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Surveillance report

Surveillance generated by nf-ncov-voc for Delta variant

Date

This report is generated on 2022-03-25 using 257885 number of genomes collected between 2020-02-25 and 2022-03-09

Pango Lineages

Pango Lineages in this report ['AY.1', 'AY.10', 'AY.100', 'AY.101', 'AY.102', 'AY.103', 'AY.103.2', 'AY.104', 'AY.106', 'AY.106', 'AY.107', 'AY.108', 'AY.109', 'AY.110', 'AY.111', 'AY.112', 'AY.113', 'AY.114', 'AY.116', 'AY.116.1', 'AY.117', 'AY.118', 'AY.119', 'AY.119.1', 'AY.119.2', 'AY.120', 'AY.120.1', 'AY.120.2', 'AY.121', 'AY.121.1', 'AY.122', 'AY.122.1', 'AY.122.4', 'AY.124', 'AY.124.1', 'AY.125', 'AY.126', 'AY.126', 'AY.127', 'AY.127.1', 'AY.128', 'AY.129', 'AY.131', 'AY.131', 'AY.133', 'AY.14', 'AY.15', 'AY.16', 'AY.16.1', 'AY.18', 'AY.19', 'AY.2', 'AY.20', 'AY.22', 'AY.23', 'AY.24', 'AY.25', 'AY.25.1', 'AY.25.3', 'AY.26', 'AY.27', 'AY.28', 'AY.29', 'AY.3', 'AY.3.1', 'AY.3.2', 'AY.3.3', 'AY.32', 'AY.34', 'AY.34.1', 'AY.35', 'AY.36', 'AY.37', 'AY.38', 'AY.39', 'AY.39.1', 'AY.4.4', 'AY.4.12', 'AY.4.2', 'AY.4.2.2', 'AY.4.2.3', 'AY.4.3', 'AY.4.4', 'AY.4.5', 'AY.4.6', 'AY.4.6.2', 'AY.4.8', 'AY.40', 'AY.41', 'AY.42', 'AY.43', 'AY.43.3', 'AY.43.4', 'AY.44', 'AY.45', 'AY.46', 'AY.46.2', 'AY.46.4', 'AY.46.5', 'AY.46.6', 'AY.47', 'AY.48', 'AY.49', 'AY.51', 'AY.53', 'AY.51', 'AY.53', 'AY.55', 'AY.55', 'AY.56', 'AY.57', 'AY.58', 'AY.59', 'AY.60', 'AY.61', 'AY.62', 'AY.64', 'AY.65', 'AY.67', 'AY.68', 'AY.7.1', 'AY.70', 'AY.71', 'AY.72', 'AY.73', 'AY.74', 'AY.75', 'AY.75.2', 'AY.76', 'AY.77', 'AY.78', 'AY.79', 'AY.82', 'AY.83', 'AY.84', 'AY.85', 'AY.86', 'AY.87', 'AY.88', 'AY.91', 'AY.92', 'AY.92', 'AY.99', 'AY.98', 'AY.99', 'AY.99.2', 'B.1.617.2']

Indicator

This table contains key indicators identified

Indicator	Sub-categories from POKAY	Mutations
Transmissibility between hu-	transmissibility	p.D614G, p.E484Q, p.L452R, p.P681R
mans		
Infection Severity	ACE2 receptor binding affinity, viral load, outcome haz-	p.D614G, p.E484K, p.E484Q, p.F490S,
	ard ratio	p.H69del, p.K417N, p.L452R, p.L5F,
		p.N501T, p.P26S, p.S494P, p.T95I,
		p.V70del
Immunity after natural infection	convalescent plasma escape, reinfection, humoral response	p.A475V, p.D614G, p.E484K, p.E484Q,
	durability	p.F490S, p.G446V, p.H69del, p.K417N,
		p.K458N, p.L452R, p.P1162S, p.S494P,
		p.V70del
Vaccines	vaccine neutralization efficacy	p.D614G, p.E484K, p.E484Q, p.K417N,
		p.L452R
Monoclonal antibodies	monoclonal antibody serial passage escape, pharmaceuti-	p.A475V, p.E484K, p.E484Q, p.F490S,
	cal effectiveness	p.G142D, p.G446V, p.K417N, p.L452R,
		p.N501T, p.P251L, p.R158G, p.S255F,
		p.S443F, p.S494P
Diagnostics	clinical indicators, antigenic test failure, symptom preva-	
	lence	

Mutation Significance

This table contains key functional impacts of mutations identified

Mutations	Sub-category	Function	Lineages	Citation	Sequence	Reference	Alternate	Alternate
					Depth	Allele	Allele	Frequency
p.E484K	ACE2 receptor bind-	This combination showed	AY.77	Collier et al.	2	G	A,C	nan
	ing affinity	extasciitilde3x increase		(2021)				
		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						

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Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.E484K	ACE2 receptor binding affinity	This variant appears twice in the experiments, with slightly different affinities (both extasciitilde1.2x decrease in binding rel- ative to D614G) using flow cytometry and ACE2 ectodomains-Fc portion IgG complex.	AY.77	Gong et al. (2021)	2	G	A,C	nan
p.E484K	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.	AY.77	Laffeber et al. (2021)	2	G	A,C	nan
p.E484K	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.	AY.77	Liu et al. (2021)	2	G	A,C	nan
p.E484K	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).	AY.77	Ramanathan et al. (2021)	2	G	A,C	nan
p.E484K	ACE2 receptor binding affinity	Experimentally, ACE2 binding affinity increased 0.06 fold	AY.77	Starr et al. (2020)	2	G	A,C	nan
p.E484K	ACE2 receptor binding affinity	Reported moderate in- crease in affinity compared to wild-type RBD on the cell surface (Kd	AY.77	Tian et al. (2021)	2	G	A,C	nan
p.E484K	ACE2 receptor binding affinity	Reported slight increase in affinity compared to wild- type RBD on the cell sur- face (Kd	AY.77	Tian et al. (2021)	2	G	A,C	nan
p.E484K	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.	AY.77	Vogel et al. (2021)	2	G	A,C	nan
p.E484K	ACE2 receptor binding affinity	Among the first selected variants in an in vitro evolution experiment for ACE2 binding.	AY.77	Zahradnik et al. (2021)	2	G	A,C	nan
p.E484K	T cell evasion	Analyzing responses to the E484K mutation seen in B.1.351 and P.1 variants, we noted that it did not fall in a region predicted to bind the HLAII alleles tested (table S4). The mutation appeared to have no substantial or differential impact on T cell responses.	AY.77	Reynolds et al. (2021)	2	G	A,C	nan
p.E484K	antibody epitope effects	Ablates Class 1 receptor- binding-motif targeting an- tibodies COV2-2050, 1B07, COVOX-384 and S2H58.	AY.77	Chen et al. (2021)	2	G	A,C	nan

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Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	e Reference Allele	Alternate Allele	Alternate Frequency
p.E484K	antibody epitope effects	Of 50 mAbs tested, major loss of neutralization observed for S2N28, S2X615, S2N12, S2X192, S2H70, S2X16, S2X58, S2H70, S2X613, S2D19, S2N22, S2D32, S2H58, S2M11, S2D106, S2X30.	AY.77	Collier et al. (2021)	2	G	A,C	nan
p.E484K	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.	AY.77	Gaebler et al. (2021)	2	G	A,C	nan
p.E484K	antibody epitope effects	Monoclonal antibodies 13G9 and 58G6 maintain fairly high neutralization potency, compared to others interfacing with E484K.	AY.77	Li et al. (2021)	2	G	A,C	nan
p.E484K	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.	AY.77	Liu et al. (2020)	2	G	A,C	nan
p.E484K	antibody epitope effects	Massive reduction in binding efficiency vs wild type for mAb LY-CoV555.	AY.77	Rappazzo et al. (2021)	2	G	A,C	nan
p.E484K	antibody epitope effects	Complete loss of binding in ELISA by the variant against monoclonal anti- body VH-Fc ab8	AY.77	Sun et al. (2021)	2	G	A,C	nan
p.E484K	antibody epitope effects	Pseudotyped virus model ablates neutralization by RBD-directed mAbs 4-20, 2-4, 2-43, 2-30, 2-15, LY-Cov555, C121. Pseudotyped virus model impairs neutralization by RBD-directed mAb COV2-2196 (somewhat more than fully pseudotyped B.1.351 or live virus)	AY.77	Wang et al. (2021)	2	G	A,C	nan
p.E484K	antibody epitope effects	Resistent to all seven class 2 (Spike 'up' or 'down' conformation, RBD targeting) antibodies tested, with 10-fold or greater reduction in neutralization (plus notable reudction in two unclassfied mAbs).	AY.77	Wang et al. (2021)	2	G	A,C	nan
p.E484K	convalescent plasma binding	1.42x increase in Spike binding (relative to D614G alone) by 5 plasma col- lected 8 months post- symptom-onset.	AY.77	Gong et al. (2021)	2	G	A,C	nan
p.E484K	convalescent plasma escape	Average extasciitilde5-fold reduction in neutralization efficacy in convalescent sera of 16 health workers infected in Spring 2020.	AY.77	Alenquer et al. (2021)	2	G	A,C	nan
p.E484K	convalescent plasma escape	This mutation occurred in 100% of sequenced virions after 12 passages and led to a 4-fold decrease in convalescent plasma neutralization activity	AY.77	Andreano et al. (2020)	2	G	A,C	nan
p.E484K	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	AY.77	Cele et al. (2021)	2	G	A,C	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.E484K	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 (triplicate experiments). Against a wider panel of 16 convalescent plasma (no replicates), all but one show major resistance.	AY.77	Liu et al. (2021)	2	G	A,C	nan
p.E484K	convalescent plasma escape	Escape mutant found after in passage in plasma pool of 26 convalescents mean 1.5 post symptom onset.	AY.77	Schmidt et al. (2021)	2	G	A,C	nan
p.E484K	convalescent plasma escape	The only mutation in the B.1.351 lineage that appears to contribute to neutralization reduction (extasciitilde1.7x across 10 convalescent sera from April 2020 infectees)	AY.77	Tada et al. (2021)	2	G	A,C	nan
p.E484K	convalescent plasma escape	Pseudotyped viruses for B.1.618 was 2.5-fold resistant to neutralization by convalescent sera compared to wild type - a finding that was similar to that of the 3-fold resistance of the South Africa B.1.351 variant using the same assay. The resistance of B.1.618 was caused by the E484K mutation, based on results from viruses pseudotyped for individual variants within B.1.618. [details on the convalescent patient sera collection are not abundantly clear in the preprint]	AY.77	Tada et al. (2021)	2	G	A,C	nan
p.E484K	convalescent plasma escape	As measured by surface plasmon resonance, RBD with the E484K mutation alone showed a mean 19.1x decrease in binding affinity for six batches of hyperimmune immunoglobulin (hCoV-2IG) preparations generated from SARS-CoV-2 convalescent plasma.	AY.77	Tang et al. (2021)	2	G	A,C	nan
p.E484K	convalescent plasma escape	The neutralizing activity of 15/20 convalescent sera was significantly lower against this pseudotyped virus model	AY.77	Wang et al. (2021)	2	G	A,C	nan
p.E484K	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	AY.77	Wibmer et al. (2021)	2	G	A,C	nan
p.E484K	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 directly 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.	AY.77	Wibmer et al. (2021)	2	G	A,C	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.E484K	convalescent plasma escape	Subtype of the B.1.526 "New York" lineage, lentivirus pseudotyped with this mutation combination in showed 3.3x reduction in IC50 serum dilution concentration for 6 convalescent sera.	AY.77	Zhou et al. (2021)	2	G	A,C	nan
p.E484K	monoclonal anti- body serial passage escape	The engineered mutation cause 10-fold or more increase in the disassociation constant with many monoclonal antibodies (C144/C002/C121/C104/C1		Barnes et al. (2020)	2	G	A,C	nan
p.E484K	monoclonal anti- body serial passage escape	Escape variant 100% appearance in 2 pas- sages against Regeneron monoclonal antibody REGN10989 @ 50ug/mL (99% after one passage)	AY.77	Baum et al. (2020)	2	G	A,C	nan
p.E484K	monoclonal anti- body serial passage escape	Mildly effective mutant against this position in the RBD for highly neutralizing COV2-2479 monoclonal antibody Effective mutant against this position in the RBD for highly neutralizing COV2-2050 monoclonal antibody	AY.77	Greaney et al. (2020)	2	G	A,C	nan
p.E484K	monoclonal anti- body serial passage escape	Escape mutation against monoclonal antibody LY- CoV555 (antibody that forms the basis for Eli Lilly's bamlanivimab)	AY.77	Starr et al. (2021)	2	G	A,C	nan
p.E484K	monoclonal anti- body serial passage escape	Class 2 antibodies C627, C602, C671, C643, and class 2/3 antibody C603 se- lected for the emergence of the E484K mutation in vitro.	AY.77	Wang et al. (2021)	2	G	A,C	nan
p.E484K	monoclonal anti- body serial passage escape	Strong positive selection (up to 50% of supernatant sequences) after C121 monoclonal antibody assay, decreasing in subsequent passages Strong positive selection (up to 44% of supernatant sequences) after after one round of C144 monoclonal antibody passage, then waning on subsequent passages	AY.77	Weisblum et al. (2020)	2	G	A,C	nan
p.E484K	pharmaceutical effectiveness	Bamlanivimab (LY-CoV555) lost extasci- itilde16x binding against this isolated mutation. Casirivimab lost extasci- itilde16x binding against this isolated mutation.	AY.77	Engelhart et al. (2021)	2	G	A,C	nan
p.E484K	pharmaceutical effectiveness	Tixagevimab, Regdan- vimab and COR-101 display reduced binding affinity to virus pseu- dotyped as RBD from B.1.351.	AY.77	Engelhart et al. (2021)	2	G	A,C	nan
p.E484K	pharmaceutical effectiveness	This mutated version of RBD completely abolishes the binding to a therapeutic antibody, Bamlanivimab, in vitro.	AY.77	Liu et al. (2021)	2	G	A,C	nan
p.E484K	trafficking	This variant alone shows a extasciitilde5x decrease in cell entry efficiency (RLU measurement in 293T cells) compared to D614G.	AY.77	Ferriera et al (2021)	2	G	A,C	nan
p.E484K	trafficking	This variant combination shows a extasciitilde4-5x decrease in cell entry efficiency (RLU measurement in 293T cells) compared to D614G, same as L452R alone.	AY.77	Ferriera et al (2021)	2	G	A,C	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.E484K	trafficking	This variant combination shows a extasciitilde3x decrease in cell entry efficiency (RLU measurement in 293T cells) compared to D614G, significantly less of a decrease than any B.1.617 lineage variants alone, suggesting a synergistic effect on cell entry while maintaining known immunity esacpe mutants.	AY.77	Ferriera et al (2021)	2	G	A,C	nan
p.E484K	trafficking	extasciitilde2x more infectivity than D614G alone in HEK293T-ACE2 cells 48h	AY.77	Kuzmina et al. (2021)	2	G	A,C	nan
p.E484K	trafficking	post-transduction. Lentiviral pseudotyped with this individual mutation from B.1.351 was tested on ACE2.293T cells. Luciferase activity was measured two days postinfection, showing no change in infection rate amongst the cells.	AY.77	Tada et al. (2021)	2	G	A,C	nan
p.E484K	vaccine neutralization efficacy	Nine stored sera from Pfizer BNT162b2 vacci- nees were tested against a range of spike muta- tion bearing PV. E484K conferred a ten-fold reduc- tion in neutralisation by vaccine sera.	AY.77	Ferreira et al. (2021)	2	G	A,C	nan
p.E484K	vaccine neutralization efficacy	E484K pseudotyped VSV was tested for neutralization in a clonal HEK-293T ACE2 TMPRSS2 cell line optimized for highly efficient S-mediated infection. A cohort of 12 Argentinian recipients of the Gamaleya Sputnik V Ad26 / Ad5 vaccine showed a mean 2.8x decrease in neutralization effiacacy.	AY.77	Ikegame et al. (2021)	2	G	A,C	nan
p.E484K	vaccine neutralization efficacy	Human sera from 5 two- dose Pfizer vaccinated in- dividuals (47-68 days post 1st-dose) neutralized this variant 3.4x less relative to reference USA-WA1/2020 strain. 8 convalescent plasma with weak IgG ELISA titre neutralized this variant 2.4x less rel- ative to reference USA- WA1/2020 strain. One plasma failed to neutral- ize at all. 11 convales- cent plasma with moderate IgG ELISA titre neutral- ized this variant 4.2x less relative to reference USA- WA1/2020 strain. 11 con- valescent plasma with high IgG ELISA titre neutral- ized this variant 2.6x less relative to reference USA- WA1/2020 strain. 2.6x less relative to reference USA- WA1/2020 strain.	AY.77	Jangra et al. (2021)	2	G	A,C	nan
p.E484K	vaccine neutraliza- tion efficacy	This variant showed only minor in Pfizer sera (one or two dose) neutralization efficiency vs D614G (using lentivirus pseudotype).	AY.77	Kuzmina et al. (2021)	2	G	A,C	nan
p.E484K	vaccine neutralization efficacy	Neutralizing antibody titers of non-human primate sera after one or two doses of Ad26.COV2.S (Jannsen vaccine) against the variants containing the E484K substitution in the RBD were present but reduced (fold reduction between 3.35–7.78, 95% confidence interval all above twofold difference, one-sample t test).	AY.77	Solfrosi et al. (2021)	2	G	A,C	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.E484K	vaccine neutralization efficacy	Pseudotyped viruses for B.1.618 was 2.7-fold resistant to neutralization by 6 BNT162b2 vaccine sera 28 days post-booster compared to wild type - a finding that was similar to that of the 3.4-fold resistance of the South Africa B.1.351 variant using the same assay. Neutralization by 3 Moderna vaccine sera 28 days post-booster was 3-fold resistant (vs. 2.2-fold for B.1.351). The resistance of B.1.618 was caused by the E484K mutation, based on results from viruses pseudotyped for individual variants within B.1.618.	AY.77	Tada et al. (2021)	2	G	A,C	nan
p.E484K	vaccine neutraliza- tion efficacy	In a cohort of 20 patients 8+ weeks after second vaccine dose of Moderna (mRNA-1273) or Pfizer- BioNTech (BNT162b2) vaccines, ELISA tests show 10x reduced efficacy of a majority of isolated anti- bodies, but only a modest decrease for vaccine plasma overall.	AY.77	Wang et al. (2021)	2	G	A,C	nan
p.E484K	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. 1.06x 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.	AY.77	Gong et al. (2021)	2	G	A,C	nan
p.E484K	virion structure	Estimated free energy change (ddG) for this variant is -0.6 kcal/mol (i.e. destabilizing relative to wild type)	AY.77	Spratt et al. (2021)	2	G	A,C	nan
p.K458N	convalescent plasma escape	Resistant to a pool of 10 convalescent sera (but less than 4x, a typical threshold for definition of escape)	AY.46.1	Li et al. (2020)	17	A	С	nan
p.G446V	antibody epitope effects	Mutant screen in neutral- ization assay with a broad range of monoclonal anti- bodies shows resistence to more than one antibody.	AY.127.1, AY.131	Liu et al. (2021)	33	G	Т	nan
p.G446V	antibody epitope effects	Massive reduction in binding efficiency vs wild type for mAb REGN10933.	AY.127.1, AY.131	Rappazzo et al. (2021)	33	G	Т	nan
p.G446V	convalescent plasma escape	In 2 of 11 subjects' convalescent sera in an early+late mutational landscape analysis of the RBD, the early serum timepoint shows significant resistance (extasciitide10x or more), but both abate by the late timepoint (extasciitide3m) presumably through immune cell somatic mutation evolution.	AY.127.1, AY.131	Greaney et al. (2021)	33	G	Т	nan
p.G446V	convalescent plasma escape	Resistant to a pool of 10 convalescent sera (but less than 4x, a typical threshold for definition of escape)	AY.127.1, AY.131	Li et al. (2020)	33	G	Т	nan
p.G446V	convalescent plasma escape	Ablation of neutralization capability of 3 convalescent sera tested, 1 improvement.	AY.127.1, AY.131	Liu et al. (2021)	33	G	Т	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.G446V	monoclonal anti- body serial passage escape	Most effective mutant against this position in the RBD for highly neutralizing COV2-2499 monoclonal antibody Most but only mildly effective mutant against this position in the RBD for highly neutralizing COV2-2096 monoclonal antibody	AY.127.1, AY.131	Greaney et al. (2020)	33	G	Т	nan
p.G446V	pharmaceutical effectiveness	Cligavimab lost extasci- itilde16x binding against this isolated mutation. Imdevimab lost extasci- itilde16x binding against this isolated mutation (the only RBD variant to do so).	AY.127.1, AY.131	Engelhart et al. (2021)	33	G	Т	nan
p.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.	AY.127.1, AY.34.1, AY.34.1, AY.1. AY.4.8, AY.125, AY.4.2.1, AY.42, AY.119, AY.36, AY.116.1, AY.100, AY.112, AY.109, AY.121, AY.43.4, AY.76, AY.4.7, AY.131, AY.4.2, AY.102, AY.116, AY.122.4, AY.119, AY.129, AY.121.1, AY.4.4, AY.4, AY.87, AY.107, AY.124.1, AY.4.3, B.1.617.2, AY.106, AY.114, AY.34, AY.114, AY.34, AY.114, AY.39.1, AY.4.6, AY.106, AY.118, AY.106, AY.118, AY.106, AY.118, AY.107, AY.108, AY.111, AY.4.104, AY.110, AY.4.104, AY.110, AY.4.124, AY.111, AY.4.124, AY.110, AY.4.124, AY.117, AY.29, AY.119, AY.120, AY.120, AY.120, AY.120, AY.29, AY.120, AY.29, AY.120, AY.29, AY.120, AY.20, AY.127, AY.120, AY.127, AY.120, AY.127, AY.120, AY.127, AY.120, AY.127, AY.120, AY.127, AY.120, AY.127, AY.120, AY.127, AY.120, AY.127, AY.120, AY.127, AY.120, AY.128, AY.127, AY.120, AY.127, AY.120, AY.128, AY.127, AY.120, AY.127,	Gong et al. (2021)	6640	C	T	nan

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Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.T95I	convalescent plasma binding	No change in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptomonset.	AY.127.1, AY.34.1, AY.34.1, AY.1., AY.4.8, AY.125, AY.4.2.1, AY.42, AY.119, AY.36, AY.116.1, AY.100, AY.112, AY.109, AY.121, AY.43.4, AY.76, AY.4.7, AY.131, AY.4.2, AY.102, AY.116, AY.119.2, AY.119.2, AY.119.2, AY.121.1, AY.4.4, AY.119.2, AY.121.1, AY.4.4, AY.114, AY.34, AY.114, AY.34, AY.114, AY.39, AY.114, AY.39, AY.118, AY.118, AY.118, AY.119, AY.4.5, AY.106, AY.118, AY.110, AY.4.5, AY.108, AY.111, AY.104, AY.111, AY.104, AY.117, AY.124, AY.117, AY.124, AY.117, AY.124, AY.117, AY.124, AY.117, AY.120, AY.29, AY.119.1, AY.4.2.3, AY.1120, AY.29, AY.120, AY.29, AY.120, AY.29, AY.120.1, AY.4.2.2	Gong et al. (2021)	6640	C	T	nan

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Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.T95I	vaccinee binding plasma	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.	AY.127.1, AY.34.1, AY.34.1, AY.34.1, AY.4.2, AY.119, AY.36, AY.116.1, AY.101, AY.100, AY.112, AY.121, AY.43.4, AY.76, AY.4.7, AY.131, AY.4.2, AY.102, AY.116, AY.119, AY.121, AY.4.109, AY.121, AY.4.3, AY.107, AY.121, AY.4.4, AY.129, AY.121, AY.4.4, AY.4, AY.4, AY.4, AY.4, AY.4, AY.4, AY.107, AY.124.1, AY.34, AY.114, AY.39.1, AY.4.3, B.1.617.2, AY.4.6, AY.118, AY.126, AY.106, AY.118, AY.126, AY.107, AY.121, AY.4.5, AY.108, AY.111, AY.104, AY.110, AY.4.5, AY.110, AY.4.5, AY.111, AY.104, AY.110, AY.4.5, AY.120, AY.120, AY.120, AY.29, AY.120, AY.120	Gong et al. (2021)	6640	C	T	nan
p.H69del	ACE2 receptor binding affinity	Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant showed a 1.51x increase in binding (KD) relative to D614G, mostly due to decreased in "off-rate" a.k.a. dissociation rate (Kdis).	AY.77	Gong et al. (2021)	2	ATACATG	A	nan
p.H69del	antibody epitope effects	Reduces neutralization by structurally unmapped mAb COVA1-21 (cluster XI).	AY.77	Rees-Spear et al. (2021)	2	ATACATG	A	nan
p.H69del	convalescent plasma binding	1.33x increase in Spike binding (relative to D614G alone) by 5 plasma col- lected 8 months post- symptom-onset.	AY.77	Gong et al. (2021)	2	ATACATG	A	nan
p.H69del	convalescent plasma escape	Fatal COVID-19 complica- tions in immunocomprim- ised patient after immune escape from convalescent plasma	AY.77	Kemp et al. (2020)	2	ATACATG	A	nan
p.H69del	convalescent plasma escape	Neutralization activity of almost all Moderna Phase 1 sera tested actually *in- creased*.	AY.77	Shen et al. (2021)	2	ATACATG	A	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.H69del	convalescent plasma escape	Viruses containing the point mutations of B.1.1.7 showed that the single point mutations ($\Delta 69$ -70 and N501Y) were neutralized as efficiently as D614G across 10 convalescent sera from April 2020 infectees.	AY.77	Tada et al. (2021)	2	ATACATG	A	nan
p.H69del	immunosuppression variant emergence	The delH69/V70 enhances viral infectivity, indicating its effect on virus fitness is independent to the N501Y RBM change [with which it is found in lineage B.1.1.7] Possibly arisen as a result of the virus evolving from immune selection pressure in infected individuals and possibly only one chronic infection in the case of lineage B.1.1.7.	AY.77	Kemp et al. (2020)	2	ATACATG	A	nan
p.H69del	vaccinee plasma binding	1.14x 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.	AY.77	Gong et al. (2021)	2	ATACATG	A	nan
p.N501T	ACE2 receptor binding affinity	Experimentally, ACE2 binding affinity increased 0.1 fold	AY.131	Starr et al. (2020)	1	A	С	nan
p.N501T	anthropozoonotic events	These variants dominate in mink infections in North America, sometime supplemented with F486L. The Y453F variant found in other jurisdictions in mink infections is notably absent in North America.	AY.131	Cai and Cai (2021)	1	A	С	nan
p.N501T	anthropozoonotic events	Observed in second of two Netherlands mink cohorts, potential adaptation.	AY.131	Oreshkova et al. (2020)	1	A	С	nan
p.N501T	anthropozoonotic events	Observed in 4 separate mink farms in Denmark, but not humans, poten- tial adaptation (diff set of farms than F486L).	AY.131	Oude Munnink et al. (2020)	1	A	С	nan
p.N501T	anthropozoonotic events	Emergent variants observed in tandem in ferrets post-serial infection.	AY.131	Richard et al. (2020)	1	A	С	nan
p.N501T	monoclonal anti- body serial passage escape	Mild in vitro selection against class 3 monoclonal antibody C670.	AY.131	Wang et al. (2021)	1	A	С	nan
p.N501T	pharmaceutical effectiveness	Estesevimab lost extasci- itilde12x binding against this isolated mutation.	AY.131	Engelhart et al. (2021)	1	A	С	nan

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p-R188G nonnecloual nataleon against MY-861, MY-86	Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
AY.99, AY.4.6, AY.40, AY.37, AY.118, AY.126, AY.122, AY.78, AY.92, AY.119.1,		monoclonal anti- body serial passage	Escape mutation against Spike N terminal domain antigenic supersite i mAb	AY.86, AY.34.1, AY.103, AY.119, AY.109, AY.28, AY.112, AY.47, AY.43.4, AY.22.4, AY.33, AY.4, AY.106, AY.85, AY.98, AY.59, AY.111, AY.75, AY.74, AY.19, AY.35, AY.45, AY.19, AY.32, AY.48, AY.88, AY.58, AY.98, AY.58, AY.98, AY.58, AY.98, AY.58, AY.98, AY.58, AY.98, AY.32, AY.45, AY.111, AY.10, AY.11, AY.11, AY.10, AY.111, AY.121, AY.103.2, AY.16.1, AY.1121, AY.53, AY.42, AY.18, AY.19, AY.108, AY.46, AY.119, AY.108, AY.119, AY.108, AY.119, AY.108, AY.411, AY.117, AY.25.3, AY.42, AY.10, AY.32, AY.10, AY.32, AY.10, AY.32, AY.110, AY.32, AY.10, AY.32, AY.117, AY.45, AY.46, AY.23, AY.124, AY.15, AY.117, AY.21, AY.117, AY.24, AY.117, AY.24, AY.117, AY.24, AY.117, AY.21, AY.117, AY.21, AY.42, AY.118, AY.117, AY.118, AY.119, AY.44, AY.79, AY.120, AY.44, AY.79, AY.121, AY.41, AY.116, AY.22, AY.118, AY.118, AY.118, AY.119, AY.41, AY.116, AY.22, AY.114, AY.116, AY.22, AY.114, AY.115, AY.117, AY.41, AY.116, AY.22, AY.114, AY.116, AY.22, AY.114, AY.116, AY.21, AY.43, AY.49, AY.126, AY.49, AY.126, AY.49, AY.126, AY.49, AY.47, AY.118, AY.11	McCallum et	Depth	Allele	Allele	Frequency

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.S494P	ACE2 receptor binding affinity	Using molecular dynamic simulation, the mildly (extasciitilde1kcal/mol) enhanced binding energy of this variant is primarily contributed by Tyr505 (-4.98 kcal/mol) which is now involved in a strong hydrogen bonding network with Arg393. Another important energetic contribution comes from the altered orientation of Tyr41 which is now involved with two hydrogen-bonding interactions with Asp355 and Thr500.	AY.108	Chakraborty (2021)	27	T	С	nan
p.S494P	ACE2 receptor binding affinity	Minor variant selected in late rounds of an in vitro evolution experiment for ACE2 binding. Shown to increase the thermostability but decrease the association rate constant of the RBD to ACE2	AY.108	Zahradnik et al. (2021)	27	Т	С	nan
p.S494P	antibody epitope effects	Mutant screen in neutral- ization assay with a broad range of monoclonal anti- bodies shows resistence to mAb SARS2-01.	AY.108	Liu et al. (2020)	27	Т	С	nan
p.S494P	antibody epitope effects	Greater than 10-fold rediuction of binding effeiency vs wild type for mAb LY-CoV555.	AY.108	Rappazzo et al. (2021)	27	Т	С	nan
p.S494P	convalescent plasma escape	S494P frequently engages in interactions with antibodies but not with ACE2. It reduces antibody neutralization of all 16 convalescent sera tested, averaging WT ratio of 0.41+0.08 (less dramatic than E484K). This amino acid emerges as an additional hotspot for immune evasion and a target for therapies, vaccines and diagnostics. It has emerged independently in multiple lineages.	AY.108	Alenquer et al. (2021)	27	T	C	nan
p.S494P	convalescent plasma escape	In 2 of 11 subjects' convalescent sera in an early+late mutational landscape analysis of the RBD, S484P shows a slightly resistent profile across both timepoints (i.e. resistant to immune cell somatic mutation evolution)	AY.108	Greaney et al. (2021)	27	T	С	nan
p.S494P	convalescent plasma escape	Mixed bag of positive and negative changes in neutralization capability of all 4 convalescent sera tested.	AY.108	Liu et al. (2021)	27	Т	C	nan
p.S494P	immunosuppression variant emergence	Combination of RBD mutations appeared (day 75) and persisted in chronic (152 day) SARS-CoV-2 infection of immunocompromised patient with severe antiphospholipid syndrome complicated by diffuse alveolar hemorrhage, who was receiving anticoagulation therapy, glucocorticoids, cyclophosphamide, and intermittent rituximab and eculizumab.	AY.108	Choi et al. (2020)	27	Т	С	nan
p.S494P	monoclonal anti- body serial passage escape	Escape mutation against monoclonal antibody LY- CoV555 (antibody that forms the basis for Eli Lilly's bamlanivimab)	AY.108	Starr et al. (2021)	27	Т	C	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.S494P	pharmaceutical effectiveness	Bamlanivimab (LY-CoV555) lost extasciitilde8x binding against this isolated mutation. Regdanvimab lost extasciitilde32x binding against this isolated mutation.	AY.108	Engelhart et al. (2021)	27	Т	С	nan
p.S255F	monoclonal anti- body serial passage escape	Escape mutation against Spike N terminal domain antigenic supersite i mAb S2L28	AY.106	McCallum et al. (2021)	236	С	Т	nan
p.P681R	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). [Inference from similar positively charged substitution P681H actually described in the work]	AY.127, AY.65, AY.88, AY.56	Maaroufi (2021)	301	CTCC	TTCG,CTC	Gnan
p.P681R	trafficking	Quantification of the band intensities showed that the P681R mutation, which lies near the proteolytic processing site, caused a small increase in proteolytic processing as measured by a 2-fold decrease in the ratio of S/S2.	AY.127, AY.65, AY.88, AY.56	Tada et al. (2021)	301	CTCC	TTCG,CTC	Gnan
p.P681R	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. [PG: Inferred by conservative AA substitution of described P681H]	AY.127, AY.65, AY.88, AY.56	Tada et al. (2021)	301	CTCC	TTCG,CTC	Gnan
p.P681R	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). [Inference from similar positively charged substitution P681H actually described in the work]	AY.46	Maaroufi (2021)	56	TCC	CCG,TCG	nan
p.P681R	trafficking	Quantification of the band intensities showed that the P681R mutation, which lies near the proteolytic processing site, caused a small increase in proteolytic processing as measured by a 2-fold decrease in the ratio of S/S2.	AY.46	Tada et al. (2021)	56	TCC	CCG,TCG	nan

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Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.P681R	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. [PG: Inferred by conservative AA substitution of described P681H]	AY.46	Tada et al. (2021)	56	TCC	CCG,TCG	nan
p.P681R	symptom prevalence	Gross examination of 3+3 hamster lung specimens showed pronounced congestion and hemorrhages on days 5 and 7 post-infection in the case of the B.1.617.1 as compared with the B.1. The lung lesions with the B.1 variant were minimal to mild whereas with B.1.617.1 they were moderate. For B.1 pneumonic changes were minimal to mild (inflammatory cell infiltration, focal consolidation and mild congestion). The pronounced changes (moderate to severe) with mononuclear infiltration in the alveolar interstitial space, interstitial septal thickening, consolidation and pneumocyte hyperplasia were observed with B.1.617.1 variant consistently.	AY.35, AY.87	Yadav et al. (2021)	9	C	G	nan
p.P681R	trafficking	This variant combination shows a extasciitilde3x decrease in cell entry efficiency (RLU measurement in 293T cells) compared to D614G, significantly less of a decrease than any B.1.617 lineage variants alone, suggesting a synergistic effect on cell entry while maintaining known immunity esacpe mutants.	AY.77	Ferriera et al (2021)	2	С	G	nan

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Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.P681R	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). [Inference from similar positively charged substitution P681H actually described in the work]	AY.86, AY.34.1, AY.103, AY.119, AY.109, AY.28, AY.112, AY.47, AY.43.4, AY.5, AY.122.4, AY.33, AY.4, AY.16, B.1.617.2, AY.106, AY.85, AY.98, AY.111, AY.75, AY.74, AY.19, AY.45, AY.48, AY.93, AY.32, AY.58, AY.93, AY.4, AY.103, AY.13, AY.4, AY.13, AY.4, AY.13, AY.1, AY.48, AY.120.2, AY.36, AY.116.1, AY.121, AY.53, AY.98.1, AY.103.2, AY.76, AY.47, AY.25.3, AY.42, AY.83, AY.119.2, AY.10, AY.44, AY.45, AY.46, AY.25, AY.46, AY.117, AY.24, AY.16, AY.121, AY.45, AY.46, AY.124, AY.117, AY.45, AY.46, AY.124, AY.161, AY.117, AY.24, AY.161, AY.117, AY.42, AY.128, AY.42, AY.129, AY.129, AY.14, AY.15, AY.10, AY.41, AY.116, AY.120, AY.44, AY.46, AY.121, AY.41, AY.116, AY.122, AY.128, AY.42, AY.129, AY.129, AY.14, AY.15, AY.114, AY.116, AY.22, AY.114, AY.116, AY.22, AY.114, AY.116, AY.22, AY.114, AY.116, AY.22, AY.114, AY.116, AY.21, AY.41, AY.116, AY.22, AY.114, AY.116, AY.22, AY.114, AY.116, AY.22, AY.114, AY.116, AY.21, AY.41, AY.116, AY.22, AY.114, AY.116, AY.21, AY.42, AY.43, AY.75.2, AY.114, AY.116, AY.22, AY.114, AY.116, AY.23, AY.40, AY.33, AY.99, AY.4.6, AY.40, AY.37, AY.118, AY.41, AY.116, AY.25, AY.49, AY.42, AY.49, AY.75, AY.49, AY.75, AY.49, AY.75, AY.40, AY.40, AY.37, AY.19, AY.40,	Maaroufi (2021)	99996 99996	Allele	CIDGOH ©	Frequency

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Mutations Sub-category F	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.P681R trafficking Q ir P lii p lii s i o o s i	Quantification of the band ntensities showed that the P681R mutation, which ies near the proteolytic processing site, caused a small increase in proteolytic processing as measured by a 2-fold decrease in the ratio of S/S2.	AY.34.1, AY.103, AY.86, AY.119, AY.109, AY.112, AY.28, AY.43.4, AY.47, AY.5, AY.122.4, AY.33, AY.85, AY.98, AY.59, AY.111, AY.75, AY.74, AY.19, AY.35, AY.43, AY.43, AY.45, AY.48, AY.93, AY.32, AY.58, AY.20, AY.13, AY.26, AY.13, AY.103.2, AY.16.1, AY.121, AY.53, AY.42, AY.83, AY.103.2, AY.6, AY.116.1, AY.121, AY.53, AY.42, AY.83, AY.119.2, AY.10, AY.46, AY.25, AY.46, AY.23, AY.66, AY.23, AY.66, AY.116, AY.117, AY.25, AY.14, AY.55, AY.31, AY.94, AY.55, AY.31, AY.94, AY.55, AY.31, AY.94, AY.16.1, AY.117, AY.24, AY.16.1, AY.117, AY.42, AY.16.1, AY.117, AY.42, AY.16.1, AY.118, AY.101, AY.41, AY.116, AY.22, AY.129, AY.131, AY.41, AY.116, AY.22, AY.131, AY.41, AY.116, AY.23, AY.75.2, AY.114, AY.39.1, AY.42, AY.75.2, AY.114, AY.116, AY.22, AY.131, AY.41, AY.116, AY.22, AY.131, AY.41, AY.116, AY.22, AY.131, AY.41, AY.116, AY.23, AY.99, AY.33, AY.99, AY.33, AY.92, AY.34, AY.75, AY.35, AY.35, AY.35, AY.36, AY.37, AY.38, AY.32, AY.39,	Tada et al. (2021)	Depth 99984	Allele	Allele G,GTCGT,	Frequency

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Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.P681R	transmissibility	Normalized for particle number, on ACE2.293T cells showed that the B.1.617 spike protein was >2-fold increase in infectiv- ity relative to D614G wild type.	AY.35, AY.87	Tada et al. (2021)	9	C	G	nan
p.P681R	viral load	In 9 infected hamsters each for B.1 and B.1.617.1, no significant change in viral load or subgenomic RNA levels were detected.	AY.35, AY.87	Yadav et al. (2021)	9	С	G	nan

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p.P681R 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. [PG: Inferred by conservative AA substitution of described P681H] Take Ratio of S2 (processed, AY.86, AY.48, AY.103, AY.411, (2021) AY.403, AY.109, AY.47, AY.47, AY.47, AY.47, AY.48, AY.4	Frequency FAGG
AY-106, AY-30, AY-30, AY-31, AY-11, AY-12, AY-13, AY-14, AY-15, AY-14, AY-15, AY-15, AY-16, AY-17, AY-18, AY-19, AY-11, AY-12, AY-12, AY-13, AY-14, AY-14, AY-15, AY-16, AY-10, AY-12, AY-12, AY-12, AY-13, AY-12, A	

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.P681R	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). [Inference from similar positively charged substitution P681H actually described in the work]	AY.127.1	Maaroufi (2021)	16	CTCGG	GTCGT	nan
p.P681R	trafficking	Quantification of the band intensities showed that the P681R mutation, which lies near the proteolytic processing site, caused a small increase in proteolytic processing as measured by a 2-fold decrease in the ratio of S/S2.	AY.127.1	Tada et al. (2021)	16	CTCGG	GTCGT	nan
p.P681R	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. [PG: Inferred by conservative AA substitution of described P681H]	AY.127.1	Tada et al. (2021)	16	CTCGG	GTCGT	nan
p.P26S	ACE2 receptor binding affinity	Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant showed a 1.58x increase in binding (KD) relative to D614G.	AY.4.3, AY.3.2	Gong et al. (2021)	37	C	Т	nan
p.P26S	convalescent plasma binding	1.08x decrease in Spike binding (relative to D614G alone) by 5 plasma col- lected 8 months post- symptom-onset.	AY.4.3, AY.3.2	Gong et al. (2021)	37	C	Т	nan
p.P26S	vaccinee plasma binding	1.23x 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. 1.37x 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.	AY.4.3, AY.3.2	Gong et al. (2021)	37	С	T	nan
p.L5F	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.	AY.35, AY.4.4, AY.77, AY.53	Gong et al. (2021)	15	C	Т	nan
p.L5F	convalescent plasma binding	No change in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptomonset.	AY.35, AY.4.4, AY.77, AY.53	Gong et al. (2021)	15	С	Т	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.L5F	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.	AY.35, AY.4.4, AY.77, AY.53	Gong et al. (2021)	15	C	T	nan
p.P1162S	convalescent plasma escape	Escape mutant found after in passage in plasma pool of 26 convalescents mean 1.5 post symptom onset.	AY.94, AY.4.12	Schmidt et al. (2021)	601	С	Т	nan
p.E484Q	ACE2 receptor binding affinity	Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant combination (representing lineage B.1.617) showed a 1.85x increase in binding (KD) relative to D614G. [exact variant list not provided in manuscript, is inferred fro common knowledge]	AY.35, AY.87	Gong et al. (2021)	8	G	С	nan
p.E484Q	antibody epitope effects	>20% (ELISA significance threshold) drop in anti- body binding by this vari- ant against monoclonal an- tibody VH-Fc ab8.	AY.35, AY.87	Sun et al. (2021)	8	G	С	nan
p.E484Q	convalescent plasma binding	This variant combination (representing lineage B.1.617) showed a 1.22x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 8 months postsymptom-onset. [exact variant list not provided in manuscript, is inferred fro common knowledge]	AY.35, AY.87	Gong et al. (2021)	8	G	С	nan
p.E484Q	convalescent plasma escape	In 3 of 11 subjects' convalescent sera in an early+late mutational landscape analysis of the RBD, E484Q shows a notably resistant profile, comparable to or even more resistant than E484K at later time points (i.e. more resistant to immune cell somatic mutation evolution), see Figure 5a,b. Subject C 32 days post-infection showed »10 fold reduction in neutralization, reducing to extasciitilde10-fold by day 104. Subject B 26 days post-infection showed extasciitilde10 fold reduction in neutralization, reducing to extasciitilde10 fold reduction in neutralization, reducing to extasciitilde4x at day 113. Notably, Subject B also showed smaller than typical (extasciitilde10 vs 30+ fold) reduction in one-month neutralization by E484K immune escape at day 104. Subject I 26 days post-infection showed extasciitilde10 fold reduction in neutralization, with no reduction in escape at day 102. Notably, Subject I also showed smaller than typical (extasciitilde10 vs 30+ fold) reduction in one-month neutralization by E484K at day 26, and no E484K immune escape at day 102.	AY.35, AY.87	Greaney et al. (2021)	8	G	C	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.E484Q	convalescent plasma escape	Pseudotyped viruses for B.1.617 was 2.3-fold resistant to neutralization by convalescent sera compared to wild type - a finding that was similar to that of the 3-fold resistance of the South Africa B.1.351 variant using the same assay. The resistance of B.1.617 was caused by the L452R and E484Q mutation, based on results from viruses pseudotyped for individual variants within B.1.617. [details on the convalescent patient sera collection are not abundantly clear in the preprint]	AY.35, AY.87	Tada et al. (2021)	8	G	C	nan
p.E484Q	monoclonal anti- body serial passage escape	Escape mutation against monoclonal antibody LY- CoV555 (antibody that forms the basis for Eli Lilly's bamlanivimab)	AY.35, AY.87	Starr et al. (2021)	8	G	С	nan
p.E484Q	pharmaceutical effectiveness	Bamlanivimab (LY-CoV555) lost extasciitilde20x binding against this isolated mutation. Casirivimab lost extasciitilde4x binding against this isolated mutation.	AY.35, AY.87	Engelhart et al. (2021)	8	G	С	nan
p.E484Q	symptom prevalence	Gross examination of 3+3 hamster lung specimens showed pronounced congestion and hemorrhages on days 5 and 7 post-infection in the case of the B.1.617.1 as compared with the B.1. The lung lesions with the B.1 variant were minimal to mild whereas with B.1.617.1 they were moderate. For B.1 pneumonic changes were minimal to mild (inflammatory cell infiltration, focal consolidation and mild congestion). The pronounced changes (moderate to severe) with mononuclear infiltration in the alveolar interstitial space, interstitial septal thickening, consolidation and pneumocyte hyperplasia were observed with B.1.617.1 variant consistently.	AY.35, AY.87	Yadav et al. (2021)	8	G	С	nan
p.E484Q	trafficking	This variant alone shows a 10x decrease in cell entry efficiency (RLU measurement in 293T cells) compared to D614G.	AY.35, AY.87	Ferriera et al (2021)	8	G	С	nan
p.E484Q	transmissibility	The combination caused a 3-fold increase in infectivity relative to D614G wild type. [compare to 3.5x for L452R alone]	AY.35, AY.87	Tada et al. (2021)	8	G	С	nan
p.E484Q	transmissibility	Normalized for particle number, on ACE2.293T cells showed that the B.1.617 spike protein was >2-fold increase in infectiv- ity relative to D614G wild type.	AY.35, AY.87	Tada et al. (2021)	8	G	С	nan

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Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.E484Q	vaccine neutralization efficacy	Nine stored sera from Pfizer BNT162b2 vaccinees were tested against a range of spike mutation bearing PV. E484Q had a extasciitilde5x drop in neutralization (vs extasciitilde10x for E484K). When E484Q and L452R were combined, the fold change was significant, but similar to that of L452R alone (extasciitilde2x), suggesting no evidence for an additive effect [perhaps even E484Q effect dilution].	AY.35, AY.87	Ferreira et al. (2021)	8	G	С	nan
p.E484Q	vaccine neutralization efficacy	1.4x reduction in neutralization (ID50) in sera 3 weeks after one dose of Pfizer/BioNTech BNT162b2 (up to 5 naive and post infection vaccinees)	AY.35, AY.87	Gong et al. (2021)	8	G	С	nan
p.E484Q	vaccine neutralization efficacy	Pseudotyped viruses for B.1.617 was 4-fold resistant to neutralization by 6 BNT162b2 vaccine sera 28 days post-booster compared to wild type - a finding that was similar to that of the 3.4-fold resistance of the South Africa B.1.351 variant using the same assay. Neutralization by 3 Moderna vaccine sera 28 days post-booster was 5-fold resistant (vs. 2.2-fold for B.1.351). The resistance of B.1.617 was caused by the L452R and E484Q mutation, based on results from viruses pseudotyped for individual variants within B.1.617.	AY.35, AY.87	Tada et al. (2021)	8	G	C	nan
p.E484Q	vaccinee plasma binding	This variant combination (representing lineage B.1.617) showed a 1.30x 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. 1.18x 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. [exact variant list not provided in manuscript, is inferred fro common knowledge]	AY.35, AY.87	Gong et al. (2021)	8	G	C	nan
p.E484Q	viral load	In 9 infected hamsters each for B.1 and B.1.617.1, no significant change in viral load or subgenomic RNA levels were detected.	AY.35, AY.87	Yadav et al. (2021)	8	G	С	nan
p.P251L	monoclonal anti- body serial passage escape	Escape mutation against Spike N terminal domain antigenic supersite i mAb S2X28	AY.98.1, AY.86	McCallum et al. (2021)	1222	С	Т	nan
p.V70del	ACE2 receptor binding affinity	Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant showed a 1.51x increase in binding (KD) relative to D614G, mostly due to decreased in "off-rate" a.k.a. dissociation rate (Kdis).	AY.77	Gong et al. (2021)	2	ATACATG	A	nan
p.V70del	antibody epitope effects	Reduces neutralization by structurally unmapped mAb COVA1-21 (cluster XI).	AY.77	Rees-Spear et al. (2021)	2	ATACATG	A	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.V70del	convalescent plasma binding	1.33x increase in Spike binding (relative to D614G alone) by 5 plasma col- lected 8 months post- symptom-onset.	AY.77	Gong et al. (2021)	2	ATACATG	A	nan
p.V70del	convalescent plasma escape	Fatal COVID-19 complica- tions in immunocomprim- ised patient after immune escape from convalescent plasma	AY.77	Kemp et al. (2020)	2	ATACATG	A	nan
p.V70del	convalescent plasma escape	Neutralization activity of almost all Moderna Phase 1 sera tested actually *increased*.	AY.77	Shen et al. (2021)	2	ATACATG	A	nan
p.V70del	convalescent plasma escape	Viruses containing the point mutations of B.1.1.7 showed that the single point mutations ($\Delta 69$ -70 and N501Y) were neutralized as efficiently as D614G across 10 convalescent sera from April 2020 infectees.	AY.77	Tada et al. (2021)	2	ATACATG	A	nan
p.V70del	immunosuppression variant emergence	The delH69/V70 enhances viral infectivity, indicating its effect on virus fitness is independent to the N501Y RBM change [with which it is found in lineage B.1.1.7] Possibly arisen as a result of the virus evolving from immune selection pressure in infected individuals and possibly only one chronic infection in the case of lineage B.1.1.7.	AY.77	Kemp et al. (2020)	2	ATACATG	A	nan
p.V70del	vaccinee plasma binding	1.14x 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.	AY.77	Gong et al. (2021)	2	ATACATG	A	nan
p.F490S	ACE2 receptor binding affinity	Among the first selected minor variants in an in vitro evolution experiment for ACE2 binding.	AY.111	Zahradnik et al. (2021)	9	Т	С	nan
p.F490S	antibody epitope effects	Mutant screen in neutral- ization assay with a broad range of monoclonal anti- bodies shows resistence to mAb SARS2-32.	AY.111	Liu et al. (2020)	9	Т	С	nan
p.F490S	antibody epitope effects	Complete loss of binding in ELISA by the variant against monoclonal antibody ab8	AY.111	Sun et al. (2021)	9	Т	С	nan
p.F490S	convalescent plasma escape	Strong reduction in neutralization capability of all 4 convalescent sera tested (3 ablations).	AY.111	Liu et al. (2021)	9	Т	С	nan
p.F490S	monoclonal anti- body serial passage escape	Ranked mildly effective mutant against this posi- tion in the RBD for highly neutralizing COV2-2496 monoclonal antibody	AY.111	Greaney et al. (2020)	9	Т	С	nan
p.F490S	monoclonal anti- body serial passage escape	Escape mutation against monoclonal antibody LY- CoV555 (antibody that forms the basis for Eli Lilly's bamlanivimab)	AY.111	Starr et al. (2021)	9	Т	С	nan
p.F490S	monoclonal anti- body serial passage escape	Class 2/3 mAb C603 modestly selected for the emergence of this mutation in vitro.	AY.111	Wang et al. (2021)	9	Т	С	nan
p.F490S	pharmaceutical effectiveness	Greater than 10-fold rediuction of binding effeiency vs wild type for mAb LY-CoV555.	AY.111	Rappazzo et al. (2021)	9	Т	С	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.K417N	ACE2 receptor binding affinity	The K417N mutation decreased the affinity extasci- itilde4 fold, mainly by de- creasing the k(on) but also by increasing the k(off) as measured by surface plas- mon resonance.	AY.1, AY.2	Barton et al. (2021)	12	G	Т	nan
p.K417N	ACE2 receptor binding affinity	This combination showed extasciitilde3x increase binding to ACE2 vs wild type, about half that of the B.1.17 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	AY.1, AY.2	Collier et al. (2021)	12	G	Т	nan
p.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.	AY.1, AY.2	Gong et al. (2021)	12	G	Т	nan
p.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.	AY.1, AY.2	Laffeber et al. (2021)	12	G	Т	nan
p.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.	AY.1, AY.2	Liu et al. (2021)	12	G	T	nan
p.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).	AY.1, AY.2	Ramanathan et al. (2021)	12	G	Т	nan
p.K417N	ACE2 receptor binding affinity	Reported 3-fold decrease in affinity compared to wild- type RBD on the cell sur- face (Kd	AY.1, AY.2	Tian et al. (2021)	12	G	Т	nan
p.K417N	ACE2 receptor binding affinity	Reported slight increase in affinity compared to wild- type RBD on the cell sur- face (Kd	AY.1, AY.2	Tian et al. (2021)	12	G	Т	nan
p.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.	AY.1, AY.2	Vogel et al. (2021)	12	G	Т	nan
p.K417N	antibody epitope effects	>20% (ELISA significance threshold) drop in anti- body binding (ELISA) by this variant against IgG1 monoclonal antibody ab1.	AY.1, AY.2	Sun et al. (2021)	12	G	Т	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.K417N	antibody epitope effects	5 antibodies tested were less potent against K417N by ten-fold or more (class 1 mAbs)	AY.1, AY.2	Wang et al. (2021)	12	G	T	nan
p.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.	AY.1, AY.2	Wang et al. (2021)	12	G	Т	nan
p.K417N	convalescent plasma binding	2.16x increase in Spike binding (relative to D614G alone) by 5 plasma col- lected 8 months post- symptom-onset.	AY.1, AY.2	Gong et al. (2021)	12	G	Т	nan
p.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	AY.1, AY.2	Cele et al. (2021)	12	G	Т	nan
p.K417N	convalescent plasma escape	In 19 convalescent hu- man sera extasciitilde1mo post infection, Two-tailed Wilcoxon matched-pairs signed-rank test shows mild resistence P	AY.1, AY.2	Chen et al. (2021)	12	G	Т	nan
p.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% re-	AY.1, AY.2	Wibmer et al. (2021)	12	G	Т	nan
p.K417N	convalescent plasma escape	tained high titres Nearly half (21 of 44, 48%) of early pandemic exposure convalescent plasma/sera failed to neutralize the 501Y.V2 ("South African") lineage pseudovirus con- struct Only 3 of 44 con- vascent sera (those with the highest titer, which correlated directly 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.	AY.1, AY.2	Wibmer et al. (2021)	12	G	T	nan
p.K417N	gene expression increase	Experimentally, Spike gene expression increased 0.1 fold	AY.1, AY.2	Starr et al. (2020)	12	G	Т	nan
p.K417N	monoclonal anti- body serial passage escape	Escape mutation against monoclonal antibody LY-CoV016	AY.1, AY.2	Starr et al. (2021)	12	G	Т	nan
p.K417N	monoclonal anti- body serial passage escape	In vitro selection against class 1 (Spike 'up' confor- mation) monoclonal anti- body C682, and to a lesser extent C614 and C660	AY.1, AY.2	Wang et al. (2021)	12	G	Т	nan
p.K417N	pharmaceutical effectiveness	COR-101 lost extasci- itilde6x binding against this isolated mutation. Estesevimab lost extasci- itilde100x binding against this isolated mutation.	AY.1, AY.2	Engelhart et al. (2021)	12	G	Т	nan
p.K417N	pharmaceutical effectiveness	Tixagevimab, Regdan- vimab and COR-101 display reduced binding affinity to virus pseu- dotyped as RBD from B.1.351.	AY.1, AY.2	Engelhart et al. (2021)	12	G	Т	nan

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Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.K417N	pharmaceutical effectiveness	This mutated version of RBD completely abolishes the binding to a ther- apeutic antibody, Bam- lanivimab, in vitro.	AY.1, AY.2	Liu et al. (2021)	12	G	Т	nan
p.K417N	trafficking	extasciitilde2x more infectivity than D614G alone in HEK293T-ACE2 cells 48h post-transduction.	AY.1, AY.2	Kuzmina et al. (2021)	12	G	Т	nan
p.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.	AY.1, AY.2	Tada et al. (2021)	12	G	Т	nan
p.K417N	vaccine neutraliza- tion efficacy	This variant showed only minor in Pfizer sera (one or two dose) neutralization efficiency vs D614G (using lentivirus pseudotype).	AY.1, AY.2	Kuzmina et al. (2021)	12	G	Т	nan
p.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.	AY.1, AY.2	Gong et al. (2021)	12	G	T	nan
p.K417N	virion structure	Estimated free energy change (ddG) for this variant is -0.86 kcal/mol (i.e. destabilizing relative to wild type)	AY.1, AY.2	Spratt et al. (2021)	12	G	Т	nan
p.G142D	anthropozoonotic events	These variants dominate in mink infections in North America, sometime supplemented with F486L. The Y453F variant found in other jurisdictions in mink infections is notably absent in North America.	AY.131	Cai and Cai (2021)	1	G	A	nan

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Mutations	Sub-category	Function	Lineages	Citation	Sequence	Reference	Alternate	Alternate	1
p.G142D	monoclonal anti-	Escape mutation against	AY.86,	McCallum et	Depth 91866	Allele	Allele	Frequency GfataTA,ATT	ATG
	body serial passage escape	Spike N terminal domain antigenic supersite i mAbs	AY.34.1, AY.103,	al. (2021)					
		S2M28, S2X28, S2X333	AY.119, AY.109,						
			AY.28, AY.112,						
			AY.47, AY.43.4, AY.5,						
			AY.122.4, AY.33,						
			AY.4, AY.16, B.1.617.2,						
			AY.46, AY.106,						
			AY.85, AY.98, AY.59,						
			AY.111, AY.75, AY.74, AY.35, AY.4.5,						
			AY.48, AY.93, AY.3.2,						
			AY.88, AY.20, AY.13, AY.26,						
			AY.133, AY.127.1,						
			AY.1, AY.4.8, AY.36,						
			AY.116.1, AY.121,						
			AY.5.3, AY.98.1,						
			AY.103.2, AY.76, AY.4.7,						
			AY.25.3, AY.4.2, AY.83,						
			AY.119.2, AY.10, AY.32,						
			AY.14, AY.54, AY.25.1,						
			AY.45, AY.46.6,						
			AY.23, AY.64, AY.108, AY.46.5,						
			AY.3.1, AY.94, AY.55, AY.51,						
			AY.3, AY.124, AY.117,						
			AY.24, AY.113,						
			AY.6, AY.120, AY.84, AY.72,						
			AY.128, AY.4.4,						
			AY.79, AY.65, AY.125,						
			AY.99.1, AY.4.2.1,						
			AY.42, AY.15, AY.101,						
			AY.44, AY.46.2, AY.122.1,						
			AY.131, AY.41,						
			AY.116, AY.22,						
			AY.129, AY.34,						
			AY.114, AY.39.1,						
			AY.4.3, AY.99, AY.4.6,						
			AY.40, AY.37, AY.118,						
			AY.126, AY.122,						
			AY.78, AY.119.1,						
			AY.4.2.3, AY.77, AY.29, AY.27, AY.39,						
			AY.3.3, AY.9.2.1,						
			AY.100, AY.5.4,						
			AY.61, AY.25, AY.62, AY.67,						
		Co	AY.102, on&&c68Us				│ CIDGOH [©]		
			AY.43.3, AY.43.						

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Depth Allele Allele F	Alternate Frequency MATTA, ATT
AY.103, AY.119, AY.109, AY.209, AY.22, AY.47, AY.43.4, AY.5, AY.42.4, AY.33, AY.4, AY.46, B.1.617.2, AY.46, AY.106, AY.85, AY.85, AY.98, AY.59, AY.111, AY.75, AY.74, AY.35, AY.48, AY.93, AY.3.2, AY.48, AY.93, AY.3.2, AY.88, AY.20, AY.13, AY.127,1, AY.13, AY.127,1, AY.1,	
AY.109, AY.28, AY.112, AY.47, AY.434, AY.5, AY.122.4, AY.33, AY.4, AY.16, B.1.617.2, AY.46, AY.106, AY.85, AY.98, AY.59, AY.111, AY.75, AY.74, AY.35, AY.4.5, AY.48, AY.93, AY.3.2, AY.48, AY.20, AY.13, AY.26, AY.133, AY.27.1, AY.1, AY.4, AY.3, AY.48, AY.3, AY.30, AY.116.1, AY.121, AY.121, AY.13, AY.20, AY.116.1, AY.121, AY.13, AY.103.2,	
AY.112, AY.43, AY.43, AY.43, AY.122.4, AY.33, AY.4, AY.16, B.1.617.2, AY.46, AY.106, AY.98, AY.98, AY.99, AY.111, AY.75, AY.74, AY.35, AY.45, AY.48, AY.93, AY.3.2, AY.48, AY.30, AY.31, AY.31, AY.31, AY.31, AY.32, AY.32, AY.33, AY.32, AY.33, AY.34, AY.35, AY.34, AY.35, AY.36, AY.37, AY.37, AY.37, AY.38, AY.39, AY.39, AY.39, AY.31, AY.48, AY.36, AY.116.1, AY.16.1, AY.16.1, AY.121, AY.53, AY.98.1, AY.90, AY.913, AY.901, A	
AY. 43.4, AY.5, AY.122.4, AY.33, AY.4, AY.16, B.1.617.2, AY.46, AY.106, AY.85, AY.98, AY.59, AY.111, AY.75, AY.45, AY.45, AY.45, AY.48, AY.93, AY.3.2, AY.88, AY.20, AY.13, AY.26, AY.133, AY.127.1, AY.1, AY.4.8, AY.36, AY.16.1, AY.116.1, AY.121, AY.121, AY.5.3, AY.98.1, AY.98.1, AY.98.1, AY.98.1, AY.98.1, AY.98.1,	
AY.33, AY.4, AY.16, B.1.617.2, AY.46, AY.106, AY.85, AY.98, AY.59, AY.111, AY.75, AY.74, AY.35, AY.4.5, AY.48, AY.93, AY.32, AY.32, AY.88, AY.20, AY.13, AY.26, AY.133, AY.127.1, AY.1, AY.4.8, AY.16.1, AY.16.1, AY.16.1, AY.103.2,	
AY.4, AY.16, B.1.617.2, AY.46, AY.46, AY.106, AY.85, AY.98, AY.59, AY.111, AY.75, AY.74, AY.35, AY.4.5, AY.93, AY.3.2, AY.88, AY.20, AY.13, AY.26, AY.133, AY.127.1, AY.1, AY.4.8, AY.36, AY.116.1, AY.116.1, AY.121, AY.5, AY.98.1, AY.98.1, AY.98.1, AY.103.2,	
AY.46, AY.106, AY.85, AY.98, AY.59, AY.111, AY.75, AY.44, AY.35, AY.4.5, AY.48, AY.93, AY.3.2, AY.88, AY.20, AY.13, AY.26, AY.133, AY.127.1, AY.1, AY.4.8, AY.36, AY.16.1, AY.16.1, AY.110.1, AY.121, AY.121, AY.121, AY.121, AY.121, AY.121, AY.121, AY.121, AY.121, AY.132, AY.133, AY.110.1	
AY.85, AY.98, AY.59, AY.111, AY.75, AY.74, AY.35, AY.4.5, AY.48, AY.93, AY.3.2, AY.88, AY.20, AY.13, AY.26, AY.133, AY.127.1, AY.1, AY.4.8, AY.36, AY.16.1, AY.16.1, AY.116.1, AY.121, AY.121, AY.121, AY.133, AY.14.8, AY.36,	
AY.111, AY.75, AY.74, AY.35, AY.4.5, AY.48, AY.93, AY.3.2, AY.88, AY.20, AY.13, AY.26, AY.133, AY.127.1, AY.1, AY.4.8, AY.36, AY.116.1, AY.121, AY.5.3, AY.98.1, AY.98.1, AY.903.2,	
AY.35, AY.4.5, AY.48, AY.93, AY.3.2, AY.88, AY.20, AY.13, AY.26, AY.133, AY.127.1, AY.1, AY.4.8, AY.36, AY.116.1, AY.16.1, AY.121, AY.5.3, AY.98.1, AY.98.1, AY.103.2,	
AY.3.2, AY.88, AY.20, AY.13, AY.26, AY.133, AY.127.1, AY.1, AY.4.8, AY.36, AY.116.1, AY.121, AY.5.3, AY.98.1, AY.98.1, AY.103.2,	
AY.13, AY.26, AY.133, AY.127.1, AY.1, AY.4.8, AY.36, AY.116.1, AY.121, AY.5.3, AY.98.1, AY.98.1, AY.103.2,	
AY.127.1, AY.1, AY.4.8, AY.36, AY.116.1, AY.121, AY.5.3, AY.98.1, AY.103.2,	
AY.36, AY.116.1, AY.121, AY.5.3, AY.98.1, AY.103.2,	
AY.121, AY.5.3, AY.98.1, AY.103.2,	
AY.98.1, AY.103.2,	
AY.76, AY.4.7, AY.25.3,	
AY.4.2, AY.83,	
AY.119.2, AY.10, AY.32, AY.11, AY.54	
AY.14, AY.54, AY.25.1,	
AY.45, AY.46.6,	
AY.23, AY.64, AY.108,	
AY.46.5, AY.3.1, AY.94,	
AY.55, AY.51, AY.3, AY.124,	
AY.117, AY.24,	
AY.113, AY.6, AY.120,	
AY.84, AY.72, AY.128,	
AY.4.4, AY.79, AY.65,	
AY.125, AY.99.1,	
AY.4.2.1, AY.42, AY.15,	
AY.101, AY.44,	
AY.46.2, AY.122.1,	
AY.131, AY.41,	
AY.116, AY.22,	
AY.129, AY.34,	
AY.114, AY.39.1,	
AY.4.3, AY.99, AY.4.6,	
AY.40, AY.37, AY.118,	
AY.126, AY.122, AY.122,	
AY.78, AY.119.1,	
AY.4.2.3, AY.77, AY.29,	
AY.27, AY.39, AY.3.3,	
AY.9.2.1, AY.100,	
AY.5.4, AY.61, AY.25,	
AY.62, AY.67, AY.102,	
Contacts Us CIDGOH O AY.43.3, AY.43.	1

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.S443F	monoclonal anti- body serial passage escape	Ranked effective escape variant in the RBD for highly neutralizing COV2- 2499 monoclonal antibody	AY.124, AY.124.1	Greaney et al. (2020)	7	С	Т	nan
p.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.	AY.5, AY.46, AY.37, AY.67, AY.4.2.3, AY.33, AY.27, AY.59, AY.9	Gong et al. (2021)	19383	GGA	TGG,GGG	nan
p.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.	AY.4.2.3	Gong et al. (2021)	3	GGA	TGG,GGG	nan
p.D614G	ACE2 receptor binding affinity	In four cell lines (including 293T-hACE2 cells), this mutation combination increases infectivity vs D614G alone	AY.5, AY.46, AY.37, AY.67, AY.4.2.3, AY.33, AY.27, AY.59, AY.9	Li et al. (2020)	19383	GGA	TGG,GGG	nan
p.D614G	convalescent plasma binding	2.15x increase in Spike binding (relative to D614G alone) by 5 plasma col- lected 8 months post- symptom-onset.	AY.5, AY.46, AY.37, AY.67, AY.4.2.3, AY.33, AY.27, AY.59, AY.9	Gong et al. (2021)	19383	GGA	TGG,GGG	nan
p.D614G	convalescent plasma binding	No change in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom- onset.	AY.4.2.3	Gong et al. (2021)	3	GGA	TGG,GGG	nan
p.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]	AY.5, AY.46, AY.37, AY.67, AY.4.2.3, AY.33, AY.27, AY.59, AY.9	Wilhelm et al. (2021)	19383	GGA	TGG,GGG	nan
p.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	AY.46, AY.37, AY.67, AY.4.2.3, AY.27, AY.59, AY.9	Brehm et al. (2021)	19118	GGA	TGG,GGG	nan
p.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.	AY.5, AY.46, AY.37, AY.67, AY.4.2.3, AY.33, AY.27, AY.59, AY.9	Landis et al. (2021)	19383	GGA	TGG,GGG	nan
p.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	AY.46, AY.37, AY.67, AY.4.2.3, AY.27, AY.59, AY.9	Brehm et al. (2021)	19118	GGA	TGG,GGG	nan
p.D614G	syncytium forma- tion	Slight increase in Vero cell- cell membrane fusion assay under infection with VSV pseudotyped virus.	AY.5, AY.46, AY.37, AY.67, AY.4.2.3, AY.33, AY.27, AY.59, AY.9	Kim et al. (2021)	19383	GGA	TGG,GGG	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.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 vacinee 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.	AY.5, AY.46, AY.37, AY.67, AY.4.2.3, AY.33, AY.27, AY.59, AY.9	Planas et al. (2021)	19383	GGA	TGG,GGG	nan
p.D614G	trafficking	Circulating variant shown in vitro to not have major defects or enhancement of cell surface protein traffick- ing (i.e. Spike cleavage or fusion required for cell en- try)	AY.5, AY.46, AY.37, AY.67, AY.4.2.3, AY.33, AY.27, AY.59, AY.9	Barrett et al. (2021)	19383	GGA	TGG,GGG	nan
p.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.	AY.5, AY.46, AY.37, AY.67, AY.4.2.3, AY.33, AY.27, AY.59, AY.9	Daniloski et al. (2021)	19383	GGA	TGG,GGG	nan
p.D614G	trafficking	No change in infectivity (24h) relative to D614G alone in Caco-2 cells, Vero or Calu-3.	AY.5, AY.46, AY.37, AY.67, AY.4.2.3, AY.33, AY.27, AY.59, AY.9	Kim et al. (2021)	19383	GGA	TGG,GGG	nan
p.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).	AY.5, AY.46, AY.37, AY.67, AY.4.2.3, AY.33, AY.27, AY.59, AY.9	Kim et al. (2021)	19383	GGA	TGG,GGG	nan
p.D614G	trafficking	Among S variants tested, the D614G mutant shows the highest cell entry (ex- tasciitilde3.5x wild type), as supported by structural and binding analyses.	AY.5, AY.46, AY.37, AY.67, AY.4.2.3, AY.33, AY.27, AY.59, AY.9	Ozono et al. (2020)	19383	GGA	TGG,GGG	nan
p.D614G	trafficking	Quantification of the band intensities showed that the P681R mutation, which lies near the proteolytic processing site, caused a small increase in proteolytic processing as measured by a 2-fold decrease in the ratio of S/S2.	AY.5, AY.46, AY.37, AY.67, AY.4.2.3, AY.33, AY.27, AY.59, AY.9	Tada et al. (2021)	19383	GGA	TGG,GGG	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.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.	AY.5, AY.46, AY.37, AY.67, AY.4.2.3, AY.33, AY.27, AY.59, AY.9	Zhang et l. (2020)	19383	GGA	TGG,GGG	nan
p.D614G	transmissibility	Increased infectivity of the B.1.617 spike was at- tributed 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]	AY.5, AY.46, AY.37, AY.67, AY.4.2.3, AY.33, AY.27, AY.59, AY.9	Tada et al. (2021)	19383	GGA	TGG,GGG	nan
p.D614G	vaccine neutraliza- tion 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.	AY.5, AY.46, AY.37, AY.67, AY.4.23, AY.33, AY.27, AY.59, AY.9	Garcia- Beltran et al. (2021)	19383	GGA	TGG,GGG	nan
p.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.	AY.5, AY.46, AY.37, AY.67, AY.4.2.3, AY.33, AY.27, AY.59, AY.9	Kuzmina et al. (2021)	19383	GGA	TGG,GGG	nan
p.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).	AY.5, AY.46, AY.37, AY.67, AY.4.2.3, AY.33, AY.27, AY.59, AY.9	Wilhelm et al. (2021)	19383	GGA	TGG,GGG	nan
p.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.	AY.5, AY.46, AY.37, AY.67, AY.4.2.3, AY.33, AY.27, AY.59, AY.9	Gong et al. (2021)	19383	GGA	TGG,GGG	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.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.	AY.4.2.3	Gong et al. (2021)	3	GGA	TGG,GGG	nan
p.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.	AY.5, AY.46, AY.37, AY.67, AY.4.2.3, AY.33, AY.27, AY.59, AY.9	Plante et al. (2020)	19383	GGA	TGG,GGG	nan
p.D614G	virion structure	Estimated free energy change (ddG) for this variant is 2.5 kcal/mol (i.e. stabilizing relative to wild type)	AY.5, AY.46, AY.37, AY.67, AY.4.2.3, AY.33, AY.27, AY.59, AY.9	Spratt et al. (2021)	19383	GGA	TGG,GGG	nan
p.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.	AY.5, AY.46, AY.37, AY.67, AY.4.2.3, AY.33, AY.27, AY.59, AY.9	Weissman et al. (2020)	19383	GGA	TGG,GGG	nan
p.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.	AY.5, AY.46, AY.37, AY.67, AY.4.2.3, AY.33, AY.27, AY.59, AY.9	Yurkovetskiy et al. (2020)	19383	GGA	TGG,GGG	nan
p.D614G	virion structure	Based on pseudotyped virus experiments, D614G may increase infectivity by assembling more func- tional S protein into the virion.	AY.5, AY.46, AY.37, AY.67, AY.4.2.3, AY.33, AY.27, AY.59, AY.9	Zhang et al. (2020)	19383	GGA	TGG,GGG	nan
p.D614G	ACE2 receptor binding affinity	This variant appears twice in the experiments, with slightly different affinities (both extasciitilde1.2x decrease in binding relative to D614G) using flow cytometry and ACE2 ectodomains-Fc portion IgG complex.	AY.77	Gong et al. (2021)	2	A	G	nan
p.D614G	ACE2 receptor binding affinity	Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant showed a 1.51x increase in binding (KD) relative to D614G, mostly due to decreased in "off-rate" a.k.a. dissociation rate (Kdis).	AY.77	Gong et al. (2021)	2	A	G	nan
p.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.	AY.1, AY.2	Gong et al. (2021)	12	A	G	nan

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p.D614G ACE2 seceptor bind- for granterity and large flowers in the la		Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
AY.100, AY.61, AY.25, AY.62, AY.102, AY.38,		ACE2 receptor bind-	Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant showed a 2.66x increase in binding (KD) relative to	AY.86, AY.34.1, AY.103, AY.119, AY.109, AY.28, AY.112, AY.47, AY.43.4, AY.122.4, AY.4, AY.16, B.1.617.2, AY.106, AY.85, AY.98, AY.111, AY.75, AY.48, AY.93, AY.4.5, AY.48, AY.93, AY.3.2, AY.88, AY.58, AY.20, AY.13, AY.127.1, AY.1, AY.1, AY.4.8, AY.120.2, AY.36, AY.116.1, AY.121, AY.5.3, AY.116.1, AY.103.2, AY.76, AY.44, AY.25.1, AY.45, AY.46.6, AY.23, AY.46.6, AY.23, AY.46.6, AY.23, AY.16.1, AY.117, AY.48, AY.108, AY.46.5, AY.416, AY.117, AY.49, AY.108, AY.46.6, AY.23, AY.14, AY.161, AY.117, AY.24, AY.113, AY.6, AY.120, AY.84, AY.120, AY.84, AY.121, AY.113, AY.41, AY.116, AY.117, AY.24, AY.113, AY.116, AY.117, AY.24, AY.113, AY.41, AY.116, AY.120, AY.84, AY.79, AY.84, AY.79, AY.84, AY.79, AY.84, AY.79, AY.84, AY.79, AY.128, AY.41, AY.116, AY.117, AY.41, AY.116, AY.129, AY.42, AY.131, AY.41, AY.116, AY.22, AY.129, AY.43, AY.75.2, AY.119, AY.41, AY.116, AY.22, AY.129, AY.34, AY.75.2, AY.119, AY.41, AY.116, AY.22, AY.129, AY.43, AY.40, AY.126, AY.121, AY.131, AY.41, AY.116, AY.22, AY.129, AY.43, AY.75.2, AY.119, AY.43, AY.99, AY.44, AY.126, AY.129, AY.39, AY.43, AY.75.2, AY.119, AY.41, AY.116, AY.22, AY.119, AY.43, AY.99, AY.44, AY.126, AY.129, AY.39, AY.43, AY.75.2, AY.119, AY.41, AY.116, AY.117, AY.41, AY.116, AY.22, AY.129, AY.31, AY.41, AY.116, AY.120, AY.41, AY.116, AY.121, AY.117, AY.41, AY.116, AY.120, AY.41, AY.4	Gong et al.	Depth	Allele	Allele	Frequency

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.D614G	ACE2 receptor binding affinity	Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant combination (representing lineage B.1.617) showed a 1.85x increase in binding (KD) relative to D614G. [exact variant list not provided in manuscript, is inferred fro common knowledge]	AY.35, AY.87	Gong et al. (2021)	9	A	G	nan
p.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.	AY.35, AY.4.4, AY.77, AY.53	Gong et al. (2021)	15	A	G	nan
p.D614G	ACE2 receptor binding affinity	Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant showed a 1.58x increase in binding (KD) relative to D614G.	AY.4.3, AY.3.2	Gong et al. (2021)	37	A	G	nan
p.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.	AY.127.1, AY.34.1, AY.34.1, AY.1.4, AY.1.5, AY.4.2.1, AY.42, AY.119, AY.36, AY.116.1, AY.100, AY.112, AY.109, AY.121, AY.43.4, AY.76, AY.4.7, AY.131, AY.4.2, AY.102, AY.116, AY.119.2, AY.119.2, AY.119.2, AY.119.3, AY.4.4, AY.114, AY.4.4, AY.4.4, AY.114, AY.34, AY.114, AY.34, AY.114, AY.34, AY.114, AY.39.1, AY.4.3, B.1.617.2, AY.4.6, AY.118, AY.118, AY.126, AY.106, AY.118, AY.110, AY.4.5, AY.108, AY.111, AY.104, AY.110, AY.4.5, AY.117, AY.120, AY.120, AY.120, AY.120, AY.120, AY.127, AY.120, AY.127, AY.120, AY.29, AY.120, AY.29, AY.120, AY.20, AY.120, AY.212, AY.120, AY.212, AY.120, AY.22, AY.120, AY.212, AY.120, AY.22, AY.120, AY.4.2.2	Gong et al. (2021)	7800	A	G	nan

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Mutations Sub-category Function	Lineages	Citation	Sequence Depth		Alternate Allele	Alternate Frequency
p.D614G ACE2 receptor bind- In four ce	Il lines (including AY.86, EE2 cells), this AY.34.1, combination AY.103, infectivity vs AY.119,	Li et a (2020)	Sequence Depth 1. 80971	Allele A	Allele G	nan

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Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.D614G	convalescent plasma binding	1.42x increase in Spike binding (relative to D614G alone) by 5 plasma col- lected 8 months post- symptom-onset.	AY.77	Gong et al. (2021)	2	A	G	nan
p.D614G	convalescent plasma binding	1.33x increase in Spike binding (relative to D614G alone) by 5 plasma col- lected 8 months post- symptom-onset.	AY.77	Gong et al. (2021)	2	A	G	nan
p.D614G	convalescent plasma binding	2.16x increase in Spike binding (relative to D614G alone) by 5 plasma col- lected 8 months post- symptom-onset.	AY.1, AY.2	Gong et al. (2021)	12	A	G	nan

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Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
Mutations p.D614G	Sub-category convalescent plasma binding	Function 2.15x increase in Spike binding (relative to D614G alone) by 5 plasma collected 8 months postsymptom-onset.	AY.86, AY.34.1, AY.103, AY.119, AY.109, AY.28, AY.112, AY.47, AY.43.4, AY.122.4, AY.4, AY.16, B.1.617.2, AY.106, AY.85, AY.84, AY.19, AY.35, AY.45, AY.48, AY.93, AY.32, AY.48, AY.19, AY.11, AY.75, AY.48, AY.93, AY.32, AY.48, AY.93, AY.120.2, AY.13, AY.16.1, AY.116.1, AY.121, AY.53, AY.42, AY.103.2, AY.64, AY.103.2, AY.64, AY.103.2, AY.64, AY.103.2, AY.64, AY.103.2, AY.65, AY.414, AY.55, AY.45, AY.46.6, AY.23, AY.46.6, AY.23, AY.46.6, AY.23, AY.46.7, AY.45, AY.46.8, AY.46.8, AY.46.8, AY.46.8, AY.4113, AY.6, AY.117, AY.44, AY.108, AY.4113, AY.6, AY.120, AY.84, AY.117, AY.41, AY.117, AY.44, AY.108, AY.42, AY.113, AY.6, AY.120, AY.84, AY.113, AY.6, AY.120, AY.84, AY.114, AY.117, AY.44, AY.117, AY.44, AY.117, AY.44, AY.79, AY.65, AY.120, AY.84, AY.79, AY.121, AY.41, AY.43, AY.75.2, AY.114, AY.43, AY.75.2, AY.118, AY.41, A	Citation Gong et al. (2021)	Sequence Depth 80971	Reference Allele A	Alternate Allele G	Alternate Frequency nan
		Ce	AY.4.3, AY.99, AY.4.6, AY.40,				CIDGOH [©]	

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.D614G	convalescent plasma binding	This variant combination (representing lineage B.1.617) showed a 1.22x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 8 months postsymptom-onset. [exact variant list not provided in manuscript, is inferred fro common knowledge]	AY.35, AY.87	Gong et al. (2021)	9	A	G	nan
p.D614G	convalescent plasma binding	No change in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom- onset.	AY.35, AY.4.4, AY.77, AY.53	Gong et al. (2021)	15	A	G	nan
p.D614G	convalescent plasma binding	1.08x decrease in Spike binding (relative to D614G alone) by 5 plasma col- lected 8 months post- symptom-onset.	AY.4.3, AY.3.2	Gong et al. (2021)	37	A	G	nan
p.D614G	convalescent plasma binding	No change in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptomonset.	AY.127.1, AY.34.1, AY.34.1, AY.1, AY.4.8, AY.125, AY.4.2.1, AY.42, AY.119, AY.36, AY.116.1, AY.101, AY.100, AY.112, AY.109, AY.121, AY.43.4, AY.76, AY.4.7, AY.131, AY.4.2, AY.102, AY.116, AY.119.2, AY.119.2, AY.119.3, AY.121.1, AY.4.4, AY.4.4, AY.4.4, AY.4.5, AY.107, AY.124.1, AY.34, AY.114, AY.39.1, AY.4.3, B.1.617.2, AY.4.6, AY.118, AY.126, AY.118, AY.126, AY.110, AY.4.5, AY.106, AY.111, AY.104, AY.110, AY.4.5, AY.110, AY.4.5, AY.110, AY.4.5, AY.111, AY.104, AY.117, AY.92, AY.119.1, AY.113, AY.77, AY.120, AY.29, AY.20, AY.20, AY.20, AY.20, AY.2128, AY.127, AY.120, AY.20, AY.20, AY.20, AY.20, AY.218, AY.127, AY.120, AY.22, AY.128, AY.127, AY.120, AY.29, AY.128, AY.127, AY.120, AY.29, AY.20, AY.39, AY.128, AY.127, AY.120, AY.29, AY.20, AY.39, AY.128, AY.127, AY.120, AY.4.2.2	Gong et al. (2021)	7800	A	G	nan

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Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.D614G	convalescent plasma escape	Pseudotyped viruses for B.1.618 was 2.5-fold resistant to neutralization by convalescent sera compared to wild type - a finding that was similar to that of the 3-fold resistance of the South Africa B.1.351 variant using the same assay. The resistance of B.1.618 was caused by the E484K mutation, based on results from viruses pseudotyped for individual variants within B.1.618. [details on the convalescent patient sera collection are not abundantly clear in the preprint]	AY.77	Tada et al. (2021)	2	A	G	nan
p.D614G	convalescent plasma escape	Pseudotyped viruses for B.1.617 was 2.3-fold resistant to neutralization by convalescent sera compared to wild type - a finding that was similar to that of the 3-fold resistance of the South Africa B.1.351 variant using the same assay. The resistance of B.1.617 was caused by the L452R and E484Q mutation, based on results from viruses pseudotyped for individual variants within B.1.617. [details on the convalescent patient sera collection are not abundantly clear in the preprint]	AY.35, AY.87	Tada et al. (2021)	9	A	G	nan

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Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
Mutations p.D614G	Sub-category 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]	AY.86, AY.34.1, AY.103, AY.119, AY.109, AY.28, AY.112, AY.47, AY.43.4, AY.122.4, AY.4, AY.16, B.1.617.2, AY.106, AY.85, AY.98, AY.111, AY.75, AY.43, AY.19, AY.35, AY.4.5, AY.48, AY.93, AY.3.2, AY.88, AY.58, AY.133, AY.127.1, AY.1, AY.1, AY.1, AY.1, AY.103.2, AY.161, AY.103.2, AY.103.2, AY.103.2, AY.14, AY.25.3, AY.119.1, AY.53, AY.119.2, AY.10, AY.25.3, AY.119.1, AY.54, AY.25.1, AY.45, AY.46.6, AY.23, AY.14, AY.55, AY.46.6, AY.23, AY.14, AY.55, AY.46.6, AY.23, AY.113, AY.6, AY.117, AY.24, AY.113, AY.16.1, AY.117, AY.24, AY.113, AY.16, AY.120, AY.84, AY.120, AY.84, AY.121, AY.45, AY.46.6, AY.23, AY.41, AY.108, AY.46.7, AY.46.8, AY.46.9, AY.113, AY.117, AY.24, AY.113, AY.116, AY.117, AY.24, AY.113, AY.116, AY.120, AY.84, AY.79, AY.65, AY.120, AY.84, AY.79, AY.121, AY.121, AY.131, AY.141, AY.116, AY.120, AY.42, AY.118, AY.121, AY.43, AY.75, AY.129, AY.44, AY.46.2, AY.49, AY.129, AY.41, AY.116, AY.120, AY.41, AY.116, AY.120, AY.41, AY.116, AY.121, AY.121, AY.131, AY.41, AY.116, AY.120, AY.43, AY.75, AY.120, AY.44, AY.45, AY.120, AY.41, AY.120, AY.41, AY.121, AY.131, AY.41, AY.116, AY.120, AY.42, AY.120, AY.43, AY.75, AY.120, AY.44, AY.45, AY.120, AY.41, AY.120, AY.41, AY.120, AY.42, AY.131, AY.41, AY.116, AY.120, AY.43, AY.72, AY.120, AY.44, AY.45, AY.120, AY.41, AY.120, AY.41, AY.120, AY.42, AY.131, AY.41, AY.116, AY.120, AY.43, AY.72, AY.120, AY.44, AY.40, AY.120, AY.41, AY.120, AY.41, AY.120, AY.41, AY.120, AY.41, AY.120, AY.41, AY.120, AY.41, AY.41, AY.120, AY.42, AY.120, AY.43, AY.72, AY.120, AY.43, AY.73, AY.43, AY	Citation Wilhelm et al. (2021)	Sequence Depth 80971	Reference Allele A	Alternate Allele G	Alternate Frequency nan
			AY.126, AY.122, AY.78, AY.92, AY.119.1, AY.2, AY.77,				CIDGOH [©]	

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Mutations	Sub-category	Function	Lineages	Citation	Sequence	Reference Allele	Alternate Allele	Alternate
D.1116	,		177.05		Depth			Frequency
p.D614G	humoral response	27yo female nurse rein-	AY.65,	Brehm et al.	12124	A	G	nan
	durability	fected in December 2020	AY.4.2.1,	(2021)				
		(B.1.177) after initial infec-	AY.61, AY.28,					
		tion in March 2020 (B.3),	AY.47, AY.62,					
		i.e. with a 9 month inter-	AY.4.2,					
		val. Both cases were mild.	AY.38, AY.10,					
		No significant differences	AY.75.2,					
		in the neutralizing capac-	AY.14, AY.57,					
		ity of the two linages were	B.1.617.2,					
		observed in 4 sera taken	AY.60,					
		(1 pre-reinfection, three	AY.4.2.2,					
		post-reinfection). Neu-	AY.64, AY.75,					
		tralizing antibody titres	AY.74, AY.71,					
		(IC50) before and imme-	AY.55, AY.73,					
		diately after re-infection	AY.9.2, AY.2,					
		were <300 against both	AY.119.1,					
		strains, and jumped >7x	AY.24, AY.70,					
		upon re-infection. Viral	AY.68, AY.56,					
		titres were also higher in	AY.72, AY.26,					
		the second case. Sec-	AY.133,					
		ond case also includes	AY.9.2.1					
		N:p.A220V						[

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AY.6, AY.120, AY.84, AY.72, AY.128, AY.44, AY.79, AY.65, AY.99.1, AY.42, AY.15, AY.101, AY.42, AY.44, AY.46, AY.44, AY.46, AY.44, AY.46, AY.41, AY.42, AY.44, AY.45, AY.44, AY.45, AY.46, AY.40, AY.41, AY.43, AY.46, AY.40, AY.41, AY.40, AY.41, AY.40, AY.41, AY.40, AY.41, AY.40, AY.41, AY.41, AY.42, AY.77, AY.29, AY.39, AY.33, AY.92, AY.39, AY.33, AY.92, AY.39, AY.33, AY.92, AY.46, AY.100, AY.61, AY.61, AY.62, AY.102, AY.62, AY.62, AY.62, AY.102,

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Mutations	Sub-category	Function	Lineages	Citation	Sequence	Reference	Alternate	Alternate
					Depth	Allele	Allele	Frequency
p.D614G	reinfection	27yo female nurse rein-	AY.65,	Brehm et al.	12124	A	G	nan
		fected in December 2020	AY.4.2.1,	(2021)				
		(B.1.177) after initial infec-	AY.61, AY.28,					
		tion in March 2020 (B.3).	AY.47, AY.62,					
		Both cases were mild. Sec-	AY.4.2,					
		ond case also includes	AY.38, AY.10,					
		N:p.A220V	AY.75.2,					
			AY.14, AY.57,					
			B.1.617.2,					
			AY.60,					
			AY.4.2.2,					
			AY.64, AY.75,					
			AY.74, AY.71,					
			AY.55, AY.73,					
			AY.9.2, AY.2,					
			AY.119.1,					
			AY.24, AY.70,					
			AY.68, AY.56,					
			AY.72, AY.26,					
			AY.133,					
			AY.9.2.1					

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Mutations Sub-category Function Lineages	Citation Sequence Reference Alternate Alternate Depth Allele Allele Frequency
p.D614G syncytium formation with five cell membrane fusion assay under infection with VSV pseudotyped virus. Slight increase in Vero cellcell membrane fusion assay Ay.34.1 (Ay.19, Ay.19, Ay.28, Ay.112, Ay.47, Ay.43.4 (Ay.47, Ay.43.4 (Ay.43.4 (Ay.43.	Name

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.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 vacinee 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.	AY.86, AY.34.1, AY.103, AY.119, AY.109, AY.28, AY.112, AY.47, AY.43.4, AY.122.4, AY.4, AY.16, B.1.617.2, AY.106, AY.85, AY.98, AY.111, AY.75, AY.48, AY.93, AY.32, AY.48, AY.93, AY.120.2, AY.13, AY.121, AY.1, AY.14, AY.121, AY.15, AY.161, AY.121, AY.53, AY.98.1, AY.103.2, AY.76, AY.47, AY.25.3, AY.42, AY.83, AY.119.2, AY.10, AY.25.1, AY.45, AY.46.6, AY.23, AY.46.6, AY.23, AY.64, AY.108, AY.65, AY.113, AY.66, AY.121, AY.13, AY.67, AY.14, AY.15, AY.46.1, AY.117, AY.24, AY.108, AY.46.1, AY.117, AY.24, AY.113, AY.6, AY.120, AY.84, AY.120, AY.84, AY.121, AY.45, AY.46.5, AY.47, AY.25.1, AY.46.1, AY.117, AY.24, AY.113, AY.61, AY.116, AY.121, AY.121, AY.131, AY.14, AY.161, AY.116, AY.120, AY.84, AY.79, AY.65, AY.121, AY.14, AY.161, AY.116, AY.120, AY.84, AY.75, AY.101, AY.44, AY.79, AY.65, AY.118, AY.116, AY.120, AY.84, AY.75, AY.114, AY.116, AY.120, AY.43, AY.75.2, AY.114, AY.116, AY.22, AY.131, AY.41, AY.116, AY.22, AY.131, AY.43, AY.75.2, AY.119, AY.43, AY.75, AY.33, AY.33, AY.32, AY.33, AY.33, AY.33, AY.33, AY.33, AY.34, AY.75.2, AY.134, AY.75, AY.62, AY.73, AY.33, AY.	Planas et al. (2021)		Allele		

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Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.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.	AY.86, AY.34.1, AY.103, AY.119, AY.109, AY.28, AY.112, AY.47, AY.43.4, AY.122.4, AY.4, AY.16, B.1.617.2, AY.106, AY.85, AY.98, AY.111, AY.75, AY.45, AY.49, AY.19, AY.35, AY.4.5, AY.48, AY.93, AY.32, AY.88, AY.58, AY.20, AY.13, AY.127.1, AY.1, AY.1, AY.1, AY.1, AY.16.1, AY.121, AY.5.3, AY.121, AY.5.3, AY.42, AY.103.2, AY.16.1, AY.119, AY.5.3, AY.45, AY.103.2, AY.16, AY.117, AY.25.3, AY.42, AY.18, AY.108, AY.46.6, AY.23, AY.14, AY.55, AY.31, AY.45, AY.46.1, AY.117, AY.45, AY.46.1, AY.117, AY.45, AY.46.1, AY.117, AY.47, AY.48, AY.120, AY.48, AY.120, AY.49, AY.118, AY.41, AY.116, AY.21, AY.41, AY.116, AY.24, AY.113, AY.42, AY.118, AY.44, AY.79, AY.65, AY.125, AY.118, AY.41, AY.116, AY.22, AY.114, AY.41, AY.116, AY.22, AY.114, AY.41, AY.116, AY.22, AY.114, AY.41, AY.116, AY.22, AY.118, AY.42, AY.118, AY.120, AY.43, AY.42, AY.118, AY.120, AY.44, AY.121, AY.41, AY.116, AY.22, AY.118, AY.42, AY.119, AY.43, AY.43, AY.40, AY.118, AY.126, AY.129, AY.34, AY.43, AY.40, AY.118, AY.120, AY.41, AY.41, AY.41, AY.41, AY.41, AY.42, AY.114, AY.43, AY.42, AY.114, AY.43, AY.45, AY.43, AY.45, AY.43, AY.40, AY.118, AY.120, AY.43, AY.43, AY.43, AY.44, AY.46, AY.118, AY.116, AY.22, AY.119, AY.43, AY	Daniloski et al. (2021)	Depth 80971	Allele	CIDGOH ©	nan

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Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
Mutations p.D614G	Sub-category trafficking	Function No change in infectivity (24h) relative to D614G alone in Caco-2 cells, Vero or Calu-3.	AY.86, AY.34.1, AY.103, AY.119, AY.109, AY.28, AY.112, AY.47, AY.43.4, AY.122.4, AY.4, AY.16, B.1.617.2, AY.106, AY.85, AY.98, AY.111, AY.75, AY.45, AY.45, AY.45, AY.45, AY.48, AY.93, AY.32, AY.88, AY.58, AY.133, AY.127.1, AY.1,	Kim et al. (2021)	Sequence Depth 80971	Reference Allele A	Alternate Allele G	Alternate Frequency nan
			AY.108, AY.46.5, AY.3.1, AY.94, AY.55, AY.51, AY.3, AY.124, AY.16.1, AY.117, AY.24, AY.113, AY.6, AY.120, AY.84, AY.72, AY.128,					
			AY.41, AY.116, AY.22, AY.129, AY.34, AY.75.2, AY.114, AY.39.1, AY.4.3, AY.99, AY.4.6, AY.40, AY.118, AY.126, AY.122, AY.122, AY.178, AY.92, AY.119.1, AY.2, AY.77, AY.29, AY.33, AY.9.2.1, AY.100, AY.61, AY.25, AY.62, AY.102, AY.102, AY.102, AY.102, AY.38,					

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Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
Mutations p.D614G	Trafficking Trafficking	Function 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).	AY.86, AY.34.1, AY.103, AY.119, AY.109, AY.28, AY.112, AY.47, AY.43.4, AY.122.4, AY.4, AY.106, B1.617.2, AY.106, AY.85, AY.98, AY.111, AY.75, AY.48, AY.93, AY.32, AY.48, AY.93, AY.32, AY.48, AY.19, AY.13, AY.26, AY.133, AY.127.1, AY.1, AY.1, AY.1, AY.1, AY.1, AY.16.1, AY.121, AY.16.1, AY.121, AY.53, AY.98.1, AY.103.2, AY.76, AY.47, AY.25.3, AY.48, AY.48, AY.19, AY.10, AY.44, AY.55, AY.45, AY.116.1, AY.117, AY.45, AY.46.6, AY.23, AY.14, AY.55, AY.113, AY.65, AY.113, AY.65, AY.113, AY.67, AY.124, AY.108, AY.46.5, AY.113, AY.41, AY.116, AY.124, AY.117, AY.24, AY.117, AY.24, AY.113, AY.6, AY.120, AY.84, AY.75, AY.124, AY.113, AY.6, AY.120, AY.84, AY.75, AY.113, AY.41, AY.116, AY.22, AY.114, AY.116, AY.21, AY.42, AY.113, AY.41, AY.42, AY.128, AY.43, AY.75, AY.129, AY.43, AY.44, AY.75, AY.114, AY.41, AY.116, AY.22, AY.118, AY.126, AY.129, AY.43, AY.41, AY.42, AY.43, AY.75, AY.101, AY.43, AY.44, AY.75, AY.101, AY.45, AY.118, AY.126, AY.129, AY.49, AY.129, AY.34, AY.75, AY.131, AY.41, AY.116, AY.22, AY.118, AY.126, AY.129, AY.34, AY.75, AY.131, AY.41,	Kim et al. (2021)	Sequence Depth 80971	Reference Allele A	Alternate Allele G	Alternate Frequency nan
		Co	AY.38, on t 3∕c#3/3s AY.43,				CIDGOH [©]	

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Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.D614G	trafficking	extasciitilde2x more infectivity than D614G alone in HEK293T-ACE2 cells 48h post-transduction.	AY.77	Kuzmina et al. (2021)	2	A	G	nan
p.D614G	trafficking	extasciitilde2x more infectivity than D614G alone in HEK293T-ACE2 cells 48h post-transduction.	AY.1, AY.2	Kuzmina et al. (2021)	12	A	G	nan

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Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
Mutations p.D614G	Sub-category trafficking	Function Among S variants tested, the D614G mutant shows the highest cell entry (extasciitide3.5x wild type), as supported by structural and binding analyses.	Lineages AY.86, AY.34.1, AY.103, AY.119, AY.109, AY.28, AY.112, AY.47, AY.43.4, AY.122.4, AY.4, AY.16, B.1.617.2, AY.106, AY.85, AY.711, AY.75, AY.74, AY.19, AY.35, AY.45, AY.48, AY.93, AY.3.2, AY.88, AY.58, AY.58, AY.20, AY.13, AY.127.1, AY.1, AY.1, AY.1, AY.1, AY.1, AY.1, AY.121, AY.16.1, AY.121, AY.16.1, AY.121, AY.53, AY.98.1, AY.103.2, AY.76, AY.47, AY.25.3, AY.42, AY.83, AY.119.2, AY.10, AY.32, AY.14, AY.55, AY.46.6, AY.23, AY.14, AY.55, AY.113, AY.46.5, AY.31, AY.94, AY.55, AY.117, AY.24, AY.108, AY.46.5, AY.117, AY.24, AY.117, AY.41, AY.116, AY.126, AY.129, AY.41, AY.42, AY.43, AY.44, AY.75, AY.114, AY.41, AY.42, AY.43, AY.75, AY.101, AY.44, AY.46, AY.49, AY.120, AY.41, A	Ozono et al. (2020)	Sequence Depth 80971	Reference Allele A	Alternate Allele G	Alternate Frequency nan
		Co	AY.38, on t 3∕c#3/3s AY.43,				CIDGOH [©]	

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Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.D614G	trafficking	Quantification of the band intensities showed that the P681R mutation, which lies near the proteolytic processing site, caused a small increase in proteolytic processing as measured by a 2-fold decrease in the ratio of S/S2.	AY.86, AY.34.1, AY.103, AY.119, AY.109, AY.28, AY.112, AY.47, AY.43.4, AY.122.4, AY.4, AY.16, B.1.617.2, AY.106, AY.85, AY.98, AY.111, AY.75, AY.45, AY.48, AY.93, AY.45, AY.48, AY.20, AY.13, AY.26, AY.13, AY.127.1, AY.1, AY.4, AY.1, AY.4, AY.100.2, AY.36, AY.116.1, AY.121, AY.5.3, AY.42, AY.18, AY.103.2, AY.76, AY.42, AY.83, AY.119.2, AY.16, AY.117, AY.45, AY.46.6, AY.23, AY.46, AY.25.1, AY.46.6, AY.23, AY.46.6, AY.23, AY.66, AY.117, AY.45, AY.46.7, AY.46.8, AY.108, AY.46.8, AY.4108, AY.46.8, AY.4108, AY.46.9, AY.117, AY.24, AY.101, AY.117, AY.24, AY.113, AY.6, AY.120, AY.84, AY.79, AY.65, AY.117, AY.24, AY.113, AY.6, AY.120, AY.84, AY.79, AY.65, AY.113, AY.14, AY.16.1, AY.117, AY.24, AY.113, AY.42, AY.113, AY.42, AY.13, AY.42, AY.131, AY.42, AY.14, AY.79, AY.46, AY.120, AY.84, AY.79, AY.42, AY.113, AY.41, AY.116, AY.126, AY.129, AY.42, AY.119, AY.42, AY.119, AY.43, AY.75.2, AY.114, AY.41, AY.42, AY.43, AY.75.2, AY.1114, AY.41, AY.41, AY.41, AY.42, AY.43, AY.75.2, AY.1114, AY.41, AY.42, AY.43, AY.75.2, AY.119, AY.43, AY.75.2, AY.119, AY.44, AY.75.2, AY.119, AY.43, AY.75.2, AY.114, AY.40, AY.118, AY.126, AY.43, AY.75.2, AY.114, AY.43, AY.75.2, AY.13, AY.42, AY.13, AY.42, AY.13, AY.42, AY.13, AY.42, AY.13, AY.43, AY.75.2, AY.14, AY.43, AY.75.2, AY.14, AY.44, AY.75, AY.44, AY.75, AY.44, AY.75, AY.44, AY.75, AY.44, AY.75, AY.44, AY.75, A	Tada et al. (2021)	Depth 80971	Allele	CIDGOH ©	nan

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Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.D614G	trafficking	We report here pseudoviruses carrying SG614 enter ACE2-expressing cells more efficiently than wild type (extasciitide9-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.	AY.86, AY.34.1, AY.103, AY.119, AY.109, AY.28, AY.112, AY.47, AY.43.4, AY.122.4, AY.4, AY.16, B.1.617.2, AY.106, AY.85, AY.98, AY.111, AY.75, AY.45, AY.49, AY.45, AY.49, AY.45, AY.48, AY.93, AY.32, AY.88, AY.58, AY.20, AY.13, AY.127.1, AY.1, AY.4, AY.120.2, AY.36, AY.116.1, AY.121, AY.5.3, AY.98.1, AY.103.2, AY.6, AY.119.2, AY.10, AY.84, AY.25.1, AY.45, AY.46.6, AY.23, AY.14, AY.55, AY.46, AY.108, AY.46.6, AY.23, AY.117, AY.16, AY.121, AY.16, AY.124, AY.161, AY.117, AY.46, AY.124, AY.161, AY.116, AY.124, AY.161, AY.116, AY.124, AY.161, AY.116, AY.125, AY.118, AY.42, AY.126, AY.43, AY.44, AY.79, AY.65, AY.126, AY.116, AY.121, AY.116, AY.121, AY.116, AY.124, AY.113, AY.161, AY.116, AY.129, AY.42, AY.118, AY.120, AY.44, AY.121, AY.41, AY.116, AY.120, AY.42, AY.131, AY.116, AY.120, AY.43, AY.41, AY.116, AY.120, AY.44, AY.15, AY.116, AY.120, AY.45, AY.118, AY.116, AY.120, AY.41, AY.116, AY.22, AY.118, AY.116, AY.120, AY.43, AY.43, AY.43, AY.43, AY.43, AY.40, AY.118, AY.118, AY.116, AY.120, AY.41, AY.116, AY.121, AY.41, AY.116, AY.121, AY.43, AY.43, AY.43, AY.43, AY.43, AY.44, AY.75, AY.38, AY.43, AY.43, AY.39, AY.38, AY.38, AY.38, AY.38, AY.43, AY.38, AY.38, AY.43, AY.38, AY.43, AY.43, AY.43, AY.43, AY.44, AY.46, AY.118, AY.118, AY.126, AY.131, AY.116, AY.121, AY.131, AY.116, AY.121, AY.131, AY.116, AY.121, AY.131, AY.116, AY.22, AY.134, AY.75, AY.34, AY.75, AY.36, AY.34, AY.75, AY.36, AY.37, AY.37, AY.37, AY.37, AY.37, AY.37	Zhang et 1. (2020)	Depth 80971	A	CIDGOH ©	nan

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Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.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]	AY. 86, AY. 34.1, AY. 103, AY. 119, AY. 109, AY. 28, AY. 112, AY. 47, AY. 43.4, AY. 122.4, AY. 4, AY. 106, AY. 85, AY. 111, AY. 75, AY. 48, AY. 19, AY. 35, AY. 48, AY. 19, AY. 26, AY. 13, AY. 26, AY. 13, AY. 121, AY. 16, AY. 16, AY. 16, AY. 16, AY. 17, AY. 18, AY. 19, AY. 103, AY. 120, AY. 13, AY. 121, AY. 16, AY. 121, AY. 121, AY. 121, AY. 25.3, AY. 42, AY. 18, AY. 19.2, AY. 10, AY. 46, AY. 19, AY. 46, AY. 108, AY. 46.5, AY. 31, AY. 46.7, AY. 108, AY. 46.8, AY. 48, AY. 108, AY. 46.8, AY. 108, AY. 46.9, AY. 113, AY. 6, AY. 120, AY. 18, AY. 121, AY. 117, AY. 24, AY. 113, AY. 161, AY. 117, AY. 24, AY. 118, AY. 126, AY. 127, AY. 127, AY. 128, AY. 144, AY. 146, AY. 129, AY. 141, AY. 141, AY. 116, AY. 129, AY. 141, AY. 118, AY. 120, AY. 43, AY. 120, AY. 44, AY. 120, AY. 44, AY. 120, AY. 45, AY. 120, AY. 46, AY. 113, AY. 47, AY. 120, AY. 48, AY. 120, AY. 49, AY. 1121, AY. 41, AY. 42, AY. 113, AY. 43, AY. 120, AY. 44, AY. 45, AY. 120, AY. 46, AY. 120, AY. 47, AY. 120, AY. 48, AY. 120, AY. 49, AY. 120, AY. 40, AY. 113, AY. 41, AY. 116, AY. 22, AY. 119, AY. 41, AY. 116, AY. 22, AY. 119, AY. 43, AY. 99, AY. 44, AY. 19, AY. 45, AY. 19, AY. 46, AY. 119, AY. 41, AY. 116, AY. 22, AY. 119, AY. 43, AY. 19, AY. 46, AY. 119, AY. 41, AY. 116, AY. 22, AY. 119, AY. 43, AY. 39, AY. 48, AY. 59, AY. 49, AY. 119, AY. 40, AY. 118, AY. 40, AY. 118, AY. 40, AY. 119, AY. 40, AY. 110, AY. 40, AY. 110, AY. 40, AY. 11	Tada et al. (2021)	Depth 80971	Allele	CIDGOH ©	requency

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Mutations	Sub-category	Function	Lineages	Citation	Sequence	Reference	Alternate	Alternate
					Depth	Allele	Allele	Frequency
p.D614G	transmissibility	The combination caused a	AY.35, AY.87	Tada et al.	9	A	G	nan
		3-fold increase in infectiv-		(2021)				
		ity relative to D614G wild		,				
		type. [compare to 3.5x for						
		L452R alone]						
p.D614G	transmissibility	Normalized for particle	AY.35, AY.87	Tada et al.	9	A	G	nan
		number, on ACE2.293T		(2021)				
		cells showed that the		,				
		B.1.617 spike protein was						
		>2-fold increase in infectiv-						
		ity relative to D614G wild						
		type.						

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Mutations Sub-category Function Linea	ages Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
D.D614G vaccine neutralization efficacy activity swild type: 1.2x Ay.3 Ay.4 Ay.	6, 4.1, 03, 19, 09, 8, 19, 09, 8, 12, 7, 3.4, 22.4, , AY.16, i17.2, 06, 5, AY.98, 11, 5, AY.74, 9, AY.35, .5, 8, AY.93, 2, AY.88, 8, AY.20, 3, AY.26, 33, 27.1, , AY.4.8, 20.2, 6, 16.1, 221, .3, 8.1, 03.2, 6, AY.4.7, 5.3, .2, AY.83, 19.2, 0, AY.32, 4, AY.54, 5.1, 5, 6.6, 6.6, 3, AY.64, 08, 6.5, .1, AY.94, 5, AY.124, 6.1, 17, 4, 13, , AY.15, 01, 4, 6.2, 29, 4, 5, 25, 9.1, .2.1, 2.2, AY.15, 01, 4, 6.2, 29, 4, 5, AY.94, 1, 16, 2, 29, 4, 5, AY.95, 3, 2, 1, 00, 1, 5, 5, 2, 14, 9, 1, 3, AY.99, .3, 1, 10, 10, 10, 10, 10, 10, 10, 10, 10,	Depth 80971	Allele	CIDGOH ©	nan Alternate Frequency nan

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Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.D614G	vaccine neutralization efficacy	1.4x reduction in neutralization (ID50) in sera 3 weeks after one dose of Pfizer/BioNTech BNT162b2 (up to 5 naive and post infection vaccinees)	AY.35, AY.87	Gong et al. (2021)	9	A	G	nan

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Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.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 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.	AY.86, AY.34.1, AY.103, AY.119, AY.109, AY.28, AY.112, AY.47, AY.43.4, AY.122.4, AY.4, AY.16, B.1.617.2, AY.106, AY.85, AY.98, AY.111, AY.75, AY.45, AY.48, AY.93, AY.32, AY.88, AY.93, AY.32, AY.88, AY.133, AY.127.1, AY.1, AY.121, AY.121, AY.121, AY.121, AY.53, AY.98.1, AY.103.2, AY.76, AY.48, AY.19.2, AY.10, AY.32, AY.19.4, AY.54, AY.19.2, AY.10, AY.32, AY.14, AY.54, AY.19.3, AY.113, AY.42, AY.14, AY.55, AY.128, AY.46.6, AY.23, AY.124, AY.113, AY.6, AY.124, AY.113, AY.124, AY.113, AY.16.1, AY.117, AY.24, AY.113, AY.41, AY.116, AY.125, AY.42, AY.118, AY.42, AY.128, AY.44, AY.79, AY.42, AY.118, AY.41, AY.116, AY.22, AY.114, AY.116, AY.22, AY.114, AY.116, AY.22, AY.118, AY.41, AY.116, AY.22, AY.118, AY.42, AY.19, AY.43, AY.99, AY.46, AY.190, AY.41, AY.116, AY.22, AY.118, AY.42, AY.43, AY.75.2, AY.114, AY.116, AY.22, AY.118, AY.41, AY.116, AY.22, AY.131, AY.41, AY.116, AY.22, AY.131, AY.41, AY.116, AY.22, AY.131, AY.41, AY.116, AY.23, AY.42, AY.43, AY.75.2, AY.114, AY.116, AY.21, AY.41, AY.116, AY.22, AY.131, AY.41, AY.116, AY.23, AY.42, AY.43, AY.75.2, AY.114, AY.39, AY.42, AY.40, A	Kuzmina et al. (2021)		Allele		

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Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.D614G	vaccine neutraliza- tion efficacy	This variant showed only minor in Pfizer sera (one or two dose) neutralization efficiency vs D614G (using lentivirus pseudotype).	AY.77	Kuzmina et al. (2021)	2	A	G	nan
p.D614G	vaccine neutraliza- tion efficacy	This variant showed only minor in Pfizer sera (one or two dose) neutralization efficiency vs D614G (using lentivirus pseudotype).	AY.1, AY.2	Kuzmina et al. (2021)	12	A	G	nan
p.D614G	vaccine neutralization efficacy	Pseudotyped viruses for B.1.618 was 2.7-fold resistant to neutralization by 6 BNT162b2 vaccine sera 28 days post-booster compared to wild type - a finding that was similar to that of the 3.4-fold resistance of the South Africa B.1.351 variant using the same assay. Neutralization by 3 Moderna vaccine sera 28 days post-booster was 3-fold resistant (vs. 2.2-fold for B.1.351). The resistance of B.1.618 was caused by the E484K mutation, based on results from viruses pseudotyped for individual variants within B.1.618.	AY.77	Tada et al. (2021)	2	A	G	nan
p.D614G	vaccine neutralization efficacy	Pseudotyped viruses for B.1.617 was 4-fold resistant to neutralization by 6 BNT162b2 vaccine sera 28 days post-booster compared to wild type - a finding that was similar to that of the 3.4-fold resistance of the South Africa B.1.351 variant using the same assay. Neutralization by 3 Moderna vaccine sera 28 days post-booster was 5-fold resistant (vs. 2.2-fold for B.1.351). The resistance of B.1.617 was caused by the L452R and E484Q mutation, based on results from viruses pseudotyped for individual variants within B.1.617.	AY.35, AY.87	Tada et al. (2021)	9	A	G	nan

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AY.100, AY.61, AY.25, AY.62,

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Mutations	Sub-category		Function	Lineages	Citation	Sequence	Reference	Alternate	Alternate
						Depth	Allele	Allele	Frequency
p.D614G	vaccinee p	lasma	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. 1.06x 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.	AY.77	Gong et al. (2021)	2	A	G	nan
p.D614G	vaccinee p binding	lasma	1.14x 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.	AY.77	Gong et al. (2021)	2	A	G	nan
p.D614G	vaccinee p binding	lasma	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.	AY.1, AY.2	Gong et al. (2021)	12	A	G	nan

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Mutations	Sub-category		Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.D614G	vaccinee binding pla	asma	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.	AY.86, AY.34.1, AY.103, AY.119, AY.109, AY.28, AY.112, AY.47, AY.43.4, AY.122.4, AY.4, AY.106, B.1.617.2, AY.106, AY.85, AY.98, AY.111, AY.75, AY.48, AY.99, AY.4.5, AY.48, AY.93, AY.3.2, AY.88, AY.58, AY.20, AY.13, AY.26, AY.133, AY.127.1, AY.1, AY.4.8, AY.120.2, AY.36, AY.116.1, AY.121, AY.5.3, AY.42, AY.83, AY.19.2, AY.103.2, AY.6, AY.119.2, AY.10, AY.25.3, AY.42, AY.36, AY.119.2, AY.10, AY.45, AY.46.6, AY.23, AY.46.7, AY.25.1, AY.46.8, AY.46.8, AY.46.9, AY.113, AY.6, AY.113, AY.6, AY.120, AY.113, AY.6, AY.108, AY.45, AY.46.5, AY.31, AY.45, AY.46.5, AY.31, AY.41, AY.116, AY.117, AY.24, AY.113, AY.6, AY.125, AY.113, AY.6, AY.126, AY.127, AY.128, AY.44, AY.79, AY.65, AY.127, AY.128, AY.44, AY.79, AY.121, AY.41, AY.116, AY.116, AY.117, AY.42, AY.118, AY.41, AY.116, AY.126, AY.127, AY.129, AY.41, AY.42, AY.131, AY.41, AY.43, AY.99, AY.44, AY.75, AY.194, AY.1126, AY.127, AY.128, AY.418, AY.429, AY.438, AY.440, AY.126, AY.127, AY.438, AY.440, AY.126, AY.127, AY.438, AY.440, AY.126, AY.129, AY.438, AY.438, AY.438, AY.438, AY.438, AY.448, AY.75, AY.458, AY.458, AY.468, AY.477, AY.29, AY.318, AY.418, AY.419, AY.419	Gong et al. (2021)	Depth 80971	A	CIDGOH ©	nan

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Mutations	Sub-catego	ry	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.D614G	vaccinee binding	plasma	This variant combination (representing lineage B.1.617) showed a 1.30x 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. 1.18x 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. [exact variant list not provided in manuscript, is inferred fro common knowledge]	AY.35, AY.87	Gong et al. (2021)	9	A	G	nan
p.D614G	vaccinee binding	plasma	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.	AY.35, AY.4.4, AY.77, AY.53	Gong et al. (2021)	15	A	G	nan
p.D614G	vaccinee binding	plasma	1.23x 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. 1.37x 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.	AY.4.3, AY.3.2	Gong et al. (2021)	37	A	G	nan

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Mutations	Sub-categor	ry	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.D614G	vaccinee binding	plasma	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.	AY.127.1, AY.34.1, AY.34.1, AY.4.8, AY.125, AY.4.2.1, AY.40, AY.119, AY.36, AY.116.1, AY.100, AY.112, AY.109, AY.121, AY.43.4, AY.6, AY.131, AY.4.2, AY.102, AY.116, AY.119.2, AY.119.2, AY.120, AY.121.1, AY.4.4, AY.4.4, AY.4.5, AY.107, AY.124.1, AY.4.6, AY.118, AY.126, AY.118, AY.126, AY.118, AY.126, AY.118, AY.118, AY.118, AY.126, AY.110, AY.4.5, AY.106, AY.111, AY.4.4, AY.110, AY.4.5, AY.111, AY.104, AY.110, AY.4.5, AY.111, AY.124, AY.117, AY.124, AY.117, AY.124, AY.117, AY.124, AY.117, AY.124, AY.117, AY.124, AY.117, AY.120, AY.29, AY.120, AY.29, AY.127, AY.120, AY.29, AY.120, AY.4.2.2	Gong et al. (2021)	7800	A	G	nan

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Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.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.	AY.86, AY.34.1, AY.103, AY.119, AY.109, AY.28, AY.112, AY.47, AY.43.4, AY.122.4, AY.4, AY.16, B.1.617.2, AY.106, AY.85, AY.98, AY.111, AY.75, AY.45, AY.49, AY.45, AY.49, AY.19, AY.26, AY.133, AY.26, AY.133, AY.127.1, AY.1, AY.48, AY.120.2, AY.36, AY.116.1, AY.121, AY.5.3, AY.98.1, AY.103.2, AY.6, AY.119.2, AY.10, AY.25.3, AY.42, AY.10, AY.45, AY.45, AY.410, AY.45, AY.46.6, AY.23, AY.46.6, AY.23, AY.14, AY.55, AY.46.7, AY.45, AY.46.8, AY.46.8, AY.46.8, AY.46.8, AY.46.9, AY.113, AY.6, AY.124, AY.117, AY.24, AY.113, AY.6, AY.120, AY.84, AY.120, AY.84, AY.121, AY.45, AY.46.8, AY.46.9, AY.118, AY.117, AY.41, AY.116, AY.22, AY.118, AY.41, AY.116, AY.22, AY.118, AY.42, AY.118, AY.43, AY.120, AY.44, AY.45, AY.118, AY.121, AY.41, AY.116, AY.22, AY.114, AY.41, AY.116, AY.22, AY.114, AY.41, AY.116, AY.22, AY.118, AY.120, AY.43, AY.42, AY.119, AY.44, AY.45, AY.118, AY.126, AY.129, AY.34, AY.75.2, AY.1114, AY.41, AY.416, AY.21, AY.42, AY.119, AY.43, AY.42, AY.119, AY.44, AY.45, AY.119, AY.45, AY.119, AY.46, AY.120, AY.47, AY.49, AY.118, AY.120, AY.41, AY.41, AY.116, AY.22, AY.119, AY.43, AY.92, AY.119, AY.43, AY.92, AY.119, AY.43, AY.92, AY.119, AY.43, AY.93, AY.43, AY.93, AY.	Plante et al. (2020)	Depth 80971	Allele	CIDGOH ©	requency

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p.D644G virion structure Estimated free energy AV.85, Spratt et al. 80971 A G nam change (delfo for this without in 2.5 learlymol [1.6, AV.85, AV.81, AV.10.] AV.10. AV.10	Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
AY.22, AY.129, AY.34, AY.75.2, AY.114, AY.39.1, AY.4.3, AY.99, AY.4.6, AY.40, AY.118, AY.126, AY.122, AY.122, AY.78, AY.92, AY.19.1, AY.2, AY.77, AY.29, AY.39, AY.3,3,			Estimated free energy change (ddG) for this variant is 2.5 kcal/mol (i.e. stabilizing relative to wild	AY.86, AY.34.1, AY.103, AY.119, AY.109, AY.28, AY.112, AY.47, AY.43.4, AY.122.4, AY.4, AY.16, B.1.617.2, AY.106, AY.85, AY.98, AY.111, AY.75, AY.44, AY.19, AY.35, AY.4.5, AY.48, AY.93, AY.3.2, AY.88, AY.58, AY.20, AY.13, AY.127.1, AY.1, AY.1, AY.16, AY.116.1, AY.121, AY.5.3, AY.116.1, AY.111, AY.55, AY.48, AY.103.2, AY.6, AY.119.2, AY.10, AY.25.3, AY.42, AY.10, AY.25.1, AY.45, AY.46.6, AY.23, AY.46.6, AY.23, AY.124, AY.108, AY.46.6, AY.23, AY.124, AY.108, AY.46.6, AY.23, AY.116, AY.117, AY.24, AY.108, AY.46.6, AY.23, AY.124, AY.108, AY.46.6, AY.23, AY.124, AY.113, AY.6, AY.124, AY.113, AY.117, AY.24, AY.113, AY.114, AY.115, AY.116, AY.117, AY.44, AY.79, AY.42, AY.129, AY.42, AY.131, AY.41, AY.116, AY.120, AY.44, AY.79, AY.42, AY.129, AY.41, AY.116, AY.120, AY.44, AY.79, AY.42, AY.118, AY.41, AY.116, AY.129, AY.43, AY.41, AY.116, AY.22, AY.119, AY.41, AY.116, AY.21, AY.41, AY.116, AY.21, AY.41, AY.116, AY.22, AY.129, AY.34, AY.75.2, AY.119, AY.43, AY.40, AY.118, AY.126, AY.129, AY.34, AY.75.2, AY.119, AY.41, AY.116, AY.21, AY.41, AY.116, AY.22, AY.119, AY.43, AY.40, AY.126, AY.129, AY.34, AY.75.2, AY.119, AY.43, AY.40, AY.118, AY.126, AY.129, AY.39, AY.44, AY.43, AY.99, AY.45, AY.75, AY.19, AY.47, AY.29, AY.39, AY.47, AY.29, AY.39, AY.47, AY.29, AY.39, AY.39, AY.49, AY.39, AY.49, AY.19, AY.40, AY.118, AY.119, AY.41, AY	Spratt et al.	Depth	Allele	Allele	Frequency

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Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.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.	AY.86, AY.34.1, AY.103, AY.119, AY.109, AY.28, AY.112, AY.47, AY.43.4, AY.16, B.1.617.2, AY.106, AY.85, AY.98, AY.111, AY.75, AY.45, AY.45, AY.48, AY.93, AY.32, AY.88, AY.58, AY.20, AY.13, AY.26, AY.133, AY.127.1, AY.1, AY.4, AY.120.2, AY.36, AY.116.1, AY.121, AY.53, AY.98.1, AY.103.2, AY.76, AY.48, AY.98.1, AY.103.2, AY.76, AY.47, AY.55, AY.46, AY.25, AY.46, AY.25, AY.46, AY.23, AY.46, AY.23, AY.46, AY.23, AY.16, AY.117, AY.24, AY.108, AY.46.5, AY.31, AY.47, AY.48, AY.49, AY.49, AY.40, AY.40, AY.40, AY.41, AY.117, AY.24, AY.108, AY.42, AY.44, AY.108, AY.42, AY.44, AY.108, AY.45, AY.126, AY.127, AY.41, AY.117, AY.24, AY.113, AY.41, AY.116, AY.120, AY.44, AY.79, AY.42, AY.49, AY.128, AY.44, AY.79, AY.42, AY.118, AY.41, AY.116, AY.22, AY.118, AY.41, AY.116, AY.22, AY.118, AY.41, AY.116, AY.22, AY.114, AY.116, AY.22, AY.118, AY.41, AY.116, AY.22, AY.114, AY.116, AY.22, AY.118, AY.41, AY.116, AY.22, AY.118, AY.41, AY.116, AY.22, AY.114, AY.116, AY.22, AY.118, AY.41, AY.116, AY.22, AY.119, AY.42, AY.118, AY.41, AY.116, AY.22, AY.119, AY.43, AY.99, AY.46, AY.120, AY.41, AY.116, AY.22, AY.119, AY.42, AY.118, AY.116, AY.22, AY.119, AY.43, AY.99, AY.46, AY.190, AY.41, AY.116, AY.22, AY.119, AY.42, AY.118, AY.116, AY.22, AY.119, AY.43, AY.75.2, AY.114, AY.116, AY.21, AY.41, AY.116, AY.22, AY.119, AY.43, AY.75.2, AY.114, AY.116, AY.22, AY.119, AY.43, AY.75.2, AY.114, AY.116, AY.210, AY.410, AY.	Yurkovetskiy et al. (2020)	Bopth 80971	Allele	CIDGOH ©	requency

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	Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
COL ANY MOTE AND ANY MARKET AND AND ANY MARKET AND AND ANY MARKET AND	p.D614G		Based on pseudotyped virus experiments, D614G may increase infectivity by assembling more functional S protein into the virion.	AY.86, AY.34.1, AY.103, AY.119, AY.109, AY.28, AY.112, AY.47, AY.43.4, AY.122.4, AY.4, AY.16, B.1.617.2, AY.106, AY.85, AY.98, AY.111, AY.75, AY.45, AY.49, AY.45, AY.49, AY.19, AY.40, AY.113, AY.26, AY.133, AY.127.1, AY.1, AY.48, AY.120.2, AY.36, AY.116.1, AY.121, AY.5.3, AY.98.1, AY.103.2, AY.6, AY.113, AY.6, AY.14, AY.53, AY.45, AY.46, AY.19.2, AY.10, AY.45, AY.46, AY.113, AY.46, AY.108, AY.46.5, AY.113, AY.6, AY.117, AY.24, AY.113, AY.6, AY.121, AY.17, AY.24, AY.113, AY.6, AY.124, AY.117, AY.44, AY.108, AY.46.5, AY.113, AY.6, AY.120, AY.84, AY.121, AY.117, AY.44, AY.108, AY.45, AY.113, AY.6, AY.120, AY.84, AY.121, AY.117, AY.24, AY.113, AY.6, AY.120, AY.84, AY.79, AY.65, AY.121, AY.113, AY.6, AY.120, AY.84, AY.79, AY.124, AY.116, AY.125, AY.116, AY.126, AY.127, AY.128, AY.41, AY.116, AY.22, AY.114, AY.39.1, AY.41,	Zhang et al.	Depth	Allele	G G	Frequency

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	ction Lineages		Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.L452R ACE2 receptor binding affinity ACH tion ant	ng flow cytometry and AY.86, E2 ectodomains-Fc por-LigG complex, this varishowed a 2.66x increase inding (KD) relative to AY.109,	Gong et al. (2021) Gong e	Sequence Depth 100341			

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Mutations	Sub-category	Function	Lineages	Citation	Sequence	Reference	Alternate	Alternate
					Depth	Allele	Allele	Frequency
p.L452R	ACE2 receptor bind-	Using flow cytometry and	AY.35, AY.87	Gong et al.	9	T	G	nan
	ing affinity	ACE2 ectodomains-Fc por-		(2021)				
		tion IgG complex, this						
		variant combination (rep-						
		resenting lineage B.1.617)						
		showed a 1.85x increase						
		in binding (KD) relative						
		to D614G. [exact vari-						
		ant list not provided in						
		manuscript, is inferred fro						
		common knowledge						

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Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
Mutations p.L452R	ACE2 receptor binding affinity	Function extasciitilde1.7-fold increase in binding affinity vs wild type.	AY.86, AY.34.1, AY.103, AY.119, AY.109, AY.28, AY.112, AY.47, AY.43.4, AY.12.4, AY.33, AY.4, AY.106, AY.85, AY.98, AY.111, AY.75, AY.74, AY.35, AY.44, AY.19, AY.35, AY.45, AY.48, AY.20, AY.13, AY.26, AY.13, AY.27, AY.16.1, AY.16.1, AY.111, AY.53, AY.48, AY.103.2, AY.66, AY.116.1, AY.111, AY.53, AY.45, AY.46.6, AY.119, AY.53, AY.47, AY.25.3, AY.48, AY.103.2, AY.66, AY.119.2, AY.10, AY.55, AY.45, AY.46, AY.25.1, AY.45, AY.46, AY.25.1, AY.45, AY.46, AY.25, AY.113, AY.54, AY.108, AY.46, AY.108, AY.47, AY.108, AY.46, AY.111, AY.117, AY.44, AY.117, AY.44, AY.113, AY.6, AY.120, AY.44, AY.113, AY.6, AY.120, AY.45, AY.46, AY.210, AY.45, AY.46, AY.210, AY.41, AY.117, AY.42, AY.113, AY.6, AY.120, AY.44, AY.113, AY.6, AY.120, AY.44, AY.117, AY.44, AY.117, AY.44, AY.113, AY.6, AY.120, AY.44, AY.113, AY.6, AY.121, AY.113, AY.6, AY.121, AY.113, AY.116, AY.41, AY.116, AY.22,	Motozono et al. (2021)	Sequence Depth 100353	Reference Allele T	Alternate Allele G	Alternate Frequency nan
			AY.113, AY.6, AY.120, AY.84, AY.72, AY.128, AY.4.4, AY.79, AY.65, AY.125, AY.99.1, AY.4.2.1, AY.4.2, AY.15, AY.101, AY.44, AY.46.2, AY.49, AY.122.1, AY.131, AY.41, AY.116, AY.22, AY.129, AY.129, AY.34,					
		Co	AY.75.2, AY.114, AY.39.1, AY.4.3, AY.99, AY.4.6, AY.126, AY.122, AY.78, AY.92, AY.119.1, AY.2, AY.4.2.3, AY.77, AY.29, AY.3.3, AY.3.3, AY.77, AY.39, AY.3.4, AY.100, AY.5.4,				CIDGOН [©]	

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Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
Mutations p.L452R	T cell evasion	Function 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).	AY.86, AY.34.1, AY.103, AY.119, AY.109, AY.28, AY.112, AY.47, AY.43.4, AY.16, B.1.617.2, AY.46, AY.106, AY.85, AY.98, AY.74, AY.19, AY.75, AY.74, AY.19, AY.33, AY.4.5, AY.111, AY.75, AY.44, AY.19, AY.35, AY.48, AY.93, AY.32, AY.48, AY.20, AY.13, AY.21, AY.14, AY.10, AY.13, AY.16, AY.116, AY.121, AY.14, AY.15, AY.16, AY.120.2, AY.16, AY.116, AY.121, AY.16, AY.121, AY.16, AY.121, AY.18, AY.120.2, AY.16, AY.1108, AY.1108, AY.1108, AY.1108, AY.1108, AY.1108, AY.1108, AY.108, AY.108, AY.46.6, AY.31, AY.108, AY.46.5, AY.31, AY.94, AY.55, AY.46.5, AY.31, AY.108, AY.46.5, AY.31, AY.104, AY.55, AY.46.6, AY.31, AY.108, AY.46.5, AY.31, AY.104, AY.55, AY.31, AY.104, AY.55, AY.31, AY.104, AY.55, AY.31, AY.104, AY.108, AY.46.5, AY.31, AY.104, AY.108, AY.46.5, AY.31, AY.104, AY.108, AY.46.5, AY.31, AY.124, AY.16.1,	Motozono et al. (2021)	Sequence Depth 100353	Reference Allele T	Alternate Allele G	Alternate Frequency nan
			AY.3.1, AY.94, AY.55, AY.51, AY.3, AY.124,					
			AY.101, AY.44, AY.46.2, AY.49, AY.122.1, AY.131, AY.116, AY.22, AY.129, AY.34, AY.75.2, AY.114,					
			AY.39.1, AY.4.3, AY.99, AY.4.6, AY.40, AY.37, AY.118, AY.126, AY.122, AY.78, AY.92, AY.119.1, AY.2, AY.4.2.3, AY.77, AY.29, AY.27, AY.39, AY.3.3, DIAMOS US,				¢idgoh [©]	

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Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.L452R	Sub-category antibody epitope effects	Resistent to some neutralizing antibodies: mAbs X593 and P2B-2F6	AY.86, AY.34.1, AY.103, AY.119, AY.109, AY.28, AY.112, AY.47, AY.43.4, AY.16, B.1.617.2, AY.46, AY.106, AY.85, AY.98, AY.111, AY.75, AY.74, AY.19, AY.35, AY.4.5, AY.48, AY.93, AY.3.2, AY.88, AY.58, AY.98, AY.111, AY.1, AY.	Li et al (2020)	Depth	Reference Allele T	Alternate Allele G	Alternate Frequency nan
		Co	AY.78, AY.92, AY.119.1, AY.2, AY.4.2.3, AY.77, AY.29, AY.27, AY.39, AY.3.3, AY.3.4				ÇIDGOH [©]	

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p.L452R					Depth	l Allele	1 Allele	Frequency
p.12-4021v	antibody epitope effects	Mutant screen in neutralization assay with a broad range of monoclonal antibodies shows resistence to more than one antibody.	AY.86, AY.86, AY.34.1, AY.103, AY.119, AY.109, AY.28, AY.112, AY.47, AY.43.4, AY.5, AY.122.4, AY.33, AY.4, AY.106, AY.85, AY.98, AY.111, AY.75, AY.47, AY.19, AY.35, AY.48, AY.93, AY.32, AY.88, AY.98, AY.19, AY.106, AY.11, AY.75, AY.48, AY.93, AY.31, AY.45, AY.48, AY.93, AY.32, AY.88, AY.58, AY.20, AY.13, AY.120.2, AY.13, AY.121, AY.1, AY.4.8, AY.121, AY.5.3, AY.42, AY.16.1, AY.121, AY.5.3, AY.42, AY.83, AY.119.2, AY.10, AY.45, AY.46, AY.25.3, AY.45, AY.46, AY.25.1, AY.45, AY.46, AY.23, AY.47, AY.25.1, AY.45, AY.46, AY.108, AY.46.5, AY.31, AY.94, AY.55, AY.51, AY.31, AY.94, AY.55, AY.117, AY.44, AY.108, AY.42, AY.113, AY.6, AY.120, AY.84, AY.121, AY.117, AY.44, AY.117, AY.44, AY.117, AY.44, AY.117, AY.41, AY.117, AY.42, AY.113, AY.6, AY.120, AY.44, AY.79, AY.65, AY.121, AY.113, AY.6, AY.120, AY.44, AY.79, AY.65, AY.114, AY.116, AY.21, AY.41, AY.116, AY.22, AY.114, AY.116, AY.21, AY.42, AY.118, AY.118, AY.118, AY.118, AY.119, AY.43, AY.49, AY.40, AY.41, AY	Liu et al (2021)	Depth 100353	Allele T	Allele G	requency
			AY.27, AY.39, AY.3.3,					

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ects effects	extasciitilde20% (ELISA significance threshold) drop in antibody binding (ELISA) by this variant against monoclonal antibody VH ab6.	AY.86, AY.34.1, AY.103, AY.119, AY.109, AY.28, AY.112, AY.47, AY.43.4, AY.5, AY.122.4, AY.33, AY.4, AY.16, B.1.617.2, AY.46, AY.106, AY.85, AY.98, AY.59, AY.111, AY.75, AY.74, AY.19, AY.35,	Sun et al. (2021)	Depth 100353	Allele T	Allele G	Frequency
		AY.4.5, AY.48, AY.93, AY.48, AY.93, AY.3.2, AY.88, AY.58, AY.20, AY.13, AY.26, AY.133, AY.127.1, AY.1, AY.4.8, AY.120.2, AY.36, AY.116.1, AY.121, AY.5.3, AY.98.1, AY.103.2, AY.76, AY.4.7, AY.25.3, AY.4.2, AY.83, AY.119.2, AY.10, AY.54, AY.25.1, AY.45, AY.46.6, AY.23, AY.64, AY.108, AY.46.5, AY.31, AY.94, AY.55, AY.51, AY.113, AY.6, AY.124, AY.117, AY.24, AY.113, AY.6, AY.120, AY.84, AY.72, AY.128, AY.4.4, AY.79, AY.65, AY.128, AY.4.4, AY.79, AY.65, AY.125, AY.113, AY.41, AY.116, AY.41, AY.116, AY.42, AY.116, AY.41, AY.116, AY.41, AY.116, AY.42, AY.118, AY.41, AY.116, AY.42, AY.118, AY.41, AY.116, AY.42, AY.118, AY.120, AY.43, AY.41, AY.116, AY.42, AY.118, AY.120, AY.43, AY.41, AY.116, AY.42, AY.118, AY.120, AY.41, AY.118, AY.121, AY.41, AY.118, AY.122, AY.418, AY.124, AY.418, AY.126, AY.49, AY.127, AY.418, AY.127, AY.427, AY.439, AY.477, AY.478, AY.478, AY.478, AY.477, AY.478, AY.488, AY.478, AY.478, AY.478, AY.478, AY.478, AY.478, AY.478, AY.4					
	Co	AY.3.3, ontact Us, AY.100,			1	CIDGOH [©]	

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Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
Mutations p.L452R	convalescent plasma binding	Function 2.15x increase in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset.	AY.86, AY.34.1, AY.103, AY.119, AY.109, AY.28, AY.112, AY.47, AY.43.4, AY.5, AY.122.4, AY.33, AY.4, AY.106, AY.85, AY.98, AY.71, AY.45, AY.45, AY.45, AY.48, AY.20, AY.13, AY.26, AY.113, AY.16, AY.106, AY.13, AY.13, AY.21, AY.14, AY.13, AY.14, AY.15, AY.45, AY.14, AY.15, AY.46, AY.113, AY.16, AY.116, AY.116, AY.119, AY.45, AY.46, AY.119, AY.45, AY.46, AY.119, AY.47, AY.25, AY.48, AY.49, AY.119, AY.41, AY.48, AY.49, AY.119, AY.41, AY.41, AY.118, AY.46, AY.108, AY.46, AY.113, AY.46, AY.113, AY.46, AY.113, AY.46, AY.113, AY.41, AY.113, AY.41, AY.114, AY.115, AY.42, AY.113, AY.46, AY.42, AY.113, AY.41, AY.114, AY.115, AY.41, AY.115, AY.41, AY.116, AY.42, AY.43, AY.44, AY.46, AY.49, AY.42, AY.41, AY	Gong et al. (2021)	Sequence Depth 100341	Reference Allele T	Alternate Allele G	Alternate Frequency nan
		Co	AY.116, AY.22, AY.129,				CIDGOH [©]	

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Mutations	Sub-category	Function	Lineages	Citation	Sequence	Reference	Alternate	Alternate
					Depth	Allele	Allele	Frequency
p.L452R	convalescent plasma	This variant combina-	AY.35, AY.87	Gong et al.	9	T	G	nan
	binding	tion (representing lineage		(2021)				
		B.1.617) showed a 1.22x						
		decrease in Spike bind-						
		ing (relative to D614G						
		alone) by 5 plasma col-						
		lected 8 months post-						
		symptom-onset. [exact						
		variant list not provided in						
		manuscript, is inferred fro						
		common knowledge						

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Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
Mutations p.L452R	Sub-category convalescent plasma escape	Function Observed extasciitilde2x decrease on average in 16 health workers' convalescent sera.	AY.86, AY.34.1, AY.103, AY.119, AY.109, AY.28, AY.112, AY.47, AY.43.4, AY.16, B.1.617.2, AY.46, AY.106, AY.85, AY.98, AY.59, AY.111, AY.75, AY.74, AY.19, AY.35, AY.4.5, AY.48, AY.93, AY.4.5, AY.48, AY.93, AY.3.2, AY.88, AY.58, AY.98, AY.59, AY.111, AY.53, AY.410, AY.101, AY.101	Alenquer et al. (2021)	Sequence Depth 100353	Reference Allele T	Alternate Allele G	Alternate Frequency nan
		Ce	AY.34, AY.75.2,				CIDGOH [©]	

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D-Li-Million of San of Land Million of San of Land Million (1997) and Million of San of Land Million (1997) and Million of San of Land Million (1997) and Million (19	Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
AY.77, AY.29, AY.27, AY.39,		convalescent plasma	Ablation of neutralization capability of 3 of 4 convalescent sera tested, the other is significantly hin-	AY.86, AY.34.1, AY.103, AY.119, AY.109, AY.28, AY.112, AY.47, AY.43.4, AY.33, AY.4, AY.16, B.1.617.2, AY.46, AY.106, AY.85, AY.98, AY.711, AY.75, AY.44, AY.19, AY.35, AY.44, AY.19, AY.35, AY.45, AY.48, AY.20, AY.13, AY.26, AY.13, AY.127.1, AY.1, AY.48, AY.120.2, AY.36, AY.116.1, AY.121, AY.53, AY.42, AY.83, AY.19.2, AY.14, AY.25.3, AY.42, AY.19, AY.45, AY.46, AY.119, AY.55, AY.46, AY.119, AY.55, AY.47, AY.25, AY.48, AY.19, AY.10, AY.31, AY.11, AY.117, AY.25, AY.46, AY.108, AY.46, AY.108, AY.46, AY.108, AY.46, AY.113, AY.66, AY.120, AY.84, AY.113, AY.61, AY.117, AY.24, AY.113, AY.61, AY.117, AY.24, AY.113, AY.63, AY.125, AY.121, AY.41, AY.116, AY.127, AY.128, AY.129, AY.129, AY.111, AY.41, AY.116, AY.22, AY.111, AY.41, AY.116, AY.22, AY.113, AY.41, AY.116, AY.22, AY.113, AY.41, AY.116, AY.22, AY.114, AY.116, AY.22, AY.113, AY.41, AY.116, AY.22, AY.114, AY.116, AY.21, AY.41, AY.116, AY.22, AY.114, AY.116, AY.21, AY.41, AY.116, AY.22, AY.118, AY.126, AY.127, AY.131, AY.41, AY.116, AY.22, AY.118, AY.129, AY.131, AY.41, AY.116, AY.22, AY.119, AY.43, AY.99, AY.4.6, AY.118, AY.129, AY.119, AY.43, AY.99, AY.4.71, AY.41, AY.116, AY.21, AY.41, AY.116, AY.22, AY.119, AY.41, AY.116, AY.21, AY.41, AY.116, AY.22, AY.119, AY.43, AY.44, AY.75, AY.114, AY.116, AY.217, AY.418, AY.129, AY.114, AY.116, AY.217, AY.418, AY.129, AY.419,	Liu et al.	Depth	Allele	Allele	Frequency
Cident of the control			Co	AY.27, AY.39, AY.3.3,				CIDGOH [©]	

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Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.L452R	convalescent plasma escape	Pseudotyped viruses for B.1.617 was 2.3-fold resistant to neutralization by convalescent sera compared to wild type - a finding that was similar to that of the 3-fold resistance of the South Africa B.1.351 variant using the same assay. The resistance of B.1.617 was caused by the L452R and E484Q mutation, based on results from viruses pseudotyped for individual variants within B.1.617. [details on the convalescent patient sera collection are not abundantly clear in the preprint]	AY.35, AY.87	Tada et al. (2021)	9	T	G	nan

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Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
Mutations p.L452R	Sub-category 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]	AY.86, AY.34.1, AY.103, AY.119, AY.109, AY.28, AY.112, AY.47, AY.43.4, AY.33, AY.4, AY.16, B.1.617.2, AY.46, AY.106, AY.85, AY.98, AY.59, AY.111, AY.75, AY.44, AY.19, AY.35, AY.45, AY.48, AY.93, AY.3.2, AY.88, AY.58, AY.98, AY.133, AY.127.1, AY.1, AY.1	Citation Wilhelm et al. (2021)	Sequence Depth 100341	Reference Allele T	Alternate Allele G	Alternate Frequency nan
		Co	AY.39.1, AY.4.3,				CIDGOH [©]	

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Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
Mutations p.L452R	Sub-category gene expression in- crease	Experimentally, Spike gene expression increased 0.32 fold	AY.86, AY.34.1, AY.103, AY.119, AY.109, AY.28, AY.112, AY.47, AY.43.4, AY.5, AY.122.4, AY.33, AY.4, AY.106, B.1.617.2, AY.46, AY.106, AY.85, AY.98, AY.59, AY.111, AY.75, AY.44, AY.19, AY.35, AY.48, AY.93, AY.3.2, AY.48, AY.20, AY.13, AY.26, AY.133, AY.127.1, AY.1, AY.14, AY.10, AY.121, AY.121, AY.121, AY.121, AY.121, AY.121, AY.121, AY.121, AY.13, AY.46, AY.116, AY.25.3, AY.46, AY.116, AY.25.1, AY.46, AY.116, AY.23, AY.46, AY.108, AY.46.5, AY.31, AY.65, AY.31, AY.65, AY.113, AY.66, AY.124, AY.113, AY.67, AY.125, AY.113, AY.67, AY.121, AY.117, AY.117, AY.117, AY.117, AY.117, AY.117, AY.118, AY.119, AY.1113, AY.66, AY.120, AY.84, AY.121, AY.113, AY.67, AY.121, AY.113, AY.68, AY.124, AY.113, AY.69, AY.125, AY.116, AY.21, AY.117, AY.117, AY.117, AY.118, AY.118, AY.119, AY.119, AY.111, AY.116, AY.21, AY.111, AY.116, AY.22, AY.114, AY.116, AY.22, AY.114, AY.116, AY.22, AY.114, AY.116, AY.22, AY.114, AY.116, AY.22, AY.131, AY.41, AY.116, AY.29, AY.43, AY.99, AY.4.6,	Citation Starr et al. (2020)	Sequence Depth 100353	Reference Allele T	Alternate Allele G	Alternate Frequency nan
		Co	AY.4.3,				CIDGOH [©]	

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Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.L452R	monoclonal antibody serial passage escape	Function Ranked effective mutant against this position in the RBD for highly neutralizing COV2-2096	AY.86, AY.34.1, AY.103, AY.119, AY.109, AY.28, AY.112, AY.47, AY.43.4, AY.16, B.1.617.2, AY.46, AY.106, AY.85, AY.98, AY.59, AY.111, AY.75, AY.74, AY.19, AY.35, AY.4.5, AY.48, AY.93, AY.3.2, AY.88, AY.58, AY.98, AY.59, AY.111, AY.75, AY.48, AY.93, AY.32, AY.88, AY.58, AY.98, AY.58, AY.98, AY.58, AY.98, AY.100.2, AY.13, AY.120.2, AY.36, AY.116.1, AY.121, AY.5.3, AY.98.1, AY.103.2, AY.76, AY.47, AY.25.3, AY.42, AY.47, AY.25.3, AY.42, AY.19, AY.55, AY.45, AY.46, AY.108, AY.46, AY.108, AY.46, AY.108, AY.46, AY.108, AY.46, AY.108, AY.46, AY.108, AY.46, AY.117, AY.41, AY.117, AY.44, AY.55, AY.113, AY.6, AY.120, AY.84, AY.120, AY.84, AY.121, AY.113, AY.6, AY.120, AY.84, AY.121, AY.113, AY.6, AY.120, AY.44, AY.114, AY.115, AY.115, AY.116, AY.22, AY.114, AY.39, AY.40, AY.75.2, AY.114, AY.39, AY.40, AY.37, AY.99, AY.40, AY.37,	Greaney et al. (2020)				
		Co	AY.4.3, AY.99, AY.4.6,				CIDGOH [©]	

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Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.L452R	monoclonal antibody serial passage escape	Escape mutation against monoclonal antibody LY-CoV555 (antibody that forms the basis for Eli Lilly's bamlanivimab)	AY.86, AY.34.1, AY.103, AY.119, AY.109, AY.28, AY.112, AY.47, AY.43.4, AY.33, AY.4, AY.16, B.1.617.2, AY.46, AY.106, AY.85, AY.98, AY.711, AY.75, AY.44, AY.19, AY.35, AY.45, AY.49, AY.31, AY.40, AY.111, AY.75, AY.48, AY.93, AY.32, AY.88, AY.58, AY.20, AY.13, AY.26, AY.13, AY.120.2, AY.16.1, AY.103.2, AY.16.1, AY.119, AY.55.3, AY.42, AY.36, AY.119.2, AY.14, AY.25.1, AY.45, AY.46, AY.19, AY.36, AY.119, AY.55, AY.46, AY.119, AY.55, AY.41, AY.54, AY.19, AY.10, AY.32, AY.14, AY.54, AY.108, AY.46.6, AY.31, AY.45, AY.46.6, AY.31, AY.45, AY.46.6, AY.31, AY.45, AY.46.6, AY.117, AY.25, AY.101, AY.45, AY.108, AY.46.6, AY.117, AY.25, AY.117, AY.25, AY.117, AY.21, AY.117, AY.24, AY.113, AY.41, AY.116, AY.117, AY.24, AY.113, AY.41, AY.116, AY.122, AY.131, AY.41, AY.116, AY.122, AY.131, AY.41, AY.116, AY.121, AY.41, AY.116, AY.122, AY.131, AY.41, AY.116, AY.121, AY.41, AY.116, AY.121, AY.41, AY.116, AY.122, AY.131, AY.41, AY.116, AY.121, AY.41, AY.116, AY.22, AY.1131, AY.41, AY.116, AY.22, AY.1131, AY.41, AY.116, AY.22, AY.121, AY.41, AY.116, AY.22, AY.121, AY.41, AY.116, AY.22, AY.121, AY.41, AY.42, AY.43, AY.75, AY.42, AY.131, AY.41, AY.116, AY.22, AY.119, AY.42, AY.1131, AY.41, AY.116, AY.22, AY.1131, AY.41, AY.116, AY.22, AY.119, AY.42, AY.131, AY.41, AY.116, AY.22, AY.119, AY.33, AY.99, AY.32, AY.3	Starr et al. (2021)	Sequence Depth 100353	Allele	Allele G	nan
			ntact.Us, AY.100, AY.5.4,				CIDGOH ®	

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Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
Mutations p.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.	Lineages AY.86, AY.34.1, AY.103, AY.119, AY.109, AY.28, AY.112, AY.47, AY.43.4, AY.5, AY.122.4, AY.33, AY.4, AY.106, AY.85, AY.98, AY.111, AY.75, AY.45, AY.19, AY.45, AY.49, AY.111, AY.75, AY.48, AY.98, AY.49, AY.111, AY.75, AY.48, AY.19, AY.48, AY.19, AY.48, AY.19, AY.103, AY.127.1, AY.1, AY.1, AY.1, AY.1, AY.103.2, AY.16.1, AY.116.1, AY.121, AY.53, AY.119.2, AY.10, AY.83, AY.119.2, AY.10, AY.84, AY.103.2, AY.14, AY.103, AY.117, AY.14, AY.15, AY.46.6, AY.23, AY.45, AY.46.6, AY.23, AY.16.1, AY.117, AY.18, AY.16.1, AY.117, AY.18, AY.16.1, AY.117, AY.118, AY.118, AY.119, AY.42, AY.118, AY.116, AY.120, AY.84, AY.79, AY.65, AY.128, AY.41, AY.117, AY.124, AY.113, AY.14, AY.15, AY.116, AY.120, AY.84, AY.79, AY.65, AY.121, AY.113, AY.114, AY.115, AY.116, AY.120, AY.84, AY.75, AY.128, AY.41, AY.116, AY.120, AY.84, AY.75, AY.121, AY.131, AY.141, AY.116, AY.120, AY.42, AY.121, AY.43, AY.75, AY.121, AY.43, AY.75, AY.128, AY.44, AY.75, AY.129, AY.42, AY.131, AY.41, AY.116, AY.22, AY.129, AY.42, AY.131, AY.41, AY.116, AY.120, AY.43, AY.75, AY.128, AY.44, AY.75, AY.128, AY.45, AY.129, AY.41, AY.118, AY.116, AY.22, AY.129, AY.31, AY.43, AY.43, AY.44, AY.75, AY.45, AY.15, AY.16, AY.129, AY.42, AY.15, AY.118, AY.129, AY.43, AY.75, AY.131, AY.41, AY.116, AY.22, AY.131, AY.41, AY.116, AY.22, AY.128, AY.42, AY.131, AY.41, AY.116, AY.22, AY.129, AY.33, AY.39, AY.39	Citation Wang et al. (2021)		Allele		
			AY.100,				1.2.3011	

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Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.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.	AY.86, AY.34.1, AY.103, AY.119, AY.109, AY.28, AY.112, AY.47, AY.43.4, AY.16, B.1.617.2, AY.46, AY.106, AY.85, AY.98, AY.111, AY.75, AY.74, AY.19, AY.33, AY.4.5, AY.19, AY.35, AY.48, AY.93, AY.32, AY.88, AY.58, AY.20, AY.13, AY.26, AY.13, AY.16.1, AY.11, AY.11, AY.48, AY.120.2, AY.36, AY.116.1, AY.111, AY.5.3, AY.98.1, AY.103.2, AY.76, AY.47, AY.25.3, AY.42, AY.45, AY.46, AY.119, AY.55, AY.47, AY.25.1, AY.45, AY.46, AY.119, AY.55, AY.14, AY.54, AY.10, AY.25, AY.110, AY.32, AY.14, AY.54, AY.108, AY.46.5, AY.31, AY.45, AY.46.6, AY.23, AY.124, AY.16.1, AY.117, AY.24, AY.113, AY.6, AY.120, AY.84, AY.113, AY.6, AY.117, AY.25, AY.110, AY.45, AY.46.5, AY.117, AY.45, AY.16.1, AY.117, AY.24, AY.118, AY.117, AY.24, AY.118, AY.116, AY.129, AY.44, AY.79, AY.65, AY.121, AY.41, AY.116, AY.121, AY.42, AY.131, AY.41, AY.131, AY.41, AY.141, AY.116, AY.22, AY.121, AY.43, AY.43, AY.40, AY.40, AY.41, AY.41, AY.41, AY.41, AY.41, AY.41, AY.42, AY.43, AY.44, AY.75, AY.42, AY.131, AY.41, AY.116, AY.22, AY.119, AY.43, AY.44, AY.75, AY.43, AY.43, AY.42, AY.75, AY.43, AY.43, AY.43, AY.43, AY.44, AY.75, AY.43, AY.44, AY.73, AY.43, AY.43, AY.43, AY.44, AY.73, AY.43, AY.43, AY.43, AY.44, AY.73, AY.43, AY.43, A	Engelhart et al. (2021)	Depth 100353	Allele	Allele G	nan
			ntact.Us, AY.100, AY.5.4,				CIDGOH ®	

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Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.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.	AY.86, AY.34.1, AY.103, AY.119, AY.109, AY.28, AY.112, AY.47, AY.43.4, AY.33, AY.4, AY.16, B.1.617.2, AY.46, AY.106, AY.85, AY.98, AY.59, AY.111, AY.75, AY.44, AY.9, AY.35, AY.48, AY.93, AY.3.2, AY.88, AY.58, AY.94, AY.13, AY.120.2, AY.16, AY.116.1, AY.121, AY.5.3, AY.119.2, AY.66, AY.116.1, AY.119.2, AY.103.2, AY.14, AY.25.3, AY.14, AY.25.3, AY.14, AY.55, AY.45, AY.46.6, AY.23, AY.14, AY.55, AY.47, AY.25, AY.48, AY.108, AY.119, AY.108, AY.119, AY.108, AY.119, AY.108, AY.119, AY.108, AY.119, AY.111, AY.111, AY.117, AY.24, AY.108, AY.46.5, AY.31, AY.45, AY.46.5, AY.31, AY.41, AY.113, AY.6, AY.120, AY.84, AY.120, AY.84, AY.121, AY.131, AY.117, AY.45, AY.46.5, AY.113, AY.66, AY.127, AY.128, AY.41, AY.117, AY.41, AY.118, AY.129, AY.129, AY.121, AY.42, AY.129, AY.42, AY.131, AY.41, AY.116, AY.22, AY.129, AY.42, AY.129, AY.43, AY.41, AY.42, AY.42, AY.43, AY.75, AY.43, AY.43, AY.43, AY.44, AY.49, AY.42, AY.114, AY.416, AY.22, AY.114, AY.116, AY.22, AY.114, AY.116, AY.22, AY.129, AY.33, AY.99, AY.4.6, AY.4.7, AY.3, AY.4.7, AY.3, AY.4.7, AY.3, AY.4.7, AY.3, AY.4, AY.4, AY.4, AY.4, AY.4	McCallum et al. (2021)	Sequence Depth 100353	T T	Allele	nan
		Ce	ontact.Us,		1		CIDGOH [©]	

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Mutations	Sub-category	Function	Lineages	Citation	Sequence	Reference	Alternate	Alternate
p.L452R	symptom prevalence	Gross examination of 3+3 hamster lung specimens showed pronounced congestion and hemorrhages on days 5 and 7 post-infection in the case of the B.1.617.1 as compared with the B.1. The lung lesions with the B.1 variant were minimal to mild whereas with B.1.617.1 they were moderate. For B.1 pneumonic changes were minimal to mild (inflammatory cell infiltration, focal consolidation and mild congestion). The pronounced changes (moderate to severe) with mononuclear infiltration in the alveolar interstitial space, interstitial septal thickening, consolidation and pneumocyte hyperplasia were observed with B.1.617.1 variant con-	AY.35, AY.87	Yadav et al. (2021)	Depth 9	Allele T	Allele G	Frequency

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Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.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.	AY.86, AY.34.1, AY.103, AY.119, AY.109, AY.28, AY.112, AY.47, AY.43.4, AY.5, AY.122.4, AY.33, AY.4, AY.16, B1.617.2, AY.46, AY.106, AY.85, AY.98, AY.59, AY.111, AY.75, AY.43, AY.98, AY.32, AY.48, AY.93, AY.3.2, AY.48, AY.13, AY.20, AY.13, AY.127.1, AY.1, AY.1, AY.4.8, AY.120.2, AY.36, AY.116.1, AY.121, AY.5.3, AY.98.1, AY.103.2, AY.76, AY.47, AY.25.3, AY.42, AY.34, AY.19, AY.45, AY.46, AY.108, AY.119, AY.55, AY.119, AY.108, AY.119, AY.108, AY.119, AY.108, AY.119, AY.111, AY.45, AY.46, AY.108, AY.41, AY.113, AY.46, AY.108, AY.46, AY.108, AY.41, AY.113, AY.46, AY.120, AY.84, AY.121, AY.131, AY.41, AY.116, AY.117, AY.42, AY.113, AY.46, AY.121, AY.41, AY.114, AY.115, AY.121, AY.131, AY.41, AY.116, AY.121, AY.42, AY.131, AY.41, AY.140, AY.42, AY.131, AY.41, AY.140, AY.42, AY.140, AY.42, AY.140, AY.42, AY.141, AY.141	Deng et al. (2021)	Sequence Depth 100353	Reference Allele T	Alternate Allele G	nan
		Co	ntace Us, AY.100,				CIDGOH [©]	

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Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
Mutations p.L452R	trafficking	This variant alone shows a extascititlde5x 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]	AY.86, AY.34.1, AY.103, AY.119, AY.109, AY.28, AY.112, AY.47, AY.43.4, AY.16, B.1.617.2, AY.46, AY.106, AY.85, AY.98, AY.59, AY.111, AY.75, AY.45, AY.48, AY.93, AY.48, AY.93, AY.32, AY.48, AY.103, AY.133, AY.127.1, AY.1, AY.133, AY.120.2, AY.36, AY.116.1, AY.121, AY.53, AY.48, AY.199.1, AY.103.2, AY.66, AY.116.1, AY.117, AY.53, AY.45, AY.46.6, AY.25.1, AY.45, AY.46.6, AY.23, AY.104, AY.108, AY.108, AY.108, AY.108, AY.119, AY.108, AY.108, AY.108, AY.119, AY.108, AY.119, AY.108, AY.1117, AY.24, AY.108, AY.45, AY.46, AY.23, AY.46, AY.108, AY.46, AY.108, AY.47, AY.48, AY.49, AY.113, AY.41, AY.117, AY.41, AY.113, AY.41, AY.114, AY.115, AY.41, AY.115, AY.42, AY.121, AY.42, AY.131, AY.41, AY.116, AY.121, AY.41, AY.116, AY.129	Citation Ferriera et al (2021)	Sequence Depth 100353	Reference Allele T	Alternate Allele G	Alternate Frequency nan
			AY.49, AY.122.1, AY.131, AY.116, AY.22, AY.129, AY.34, AY.75.2, AY.114, AY.39.1, AY.4.3, AY.99, AY.4.6, AY.40, AY.37, AY.118, AY.126, AY.122, AY.78, AY.92, AY.119.1, AY.2, AY.4.2.3,					
		Co	AY.77, AY.29, AY.27, AY.39, AY.3.3, AY.400, AY.100,				CIDGOH [©]	

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Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.L452R	trafficking	This variant combination shows a extasciitilde4-5x decrease in cell entry efficiency (RLU measurement in 293T cells) compared to D614G, same as L452R alone.	AY.77	Ferriera et al (2021)	4	Т	G	nan
p.L452R	trafficking	This variant combination shows a extasciitilde3x decrease in cell entry efficiency (RLU measurement in 293T cells) compared to D614G, significantly less of a decrease than any B.1.617 lineage variants alone, suggesting a synergistic effect on cell entry while maintaining known immunity esacpe mutants.	AY.77	Ferriera et al (2021)	4	Т	G	nan

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Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.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]	AY.86, AY.34.1, AY.103, AY.119, AY.109, AY.28, AY.112, AY.47, AY.43.4, AY.5, AY.122.4, AY.33, AY.4, AY.16, B.1.617.2, AY.46, AY.106, AY.85, AY.98, AY.59, AY.111, AY.75, AY.74, AY.19, AY.35, AY.48, AY.93, AY.3.2, AY.88, AY.58, AY.20, AY.13, AY.26, AY.133, AY.127.1, AY.1, AY.4.8, AY.120.2, AY.36, AY.116.1, AY.121, AY.5.3, AY.98.1, AY.103.2, AY.76, AY.4.7, AY.25.3, AY.42, AY.83, AY.119.2, AY.10, AY.32, AY.14, AY.54, AY.25.1, AY.45, AY.46.6, AY.23, AY.64, AY.108, AY.46.5, AY.31, AY.94, AY.55, AY.51, AY.46, AY.108, AY.46.5, AY.31, AY.94, AY.108, AY.46.5, AY.31, AY.94, AY.107, AY.41, AY.113, AY.6, AY.120, AY.84, AY.108, AY.46.5, AY.31, AY.94, AY.108, AY.46.5, AY.31, AY.94, AY.108, AY.46.5, AY.31, AY.94, AY.108, AY.46.5, AY.31, AY.94, AY.113, AY.6, AY.120, AY.84, AY.72, AY.128, AY.41, AY.116, AY.117, AY.42, AY.113, AY.41, AY.116, AY.129, AY.42, AY.131, AY.41, AY.116, AY.129, AY.42, AY.131, AY.41, AY.116, AY.129, AY.42, AY.131, AY.41, AY.116, AY.22, AY.129, AY.34, AY.75.2, AY.114, AY.116, AY.129, AY.42, AY.131, AY.41, AY.116, AY.129, AY.42, AY.131, AY.41, AY.116, AY.212, AY.42, AY.43, AY.75.2, AY.114, AY.116, AY.129, AY.42, AY.131, AY.41, AY.116, AY.212, AY.42, AY.131, AY.41, AY.116, AY.22, AY.43, AY.75.2, AY.114, AY.39.1, AY.42, AY.131, AY.41, AY.116, AY.22, AY.43, AY.75.2, AY.129, AY.39, A	Tada et al. (2021)	Depth 100341	T	CIDGOH ©	requency

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Mutations	Sub-category	Function	Lineages	Citation	Sequence	Reference	Alternate	Alternate
					Depth	Allele	Allele	Frequency
p.L452R	transmissibility	The combination caused a 3-fold increase in infectivity relative to D614G wild type. [compare to 3.5x for L452R alone]	AY.35, AY.87	Tada et al. (2021)	9	Т	G	nan
p.L452R	transmissibility	Normalized for particle number, on ACE2.293T cells showed that the B.1.617 spike protein was >2-fold increase in infectivity relative to D614G wild type.	AY.35, AY.87	Tada et al. (2021)	9	Т	G	nan

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Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.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.	AY.86, AY.34.1, AY.103, AY.119, AY.109, AY.28, AY.112, AY.47, AY.43.4, AY.16, B.1.617.2, AY.46, AY.106, AY.85, AY.98, AY.111, AY.75, AY.45, AY.48, AY.93, AY.32, AY.48, AY.93, AY.32, AY.48, AY.19, AY.133, AY.127.1, AY.1, AY.1, AY.1, AY.1, AY.120.2, AY.36, AY.116.1, AY.121, AY.5.3, AY.98.1, AY.103.2, AY.76, AY.47, AY.25.3, AY.48, AY.192, AY.10, AY.25.3, AY.46.6, AY.23, AY.119.2, AY.10, AY.32, AY.119.2, AY.10, AY.25.1, AY.45, AY.46.6, AY.23, AY.119.2, AY.10, AY.25.1, AY.45, AY.46.5, AY.31, AY.45, AY.46.6, AY.23, AY.117, AY.45, AY.46.6, AY.23, AY.117, AY.45, AY.46.6, AY.113, AY.46, AY.113, AY.46, AY.113, AY.41, AY.116, AY.117, AY.44, AY.117, AY.44, AY.118, AY.117, AY.41, AY.116, AY.120, AY.84, AY.79, AY.121, AY.41, AY.116, AY.121, AY.41, AY.116, AY.121, AY.42, AY.131, AY.41, AY.116, AY.121, AY.41, AY.116, AY.121, AY.42, AY.121, AY.43, AY.124, AY.131, AY.41, AY.116, AY.127, AY.43, AY.141, AY.116, AY.129, AY.41, AY.116, AY.129, AY.41, AY.118, AY.119, AY.42, AY.119, AY.43, AY.120, AY.41, AY.116, AY.121, AY.41, AY.116, AY.121, AY.41, AY.116, AY.121, AY.42, AY.131, AY.41, AY.116, AY.121, AY.43, AY.124, AY.131, AY.41, AY.116, AY.127, AY.43, AY.128, AY.44, AY.752, AY.131, AY.41, AY.116, AY.129, AY.43, AY.140, AY.44, AY.45, AY.150, AY.41, AY.116, AY.212, AY.42, AY.113, AY.41, AY.116, AY.22, AY.114, AY.116, AY.22, AY.114, AY.116, AY.22, AY.114, AY.116, AY.23, AY.24, AY.129, AY.33, AY.99, AY.33, AY.99, AY.33, AY.99, AY.33, AY.99, AY.33, AY.99, AY.33, AY.39, AY.33, AY.33, AY.39, AY.31, AY.31, AY.42, AY.33, AY.39, AY.32, AY.32, AY.32, AY.33, AY.34, AY.35, AY.34, AY.35, AY.35, AY.35, AY.35, AY.35, AY.3	Ferreira et al. (2021)		Allele	Allele G	
		Co	n t actv.Us, AY.100,				CIDGOH [©]	

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Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.L452R	vaccine neutraliza- tion efficacy	Nine stored sera from Pfizer BNT162b2 vaccinees were tested against a range of spike mutation bearing PV. E484Q had a extasciitilde5x drop in neutralization (vs extasciitilde10x for E484K). When E484Q and L452R were combined, the fold change was significant, but similar to that of L452R alone (extasciitilde2x), suggesting no evidence for an additive effect [perhaps even E484Q effect dilution].	AY.35, AY.87	Ferreira et al. (2021)	9	T	G	nan
p.L452R	vaccine neutraliza- tion efficacy	1.4x reduction in neutralization (ID50) in sera 3 weeks after one dose of Pfizer/BioNTech BNT162b2 (up to 5 naive and post infection vaccinees)	AY.35, AY.87	Gong et al. (2021)	9	T	G	nan

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Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.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.	AY.86, AY.34.1, AY.103, AY.119, AY.109, AY.28, AY.112, AY.47, AY.43.4, AY.16, B.1.617.2, AY.46, AY.106, AY.85, AY.98, AY.59, AY.111, AY.75, AY.47, AY.48, AY.93, AY.32, AY.48, AY.93, AY.32, AY.48, AY.93, AY.32, AY.13, AY.120.2, AY.13, AY.13, AY.120.2, AY.16, AY.116.1, AY.121, AY.53, AY.98.1, AY.103.2, AY.76, AY.47, AY.25.3, AY.42, AY.34, AY.25.1, AY.45, AY.46, AY.19, AY.45, AY.46, AY.19, AY.41, AY.55, AY.46, AY.19, AY.41, AY.55, AY.41, AY.55, AY.42, AY.19, AY.19, AY.19, AY.19, AY.19, AY.10, AY.25, AY.110, AY.45, AY.46, AY.108, AY.46, AY.117, AY.24, AY.113, AY.66, AY.120, AY.84, AY.117, AY.24, AY.113, AY.66, AY.120, AY.84, AY.121, AY.45, AY.113, AY.66, AY.120, AY.84, AY.117, AY.24, AY.113, AY.66, AY.120, AY.84, AY.79, AY.121, AY.41, AY.116, AY.117, AY.41, AY.116, AY.117, AY.41, AY.116, AY.117, AY.41, AY.116, AY.117, AY.41, AY.116, AY.121, AY.42, AY.131, AY.41, AY.116, AY.121, AY.43, AY.43, AY.75.2, AY.131, AY.41, AY.116, AY.22, AY.118, AY.41, AY.116, AY.22, AY.119, AY.33, AY.99, AY.33, AY.99, AY.33, AY.39, AY.33, AY.34, AY.34, AY.34, AY.34, AY.35, AY.34, AY.35, AY.34, AY.35, AY.34, AY.35, AY.34, AY.35, AY.34, A	Jacobson et al. (2021)				
		Co	ontact Us,		1		CIDGOH [©]	1

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Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.L452R	vaccine neutralization efficacy	Pseudotyped viruses for B.1.617 was 4-fold resistant to neutralization by 6 BNT162b2 vaccine sera 28 days post-booster compared to wild type - a finding that was similar to that of the 3.4-fold resistance of the South Africa B.1.351 variant using the same assay. Neutralization by 3 Moderna vaccine sera 28 days post-booster was 5-fold resistant (vs. 2.2-fold for B.1.351). The resistance of B.1.617 was caused by the L452R and E484Q mutation, based on results from viruses pseudotyped for individual vari-	AY.35, AY.87	Tada et al. (2021)	9	T	G	nan

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Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
Mutations p.L452R	Sub-category 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).	AY.86, AY.34.1, AY.103, AY.119, AY.109, AY.28, AY.112, AY.47, AY.43.4, AY.33, AY.4, AY.106, AY.85, AY.98, AY.111, AY.75, AY.74, AY.35, AY.44, AY.31, AY.45, AY.19, AY.35, AY.45, AY.48, AY.98, AY.58, AY.98, AY.58, AY.98, AY.58, AY.98, AY.58, AY.101, AY.120.2, AY.13, AY.120.2, AY.36, AY.116.1, AY.121, AY.5.3, AY.98.1, AY.103.2, AY.76, AY.47, AY.25.3, AY.42, AY.48, AY.54, AY.19, AY.55, AY.45, AY.46, AY.10, AY.47, AY.25.1, AY.45, AY.46, AY.10, AY.32, AY.111, AY.55, AY.45, AY.46, AY.108, AY.46, AY.108, AY.46, AY.108, AY.46, AY.108, AY.46, AY.108, AY.46, AY.117, AY.41, AY.41, AY.117, AY.44, AY.55, AY.120, AY.42, AY.113, AY.6, AY.120, AY.44, AY.117, AY.44, AY.117, AY.44, AY.116, AY.117, AY.44, AY.116, AY.42, AY.113, AY.41, AY.116, AY.42, AY.114, AY.41, AY.42, AY.114, AY.43, AY.43, AY.75, AY.44, AY.75, AY.114, AY.41, AY.42, AY.43, AY.75, AY.43, AY.44, AY.75, AY.44, AY.75, AY.44, AY.75, AY.41, A	Citation Wilhelm et al. (2021)	Sequence Depth 100341	Reference Allele T	Alternate Allele G	Alternate Frequency nan
		Co	AY.99, AY.4.6,				CIDGOH [©]	

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Mutations	Sub-categor	·y	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.L452R	vaccinee binding	plasma	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.	AY.86, AY.34.1, AY.103, AY.119, AY.109, AY.28, AY.112, AY.47, AY.43.4, AY.5, AY.122.4, AY.33, AY.4, AY.106, AY.85, AY.98, AY.111, AY.75, AY.47, AY.48, AY.98, AY.19, AY.49, AY.19, AY.20, AY.13, AY.20, AY.13, AY.20, AY.13, AY.121, AY.48, AY.120.2, AY.36, AY.116.1, AY.121, AY.5.3, AY.42, AY.103.2, AY.6, AY.119, AY.83, AY.121, AY.53, AY.42, AY.103, AY.45, AY.103.2, AY.46, AY.116, AY.25.3, AY.45, AY.45, AY.41, AY.10, AY.45, AY.117, AY.45, AY.117, AY.45, AY.119, AY.45, AY.119, AY.45, AY.119, AY.45, AY.119, AY.45, AY.119, AY.45, AY.119, AY.45, AY.46, AY.23, AY.47, AY.124, AY.113, AY.46.1, AY.117, AY.44, AY.108, AY.47, AY.128, AY.44, AY.129, AY.44, AY.120, AY.44, AY.121, AY.41, AY.116, AY.22, AY.131, AY.41, AY.116, AY.22, AY.44, AY.79, AY.45, AY.118, AY.41, AY.116, AY.22, AY.44, AY.79, AY.45, AY.118, AY.41, AY.116, AY.22, AY.41, AY.116, AY.22, AY.41, AY.116, AY.22, AY.43, AY.75, AY.41, AY.116, AY.22, AY.44, AY.75, AY.41, AY.116, AY.22, AY.41, AY.116, AY.22, AY.43, AY.75, AY.41, AY.116, AY.22, AY.41, AY.116, AY.22, AY.41, AY.116, AY.22, AY.41, AY.116, AY.22, AY.43, AY.75, AY.43, AY.75, AY.43, AY.75, AY.41, AY.116, AY.22, AY.43, AY.75,	Gong et al. (2021)	Depth 100341	T	CIDGOH ©	nan

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Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.L452R	vaccinee plasma binding	This variant combination (representing lineage B.1.617) showed a 1.30x 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. 1.18x 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. [exact variant list not provided in manuscript, is inferred fro common knowledge]	AY.35, AY.87	Gong et al. (2021)	9	T	G	nan
p.L452R	viral load	In 9 infected hamsters each for B.1 and B.1.617.1, no significant change in viral load or subgenomic RNA levels were detected.	AY.35, AY.87	Yadav et al. (2021)	9	Т	G	nan

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Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
P.L452R	virion structure	Estimated free energy change (ddG) for this variant is -0.67 kcal/mol (i.e. destabilizing relative to wild type)	AY.86, AY.34.1, AY.103, AY.119, AY.109, AY.28, AY.112, AY.47, AY.43.4, AY.33, AY.4, AY.16, B.1.617.2, AY.46, AY.106, AY.85, AY.98, AY.59, AY.111, AY.75, AY.74, AY.19, AY.35, AY.4.5, AY.48, AY.93, AY.20, AY.13, AY.26, AY.133, AY.127.1, AY.1, AY.120.2, AY.36, AY.116.1, AY.121, AY.5.3, AY.98.1, AY.103.2, AY.6, AY.119.2, AY.14, AY.55, AY.48, AY.120.2, AY.36, AY.110.1, AY.121, AY.55, AY.46, AY.121, AY.125, AY.14, AY.15, AY.108, AY.1108, AY.1117, AY.25, AY.118, AY.108, AY.46.6, AY.23, AY.14, AY.15, AY.117, AY.24, AY.118, AY.117, AY.24, AY.117, AY.24, AY.117, AY.24, AY.118, AY.117, AY.24, AY.117, AY.24, AY.118, AY.116, AY.120, AY.84, AY.72, AY.121, AY.116, AY.121, AY.117, AY.24, AY.116, AY.121, AY.117, AY.24, AY.118, AY.116, AY.121, AY.116, AY.22, AY.129, AY.34, AY.120, AY.41, AY.116, AY.22, AY.129, AY.34, AY.120, AY.43, AY.120, AY.44, AY.131, AY.41, AY.116, AY.22, AY.121, AY.131, AY.41, AY.121, AY.42, AY.131, AY.41, AY.131, AY.41, AY.121, AY.42, AY.131, AY.41, AY.120, AY.43, AY.44, AY.49, AY.120, AY.43, AY.43, AY.43, AY.43, AY.43, AY.43, AY.44, AY.49, AY.120, AY.43, AY.43, AY.43, AY.43, AY.43, AY.43, AY.44, AY.44, AY.49, AY.120, AY.43, AY.43, AY.43, AY.43, AY.43, AY.44, AY.44, AY.49, AY.49, AY.120, AY.43, AY.43, AY.43, AY.43, AY.44, AY.49, AY.49, AY.120, AY.43, AY.43, AY.43, AY.43, AY.43, AY.44, AY.44, AY.49,	Spratt et al. (2021)	Sequence Depth 100353	Reference Allele T	Alternate Allele G	Alternate Frequency nan
		Co	AY.3.3, on t act. Us,				CIDGOH ®	

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Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.A475V	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.	AY.111	Gaebler et al. (2021)	9	C	Т	nan
p.A475V	antibody epitope effects	Resistent to some neutralizing antibodies: mAbs 157, 247, CB6, P2C-1F11, B38, and CA1	AY.111	Li et al. (2020)	9	C	Т	nan
p.A475V	antibody epitope effects	Resistent to some class 1 (Spike 'up' conformation) antibodies tested.	AY.111	Wang et al. (2021)	9	С	Т	nan
p.A475V	convalescent plasma escape	Resistant to a pool of 10 convalescent sera (but less than 4x, a typical threshold for definition of escape)	AY.111	Li et al. (2020)	9	С	Т	nan
p.A475V	monoclonal anti- body serial passage escape	The engineered mutation cause 10-fold or more increase in the disassociation constant with C102, C105 and C144 monoclonal antibodies vs. wild type Spike protein RBD domain AAs.	AY.111	Barnes et al. (2020)	9	С	Т	nan
p.A475V	monoclonal anti- body serial passage escape	Escape mutation against monoclonal antibody LY- CoV016, minimal ACE2 binding affinity loss	AY.111	Starr et al. (2021)	9	С	Т	nan
p.A475V	pharmaceutical effectiveness	COR-101 lost extasci- itilde50x binding against this isolated mutation. Estesevimab lost extasci- itilde8x binding against this isolated mutation. Sotrovimab lost extasci- itilde30x binding against this isolated mutation. Tixagevimab lost extasci- itilde15x binding against this isolated mutation. m396 lost extasci- itilde8x binding against this iso- lated mutation.	AY.111	Engelhart et al. (2021)	9	С	T	nan

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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)