

Table S1. Sequence alignment and identification of recurrent mutations identified in the SARS-CoV-2 genome.

	Sequence identifiers	% Pairwise identity	Country	Conserved mutation(s)
Ref	NC_045512.2		China	
1	MT276598.1	99.97	Israel	C241U/C313U/C3037U/C14408U/A23403G/GGG28881-4AAC
2	MT066176.1	99.99	Taiwan	
3	MT262993.1	99.9	Pakistan	
4	MT344962.1	99.98	USA/Minnesota	Del 1606-1609
5	MT344959.1	99.98	USA/Pennsylvania	C241U/C1059U/C3037U/C14408U/A23403G/G25563U
6	MT304476.1	99.98	South Korea	G11083U/C14805U/G26144U/C28311U
7	MT276326.1	99.98	USA/Georgia	G11083U/C14805U/G26144U
8	MT320538.2	99.98	France	C241U/C3037U/C14408U/A23403G
9	MT344960.1	99.98	USA/Rhode Island	C241U/C1059U/C3037U/C14408U/A23403G/G25563U/C27964U
10	MT344961.1	99.98	USA/Nevada	Del 1606-1609
11	MT328034.1	99.97	Greece	C8782U/C14805U/ U28134C
12	MT093571.1	99.98	Sweden	G26144U
13	MT114415.1	99.99	Hong Kong	G1397A/G11083U/U28688C/G29742U
14	MT350282.1	99.98	Brazil	G11083U/C14408U/C14805U/U17247C/G26144U
15	MT470156.1	99.97	France	C241U/C313U/C3037U/A23403G/GGG28881-4AAC
16	MT328035.1	99.97	Greece	C241U/C3037U/C14408U/A23403G/GGG28881-4AAC
17	MT371050.1	99.99	Sri Lanka	C14805U/U17247C/G26144U
18	MT370518.1	99.98	Taiwan	C1059U/G1397A/G11083U/U28688C/G29742U
19	LC542976.1	99.99	Japan	C8782U/ U28134C
20	MT371047.1	99.97	Sri Lanka	G1397A/G11083U/U28688C/G29742U
21	MT324062.1	99.98	South Africa	C241U/C3037U/C14408U/A23403G
22	MT396241.1	99.99	China	
23	MT007544.1	99.96	Australia	G26144U
24	MT385418.1	99.97	USA/California	C241U/C313U/C3037U/C14408U/A23403G/GGG28881-4AAC
25	MT374105.1	99.99	Taiwan	G11083U/C14805U/U17247C/G26144U
26	MT374116.1	99.97	Taiwan	C241U/C3037U/C14408U/A23403G/GGG28881-4AAC
27	MT327745.1	99.98	Turkey	G1397A/G11083U/U28688C/G29742U
28	MT358402.1	99.97	USA/Louisiana	C241U/C1059U/C3037U/C14408U/A23403G/G25563U/C27964U
29	MT263074.1	99.97	Peru	C241U/C3037U/C14408U/A23403G/GGG28881-4AAC
30	MT359866.1	99.97	Spain	C241U/C313U/C3037U/C14408U/A23403G/GGG28881-4AAC
31	MT385486.1	98.6	USA/California	G11083U/C28311U
32	MT072688.1	99.99	Nepal	C24023U
33	LC553263.1	99.97	Japan	C241U/C313U/C3037U/C14408U/A23403G/GGG28881-4AAC
34	MT114419.1	99.99	Hong Kong	G11083U
35	MT396242.1	99.5	India	C241U/C313U/C3037U/C14408U/A23403G/GGG28881-4AAC
36	MT375478.1	99.97	USA/Washington	C241U/C1059U/C3037U/C14408U/A23403G/G25563U
37	MT240479.1	99.98	Pakistan	C241U/G1397A/G11083U
38	MT372482.1	99.1	Malaysia	G11083U/C28311U
39	MT350242.1	99.9	USA/Virginia	C241U/C1059U/C14408U/A23403G/G25563U
40	MT320891.2	99.98	Iran	G1397A/G11083U/G29742U
41	MT198651.1	96.4	Spain	C8782U/C14805U/U28134C
42	MT292575.1	99.98	Spain	C241U/C3037U/C14408U/A23403G
43	MT582453.1	99.97	Germany	C241U/C1059U/C3037U/C14408U/A23403G/G25563U
44	MT371035.1	99.97	USA/New York	C241U/C1059U/C3037U/C14408U/A23403G/G25563U
45	MT370841.1	99.96	USA/New York	C8782U/A23403G/C24023U/U28134C
46	MT077125.1	99.99	Italy	G11083U/G26144U
47	MT370933.1	99.98	USA/New Jersey	C241U/C1059U/C3037U/C14408U/A23403G/G25563U
48	MT358731.1	99.97	USA/Washington	C241U/C1059U/C3037U/C14408U/A23403G/G25563U
49	MT371574.1	99.98	Czech Republic	C241U/C3037U/C14408U/A23403G/GGG28881-4AAC
50	MT375471.1	99.98	USA/Connecticut	C1059U/C3037U/C14408U/A23403G/G25563U
51	MT451006.1	99.99	Australia	Del 1606-1609
52	MT457394.1	99.95	Nederland	Del 1606-1609
53	MT451263.1	99.5	Australia	C241U/C3037U/G9802U/C14408U/A23403G
54	MT496988.1	99.98	India	C241U/C3037U/G9802U/C14408U/A23403G/G25563U
55	EPI_ISL_416425	99.9	China	G9802U
56	EPI_ISL_417211	99.98	New Zealand	Del 1606-1609
57	EPI_ISL_416429	99.98	Vietnam	C8782U/C24023U/U28134C
58	EPI_ISL_419222	99.6	Hong Kong	G26144U
59	EPI_ISL_422940	99.5	Netherlands	C241U/C3037U/G9803U/C14408U/A23403G/GGG28881-4AAC/
60	MT451063.1	99.3	Australia	C8781U/G9803U
61	MT380727.1	99.9	Iran	U28688C
62	MT512430.1	99.99	USA/Atlanta	G9803U
63	EPI_ISL_417212	99.97	New Zealand	C14805U/G26144U
64	EPI_ISL_429691	90.2	Brazil	C3037U/C14408U/A23403G/GGG28881-4AAC
65	EPI_ISL_416538	99.6	New Zealand	C8781U/C24034U

Table S2. Mutational analysis of SAR-CoV-2 sequences analyzed in the current study.

Sequence identifiers	Sd	Sn	S	N	ps	pn	ds	dn	ds/dn	ps/pn
China-EPI_ISL_416425	5.0000	5.0000	6559.3333	23341.6667	0.0008	0.0002	0.0008	0.0002	3.5598	3.5585
Israel-MT276598.1	5.0000	3.0000	6556.0000	23309.0000	0.0008	0.0001	0.0008	0.0001	5.9281	5.9256
Taiwan-MT066176.1	1.0000	1.0000	6556.3333	23311.6667	0.0002	0.0000	0.0002	0.0000	3.5559	3.5556
Vietnam-EPI_ISL_416429	4.0000	3.0000	6556.6667	23311.3333	0.0006	0.0001	0.0006	0.0001	4.7420	4.7405
USA-MT344962.1	2.0000	0.0000	6556.6667	23314.3333	0.0003	0.0000	0.0003	0.0000	nan	nan
USA-MT512430.1	1.0000	0.0000	6557.3333	23322.6667	0.0002	0.0000	0.0002	0.0000	nan	nan
France-MT320538.2	3.0000	3.0000	6557.5000	23322.5000	0.0005	0.0001	0.0005	0.0001	3.5574	3.5566
USA-MT276326.1	1.0000	5.0000	6557.3333	23322.6667	0.0002	0.0002	0.0002	0.0002	0.7113	0.7113
USA-MT344960.1	4.0000	3.0000	6557.5000	23322.5000	0.0006	0.0001	0.0006	0.0001	4.7437	4.7422
USA-MT344959.1	3.0000	3.0000	6556.5000	23320.5000	0.0005	0.0001	0.0005	0.0001	3.5576	3.5569
USA-MT344961.1	1.0000	1.0000	6556.5000	23317.5000	0.0002	0.0000	0.0002	0.0000	3.5567	3.5564
South_Korea-MT304476.1	0.0000	5.0000	6557.3333	23322.6667	0.0000	0.0002	0.0000	0.0002	nan	nan
Greece-MT328034.1	4.0000	5.0000	6557.8333	23325.1667	0.0006	0.0002	0.0006	0.0002	2.8462	2.8455
Sweden-MT093571.1	2.0000	5.0000	6558.1667	23324.8333	0.0003	0.0002	0.0003	0.0002	1.4227	1.4226
Hong Kong-MT114415.1	1.0000	3.0000	6558.6667	23330.3333	0.0002	0.0001	0.0002	0.0001	1.1857	1.1857
Brazil-MT350282.1	0.0000	6.0000	6559.1667	23341.8333	0.0000	0.0003	0.0000	0.0003	nan	nan
France-MT470156.1	5.0000	3.0000	6560.0000	23341.0000	0.0008	0.0001	0.0008	0.0001	5.9326	5.9301
Greece-MT328035.1	4.0000	4.0000	6559.8333	23341.1667	0.0006	0.0002	0.0006	0.0002	3.5592	3.5582
Hong Kong-EPI_ISL_419222	1.0000	3.0000	6537.0000	23244.0000	0.0002	0.0001	0.0002	0.0001	1.1853	1.1853
Japan-LC542976.1	4.0000	0.0000	6559.3333	23341.6667	0.0006	0.0000	0.0006	0.0000	nan	nan
NewZealand-EPI_ISL_416538	4.0000	7.0000	6537.8333	23243.1667	0.0006	0.0003	0.0006	0.0003	2.0320	2.0315
Sri Lanka-MT371047.1	4.0000	6.0000	6560.1667	23340.8333	0.0006	0.0003	0.0006	0.0003	2.3725	2.3720
South Africa-MT324062.1	4.0000	2.0000	6559.5000	23341.5000	0.0006	0.0001	0.0006	0.0001	7.1193	7.1169
Taiwan-MT370518.1	2.0000	5.0000	6559.6667	23341.3333	0.0003	0.0002	0.0003	0.0002	1.4234	1.4233
Sri Lanka_-MT371050.1	1.0000	3.0000	6559.5000	23341.5000	0.0002	0.0001	0.0002	0.0001	1.1862	1.1861
China-MT396241.1	1.0000	0.0000	6559.3333	23335.6667	0.0002	0.0000	0.0002	0.0000	nan	nan
Australia-MT007544.1	0.0000	3.0000	6556.1667	23332.8333	0.0000	0.0001	0.0000	0.0001	nan	nan
USA-MT385418.1	5.0000	4.0000	6560.0000	23341.0000	0.0008	0.0002	0.0008	0.0002	4.4494	4.4476
Taiwan-MT374105.1	0.0000	4.0000	6558.6667	23339.3333	0.0000	0.0002	0.0000	0.0002	nan	nan
Taiwan-MT374116.1	5.0000	3.0000	6559.3333	23338.6667	0.0008	0.0001	0.0008	0.0001	5.9326	5.9301
Turkey-MT327745.1	2.0000	4.0000	6550.1667	23281.8333	0.0003	0.0002	0.0003	0.0002	1.7774	1.7772
USA-MT358402.1	5.0000	5.0000	6558.6667	23336.3333	0.0008	0.0002	0.0008	0.0002	3.5594	3.5581
Peru-MT263074.1	5.0000	4.0000	6553.6667	23299.3333	0.0008	0.0002	0.0008	0.0002	4.4457	4.4439
Nederland-MT457394.1	5.0000	6.0000	6556.0000	23318.0000	0.0008	0.0003	0.0008	0.0003	2.9650	2.9640
Spain-MT359866.1	5.0000	4.0000	6558.0000	23334.0000	0.0008	0.0002	0.0008	0.0002	4.4494	4.4476
USA-MT385486.1	3.0000	4.0000	6466.3333	23002.6667	0.0005	0.0002	0.0005	0.0002	2.6685	2.6680
Nepal-MT072688.1	1.0000	0.0000	6543.3333	23264.6667	0.0002	0.0000	0.0002	0.0000	nan	nan
Japan-LC553263.1	6.0000	4.0000	6556.3333	23326.6667	0.0009	0.0002	0.0009	0.0002	5.3395	5.3368
Hong-Kong-MT114419.1	1.0000	1.0000	6552.5000	23309.5000	0.0002	0.0000	0.0002	0.0000	3.5576	3.5573
India-MT396242.1	5.0000	8.0000	6511.5000	23149.5000	0.0008	0.0003	0.0008	0.0003	2.2226	2.2220
USA-MT375478.1	3.0000	6.0000	6552.0000	23316.0000	0.0005	0.0003	0.0005	0.0003	1.7795	1.7793
Pakistan-MT240479.1	2.0000	4.0000	6547.6667	23287.3333	0.0003	0.0002	0.0003	0.0002	1.7785	1.7783
Australia-MT451263.1	4.0000	2.0000	6448.8333	22987.1667	0.0006	0.0001	0.0006	0.0001	7.1316	7.1291
USA-MT350242.1	3.0000	4.0000	6548.8333	23301.1667	0.0005	0.0002	0.0005	0.0002	2.6691	2.6685
Malaysia-MT372482.1	6.5000	30.5000	6488.8333	23121.1667	0.0010	0.0013	0.0010	0.0013	0.7592	0.7594
Australia-MT451006.1	0.0000	1.0000	6543.0000	23253.0000	0.0000	0.0000	0.0000	0.0000	nan	nan
India-MT496988.1	6.0000	4.0000	6543.1667	23255.8333	0.0009	0.0002	0.0009	0.0002	5.3340	5.3313
Iran-MT320891.2	1.0000	4.0000	6545.3333	23274.6667	0.0002	0.0002	0.0002	0.0002	0.8890	0.8890
Australia-MT451063.1	5.0000	2.0000	6473.8333	23025.1667	0.0008	0.0001	0.0008	0.0001	8.8957	8.8916
Spain-MT198651.1	3.0000	5.0000	6155.0000	21958.0000	0.0005	0.0002	0.0005	0.0002	2.1409	2.1405
Netherlands-EPI_ISL_422940	6.0000	4.0000	6492.0000	23100.0000	0.0009	0.0002	0.0009	0.0002	5.3400	5.3373
Spain-MT292575.1	3.0000	2.0000	6536.5000	23238.5000	0.0005	0.0001	0.0005	0.0001	5.3341	5.3328
Germany-MT394864.1	3.0000	3.0000	6284.1667	22371.8333	0.0005	0.0001	0.0005	0.0001	3.5608	3.5600
Germany-MT582453.1	3.0000	4.0000	6536.8333	23238.1667	0.0005	0.0002	0.0005	0.0002	2.6667	2.6662
USA-NY-MT371035.1	3.0000	7.0000	6524.3333	23199.6667	0.0005	0.0003	0.0005	0.0003	1.5241	1.5239
USA-MT370841.1	5.0000	7.0000	6524.8333	23199.1667	0.0008	0.0003	0.0008	0.0003	2.5404	2.5397
Italy-MT077125.1	0.0000	2.0000	6537.8333	23243.1667	0.0000	0.0001	0.0000	0.0001	nan	nan
USA-MT370933.1	3.0000	3.0000	6522.1667	23192.8333	0.0005	0.0001	0.0005	0.0001	3.5568	3.5560
USA-MT358731.1	4.0000	4.0000	6534.5000	23267.5000	0.0006	0.0002	0.0006	0.0002	3.5618	3.5607
Czech Republic-MT371574.1	4.0000	3.0000	6529.0000	23225.0000	0.0006	0.0001	0.0006	0.0001	4.7445	4.7429
NewZealand-EPI_ISL_417211	2.0000	0.0000	6513.0000	23166.0000	0.0003	0.0000	0.0003	0.0000	nan	nan
Brazil-EPI_ISL_429691	4.0000	9.0000	5614.5000	20026.5000	0.0007	0.0004	0.0007	0.0004	1.5856	1.5853
NewZealand-EPI_ISL_417212	1.0000	6.0000	6511.3333	23170.6667	0.0002	0.0003	0.0002	0.0003	0.5930	0.5931
USA-MT375471.1	2.0000	5.0000	6491.6667	23151.3333	0.0003	0.0002	0.0003	0.0002	1.4266	1.4265
Iran-MT380727.1	1.0000	0.0000	300.3333	1016.6667	0.0033	0.0000	0.0033	0.0000	nan	nan

Sd: the number of observed synonymous substitutions / Sn: The number of observed non-synonymous substitutions / S: The number of potential synonymous substitutions (the average for the two compared sequences) / N: The number of potential non-synonymous substitutions (the average for the two compared sequences) ps: The proportion of observed synonymous substitutions (Sd/S) / pn: The proportion of observed non-synonymous substitutions (Sn/N) / ds: The Jukes-Cantor correction for multiple hits of ps / dn: The Jukes-Cantor correction for multiple hits of pn/ ds/dn: The ratio of synonymous to non-synonymous substitutions. Note, the total number of mutations in a virus sequence is the sum of synonymous and non-synonymous substitutions (Sd+Sn).

Table S3. Nucleotide substitutions that have the greatest impact on RNA secondary structure in the 200 bp surrounding region of 1059 position in Nsp2 based on RNAsnp mode-3.

Nsp2	Mode 2		Mode 1		
Mutation	Interval	p-value1	Folding Window	Local region	p-value2
G960A	20-50	0.0975	1-200	1-50	0.0467
G960C	1-33	0.0047	1-200	1-50	0.0297
G960U	20-50	0.0962	1-200	1-50	0.0395
U961G	1-31	0.0238	1-200	132-199	0.0282
G970C	1-31	0.0010	1-200	1-50	0.0379
G1018U	53-125	0.0163	1-200	55-124	0.0299
A1020C	56-125	0.0060	1-200	57-125	0.0203
A1022C	61-124	0.0134	1-200	62-124	0.0331
C1026G	30-71	0.0097	1-200	32-125	0.0384
U1029C	59-125	0.0198	1-200	55-124	0.0372
A1032C	53-125	0.0087	1-200	55-124	0.0267
A1032U	53-125	0.0088	1-200	55-124	0.0269
A1037C	52-125	0.0117	1-200	53-125	0.0313
A1037U	52-125	0.0157	1-200	53-125	0.0394
A1038C	52-125	0.0136	1-200	52-125	0.0383
C1044G	77-134	0.0093	1-200	62-134	0.0211
A1047C	78-127	0.0195	1-200	60-127	0.0335
A1051G	52-106	0.0108	1-200	53-106	0.0334
U1053C	52-106	0.0067	1-200	53-106	0.0248
U1054G	61-120	0.0127	1-200	62-120	0.0381
U1062G	55-110	0.0117	1-200	56-110	0.0343
U1062C	61-124	0.0168	1-200	62-124	0.0449
A1064C	61-124	0.0168	1-200	62-124	0.0471
U1073G	83-124	0.0170	1-200	62-124	0.0265
U1086G	99-135	0.0132	1-200	53-135	0.0480
U1090G	77-133	0.0246	1-200	62-133	0.0439
C1091G	77-134	0.0074	1-200	62-134	0.0224
C1121G	142-198	0.0022	1-200	142-198	0.0126

Table S4. Nucleotide substitutions that have the most impact on RNA secondary structure on the 3'UTR based on RNAsnp mode-3.

3' UTR	Mode 2		Mode 1		
Mutation	Interval	p-value1	Folding Window	Local region	p-value2
A29700C	15-99	0.0860	1-226	11-93	0.0306
G297003U	15-99	0.0813	1-229	11-93	0.0406
U29709C	15-46	0.0446	1-229	1-50	0.0431
A29749C	15-99	0.0886	1-229	11-93	0.0224

Table S5. Nucleotide substitutions that have the greatest impact on RNA secondary structure on 3'UTR based on RaSE program. The dot-bracket-notation of MFE structure of mutated sequence is presented.

[illegible]

Table S6. Nucleotide substitutions that have the greatest impact on RNA secondary structure of 200 bp flanking region of 1059 nucleotide in Nsp2 based on RaSE program. The dot-bracket-notation of MFE structure of mutated sequence is presented.

[illegible]

Table S7. The effect of mutations in SARS-CoV-2 genes on prediction of host miRNA binding and total free energy of binding miRNA binding using ltaRNA and RNAup tools. Conserved mutations are indicated with asterisks.

Target		Predicted miRNA	Total free energy of binding	
			ltaRNA	RNAup
Nsp3	WT	miR-197-5p	-12.24	-13.37
	*C3037U	-	-8.53	-9.75
Nsp4	WT	miR-3935	-13.39	-14.73
	A9259G	-	-13.48	-14.78
Nsp4	WT	miR-18b-5p	-13.72	-13.5
	*G9802U	-	-10.13	-9.6
	*C9803U	-	-8.7	-8.85
Nsp12	WT	miR-1273d	-16.42	-16.61
	C15293U	miR-1273d	-15.22	-15.48
S	WT	miR-338-3p	-6.98	-6.54
	C24034U	-	-6.98	-6.54
	G24057A	-	-8	-7.83
S	WT	miR-4661-3p	-19.2	-14.41
	G25311U	-	-17.23	-13.14

Table S8. Putative donor and acceptor splice sites and splice motifs in SARS-CoV-2 genome.

Region	5' Donor site	3' Acceptor site	ESE	ESS	ISE	ISS
5' UTR	-	1	-	-	-	-
Nsp1	2	-	1	1	8	-
Nsp2	1	1	3	2	6	1
Nsp3	3	3	25	12	25	-
Nsp4	4	-	6	1	6	-
Nsp5	2	1	3	3	6	-
Nsp6	-	3	-	1	5	-
Nsp7	-	-	2	2	-	-
Nsp8	1	-	5	1	2	-
Nsp9	1	-	2	-	2	-
Nsp10	1	-	2	-	1	-
Nsp11	-	-	-	-	1	-
Nsp12	1	5	9	7	10	-
Nsp13	2	2	5	1	9	-
Nsp14	1	3	4	1	7	-
Nsp15	-	-	1	1	-	-
Nsp16	-	1	1	1	-	-
S	-	6	6	3	14	1
ORF3a	-	3	4	3	3	-
E	1	1	-	-	4	-
M	-	1	1	2	5	-
ORF6	-	-	-	1	1	-
ORF7a	-	1	1	-	3	-
ORF7b	-	-	-	-	-	-
ORF8	1	-	1	-	1	-
N	2	3	7	7	6	-
ORF10	-	-	-	-	-	-
3' UTR	-	-	-	1	-	-

ESE; exon splicing enhancer, ESS; exon splicing silencer, ISE; intron splicing enhancer, ISS; intron splicing silencer.