Figure S2

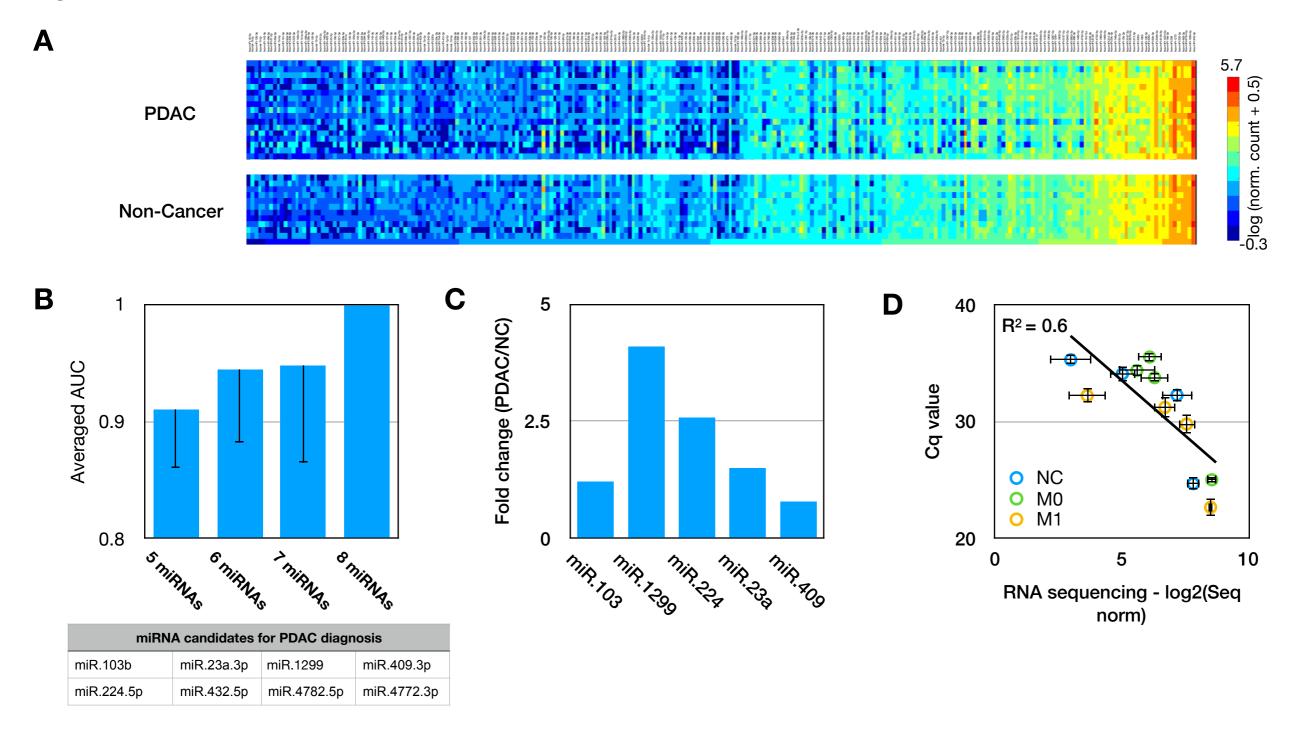


Figure S2. miRNA sequencing to discover miRNA biomarkers to discern PDAC from non-cancer. (A) Raw miRNA sequencing data from 6 healthy controls, 6 non-cancer disease controls, 5 M0 PDAC patients, and 12 M1 PDAC patients. (B) 8 potential miRNA candidates were selected using least absolute shrinkage and selection operator (LASSO) for cancer versus non-cancer, achieving AUC=1 within discovery cohort. (C) We selected 5 out of 8 miRNA candidates based on their abundance as detected by qPCR (Cq < 40) and show the average fold changes of these 5 miRNAs between patient groups. (D) We validated these miRNAs by calculating the correlation coefficient between their qPCR data and the miRNA sequencing data. The overall $R^2 = 0.6$