**Figure S3. ND-fed p38αFab-KO** **mice present increased expression of metabolic genes.**

**(a)** qRT-PCR analysis of mRNA expression of browning, adipogenic, glycolytic, β-oxidation, and lipogenic genes from BAT of ND-fed Fab-Cre and p38αFab-KO mice. mRNA expression was normalized to the amount of *Gapdh* mRNA. **(b)** Immunoblot analysis of PGC1α protein levels in BAT of ND-fed Fab-Cre and p38αFab-KO mice **(c)** qRT-PCR analysis of mRNA expression of browning, adipogenic, glycolytic, β-oxidation, and lipogenic genes from eWAT of ND-fed Fab-Cre and p38αFab-KO mice. mRNA expression was normalized to the amount of *Gapdh* mRNA (mean±SEM, Fab-Cre n=7 mice; p38αFab-KO n=7 mice). \*p < 0.05; \*\*p < 0.01. Fab-Cre vs p38αFab-KO (*t*-test or Welch’s test when variances were different). See also S1 Data.