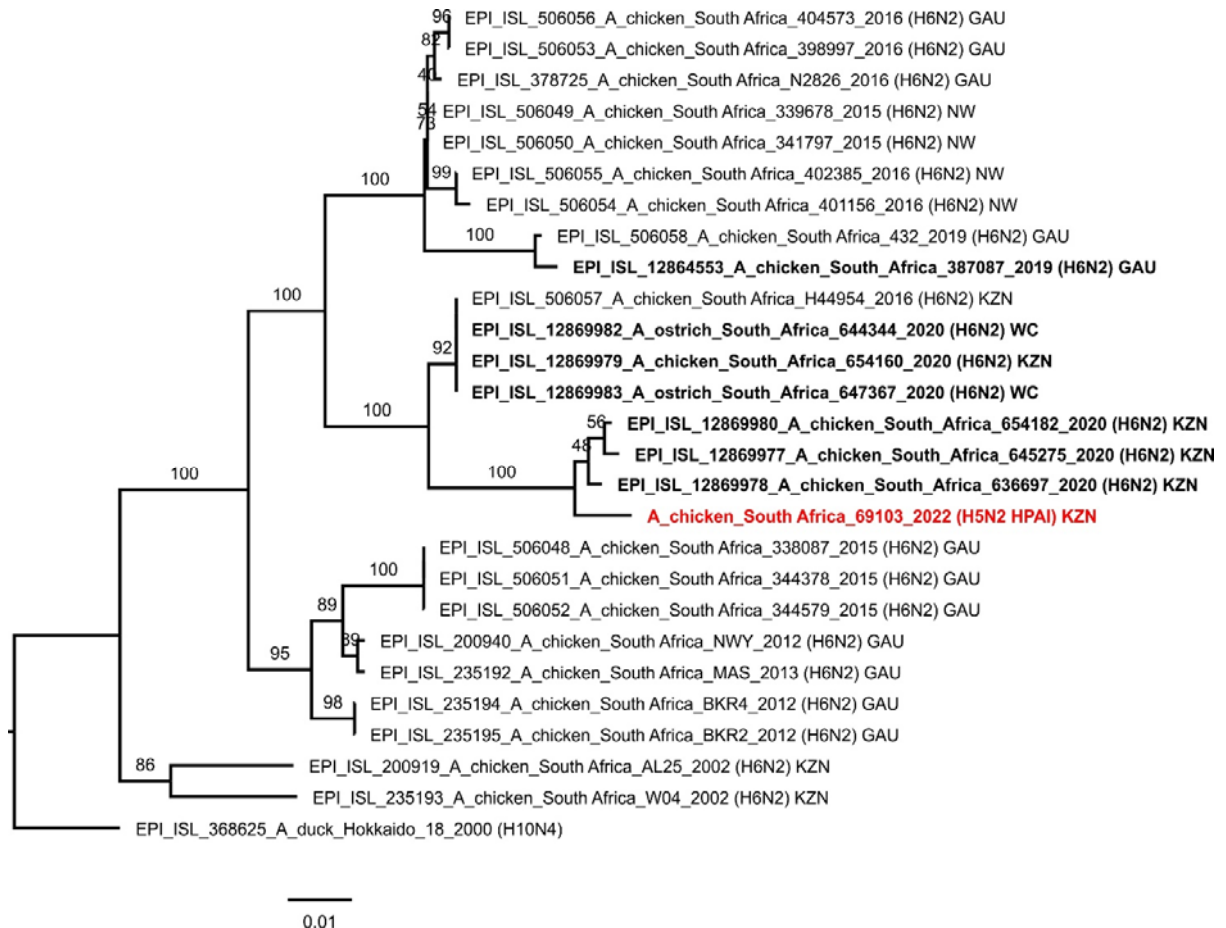
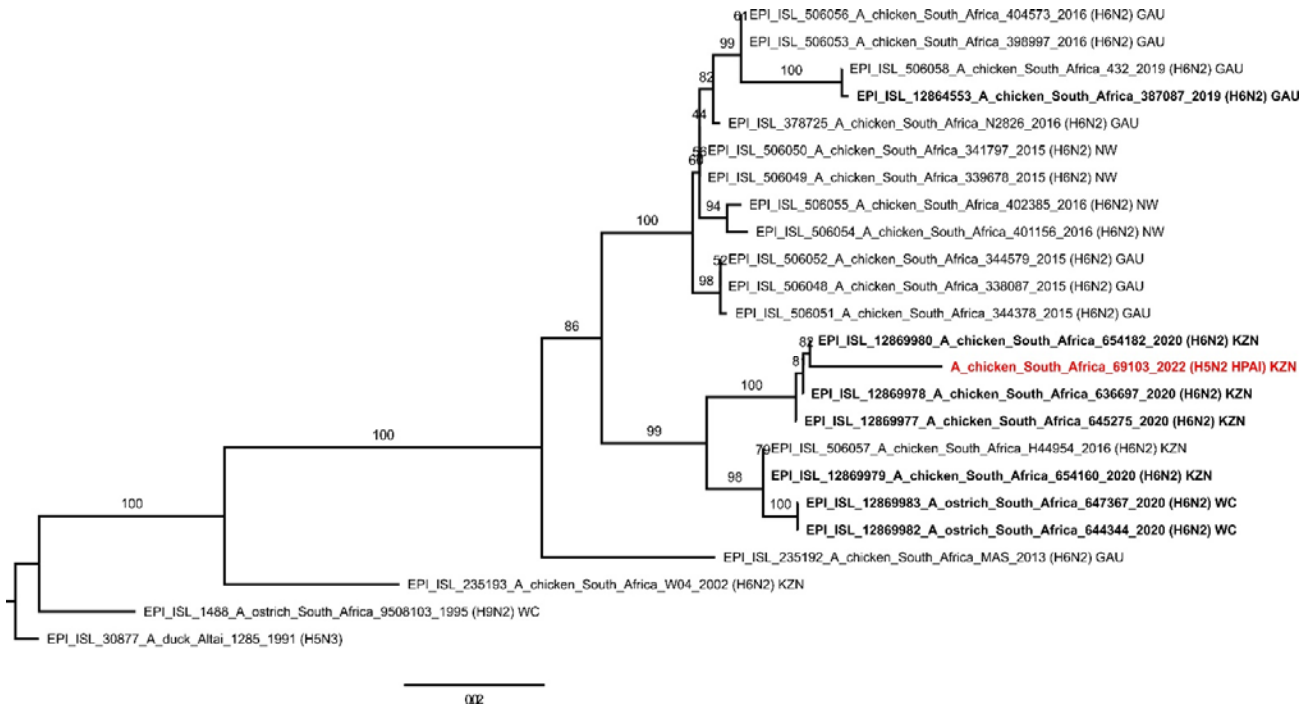


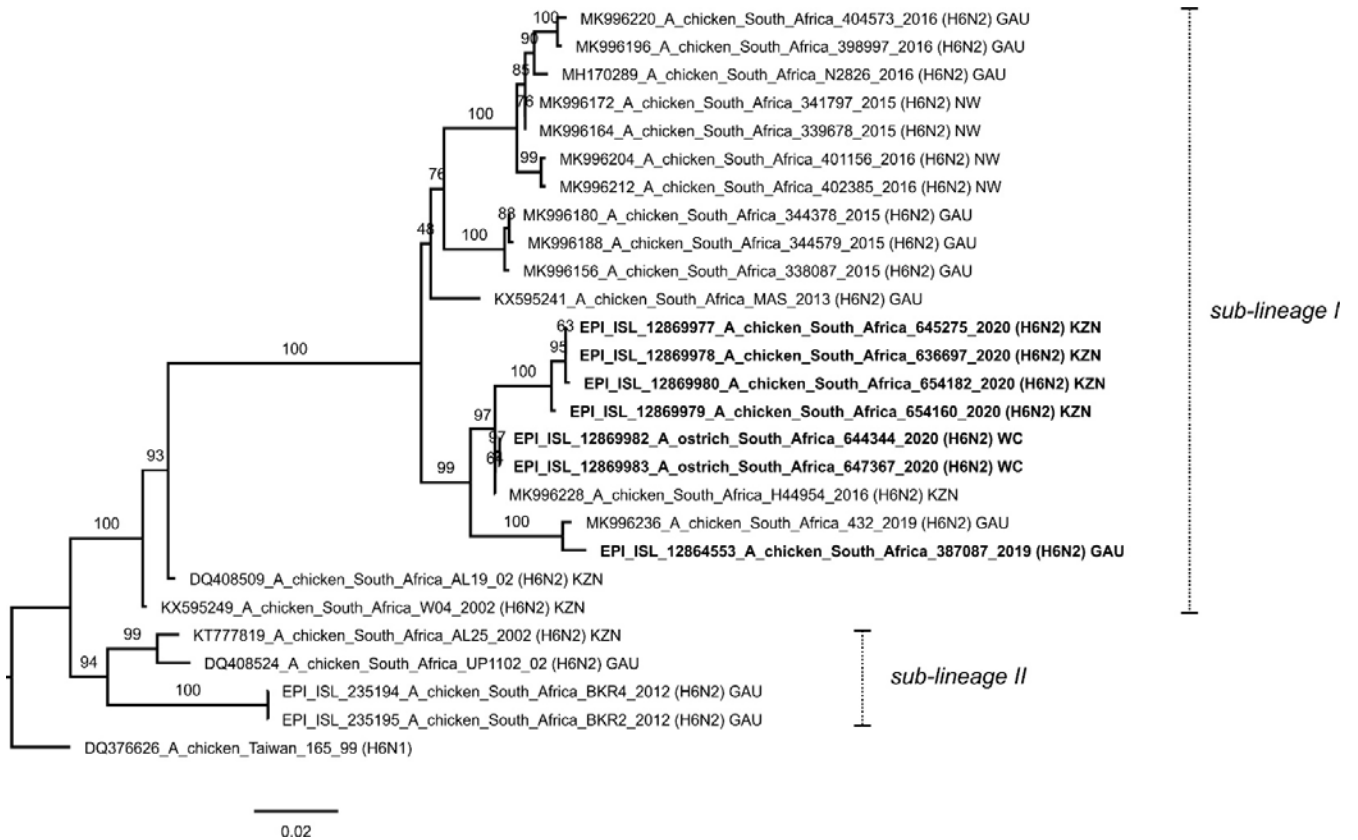
(i) PB2



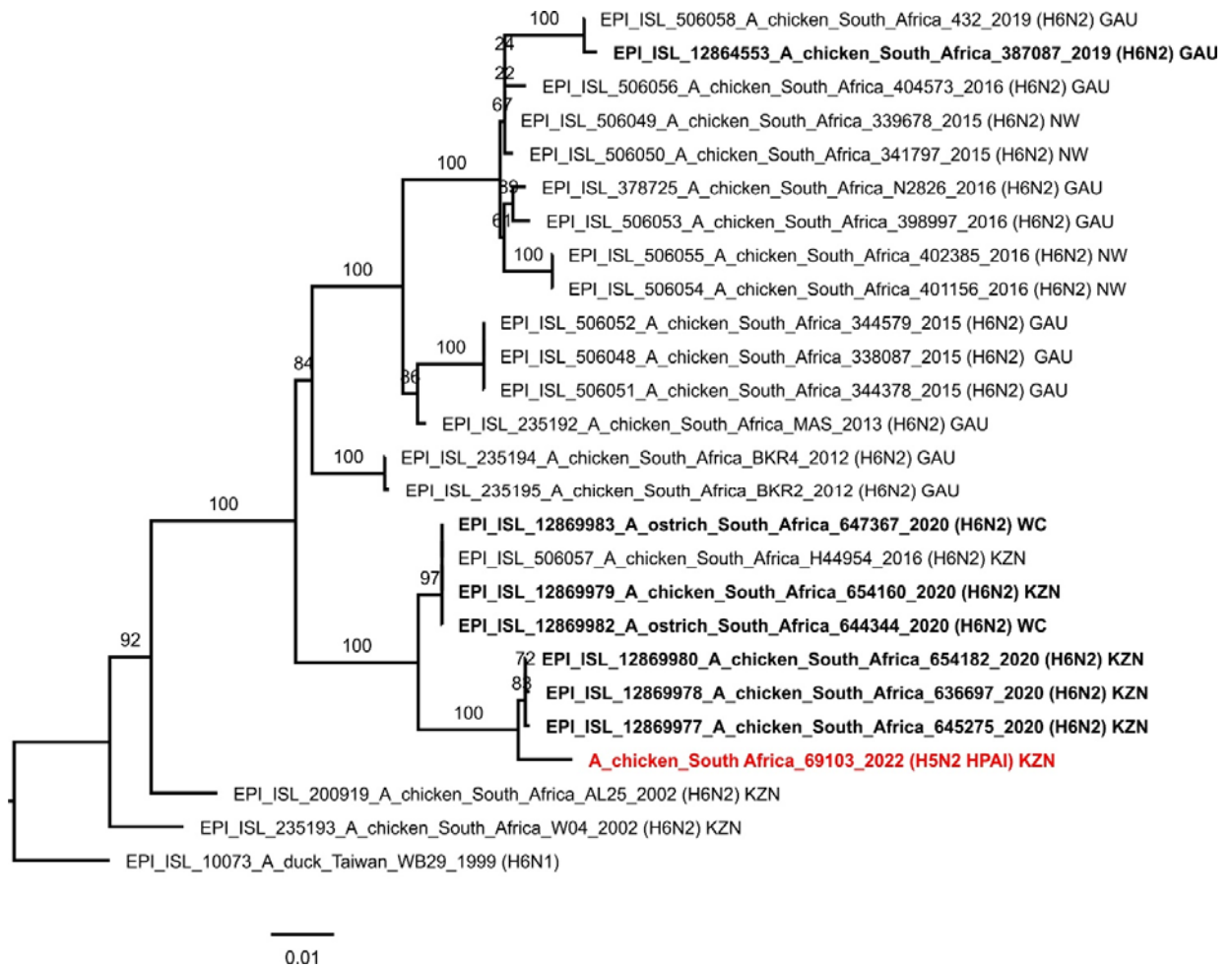
(ii) PB1



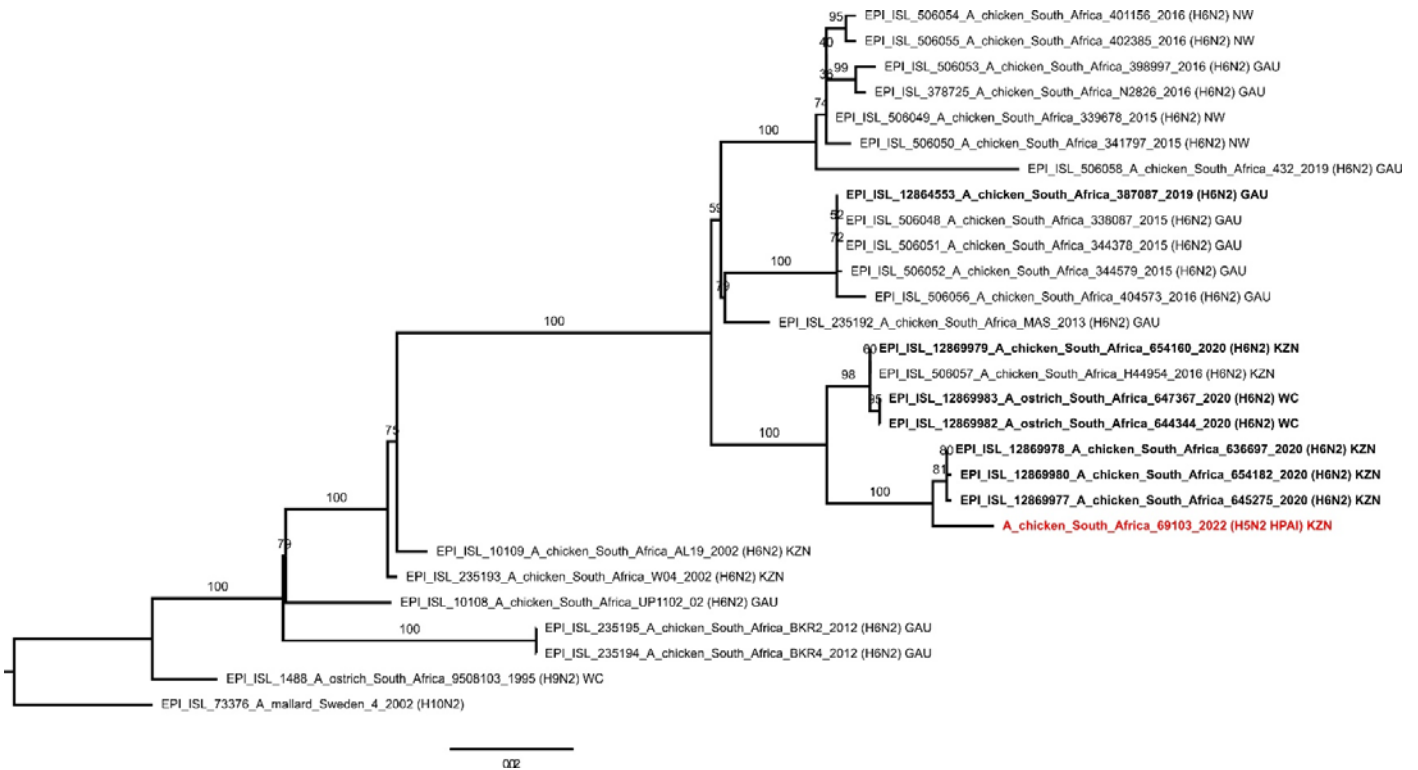
(iii) PA



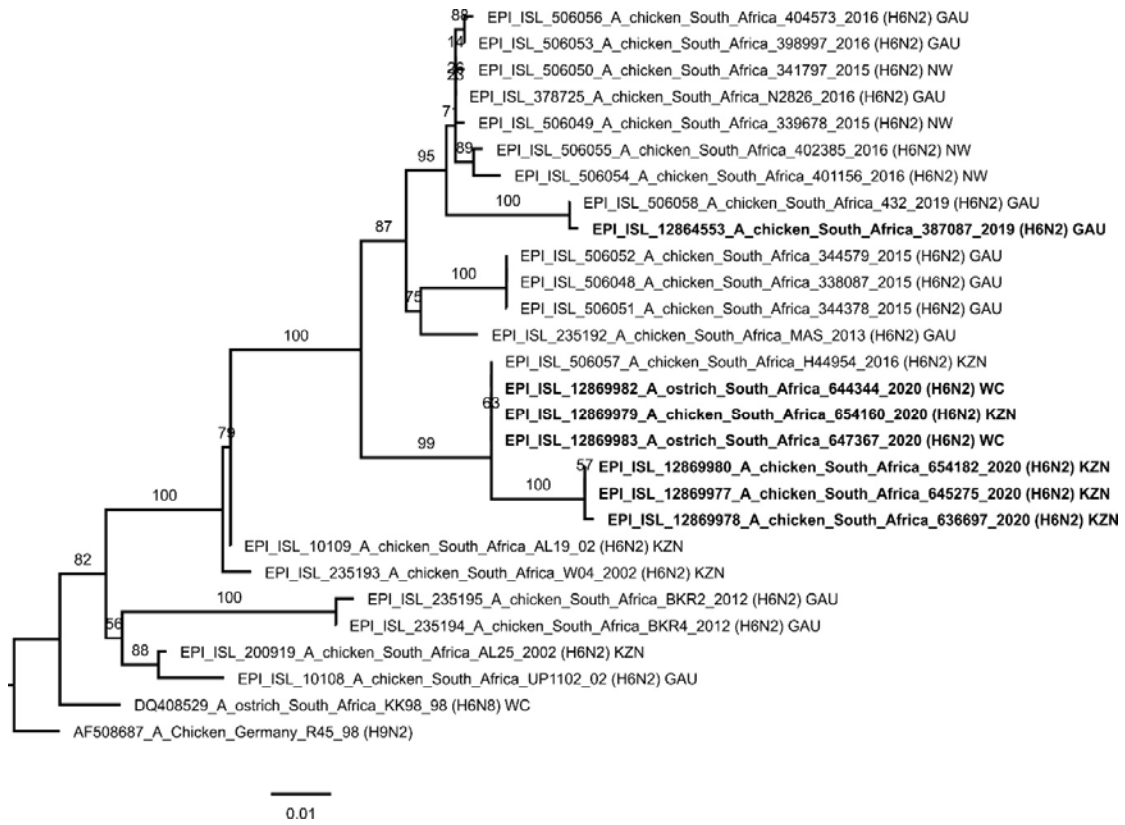
(iv) HA



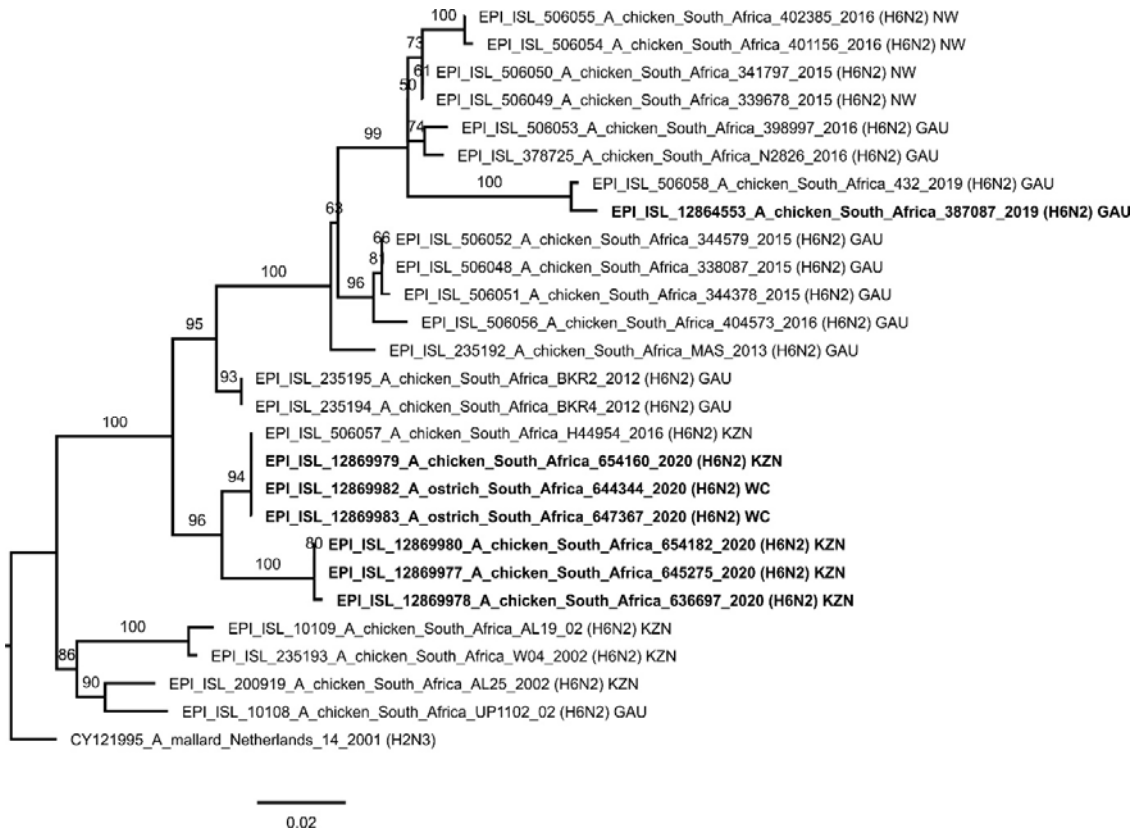
(v) NP



(vi) NA



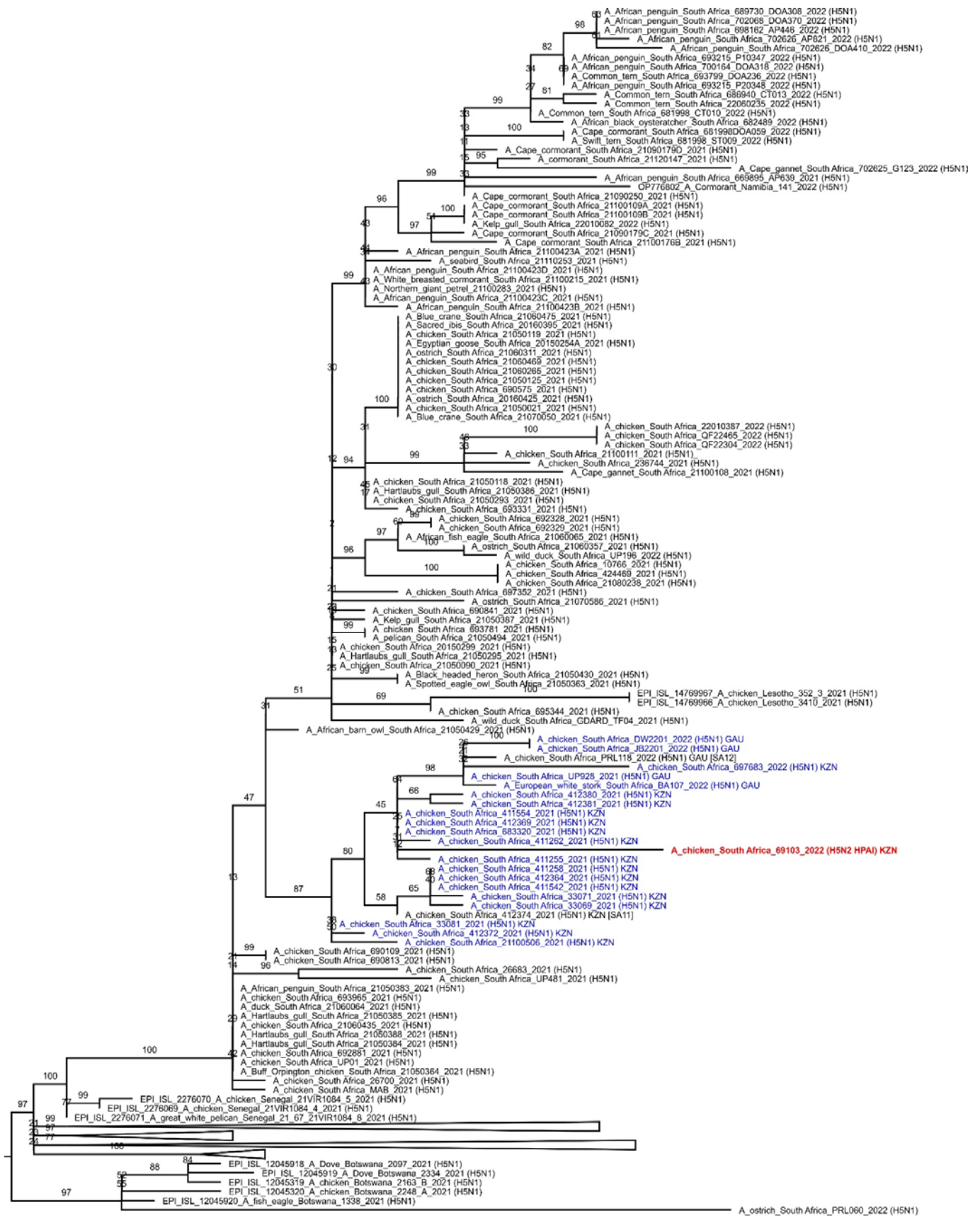
(vii) M

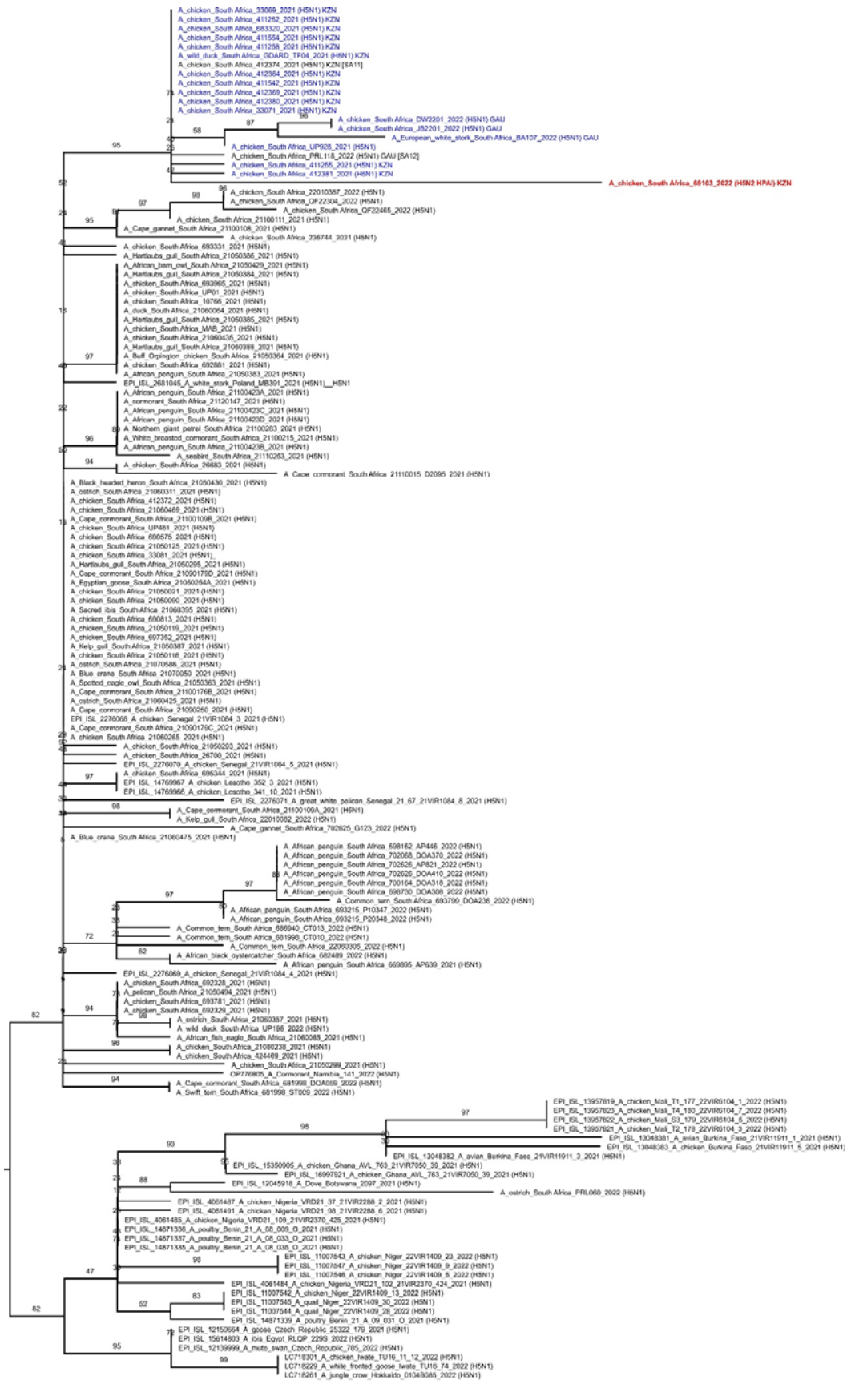


(viii) NS

**Supplemental Figure 1(a).** Maximum likelihood phylogenetic trees for the eight genome segments of South African H6N2 viruses and the H5N2 HPAI reassortant virus from KwaZulu-Natal province (in red). Viruses sequenced in this study are in boldface. A/chicken/South Africa/654160/2020 and A/ostrich/South Africa/647367/2020 are omitted from the PB2 tree due to their partial sequences. The provincial locations for each virus are abbreviated as follows: GAU- Gauteng; KZN- KwaZulu-Natal; NW- North-West; WC-Western Cape.







(ii) M



(iii) NS

**Supplemental Figure 1(b).** Maximum likelihood phylogenetic trees for the HA, M and NS genome segments of South African clade 2.3.4.4b H5N1 viruses and the H5N2 HPAI reassortant virus (in red). The members of



sub-genotype SA10 are in blue. The provincial locations for the viruses in sub-genotype SA10 are abbreviated as follows: GAU- Gauteng; KZN- KwaZulu-Natal; WC-Western Cape.