



**Supplementary Figure S7. Phylogenetic tree for the full length HA of H1N2 viruses isolated in a slaughterhouse in Vietnam in 2013-2014**

Trees were constructed with PhyML. Branch support aLRT statistics were shown at major nodes with values larger or equal to 0.8. GenBank accession numbers of retrieved sequences are indicated. Red: sequences from our study; Blue: sequences from Takemae et al. (Ref. 28); Green: viruses from Vietnam from other studies.