

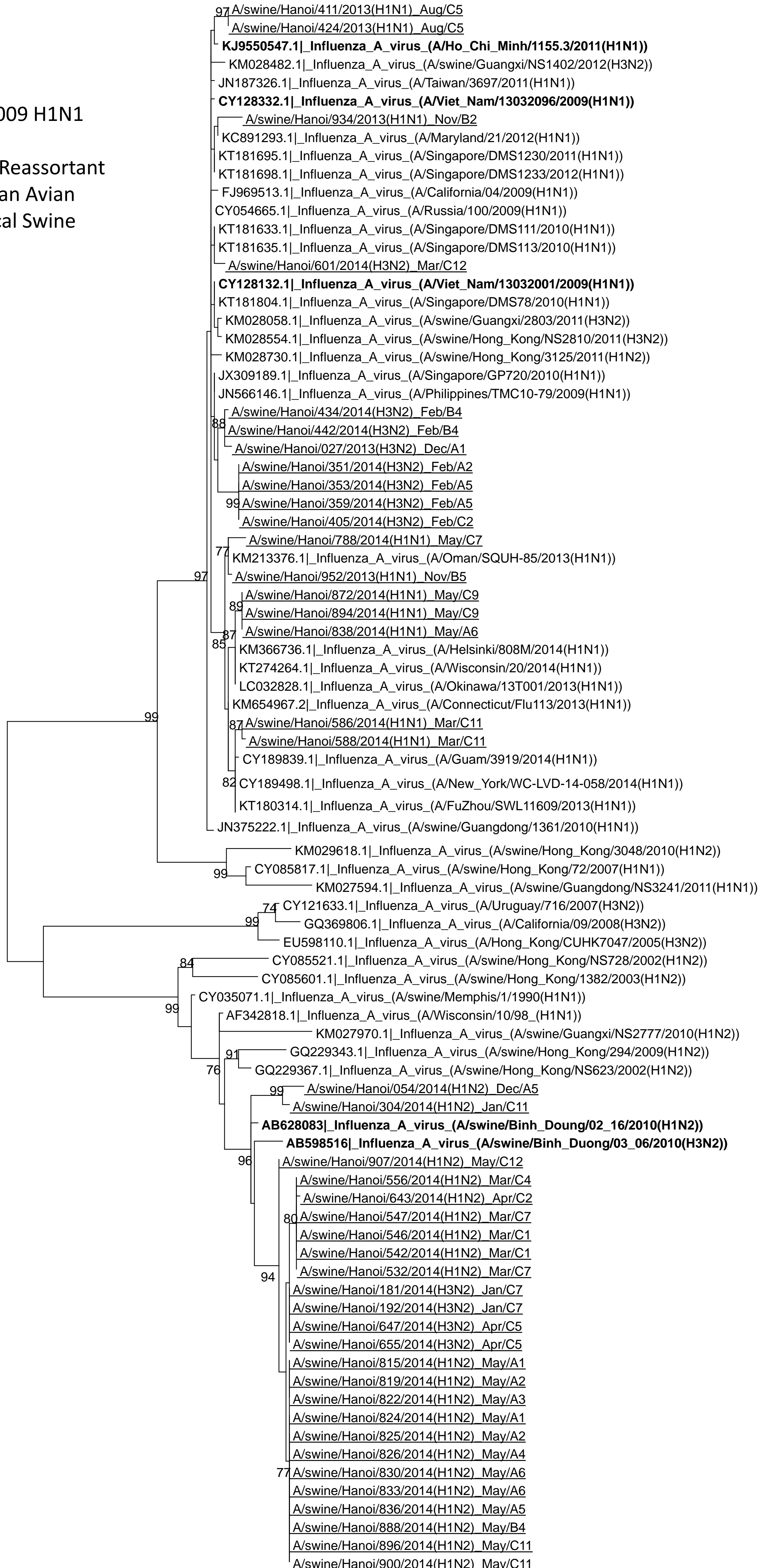
Supplementary Figure S6. Phylogenetic tree for the full length M of viruses isolated in a slaughterhouse in Vietnam in 2013-2014

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.

M

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



Pdm09

EA

Human

CS

TR

0.02