Diagram

Description automatically generated

**Extended Data Figure XX**. **Representative** **phylogenetic relationships of North American swine H1 1A classical swine lineage influenza A viruses from 2019 to 2021**. Each genetic clade was proportionately down sampled using smotXX and branches were colored. Swine influenza A virus strains characterized are marked by hash signs (#) and colored purple with the genetic clade consensus colored gray. The numbers in parentheses in the color key indicate number of each genetic clade detected between 2019 and 2021. Human seasonal H1 vaccine strains were colored gray; candidate vaccine viruses were colored red; and reported H1 variant cases detected between 2019 and 2021 were colored orange. The tree was midpoint rooted; all branch lengths are drawn to scale, and the scale bar indicates the number of nucleotide substitutions per site. The complete H1 phylogeny and input data are presented at <https://github.com/flu-crew/datasets>.

XXArendsee, Z.W., Baker, A.L.V. and Anderson, T.K., 2022. smot: a python package and CLI tool for contextual phylogenetic subsampling. *Journal of Open Source Software*, *7*(80), p.4193.