

## **Supplementary File Information**

All Supplementary files have been uploaded in Google Drive and can be accessed using the following link:

<https://drive.google.com/drive/folders/11kdpXbS1KAd9dfWS9ZfyT3D9Y2GN>

[UnAb?usp=sharing](https://drive.google.com/drive/folders/11kdpXbS1KAd9dfWS9ZfyT3D9Y2GN?usp=sharing)

**Supplementary Figure-1:** Schematic diagram showing details of proteome analysis

**Supplementary Table-1:** List of downregulated genes along with their fold changes, as resulted from meta-analysis.

**Supplementary Table-2:** List of upregulated genes along with their fold changes, as resulted from meta-analysis.

**Supplementary Table-3:** Information of deregulated miRNAs reported in literature.

**Supplementary Table-4:** Total list of target genes obtained from miRNet, corresponding to all the miRNAs reported to be altered in high risk IPMN.

**Supplementary Table-5:** List of upregulated genes interacting with downregulated miRNAs.

**Supplementary Table-6:** List of downregulated genes interacting with upregulated miRNAs.

**Supplementary Table-7:** List of long noncoding RNAs altered in high risk IPMN.

**Supplementary Table-8:** List of most significant deregulated KEGG biological pathways.

**Supplementary Table-9:** List of reported cyst fluid proteins altered in high risk IPMN.