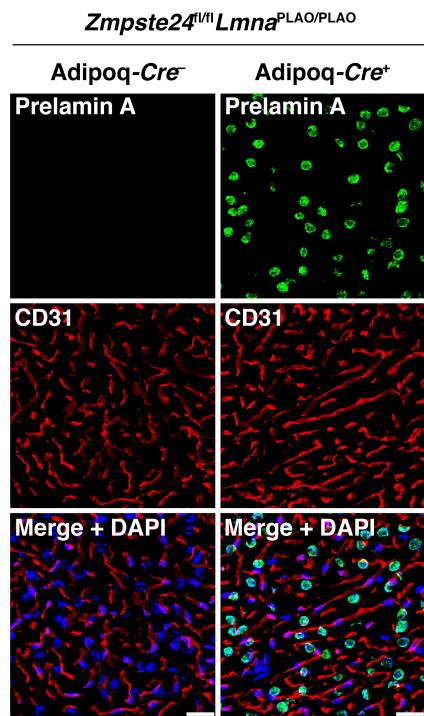
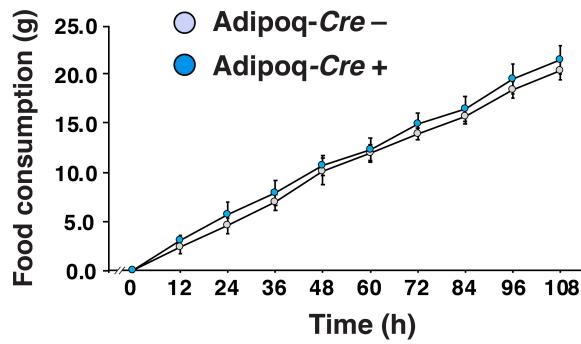


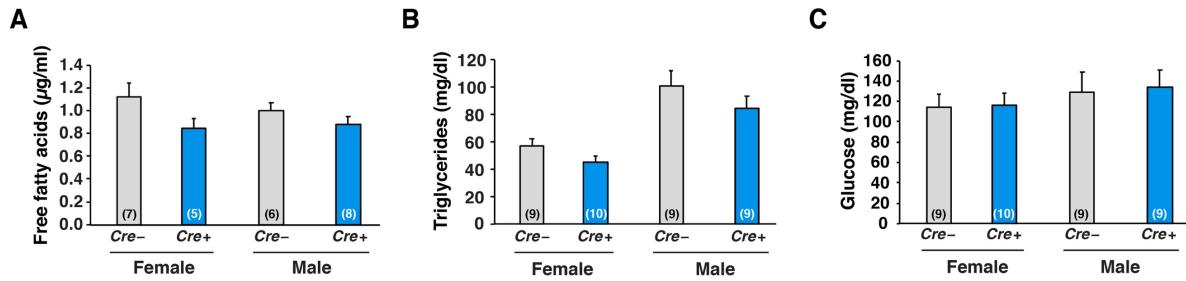
Supplemental Figure S1. Specificity of the Adipoq-Cre transgene. (A) Quantitative RT-PCR studies of *Cre* expression in gonadal WAT and liver in male and female *Lmna^{PLAO/PLAO}Zmpste24^{f/f}*Adipoq-Cre⁻ (grey) and *Lmna^{PLAO/PLAO}Zmpste24^{f/f}*Adipoq-Cre⁺ (blue) mice. Gene expression was normalized to cyclophilin A. Graphs show mean ± SEM; 3 mice/group. *P < 0.01. (B) Adipoq-Cre expression in adipose tissue detected with the *Rosa^{mT/mG}* reporter mouse. The expression of *Cre* in *Rosa^{mT/mG}* mice results in the loss of tdTomato fluorescence (red) and the appearance of EGFP fluorescence (green). Gonadal WAT and kidney (with attached perirenal fat) were collected from *Rosa^{mT/mG}*Adipoq-Cre⁻ and *Rosa^{mT/mG}*Adipoq-Cre⁺ mice, and tissue sections were imaged by fluorescence microscopy. Nuclei were stained with DAPI (white). The border between perirenal fat and kidney is marked with a dashed line. Scale bars; 50 µm for WAT and 25 µm for kidney. (C) Detection of Adipoq-Cre expression in peritoneal macrophages using the *Rosa^{mT/mG}* reporter mouse. Macrophages isolated from a *Rosa^{mT/mG}*Adipoq-Cre⁺ mouse were stained with DAPI to identify nuclei (white) and examined by fluorescence microscopy. The macrophages expressed tdTomato fluorescence (red) but not EGFP (green). Scale bar, 20 µm. (D) Measurement of *Zmpste24* expression in peritoneal macrophages isolated from male *Lmna^{PLAO/PLAO}Zmpste24^{f/f}*Adipoq-Cre⁻ (grey) and *Lmna^{PLAO/PLAO}Zmpste24^{f/f}*Adipoq-Cre⁺ (blue) mice. Gene expression was normalized to cyclophilin A; graphs show mean ± SEM; n = 3 mice/group. *P < 0.05. (E and F) Measurement of *Zmpste24* expression by qRT-PCR in liver (E) and kidney (F) from male and female *Lmna^{PLAO/PLAO}Zmpste24^{f/f}*Adipoq-Cre⁻ (grey) and *Lmna^{PLAO/PLAO}Zmpste24^{f/f}*Adipoq-Cre⁺ (blue) mice. Data were normalized to cyclophilin A. The mean ± SEM are shown for 5–7 male mice and 4–5 female mice/genotype. *Zmpste24* expression was not reduced in the liver and kidney of *Lmna^{PLAO/PLAO}Zmpste24^{f/f}*Adipoq-Cre⁺ mice (P > 0.250).



Supplemental Figure S2. Detection of prelamin A in adipocytes but not endothelial cells of *Lmna*^{PLAO/PLAO}*Zmpste24*^{f/f}*Adipoq-Cre*⁺ mice. Frozen tissue sections of BAT from a *Lmna*^{PLAO/PLAO}*Zmpste24*^{f/f}*Adipoq-Cre*⁻ mouse and a *Lmna*^{PLAO/PLAO}*Zmpste24*^{f/f}*Adipoq-Cre*⁺ mouse were stained with antibodies against prelamin A (green) and CD31 (red). DNA was stained with DAPI (blue). Images were recorded with a confocal microscope using a 20× objective and a 2× digital zoom. Identical microscope settings were used for all tissue samples. Scale bar, 20 μm.



Supplemental Figure S3. Inactivating *Zmpste24* in adipose tissue does not affect food consumption. Food consumption in 24–26-week-old male $Lmna^{PLAO/PLAO}Zmpste24^{fl/fl}$ Adipoq-*Cre*⁻ (grey; $n = 5$) and $Lmna^{PLAO/PLAO}Zmpste24^{fl/fl}$ Adipoq-*Cre*⁺ (blue; $n = 6$) mice was measured for five consecutive days. The amount of food consumed was measured every 12 h. Graphs depict mean \pm SD. Food consumption was analyzed by repeated measures ANOVA.



Supplemental Figure S4. Inactivating *Zmpste24* in adipocytes does not alter free fatty acid, triglyceride, or glucose levels in the plasma. Free fatty acids (A), triglyceride (B), and glucose (C) levels were measured in male and female *Lmna^{PLAO/PLAO}Zmpste24^{f/f}Adipoq-Cre-* (grey) and *Lmna^{PLAO/PLAO}Zmpste24^{f/f}Adipoq-Cre⁺* (blue) mice. Graphs show mean \pm SEM. The numbers of mice per group are shown in parentheses. Free fatty acid, triglycerides and glucose levels were not different ($P > 0.10$).

Supplemental Table 1. Expression of adipose-related genes in gonadal WAT. Quantitative RT-PCR studies of adipose-related genes in gonadal WAT from male and female *Lmna^{PLAO/PLAO}Zmpste24^{f/f}Adipoq-Cre*⁻ (*-Cre*) and *Lmna^{PLAO/PLAO}Zmpste24^{f/f}Adipoq-Cre*⁺ (*+Cre*) mice. Data were normalized to cyclophilin A. The mean ± SEM are shown for 5–7 male mice/genotype and 4–5 female mice/genotype. **P* < 0.05.

Gene	Male		Female	
	<i>-Cre</i> (<i>n</i> = 5)	<i>+Cre</i> (<i>n</i> = 7)	<i>-Cre</i> (<i>n</i> = 4)	<i>+Cre</i> (<i>n</i> = 5)
<i>Pparg2</i>	0.074 ± 0.014	0.070 ± 0.009	0.113 ± 0.007	0.086 ± 0.004*
<i>Adipoq</i>	1.951 ± 0.200	1.681 ± 0.204	3.073 ± 0.436	2.310 ± 0.235
<i>Srebf1c</i>	0.114 ± 0.016	0.103 ± 0.010	0.100 ± 0.012	0.142 ± 0.042
<i>Fasn</i>	1.041 ± 0.104	1.044 ± 0.197	2.248 ± 0.662	2.922 ± 1.336
<i>Acc</i>	0.273 ± 0.044	0.216 ± 0.037	0.738 ± 0.196	0.851 ± 0.361
<i>Cebpa</i>	0.575 ± 0.076	0.436 ± 0.034	0.569 ± 0.034	0.424 ± 0.034*
<i>Cebpb</i>	0.030 ± 0.004	0.023 ± 0.002	0.020 ± 0.001	0.014 ± 0.002*
<i>Fabp4</i>	21.818 ± 1.339	21.271 ± 1.627	26.198 ± 1.324	21.631 ± 2.789
<i>Ucp1</i>	0.003 ± 0.001	0.001 ± 0.000*	0.031 ± 0.012	0.011 ± 0.011
<i>Pnpla2</i>	1.665 ± 0.219	1.285 ± 0.118	1.852 ± 0.305	1.480 ± 0.171
<i>Gpam</i>	0.174 ± 0.030	0.124 ± 0.014	0.377 ± 0.032	0.301 ± 0.053
<i>Hsl</i>	1.131 ± 0.133	0.892 ± 0.078	1.143 ± 0.089	0.802 ± 0.041*
<i>Lpin1</i>	0.123 ± 0.013	0.100 ± 0.009	0.088 ± 0.004	0.073 ± 0.012

Supplemental Table 2. Expression of extracellular matrix- and p53-related genes in gonadal WAT.
Quantitative RT-PCR studies of extracellular matrix- and p53-related genes in gonadal WAT from male and female *Lmna*^{PLAO/PLAO}*Zmpste24*^{f/f}*Adipoq-Cre*⁻(-*Cre*) and *Lmna*^{PLAO/PLAO}*Zmpste24*^{f/f}*Adipoq-Cre*⁺(+*Cre*) mice. Data were normalized to cyclophilin A. The mean ± SEM are shown for 5–7 male mice/genotype and 4–5 female mice/genotype.

Gene	Male		Female	
	<i>-Cre</i> (n = 5)	<i>+Cre</i> (n = 7)	<i>-Cre</i> (n = 4)	<i>+Cre</i> (n = 5)
<i>Col4a1</i>	0.391 ± 0.064	0.432 ± 0.058	0.273 ± 0.025	0.222 ± 0.024
<i>Colla1</i>	0.214 ± 0.034	0.269 ± 0.047	0.259 ± 0.037	0.256 ± 0.037
<i>Col6a3</i>	0.064 ± 0.018	0.082 ± 0.020	0.098 ± 0.013	0.092 ± 0.015
<i>Gadd45a</i>	0.021 ± 0.002	0.023 ± 0.003	0.034 ± 0.002	0.042 ± 0.012
<i>Gadd45b</i>	0.018 ± 0.006	0.015 ± 0.002	0.010 ± 0.001	0.011 ± 0.002
<i>Cdkn1a</i>	0.046 ± 0.012	0.047 ± 0.010	0.031 ± 0.010	0.019 ± 0.003

Supplemental Table 3. Primer sequences for quantitative RT-PCR studies. All sequences 5' to 3'.

Gene	Forward	Reverse
<i>Col4a1</i>	ATGGCTTGCCTGGAGAGATAGG	TGGTTGCCCTTGAGTCCTGGA
<i>Colla1</i>	TGACTGGAAGAGCGGAGAGT	GACGGCTGAGTAGGAAACAC
<i>Col6a3</i>	CAGAACCATTTGTTCTCACT	AGGACTACACATCTTTCAC
<i>Gadd45a</i>	ACTGTGTGCTGGTGACGAAC	TGATCCATGTAGCGACTTCC
<i>Gadd45b</i>	GCTGTGGAGTGTGACTGCAT	GGTGAGGCGATCCTGACG
<i>Cdkn1a</i>	CCACAGCGATATCCAGACATT	AAGAGACAACGGCACACTTG
<i>Pparg2</i>	AACTCTGGGAGATTCTCCTGTTGA	TGGTAATTCTTGTGAAGTGCTATA
<i>Adipoq</i>	GATGGCACTCCTGGAGAGAAG	CAGCTCCTGTCATTCCAACAT
<i>Pnpla2</i>	TCCGTGGCTGTCTACTAAAGA	TGGGATATGATGACGTTCTCTCC
<i>Cre</i>	ACCTGAAGATGTTCGCGATT	ATGTTAGCTGGCCCAAATG
Prelamin A	GGTTGAGGACAATGAGGATGA	TGAGCGCAGGTTGACTCAG
Prelamin A (set 2)	CTAGTCACCCGCTCCTACCTC	CTGCCTGGCAGGTCCCAGAT
<i>Lmna</i>	CCTATCGAAAGCTGCTGGAG	CCTGAGACTGGGATGAGTGG
<i>Lmna</i> (set 2)	GGACCAGGTGGAACAGTATAAGA	TGCTGTTCCCTCTCAGCAGACT
<i>Lmnb1</i>	CAACTGACCTCATCTGGAAAGAAC	TGAAGACTGTGCTTCTGAGC
<i>Cd11c</i>	TGCCAGGATGACCTTAGTGTG	CAGAGTGAUTGTGGTTCCGTAG
<i>Il1b</i>	AGAAGCTGTGGCAGCTACCTG	GGAAAAGAAGGTGCTCATGTCC
<i>Tnfa</i>	CAGGCAGGTGCCTATGTCTC	CGATCACCCGAAGTTCACTAG
<i>Fasn</i>	GTCGTCTGCCTCCAGAGC	GTTGGCCCAGAACTCCTGTA
<i>Acaca</i>	GCCTCTCCTGACAAACGAG	TGACTGCCAACATCTCTG
<i>Cebpa</i>	GCAAAGCCAAGAAGTCGGTGG	TTCTGTTGCGTCTCCACGTTGC
<i>Cebpb</i>	TTTAGACCCATGGAAAGTGGC	CTCCAGGTAGGGCTGAAGT
<i>Fabp4</i>	AACCTGGAAGCTGTCTCCA	CACGCCAGTTGAAGGAAA
<i>Ucp1</i>	GGGCCCTGTAAACAAACAAA	GTCGGTCCTCCTGGTGT
<i>Cd11b</i>	TACTCGGGCAGTCTCTGAGTG	ATGGTTGCCTCCAGTCTCAGCA
<i>Ly71</i>	CGTGTGTTGGTGGCACTGTGA	CCACATCAGTGTCCAGGAGAC
<i>Gpam</i>	AGCAAGTCCTGCGCTATCAT	CTCGTGTGGTGATTGTGAC
<i>Hsl</i>	GGAACTAAGTGGACGCAAGC	CCAGGGCTGCCTCAGACAC
<i>Lpin1</i>	CTATGCTGCTTGGAACCG	GGACACTCCCAC TGCTTGT
<i>Srebflc</i>	CGCGGACACGGAGCCATG	GAGAAGCTCTCAGGAGAGTTGG
<i>Zmpste24</i>	CCTCTGTTGACAAATTACACC	AACGCTTAGATCCTCAACAAACA