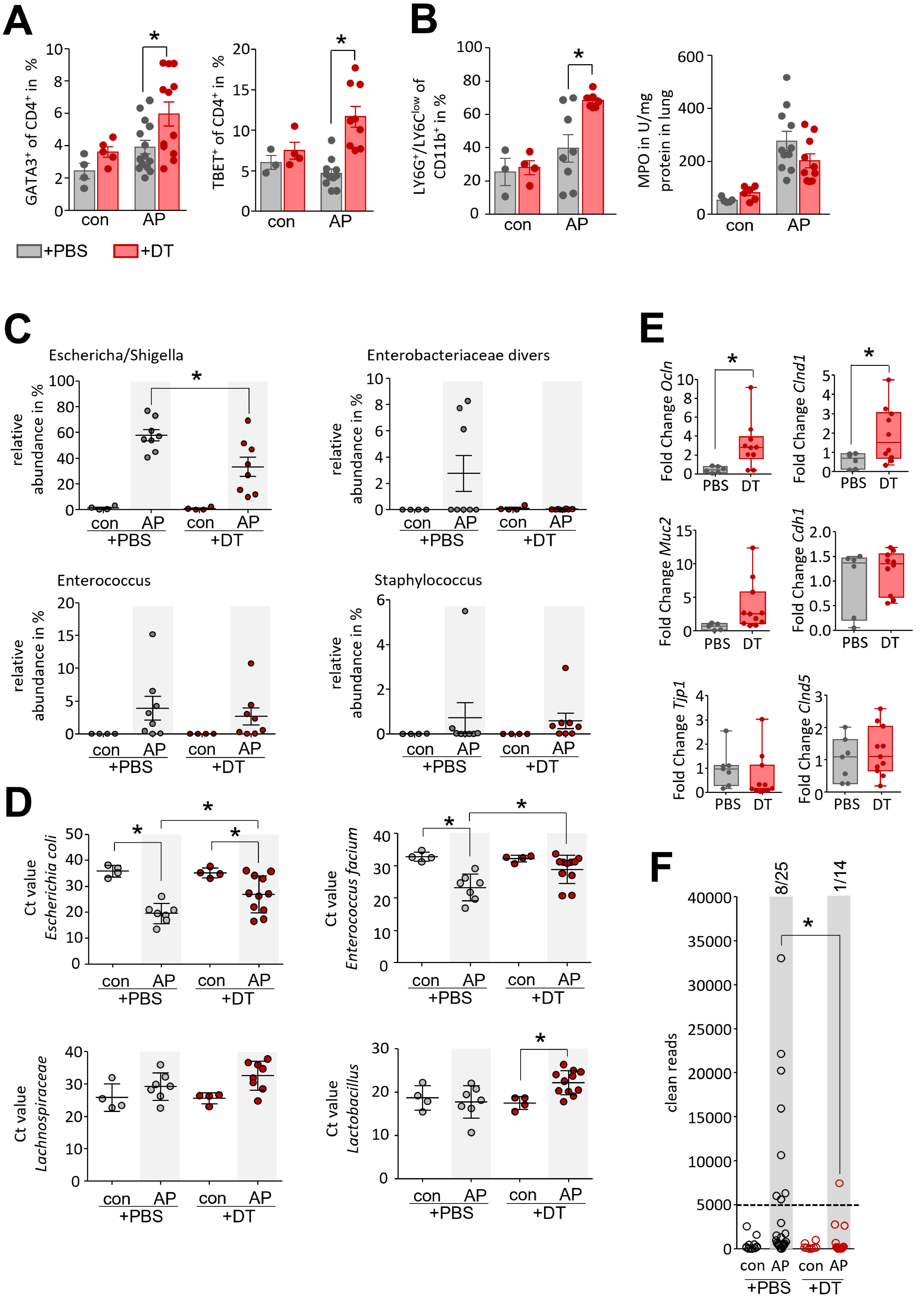

Figure S10: *Effects of Treg depletion on immune response and duodenal microbiome composition.* (**A**) Flow cytometry analysis of splenocytes showed an increased T_{eff} response marked by $TBET^+$ and $GATA3^+$ $CD4^+$ T-cells. (**B**) The percentage of $LY6G^+/LY6C^{low}$ of $CD11b^+$ cells in spleen 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 DEREG mice showed a significant reduction in the AP associated overgrowth of facultative bacterial pathogens *Eschericha/Shigella* in the T_{reg} 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.