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AMOVA AND PHILOGENY IN SARS-COV- 2 PROTOCOLS

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METHODOLOGY

1 1.METHODOLOGY

2 DATABANK

3 The 153 gene sequences of the integrase gene of human immunodeficiency virus 1 were collected from GENBANK (<https://www.ncbi.nlm.nih.gov/popset/?term=MN888087.1>) and participate in a PopSet dipped by Totmenin and collaborators on March 25, 2020 (Popset:1822236350).

4 **PHYLOGENETICS ANALYSES:** For phylogenetic analyses, the previously described nucleotide sequences were used. The sequences were aligned using the MEGA X program (TAMURA et al., 2018) and gaps were extracted for the construction of phylogenetic trees.

5 **GENETIC STRUCTURING ANALYSES:** Paired FST estimators were obtained with the software Arlequin v. 3.5 (EXCOFFIER et al., 2005) using 1000 random permutations. The FST matrix generated by the software was used in the

construction of a dendrogram based on the UPGMA distance method with the MEGA X software (TAMURA et al., 2018) and the FST and geographic distance matrices were not compared.