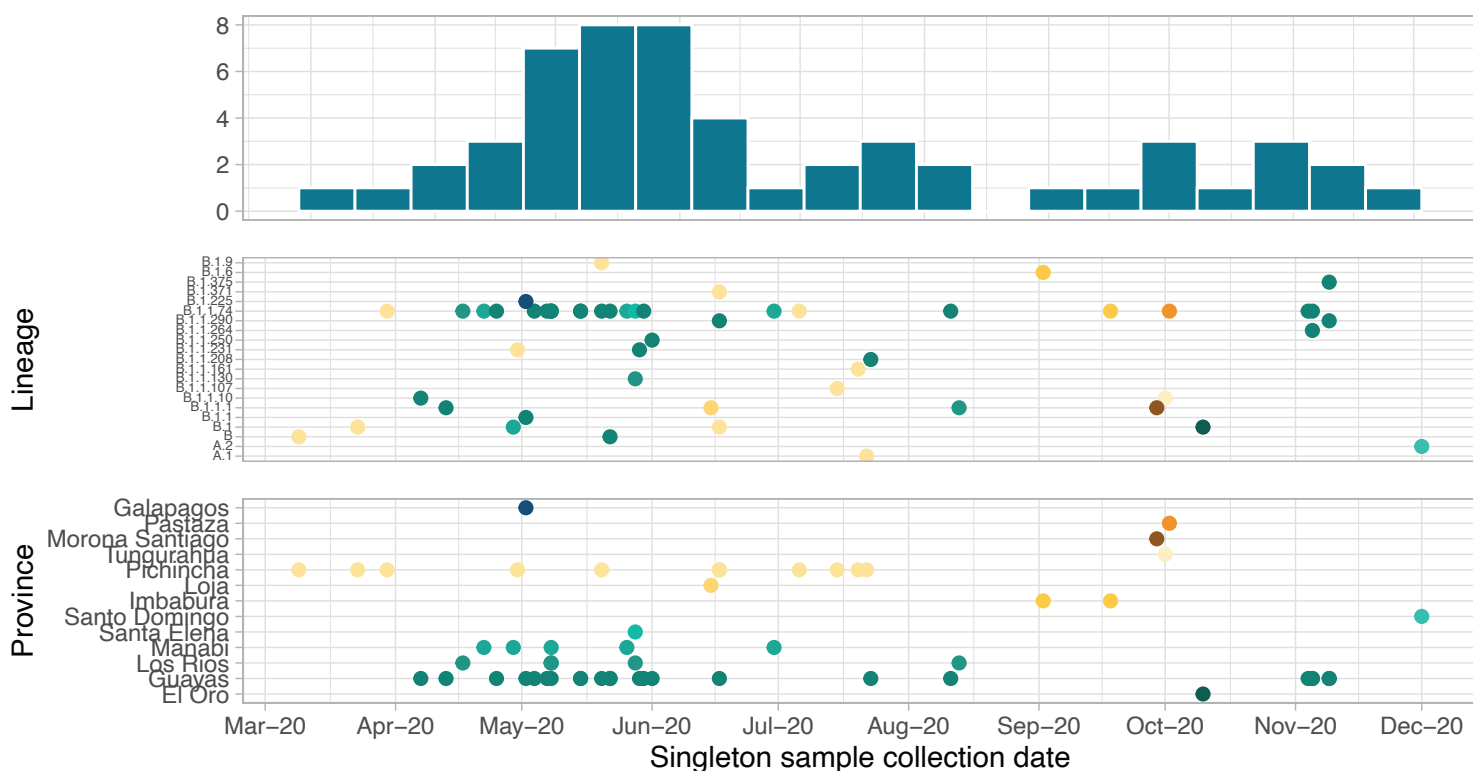
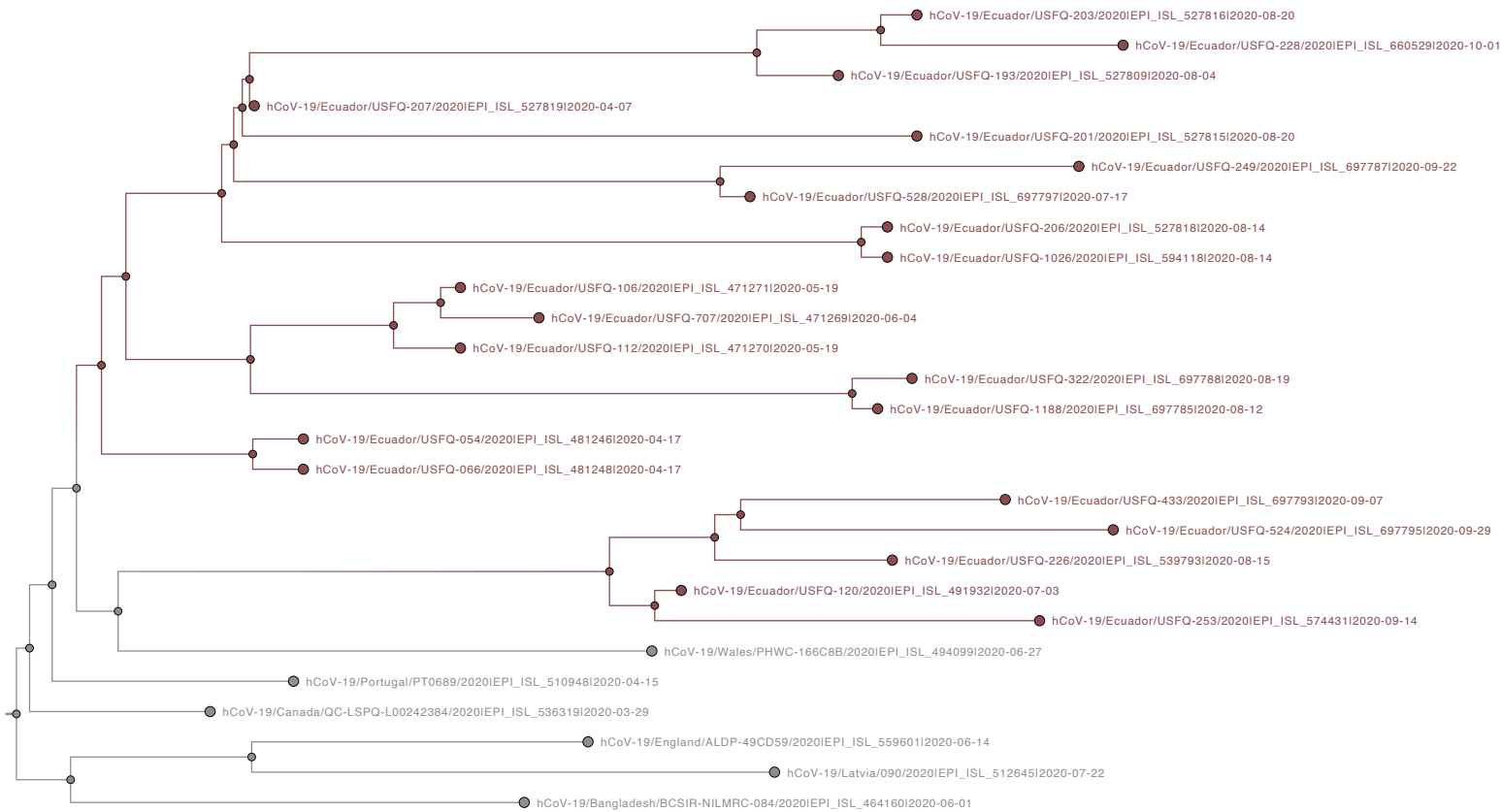


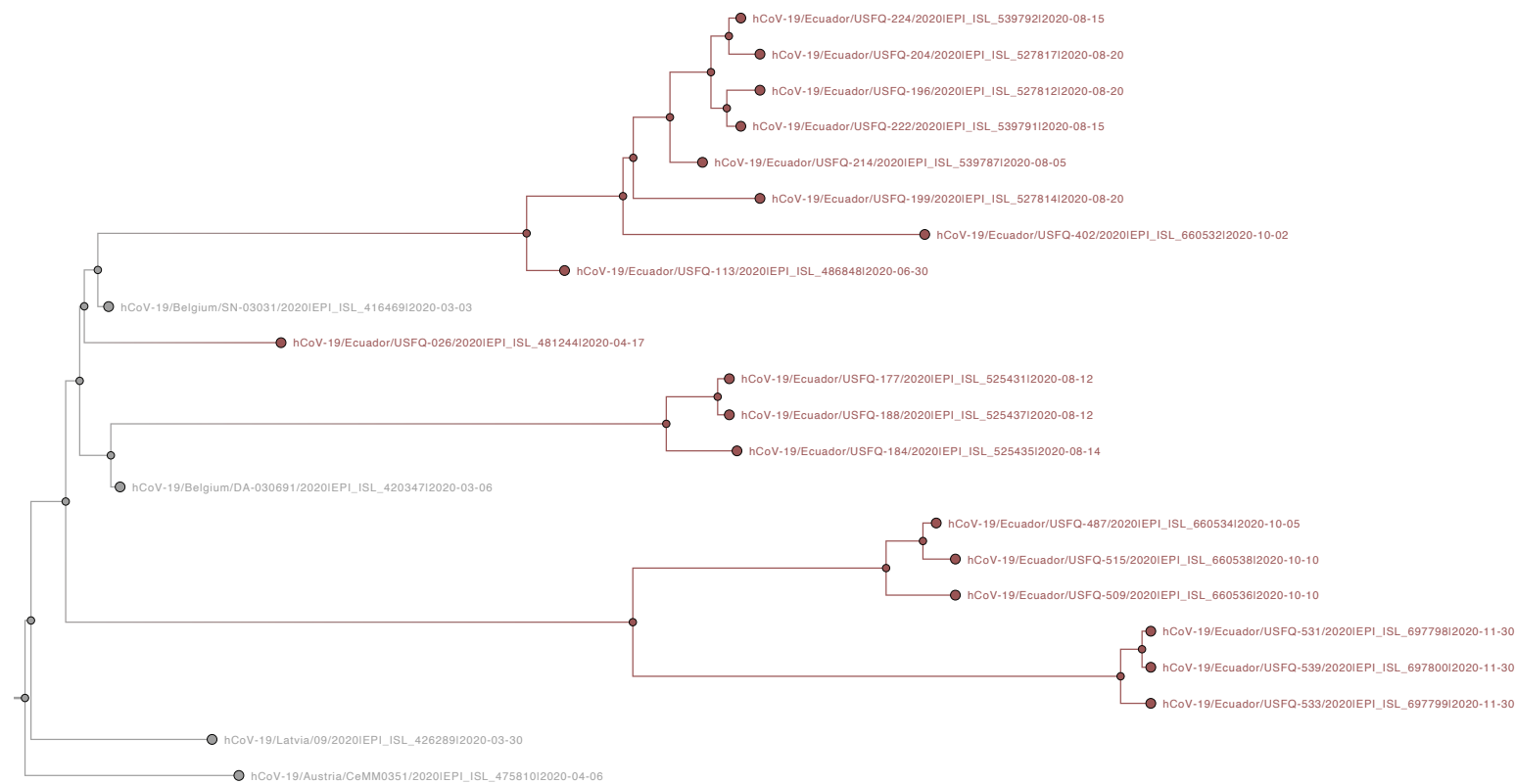
**Fig S1.** Comparison of the reported numbers of cases and deaths and the publicly available SARS-CoV-2 genomes generated per country in South America. Numbers of sequences were taken from the GISAID database, and the reported numbers of cases and deaths were taken from Our World in Data. Data retrieved on February 14 2021, with a cutoff date on 2020-12-10. Lower panels show data from countries at a different scale compared to the upper panels for visualisation purposes. Color scheme shows the (logarithmic) numbers of sequences per cumulative number of reported death.



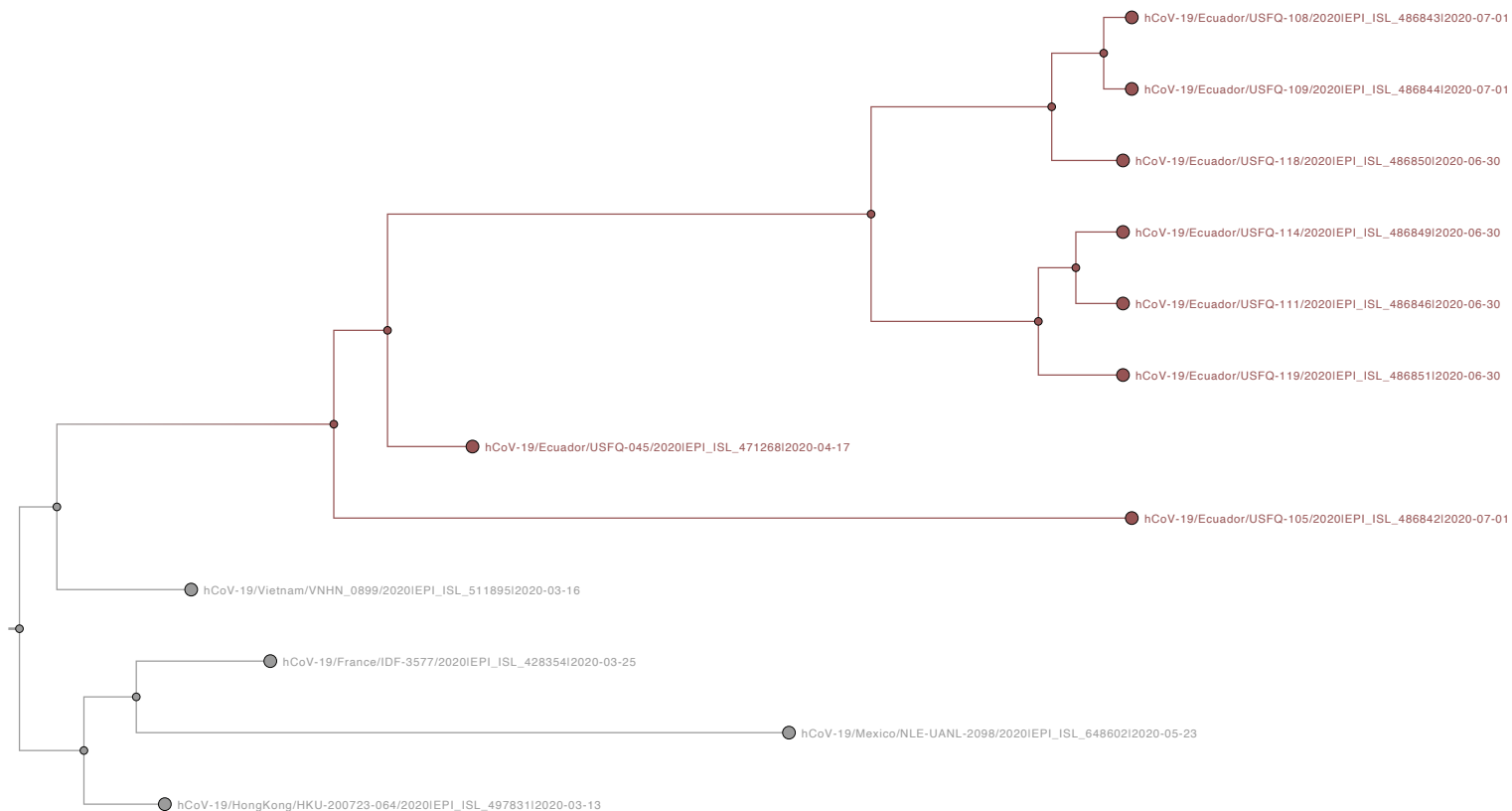
**Fig S2.** Summary of singletons identified in Ecuador. The upper panel shows the number of singletons per two-week epidemiological weeks. The middle panel shows the Pango lineages to which singletons were assigned, and the lower panel shows the province where singletons were identified by sample collection date. Dot colours correspond to the province where the samples were collected.



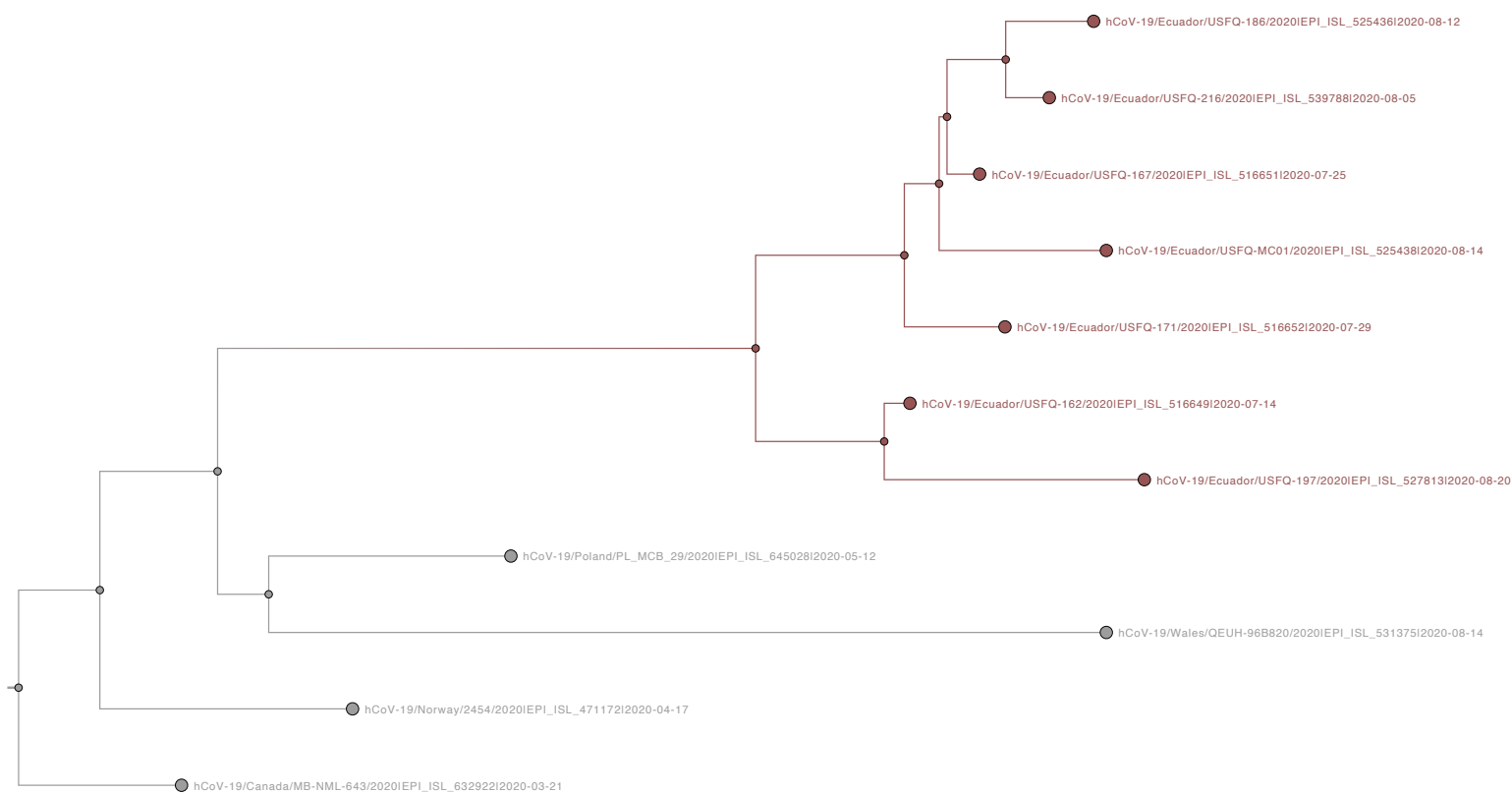
**Fig S3.** Subtree from MCC corresponding to transmission lineages group D.



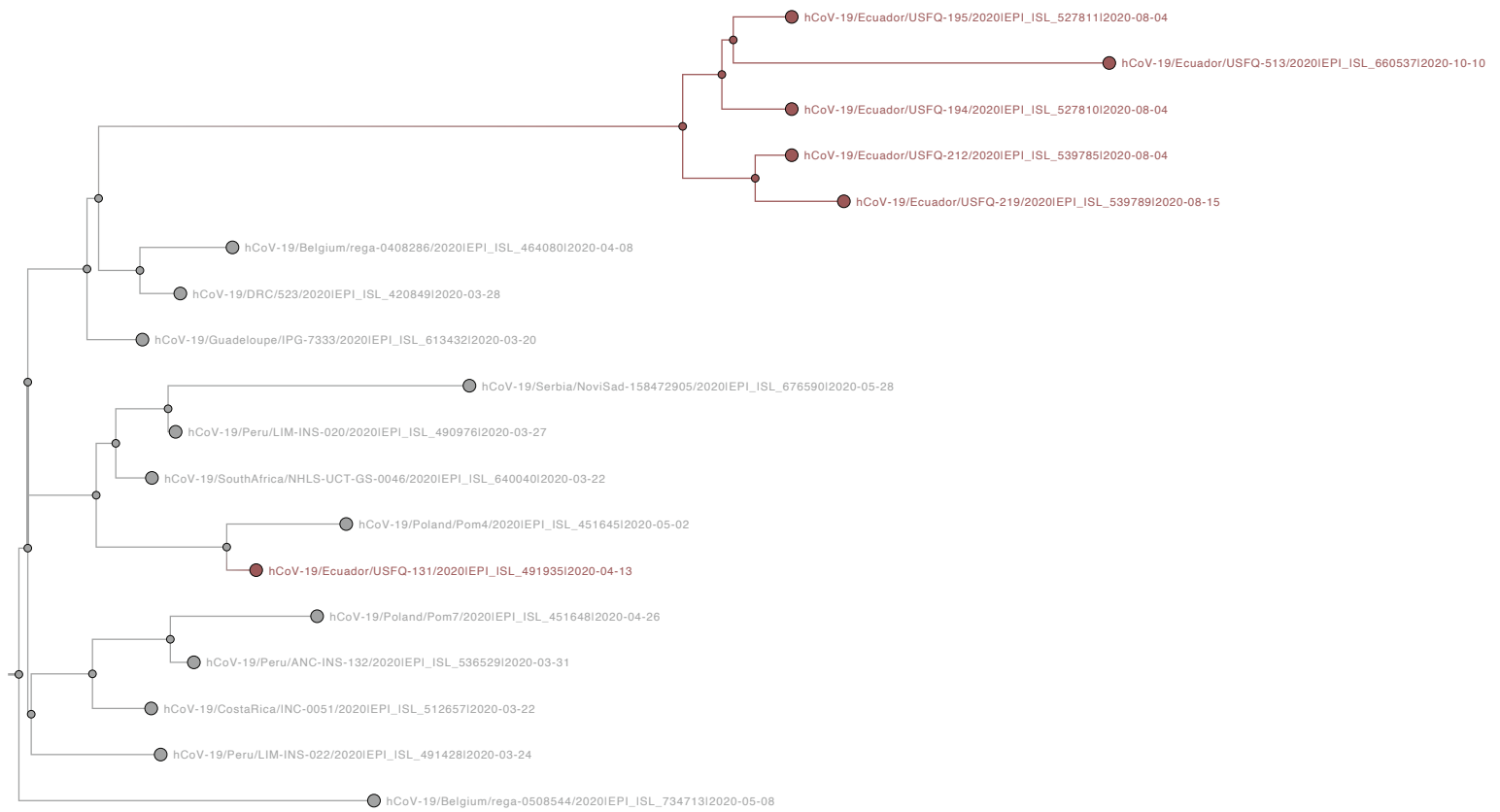
**Fig S4.** Subtree from MCC corresponding to transmission lineages group H.



**Fig S5.** Subtree from MCC corresponding to transmission lineage G.



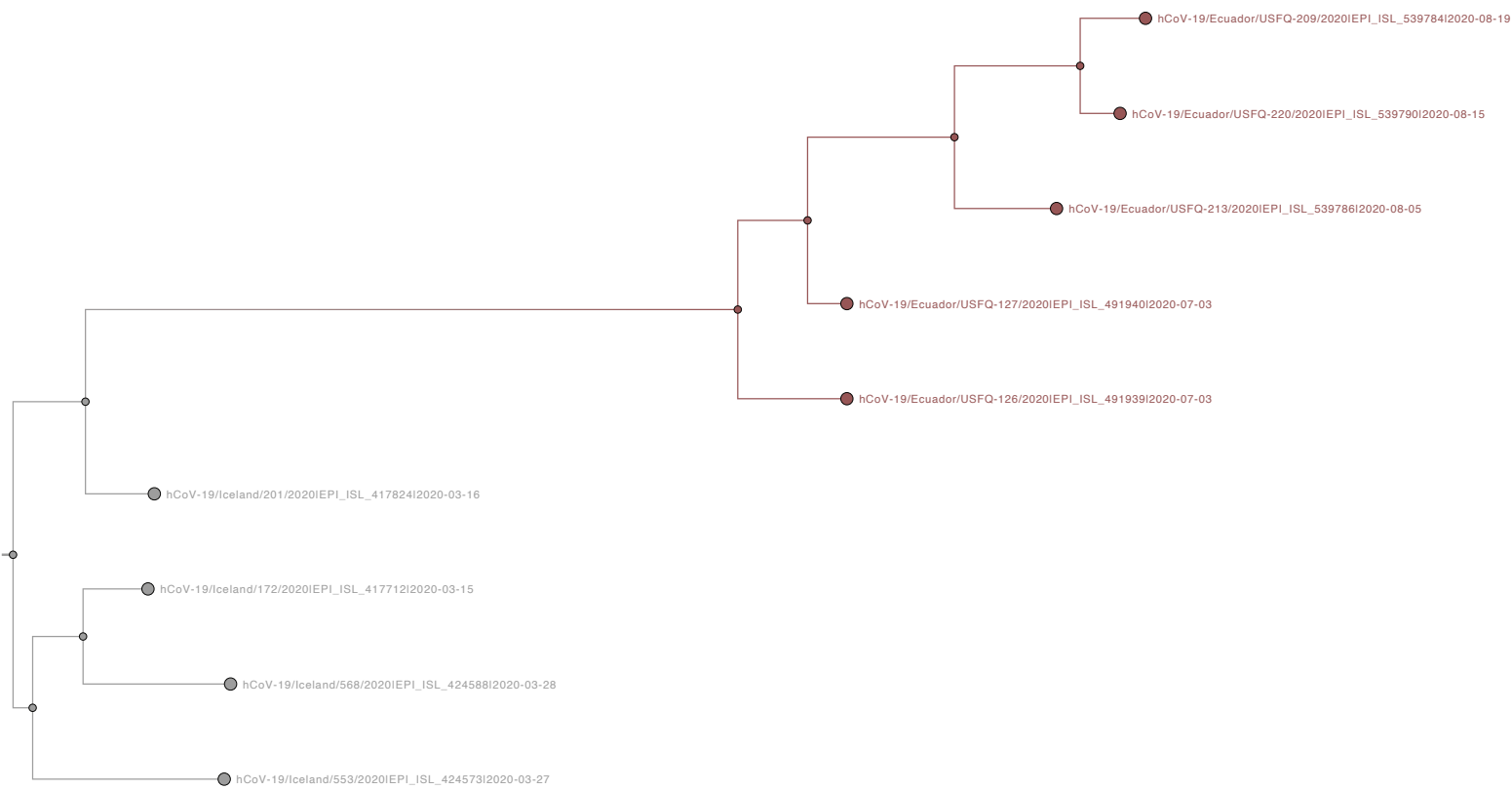
**Fig S6.** Subtree from MCC corresponding to transmission lineage O.



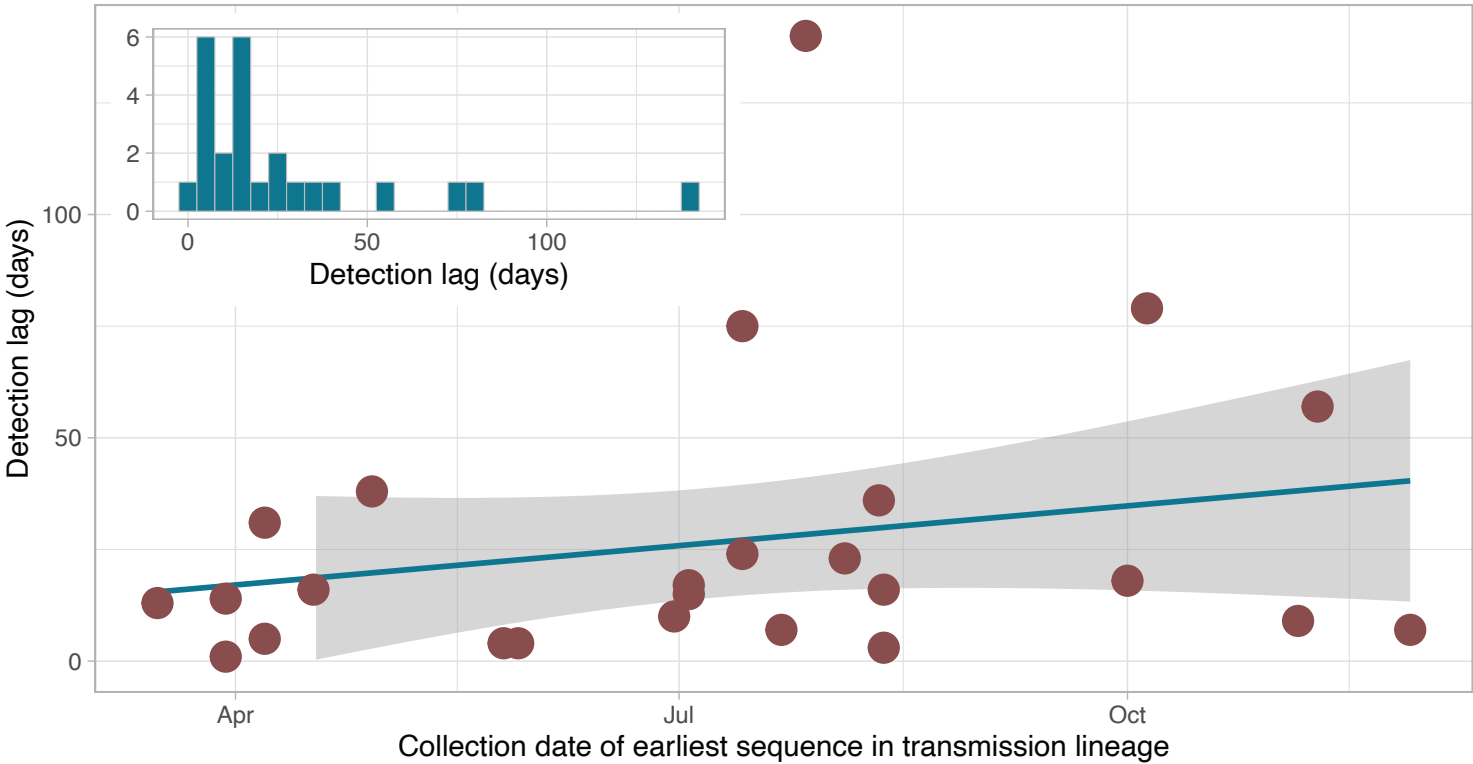
**Fig S7.** Subtree from MCC corresponding to transmission lineage F.



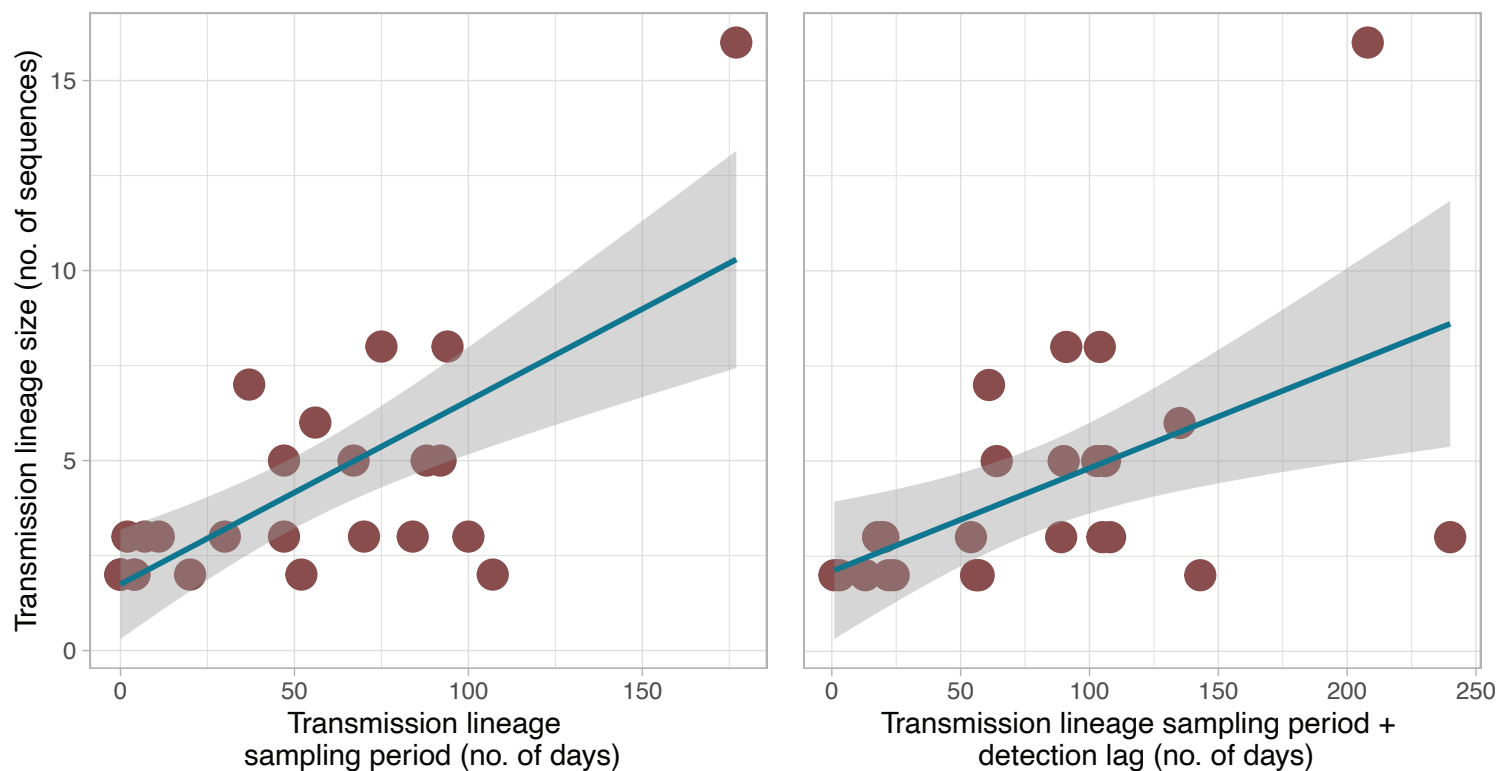
**Fig S8.** Subtree from MCC corresponding to transmission lineage B.



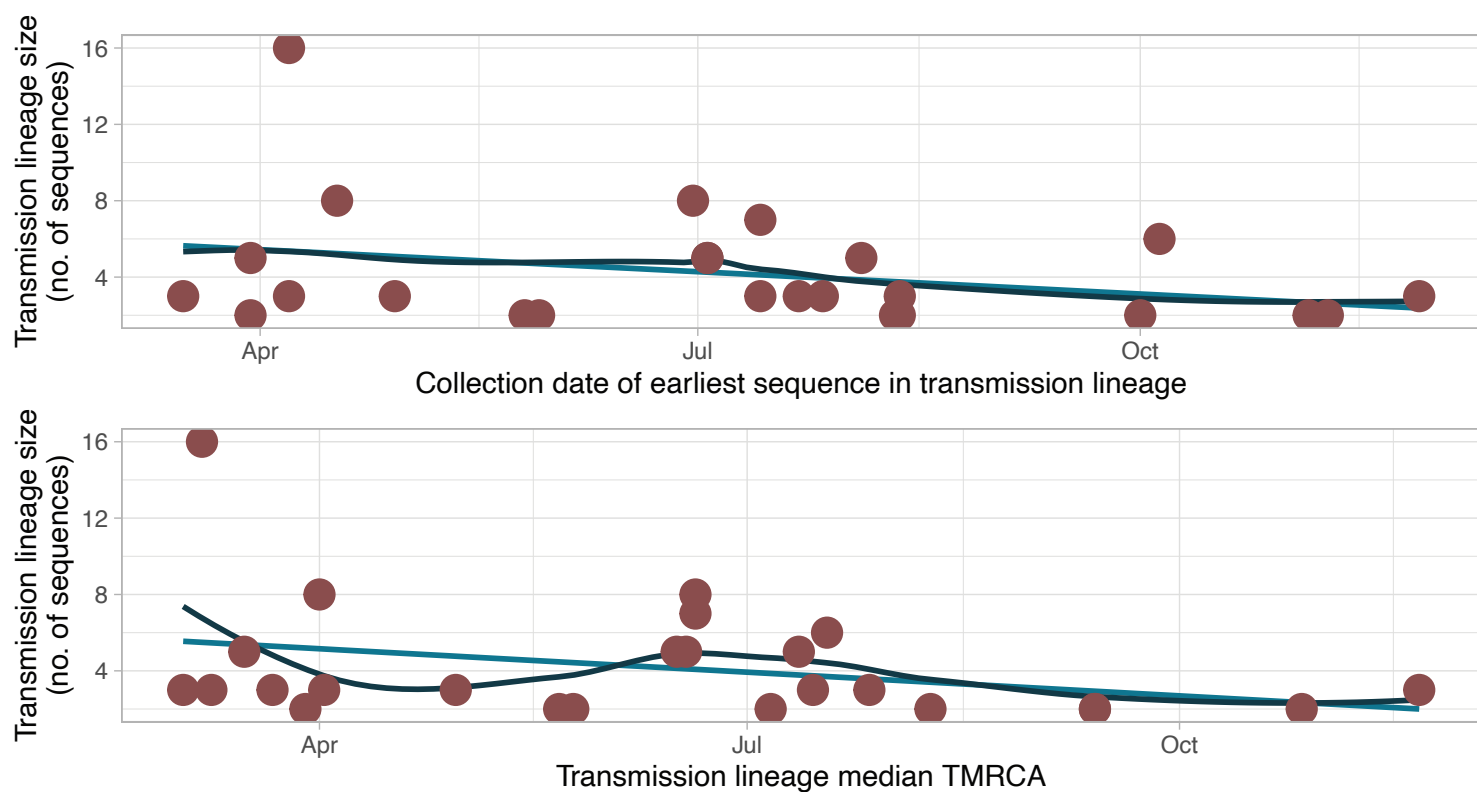
**Fig S9.** Subtree from MCC corresponding to transmission lineage M.



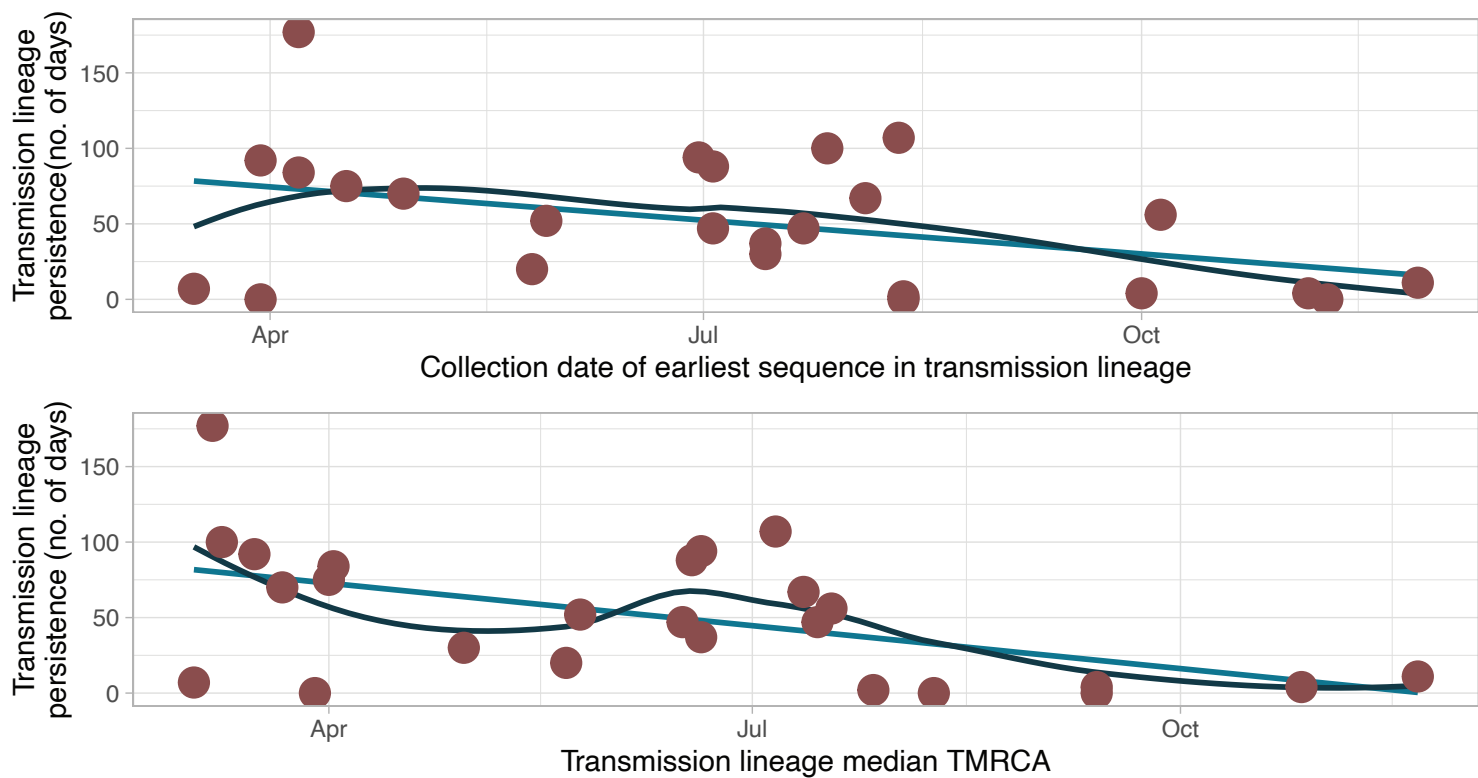
**Fig S10.** Changes of detection lag over time. Figure shows the detection lag of every transmission lineage (time between the TMRCA of a transmission lineage and the collection date of its earliest sequence), plotted by the collection date of the earliest sequence in said lineage. The inset shows the distribution of detection lag times in the data set.



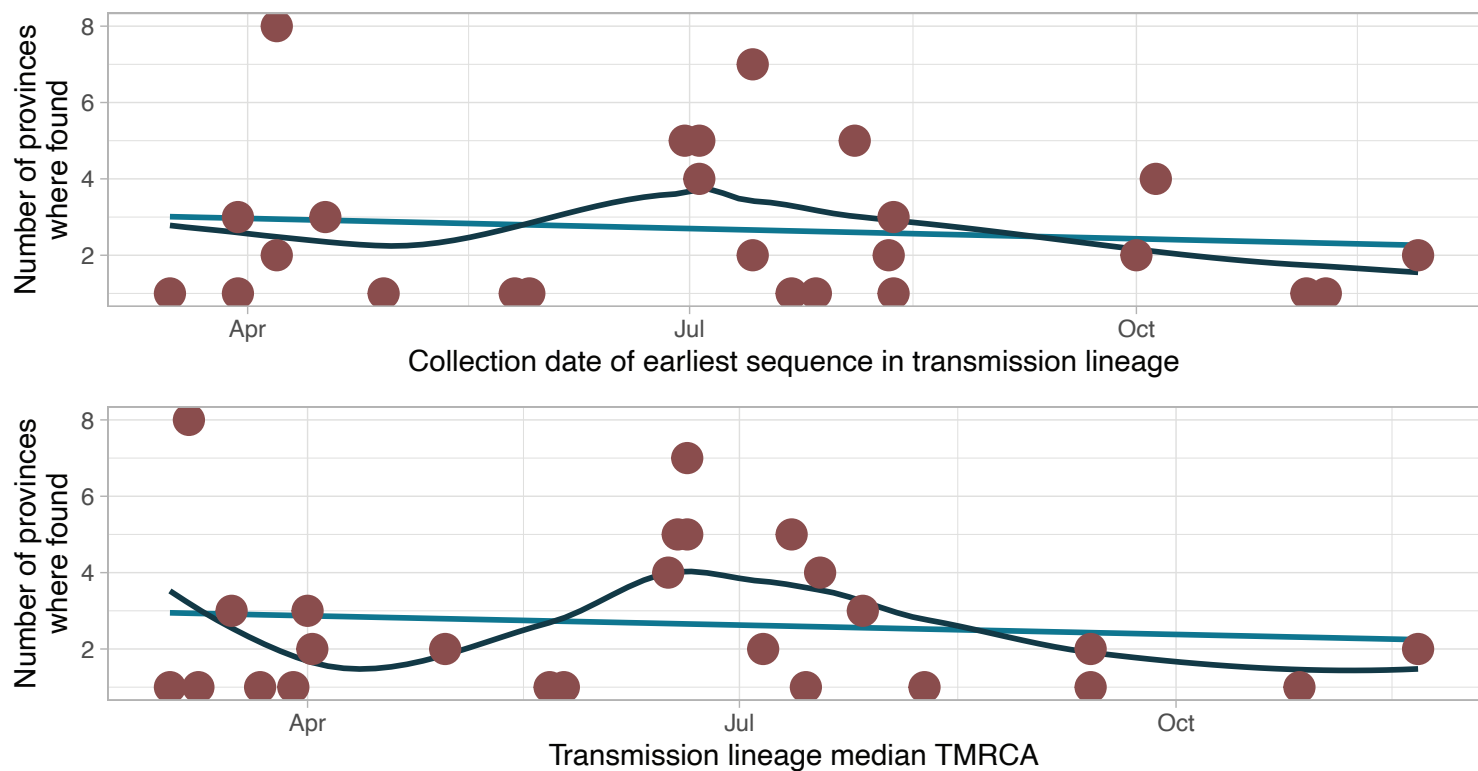
**Fig S11.** Comparison between the size of transmission lineages (i.e. number of sequences assigned to a transmission lineage) and their persistence in time estimated as either the number of days between the earliest and most recent sequences in said lineage (left) or the number of days between the transmission lineage TMRCA and the most recent sequence (right).



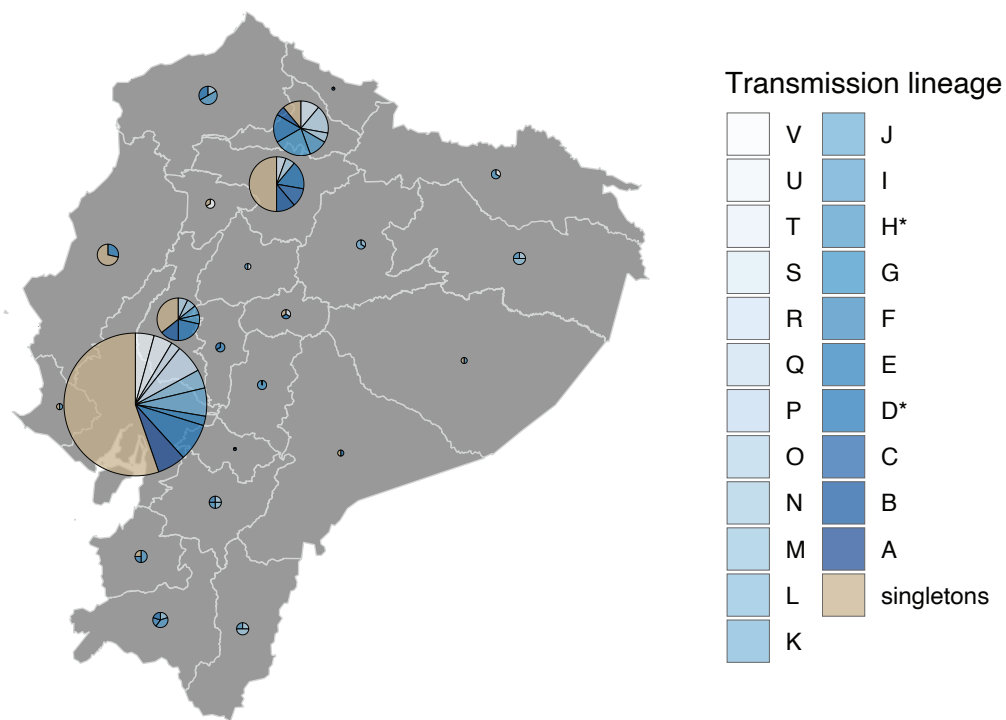
**Fig S12.** Comparison between the size of transmission lineages (i.e. number of sequences assigned to a transmission lineage) and the collection date of the first sequence identified in said lineage (upper panel) or the TMRCA for said transmission lineage (lower panel). Trend lines show a linear regression (green) and a fitted local polynomial regression (R function stats::loess, black).



**Fig S13.** Comparison between the persistence in time of transmission lineages (number of days between the earliest and most recent sequences in said lineage) and the collection date of the first sequence identified in said lineage (upper panel) or the TMRCA for said transmission lineage (lower panel). Trend lines show a linear regression (green) and a fitted local polynomial regression (R function `stat::loess`, black).

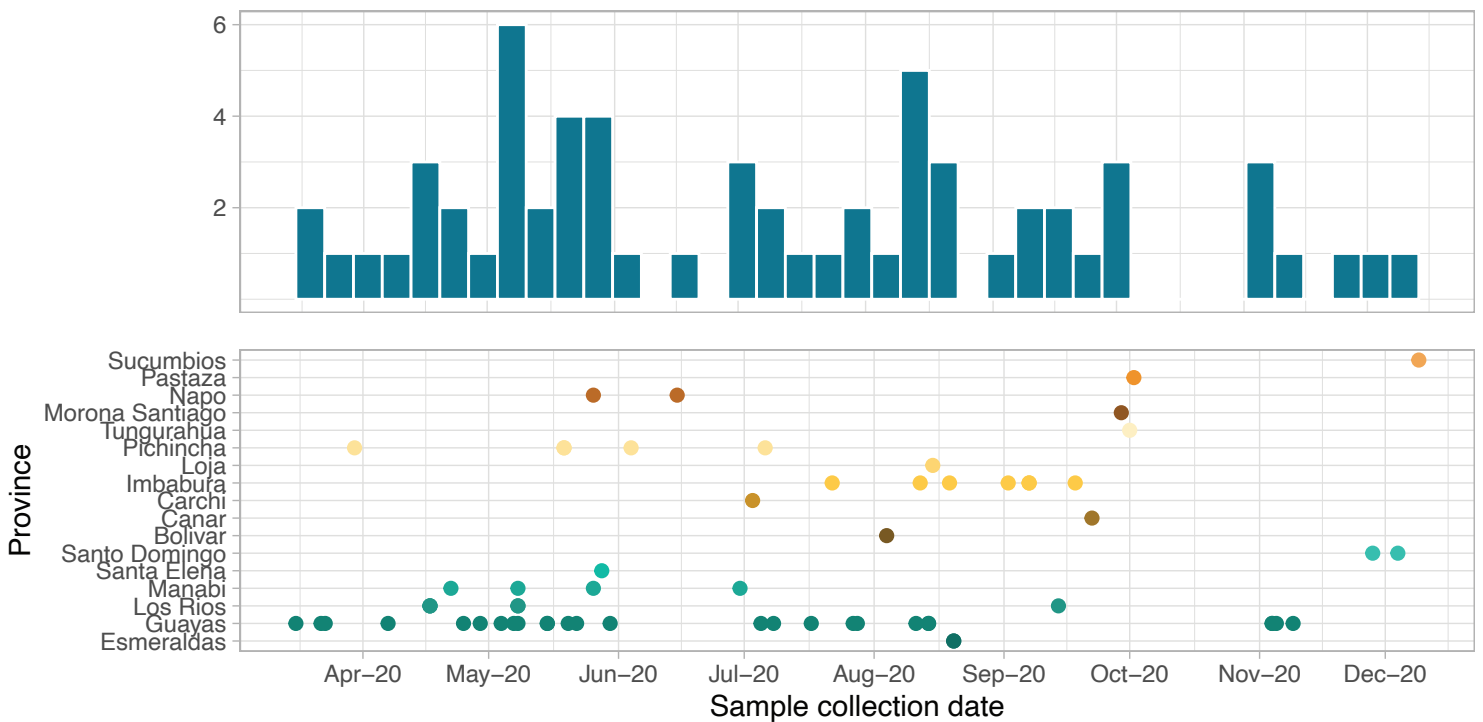


**Fig S14.** Comparison between the geographic spread of transmission lineages (number of provinces where they've been detected) and the collection date of the first sequence identified in said lineage (upper panel) or the TMRCA for said transmission lineage (lower panel). Trend lines show a linear regression (green) and a fitted local polynomial regression (R function `stat::loess`, black).



**Fig S15.** Map of Ecuador showing the contribution of individual transmission lineages (shades of blue) and sequences not associated with them (singletons) in each province. Circle radii represent the number of sequences per province.

#### B.1.1.74



**Fig S16.** Summary of the identification of Pango lineage B.1.1.74 in Ecuador. The upper panel shows the number of sequences assigned to B.1.1.74 per 7-day time period, and the lower panel shows the province where these sequences were identified by sample collection date. Dot colours correspond to the province where the samples were collected.