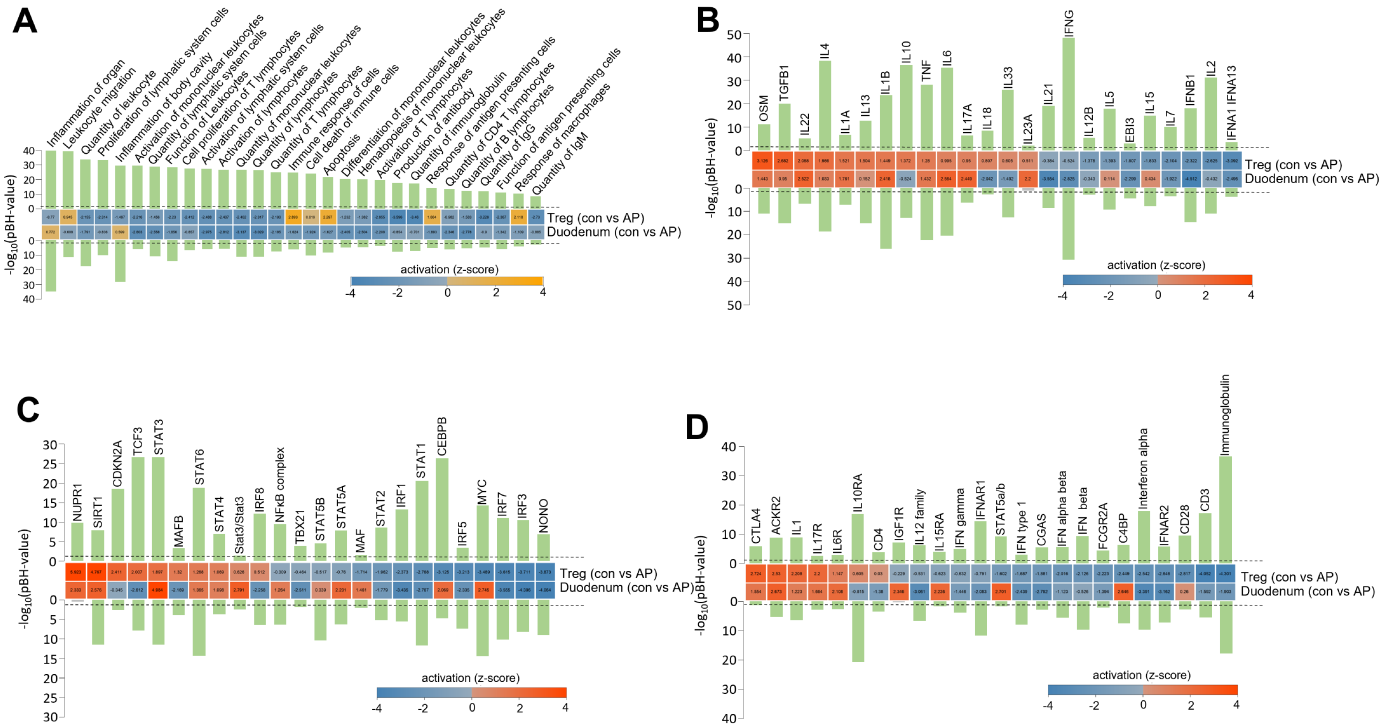

Figure S9: *Analysis of AP induced transcriptional changes in splenic T_{regs} and duodenal tissue samples.* (**A**) Comparative pathway analysis of the transcriptome data showed similar immune pathway and disease pattern alterations in isolated T_{reg} (top) and duodenal tissue (bottom). (**B-D**) Comparative analysis of AP-associated predicted upstream regulators in T_{regs} (top) and duodenal tissue (bottom) of selected individual genes in the group of cytokines (**B**), transcriptional regulators (**C**) and downstream target genes (**D**). Important upstream regulators showed a similar activation pattern at the mRNA level in both sample sets. Whereas transcripts of the anti-inflammatory cytokines TGFB1, IL-4, and IL-13 were more abundant, type I cytokines IL-12B, IL-2 and IFNγ mRNAs were decreased. Interestingly, gene expression of the IL-6 cytokine family like IL-6 or oncostatin M (OSM) was activated in both sample sets (**B**). The expression pattern of transcriptional regulator genes such as *Stat3* and *Stat6,* which were significantly induced, indicated a type 2 immune response. *Tbx21*, *Stat1* or *Irf1*, *Irf7* and *Irf3, which* were significantly repressed suggested a general pancreatitis-associated anti-inflammatory reaction (**C**). Gene expression alterations of other downstream regulators, such as CTLA4, IL10RA, IL6R, the IL-12 family pathway and the IFNγ pathway support the notion of a general SAP-induced immune suppression, which is mediated by CD25⁺/FOXP3⁺ Tregs (**D**). Heatmaps illustrate activation z-scores, whereas bar graphs depict Benjamini-Hochberg corrected *p*-values ($-\log_{10}$(*p*BH-value).