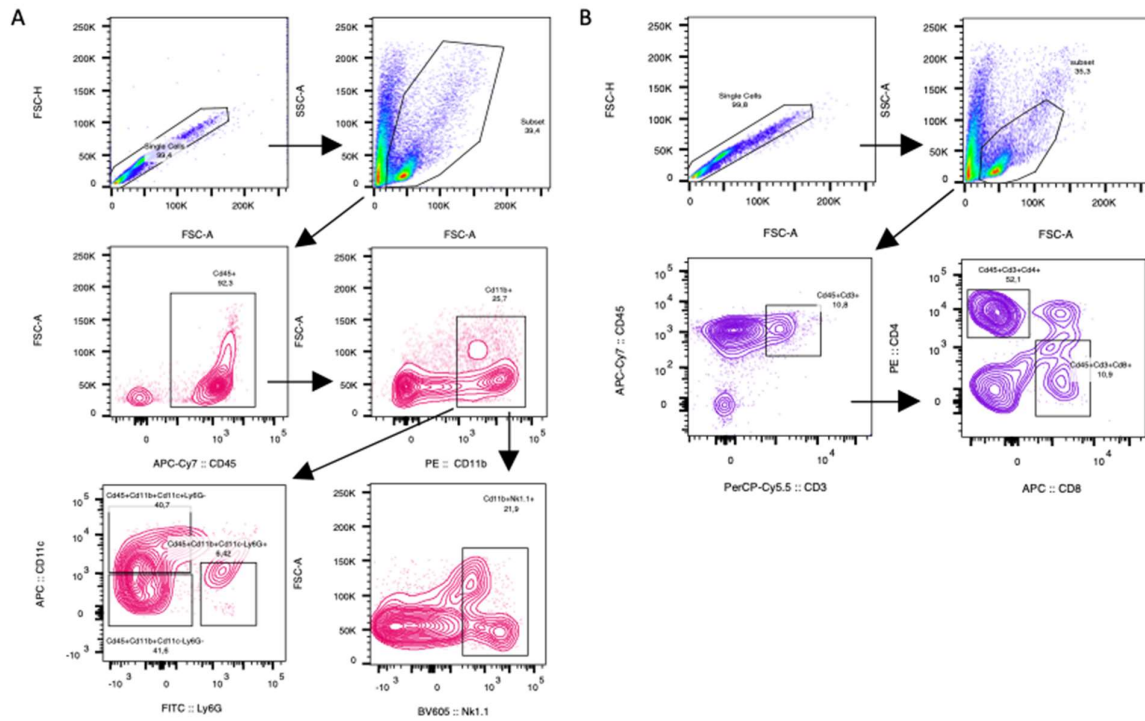
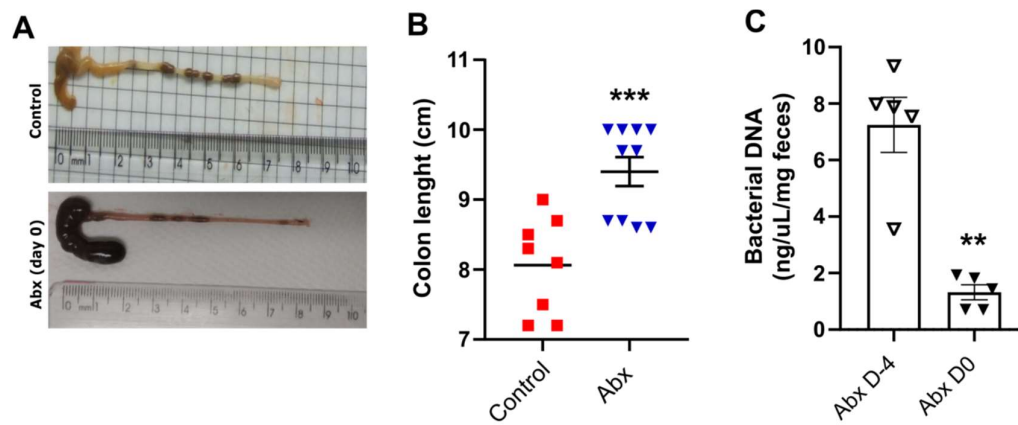


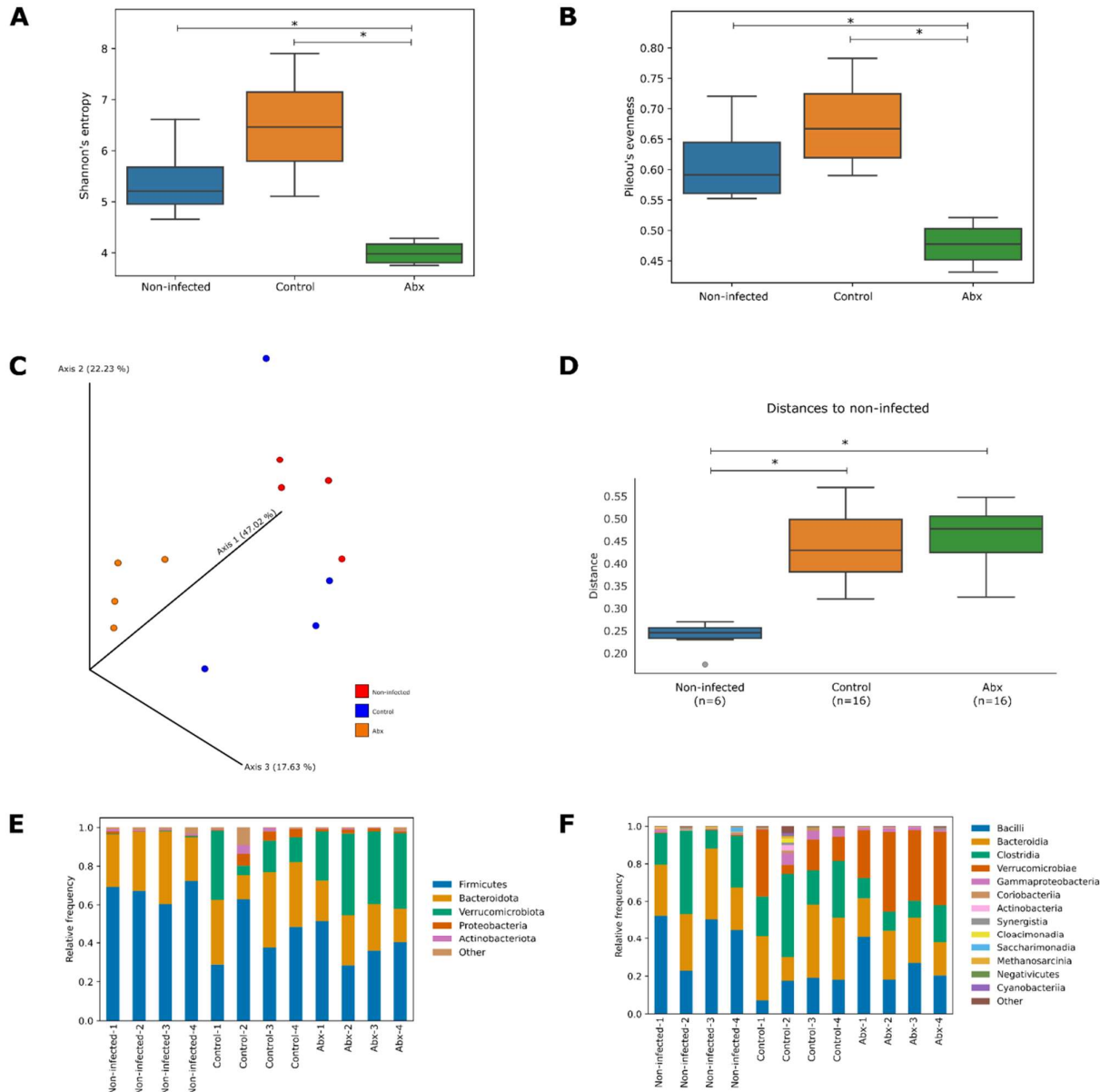
## Supplementary Materials



**Supplementary Figure S1. Gating strategies used to define the leukocyte populations of the BAL. (A)** Gating strategy used for analysis of myeloid and NK cells. **(B)** Gating strategy used for the analysis of lymphocytes.



**Supplementary Figure S2. Effect of oral antibiotics on the length of large intestine and fecal bacterial load.** (A) Representative images of cecum and colon. Female K18-hACE2 mice were treated for 3 days with antibiotic cocktail before infection (Abx day 0). (B) Colon length of mice treated or not with antibiotics. \*\*\* $p < 0.001$  by Student's  $t$ -test ( $n = 8-11$ ). (C) Bacterial DNA from feces samples of mice before (Abx D-4) and after 3 days of antibiotic treatment (Abx D0). \*\* $p < 0.005$  by Student's  $t$ -test ( $n = 5$ ).



**Supplementary Figure S3. Microbiota changes after infection of K18-hACE2 mice.** Female K18-hACE2 mice were either treated (Abx) or not treated (Control) for 3 days before SARS-CoV-2 infection. Mice were euthanized at 5 dpi and the luminal contents were collected for microbiota analysis. A non-infected group was also included in this analysis. Comparisons of alpha diversity between experimental groups. (A) Shannon's entropy index, (B) Pielou's evenness index.  $*p < 0.05$  by Kruskal-Wallis test ( $n = 4$  samples/group). (C) PCoA plot using weighted UniFrac dissimilarity based on ASVs of the different experimental groups. Comparisons of beta diversity between experimental groups. (D) Distance from the non-infected group using pairwise PERMANOVA test and weighted UniFrac distance matrix.  $*p < 0.05$  ( $n = 4$  samples/group). (E-F) Comparison of gut bacterial composition among experimental groups. (E) Bacterial abundance at the phylum level and (F) class distribution.