***Phylogenetic Tree Construction***

29,287 SARS-CoV-2 genomes were downloaded as a MAFFT-produced multiple sequence alignment (-FFT-NS-2) from the GISAID EpiCoV database on May 26th, 2020 at 9:57AM (Katoh; https://www.gisaid.org/). The alignment was manually inspected and trimmed to remove positions without a corresponding base in the 29,903 nt Wuhan-Hu-1 reference sequence (NC\_045512.2). The alignment was processed to remove genomic assemblies of less than 29,400 nt. Sequences from non-human hosts, sequences without a discrete sampling date, and sequences that could not be matched to an entry in metadata from EpiCoV were additionally removed from the alignment in R 3.6.1 (https://www.gisaid.org/). To remove positions that have been reported to experience high rates of sequencing error or hypermutability, the alignment was masked according to recommendations from EMBL (http://virological.org/t/issues-with-sars-cov-2-sequencing-data/473). Duplicate sequences were removed from the masked alignment in CD-HIT (-c 1.0) (Li). The processed alignment of 15,028 SARS-CoV-2 genomes was used to build a phylogenetic tree in IQ-TREE with gamma substitution and invariable site options (-m HKY+I+G) (Nguyen).