



**Figure S2: Microbiota composition changes in a second mouse model of acute pancreatitis.** AP was induced by 8 hourly repetitive injections of caerulein (50 µg/kg/bodyweight) for three consecutive days in C57Bl/6 mice (Cae, n=15), controls (PBS, n=5) received PBS instead of caerulein. Mice were sacrificed one day after the last injection. (A) The stacked bar graph illustrates prominent taxa identified by 16S RNA gene sequencing of duodenal and colon samples of caerulein treated AP mice and PBS treated controls. Facultative pathogenic were marked in red, beneficial commensal bacteria were marked in green. (B) Principal coordinate analysis showed significant AP-associated changes of the microbiome pattern in colon ( $p < 0.001$ ,  $R^2 = 22.1\%$ ) and duodenum ( $p < 0.001$ ,  $R^2 = 30.5\%$ ), significance was tested by permutational Multivariate Analysis of Variance. (C) Taxa from the phylum Proteobacteria were significantly increased in duodenal samples whereas beneficial bacteria such as *Lactobacillaceae* were decreased. (D) H&E staining illustrates pancreatic damage. (E) At day 4 serum amylase and lipase activity as well as MPO activity in lung tissue had returned to basal levels. (F-G) Immunofluorescent labelling of CD3<sup>+</sup> T-cells and CD8α<sup>+</sup> IELs showed no differences between AP mice and controls. (H) Flow cytometry analysis of splenocytes also showed no increase of FOXP3<sup>+</sup>/CD25<sup>+</sup> regulatory T-cells. Statistically significant differences of taxa of interest were tested by unpaired Mann-Whitney test for independent samples, significance levels of  $p < 0.05$  are marked by an asterisk.