Supplementary Data

Clinically validated nasopharyngeal SARS-CoV-2 real time reverse transcription polymerase chain reaction (RT-PCR) test were performed in Fimlab laboratories (Tampere, Finland) with commercial RT-PCR kits by GenomEra®, Abacus Diagnostica; Cobas 8800®, Roche Diagnostics, and Allplex™, Seegene and in Synlab laboratories (Helsinki, Finland) by TaqPath, Thermo Fisher Scientific. Sequencing was done by Fimlab laboratories using Clean-plex SARS-CoV-2 FLEX-panel by Paragon Genomics (1) and the Finnish Institute for Health and Welfare using ARTIC primers (2, 3). The B.1.617.2 variants were assigned with the Pangolin COVID-19 Lineage Assigner (https://pangolin.cog-uk.io/, (4)). The strains had B.1.617.2 lineage defining spike mutations T19R, L452R, T478K and P681R and, in addition, deletion F157-R158 and mutations T95I, E156G and D614G.

COVID-19 cases are notified to the National Infectious Diseases Register (NIDR) by both laboratories and physicians. The laboratory notification also includes sequencing data.

References

1. PS7004-02_CleanPlex-SARS-CoV-2-FLEX-Panels.v3 [Internet]. [cited 28.6.2021].

2. COVID-19 ARTIC v3 Illumina library construction and sequencing protocol V.4 [Internet].; 2020 [updated May 29,; cited June 23, 2021]. Available from: https://www.protocols.io/view/covid-19-artic-v3-illumina-library-construction-an-bgxjjxkn?version_warning=no.

3. Quick Josh, Loman Nick, ARTIC Consortium. hCoV-2019/nCoV-2019 Version 3 Amplicon Set. 2020 Mar 24,.

4. Rambaut A, Holmes EC, O'Toole Á, Hill V, McCrone JT, Ruis C, du Plessis L, Pybus OG. A dynamic nomenclature proposal for SARS-CoV-2 lineages to assist genomic epidemiology. Nat Microbiol. 2020 Nov;5(11):1403-1407. doi: 10.1038/s41564-020-0770-5. Epub 2020 Jul 15. PMID: 32669681; PMCID: PMC7610519.