**Supplementary Material**

Nanopore sequencing

Midnight amplicons (~2.5 kb) from total DNA extracts were prepared for nanopore using the ONT Rapid Barcoding Kit (SQK-RBK004) according to the manufacturer’s protocol. Up to 12 samples were multiplexed on a flow-cell and sequenced on a MinION device. In addition, a no-template negative control was sequenced on each run. The *RAMPART* (v1.2.0) software package was used to monitor sequencing performance in real-time, with runs proceeding until a minimum ~20-fold coverage across at least 90% of the genome. All sequences underwent subsequent analysis provided the negative control met quality metrics.

The reads were demultiplexed with bases called using *Guppy* and aligned to the Wuhan-Hu-1 reference genome (MN908947.3) using *minimap2* (2.17-r941) with consensus genomes generated using bedtools. SARS-CoV-2 genomic lineages were inferred using Phylogenetic Assignment of Named Global Outbreak Lineages (PANGOLIN)[1]. A sequence was included for phylogenetic analysis if they met the following criteria 1) passed pangolin Qc; 2) was assigned to a lineage; and 3) contained less than 1000 ambiguous sites following masking of known problematic sites.

In total sequences pertaining to the identified outbreaks (n=84) and a random selection of community isolates (n=47) were included in a cluster analysis. A maximum likelihood tree was generated using *iqtree* v2.2.0 (substitution model: GTR+F+R2)[2] with genomic linkages inferred using *fasttranscluster v0.0.1*[3]using previously defined thresholds (K=2 and P=0.25).

**References**

1. cov-lineages/pangolin. Available at: https://github.com/cov-lineages/pangolin. Accessed 12 May 2022.

2. Minh B, Schmidt H, Chernomor O, et al. IQ-TREE 2: New models and efficient methods for phylogenetic inference in the genomic era. Mol Biol Evol **2020**; 37:1530–1534.

3. Stimson J, Gardy J, Mathema B, Crudu V, Cohen T, Colijn C. Beyond the SNP Threshold: Identifying Outbreak Clusters Using Inferred Transmissions. Mol Biol Evol **2019**; 36:587–603.