Supplementary Figure 8. Maximum-Likelihood global phylogeny of SARS-CoV-2. To ensure that the patient case was not resultant of a superinfection event, all patient sequences were aligned with a snapshot of global SARS-CoV-2 sequences downloaded from the GISAID database between 1st April and 5th May (26472 sequences, only full sequences and excluding all low coverage sequences). Sequences were aligned using MAFFT and a maximum-likelihood tree inferred with IQTREE v2.1.3. All 23 sequenced from the patient case (red) formed a distinct clade, suggesting that all viral populations diversified within-host.