SUPPLEMENTARY DATA

Sequences of the Real-Time PCR Primers (5'>3') used at 60°C:

RPLP0 (H)	SS :	ACCTCCTTTTTCCAGGCTTT
	AS :	CCCACTTTGTCTCCAGTCTTG
Rplp0 (m)	SS :	ACCTCCTTCTTCCAGGCTTT
	AS :	ACCTCTTTCTTCCAAGCTTT
ICER (H)	SS :	ATGGCTGTAACTGGAGATGACACAG
	AS :	CTCCCTGTGGCAAAGCAGCA
Icer (m)	SS :	ATGGCTGTAACTGGAGATGAAACTG
	AS :	CACCTTGTGGCAAAGCAGTA
ATF3 (H)	SS :	CTCCTGGGTCACTGGTGTTT
	AS :	GTTCTCTGCTGCTGGGATTC
Atf3 (m)	SS :	AAGACAGAGTGCCTGCAGAA
	AS :	GTGCCACCTCTGCTTAGCTC
GLUT4 (H)	SS :	CATTCCTTGGTTCATCGTG
	AS :	ATAGCCTCCGCAACATAC
Glut4 (m)	SS :	AGAGTCTAAAGCGCCT
	AS :	CCGAGACCAACGTGAA
ADIPOQ (H)	SS :	GGTCTCGAACTCCTGGCCTA
	AS :	TGAGATATCGACTGGGCATGGT
Adipoq (m)	SS :	AGGAAAGGAGAGCCTGGAGAA
	AS :	CCGTGATGTGGTAAGAGAAGTAG

H: Human; M: Mouse

Supplementary Table 1. Metabolic characteristic of control and high fat diet-induced obese mice

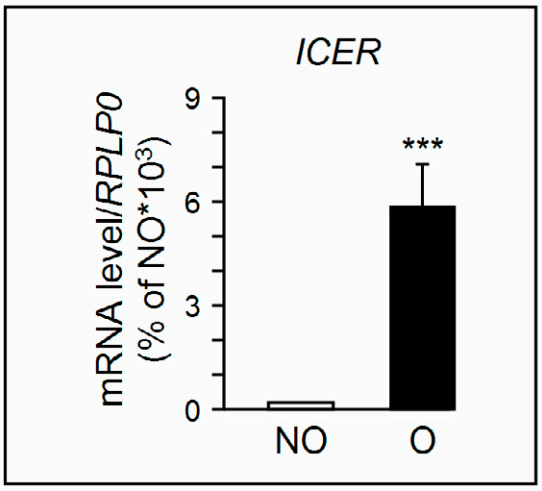
	Control (n=8)	HFD (n=8)
Age (weeks)	36	36
Body weight (grams)	23.1±6.1	32.1±1*
Insulin (μU/ml)	15±7	53±9*
Glucose (mg/dl)	134±13.5	168±17*
GIR (mg/kg/min)	94±19	33±5*

Data are mean ± SEM

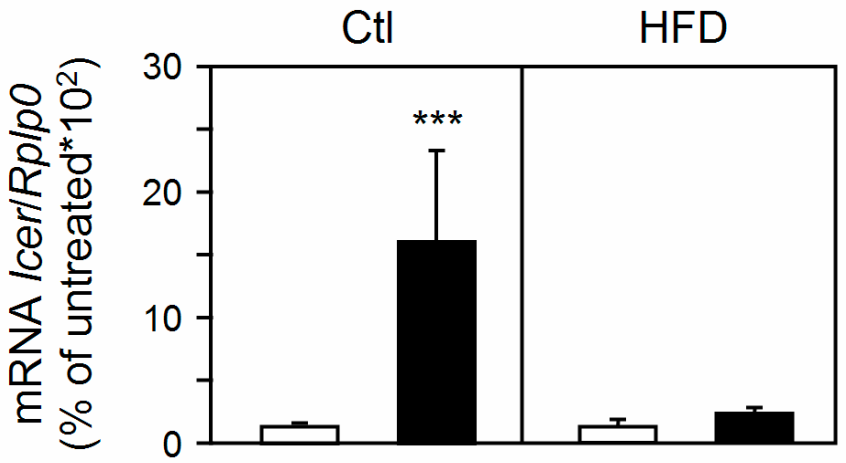
*$p<0.05$, GIR: Glucose infusion rate.

SUPPLEMENTARY DATA

Supplementary Figure 1. Measurement of ICER level in the human subcutaneous adipose tissue (SAT). The mRNA level of *ICER* was quantified by quantitative real-time PCR in 5 SAT of human non obese (NO, *white bars*) and 5 obese individuals (O, *filled bars*). The mRNA level was normalized against the *RPLP0* and the expression level from non obese was set to 100%. Data are the mean of ± SEM that were repeated 3 times (***, P<0.001).

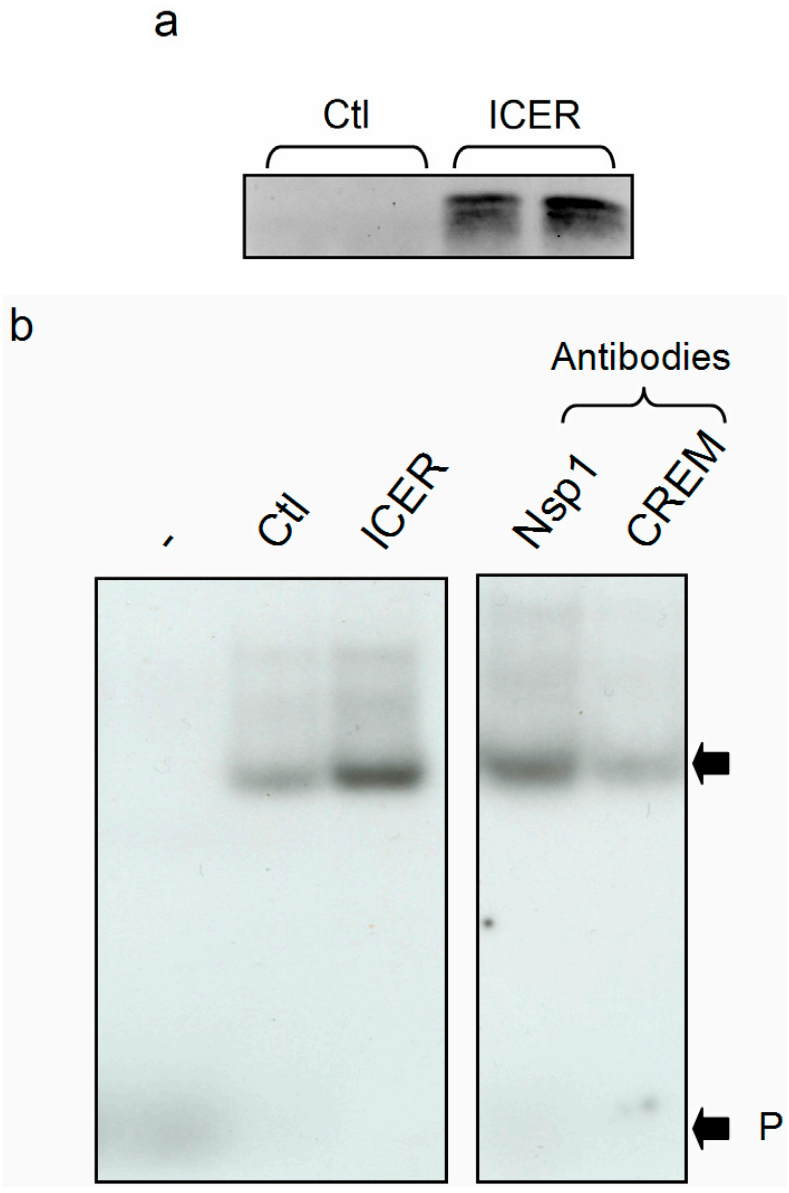


Supplementary Figure 2. Effect of insulin on the expression of Icer in WAT. On the day of the clamp, glucose and insulin (18 $mU \cdot kg^{-1} \cdot min^{-1}$) were infused into the femoral vein for 3 h. Euglycemia was maintained by periodically adjusting a variable infusion of 16.5% glucose. Insulin (*filled bar*) was infused in control (Ctl) and obese mice (HFD). Animals were thereafter euthanized and WAT were extracted. Total RNAs were prepared from WAT of animals and the level of Icer was quantified by quantitative real-time PCR. The mRNA level was normalized against the *Rplp0* and the expression level from mice that were fasted for 10 h (*white bars*) was set to 100%. Data are the mean of ± SEM for 4 mice in each groups that were repeated 3 times (***, P<0.001).



SUPPLEMENTARY DATA

Supplementary Figure 3. Overexpression of Icer in 3T3-L1 adipocytes. The 3T3-L1 adipocytes were electroporated with 250 μg of the plasmid coding for Icer-Iγ (ICER) or the empty vector (Ctl). (**a**) 48h after electroporation, the expression of Icer was detected by Western blotting experiments using the anti-Crem antibody. (**b**) Measurement of the Icer activity by EMSA. Nuclear protein extracts (NEs) were prepared from 3T3-L1 adipocytes 48h after electroporation. NEs were incubated with the CRE sequence as the labelled probe (P). To determine the binding activity of ICER, NEs were pre-incubated with the anti-CREM (CREM) or the anti-HES-1 (Nsp1) antibodies as a negative control. The figures are representative of three independent experiments.



SUPPLEMENTARY DATA

Supplementary Figure 4. Silencing of Icer in 3T3-L1 fibroblasts. The 3T3-L1 undifferentiated cells were transfected with a control RNA duplex (Ctl, *white bars*) or with siICER (*filled bars*). (**a**) Nuclear proteins were prepared 48h after transfection and subjected to western blotting analysis for the quantification of Icer and Atf3 levels. To control the specificity of the silencing the expression of Creb1 is shown. The figure shows the results of a representative experiment out of three. (**b**) Quantification of the *Atf3*, *Adipoq* and *Glut4* levels by quantitative real-time PCR. Total RNAs were prepared 48h (*Atf3)* and 96h (*Adipoq* and *Glut4*) after transfection. The mRNA levels of *Atf3*, *Adipoq* and *Glut4* were normalised against the *Rplp0* and the expression levels from control cells were set to 100%. Data are the mean of ± SEM of 3 independent experiments (***, P<0.001).