Supplemental Figure 1.
Supplemental Figure 2.

**FFPE Tissue Study (FTS)**

**FTS1. miRNA Identification and Verification in 22 specimens:** LG IPMN (10), HG IPMN (12)
- a. Specimen Microdissection
- b. Total RNA Extraction
- c. HT miRNA Expression Analysis (TaqMan® MicroRNA Arrays)¹
- d. Identification of miRNA candidates using bioinformatics¹ → 26 tissue miRNAs
- e. RT-qPCR verification of tissue miRNAs (singleplex TaqMan RT-qPCR)¹

**FTS2. Independent miRNA Validation in 33 specimens:** LG IPMN (6), HG IPMN (14), HG IPMN w/cancer (13).
- a. Specimen Microdissection
- b. Total RNA Extraction
- c. RT-qPCR validation of tissue miRNAs from FTS1 using singleplex TaqMan RT-qPCR¹
- d. Identification of miRNA candidates by bioinformatics using 23 specimens → 13 “verified” tissue miRNAs²

**Cystic Fluid Study (CFS)**

**CFS1. miRNA Identification and Verification in 15 specimens:** SCA (5), LG IPMN (5), HG IPMN (5)
- a. Specimen Microdissection
- b. Total RNA Extraction
- c. HT miRNA Expression Analysis (TaqMan MicroRNA Arrays)¹
- d. Identification of miRNA candidates by bioinformatics using 11 specimens² → 37 cyst fluid miRNAs, containing top 13 miRNAs from 26 tissue miRNAs (FTS1.d)
- e. RT-qPCR verification of cyst fluid miRNAs by singleplex TaqMan RT-qPCR → 18 “verified” cyst fluid miRNAs²

**CFS2. Independent miRNA Validation in 50 specimens:** LG IPMN (2), IG IPMN (12), HG IPMN (5), HG IPMN w/cancer (1), SCA (20), NET (5), SPN (5)
- a. Specimen Microdissection
- b. Total RNA Extraction
- c. RT-qPCR validation of 18 “verified” cyst fluid miRNAs + miR-21 by singleplex TaqMan RT-qPCR using 49 specimens²
- d. Logistic regression model: combined specimens from CFS1 (9) + CFS2 (12) for training set, and CFS2 (37) for test set → 9 miRNA model²
Supplemental Figure 4.

A. 

B.
Supplemental Figure 5.
Supplemental Figure 6.

A. 

B.
Supplemental Figure 8.