**Supplementary file legends:**

**Supplementary Figure S1. Heatmap shows the cytobands amplified and deleted in OUH and TCGA cohort. 1a)** Amplification and deletion of cytobands in OUH cohort. 1b) Amplification and deletion of cytobands in TCGA cohort. The rows represent the cytobands while the columns represent the samples. The color bars on y-axis represent the chromosomes. The red color in the heatmap represents the amplification, green color represent the deletion while black represent the normal state.

**Supplementary Figure S2.****CNA profile of the two xenografts cell lines and their original tumors.** The minor allele frequency is in blue and purple is the total copy number.

**Supplementary Figure S3. The figure shows CNA profile of three IPMN samples.** The minor allele frequency is in blue and purple is the total copy number.

**Supplementary Figure S4. Correlation between genome instability index (GII) and ploidy.** 4A) Scatter plot shows the correlation between GII and ploidy of the tumors in OUH cohort. 4B) Scatter plot shows the correlation between GII and ploidy of the tumors in TCGA cohort. The x-axis represent the genome instability index while the y-axis represent the ploidy of the tumors.

**Supplementary** **Figure S5. Frequency plot of the CNAs of periampullary adenocarcinomas based on site of origin.** The x-axis represents the genomic position and is divided into 22 facets for 22 chromosomes. The y-axis represents the frequency of chromosomal gain and losses for five subtypes based on site of origin. The number of samples in each subtypes are PDAC: 28, bile duct: 4, ampulla P: 6, ampulla I: 7, duodenum: 9.