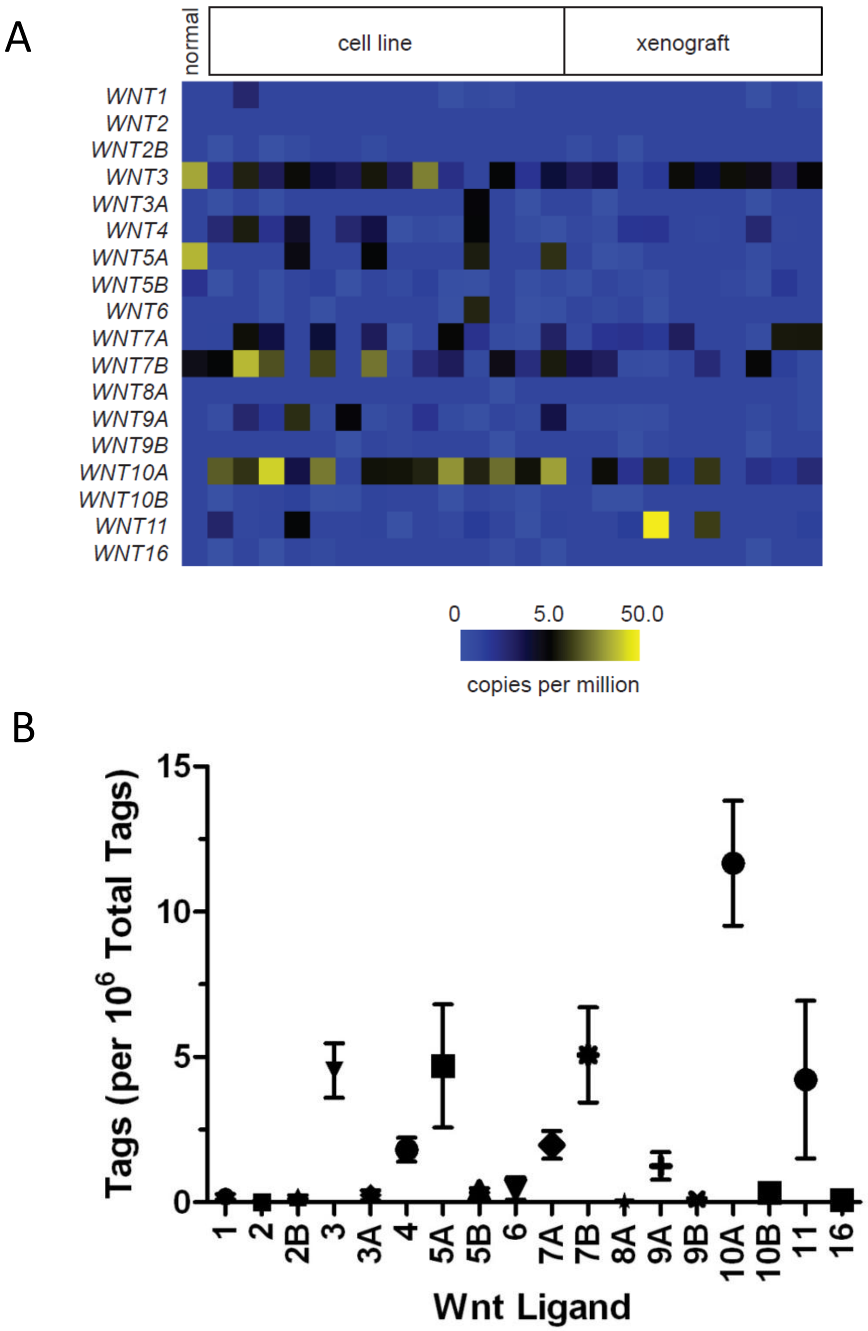
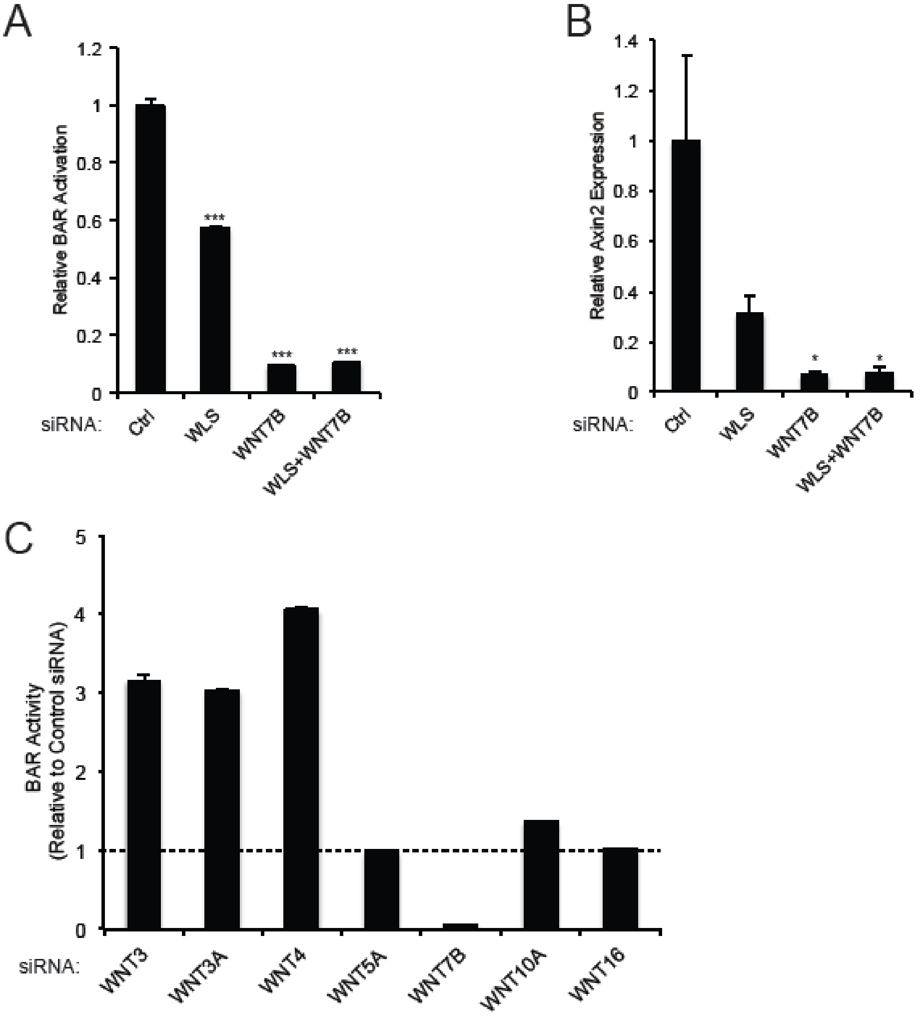


Supplemental Figure 1. *In silico* analysis of Wnt ligand expression of pancreatic cancer based on a published SAGE (serial analysis of gene expression) dataset of 24 PDAC tumors passaged either as *in vitro* cell lines or xenografts in nude mice to remove contaminating non-malignant cells (Jones, et al., 2008, Science **321**:1801-6). Shown here are the number of specific sequence tags for each Wnt gene per million sequence tags matching known transcripts. The data for each Wnt gene is represented as a (A) heatmap of individual tumor samples and (B) the overall combined average ± standard deviation across all tumor samples. Normal is from microdissected normal pancreatic ductal epithelial cells.



Supplemental Figure 2. AsPC-1 with stable BAR-luciferase reporter were transiently transfected with 10nM each of the indicated individual or combinations of siRNAs. At 48 hours post-transfection, cells were analyzed for (a, c) BAR-luciferase reporter activity or (b) AXIN2 expression by QPCR with ACTB as normalization control for QPCR. All data were normalized to measurements observed with corresponding control siRNAs. The dashed line in panel c indicates position of normalized control siRNA and shows that only WNT7B siRNA transfection led to appreciable inhibition of BAR-luciferase reporter. At least 75% knockdown of each gene by its corresponding siRNA was confirmed by qPCR (data not shown). *P<0.05, *** P<0.001.