









Supplementary Figure S1 Phylogenetic trees based on the full-length nucleotide sequences of the surface glycoprotein genes *HA* and *NA* (A-B) and internal genes *PB2*, *PB1*, *PA*, *NP*, *M*, and *NS* (C-H) of MDk/W452(H5N8). Phylogenetic trees were generated from published sequences available in GenBank by using the Meg Align function of DNASTar 5.0, aligned and bootstrapped in Clustal X [44], and then viewed in NJ plot [45]. The scale represents the number of substitutions per nucleotide. Bootstrap values $\geq 60\%$ from 1000 bootstrap replicates performed to assign confidence to the grouping.