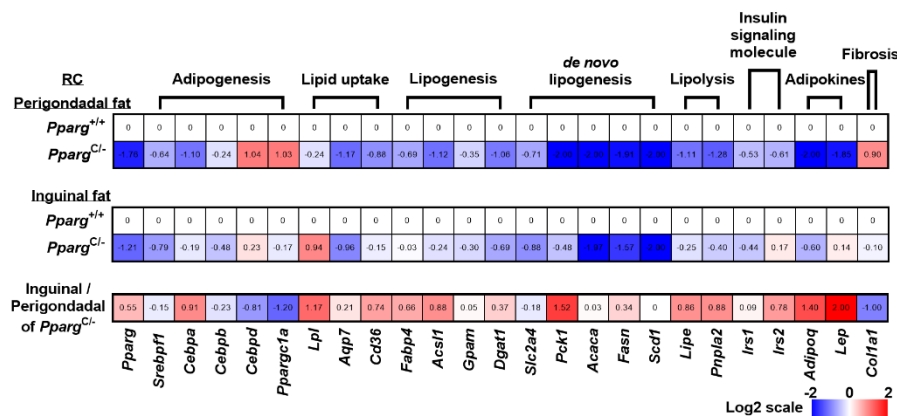
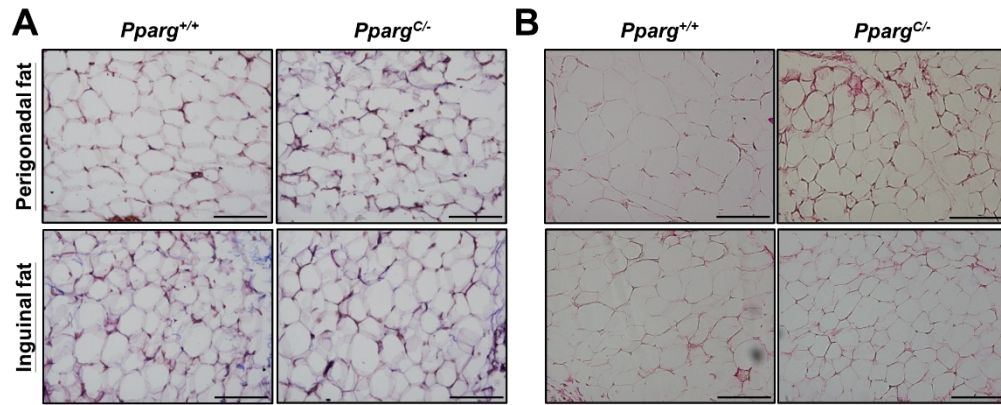


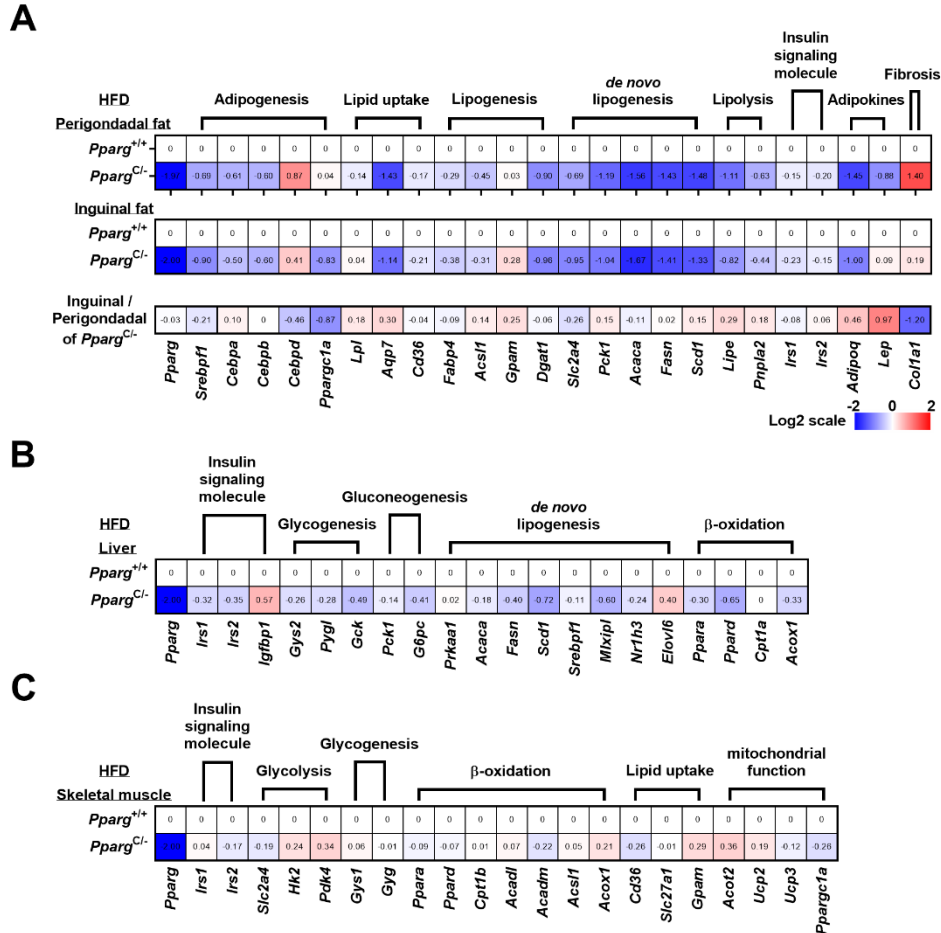
Supplemental Figures



Supplemental Figure S1. mRNA levels of metabolic genes in adipose tissues of chow-fed *Pparg*<sup>C/-</sup> mice. The heat-map represents mRNA levels of metabolic genes analyzed by quantitative real-time PCR in perigonadal and inguinal fat of chow-fed *Pparg*<sup>C/-</sup> mice relative to *Pparg*<sup>+/+</sup> mice. The ratio of mRNA level of inguinal to perigonadal fat in *Pparg*<sup>C/-</sup> mice is also shown. The average log 2 fold-change values are inside squares. The log 2 expression scales represent the values in terms of logarithmic fold, blue (lowest), white (medium), and red (highest) expression levels. RC, regular chow.



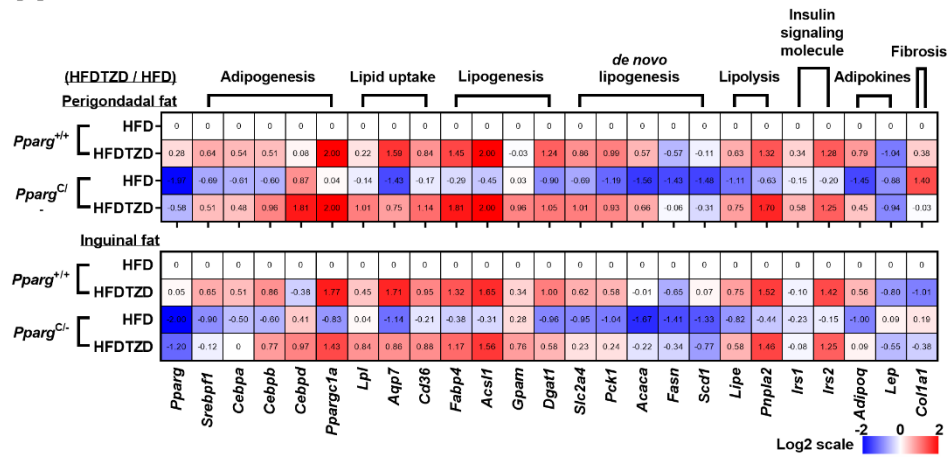
**Supplemental Figure S2. Fibrosis staining of *Pparg*<sup>C/-</sup> adipose tissue.** Masson's trichrome (A) and picrosirius red (B) staining in the perigonadal and inguinal fat of *Pparg*<sup>C/-</sup> mice and wild-type mice. Scale bar = 100 μm.



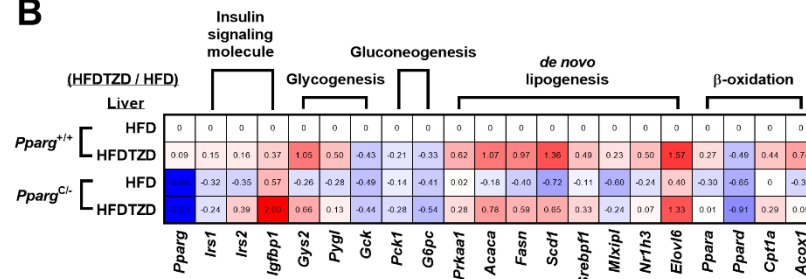
Supplemental Figure S3. mRNA levels of metabolic genes in metabolic tissues of HFD-fed *Pparg*<sup>-/-</sup> mice. The heat-map represents mRNA levels of metabolic genes analyzed by quantitative real-time PCR in perigonadal and inguinal fat (A), liver (B), and skeletal muscle (C) of HFD-fed *Pparg*<sup>-/-</sup> mice relative to *Pparg*<sup>+/+</sup> mice. The ratio of mRNA level of inguinal to perigonadal fat in *Pparg*<sup>-/-</sup> mice is also shown in (A). The average log 2 fold-change values are inside squares. The log 2 expression scales represent the values in terms of logarithmic fold, blue (lowest), white (medium), and red (highest) expression levels. HFD, high-fat diet.



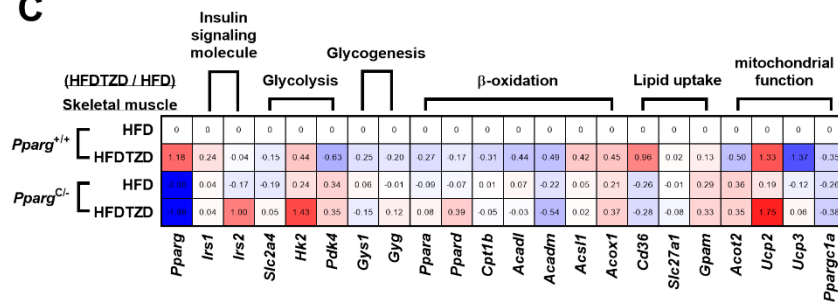
**A**



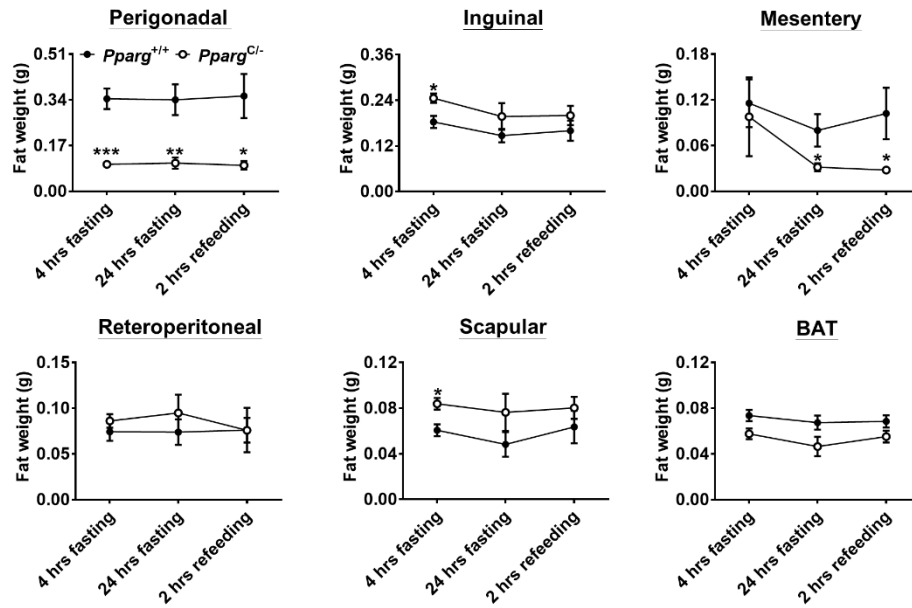
**B**



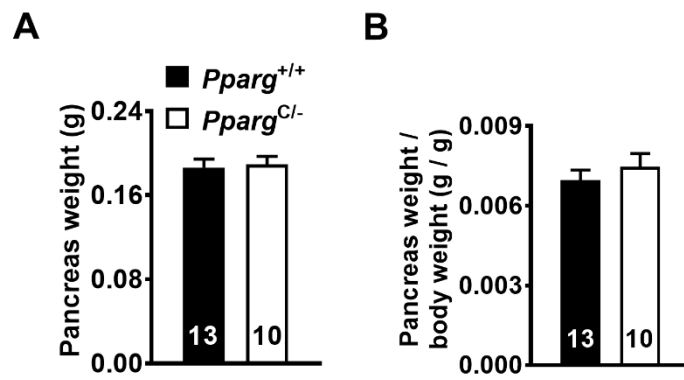
**C**



**Supplemental Figure S5. mRNA levels of metabolic genes in metabolic tissues of both HFD-fed and HFDTZD-fed *Pparg*<sup>C/-</sup> mice.** The heat-map represents mRNA levels of metabolic genes analyzed by quantitative real-time PCR in perigonadal and inguinal fat (A), liver (B), and skeletal muscle (C) of both HFD-fed and HFDTZD-fed *Pparg*<sup>C/-</sup> and *Pparg*<sup>+/+</sup> mice. The mRNA levels of HFD-fed *Pparg*<sup>+/+</sup> mice were used as the relative reference. The average log 2 fold-change values are inside squares. The log 2 expression scales represent the values in terms of logarithmic fold, blue (lowest), white (medium), and red (highest) expression levels. This illustration emphasizes the TZD effect.



**Supplemental Figure S6. Dynamics of fat weights during the 24 hrs of fasting and 2 hrs of refeeding course.** The fat weight of various depots in *Pparg*<sup>Cl-</sup> mice and *Pparg*<sup>+/+</sup> mice after 4 hrs fasting, 24 hrs fasting, or 2 hrs refeeding. \*  $p < 0.05$ , \*\*  $p < 0.01$ , and \*\*\*  $p < 0.001$  compared with *Pparg*<sup>+/+</sup> mice. This panel is associated with the experiment in Figure 2A



Supplemental Figure S7. Pancreas weight of *Pparg*<sup>C/-</sup> mice. Pancreas weight (A) and pancreas to body weight (B) in *Pparg*<sup>+/+</sup> and *Pparg*<sup>C/-</sup> mice.