

Supplementary Information

Supplementary Figure 1. Screen shot of inquire about KRAS, TP53, CDKN2A and CDKN2B in TCGA pancreatic cancer samples on the website <http://www.cbioportal.org/>.

Supplementary Figure 2. Lentiviral vectors used in this study. **a**, Diagram of the lentiviral vectors. **b**, The knockdown efficiency of the shRNAs tested in MEFs by real-time PCR.

Supplementary Figure 3. Gross appearance of the mouse pancreatic cancers. **a**, All of the mouse pancreatic ductal adenocarcinomas were located in the head of the pancreas. **b**, The size of most tumors ranged from 0.5 to 1.5 cm. **c**, The cut surfaces were yellow to white and exhibited little hemorrhage and necrosis. **d**, Obstruction of the common bile duct and/or the main pancreatic duct cause by tumor mass. **e**, Additional abnormalities were observed in the digestive organs.

Supplementary Figure 4. The whole appearance of HE staining and CK-19 of pancreatic cancer. The frame region in “a” was shown as “b” and the frame region in “b” was shown as “c”. N: normal tissue; T: tumor.

Supplementary Figure 5. Cellular proliferation in pancreatic cancer. **a**, PCNA

expression. PCNA expression was not detected in normal pancreatic ducts and was significantly enhanced in pancreatic cancer. **b**, the quantification of ki67 positive cells in normal tissue, pancreatic cancer, adjacent tissues and distal tissues.

Supplementary Figure 6. Cell types infected by lentivirus. The lentivirus KRAS-shTp53-EGFP, KRAS-shTp53-EGFP-shCdkn2a, KRAS-shTp53-EGFP-shCdkn2b were injected and collect samples at day 7 for staining. The sections were staining with CK19 antibody and GFP antibody. Most EGFP positive cells are also CK-19 positive.

Supplementary Figure 7. Hematoxylin and eosin (H&E) staining of pancreatic cancer induced by cytokeatin-19 promoter-driven KRAS^{G12D} expression. Duct-like structure was observed in tumor. Two fields (10x and 20x) were shown.

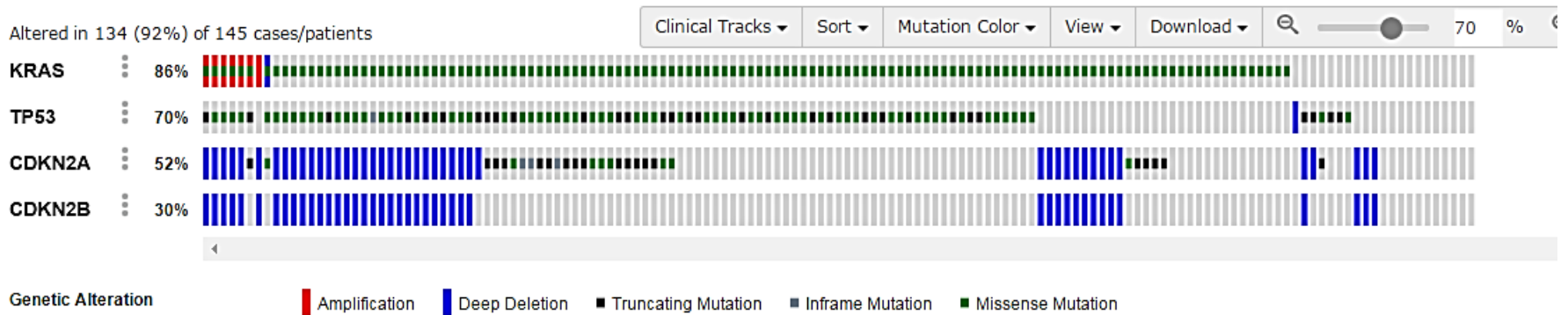
Supplementary Table 1. The quality of RNA-seq, reads mapping rate, and the correlation of 3 biological replicates.

Supplementary Table 2. The enrichment of human pancreatic cancers core regulatory process or pathway of human pancreatic cancers.

Supplementary Table 3. Sequence of all primers used in this study and target sequence of shRNA.

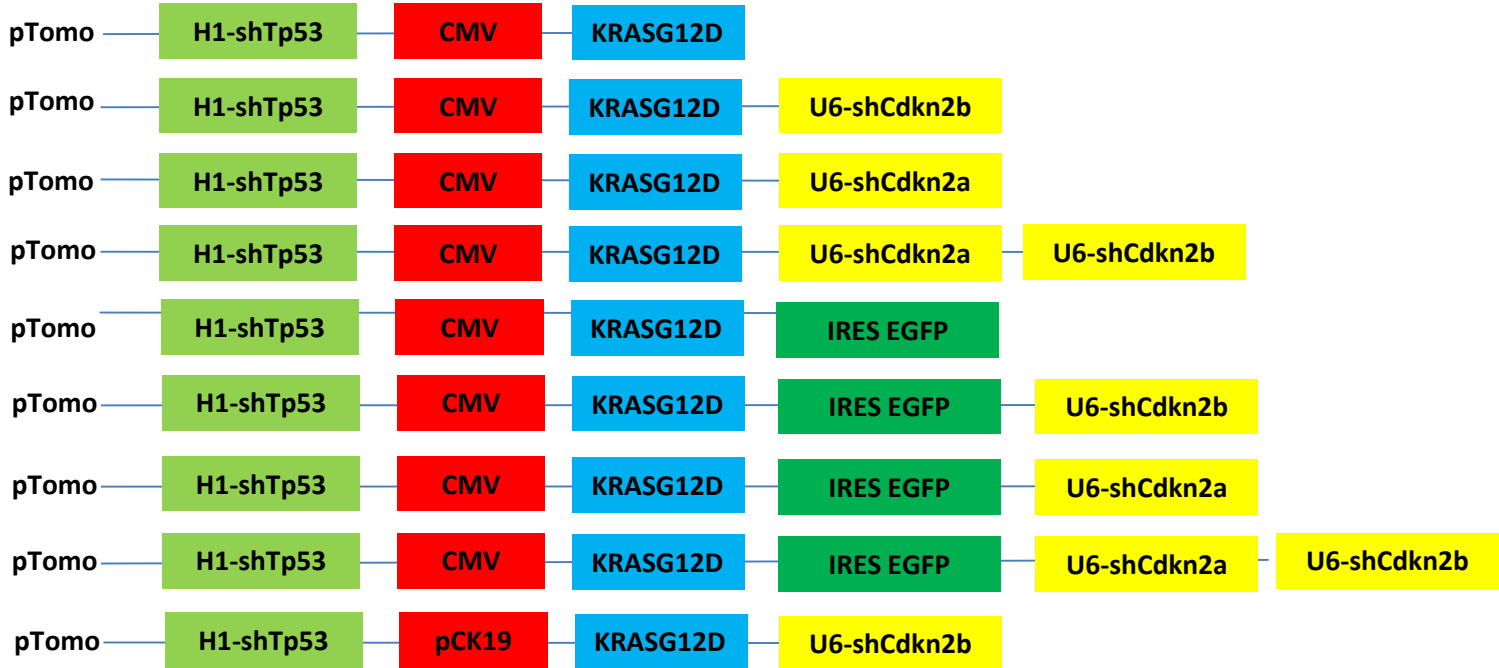
Supplementary Fig 1

Case Set: Tumor Samples with sequencing and CNA data All tumor samples that have CNA and sequencing data (145 samples)(145 patients / 145 samples)

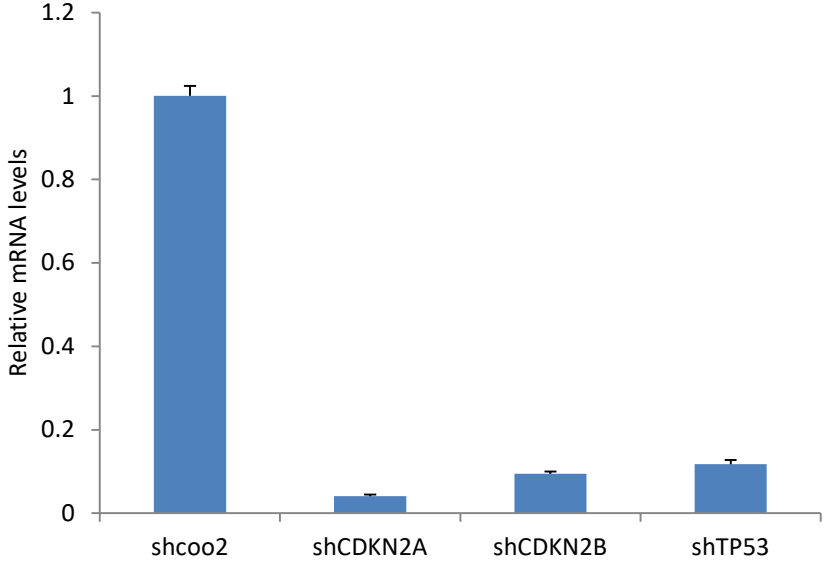


Supplementary Fig 2

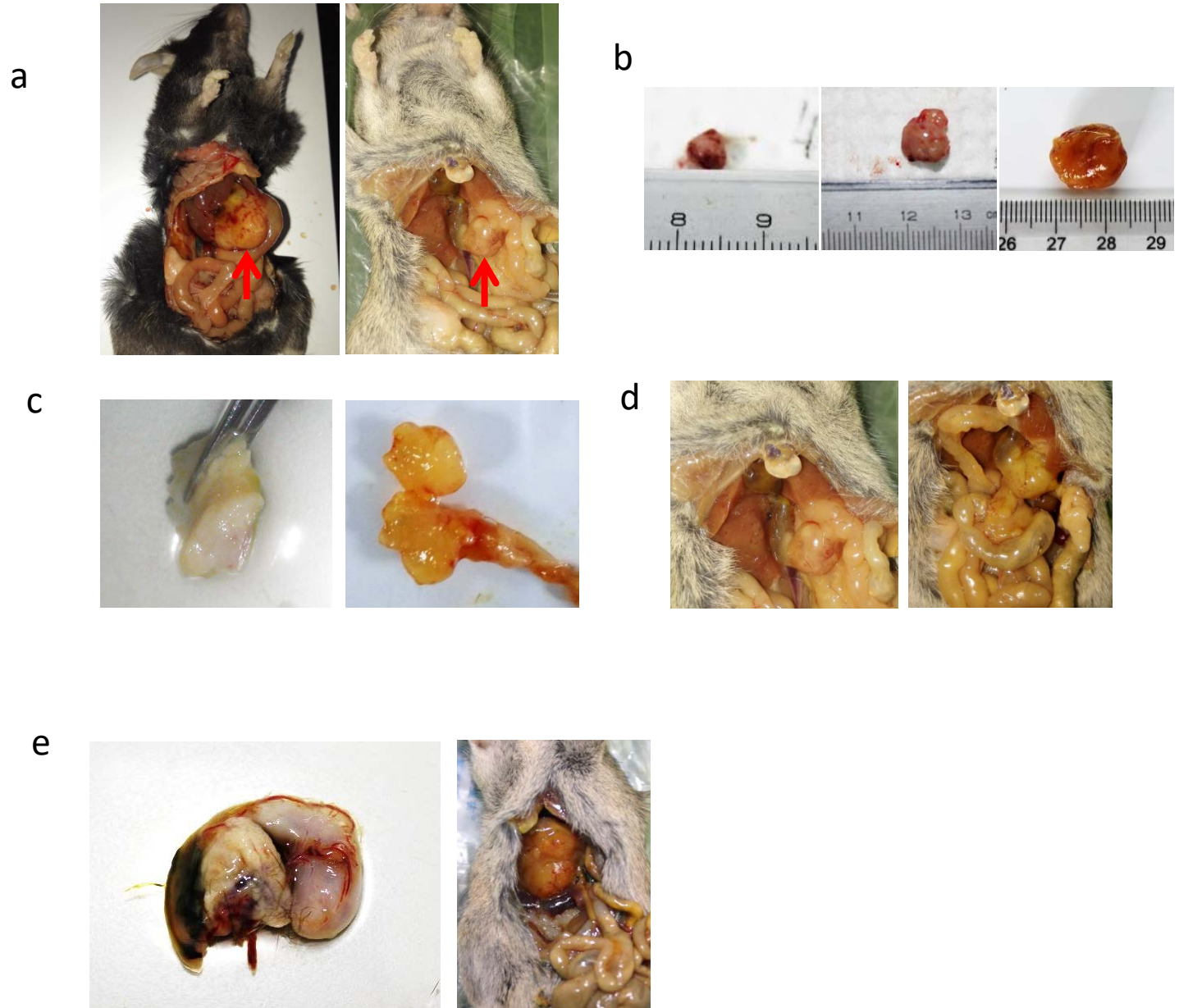
a



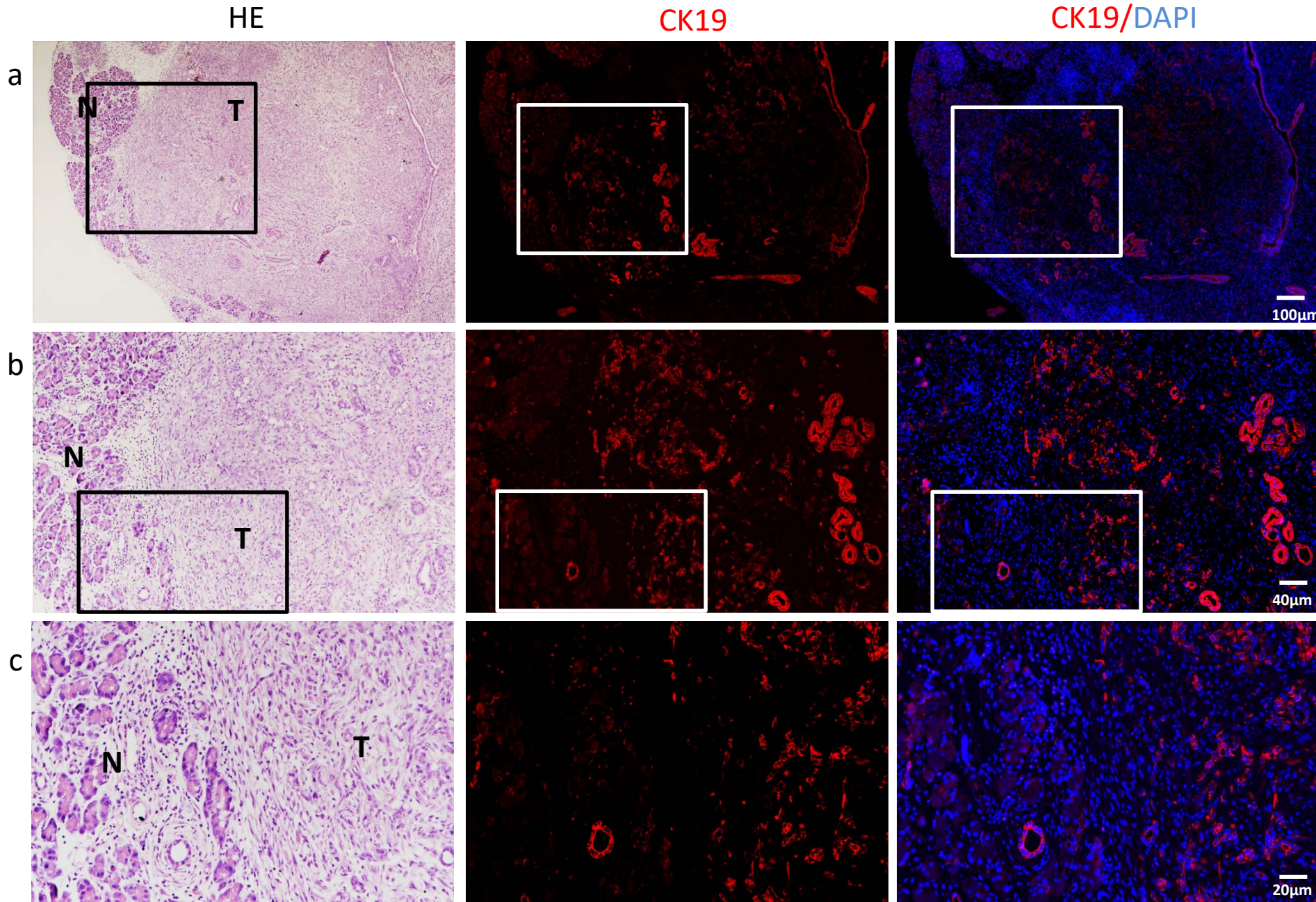
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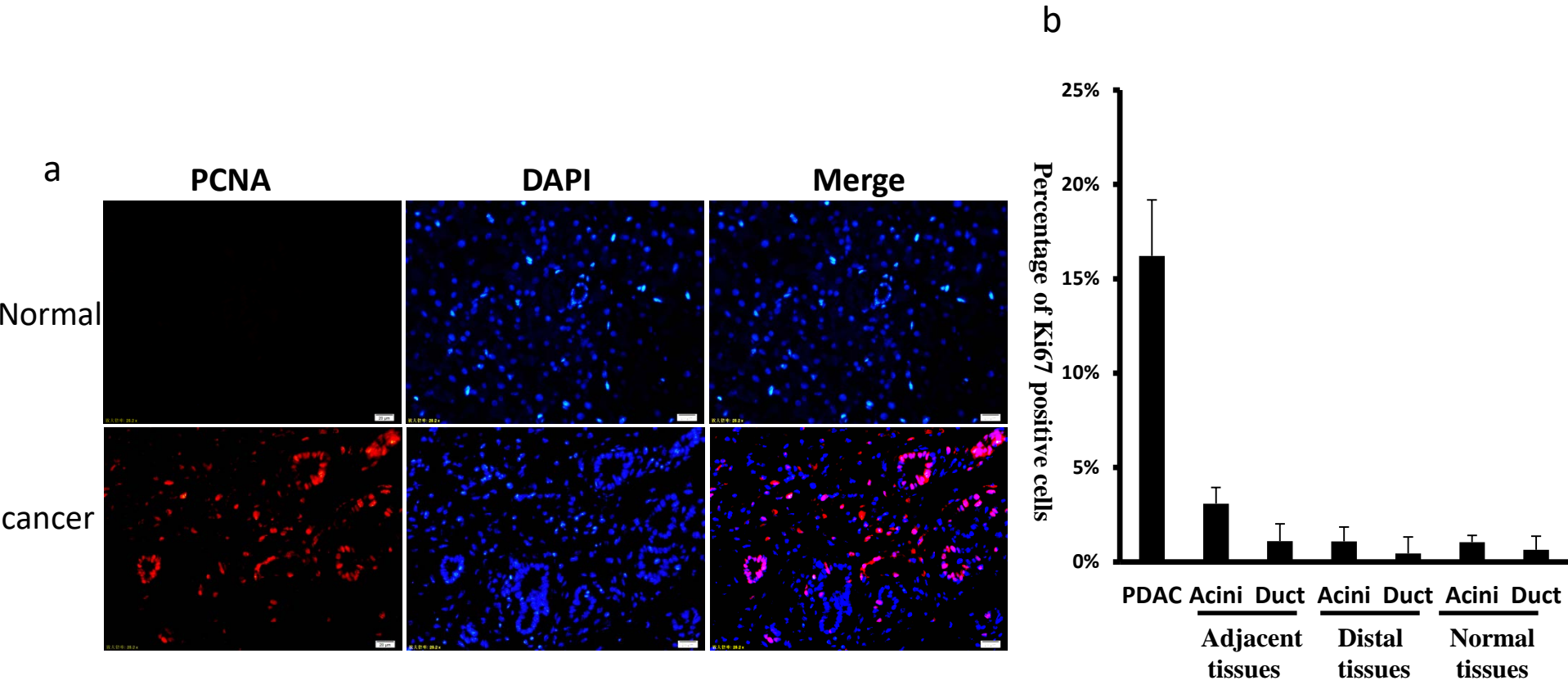
Supplementary Fig 3



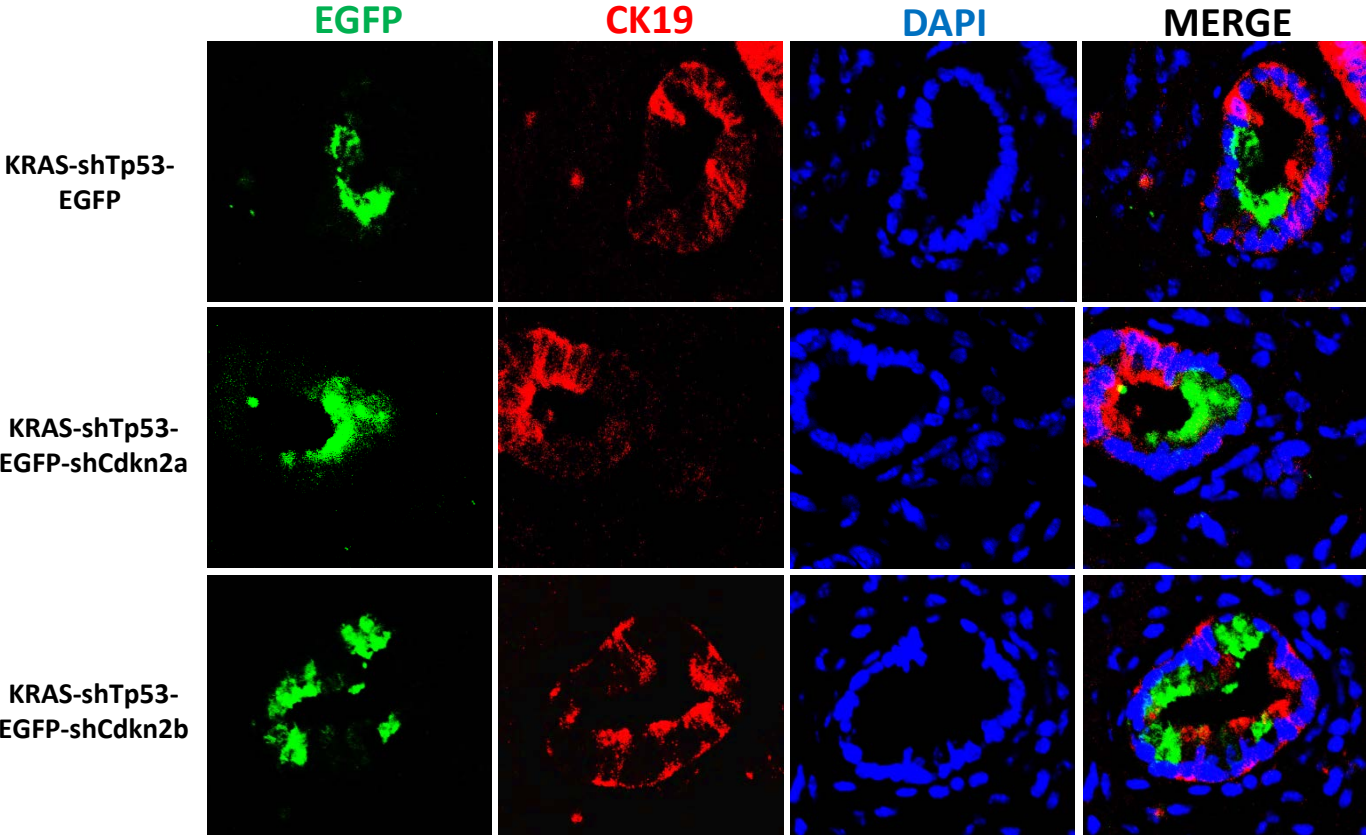
Supplementary Fig 4



Supplementary Fig 5

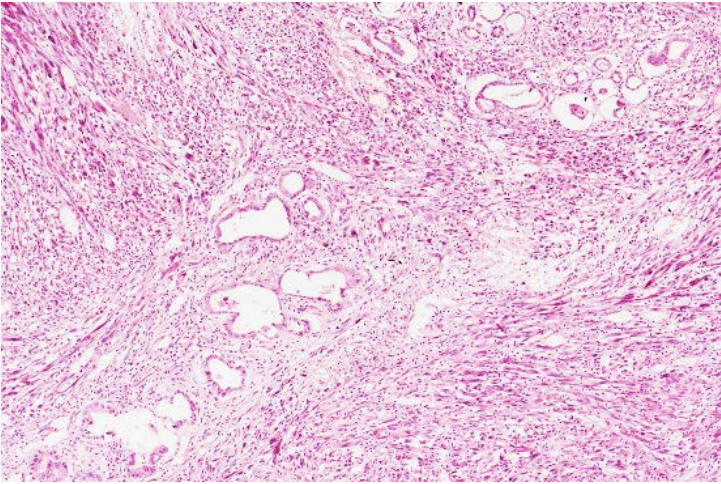


Supplementary Fig 6

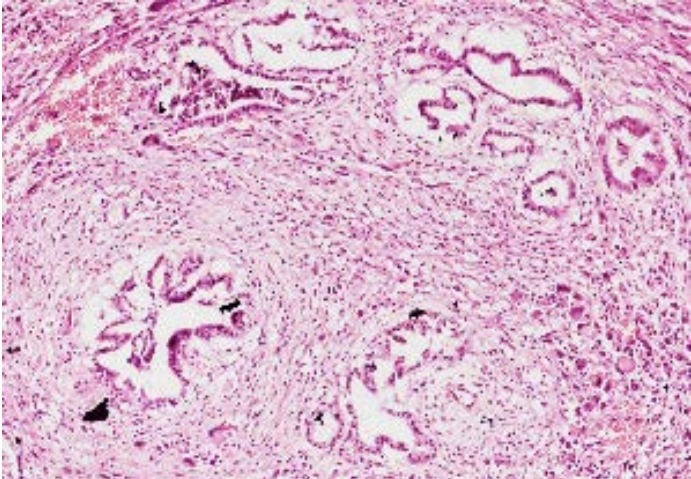
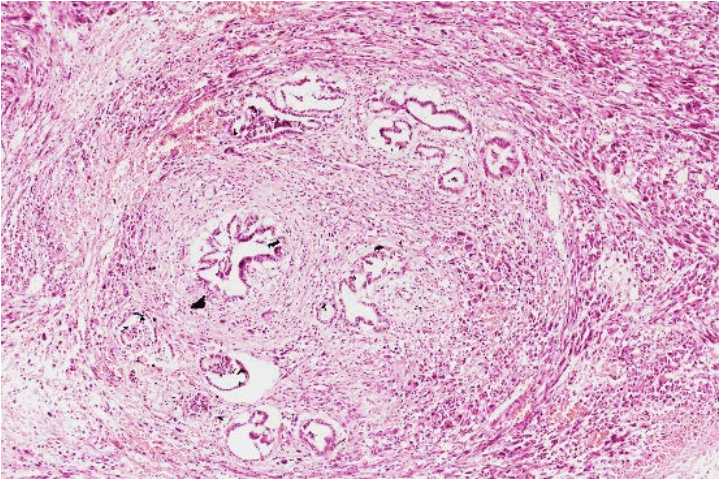
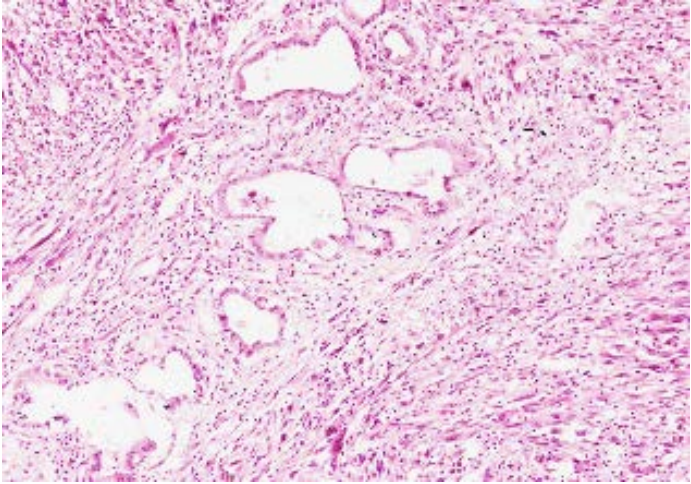


Supplementary Fig 7

10x



20x



Supplementary Table 1. The quality of RNA-seq, reads mapping rate, and the correlation of 3 biological replicates.

Sample	Raw bases(G)	Clean bases(G)	Clean bases(%)	Clean Q20(%)	Clean Q30(%)	Overall read mapping rate*(%)	Mean correlation #(R)
newborn-1	11.99	11.8	0.9842	97.92	95.06	91.60	0.9823
newborn-2	10.06	9.91	0.9851	97.66	94.51	91.70	
newborn-3	10.61	10.45	0.9849	97.92	95.05	92.80	
9-wk-1	12.08	11.83	0.9793	97.84	94.91	91.10	0.9690
9-wk-2	10.42	10.22	0.9808	97.81	94.85	91.00	
9-wk-3	9.98	9.79	0.9810	97.84	94.88	91.40	
PDAC-1	9.36	9.15	0.9776	97.16	93.79	86.30	0.9108
PDAC-2	9.83	9.62	0.9786	97.22	93.82	88.20	
PDAC-3	10.95	10.72	0.9790	97.23	93.84	87.60	

* The reads were mapped to the mouse genome (GRCm38.p4).

Mean Pearson correlation of 3 biological replicates, and p-value < 2.2E-16 with cor.test and Pearson's product-moment correlation in all pairwise.

Supplementary Table 3. Sequence of primers used in this study and target sequence of shRNA.

primer name	sequence(5'-3')
<i>TP53</i> RT-Forward	CTC TCC CCC GCA AAA GAA AAA
<i>TP53</i> RT-Reverse	CGG AAC ATC TCG AAG CGT TTA
<i>CDKN2A</i> RT-Forward	ACA TCA AGA CAT CGT GCG ATA TT
<i>CDKN2A</i> RT-Reverse	CCA GCG GTA CAC AAA GAC CA
<i>CDKN2B</i> RT-Forward	CCC TGC CAC CCT TAC CAG A
<i>CDKN2B</i> RT-Reverse	CAG ATA CCT CGC AAT GTC ACG
<i>Xba</i> I- <i>KRAS</i> ^{G12D} -Forward	TAG CTC TAG AGC CAC CAT GAC TGA ATA TAA ACT TGT GGT AGT TGG AGC TGA TGG CGT AGG C
<i>Sal</i> I- <i>Age</i> I- <i>KRAS</i> ^{G12D} -Reverse	CAG CAT TTA AGG TAA AAG CT
<i>Cla</i> I-sh <i>TP53</i> -Forward	CCA TCG ATG CGG AAT TCG AAC GCT GAC GTC
<i>Cla</i> I-sh <i>TP53</i> -Reverse	CCA TCG ATG CAA AAA GTA CAT GTG TAA T
<i>Kpn</i> 2I-sh <i>Cdkn2b</i> -Forward	ATC GTC CGG AGA GGG CCT ATT TCC CAT GAT
<i>Sal</i> I-sh <i>Cdkn2b</i> -Reverse	ACG TGT CGA CAT GAA TAC TGC CAT TTG TCT
<i>Sal</i> I-sh <i>Cdkn2a</i> -Forward	ATC GGT CGA CGA GGG CCT ATT TCC CAT GAT
<i>Sal</i> I-sh <i>Cdkn2a</i> -Reverse	ACG TGT CGA CAT GAA TAC TGC CAT TTG TCT
target sequences of sh <i>TP53</i>	GTA CAT GTG TAA TAG CTC CTT
target sequences of sh <i>Cden2a</i>	CGG GCA TAG CTT CAG CTC AAC
target sequences of sh <i>Cden2b</i>	CAC CTC CAG CTC GAC AAG GAA ATA GTG AT