

Supplementary information

Tables S1 – S3

Figures S1 – S6

Table S1. Substitutions of more than 90% frequency of Japan-related B.1.1 variants and those of the other B.1.1 variants

| Substitution | Japan-related B.1.1 variants (%) | The other B.1.1 variants (%) |
|---------------------|---|-------------------------------------|
| A23403G | 100.0 | 98.8 |
| C3037T | 100.0 | 96.2 |
| C14408T | 99.9 | 98.0 |
| C241T | 99.7 | 95.8 |
| GGG28881AAC | 98.3 | 93.3 |
| C313T | 90.3 | 5.5 |

Japan-related variants include “Domestic” and “International” B.1.1 lineage genomes, and the other variants include “Quarantine” and non-Japan-related B.1.1 lineage genomes.

Table S2. Substitutions of more than 90% frequency of Japan-related AY.29 variants and those of the other Delta variants

| Substitution | Japan-related AY.29 variants (%) | The other Delta variants (%) |
|---------------------|---|-------------------------------------|
| A23403G | 100.0 | 99.7 |
| C3037T | 100.0 | 99.3 |
| C8986T | 100.0 | 89.9 |
| G15451A | 100.0 | 97.6 |
| G9053T | 100.0 | 89.4 |
| C19220T | 100.0 | 89.6 |
| C5239T | 100.0 | 0.0 |
| G4181T | 100.0 | 89.2 |
| C16466T | 100.0 | 98.9 |
| C25469T | 100.0 | 99.4 |
| T26767C | 100.0 | 99.2 |
| G29402T | 99.9 | 97.5 |
| G210T | 99.9 | 95.4 |
| C10029T | 99.9 | 89.4 |
| C241T | 99.9 | 96.1 |
| G28916T | 99.9 | 88.8 |
| C7124T | 99.9 | 86.9 |
| C23604G | 99.9 | 99.3 |
| C6402T | 99.9 | 87.4 |
| G28881T | 99.9 | 98.6 |
| C27874T | 99.9 | 88.3 |
| C21618G | 99.9 | 98.0 |
| C27752T | 99.9 | 94.6 |
| A28461G | 99.8 | 97.1 |
| T5514C | 99.8 | 0.0 |
| G24410A | 99.8 | 95.2 |
| G29742T | 99.8 | 91.2 |
| A11332G | 99.7 | 89.1 |
| C14408T | 99.7 | 99.3 |
| T27638C | 99.7 | 92.7 |
| A28271- | 99.6 | 92.9 |
| AGTTCA22029- | 99.4 | 91.1 |
| C22995A | 99.4 | 96.9 |
| T22917G | 99.4 | 96.5 |
| A11201G | 98.9 | 89.6 |
| GATTTC28248- | 98.7 | 96.0 |
| C21846T | 98.1 | 36.6 |
| G21987A | 93.3 | 64.8 |

Table S3. “Domestic” R.1 entries during the five epidemic waves of COVID-19 in Japan

| Epidemic wave | 1st | 2nd | 3rd | 4th | 5th |
|---|--------------|------------|-----------------|-------------------|---------------|
| Starting date | 2020-01-01 | 2020-06-14 | 2020-10-10 | 2021-03-01 | 2021-06-21 |
| Ending date | 2020-06-13 | 2020-10-09 | 2021-02-28 | 2021-06-20 | 2021-12-16 |
| # of R.1 genome (Proportion %) | 4 (0.05%) | 0 (0%) | 932 (12.24%) | 6,639 (87.17%) | 41 (0.54%) |

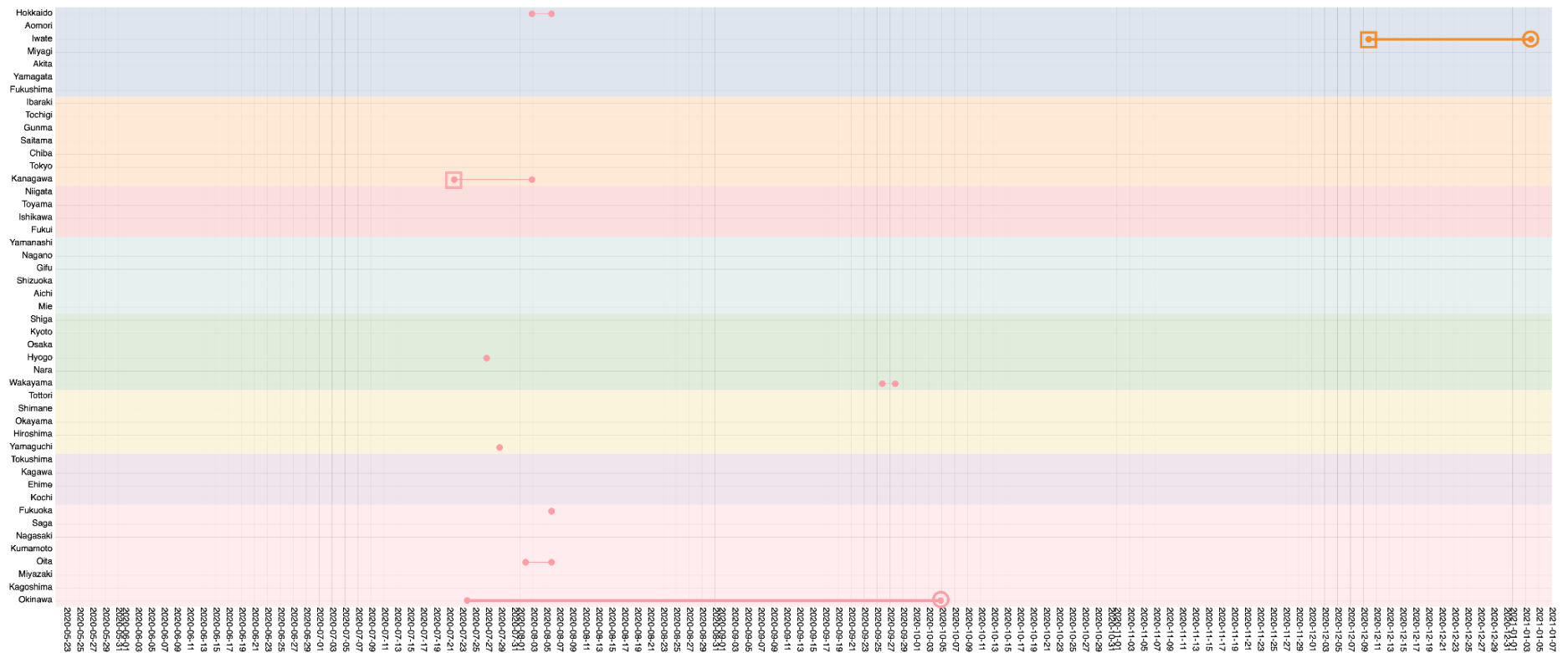


Figure S1 HaploGraph visualization for the haplotypes “1.45.4” and “1.70.13.20.1.9.2” of the second epidemic wave that showed prefectural preference. Dots and lines in pink and orange indicate the haplotypes “1.45.4” and “1.70.13.20.1.9.2”, respectively. The earliest or latest entry of each haplotype is surrounded by a square or a circle of the corresponding color. The haplotype “1.45.4” was mostly sampled in Okinawa prefecture, and “1.70.13.20.1.9.2” was all sampled in Iwate prefecture. For the details of the “HaploGraph”, please see Figure 1.

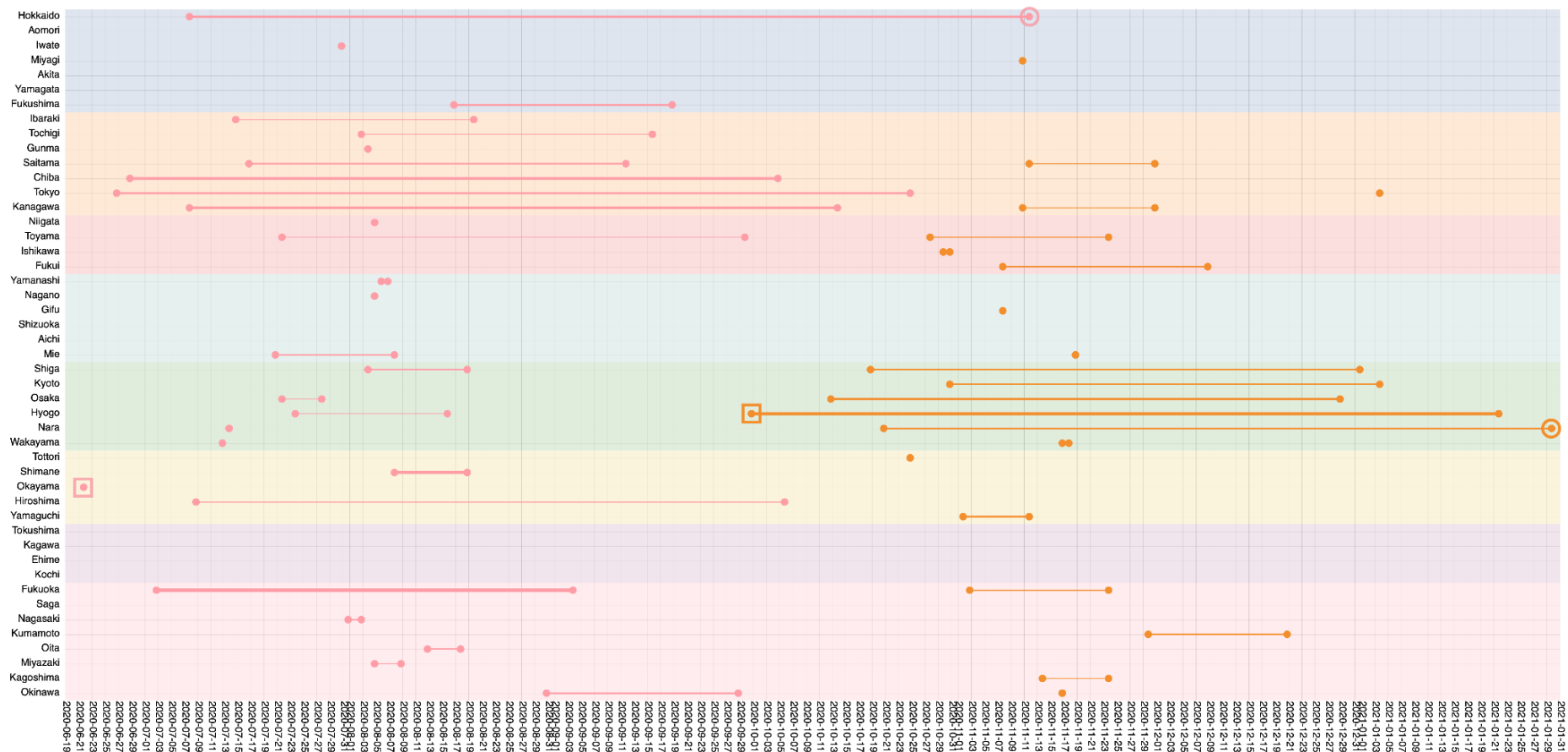


Figure S2. HaploGraph visualization for the haplotypes “1.7” and “c.1.x.10” of the third epidemic wave. Dots and lines in pink and orange indicate the second largest haplotype “1.7” and the third largest haplotype “c.1.x.10”, respectively. The earliest or latest entry of each haplotype is surrounded by a square or a circle of the corresponding color.

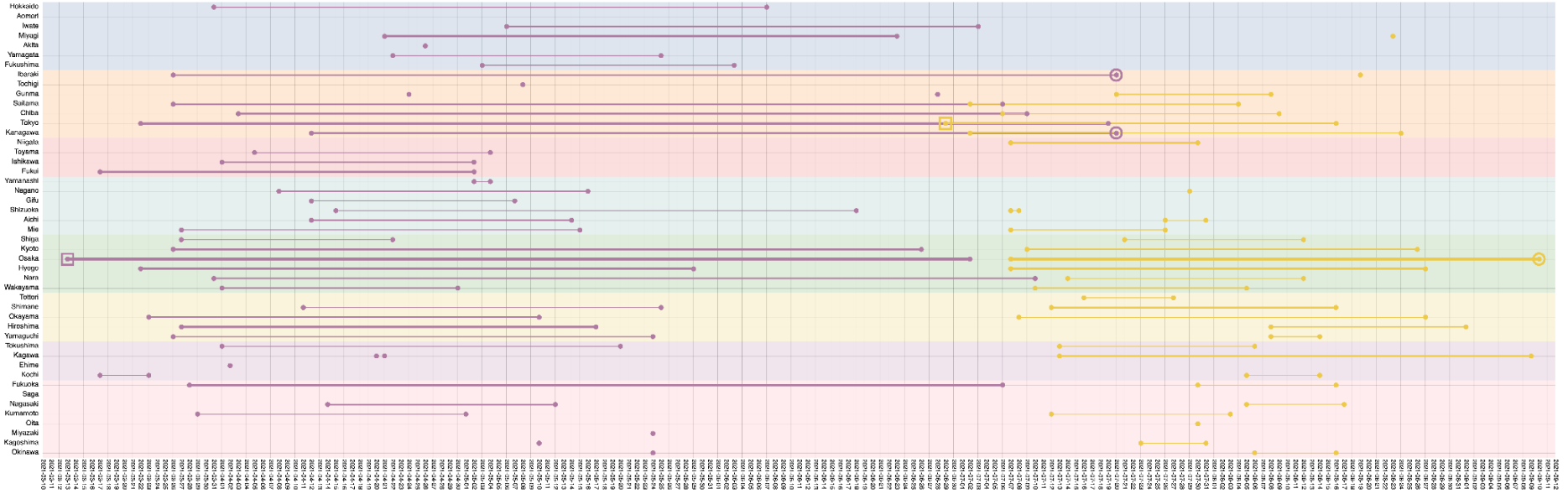


Figure S3. HaploGraph visualization for the haplotypes “1.265.2” and “2.112.5” of the fourth epidemic wave. Dots and lines in purple and yellow indicate the second largest haplotype “1.265.2” and the fourth largest haplotype “2.112.5”, respectively. The earliest or latest entry of each haplotype is surrounded by a square or a circle of the corresponding color.

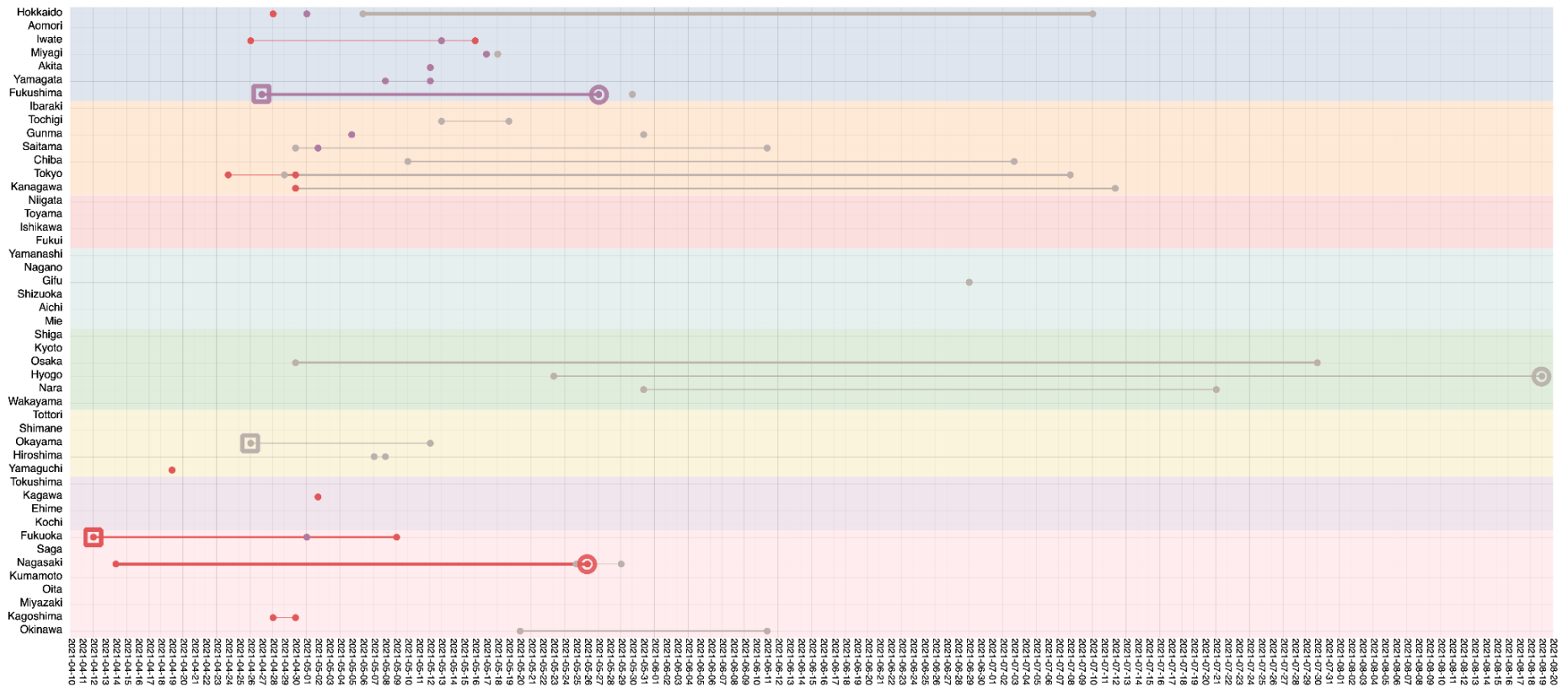


Figure S4. HaploGraph visualization for the haplotypes “1.265.2.145.3”, “1.265.2.454”, and “1.265.2.483.1.4.x.1” of the fourth epidemic wave that showed prefectural preference. Dots and lines in grey, red, and purple indicate the haplotypes “1.265.2.145.3”, “1.265.2.454”, and “1.265.2.483.1.4.x.1”, respectively. The earliest or latest entry of each haplotype is surrounded by a square or a circle of the corresponding color. The haplotype “1.265.2.145.3” was mostly sampled in Hokkaido, the “1.265.2.454” was mostly sampled in Nagasaki, and the “1.265.2.483.1.4.x.1” was mostly sampled in Fukushima.

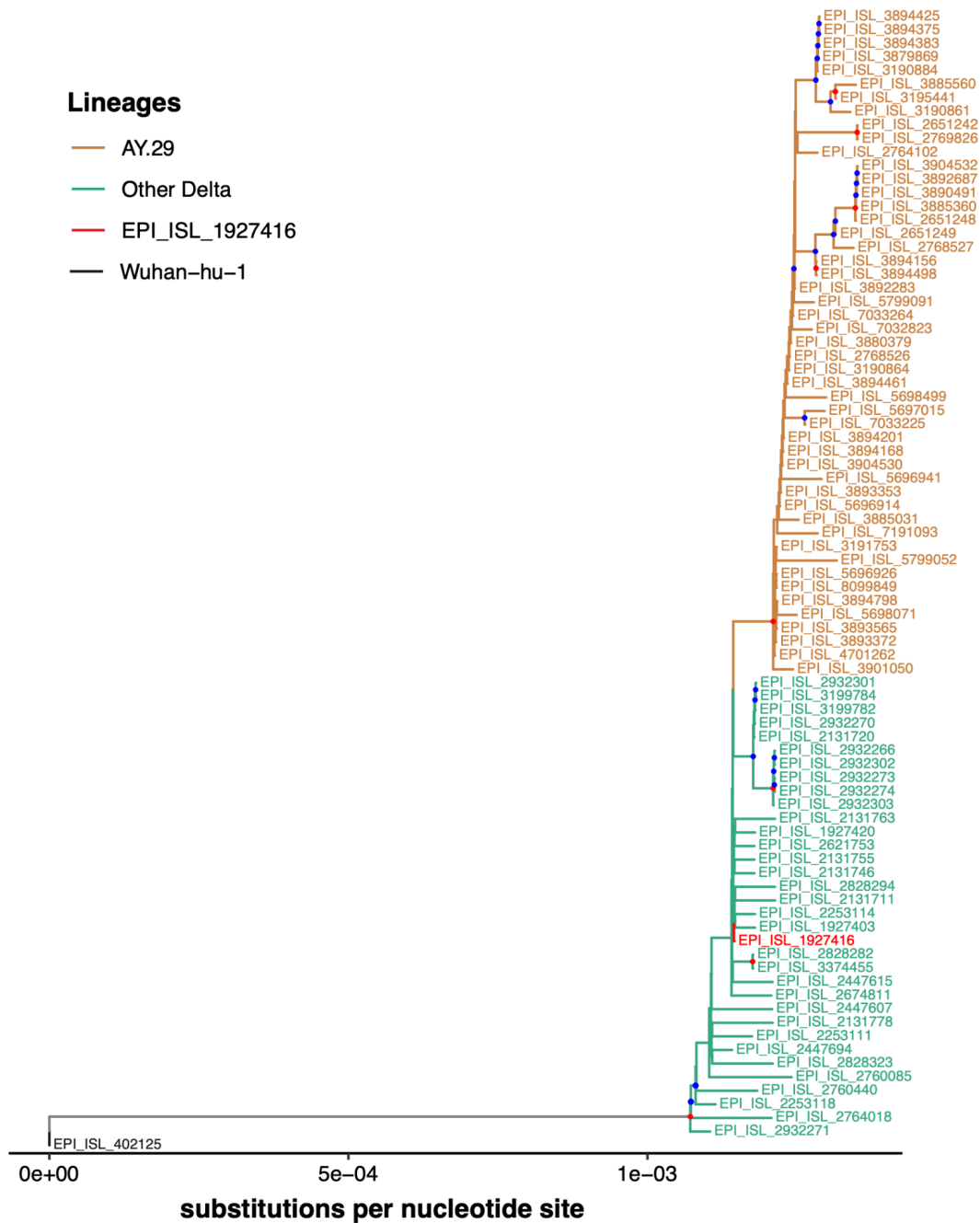
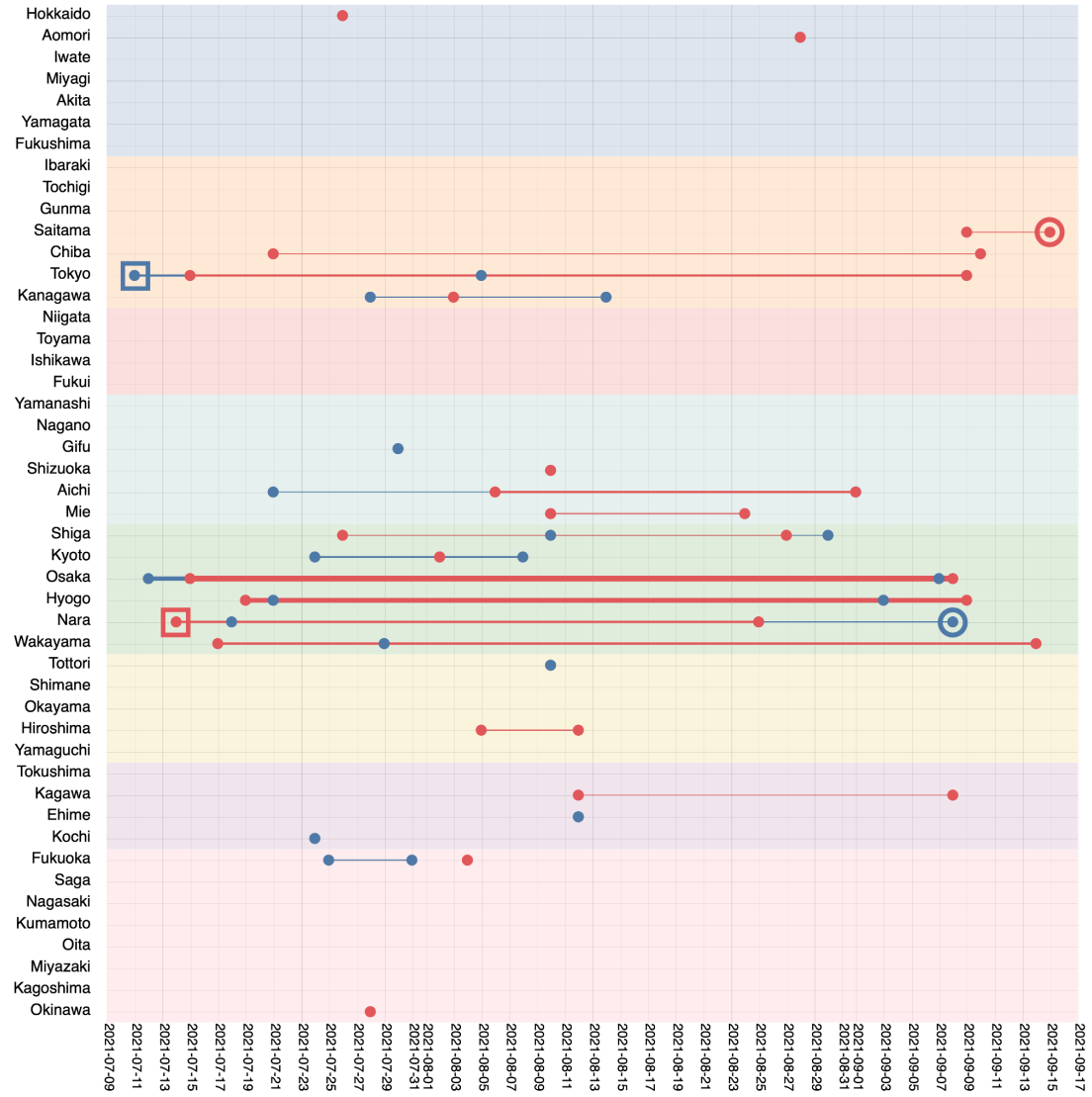
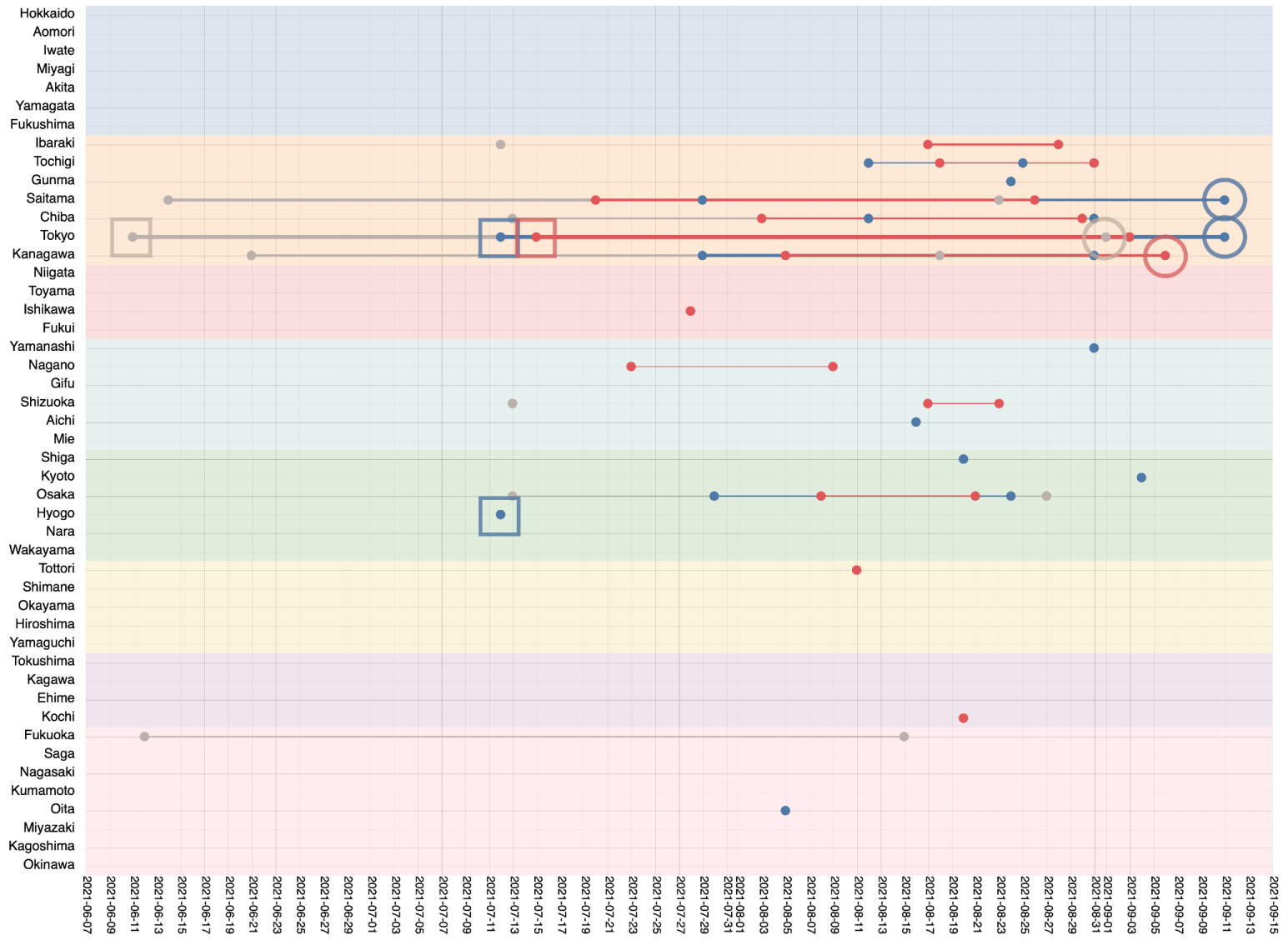


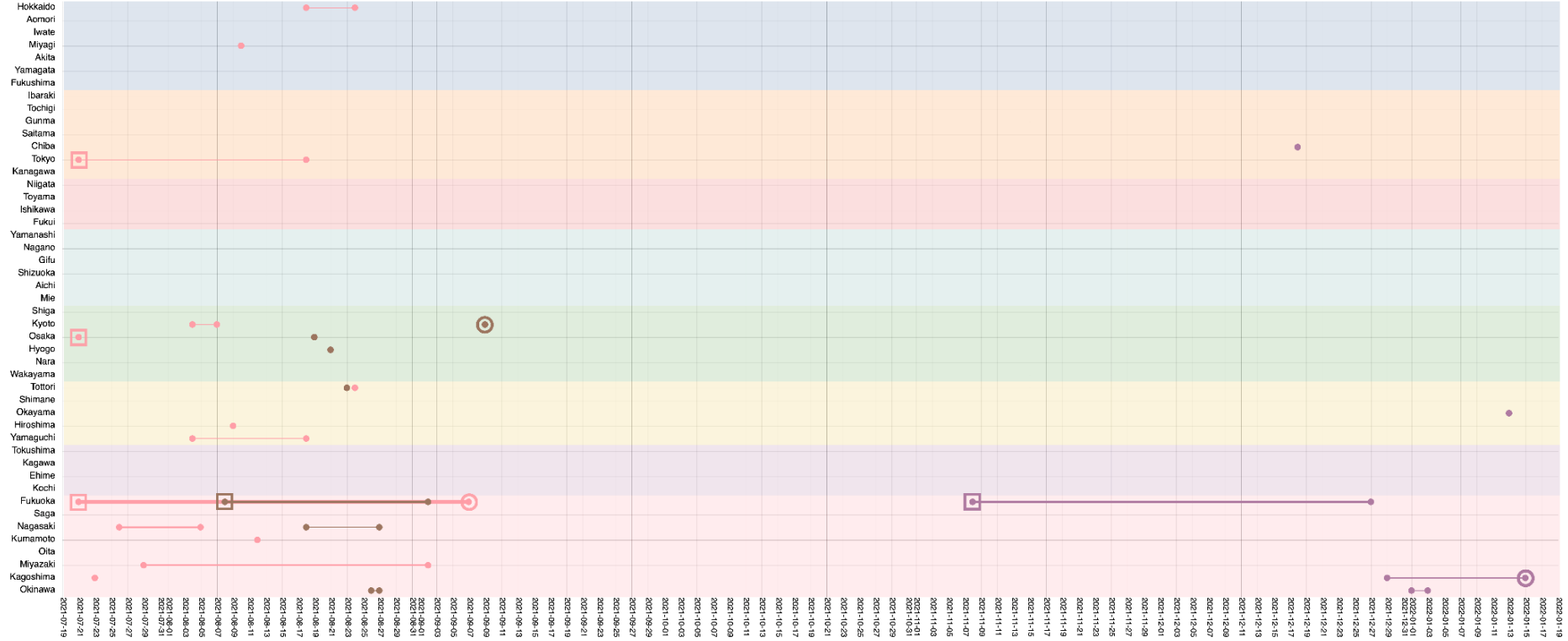
Figure S5. Maximum-likelihood (ML) phylogenetic tree of the 83 early Japan-related Delta and the Wuhan-Hu-1 reference genomes. The reference (EPI_ISL_40215), B.1.617.2, and AY.29 genomes were shown in black, green, and brown, respectively. Note that EPI_ISL_1927416 (belonging to B.1.617.2) shown in red is located at the base of the main B.1.617.2 cluster and appears to be a direct ancestor of the AY.29 cluster. A red or blue circle in the internal node is shown if the bootstrap value (1000 times ultrafast bootstrap test) is $\geq 80\%$ or $\geq 50\%$, respectively.



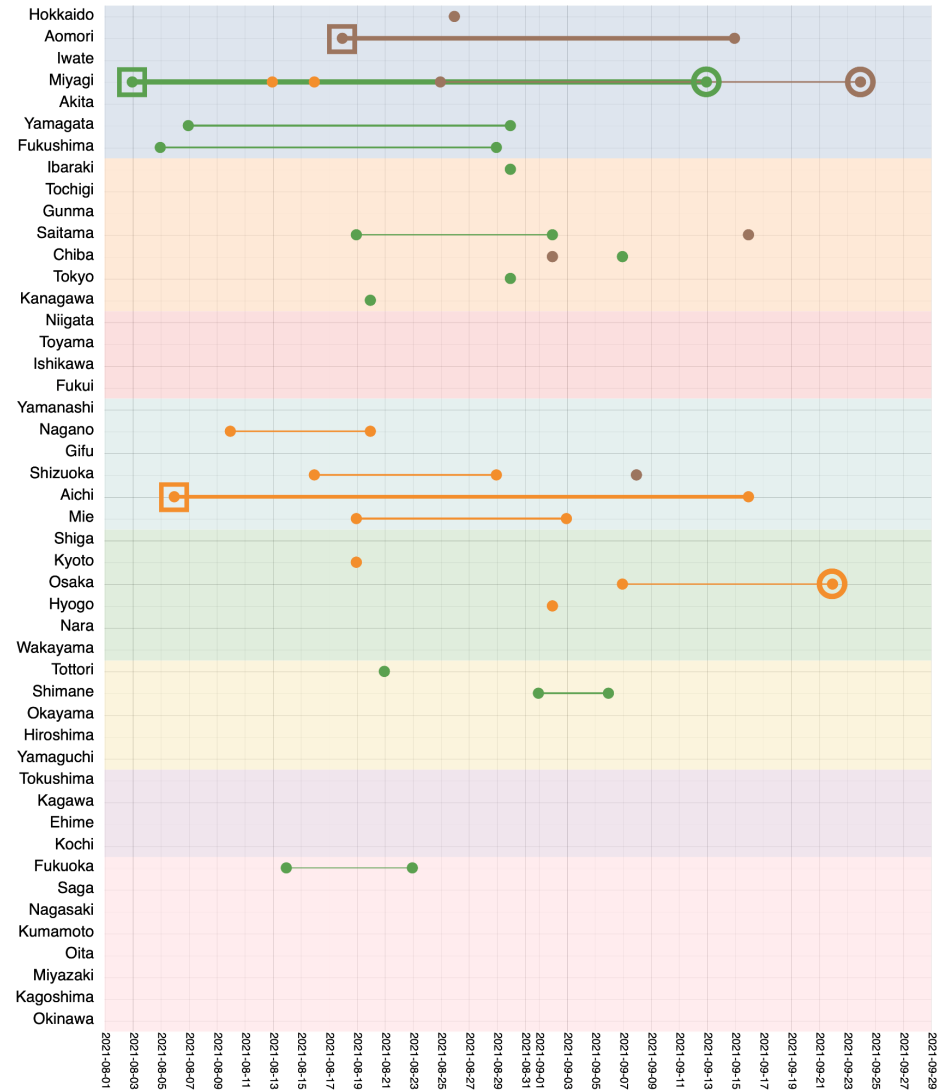
(A)



(B)



(C)



(D)

Figure S6. HaploGraph visualization for the eleven haplotypes of the fifth epidemic wave that showed regional preference. The earliest or latest entry of each haplotype is surrounded by a square or a circle of corresponding color. (A) The haplotypes “1.554.53” (red) and “1.501.7.212.25” (blue) were mostly sampled (the thick lines of red and blue) in the Kinki area (the midwest part of Japan). (B) The haplotypes “1.554.80.47” (red), “1.554.80” (blue), and “1.501.7.1119” (grey) were mostly sampled (the thick lines of red, blue and grey) in the Kanto area (the southeast part of Japan). (C) The haplotypes “1.207.75” (pink), “i.259” (grey), and “1.501.7.278.3.1.x.2” (purple) were mostly sampled (the thick lines of pink, grey and purple) in the Kyushu area (the southwest part of Japan). (D) The haplotypes “1.501.7.439.37.1.2” (brown) and “1.501.7.291.2.17.2” (green) were mostly sampled (the thick lines of brown and green) in the Tohoku area (the northeast part of Japan). The haplotype “1.240.2.166” (orange) was mostly sampled (the thick lines of orange) in the Chubu area (the middle part of Japan).