Figures and figure supplements

The global antigenic diversity of swine influenza A viruses
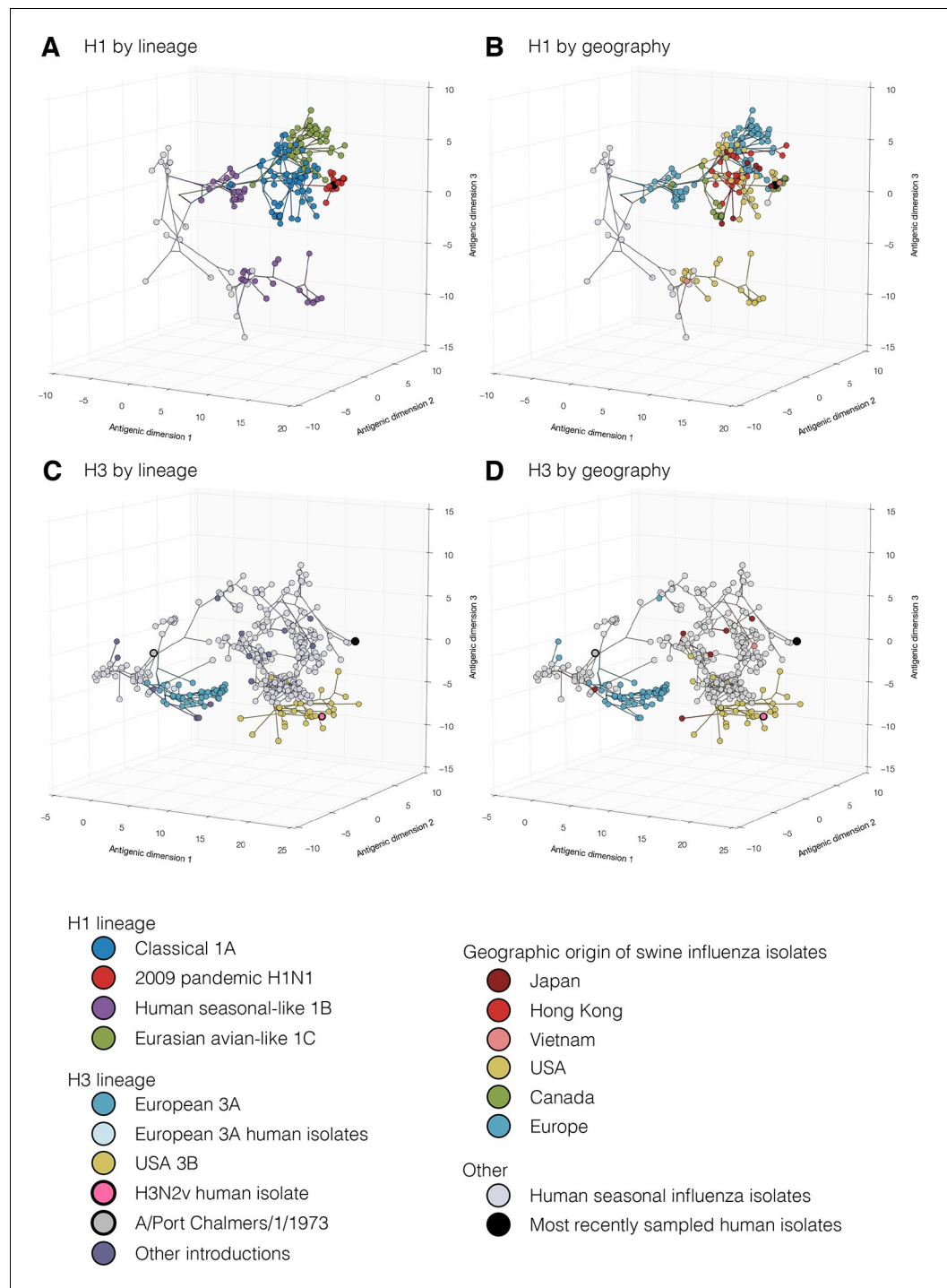
Nicola S Lewis *et al*

Figure 1. Evolutionary relationships of H1 (A, B) and H3 (C, D) influenza viruses circulating in swine and humans inferred by Bayesian Multi-dimensional scaling (BMDS). Each colored ball represents a single virus. Viruses are colored by lineage (A,C) and by geography (B,D). Lines connecting each virus represent inferred phylogenetic relationships. Distances for antigenic dimensions are measured in antigenic units (AU) and each unit is equivalent to a two-fold dilution in HI assay data. Antigenic distance can be interpreted as a measure of antigenic similarity – viruses close to one another are more antigenically similar than viruses further apart. Interactive visualizations are available at https://phylogeography.github.io/influenzaH1/ and https://phylogeography.github.io/influenzaH3/. Source data and GIF files for rotational views of 3D antigenic maps in *Figure 1* have been deposited in Dryad (*Lewis et al., 2016*).

Figure 1 continued on next page
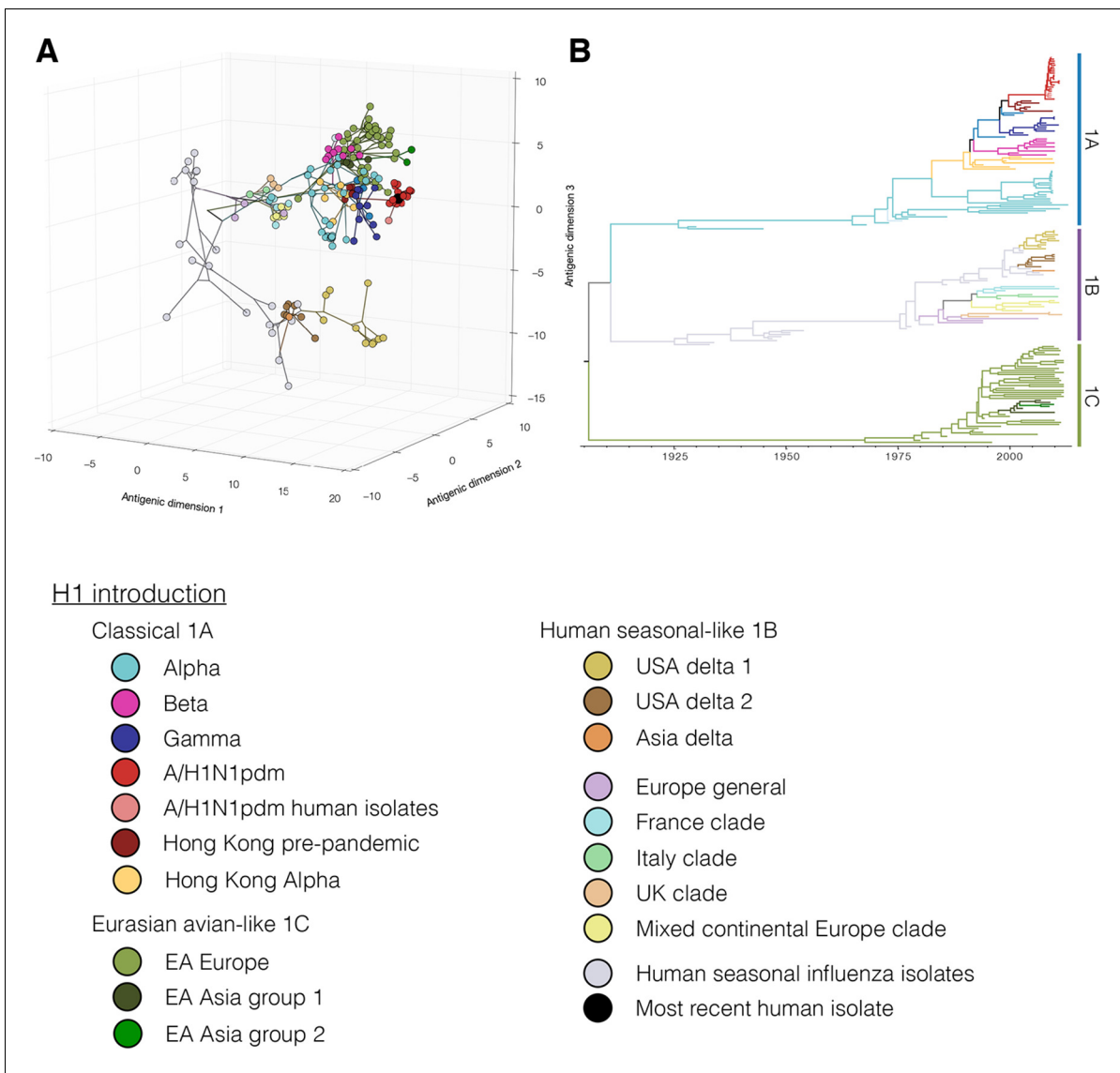
Figure 1 continued

Figure 1—figure supplement 1. *Figure 1A,B* colored by H1 genetic sub lineages in the Bayesian MCC tree.
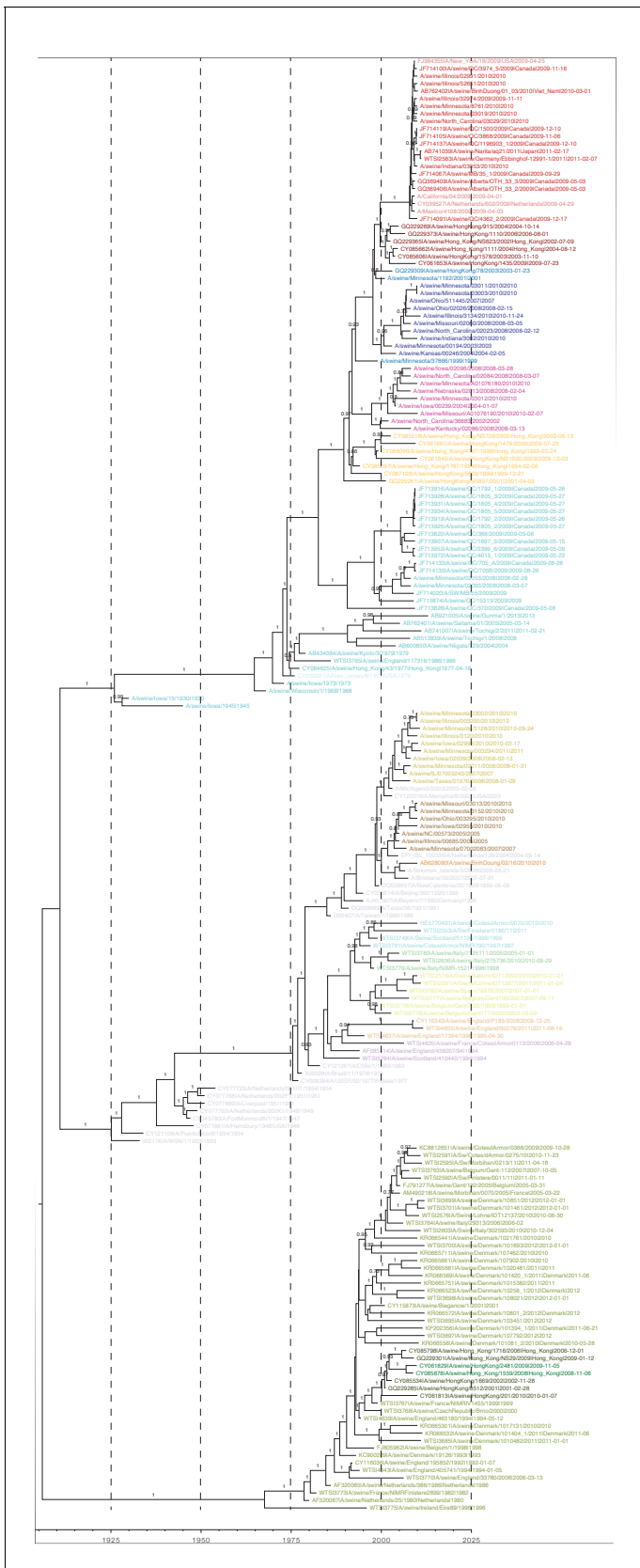DOI: 10.7554/eLife.12217.004

Figure 1—figure supplement 2. Bayesian H1 MCC tree with taxa labels and posterior support values
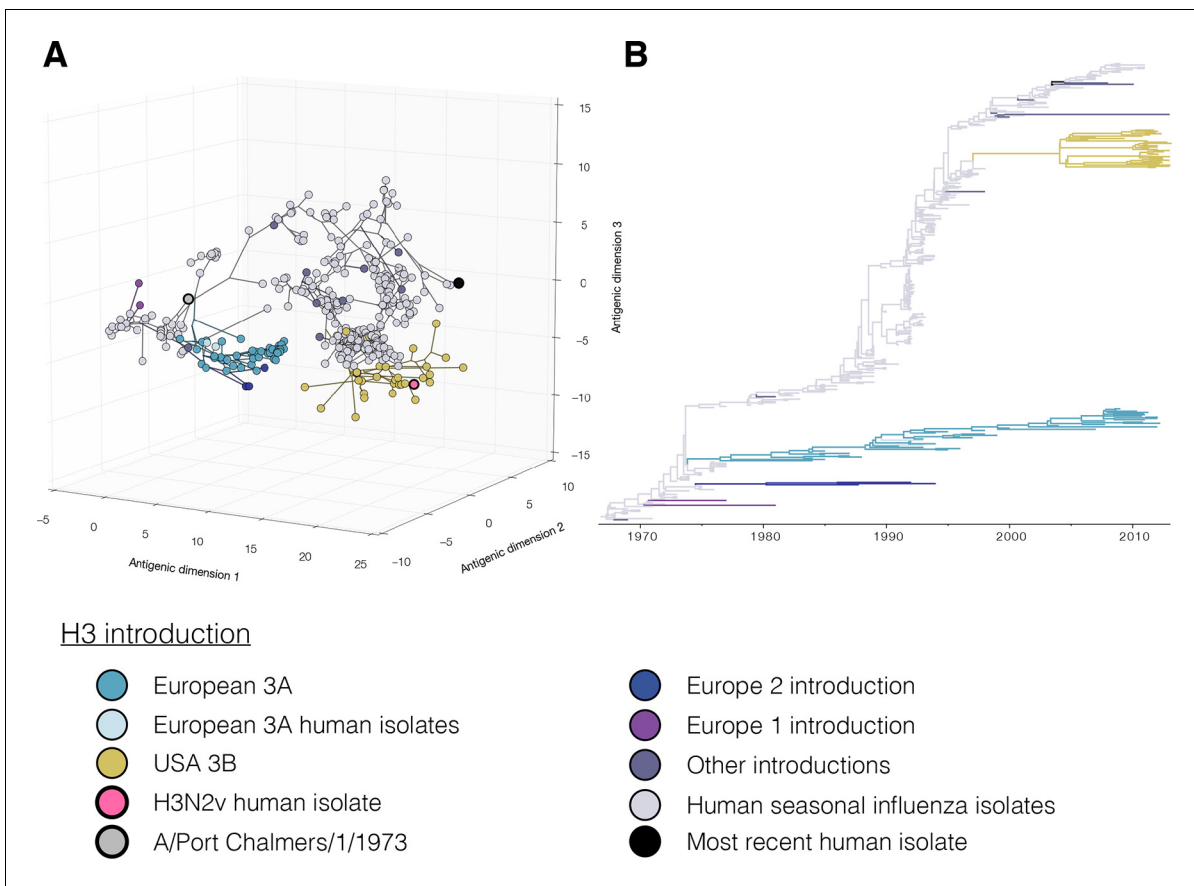DOI: 10.7554/eLife.12217.005

Figure 1—figure supplement 3. *Figure 1C,D* colored by H3 genetic sub lineages in the Bayesian MCC tree.
DOI: 10.7554/eLife.12217.006

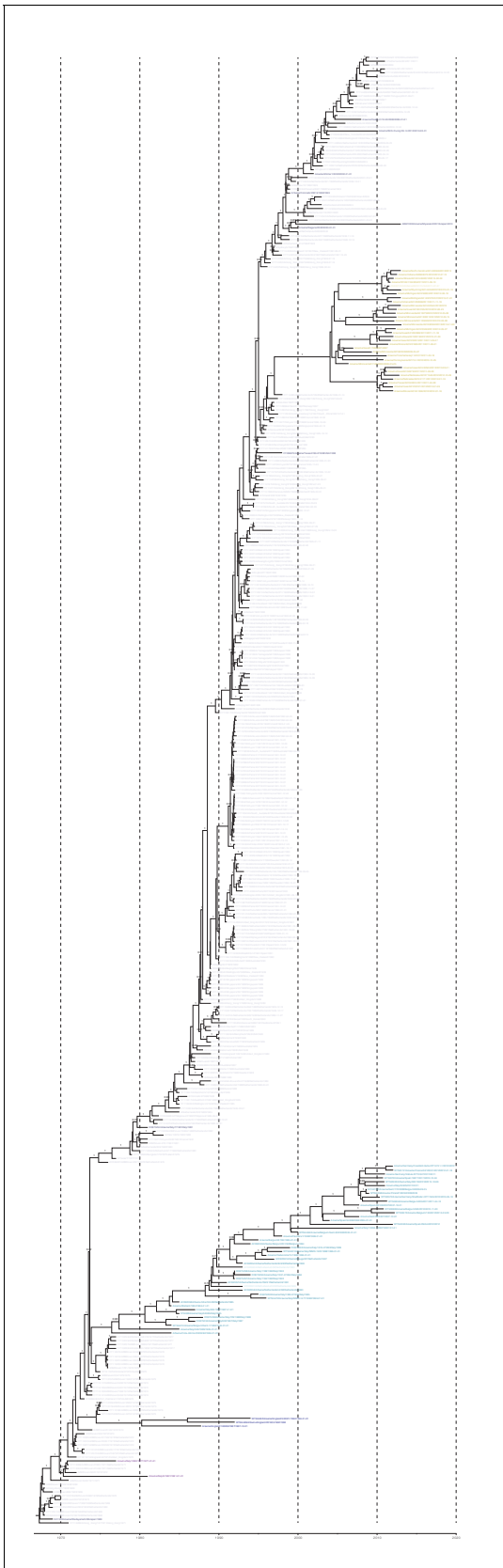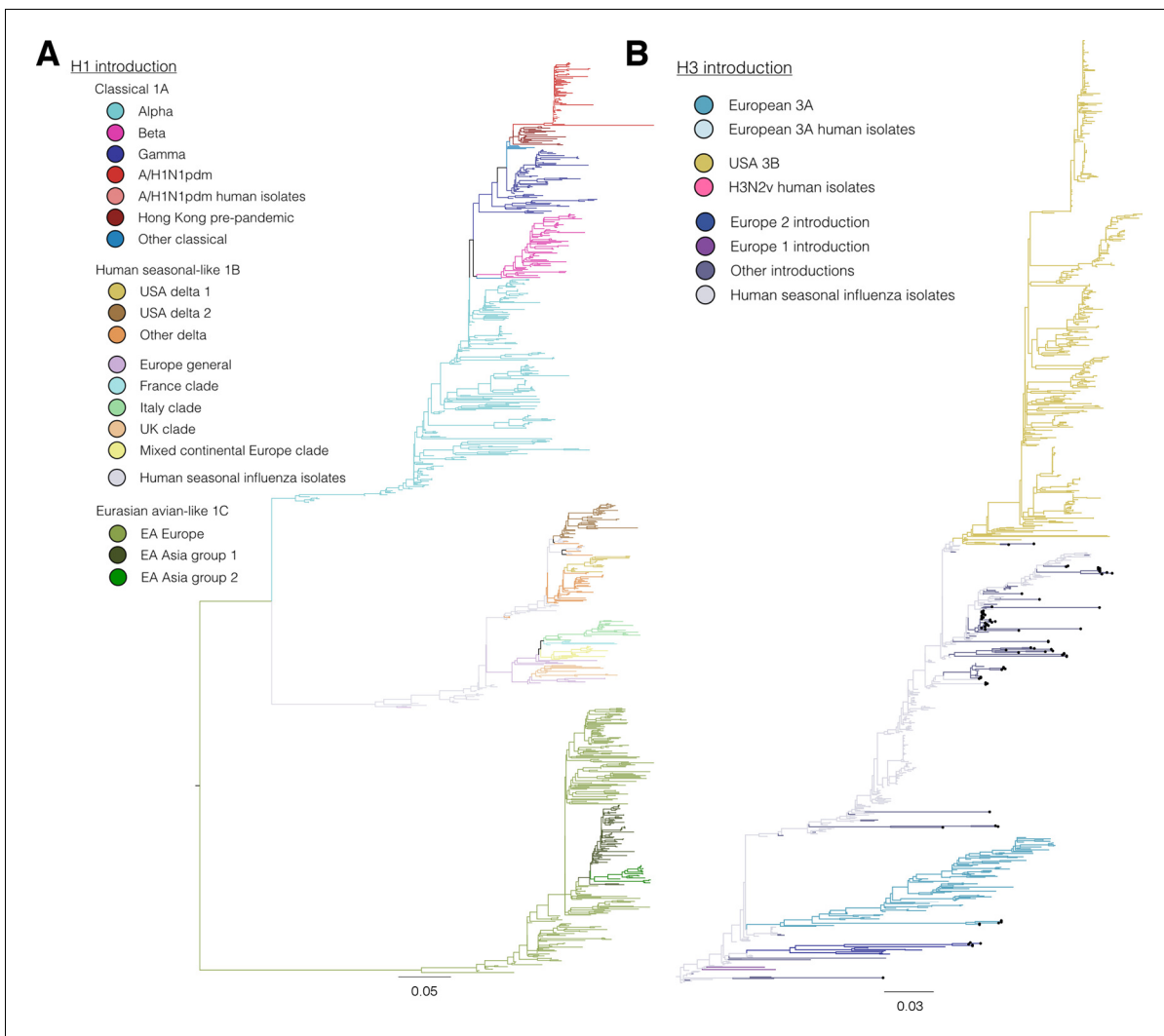**Figure 1—figure supplement 4.** Bayesian H3 MCC tree with taxa labels and posterior support values
DOI: 10.7554/eLife.12217.007

Figure 1—figure supplement 5. Maximum likelihood phylogenetic trees colored by lineage.
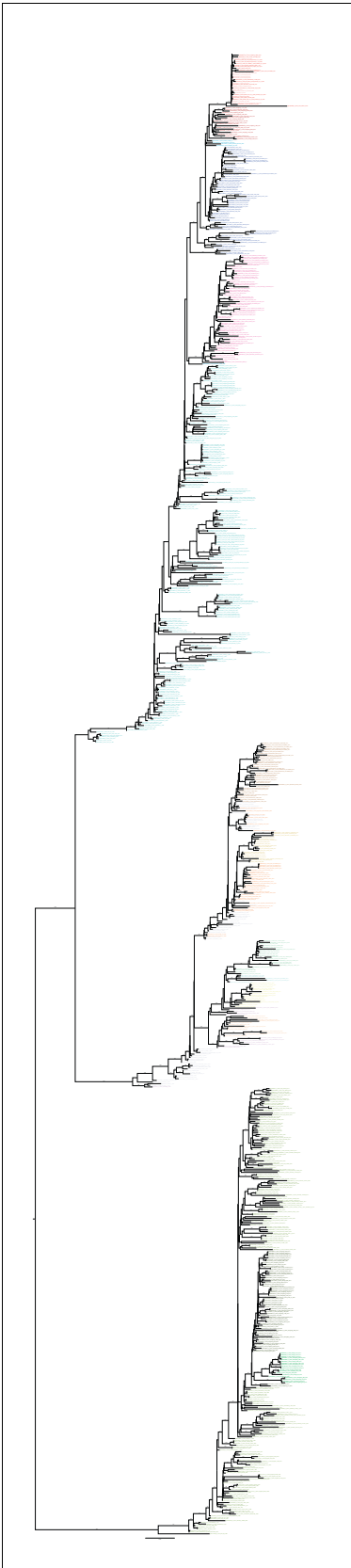DOI: 10.7554/eLife.12217.008

Figure 1—figure supplement 6. Maximum likelihood H1 phylogenetic tree with taxa labels and bootstrap support values
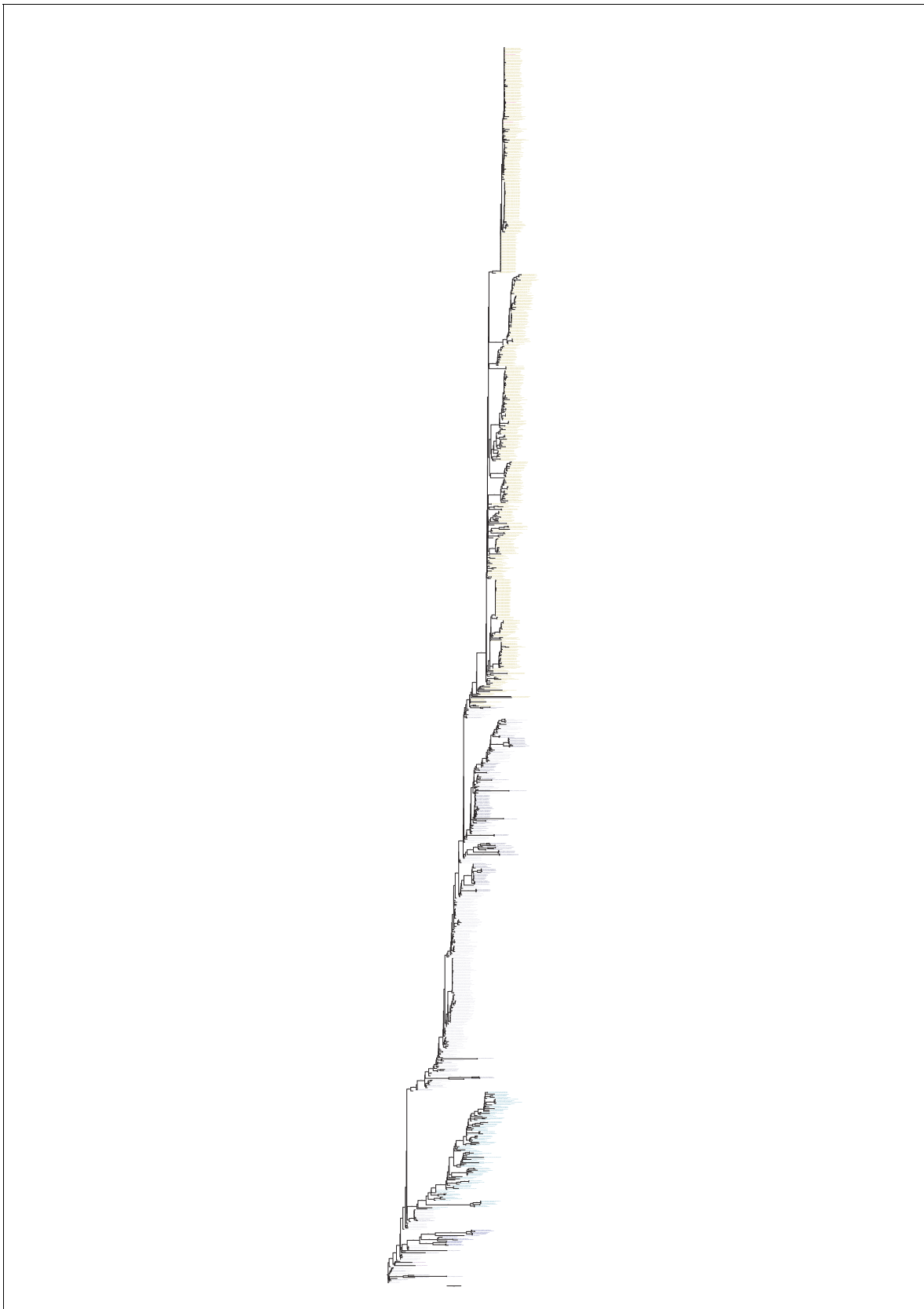DOI: 10.7554/eLife.12217.009

Figure 1—figure supplement 7. Maximum likelihood H3 phylogenetic tree with taxa labels and bootstrap support values.
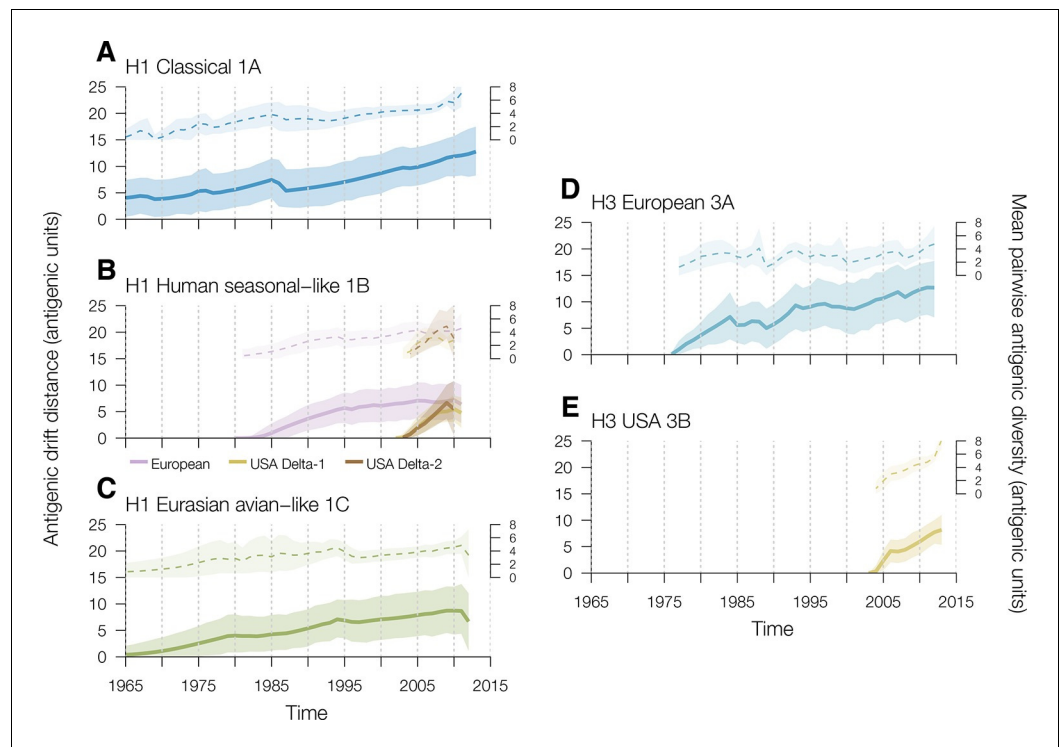DOI: 10.7554/eLife.12217.010

Figure 2. Time series of year-to-year rates of antigenic drift distance and antigenic diversity of H1 and H3 viruses in swine by genetic lineage. Solid colored lines represent year-to-year antigenic drift distance, where drift for year *i* is measured as the mean of Euclidean distances among strains in a phylogenetic lineage in year *i* compared to the mean of Euclidean distances among strains of that phylogenetic lineage from the previous year (*i*–1). The dotted line represents antigenic diversity among H1 and H3 strains by lineage through time. For the solid and dotted lines, the shaded region represents the range of the highest posterior density estimates. Multiple introductions which circulate for >5 years of the human seasonal-like swine H1 lineage in European (purple) and USA (gold) swine were calculated separately. Source data for *Figure 2* has been deposited in Dryad (*Lewis et al., 2016*).
DOI: 10.7554/eLife.12217.011