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Supplemental Data

AMPK and PPARδ Agonists Are Exercise Mimetics

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Table S1. Gene targets unique to combined GW1516 treatment and exercise training. The following genes were identified in microarray analysis as unique targets of combined GW1516 and exercise training. Down-regulated genes are in bold italics. (N=3, each pooled from 3 mice, $p<0.05$).

DESCRIPTION	LOCUS	GW+Tr
ANGIOGENESIS		
CD55 antigen	***Cd55***	***0.56***
CARBOHYDRATE METABOLISM		
phosphoenolpyruvate carboxykinase 1, cytosolic	Pck1	3.518
CYTOKINES		
interferon, alpha-inducible protein 27	Ifi27	1.714
FAT METABOLISM		
adipose differentiation related protein	Adfp	2.009
stearoyl-Coenzyme A desaturase 2	Scd2	1.849
acetyl-Coenzyme A acetyltransferase 2	Acat2	1.625
ATP citrate lyase	Acly	2.606
adiponectin, C1Q and collagen domain containing	Adipoq	3.082
diacylglycerol O-acyltransferase 2	Dgat2	2.784
gamma-glutamyl carboxylase	***Ggcx***	***0.575***
lipase, hormone sensitive	Lipe	3.032
monoglyceride lipase	Mgll	1.907
resistin	Retn	4.114
CD36 antigen	Cd36	1.584
fatty acid binding protein 4, adipocyte	Fabp4	2.189
lipoprotein lipase	Lpl	1.659
HEAT SHOCK RESPONSE		
haptoglobin	Hp	1.679
MITOCHONDRIAL PROTEINS		
3-oxoacid CoA transferase 1	***Oxct1***	***0.574***
microsomal glutathione S-transferase 1	Mgst1	1.916
OTHERS		
carbonic anhydrase 3	Car3	2.339
cysteine dioxygenase 1, cytosolic	Cdo1	3.266
DNA segment, Chr 4, Wayne State University 53, expressed	D4Wsu53e	1.586
dynein cytoplasmic 1 intermediate chain 2	Dync1i2	1.705
fusion, derived from t(12;16) malignant liposarcoma (human)	***Fus***	***0.605***
Kruppel-like factor 3 (basic)	Klf3	1.901
lysosomal membrane glycoprotein 2	***Lamp2***	***0.608***
neighbor of Punc E11	***Nope***	***0.452***
thyroid hormone responsive SPOT14 homolog (Rattus)	Thrsp	2.685

cytochrome P450, family 2, subfamily e, polypeptide 1	Cyp2e1	2.941
complement factor D (adipsin)	Cfd	2.828
transketolase	Tkt	2.256
OXYGEN CARRIERS		
GPI-anchored membrane protein 1	Gpiap1	1.83
solute carrier family 38, member 4	***Slc38a4***	***0.579***
PROLIFERATION & APOPTOSIS		
RIKEN cDNA 1190002H23 gene	***1190002H23Rik***	***0.543***
cell death-inducing DFFA-like effector c	Cidec	4.771
SIGNAL TRANSDUCTION		
annexin A7	***Anxa7***	***0.544***
dual specificity phosphatase 7	Dusp7	1.661
homeodomain interacting protein kinase 3	Hipk3	1.694
insulin-like growth factor binding protein 5	Igfbp5	1.772
protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), beta isoform	Ppp2r1b	2.509
protein tyrosine phosphatase-like (proline instead of catalytic arginine), member b	Ptplb	2.38
STEROID BIOGENESIS		
retinol binding protein 4, plasma	Rbp4	2.065
TRANSCRIPTION		
CCAAT/enhancer binding protein (C/EBP), alpha	Cebpa	2.168
nuclear receptor subfamily 1, group D, member 2(Reverb-b)	Nr1d2	1.794
TRANSPORT		
transferrin	Trf	1.907
archain 1	Arcn1	1.617
solute carrier family 1 (neutral amino acid transporter), member 5	Slc1a5	1.939
RIKEN cDNA 1810073N04 gene	1810073N04Rik	2.326

Table S2. Genes regulated by combination of GW1516 treatment and exercise training in quadriceps. The following is a list of target genes identified by microarray analysis and categorized into functional classes. The down-regulated genes are in bold italics. Data is average of N=3 samples in each group ($p<0.05$). Combination of drug treatment and exercise created a gene signature in muscles that was unique from either treatment alone. Thirty-two percent of these genes encode enzymes of metabolic pathways such as fatty acid biosynthesis/storage (e.g. *Fasn*, *Scd 1 & 2*), uptake [e.g. *Cd36*, fatty acid binding proteins (*Fabp*) and *Lpl*] and oxidation [e.g. adiponectin, hormone sensitive lipase (*Lipe*), *Pdk4*, *Ucp3*]; and carbohydrate metabolism [e.g. fructose bisphosphate 2 (*Fbp2*), phosphoenolpyruvate carboxykinase 1 (*Pck1*), lactate dehydrogenase B], which along with oxygen transporters and mitochondrial proteins form the largest class of genes directly linked to muscle performance (Ikeda et al., 2002; Achten and Jeukendrup, 2004; Hittel et al., 2005; Civitarese et al., 2006; Nadeau et al., 2006; Kiens, 2006; Yamauchi et al., 2006). All but 4 of these genes were induced, suggestive of a general increase in oxidative capacity. Furthermore, additional pathways including angiogenesis (e.g. angiopoietin-like 4 protein/also a known regulator of lipid metabolism), signal transduction (e.g. adrenergic receptor β3, insulin-like growth factor, insulin-like growth factor binding protein 5), transcription (e.g. *Cebpa*, *Nr1d2*, *Nr4a2*) and substrate transport (e.g. transferrin, chloride channel 5) were identified, implicating relevance to muscle remodeling and endurance (Nagase et al., 1996; Singleton and Feldman, 2001; Adams, 2002; Centrella et al., 2004; Lundby et al., 2005; Mahoney et al., 2005a and b; Ramakrishnan et al., 2005).

DESCRIPTION	LOCUS	TR+GW
ANGIOGENESIS		
angiopoietin-like 4	Angptl4	5.495
CD55 antigen	***Cd55***	***0.56***
CARBOHYDRATE METABOLISM		
fructose bisphosphatase 2	Fbp2	2.808
phosphoenolpyruvate carboxykinase 1, cytosolic	Pck1	3.518
lactate dehydrogenase B	Ldhb	2.541
CYTOKINES		
interferon, alpha-inducible protein 27	Ifi27	1.714
interleukin 6 signal transducer	Il6st	1.972
FAT METABOLISM		
adipose differentiation related protein	Adfp	2.009
cDNA sequence BC054059	BC054059	5.08
RIKEN cDNA 2310076L09 gene	2310076L09Rik	1.868
hydroxysteroid (17-beta) dehydrogenase 12	Hsd17b12	2.376
stearoyl-Coenzyme A desaturase 1	Scd1	6.494
stearoyl-Coenzyme A desaturase 2	Scd2	1.849
fatty acid synthase	Fasn	6.323
acetyl-Coenzyme A acyltransferase 2 (mitochondrial 3-oxoacyl-Coenzyme A thiolase)	Acaa2	1.926
acetyl-Coenzyme A dehydrogenase, long-chain	Acadl	2.549
adiponectin, C1Q and collagen domain containing	Adipoq	3.082
lipase, hormone sensitive	Lipe	3.032
malonyl-CoA decarboxylase	Mlycd	1.781
monoglyceride lipase	Mgll	1.907
uncoupling protein 3 (mitochondrial, proton carrier)	Ucp3	2.943

ATP citrate lyase	Acly	2.606
carnitine palmitoyltransferase 1a, liver	Cpt1a	2.753
diacylglycerol O-acyltransferase 2	Dgat2	2.784
gamma-glutamyl carboxylase	***Ggcx***	***0.575***
glycerol-3-phosphate acyltransferase, mitochondrial	Gpam	2.207
pyruvate dehydrogenase kinase, isoenzyme 4	Pdk4	2.27
resistin	Retn	4.114
acetyl-Coenzyme A acetyltransferase 2	Acat2	1.625
ATP-binding cassette, sub-family B (MDR/TAP), member 1A	Abcb1a	10.322
CD36 antigen	Cd36	1.584
solute carrier family 27 (fatty acid transporter), member 1	Slc27a1	3.58
fatty acid binding protein 3, muscle and heart	Fabp3	1.833
fatty acid binding protein 4, adipocyte	Fabp4	2.189
lipoprotein lipase	Lpl	1.659
diazepam binding inhibitor	Dbi	1.936
solute carrier family 27 (fatty acid transporter), 1	Slc27a1	
HEAT SHOCK RESPONSE		
haptoglobin	Hp	1.679
heat shock protein 1B	Hspa1b	8.845
heat shock protein 90kDa alpha (cytosolic), class A member 1	Hsp90aa1	1.513
heat shock protein 9A	Hspa9a	1.61
DnaJ (Hsp40) homolog, subfamily B, member 1	Dnajb1	3.59
OTHERS		
carbonic anhydrase 3	Car3	2.339
dynein cytoplasmic 1 intermediate chain 2	Dync1i2	1.705
amyloid beta (A4) precursor-like protein 2	Aplp2	1.937
catalase	Cat	1.82
crystallin, beta B1	Crybb1	2.457
cysteine dioxygenase 1, cytosolic	Cdo1	3.266
lysosomal membrane glycoprotein 2	***Lamp2***	***0.608***
neighbor of Punc E11	***Nope***	***0.452***
neuralized-like homolog (Drosophila)	Neurl	1.941
retbindin	Rtbdn	2.32
serine (or cysteine) peptidase inhibitor, clade F, member 1	Serpinf1	7.765
serine (or cysteine) proteinase inhibitor, clade A, member 1a	***Serpina1a***	***0.396***
surfeit gene 4	Surf4	2.091
thyroid hormone responsive SPOT14 homolog (Rattus)	Thrsp	2.685
acid phosphatase 5, tartrate resistant	Acp5	3.91
DNA segment, Chr 4, Wayne State University 53, expressed	D4Wsu53e	1.586
erythroid differentiation regulator 1		***0.619***
fusion, derived from t(12;16) malignant liposarcoma (human)	***Fus***	***0.605***
huntingtin interacting protein 1 related	Hip1r	1.75
kelch-like 7 (Drosophila)	***Klhl7***	***0.5***
Kruppel-like factor 3 (basic)	Klf3	1.901
Mpv17 transgene, kidney disease mutant-like	Mpv17l	1.988
RIKEN cDNA C530043G21 gene	C530043G21Rik	1.5
ligase III, DNA, ATP-dependent	Lig3	2.693
cytochrome P450, family 2, subfamily e, polypeptide 1	Cyp2e1	2.941
complement factor D (adipsin)	Cfd	2.828
Transketolase	Tkt	2.256
amyloid beta (A4) precursor-like protein 2	Aplp2	1.937
Myosin binding protein H	Mybph	1.578
MITOCHONDRIAL PROTEINS		

3-oxoacid CoA transferase 1	***Oxct1***	***0.574***
microsomal glutathione S-transferase 1	Mgst1	1.916
mitochondrial ribosomal protein L15	***Mrpl15***	***0.61***
solute carrier family 25 (mitochondrial carnitine/acylcarnitine translocase), member 20	Slc25a20	1.865
ATP-binding cassette, sub-family E (OABP), member 1	***Abce1***	***0.556***
OXYGEN CARRIERS		
GPI-anchored membrane protein 1	Gpiap1	1.83
myoglobin	Mb	1.578
solute carrier family 38, member 4	***Slc38a4***	***0.579***
hemoglobin alpha, adult chain 1	Hba-a1	1.632
hemoglobin, beta adult minor chain | hemoglobin Y, beta-like embryonic chain	Hbb-b2 | Hbb-y	1.626
PROLIFERATION & APOPTOSIS		
tripartite motif-containing 35	Trim35	1.856
RIKEN cDNA 1190002H23 gene	***1190002H23Rik***	***0.543***
B-cell translocation gene 2, anti-proliferative	Btg2	1.601
cell death-inducing DFFA-like effector c	Cidec	4.771
cell death-inducing DNA fragmentation factor, alpha subunit-like effector A	Cidea	49.625
SIGNAL TRANSDUCTION		
annexin A7	***Anxa7***	***0.544***
adrenergic receptor, beta 3	Adrb3	3.83
dual specificity phosphatase 10	***Dusp10***	***0.579***
dual specificity phosphatase 7	Dusp7	1.661
homeodomain interacting protein kinase 3	Hipk3	1.694
insulin-like growth factor 2	Igf2	1.635
insulin-like growth factor binding protein 5	Igfbp5	1.772
protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), beta isoform	Ppp2r1b	2.509
protein tyrosine phosphatase, non-receptor type 2	***Ptpn2***	***0.432***
protein tyrosine phosphatase-like (proline instead of catalytic arginine), member b	Ptplb	2.38
RAB5B, member RAS oncogene family	Rab5b	1.603
RAP2C, member of RAS oncogene family	***Rap2c***	***0.601***
transforming growth factor, beta receptor II	Tgfbr2	2.13
Ras-related GTP binding D	Rragd	2.101
3-monooxygenase/tryptophan 5-monooxygenase activation protein, gamma polypeptide	Ywhag	1.87
STEROID BIOGENESIS		
aldehyde dehydrogenase family 1, subfamily A7	Aldh1a7	3.862
retinol binding protein 4, plasma	Rbp4	2.065
transthyretin	***Ttr***	***0.026***
myosin binding protein H	Mybph	1.578
TRANSCRIPTION		
zinc finger protein 261	Zfp261	1.847
notchless homolog 1 (Drosophila)	Nle1	1.831
retinoblastoma binding protein 4	Rbbp4	2.865
ankyrin repeat and SOCS box-containing protein 15	Asb15	1.78
activating transcription factor 3	Atf3	1.802
CCAAT/enhancer binding protein (C/EBP), alpha	Cebpa	2.168
early growth response 1	Egr1	2.577
forkhead box O3a	***Foxo3a***	***0.634***
Jun-B oncogene	Junb	1.792
LIM homeobox transcription factor 1 alpha	Lmx1a	4.106
nuclear receptor subfamily 1, group D, member 2(Reverb-b)	Nr1d2	1.794
nuclear receptor subfamily 4, group A, member 2 (NURR1)	Nr4a2	1.776

RNA polymerase 1-4	Rpo1-4	2.498
sin3 associated polypeptide	***Sap30***	***0.551***
wingless-related MMTV integration site 7B	Wnt7b	4.449
FBJ osteosarcoma oncogene	Fos	3.9
TRANSPORT		
seminal vesicle protein 2	***Svp2***	***0.014***
seminal vesicle secretion 5	***Svs5***	***0.095***
transferrin	Trf	1.907
archain 1	Arcn1	1.617
two pore channel 1	Tpcn1	2.842
solute carrier family 1 (neutral amino acid transporter), member 5	Slc1a5	1.939
chloride channel 5	Clcn5	2.333
claudin 5	Cldn5	1.545
albumin 1	***Alb1***	***0.245***
RIKEN cDNA 1810073N04 gene	1810073N04Rik	2.326

Table S3. Selective GW1516 and/or exercise induced genes including heat shock proteins, metallothioneins and other stress biomarkers are not changed by the combination possibly reflecting a potential lessening of exercise-based damage (Liu and Steinacker, 2001; Jagoe et al., 2002; Koh, 2002; McArdle et al., 2002; Lecker et al., 2004). Data is average of N=3 samples in each group ($p<0.05$).

DESCRIPTION	**LOCUS**	**GW**	**Tr**	**Tr+GW**
heat shock protein 1	Hspb1	1.815	1.965	-
heat shock protein family, 7 (cardiovascular)	Hspb7	3.414	1.753	-
DnaJ (Hsp40) homolog, subfamily A, 1	Dnaja1	-	1.545	-
heat shock protein 110	Hsp110	-	1.587	-
serine (or cysteine) peptidase inhibitor H1	Serpinh1	-	2.198	-
DnaJ (Hsp40) homolog, subfamily A, 4	Dnaja4	1.756	1.545	-
metallothionein 1	Mt1	2.364	-	-
metallothionein 2	Mt2	2.151	-	-
crystallin, alpha B	Cryab	1.561	1.52	-
crystallin, gamma F	Crygf	1.801	3.56	-
MAD homolog 3 (Drosophila)	Smad3	1.841	1.886	-
ankyrin repeat domain 1 (cardiac muscle)	Ankrd1	4.235	-	-
TNF receptor superfamily, 12a	Tnfrsf12a	1.759	1.782	-
Jun oncogene	Jun	-	1.521	-

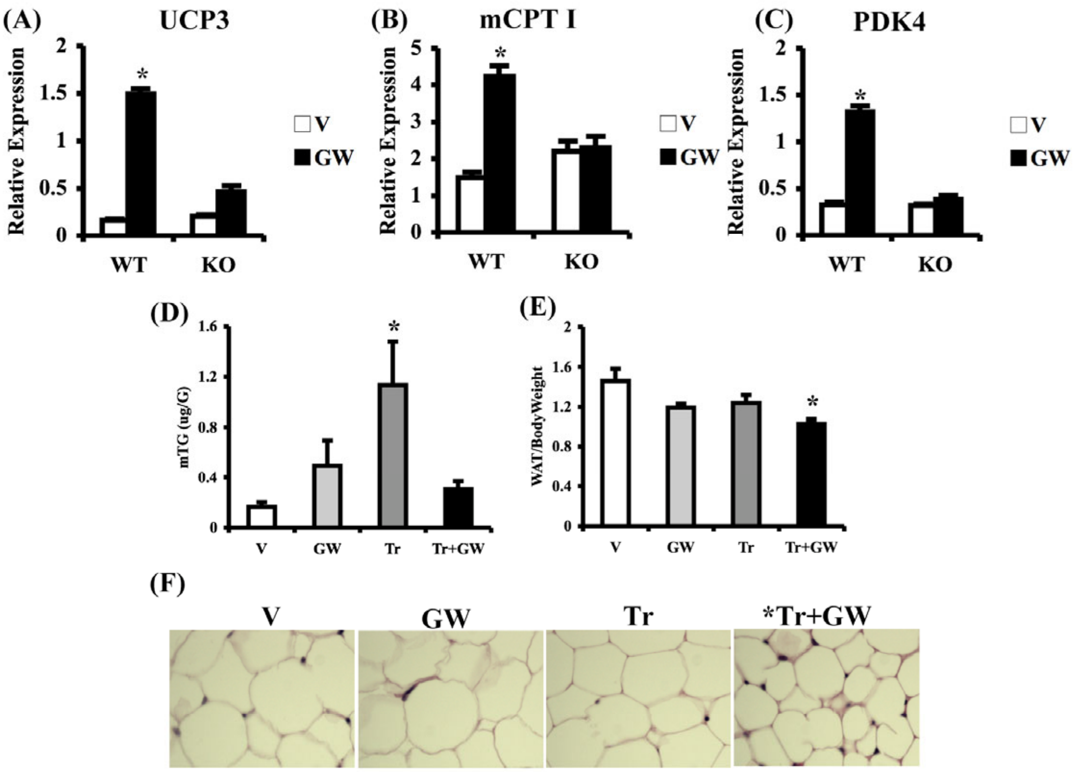
Table S4. Targets common to exercise-PPARδ and AMPK-PPARδ gene signatures. Comparison of gene signature generated by either combined PPARδ activation and exercise with that of PPARδ and AMPK co-activation revealed 52 common target genes listed below. Data is average of N=3 samples in each group ($p<0.05$).

DESCRIPTION	LOCUS	TR+GW	AI+GW
ANGIOGENESIS			
angiopoietin-like 4	Angptl4	5.495	2.917
APOPTOSIS			
cell death-inducing DFFA-like effector c	Cidec	4.771	1.838
cell death-inducing DNA fragmentation factor, alpha subunit-like effector A	Cidea	49.625	1.842
CARBOHYDRATE METABOLISM			
lactate dehydrogenase B	Ldhb	2.541	1.917
fructose bisphosphatase 2	Fbp2	2.808	2.478
FAT METABOLISM			
stearoyl-Coenzyme A desaturase 1	Scd1	6.494	1.78
fatty acid binding protein 3, muscle and heart	Fabp3	1.833	1.5
pyruvate dehydrogenase kinase, isoenzyme 4	Pdk4	2.27	2.486
uncoupling protein 3 (mitochondrial, proton carrier)	Ucp3	2.943	2.792
adiponectin, C1Q and collagen domain containing	Adipoq	3.082	1.56
diacylglycerol O-acyltransferase 2	Dgat2	2.784	2.14
solute carrier family 27 (fatty acid transporter), member 1	Slc27a1	3.58	2.195
lipase, hormone sensitive	Lipe	3.032	1.746
solute carrier family 25 (mitochondrial carnitine/acylcarnitine translocase), member 20	Slc25a20	1.704	1.697
CD36 antigen	Cd36	1.584	1.513
phosphoenolpyruvate carboxykinase 1, cytosolic	Pck1	3.518	1.781
fatty acid synthase	Fasn	6.323	2.24
fatty acid binding protein 4, adipocyte	Fabp4	2.189	1.81
monoglyceride lipase	Mgll	1.907	1.51
acetyl-Coenzyme A acetyltransferase 2	Acat2	1.625	1.563
acetyl-Coenzyme A dehydrogenase, long-chain	Acadl	2.549	1.992
resistin	Retn	4.114	1.756
malonyl-CoA decarboxylase	Mlycd	1.781	1.962
transketolase	Tkt	2.256	1.983
ATP citrate lyase	Acly	2.458	1.91
HEAT SHOCK			
heat shock protein 90kDa alpha (cytosolic), class A member 1	Hsp90aa1	1.455	0.616
DnaJ (Hsp40) homolog, subfamily B, member 1	Dnajb1	3.59	0.604
CYTOKINES			
interferon, alpha-inducible protein 27	Ifi27	1.714	1.537

OTHERS			
sarcolipin	Sln	0.363	4.576
thyroid hormone responsive SPOT14 homolog (Rattus)	Thrsp	2.685	1.766
RIKEN cDNA 2310076L09 gene	2310076L09 Rik	1.868	2.117
myosin, heavy polypeptide 2, skeletal muscle, adult	Myh2	2.194	1.797
surfeit gene 4	Surf4	2.091	0.654
acid phosphatase 5, tartrate resistant	Acp5	3.91	1.477
serine (or cysteine) proteinase inhibitor, clade A, member 1a	Serpina1a	0.396	3.891
cysteine dioxygenase 1, cytosolic	Cdo1	3.266	1.678
erythroid differentiation regulator 1		0.619	1.805
RIKEN cDNA 1810073N04 gene	1810073N04 Rik	2.326	1.628
superoxide dismutase 3, extracellular	Sod3	1.606	1.617
complement factor D (adipsin)	Cfd	2.828	1.5
cytochrome P450, family 2, subfamily e, polypeptide 1	Cyp2e1	2.941	1.743
catalase	Cat	1.728	1.902
early growth response 1	Egr1	2.577	0.65
OXYGEN CARRIER			
hemoglobin, beta adult minor chain | hemoglobin Y, beta-like embryonic chain	Hbb-b2 | Hbb-y	1.626	1.503
STEROID BIOGENESIS			
retinol binding protein 4, plasma	Rbp4	2.065	2.225
SIGNAL TRANSDUCTION			
adrenergic receptor, beta 3	Adrb3	3.83	1.56
protein tyrosine phosphatase-like (proline instead of catalytic arginine), member b	Ptplb	2.38	1.569
dual specificity phosphatase 7	Dusp7	1.661	1.672
TRANSCRIPTION			
nuclear receptor subfamily 4, group A, member 2	Nr4a2	1.776	0.437
TRANSPORT			
solute carrier family 1 (neutral amino acid transporter), member 5	Slc1a5	1.939	1.511
two pore channel 1	Tpcn1	2.842	1.487
seminal vesicle secretion 5	Svs5	0.095	2.243

Table S5. Oxidative genes induced by AMPK agonist AICAR as well as by transgenic over-expression of VP16-PPARδ in quadriceps of untrained mice. Data is average of N=3 mice in each group ($p<0.5$).

Locus	**Description**	**AICAR**	**VP-PPARd**
Aacs	acetoacetyl-CoA synthetase	1.875	2.771
Acly	ATP citrate lyase	1.687	2.429
Adipoq	adiponectin	2.043	2.122
Ak2	adenylate kinase 2	1.486	1.173
Apoe	apolipoprotein E	1.403	1.959
Cd36	CD36 antigen	1.386	3.66
Ces3	carboxylesterase 3	1.516	1.869
Cidea	cell death-inducing DNA fragmentation factor, alpha subunit-like effector A	5.021	2.356
Dgat2	diacylglycerol O-acyltransferase 2	2.034	2.147
Elovl6	ELOVL family member 6	2.134	4.43
Fabp4	fatty acid binding protein 4, adipocyte	1.709	1.23
Fasn	fatty acid synthase	2.098	2.749
Lep	leptin	2.047	3.579
Lipe	lipase, hormone sensitive	1.64	2.203
Lpl	lipoprotein lipase	1.386	1.285
Mgll	monoglyceride lipase	1.503	2.816
Mgst1	microsomal glutathione S-transferase 1	1.602	1.905
Nrip1	nuclear receptor interacting protein 1	1.474	1.887
Pck1	phosphoenolpyruvate carboxykinase 1	2.68	2.169
Pcx	pyruvate carboxylase	1.393	-
Pdk4	pyruvate dehydrogenase kinase, isoenzyme 4	1.321	5.06
Pparg	peroxisome proliferator activated receptor gamma	3.027	2.334
Retn	resistin	1.891	1.641
Scd1	stearoyl-Coenzyme A desaturase 1	1.931	7.353
Sdhd	succinate dehydrogenase complex, subunit D	1.529	1.349
Sfxn1	sideroflexin 1	1.713	1.494
Slc25a5		1.372	1.348
Sult1a1	sulfotransferase family 1A	2.021	1.996
Tspo	translocator protein	1.441	2.133
Ucp1	uncoupling protein 1	3.623	0.695
Ucp3	uncoupling protein 3	1.258	4.107



(G)

Description	Locus	GW+AI	VP-PPARδ
ATP citrate lyase	Acly	1.648	3.095
carnitine palmitoyltransferase 1b, muscle	Cpt1b	1.371	1.678
fatty acid binding protein 3, muscle and heart	Fabp3	1.447	5.904
fatty acid synthase	Fasn	2.24	2.749
lipoprotein lipase	Lpl	1.113	1.72
lipase, hormone sensitive	Lipe	1.746	2.203
pyruvate dehydrogenase kinase, isoenzyme 4	Pdk4	2.486	5.06
stearoyl-Coenzyme A desaturase 1	Scd1	1.78	7.353
uncoupling protein 3	Ucp3	2.792	4.107

Figure S1. PPARδ activation in muscle. (A-C) Regulation of oxidative genes by GW1516 in wild type and PPARδ null primary muscle cells. **(D)** Muscle triglycerdise levels. **(E-F)** Epididymal fat to body weight ratio **(E)** and cross-sectional area **(F)** in indicated groups of mice. **(G)** List of selective oxidative genes induced in muscle by combined PPARδ and AMPK activation as well as VP16-PPARδ over-expression determined by microarray analysis. * represents statistical significance between V and indicated groups ($p<0.05$, One Way ANOVA; post hoc: Dunnett’s Multiple Comparison Test).

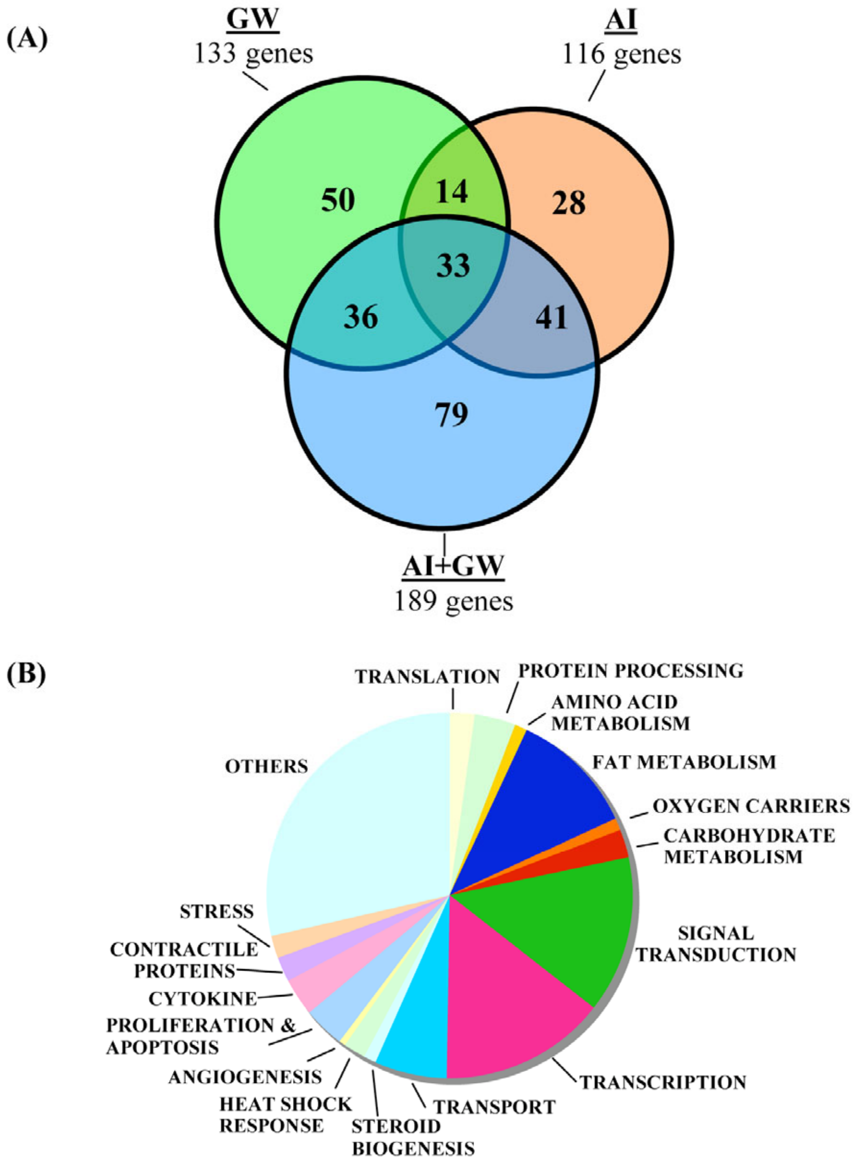


Figure S2. Synergistic regulation of muscle gene expression by PPARδ and AMPK. (A) Venn diagram comparing GW, Tr and AI+GW target genes identified in microarray analysis of quadriceps. Data is an average of N=3 samples in each group. The selection criteria used a $p<0.05$ on Bonferroni's multiple comparison test. **(B)** Classification of AI+GW target genes.

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