

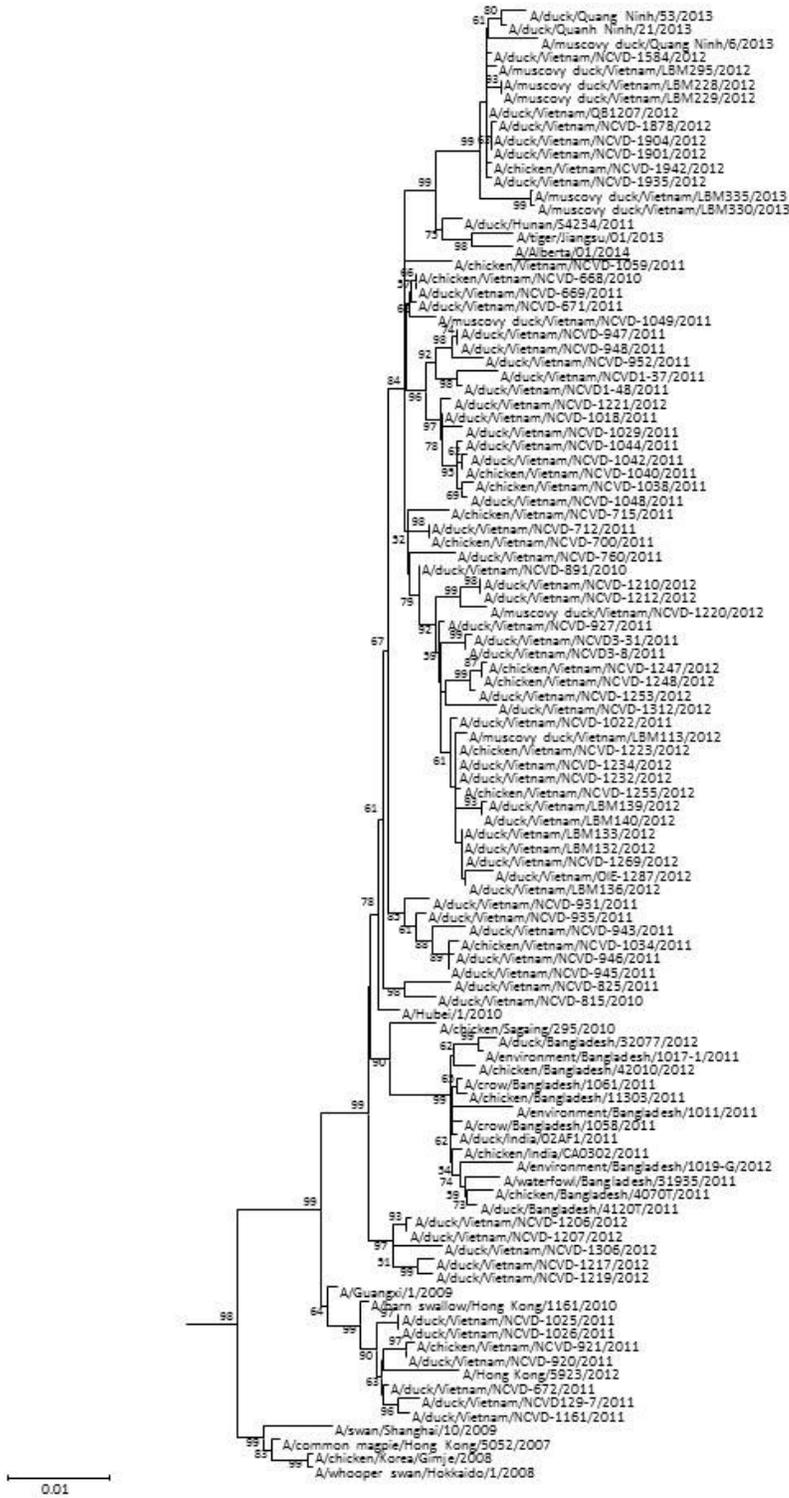
# Full-Genome Analysis of Avian Influenza A(H5N1) Virus from a Human, North America, 2013

## Technical Appendix 2

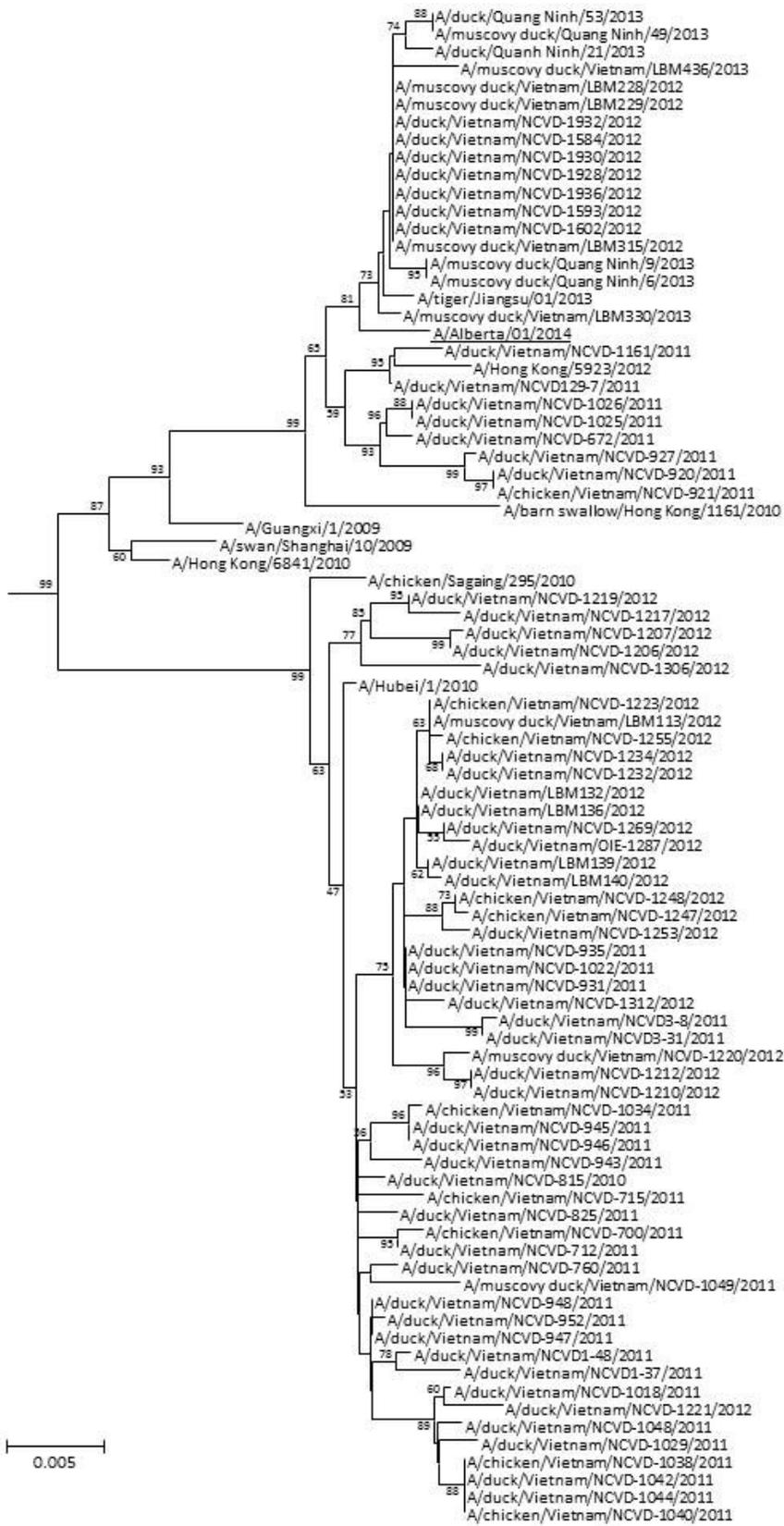
PB1



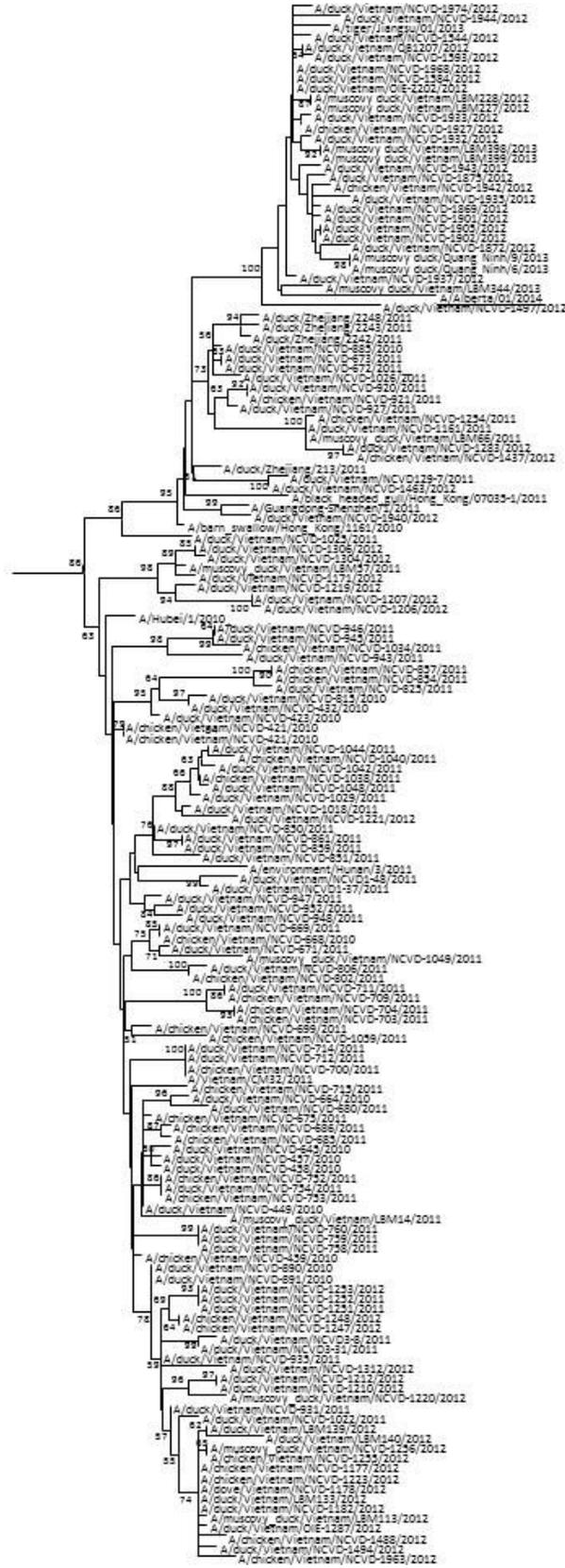
PA



NP



NA



M



NS

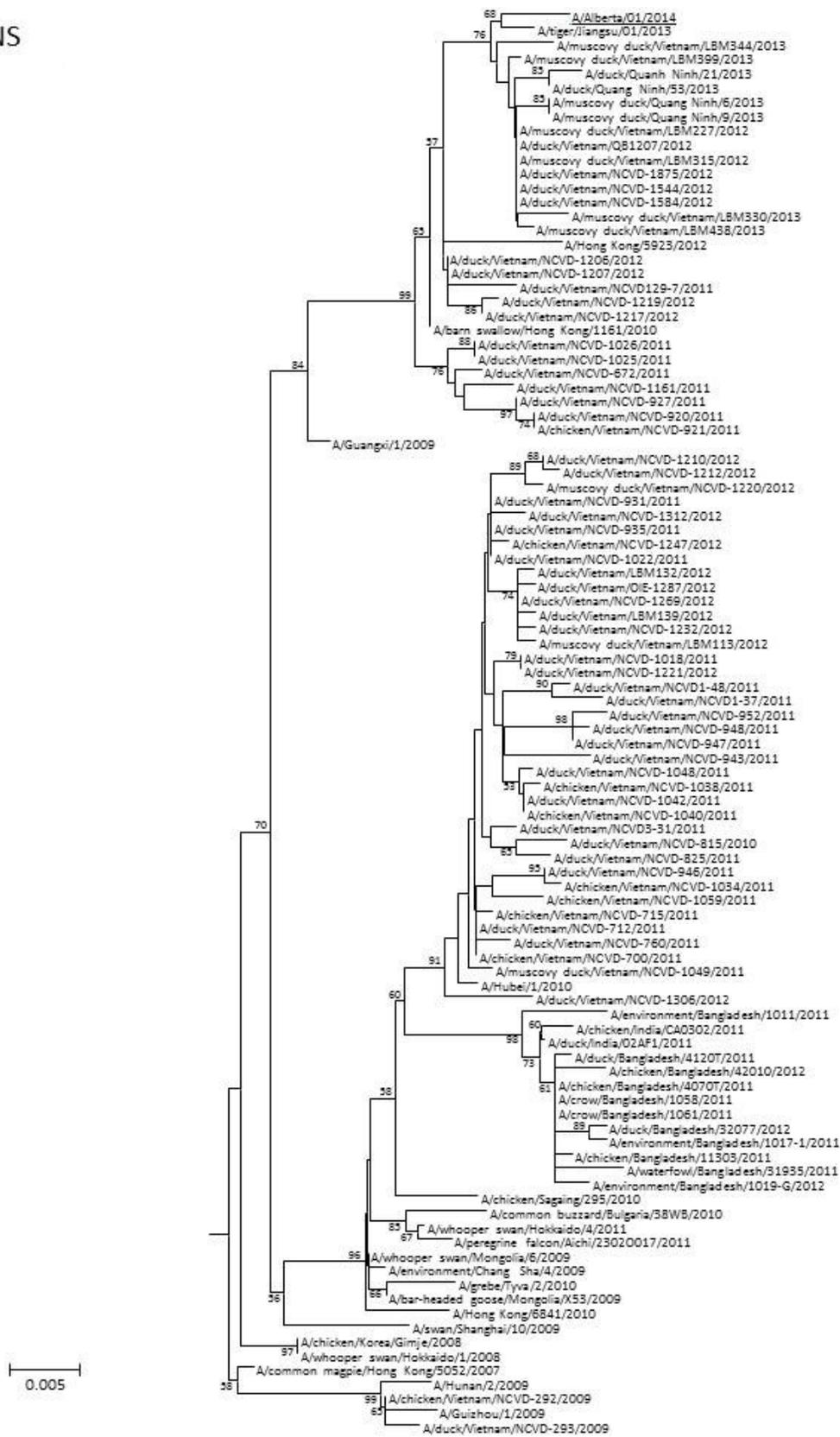


Figure. Neighbor-joining phylogenetic trees of the polymerase basic 1 (PB1) (GSAID accession no. EPI500777), polymerase (PA) (GSAID accession no. EPI500776), nucleoprotein (NP) (GSAID accession no. EPI500774), neuraminidase (NA) (GSAID accession no. EPI500773), matrix (M) (GSAID accession no. EPI500772), and nonstructural protein (NS) (GSAID accession no. EPI500775) genes of highly pathogenic avian influenza A(H5N1) viruses with A/Alberta/01/2014. The H5N1 virus detected in Canada is underlined. Bootstraps generated from 1,000 replicates are shown at branch nodes. Scale bar represents nucleotide substitutions per site. GSAID, Global Initiative on Sharing Avian Influenza Data.