**Supplementary Figure 1: (A)** Correlation of gene expression levels in a pancreatic cancer cell line between single cells, bulk cells, and across independent replicates. (Single cell vs Bulk, R2: 0.915 and R2:0.9 for genesBoth ≥1 (N=14,922) and ≥10 (N=11,574) respectively. Independent Cell Replicates, R2: 0.937 and R2: 0.955 for genesBoth ≥1 (N=13,791) and ≥10 (N=10,609) respectively). **(B)** Scatter plots of number of UMIs against number of genes expressed and percentage of mitochondrial genes expressed per single cell across independent tissue samples from pancreatic lesions (different colors). **(C)** Violin plots of number of genes, UMIs, and percentage of mitochondrial genes expressed per single cell from tissue samples profiled in this study. **(D)** Principal components (PC) elbow plot to determine the elbow between the standard deviation of the PC and the number of PCs (11).

**Supplementary Figure 2 (A)** Gross pathology of a HGD-IPMN lesion with concomitant PDAC included in this study. **(B)** Paraffin fixed tissue H&E sections of representative LGD-IPMN and HGD-IPMN lesions included in this study (20x magnification).

**Supplementary Figure 3:** Feature Plot of characteristic genes plotted across tSNE clusters demonstrating stromal phenotypes.

**Supplementary Figure 4:** Correlation heatmap of Pearson correlation coefficients of hierarchically clustered individual cells across stromal populations identified by originating lesion type and tSNE cluster suggests multiple unique subtypes.

**Supplementary Figure 5:** Tapestation traces following (A) cDNA amplification of single cell and (B) library construction demonstrating sufficient quality and yield of material. Vertical lines demonstrate regions utilized to calculate cDNA and library yield through area under the curve.

**Supplementary Table 1:** Patient characteristics

**Supplementary Table 2:** Cell phenotype gene list

**Supplementary Table 3:** Differentially expressed genes across all clusters

**Supplementary Table 4:** Pancreatic cancer core signaling pathways across lesion types

**Supplementary Table 5:** Pathway analysis among lesion types