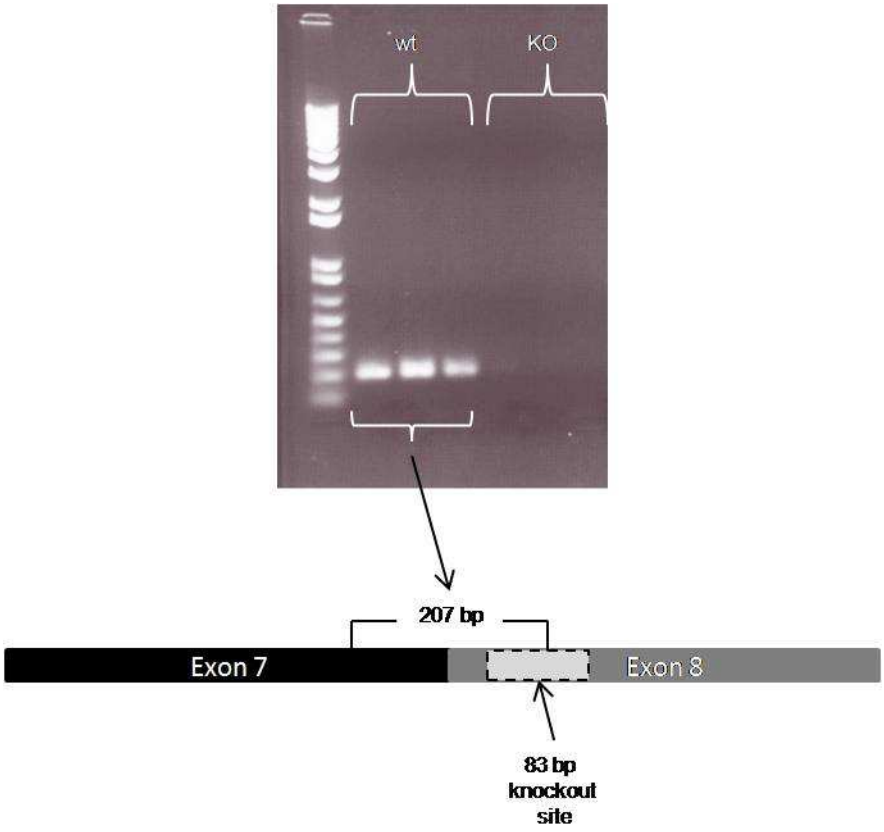
Suppl. Table 1

Primer sequences and miRNA assay.

Gene	Forward Primer	Reverse Primer
Myf5	CCACCTCCAACTGCTCTGA	GCTGTCAAAGCTGCTGTTCTT
MyHC	TCCAAACCGTCTCTGCACTGTT	AGCGTACAAAGTGTGGGTGTGT
MyoD	AGCACTACAGTGGCGATCA	GGCCGCTGTAATCCATCAT
myogenin	CTACAGGCCTTGCTCAGCTC	TGGGAGTTGCATTCACTG
Myl3	GGCTCTGGGTCAGAATCCTA	CATCATCTTGGAATTGAGCTCTT
Mylpf	TGACCATGTTTGGGGAAAAG	GGTAAGCAGCTCCTCCAAGA
TFIIB	TGGAGATTTGTCCACCATGA	GAATTGCCAAACTCATCAAAACT
TPM2	AAAACCATTGATGATCTGGAAGA	TGATGTCATTGAGTGCGTTG

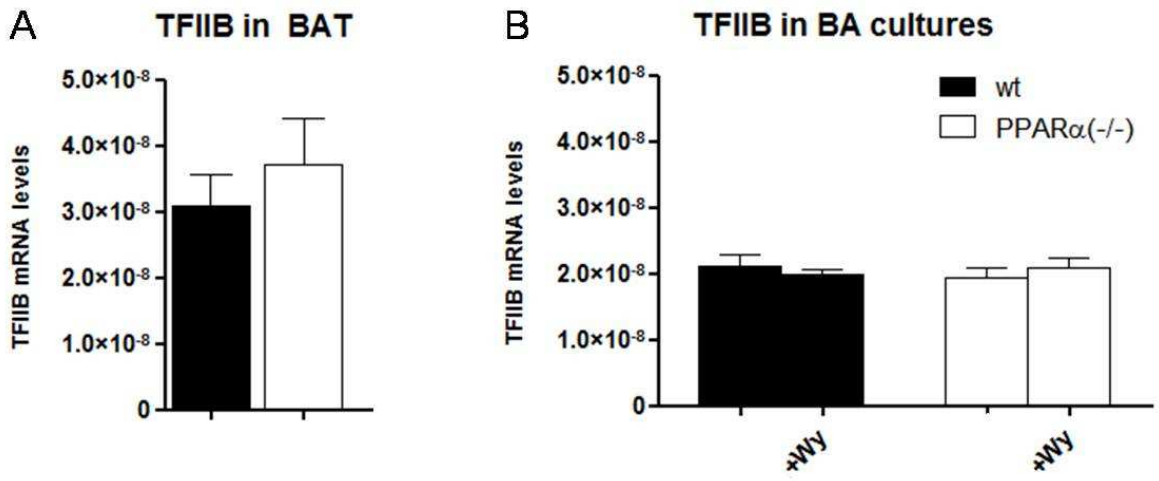
microRNA	Targeted sequence	Assay ID
hsa-miR-206	UGGAAUGUAAGGAAGUGUGUGG	000510

Suppl. Table 1. qPCR primer sequences. Before the measurements, the intron-spanning primer pairs for each mRNA, designed and obtained from the Universal Probe Library, were validated by a standard curve to verify the amplification efficiency and the linear range of amplification (not shown). The miRNA assay from Applied Biosystems consisted of a miRNA-specific RT primer and a miRNA-specific qPCR probe/primer mix.



Suppl. Figure 1. Confirmation of PPARα ablation.
cDNA samples from 3 mice from each genotype (from the same experiment as in Fig. 1 and Suppl. Fig. 2) were analyzed with Reverse-Transcriptase PCR. The PPARα-ablated mice were originally generated by removing an 83 bp sequence in exon 8 [1]. To amplify PPARα cDNA, we used a forward primer annealing in exon 7 and a reverse primer annealing in exon 8 within the 83 bp knockout site. The PCR product was predicted to be 207 bp long in the PPARα-wildtype mice and not existing in PPARα-knockout mice. As seen, the PPARα-wildtype and PPARα-ablated genetic identities were confirmed.
PPARα forward primer: AATGCCTTAGAACTGGATGACAG
PPARα reverse primer : AAAAATGGTGGACCTTCGG

Reference:
[1] S.S. Lee, T. Pineau, J. Drago, E.J. Lee, J.W. Owens, D.L. Kroetz, P.M. Fernandez-Salguero, H. Westphal, F.J. Gonzalez. Targeted disruption of the alpha isoform of the peroxisome proliferator-activated receptor gene in mice results in abolishment of the pleiotropic effects of peroxisome proliferators, Mol. Cell. Biol. 15 (1995) 3012-3022.



Suppl. Figure 2. Expression of TFIIB in BAT and primary brown adipocytes.
(A) TFIIB mRNA levels in interscapular BAT and **(B)** in primary brown adipocytes were measured with Real-Time qPCR. Black bars: wildtype, white bars: PPARα-ablated. The TFIIB mRNA levels were linearized by the formula 2^{-Ct} and presented in **(A)** and **(B)** as means ± SE from 7-8 mice and from 6 cell cultures. The TFIIB expression levels were used to normalize GOI mRNA levels.