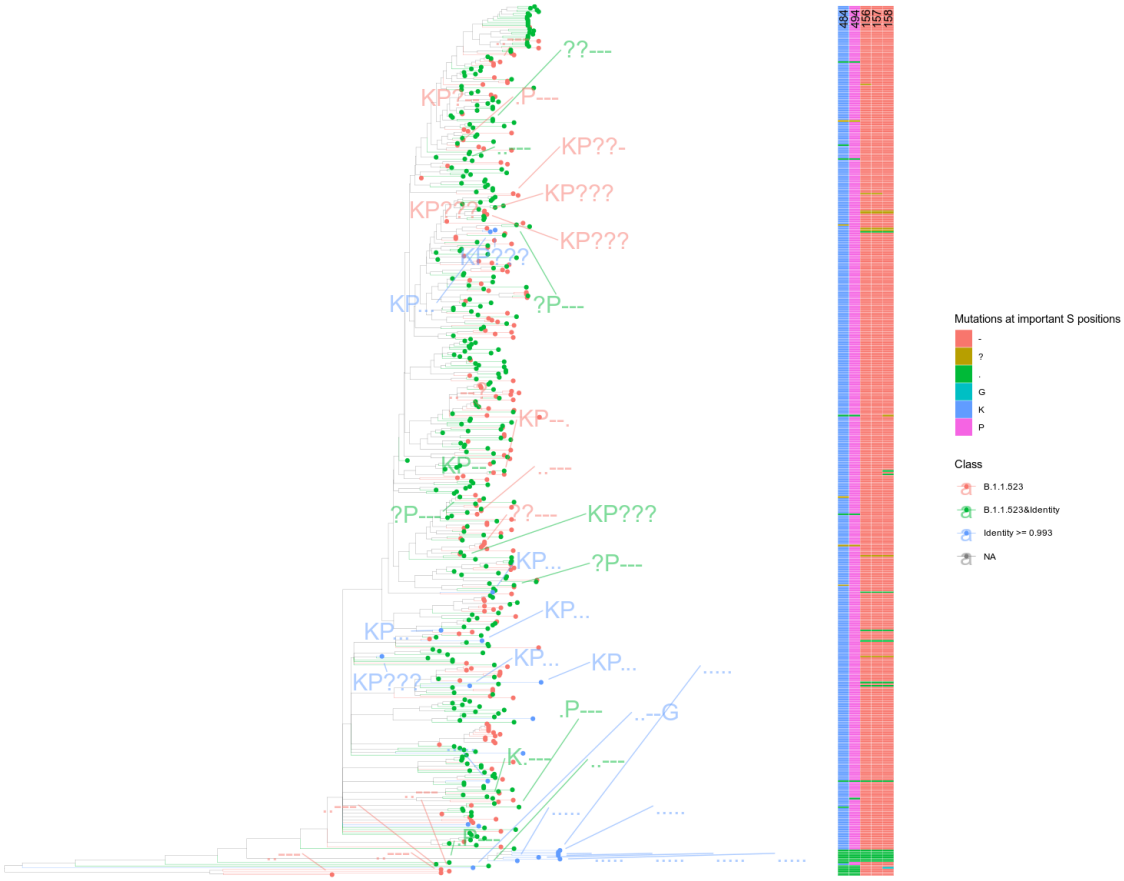

Figure S1. Maximum likelihood tree based on the genomic sequences that are classifiable as B.1.1.523 lineage together with the closest sequences based on identity search. The heatmap indicates residues at the 484,494 and 156-158 positions. The five letter length labels indicate cases and corresponding haplotypes where the residues do not match the expected ones for the B.1.1.523 lineage.