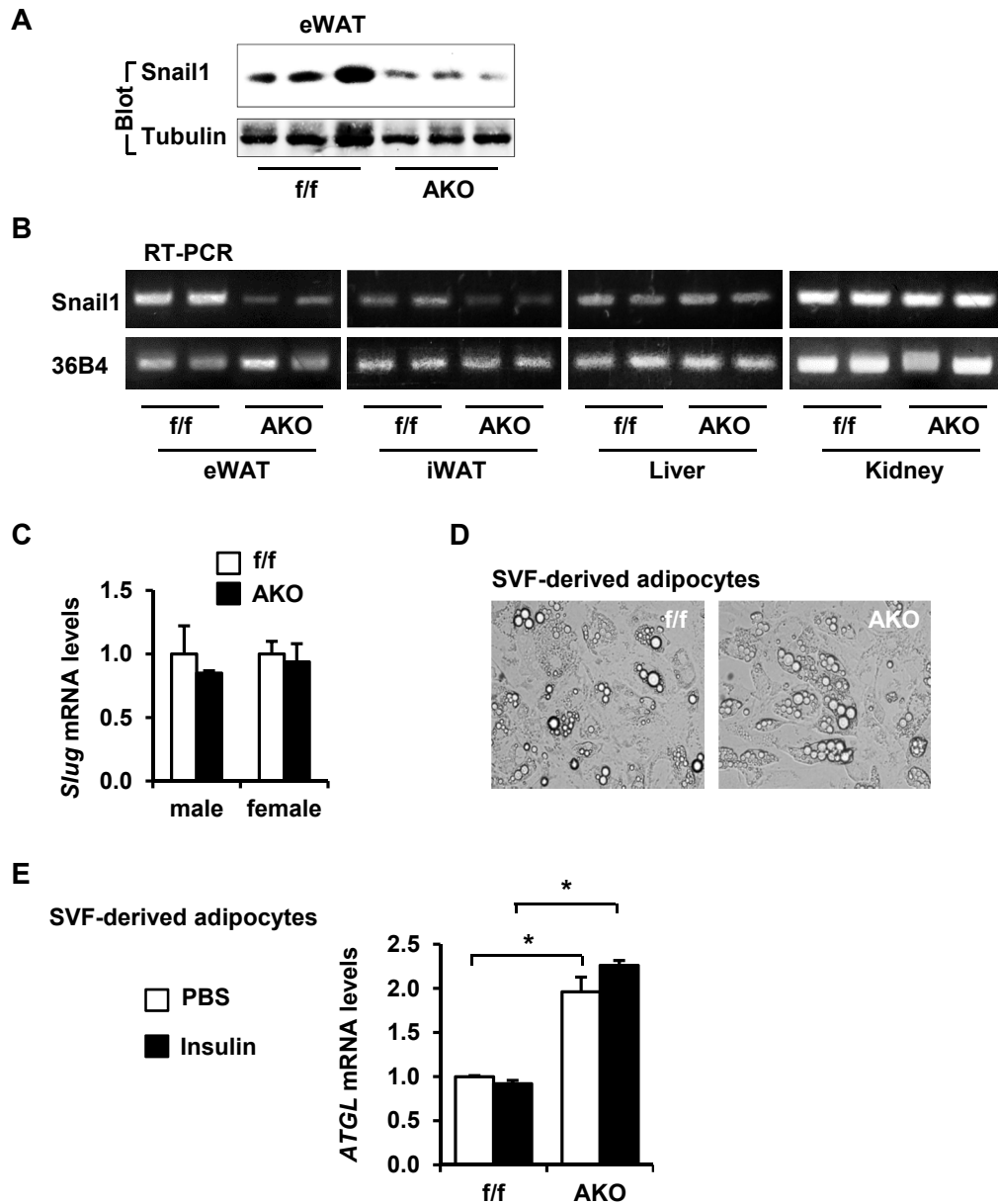
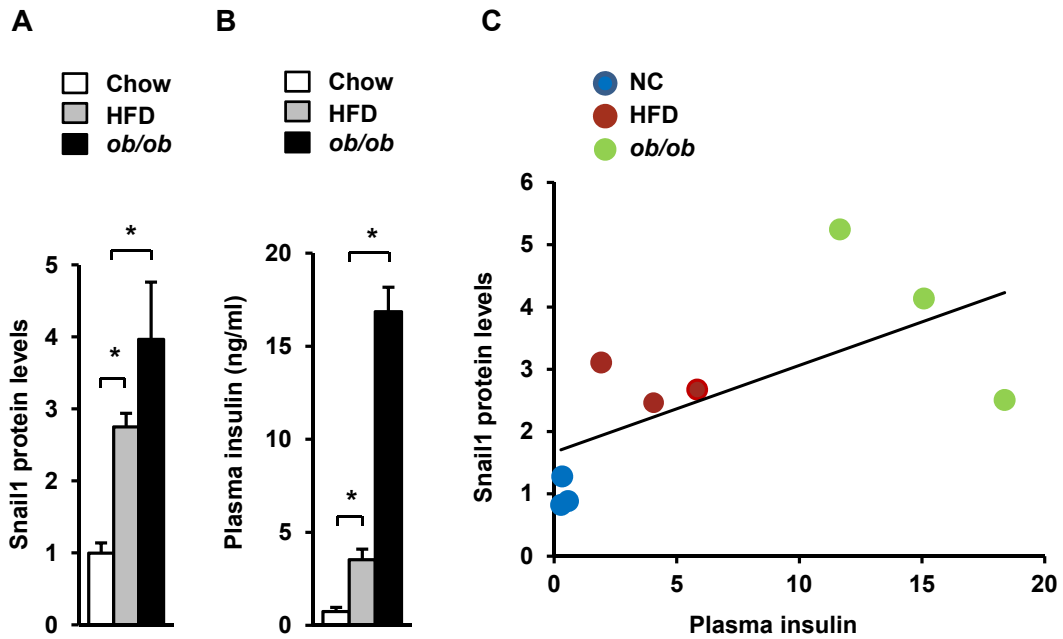


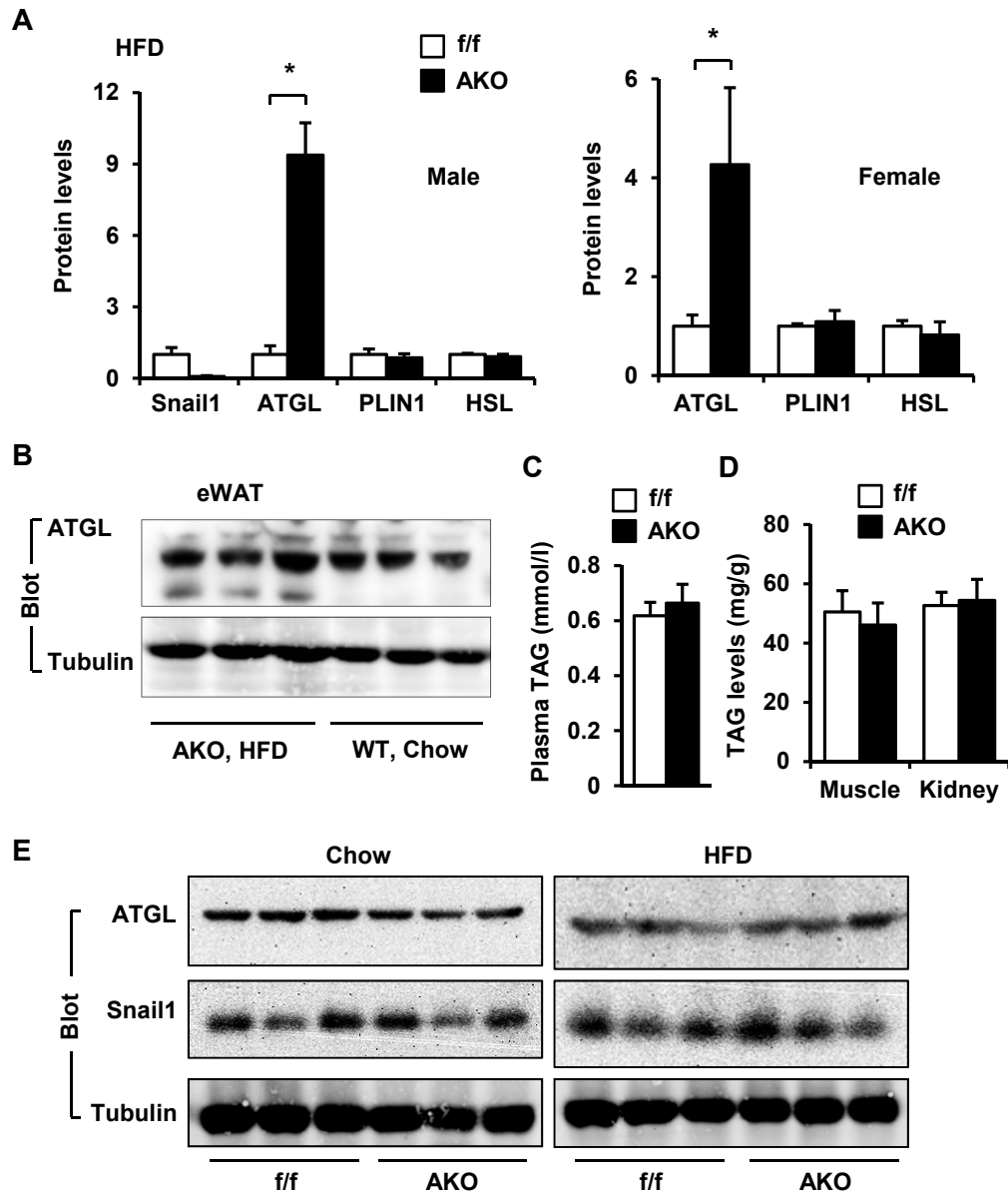
**Figure S1. Insulin increases Snail1 levels in adipocytes.** **A.** 3T3-L1 adipocytes were stimulated with insulin at 0-100 nM for 60 min. Cell extracts were immunoblotted with antibodies against Snail1, phospho-Akt (pSer473), Akt, phospho-GSK3 $\alpha/\beta$  (pSer21/9), GSK3 $\alpha/\beta$ , or tubulin. **B.** Snail1 proteins in Fig. 1F (normalized to p85 levels) were quantified. **C.** C57BL male mice (12 weeks) were injected with insulin (2 units/kg body weight i.p.) and eWAT was harvested 2 and 4 h after stimulation. *Snail1* mRNA levels were measured by qPCR and normalized to 36B4 expression. The values are mean  $\pm$  sem. \* $p$ <0.05. (Related to Figure 1).



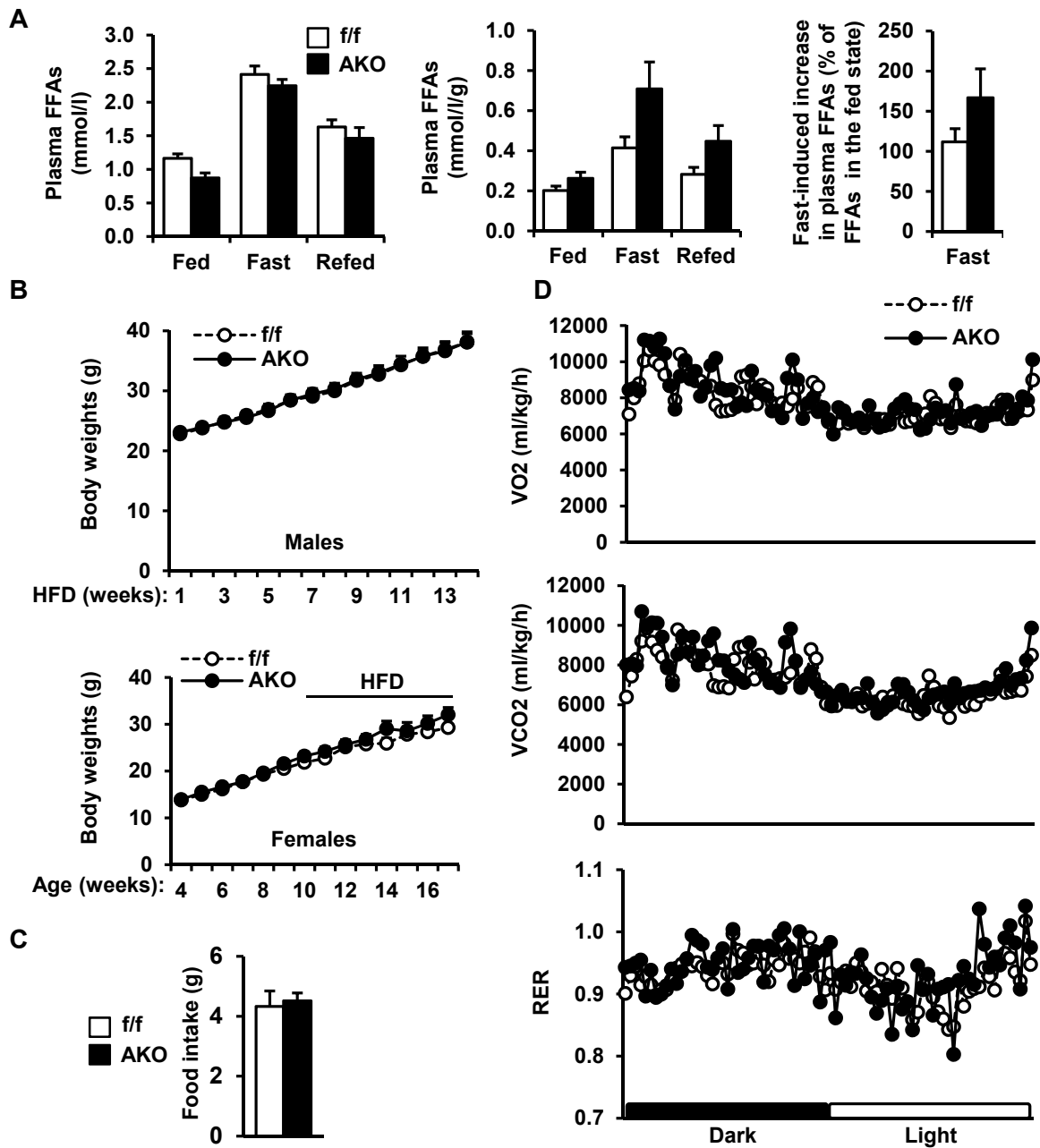
**Figure S2. Verification of AKO mice.** **A.** eWAT extracts were immunoblotted with the indicated antibodies. **B.** Total mRNAs were prepared from AKO and *Snail1<sup>flox/flox</sup>* males, and *Snail1* and *36B4* mRNA levels were measured by RT-PCR. **C.** *Slug* expression (normalized 36B4 levels) was measured in gonadal WAT by qPCR. Males (12 weeks): f/f: n=5; AKO: n=3; females (20 weeks): f/f: n=6, AKO: n=4. **D.** SVFs were isolated from eWAT and differentiated into adipocytes. Representative images of SVF-derived adipocytes. **E.** SVF-derived adipocytes were deprived of serum overnight and stimulated with insulin (100 nM) or PBS (control) for 6 h. *ATGL* mRNA levels were measured by qPCR and normalized to 36B4 levels. N=3. The values are mean  $\pm$  sem. \*p<0.05. (Related to Figure 2).



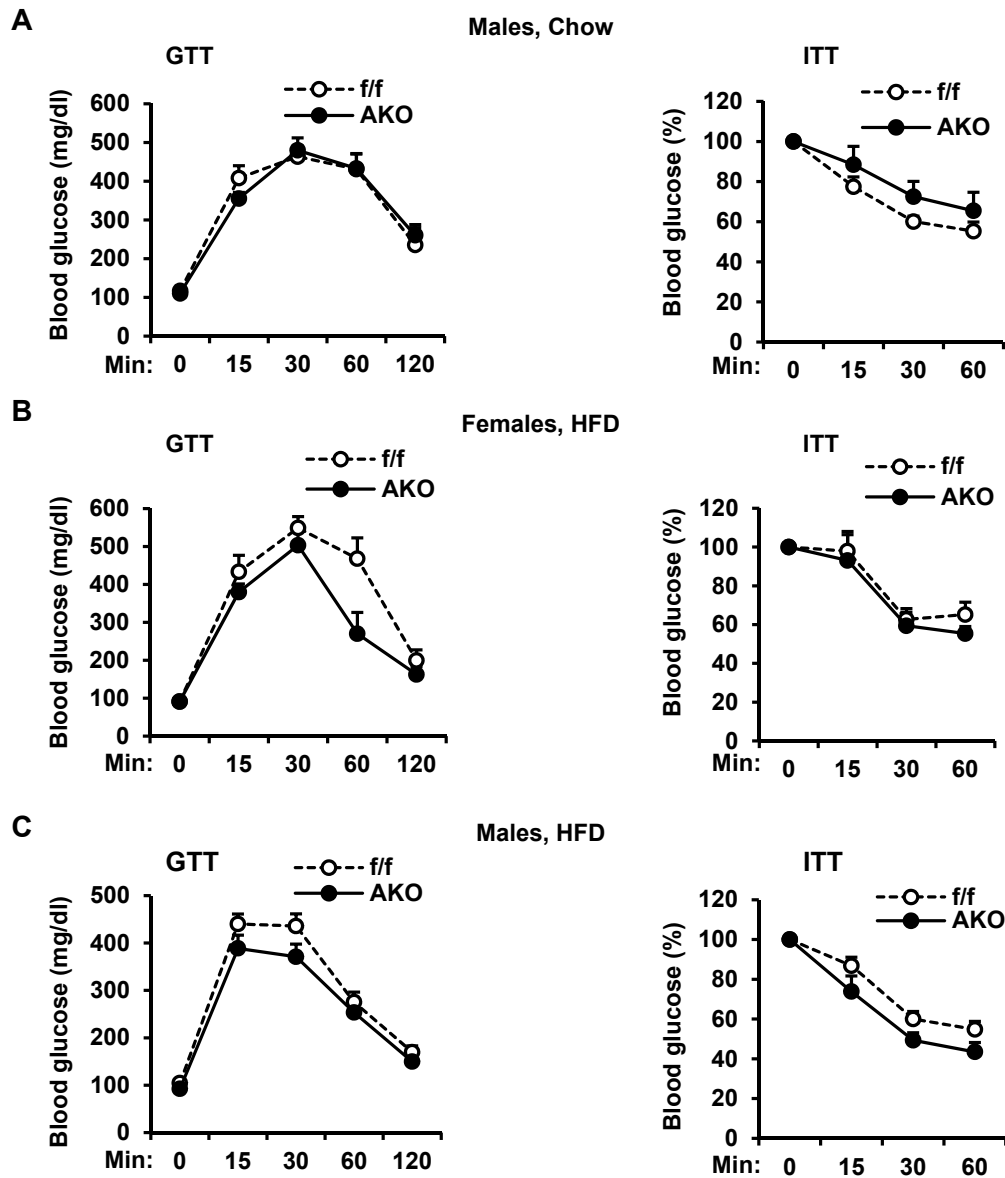
**Figure S3. eWAT Snail1 levels correlate with plasma insulin levels in mice. A.** Snail1 protein levels in Fig. 5B were quantified (normalized to tubulin levels). **B.** Overnight fasting plasma insulin levels. **C.** eWAT Snail1 protein levels (A) were plotted against fasting plasma insulin levels (B). The values are mean  $\pm$  sem. \* $p < 0.05$ . (Related to Figure 3).



**Figure S4. Characterization of AKO mice.** **A.** Protein levels in Fig. 5C were quantified (normalized to tubulin levels). **B.** eWAT extracts were prepared from AKO males fed a HFD for 30 weeks or WT mice (14 weeks) fed a standard chow diet, and immunoblotted with the indicated antibodies. **C-D.** AKO and *Snail1<sup>flox/flox</sup>* males were fed a HFD for 30 weeks. Plasma (n=12-15), muscle (n=6), and kidney (n=6) TAG levels were measured in mice fasted overnight. **E.** Males were fed either a normal chow diet (10 week-old) or a HFD for 30 weeks. Liver extracts were immunoblotted with the indicated antibodies. The values are mean  $\pm$  sem. \*p<0.05. (Related to Figure 5)



**Figure S5. Lipolysis, Body weight, and energy balance in *Snail1<sup>flox/flox</sup>* and AKO mice.** **A.** AKO (n=4) and *Snail1<sup>flox/flox</sup>* (n=8) males (6 wks) were fed a HFD for 2 wks. Blood samples were collected under fed, fasted (overnight), or refed (for 3 h) conditions and used to measure FFAs. Fat mass was measured using pDEXA. Plasma FFA levels were normalized to fat mass (left panels), and the difference between the fasted and fed states was further normalized to the values in the fed state (right panels). **B.** Male (n=20) and female (n=3-6) growth curves. Males were fed a HFD at 7 weeks of age. **C-D.** Males (10 weeks, n=3) were fed a normal chow diet. **C.** Food intake. **D.** O<sub>2</sub> consumption and CO<sub>2</sub> production were measured using metabolic cages and normalized to lean mass. The values are mean ± sem. (Related to Figure 6).



**Figure S6. Glucose metabolism in AKO mice.** **A.** GTT (glucose: 2 g/kg body weight) and ITT (insulin: 1 unit/kg) were performed in male mice at 8 weeks of age (AKO: n=5-7; *Snail1*<sup>flox/flox</sup>: n=7-10). **B.** GTT (glucose: 2 g/kg body weight) and ITT (insulin: 0.7 units/kg) were performed in female mice fed a HFD for 8 weeks (AKO: n=6; *Snail1*<sup>flox/flox</sup>: n=3). **C.** GTT (glucose: 1 g/kg body weight) and ITT (insulin: 1 unit/kg) were performed in male mice fed a HFD for 30 weeks (AKO: n=17; *Snail1*<sup>f/f</sup>: n=12). The values are mean ± sem. (Related to Figure 7).

<b>Antibody</b>	<b>Inc.</b>	<b>CAT#</b>	<b>Dilution</b>
AKT	Cell Signaling Technology	2920	5,000
pAkt (Ser473)	Cell Signaling Technology	4060	5,000
GSK3 $\alpha/\beta$	Cell Signaling Technology	5676	5,000
pGSK3 $\alpha/\beta$	Cell Signaling Technology	8566	5,000
Tubulin	Santa Cruz	sc-5286	5,000
ERK	Santa Cruz	sc-154	5,000
pMAPK	Cell Signaling Technology	4370	5,000
Snail1	Cell Signaling Technology	3895	2,500
ATGL	Cell Signaling Technology	2439	5,000
PLIN1	Cell Signaling Technology	2178	5,000
Snail1	Cell Signaling Technology	3879	ChIP
H3K9ac	EMD Millipore	04-1003	ChIP

**Table S1. Antibodies, Related to Figures 1-5**

### ChIP primers

Genes	Forward	Reverse
<i>ATGL</i>	AGGAGGAGACACCTGTTAC	GATTCCCAGGCTTCAGCTTC
<i>NIK</i>	CGAGGTCCACAGAATGAAGGAC	CAAGTCAGGGTCTCACAGCATAG
<i>CDH1</i>	CATGTCTCCGTGGGTCAGA	AGGTGGCAGCCAAGGAACT

### qPCR primers

Genes	Forward	Reverse
<i>Snail1</i>	CCTTGTGTCTGCACGACCTGT	CACTGGTATCTCTTCACATCCG
<i>adiponectin</i>	AAGGACAAGGCCGTTCTCT	TATGGGTAGTTGCAGTCAGTTGG
<i>ATGL</i>	TTCACCATCCGCTTGTGGAG	AGATGGTCACCCAATTCCTC
<i>HSL</i>	ACGCTACACAAAGGCTGCTT	TCGTTGCGTTTGTAGTGCTC
<i>PLIN1</i>	CACTCTCTGGCCATGTGGAT	AGAGGCTGCCAGGTTGTG
<i>PPAR<math>\gamma</math></i>	CCAGAGTCTGCTGATCTGCG	GCCACCTCTTTGCTCTGATC
<i>ChREBP</i>	CTGGGGACCTAACAGGAGC	GAAGCCACCCTATAGCTCCC
<i>SREBP1</i>	AACGTCACCTCCAGCTAGAC	CCACTAAGGTGCCTACAGAGC
<i>Fasn</i>	TTGACGGCTCACACACCTAC	CGATCTTCCAGGCTCTTCAG
<i>PGC1<math>\alpha</math></i>	TGGACGGAAGCAATTTTCA	TTACCTGCGCAAGCTTCTCT
<i>LCAD</i>	CACTCAGATATTGTCATGCCCT	TCCATTGAGAATCCAATCACTC
<i>MCAD</i>	ACCCTGTGGAGAAGCTGATG	AGCAACAGTGCTTGGAGCTT
<i>ApoB</i>	CCAGAGTGTGGAGCTGAATGT	TTGCTTTTATGGGAGCCTAGC
<i>MTP</i>	CTCCACAGTGCAGTTCTCACA	AGAGACATATCCCCTGCCTGT
<i>DGAT1</i>	CGTGGTATCCTGAATTGGTG	GGCGTTCTCAATCTGAAAT
<i>DGAT2</i>	ATCTTCTCTGTCACCTGGCT	ACCTTTCTTGGGCGTGTCC
<i>36B4</i>	AAGCGCGTCCTGGCATTGTCT	CCGCAGGGGCAGCAGTGGT
<i>Slug (mouse)</i>	ATTGCCTTGTGTCTGCAAGAT	TTTTGGAGCAGTTTTTGC ACT
<i>Slug (human)</i>	ACTGGACACACATACAGTGATT	GGAGAGAGGCCATTGGGTAG
<i>GAPDH (human)</i>	CGACCACTTTGTCAAGCTCA	AGGGGTCTACATGGCAACTG

**Table S2. Primer Sequences, Related to Figures 1, 3-5, and 7.**