**Supplementary Figure legends**

**Supplementary Figure S1.**

The images of laser capture microdissection (LMD) for PanIN tissue of *AID* Tg mouse (left panel; before LMD, right panel: after LMD).

**Supplementary Figure S2.** Whole exome sequencing of *AID* Tg pancreatic tissue

1. Whole exome sequencing revealed 111 somatic mutations in 42 genes, according to the variant filtering process.
2. C:G>T:A transitions occupied 37% of all mutations found in whole exome sequencing.

**Supplementary Figure S3.**

RNAseq data sets derived from The Cancer Genome Atlas (TCGA) showed various levels of *AID* mRNA expression in human pancreatic adenocarcinomas (N: Number). In addition, *AID* mRNA expression level in human pancreatic adenocarcinoma was higher than the mean *AID* mRNA expression level in all cancer types.1