Table S1: Sequences of qPCR Primers

Gene	Forward $(5' \rightarrow 3')$	Reverse $(5' \rightarrow 3')$
ACAD-L	TCTTTCCTCGGAGCATGACA	GACCTCTCTACTCACTTCTCCAG
ACAD-M	AAGCCACGAAGTATGCCCTG	CCATAGCCTCCGAAAATCTG
ACC	TGAGGAGGACCGCATTTATC	GCATGGAATGGCAGTAAGGT
Aconitase	TCTCTAACAACCTGCTCATCGG	TCATCTCCAATCACCACCCACC
ADH1	ACAAACCCTTCACCATCGAG	CCTTCTCCAACGCTCTCAAC
Adiponectin	TGTTGGAATGACAGGAGCTG	CGAATGGGTACATTGGGAAC
COX 8b	GAACCATGAAGCCAACGACT	GCGAAGTTCACAGTGGTTCC
COX II	TCTCCCCTCTCTACGCATTCTA	ACGGATTGGAAGTTCTATTGGC
CPT-1β	GATCTGGGCTATCTGTGTCCG	ACGTTTGGAAGCTGTAGAGCATG
CRBP-I	GCTGAGCACTTTTCGGAACT	CCCTCAGCTCTCATTTCCAG
CYC	ATTTCAACCCTTACTTTCCCG	CCACTTATGCCGCTTCATGGC
Cyclophilin	CAAGACTGAATGGCTGGATG	ATGGGGTAGGGACGCTCTCC
FAS	TACTCAGCAGAAGATGTGCGG	TTTGCCAAGGAGGTGCGAAC
G6P	TGCAAGGGAGAACTCAGCAA	GGACCAAGGAAGCCACAATG
GLUT2	ACGGATGCCAATTACCGACA	TGCTGGGCCATGTGCA
Lpl	TCTGTACGGCACAGTGG	CCTCTCGATGACGAAGC
MGL	CAGAGAGGCCAACCTACTTTTC	ATGCGCCCCAAGGTCATATTT
PEPCK	TTGAACTGACAGACTCGCCCT	TGCCCATCCGAGTCATGA
PPARα	GACAAGGCCTCAGGGTACCA	GCCGAATAGTTCGCCGAAA
PPARγ	AACTCTGGGAGATTCTCCTGTTGA	TGGTAATTTCTTGTGAAGTGCTCATA
RALDH1	TTTGGCCACACACTCCAATA	GGGCTGACAAGATTCATGGT
RBP4	TCTGTGGACGAGAAGGGTCAT	CCAGTTGCTCAGAAGACGGAC
RetSDR1	CCAAAGCTGTCCGAGAGAAG	CAATATGGCCGTTCTGGAGT
SCD-1	CTACAAGCCTGGCCTCCTGC	GGACCCCAGGGAAACCAGGA
SREBP-1c	GCAGACTCACTGCTGCTGAC	AGGTACTGTGGCCAAGATGG
TGM2	ACAGCATCCCACTTCGAATC	CTTGATTTCGGGATTCTCCA
UCP-1	CAGAATGCAAGCCCAGAGC	AAGCATTGTAGGTCCCCGTGT

Table S2: Expression levels of genes in soleus muscle in

Gene	WT	C-III-KO	
CPT-1β	0.89±0.31	0.80±0.16	n.d.
PPARα	0.48±0.19	0.48±0.19	n.d.
PGC1a	0.46±0.15	0.46±0.11	n.d.
ACAD-M	0.43±0.12	0.46±0.10	n.d.
ACAD-L	0.83±0.20	0.78±0.15	n.d.

wild-type (WT) and C-III-KO mice after being fed a high fat diet.

Gene expression is presented as relative expression level (mean $\pm$ SEM). n=4 each genotype; n.d., not different. CPT-1 $\beta$ , Carnitine palmitoyltransferase-1 $\beta$ ; PPAR $\alpha$ , peroxisome proliferator-activated receptor alpha; PGC1 $\alpha$ , PPAR $\gamma$  coactivator 1 $\alpha$ ; ACAD, acyl-Coenzyme A dehydrogenase (M-medium; L-long).

## **Online Supplementary Data**

## Figure Legends for supplementary figures

Fig. S1. CRBP-III expression is regulated by PPAR $\gamma$ . (A) Luciferase assays using different CRBP-III promoter constructs transfected into COS7 cells. Cells were co-transfected with expression vectors for PPAR $\gamma$  and RXR $\alpha$ . Relative luciferase activity was assessed after treatment with vehicle (dark bar) or rosiglitazone (light bar). (B) The protein-DNA complex for PPRE1 and PPRE3 can be supershifted (light arrow) using specific antibodies against PPAR $\gamma$  or RXR $\alpha$ . aP2-PPRE was used as a positive control.

## Fig S2

CRBP-III is not expressed in the brain. Northern Blot Analysis of different regions of the brain. Top panel shows lack of expression of CRBP-III; bottom panel shows the ethidium stained RNA gel as loading control. 1, liver, 2, whole brain; 3, cerebral cortex; 4, basal ganglia; 5, hippocampus; 6, hypothalamus; 7, cerebellum; 8, brain stem.

## Fig. S3

CRBP-III is expressed in brown adipose tissue (BAT). Expression of CRBP-III in BAT was analyzed in protein extracts from total BAT (whole), BAT stromal vascular fraction (SVF), BAT adipocytes (ADIPO) and white adipose tissue (WAT) as comparison. 75  $\mu$ g protein was loaded for each sample.