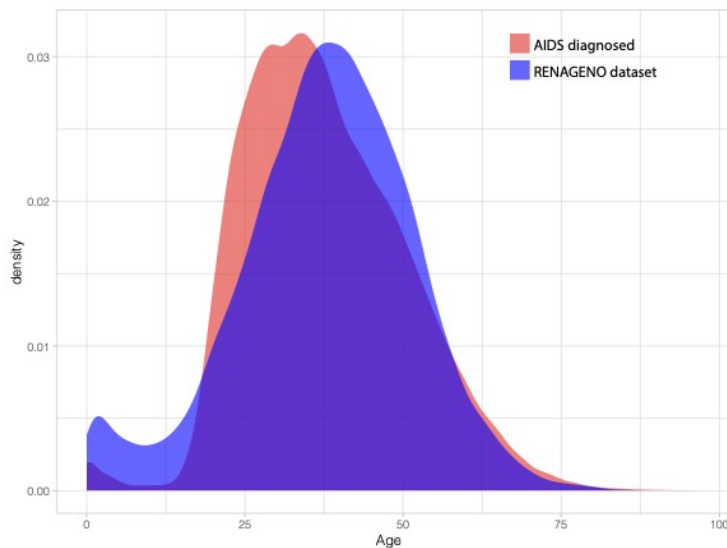


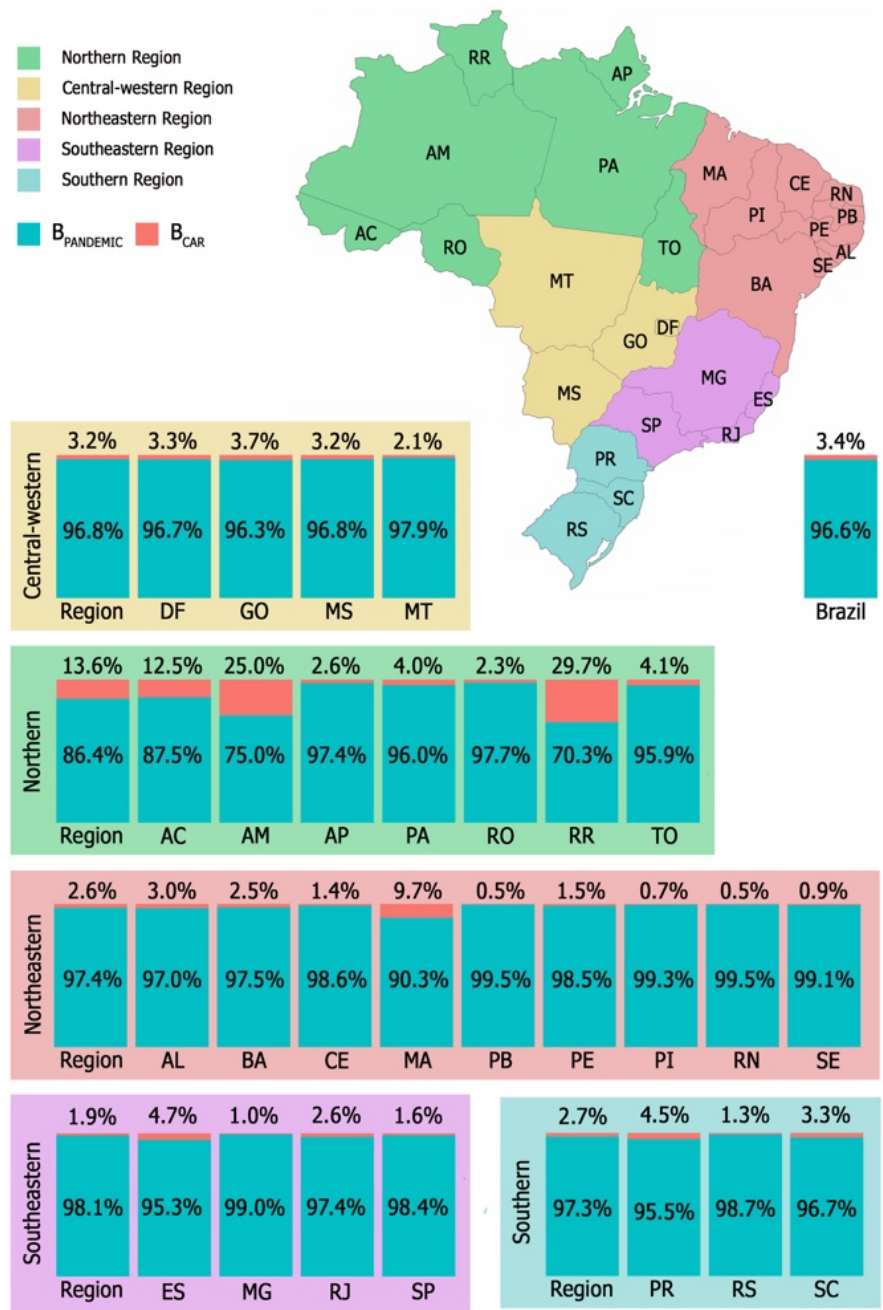
Supplementary Material:

HIV-1 molecular diversity in Brazil unveiled by 10 years of sampling by the national genotyping network

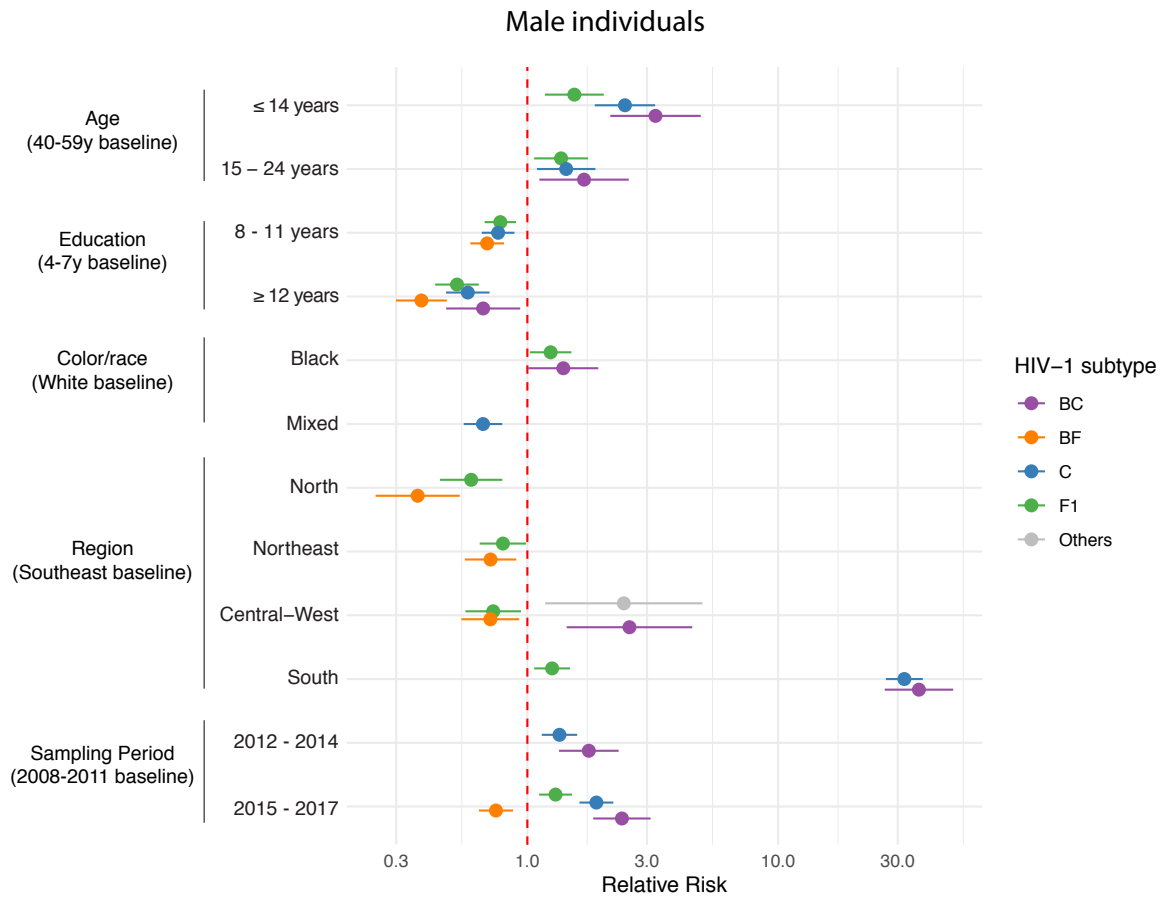
Tiago Gräf^{1*}; Gonzalo Bello²; Paula Andrade²; Ighor Arantes²; João Pereira^{3,4}; Alexandre Bonfim Pinheiro da Silva^{3,4}; Rafael V. Veiga^{5,6}; Diana Mariani³; Lídia Theodoro Boullosa³; Mônica B. Arruda³; José Carlos Couto Fernandez²; Ann M. Dennis⁷; David A. Rasmussen^{8,9}; Amilcar Tanuri³.



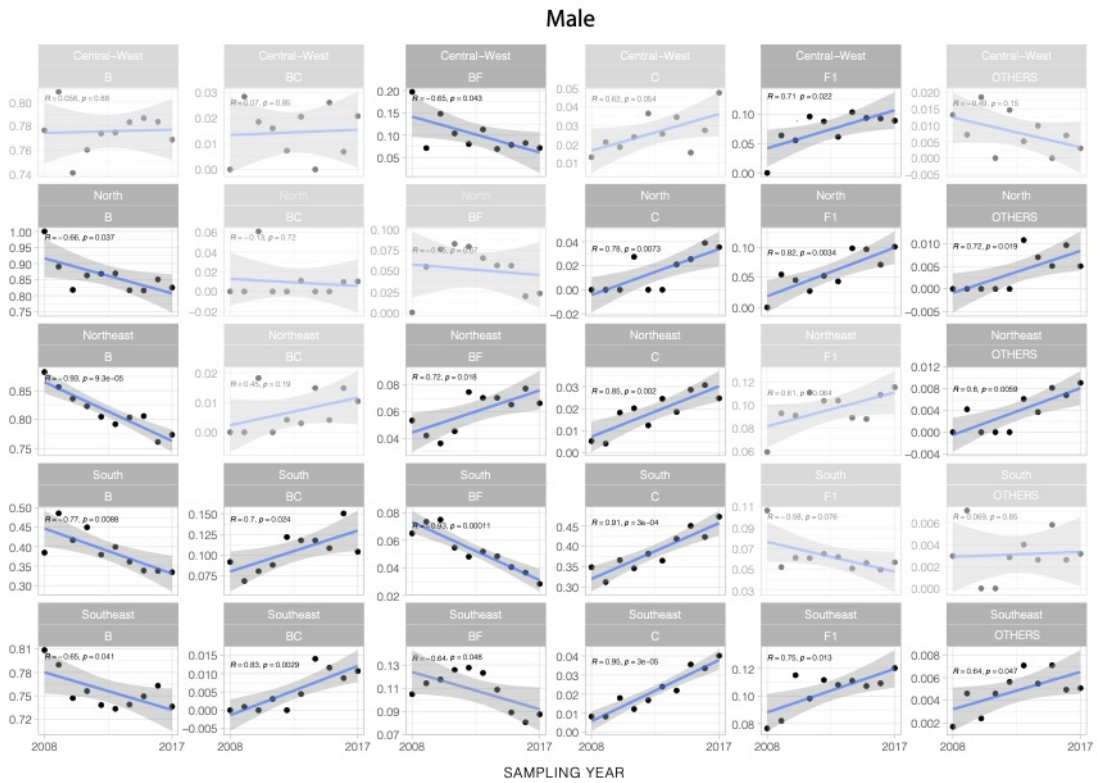
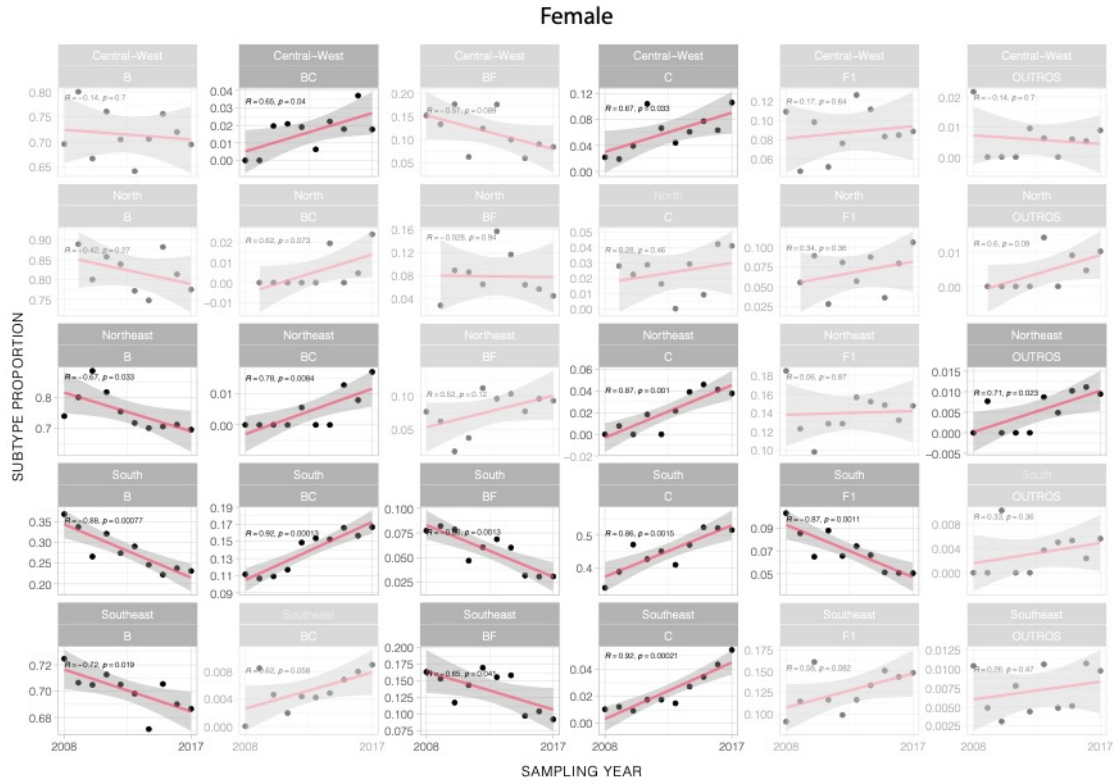
Supplementary figure 1. Age density distribution of all individuals diagnosed with AIDS in Brazil (red) between 2015-2017 and in the RENAGENO dataset (blue) in the same period.



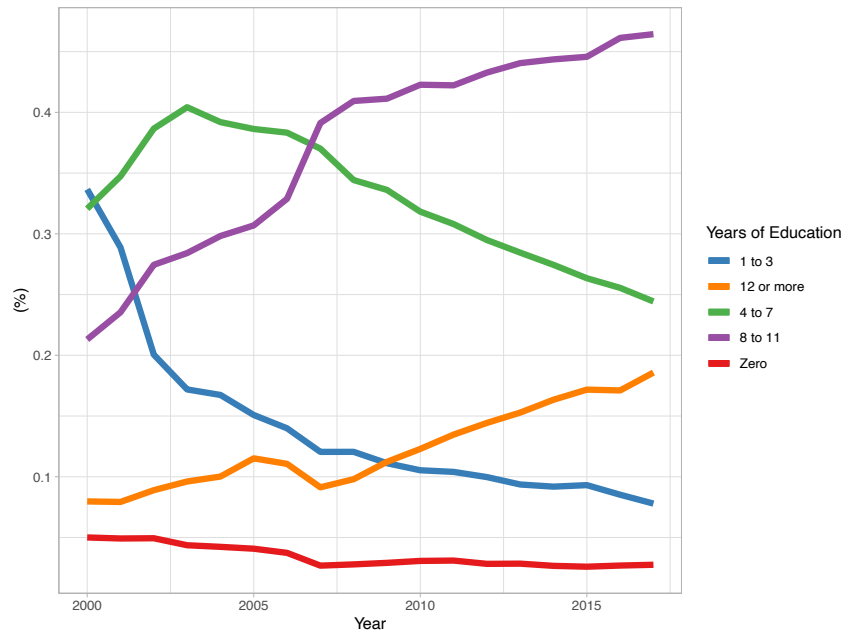
Supplementary figure 2. Proportion of the HIV-1B pandemic (B_{PANDEMIC}) and Caribbean (B_{CAR}) lineages per Brazilian states and regions. Plots and maps were drawn in R (version 4.0.3 - <https://www.r-project.org>) using the libraries ggplot2, tmap, sf and brazilmaps.



Supplementary figure 3. Relative risk of HIV-1 subtypes and main recombinant forms among RENAGENO male sampled population.



Supplementary figure 4. Pearson correlation between HIV-1 variant proportion and sampling year. Panels are organized by viral variant (columns) and country region (rows). Significant correlations are highlighted and coefficients and p values are shown.



Supplementary figure 5. New AIDS diagnosed individuals in Brazil per education status.