A

hPDA2   hPDA3   hPDA1-4

- Myeloid cell (CD16⁺)
- CD4 T cell
- CD4⁺CD25⁺
- CD8 T Cell
- CD8⁺CD33⁺
- CD66a/c/e⁺
- B cell
- Myeloid cell (HLA-DR⁺)
- Myeloid cell (CD11c⁺)
- Myeloid cell
- Undefined

B hPDA

C Correlation Treg : Macrophage

$R^2 = 0.1754$
$p = 0.008$

Correlation Treg : CD8

$R^2 = 0.00029$
$p = 0.918$

D hPanIN

E Correlation Treg : Macrophage

$R^2 = 0.416$
$p < 0.0001$

Correlation Treg : CD8

$R^2 = 0.3822$
$p < 0.0001$

F

Average Expression

Percent Expressed

G TCGA PDAC

FOXP3 low [n=75]   FOXP3 high [n=75]

H

$r = 0.3219$
$P < 0.0001$

I

$r = 0.2736$
$P = 0.0007$

$r = 0.1142$
$P = 0.1642$

$r = 0.4581$
$P < 0.0001$

$r = 0.3870$
$P < 0.0001$

Supplemental Figure 1

Supplemental Figure 1. Prevalence analysis of Regulatory T cells in human PDA patient samples. (A) CyTOF immune profiling of human pancreatic tumors. Left: FlowSOM-viSNE analysis of immune infiltration (CD25+ cells colored in green); Right: Quantification of immune cell types in 4 human pancreatic tumors. **(B)** Quantitative analysis of Tregs, Macrophages and CD8 T cells present in 39 human PDA samples. **(C)** Pearson's correlation coefficient analysis between the frequency of Treg and Macrophage or between Treg and CD8 T cells in human PDA. **(D)** Quantitative analysis of Tregs, Macrophages and CD8 T cells present in 37 human PanIN samples. **(E)** Pearson's correlation coefficient analysis between the frequency of Treg and Macrophage or between Treg and CD8 T cells in human PanIN samples. Tregs positively correlate with macrophages in human PanIN and cancer, and with CD8+ T cells in human PanIN **(F)** Bubble plots showing selected cell type-specific markers across all clusters identified in the single-cell analysis of mouse PanIN lesions. Size of dots represents percentage of cells expressing a particular maker and intensity of color indicates level of mean expression. **(G)** Heatmap showing differentially expressed myCAF genes and TGFβ signaling genes (adjusted P<0.05) in human pancreatic cancer tissues expressing low versus high FOXP3. Based on the tumor RNA-Seq data from the TCGA. FOXP3 low = 75 samples and high = 75 samples. **(H)** TCGA data analysis showing correlation between FOXP3 and ACTA2 gene expression in human pancreatic cancer tissues. **(I)** TCGA data analysis showing positive correlation between FOXP3 and TGFβ signaling genes expression in human pancreatic cancer tissues. Pearson's correlation analysis was used. n=150.