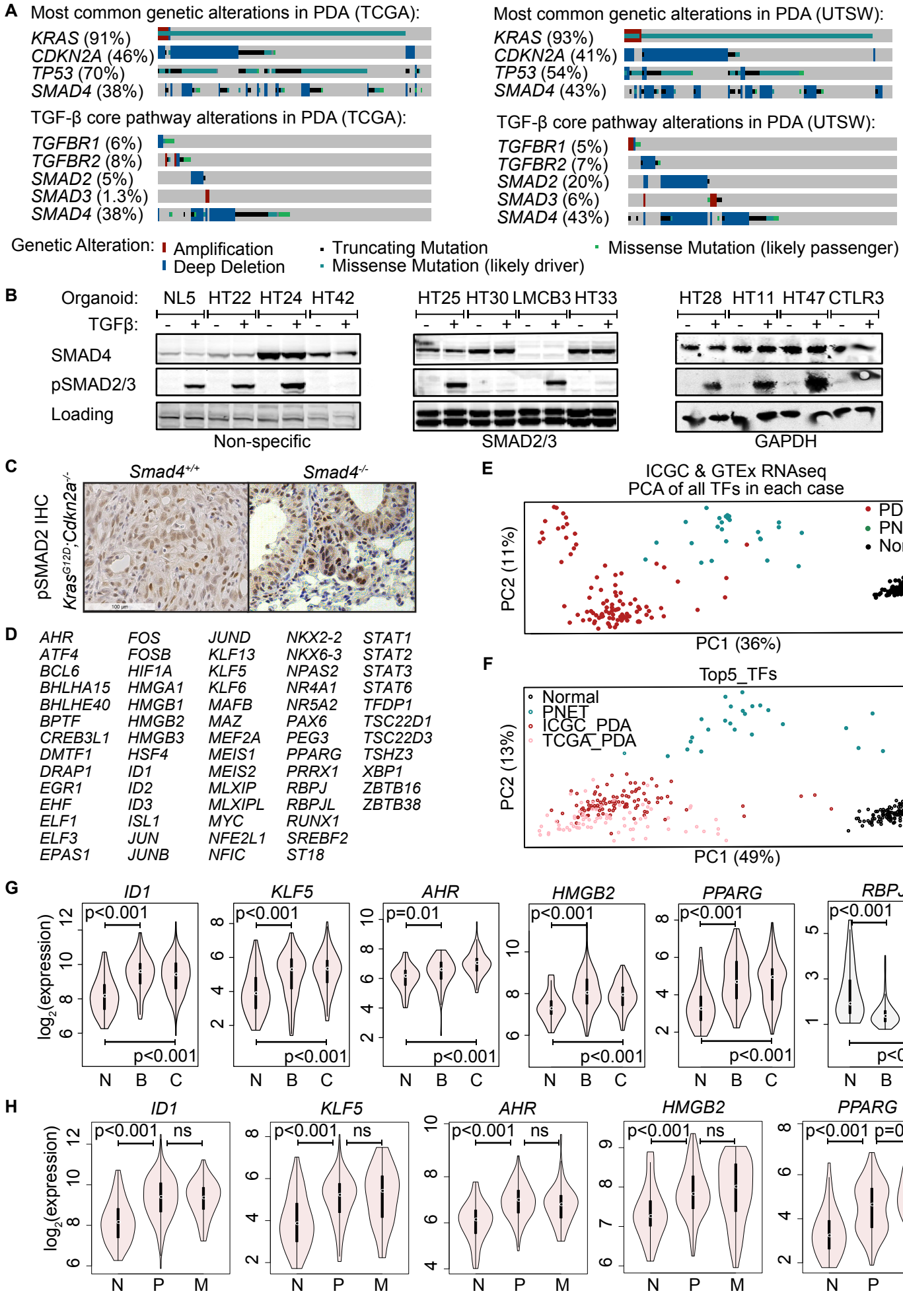
Supplementary Fig. S1



Supplementary Fig. S1: TGF-β signaling and transcriptional networks in PDA

A) cBioportal oncoprints of common genetic alterations and TGF-β pathway alterations in PDA. Each column represents one case.

B) Western immunoblot analysis of pSMAD2 and SMAD4 in human PDA organoids treated with or without 100 pM TGF-β for 2h.

C) pSMAD2 immunohistochemistry (IHC) of mouse *Kras^{G12D};Cdkn2a$^{-/-}$* PDA in the pancreas (*right*) and *Kras^{G12D}; Cdkn2a$^{-/-}$;Smad4$^{-/-}$* PDA metastasis in the lung (*left*).

D) Genes represented within the top 5 expressed transcription factors of at least one sample in 225 samples of normal pancreas, PNET, and PDA.

E) PCA of GTEx and ICGC RNA-seq datasets from using the complete list of transcription factors expressed in these samples.

F) PCA of GTEx, ICGC, and TCGA RNA-seq datasets using the gene set in Supplementary Fig. S1D.

G) GEO2R analysis of the expression of the top PDA-enriched PC1 genes (refer to Figure 1E) in the pancreatic microarray dataset GSE71729. N=Normal pancreas, B=Basal PDA, C=Classical PDA. p-values are from two-sided, unpaired t-tests of B versus N, and C versus N.

H) GEO2R analysis of the expression of PDA-enriched PC1 genes in pancreatic microarray dataset GSE71729. N=Normal pancreas, P=Primary PDA tumor, M=Metastasis of PDA. P-values from two-sided, unpaired t-tests of P versus N, and M versus P.