SUPPLEMENTAL MATERIAL

"Young at Heart":

Regenerative Potential Linked to Immature Cardiac Phenotypes

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Extended Methods

RNA extraction, reverse transcription and quantitative real-time PCR

Single mouse hearts or pools of two zebrafish hearts were homogenized in QIAzol Lysis reagent using FastPrep Tubes, Lysing Matrix D (MP Biomedicals Europe, France) and total RNA was subsequently isolated with the miRNeasy mini RNA extraction kit (QIAgen, Germany) (1). For gene expression analysis, 200ng RNA was reverse transcribed using the VILO Superscript cDNA synthesis kit (Life Technologies). The qPCR reaction mix was comprised of 2.5µl TaqMan® Universal PCR Master Mix, No AmpErase® UNG (Life Technologies, UK), 0.25µl of the respective FAM-labelled Taqman assay (Life Technologies, UK), and 2.25µl diluted RT product corresponding to 1ng RNA. MiRNAs (50 ng input material) were reverse transcribed using the TaqMan® MicroRNA Reverse Transcription Kit, Megaplex rodent primers Pool A (Life Technologies, UK). 2.25µl diluted RT product corresponding to 0.225ng RNA were used for qPCR. QPCRs were run on a ViiA7 qPCR machine (Life Technologies, UK) and the $\Delta\Delta$ Ct method was used to determine the relative quantification of targets. Taqman assays used for qPCR are listed in **Supplementary Table 1.**

Protein extraction and immunoblot analysis

Hearts were weighed and powdered in liquid nitrogen and crushed using a mortar and pestle. Ice-cold lysis buffer, at a ratio of 100µl per 10mg of tissue was added. The lysis buffer consisted of a combination of 100mM Tris-HCl pH 7.4, 1% Triton X-100, protease and phosphatase inhibitors (Sigma, UK) (2). Samples were centrifuged at 14,000g for 10 minutes at 4 °C. The soluble and non-soluble fractions were separated and added to Laemmli buffer and denatured at 98°C for 5min before being briefly

centrifuged, this after quantification of protein concentration using the BCA assay (Thermo Scientific, USA). 10µg of protein were loaded per lane, separated on 4-12% gradient gels (Life Technologies, UK) at 130-170V for 100-120min in NuPage MOPS SDS Running Buffer (Life Technologies, UK) diluted with distilled water. Subsequently, the samples were transferred to nitrocellulose membranes (GE Healthcare, USA) in ice-cold transfer buffer (25mM Tris Base and 200mM Glycine dissolved in 20% methanol) (3). Next, membranes were blocked in 5% milk in PBS (PBS, Lonza, UK) with 0.1% Tween (PBST) for 1hr on a shaker at room temperature. After a brief wash in PBST, they were incubated overnight with primary antibodies in 5% BSA (Sigma Aldrich, UK) with 0.01% sodium azide (Sigma Aldrich, UK) (Table 2). The following day, after 3 washes in PBST, 15 min each, the membranes were incubated for 1hr at room temperature with the HRP-labelled secondary antibody diluted in 5% milk in PBST, according to the source of the primary antibody. The membranes were washed in PBST 3 times for 15 min and developed using ECL western blotting detection reagent using X-ray films (FUJIFILM, USA). Immunoblots were quantified by densitometry using Image-J software. The following primary antibodies were purchased from Abcam, UK: monoclonal Troponin T (ab130003) and polyclonal nebulette (ab99420) both used at 4 µg/ml. Monoclonal myozenin 2 (sc-377359) from Santa Cruz was used at 1:100 dilution. Immunoreactivity was visualized with horseradish peroxidase-linked rabbit anti-mouse or swine anti-rabbit (DAKO) at 1:2000.

Difference in-gel electrophoresis

The heart tissue was homogenized in lysis buffer (9.5M urea, 2% w/v CHAPS, 1% w/v DTT and 0.8% Pharmalyte pH3-10) with Lysing matrix D (MP Biomedicals, Solon, USA) using FastPrep 120 (Krackeler Scientific Inc, USA) (4). Samples were

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further processed using ReadyPrep 2D Cleanup kit (Bio-Rad, UK). The samples were then resuspended in DIGE lysis buffer (8M urea, 4% w/v CHAPS, 30mM TrisHCl, pH 8.5). Protein samples were labelled with Cy3 or Cy5 fluorescent dye (DIGE Fluor minimal dyes, GE Healthcare, USA) and mixed with Cy2-labelled internal standard. Following overnight rehydration, IPG dry strips (pH3-10, nonlinear, 18cm, GE Healthcare, USA) were focused on the IPGphor for 29kVhr. The strips were subsequently reduced in equilibration solution (6M urea, 2% w/v SDS, 30% w/v glycerol, 50mM Tris, pH 8.8) with 10mg/mL DTT for 15min, and alkylated in equilibration solution with 48mg/mL iodoacetamide for another 15min before put on top of large format 12% polyacrylamide gels. SDS-PAGE was performed in Ettan Dalt six electrophoresis system (GE Healthcare, USA) at 30W/gel. The gels were then scanned in Ettan DIGE imager (GE Healthcare, USA) and the images were analysed using DeCyder version 7.0 (GE Healthcare, USA). Differentially expressed spots of interest were manually excised for further MS analysis.

Liquid chromatography tandem mass spectrometry (LC-MS/MS)

Tryptic in-gel digestion was performed overnight using the Investigator ProGest (DigiLab,USA) robotic digestion system (5). The digested peptide solution was dried using a SpeedVac concentrator (Thermo Fisher Scientific, UK) and resuspended in 20µl of 0.1% formic acid. The samples were separated by nano-flow HPLC on a reverse phase column (C18 PepMap100, 3µm, 100 Å, 25cm; Thermo Scientific, USA) before injected to an LTQ Orbitrap XL mass spectrometer (Thermo Scientific, USA). Spectra were collected from the mass analyzer (Orbitrap) using full ion scan mode over the m/z range 450-1600 followed by data-dependent MS/MS scans on 6 most abundant ions with dynamic exclusion. Database searches were performed using Mascot version 2.3.01 against the IPI mouse database version 3.87 (59534 entries)

and the IPI zebrafish database version 3.86 (40470 entries), or UniProt/SwissProt mouse database version 2013_08 (16619 entries), with the following parameters: precursor tolerance 10ppm, fragment tolerance 0.8Da, carbamidomethylation on cysteines as fixed modification and oxidation on methionine as variable modification, 2 missed cleavages were allowed. Scaffold software (Version 4.3.2, Proteome Software inc, Portland, OR) was then used to validate MS/MS based peptides and protein identification and assign spectral counts across the individual samples. Protein identifications were accepted if they could be established at greater than 99.0% probability with at least 2 unique peptides.

Statistical and bioinformatic analysis

Principal component analysis (PCA) was used to visualize multidimensional DIGE data using DeCyder version 7.0 (GE Healthcare, USA). Significance of differential transcript or protein expression was assessed using unpaired Student's t-test with unequal variance. Results were given as means \pm SD. P-values ≤ 0.05 were considered significant.

Online References

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- 4. Yin X, Dwyer J, Langley S, Mayr U, Xing Q, Drozdov I, et al. Effects of perhexiline-induced fuel switch on the cardiac proteome and metabolome. J Mol Cell Cardiol 2013;55:27-30.
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Gene	Species	Taqman Assay ID
18S	Mouse	Mm03928990_g1
Myh6	Mouse	Mm00440359_m1
Myh7	Mouse	Mm01319006_g1
Myh7b	Mouse	Mm01249941_m1
Myl2	Mouse	Mm00440384_m1
Myl3	Mouse	Mm00803034_m1
Myl7	Mouse	Mm01183005_g1
tnnc1	Mouse	Mm00437115_g1
tnnc2	Mouse	Mm01243775_g1
tnni1	Mouse	Mm00502426_m1
tnni2	Mouse	Mm00437157_g1
tnni3	Mouse	Mm00437164_m1
tnnt1	Mouse	Mm00449089_m1
Tnnt2	Mouse	Mm01290256_m1
Tnnt3	Mouse	Mm01137842_g1
Tnnt3	Mouse	Mm01268863_m1
miR-1	Mouse/Zebrafish	2222
miR-499	Mouse/Zebrafish	1352
miR-133a	Mouse/Zebrafish	2246
miR-133b	Mouse/Zebrafish	2247
18S	Zebrafish	Hs99999901_s1
myh6	Zebrafish	Dr03112899_s1
myl2	Zebrafish	Dr03142386_m1
myl7	Zebrafish	Dr03105697_m1
tnnc1a	Zebrafish	Dr03106128_mH
tnnc1b	Zebrafish	Dr03089208_g1
tnnc2	Zebrafish	Dr03432983_g1
tnni1al	Zebrafish	Dr03146635_m1

Supplementary Table 1. Taqman assays used for qPCR.

tnni1b	Zebrafish	Dr03090193_m1	
tnni2a.1	Zebrafish	Dr03102546_m1	
tnni2b.1	Zebrafish	Dr03083605_g1	
tnnt1	Zebrafish	Dr03201591_s1	
tnnt2a	Zebrafish	Dr03131740_g1	
tnnt2d	Zebrafish	Dr03090816_g1	
tnnt3a	Zebrafish	Dr03150378_g1	
tnnt3b	Zebrafish	Dr03086581_m1	
vmhc/myh7bb	Zebrafish	Dr03431115_g1	
zgc:66286	Zebrafish	Dr03113522_m1	

Supplementary Table 2. Identifications of selected protein spots of adult mice hearts.

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G17NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrialIPI0030888279,778100.0%20285130.1G18Stress-70 protein, mitochondrialIPI0013390373,529100.0%10111820.3G18Heat shock cognate 71 kDa proteinIPI0032335770,873100.0%9121818.4G19Stress-70 protein, mitochondrialIPI0013390373,529100.0%11132318.9G20Stress-70 protein, mitochondrialIPI0013390373,529100.0%2234.3G20Stress-70 protein, mitochondrialIPI0013390373,529100.0%2234.3G20Heat shock cognate 71 kDa proteinIPI0013390373,529100.0%2234.3G20Heat shock cognate 71 kDa proteinIPI0013390373,529100.0%2234.3G21Serum albuminIPI001356067,943100.0%14152320.4G22Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrialIPI0013360367,943100.0%6101810.4G23SerotransferrinIPI0013978876,724100.0%691512.2
G18Stress-70 protein, mitochondrialIPI0013390373,529100.0%10111820.2G18Heat shock cognate 71 kDa proteinIPI0032335770,873100.0%9121818.4G19Stress-70 protein, mitochondrialIPI0013390373,529100.0%11132318.9G20Stress-70 protein, mitochondrialIPI0013390373,529100.0%2234.3G20Heat shock cognate 71 kDa proteinIPI003235770,873100.0%2234.3G20Heat shock cognate 71 kDa proteinIPI003235770,873100.0%2234.3G20Heat shock cognate 71 kDa proteinIPI0013160568,693100.0%14152320.4G21Serum albuminIPI001356067,943100.0%6101810.4G22Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrialIPI0013978876,724100.0%691512.2G23SerotransferrinIPI0013978876,724100.0%691512.2
G18Heat shock cognate 71 kDa proteinIPI0032335770,873100.0%9121818.4G19Stress-70 protein, mitochondrialIPI0013390373,529100.0%11132318.9G20Stress-70 protein, mitochondrialIPI0013390373,529100.0%2234.3G20Heat shock cognate 71 kDa proteinIPI0032335770,873100.0%2234.3G20Heat shock cognate 71 kDa proteinIPI003235770,873100.0%2232.9G21Serum albuminIPI0013165568,693100.0%14152320.4G22Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrialIPI0013360667,943100.0%6101810.4G23SerotransferrinIPI0013978876,724100.0%691512.2
G19 Stress-70 protein, mitochondrial IPI00133903 73,529 100.0% 11 13 23 18.5 G20 Stress-70 protein, mitochondrial IPI00133903 73,529 100.0% 2 2 3 4.3 G20 Heat shock cognate 71 kDa protein IPI00323357 70,873 100.0% 2 2 3 2.9 G21 Serum albumin IPI00131695 68,693 100.0% 14 15 23 20.4 G22 Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial IPI00133606 67,943 100.0% 6 10 18 104.4 G23 Serotransferrin IPI00139788 76,724 100.0% 6 9 15 12.2
G20 Stress-70 protein, mitochondrial IPI00133903 73,529 100.0% 2 2 3 4.3 G20 Heat shock cognate 71 kDa protein IPI00323357 70,873 100.0% 2 2 3 2.5 G21 Serum albumin IPI00131695 68,693 100.0% 14 15 23 20.4 G22 Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial IPI0013360 67,943 100.0% 6 10 18 10.4 G23 Serotransferrin IPI00139788 76,724 100.0% 6 9 15 12.2
G20 Heat shock cognate 71 kDa protein IPI00323357 70,873 100.0% 2 2 3 2.5 G21 Serum albumin IPI00131695 68,693 100.0% 14 15 23 20.4 G22 Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial IPI00133660 67,943 100.0% 6 10 18 10.4 G23 Serotransferrin IPI00139788 76,724 100.0% 6 9 15 12.2
G21 Serum albumin IPI00131695 68,693 100.0% 14 15 23 20.4 G22 Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial IPI00153660 67,943 100.0% 6 10 18 10.4 G23 Serotransferrin IPI00139788 76,724 100.0% 6 9 15 12.2
G22 Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial IPI00153660 67,943 100.0% 6 10 18 10.4 G23 Serotransferrin IPI00139788 76,724 100.0% 6 9 15 12.2
G23 Serotransferrin IPI00139788 76,724 100.0% 6 9 15 12.2
G24 Serotransferrin IPI00139788 76.724 100.0% 16 21 37 31.1
G25 Serotransferrin IPI00139788 76.724 100.0% 14 15 26 24.0
G26 Aconitate hydratase, mitochondrial IPI00116074 85,466 100.0% 24 33 58 32.4
G27 Succinate dehydrogenase [ubiquinone] flavoprotein subunit. mitochondrial IPI00230351 72.586 100.0% 18 22 35 31.6
G28 Unidentified
G29 Dihydrolioovl dehydrogenase, mitochondrial IPI00874456 54.599 100.0% 3 3 3 5.7
G29 Isoform M1 of Pyruvate kinase isozymes M1/M2 IP100845840 57.986 100.0% 2 2 4 3.4
G30 Isoform M1 of Pyruvate kinase isozymes M1/M2 IPI00845840 57,986 100.0% 14 18 34 35.2
G31 Trifunctional enzyme subunit beta, mitochondrial IPI00115607 51,388 100.0% 18 23 37 37.9
G32 Alpha-englase IPI00462072 47.142 100.0% 6 8 17 27.6
G33 Beta-enolase IPI00228548 47.026 100.0% 6 8 13 24.2
G34 Malate debudrogenase, mitochondrial IPI00323592 35.612 100.0% 8 9 16 43.6
G35 Succinvl-CoA ligase [GDP-formine] subunit alpha. mitochondrial IPI0040642 36.155 100.0% 3 3 6 11.6
G36 Aldose reductase IPI00223757 35 733 100.0% 10 12 19 31 6
G37 Myosin light chain 3 IPI00133392 22.422 100.0% 2 2 3 20.6
G37 Hydroxyacyl-cenzyme A dehydrogenase mitochondrial IPI00121105 34 465 100 0% 3 3 3 13 4
G38 Hydroxyacyl-cenzyme A dehydrogenase, mitochondrial IPI00121105 34,465 100.0% 5 5 7 13.7
G39 Electron transfer flavoorotein subunit beta IPI00121440 27.623 100.0% 14 18 31 55.7
G40 Peroxiredoxin-1 IPI00121788 22 178 100 0% 7 8 15 33 2
G41 ATP synthase subunit 0, mitochondrial IPI00118986 23,364 100.0% 4 5 12 22 1
G42 Superovide dismutase [Mn] mitochondrial [PI00109109 24 603 100.0% 5 8 13 25 7
G43 Alpha-rrystallin 8 chain 1900/05/05 20,000 5 6 7 14 297
G44 Nucleoside diphosphate kinase B [I] 00132274 20,003 100.0% 0 / 14 23/
G45 Mixediaha [PI002760 17 070 100.0% 4 5 0 37 0
G46 Mixadiohin [PI00230760 17,070 100.0% 14 5 5 57.0
G47 Hemotobin Joha adult chain 2 Dio 14 C 0 14 C 0 16 C 0 17,010 100.0% 11 14 C 0 004
G48 Cytochrome c oxidase subunit 6B1

Supplementary Table 3. Identifications of selected protein spots of adult zebrafish hearts.

Bit Candia: myoni light chain 2 PHOAMB18/9 50,001 10,006 6 8 1 88.4 Bit Candia: myoni light chain 2 PHOAMB18/9 50,007 110,006 11 18 28.4 43.8 Bit Candia: myoni light chain 1 PHOAMB18/9 50,007 11 18 24 42.8 52.8 Bit Candia: myoni light chain 1 PHOAMB18/9 50,007 12 2 4.4 65.8 Bit Statis Additional 1 PHOAMB18/9 50,507 100,005 4 4 6 2.5 Bit Statis Additional 1 PHOAMB18/9 50,507 100,005 4 4 6 2.5 Bit Statis Additional 1 PHOAMB18/9 50,507 100,005 4 4 7 4.2 Bit Candia: myoni light chain 2 Statis Additional 1 PHOAMB18/9 50,507 100,005 4 4 7 4.2 Bit Statis Additional 1 PHOAMB18/9 50,407	Spot	Protein name	Accession Number	Mw (Da)	Protein identification probability	#unique peptides	#unique spectra	#total spectra	Percentage sequence coverage
N21 Cardia: myoin light chain 2 100.08 9 1.3 2.6 4.3. B3 Cardia: myoin light chain 1 100.08 1.0 1.0 1.0 2.6 2.8. B30 Cardia: myoin light chain 1 100.08 7.1 1.0 2.6 2.8. 1.00.08 7.1 1.0 5.0 2.6 2.8. 2.0.0 4.6 2.0 3.0 4.6 2.0 3.0 4.6 2.0 3.0 4.6 2.0 3.0 4.6 2.0 3.0 4.0 2.0 3.0 4.0 4.0 2.0 3.0 4.0 4.0 2.0 3.0 4.0 4.0 2.0 3.0 4.0 4.0 2.0 3.0 4.0 4.0 2.0 3.0 4.0 4.0 2.0 3.0 4.0 4.0 2.0 3.0 4.0 4.0 2.0 3.0 4.0 4.0 2.0 3.0 4.0 4.0 2.0 3.0 4.0 4.0 4.0 4.0 4.0 4.0 4.0 4.0 4.0 4.0 4.0 4.0 4.0	R01	Cardiac myosin light chain 2	IPI00481849	19,021	100.0%	6	8	15	38.4%
B33 Cardiac myoin light chain 1 B38 B36 Cardiac myoin light chain 1 B38 B38 Cardiac myoin light chain 1 B38 B38 Cardiac myoin light chain 1 B38	R02	Cardiac myosin light chain 2	IPI00481849	19,021	100.0%	9	13	25	45.3%
B01 Cardiac myosh light chan 1 100 <	R03	Cardiac myosin light chain 2	IPI00481849	19,021	100.0%	11	18	26	62.8%
NBS Cardiac myosh light than 1 Dit Notes	R04	Cardiac myosin light chain 1	IPI00616566	21,865	100.0%	11	16	24	56.6%
Note Indextified INDEX	R05	Cardiac myosin light chain 1	IPI00616566	21,865	100.0%	15	27	44	65.8%
807 Cybachrone contase submit Vas 19.00% 2 2 3 84.84 808 Fitt stating freid mangen and submit Vas 10.00% 4 4 7 42.84 809 Fitt stating freid mangen and submit Vas 10.00% 4 4 7 42.84 809 Fitt stating freid mangen and submit Vas 10.00% 2 4 6 1.84 801 Cardiac machine submit Vas 10.00% 4 1.6 4 4.8 4.9 <td< td=""><td>R06</td><td>Unidentified</td><td>-</td><td>-</td><td>-</td><td>-</td><td>-</td><td>-</td><td>-</td></td<>	R06	Unidentified	-	-	-	-	-	-	-
R88 Faty and binding motent 3, mance and beart. PP00091514 14,882 11,800,70 4 4 6 6,238 R10 NADM dehydrogenses (Ubiquinone) Fe S protein 3 PP00050456 29,484 100,07 2 4 7 538 R11 Carlia convening dr. dan 1 PP00050456 29,484 100,07 4 1 5 358 R13 Adf eynthase values bein PP00050456 29,484 100,07 4 1 5 358 R13 Adf eynthase values bein PP00050403 61,197 100,07 1 4 6 5 35 R14 Hest shock 60/0 protein (Chaperonin) PP00050400 71,37 100,07 1 1 2 3 2 3 2 3	R07	Cytochrome c oxidase subunit Vaa	IP100488350	15,897	100.0%	2	2	3	18.4%
190 Hotors H4 11.368<	R08	Fatty acid binding protein 3, muscle and heart	IPI00491514	14,882	100.0%	4	4	6	26.3%
NADP dehydrogenase (Ublguinoe) Fe Sprichs 3 MADP dehydrogenase (Ublguinoe) Fe Sprichs 3 MP (M05556 22.84 100.0% 3 4 6 6.88 NADP dehydrogenase (Ublguinoe) Fe Sprichs 3 AP (M1556 10.00% 3 4 6.1 8.88 NADP dehydrogenase (Ublguinoe) Fe Sprichs 3 NADP dehydrogenase (Ublguinoe) Fe Sprichs 1 NADP dehydrogenase (Ublguinoe) Fe Sprichs 3 NADP dehydrogenase (Ublguinoe) Fe Sprichs 1 NADP d	R09	Histone H4	IP100482809	11,368	100.0%	4	4	7	40.8%
R11 Cardiac myosin light chain 1 PIODE SEGS 21,865 100,078 3 4 6 6 2	R10	NADH dehydrogenase (Ubiquinone) Fe-S protein 3	IPI00503659	29,484	100.0%	2	4	7	9.8%
III 2 Applipportein A (paperatin) PI0095800 Sol.40 U00.75 Sol.50	R11	Cardiac myosin light chain 1	IPI00616566	21,865	100.0%	3	4	6	14.8%
R13 ATP synthase subunit beta IPPO058905 56,475 10,00% 4 5 6 7 R14 Heat shock 600 protein 1 (Chaperonin) IPPO058003 61,197 100,00% 17 21 6 14,00 R15 Genoin A IPPO058003 61,197 100,00% 17 21 30 15 26 7,574 R17 Genoin A IPPO058004 61,007 24,313 100,00% 18 10 20 12,225 R18 Mohd dehydroganase (Ubquinong) fe S protein 1 IPPO050046 7,433 100,00% 21 24 2 25 27 R20 NADH dehydroganase (Ubquinong) fe S protein 1 IPPO050046 7,433 100,00% 21 24 2 27 28 R20 NADH dehydroganase (Ubquinong) fe S protein 1 IPPO050046 7,433 100,00% 13 13 23 24 24 25 27 R20 NADH dehydroganase (Ubquinon) fe S protein 1 IPPO050046 7,433 100,00% 13 13 23 24 24 25 25	R12	Apolipoprotein A (apoa1b)	IP100994508	30,140	100.0%	9	12	22	26.1%
R14 Heat shock 60k0 protein 1 (Chaperonin) IPID058003 61,137 100.0% 14 61 21 34 44.7 R15 Heat shock 60k0 protein 1 (Chaperonin) IPID058003 72,714 100.0% 4 4 7 57.7 R16 IPID016665 72,713 100.0% 15 15 26 32.2 R18 NADF dehydrogenase (Ubiquinone) Fes protein 1 IPID016615 72,413 100.0% 13 22 4 26.3 30.00 R19 NADF dehydrogenase (Ubiquinone) Fes protein 1 IPID0506167 72,413 100.0% 13 16 24 2.7 8 R19 NADF dehydrogenase (Ubiquinone) Fes protein 1 IPID0506167 72,413 100.0% 13 16 2.4 2.7 75.3 R20 Acontase 2, michondrial IPID0508167 2.4862 100.0% 18 9 <td>R13</td> <td>ATP synthase subunit beta</td> <td>IPI00897805</td> <td>56,476</td> <td>100.0%</td> <td>4</td> <td>5</td> <td>5</td> <td>20.2%</td>	R13	ATP synthase subunit beta	IPI00897805	56,476	100.0%	4	5	5	20.2%
R15 Heat shock 600 protein 1 (Chaperonin) P100022002 P100022002 P27,174 P100022002 P27,174 P100022002 P27,174 P100022002 P27,174 P100020020 P27,174 P100020020 P27,174 P20002002 P27,174 P200020020 P27,174 P200020020 P27,174 P200020020 P200020000 P200020000 P200020000 P200020000 P2000200000 P2000200000 P2000200000 P20002000000 P2000200000000000000000000000000000000	R14	Heat shock 60kD protein 1 (Chaperonin)	IPI00508003	61,197	100.0%	14	16	24	24.0%
R16 Uncharacterized protein IPI001062805 R17, R2 IDI0052805 R17, R2 IDI00520056 R17, R2 IDI0050046 R17, R2	R15	Heat shock 60kD protein 1 (Chaperonin)	IPI00508003	61,197	100.0%	17	21	36	41.7%
R17 Gesolin A IPI0016654 80,625 10.00% 88 10 20 12.22 R18 MADH derbydrogenset (Ubiquinone) F-5 protein 1 IPI0056127 22.122 10.00% 12 24 21.22 R18 Ventricular myoin heavy chain-like protein IPI0056127 22.4172 10.00% 13 16 24 72.84 R19 Ventricular myoin heavy chain-like protein IPI0050666 79.433 10.00% 3 3 5 4.14 R21 NADH derbydrogenset (Ubiquinone) F-5 protein 1 IPI0050666 79.433 10.00% 8 9 17 19.33 R23 Accontase 2, mitchchondrial IPI0048652 84.862 10.00% 8 9 17 19.33 R24 Acontase 2, mitchchondrial IPI0048652 84.862 10.00% 18 18 20 23.72 23.72 23.72 23.72 23.72 23.72 23.72 23.72 23.72 23.72 23.72 24.72 24.72 24.72 24.72 24.72 24.72 24.72 24.72 24.72 24.72 24.72 <td>R16</td> <td>Uncharacterized protein</td> <td>IPI00628054</td> <td>72,714</td> <td>100.0%</td> <td>4</td> <td>4</td> <td>7</td> <td>5.7%</td>	R16	Uncharacterized protein	IPI00628054	72,714	100.0%	4	4	7	5.7%
BADH dehydrogenase (Ubiquinone) fes protein 1 PI005012 72,433 91,000% 91 91 94,33 91,000% 92 94 91,000% 92 94	R17	Gesolin A	IPI01016654	80,625	100.0%	8	10	20	19.2%
R13 Ventricular mycsin heavy chain-fike protein IPI0056167 224,172 100.0% 12 24 43 424.8% R19 Ventricular mycsin heavy chain-fike protein IPI0056167 224,172 100.0% 13 16 24 74.8 R19 Ventricular mycsin heavy chain-fike protein IPI005066 79.43 100.0% 23 14 74.8 75.7 R21 ADDH dehydrogenase (Ubiquinone) Fe-Sprotein 1 IPI005066 79.43 100.0% 8 9 17 19.3 R22 Aconitase 2, mitochondrial IPI0048352 84.862 100.0% 18 10 19 19.3 12.8	R18	NADH dehydrogenase (Ubiquinone) Fe-S protein 1	IPI00500466	79,433	100.0%	15	15	26	21.2%
R19 MADH dehydrogenase (Ubiquinne) Fe-Sprotein 1 IPI00500466 79.433 100.0% 12 24 44 27.88 R20 MADH dehydrogenase (Ubiquinne) Fe-Sprotein 1 IPI00500466 79.433 100.0% 21 24 44 27.87 R21 MADH dehydrogenase (Ubiquinne) Fe-Sprotein 1 IPI00500466 79.433 100.0% 21 24 44 25.77 R22 Acetyltransferase component of pryvate dehydrogenase (ubiquinne) Fe-Sprotein 1 IPI0043210 69.208 100.0% 8 8 9 17 93.37 R23 Aconitase 2, mitochondrial IPI0043102 84.862 100.0% 13 15 27 67.85 R25 Aconitase 2, mitochondrial IPI0043105 24.862 100.0% 18 8 10 92.22 27.353 R26 Aconitase 2, mitochondrial IPI0043105 24.862 100.0% 18 28.4 19.86 R27 Aconitase 2, mitochondrial IPI0043105 24.862 100.0% 18 24.9 24.9 24.9 24.9 24.9 24.9 24.9 24.9 24	R18	Ventricular myosin heavy chain-like protein	IPI00616127	224,172	100.0%	22	26	43	10.6%
F19 Ventricular myosin heavy chain-like protein IP10051046 IP24, 122 IP24, 122 IP24, 122 IP24, 122 IP24, 122 IP24, 122 IP24, 124 IP24 IP24 <	R19	NADH dehydrogenase (Ubiquinone) Fe-S protein 1	IPI00500466	79,433	100.0%	19	23	41	24.8%
NADH dehydrogenase (Ubiquinone) Fe-S protein 1 IPI0050466 79,433 100.0% 21 24 44.18 NADH dehydrogenase (Ubiquinone) Fe-S protein 1 IPI0050466 79,433 100.0% 4 6 12 97,33 NADH dehydrogenase (Ubiquinone) Fe-S protein 1 IPI00504566 84,662 100.0% 4 6 12 97,33 R2A Accinitase 2, mitochondrial IPI00504566 84,662 100.0% 13 15 16 10 12 12,33 R2A Aconitase 2, mitochondrial IPI00501169 84,462 100.0% 13 14 24 <	R19	Ventricular myosin heavy chain-like protein	IPI00616127	224,172	100.0%	13	16	24	7.8%
R21 NADH dehydrogenase (Ubiquinone) Fe S protein 1 IPI003 IPI0042 IPI00423162 IPI00423162 <thipi00423162< th=""> <thipi00423162< th=""> I</thipi00423162<></thipi00423162<>	R20	NADH dehydrogenase (Ubiquinone) Fe-S protein 1	IP100500466	79,433	100.0%	21	24	44	25.7%
R22 Acetyttransfersae component of pruvate dehydrogenase complex IPI0043326 89,208 100.0% 8 9 72 93.38 R24 Aconitase 2, mitochondrial IPI0043362 84,862 100.0% 8 9 72 73.53 R25 Aconitase 2, mitochondrial IPI0043362 84,862 100.0% 15 18 30 29.2% R27 Transferrin IPI0043362 84,862 100.0% 15 18 30 29.2% R27 Transferrin IPI0043362 84,862 100.0% 15 84 8 4 49.35 R20 Indentified	R21	NADH dehydrogenase (Ubiquinone) Fe-S protein 1	IP100500466	79,433	100.0%	3	3	5	4.1%
R23 Acontase 2, mitochondrial IPI00433552 84,862 ID0.0% 8 9 1 9 13.78 R25 Acontase 2, mitochondrial IPI00433552 84,862 ID0.0% 13 15 16 20 25.58 R25 Acontase 2, mitochondrial IPI00433552 84,862 ID0.0% 13 15 16 20 25.58 R27 Transferrin IPI00501169 54,408 ID0.0% 8 8 10 8.0 12 14 15.58 15.58 R30 Fibringen, B beta polyneptide IPI00501169 54,408 ID0.0% 8 8 10 8.1 2.7 2.7.38 R31 Elongation factor 1-alpha IPI00492077 47,473 ID0.0% 8 9 17 2.7.38 R32 Enclase IPI00492077 47,473 ID0.0% 8 9 17 2.7.38 R33 Bitoringen, B beta polyneptide IPI00492077 47,473 ID0.0% 8 9 17 2.7.38 R33 Bitoringen, B beta polyneptide IPI00492077 <td>R22</td> <td>Acetyltransferase component of pyruvate dehydrogenase complex</td> <td>IPI00492140</td> <td>69,208</td> <td>100.0%</td> <td>4</td> <td>6</td> <td>12</td> <td>9.7%</td>	R22	Acetyltransferase component of pyruvate dehydrogenase complex	IPI00492140	69,208	100.0%	4	6	12	9.7%
R2A Acontase 2, mitochondrial IPI00483652 84,862 ID0.0% 10	R23	Aconitase 2, mitochondrial	IPI00483652	84,862	100.0%	8	9	17	19.3%
R25 Aconitase 2, mitochondrial IPI00483652 84,862 100.0% 13 15 15 18 02 25.3 R26 Aconitase 2, mitochondrial IPI00483652 84,862 100.0% 12 14 29.2% R27 Transferrin IPI00501169 54,408 100.0% 8 8 1 19.6% R30 Fibrinogen, B beta polypeptide IPI00501169 54,408 100.0% 6 8 9 17.2 73.533 R31 Elongation factor 1-alpha IPI00501169 54,408 100.0% 6 8 9 17 23.0% R32 beta-enolase IPI00493877 47.473 100.0% 8 9 17 23.0% R33 beta-enolase IPI00493877 47.473 100.0% 8 11 21 32.0% R34 Giyceraldehydrogenase IPI0049773 35.744 100.0% 8 12 24.3% R34 Alle dehydrogenase IPI0049773 35.740 100.0% 4 4 7 14.7% R34	R24	Aconitase 2, mitochondrial	IPI00483652	84,862	100.0%	10	10	19	18.7%
R25 Aconitase 2, mitochondrial IPI0043822 84,82 10.0% 12 14 20 22.3.1% R28 Unidentified 7.5.33 100.0% 16 8.8 19.6% R29 Fibringer, B beta polypeptide 100051169 54,408 100.0% 6 8 13 20.1% R31 Elongation factor 1-alpha 100051169 54,408 100.0% 6 8 13 20.3% R31 Elongation factor 1-alpha 100048321 47,075 100.0% 6 8 13 20.3% R32 beta-enolase 100048377 47,473 100.0% 9 14 23 24 24 28 37.4% R33 beta-enolase 100049977 47,473 100.0% 8 11 21 24 28 24 27 28 27 28 27 28 23 24 24 28 24 24 24 28 24 24 24 24 24 24 24 24 24 24 24 24 2	R25	Aconitase 2, mitochondrial	IPI00483652	84,862	100.0%	13	15	27	26.5%
R22 Transferrin IPI0097272 73,533 100.0% 12 14 22 22. R30 Hibrinogen, B beta polypeptide IPI00501169 54,408 100.0% 8 8 14 13.65 R30 Fibrinogen, B beta polypeptide IPI00501169 54,408 100.0% 6 8 13 20.1% R31 Elongation factor 1-alpha IPI00483215 47,075 100.0% 6 8 13 20.1% R32 beta-enolase IPI00490877 47,473 100.0% 9 14 22 23.8 R33 beta-enolase IPI00490877 47,473 100.0% 8 11 21 24.0% R34 Glyceralehyde-3-phosphate dehydrogenase IPI00490877 47,473 100.0% 8 11 21 23.2 24.0% R34 Glyceralehyde-3-phosphate dehydrogenase IPI00490877 47,473 100.0% 15 5 10.2 23.2 24.0% R34 Glyceralehyde-3-phosphate dehydrogenase IPI00491775 35,764 100.0% 14 4 7	R26	Aconitase 2, mitochondrial	IPI00483652	84,862	100.0%	15	18	30	29.2%
R28 Unidentified I I I I I I R29 Fibrinogen, B beta polypeptide IPI00501169 54,408 100.0% 16 20 34 37.5% R31 Elongation factor 1-alpha IPI00431240 50,048 100.0% 6 8 13 20.1% R32 Enolase IPI0043225 47,075 100.0% 6 8 24.2% R33 beta-enolase IPI0049877 47,473 100.0% 14 22 24.0% R33 beta-enolase IPI00497753 35,784 100.0% 8 11 32.4% R34 Glyceraldehyde-3-phosphate dehydrogenase IPI00497753 35,784 100.0% 8 12 23.2% R35 Voltage-dependent anion channel 3 IPI0049720 33,620 100.0% 4 4 7 13.7% R36 Malate dehydrogenase IPI0049720 35,420 100.0% 4 4 7 13.4% R38 Malate dehydrogenase IPI0049755 35,420 100.0% 5 5 <	R27	Transferrin	IPI00972722	73,533	100.0%	12	14	22	23.1%
R2P Fibrinagen, B beta polyapetide 1P100501169 54,408 100.0% 8 8 14 19.0% R3D Fibrinagen, B beta polyapetide 1P100511240 50,048 100.0% 66 8 13 37.5% R31 Elongation factor 1-alpha 1P100432121 47,075 100.0% 8 9 17 27.3% R32 beta-enolase 1P10049077 47,473 100.0% 14 22 38 24.0% R33 beta-enolase 1P10049077 47,473 100.0% 14 22 38 37.4% R34 Glyceraldehydre-3-posphate dehydrogenase 1P10049077 47,473 100.0% 14 22 38 7.408 R35 Voltage-dependent anion channel 3 1P100497720 35,784 100.0% 15 23 32 22.8% R36 Four ad a half LIM domains protein a 1P100497720 39,095 100.0% 4 4 7 13.4% R38 Four ad a half LIM domains protein a 1P100491775 55,402 100.0% 5 5 9 10.7%	R28	Unidentified	-	-	-	-	-	-	-
R30 Fibrinagen, B beta polypeptide IPI00511240 S4,408 100.0% 6 20 34 37.5% R31 Elionagtion factor 1-alpha IPI00512240 S0,048 100.0% 6 8 13 20.1% R32 Enolase IPI00438215 47,075 100.0% 8 9 17 27.3% R33 beta-enolase IPI00490877 47,473 100.0% 14 22 38 37.4% R34 Glyceraldehyde-3-phosphate dehydrogenase IPI00490877 47,473 100.0% 8 11 21 32.4% R35 Voltage-dependent anion channel 3 IPI00497703 35,784 100.0% 7 12 23 22.6% R36 Malate dehydrogenase IPI0049720 35,420 100.0% 4 4 7 13.4% R37 Malate dehydrogenase IPI00512157 35,420 100.0% 4 4 7 14.3% R38 Four and a haf Liff Und omains protein a IPI00491720 35,420 100.0% 8 11 19 76.2% R3	R29	Fibrinogen, B beta polypeptide	IPI00501169	54,408	100.0%	8	8	14	19.6%
R31 Elongation factor 1-alpha IPI00512240 S50,48 ID0.0% G 8 R32 D103se R32 beta-enolase IPI00498215 47,073 ID0.0% 9 14 22 32 R33 beta-enolase IPI00490877 47,473 ID0.0% 9 14 22 33 34 R34 Glyceraldehydrogenase IPI00490877 47,473 ID0.0% 14 22 33 37.4% R35 Voltage-dependent anion channel 3 IPI0049753 35,784 ID0.0% 15 26 10 26.0% R36 Malate dehydrogenase IPI00512157 35,420 ID0.0% 4 4 7 11.4% R38 ATP synthase suburit alpha IPI004997720 39,095 ID0.0% 4 4 7 13.4% R39 Moglobin IPI0049175 35,740 ID0.0% 4 4 7 13.4% R34 ATP synthase suburit alpha IPI0049175 35,740 ID0.0% 4 4 7 13.4% R34 Malate dehydrogen	R30	Fibrinogen, B beta polypeptide	IPI00501169	54,408	100.0%	16	20	34	37.5%
R32 Enclase IPI00483215 47,075 100.0% 8 9 17 27.3% R32 beta-enclase IPI00490877 47,473 100.0% 9 14 22.3% R33 beta-enclase IPI00490877 47,473 100.0% 14 22 38 74.473 R34 Glyceraldehyde-3-phosphate dehydrogenase IPI00490877 47,473 100.0% 8 11 21 32.47% R35 Voltage-dependent anion channel 3 IPI0049753 35,784 100.0% 8 11 21 32.48% R36 Malate dehydrogenase IPI0049770 35,784 100.0% 4 4 7 11.34% R38 Four and a half LIM domains protein a IPI00497120 39,095 100.0% 4 4 7 13.4% R38 Malate dehydrogenase IPI00491257 35,420 100.0% 4 4 7 13.4% R39 Myoglobin IPI00491257 35,420 100.0% 4 4 9 13.4% R40 Glutathione S-transferase kappa 1	R31	Elongation factor 1-alpha	IPI00512240	50,048	100.0%	6	8	13	20.1%
B32 beta-enolase IPI00490877 47,473 100.0% 9 14 23 24.0% B33 beta-enolase IPI00490877 47,473 100.0% 9 14 23 24.0% R33 beta-enolase IPI00490877 47,473 100.0% 8 11 21 32.4% R34 Giveraldehyde-3-phosphate dehydrogenase IPI00495240 36,584 100.0% 8 10 22.60% R36 Malate dehydrogenase IPI00512157 35,420 100.0% 15 23 32 22.8% R38 Four and a half LIM domains protein a IPI00491275 35,420 100.0% 4 4 7 11.7% R38 ATP synthase subunit alpha IPI00491975 55,420 100.0% 4 4 7 13.4% R40 Glutathione S-transferase kappa 1 IPI00491975 55,420 100.0% 4 4 9 14.7% R41 ATP synthase oligomycin sensitivity conferral protein IPI00491975 55,420 100.0% 4 4 9 12.3% R42<	R32	Enolase	IPI00483215	47,075	100.0%	8	9	17	27.3%
R33beta-enclaseIPI004987747,473100.0%14223837.48R34Glyceraldehyde-3-phosphate dehydrogenaseIPI004977335,784100.0%8112132.48R35Voltage-dependent anion channel 3IPI0085192632,854100.0%7122322.8%R36Malate dehydrogenaseIPI004972036,258100.0%7122322.8%R37Malate dehydrogenaseIPI004972039,095100.0%44713.4%R38Four and a half LIM domains protein aIPI004972039,095100.0%44713.4%R38Malate dehydrogenaseIPI004972039,095100.0%44713.4%R38ATP synthase subunit alphaIPI0049072059,745100.0%55810.7%R40Glutathione S-transferase piIPI00490091515,584100.0%45912.4%R41ATP synthase oligomycin sensitivity conferral proteinIPI004807022,483100.0%4710.5%R41ATP synthase, H+ transporting, mitochondrial F0 complex, subunit dIPI004971218,771100.0%33623.5%R44Muscle colfilin 2IPI0049799817,714100.0%471115%R44Muscle colfilin 2IPI0049791515,584100.0%55623.6%R44Muscle colfilin 2	R32	beta-enolase	IP100490877	47,473	100.0%	9	14	23	24.0%
R34Glyceraldehyde-3-phosphate dehydrogenaseIPI0049775335,784100.%8112132.4%R35Voltage-dependent anion channel 3IPI0049775335,784100.0%561026.0%R36Malate dehydrogenaseIPI004972033,252100.0%712233725.5%R37Malate dehydrogenaseIPI0049772039,095100.0%44711.4%R38Alter dehydrogenaseIPI0049775335,420100.0%44711.4%R38Alter dehydrogenaseIPI0049975557,45100.0%44711.4%R39MyoglobinIPI004991515,584100.0%44711.4%R40Glutathione S-transferase piIPI004991515,584100.0%455923.1%R41ATP synthase oligomycin sensitivity conferral proteinIPI004807022,483100.0%44711.9%R43ATP synthase, H+ transporting, mitochondrial F0 complex, subunit dIPI004871218,259100.0%8142336.0%R44Mucleoside diphosphate kinaseIPI0049977417,489100.0%7142136.0%R44Mucleoside diphosphate kinaseIPI0049977417,489100.0%7142136.0%R45Nucleoside diphosphate kinaseIPI0049977417,489100.0%7142156.0%<	R33	beta-enolase	IP100490877	47,473	100.0%	14	22	38	37.4%
R35 Voltage-dependent anion channel 3 IPI00851926 32,854 100.0% 5 6 10 22.8% R36 Malate dehydrogenase IPI00495240 36,258 100.0% 7 12 23 22.8% R37 Malate dehydrogenase IPI00495240 36,258 100.0% 4 4 7 14.7% R38 Four and a half LIM domains protein a IPI00497720 39,095 100.0% 4 4 7 13.4% R38 Malate dehydrogenase IPI00491757 35,420 100.0% 4 4 7 13.4% R39 Myoglobin IPI00491975 59,745 100.0% 8 11 19 76.2% R40 Glutathione S-transferase kappa 1 IPI0049015 15,584 100.0% 4 5 9 23.1% R41 ATP synthase oligomycin sensitivity conferral protein IPI0048672 25,008 100.0% 4 7 14 16.2% R43 ATP synthase, H+ transporting, mitochondrial F0 complex, subunit d IPI0048672 25,008 100.0% 8 14 23 </td <td>R34</td> <td>Glyceraldehyde-3-phosphate dehydrogenase</td> <td>IPI00497753</td> <td>35,784</td> <td>100.0%</td> <td>8</td> <td>11</td> <td>21</td> <td>32.4%</td>	R34	Glyceraldehyde-3-phosphate dehydrogenase	IPI00497753	35,784	100.0%	8	11	21	32.4%
R36Malate dehydrogenaseIP10049524036,258100.0%7122322.8%R37Malate dehydrogenaseIP1004972036,258100.0%15233752.5%R38Four and a half LIM domains protein aIP1004972039,020100.0%44713.4%R38Malate dehydrogenaseIP1004972735,420100.0%44713.4%R38ATP synthase subunit alphaIP10049197559,745100.0%8111976.2%R40Glutathione S-transferase piIP10049091515,584100.0%8111976.2%R40Glutathione S-transferase kappa 1IP1004807022,483100.0%45916.2%R41ATP synthase oligomycin sensitivity conferral proteinIP1004807022,483100.0%471119.6%R43ATP synthase, H+ transporting, mitochondrial F0 complex, subunit dIP1004911518,271100.0%8142336.0%R44Muscle cofilin 2IP1004977417,489100.0%8142336.0%R44Muscle cofilin 2IP1004977417,489100.0%55831.1%R45Nucleoside diphosphate kinaseIP1004977417,489100.0%55831.1%R47MyoglobinIP1004901515,584100.0%18274980.0%R47MyoglobinIP100490	R35	Voltage-dependent anion channel 3	IPI00851926	32,854	100.0%	5	6	10	26.0%
R37Malate dehydrogenaseIPI0051215735,420100.0%15233752.5%R38Four and a half LIM domains protein aIPI0049772039,095100.0%44714.7%R38Malate dehydrogenaseIPI0049172555,420100.0%44713.4%R38ATP synthase subunit alphaIPI0049197559,745100.0%55810.7%R39MyoglobinIPI0049091515,584100.0%8111976.2%R40Glutathione S-transferase piIPI004807225,908100.0%45923.5%R41ATP synthase oligomycin sensitivity conferral proteinIPI004867225,908100.0%471119.6%R43ATP synthase, H+ transporting, mitochondrial F0 complex, subunit dIPI004867218,771100.0%8142336.0%R44Muscle cofilin 2IR,071100.0%471119.6%R45Nucleoside diphosphate kinaseIPI0049789317,124100.0%33623.0%R46Peptidyl-prolyl cis-trans isomeraseIPI004977417,489100.0%55831.1%R47MyoglobinIPI004977415,584100.0%55831.1%R47MyoglobinIPI004977417,489100.0%55831.1%R47MyoglobinIPI004977415,584100.0% <td< td=""><td>R36</td><td>Malate dehydrogenase</td><td>IPI00495240</td><td>36,258</td><td>100.0%</td><td>7</td><td>12</td><td>23</td><td>22.8%</td></td<>	R36	Malate dehydrogenase	IPI00495240	36,258	100.0%	7	12	23	22.8%
R38Four and a half LIM domains protein aIPI0049772039,950100.0%444714.7%R38Malate dehydrogenaseIPI0051215735,420100.0%44713.4%R38ATP synthase subunit alphaIPI0049197559,745100.0%44713.4%R39MyoglobinIPI00491917559,745100.0%555810.7%R40Glutathione S-transferase piIPI0050266823,528100.0%45923.1%R41ATP synthase oligomycin sensitivity conferral proteinIPI0048967225,908100.0%45916.2%R41ATP synthase oligomycin sensitivity conferral proteinIPI004807022,483100.0%45916.2%R42Superoxide dismutaseIPI0048070225,908100.0%471119.6%R43ATP synthase oligomycin sensitivity conferral proteinIPI0048071218,259100.0%471119.6%R43ATP synthase, H+ transporting, mitochondrial F0 complex, subunit dIPI0051134518,771100.0%333623.0%R44Muscle cofilin 2IPI00497798917,124100.0%7142153.6%R45Nucleoside diphosphate kinaseIPI0049777417,489100.0%55831.1%R47MyoglobinIPI0049091515,584100.0%1827 <td>R37</td> <td>Malate dehydrogenase</td> <td>IPI00512157</td> <td>35,420</td> <td>100.0%</td> <td>15</td> <td>23</td> <td>37</td> <td>52.5%</td>	R37	Malate dehydrogenase	IPI00512157	35,420	100.0%	15	23	37	52.5%
R38Malate dehydrogenaseIPI0051215735, 420100.0%444713.4%R38ATP synthase subunit alphaIPI0049197559,745100.0%55810.7%R39MyoglobinIPI0049091515,584100.0%555923.1%R40Glutathione S-transferase piIPI0050266823,528100.0%45916.2%R41ATP synthase oligomycin sensitivity conferral proteinIPI0048967225,908100.0%45916.2%R41ATP synthase oligomycin sensitivity conferral proteinIPI0048807022,483100.0%471119.6%R43ATP synthase oligomycin sensitivity conferral proteinIPI0048807225,908100.0%471119.6%R44Muscle coflin 2IPI0048671218,259100.0%471119.6%R45Nucleoside diphosphate kinaseIPI0049798917,124100.0%33623.0%R46Peptidyl-prolyl cis-trans isomeraseIPI0049777417,489100.0%55831.1%R47MyoglobinIPI0049091515,584100.0%18274988.0%	R38	Four and a half LIM domains protein a	IPI00497720	39,095	100.0%	4	4	7	14.7%
R38ATP synthase subunit alphaIPI0049197559,785100.0%55810.7%R39MyoglobinIPI0049091515,584100.0%8111976.2%R40Glutathione S-transferase piIPI005206823,528100.0%811976.2%R40Glutathione S-transferase kappa 1IPI0048907225,908100.0%45916.2%R41ATP synthase oligomycin sensitivity conferral proteinIPI0048307022,483100.0%471119.6%R42Superoxide dismutaseIPI004867225,008100.0%471119.6%R43ATP synthase, H+ transporting, mitochondrial F0 complex, subunit dIPI0051134518,771100.0%8142336.0%R44Muscle cofilin 2Nucleoside diphosphate kinaseIPI0049798917,124100.0%7142153.6%R45Nucleoside diphosphate kinaseIPI0049777417,489100.0%55831.1%R47MyoglobinIPI004901515,584100.0%18274980.0%R47MyoglobinIPI004901515,584100.0%18274980.0%	R38	Malate dehydrogenase	IPI00512157	35,420	100.0%	4	4	7	13.4%
R39 Myoglobin IPI00490915 15,584 100.0% 8 11 19 76.2% R40 Glutathione S-transferase pi IPI00502668 23,528 100.0% 5 5 9 23.1% R40 Glutathione S-transferase kappa 1 IPI00489672 25,908 100.0% 4 5 9 21.1% R41 ATP synthase oligomycin sensitivity conferral protein IPI00489672 25,908 100.0% 6 9 17 40.7% R42 Superoxide dismutase IPI00486725 25,008 100.0% 4 7 11 19.6% R43 ATP synthase, H+ transporting, mitochondrial F0 complex, subunit d IPI0048712 18,271 100.0% 8 14 23 36.0% R44 Muscle cofilin 2 IR/0112 18,771 100.0% 3 3 6 23.0% R45 Nucleoside diphosphate kinase IPI004979789 17,124 100.0% 7 14 21 53.6% R46 Peptidyl-prolyl cis-trans isomerase IPI00490774 17,489 100.0% 5 5 8	R38	ATP synthase subunit alpha	IPI00491975	59,745	100.0%	5	5	8	10.7%
R40 Glutathione S-transferase pi IPI00502668 23,528 100.0% 5 5 9 23.1% R40 Glutathione S-transferase kappa 1 Glutathione S-transferase kappa 1 IPI00489672 25,908 100.0% 4 5 9 16.2% R41 ATP synthase oligomycin sensitivity conferral protein IPI00483070 22,483 100.0% 6 9 17 40.7% R42 Superoxide dismutase IPI00486525 25,008 100.0% 4 7 11 9.6% R43 ATP synthase, H+ transporting, mitochondrial F0 complex, subunit d IPI00486721 18,259 100.0% 4 4 23 36.0% R44 Muscle cofilin 2 IPI00481712 18,259 100.0% 3 3 6 23.0% R45 Nucleoside diphosphate kinase IPI00497789 17,124 100.0% 7 14 21 53.6% R46 Peptidyl-prolyl cis-trans isomerase IPI004997774 17,489 100.0% 18 27 49 86.0% R47 Myoglobin IPI00499015 15,584 100.0% <td>R39</td> <td>Myoglobin</td> <td>IPI00490915</td> <td>15,584</td> <td>100.0%</td> <td>8</td> <td>11</td> <td>19</td> <td>76.2%</td>	R39	Myoglobin	IPI00490915	15,584	100.0%	8	11	19	76.2%
R40 Glutathione S-transferase kappa 1 IPI00489672 25,908 100.0% 4 5 9 16.2% R41 ATP synthase oligomycin sensitivity conferral protein IPI00483070 22,908 100.0% 6 9 17 40.7% R42 Superoxide dismutase IPI00483072 25,008 100.0% 4 7 11 19.6% R43 ATP synthase, H+ transporting, mitochondrial F0 complex, subunit d IPI00486525 25,008 100.0% 4 4 23 36.0% R44 Muscle cofilin 2 IPI00484712 18,259 100.0% 3 3 6 23.0% R45 Nucleoside diphosphate kinase IPI00497989 17,124 100.0% 7 14 21 53.6% R46 Peptidyl-prolyl cis-trans isomerase IPI004997774 17,489 100.0% 5 5 8 31.1% R47 Myoglobin IPI00490915 15,584 100.0% 18 27 49 85.0%	R40	Glutathione S-transferase pi	IP100502668	23,528	100.0%	5	5	9	23.1%
R41 ATP synthase oligomycin sensitivity conferral protein IPI00483070 22,483 100.0% 6 9 17 40.7% R42 Superoxide dismutase IPI00483070 22,483 100.0% 4 7 11 19.0% R43 ATP synthase, H+ transporting, mitochondrial F0 complex, subunit d IPI00486712 18,259 100.0% 4 7 11 19.6% R44 Muscle cofilin 2 IPI00484712 18,259 100.0% 8 14 23 36.0% R45 Nucleoside diphosphate kinase IPI00497989 17,124 100.0% 7 14 21 53.6% R46 Peptidyl-prolyl cis-trans isomerase IPI00497774 17,489 100.0% 5 5 8 31.1% R47 Myoglobin IPI00490915 15,584 100.0% 18 27 49 85.0%	R40	Glutathione S-transferase kappa 1	IPI00489672	25,908	100.0%	4	5	9	16.2%
R42 Superoxide dismutase IPI00480525 25,008 100.0% 4 7 11 19.0% R43 ATP synthase, H+ transporting, mitochondrial F0 complex, subunit d IPI00480712 18,259 100.0% 8 14 23 36.0% R44 Muscle coflin 2 IPI00511345 18,771 100.0% 3 3 6 23.0% R45 Nucleoside diphosphate kinase IPI00497989 17,124 100.0% 7 14 21 53.6% R46 Peptidyl-prolyl cis-trans isomerase IPI00499774 17,489 100.0% 5 5 8 31.1% R47 Myoglobin IPI00499015 15,584 100.0% 18 27 49 85.0%	R41	A IP synthase oligomycin sensitivity conferral protein	IPI00483070	22,483	100.0%	6	9	1/	40.7%
R43 A1P synthase, H+ transporting, mitochondrial FU complex, subunit d IP100484/12 18,259 100.0% 8 14 23 36.0% R44 Muscle cofilin 2 IP100511345 18,771 100.0% 3 3 6 23.0% R45 Nucleoside diphosphate kinase IP100497989 17,124 100.0% 7 14 21 53.6% R46 Peptidyl-prolyl cis-trans isomerase IP100497774 17,489 100.0% 5 5 8 31.1% R47 Myoglobin IP100490915 15,584 100.0% 18 27 49 85.0%	K42	Superoxide dismutase	IP100486525	25,008	100.0%	4	7	11	19.6%
R44 Muscle comin 2 IP100511345 18, / 1 100.0% 3 3 6 23.0% R45 Nucleoside diphosphate kinase IP100497989 17,124 100.0% 7 14 21 53.6% R46 Peptidyl-prolyl cis-trans isomerase IP100497774 17,489 100.0% 5 5 8 31.1% R47 Myoglobin IP100490915 15,584 100.0% 18 27 49 85.0%	K43	ATP synthase, H+ transporting, mitochondrial FU complex, subunit d	IPI00484712	18,259	100.0%	8	14	23	36.0%
R45 Nucleoside dipriosprate kinase IP100497989 17,124 100.0% 7 14 21 53.6% R46 Peptidyl-prolyl cis-trans isomerase IP100497774 17,489 100.0% 5 5 8 31.1% R47 Myoglobin IP100490915 15,584 100.0% 18 27 49 85.0%	K44	Musice comm 2	IP100511345	18,//1	100.0%	3	3	6	23.0%
R40 Peptidyi-prolyl cis-trans isomerase IPI00497/74 17,489 100.0% 5 5 8 31.1% R47 Myoglobin IPI00490915 15,584 100.0% 18 27 49 85.0% D40 Listentified IPI00490915 15,584 100.0% 18 27 49 85.0%	K45	Nucleoside dipnosphate kinase	IPI00497989	17,124	100.0%	7	14	21	53.6%
K4/ INVOGIODIN IPIUU490915 15,584 100.0% 18 27 49 85.0%	K46	Peptidyi-proiyi cis-trans isomerase	IP100497774	17,489	100.0%	5	5	8	31.1%
	K47	Myogiopin	IPI00490915	15,584	100.0%	18	27	49	85.0%

Supplementary Table 4. Identifications of differentially expressed protein spots between cardiomyocytes from Day 0 and adult mice.

				# Unique	# Unique	# Total	Sequence	Day 0 v	vs Adult
No. Protein name	UniProt ID	pl	Mw (Da)	peptide	spectrum	spectrum	coverage	T-test	Av. Ratio
1 Calreticulin	CALR_MOUSE	4.33	46,347	11	12	20	27.90%	9.70E-07	-3.66
2 Tropomyosin alpha-1 chain	TPM1_MOUSE	4.69	32,681	5	5	9	18.30%	0.00012	-2.91
3 78 kDa glucose-regulated protein	GRP78_MOUSE	5.01	70,465	19	24	37	37.40%	4.30E-06	-1.89
4 Desmin	DESM_MOUSE	5.21	53,498	12	12	22	27.70%	8.20E-05	-2.84
4 Vimentin	VIME_MOUSE	5.05	53,556	14	16	23	41.20%	8.20E-05	-2.84
4 Myosin-6	MYH6_MOUSE	5.57	223,565	20	21	34	11.70%	8.20E-05	-2.84
5 ATP synthase subunit beta, mitochondrial	ATPB_MOUSE	4.99	51,749	13	18	29	36.30%	6.30E-05	-4.20
5 Myosin-6	MYH6_MOUSE	5.57	223,565	17	19	28	10.60%	6.30E-05	-4.20
6 Unidentified	-	-	-	-	-	-	-	0.0051	-3.17
7 Alpha-fetoprotein	FETA_MOUSE	5.54	65,343	20	24	41	38.50%	0.00023	-6.50
8 Alpha-fetoprotein	FETA MOUSE	5.54	65,343	23	29	47	45.30%	0.0002	-7.71
8 Myosin-6	MYH6 MOUSE	5.57	223,565	23	28	48	10.70%	0.0002	-7.71
9 Heterogeneous nuclear ribonucleoprotein K	HNRPK MOUSE	5.39	50,976	10	11	17	27.40%	0.03	-2.55
9 Desmin		5.21	53,498	14	14	23	32.00%	0.03	-2.55
9 Myosin-6	MYH6 MOUSE	5.57	223.565	15	15	24	8.36%	0.03	-2.55
10 Alpha-fetoprotein	FETA MOUSE	5.54	65.343	20	28	47	44.80%	0.00054	-6.30
10 Myosin-6	MYH6 MOUSE	5.57	223,565	22	26	43	11.10%	0.00054	-6.30
11 Gelsolin	GELS MOUSE	5.72	83.344	14	15	23	23.30%	0.0011	-4.19
11 Myosin-6	MYH6 MOUSE	5.57	223 565	17	18	27	10 40%	0.0011	-4 19
12 Gelsolin	GELS MOUSE	5.72	83 344	22	27	44	36.80%	0.00036	-6.01
13 Dihydrollovilysine-residue acetyltransferase component of nyruvate dehydrogenase complex mitochondrial	ODP2 MOUSE	5 70	58 778	14	22	35	29 10%	0.0081	1 75
19 Anonitate hydratase mitochondrial		8.08	85 464	12	12	17	19.00%	0.0001	1.75
15 Unidentified	-	-	- 00,404	- 12		- 17	-	9 20F-06	-3.36
16 Tubulin beta-AB chain	TBB4B MOUSE	4 79	49 831	18	22	33	58 20%	6 50E-05	-3 14
17 ATD synthace subunit beta mitochondrial	ATPR MOUSE	1 99	51 7/9	16	29	55	11 A0%	5 70E-06	3 39
12 Protein disulfide.icomerse A3		5.69	54 267	13	14	18	28 10%	1 /0E-05	-2.91
19 T-complex protein 1 submitted Asi		5 72	59,207	15	7	10	14.00%	6 30F-06	-2.91
20 T complex protein 1 subunit epsilon		5 72	50 /02	16	, 10	20	27 00%	4 20E-05	-2.55
20 Frompies protein Establish epsilon 21 Inidantifica		5.72	33,433	- 10	- 19	- 50	37.30%	7 20E-06	-3.10
21 Onderstelling ordere associated protein 2			- E 2 0 6 2	- 0	- 0	- 12	20 20%	0 00000	-3.05
22 Aueriyiyi cyclase-associated protein 2		0.00 E 9E	52,002 67 E1E	11	12	15	20.20%	0.00082	-2.13
22 Diraidantified	ITTES_WOOSE	5.65	02,515	11	15	25	22.00%	0.00082	-2.15
23 Onligentined		-	- 61.026	- 0	-	- 10	-	4 205 05	-3.33
24 Diriyu opyrimiunase-relateu protein 5		6.04	44.071	10	ہ جد	13	20.20%	4.30E-05	-5.09
25 Elongation ractor nu, initionolitata		0.20	44,971	10	27	42	51.80%	9.60E-05	-2.89
26 Hydroxysterold denydrogenase-like protein 2	HSDL2_MOUSE	6.31	54,208	10	11	14	23.30%	0.01	-2.61
26 F-complex protein 1 subunit gamma		6.28	60,630	10	10	15	26.10%	0.01	-2.61
26 Stress-inauced-phosphoprotein 1		6.40	62,582	12	12	14	26.00%	0.01	-2.61
27 Aldenyde denydrogenase x, mitochondrial	ALIB1_MOUSE	6.13	55,401	13	15	24	28.10%	0.0019	-3.13
28 Aldenyde denydrogenase x, mitochondrial	ALIBI_MOUSE	6.13	55,401	5	6	12	10.60%	0.00014	-4.75
29 ATP synthase subunit alpha, mitochondrial	ATPA_MOUSE	8.28	55,310	18	22	39	40.50%	3.90E-05	2.94
30 Actin, alpha cardiac muscle 1	ACIC_MOUSE	5.23	41,785	12	18	46	34.70%	0.019	1.24
31 Troponin T, cardiac muscle	TNNT2_MOUSE	4.98	35,694	12	17	28	32.20%	9.20E-07	3.60
32 Creatine kinase B-type	KCRB_MOUSE	5.40	42,582	12	16	26	42.00%	0.00031	-3.16
33 Alpha-enolase	ENOA_MOUSE	6.36	47,010	14	17	31	35.90%	6.80E-06	-3.89
34 Alpha-enolase	ENOA_MOUSE	6.36	47,010	18	24	40	49.50%	5.20E-05	-4.12
35 Alpha-enolase	ENOA_MOUSE	6.36	47,010	18	30	48	46.50%	1.40E-05	-4.20
36 Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	ODPA_MOUSE	6.78	40,181	5	6	8	14.40%	0.0077	-2.01
36 Alpha-centractin	ACTZ_MOUSE	6.19	42,614	6	7	11	23.90%	0.0077	-2.01
37 Fumarate hydratase, mitochondrial	FUMH_MOUSE	7.88	49,921	13	14	19	39.60%	1.30E-05	2.81

38 3-ketoacyl-CoA thiolase, mitochondrial	THIM_MOUSE	8.33	41,830	8	11	20	32.70%	4.40E-05	4.40
38 Creatine kinase S-type, mitochondrial	KCRS_MOUSE	7.72	43,387	11	14	20	32.00%	4.40E-05	4.40
38 Medium-chain specific acyl-CoA dehydrogenase, mitochondrial	ACADM_MOUSE	7.69	43,593	9	12	21	24.20%	4.40E-05	4.40
38 Phosphoglycerate kinase 1	PGK1_MOUSE	8.02	44,419	11	17	29	37.20%	4.40E-05	4.40
39 3-ketoacyl-CoA thiolase, mitochondrial	THIM_MOUSE	8.33	41,830	12	17	26	52.10%	0.0011	4.18
40 3-ketoacyl-CoA thiolase, mitochondrial	THIM_MOUSE	8.33	41,830	12	16	26	49.40%	0.00023	5.56
40 Creatine kinase S-type, mitochondrial	KCRS_MOUSE	7.72	43,387	13	19	29	39.90%	0.00023	5.56
40 Phosphoglycerate kinase 1	PGK1_MOUSE	8.02	44,419	17	24	36	49.40%	0.00023	5.56
41 3-ketoacyl-CoA thiolase, mitochondrial	THIM_MOUSE	8.33	41,830	21	33	46	73.80%	0.0013	2.86
42 Tropomyosin alpha-1 chain	TPM1_MOUSE	4.69	32,681	21	32	58	54.20%	2.40E-05	2.03
43 Elongation factor 1-delta	EF1D_MOUSE	4.91	31,162	9	10	18	37.70%	0.0001	-2.68
44 Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	ODPB_MOUSE	5.39	35,768	12	17	33	44.80%	0.00023	2.14
46 Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	IDH3A_MOUSE	5.59	36,707	2	3	5	6.83%	3.20E-05	2.79
46 Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	IDH3A_MOUSE	5.59	36,707	11	13	19	35.20%	0.011	1.24
47 Malate dehydrogenase, cytoplasmic	MDHC_MOUSE	6.16	36,380	10	12	27	35.90%	0.00025	1.59
48 Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial	ECH1 MOUSE	6.01	32,433	8	12	23	37.00%	4.10E-06	5.39
49 Myozenin-2	MYOZ2_MOUSE	8.53	29,762	5	5	9	20.80%	2.40E-05	4.64
49 Four and a half LIM domains protein 2	FHL2 MOUSE	7.31	32,073	5	5	6	20.80%	2.40E-05	4.64
49 Malate dehydrogenase, cytoplasmic	MDHC MOUSE	6.16	36,380	4	4	7	14.40%	2.40E-05	4.64
50 Unidentified			-	-	-	-		0.0001	4.22
51 Electron transfer flavoprotein subunit alpha, mitochondrial	ETFA MOUSE	8.62	35.009	8	14	25	35.70%	8.20E-07	4.64
52 Aldose reductase	ALDR MOUSE	6.79	35.601	9	10	14	32.00%	0.029	-2.08
52 Annexin A2	ANXA2 MOUSE	7.53	38.545	13	15	23	38.30%	0.029	-2.08
53 Malate dehydrogenase, mitochondrial	MDHM MOUSE	8.55	33,139	10	10	15	39.60%	9.80E-06	-1.79
53 Glyceraldebyde-3-phosphate debydrogenase	G3P_MOUSE	8 4 5	35 679	9	11	19	30 30%	9 80F-06	-1.79
Sa Annevin A2		7 53	38 545	12	14	20	42 80%	9 80F-06	-1 79
54 Flectron transfer flavonrotein subunit alnha mitochondrial	FTFA MOUSE	8.62	35,009	8	17	19	32 70%	7 20F-07	3.09
55 Voltage-dependent anion-selective channel protein 1		8 55	32 351	11	14	21	48 30%	0.0081	2 01
S6 Carbonyl reductase [MADDell 1		8 5 3	30 510	6	6	7	2/ 90%	0.0074	1 50
56 Voltage-denendent anion-selective channel protein 1		8 55	32 351	5	5	, 8	24.50%	0.0074	1.50
57.2.4.dianoul.CoA reductase mitochondrial		0.55 9.79	22,351	5	5	0	24.70%	0.0074	1.50
57 2,4-dielogi-con reductase, inicologinalia		8 55	22,451	2	0	16	20.00%	6.00E-05	2.07
So votage dependent and inscretive channel protein 1		4.62	20 174	8	10	10	26 10%	1.40E.06	2.07
55 14-5-5 protein epsilon		4.05	29,174	o F	01	15	24 000/	0.00015	-2.94
61 Clothern transfer flowards submit beta		4.41	23,700	11	10	20	42 100/	0.00013	-2.00
		6.29 F 21	27,492	11	10	29	45.10%	2 105 05	-2.92
62 Algoripoprotein A-i		5.51	27,950	9	11	10	30.70%	3.10E-05	-2.70
53 Wilcrotubule-associated protein RP/EB family member 1	MARE1_MOUSE	5.12	29,885	3	3	5	14.60%	0.00044	-2.30
63 bolquinone biosynthesis protein COQ9, mitochondria		4.93	30,241	3	3	5	12.80%	0.00044	-2.30
64 Apolipoprotein A-i	APOA1_MOUSE	5.31	27,950	/	9	14	29.20%	1.30E-05	-4.06
64 Microtubule-associated protein RP/EB ramily member 1	MARE1_MOUSE	5.12	29,885	/	9	18	36.20%	1.30E-05	-4.06
65 Chioride intracellular channel protein 1		5.09	26,882	10	12	18	52.30%	0.00015	-3.84
be Carbonic anyorase 2	CAH2_MOUSE	6.48	28,901	5	6	11	24.60%	0.01	1.50
66 Bisphosphoglycerate mutase	PMGE_MOUSE	6.56	29,847	5	5	8	24.30%	0.01	1.50
6/ Phosphoglycerate mutase 1	PGAM1_MOUSE	6.75	28,701	10	1/	26	50.00%	1.60E-07	-3.49
68 Adenylate kinase 2, mitochondrial	KAD2_MOUSE	6.96	26,469	5	6	9	24.70%	0.013	1.16
68 Phosphoglycerate mutase 1	PGAM1_MOUSE	6.75	28,701	5	6	8	33.50%	0.013	1.16
69 Adenylate kinase 2, mitochondrial	KAD2_MOUSE	6.96	26,469	5	6	10	28.00%	0.00053	1.71
69 Electron transfer flavoprotein subunit beta	ETFB_MOUSE	8.29	27,492	8	8	11	31.40%	0.00053	1.71
69 Enoyl-CoA hydratase, mitochondrial	ECHM_MOUSE	7.78	28,475	4	5	8	19.70%	0.00053	1.71
70 Enoyl-CoA hydratase, mitochondrial	ECHM_MOUSE	7.78	28,475	9	11	18	30.00%	0.0021	1.86
71 Electron transfer flavoprotein subunit beta	ETFB_MOUSE	8.29	27,492	6	6	10	26.30%	5.10E-06	2.00
71 Enoyl-CoA hydratase, mitochondrial	ECHM_MOUSE	7.78	28,475	6	7	12	19.70%	5.10E-06	2.00
72 Ubiquitin-conjugating enzyme E2 R1	UB2R1_MOUSE	4.44	26,622	2	2	4	9.36%	5.60E-06	2.31
73 Electron transfer flavoprotein subunit beta	ETFB_MOUSE	8.29	27,492	9	12	22	41.60%	2.70E-06	2.73

73 Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial	DHSB_MOUSE	8.69	28,770	6	8	12	28.00%	2.70E-06	2.73
73 Phosphoglycerate mutase 2	PGAM2_MOUSE	8.65	28,827	8	10	16	30.40%	2.70E-06	2.73
73 Enoyl-CoA delta isomerase 1, mitochondrial	ECI1_MOUSE	8.23	29,224	6	9	15	26.00%	2.70E-06	2.73
74 Coiled-coil-helix-coiled-coil-helix domain-containing protein 3, mitochondrial	CHCH3 MOUSE	8.57	26,203	8	9	13	25.60%	4.60E-05	1.77
74 Proteasome subunit alpha type-7	PSA7 MOUSE	8.59	27,855	6	7	11	34.30%	4.60E-05	1.77
74 Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial	DHSB MOUSE	8.69	28,770	10	13	16	43.60%	4.60E-05	1.77
75 Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial	DHSB_MOUSE	8.69	28,770	11	16	28	43.60%	0.011	1.39
75 Phosphoglycerate mutase 2	PGAM2 MOUSE	8.65	28,827	9	12	20	30.80%	0.011	1.39
76 Translationally-controlled tumor protein	TCTP MOUSE	4.76	19.462	6	9	14	34.90%	1.60E-05	-2.42
77 Translationally-controlled tumor protein	TCTP MOUSE	4.76	19.462	7	10	19	41.90%	7.80E-06	-2.59
78 Myosin light chain 3	MYL3 MOUSE	5.03	22,290	8	13	23	52.50%	6.40E-06	1.94
79 Myosin light chain 3	MYL3 MOUSE	5.03	22.290	13	21	53	70.60%	1.60E-05	1.69
80 Myosin light chain 3	MYL3 MOUSE	5.03	22.290	10	13	22	57.40%	0.00042	1.59
81 NADH dehvdrogenase [ubiquinone] iron-sulfur protein 8 mitochondrial	NDUS8 MOUSE	5.13	20 442	4		11	25 90%	0.0013	1.93
82 Osteorelast-stimulating factor 1	OSTE1 MOUSE	5 44	23 783	2	2	3	9 30%	0.001	-2.42
82 Pre-mRNA-snlicing factor SPE77	SPE27 MOUSE	5.48	26,000	3	3	3	13 80%	0.001	-2.42
82 NADH dehvdrogenase [ubinuinone] iron-sulfur protein 3_mitochondrial	NDUS3 MOUSE	5.45	26,000	3	3	3	14 10%	0.001	-2.42
83 Chloride intracellular channel protein A		5.45	28 598	12	16	24	52 60%	1 50F-06	-3.88
84 Serum anvloid P-component	SAMP MOUSE	5.45	26,330	6	8	15	24 10%	0.0049	-3.28
45 NADH day/drogenase [ubinuinona] flavorrotein 2. mitochondria]		5.31	23,247	11	20	33	55 60%	1 40E-05	1 77
SS Applingerstal Al		5.31	23,047	1/	20	3/	45 80%	1.40E-05	1.77
Se Thioredoxin down and ant perovide reductase mitochondrial	PRDY2 MOUSE	5.51	21,550	14	20	12	28 00%	1.40E-05	2.77
Se BAG family molecular changerone regulator 2	PROXS_WOUSE	5.75 6.01	21,303	5	5	13	20.00%	1.10E-05	2.22
	BAGZ_WOUSE	0.01 E 02	25,474	0	0	12	24.30%	1.10E-05	2.22 E 27
o/ return equivalin-4		5.05	20,470	0 2	2	15	43.30%	1 205 05	-5.27
		6.40	20,005	3	5	с 0	19.30%	1.202-05	-2.14
80 Alaba gardellin Babaja		0.12	23,014	5	5	0	24.90%	1.20E-05	-2.14
69 Alpha-trystainin 6 thaini		0.70	20,009	/	16	10	40.90%	1.30E-05	1.99
90 Eletetein nomolog, mitocnononal	ESI_MOUSE	7.31	23,920	9	10	29	44.00%	6.80E-06	3.11
90 Guidathione S-transferase Mu 2	GSTIVIZ_IVIOUSE	7.31	25,580	10	13	22	44.50%	6.80E-06	3.11
91 NAUH denydrogenase [ubiquinone] 1 beta subcomplex subunit 9	NDUB9_MOUSE	7.84	21,853	3	5	8	21.20%	1.40E-06	2.76
91 Glutatnione S-transferase P 1	GSTP1_MOUSE	8.13	23,478	5	6	14	31.90%	1.40E-06	2.76
92 Peroxireaoxin-1	PRDX1_MOUSE	8.26	22,045	/	9	15	45.70%	4.80E-06	2.91
93 Glutathione S-transferase Mu 1	GSTM1_MOUSE	8.14	25,839	6	9	16	40.40%	0.00044	2.78
94 NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10	NDUBA_MOUSE	8.19	21,024	8	11	1/	46.00%	0.00018	1.95
94 Glutathione S-transferase P1	GSTP1_MOUSE	8.13	23,478	8	9	16	48.10%	0.00018	1.95
95 Protein NipSnap homolog 2	NIPS2_MOUSE	9.31	32,933	3	5	9	11.70%	3.40E-05	2.06
96 GTP:AMP phosphotransferase AK3, mitochondrial	KAD3_MOUSE	8.88	25,295	3	3	6	16.70%	0.0029	1.76
96 Protein NipSnap homolog 2	NIPS2_MOUSE	9.31	32,933	4	4	8	17.40%	0.0029	1.76
97 Myosin light chain 4	MYL4_MOUSE	4.96	21,159	8	11	17	50.30%	0.001	-2.20
98 Myosin light chain 4	MYL4_MOUSE	4.96	21,159	5	9	15	32.10%	0.033	-1.26
99 Myosin light chain 4	MYL4_MOUSE	4.96	21,159	6	7	10	36.80%	0.00038	-1.74
99 Peroxiredoxin-2	PRDX2_MOUSE	5.20	21,647	7	8	13	49.00%	0.00038	-1.74
100 Chromobox protein homolog 3	CBX3_MOUSE	5.13	20,855	6	8	14	36.60%	0.00072	-3.55
101 39S ribosomal protein L12, mitochondrial	RM12_MOUSE	5.35	16,653	4	4	7	24.40%	5.30E-05	-3.13
102 ATP synthase subunit d, mitochondrial	ATP5H_MOUSE	5.53	18,618	8	8	15	53.40%	8.60E-07	3.32
103 Adenylate kinase isoenzyme 1	KAD1_MOUSE	5.67	21,540	8	9	17	50.00%	1.10E-05	2.29
104 ATP synthase subunit d, mitochondrial	ATP5H_MOUSE	5.53	18,618	2	2	2	18.00%	0.0038	2.17
105 ATP synthase subunit d, mitochondrial	ATP5H_MOUSE	5.53	18,618	14	20	36	80.70%	2.70E-06	2.19
106 Ferritin heavy chain	FRIH_MOUSE	5.53	21,067	4	5	8	27.50%	0.0015	1.56
107 Putative hydrolase RBBP9	RBBP9_MOUSE	5.62	20,912	5	6	10	26.90%	0.0034	-2.53
108 Ferritin light chain 1	FRIL1_MOUSE	5.65	20,802	9	14	26	61.20%	0.011	-1.85
109 Coactosin-like protein	COTL1_MOUSE	5.23	15,813	1	1	1	5.63%	0.00015	-2.96
110 Tubulin-specific chaperone A	TBCA_MOUSE	5.25	12,626	6	9	14	38.90%	0.0077	-2.04
111 Programmed cell death protein 5	PDCD5_MOUSE	5.56	14,144	4	6	10	37.30%	1.70E-06	-3.30

112 Retinol-binding protein 1	RET1_MOUSE	5.11	15,715	8	12	22	54.80%	6.50E-06	-3.23
113 Retinol-binding protein 1	RET1_MOUSE	5.11	15,715	6	8	10	47.40%	0.0018	2.40
114 Cytochrome c oxidase subunit 5A, mitochondrial	COX5A_MOUSE	5.01	12,436	5	6	12	43.20%	6.70E-06	2.30
115 Cytochrome c oxidase subunit 5A, mitochondrial	COX5A_MOUSE	5.01	12,436	3	4	8	21.90%	0.0011	2.29
116 Unidentified	-		-	-	-	-		1.20E-06	2.90
117 Fatty acid-binding protein, heart	FABPH_MOUSE	6.15	14,688	7	11	16	55.60%	3.80E-07	6.93
118 Fatty acid-binding protein, heart	FABPH_MOUSE	6.15	14,688	2	3	4	21.10%	0.00072	2.67
119 Costars family protein ABRACL	ABRAL_MOUSE	5.49	9,030	1	1	2	11.10%	5.60E-05	2.66
120 Fatty acid-binding protein, epidermal	FABP5_MOUSE	6.18	15,006	2	2	4	25.20%	0.004	-2.82
121 Fatty acid-binding protein, heart	FABPH_MOUSE	6.15	14,688	4	4	7	28.60%	1.30E-07	6.74
122 Fatty acid-binding protein, heart	FABPH_MOUSE	6.15	14,688	4	5	7	31.60%	0.0054	4.31
123 Fatty acid-binding protein, heart	FABPH_MOUSE	6.15	14,688	11	16	30	72.20%	7.00E-08	6.94
124 Enhancer of rudimentary homolog	ERH_MOUSE	5.62	12,128	2	4	7	26.90%	3.90E-08	-5.03
125 Cytochrome c oxidase subunit 5B, mitochondrial	COX5B_MOUSE	5.74	10,718	3	4	7	24.20%	1.40E-06	2.89
126 Cytochrome c oxidase subunit 5B, mitochondrial	COX5B_MOUSE	5.74	10,718	5	6	8	29.70%	8.70E-06	2.74
127 Stathmin	STMN1_MOUSE	5.76	17,143	7	10	17	32.20%	1.80E-09	-23.63
128 Heat shock protein beta-7	HSPB7_MOUSE	5.95	18,635	5	7	13	37.30%	0.0014	-1.92
129 Ubiquitin-conjugating enzyme E2 N	UBE2N_MOUSE	6.13	17,138	5	6	10	40.80%	0.00013	-2.02
130 Fatty acid-binding protein, epidermal	FABP5_MOUSE	6.18	15,006	2	2	2	14.80%	4.70E-05	-4.33
131 Fatty acid-binding protein, epidermal	FABP5_MOUSE	6.18	15,006	7	10	17	73.30%	4.10E-07	-6.69
132 Transthyretin	TTHY_MOUSE	5.77	15,776	5	7	14	28.60%	0.0078	-1.61
133 40S ribosomal protein S12	RS12_MOUSE	7.02	14,394	2	2	2	20.50%	6.60E-05	-2.36
134 40S ribosomal protein S12	RS12_MOUSE	7.02	14,394	3	4	7	22.00%	5.60E-06	-4.18
135 Nucleoside diphosphate kinase B	NDKB_MOUSE	7.17	17,232	6	9	15	46.10%	0.00042	5.60
136 Peptidyl-prolyl cis-trans isomerase A	PPIA_MOUSE	7.73	17,971	11	17	31	74.40%	0.05	-1.73
137 Myoglobin	MYG_MOUSE	7.23	16,938	6	9	12	48.70%	0.0003	3.06
138 Unidentified	-		-	-	-	-		2.20E-05	2.90
139 Cofilin-1	COF1_MOUSE	8.26	18,428	8	9	13	47.60%	1.80E-05	-4.65
140 Peptidyl-prolyl cis-trans isomerase A	PPIA_MOUSE	7.73	17,971	10	16	27	66.50%	4.20E-05	5.86
141 NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 7	NDUB7_MOUSE	8.38	16,200	5	5	9	44.50%	0.0032	-1.88
141 Destrin	DEST_MOUSE	8.19	18,390	6	7	10	40.60%	0.0032	-1.88
142 Myoglobin	MYG_MOUSE	7.23	16,938	10	16	30	65.60%	6.50E-06	9.75
143 Peroxiredoxin-5, mitochondrial	PRDX5_MOUSE	7.70	17,015	10	12	20	49.00%	2.90E-05	3.49
144 Myoglobin	MYG_MOUSE	7.23	16,938	7	10	14	61.70%	0.00027	4.38
145 Unidentified	-		-	-	-	-		5.10E-05	2.19
146 Unidentified	-		-	-	-	-		2.40E-07	9.14
147 Protein S100-A13	S10AD_MOUSE	5.89	11,158	2	2	4	20.40%	0.00031	5.02
148 ATP synthase-coupling factor 6, mitochondrial	ATP5J_MOUSE	5.40	8,945	4	5	7	40.70%	1.60E-05	4.73
149 NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial	NDUS6_MOUSE	8.86	13,020	7	10	18	65.50%	0.023	2.16
150 Acylphosphatase-2	ACYP2_MOUSE	9.30	11,878	5	5	6	34.00%	0.00075	2.65
151 Cytochrome c oxidase subunit 6B1	CX6B1 MOUSE	8.97	9,940	7	7	12	66.30%	0.0049	3.17

Supplementary Figure 1. DIGE Analysis. A) Differentially expressed proteins between the adult mouse heart versus zebrafish (ZF) heart (**Supplementary Tables 2** and **3**, respectively). **B)** Differentially expressed proteins between the neonatal and adult mouse heart. Note that in panel B results of **Fig. 1B** were reproduced with different biological replicates using a dye swap. The numbered spots were analysed by LC-MS/MS.



Supplementary Figure 2. Enrichment Analysis. Enrichment for biological processes, cellular localisation and molecular function for the proteins identified by DIGE, in adult mice and adult zebrafish (ZF) hearts (**Supplementary Tables 2 and 3**).

Adult Mouse Heart



Adult ZF Heart



Supplementary Figure 3. Western Blot Analysis. A) Myozenin, nebulette and troponin T were proteins of interest in the DIGE analysis. Further immunoblot analyses were performed to corroborate the proteomics data. However, most antibodies are not validated for zebrafish. Thus, we cannot determine if the protein is absent or simply not recognised by the antibody. Note the different troponin T isoform in zebrafish at 25kDa. B) Densitometry quantitation. ****** P<0.01, ******* P<0.001. ZF, denotes "adult zebrafish".



В



Nebulette



Tnnt2 (37 kDa)



Tnnt3 (25 kDa)



Supplementary Figure 4. qPCR Analysis. In order to compare gene expression between two species in a given gene family, a gene from that family that did not change significantly over time was used as the normalisation control as indicated. For myoz1 and myoz2, 18S RNA was used as an endogenous control. The relative abundance was ranked from lowest to highest expression (+, ++, +++) in neonatal mouse, adult mouse and adult zebrafish (ZF) hearts. The absence of expression or very low levels was denoted by (-). Summary in Fig. 2A.



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D14-

Adult-

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