Ancestral area reconstruction of SARS-CoV-2 indicates multiple sources of entry into Australia

Supplementary materials

**Supplementary table 1.** Dispersal events of SARS-CoV-2 isolates from Australia to other (sub)continents identified for the IQ-tree, BEAST and FastTree phylogenies\*

|  |  |  |  |
| --- | --- | --- | --- |
| Phylogeny  (Methods) | On IQ-tree phylogeny  (S-DIVA)\*\* | On BEAST phylogeny  (S-DIVA)\*\* | On FastTree phylogeny  (BayArea) |
| Dispersal routes from Australia | A->B:2.5  A->C:3.5  A->D:2.583333  A->E:1.25  A->F:0.5  A->G:3.5  A->H:1.5  A->J:9.666667  A->K:5 | A->B:4.5  A->C:2.5  A->D:0.5  A->E:4  A->F:2.5  A->G:1.833333  A->H:2.5  A->I:0.5  A->J:11  A->K:4.5 | A->B  A->C  A->D  A->E  A->F  A->G:  A->H  A->I  A->J  A->K |
| Cost of dispersals from Australia | 30 | 34.33 |  |

\* (A) Australia, (B) Southeast Asia, (C) West Asia, (D) East Asia, (E) South Asia, (F) North Asia, (G) North America, (H) South America, (I) Central Asia, (J) Europe. \*\* Dispersal costs estimated by S-DIVA for corresponding dispersal events.

**Supplementary file 1.** The clusters and representative sequences generated by CD-HIT redundancy reduction at a threshold of 99.5% nucleotide similarity

The results were described in a separate excel document.