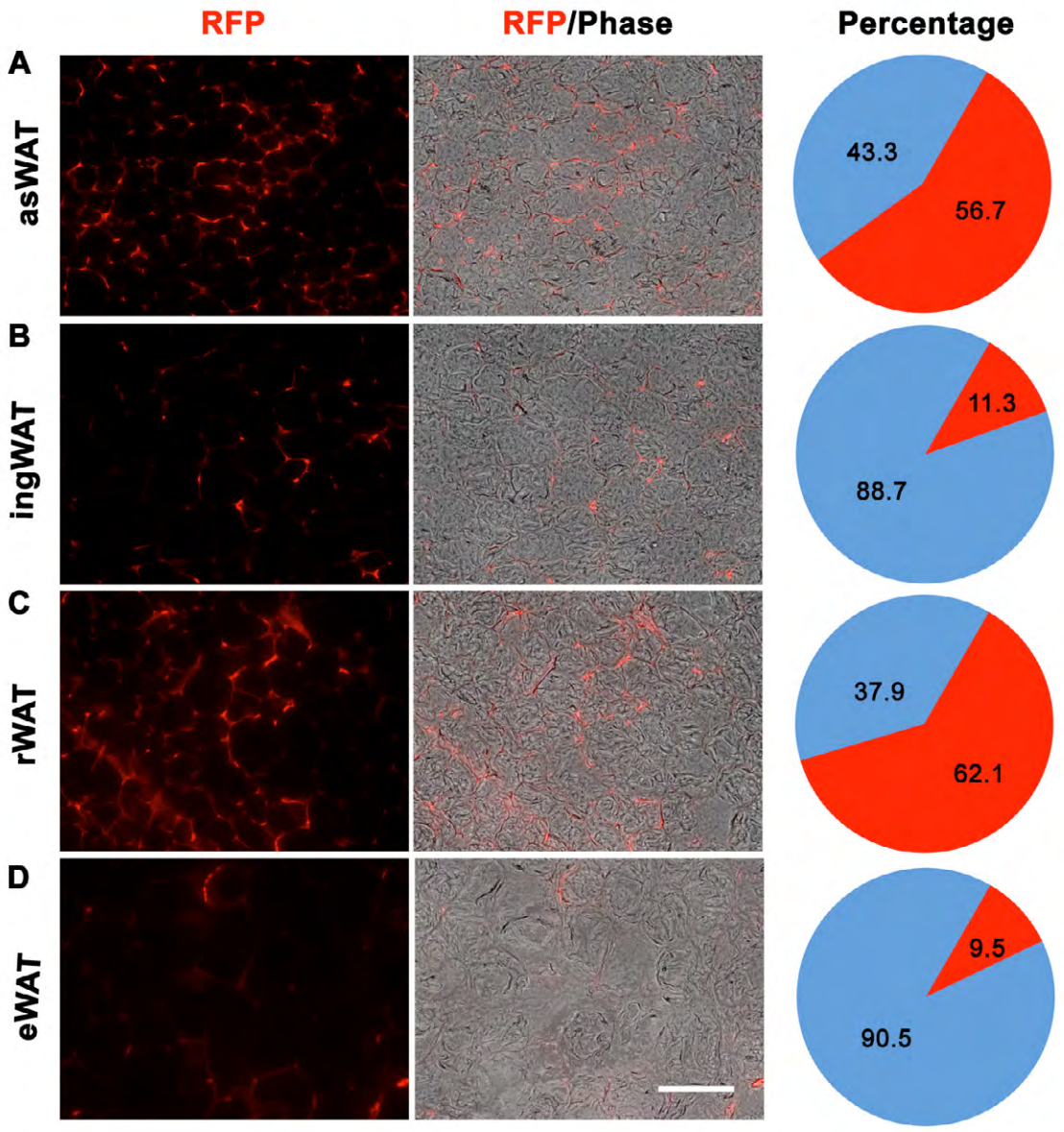

Fig. S1. Pax3 lineage tracing *in vivo*. (A) asWAT, (B) ingWAT, (C) rWAT, and (D) eWAT were isolated from adult (2–3 month old) $Pax3^{Cre/+}$/Rosa26-tdTomato mice, fixed, cryosectioned and imaged based on red fluorescence (tdTomato, left panels) and phase contrast (right panels, merged with the fluorescent images). Scale bar: 100 ∀m.

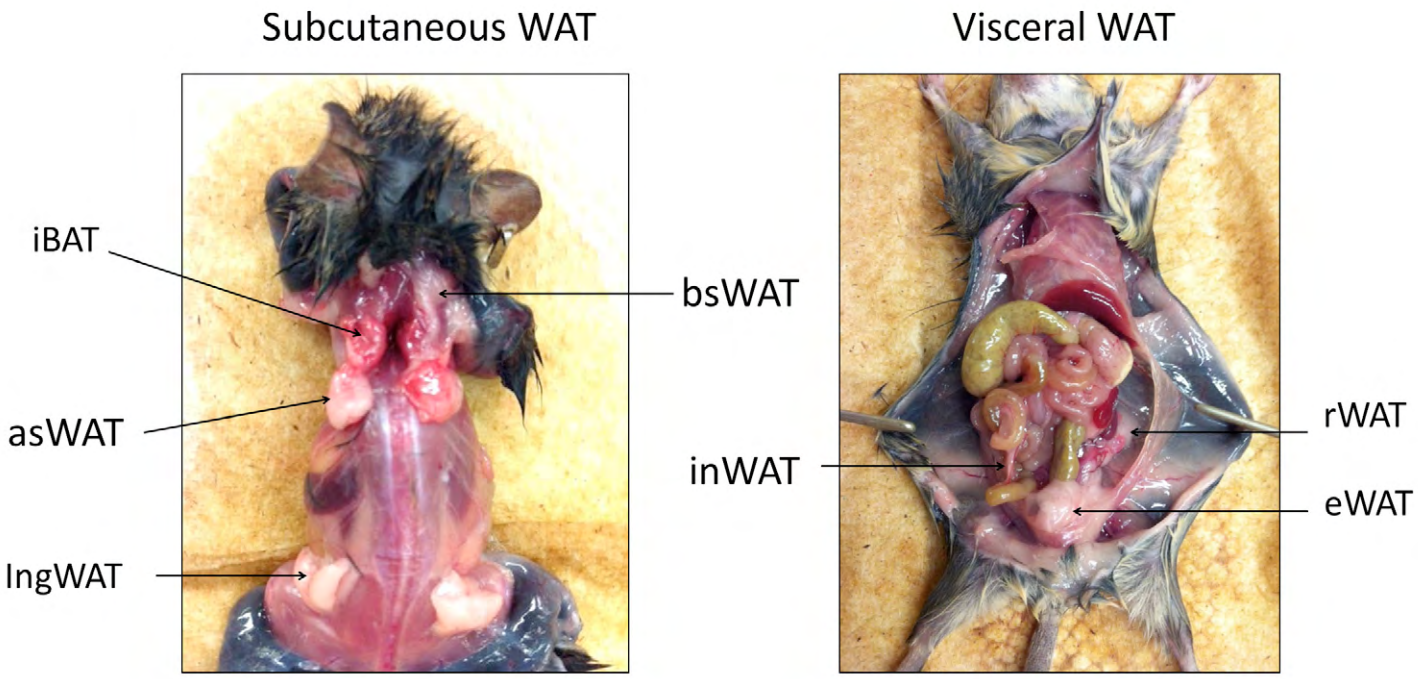

Fig. S2. Nomenclatures of WAT depots used in this study. asWAT: anterior subcutaneous WAT; bsWAT: back subcutaneous WAT; ingWAT: inguinal WAT; iBAT: intrascapular brown adipose tissue; inWAT: intestinal WAT, rWAT: retroperitoneal WAT; eWAT: epididymal WAT.

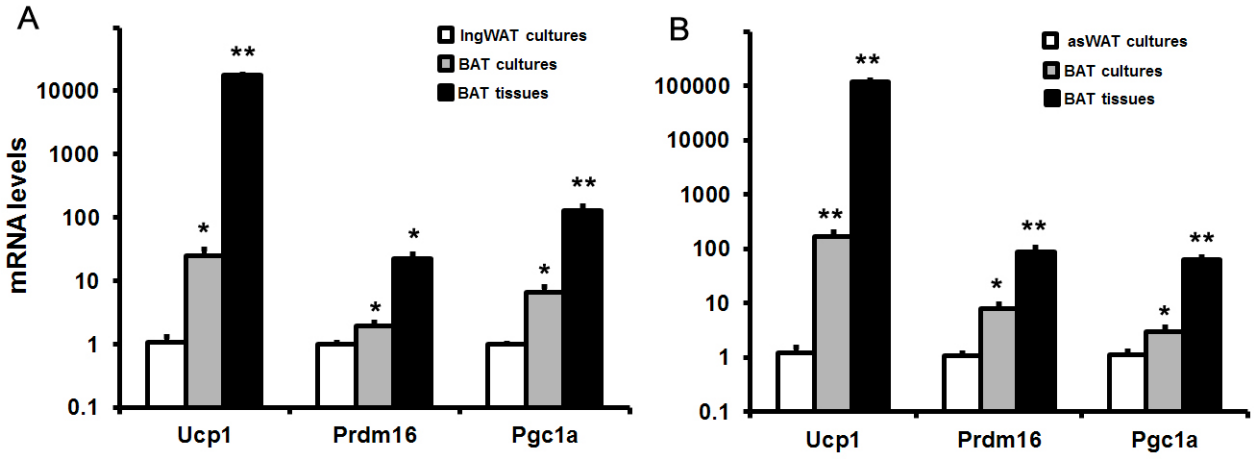

Fig. S3. Relative mRNA levels of brown-fat specific genes in white and brown adipocyte cultures. (A) Relative expression level of ingWAT SVF culture, BAT SVF culture and iBAT tissue. (B) Relative expression level of asWAT SVF culture, BAT SVF culture and iBAT tissue. N=3. *P<0.05, **P<0.01.

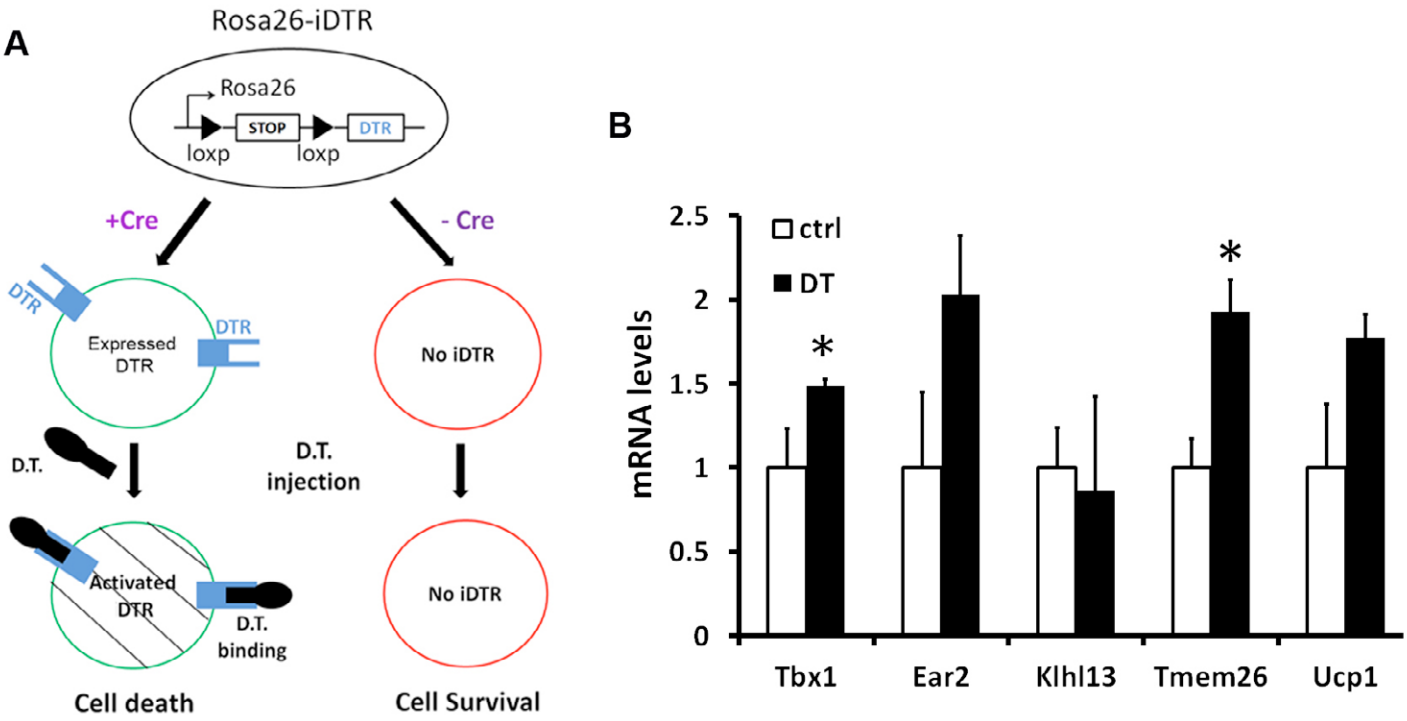

Fig. S4. Ablation of Pax3 lineage cells promotes beige adipocyte gene expression in SVF cultures. (H) Strategy for genetic ablation of Pax3 lineage cells using $Pax3^{Cre/+}$/Rosa26-iDTR mice. (I) Relative mRNA levels of beige and BAT markers in control (vehicle treated) and DT treated SVF cultures.