

SUPPLEMENTAL MATERIAL

RNA analyses

Total RNA was isolated and reverse transcribed with AffinityScript QPCR cDNA Synthesis Kit (Agilent Technologies). PCR reactions were performed in triplicate in a 96-well format using the MX3005P (Stratagene). The primer sets (SYBR green) used to detect specific gene expression are as follows: mBDH1 fwd-TCTCGGACTGCCTGCGCTAT, rev-ACCGCTGTTGCAGTAGGTTT; m36B4 fwd-TGGAAGTCCAACACTTTCCTCAA m36B4 rev-ATCTGCTGCATCTGCTTGGAG; mMCT1 fwd-TGCAACGACCAGTGAAGTATC, rev-GACAACCACCAGCGATCATTA; mMCT2 fwd-ATACTTGCAGGTCCTCTCATTC, rev-GGAAGAGGCAGACAACGATAA. 36B4 primer set was included in a separate well (in triplicate) and used to normalize the gene expression data.

Proteomics using Stable Isotope Labeling by Amino Acids (SILAC)

Crude mitochondrial fractions were prepared from cardiac tissue of Lys6 (¹³C6-Lysine, Silantes) labeled (heavy) and non-labeled (light) mice. Mitochondrial fractions were prepared as previously described.¹ Briefly, immediately following euthanasia, the mouse ventricles were dissected, washed and placed in ice-cold isolation buffer (220 mM mannitol, 70 mM sucrose, 5mM HEPES-KOH, pH 7.4, 1mM EGTA, 1mg/ml BSA and protease inhibitor cocktail). The tissue was then minced and homogenized using a Potter-Elvehjem glass/Teflon homogenizer. A crude mitochondrial fraction was extracted from the homogenate using differential centrifugation and resuspended in small amount of the isolation buffer (300 µl).

A 1:1 mixture of heavy and light heart mitochondrial fractions were then separated by gel electrophoresis on precast 4–12% NuPAGE gradient gels (Invitrogen) and stained with the

Colloidal Blue Staining Kit (Invitrogen). Evenly sized gel pieces were excised and processed for mass spectrometry. The gel pieces were subjected to in-gel reduction and alkylation, followed by LysC (Wako) digestion as described previously.² In brief, trypsin digested gel pieces were washed twice with 50% 50 mM NH_4HCO_3 eluent additive for LC-MS (Sigma-Aldrich) / 50% ethanol for 20 min, and dehydrated with 100% ethanol for 10 min, and then vacuum centrifuged. Gel pieces were reduced with 10 mM DTT for 45 min at 56°C and alkylated with 55 mM iodoacetamide for 30 min at RT in the dark. After two cycles of washing and dehydration, samples were dehydrated twice with 100% ethanol for 15 min and vacuum centrifuged. Gel pieces were digested overnight at 37°C in 50 μl of digestion buffer containing 12.5 ng/ μl of LysC (Wako).

Released peptides were extracted once with 30% acetonitrile/ 3% trifluoroacetic acid (TFA), twice with 70% acetonitrile, followed by two final extractions with 100% acetonitrile. Extracts were vacuum centrifuged to remove acetonitrile and subsequently acidified with 0.5% TFA. Peptides were desalted and concentrated with homemade "STAGE" tips (Stop and Go extraction tips) filled with C-18 (C18 Empore Disks, 3M) as described.³

Mass spectrometric experiments were performed on a nano-flow HPLC system (Agilent) connected to a LTQ-Orbitrap XL instrument (Thermo Scientific) equipped with a nanoelectrospray source (Proxeon). The mass spectrometer was operated in the data dependent mode to monitor MS and MS/MS spectra. Survey full-scan MS spectra (from m/z 300–2000) were acquired in the Orbitrap with a resolution of $R=60,000$ at m/z 400 after accumulation of 1,000,000 ions. The five most intense ions from the preview survey scan delivered by the Orbitrap were sequenced by collision-induced dissociation (CID) in the LTQ. Mass spectra were analyzed using MaxQuant software (Version 1.0.14.10)⁴ and all tandem mass spectra were

searched against the mouse International Protein Index protein sequence database (IPI version 3.54) and concatenated with reversed copies of all sequences. The required false positive rate was set to 1% at the protein and peptide level. Maximum allowed mass deviation was set to 7 ppm in MS mode and 0.5 Da for MS/MS peaks. The parameter settings were: LysC as digesting enzyme, a maximum of two missed cleavages, a minimum of six amino acids, carbamidomethylation at cysteine residues as fixed and oxidation at methionine residues as variable modifications.

Metabolomic analysis of organic acids and acylcarnitines

Immediately following deep anesthesia by intraperitoneal injection of pentobarbital (100 mg/kg body weight), bi-ventricle was excised and frozen. Specimens of powdered bi-ventricle tissue were diluted 20-fold (mass:volume) in 50% acetonitrile supplemented with 0.3% formate (acylcarnitines, amino acids, and organic acids). Samples were homogenized in a TissueLyser II (Qiagen). Tissue extracts were derivatized and analyzed as previously described.⁵ Levels of succinate, C4OH-carnitine, and C2-carnitine were determined using stable isotope dilution techniques. The data were acquired using a Waters AcquityTM UPLC system equipped with a TQ (triple quadrupole) detector and a data system controlled by MassLynx 4.1 operating system (Waters Corporation). Metabolites were quantified using methods described previously.⁶

Supplemental Table 1: Mitochondrial proteins identified by proteomic profiling in compensated hypertrophy (CH) and/or heart failure (HF) samples.

ID	Gene Name
IPI00387379	2,4-dienoyl CoA reductase 1, mitochondrial
IPI00379694, IPI00127625	3-hydroxy-3-methylglutaryl-Coenzyme A lyase
IPI00330754, IPI00890322, IPI00857778	3-hydroxybutyrate dehydrogenase, type 1
IPI00885424, IPI00154047	3-hydroxyisobutyryl-Coenzyme A hydrolase
IPI00132653, IPI00856651, IPI00858156	3-oxoacid CoA transferase 1
IPI00606168, IPI00856229, IPI00227445, IPI00407499	4-aminobutyrate aminotransferase
IPI00648312	5'-nucleotidase domain containing 3
IPI00648235, IPI00187512	5'-nucleotidase, cytosolic III
IPI00230589, IPI00230591, IPI00230590, IPI00894854,	A kinase (PRKA) anchor protein 1
IPI00890007, IPI00230593, IPI00115506, IPI00230592	
IPI00323406	ATP synthase mitochondrial F1 complex assembly factor 1
IPI00336348	ATP synthase mitochondrial F1 complex assembly factor 2; similar to ATP synthase mitochondrial F1 complex assembly factor 2
IPI00468481	ATP synthase, H ⁺ transporting mitochondrial F1 complex, beta subunit
IPI00856424, IPI00125460	ATP synthase, H ⁺ transporting, mitochondrial F0 complex, subunit F pseudogene; similar to ATP synthase coupling factor 6, mitochondrial precursor (ATPase subunit F6); ATP synthase, H ⁺ transporting, mitochondrial F0 complex, subunit F
IPI00341282	ATP synthase, H ⁺ transporting, mitochondrial F0 complex, subunit b, isoform 1; predicted gene 12231
IPI00857439, IPI00130280	ATP synthase, H ⁺ transporting, mitochondrial F1 complex, alpha subunit, isoform 1
IPI00750074, IPI00313475, IPI00775853, IPI00776084,	ATP synthase, H ⁺ transporting, mitochondrial F1 complex, gamma polypeptide 1
IPI00776275, IPI00751391, IPI00776312	
IPI00761646, IPI00672663, IPI00816848	ATP-binding cassette, sub-family B (MDR/TAP), member 7
IPI00856267, IPI00856425, IPI00123422, IPI00459383	ATP-binding cassette, sub-family B (MDR/TAP), member 8
IPI00135646, IPI00553576	ATP-binding cassette, sub-family D (ALD), member 3
IPI00108410	ATPase family, AAA domain containing 1
IPI00126913, IPI00464208	ATPase family, AAA domain containing 3A
IPI00127598, IPI00331463	ATPase inhibitory factor 1
IPI00880712, IPI00880589, IPI00880341, IPI00357510,	AU RNA binding protein/enoyl-coenzyme A hydratase
IPI00357511, IPI00124900	
IPI00606647, IPI00321499	BCL2-like 13 (apoptosis facilitator)
IPI00128346	CDGSH iron sulfur domain 1
IPI00345740, IPI00649328, IPI00649725	CDGSH iron sulfur domain 3
IPI00222203, IPI00874655, IPI00267596	COX15 homolog, cytochrome c oxidase assembly protein (yeast)
IPI00830383, IPI00830273, IPI00467840, IPI00830443	ClpB caseinolytic peptidase B homolog (E. coli)
IPI00128261	Cytochrome b
IPI00130376, IPI00355248	Cytochrome c oxidase subunit 1
IPI00116896	Cytochrome c oxidase subunit 3; ATP synthase subunit a; ATP synthase protein 8
IPI00347634, IPI00120414, IPI00279858	DnaJ (Hsp40) homolog, subfamily A, member 3
IPI00648191, IPI00226466, IPI00828649	DnaJ (Hsp40) homolog, subfamily C, member 11
IPI00624902, IPI00468992, IPI00111111, IPI00881254	DnaJ (Hsp40) homolog, subfamily C, member 19
IPI00137424	ECSIT homolog (Drosophila)
IPI00828369, IPI00474134, IPI00153350	FAD-dependent oxidoreductase domain containing 1
IPI00267299, IPI00460703	FAST kinase domains 2
IPI00881994, IPI00230283	G elongation factor, mitochondrial 1
IPI00338876, IPI00269240	G elongation factor, mitochondrial 2
IPI00622170, IPI00225294, IPI00336569	GUF1 GTPase homolog (S. cerevisiae)
IPI00117083	GrpE-like 1, mitochondrial
IPI00115598, IPI00230550	H2-K region expressed gene 6
IPI00331517	HIG1 domain family, member 1A
IPI00170051, IPI00881059	HscB iron-sulfur cluster co-chaperone homolog (E. coli)
IPI00110578, IPI00856218, IPI00856829	IscU iron-sulfur cluster scaffold homolog (E. coli); similar to nitrogen fixation cluster-like
IPI00130331	L-2-hydroxyglutarate dehydrogenase; predicted gene 7842
IPI00471097	LYR motif containing 5
IPI00117832, IPI00918067	LYR motif containing 7
IPI00122740	MACRO domain containing 1
IPI00123276	MOCO sulphurase C-terminal domain containing 2
IPI00222753	MTERF domain containing 3
IPI00116748	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 1C
IPI00318645	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 11
IPI00344004	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 12
IPI00230715	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 13
IPI00315302	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2
IPI00858238, IPI00132216	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 3
IPI00125929	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4
IPI00880753, IPI00331332	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5
IPI00133399	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 6 (B14)
IPI00130322	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 7 (B14.5a)

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 IPI00122633
 IPI00654091, IPI00762636

 NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 8
 NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9
 NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, assembly factor 1
 NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, assembly factor 2
 NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, assembly factor 4
 NADH dehydrogenase (ubiquinone) 1 beta subcomplex 3; predicted gene 3192
 NADH dehydrogenase (ubiquinone) 1 beta subcomplex 4; predicted gene 3873; predicted gene 3244
 NADH dehydrogenase (ubiquinone) 1 beta subcomplex 8
 NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 10
 NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5

 NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 6
 NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 7
 NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9
 NADH dehydrogenase (ubiquinone) 1, alpha/beta subcomplex, 1; predicted gene 4455
 NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 2; similar to NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 2
 NADH dehydrogenase (ubiquinone) Fe-S protein 1
 NADH dehydrogenase (ubiquinone) Fe-S protein 2
 NADH dehydrogenase (ubiquinone) Fe-S protein 4
 NADH dehydrogenase (ubiquinone) Fe-S protein 5; cDNA sequence BC002163
 NADH dehydrogenase (ubiquinone) Fe-S protein 7
 NADH dehydrogenase (ubiquinone) Fe-S protein 8
 NADH dehydrogenase (ubiquinone) flavoprotein 1
 NADH dehydrogenase (ubiquinone) flavoprotein 2
 NADH dehydrogenase (ubiquinone) flavoprotein 3
 NADH-ubiquinone oxidoreductase chain 1
 NADH-ubiquinone oxidoreductase chain 4L; NADH-ubiquinone oxidoreductase chain 4
 NFU1 iron-sulfur cluster scaffold homolog (*S. cerevisiae*); predicted gene 7855
 NLR family member X1
 OCIA domain containing 1
 OMA1 homolog, zinc metallopeptidase (*S. cerevisiae*)
 PET112-like (yeast)
 Parkinson disease (autosomal recessive, early onset) 7

 RAB1B, member RAS oncogene family
 RIKEN cDNA 1300010F03 gene
 RIKEN cDNA 1500001M20 gene
 RIKEN cDNA 1700021F05 gene
 RIKEN cDNA 1700034H14 gene
 RIKEN cDNA 1700034I23 gene; predicted gene 10731
 RIKEN cDNA 1810020G14 gene; synaptojanin 2 binding protein; predicted gene 4116

 RIKEN cDNA 2010107E04 gene
 RIKEN cDNA 2310003L22 gene
 RIKEN cDNA 2310005E10 gene
 RIKEN cDNA 2310028O11 gene
 RIKEN cDNA 2410015M20 gene
 RIKEN cDNA 2410091C18 gene
 RIKEN cDNA 4930402E16 gene
 RIKEN cDNA 4933403F05 gene
 RIKEN cDNA 9030617O03 gene
 RIKEN cDNA 9330129D05 gene
 RIKEN cDNA 9430016H08 gene
 RIKEN cDNA A230051G13 gene
 RNA (guanine-9-) methyltransferase domain containing 1
 SCO cytochrome oxidase deficient homolog 1 (yeast)
 TNF receptor-associated protein 1
 Ts translation elongation factor, mitochondrial
 YME1-like 1 (*S. cerevisiae*)
 aarF domain containing kinase 1
 abhydrolase domain containing 10
 abhydrolase domain containing 11
 acetyl-Coenzyme A acetyltransferase 1
 acetyl-Coenzyme A acyltransferase 2 (mitochondrial 3-oxoacyl-Coenzyme A thiolase
 acid phosphatase 6, lysophosphatidic
 aconitase 2, mitochondrial
 acyl-CoA synthetase family member 2
 acyl-CoA synthetase family member 2

IPI00856216, IPI00112549, IPI00857822, IPI00556840,
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 IPI00655156, IPI00353887

acyl-CoA synthetase long-chain family member 1
 acyl-CoA synthetase long-chain family member 2
 acyl-CoA synthetase short-chain family member 1
 acyl-CoA thioesterase 1
 acyl-CoA thioesterase 10
 acyl-CoA thioesterase 13
 acyl-CoA thioesterase 2
 acyl-CoA thioesterase 9
 acyl-Coenzyme A dehydrogenase family, member 10
 acyl-Coenzyme A dehydrogenase family, member 11
 acyl-Coenzyme A dehydrogenase family, member 12
 acyl-Coenzyme A dehydrogenase, long-chain
 acyl-Coenzyme A dehydrogenase, medium chain
 acyl-Coenzyme A dehydrogenase, short chain
 acyl-Coenzyme A dehydrogenase, short/branched chain
 acyl-Coenzyme A dehydrogenase, very long chain
 acyl-Coenzyme A oxidase 1, palmitoyl
 adenylate kinase 1
 adenylate kinase 3
 alcohol dehydrogenase, iron containing, 1
 aldehyde dehydrogenase 1 family, member B1
 aldehyde dehydrogenase 1 family, member L2
 aldehyde dehydrogenase 2, mitochondrial
 aldehyde dehydrogenase 4 family, member A1
 aldehyde dehydrogenase 9, subfamily A1
 aldehyde dehydrogenase family 6, subfamily A1
 aldehyde dehydrogenase family 7, member A1
 aldehyde dehydrogenase family 5, subfamily A1
 aldo-keto reductase family 1, member B7
 aldolase C, fructose-bisphosphate
 alkylglycerone phosphate synthase
 alpha-methylacyl-CoA racemase
 aminolevulinic acid synthase 1
 apolipoprotein A-I binding protein
 apolipoprotein O-like
 apoptosis-inducing factor, mitochondrion-associated 1
 arginyl-tRNA synthetase 2, mitochondrial
 asparaginyl-tRNA synthetase 2 (mitochondrial)(putative)
 aspartyl-tRNA synthetase 2 (mitochondrial)
 biphenyl hydrolase-like (serine hydrolase, breast epithelial mucin-associated antigen
 brain protein 44; similar to brain protein 44; predicted gene 3982
 branched chain aminotransferase 2, mitochondrial
 branched chain ketoacid dehydrogenase E1, alpha polypeptide
 branched chain ketoacid dehydrogenase E1, beta polypeptide; similar to 3-methyl-2-oxobutanoate dehydrogenase
 cDNA sequence AK157302
 carbonyl reductase 2
 carbonyl reductase 4
 carnitine acetyltransferase

 carnitine palmitoyltransferase 1a, liver
 carnitine palmitoyltransferase 1b, muscle
 carnitine palmitoyltransferase 2

 caseinolytic peptidase X (E.coli)
 caseinolytic peptidase, ATP-dependent, proteolytic subunit homolog (E. coli)
 catalase
 cathepsin B
 cathepsin D
 caveolin 1, caveolae protein
 chaperone, ABC1 activity of bc1 complex like (S. pombe)
 chaperonin containing Tcp1, subunit 7 (eta)
 citrate lyase beta like
 citrate synthase
 citrate synthase like
 clathrin, heavy polypeptide (Hc)
 coenzyme Q3 homolog, methyltransferase (yeast)
 coenzyme Q5 homolog, methyltransferase (yeast)
 coenzyme Q6 homolog (yeast)
 coenzyme Q9 homolog (yeast)
 coiled-coil domain containing 109A

IPI00137601
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 IPI00117281, IPI00660262, IPI00463220, IPI00227783

coiled-coil domain containing 44
 coiled-coil domain containing 58
 coiled-coil domain containing 90A
 coiled-coil-helix-coiled-coil-helix domain containing 3; similar to coiled-coil-helix-coiled-coil-helix domain containing
 coiled-coil-helix-coiled-coil-helix domain containing 4
 complement component 1, q subcomponent binding protein
 coproporphyrinogen oxidase
 creatine kinase, mitochondrial 1, ubiquitous
 creatine kinase, mitochondrial 2
 cysteine conjugate-beta lyase 2
 cysteinyl-tRNA synthetase 2 (mitochondrial)(putative)
 cytochrome P450, family 27, subfamily a, polypeptide 1
 cytochrome b5 reductase 1
 cytochrome b5 reductase 3
 cytochrome c oxidase subunit IV isoform 1
 cytochrome c oxidase subunit VIIa polypeptide 2-like; predicted gene 6965
 cytochrome c oxidase, subunit VI a, polypeptide 2
 cytochrome c oxidase, subunit VIIa 1
 cytochrome c oxidase, subunit VIIb polypeptide 1
 cytochrome c oxidase, subunit Va
 cytochrome c oxidase, subunit XVII assembly protein homolog (yeast
 cytochrome c, testis
 cytochrome c-1
 death associated protein 3
 dehydrogenase/reductase (SDR family) member 1
 dehydrogenase/reductase (SDR family) member 4
 demethyl-Q 7
 dihydrolipoamide S-acetyltransferase (E2 component of pyruvate dehydrogenase complex
 dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex
 dihydrolipoamide branched chain transacylase E2
 dihydrolipoamide dehydrogenase
 dihydroorotate dehydrogenase

 dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenzyme A isomerase
 electron transferring flavoprotein, dehydrogenase
 enoyl Coenzyme A hydratase domain containing 3
 enoyl Coenzyme A hydratase, short chain, 1, mitochondria
 enoyl coenzyme A hydratase 1, peroxisoma
 enoyl-Coenzyme A, hydratase/3-hydroxyacyl Coenzyme A dehydrogenase
 ethylmalonic encephalopathy 1
 family with sequence similarity 162, member A
 family with sequence similarity 82, member B
 ferredoxin reductase
 ferrochelataase
 fission 1 (mitochondrial outer membrane) homolog (yeast)
 frataxin
 fumarate hydratase 1
 fumarylacetoacetate hydrolase domain containing 1
 fumarylacetoacetate hydrolase domain containing 2A
 glioblastoma amplified sequence
 glutamate dehydrogenase 1; predicted gene 5902
 glutamate oxaloacetate transaminase 2, mitochondrial
 glutaryl-Coenzyme A dehydrogenase
 glutathione S-transferase kappa 1
 glutathione transferase zeta 1 (maleylacetoacetate isomerase)
 glycerol kinase
 glycerol kinase 2
 glycerol phosphate dehydrogenase 2, mitochondrial
 glycerol-3-phosphate dehydrogenase 1 (soluble)
 glycyl-tRNA synthetase
 glyoxalase domain containing 4
 growth factor, erv1 (S. cerevisiae)-like (augmenter of liver regeneration)
 growth hormone inducible transmembrane protein
 heat shock protein 1 (chaperonin 10); predicted gene, EG628438; heat shock protein 1 (chaperonin 10), related sequence 1;
 predicted gene 2903
 heat shock protein 1B; heat shock protein 1A; heat shock protein 1-like
 heat shock protein 2
 heat shock protein 9
 heat shock protein 90 alpha (cytosolic), class B member 1
 heterogeneous nuclear ribonucleoprotein L-like; glutathione peroxidase 4

IPI00762858, IPI00283612, IPI00759938, IPI00468553,
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 IPI00111211
 IPI00322422
 IPI00274131, IPI00874379
 IPI00131988, IPI00271430
 IPI00132170
 IPI00654010, IPI00284978

 hexokinase 1

 hexokinase 2
 histidine triad nucleotide binding protein 2
 histidyl-tRNA synthetase 2, mitochondrial (putative)
 holocytochrome c synthetase
 hydroxyacyl glutathione hydrolase
 hydroxyacyl-Coenzyme A dehydrogenase
 hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), alpha subunit
 hydroxysteroid (17-beta) dehydrogenase 1C
 hydroxysteroid (17-beta) dehydrogenase 4
 hydroxysteroid dehydrogenase like 2
 hypothetical protein LOC675054; RIKEN cDNA 2900010M23 gene
 inner membrane protein, mitochondrial

 insulin degrading enzyme
 iron-sulfur cluster assembly 1 homolog (*S. cerevisiae*)
 isocitrate dehydrogenase 2 (NADP+), mitochondrial
 isocitrate dehydrogenase 3 (NAD+) alpha
 isocitrate dehydrogenase 3 (NAD+) beta
 isocitrate dehydrogenase 3 (NAD+), gamma
 isoleucine-tRNA synthetase 2, mitochondrial; similar to isoleucine-tRNA synthetase 2, mitochondria
 isovaleryl coenzyme A dehydrogenase
 lactate dehydrogenase B; predicted gene 5514
 lactation elevated 1
 leucine aminopeptidase 3
 leucine zipper-EF-hand containing transmembrane protein 1
 leucine-rich PPR-motif containing
 leucyl-tRNA synthetase, mitochondrial
 lon peptidase 1, mitochondrial
 lysophospholipase 1
 malate dehydrogenase 1, NAD (soluble)
 malate dehydrogenase 2, NAD (mitochondrial)
 malic enzyme 3, NADP(+)-dependent, mitochondrial
 malonyl-CoA decarboxylase
 metaxin 2
 methionine sulfoxide reductase A
 methionine sulfoxide reductase B2
 methylcrotonoyl-Coenzyme A carboxylase 1 (alpha
 methylcrotonoyl-Coenzyme A carboxylase 2 (beta
 methylenetetrahydrofolate dehydrogenase (NADP+ dependent), methylenetetrahydrofolate cyclohydrolase,
 formyltetrahydrofolate synthase
 methylmalonic aciduria (cobalamin deficiency) type A
 methylmalonic aciduria (cobalamin deficiency) type B homolog (human
 methylmalonyl CoA epimerase
 methylmalonyl-Coenzyme A mutase
 mitochondrial ribosomal protein S7
 mitochondrial antiviral signaling protein
 mitochondrial carrier homolog 2 (*C. elegans*); predicted gene, 100039384; predicted gene, 100039506
 mitochondrial intermediate peptidase; similar to Mipep protein
 mitochondrial poly(A) polymerase
 mitochondrial ribosomal protein L1
 mitochondrial ribosomal protein L10
 mitochondrial ribosomal protein L11
 mitochondrial ribosomal protein L12
 mitochondrial ribosomal protein L13
 mitochondrial ribosomal protein L15
 mitochondrial ribosomal protein L16
 mitochondrial ribosomal protein L28
 mitochondrial ribosomal protein L3
 mitochondrial ribosomal protein L39
 mitochondrial ribosomal protein L40
 mitochondrial ribosomal protein L44
 mitochondrial ribosomal protein L45
 mitochondrial ribosomal protein L46
 mitochondrial ribosomal protein L47
 mitochondrial ribosomal protein L48
 mitochondrial ribosomal protein L49; similar to mitochondrial ribosomal protein L45
 mitochondrial ribosomal protein L51
 mitochondrial ribosomal protein L9

IPI00895548, IPI00895482, IPI00348248, IPI00895361
 IPI00321858
 IPI00320963, IPI00880873, IPI00556725
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 IPI00654405, IPI00117689
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 IPI00666165, IPI00125035, IPI00648501, IPI00649018,
 IPI00651878
 IPI00858282, IPI00474281, IPI00115607, IPI00850941

 IPI00115040, IPI00850545, IPI00677484

 mitochondrial ribosomal protein S10
 mitochondrial ribosomal protein S15
 mitochondrial ribosomal protein S18A
 mitochondrial ribosomal protein S18B
 mitochondrial ribosomal protein S22
 mitochondrial ribosomal protein S23; similar to Mrps23 protein

 mitochondrial ribosomal protein S27
 mitochondrial ribosomal protein S28
 mitochondrial ribosomal protein S30
 mitochondrial ribosomal protein S31
 mitochondrial ribosomal protein S35
 mitochondrial ribosomal protein S6
 mitochondrial ribosomal protein S9
 mitochondrial ribosome recycling factor; similar to mitochondrial ribosome recycling factor; predicted gene 637
 mitochondrial trans-2-enoyl-CoA reductase
 mitochondrial translational initiation factor 2

 mitochondrial ubiquitin ligase activator of NFKB 1
 mitofusin 1
 monoamine oxidase B
 myosin, light chain 10, regulatory
 nephronophthysis 3 (adolescent); acyl-Coenzyme A dehydrogenase family, member 1
 neurolysin (metallopeptidase M3 family)
 nicotinamide nucleotide adenyltransferase 3
 nicotinamide nucleotide transhydrogenase
 nitrilase family, member 2
 nitrogen fixation gene 1 (S. cerevisiae); similar to Nitrogen fixation gene 1 (S. cerevisiae)
 nudix (nucleoside diphosphate linked moiety X)-type motif 13
 optic atrophy 3 (human)
 ornithine aminotransferase
 oxidase assembly 1-like
 oxidoreductase NAD-binding domain containing 1
 oxoglutarate dehydrogenase (lipoamide)

 pentatricopeptide repeat domain 2
 pentatricopeptide repeat domain 3
 peptidase (mitochondrial processing) alpha
 peptidase (mitochondrial processing) beta
 peptidylprolyl isomerase F (cyclophilin F)
 peroxiredoxin 1; predicted gene 7204

 peroxiredoxin 3
 peroxiredoxin 4
 peroxiredoxin 5
 peroxisomal delta3, delta2-enoyl-Coenzyme A isomerase
 phenylalanine-tRNA synthetase 2 (mitochondrial)
 pitrilysin metallopeptidase 1
 polymerase I and transcript release factor
 predicted gene 10078; predicted gene 3544; similar to mitochondrial ribosomal protein S36; mitochondrial ribosomal
 protein S36; predicted gene 7258; predicted gene 4676
 predicted gene 10108; cytochrome c, somatic; predicted gene 10053; similar to cytochrome c
 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 FO complex, subunit g; predicted gene 4045
 predicted gene 10250; hypothetical protein LOC676483; predicted gene 5051; ATP synthase, H⁺ transporting,
 mitochondrial FO complex, subunit d; predicted gene 4953; similar to ATP synthase, H⁺ transporting, mitochondrial FO
 complex, subunit d
 predicted gene 11225; 3-hydroxyisobutyrate dehydrogenase
 predicted gene 11945; predicted gene 6238; mitochondrial ribosomal protein L3C
 predicted gene 12115; single-stranded DNA binding protein 1
 predicted gene 12141; heat shock protein 1 (chaperonin)

 predicted gene 13328; mitochondrial ribosomal protein S5
 predicted gene 13639; similar to adenylate kinase 4; adenylate kinase 3-like 1

 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 910
 predicted gene 14506; BCL2/adenovirus E1B interacting protein 3; predicted gene 6532; similar to E1B 19K/Bcl-2-binding
 protein homolog

IPI00110385
 IPI00116753
 IPI00132347, IPI00555000
 IPI00111770, IPI00875971
 IPI00453724, IPI00556699, IPI00755768

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 IPI00133167

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 IPI00408727, IPI00881534, IPI00881722, IPI00881568,
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 IPI00753072, IPI00222767, IPI00752455
 IPI00221407, IPI00776169
 IPI00122251
 IPI00881473, IPI00881737, IPI00459279
 IPI00222930, IPI00307931, IPI00515349, IPI00123186
 IPI00875863, IPI00474370, IPI00473646
 IPI00858050, IPI00320716

 predicted gene 15683; RIKEN cDNA 2310005N03 gene; similar to RIKEN cDNA 2310005N03
 predicted gene 2893; electron transferring flavoprotein, alpha polypeptide
 predicted gene 2962; ubiquinol-cytochrome c reductase binding protein
 predicted gene 2972; ATP synthase, H⁺ transporting, mitochondrial F1F0 complex, subunit c
 predicted gene 3672; similar to Glycine cleavage system H protein, mitochondrial precursor; glycine cleavage system
 protein H (aminomethyl carrier)
 predicted gene 4237; NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 1
 predicted gene 4691; predicted gene 6944; predicted gene 10290; predicted gene 10566; predicted gene 10291; predicted
 gene 3200; predicted gene 12070; predicted gene 7286; predicted gene 6946; predicted gene 8825; predicted gene 9081;
 glyceraldehyde-3-phosphate dehydrogenase; predicted gene 10359; predicted gene 10358; predicted gene 7784; predicted
 gene 12416; predicted gene 14148; predicted gene 13882; predicted gene 4217; predicted gene 7183; predicted gene 10313;
 predicted gene 2467; predicted gene 5787; predicted gene 2193; predicted gene 13292; predicted gene 380687; predicted
 gene 2076; predicted gene 3222; predicted gene 7507; predicted gene 7293; predicted gene 15191; predicted gene 674324;
 predicted gene 10284; predicted gene 8055; similar to hCG1978856; predicted gene 2574; similar to glyceraldehyde-3-
 phosphate dehydrogenase; predicted gene 7545; predicted gene 12033; predicted gene 3272; predicted gene 3534; predicted
 gene 2308; predicted gene 3839; predicted gene 9061; predicted gene 3671; predicted gene 8513; predicted gene 4654;
 predicted gene 12537; predicted gene 4929; predicted gene 5652; predicted gene 9568; predicted gene 8349; predicted gene
 2546; predicted gene 7129; similar to Glyceraldehyde-3-phosphate dehydrogenase (GAPDH); predicted gene 8318;
 glyceraldehyde-3-phosphate dehydrogenase pseudogene; predicted gene 7611; predicted gene 2445; predicted gene 6283;
 predicted gene 11557; predicted gene 4335; predicted gene 9127; predicted gene 3695; predicted gene 5507; predicted gene
 8174; predicted gene 4609; predicted gene 3809; predicted gene 9034; predicted gene 2606; predicted gene 4575; predicted
 gene 12286; predicted gene 11658; predicted gene 5732; predicted gene 16374; predicted gene 8100; predicted gene 11953;
 predicted gene, EG545741; predicted gene 2451; predicted gene 14130

 predicted gene 5436; similar to ATP synthase, H⁺ transporting, mitochondrial F1 complex, O subunit; ATP synthase, H⁺
 transporting, mitochondrial F1 complex, O subunit
 predicted gene 5626; stomatin (Epb7.2)-like 2
 predicted gene 6123; pyruvate dehydrogenase (lipoamide) beta
 predicted gene 6265; similar to cytochrome c oxidase, subunit VIc; cytochrome c oxidase, subunit VIc
 predicted gene 6444; NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 11
 predicted gene 6560; predicted gene 2124; predicted gene 6992; pyruvate kinase, muscle; similar to M2-type pyruvate
 kinase
 predicted gene 6835; ATP synthase, H⁺ transporting, mitochondrial F0 complex, subunit f, isoform 2; predicted gene 6581

 predicted gene 6997; mitochondrial ribosomal protein L22
 predicted gene 7049; similar to NADP-dependent malic enzyme (NADP-ME) (Malic enzyme 1); malic enzyme 1, NADP(+)-
 dependent, cytosolic
 predicted gene 7591; voltage-dependent anion channel 3
 predicted gene 7730; non-metastatic cells 2, protein (NM23B) expressed in; predicted gene 5566; predicted gene 5425;
 similar to Nucleoside diphosphate kinase B (NDK B) (NDP kinase B) (P18)
 predicted gene 7997; lactate dehydrogenase A; predicted gene 5452
 predicted gene 8546; acylglycerol kinase
 predicted gene 8566; superoxide dismutase 1, soluble; similar to Superoxide dismutase
 predicted gene 9481; mitochondrial ribosomal protein L41
 predicted gene 9755; Tu translation elongation factor, mitochondrial
 predicted gene 9803; mitochondria-associated protein involved in granulocyte-macrophage colony-stimulating factor signal
 transduction
 presenilin associated, rhomboid-like
 prohibitin 2
 prohibitin; predicted gene 4773; RIKEN cDNA 1700071K01 gene
 proline dehydrogenase
 proline synthetase co-transcribed
 propionyl Coenzyme A carboxylase, beta polypeptide
 propionyl-Coenzyme A carboxylase, alpha polypeptide
 prosaposin
 prostaglandin E synthase 2
 protein phosphatase 1K (PP2C domain containing)
 protein phosphatase 2C, magnesium dependent, catalytic subunit
 pyrophosphatase (inorganic) 2

 pyruvate carboxylase
 pyruvate dehydrogenase E1 alpha 1
 pyruvate dehydrogenase E1 alpha 2
 pyruvate dehydrogenase complex, component X; similar to pyruvate dehydrogenase complex, component X
 pyruvate dehydrogenase kinase, isoenzyme 1
 pyruvate dehydrogenase kinase, isoenzyme 2
 quinoid dihydropteridine reductase; similar to Quinoid dihydropteridine reductase
 ras homolog gene family, member T1
 ras homolog gene family, member T2
 reticulon 4 interacting protein 1

IPI00895515, IPI00229040, IPI00857145
IPI00129164
IPI00318006
IPI00454008
IPI00109354
IPI00170357, IPI00850215
IPI00225288, IPI00471416
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IPI00125652, IPI00828588
IPI00471266, IPI00350590, IPI00124699, IPI00271280
IPI00223216, IPI00762128
IPI00895166, IPI00112822, IPI00895392, IPI00230512

retinol dehydrogenase 13 (all-trans and 9-cis)
sepiapterin reductase
serine hydrolase-like
serine hydroxymethyltransferase 2 (mitochondrial)
seryl-aminoacyl-tRNA synthetase 2
similar to AFG3(ATPase family gene 3)-like 2 (yeast); AFG3(ATPase family gene 3)-like 2 (yeast)
similar to Coiled-coil domain containing 90B; coiled-coil domain containing 90B
similar to Electron transferring flavoprotein, beta polypeptide; electron transferring flavoprotein, beta polypeptid
similar to NADH dehydrogenase (ubiquinone) Fe-S protein 3; NADH dehydrogenase (ubiquinone) Fe-S protein 3; predicted
gene 12251
similar to NADH dehydrogenase (ubiquinone) Fe-S protein 6; NADH dehydrogenase (ubiquinone) Fe-S protein 6; predicted
gene 6415
similar to Saccharopine dehydrogenase (putative); saccharopine dehydrogenase (putative)

similar to Solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 3; solute carrier family 25
(mitochondrial carrier, phosphate carrier), member 3
similar to Unknown (protein for IMAGE:4910858); predicted gene 4076
similar to Voltage-dependent anion-selective channel protein 2 (VDAC-2) (mVDAC2) (mVDAC6) (Outer mitochondrial
membrane protein porin 2); predicted gene 7832; voltage-dependent anion channel 2
similar to adenylate kinase 2; adenylate kinase 2
similar to brain protein 44-like protein; brain protein 44-like; predicted gene 3452; predicted gene 8219
similar to cytochrome b5 outer mitochondrial membrane precursor; cytochrome b5 type I
similar to cytochrome c oxidase, subunit VIIc; predicted gene 3386; cytochrome c oxidase, subunit VIIc
similar to cytochrome c oxidase, subunit Vb; predicted gene 11273; cytochrome c oxidase, subunit Vb
similar to es1 protein; DNA segment, Chr 10, Johns Hopkins University 81 expressed
similar to lactamase, beta; lactamase, beta
similar to lysyl-tRNA synthetase; lysyl-tRNA synthetase
similar to mitochondrial malonyltransferase isoform b precursor; malonyl CoA:ACP acyltransferase (mitochondrial)
similar to mitofusin 2; mitofusin 2

similar to optic atrophy 1 (autosomal dominant); optic atrophy 1 homolog (human)

similar to polynucleotide phosphorylase-like protein; polyribonucleotide nucleotidyltransferase
sirtuin 5 (silent mating type information regulation 2 homolog) 5 (S. cerevisiae)
solute carrier family 16 (monocarboxylic acid transporters), member 1
solute carrier family 25 (mitochondrial carnitine/acylcarnitine translocase), member 20
solute carrier family 25 (mitochondrial carrier oxoglutarate carrier), member 11
solute carrier family 25 (mitochondrial carrier, Aralar), member 12
solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 13
solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 4
solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 5; similar to ADP/ATP translocase
2 (Adenine nucleotide translocator 2) (ANT 2) (ADP,ATP carrier protein 2) (Solute carrier family 25 member 5); predicted
gene 5529; predicted gene 8429; predicted gene 5256
solute carrier family 25 (mitochondrial carrier, citrate transporter), member 1
solute carrier family 25 (mitochondrial carrier, dicarboxylate transporter), member 10
solute carrier family 25 (mitochondrial carrier, glutamate), member 22

solute carrier family 25, member 40
solute carrier family 25, member 42
solute carrier family 25, member 46
sorting and assembly machinery component 50 homolog (S. cerevisiae)
spastic paraplegia 7 homolog (human)
staphylococcal nuclease and tudor domain containing 1
sterol carrier protein 2, liver
succinate dehydrogenase complex, subunit A, flavoprotein (Fp)
succinate dehydrogenase complex, subunit B, iron sulfur (Ip); similar to succinate dehydrogenase Ip subunit
succinate dehydrogenase complex, subunit C, integral membrane protein
succinate-CoA ligase, GDP-forming, alpha subunit
succinate-Coenzyme A ligase, ADP-forming, beta subunit
succinate-Coenzyme A ligase, GDP-forming, beta subunit
sulfide quinone reductase-like (yeast)
sulfite oxidase
superoxide dismutase 2, mitochondrial
suppressor of var1, 3-like 1 (S. cerevisiae)
tRNA 5-methylaminomethyl-2-thiouridylyl methyltransferase
tRNA nucleotidyl transferase, CCA-adding, 1
thioredoxin 2
thioredoxin reductase 2; similar to thioredoxin reductase 2
thiosulfate sulfurtransferase, mitochondrial
transcription factor A, mitochondrial

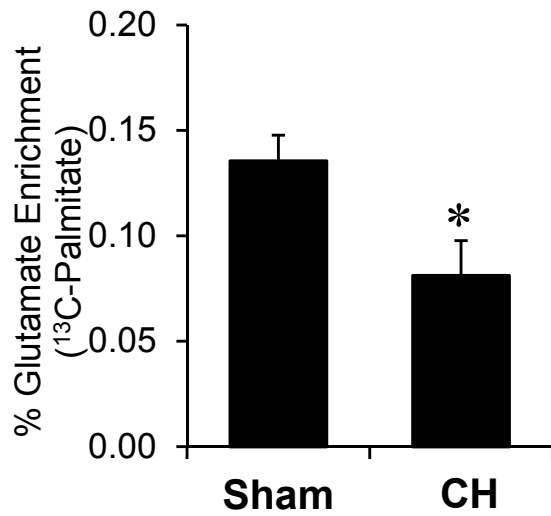
IPI00649594, IPI00848390, IPI00453815, IPI00828226, IPI00881541, IPI00648278	transforming growth factor beta regulated gene 4; similar to Transforming growth factor beta regulated gene 4
IPI00126861	transglutaminase 2, C polypeptide
IPI00165902	translocase of inner mitochondrial membrane 10 homolog (yeast)
IPI00134484	translocase of inner mitochondrial membrane 13 homolog (yeast)
IPI00885780, IPI00315325, IPI00515156	translocase of inner mitochondrial membrane 22 homolog (yeast)
IPI00135068, IPI00889924	translocase of inner mitochondrial membrane 44
IPI00111045	translocase of inner mitochondrial membrane 50 homolog (yeast)
IPI00125513	translocase of inner mitochondrial membrane 9 homolog (yeast)
IPI00474157, IPI00875326	translocase of outer mitochondrial membrane 40 homolog (yeast)
IPI00751137, IPI00377728	translocase of outer mitochondrial membrane 70 homolog A (yeast)
IPI00122499, IPI00885696, IPI00830213	transmembrane protein 143
IPI00130661	tripeptidyl peptidase I
IPI00460008, IPI00111613, IPI00307938	tryptophanyl tRNA synthetase 2 (mitochondrial)
IPI00118384, IPI00828266, IPI00885651	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide
IPI00119138	ubiquinol cytochrome c reductase core protein 2
IPI00857580, IPI00109603, IPI00857713, IPI00919103, IPI00858246, IPI00858043, IPI00857602, IPI00230305, IPI00749564	ubiquinol-cytochrome c reductase complex chaperone, CBP3 homolog (yeast)
IPI00653598, IPI00111885	ubiquinol-cytochrome c reductase core protein 1
IPI00133240	ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1
IPI00648640, IPI00224210	ubiquinol-cytochrome c reductase, complex III subunit VII
IPI00114153	uncoupling protein 3 (mitochondrial, proton carrier)
IPI00624653	upregulated during skeletal muscle growth 5
IPI00222180	valyl-tRNA synthetase 2, mitochondrial (putative); similar to valyl-tRNA synthetase 2-lik
IPI00230540, IPI00122549, IPI00857067	voltage-dependent anion channel 1
IPI00221569	zinc binding alcohol dehydrogenase, domain containing 2

Mitochondrial proteomic profiling in compensated hypertrophy (CH) and heart failure (HF). Quantitative proteomic analysis was done using the Stable Isotope Labeling by Amino ACids (SILAC) method in mitochondria isolated from the ventricles of sham-operated, CH, and HF animals. Mitochondrial proteins identified in all samples are listed. GOCC annotation in DAVID and the Mitocarta were used to define proteins as mitochondrial.

Supplemental Table 2: Proteins regulated in compensated hypertrophy (CH) and heart failure (HF) samples.

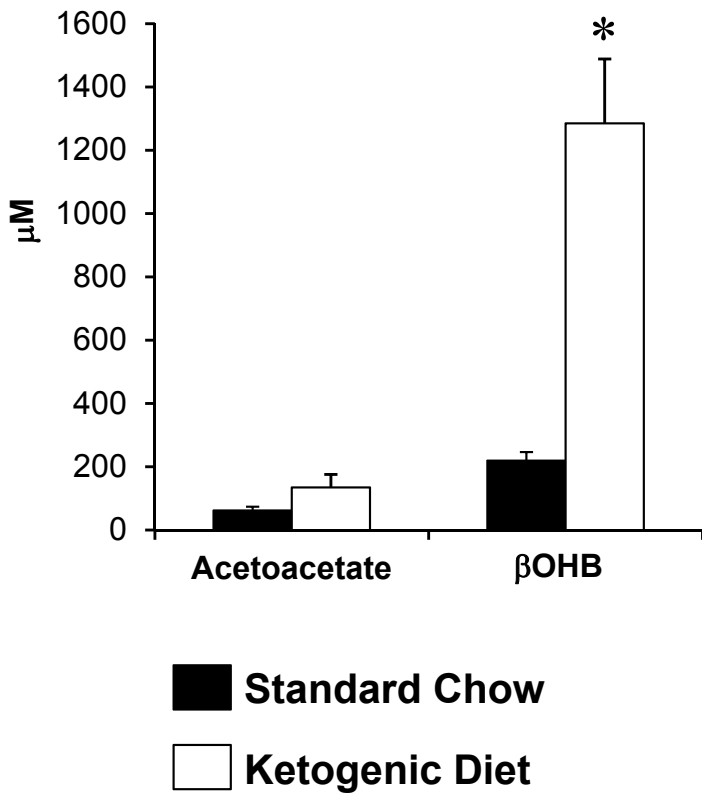
Gene Symbol	Protein Names	CH/CTRL	HF/CTRL
Abhd11	Abhydrolase domain-containing protein 11	1.28	3.45
Nfu1	Putative uncharacterized protein	1.19	2.71
Fahd2a	Fumarylacetoacetate hydrolase domain-containing protein 2A	-1.07	2.02
Abat	4-aminobutyrate aminotransferase	1.84	1.95
Bdh1	3-hydroxybutyrate dehydrogenase	2.74	1.89
Hagh	Hydroxyacylglutathione hydrolase	1.73	1.80
Cltc	Clathrin heavy chain	1.38	1.78
Nln	Neurolysin	1.63	1.65
Slc25a10	Mitochondrial dicarboxylate carrier	1.17	1.55
Rars2	Probable arginyl-tRNA synthetase	1.43	1.52
Cbr2	Carbonyl reductase [NADPH] 2	1.68	1.49
Ccdc58	Coiled-coil domain-containing protein 58	1.51	1.44
Hk1	Hexokinase 1	1.65	1.44
Ctsb	Cathepsin B;Cathepsin B1;Cathepsin B light chain;Cathepsin B heavy chair	1.53	1.43
Slc25a1	Solute carrier family 25	1.75	1.43
Cyb5r3	Cytochrome b5 reductase 3	1.84	1.38
Nudt13	Nucleoside diphosphate-linked moiety X motif 13	1.62	1.37
Acot9	Acyl-coenzyme A thioesterase 9	1.67	1.37
Cyb5r1	NADH-cytochrome b5 reductase 1	1.76	1.37
Cpox	Coproporphyrinogen-III oxidase	1.68	1.33
Hk2	Hexokinase-2	1.69	1.32
Ghitm	Growth hormone-inducible transmembrane protein	1.53	1.31
Gyk	Glycerol kinase	1.54	1.31
Tomm70a	Translocase of outer membrane 70 kDa subunit	1.65	1.28
Gfer	FAD-linked sulfhydryl oxidase ALR	1.69	1.20
Acsf2	Acyl-CoA synthetase family member 2	1.59	1.14
Tmem126a	Transmembrane protein 126A	3.00	1.13
Mrps30	28S ribosomal protein S30	1.54	1.10
Timm22	Mitochondrial import inner membrane translocase subunit	-1.27	1.02
Slc25a42	Solute carrier family 25 member 42	-1.44	-1.18
Acss1	Acetyl-coenzyme A synthetase 2-like	-1.27	-1.19
Agps	Alkylglycerone phosphate synthase	-1.73	-1.19
Cat	Catalase	-1.37	-1.21
Gstk1	Glutathione S-transferase kappa 1	-1.37	-1.25
Opa3	Optic atrophy 3 protein homolog	1.13	-1.26
Tmem143	Transmembrane protein 143	1.06	-1.26
Cisd1	CDGSH iron sulfur domain-containing protein 1	1.27	-1.26
Acaa2	Acetyl-Coenzyme A acyltransferase 2	-1.32	-1.27
9030617O03Rik	Probable 10-formyltetrahydrofolate dehydrogenase	-1.55	-1.29
Slc25a22	Mitochondrial glutamate carrier 1	-1.39	-1.32
Cox6a2	Cytochrome c oxidase subunit 6A2	-1.38	-1.35
Scp2	Non-specific lipid-transfer protein	-1.33	-1.37
Ak1	Adenylate kinase isoenzyme 1	-1.29	-1.38
Hsd17b4	17-beta-hydroxysteroid dehydrogenase 4	-1.46	-1.38
Ech1	Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase	-1.47	-1.39
Gpd1	Glycerol-3-phosphate dehydrogenase [NAD+]	-1.35	-1.39
Abcd3	ATP-binding cassette, sub-family D (ALD), member 3	-1.64	-1.41
Acad11	Acyl-CoA dehydrogenase family member 11	-1.66	-1.42
Ppm1k	Protein phosphatase 1K	-1.61	-1.42
Acox1	Acyl-Coenzyme A oxidase 1	-1.71	-1.54
Mdh1	Malate dehydrogenase	-1.51	-1.54
Ehhadh	Enoyl-CoA hydratase/3,2-trans-enoyl-CoA isomerase	-1.36	-1.60
Ldhb	L-lactate dehydrogenase B chain	-1.75	-1.83
Ucp3	Mitochondrial uncoupling protein 3	-1.56	-1.84
Pkm2	Pyruvate kinase isozymes M1/M2;Pyruvate kinase muscle isozyme	-1.10	-1.91

Quantitative proteomic analysis was done using the St¹³able Isotope Labeling by Amino ACids (SILAC) method in mitochondria isolated from the ventricles of sham-operated, CH, and HF animals. Proteins that exhibited a significant difference in the CH and/or HF models vs. corresponding sham-operated controls as determined using mass spectrometry-based quantitative proteomic analysis (MS/MS processing; Thermo Scientific LTQ Orbitrap Velos) are listed. A cut-off of < -1.25 or > 1.5 FC was used to identify regulated proteins.

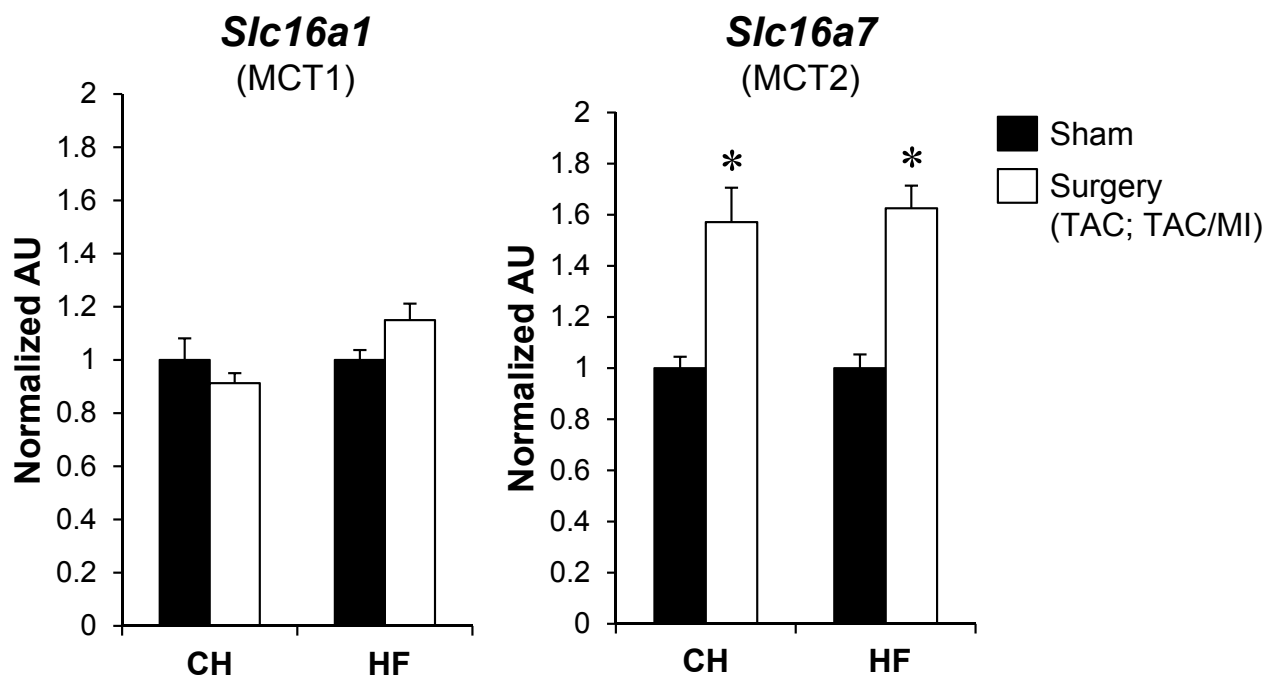


Supplemental Figure 1. Reduced palmitate oxidation in the hypertrophied heart. The relative contribution of palmitate to TCA carbon cycle flux is shown for CH and sham-operated controls. Data are shown as mean \pm SEM (n=6, Sham and 7, CH).

Plasma Ketones



Supplemental Figure 2. Ketogenic diet results in an increase in circulating ketone bodies. Plasma ketone levels measured in wild-type C57BL/6J mice fed a ketogenic diet for 4 weeks compared to control diet fed mice. Bars represent mean \pm SEM values (n=6-7 per group) * $p < 0.05$.



Supplemental Figure 3. *Slc16a1* expression is induced in the hypertrophied and failing mouse heart. *Slc16a1* (MCT1) and *Slc16a7* (MCT2) mRNA levels in cardiac ventricular tissue from mice 4 weeks after sham, TAC (CH), or TAC/MI (HF) surgeries. Samples were taken 24 h (Fasted) after feeding. Expression is normalized to *Rplp0* (36B4). Bars represent mean \pm SEM values (n=6-21 per group) *p<0.05.

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