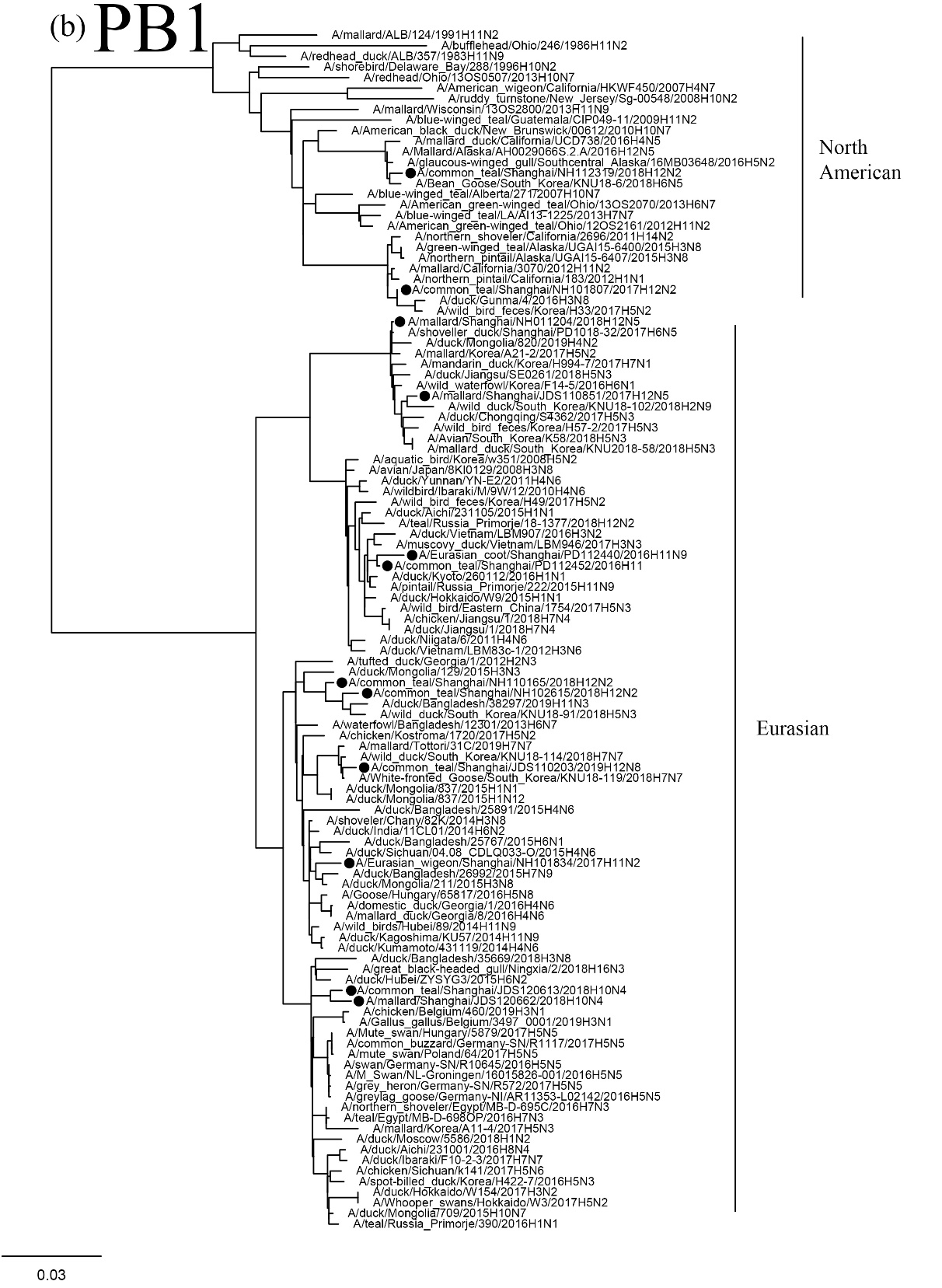
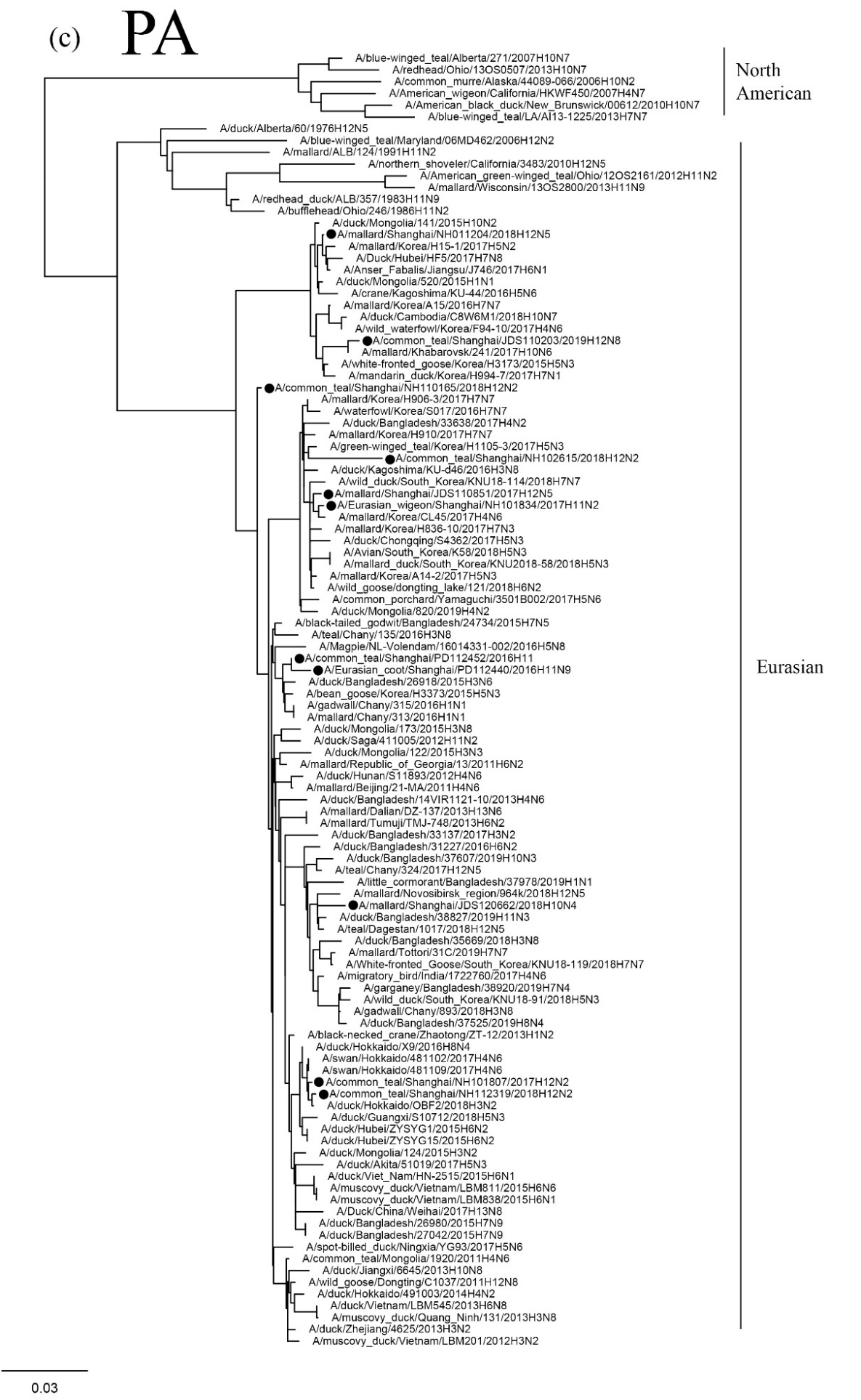


**Supplementary Figure S1a.** Phylogenetic trees of the PB2 genes of the H10-H12 subtype isolates found in Shanghai, China. PB2 genes are 21-2303 bp. The maximum likelihood (ML) tree was constructed using the GTR+G model in PhyML software version 3.0. Bootstrap values were calculated for 1,000 replicates, and values less than 75% are not shown. Number indicate the ML bootstrap values. The viruses characterized in this study are indicated by black circles.



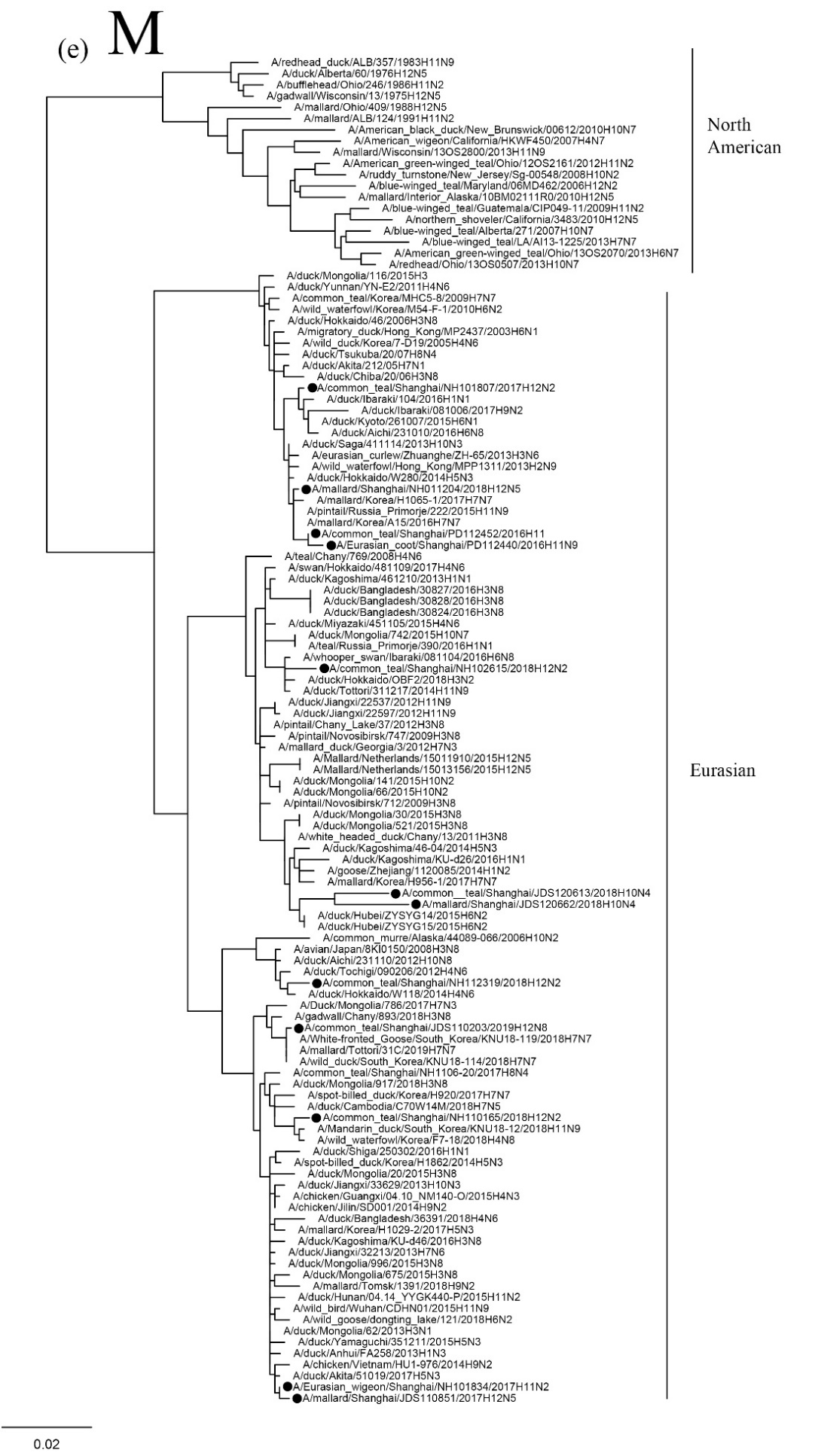
**Supplementary Figure S1b.** Phylogenetic trees of the PB1 genes of the H10-H12 subtype strains isolated in Shanghai, China. PB1 genes are 18-2291 bp. The analysis methods were the same as described in Figure S1a.



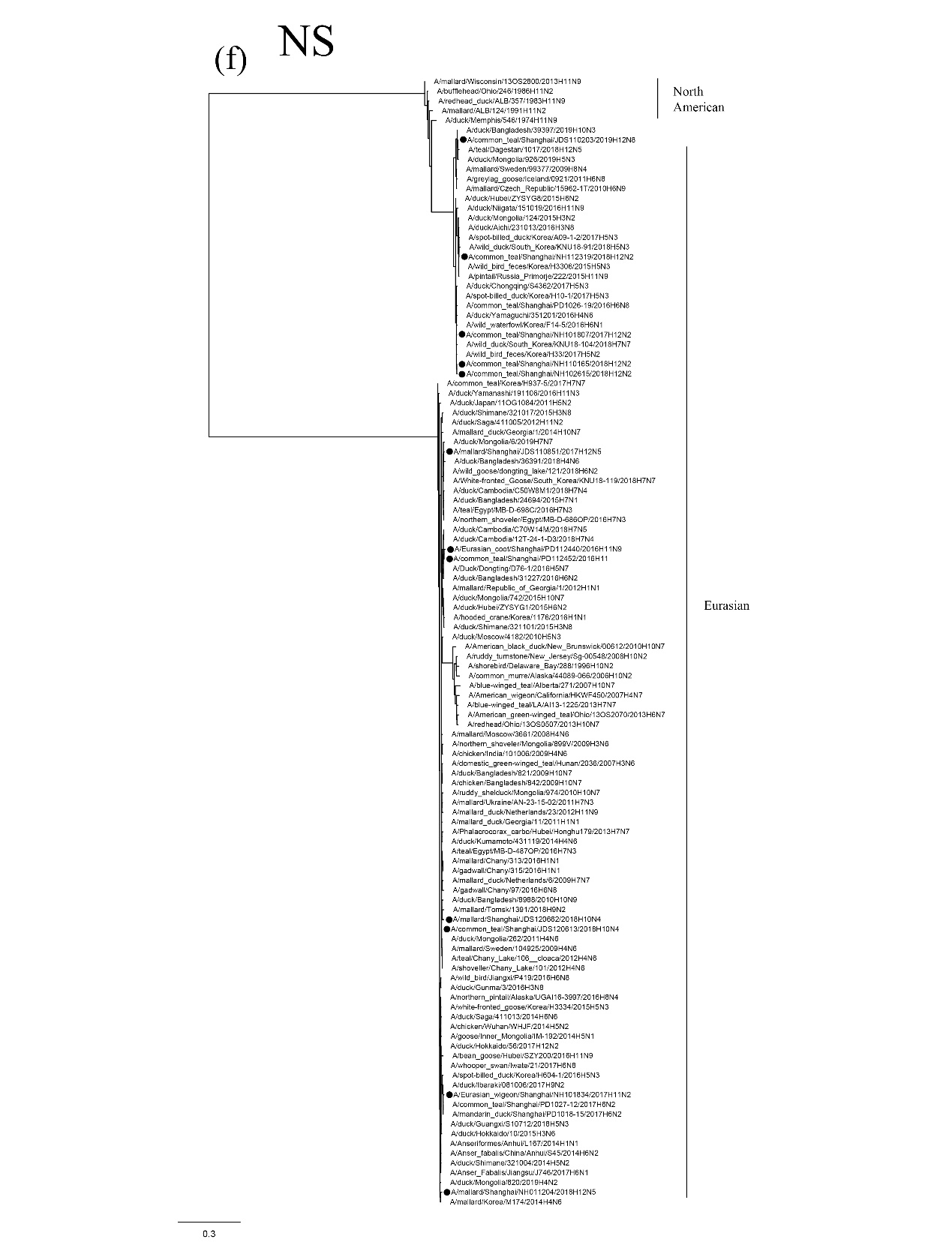
**Supplementary Figure S1c.** Phylogenetic trees of the PA genes of the H10-H12 subtype strains isolated in Shanghai, China. PA genes are 18-2167 bp. The analysis methods were the same as described in Figure S1a.



**Supplementary Figure S1d.** Phylogenetic trees of the NP genes of the H10-H12 subtype strains isolated in Shanghai, China. PB2 genes are 46-1543 bp. The maximum likelihood (ML) tree was constructed using the GTR+I+G model in PhyML software version 3.0. Bootstrap values were calculated for 1,000 replicates, and values less than 75% are not shown. Number indicate the ML bootstrap values. The viruses characterized in this study are indicated by black circles.



**Supplementary Figure S1e.** Phylogenetic trees of the M genes of the H10-H12 subtype strains isolated in Shanghai, China. M genes are 19-1000 bp. The analysis methods were the same as described in Figure S1d.



**Supplementary Figure S1f.** Phylogenetic trees of the NS genes of the H10-H12 subtype strains isolated in Shanghai, China. NS genes are 1-838 bp. The maximum likelihood (ML) tree was constructed using the TPM2uf+I+G model in PhyML software version 3.0. Bootstrap values were calculated for 1,000 replicates, and values less than 75% are not shown. Number indicate the ML bootstrap values. The viruses characterized in this study are indicated by black circles.