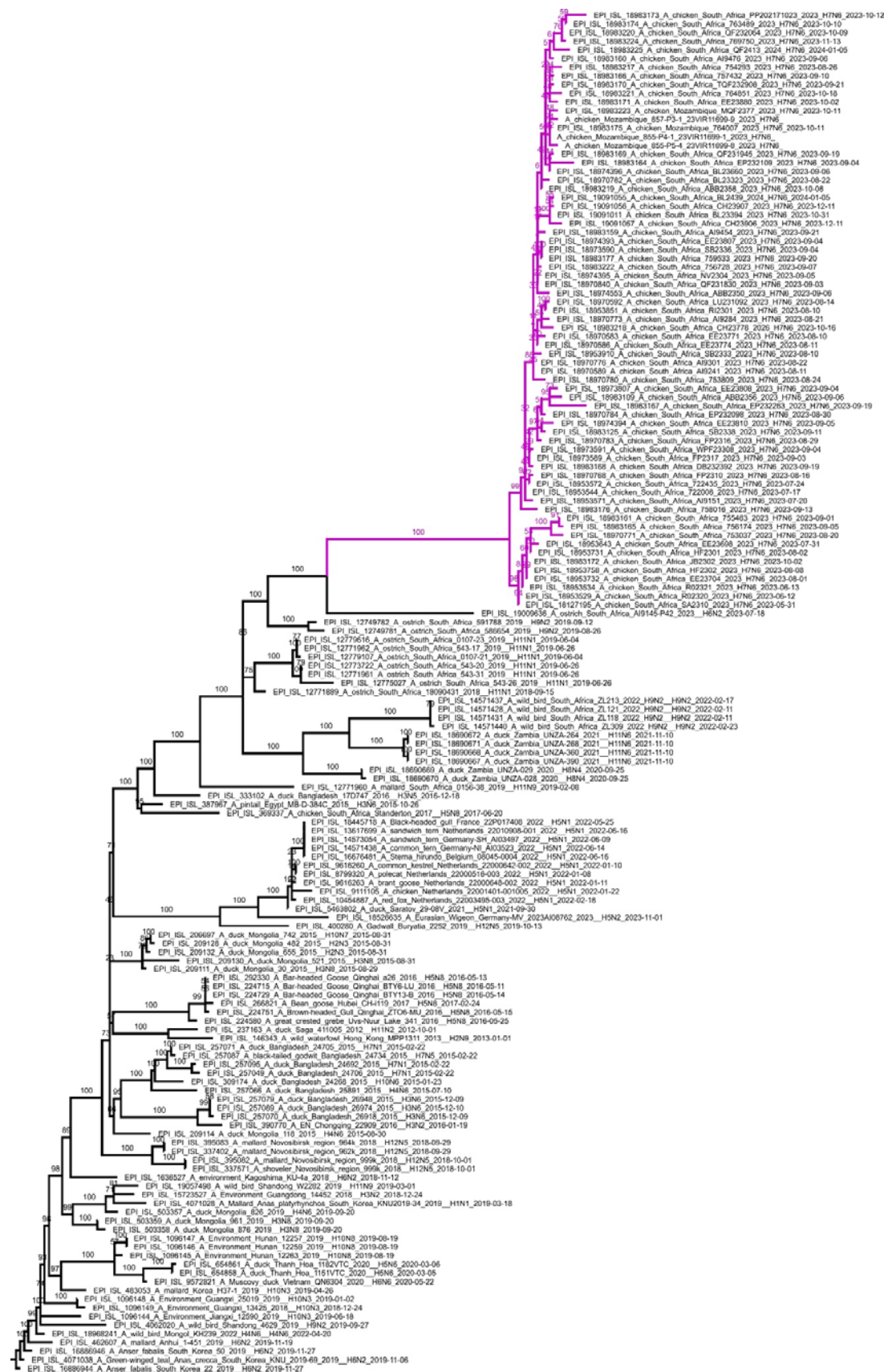


Supplemental Figure 1.

Maximum likelihood phylogenetic trees of the complete genome sequences of southern African H7N6 high pathogenicity avian influenza viruses (in magenta), and the closest relatives retrieved from public sequence databases. Bootstrap values are indicated.

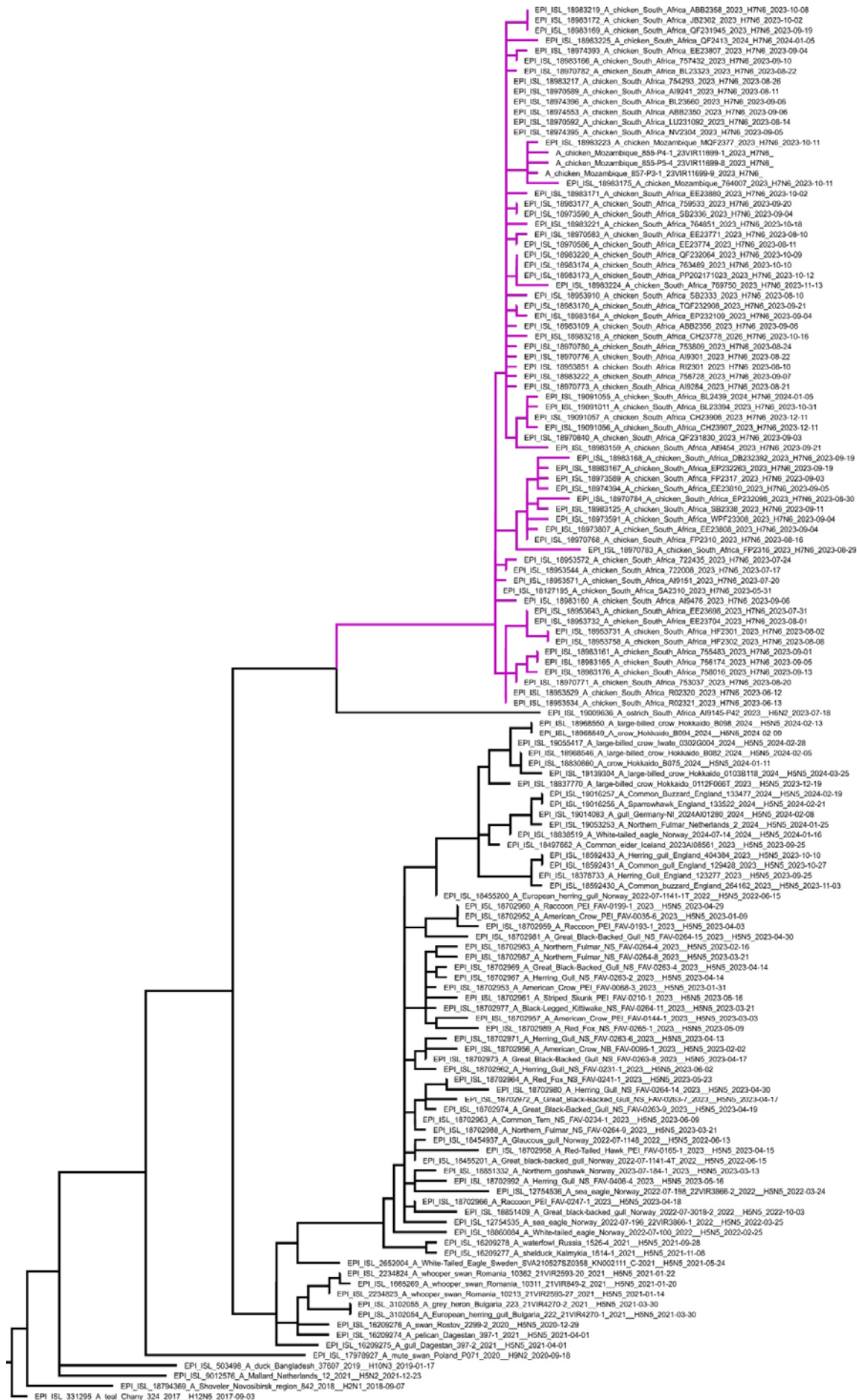


0.007

Segment 1-PB2

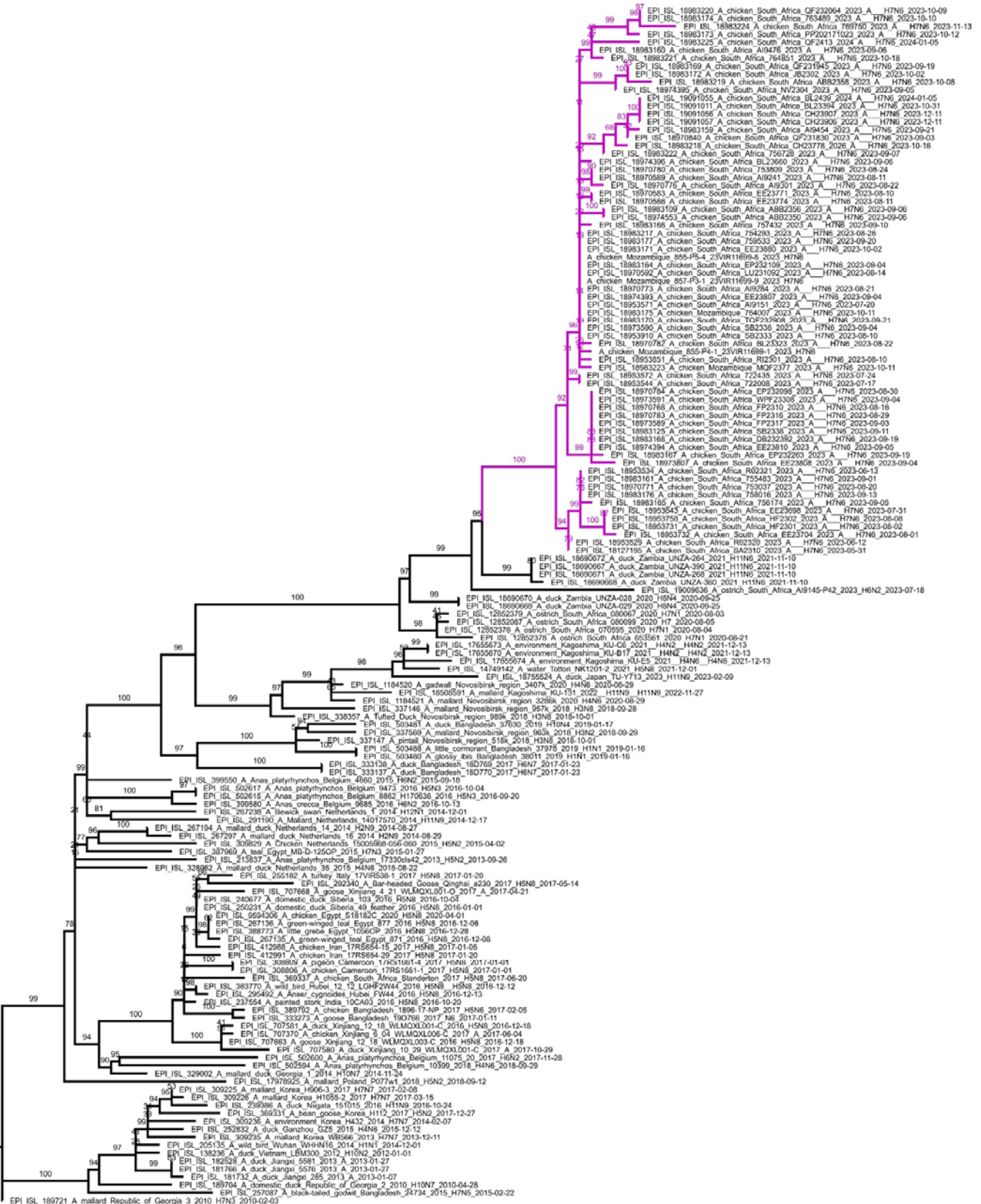


Segment 2-PB1



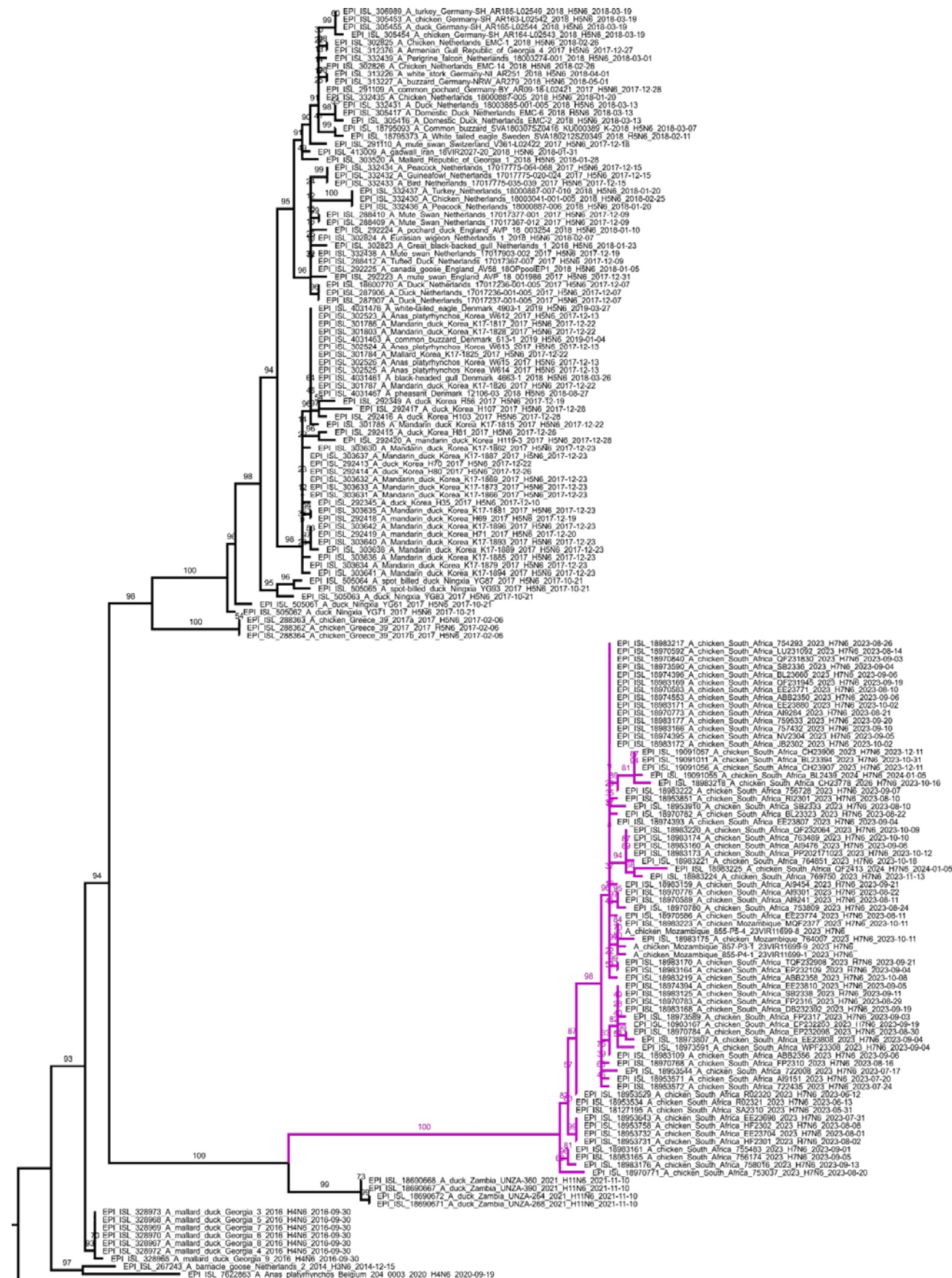
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Segment 3-PA

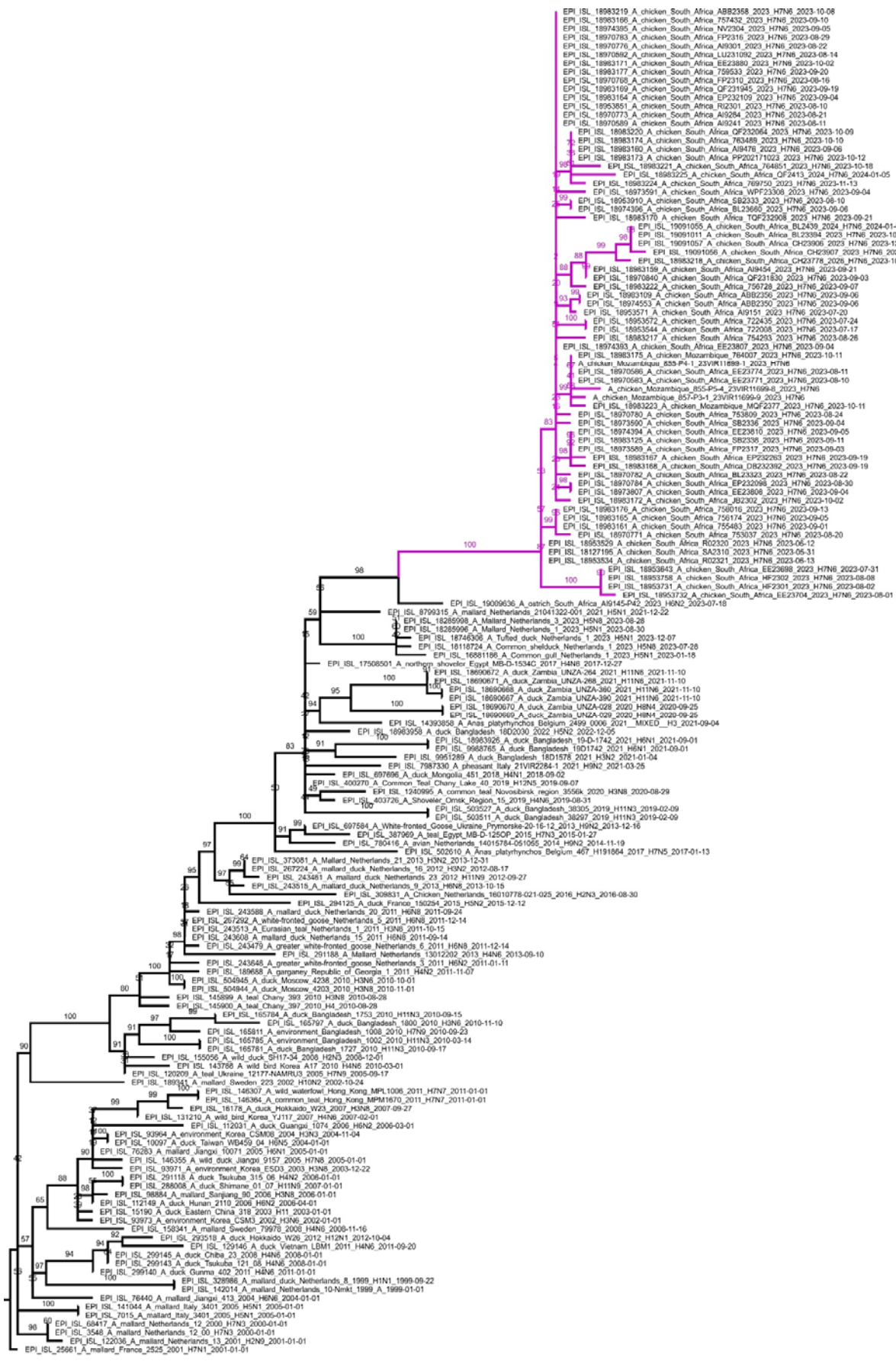


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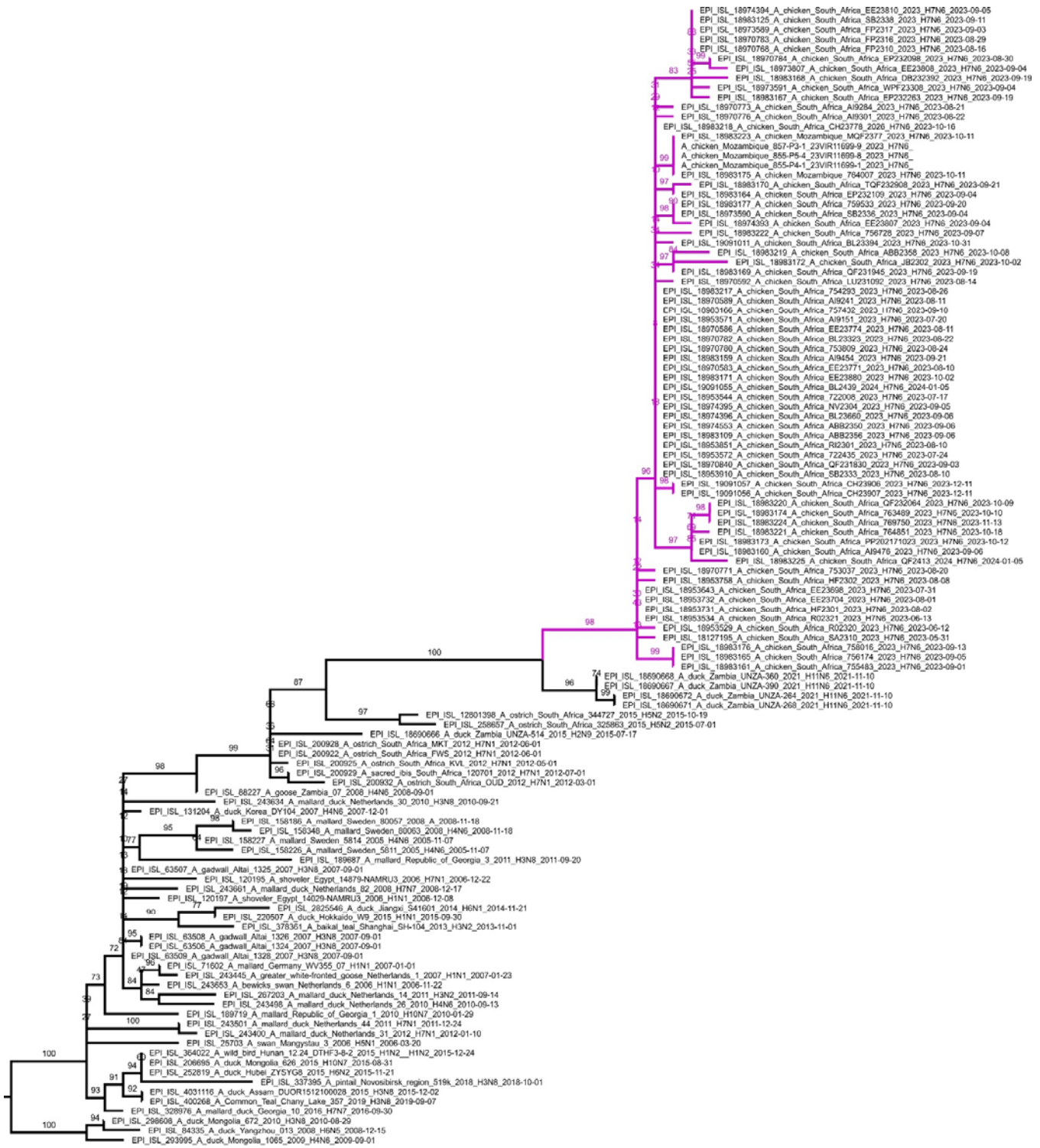
Segment 5:NP



Segment 6-NA



0.005
Segment 7-M



Segment 8-NS