

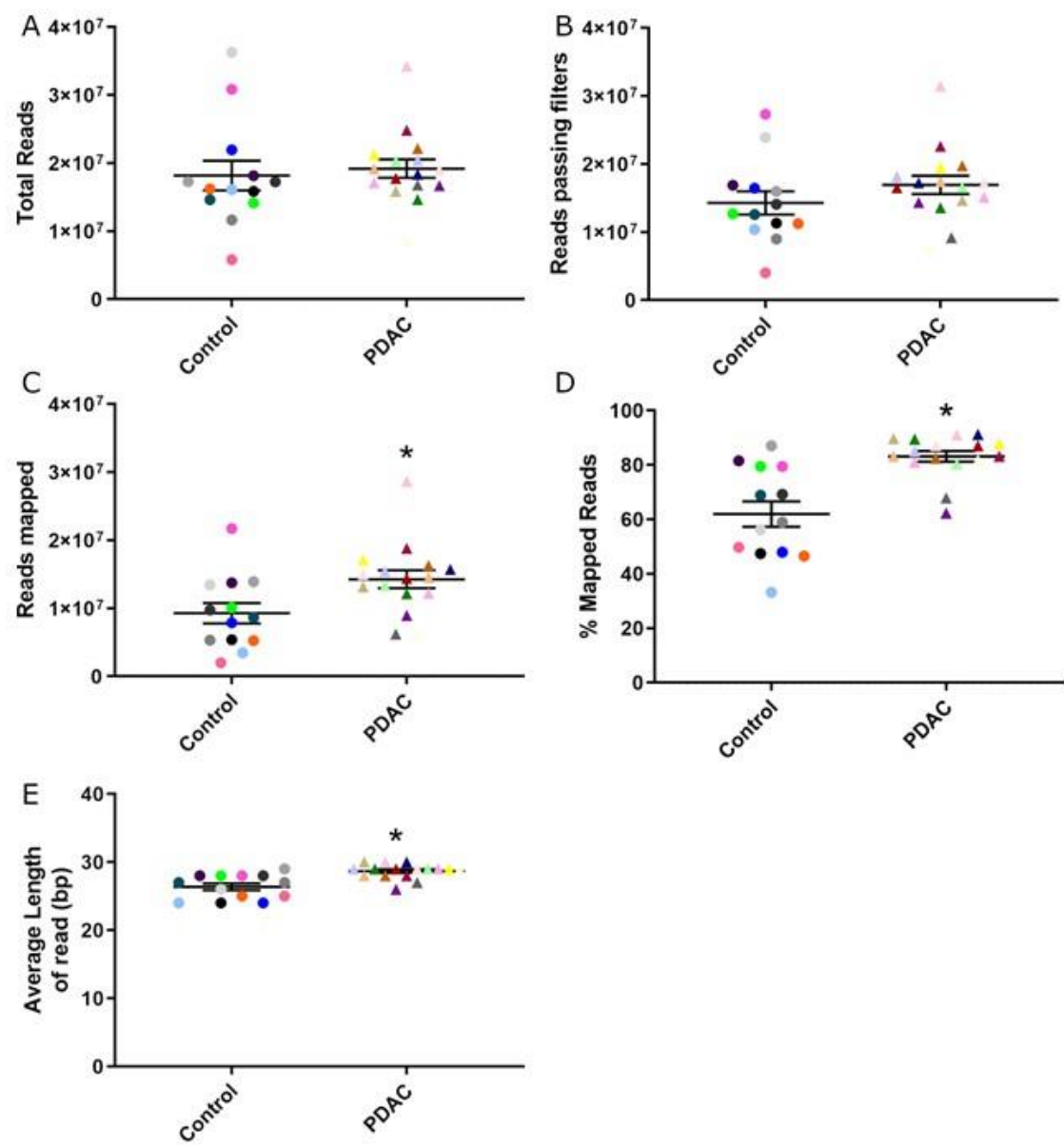
## **SUPPLEMENTARY DATA**

**Title:** Small RNA sequencing analysis of peptide-affinity isolated plasma extracellular vesicles distinguishes pancreatic cancer patients from non-affected individuals

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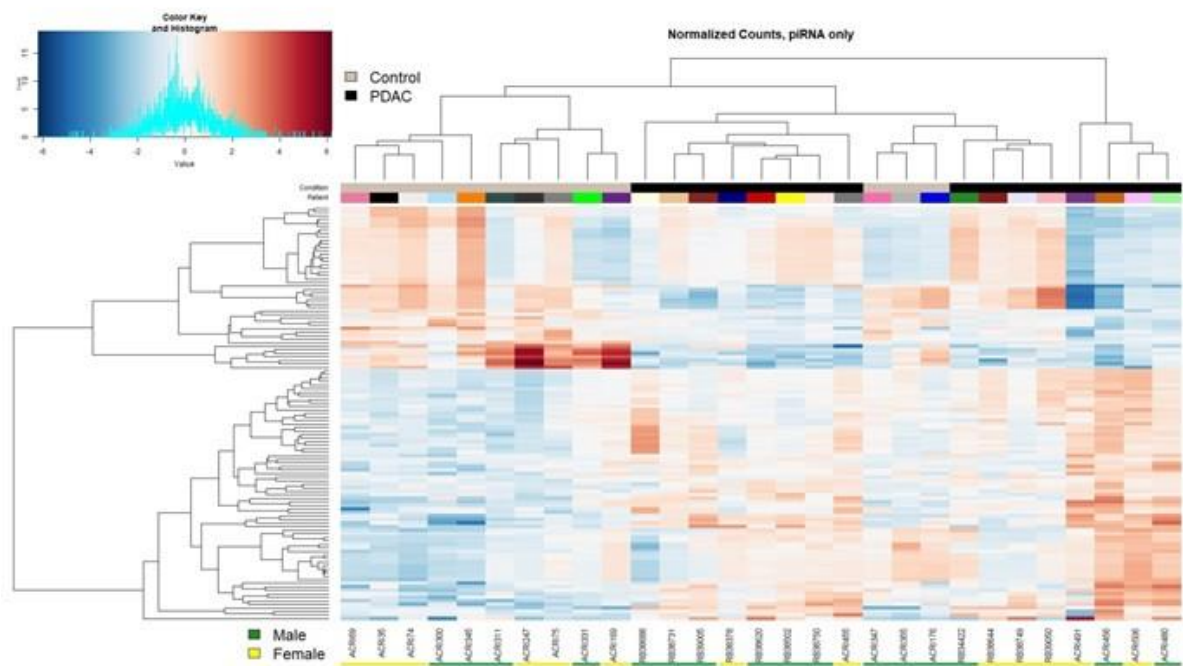
SUPPLEMENTAL FIGURES

Supplemental Figure 1



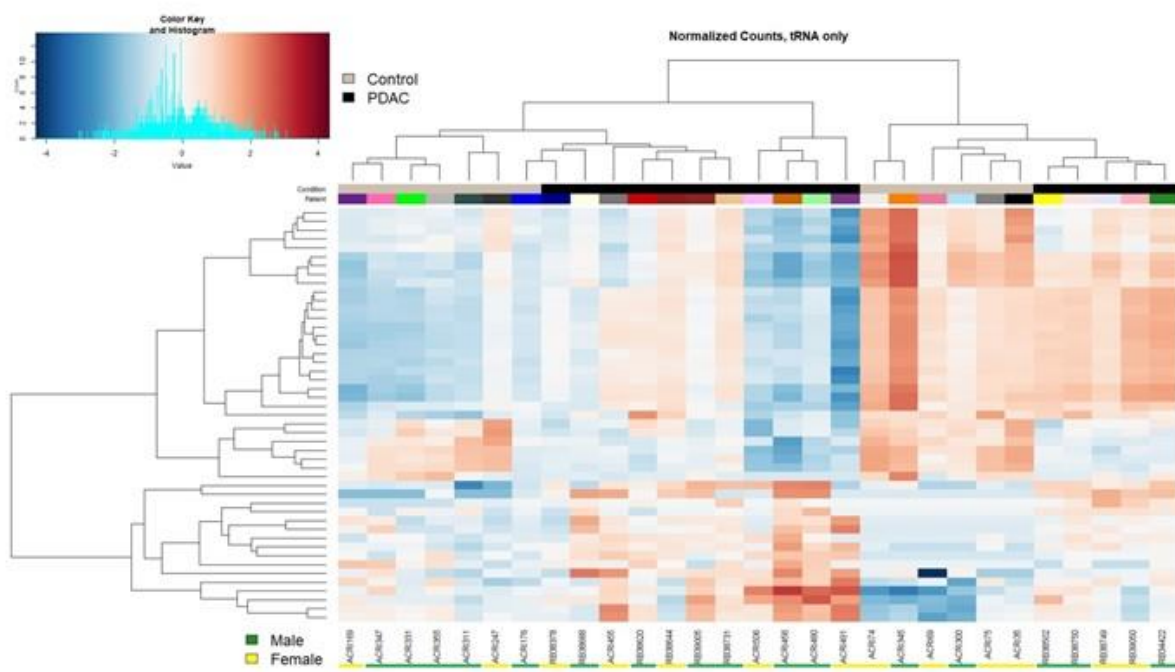
**Supplemental Figure 1. Histograms depicting sRNAseq quality control characteristics.** A) Total sRNA Reads, B) Reads passing filters, C) Reads mapped, D) % of mapped reads and E) average length (bp) of mapped reads in non-affected individuals and PDAC patient samples. (\*p<0.05).

Supplemental Figure 2



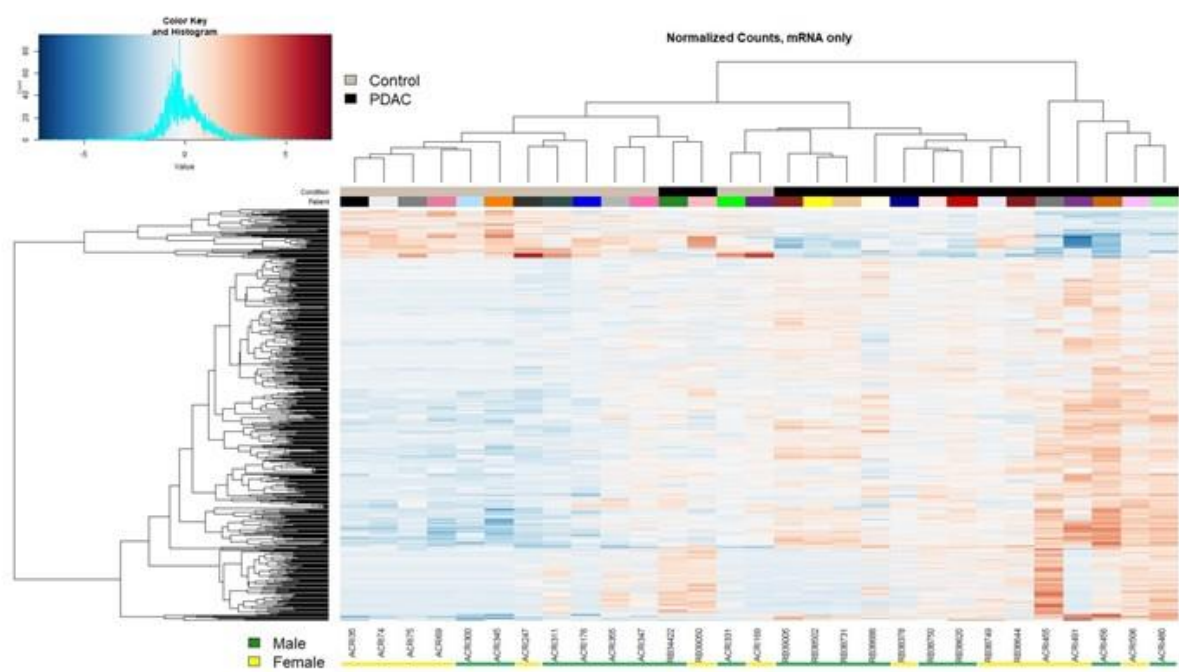
**Supplemental Figure 2. Heatmap of annotated piRNA for non-affected individuals (Control; grey) and PDAC patients (black).** The heatmap represents log transformed normalized (TMM) reads. Heatmap colors correspond to RNA expression as indicated in the color key: blue (down-regulated) and red (up-regulated).

Supplemental Figure 3



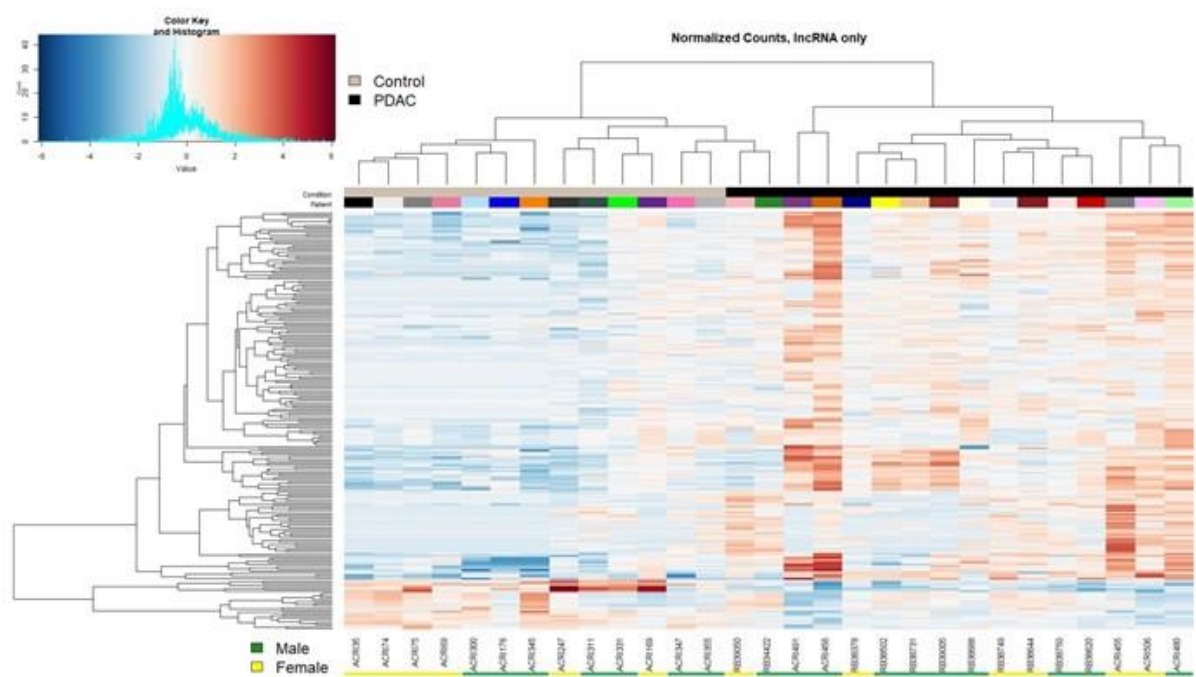
**Supplemental Figure 3. Heatmap of annotated tRNA for non-affected individuals (Control; grey) and PDAC patients (black).** The heatmap represents log transformed normalized (TMM) reads. Heatmap colors correspond to RNA expression as indicated in the color key: blue (down-regulated) and red (up-regulated).

Supplemental Figure 4



**Supplemental Figure 4. Heatmap of annotated mRNA fragments for non-affected individuals (Control; grey) and PDAC patients (black).** The heatmap represents log transformed normalized (TMM) reads. Heatmap colors correspond to RNA expression as indicated in the color key: blue (down-regulated) and red (up-regulated).

Supplemental Figure 5



**Supplemental Figure 5. Unsupervised hierarchical clustering analysis of annotated lncRNA fragments for non-affected individuals (Control; grey) and PDAC patients (black).** The heatmap represents log transformed normalized (TMM) reads. Heatmap colors correspond to RNA expression as indicated in the color key: blue (down-regulated) and red (up-regulated).