



Figure S1. Maximum-likelihood phylogeny inferred from 388 SARS-CoV-2 genomes, including 84 from Arizona and 304 representatives from around the world. Tips are colored by origin of sequence, and major lineages assigned by Pangolin, with more than 2 sequence representatives from Arizona, are labeled and indicated by black vertical bars (Note: vertical bars do not necessarily cover all genomes from a given Pangolin lineage, only those from Arizona). B.1.X is a well-supported sublineage of B.1 that has not been named by Pangolin. Genomes from Arizona are labeled with the associated GISAID accession number and Arizona County of origin, when available. The tree was visualized with a custom Python script that utilized the software package BALTIC (<https://github.com/evogytis/baltic>).