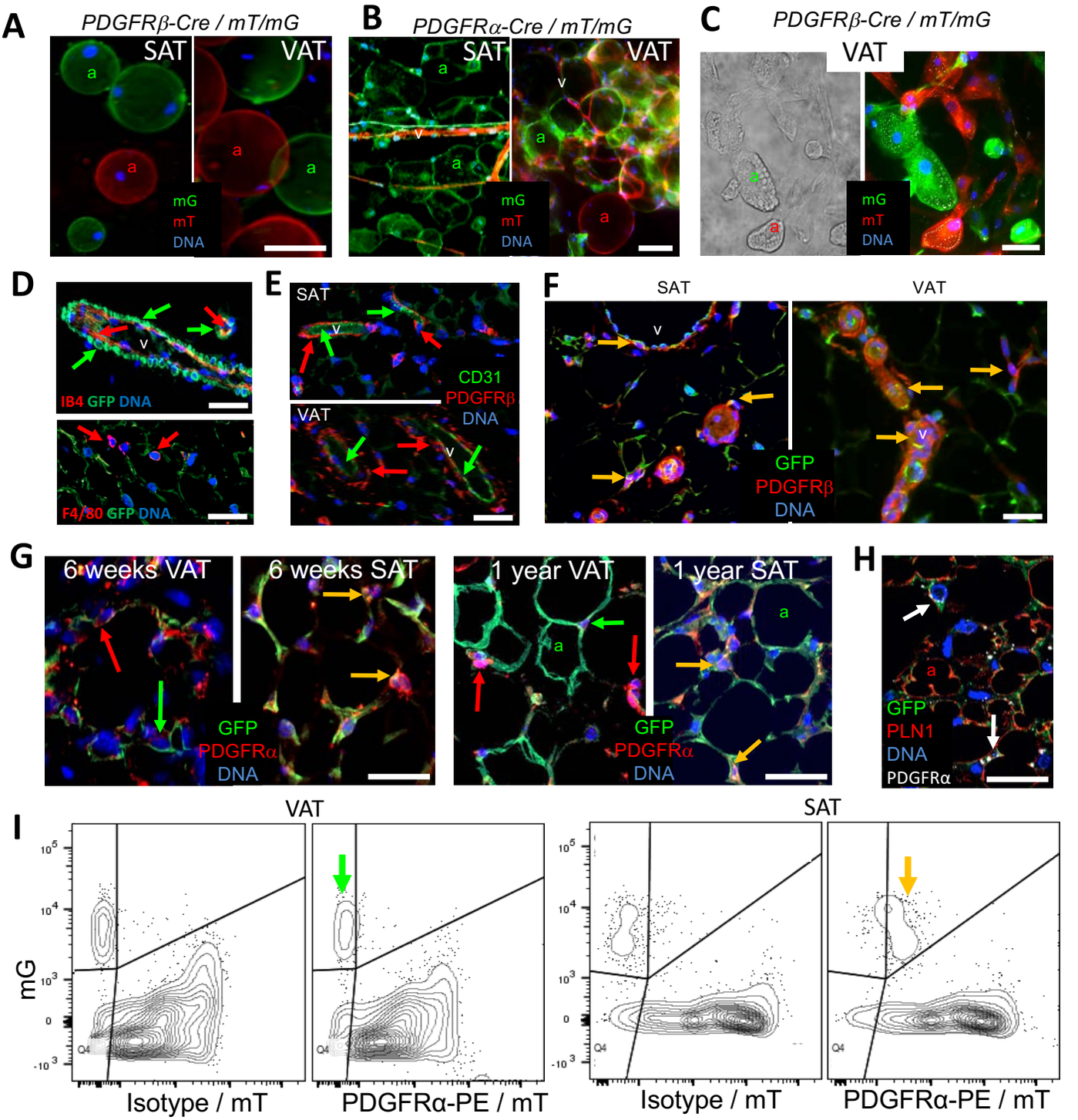

Fig. S1. Distinct PDGFRβ+ lineages generate white adipocytes in SAT and VAT.
(A) Suspended mT+ and mG+ adipocytes (a) from disaggregated SAT and VAT of an adult *Pdgfrβ-Cre*; *mT/mG* mouse. (B) A whole mount of SAT and VAT from an adult *Pdgfrα-Cre; mT/mG* mouse showing mT+ and mG+ adipocytes and mT+ vasculature (v). (C) Cultured SVF from VAT of an adult *Pdgfrβ-Cre*; *mT/mG* mouse subjected to white adipogenesis induction. Note lipid droplets in mT+ and mG+ adipocytes. (D-H) Paraffin sections of SAT and VAT from *Pdgfrβ-Cre*; *mT/mG* mice. (D) F4/80 IF / Isolectin B4 staining showing perivascular mG lineage tracing and that macrophages and endothelial cells are not lineage-traced in SAT. (E) PDGFRβ / CD31 IF showing that , like Pdgfrβ-Cre, PDGFRβ is perivascular in SAT and VAT. (F) GFP / PDGFRβ IF confirming that perivascular PDGFRβ+ cells are lineage-traced with Pdgfrβ-Cre in SAT and VAT. Colocalization is indicated (yellow arrows). v: blood vessels. (G) GFP / PDGFRα IF showing PDGFRα / mG colocalization in SAT and lack of PDGFRα / mG colocalization in VAT of 6 week-old and 1 year old mice. (H) GFP / perilipin-1 / PDGFRα IF showing PDGFRα / mG colocalization outside adipocytes in SAT. (I) Flow cytometric analysis of SVF from SAT and VAT of a *Pdgfrβ-Cre*; *mT/mG* mouse with anti-PDGFRα PE-conjugated antibody. The PDGFRα gate is set using the IgG-PE isotype control on SVF from C57BL/6 mice (not shown). The mG gate is set based on autofluorescence of SVF from C57BL/6 mice (not shown). Note the PDGFRα signal on mG+ cells only in SAT (yellow arrow). In all panels, scale bar=50 μm; nuclei are blue.

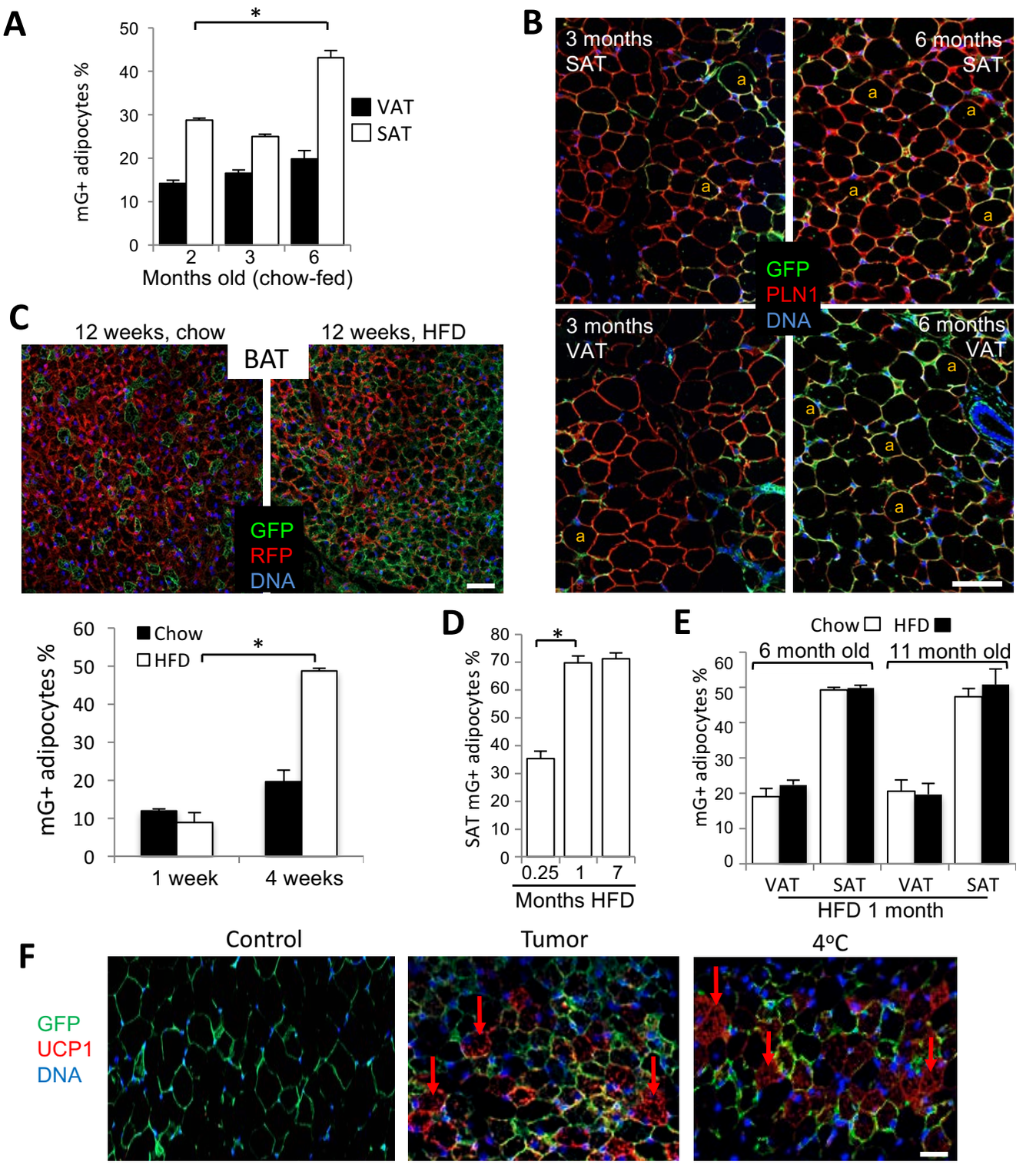

Fig. S2. The PDGFRβ+ lineage contribution to the beige adipocyte pool is minimal.
(A) Frequency of mG+ adipocytes in VAT and SAT of 2, 3, and 6 month-old *Pdgfrβ-Cre*; *mT/mG* mice raised on chow diet. (B) Confocal IF on paraffin sections of SAT and VAT from 3-month-old and 6-month-old *Pdgfrβ-Cre*; *mT/mG* mice subjected to perilipin-1 labeling adipocytes / GFP labeling ASC and adipocytes. Yellow: mG / perilipin-1 co-localization in adipocytes (a). (C) Paraffin sections of interscapular BAT from 12 week-old *Pdgfrβ-Cre*; *mT/mG* mice fed chow or high fat diet for 4 weeks were subjected to RFP (red) and GFP (green) IF. Below: quantification of mG+ adipocyte frequency after 1 and 4 weeks of feeding. (D) Frequency of mG+ adipocytes in SAT of *Pdgfrβ-Cre*; *mT/mG* mice fed HFD for 1 week, 1 month or 7 months starting at week 8 of age. (E) Frequency of mG+ adipocytes in VAT and SAT of *Pdgfrβ-Cre*; *mT/mG* mice fed chow or HFD for 1 month starting at month 6 or 11 of age. (F) Paraffin sections of SAT from *Pdgfrβ-Cre*; *mT/mG* mice untreated (control), subcutaneously allografted with prostate RM1 adenocarcinoma cells (tumor) or exposed to cold (4ºC) for 10 days subjected to UCP1 (red) and GFP (green) IF. UCP1 expression in adipocytes not traced with *Pdgfrβ* lineage is indicated. In all panels, scale bar=50 μm; nuclei are blue. In all graphs, plotted are mean ± s.e.m. for multiple fields (n=10). **P*<0.05 (Student's t-test).

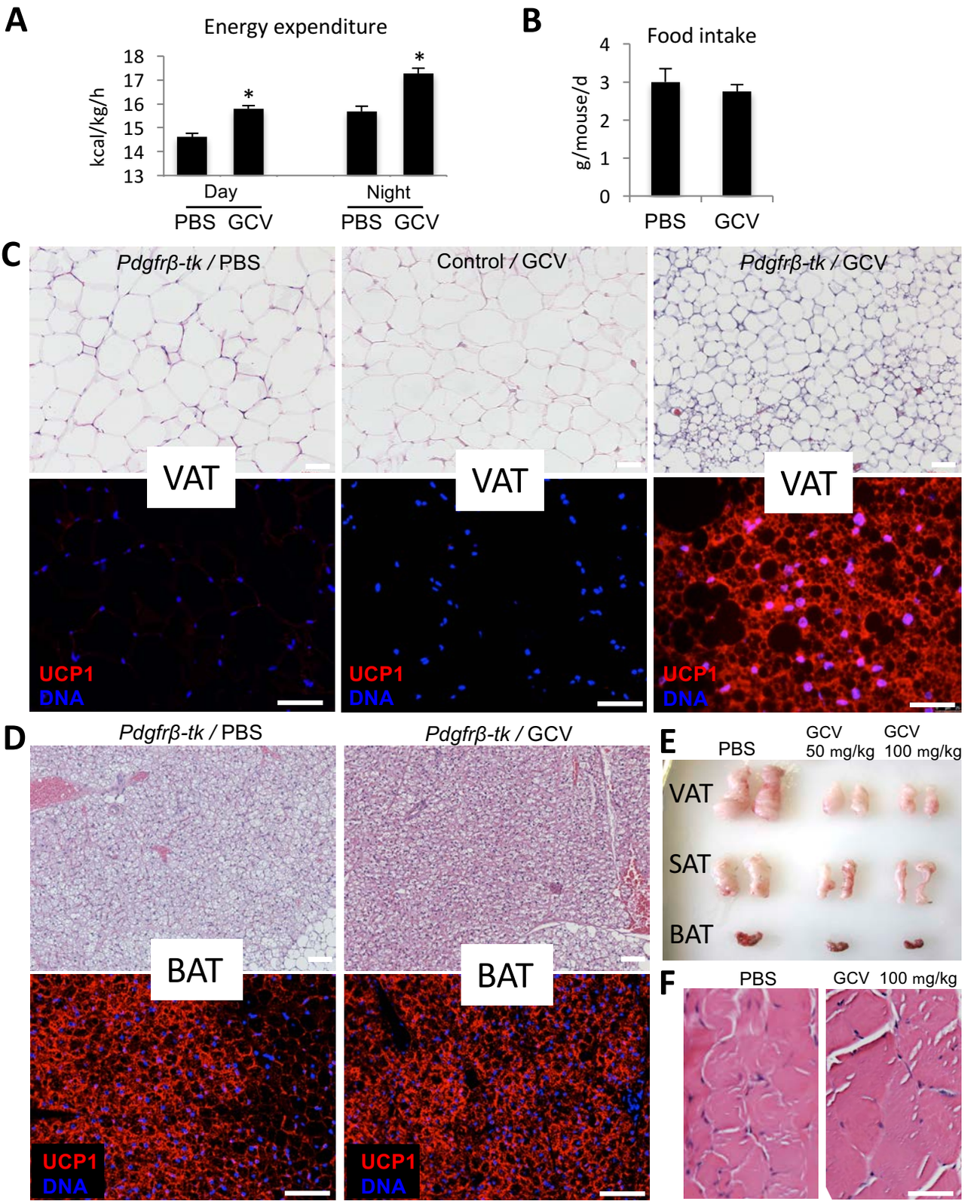

Fig. S3. Depletion of the PDGFRβ+ lineage results in AT beiging.
(A) Heat production by *Pdgfrβ-tk* mice 1 month after GCV or PBS treatment analyzed over a 4-day/night period (mean dark and light cycle values are plotted) shows that PDGFRβ+ lineage depletion results in increased energy expenditure. (B) Mean grams of food consumed per day over a 4-day/night period by *Pdgfrβ-tk* mice 1 month post GCV or PBS treatment. Plotted are mean ± s.e.m. for multiple mice; **P*<0.05 (Student's t-test) as compared to PBS. (C, D) Paraffin sections of VAT (C) and interscapular BAT (D) from *Pdgfrβ-tk* or C57BL/6 (control) mice 1 month post-treatment with PBS (control) or 100 mg/kg GCV were subjected to H/E staining and UCP1 IF (red). (E) Perigonadal VAT, inguinal SAT and interscapular BAT depots from *Pdgfrβ-tk* mice 1 month after GCV or PBS (Control) treatment. (F) H/E staining of skeletal muscle from *Pdgfrβ-tk* mice 1 month after GCV or PBS (Control) treatment showing the lack of fiber thickness reduction. Scale bar = 50 μm; nuclei are blue.

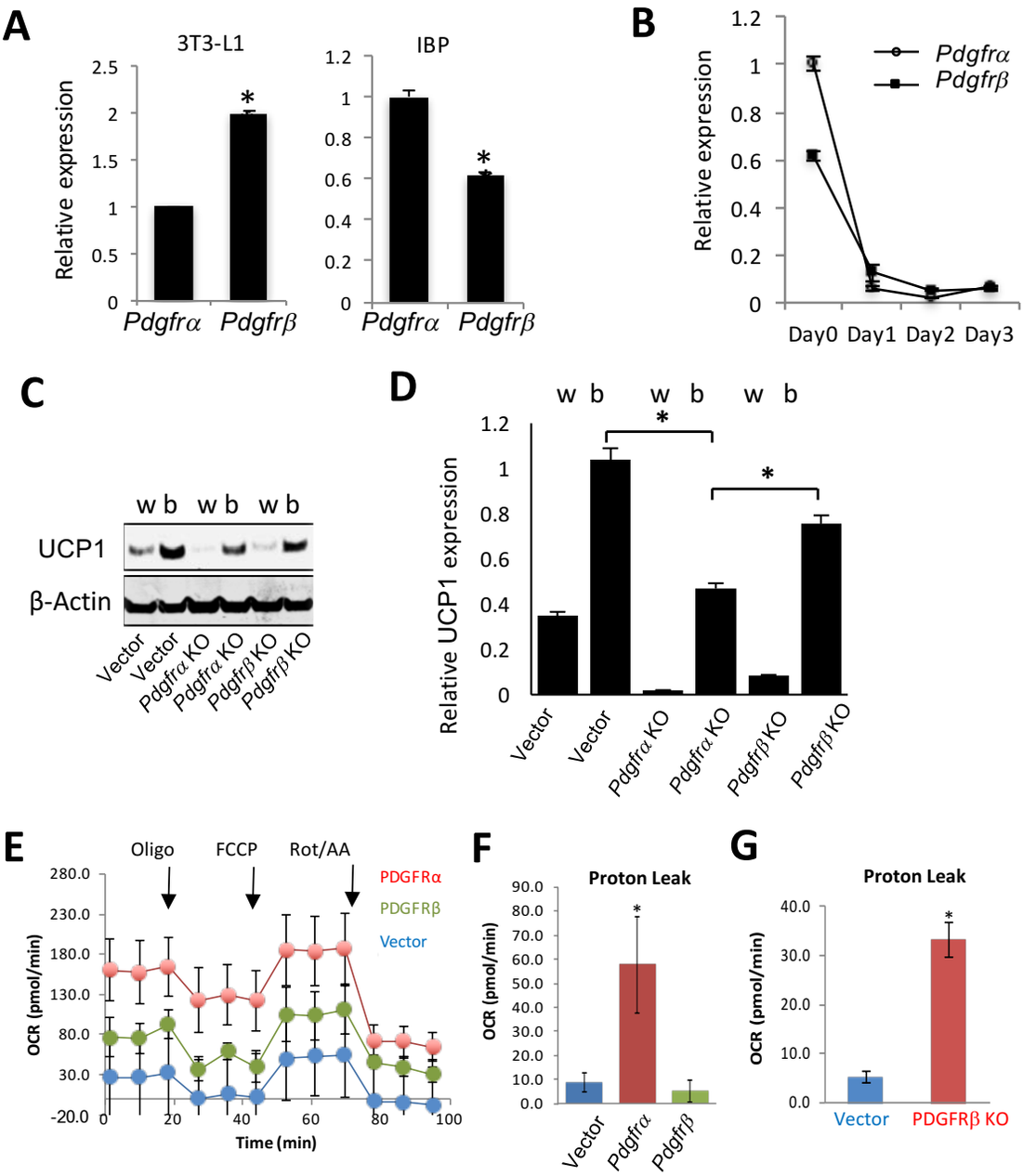

Fig. S4. PDGFRα / PDGFRβ signaling controls beige / white adipocyte balance.
(A) Quantitative RT-PCR analysis of *Pdgfra* and *Pdgfrβ* mRNA expression, normalized to *18S* RNA, in 3T3-L1 cells and immortalized brown preadipocytes (IBP) grown in regular culture medium without differentiation induction. (B) *Pdgfra* and *Pdgfrβ* mRNA expression reduction in IBP over the first 3 days after white adipogenesis induction. (C) UCP1 immunoblotting of extracts from IBP KO for *Pdgfra* or *Pdgfrβ* compared to control cells transduced with CRISPR/Cas9 vector. Cells were induced to undergo brown (b) or white (w) adipogenesis for 8 days prior to analysis. (D) Quantification of data from C. Plotted are mean band intensity measurements ± s.e.m. for three samples; **P*<0.05 (Student's t-test). (E-G) Seahorse XFe24 / Flux Assay Kit was used to analyze mitochondrial respiration in 3T3-L1 adipocytes overexpressing *Pdgfra* or *Pdgfrβ* (E-F) or in 3T3-L1 *Pdgfrβ KO* cells (G). Oxygen consumption rate (OCR) was measured upon successive treatment with oligomycin, FCCP (Carbonyl cyanide-p-trifluoromethoxyphenylhydrazone) and rotenone / antimycin A. Plotted in H and I is oligomycin-resistant OCR, which reflects ATP-uncoupled respiration.

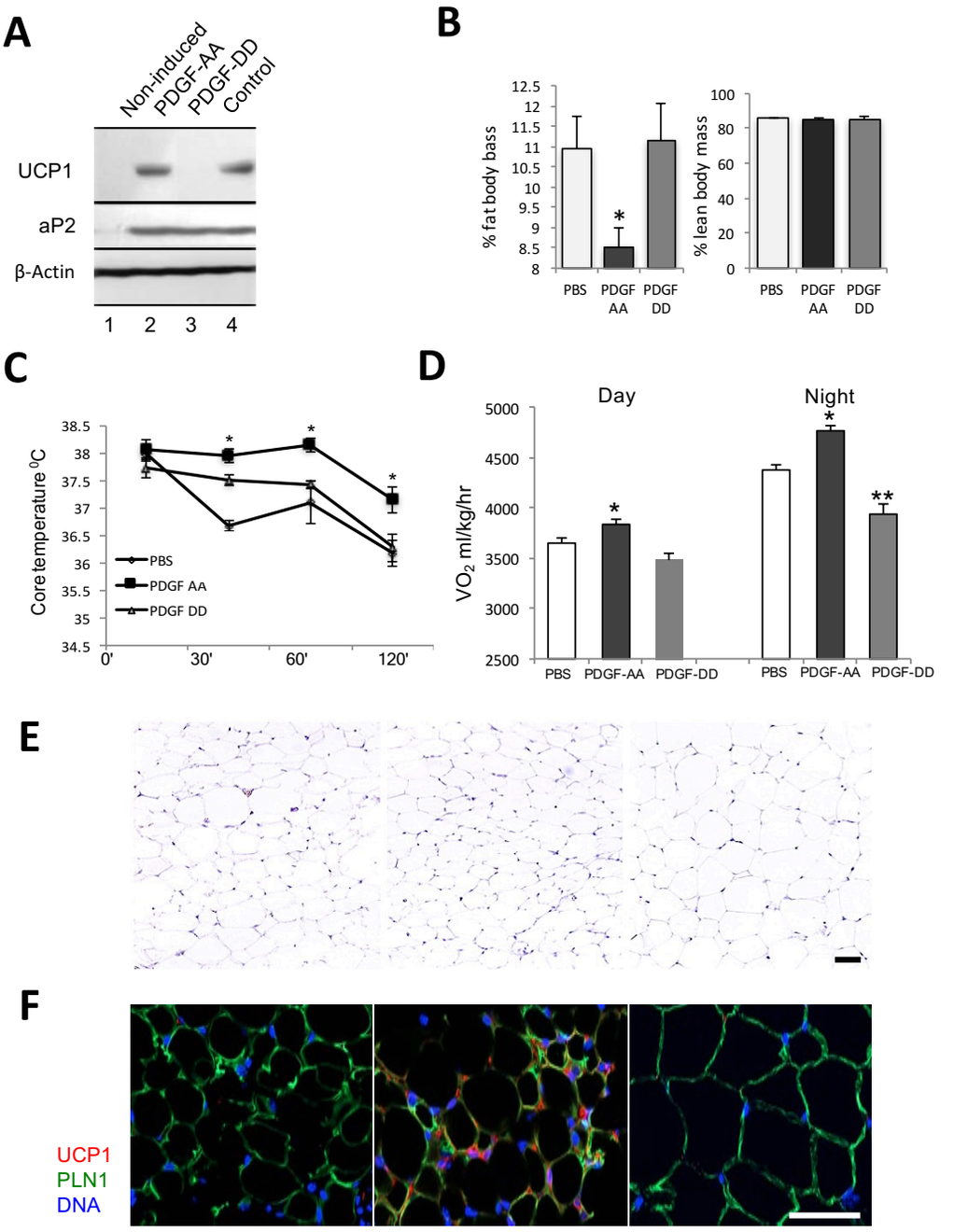

Fig. S5. Effects of PDGF ligands on adipocyte development.
(A) Immunoblotting of extracts from IBP grown in regular medium (1), or brown adipogenesis induction medium (2-3) supplemented with 30 ng/ml PDGF-AA, (R&D, Cat.#221-AA) 30 ng/ml PDGF-DD (R&D, Cat.#1159-SB/CF), or not supplemented (4). Adipogenesis is confirmed by aP2 immunoblotting. Note UCP1 expression absence upon PDGF-DD treatment. (B-F) Data from mice treated with PDGF-AA (R&D, Cat.#221-AA) or PDGF-DD; control mice were injected with PBS. (B) Fat and lean body mass measured by EchoMRI. Note reduced fat content upon PDGF-AA treatment. (C) Body temperature of treated mice measured over 120 min, at 4°C. Note increased cold tolerance of PDGF-AA-treated mice. (D) Oxygen consumption (VO_2) measured in metabolic chambers over 3 days indicates increased metabolic rate in PDGF-AA-treated mice. In B-D, plotted are mean ± s.e.m. for multiple mice; Student's t-test was used to identify $P<0.05$ * increase and ** decrease compared to control (PBS). (E) H/E-stained paraffin sections reveal decreased VAT adipocyte size in PDGF-AA-treated mice. (F) anti-UCP1 (red) /anti-perilipin-1 (green) IF reveals UCP1 expression in VAT of PDGF-AA-treated mice. Scale bars: 50 μm; nuclei are blue.