



Figure S1: Analysis of the murine intestinal microbiome during AP. (A) 16S rRNA gene sequencing was performed using faecal samples of colon, caecum and duodenum of C57Bl/6 mice (control n=10 vs. AP n=24). Principal coordinate analysis showed AP-associated changes of the microbiome pattern (AP in red, controls in blue) in all three parts of the gut. Permutational multivariate analysis of variance confirmed significant differences (colon: $p < 0.001$, $R^2 = 32.7\%$, caecum: $p < 0.001$, $R^2 = 26.0\%$ and duodenum: $p < 0.001$, $R^2 = 35.3\%$) (B) Jaccard coefficient index suggested high similarity between colon and caecum samples, but differences for duodenum samples. (C) The abundance and specific localization of the facultative pathogenic bacteria *Escherichia/Shigella*, *Enterococcus*, *Staphylococcus*, and *Enterobacteriaceae* divers within the gut is shown.