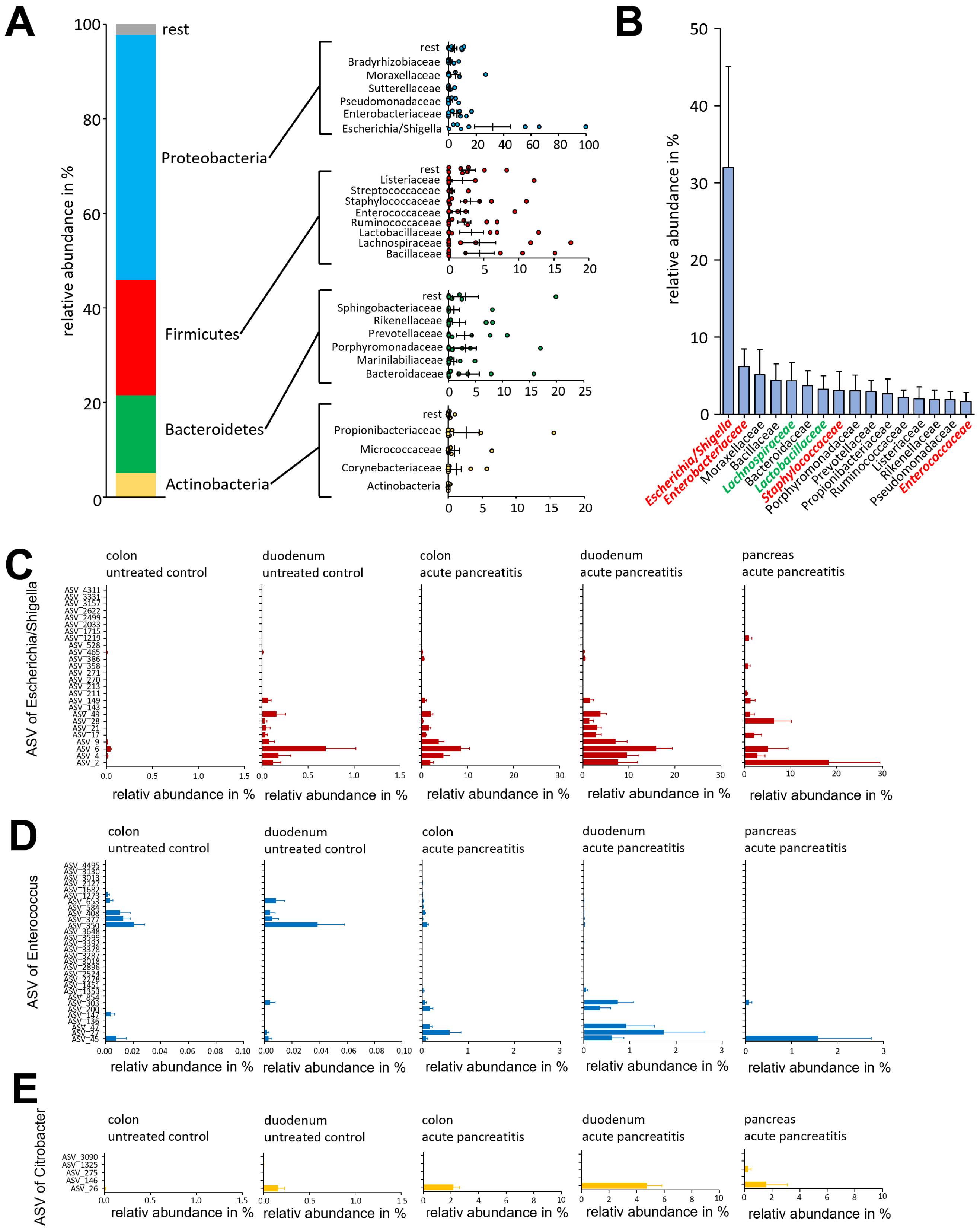

Figure S11: *A detailed analysis of the 16S rRNA gene sequencing of mouse pancreatic necrosis tissue.* (**A**) The stacked bar graph shows the mean relative abundance of the phyla Actinobacteria, Bacteroidetes, Firmicutes and Proteobacteria of murine necrosis samples (n=8). The dot plots illustrate the relative abundance of major taxa within these four phyla. (**B**) Bar graph showed the 15 most abundant families + Escherichia/Shigella identified in murine necrosis samples. (**C-E**) Bar graphs represent the different amplicon sequence variants (ASVs) of the taxa *Escherichia/Shigella* (**C**), *Enterococcus* (**D**) and *Citrobacter* (**E**) in colon and duodenal samples of mice with and without AP as well as of murine necrosis samples. This analysis shows that the same taxa we detected in duodenal samples could also be found in the necrosis.