

## Supplemental Material

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

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

**Figure S2.** Features of HQ *versus* LQ datasets related to quality of the 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/> that 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 indexes in the different Spanish regions. (A) Haplotype diversity, (B) nucleotide diversity, and (C) Accumulated sequences; note that there is discontinuity in sampling from 15 April; which however, does not have impact in our study because most of the analysis focus on the beginning of the pandemic and the time right after the lockdown on 15 March.

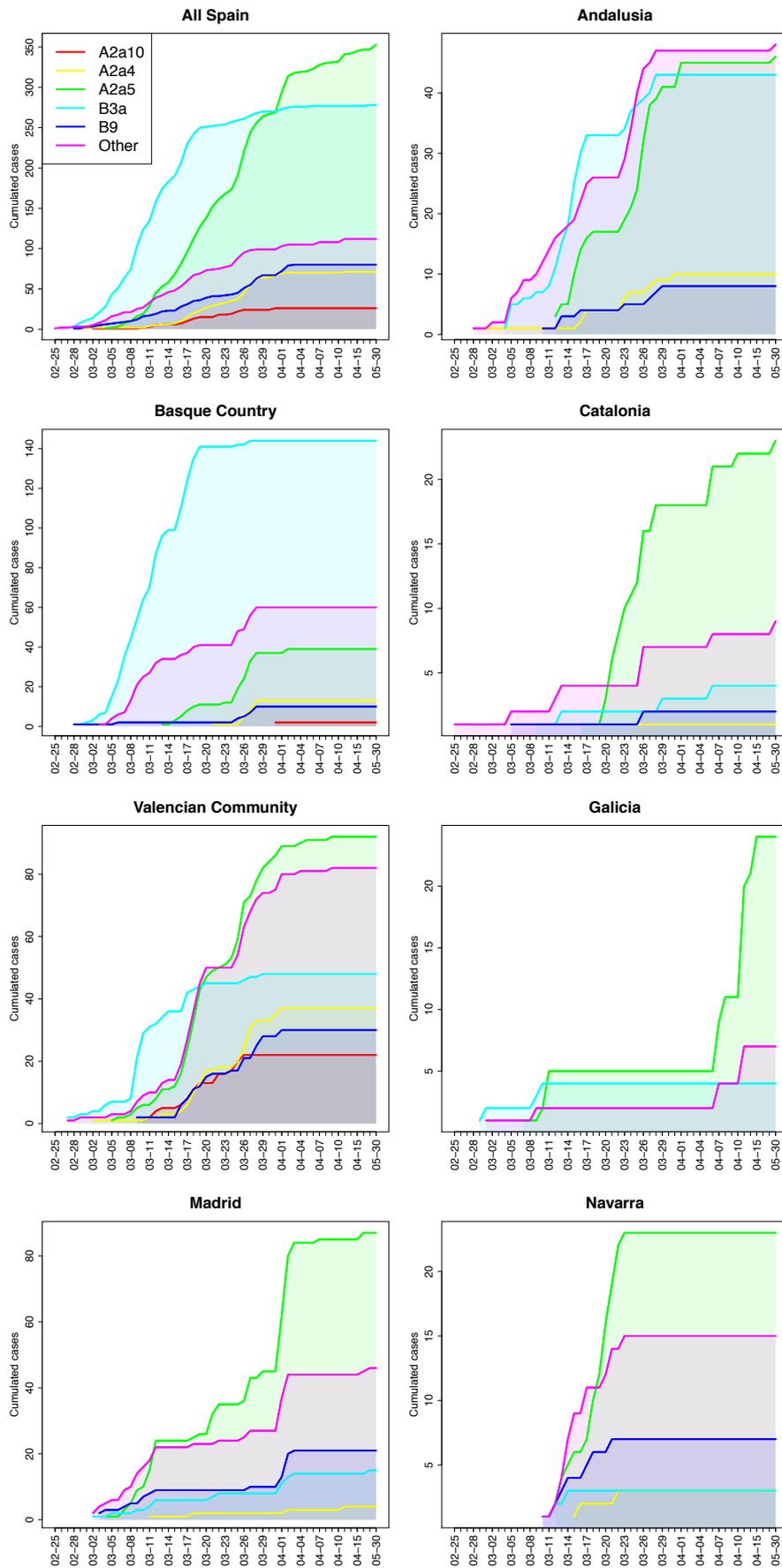
**Figure S13.** Network of all Spanish genomes.

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

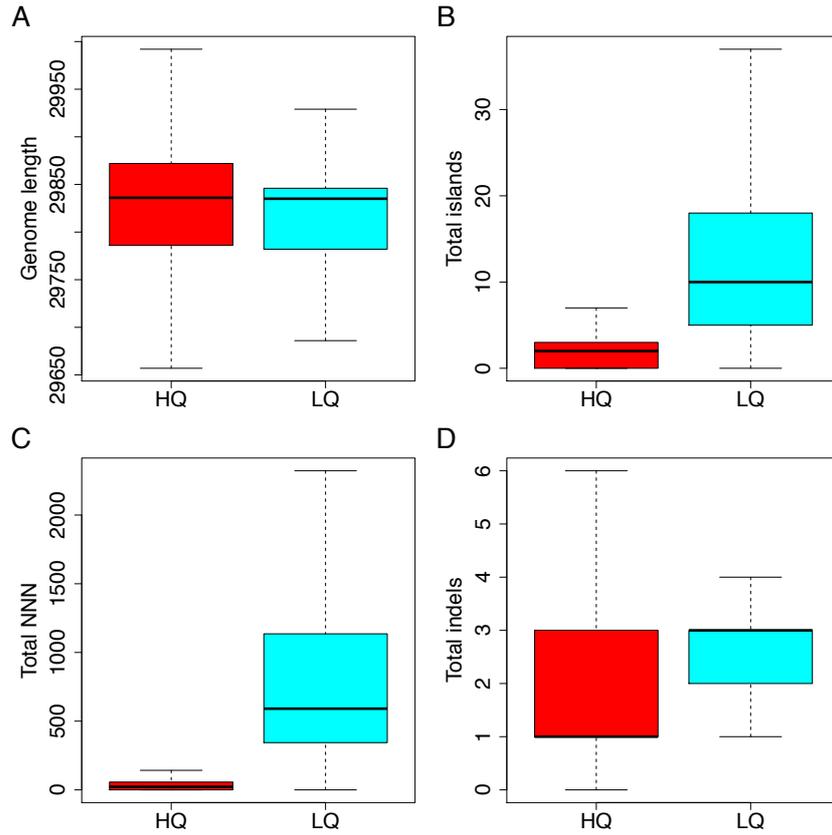
**Figure S15.** Interpolation map of Spanish haplogroup A2 frequencies, which roughly matches the frequency of D614G. The map on the top indicates the sampling points.

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

Figure S1.



**Figure S2.**



**Figure S3.**

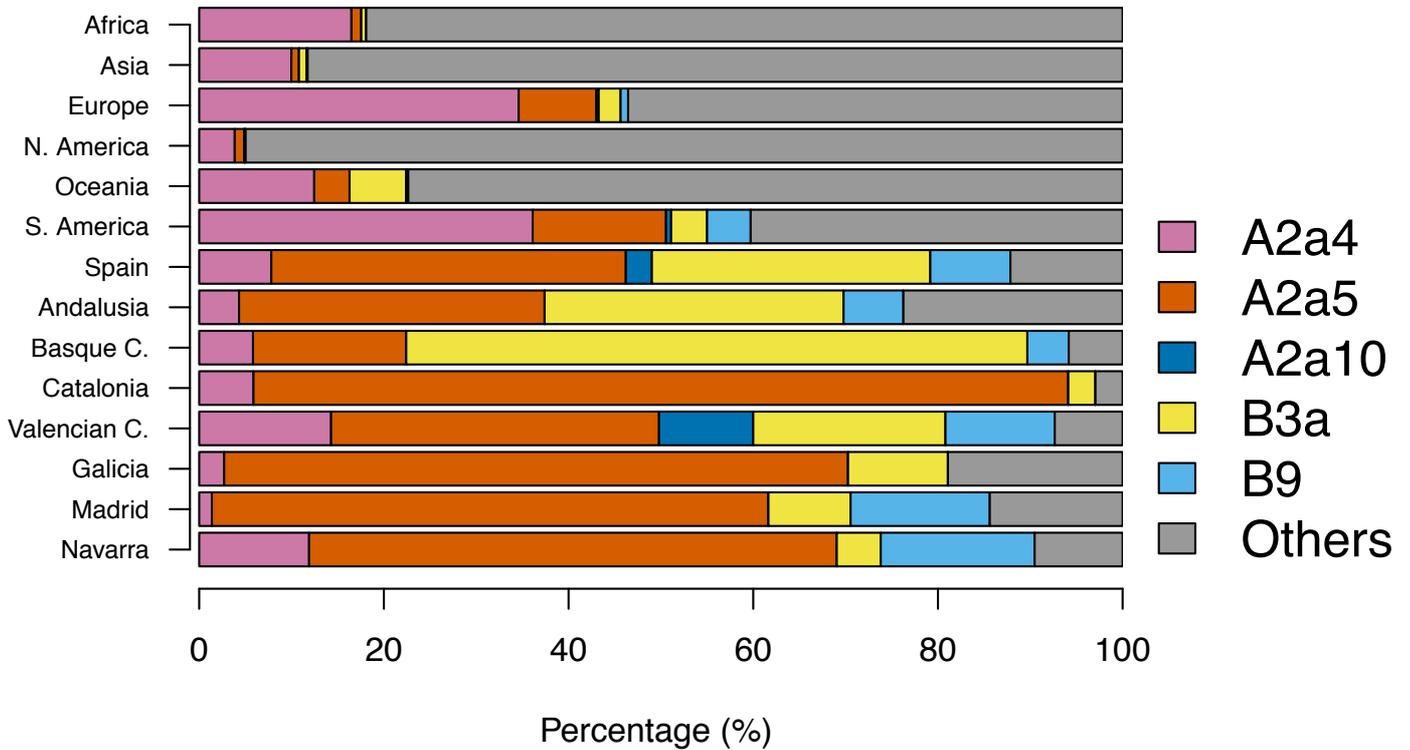


Figure S4

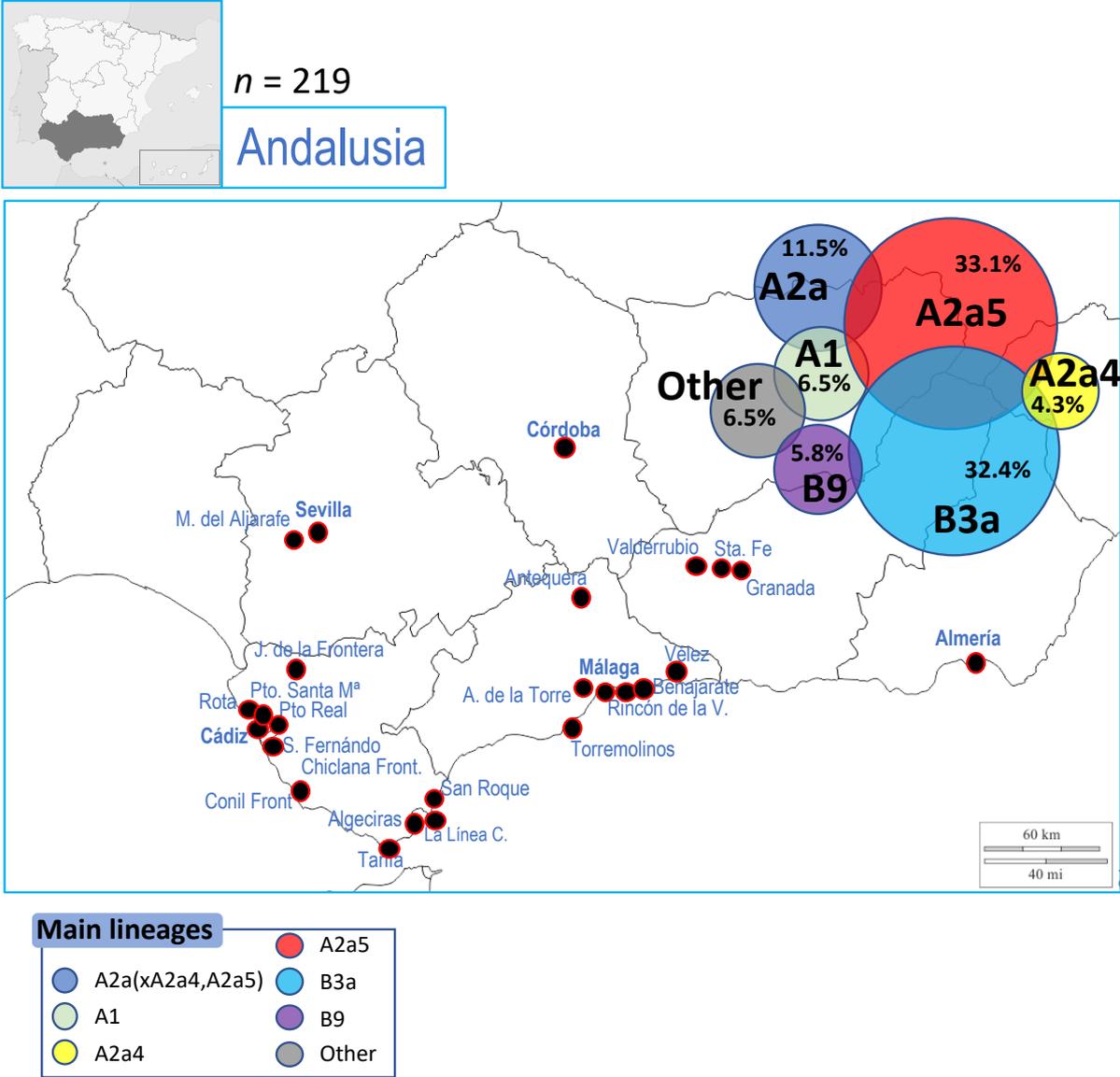


Figure S5

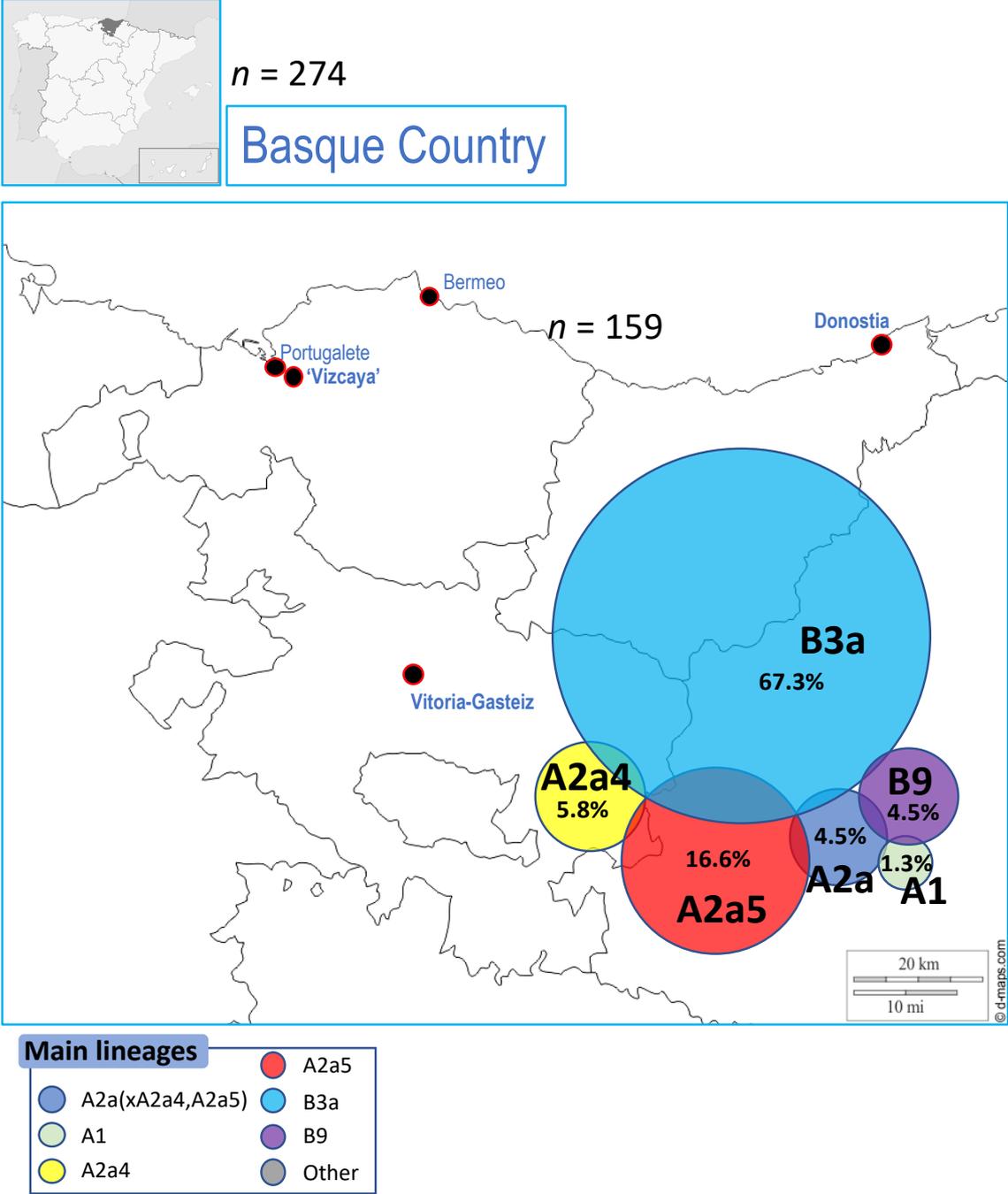


Figure S6



Figure S7

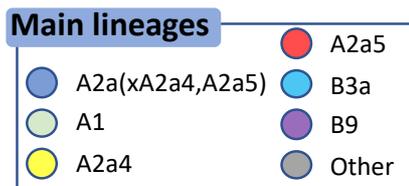
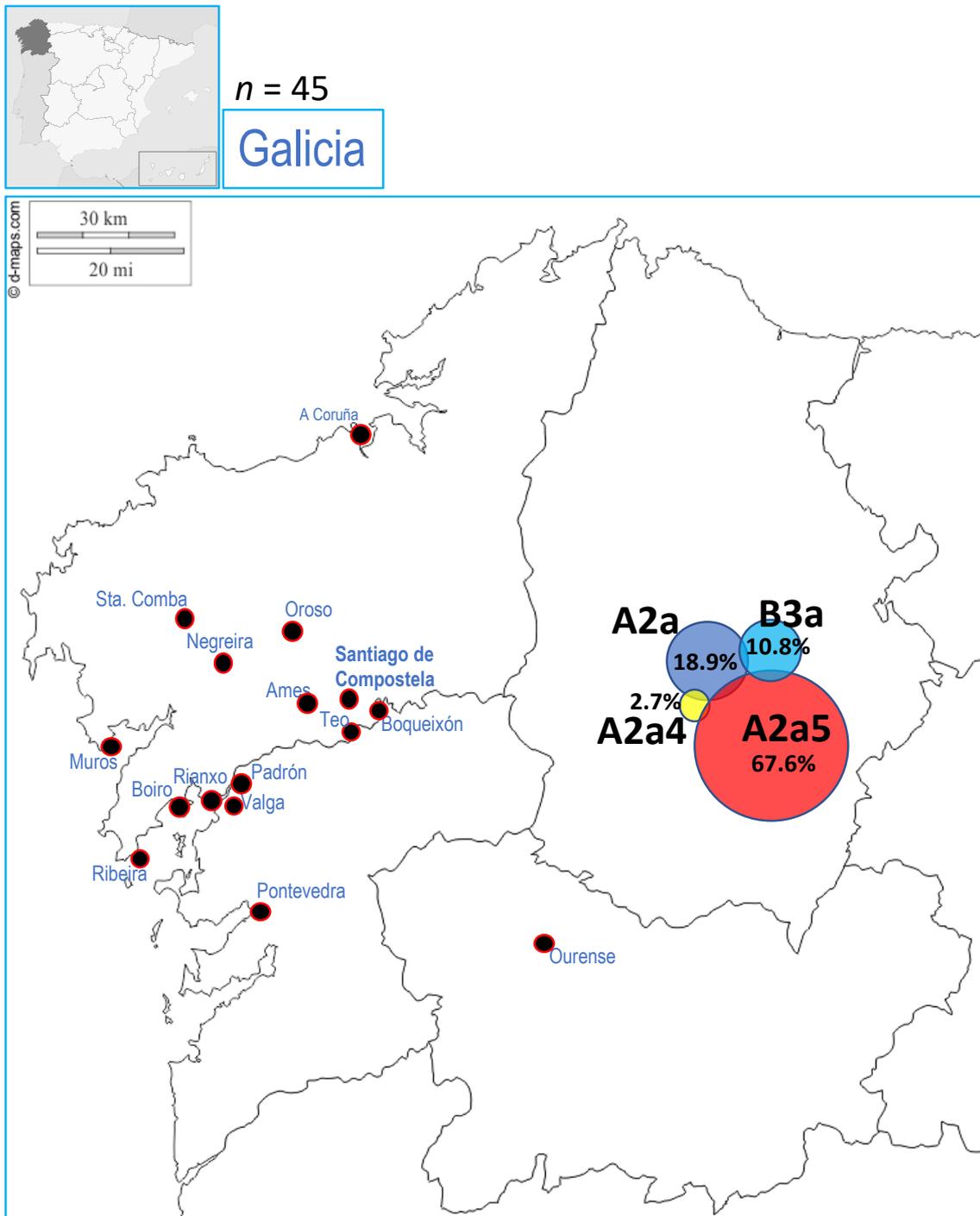


Figure S8

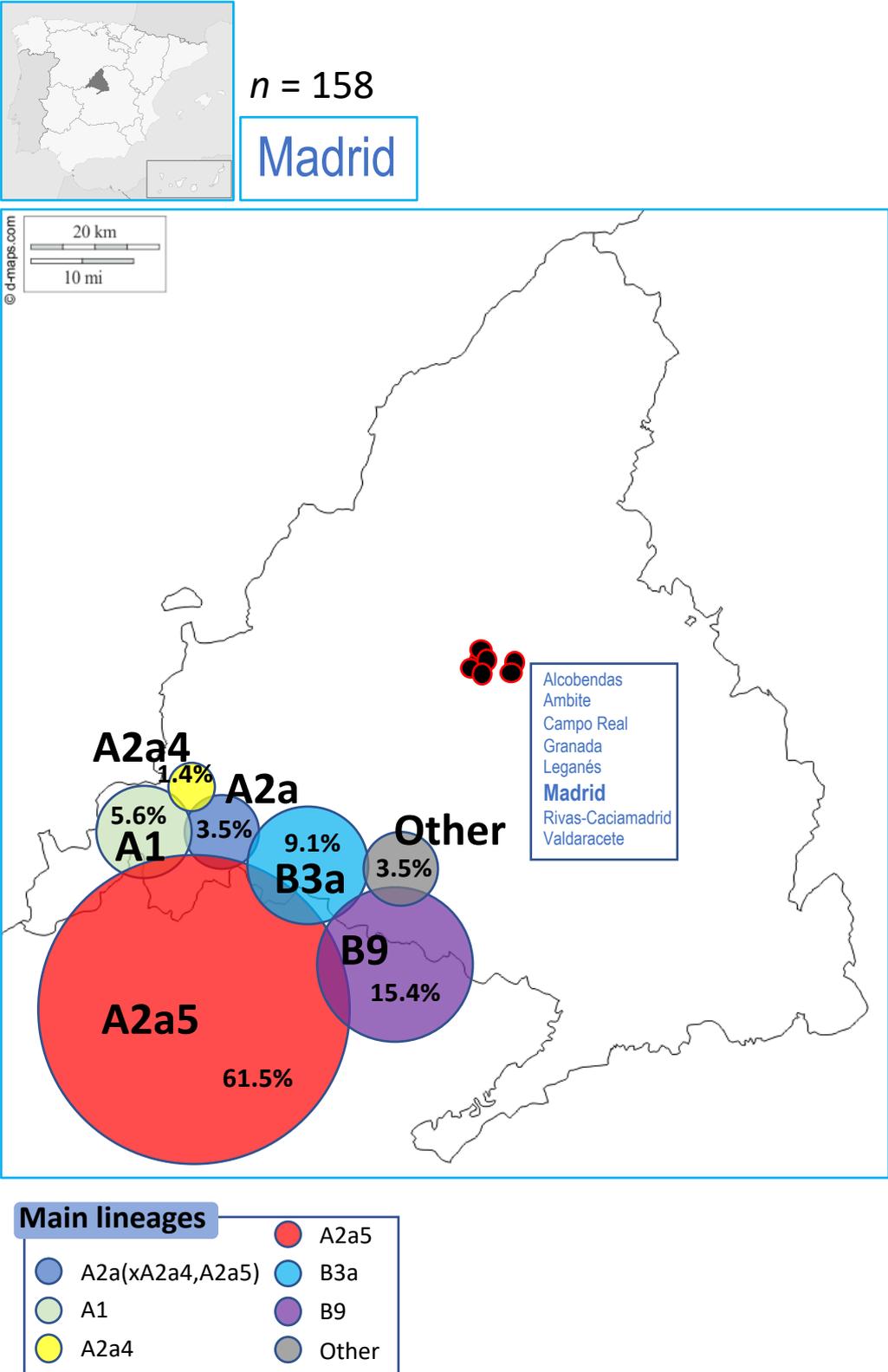


Figure S9

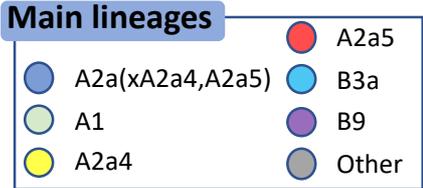
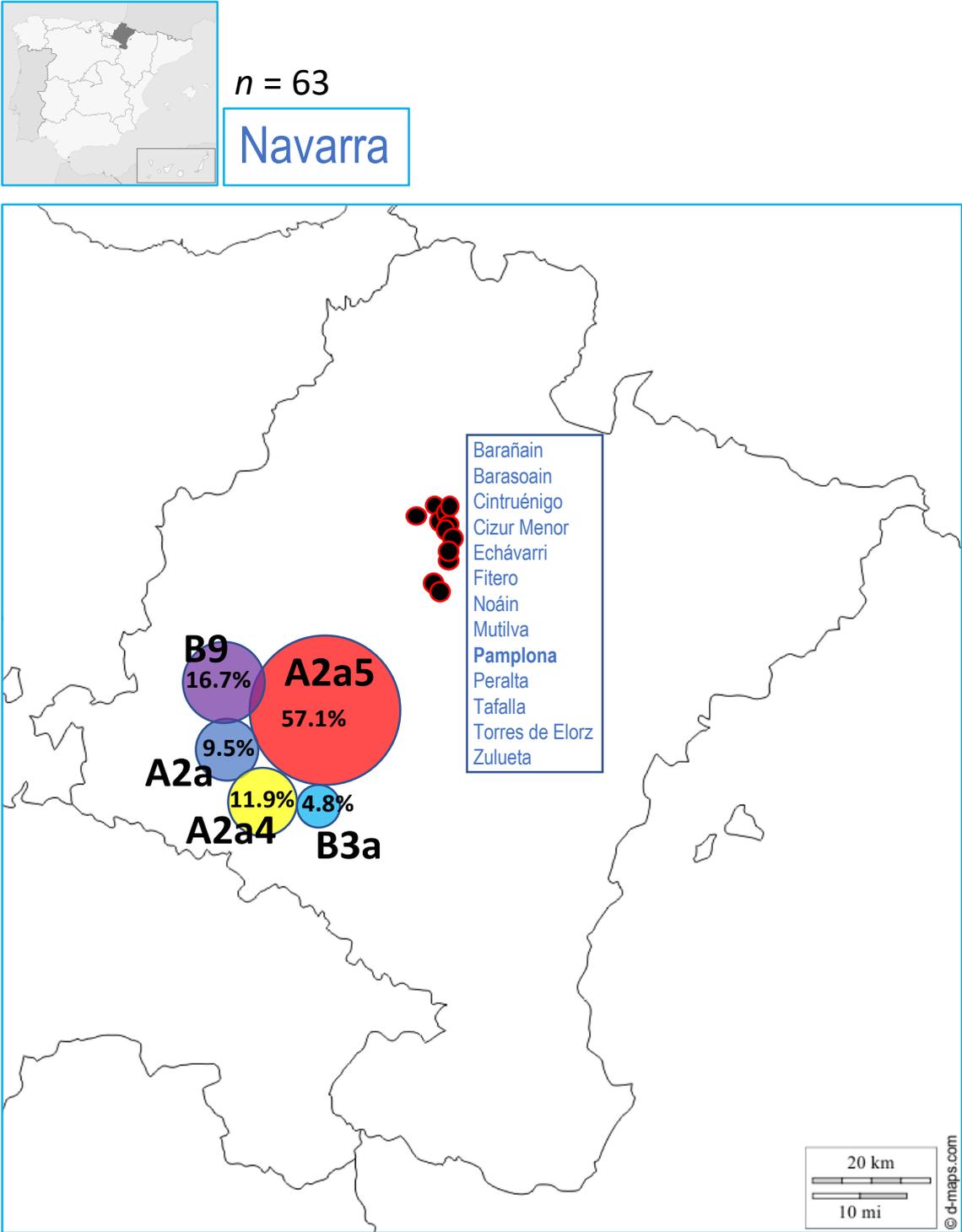


Figure S10

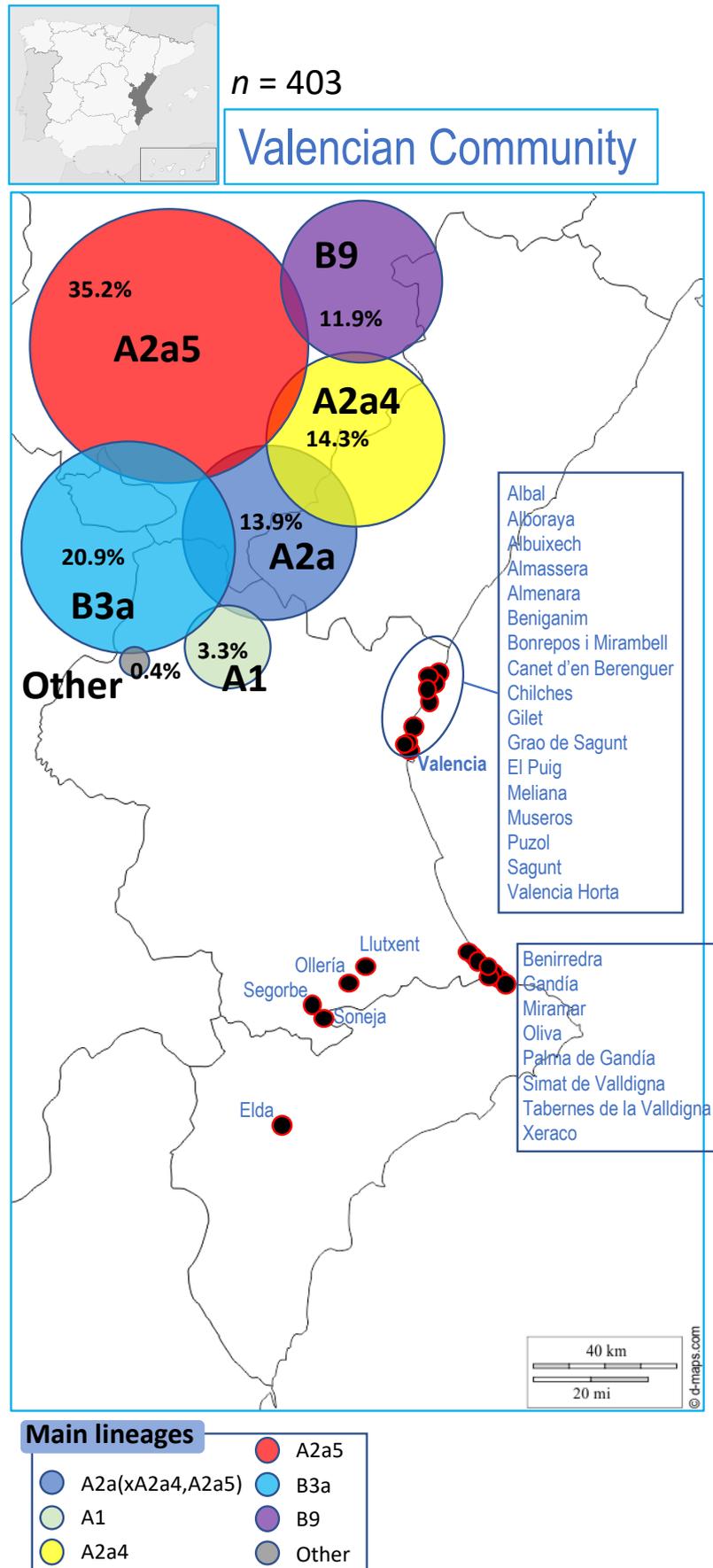


Figure S11.

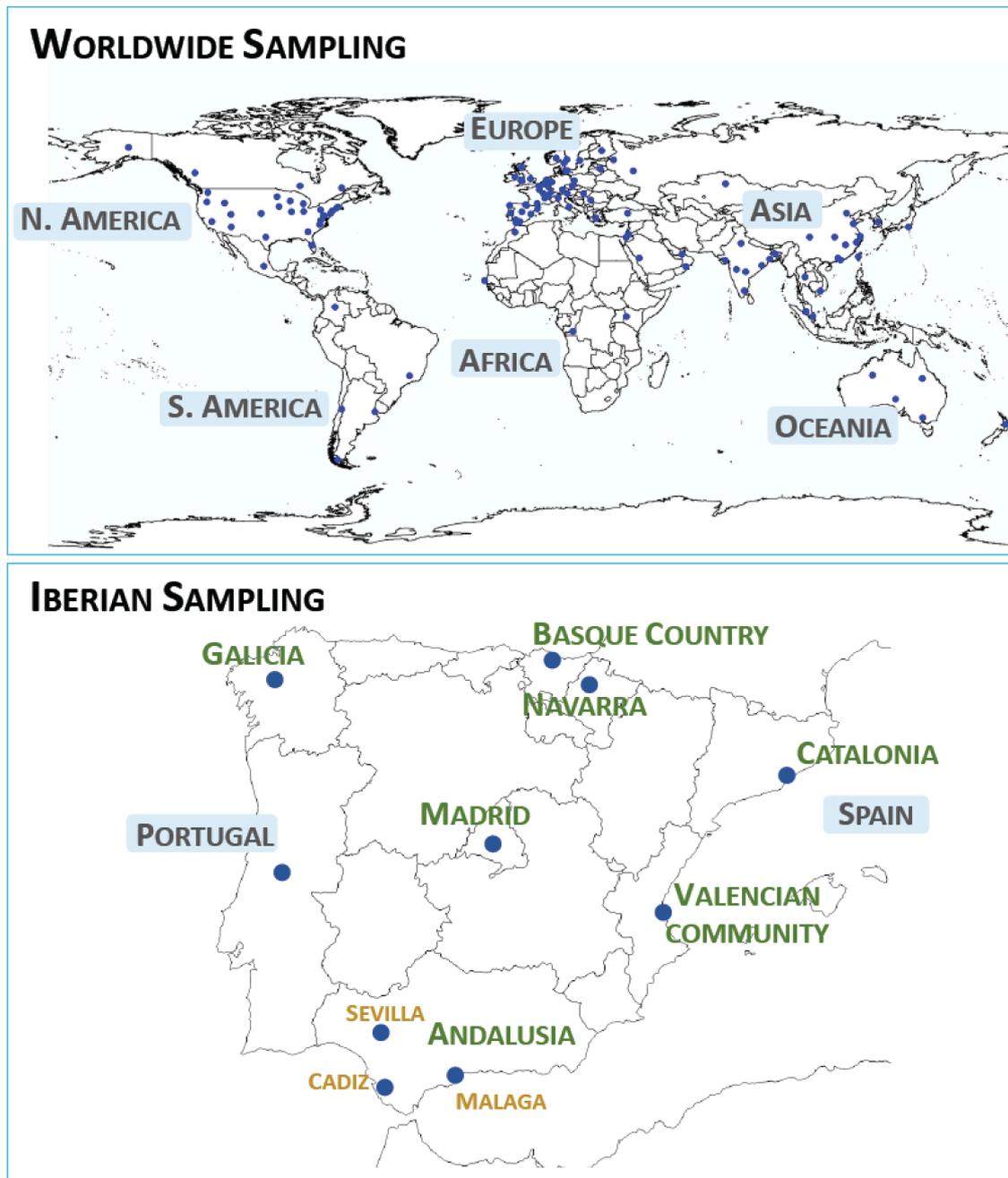


Figure S12.

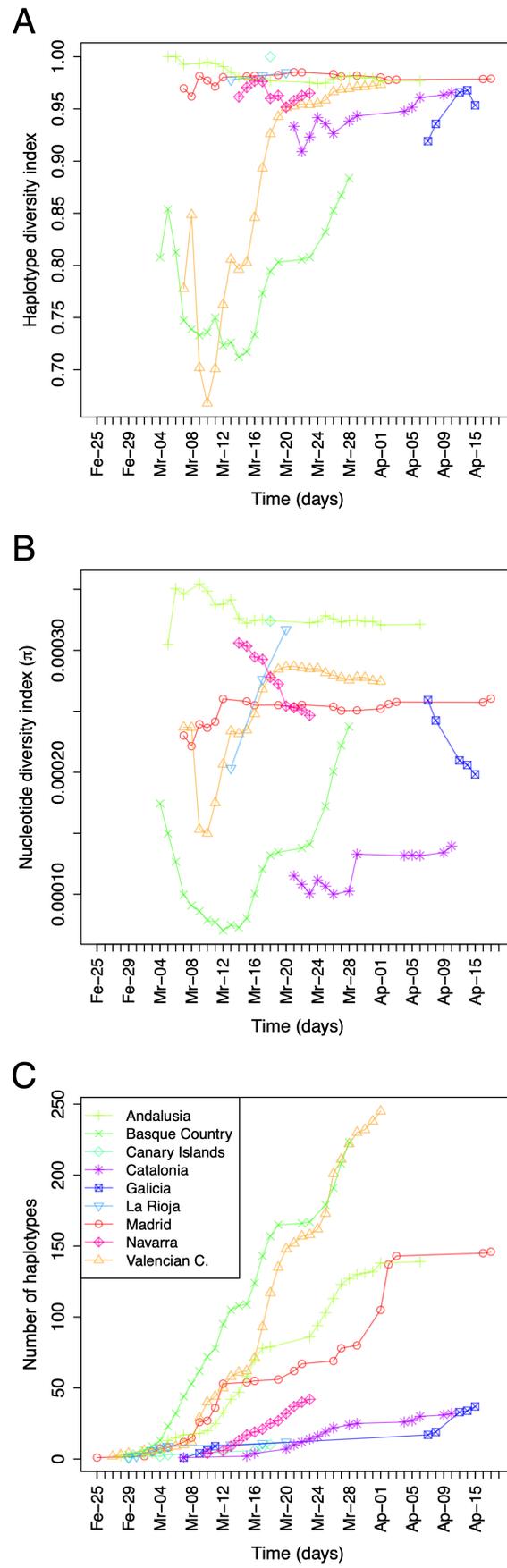


Figure S13.

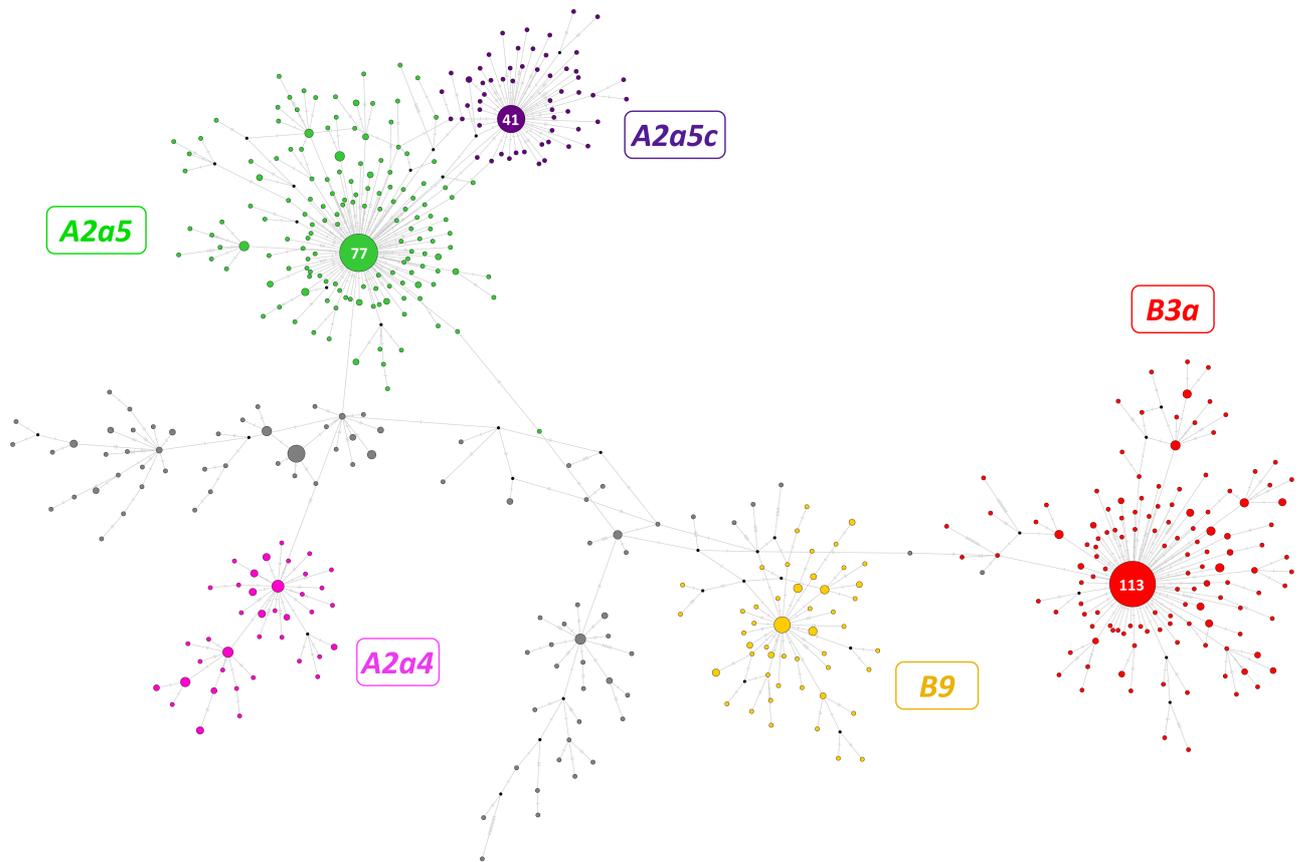


Figure S14.

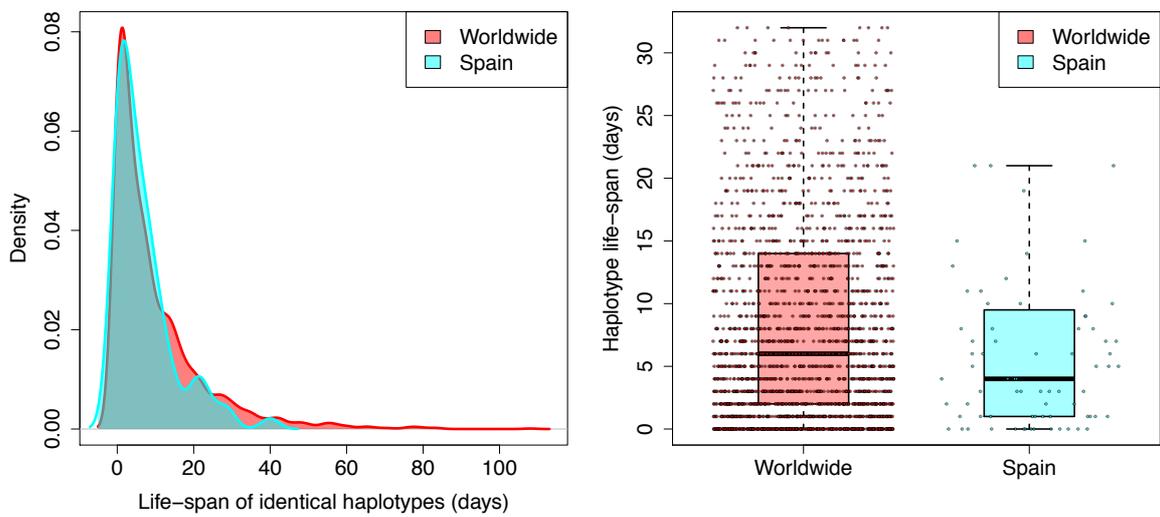


Figure S15.

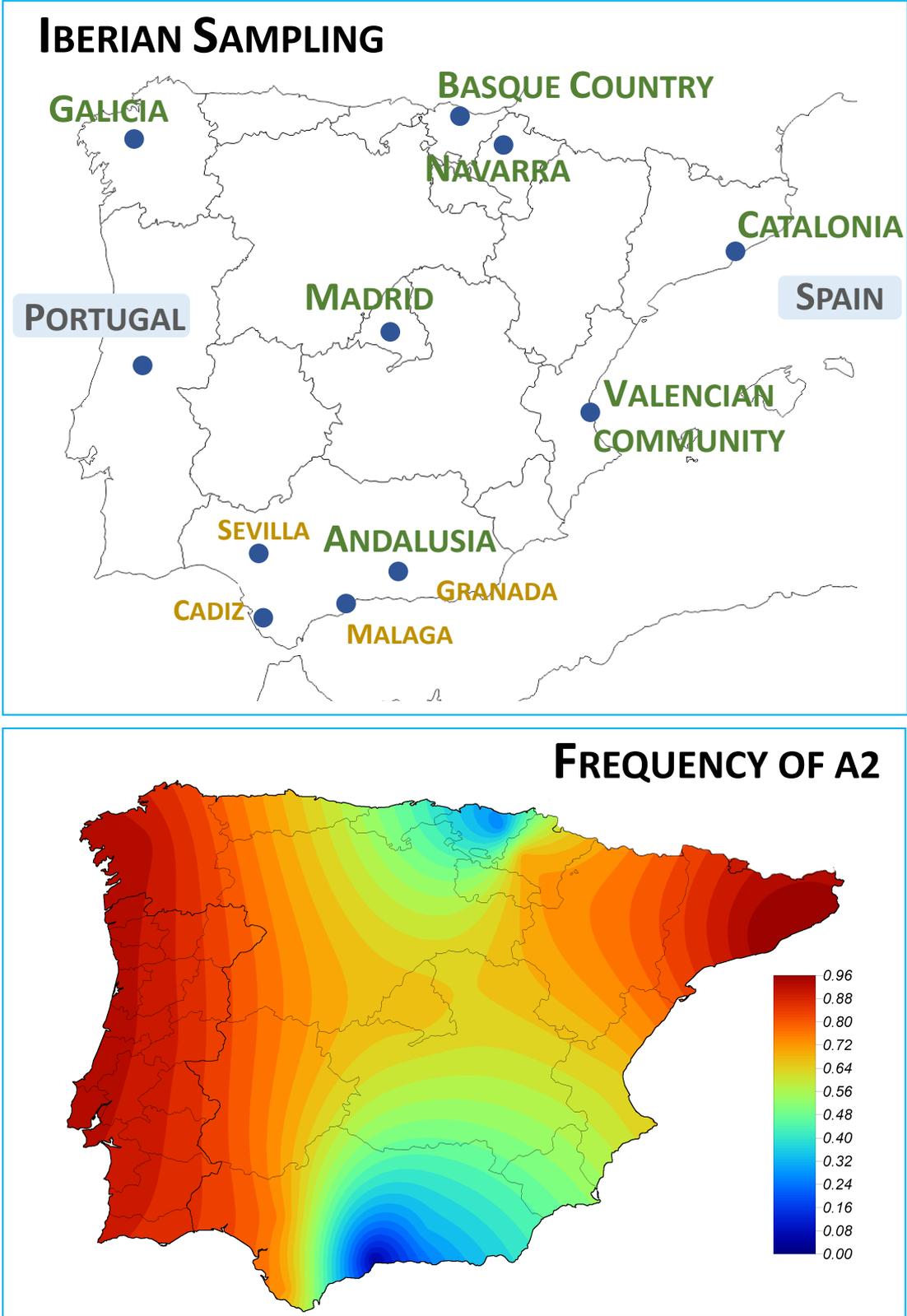


Figure S16.

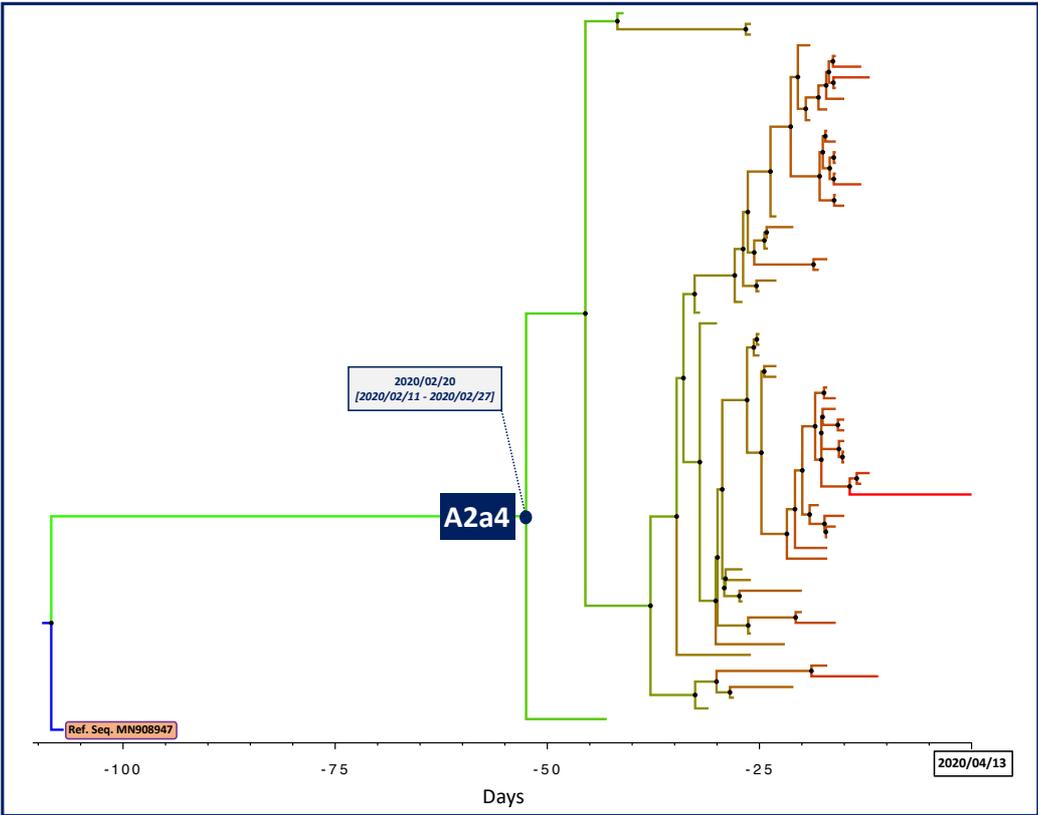


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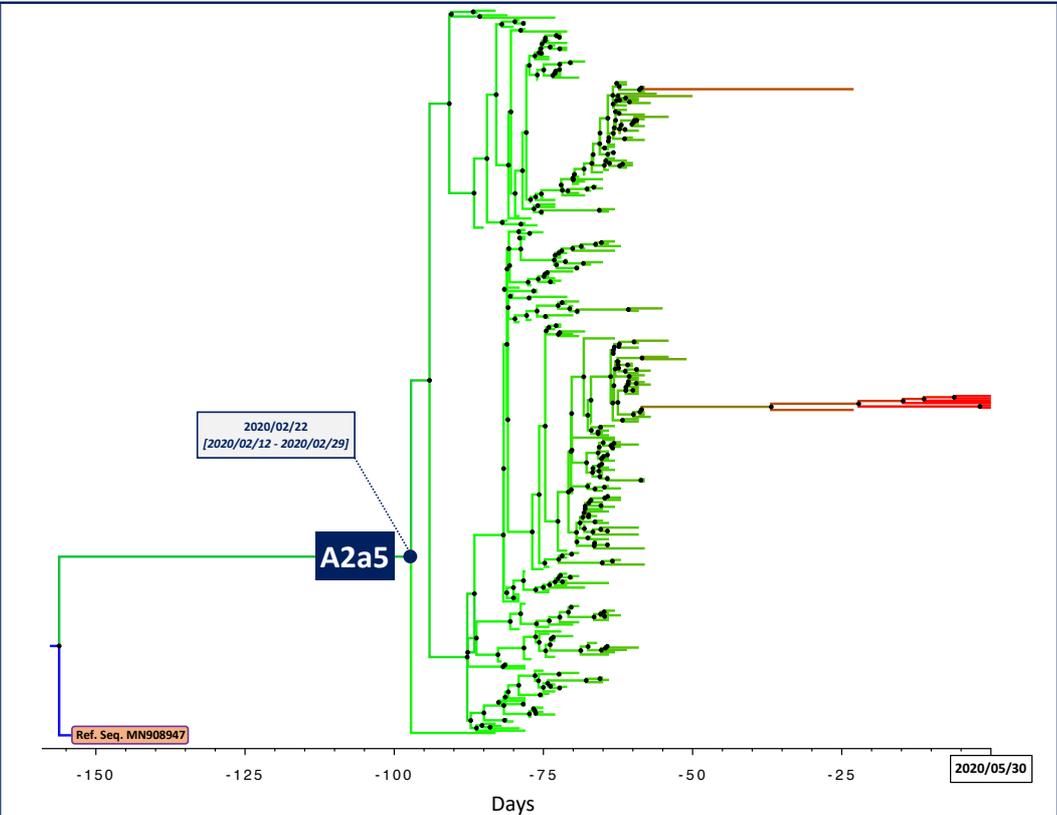


Figure S18.

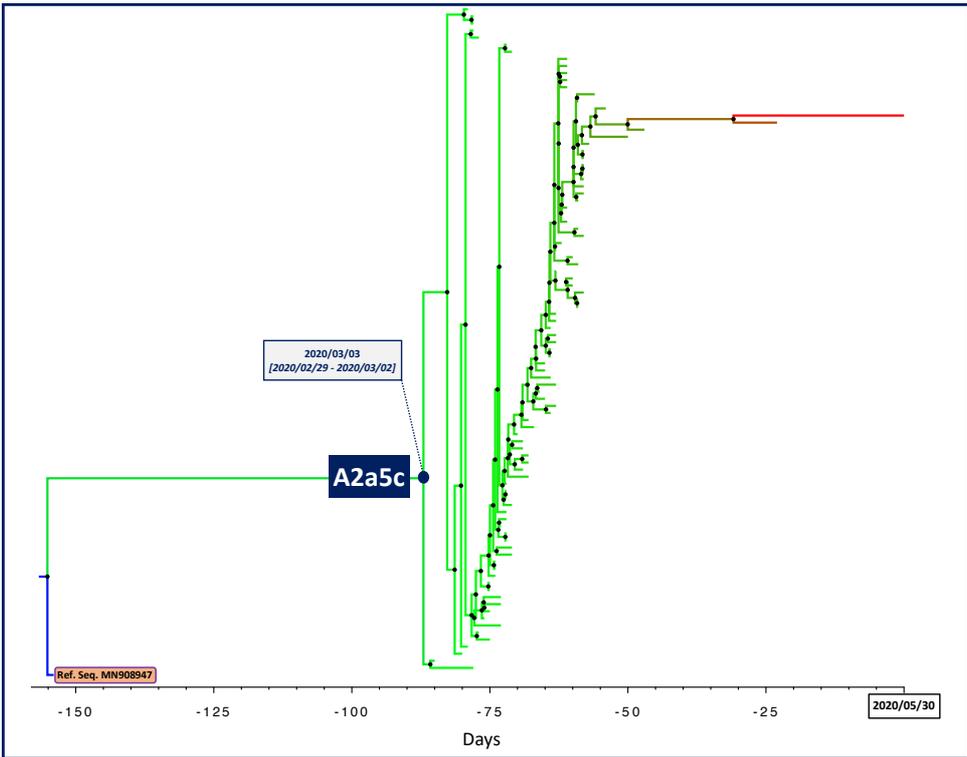


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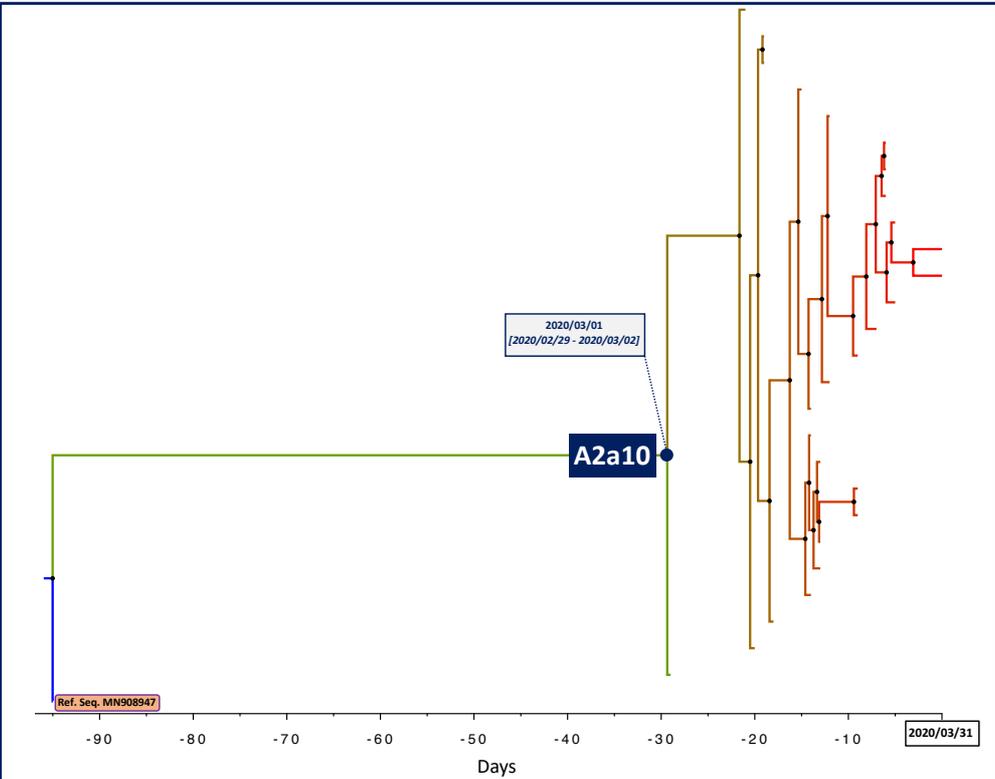


Figure S20.

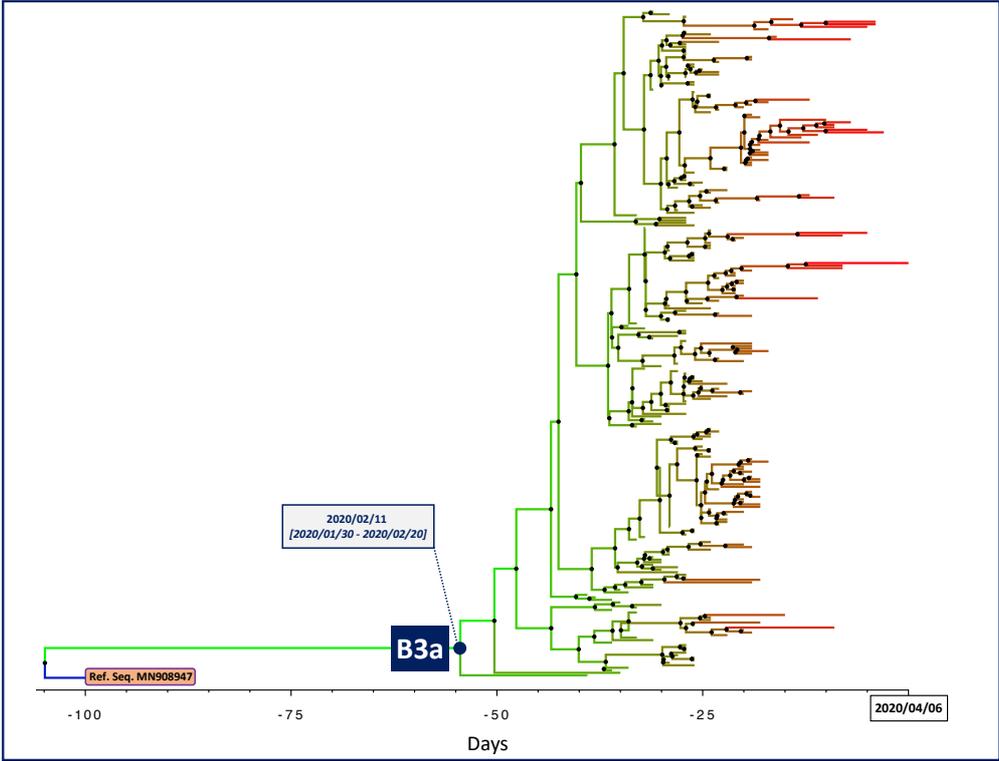


Figure S21.

