**SUPPLEMENTARY INFORMATION**

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**Supplementary Table 1. Accession IDs and sampling dates of sequences included in the dataset**

600_Figure S1.tif

**Supplementary Figure 1. Ancestral reconstruction of SARS-CoV-2 lineages B.1 using the European dataset.** **a**, **b**, The figure shows the full tree (**a**) and compressed visualization produced by PastML (**b**) using marginal posterior probability approximation (MPPA) with an F81-like model. Different colours correspond to different European countries and lineages. Numbers inside (or next to) the circles indicate the number of strains assigned to the specific node. AT, Austria; IT, Italy; DK, Denmark; NO, Norway; BA, Bosnia and Herzegovina; BE, Belgium; BG, Bulgaria; CH, Swiss; CN, China; CZ, Czech Republic; DE, Germany; ES, Spain; HU, Hungary; FI, Finland; FR, France; GB, United Kingdom; GR, Greece; HR, Croatia; IE, Ireland; IS, Iceland; PL, Poland; LT, Lithuania; LU, Luxembourg; LV, Latvia; NL, Netherlands; PT, Portugal; RO, Romania; RS, Serbia; RU, Russia; SE, Sweden; TR, Turkey.

600_Figure S2.tif

**Supplementary Figure 2.** **Ancestral reconstruction of SARS-CoV-2 lineages B using European dataset.** **a**, **b**, The figure shows the full tree (**a**) and compressed visualization produced by PastML (**b**) using marginal posterior probability approximation (MPPA) with an F81-like model. Different colours correspond to different European countries and lineages. Numbers inside (or next to) the circles indicate the number of strains assigned to the specific node. AT, Austria; GB, United Kingdom; BE, Belgium; CH, Swiss; CN, China; IT, Italy; DE, Germany; ES, Spain; GR, Greece; NL, Netherlands; PT, Portugal; FI, Finland; FR, France; IE, Ireland; IS, Iceland; LV, Latvia.