

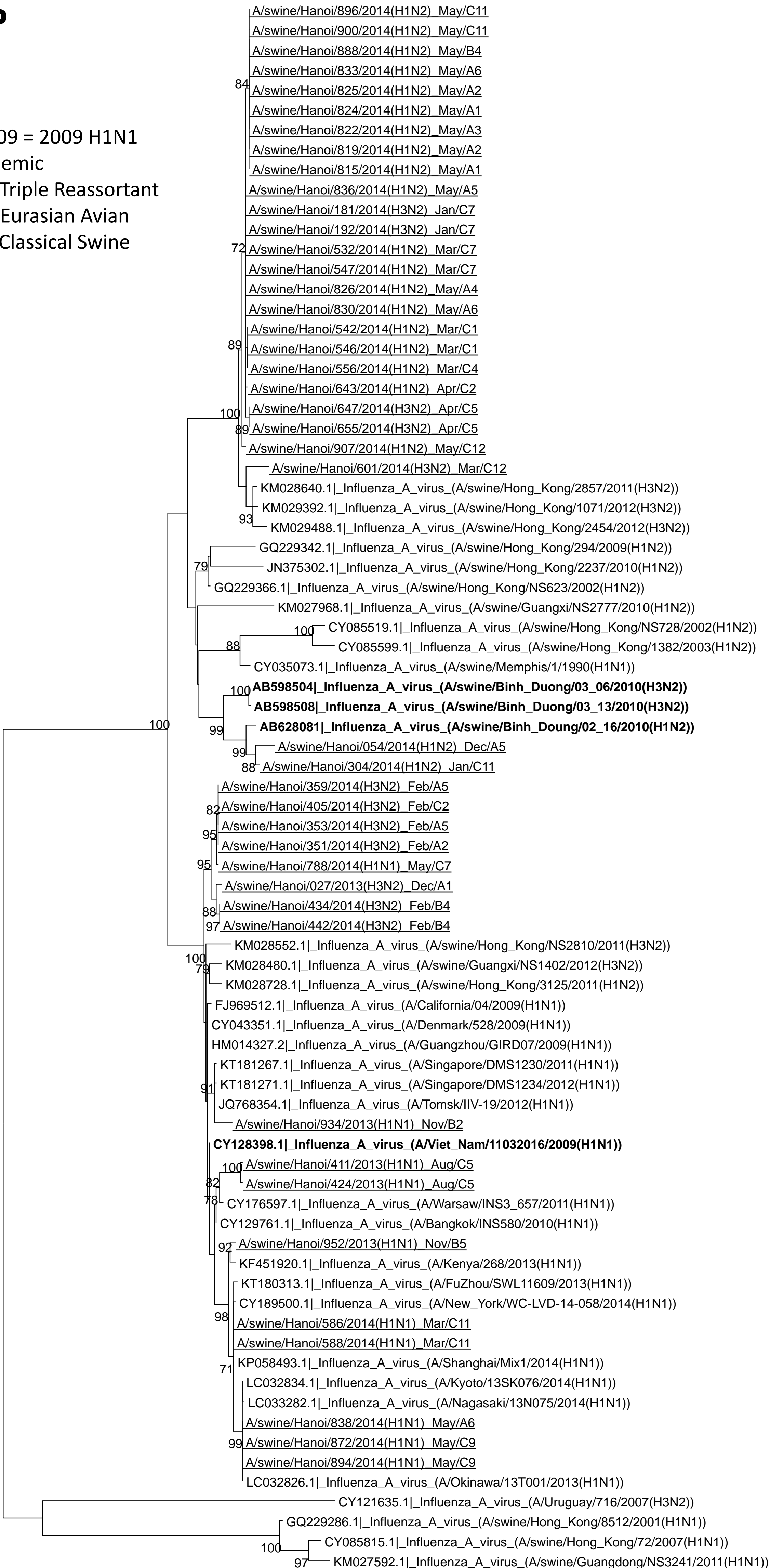
Supplementary Figure S5. Phylogenetic tree for the full length NP of viruses isolated in a slaughterhouse in Vietnam in 2013-2014

The trees were constructed with MEGA 6.06. Bootstrap values greater or equal to 70 are shown. GenBank accession numbers of retrieved sequences are indicated.

Underlined: Viruses from our study. **Bold**: Viruses from Vietnam from other studies.

# NP

Pdm09 = 2009 H1N1  
pandemic  
TR = Triple Reassortant  
EA = Eurasian Avian  
CS = Classical Swine



TR

CS

TR

Pdm09

Human

EA

0.02