Supplementary Figures

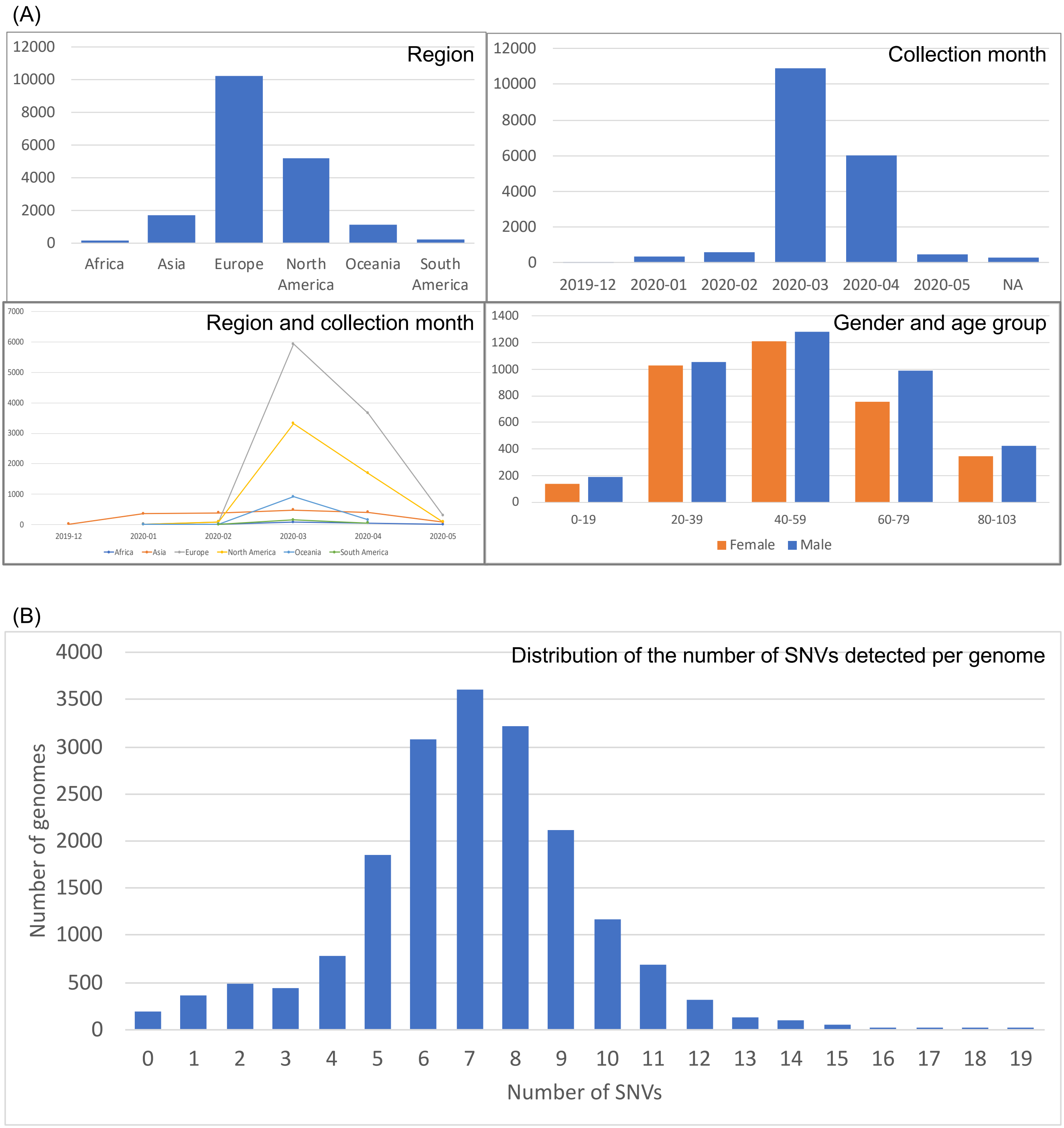


Fig. S1. Summary of the 18,599 GISAID SARS-CoV-2 genomes analyzed. (A) Genome distribution by region, collection month, gender, and age group. (B) Distribution of the number of SNVs detected per genome, only including variants detected in two or more genomes (i.e. excluding SNVs unique to a single genome).

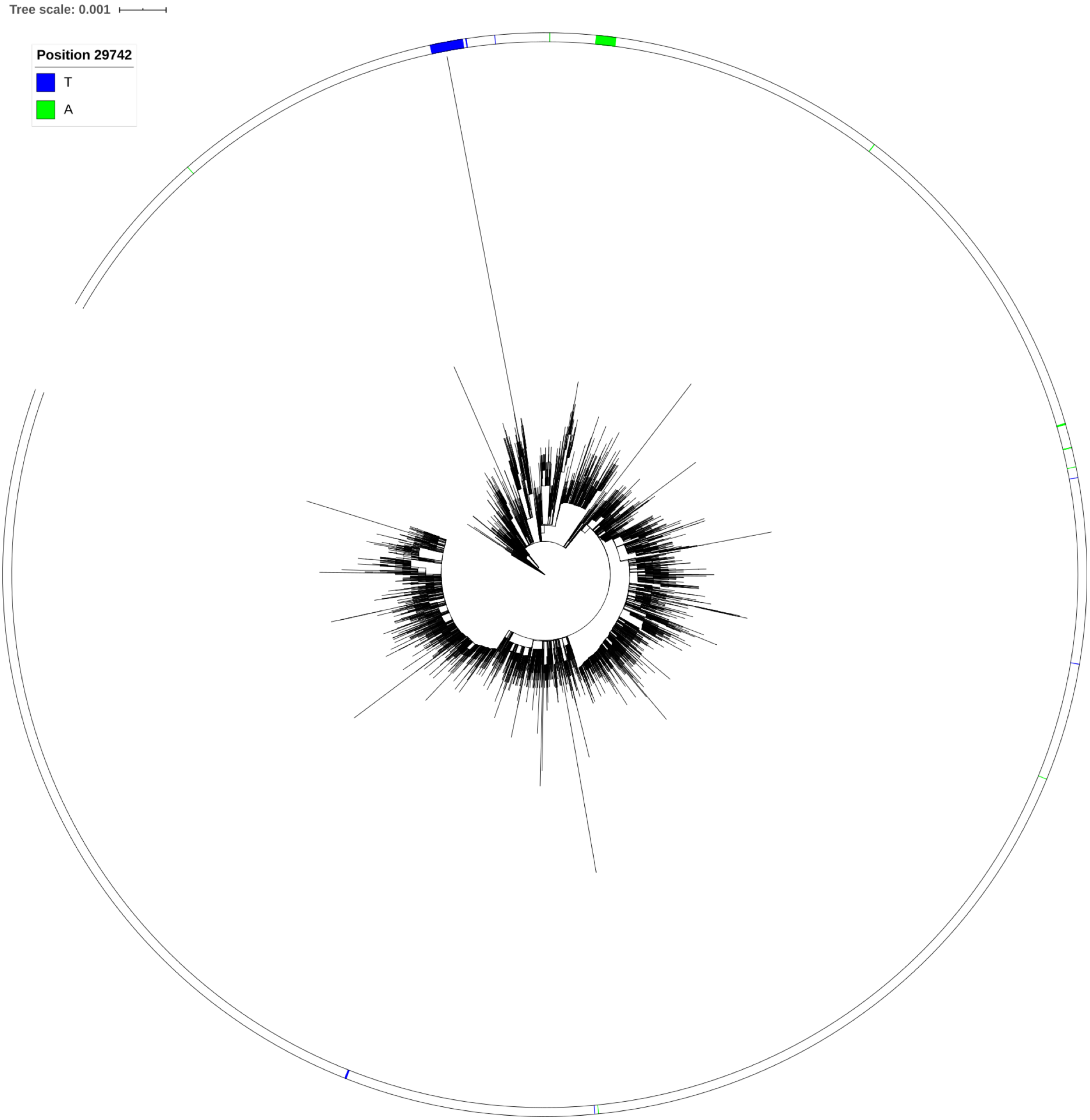


Fig. S2. Whole genome phylogeny analysis of SARS-CoV-2 genomes. A maximum likelihood phylogeny tree was constructed from 18k GISAID genomes using RAxML. Genomes carrying the g.29742G>T (blue) and g.29742G>A (green) variants are shown.

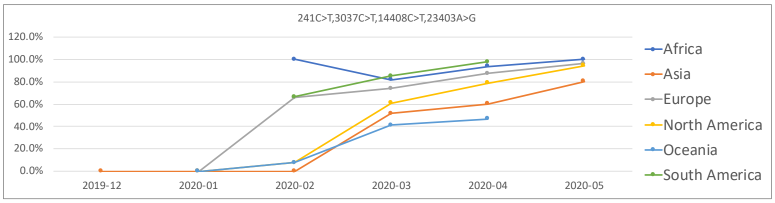
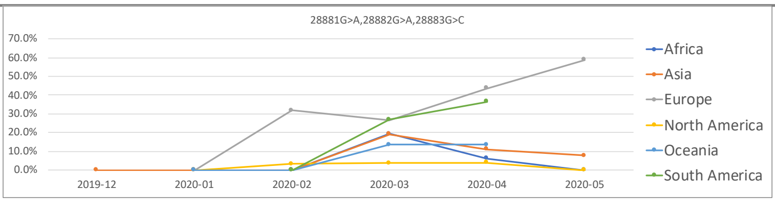
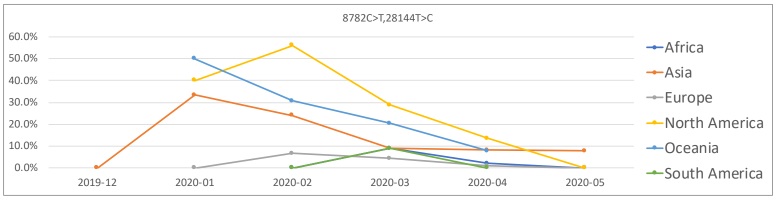
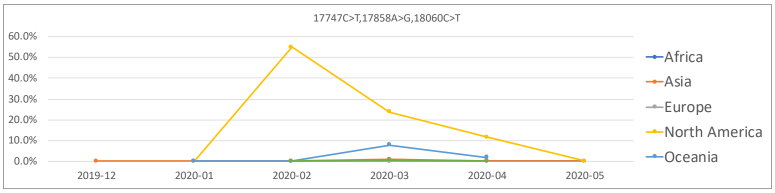
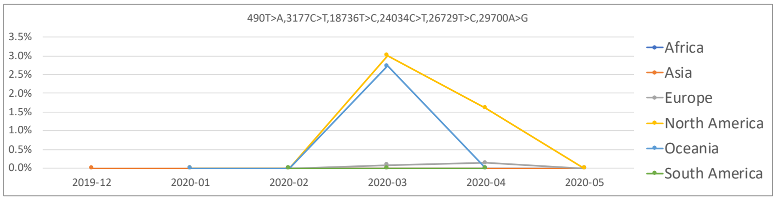
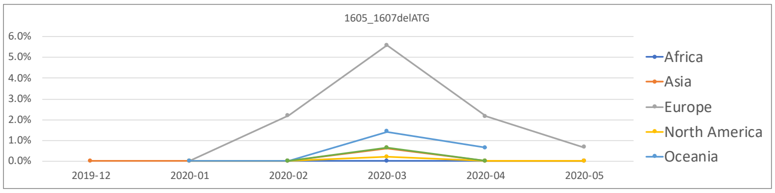
<table>
<tr><th>Type</th><th>Variants</th><th>Geolocation and collection month</th></tr>
<tr><td>CEV group1</td><td>241C>T
3037C>T
14408C>T
23403A>G</td><td>
</td></tr>
<tr><td>CEV group2</td><td>28881G>A
28882G>A
28883G>C</td><td>
</td></tr>
<tr><td>CEV group3</td><td>8782C>T
28144T>C</td><td>
</td></tr>
<tr><td>CEV group4</td><td>17747C>T
17858A>G
18060C>T</td><td>
</td></tr>
<tr><td>CEV group5</td><td>490T>A
3177C>T
18736T>C
24034C>T
26729T>C
29700A>G</td><td>
</td></tr>
<tr><td>A 3nt deletion</td><td>1605_1607delATG</td><td>
</td></tr>
</table>

Fig. S3. Geographical and temporal distribution of genomes harboring SARS-CoV-2 co-evolving variants. Genome distribution is shown for five co-evolving variant groups and a group of 3 nt deletion.