

File Name: Supplementary Data 1

Description: These data include the sliding window views showing the genetic differentiation, nucleotide diversity and Tajima's D of the 90-day and 45-day runs (Files: "SW_90.jpg" and "SW_45.jpg"); phylogenetic trees of the constructed virus strains in the populations of the 90-day and 45-day runs (Files: "PT_90.jpg" and "PT_45.jpg"); the sequence of the wild-type reference (MT020880) downloaded from CoVdb (File: "ref.fasta"); pSARS-CoV-2 Delta (BAC clone, File: "Delta_Seq.pdf"); the information of the Omicron-like strains shown in Supplementary Fig. 4a (File: "Early_Omicron_Like_variants.xlsx"); the results of the surface plasmon resonance (SPR) experiments for measuring the hACE2 affinities of the estimated dominant strains in different populations of the 90-day runs (File: "SPR.jpg"), the plots on the left are the results of measuring the affinity of the ligand for the receptor, K_D , and the plots on the right are the results of measuring the response in resonance units, RUs); the Molecular docking results of the hACE2/evolved RBD complex for the estimated dominant strains of the 90-day 492I populations and the control strains (File: "Molecular_docking.jpg"); the information of high-frequency mutations (File: "HF_mutations.xlsx"); the primers used in the study (File: "Primers.docx"); the List of Omicron mutations shared by Omicron sublineages (File: "Omicron_Spike_Muts.xlsx"); the accession numbers of the sequences accessed in Nextstrain (File: "nextstrain_accessions.xls.gz"); the scripts used in the analyses in the manuscript (File: "Pipeline.zip"); the resources utilized in this work (File: "Resource_Table.docx"); and the quality control reports of the source data (File: "FASTQC.zip").