Description of Additional Supplementary Files

Supplementary Data 1: Raw read counts for RNA-seq analysis of fluorescence-activated cell sorted E13.5 intestine, stomach, pancreas, and $Bapx1^{Cre/+}$;$ROSA26^{mT/mG}$;$Sufu^{f/f}$;$Spop^{f/f}$ mutant pancreas mesenchyme.

Supplementary Data 2: FPKM values derived from RNA-seq raw read counts of fluorescence-activated cell sorted E13.5 intestine, stomach, pancreas, and $Bapx1^{Cre/+}$;$ROSA26^{mT/mG}$;$Sufu^{f/f}$;$Spop^{f/f}$ mutant pancreas mesenchyme.

Supplementary Data 3: DESeq2 results table for differential gene analyses between intestine, stomach, and pancreas tissue pairs as well as control versus E13.5 $Bapx1^{Cre/+}$;$ROSA26^{mT/mG}$;$Sufu^{f/f}$;$Spop^{f/f}$ pancreatic mesenchyme. Sheets described as follows: panc_vs_int_deTab: Differential comparison between control pancreatic and intestinal mesenchyme. Positive fold change values indicate relative enrichment in pancreas. Negative values indicate relative enrichment in intestine. panc_vs_st_deTab: Differential comparison between control pancreatic and stomach mesenchyme. Positive fold change values indicate relative enrichment in pancreas. Negative values indicate relative enrichment in stomach. st_vs_int_deTab: Differential comparison between control stomach and intestinal mesenchyme. Positive fold change values indicate relative enrichment in stomach. Negative values indicate relative enrichment in intestine. panc_vs_pancMut_deTab: Differential comparison between E13.5 control versus $Bapx1^{Cre/+}$;$ROSA26^{mT/mG}$;$Sufu^{f/f}$;$Spop^{f/f}$ pancreatic mesenchyme. Positive fold change values indicate relative enrichment in control pancreatic mesenchyme. Negative values indicate relative enrichment in mutant pancreatic mesenchyme.

Supplementary Data 4: gProfilerR output of GO enrichment analysis in Generic Enrichment Map (GEM) format, used as input for generating enrichment maps in Fig. 1D.