



**Figure S8:** Pathway analysis of  $T_{regs}$  during AP based on microarray-based transcriptome analysis. (A-D) GFP expression of  $T_{regs}$  in DERE mice (AP and controls) was used to isolate  $T_{regs}$  by FACS. RNA prepared from 4 SAP and 4 control animals was used for microarray-based transcriptome analysis. (A) Bar graphs show AP-induced overrepresented pathways ( $-\log_{10}(pBH\text{-value})$ ) based on differentially expressed genes which were identified by QIAGEN's Ingenuity Pathway Analysis (IPA) software. Heatmap illustrates the z-score which indicates activation (positive z-score, red) or inhibition (negative z-score, blue) of this pathway. (B-D) Selected pathways were shown for the group of cytokines (B), transmembrane receptors (C) and transcriptional regulators (D). Heatmap illustrates the z-score which indicates activation (positive z-score, red) or inhibition (negative z-score, blue) of the respective regulator.