

## Supplemental Material

### **Phylogeography of SARS-CoV-2 pandemic in Spain: a story of multiple introductions, micro-geographic stratification, founder effects, and super-spreaders**

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**Figure S1.** Accumulative counts of Spanish genomes in GISAID.

**Figure S2.** Features of HQ vs LQ datasets related to quality of sequence data.

**Figure S3.** Frequency of main haplogroups by Spanish regions.

**Figure S4 to S10.** Lineages observed in Spanish regions. Only those with >30 genomes analyzed are shown. Large regional maps were downloaded from <https://d-maps.com/> and can be used freely according to <https://d-maps.com/conditions.php?lang=es>. Map of a) Andalusia: [https://d-maps.com/carte.php?num\\_car=13251&lang=es](https://d-maps.com/carte.php?num_car=13251&lang=es); b) Basque Country: [https://d-maps.com/carte.php?num\\_car=13481&lang=pt](https://d-maps.com/carte.php?num_car=13481&lang=pt); c) Catalonia: [https://d-maps.com/carte.php?num\\_car=13853&lang=es](https://d-maps.com/carte.php?num_car=13853&lang=es); d) Galicia: [https://d-maps.com/carte.php?num\\_car=14017&lang=es](https://d-maps.com/carte.php?num_car=14017&lang=es); e) Madrid: [https://d-maps.com/carte.php?num\\_car=14101&lang=es](https://d-maps.com/carte.php?num_car=14101&lang=es); f) Navarra: [https://d-maps.com/carte.php?num\\_car=14301&lang=es](https://d-maps.com/carte.php?num_car=14301&lang=es); and g) Valencian Community: [https://d-maps.com/carte.php?num\\_car=14399&lang=es](https://d-maps.com/carte.php?num_car=14399&lang=es). Small Spanish maps were downloaded from Wikipedia.

**Figure S11.** Sampling points of interpolated maps shown in Figure 2 (main text).

**Figure S12.** Diversity indices for different Spanish regions. (A) Haplotype diversity, (B) nucleotide diversity, and (C) accumulated sequences. Note, discontinuity in sampling occurred from 15 April, however this did not impact our study as most analyses focused on the beginning of the pandemic and the time right after lockdown on 15 March.

**Figure S13.** Network of all Spanish genomes.

**Figure S14.** Boxplot and density plot of genome lifespan of identical haplotypes in GISAID database.

**Figure S15.** Interpolation map of Spanish haplogroup A2 frequencies, which roughly matches frequency of D614G. Map on top indicates sampling points.

**Figure S16 to S21.** ML phylogenies and TMRCA for most common Spanish clades.

Figure S1.

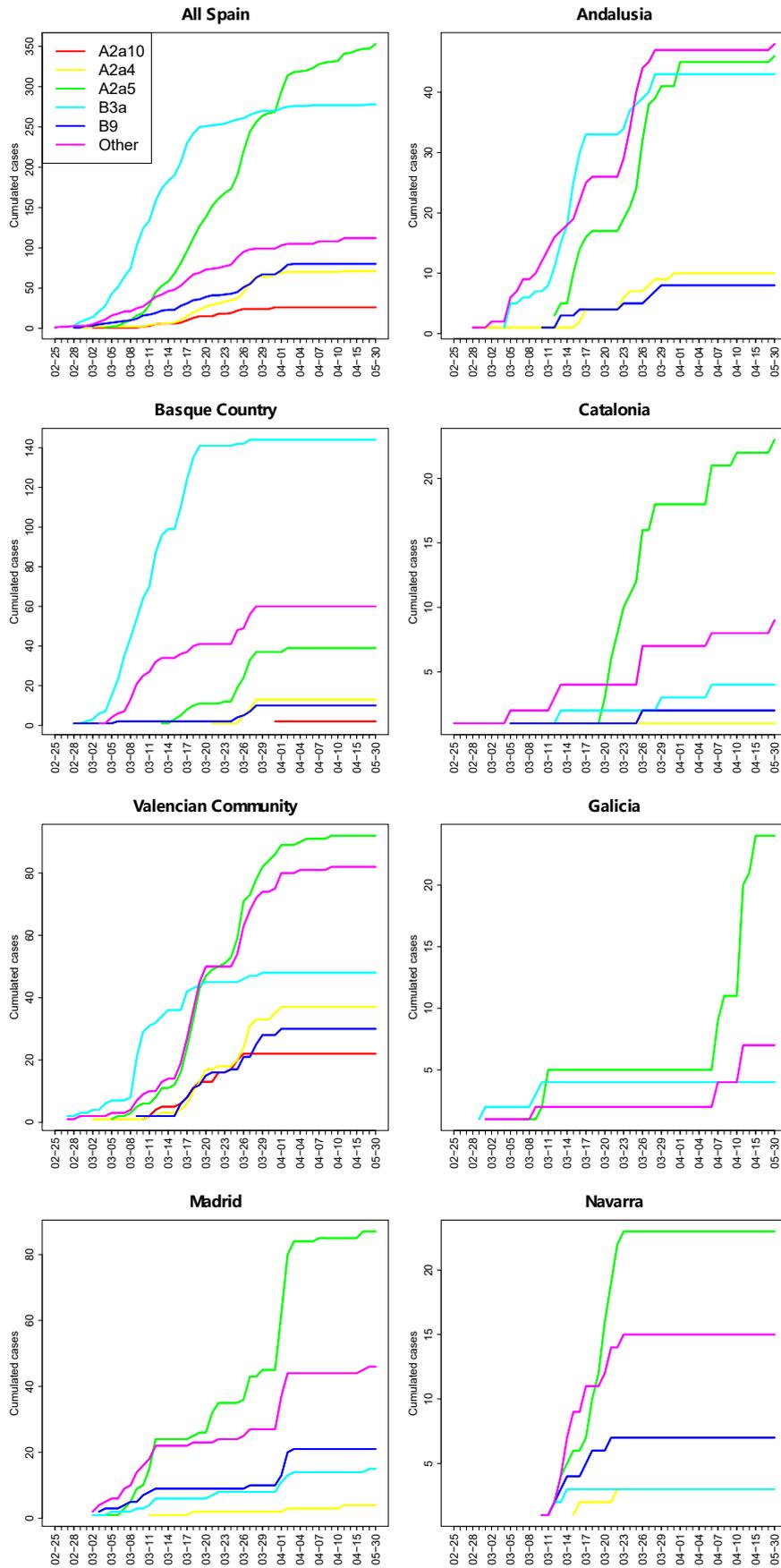
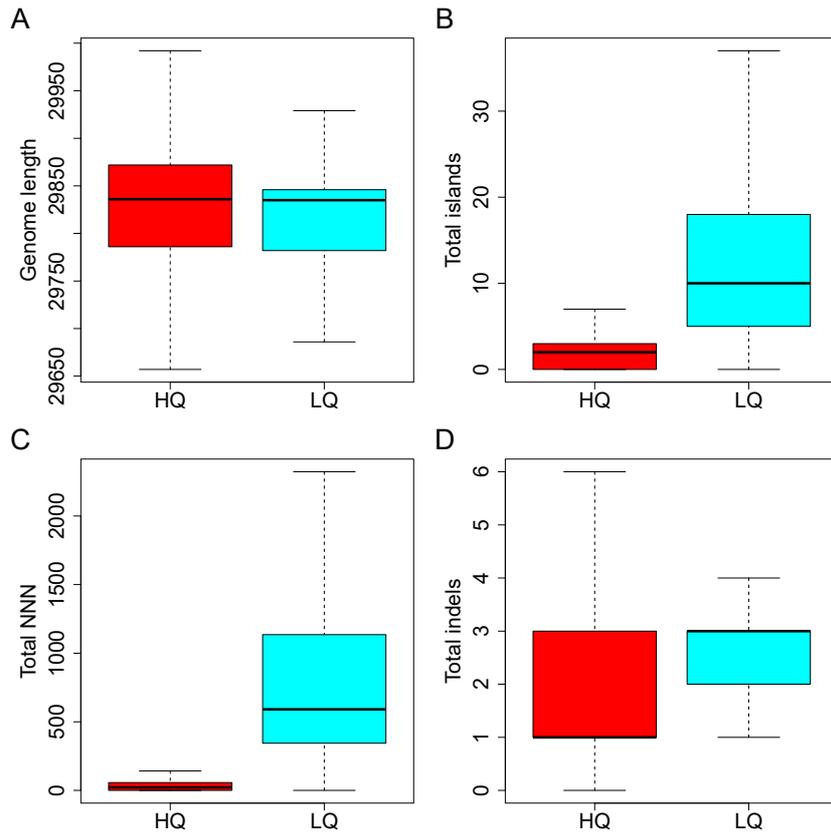


Figure S2.



**Figure S3.**

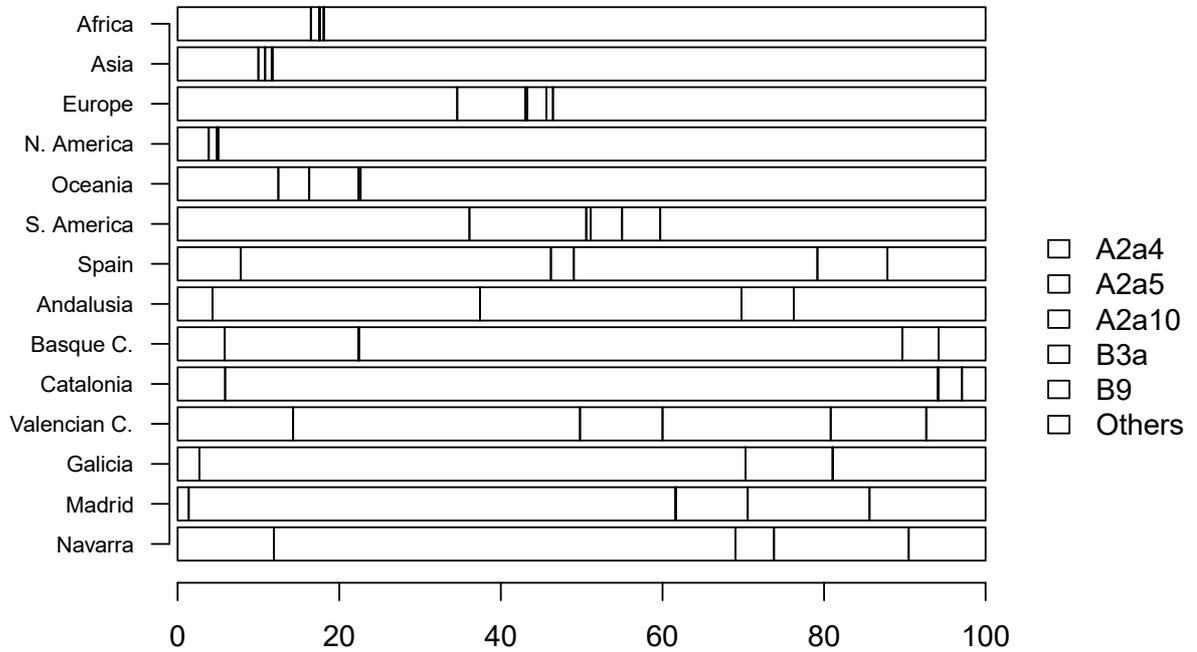


Figure S4

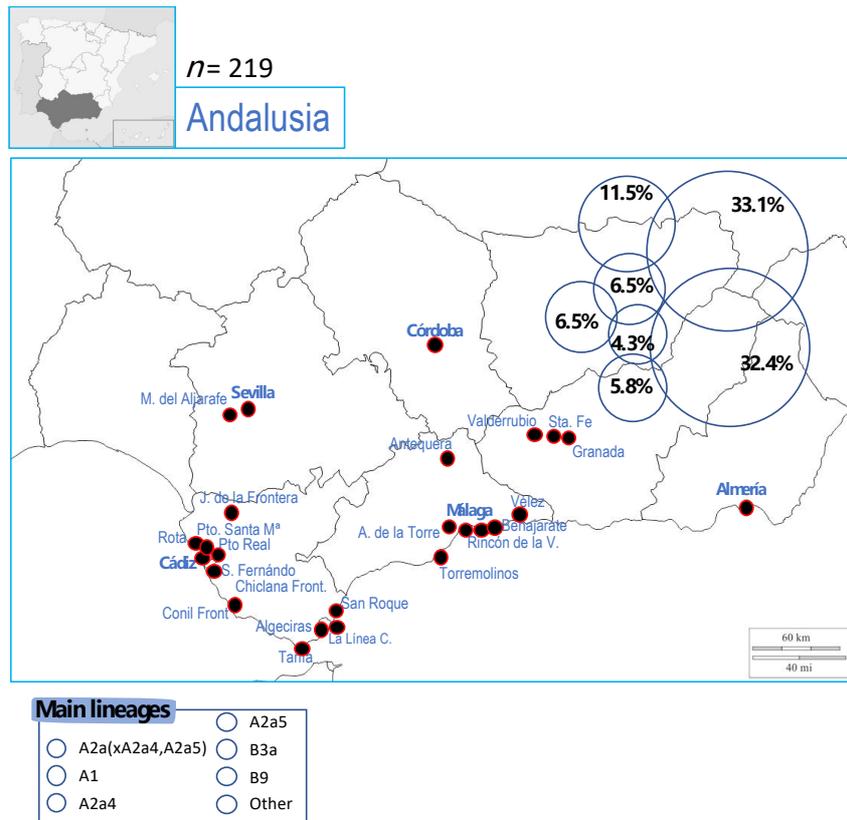


Figure S5

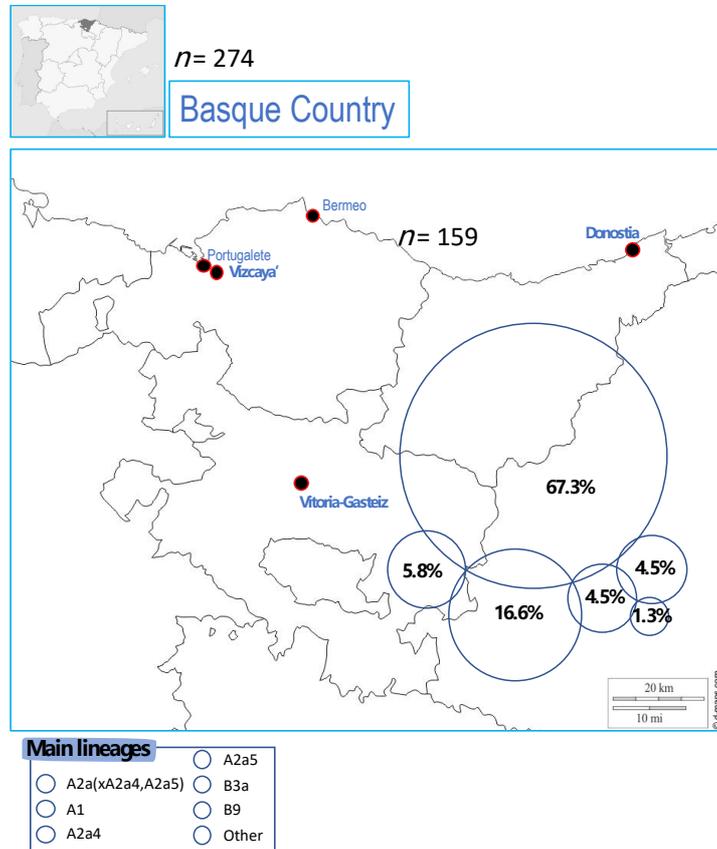


Figure S6

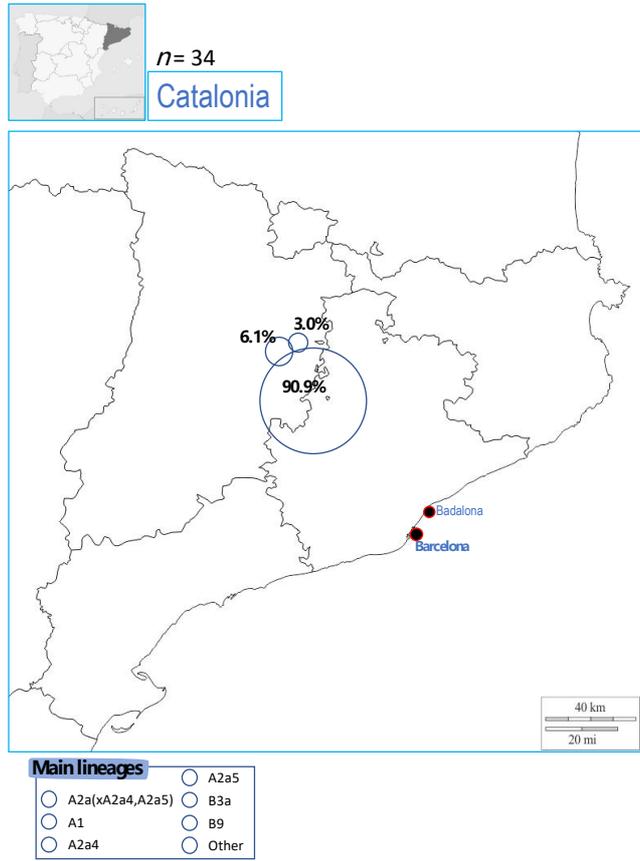


Figure S7

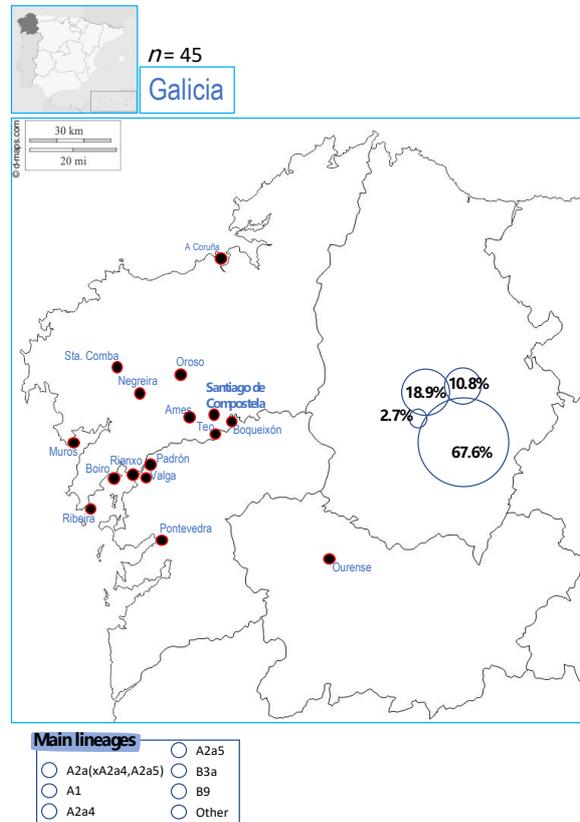


Figure S8

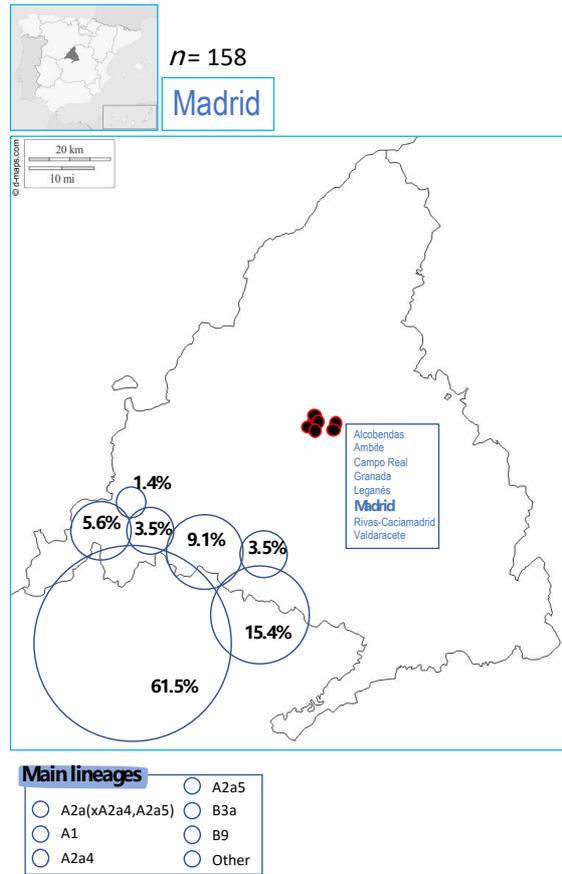


Figure S9

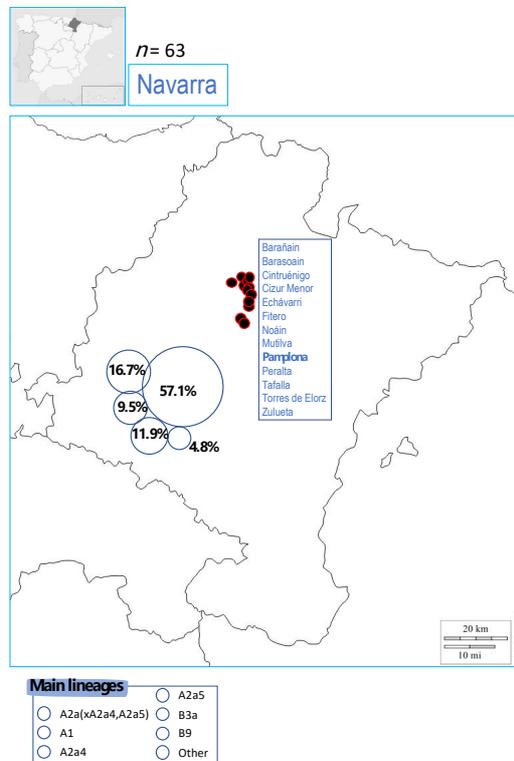


Figure S10

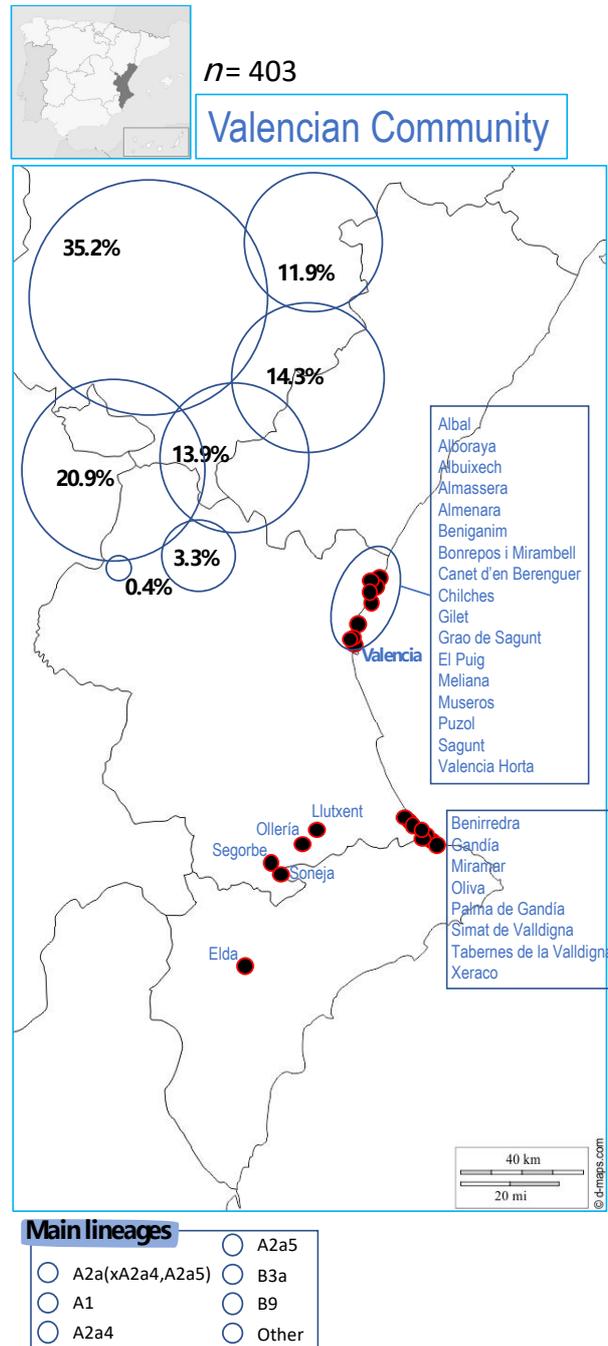


Figure S11.

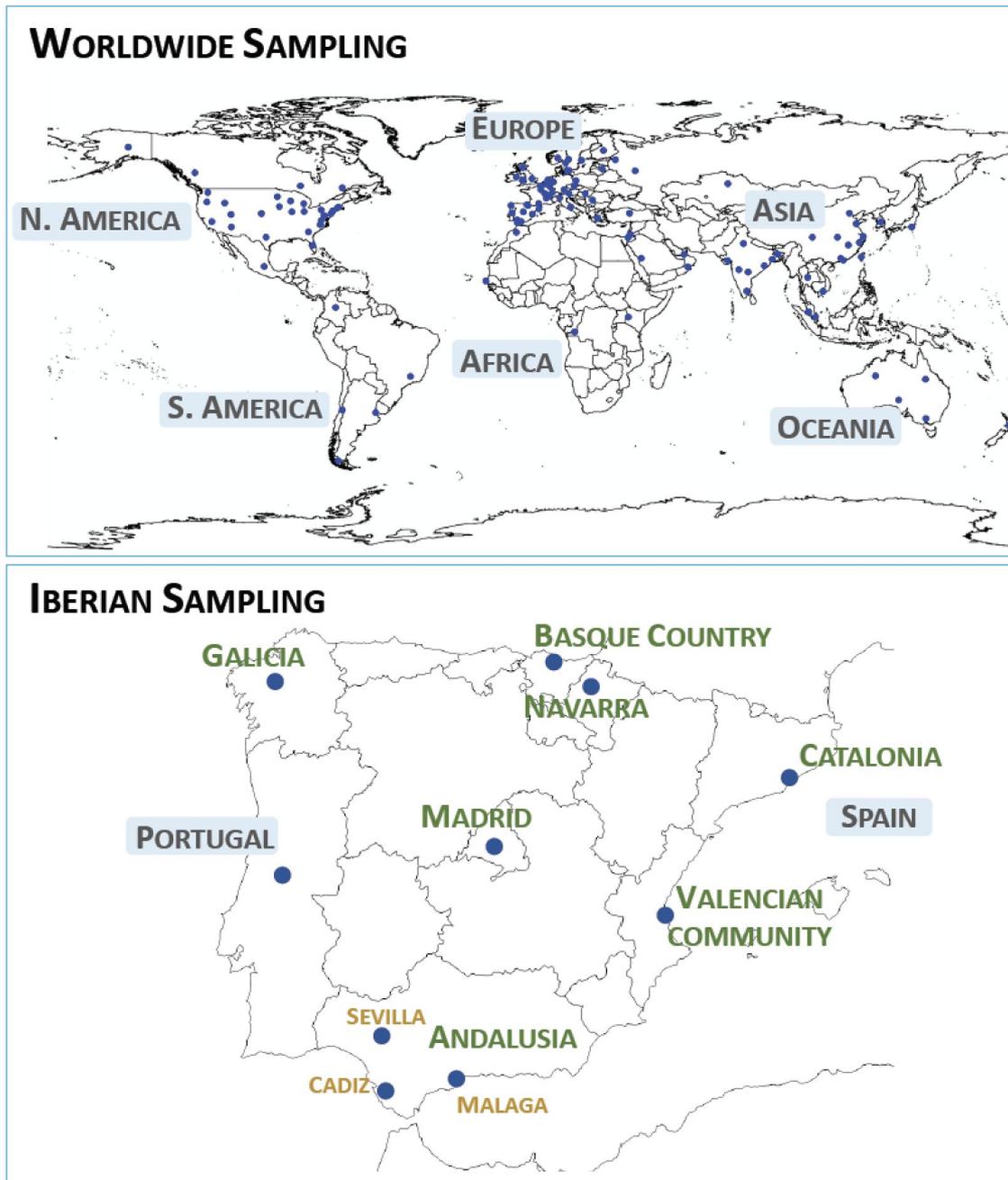


Figure S12.

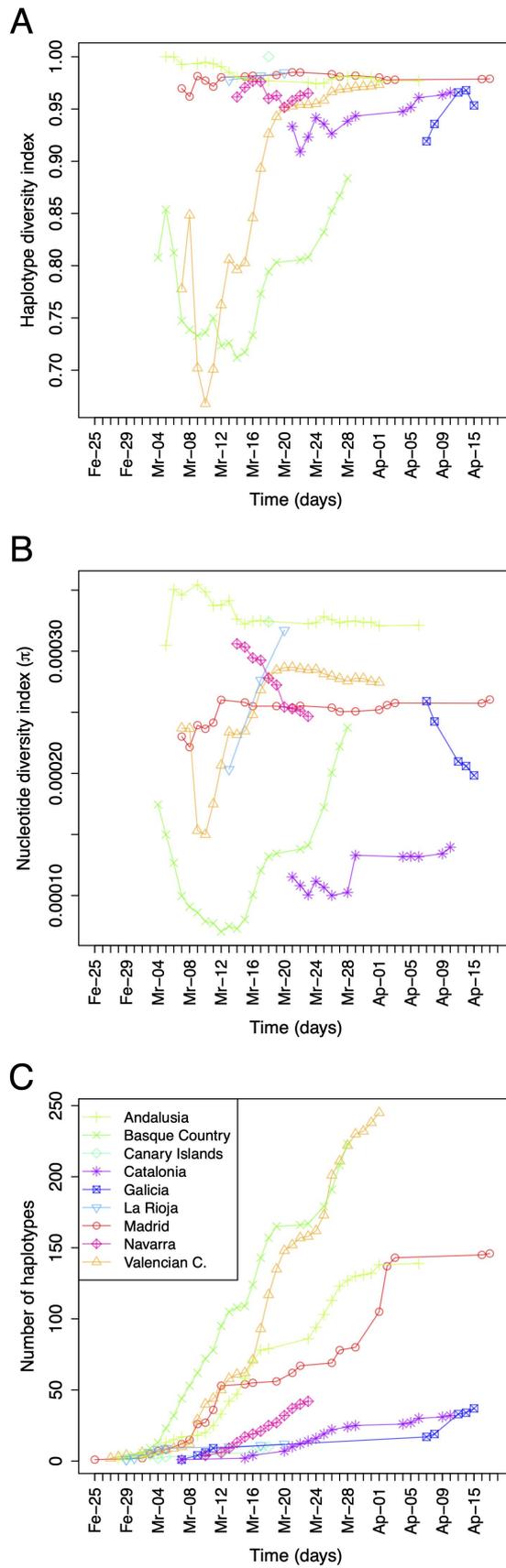


Figure S13.

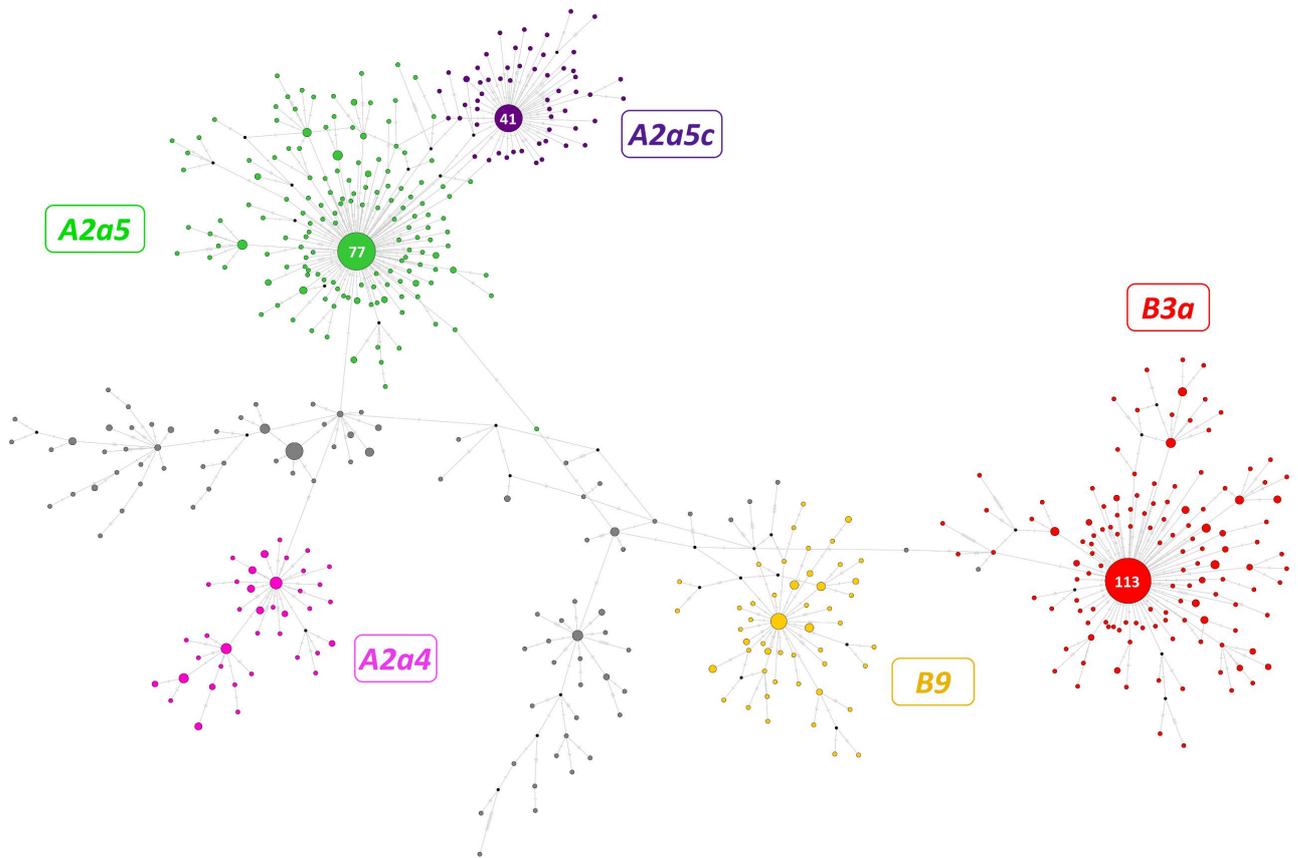


Figure S14.

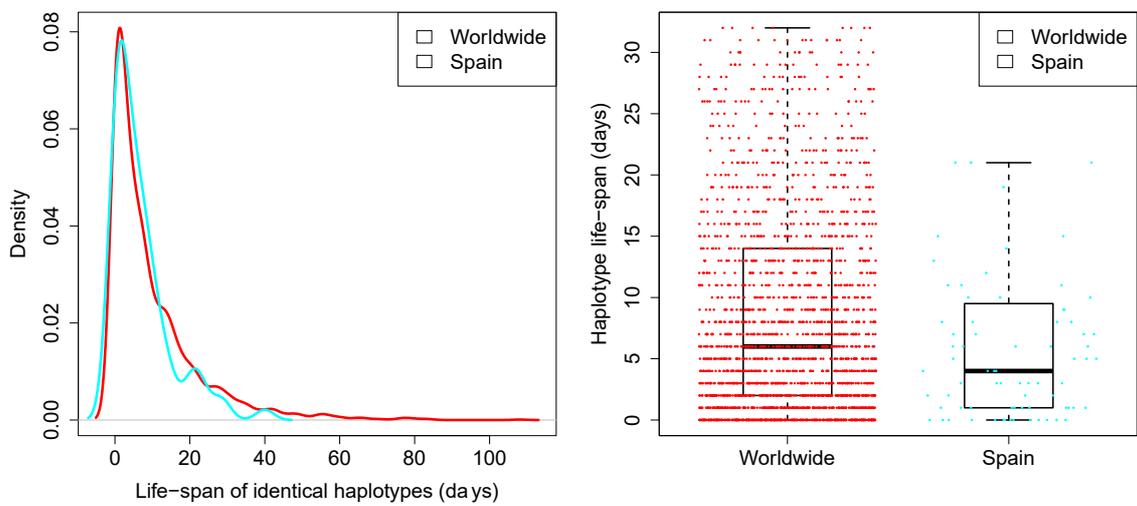


Figure S15.

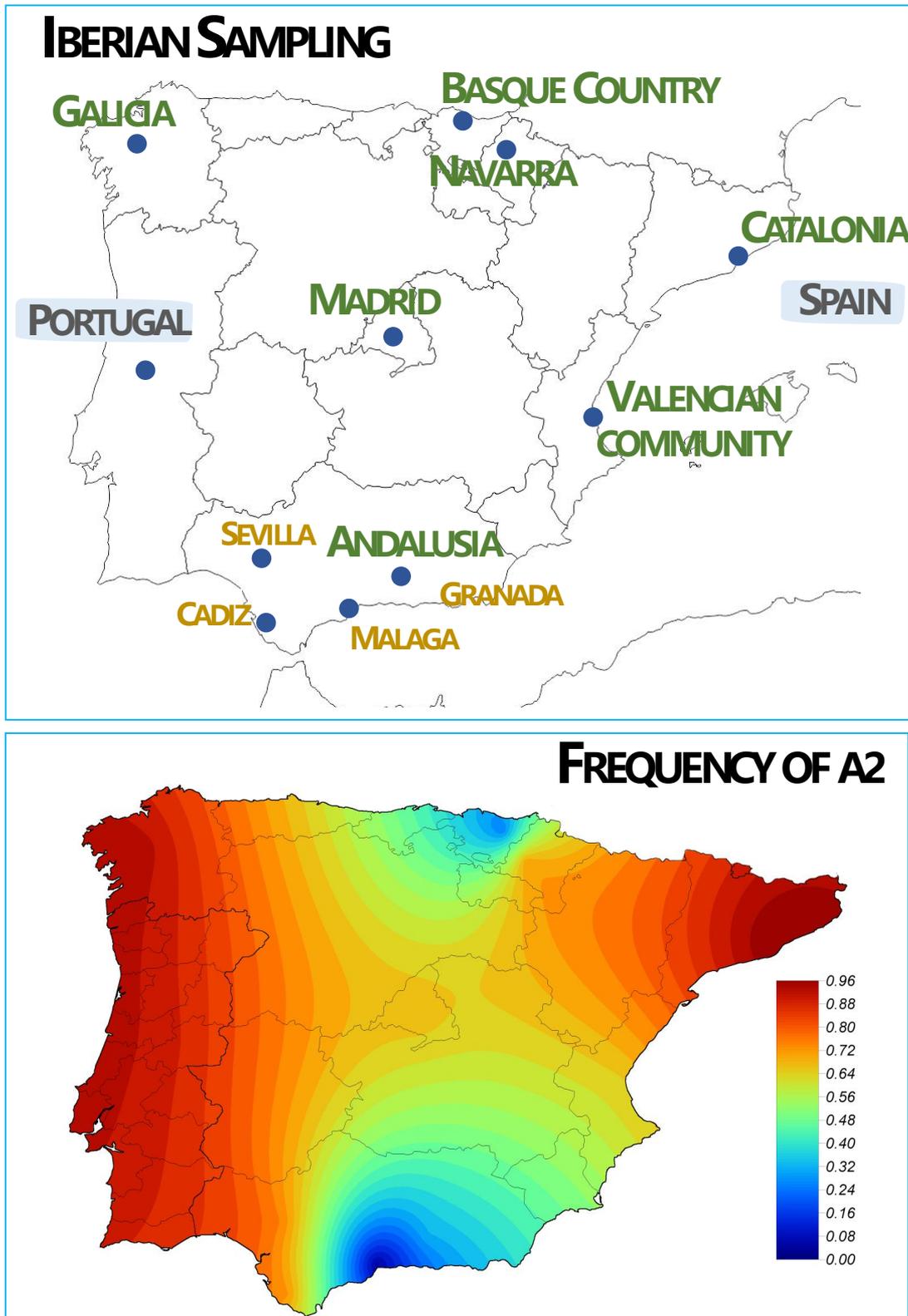


Figure S16.

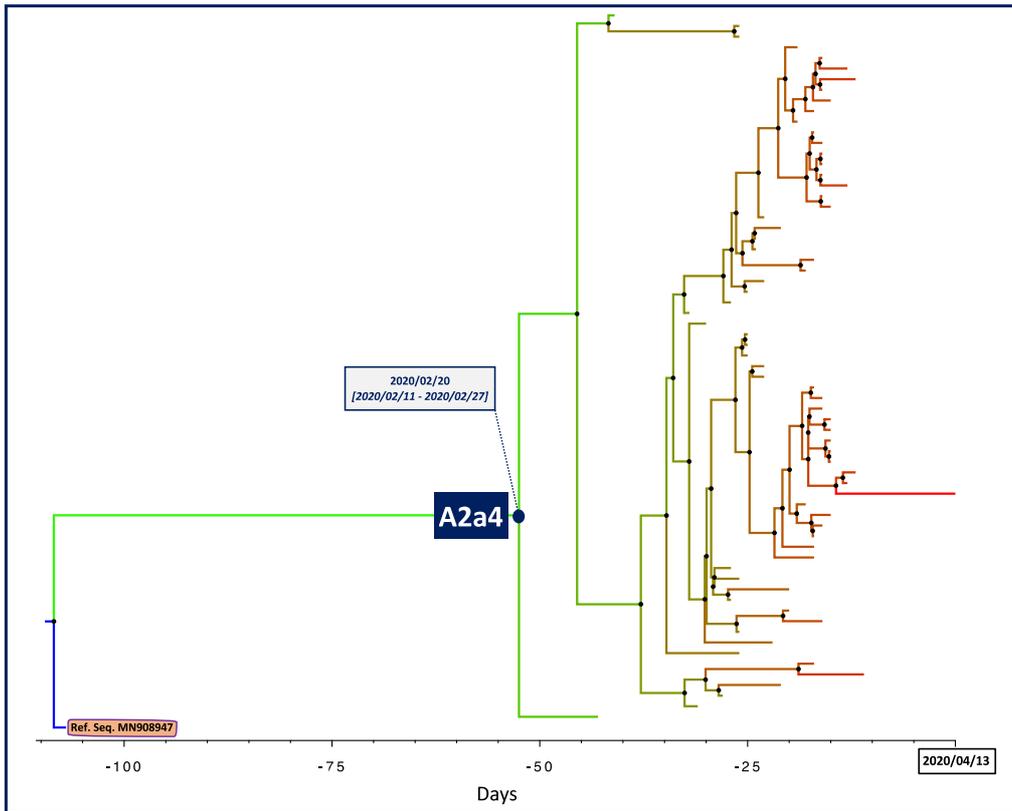


Figure S17.

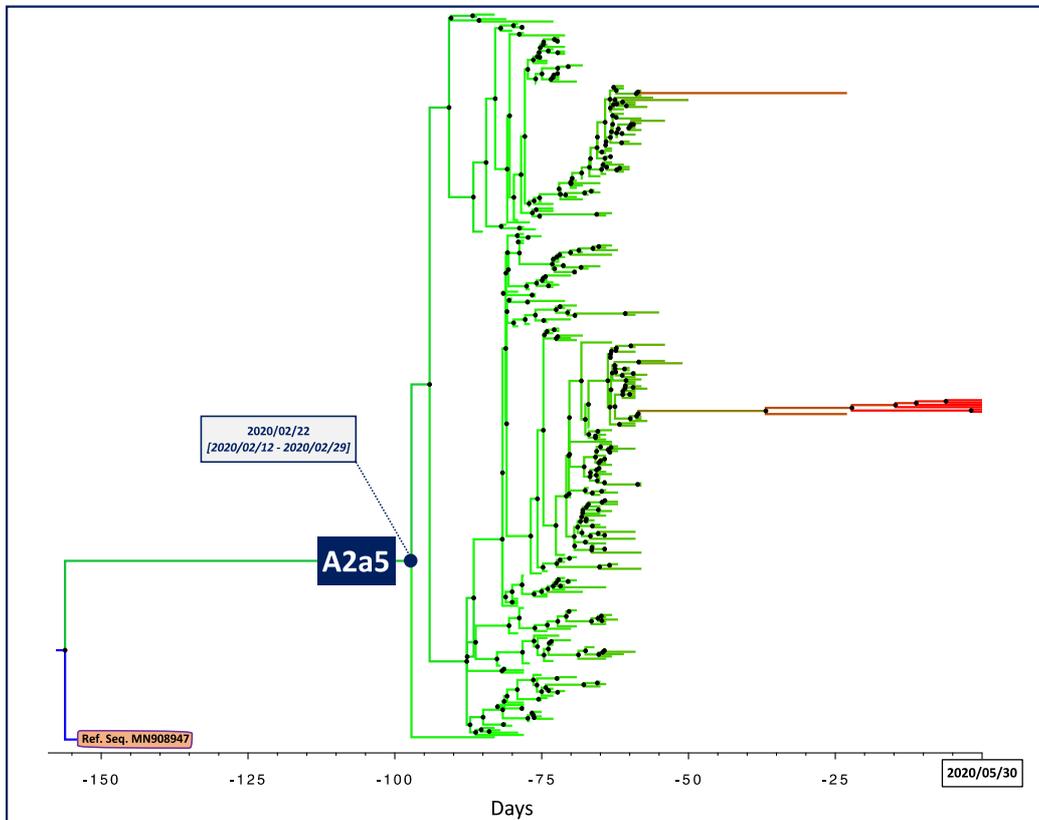


Figure S18.

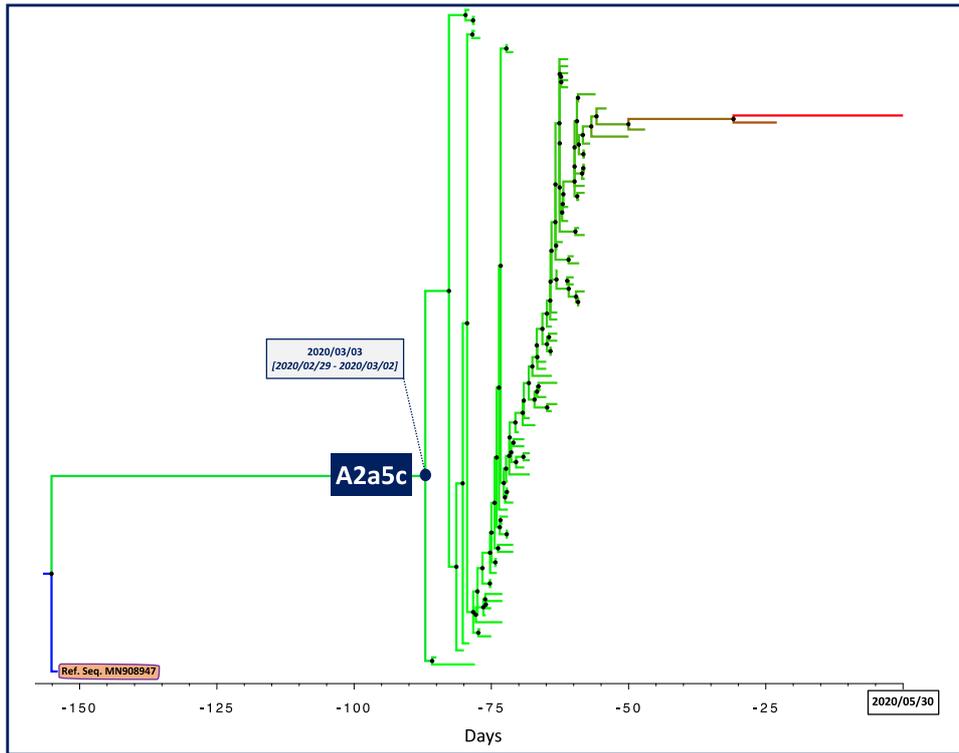


Figure S19.

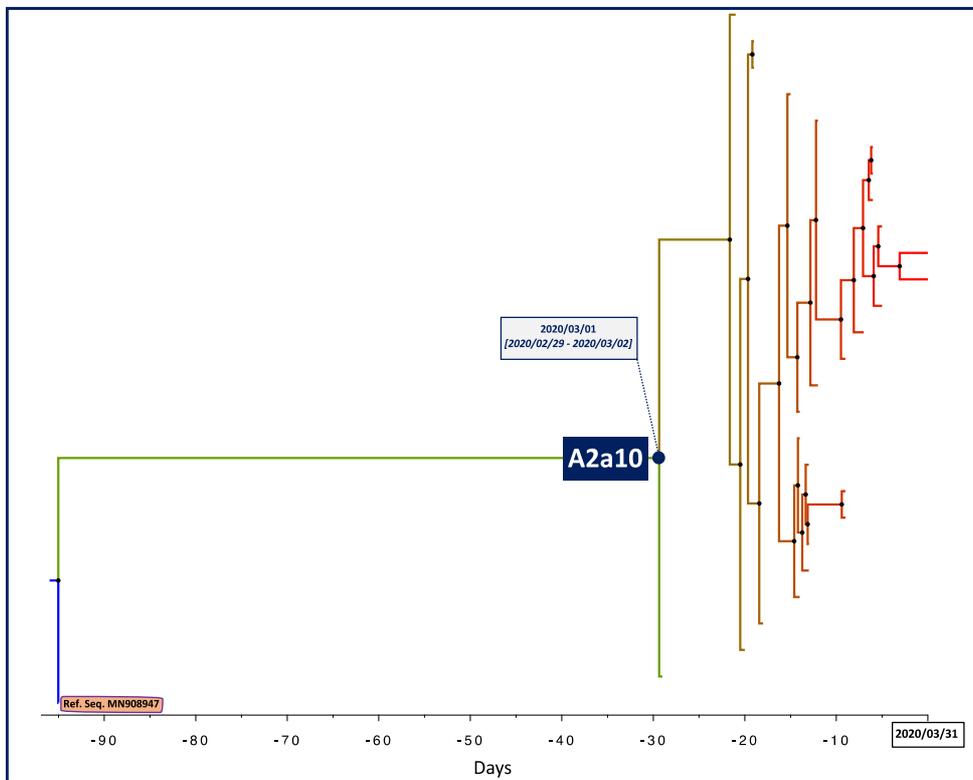


Figure S20.

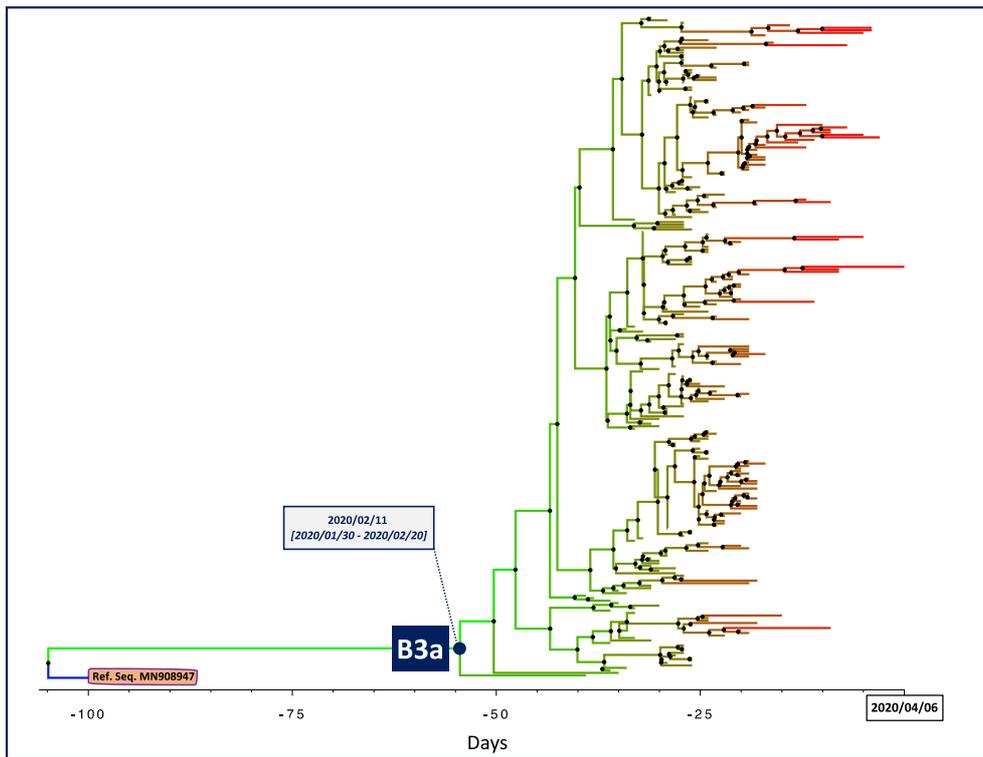


Figure S21.

