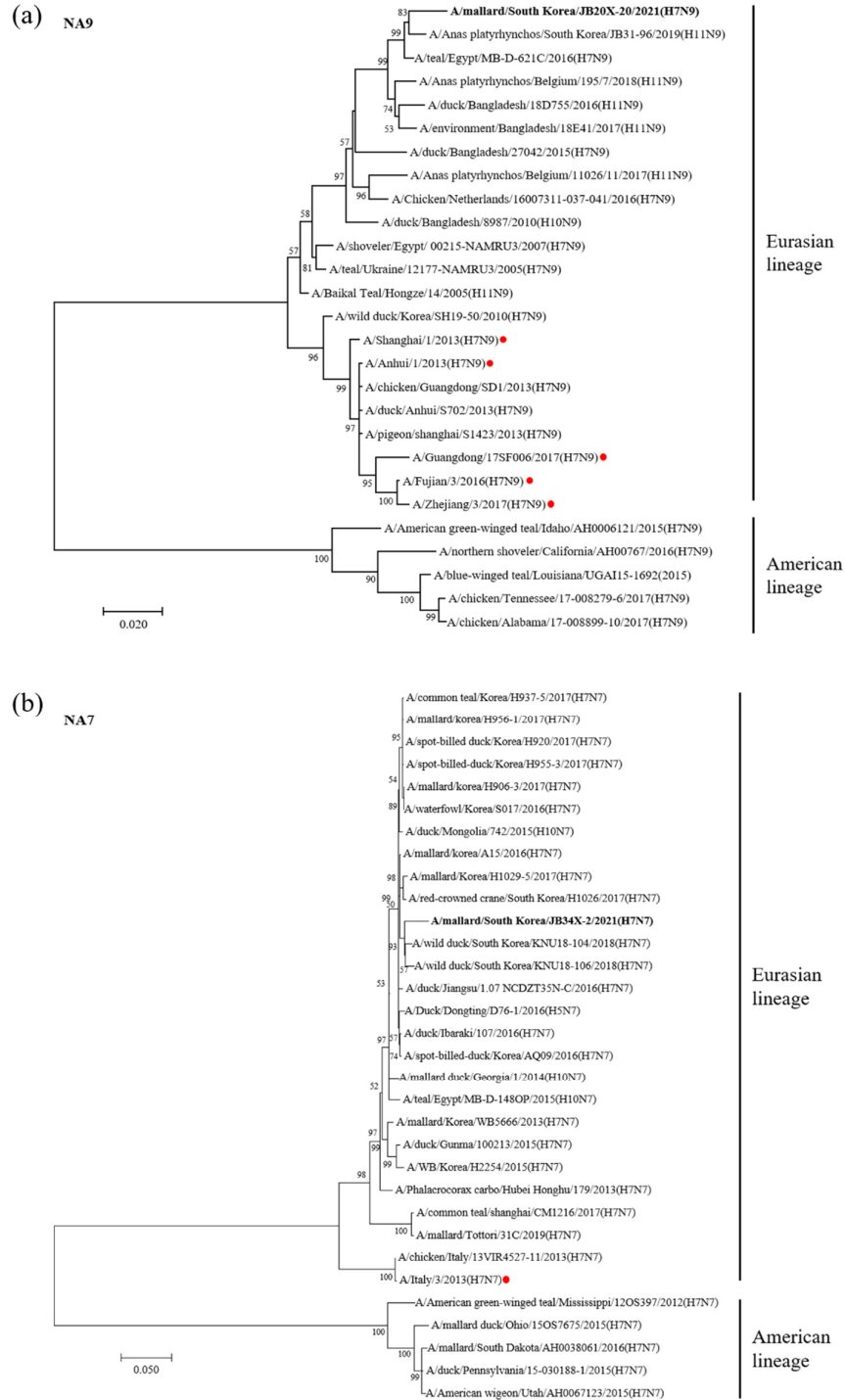
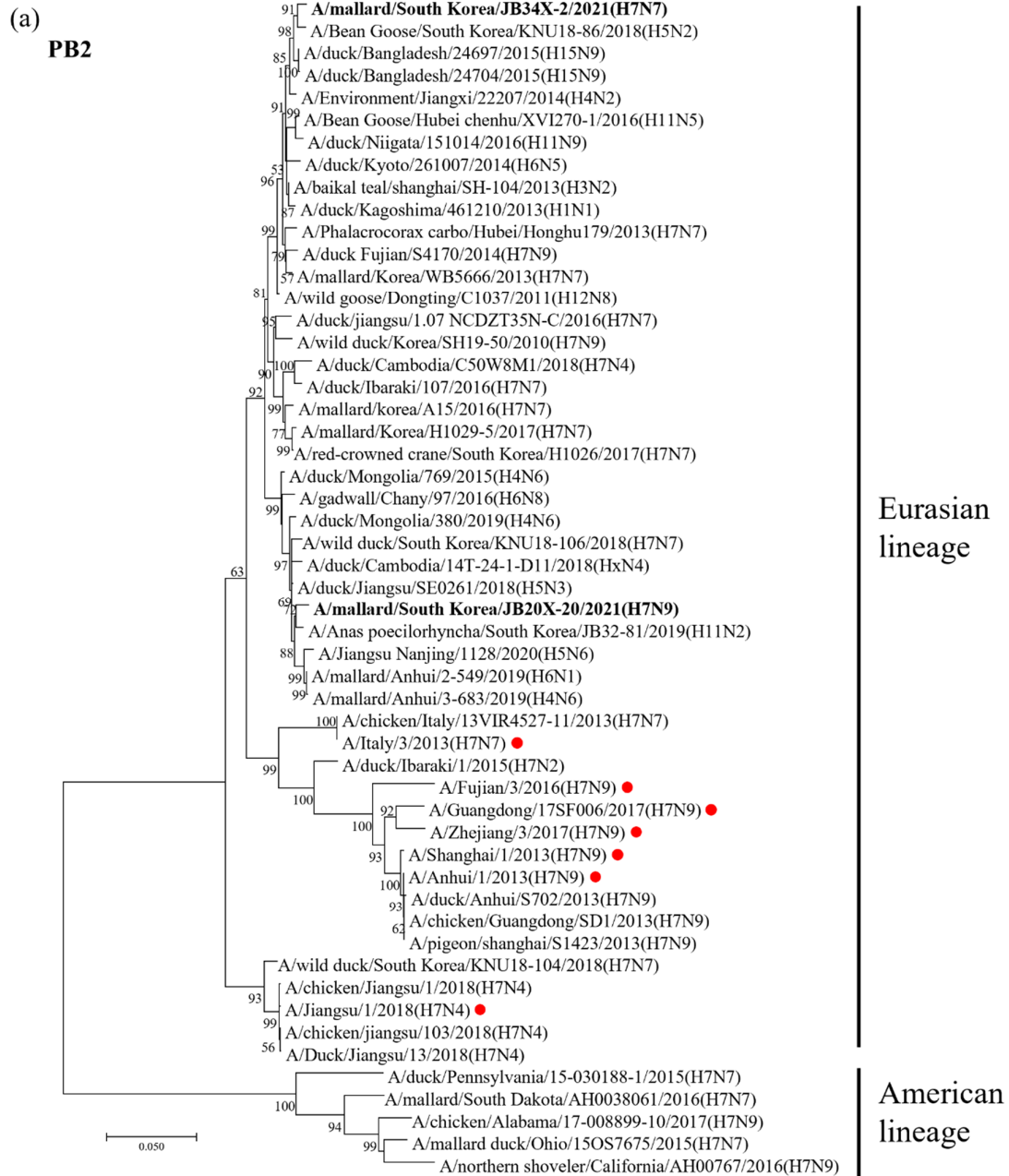


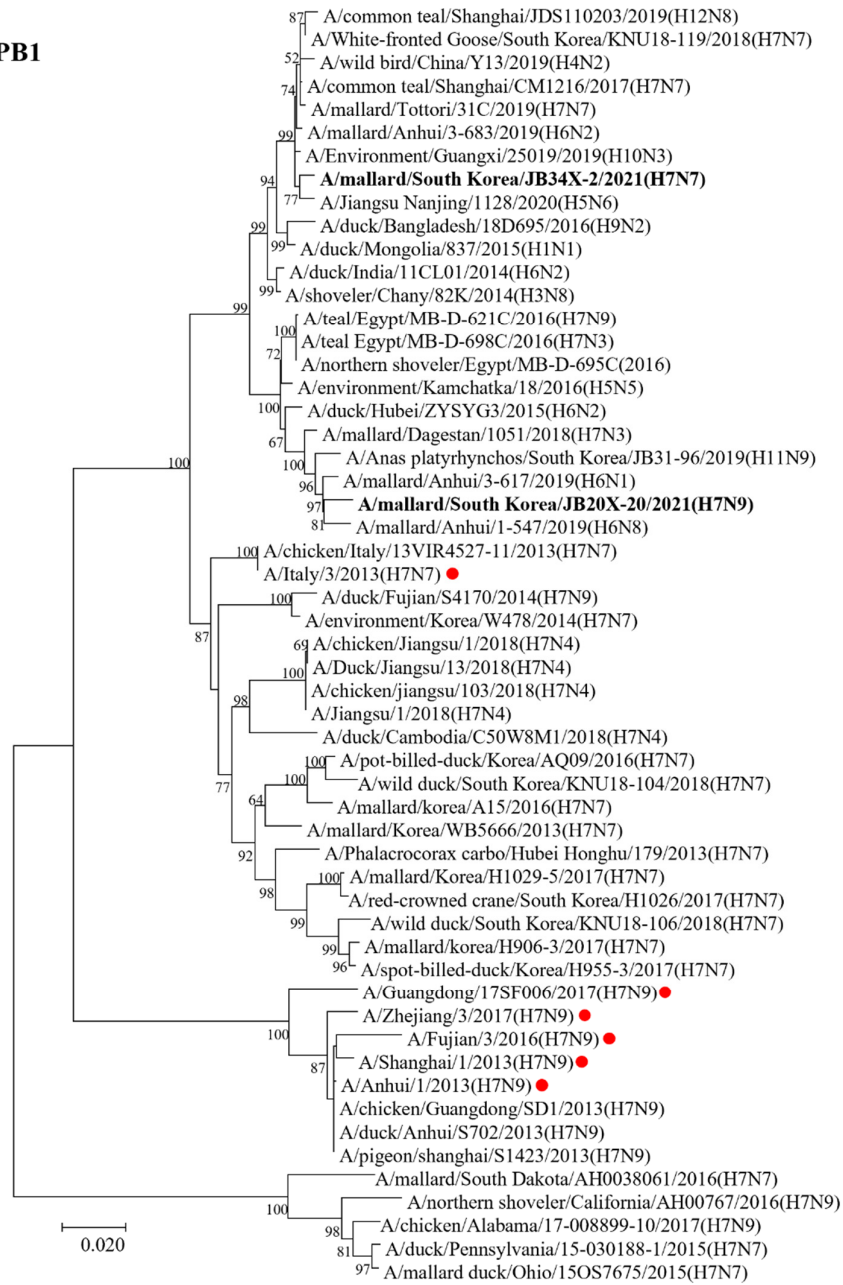
Supplementary Figure S1. Phylogenetic tree of the NA9 (a) and NA7 (b) gene based on nucleotides. The tree was analyzed using the maximum-likelihood (ML) method with 1,000 bootstrap replication and only bootstrap values more than 50% are shown. The two H7 Korean avian influenza viruses (AIVs) isolated in this study are shown in bold. The human influenza viruses are indicated by red circles.



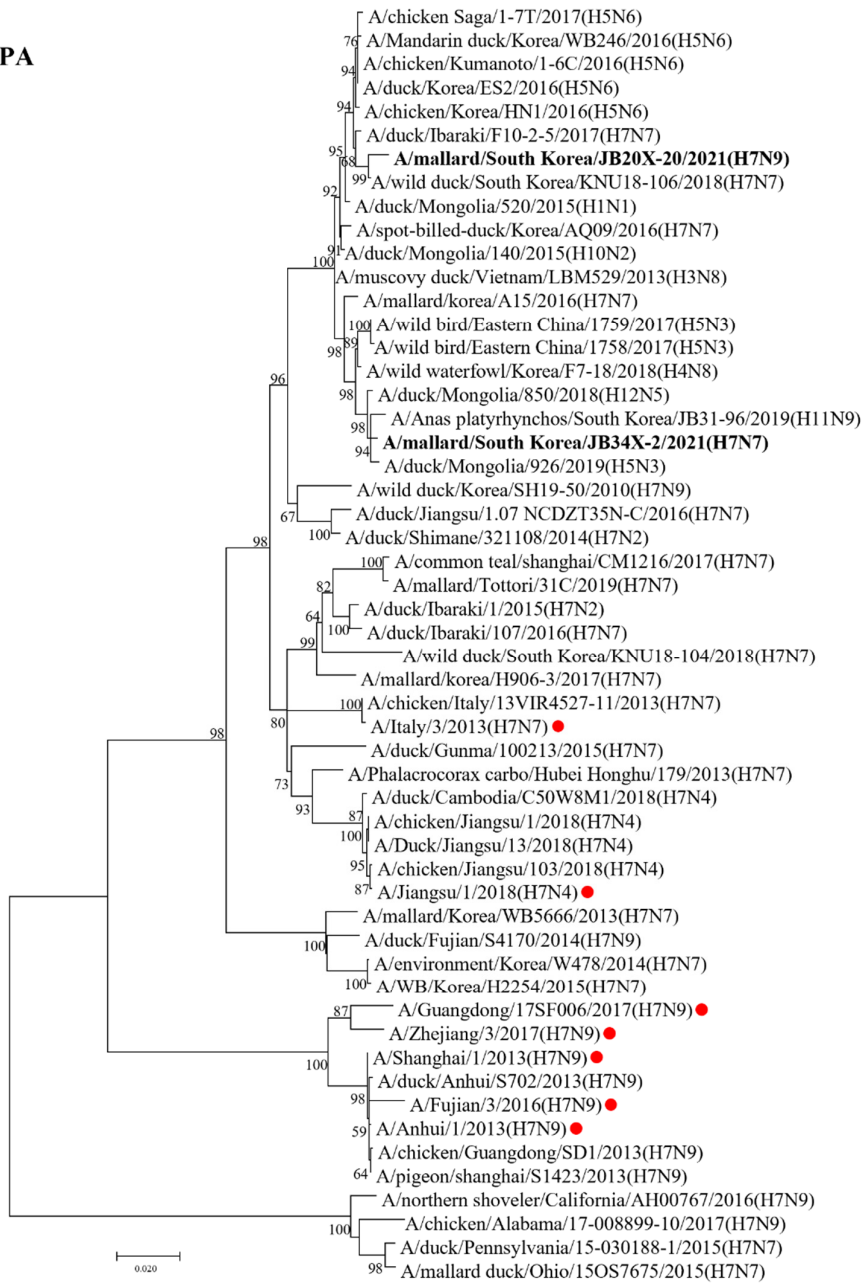
Supplementary Figure S2. Phylogenetic tree of the PB2 (a), PB1 (b), PA (c), NP (d), M (e), and NS (f) genes based on nucleotides. The tree was analyzed using the maximum-likelihood (ML) method with 1,000 bootstrap replication and only bootstrap values more than 50% are shown. The two H7 Korean AIVs isolated in this study are shown in bold. The human influenza viruses are indicated by red circles.



(b) PB1

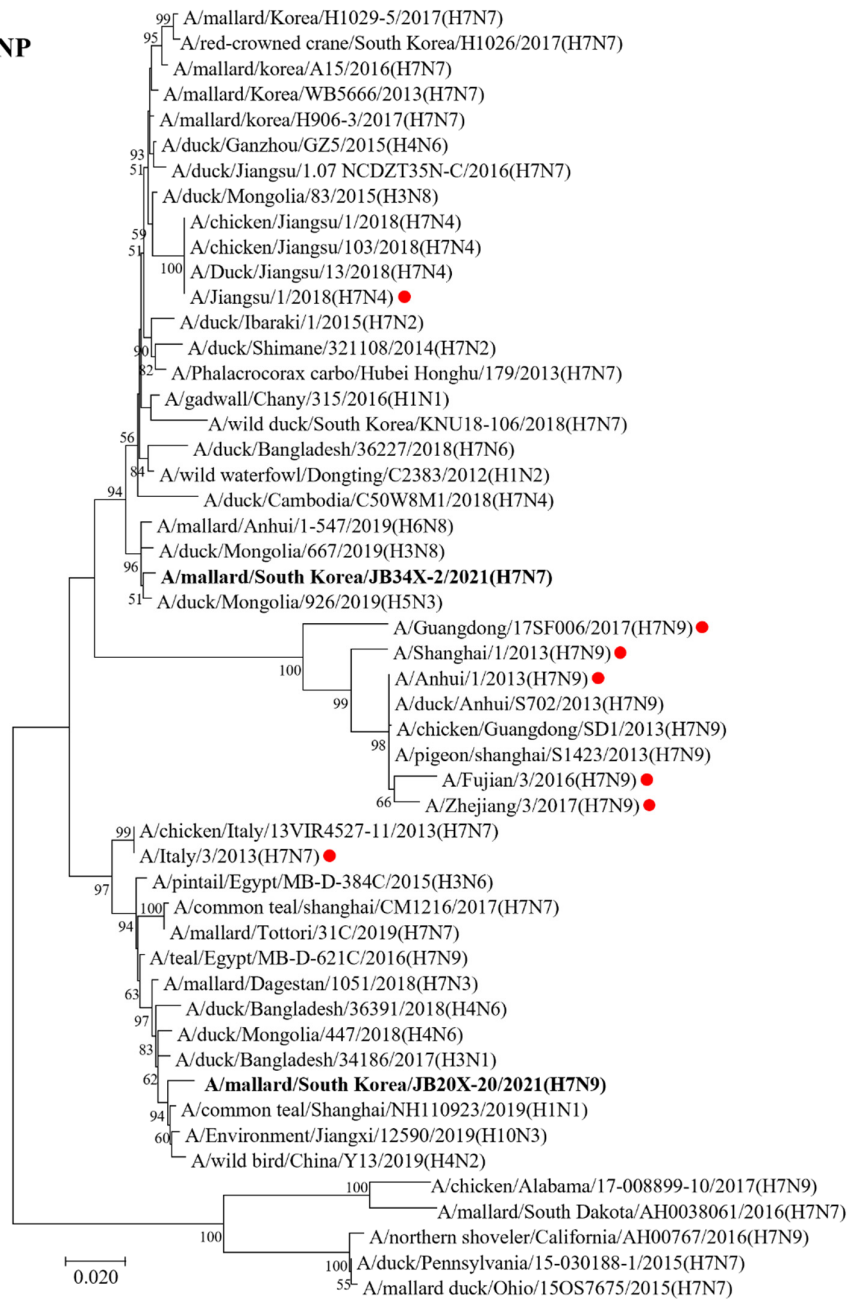


(c)
PA



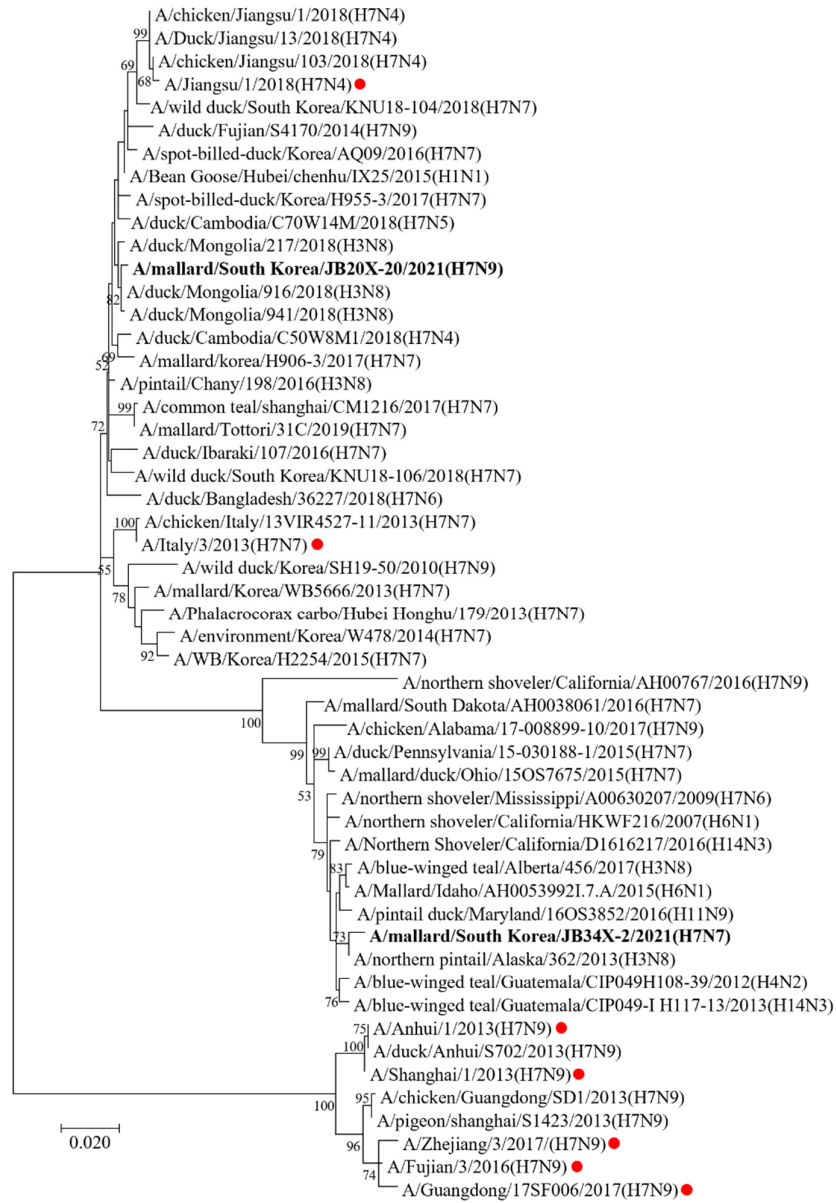
(d)

NP

Eurasian
lineageAmerican
lineage

(e)

M



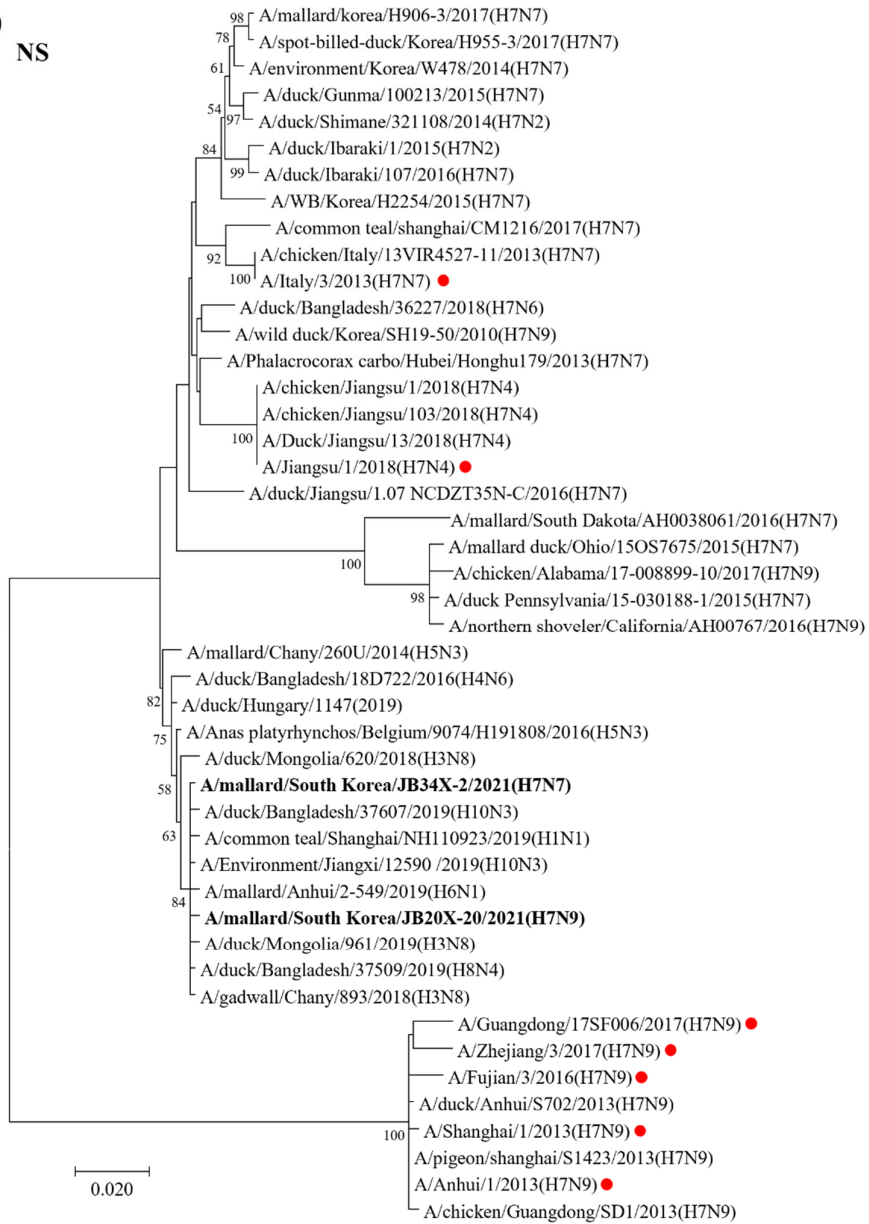
Eurasian
lineage

American
lineage

Eurasian
lineage

(f)

NS

Eurasian
lineageAmerican
lineageEurasian
lineage