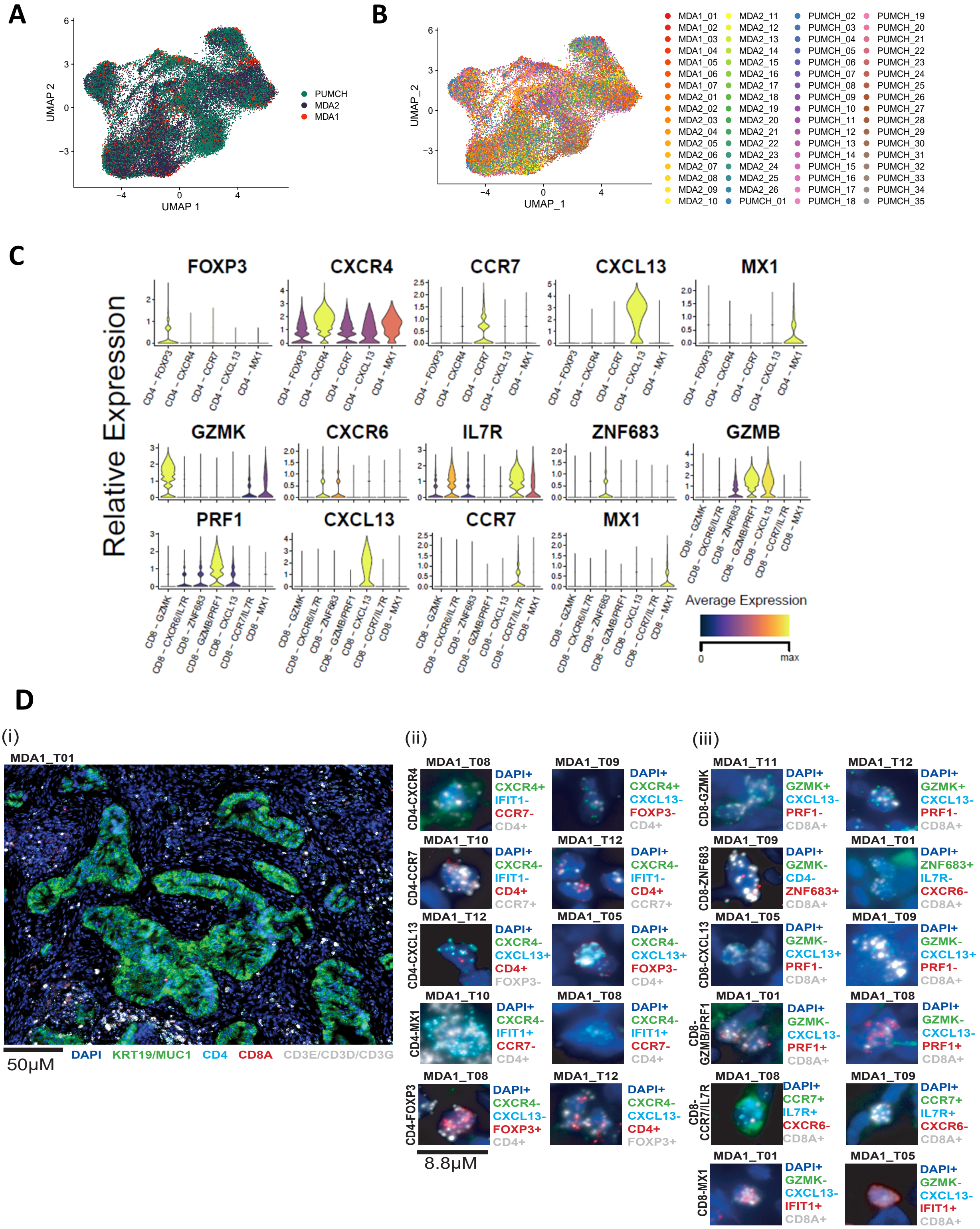
# SUPPLEMENTARY FIGURE S1

## Single cell sequencing reveals trajectory of tumor-infiltrating lymphocyte states in pancreatic cancer

# Supplementary Figure S1



**Supplementary Figure S1.** The uniform manifold approximation and projection (UMAP) of 39,694 single T-cells from 57 pancreatic ductal adenocarcinoma (PDAC) samples and 22 uninvolved samples, color coded by **(A)** cohort and **(B)** patient. Each dot is a single cell and is colored according to dataset/patient and transcriptomic cell state respectively. **(C)** Violin plots showing relative expression of the defining gene for each tumor-infiltrating lymphocyte (TIL) cell state. Plots are color coded according to level of expression as indicated by the color key. **(D)** RNAscope of cells in the PDAC TME: (i) Field view of tumor cells (KRT19/MUC1+) and CD3/CD4/CD8-expressing T cells from a highly T cell-infiltrated PDAC sample, and examples of (ii) CD4$^+$ cells and (iii) CD8$^+$ cells expressing markers of the single-cell RNAseq-defined T-cell states (left label) present in the PDAC TME (top label). Labels on the right indicate all markers in the panel for the slide and their associated pseudo-coloring. Each cell state is depicted for one cell, in two patients.