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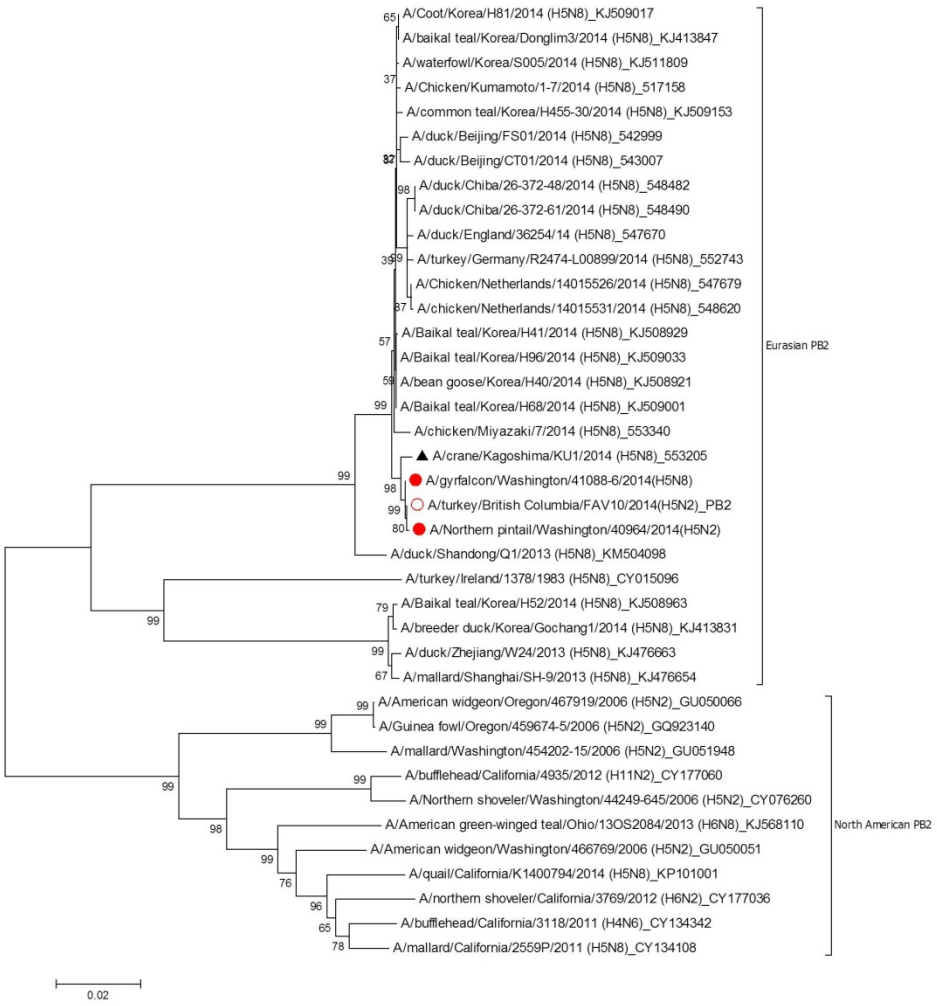
Novel Eurasian Highly Pathogenic Influenza A(H5) Viruses in Wild Birds, Washington State, USA, 2014

Technical Appendix

A



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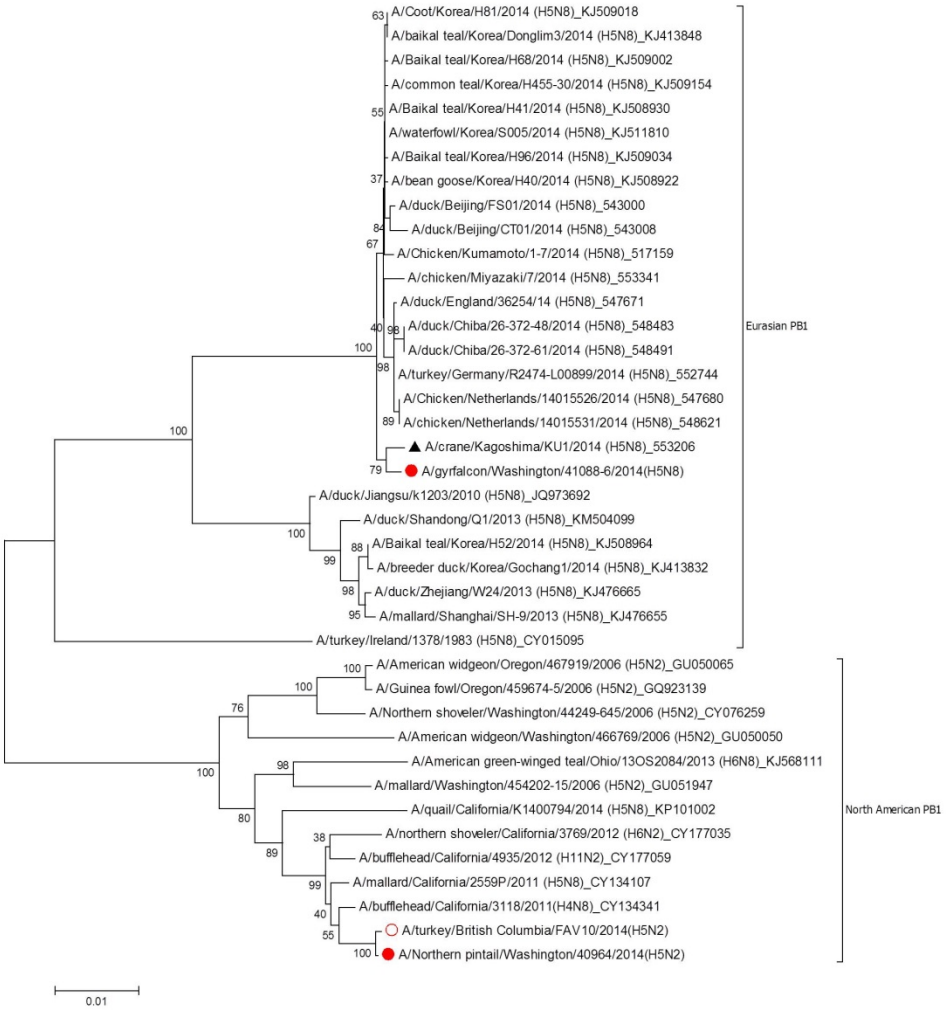
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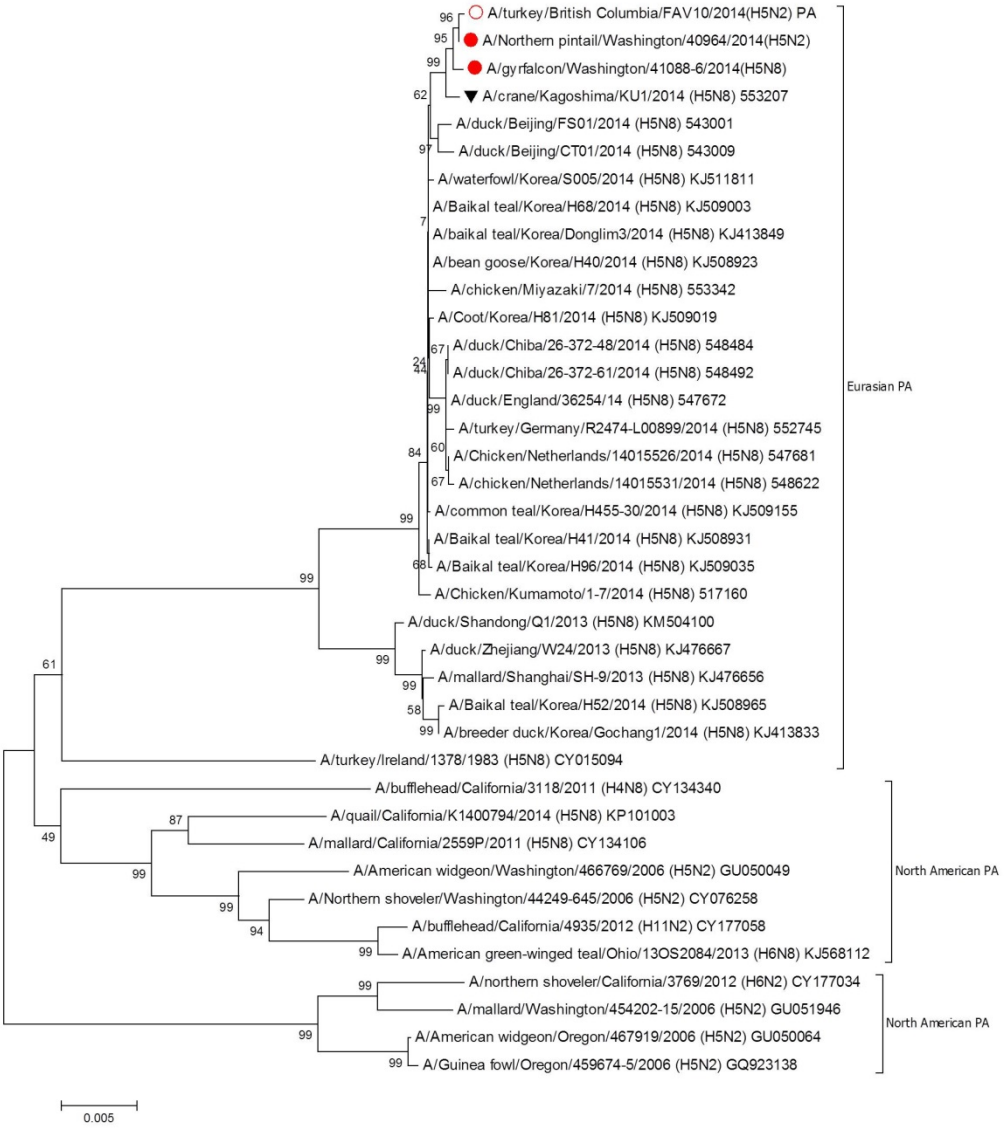
0.01

C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Eurasian PA
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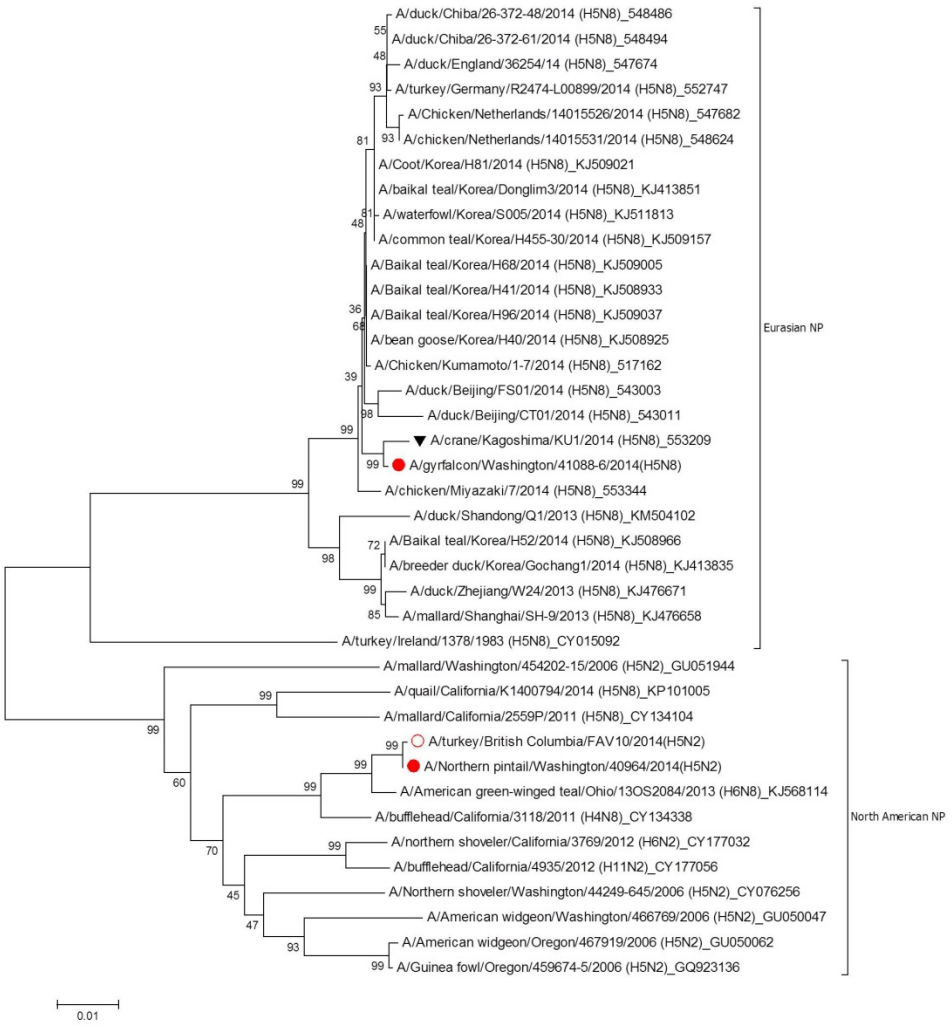
0.005

D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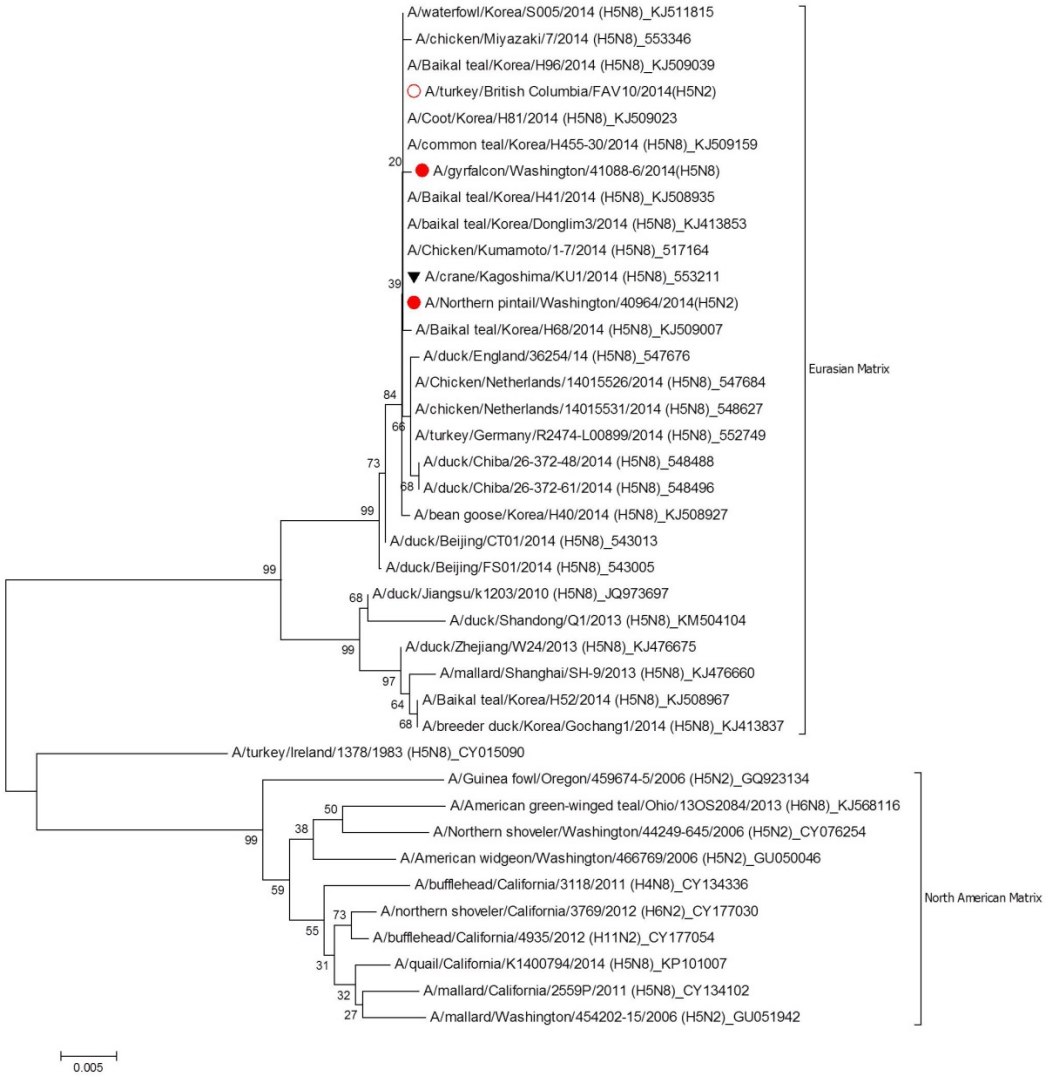
North American NP
0.01

E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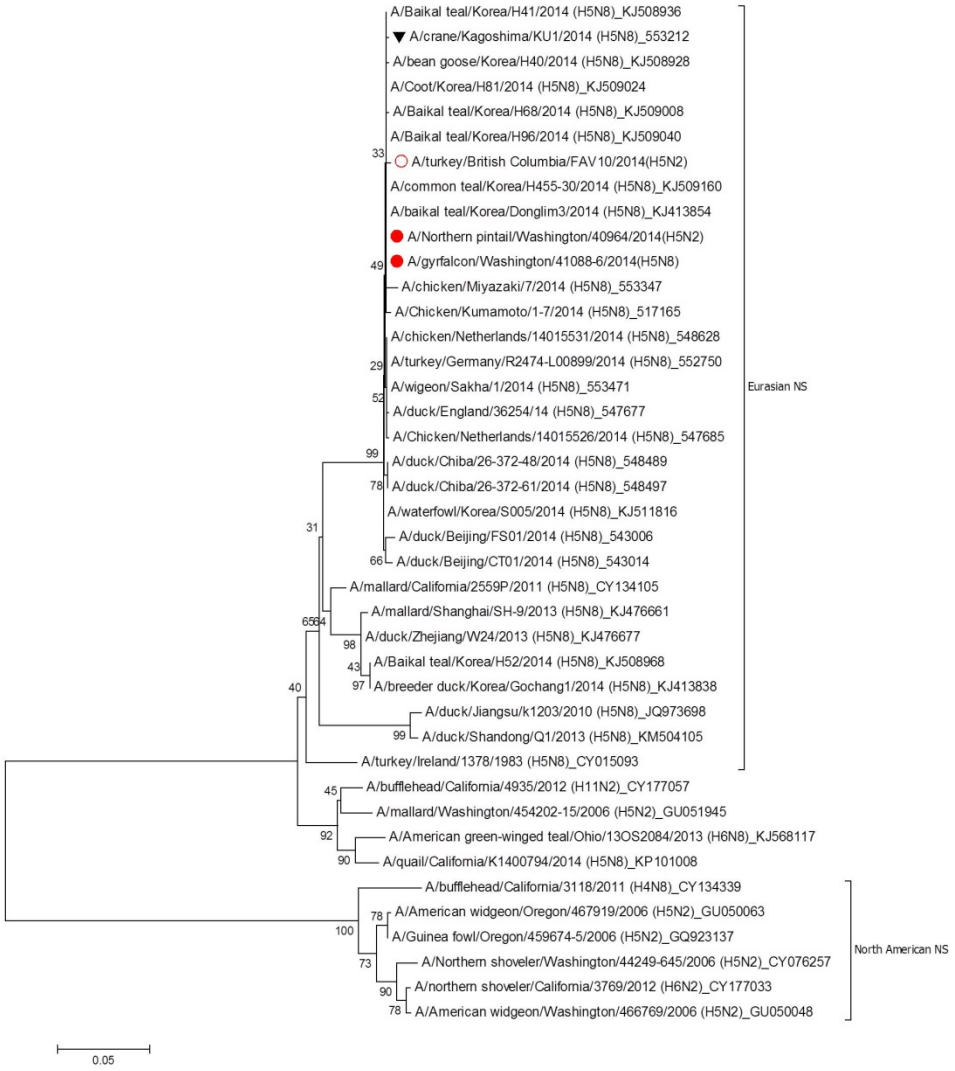
Eurasian Matrix
North American Matrix
0.005

F



Technical Appendix Figure, panels A–F. Phylogenetic analysis of the 6 internal genes of the influenza A(H5N2) and (H5N8) viruses: A, polymerase basic (PB) 2; B, PB1; C, polymerase acidic (PA); D, nucleoprotein (NP); E, matrix (M); and F, nonstructural (NS). Red circles indicate highly pathogenic avian influenza (HPAI) subtype H5N2 and H5N8 strains from the United States; open red circle indicates HPAI subtype H5N2 virus from Canada; black triangle represents HPAI subtype H5N8 derived from A/crane/Kagoshima/KU1/2014(H5N8) in Japan. Sequences were aligned by using MUSCLE, and phylogenetic and molecular evolutionary analyses were conducted by using MEGA version 5, using the neighbor-joining tree-building method, with 1,000 bootstrap replicates (*1*). Analysis was done with viruses that were phylogenetically representative of appropriate lineages (Influenza Virus Resource database, http://www.ncbi.nlm.nih.gov/genomes/FLU/FLU.html).

Reference

<jrn>1. Tamura K, Peterson D, Peterson N, Stecher G, Nei M, Kumar S. MEGA5: Molecular Evolutionary Genetics Analysis using Maximum Likelihood, Evolutionary Distance, and Maximum Parsimony Methods. Mol Biol Evol. 2011;28:2731–9. PubMed http://dx.doi.org/10.1093/molbev/msr121</jrn>