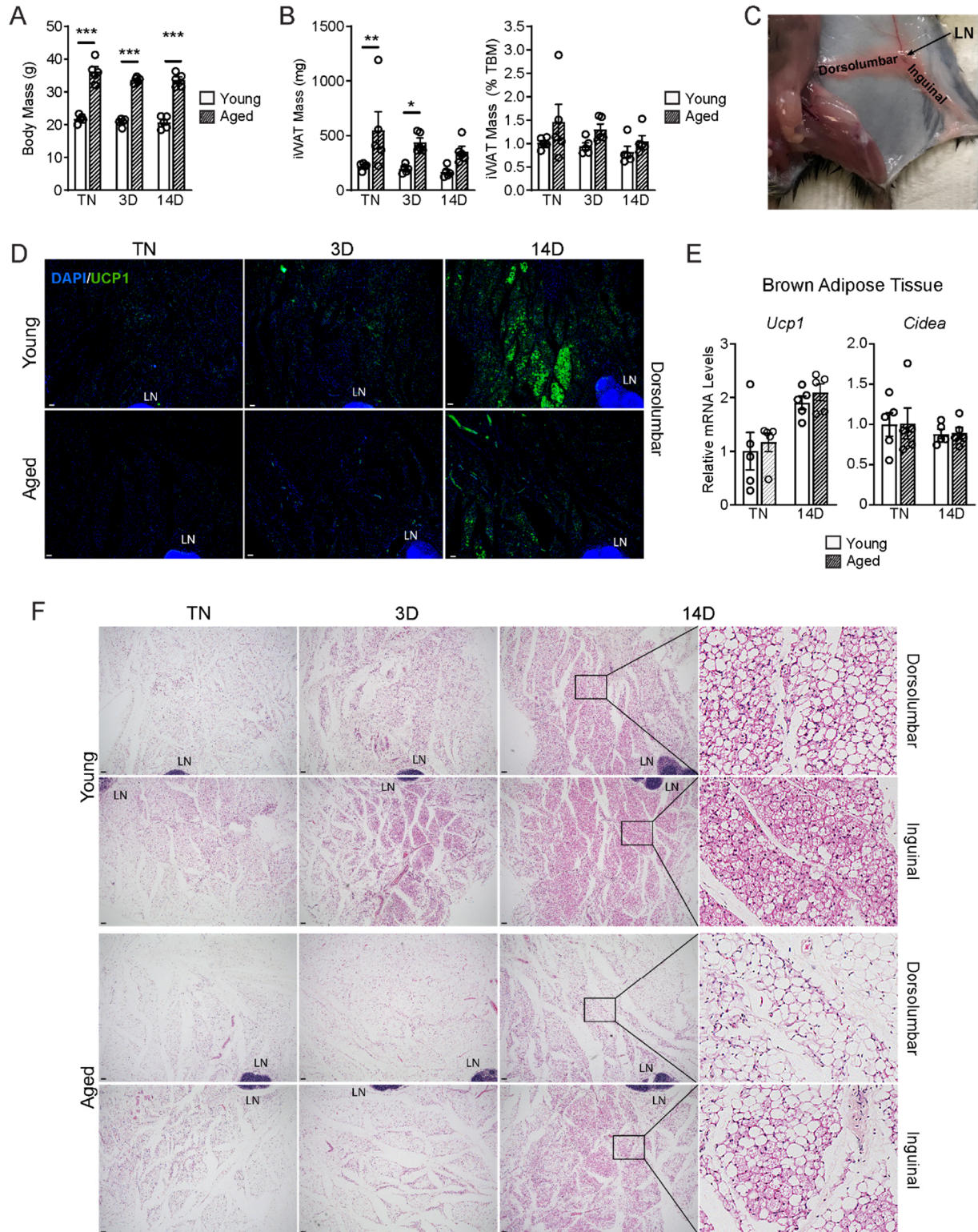


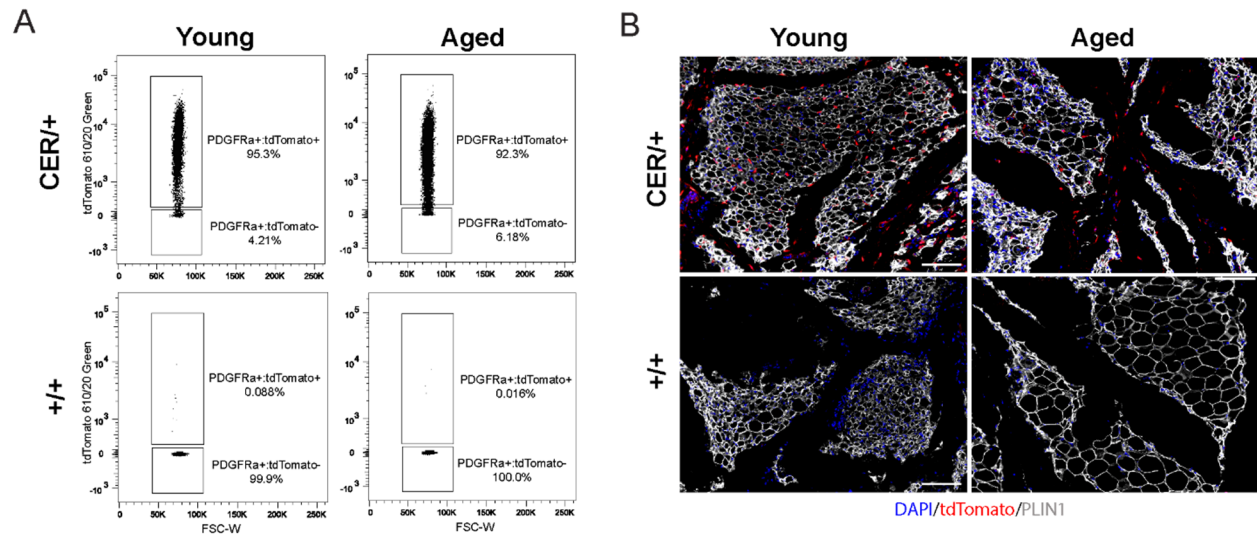
431 **Supplemental Figures**
Figure S1



432

433 **Figure S1, related to Figure 1. (A-B)** Body mass and iWAT mass of mice described in Figure 1A, n=5. **(C)** Mouse dissection
434 with lymph node (LN) orientation showing the dorsolumbar and inguinal regions of the iWAT pad. **(D)** Immunofluorescence
435 analysis of iWAT with UCP1 (green) and DAPI (blue). LN=lymph node. Scale bar 100 μ m. **(E)** mRNA levels of *Ucp1* and *Cidea*
436 in BAT of young and aged mice housed at TN, and either maintained at TN or exposed to cold for 2 weeks. **(F)** H&E staining
437 of serial sections of iWAT from D (above) and Figure 1C, LN=lymph node. Scale bar 100 μ m. Data represent mean \pm SEM,
438 points represent biological replicates, analyzed using a Student's t-test with a two-way ANOVA with a Tukey correction for
439 multiple comparisons. Significance: not significant, $P > 0.05$; * $P < 0.05$ ** $P < 0.01$; *** $P < 0.001$.
440

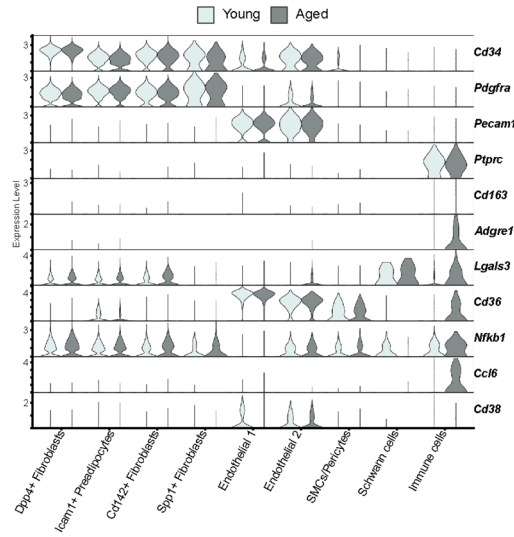
Figure S2



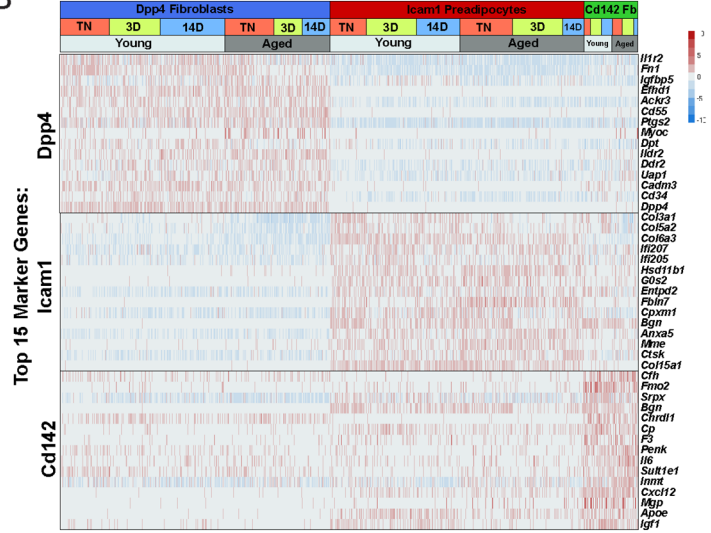
441 **Figure S2, related to Figure 2. (A)** Representative flow cytometry plots showing expression of tdTomato in gated Live, Lin⁻;
442 PDGFR α ⁺ stromal vascular cells isolated from young and aged reporter mice (described in Figure 2) immediately after
443 treatment with tamoxifen (tmx, pulse). **(B)** Immunofluorescence analysis of iWAT from young and aged reporter mice with
444 tdTomato (red), PLIN1 (white) and DAPI (blue) after the tmx pulse, scale bar 100 μ m.
445
446

Figure S3

A



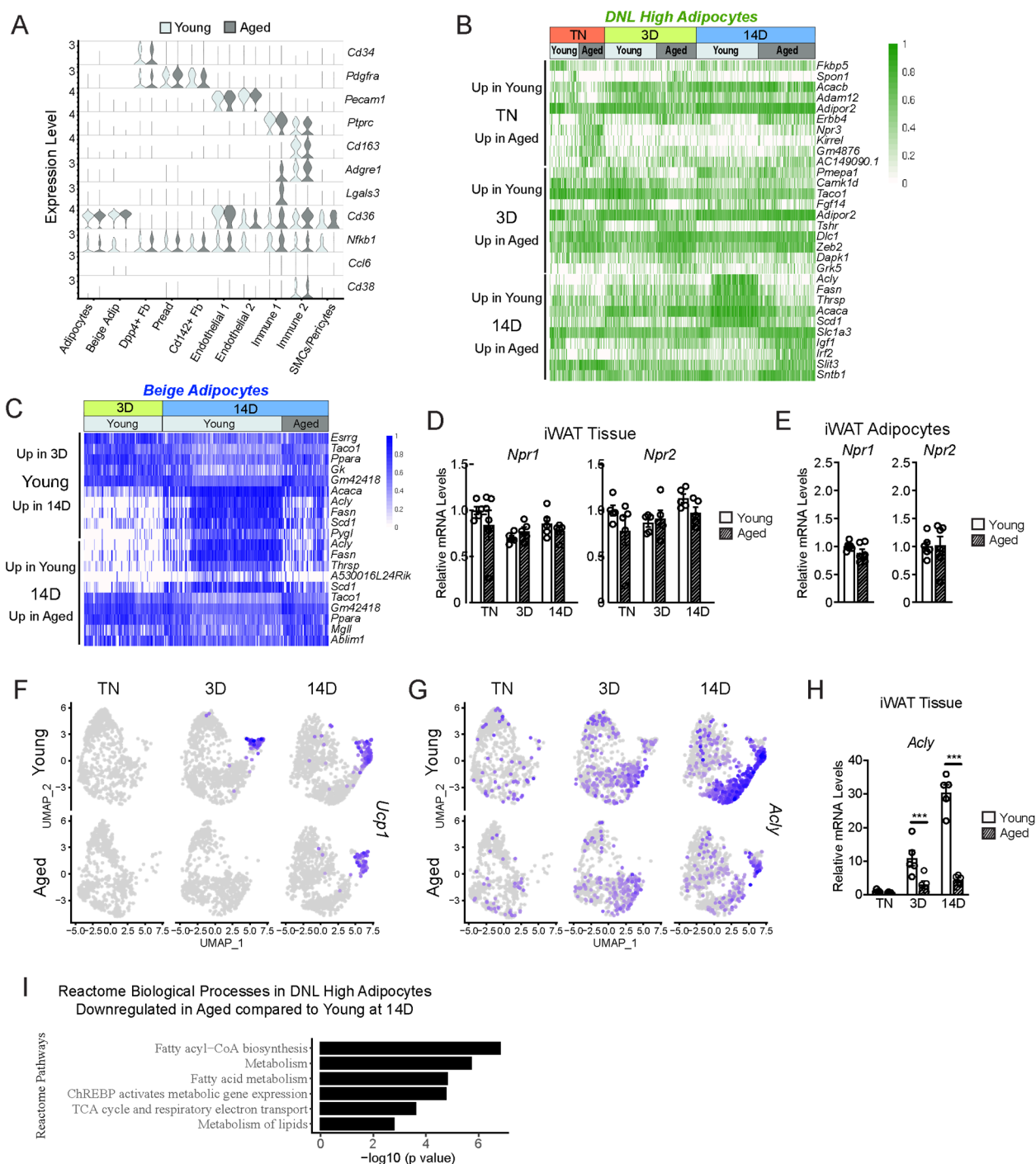
B



447
448
449
450

Figure S3, related to Figure 3. (A) Violin plot showing expression of ARC marker genes in cell clusters split by age, Y-axis = log-scale normalized read count. **(B)** Expression heatmap of top ASPC marker genes across age and housing conditions.

Figure S4



451
 452 **Figure S4, related to Figures 5,6.** (A) Violin plot showing expression levels of ARC marker genes split by age, y-axis = log-
 453 scale normalized read count. (B) Expression heatmap of the top aging-regulated genes in DNL-high adipocytes. (C)
 454 Expression heatmap of the top aging-regulated and cold-regulated genes in beige adipocytes. (D-E) *Npr1* and *Npr2* mRNA
 455 levels in (D) iWAT from mouse groups described in Figure 1A, n=5 and (E) isolated adipocytes from iWAT from TN-acclimated
 456 young and aged mice, n=6. (E-F) UMAP of *Ucp1* (E) and *Acly* (F) mRNA levels in adipocyte populations (from Figure 5D). (H)

457 *Acy* mRNA levels in iWAT from mouse groups described in Figure 1A, n=5. (G) Enrichment analysis displaying the top six
458 Reactome pathways in DNL high adipocytes downregulated in aged at 14 days. Data represent mean \pm SEM, points represent
459 biological replicates, 2 groups analyzed using a Student's t-test, and multiple conditions analyzed with a two-way ANOVA with
460 a Tukey correction for multiple comparisons. Significance: not significant, $P > 0.05$; * $P < 0.05$ ** $P < 0.01$; *** $P < 0.001$.