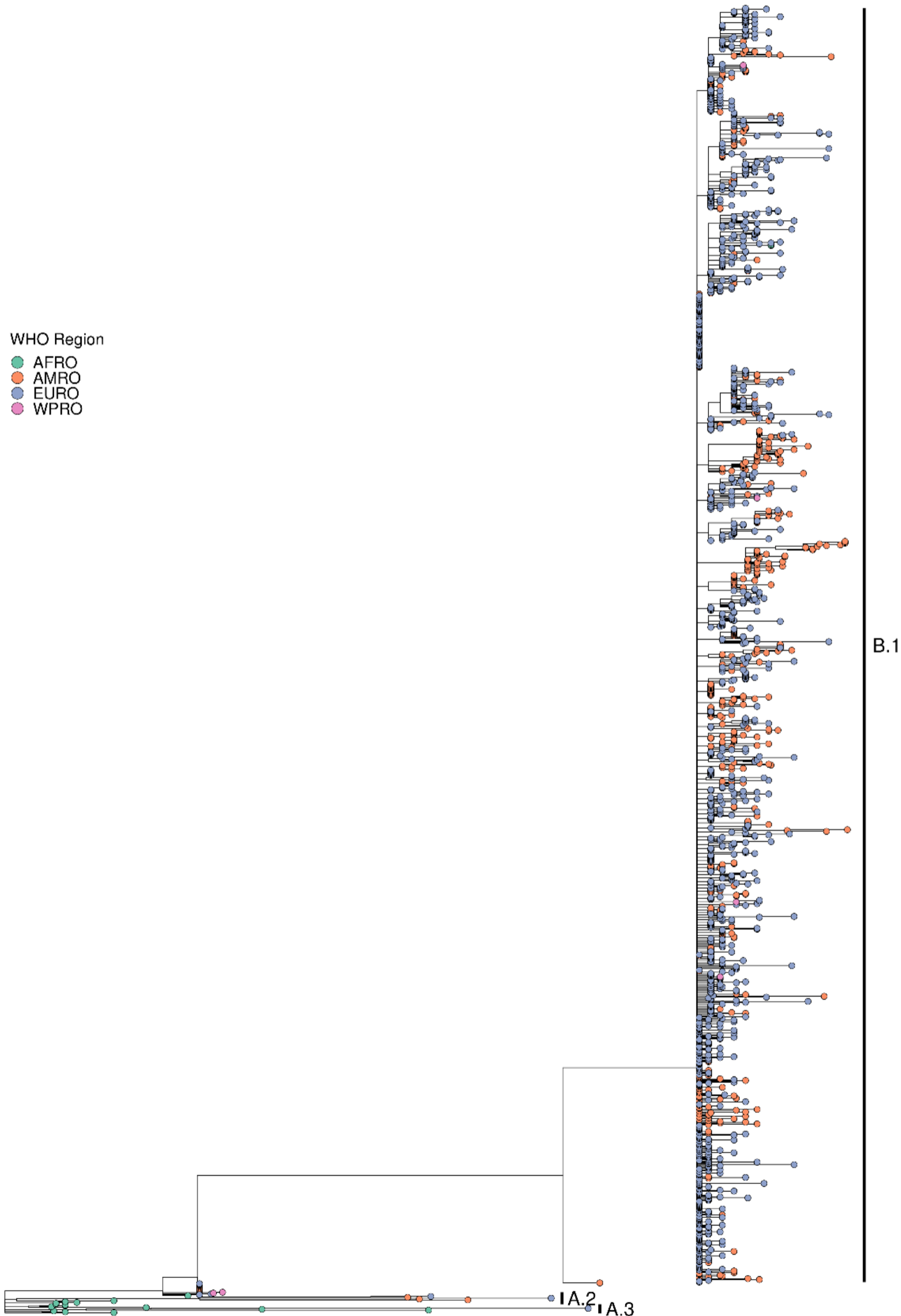


Phylogenetic trees from 'Investigation into monkeypox outbreak in England: technical briefing 8'

Figure 9. Phylogenetic tree of Clade IIb sequences

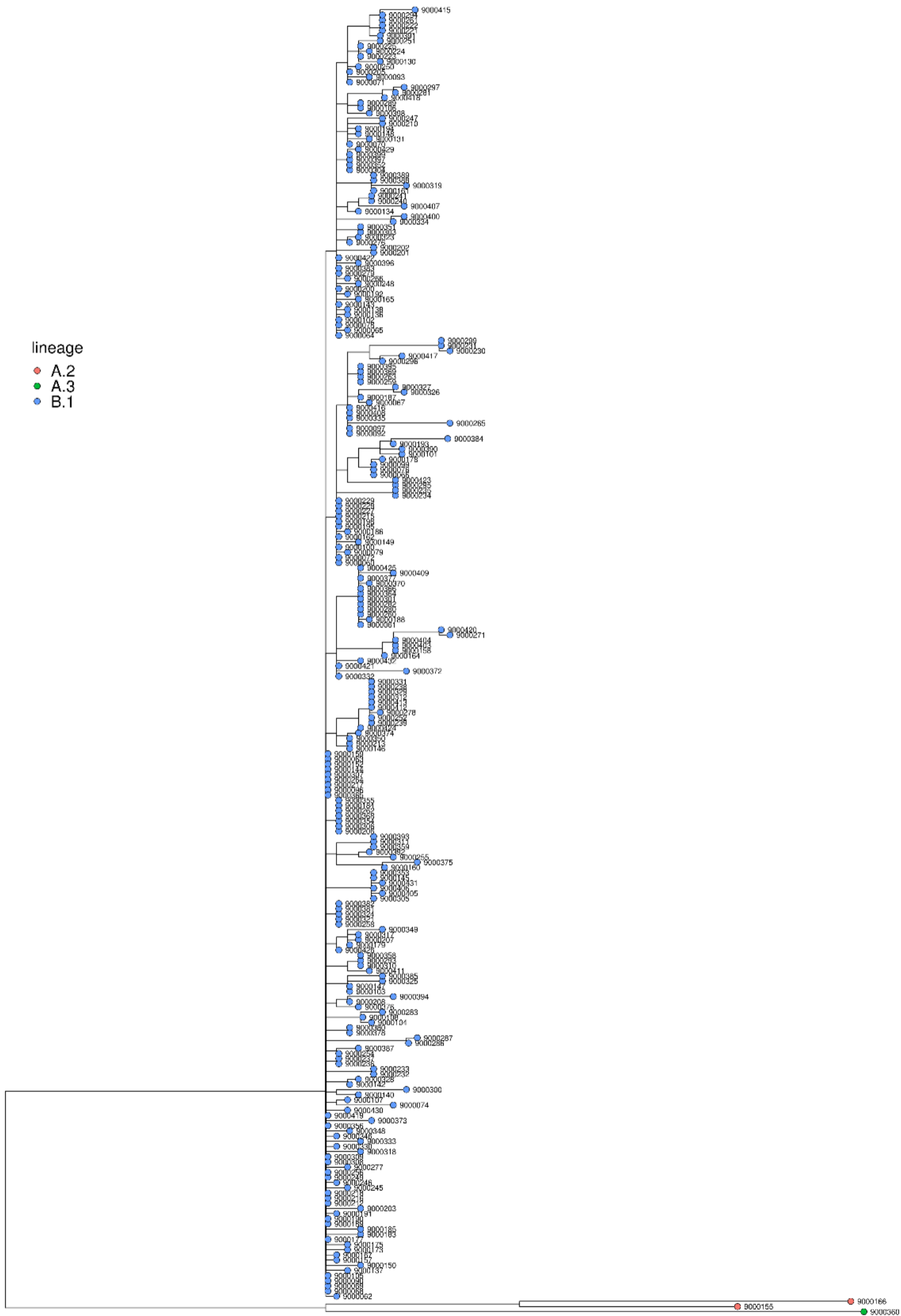
All UK sequences that have passed QC are included in the tree. Clade IIb genomes in Genbank that are not from the 2022 UK cases and are at least 180 kb (kilobases) in length are also included. The sequences are processed using [squirrel](#) to align to reference NC_063383 and mask repetitive regions. The 5' inverted terminal repeat (ITR) sequence is also masked. The tree was generated using the Jukes-Cantor method in [iqtree](#). Sequences are coloured by WHO region and lineages B.1, A.2, and A.3 are labelled.



Supplementary data is not available for this figure.

Figure 10. Phylogeny of Clade IIb UK sequences

Sequences are coloured by lineage and labelled by the sample identifier used in the isolate field for Genbank. The sequences are processed using squirrel to align to NC_063383 and mask repetitive regions. The 5' ITR is also masked. The tree was generated using the Jukes-Cantor method in [iqtree](#).



Supplementary data is not available for this figure.