

## Supplementary Data

### Supplementary Methods

#### Heart hydrogen peroxide real-time measurement

For *in situ* detection of hydrogen peroxide ( $H_2O_2$ ) in the heart, experiments have been optimized based on the procedure of Duparc *et al.* (1, 2) for real-time measurement of NO release in the hypothalamus of mice with an amperometric probe. The  $H_2O_2$ -specific amperometric probe was calibrated as referred to manufacturer's instructions (ISO-HPO-100; World Precision Instruments, Aston, UK). Briefly, the probe was left in 20 ml of PBS buffer. After the sensor had stabilized, solution of  $H_2O_2$  (from 100 to 800 nM) was added in PBS. The current observed was directly proportional to  $H_2O_2$  concentration. The sensitivity of a fresh probe was at least 1 pA/nM. Probes were tested before each experiment to validate their sensitivity. Then, 1.5-month-old mice were given pentobarbital (100 mg/kg ip) and were placed on a heating plate at 37°C. The chest was opened quickly and the probe was implanted in the left ventricle, without mechanical ventilation, to monitor  $H_2O_2$  release. After 20 min of stabilization of the probe,  $H_2O_2$  concentration in the tissue was measured for 15 min in real-time with the data acquisition system LabTrax

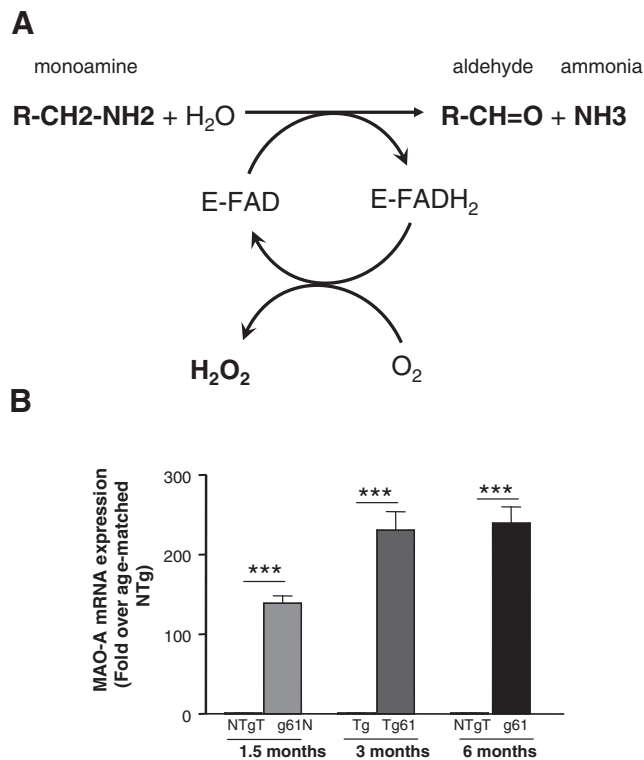
(WPI) connected to the free radical analyzer Apollo1000 (WPI). Data were acquired and analyzed using DataTrax2 software (WPI).

#### GSH measurements

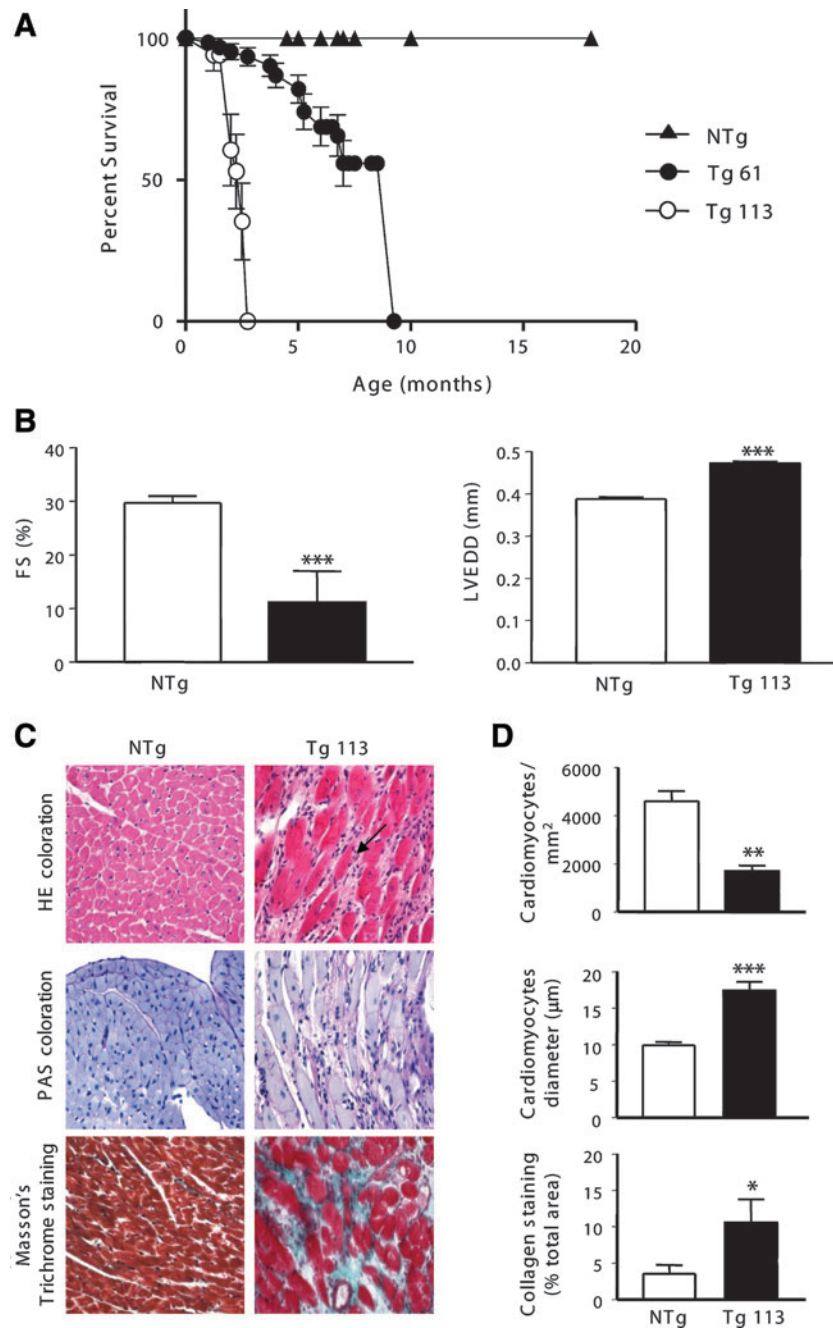
GSH content was evaluated in ventricle samples and neonatal cardiomyocytes using "Total Glutathione detection kit" from Assay Designs.

#### Supplementary References

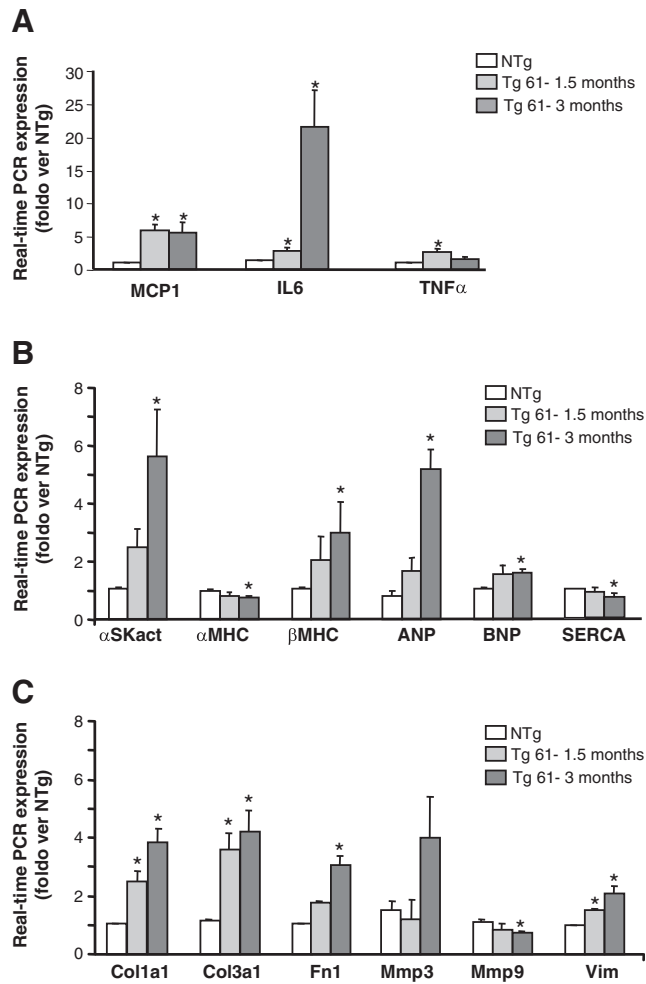
- Duparc T, Colom A, Cani PD, Massaly N, Rastrelli S, Drougard A, Le Gonidec S, Mouldous L, Frances B, Leclercq I, Llorens-Cortes C, Pospisilik JA, Delzenne NM, Valet P, Castan-Laurell I, and Knauf C. Central apelin controls glucose homeostasis via a nitric oxide-dependent pathway in mice. *Antioxid Redox Signal* 15: 1477–1496, 2011.
- Duparc T, Naslain D, Colom A, Muccioli GG, Massaly N, Delzenne NM, Valet P, Cani PD, and Knauf C. Jejunum inflammation in obese and diabetic mice impairs enteric glucose detection and modifies nitric oxide release in the hypothalamus. *Antioxid Redox Signal* 14: 415–423, 2011.



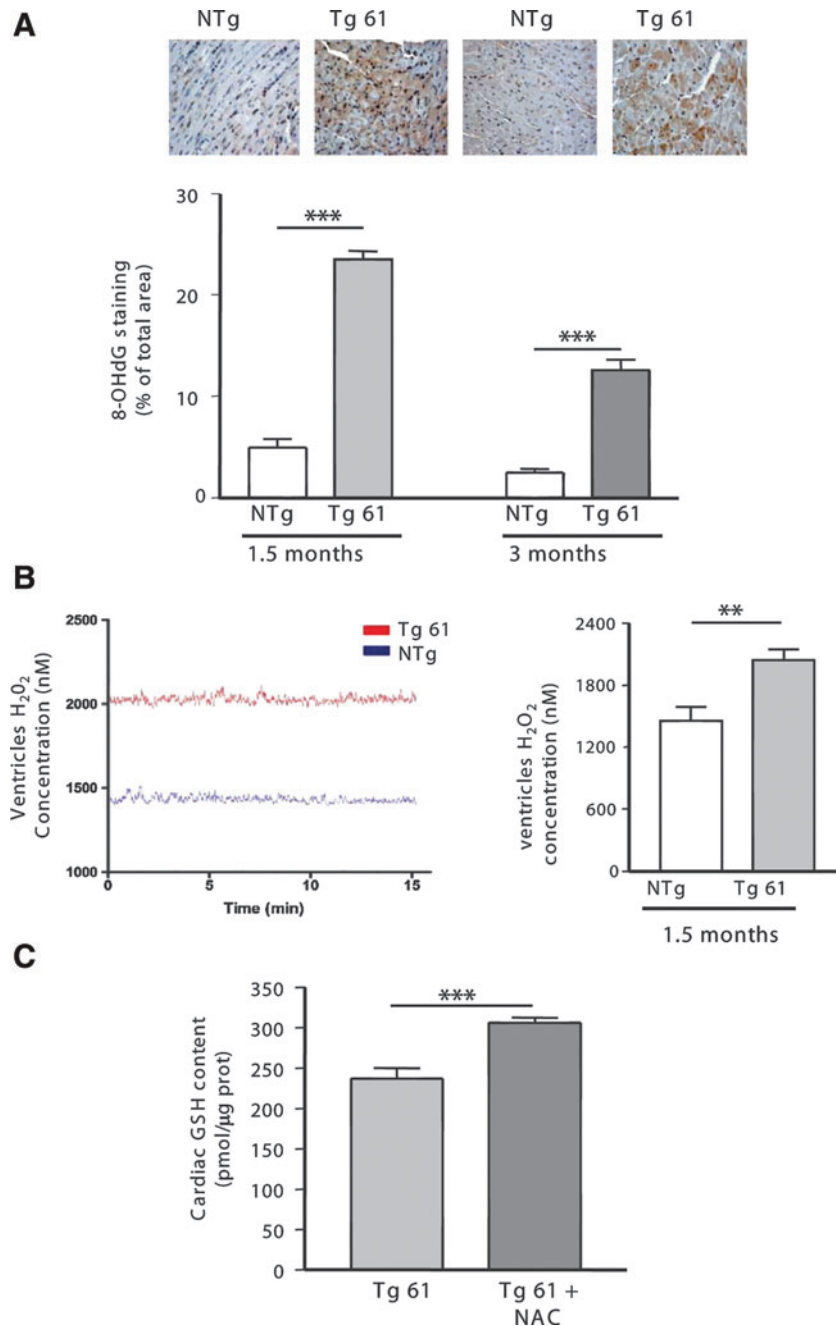
**SUPPLEMENTARY FIG. S1. Enzymatic reaction for MAO-A and mRNA expression of MAO-A in Tg mice. (A)** Oxidative deamination of monoamines by the flavoenzyme monoamine oxidase-A (MAO-A). In the first step, binding of the monoamine to the enzyme (E) yields an aldehyde and ammonia by reduction of FAD cofactor. In the second step, the oxidized form of the prosthetic group is restored by the binding of oxygen and the concomitant production of hydrogen peroxide ( $H_2O_2$ ). FAD, Flavin-Adenine-Dinucleotide. **(B)** MAO-A mRNA expression in transgenic (Tg) 61 mice at different ages. Expression was normalized to age-matched nontransgenic (NTg) mice ( $n=4$ ). \*\*\* $p < 0.001$  compared to NTg mice.



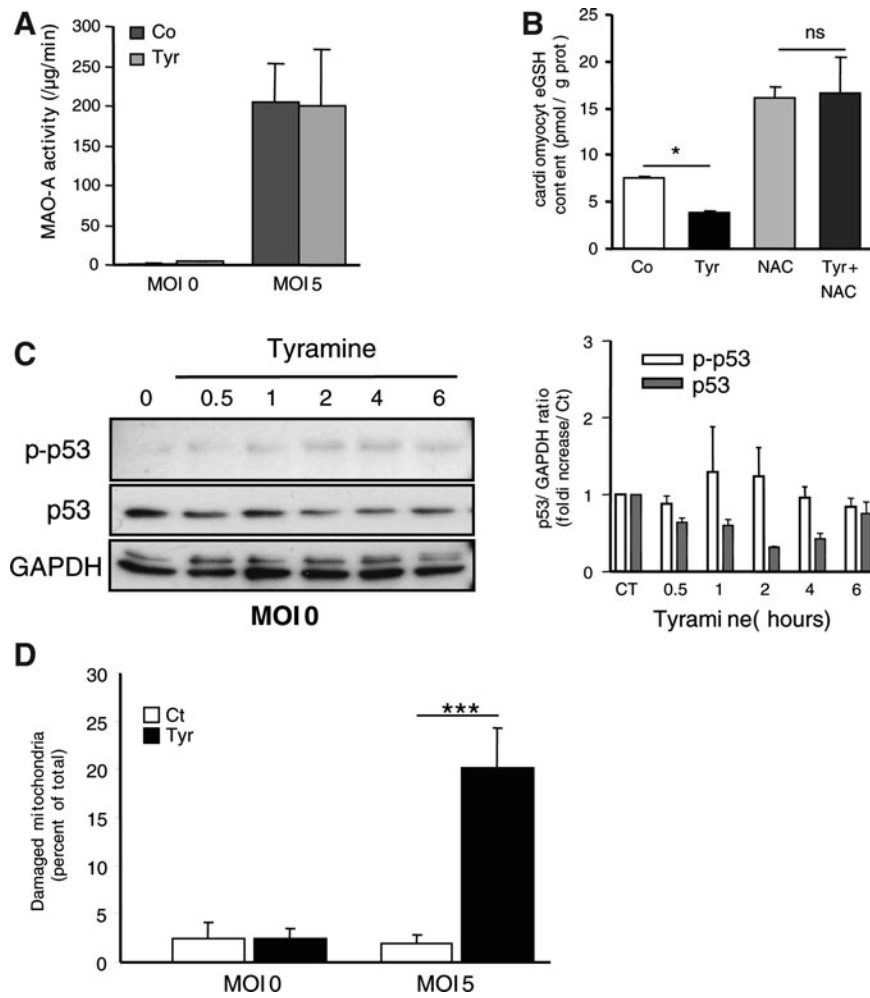
**SUPPLEMENTARY FIG. S2. Survival in MAO-A Tg mice and characterization of Tg 113 mice.** (A) MAO-A cardiac overexpression triggers mice premature death. Kaplan-Meier analysis of death with aging in NTg ( $n=26$ ), Tg 61 ( $n=38$ ), and Tg 113 mice ( $n=17$ ). (B) MAO-A Tg line 113 develops dilated cardiomyopathy and heart failure. Fractional shortening (FS) and left-ventricular diastolic diameter (LVEDD) assessment by echocardiography in 2-month-old Ntg or Tg 113 mice ( $n=2-6$ ) ( $***p < 0.001$  vs. NTg). (C) MAO-A Tg line 113 develops cardiomyocytes loss and compensative hypertrophy and fibrosis. Histological characterization ( $\times 400$ ) of ventricular pathology by hematoxylin-eosin (HE), periodic acid Schiff (PAS), and Masson's trichrome (green) staining in cardiac sections of NTg and Tg 113 at 2 months. *Arrow* indicates necrotic area. (D) Quantification of cardiomyocyte number per mm<sup>2</sup> ( $n=4$ ), cardiomyocyte diameter ( $n=4$ ), and collagen content on cardiac sections ( $n=4$ ) ( $*p < 0.05$ ,  $**p < 0.01$  or  $***p < 0.001$  vs. Ntg).



**SUPPLEMENTARY FIG. S3. Transcriptome analysis in MAO-A-overexpressing mice at the ages of 1.5 and 3 months.** Expression of genes involved in inflammation (**A**), cardiac remodelling (**B**), and cardiac fibrosis (**C**). Expression of the gene of interest is normalized to the expression of three housekeeping genes and results are expressed as fold over NTg mice ( $n=4$ ). ( $*p < 0.05$  vs. NTg). MCP1, monocyte chemoattractant protein 1 (Ccl2); IL6, interleukin 6; TNF $\alpha$ , tumor necrosis factor  $\alpha$ ;  $\alpha$ SKact, skeletal alpha actin;  $\alpha$ MHC, myosin heavy chain alpha;  $\beta$ MHC, myosin heavy chain beta; ANP, atrial natriuretic peptide; BNP, B-type natriuretic peptide; SERCA, sarco/endoplasmic reticulum calcium ATPase; Col1a1, collagen type I alpha 1; Col3a1, collagen type III alpha 1; Fn1, fibronectin 1; Mmp9, matrix metalloprotease 9; Vim, vimentin ( $*p < 0.05$  vs. NTg).



**SUPPLEMENTARY FIG. S4. Oxidative stress measurements in MAO-A Tg mice. (A)** 8-OH-dG immunohistochemistry on cardiac sections from 1.5-month-old and 3-month-old NTg and Tg 61 mice ( $\times 400$ ). Quantification of 8-OH-dG staining was expressed as percent of total area ( $n=4$ ). **(B)** Real-time *in situ* measurements of H<sub>2</sub>O<sub>2</sub> in ventricles from anesthetized Tg and NTg mice at 1.5 months. Histogram represents average H<sub>2</sub>O<sub>2</sub> concentration from  $n=5$  mice **(C)** glutathione reduced (GSH) content in ventricle extracts from 5-month-old Tg 61-untreated, and N-acetyl-cystein (NAC)-treated Tg 61 (Tg61 + NAC) mice ( $n=6$ ).  $**p < 0.01$ ,  $***p < 0.001$  vs. indicated value.



**SUPPLEMENTARY FIG. S5. MAO-A activity, GSH measurements, p53 activation, and mitochondrial damage in neonatal cardiomyocytes.** (A) Quantification of MAO-A activity by luminescence in the presence of tyramine ( $500 \mu\text{M}$ ) for 24 h in untransduced or Ade-MAO-A-transduced neonatal cardiomyocytes ( $n=3$ ). (B) GSH content in neonatal cardiomyocytes transduced with Ade-MAO-A and treated with tyramine ( $500 \mu\text{M}$ ) for 2 h in the presence of NAC ( $5 \text{mM}$ ). ( $*p < 0.05$ ,  $***p < 0.001$  vs. indicated value; ns, nonsignificant). (C) Analysis of total or phospho(ser15)-p53 and total p53 levels by immunoblot in untransduced neonatal cardiomyocytes (multiplicity of infection [MOI] 0) stimulated with  $500 \mu\text{M}$  tyramine for the indicated time ( $n=3$ ). (D) Number of damaged mitochondria expressed as percent of total mitochondria in untransduced or ade-MAO-A-transduced cardiomyocytes treated with tyramine for 4 h.

SUPPLEMENTARY TABLE S1. UPREGULATED GENES ENCODING MITOCHONDRIAL PROTEINS

<i>Symbol</i>	<i>Protein name</i>	<i>Accession number</i>	<i>Fold over NTg</i>	<i>p-value</i>
TSPO	Translocator protein (18 kDa)	P222657	2.26	7.30E-09
HCLS1	Hematopoietic cell-specific Lyn substrate 1	P297679	2.22	5.70E-07
MTCH1	Mitochondrial carrier homolog 1 ( <i>C. elegans</i> )	P458242	2.19	1.13E-04
UCP2	Uncoupling protein 2 (mitochondrial, proton carrier)	P297105	2.07	2.58E-05
CYBB	Cytochrome b-245, beta polypeptide	P444628	1.99	6.30E-08
RAB32	RAB32, member RAS oncogene family	P293688	1.97	4.69E-08
SLC25A45	Solute carrier family 25, member 45	P349727	1.92	1.64E-07
GPRC5C	G protein-coupled receptor, family C, group 5, member C	P309988	1.85	4.54E-06
ASS1	Argininosuccinate synthetase 1	P361165	1.85	1.77E-06
GPX1	Glutathione peroxidase 1	P684378	1.78	1.59E-06
SLC25A1	Solute carrier family 25 (mitochondrial carrier; citrate transporter), member 1	P350922	1.77	1.79E-06
GRN	Granulin	P192800	1.75	3.94E-05
PISD	Phosphatidylserine decarboxylase	P422338	1.69	3.28E-05
VARS	Valyl-tRNA synthetase	P203501	1.69	1.12E-04
PRELID1	PRELI domain containing 1	P505337	1.67	3.15E-06
SARDH	Sarcosine dehydrogenase	P492676	1.67	1.31E-04
CPT1C	Carnitine palmitoyltransferase 1C	P269942	1.64	9.29E-07
RNASEL	Ribonuclease L (2',5'-oligoadenylate synthetase-dependent)	P377760	1.62	9.56E-07
PRDX4	Peroxiredoxin 4	P200819	1.62	1.61E-06
HK1	Hexokinase 1	P479599	1.60	2.66E-03
CKB	Creatine kinase, brain	P425772	1.57	1.56E-03
SFXN1	Sideroflexin 1	P418526	1.55	2.90E-07
PYCR1	Pyrroline-5-carboxylate reductase 1	P503896	1.54	2.48E-05
TK2	Thymidine kinase 2, mitochondrial	P310398	1.50	7.31E-05
CYB5R3	Cytochrome b5 reductase 3	P153170	1.48	1.19E-03
CYBA	Cytochrome b-245, alpha polypeptide	P131800	1.47	1.92E-03
SLC25A10	Solute carrier family 25 (mitochondrial carrier; dicarboxylate transporter), member 10	P404904	1.43	1.39E-03
STAR	Steroidogenic acute regulatory protein	P274436	1.42	3.04E-04

NTg, nontransgenic.

SUPPLEMENTARY TABLE S2. DOWNREGULATED GENES ENCODING MITOCHONDRIAL PROTEINS

<i>Symbol</i>	<i>Protein name</i>	<i>Accession number</i>	<i>Fold over NTg</i>	<i>p-value</i>
MRPS33	Mitochondrial ribosomal protein S33	P342896	0.37	1.29E-06
LAP3	Leucine aminopeptidase 3	P431662	0.38	8.45E-06
MRPS18C	Mitochondrial ribosomal protein S18C	P108484	0.39	1.99E-07
MRPL1	Mitochondrial ribosomal protein L1	P86073	0.39	7.22E-08
PITRM1	Pitrilysin metallopeptidase 1	P474960	0.39	9.45E-07
PPM1K	Protein phosphatase 1K (PP2C domain containing)	P265219	0.40	2.52E-07
PDK4	Pyruvate dehydrogenase kinase, isozyme 4	P350453	0.40	8.20E-05
DBT	Dihydrolipoamide branched chain transacylase E2	P569348	0.42	3.90E-08
SH3GLB1	SH3-domain GRB2-like endophilin B1	P32249	0.43	6.40E-06
MLYCD	Malonyl-CoA decarboxylase	P222283	0.43	9.04E-09
MCEE	Methylmalonyl CoA epimerase	P320481	0.43	2.07E-06
TFB2M	Transcription factor B2, mitochondrial	P374499	0.45	1.52E-05
UCP3	Uncoupling protein 3 (mitochondrial, proton carrier)	P380379	0.45	1.25E-04
ND4L	NADH dehydrogenase, subunit 4L (complex I)	P245525	0.45	7.44E-05
MAOB	Monoamine oxidase B	P302566	0.48	1.00E-05
COX16	COX16 cytochrome c oxidase assembly homolog ( <i>S. cerevisiae</i> )	P404300	0.49	1.07E-06
ATP5F1	ATP synthase, H <sup>+</sup> transporting, mitochondrial F0 complex, subunit B1	P106929	0.50	6.53E-04
MRPL47	Mitochondrial ribosomal protein L47	P302291	0.50	7.80E-09
MRPS35	Mitochondrial ribosomal protein S35	P110841	0.51	7.67E-09
CPOX	Coproporphyrinogen oxidase	P257258	0.51	3.10E-05
HSDL2	Hydroxysteroid dehydrogenase like 2	P281930	0.51	1.24E-07
MRPS25	Mitochondrial ribosomal protein S25	P121325	0.51	2.63E-07
ACSS1	Acyl-CoA synthetase short-chain family member 1	P479321	0.51	1.67E-06
PINK1	PTEN induced putative kinase 1	P196605	0.51	7.29E-07
C5ORF33	Chromosome 5 open reading frame 33	P243323	0.52	1.13E-06
DECR1	2,4-dienoyl CoA reductase 1, mitochondrial	P208555	0.52	1.57E-06
CHCHD3	Coiled-coil-helix-coiled-coil-helix domain containing 3	P526335	0.52	8.93E-04
MTFR1	Mitochondrial fission regulator 1	P143002	0.55	9.63E-07
MRPS22	Mitochondrial ribosomal protein S22	P362903	0.55	6.63E-06
SLC25A46	Solute carrier family 25, member 46	P176711	0.55	1.14E-05
MRS2	MRS2 magnesium homeostasis factor homolog ( <i>S. cerevisiae</i> )	P618187	0.55	5.91E-06
AUH	AU RNA binding protein/enoyl-Coenzyme A hydratase	P372473	0.55	9.13E-07
NDUFB11	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 11, 17.3kDa	P205573	0.55	5.04E-05
DARS2	Aspartyl-tRNA synthetase 2, mitochondrial	P102559	0.55	1.06E-08
SLC25A36	Solute carrier family 25, member 36	P124121	0.56	1.83E-04
PDHA1	Pyruvate dehydrogenase (lipoamide) alpha 1	P581435	0.56	6.01E-06
COQ7	Coenzyme Q7 homolog, ubiquinone (yeast)	P161691	0.56	1.39E-07
NNT	Nicotinamide nucleotide transhydrogenase	P113395	0.56	4.98E-06
MARCH5	Membrane-associated ring finger (C3HC4) 5	P405668	0.56	2.00E-07
COX7A2	Cytochrome c oxidase subunit VIIa polypeptide 2 (liver)	P319031	0.56	2.50E-05
NDUFA6	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 6, 14kDa	P217474	0.57	2.89E-07
PDHX	Pyruvate dehydrogenase complex, component X	P149946	0.57	1.34E-04
MFN1	Mitofusin 1	P2732	0.57	5.50E-08
ADH5	Alcohol dehydrogenase 5 (class III), chi polypeptide	P404275	0.57	3.60E-06
YARS2	Tyrosyl-tRNA synthetase 2, mitochondrial	P373609	0.58	4.37E-07
MUT	Methylmalonyl Coenzyme A mutase	P633163	0.58	7.62E-06
MRPS21	Mitochondrial ribosomal protein S21	P509012	0.58	1.96E-06
NDUFS6	NADH dehydrogenase (ubiquinone) Fe-S protein 6, 13kDa (NADH-coenzyme Q reductase)	P335077	0.58	4.48E-08
SLC25A11	Solute carrier family 25 (mitochondrial carrier; oxoglutarate carrier), member 11	P267454	0.58	7.32E-06
TOMM7	Translocase of outer mitochondrial membrane 7 homolog (yeast)	P206547	0.58	5.44E-05
COX15	COX15 homolog, cytochrome c oxidase assembly protein (yeast)	P354744	0.58	6.47E-04
TIMM8A	Translocase of inner mitochondrial membrane 8 homolog A (yeast)	P373043	0.59	4.87E-07
DUT	Deoxyuridine triphosphatase	P480360	0.59	8.03E-04
LYPLA1	Lysophospholipase I	P8227	0.59	3.20E-05
MRPL22	Mitochondrial ribosomal protein L22	P322994	0.59	9.60E-07
CLPX	ClpX caseinolytic peptidase X homolog ( <i>E. coli</i> )	P304683	0.59	3.40E-05
MTERFD3	MTERF domain containing 3	P202623	0.60	2.05E-05
NDUFA8	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 8, 19kDa	P475501	0.60	3.78E-03
PHB	Prohibitin	P165934	0.60	6.26E-06

(continued)

SUPPLEMENTARY TABLE S2. (CONTINUED)

<i>Symbol</i>	<i>Protein name</i>	<i>Accession number</i>	<i>Fold over NTg</i>	<i>p-value</i>
KIAA0564	KIAA0564	P221144	0.60	1.07E-04
SUCLA2	Succinate-CoA ligase, ADP-forming, beta subunit	P111554	0.60	5.00E-05
FECH	Ferrochelatase (protoporphyrin)	P266763	0.60	2.51E-04
NDUFA12	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 12	P458540	0.60	1.73E-04
COX7B	Cytochrome c oxidase subunit VIIb	P160664	0.61	1.11E-05
MRPL19	Mitochondrial ribosomal protein L19	P604526	0.61	4.45E-07
ADHFE1	Alcohol dehydrogenase, iron containing, 1	P116264	0.61	1.08E-04
UQCRH	Ubiquinol-cytochrome c reductase hinge protein	P350301	0.61	4.20E-05
ATP5G3	ATP synthase, H <sup>+</sup> transporting, mitochondrial F0 complex, subunit C3 (subunit 9)	P294849	0.61	5.88E-06
MTERFD1	MTERF domain containing 1	P507204	0.62	3.94E-04
SYNJ2BP	Synaptojanin 2 binding protein	P662001	0.62	5.12E-04
ACOT2	Acyl-CoA thioesterase 2	P525183	0.62	2.53E-04
SLC25A37	Solute carrier family 25, member 37	P343429	0.62	4.87E-04
ATP5S	ATP synthase, H <sup>+</sup> transporting, mitochondrial F0 complex, subunit s (factor B)	P195798	0.62	1.28E-06
RAB11FIP5	RAB11 family interacting protein 5 (class I)	P529360	0.62	2.83E-05
OXCT1	3-oxoacid CoA transferase 1	P107321	0.62	7.76E-07
SDHA	Succinate dehydrogenase complex, subunit A, flavoprotein (Fp)	P458708	0.62	3.51E-03
COX7A2L	Cytochrome c oxidase subunit VIIa polypeptide 2 like	P434803	0.62	2.19E-06
L2HGDH	L-2-hydroxyglutarate dehydrogenase	P221132	0.62	2.57E-05
ETFDH	Electron-transferring-flavoprotein dehydrogenase	P161574	0.62	2.21E-04
SLC25A26	Solute carrier family 25, member 26	P71544	0.62	1.35E-06
TOMM20	Translocase of outer mitochondrial membrane 20 homolog (yeast)	P310930	0.62	1.82E-07
C18ORF55	Chromosome 18 open reading frame 55	P395842	0.62	5.85E-06
YWHAZ	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide	P480709	0.63	1.65E-03
ACSL1	Acyl-CoA synthetase long-chain family member 1	P496432	0.63	9.37E-05
PTPMT1	Protein tyrosine phosphatase, mitochondrial 1	P226341	0.63	4.09E-08
SLC25A16	Solute carrier family 25 (mitochondrial carrier; Graves disease autoantigen), member 16	P458870	0.63	6.08E-06
MRPL50	Mitochondrial ribosomal protein L50	P112677	0.63	2.35E-05
DLAT	Dihydrolipoamide S-acetyltransferase	P265106	0.63	2.05E-05
MCAT	Malonyl CoA:ACP acyltransferase (mitochondrial)	P314855	0.63	3.36E-05
AFG3L1	AFG3 ATPase family gene 3-like 1 ( <i>S. cerevisiae</i> )	P598714	0.64	4.11E-04
OGG1	8-oxoguanine DNA glycosylase	P489903	0.64	2.16E-03
ACSL6	Acyl-CoA synthetase long-chain family member 6	P380699	0.64	9.22E-04
SSBP1	Single-stranded DNA binding protein 1	P289685	0.64	4.11E-05
PPP1CC	Protein phosphatase 1, catalytic subunit, gamma isoform	P519508	0.65	1.08E-04
NDUFV3	NADH dehydrogenase (ubiquinone) flavoprotein 3, 10kDa	P170054	0.65	9.40E-06
OXSM	3-oxoacyl-ACP synthase, mitochondrial	P312748	0.65	2.31E-05
SLC25A12	Solute carrier family 25 (mitochondrial carrier, Aralar), member 12	P1196751	0.65	1.32E-03
MTRF1L	Mitochondrial translational release factor 1-like	P397548	0.65	2.98E-08
MRPL40	Mitochondrial ribosomal protein L40	P420627	0.65	4.15E-05
REEP1	Receptor accessory protein 1	P508341	0.66	2.29E-06
SUOX	Sulfite oxidase	P249360	0.66	1.20E-04
IMMP1L	IMP1 inner mitochondrial membrane peptidase-like ( <i>S. cerevisiae</i> )	P3754	0.66	1.30E-04
PACS2	Phosphofurin acidic cluster sorting protein 2	P439520	0.66	6.59E-07
MTIF2	Mitochondrial translational initiation factor 2	P455597	0.66	3.67E-05
TOMM22	Translocase of outer mitochondrial membrane 22 homolog (yeast)	P105339	0.66	1.86E-06
COX11	COX11 homolog, cytochrome c oxidase assembly protein (yeast)	P214319	0.66	3.00E-06
MRPL18	Mitochondrial ribosomal protein L18	P210474	0.66	1.09E-03
CPT1B	Carnitine palmitoyltransferase 1B (muscle)	P232913	0.66	2.28E-04
MCCC1	Methylcrotonoyl-Coenzyme A carboxylase 1 (alpha)	P282975	0.66	3.81E-05
ACOT13	Acyl-CoA thioesterase 13	P502422	0.67	8.22E-06
ATP5B	ATP synthase, H <sup>+</sup> transporting, mitochondrial F1 complex, beta polypeptide	P328078	0.67	2.13E-04
NDUFA4	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4, 9kDa	P552832	0.67	1.53E-05
CAPRIN2	Caprin family member 2	P204944	0.67	4.57E-05
MMADHC	methylmalonic aciduria (cobalamin deficiency) cblD type, with homocystinuria	P236721	0.67	2.31E-04

(continued)



SUPPLEMENTARY TABLE S2. (CONTINUED)

<i>Symbol</i>	<i>Protein name</i>	<i>Accession number</i>	<i>Fold over NTg</i>	<i>p-value</i>
ABCD3	ATP-binding cassette, sub-family D (ALD), member 3	P394395	0.67	1.54E-05
USMG5	Up-regulated during skeletal muscle growth 5 homolog (mouse)	P181365	0.68	3.78E-03
C2ORF56	Chromosome 2 open reading frame 56	P180826	0.68	6.56E-07
ECSIT	ECSIT homolog (Drosophila)	P348548	0.68	3.94E-05
MRPL32	Mitochondrial ribosomal protein L32	P141818	0.68	2.28E-04
BCAT2	Branched chain aminotransferase 2, mitochondrial	P448266	0.68	3.65E-05
ECHDC3	Enoyl Coenzyme A hydratase domain containing 3	P475378	0.68	1.14E-03
RNASET2	Ribonuclease T2	P477019	0.68	8.88E-06
SLC25A33	Solute carrier family 25, member 33	P156434	0.68	1.86E-03
SDHD	Succinate dehydrogenase complex, subunit D, integral membrane protein	P260871	0.69	1.31E-05
MRPS31	Mitochondrial ribosomal protein S31	P319732	0.69	2.80E-05
NDUFS8	NADH dehydrogenase (ubiquinone) Fe-S protein 8, 23 kDa (NADH-coenzyme Q reductase)	P247441	0.69	6.35E-04
TUSC3	Tumor suppressor candidate 3	P515347	0.69	1.32E-03
PARL	Presenilin associated, rhomboid-like	P247943	0.69	5.87E-05
PDPR	Pyruvate dehydrogenase phosphatase regulatory subunit	P137829	0.69	4.66E-04
ABCE1	ATP-binding cassette, sub-family E (OABP), member 1	P332822	0.69	9.62E-06
COX6B2	Cytochrome c oxidase subunit VIb polypeptide 2 (testis)	P300506	0.69	3.58E-04
ACN9	ACN9 homolog ( <i>S. cerevisiae</i> )	P376337	0.70	6.36E-04
RG9MTD1	RNA (guanine-9-) methyltransferase domain containing 1	P301994	0.70	1.88E-04
OXA1L	Oxidase (cytochrome c) assembly 1-like	P531829	0.70	3.27E-04
MRPL49	Mitochondrial ribosomal protein L49	P261351	0.70	4.52E-06
MTCP1	Mature T-cell proliferation 1	P452280	0.70	6.41E-05
TOMM40L	Translocase of outer mitochondrial membrane 40 homolog (yeast)-like	P86003	0.70	2.06E-04
MRPL42	Mitochondrial ribosomal protein L42	P40367	0.71	1.11E-03
GLRX2	Glutaredoxin 2	P514107	0.71	8.98E-04