Table S1: Determination of clade, variant and lineage by Audacity*instant* and Nextclade.

ID	**NCBI acc. No.**	**GISAID acc. No.**	**Clade[1]**	**Clade[2]**	**Lineage[1]**	**Lineage[2]**	**Variant[1]**	**Variant[2]**
EGY1[*]	QQ346382	EPI_ISL_16713842	GR	20B	C.36.3	B.1.1	Unassigned	Unassigned
EGY2[#]	QQ347969	EPI_ISL_16743975	GR	20D	C.36	C.36.3	Unassigned	Unassigned
EGY3[#]	QQ346383	EPI_ISL_16713843	GR	20I	C.36.3	B.1.1.7	Unassigned	Alpha[**]
EGY4[#]	QQ346384	EPI_ISL_16713844	GR	20D	C.36.3	C.36.3	Unassigned	Unassigned
EGY5[$]	QQ346385	EPI_ISL_16713845	GR	20I	C.36	B.1.1.7	Unassigned	Alpha
EGY6[#]	QQ346386	EPI_ISL_16713846	GR	20I	C.36	B.1.1.7	Unassigned	Alpha
EGY7[*]	QQ346387	EPI_ISL_16713847	GR	20D	C.36	C.36.3	Unassigned	Unassigned
EGY8[#]	QQ346388	EPI_ISL_16713848	GR	20D	C.36	C.36.3	Unassigned	Unassigned
EGY9[#]	QQ346389	EPI_ISL_16713849	GR	20I	C.36	B.1.1.7	Unassigned	Alpha
EGY10[#]	QQ346390	EPI_ISL_16713850	G	20D	B.1	C.36.3	Unassigned	Unassigned
EGY11[#]	QQ346391	EPI_ISL_16713851	GR	20D	C.36.3	C.36.3	Unassigned	Unassigned
EGY12[#]	QQ346392	EPI_ISL_16713852	GR	20I	C.36	B.1.1.7	Unassigned	Alpha
EGY13[*]	QQ346393	EPI_ISL_16713853	GRY	20D	B.1.1.7	C.36.3	Alpha	Unassigned
EGY14[$]	QQ346394	EPI_ISL_16713854	GRY	20D	B.1.1.7	C.36.3	Alpha	Unassigned
EGY15[#]	QQ346395	EPI_ISL_16743976	GR	20I	C.36.3	B.1.1.7	Unassigned	Alpha
EGY16[#]	QQ346396	EPI_ISL_16713855	GR	20I	C.36.3	B.1.1.7	Unassigned	Alpha
EGY17[#]	QQ346397	EPI_ISL_16713856	GRY	20I	B.1.1.7	B.1.1.7	Alpha	Alpha
EGY18[#]	QQ346398	EPI_ISL_16713857	G	20I	None	B.1.1.7	Unassigned	Alpha
EGY19[#]	QQ346399	EPI_ISL_16713858	G	20D	B.1.1.7	C.36.3	Alpha	Unassigned
EGY20[*]	QQ346400	EPI_ISL_16713859	GRY	20D	B.1.1.7	C.36.3	Alpha	Unassigned
EGY21[#]	QQ346401	EPI_ISL_16713860	GRY	20D	B.1.1.7	C.36.3	Alpha	Unassigned
EGY22[#]	QQ346402	EPI_ISL_16713861	GRY	20D	B.1.1.7	C.36.3	Alpha	Unassigned
EGY23[#]	QQ346403	EPI_ISL_16713862	G	20D	None	C.36.3	Unassigned	Unassigned

[#]Old: This variant last occurred >100 days ago. [*]Recent (not ranked): This variant was detected in the past 100 days but has not shown signs of spreading in the past 30 days. [$]Rare: This variant only occurred 0 or 1 times. ** Variants of concern (VOC) according to WHO. [1] by to Audacity*instant* (v.5.0.1) through GISAID, [2] by Nextclade. Last accessed 28/2/2023.

Table S2: Count of detected mutation per isolate.

NCBI acc. No.	**GISAID acc. No.**	**Detected Mutations##**	**N**
QQ346382*	EPI_ISL_16713842	D614G, Q677H	**2**
QQ346387*	EPI_ISL_16713847	D614G, Q677H	**2**
QQ346400*	EPI_ISL_16713859	D614G, Q677H	**2**
QQ347969#	EPI_ISL_16743975	L452R, D614G, Q677H	**3**
QQ346388#	EPI_ISL_16713848	L452R, D614G, Q677H	**3**
QQ346384#	EPI_ISL_16713844	L452R, D614G, Q677H	**3**
QQ346390#	EPI_ISL_16713850	L452R, D614G, Q677H	**3**
QQ346391#	EPI_ISL_16713851	L452R, D614G, Q677H	**3**
QQ346393*	EPI_ISL_16713853	D614G, Y660H, Q677H	**3**
QQ346399#	EPI_ISL_16713858	L452R, D614G, Q677H, I720N	**4**
QQ346401#	EPI_ISL_16713860	L452R, D614G, Q677H, T747P	**4**
QQ346403#	EPI_ISL_16713862	L452R, D614G, Y660H, Q677H	**4**
QQ346386#	EPI_ISL_16713846	N501Y, A570D, D614G, P681H, T716I	**5**
QQ346396#	EPI_ISL_16713855	N501Y, A570D, D614G, P681H, T716I	**5**
QQ346394$	EPI_ISL_16713854	L452R, D614G, Q677H, T719S, S721T	**5**
QQ346402#	EPI_ISL_16713861	L452R, D614G, Q677H, T747P, S750K	**5**
QQ346385$	EPI_ISL_16713845	V445G, N501Y, A570D, D614G, P681H, T716I	**6**
QQ346392#	EPI_ISL_16713852	N501Y, A570D, D614G, D627N, P681H, T716I	**6**
QQ346383#	EPI_ISL_16713843	N501Y, A570D, D614G, D627N, P681H, T716I	**6**
QQ346398#	EPI_ISL_16713857	N501Y, A570D, D614G, D627N, P681H, T716I	**6**
QQ346389#	EPI_ISL_16713849	N501Y, A570D, D614G, D627N, P681H, T716I, T747P	**7**
QQ346395#	EPI_ISL_16743976	N501Y, R567K, A570D, D614G, D627N, P681H, T716I	**7**
QQ346397#	EPI_ISL_16713856	N501Y, R567K, A570D, D614G, E619K, D627N, P681H, T716I	**8**

[#]Old: This variant last occurred >100 days ago. [*]Recent (not ranked): This variant was detected in the past 100 days but has not shown signs of spreading in the past 30 days. [$]Rare: This variant only occurred 0 or 1 times. N: number of mutations per isolate. ## Detection of mutations was done by CoVsurver online tool endorsed by GISAID.

Table S3: Mutation frequency among the 23 partial spike sequences.

Mutation	**Old (n= 17)**	**Recent (n= 4)**	**Rare (n= 2)**	**Total (N= 23)**	**Percent (%)**	^{MC}p**-value**
D614G	17	4	2	23	100.0%	1.000
Q677H	9	4	1	14	61.0%	0.578
L452R	9	0	1	10	43.5%	0.28
N501Y	8	0	1	9	39.0%	0.471
A570D	8	0	1	9	39.0%	0.506
P681H	8	0	1	9	39.0%	0.497
T716I	8	0	1	9	39.0%	0.481
D627N	6	0	0	6	26.0%	0.301
T747P	3	0	0	3	13.0%	0.727
R567K	2	0	0	2	8.7%	1.000
Y660H	1	1	0	2	8.7%	0.439
V445G	0	0	1	1	4.3%	0.089
E619K	1	0	0	1	4.3%	1.000
T719S	0	0	1	1	4.3%	1.000
I720N	1	0	0	1	4.3%	0.091
S721T	0	0	1	1	4.3%	0.082
S750K	1	0	0	1	4.3%	1.000

According to CoVsurver tool, a total of 17 mutations with a total frequency of 102 were detected among our 23 sequences. ^{MC}p: obtained by chi-square test with Monto Carlo simulation.

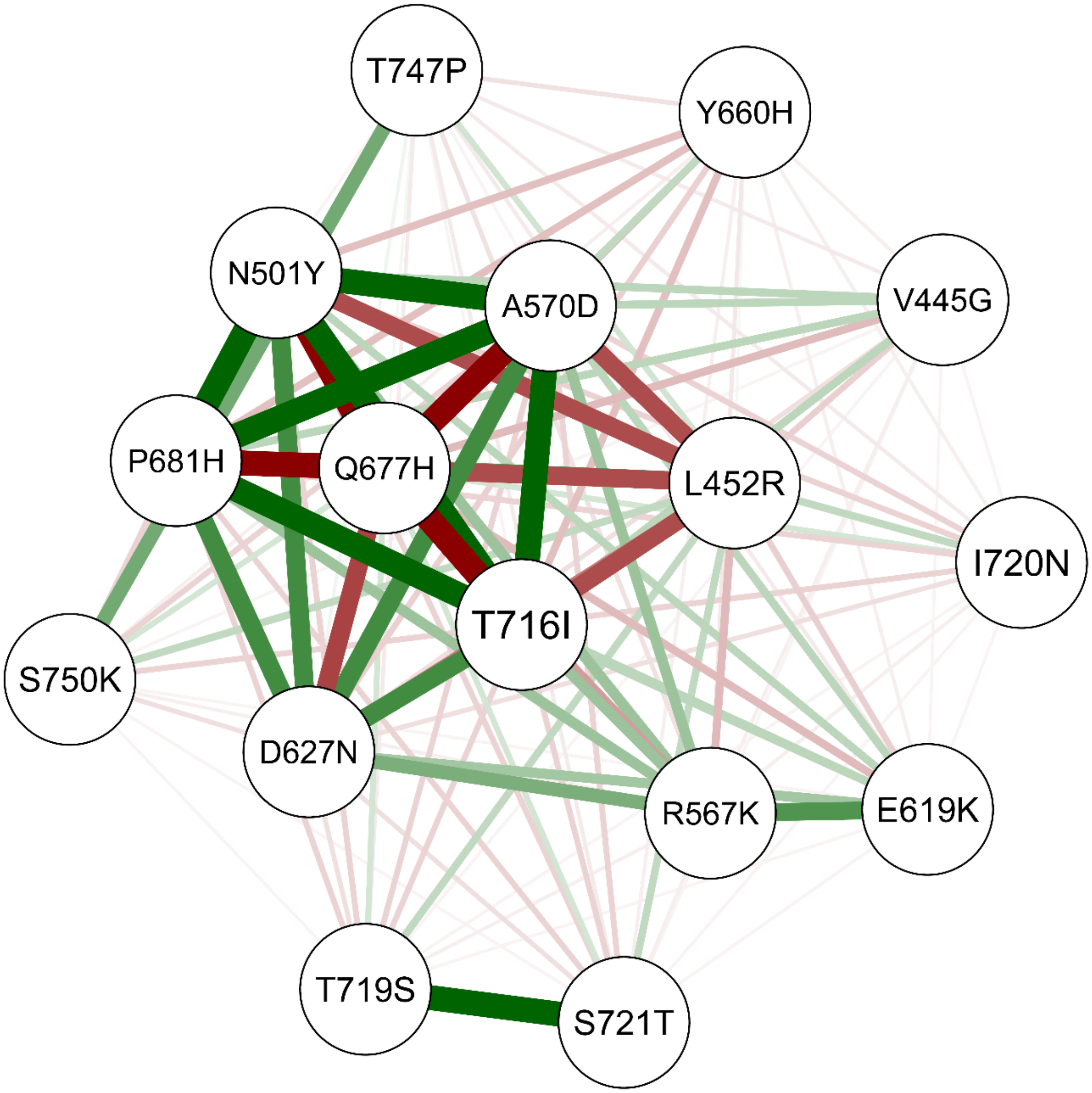

Figure S1: Network graph based on Spearman's correlation matrix between detected mutations.

The green lines represent positive correlation coefficients while the red lines represent negative correlation coefficients. The more intense color indicates a higher correlation while faded colors describe low or no correlation.