**Suppl 4. Phylogenetic Analysis and Annotation:** Reference genomes and amino acids of hemagglutinin (HA) from H1N1 virus, H5N1, Indonesian H1N1 (called as Indonesian H1), Bovine H5N1 (called as Bovine H5) were obtained from the National Center for Biotechnology Information (NCBI) Orthologs of the National Library of Medicine. Amino acid homological analysis was performed using Align Sequences Protein BLAST (algorithm protein–protein BLAST) with the protein accession numbers of HAs listed in the NCBI Reference Sequence Database in order to determine the whole amino acid homology of HAs between humans and other animals. Phylogenetic analyses of the complete protein and major coding regions were performed with RAxML software (version 8.2.9)(Karlsruhe Institute of Technology: KIT), Karlsruhe, Baden-Württemberg, German) with 1000 bootstrap replicates using the general time reversible nucleotide substitution model. Details of the protein accession numbers of HAs are available in the supplementary materials.