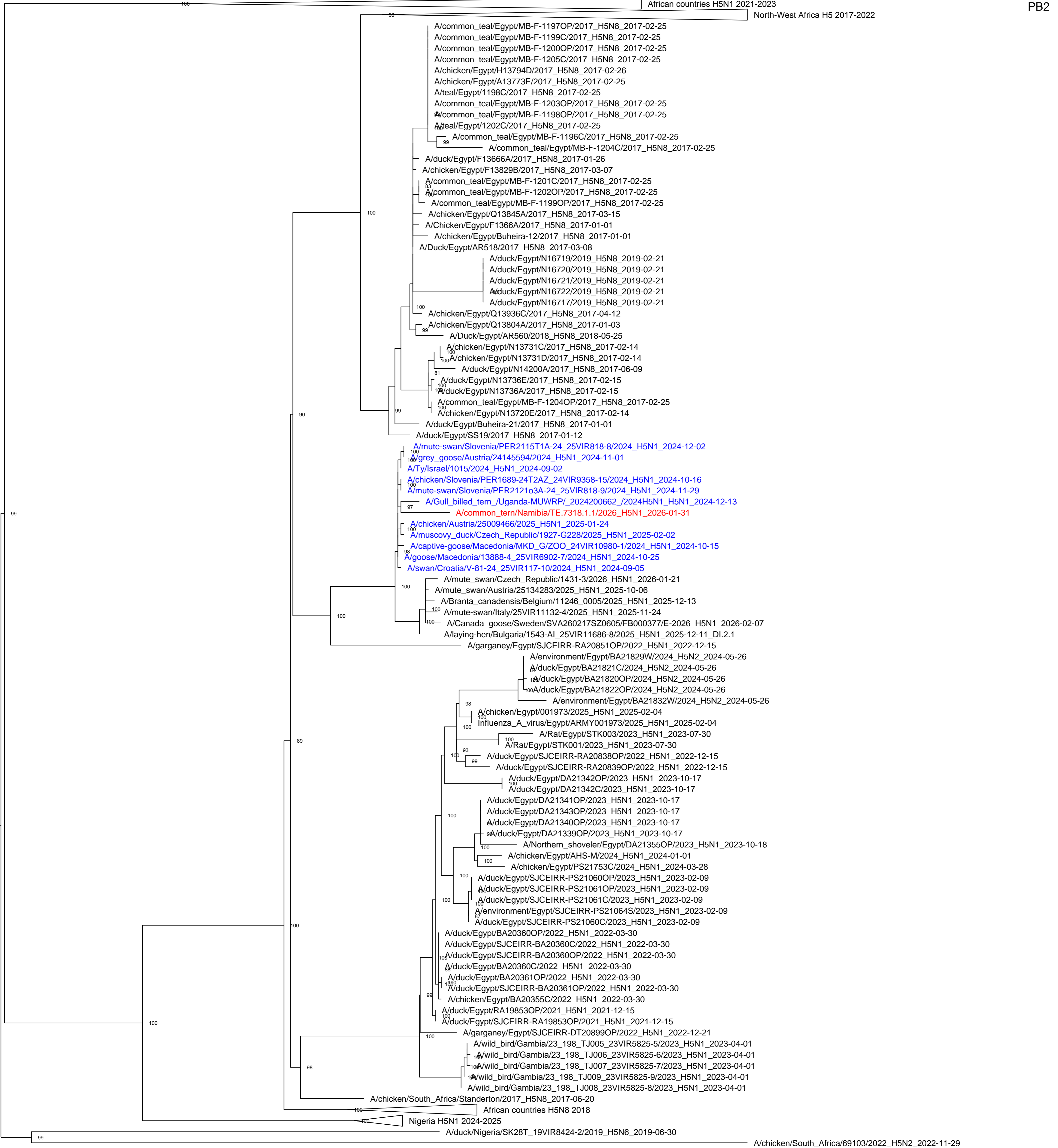
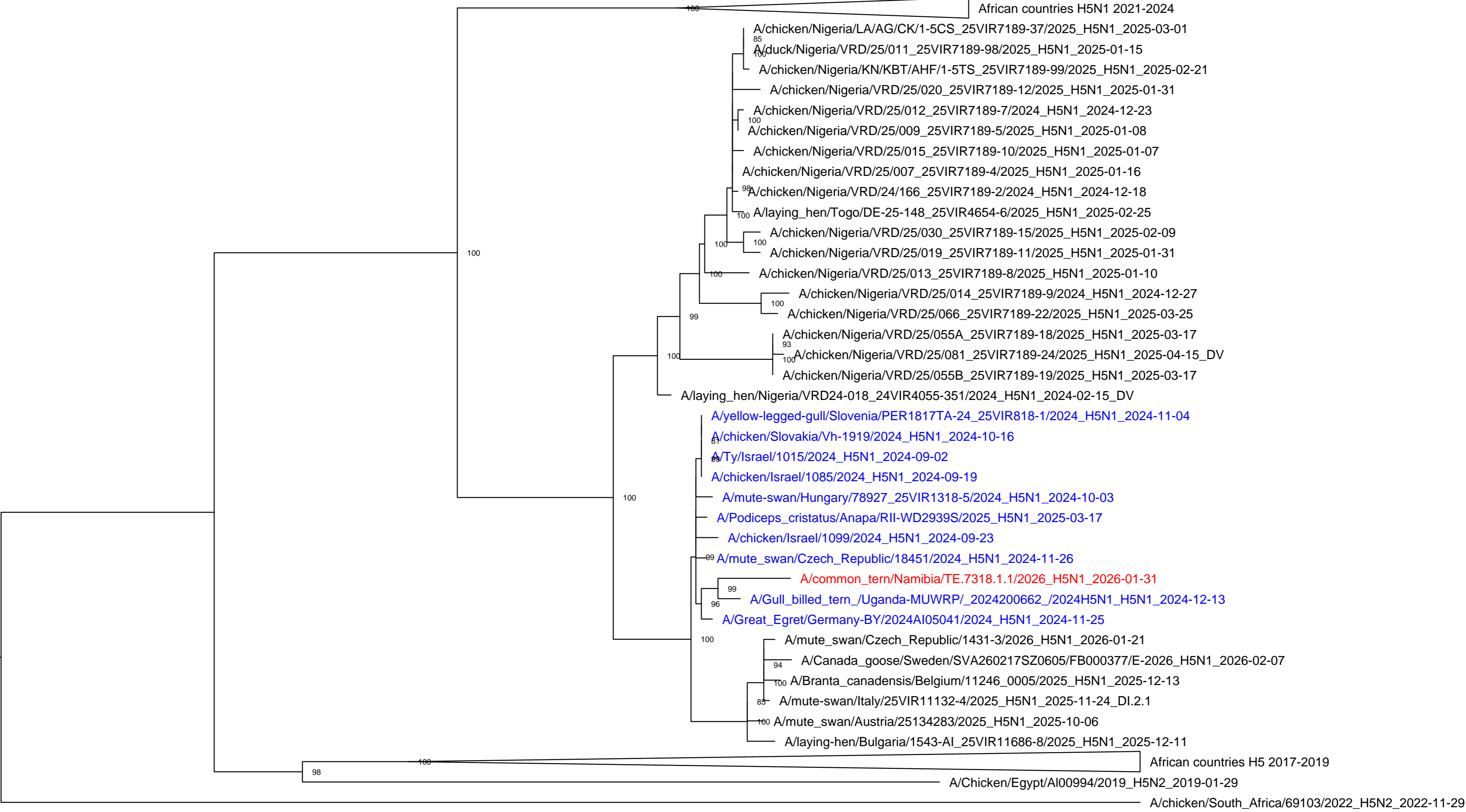


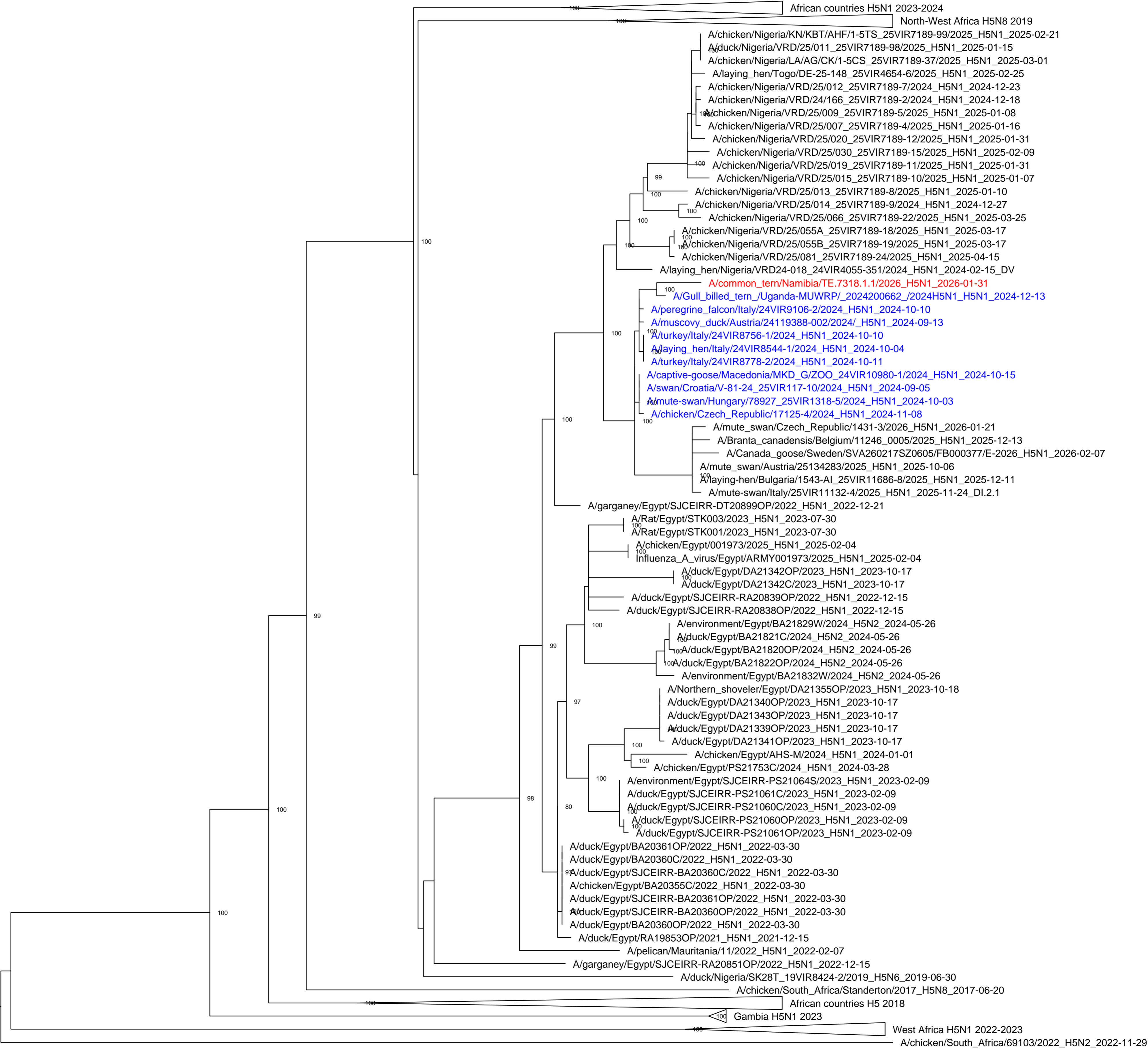
# VETERINARIA RIVISTA DI SANITÀ PUBBLICA VETERINARIA **ITALIANA**

**Supplementary material**



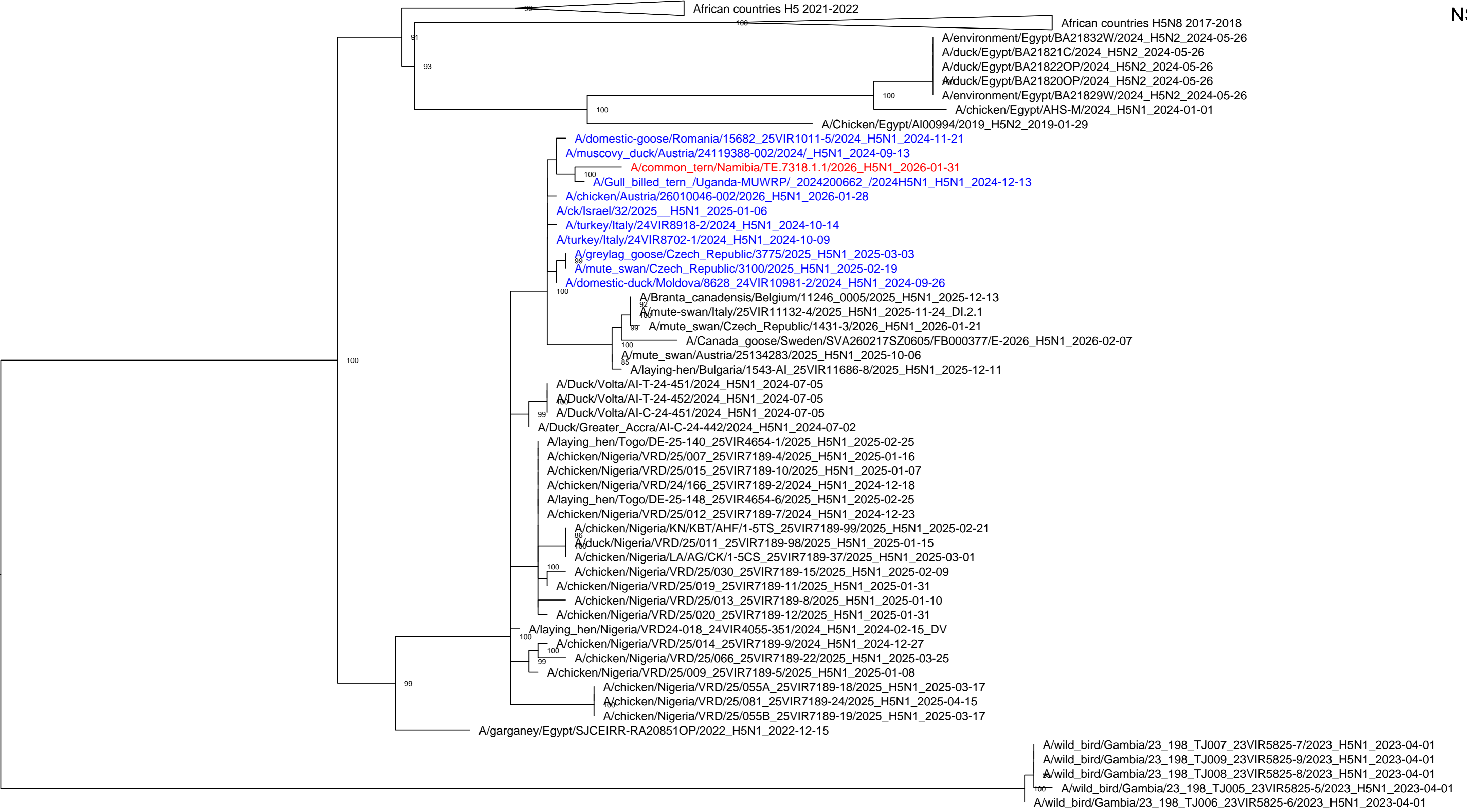












SM Figure 1. Maximum-likelihood phylogenetic trees based on the PB1, PB2, PA, NP, MP, and NS gene segments of the HPAI A(H5N1) virus detected in Namibia in January 2026, highlighted in red, and related EA-2024-DI strains identified by BLAST analysis, highlighted in blue. Ultrafast bootstrap values greater than 80 are indicated next to the nodes.