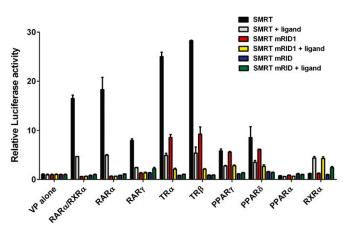
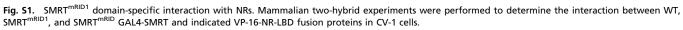
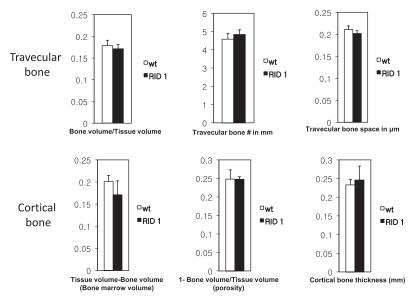
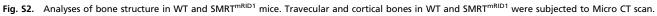
Supporting Information

Fang et al. 10.1073/pnas.1017707108









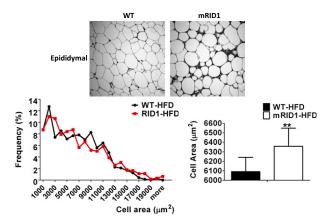


Fig. S3. Analyses of epididymal fat depots in WT and SMRT^{mRID1} mice. Epididymal fat depot was subject to analysis of adipocyte cross-sectional area in WT and SMRT^{mRID1} mice. All error bars are SE. **P < 0.01.

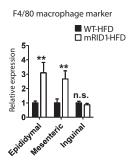


Fig. 54. Gene expression of macrophage-specific markers in various white adipose tissue (WAT) depots. Macrophage-specific marker F4/80 expression was examined by quantitative real-time PCR. All error bars are SD. **P < 0.01.

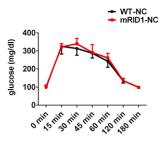


Fig. S5. Glucose tolerance test (GTT) in normal chow-fed WT and SMRT^{mRID1}. Age-matched WT and SMRT^{mRID1} mice were subjected to GTT under normal chow diet.

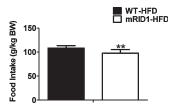


Fig. S6. Comparison of food intake WT and SMRT^{mRID1}. Food intake was normalized by body weight in WT and SMRT^{mRID1} mice on a high-fat diet (HFD). All error bars are SD. **P < 0.01.

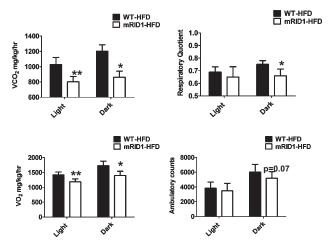


Fig. S7. Comparison of metabolic rates in body-weight–matched WT and SMRT^{mRID1} mice on a high-fat diet (HFD). Carbon dioxide production (VCO₂), oxygen consumption (VO₂), respiratory quotient, and ambulatory counts were measured in body-weight–matched WT and SMRT^{mRID1} mice on a HFD. All error bars are SD. *P < 0.05, **P < 0.01.

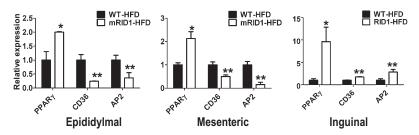


Fig. S8. Comparison of expression levels of PPAR_Y target genes in different WAT depots of WT and SMRT^{mRID1} mice. Well-known PPAR_Y target genes, such as AP2 and CD36, were subjected to RT-quantitative PCR to determine their expression levels in different white adipose tissue (WAT) depots of WT and SMRT^{mRID1} mice. All error bars are SD. **P* < 0.05, ***P* < 0.01.