Surveillance report

Surveillance generated by nf-ncov-voc for Omicron variant

Date

This report is generated on 2023-03-04 using 459574 number of genomes collected between 2020-02-25 and 2023-02-16

Pango Lineages

Pango Lineages in this report ['BA.1', 'BA.1.1', 'BA.1.1.1', 'BA.1.1.10', 'BA.1.1.11', 'BA.1.1.13', 'BA.1.1.14', 'BA.1.1.15', 'BA.1.1.16', 'BA.1.1.17', 'BA.1.1.18', 'BA.1.1.2', 'BA.1.1.3', 'BA.1.1.4', 'BA.1.1.6', 'BA.1.1.7', 'BA.1.1.8', 'BA.1.1.9', 'BA.1.10', 'BA.1.12', 'BA.1.13', 'BA.1.13.1', 'BA.1.14', 'BA.1.14.1', 'BA.1.14.2', 'BA.1.15', 'BA.1.15.1', 'BA.1.15.2', 'BA.1.15.3', 'BA.1.16', 'BA.1.17', 'BA.1.17.1', 'BA.1.17.2', 'BA.1.18', 'BA.1.19', 'BA.1.20', 'BA.1.21', 'BA.1.3', 'BA.1.5', 'BA.1.6', 'BA.1.7', 'BA.1.8', 'BA.1.9', 'BA.2', 'BA.2.1', 'BA.2.10', 'BA.2.10.1', 'BA.2.10.3', 'BA.2.11', 'BA.2.12', 'BA.2.12.1', 'BA.2.12.2', 'BA.2.13', 'BA.2.13.1', 'BA.2.14', 'BA.2.15', 'BA.2.16', 'BA.2.17', 'BA.2.18', 'BA.2.2', 'BA.2.2.1', 'BA.2.20', 'BA.2.21', 'BA.2.22', 'BA.2.23', 'BA.2.23.1', 'BA.2.24', 'BA.2.25', 'BA.2.26', 'BA.2.27', 'BA.2.29', 'BA.2.3', 'BA.2.3.1', 'BA.2.3.10', 'BA.2.3.11', 'BA.2.3.12', 'BA.2.3.13', 'BA.2.3.14', 'BA.2.3.15', 'BA.2.3.16', 'BA.2.3.17', 'BA.2.3.2', 'BA.2.3.20', 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'CD.1', 'CE.1', 'CG.1', 'CH.1', 'CH.1.1', 'CH.1.1.1', 'CH.1.1.2', 'CH.2', 'CJ.1', 'CK.1', 'CK.2', 'CK.2.1', 'CK.2.1.1', 'CK.3', 'CL.1', 'CM.1', 'CM.2', 'CM.3', 'CM.4', 'CM.5', 'CM.8', 'CM.8.1', 'CM.9', 'CN.1', 'CP.1', 'CQ.1', 'CQ.1.1', 'CQ.2', 'CR.1', 'CR.1.1', 'CR.1.2', 'CR.2', 'CV.1', 'DB.1', 'DC.1', 'DE.1', 'DE.2', 'DF.1', 'DG.1', 'XAC', 'XAE', 'XAF', 'XAG', 'XAM', 'XAN', 'XAP', 'XAQ', 'XAS', 'XAZ', 'XBB', 'XBB.1', 'XBB.1.1', 'XBB.1.3', 'XBB.1.4', 'XBB.1.5', 'XBB.2', 'XBB.3', 'XBB.4', 'XBD', 'XBE', 'XBF', 'XBH', 'XE', 'XM', 'XN', 'XQ', 'XW', 'XZ']

Indicator

This table contains key indicators identified

Indicator	Sub-categories from POKAY	Mutations
Transmissibility between humans	transmissibility	D614G, L452R, N440K
Infection Severity	ACE2 receptor binding affinity, viral load, outcome hazard ratio	A701V, D215G, D253G, D614G, E484R, F490S, F490Y, G339D, H655Y, K417N, K417T, K458R, L18F, L452M, L452Q, L452R, L5F, N440K, N448S, N460K, N501Y, P681H, Q677H, R346T, S13I, S477N, S494P, T1027I, T716I, T95I
Immunity after natural infection	convalescent plasma escape, reinfection, humoral response durability	A260T, A260V, A623T, A831V, D215G, D614G, D796H, E484A, F486S, F490L, F490S, G446D, H146del, K147E, K147N, K150E, K150R, K417N, K444N, K444R, K444T, L18F, L452R, L5F, N450D, N450Y, N501Y, P1162S, P25L, Q1208H, Q14H, Q493R, Q677H, S477N, S494P, T604I, W64R, Y248H
Vaccines	vaccine neutralization efficacy	D614G, K417N, L452R, N501Y, P681H
Monoclonal antibodies	monoclonal antibody serial passage escape, pharmaceutical effectiveness	C15F, D253G, D420N, D80N, E484A, E484R, E484T, E484V, F456V, F486A, F486I, F486L, F486P, F486S, F486V, F490L, F490S, F490V, G142D, G252D, G257S, G446D, K147E, K147Q, K417H, K417I, K417N, K417T, K444R, L244S, L452R, N440K, N450D, N450Y, N460I, N460K, N460S, N460Y, N487K, N501Y, P139S, P251L, Q493R, Q779K, R346I, R346K, R346S, S255F, S373P, S443F, S494P, V445A
Diagnostics	clinical indicators, antigenic test failure, symptom prevalence	

Mutation Significance

This table contains key functional impacts of mutations identified

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
L452Q	ACE2 receptor binding affinity	Experimentally, ACE2 binding affinity increased 0.07 fold	BA.2.38, BG.2, BG.4, BA.5.2.28, BA.2.12.1, BA.2.12, BG.6, BG.5, BH.1	Starr et al. (2020)	13079	T	A	0.97
L452Q	gene expression increase	Experimentally, Spike gene expression increased 0.27 fold	BA.2.38, BG.2, BG.4, BA.5.2.28, BA.2.12.1, BA.2.12, BG.6, BG.5, BH.1	Starr et al. (2020)	13079	T	A	0.97
K150E	convalescent plasma escape	Strong positive selection (up to 40% of supernatant sequences) under three rounds of COV47 convalescent plasma passage	CL.1	Weisblum et al. (2020)	12	A	G	1.0
F490L	antibody epitope effects	Resistent to some neutralizing antibodies: mAbs X593, 261-262, H4, and P2B-2F6	BL.1.3	Li et al. (2020)	1	T	C	1.0
F490L	antibody epitope effects	Complete loss of binding in ELISA by the variant against monoclonal antibody ab8	BL.1.3	Sun et al. (2021)	1	T	C	1.0
F490L	convalescent plasma escape	Resistant to a pool of 10 convalescent sera (but less than 4x, a typical threshold for definition of escape) Resistent to 3 individual sera at >4x	BL.1.3	Li et al. (2020)	1	T	C	1.0
F490L	monoclonal antibody serial passage escape	Positive selection (up to 23% of supernatant sequences) after C121 monoclonal antibody assay	BL.1.3	Weisblum et al. (2020)	1	T	C	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
T95I	ACE2 receptor binding affinity	Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant showed a 1.33x decrease in binding (KD) relative to D614G.	BA.1.13.1, BA.1.1.7, BA.1.1.11, BA.1.1.18, BA.1.1.4, BA.1.15.3, BA.1.7, BA.1.8, BA.1.14, BA.1.15.1, BA.1.1.6, BA.1.1.14, BA.1.1.15, BA.1.14.2, BA.1.15, BA.1.1.2, BA.5.2.28, BA.4.6.3, BA.1.5, BA.1.1.3, BD.1, BA.1.13, BA.1.1, BA.1.1.17, XM, BA.1.17.1, BA.1.1.13, BA.1.18, BA.1.3, BA.1.17, BC.2, BQ.1.11, BA.1.1.9, BA.1.15.2, BA.1.21, BA.1.9, BQ.1.25, BA.1.1.16, BA.1.10, CH.1.1, BA.1.16, BA.1.17.2, BA.1.1.8, BA.1.1.10, BA.1, BA.1.12, BA.1.1.1, BA.1.20, BA.1.14.1, BA.1.19, BA.1.6	Gong et al. (2021)	64136	C	T	0.99

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
T95I	convalescent plasma binding	No change in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset.	BA.1.13.1, BA.1.1.7, BA.1.1.11, BA.1.1.18, BA.1.1.4, BA.1.15.3, BA.1.7, BA.1.8, BA.1.14, BA.1.15.1, BA.1.1.6, BA.1.1.14, BA.1.1.15, BA.1.14.2, BA.1.15, BA.1.1.2, BA.5.2.28, BA.4.6.3, BA.1.5, BA.1.1.3, BD.1, BA.1.13, BA.1.1, BA.1.1.17, XM, BA.1.17.1, BA.1.1.13, BA.1.18, BA.1.3, BA.1.17, BC.2, BQ.1.11, BA.1.1.9, BA.1.15.2, BA.1.21, BA.1.9, BQ.1.25, BA.1.1.16, BA.1.10, CH.1.1, BA.1.16, BA.1.17.2, BA.1.1.8, BA.1.1.10, BA.1, BA.1.12, BA.1.1.1, BA.1.20, BA.1.14.1, BA.1.19, BA.1.6	Gong et al. (2021)	64136	C	T	0.99

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
T95I	vaccinee plasma binding	1.16x increase in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in previously non-seroconverted subjects. 1.02x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in post-infection vaccinees.	BA.1.13.1, BA.1.1.7, BA.1.1.11, BA.1.1.18, BA.1.1.4, BA.1.15.3, BA.1.7, BA.1.8, BA.1.14, BA.1.15.1, BA.1.1.6, BA.1.1.14, BA.1.1.15, BA.1.14.2, BA.1.15, BA.1.1.2, BA.5.2.28, BA.4.6.3, BA.1.5, BA.1.1.3, BD.1, BA.1.13, BA.1.1, BA.1.1.17, XM, BA.1.17.1, BA.1.1.13, BA.1.18, BA.1.3, BA.1.17, BC.2, BQ.1.11, BA.1.1.9, BA.1.15.2, BA.1.21, BA.1.9, BQ.1.25, BA.1.1.16, BA.1.10, CH.1.1, BA.1.16, BA.1.17.2, BA.1.1.8, BA.1.1.10, BA.1, BA.1.12, BA.1.1.1, BA.1.20, BA.1.14.1, BA.1.19, BA.1.6	Gong et al. (2021)	64136	C	T	0.99
N440K	ACE2 receptor binding affinity	Experimentally, ACE2 binding affinity increased 0.07 fold	BF.1, BA.2.56, BQ.1.1.1, BA.2.3.20, BF.1.1	Starr et al. (2020)	1054	CAAT	CAAG,TAAG	0.96
N440K	antibody epitope effects	N501Y substitution decreased the neutralizing and binding activities of CB6 and increased that of BD-23	BF.1, BA.2.56, BQ.1.1.1, BA.2.3.20, BF.1.1	Cheng et al. (2021)	1054	CAAT	CAAG,TAAG	0.96
N440K	antibody epitope effects	Ablates binding by class 3 mAbs such as C135 that do not directly interfere with ACE2 binding, but clonal somatic mutations of memory B cells at 6.2 months (evolving humoral immune response) show pronounced increase in binding to the variant.	BF.1, BA.2.56, BQ.1.1.1, BA.2.3.20, BF.1.1	Gaebler et al. (2021)	1054	CAAT	CAAG,TAAG	0.96
N440K	antibody epitope effects	Greater than 10-fold reduction of binding effeiency vs wild type for mAb LY-CoV555. Abolishes binding of mAb ADG-1.	BF.1, BA.2.56, BQ.1.1.1, BA.2.3.20, BF.1.1	Rappazzo et al. (2021)	1054	CAAT	CAAG,TAAG	0.96
N440K	antibody epitope effects	Resistent to class 3 antibodies (i.e. Abs that do not directly interfere with ACE2 binding).	BF.1, BA.2.56, BQ.1.1.1, BA.2.3.20, BF.1.1	Wang et al. (2021)	1054	CAAT	CAAG,TAAG	0.96
N440K	monoclonal antibody serial passage escape	Class 3 antibody C669 mildly selected for the emergence of the N440K mutation in vitro (in contrast to N440H which caused mild escape in Class 1/2 mAb C653).	BF.1, BA.2.56, BQ.1.1.1, BA.2.3.20, BF.1.1	Wang et al. (2021)	1054	CAAT	CAAG,TAAG	0.96

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
N440K	monoclonal antibody serial passage escape	Positive selection (up to 45% of supernatant sequences) under two rounds of C135 monoclonal antibody passage, eliminated in subsequent passages	BF.1, BA.2.56, BQ.1.1.1, BA.2.3.20, BF.1.1	Weisblum et al. (2020)	1054	CAAT	CAAG,TAAG	0.96
N440K	reinfection	A 47yo Indian male was reinfected with B.1.36 lineage virus in September 2020 after infection with genetically distinct B.1.36 virus in July, with negative PCR tests in between. While the forst episode was asymptomatic, the second included fever, cough, and malaise. The second case additionally contained stopgain ORF3a:E261*	BF.1, BA.2.56, BQ.1.1.1, BA.2.3.20, BF.1.1	Rani et al. (2021)	1054	CAAT	CAAG,TAAG	0.96
N440K	transmissibility	The N440K variant produced ten times higher infectious viral titers than a prevalent A2a strain, and over 1000 folds higher titers than a much less prevalent A3i strain prototype in Caco2 cells. Interestingly, A3i strain showed the highest viral RNA levels, but the lowest infectious titers in the culture supernatants, indicating the absence of correlation between the RNA content and the infectivity of the sample.	BF.1, BA.2.56, BQ.1.1.1, BA.2.3.20, BF.1.1	Tandel et al. (2021)	1054	CAAT	CAAG,TAAG	0.96

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
N440K	ACE2 receptor binding affinity	Experimentally, ACE2 binding affinity increased 0.07 fold	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BU.2, BA.5.2.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, CA.5, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.2.76, BA.5.2.6, BT.1, XAE, BG.2, BA.1.18, BF.25,	Starr et al. (2020)	186826	T	G,GCTC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
N440K	antibody epitope effects	N501Y substitution decreased the neutralizing and binding activities of CB6 and increased that of BD-23	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BU.2, BA.5.2.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, CA.5, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.2.76, BA.5.2.6, BT.1, XAE, BG.2, BA.1.18, BF.25,	Cheng et al. (2021)	186826	T	G,GCTC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
N440K	antibody epitope effects	Ablates binding by class 3 mAbs such as C135 that do not directly interfere with ACE2 binding, but clonal somatic mutations of memory B cells at 6.2 months (evolving humoral immune response) show pronounced increase in binding to the variant.	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BU.2, BA.5.2.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, CA.5, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.2.76, BA.5.2.6, BT.1, XAE, BG.2, BA.1.18, BF.25,	Gaebler et al. (2021)	186826	T	G,GCTC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
N440K	antibody epitope effects	Greater than 10-fold reduction of binding effeiency vs wild type for mAb LY-CoV555. Abolishes binding of mAb ADG-1.	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BU.2, BA.5.2.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, CA.5, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.2.76, BA.5.2.6, BT.1, XAE, BG.2, BA.1.18, BF.25,	Rappazzo et al. (2021)	186826	T	G,GCTC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
N440K	antibody epitope effects	Resistent to class 3 antibodies (i.e. Abs that do not directly interfere with ACE2 binding).	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BU.2, BA.5.2.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, CA.5, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.2.76, BA.5.2.6, BT.1, XAE, BG.2, BA.1.18, BF.25,	Wang et al. (2021)	186826	T	G,GCTC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
N440K	monoclonal antibody serial passage escape	Class 3 antibody C669 mildly selected for the emergence of the N440K mutation in vitro (in contrast to N440H which caused mild escape in Class 1/2 mAb C653).	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BU.2, BA.5.2.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, CA.5, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.2.76, BA.5.2.6, BT.1, XAE, BG.2, BA.1.18, BF.25,	Wang et al. (2021)	186826	T	G,GCTC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
N440K	monoclonal antibody serial passage escape	Positive selection (up to 45% of supernatant sequences) under two rounds of C135 monoclonal antibody passage, eliminated in subsequent passages	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BU.2, BA.5.2.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, CA.5, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.2.76, BA.5.2.6, BT.1, XAE, BG.2, BA.1.18, BF.25,	Weisblum et al. (2020)	186826	T	G,GCTC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
N440K	reinfection	A 47yo Indian male was reinfected with B.1.36 lineage virus in September 2020 after infection with genetically distinct B.1.36 virus in July, with negative PCR tests in between. While the forst episode was asymptomatic, the second included fever, cough, and malaise. The second case additionally contained stopgain ORF3a:E261*	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BA.5.2.2, BU.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.2.76, BA.5.2.6, BT.1, XAE, BG.2, BA.1.1.18, BA.2.25, BY.1.1.1,	Rani et al. (2021)	186804	T	G,GCTC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
N440K	transmissibility	The N440K variant produced ten times higher infectious viral titers than a prevalent A2a strain, and over 1000 folds higher titers than a much less prevalent A3i strain prototype in Caco2 cells. Interestingly, A3i strain showed the highest viral RNA levels, but the lowest infectious titers in the culture supernatants, indicating the absence of correlation between the RNA content and the infectivity of the sample.	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BU.2, BA.5.2.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, CA.5, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.2.76, BA.5.2.6, BT.1, XAE, BG.2, BA.1.18, BF.25,	Tandel et al. (2021)	186826	T	G,GCTC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
N440K	ACE2 receptor binding affinity	Experimentally, ACE2 binding affinity increased 0.07 fold	BA.2.36	Starr et al. (2020)	59	TCTT	GCTT	0.98
N440K	antibody epitope effects	N501Y substitution decreased the neutralizing and binding activities of CB6 and increased that of BD-23	BA.2.36	Cheng et al. (2021)	59	TCTT	GCTT	0.98
N440K	antibody epitope effects	Ablates binding by class 3 mAbs such as C135 that do not directly interfere with ACE2 binding, but clonal somatic mutations of memory B cells at 6.2 months (evolving humoral immune response) show pronounced increase in binding to the variant.	BA.2.36	Gaebler et al. (2021)	59	TCTT	GCTT	0.98
N440K	antibody epitope effects	Greater than 10-fold reduction of binding effeiency vs wild type for mAb LY-CoV555. Abolishes binding of mAb ADG-1.	BA.2.36	Rappazzo et al. (2021)	59	TCTT	GCTT	0.98
N440K	antibody epitope effects	Resistent to class 3 antibodies (i.e. Abs that do not directly interfere with ACE2 binding).	BA.2.36	Wang et al. (2021)	59	TCTT	GCTT	0.98
N440K	monoclonal antibody serial passage escape	Class 3 antibody C669 mildly selected for the emergence of the N440K mutation in vitro (in contrast to N440H which caused mild escape in Class 1/2 mAb C653).	BA.2.36	Wang et al. (2021)	59	TCTT	GCTT	0.98
N440K	monoclonal antibody serial passage escape	Positive selection (up to 45% of supernatant sequences) under two rounds of C135 monoclonal antibody passage, eliminated in subsequent passages	BA.2.36	Weisblum et al. (2020)	59	TCTT	GCTT	0.98
N440K	reinfection	A 47yo Indian male was reinfected with B.1.36 lineage virus in September 2020 after infection with genetically distinct B.1.36 virus in July, with negative PCR tests in between. While the forst episode was asymptomatic, the second included fever, cough, and malaise. The second case additionally contained stopgain ORF3a:E261*	BA.2.36	Rani et al. (2021)	59	TCTT	GCTT	0.98
N440K	transmissibility	The N440K variant produced ten times higher infectious viral titers than a prevalent A2a strain, and over 1000 folds higher titers than a much less prevalent A3i strain prototype in Caco2 cells. Interestingly, A3i strain showed the highest viral RNA levels, but the lowest infectious titers in the culture supernatants, indicating the absence of correlation between the RNA content and the infectivity of the sample.	BA.2.36	Tandel et al. (2021)	59	TCTT	GCTT	0.98

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
K417N	ACE2 receptor binding affinity	The K417N mutation decreased the affinity extasciitilde4 fold, mainly by decreasing the k(on) but also by increasing the k(off) as measured by surface plasmon resonance.	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BA.5.2.2, BU.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, CA.5, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.64, BA.1.6, BA.2.76, BA.5.2.6, XAE, BT.1, BG.2, BA.1.1.18, BF.25, BV.1.1, BA.1.7,	Barton et al. (2021)	187577	G	T,TATC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
K417N	ACE2 receptor binding affinity	This combination showed extasciitilde3x increase binding to ACE2 vs wild type, about half that of the B.1.1.7 lineage, suggesting that the K417N mutation is slightly detrimental to ACE2 binding, probably as a result of disrupting the salt bridge formed with ACE2 residue D30	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BA.5.2.2, BU.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, CA.5, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.64, BA.1.6, BA.2.76, BA.5.2.6, XAE, BT.1, BG.2, BA.1.1.18, BF.25, BX.1.1, BA.1.7,	Collier et al. (2021)	187577	G	T,TATC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
K417N	ACE2 receptor binding affinity	Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant showed a 1.5x decrease in binding (KD) relative to D614G.	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BA.5.2.2, BU.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.64, BA.1.6, BA.2.76, BA.5.2.6, XAE, BT.1, BG.2, BA.1.1.18, BF.25, BA.1.1, BA.1.7,	Gong et al. (2021)	187555	G	T,TATC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
K417N	ACE2 receptor binding affinity	RBD containing the N501Y mutation results in 9-fold stronger binding to the hACE2 receptor than wild type RBD. The E484K mutation does not significantly influence the affinity for the receptor, while K417N attenuates affinity. As a result, RBD from B.1.351 containing all three mutations binds 3-fold stronger to hACE2 than wild type RBD but 3-fold weaker than N501Y.	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BA.5.2.2, BU.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, CA.5, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.64, BA.1.6, BA.2.76, BA.5.2.6, XAE, BT.1, BG.2, BA.1.1.18, BF.25, BV.1.1, BA.1.7,	Laffeber et al. (2021)	187577	G	T,TATC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
K417N	ACE2 receptor binding affinity	Studying the key covariants in lineage of concern 501Y.V2, observed about 2-fold increase in ACE2 binding vs wildtype, but greatly decreased mAb binding, suggesting evolutionary optimum tension between immune evasion and ACE2 binding affinity as the N501Y variant alone has 10x increase in affinity but no effect on tested mAb binding.	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BA.5.2.2, BU.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, CA.5, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.64, BA.1.6, BA.2.76, BA.5.2.6, XAE, BT.1, BG.2, BA.1.1.18, BF.25, BX.1.1, BA.1.7,	Liu et al. (2021)	187577	G	T,TATC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
K417N	ACE2 receptor binding affinity	Using Mircoscale Thermopheresis, the B.1.351 variant harboring three mutations, binds ACE2 at nearly five-fold greater affinity than the original SARS-COV-2 RBD (Kd 87.6, vs 402.5 nM).	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BA.5.2.2, BU.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, CA.5, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.64, BA.1.6, BA.2.76, BA.5.2.6, XAE, BT.1, BG.2, BA.1.1.18, BF.25, BA.1.1, BA.1.7,	Ramanathan et al. (2021)	187577	G	T,TATC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
K417N	ACE2 receptor binding affinity	Reported 3-fold decrease in affinity compared to wild-type RBD on the cell surface (Kd	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BA.5.2.2, BU.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, CA.5, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.64, BA.1.6, BA.2.76, BA.5.2.6, XAE, BT.1, BG.2, BA.1.1.18, BF.25, BA.1.1, BA.1.7,	Tian et al. (2021)	187577	G	T,TATC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
K417N	ACE2 receptor binding affinity	Reported slight increase in affinity compared to wild-type RBD on the cell surface (Kd	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BA.5.2.2, BU.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, CA.5, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.64, BA.1.6, BA.2.76, BA.5.2.6, XAE, BT.1, BG.2, BA.1.1.18, BF.25, BA.1.1, BA.1.7,	Tian et al. (2021)	187577	G	T,TATC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
K417N	ACE2 receptor binding affinity	The affinity of ACE2 for this mutation combination was twice as high as for wild type. Having in mind that the affinity of SARS-CoV-2 for ACE2 is only 4-fold higher compared to SARS-CoV-1, this factor of 2 is expected to be biologically significant.	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BA.5.2.2, BU.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, CA.5, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.64, BA.1.6, BA.2.76, BA.5.2.6, XAE, BT.1, BG.2, BA.1.1.18, BF.25, BX.1.1, BA.1.7,	Vogel et al. (2021)	187577	G	T,TATC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
K417N	antibody epitope effects	>20% (ELISA significance threshold) drop in antibody binding (ELISA) by this variant against IgG1 monoclonal antibody ab1.	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BA.5.2.2, BU.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, CA.5, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.64, BA.1.6, BA.2.76, BA.5.2.6, XAE, BT.1, BG.2, BA.1.1.18, BF.25, BV.1.1, BA.1.7,	Sun et al. (2021)	187577	G	T,TATC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
K417N	antibody epitope effects	5 antibodies tested were less potent against K417N by ten-fold or more (class 1 mAbs)	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BA.5.2.2, BU.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, CA.5, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.64, BA.1.6, BA.2.76, BA.5.2.6, XAE, BT.1, BG.2, BA.1.1.18, BF.25, BA.1.1, BA.1.7,	Wang et al. (2021)	187577	G	T,TATC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
K417N	antibody epitope effects	Pseudotyped virus model ablates binding by RBD-directed mAbs CB6 and 910-30 (targeting the inner side of the RBD). Pseudotyped virus model impairs binding by RBD-directed mAbs 4-20 and REGN10933.	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BA.5.2.2, BU.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, CA.5, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.64, BA.1.6, BA.2.76, BA.5.2.6, XAE, BT.1, BG.2, BA.1.1.18, BF.25, BX.1.1, BA.1.7,	Wang et al. (2021)	187577	G	T,TATC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
K417N	convalescent plasma binding	2.16x increase in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset.	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BA.5.2.2, BU.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.64, BA.1.6, BA.2.76, BA.5.2.6, XAE, BT.1, BG.2, BA.1.1.18, BF.25, BA.1.1, BA.1.7,	Gong et al. (2021)	187555	G	T,TATC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
K417N	convalescent plasma escape	The 501Y.V2 to first wave IC50 ratio ranged from 6 to 200-fold. Averaging across all 7 participant convalescent sera highlighted the dramatic decrease in sensitivity to neutralization of authentic 501Y.V2 variants. PG: I'm purposefully ignoring D614G and A701V as contributors	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BA.5.2.2, BU.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, CA.5, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.64, BA.1.6, BA.2.76, BA.5.2.6, XAE, BT.1, BG.2, BA.1.1.18, BF.25, BX.1.1, BA.1.7,	Cele et al. (2021)	187577	G	T,TATC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
K417N	convalescent plasma escape	In 19 convalescent human sera extasciitilde1mo post infection, Two-tailed Wilcoxon matched-pairs signed-rank test shows mild resistence P	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BA.5.2.2, BU.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, CA.5, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.64, BA.1.6, BA.2.76, BA.5.2.6, XAE, BT.1, BG.2, BA.1.1.18, BF.25, BV.1.1, BA.1.7,	Chen et al. (2021)	187577	G	T,TATC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
K417N	convalescent plasma escape	27% of 44 early pandemic exposure convalescent plasma/sera lose all activity against a RBD triple mutant pseudovirus (RBD mutatants of the 501Y.V2 "South African" lineage), while only 23% retained high titres	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BA.5.2.2, BU.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, CA.5, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.64, BA.1.6, BA.2.76, BA.5.2.6, XAE, BT.1, BG.2, BA.1.1.18, BF.25, BA.1.1, BA.1.7,	Wibmer et al. (2021)	187577	G	T,TATC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
K417N	convalescent plasma escape	Nearly half (21 of 44, 48%) of early pandemic exposure convalescent plasma/sera failed to neutralize the 501Y.V2 (”South African”) lineage pseudovirus construct Only 3 of 44 convascent sera (those with the highest titer, which correlated direectly with initial infection severity) had high neutralization against this 501Y.V2 PG: note that lineage variant R246I was excluded from the text in reference to these sera assays, not sure if that was an oversight.	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BA.5.2.2, BU.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, CA.5, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.64, BA.1.6, BA.2.76, BA.5.2.6, XAE, BT.1, BG.2, BA.1.1.18, BF.25, BA.1.1, BA.1.7,	Wibmer et al. (2021)	187577	G	T,TATC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
K417N	gene expression increase	Experimentally, Spike gene expression increased 0.1 fold	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BA.5.2.2, BU.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, CA.5, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.64, BA.1.6, BA.2.76, BA.5.2.6, XAE, BT.1, BG.2, BA.1.1.18, BF.25, BV.1.1, BA.1.7,	Starr et al. (2020)	187577	G	T,TATC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
K417N	monoclonal antibody serial passage escape	Escape mutation against monoclonal antibody LY-CoV016	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BA.5.2.2, BU.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, CA.5, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.64, BA.1.6, BA.2.76, BA.5.2.6, XAE, BT.1, BG.2, BA.1.1.18, BF.25, BA.1.1, BA.1.7,	Starr et al. (2021)	187577	G	T,TATC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
K417N	monoclonal antibody serial passage escape	In vitro selection against class 1 (Spike 'up' conformation) monoclonal antibody C682, and to a lesser extent C614 and C660	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BA.5.2.2, BU.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, CA.5, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.64, BA.1.6, BA.2.76, BA.5.2.6, XAE, BT.1, BG.2, BA.1.1.18, BF.25, BA.1.1, BA.1.7,	Wang et al. (2021)	187577	G	T,TATC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
K417N	pharmaceutical effectiveness	COR-101 lost extasciitilde6x binding against this isolated mutation. Estesevimab lost extasciitilde100x binding against this isolated mutation.	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BA.5.2.2, BU.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, CA.5, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.64, BA.1.6, BA.2.76, BA.5.2.6, XAE, BT.1, BG.2, BA.1.1.18, BF.25, BX.1.1, BA.1.7,	Engelhart et al. (2021)	187577	G	T,TATC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
K417N	pharmaceutical effectiveness	Tixagevimab, Regdanvimab and COR-101 display reduced binding affinity to virus pseudotyped as RBD from B.1.351.	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BA.5.2.2, BU.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, CA.5, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.64, BA.1.6, BA.2.76, BA.5.2.6, XAE, BT.1, BG.2, BA.1.1.18, BF.25, BX.1.1, BA.1.7,	Engelhart et al. (2021)	187577	G	T,TATC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
K417N	pharmaceutical effectiveness	COR-101 lost extasciitilde20x binding against this double mutation. Estesevimab lost extasciitilde16x binding against this double mutation. Regdanvimab lost extasciitilde6x binding against this double mutation. M396 lost extasciitilde10x binding against this double mutation.	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BA.5.2.2, BU.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, CA.5, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.64, BA.1.6, BA.2.76, BA.5.2.6, XAE, BT.1, BG.2, BA.1.1.18, BF.25, BX.1.1, BA.1.7,	Engelhart et al. (2021)	187549	G	T,TATC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
K417N	pharmaceutical effectiveness	This mutated version of RBD completely abolishes the binding to a therapeutic antibody, Bamlanivimab, in vitro.	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BA.5.2.2, BU.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, CA.5, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.64, BA.1.6, BA.2.76, BA.5.2.6, XAE, BT.1, BG.2, BA.1.1.18, BF.25, BX.1.1, BA.1.7,	Liu et al. (2021)	187577	G	T,TATC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
K417N	trafficking	extasciitilde2x more infectivity than D614G alone in HEK293T-ACE2 cells 48h post-transduction.	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BA.5.2.2, BU.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.64, BA.1.6, BA.2.76, BA.5.2.6, XAE, BT.1, BG.2, BA.1.1.18, BF.25, BA.1.1, BA.1.7,	Kuzmina et al. (2021)	187555	G	T,TATC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
K417N	trafficking	extasciitilde9x more infectivity than D614G alone in HEK293T-ACE2 cells 48h post-transduction (no synergy as level approx. that of N501Y alone).	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BU.2, BA.5.2.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.64, BA.1.6, BA.2.76, BA.5.2.6, XAE, BT.1, BG.2, BA.1.1.18, BA.2.25, BY.1.1.1,	Kuzmina et al. (2021)	187527	G	T,TATC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
K417N	trafficking	Lentiviral pseudotyped with this individual mutation from B.1.351 was tested on ACE2.293T cells. Luciferase activity was measured two days postinfection, showing mild decrease in infection rate amongst the cells, suggesting that this mutation does not contributing to cell entry fitness.	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BA.5.2.2, BU.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, CA.5, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.64, BA.1.6, BA.2.76, BA.5.2.6, XAE, BT.1, BG.2, BA.1.1.18, BF.25, BX.1.1, BA.1.7,	Tada et al. (2021)	187577	G	T,TATC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
K417N	vaccine neutralization efficacy	This variant showed only minor in Pfizer sera (one or two dose) neutralization efficiency vs D614G (using lentivirus pseudotype).	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BA.5.2.2, BU.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.64, BA.1.6, BA.2.76, BA.5.2.6, XAE, BT.1, BG.2, BA.1.1.18, BF.25, BX.1.1, BA.1.7,	Kuzmina et al. (2021)	187555	G	T,TATC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
K417N	vaccine neutralization efficacy	This variant showed >5x decrease in Pfizer sera (3 weeks post-first dose: n	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BU.2, BA.5.2.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.64, BA.1.6, BA.2.76, BA.5.2.6, XAE, BT.1, BG.2, BA.1.1.18, BE.2.1, BY.1.1.1,	Kuzmina et al. (2021)	187527	G	T,TATC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
K417N	vaccinee plasma binding	1.76x increase in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in previously non-seroconverted subjects. 1.75x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in post-infection vaccinees.	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BA.5.2.2, BU.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.64, BA.1.6, BA.2.76, BA.5.2.6, XAE, BT.1, BG.2, BA.1.1.18, BF.25, BX.1.1, BA.1.7,	Gong et al. (2021)	187555	G	T,TATC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
K417N	virion structure	Estimated free energy change (ddG) for this variant is -0.86 kcal/mol (i.e. destabilizing relative to wild type)	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BA.5.2.2, BU.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, CA.5, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.64, BA.1.6, BA.2.76, BA.5.2.6, XAE, BT.1, BG.2, BA.1.1.18, BF.25, BA.1.1, BA.1.7,	Spratt et al. (2021)	187577	G	T,TATC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
K417N	ACE2 receptor binding affinity	The K417N mutation decreased the affinity extasciitilde4 fold, mainly by decreasing the k(on) but also by increasing the k(off) as measured by surface plasmon resonance.	BA.2.3.6	Barton et al. (2021)	767	GATT	TATT	0.97
K417N	ACE2 receptor binding affinity	This combination showed extasciitilde3x increase binding to ACE2 vs wild type, about half that of the B.1.1.7 lineage, suggesting that the K417N mutation is slightly detrimental to ACE2 binding, probably as a result of disrupting the salt bridge formed with ACE2 residue D30	BA.2.3.6	Collier et al. (2021)	767	GATT	TATT	0.97
K417N	ACE2 receptor binding affinity	Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant showed a 1.5x decrease in binding (KD) relative to D614G.	BA.2.3.6	Gong et al. (2021)	767	GATT	TATT	0.97
K417N	ACE2 receptor binding affinity	RBD containing the N501Y mutation results in 9-fold stronger binding to the hACE2 receptor than wild type RBD. The E484K mutation does not significantly influence the affinity for the receptor, while K417N attenuates affinity. As a result, RBD from B.1.351 containing all three mutations binds 3-fold stronger to hACE2 than wild type RBD but 3-fold weaker than N501Y.	BA.2.3.6	Laffeber et al. (2021)	767	GATT	TATT	0.97
K417N	ACE2 receptor binding affinity	Studying the key covariants in lineage of concern 501Y.V2, observed about 2-fold increase in ACE2 binding vs wildtype, but greatly decreased mAb binding, suggesting evolutionary optimum tension between immune evasion and ACE2 binding affinity as the N501Y variant alone has 10x increase in affinity but no effect on tested mAb binding.	BA.2.3.6	Liu et al. (2021)	767	GATT	TATT	0.97
K417N	ACE2 receptor binding affinity	Using Mircoscale Thermopheresis, the B.1.351 variant harboring three mutations, binds ACE2 at nearly five-fold greater affinity than the original SARS-COV-2 RBD (Kd 87.6, vs 402.5 nM).	BA.2.3.6	Ramanathan et al. (2021)	767	GATT	TATT	0.97
K417N	ACE2 receptor binding affinity	Reported 3-fold decrease in affinity compared to wild-type RBD on the cell surface (Kd	BA.2.3.6	Tian et al. (2021)	767	GATT	TATT	0.97
K417N	ACE2 receptor binding affinity	Reported slight increase in affinity compared to wild-type RBD on the cell surface (Kd	BA.2.3.6	Tian et al. (2021)	767	GATT	TATT	0.97
K417N	ACE2 receptor binding affinity	The affinity of ACE2 for this mutation combination was twice as high as for wild type. Having in mind that the affinity of SARS-CoV-2 for ACE2 is only 4-fold higher compared to SARS-CoV-1, this factor of 2 is expected to be biologically significant.	BA.2.3.6	Vogel et al. (2021)	767	GATT	TATT	0.97
K417N	antibody epitope effects	>20% (ELISA significance threshold) drop in antibody binding (ELISA) by this variant against IgG1 monoclonal antibody ab1.	BA.2.3.6	Sun et al. (2021)	767	GATT	TATT	0.97

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
K417N	antibody epitope effects	5 antibodies tested were less potent against K417N by ten-fold or more (class 1 mAbs)	BA.2.3.6	Wang et al. (2021)	767	GATT	TATT	0.97
K417N	antibody epitope effects	Pseudotyped virus model ablates binding by RBD-directed mAbs CB6 and 910-30 (targeting the inner side of the RBD). Pseudotyped virus model impairs binding by RBD-directed mAbs 4-20 and REGN10933.	BA.2.3.6	Wang et al. (2021)	767	GATT	TATT	0.97
K417N	convalescent plasma binding	2.16x increase in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset.	BA.2.3.6	Gong et al. (2021)	767	GATT	TATT	0.97
K417N	convalescent plasma escape	The 501Y.V2 to first wave IC50 ratio ranged from 6 to 200-fold. Averaging across all 7 participant convalescent sera highlighted the dramatic decrease in sensitivity to neutralization of authentic 501Y.V2 variants. PG: I'm purposefully ignoring D614G and A701V as contributors	BA.2.3.6	Cele et al. (2021)	767	GATT	TATT	0.97
K417N	convalescent plasma escape	In 19 convalescent human sera extasciitilde1mo post infection, Two-tailed Wilcoxon matched-pairs signed-rank test shows mild resistence P	BA.2.3.6	Chen et al. (2021)	767	GATT	TATT	0.97
K417N	convalescent plasma escape	27% of 44 early pandemic exposure convalescent plasma/sera lose all activity against a RBD triple mutant pseudovirus (RBD mutatants of the 501Y.V2 "South African" lineage), while only 23% retained high titres	BA.2.3.6	Wibmer et al. (2021)	767	GATT	TATT	0.97
K417N	convalescent plasma escape	Nearly half (21 of 44, 48%) of early pandemic exposure convalescent plasma/sera failed to neutralize the 501Y.V2 ("South African") lineage pseudovirus construct Only 3 of 44 convascent sera (those with the highest titer, which correlated direectly with initial infection severity) had high neutralization against this 501Y.V2 PG: note that lineage variant R246I was excluded from the text in reference to these sera assays, not sure if that was an oversight.	BA.2.3.6	Wibmer et al. (2021)	767	GATT	TATT	0.97
K417N	gene expression increase	Experimentally, Spike gene expression increased 0.1 fold	BA.2.3.6	Starr et al. (2020)	767	GATT	TATT	0.97
K417N	monoclonal antibody serial passage escape	Escape mutation against monoclonal antibody LY-CoV016	BA.2.3.6	Starr et al. (2021)	767	GATT	TATT	0.97
K417N	monoclonal antibody serial passage escape	In vitro selection against class 1 (Spike 'up' conformation) monoclonal antibody C682, and to a lesser extent C614 and C660	BA.2.3.6	Wang et al. (2021)	767	GATT	TATT	0.97
K417N	pharmaceutical effectiveness	COR-101 lost extasciitilde6x binding against this isolated mutation. Estesevimab lost extasciitilde100x binding against this isolated mutation.	BA.2.3.6	Engelhart et al. (2021)	767	GATT	TATT	0.97
K417N	pharmaceutical effectiveness	Tixagevimab, Regdanvimab and COR-101 display reduced binding affinity to virus pseudotyped as RBD from B.1.351.	BA.2.3.6	Engelhart et al. (2021)	767	GATT	TATT	0.97

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
K417N	pharmaceutical effectiveness	COR-101 lost extasciitilde20x binding against this double mutation. Estesevimab lost extasciitilde16x binding against this double mutation. Regdanvimab lost extasciitilde6x binding against this double mutation. M396 lost extasciitilde10x binding against this double mutation.	BA.2.3.6	Engelhart et al. (2021)	767	GATT	TATT	0.97
K417N	pharmaceutical effectiveness	This mutated version of RBD completely abolishes the binding to a therapeutic antibody, Bamlanivimab, in vitro.	BA.2.3.6	Liu et al. (2021)	767	GATT	TATT	0.97
K417N	trafficking	extasciitilde2x more infectivity than D614G alone in HEK293T-ACE2 cells 48h post-transduction.	BA.2.3.6	Kuzmina et al. (2021)	767	GATT	TATT	0.97
K417N	trafficking	extasciitilde9x more infectivity than D614G alone in HEK293T-ACE2 cells 48h post-transduction (no synergy as level approx. that of N501Y alone).	BA.2.3.6	Kuzmina et al. (2021)	767	GATT	TATT	0.97
K417N	trafficking	Lentiviral pseudotyped with this individual mutation from B.1.351 was tested on ACE2.293T cells. Luciferase activity was measured two days postinfection, showing mild decrease in infection rate amongst the cells, suggesting that this mutation does not contributing to cell entry fitness.	BA.2.3.6	Tada et al. (2021)	767	GATT	TATT	0.97
K417N	vaccine neutralization efficacy	This variant showed only minor in Pfizer sera (one or two dose) neutralization efficiency vs D614G (using lentivirus pseudotype).	BA.2.3.6	Kuzmina et al. (2021)	767	GATT	TATT	0.97
K417N	vaccine neutralization efficacy	This variant showed >5x decrease in Pfizer sera (3 weeks post-first dose: n	BA.2.3.6	Kuzmina et al. (2021)	767	GATT	TATT	0.97
K417N	vaccinee plasma binding	1.76x increase in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in previously non-seroconverted subjects. 1.75x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in post-infection vaccinees.	BA.2.3.6	Gong et al. (2021)	767	GATT	TATT	0.97
K417N	virion structure	Estimated free energy change (ddG) for this variant is -0.86 kcal/mol (i.e. destabilizing relative to wild type)	BA.2.3.6	Spratt et al. (2021)	767	GATT	TATT	0.97
A701V	ACE2 receptor binding affinity	Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant showed essentially no change in binding (KD) relative to D614G.	BA.5.1.18, BA.4.1, BA.5.5, BA.5.1.23, BA.1.17.2, BQ.1.1.4, BA.4.4, BA.1.17, BF.31.1, BF.7.4.1, BE.1.4.1, BN.1, BD.1	Gong et al. (2021)	11882	C	T	0.61

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
A701V	convalescent plasma binding	1.11x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset.	BA.5.1.18, BA.4.1, BA.5.5, BA.5.1.23, BA.1.17.2, BQ.1.1.4, BA.4.4, BA.1.17, BF.31.1, BF.7.4.1, BE.1.4.1, BN.1, BD.1	Gong et al. (2021)	11882	C	T	0.61
A701V	trafficking	Lentiviral pseudotyped with this individual mutation from B.1.351 was tested on ACE2.293T cells. Luciferase activity was measured two days postinfection, showing mild decrease in infection rate amongst the cells, suggesting that this mutation does not contributing to cell entry fitness.	BA.5.1.18, BA.4.1, BA.5.5, BA.5.1.23, BA.1.17.2, BQ.1.1.4, BA.4.4, BA.1.17, BF.31.1, BF.7.4.1, BE.1.4.1, BN.1, BD.1	Tada et al. (2021)	11882	C	T	0.61
A701V	vaccinee plasma binding	1.19x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in previously non-seroconverted subjects. 1.1x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in post-infection vaccinees.	BA.5.1.18, BA.4.1, BA.5.5, BA.5.1.23, BA.1.17.2, BQ.1.1.4, BA.4.4, BA.1.17, BF.31.1, BF.7.4.1, BE.1.4.1, BN.1, BD.1	Gong et al. (2021)	11882	C	T	0.61
A701V	virion structure	Estimated free energy change (ddG) for this variant is -0.33 kcal/mol (i.e. destabilizing relative to wild type)	BA.5.1.18, BA.4.1, BA.5.5, BA.5.1.23, BA.1.17.2, BQ.1.1.4, BA.4.4, BA.1.17, BF.31.1, BF.7.4.1, BE.1.4.1, BN.1, BD.1	Spratt et al. (2021)	11882	C	T	0.61
F486S	antibody epitope effects	Mutant screen in neutralization assay with a broad range of monoclonal antibodies shows high resistence to 5 antibodies.	CH.1.1.2, XBB.4, BA.2.75.7, BY.1.1.1, BM.4.1.1, BM.1, CA.3, XBB.1.3, CH.2, BN.1.3.1, CH.1, BM.1.1, BM.4.1, BY.1.2, BR.1.2, BY.1, CM.8.1, CA.5, XBB.3, CM.2, XBB.1.4, CA.1, CA.3.1, XBD, BA.2.75.2, XBH, CA.7, XBB, CH.1.1, XBB.1.1, CV.1	Liu et al. (2020)	1101	T	C,CC	0.85

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
F486S	antibody epitope effects	>60% drop in antibody binding (ELISA) by this variant against monoclonal antibody VH-Fc ab8.	CH.1.1.2, XBB.4, BA.2.75.7, BY.1.1.1, BM.4.1.1, BM.1, CA.3, XBB.1.3, CH.2, BN.1.3.1, CH.1, BM.1.1, BM.4.1, BY.1.2, BR.1.2, BY.1, CM.8.1, CA.5, XBB.3, CM.2, XBB.1.4, CA.1, CA.3.1, XBD, BA.2.75.2, XBH, CA.7, XBB, CH.1.1, XBB.1.1, CV.1	Sun et al. (2021)	1101	T	C,CC	0.85
F486S	convalescent plasma escape	Modest decrease in in neutralization capability of all 4 convalescent sera tested.	CH.1.1.2, XBB.4, BA.2.75.7, BY.1.1.1, BM.4.1.1, BM.1, CA.3, XBB.1.3, CH.2, BN.1.3.1, CH.1, BM.1.1, BM.4.1, BY.1.2, BR.1.2, BY.1, CM.8.1, CA.5, XBB.3, CM.2, XBB.1.4, CA.1, CA.3.1, XBD, BA.2.75.2, XBH, CA.7, XBB, CH.1.1, XBB.1.1, CV.1	Liu et al. (2021)	1101	T	C,CC	0.85
F486S	gene expression increase	Experimentally, Spike gene expression increased 0.13 fold	CH.1.1.2, XBB.4, BA.2.75.7, BY.1.1.1, BM.4.1.1, BM.1, CA.3, XBB.1.3, CH.2, BN.1.3.1, CH.1, BM.1.1, BM.4.1, BY.1.2, BR.1.2, BY.1, CM.8.1, CA.5, XBB.3, CM.2, XBB.1.4, CA.1, CA.3.1, XBD, BA.2.75.2, XBH, CA.7, XBB, CH.1.1, XBB.1.1, CV.1	Starr et al. (2020)	1101	T	C,CC	0.85

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
F486S	monoclonal antibody serial passage escape	Ranked moderately effective mutant against this position in the RBD for highly neutralizing COV2-2832 monoclonal antibody	CH.1.1.2, XBB.4, BA.2.75.7, BY.1.1.1, BM.4.1.1, BM.1, CA.3, XBB.1.3, CH.2, BN.1.3.1, CH.1, BM.1.1, BM.4.1, BY.1.2, BR.1.2, BY.1, CM.8.1, CA.5, XBB.3, CM.2, XBB.1.4, CA.1, CA.3.1, XBD, BA.2.75.2, XBH, CA.7, XBB, CH.1.1, XBB.1.1, CV.1	Greaney et al. (2020)	1101	T	C,CC	0.85
F486S	antibody epitope effects	Mutant screen in neutralization assay with a broad range of monoclonal antibodies shows high resistence to 5 antibodies.	BM.1.1, CM.4	Liu et al. (2020)	33	TT	CT,CC	0.61
F486S	antibody epitope effects	>60% drop in antibody binding (ELISA) by this variant against monoclonal antibody VH-Fc ab8.	BM.1.1, CM.4	Sun et al. (2021)	33	TT	CT,CC	0.61
F486S	convalescent plasma escape	Modest decrease in in neutralization capability of all 4 convalescent sera tested.	BM.1.1, CM.4	Liu et al. (2021)	33	TT	CT,CC	0.61
F486S	gene expression increase	Experimentally, Spike gene expression increased 0.13 fold	BM.1.1, CM.4	Starr et al. (2020)	33	TT	CT,CC	0.61
F486S	monoclonal antibody serial passage escape	Ranked moderately effective mutant against this position in the RBD for highly neutralizing COV2-2832 monoclonal antibody	BM.1.1, CM.4	Greaney et al. (2020)	33	TT	CT,CC	0.61
K417I	gene expression increase	Experimentally, Spike gene expression increased 0.39 fold	BA.2.9.1	Starr et al. (2020)	6	AG	AT	0.5
K417I	monoclonal antibody serial passage escape	Escape mutation against monoclonal antibody LY-CoV016	BA.2.9.1	Starr et al. (2021)	6	AG	AT	0.5
R346K	gene expression increase	Experimentally, Spike gene expression increased 0.12 fold	BA.1.1.7, BA.1.1.11, BA.1.1.18, BA.1.1.4, BA.1.1.6, BA.1.1.14, BA.1.1.15, BA.1.15, BA.1.1.2, BA.5.1.22, BA.1.1.3, BA.1.1, BA.1.1.17, XM, BE.1.1, BA.1.1.13, BC.2, BA.1.1.9, BA.1.1.16, BA.1.1.8, BA.1.1.10, BA.1, BA.1.1.1	Starr et al. (2020)	53566	G	A	0.69

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
R346K	monoclonal antibody serial passage escape	Strong positive selection (up to 53% of supernatant sequences) under two rounds of C135 monoclonal antibody passage, overall 70% switch away from R346 to S, K or M	BA.1.1.7, BA.1.1.11, BA.1.1.18, BA.1.1.4, BA.1.1.6, BA.1.1.14, BA.1.1.15, BA.1.15, BA.1.1.2, BA.5.1.22, BA.1.1.3, BA.1.1, BA.1.1.17, XM, BE.1.1, BA.1.1.13, BC.2, BA.1.1.9, BA.1.1.16, BA.1.1.8, BA.1.1.10, BA.1, BA.1.1.1	Weisblum et al. (2020)	53566	G	A	0.69

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
E484A	antibody epitope effects	Mutant screen in neutralization assay with a broad range of monoclonal antibodies shows high resistence to 4 antibodies, and broad low level resistence against much of the rest of the panel.	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BU.2, BA.5.2.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, CA.5, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.2.76, BA.5.2.6, BT.1, XAE, BG.2, BA.1.1.18, BF.25, BY.1.1.1,	Liu et al. (2020)	185921	A	C,CAA	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
E484A	convalescent plasma escape	Remarkably, several of the E484 escape mutants were resistant to neutralization at the highest concentration (1:80 initial dilution) of all 4 convalescent sera tested. Against a wider panel of 16 convalescent plasma (no replicates), all but one show major resistance.	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BU.2, BA.5.2.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, CA.5, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.2.76, BA.5.2.6, BT.1, XAE, BG.2, BA.1.1.18, BA.2.75, BY.1.1.1,	Liu et al. (2021)	185921	A	C,CAA	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
E484A	monoclonal antibody serial passage escape	Ranked moderately effective mutant against this position in the RBD for highly neutralizing COV2-2050 monoclonal antibody	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BU.2, BA.5.2.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, CA.5, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.2.76, BA.5.2.6, BT.1, XAE, BG.2, BA.1.1.18, BF.25, BY.1.1.1,	Greaney et al. (2020)	185921	A	C,CAA	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
E484A	monoclonal antibody serial passage escape	"E484A rose in frequency in linkage with F486I, but since E484A is not an escape mutation in our maps it is not shown in other panels"	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BU.2, BA.5.2.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, CA.5, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.2.76, BA.5.2.6, BT.1, XAE, BG.2, BA.1.1.18, BF.25, BY.1.1.1,	Starr et al. (2020)	185921	A	C,CAA	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
E484A	monoclonal antibody serial passage escape	Escape mutation against monoclonal antibody LY-CoV555 (antibody that forms the basis for Eli Lilly's bamlanivimab)	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BU.2, BA.5.2.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, CA.5, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.2.76, BA.5.2.6, BT.1, XAE, BG.2, BA.1.1.18, BA.2.25, BY.1.1.1,	Starr et al. (2021)	185921	A	C,CAA	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
E484A	pharmaceutical effectiveness	Bamlanivimab (LY-CoV555) lost extasciitilde8x binding against this isolated mutation.	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BU.2, BA.5.2.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, CA.5, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.2.76, BA.5.2.6, BT.1, XAE, BG.2, BA.1.1.18, BF.25, BY.1.1.1,	Engelhart et al. (2021)	185921	A	C,CAA	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
K417H	gene expression increase	Experimentally, Spike gene expression increased 0.1 fold	BA.5.2.28	Starr et al. (2020)	120	AAG	AAT	0.98
K417H	monoclonal antibody serial passage escape	Escape mutation against monoclonal antibody LY-CoV016	BA.5.2.28	Starr et al. (2021)	120	AAG	AAT	0.98
F486A	gene expression increase	Experimentally, Spike gene expression increased 0.1 fold	BW.1.1, CQ.2, BA.5.1.12	Starr et al. (2020)	400	TT	GT,GC	1.0
F486A	monoclonal antibody serial passage escape	Most effective mutant against this position in the RBD for highly neutralizing COV2-2832 monoclonal antibody	BW.1.1, CQ.2, BA.5.1.12	Greaney et al. (2020)	400	TT	GT,GC	1.0
L452R	ACE2 receptor binding affinity	Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant showed a 2.66x increase in binding (KD) relative to D614G.	BQ.1.1.13, BQ.1.22	Gong et al. (2021)	186	CCT	CCG	0.96
L452R	ACE2 receptor binding affinity	extasciitilde1.7-fold increase in binding affinity vs wild type.	BQ.1.1.13, BQ.1.22	Motozono et al. (2021)	186	CCT	CCG	0.96
L452R	T cell evasion	L452R derivative virus did not induce IFN-gamma expression even at the highest concentration tested (10 nM) in two different A*24:02 convalescent sera donor plasma (linear epitope NYNYLYRLF 448,456).	BQ.1.1.13, BQ.1.22	Motozono et al. (2021)	186	CCT	CCG	0.96
L452R	antibody epitope effects	Resistent to some neutralizing antibodies: mAbs X593 and P2B-2F6	BQ.1.1.13, BQ.1.22	Li et al. (2020)	186	CCT	CCG	0.96
L452R	antibody epitope effects	Mutant screen in neutralization assay with a broad range of monoclonal antibodies shows resistence to more than one antibody.	BQ.1.1.13, BQ.1.22	Liu et al. (2021)	186	CCT	CCG	0.96
L452R	antibody epitope effects	10 of 14 RBD-specific mAbs that showed at least 10-fold reduced neutralization of B.1.427/B.1.429 variant pseudotype (S13I, W152C, and L452R) were also found to poorly bind to just a L452R RBD mutant, demonstrating a role for this mutation as an escape mechanism for certain RBD-targeting mAbs.	BQ.1.1.13, BQ.1.22	McCallum et al. (2021)	186	CCT	CCG	0.96
L452R	antibody epitope effects	extasciitilde20% (ELISA significance threshold) drop in antibody binding (ELISA) by this variant against monoclonal antibody VH ab6.	BQ.1.1.13, BQ.1.22	Sun et al. (2021)	186	CCT	CCG	0.96
L452R	convalescent plasma binding	2.15x increase in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset.	BQ.1.1.13, BQ.1.22	Gong et al. (2021)	186	CCT	CCG	0.96
L452R	convalescent plasma escape	Observed extasciitilde2x decrease on average in 16 health workers' convalescent sera.	BQ.1.1.13, BQ.1.22	Alenquer et al. (2021)	186	CCT	CCG	0.96
L452R	convalescent plasma escape	Ablation of neutralization capability of 3 of 4 convalescent sera tested, the other is significantly hindered.	BQ.1.1.13, BQ.1.22	Liu et al. (2021)	186	CCT	CCG	0.96
L452R	convalescent plasma escape	Relative to B.1, Epsilon (B.1.417/429) shows 1.74x-2.35x decrease in neutralization efficiency by convalescent plasma [no cohort details provided]	BQ.1.1.13, BQ.1.22	Wilhelm et al. (2021)	186	CCT	CCG	0.96
L452R	gene expression increase	Experimentally, Spike gene expression increased 0.32 fold	BQ.1.1.13, BQ.1.22	Starr et al. (2020)	186	CCT	CCG	0.96
L452R	monoclonal antibody serial passage escape	Ranked effective mutant against this position in the RBD for highly neutralizing COV2-2096	BQ.1.1.13, BQ.1.22	Greaney et al. (2020)	186	CCT	CCG	0.96

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
L452R	monoclonal antibody serial passage escape	Escape mutation against monoclonal antibody LY-CoV555 (antibody that forms the basis for Eli Lilly's bamlanivimab)	BQ.1.1.13, BQ.1.22	Starr et al. (2021)	186	CCT	CCG	0.96
L452R	monoclonal antibody serial passage escape	Class 2/3 antibody C628 and class 2 antibody C643 selected for the emergence of the L452R mutation in vitro.	BQ.1.1.13, BQ.1.22	Wang et al. (2021)	186	CCT	CCG	0.96
L452R	pharmaceutical effectiveness	Bamlanivimab (LY-CoV555) lost extasciitilde5x binding against this isolated mutation. Cligavimab lost extasciitilde4x binding against this isolated mutation. Regdanvimab lost extasciitilde4x binding against this isolated mutation.	BQ.1.1.13, BQ.1.22	Engelhart et al. (2021)	186	CCT	CCG	0.96
L452R	pharmaceutical effectiveness	Bamlanivimab (LY-CoV555) entirely lost its neutralizing activity due to the central location of L452R in the epitopes recognized by this mAb. Regdanvimab (CT-P59), and to a smaller extent etesevimab, showed a reduction in neutralization potency.	BQ.1.1.13, BQ.1.22	McCallum et al. (2021)	186	CCT	CCG	0.96
L452R	trafficking	We observed increased entry by pseudoviruses carrying the L452R mutation compared to D614G alone, with a 6.7 to 22.5-fold increase in 293T cells and a 5.8 to 14.7-fold increase in human airway organoids.	BQ.1.1.13, BQ.1.22	Deng et al. (2021)	186	CCT	CCG	0.96
L452R	trafficking	This variant alone shows a extasciitilde5x decrease in cell entry efficiency (RLU measurement in 293T cells) compared to D614G. [listed as L454R in Figure, but L452R in text, also text suggests not statistucally significant, but error bars say otherwise in Figure 4]	BQ.1.1.13, BQ.1.22	Ferriera et al (2021)	186	CCT	CCG	0.96
L452R	trafficking	Increased stability of RBD expression in yeast, suggesting increased Spike protein stability.	BQ.1.1.13, BQ.1.22	Motozono et al. (2021)	186	CCT	CCG	0.96
L452R	transmissibility	Increased infectivity of the B.1.617 spike was attributed to L452R, which itself caused a 3.5-fold increase in infectivity relative to D614G wild type. [In combination with E484Q caused a lower 3-fold increase]	BQ.1.1.13, BQ.1.22	Tada et al. (2021)	186	CCT	CCG	0.96
L452R	vaccine neutralization efficacy	Nine stored sera from Pfizer BNT162b2 vaccinees were tested against a range of spike mutation bearing PV. L452R conferred about a two-fold reduction in neutralisation by vaccine sera, but was not statistically significant with this sample size.	BQ.1.1.13, BQ.1.22	Ferreira et al. (2021)	186	CCT	CCG	0.96
L452R	vaccine neutralization efficacy	The presence of this variant in 189 post-mRNA-vaccination COVID-19 cases was proportionally in line with lineage prevalence in Northen California during the study period, suggesting no effect of these variants on immune escape.	BQ.1.1.13, BQ.1.22	Jacobson et al. (2021)	186	CCT	CCG	0.96

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
L452R	vaccine neutralization efficacy	The presence of these B.1.417/B.1.429 defining variants in 189 post-mRNA-vaccination COVID-19 cases was proportionally in line with lineage prevalence in Northen California during the study period, suggesting no effect of these variants on immune escape.	BQ.1.1.13, BQ.1.22	Jacobson et al. (2021)	186	CCT	CCG	0.96
L452R	vaccine neutralization efficacy	Relative to B.1, Epsilon (B.1.417/429) shows 1.74x-2.35x decrease in neutralization efficiency by 18 vaccinee sera (BNT162b2 and mRNA1273).	BQ.1.1.13, BQ.1.22	Wilhelm et al. (2021)	186	CCT	CCG	0.96
L452R	vaccinee plasma binding	1.05x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in previously non-seroconverted subjects. 1.16x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in post-infection vaccinees.	BQ.1.1.13, BQ.1.22	Gong et al. (2021)	186	CCT	CCG	0.96
L452R	virion structure	Estimated free energy change (ddG) for this variant is -0.67 kcal/mol (i.e. destabilizing relative to wild type)	BQ.1.1.13, BQ.1.22	Spratt et al. (2021)	186	CCT	CCG	0.96

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
L452R	ACE2 receptor binding affinity	Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant showed a 2.66x increase in binding (KD) relative to D614G.	BA.5.1.2, BQ.1.1.15, BA.5.2.14, DE.2, BE.4.2, CN.1, BF.5, BF.7.1, BA.5.2.3, BA.2.75, BA.4.4, BA.5.1.9, BA.5.2.23, BQ.1.1.19, BQ.1.1.3, BA.5.2.34, CQ.1.1, BA.4.1.9, BA.5.2.18, BE.1.1.2, BF.12, BR.2.1, BF.26, BA.5.1.21, BA.5.1.16, CG.1, BA.5.1.3, BF.17, BQ.1.16, BA.5.3.3, CE.1, BA.5.2.26, BQ.1.1.14, BQ.1.1.2, BQ.1.8.2, BR.1.2, BA.5.2.28, BT.2, BQ.1.1.5, CR.1.2, BA.5.1.4, BA.4.1.5, BQ.1.1.25, BA.5.1.22, BQ.1.3, BA.5.1.19, BA.4.1.1, BF.7.5, BF.1, BA.4.1.10, BA.5.2.21, BQ.1.1.7, BQ.1.1.6, BQ.1.10.1, BR.1, BQ.1.1.28, CA.1, BF.4, CK.3, BF.7.4.1, CR.2, XBE, BA.2.75.4, BQ.1.1.27, BA.5.2.37, CA.7, BQ.1.1, BQ.1.12, BA.4.7, BF.19, BA.5.10, BF.31, BF.7.3, BF.7.7, BA.5.1.31, BF.7.8, XAS, BA.5.2.33, CC.1, BQ.1.1.24, BA.5.6.2, BA.5.2.2, BQ.1.6, BU.2, CV.1, CQ.2, BE.4, BA.5.1.25, BQ.1.26, BQ.1.10, BV.2, BE.3, BA.5.2.22, BF.15, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BF.29, BQ.1.23, BA.4.5, BE.4.1.1, BF.32, BQ.1.2, BA.5.1.24, BF.3.1,	Gong et al. (2021)	84146	T	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
L452R	ACE2 receptor binding affinity	extasciitilde1.7-fold increase in binding affinity vs wild type.	BA.5.1.2, BQ.1.1.15, BA.5.2.14, DE.2, BE.4.2, CN.1, BF.5, BF.7.1, BA.5.2.3, BA.2.75, BA.4.4, BA.5.1.9, BA.5.2.23, BQ.1.1.19, BQ.1.1.3, BA.5.2.34, CQ.1.1, BA.4.1.9, BA.5.2.18, BE.1.1.2, BF.12, BR.2.1, BF.26, BA.5.1.21, BA.5.1.16, CG.1, BA.5.1.3, BF.17, BQ.1.16, BA.5.3.3, CE.1, BA.5.2.26, BQ.1.1.14, BQ.1.1.2, BQ.1.8.2, BR.1.2, BA.5.2.28, BT.2, BQ.1.1.5, CR.1.2, BA.5.1.4, BA.4.1.5, BQ.1.1.25, BA.5.1.22, BQ.1.3, BA.5.1.19, BA.4.1.1, BF.7.5, BF.1, BA.4.1.10, BA.5.2.21, BQ.1.1.7, BQ.1.1.6, BQ.1.10.1, BR.1, BQ.1.1.28, CA.1, BF.4, CK.3, BF.7.4.1, CR.2, XBE, BA.2.75.4, BQ.1.1.27, BA.5.2.37, CA.7, BQ.1.1, BQ.1.12, BA.4.7, BF.19, BA.5.10, BF.31, BF.7.3, BF.7.7, BA.5.1.31, BF.7.8, XAS, BA.5.2.33, CC.1, BQ.1.1.24, BA.5.6.2, BA.5.2.2, BQ.1.6, BU.2, CV.1, CQ.2, BE.4, BA.5.1.25, BQ.1.26, BQ.1.10, BV.2, BE.3, BA.5.2.22, BF.15, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BF.29, BQ.1.23, BA.4.5, BE.4.1.1, BF.32, BQ.1.2, BA.5.1.24, BF.3.1,	Motozono et al. (2021)	84146	T	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
L452R	T cell evasion	L452R derivative virus did not induce IFN-gamma expression even at the highest concentration tested (10 nM) in two different A*24:02 convalescent sera donor plasma (linear epitope NYNYLYRLF 448,456).	BA.5.1.2, BQ.1.1.15, BA.5.2.14, DE.2, BE.4.2, CN.1, BF.5, BF.7.1, BA.5.2.3, BA.2.75, BA.4.4, BA.5.1.9, BA.5.2.23, BQ.1.1.19, BQ.1.1.3, BA.5.2.34, CQ.1.1, BA.4.1.9, BA.5.2.18, BE.1.1.2, BF.12, BR.2.1, BF.26, BA.5.1.21, BA.5.1.16, CG.1, BA.5.1.3, BF.17, BQ.1.16, BA.5.3.3, CE.1, BA.5.2.26, BQ.1.1.14, BQ.1.1.2, BQ.1.8.2, BR.1.2, BA.5.2.28, BT.2, BQ.1.1.5, CR.1.2, BA.5.1.4, BA.4.1.5, BQ.1.1.25, BA.5.1.22, BQ.1.3, BA.5.1.19, BA.4.1.1, BF.7.5, BF.1, BA.4.1.10, BA.5.2.21, BQ.1.1.7, BQ.1.1.6, BQ.1.10.1, BR.1, BQ.1.1.28, CA.1, BF.4, CK.3, BF.7.4.1, CR.2, XBE, BA.2.75.4, BQ.1.1.27, BA.5.2.37, CA.7, BQ.1.1, BQ.1.12, BA.4.7, BF.19, BA.5.10, BF.31, BF.7.3, BF.7.7, BA.5.1.31, BF.7.8, XAS, BA.5.2.33, CC.1, BQ.1.1.24, BA.5.6.2, BA.5.2.2, BQ.1.6, BU.2, CV.1, CQ.2, BE.4, BA.5.1.25, BQ.1.26, BQ.1.10, BV.2, BE.3, BA.5.2.22, BF.15, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BF.29, BQ.1.23, BA.4.5, BE.4.1.1, BF.32, BQ.1.2, BA.5.1.24, BF.3.1,	Motozono et al. (2021)	84146	T	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
L452R	antibody epitope effects	Resistent to some neutralizing antibodies: mAbs X593 and P2B-2F6	BA.5.1.2, BQ.1.1.15, BA.5.2.14, DE.2, BE.4.2, CN.1, BF.5, BF.7.1, BA.5.2.3, BA.2.75, BA.4.4, BA.5.1.9, BA.5.2.23, BQ.1.1.19, BQ.1.1.3, BA.5.2.34, CQ.1.1, BA.4.1.9, BA.5.2.18, BE.1.1.2, BF.12, BR.2.1, BF.26, BA.5.1.21, BA.5.1.16, CG.1, BA.5.1.3, BF.17, BQ.1.16, BA.5.3.3, CE.1, BA.5.2.26, BQ.1.1.14, BQ.1.1.2, BQ.1.8.2, BR.1.2, BA.5.2.28, BT.2, BQ.1.1.5, CR.1.2, BA.5.1.4, BA.4.1.5, BQ.1.1.25, BA.5.1.22, BQ.1.3, BA.5.1.19, BA.4.1.1, BF.7.5, BF.1, BA.4.1.10, BA.5.2.21, BQ.1.1.7, BQ.1.1.6, BQ.1.10.1, BR.1, BQ.1.1.28, CA.1, BF.4, CK.3, BF.7.4.1, CR.2, XBE, BA.2.75.4, BQ.1.1.27, BA.5.2.37, CA.7, BQ.1.1, BQ.1.12, BA.4.7, BF.19, BA.5.10, BF.31, BF.7.3, BF.7.7, BA.5.1.31, BF.7.8, XAS, BA.5.2.33, CC.1, BQ.1.1.24, BA.5.6.2, BA.5.2.2, BQ.1.6, BU.2, CV.1, CQ.2, BE.4, BA.5.1.25, BQ.1.26, BQ.1.10, BV.2, BE.3, BA.5.2.22, BF.15, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BF.29, BQ.1.23, BA.4.5, BE.4.1.1, BF.32, BQ.1.2, BA.5.1.24, BF.3.1,	Li et al. (2020)	84146	T	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
L452R	antibody epitope effects	Mutant screen in neutralization assay with a broad range of monoclonal antibodies shows resistence to more than one antibody.	BA.5.1.2, BQ.1.1.15, BA.5.2.14, DE.2, BE.4.2, CN.1, BF.5, BF.7.1, BA.5.2.3, BA.2.75, BA.4.4, BA.5.1.9, BA.5.2.23, BQ.1.1.19, BQ.1.1.3, BA.5.2.34, CQ.1.1, BA.4.1.9, BA.5.2.18, BE.1.1.2, BF.12, BR.2.1, BF.26, BA.5.1.21, BA.5.1.16, CG.1, BA.5.1.3, BF.17, BQ.1.16, BA.5.3.3, CE.1, BA.5.2.26, BQ.1.1.14, BQ.1.1.2, BQ.1.8.2, BR.1.2, BA.5.2.28, BT.2, BQ.1.1.5, CR.1.2, BA.5.1.4, BA.4.1.5, BQ.1.1.25, BA.5.1.22, BQ.1.3, BA.5.1.19, BA.4.1.1, BF.7.5, BF.1, BA.4.1.10, BA.5.2.21, BQ.1.1.7, BQ.1.1.6, BQ.1.10.1, BR.1, BQ.1.1.28, CA.1, BF.4, CK.3, BF.7.4.1, CR.2, XBE, BA.2.75.4, BQ.1.1.27, BA.5.2.37, CA.7, BQ.1.1, BQ.1.12, BA.4.7, BF.19, BA.5.10, BF.31, BF.7.3, BF.7.7, BA.5.1.31, BF.7.8, XAS, BA.5.2.33, CC.1, BQ.1.1.24, BA.5.6.2, BA.5.2.2, BQ.1.6, BU.2, CV.1, CQ.2, BE.4, BA.5.1.25, BQ.1.26, BQ.1.10, BV.2, BE.3, BA.5.2.22, BF.15, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BF.29, BQ.1.23, BA.4.5, BE.4.1.1, BF.32, BQ.1.2, BA.5.1.24, BF.3.1,	Liu et al. (2021)	84146	T	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
L452R	antibody epitope effects	10 of 14 RBD-specific mAbs that showed at least 10-fold reduced neutralization of B.1.427/B.1.429 variant pseudotype (S13I, W152C, and L452R) were also found to poorly bind to just a L452R RBD mutant, demonstrating a role for this mutation as an escape mechanism for certain RBD-targeting mAbs.	BA.5.1.2, BQ.1.1.15, BA.5.2.14, DE.2, BE.4.2, CN.1, BF.5, BF.7.1, BA.5.2.3, BA.2.75, BA.4.4, BA.5.1.9, BA.5.2.23, BQ.1.1.19, BQ.1.1.3, BA.5.2.34, CQ.1.1, BA.4.1.9, BA.5.2.18, BE.1.1.2, BF.12, BR.2.1, BF.26, BA.5.1.21, BA.5.1.16, CG.1, BA.5.1.3, BF.17, BQ.1.16, BA.5.3.3, CE.1, BA.5.2.26, BQ.1.1.14, BQ.1.1.2, BQ.1.8.2, BR.1.2, BA.5.2.28, BT.2, BQ.1.1.5, CR.1.2, BA.5.1.4, BA.4.1.5, BQ.1.1.25, BA.5.1.22, BQ.1.3, BA.5.1.19, BA.4.1.1, BF.7.5, BF.1, BA.4.1.10, BA.5.2.21, BQ.1.1.7, BQ.1.1.6, BQ.1.10.1, BR.1, BQ.1.1.28, CA.1, BF.4, CK.3, BF.7.4.1, CR.2, XBE, BA.2.75.4, BQ.1.1.27, BA.5.2.37, CA.7, BQ.1.1, BQ.1.12, BA.4.7, BF.19, BA.5.10, BF.31, BF.7.3, BF.7.7, BA.5.1.31, BF.7.8, XAS, BA.5.2.33, CC.1, BQ.1.1.24, BA.5.6.2, BA.5.2.2, BQ.1.6, BU.2, CV.1, CQ.2, BE.4, BA.5.1.25, BQ.1.26, BQ.1.10, BV.2, BE.3, BA.5.2.22, BF.15, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BF.29, BQ.1.23, BA.4.5, BE.4.1.1, BF.32, BQ.1.2, BA.5.1.24, BF.3.1,	McCallum et al. (2021)	84146	T	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
L452R	antibody epitope effects	extasciitilde20% (ELISA significance threshold) drop in antibody binding (ELISA) by this variant against monoclonal antibody VH ab6.	BA.5.1.2, BQ.1.1.15, BA.5.2.14, DE.2, BE.4.2, CN.1, BF.5, BF.7.1, BA.5.2.3, BA.2.75, BA.4.4, BA.5.1.9, BA.5.2.23, BQ.1.1.19, BQ.1.1.3, BA.5.2.34, CQ.1.1, BA.4.1.9, BA.5.2.18, BE.1.1.2, BF.12, BR.2.1, BF.26, BA.5.1.21, BA.5.1.16, CG.1, BA.5.1.3, BF.17, BQ.1.16, BA.5.3.3, CE.1, BA.5.2.26, BQ.1.1.14, BQ.1.1.2, BQ.1.8.2, BR.1.2, BA.5.2.28, BT.2, BQ.1.1.5, CR.1.2, BA.5.1.4, BA.4.1.5, BQ.1.1.25, BA.5.1.22, BQ.1.3, BA.5.1.19, BA.4.1.1, BF.7.5, BF.1, BA.4.1.10, BA.5.2.21, BQ.1.1.7, BQ.1.1.6, BQ.1.10.1, BR.1, BQ.1.1.28, CA.1, BF.4, CK.3, BF.7.4.1, CR.2, XBE, BA.2.75.4, BQ.1.1.27, BA.5.2.37, CA.7, BQ.1.1, BQ.1.12, BA.4.7, BF.19, BA.5.10, BF.31, BF.7.3, BF.7.7, BA.5.1.31, BF.7.8, XAS, BA.5.2.33, CC.1, BQ.1.1.24, BA.5.6.2, BA.5.2.2, BQ.1.6, BU.2, CV.1, CQ.2, BE.4, BA.5.1.25, BQ.1.26, BQ.1.10, BV.2, BE.3, BA.5.2.22, BF.15, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BF.29, BQ.1.23, BA.4.5, BE.4.1.1, BF.32, BQ.1.2, BA.5.1.24, BF.3.1,	Sun et al. (2021)	84146	T	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
L452R	convalescent plasma binding	2.15x increase in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset.	BA.5.1.2, BQ.1.1.15, BA.5.2.14, DE.2, BE.4.2, CN.1, BF.5, BF.7.1, BA.5.2.3, BA.2.75, BA.4.4, BA.5.1.9, BA.5.2.23, BQ.1.1.19, BQ.1.1.3, BA.5.2.34, CQ.1.1, BA.4.1.9, BA.5.2.18, BE.1.1.2, BF.12, BR.2.1, BF.26, BA.5.1.21, BA.5.1.16, CG.1, BA.5.1.3, BF.17, BQ.1.16, BA.5.3.3, CE.1, BA.5.2.26, BQ.1.1.14, BQ.1.1.2, BQ.1.8.2, BR.1.2, BA.5.2.28, BT.2, BQ.1.1.5, CR.1.2, BA.5.1.4, BA.4.1.5, BQ.1.1.25, BA.5.1.22, BQ.1.3, BA.5.1.19, BA.4.1.1, BF.7.5, BF.1, BA.4.1.10, BA.5.2.21, BQ.1.1.7, BQ.1.1.6, BQ.1.10.1, BR.1, BQ.1.1.28, CA.1, BF.4, CK.3, BF.7.4.1, CR.2, XBE, BA.2.75.4, BQ.1.1.27, BA.5.2.37, CA.7, BQ.1.1, BQ.1.12, BA.4.7, BF.19, BA.5.10, BF.31, BF.7.3, BF.7.7, BA.5.1.31, BF.7.8, XAS, BA.5.2.33, CC.1, BQ.1.1.24, BA.5.6.2, BA.5.2.2, BQ.1.6, BU.2, CV.1, CQ.2, BE.4, BA.5.1.25, BQ.1.26, BQ.1.10, BV.2, BE.3, BA.5.2.22, BF.15, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BF.29, BQ.1.23, BA.4.5, BE.4.1.1, BF.32, BQ.1.2, BA.5.1.24, BF.3.1,	Gong et al. (2021)	84146	T	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
L452R	convalescent plasma escape	Observed extasciitilde2x decrease on average in 16 health workers' convalescent sera.	BA.5.1.2, BQ.1.1.15, BA.5.2.14, DE.2, BE.4.2, CN.1, BF.5, BF.7.1, BA.5.2.3, BA.2.75, BA.4.4, BA.5.1.9, BA.5.2.23, BQ.1.1.19, BQ.1.1.3, BA.5.2.34, CQ.1.1, BA.4.1.9, BA.5.2.18, BE.1.1.2, BF.12, BR.2.1, BF.26, BA.5.1.21, BA.5.1.16, CG.1, BA.5.1.3, BF.17, BQ.1.16, BA.5.3.3, CE.1, BA.5.2.26, BQ.1.1.14, BQ.1.1.2, BQ.1.8.2, BR.1.2, BA.5.2.28, BT.2, BQ.1.1.5, CR.1.2, BA.5.1.4, BA.4.1.5, BQ.1.1.25, BA.5.1.22, BQ.1.3, BA.5.1.19, BA.4.1.1, BF.7.5, BF.1, BA.4.1.10, BA.5.2.21, BQ.1.1.7, BQ.1.1.6, BQ.1.10.1, BR.1, BQ.1.1.28, CA.1, BF.4, CK.3, BF.7.4.1, CR.2, XBE, BA.2.75.4, BQ.1.1.27, BA.5.2.37, CA.7, BQ.1.1, BQ.1.12, BA.4.7, BF.19, BA.5.10, BF.31, BF.7.3, BF.7.7, BA.5.1.31, BF.7.8, XAS, BA.5.2.33, CC.1, BQ.1.1.24, BA.5.6.2, BA.5.2.2, BQ.1.6, BU.2, CV.1, CQ.2, BE.4, BA.5.1.25, BQ.1.26, BQ.1.10, BV.2, BE.3, BA.5.2.22, BF.15, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BF.29, BQ.1.23, BA.4.5, BE.4.1.1, BF.32, BQ.1.2, BA.5.1.24, BF.3.1,	Alenquer et al. (2021)	84146	T	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
L452R	convalescent plasma escape	Ablation of neutralization capability of 3 of 4 convalescent sera tested, the other is significantly hindered.	BA.5.1.2, BQ.1.1.15, BA.5.2.14, DE.2, BE.4.2, CN.1, BF.5, BF.7.1, BA.5.2.3, BA.2.75, BA.4.4, BA.5.1.9, BA.5.2.23, BQ.1.1.19, BQ.1.1.3, BA.5.2.34, CQ.1.1, BA.4.1.9, BA.5.2.18, BE.1.1.2, BF.12, BR.2.1, BF.26, BA.5.1.21, BA.5.1.16, CG.1, BA.5.1.3, BF.17, BQ.1.16, BA.5.3.3, CE.1, BA.5.2.26, BQ.1.1.14, BQ.1.1.2, BQ.1.8.2, BR.1.2, BA.5.2.28, BT.2, BQ.1.1.5, CR.1.2, BA.5.1.4, BA.4.1.5, BQ.1.1.25, BA.5.1.22, BQ.1.3, BA.5.1.19, BA.4.1.1, BF.7.5, BF.1, BA.4.1.10, BA.5.2.21, BQ.1.1.7, BQ.1.1.6, BQ.1.10.1, BR.1, BQ.1.1.28, CA.1, BF.4, CK.3, BF.7.4.1, CR.2, XBE, BA.2.75.4, BQ.1.1.27, BA.5.2.37, CA.7, BQ.1.1, BQ.1.12, BA.4.7, BF.19, BA.5.10, BF.31, BF.7.3, BF.7.7, BA.5.1.31, BF.7.8, XAS, BA.5.2.33, CC.1, BQ.1.1.24, BA.5.6.2, BA.5.2.2, BQ.1.6, BU.2, CV.1, CQ.2, BE.4, BA.5.1.25, BQ.1.26, BQ.1.10, BV.2, BE.3, BA.5.2.22, BF.15, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BF.29, BQ.1.23, BA.4.5, BE.4.1.1, BF.32, BQ.1.2, BA.5.1.24, BF.3.1,	Liu et al. (2021)	84146	T	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
L452R	convalescent plasma escape	Relative to B.1, Epsilon (B.1.417/429) shows 1.74x-2.35x decrease in neutralization efficiency by convalescent plasma [no cohort details provided]	BA.5.1.2, BQ.1.1.15, BA.5.2.14, DE.2, BE.4.2, CN.1, BF.5, BF.7.1, BA.5.2.3, BA.2.75, BA.4.4, BA.5.1.9, BA.5.2.23, BQ.1.1.19, BQ.1.1.3, BA.5.2.34, CQ.1.1, BA.4.1.9, BA.5.2.18, BE.1.1.2, BF.12, BR.2.1, BF.26, BA.5.1.21, BA.5.1.16, CG.1, BA.5.1.3, BF.17, BQ.1.16, BA.5.3.3, CE.1, BA.5.2.26, BQ.1.1.14, BQ.1.1.2, BQ.1.8.2, BR.1.2, BA.5.2.28, BT.2, BQ.1.1.5, CR.1.2, BA.5.1.4, BA.4.1.5, BQ.1.1.25, BA.5.1.22, BQ.1.3, BA.5.1.19, BA.4.1.1, BF.7.5, BF.1, BA.4.1.10, BA.5.2.21, BQ.1.1.7, BQ.1.1.6, BQ.1.10.1, BR.1, BQ.1.1.28, CA.1, BF.4, CK.3, BF.7.4.1, CR.2, XBE, BA.2.75.4, BQ.1.1.27, BA.5.2.37, CA.7, BQ.1.1, BQ.1.12, BA.4.7, BF.19, BA.5.10, BF.31, BF.7.3, BF.7.7, BA.5.1.31, BF.7.8, XAS, BA.5.2.33, CC.1, BQ.1.1.24, BA.5.6.2, BA.5.2.2, BQ.1.6, BU.2, CV.1, CQ.2, BE.4, BA.5.1.25, BQ.1.26, BQ.1.10, BV.2, BE.3, BA.5.2.22, BF.15, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BF.29, BQ.1.23, BA.4.5, BE.4.1.1, BF.32, BQ.1.2, BA.5.1.24, BF.3.1,	Wilhelm et al. (2021)	84146	T	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
L452R	gene expression increase	Experimentally, Spike gene expression increased 0.32 fold	BA.5.1.2, BQ.1.1.15, BA.5.2.14, DE.2, BE.4.2, CN.1, BF.5, BF.7.1, BA.5.2.3, BA.2.75, BA.4.4, BA.5.1.9, BA.5.2.23, BQ.1.1.19, BQ.1.1.3, BA.5.2.34, CQ.1.1, BA.4.1.9, BA.5.2.18, BE.1.1.2, BF.12, BR.2.1, BF.26, BA.5.1.21, BA.5.1.16, CG.1, BA.5.1.3, BF.17, BQ.1.16, BA.5.3.3, CE.1, BA.5.2.26, BQ.1.1.14, BQ.1.1.2, BQ.1.8.2, BR.1.2, BA.5.2.28, BT.2, BQ.1.1.5, CR.1.2, BA.5.1.4, BA.4.1.5, BQ.1.1.25, BA.5.1.22, BQ.1.3, BA.5.1.19, BA.4.1.1, BF.7.5, BF.1, BA.4.1.10, BA.5.2.21, BQ.1.1.7, BQ.1.1.6, BQ.1.10.1, BR.1, BQ.1.1.28, CA.1, BF.4, CK.3, BF.7.4.1, CR.2, XBE, BA.2.75.4, BQ.1.1.27, BA.5.2.37, CA.7, BQ.1.1, BQ.1.12, BA.4.7, BF.19, BA.5.10, BF.31, BF.7.3, BF.7.7, BA.5.1.31, BF.7.8, XAS, BA.5.2.33, CC.1, BQ.1.1.24, BA.5.6.2, BA.5.2.2, BQ.1.6, BU.2, CV.1, CQ.2, BE.4, BA.5.1.25, BQ.1.26, BQ.1.10, BV.2, BE.3, BA.5.2.22, BF.15, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BF.29, BQ.1.23, BA.4.5, BE.4.1.1, BF.32, BQ.1.2, BA.5.1.24, BF.3.1,	Starr et al. (2020)	84146	T	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
L452R	monoclonal antibody serial passage escape	Ranked effective mutant against this position in the RBD for highly neutralizing COV2-2096	BA.5.1.2, BQ.1.1.15, BA.5.2.14, DE.2, BE.4.2, CN.1, BF.5, BF.7.1, BA.5.2.3, BA.2.75, BA.4.4, BA.5.1.9, BA.5.2.23, BQ.1.1.19, BQ.1.1.3, BA.5.2.34, CQ.1.1, BA.4.1.9, BA.5.2.18, BE.1.1.2, BF.12, BR.2.1, BF.26, BA.5.1.21, BA.5.1.16, CG.1, BA.5.1.3, BF.17, BQ.1.16, BA.5.3.3, CE.1, BA.5.2.26, BQ.1.1.14, BQ.1.1.2, BQ.1.8.2, BR.1.2, BA.5.2.28, BT.2, BQ.1.1.5, CR.1.2, BA.5.1.4, BA.4.1.5, BQ.1.1.25, BA.5.1.22, BQ.1.3, BA.5.1.19, BA.4.1.1, BF.7.5, BF.1, BA.4.1.10, BA.5.2.21, BQ.1.1.7, BQ.1.1.6, BQ.1.10.1, BR.1, BQ.1.1.28, CA.1, BF.4, CK.3, BF.7.4.1, CR.2, XBE, BA.2.75.4, BQ.1.1.27, BA.5.2.37, CA.7, BQ.1.1, BQ.1.12, BA.4.7, BF.19, BA.5.10, BF.31, BF.7.3, BF.7.7, BA.5.1.31, BF.7.8, XAS, BA.5.2.33, CC.1, BQ.1.1.24, BA.5.6.2, BA.5.2.2, BQ.1.6, BU.2, CV.1, CQ.2, BE.4, BA.5.1.25, BQ.1.26, BQ.1.10, BV.2, BE.3, BA.5.2.22, BF.15, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BF.29, BQ.1.23, BA.4.5, BE.4.1.1, BF.32, BQ.1.2, BA.5.1.24, BF.3.1,	Greaney et al. (2020)	84146	T	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
L452R	monoclonal antibody serial passage escape	Escape mutation against monoclonal antibody LY-CoV555 (antibody that forms the basis for Eli Lilly's bamlanivimab)	BA.5.1.2, BQ.1.1.15, BA.5.2.14, DE.2, BE.4.2, CN.1, BF.5, BF.7.1, BA.5.2.3, BA.2.75, BA.4.4, BA.5.1.9, BA.5.2.23, BQ.1.1.19, BQ.1.1.3, BA.5.2.34, CQ.1.1, BA.4.1.9, BA.5.2.18, BE.1.1.2, BF.12, BR.2.1, BF.26, BA.5.1.21, BA.5.1.16, CG.1, BA.5.1.3, BF.17, BQ.1.16, BA.5.3.3, CE.1, BA.5.2.26, BQ.1.1.14, BQ.1.1.2, BQ.1.8.2, BR.1.2, BA.5.2.28, BT.2, BQ.1.1.5, CR.1.2, BA.5.1.4, BA.4.1.5, BQ.1.1.25, BA.5.1.22, BQ.1.3, BA.5.1.19, BA.4.1.1, BF.7.5, BF.1, BA.4.1.10, BA.5.2.21, BQ.1.1.7, BQ.1.1.6, BQ.1.10.1, BR.1, BQ.1.1.28, CA.1, BF.4, CK.3, BF.7.4.1, CR.2, XBE, BA.2.75.4, BQ.1.1.27, BA.5.2.37, CA.7, BQ.1.1, BQ.1.12, BA.4.7, BF.19, BA.5.10, BF.31, BF.7.3, BF.7.7, BA.5.1.31, BF.7.8, XAS, BA.5.2.33, CC.1, BQ.1.1.24, BA.5.6.2, BA.5.2.2, BQ.1.6, BU.2, CV.1, CQ.2, BE.4, BA.5.1.25, BQ.1.26, BQ.1.10, BV.2, BE.3, BA.5.2.22, BF.15, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BF.29, BQ.1.23, BA.4.5, BE.4.1.1, BF.32, BQ.1.2, BA.5.1.24, BF.3.1,	Starr et al. (2021)	84146	T	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
L452R	monoclonal antibody serial passage escape	Class 2/3 antibody C628 and class 2 antibody C643 selected for the emergence of the L452R mutation in vitro.	BA.5.1.2, BQ.1.1.15, BA.5.2.14, DE.2, BE.4.2, CN.1, BF.5, BF.7.1, BA.5.2.3, BA.2.75, BA.4.4, BA.5.1.9, BA.5.2.23, BQ.1.1.19, BQ.1.1.3, BA.5.2.34, CQ.1.1, BA.4.1.9, BA.5.2.18, BE.1.1.2, BF.12, BR.2.1, BF.26, BA.5.1.21, BA.5.1.16, CG.1, BA.5.1.3, BF.17, BQ.1.16, BA.5.3.3, CE.1, BA.5.2.26, BQ.1.1.14, BQ.1.1.2, BQ.1.8.2, BR.1.2, BA.5.2.28, BT.2, BQ.1.1.5, CR.1.2, BA.5.1.4, BA.4.1.5, BQ.1.1.25, BA.5.1.22, BQ.1.3, BA.5.1.19, BA.4.1.1, BF.7.5, BF.1, BA.4.1.10, BA.5.2.21, BQ.1.1.7, BQ.1.1.6, BQ.1.10.1, BR.1, BQ.1.1.28, CA.1, BF.4, CK.3, BF.7.4.1, CR.2, XBE, BA.2.75.4, BQ.1.1.27, BA.5.2.37, CA.7, BQ.1.1, BQ.1.12, BA.4.7, BF.19, BA.5.10, BF.31, BF.7.3, BF.7.7, BA.5.1.31, BF.7.8, XAS, BA.5.2.33, CC.1, BQ.1.1.24, BA.5.6.2, BA.5.2.2, BQ.1.6, BU.2, CV.1, CQ.2, BE.4, BA.5.1.25, BQ.1.26, BQ.1.10, BV.2, BE.3, BA.5.2.22, BF.15, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BF.29, BQ.1.23, BA.4.5, BE.4.1.1, BF.32, BQ.1.2, BA.5.1.24, BF.3.1,	Wang et al. (2021)	84146	T	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
L452R	pharmaceutical effectiveness	Bamlanivimab (LY-CoV555) lost extasci-itilde5x binding against this isolated mutation. Cligavimab lost extasci-itilde4x binding against this isolated mutation. Regdanvimab lost extasci-itilde4x binding against this isolated mutation.	BA.5.1.2, BQ.1.1.15, BA.5.2.14, DE.2, BE.4.2, CN.1, BF.5, BF.7.1, BA.5.2.3, BA.2.75, BA.4.4, BA.5.1.9, BA.5.2.23, BQ.1.1.19, BQ.1.1.3, BA.5.2.34, CQ.1.1, BA.4.1.9, BA.5.2.18, BE.1.1.2, BF.12, BR.2.1, BF.26, BA.5.1.21, BA.5.1.16, CG.1, BA.5.1.3, BF.17, BQ.1.16, BA.5.3.3, CE.1, BA.5.2.26, BQ.1.1.14, BQ.1.1.2, BQ.1.8.2, BR.1.2, BA.5.2.28, BT.2, BQ.1.1.5, CR.1.2, BA.5.1.4, BA.4.1.5, BQ.1.1.25, BA.5.1.22, BQ.1.3, BA.5.1.19, BA.4.1.1, BF.7.5, BF.1, BA.4.1.10, BA.5.2.21, BQ.1.1.7, BQ.1.1.6, BQ.1.10.1, BR.1, BQ.1.1.28, CA.1, BF.4, CK.3, BF.7.4.1, CR.2, XBE, BA.2.75.4, BQ.1.1.27, BA.5.2.37, CA.7, BQ.1.1, BQ.1.12, BA.4.7, BF.19, BA.5.10, BF.31, BF.7.3, BF.7.7, BA.5.1.31, BF.7.8, XAS, BA.5.2.33, CC.1, BQ.1.1.24, BA.5.6.2, BA.5.2.2, BQ.1.6, BU.2, CV.1, CQ.2, BE.4, BA.5.1.25, BQ.1.26, BQ.1.10, BV.2, BE.3, BA.5.2.22, BF.15, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BF.29, BQ.1.23, BA.4.5, BE.4.1.1, BF.32, BQ.1.2, BA.5.1.24, BF.3.1,	Engelhart et al. (2021)	84146	T	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
L452R	pharmaceutical effectiveness	Bamlanivimab (LY-CoV555) entirely lost its neutralizing activity due to the central location of L452R in the epitopes recognized by this mAb. Regdanvimab (CT-P59), and to a smaller extent etesevimab, showed a reduction in neutralization potency.	BA.5.1.2, BQ.1.1.15, BA.5.2.14, DE.2, BE.4.2, CN.1, BF.5, BF.7.1, BA.5.2.3, BA.2.75, BA.4.4, BA.5.1.9, BA.5.2.23, BQ.1.1.19, BQ.1.1.3, BA.5.2.34, CQ.1.1, BA.4.1.9, BA.5.2.18, BE.1.1.2, BF.12, BR.2.1, BF.26, BA.5.1.21, BA.5.1.16, CG.1, BA.5.1.3, BF.17, BQ.1.16, BA.5.3.3, CE.1, BA.5.2.26, BQ.1.1.14, BQ.1.1.2, BQ.1.8.2, BR.1.2, BA.5.2.28, BT.2, BQ.1.1.5, CR.1.2, BA.5.1.4, BA.4.1.5, BQ.1.1.25, BA.5.1.22, BQ.1.3, BA.5.1.19, BA.4.1.1, BF.7.5, BF.1, BA.4.1.10, BA.5.2.21, BQ.1.1.7, BQ.1.1.6, BQ.1.10.1, BR.1, BQ.1.1.28, CA.1, BF.4, CK.3, BF.7.4.1, CR.2, XBE, BA.2.75.4, BQ.1.1.27, BA.5.2.37, CA.7, BQ.1.1, BQ.1.12, BA.4.7, BF.19, BA.5.10, BF.31, BF.7.3, BF.7.7, BA.5.1.31, BF.7.8, XAS, BA.5.2.33, CC.1, BQ.1.1.24, BA.5.6.2, BA.5.2.2, BQ.1.6, BU.2, CV.1, CQ.2, BE.4, BA.5.1.25, BQ.1.26, BQ.1.10, BV.2, BE.3, BA.5.2.22, BF.15, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BF.29, BQ.1.23, BA.4.5, BE.4.1.1, BF.32, BQ.1.2, BA.5.1.24, BF.3.1,	McCallum et al. (2021)	84146	T	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
L452R	trafficking	We observed increased entry by pseudoviruses carrying the L452R mutation compared to D614G alone, with a 6.7 to 22.5-fold increase in 293T cells and a 5.8 to 14.7-fold increase in human airway organoids.	BA.5.1.2, BQ.1.1.15, BA.5.2.14, DE.2, BE.4.2, CN.1, BF.5, BF.7.1, BA.5.2.3, BA.2.75, BA.4.4, BA.5.1.9, BA.5.2.23, BQ.1.1.19, BQ.1.1.3, BA.5.2.34, CQ.1.1, BA.4.1.9, BA.5.2.18, BE.1.1.2, BF.12, BR.2.1, BF.26, BA.5.1.21, BA.5.1.16, CG.1, BA.5.1.3, BF.17, BQ.1.16, BA.5.3.3, CE.1, BA.5.2.26, BQ.1.1.14, BQ.1.1.2, BQ.1.8.2, BR.1.2, BA.5.2.28, BT.2, BQ.1.1.5, CR.1.2, BA.5.1.4, BA.4.1.5, BQ.1.1.25, BA.5.1.22, BQ.1.3, BA.5.1.19, BA.4.1.1, BF.7.5, BF.1, BA.4.1.10, BA.5.2.21, BQ.1.1.7, BQ.1.1.6, BQ.1.10.1, BR.1, BQ.1.1.28, CA.1, BF.4, CK.3, BF.7.4.1, CR.2, XBE, BA.2.75.4, BQ.1.1.27, BA.5.2.37, CA.7, BQ.1.1, BQ.1.12, BA.4.7, BF.19, BA.5.10, BF.31, BF.7.3, BF.7.7, BA.5.1.31, BF.7.8, XAS, BA.5.2.33, CC.1, BQ.1.1.24, BA.5.6.2, BA.5.2.2, BQ.1.6, BU.2, CV.1, CQ.2, BE.4, BA.5.1.25, BQ.1.26, BQ.1.10, BV.2, BE.3, BA.5.2.22, BF.15, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BF.29, BQ.1.23, BA.4.5, BE.4.1.1, BF.32, BQ.1.2, BA.5.1.24, BF.3.1,	Deng et al. (2021)	84146	T	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
L452R	trafficking	This variant alone shows a extasciitilde5x decrease in cell entry efficiency (RLU measurement in 293T cells) compared to D614G. [listed as L454R in Figure, but L452R in text, also text suggests not statistucally significant, but error bars say otherwise in Figure 4]	BA.5.1.2, BQ.1.1.15, BA.5.2.14, DE.2, BE.4.2, CN.1, BF.5, BF.7.1, BA.5.2.3, BA.2.75, BA.4.4, BA.5.1.9, BA.5.2.23, BQ.1.1.19, BQ.1.1.3, BA.5.2.34, CQ.1.1, BA.4.1.9, BA.5.2.18, BE.1.1.2, BF.12, BR.2.1, BF.26, BA.5.1.21, BA.5.1.16, CG.1, BA.5.1.3, BF.17, BQ.1.16, BA.5.3.3, CE.1, BA.5.2.26, BQ.1.1.14, BQ.1.1.2, BQ.1.8.2, BR.1.2, BA.5.2.28, BT.2, BQ.1.1.5, CR.1.2, BA.5.1.4, BA.4.1.5, BQ.1.1.25, BA.5.1.22, BQ.1.3, BA.5.1.19, BA.4.1.1, BF.7.5, BF.1, BA.4.1.10, BA.5.2.21, BQ.1.1.7, BQ.1.1.6, BQ.1.10.1, BR.1, BQ.1.1.28, CA.1, BF.4, CK.3, BF.7.4.1, CR.2, XBE, BA.2.75.4, BQ.1.1.27, BA.5.2.37, CA.7, BQ.1.1, BQ.1.12, BA.4.7, BF.19, BA.5.10, BF.31, BF.7.3, BF.7.7, BA.5.1.31, BF.7.8, XAS, BA.5.2.33, CC.1, BQ.1.1.24, BA.5.6.2, BA.5.2.2, BQ.1.6, BU.2, CV.1, CQ.2, BE.4, BA.5.1.25, BQ.1.26, BQ.1.10, BV.2, BE.3, BA.5.2.22, BF.15, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BF.29, BQ.1.23, BA.4.5, BE.4.1.1, BF.32, BQ.1.2, BA.5.1.24, BF.3.1,	Ferriera et al (2021)	84146	T	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
L452R	trafficking	Increased stability of RBD expression in yeast, suggesting increased Spike protein stability.	BA.5.1.2, BQ.1.1.15, BA.5.2.14, DE.2, BE.4.2, CN.1, BF.5, BF.7.1, BA.5.2.3, BA.2.75, BA.4.4, BA.5.1.9, BA.5.2.23, BQ.1.1.19, BQ.1.1.3, BA.5.2.34, CQ.1.1, BA.4.1.9, BA.5.2.18, BE.1.1.2, BF.12, BR.2.1, BF.26, BA.5.1.21, BA.5.1.16, CG.1, BA.5.1.3, BF.17, BQ.1.16, BA.5.3.3, CE.1, BA.5.2.26, BQ.1.1.14, BQ.1.1.2, BQ.1.8.2, BR.1.2, BA.5.2.28, BT.2, BQ.1.1.5, CR.1.2, BA.5.1.4, BA.4.1.5, BQ.1.1.25, BA.5.1.22, BQ.1.3, BA.5.1.19, BA.4.1.1, BF.7.5, BF.1, BA.4.1.10, BA.5.2.21, BQ.1.1.7, BQ.1.1.6, BQ.1.10.1, BR.1, BQ.1.1.28, CA.1, BF.4, CK.3, BF.7.4.1, CR.2, XBE, BA.2.75.4, BQ.1.1.27, BA.5.2.37, CA.7, BQ.1.1, BQ.1.12, BA.4.7, BF.19, BA.5.10, BF.31, BF.7.3, BF.7.7, BA.5.1.31, BF.7.8, XAS, BA.5.2.33, CC.1, BQ.1.1.24, BA.5.6.2, BA.5.2.2, BQ.1.6, BU.2, CV.1, CQ.2, BE.4, BA.5.1.25, BQ.1.26, BQ.1.10, BV.2, BE.3, BA.5.2.22, BF.15, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BF.29, BQ.1.23, BA.4.5, BE.4.1.1, BF.32, BQ.1.2, BA.5.1.24, BF.3.1,	Motozono et al. (2021)	84146	T	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
L452R	transmissibility	Increased infectivity of the B.1.617 spike was attributed to L452R, which itself caused a 3.5-fold increase in infectivity relative to D614G wild type. [In combination with E484Q caused a lower 3-fold increase]	BA.5.1.2, BQ.1.1.15, BA.5.2.14, DE.2, BE.4.2, CN.1, BF.5, BF.7.1, BA.5.2.3, BA.2.75, BA.4.4, BA.5.1.9, BA.5.2.23, BQ.1.1.19, BQ.1.1.3, BA.5.2.34, CQ.1.1, BA.4.1.9, BA.5.2.18, BE.1.1.2, BF.12, BR.2.1, BF.26, BA.5.1.21, BA.5.1.16, CG.1, BA.5.1.3, BF.17, BQ.1.16, BA.5.3.3, CE.1, BA.5.2.26, BQ.1.1.14, BQ.1.1.2, BQ.1.8.2, BR.1.2, BA.5.2.28, BT.2, BQ.1.1.5, CR.1.2, BA.5.1.4, BA.4.1.5, BQ.1.1.25, BA.5.1.22, BQ.1.3, BA.5.1.19, BA.4.1.1, BF.7.5, BF.1, BA.4.1.10, BA.5.2.21, BQ.1.1.7, BQ.1.1.6, BQ.1.10.1, BR.1, BQ.1.1.28, CA.1, BF.4, CK.3, BF.7.4.1, CR.2, XBE, BA.2.75.4, BQ.1.1.27, BA.5.2.37, CA.7, BQ.1.1, BQ.1.12, BA.4.7, BF.19, BA.5.10, BF.31, BF.7.3, BF.7.7, BA.5.1.31, BF.7.8, XAS, BA.5.2.33, CC.1, BQ.1.1.24, BA.5.6.2, BA.5.2.2, BQ.1.6, BU.2, CV.1, CQ.2, BE.4, BA.5.1.25, BQ.1.26, BQ.1.10, BV.2, BE.3, BA.5.2.22, BF.15, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BF.29, BQ.1.23, BA.4.5, BE.4.1.1, BF.32, BQ.1.2, BA.5.1.24, BF.3.1,	Tada et al. (2021)	84146	T	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
L452R	vaccine neutralization efficacy	Nine stored sera from Pfizer BNT162b2 vaccinees were tested against a range of spike mutation bearing PV. L452R conferred about a two-fold reduction in neutralisation by vaccine sera, but was not statistically significant with this sample size.	BA.5.1.2, BQ.1.1.15, BA.5.2.14, DE.2, BE.4.2, CN.1, BF.5, BF.7.1, BA.5.2.3, BA.2.75, BA.4.4, BA.5.1.9, BA.5.2.23, BQ.1.1.19, BQ.1.1.3, BA.5.2.34, CQ.1.1, BA.4.1.9, BA.5.2.18, BE.1.1.2, BF.12, BR.2.1, BF.26, BA.5.1.21, BA.5.1.16, CG.1, BA.5.1.3, BF.17, BQ.1.16, BA.5.3.3, CE.1, BA.5.2.26, BQ.1.1.14, BQ.1.1.2, BQ.1.8.2, BR.1.2, BA.5.2.28, BT.2, BQ.1.1.5, CR.1.2, BA.5.1.4, BA.4.1.5, BQ.1.1.25, BA.5.1.22, BQ.1.3, BA.5.1.19, BA.4.1.1, BF.7.5, BF.1, BA.4.1.10, BA.5.2.21, BQ.1.1.7, BQ.1.1.6, BQ.1.10.1, BR.1, BQ.1.1.28, CA.1, BF.4, CK.3, BF.7.4.1, CR.2, XBE, BA.2.75.4, BQ.1.1.27, BA.5.2.37, CA.7, BQ.1.1, BQ.1.12, BA.4.7, BF.19, BA.5.10, BF.31, BF.7.3, BF.7.7, BA.5.1.31, BF.7.8, XAS, BA.5.2.33, CC.1, BQ.1.1.24, BA.5.6.2, BA.5.2.2, BQ.1.6, BU.2, CV.1, CQ.2, BE.4, BA.5.1.25, BQ.1.26, BQ.1.10, BV.2, BE.3, BA.5.2.22, BF.15, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BF.29, BQ.1.23, BA.4.5, BE.4.1.1, BF.32, BQ.1.2, BA.5.1.24, BF.3.1,	Ferreira et al. (2021)	84146	T	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
L452R	vaccine neutralization efficacy	The presence of this variant in 189 post-mRNA-vaccination COVID-19 cases was proportionally in line with lineage prevalence in Northen California during the study period, suggesting no effect of these variants on immune escape.	BA.5.1.2, BQ.1.1.15, BA.5.2.14, DE.2, BE.4.2, CN.1, BF.5, BF.7.1, BA.5.2.3, BA.2.75, BA.4.4, BA.5.1.9, BA.5.2.23, BQ.1.1.19, BQ.1.1.3, BA.5.2.34, CQ.1.1, BA.4.1.9, BA.5.2.18, BE.1.1.2, BF.12, BR.2.1, BF.26, BA.5.1.21, BA.5.1.16, CG.1, BA.5.1.3, BF.17, BQ.1.16, BA.5.3.3, CE.1, BA.5.2.26, BQ.1.1.14, BQ.1.1.2, BQ.1.8.2, BR.1.2, BA.5.2.28, BT.2, BQ.1.1.5, CR.1.2, BA.5.1.4, BA.4.1.5, BQ.1.1.25, BA.5.1.22, BQ.1.3, BA.5.1.19, BA.4.1.1, BF.7.5, BF.1, BA.4.1.10, BA.5.2.21, BQ.1.1.7, BQ.1.1.6, BQ.1.10.1, BR.1, BQ.1.1.28, CA.1, BF.4, CK.3, BF.7.4.1, CR.2, XBE, BA.2.75.4, BQ.1.1.27, BA.5.2.37, CA.7, BQ.1.1, BQ.1.12, BA.4.7, BF.19, BA.5.10, BF.31, BF.7.3, BF.7.7, BA.5.1.31, BF.7.8, XAS, BA.5.2.33, CC.1, BQ.1.1.24, BA.5.6.2, BA.5.2.2, BQ.1.6, BU.2, CV.1, CQ.2, BE.4, BA.5.1.25, BQ.1.26, BQ.1.10, BV.2, BE.3, BA.5.2.22, BF.15, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BF.29, BQ.1.23, BA.4.5, BE.4.1.1, BF.32, BQ.1.2, BA.5.1.24, BF.3.1,	Jacobson et al. (2021)	84146	T	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
L452R	vaccine neutralization efficacy	The presence of these B.1.417/B.1.429 defining variants in 189 post-mRNA-vaccination COVID-19 cases was proportionally in line with lineage prevalence in Northen California during the study period, suggesting no effect of these variants on immune escape.	BA.5.1.2, BQ.1.1.15, BA.5.2.14, DE.2, BE.4.2, CN.1, BF.5, BF.7.1, BA.5.2.3, BA.2.75, BA.4.4, BA.5.1.9, BA.5.2.23, BQ.1.1.19, BQ.1.1.3, BA.5.2.34, CQ.1.1, BA.4.1.9, BA.5.2.18, BE.1.1.2, BF.12, BR.2.1, BF.26, BA.5.1.21, BA.5.1.16, CG.1, BA.5.1.3, BF.17, BQ.1.16, BA.5.3.3, CE.1, BA.5.2.26, BQ.1.1.14, BQ.1.1.2, BQ.1.8.2, BR.1.2, BA.5.2.28, BT.2, BQ.1.1.5, CR.1.2, BA.5.1.4, BA.4.1.5, BQ.1.1.25, BA.5.1.22, BQ.1.3, BA.5.1.19, BA.4.1.1, BF.7.5, BF.1, BA.4.1.10, BA.5.2.21, BQ.1.1.7, BQ.1.1.6, BQ.1.10.1, BR.1, BQ.1.1.28, CA.1, BF.4, CK.3, BF.7.4.1, CR.2, XBE, BA.2.75.4, BQ.1.1.27, BA.5.2.37, BQ.1.1.23, BQ.1.1, CA.7, BQ.1.12, BA.4.7, BF.19, BA.5.10, BF.31, BF.7.3, BF.7.7, BA.5.1.31, BF.7.8, XAS, BA.5.2.33, CC.1, BQ.1.1.24, BA.5.6.2, BA.5.2.2, BQ.1.6, BU.2, CV.1, CQ.2, BE.4, BA.5.1.25, BQ.1.26, BQ.1.10, BV.2, BE.3, BA.5.2.22, BF.15, BR.3, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BF.29, BQ.1.23, BA.4.5, BE.4.1.1, BE.3.2, BQ.1.2, BA.5.1.24, BF.3.1,	Jacobson et al. (2021)	84135	T	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
L452R	vaccine neutralization efficacy	Relative to B.1, Epsilon (B.1.417/429) shows 1.74x-2.35x decrease in neutralization efficiency by 18 vaccinee sera (BNT162b2 and mRNA1273).	BA.5.1.2, BQ.1.1.15, BA.5.2.14, DE.2, BE.4.2, CN.1, BF.5, BF.7.1, BA.5.2.3, BA.2.75, BA.4.4, BA.5.1.9, BA.5.2.23, BQ.1.1.19, BQ.1.1.3, BA.5.2.34, CQ.1.1, BA.4.1.9, BA.5.2.18, BE.1.1.2, BF.12, BR.2.1, BF.26, BA.5.1.21, BA.5.1.16, CG.1, BA.5.1.3, BF.17, BQ.1.16, BA.5.3.3, CE.1, BA.5.2.26, BQ.1.1.14, BQ.1.1.2, BQ.1.8.2, BR.1.2, BA.5.2.28, BT.2, BQ.1.1.5, CR.1.2, BA.5.1.4, BA.4.1.5, BQ.1.1.25, BA.5.1.22, BQ.1.3, BA.5.1.19, BA.4.1.1, BF.7.5, BF.1, BA.4.1.10, BA.5.2.21, BQ.1.1.7, BQ.1.1.6, BQ.1.10.1, BR.1, BQ.1.1.28, CA.1, BF.4, CK.3, BF.7.4.1, CR.2, XBE, BA.2.75.4, BQ.1.1.27, BA.5.2.37, CA.7, BQ.1.1, BQ.1.12, BA.4.7, BF.19, BA.5.10, BF.31, BF.7.3, BF.7.7, BA.5.1.31, BF.7.8, XAS, BA.5.2.33, CC.1, BQ.1.1.24, BA.5.6.2, BA.5.2.2, BQ.1.6, BU.2, CV.1, CQ.2, BE.4, BA.5.1.25, BQ.1.26, BQ.1.10, BV.2, BE.3, BA.5.2.22, BF.15, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BF.29, BQ.1.23, BA.4.5, BE.4.1.1, BF.32, BQ.1.2, BA.5.1.24, BF.3.1,	Wilhelm et al. (2021)	84146	T	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
L452R	vaccinee plasma binding	1.05x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in previously non-seroconverted subjects. 1.16x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in post-infection vaccinees.	BA.5.1.2, BQ.1.1.15, BA.5.2.14, DE.2, BE.4.2, CN.1, BF.5, BF.7.1, BA.5.2.3, BA.2.75, BA.4.4, BA.5.1.9, BA.5.2.23, BQ.1.1.19, BQ.1.1.3, BA.5.2.34, CQ.1.1, BA.4.1.9, BA.5.2.18, BE.1.1.2, BF.12, BR.2.1, BF.26, BA.5.1.21, BA.5.1.16, CG.1, BA.5.1.3, BF.17, BQ.1.16, BA.5.3.3, CE.1, BA.5.2.26, BQ.1.1.14, BQ.1.1.2, BQ.1.8.2, BR.1.2, BA.5.2.28, BT.2, BQ.1.1.5, CR.1.2, BA.5.1.4, BA.4.1.5, BQ.1.1.25, BA.5.1.22, BQ.1.3, BA.5.1.19, BA.4.1.1, BF.7.5, BF.1, BA.4.1.10, BA.5.2.21, BQ.1.1.7, BQ.1.1.6, BQ.1.10.1, BR.1, BQ.1.1.28, CA.1, BF.4, CK.3, BF.7.4.1, CR.2, XBE, BA.2.75.4, BQ.1.1.27, BA.5.2.37, CA.7, BQ.1.1, BQ.1.12, BA.4.7, BF.19, BA.5.10, BF.31, BF.7.3, BF.7.7, BA.5.1.31, BF.7.8, XAS, BA.5.2.33, CC.1, BQ.1.1.24, BA.5.6.2, BA.5.2.2, BQ.1.6, BU.2, CV.1, CQ.2, BE.4, BA.5.1.25, BQ.1.26, BQ.1.10, BV.2, BE.3, BA.5.2.22, BF.15, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BF.29, BQ.1.23, BA.4.5, BE.4.1.1, BF.32, BQ.1.2, BA.5.1.24, BF.3.1,	Gong et al. (2021)	84146	T	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
L452R	virion structure	Estimated free energy change (ddG) for this variant is -0.67 kcal/mol (i.e. destabilizing relative to wild type)	BA.5.1.2, BQ.1.1.15, BA.5.2.14, DE.2, BE.4.2, CN.1, BF.5, BF.7.1, BA.5.2.3, BA.2.75, BA.4.4, BA.5.1.9, BA.5.2.23, BQ.1.1.19, BQ.1.1.3, BA.5.2.34, CQ.1.1, BA.4.1.9, BA.5.2.18, BE.1.1.2, BF.12, BR.2.1, BF.26, BA.5.1.21, BA.5.1.16, CG.1, BA.5.1.3, BF.17, BQ.1.16, BA.5.3.3, CE.1, BA.5.2.26, BQ.1.1.14, BQ.1.1.2, BQ.1.8.2, BR.1.2, BA.5.2.28, BT.2, BQ.1.1.5, CR.1.2, BA.5.1.4, BA.4.1.5, BQ.1.1.25, BA.5.1.22, BQ.1.3, BA.5.1.19, BA.4.1.1, BF.7.5, BF.1, BA.4.1.10, BA.5.2.21, BQ.1.1.7, BQ.1.1.6, BQ.1.10.1, BR.1, BQ.1.1.28, CA.1, BF.4, CK.3, BF.7.4.1, CR.2, XBE, BA.2.75.4, BQ.1.1.27, BA.5.2.37, CA.7, BQ.1.1, BQ.1.12, BA.4.7, BF.19, BA.5.10, BF.31, BF.7.3, BF.7.7, BA.5.1.31, BF.7.8, XAS, BA.5.2.33, CC.1, BQ.1.1.24, BA.5.6.2, BA.5.2.2, BQ.1.6, BU.2, CV.1, CQ.2, BE.4, BA.5.1.25, BQ.1.26, BQ.1.10, BV.2, BE.3, BA.5.2.22, BF.15, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BF.29, BQ.1.23, BA.4.5, BE.4.1.1, BF.32, BQ.1.2, BA.5.1.24, BF.3.1,	Spratt et al. (2021)	84146	T	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
E484T	monoclonal antibody serial passage escape	Ranked moderately effective mutant against this position in the RBD for highly neutralizing COV2-2050 monoclonal antibody	XBB.1.3	Greaney et al. (2020)	1	GA	AC	1.0
E484T	monoclonal antibody serial passage escape	Escape mutation against monoclonal antibody LY-CoV555 (antibody that forms the basis for Eli Lilly's bamlanivimab)	XBB.1.3	Starr et al. (2021)	1	GA	AC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
Q493R	antibody epitope effects	Ablates binding by class 2 mAbs such as C144 that directly interfere with ACE2 binding, but clonal somatic mutations of memory B cells at 6.2 months (evolving humoral immune response) show pronounced increase in binding to the variant.	BA.2.52, BA.2.17, BA.1.1.7, XAQ, BA.2.9.2, BA.1.15.3, XZ, BA.2.43, BA.1.14, BA.1.15.1, BA.2.63, BA.1.1.14, BA.2.45, BA.1.14.2, BP.1, BA.2.3.17, BA.2.31.1, BA.1.1.2, BA.2.14, BA.5.2.28, BA.2.2.1, BA.2.3.13, BA.2.49, BA.2.12, BA.2.3.16, BA.1.13, BA.2.53, BA.2.34, BA.2.82, BA.2.9.3, BA.2.3.1, BA.2.3.8, BA.1.3, BA.1.17, BC.2, BA.2.81, BA.2.3.7, BA.2.2, BA.1.1.16, BA.1.10, BA.1.16, BA.1.17.2, BA.2.37, BA.2.55, BA.2.61, BA.2.3.14, XQ, BG.6, BA.2.50, BA.2.9, BA.1.1.4, BA.2.40.1, BA.2.72, BA.2.9.7, BA.2.13.1, BA.1.15, BA.2.54, BA.2.9.1, BA.2.23, BA.1.1.3, BA.2.18, BA.1.1, BA.2.32, BA.2.10, XAM, XM, BA.2.35, BA.2.21, BA.2.47, BA.1.18, BA.2.41, BA.2.20, BA.2.65, BA.2.27, BA.1.21, BA.1.9, BA.2.59, BA.2.3.12, BA.2.3.6, BA.2, BA.2.25, BA.2.3.15, BA.2.5, BA.2.11, BA.1.19, BH.1, BA.2.48, BA.1.13.1, BA.1.1.11, BA.2.42, BA.2.70, BA.2.3.10, BA.1.8, BA.2.23.1, BA.2.60, BA.2.12.1, BA.2.74, BA.2.44, BA.1.1.15,	Gaebler et al. (2021)	111372	A	G,GAC	0.99

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
Q493R	antibody epitope effects	Massive reduction in binding efficiency vs wild type for mAbs CB6/LY-CoV16 and LY-CoV555.	BA.2.52, BA.2.17, BA.1.1.7, XAQ, BA.2.9.2, BA.1.15.3, XZ, BA.2.43, BA.1.14, BA.1.15.1, BA.2.63, BA.1.1.14, BA.2.45, BA.1.14.2, BP.1, BA.2.3.17, BA.2.31.1, BA.1.1.2, BA.2.14, BA.5.2.28, BA.2.2.1, BA.2.3.13, BA.2.49, BA.2.12, BA.2.3.16, BA.1.13, BA.2.53, BA.2.34, BA.2.82, BA.2.9.3, BA.2.3.1, BA.2.3.8, BA.1.3, BA.1.17, BC.2, BA.2.81, BA.2.3.7, BA.2.2, BA.1.1.16, BA.1.10, BA.1.16, BA.1.17.2, BA.2.37, BA.2.55, BA.2.61, BA.2.3.14, XQ, BG.6, BA.2.50, BA.2.9, BA.1.1.4, BA.2.40.1, BA.2.72, BA.2.9.7, BA.2.13.1, BA.1.15, BA.2.54, BA.2.9.1, BA.2.23, BA.1.1.3, BA.2.18, BA.1.1, BA.2.32, BA.2.10, XAM, XM, BA.2.35, BA.2.21, BA.2.47, BA.1.18, BA.2.41, BA.2.20, BA.2.65, BA.2.27, BA.1.21, BA.1.9, BA.2.59, BA.2.3.12, BA.2.3.6, BA.2, BA.2.25, BA.2.3.15, BA.2.5, BA.2.11, BA.1.19, BH.1, BA.2.48, BA.1.13.1, BA.1.1.11, BA.2.42, BA.2.70, BA.2.3.10, BA.1.8, BA.2.23.1, BA.2.60, BA.2.12.1, BA.2.74, BA.2.44, BA.1.1.15,	Rappazzo et al. (2021)	111372	A	G,GAC	0.99

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
Q493R	antibody epitope effects	Somewhat resistent to some class 1 (Spike 'up') antibodies tested. Mix of non- to strongly resistent in class 2 antibodies tested.	BA.2.52, BA.2.17, BA.1.1.7, XAQ, BA.2.9.2, BA.1.15.3, XZ, BA.2.43, BA.1.14, BA.1.15.1, BA.2.63, BA.1.1.14, BA.2.45, BA.1.14.2, BP.1, BA.2.3.17, BA.2.31.1, BA.1.1.2, BA.2.14, BA.5.2.28, BA.2.2.1, BA.2.3.13, BA.2.49, BA.2.12, BA.2.3.16, BA.1.13, BA.2.53, BA.2.34, BA.2.82, BA.2.9.3, BA.2.3.1, BA.2.3.8, BA.1.3, BA.1.17, BC.2, BA.2.81, BA.2.3.7, BA.2.2, BA.1.1.16, BA.1.10, BA.1.16, BA.1.17.2, BA.2.37, BA.2.55, BA.2.61, BA.2.3.14, XQ, BG.6, BA.2.50, BA.2.9, BA.1.1.4, BA.2.40.1, BA.2.72, BA.2.9.7, BA.2.13.1, BA.1.15, BA.2.54, BA.2.9.1, BA.2.23, BA.1.1.3, BA.2.18, BA.1.1, BA.2.32, BA.2.10, XAM, XM, BA.2.35, BA.2.21, BA.2.47, BA.1.18, BA.2.41, BA.2.20, BA.2.65, BA.2.27, BA.1.21, BA.1.9, BA.2.59, BA.2.3.12, BA.2.3.6, BA.2, BA.2.25, BA.2.3.15, BA.2.5, BA.2.11, BA.1.19, BH.1, BA.2.48, BA.1.13.1, BA.1.1.11, BA.2.42, BA.2.70, BA.2.3.10, BA.1.8, BA.2.23.1, BA.2.60, BA.2.12.1, BA.2.74, BA.2.44, BA.1.1.15,	Wang et al. (2021)	111372	A	G,GAC	0.99

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
Q493R	convalescent plasma escape	Escape mutant found after in passage in plasma pool of 26 convalescents mean 1.5 post symptom onset.	BA.2.52, BA.2.17, BA.1.1.7, XAQ, BA.2.9.2, BA.1.15.3, XZ, BA.2.43, BA.1.14, BA.1.15.1, BA.2.63, BA.1.1.14, BA.2.45, BA.1.14.2, BP.1, BA.2.3.17, BA.2.31.1, BA.1.1.2, BA.2.14, BA.5.2.28, BA.2.2.1, BA.2.3.13, BA.2.49, BA.2.12, BA.2.3.16, BA.1.13, BA.2.53, BA.2.34, BA.2.82, BA.2.9.3, BA.2.3.1, BA.2.3.8, BA.1.3, BA.1.17, BC.2, BA.2.81, BA.2.3.7, BA.2.2, BA.1.1.16, BA.1.10, BA.1.16, BA.1.17.2, BA.2.37, BA.2.55, BA.2.61, BA.2.3.14, XQ, BG.6, BA.2.50, BA.2.9, BA.1.1.4, BA.2.40.1, BA.2.72, BA.2.9.7, BA.2.13.1, BA.1.15, BA.2.54, BA.2.9.1, BA.2.23, BA.1.1.3, BA.2.18, BA.1.1, BA.2.32, BA.2.10, XAM, XM, BA.2.35, BA.2.21, BA.2.47, BA.1.18, BA.2.41, BA.2.20, BA.2.65, BA.2.27, BA.1.21, BA.1.9, BA.2.59, BA.2.3.12, BA.2.3.6, BA.2, BA.2.25, BA.2.3.15, BA.2.5, BA.2.11, BA.1.19, BH.1, BA.2.48, BA.1.13.1, BA.1.1.11, BA.2.42, BA.2.70, BA.2.3.10, BA.1.8, BA.2.23.1, BA.2.60, BA.2.12.1, BA.2.74, BA.2.44,	Schmidt et al. (2021)	111372	A	G,GAC	0.99

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
Q493R	monoclonal antibody serial passage escape	The engineered mutation cause 10-fold or more increase in the disassociation constant with C144, C002 and C121 monoclonal antibodies vs. wild type Spike protein RBD domain AAs.	BA.2.52, BA.2.17, BA.1.1.7, XAQ, BA.2.9.2, BA.1.15.3, XZ, BA.2.43, BA.1.14, BA.1.15.1, BA.2.63, BA.1.1.14, BA.2.45, BA.1.14.2, BP.1, BA.2.3.17, BA.2.31.1, BA.1.1.2, BA.2.14, BA.5.2.28, BA.2.2.1, BA.2.3.13, BA.2.49, BA.2.12, BA.2.3.16, BA.1.13, BA.2.53, BA.2.34, BA.2.82, BA.2.9.3, BA.2.3.1, BA.2.3.8, BA.1.3, BA.1.17, BC.2, BA.2.81, BA.2.3.7, BA.2.2, BA.1.1.16, BA.1.10, BA.1.16, BA.1.17.2, BA.2.37, BA.2.55, BA.2.61, BA.2.3.14, XQ, BG.6, BA.2.50, BA.2.9, BA.1.1.4, BA.2.40.1, BA.2.72, BA.2.9.7, BA.2.13.1, BA.1.15, BA.2.54, BA.2.9.1, BA.2.23, BA.1.1.3, BA.2.18, BA.1.1, BA.2.32, BA.2.10, XAM, XM, BA.2.35, BA.2.21, BA.2.47, BA.1.18, BA.2.41, BA.2.20, BA.2.65, BA.2.27, BA.1.21, BA.1.9, BA.2.59, BA.2.3.12, BA.2.3.6, BA.2, BA.2.25, BA.2.3.15, BA.2.5, BA.2.11, BA.1.19, BH.1, BA.2.48, BA.1.13.1, BA.1.1.11, BA.2.42, BA.2.70, BA.2.3.10, BA.1.8, BA.2.23.1, BA.2.60, BA.2.12.1, BA.2.74, BA.2.44, BA.1.1.15,	Barnes et al. (2020)	111372	A	G,GAC	0.99

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
Q493R	monoclonal antibody serial passage escape	Escape mutation against monoclonal antibody LY-CoV555 (antibody that forms the basis for Eli Lilly's bamlanivimab)	BA.2.52, BA.2.17, BA.1.1.7, XAQ, BA.2.9.2, BA.1.15.3, XZ, BA.2.43, BA.1.14, BA.1.15.1, BA.2.63, BA.1.1.14, BA.2.45, BA.1.14.2, BP.1, BA.2.3.17, BA.2.31.1, BA.1.1.2, BA.2.14, BA.5.2.28, BA.2.2.1, BA.2.3.13, BA.2.49, BA.2.12, BA.2.3.16, BA.1.13, BA.2.53, BA.2.34, BA.2.82, BA.2.9.3, BA.2.3.1, BA.2.3.8, BA.1.3, BA.1.17, BC.2, BA.2.81, BA.2.3.7, BA.2.2, BA.1.1.16, BA.1.10, BA.1.16, BA.1.17.2, BA.2.37, BA.2.55, BA.2.61, BA.2.3.14, XQ, BG.6, BA.2.50, BA.2.9, BA.1.1.4, BA.2.40.1, BA.2.72, BA.2.9.7, BA.2.13.1, BA.1.15, BA.2.54, BA.2.9.1, BA.2.23, BA.1.1.3, BA.2.18, BA.1.1, BA.2.32, BA.2.10, XAM, XM, BA.2.35, BA.2.21, BA.2.47, BA.1.18, BA.2.41, BA.2.20, BA.2.65, BA.2.27, BA.1.21, BA.1.9, BA.2.59, BA.2.3.12, BA.2.3.6, BA.2, BA.2.25, BA.2.3.15, BA.2.5, BA.2.11, BA.1.19, BH.1, BA.2.48, BA.1.13.1, BA.1.1.11, BA.2.42, BA.2.70, BA.2.3.10, BA.1.8, BA.2.23.1, BA.2.60, BA.2.12.1, BA.2.74, BA.2.44, BA.1.1.15,	Starr et al. (2021)	111372	A	G,GAC	0.99

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
Q493R	monoclonal antibody serial passage escape	Class 2 mAb C627 modestly selected for the emergence of this mutation in vitro.	BA.2.52, BA.2.17, BA.1.1.7, XAQ, BA.2.9.2, BA.1.15.3, XZ, BA.2.43, BA.1.14, BA.1.15.1, BA.2.63, BA.1.1.14, BA.2.45, BA.1.14.2, BP.1, BA.2.3.17, BA.2.31.1, BA.1.1.2, BA.2.14, BA.5.2.28, BA.2.2.1, BA.2.3.13, BA.2.49, BA.2.12, BA.2.3.16, BA.1.13, BA.2.53, BA.2.34, BA.2.82, BA.2.9.3, BA.2.3.1, BA.2.3.8, BA.1.3, BA.1.17, BC.2, BA.2.81, BA.2.3.7, BA.2.2, BA.1.1.16, BA.1.10, BA.1.16, BA.1.17.2, BA.2.37, BA.2.55, BA.2.61, BA.2.3.14, XQ, BG.6, BA.2.50, BA.2.9, BA.1.1.4, BA.2.40.1, BA.2.72, BA.2.9.7, BA.2.13.1, BA.1.15, BA.2.54, BA.2.9.1, BA.2.23, BA.1.1.3, BA.2.18, BA.1.1, BA.2.32, BA.2.10, XAM, XM, BA.2.35, BA.2.21, BA.2.47, BA.1.18, BA.2.41, BA.2.20, BA.2.65, BA.2.27, BA.1.21, BA.1.9, BA.2.59, BA.2.3.12, BA.2.3.6, BA.2, BA.2.25, BA.2.3.15, BA.2.5, BA.2.11, BA.1.19, BH.1, BA.2.48, BA.1.13.1, BA.1.1.11, BA.2.42, BA.2.70, BA.2.3.10, BA.1.8, BA.2.23.1, BA.2.60, BA.2.12.1, BA.2.74, BA.2.44,	Wang et al. (2021)	111372	A	G,GAC	0.99

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
Q493R	monoclonal antibody serial passage escape	Strong positive selection (up to 37% of supernatant sequences) after two rounds of C135 monoclonal antibody passage, overall 76% switch away from Q493 to K or R	BA.2.52, BA.2.17, BA.1.1.7, XAQ, BA.2.9.2, BA.1.15.3, XZ, BA.2.43, BA.1.14, BA.1.15.1, BA.2.63, BA.1.1.14, BA.2.45, BA.1.14.2, BP.1, BA.2.3.17, BA.2.31.1, BA.1.1.2, BA.2.14, BA.5.2.28, BA.2.2.1, BA.2.3.13, BA.2.49, BA.2.12, BA.2.3.16, BA.1.13, BA.2.53, BA.2.34, BA.2.82, BA.2.9.3, BA.2.3.1, BA.2.3.8, BA.1.3, BA.1.17, BC.2, BA.2.81, BA.2.3.7, BA.2.2, BA.1.1.16, BA.1.10, BA.1.16, BA.1.17.2, BA.2.37, BA.2.55, BA.2.61, BA.2.3.14, XQ, BG.6, BA.2.50, BA.2.9, BA.1.1.4, BA.2.40.1, BA.2.72, BA.2.9.7, BA.2.13.1, BA.1.15, BA.2.54, BA.2.9.1, BA.2.23, BA.1.1.3, BA.2.18, BA.1.1, BA.2.32, BA.2.10, XAM, XM, BA.2.35, BA.2.21, BA.2.47, BA.1.18, BA.2.41, BA.2.20, BA.2.65, BA.2.27, BA.1.21, BA.1.9, BA.2.59, BA.2.3.12, BA.2.3.6, BA.2, BA.2.25, BA.2.3.15, BA.2.5, BA.2.11, BA.1.19, BH.1, BA.2.48, BA.1.13.1, BA.1.1.11, BA.2.42, BA.2.70, BA.2.3.10, BA.1.8, BA.2.23.1, BA.2.60, BA.2.12.1, BA.2.74, BA.2.44, BA.1.1.15,	Weisblum et al. (2020)	111372	A	G,GAC	0.99

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
Q493R	antibody epitope effects	Ablates binding by class 2 mAbs such as C144 that directly interfere with ACE2 binding, but clonal somatic mutations of memory B cells at 6.2 months (evolving humoral immune response) show pronounced increase in binding to the variant.	BA.2.13	Gaebler et al. (2021)	40	CA	CG	0.98
Q493R	antibody epitope effects	Massive reduction in binding efficiency vs wild type for mAbs CB6/LY-CoV16 and LY-CoV555.	BA.2.13	Rappazzo et al. (2021)	40	CA	CG	0.98
Q493R	antibody epitope effects	Somewhat resistent to some class 1 (Spike 'up') antibodies tested. Mix of non- to strongly resistent in class 2 antibodies tested.	BA.2.13	Wang et al. (2021)	40	CA	CG	0.98
Q493R	convalescent plasma escape	Escape mutant found after in passage in plasma pool of 26 convalescents mean 1.5 post symptom onset.	BA.2.13	Schmidt et al. (2021)	40	CA	CG	0.98
Q493R	monoclonal antibody serial passage escape	The engineered mutation cause 10-fold or more increase in the disassociation constant with C144, C002 and C121 monoclonal antibodies vs. wild type Spike protein RBD domain AAs.	BA.2.13	Barnes et al. (2020)	40	CA	CG	0.98
Q493R	monoclonal antibody serial passage escape	Escape mutation against monoclonal antibody LY-CoV555 (antibody that forms the basis for Eli Lilly's bamlanivimab)	BA.2.13	Starr et al. (2021)	40	CA	CG	0.98
Q493R	monoclonal antibody serial passage escape	Class 2 mAb C627 modestly selected for the emergence of this mutation in vitro.	BA.2.13	Wang et al. (2021)	40	CA	CG	0.98
Q493R	monoclonal antibody serial passage escape	Strong positive selection (up to 37% of supernatant sequences) after two rounds of C135 monoclonal antibody passage, overall 76% switch away from Q493 to K or R	BA.2.13	Weisblum et al. (2020)	40	CA	CG	0.98
D614G	ACE2 receptor binding affinity	Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant showed essentially no change in binding (KD) relative to D614G.	BA.5.1.18, BA.4.1, BA.5.5, BA.5.1.23, BA.1.17.2, BQ.1.1.4, BA.4.4, BA.1.17, BF.31.1, BF.7.4.1, BE.1.4.1, BN.1, BD.1	Gong et al. (2021)	13000	A	G	1.0
D614G	ACE2 receptor binding affinity	Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant showed a 1.19x increase in binding (KD) relative to D614G.	BA.5.1.16, BQ.1.1.11, BQ.1.1.13, BA.2.66, BA.2.1	Gong et al. (2021)	324	A	G	1.0
D614G	ACE2 receptor binding affinity	Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant showed a 1.08x decrease in binding (KD) relative to D614G.	BQ.1.1.15, CM.2, BA.5.2.14, BN.1.1, CR.1, BQ.1.1.2, BR.2.1, BF.10	Gong et al. (2021)	2347	A	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
D614G	ACE2 receptor binding affinity	Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant showed a 1.21x increase in binding (KD) relative to D614G.	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BU.2, BA.5.2.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.5.2.6, XAE, BT.1, BG.2, BA.1.1.18, BF.25, BV.1.1, BA.1.7,	Gong et al. (2021)	196875	A	G,GTA	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
D614G	ACE2 receptor binding affinity	Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant showed a 1.5x decrease in binding (KD) relative to D614G.	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BA.5.2.2, BU.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.64, BA.1.6, BA.5.2.6, XAE, BT.1, BG.2, BA.1.1.18, BF.25, BY.1.1.1, BA.1.7, BA.5.1, BF.20, BA.5.1.5, CJ.1,	Gong et al. (2021)	196601	A	G,GTA	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
D614G	ACE2 receptor binding affinity	Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant showed a 1.28x increase in binding (KD) relative to D614G.	BA.2.38, BA.2.38.2, BA.2.38.1, BA.2.40.1, BA.2.1, BA.2.18, BH.1	Gong et al. (2021)	363	A	G	1.0
D614G	ACE2 receptor binding affinity	Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant showed a 1.07x decrease in binding (KD) relative to D614G. Compare to increased binding in full Spike variant complements for major lineages containing this variant subset: 3.56x (B.1.351 aka Beta), 4.24x (P.1 aka Gamma).	CM.2	Gong et al. (2021)	86	A	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
D614G	ACE2 receptor binding affinity	Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant showed a 2.66x increase in binding (KD) relative to D614G.	BA.5.1.2, BQ.1.1.15, BA.5.2.14, DE.2, BE.4.2, CN.1, BF.5, BF.7.1, BA.5.2.3, BA.2.75, BA.4.4, BA.5.1.9, BA.5.2.23, BQ.1.1.19, BQ.1.1.3, BA.5.2.34, CQ.1.1, BA.4.1.9, BA.5.2.18, BE.1.1.2, BF.12, BR.2.1, BF.26, BA.5.1.21, BA.5.1.16, CG.1, BA.5.1.3, BF.17, BQ.1.16, BA.5.3.3, CE.1, BA.5.2.26, BQ.1.1.14, BQ.1.1.2, BQ.1.8.2, BR.1.2, BA.5.2.28, BT.2, BQ.1.1.5, CR.1.2, BA.5.1.4, BA.4.1.5, BQ.1.1.25, BA.5.1.22, BQ.1.3, BA.5.1.19, BA.4.1.1, BF.7.5, BF.1, BA.4.1.10, BA.5.2.21, BQ.1.1.7, BQ.1.1.6, BQ.1.10.1, BR.1, BQ.1.1.28, CA.1, BF.4, CK.3, BF.7.4.1, CR.2, XBE, BA.2.75.4, BQ.1.1.27, BA.5.2.37, CA.7, BQ.1.1, BQ.1.12, BA.4.7, BF.19, BA.5.10, BF.31, BF.7.3, BF.7.7, BA.5.1.31, BF.7.8, XAS, BA.5.2.33, CC.1, BQ.1.1.24, BA.5.6.2, BA.5.2.2, BQ.1.6, BU.2, CV.1, CQ.2, BE.4, BA.5.1.25, BQ.1.26, BQ.1.10, BV.2, BE.3, BA.5.2.22, BF.15, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BF.29, BQ.1.1.13, BQ.1.23, BA.4.5, BE.4.1.1, BE.3.2, BQ.1.2, BA.5.1.24, BF.3.1,	Gong et al. (2021)	81115	A	G,GTA	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
D614G	ACE2 receptor binding affinity	Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant showed a 1.1x decrease in binding (KD) relative to D614G.	BA.5.1.2, XAQ, XBB.1.5, BA.2.75, BQ.1.1.3, BA.1.15.1, BA.5.2.34, BF.12, BR.2.1, BF.26, BA.1.1.14, BA.5.1.3, CE.1, BA.5.2.26, BR.1.2, BA.1.1.2, BA.2.75.1, BA.5.2.28, BY.1, BA.2.12, BQ.1.3, BA.1.13, BA.5.2.21, BQ.1.1.6, BA.2.9.3, BQ.1.1.28, BF.4, BF.7.4.1, BA.1.1.16, BQ.1.1, BA.4.7, BA.1.17.2, BA.5.2.2, BA.2.9, BA.5.1.25, BA.2.40.1, BQ.1.10, BA.5.2.22, BQ.1.1.13, BA.2.18, BA.5.2.25, BA.1.1, BA.2.10, BE.1.1, BQ.1.1.18, BA.2.21, BA.1.18, BA.5.2.27, BE.1.2.1, BF.7, BA.2.3.12, BA.2, BA.5.2.36, BF.13, BH.1, BA.5.1.12, BF.7.4, BQ.1.5, BA.2.42, BA.2.70, BA.2.3.10, BN.1.5, BA.2.12.1, BA.2.74, BA.2.56, BQ.1.20, BJ.1, BA.2.10.1, BQ.1.19, BF.23, BE.1.2, BQ.1.11, BE.5, BA.2.3, BA.5.1.23, BK.1, BA.2.3.2, BA.1.1.10, BA.4.6.5, BA.1.1.1, BA.1.20, BF.16, BA.5.2.6, BA.2.38.2, BF.7.6, BA.2.9.4, BQ.1.8, BG.2, BA.1.1.18, DB.1, BA.5.1, BA.5.1.5, BF.11, BA.5.1.10, BA.2.66, BA.5.1.7, BA.5.5, BF.11.3, BA.5, BF.8.1, BA.4.6, XAC, BA.2.38, BA.5.2.20,	Gong et al. (2021)	163974	A	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
D614G	ACE2 receptor binding affinity	Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant showed a 2.52x increase in binding (KD) relative to D614G, mostly due to decreased in "off-rate" a.k.a. dissociation rate (Kdis). Compare to full Spike variant complements for major lineages containing this variant subset: 5.43x (B.1.1.7 aka Alpha), 3.56x (B.1.351 aka Beta), 4.24x (P.1 aka Gamma).	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BA.5.2.2, BU.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.5.2.6, XAE, BT.1, BG.2, BA.1.1.18, BF.25, BY.1.1.1, BA.1.1, BA.5.1, BF.20, BA.5.1.5,	Gong et al. (2021)	196845	A	G,GTA	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
D614G	ACE2 receptor binding affinity	Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant showed a 1.23x decrease in binding (KD) relative to D614G.	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BU.2, BA.5.2.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.5.2.6, XAE, BT.1, BG.2, BA.1.1.18, BF.25, BX.1.1, BA.1.7,	Gong et al. (2021)	194135	A	G,GTA	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
D614G	ACE2 receptor binding affinity	Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant showed a 1.42x increase in binding (KD) relative to D614G.	BA.1.1.2	Gong et al. (2021)	258	A	G	1.0
D614G	ACE2 receptor binding affinity	Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant showed a 1.69x decrease in binding (KD) relative to D614G.	BA.5.2.22	Gong et al. (2021)	596	A	G	1.0
D614G	ACE2 receptor binding affinity	Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant showed a 1.33x decrease in binding (KD) relative to D614G.	BA.1.13.1, BA.1.1.7, BA.1.1.11, BA.1.1.18, BA.1.1.4, BA.1.15.3, BA.1.7, BA.1.8, BA.1.14, BA.1.15.1, BA.1.1.6, BA.1.1.14, BA.1.1.15, BA.1.14.2, BA.1.15, BA.1.1.2, BA.5.2.28, BA.4.6.3, BA.1.5, BA.1.1.3, BD.1, BA.1.13, BA.1.1, BA.1.1.17, XM, BA.1.17.1, BA.1.1.13, BA.1.18, BA.1.3, BA.1.17, BC.2, BQ.1.11, BA.1.1.9, BA.1.15.2, BA.1.21, BA.1.9, BQ.1.25, BA.1.1.16, BA.1.10, BA.1.16, BA.1.17.2, BA.1.1.8, BA.1.1.10, BA.1, BA.1.12, BA.1.1.1, BA.1.20, BA.1.14.1, BA.1.19, BA.1.6	Gong et al. (2021)	64881	A	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
D614G	ACE2 receptor binding affinity	In four cell lines (including 293T-hACE2 cells), this mutation combination increases infectivity vs D614G alone	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BU.2, BA.5.2.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.5.2.6, XAE, BT.1, BG.2, BA.1.1.18, BF.25, BX.1.1, BA.1.7,	Li et al. (2020)	196875	A	G,GTA	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
D614G	ACE2 receptor binding affinity	Lentiviral pseudotyped with the key mutations from COH.20G/677H lineage was tested on ACE2.293T cells for ACE2 affinity changes vs D614G alone, showing a extasciitilde70% drop in IC50 (i.e. increased affinity).	BQ.1.1.22, BA.5.5.2, XBF, BL.1, BE.9, BA.5.2.6	Tada et al. (2021)	404	A	G	1.0
D614G	convalescent plasma binding	1.11x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset.	BA.5.1.18, BA.4.1, BA.5.5, BA.5.1.23, BA.1.17.2, BQ.1.1.4, BA.4.4, BA.1.17, BF.31.1, BF.7.4.1, BE.1.4.1, BN.1, BD.1	Gong et al. (2021)	13000	A	G	1.0
D614G	convalescent plasma binding	2.29x increase in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset.	BA.5.1.16, BQ.1.1.11, BQ.1.1.13, BA.2.66, BA.2.1	Gong et al. (2021)	324	A	G	1.0
D614G	convalescent plasma binding	1.19x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset.	BQ.1.1.15, CM.2, BA.5.2.14, BN.1.1, CR.1, BQ.1.1.2, BR.2.1, BF.10	Gong et al. (2021)	2347	A	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
D614G	convalescent plasma binding	1.48x increase in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset.	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BU.2, BA.5.2.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.5.2.6, XAE, BT.1, BG.2, BA.1.1.18, BF.25, BX.1.1, BA.1.7,	Gong et al. (2021)	196875	A	G,GTA	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
D614G	convalescent plasma binding	2.16x increase in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset.	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BA.5.2.2, BU.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.64, BA.1.6, BA.5.2.6, XAE, BT.1, BG.2, BA.1.1.18, BF.25, BY.1.1.1, BA.1.7, BA.5.1, BF.20, BA.5.1.5, CJ.1,	Gong et al. (2021)	196601	A	G,GTA	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
D614G	convalescent plasma binding	1.65x increase in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset.	BA.2.38, BA.2.38.2, BA.2.38.1, BA.2.40.1, BA.2.1, BA.2.18, BH.1	Gong et al. (2021)	363	A	G	1.0
D614G	convalescent plasma binding	1.66x increase in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset. Compare to decreased binding in full Spike variant complements for major lineages containing this variant subset: 0.96x (B.1.351 aka Beta), 0.77x (P.1 aka Gamma).	CM.2	Gong et al. (2021)	86	A	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
D614G	convalescent plasma binding	2.15x increase in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset.	BA.5.1.2, BQ.1.1.15, BA.5.2.14, DE.2, BE.4.2, CN.1, BF.5, BF.7.1, BA.5.2.3, BA.2.75, BA.4.4, BA.5.1.9, BA.5.2.23, BQ.1.1.19, BQ.1.1.3, BA.5.2.34, CQ.1.1, BA.4.1.9, BA.5.2.18, BE.1.1.2, BF.12, BR.2.1, BF.26, BA.5.1.21, BA.5.1.16, CG.1, BA.5.1.3, BF.17, BQ.1.16, BA.5.3.3, CE.1, BA.5.2.26, BQ.1.1.14, BQ.1.1.2, BQ.1.8.2, BR.1.2, BA.5.2.28, BT.2, BQ.1.1.5, CR.1.2, BA.5.1.4, BA.4.1.5, BQ.1.1.25, BA.5.1.22, BQ.1.3, BA.5.1.19, BA.4.1.1, BF.7.5, BF.1, BA.4.1.10, BA.5.2.21, BQ.1.1.7, BQ.1.1.6, BQ.1.10.1, BR.1, BQ.1.1.28, CA.1, BF.4, CK.3, BF.7.4.1, CR.2, XBE, BA.2.75.4, BQ.1.1.27, BA.5.2.37, CA.7, BQ.1.1, BQ.1.12, BA.4.7, BF.19, BA.5.10, BF.31, BF.7.3, BF.7.7, BA.5.1.31, BF.7.8, XAS, BA.5.2.33, CC.1, BQ.1.1.24, BA.5.6.2, BA.5.2.2, BQ.1.6, BU.2, CV.1, CQ.2, BE.4, BA.5.1.25, BQ.1.26, BQ.1.10, BV.2, BE.3, BA.5.2.22, BF.15, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BF.29, BQ.1.1.13, BQ.1.23, BA.4.5, BE.4.1.1, BE.3.2, BQ.1.2, BA.5.1.24, BF.3.1,	Gong et al. (2021)	81115	A	G,GTA	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
D614G	convalescent plasma binding	No change in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset.	BA.5.1.2, XAQ, XBB.1.5, BA.2.75, BQ.1.1.3, BA.1.15.1, BA.5.2.34, BF.12, BR.2.1, BF.26, BA.1.1.14, BA.5.1.3, CE.1, BA.5.2.26, BR.1.2, BA.1.1.2, BA.2.75.1, BA.5.2.28, BY.1, BA.2.12, BQ.1.3, BA.1.13, BA.5.2.21, BQ.1.1.6, BA.2.9.3, BQ.1.1.28, BF.4, BF.7.4.1, BA.1.1.16, BQ.1.1, BA.4.7, BA.1.17.2, BA.5.2.2, BA.2.9, BA.5.1.25, BA.2.40.1, BQ.1.10, BA.5.2.22, BQ.1.1.13, BA.2.18, BA.5.2.25, BA.1.1, BA.2.10, BE.1.1, BQ.1.1.18, BA.2.21, BA.1.18, BA.5.2.27, BE.1.2.1, BF.7, BA.2.3.12, BA.2, BA.5.2.36, BF.13, BH.1, BA.5.1.12, BF.7.4, BQ.1.5, BA.2.42, BA.2.70, BA.2.3.10, BN.1.5, BA.2.12.1, BA.2.74, BA.2.56, BQ.1.20, BJ.1, BA.2.10.1, BQ.1.19, BF.23, BE.1.2, BQ.1.11, BE.5, BA.2.3, BA.5.1.23, BK.1, BA.2.3.2, BA.1.1.10, BA.4.6.5, BA.1.1.1, BA.1.20, BF.16, BA.5.2.6, BA.2.38.2, BF.7.6, BA.2.9.4, BQ.1.8, BG.2, BA.1.1.18, DB.1, BA.5.1, BA.5.1.5, BF.11, BA.5.1.10, BA.2.66, BA.5.1.7, BA.5.5, BF.11.3, BA.5, BF.8.1, BA.4.6, XAC, BA.2.38, BA.5.2.20,	Gong et al. (2021)	163974	A	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
D614G	convalescent plasma binding	1.65x increase in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset.	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BA.5.2.2, BU.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.5.2.6, XAE, BT.1, BG.2, BA.1.1.18, BF.25, BY.1.1.1, BA.1.1, BA.5.1, BF.20, BA.5.1.5,	Gong et al. (2021)	196845	A	G,GTA	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
D614G	convalescent plasma binding	1.26x increase in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset.	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BU.2, BA.5.2.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.5.2.6, XAE, BT.1, BG.2, BA.1.1.18, BF.25, BX.1.1, BA.1.7,	Gong et al. (2021)	194135	A	G,GTA	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
D614G	convalescent plasma binding	1.19x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset.	BA.1.1.2	Gong et al. (2021)	258	A	G	1.0
D614G	convalescent plasma binding	1.56x increase in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset.	BA.5.2.22	Gong et al. (2021)	596	A	G	1.0
D614G	convalescent plasma binding	No change in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset.	BA.1.13.1, BA.1.1.7, BA.1.1.11, BA.1.1.18, BA.1.1.4, BA.1.15.3, BA.1.7, BA.1.8, BA.1.14, BA.1.15.1, BA.1.1.6, BA.1.1.14, BA.1.1.15, BA.1.14.2, BA.1.15, BA.1.1.2, BA.5.2.28, BA.4.6.3, BA.1.5, BA.1.1.3, BD.1, BA.1.13, BA.1.1, BA.1.1.17, XM, BA.1.17.1, BA.1.1.13, BA.1.18, BA.1.3, BA.1.17, BC.2, BQ.1.11, BA.1.1.9, BA.1.15.2, BA.1.21, BA.1.9, BQ.1.25, BA.1.1.16, BA.1.10, BA.1.16, BA.1.17.2, BA.1.1.8, BA.1.1.10, BA.1, BA.1.12, BA.1.1.1, BA.1.20, BA.1.14.1, BA.1.19, BA.1.6	Gong et al. (2021)	64881	A	G	1.0
D614G	convalescent plasma escape	Lentiviral pseudotyped with the key mutations from COH.20G/677H ("Ohio") lineage was neutralized similarly to D614G in 10 convalescent sera from April 2020 infectees.	BQ.1.1.22, BA.5.5.2, XBF, BL.1, BE.9, BA.5.2.6	Tada et al. (2021)	404	A	G	1.0
D614G	convalescent plasma escape	Lentiviral pseudotyped with the key mutations from 20A.EU2 lineage was neutralized slightly less than D614G in 10 convalescent sera from April 2020 infectees.	BA.2.3.20, BL.1	Tada et al. (2021)	142	A	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
D614G	convalescent plasma escape	Relative to B.1, Epsilon (B.1.417/429) shows 1.74x-2.35x decrease in neutralization efficiency by convalescent plasma [no cohort details provided]	BA.5.1.2, BQ.1.1.15, BA.5.2.14, DE.2, BE.4.2, CN.1, BF.5, BF.7.1, BA.5.2.3, BA.2.75, BA.4.4, BA.5.1.9, BA.5.2.23, BQ.1.1.19, BQ.1.1.3, BA.5.2.34, CQ.1.1, BA.4.1.9, BA.5.2.18, BE.1.1.2, BF.12, BR.2.1, BF.26, BA.5.1.21, BA.5.1.16, CG.1, BA.5.1.3, BF.17, BQ.1.16, BA.5.3.3, CE.1, BA.5.2.26, BQ.1.1.14, BQ.1.1.2, BQ.1.8.2, BR.1.2, BA.5.2.28, BT.2, BQ.1.1.5, CR.1.2, BA.5.1.4, BA.4.1.5, BQ.1.1.25, BA.5.1.22, BQ.1.3, BA.5.1.19, BA.4.1.1, BF.7.5, BF.1, BA.4.1.10, BA.5.2.21, BQ.1.1.7, BQ.1.1.6, BQ.1.10.1, BR.1, BQ.1.1.28, CA.1, BF.4, CK.3, BF.7.4.1, CR.2, XBE, BA.2.75.4, BQ.1.1.27, BA.5.2.37, CA.7, BQ.1.1, BQ.1.12, BA.4.7, BF.19, BA.5.10, BF.31, BF.7.3, BF.7.7, BA.5.1.31, BF.7.8, XAS, BA.5.2.33, CC.1, BQ.1.1.24, BA.5.6.2, BA.5.2.2, BQ.1.6, BU.2, CV.1, CQ.2, BE.4, BA.5.1.25, BQ.1.26, BQ.1.10, BV.2, BE.3, BA.5.2.22, BF.15, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BF.29, BQ.1.1.13, BQ.1.23, BA.4.5, BE.4.1.1, BE.3.2, BQ.1.2, BA.5.1.24, BF.3.1,	Wilhelm et al. (2021)	81115	A	G,GTA	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
D614G	humoral response durability	27yo female nurse reinfected in December 2020 (B.1.177) after initial infection in March 2020 (B.3), i.e. with a 9 month interval. Both cases were mild. No significant differences in the neutralizing capacity of the two linages were observed in 4 sera taken (1 pre-reinfection, three post-reinfection). Neutralizing antibody titres (IC50) before and immediately after re-infection were <300 against both strains, and jumped >7x upon re-infection. Viral titres were also higher in the second case. Second case also includes N:p.A220V	BF.26, BA.5.1.3, BQ.1.5, BA.2.21, BA.2.65, BQ.1.14	Brehm et al. (2021)	3067	A	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
D614G	immunosuppression variant emergence	Studying 94 COVID-19 extended infection cases with genomics April 1 to October 17, 2020, one case developed 23 mutations in a 19 day period, including this combination in Spike.	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BU.2, BA.5.2.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.5.2.6, XAE, BT.1, BG.2, BA.1.1.18, BF.25, BX.1.1, BA.1.7,	Landis et al. (2021)	196875	A	G,GTA	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
D614G	reinfection	27yo female nurse reinfected in December 2020 (B.1.177) after initial infection in March 2020 (B.3). Both cases were mild. Second case also includes N:p.A220V	BF.26, BA.5.1.3, BQ.1.5, BA.2.21, BA.2.65, BQ.1.14	Brehm et al. (2021)	3067	A	G	1.0
D614G	reinfection	11 cases of re-infection with the "Marseille-4" variant found within 1028 positive tests, where all of the earlier infections were from different strains. This lineage is also characterized by N:p.M234I:A376T	BA.2.3.20, BL.1	Fournier et al. (2021)	142	A	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
D614G	reinfection	A 47yo Indian male was reinfected with B.1.36 lineage virus in September 2020 after infection with genetically distinct B.1.36 virus in July, with negative PCR tests in between. While the forst episode was asymptomatic, the second included fever, cough, and malaise. The second case additionally contained stopgain ORF3a:E261*	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BA.5.2.2, BU.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.5.2.6, XAE, BT.1, BG.2, BA.1.1.18, BF.25, BY.1.1.1, BA.1.1, BA.5.1, BF.20, BA.5.1.5,	Rani et al. (2021)	196872	A	G,GTA	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
D614G	symptom prevalence	Compared to the clade 20A strains that predominated during phase 1 between March and May 2020, the Marseille-4 variant (characterized by this mutation plus N:p.M234I:A376T) was associated with a lower frequency of cough, rhinitis, and olfactory and gustatory disorders. By contrast, hypoxemia was more frequent in patients infected with the Marseille-4 variant.	BA.2.3.20, BL.1	Fournier et al. (2021)	142	A	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
D614G	syncytium formation	Slight increase in Vero cell-cell membrane fusion assay under infection with VSV pseudotyped virus.	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BU.2, BA.5.2.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.5.2.6, XAE, BT.1, BG.2, BA.1.1.18, BF.25, BX.1.1, BA.1.7,	Kim et al. (2021)	196875	A	G,GTA	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
D614G	syncytium formation	Slight increase in Vero cell-cell membrane fusion assay under infection with VSV pseudotyped virus relative to wild type, no change relative to D614G.	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BA.5.2.2, BU.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.5.2.6, XAE, BT.1, BG.2, BA.1.1.18, BF.25, BY.1.1.1, BA.1.1, BA.5.1, BF.20, BA.5.1.5,	Kim et al. (2021)	196845	A	G,GTA	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
D614G	tissue specific neutralization	The nasal mucosa of Pfizer vaccinees with time course collection was evaluated against VSV pseudotypes: results (only one nasal swab from different previously infected vaccinee neutralizing at weeks 3 and 6 against B.1.1.7 and D614G) suggest that vaccinees probably do not elicit an early humoral response detectable at mucosal surfaces even though sera neutralization was observed. They strengthen the hypothesis that some vaccines may not protect against viral acquisition and infection of the oral–nasal region, but may prevent severe disease associated with viral dissemination in the lower respiratory tract.	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BU.2, BA.5.2.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.5.2.6, XAE, BT.1, BG.2, BA.1.1.18, BF.25, BX.1.1, BA.1.7,	Planas et al. (2021)	196875	A	G,GTA	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
D614G	trafficking	Circulating variant shown in vitro to not have major defects or enhancement of cell surface protein trafficking (i.e. Spike cleavage or fusion required for cell entry)	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BU.2, BA.5.2.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.5.2.6, XAE, BT.1, BG.2, BA.1.1.18, BF.25, BX.1.1, BA.1.7,	Barrett et al. (2021)	196875	A	G,GTA	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
D614G	trafficking	The increased transduction with Spike D614G ranged from 1.3- to 2.4-fold in Caco-2 and Calu-3 cells expressing endogenous ACE2 and from 1.5- to 7.7-fold in A549ACE2 and Huh7.5ACE2 overexpressing ACE2. Although there is minimal difference in ACE2 receptor binding between the D614 and G614 Spike variants, the G614 variant is more resistant to proteolytic cleavage, suggesting a possible mechanism for the increased transduction.	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BU.2, BA.5.2.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.5.2.6, XAE, BT.1, BG.2, BA.1.1.18, BF.25, BX.1.1, BA.1.7,	Daniloski et al. (2021)	196875	A	G,GTA	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
D614G	trafficking	No change in infectivity (24h) relative to D614G alone in Caco-2 cells, Vero or Calu-3.	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BU.2, BA.5.2.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.5.2.6, XAE, BT.1, BG.2, BA.1.1.18, BF.25, BX.1.1, BA.1.7,	Kim et al. (2021)	196875	A	G,GTA	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
D614G	trafficking	extasciitilde4x more efficient S2 domain cleavage compared to wild type in Caco-2 cells, mid-range of three cell line tested (Vero and Calu-3).	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BU.2, BA.5.2.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.5.2.6, XAE, BT.1, BG.2, BA.1.1.18, BF.25, BX.1.1, BA.1.7,	Kim et al. (2021)	196875	A	G,GTA	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
D614G	trafficking	More efficient infectivity (24h) compared to wild type, in Caco-2 cells extasciitilde9x, Vero extasciitilde8x, and Calu-3 extasciitilde8x. Compare to wild type at extasciitilde5x across cell types.	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BA.5.2.2, BU.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.5.2.6, XAE, BT.1, BG.2, BA.1.1.18, BF.25, BY.1.1.1, BA.1.1, BA.5.1, BF.20, BA.5.1.5,	Kim et al. (2021)	196845	A	G,GTA	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
D614G	trafficking	extasciitilde4x more efficient S2 domain cleavage compared to wild type, no change relative to D614G alone in Caco-2 cells, mid-range of three cell line tested (Vero and Calu-3).	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BA.5.2.2, BU.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.5.2.6, XAE, BT.1, BG.2, BA.1.1.18, BF.25, BY.1.1.1, BA.1.1, BA.5.1, BF.20, BA.5.1.5,	Kim et al. (2021)	196845	A	G,GTA	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
D614G	trafficking	extasciitilde2x more infectivity than D614G alone in HEK293T-ACE2 cells 48h post-transduction.	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BA.5.2.2, BU.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.64, BA.1.6, BA.5.2.6, XAE, BT.1, BG.2, BA.1.1.18, BF.25, BY.1.1.1, BA.1.7, BA.5.1, BF.20, BA.5.1.5, CJ.1,	Kuzmina et al. (2021)	196601	A	G,GTA	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
D614G	trafficking	extasciitilde9x more infectivity than D614G alone in HEK293T-ACE2 cells 48h post-transduction (no synergy as level approx. that of N501Y alone).	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BU.2, BA.5.2.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.64, BA.1.6, BA.5.2.6, XAE, BT.1, BG.2, BA.1.1.18, BF.25, BY.1.1.1, BA.1.1, BA.5.1, BF.20, BA.5.1.5,	Kuzmina et al. (2021)	196571	A	G,GTA	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
D614G	trafficking	9x more infectivity than D614G alone in HEK293T-ACE2 cells 48h post-transduction.	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BA.5.2.2, BU.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.5.2.6, XAE, BT.1, BG.2, BA.1.1.18, BF.25, BY.1.1.1, BA.1.1, BA.5.1, BF.20, BA.5.1.5,	Kuzmina et al. (2021)	198604	A	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
D614G	trafficking	Among S variants tested, the D614G mutant shows the highest cell entry (extasciitilde3.5x wild type), as supported by structural and binding analyses.	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BU.2, BA.5.2.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.5.2.6, XAE, BT.1, BG.2, BA.1.1.18, BF.25, BV.1.1, BA.1.7,	Ozono et al. (2020)	196875	A	G,GTA	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
D614G	trafficking	Lentiviral pseudotyped with the key mutations from COH.20G/677H lineage was tested on ACE2.293T cells. Luciferase activity was measured two days postinfection, showing no significant change in infection rate amongst the cells, suggesting that this mutation does not contributing to cell entry fitness.	BQ.1.1.22, BA.5.5.2, XBF, BL.1, BE.9, BA.5.2.6	Tada et al. (2021)	404	A	G	1.0
D614G	trafficking	Lentiviral pseudotyped with the key mutations from 20A.EU2 lineage was tested on ACE2.293T cells. Luciferase activity was measured two days postinfection, showing no significant change in infection rate amongst the cells, suggesting that this mutation does not contributing to cell entry fitness.	BA.2.3.20, BL.1	Tada et al. (2021)	142	A	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
D614G	trafficking	We report here pseudoviruses carrying SG614 enter ACE2-expressing cells more efficiently than wild type (extasciitilde9-fold). This increased entry correlates with less S1-domain shedding and higher S-protein incorporation into the virion. D614G does not alter S-protein binding to ACE2 or neutralization sensitivity of pseudoviruses. Thus, D614G may increase infectivity by assembling more functional S protein into the virion.	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BU.2, BA.5.2.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.5.2.6, XAE, BT.1, BG.2, BA.1.1.18, BF.25, BX.1.1, BA.1.7,	Zhang et l. (2020)	196875	A	G,GTA	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
D614G	transmissibility	Increased infectivity of the B.1.617 spike was attributed to L452R, which itself caused a 3.5-fold increase in infectivity relative to D614G wild type. [In combination with E484Q caused a lower 3-fold increase]	BA.5.1.2, BQ.1.1.15, BA.5.2.14, DE.2, BE.4.2, CN.1, BF.5, BF.7.1, BA.5.2.3, BA.2.75, BA.4.4, BA.5.1.9, BA.5.2.23, BQ.1.1.19, BQ.1.1.3, BA.5.2.34, CQ.1.1, BA.4.1.9, BA.5.2.18, BE.1.1.2, BF.12, BR.2.1, BF.26, BA.5.1.21, BA.5.1.16, CG.1, BA.5.1.3, BF.17, BQ.1.16, BA.5.3.3, CE.1, BA.5.2.26, BQ.1.1.14, BQ.1.1.2, BQ.1.8.2, BR.1.2, BA.5.2.28, BT.2, BQ.1.1.5, CR.1.2, BA.5.1.4, BA.4.1.5, BQ.1.1.25, BA.5.1.22, BQ.1.3, BA.5.1.19, BA.4.1.1, BF.7.5, BF.1, BA.4.1.10, BA.5.2.21, BQ.1.1.7, BQ.1.1.6, BQ.1.10.1, BR.1, BQ.1.1.28, CA.1, BF.4, CK.3, BF.7.4.1, CR.2, XBE, BA.2.75.4, BQ.1.1.27, BA.5.2.37, CA.7, BQ.1.1, BQ.1.12, BA.4.7, BF.19, BA.5.10, BF.31, BF.7.3, BF.7.7, BA.5.1.31, BF.7.8, XAS, BA.5.2.33, CC.1, BQ.1.1.24, BA.5.6.2, BA.5.2.2, BQ.1.6, BU.2, CV.1, CQ.2, BE.4, BA.5.1.25, BQ.1.26, BQ.1.10, BV.2, BE.3, BA.5.2.22, BF.15, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BF.29, BQ.1.1.13, BQ.1.23, BA.4.5, BE.4.1.1, BE.3.2, BQ.1.2, BA.5.1.24, BF.3.1,	Tada et al. (2021)	81115	A	G,GTA	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
D614G	vaccine neutralization efficacy	Pseudotyped D614G virus has reduced neutralization activity vs wild type: 1.2x (37 sera Pfizer median 9 days post 2nd dose, 37 sera Moderna median 18 days post 2nd dose). This was NOT significant by ANOVA.	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BU.2, BA.5.2.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.5.2.6, XAE, BT.1, BG.2, BA.1.1.18, BF.25, BX.1.1, BA.1.7,	Garcia-Beltran et al. (2021)	196875	A	G,GTA	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
D614G	vaccine neutralization efficacy	Using a lentivirus virus pseudotyped with D614G Spike, sera from vaccinated individuals who received the second dose (9–11 days post-second dose of Pfizer) exhibited a robust neutralizing potential, with a mean NT50 value of 99,000. This was an average of a 2-fold increase, relative to sera drawn from the individuals who received one dose of vaccination—mean NT50 dilution of 51,300. Importantly, a 6-fold increase in mean NT50 dilution was obtained when sera from the first vaccination dose was compared to convalescent sera from cohort with severe disease (NT50 51,000 vs 8,700) 21 to 63 days post-onset.	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BU.2, BA.5.2.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.5.2.6, XAE, BT.1, BG.2, BA.1.1.18, BF.25, BX.1.1, BA.1.7,	Kuzmina et al. (2021)	196875	A	G,GTA	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
D614G	vaccine neutralization efficacy	This variant showed only minor in Pfizer sera (one or two dose) neutralization efficiency vs D614G (using lentivirus pseudotype).	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BA.5.2.2, BU.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.64, BA.1.6, BA.5.2.6, XAE, BT.1, BG.2, BA.1.1.18, BF.25, BY.1.1.1, BA.1.7, BA.5.1, BF.20, BA.5.1.5, CJ.1,	Kuzmina et al. (2021)	196601	A	G,GTA	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
D614G	vaccine neutralization efficacy	This variant showed >5x decrease in Pfizer sera (3 weeks post-first dose: n	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BU.2, BA.5.2.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.64, BA.1.6, BA.5.2.6, XAE, BT.1, BG.2, BA.1.1.18, BF.25, BY.1.1.1, BA.1.1, BA.5.1, BF.20, BA.5.1.5,	Kuzmina et al. (2021)	196571	A	G,GTA	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
D614G	vaccine neutralization efficacy	This variant showed no change in Pfizer sera (one or two dose) neutralization efficiency vs D614G (using lentivirus pseudotype).	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BA.5.2.2, BU.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.5.2.6, XAE, BT.1, BG.2, BA.1.1.18, BF.25, BY.1.1.1, BA.1.1, BA.5.1, BF.20, BA.5.1.5,	Kuzmina et al. (2021)	196845	A	G,GTA	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
D614G	vaccine neutralization efficacy	Relative to B.1, Epsilon (B.1.417/429) shows 1.74x-2.35x decrease in neutralization efficiency by 18 vaccinee sera (BNT162b2 and mRNA1273).	BA.5.1.2, BQ.1.1.15, BA.5.2.14, DE.2, BE.4.2, CN.1, BF.5, BF.7.1, BA.5.2.3, BA.2.75, BA.4.4, BA.5.1.9, BA.5.2.23, BQ.1.1.19, BQ.1.1.3, BA.5.2.34, CQ.1.1, BA.4.1.9, BA.5.2.18, BE.1.1.2, BF.12, BR.2.1, BF.26, BA.5.1.21, BA.5.1.16, CG.1, BA.5.1.3, BF.17, BQ.1.16, BA.5.3.3, CE.1, BA.5.2.26, BQ.1.1.14, BQ.1.1.2, BQ.1.8.2, BR.1.2, BA.5.2.28, BT.2, BQ.1.1.5, CR.1.2, BA.5.1.4, BA.4.1.5, BQ.1.1.25, BA.5.1.22, BQ.1.3, BA.5.1.19, BA.4.1.1, BF.7.5, BF.1, BA.4.1.10, BA.5.2.21, BQ.1.1.7, BQ.1.1.6, BQ.1.10.1, BR.1, BQ.1.1.28, CA.1, BF.4, CK.3, BF.7.4.1, CR.2, XBE, BA.2.75.4, BQ.1.1.27, BA.5.2.37, CA.7, BQ.1.1, BQ.1.12, BA.4.7, BF.19, BA.5.10, BF.31, BF.7.3, BF.7.7, BA.5.1.31, BF.7.8, XAS, BA.5.2.33, CC.1, BQ.1.1.24, BA.5.6.2, BA.5.2.2, BQ.1.6, BU.2, CV.1, CQ.2, BE.4, BA.5.1.25, BQ.1.26, BQ.1.10, BV.2, BE.3, BA.5.2.22, BF.15, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BF.29, BQ.1.1.13, BQ.1.23, BA.4.5, BE.4.1.1, BE.3.2, BQ.1.2, BA.5.1.24, BF.3.1,	Wilhelm et al. (2021)	81115	A	G,GTA	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
D614G	vaccine neutralization efficacy	No significant change in virus neutralzation by 18 Pfizer two dose vaccinee sera compared to B.1.1.7. [results without including the used mutation A27S likely generalizable, as this is not a lineage defining mutation]	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BU.2, BA.5.2.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.5.2.6, XAE, BT.1, BG.2, BA.1.1.18, BF.25, BX.1.1, BA.1.7,	Zuckerman et al. (2021)	194135	A	G,GTA	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
D614G	vaccinee plasma binding	1.19x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in previously non-seroconverted subjects. 1.1x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in post-infection vaccinees.	BA.5.1.18, BA.4.1, BA.5.5, BA.5.1.23, BA.1.17.2, BQ.1.1.4, BA.4.4, BA.1.17, BF.31.1, BF.7.4.1, BE.1.4.1, BN.1, BD.1	Gong et al. (2021)	13000	A	G	1.0
D614G	vaccinee plasma binding	1.79x increase in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in previously non-seroconverted subjects. 1.3x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in post-infection vaccinees.	BA.5.1.16, BQ.1.1.11, BQ.1.1.13, BA.2.66, BA.2.1	Gong et al. (2021)	324	A	G	1.0
D614G	vaccinee plasma binding	No significant change in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in previously non-seroconverted subjects. 1.19x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in post-infection vaccinees.	BQ.1.1.15, CM.2, BA.5.2.14, BN.1.1, CR.1, BQ.1.1.2, BR.2.1, BF.10	Gong et al. (2021)	2347	A	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
D614G	vaccinee plasma binding	1.04x increase in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in previously non-seroconverted subjects. 1.09x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in post-infection vaccinees.	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BU.2, BA.5.2.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.5.2.6, XAE, BT.1, BG.2, BA.1.1.18, BF.25, BX.1.1, BA.1.7,	Gong et al. (2021)	196875	A	G,GTA	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
D614G	vaccinee plasma binding	1.76x increase in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in previously non-seroconverted subjects. 1.75x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in post-infection vaccinees.	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BA.5.2.2, BU.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.64, BA.1.6, BA.5.2.6, XAE, BT.1, BG.2, BA.1.1.18, BF.25, BY.1.1.1, BA.1.7, BA.5.1, BF.20, BA.5.1.5, CJ.1,	Gong et al. (2021)	196601	A	G,GTA	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
D614G	vaccinee plasma binding	1.04x increase in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in previously non-seroconverted subjects. 1.1x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in post-infection vaccinees.	BA.2.38, BA.2.38.2, BA.2.38.1, BA.2.40.1, BA.2.1, BA.2.18, BH.1	Gong et al. (2021)	363	A	G	1.0
D614G	vaccinee plasma binding	1.30x increase in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in previously non-seroconverted subjects. Compare to varied binding in full Spike variant complements for major lineages containing this variant subset: 1.28x increase (B.1.351 aka Beta), and 1.14x decrease (P.1 aka Gamma). 1.47x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in post-infection vaccinees. Compare to varied binding in full Spike variant complements for major lineages containing this variant subset: 1.17x increase (B.1.351 aka Beta), and 1.47x decrease (P.1 aka Gamma).	CM.2	Gong et al. (2021)	86	A	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
D614G	vaccinee plasma binding	1.05x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in previously non-seroconverted subjects. 1.16x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in post-infection vaccinees.	BA.5.1.2, BQ.1.1.15, BA.5.2.14, DE.2, BE.4.2, CN.1, BF.5, BF.7.1, BA.5.2.3, BA.2.75, BA.4.4, BA.5.1.9, BA.5.2.23, BQ.1.1.19, BQ.1.1.3, BA.5.2.34, CQ.1.1, BA.4.1.9, BA.5.2.18, BE.1.1.2, BF.12, BR.2.1, BF.26, BA.5.1.21, BA.5.1.16, CG.1, BA.5.1.3, BF.17, BQ.1.16, BA.5.3.3, CE.1, BA.5.2.26, BQ.1.1.14, BQ.1.1.2, BQ.1.8.2, BR.1.2, BA.5.2.28, BT.2, BQ.1.1.5, CR.1.2, BA.5.1.4, BA.4.1.5, BQ.1.1.25, BA.5.1.22, BQ.1.3, BA.5.1.19, BA.4.1.1, BF.7.5, BF.1, BA.4.1.10, BA.5.2.21, BQ.1.1.7, BQ.1.1.6, BQ.1.10.1, BR.1, BQ.1.1.28, CA.1, BF.4, CK.3, BF.7.4.1, CR.2, XBE, BA.2.75.4, BQ.1.1.27, BA.5.2.37, CA.7, BQ.1.1, BQ.1.12, BA.4.7, BF.19, BA.5.10, BF.31, BF.7.3, BF.7.7, BA.5.1.31, BF.7.8, XAS, BA.5.2.33, CC.1, BQ.1.1.24, BA.5.6.2, BA.5.2.2, BQ.1.6, BU.2, CV.1, CQ.2, BE.4, BA.5.1.25, BQ.1.26, BQ.1.10, BV.2, BE.3, BA.5.2.22, BF.15, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BF.29, BQ.1.1.13, BQ.1.23, BA.4.5, BE.4.1.1, BE.3.2, BQ.1.2, BA.5.1.24, BF.3.1,	Gong et al. (2021)	81115	A	G,GTA	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
D614G	vaccinee plasma binding	1.23x increase in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in previously non-seroconverted subjects. 1.1x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in post-infection vaccinees.	BA.5.1.2, XAQ, XBB.1.5, BA.2.75, BQ.1.1.3, BA.1.15.1, BA.5.2.34, BF.12, BR.2.1, BF.26, BA.1.1.14, BA.5.1.3, CE.1, BA.5.2.26, BR.1.2, BA.1.1.2, BA.2.75.1, BA.5.2.28, BY.1, BA.2.12, BQ.1.3, BA.1.13, BA.5.2.21, BQ.1.1.6, BA.2.9.3, BQ.1.1.28, BF.4, BF.7.4.1, BA.1.1.16, BQ.1.1, BA.4.7, BA.1.17.2, BA.5.2.2, BA.2.9, BA.5.1.25, BA.2.40.1, BQ.1.10, BA.5.2.22, BQ.1.1.13, BA.2.18, BA.5.2.25, BA.1.1, BA.2.10, BE.1.1, BQ.1.1.18, BA.2.21, BA.1.18, BA.5.2.27, BE.1.2.1, BF.7, BA.2.3.12, BA.2, BA.5.2.36, BF.13, BH.1, BA.5.1.12, BF.7.4, BQ.1.5, BA.2.42, BA.2.70, BA.2.3.10, BN.1.5, BA.2.12.1, BA.2.74, BA.2.56, BQ.1.20, BJ.1, BA.2.10.1, BQ.1.19, BF.23, BE.1.2, BQ.1.11, BE.5, BA.2.3, BA.5.1.23, BK.1, BA.2.3.2, BA.1.1.10, BA.4.6.5, BA.1.1.1, BA.1.20, BF.16, BA.5.2.6, BA.2.38.2, BF.7.6, BA.2.9.4, BQ.1.8, BG.2, BA.1.1.18, DB.1, BA.5.1, BA.5.1.5, BF.11, BA.5.1.10, BA.2.66, BA.5.1.7, BA.5.5, BF.11.3, BA.5, BF.8.1, BA.4.6, XAC, BA.2.38, BA.5.2.20,	Gong et al. (2021)	163974	A	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
D614G	vaccinee plasma binding	1.17x increase in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in previously non-seroconverted subjects. 1.09x increase in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in post-infection vaccinees.	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BA.5.2.2, BU.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.5.2.6, XAE, BT.1, BG.2, BA.1.1.18, BF.25, BY.1.1.1, BA.1.1, BA.5.1, BF.20, BA.5.1.5,	Gong et al. (2021)	196845	A	G,GTA	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
D614G	vaccinee plasma binding	1.14x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in previously non-seroconverted subjects. 1.11x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in post-infection vaccinees.	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BU.2, BA.5.2.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.5.2.6, XAE, BT.1, BG.2, BA.1.1.18, BF.25, BX.1.1, BA.1.7,	Gong et al. (2021)	194135	A	G,GTA	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
D614G	vaccinee plasma binding	1.08x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in previously non-seroconverted subjects. 1.27x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in post-infection vaccinees.	BA.1.1.2	Gong et al. (2021)	258	A	G	1.0
D614G	vaccinee plasma binding	1.32x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in previously non-seroconverted subjects. 1.22x increase in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in post-infection vaccinees.	BA.5.2.22	Gong et al. (2021)	596	A	G	1.0
D614G	vaccinee plasma binding	1.16x increase in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in previously non-seroconverted subjects. 1.02x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in post-infection vaccinees.	BA.1.13.1, BA.1.1.7, BA.1.1.11, BA.1.1.18, BA.1.1.4, BA.1.15.3, BA.1.7, BA.1.8, BA.1.14, BA.1.15.1, BA.1.1.6, BA.1.1.14, BA.1.1.15, BA.1.14.2, BA.1.15, BA.1.1.2, BA.5.2.28, BA.4.6.3, BA.1.5, BA.1.1.3, BD.1, BA.1.13, BA.1.1, BA.1.1.17, XM, BA.1.17.1, BA.1.1.13, BA.1.18, BA.1.3, BA.1.17, BC.2, BQ.1.11, BA.1.1.9, BA.1.15.2, BA.1.21, BA.1.9, BQ.1.25, BA.1.1.16, BA.1.10, BA.1.16, BA.1.17.2, BA.1.1.8, BA.1.1.10, BA.1, BA.1.12, BA.1.1.1, BA.1.20, BA.1.14.1, BA.1.19, BA.1.6	Gong et al. (2021)	64881	A	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
D614G	viral load	Hamsters infected with SARS-CoV-2 expressing spike(D614G) (G614 virus) produced higher infectious titres in nasal washes and the trachea, but not in the lungs, supporting clinical evidence showing that the mutation enhances viral loads in the upper respiratory tract of COVID-19 patients and may increase transmission.	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BU.2, BA.5.2.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.5.2.6, XAE, BT.1, BG.2, BA.1.1.18, BF.25, BX.1.1, BA.1.7,	Plante et al. (2020)	196875	A	G,GTA	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
D614G	virion structure	Estimated free energy change (ddG) for this variant is 2.5 kcal/mol (i.e. stabilizing relative to wild type)	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BU.2, BA.5.2.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.5.2.6, XAE, BT.1, BG.2, BA.1.1.18, BF.25, BA.1.1, BA.1.7,	Spratt et al. (2021)	196875	A	G,GTA	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
D614G	virion structure	Negative stain EM shows increased proportion of "one-up" trimer conformation of Spike proteins on the surface of virions, where the up conformation is presumed to be more likely to bind ACE2.	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BU.2, BA.5.2.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.5.2.6, XAE, BT.1, BG.2, BA.1.1.18, BF.25, BX.1.1, BA.1.7,	Weissman et al. (2020)	196875	A	G,GTA	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
D614G	virion structure	CryoEM shows increased proportion of "one-up" trimer conformation of Spike proteins on the surface of virions, where the up conformation is presumed to be more likely to bind ACE2.	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BU.2, BA.5.2.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.5.2.6, XAE, BT.1, BG.2, BA.1.1.18, BF.25, BX.1.1, BA.1.7,	Yurkovetskiy et al. (2020)	196875	A	G,GTA	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
D614G	virion structure	Based on pseudotyped virus experiments, D614G may increase infectivity by assembling more functional S protein into the virion.	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BU.2, BA.5.2.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.5.2.6, XAE, BT.1, BG.2, BA.1.1.18, BF.25, BX.1.1, BA.1.7,	Zhang et al. (2020)	196875	A	G,GTA	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
L452M	ACE2 receptor binding affinity	Experimentally, ACE2 binding affinity increased 0.06 fold	BA.2.13	Starr et al. (2020)	40	TTACC	TTACA	0.95
L452M	gene expression increase	Experimentally, Spike gene expression increased 0.16 fold	BA.2.13	Starr et al. (2020)	40	TTACC	TTACA	0.95
K444N	antibody epitope effects	Mutant screen in neutralization assay with a broad range of monoclonal antibodies shows resistence to more than one antibody.	BA.4.6.3, BA.2.38.2	Liu et al. (2021)	22	G	C,CGC	0.55
K444N	antibody epitope effects	Abolishes binding efficiency vs wild type for mAb REGN10933.	BA.4.6.3, BA.2.38.2	Rappazzo et al. (2021)	22	G	C,CGC	0.55
K444N	antibody epitope effects	extasciitilde20% (ELISA significance threshold) drop in antibody binding (ELISA) by this variant against monoclonal antibody VH ab6.	BA.4.6.3, BA.2.38.2	Sun et al. (2021)	22	G	C,CGC	0.55
K444N	convalescent plasma escape	Improvement in neutralization capability of all 4 convalescent sera tested.	BA.4.6.3, BA.2.38.2	Liu et al. (2021)	22	G	C,CGC	0.55
K444N	convalescent plasma escape	Positive selection (up to 14% of supernatant sequences) after COV-NY convalescent plasma assay	BA.4.6.3, BA.2.38.2	Weisblum et al. (2020)	22	G	C,CGC	0.55
K444N	antibody epitope effects	Mutant screen in neutralization assay with a broad range of monoclonal antibodies shows resistence to more than one antibody.	CL.1, BA.2.38, BF.1, CK.1, BA.2.38.1, CK.2, BE.4.2, CK.2.1, CK.3, BV.2, BA.5.2.24, CK.2.1.1, BA.2.18, DG.1	Liu et al. (2021)	784	G	T,TA	0.45
K444N	antibody epitope effects	Abolishes binding efficiency vs wild type for mAb REGN10933.	CL.1, BA.2.38, BF.1, CK.1, BA.2.38.1, CK.2, BE.4.2, CK.2.1, CK.3, BV.2, BA.5.2.24, CK.2.1.1, BA.2.18, DG.1	Rappazzo et al. (2021)	784	G	T,TA	0.45
K444N	antibody epitope effects	extasciitilde20% (ELISA significance threshold) drop in antibody binding (ELISA) by this variant against monoclonal antibody VH ab6.	CL.1, BA.2.38, BF.1, CK.1, BA.2.38.1, CK.2, BE.4.2, CK.2.1, CK.3, BV.2, BA.5.2.24, CK.2.1.1, BA.2.18, DG.1	Sun et al. (2021)	784	G	T,TA	0.45
K444N	convalescent plasma escape	Improvement in neutralization capability of all 4 convalescent sera tested.	CL.1, BA.2.38, BF.1, CK.1, BA.2.38.1, CK.2, BE.4.2, CK.2.1, CK.3, BV.2, BA.5.2.24, CK.2.1.1, BA.2.18, DG.1	Liu et al. (2021)	784	G	T,TA	0.45
K444N	convalescent plasma escape	Positive selection (up to 14% of supernatant sequences) after COV-NY convalescent plasma assay	CL.1, BA.2.38, BF.1, CK.1, BA.2.38.1, CK.2, BE.4.2, CK.2.1, CK.3, BV.2, BA.5.2.24, CK.2.1.1, BA.2.18, DG.1	Weisblum et al. (2020)	784	G	T,TA	0.45
W64R	convalescent plasma escape	Mutant found after in passage in plasma pool of 26 convalescents mean 1.5 post symptom onset, but also in cell culture without plasma, therefore likely a replication cycle fitness rather than polyclonal iummnuity escape variant.	BA.2.61	Schmidt et al. (2021)	9	T	A	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
W64R	convalescent plasma escape	Mutant found after in passage in plasma pool of 26 convalescents mean 1.5 post symptom onset, but also in cell culture without plasma, therefore likely a replication cycle fitness rather than polyclonal iummnuity escape variant.	BA.2.9.3, BA.2.71, BA.5.2.18	Schmidt et al. (2021)	66	T	C	0.38
R346T	ACE2 receptor binding affinity	Experimentally, ACE2 binding affinity increased 0.06 fold	XBB.1	Starr et al. (2020)	346	CAG	CAC	0.99
R346T	gene expression increase	Experimentally, Spike gene expression increased 0.15 fold	XBB.1	Starr et al. (2020)	346	CAG	CAC	0.99

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
R346T	ACE2 receptor binding affinity	Experimentally, ACE2 binding affinity increased 0.06 fold	BQ.1.1.15, XBB.4, DE.2, XBB.1.5, BF.7.1, BA.4.4, BQ.1.1.19, CQ.1.1, BQ.1.1.3, XBB.1.3, BA.5.2.34, BA.4.1.9, BN.1.3, BR.2.1, CH.1, BF.26, BA.5.1.21, BN.5, BM.1.1, BP.1, BQ.1.1.14, BQ.1.1.2, BA.5.2.28, CR.1.2, BQ.1.1.5, BY.1, BQ.1.1.25, BA.5.1.22, BA.4.1.1, BF.7.5, BA.4.1.10, BA.1.13, BA.5.2.21, BA.2.82, BQ.1.1.6, BQ.1.1.7, BQ.1.1.28, CA.1, XBD, BF.7.4.1, XBE, XBH, BA.2.75.4, BQ.1.1.27, CA.7, BQ.1.1, BF.7.3, BF.7.7, BF.7.8, BL.1.3, CV.1, BQ.1.1.24, CQ.2, BA.5.1.25, BN.1.1.1, DF.1, BM.1.1.3, BA.5.1.6, BQ.1.1.22, BQ.1.1.13, BE.4.1.1, CA.5, BA.5.3.1, BA.4.6.3, XBB.1.4, BA.4.1.8, BA.2.10, BE.1.1, BQ.1.1.18, BA.4.6.1, CA.3.1, BA.4.6.4, BE.1.4, BA.2.75.5, BE.1.2.1, BA.5.1.26, BA.5.1.18, BA.5.1.20, BF.7, BQ.1.1.9, BQ.1.24, BQ.1.9, BL.1, CB.1, BA.5.2.44, BS.1.1, BN.1.9, CQ.1, BF.7.4, BF.3, BQ.1.5, BA.5.2.9, BN.1.5, CA.3, BQ.1.22, BA.2.74, CH.2, BF.30, BN.1.2.1, BQ.1.1.11, BY.1.2, BJ.1, BA.2.10.1, BN.1.1, BL.2, BQ.1.19,	Starr et al. (2020)	67241	G	C	0.43

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
R346T	gene expression increase	Experimentally, Spike gene expression increased 0.15 fold	BQ.1.1.15, XBB.4, DE.2, XBB.1.5, BF.7.1, BA.4.4, BQ.1.1.19, CQ.1.1, BQ.1.1.3, XBB.1.3, BA.5.2.34, BA.4.1.9, BN.1.3, BR.2.1, CH.1, BF.26, BA.5.1.21, BN.5, BM.1.1, BP.1, BQ.1.1.14, BQ.1.1.2, BA.5.2.28, CR.1.2, BQ.1.1.5, BY.1, BQ.1.1.25, BA.5.1.22, BA.4.1.1, BF.7.5, BA.4.1.10, BA.1.13, BA.5.2.21, BA.2.82, BQ.1.1.6, BQ.1.1.7, BQ.1.1.28, CA.1, XBD, BF.7.4.1, XBE, XBH, BA.2.75.4, BQ.1.1.27, CA.7, BQ.1.1, BF.7.3, BF.7.7, BF.7.8, BL.1.3, CV.1, BQ.1.1.24, CQ.2, BA.5.1.25, BN.1.1.1, DF.1, BM.1.1.3, BA.5.1.6, BQ.1.1.22, BQ.1.1.13, BE.4.1.1, CA.5, BA.5.3.1, BA.4.6.3, XBB.1.4, BA.4.1.8, BA.2.10, BE.1.1, BQ.1.1.18, BA.4.6.1, CA.3.1, BA.4.6.4, BE.1.4, BA.2.75.5, BE.1.2.1, BA.5.1.26, BA.5.1.18, BA.5.1.20, BF.7, BQ.1.1.9, BQ.1.24, BQ.1.9, BL.1, CB.1, BA.5.2.44, BS.1.1, BN.1.9, CQ.1, BF.7.4, BF.3, BQ.1.5, BA.5.2.9, BN.1.5, CA.3, BQ.1.22, BA.2.74, CH.2, BF.30, BN.1.2.1, BQ.1.1.11, BY.1.2, BJ.1, BA.2.10.1, BN.1.1, BL.2, BQ.1.19, BQ.1.18,	Starr et al. (2020)	67241	G	C	0.43

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
F486I	monoclonal antibody serial passage escape	Escapes mAb REGN10933 (part of Regeneron's antibody cocktail)	BF.12, BR.2.1	Starr et al. (2020)	99	T	A	1.0
F486I	monoclonal antibody serial passage escape	Escape mutation against monoclonal antibody LY-CoV555 (antibody that forms the basis for Eli Lilly's bamlanivimab)	BF.12, BR.2.1	Starr et al. (2021)	99	T	A	1.0
K147E	convalescent plasma escape	Escape mutant found after in passage in plasma pool of 26 convalescents mean 1.5 post symptom onset.	BM.1.1, BN.1	Schmidt et al. (2021)	168	CA	CG	0.99
K147E	monoclonal antibody serial passage escape	Escape mutation against Spike N terminal domain antigenic supersite i mAbs S2X28, S2X333	BM.1.1, BN.1	McCallum et al. (2021)	168	CA	CG	0.99

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
G339D	ACE2 receptor binding affinity	Experimentally, ACE2 binding affinity increased 0.06 fold	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, BF.19, BA.1.17.2, BA.2.61, CC.1, BA.5.6.2, BU.2, BA.5.2.2, BE.4, BA.5.1.25, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BU.3, BA.1.8, BA.2.23.1, BF.18, BA.5.8, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BA.1.1.9, BA.1.15.2, BQ.1.1.20, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.2.64, BA.2.76, BA.5.2.6, XAE, BG.2, BA.1.1.18, BF.25, BA.1.7, BA.5.1, BF.20, BA.5.1.5, BA.5.1.10, BA.2.66, BA.5.10.1, BA.1.1.6, BA.5.5, BQ.1.15, BA.2.9.5, BA.5, BA.4.6, BF.7.4.2, XAZ, BA.1.5, CM.2, BA.5.1.30, BA.2.3.9, BQ.1.4,	Starr et al. (2020)	193061	G	A,ATC,AT	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
G339D	gene expression increase	Experimentally, Spike gene expression increased 0.3 fold	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, BF.19, BA.1.17.2, BA.2.61, CC.1, BA.5.6.2, BU.2, BA.5.2.2, BE.4, BA.5.1.25, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BU.3, BA.1.8, BA.2.23.1, BF.18, BA.5.8, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BA.1.1.9, BA.1.15.2, BQ.1.1.20, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.2.64, BA.2.76, BA.5.2.6, XAE, BG.2, BA.1.1.18, BF.25, BA.1.7, BA.5.1, BF.20, BA.5.1.5, BA.5.1.10, BA.2.66, BA.5.10.1, BA.1.1.6, BA.5.5, BQ.1.15, BA.2.9.5, BA.5, BA.4.6, BF.7.4.2, XAZ, BA.1.5, CM.2, BA.5.1.30, BA.2.3.9, BQ.1.4,	Starr et al. (2020)	193061	G	A,ATC,AT	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
F490S	ACE2 receptor binding affinity	Among the first selected minor variants in an in vitro evolution experiment for ACE2 binding.	XBB.1, XBB.4, BQ.1.8, XBB.1.5, BN.1.5, CJ.1, BA.2.75, BN.3.1, BN.1.1.1, XBB.1.3, BN.1.3.1, BN.1.2.1, BA.2.10.1, BN.1.7, BN.2.1, BL.2, BQ.1.1.25, XBB.3, BN.1, XBB.2, XBB.1.4, BN.1.1, XBF, BN.1.2, XBB, BM.1.1.1, XBB.1.1, BN.1.9, BA.2.75.6	Zahradnik et al. (2021)	3954	T	C	0.92
F490S	antibody epitope effects	Mutant screen in neutralization assay with a broad range of monoclonal antibodies shows resistence to mAb SARS2-32.	XBB.1, XBB.4, BQ.1.8, XBB.1.5, BN.1.5, CJ.1, BA.2.75, BN.3.1, BN.1.1.1, XBB.1.3, BN.1.3.1, BN.1.2.1, BA.2.10.1, BN.1.7, BN.2.1, BL.2, BQ.1.1.25, XBB.3, BN.1, XBB.2, XBB.1.4, BN.1.1, XBF, BN.1.2, XBB, BM.1.1.1, XBB.1.1, BN.1.9, BA.2.75.6	Liu et al. (2020)	3954	T	C	0.92
F490S	antibody epitope effects	Complete loss of binding in ELISA by the variant against monoclonal antibody ab8	XBB.1, XBB.4, BQ.1.8, XBB.1.5, BN.1.5, CJ.1, BA.2.75, BN.3.1, BN.1.1.1, XBB.1.3, BN.1.3.1, BN.1.2.1, BA.2.10.1, BN.1.7, BN.2.1, BL.2, BQ.1.1.25, XBB.3, BN.1, XBB.2, XBB.1.4, BN.1.1, XBF, BN.1.2, XBB, BM.1.1.1, XBB.1.1, BN.1.9, BA.2.75.6	Sun et al. (2021)	3954	T	C	0.92

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
F490S	convalescent plasma escape	Strong reduction in neutralization capability of all 4 convalescent sera tested (3 ablations).	XBB.1, XBB.4, BQ.1.8, XBB.1.5, BN.1.5, CJ.1, BA.2.75, BN.3.1, BN.1.1.1, XBB.1.3, BN.1.3.1, BN.1.2.1, BA.2.10.1, BN.1.7, BN.2.1, BL.2, BQ.1.1.25, XBB.3, BN.1, XBB.2, XBB.1.4, BN.1.1, XBF, BN.1.2, XBB, BM.1.1.1, XBB.1.1, BN.1.9, BA.2.75.6	Liu et al. (2021)	3954	T	C	0.92
F490S	monoclonal antibody serial passage escape	Ranked mildly effective mutant against this position in the RBD for highly neutralizing COV2-2496 monoclonal antibody	XBB.1, XBB.4, BQ.1.8, XBB.1.5, BN.1.5, CJ.1, BA.2.75, BN.3.1, BN.1.1.1, XBB.1.3, BN.1.3.1, BN.1.2.1, BA.2.10.1, BN.1.7, BN.2.1, BL.2, BQ.1.1.25, XBB.3, BN.1, XBB.2, XBB.1.4, BN.1.1, XBF, BN.1.2, XBB, BM.1.1.1, XBB.1.1, BN.1.9, BA.2.75.6	Greaney et al. (2020)	3954	T	C	0.92
F490S	monoclonal antibody serial passage escape	Escape mutation against monoclonal antibody LY-CoV555 (antibody that forms the basis for Eli Lilly's bamlanivimab)	XBB.1, XBB.4, BQ.1.8, XBB.1.5, BN.1.5, CJ.1, BA.2.75, BN.3.1, BN.1.1.1, XBB.1.3, BN.1.3.1, BN.1.2.1, BA.2.10.1, BN.1.7, BN.2.1, BL.2, BQ.1.1.25, XBB.3, BN.1, XBB.2, XBB.1.4, BN.1.1, XBF, BN.1.2, XBB, BM.1.1.1, XBB.1.1, BN.1.9, BA.2.75.6	Starr et al. (2021)	3954	T	C	0.92

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
F490S	monoclonal antibody serial passage escape	Class 2/3 mAb C603 modestly selected for the emergence of this mutation in vitro.	XBB.1, XBB.4, BQ.1.8, XBB.1.5, BN.1.5, CJ.1, BA.2.75, BN.3.1, BN.1.1.1, XBB.1.3, BN.1.3.1, BN.1.2.1, BA.2.10.1, BN.1.7, BN.2.1, BL.2, BQ.1.1.25, XBB.3, BN.1, XBB.2, XBB.1.4, BN.1.1, XBF, BN.1.2, XBB, BM.1.1.1, XBB.1.1, BN.1.9, BA.2.75.6	Wang et al. (2021)	3954	T	C	0.92
F490S	pharmaceutical effectiveness	Greater than 10-fold rediuction of binding effeiency vs wild type for mAb LY-CoV555.	XBB.1, XBB.4, BQ.1.8, XBB.1.5, BN.1.5, CJ.1, BA.2.75, BN.3.1, BN.1.1.1, XBB.1.3, BN.1.3.1, BN.1.2.1, BA.2.10.1, BN.1.7, BN.2.1, BL.2, BQ.1.1.25, XBB.3, BN.1, XBB.2, XBB.1.4, BN.1.1, XBF, BN.1.2, XBB, BM.1.1.1, XBB.1.1, BN.1.9, BA.2.75.6	Rappazzo et al. (2021)	3954	T	C	0.92
F490S	ACE2 receptor binding affinity	Among the first selected minor variants in an in vitro evolution experiment for ACE2 binding.	BN.1.3	Zahradnik et al. (2021)	147	TACTTT	TACTCT	0.99
F490S	antibody epitope effects	Mutant screen in neutralization assay with a broad range of monoclonal antibodies shows resistence to mAb SARS2-32.	BN.1.3	Liu et al. (2020)	147	TACTTT	TACTCT	0.99
F490S	antibody epitope effects	Complete loss of binding in ELISA by the variant against monoclonal antibody ab8	BN.1.3	Sun et al. (2021)	147	TACTTT	TACTCT	0.99
F490S	convalescent plasma escape	Strong reduction in neutralization capability of all 4 convalescent sera tested (3 ablations).	BN.1.3	Liu et al. (2021)	147	TACTTT	TACTCT	0.99
F490S	monoclonal antibody serial passage escape	Ranked mildly effective mutant against this position in the RBD for highly neutralizing COV2-2496 monoclonal antibody	BN.1.3	Greaney et al. (2020)	147	TACTTT	TACTCT	0.99
F490S	monoclonal antibody serial passage escape	Escape mutation against monoclonal antibody LY-CoV555 (antibody that forms the basis for Eli Lilly's bamlanivimab)	BN.1.3	Starr et al. (2021)	147	TACTTT	TACTCT	0.99
F490S	monoclonal antibody serial passage escape	Class 2/3 mAb C603 modestly selected for the emergence of this mutation in vitro.	BN.1.3	Wang et al. (2021)	147	TACTTT	TACTCT	0.99
F490S	pharmaceutical effectiveness	Greater than 10-fold rediuction of binding effeiency vs wild type for mAb LY-CoV555.	BN.1.3	Rappazzo et al. (2021)	147	TACTTT	TACTCT	0.99

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
S373P	monoclonal antibody serial passage escape	Reduce affinity for mildly cross-reactive CR3022 (2003 pandemic SARS monoclonal antibody cross-reactive to SARS-CoV-2)	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BA.5.2.2, BU.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, CA.5, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.2.76, BA.5.2.6, BT.1, XAE, BG.2, BA.1.1.18, BF.25, BA.1.1, BA.1.7,	Long et al. (2020)	196119	T	C,CCG	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
S373P	monoclonal antibody serial passage escape	Reduce affinity for mildly cross-reactive CR3022 (2003 pandemic SARS monoclonal antibody cross-reactive to SARS-CoV-2)	DC.1	Long et al. (2020)	4	TCA	CCA	0.75
K417T	ACE2 receptor binding affinity	The K417T mutation decreased the affinity extasciitilde2 fold, mainly by decreasing the k(on) but also by increasing the k(off) as measured by surface plasmon resonance.	BA.2.38, BA.2.38.2, BA.2.38.1, BA.2.40.1, BA.2.1, BA.2.18, BH.1	Barton et al. (2021)	352	AG	CT,AT	1.0
K417T	ACE2 receptor binding affinity	Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant showed a 1.28x increase in binding (KD) relative to D614G.	BA.2.38, BA.2.38.2, BA.2.38.1, BA.2.40.1, BA.2.1, BA.2.18, BH.1	Gong et al. (2021)	352	AG	CT,AT	1.0
K417T	convalescent plasma binding	1.65x increase in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset.	BA.2.38, BA.2.38.2, BA.2.38.1, BA.2.40.1, BA.2.1, BA.2.18, BH.1	Gong et al. (2021)	352	AG	CT,AT	1.0
K417T	gene expression increase	Experimentally, Spike gene expression increased 0.25 fold	BA.2.38, BA.2.38.2, BA.2.38.1, BA.2.40.1, BA.2.1, BA.2.18, BH.1	Starr et al. (2020)	352	AG	CT,AT	1.0
K417T	monoclonal antibody serial passage escape	Escape mutation against monoclonal antibody LY-CoV016	BA.2.38, BA.2.38.2, BA.2.38.1, BA.2.40.1, BA.2.1, BA.2.18, BH.1	Starr et al. (2021)	352	AG	CT,AT	1.0
K417T	monoclonal antibody serial passage escape	In vitro selection against class 1 antibody C682	BA.2.38, BA.2.38.2, BA.2.38.1, BA.2.40.1, BA.2.1, BA.2.18, BH.1	Wang et al. (2021)	352	AG	CT,AT	1.0
K417T	pharmaceutical effectiveness	COR-101 lost extasciitilde16x binding against this isolated mutation. Estesevimab lost extasciitilde16x binding against this isolated mutation. m396 lost extasciitilde8x binding against this isolated mutation.	BA.2.38, BA.2.38.2, BA.2.38.1, BA.2.40.1, BA.2.1, BA.2.18, BH.1	Engelhart et al. (2021)	352	AG	CT,AT	1.0
K417T	vaccinee plasma binding	1.04x increase in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in previously non-seroconverted subjects. 1.1x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in post-infection vaccinees.	BA.2.38, BA.2.38.2, BA.2.38.1, BA.2.40.1, BA.2.1, BA.2.18, BH.1	Gong et al. (2021)	352	AG	CT,AT	1.0
K417T	virion structure	Estimated free energy change (ddG) for this variant is -0.64 kcal/mol (i.e. destabilizing relative to wild type)	BA.2.38, BA.2.38.2, BA.2.38.1, BA.2.40.1, BA.2.1, BA.2.18, BH.1	Spratt et al. (2021)	352	AG	CT,AT	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
H655Y	ACE2 receptor binding affinity	Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant showed a 1.21x increase in binding (KD) relative to D614G.	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BA.5.2.2, BU.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.2.76, BA.5.2.6, BT.1, XAE, BG.2, BA.1.1.18, BF.25, BY.1.1.1,	Gong et al. (2021)	199697	C	T,TATA	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
H655Y	anthropozoonotic events	Six minks were intranasally infected with WA1 isolate, all developed this mutation during infection.	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BA.5.2.2, BU.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, CA.5, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.2.76, BA.5.2.6, BT.1, XAE, BG.2, BA.1.1.18, BF.25, BY.1.1.1,	Esclera et al. (2021)	199719	C	T,TATA	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
H655Y	convalescent plasma binding	1.48x increase in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset.	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BA.5.2.2, BU.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.2.76, BA.5.2.6, BT.1, XAE, BG.2, BA.1.1.18, BA.2.25, BY.1.1.1,	Gong et al. (2021)	199697	C	T,TATA	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
H655Y	homoplasy	In experimental models of SARS-CoV-2 mutational evolution (without immune pressure), this mutation in the N terminal domain appears convergent.	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BA.5.2.2, BU.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, CA.5, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.2.76, BA.5.2.6, BT.1, XAE, BG.2, BA.1.1.18, BA.2.25, BY.1.1.1,	Borges et al. (2021)	199719	C	T,TATA	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
H655Y	vaccinee plasma binding	1.04x increase in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in previously non-seroconverted subjects. 1.09x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in post-infection vaccinees.	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BA.5.2.2, BU.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.2.76, BA.5.2.6, BT.1, XAE, BG.2, BA.1.1.18, BE.2.1, BY.1.1.1,	Gong et al. (2021)	199697	C	T,TATA	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
H655Y	virion structure	Estimated free energy change (ddG) for this variant is 0.87 kcal/mol (i.e. stabilizing relative to wild type)	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BA.5.2.2, BU.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, CA.5, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.2.76, BA.5.2.6, BT.1, XAE, BG.2, BA.1.1.18, BF.25, BY.1.1.1,	Spratt et al. (2021)	199719	C	T,TATA	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
H655Y	ACE2 receptor binding affinity	Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant showed a 1.21x increase in binding (KD) relative to D614G.	BA.1.1.6	Gong et al. (2021)	688	TGAAC	TGAAT	0.96
H655Y	anthropozoonotic events	Six minks were intranasally infected with WA1 isolate, all developed this mutation during infection.	BA.1.1.6	Esclera et al. (2021)	688	TGAAC	TGAAT	0.96
H655Y	convalescent plasma binding	1.48x increase in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset.	BA.1.1.6	Gong et al. (2021)	688	TGAAC	TGAAT	0.96
H655Y	homoplasy	In experimental models of SARS-CoV-2 mutational evolution (without immune pressure), this mutation in the N terminal domain appears convergent.	BA.1.1.6	Borges et al. (2021)	688	TGAAC	TGAAT	0.96
H655Y	vaccinee plasma binding	1.04x increase in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in previously non-seroconverted subjects. 1.09x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in post-infection vaccinees.	BA.1.1.6	Gong et al. (2021)	688	TGAAC	TGAAT	0.96
H655Y	virion structure	Estimated free energy change (ddG) for this variant is 0.87 kcal/mol (i.e. stabilizing relative to wild type)	BA.1.1.6	Spratt et al. (2021)	688	TGAAC	TGAAT	0.96

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
N501Y	ACE2 receptor binding affinity	The N501Y mutation had the biggest effect on ACE2 affinity of any VOC mutation tested, increasing the affinity extasciitilde10 fold to KD extasciitilde7 nM, by increasing the k(on) extasciitilde1.8 fold and decreasing the k(off) by extasciitilde 7 fold as measured by surface plasmon resonance.	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BU.2, BA.5.2.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, CA.5, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.2.76, BA.5.2.6, BT.1, XAE, BG.2, BA.1.18, BF.25,	Barton et al. (2021)	200193	A	T,TAC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
N501Y	ACE2 receptor binding affinity	This combination showed extasciitilde3x increase binding to ACE2 vs wild type, about half that of the B.1.1.7 lineage, suggesting that the K417N mutation is slightly detrimental to ACE2 binding, probably as a result of disrupting the salt bridge formed with ACE2 residue D30	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BU.2, BA.5.2.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, CA.5, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.2.76, BA.5.2.6, BT.1, XAE, BG.2, BA.1.18, BF.25,	Collier et al. (2021)	200193	A	T,TAC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
N501Y	ACE2 receptor binding affinity	The most frequent RBM mutation N501Y (165,519 instances) makes defective the atypical N-glycosylation sequon NGV 501-503, becoming a key RBM position for the interaction with hACE2-binding hotspot 353.	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BU.2, BA.5.2.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, CA.5, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.2.76, BA.5.2.6, BT.1, XAE, BG.2, BA.1.18, BF.25,	Gamez et al. (2021)	200193	A	T,TAC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
N501Y	ACE2 receptor binding affinity	Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant showed a 2.52x increase in binding (KD) relative to D614G, mostly due to decreased in "off-rate" a.k.a. dissociation rate (Kdis). Compare to full Spike variant complements for major lineages containing this variant subset: 5.43x (B.1.1.7 aka Alpha), 3.56x (B.1.351 aka Beta), 4.24x (P.1 aka Gamma).	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BA.5.2.2, BU.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.2.76, BA.5.2.6, BT.1, XAE, BG.2, BA.1.1.18, BF.25, BY.1.1.1,	Gong et al. (2021)	200171	A	T,TAC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
N501Y	ACE2 receptor binding affinity	RBD containing the N501Y mutation results in 9-fold stronger binding to the hACE2 receptor than wild type RBD. The E484K mutation does not significantly influence the affinity for the receptor, while K417N attenuates affinity. As a result, RBD from B.1.351 containing all three mutations binds 3-fold stronger to hACE2 than wild type RBD but 3-fold weaker than N501Y.	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BU.2, BA.5.2.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, CA.5, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.2.76, BA.5.2.6, BT.1, XAE, BG.2, BA.1.18, BF.25,	Laffeber et al. (2021)	200193	A	T,TAC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
N501Y	ACE2 receptor binding affinity	Reported 10-fold increase in ACE2 binding vs wild-type (Kd	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BU.2, BA.5.2.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, CA.5, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.2.76, BA.5.2.6, BT.1, XAE, BG.2, BA.1.18, BF.25,	Liu et al. (2021)	200193	A	T,TAC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
N501Y	ACE2 receptor binding affinity	Studying the key covariants in lineage of concern 501Y.V2, observed about 2-fold increase in ACE2 binding vs wildtype, but greatly decreased mAb binding, suggesting evolutionary optimum tension between immune evasion and ACE2 binding affinity as the N501Y variant alone has 10x increase in affinity but no effect on tested mAb binding.	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BU.2, BA.5.2.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, CA.5, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.2.76, BA.5.2.6, BT.1, XAE, BG.2, BA.1.18, BF.25,	Liu et al. (2021)	200193	A	T,TAC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
N501Y	ACE2 receptor binding affinity	extasciitilde4-fold increase in binding affinity vs wild type.	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BU.2, BA.5.2.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, CA.5, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.2.76, BA.5.2.6, BT.1, XAE, BG.2, BA.1.18, BF.25,	Motozono et al. (2021)	200193	A	T,TAC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
N501Y	ACE2 receptor binding affinity	Using Microscale Thermopheresis, this variant binds ACE2 at nearly two-fold greater affinity than the original SARS-COV-2 RBD (203.7 nM vs 402.5 nM).	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BU.2, BA.5.2.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, CA.5, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.2.76, BA.5.2.6, BT.1, XAE, BG.2, BA.1.18, BF.25,	Ramanathan et al. (2021)	200193	A	T,TAC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
N501Y	ACE2 receptor binding affinity	Using Mircoscale Thermopheresis, the B.1.351 variant harboring three mutations, binds ACE2 at nearly five-fold greater affinity than the original SARS-COV-2 RBD (Kd 87.6, vs 402.5 nM).	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BU.2, BA.5.2.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, CA.5, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.2.76, BA.5.2.6, BT.1, XAE, BG.2, BA.1.18, BF.25,	Ramanathan et al. (2021)	200193	A	T,TAC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
N501Y	ACE2 receptor binding affinity	In silico methods (PyMOL and PDBePISA) involving mutagenesis (N501Y mutation) and interface analysis focusing on the Spike RDB-ACE2 interaction showed that the SARS-CoV-2 N501Y mutant (lineage B.1.1.7) establishes a more significant number of interactions relating to the mutant residue Y501 (Spike RDB) with residues Y41 and K353 (ACE2). This finding shows that the increased infectivity of SARS-CoV-2 lineage B.1.1.7 is associated with the interaction force between the Spike RBD Y501 mutant residue with the ACE2 receptor, which in this strain is increased.	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BU.2, BA.5.2.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, CA.5, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.2.76, BA.5.2.6, BT.1, XAE, BG.2, BA.1.18, BF.25,	Santos and Passos (2021)	200193	A	T,TAC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
N501Y	ACE2 receptor binding affinity	Experimentally, ACE2 binding affinity increased 0.24 fold	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BU.2, BA.5.2.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, CA.5, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.2.76, BA.5.2.6, BT.1, XAE, BG.2, BA.1.18, BF.25,	Starr et al. (2020)	200193	A	T,TAC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
N501Y	ACE2 receptor binding affinity	This single mutation causes major increase in binding affinity vs. wild type as measured by IC50 vs pseudotyped lentivirus, but combined with the complete set of B.1.1.7 lineage variants no major change vs wild type affnity is observed.	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BU.2, BA.5.2.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, CA.5, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.2.76, BA.5.2.6, BT.1, XAE, BG.2, BA.1.18, BF.25,	Tada et al. (2021)	200193	A	T,TAC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
N501Y	ACE2 receptor binding affinity	Lentiviral pseudotyped with the key mutations from COH.20G/677H lineage was tested on ACE2.293T cells for ACE2 affinity changes vs D614G alone, showing a extasci-itilde70% drop in IC50 (i.e. increased affinity).	BQ.1.1.22, BA.5.5.2, XBF, BL.1, BE.9, BA.5.2.6	Tada et al. (2021)	404	A	T	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
N501Y	ACE2 receptor binding affinity	Reported 4-fold increase in affinity compared to wild-type RBD on the cell surface (Kd	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BU.2, BA.5.2.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, CA.5, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.2.76, BA.5.2.6, BT.1, XAE, BG.2, BA.1.18, BF.25,	Tian et al. (2021)	200193	A	T,TAC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
N501Y	ACE2 receptor binding affinity	Reported slight increase in affinity compared to wild-type RBD on the cell surface (Kd	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BU.2, BA.5.2.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, CA.5, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.2.76, BA.5.2.6, BT.1, XAE, BG.2, BA.1.18, BF.25,	Tian et al. (2021)	200193	A	T,TAC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
N501Y	ACE2 receptor binding affinity	The affinity of ACE2 for this mutation combination was twice as high as for wild type. Having in mind that the affinity of SARS-CoV-2 for ACE2 is only 4-fold higher compared to SARS-CoV-1, this factor of 2 is expected to be biologically significant.	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BU.2, BA.5.2.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, CA.5, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.2.76, BA.5.2.6, BT.1, XAE, BG.2, BA.1.18, BF.25,	Vogel et al. (2021)	200193	A	T,TAC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
N501Y	ACE2 receptor binding affinity	Among the first selected and fixed variants in an in vitro evolution experiment for ACE2 binding. Calculated disassociation constant for this variant is nearly four fold lower than wild type (Kd	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BU.2, BA.5.2.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, CA.5, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.2.76, BA.5.2.6, BT.1, XAE, BG.2, BA.1.18, BF.25,	Zahradnik et al. (2021)	200193	A	T,TAC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
N501Y	ACE2 receptor binding affinity	N501Y residue inserts into a cavity at the binding interface near Y41 of ACE2. The additional interactions result in increased affinity of ACE2 for the N501Y mutant, accounting for its increased infectivity.	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BU.2, BA.5.2.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, CA.5, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.2.76, BA.5.2.6, BT.1, XAE, BG.2, BA.1.18, BF.25,	Zhu et al. (2021)	200193	A	T,TAC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
N501Y	T cell evasion	Vaccinated, but not post-infection sera, show decreased average T cell response to an N501Y peptide. When we primed transgenic mice expressing human HLA-DRB1*0401 with the Wuhan Hu-1 peptide pool, T cell responses to the B.1.1.7 variant peptide pool were significantly reduced (p	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BU.2, BA.5.2.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, CA.5, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.2.76, BA.5.2.6, BT.1, XAE, BG.2, BA.1.18, BF.25,	Reynolds et al. (2021)	200193	A	T,TAC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
N501Y	antibody epitope effects	Ablates Class 3 N-terminal domain targeting antibody COV2-2489, diminishes COV2-2676.	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BU.2, BA.5.2.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, CA.5, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.2.76, BA.5.2.6, BT.1, XAE, BG.2, BA.1.18, BF.25,	Chen et al. (2021)	200193	A	T,TAC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
N501Y	antibody epitope effects	Of 50 mAbs tested, major loss of neutralization observed for S2X128, S2D8, S2X192, S2D19, S2H14, S2H19.	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BU.2, BA.5.2.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, CA.5, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.2.76, BA.5.2.6, BT.1, XAE, BG.2, BA.1.18, BF.25,	Collier et al. (2021)	200193	A	T,TAC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
N501Y	antibody epitope effects	Wildtype elicits immune response, COVID-19 cohort epitope score > 99th percentile of the 497 pre-pandemic controls, mutant drops PIWAS epitope score from 3% to 1.2% (poorer immune recognition) Together with other B1.1.7 lineage mutational changes (Spike: Y144del, A570D, P681H, Nucleoprotein: D3L, S235F) resulted in only 2 or 579 individuals (0.3% of the population) having a dramatic reduction in PIWAS antigen scores, which reflects the peak epitope signal along the entire antigen.	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BU.2, BA.5.2.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, CA.5, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.2.76, BA.5.2.6, BT.1, XAE, BG.2, BA.1.18, BF.25,	Haynes et al. (2021)	200193	A	T,TAC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
N501Y	antibody epitope effects	Contrary to other reports on N501Y containing lineages (i.e. with additional mutations), N501Y alone may have an even greater affinity for a human monoclonal antibody specific for wild type. These results suggest that the individual N501Y mutation does not contribute to altered viral properties by itself, but may contribute to a collective conformational shift produced by multiple mutations.	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BU.2, BA.5.2.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, CA.5, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.2.76, BA.5.2.6, BT.1, XAE, BG.2, BA.1.18, BF.25,	Klegerman et al. (2021)	200193	A	T,TAC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
N501Y	antibody epitope effects	Lowered the neutralization potency of mAb COVA1-12 to the limit of the assay. Decrease in potency was observed against the N501Y pseudotype for the cluster IX mAb COVA2-17.	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BU.2, BA.5.2.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, CA.5, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.2.76, BA.5.2.6, BT.1, XAE, BG.2, BA.1.18, BF.25,	Rees-Spear et al. (2021)	200193	A	T,TAC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
N501Y	antibody epitope effects	Reduction in neutralization by mAbs COVA1-18 (extasciitilde4x), COVA2-15 (extasciitilde9x), S309 (extasciitilde3x)	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BU.2, BA.5.2.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, CA.5, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.2.76, BA.5.2.6, BT.1, XAE, BG.2, BA.1.18, BF.25,	Shen et al. (2021)	200193	A	T,TAC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
N501Y	antibody epitope effects	4 antibodies tested were less potent against K417N by ten-fold or more, in both mAb classes 1 and 3	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BU.2, BA.5.2.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, CA.5, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.2.76, BA.5.2.6, BT.1, XAE, BG.2, BA.1.18, BF.25,	Wang et al. (2021)	200193	A	T,TAC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
N501Y	convalescent plasma binding	1.65x increase in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset.	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BA.5.2.2, BU.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.2.76, BA.5.2.6, BT.1, XAE, BG.2, BA.1.1.18, BF.25, BY.1.1.1,	Gong et al. (2021)	200171	A	T,TAC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
N501Y	convalescent plasma escape	The 501Y.V2 to first wave IC50 ratio ranged from 6 to 200-fold. Averaging across all 7 participant convalescent sera highlighted the dramatic decrease in sensitivity to neutralization of authentic 501Y.V2 variants. PG: I'm purposefully ignoring D614G and A701V as contributors	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BU.2, BA.5.2.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, CA.5, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.2.76, BA.5.2.6, BT.1, XAE, BG.2, BA.1.18, BF.25,	Cele et al. (2021)	200193	A	T,TAC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
N501Y	convalescent plasma escape	0.7x reduction in neutralization by key variant in several variants of concern in sera collected from cohort of 10 with severe disease 21 to 63 days post-onset.	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BU.2, BA.5.2.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, CA.5, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.2.76, BA.5.2.6, BT.1, XAE, BG.2, BA.1.18, BF.25,	Kuzmina et al. (2021)	200193	A	T,TAC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
N501Y	convalescent plasma escape	In 30 samples collected 111 to 260 days post onset of symptoms, the covalescent plasma can neutralize both the reference USA-WA1/2020 strain and the mouse adapted strain that contains the N501Y spike mutation with similar efficiency.	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BU.2, BA.5.2.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, CA.5, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.2.76, BA.5.2.6, BT.1, XAE, BG.2, BA.1.18, BF.25,	Rathnasinghe et al. (2021)	200193	A	T,TAC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
N501Y	convalescent plasma escape	Neutralization activity of convalescent sera tested decreased extasciitilde2x with this B.1.1.7 pseudotyped virus.	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BU.2, BA.5.2.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, CA.5, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.2.76, BA.5.2.6, BT.1, XAE, BG.2, BA.1.18, BF.25,	Shen et al. (2021)	200193	A	T,TAC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
N501Y	convalescent plasma escape	Viruses containing the point mutations of B.1.1.7 showed that the single point mutations (Δ69-70 and N501Y) were neutralized as efficiently as D614G across 10 convalescent sera from April 2020 infectees.	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BU.2, BA.5.2.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, CA.5, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.2.76, BA.5.2.6, BT.1, XAE, BG.2, BA.1.18, BF.25,	Tada et al. (2021)	200193	A	T,TAC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
N501Y	convalescent plasma escape	Lentiviral pseudotyped with the key mutations from COH.20G/677H ("Ohio") lineage was neutralized similarly to D614G in 10 convalescent sera from April 2020 infectees.	BQ.1.1.22, BA.5.5.2, XBF, BL.1, BE.9, BA.5.2.6	Tada et al. (2021)	404	A	T	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
N501Y	convalescent plasma escape	As measured by surface plasmon resonance, RBD with the N501Y mutation alone showed a mean 2.1x decrease in binding affinity for six batches of hyper-immune immunoglobulin (hCoV-2IG) preparations generated from SARS-CoV-2 convalescent plasma.	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BU.2, BA.5.2.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, CA.5, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.2.76, BA.5.2.6, BT.1, XAE, BG.2, BA.1.18, BF.25,	Tang et al. (2021)	200193	A	T,TAC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
N501Y	convalescent plasma escape	27% of 44 early pandemic exposure convalescent plasma/sera lose all activity against a RBD triple mutant pseudovirus (RBD mutatants of the 501Y.V2 "South African" lineage), while only 23% retained high titres	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BU.2, BA.5.2.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, CA.5, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.2.76, BA.5.2.6, BT.1, XAE, BG.2, BA.1.18, BF.25,	Wibmer et al. (2021)	200193	A	T,TAC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
N501Y	convalescent plasma escape	Nearly half (21 of 44, 48%) of early pandemic exposure convalescent plasma/sera failed to neutralize the 501Y.V2 (”South African”) lineage pseudovirus construct Only 3 of 44 convascent sera (those with the highest titer, which correlated direectly with initial infection severity) had high neutralization against this 501Y.V2 PG: note that lineage variant R246I was excluded from the text in reference to these sera assays, not sure if that was an oversight.	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BU.2, BA.5.2.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, CA.5, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.2.76, BA.5.2.6, BT.1, XAE, BG.2, BA.1.18, BF.25,	Wibmer et al. (2021)	200193	A	T,TAC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
N501Y	environmental condition stability	Relative to D614G, this mutation demonstrated significant increase in infectivity (i.e. heat stability) after incubation at 50C after 30 minutes or 1 hour	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BU.2, BA.5.2.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, CA.5, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.2.76, BA.5.2.6, BT.1, XAE, BG.2, BA.1.18, BF.25,	Tada et al. (2021)	200193	A	T,TAC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
N501Y	homoplasy	Variant within the six key residues in the receptor binding domain (RBD). Independently reported in UK, Australia (same origin as UK), and South Africa (independent origin).	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BU.2, BA.5.2.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, CA.5, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.2.76, BA.5.2.6, BT.1, XAE, BG.2, BA.1.18, BF.25,	Flores-Alanis et al. (2021)	200193	A	T,TAC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
N501Y	immunosuppression variant emergence	Appeared (day 128) and persisted in chronic (152 day) SARS-CoV-2 infection of immunocompromised patient with severe antiphospholipid syndrome	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BU.2, BA.5.2.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, CA.5, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.2.76, BA.5.2.6, BT.1, XAE, BG.2, BA.1.18, BF.25,	Choi et al. (2020)	200193	A	T,TAC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
N501Y	monoclonal antibody serial passage escape	In vitro selection against class 1 (Spike 'up' conformation) monoclonal antibody C663, and to a lesser extent C613.	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BU.2, BA.5.2.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, CA.5, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.2.76, BA.5.2.6, BT.1, XAE, BG.2, BA.1.18, BF.25,	Wang et al. (2021)	200193	A	T,TAC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
N501Y	pharmaceutical effectiveness	COR-101 lost extasci-itilde8x binding against this isolated mutation. Regdanvimab lost extasci-itilde6x binding against this isolated mutation.	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BU.2, BA.5.2.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, CA.5, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.2.76, BA.5.2.6, BT.1, XAE, BG.2, BA.1.18, BF.25,	Engelhart et al. (2021)	200193	A	T,TAC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
N501Y	pharmaceutical effectiveness	Tixagevimab, Regdanvimab and COR-101 display reduced binding affinity to virus pseudotyped as RBD from B.1.351.	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BU.2, BA.5.2.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, CA.5, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.2.76, BA.5.2.6, BT.1, XAE, BG.2, BA.1.18, BF.25,	Engelhart et al. (2021)	200193	A	T,TAC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
N501Y	pharmaceutical effectiveness	COR-101 lost extasciitilde20x binding against this double mutation. Estesevimab lost extasciitilde16x binding against this double mutation. Regdanvimab lost extasciitilde6x binding against this double mutation. M396 lost extasciitilde10x binding against this double mutation.	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BA.5.2.2, BU.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, CA.5, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.64, BA.1.6, BA.2.76, BA.5.2.6, XAE, BT.1, BG.2, BA.1.1.18, BF.25, BX.1.1, BA.1.7,	Engelhart et al. (2021)	199919	A	T,TAC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
N501Y	pharmaceutical effectiveness	This mutated version of RBD completely abolishes the binding to a therapeutic antibody, Bamlanivimab, in vitro.	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BU.2, BA.5.2.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, CA.5, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.2.76, BA.5.2.6, BT.1, XAE, BG.2, BA.1.18, BF.25,	Liu et al. (2021)	200193	A	T,TAC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
N501Y	syncytium formation	Slight increase in Vero cell-cell membrane fusion assay under infection with VSV pseudotyped virus relative to wild type, no change relative to D614G.	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BA.5.2.2, BU.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.2.76, BA.5.2.6, BT.1, XAE, BG.2, BA.1.1.18, BF.25, BY.1.1.1,	Kim et al. (2021)	200171	A	T,TAC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
N501Y	trafficking	More efficient infectivity (24h) compared to wild type, in Caco-2 cells extasciitilde9x, Vero extasciitilde8x, and Calu-3 extasciitilde8x. Compare to wild type at extasciitilde5x across cell types.	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BA.5.2.2, BU.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.2.76, BA.5.2.6, BT.1, XAE, BG.2, BA.1.1.18, BA.2.25, BY.1.1.1,	Kim et al. (2021)	200171	A	T,TAC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
N501Y	trafficking	extasciitilde4x more efficient S2 domain cleavage compared to wild type, no change relative to D614G alone in Caco-2 cells, mid-range of three cell line tested (Vero and Calu-3).	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BA.5.2.2, BU.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.2.76, BA.5.2.6, BT.1, XAE, BG.2, BA.1.1.18, BF.25, BY.1.1.1,	Kim et al. (2021)	200171	A	T,TAC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
N501Y	trafficking	9x more infectivity than D614G alone in HEK293T-ACE2 cells 48h post-transduction.	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BA.5.2.2, BU.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.2.76, BA.5.2.6, BT.1, XAE, BG.2, BA.1.1.18, BA.2.75, BY.1.1.1,	Kuzmina et al. (2021)	201926	A	T	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
N501Y	trafficking	extasciitilde9x more infectivity than D614G alone in HEK293T-ACE2 cells 48h post-transduction (no synergy as level approx. that of N501Y alone).	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BU.2, BA.5.2.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.64, BA.1.6, BA.2.76, BA.5.2.6, XAE, BT.1, BG.2, BA.1.1.18, BA.2.25, BY.1.1.1,	Kuzmina et al. (2021)	199897	A	T,TAC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
N501Y	trafficking	Decreased stability of RBD expression in yeast, suggesting decreased Spike protein stability.	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BU.2, BA.5.2.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, CA.5, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.2.76, BA.5.2.6, BT.1, XAE, BG.2, BA.1.18, BF.25,	Motozono et al. (2021)	200193	A	T,TAC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
N501Y	trafficking	Lentiviral pseudotyped with this individual mutation from B.1.1.7 was tested on ACE2.293T cells. Luciferase activity was measured two days postinfection, showing slightly increased infection rate amongst the cells. [in what is essentially a replicate experiment in the same paper, because each B.1.351 lineage variant was indepedetly evaluated and N501 is in both lineages, a significant decrease was observed, therefore the error bars described in this paper should be interpreted carefully]	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BU.2, BA.5.2.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, CA.5, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.2.76, BA.5.2.6, BT.1, XAE, BG.2, BA.1.18, BF.25,	Tada et al. (2021)	200193	A	T,TAC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
N501Y	trafficking	Lentiviral pseudotyped with the key mutations from COH.20G/677H lineage was tested on ACE2.293T cells. Luciferase activity was measured two days postinfection, showing no significant change in infection rate amongst the cells, suggesting that this mutation does not contributing to cell entry fitness.	BQ.1.1.22, BA.5.5.2, XBF, BL.1, BE.9, BA.5.2.6	Tada et al. (2021)	404	A	T	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
N501Y	vaccine neutralization efficacy	Observed 1.3-fold reduction in neutralization efficiency of Pfizer vaccinee sera (collected 14 days after second dose) against pseudotype B.1.1.7 key variant lentivirus. Compare to 2.6-fold reduction against cultured B.1.1.7 virus.	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BU.2, BA.5.2.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, CA.5, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.2.76, BA.5.2.6, BT.1, XAE, BG.2, BA.1.18, BF.25,	Bates et al. (2021)	200193	A	T,TAC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
N501Y	vaccine neutralization efficacy	1.2x drop in neutralization using sera collected from 14 healthy adult participants that received two injections of the mRNA-1273 (Moderna) vaccine at a dose of 100 µg (18-55 years: day 1 and day 14 post-2nd dose) against a recombinant single variant virus (modified replicating WA-1 cDNA clone) relative to contemporary circulating D614G variant (USA/GA-EHC-083E/2020) using a live-virus Focus Reduction Neutralization Test (FRNT) assay.	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BU.2, BA.5.2.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, CA.5, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.2.76, BA.5.2.6, BT.1, XAE, BG.2, BA.1.18, BF.25,	Edara et al. (2021)	200193	A	T,TAC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
N501Y	vaccine neutralization efficacy	The presence of this variant in 189 post-mRNA-vaccination COVID-19 cases was proportionally in line with lineage prevalence in Northen California during the study period, suggesting no effect of these variants on immune escape.	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BU.2, BA.5.2.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, CA.5, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.2.76, BA.5.2.6, BT.1, XAE, BG.2, BA.1.18, BF.25,	Jacobson et al. (2021)	200193	A	T,TAC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
N501Y	vaccine neutralization efficacy	The presence of these B.1.417/B.1.429 defining variants in 189 post-mRNA-vaccination COVID-19 cases was proportionally in line with lineage prevalence in Northen California during the study period, suggesting no effect of these variants on immune escape.	BA.5.1.2, BQ.1.1.15, BA.5.2.14, DE.2, BE.4.2, CN.1, BF.5, BF.7.1, BA.5.2.3, BA.2.75, BA.4.4, BA.5.1.9, BA.5.2.23, BQ.1.1.19, BQ.1.1.3, BA.5.2.34, CQ.1.1, BA.4.1.9, BA.5.2.18, BE.1.1.2, BF.12, BR.2.1, BF.26, BA.5.1.21, BA.5.1.16, CG.1, BA.5.1.3, BF.17, BQ.1.16, BA.5.3.3, CE.1, BA.5.2.26, BQ.1.1.14, BQ.1.1.2, BQ.1.8.2, BR.1.2, BA.5.2.28, BT.2, BQ.1.1.5, CR.1.2, BA.5.1.4, BA.4.1.5, BQ.1.1.25, BA.5.1.22, BQ.1.3, BA.5.1.19, BA.4.1.1, BF.7.5, BF.1, BA.4.1.10, BA.5.2.21, BQ.1.1.7, BQ.1.1.6, BQ.1.10.1, BR.1, BQ.1.1.28, CA.1, BF.4, CK.3, BF.7.4.1, CR.2, XBE, BA.2.75.4, BQ.1.1.27, BA.5.2.37, BQ.1.1.23, BQ.1.1, CA.7, BQ.1.12, BA.4.7, BF.19, BA.5.10, BF.31, BF.7.3, BF.7.7, BA.5.1.31, BF.7.8, XAS, BA.5.2.33, CC.1, BQ.1.1.24, BA.5.6.2, BA.5.2.2, BQ.1.6, BU.2, CV.1, CQ.2, BE.4, BA.5.1.25, BQ.1.26, BQ.1.10, BV.2, BE.3, BA.5.2.22, BF.15, BR.3, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BF.29, BQ.1.1.13, BQ.1.23, BA.4.5, BE.4.1, BF.32, BQ.1.2, BA.5.1.24,	Jacobson et al. (2021)	84453	A	T,TAC	0.99

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
N501Y	vaccine neutralization efficacy	This variant showed no change in Pfizer sera (one or two dose) neutralization efficiency vs D614G (using lentivirus pseudotype).	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BA.5.2.2, BU.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.2.76, BA.5.2.6, BT.1, XAE, BG.2, BA.1.1.18, BF.25, BY.1.1.1,	Kuzmina et al. (2021)	200171	A	T,TAC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
N501Y	vaccine neutralization efficacy	This variant showed >5x decrease in Pfizer sera (3 weeks post-first dose: n	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BU.2, BA.5.2.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.64, BA.1.6, BA.2.76, BA.5.2.6, XAE, BT.1, BG.2, BA.1.1.18, BA.2.75, BY.1.1.1,	Kuzmina et al. (2021)	199897	A	T,TAC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
N501Y	vaccine neutralization efficacy	Human sera from 6 two-dose Pfizer vaccinated individuals (47-68 days post 1st-dose) can neutralize both the reference USA-WA1/2020 strain and the mouse adapted SARS-CoV-2 strain that contains the N501Y spike mutation with similar efficiency.	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BU.2, BA.5.2.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, CA.5, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.2.76, BA.5.2.6, BT.1, XAE, BG.2, BA.1.18, BF.25,	Rathnasinghe et al. (2021)	200193	A	T,TAC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
N501Y	vaccine neutralization efficacy	In a cohort of 20 patients 8+ weeks after second vaccine dose of Moderna (mRNA-1273) or Pfizer-BioNTech (BNT162b2) vaccines, a modest decrease in neutralization by vaccine plasma was observed.	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BU.2, BA.5.2.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, CA.5, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.2.76, BA.5.2.6, BT.1, XAE, BG.2, BA.1.18, BF.25,	Wang et al. (2021)	200193	A	T,TAC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
N501Y	vaccinee plasma binding	1.17x increase in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in previously non-seroconverted subjects. 1.09x increase in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in post-infection vaccinees.	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BA.5.2.2, BU.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.2.76, BA.5.2.6, BT.1, XAE, BG.2, BA.1.1.18, BA.2.75, BY.1.1.1,	Gong et al. (2021)	200171	A	T,TAC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
N501Y	virion structure	Estimated free energy change (ddG) for this variant is 0.69 kcal/mol (i.e. stabilizing relative to wild type)	BA.2.17, BF.7.1, CQ.1.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BU.2, BA.5.2.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BE.4.1.1, BA.1.15, BF.3.1, BA.2.54, BA.5.7, CA.5, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.2.76, BA.5.2.6, BT.1, XAE, BG.2, BA.1.18, BF.25,	Spratt et al. (2021)	200193	A	T,TAC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
N501Y	ACE2 receptor binding affinity	The N501Y mutation had the biggest effect on ACE2 affinity of any VOC mutation tested, increasing the affinity extasciitilde10 fold to KD extasciitilde7 nM, by increasing the k(on) extasciitilde1.8 fold and decreasing the k(off) by extasciitilde 7 fold as measured by surface plasmon resonance.	BA.5	Barton et al. (2021)	578	AAT	TAT	0.99
N501Y	ACE2 receptor binding affinity	This combination showed extasciitilde3x increase binding to ACE2 vs wild type, about half that of the B.1.1.7 lineage, suggesting that the K417N mutation is slightly detrimental to ACE2 binding, probably as a result of disrupting the salt bridge formed with ACE2 residue D30	BA.5	Collier et al. (2021)	578	AAT	TAT	0.99
N501Y	ACE2 receptor binding affinity	The most frequent RBM mutation N501Y (165,519 instances) makes defective the atypical N-glycosylation sequon NGV 501-503, becoming a key RBM position for the interaction with hACE2-binding hotspot 353.	BA.5	Gamez et al. (2021)	578	AAT	TAT	0.99
N501Y	ACE2 receptor binding affinity	Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant showed a 2.52x increase in binding (KD) relative to D614G, mostly due to decreased in "off-rate" a.k.a. dissociation rate (Kdis). Compare to full Spike variant complements for major lineages containing this variant subset: 5.43x (B.1.1.7 aka Alpha), 3.56x (B.1.351 aka Beta), 4.24x (P.1 aka Gamma).	BA.5	Gong et al. (2021)	578	AAT	TAT	0.99
N501Y	ACE2 receptor binding affinity	RBD containing the N501Y mutation results in 9-fold stronger binding to the hACE2 receptor than wild type RBD. The E484K mutation does not significantly influence the affinity for the receptor, while K417N attenuates affinity. As a result, RBD from B.1.351 containing all three mutations binds 3-fold stronger to hACE2 than wild type RBD but 3-fold weaker than N501Y.	BA.5	Laffeber et al. (2021)	578	AAT	TAT	0.99
N501Y	ACE2 receptor binding affinity	Reported 10-fold increase in ACE2 binding vs wild-type (Kd	BA.5	Liu et al. (2021)	578	AAT	TAT	0.99
N501Y	ACE2 receptor binding affinity	Studying the key covariants in lineage of concern 501Y.V2, observed about 2-fold increase in ACE2 binding vs wildtype, but greatly decreased mAb binding, suggesting evolutionary optimum tension between immune evasion and ACE2 binding affinity as the N501Y variant alone has 10x increase in affinity but no effect on tested mAb binding.	BA.5	Liu et al. (2021)	578	AAT	TAT	0.99
N501Y	ACE2 receptor binding affinity	extasciitilde4-fold increase in binding affinity vs wild type.	BA.5	Motozono et al. (2021)	578	AAT	TAT	0.99

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
N501Y	ACE2 receptor binding affinity	Using Microscale Thermopheresis, this variant binds ACE2 at nearly two-fold greater affinity than the original SARS-COV-2 RBD (203.7 nM vs 402.5 nM).	BA.5	Ramanathan et al. (2021)	578	AAT	TAT	0.99
N501Y	ACE2 receptor binding affinity	Using Mircoscale Thermopheresis, the B.1.351 variant harboring three mutations, binds ACE2 at nearly five-fold greater affinity than the original SARS-COV-2 RBD (Kd 87.6, vs 402.5 nM).	BA.5	Ramanathan et al. (2021)	578	AAT	TAT	0.99
N501Y	ACE2 receptor binding affinity	In silico methods (PyMOL and PDBePISA) involving mutagenesis (N501Y mutation) and interface analysis focusing on the Spike RDB-ACE2 interaction showed that the SARS-CoV-2 N501Y mutant (lineage B.1.1.7) establishes a more significant number of interactions relating to the mutant residue Y501 (Spike RDB) with residues Y41 and K353 (ACE2). This finding shows that the increased infectivity of SARS-CoV-2 lineage B.1.1.7 is associated with the interaction force between the Spike RBD Y501 mutant residue with the ACE2 receptor, which in this strain is increased.	BA.5	Santos and Passos (2021)	578	AAT	TAT	0.99
N501Y	ACE2 receptor binding affinity	Experimentally, ACE2 binding affinity increased 0.24 fold	BA.5	Starr et al. (2020)	578	AAT	TAT	0.99
N501Y	ACE2 receptor binding affinity	This single mutation causes major increase in binding affinity vs. wild type as measured by IC50 vs pseudotyped lentivirus, but combined with the complete set of B.1.1.7 lineage variants no major change vs wild type affnity is observed.	BA.5	Tada et al. (2021)	578	AAT	TAT	0.99
N501Y	ACE2 receptor binding affinity	Reported 4-fold increase in affinity compared to wild-type RBD on the cell surface (Kd	BA.5	Tian et al. (2021)	578	AAT	TAT	0.99
N501Y	ACE2 receptor binding affinity	Reported slight increase in affinity compared to wild-type RBD on the cell surface (Kd	BA.5	Tian et al. (2021)	578	AAT	TAT	0.99
N501Y	ACE2 receptor binding affinity	The affinity of ACE2 for this mutation combination was twice as high as for wild type. Having in mind that the affinity of SARS-CoV-2 for ACE2 is only 4-fold higher compared to SARS-CoV-1, this factor of 2 is expected to be biologically significant.	BA.5	Vogel et al. (2021)	578	AAT	TAT	0.99
N501Y	ACE2 receptor binding affinity	Among the first selected and fixed variants in an in vitro evolution experiment for ACE2 binding. Calculated disassociation constant for this variant is nearly four fold lower than wild type (Kd	BA.5	Zahradnik et al. (2021)	578	AAT	TAT	0.99
N501Y	ACE2 receptor binding affinity	N501Y residue inserts into a cavity at the binding interface near Y41 of ACE2. The additional interactions result in increased affinity of ACE2 for the N501Y mutant, accounting for its increased infectivity.	BA.5	Zhu et al. (2021)	578	AAT	TAT	0.99

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
N501Y	T cell evasion	Vaccinated, but not post-infection sera, show decreased average T cell response to an N501Y peptide. When we primed transgenic mice expressing human HLA-DRB1*0401 with the Wuhan Hu-1 peptide pool, T cell responses to the B.1.1.7 variant peptide pool were significantly reduced (p	BA.5	Reynolds et al. (2021)	578	AAT	TAT	0.99
N501Y	antibody epitope effects	Ablates Class 3 N-terminal domain targeting antibody COV2-2489, diminishes COV2-2676.	BA.5	Chen et al. (2021)	578	AAT	TAT	0.99
N501Y	antibody epitope effects	Of 50 mAbs tested, major loss of neutralization observed for S2X128, S2D8, S2X192, S2D19, S2H14, S2H19.	BA.5	Collier et al. (2021)	578	AAT	TAT	0.99
N501Y	antibody epitope effects	Wildtype elicits immune response, COVID-19 cohort epitope score > 99th percentile of the 497 pre-pandemic controls, mutant drops PIWAS epitope score from 3% to 1.2% (poorer immune recognition) Together with other B1.1.7 lineage mutational changes (Spike: Y144del, A570D, P681H, Nucleoprotein: D3L, S235F) resulted in only 2 or 579 individuals (0.3% of the population) having a dramatic reduction in PIWAS antigen scores, which reflects the peak epitope signal along the entire antigen.	BA.5	Haynes et al. (2021)	578	AAT	TAT	0.99
N501Y	antibody epitope effects	Contrary to other reports on N501Y containing lineages (i.e. with additional mutations), N501Y alone may have an even greater affinity for a human monoclonal antibody specific for wild type. These results suggest that the individual N501Y mutation does not contribute to altered viral properties by itself, but may contribute to a collective conformational shift produced by multiple mutations.	BA.5	Klegerman et al. (2021)	578	AAT	TAT	0.99
N501Y	antibody epitope effects	Lowered the neutralization potency of mAb COVA1-12 to the limit of the assay. Decrease in potency was observed against the N501Y pseudotype for the cluster IX mAb COVA2-17.	BA.5	Rees-Spear et al. (2021)	578	AAT	TAT	0.99
N501Y	antibody epitope effects	Reduction in neutralization by mAbs COVA1-18 (extasciitilde4x), COVA2-15 (extasciitilde9x), S309 (extasciitilde3x)	BA.5	Shen et al. (2021)	578	AAT	TAT	0.99
N501Y	antibody epitope effects	4 antibodies tested were less potent against K417N by ten-fold or more, in both mAb classes 1 and 3	BA.5	Wang et al. (2021)	578	AAT	TAT	0.99
N501Y	convalescent plasma binding	1.65x increase in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset.	BA.5	Gong et al. (2021)	578	AAT	TAT	0.99

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
N501Y	convalescent plasma escape	The 501Y.V2 to first wave IC50 ratio ranged from 6 to 200-fold. Averaging across all 7 participant convalescent sera highlighted the dramatic decrease in sensitivity to neutralization of authentic 501Y.V2 variants. PG: I'm purposefully ignoring D614G and A701V as contributors	BA.5	Cele et al. (2021)	578	AAT	TAT	0.99
N501Y	convalescent plasma escape	0.7x reduction in neutralization by key variant in several variants of concern in sera collected from cohort of 10 with severe disease 21 to 63 days post-onset.	BA.5	Kuzmina et al. (2021)	578	AAT	TAT	0.99
N501Y	convalescent plasma escape	In 30 samples collected 111 to 260 days post onset of symptoms, the covalescent plasma can neutralize both the reference USA-WA1/2020 strain and the mouse adapted strain that contains the N501Y spike mutation with similar efficiency.	BA.5	Rathnasinghe et al. (2021)	578	AAT	TAT	0.99
N501Y	convalescent plasma escape	Neutralization activity of convalescent sera tested decreased extasciitilde2x with this B.1.1.7 pseudotyped virus.	BA.5	Shen et al. (2021)	578	AAT	TAT	0.99
N501Y	convalescent plasma escape	Viruses containing the point mutations of B.1.1.7 showed that the single point mutations (Δ69-70 and N501Y) were neutralized as efficiently as D614G across 10 convalescent sera from April 2020 infectees.	BA.5	Tada et al. (2021)	578	AAT	TAT	0.99
N501Y	convalescent plasma escape	As measured by surface plasmon resonance, RBD with the N501Y mutation alone showed a mean 2.1x decrease in binding affinity for six batches of hyperimmune immunoglobulin (hCoV-2IG) preparations generated from SARS-CoV-2 convalescent plasma.	BA.5	Tang et al. (2021)	578	AAT	TAT	0.99
N501Y	convalescent plasma escape	27% of 44 early pandemic exposure convalescent plasma/sera lose all activity against a RBD triple mutant pseudovirus (RBD mutatants of the 501Y.V2 "South African" lineage), while only 23% retained high titres	BA.5	Wibmer et al. (2021)	578	AAT	TAT	0.99
N501Y	convalescent plasma escape	Nearly half (21 of 44, 48%) of early pandemic exposure convalescent plasma/sera failed to neutralize the 501Y.V2 ("South African") lineage pseudovirus construct Only 3 of 44 convascent sera (those with the highest titer, which correlated direectly with initial infection severity) had high neutralization against this 501Y.V2 PG: note that lineage variant R246I was excluded from the text in reference to these sera assays, not sure if that was an oversight.	BA.5	Wibmer et al. (2021)	578	AAT	TAT	0.99
N501Y	environmental condition stability	Relative to D614G, this mutation demonstrated significant increase in infectivity (i.e. heat stability) after incubation at 50C after 30 minutes or 1 hour	BA.5	Tada et al. (2021)	578	AAT	TAT	0.99

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
N501Y	homoplasy	Variant within the six key residues in the receptor binding domain (RBD). Independently reported in UK, Australia (same origin as UK), and South Africa (independent origin).	BA.5	Flores-Alanis et al. (2021)	578	AAT	TAT	0.99
N501Y	immunosuppression variant emergence	Appeared (day 128) and persisted in chronic (152 day) SARS-CoV-2 infection of immunocompromised patient with severe antiphospholipid syndrome	BA.5	Choi et al. (2020)	578	AAT	TAT	0.99
N501Y	monoclonal antibody serial passage escape	In vitro selection against class 1 (Spike 'up' conformation) monoclonal antibody C663, and to a lesser extent C613.	BA.5	Wang et al. (2021)	578	AAT	TAT	0.99
N501Y	pharmaceutical effectiveness	COR-101 lost extasciitilde8x binding against this isolated mutation. Regdanvimab lost extasciitilde6x binding against this isolated mutation.	BA.5	Engelhart et al. (2021)	578	AAT	TAT	0.99
N501Y	pharmaceutical effectiveness	Tixagevimab, Regdanvimab and COR-101 display reduced binding affinity to virus pseudotyped as RBD from B.1.351.	BA.5	Engelhart et al. (2021)	578	AAT	TAT	0.99
N501Y	pharmaceutical effectiveness	COR-101 lost extasciitilde20x binding against this double mutation. Estesevimab lost extasciitilde16x binding against this double mutation. Regdanvimab lost extasciitilde6x binding against this double mutation. M396 lost extasciitilde10x binding against this double mutation.	BA.5	Engelhart et al. (2021)	578	AAT	TAT	0.99
N501Y	pharmaceutical effectiveness	This mutated version of RBD completely abolishes the binding to a therapeutic antibody, Bamlanivimab, in vitro.	BA.5	Liu et al. (2021)	578	AAT	TAT	0.99
N501Y	syncytium formation	Slight increase in Vero cell-cell membrane fusion assay under infection with VSV pseudotyped virus relative to wild type, no change relative to D614G.	BA.5	Kim et al. (2021)	578	AAT	TAT	0.99
N501Y	trafficking	More efficient infectivity (24h) compared to wild type, in Caco-2 cells extasciitilde9x, Vero extasciitilde8x, and Calu-3 extasciitilde8x. Compare to wild type at extasciitilde5x across cell types.	BA.5	Kim et al. (2021)	578	AAT	TAT	0.99
N501Y	trafficking	extasciitilde4x more efficient S2 domain cleavage compared to wild type, no change relative to D614G alone in Caco-2 cells, mid-range of three cell line tested (Vero and Calu-3).	BA.5	Kim et al. (2021)	578	AAT	TAT	0.99
N501Y	trafficking	9x more infectivity than D614G alone in HEK293T-ACE2 cells 48h post-transduction.	BA.5	Kuzmina et al. (2021)	1156	AAT	TAT	0.99
N501Y	trafficking	extasciitilde9x more infectivity than D614G alone in HEK293T-ACE2 cells 48h post-transduction (no synergy as level approx. that of N501Y alone).	BA.5	Kuzmina et al. (2021)	578	AAT	TAT	0.99
N501Y	trafficking	Decreased stability of RBD expression in yeast, suggesting decreased Spike protein stability.	BA.5	Motozono et al. (2021)	578	AAT	TAT	0.99

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
N501Y	trafficking	Lentiviral pseudotyped with this individual mutation from B.1.1.7 was tested on ACE2.293T cells. Luciferase activity was measured two days postinfection, showing slightly increased infection rate amongst the cells. [in what is essentially a replicate experiment in the same paper, because each B.1.351 lineage variant was indepedetly evaluated and N501 is in both lineages, a significant decrease was observed, therefore the error bars described in this paper should be interpreted carefully]	BA.5	Tada et al. (2021)	578	AAT	TAT	0.99
N501Y	vaccine neutralization efficacy	Observed 1.3-fold reduction in neutralization efficiency of Pfizer vaccinee sera (collected 14 days after second dose) against pseudotype B.1.1.7 key variant lentivirus. Compare to 2.6-fold reduction against cultured B.1.1.7 virus.	BA.5	Bates et al. (2021)	578	AAT	TAT	0.99
N501Y	vaccine neutralization efficacy	1.2x drop in neutralization using sera collected from 14 healthy adult participants that received two injections of the mRNA-1273 (Moderna) vaccine at a dose of 100 µg (18-55 years: day 1 and day 14 post-2nd dose) against a recombinant single variant virus (modified replicating WA-1 cDNA clone) relative to contemporary circulating D614G variant (USA/GA-EHC-083E/2020) using a live-virus Focus Reduction Neutralization Test (FRNT) assay.	BA.5	Edara et al. (2021)	578	AAT	TAT	0.99
N501Y	vaccine neutralization efficacy	The presence of this variant in 189 post-mRNA-vaccination COVID-19 cases was proportionally in line with lineage prevalence in Northen California during the study period, suggesting no effect of these variants on immune escape.	BA.5	Jacobson et al. (2021)	578	AAT	TAT	0.99
N501Y	vaccine neutralization efficacy	The presence of these B.1.417/B.1.429 defining variants in 189 post-mRNA-vaccination COVID-19 cases was proportionally in line with lineage prevalence in Northen California during the study period, suggesting no effect of these variants on immune escape.	BA.5	Jacobson et al. (2021)	578	AAT	TAT	0.99
N501Y	vaccine neutralization efficacy	This variant showed no change in Pfizer sera (one or two dose) neutralization efficiency vs D614G (using lentivirus pseudotype).	BA.5	Kuzmina et al. (2021)	578	AAT	TAT	0.99
N501Y	vaccine neutralization efficacy	This variant showed >5x decrease in Pfizer sera (3 weeks post-first dose: n	BA.5	Kuzmina et al. (2021)	578	AAT	TAT	0.99

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
N501Y	vaccine neutralization efficacy	Human sera from 6 two-dose Pfizer vaccinated individuals (47-68 days post 1st-dose) can neutralize both the reference USA-WA1/2020 strain and the mouse adapted SARS-CoV-2 strain that contains the N501Y spike mutation with similar efficiency.	BA.5	Rathnasinghe et al. (2021)	578	AAT	TAT	0.99
N501Y	vaccine neutralization efficacy	In a cohort of 20 patients 8+ weeks after second vaccine dose of Moderna (mRNA-1273) or Pfizer-BioNTech (BNT162b2) vaccines, a modest decrease in neutralization by vaccine plasma was observed.	BA.5	Wang et al. (2021)	578	AAT	TAT	0.99
N501Y	vaccinee plasma binding	1.17x increase in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in previously non-seroconverted subjects. 1.09x increase in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in post-infection vaccinees.	BA.5	Gong et al. (2021)	578	AAT	TAT	0.99
N501Y	virion structure	Estimated free energy change (ddG) for this variant is 0.69 kcal/mol (i.e. stabilizing relative to wild type)	BA.5	Spratt et al. (2021)	578	AAT	TAT	0.99

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
N460K	ACE2 receptor binding affinity	Experimentally, ACE2 binding affinity increased 0.09 fold	BQ.1.1.15, BQ.1.1.17, BQ.1.8, BA.5.2.14, BQ.1.5, BQ.1.26, BQ.1.1.19, BQ.1.1.3, BV.2, BQ.1, BQ.1.10, BQ.1.22, BQ.1.13, BQ.1.1.22, BQ.1.1.11, BQ.1.1.13, BQ.1.15, BQ.1.16, BQ.1.23, BQ.1.20, BQ.1.7, BQ.1.1.14, BQ.1.1.2, BQ.1.1.10, BQ.1.2, BQ.1.8.2, BQ.1.1.5, BQ.1.19, BQ.1.1.25, BQ.1.18, BQ.1.3, CL.1, BQ.1.10.1, BQ.1.1.7, BQ.1.1.6, BQ.1.1.28, BQ.1.1.4, BQ.1.1.18, BE.1.1.1, BQ.1.1.1, BQ.1.4, CK.3, BQ.1.11, BQ.1.14, BA.5.2.24, BQ.1.25, BQ.1.24, BQ.1.1.27, BQ.1.1.20, BQ.1.1.8, BQ.1.1.9, BQ.1.12, BQ.1.1, BQ.1.9, BQ.1.1.23, BQ.1.1.24, BQ.1.1.26, BQ.1.6, BE.9	Starr et al. (2020)	22080	T	A,AA,ACTG,AGTT	0.98

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
N460K	ACE2 receptor binding affinity	Selected with increasing proportion during in vitro evolution of Spike against ACE2 receptor	BQ.1.1.15, BQ.1.1.17, BQ.1.8, BA.5.2.14, BQ.1.5, BQ.1.26, BQ.1.1.19, BQ.1.1.3, BV.2, BQ.1, BQ.1.10, BQ.1.22, BQ.1.13, BQ.1.1.22, BQ.1.1.11, BQ.1.1.13, BQ.1.15, BQ.1.16, BQ.1.23, BQ.1.20, BQ.1.7, BQ.1.1.14, BQ.1.1.2, BQ.1.1.10, BQ.1.2, BQ.1.8.2, BQ.1.1.5, BQ.1.19, BQ.1.1.25, BQ.1.18, BQ.1.3, CL.1, BQ.1.10.1, BQ.1.1.7, BQ.1.1.6, BQ.1.1.28, BQ.1.1.4, BQ.1.1.18, BE.1.1.1, BQ.1.1.1, BQ.1.4, CK.3, BQ.1.11, BQ.1.14, BA.5.2.24, BQ.1.25, BQ.1.24, BQ.1.1.27, BQ.1.1.20, BQ.1.1.8, BQ.1.1.9, BQ.1.12, BQ.1.1, BQ.1.9, BQ.1.1.23, BQ.1.1.24, BQ.1.1.26, BQ.1.6, BE.9	Zahradnik et al. (2021)	22080	T	A,AA,ACTG,AGTT	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
N460K	gene expression increase	Experimentally, Spike gene expression increased 0.16 fold	BQ.1.1.15, BQ.1.1.17, BQ.1.8, BA.5.2.14, BQ.1.5, BQ.1.26, BQ.1.1.19, BQ.1.1.3, BV.2, BQ.1, BQ.1.10, BQ.1.22, BQ.1.13, BQ.1.1.22, BQ.1.1.11, BQ.1.1.13, BQ.1.15, BQ.1.16, BQ.1.23, BQ.1.20, BQ.1.7, BQ.1.1.14, BQ.1.1.2, BQ.1.1.10, BQ.1.2, BQ.1.8.2, BQ.1.1.5, BQ.1.19, BQ.1.1.25, BQ.1.18, BQ.1.3, CL.1, BQ.1.10.1, BQ.1.1.7, BQ.1.1.6, BQ.1.1.28, BQ.1.1.4, BQ.1.1.18, BE.1.1.1, BQ.1.1.1, BQ.1.4, CK.3, BQ.1.11, BQ.1.14, BA.5.2.24, BQ.1.25, BQ.1.24, BQ.1.1.27, BQ.1.1.20, BQ.1.1.8, BQ.1.1.9, BQ.1.12, BQ.1.1, BQ.1.9, BQ.1.1.23, BQ.1.1.24, BQ.1.1.26, BQ.1.6, BE.9	Starr et al. (2020)	22080	T	A,AA,ACTG,AGT	0.98

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
N460K	monoclonal antibody serial passage escape	Escape mutation against monoclonal antibody LY-CoV016	BQ.1.1.15, BQ.1.1.17, BQ.1.8, BA.5.2.14, BQ.1.5, BQ.1.26, BQ.1.1.19, BQ.1.1.3, BV.2, BQ.1, BQ.1.10, BQ.1.22, BQ.1.13, BQ.1.1.22, BQ.1.1.11, BQ.1.1.13, BQ.1.15, BQ.1.16, BQ.1.23, BQ.1.20, BQ.1.7, BQ.1.1.14, BQ.1.1.2, BQ.1.1.10, BQ.1.2, BQ.1.8.2, BQ.1.1.5, BQ.1.19, BQ.1.1.25, BQ.1.18, BQ.1.3, CL.1, BQ.1.10.1, BQ.1.1.7, BQ.1.1.6, BQ.1.1.28, BQ.1.1.4, BQ.1.1.18, BE.1.1.1, BQ.1.1.1, BQ.1.4, CK.3, BQ.1.11, BQ.1.14, BA.5.2.24, BQ.1.25, BQ.1.24, BQ.1.1.27, BQ.1.1.20, BQ.1.1.8, BQ.1.1.9, BQ.1.12, BQ.1.1, BQ.1.9, BQ.1.1.23, BQ.1.1.24, BQ.1.1.26, BQ.1.6, BE.9	Starr et al. (2021)	22080	T	A,AA,ACTG,AGTT	0.998

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
N460K	ACE2 receptor binding affinity	Experimentally, ACE2 binding affinity increased 0.09 fold	BN.6, XBB.4, BE.4.2, XBB.1.5, BA.2.75, XBB.1.3, BL.5, BN.1.3, BR.2.1, CH.1, BN.5, BM.1.1, BR.1.2, BA.2.75.1, BY.1, BR.1, CA.1, CM.9, XBD, XBH, BA.2.75.4, CA.7, BL.1.3, CV.1, BN.1.1.1, CK.2.1.1, BM.1.1.3, BN.2, BA.2.75.3, CA.5, BA.5.3.1, BA.4.6.3, XBB.1.4, CK.2.1, CA.3.1, CM.4, BA.2.75.5, BL.1, BA.5.2.36, CB.1, BS.1.1, BN.1.9, XBB.1, CM.5, BN.1.5, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, CK.2, BY.1.2, BW.1, BA.2.10.1, BN.1.7, BN.2.1, BL.2, CM.8.1, CH.1.1.1, XBB.3, BN.1, XBB.2, CM.1, BN.1.4, BE.1.1.1, BR.4, CH.1.1, BA.2.75.10, BW.1.1, CM.3, CK.1, BA.5.9, CH.1.1.2, BA.2.75.7, BM.2.1, BY.1.1.1, DB.1, CJ.1, BN.3.1, BM.4.1.1, DG.1, BN.1.3.1, BM.4.1, BU.1, BA.2.3.20, BM.2, BA.2.75.9, CM.2, BN.1.1, BL.4, XBF, BF.11.1, BN.1.2, BA.2.75.2, XBB, BM.1.1.1, XBB.1.1, BA.5.2.16, CM.8, BA.2.75.6, BR.3	Starr et al. (2020)	6536	T	G,GCTT	0.52

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
N460K	ACE2 receptor binding affinity	Selected with increasing proportion during in vitro evolution of Spike against ACE2 receptor	BN.6, XBB.4, BE.4.2, XBB.1.5, BA.2.75, XBB.1.3, BL.5, BN.1.3, BR.2.1, CH.1, BN.5, BM.1.1, BR.1.2, BA.2.75.1, BY.1, BR.1, CA.1, CM.9, XBD, XBH, BA.2.75.4, CA.7, BL.1.3, CV.1, BN.1.1.1, CK.2.1.1, BM.1.1.3, BN.2, BA.2.75.3, CA.5, BA.5.3.1, BA.4.6.3, XBB.1.4, CK.2.1, CA.3.1, CM.4, BA.2.75.5, BL.1, BA.5.2.36, CB.1, BS.1.1, BN.1.9, XBB.1, CM.5, BN.1.5, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, CK.2, BY.1.2, BW.1, BA.2.10.1, BN.1.7, BN.2.1, BL.2, CM.8.1, CH.1.1.1, XBB.3, BN.1, XBB.2, CM.1, BN.1.4, BE.1.1.1, BR.4, CH.1.1, BA.2.75.10, BW.1.1, CM.3, CK.1, BA.5.9, CH.1.1.2, BA.2.75.7, BM.2.1, BY.1.1.1, DB.1, CJ.1, BN.3.1, BM.4.1.1, DG.1, BN.1.3.1, BM.4.1, BU.1, BA.2.3.20, BM.2, BA.2.75.9, CM.2, BN.1.1, BL.4, XBF, BF.11.1, BN.1.2, BA.2.75.2, XBB, BM.1.1.1, XBB.1.1, BA.5.2.16, CM.8, BA.2.75.6, BR.3	Zahradnik et al. (2021)	6536	T	G,GCTT	0.52

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
N460K	gene expression increase	Experimentally, Spike gene expression increased 0.16 fold	BN.6, XBB.4, BE.4.2, XBB.1.5, BA.2.75, XBB.1.3, BL.5, BN.1.3, BR.2.1, CH.1, BN.5, BM.1.1, BR.1.2, BA.2.75.1, BY.1, BR.1, CA.1, CM.9, XBD, XBH, BA.2.75.4, CA.7, BL.1.3, CV.1, BN.1.1.1, CK.2.1.1, BM.1.1.3, BN.2, BA.2.75.3, CA.5, BA.5.3.1, BA.4.6.3, XBB.1.4, CK.2.1, CA.3.1, CM.4, BA.2.75.5, BL.1, BA.5.2.36, CB.1, BS.1.1, BN.1.9, XBB.1, CM.5, BN.1.5, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, CK.2, BY.1.2, BW.1, BA.2.10.1, BN.1.7, BN.2.1, BL.2, CM.8.1, CH.1.1.1, XBB.3, BN.1, XBB.2, CM.1, BN.1.4, BE.1.1.1, BR.4, CH.1.1, BA.2.75.10, BW.1.1, CM.3, CK.1, BA.5.9, CH.1.1.2, BA.2.75.7, BM.2.1, BY.1.1.1, DB.1, CJ.1, BN.3.1, BM.4.1.1, DG.1, BN.1.3.1, BM.4.1, BU.1, BA.2.3.20, BM.2, BA.2.75.9, CM.2, BN.1.1, BL.4, XBF, BF.11.1, BN.1.2, BA.2.75.2, XBB, BM.1.1.1, XBB.1.1, BA.5.2.16, CM.8, BA.2.75.6, BR.3	Starr et al. (2020)	6536	T	G,GCTT	0.52

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
N460K	monoclonal antibody serial passage escape	Escape mutation against monoclonal antibody LY-CoV016	BN.6, XBB.4, BE.4.2, XBB.1.5, BA.2.75, XBB.1.3, BL.5, BN.1.3, BR.2.1, CH.1, BN.5, BM.1.1, BR.1.2, BA.2.75.1, BY.1, BR.1, CA.1, CM.9, XBD, XBH, BA.2.75.4, CA.7, BL.1.3, CV.1, BN.1.1.1, CK.2.1.1, BM.1.1.3, BN.2, BA.2.75.3, CA.5, BA.5.3.1, BA.4.6.3, XBB.1.4, CK.2.1, CA.3.1, CM.4, BA.2.75.5, BL.1, BA.5.2.36, CB.1, BS.1.1, BN.1.9, XBB.1, CM.5, BN.1.5, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, CK.2, BY.1.2, BW.1, BA.2.10.1, BN.1.7, BN.2.1, BL.2, CM.8.1, CH.1.1.1, XBB.3, BN.1, XBB.2, CM.1, BN.1.4, BE.1.1.1, BR.4, CH.1.1, BA.2.75.10, BW.1.1, CM.3, CK.1, BA.5.9, CH.1.1.2, BA.2.75.7, BM.2.1, BY.1.1.1, DB.1, CJ.1, BN.3.1, BM.4.1.1, DG.1, BN.1.3.1, BM.4.1, BU.1, BA.2.3.20, BM.2, BA.2.75.9, CM.2, BN.1.1, BL.4, XBF, BF.11.1, BN.1.2, BA.2.75.2, XBB, BM.1.1.1, XBB.1.1, BA.5.2.16, CM.8, BA.2.75.6, BR.3	Starr et al. (2021)	6536	T	G,GCTT	0.52
N460K	ACE2 receptor binding affinity	Experimentally, ACE2 binding affinity increased 0.09 fold	BQ.1.10	Starr et al. (2020)	238	TCTC	ACTC	0.99
N460K	ACE2 receptor binding affinity	Selected with increasing proportion during in vitro evolution of Spike against ACE2 receptor	BQ.1.10	Zahradnik et al. (2021)	238	TCTC	ACTC	0.99
N460K	gene expression increase	Experimentally, Spike gene expression increased 0.16 fold	BQ.1.10	Starr et al. (2020)	238	TCTC	ACTC	0.99

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
N460K	monoclonal antibody serial passage escape	Escape mutation against monoclonal antibody LY-CoV016	BQ.1.10	Starr et al. (2021)	238	TCTC	ACTC	0.99
N460K	ACE2 receptor binding affinity	Experimentally, ACE2 binding affinity increased 0.09 fold	BQ.1.18	Starr et al. (2020)	7	TCTC	ACTC	0.86
N460K	ACE2 receptor binding affinity	Selected with increasing proportion during in vitro evolution of Spike against ACE2 receptor	BQ.1.18	Zahradnik et al. (2021)	7	TCTC	ACTC	0.86
N460K	gene expression increase	Experimentally, Spike gene expression increased 0.16 fold	BQ.1.18	Starr et al. (2020)	7	TCTC	ACTC	0.86
N460K	monoclonal antibody serial passage escape	Escape mutation against monoclonal antibody LY-CoV016	BQ.1.18	Starr et al. (2021)	7	TCTC	ACTC	0.86
N460K	ACE2 receptor binding affinity	Experimentally, ACE2 binding affinity increased 0.09 fold	XBB.1.5, BR.2.1	Starr et al. (2020)	2652	TCTC	GCTC	0.99
N460K	ACE2 receptor binding affinity	Selected with increasing proportion during in vitro evolution of Spike against ACE2 receptor	XBB.1.5, BR.2.1	Zahradnik et al. (2021)	2652	TCTC	GCTC	0.99
N460K	gene expression increase	Experimentally, Spike gene expression increased 0.16 fold	XBB.1.5, BR.2.1	Starr et al. (2020)	2652	TCTC	GCTC	0.99
N460K	monoclonal antibody serial passage escape	Escape mutation against monoclonal antibody LY-CoV016	XBB.1.5, BR.2.1	Starr et al. (2021)	2652	TCTC	GCTC	0.99
G446D	antibody epitope effects	Mutant screen in neutralization assay with a broad range of monoclonal antibodies shows resistence to more than one antibody.	CD.1	Liu et al. (2021)	1	G	A	1.0
G446D	convalescent plasma escape	Decrease in neutralization capability of all 4 convalescent sera tested (1 ablated).	CD.1	Liu et al. (2021)	1	G	A	1.0
G446D	monoclonal antibody serial passage escape	Ranked effective mutant against this position in the RBD for highly neutralizing COV2-2499 monoclonal antibody	CD.1	Greaney et al. (2020)	1	G	A	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
G142D	monoclonal antibody serial passage escape	Escape mutation against Spike N terminal domain antigenic supersite i mAbs S2M28, S2X28, S2X333	BA.2.17, BF.7.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.2.75.1, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, CR.2, BA.5.2.37, CA.7, BF.19, BA.2.61, CC.1, CV.1, BA.5.6.2, BU.2, BA.5.2.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, BA.5.1.6, XAN, BE.4.1.1, BF.3.1, BA.2.54, BA.5.7, CA.5, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, BQ.1.1.4, BR.4, CH.1.1, BA.5.1.23, BF.7.12, BF.16, BA.5.2.6, BA.2.64, BA.2.76, BA.2.38.2, XAE, BT.1, BG.2, BF.25, BY.1.1.1, BA.5.1, BF.20, BA.5.1.5, CJ.1, BA.5.1.10, BA.2.66, BA.5.10.1, BA.5.5, BQ.1.15, BM.4.1, BA.2.9.5, BA.5, BA.4.6, BF.7.4.2, XAZ, CM.2, BA.5.2.20, BA.2.3.9, XBF, BQ.1.4, BA.2.75.2, BA.5.2, BF.9, BE.1, DE.1, XN, BA.5.2.16, BE.2, BQ.1.1.23, BA.5.1.27,	McCallum et al. (2021)	131739	GTGTTTATTAC	ATGTTTAC,A,ATGTTTACCA,A	0.52

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
G142D	monoclonal antibody serial passage escape	Selected twice in passage with mAb COV2-2489.	BA.2.17, BF.7.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.2.75.1, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, CR.2, BA.5.2.37, CA.7, BF.19, BA.2.61, CC.1, CV.1, BA.5.6.2, BU.2, BA.5.2.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, BA.5.1.6, XAN, BE.4.1.1, BF.3.1, BA.2.54, BA.5.7, CA.5, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, BQ.1.1.4, BR.4, CH.1.1, BA.5.1.23, BF.7.12, BF.16, BA.5.2.6, BA.2.64, BA.2.76, BA.2.38.2, XAE, BT.1, BG.2, BF.25, BY.1.1.1, BA.5.1, BF.20, BA.5.1.5, CJ.1, BA.5.1.10, BA.2.66, BA.5.10.1, BA.5.5, BQ.1.15, BM.4.1, BA.2.9.5, BA.5, BA.4.6, BF.7.4.2, XAZ, CM.2, BA.5.2.20, BA.2.3.9, XBF, BQ.1.4, BA.2.75.2, BA.5.2, BF.9, BE.1, DE.1, XN, BA.5.2.16, BE.2, BQ.1.1.23, BA.5.1.27,	Suryadevara et al. (2021)	131739	GTGTTTATTAC	ATGTTTAC,A,ATGTTTACCA,A	0.52

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
G142D	monoclonal antibody serial passage escape	Escape mutation against Spike N terminal domain antigenic supersite i mAbs S2M28, S2X28, S2X333	BA.5.3.1, BA.4.6	McCallum et al. (2021)	3390	GTGTTTATTAC	GTGTTTATTAC	1.0
G142D	monoclonal antibody serial passage escape	Selected twice in passage with mAb COV2-2489.	BA.5.3.1, BA.4.6	Suryadevara et al. (2021)	3390	GTGTTTATTAC	GTGTTTATTAC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
F486V	gene expression increase	Experimentally, Spike gene expression increased 0.07 fold	BA.5.1.2, BQ.1.1.15, BA.5.2.14, DE.2, BE.4.2, CN.1, BF.5, BF.7.1, BA.5.2.3, BA.5.2.23, BA.4.4, BA.5.1.9, BQ.1.1.19, BQ.1.1.3, CQ.1.1, BA.5.2.34, BA.4.1.9, BE.1.1.2, BA.5.2.18, BF.26, BA.5.1.21, BA.5.1.16, CG.1, BA.5.1.3, BF.17, BQ.1.16, BA.5.3.3, CE.1, BA.5.2.26, BQ.1.1.14, BQ.1.1.2, BQ.1.8.2, BT.2, BA.5.2.28, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.4.1.5, BQ.1.1.25, BA.5.1.22, BQ.1.3, BA.5.1.19, BA.4.1.1, BF.7.5, BF.1, BA.4.1.10, BA.5.2.21, BQ.1.1.7, BQ.1.1.6, BQ.1.10.1, BQ.1.1.28, BF.4, CK.3, BF.7.4.1, CR.2, XBE, BQ.1.1.27, BA.5.2.37, BQ.1.1, BQ.1.12, BA.4.7, BF.19, BA.5.10, BF.31, BF.7.3, BF.7.7, BA.5.1.31, BF.7.8, XAS, BA.5.2.33, CC.1, BQ.1.1.24, BA.5.6.2, BA.5.2.2, BQ.1.6, BU.2, CQ.2, BE.4, BA.5.1.25, BQ.1.26, BQ.1.10, BV.2, BE.3, BA.5.2.22, BF.15, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BF.29, BQ.1.1.13, BQ.1.23, BA.4.5, BE.4.1.1, BF.32, BQ.1.2, BA.5.1.24, BF.3.1, BA.5.7, BE.6, BA.5.3.1, BA.4.6.3, BE.1.4.1, BA.5.2.25, BA.4.1.8,	Starr et al. (2020)	83167	T	G,GC,CC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
F486V	monoclonal antibody serial passage escape	Escape variant 88% appearance in 2 passages against Regeneron monoclonal antibody RGN10933 @ 50ug/mL	BA.5.1.2, BQ.1.1.15, BA.5.2.14, DE.2, BE.4.2, CN.1, BF.5, BF.7.1, BA.5.2.3, BA.5.2.23, BA.4.4, BA.5.1.9, BQ.1.1.19, BQ.1.1.3, CQ.1.1, BA.5.2.34, BA.4.1.9, BE.1.1.2, BA.5.2.18, BF.26, BA.5.1.21, BA.5.1.16, CG.1, BA.5.1.3, BF.17, BQ.1.16, BA.5.3.3, CE.1, BA.5.2.26, BQ.1.1.14, BQ.1.1.2, BQ.1.8.2, BT.2, BA.5.2.28, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.4.1.5, BQ.1.1.25, BA.5.1.22, BQ.1.3, BA.5.1.19, BA.4.1.1, BF.7.5, BF.1, BA.4.1.10, BA.5.2.21, BQ.1.1.7, BQ.1.1.6, BQ.1.10.1, BQ.1.1.28, BF.4, CK.3, BF.7.4.1, CR.2, XBE, BQ.1.1.27, BA.5.2.37, BQ.1.1, BQ.1.12, BA.4.7, BF.19, BA.5.10, BF.31, BF.7.3, BF.7.7, BA.5.1.31, BF.7.8, XAS, BA.5.2.33, CC.1, BQ.1.1.24, BA.5.6.2, BA.5.2.2, BQ.1.6, BU.2, CQ.2, BE.4, BA.5.1.25, BQ.1.26, BQ.1.10, BV.2, BE.3, BA.5.2.22, BF.15, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BF.29, BQ.1.1.13, BQ.1.23, BA.4.5, BE.4.1.1, BF.32, BQ.1.2, BA.5.1.24, BF.3.1, BA.5.7, BE.6, BA.5.3.1, BA.4.6.3, BE.1.4.1, BA.5.2.25, BA.4.1.8,	Baum et al. (2020)	83167	T	G,GC,CC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
F486V	monoclonal antibody serial passage escape	Ranked modestly effective mutant against this position in the RBD for highly neutralizing COV2-2832 monoclonal antibody	BA.5.1.2, BQ.1.1.15, BA.5.2.14, DE.2, BE.4.2, CN.1, BF.5, BF.7.1, BA.5.2.3, BA.5.2.23, BA.4.4, BA.5.1.9, BQ.1.1.19, BQ.1.1.3, CQ.1.1, BA.5.2.34, BA.4.1.9, BA.5.2.18, BE.1.1.2, BF.26, BA.5.1.21, BA.5.1.16, CG.1, BA.5.1.3, BF.17, BQ.1.16, BA.5.3.3, CE.1, BA.5.2.26, BQ.1.1.14, BQ.1.1.2, BQ.1.8.2, BT.2, BA.5.2.28, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.4.1.5, BQ.1.1.25, BA.5.1.22, BQ.1.3, BA.5.1.19, BA.4.1.1, BF.7.5, BF.1, BA.4.1.10, BA.5.2.21, BQ.1.1.7, BQ.1.1.6, BQ.1.10.1, BQ.1.1.28, BF.4, CK.3, BF.7.4.1, CR.2, XBE, BQ.1.1.27, BA.5.2.37, BQ.1.1.23, BQ.1.1, BQ.1.12, BA.4.7, BF.19, BA.5.10, BF.31, BF.7.3, BF.7.7, BA.5.1.31, BF.7.8, XAS, BA.5.2.33, CC.1, BQ.1.1.24, BA.5.6.2, BA.5.2.2, BQ.1.6, BU.2, CQ.2, BE.4, BA.5.1.25, BQ.1.26, BQ.1.10, BV.2, BE.3, BA.5.2.22, BF.15, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BF.29, BQ.1.1.13, BQ.1.23, BA.4.5, BE.4.1.1, BF.32, BQ.1.2, BA.5.1.24, BF.3.1, BA.5.7, BE.6, BA.5.3.1, BA.4.6.3, BE.1.1, BA.5.2.25, BA.4.1.8,	Greaney et al. (2020)	83170	T	G,GC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
F486V	monoclonal antibody serial passage escape	Escape mutation against monoclonal antibody LY-CoV555 (antibody that forms the basis for Eli Lilly's bamlanivimab)	BA.5.1.2, BQ.1.1.15, BA.5.2.14, DE.2, BE.4.2, CN.1, BF.5, BF.7.1, BA.5.2.3, BA.5.2.23, BA.4.4, BA.5.1.9, BQ.1.1.19, BQ.1.1.3, CQ.1.1, BA.5.2.34, BA.4.1.9, BE.1.1.2, BA.5.2.18, BF.26, BA.5.1.21, BA.5.1.16, CG.1, BA.5.1.3, BF.17, BQ.1.16, BA.5.3.3, CE.1, BA.5.2.26, BQ.1.1.14, BQ.1.1.2, BQ.1.8.2, BT.2, BA.5.2.28, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.4.1.5, BQ.1.1.25, BA.5.1.22, BQ.1.3, BA.5.1.19, BA.4.1.1, BF.7.5, BF.1, BA.4.1.10, BA.5.2.21, BQ.1.1.7, BQ.1.1.6, BQ.1.10.1, BQ.1.1.28, BF.4, CK.3, BF.7.4.1, CR.2, XBE, BQ.1.1.27, BA.5.2.37, BQ.1.1, BQ.1.12, BA.4.7, BF.19, BA.5.10, BF.31, BF.7.3, BF.7.7, BA.5.1.31, BF.7.8, XAS, BA.5.2.33, CC.1, BQ.1.1.24, BA.5.6.2, BA.5.2.2, BQ.1.6, BU.2, CQ.2, BE.4, BA.5.1.25, BQ.1.26, BQ.1.10, BV.2, BE.3, BA.5.2.22, BF.15, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BF.29, BQ.1.1.13, BQ.1.23, BA.4.5, BE.4.1.1, BF.32, BQ.1.2, BA.5.1.24, BF.3.1, BA.5.7, BE.6, BA.5.3.1, BA.4.6.3, BE.1.4.1, BA.5.2.25, BA.4.1.8,	Starr et al. (2021)	83167	T	G,GC,CC	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
G257S	monoclonal antibody serial passage escape	Escape mutation against Spike N terminal domain antigenic supersite i mAb S2L28	BN.6, CH.1.1.2, BA.2.75.7, BM.2.1, BY.1.1.1, BN.1.5, CJ.1, BA.2.75, BN.3.1, BM.1, BM.4.1.1, BN.1.1.1, BL.5, BL.3, CA.3, CH.2, BN.1.3.1, BN.1.3, BN.1.2.1, BR.2.1, BM.1.1.3, BN.2, CH.1, BA.2.75.3, BN.5, BM.1.1, BM.4.1, BY.1.2, BA.2.10.1, BN.1.7, BR.1.2, BA.2.75.1, BN.2.1, BL.2, BQ.1.19, BM.2, BY.1, CA.5, CH.1.1.1, BA.2.75.9, BN.1, BR.1, BN.1.4, BA.5.2.20, BL.4, BN.1.1, CA.1, XBF, BR.4, CA.3.1, BF.34, XBD, BN.1.2, BA.2.75.2, BA.2.75.5, XBH, BA.2.75.4, CA.7, BM.1.1.1, CH.1.1, BA.2.75.10, BA.2.73, BL.1, CB.1, BN.1.9, BL.1.3, BA.2.75.6, CV.1, BR.3	McCallum et al. (2021)	2808	G	A	0.7

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
K444T	convalescent plasma escape	Escape mutant found after in passage in plasma pool of 26 convalescents mean 1.5 post symptom onset.	BQ.1.1.15, CH.1.1.2, BQ.1.1.17, BQ.1.8, BQ.1.5, DB.1, BQ.1.26, BQ.1.1.19, BQ.1.1.3, BQ.1, BQ.1.10, BE.3, BQ.1.22, CH.1, BQ.1.13, BQ.1.1.22, BQ.1.1.11, BQ.1.1.13, BQ.1.15, BQ.1.16, BQ.1.23, BA.5.6.2, BQ.1.20, BQ.1.7, BQ.1.1.14, BQ.1.1.2, BQ.1.1.10, BQ.1.2, BQ.1.8.2, BW.1, BQ.1.19, BQ.1.1.25, BQ.1.18, BA.5.3.1, BQ.1.3, BA.5.2.25, BQ.1.10.1, BQ.1.1.7, BQ.1.1.6, BQ.1.1.28, BQ.1.1.4, BQ.1.1.18, BE.1.1.1, BQ.1.1.1, BQ.1.4, BR.4, BQ.1.11, BQ.1.14, BQ.2, BQ.1.25, BQ.1.24, BQ.1.1.27, BQ.1.1.20, BQ.1.1.8, BQ.1.1.9, BQ.1.12, BQ.1.1, CH.1.1, BQ.1.9, BA.5.2.36, BW.1.1, BQ.1.1.23, BQ.1.1.24, BQ.1.1.26, BQ.1.6, BE.9	Schmidt et al. (2021)	22746	A	C,CGGC,CT	0.53

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
K444T	gene expression increase	Experimentally, Spike gene expression increased 0.07 fold	BQ.1.1.15, CH.1.1.2, BQ.1.1.17, BQ.1.8, BQ.1.5, DB.1, BQ.1.26, BQ.1.1.19, BQ.1.1.3, BQ.1, BQ.1.10, BE.3, BQ.1.22, CH.1, BQ.1.13, BQ.1.1.22, BQ.1.1.11, BQ.1.1.13, BQ.1.15, BQ.1.16, BQ.1.23, BA.5.6.2, BQ.1.20, BQ.1.7, BQ.1.1.14, BQ.1.1.2, BQ.1.1.10, BQ.1.2, BQ.1.8.2, BW.1, BQ.1.19, BQ.1.1.25, BQ.1.18, BA.5.3.1, BQ.1.3, BA.5.2.25, BQ.1.10.1, BQ.1.1.7, BQ.1.1.6, BQ.1.1.28, BQ.1.1.4, BQ.1.1.18, BE.1.1.1, BQ.1.1.1, BQ.1.4, BR.4, BQ.1.11, BQ.1.14, BQ.2, BQ.1.25, BQ.1.24, BQ.1.1.27, BQ.1.1.20, BQ.1.1.8, BQ.1.1.9, BQ.1.12, BQ.1.1, CH.1.1, BQ.1.9, BA.5.2.36, BW.1.1, BQ.1.1.23, BQ.1.1.24, BQ.1.1.26, BQ.1.6, BE.9	Starr et al. (2020)	22746	A	C,CGGC,CT	0.53
K444T	convalescent plasma escape	Escape mutant found after in passage in plasma pool of 26 convalescents mean 1.5 post symptom onset.	BW.1	Schmidt et al. (2021)	49	AG	CG	0.98
K444T	gene expression increase	Experimentally, Spike gene expression increased 0.07 fold	BW.1	Starr et al. (2020)	49	AG	CG	0.98
K444T	convalescent plasma escape	Escape mutant found after in passage in plasma pool of 26 convalescents mean 1.5 post symptom onset.	BQ.1.1.5	Schmidt et al. (2021)	260	TAA	TAC	0.99
K444T	gene expression increase	Experimentally, Spike gene expression increased 0.07 fold	BQ.1.1.5	Starr et al. (2020)	260	TAA	TAC	0.99
N450Y	antibody epitope effects	Mutant screen in neutralization assay with a broad range of monoclonal antibodies shows resistence to more than one antibody.	CM.2	Liu et al. (2021)	86	GTAATTATAATTAC	GTACATTATGATAC	0.98

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
N450Y	convalescent plasma escape	Strong reduction in neutralization capability of all 4 convalescent sera tested (2 ablations), triple replicates. Against a broader panel of 16 convalescent plasma (no replicates), reductions in neutralization are considerably less dramatic in pattern, and sometime neutralization increases.	CM.2	Liu et al. (2021)	86	GTAATTATAATCTAC	GTAATTATATTATAC	0.98
N450Y	monoclonal antibody serial passage escape	Most effective mutant against this position in the RBD for highly neutralizing COV2-2096	CM.2	Greaney et al. (2020)	86	GTAATTATAATCTAC	GTAATTATATTATAC	0.98
N450D	antibody epitope effects	Mutant screen in neutralization assay with a broad range of monoclonal antibodies shows resistence to more than one antibody.	CM.5, CN.1, BA.2.75, BN.3.1, BM.1, BF.28, BA.5.5.1, BM.1.1.3, BA.2.56, BF.32, CM.8.1, BA.2.3.20, BA.5.1.22, BA.2.79, CM.1, CM.9, CM.4, BA.5.2.32, CC.1, CM.8, BF.14, BU.3, CM.3, BA.5.2.19	Liu et al. (2021)	1719	A	G	0.34
N450D	convalescent plasma escape	Strong reduction in neutralization capability of all 4 convalescent sera tested (2 ablations).	CM.5, CN.1, BA.2.75, BN.3.1, BM.1, BF.28, BA.5.5.1, BM.1.1.3, BA.2.56, BF.32, CM.8.1, BA.2.3.20, BA.5.1.22, BA.2.79, CM.1, CM.9, CM.4, BA.5.2.32, CC.1, CM.8, BF.14, BU.3, CM.3, BA.5.2.19	Liu et al. (2021)	1719	A	G	0.34
N450D	convalescent plasma escape	Escape mutant found after in passage in plasma pool of 26 convalescents mean 1.5 post symptom onset.	CM.5, CN.1, BA.2.75, BN.3.1, BM.1, BF.28, BA.5.5.1, BM.1.1.3, BA.2.56, BF.32, CM.8.1, BA.2.3.20, BA.5.1.22, BA.2.79, CM.1, CM.9, CM.4, BA.5.2.32, CC.1, CM.8, BF.14, BU.3, CM.3, BA.5.2.19	Schmidt et al. (2021)	1719	A	G	0.34

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
N450D	monoclonal antibody serial passage escape	Escape variant 95% appearance in 2 passages against Regeneron monoclonal antibody RGN10934 @ 50ug/mL	CM.5, CN.1, BA.2.75, BN.3.1, BM.1, BF.28, BA.5.5.1, BM.1.1.3, BA.2.56, BF.32, CM.8.1, BA.2.3.20, BA.5.1.22, BA.2.79, CM.1, CM.9, CM.4, BA.5.2.32, CC.1, CM.8, BF.14, BU.3, CM.3, BA.5.2.19	Baum et al. (2020)	1719	A	G	0.34
F486P	gene expression increase	Experimentally, Spike gene expression increased 0.22 fold	BM.1.1.3, XBB.1, BQ.1.8, XBB.2, BM.1.1.1, XBB.1.5, XBF, BA.2.10.1, CJ.1, CH.1.1.1	Starr et al. (2020)	3482	TT	TC,GT,CC	0.94
F486P	monoclonal antibody serial passage escape	Ranked modestly effective mutant against this position in the RBD for highly neutralizing COV2-2832 monoclonal antibody	BM.1.1.3, XBB.1, BQ.1.8, XBB.2, BM.1.1.1, XBB.1.5, XBF, BA.2.10.1, CJ.1, CH.1.1.1	Greaney et al. (2020)	3482	TT	TC,GT,CC	0.94
F486P	monoclonal antibody serial passage escape	Escape mutation against monoclonal antibody LY-CoV555 (antibody that forms the basis for Eli Lilly's bamlanivimab)	BM.1.1.3, XBB.1, BQ.1.8, XBB.2, BM.1.1.1, XBB.1.5, XBF, BA.2.10.1, CJ.1, CH.1.1.1	Starr et al. (2021)	3482	TT	TC,GT,CC	0.94

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
P681H	ACE2 receptor binding affinity	Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant showed a 1.23x decrease in binding (KD) relative to D614G.	BA.2.17, BF.7.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BU.2, BA.5.2.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BA.1.15, BF.3.1, BA.2.54, BA.5.7, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.2.76, BA.5.2.6, BT.1, XAE, BG.2, BA.1.1.18, BF.25, BY.1.1.1, BA.1.1, BA.5.1, BF.20, BA.5.1.5,	Gong et al. (2021)	187008	C	A,ATCGT,ACGTCGA	0.98

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
P681H	antibody epitope effects	Ablates Class 3 N-terminal domain targeting antibody COV2-2489, diminishes COV2-2676.	BA.2.17, BF.7.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BA.5.2.2, BU.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BA.1.15, BF.3.1, BA.2.54, BA.5.7, CA.5, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.2.76, BA.5.2.6, BT.1, XAE, BG.2, BA.1.1.18, BF.25, BY.1.1.1, BA.1.7, BA.5.1, BF.20, BA.5.1.5, CJ.1,	Chen et al. (2021)	187030	C	A,ATCGT,ACGCGA	0.98

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
P681H	antibody epitope effects	Wildtype elicits immune response, COVID-19 cohort epitope score > 99th percentile of the 497 pre-pandemic controls, mutant drops PIWAS epitope score from 7.8% to 1.2% (significantly poorer immune recognition) Together with other B1.1.7 lineage mutational changes (Spike: Y144del,N501Y, A570D Nucleoprotein: D3L, S235F) resulted in only 2 of 579 individuals (0.3% of the population) having a dramatic reduction in PIWAS antigen scores, which reflects the peak epitope signal along the entire antigen.	BA.2.17, BF.7.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BA.5.2.2, BU.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BA.1.15, BF.3.1, BA.2.54, BA.5.7, CA.5, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.2.76, BA.5.2.6, BT.1, XAE, BG.2, BA.1.1.18, BF.25, BY.1.1.1, BA.1.7, BA.5.1, BF.20, BA.5.1.5, CJ.1,	Haynes et al. (2021)	187030	C	A,ATCGT,ACATCGA	0.98

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
P681H	antibody epitope effects	This variant is adjacent to the Spike protein furin cleavage site (cleavage of S into S1 and S2 subunits is required for viral membrane fusion and subsequent entry into host cells), a site shown to be highly immunogenic.	BA.2.17, BF.7.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BA.5.2.2, BU.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BA.1.15, BF.3.1, BA.2.54, BA.5.7, CA.5, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.2.76, BA.5.2.6, BT.1, XAE, BG.2, BA.1.1.18, BF.25, BY.1.1.1, BA.1.7, BA.5.1, BF.20, BA.5.1.5, CJ.1,	Johnson et al. (2020)	187030	C	A,ATCGT,ACGCGA	0.95

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
P681H	convalescent plasma binding	1.26x increase in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset.	BA.2.17, BF.7.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BU.2, BA.5.2.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BA.1.15, BF.3.1, BA.2.54, BA.5.7, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.2.76, BA.5.2.6, BT.1, XAE, BG.2, BA.1.1.18, BF.25, BY.1.1.1, BA.1.1, BA.5.1, BF.20, BA.5.1.5,	Gong et al. (2021)	187008	C	A,ATCGT,ACGCGA	0.95

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
P681H	trafficking	While the introduction of P681H in the SARS-CoV-2 B.1.1.7 variant may increase spike cleavage by furin-like proteases, this does not significantly impact viral entry or cell-cell spread. We consider that other factors are at play to account for the increased in transmission and disease severity attributed to this variant of concern (VOC).	BA.2.17, BF.7.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BA.5.2.2, BU.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BA.1.15, BF.3.1, BA.2.54, BA.5.7, CA.5, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.2.76, BA.5.2.6, BT.1, XAE, BG.2, BA.1.1.18, BF.25, BY.1.1.1, BA.1.7, BA.5.1, BF.20, BA.5.1.5, CJ.1,	Lubinski et al. (2021)	187030	C	A,ATCGT,ACGCGA	0.98

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
P681H	trafficking	This mutation in the first base of the furin clevage site maintains the RXXR recognition motif, and is presumed to enhance cleavage based on the removal of a proline-directed phosphotase recognition site at S680. In a homologuous site in Infectious Bronchitis Virus (IBV, Gammacoronaviruses), abolition of S680 phosphorylation improves furin cleavage (and presumably cell entry).	BA.2.17, BF.7.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BA.5.2.2, BU.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BA.1.15, BF.3.1, BA.2.54, BA.5.7, CA.5, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.2.76, BA.5.2.6, BT.1, XAE, BG.2, BA.1.1.18, BF.25, BY.1.1.1, BA.1.7, BA.5.1, BF.20, BA.5.1.5, CJ.1,	Maaroufi (2021)	187030	C	A,ATCGT,ACGTC,ATCGA	0.98,0.01,0.01,0.01

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
P681H	trafficking	Lentiviral pseudotyped with this individual mutation from B.1.1.7 was tested on ACE2.293T cells. Luciferase activity was measured two days postinfection, showing NO statistically significant infection rate change amongst the cells, suggesting that furin cleavage typically used for cell entry is not affected by this change one amino acid upstream of the RXXR recognition pattern.	BA.2.17, BF.7.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BA.5.2.2, BU.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BA.1.15, BF.3.1, BA.2.54, BA.5.7, CA.5, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.2.76, BA.5.2.6, BT.1, XAE, BG.2, BA.1.1.18, BF.25, BY.1.1.1, BA.1.7, BA.5.1, BF.20, BA.5.1.5, CJ.1,	Tada et al. (2021)	187030	C	A,ATCGT,ACATCGA	0.98

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
P681H	vaccine neutralization efficacy	No significant change in virus neutralzation by 18 Pfizer two dose vaccinee sera compared to B.1.1.7. [results without including the used mutation A27S likely generalizable, as this is not a lineage defining mutation]	BA.2.17, BF.7.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BU.2, BA.5.2.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BA.1.15, BF.3.1, BA.2.54, BA.5.7, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.2.76, BA.5.2.6, BT.1, XAE, BG.2, BA.1.1.18, BF.25, BY.1.1.1, BA.1.1, BA.5.1, BF.20, BA.5.1.5,	Zuckerman et al. (2021)	187008	C	A,ATCGT,ACGCGA	0.95

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
P681H	vaccinee plasma binding	1.14x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in previously non-seroconverted subjects. 1.11x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in post-infection vaccinees.	BA.2.17, BF.7.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BU.2, BA.5.2.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BA.1.15, BF.3.1, BA.2.54, BA.5.7, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.2.76, BA.5.2.6, BT.1, XAE, BG.2, BA.1.1.18, BF.25, BY.1.1.1, BA.1.1, BA.5.1, BF.20, BA.5.1.5,	Gong et al. (2021)	187008	C	A,ATCGT,ACGCGA	0.95

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
P681H	virion structure	The Ratio of S2 (processed Spike) to full length Spike is higher for this mutation, due to a drop in the full length Spike measured, suggesting that this mutation compensates for decreased Spike production by improved proteolytic processing.	BA.2.17, BF.7.1, BQ.1.1.19, BA.5.2.34, BN.5, BM.1.1, BQ.1.16, BA.1.14.2, BA.5.3.3, CE.1, BP.1, BA.2.31.1, BA.1.1.2, BA.2.75.1, CR.1.2, BQ.1.1.5, BA.5.1.4, BA.2.12, BF.1, BQ.1.10.1, BA.5.2.21, BA.2.82, BA.2.9.3, BQ.1.1.6, BA.1.3, CK.3, CR.2, BA.5.2.37, CA.7, BF.19, BA.1.17.2, BA.2.61, CC.1, CV.1, BA.5.6.2, BA.5.2.2, BU.2, BE.4, BA.5.1.25, BN.1.1.1, BQ.1.10, CK.2.1.1, DF.1, BA.5.1.6, BQ.1.1.22, XAN, BA.1.15, BF.3.1, BA.2.54, BA.5.7, CA.5, XBB.1.4, XAM, BA.2.35, BE.1.1, BA.2.21, BA.5.2.24, BA.2.27, BA.1.21, BA.5.2.36, BA.2.3.15, BF.14, BF.13, BU.3, BA.1.8, BA.2.23.1, BF.18, BM.1, CA.3, BL.3, CH.2, BN.1.2.1, BA.5.8, BY.1.2, BA.4.8, BA.2.30, BG.5, BA.2.51, CR.1.1, BQ.1.1.4, BA.1.17.1, BR.4, BA.1.1.9, BA.1.15.2, BQ.1.1.20, CH.1.1, BA.5.1.23, BA.1.1.10, BF.7.12, BW.1.1, BA.1.20, BF.16, BA.2.38.2, BA.1.6, BA.2.64, BA.2.76, BA.5.2.6, BT.1, XAE, BG.2, BA.1.1.18, BF.25, BY.1.1.1, BA.1.7, BA.5.1, BF.20, BA.5.1.5, CJ.1,	Tada et al. (2021)	187030	C	A,ATCGT,ACATCGA	0.98

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
P681H	ACE2 receptor binding affinity	Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant showed a 1.23x decrease in binding (KD) relative to D614G.	BA.2.75.6, BA.2.9, BR.2.1, BE.1.2.1	Gong et al. (2021)	2163	CT	AT	0.85
P681H	antibody epitope effects	Ablates Class 3 N-terminal domain targeting antibody COV2-2489, diminishes COV2-2676.	BA.2.75.6, BA.2.9, BR.2.1, BE.1.2.1	Chen et al. (2021)	2163	CT	AT	0.85
P681H	antibody epitope effects	Wildtype elicits immune response, COVID-19 cohort epitope score > 99th percentile of the 497 pre-pandemic controls, mutant drops PIWAS epitope score from 7.8% to 1.2% (significantly poorer immune recognition) Together with other B1.1.7 lineage mutational changes (Spike: Y144del,N501Y, A570D Nucleoprotein: D3L, S235F) resulted in only 2 of 579 individuals (0.3% of the population) having a dramatic reduction in PIWAS antigen scores, which reflects the peak epitope signal along the entire antigen.	BA.2.75.6, BA.2.9, BR.2.1, BE.1.2.1	Haynes et al. (2021)	2163	CT	AT	0.85
P681H	antibody epitope effects	This variant is adjacent to the Spike protein furin cleavage site (cleavage of S into S1 and S2 subunits is required for viral membrane fusion and subsequent entry into host cells), a site shown to be highly immunogenic.	BA.2.75.6, BA.2.9, BR.2.1, BE.1.2.1	Johnson et al. (2020)	2163	CT	AT	0.85
P681H	convalescent plasma binding	1.26x increase in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset.	BA.2.75.6, BA.2.9, BR.2.1, BE.1.2.1	Gong et al. (2021)	2163	CT	AT	0.85
P681H	trafficking	While the introduction of P681H in the SARS-CoV-2 B.1.1.7 variant may increase spike cleavage by furin-like proteases, this does not significantly impact viral entry or cell-cell spread. We consider that other factors are at play to account for the increased in transmission and disease severity attributed to this variant of concern (VOC).	BA.2.75.6, BA.2.9, BR.2.1, BE.1.2.1	Lubinski et al. (2021)	2163	CT	AT	0.85
P681H	trafficking	This mutation in the first base of the furin clevage site maintains the RXXR recognition motif, and is presumed to enhance cleavage based on the removal of a proline-directed phosphotase recognition site at S680. In a homologuous site in Infectious Bronchitis Virus (IBV, Gammacoronaviruses), abolition of S680 phosphorylation improves furin cleavage (and presumably cell entry).	BA.2.75.6, BA.2.9, BR.2.1, BE.1.2.1	Maaroufi (2021)	2163	CT	AT	0.85

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
P681H	trafficking	Lentiviral pseudotyped with this individual mutation from B.1.1.7 was tested on ACE2.293T cells. Luciferase activity was measured two days postinfection, showing NO statistically significant infection rate change amongst the cells, suggesting that furin cleavage typically used for cell entry is not affected by this change one amino acid upstream of the RXXR recognition pattern.	BA.2.75.6, BA.2.9, BR.2.1, BE.1.2.1	Tada et al. (2021)	2163	CT	AT	0.85
P681H	vaccine neutralization efficacy	No significant change in virus neutralzation by 18 Pfizer two dose vaccinee sera compared to B.1.1.7. [results without including the used mutation A27S likely generalizable, as this is not a lineage defining mutation]	BA.2.75.6, BA.2.9, BR.2.1, BE.1.2.1	Zuckerman et al. (2021)	2163	CT	AT	0.85
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P681H	virion structure	The Ratio of S2 (processed Spike) to full length Spike is higher for this mutation, due to a drop in the full length Spike measured, suggesting that this mutation compensates for decreased Spike production by improved proteolytic processing.	BA.2.75.6, BA.2.9, BR.2.1, BE.1.2.1	Tada et al. (2021)	2163	CT	AT	0.85
P681H	ACE2 receptor binding affinity	Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant showed a 1.23x decrease in binding (KD) relative to D614G.	BQ.1.1.4	Gong et al. (2021)	788	CTCGG	ATCGG	0.97
P681H	antibody epitope effects	Ablates Class 3 N-terminal domain targeting antibody COV2-2489, diminishes COV2-2676.	BQ.1.1.4	Chen et al. (2021)	788	CTCGG	ATCGG	0.97
P681H	antibody epitope effects	Wildtype elicits immune response, COVID-19 cohort epitope score > 99th percentile of the 497 pre-pandemic controls, mutant drops PIWAS epitope score from 7.8% to 1.2% (significantly poorer immune recognition) Together with other B1.1.7 lineage mutational changes (Spike: Y144del,N501Y, A570D Nucleoprotein: D3L, S235F) resulted in only 2 of 579 individuals (0.3% of the population) having a dramatic reduction in PIWAS antigen scores, which reflects the peak epitope signal along the entire antigen.	BQ.1.1.4	Haynes et al. (2021)	788	CTCGG	ATCGG	0.97

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P681H	ACE2 receptor binding affinity	Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant showed a 1.23x decrease in binding (KD) relative to D614G.	CQ.2, BE.4, BE.4.2, BE.4.1.1, BQ.1.1.14, BA.2.31, CQ.1.1, CQ.1, BA.5.2.34, BE.4.1	Gong et al. (2021)	445	CTCGG	ATCGG,ATCGG	0.94
P681H	antibody epitope effects	Ablates Class 3 N-terminal domain targeting antibody COV2-2489, diminishes COV2-2676.	CQ.2, BE.4, BE.4.2, BE.4.1.1, BQ.1.1.14, BA.2.31, CQ.1.1, CQ.1, BA.5.2.34, BE.4.1	Chen et al. (2021)	445	CTCGG	ATCGG,ATCGG	0.94
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P681H	antibody epitope effects	This variant is adjacent to the Spike protein furin cleavage site (cleavage of S into S1 and S2 subunits is required for viral membrane fusion and subsequent entry into host cells), a site shown to be highly immunogenic.	CQ.2, BE.4, BE.4.2, BE.4.1.1, BQ.1.1.14, BA.2.31, CQ.1.1, CQ.1, BA.5.2.34, BE.4.1	Johnson et al. (2020)	445	CTCGG	ATCGG,ATCGG	0.94
P681H	convalescent plasma binding	1.26x increase in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset.	CQ.2, BE.4, BE.4.2, BE.4.1.1, BQ.1.1.14, BA.2.31, CQ.1.1, CQ.1, BA.5.2.34, BE.4.1	Gong et al. (2021)	445	CTCGG	ATCGG,ATCGG	0.94
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P681H	trafficking	Lentiviral pseudotyped with this individual mutation from B.1.1.7 was tested on ACE2.293T cells. Luciferase activity was measured two days postinfection, showing NO statistically significant infection rate change amongst the cells, suggesting that furin cleavage typically used for cell entry is not affected by this change one amino acid upstream of the RXXR recognition pattern.	CQ.2, BE.4, BE.4.2, BE.4.1.1, BQ.1.1.14, BA.2.31, CQ.1.1, CQ.1, BA.5.2.34, BE.4.1	Tada et al. (2021)	445	CTCGG	ATCGG,ATCGG	0.94
P681H	vaccine neutralization efficacy	No significant change in virus neutralzation by 18 Pfizer two dose vaccinee sera compared to B.1.1.7. [results without including the used mutation A27S likely generalizable, as this is not a lineage defining mutation]	CQ.2, BE.4, BE.4.2, BE.4.1.1, BQ.1.1.14, BA.2.31, CQ.1.1, CQ.1, BA.5.2.34, BE.4.1	Zuckerman et al. (2021)	445	CTCGG	ATCGG,ATCGG	0.94
P681H	vaccinee plasma binding	1.14x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in previously non-seroconverted subjects. 1.11x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in post-infection vaccinees.	CQ.2, BE.4, BE.4.2, BE.4.1.1, BQ.1.1.14, BA.2.31, CQ.1.1, CQ.1, BA.5.2.34, BE.4.1	Gong et al. (2021)	445	CTCGG	ATCGG,ATCGG	0.94
P681H	virion structure	The Ratio of S2 (processed Spike) to full length Spike is higher for this mutation, due to a drop in the full length Spike measured, suggesting that this mutation compensates for decreased Spike production by improved proteolytic processing.	CQ.2, BE.4, BE.4.2, BE.4.1.1, BQ.1.1.14, BA.2.31, CQ.1.1, CQ.1, BA.5.2.34, BE.4.1	Tada et al. (2021)	445	CTCGG	ATCGG,ATCGG	0.94
E484R	ACE2 receptor binding affinity	Experimentally, ACE2 binding affinity increased 0.15 fold	BA.2.3.20	Starr et al. (2020)	107	GTTGA	GTTAG	0.99
E484R	ACE2 receptor binding affinity	This is a two point mutation change giving this position the highest possible fitness, has higher affinity than circulating E484K variant.	BA.2.3.20	Zahradnik et al. (2021)	107	GTTGA	GTTAG	0.99
E484R	monoclonal antibody serial passage escape	Ranked mildly effective mutant against this position in the RBD for highly neutralizing COV2-2050 monoclonal antibody Ranked mildly effective mutant against this position in the RBD for highly neutralizing COV2-2479 monoclonal antibody	BA.2.3.20	Greaney et al. (2020)	107	GTTGA	GTTAG	0.99

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
E484R	monoclonal antibody serial passage escape	Escape mutation against monoclonal antibody LY-CoV555 (antibody that forms the basis for Eli Lilly's bamlanivimab)	BA.2.3.20	Starr et al. (2021)	107	GTTGA	GTTAG	0.99
E484R	ACE2 receptor binding affinity	Experimentally, ACE2 binding affinity increased 0.15 fold	CM.2, CM.1, CM.5, CM.9, CM.4, CM.8.1, CM.8	Starr et al. (2020)	208	GA	AG	1.0
E484R	ACE2 receptor binding affinity	This is a two point mutation change giving this position the highest possible fitness, has higher affinity than circulating E484K variant.	CM.2, CM.1, CM.5, CM.9, CM.4, CM.8.1, CM.8	Zahradnik et al. (2021)	208	GA	AG	1.0
E484R	monoclonal antibody serial passage escape	Ranked mildly effective mutant against this position in the RBD for highly neutralizing COV2-2050 monoclonal antibody Ranked mildly effective mutant against this position in the RBD for highly neutralizing COV2-2479 monoclonal antibody	CM.2, CM.1, CM.5, CM.9, CM.4, CM.8.1, CM.8	Greaney et al. (2020)	208	GA	AG	1.0
E484R	monoclonal antibody serial passage escape	Escape mutation against monoclonal antibody LY-CoV555 (antibody that forms the basis for Eli Lilly's bamlanivimab)	CM.2, CM.1, CM.5, CM.9, CM.4, CM.8.1, CM.8	Starr et al. (2021)	208	GA	AG	1.0

The results here are in whole or part based upon data hosted at the Canadian VirusSeq Data Portal: https://virusseq-dataportal.ca/.We wish to acknowledge the following organisations/laboratories for contributing data to the Portal: Canadian Public Health Laboratory Network (CPHLN), CanCOGGeN VirusSeq and the list of labs available at https://virusseq-dataportal.ca/acknowledgements)