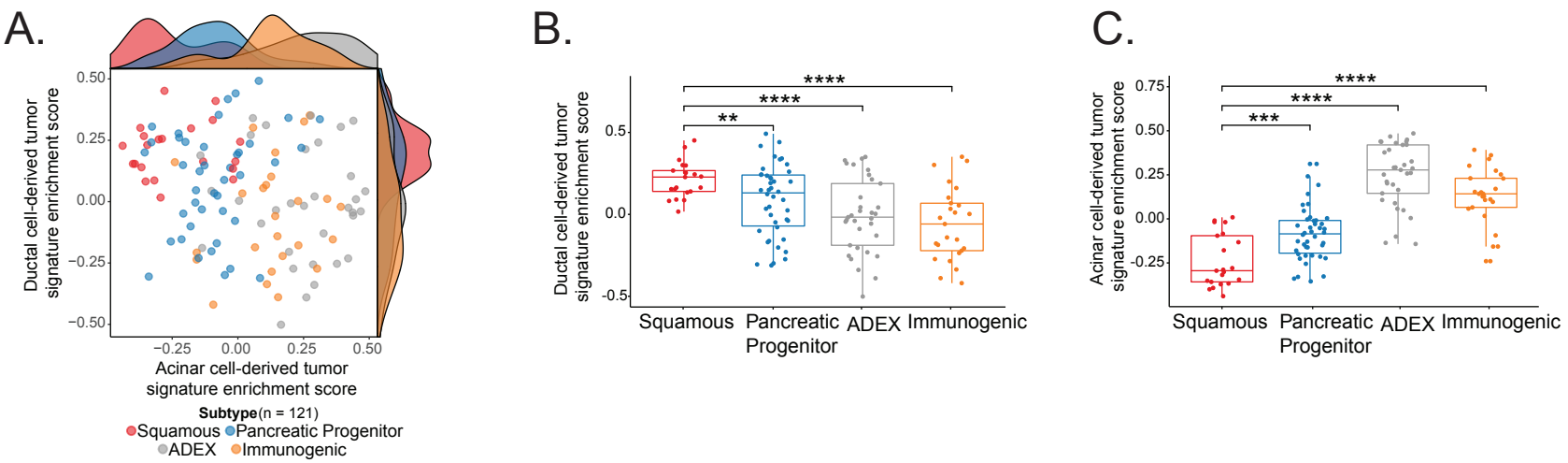

Supplementary Figure 5: Acinar and ductal cell-derived tumor signature enrichment in TCGA cohort

(A) Scatter plot of acinar cell-derived tumor and ductal cell-derived tumor signature enrichment in primary PDAC samples (TCGA, n = 121) classified as squamous, pancreatic progenitor, immunogenic, or ADEX molecular subtypes. Each dot represents a tumor sample, color coded by molecular subtype. **(B)** Box plot of the ductal cell-derived tumor signature enrichment score in primary PDAC samples (TCGA, n = 121) classified as squamous, pancreatic progenitor, immunogenic, or ADEX molecular subtypes. The ductal cell-derived signature enrichment score is significantly different in tumors classified as the pancreatic progenitor (n = 42), ADEX (n = 33), or immunogenic (n = 25) subtypes than the squamous subtype (n = 21), using a two-tailed Student's t-test. ** p-value < 0.01, ****p-value <0.0001. **(C)** Box plot of the acinar cell-derived tumor signature enrichment score in primary PDAC samples (TCGA, n = 121) classified as squamous, pancreatic progenitor, immunogenic, or ADEX molecular subtypes. The acinar cell-derived signature enrichment score is significantly different in tumors classified as the pancreatic progenitor (n = 42), ADEX (n = 33), or immunogenic (n = 25) subtypes than the squamous subtype (n = 21), p-values based on a two-tailed Student's t-test. ***p-value < 0.001, ****p-value < 0.0001.