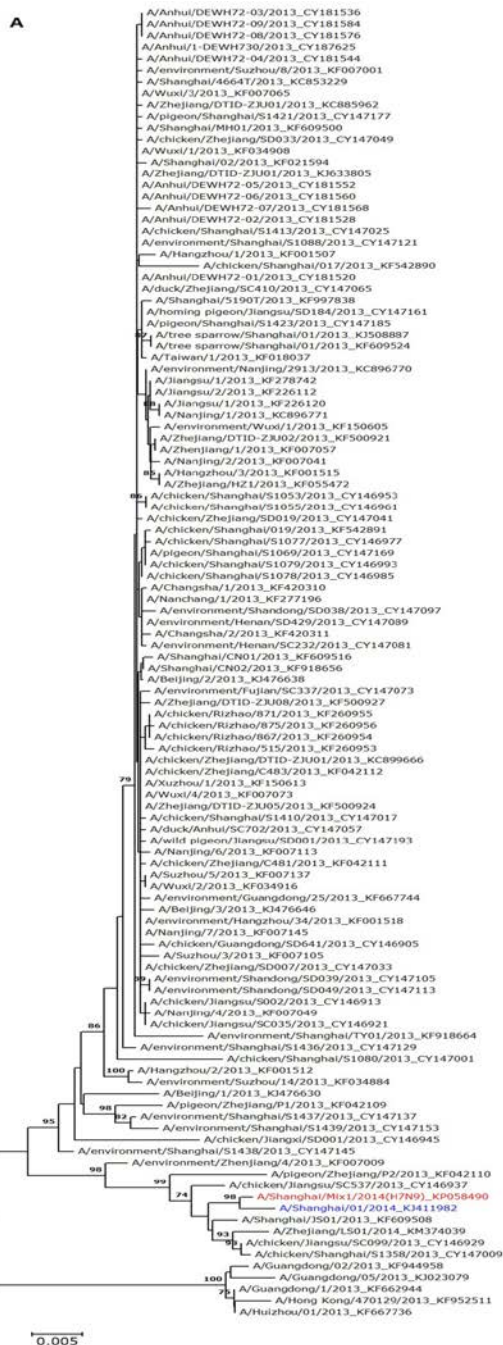
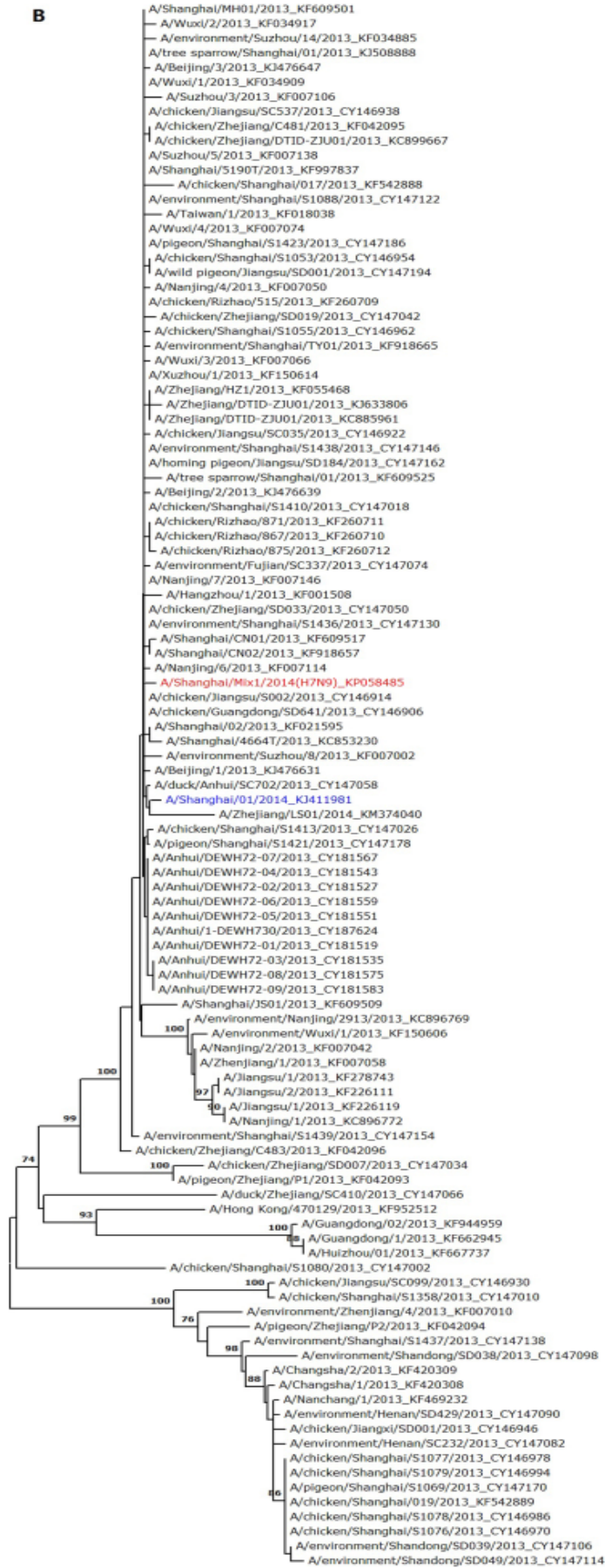


# Co-infection with Avian (H7N9) and Pandemic (H1N1) 2009 Influenza Viruses, China

## Technical Appendix



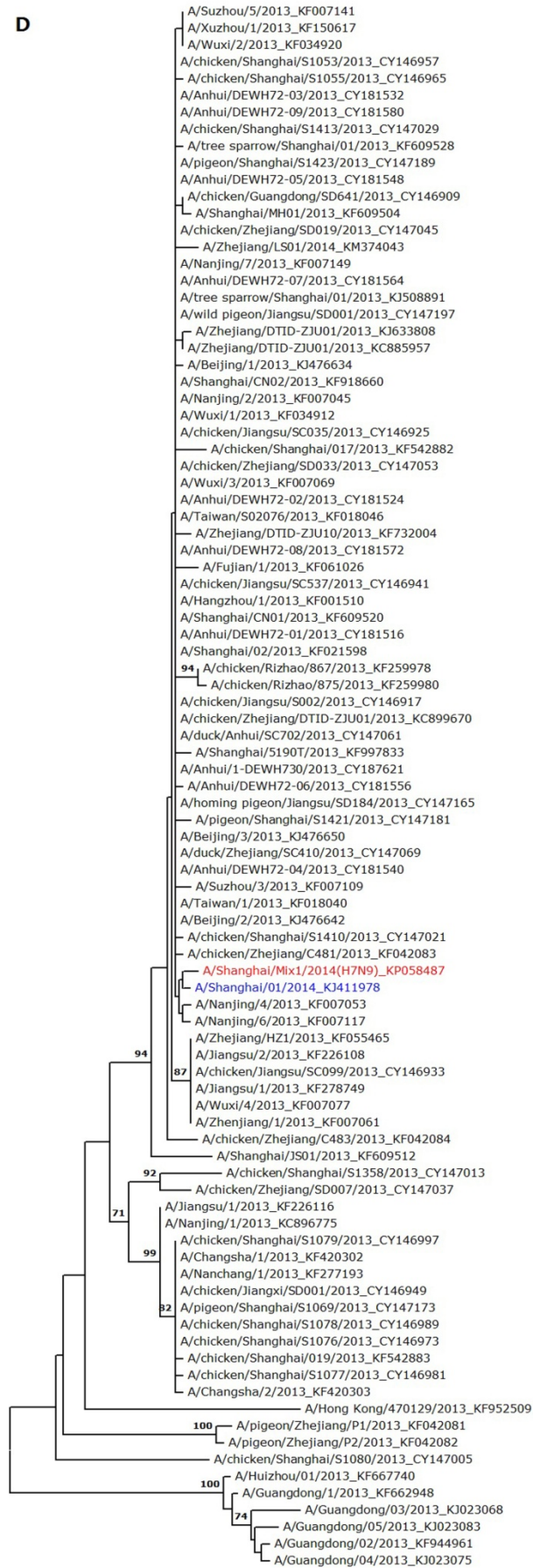
**B**



0.005

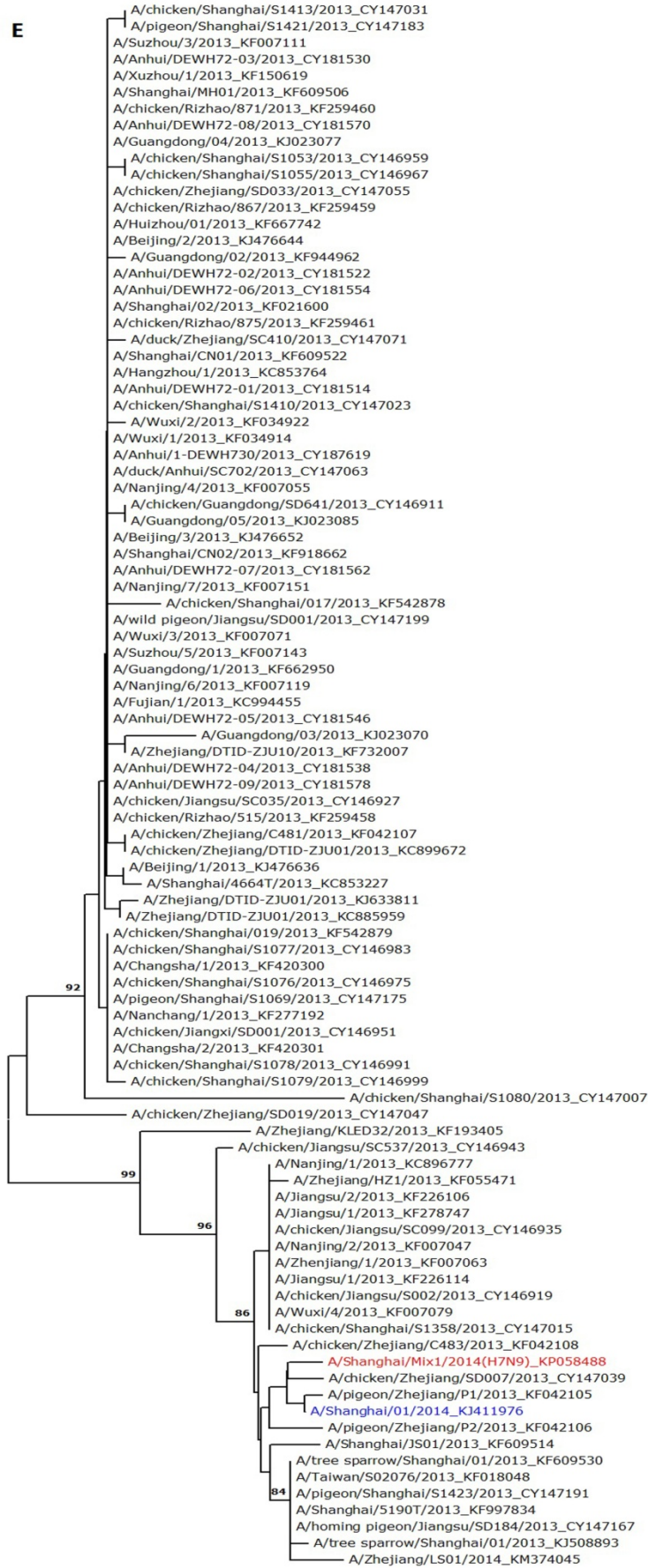


D



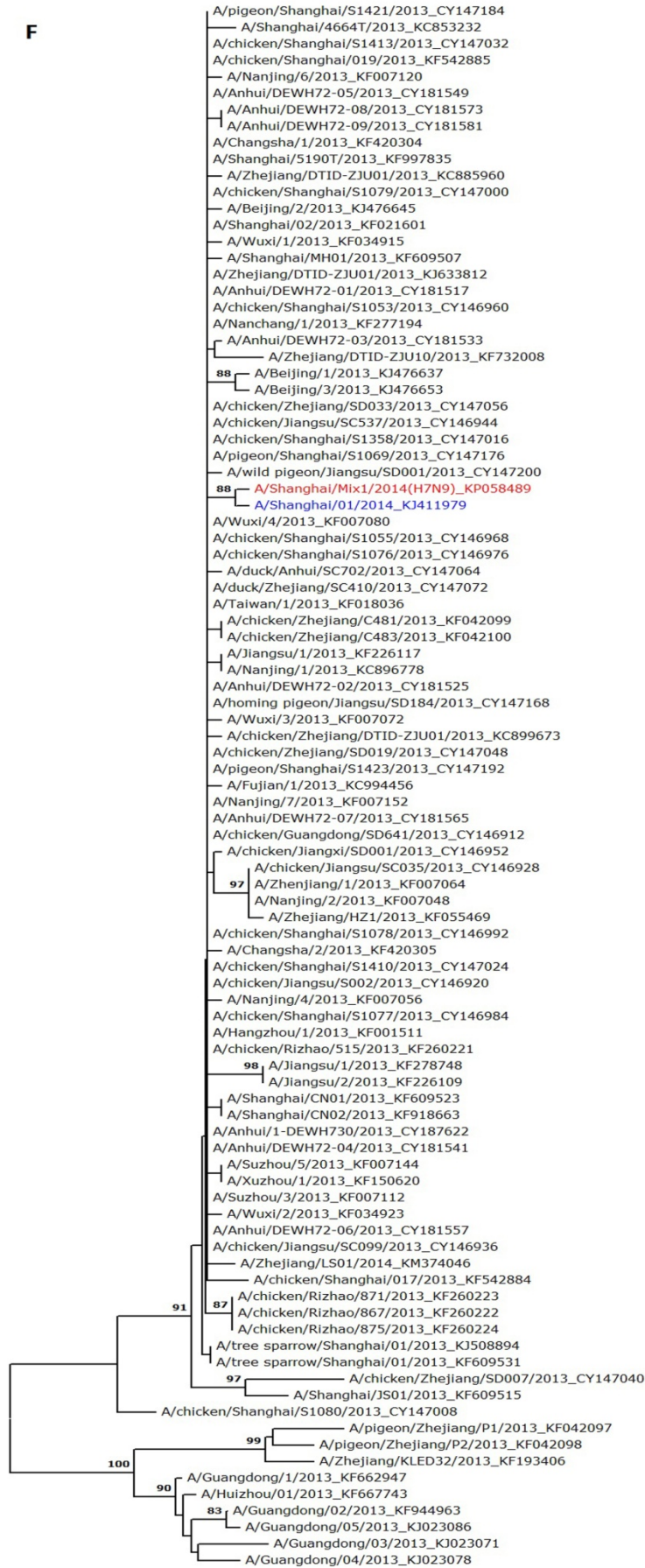
0.005

E



0.002

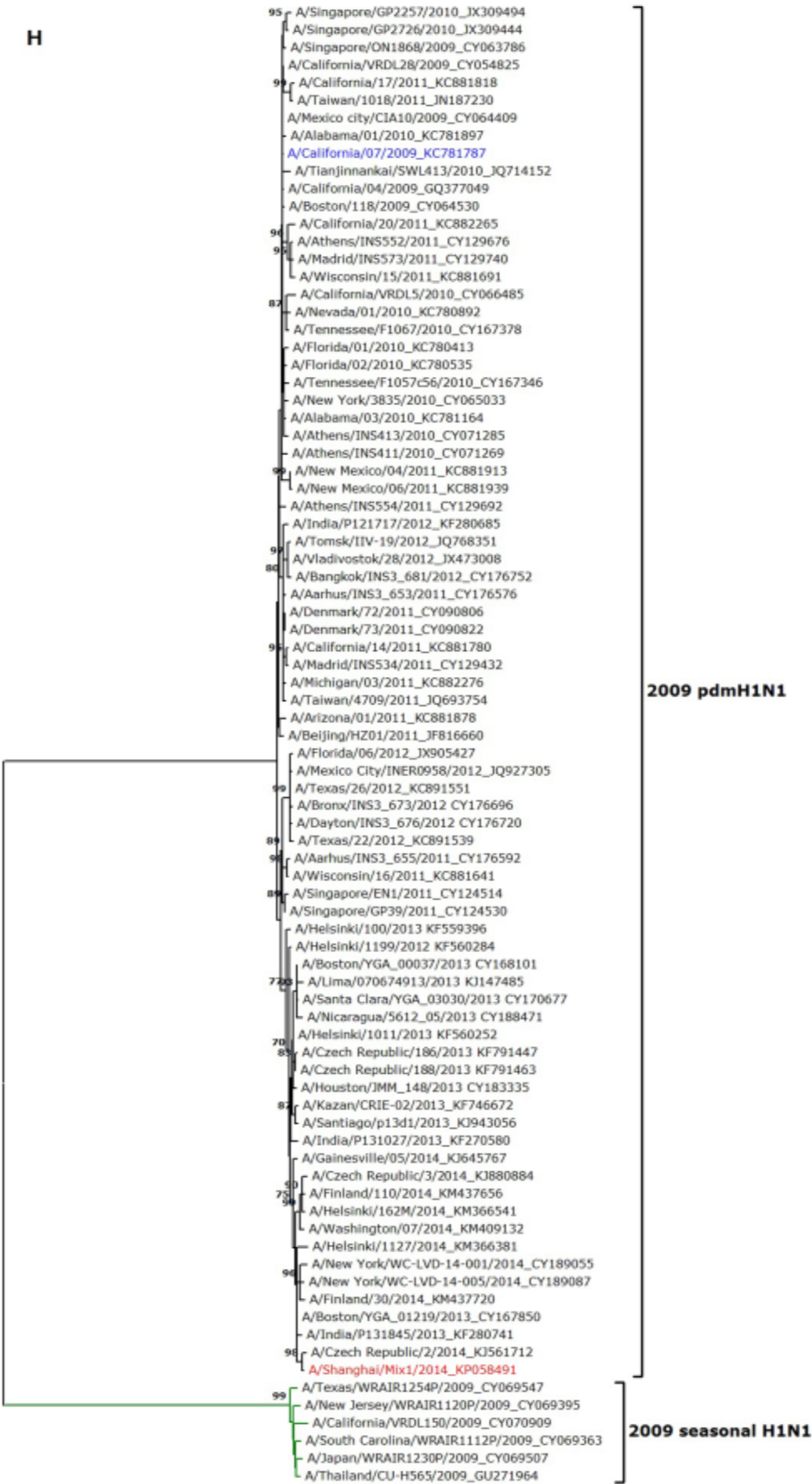
F



0.005

G

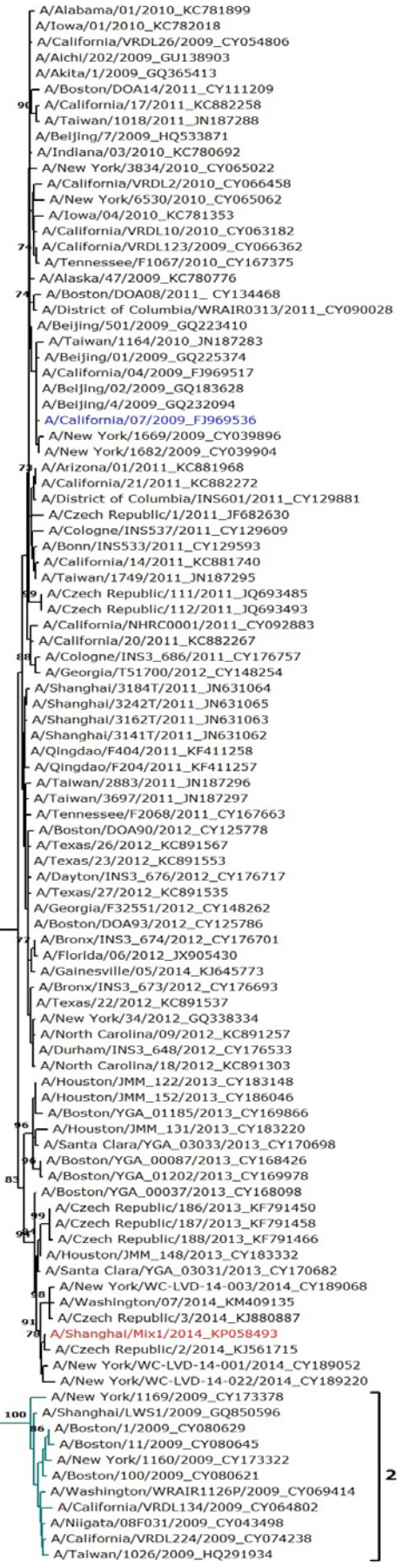








J



2009 pdmH1N1

2009 seasonal H1N1

0.02

K

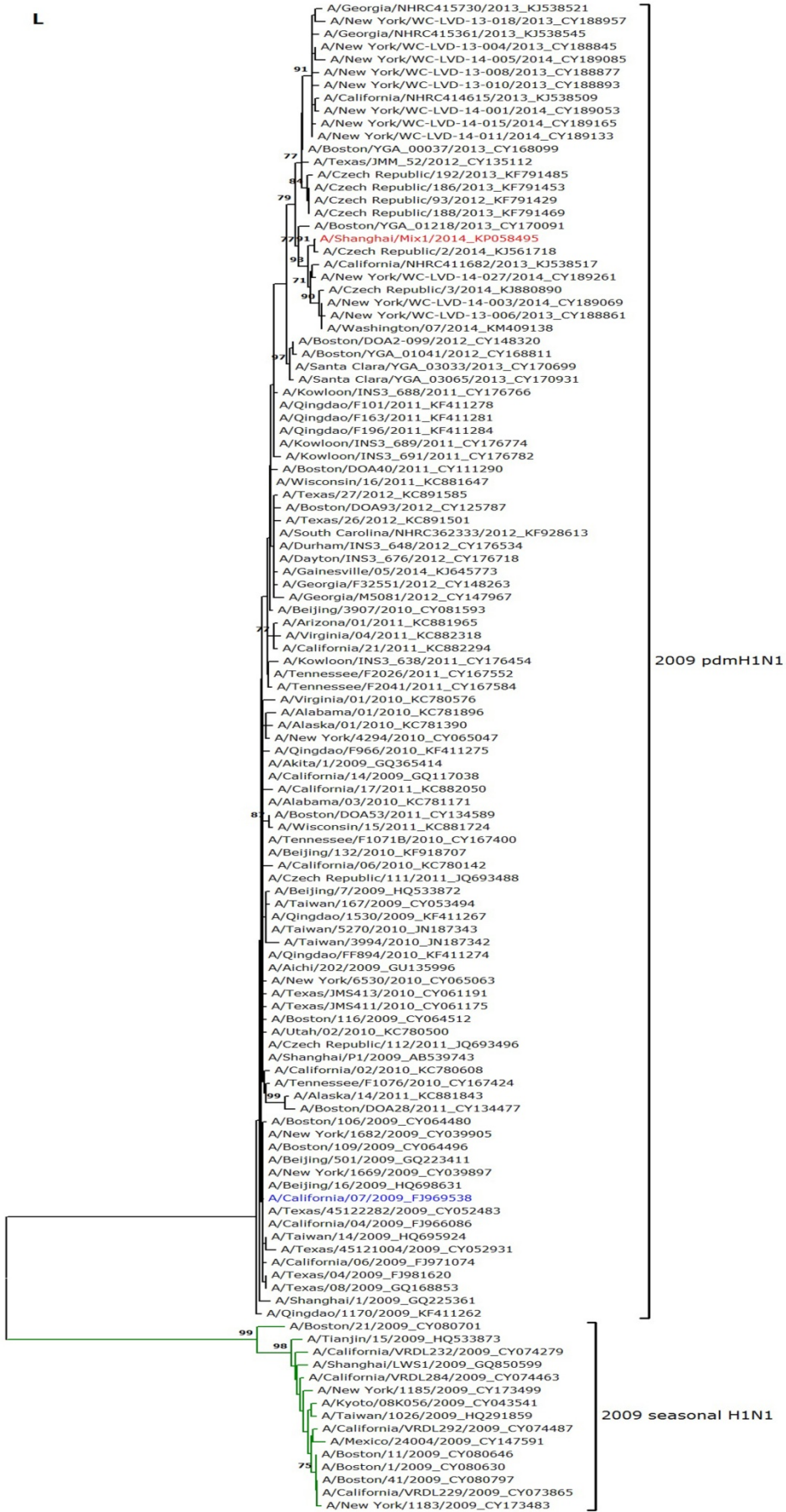


2009 pdmH1N1

2009 seasonal H1N1

0.01

L



**Technical Appendix Figure.** Phylogenetic analysis of 12 internal genes of the co-infection viruses in Shanghai, China. Phylogenetic trees were constructed by using the neighbor-joining method with bootstrap analysis of 1,000 replicates in MEGA 5.1 program. Numbers next to nodes indicate bootstrap value percentages (>70%). Panels A, B, C, D, E, F were the PB2, PB1, PA, NP, MP, NS phylogenetic trees of the A/Shanghai/Mix1/2014(H7N9) strain, respectively, and panels G, H, J, K, L, M were the PB2, PB1, PA, NP, MP, NS phylogenetic trees of the A/Shanghai/Mix1/2014(H1N1) strain, respectively. Red font indicates the A/Shanghai/Mix1/2014(H7N9) and A/Shanghai/Mix1/2014(H1N1) strains isolated from the co-infection patient from Shanghai, China. Blue font in the phylogenetic trees of the A/Shanghai/Mix1/2014(H7N9) strain indicates the representative strains of Shanghai area during the same wave of the H7N9 outbreak in China (1). Blue font in the phylogenetic trees of the A/Shanghai/Mix1/2014(H1N1) strain indicates the recommended influenza vaccine strain in the 2013–14 Northern Hemisphere influenza season ([http://www.who.int/influenza/vaccines/virus/recommendations/2013\\_14\\_north/en/](http://www.who.int/influenza/vaccines/virus/recommendations/2013_14_north/en/)). Scale bars indicate nucleotide substitutions per site. The GISAID or GenBank accession numbers of the influenza viruses in the construction of the phylogenetic analyses are displayed in the phylogenetic trees, which followed the taxon names.