Supplemental Figure 1



Supplemental Figure 1. Correlation and categorical analyses of ATMs and ATDCs. (**A**)-(**B**) Correlation scatter plots for ATM and ATDC frequencies and clinical measures for VAT and SAT. Best fit lines are shown based on linear regression, and dotted lines indicate the 95% confidence bands. Red asterisks indicate p<0.05 by Spearman correlation. (**C**) Multiple regression results examining VAT ATMs and ATDCs as predictors of HbA1c adjusting for age, sex, and BMI (**D**) Subjects stratified by diagnosis of diabetes, with indicated SVC frequencies in VAT normalized to frequencies in SAT for each individual. (**E**) SAT SVC frequencies in patients stratified by clinical criteria. (**F**) Subjects stratified by diagnosis of diabetes and sex. NDM female n=9; NDM male n=17; DM female n=6; DM male n=12.

Supplemental Figure 2

Α





Supplemental Figure 2. Top differentially expressed genes in human ATM subtypes and overlap with published data. (A) Number of unique DE genes increased for each ATM subtype compared to both other subtypes, with at least five-fold difference in expression. (B) DE genes up in each subtype compared to both other subtypes, with at least five-fold difference in expression. (C) The most highly expressed DE genes with at least 10-fold change comparing CD206+ to CD11c+ ATMs. (D) DE transcription factors with the highest fold change comparing CD206+ ATMs to CD11c+ ATMs. (E) The most highly expressed DE genes with at least 10-fold change comparing CD206+ to DP ATMs. (F) DE transcription factors with the highest fold change comparing CD206+ ATMs to DP ATMs. (G) Overlap of human ATM subtypes with putative dendritic cells and monocyte gene expression from Vijay et al. 2020. Data shown as log2 (FPKM) unless otherwise indicated.

Supplemental Figure 3



Supplemental Figure 3. Gene set expression shown in mean FPKM for VAT and ATM subtypes. Gene sets represent scavenger receptors (A), HLA-D genes (B), lipid-laden macrophages (C), lipid antigen presentation (D), and cytokines (E).



Cytokine interaction networks in two prominent human visceral ATM subtypes in obesity

Supplemental Figure 4. Supplemental analysis related to Figure 6. Cytokine gene expression networks constructed for CD206⁺ vs. CD11c⁺ ATMs. Nodes are genes, where the size of the node indicates relative expression. Edges between genes represent a known protein-protein interaction, where edge weight is the average of each pair of genes' expressions. Red nodes indicate DE genes in the networks.