Figure 1 - figure supplement 1. Genomic vRNA segment trees. Maximum-likelihood phylogenetic reconstruction of each vRNA segment from H3N2 and H1N1 virus sequences shown in Supplementary Files 1-4. Representative trees from replicate 2 for H3N2 viruses from 1995-2004 **(A)**, replicate 7 for H3N2 viruses from 2005-2014 **(B)**, replicate 6 for H1N1 viruses from 2000-2008 **(C)**, and replicate 3 for H1N1 viruses from 2010-2018 **(D)**. Sequences are coded by cluster. Bootstrapping was performed with 100 replicates (bootstrap values greater than 70 are shown in red). Scale bars indicate percent divergence.