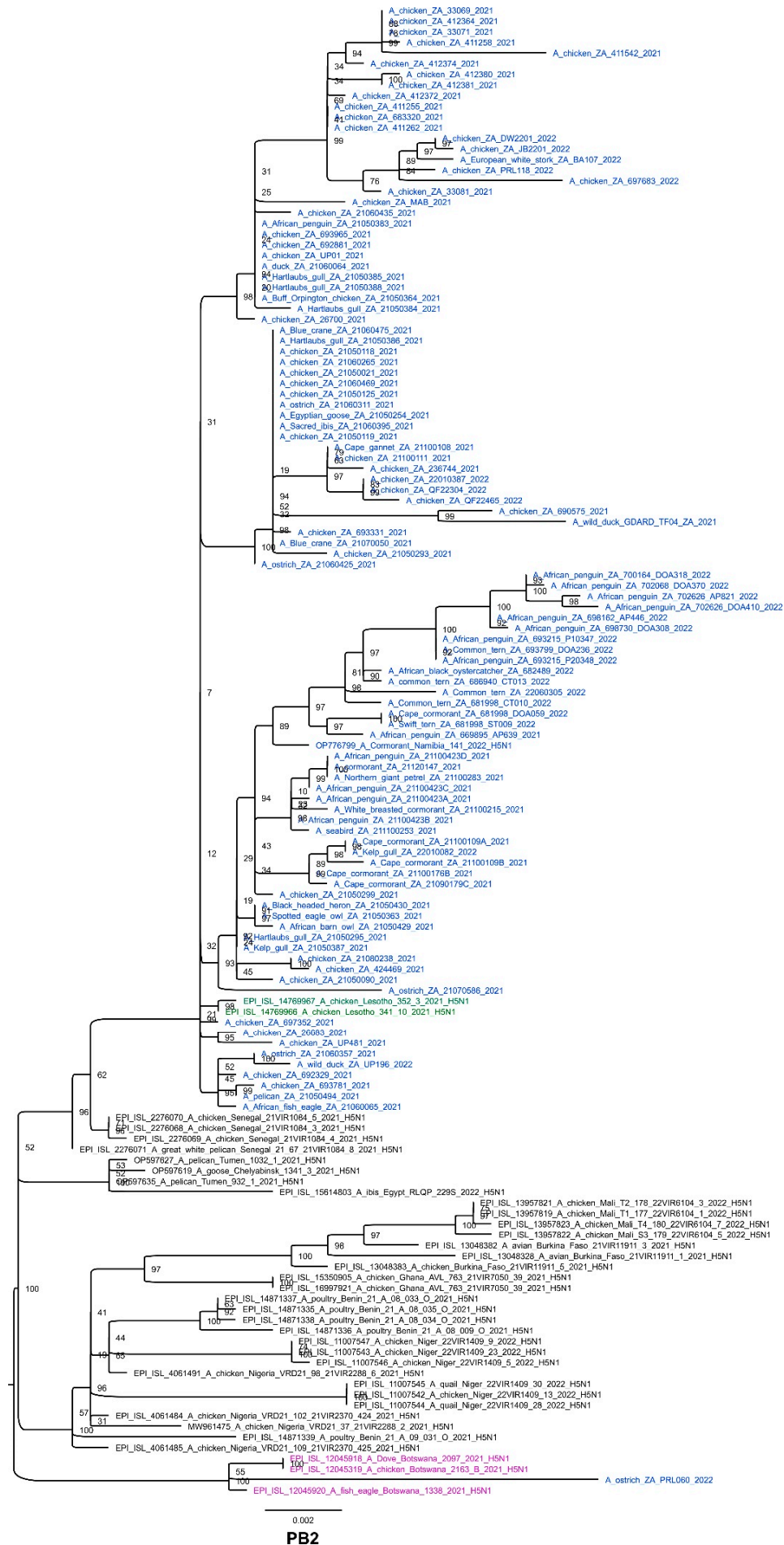
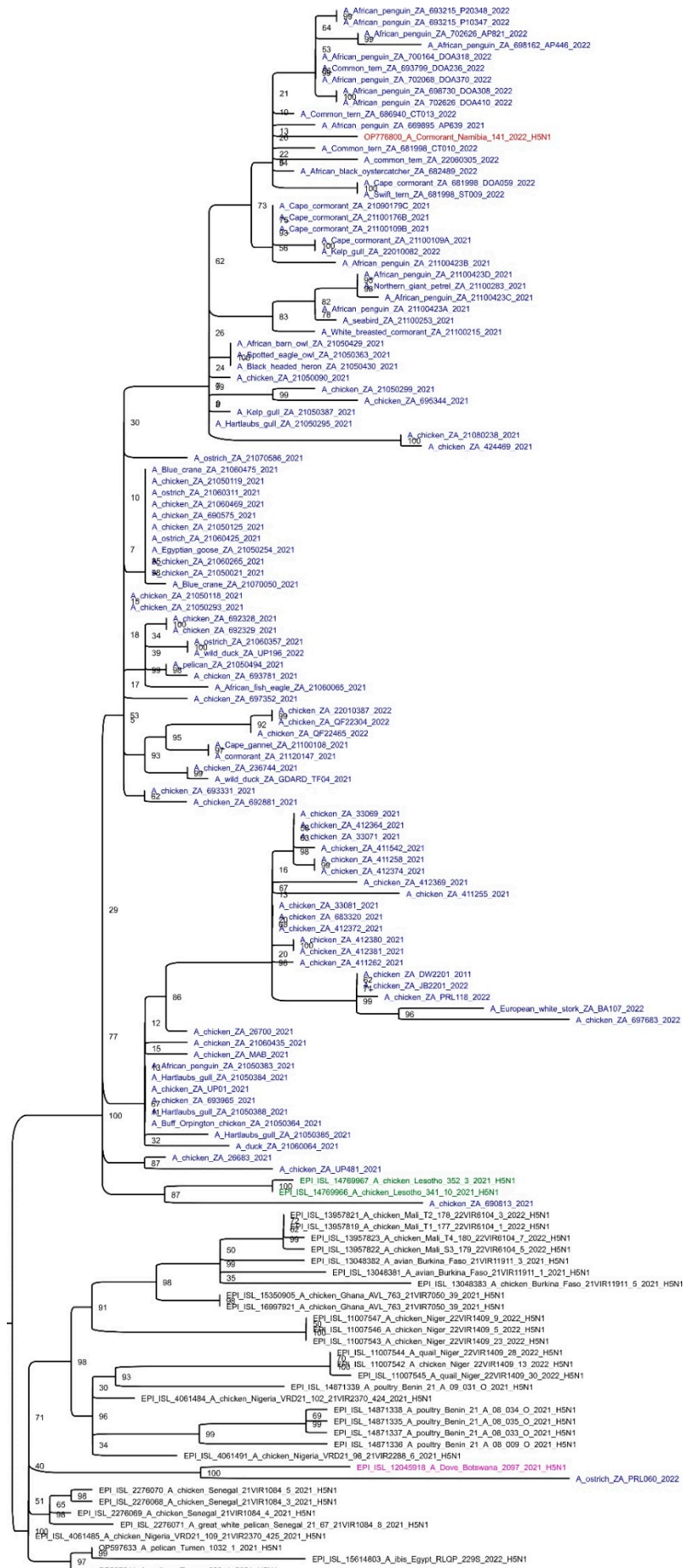


Figure S1.(a) to (h).

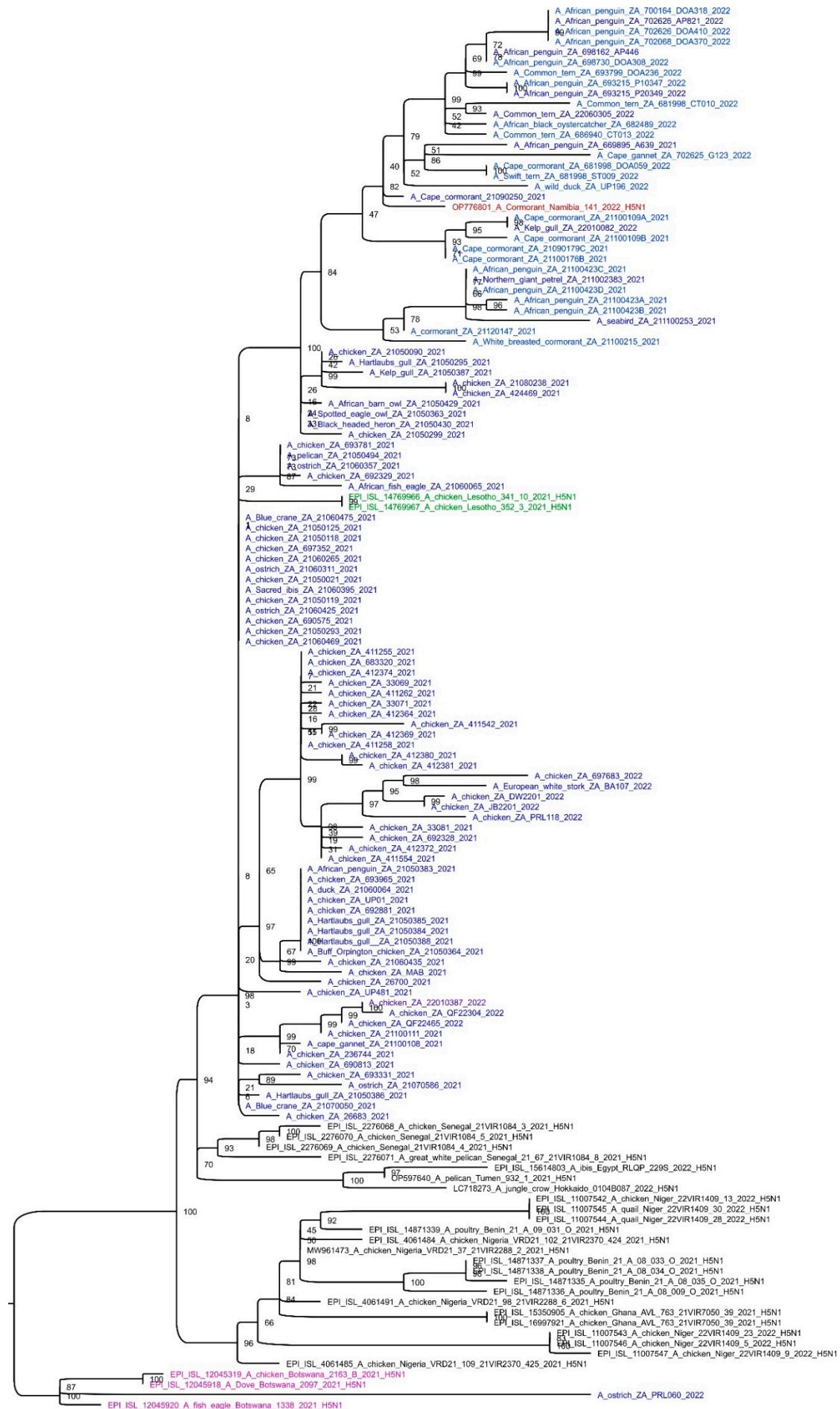
1(a)



1(b)



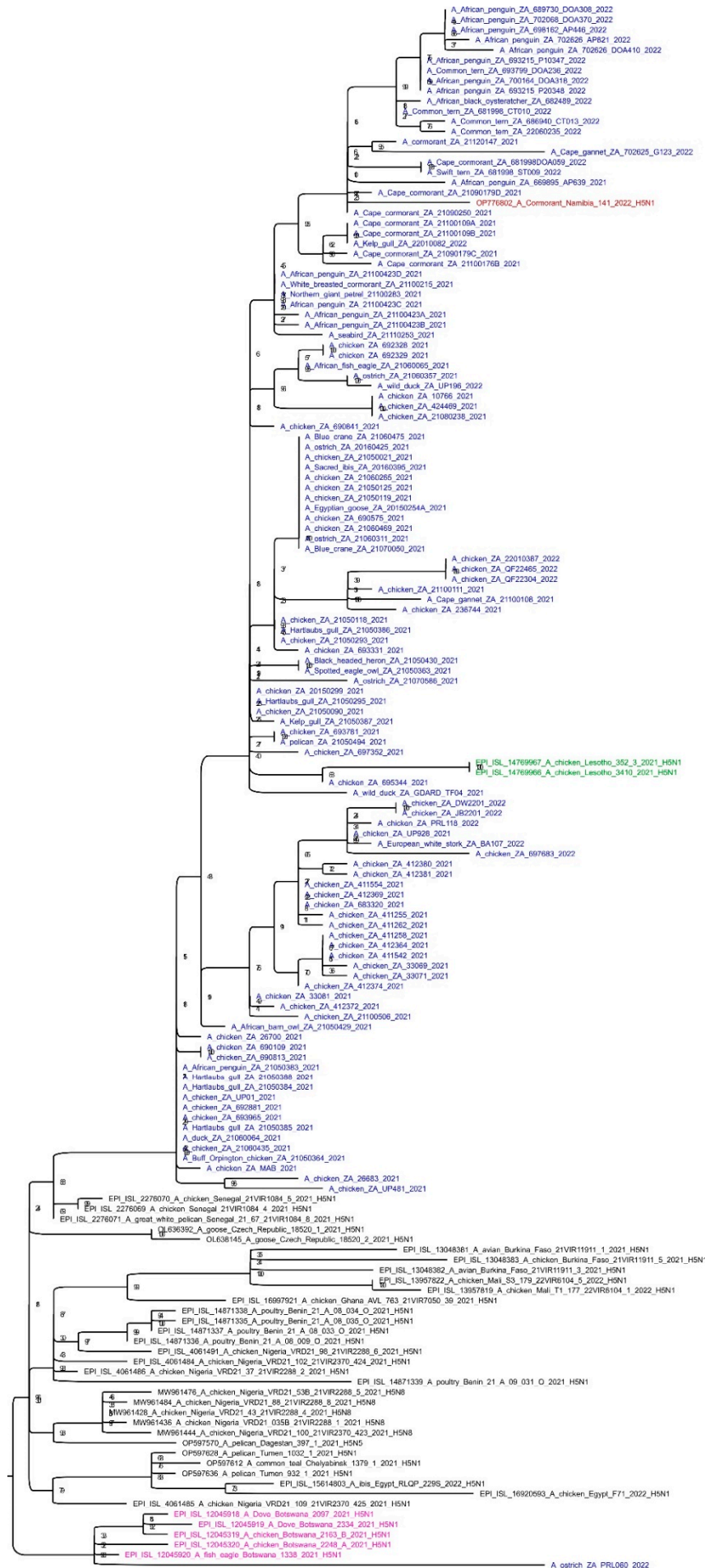
1(c)



0.002

PA

1(d)

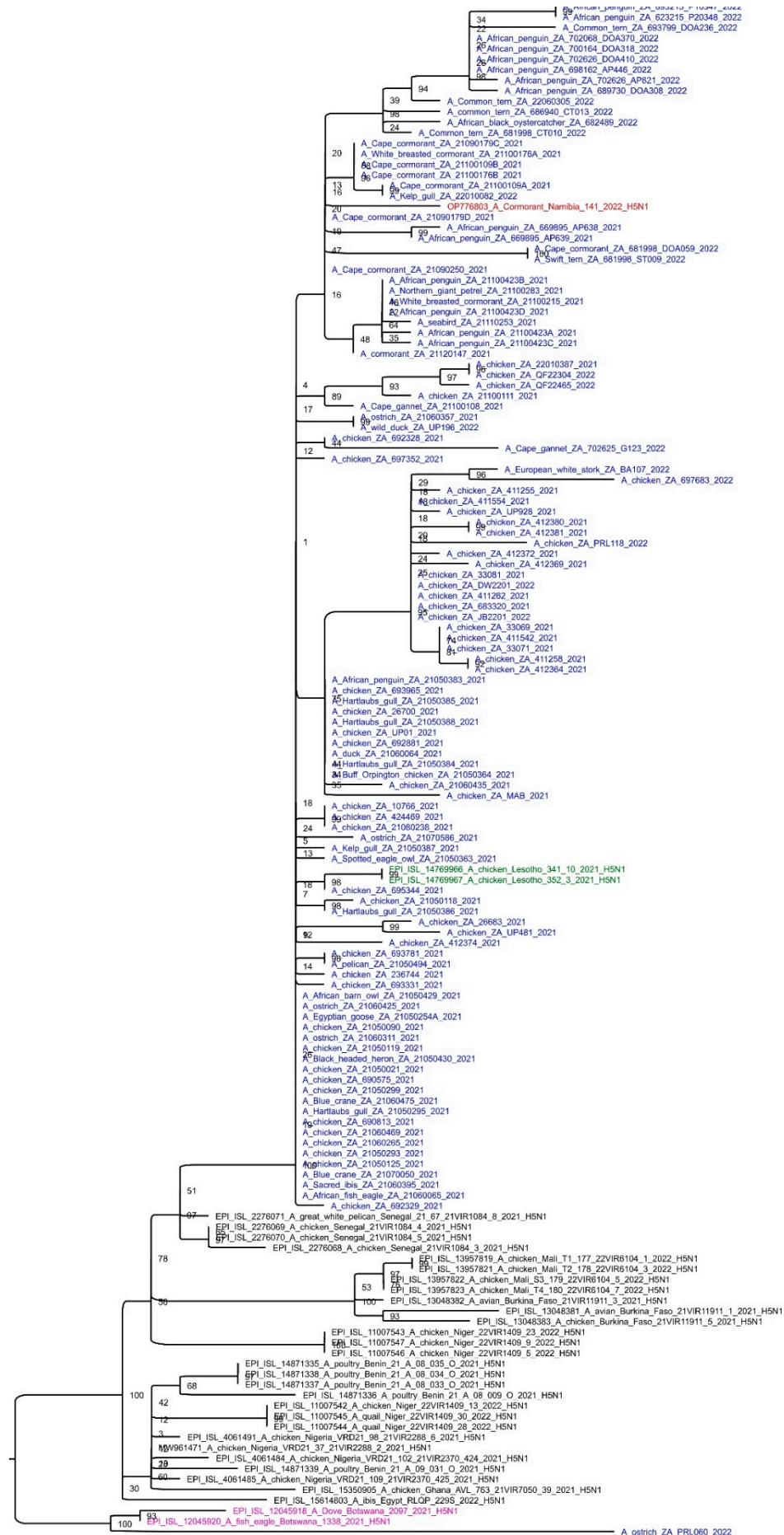


0.002

HA



1(e)



0.002

NP

1(f)



0.003

NA

**A**

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A\_Common\_tern\_ZA\_681998\_CT010\_2022  
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LC718301\_A\_chicken\_Ivate\_TU16\_11\_12\_2022\_HSN1  
LC718229\_A\_white-fronted\_goose\_Ivate\_TU16\_74\_2022\_HSN1  
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07545\_A\_quail\_Niger\_22VIR1409\_30\_2022\_HSN1  
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M

**Supplemental Figure S1a–h.** Maximum Likelihood phylogenetic trees of the individual genome segments of H5N1 HPAI viruses. All trees are midpoint-rooted and bootstrap values are indicated. South African viruses are highlighted in blue, Namibia in red, Lesotho in green, and Botswana in magenta.

