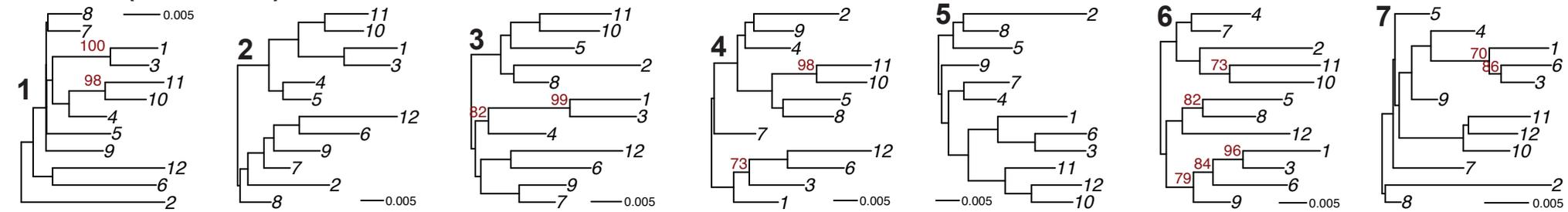
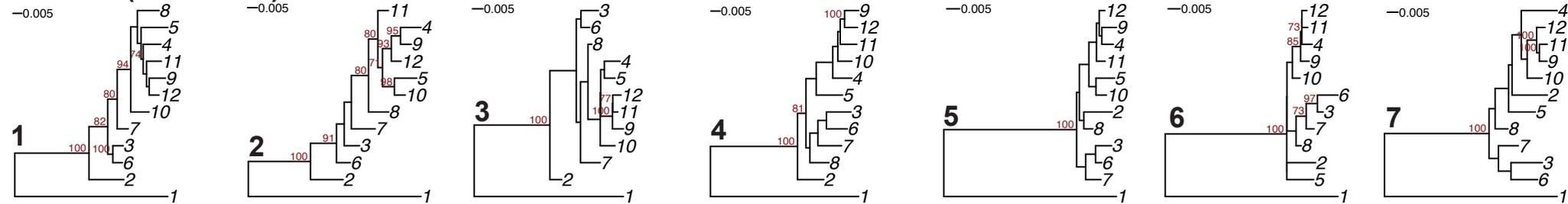


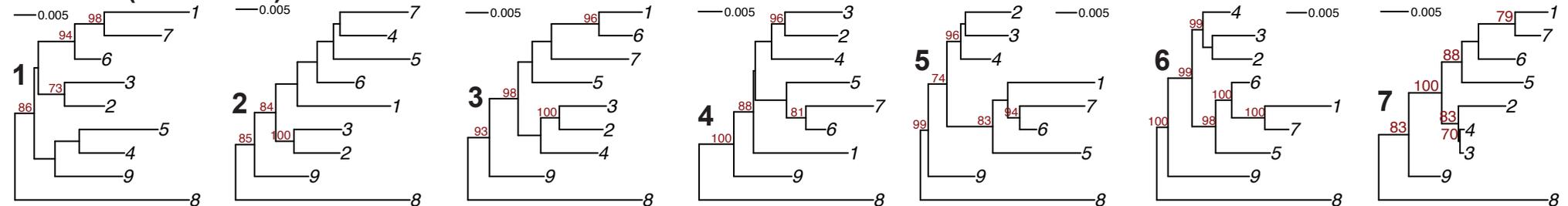
A H3N2 (1995-2004)



B H3N2 (2005-2014)



C H1N1 (2000-2008)



D H1N1 (2010-2018)

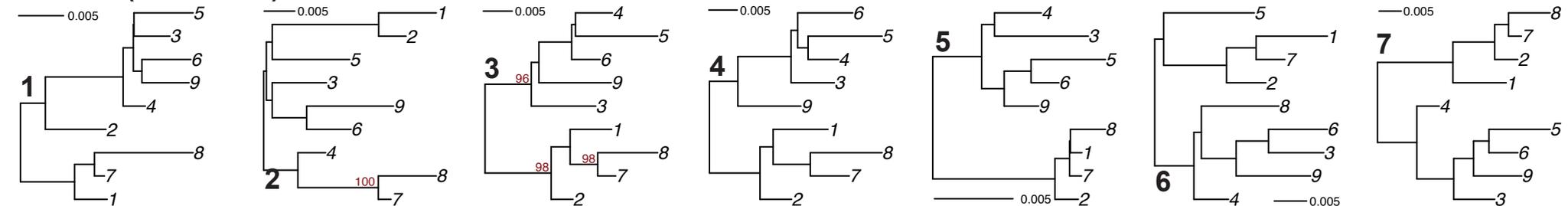


Figure 1 - figure supplement 2. Full-length concatenated genome trees. Maximum-likelihood phylogenetic reconstruction of full-length H3N2 virus (A-B) and H1N1 virus (C-D) genomic sequences shown in Supplementary Files 1-4. Sequences are coded by cluster. The numbers 1-7 in bold indicate replicates. Bootstrapping was performed with 1,000 replicates (bootstrap values greater than 70 are shown in red). Scale bars indicate percent divergence.