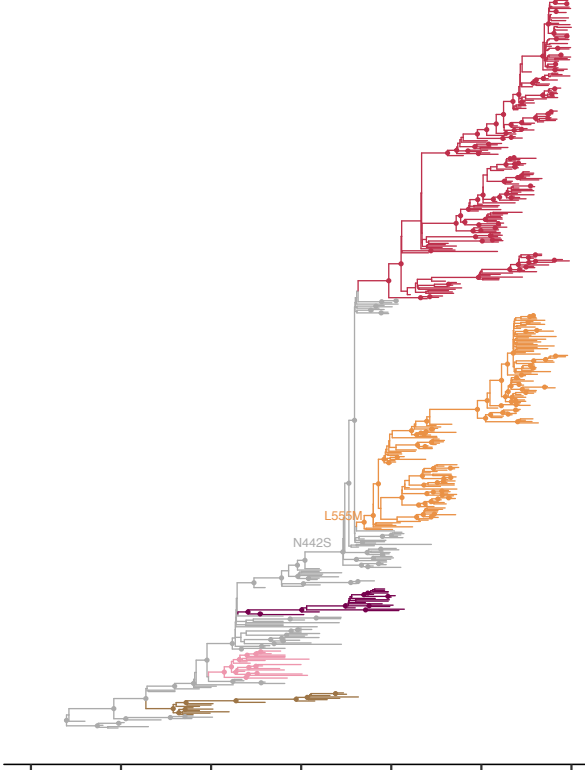
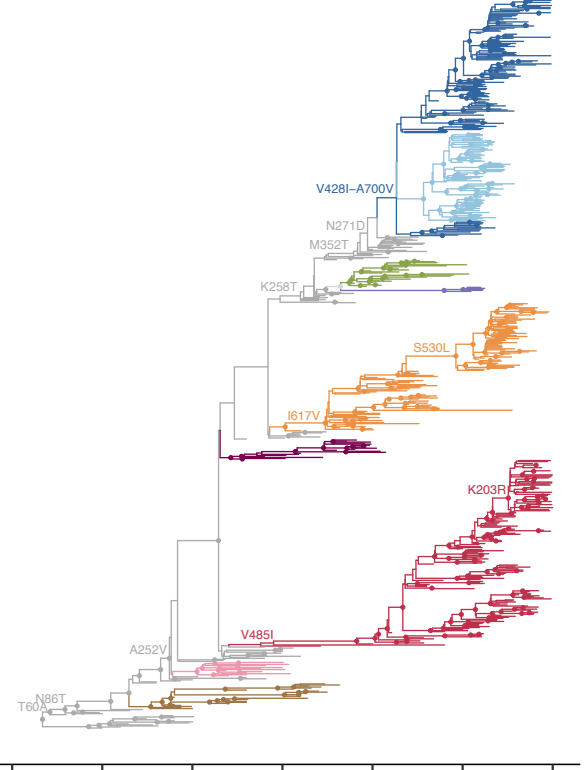
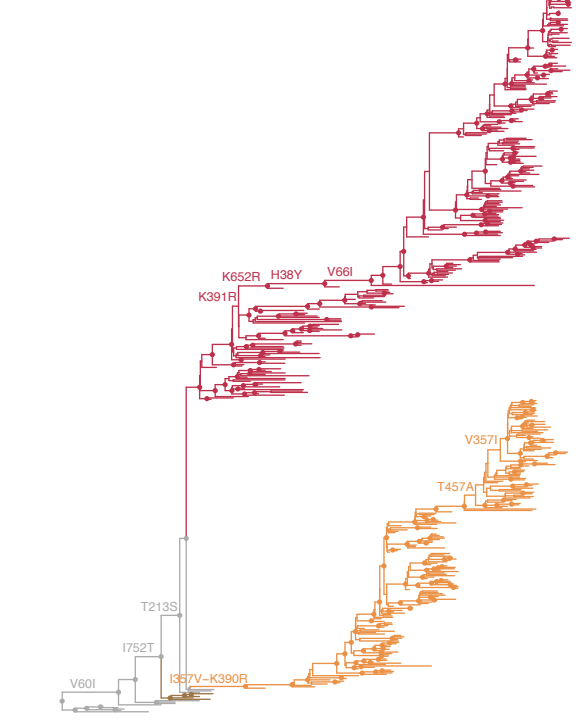
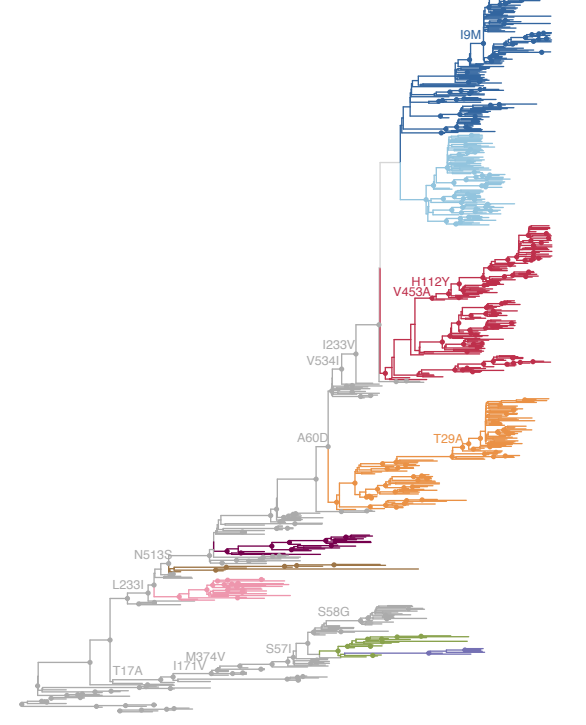
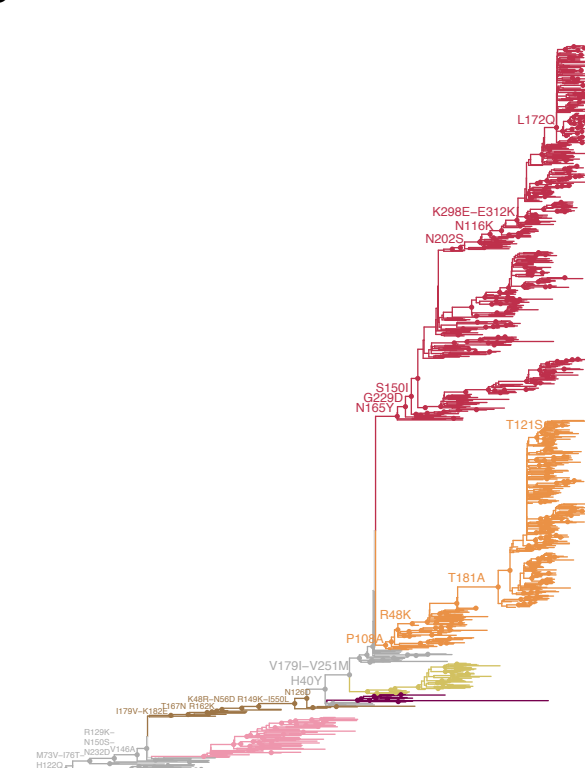
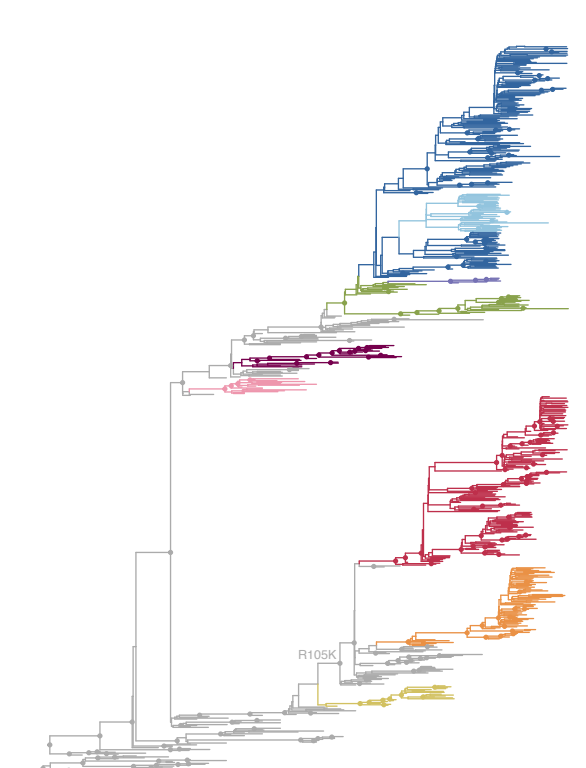
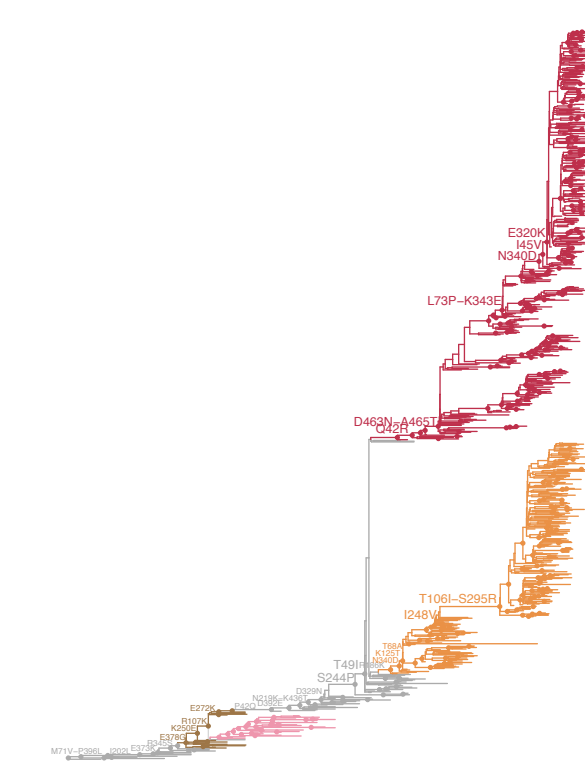
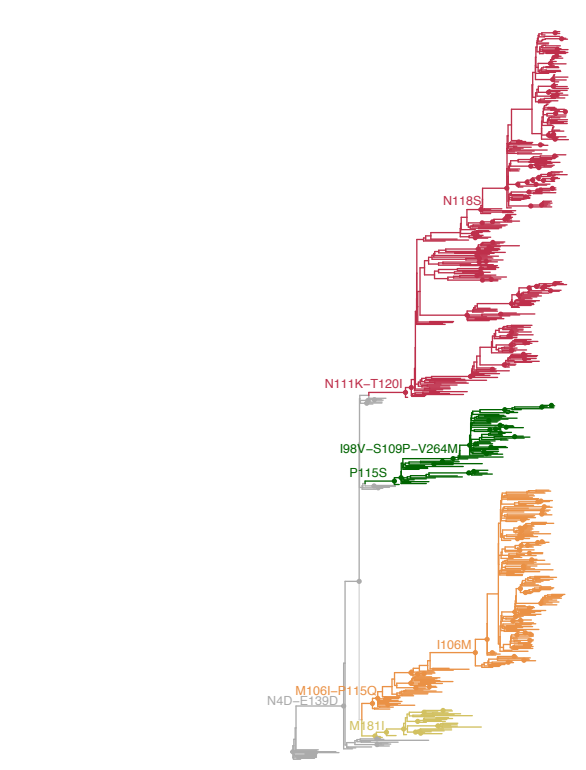
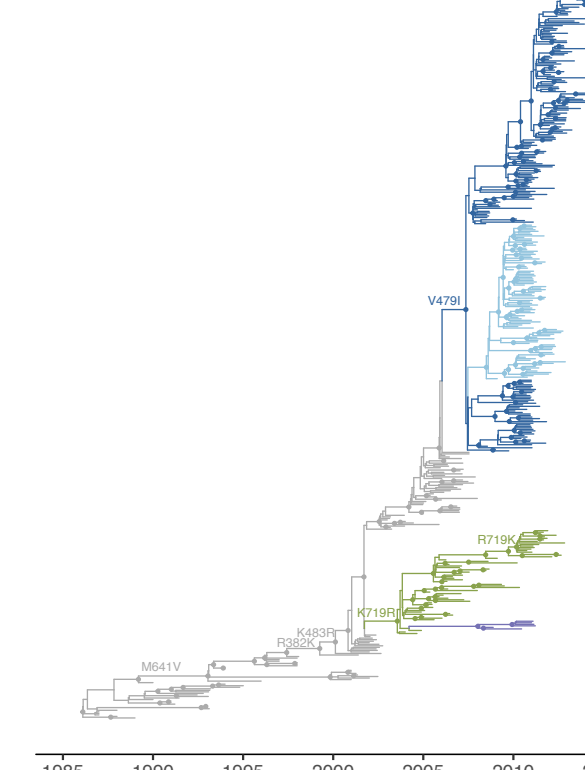
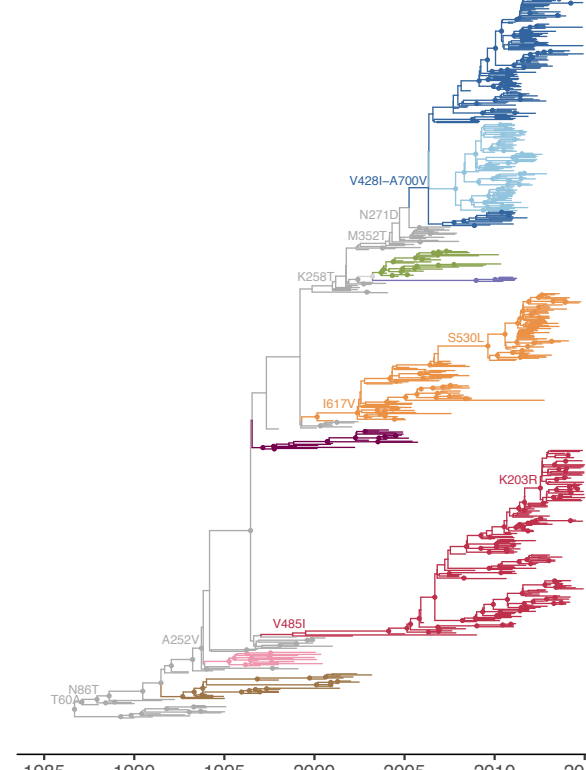
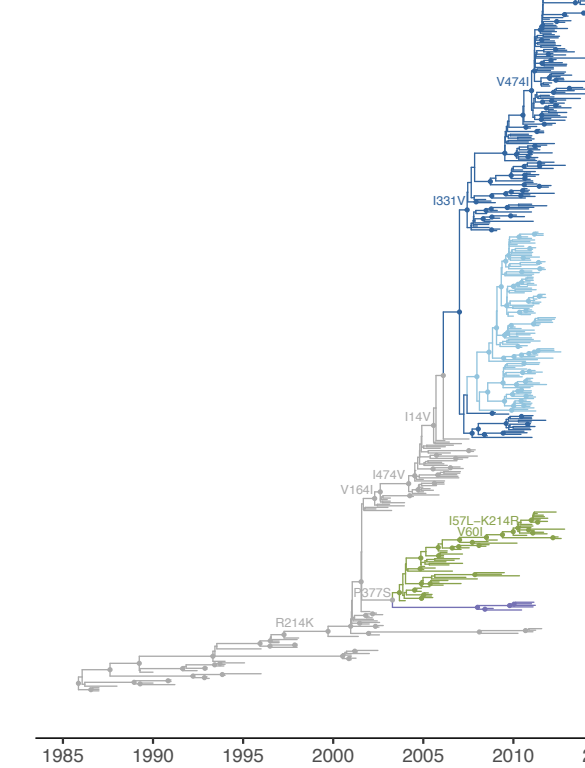
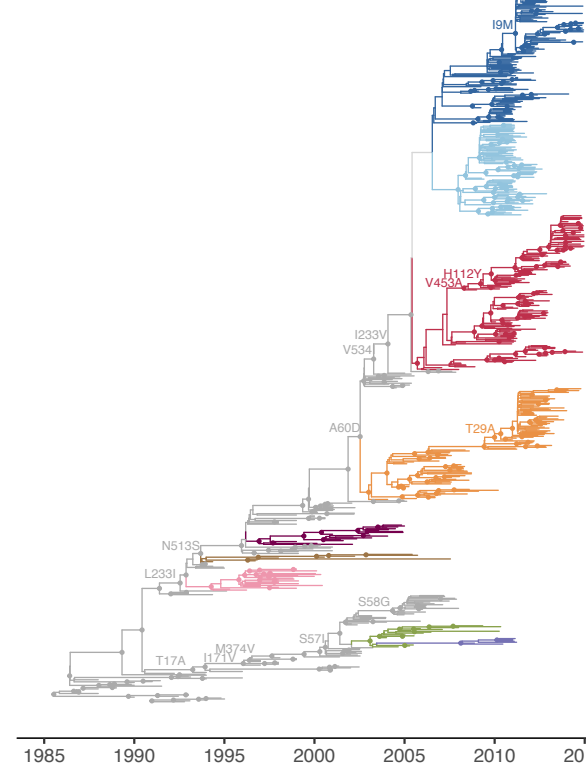
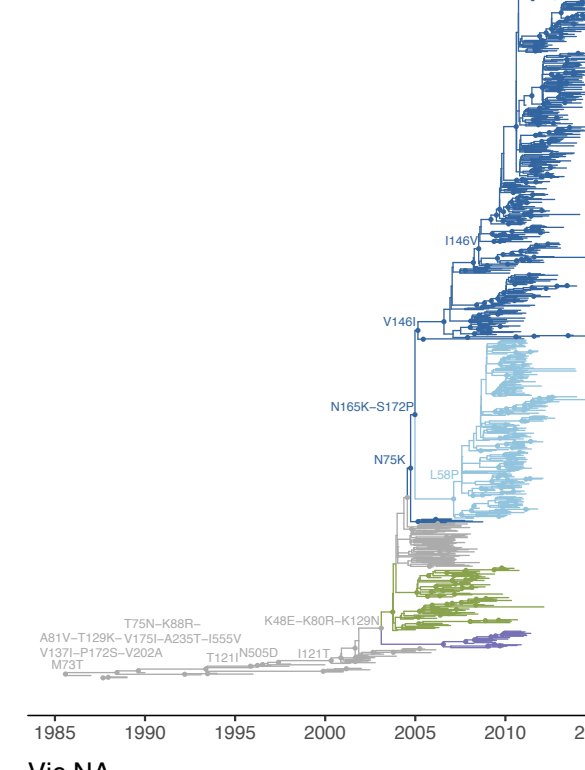
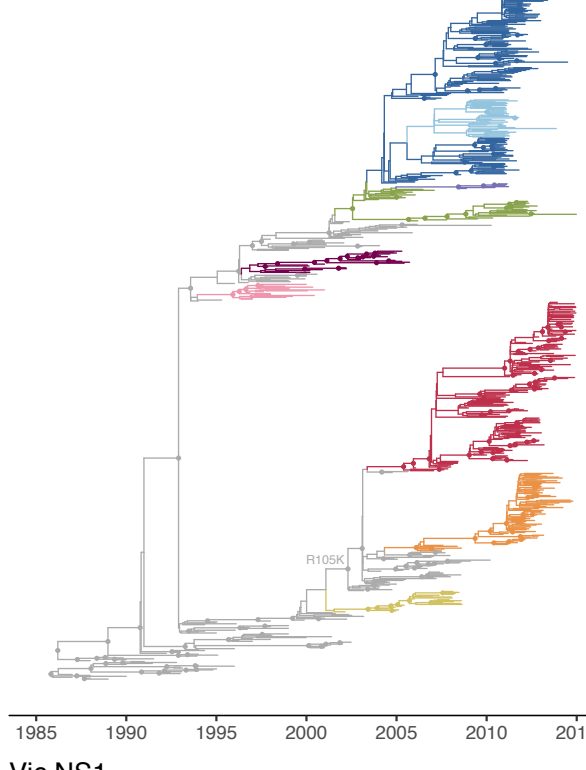
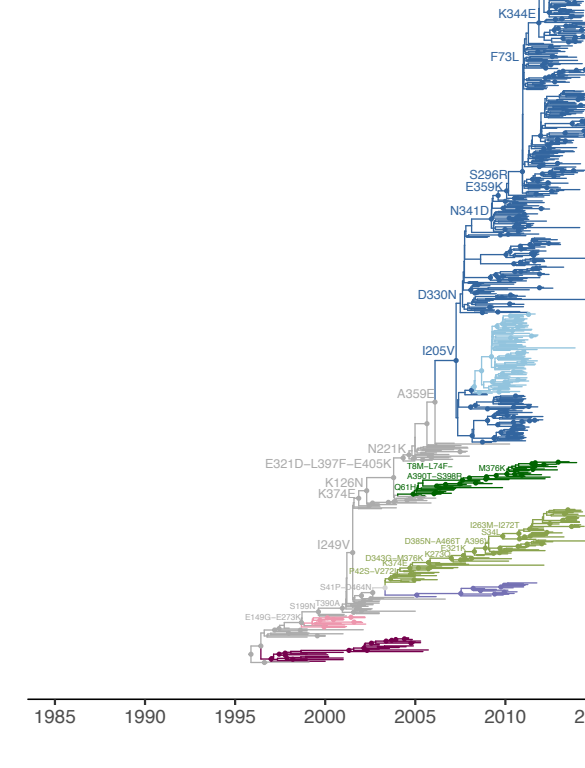
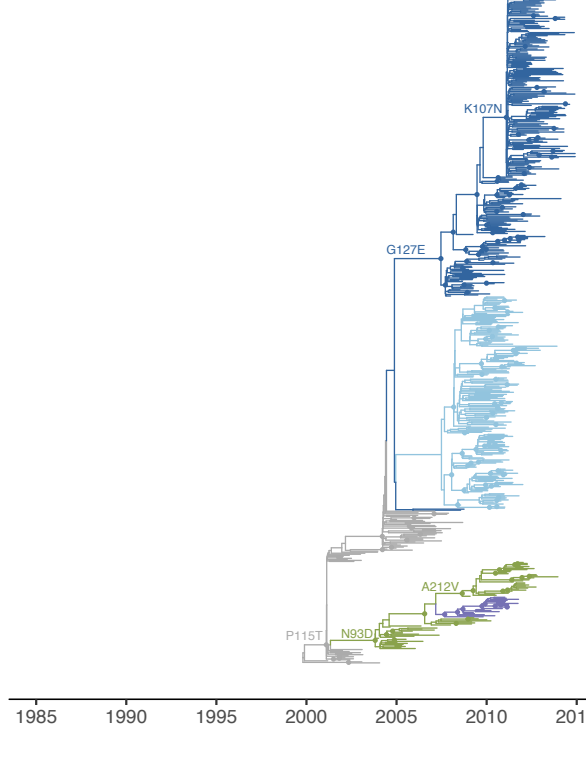


A Yam PB2**Yam/Vic PA****Yam PB1****Yam/Vic NP****B Yam HA****Yam/Vic M1****Yam NA****Yam NS1****C Vic PB2****Yam/Vic PA****Vic PB1****Yam/Vic NP****D Vic HA****Yam/Vic M1****Vic NA****Vic NS1**

S1 Fig. Maximum-clade credibility trees for all major influenza B virus genes. Lineage-specific gene phylogenies shown for (A) Yamagata PB2, PB1, PA, NP, (B) Yamagata HA, NA, M1, NS1, (C) Victoria PB2, PB1, PA, NP, and (D) Victoria HA, NA, M1, NS1. Branches of phylogenies are labeled with amino acid substitutions occurring along the phylogenetic ‘trunk’ and are colored by well-supported clade distinctions. Nodes with greater than 0.70 posterior probability support are shown with circle node shapes.