

Supplementary Figures

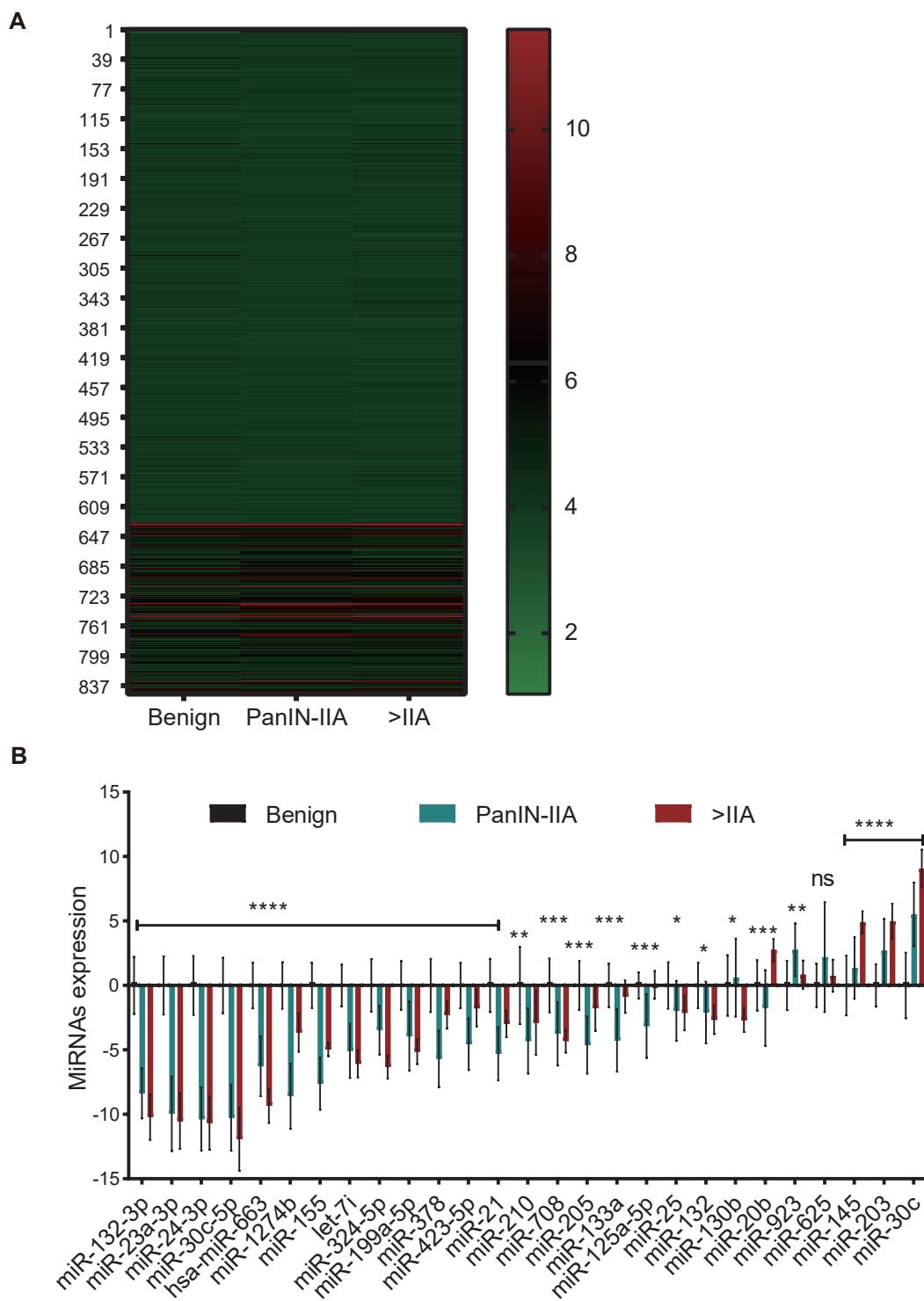


Figure S1. Biomarker discovery of miRNAs in FFPE tissues. **(A)** Heat map of all miRNAs identified by microarray expression profiling in FFPE tissues ($n = 300$) from benign, early lesions (PanIN-TNM stage IIA), and advanced stages (>IIA). Each group contained 100 tissue cores, with statistical power $\geq 95\%$. $p < 0.05$. **(B)** Quantitative polymerase chain reaction analysis of differentially expressed miRNAs in benign, early lesions and advanced stage tissues. Each group was duplicated with nine samples. Delta delta Ct value was the relative delta Ct value of each group normalized to the mean delta Ct value of benign group. The column and bar represents mean with \pm SD. The significance was analyzed with one-way ANOVA: * $p < 0.05$; ** $p < 0.01$; *** $p < 0.001$; **** $p < 0.0001$.

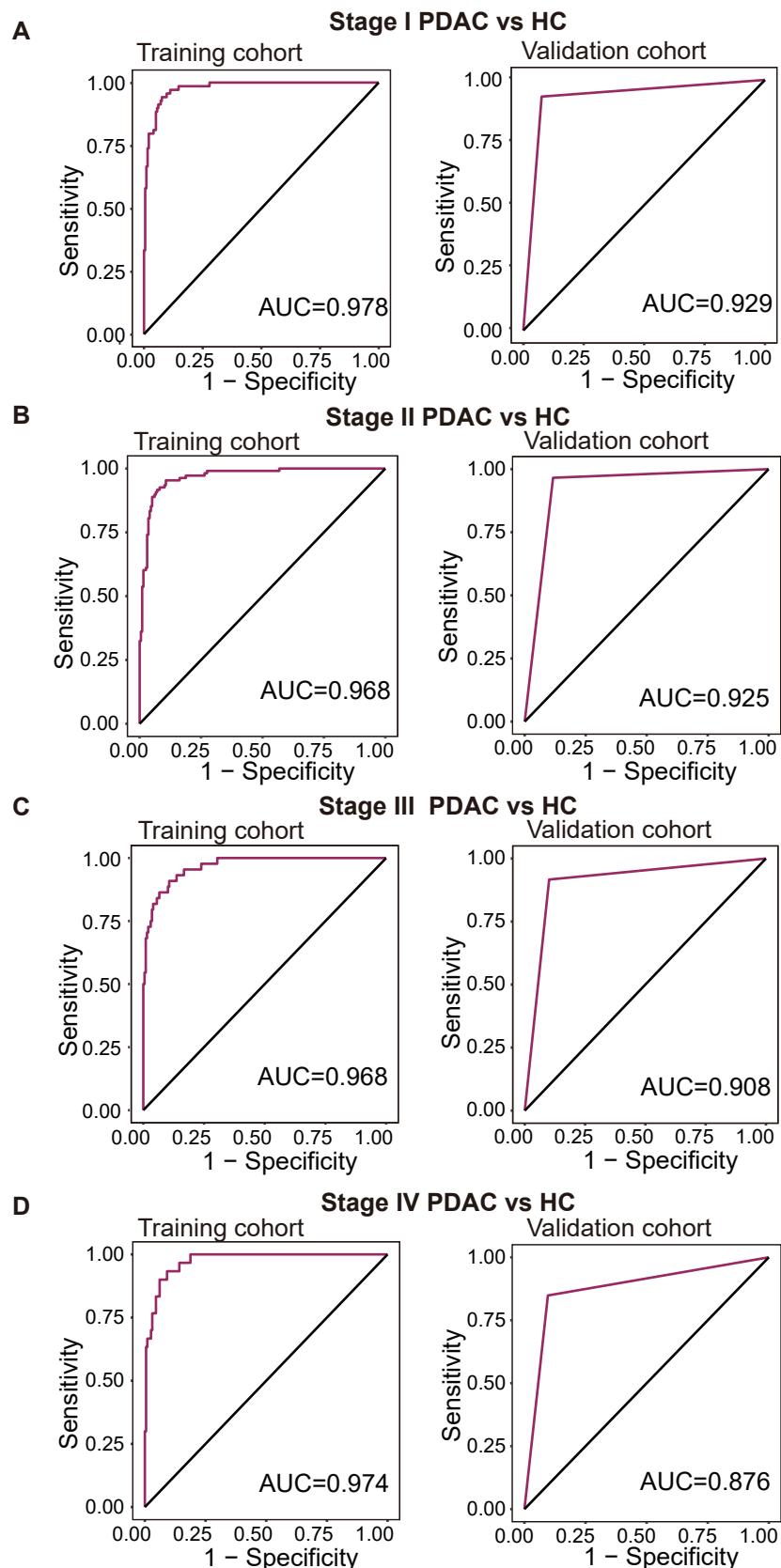


Figure S2. ROC curves of the miRNA panel in distinguishing patients with pancreatic ductal adenocarcinoma (PDAC) at TNM stage I (**A**), II (**B**), III (**C**), and IV (**D**) from healthy controls (HC) in the training and validation cohorts.

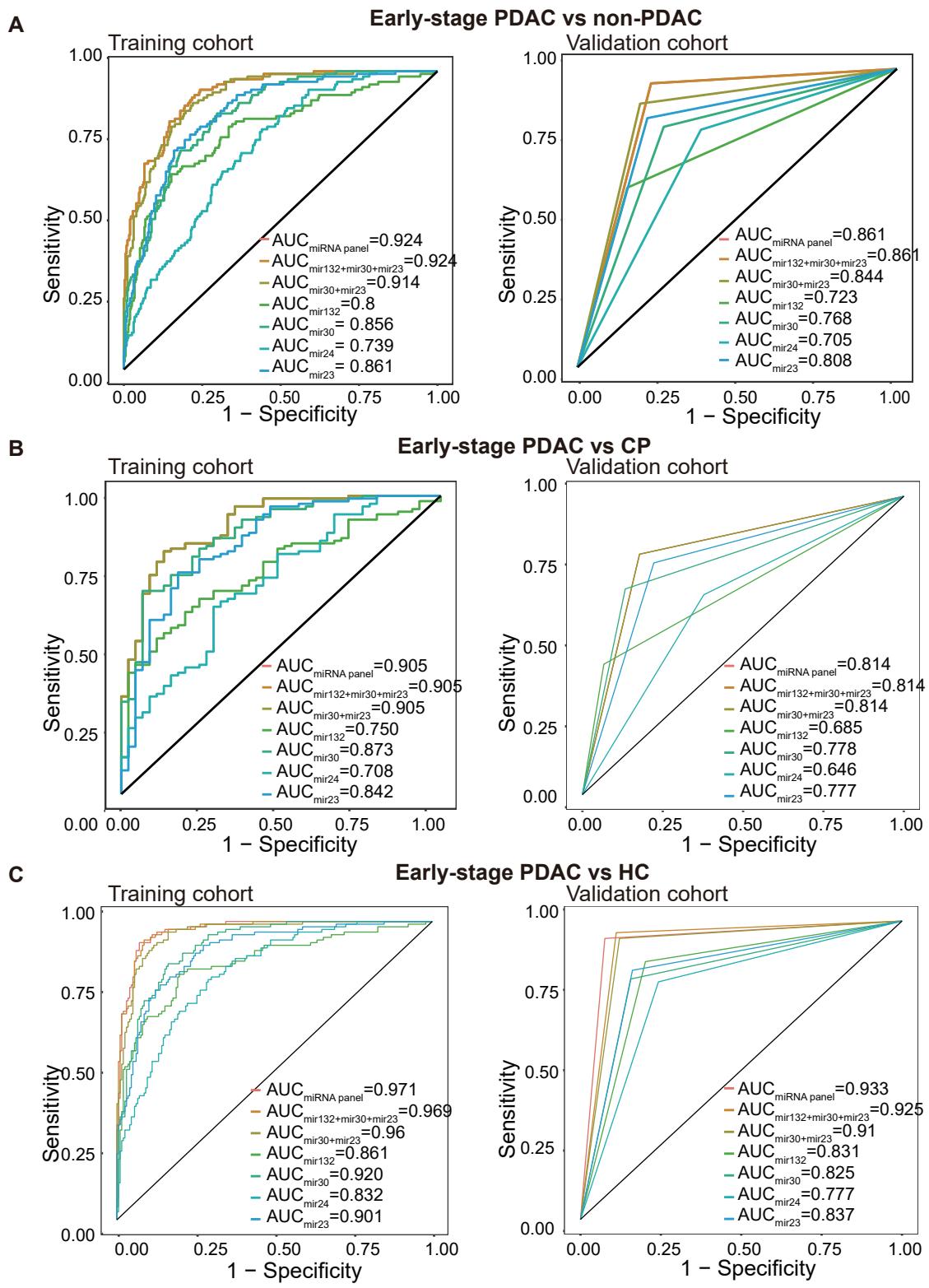


Figure S3. ROC curves of the four miRNAs individually or in combination in distinguishing patients with early-stage pancreatic ductal adenocarcinoma (PDAC) (TNM stage≤ IIA) from non-PDAC (healthy controls and individuals with chronic pancreatitis and pancreatic cystic neoplasms) (A), chronic pancreatitis (CP) (B), and healthy controls (HC) (C) in the training and validation cohorts.

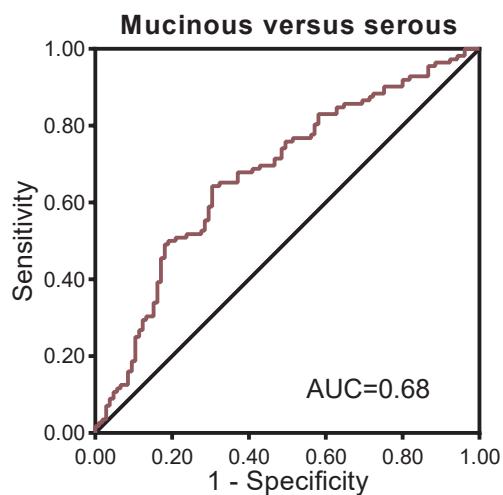


Figure S4. ROC curve of the four-miRNA panel in distinguishing patients with pancreatic mucinous tumors from serous tumors.

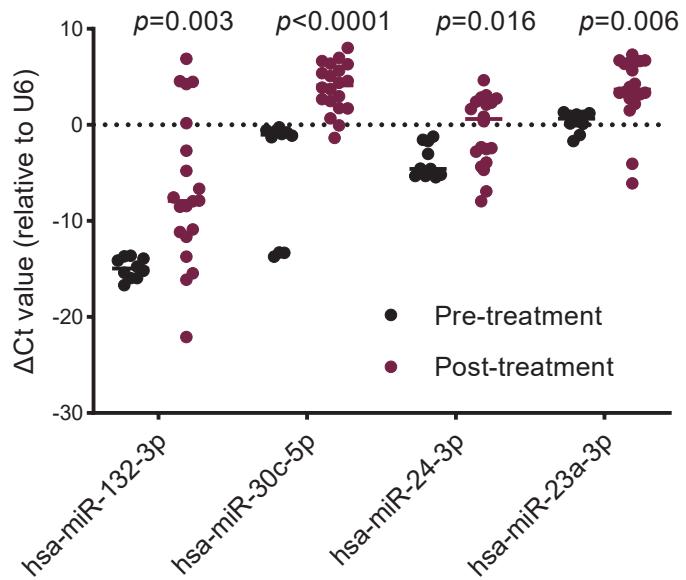


Figure S5. Expression levels of four individual miRNAs in patients with PCa before or after receiving treatment. 10 pre-treatment patients and 20 post-treatment patients with PCa were detected with dual-channel RT-PCR. MiRNA expression levels were represented as the delta Ct value, which was the relative Ct value of each miRNA normalized to U6. The significance was analyzed with unpaired t-test.