ACGGCTGGATTCCGAGAAC	5'-TCCTGCTCAACCCTAGTAGATTC
<i>Esrrg</i>	5'-TGACTTGGCTGACCGAG	5'-CCGAGGATCAGAATCTCC
<i>Ppara</i>	5'-ACTACGGAGTTCACGCATGTG	5'-TTGTCGTACACCAGCTTCAGC
<i>Ppard</i>	5'-TCACCGGAAGTCCAGCCA	5'-ACACCAGGCCCTTCTCTGCCT
<i>Myh7</i>	5'-GCCAACTATGCTGGAGCTGATGCC	5'-GGTGCCTGGAGCGCAAGTTTGTGATAAG
<i>Myh7b</i>	5'-GCCTCTGCGGACATTGATAG	5'-GGGCAGCTGGAAGATCACT
<i>Tnmi1</i>	5'-TGAAGCCAAATGCCTCCACAACAC	5'-ACACCTTGTGCTTAGAGCCAGTA
<i>Tnnc1</i>	5'-AGCTCATGAAGGACGGTGACAAGA	5'-AACCCTGCAAGACCAGCATCTACT
<i>Tnnt1</i>	5'-TGGATCCACCAGCTGGAATCAGAA	5'-GCTGATGCGGTTGTAGAGCACATT
<i>Tnmi2</i>	5'-AGCAGCAAGGAGCTGGAAGA	5'-ATGGCGTCCGACAGACATAC
<i>Tnnc2</i>	5'-CCATCATCGAGGAGGTGGAC	5'-CTTCCCCTTCGCATCCTCTT
<i>Tnnt3</i>	5'-AACTGGAGACTGACAAATTCGAGT	5'-GCTGTGCTTCTGGGTTTGGT
<i>Sox6</i>	5'- TCTACAGCAGCAGCACAAGATTA	5'- CATGTGGAAAAATTGGGATCA
<i>Fnip1</i>	5'- TCCGTCAGTGCTGGTATC	5'- ACAGCTTCTGCTATTGGTTCATC
<i>Fnip2</i>	5'- TTGACTCCAGAGCCGTTCA	5'- GGAACATCCTCTGCTTTCTGA
Primers for quantification of mtDNA		
<i>mt-Nd1</i>	5'-CCCATTTCGCGTTATCTT	5'-AAGTTGATCGTAACGGAAGC
<i>Lpl</i>	5'-GATGGACGGTAAGAGTGATTC	5'-ATCCAAGGGTAGCAGACAGGT