**Supplementary Methods – Reanalysis of EPI\_ISL\_1314265**

FAST5 data was basecalled and demultiplexed using Guppy (v6.3.8) using the super-high accuracy model. The basecalled reads were mapped to SARS-CoV-2 reference genome Wuhan-Hu-1 (MN908947.3) with Minimap2 (v2.18) and ARTIC V3 primers were trimmed using iVar (v1.3.1) 31,32. Variant calling was performed with Clair3 (version 0.1.11) using the ‘r941\_prom\_sup\_g5014’ model and variant effect analysis was performed and summarized with SnpEff (v5.0) and SnpSift (v4.3.1t) 33–35. Depth-masked consensus sequences were generated using Bcftools (v1.12) and consensus sequences were generated using Bcftools depth-masked consensus sequence generation 36.

**References**

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