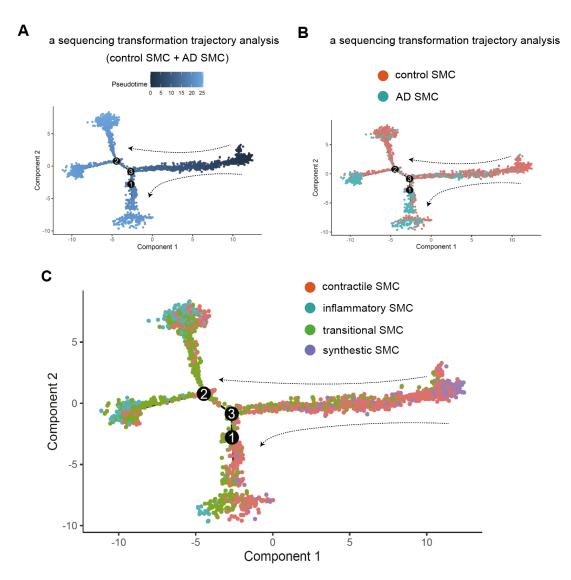


Supplemental Figure 1 Subcellular reclustering and signaling pathway enrichment analysis of CD4 immune T cells

- (A) The expression level of $CD4^+T$ cells.
- (B) Gene ontology (GO) analysis indicated significant enrichment processes.
- (C) The expression of typical CD4+ T cell markers.
- (D) The expression of myeloid cell markers, such as those associated with Dendritic Cells (pDCs).



Supplemental Figure 2 Sequencing transformation trajectory analysis of SMC

- (A) Sequencing transformation trajectory analysis of control-SMC and AD-SMC.
- (B) The differences in cell transformation between AD-SMC and control-SMC.
- (C) Detailed analysis based on gene expression profiles of different type of SMC.

GO biological process complete		
events	P value	FDR
response to oxidative stress	2.20E-05	4.93E-04
detoxification of inorganic compound	3.34E-04	5.52E-03
detoxification	7.08E-04	1.05E-02
positive regulation of T cell mediated cytotoxicity	4.43E-03	4.68E-02

ControlVSCS Control-VSCS ADVSCS AD. VSCS log₂ fold change log₂ fold change APOE NET1 CD36 SOD2 CYP1B1 KLF2 CYGB GPX3 RHOB COL1A1 RCAN1 NDUFA12 PRNP PPP2CB HSPA1A SELK TXNIP PRKAA2 PRDX2 BTC1 0.3 2 PRDX2 BTG1 PSIP1 FYN EPAS1 FOS CHCHD2 KDM6B RHOB COL1A1 CRYAB TNFAIP3 RBPMS KCNA5 NCOA7 APOD MSRB3 DDIMM 0.2 KDM6B SEPP1 COL6A1 HSPA1B NR4A2 GPX4 PRDX4 STAT1 ATP2A2 MT-ND3 GSTP1 1 MSRB3 PDLIM1 HBB EDNRA SOD3 IL6 HBA2 TPM1 TXN 0.1 0 0

Supplemental Figure 3 The heat map of the expression levels of genes involved in oxidative stress events in AD

response to oxidative stress