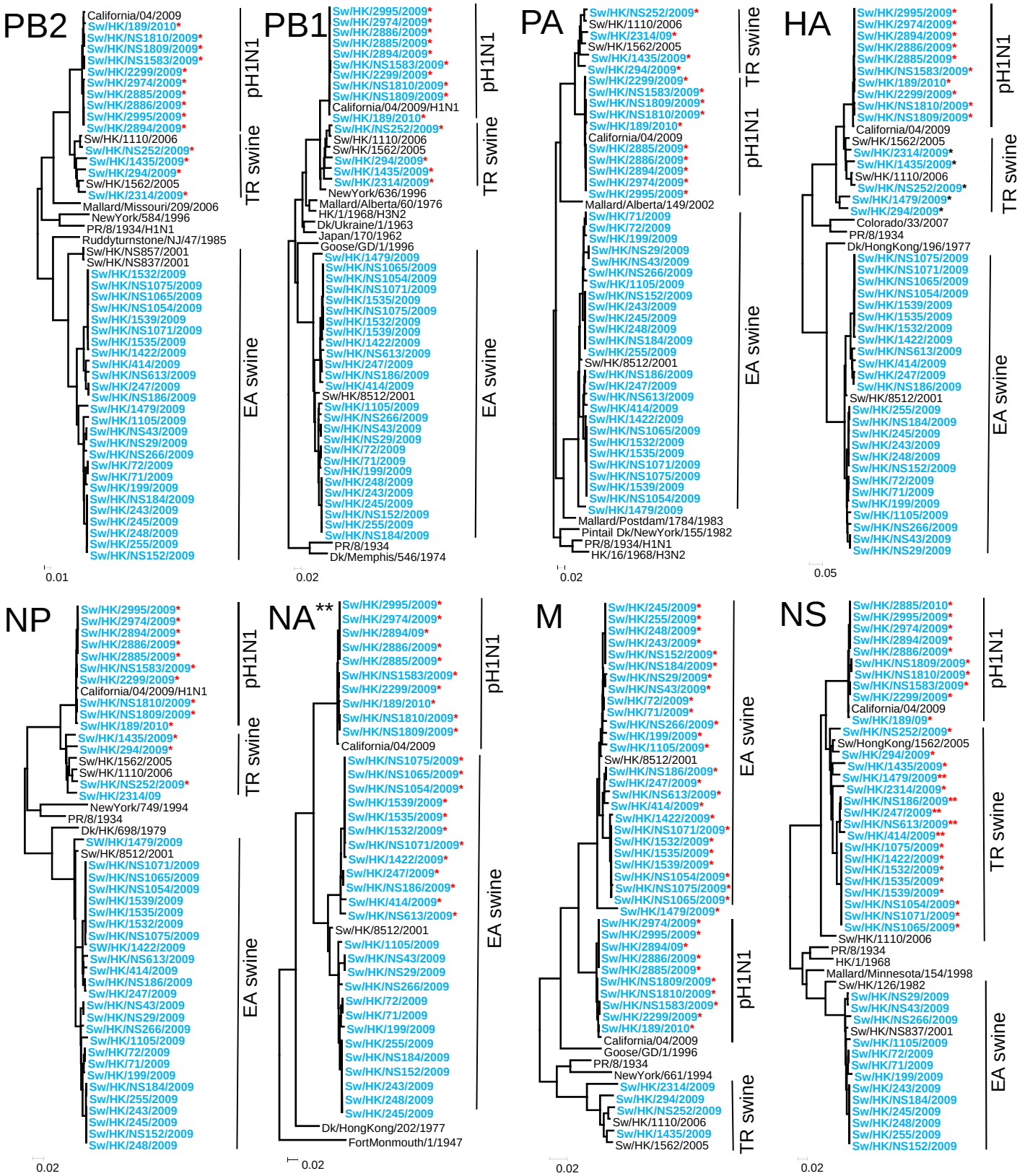

Supplementary Figure 2. Phylogenetic tree of swine influenza viruses constructed by the neighbor-joining method. Swine influenza viruses tested by the established quantitative PCR assays are highlighted in blue. Representative human, avian, classical swine, EA swine and TR swine influenza virus sequences from Genbank (in black) are included as references. Viral sequences from viruses determined in this study were described elsewhere (11). The scale bar shows the estimated genetic distance of these viruses. * Viruses positive in the corresponding melting curve analyses; ** weak positive; * HA sequences with a melting curve signal that is different from the one of pandemic H1N1/09; ** N2 sequences were excluded in the analysis.