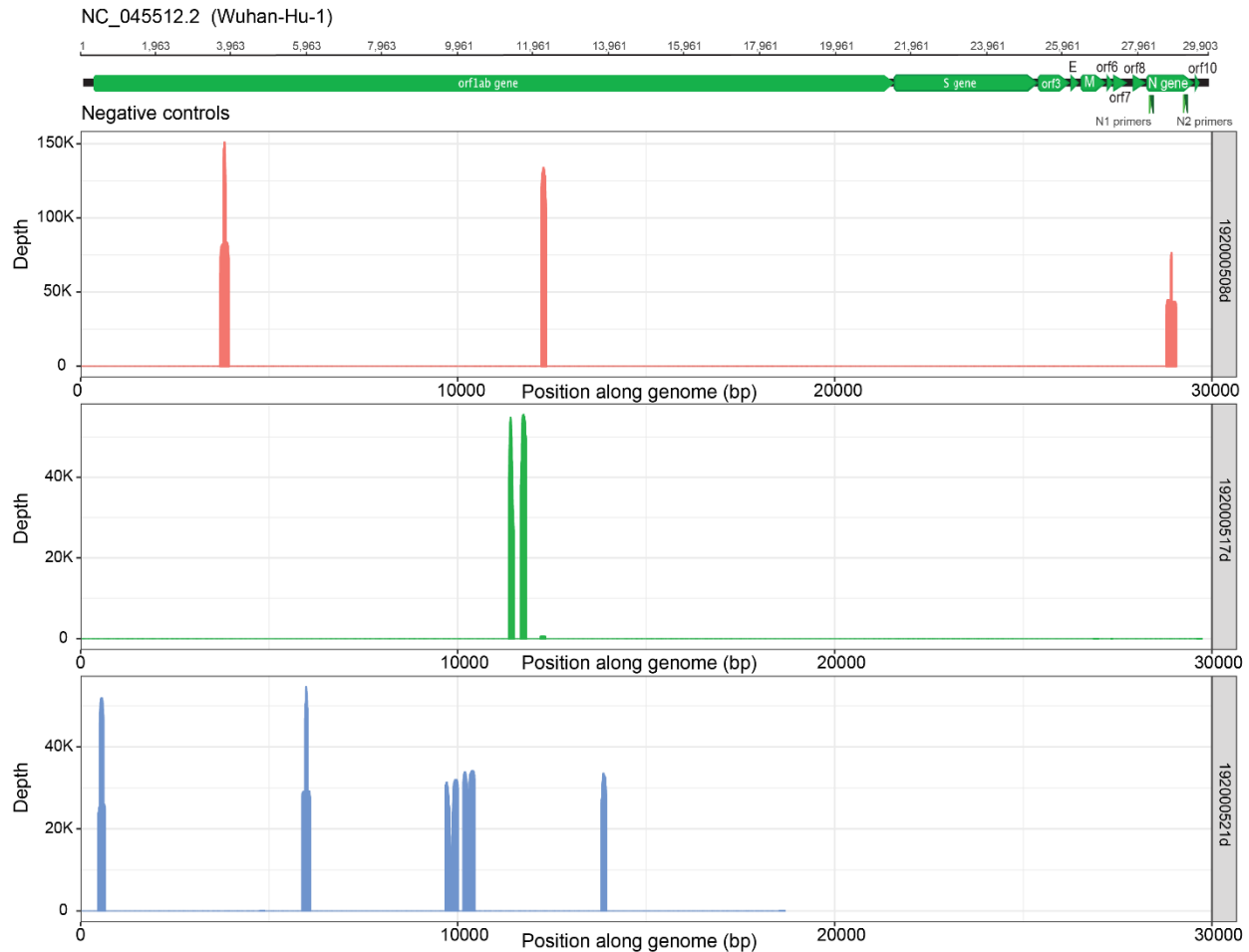
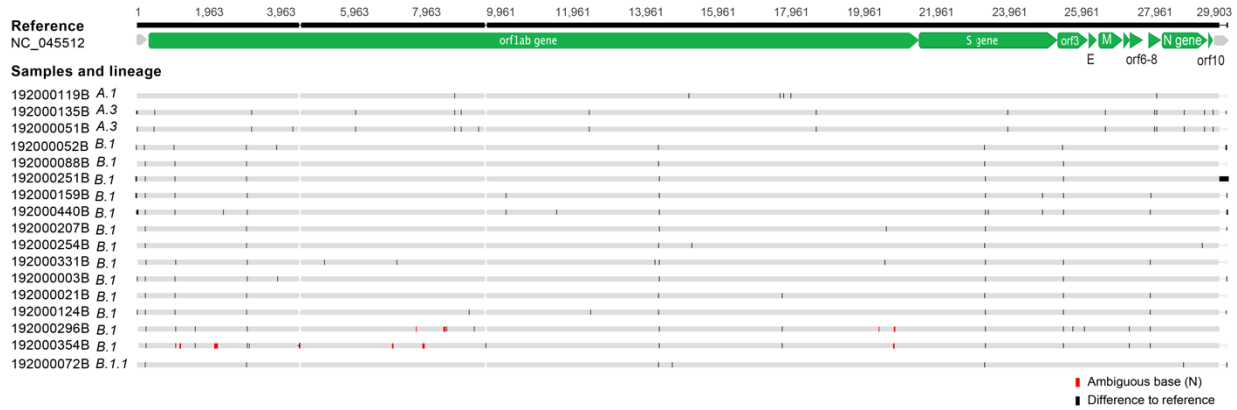


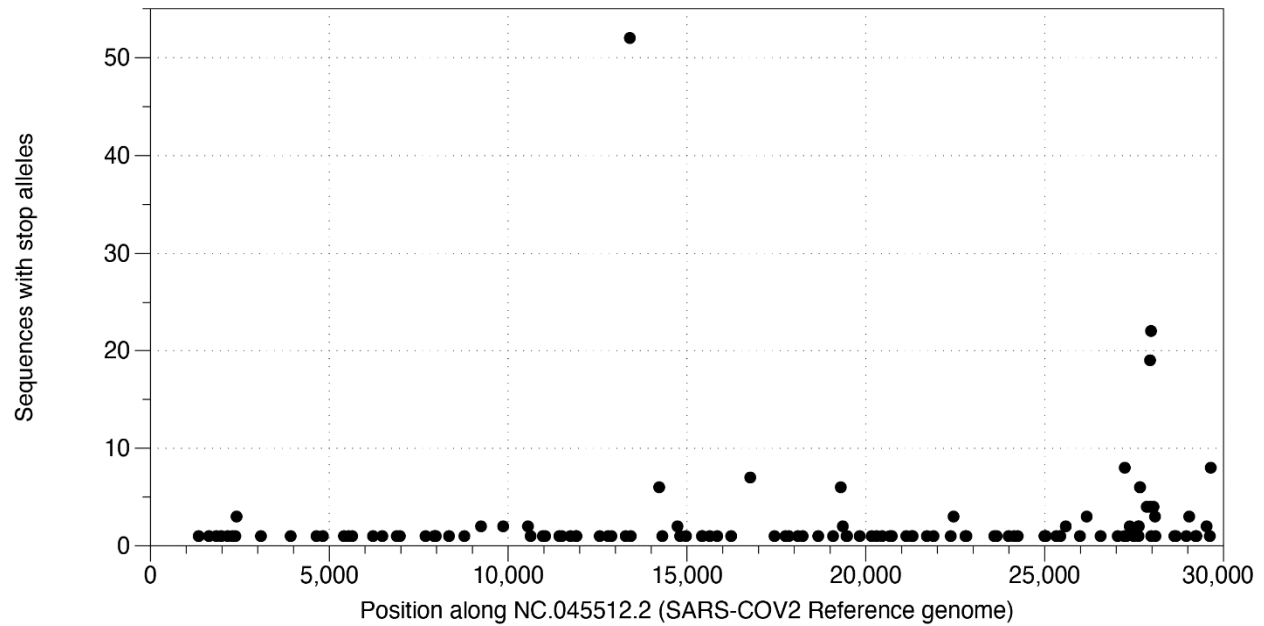
## Supplementary Figures (1-4)



**Supplementary Fig. 1.** Genome coverage plots for the three SARS-CoV-2 negative samples. Coverage is localized despite the 45-91 M reads that these samples obtained post-capture.



**Supplementary Fig. 2.** A multiple sequence alignment (using MAFFT) of 17 reconstructed SARS-CoV-2 genomes and Wuhan-Hu-1 reference genome (NC\_045512). Grey indicates agreement with the reference, black is a disagreement, and pink marks areas in the reconstruction with an ambiguous nucleotide, “N”. The pangolin lineage assignment is listed next to the sample name. The extra length of the 192000251B seen here is an assembly artifact and was excluded from analysis.



**Supplementary Fig. 3.** Stop codon variants in sampled SARS-CoV-2 genomic assemblies. A snapshot of full length SARS-CoV-2 genome assemblies from GISAID and NCBI on 27 May 2020 was downloaded (comprising 39246 entries), and processed to detect single nucleotide variant alleles that introduced a stop codon. Introduced stop codons were detected in 270 entries, and the frequency of these alleles are plotted along the SARS-CoV-2 reference genome position. Introduced stop codons are rare but are distributed throughout the genomic sequences. Multiple loci harbor stop codons in unrelated assemblies.



**Supplementary Fig. 4.** Junctions reads to support expression of ORF10 19200052B, 19200251B and 19200440B. Expression values were calculated as 0.13, 0.13 and 0.02 reads/million. Few examples of those junction reads are shown in the figure (purple arrows).

## **Supplementary Tables (1-4)**

**Supplementary Table 1.** Sample information, capture pools and sequencing metrics details.

**Supplementary. Table 2.** Lineage analysis of the 17 full-length genomes.

**Supplementary Table 3.** Junction read counts is reads/million identified in the post capture data of 17 samples with full-length genomes.

**Supplementary Table 4.** Junction read counts in reads/million identified in the nine samples sequenced before (IDxxxxB-2) and after capture (IDxxxxB) enrichment.