Materials and Methods

All 17 SARS-CoV-2 genome sequences for isolates listed under the location "Europe / Turkey" in the EpiCoV database of GISAID (https://www.epicov.org/epi3/frontend#) were downloaded in a FASTA file. The nucleotide sequence for the surface glycoprotein (AKA S protein, spike protein) extracted from the reference genome for SARS-CoV-2 found in the Nucleotide database of NCBI was aligned to the isolate genomes using nucleotide BLAST (BLASTn, https://blast.ncbi.nlm.nih.gov/Blast.cgi), with the reference sequence as the query sequence, and the isolate genome sequences as the subject sequence, optimized for highly similar sequences using the megablast preset settings. The sites in the isolate genomes aligning to the surface glycoprotein nucleotide sequence were downloaded in a FASTA file. The nucleotide sequences were translated into amino acid sequences using the EMBOSS Transeq online translation tool (https://www.ebi.ac.uk/Tools/st/emboss_transeq/). The resulting amino acid sequences, along with the reference protein sequence for the surface glycoprotein, were collected in a single file, and subjected to multiple sequence alignment using the MUSCLE online MSA tool (https://www.ebi.ac.uk/Tools/msa/muscle/). The results were downloaded in a FASTA file, and visualized using the Jalview multiple sequence alignment analysis software.