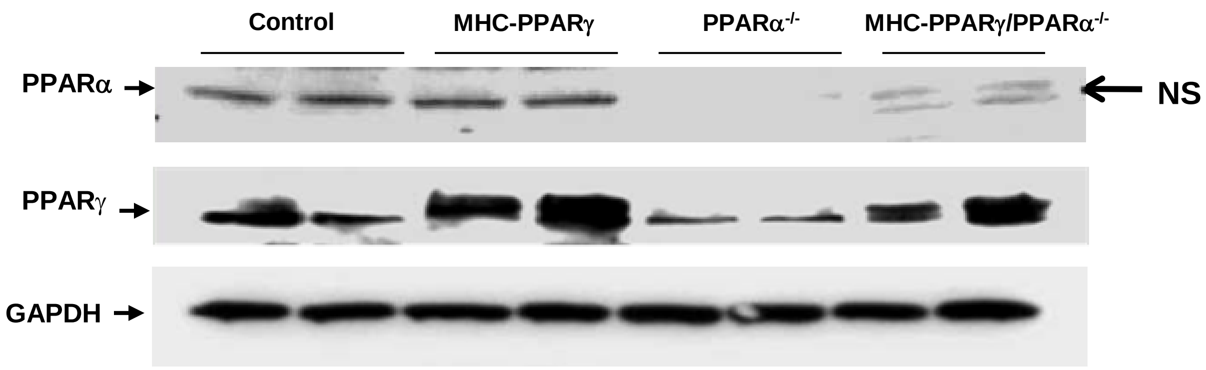
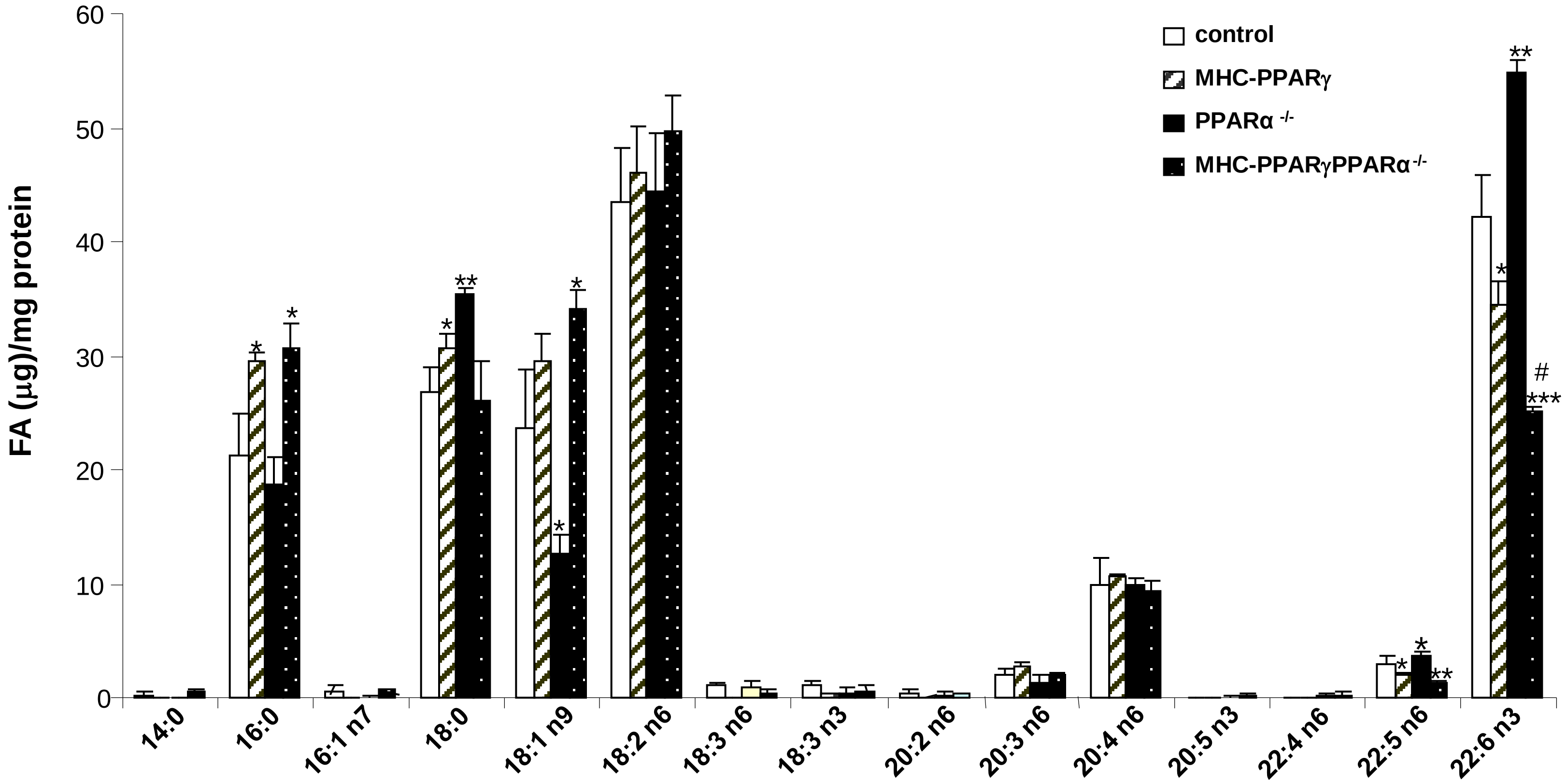
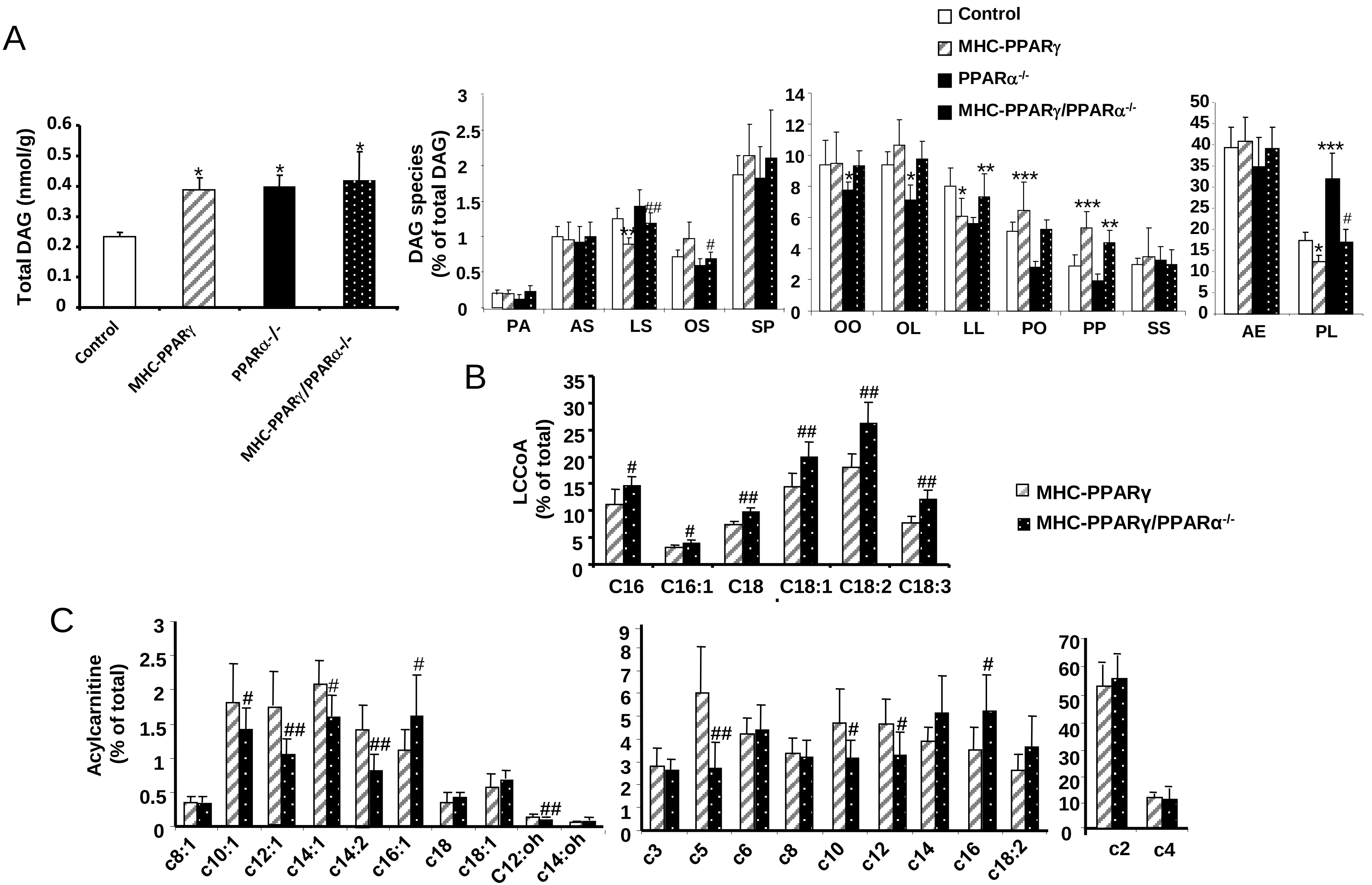


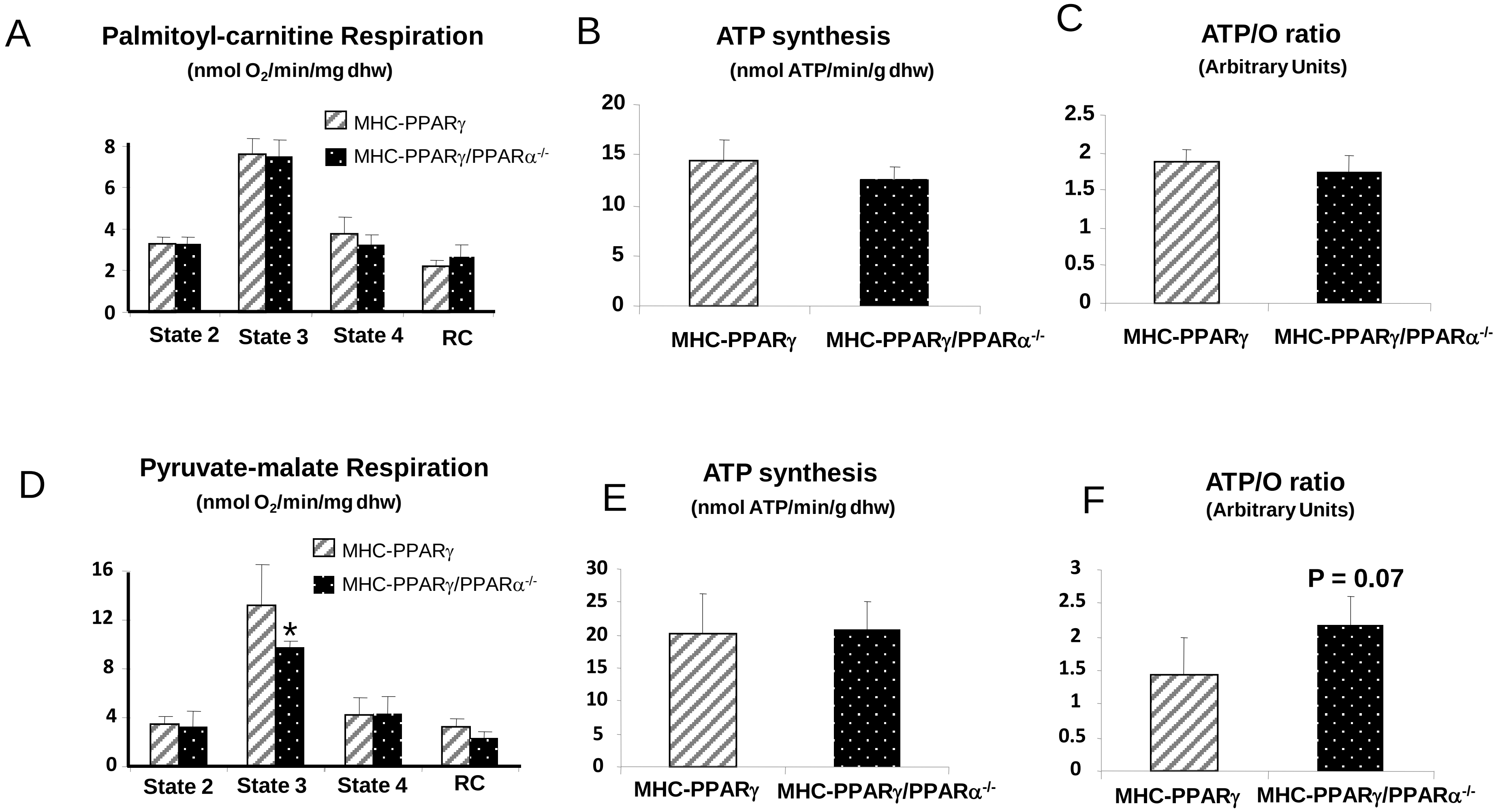
Supplemental Figure1. Western blotting detecting PPARα and PPARγ proteins in each genotype. Abbreviation: NS, non-specific bands.



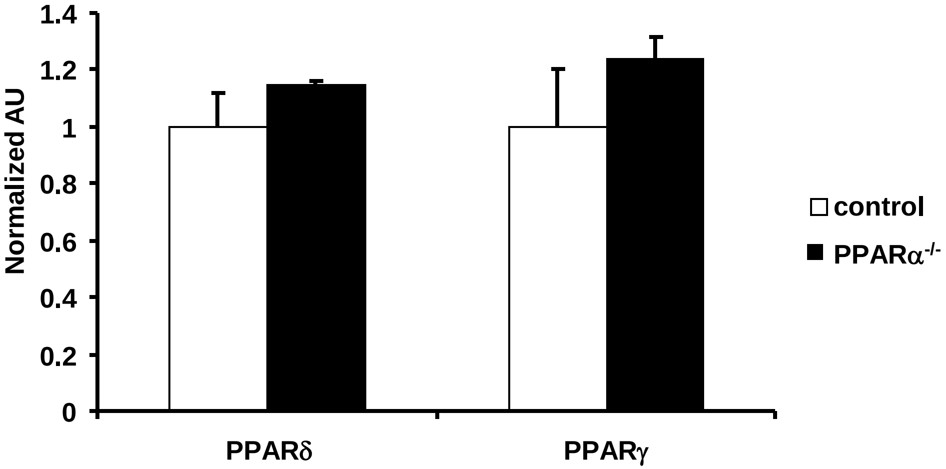
Supplementary Figure 2. Gas chromatographic analysis heart FA composition. Data are shown as means ± S.D (n = 5 per group). * $P < 0.05$, ** $P < 0.01$ and ***$P < 0.001$ compared with littermates controls; # $P < 0.05$ compared with MHC-PPARγ mice.



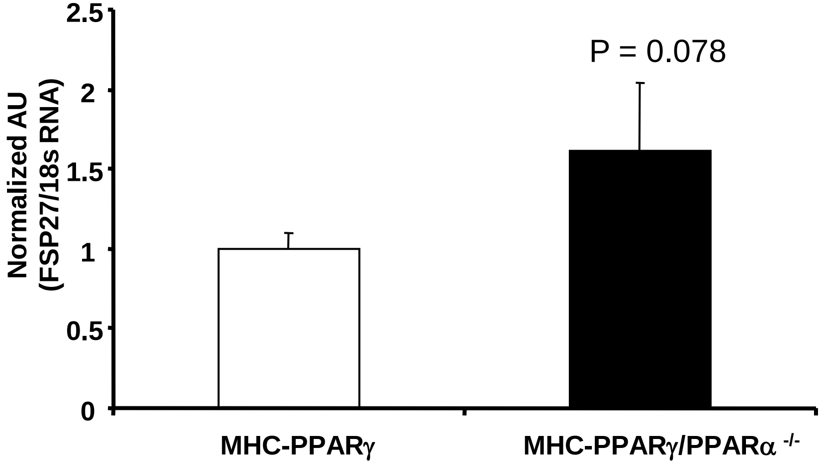
Supplementary Figure 3. Heart tissue DAG, Long chain acyl-CoA and acylcarnitine profiles. (a) Total DAG content and species. DAG species were abbreviated as two contributing fatty acyl groups. A, E, S, O, L, and P denote arachidonoyl, eicosapentanoyl, stearoyl, oleoyl, linoleoyl, and palmitoyl groups, respectively. **(b)** Individual long chain acyl-CoA and **(c)** acylcarnitine species. Values represent % of total LCCoA and acylcarnitine contents. Data are shown as means ± S.D (n = 6-7 per group). * $P < 0.05$, ** $P < 0.01$ and ***$P < 0.001$ compared with controls. $^{\#}P < 0.05$ and $^{\#\#}P < 0.01$ compared with MHC-PPARγ mice.



Supplementary Figure 4. Mitochondrial function in the heart. Respiration rates (*A* and D) and ATP synthesis rates (*B and E*) of mitochondria isolated from hearts of 12-week-old female MHC-PPARγ and MHC-PPARγ/PPARα$^{-/-}$ mice, measured in the presence of palmitoyl-carnitine(A and B) or pyruvate-malate (D and E) as a substrate (*n = 5*). (*C and F):* State 3 respiration and ATP synthesis rates were used to calculate ATP-to-O ratios for each substrate. Abbreviations: O, oxygen.



Supplementary Figure 5. qRT-PCR analysis of heart PPARδ and PPARγ mRNA expression in control and PPARα$^{-/-}$ mice. Data are shown as means ± S.D (n = 7 per group)



Supplementary Figure 6. qRT-PCR analysis of heart cell death-inducing DFFA-like effector c (FSP27) mRNA expression in MHC-PPARγ and MHC-PPARγ/PPARα$^{-/-}$ mice. Data was normalized to 18s RNA. Values present fold change relative to wild type controls, which was assigned as one. Data are shown as means ± S.D.

Supplementary Table 1 Microarray Analysis of relevant genes expressed in heart of MHC-PPARγ/PPAR$\alpha^{-/-}$ *vs*. MHC-PPARγ mice.

Gene Description	Gene symbol	Accession Number	Fold Change (MHC-PPARγ/PPAR$\alpha^{-/-}$ vs MHC-PPARγ)
Lipid Metabolism			
adipose differentiation related protein	Adrp	NM_007408	1.31*
CD36 antigen	Cd36	NM_007643	1.84*
lipase, gastric	Lipf	NM_026334	2.01*
adiponutrin	Adpn	NM_054088	5.86**
diacylglycerol O-acyltransferase 1	Dgat1	NM_010046	1.64*
patatin-like phospholipase domain containing 2	Atgl	NM_025802	1.42*
acyl-CoA synthetase long-chain family member 4	Acsl4	NM_019477	1.25*
lipase, hormone sensitive	Hsl	NM_010719	1.66*
angiopoietin-like 4	Angptl4	NM_020581	5.40*
fatty acid synthase	Fasn	NM_007988	1.06
Lipoprotein lipase	lpl	NM_008509	0.72
plasma membrane associated protein, S3-12	Plin4	NM_020568	1.37*
Glucose Metabolism			
solute carrier family 2 (facilitated glucose transporter), member 1	Glut1	NM_011400	1.31
solute carrier family 2 (facilitated glucose transporter), member 4	Glut4	NM_009204	0.83
pyruvate dehydrogenase kinase, isoenzyme 4	Pdk4	NM_013743	1.56 ($P = 0.06$)
pyruvate carboxylase	Pcx	NM_008797	0.90
glyoxylate reductase/hydroxypyruvate reductase	Grhpr	NM_080289	1.26*
pyruvate dehydrogenase (lipoamide) beta	Pdhb	NM_024221	1.09

* $P < 0.05$ and ** $P < 0.01$in MHC-PPARγ/PPAR$\alpha^{-/-}$ mice compared to MHC-PPARγ mice.

Supplementary Table 1 (Continued). Genes expressed in heart of MHC-PPARγ/PPAR$\alpha^{-/-}$ *vs*. MHC-PPARγ mice.

Gene Description	Gene symbol	Accession Number	Fold Change (MHC-PPARγ/PPAR$\alpha^{-/-}$ vs MHC-PPARγ)
oxidative phosphorylation			
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 8	Nadfa8	NM_026703	0.87
NADH dehydrogenase (ubiquinone) Fe-s protein 4	Ndufs4	NM_010887	0.92
NADH dehydrogenase (ubiquinone) 1 Fe-s protein 2	Ndufs2	NM_153064	0.89
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 11	Ndufa11	XM_128696	0.93
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 4	Ndufa4	NM_010886	1.07
NADH dehydrogenase (ubiquinone) 1 alphasubcomplex 3	Ndufa3	NM_025348	0.97
NADH dehydrogenase (ubiquinone) 1 beta subcomplex 10	Ndufb10	XM_128594	1.30
NADH dehydrogenase (ubiquinone) flavoprotein 2	Ndugv2	NM_026612	1.43*
ATP synthase H+ transporter, mitochondrial F0complex, subunit F	Atp5j	NM_016755	0.81
ATP synthase H+ transporter, mitochondrial F0complex, subunit S	Atp5s	AK009141	1.07
Others			
calcium channel, voltage-dependent, alpha2/delta subunit 1	Cacan2d1	NM_009784	1.18*
retinol binding protein 1, cellular	CRBPIII	NM_022020	5.91**
peroxisome proliferator activated receptor, gamma, coactivator 1 alpha	Ppargc1a	NM_008904	0.75
acyl-Coenzyme A thioesterase 2, mitochondrial	Acate2	NM_019736	1.19*
DNA-damage inducible transcript 3	Ddit3	NM_007837	0.80*
heat shock 70kD protein 5 (glucose-regulated protein)	Grp78	NM_022310	0.98
caspase 6	casp6	NM_009811	0.78*
natriuretic peptide precursor type B	BNP	NM_008726	0.48**
serine hydrolase-like	Serh1	NM_023475	0.55**

* $P < 0.05$ and ** $P < 0.01$in MHC-PPARγ/PPAR$\alpha^{-/-}$ mice compared to MHC-PPARγ mice.

Supplementary Table 2. Primers used for qRT-PCR amplification

Gene	Genebank Accession No	Primer sequences	Amplication length (bass pair)
Cd36	NM_007643	Sense; 5’ - ATTGGTCAAGCCAGCT- 3’ Antisense; 5’- TGTAGGCTCATCCACTAC - 3’	266
Aox	NM_015729	Sense; 5’ - ATCACGGGCACTTATGC - 3’ Antisense; 5’ - TCTCACGGATAGGGACA - 3’	241
Dgat1	NM_010046	Sense; 5’ - GAGTCTATCACTCCAGTGGG -3’ Antisense; 5’ - GGCGGCACCACAGGTTGACA -3’	100
Adrp	NM_007408	Sense; 5’ - CTACGACGACACCGAT - 3’ Antisense; 5’ - CATTGCGGAATACGGAG - 3’	200
Cpt1	NM_009948	Sense; 5’ - CCGCACAGAGACTATCT - 3 Antisense; 5’ - TGTTGTGGTTTATCCGC - 3’	266
Fas	X13135	Sense; 5’ - CGTATATGTGAACAGCGC - 3’ Antisense; 5’- AGGTCTCGGATGCCTA - 3’	296
Lpl	NM_008509	Sense; 5’ - TCTGTACGGCACAGTGG - 3’ Antisense; 5’ - CCTCTCGATGACGAAGC - 3’	196
mtTfa	NM-009360	Sense; 5’ - TATGGAGAAGGAGGCCC - 3’ Antisense; 5’ - ATTGTCGTAACGAATCCTATCA - 3’	254
Sod1	NM_011434	Sense; 5’ - CAAGCGGTGAACCAGTTGTG - 3’ Antisense; 5’ - TGAGGTCCTGCACTGGTAC - 3	216
Sod2	NM_013671	Sense; 5’ - TCTCAACGCCACCGAG - 3’ Antisense; 5’ - AGTCACGCTTGATAGCC - 3’	191
Gpx1	NM_008160	Sense; 5’ - GTCTCTCTGAGGCACGATCCG - 3’ Antisense; 5’ - TTCCGCAGGAAGGTAAACAGC - 3’	216

Supplementary Table 2 (continued). Primers used for qRT-PCR amplification

Gene	Genebank Accession No	Primer sequences	Amplication length (bass pair)
Catalase	NM_009804	Sense; 5’ - ACCCTCTTATACCAGTTGGC - 3’	321
		Antisense; 5’ - GCATGCACATGGGGCCATCA - 3’	
Chop	X67083	Sense; 5’- AGTGGCACAGCTAGCTGAAGAG - 3’	361
		Antisense; 5’ - ATGCCCACTGTTCATGCTTGGTG- 3’	
Xbp1	NM_013842	Sense; 5’ - GAACACGCTTGGGAATG - 3’	248
		Antisense; 5’ - TGACAGGGTCCAACTT - 3’	
BNP	D82049	Sense; 5’ - AGGTTTGCTATCTGGCA - 3’	259
		Antisense; 5’ - ATGTCGAAGTTTAAGGCTCTGGA - 3’	
Ucp2	NM_011671	Sense; 5’ - AAAAGATACTCTCCTGAAAGC- 3	102
		Antisense; 5’ - TGACGGTGGTGCAGAAGC- 3’	
CRBPIII	NM_022020	Sense; 5’ - AAATGCACGAGCCTGGTTAC - 3’	166
		Antisense; 5’- CAGGCTCTCTGGAAGGTTTG - 3’	
Pdk4	NM_013743	Sense; 5’ - GACCGCTTAGTGAACAC - 3’	224
		Antisense; 5’ - GTAACGGGGTCCACTG - 3’	
Fsp27	NM_178373	Sense; 5’ - GACCTGTACAAGCTGAACCCTC- 3’	198
		Antisense; 5’ - ATTGTCGTAACGAATCCTATCA - 3’	
Ppargc1a	NM_008904	Sense; 5’ - CACGCAGCCCTATTCA - 3’	286
		Antisense; 5’ - GTCGTACCTGGGCCTA - 3	