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AMOVA AND PHILOGENY IN HIV-1 PROTOCOLS

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METHODOLOGY

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2 **DATABANK:** 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).

3 **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.

4 **GENETIC STRUCTURING ANALYSES:** Paired F_{ST} estimators were obtained with the software Arlequin v. 3.5 (EXCOFFIER et al., 2005) using 1000 random permutations. The F_{ST} 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 F_{ST} and geographic distance matrices were not compared.