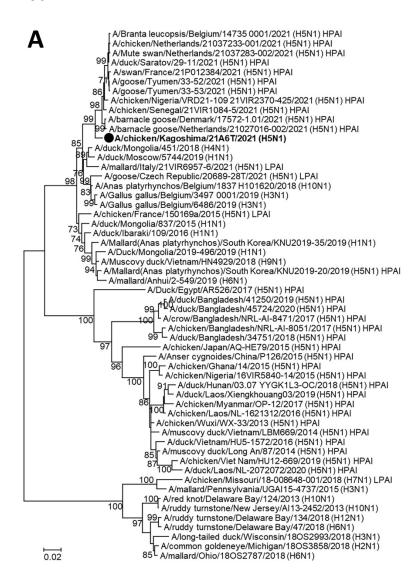
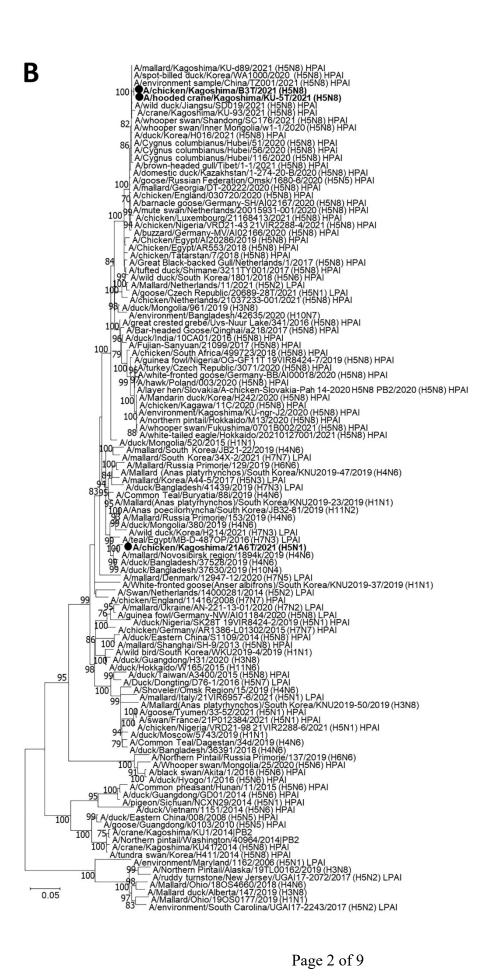
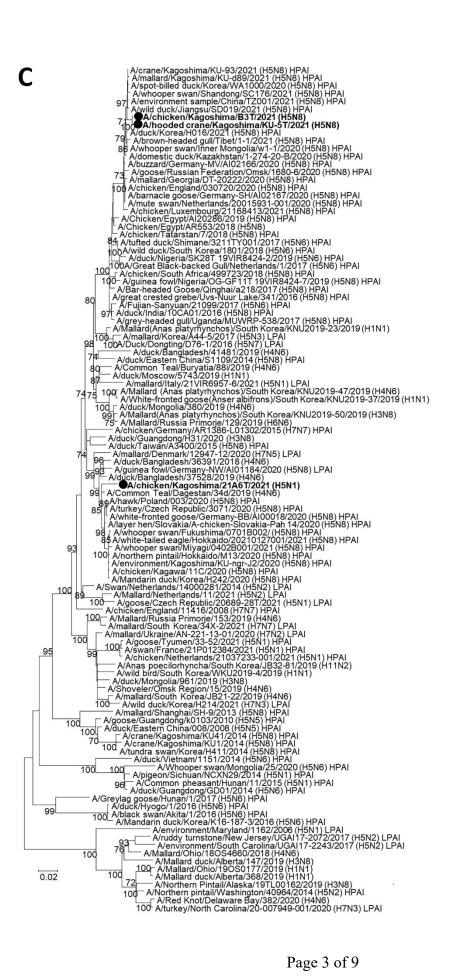
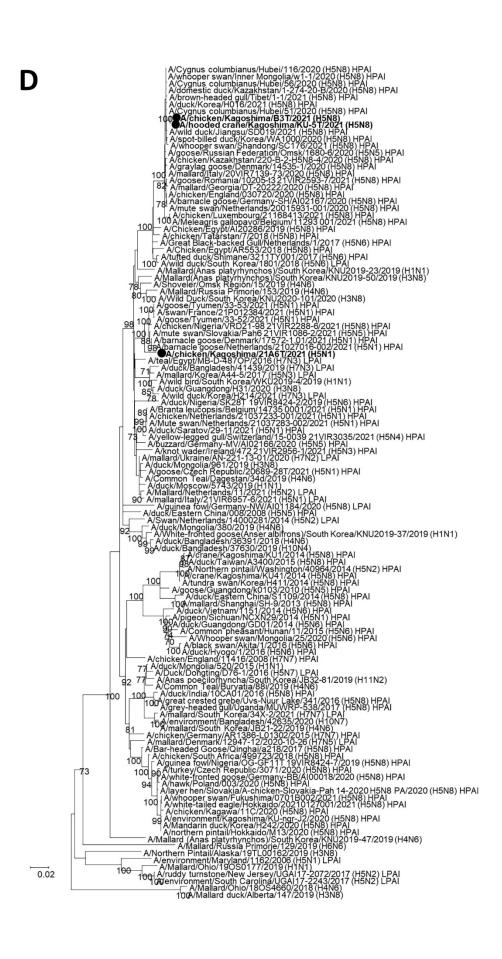
Genetically Diverse Highly Pathogenic Avian Influenza A(H5N1/H5N8) Viruses among Wild Waterfowl and Domestic Poultry, Japan, 2021

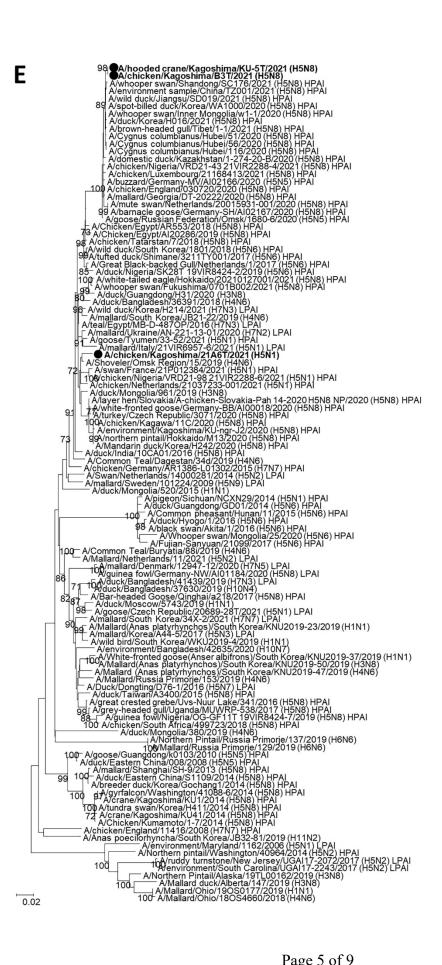
Appendix

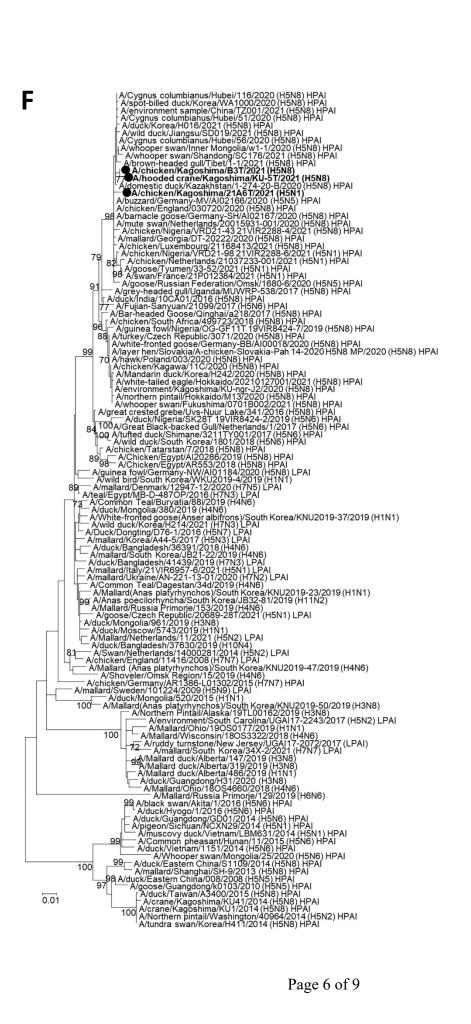








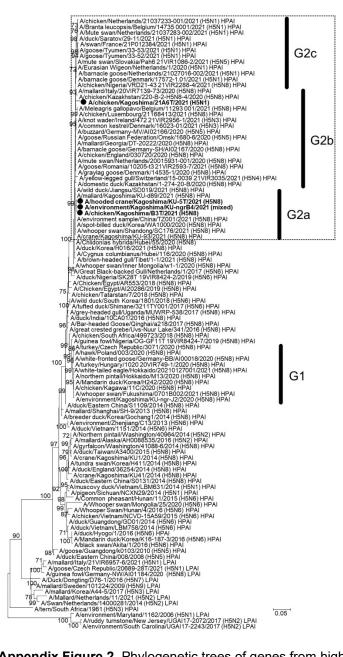




Awhooper swan/Shardong/SC176/2021 (HSN8) HPAI Awild dusk/Jaingays/South/Sc070000 (HSN8) HPAI Awild dusk/Jaingays/South/Sc07000 (HSN8) HPAI Awild dusk/Jaingays/Sc0700 (HSN8) HPAI Awild dusk/Jaingays/Jaing G 0.1



Appendix Figure 1. Phylogenetic tree of hemagglutinin genes of highly pathogenic avian influenza A(H5N1/H5N8) viruses isolated among wild waterfowl and domestic poultry on the Izumi plain, Japan in November 2021. We phylogenetically analyzed the nucleotide sequences of the genes from A/environment/Kagoshima/KU-ngrB4/2021 (mixed), A/chicken/Kagoshima/21A6T/2021 (H5N1), A/chicken/Kagoshima/B3T/2021 (H5N8), and A/hooded crane/Kagoshima/KU-5T/2021 (H5N8) with representative counterparts by using the maximum-likelihood method with a bootstrapping set of 1,000 replicates. Black circles with bold text indicate viruses isolated in this study. Area inside dotted box indicates genetic group 2 shown in Figure 2. Bootstrap values >70% are shown at the nodes. Scale bar indicates nucleotide substitutions per site. HPAI, highly pathogenic avian influenza; LPAI, low pathogenicity avian influenza.



Appendix Figure 2. Phylogenetic trees of genes from highly pathogenic avian influenza A(H5N1/H5N8) viruses isolated on the Izumi plain, Japan in November 2021. Trees represent H5N1 genes NA (A), PB2 (B), PB1 (C), PA (D), NP (E), M (F), and NSP (G); and the H5N8 NA gene (H). Genes from A/chicken/Kagoshima/21A6T/2021 (H5N1), A/chicken/Kagoshima/B3T/2021 (H5N8), and A/hooded crane/Kagoshima/KU-5T/2021 (H5N8) were phylogenetically analyzed with representative counterparts using the maximum-likelihood method with a bootstrapping set of 1,000 replicates. Black circles and bold text indicate viruses isolated in this study. Bootstrap values >70% are shown at the nodes. Scale bar indicates nucleotide substitutions per site. HA, hemagglutinin; HPAI, highly pathogenic avian influenza; LPAI, low pathogenicity avian influenza; M, matrix; NA, neuraminidase; NP, nucleoprotein; NSP, nonstructural protein; PA, polymerase; PB1, polymerase basic 1; PB2, polymerase basic 2.