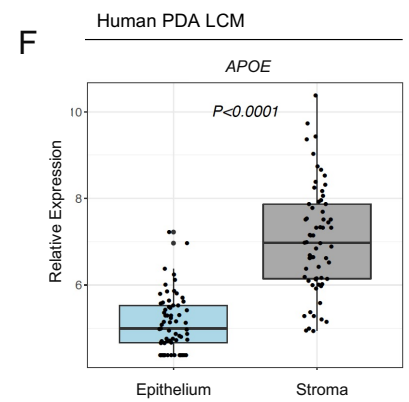
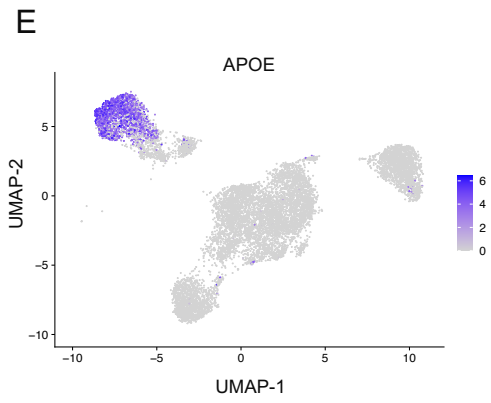
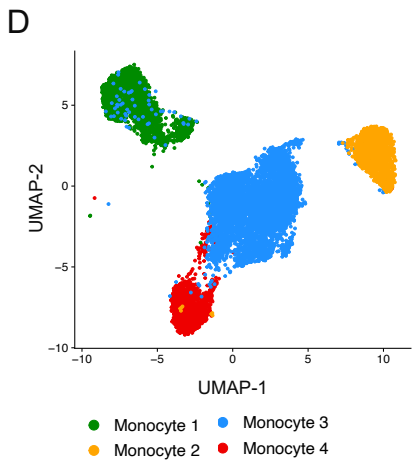
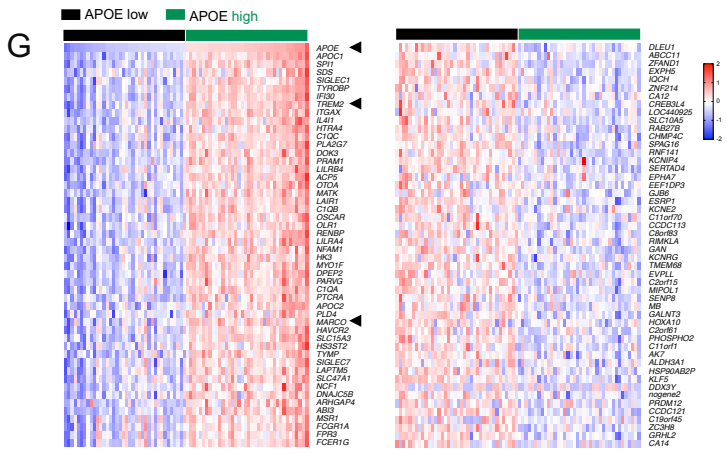


Circulating monocytes



Human PDA - TCGA



Supplementary Figure 1. *APOE* is highly expressed in the human PDA microenvironment. (A) Feature plot of *APOE* in human PDA tumor cell populations. Low expression is in grey, while high expression for *APOE* is in blue. (B) Dot plot of lineage markers used to define identified myeloid populations in human PDA. Color of the dot represents average expression. Size of the dot represents expression frequency. (C) Average expression heatmap of myCAF (*TAGLN*, *ACTA2*, *POSTN*) and iCAF (*C3*, *DPT*, *APOE*) lineage markers. Low expression (blue) and high expression (red) of selected genes. (D) UMAP visualization of 4 identified monocyte populations in human PDA. (E) Feature plot of *APOE* in human PDA monocyte populations. Low expression is in grey, while high expression for *APOE* is in blue. (F) Relative *APOE* expression in epithelium (n=65) and stroma (n=65) compartments in human PDA samples from Laser Capture Microdissection PDA dataset. (G) Heatmaps of the top correlated genes in *APOE* low (n=38) and *APOE* high (n=38) (top and bottom quartile) patients from TCGA pancreatic cancer data. Arrowheads denote *APOE*, *TREM2*, and *MARCO*. Low expression is in blue. High expression is in red.