Supplemental Figure 1.

A.

B.

C.

Supplemental Figure 2.

FFPE Tissue Study (FTS)

Cystic Fluid Study (CFS)

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 bioinformatics[1] → 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-qPCR[1]

d. Identification of miRNA candidates by bioinformatics using 23 specimens → 13 "verified" *tissue* miRNAs[2]

CFS1. miRNA Identification and Verification in 15 specimens: SCA (5), LG IPMN (5), HG IPMN (5)

b. Total RNA Extraction

c. HT miRNA Expression Analysis (TaqMan MicroRNA Arrays)[1]

d. Identification of miRNA candidates by bioinformatics using 11 specimens[2] → 37 *cyst fluid* miRNAs, containing top 13 miRNAs from 26 *tissue* miRNAs (FTS1.d)

f. RT-qPCR verification of *cyst fluid* miRNAs by singleplex TaqMan RT-qPCR → 18 "verified" *cyst fluid* miRNAs[2]

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)
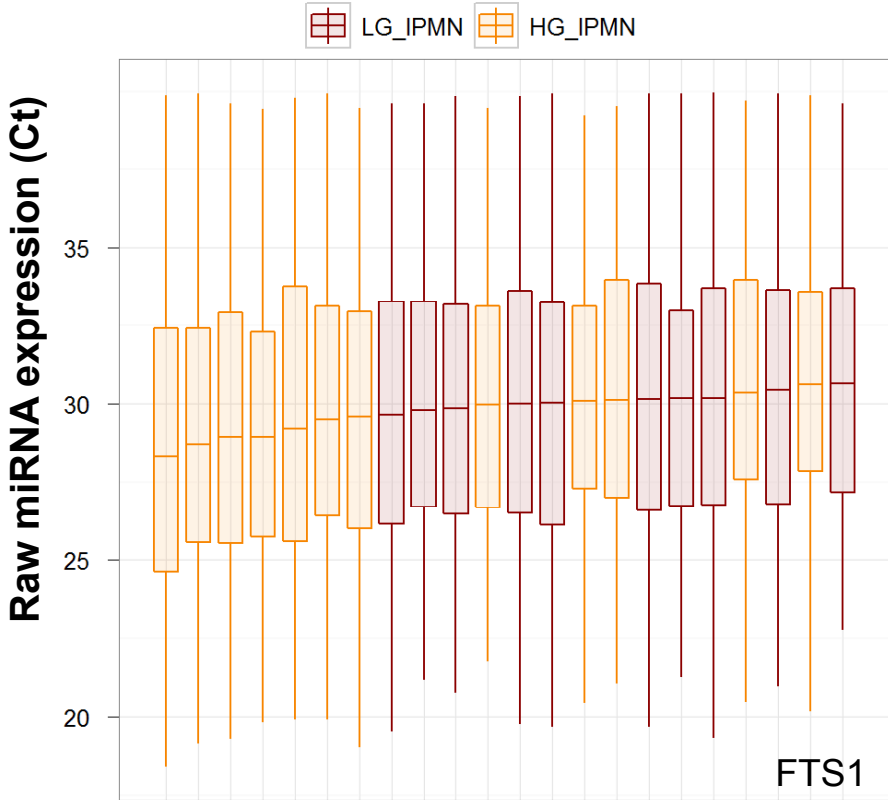
b. Total RNA Extraction

c. RT-qPCR validation of 18 "verified" *cyst fluid* miRNAs + miR-21 by singleplex TaqMan RT-qPCR using 49 specimens[2]

d . Logistic regression model: combined specimens from CFS1 (9) + CFS2 (12) for training set, and CFS2 (37) for test set → 9 miRNA model[2]
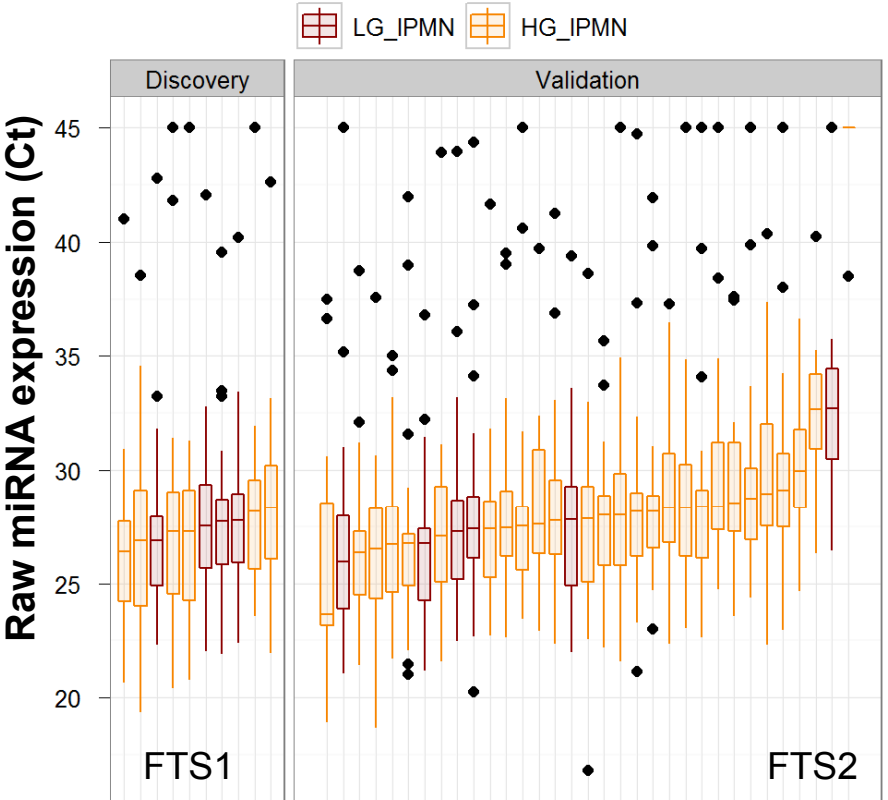
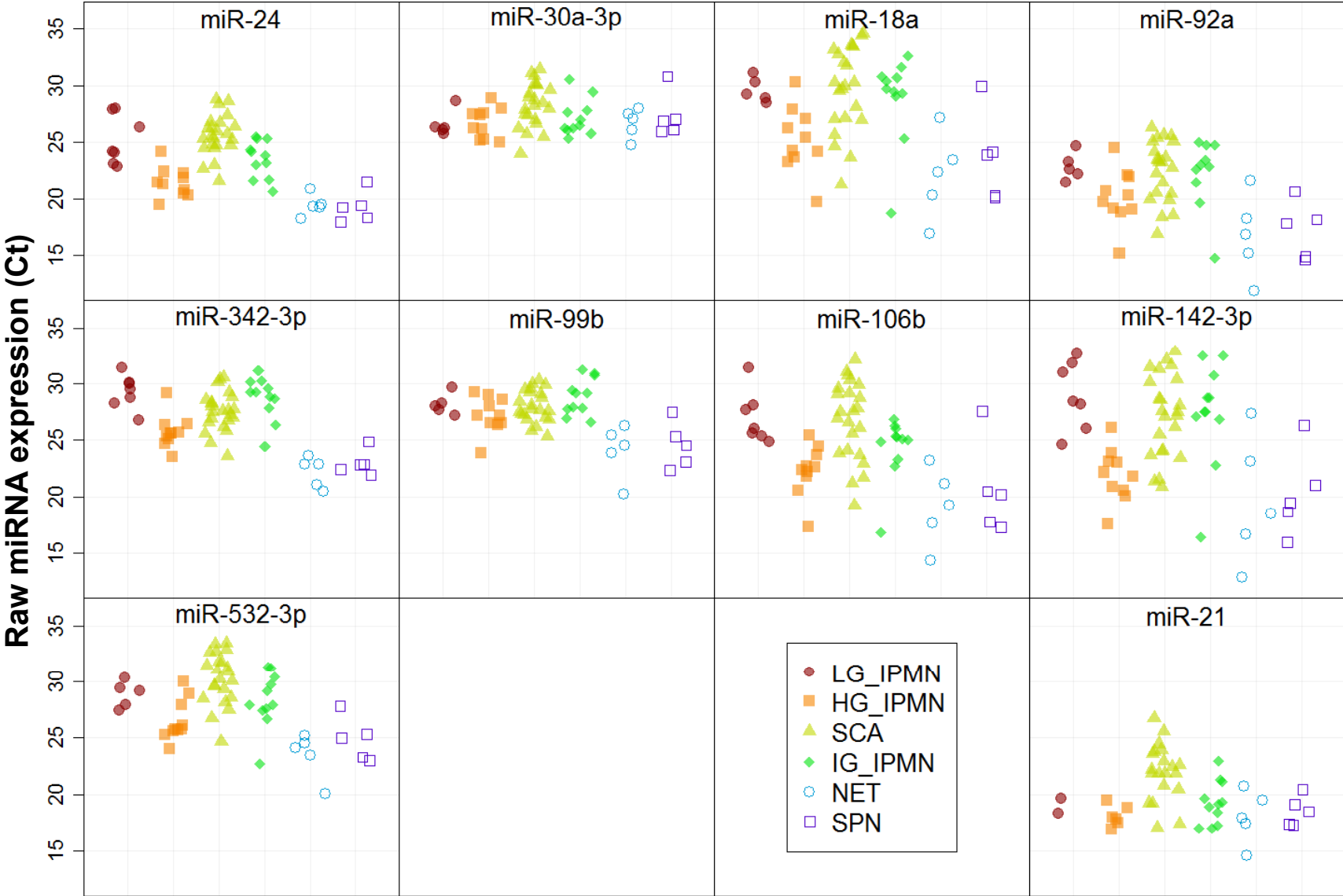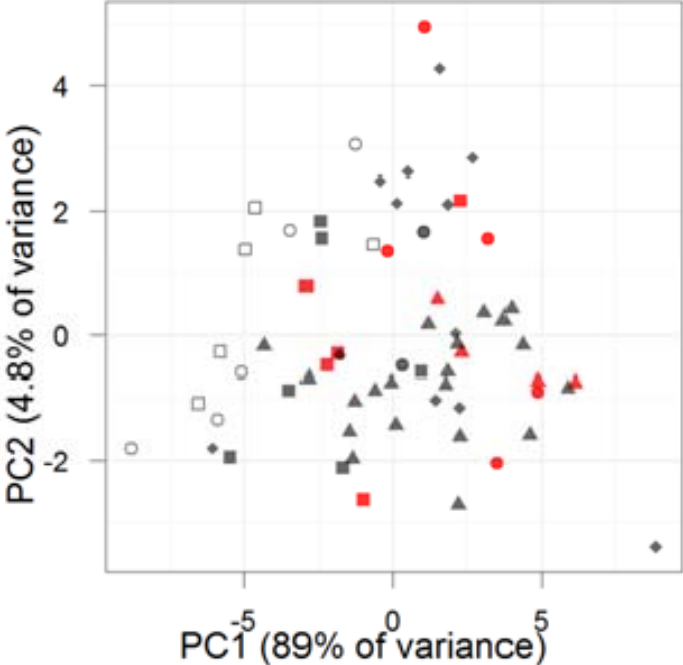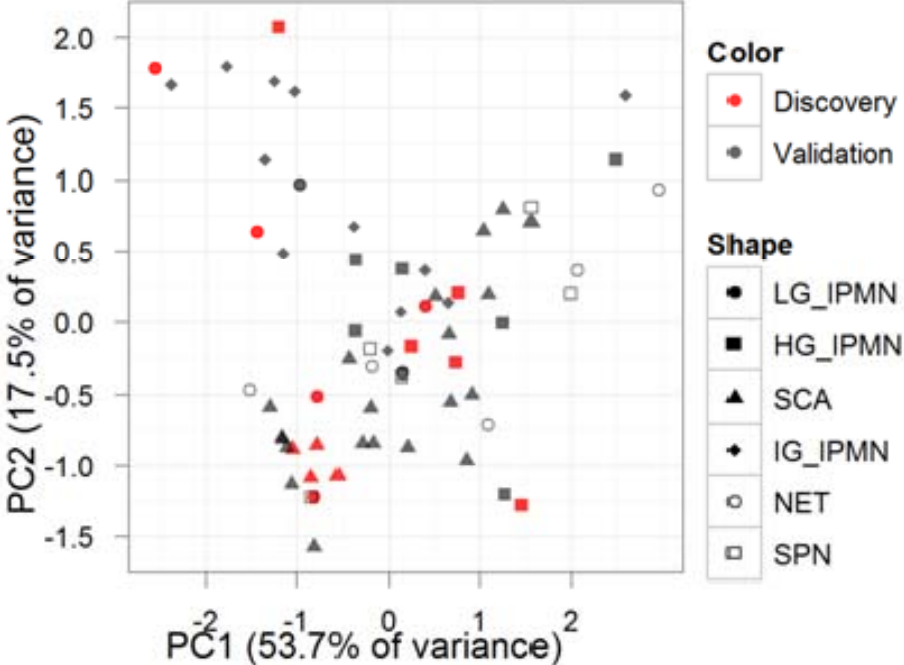# Supplemental Figure 3.
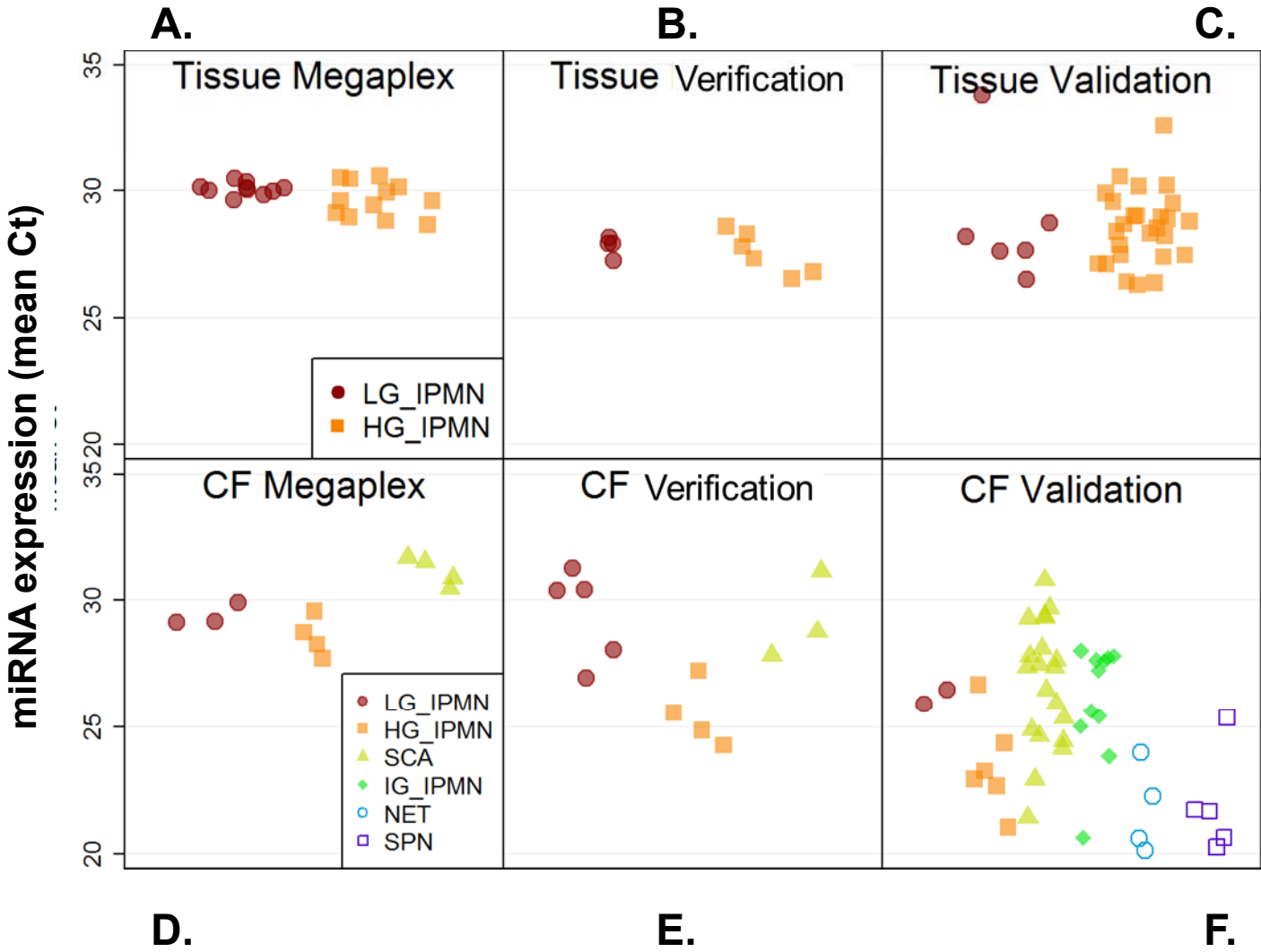
Supplemental Figure 4.

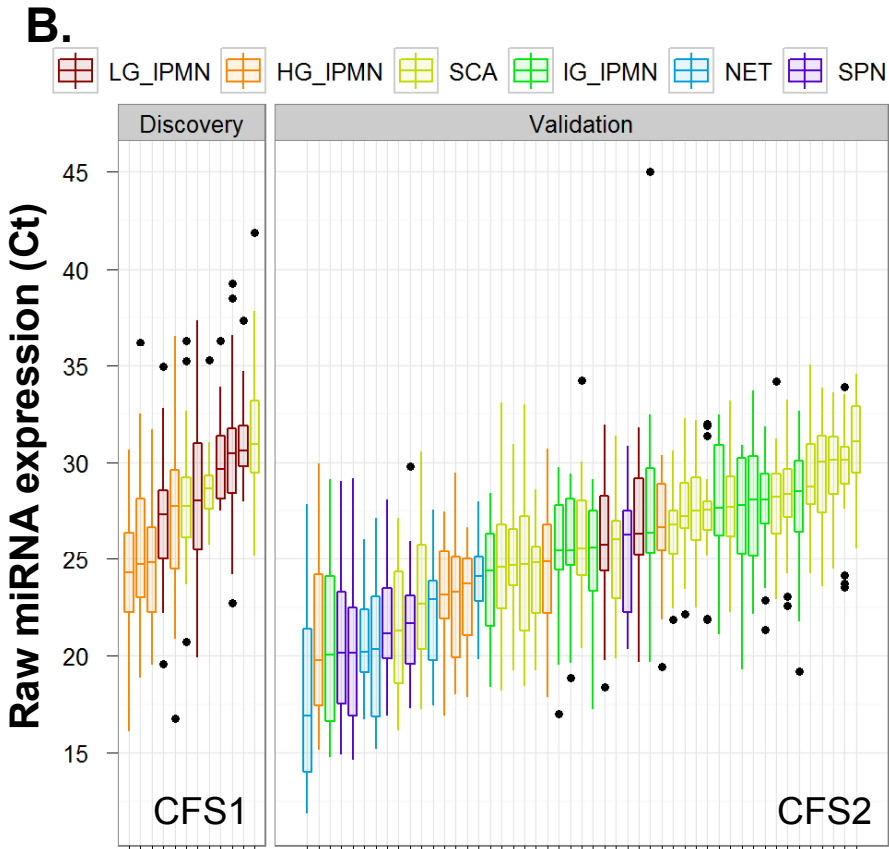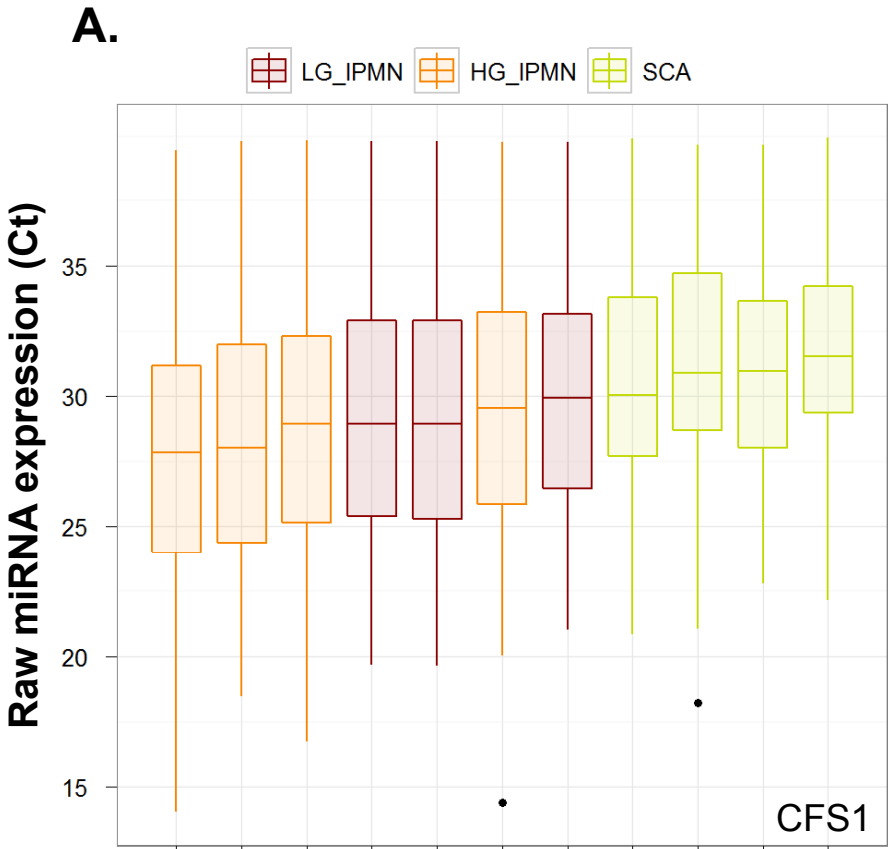**Supplemental Figure 5.**

Supplemental Figure 6.

A.

B.

Supplemental Figure 7.

Supplemental Figure 8.