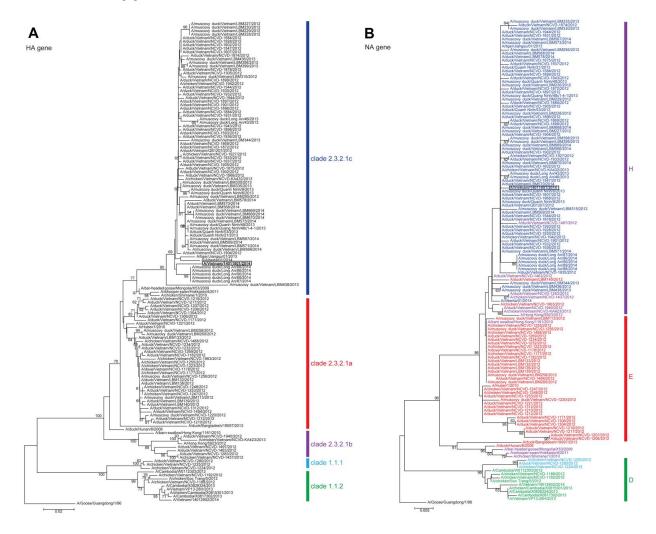
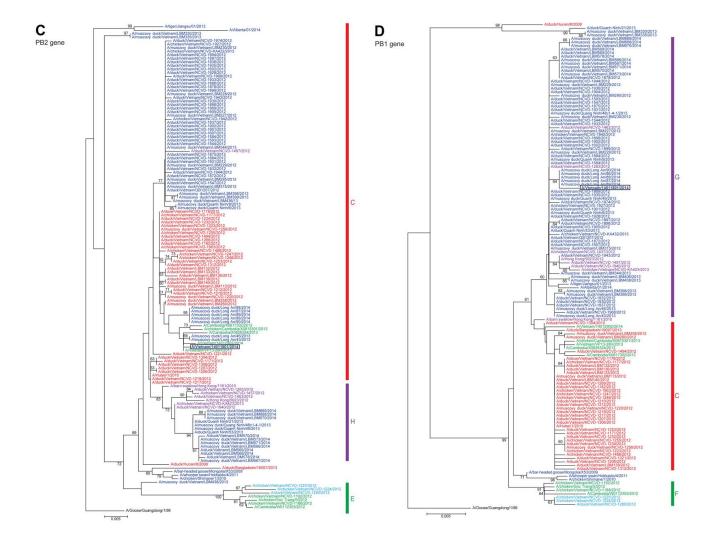
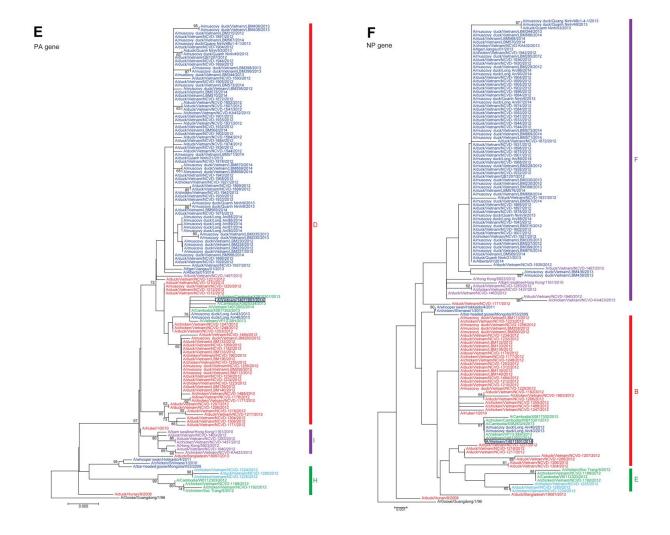
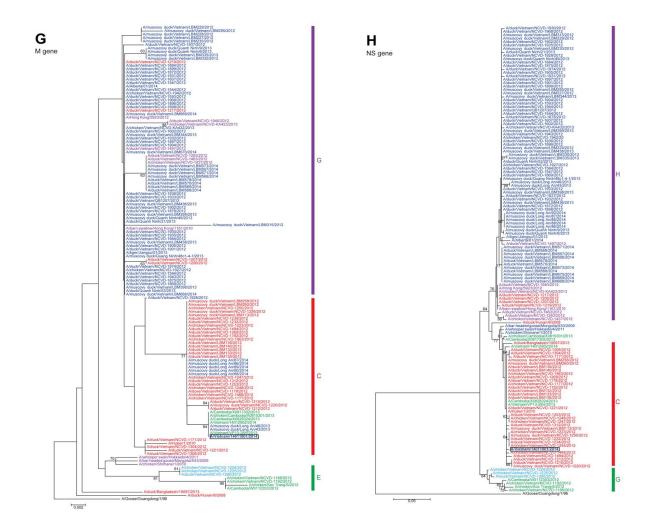
Novel Reassortant Avian Influenza A(H5N1) Virus in Human, Southern Vietnam, 2014

Technical Appendix









Technical Appendix Figure. Phylogenetic analyses of the genes of the avian influenza A(H5N1) virus described in this study: A) hemagglutinin (HA) gene; B) neuraminidase (NA) gene; C) polymerase basic (PB) 2 gene; D) PB1 gene; E) polymerase acid (PA) protein gene; F) nucleoprotein (NP) gene; G) matrix (M) gene; and H) nonstructural (NS) gene. Trees were constructed by using the neighbor-joining method. The evolutionary distances were computed by using the Kimura 2–parameter method. Bootstrap values were calculated from 1,000 replicates and values >60% are shown next to branches. Sequences of the A(H5N1) virus isolated in this study are in bold font and inside a box. Viruses are colored on the basis of their hemagglutinin clade: 1.1.1 in light blue; 1.1.2 in green; 2.3.2.1a in red; 2.3.2.1b in purple; and 2.3.2.1c in dark blue. Scale bars indicate nucleotide substitutions per site.