SUPPLEMENTARY DATA

Supplementary Table 1. Primer sequences used for quantitative real time PCR analysis.

Gene	Forward Primer	Reverse Primer	Gene Bank
Acadl	GGCTTGCTTGGCATCAACA	CGCAGAGAAACATGG	NM_007381.3
Acadm	AGAGCTCTAGACGAAGCCACGA	GAGTTCAACCTTCATCGCCATT	NM_007382.4
Agrp	CCCAGGTCTAAGTCTGAATGGC	TTCTGTGGATCTAGCACCTCCG	NM_007427.2
Cart	AACGCATTCCGATCTACGAGA	ACAGTCACACAGCTTCCCGAT	NM_013732.6
Ccl2	TCTCTCTTCCTCCACCACCATG	GCGTTAACTGCATCTGGCTGA	NM_011333.3
Ccl3	GCGGCTGATGATTGGACAA	ATCTCCAGCTCGAGCAATGG	NM_011337.2
Cnr1	GGCACCTCTTTCTCAGTCACGT	GGTGATGGTACGGAAGGTGGTA	NM_007726.3
Cd36	GGACATACTTAGATGTGGAACCCATA	TGTTGACCTGCAGTCGTTTTG	NM_001159558.1
Cpt1a	CACCAACGGGCTCATCTTCT	CCTTCTATCGAATTTGCTCTGGTT	NM_013495.2
Cpt1b	TGGGACTGGTCGATTGCAT	AGTGGCCATACCTTTCCGG	NM_009948.2
Crh	ATTTCACACACGCAGTCGGTAT	AAGCCCAGGAATGAAGTCCA	NM_205769.2
Emr1	GGATGGATAATGGCTGCTGGT	CCAGGCAAGGAGGACAGAGTTT	NM_010130.4
Hprt	CAGTCCCAGCGTCGTGATTA	AGCAAGTCTTTCAGTCCTGTC	NM_013556
Il6	TCTGCAAGAGACTTCCATCCAGT	TGTCACCAGCATCAGTCCCA	NM_031168.1
Lepr	CGGAGAGCCACGCAACTT	CAGCCCCGGGCAGTTT	NM_146146.2
Lpl	GGACTGAGGATGGCAAGCAA	GCCACTGTGCCGTACAGAGA	NM_008509.2
Mch	TTCAAAGAACACAGGCTCCAAA	ACTCAGCATTCTGAACTCCATTCTC	NM_029971.2
Npy	ACTCCGCTCTGCGACACTACAT	GCGTTTTCTGTGCTTTCCTTCA	NM_023456.2
Npy1r	CTGCAGTATTTCGGCCCACTCT	ACTGTCCCGGATCTTGTCCATC	NM_010934
Pik3ca	ACCTCAGGCTTGAAGAGTGTCG	CCGTAAGTCGTCGCCATTTTTA	NM_008839.2
Pik3r1	AACCGAAACAAAGCGGAGAA	TTGACTTCGCCGTCTACCACT	NM_001024955.1
Pomc	GCCACTGAACATCTTTGTCCC	AATCTCGGCATCTTCCACGT	NM_008895.3
Ppara	GTCACACAATGCAATTCGCTTT	TTTGCTTTTTCAGATCTTGGCA	NM_011144.6
Ppargc1c	ACAGCCGTAGGCCCAGGTAC	GCCTTTCGTGCTCATAGGCTT	NM_008904.2
Stat3	ATCTGTGTGACACCAACGACCT	TCAGCACCTTCACCGTTATTTC	NM_213659.2
Tnf	ATGAGAAGTTCCCAAATGGCCT	GGGTCTGGGCCATAGAACTGA	NM_013693.2
Trh	GTGCCAACCAAGACAAGGAT	TTCTTCCCAGCTTCTTTGGA	NM_009426.2

SUPPLEMENTARY DATA

Supplementary Table 2. Sequences of PCR primers used for EpiTYPER methylation analysis and product size of each amplicon.

Amplicon	Primer	Sequence	Product size (bp)
Ppara_#3	forward	aggaagagagGGTAGAGTTTTAGTGTTTGAGTTGGA	491
	reverse	cagtaatacgactcactatagggagaaggctATAAAAAAACTACCCAAAATCACCC	
Ppara_#4	forward	aggaagagagGGGTGATTTTGGGTAGTTTTTTTAT	445
	reverse	cagtaatacgactcactatagggagaaggctCCAACCCCTAAACACCTAAAACT	
Ppara_#7	forward	aggaagagagTGTAGTTTTAGGTGTTTAGGGGTTG	491
	reverse	cagtaatacgactcactatagggagaaggctAAATCAATCTATCAAAAAACCTCCA	
Pik3r1_#1	forward	aggaagagagGTAGTTTTTGTTTTTGGGAAGGAA	346
	reverse	cagtaatacgactcactatagggagaaggctACCAAACTAAACCATAATAATCCCC	
Pik3r1_#8	forward	aggaagagagGGGGATTATTATGGTTTAGTTTGG	354
	reverse	cagtaatacgactcactatagggagaaggctAACAAACTACCAACTCCCAAT	
Pik3r1_#9	forward	aggaagagagGATTGGGAGTTGGTAGTTTGT	183
	reverse	cagtaatacgactcactatagggagaaggctTAAAACCCAAACTAAACAAAAAAAA	
Pik3r1_#10	forward	aggaagagagTTTTTTTTGTTTAGTTTGGGTTTTA	358
	reverse	cagtaatacgactcactatagggagaaggctAACTCCTAAACCTTAATAACCCTCC	
Pik3r1_#11	forward	aggaagagagGGGAGGGTTATTAAGGTTTAGGAG	385
	reverse	cagtaatacgactcactatagggagaaggctACAAACAAAACCAAAAATTACAAAA	
Ppargc1a_#1	forward	aggaagagagTTTATGTTATTTTATATAGAGTTTTGGTTG	356
	reverse	cagtaatacgactcactatagggagaaggctAACCAAATATTTCCTTTTCTTTCTTC	
Ppargc1a_#3	forward	aggaagagagAAGTTATTAAAAAGTAGGTTGGGTTGTT	489
	reverse	cagtaatacgactcactatagggagaaggctCCTTCAAACACTCCTCTAATAAAAAAA	
Ppargc1a_#4	forward	aggaagagagTTTTATTATTGTTTATGGTGTTTGGTT	373
	reverse	cagtaatacgactcactatagggagaaggctAAAATCCCTCCTTTCAATAATTCTA	
Cpt1b_#1	forward	aggaagagagAGTGAATTGGAAAGTTATTGTTTGG	408
	reverse	cagtaatacgactcactatagggagaaggctATACTAAAACCACTCCCTTCCCTAA	
Cpt1b_#8	forward	aggaagagagTTAGGGAAGGGAGTGGTTTTAGTAT	266
	reverse	cagtaatacgactcactatagggagaaggctTTCTCCACCCCAATTTAAAAATAA	
Cpt1b_#10	forward	aggaagagagTTTGGTTTTTTTGGTTTATGTTTTT	462
	reverse	cagtaatacgactcactatagggagaaggctAATCTCCTATCCCATAATACTCCCTAA	
Cpt1b_#12	forward	aggaagagagAAGTAAATTTGAGTTGTGAGTTGGG	488
	reverse	cagtaatacgactcactatagggagaaggctCCATCCTAAAATTTATTCAACACCT	
Cpt1b_#22	forward	aggaagagagGTTGGAGTAGTAGTGGTTTTTGAGG	416
	reverse	cagtaatacgactcactatagggagaaggctCCTATACTAATCCCCAACTCACAAC	
Cpt1a_#5	forward	aggaagagagGAAAGATGGAGGTAAATAGGGTTTT	482
	reverse	cagtaatacgactcactatagggagaaggctCCAAAAACCAACACACTCATAATC	
Cpt1a_#7	forward	aggaagagagGAGATTATGAGTGTGTTGGTTTTTG	364
	reverse	cagtaatacgactcactatagggagaaggctTTCCTTACCCTAAAAACCTCAATTT	
Cpt1a_#15	forward	aggaagagagGGTTTTTAGGGTAAGGAATGTTGTT	383
	reverse	cagtaatacgactcactatagggagaaggctAAAAAAAATACCCTCTACTTCTCCA	

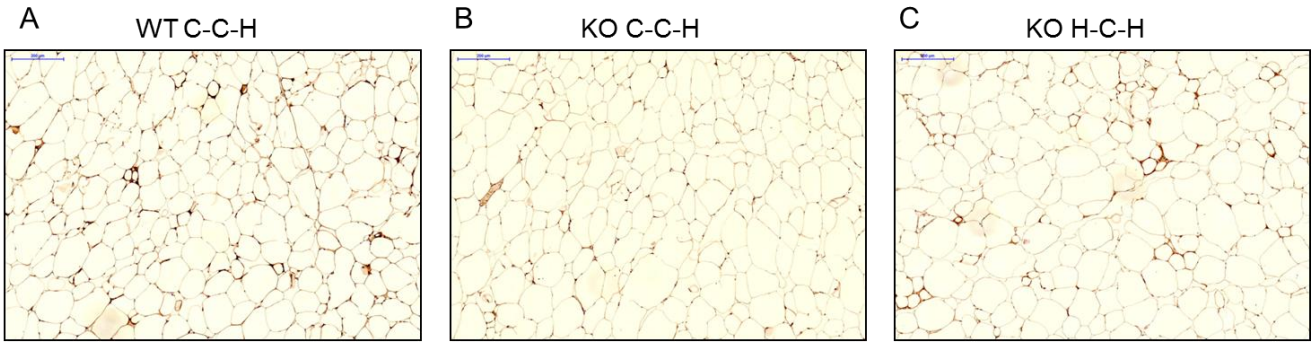
SUPPLEMENTARY DATA

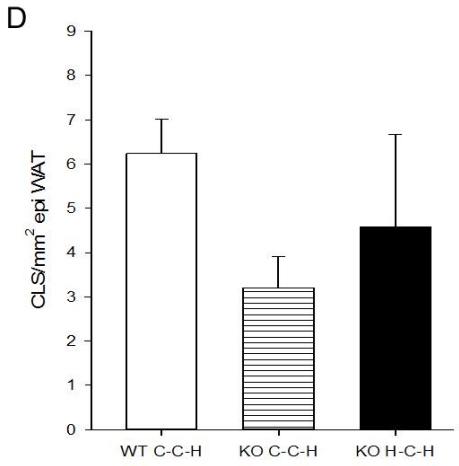
Supplementary Table 3. Sequences of oligonucleotide used for EMSA

Name	Primer	Sequence
CG_Cpt1b+227,+224	forward	AAGCCTGGCCAACCGCCGCTGCCACCGAACC
CG_Cpt1b+227,+224	reverse	GGTTCGGTGGCAGCGGCGGTTGGCCAGGCTT
F_CG_Cpt1b+227,+224	competition	AAGCCTGGCCAACCGCCGCTGCCACCGAACC
(me)CG_Cpt1b+227,+224	forward	AAGCCTGGCCAAC-(me)CGC-(me)CGCTGCCACCGAACC
(me)CG_Cpt1b+227,+224	reverse	GGTTCGGTGGCAG-(me)CGG-(me)CGGTTGGCCAGGCTT
F_(me)CG_Cpt1b+227,+224	competition	AAGCCTGGCCAAC-(me)CGC-(me)CGCTGCCACCGAACC
CG_Cpt1b-72	forward	GGCCCATGTCCCCACGTCCTTCAGGCCTGG
CG_Cpt1b-72	reverse	CCAGGCCTGAAGGACGTGGGGACATGGGCC
F_CG_Cpt1b-72	competition	GGCCCATGTCCCCACGTCCTTCAGGCCTGG
(me)CG_Cpt1b-72	forward	GGCCCATGTCCCCA-(me)CGTCCTTCAGGCCTGG
(me)CG_Cpt1b-72	reverse	CCAGGCCTGAAGGA-(me)CGTGGGGACATGGGCC
F_(me)CG_Cpt1b-72	competition	GGCCCATGTCCCCA-(me)CGTCCTTCAGGCCTGG
CG_Cpt1b-202	forward	TCCTTTTGGGGGAGCGCCTAGGGAGGGTGG
CG_Cpt1b-202	reverse	CCACCCTCCCTAGGCGCTCCCCCAAAAGGA
F_CG_Cpt1b-202	competition	TCCTTTTGGGGGAGCGCCTAGGGAGGGTGG
(me)CG_Cpt1b-202	forward	TCCTTTTGGGGGAG-(me)CGCCTAGGGAGGGTGG
(me)CG_Cpt1b-202	reverse	CCACCCTCCCTAGG-(me)CGCTCCCCCAAAAGGA
F_(me)CG_Cpt1b-202	competition	TCCTTTTGGGGGAG-(me)CGCCTAGGGAGGGTGG
CG_Ppara-140	forward	TGGCCCTGCGGACCCGCAGGCGGAGTGCAG
CG_Ppara-140	reverse	CTGCACTCCGCCTGCGGGTCCGCAGGGCCA
F_CG_Ppara-140	competition	TGGCCCTGCGGACCCGCAGGCGGAGTGCAG
(me)CG_Ppara-140	forward	TGGCCCTGCGGACC-(me)CGCAGGCGGAGTGCAG
(me)CG_Ppara-140	reverse	CTGCACTCCGCCTG-(me)CGGGTCCGCAGGGCCA
F_(me)CG_Ppara-140	competition	TGGCCCTGCGGACC-(me)CGCAGGCGGAGTGCAG
Oct1	forward	TGTCGAATGCAAATCACTAGAA
Oct1	reverse	TTCTAGTGATTTGCATTCGACA
NFkB	forward	AGTTGAGGGGACTTTCCCAGGC
NFkB	reverse	GCCTGGGAAAGTCCCCTCAACT

SUPPLEMENTARY DATA

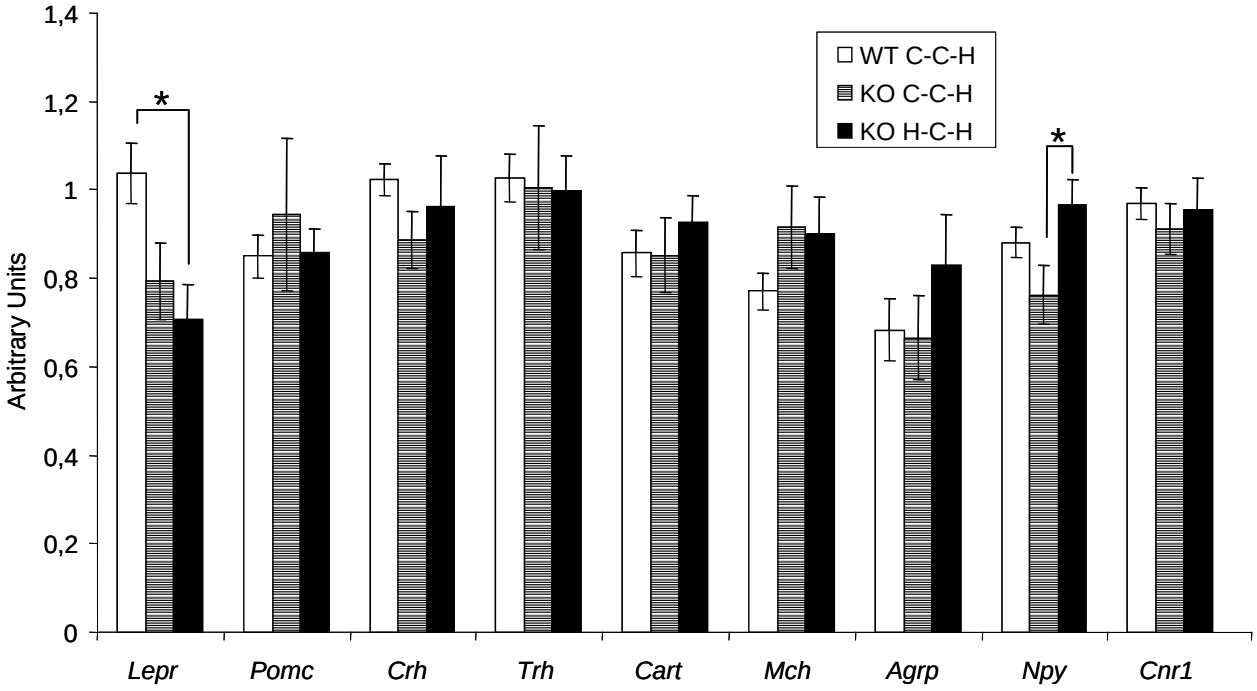
Supplementary Figure 1. Crown-like structures (CLS) in white adipose tissue. Tissues were stained with an F4/80 anti-mouse antibody. Crown-like structures were determined in three randomly chosen areas within the slides. Slightly fewer CLS were observed in KO C-C-H compared to WT C-C-H and KO H-C-H, respectively. However, this was not statistically significant (**D**). n=4-13 per group. CLS: Crown-like structure, WAT: White adipose tissue.





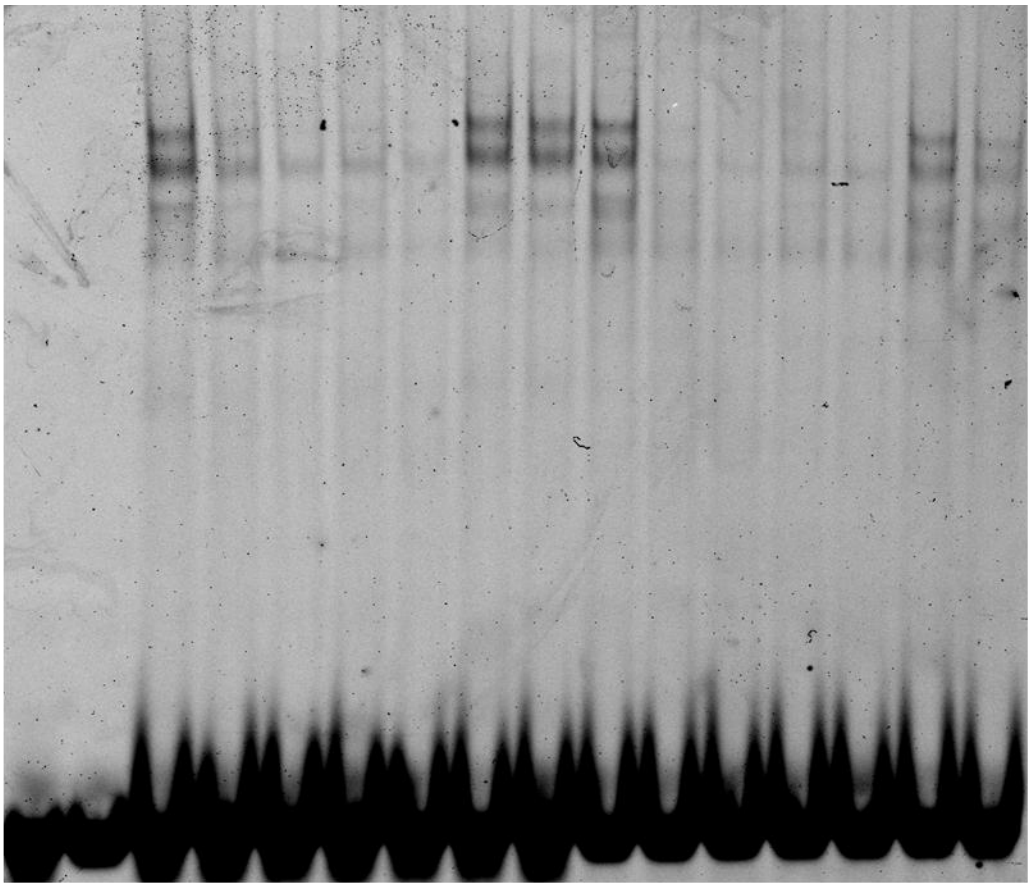
SUPPLEMENTARY DATA

Supplementary Figure 2. Gene expression levels in hypothalamus of leptin receptor – long form (LEPR), proopiomelanocortin (POMC), corticotropin releasing hormone (CRH), thyrotropin-releasing hormone (TRH), cocaine and amphetamine-regulated transcript (CART), melanin-concentrating hormone (MCH), agouti-related protein (AgRP), neuropeptide Y (NPY), cannabinoid receptor 1 (CNR1) and suppressor of cytokine signaling 3 (SOCS3). *P<0.05, n=4-13 per group.



SUPPLEMENTARY DATA

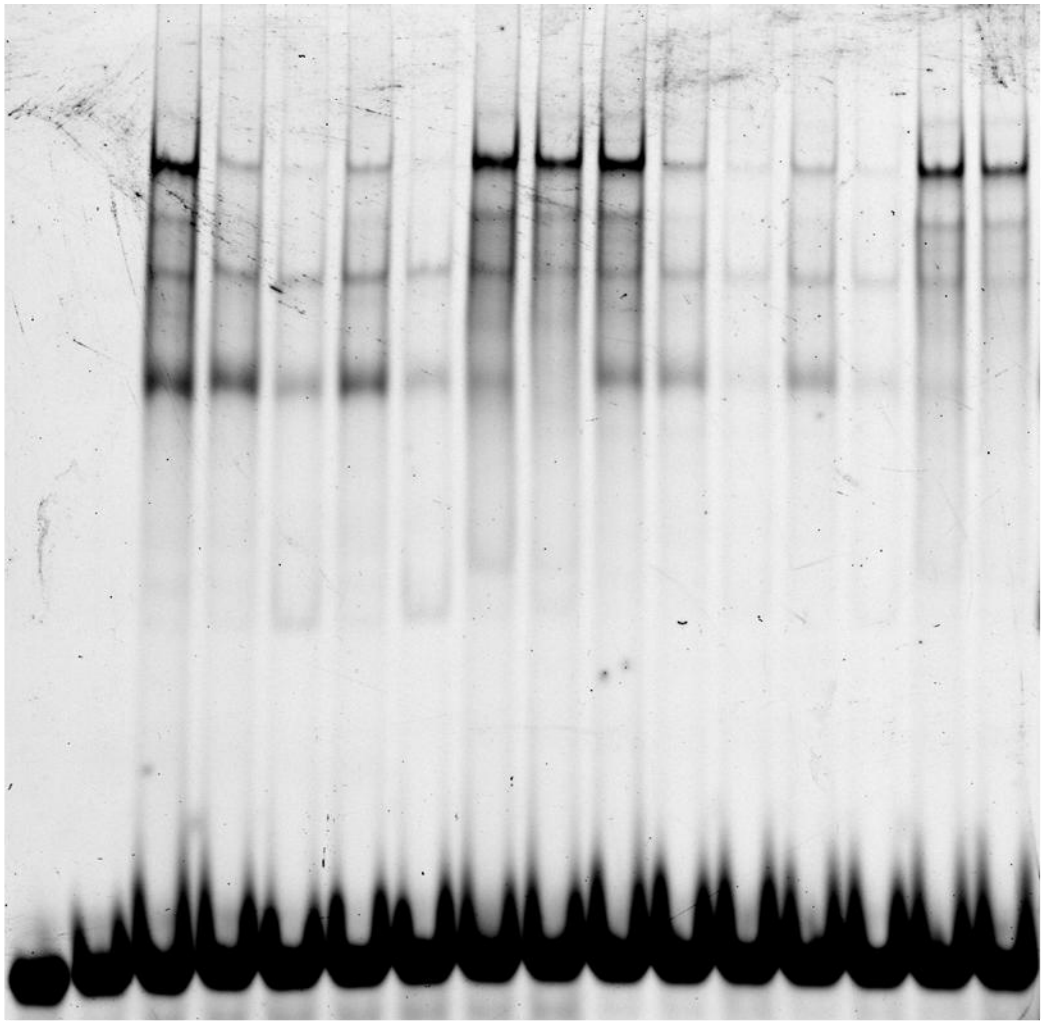
Supplementary Figure 3. No methylation specific formation of a protein-DNA complex at the Cpt1b CpG_{-72} site in mouse C2C12 myoblasts. Methylated (m) and unmethylated (um) Cy5-labelled probes carrying the CpG_{-72} site, were investigated in competition EMSAs using C2C12 mouse myoblast nuclear extracts. Lane 1 and 2 represent oligonucleotides without incubation with nuclear extract. Lane 3 and 10 represent protein-DNA complex formation at the unmethylated and methylated CpG. In lane 4, 5, 13, 14 competition with unlabeled methylated oligonucleotides was performed, whereas in lane 6, 7, 11, 12 competition with unlabeled unmethylated oligonucleotides was performed. Specificity was assured by competition experiments with unlabeled Oct1/NfKB consensus oligonucleotides (lanes 8, 9, 15, 16).



	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
Labelled Oligo	um	m	um							m						
Competitor	-	-	-	10x m	50x m	10x um	50x um	10x NFkB	50x NFkB	-	10x um	50x um	10x m	50x m	10x NFkB	50x NFkB
NE	-	-	+	+	+	+	+	+	+	+	+	+	+	+	+	+

SUPPLEMENTARY DATA

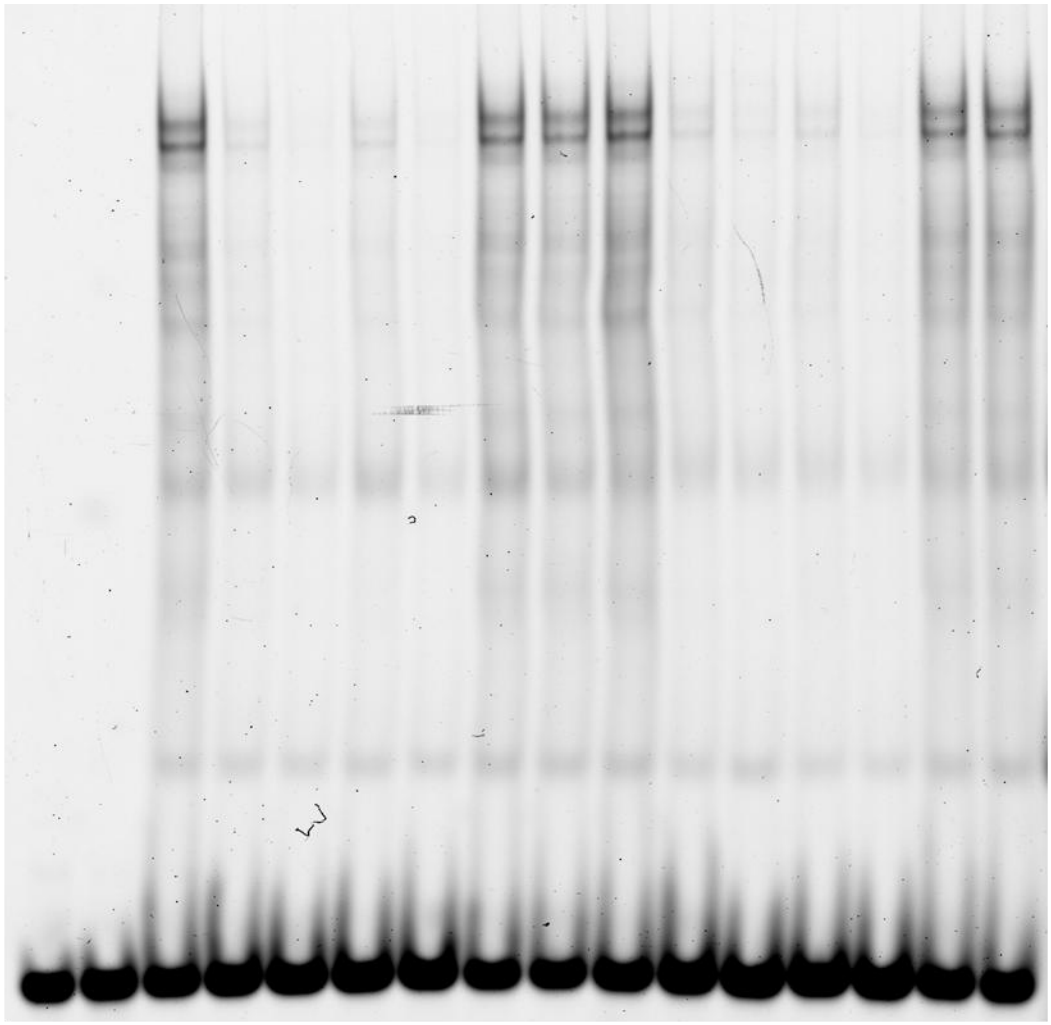
Supplementary Figure 4. No methylation specific formation of a protein-DNA complex at the Cpt1b $CpG_{+227/+224}$ site in mouse C2C12 myoblasts. Methylated (m) and unmethylated (um) Cy5-labelled probes carrying the $CpG_{+227/+224}$ site, were investigated in competition EMSAs using C2C12 mouse myoblast nuclear extracts. Lane 1 and 2 represent oligonucleotides without incubation with nuclear extract. Lane 3 and 10 represent protein-DNA complex formation at the unmethylated and methylated CpG. In lane 4, 5, 13, 14 competition with unlabeled methylated oligonucleotides was performed, whereas in lane 6, 7, 11, 12 competition with unlabeled unmethylated oligonucleotides was performed. Specificity was assured by competition experiments with unlabeled Oct1/NfKB consensus oligonucleotides (lanes 8, 9, 15, 16).



	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
Labelled Oligo	um	m	um							m						
Competitor	-	-	-	10x m	50x m	10x um	50x um	10x Oct1	50x Oct1	-	10x um	50x um	10x m	50x m	10x Oct1	50x Oct1
NE	-	-	+	+	+	+	+	+	+	+	+	+	+	+	+	+

SUPPLEMENTARY DATA

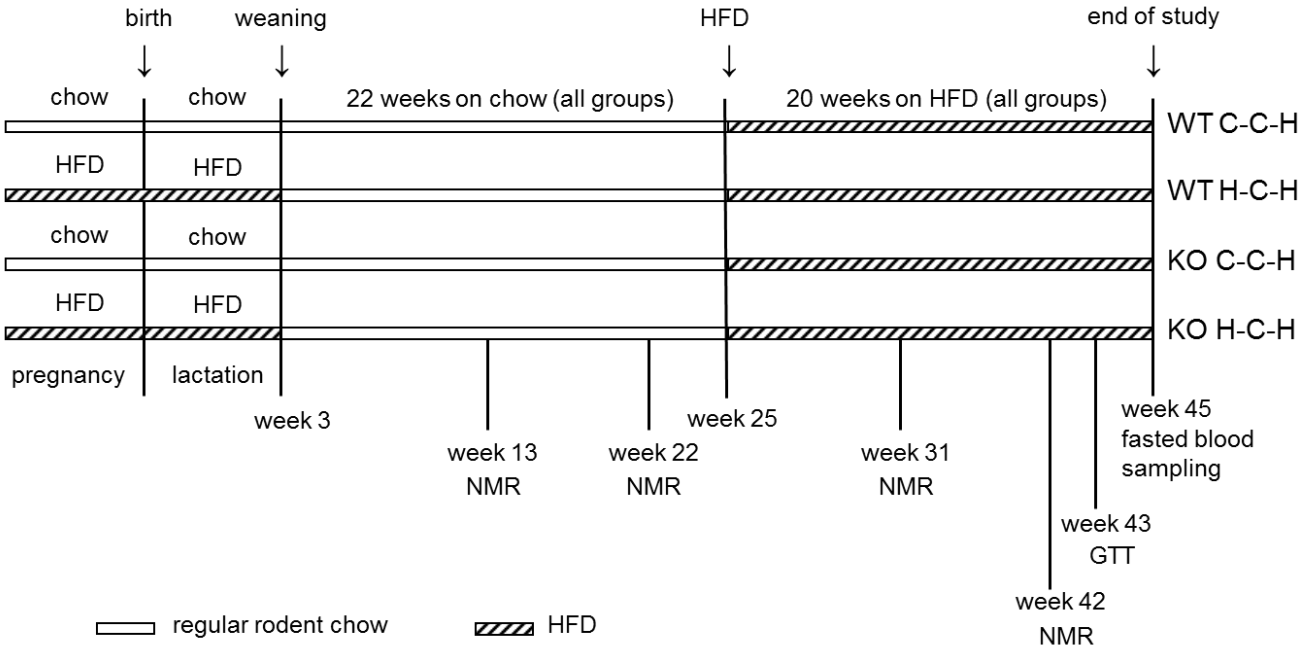
Supplementary Figure 5. No methylation specific formation of a protein-DNA complex at the Cpt1b CpG_{-202} site in mouse C2C12 myoblasts. Methylated (m) and unmethylated (um) Cy5-labelled probes carrying the CpG_{-202} site, were investigated in competition EMSAs using C2C12 mouse myoblast nuclear extracts. Lane 1 and 2 represent oligonucleotides without incubation with nuclear extract. Lane 3 and 10 represent protein-DNA complex formation at the unmethylated and methylated CpG. In lane 4, 5, 13, 14 competition with unlabeled methylated oligonucleotides was performed, whereas in lane 6, 7, 11, 12 competition with unlabeled unmethylated oligonucleotides was performed. Specificity was assured by competition experiments with unlabeled Oct1/NfKB consensus oligonucleotides (lanes 8, 9, 15, 16).



	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
Labelled Oligo	um	m	um							m						
Competitor	-	-	-	10x m	50x m	10x um	50x um	10x Oct1	50x Oct1	-	10x um	50x um	10x m	50x m	10x Oct1	50x Oct1
NE	-	-	+	+	+	+	+	+	+	+	+	+	+	+	+	+

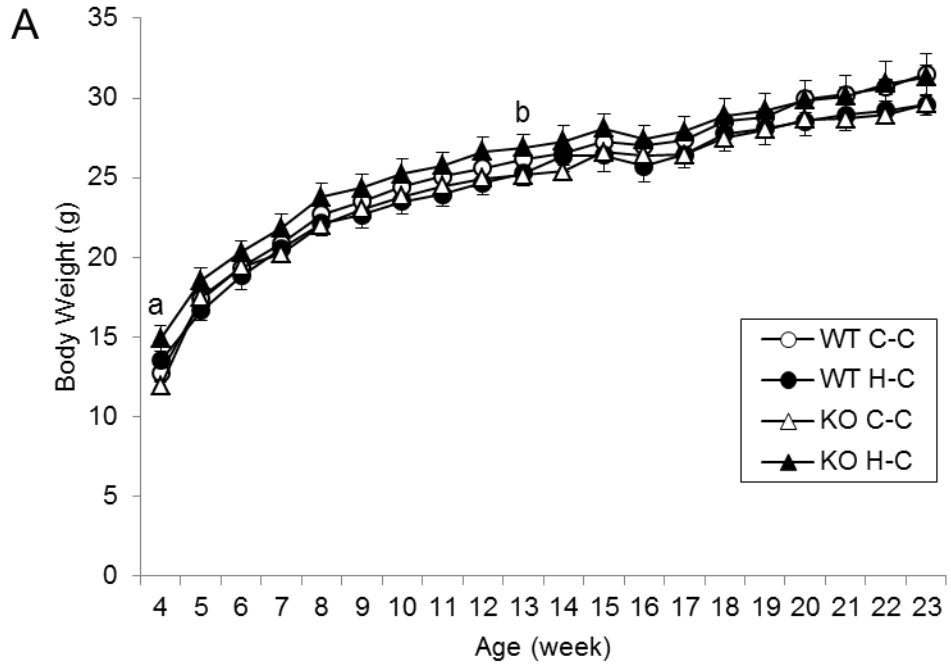
SUPPLEMENTARY DATA

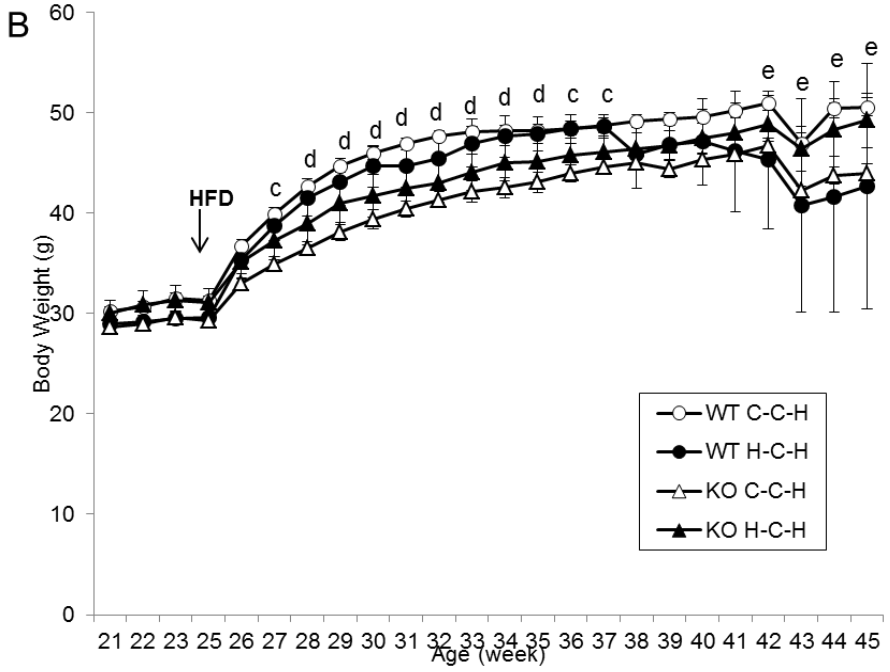
Supplementary Figure 6. Schematic representation of the study including an additional group of wild type mice that received a high fat diet during pregnancy and lactation and between week 25 and 45 of life (WT H-C-H). Open bars indicate periods of food exposition with a regular rodent chow, hatched bars indicate periods of food exposition with a high fat diet. HFD: High fat diet; NMR: Nuclear magnetic resonance spectroscopy; GTT: Intra peritoneal glucose tolerance test; WT: Wild type offspring; KO: *Gipr*$^{-/-}$ offspring. For further details see also Figure 1 in the main text.
Results of key experiments of the study with these for groups are shown in Supplementary Figures 7-11. A two-way ANOVA analysis with genotype and maternal diet as the independent variables was performed. Significance was accepted at $P<0.05$.



SUPPLEMENTARY DATA

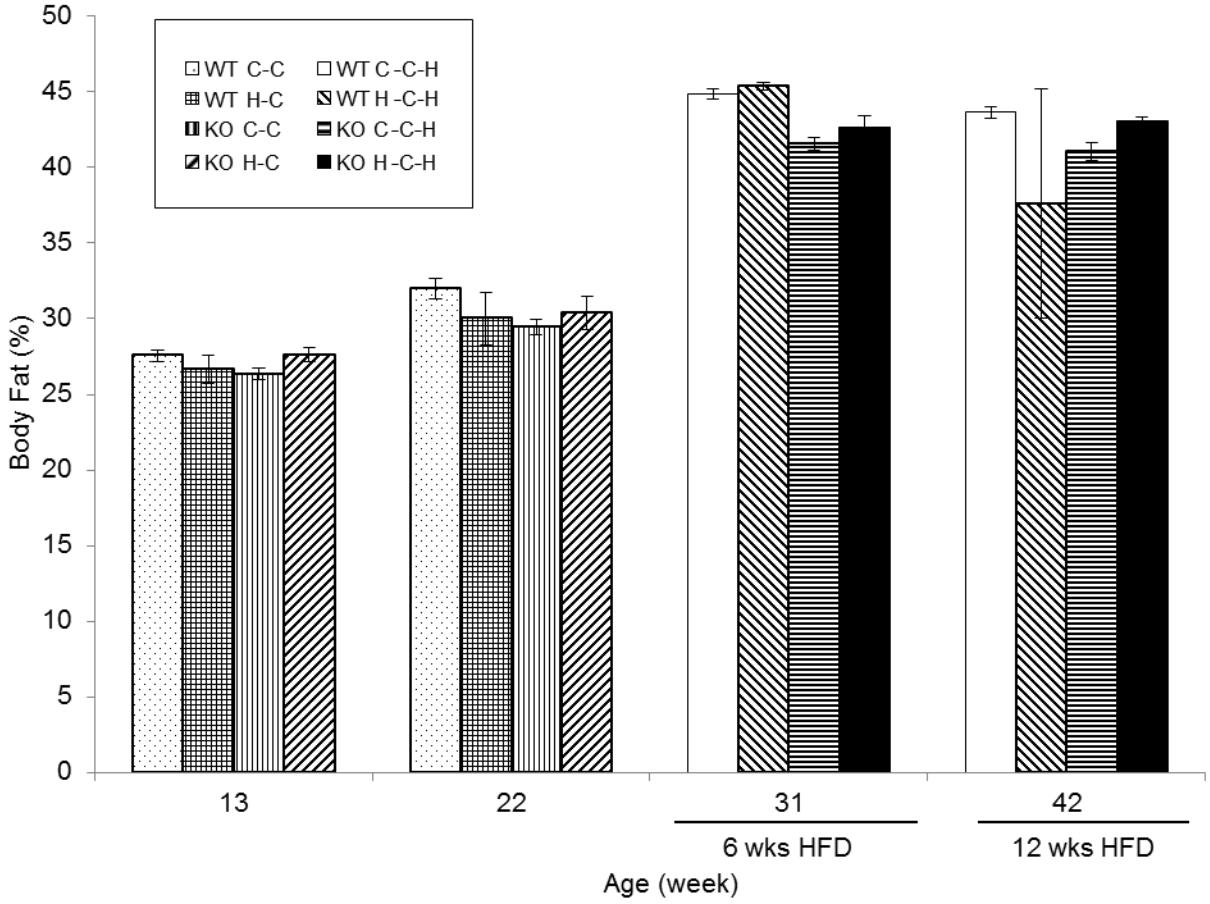
Supplementary Figure 7. A: Growth curve of offspring from 4 weeks until 23 weeks of age on a standard rodent chow. WT C-C: Wild type offspring exposed to a regular chow during pregnancy/ lactation and post weaning; WT H-C: Wild type offspring exposed to HFD during pregnancy/ lactation and post weaning; KO C-C: *Gipr*$^{-/-}$ offspring exposed to a regular chow during pregnancy/ lactation and post weaning; KO H-C: *Gipr*$^{-/-}$ offspring exposed to a HFD during pregnancy/ lactation and switched to a regular diet post weaning; n= 3-13 per group, a = two-way ANOVA P<0.05 for maternal diet, b = two-way ANOVA P<0.05 for interaction genotype x maternal diet.
B: Growth curve of offspring after a HFD was started at 25 weeks of age; n= 3-13 per group, for WT H-C-H n= 2 for week 42-45, c = two-way ANOVA P<0.05 for genotype, d = two-way ANOVA P<0.01 for genotype, e = two-way ANOVA P<0.05 for interaction genotype x maternal diet.





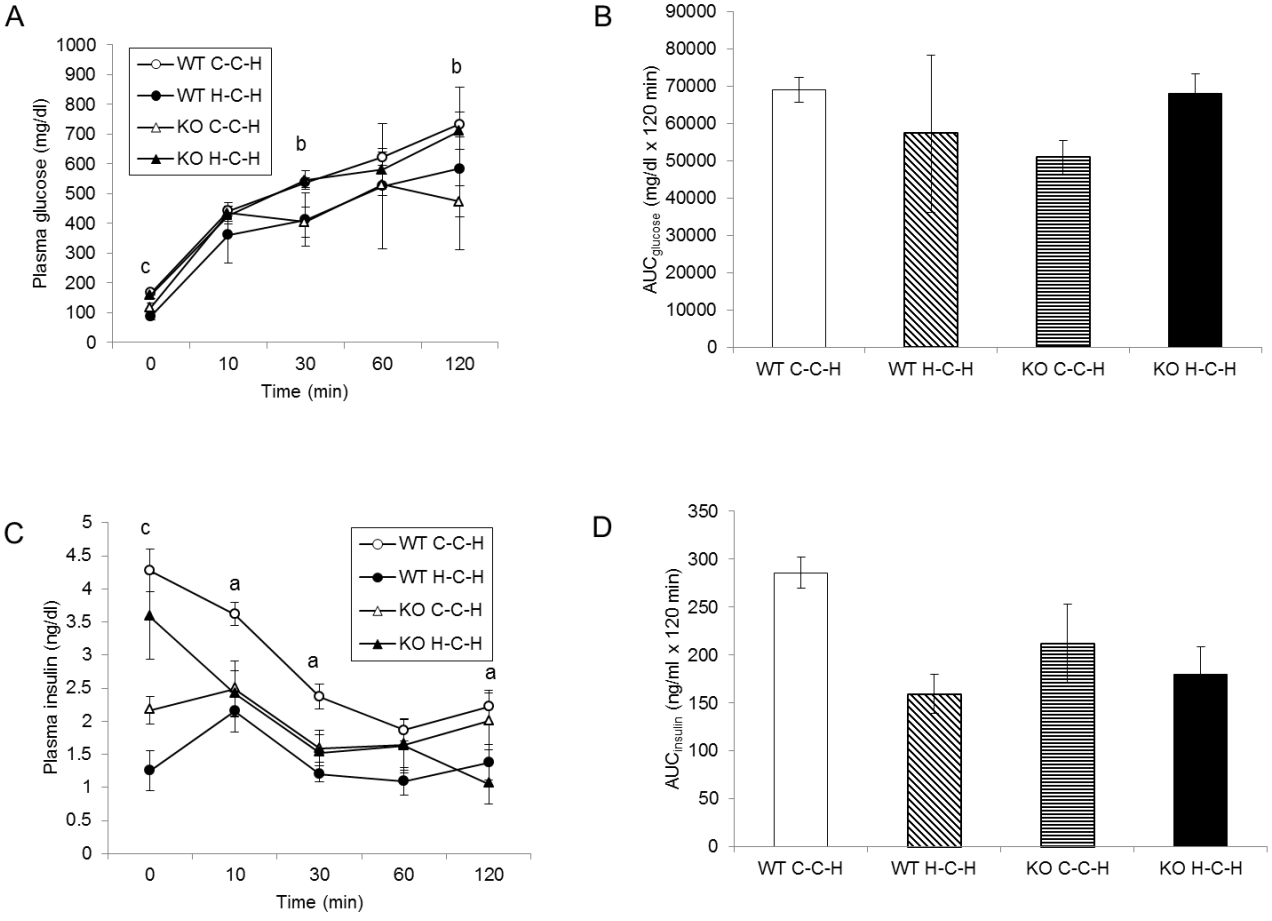
SUPPLEMENTARY DATA

Supplementary Figure 8. Adiposity was measured by nuclear magnetic resonance spectroscopy, n= 3-13 per group, for WT H-C-H n=2 at week 42. Two-way ANOVA: P<0.001 for genotype at 31 weeks and P<0.01 for interaction genotype x maternal diet at 42 weeks.



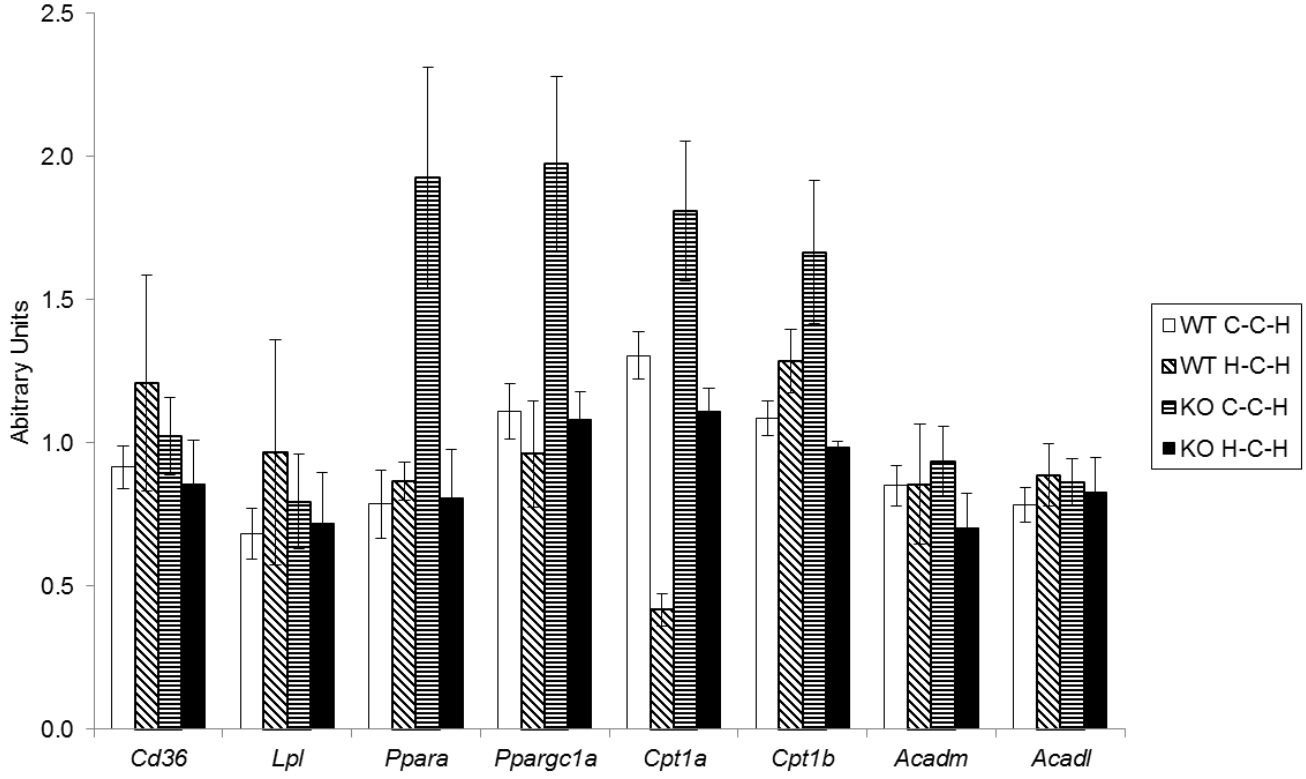
SUPPLEMENTARY DATA

Supplementary Figure 9. Glucose tolerance test at 43 weeks of age (18 weeks on HFD). After an overnight fast, mice received an i.p. injection of 2.0 g glucose per kg body weight. **A:** Plasma glucose levels. **B:** AUC: Area under the curve for glucose, two-way ANOVA: P<0.05 for interaction genotype x maternal diet. **C:** Plasma insulin levels. **D:** AUC: Area under the curve for insulin, two-way ANOVA: P<0.05 for maternal diet.
n=3-13 per group, a = two-way ANOVA P<0.05 for maternal diet, b = two-way ANOVA P<0.05 for interaction genotype x maternal diet, c = two-way ANOVA P<0.01 for interaction genotype x maternal diet.



SUPPLEMENTARY DATA

Supplementary Figure 10. Gene expression levels in gastrocnemius muscle. *Cd36*: Cluster of differation 36 fatty acid transporter, *Lpl*: Lipoprotein lipase, *Ppara*: Peroxisome proliferator-activated receptor α, *Ppargc1a*: Peroxisome proliferator-activated receptor gamma coactivator 1-α, *Cpt1a*: Carnitine palmitoyltransferase-1 α, *Cpt1b*: Carnitine palmitoyltransferase-1 β, *Acadm*: Medium-chain acyl-CoA dehydrogenase, *Acadl*: Long-chain acyl-CoA dehydrogenase. n=4-13 per group; n=2 for WT H-C-H.
Two-way ANOVA: *Ppara*: P<0.05 for interaction genotype x maternal diet. *Ppargc1a*: P<0.05 for genotype and for maternal diet. *Cpt1a*: P<0.01 for genotype, P<0.001 for maternal diet and P<0.01 for interaction genotype x maternal diet. *Cpt1b*: P<0.01 for interaction genotype x maternal diet.



SUPPLEMENTARY DATA

Supplementary Figure 11. Gene expression levels in hypothalamus of phosphatidylinositol 3-kinase catalytic subunit p110 (*Pik3ca)*, phosphatidylinositol 3-kinase regulatory subunit p85α *(Pik3r1*), signal transducer and activator of transcription 3 (*Stat3*) and neuropeptide Y receptor 1 *(Npy1r*). n=4-13 per group; n=2 for WT H-C-H.
Two-way ANOVA: *Pik3r1*: P<0.05 for genotype and for maternal diet.