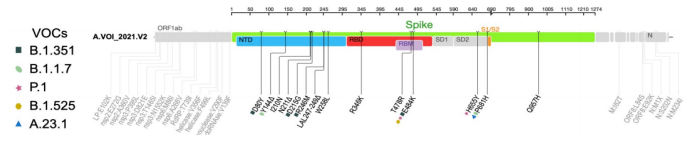


Table with columns for NCLP kód (PCR) →, NCLP kód (SEGS) →, NCLP kód (404), WHO, Pangolin lineage, Nextstrain, ECDC/CDC, and various amino acid positions (51354 to 51577). Rows list different SARS-CoV-2 variants like B.1.1.7, B.1.1.7+484K, B.1.1.7+549P, B.1.1.7+452K, B.1.351, B.1.28, P.1, A.23.1, B.1.318, B.1.324.1, B.1.615, B.1.617, B.1.617.1, B.1.617.2, B.1.617.3, B.1.618, B.1.620, B.1.621, B.1.1.519, B.1.214.2, A.23.1, C.16, C.36, B.1.351+P398L, B.1.351+ES16Q, AT.1, AV.1, and AV01V2. The table indicates the presence of specific mutations (marked with '+') across these variants.

trans - zvýšení transmissibility  
esc - únik před tlakem protilátek  
del11 mutace v individuálních lótech  
D614G - tabulka Q675H  
alelní změna  
N termínální doména - vazba protilátek  
blízko furinového štěpného místa - ovlivnění vazby na receptor  
dle jedné práce zvýšení patogenicity  
receptor binding doména  
INS = inserce  
spike mutation of interest



Supplemental Fig S4: Genome map of the A.VOI.V2, with mutations annotated by presence in other VOCs

A novel variant of interest of SARS-CoV-2 with multiple spike mutations detected through travel surveillance in Africa  
Auteurs: de Oliveira T, Lutsaruta S, Niengrong J, Morais J, Pissao JP, Neto Z, Afonso P, Miranda J, David K, Ingles L, Amilton P, A P R R C, Freitas H R, Mufinda F, Tessema K S, Tegally H, San E I, Wilkinson E, Giandhari J, Pillay S, Giovannetti M, Naidoo V, Katzourakis A, Ghafari M, Singh L, Tshibangu D, Martin D, Lessells B.