

Supplementary Material

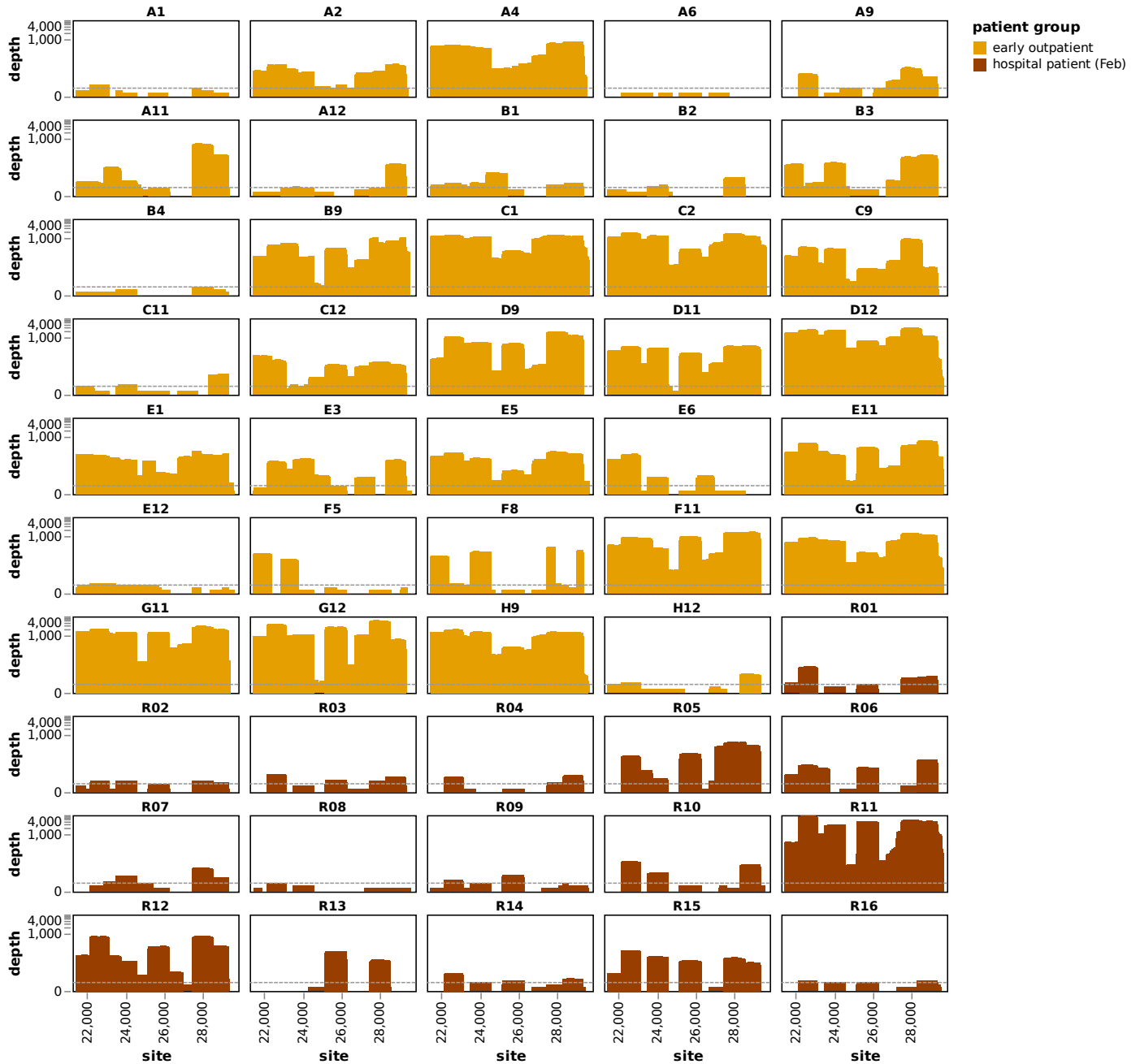


Figure S1 Sequencing depth over the SARS-CoV-2 genome from site 21,570 to 29,550 for the 34 virus-positive early epidemic samples and the 16 samples from hospitalized patients in February. Depth is the number of aligned reads that cover that site with a quality score ≥ 20 . The dashed gray line is the minimum coverage required to call a consensus identity at a site. Note that the y-axis uses a symlog scale. An interactive version of this plot that enables zooming into specific site ranges and mouseovers to see read count statistics at each site is at https://jbloom.github.io/SARS-CoV-2_PRJNA612766/coverage_region.html. A version of the plot where the x-axis spans the entire SARS-CoV-2 genome is in Figure S2.

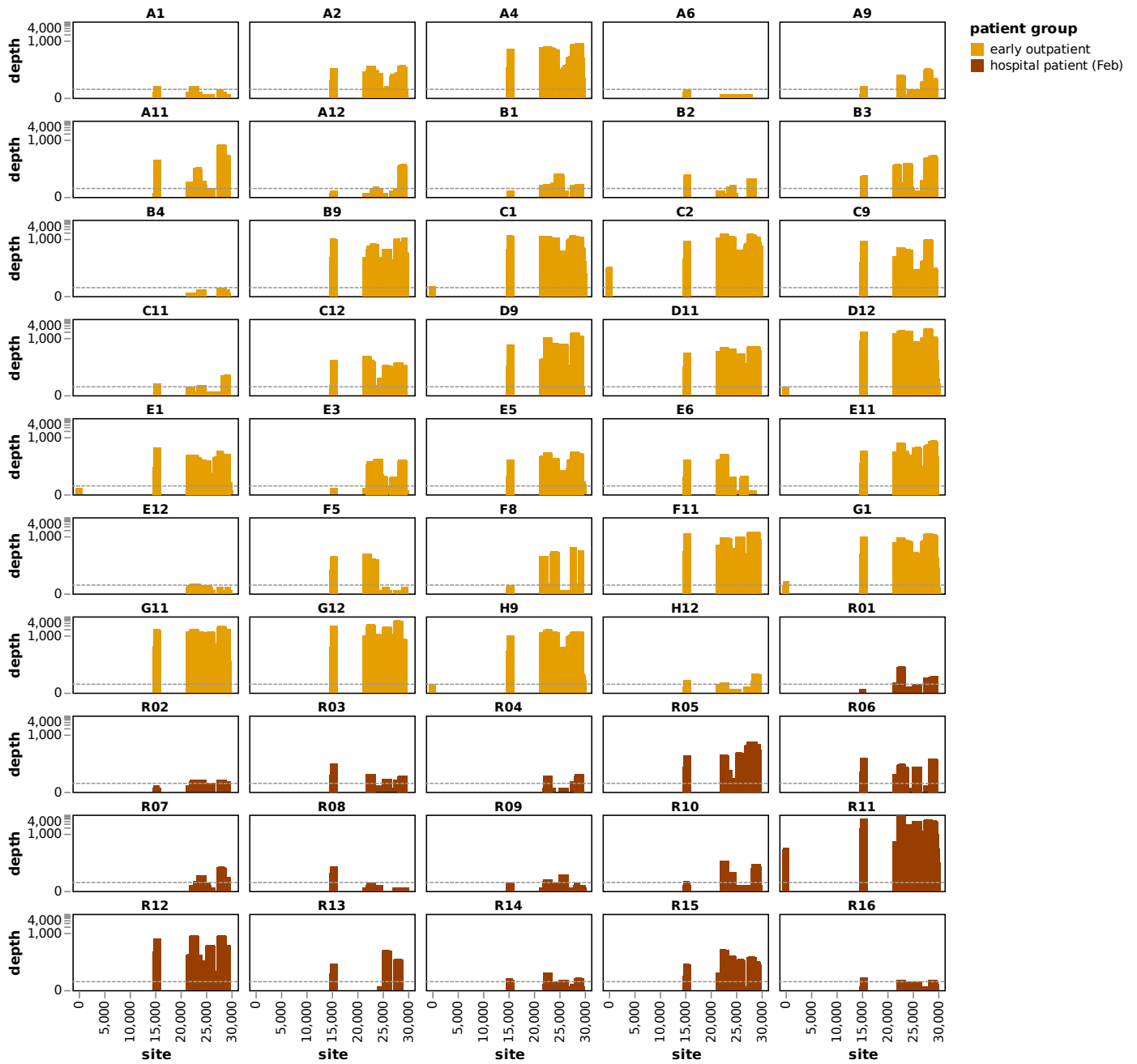


Figure S2 A version of Figure ?? that shows coverage over the full length of the SARS-CoV-2 genome. An interactive version of this plot is at https://jbloom.github.io/SARS-CoV-2_PRJNA612766/coverage_all.html.

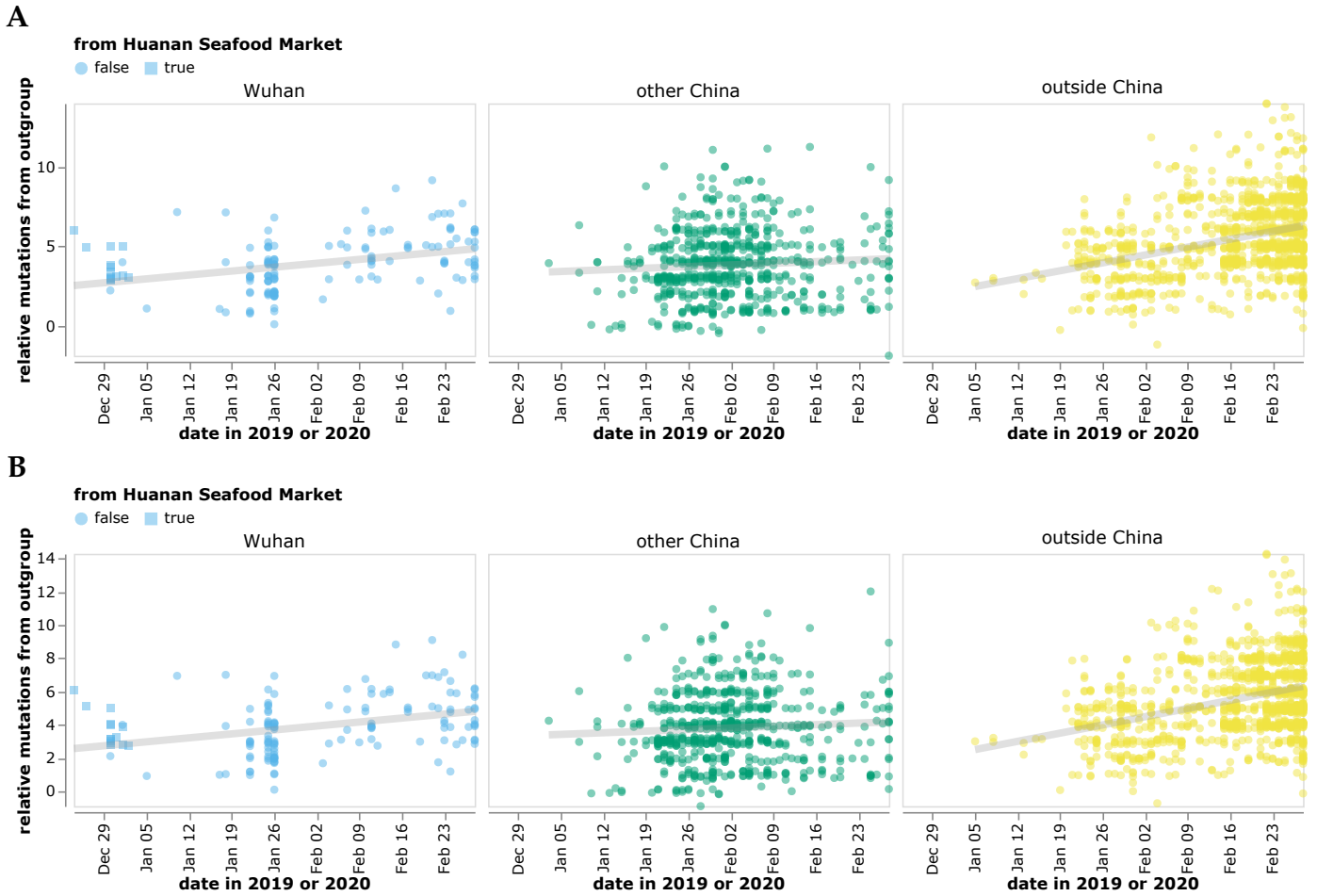


Figure S3 Versions of Figure 3 but calculating the relative mutational distances using an outgroup of (A) RpYN06 or (B) RmYN02.

A

progenitor as USA/WA1/2020 (2020-01-19)
 mutations from proCoV2 (Kumar et al): none
 mutations from Wuhan-Hu-1: C8782T, C18060T, T28144C

progenitor as Guangdong/HKU-SZ-002/2020 (2020-01-10)
 mutations from proCoV2 (Kumar et al): T18060C, C29095T
 mutations from Wuhan-Hu-1: C8782T, T28144C, C29095T

progenitor as Shandong/LY005-2/2020 (2020-01-24)
 mutations from proCoV2 (Kumar et al): T3171C, T18060C
 mutations from Wuhan-Hu-1: T3171C, C8782T, T28144C



B

progenitor as USA/WA1/2020 (2020-01-19)
 mutations from proCoV2 (Kumar et al): none
 mutations from Wuhan-Hu-1: C8782T, C18060T, T28144C

progenitor as Guangdong/HKU-SZ-002/2020 (2020-01-10)
 mutations from proCoV2 (Kumar et al): T18060C, C29095T
 mutations from Wuhan-Hu-1: C8782T, T28144C, C29095T

progenitor as Shandong/LY005-2/2020 (2020-01-24)
 mutations from proCoV2 (Kumar et al): T3171C, T18060C
 mutations from Wuhan-Hu-1: T3171C, C8782T, T28144C

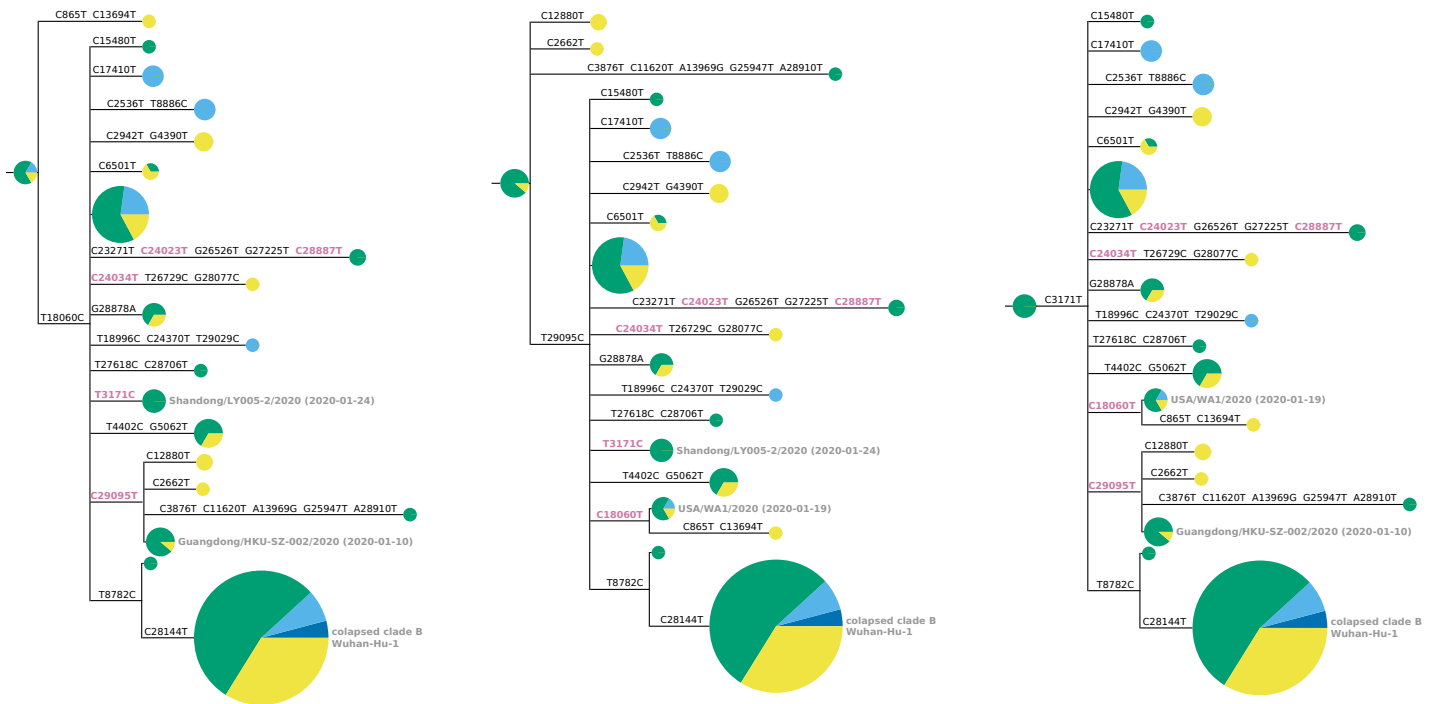


Figure S4 A version of Figure 4 but rooting using an outgroup of (A) RpYN06 or (B) RmYN02 outgroups. The tree topologies are identical to those obtained using RaTG13 in Figure 4, with the only differences being a few minor changes in which mutations on branches are towards the outgroup (purple mutation labels).