



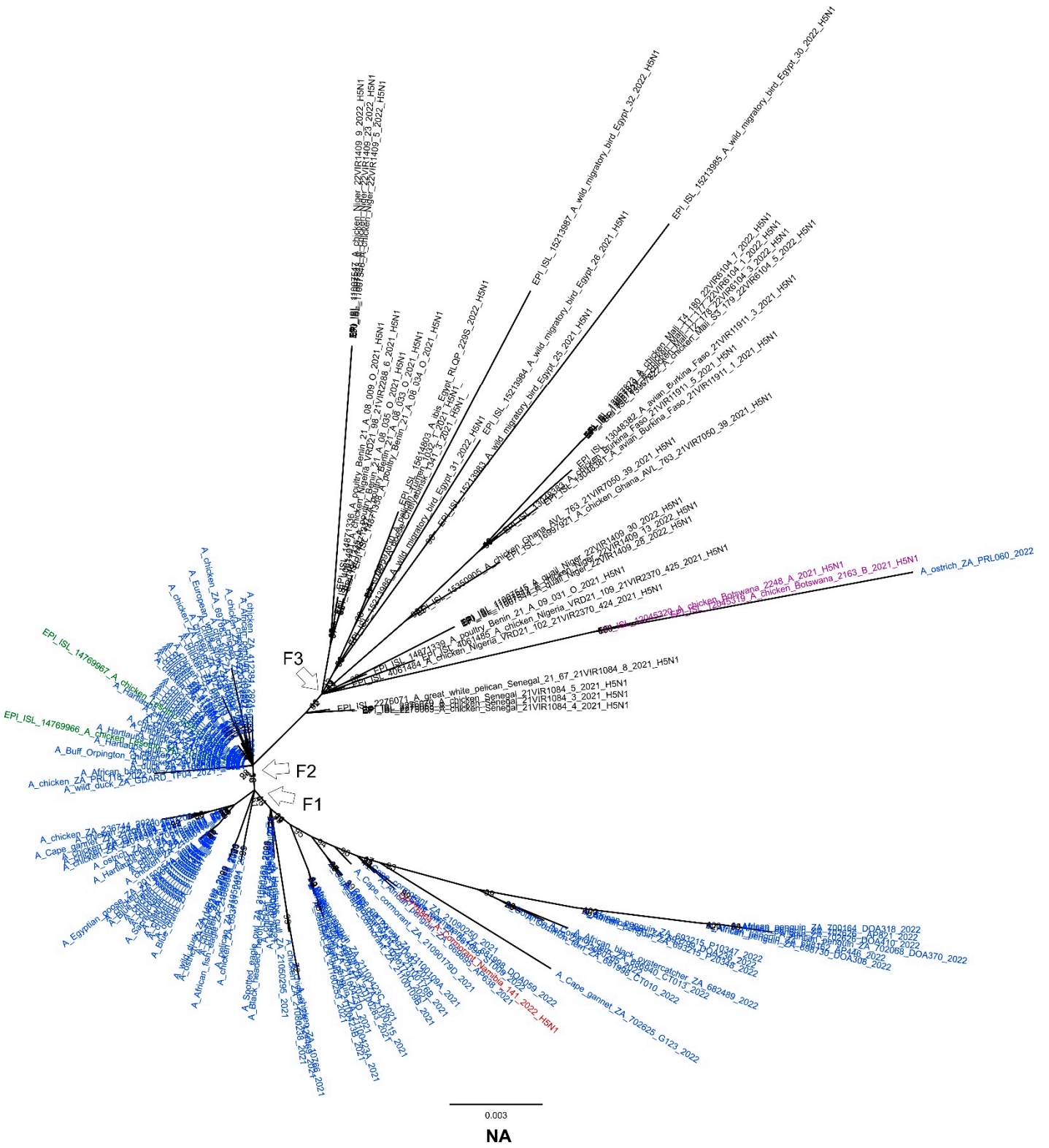






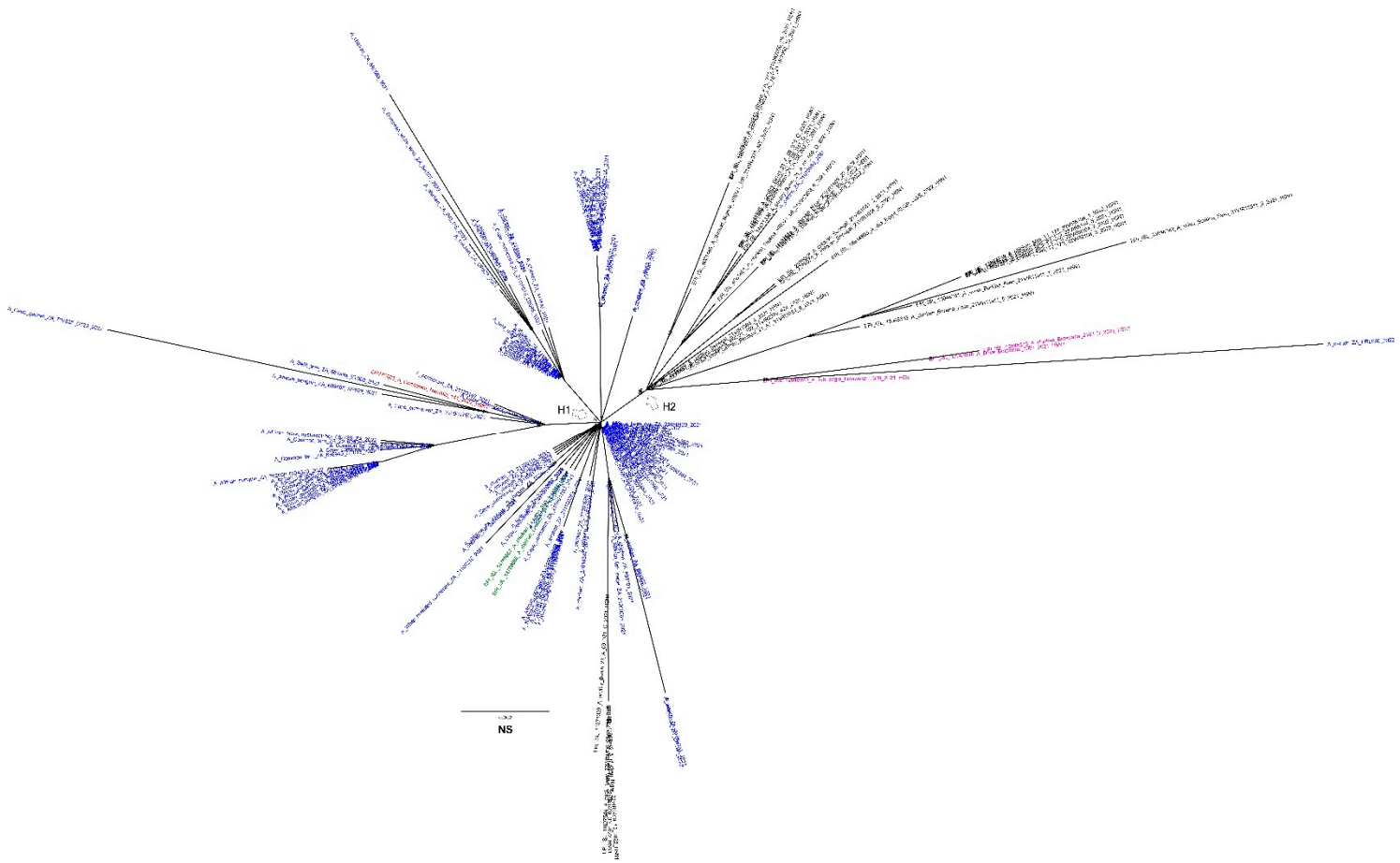


3(f)





3(h)



**Figure S3a–h.** Radial views of the Maximum Likelihood phylogenetic trees of the individual genome segments of H5N1 HPAI viruses used to identify subclades, as shown by the arrows. Letters A to H were used for the PB2, PB2, PA, HA, NP, NA, M and NS genes, respectively. South African viruses are highlighted in blue, Namibia in red, Lesotho in green and Botswana in magenta.