Supplementary Table 1. Mutations in Delta and Omicron isolates.

Mutations detected in a Delta isolate (B.1.617.2 lineage, strain TKYTK1734, GISAID ID: EPI_ISL_2378732) compared to an original SARS-CoV-2 (B lineage, strain Wuhan-Hu-1, GenBank accession no. NC_045512.2)

Nucleotide position	Reference	Mutation	Mutation type	ORF	Amino acid substitution
210	G	T	upstream_gene_variant	NSP1	
241	C	T	upstream_gene_variant	NSP1	
1191	C	T	missense_variant	NSP2	P129L
1267	C	T	synonymous_variant	NSP2	G154G
3037	C	T	synonymous_variant	NSP3	F106F
5184	C	T	missense_variant	NSP3	P822L
9891	C	T	missense_variant	NSP4	A446V
11418	T	C	missense_variant	NSP6	V149A
12102	C	T	missense_variant	NSP8	S4L
12946	T	C	synonymous_variant	NSP9	Y87Y
14408	C	T	missense_variant	NSP12	P303L
15451	G	A	missense_variant	NSP12	G651S
16466	C	T	missense_variant	NSP13	P77L
18176	C	T	missense_variant	NSP14	P46L
20148	C	T	synonymous_variant	NSP15	F176F
20262	A	G	synonymous_variant	NSP15	L214L
21618	C	G	missense_variant	S	T19R
21987	G	A	missense_variant	S	G142D
22028	GAGTTCA	G	disruptive_inframe_deletion	S	EFR156-158G
22917	T	G	missense_variant	S	L452R
22995	C	A	missense_variant	S	T478K
23403	A	G	missense_variant	S	D614G
23604	C	G	missense_variant	S	P681R
24410	G	A	missense_variant	S	D950N
25469	C	T	missense_variant	ORF3a	S26L
26767	T	C	missense_variant	M	I82T
27638	T	C	missense_variant	ORF7a	V82A
27739	C	T	missense_variant	ORF7a	L116F
27752	C	T	missense_variant	ORF7a	T120I
28247	AGATTTC	A	conservative_inframe_deletion	ORF8	DF119-120del
28270	TA	T	upstream_gene_variant	N	
28461	A	G	missense_variant	N	D63G
28881	G	T	missense_variant	N	R203M
29402	G	T	missense_variant	N	D377Y
29742	G	T	downstream_gene_variant		

Mutations detected in an Omicron isolate (BA.1 lineage, strain TY38-873, GISAID ID: EPI_ISL_7418017) compared to an original SARS-CoV-2 (B lineage, strain Wuhan-Hu-1, GenBank accession no. NC_045512.2)

Nucleotide position	Reference	Mutation	Mutation type	ORF	Amino acid substitution
241	C	T	upstream_gene_variant	NSP1	
2832	A	G	missense_variant	NSP3	K38R
3037	C	T	synonymous_variant	NSP3	F106F
5386	T	G	synonymous_variant	NSP3	A889A
5673	C	T	missense_variant	NSP3	P985L
5730	C	T	missense_variant	NSP3	T1004I
6512	AGTT	A	disruptive_inframe_deletion	NSP3	SL1265-1266I
8393	G	A	missense_variant	NSP3	A1892T
10029	C	T	missense_variant	NSP4	T492I
10447	GCC	GTA	missense_variant	NSP5	P132Y
11282	AGTTTGTCTG	A	disruptive_inframe_deletion	NSP6	LSG105-107del
11537	A	G	missense_variant	NSP6	I189V
13195	T	C	synonymous_variant	NSP10	V57V
14408	C	T	missense_variant	NSP12	P303L
15240	C	T	synonymous_variant	NSP12	N580N
18163	A	G	missense_variant	NSP14	I42V
21762	C	T	missense_variant	S	A67V
21764	ATACATG	A	disruptive_inframe_deletion	S	HV69-70del
21846	C	T	missense_variant	S	T95I
21986	GGTGTTTATT	G	disruptive_inframe_deletion	S	GVYY142-145D
22193	AATT	A	disruptive_inframe_deletion	S	NL211-212I
22204	T	TGAGCCAGAA	disruptive_inframe_insertion	S	RD214-215EPE
22578	G	A	missense_variant	S	G339D
22672	TTC	TCT	missense_variant	S	S371L
22679	T	C	missense_variant	S	S373P
22686	C	T	missense_variant	S	S375F
22813	G	T	missense_variant	S	K417N
22882	T	G	missense_variant	S	N440K
22898	G	A	missense_variant	S	G446S
22992	G	A	missense_variant	S	S477N
22995	C	A	missense_variant	S	T478K
23013	A	C	missense_variant	S	E484A
23040	A	G	missense_variant	S	Q493R
23048	G	A	missense_variant	S	G496S
23055	A	G	missense_variant	S	Q498R
23063	A	T	missense_variant	S	N501Y
23075	T	C	missense_variant	S	Y505H
23202	C	A	missense_variant	S	T547K
23403	A	G	missense_variant	S	D614G
23525	C	T	missense_variant	S	H655Y
23599	T	G	missense_variant	S	N679K
23604	C	A	missense_variant	S	P681H
23854	C	A	missense_variant	S	N764K
23948	G	T	missense_variant	S	D796Y
24130	C	A	missense_variant	S	N856K
24424	A	T	missense_variant	S	Q954H
24469	T	A	missense_variant	S	N969K
24503	C	T	missense_variant	S	L981F
25000	C	T	synonymous_variant	S	D1146D
25584	C	T	synonymous_variant	ORF3a	T64T
26270	C	T	missense_variant	E	T9I
26530	A	G	missense_variant	M	D3G
26577	C	G	missense_variant	M	Q19E
26709	G	A	missense_variant	M	A63T
27259	A	C	synonymous_variant	ORF6	R20R
27807	C	T	synonymous_variant	ORF7b	L18L
28271	A	T	upstream_gene_variant	N	
28311	C	T	missense_variant	N	P13L
28361	GGAGAACGCA	G	disruptive_inframe_deletion	N	ERS31-33del
28880	AGGG	AAAC	missense_variant	N	RG203-204KR
29645	G	T	missense_variant	ORF10	V30L