1875-0362/21

Send Orders for Reprints to reprints@benthamscience.net

The Open Bioinformatics Journal

Supplementary Material

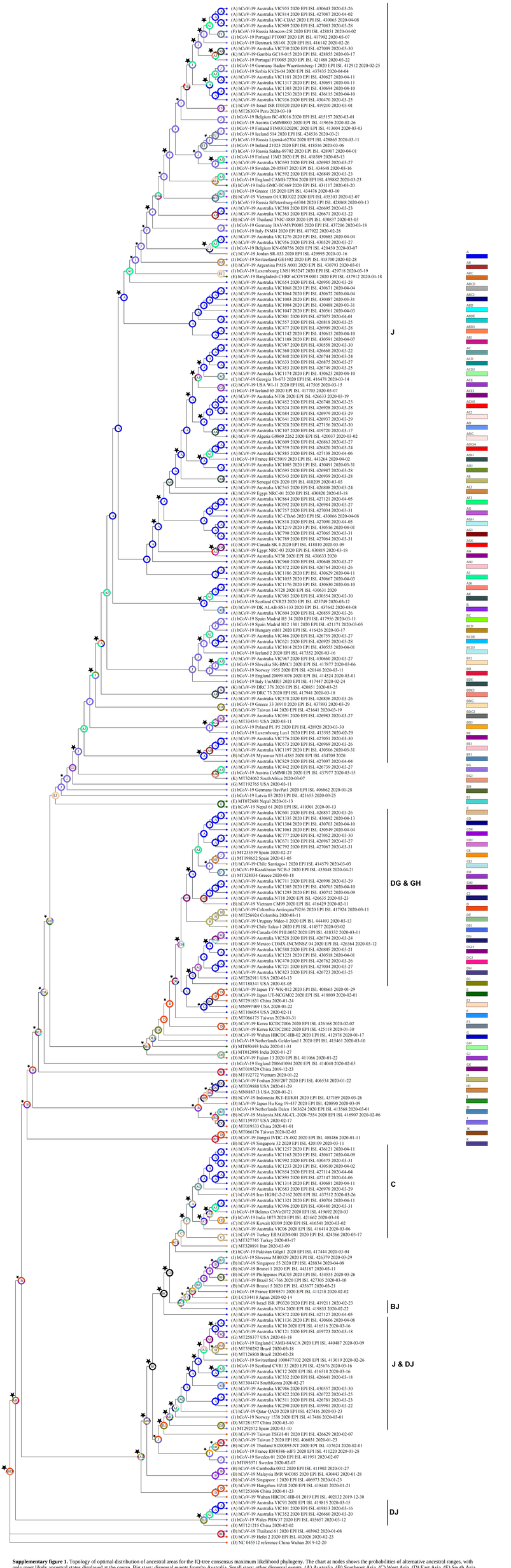
Content list available at: https://openbioinformaticsjournal.com

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

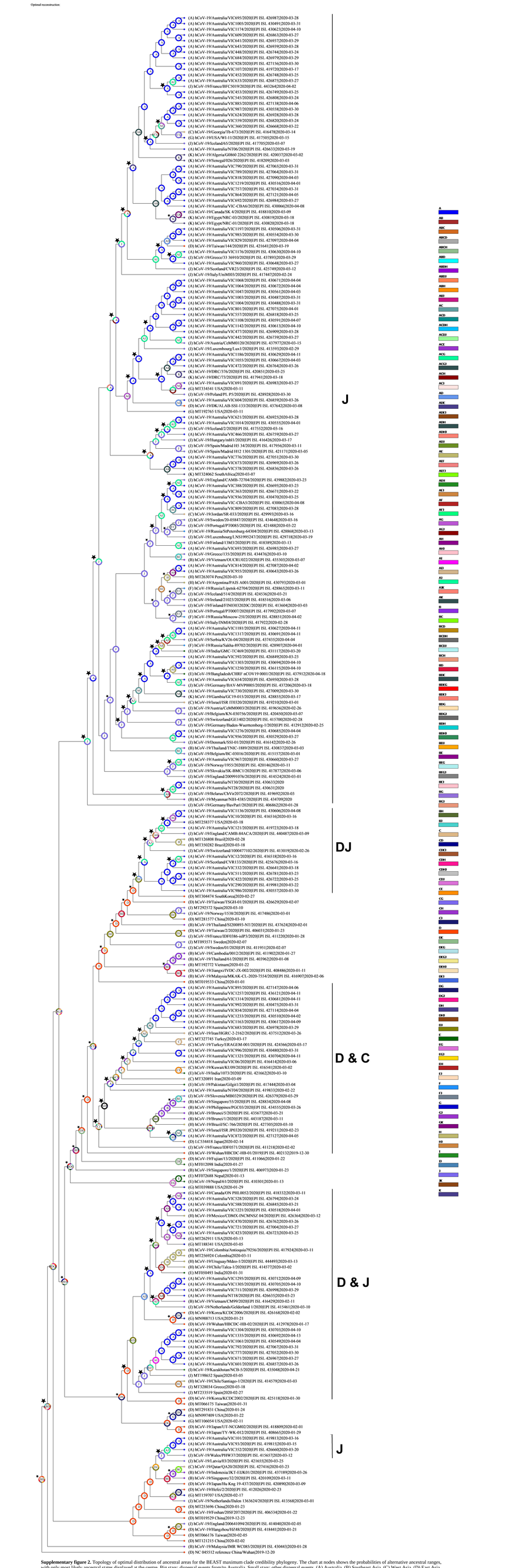
Supplementary Table 1. Dispersal events of SARS-CoV-2 isolates from Australia to other (sub)continents identified for the IQ-tree, BEAST and FastTree phylogenies*

Phylogeny (Methods)	On IQ-tree Phylogeny (S-DIVA)**	On Beast Phylogeny (S-DIVA)**	On Fast Tree 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	N/A

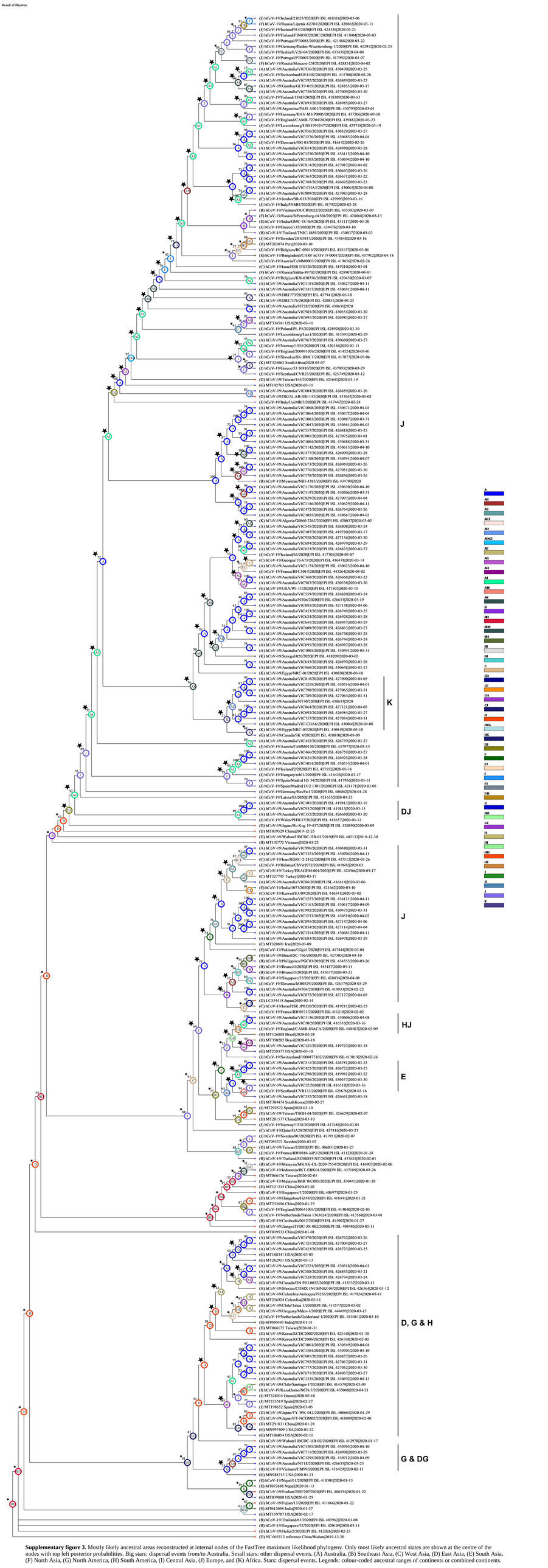
* (A) Australia, (B) Southeast Asia, (C) West Asia, (D) East Asia, (E) South Asia, (F) North Asia, (G) North America, (H) South America, (I) Central Asia, (J) Europe. ** Dispersal costs estimated by S-DIVA for corresponding dispersal events.



Supplementary figure 1. Topology of optimal distribution of ancestral areas for the IQ-tree consensus maximum likelihood phylogeny. The chart at nodes shows the probabilities of alternative ancestral ranges, with only most likely ancestral states displayed at the centre. Big stars: dispersal events from/to Australia. Small stars: other dispersal events. (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, and (K) Africa. Legends: colour-coded ancestral ranges of continents or combined continents.



Supplementary figure 2. Topology of optimal distribution of ancestral areas for the BEAST maximum clade credibility phylogeny. The chart at nodes shows the probabilities of alternative ancestral ranges, with only most likely ancestral states displayed at the centre. Big stars: dispersal events from/to Australia. Small stars: other dispersal events. (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, and (K) Africa. Legends: colour-coded ancestral ranges of continents or combined continents.



Supplementary figure 3. Mostly likely ancestral areas reconstructed at internal nodes of the FastTree maximum likelihood phylogeny. Only most likely ancestral states are shown at the centre of the nodes with top left posterior probabilities. Big stars: dispersal events from/to Australia. Small stars: other dispersal events. (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, and (K) Africa. Stars: dispersal events. Legends: colour-coded ancestral ranges of continents or combined continents.