

B

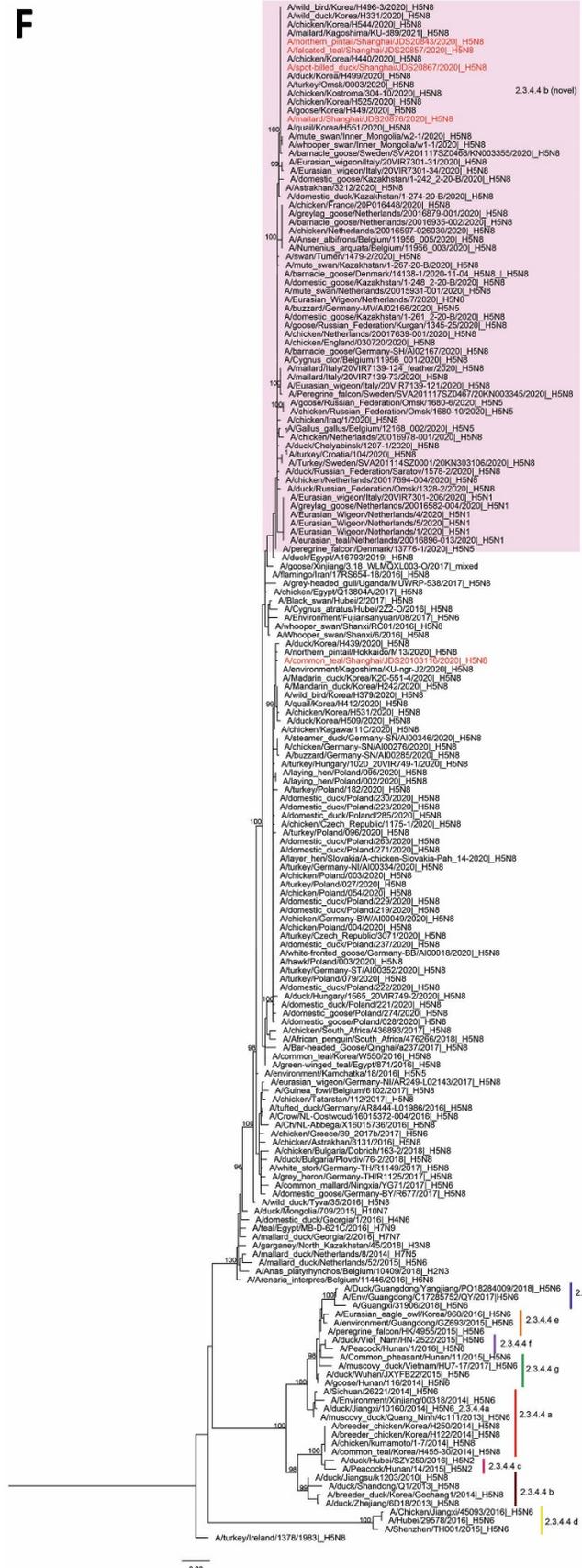


0.02

D



F



G



Appendix Figure. Phylogenetic trees of highly pathogenic avian influenza A(H5N8) isolated in Shanghai, China during 2020 (red text), and reference sequences in GISAID (<https://www.gisaid.org>). Tree was based on 7 gene segments; it was constructed using IQ-TREE (1) with 1,000 bootstrap replicates. Labels indicate subclades 2.3.4.4a–h. Pink shading indicates novel genotypes of clade 2.3.4.4b. Numbers to the left of node indicate bootstrap values. Scale bars indicate average number of nucleotide substitutions per site.

Reference

1. Minh BQ, Schmidt HA, Chernomor O, Schrempf D, Woodhams MD, von Haeseler A, et al. IQ-TREE 2: new models and efficient methods for phylogenetic inference in the genomic era. *Mol Biol Evol.* 2020;37:1530–4. [PubMed https://doi.org/10.1093/molbev/msaa015](https://doi.org/10.1093/molbev/msaa015)