Comparative Genomics: SARS-CoV-2 vs SARS-CoV Tor2

Sequences:
- SARS-CoV-2 (MN908947.3)
- SARS-CoV Tor2 (AY274119.3)

Alignment Method:
- Full genome alignment using MAFFT (FFT-NS-2 strategy).
- Alignment length: 30,016 bases.

Results:
- Mutations detected: 6,319.
- Genomic divergence: 21.05%.

First few differences (Position, SARS-CoV-2 base, SARS-CoV Tor2 base):
3 t a
4 a t
5 a t
12 a t
18 t a
25 t -
26 a -
28 c a
31 a g
41 t -
42 t c
90 g a
97 a g
111 t c
120 t c
121 c t
133 t a
134 t c
140 c t
141 t a

Interpretation:
- SARS-CoV-2 diverges significantly from SARS-CoV (2003).
- Early genome region shows substitution and indel hotspots.
- Divergence suggests changes in regulatory RNA regions and spike-mediated host interaction.

Tools Used:
- Ubuntu (WSL)
- MAFFT v7.505
- Python (Biopython)
- Custom mutation counting script

Conclusion:
The alignment confirms substantial sequence evolution between the two viral genomes and highlights regions potentially associated with biochemical/functional differences.