Supplemental material

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Gut

Figure S8: *Pathway analysis of T$_{regs}$ during AP based on microarray-based transcriptome analysis.* (**A-D**) GFP expression of T$_{regs}$ in DEREG 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-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-scroe, 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-scroe, red) or inhibition (negative z-score, blue) of the respective regulator.