Fig. S1. Impact of CP treatment on viral burden. (A, B) Median vRNA and full-length (gRNA) levels in nasal lavages (A) and tracheal aspirates (B). The dashed line indicates limit of detection. (C) Results of Area under the curve analysis of total vRNA, full-length (gRNA) and sgRNA levels in nasal lavages and tracheal aspirates. Bars show mean with SEM. $n=2$ (CP treatment), $n=2$ (NP treatment), and $n=4$ (not treated).
Fig. S2. Clinical markers of infection and COVID-19. Graphs show measurements in individual animals over time.
Fig. S3. Analysis of intra-host polymorphisms. (A) Read depths between the amplicon sequence approach (ARTIC) and metagenomic sequencing (mNGS). (B) Relationship between nucleotide diversity and viral loads. (C) Allele frequencies in recovered viral genomes.