

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. These genome sequences and the reference genome sequence for SARS-CoV-2 found in the Nucleotide database of NCBI were collected in a single file, and subjected to multiple sequence alignment using the Clustal Omega online MSA tool (<https://www.ebi.ac.uk/Tools/msa/clustalo/>). The results were downloaded in FASTA and CLUSTALW files.