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**Supplementary Figure. 2. Single-cell transcriptomic atlas and cell typing in primary PDAC and hepatic metastatic tumor.** (A) Dot plot showing representative marker genes across 22 cell clusters in our cohort. Dot size is proportional to the fraction of cells expressing specific genes. Color intensity corresponds to the relative expression of specific genes. (B and C), tSNE plots displaying the integrated scRNA-seq cell map before and after batch correction using the Harmony package. (D) The UMAP plot displaying the scRNA-seq cell map consisting of 12 annotated cell types (n = 32,504 cells). The UMAP plot illustrates the distribution of all sequenced cells categorized by tissue origin. (E) The UMAP plot displaying the cell map in LNN, LNP, and HM groups. (F) The bar plot showing cell type abundance from different groups, including three LNN, three LNP, and one HM PDAC tissues. (G) The bar plot showing cell type abundance in scRNA-seq, including seven samples from our cohort. PDAC, pancreatic ductal adenocarcinoma; LNN, lymph node-negative; LNP, lymph node-positive; HM, hepatic metastasis.