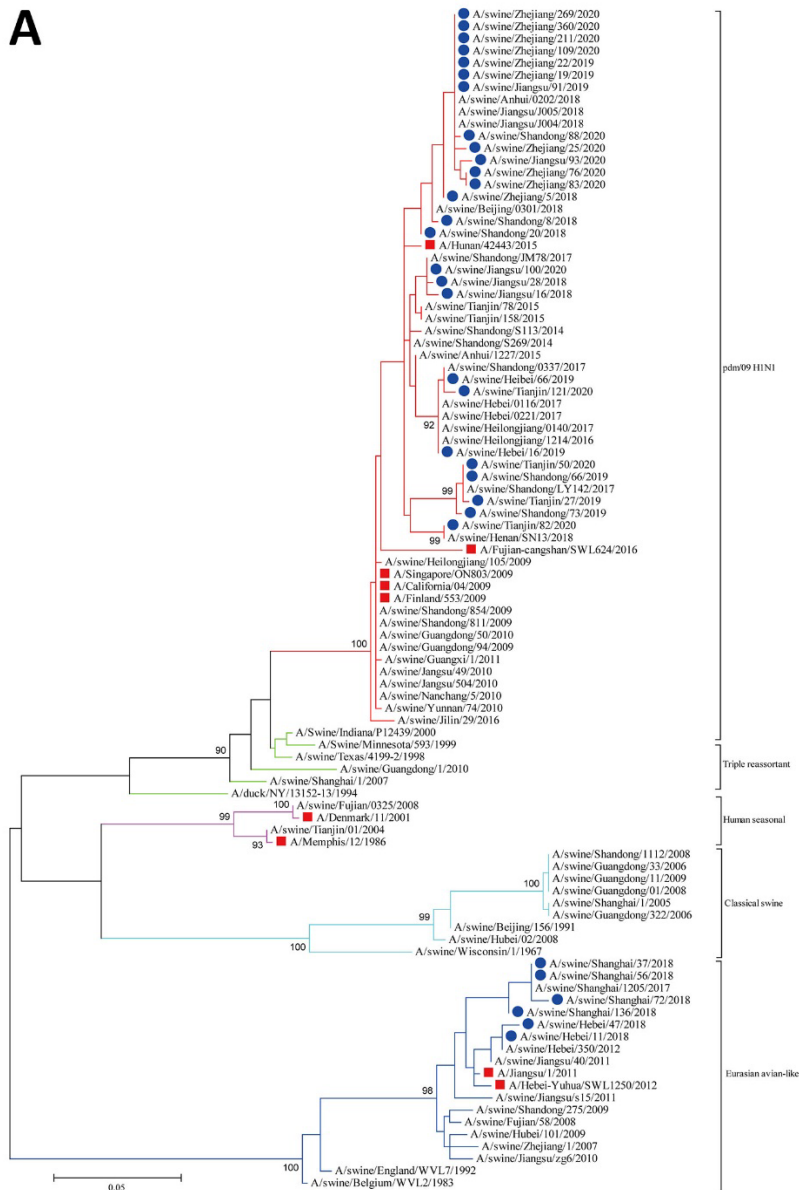


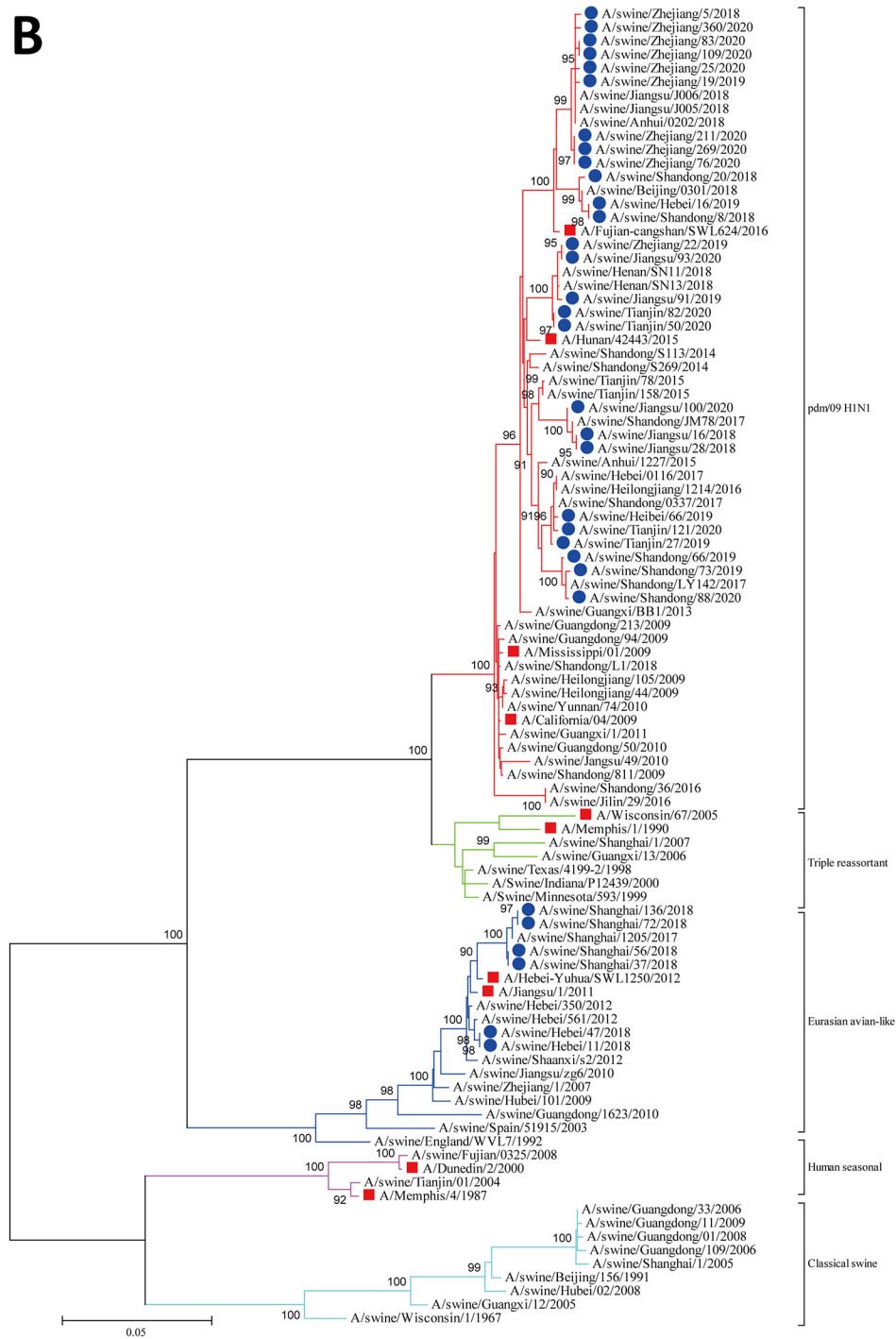
# Potential Threats to Human Health from Eurasian Avian-Like Swine Influenza A(H1N1) Virus and Its Reassortants

## Appendix

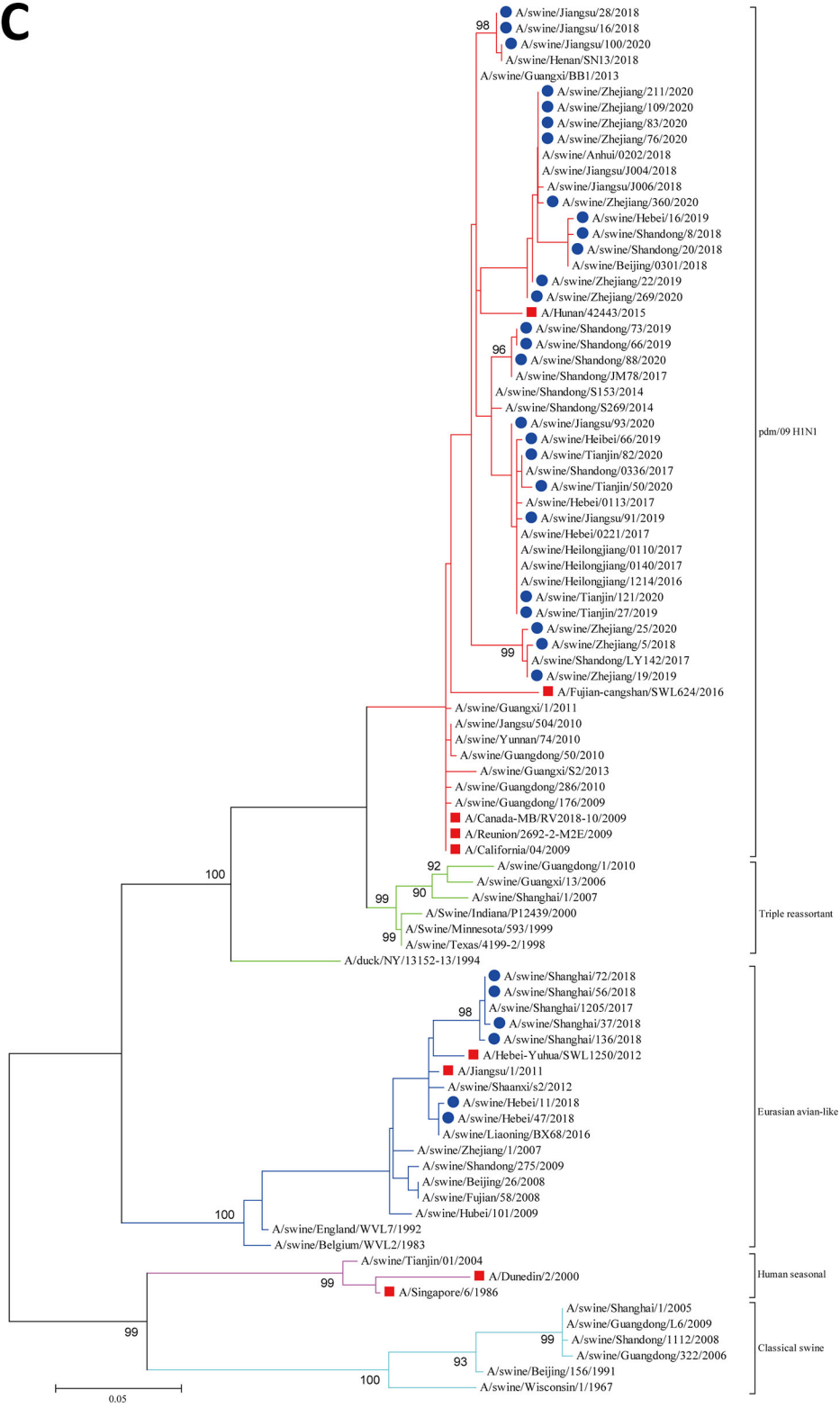
**A**



B

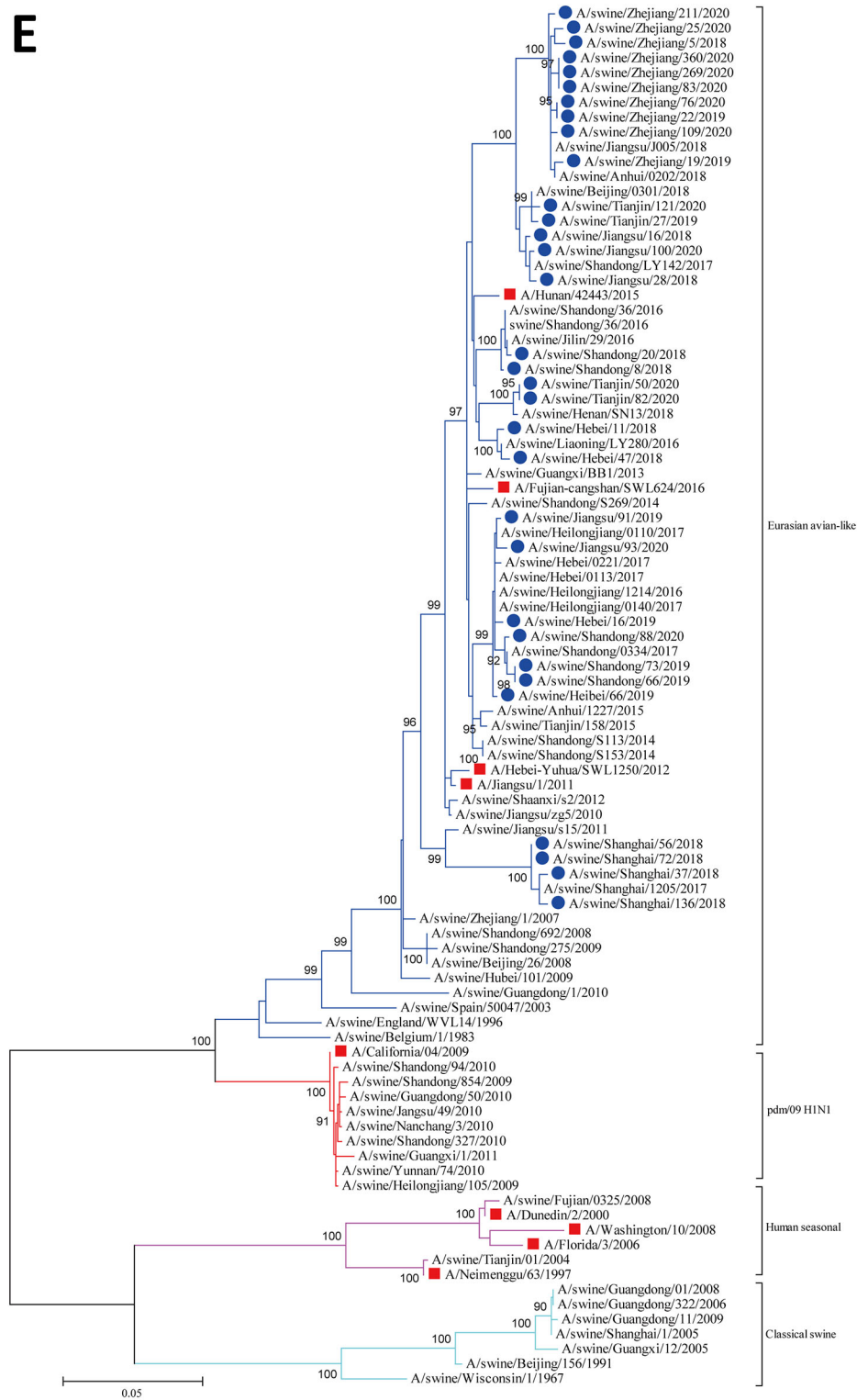


C



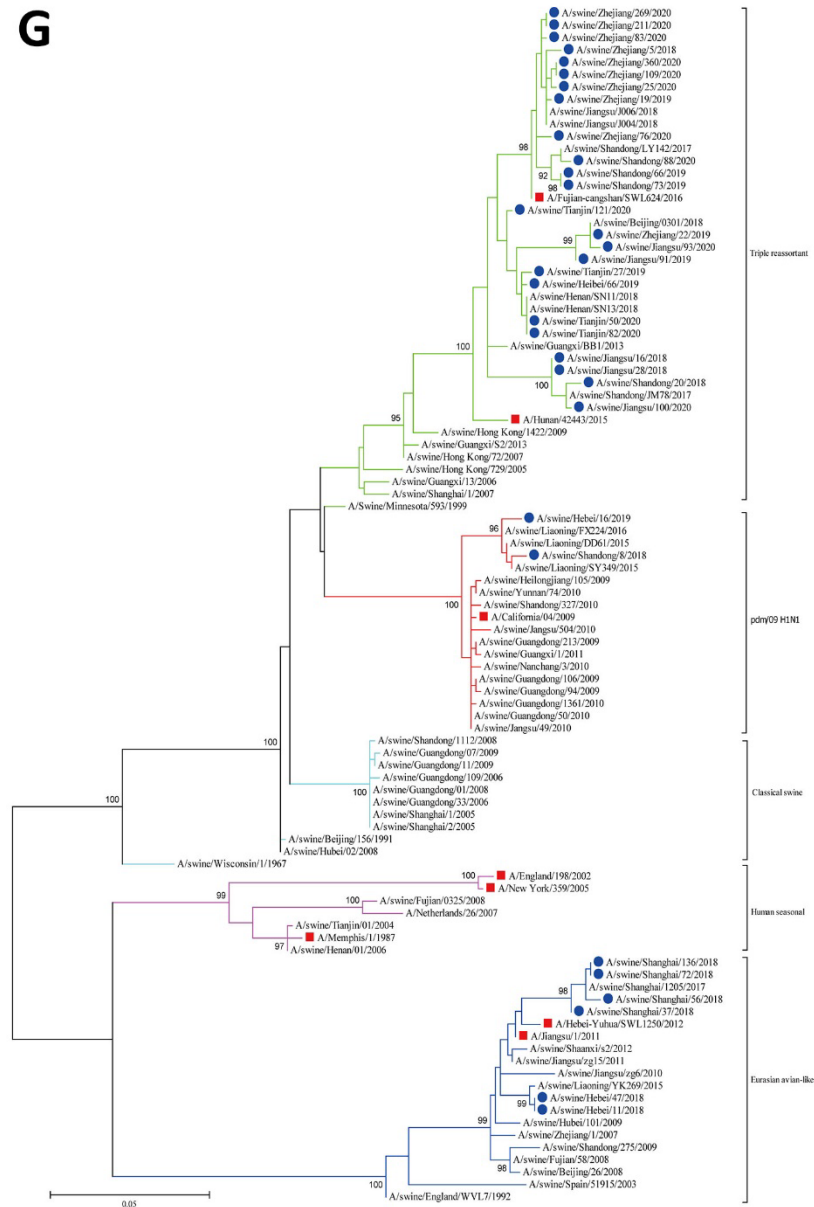


E





G



**Appendix Figure.** Maximum-likelihood phylogenetic tree of the A) PB2, B) PB1, C) PA, D) NP, E) NA, F) M, and G) NS genes. The phylogeny of available sequences of related viruses from GenBank and GISAID database (<https://www.gisaid.org>), and the sequences of 32 isolates in this study were inferred by using MEGA version 7 (<https://www.megasoftware.net>) under the general time-reversible plus gamma distribution model with 1,000 bootstrap replicates. Red triangles indicate reference sequences from humans. Blue circles indicate isolates sequenced in this study. Scale bar indicates substitutions per nucleotide.