

Supplementary Figure S1A.

N2

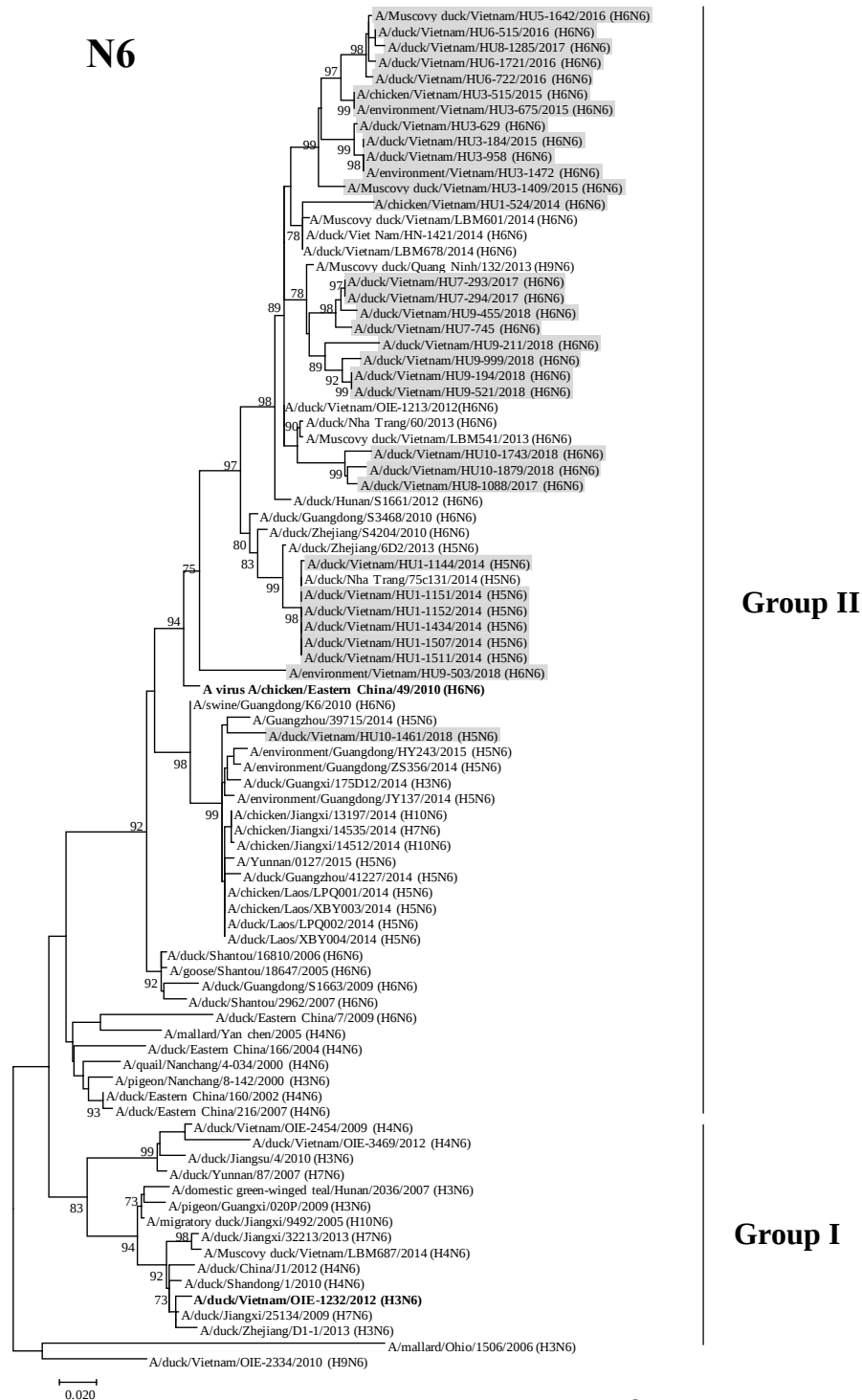


Y280/
BJ94

Group II

Supplementary Figure S1. Phylogenetic tree of the NA and internal gene segments of H9 and H6 avian influenza viruses. The N2, N6, PB2, PB1, PA, NP, M, and NS genes were used for ML phylogenetic analysis using MEGA 7.0 software. The digits at the nodes indicate the probability of the confidence levels from 1,000 bootstrap replicates. The studied viruses are highlighted in gray and the representative of each sublineage is indicated in bold.

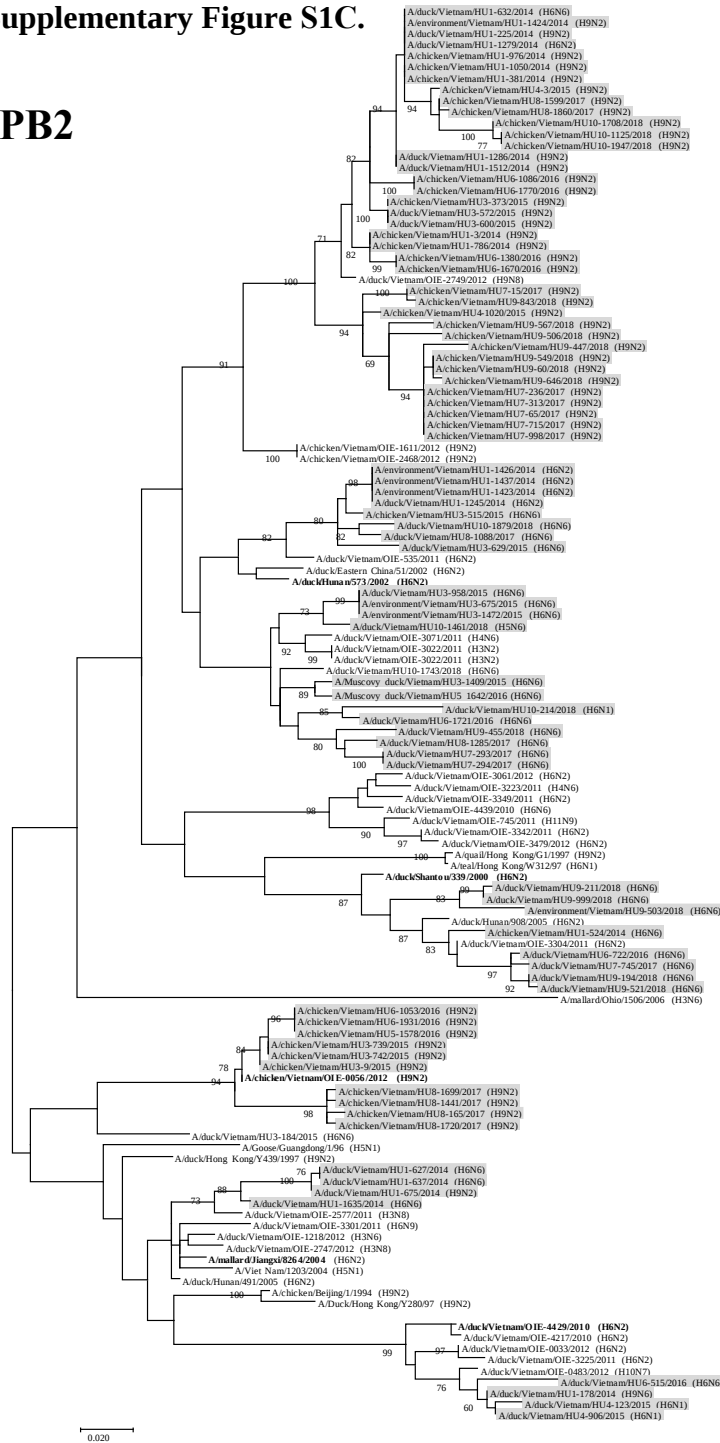
Supplementary Figure S1B.



Supplementary Figure S1 (cont). Phylogenetic tree of the NA and internal gene segments of H9 and H6 avian influenza viruses. The N2, N6, PB2, PB1, PA, NP, M, and NS genes were used for ML phylogenetic analysis using MEGA 7.0 software. The digits at the nodes indicate the probability of the confidence levels from 1,000 bootstrap replicates. The studied viruses are highlighted in gray and the representative of each sublineage is indicated in bold.

Supplementary Figure S1C.

PB2



H6
group III

H6
group I

H9 China

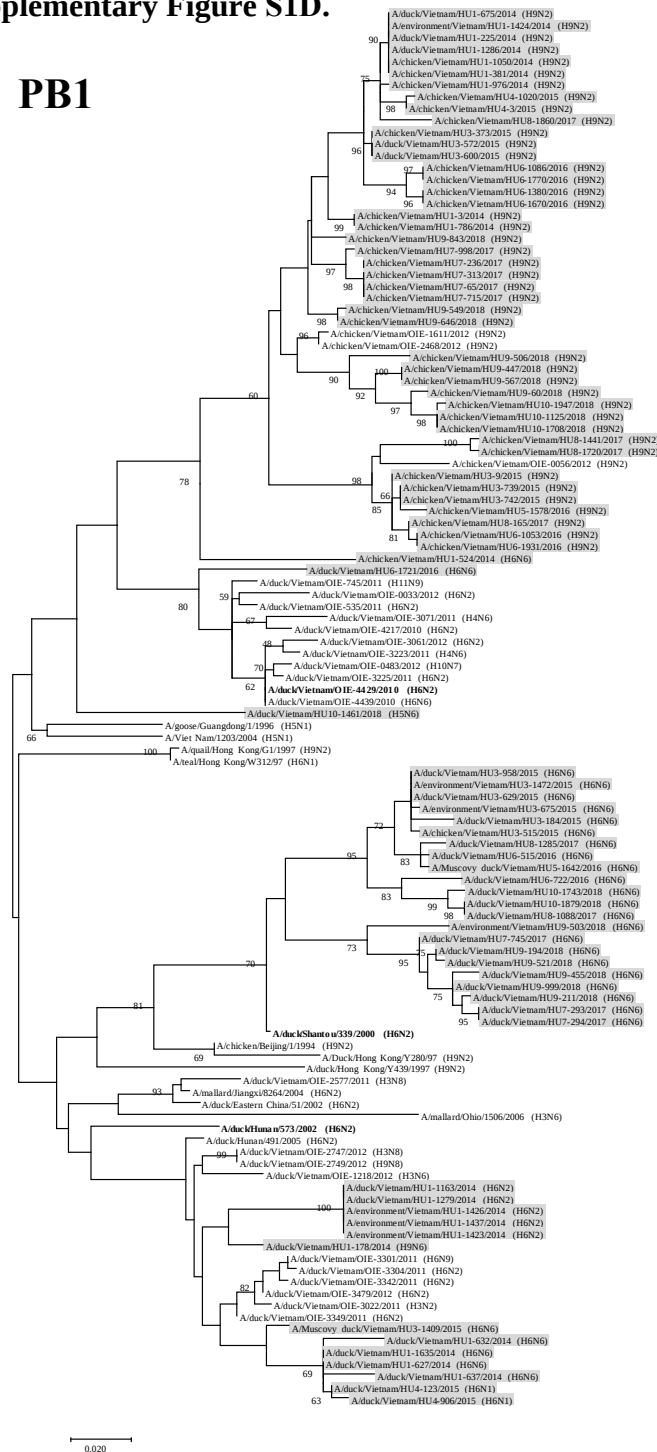
JX8264-like

Vietnam

Supplementary Figure S1 (cont). Phylogenetic tree of the NA and internal gene segments of H9 and H6 avian influenza viruses. The N2, N6, PB2, PB1, PA, NP, M, and NS genes were used for ML phylogenetic analysis using MEGA 7.0 software. The digits at the nodes indicate the probability of the confidence levels from 1,000 bootstrap replicates. The studied viruses are highlighted in gray and the representative of each sublineage is indicated in bold.

Supplementary Figure S1D.

PB1



Vietnam

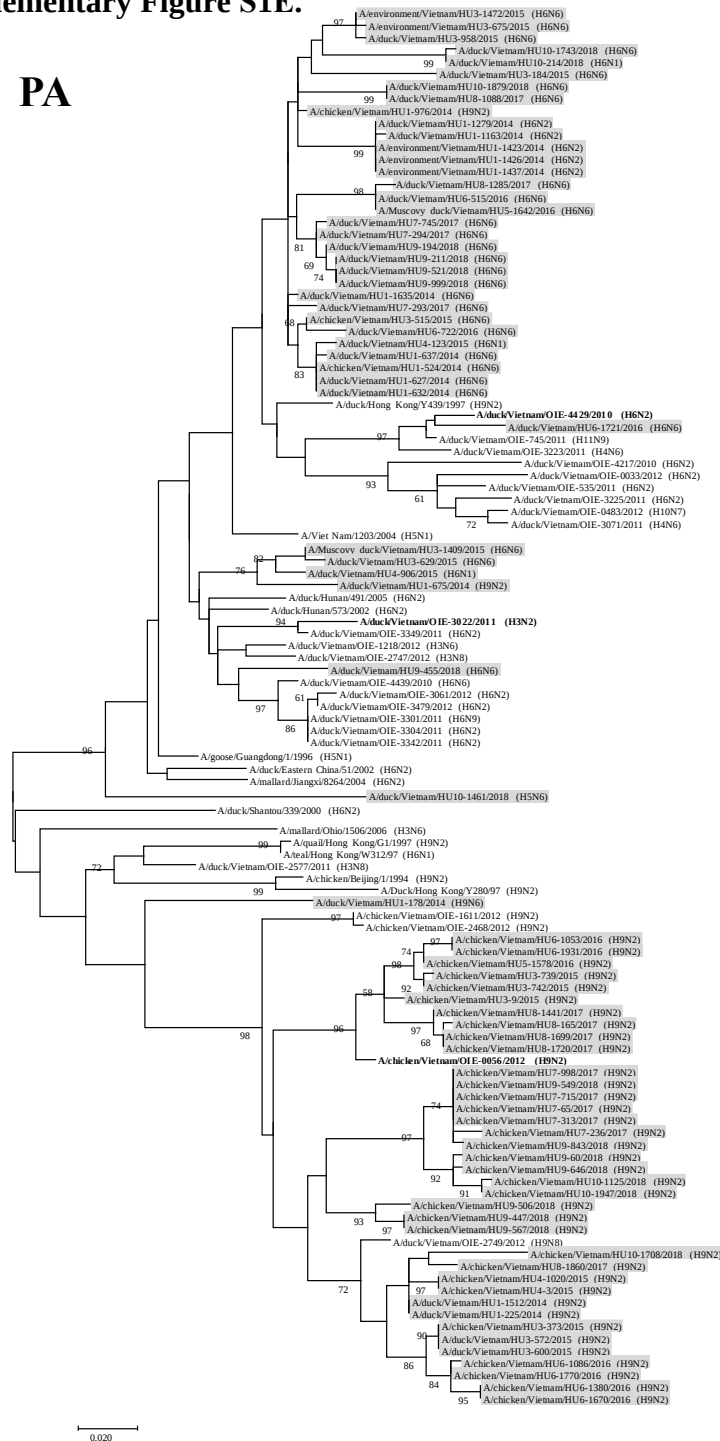
H6 group I

Hunan491-like

Supplementary Figure S1 (cont). Phylogenetic tree of the NA and internal gene segments of H9 and H6 avian influenza viruses. The N2, N6, PB2, PB1, PA, NP, M, and NSgenes were used for ML phylogenetic analysis using MEGA 7.0 software. The digits at the nodes indicate the probability of the confidence levels from 1,000 bootstrap replicates. The studied viruses are highlighted in gray and the representative of each sublineage is indicated in bold.

Supplementary Figure S1E.

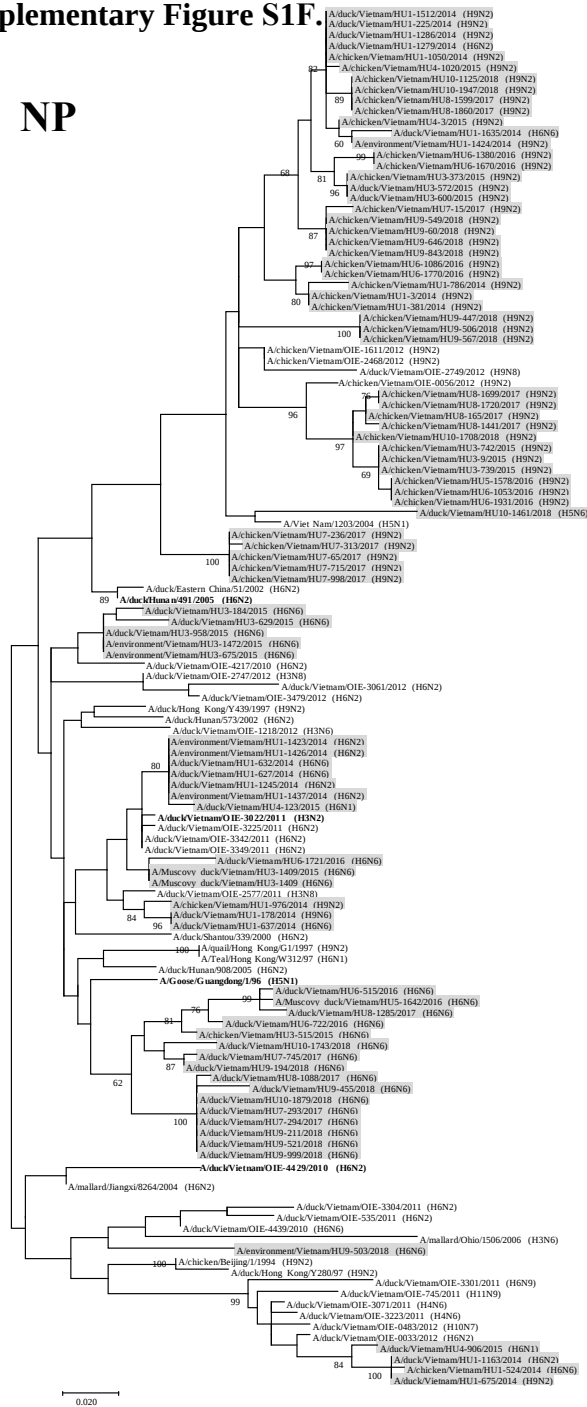
PA



Supplementary Figure S1 (cont). Phylogenetic tree of the NA and internal gene segments of H9 and H6 avian influenza viruses. The N2, N6, PB2, PB1, PA, NP, M, and NS genes were used for ML phylogenetic analysis using MEGA 7.0 software. The digits at the nodes indicate the probability of the confidence levels from 1,000 bootstrap replicates. The studied viruses are highlighted in gray and the representative of each sublineage is indicated in bold.

Supplementary Figure S1F.

NP



Hunan491-like

Wild bird

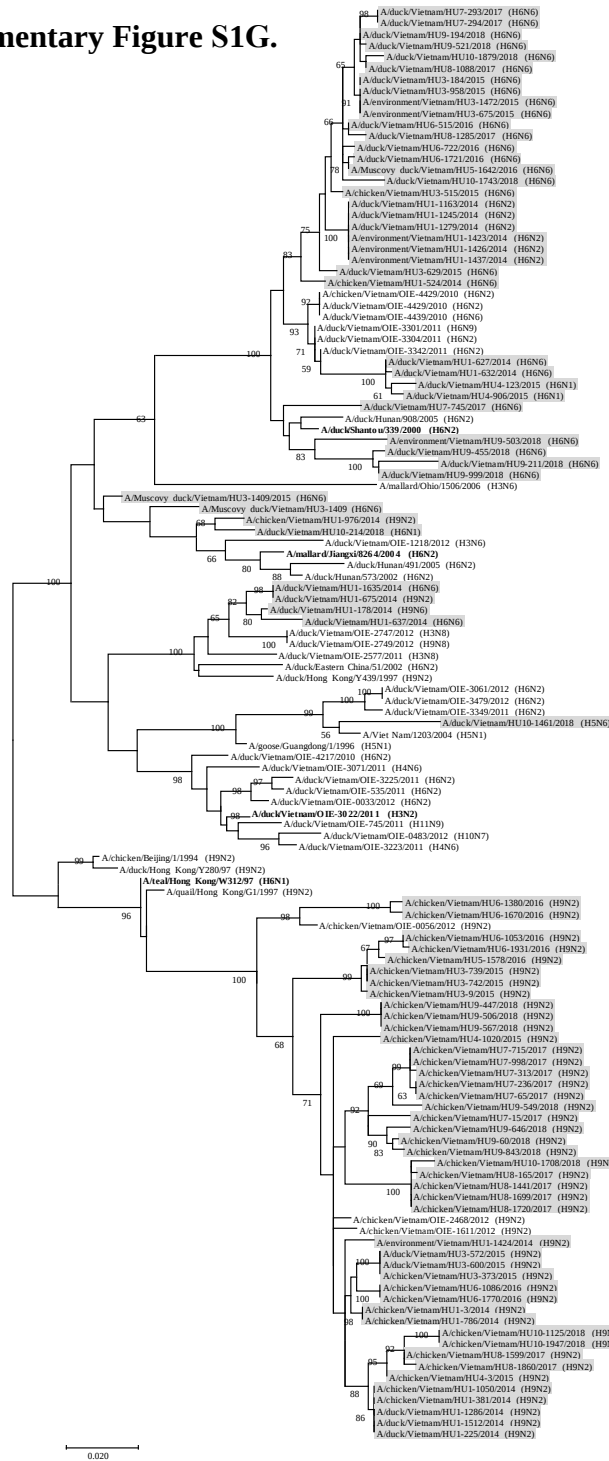
Gs/Gd-like

Vietnam

Supplementary Figure S1 (cont). Phylogenetic tree of the NA and internal gene segments of H9 and H6 avian influenza viruses. The N2, N6, PB2, PB1, PA, NP, M, and NSgenes were used for ML phylogenetic analysis using MEGA 7.0 software. The digits at the nodes indicate the probability of the confidence levels from 1,000 bootstrap replicates. The studied viruses are highlighted in gray and the representative of each sublineage is indicated in bold.

Supplementary Figure S1G.

M



H6 group I

JX8264-like

Wild bird

H6 W312

Supplementary Figure S1 (cont). Phylogenetic tree of the NA and internal gene segments of H9 and H6 avian influenza viruses. The N2, N6, PB2, PB1, PA, NP, M, and NSgenes were used for ML phylogenetic analysis using MEGA 7.0 software. The digits at the nodes indicate the probability of the confidence levels from 1,000 bootstrap replicates. The studied viruses are highlighted in gray and the representative of each sublineage is indicated in bold.

Supplementary Figure S1H.

NS

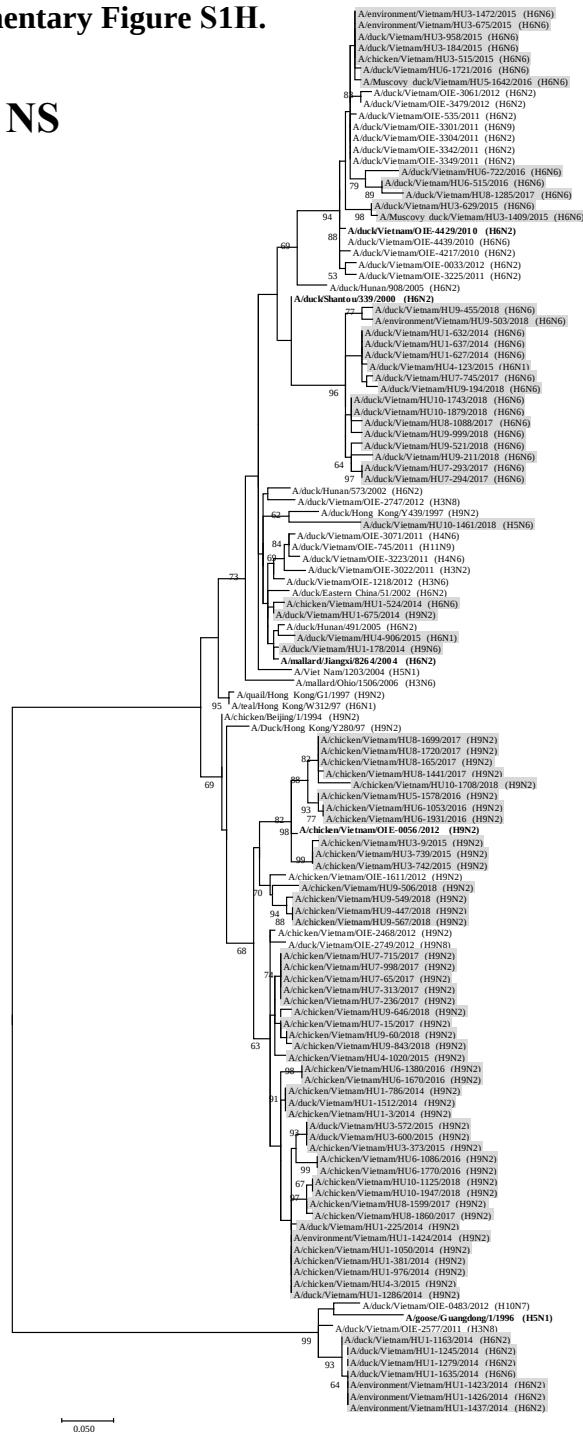
Vietnam

H6 group I

JX8264-like

H9 China

Gs/Gd-like



Supplementary Figure S1 (cont). Phylogenetic tree of the NA and internal gene segments of H9 and H6 avian influenza viruses. The N2, N6, PB2, PB1, PA, NP, M, and NS genes were used for ML phylogenetic analysis using MEGA 7.0 software. The digits at the nodes indicate the probability of the confidence levels from 1,000 bootstrap replicates. The studied viruses are highlighted in gray and the representative of each sublineage is indicated in bold.