Supplementary Materials for “Genome-wide mutation landscape of SARS-CoV-2”

**Supplementary Figure Legenes**

**Supplementary Fig. S1.** The distribution of SNP frequency.

**Supplementary Fig. S2.** The distribution of different SNP types.

**Supplementary Fig. S3.** The distribution of different SNP annotation types.

**Supplementary Fig. S4.** The fold change (FC) of each continent on each SNP hotspot.

**Supplementary Fig. S5.** The continent distribution of 3,159 genome sequence.

**Supplementary Tables.**

**Supplementary Table S1.** The frequency of each SNV

**Supplementary Table S2.** The genomic bin enrichment of 244 high frequent SNVs

**Supplementary Table S3.** The 22 SNP hotspots with its annotation type

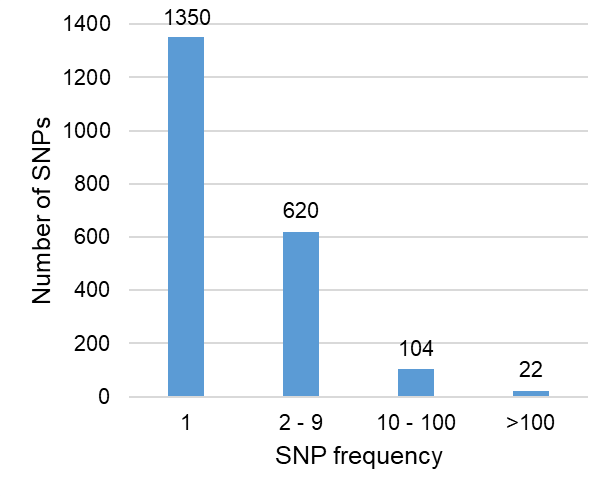
**Supplementary Table S4.** The enrichment analysis of each continent on each SNP hotspot.

**Supplementary Table S5.** The information of 1,656 genome sequences that containing SNP at locus 23,403.

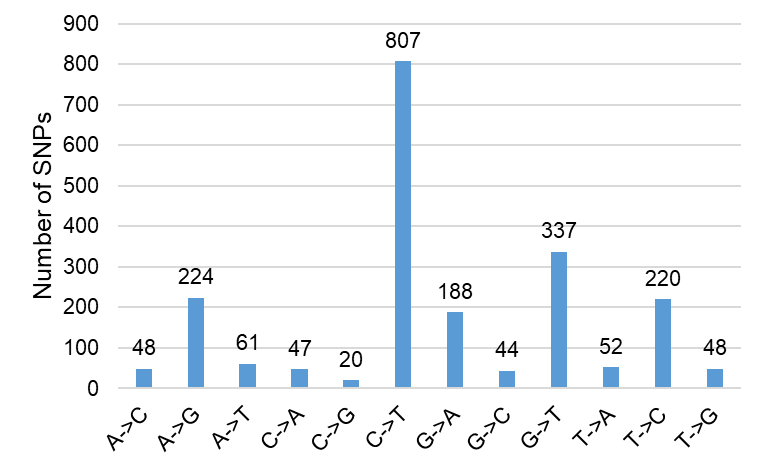
**Supplementary Table S6.** Mutation sensitivity score of each amino acid in spike glycoprotein

**Supplementary Table S7.** The 3,160 genome sequences information

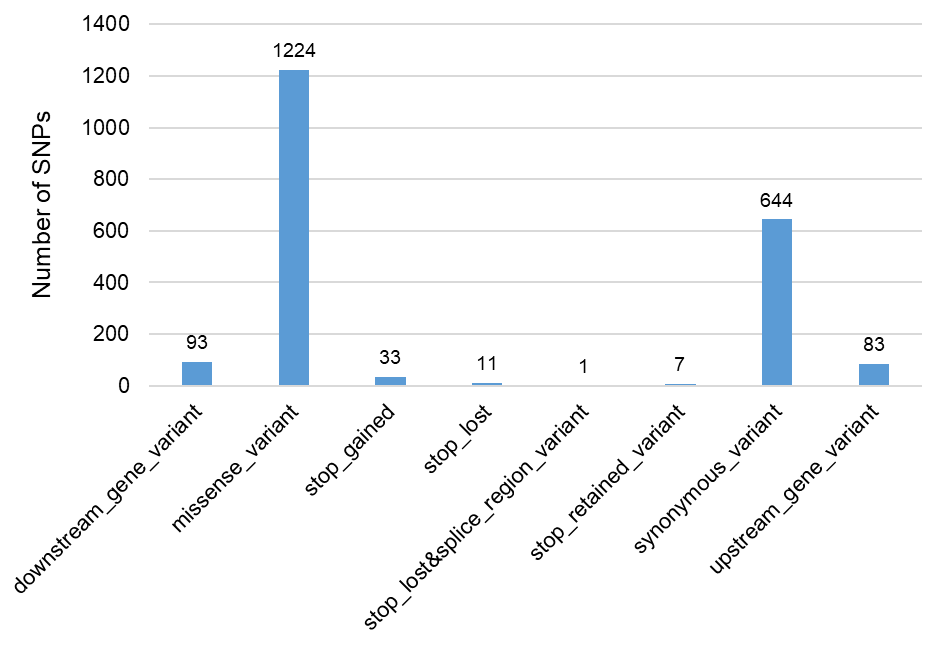
**Supplementary Figures**



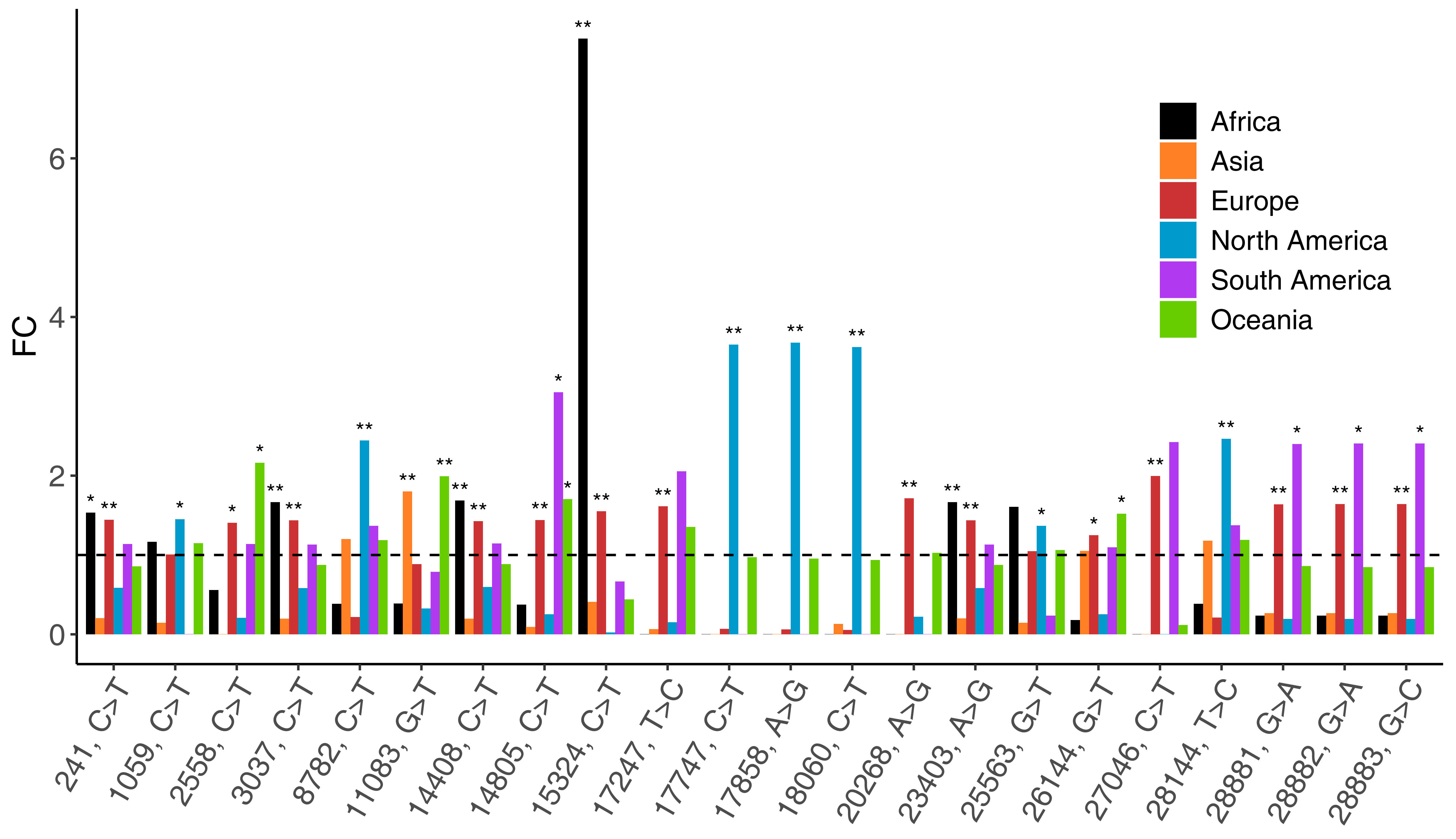
**Supplementary Fig. S1.** The distribution of SNP frequency.



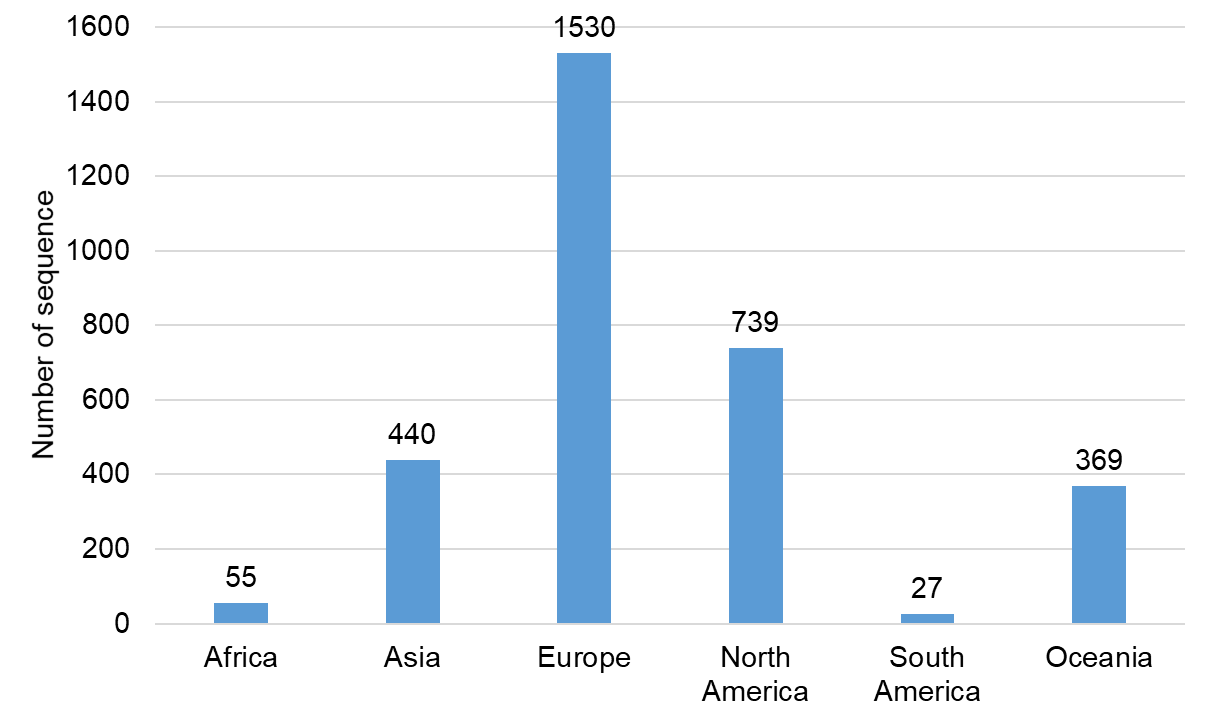
**Supplementary Fig. S2.** The distribution of different SNP types.



**Supplementary Fig. S3.** The distribution of different SNP annotation types.



**Supplementary Fig. S4.** The fold change (FC) of each continent on each SNP hotspot. The black dash line indicates FC = 1, \* means 1e-6 < *p* < 0.01, .\*\* means *p* < 1e-6.



**Supplementary Fig. S5.** The continent distribution of 3,159 genome sequence.