

(A)



(B)

Description: MN908947.3:21563-25384_0 0-1646
Molecule type: dna
Query Length: 1598
Other reports: [Distance tree of results](#) [MSA viewer](#) ?

to to to

[Filter](#) [Reset](#)

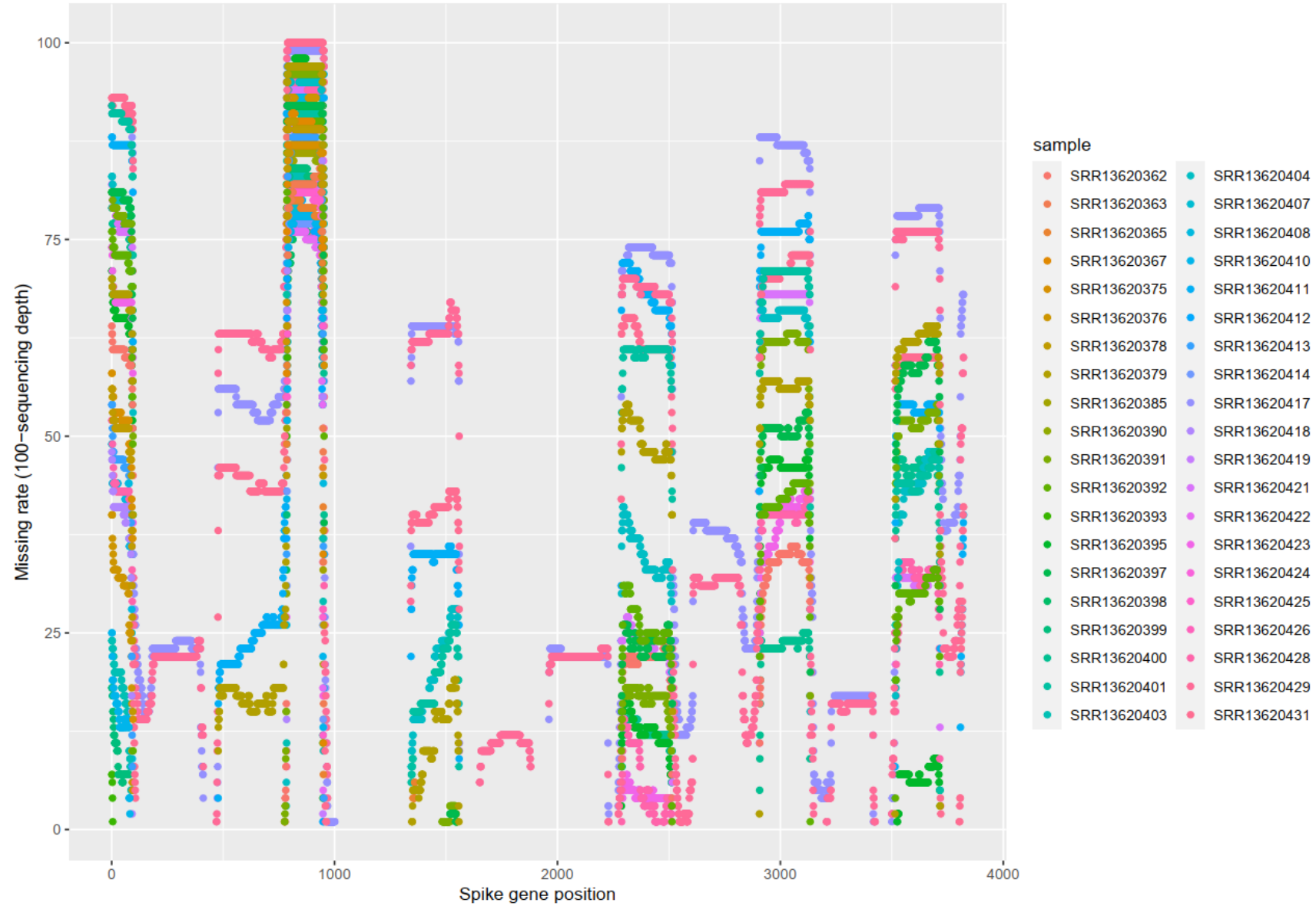
Descriptions Graphic Summary Alignments Taxonomy

Sequences producing significant alignments Download [New](#) Select columns Show 100 ?

☒ select all 100 sequences selected [GenBank](#) [Graphics](#) [Distance tree of results](#) [New](#) [MSA Viewer](#)

	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input checked="" type="checkbox"/>	Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/human/TWN/CGMH-CGU-22/2020_co...	Severe acute res...	2599	2823	95%	0.0	100.00%	29857	MT479224.1
<input checked="" type="checkbox"/>	Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/human/RUS/Dubrovka/2020_complete...	Severe acute res...	2599	2823	95%	0.0	100.00%	29785	MW514307.1
<input checked="" type="checkbox"/>	Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/human/BEL/GHB-03021/2020_complet...	Severe acute res...	2599	2823	95%	0.0	100.00%	29740	MW368439.1
<input checked="" type="checkbox"/>	Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/human/RUS/Dubrovka/2020_ORF1ab p...	Severe acute res...	2599	2823	95%	0.0	100.00%	4043	MW161041.1
<input checked="" type="checkbox"/>	Severe acute respiratorv svndrome coronavirus 2 isolate SARS-CoV-2/human/DNK/SARS-CoV-2 DK-AHH1 c...	Severe acute res...	2588	2812	95%	0.0	99.86%	29778	MZ049598.1

Supplementary Figure S1 (A) Read alignment of a diluted viral solution (Ct=31.79). (B) BLAST result of a consensus sequence.



Supplementary Figure S2 Read depth distribution across spike gene. In order to highlight low sequencing depth, missing rate is defined by $100 - \text{SD}$ and the SD is set as 100 when sequencing depth ≥ 100 , otherwise $\text{SD} = \text{sequencing depth}$.