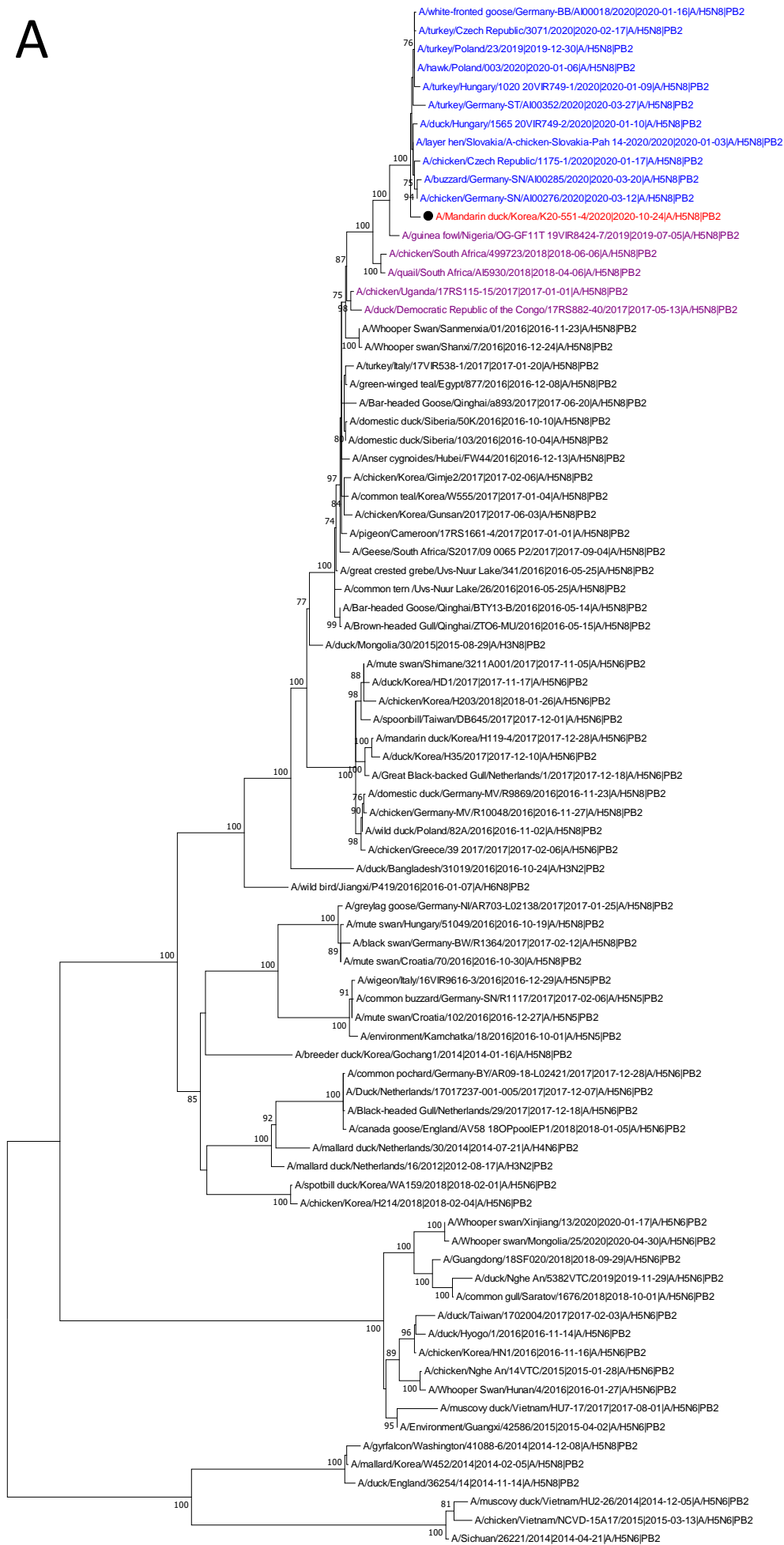


Supplementary Figure S1. Maximum-likelihood phylogenetic trees of the PB2, PB1, PA, HA, NP, NA, MP, and NS genes. Taxa was colored according to the isolation location (red, Mongolia; blue, Xinjiang, China). The subgroup B H5N8 isolates that are closely related to the 551-4/2020 virus are colored according to the isolation location. Bootstrap values over 70% are shown next to the branches Each cluster is labeled according to the genotype classification by King et al. [1] and Baek and Lee et al. [2]. A, polymerase basic 2 (PB2); B, polymerase basic 1 (PB1); C, polymerase acidic (PA); D, haemagglutinin (HA); E, nucleoprotein (NP); F, neuraminidase (NA); G, matrix (M); H, nonstructural (NS).

References

1. King, J.; Harder, T.; Conraths, F. J.; Beer, M.; Pohlmann, A., The genetics of highly pathogenic avian influenza viruses of subtype H5 in Germany, 2006-2020. *Transbound Emerg Dis* 2020.
2. Baek, Y. G.; Lee, Y. N.; Lee, D. H.; Cheon, S. H.; Kye, S. J.; Park, Y. R.; Si, Y. J.; Lee, M. H.; Lee, Y. J., A novel reassortant clade 2.3.4.4 highly pathogenic avian influenza H5N6 virus identified in South Korea in 2018. *Infect Genet Evol* 2020, 78, 104056.

A



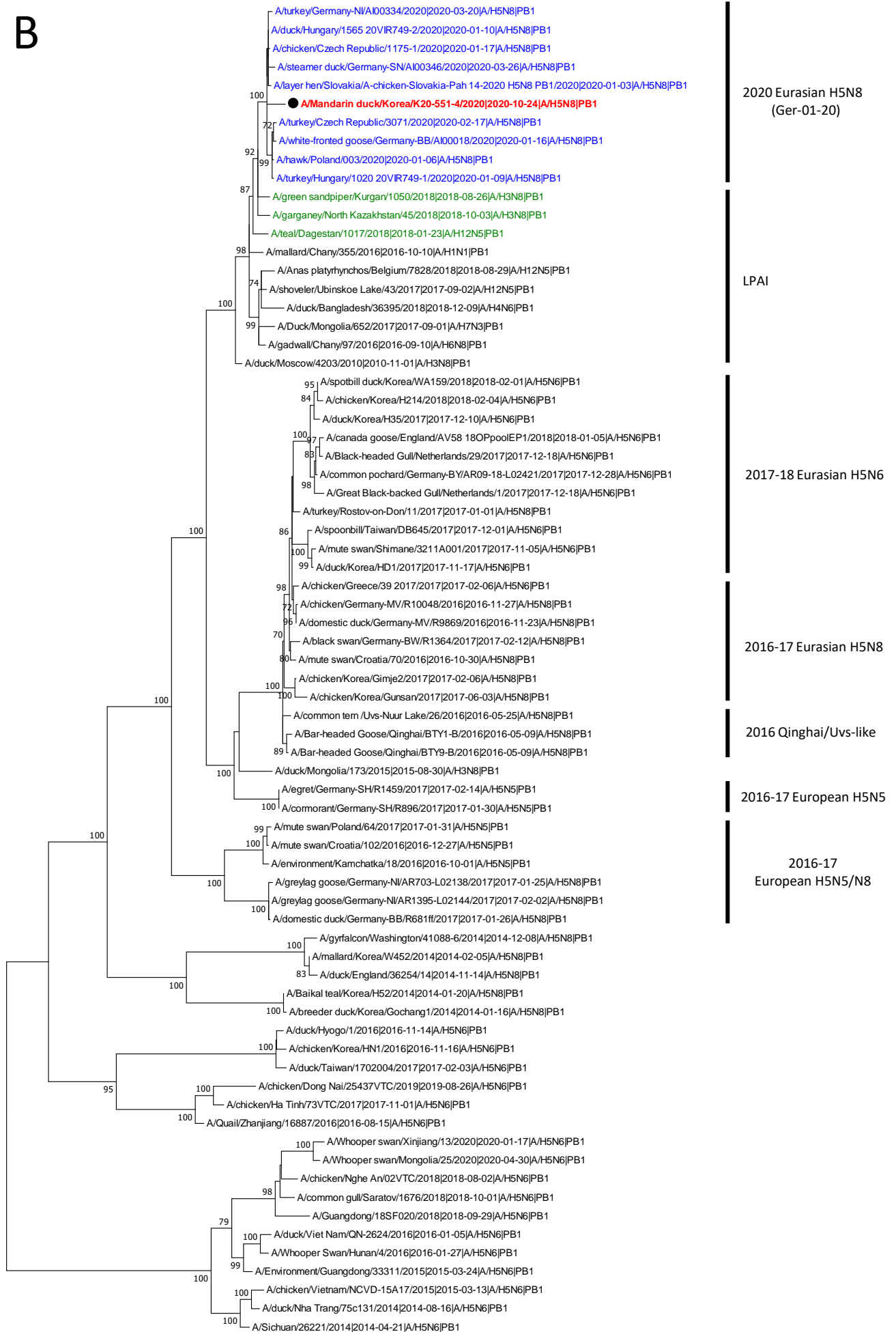
2016 Qinghai/Uvs-like

2016-18 Eurasian
H5N6/N82016-17 European
H5N5/N8

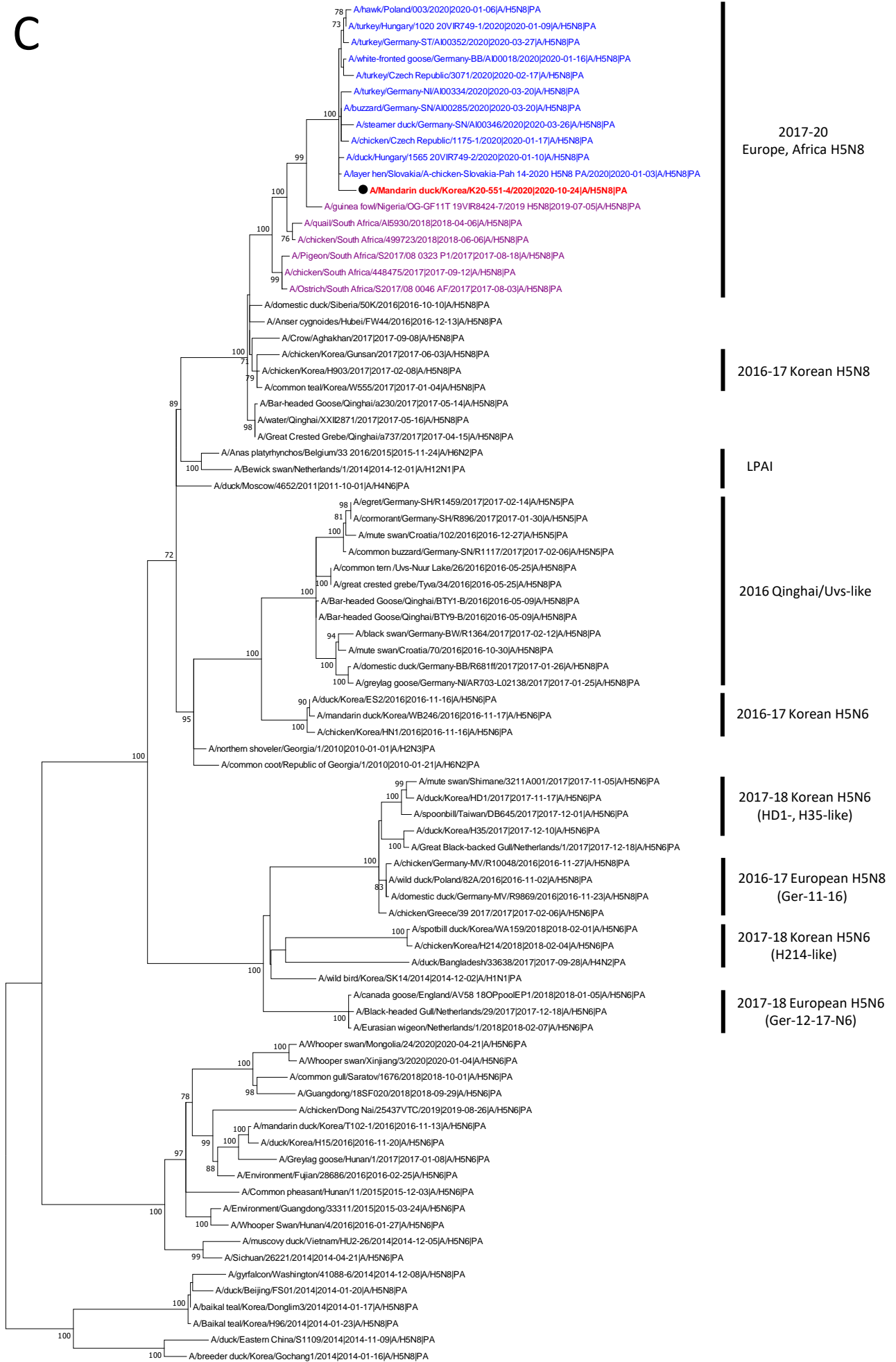
2017-18 Eurasian H5N6

0.01

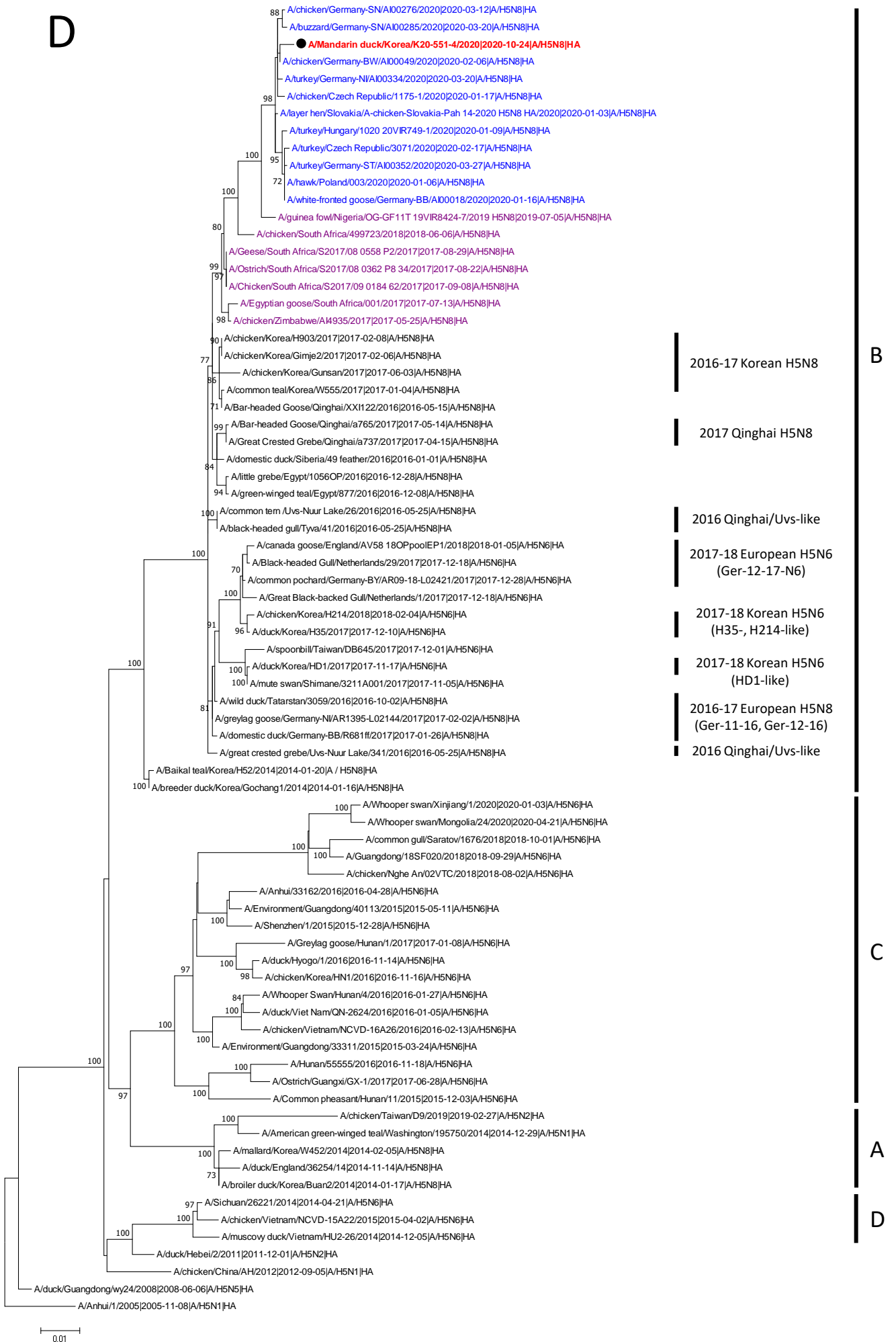
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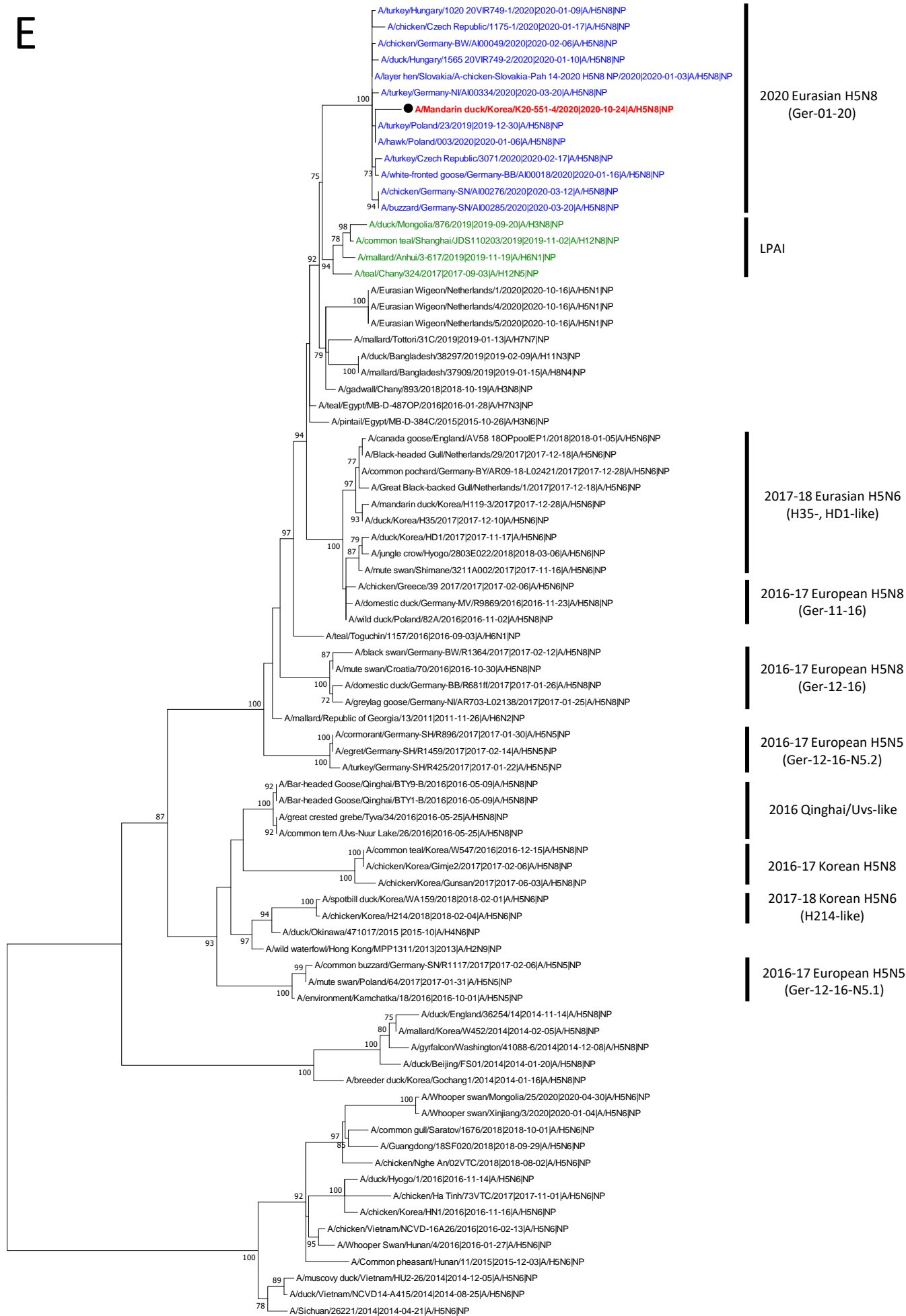


C

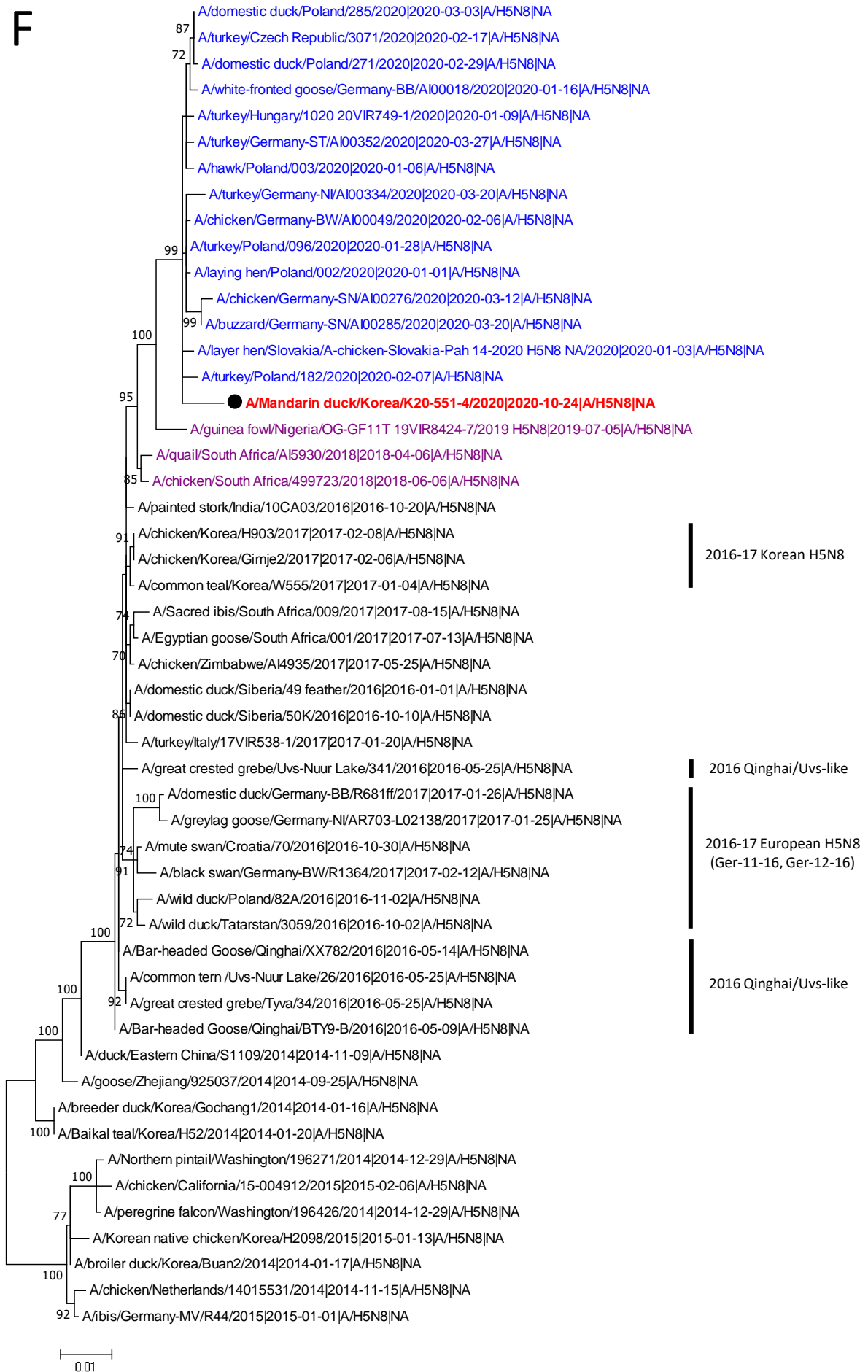


D





F



B

A

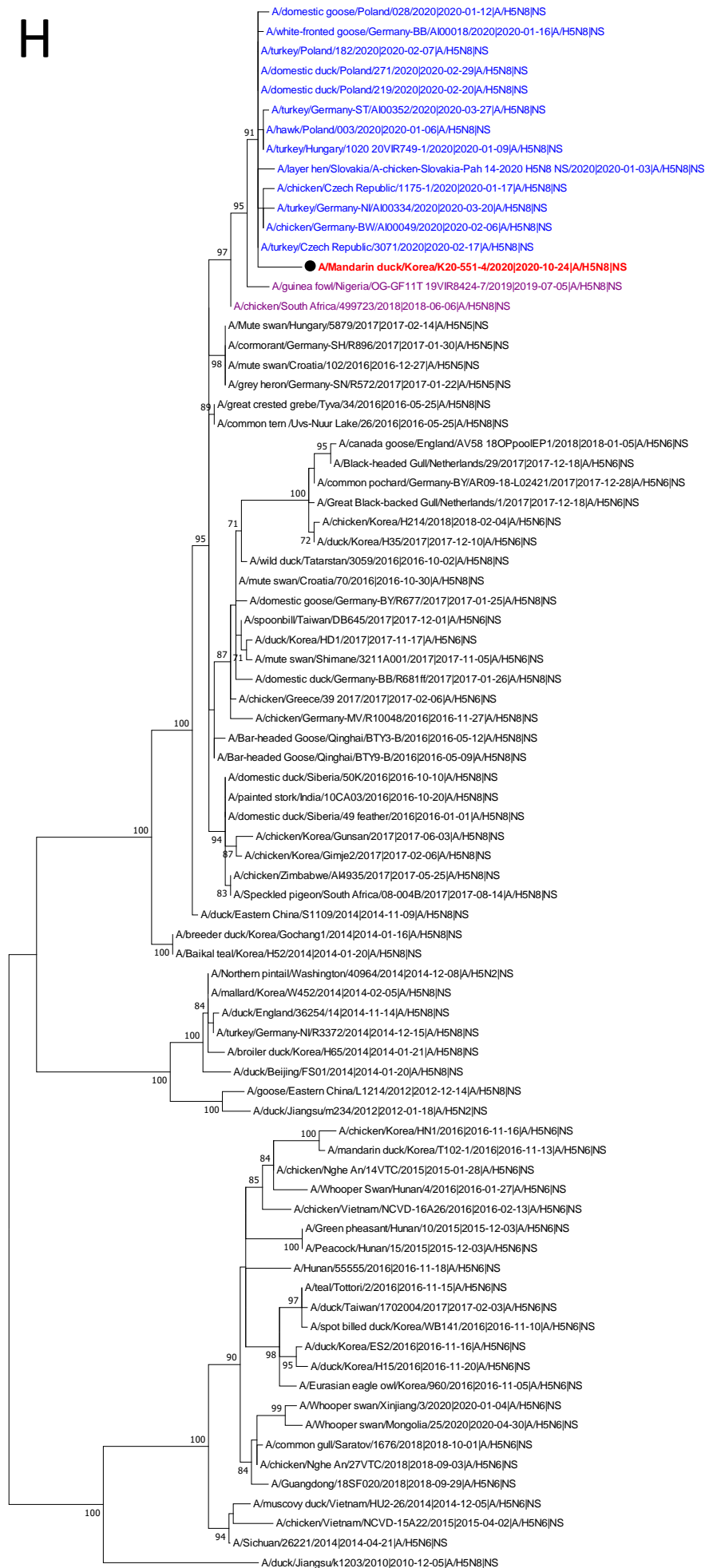
G



2016 Qinghai/Uvs-like

0.01

H



2016 Qinghai/Uvs-like