



Supplementary Figure 1

Supplementary Figure 1. Characterization of the *KP^{wm/+}C* mouse model and derived cell lines. **A and B,** The overall survival and disease-specific survival between *KP^{wm/+}C* and *KP^{f1/+}C* PDAC models as determined by the log-rank (Mantel-Cox) test. **C and D,** The overall survival and disease-specific survival between *KP^{wm/+}C* and *KP^{LSL/+}C* PDAC models as determined by the log-rank (Mantel-Cox) test. **E,** The timeline of PDAC progression is histologically similar between *KP^{wm/+}C* and *KP^{f1/+}C* PDAC models. Scale bars, 200μM. **F,** All murine and human PDAC cell lines underwent Sanger sequencing to confirm *p53* missense mutations (listed) and to exclude the presence of wildtype *p53* alleles. **G,** Transwell migration/invasion assays of PDAC cell lines derived from pancreas tumors in *KP^{wm/+}C* mice and human PDAC cell lines (MDA-PATC) following mutant *p53* knockdown. **H,** The effects of ectopic mutant *p53^{R172H}* expression on PDAC cell migration and invasion in *p53*-null, *KP^{f1/C}* cell lines. **I,** GSEA analysis of hallmark pathways in *KP^{wm/+}C* tumors reveals dysregulated pathways similar to human PDAC. **(G, H)** Data are quantified by 20X fields as mean±s.d. and pooled from at least two independent experiments performed in triplicate. P values determined by unpaired two-tailed t-tests.