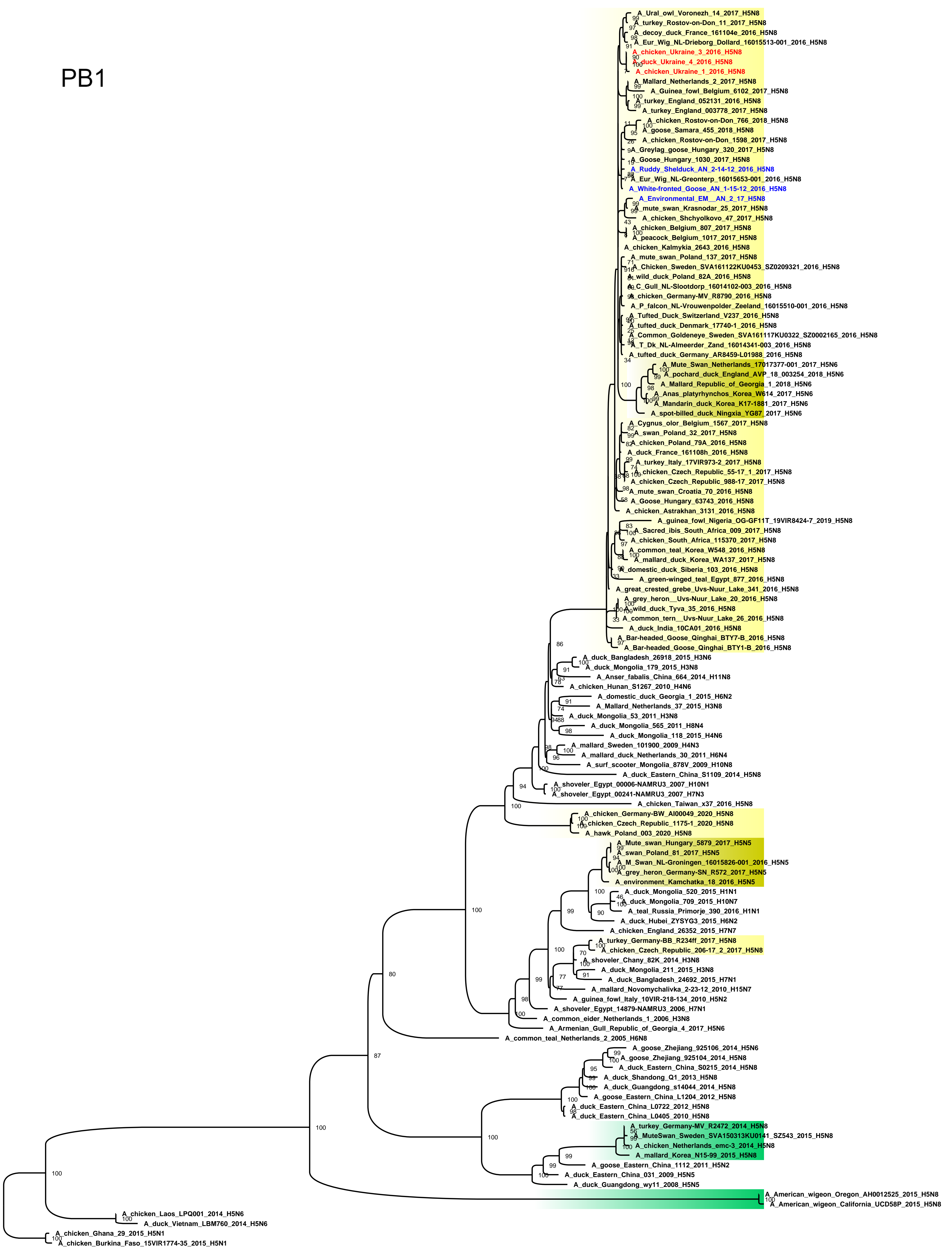


**Figures S1. Maximum Likelihood phylogenetic trees of the PB2, PB1, PA, NP, MP and NS genes.** H5N8 HPAIV collected in Ukraine from domestic (red) and wild (blue) (Muzyka et al. 2018) birds. Bootstrap supports are indicated next to the nodes, while branch lengths are scaled according to the number of nucleotide substitutions per site. H5N8 clade 2.3.4.4b is highlighted in yellow; H5N8 clade 2.3.4.4a – in green; dark yellow marked H5N6 and H5N5 subtypes.



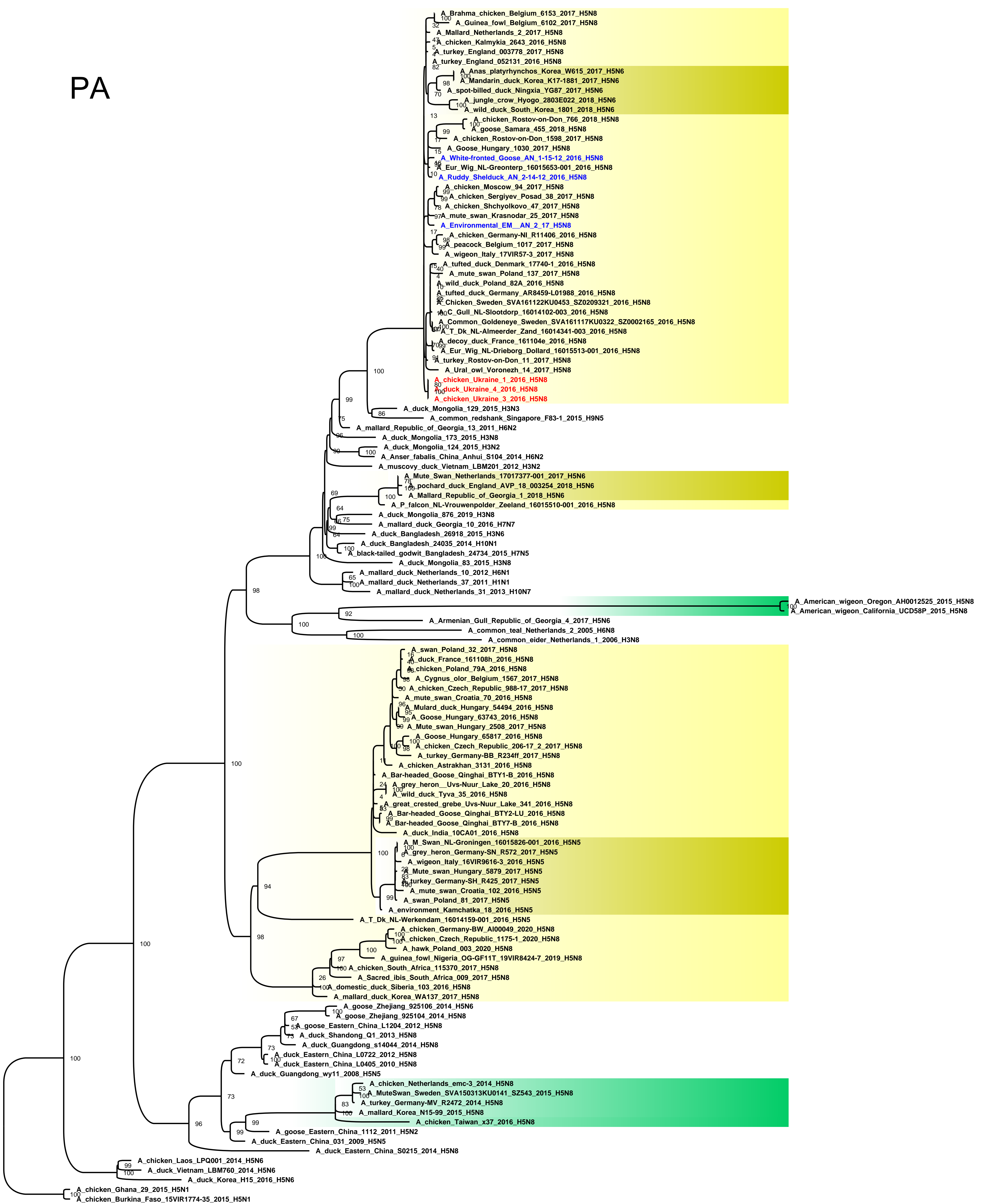


PB1



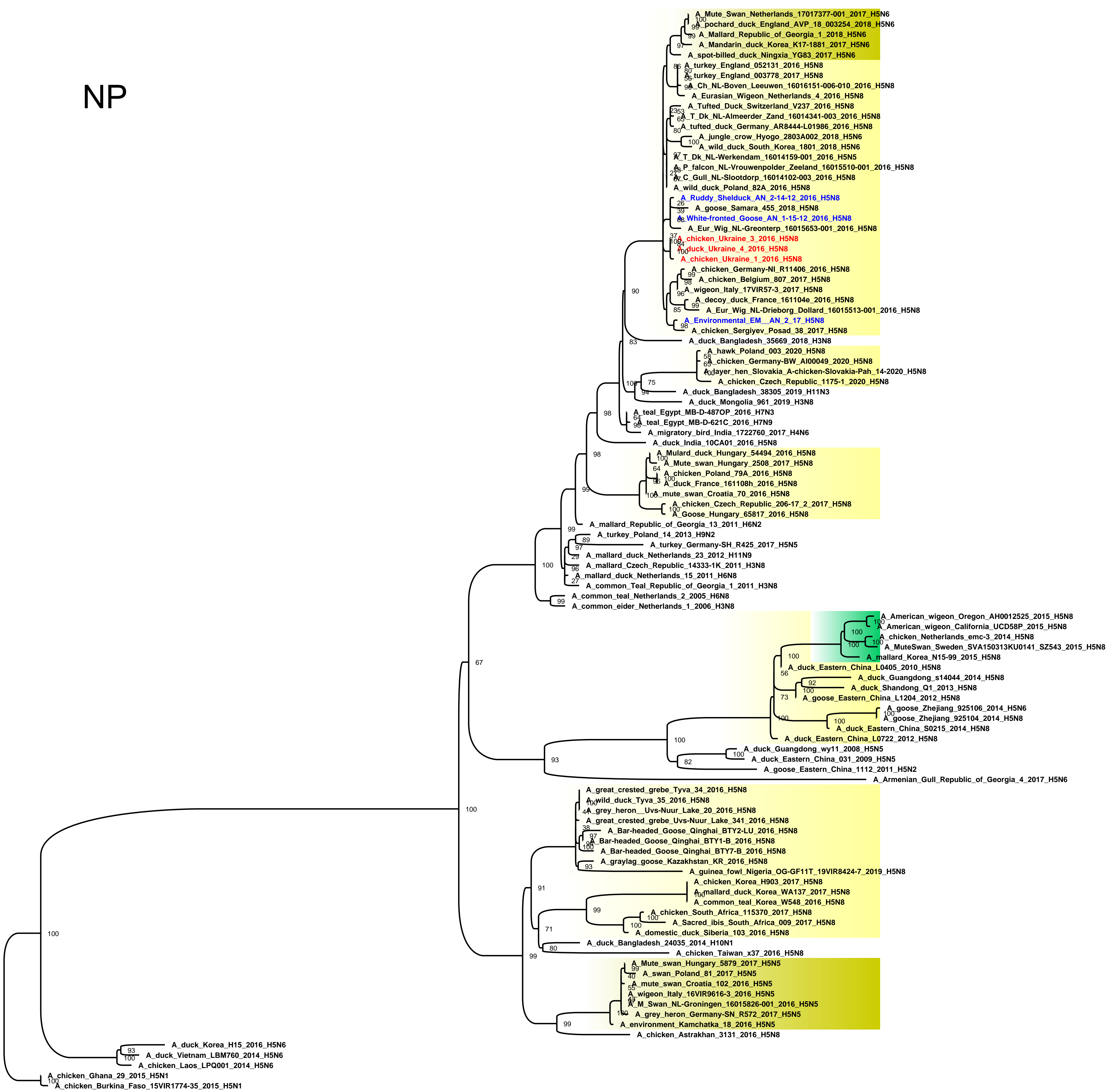


PA

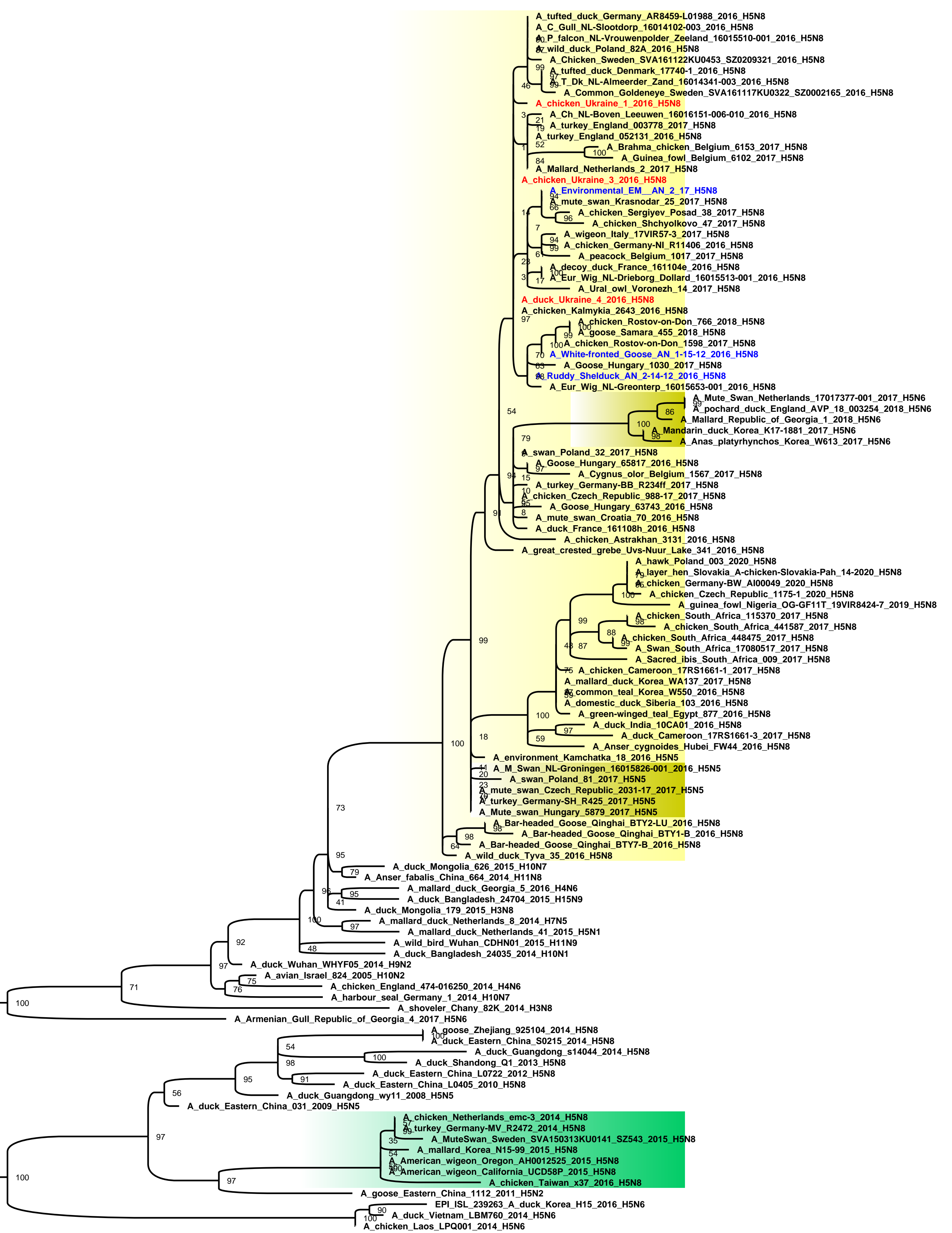




NP



MP



0.008



NS

