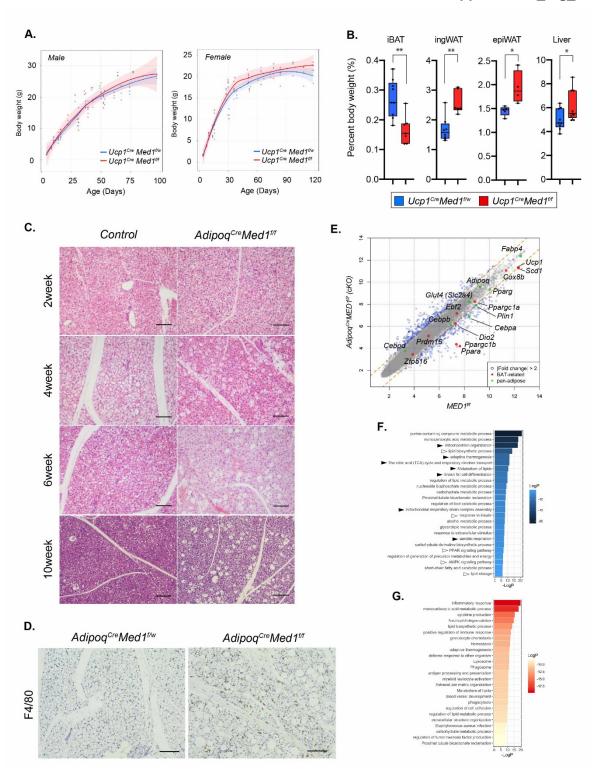
## Supplemental\_Fig\_S5



## Figure S5: Analysis of adult BAT in the absence of MED1

A) Body weight transition of Ucp1<sup>Cre</sup>Med1<sup>f/w</sup> and Ucp1<sup>Cre</sup>Med1<sup>f/f</sup> mice (Mean, Confidence interval 0.95). Both male and female *Ucp1*<sup>Cre</sup>*Med1*<sup>ff</sup> mice showed a trend toward an increase in body weight in young adults. B) Percentage of tissue weight over body weight values are shown. Note that while BAT is smaller in Ucp1<sup>Cre</sup>Med1<sup>fff</sup> mice compared to Ucp1<sup>Cre</sup>Med1<sup>f/w</sup>mice, WAT and liver show increase masses in Ucp1<sup>Cre</sup>Med1<sup>f/f</sup> mice (mean, ± SD, \*p<0.05, \*\*p<0.005 (T-test)). C) H&E staining of paraffin sections of BAT tissues harvested postnatally from control and Adipoq<sup>Cre</sup>Med1<sup>ff</sup> mice at 2, 4, 6, and 10 weeks of age. Bars indicate 100 µm. D) Immunohistochemistry of F4/80 antigen in 10-week old BAT of Adipoq<sup>Cre</sup>Med1<sup>f/w</sup> and Adipoq<sup>Cre</sup>Med1<sup>f/f</sup> mice. Bars indicate 100 µm. **E**) microarray analysis of BAT isolated from Med1<sup>ff</sup> (n=2) and Adipoq<sup>Cre</sup>Med1<sup>ff</sup> (n=2) mice. Genes with changes >2-fold between conditions are plotted in blue. Representative pan-adipose genes are plotted in green, and representative BAT-genes are plotted in red. F) GO enrichment analysis of down-regulated genes in BAT of *Adipoq*<sup>Cre</sup>*Med1*<sup>ff</sup> mice are shown. Top 25 categories are shown. White arrowheads correspond to pan-adipose-related terms and black arrowheads correspond to BAT-related terms. G) GO enrichment analysis of upregulated genes in BAT of Adipog<sup>Cre</sup>Med1<sup>f/f</sup> mice is shown.