Supplemental materials

\textbf{Figure S1.} Maximum clade credibility phylogenetic trees for eight gene segments. H7N8 strains associated with the outbreak of disease in Indiana turkeys are highlighted by a red box. Clade posterior probabilities $\geq 0.7$ are shown. Horizontal bars indicate 95% highest posterior density of age estimates of tree nodes.

\textbf{Figure S2.} Maximum clade credibility phylogenetic trees for eight gene segments. H7N8 strains associated with the outbreak of disease in Indiana turkeys are highlighted by a red box. Branches are colored according to the estimated ancestral state of host group from discrete trait reconstruction. Clade posterior probabilities $\geq 0.7$ are shown. Horizontal bars indicate 95% highest posterior density of age estimates of tree nodes.
Figure S1
HA
Figure S2
PB1