**Supplementary Material**

**Figure description:**

**Maximum likelihood phylogenetic tree (ML, GTR, 1,000 bootstrap) of the C.37 lineage.** The phylogenetic tree was constructed using the 203\_LABRESIS sequence obtained from this study, 16 sequences from Argentina, 24 from Chile, 26 from Peru and 1 from São Paulo State of Brazil. All sequences were available in EpiCoV database in GISAID. This dataset was aligned using MAFFT v7.475 and subjected to maximum likelihood (ML) phylogenetic analysis using IQ-TREE v2.1.2 (GTR+F+R4, SHaLRT with 1,000 replicates). Branches are colored according to the countries (Chile in grey, Brazil in yellow, Peru in pink, and Argentina in blue). The scale of the phylogenetic branches is given as substitutions per nucleotide site. All mutations identified in the 203\_LABRESIS sequence (deletions in the ORF1a and Spike genes are shown in bold) are listed in the box.