

Supplementary Figure S4. Phylogenetic tree for the full length PB2 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.

PB2

Pdm09 = 2009 H1N1

pandemic

TR = Triple Reassortant

EA = Eurasian Avian

CS = Classical Swine



Pdm09

TR

EA
Human
CS

0.02