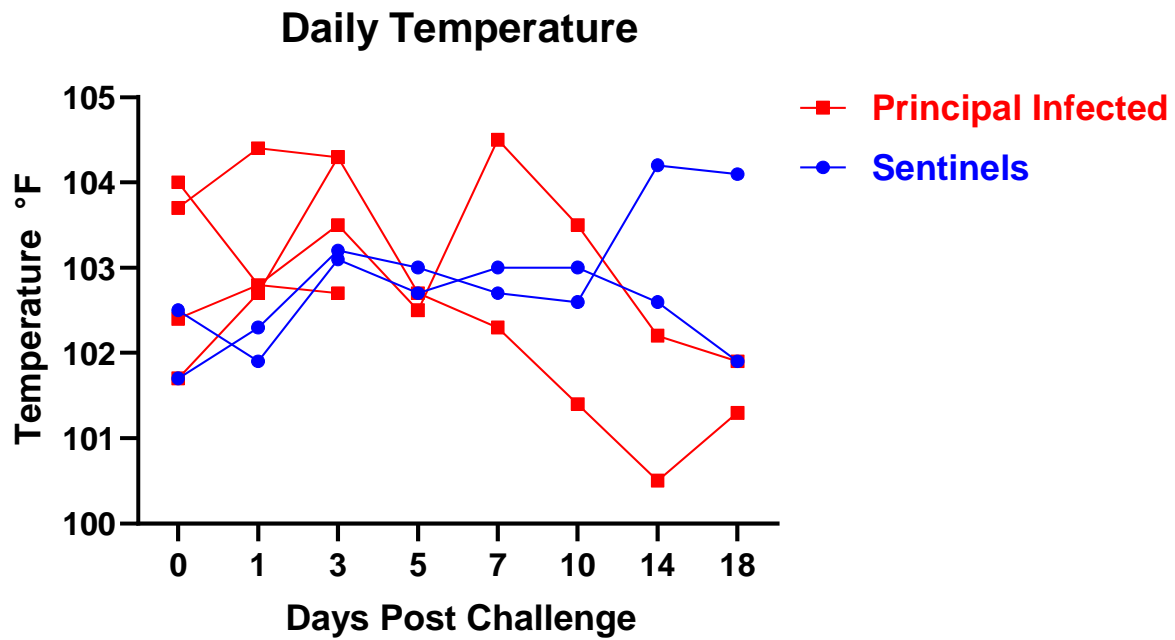
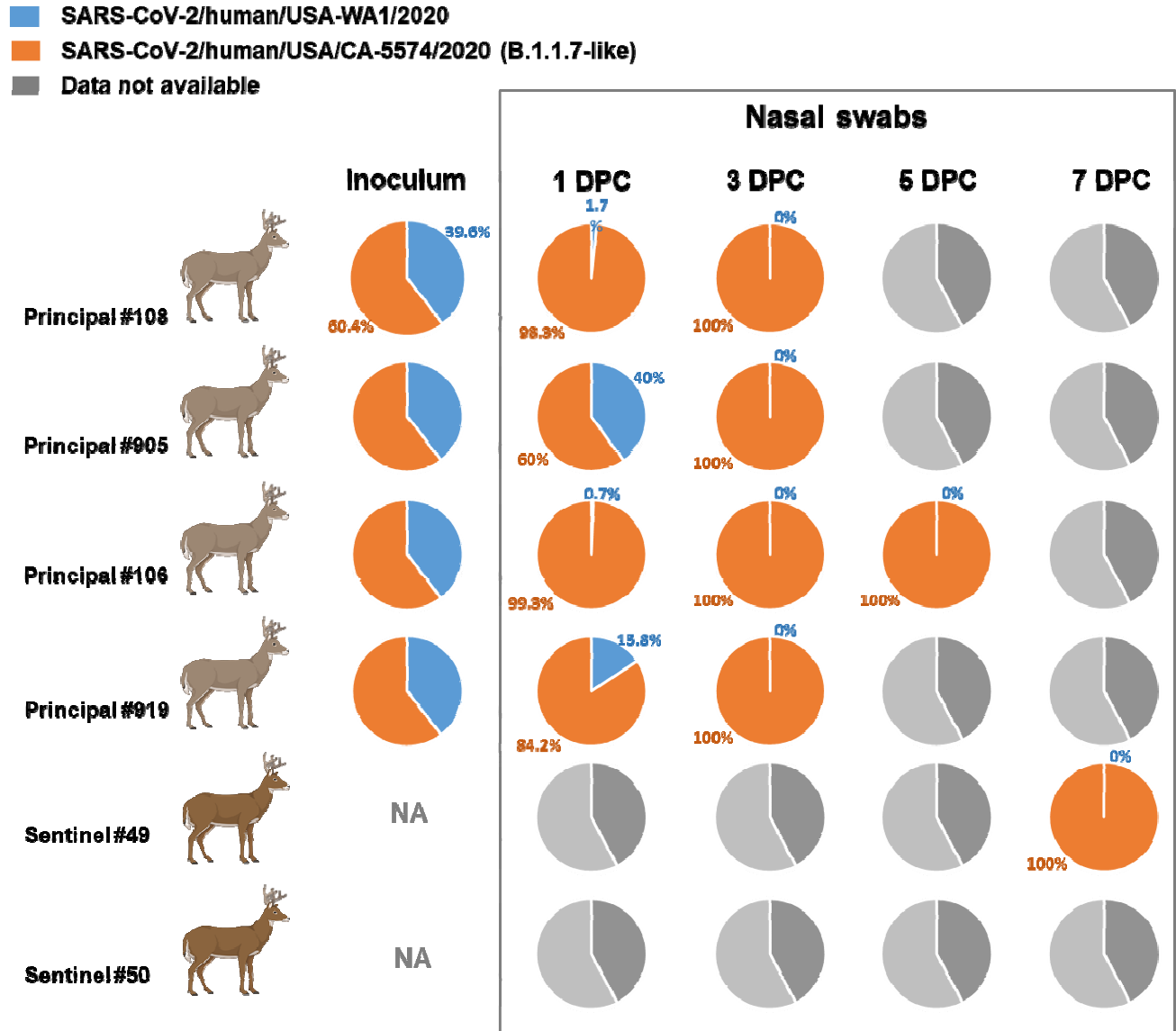


**Supplementary Figure 1. Read coverage of sequenced samples from SARS-CoV-2 co-infected white-tailed deer.** Swab and tissue homogenate samples from white-tailed deer co-infected with the SARS-CoV-2/human/USA/WA1/2020 (lineage A WA1) and SARS-CoV-2/human/USA/CA-5574/2020 (alpha VOC B.1.1.7) strains were analyzed using next generation sequencing.



**Supplementary Figure 2. Daily Temperatures.** Rectal temperatures were taken from sedated deer on 0, 1, 3, 5, 7, 10, 14, 18 DPC.



**Supplementary Figure 3. Next-generation sequencing of swabs collected from SARS-CoV-2 co-infected white-tailed deer.** cDNA products of SARS-CoV-2 RNA extracted from nasal swabs were sequenced on the Illumina NextSeq platform to evaluate the *in vivo* competition between the ancestral lineage A WA1 (SARS-CoV-2/human/USA/WA1/2020) and the alpha VOC B.1.1.7 (SARS-CoV-2/human/ USA/CA-5574/2020) strains.