

A/H3N2

A/H1N1pdm09

**Supplementary Figure 2.** Phylogenetic tree based on NA1pdm09 and NA2 sequences, generated in MEGA 6 (18) by using the Maximum Likelihood method based on the Hasegawa-Kishino-Yano model. The numbers next to the branches indicate the percentage of 1,000 bootstrap replicates that support each phylogenetic branch. The tree is drawn to scale, with branch lengths measured in the number of substitutions per site.

Vaccine strains in 2014: A/Texas/50/2012 (A/H3N2), A/California/07/2009 (A/H1N1pdm09)

A/H3N2 reassortant virus clone on MDCK, passage 1 and 2

A/H3N2 virus clone on MDCK, passage 1

A/H1N1pdm09 and A/H3N2 virus strains from original samples