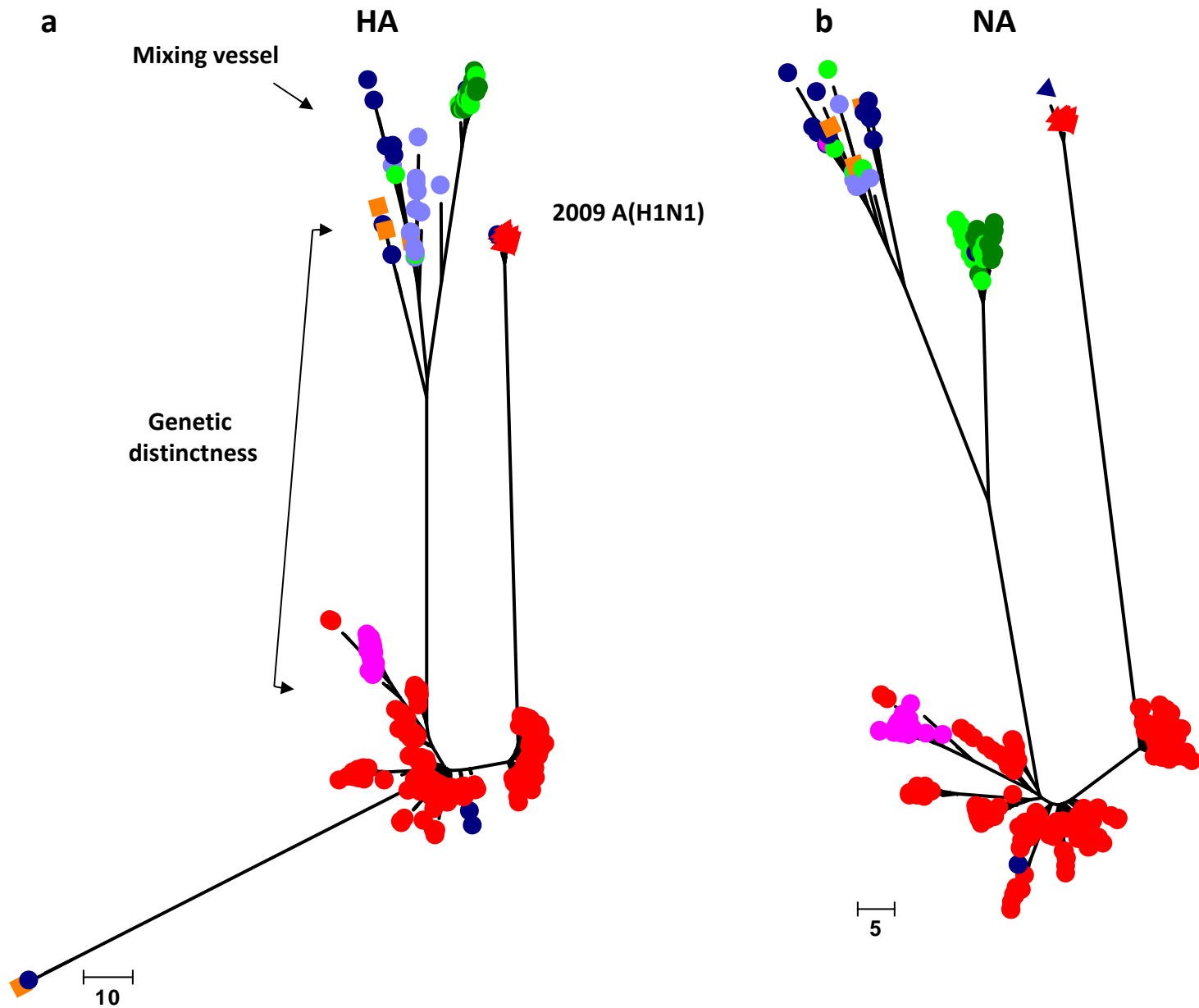
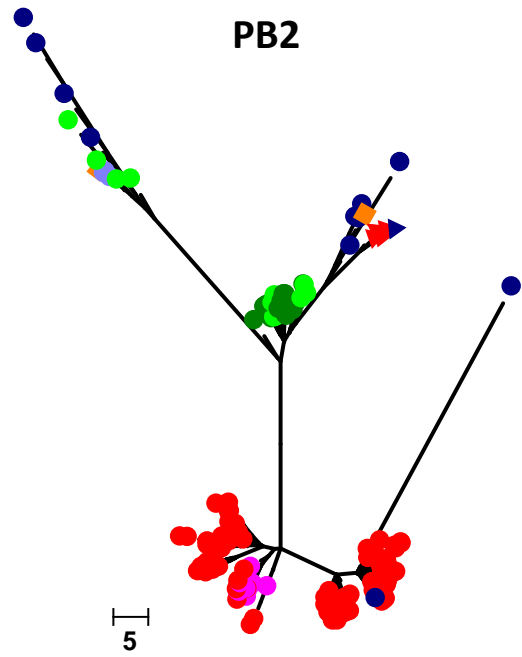
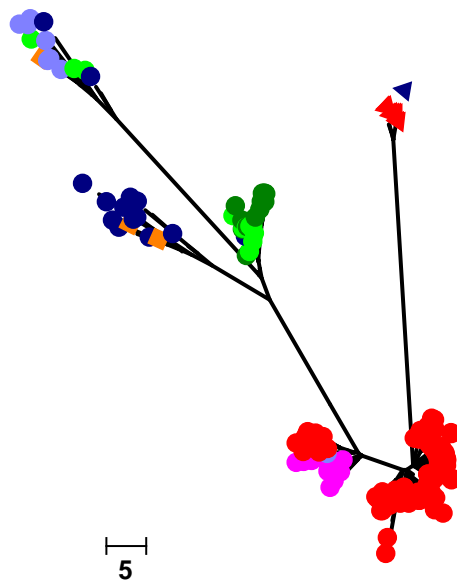
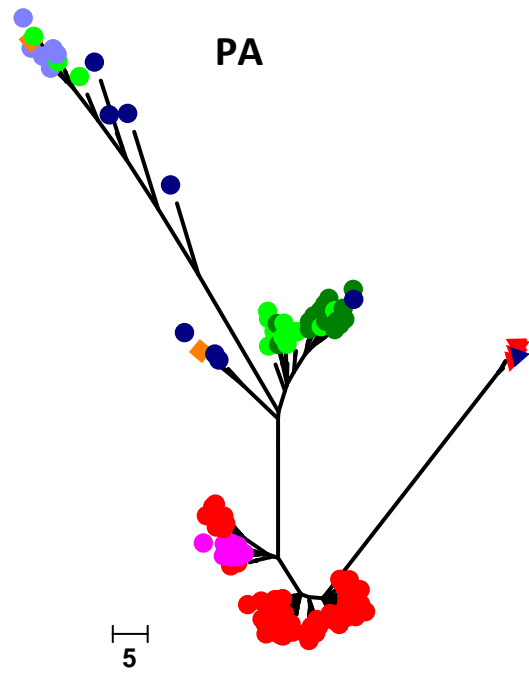
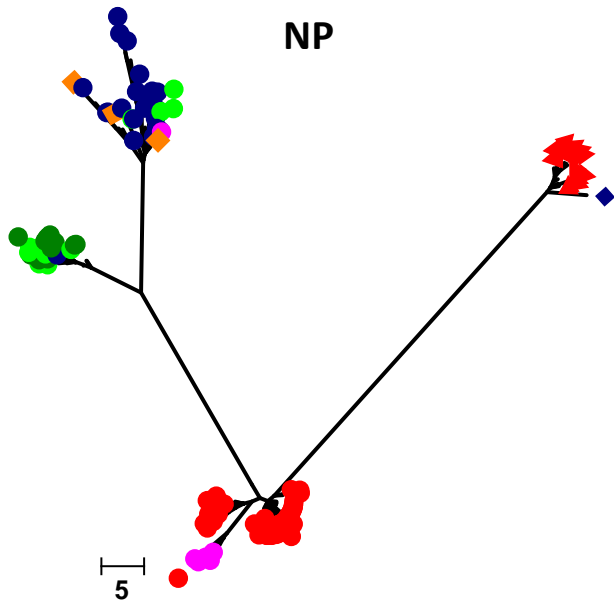
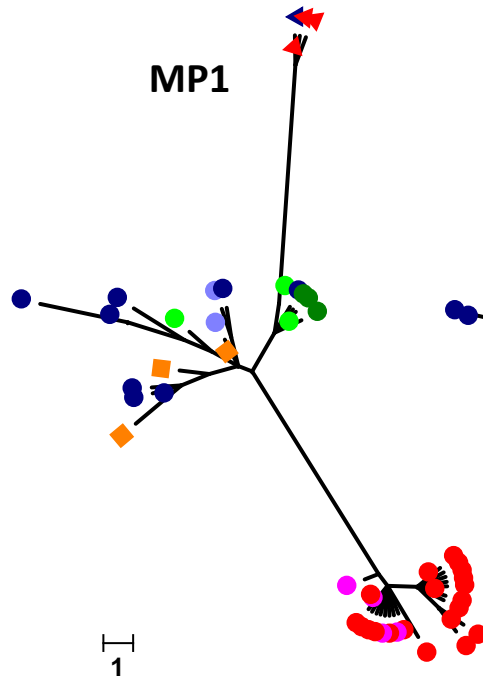
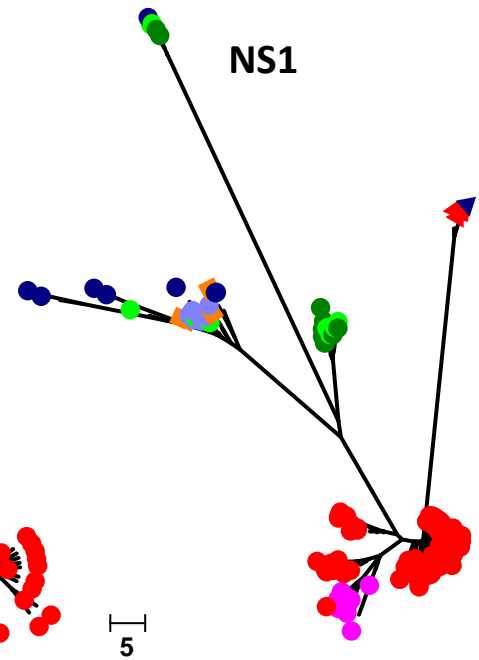


Figure 2. Genetic distinctness of the influenza 2009 A(H1N1) virus: a) hemagglutinin (HA) and b) neuraminidase (NA) proteins; c) phylogenetic trees for PB2, PB1, PA, NP, MP1, and NS1 proteins



C**PB2****PB1****PA****NP****MP1****NS1**

Legend:

a) and b)

Protein sequences from avian, swine and human influenza A(H1N1) viruses circulating in North America from 1989 to 2009 were retrieved from the Influenza Virus Resource. Sequences were used for the reconstruction of unrooted phylogenetic trees with the maximum parsimony method. Proteins from the influenza 2009 A(H1N1) virus (red triangles), earlier human (red and pink circles) swine (navy blue and purple circles) and avian (green circles) viruses are shown. Light colors (pink, purple and green) correspond to viruses found between 1989 and 1999 and dark (red, navy blue and green) colors to viruses found between 2000 and 2009. Arrow indicates the influenza swine cluster containing an assortment of avian and human viruses. Genetic distinctness between pig-human interspecies transmission of influenza A viruses (orange squares; cases occurred in Iowa, Maryland and Wisconsin, US between 1991 and 2006) and the main cluster of human influenza viruses are indicated with the left bracket. Similar noticeable phylogenetic differences are observed between the influenza 2009 A(H1N1) virus and the main human influenza virus cluster. Scale bar indicates the number of changes over the whole sequence.

c)

Detailed phylogenetic tree topology, protein accession numbers, virus strains and serotypes, and statistical significance of branch order are presented in Supplementary Materials - Figure 1.