



**Figure S10:** Effects of Treg depletion on immune response and duodenal microbiome composition. (A) Flow cytometry analysis of splenocytes showed an increased T<sub>eff</sub> response marked by TBET<sup>+</sup> and GATA3<sup>+</sup> CD4<sup>+</sup> T-cells. (B) The percentage of LY6G<sup>+</sup>/LY6C<sup>low</sup> of CD11b<sup>+</sup> cells in spleen was significantly higher in DT treated mice compared to PBS treated animals. In contrast the MPO activity in lung was not different. (C) Analysis of duodenal faecal samples of DEREK mice showed a significant reduction in the AP associated overgrowth of facultative bacterial pathogens *Escherichia/Shigella* in the T<sub>reg</sub> depleted group. (D) Specific RT-qPCR analysis of *Escherichia coli*, *Enterococcus faecium*, *Lachnospiraceae* and *Lactobacillus* showed increased Ct values of facultative pathogenic bacteria in DT treated mice and confirmed the results of the 16S RNA gene sequencing approach. (E) By RT-qPCR analysis of DNA prepared from duodenal tissue we detected slightly increased mRNA levels for genes encoding cell-cell contact proteins. (F) Read numbers of the 16S rRNA gene in sequencing analysis of bacterial DNA from mouse pancreatic necrosis tissue (significance was tested using the Mann-Whitney test). Statistically significant differences were tested by unpaired student's t-test for independent samples and significance levels of  $p < 0.05$  are marked by an asterisk.