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Supplementary Fig. 1. The estimated maximum-clade-credibility phylogeny of eight genetic segments of clade 2.3.4.4b H5Nx viruses in Eurasia. Time-scaled phylogenies (dates shown on the horizontal axis) were inferred using relaxed-clock Bayesian Markov chain Monte Carlo analysis for each gene segment separately. (A) H5. (B) N6. (C) N8. (D) Polymerase basic 2 (PB2). (E) Polymerase basic 1 (PB1). (F) Polymerase acidic (PA). (G) Nucleoprotein (NP). (H) Matrix protein (MP). (I) Nonstructural (NS). The SRD06 nucleotide-substitution model and a Bayesian skyline coalescent tree prior were used in the analyses. For each gene segment, two independent runs were performed with a chain length of 100 million steps, with sampling every 10,000 steps. Tracer v1.6[1] was used for visual inspection of effective sample size (ESS) and chain convergence. The results from two runs were combined for analyses to ensure that an adequate ESS value (> 200) was reached for relevant parameters using Logcombiner v1.8.1 with 10% burn-in. The maximum-clade-credibility trees were generated with TreeAnnotator v1.8.1 and visualized with FigTree v1.4.2. The clade 2.3.4.4b H5N6 isolates in South Korea and other countries are labeled in red and blue, respectively. The isolates in this study are indicated by dots. Several clusters of the PB2, PB1, PA, and NP genes were indicated by different color. Branch lengths represent time. Posterior probabilities of > 0.7 are provided for key nodes.

1. **Rambaut A, Drummond AJ, Xie D, Baele G, Suchard MA.** Posterior summarization in Bayesian phylogenetics using Tracer 1.7. Syst Biol 2018, **67**, 901-904.
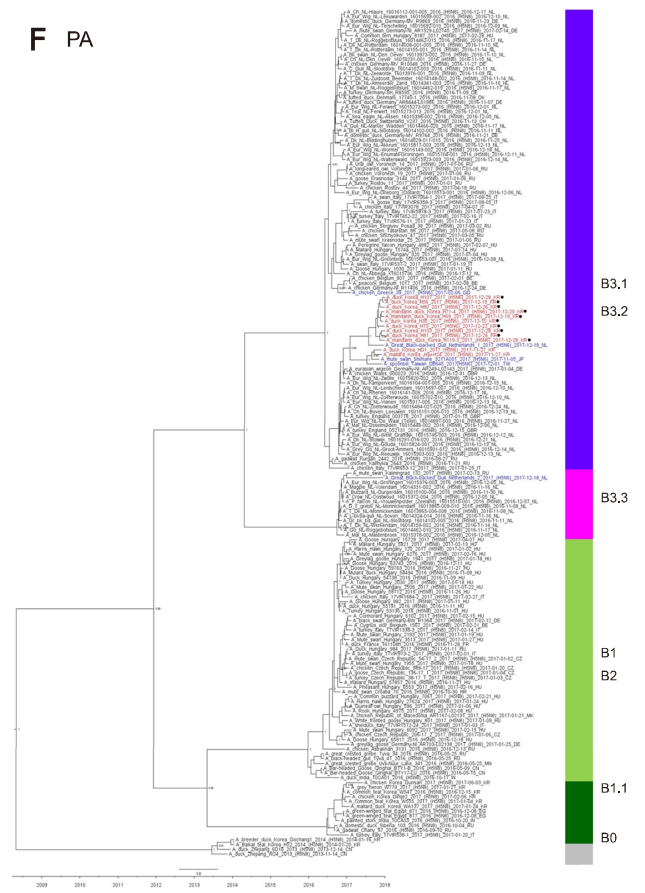
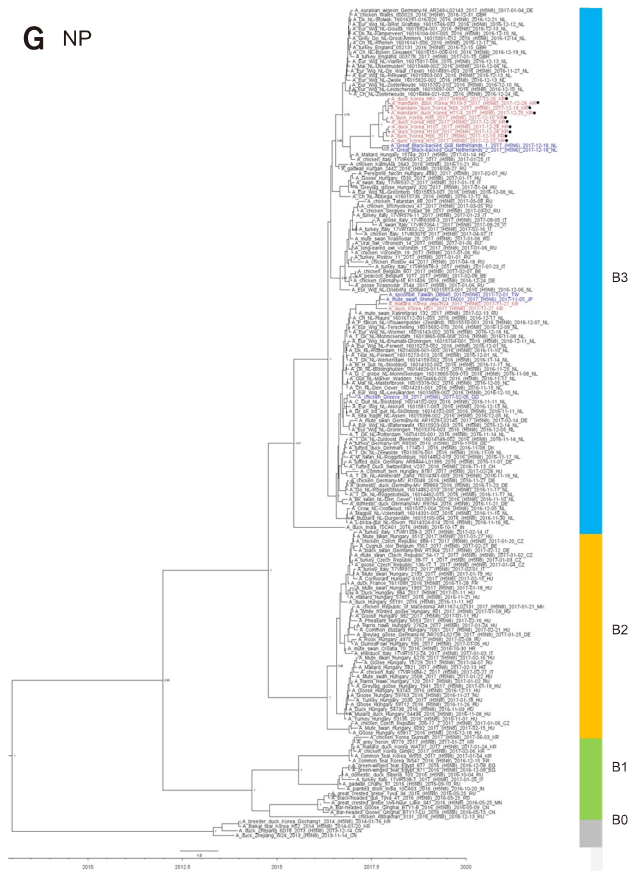**C** N8

D PB2
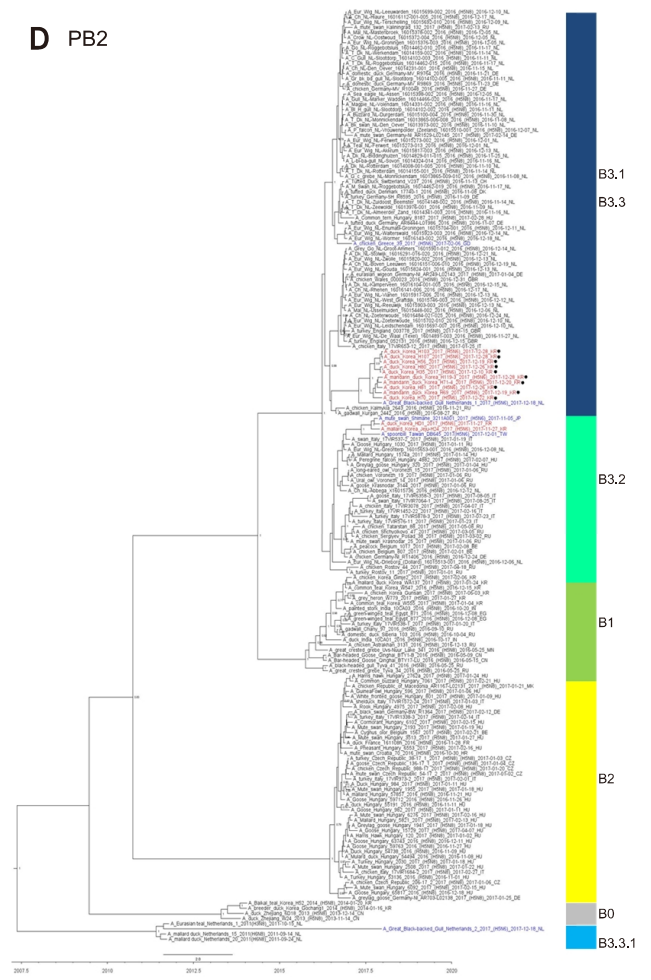
Supplementary Fig. 1. Continued.
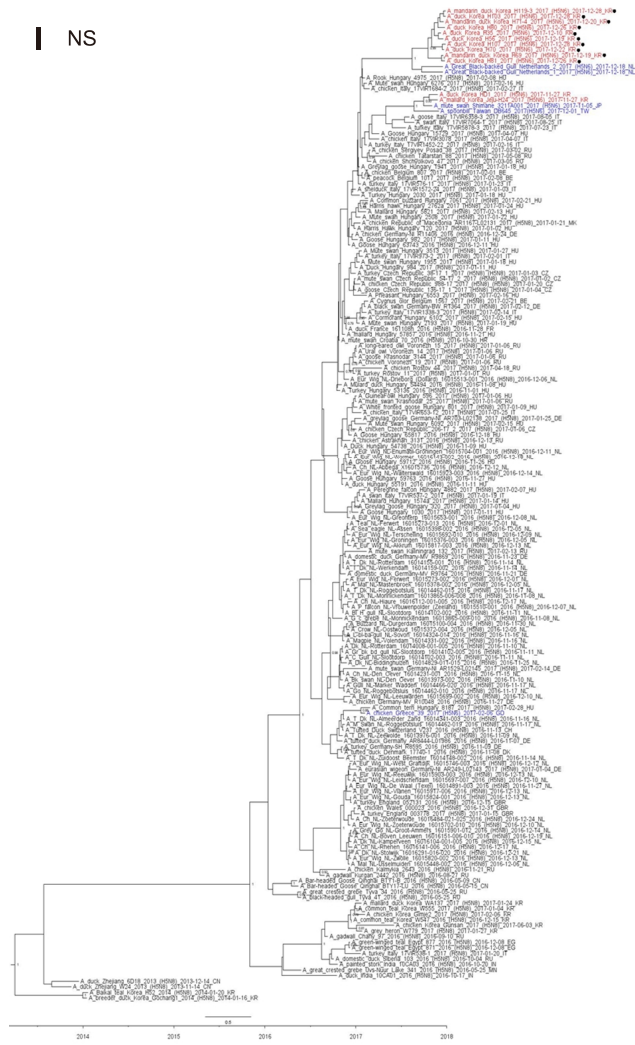
E PB1

F PA

Supplementary Fig. 1. Continued.

G NP

H MP

Supplementary Fig. 1. Continued.

Supplementary Fig. 1. Continued.