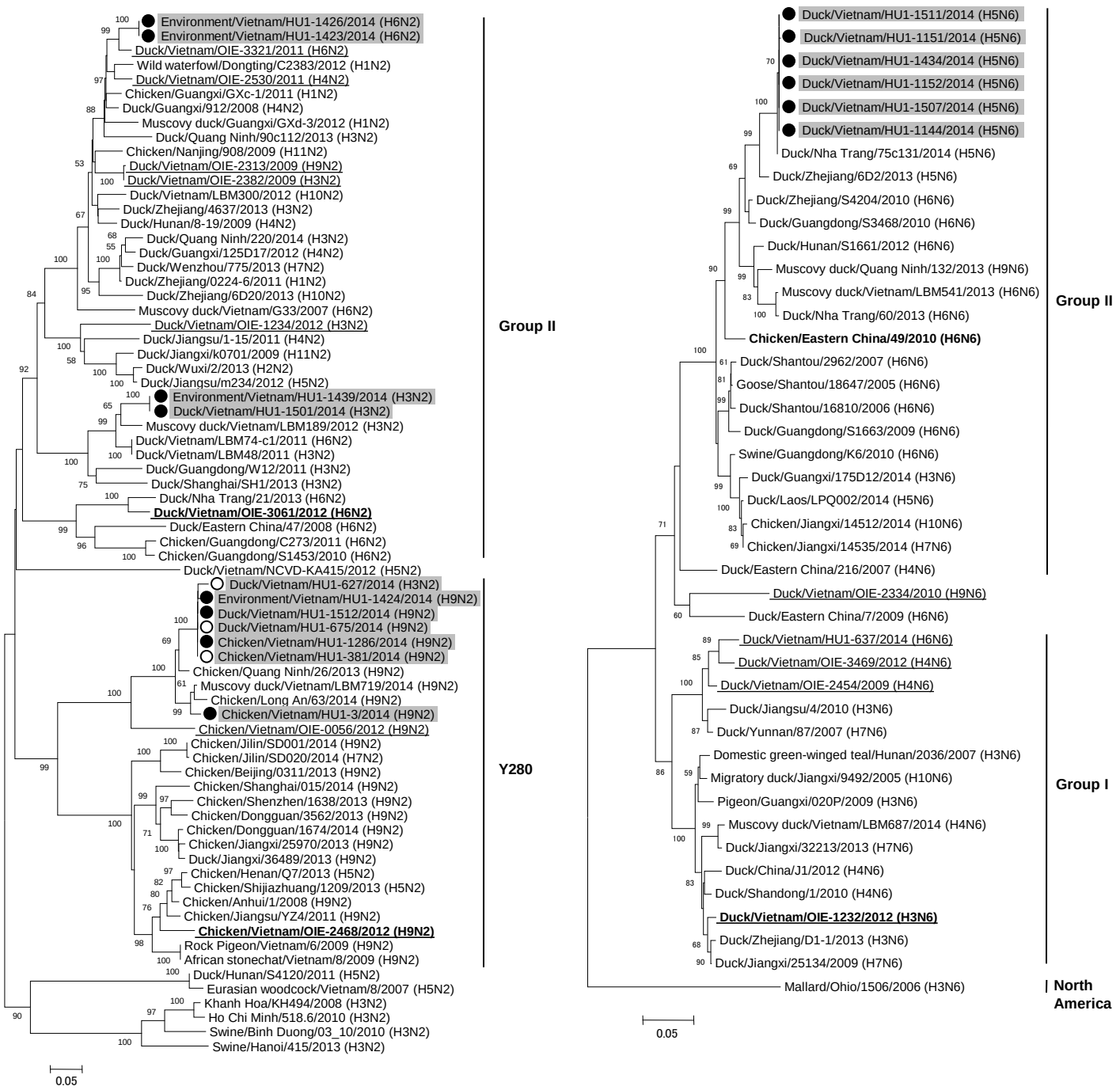
(a)

(b)

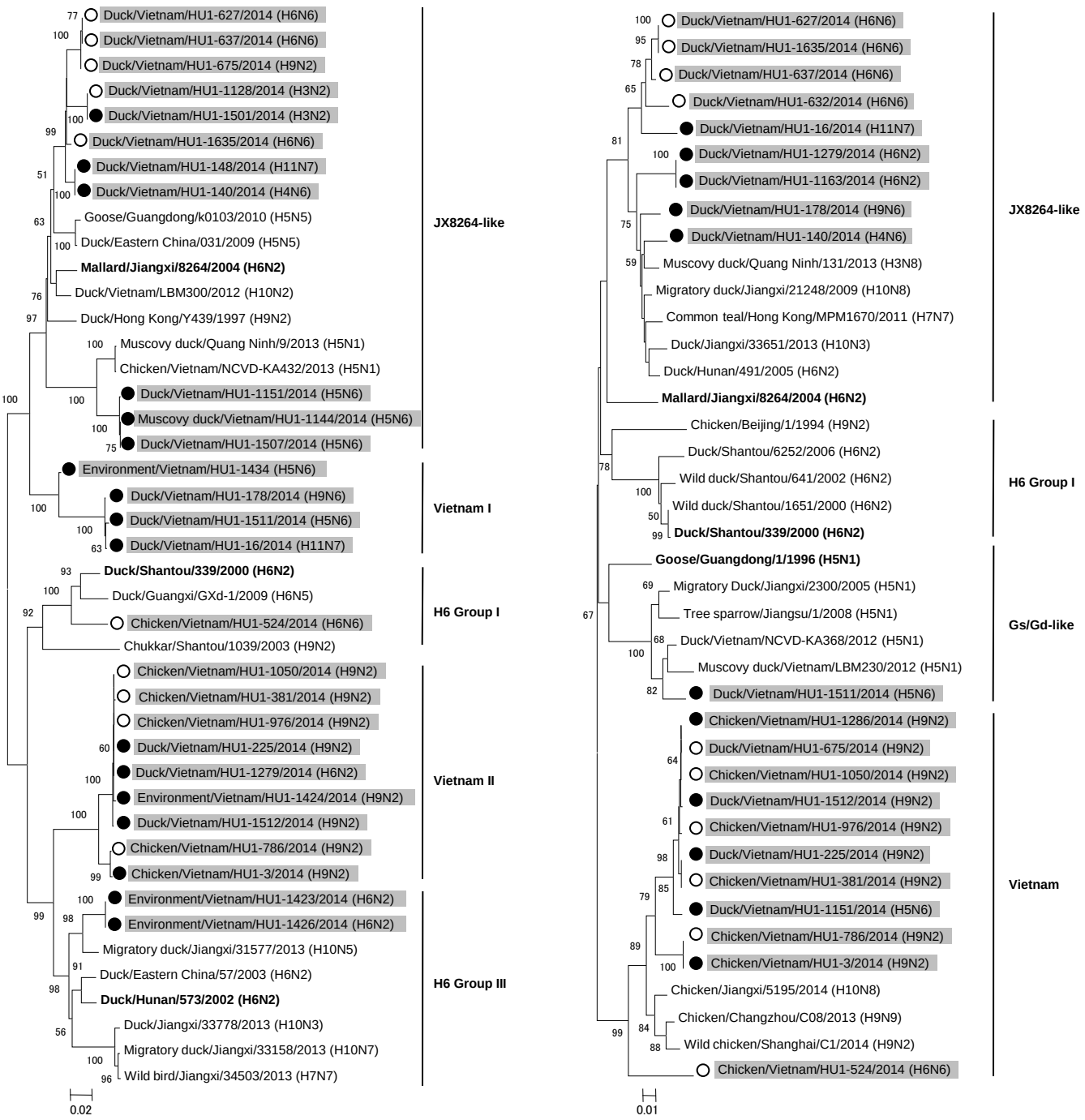
Supplemental Fig. 1. Representative pictures of the intervention LBM and non-intervention LBM in Thua Thien Hue province, Vietnam.

(a) Intervention LBM was deployed by VAHIP project, which has a good infrastructure with the biosecurity equipments. Only poultry with high density was gathered for selling in intervention LBM. (b) Non-intervention LBM is the conventional market where no paticular biosecurity infrastructure was established and at where poultry and other animals were usually mixed together in low biosecurity condition.



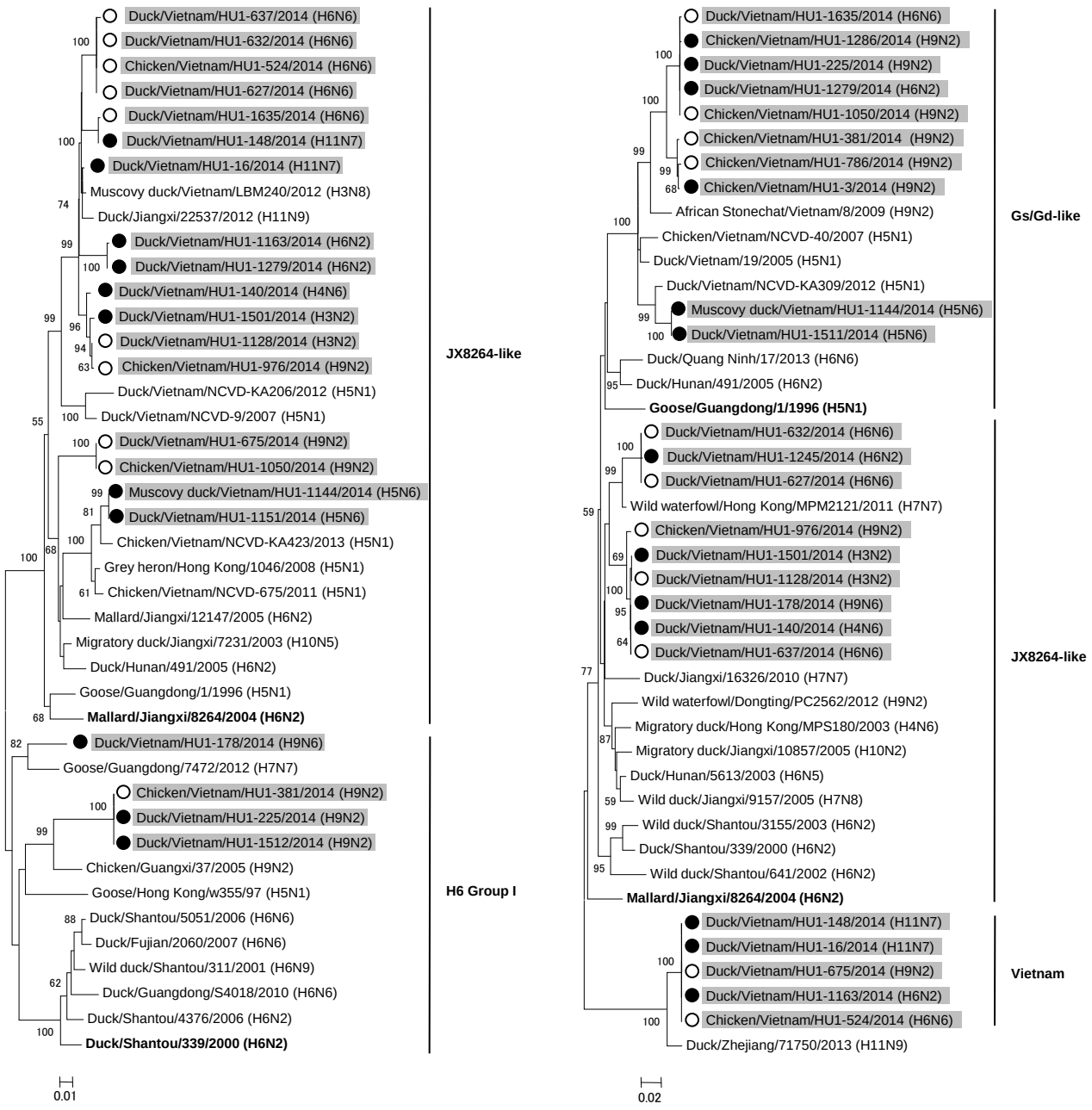
Supplemental Fig. 2. Phylogenetic tree for the NA genes of influenza viruses isolated in LBMs.

Nucleotide 29–1411 (1383 bp) of N2 (a) and 83–740 (658 bp) of N6 (b) were used for the ML phylogenetic analysis. The NA genes of viruses isolated in LBMs were clustered into two different sublineages: Y280 and Group II for N2 genes and Group I and Group II for N6 genes. Horizontal distances are proportional to the minimum number of nucleotide differences required to join nodes and sequences. Digits at the nodes indicate the probability of confidence levels in a bootstrap analysis with 1,000 replications. The viruses isolated in this study are highlighted in gray, and the representative of each sublineage is indicated in bold. The virus isolated in our previous study is underlined. The viruses isolated at intervention LBMs are indicated by black circles, and the virus isolated at a non-intervention LBM is indicated by a white circle.

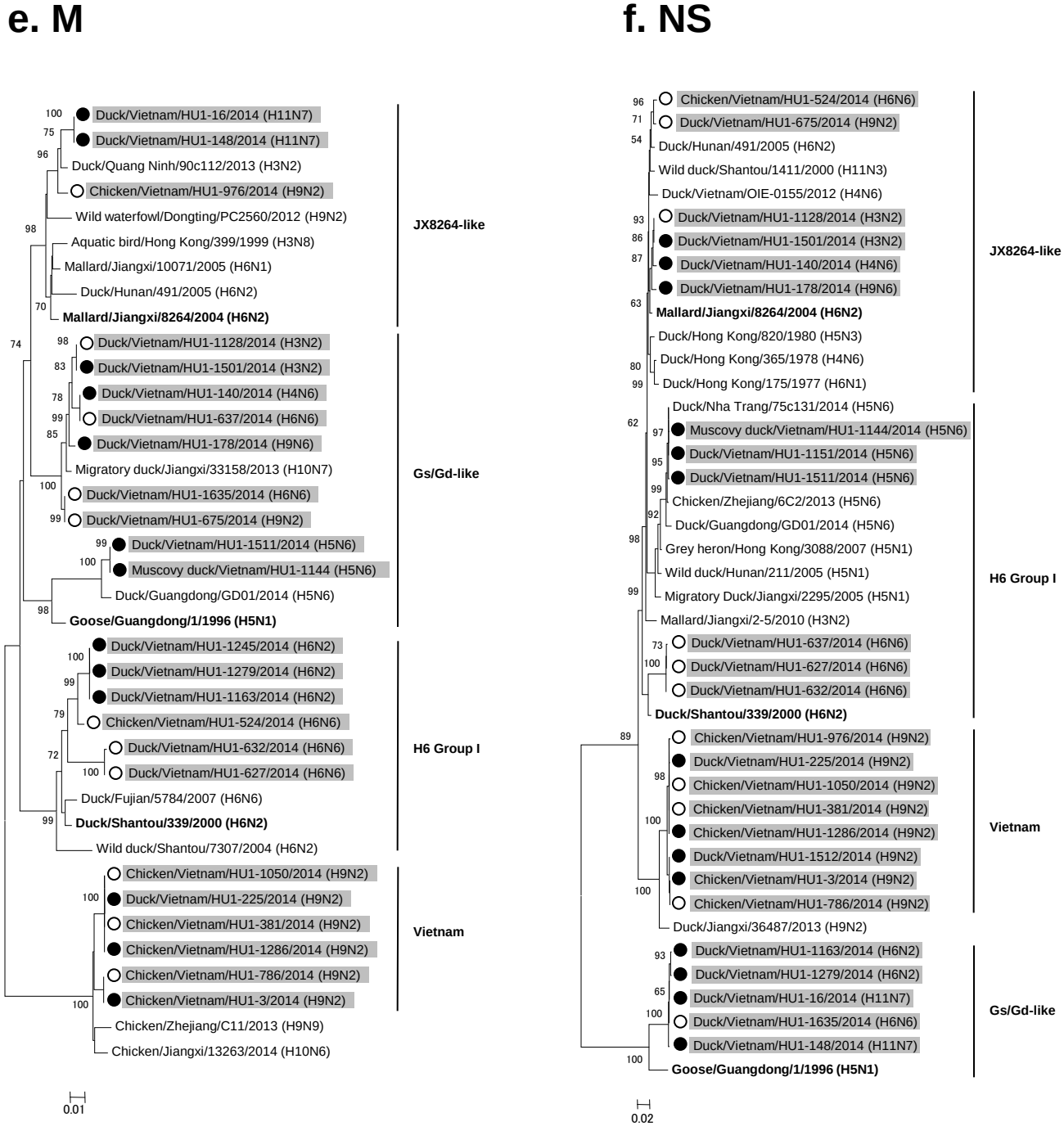


Supplemental Fig. 3. Phylogenetic tree for the six internal genes of influenza viruses isolated in LBMs.

Nucleotide 1089–1923 (835 bp) of PB2 (a), 1169–1883 (715 bp) of PB1 (b), 813–1520 (708 bp) of PA (c), 1–643 (643 bp) of NP (d), 1–825 (825 bp) of M (e), and 27–839 (813 bp) of NS (f) were used for the ML phylogenetic analysis. Horizontal distances are proportional to the minimum number of nucleotide differences required to join nodes and sequences. Digits at the nodes indicate the probability of confidence levels in a bootstrap analysis with 1,000 replications. The viruses isolated in this study are indicated are highlighted in gray, and the representative of each sublineage is indicated in bold. The viruses isolated at intervention LBMs are indicated by black circles, and the virus isolated at a non-intervention LBM is indicated by a white circle.



Supplemental Fig. 3 ***(cont.).*** Phylogenetic tree for the six internal genes of influenza viruses isolated in LBMs.



Supplemental Fig. 3 ***(cont.).*** Phylogenetic tree for the six internal genes of influenza viruses isolated in LBMs.