Surveillance report

Surveillance generated by nf-ncov-voc for Delta variant

Date

This report is generated on 2022-01-21 using 164953 number of genomes collected between 2020-02-25 and 2021-12-29

Pango Lineages

Pango Lineages in this report ['AY.1', 'AY.10', 'AY.100', 'AY.101', 'AY.102', 'AY.103', 'AY.104', 'AY.105', 'AY.106', 'AY.107', 'AY.108', 'AY.109', 'AY.11', 'AY.110', 'AY.111', 'AY.113', 'AY.114', 'AY.116', 'AY.116.1', 'AY.117', 'AY.118', 'AY.119', 'AY.119.1', 'AY.120', 'AY.120.1', 'AY.121', 'AY.121.1', 'AY.122', 'AY.122.1', 'AY.124', 'AY.125', 'AY.126', 'AY.127', 'AY.13', 'AY.14', 'AY.15', 'AY.16', 'AY.16.1', 'AY.17', 'AY.18', 'AY.19', 'AY.2', 'AY.20', 'AY.21', 'AY.23', 'AY.24', 'AY.25', 'AY.25.1', 'AY.26', 'AY.27', 'AY.28', 'AY.29', 'AY.3', 'AY.3.1', 'AY.32', 'AY.33', 'AY.34', 'AY.34.1', 'AY.35', 'AY.36', 'AY.37', 'AY.38', 'AY.39', 'AY.39.1', 'AY.4', 'AY.4.2', 'AY.4.2.1', 'AY.4.2.2', 'AY.4.3', 'AY.4.4', 'AY.4.5', 'AY.4.6', 'AY.40', 'AY.41', 'AY.42', 'AY.43', 'AY.43.3', 'AY.43.4', 'AY.44', 'AY.45', 'AY.46', 'AY.46.1', 'AY.46.2', 'AY.46.4', 'AY.46.6', 'AY.47', 'AY.48', 'AY.49', 'AY.5', 'AY.5.3', 'AY.51', 'AY.53', 'AY.54', 'AY.55', 'AY.56', 'AY.57', 'AY.59', 'AY.6', 'AY.60', 'AY.61', 'AY.62', 'AY.64', 'AY.65', 'AY.66', 'AY.67', 'AY.68', 'AY.7.1', 'AY.70', 'AY.72', 'AY.73', 'AY.74', 'AY.75', 'AY.77', 'AY.78', 'AY.82', 'AY.83', 'AY.84', 'AY.85', 'AY.86', 'AY.87', 'AY.88', 'AY.89', 'AY.9', 'AY.9.2', 'AY.9.2.1', 'AY.92', 'AY.93', 'AY.94', 'AY.98', 'AY.98.1', 'AY.99', 'AY.99.2', 'B.1.617.2']

Indicator

This table contains key indicators identified

Indicator	Sub-categories from POKAY	Mutations
Transmissibility between humans	transmissibility	p.D614G, p.E484Q, p.L452R, p.P681R
Infection Severity	ACE2 receptor binding affinity, viral load, outcome hazard ratio	p.D138Y, p.D614G, p.E484K, p.E484Q, p.H69del, p.K417N, p.L452R, p.L5F, p.P26S, p.P681H, p.S494P, p.T95I, p.V70del
Immunity after natural infection	convalescent plasma escape, reinfection, humoral response durability	p.D614G, p.E484K, p.E484Q, 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, p.P681H
Monoclonal antibodies	monoclonal antibody serial passage escape, pharmaceutical effectiveness	p.E484K, p.E484Q, p.G142D, p.K417N, p.L452R, p.P251L, p.R158G, p.S255F, p.S443F, p.S494P
Diagnostics	clinical indicators, antigenic test failure, symptom prevalence	

Mutation Significance

This table contains key functional impacts of mutations identified

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Alternate Allele	Alternate Frequency
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	A	0.5
p.V70del	antibody epitope effects	Reduces neutralization by structurally unmapped mAb COVA1-21 (cluster XI).	AY.77	Rees-Spear et al. (2021)	2	A	0.5

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Alternate Allele	Alternate Frequency
p.V70del	convalescent plasma binding	1.33x increase in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset.	AY.77	Gong et al. (2021)	2	A	0.5
p.V70del	convalescent plasma escape	Fatal COVID-19 complications in immunocompromised patient after immune escape from convalescent plasma	AY.77	Kemp et al. (2020)	2	A	0.5
p.V70del	convalescent plasma escape	Neutralization activity of almost all Moderna Phase 1 sera tested actually *increased*.	AY.77	Shen et al. (2021)	2	A	0.5
p.V70del	convalescent plasma escape	Viruses containing the point mutations of B.1.1.7 showed that the single point mutations (Δ69-70 and N501Y) were neutralized as efficiently as D614G across 10 convalescent sera from April 2020 infectees.	AY.77	Tada et al. (2021)	2	A	0.5
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	A	0.5
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	A	0.5

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Alternate Allele	Alternate Frequency
p.G142D	monoclonal antibody serial passage escape	Escape mutation against Spike N terminal domain antigenic supersite i mAbs S2M28, S2X28, S2X333	AY.54, AY.46.2, AY.45, AY.88, AY.108, AY.11, AY.113, AY.118, AY.13, AY.3.1, AY.53, AY.73, AY.103, AY.43.4, AY.124, AY.109, AY.84, AY.23, AY.89, AY.36, AY.44, AY.34.1, AY.46.1, AY.119.1, AY.77, AY.27, AY.75, AY.4, AY.125, AY.59, B.1.617.2, AY.86, AY.116.1, AY.117, AY.102, AY.15, AY.32, AY.34, AY.116, AY.9, AY.70, AY.9.2.1, AY.37, AY.121.1, AY.43.3, AY.4.4, AY.47, AY.5, AY.65, AY.25, AY.120.1, AY.42, AY.74, AY.105, AY.120, AY.104, AY.126, AY.106, AY.114, AY.51, AY.46.4, AY.43, AY.64, AY.78, AY.3, AY.107, AY.6, AY.7.1, AY.99, AY.26, AY.68, AY.38, AY.46.6, AY.41, AY.99.2, AY.46, AY.39, AY.4.2.1, AY.4.3, AY.35, AY.20, AY.110, AY.111, AY.127, AY.33, AY.57, AY.14, AY.4.2, AY.72, AY.85, AY.39.1, AY.21, AY.94, AY.98, AY.60, AY.25.1, AY.1, AY.119, AY.4.5, AY.82, AY.121, AY.18, AY.4.2.2, AY.28, AY.93, AY.10, AY.5.3, AY.24, AY.16, AY.62, AY.122, AY.29, AY.83, AY.98.1, AY.9.2, AY.48, AY.4.6, AY.122.1, AY.55, AY.101, AY.100	McCallum et al. (2021)	53643	A,ATGT,ATGTTA,ATT,ATG	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Alternate Allele	Alternate Frequency
p.G142D	monoclonal antibody serial passage escape	Selected twice in passage with mAb COV2-2489.	AY.54, AY.46.2, AY.45, AY.88, AY.108, AY.11, AY.113, AY.118, AY.13, AY.3.1, AY.53, AY.73, AY.103, AY.43.4, AY.124, AY.109, AY.84, AY.23, AY.89, AY.36, AY.44, AY.34.1, AY.46.1, AY.119.1, AY.77, AY.27, AY.75, AY.4, AY.125, AY.59, B.1.617.2, AY.86, AY.116.1, AY.117, AY.102, AY.15, AY.32, AY.34, AY.116, AY.9, AY.70, AY.9.2.1, AY.37, AY.121.1, AY.43.3, AY.4.4, AY.47, AY.5, AY.65, AY.25, AY.120.1, AY.42, AY.74, AY.105, AY.120, AY.104, AY.126, AY.106, AY.114, AY.51, AY.46.4, AY.43, AY.64, AY.78, AY.3, AY.107, AY.6, AY.7.1, AY.99, AY.26, AY.68, AY.38, AY.46.6, AY.41, AY.99.2, AY.46, AY.39, AY.4.2.1, AY.4.3, AY.35, AY.20, AY.110, AY.111, AY.127, AY.33, AY.57, AY.14, AY.4.2, AY.72, AY.85, AY.39.1, AY.21, AY.94, AY.98, AY.60, AY.25.1, AY.1, AY.119, AY.4.5, AY.82, AY.121, AY.18, AY.4.2.2, AY.28, AY.93, AY.10, AY.5.3, AY.24, AY.16, AY.62, AY.122, AY.29, AY.83, AY.98.1, AY.9.2, AY.48, AY.4.6, AY.122.1, AY.55, AY.101, AY.100	Suryadevara et al. (2021)	53643	A,ATGT,ATGTTA,ATT,ATG	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Alternate Allele	Alternate Frequency
p.P251L	monoclonal antibody serial passage escape	Escape mutation against Spike N terminal domain antigenic supersite i mAb S2X28	AY.86, AY.98.1	McCallum et al. (2021)	403	T	0.4
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.77, AY.46.4, AY.6, AY.35, AY.4.4	Gong et al. (2021)	31	T	0.26
p.L5F	convalescent plasma binding	No change in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset.	AY.77, AY.46.4, AY.6, AY.35, AY.4.4	Gong et al. (2021)	31	T	0.26
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.77, AY.46.4, AY.6, AY.35, AY.4.4	Gong et al. (2021)	31	T	0.26
p.D614G	ACE2 receptor binding affinity	Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant showed a 1.32x increase in binding (KD) relative to D614G.	AY.70	Gong et al. (2021)	8	TGG,GGG	1.0
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.27, AY.33, AY.38, AY.57, AY.70, AY.46	Gong et al. (2021)	13662	TGG,GGG	1.0
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.70	Gong et al. (2021)	8	TGG,GGG	1.0
p.D614G	ACE2 receptor binding affinity	In four cell lines (including 293T-hACE2 cells), this mutation combination increases infectivity vs D614G alone	AY.27, AY.33, AY.38, AY.57, AY.70, AY.46	Li et al. (2020)	13662	TGG,GGG	1.0
p.D614G	convalescent plasma binding	1.56x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset.	AY.70	Gong et al. (2021)	8	TGG,GGG	1.0
p.D614G	convalescent plasma binding	2.15x increase in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset.	AY.27, AY.33, AY.38, AY.57, AY.70, AY.46	Gong et al. (2021)	13662	TGG,GGG	1.0
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 post-symptom-onset. [exact variant list not provided in manuscript, is inferred fro common knowledge]	AY.70	Gong et al. (2021)	8	TGG,GGG	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Alternate Allele	Alternate Frequency
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.70	Tada et al. (2021)	8	TGG,GGG	1.0
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.27, AY.33, AY.38, AY.57, AY.70, AY.46	Wilhelm et al. (2021)	13662	TGG,GGG	1.0
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.27, AY.38, AY.57, AY.70, AY.46	Brehm et al. (2021)	13501	TGG,GGG	1.0
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.27, AY.33, AY.38, AY.57, AY.70, AY.46	Landis et al. (2021)	13662	TGG,GGG	1.0
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.27, AY.38, AY.57, AY.70, AY.46	Brehm et al. (2021)	13501	TGG,GGG	1.0
p.D614G	syncytium formation	Slight increase in Vero cell-cell membrane fusion assay under infection with VSV pseudotyped virus.	AY.27, AY.33, AY.38, AY.57, AY.70, AY.46	Kim et al. (2021)	13662	TGG,GGG	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	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 vaccinee neutralizing at weeks 3 and 6 against B.1.1.7 and D614G) suggest that vaccinees probably do not elicit an early humoral response detectable at mucosal surfaces even though sera neutralization was observed. They strengthen the hypothesis that some vaccines may not protect against viral acquisition and infection of the oral–nasal region, but may prevent severe disease associated with viral dissemination in the lower respiratory tract.	AY.27, AY.33, AY.38, AY.57, AY.70, AY.46	Planas et al. (2021)	13662	TGG,GGG	1.0
p.D614G	trafficking	Circulating variant shown in vitro to not have major defects or enhancement of cell surface protein trafficking (i.e. Spike cleavage or fusion required for cell entry)	AY.27, AY.33, AY.38, AY.57, AY.70, AY.46	Barrett et al. (2021)	13662	TGG,GGG	1.0
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.27, AY.33, AY.38, AY.57, AY.70, AY.46	Daniloski et al. (2021)	13662	TGG,GGG	1.0
p.D614G	trafficking	No change in infectivity (24h) relative to D614G alone in Caco-2 cells, Vero or Calu-3.	AY.27, AY.33, AY.38, AY.57, AY.70, AY.46	Kim et al. (2021)	13662	TGG,GGG	1.0
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.27, AY.33, AY.38, AY.57, AY.70, AY.46	Kim et al. (2021)	13662	TGG,GGG	1.0
p.D614G	trafficking	Among S variants tested, the D614G mutant shows the highest cell entry (extasciitilde3.5x wild type), as supported by structural and binding analyses.	AY.27, AY.33, AY.38, AY.57, AY.70, AY.46	Ozono et al. (2020)	13662	TGG,GGG	1.0
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.27, AY.33, AY.38, AY.57, AY.70, AY.46	Tada et al. (2021)	13662	TGG,GGG	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	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.27, AY.33, AY.38, AY.57, AY.70, AY.46	Zhang et l. (2020)	13662	TGG,GGG	1.0
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.27, AY.33, AY.38, AY.57, AY.70, AY.46	Tada et al. (2021)	13662	TGG,GGG	1.0
p.D614G	transmissibility	The combination caused a 3-fold increase in infectivity relative to D614G wild type. [compare to 3.5x for L452R alone]	AY.70	Tada et al. (2021)	8	TGG,GGG	1.0
p.D614G	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.70	Tada et al. (2021)	8	TGG,GGG	1.0
p.D614G	vaccine neutralization efficacy	Pseudotyped D614G virus has reduced neutralization activity vs wild type: 1.2x (37 sera Pfizer median 9 days post 2nd dose, 37 sera Moderna median 18 days post 2nd dose). This was NOT significant by ANOVA.	AY.27, AY.33, AY.38, AY.57, AY.70, AY.46	Garcia-Beltran et al. (2021)	13662	TGG,GGG	1.0
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.70	Gong et al. (2021)	8	TGG,GGG	1.0
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.27, AY.33, AY.38, AY.57, AY.70, AY.46	Kuzmina et al. (2021)	13662	TGG,GGG	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Alternate Allele	Alternate Frequency
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.70	Tada et al. (2021)	8	TGG,GGG	1.0
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.27, AY.33, AY.38, AY.57, AY.70, AY.46	Wilhelm et al. (2021)	13662	TGG,GGG	1.0
p.D614G	vaccinee plasma binding	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 previously non-seroconverted subjects. 1.56x 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.70	Gong et al. (2021)	8	TGG,GGG	1.0
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.27, AY.33, AY.38, AY.57, AY.70, AY.46	Gong et al. (2021)	13662	TGG,GGG	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Alternate Allele	Alternate Frequency
p.D614G	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.70	Gong et al. (2021)	8	TGG,GGG	1.0
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.27, AY.33, AY.38, AY.57, AY.70, AY.46	Plante et al. (2020)	13662	TGG,GGG	1.0
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.27, AY.33, AY.38, AY.57, AY.70, AY.46	Spratt et al. (2021)	13662	TGG,GGG	1.0
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.27, AY.33, AY.38, AY.57, AY.70, AY.46	Weissman et al. (2020)	13662	TGG,GGG	1.0
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.27, AY.33, AY.38, AY.57, AY.70, AY.46	Yurkovetskiy et al. (2020)	13662	TGG,GGG	1.0
p.D614G	virion structure	Based on pseudotyped virus experiments, D614G may increase infectivity by assembling more functional S protein into the virion.	AY.27, AY.33, AY.38, AY.57, AY.70, AY.46	Zhang et al. (2020)	13662	TGG,GGG	1.0
p.D614G	ACE2 receptor binding affinity	This variant appears twice in the experiments, with slightly different affinities (both extasci-itilde1.2x decrease in binding relative to D614G) using flow cytometry and ACE2 ectodomains-Fc portion IgG complex.	AY.77	Gong et al. (2021)	2	G	1.0
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	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Alternate Allele	Alternate Frequency
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.2, AY.1	Gong et al. (2021)	10	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Alternate Allele	Alternate Frequency
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.54, AY.46.2, AY.45, AY.88, AY.108, AY.11, AY.113, AY.118, AY.13, AY.3.1, AY.53, AY.73, AY.103, AY.43.4, AY.124, AY.109, AY.84, AY.23, AY.89, AY.36, AY.44, AY.34.1, AY.46.1, AY.119.1, AY.77, AY.75, AY.4, AY.125, AY.59, B.1.617.2, AY.86, AY.19, AY.116.1, AY.117, AY.102, AY.15, AY.32, AY.34, AY.116, AY.9, AY.9.2.1, AY.37, AY.121.1, AY.43.3, AY.2, AY.4.4, AY.47, AY.5, AY.65, AY.25, AY.120.1, AY.42, AY.74, AY.105, AY.120, AY.104, AY.126, AY.106, AY.114, AY.51, AY.46.4, AY.43, AY.64, AY.78, AY.3, AY.107, AY.6, AY.7.1, AY.99, AY.26, AY.68, AY.46.6, AY.41, AY.99.2, AY.67, AY.39, AY.4.2.1, AY.4.3, AY.35, AY.20, AY.110, AY.111, AY.127, AY.49, AY.92, AY.14, AY.4.2, AY.40, AY.72, AY.85, AY.39.1, AY.21, AY.94, AY.17, AY.98, AY.60, AY.25.1, AY.1, AY.119, AY.4.5, AY.61, AY.82, AY.121, AY.16.1, AY.56, AY.18, AY.4.2.2, AY.28, AY.93, AY.10, AY.5.3, AY.24, AY.16, AY.62, AY.122, AY.29, AY.83, AY.98.1, AY.9.2, AY.48, AY.4.6, AY.122.1, AY.55, AY.87, AY.101, AY.100	Gong et al. (2021)	45770	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	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.98, AY.35	Gong et al. (2021)	12	G	1.0
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.77, AY.46.4, AY.6, AY.35, AY.4.4	Gong et al. (2021)	31	G	1.0
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	Gong et al. (2021)	1	G	1.0
p.D614G	ACE2 receptor binding affinity	Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant showed a 1.23x decrease in binding (KD) relative to D614G.	AY.5	Gong et al. (2021)	18	G	1.0
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.106, AY.114, AY.119.1, AY.77, AY.78, AY.107, AY.4, AY.1, AY.119, AY.4.5, AY.125, B.1.617.2, AY.121, AY.88, AY.4.2.2, AY.116.1, AY.117, AY.108, AY.5.3, AY.102, AY.113, AY.118, AY.34, AY.116, AY.39, AY.4.2.1, AY.4.3, AY.121.1, AY.29, AY.124, AY.4.4, AY.20, AY.43.4, AY.109, AY.110, AY.111, AY.127, AY.89, AY.36, AY.34.1, AY.4.6, AY.92, AY.120.1, AY.4.2, AY.42, AY.120, AY.85, AY.104, AY.39.1, AY.101, AY.126, AY.100	Gong et al. (2021)	4594	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Alternate Allele	Alternate Frequency
p.D614G	ACE2 receptor binding affinity	In four cell lines (including 293T-hACE2 cells), this mutation combination increases infectivity vs D614G alone	AY.54, AY.46.2, AY.45, AY.88, AY.108, AY.11, AY.113, AY.118, AY.13, AY.3.1, AY.53, AY.73, AY.103, AY.43.4, AY.124, AY.109, AY.84, AY.23, AY.89, AY.36, AY.44, AY.34.1, AY.46.1, AY.119.1, AY.77, AY.75, AY.4, AY.125, AY.59, B.1.617.2, AY.86, AY.19, AY.116.1, AY.117, AY.102, AY.15, AY.32, AY.34, AY.116, AY.9, AY.9.2.1, AY.37, AY.121.1, AY.43.3, AY.2, AY.4.4, AY.47, AY.5, AY.65, AY.25, AY.120.1, AY.42, AY.74, AY.105, AY.120, AY.104, AY.126, AY.106, AY.114, AY.51, AY.46.4, AY.43, AY.64, AY.78, AY.3, AY.107, AY.6, AY.7.1, AY.99, AY.26, AY.68, AY.46.6, AY.41, AY.99.2, AY.67, AY.39, AY.4.2.1, AY.4.3, AY.35, AY.20, AY.110, AY.111, AY.127, AY.49, AY.92, AY.14, AY.4.2, AY.40, AY.72, AY.85, AY.39.1, AY.21, AY.94, AY.17, AY.98, AY.60, AY.25.1, AY.1, AY.119, AY.4.5, AY.61, AY.82, AY.121, AY.16.1, AY.56, AY.18, AY.4.2.2, AY.28, AY.93, AY.10, AY.5.3, AY.24, AY.16, AY.62, AY.122, AY.29, AY.83, AY.98.1, AY.9.2, AY.48, AY.4.6, AY.122.1, AY.55, AY.87, AY.101, AY.100	Li et al. (2020)	45770	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Alternate Allele	Alternate Frequency
p.D614G	convalescent plasma binding	1.42x increase in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset.	AY.77	Gong et al. (2021)	2	G	1.0
p.D614G	convalescent plasma binding	1.33x increase in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset.	AY.77	Gong et al. (2021)	2	G	1.0
p.D614G	convalescent plasma binding	2.16x increase in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset.	AY.2, AY.1	Gong et al. (2021)	10	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Alternate Allele	Alternate Frequency
p.D614G	convalescent plasma binding	2.15x increase in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset.	AY.54, AY.46.2, AY.45, AY.88, AY.108, AY.11, AY.113, AY.118, AY.13, AY.3.1, AY.53, AY.73, AY.103, AY.43.4, AY.124, AY.109, AY.84, AY.23, AY.89, AY.36, AY.44, AY.34.1, AY.46.1, AY.119.1, AY.77, AY.75, AY.4, AY.125, AY.59, B.1.617.2, AY.86, AY.19, AY.116.1, AY.117, AY.102, AY.15, AY.32, AY.34, AY.116, AY.9, AY.9.2.1, AY.37, AY.121.1, AY.43.3, AY.2, AY.4.4, AY.47, AY.5, AY.65, AY.25, AY.120.1, AY.42, AY.74, AY.105, AY.120, AY.104, AY.126, AY.106, AY.114, AY.51, AY.46.4, AY.43, AY.64, AY.78, AY.3, AY.107, AY.6, AY.7.1, AY.99, AY.26, AY.68, AY.46.6, AY.41, AY.99.2, AY.67, AY.39, AY.4.2.1, AY.4.3, AY.35, AY.20, AY.110, AY.111, AY.127, AY.49, AY.92, AY.14, AY.4.2, AY.40, AY.72, AY.85, AY.39.1, AY.21, AY.94, AY.17, AY.98, AY.60, AY.25.1, AY.1, AY.119, AY.4.5, AY.61, AY.82, AY.121, AY.16.1, AY.56, AY.18, AY.4.2.2, AY.28, AY.93, AY.10, AY.5.3, AY.24, AY.16, AY.62, AY.122, AY.29, AY.83, AY.98.1, AY.9.2, AY.48, AY.4.6, AY.122.1, AY.55, AY.87, AY.101, AY.100	Gong et al. (2021)	45770	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	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 post-symptom-onset. [exact variant list not provided in manuscript, is inferred fro common knowledge]	AY.98, AY.35	Gong et al. (2021)	12	G	1.0
p.D614G	convalescent plasma binding	No change in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset.	AY.77, AY.46.4, AY.6, AY.35, AY.4.4	Gong et al. (2021)	31	G	1.0
p.D614G	convalescent plasma binding	1.08x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset.	AY.4.3	Gong et al. (2021)	1	G	1.0
p.D614G	convalescent plasma binding	1.26x increase in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset.	AY.5	Gong et al. (2021)	18	G	1.0
p.D614G	convalescent plasma binding	No change in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset.	AY.106, AY.114, AY.119.1, AY.77, AY.78, AY.107, AY.4, AY.1, AY.119, AY.4.5, AY.125, B.1.617.2, AY.121, AY.88, AY.4.2.2, AY.116.1, AY.117, AY.108, AY.5.3, AY.102, AY.113, AY.118, AY.34, AY.116, AY.39, AY.4.2.1, AY.4.3, AY.121.1, AY.29, AY.124, AY.4.4, AY.20, AY.43.4, AY.109, AY.110, AY.111, AY.127, AY.89, AY.36, AY.34.1, AY.4.6, AY.92, AY.120.1, AY.4.2, AY.42, AY.120, AY.85, AY.104, AY.39.1, AY.101, AY.126, AY.100	Gong et al. (2021)	4594	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	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	G	1.0
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.98, AY.35	Tada et al. (2021)	12	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Alternate Allele	Alternate Frequency
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.54, AY.46.2, AY.45, AY.88, AY.108, AY.11, AY.113, AY.118, AY.13, AY.3.1, AY.53, AY.73, AY.103, AY.43.4, AY.124, AY.109, AY.84, AY.23, AY.89, AY.36, AY.44, AY.34.1, AY.46.1, AY.119.1, AY.77, AY.75, AY.4, AY.125, AY.59, B.1.617.2, AY.86, AY.19, AY.116.1, AY.117, AY.102, AY.15, AY.32, AY.34, AY.116, AY.9, AY.9.2.1, AY.37, AY.121.1, AY.43.3, AY.2, AY.4.4, AY.47, AY.5, AY.65, AY.25, AY.120.1, AY.42, AY.74, AY.105, AY.120, AY.104, AY.126, AY.106, AY.114, AY.51, AY.46.4, AY.43, AY.64, AY.78, AY.3, AY.107, AY.6, AY.7.1, AY.99, AY.26, AY.68, AY.46.6, AY.41, AY.99.2, AY.67, AY.39, AY.4.2.1, AY.4.3, AY.35, AY.20, AY.110, AY.111, AY.127, AY.49, AY.92, AY.14, AY.4.2, AY.40, AY.72, AY.85, AY.39.1, AY.21, AY.94, AY.17, AY.98, AY.60, AY.25.1, AY.1, AY.119, AY.4.5, AY.61, AY.82, AY.121, AY.16.1, AY.56, AY.18, AY.4.2.2, AY.28, AY.93, AY.10, AY.5.3, AY.24, AY.16, AY.62, AY.122, AY.29, AY.83, AY.98.1, AY.9.2, AY.48, AY.4.6, AY.122.1, AY.55, AY.87, AY.101, AY.100	Wilhelm et al. (2021)	45770	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Alternate Allele	Alternate Frequency
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.119.1, AY.64, AY.75, AY.60, AY.61, AY.26, AY.59, B.1.617.2, AY.68, AY.88, AY.4.2.2, AY.28, AY.67, AY.10, AY.24, AY.62, AY.9, AY.4.2.1, AY.9.2.1, AY.37, AY.73, AY.2, AY.47, AY.9.2, AY.65, AY.14, AY.4.2, AY.74, AY.55, AY.72, AY.21	Brehm et al. (2021)	10039	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Alternate Allele	Alternate Frequency
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.54, AY.46.2, AY.45, AY.88, AY.108, AY.11, AY.113, AY.118, AY.13, AY.3.1, AY.53, AY.73, AY.103, AY.43.4, AY.124, AY.109, AY.84, AY.23, AY.89, AY.36, AY.44, AY.34.1, AY.46.1, AY.119.1, AY.77, AY.75, AY.4, AY.125, AY.59, B.1.617.2, AY.86, AY.19, AY.116.1, AY.117, AY.102, AY.15, AY.32, AY.34, AY.116, AY.9, AY.9.2.1, AY.37, AY.121.1, AY.43.3, AY.2, AY.4.4, AY.47, AY.5, AY.65, AY.25, AY.120.1, AY.42, AY.74, AY.105, AY.120, AY.104, AY.126, AY.106, AY.114, AY.51, AY.46.4, AY.43, AY.64, AY.78, AY.3, AY.107, AY.6, AY.7.1, AY.99, AY.26, AY.68, AY.46.6, AY.41, AY.99.2, AY.67, AY.39, AY.4.2.1, AY.4.3, AY.35, AY.20, AY.110, AY.111, AY.127, AY.49, AY.92, AY.14, AY.4.2, AY.40, AY.72, AY.85, AY.39.1, AY.21, AY.94, AY.17, AY.98, AY.60, AY.25.1, AY.1, AY.119, AY.4.5, AY.61, AY.82, AY.121, AY.16.1, AY.56, AY.18, AY.4.2.2, AY.28, AY.93, AY.10, AY.5.3, AY.24, AY.16, AY.62, AY.122, AY.29, AY.83, AY.98.1, AY.9.2, AY.48, AY.4.6, AY.122.1, AY.55, AY.87, AY.101, AY.100	Landis et al. (2021)	45770	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Alternate Allele	Alternate Frequency
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.119.1, AY.64, AY.75, AY.60, AY.61, AY.26, AY.59, B.1.617.2, AY.68, AY.88, AY.4.2.2, AY.28, AY.67, AY.10, AY.24, AY.62, AY.9, AY.4.2.1, AY.9.2.1, AY.37, AY.73, AY.2, AY.47, AY.9.2, AY.65, AY.14, AY.4.2, AY.74, AY.55, AY.72, AY.21	Brehm et al. (2021)	10039	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Alternate Allele	Alternate Frequency
p.D614G	syncytium formation	Slight increase in Vero cell-cell membrane fusion assay under infection with VSV pseudotyped virus.	AY.54, AY.46.2, AY.45, AY.88, AY.108, AY.11, AY.113, AY.118, AY.13, AY.3.1, AY.53, AY.73, AY.103, AY.43.4, AY.124, AY.109, AY.84, AY.23, AY.89, AY.36, AY.44, AY.34.1, AY.46.1, AY.119.1, AY.77, AY.75, AY.4, AY.125, AY.59, B.1.617.2, AY.86, AY.19, AY.116.1, AY.117, AY.102, AY.15, AY.32, AY.34, AY.116, AY.9, AY.9.2.1, AY.37, AY.121.1, AY.43.3, AY.2, AY.4.4, AY.47, AY.5, AY.65, AY.25, AY.120.1, AY.42, AY.74, AY.105, AY.120, AY.104, AY.126, AY.106, AY.114, AY.51, AY.46.4, AY.43, AY.64, AY.78, AY.3, AY.107, AY.6, AY.7.1, AY.99, AY.26, AY.68, AY.46.6, AY.41, AY.99.2, AY.67, AY.39, AY.4.2.1, AY.4.3, AY.35, AY.20, AY.110, AY.111, AY.127, AY.49, AY.92, AY.14, AY.4.2, AY.40, AY.72, AY.85, AY.39.1, AY.21, AY.94, AY.17, AY.98, AY.60, AY.25.1, AY.1, AY.119, AY.4.5, AY.61, AY.82, AY.121, AY.16.1, AY.56, AY.18, AY.4.2.2, AY.28, AY.93, AY.10, AY.5.3, AY.24, AY.16, AY.62, AY.122, AY.29, AY.83, AY.98.1, AY.9.2, AY.48, AY.4.6, AY.122.1, AY.55, AY.87, AY.101, AY.100	Kim et al. (2021)	45770	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	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 vaccinee neutralizing at weeks 3 and 6 against B.1.1.7 and D614G) suggest that vaccinees probably do not elicit an early humoral response detectable at mucosal surfaces even though sera neutralization was observed. They strengthen the hypothesis that some vaccines may not protect against viral acquisition and infection of the oral–nasal region, but may prevent severe disease associated with viral dissemination in the lower respiratory tract.	AY.54, AY.46.2, AY.45, AY.88, AY.108, AY.11, AY.113, AY.118, AY.13, AY.3.1, AY.53, AY.73, AY.103, AY.43.4, AY.124, AY.109, AY.84, AY.23, AY.89, AY.36, AY.44, AY.34.1, AY.46.1, AY.119.1, AY.77, AY.75, AY.4, AY.125, AY.59, B.1.617.2, AY.86, AY.19, AY.116.1, AY.117, AY.102, AY.15, AY.32, AY.34, AY.116, AY.9, AY.9.2.1, AY.37, AY.121.1, AY.43.3, AY.2, AY.4.4, AY.47, AY.5, AY.65, AY.25, AY.120.1, AY.42, AY.74, AY.105, AY.120, AY.104, AY.126, AY.106, AY.114, AY.51, AY.46.4, AY.43, AY.64, AY.78, AY.3, AY.107, AY.6, AY.7.1, AY.99, AY.26, AY.68, AY.46.6, AY.41, AY.99.2, AY.67, AY.39, AY.4.2.1, AY.4.3, AY.35, AY.20, AY.110, AY.111, AY.127, AY.49, AY.92, AY.14, AY.4.2, AY.40, AY.72, AY.85, AY.39.1, AY.21, AY.94, AY.17, AY.98, AY.60, AY.25.1, AY.1, AY.119, AY.4.5, AY.61, AY.82, AY.121, AY.16.1, AY.56, AY.18, AY.4.2.2, AY.28, AY.93, AY.10, AY.5.3, AY.24, AY.16, AY.62, AY.122, AY.29, AY.83, AY.98.1, AY.9.2, AY.48, AY.4.6, AY.122.1, AY.55, AY.87, AY.101, AY.100	Planas et al. (2021)	45770	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Alternate Allele	Alternate Frequency
p.D614G	trafficking	Circulating variant shown in vitro to not have major defects or enhancement of cell surface protein trafficking (i.e. Spike cleavage or fusion required for cell entry)	AY.54, AY.46.2, AY.45, AY.88, AY.108, AY.11, AY.113, AY.118, AY.13, AY.3.1, AY.53, AY.73, AY.103, AY.43.4, AY.124, AY.109, AY.84, AY.23, AY.89, AY.36, AY.44, AY.34.1, AY.46.1, AY.119.1, AY.77, AY.75, AY.4, AY.125, AY.59, B.1.617.2, AY.86, AY.19, AY.116.1, AY.117, AY.102, AY.15, AY.32, AY.34, AY.116, AY.9, AY.9.2.1, AY.37, AY.121.1, AY.43.3, AY.2, AY.4.4, AY.47, AY.5, AY.65, AY.25, AY.120.1, AY.42, AY.74, AY.105, AY.120, AY.104, AY.126, AY.106, AY.114, AY.51, AY.46.4, AY.43, AY.64, AY.78, AY.3, AY.107, AY.6, AY.7.1, AY.99, AY.26, AY.68, AY.46.6, AY.41, AY.99.2, AY.67, AY.39, AY.4.2.1, AY.4.3, AY.35, AY.20, AY.110, AY.111, AY.127, AY.49, AY.92, AY.14, AY.4.2, AY.40, AY.72, AY.85, AY.39.1, AY.21, AY.94, AY.17, AY.98, AY.60, AY.25.1, AY.1, AY.119, AY.4.5, AY.61, AY.82, AY.121, AY.16.1, AY.56, AY.18, AY.4.2.2, AY.28, AY.93, AY.10, AY.5.3, AY.24, AY.16, AY.62, AY.122, AY.29, AY.83, AY.98.1, AY.9.2, AY.48, AY.4.6, AY.122.1, AY.55, AY.87, AY.101, AY.100	Barrett et al. (2021)	45770	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	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.54, AY.46.2, AY.45, AY.88, AY.108, AY.11, AY.113, AY.118, AY.13, AY.3.1, AY.53, AY.73, AY.103, AY.43.4, AY.124, AY.109, AY.84, AY.23, AY.89, AY.36, AY.44, AY.34.1, AY.46.1, AY.119.1, AY.77, AY.75, AY.4, AY.125, AY.59, B.1.617.2, AY.86, AY.19, AY.116.1, AY.117, AY.102, AY.15, AY.32, AY.34, AY.116, AY.9, AY.9.2.1, AY.37, AY.121.1, AY.43.3, AY.2, AY.4.4, AY.47, AY.5, AY.65, AY.25, AY.120.1, AY.42, AY.74, AY.105, AY.120, AY.104, AY.126, AY.106, AY.114, AY.51, AY.46.4, AY.43, AY.64, AY.78, AY.3, AY.107, AY.6, AY.7.1, AY.99, AY.26, AY.68, AY.46.6, AY.41, AY.99.2, AY.67, AY.39, AY.4.2.1, AY.4.3, AY.35, AY.20, AY.110, AY.111, AY.127, AY.49, AY.92, AY.14, AY.4.2, AY.40, AY.72, AY.85, AY.39.1, AY.21, AY.94, AY.17, AY.98, AY.60, AY.25.1, AY.1, AY.119, AY.4.5, AY.61, AY.82, AY.121, AY.16.1, AY.56, AY.18, AY.4.2.2, AY.28, AY.93, AY.10, AY.5.3, AY.24, AY.16, AY.62, AY.122, AY.29, AY.83, AY.98.1, AY.9.2, AY.48, AY.4.6, AY.122.1, AY.55, AY.87, AY.101, AY.100	Daniloski et al. (2021)	45770	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Alternate Allele	Alternate Frequency
p.D614G	trafficking	No change in infectivity (24h) relative to D614G alone in Caco-2 cells, Vero or Calu-3.	AY.54, AY.46.2, AY.45, AY.88, AY.108, AY.11, AY.113, AY.118, AY.13, AY.3.1, AY.53, AY.73, AY.103, AY.43.4, AY.124, AY.109, AY.84, AY.23, AY.89, AY.36, AY.44, AY.34.1, AY.46.1, AY.119.1, AY.77, AY.75, AY.4, AY.125, AY.59, B.1.617.2, AY.86, AY.19, AY.116.1, AY.117, AY.102, AY.15, AY.32, AY.34, AY.116, AY.9, AY.9.2.1, AY.37, AY.121.1, AY.43.3, AY.2, AY.4.4, AY.47, AY.5, AY.65, AY.25, AY.120.1, AY.42, AY.74, AY.105, AY.120, AY.104, AY.126, AY.106, AY.114, AY.51, AY.46.4, AY.43, AY.64, AY.78, AY.3, AY.107, AY.6, AY.7.1, AY.99, AY.26, AY.68, AY.46.6, AY.41, AY.99.2, AY.67, AY.39, AY.4.2.1, AY.4.3, AY.35, AY.20, AY.110, AY.111, AY.127, AY.49, AY.92, AY.14, AY.4.2, AY.40, AY.72, AY.85, AY.39.1, AY.21, AY.94, AY.17, AY.98, AY.60, AY.25.1, AY.1, AY.119, AY.4.5, AY.61, AY.82, AY.121, AY.16.1, AY.56, AY.18, AY.4.2.2, AY.28, AY.93, AY.10, AY.5.3, AY.24, AY.16, AY.62, AY.122, AY.29, AY.83, AY.98.1, AY.9.2, AY.48, AY.4.6, AY.122.1, AY.55, AY.87, AY.101, AY.100	Kim et al. (2021)	45770	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Alternate Allele	Alternate Frequency
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.54, AY.46.2, AY.45, AY.88, AY.108, AY.11, AY.113, AY.118, AY.13, AY.3.1, AY.53, AY.73, AY.103, AY.43.4, AY.124, AY.109, AY.84, AY.23, AY.89, AY.36, AY.44, AY.34.1, AY.46.1, AY.119.1, AY.77, AY.75, AY.4, AY.125, AY.59, B.1.617.2, AY.86, AY.19, AY.116.1, AY.117, AY.102, AY.15, AY.32, AY.34, AY.116, AY.9, AY.9.2.1, AY.37, AY.121.1, AY.43.3, AY.2, AY.4.4, AY.47, AY.5, AY.65, AY.25, AY.120.1, AY.42, AY.74, AY.105, AY.120, AY.104, AY.126, AY.106, AY.114, AY.51, AY.46.4, AY.43, AY.64, AY.78, AY.3, AY.107, AY.6, AY.7.1, AY.99, AY.26, AY.68, AY.46.6, AY.41, AY.99.2, AY.67, AY.39, AY.4.2.1, AY.4.3, AY.35, AY.20, AY.110, AY.111, AY.127, AY.49, AY.92, AY.14, AY.4.2, AY.40, AY.72, AY.85, AY.39.1, AY.21, AY.94, AY.17, AY.98, AY.60, AY.25.1, AY.1, AY.119, AY.4.5, AY.61, AY.82, AY.121, AY.16.1, AY.56, AY.18, AY.4.2.2, AY.28, AY.93, AY.10, AY.5.3, AY.24, AY.16, AY.62, AY.122, AY.29, AY.83, AY.98.1, AY.9.2, AY.48, AY.4.6, AY.122.1, AY.55, AY.87, AY.101, AY.100	Kim et al. (2021)	45770	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	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	G	1.0
p.D614G	trafficking	extasciitilde2x more infectivity than D614G alone in HEK293T-ACE2 cells 48h post-transduction.	AY.2, AY.1	Kuzmina et al. (2021)	10	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Alternate Allele	Alternate Frequency
p.D614G	trafficking	Among S variants tested, the D614G mutant shows the highest cell entry (extascitilde3.5x wild type), as supported by structural and binding analyses.	AY.54, AY.46.2, AY.45, AY.88, AY.108, AY.11, AY.113, AY.118, AY.13, AY.3.1, AY.53, AY.73, AY.103, AY.43.4, AY.124, AY.109, AY.84, AY.23, AY.89, AY.36, AY.44, AY.34.1, AY.46.1, AY.119.1, AY.77, AY.75, AY.4, AY.125, AY.59, B.1.617.2, AY.86, AY.19, AY.116.1, AY.117, AY.102, AY.15, AY.32, AY.34, AY.116, AY.9, AY.9.2.1, AY.37, AY.121.1, AY.43.3, AY.2, AY.4.4, AY.47, AY.5, AY.65, AY.25, AY.120.1, AY.42, AY.74, AY.105, AY.120, AY.104, AY.126, AY.106, AY.114, AY.51, AY.46.4, AY.43, AY.64, AY.78, AY.3, AY.107, AY.6, AY.7.1, AY.99, AY.26, AY.68, AY.46.6, AY.41, AY.99.2, AY.67, AY.39, AY.4.2.1, AY.4.3, AY.35, AY.20, AY.110, AY.111, AY.127, AY.49, AY.92, AY.14, AY.4.2, AY.40, AY.72, AY.85, AY.39.1, AY.21, AY.94, AY.17, AY.98, AY.60, AY.25.1, AY.1, AY.119, AY.4.5, AY.61, AY.82, AY.121, AY.16.1, AY.56, AY.18, AY.4.2.2, AY.28, AY.93, AY.10, AY.5.3, AY.24, AY.16, AY.62, AY.122, AY.29, AY.83, AY.98.1, AY.9.2, AY.48, AY.4.6, AY.122.1, AY.55, AY.87, AY.101, AY.100	Ozono et al. (2020)	45770	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	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.54, AY.46.2, AY.45, AY.88, AY.108, AY.11, AY.113, AY.118, AY.13, AY.3.1, AY.53, AY.73, AY.103, AY.43.4, AY.124, AY.109, AY.84, AY.23, AY.89, AY.36, AY.44, AY.34.1, AY.46.1, AY.119.1, AY.77, AY.75, AY.4, AY.125, AY.59, B.1.617.2, AY.86, AY.19, AY.116.1, AY.117, AY.102, AY.15, AY.32, AY.34, AY.116, AY.9, AY.9.2.1, AY.37, AY.121.1, AY.43.3, AY.2, AY.4.4, AY.47, AY.65, AY.25, AY.120.1, AY.42, AY.74, AY.105, AY.120, AY.104, AY.126, AY.106, AY.114, AY.51, AY.46.4, AY.43, AY.64, AY.78, AY.3, AY.107, AY.6, AY.7.1, AY.99, AY.26, AY.68, AY.46.6, AY.41, AY.99.2, AY.67, AY.39, AY.4.2.1, AY.4.3, AY.35, AY.20, AY.110, AY.111, AY.127, AY.49, AY.92, AY.14, AY.4.2, AY.40, AY.72, AY.85, AY.39.1, AY.21, AY.94, AY.17, AY.98, AY.60, AY.25.1, AY.1, AY.119, AY.4.5, AY.61, AY.82, AY.121, AY.16.1, AY.56, AY.18, AY.4.2.2, AY.28, AY.93, AY.10, AY.5.3, AY.24, AY.16, AY.62, AY.122, AY.29, AY.83, AY.98.1, AY.9.2, AY.48, AY.4.6, AY.122.1, AY.55, AY.87, AY.101, AY.100	Tada et al. (2021)	45752	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	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.54, AY.46.2, AY.45, AY.88, AY.108, AY.11, AY.113, AY.118, AY.13, AY.3.1, AY.53, AY.73, AY.103, AY.43.4, AY.124, AY.109, AY.84, AY.23, AY.89, AY.36, AY.44, AY.34.1, AY.46.1, AY.119.1, AY.77, AY.75, AY.4, AY.125, AY.59, B.1.617.2, AY.86, AY.19, AY.116.1, AY.117, AY.102, AY.15, AY.32, AY.34, AY.116, AY.9, AY.9.2.1, AY.37, AY.121.1, AY.43.3, AY.2, AY.4.4, AY.47, AY.5, AY.65, AY.25, AY.120.1, AY.42, AY.74, AY.105, AY.120, AY.104, AY.126, AY.106, AY.114, AY.51, AY.46.4, AY.43, AY.64, AY.78, AY.3, AY.107, AY.6, AY.7.1, AY.99, AY.26, AY.68, AY.46.6, AY.41, AY.99.2, AY.67, AY.39, AY.4.2.1, AY.4.3, AY.35, AY.20, AY.110, AY.111, AY.127, AY.49, AY.92, AY.14, AY.4.2, AY.40, AY.72, AY.85, AY.39.1, AY.21, AY.94, AY.17, AY.98, AY.60, AY.25.1, AY.1, AY.119, AY.4.5, AY.61, AY.82, AY.121, AY.16.1, AY.56, AY.18, AY.4.2.2, AY.28, AY.93, AY.10, AY.5.3, AY.24, AY.16, AY.62, AY.122, AY.29, AY.83, AY.98.1, AY.9.2, AY.48, AY.4.6, AY.122.1, AY.55, AY.87, AY.101, AY.100	Zhang et l. (2020)	45770	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	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.54, AY.46.2, AY.45, AY.88, AY.108, AY.11, AY.113, AY.118, AY.13, AY.3.1, AY.53, AY.73, AY.103, AY.43.4, AY.124, AY.109, AY.84, AY.23, AY.89, AY.36, AY.44, AY.34.1, AY.46.1, AY.119.1, AY.77, AY.75, AY.4, AY.125, AY.59, B.1.617.2, AY.86, AY.19, AY.116.1, AY.117, AY.102, AY.15, AY.32, AY.34, AY.116, AY.9, AY.9.2.1, AY.37, AY.121.1, AY.43.3, AY.2, AY.4.4, AY.47, AY.5, AY.65, AY.25, AY.120.1, AY.42, AY.74, AY.105, AY.120, AY.104, AY.126, AY.106, AY.114, AY.51, AY.46.4, AY.43, AY.64, AY.78, AY.3, AY.107, AY.6, AY.7.1, AY.99, AY.26, AY.68, AY.46.6, AY.41, AY.99.2, AY.67, AY.39, AY.4.2.1, AY.4.3, AY.35, AY.20, AY.110, AY.111, AY.127, AY.49, AY.92, AY.14, AY.4.2, AY.40, AY.72, AY.85, AY.39.1, AY.21, AY.94, AY.17, AY.98, AY.60, AY.25.1, AY.1, AY.119, AY.4.5, AY.61, AY.82, AY.121, AY.16.1, AY.56, AY.18, AY.4.2.2, AY.28, AY.93, AY.10, AY.5.3, AY.24, AY.16, AY.62, AY.122, AY.29, AY.83, AY.98.1, AY.9.2, AY.48, AY.4.6, AY.122.1, AY.55, AY.87, AY.101, AY.100	Tada et al. (2021)	45770	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Alternate Allele	Alternate Frequency
p.D614G	transmissibility	The combination caused a 3-fold increase in infectivity relative to D614G wild type. [compare to 3.5x for L452R alone]	AY.98, AY.35	Tada et al. (2021)	12	G	1.0
p.D614G	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.98, AY.35	Tada et al. (2021)	12	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Alternate Allele	Alternate Frequency
p.D614G	vaccine neutralization efficacy	Pseudotyped D614G virus has reduced neutralization activity vs wild type: 1.2x (37 sera Pfizer median 9 days post 2nd dose, 37 sera Moderna median 18 days post 2nd dose). This was NOT significant by ANOVA.	AY.54, AY.46.2, AY.45, AY.88, AY.108, AY.11, AY.113, AY.118, AY.13, AY.3.1, AY.53, AY.73, AY.103, AY.43.4, AY.124, AY.109, AY.84, AY.23, AY.89, AY.36, AY.44, AY.34.1, AY.46.1, AY.119.1, AY.77, AY.75, AY.4, AY.125, AY.59, B.1.617.2, AY.86, AY.19, AY.116.1, AY.117, AY.102, AY.15, AY.32, AY.34, AY.116, AY.9, AY.9.2.1, AY.37, AY.121.1, AY.43.3, AY.2, AY.4.4, AY.47, AY.5, AY.65, AY.25, AY.120.1, AY.42, AY.74, AY.105, AY.120, AY.104, AY.126, AY.106, AY.114, AY.51, AY.46.4, AY.43, AY.64, AY.78, AY.3, AY.107, AY.6, AY.7.1, AY.99, AY.26, AY.68, AY.46.6, AY.41, AY.99.2, AY.67, AY.39, AY.4.2.1, AY.4.3, AY.35, AY.20, AY.110, AY.111, AY.127, AY.49, AY.92, AY.14, AY.4.2, AY.40, AY.72, AY.85, AY.39.1, AY.21, AY.94, AY.17, AY.98, AY.60, AY.25.1, AY.1, AY.119, AY.4.5, AY.61, AY.82, AY.121, AY.16.1, AY.56, AY.18, AY.4.2.2, AY.28, AY.93, AY.10, AY.5.3, AY.24, AY.16, AY.62, AY.122, AY.29, AY.83, AY.98.1, AY.9.2, AY.48, AY.4.6, AY.122.1, AY.55, AY.87, AY.101, AY.100	Garcia-Beltran et al. (2021)	45770	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	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.98, AY.35	Gong et al. (2021)	12	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	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 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.54, AY.46.2, AY.45, AY.88, AY.108, AY.11, AY.113, AY.118, AY.13, AY.3.1, AY.53, AY.73, AY.103, AY.43.4, AY.124, AY.109, AY.84, AY.23, AY.89, AY.36, AY.44, AY.34.1, AY.46.1, AY.119.1, AY.77, AY.75, AY.4, AY.125, AY.59, B.1.617.2, AY.86, AY.19, AY.116.1, AY.117, AY.102, AY.15, AY.32, AY.34, AY.116, AY.9, AY.9.2.1, AY.37, AY.121.1, AY.43.3, AY.2, AY.4.4, AY.47, AY.5, AY.65, AY.25, AY.120.1, AY.42, AY.74, AY.105, AY.120, AY.104, AY.126, AY.106, AY.114, AY.51, AY.46.4, AY.43, AY.64, AY.78, AY.3, AY.107, AY.6, AY.7.1, AY.99, AY.26, AY.68, AY.46.6, AY.41, AY.99.2, AY.67, AY.39, AY.4.2.1, AY.4.3, AY.35, AY.20, AY.110, AY.111, AY.127, AY.49, AY.92, AY.14, AY.4.2, AY.40, AY.72, AY.85, AY.39.1, AY.21, AY.94, AY.17, AY.98, AY.60, AY.25.1, AY.1, AY.119, AY.4.5, AY.61, AY.82, AY.121, AY.16.1, AY.56, AY.18, AY.4.2.2, AY.28, AY.93, AY.10, AY.5.3, AY.24, AY.16, AY.62, AY.122, AY.29, AY.83, AY.98.1, AY.9.2, AY.48, AY.4.6, AY.122.1, AY.55, AY.87, AY.101, AY.100	Kuzmina et al. (2021)	45770	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Alternate Allele	Alternate Frequency
p.D614G	vaccine neutralization 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	1.0
p.D614G	vaccine neutralization efficacy	This variant showed only minor in Pfizer sera (one or two dose) neutralization efficiency vs D614G (using lentivirus pseudotype).	AY.2, AY.1	Kuzmina et al. (2021)	10	G	1.0
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	G	1.0
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.98, AY.35	Tada et al. (2021)	12	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Alternate Allele	Alternate Frequency
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.54, AY.46.2, AY.45, AY.88, AY.108, AY.11, AY.113, AY.118, AY.13, AY.3.1, AY.53, AY.73, AY.103, AY.43.4, AY.124, AY.109, AY.84, AY.23, AY.89, AY.36, AY.44, AY.34.1, AY.46.1, AY.119.1, AY.77, AY.75, AY.4, AY.125, AY.59, B.1.617.2, AY.86, AY.19, AY.116.1, AY.117, AY.102, AY.15, AY.32, AY.34, AY.116, AY.9, AY.9.2.1, AY.37, AY.121.1, AY.43.3, AY.2, AY.4.4, AY.47, AY.5, AY.65, AY.25, AY.120.1, AY.42, AY.74, AY.105, AY.120, AY.104, AY.126, AY.106, AY.114, AY.51, AY.46.4, AY.43, AY.64, AY.78, AY.3, AY.107, AY.6, AY.7.1, AY.99, AY.26, AY.68, AY.46.6, AY.41, AY.99.2, AY.67, AY.39, AY.4.2.1, AY.4.3, AY.35, AY.20, AY.110, AY.111, AY.127, AY.49, AY.92, AY.14, AY.4.2, AY.40, AY.72, AY.85, AY.39.1, AY.21, AY.94, AY.17, AY.98, AY.60, AY.25.1, AY.1, AY.119, AY.4.5, AY.61, AY.82, AY.121, AY.16.1, AY.56, AY.18, AY.4.2.2, AY.28, AY.93, AY.10, AY.5.3, AY.24, AY.16, AY.62, AY.122, AY.29, AY.83, AY.98.1, AY.9.2, AY.48, AY.4.6, AY.122.1, AY.55, AY.87, AY.101, AY.100	Wilhelm et al. (2021)	45770	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Alternate Allele	Alternate Frequency
p.D614G	vaccine neutralization efficacy	No significant change in virus neutralzation by 18 Pfizer two dose vaccinee sera compared to B.1.1.7. [results without including the used mutation A27S likely generalizable, as this is not a lineage defining mutation]	AY.5	Zuckerman et al. (2021)	18	G	1.0
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. 1.06x 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	1.0
p.D614G	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	G	1.0
p.D614G	vaccinee plasma binding	1.76x increase in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in previously non-seroconverted subjects. 1.75x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in post-infection vaccinees.	AY.2, AY.1	Gong et al. (2021)	10	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Alternate Allele	Alternate Frequency
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.54, AY.46.2, AY.45, AY.88, AY.108, AY.11, AY.113, AY.118, AY.13, AY.3.1, AY.53, AY.73, AY.103, AY.43.4, AY.124, AY.109, AY.84, AY.23, AY.89, AY.36, AY.44, AY.34.1, AY.46.1, AY.119.1, AY.77, AY.75, AY.4, AY.125, AY.59, B.1.617.2, AY.86, AY.19, AY.116.1, AY.117, AY.102, AY.15, AY.32, AY.34, AY.116, AY.9, AY.9.2.1, AY.37, AY.121.1, AY.43.3, AY.2, AY.4.4, AY.47, AY.5, AY.65, AY.25, AY.120.1, AY.42, AY.74, AY.105, AY.120, AY.104, AY.126, AY.106, AY.114, AY.51, AY.46.4, AY.43, AY.64, AY.78, AY.3, AY.107, AY.6, AY.7.1, AY.99, AY.26, AY.68, AY.46.6, AY.41, AY.99.2, AY.67, AY.39, AY.4.2.1, AY.4.3, AY.35, AY.20, AY.110, AY.111, AY.127, AY.49, AY.92, AY.14, AY.4.2, AY.40, AY.72, AY.85, AY.39.1, AY.21, AY.94, AY.17, AY.98, AY.60, AY.25.1, AY.1, AY.119, AY.4.5, AY.61, AY.82, AY.121, AY.16.1, AY.56, AY.18, AY.4.2.2, AY.28, AY.93, AY.10, AY.5.3, AY.24, AY.16, AY.62, AY.122, AY.29, AY.83, AY.98.1, AY.9.2, AY.48, AY.4.6, AY.122.1, AY.55, AY.87, AY.101, AY.100	Gong et al. (2021)	45770	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Alternate Allele	Alternate Frequency
p.D614G	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.98, AY.35	Gong et al. (2021)	12	G	1.0
p.D614G	vaccinee plasma binding	1.23x increase in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in previously non-seroconverted subjects. 1.1x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in post-infection vaccinees.	AY.77, AY.46.4, AY.6, AY.35, AY.4.4	Gong et al. (2021)	31	G	1.0
p.D614G	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	Gong et al. (2021)	1	G	1.0
p.D614G	vaccinee plasma binding	1.14x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in previously non-seroconverted subjects. 1.11x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in post-infection vaccinees.	AY.5	Gong et al. (2021)	18	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	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.106, AY.114, AY.119.1, AY.77, AY.78, AY.107, AY.4, AY.1, AY.119, AY.4.5, AY.125, B.1.617.2, AY.121, AY.88, AY.4.2.2, AY.116.1, AY.117, AY.108, AY.5.3, AY.102, AY.113, AY.118, AY.34, AY.116, AY.39, AY.4.2.1, AY.4.3, AY.121.1, AY.29, AY.124, AY.4.4, AY.20, AY.43.4, AY.109, AY.110, AY.111, AY.127, AY.89, AY.36, AY.34.1, AY.4.6, AY.92, AY.120.1, AY.4.2, AY.42, AY.120, AY.85, AY.104, AY.39.1, AY.101, AY.126, AY.100	Gong et al. (2021)	4594	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	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.54, AY.46.2, AY.45, AY.88, AY.108, AY.11, AY.113, AY.118, AY.13, AY.3.1, AY.53, AY.73, AY.103, AY.43.4, AY.124, AY.109, AY.84, AY.23, AY.89, AY.36, AY.44, AY.34.1, AY.46.1, AY.119.1, AY.77, AY.75, AY.4, AY.125, AY.59, B.1.617.2, AY.86, AY.19, AY.116.1, AY.117, AY.102, AY.15, AY.32, AY.34, AY.116, AY.9, AY.9.2.1, AY.37, AY.121.1, AY.43.3, AY.2, AY.4.4, AY.47, AY.5, AY.65, AY.25, AY.120.1, AY.42, AY.74, AY.105, AY.120, AY.104, AY.126, AY.106, AY.114, AY.51, AY.46.4, AY.43, AY.64, AY.78, AY.3, AY.107, AY.6, AY.7.1, AY.99, AY.26, AY.68, AY.46.6, AY.41, AY.99.2, AY.67, AY.39, AY.4.2.1, AY.4.3, AY.35, AY.20, AY.110, AY.111, AY.127, AY.49, AY.92, AY.14, AY.4.2, AY.40, AY.72, AY.85, AY.39.1, AY.21, AY.94, AY.17, AY.98, AY.60, AY.25.1, AY.1, AY.119, AY.4.5, AY.61, AY.82, AY.121, AY.16.1, AY.56, AY.18, AY.4.2.2, AY.28, AY.93, AY.10, AY.5.3, AY.24, AY.16, AY.62, AY.122, AY.29, AY.83, AY.98.1, AY.9.2, AY.48, AY.4.6, AY.122.1, AY.55, AY.87, AY.101, AY.100	Plante et al. (2020)	45770	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Alternate Allele	Alternate Frequency
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.54, AY.46.2, AY.45, AY.88, AY.108, AY.11, AY.113, AY.118, AY.13, AY.3.1, AY.53, AY.73, AY.103, AY.43.4, AY.124, AY.109, AY.84, AY.23, AY.89, AY.36, AY.44, AY.34.1, AY.46.1, AY.119.1, AY.77, AY.75, AY.4, AY.125, AY.59, B.1.617.2, AY.86, AY.19, AY.116.1, AY.117, AY.102, AY.15, AY.32, AY.34, AY.116, AY.9, AY.9.2.1, AY.37, AY.121.1, AY.43.3, AY.2, AY.4.4, AY.47, AY.5, AY.65, AY.25, AY.120.1, AY.42, AY.74, AY.105, AY.120, AY.104, AY.126, AY.106, AY.114, AY.51, AY.46.4, AY.43, AY.64, AY.78, AY.3, AY.107, AY.6, AY.7.1, AY.99, AY.26, AY.68, AY.46.6, AY.41, AY.99.2, AY.67, AY.39, AY.4.2.1, AY.4.3, AY.35, AY.20, AY.110, AY.111, AY.127, AY.49, AY.92, AY.14, AY.4.2, AY.40, AY.72, AY.85, AY.39.1, AY.21, AY.94, AY.17, AY.98, AY.60, AY.25.1, AY.1, AY.119, AY.4.5, AY.61, AY.82, AY.121, AY.16.1, AY.56, AY.18, AY.4.2.2, AY.28, AY.93, AY.10, AY.5.3, AY.24, AY.16, AY.62, AY.122, AY.29, AY.83, AY.98.1, AY.9.2, AY.48, AY.4.6, AY.122.1, AY.55, AY.87, AY.101, AY.100	Spratt et al. (2021)	45770	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Alternate Allele	Alternate Frequency
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.54, AY.46.2, AY.45, AY.88, AY.108, AY.11, AY.113, AY.118, AY.13, AY.3.1, AY.53, AY.73, AY.103, AY.43.4, AY.124, AY.109, AY.84, AY.23, AY.89, AY.36, AY.44, AY.34.1, AY.46.1, AY.119.1, AY.77, AY.75, AY.4, AY.125, AY.59, B.1.617.2, AY.86, AY.19, AY.116.1, AY.117, AY.102, AY.15, AY.32, AY.34, AY.116, AY.9, AY.9.2.1, AY.37, AY.121.1, AY.43.3, AY.2, AY.4.4, AY.47, AY.5, AY.65, AY.25, AY.120.1, AY.42, AY.74, AY.105, AY.120, AY.104, AY.126, AY.106, AY.114, AY.51, AY.46.4, AY.43, AY.64, AY.78, AY.3, AY.107, AY.6, AY.7.1, AY.99, AY.26, AY.68, AY.46.6, AY.41, AY.99.2, AY.67, AY.39, AY.4.2.1, AY.4.3, AY.35, AY.20, AY.110, AY.111, AY.127, AY.49, AY.92, AY.14, AY.4.2, AY.40, AY.72, AY.85, AY.39.1, AY.21, AY.94, AY.17, AY.98, AY.60, AY.25.1, AY.1, AY.119, AY.4.5, AY.61, AY.82, AY.121, AY.16.1, AY.56, AY.18, AY.4.2.2, AY.28, AY.93, AY.10, AY.5.3, AY.24, AY.16, AY.62, AY.122, AY.29, AY.83, AY.98.1, AY.9.2, AY.48, AY.4.6, AY.122.1, AY.55, AY.87, AY.101, AY.100	Weissman et al. (2020)	45770	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	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.54, AY.46.2, AY.45, AY.88, AY.108, AY.11, AY.113, AY.118, AY.13, AY.3.1, AY.53, AY.73, AY.103, AY.43.4, AY.124, AY.109, AY.84, AY.23, AY.89, AY.36, AY.44, AY.34.1, AY.46.1, AY.119.1, AY.77, AY.75, AY.4, AY.125, AY.59, B.1.617.2, AY.86, AY.19, AY.116.1, AY.117, AY.102, AY.15, AY.32, AY.34, AY.116, AY.9, AY.9.2.1, AY.37, AY.121.1, AY.43.3, AY.2, AY.4.4, AY.47, AY.5, AY.65, AY.25, AY.120.1, AY.42, AY.74, AY.105, AY.120, AY.104, AY.126, AY.106, AY.114, AY.51, AY.46.4, AY.43, AY.64, AY.78, AY.3, AY.107, AY.6, AY.7.1, AY.99, AY.26, AY.68, AY.46.6, AY.41, AY.99.2, AY.67, AY.39, AY.4.2.1, AY.4.3, AY.35, AY.20, AY.110, AY.111, AY.127, AY.49, AY.92, AY.14, AY.4.2, AY.40, AY.72, AY.85, AY.39.1, AY.21, AY.94, AY.17, AY.98, AY.60, AY.25.1, AY.1, AY.119, AY.4.5, AY.61, AY.82, AY.121, AY.16.1, AY.56, AY.18, AY.4.2.2, AY.28, AY.93, AY.10, AY.5.3, AY.24, AY.16, AY.62, AY.122, AY.29, AY.83, AY.98.1, AY.9.2, AY.48, AY.4.6, AY.122.1, AY.55, AY.87, AY.101, AY.100	Yurkovetskiy et al. (2020)	45770	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Alternate Allele	Alternate Frequency
p.D614G	virion structure	Based on pseudotyped virus experiments, D614G may increase infectivity by assembling more functional S protein into the virion.	AY.54, AY.46.2, AY.45, AY.88, AY.108, AY.11, AY.113, AY.118, AY.13, AY.3.1, AY.53, AY.73, AY.103, AY.43.4, AY.124, AY.109, AY.84, AY.23, AY.89, AY.36, AY.44, AY.34.1, AY.46.1, AY.119.1, AY.77, AY.75, AY.4, AY.125, AY.59, B.1.617.2, AY.86, AY.19, AY.116.1, AY.117, AY.102, AY.15, AY.32, AY.34, AY.116, AY.9, AY.9.2.1, AY.37, AY.121.1, AY.43.3, AY.2, AY.4.4, AY.47, AY.5, AY.65, AY.25, AY.120.1, AY.42, AY.74, AY.105, AY.120, AY.104, AY.126, AY.106, AY.114, AY.51, AY.46.4, AY.43, AY.64, AY.78, AY.3, AY.107, AY.6, AY.7.1, AY.99, AY.26, AY.68, AY.46.6, AY.41, AY.99.2, AY.67, AY.39, AY.4.2.1, AY.4.3, AY.35, AY.20, AY.110, AY.111, AY.127, AY.49, AY.92, AY.14, AY.4.2, AY.40, AY.72, AY.85, AY.39.1, AY.21, AY.94, AY.17, AY.98, AY.60, AY.25.1, AY.1, AY.119, AY.4.5, AY.61, AY.82, AY.121, AY.16.1, AY.56, AY.18, AY.4.2.2, AY.28, AY.93, AY.10, AY.5.3, AY.24, AY.16, AY.62, AY.122, AY.29, AY.83, AY.98.1, AY.9.2, AY.48, AY.4.6, AY.122.1, AY.55, AY.87, AY.101, AY.100	Zhang et al. (2020)	45770	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Alternate Allele	Alternate Frequency
p.L452R	ACE2 receptor binding affinity	Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant showed a 2.66x increase in binding (KD) relative to D614G.	AY.3.1	Gong et al. (2021)	22	TG,CG	1.0
p.L452R	ACE2 receptor binding affinity	extasciitilde1.7-fold increase in binding affinity vs wild type.	AY.3.1	Motozono et al. (2021)	22	TG,CG	1.0
p.L452R	T cell evasion	L452R derivative virus did not induce IFN-gamma expression even at the highest concentration tested (10 nM) in two different A*24:02 convalescent sera donor plasma (linear epitope NYNYLYRLF 448,456).	AY.3.1	Motozono et al. (2021)	22	TG,CG	1.0
p.L452R	antibody epitope effects	Resistent to some neutralizing antibodies: mAbs X593 and P2B-2F6	AY.3.1	Li et al. (2020)	22	TG,CG	1.0
p.L452R	antibody epitope effects	Mutant screen in neutralization assay with a broad range of monoclonal antibodies shows resistence to more than one antibody.	AY.3.1	Liu et al. (2021)	22	TG,CG	1.0
p.L452R	antibody epitope effects	10 of 14 RBD-specific mAbs that showed at least 10-fold reduced neutralization of B.1.427/B.1.429 variant pseudotype (S13I, W152C, and L452R) were also found to poorly bind to just a L452R RBD mutant, demonstrating a role for this mutation as an escape mechanism for certain RBD-targeting mAbs.	AY.3.1	McCallum et al. (2021)	22	TG,CG	1.0
p.L452R	antibody epitope effects	extasciitilde20% (ELISA significance threshold) drop in antibody binding (ELISA) by this variant against monoclonal antibody VH ab6.	AY.3.1	Sun et al. (2021)	22	TG,CG	1.0
p.L452R	convalescent plasma binding	2.15x increase in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset.	AY.3.1	Gong et al. (2021)	22	TG,CG	1.0
p.L452R	convalescent plasma escape	Observed extasciitilde2x decrease on average in 16 health workers' convalescent sera.	AY.3.1	Alenquer et al. (2021)	22	TG,CG	1.0
p.L452R	convalescent plasma escape	Ablation of neutralization capability of 3 of 4 convalescent sera tested, the other is significantly hindered.	AY.3.1	Liu et al. (2021)	22	TG,CG	1.0
p.L452R	convalescent plasma escape	Relative to B.1, Epsilon (B.1.417/429) shows 1.74x-2.35x decrease in neutralization efficiency by convalescent plasma [no cohort details provided]	AY.3.1	Wilhelm et al. (2021)	22	TG,CG	1.0
p.L452R	gene expression increase	Experimentally, Spike gene expression increased 0.32 fold	AY.3.1	Starr et al. (2020)	22	TG,CG	1.0
p.L452R	monoclonal antibody serial passage escape	Ranked effective mutant against this position in the RBD for highly neutralizing COV2-2096	AY.3.1	Greaney et al. (2020)	22	TG,CG	1.0
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.3.1	Starr et al. (2021)	22	TG,CG	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Alternate Allele	Alternate Frequency
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.	AY.3.1	Wang et al. (2021)	22	TG,CG	1.0
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.3.1	Engelhart et al. (2021)	22	TG,CG	1.0
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.3.1	McCallum et al. (2021)	22	TG,CG	1.0
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.3.1	Deng et al. (2021)	22	TG,CG	1.0
p.L452R	trafficking	This variant alone shows a extasciitilde5x decrease in cell entry efficiency (RLU measurement in 293T cells) compared to D614G. [listed as L454R in Figure, but L452R in text, also text suggests not statistucally significant, but error bars say otherwise in Figure 4]	AY.3.1	Ferriera et al (2021)	22	TG,CG	1.0
p.L452R	trafficking	Increased stability of RBD expression in yeast, suggesting increased Spike protein stability.	AY.3.1	Motozono et al. (2021)	22	TG,CG	1.0
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.3.1	Tada et al. (2021)	22	TG,CG	1.0
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.3.1	Ferreira et al. (2021)	22	TG,CG	1.0
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.3.1	Jacobson et al. (2021)	22	TG,CG	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Alternate Allele	Alternate Frequency
p.L452R	vaccine neutralization efficacy	Relative to B.1, Epsilon (B.1.417/429) shows 1.74x-2.35x decrease in neutralization efficiency by 18 vaccinee sera (BNT162b2 and mRNA1273).	AY.3.1	Wilhelm et al. (2021)	22	TG,CG	1.0
p.L452R	vaccinee plasma binding	1.05x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in previously non-seroconverted subjects. 1.16x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in post-infection vaccinees.	AY.3.1	Gong et al. (2021)	22	TG,CG	1.0
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.3.1	Spratt et al. (2021)	22	TG,CG	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Alternate Allele	Alternate Frequency
p.L452R	ACE2 receptor binding affinity	Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant showed a 2.66x increase in binding (KD) relative to D614G.	AY.54, AY.46.2, AY.45, AY.88, AY.108, AY.11, AY.113, AY.118, AY.13, AY.53, AY.73, AY.103, AY.43.4, AY.124, AY.109, AY.84, AY.23, AY.89, AY.36, AY.44, AY.34.1, AY.46.1, AY.119.1, AY.77, AY.27, AY.75, AY.4, AY.125, AY.59, B.1.617.2, AY.86, AY.19, AY.116.1, AY.117, AY.102, AY.15, AY.32, AY.34, AY.116, AY.9, AY.70, AY.9.2.1, AY.37, AY.121.1, AY.43.3, AY.2, AY.4.4, AY.47, AY.5, AY.65, AY.25, AY.120.1, AY.42, AY.74, AY.105, AY.120, AY.104, AY.126, AY.106, AY.114, AY.51, AY.46.4, AY.43, AY.64, AY.78, AY.3, AY.107, AY.6, AY.7.1, AY.99, AY.26, AY.68, AY.38, AY.46.6, AY.41, AY.99.2, AY.46, AY.67, AY.39, AY.4.2.1, AY.4.3, AY.35, AY.20, AY.110, AY.111, AY.127, AY.33, AY.49, AY.57, AY.92, AY.14, AY.4.2, AY.40, AY.72, AY.85, AY.39.1, AY.21, AY.94, AY.17, AY.98, AY.60, AY.25.1, AY.1, AY.119, AY.4.5, AY.61, AY.82, AY.121, AY.16.1, AY.56, AY.18, AY.4.2.2, AY.28, AY.93, AY.10, AY.5.3, AY.24, AY.16, AY.62, AY.122, AY.29, AY.83, AY.98.1, AY.3.1, AY.48, AY.4.6, AY.122.1,	Gong et al. (2021)	59423	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Alternate Allele	Alternate Frequency
p.L452R	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.98, AY.35, AY.70	Gong et al. (2021)	24	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Alternate Allele	Alternate Frequency
p.L452R	ACE2 receptor binding affinity	extasciitilde1.7-fold increase in binding affinity vs wild type.	AY.54, AY.46.2, AY.45, AY.88, AY.108, AY.11, AY.113, AY.118, AY.13, AY.53, AY.73, AY.103, AY.43.4, AY.124, AY.109, AY.84, AY.23, AY.89, AY.36, AY.44, AY.34.1, AY.46.1, AY.119.1, AY.77, AY.27, AY.75, AY.4, AY.66, AY.125, AY.59, B.1.617.2, AY.86, AY.19, AY.116.1, AY.117, AY.102, AY.15, AY.32, AY.34, AY.116, AY.9, AY.70, AY.9.2.1, AY.37, AY.121.1, AY.43.3, AY.2, AY.4.4, AY.47, AY.5, AY.65, AY.25, AY.120.1, AY.42, AY.74, AY.105, AY.120, AY.104, AY.126, AY.106, AY.114, AY.51, AY.46.4, AY.43, AY.64, AY.78, AY.3, AY.107, AY.6, AY.7.1, AY.99, AY.26, AY.68, AY.38, AY.46.6, AY.41, AY.99.2, AY.46, AY.67, AY.39, AY.4.2.1, AY.4.3, AY.35, AY.20, AY.110, AY.111, AY.127, AY.33, AY.49, AY.57, AY.92, AY.14, AY.4.2, AY.40, AY.72, AY.85, AY.39.1, AY.21, AY.94, AY.17, AY.98, AY.60, AY.25.1, AY.1, AY.119, AY.4.5, AY.61, AY.82, AY.121, AY.16.1, AY.56, AY.18, AY.4.2.2, AY.28, AY.93, AY.10, AY.5.3, AY.24, AY.16, AY.62, AY.122, AY.29, AY.83, AY.98.1, AY.9.2, AY.48, AY.4.6,	Motozono et al. (2021)	59425	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Alternate Allele	Alternate Frequency
p.L452R	T cell evasion	L452R derivative virus did not induce IFN-gamma expression even at the highest concentration tested (10 nM) in two different A*24:02 convalescent sera donor plasma (linear epitope NYNYLYRLF 448,456).	AY.54, AY.46.2, AY.45, AY.88, AY.108, AY.11, AY.113, AY.118, AY.13, AY.53, AY.73, AY.103, AY.43.4, AY.124, AY.109, AY.84, AY.23, AY.89, AY.36, AY.44, AY.34.1, AY.46.1, AY.119.1, AY.77, AY.27, AY.75, AY.4, AY.66, AY.125, AY.59, B.1.617.2, AY.86, AY.19, AY.116.1, AY.117, AY.102, AY.15, AY.32, AY.34, AY.116, AY.9, AY.70, AY.9.2.1, AY.37, AY.121.1, AY.43.3, AY.2, AY.4.4, AY.47, AY.5, AY.65, AY.25, AY.120.1, AY.42, AY.74, AY.105, AY.120, AY.104, AY.126, AY.106, AY.114, AY.51, AY.46.4, AY.43, AY.64, AY.78, AY.3, AY.107, AY.6, AY.7.1, AY.99, AY.26, AY.68, AY.38, AY.46.6, AY.41, AY.99.2, AY.46, AY.67, AY.39, AY.4.2.1, AY.4.3, AY.35, AY.20, AY.110, AY.111, AY.127, AY.33, AY.49, AY.57, AY.92, AY.14, AY.4.2, AY.40, AY.72, AY.85, AY.39.1, AY.21, AY.94, AY.17, AY.98, AY.60, AY.25.1, AY.1, AY.119, AY.4.5, AY.61, AY.82, AY.121, AY.16.1, AY.56, AY.18, AY.4.2.2, AY.28, AY.93, AY.10, AY.5.3, AY.24, AY.16, AY.62, AY.122, AY.29, AY.83, AY.98.1, AY.9.2, AY.48, AY.4.6,	Motozono et al. (2021)	59425	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Alternate Allele	Alternate Frequency
p.L452R	antibody epitope effects	Resistent to some neutralizing antibodies: mAbs X593 and P2B-2F6	AY.54, AY.46.2, AY.45, AY.88, AY.108, AY.11, AY.113, AY.118, AY.13, AY.53, AY.73, AY.103, AY.43.4, AY.124, AY.109, AY.84, AY.23, AY.89, AY.36, AY.44, AY.34.1, AY.46.1, AY.119.1, AY.77, AY.27, AY.75, AY.4, AY.66, AY.125, AY.59, B.1.617.2, AY.86, AY.19, AY.116.1, AY.117, AY.102, AY.15, AY.32, AY.34, AY.116, AY.9, AY.70, AY.9.2.1, AY.37, AY.121.1, AY.43.3, AY.2, AY.4.4, AY.47, AY.5, AY.65, AY.25, AY.120.1, AY.42, AY.74, AY.105, AY.120, AY.104, AY.126, AY.106, AY.114, AY.51, AY.46.4, AY.43, AY.64, AY.78, AY.3, AY.107, AY.6, AY.7.1, AY.99, AY.26, AY.68, AY.38, AY.46.6, AY.41, AY.99.2, AY.46, AY.67, AY.39, AY.4.2.1, AY.4.3, AY.35, AY.20, AY.110, AY.111, AY.127, AY.33, AY.49, AY.57, AY.92, AY.14, AY.4.2, AY.40, AY.72, AY.85, AY.39.1, AY.21, AY.94, AY.17, AY.98, AY.60, AY.25.1, AY.1, AY.119, AY.4.5, AY.61, AY.82, AY.121, AY.16.1, AY.56, AY.18, AY.4.2.2, AY.28, AY.93, AY.10, AY.5.3, AY.24, AY.16, AY.62, AY.122, AY.29, AY.83, AY.20.1, AY.9.2, AY.48, AY.4.6,	Li et al. (2020)	59425	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Alternate Allele	Alternate Frequency
p.L452R	antibody epitope effects	Mutant screen in neutralization assay with a broad range of monoclonal antibodies shows resistence to more than one antibody.	AY.54, AY.46.2, AY.45, AY.88, AY.108, AY.11, AY.113, AY.118, AY.13, AY.53, AY.73, AY.103, AY.43.4, AY.124, AY.109, AY.84, AY.23, AY.89, AY.36, AY.44, AY.34.1, AY.46.1, AY.119.1, AY.77, AY.27, AY.75, AY.4, AY.66, AY.125, AY.59, B.1.617.2, AY.86, AY.19, AY.116.1, AY.117, AY.102, AY.15, AY.32, AY.34, AY.116, AY.9, AY.70, AY.9.2.1, AY.37, AY.121.1, AY.43.3, AY.2, AY.4.4, AY.47, AY.5, AY.65, AY.25, AY.120.1, AY.42, AY.74, AY.105, AY.120, AY.104, AY.126, AY.106, AY.114, AY.51, AY.46.4, AY.43, AY.64, AY.78, AY.3, AY.107, AY.6, AY.7.1, AY.99, AY.26, AY.68, AY.38, AY.46.6, AY.41, AY.99.2, AY.46, AY.67, AY.39, AY.4.2.1, AY.4.3, AY.35, AY.20, AY.110, AY.111, AY.127, AY.33, AY.49, AY.57, AY.92, AY.14, AY.4.2, AY.40, AY.72, AY.85, AY.39.1, AY.21, AY.94, AY.17, AY.98, AY.60, AY.25.1, AY.1, AY.119, AY.4.5, AY.61, AY.82, AY.121, AY.16.1, AY.56, AY.18, AY.4.2.2, AY.28, AY.93, AY.10, AY.5.3, AY.24, AY.16, AY.62, AY.122, AY.29, AY.83, AY.20.1, AY.9.2, AY.48, AY.4.6,	Liu et al. (2021)	59425	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Alternate Allele	Alternate Frequency
p.L452R	antibody epitope effects	10 of 14 RBD-specific mAbs that showed at least 10-fold reduced neutralization of B.1.427/B.1.429 variant pseudotype (S13I, W152C, and L452R) were also found to poorly bind to just a L452R RBD mutant, demonstrating a role for this mutation as an escape mechanism for certain RBD-targeting mAbs.	AY.54, AY.46.2, AY.45, AY.88, AY.108, AY.11, AY.113, AY.118, AY.13, AY.53, AY.73, AY.103, AY.43.4, AY.124, AY.109, AY.84, AY.23, AY.89, AY.36, AY.44, AY.34.1, AY.46.1, AY.119.1, AY.77, AY.27, AY.75, AY.4, AY.66, AY.125, AY.59, B.1.617.2, AY.86, AY.19, AY.116.1, AY.117, AY.102, AY.15, AY.32, AY.34, AY.116, AY.9, AY.70, AY.9.2.1, AY.37, AY.121.1, AY.43.3, AY.2, AY.4.4, AY.47, AY.5, AY.65, AY.25, AY.120.1, AY.42, AY.74, AY.105, AY.120, AY.104, AY.126, AY.106, AY.114, AY.51, AY.46.4, AY.43, AY.64, AY.78, AY.3, AY.107, AY.6, AY.7.1, AY.99, AY.26, AY.68, AY.38, AY.46.6, AY.41, AY.99.2, AY.46, AY.67, AY.39, AY.4.2.1, AY.4.3, AY.35, AY.20, AY.110, AY.111, AY.127, AY.33, AY.49, AY.57, AY.92, AY.14, AY.4.2, AY.40, AY.72, AY.85, AY.39.1, AY.21, AY.94, AY.17, AY.98, AY.60, AY.25.1, AY.1, AY.119, AY.4.5, AY.61, AY.82, AY.121, AY.16.1, AY.56, AY.18, AY.4.2.2, AY.28, AY.93, AY.10, AY.5.3, AY.24, AY.16, AY.62, AY.122, AY.29, AY.83, AY.98.1, AY.9.2, AY.48, AY.4.6,	McCallum et al. (2021)	59425	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Alternate Allele	Alternate Frequency
p.L452R	antibody epitope effects	extasciitilde20% (ELISA significance threshold) drop in antibody binding (ELISA) by this variant against monoclonal antibody VH ab6.	AY.54, AY.46.2, AY.45, AY.88, AY.108, AY.11, AY.113, AY.118, AY.13, AY.53, AY.73, AY.103, AY.43.4, AY.124, AY.109, AY.84, AY.23, AY.89, AY.36, AY.44, AY.34.1, AY.46.1, AY.119.1, AY.77, AY.27, AY.75, AY.4, AY.66, AY.125, AY.59, B.1.617.2, AY.86, AY.19, AY.116.1, AY.117, AY.102, AY.15, AY.32, AY.34, AY.116, AY.9, AY.70, AY.9.2.1, AY.37, AY.121.1, AY.43.3, AY.2, AY.4.4, AY.47, AY.5, AY.65, AY.25, AY.120.1, AY.42, AY.74, AY.105, AY.120, AY.104, AY.126, AY.106, AY.114, AY.51, AY.46.4, AY.43, AY.64, AY.78, AY.3, AY.107, AY.6, AY.7.1, AY.99, AY.26, AY.68, AY.38, AY.46.6, AY.41, AY.99.2, AY.46, AY.67, AY.39, AY.4.2.1, AY.4.3, AY.35, AY.20, AY.110, AY.111, AY.127, AY.33, AY.49, AY.57, AY.92, AY.14, AY.4.2, AY.40, AY.72, AY.85, AY.39.1, AY.21, AY.94, AY.17, AY.98, AY.60, AY.25.1, AY.1, AY.119, AY.4.5, AY.61, AY.82, AY.121, AY.16.1, AY.56, AY.18, AY.4.2.2, AY.28, AY.93, AY.10, AY.5.3, AY.24, AY.16, AY.62, AY.122, AY.29, AY.83, AY.9.2, AY.48, AY.4.6,	Sun et al. (2021)	59425	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Alternate Allele	Alternate Frequency
p.L452R	convalescent plasma binding	2.15x increase in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset.	AY.54, AY.46.2, AY.45, AY.88, AY.108, AY.11, AY.113, AY.118, AY.13, AY.53, AY.73, AY.103, AY.43.4, AY.124, AY.109, AY.84, AY.23, AY.89, AY.36, AY.44, AY.34.1, AY.46.1, AY.119.1, AY.77, AY.27, AY.75, AY.4, AY.125, AY.59, B.1.617.2, AY.86, AY.19, AY.116.1, AY.117, AY.102, AY.15, AY.32, AY.34, AY.116, AY.9, AY.70, AY.9.2.1, AY.37, AY.121.1, AY.43.3, AY.2, AY.4.4, AY.47, AY.5, AY.65, AY.25, AY.120.1, AY.42, AY.74, AY.105, AY.120, AY.104, AY.126, AY.106, AY.114, AY.51, AY.46.4, AY.43, AY.64, AY.78, AY.3, AY.107, AY.6, AY.7.1, AY.99, AY.26, AY.68, AY.38, AY.46.6, AY.41, AY.99.2, AY.46, AY.67, AY.39, AY.4.2.1, AY.4.3, AY.35, AY.20, AY.110, AY.111, AY.127, AY.33, AY.49, AY.57, AY.92, AY.14, AY.4.2, AY.40, AY.72, AY.85, AY.39.1, AY.21, AY.94, AY.17, AY.98, AY.60, AY.25.1, AY.1, AY.119, AY.4.5, AY.61, AY.82, AY.121, AY.16.1, AY.56, AY.18, AY.4.2.2, AY.28, AY.93, AY.10, AY.5.3, AY.24, AY.16, AY.62, AY.122, AY.29, AY.83, AY.98.1, AY.3.1, AY.48, AY.4.6, AY.122.1,	Gong et al. (2021)	59423	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Alternate Allele	Alternate Frequency
p.L452R	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 post-symptom-onset. [exact variant list not provided in manuscript, is inferred fro common knowledge]	AY.98, AY.35, AY.70	Gong et al. (2021)	24	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Alternate Allele	Alternate Frequency
p.L452R	convalescent plasma escape	Observed extasciitilde2x decrease on average in 16 health workers' convalescent sera.	AY.54, AY.46.2, AY.45, AY.88, AY.108, AY.11, AY.113, AY.118, AY.13, AY.53, AY.73, AY.103, AY.43.4, AY.124, AY.109, AY.84, AY.23, AY.89, AY.36, AY.44, AY.34.1, AY.46.1, AY.119.1, AY.77, AY.27, AY.75, AY.4, AY.66, AY.125, AY.59, B.1.617.2, AY.86, AY.19, AY.116.1, AY.117, AY.102, AY.15, AY.32, AY.34, AY.116, AY.9, AY.70, AY.9.2.1, AY.37, AY.121.1, AY.43.3, AY.2, AY.4.4, AY.47, AY.5, AY.65, AY.25, AY.120.1, AY.42, AY.74, AY.105, AY.120, AY.104, AY.126, AY.106, AY.114, AY.51, AY.46.4, AY.43, AY.64, AY.78, AY.3, AY.107, AY.6, AY.7.1, AY.99, AY.26, AY.68, AY.38, AY.46.6, AY.41, AY.99.2, AY.46, AY.67, AY.39, AY.4.2.1, AY.4.3, AY.35, AY.20, AY.110, AY.111, AY.127, AY.33, AY.49, AY.57, AY.92, AY.14, AY.4.2, AY.40, AY.72, AY.85, AY.39.1, AY.21, AY.94, AY.17, AY.98, AY.60, AY.25.1, AY.1, AY.119, AY.4.5, AY.61, AY.82, AY.121, AY.16.1, AY.56, AY.18, AY.4.2.2, AY.28, AY.93, AY.10, AY.5.3, AY.24, AY.16, AY.62, AY.122, AY.29, AY.83, AY.9.2, AY.48, AY.4.6,	Alenquer et al. (2021)	59425	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Alternate Allele	Alternate Frequency
p.L452R	convalescent plasma escape	Ablation of neutralization capability of 3 of 4 convalescent sera tested, the other is significantly hindered.	AY.54, AY.46.2, AY.45, AY.88, AY.108, AY.11, AY.113, AY.118, AY.13, AY.53, AY.73, AY.103, AY.43.4, AY.124, AY.109, AY.84, AY.23, AY.89, AY.36, AY.44, AY.34.1, AY.46.1, AY.119.1, AY.77, AY.27, AY.75, AY.4, AY.66, AY.125, AY.59, B.1.617.2, AY.86, AY.19, AY.116.1, AY.117, AY.102, AY.15, AY.32, AY.34, AY.116, AY.9, AY.70, AY.9.2.1, AY.37, AY.121.1, AY.43.3, AY.2, AY.4.4, AY.47, AY.5, AY.65, AY.25, AY.120.1, AY.42, AY.74, AY.105, AY.120, AY.104, AY.126, AY.106, AY.114, AY.51, AY.46.4, AY.43, AY.64, AY.78, AY.3, AY.107, AY.6, AY.7.1, AY.99, AY.26, AY.68, AY.38, AY.46.6, AY.41, AY.99.2, AY.46, AY.67, AY.39, AY.4.2.1, AY.4.3, AY.35, AY.20, AY.110, AY.111, AY.127, AY.33, AY.49, AY.57, AY.92, AY.14, AY.4.2, AY.40, AY.72, AY.85, AY.39.1, AY.21, AY.94, AY.17, AY.98, AY.60, AY.25.1, AY.1, AY.119, AY.4.5, AY.61, AY.82, AY.121, AY.16.1, AY.56, AY.18, AY.4.2.2, AY.28, AY.93, AY.10, AY.5.3, AY.24, AY.16, AY.62, AY.122, AY.29, AY.83, AY.98.1, AY.9.2, AY.48, AY.4.6,	Liu et al. (2021)	59425	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	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.98, AY.35, AY.70	Tada et al. (2021)	24	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Alternate Allele	Alternate Frequency
p.L452R	convalescent plasma escape	Relative to B.1, Epsilon (B.1.417/429) shows 1.74x-2.35x decrease in neutralization efficiency by convalescent plasma [no cohort details provided]	AY.54, AY.46.2, AY.45, AY.88, AY.108, AY.11, AY.113, AY.118, AY.13, AY.53, AY.73, AY.103, AY.43.4, AY.124, AY.109, AY.84, AY.23, AY.89, AY.36, AY.44, AY.34.1, AY.46.1, AY.119.1, AY.77, AY.27, AY.75, AY.4, AY.125, AY.59, B.1.617.2, AY.86, AY.19, AY.116.1, AY.117, AY.102, AY.15, AY.32, AY.34, AY.116, AY.9, AY.70, AY.9.2.1, AY.37, AY.121.1, AY.43.3, AY.2, AY.4.4, AY.47, AY.5, AY.65, AY.25, AY.120.1, AY.42, AY.74, AY.105, AY.120, AY.104, AY.126, AY.106, AY.114, AY.51, AY.46.4, AY.43, AY.64, AY.78, AY.3, AY.107, AY.6, AY.7.1, AY.99, AY.26, AY.68, AY.38, AY.46.6, AY.41, AY.99.2, AY.46, AY.67, AY.39, AY.4.2.1, AY.4.3, AY.35, AY.20, AY.110, AY.111, AY.127, AY.33, AY.49, AY.57, AY.92, AY.14, AY.4.2, AY.40, AY.72, AY.85, AY.39.1, AY.21, AY.94, AY.17, AY.98, AY.60, AY.25.1, AY.1, AY.119, AY.4.5, AY.61, AY.82, AY.121, AY.16.1, AY.56, AY.18, AY.4.2.2, AY.28, AY.93, AY.10, AY.5.3, AY.24, AY.16, AY.62, AY.122, AY.29, AY.83, AY.98.1, AY.3.1, AY.48, AY.4.6, AY.122.1,	Wilhelm et al. (2021)	59423	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Alternate Allele	Alternate Frequency
p.L452R	gene expression increase	Experimentally, Spike gene expression increased 0.32 fold	AY.54, AY.46.2, AY.45, AY.88, AY.108, AY.11, AY.113, AY.118, AY.13, AY.53, AY.73, AY.103, AY.43.4, AY.124, AY.109, AY.84, AY.23, AY.89, AY.36, AY.44, AY.34.1, AY.46.1, AY.119.1, AY.77, AY.27, AY.75, AY.4, AY.66, AY.125, AY.59, B.1.617.2, AY.86, AY.19, AY.116.1, AY.117, AY.102, AY.15, AY.32, AY.34, AY.116, AY.9, AY.70, AY.9.2.1, AY.37, AY.121.1, AY.43.3, AY.2, AY.4.4, AY.47, AY.5, AY.65, AY.25, AY.120.1, AY.42, AY.74, AY.105, AY.120, AY.104, AY.126, AY.106, AY.114, AY.51, AY.46.4, AY.43, AY.64, AY.78, AY.3, AY.107, AY.6, AY.7.1, AY.99, AY.26, AY.68, AY.38, AY.46.6, AY.41, AY.99.2, AY.46, AY.67, AY.39, AY.4.2.1, AY.4.3, AY.35, AY.20, AY.110, AY.111, AY.127, AY.33, AY.49, AY.57, AY.92, AY.14, AY.4.2, AY.40, AY.72, AY.85, AY.39.1, AY.21, AY.94, AY.17, AY.98, AY.60, AY.25.1, AY.1, AY.119, AY.4.5, AY.61, AY.82, AY.121, AY.16.1, AY.56, AY.18, AY.4.2.2, AY.28, AY.93, AY.10, AY.5.3, AY.24, AY.16, AY.62, AY.122, AY.29, AY.83, AY.21.1, AY.9.2, AY.48, AY.4.6,	Starr et al. (2020)	59425	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Alternate Allele	Alternate Frequency
p.L452R	monoclonal antibody serial passage escape	Ranked effective mutant against this position in the RBD for highly neutralizing COV2-2096	AY.54, AY.46.2, AY.45, AY.88, AY.108, AY.11, AY.113, AY.118, AY.13, AY.53, AY.73, AY.103, AY.43.4, AY.124, AY.109, AY.84, AY.23, AY.89, AY.36, AY.44, AY.34.1, AY.46.1, AY.119.1, AY.77, AY.27, AY.75, AY.4, AY.66, AY.125, AY.59, B.1.617.2, AY.86, AY.19, AY.116.1, AY.117, AY.102, AY.15, AY.32, AY.34, AY.116, AY.9, AY.70, AY.9.2.1, AY.37, AY.121.1, AY.43.3, AY.2, AY.4.4, AY.47, AY.5, AY.65, AY.25, AY.120.1, AY.42, AY.74, AY.105, AY.120, AY.104, AY.126, AY.106, AY.114, AY.51, AY.46.4, AY.43, AY.64, AY.78, AY.3, AY.107, AY.6, AY.7.1, AY.99, AY.26, AY.68, AY.38, AY.46.6, AY.41, AY.99.2, AY.46, AY.67, AY.39, AY.4.2.1, AY.4.3, AY.35, AY.20, AY.110, AY.111, AY.127, AY.33, AY.49, AY.57, AY.92, AY.14, AY.4.2, AY.40, AY.72, AY.85, AY.39.1, AY.21, AY.94, AY.17, AY.98, AY.60, AY.25.1, AY.1, AY.119, AY.4.5, AY.61, AY.82, AY.121, AY.16.1, AY.56, AY.18, AY.4.2.2, AY.28, AY.93, AY.10, AY.5.3, AY.24, AY.16, AY.62, AY.122, AY.29, AY.83, AY.9.2, AY.48, AY.4.6,	Greaney et al. (2020)	59425	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	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.54, AY.46.2, AY.45, AY.88, AY.108, AY.11, AY.113, AY.118, AY.13, AY.53, AY.73, AY.103, AY.43.4, AY.124, AY.109, AY.84, AY.23, AY.89, AY.36, AY.44, AY.34.1, AY.46.1, AY.119.1, AY.77, AY.27, AY.75, AY.4, AY.66, AY.125, AY.59, B.1.617.2, AY.86, AY.19, AY.116.1, AY.117, AY.102, AY.15, AY.32, AY.34, AY.116, AY.9, AY.70, AY.9.2.1, AY.37, AY.121.1, AY.43.3, AY.2, AY.4.4, AY.47, AY.5, AY.65, AY.25, AY.120.1, AY.42, AY.74, AY.105, AY.120, AY.104, AY.126, AY.106, AY.114, AY.51, AY.46.4, AY.43, AY.64, AY.78, AY.3, AY.107, AY.6, AY.7.1, AY.99, AY.26, AY.68, AY.38, AY.46.6, AY.41, AY.99.2, AY.46, AY.67, AY.39, AY.4.2.1, AY.4.3, AY.35, AY.20, AY.110, AY.111, AY.127, AY.33, AY.49, AY.57, AY.92, AY.14, AY.4.2, AY.40, AY.72, AY.85, AY.39.1, AY.21, AY.94, AY.17, AY.98, AY.60, AY.25.1, AY.1, AY.119, AY.4.5, AY.61, AY.82, AY.121, AY.16.1, AY.56, AY.18, AY.4.2.2, AY.28, AY.93, AY.10, AY.5.3, AY.24, AY.16, AY.62, AY.122, AY.29, AY.83, AY.98.1, AY.9.2, AY.48, AY.4.6,	Starr et al. (2021)	59425	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Alternate Allele	Alternate Frequency
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.	AY.54, AY.46.2, AY.45, AY.88, AY.108, AY.11, AY.113, AY.118, AY.13, AY.53, AY.73, AY.103, AY.43.4, AY.124, AY.109, AY.84, AY.23, AY.89, AY.36, AY.44, AY.34.1, AY.46.1, AY.119.1, AY.77, AY.27, AY.75, AY.4, AY.66, AY.125, AY.59, B.1.617.2, AY.86, AY.19, AY.116.1, AY.117, AY.102, AY.15, AY.32, AY.34, AY.116, AY.9, AY.70, AY.9.2.1, AY.37, AY.121.1, AY.43.3, AY.2, AY.4.4, AY.47, AY.5, AY.65, AY.25, AY.120.1, AY.42, AY.74, AY.105, AY.120, AY.104, AY.126, AY.106, AY.114, AY.51, AY.46.4, AY.43, AY.64, AY.78, AY.3, AY.107, AY.6, AY.7.1, AY.99, AY.26, AY.68, AY.38, AY.46.6, AY.41, AY.99.2, AY.46, AY.67, AY.39, AY.4.2.1, AY.4.3, AY.35, AY.20, AY.110, AY.111, AY.127, AY.33, AY.49, AY.57, AY.92, AY.14, AY.4.2, AY.40, AY.72, AY.85, AY.39.1, AY.21, AY.94, AY.17, AY.98, AY.60, AY.25.1, AY.1, AY.119, AY.4.5, AY.61, AY.82, AY.121, AY.16.1, AY.56, AY.18, AY.4.2.2, AY.28, AY.93, AY.10, AY.5.3, AY.24, AY.16, AY.62, AY.122, AY.29, AY.83, AY.20.1, AY.9.2, AY.48, AY.4.6,	Wang et al. (2021)	59425	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Alternate Allele	Alternate Frequency
p.L452R	pharmaceutical effectiveness	Bamlanivimab (LY-CoV555) lost extasci-itilde5x binding against this isolated mutation. Cligavimab lost extasci-itilde4x binding against this isolated mutation. Regdanvimab lost ex-tasciitilde4x binding against this isolated mutation.	AY.54, AY.46.2, AY.45, AY.88, AY.108, AY.11, AY.113, AY.118, AY.13, AY.53, AY.73, AY.103, AY.43.4, AY.124, AY.109, AY.84, AY.23, AY.89, AY.36, AY.44, AY.34.1, AY.46.1, AY.119.1, AY.77, AY.27, AY.75, AY.4, AY.66, AY.125, AY.59, B.1.617.2, AY.86, AY.19, AY.116.1, AY.117, AY.102, AY.15, AY.32, AY.34, AY.116, AY.9, AY.70, AY.9.2.1, AY.37, AY.121.1, AY.43.3, AY.2, AY.4.4, AY.47, AY.5, AY.65, AY.25, AY.120.1, AY.42, AY.74, AY.105, AY.120, AY.104, AY.126, AY.106, AY.114, AY.51, AY.46.4, AY.43, AY.64, AY.78, AY.3, AY.107, AY.6, AY.7.1, AY.99, AY.26, AY.68, AY.38, AY.46.6, AY.41, AY.99.2, AY.46, AY.67, AY.39, AY.4.2.1, AY.4.3, AY.35, AY.20, AY.110, AY.111, AY.127, AY.33, AY.49, AY.57, AY.92, AY.14, AY.4.2, AY.40, AY.72, AY.85, AY.39.1, AY.21, AY.94, AY.17, AY.98, AY.60, AY.25.1, AY.1, AY.119, AY.4.5, AY.61, AY.82, AY.121, AY.16.1, AY.56, AY.18, AY.4.2.2, AY.28, AY.93, AY.10, AY.5.3, AY.24, AY.16, AY.62, AY.122, AY.29, AY.83, AY.9.2, AY.48, AY.4.6,	Engelhart et al. (2021)	59425	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	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.54, AY.46.2, AY.45, AY.88, AY.108, AY.11, AY.113, AY.118, AY.13, AY.53, AY.73, AY.103, AY.43.4, AY.124, AY.109, AY.84, AY.23, AY.89, AY.36, AY.44, AY.34.1, AY.46.1, AY.119.1, AY.77, AY.27, AY.75, AY.4, AY.66, AY.125, AY.59, B.1.617.2, AY.86, AY.19, AY.116.1, AY.117, AY.102, AY.15, AY.32, AY.34, AY.116, AY.9, AY.70, AY.9.2.1, AY.37, AY.121.1, AY.43.3, AY.2, AY.4.4, AY.47, AY.5, AY.65, AY.25, AY.120.1, AY.42, AY.74, AY.105, AY.120, AY.104, AY.126, AY.106, AY.114, AY.51, AY.46.4, AY.43, AY.64, AY.78, AY.3, AY.107, AY.6, AY.7.1, AY.99, AY.26, AY.68, AY.38, AY.46.6, AY.41, AY.99.2, AY.46, AY.67, AY.39, AY.4.2.1, AY.4.3, AY.35, AY.20, AY.110, AY.111, AY.127, AY.33, AY.49, AY.57, AY.92, AY.14, AY.4.2, AY.40, AY.72, AY.85, AY.39.1, AY.21, AY.94, AY.17, AY.98, AY.60, AY.25.1, AY.1, AY.119, AY.4.5, AY.61, AY.82, AY.121, AY.16.1, AY.56, AY.18, AY.4.2.2, AY.28, AY.93, AY.10, AY.5.3, AY.24, AY.16, AY.62, AY.122, AY.29, AY.83, AY.98.1, AY.9.2, AY.48, AY.4.6,	McCallum et al. (2021)	59425	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Alternate Allele	Alternate Frequency
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 consistently.	AY.98, AY.35, AY.70	Yadav et al. (2021)	24	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	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.54, AY.46.2, AY.45, AY.88, AY.108, AY.11, AY.113, AY.118, AY.13, AY.53, AY.73, AY.103, AY.43.4, AY.124, AY.109, AY.84, AY.23, AY.89, AY.36, AY.44, AY.34.1, AY.46.1, AY.119.1, AY.77, AY.27, AY.75, AY.4, AY.66, AY.125, AY.59, B.1.617.2, AY.86, AY.19, AY.116.1, AY.117, AY.102, AY.15, AY.32, AY.34, AY.116, AY.9, AY.70, AY.9.2.1, AY.37, AY.121.1, AY.43.3, AY.2, AY.4.4, AY.47, AY.5, AY.65, AY.25, AY.120.1, AY.42, AY.74, AY.105, AY.120, AY.104, AY.126, AY.106, AY.114, AY.51, AY.46.4, AY.43, AY.64, AY.78, AY.3, AY.107, AY.6, AY.7.1, AY.99, AY.26, AY.68, AY.38, AY.46.6, AY.41, AY.99.2, AY.46, AY.67, AY.39, AY.4.2.1, AY.4.3, AY.35, AY.20, AY.110, AY.111, AY.127, AY.33, AY.49, AY.57, AY.92, AY.14, AY.4.2, AY.40, AY.72, AY.85, AY.39.1, AY.21, AY.94, AY.17, AY.98, AY.60, AY.25.1, AY.1, AY.119, AY.4.5, AY.61, AY.82, AY.121, AY.16.1, AY.56, AY.18, AY.4.2.2, AY.28, AY.93, AY.10, AY.5.3, AY.24, AY.16, AY.62, AY.122, AY.29, AY.83, AY.98.1, AY.9.2, AY.48, AY.4.6,	Deng et al. (2021)	59425	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Alternate Allele	Alternate Frequency
p.L452R	trafficking	This variant alone shows a extasciitilde5x decrease in cell entry efficiency (RLU measurement in 293T cells) compared to D614G. [listed as L454R in Figure, but L452R in text, also text suggests not statistucally significant, but error bars say otherwise in Figure 4]	AY.54, AY.46.2, AY.45, AY.88, AY.108, AY.11, AY.113, AY.118, AY.13, AY.53, AY.73, AY.103, AY.43.4, AY.124, AY.109, AY.84, AY.23, AY.89, AY.36, AY.44, AY.34.1, AY.46.1, AY.119.1, AY.77, AY.27, AY.75, AY.4, AY.66, AY.125, AY.59, B.1.617.2, AY.86, AY.19, AY.116.1, AY.117, AY.102, AY.15, AY.32, AY.34, AY.116, AY.9, AY.70, AY.9.2.1, AY.37, AY.121.1, AY.43.3, AY.2, AY.4.4, AY.47, AY.5, AY.65, AY.25, AY.120.1, AY.42, AY.74, AY.105, AY.120, AY.104, AY.126, AY.106, AY.114, AY.51, AY.46.4, AY.43, AY.64, AY.78, AY.3, AY.107, AY.6, AY.7.1, AY.99, AY.26, AY.68, AY.38, AY.46.6, AY.41, AY.99.2, AY.46, AY.67, AY.39, AY.4.2.1, AY.4.3, AY.35, AY.20, AY.110, AY.111, AY.127, AY.33, AY.49, AY.57, AY.92, AY.14, AY.4.2, AY.40, AY.72, AY.85, AY.39.1, AY.21, AY.94, AY.17, AY.98, AY.60, AY.25.1, AY.1, AY.119, AY.4.5, AY.61, AY.82, AY.121, AY.16.1, AY.56, AY.18, AY.4.2.2, AY.28, AY.93, AY.10, AY.5.3, AY.24, AY.16, AY.62, AY.122, AY.29, AY.83, AY.98.1, AY.9.2, AY.48, AY.4.6,	Ferriera et al (2021)	59425	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	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	G	1.0
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	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Alternate Allele	Alternate Frequency
p.L452R	trafficking	Increased stability of RBD expression in yeast, suggesting increased Spike protein stability.	AY.54, AY.46.2, AY.45, AY.88, AY.108, AY.11, AY.113, AY.118, AY.13, AY.53, AY.73, AY.103, AY.43.4, AY.124, AY.109, AY.84, AY.23, AY.89, AY.36, AY.44, AY.34.1, AY.46.1, AY.119.1, AY.77, AY.27, AY.75, AY.4, AY.66, AY.125, AY.59, B.1.617.2, AY.86, AY.19, AY.116.1, AY.117, AY.102, AY.15, AY.32, AY.34, AY.116, AY.9, AY.70, AY.9.2.1, AY.37, AY.121.1, AY.43.3, AY.2, AY.4.4, AY.47, AY.5, AY.65, AY.25, AY.120.1, AY.42, AY.74, AY.105, AY.120, AY.104, AY.126, AY.106, AY.114, AY.51, AY.46.4, AY.43, AY.64, AY.78, AY.3, AY.107, AY.6, AY.7.1, AY.99, AY.26, AY.68, AY.38, AY.46.6, AY.41, AY.99.2, AY.46, AY.67, AY.39, AY.4.2.1, AY.4.3, AY.35, AY.20, AY.110, AY.111, AY.127, AY.33, AY.49, AY.57, AY.92, AY.14, AY.4.2, AY.40, AY.72, AY.85, AY.39.1, AY.21, AY.94, AY.17, AY.98, AY.60, AY.25.1, AY.1, AY.119, AY.4.5, AY.61, AY.82, AY.121, AY.16.1, AY.56, AY.18, AY.4.2.2, AY.28, AY.93, AY.10, AY.5.3, AY.24, AY.16, AY.62, AY.122, AY.29, AY.83, AY.9.2, AY.48, AY.4.6,	Motozono et al. (2021)	59425	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	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.54, AY.46.2, AY.45, AY.88, AY.108, AY.11, AY.113, AY.118, AY.13, AY.53, AY.73, AY.103, AY.43.4, AY.124, AY.109, AY.84, AY.23, AY.89, AY.36, AY.44, AY.34.1, AY.46.1, AY.119.1, AY.77, AY.27, AY.75, AY.4, AY.125, AY.59, B.1.617.2, AY.86, AY.19, AY.116.1, AY.117, AY.102, AY.15, AY.32, AY.34, AY.116, AY.9, AY.70, AY.9.2.1, AY.37, AY.121.1, AY.43.3, AY.2, AY.4.4, AY.47, AY.5, AY.65, AY.25, AY.120.1, AY.42, AY.74, AY.105, AY.120, AY.104, AY.126, AY.106, AY.114, AY.51, AY.46.4, AY.43, AY.64, AY.78, AY.3, AY.107, AY.6, AY.7.1, AY.99, AY.26, AY.68, AY.38, AY.46.6, AY.41, AY.99.2, AY.46, AY.67, AY.39, AY.4.2.1, AY.4.3, AY.35, AY.20, AY.110, AY.111, AY.127, AY.33, AY.49, AY.57, AY.92, AY.14, AY.4.2, AY.40, AY.72, AY.85, AY.39.1, AY.21, AY.94, AY.17, AY.98, AY.60, AY.25.1, AY.1, AY.119, AY.4.5, AY.61, AY.82, AY.121, AY.16.1, AY.56, AY.18, AY.4.2.2, AY.28, AY.93, AY.10, AY.5.3, AY.24, AY.16, AY.62, AY.122, AY.29, AY.83, AY.98.1, AY.34.2, AY.48, AY.4.6, AY.122.1,	Tada et al. (2021)	59423	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Alternate Allele	Alternate 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.98, AY.35, AY.70	Tada et al. (2021)	24	G	1.0
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.98, AY.35, AY.70	Tada et al. (2021)	24	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	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.54, AY.46.2, AY.45, AY.88, AY.108, AY.11, AY.113, AY.118, AY.13, AY.53, AY.73, AY.103, AY.43.4, AY.124, AY.109, AY.84, AY.23, AY.89, AY.36, AY.44, AY.34.1, AY.46.1, AY.119.1, AY.77, AY.27, AY.75, AY.4, AY.66, AY.125, AY.59, B.1.617.2, AY.86, AY.19, AY.116.1, AY.117, AY.102, AY.15, AY.32, AY.34, AY.116, AY.9, AY.70, AY.9.2.1, AY.37, AY.121.1, AY.43.3, AY.2, AY.4.4, AY.47, AY.5, AY.65, AY.25, AY.120.1, AY.42, AY.74, AY.105, AY.120, AY.104, AY.126, AY.106, AY.114, AY.51, AY.46.4, AY.43, AY.64, AY.78, AY.3, AY.107, AY.6, AY.7.1, AY.99, AY.26, AY.68, AY.38, AY.46.6, AY.41, AY.99.2, AY.46, AY.67, AY.39, AY.4.2.1, AY.4.3, AY.35, AY.20, AY.110, AY.111, AY.127, AY.33, AY.49, AY.57, AY.92, AY.14, AY.4.2, AY.40, AY.72, AY.85, AY.39.1, AY.21, AY.94, AY.17, AY.98, AY.60, AY.25.1, AY.1, AY.119, AY.4.5, AY.61, AY.82, AY.121, AY.16.1, AY.56, AY.18, AY.4.2.2, AY.28, AY.93, AY.10, AY.5.3, AY.24, AY.16, AY.62, AY.122, AY.29, AY.83, AY.98.1, AY.9.2, AY.48, AY.4.6,	Ferreira et al. (2021)	59425	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	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. 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.98, AY.35, AY.70	Ferreira et al. (2021)	24	G	1.0
p.L452R	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.98, AY.35, AY.70	Gong et al. (2021)	24	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	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.54, AY.46.2, AY.45, AY.88, AY.108, AY.11, AY.113, AY.118, AY.13, AY.53, AY.73, AY.103, AY.43.4, AY.124, AY.109, AY.84, AY.23, AY.89, AY.36, AY.44, AY.34.1, AY.46.1, AY.119.1, AY.77, AY.27, AY.75, AY.4, AY.66, AY.125, AY.59, B.1.617.2, AY.86, AY.19, AY.116.1, AY.117, AY.102, AY.15, AY.32, AY.34, AY.116, AY.9, AY.70, AY.9.2.1, AY.37, AY.121.1, AY.43.3, AY.2, AY.4.4, AY.47, AY.5, AY.65, AY.25, AY.120.1, AY.42, AY.74, AY.105, AY.120, AY.104, AY.126, AY.106, AY.114, AY.51, AY.46.4, AY.43, AY.64, AY.78, AY.3, AY.107, AY.6, AY.7.1, AY.99, AY.26, AY.68, AY.38, AY.46.6, AY.41, AY.99.2, AY.46, AY.67, AY.39, AY.4.2.1, AY.4.3, AY.35, AY.20, AY.110, AY.111, AY.127, AY.33, AY.49, AY.57, AY.92, AY.14, AY.4.2, AY.40, AY.72, AY.85, AY.39.1, AY.21, AY.94, AY.17, AY.98, AY.60, AY.25.1, AY.1, AY.119, AY.4.5, AY.61, AY.82, AY.121, AY.16.1, AY.56, AY.18, AY.4.2.2, AY.28, AY.93, AY.10, AY.5.3, AY.24, AY.16, AY.62, AY.122, AY.29, AY.83, AY.98.1, AY.9.2, AY.48, AY.4.6,	Jacobson et al. (2021)	59425	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	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 variants within B.1.617.	AY.98, AY.35, AY.70	Tada et al. (2021)	24	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Alternate Allele	Alternate Frequency
p.L452R	vaccine neutralization efficacy	Relative to B.1, Epsilon (B.1.417/429) shows 1.74x-2.35x decrease in neutralization efficiency by 18 vaccinee sera (BNT162b2 and mRNA1273).	AY.54, AY.46.2, AY.45, AY.88, AY.108, AY.11, AY.113, AY.118, AY.13, AY.53, AY.73, AY.103, AY.43.4, AY.124, AY.109, AY.84, AY.23, AY.89, AY.36, AY.44, AY.34.1, AY.46.1, AY.119.1, AY.77, AY.27, AY.75, AY.4, AY.125, AY.59, B.1.617.2, AY.86, AY.19, AY.116.1, AY.117, AY.102, AY.15, AY.32, AY.34, AY.116, AY.9, AY.70, AY.9.2.1, AY.37, AY.121.1, AY.43.3, AY.2, AY.4.4, AY.47, AY.5, AY.65, AY.25, AY.120.1, AY.42, AY.74, AY.105, AY.120, AY.104, AY.126, AY.106, AY.114, AY.51, AY.46.4, AY.43, AY.64, AY.78, AY.3, AY.107, AY.6, AY.7.1, AY.99, AY.26, AY.68, AY.38, AY.46.6, AY.41, AY.99.2, AY.46, AY.67, AY.39, AY.4.2.1, AY.4.3, AY.35, AY.20, AY.110, AY.111, AY.127, AY.33, AY.49, AY.57, AY.92, AY.14, AY.4.2, AY.40, AY.72, AY.85, AY.39.1, AY.21, AY.94, AY.17, AY.98, AY.60, AY.25.1, AY.1, AY.119, AY.4.5, AY.61, AY.82, AY.121, AY.16.1, AY.56, AY.18, AY.4.2.2, AY.28, AY.93, AY.10, AY.5.3, AY.24, AY.16, AY.62, AY.122, AY.29, AY.83, AY.98.1, AY.3.1, AY.48, AY.4.6, AY.122.1,	Wilhelm et al. (2021)	59423	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Alternate Allele	Alternate Frequency
p.L452R	vaccinee plasma binding	1.05x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in previously non-seroconverted subjects. 1.16x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in post-infection vaccinees.	AY.54, AY.46.2, AY.45, AY.88, AY.108, AY.11, AY.113, AY.118, AY.13, AY.53, AY.73, AY.103, AY.43.4, AY.124, AY.109, AY.84, AY.23, AY.89, AY.36, AY.44, AY.34.1, AY.46.1, AY.119.1, AY.77, AY.27, AY.75, AY.4, AY.125, AY.59, B.1.617.2, AY.86, AY.19, AY.116.1, AY.117, AY.102, AY.15, AY.32, AY.34, AY.116, AY.9, AY.70, AY.9.2.1, AY.37, AY.121.1, AY.43.3, AY.2, AY.4.4, AY.47, AY.5, AY.65, AY.25, AY.120.1, AY.42, AY.74, AY.105, AY.120, AY.104, AY.126, AY.106, AY.114, AY.51, AY.46.4, AY.43, AY.64, AY.78, AY.3, AY.107, AY.6, AY.7.1, AY.99, AY.26, AY.68, AY.38, AY.46.6, AY.41, AY.99.2, AY.46, AY.67, AY.39, AY.4.2.1, AY.4.3, AY.35, AY.20, AY.110, AY.111, AY.127, AY.33, AY.49, AY.57, AY.92, AY.14, AY.4.2, AY.40, AY.72, AY.85, AY.39.1, AY.21, AY.94, AY.17, AY.98, AY.60, AY.25.1, AY.1, AY.119, AY.4.5, AY.61, AY.82, AY.121, AY.16.1, AY.56, AY.18, AY.4.2.2, AY.28, AY.93, AY.10, AY.5.3, AY.24, AY.16, AY.62, AY.122, AY.29, AY.83, AY.98.1, AY.34.2, AY.48, AY.4.6, AY.122.1,	Gong et al. (2021)	59423	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	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.98, AY.35, AY.70	Gong et al. (2021)	24	G	1.0
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.98, AY.35, AY.70	Yadav et al. (2021)	24	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	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.54, AY.46.2, AY.45, AY.88, AY.108, AY.11, AY.113, AY.118, AY.13, AY.53, AY.73, AY.103, AY.43.4, AY.124, AY.109, AY.84, AY.23, AY.89, AY.36, AY.44, AY.34.1, AY.46.1, AY.119.1, AY.77, AY.27, AY.75, AY.4, AY.66, AY.125, AY.59, B.1.617.2, AY.86, AY.19, AY.116.1, AY.117, AY.102, AY.15, AY.32, AY.34, AY.116, AY.9, AY.70, AY.9.2.1, AY.37, AY.121.1, AY.43.3, AY.2, AY.4.4, AY.47, AY.5, AY.65, AY.25, AY.120.1, AY.42, AY.74, AY.105, AY.120, AY.104, AY.126, AY.106, AY.114, AY.51, AY.46.4, AY.43, AY.64, AY.78, AY.3, AY.107, AY.6, AY.7.1, AY.99, AY.26, AY.68, AY.38, AY.46.6, AY.41, AY.99.2, AY.46, AY.67, AY.39, AY.4.2.1, AY.4.3, AY.35, AY.20, AY.110, AY.111, AY.127, AY.33, AY.49, AY.57, AY.92, AY.14, AY.4.2, AY.40, AY.72, AY.85, AY.39.1, AY.21, AY.94, AY.17, AY.98, AY.60, AY.25.1, AY.1, AY.119, AY.4.5, AY.61, AY.82, AY.121, AY.16.1, AY.56, AY.18, AY.4.2.2, AY.28, AY.93, AY.10, AY.5.3, AY.24, AY.16, AY.62, AY.122, AY.29, AY.83, AY.9.2, AY.48, AY.4.6,	Spratt et al. (2021)	59425	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Alternate Allele	Alternate Frequency
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	A	0.5
p.H69del	antibody epitope effects	Reduces neutralization by structurally unmapped mAb COVA1-21 (cluster XI).	AY.77	Rees-Spear et al. (2021)	2	A	0.5
p.H69del	convalescent plasma binding	1.33x increase in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset.	AY.77	Gong et al. (2021)	2	A	0.5
p.H69del	convalescent plasma escape	Fatal COVID-19 complications in immunocompromised patient after immune escape from convalescent plasma	AY.77	Kemp et al. (2020)	2	A	0.5
p.H69del	convalescent plasma escape	Neutralization activity of almost all Moderna Phase 1 sera tested actually *increased*.	AY.77	Shen et al. (2021)	2	A	0.5
p.H69del	convalescent plasma escape	Viruses containing the point mutations of B.1.1.7 showed that the single point mutations (Δ69-70 and N501Y) were neutralized as efficiently as D614G across 10 convalescent sera from April 2020 infectees.	AY.77	Tada et al. (2021)	2	A	0.5
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	A	0.5
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	A	0.5
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)	4	C	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Alternate Allele	Alternate Frequency
p.R158G	monoclonal antibody serial passage escape	Escape mutation against Spike N terminal domain antigenic supersite i mAb S2X28	AY.54, AY.46.2, AY.45, AY.88, AY.108, AY.11, AY.113, AY.118, AY.13, AY.3.1, AY.53, AY.103, AY.43.4, AY.124, AY.109, AY.84, AY.23, AY.89, AY.36, AY.44, AY.34.1, AY.46.1, AY.119.1, AY.77, AY.27, AY.75, AY.4, AY.66, AY.125, AY.59, B.1.617.2, AY.86, AY.19, AY.116.1, AY.117, AY.102, AY.15, AY.32, AY.34, AY.116, AY.9, AY.70, AY.9.2.1, AY.37, AY.121.1, AY.43.3, AY.2, AY.4.4, AY.47, AY.5, AY.65, AY.25, AY.120.1, AY.42, AY.74, AY.105, AY.120, AY.104, AY.126, AY.106, AY.114, AY.51, AY.46.4, AY.43, AY.64, AY.78, AY.3, AY.107, AY.6, AY.7.1, AY.99, AY.26, AY.68, AY.38, AY.46.6, AY.41, AY.99.2, AY.46, AY.67, AY.39, AY.4.2.1, AY.4.3, AY.35, AY.20, AY.110, AY.111, AY.127, AY.33, AY.49, AY.57, AY.92, AY.14, AY.4.2, AY.40, AY.72, AY.85, AY.39.1, AY.21, AY.94, AY.17, AY.98, AY.60, AY.25.1, AY.1, AY.119, AY.4.5, AY.61, AY.82, AY.121, AY.16.1, AY.56, AY.18, AY.4.2.2, AY.28, AY.93, AY.10, AY.5.3, AY.24, AY.16, AY.62, AY.122, AY.29, AY.83, AY.9.2, AY.48, AY.4.6,	McCallum et al. (2021)	58632	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Alternate Allele	Alternate Frequency
p.S255F	monoclonal antibody serial passage escape	Escape mutation against Spike N terminal domain antigenic supersite i mAb S2L28	AY.106	McCallum et al. (2021)	116	T	0.69
p.S443F	monoclonal antibody serial passage escape	Ranked effective escape variant in the RBD for highly neutralizing COV2-2499 monoclonal antibody	AY.124	Greaney et al. (2020)	1	T	1.0
p.E484K	ACE2 receptor binding affinity	This combination showed extasciitilde3x increase binding to ACE2 vs wild type, about half that of the B.1.1.7 lineage, suggesting that the K417N mutation is slightly detrimental to ACE2 binding, probably as a result of disrupting the salt bridge formed with ACE2 residue D30	AY.77	Collier et al. (2021)	2	A,C	1.0
p.E484K	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,C	1.0
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	A,C	1.0
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	A,C	1.0
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	A,C	1.0
p.E484K	ACE2 receptor binding affinity	Experimentally, ACE2 binding affinity increased 0.06 fold	AY.77	Starr et al. (2020)	2	A,C	1.0
p.E484K	ACE2 receptor binding affinity	Reported moderate increase in affinity compared to wild-type RBD on the cell surface (Kd	AY.77	Tian et al. (2021)	2	A,C	1.0
p.E484K	ACE2 receptor binding affinity	Reported slight increase in affinity compared to wild-type RBD on the cell surface (Kd	AY.77	Tian et al. (2021)	2	A,C	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Alternate Allele	Alternate Frequency
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	A,C	1.0
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	A,C	1.0
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	A,C	1.0
p.E484K	antibody epitope effects	Ablates Class 1 receptor-binding-motif targeting antibodies COV2-2050, 1B07, COVOX-384 and S2H58.	AY.77	Chen et al. (2021)	2	A,C	1.0
p.E484K	antibody epitope effects	Of 50 mAbs tested, major loss of neutralization observed for S2N28, S2X615, S2N12, S2X192, S2H7, S2X16, S2X58, S2H70, S2X613, S2D19, S2N22, S2D32, S2H58, S2M11, S2D106, S2X30.	AY.77	Collier et al. (2021)	2	A,C	1.0
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	A,C	1.0
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	A,C	1.0
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	A,C	1.0
p.E484K	antibody epitope effects	Massive reduction in binding efficiency vs wild type for mAb LY-CoV555.	AY.77	Rappazzo et al. (2021)	2	A,C	1.0
p.E484K	antibody epitope effects	Complete loss of binding in ELISA by the variant against monoclonal antibody VH-Fc ab8	AY.77	Sun et al. (2021)	2	A,C	1.0
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	A,C	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Alternate Allele	Alternate Frequency
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	A,C	1.0
p.E484K	convalescent plasma binding	1.42x increase in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset.	AY.77	Gong et al. (2021)	2	A,C	1.0
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	A,C	1.0
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	A,C	1.0
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	A,C	1.0
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	A,C	1.0
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	A,C	1.0
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	A,C	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Alternate Allele	Alternate Frequency
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	A,C	1.0
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	A,C	1.0
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	A,C	1.0
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	A,C	1.0
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 direectly with initial infection severity) had high neutralization against this 501Y.V2 PG: note that lineage variant R246I was excluded from the text in reference to these sera assays, not sure if that was an oversight.	AY.77	Wibmer et al. (2021)	2	A,C	1.0
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	A,C	1.0
p.E484K	monoclonal antibody serial passage escape	The engineered mutation cause 10-fold or more increase in the disassociation constant with many monoclonal antibodies (C144/C002/C121/C104/C110).	AY.77	Barnes et al. (2020)	2	A,C	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Alternate Allele	Alternate Frequency
p.E484K	monoclonal antibody serial passage escape	Escape variant 100% appearance in 2 passages against Regeneron monoclonal antibody REGN10989 @ 50ug/mL (99% after one passage)	AY.77	Baum et al. (2020)	2	A,C	1.0
p.E484K	monoclonal antibody 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	A,C	1.0
p.E484K	monoclonal antibody 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	A,C	1.0
p.E484K	monoclonal antibody serial passage escape	Class 2 antibodies C627, C602, C671, C643, and class 2/3 antibody C603 selected for the emergence of the E484K mutation in vitro.	AY.77	Wang et al. (2021)	2	A,C	1.0
p.E484K	monoclonal antibody 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	A,C	1.0
p.E484K	pharmaceutical effectiveness	Bamlanivimab (LY-CoV555) lost extasciitilde16x binding against this isolated mutation. Casirivimab lost extasciitilde16x binding against this isolated mutation.	AY.77	Engelhart et al. (2021)	2	A,C	1.0
p.E484K	pharmaceutical effectiveness	Tixagevimab, Regdanvimab and COR-101 display reduced binding affinity to virus pseudotyped as RBD from B.1.351.	AY.77	Engelhart et al. (2021)	2	A,C	1.0
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	A,C	1.0
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	A,C	1.0
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	A,C	1.0
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	A,C	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Alternate Allele	Alternate Frequency
p.E484K	trafficking	extasciitilde2x more infectivity than D614G alone in HEK293T-ACE2 cells 48h post-transduction.	AY.77	Kuzmina et al. (2021)	2	A,C	1.0
p.E484K	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 no change in infection rate amongst the cells.	AY.77	Tada et al. (2021)	2	A,C	1.0
p.E484K	vaccine neutralization efficacy	Nine stored sera from Pfizer BNT162b2 vaccinees were tested against a range of spike mutation bearing PV. E484K conferred a ten-fold reduction in neutralisation by vaccine sera.	AY.77	Ferreira et al. (2021)	2	A,C	1.0
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	A,C	1.0
p.E484K	vaccine neutralization efficacy	Human sera from 5 two-dose Pfizer vaccinated individuals (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 relative to reference USA-WA1/2020 strain. One plasma failed to neutralize at all. 11 convalescent plasma with moderate IgG ELISA titre neutralized this variant 4.2x less relative to reference USA-WA1/2020 strain. 11 convalescent plasma with high IgG ELISA titre neutralized this variant 2.6x less relative to reference USA-WA1/2020 strain.	AY.77	Jangra et al. (2021)	2	A,C	1.0
p.E484K	vaccine neutralization 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,C	1.0
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	A,C	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	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	A,C	1.0
p.E484K	vaccine neutralization 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 antibodies, but only a modest decrease for vaccine plasma overall.	AY.77	Wang et al. (2021)	2	A,C	1.0
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	A,C	1.0
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	A,C	1.0
p.D138Y	ACE2 receptor binding affinity	Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant showed a 1.32x increase in binding (KD) relative to D614G.	AY.70	Gong et al. (2021)	3	T	0.33
p.D138Y	convalescent plasma binding	1.56x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset.	AY.70	Gong et al. (2021)	3	T	0.33
p.D138Y	vaccinee plasma binding	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 previously non-seroconverted subjects. 1.56x 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.70	Gong et al. (2021)	3	T	0.33

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Alternate Allele	Alternate Frequency
p.D138Y	virion structure	Estimated free energy change (ddG) for this variant is 0.43 kcal/mol (i.e. stabilizing relative to wild type)	AY.70	Spratt et al. (2021)	3	T	0.33
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.88, AY.114, AY.65	Maaroufi (2021)	217	TTCG,CTCG,TTCGTCGG,CTCGTCGT,CTCGT	
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.88, AY.114, AY.65	Tada et al. (2021)	217	TTCG,CTCG,TTCGTCGG,CTCGTCGT,CTCGT	
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.88, AY.114, AY.65	Tada et al. (2021)	217	TTCG,CTCG,TTCGTCGG,CTCGTCGT,CTCGT	
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.98, AY.35, AY.70	Yadav et al. (2021)	20	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Alternate Allele	Alternate Frequency
p.P681R	trafficking	This variant combination shows a extasci-itilde3x 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	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	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.54, AY.46.2, AY.45, AY.108, AY.11, AY.113, AY.118, AY.13, AY.3.1, AY.53, AY.73, AY.103, AY.43.4, AY.124, AY.109, AY.84, AY.23, AY.89, AY.36, AY.44, AY.34.1, AY.46.1, AY.119.1, AY.77, AY.27, AY.75, AY.4, AY.66, AY.125, AY.59, B.1.617.2, AY.86, AY.19, AY.116.1, AY.117, AY.102, AY.15, AY.32, AY.34, AY.116, AY.9, AY.70, AY.9.2.1, AY.37, AY.121.1, AY.43.3, AY.2, AY.4.4, AY.47, AY.25, AY.120.1, AY.42, AY.74, AY.105, AY.120, AY.104, AY.126, AY.106, AY.51, AY.46.4, AY.43, AY.64, AY.78, AY.3, AY.107, AY.6, AY.7.1, AY.99, AY.26, AY.68, AY.38, AY.46.6, AY.41, AY.99.2, AY.46, AY.67, AY.39, AY.4.2.1, AY.4.3, AY.35, AY.20, AY.110, AY.111, AY.33, AY.49, AY.57, AY.92, AY.14, AY.4.2, AY.40, AY.72, AY.85, AY.39.1, AY.21, AY.94, AY.17, AY.98, AY.60, AY.25.1, AY.1, AY.119, AY.4.5, AY.61, AY.82, AY.121, AY.16.1, AY.56, AY.18, AY.4.2.2, AY.28, AY.93, AY.10, AY.5.3, AY.24, AY.16, AY.62, AY.122, AY.29, AY.83, AY.98.1, AY.9.2, AY.48, AY.4.6, AY.122.1, AY.55, AY.87, AY.101,	Maaroufi (2021)	59202	G,GTCGT,GTCGG	0.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Alternate Allele	Alternate Frequency
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.54, AY.46.2, AY.45, AY.108, AY.11, AY.113, AY.118, AY.13, AY.3.1, AY.53, AY.73, AY.103, AY.43.4, AY.124, AY.109, AY.84, AY.23, AY.89, AY.36, AY.44, AY.34.1, AY.46.1, AY.119.1, AY.77, AY.27, AY.75, AY.4, AY.125, AY.59, B.1.617.2, AY.86, AY.19, AY.116.1, AY.117, AY.102, AY.15, AY.32, AY.34, AY.116, AY.9, AY.70, AY.9.2.1, AY.37, AY.121.1, AY.43.3, AY.2, AY.4.4, AY.47, AY.25, AY.120.1, AY.42, AY.74, AY.105, AY.120, AY.104, AY.126, AY.106, AY.51, AY.46.4, AY.43, AY.64, AY.78, AY.3, AY.107, AY.6, AY.7.1, AY.99, AY.26, AY.68, AY.38, AY.46.6, AY.41, AY.99.2, AY.46, AY.67, AY.39, AY.4.2.1, AY.4.3, AY.35, AY.20, AY.110, AY.111, AY.33, AY.49, AY.57, AY.92, AY.14, AY.4.2, AY.40, AY.72, AY.85, AY.39.1, AY.21, AY.94, AY.17, AY.98, AY.60, AY.25.1, AY.1, AY.119, AY.4.5, AY.61, AY.82, AY.121, AY.16.1, AY.56, AY.18, AY.4.2.2, AY.28, AY.93, AY.10, AY.5.3, AY.24, AY.16, AY.62, AY.122, AY.29, AY.83, AY.98.1, AY.9.2, AY.48, AY.4.6, AY.122.1, AY.52, AY.87, AY.101, AY.100	Tada et al. (2021)	59200	G,GTCGT,GTCGG	0.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	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 infectivity relative to D614G wild type.	AY.98, AY.35, AY.70	Tada et al. (2021)	20	G	1.0
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.98, AY.35, AY.70	Yadav et al. (2021)	20	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	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.54, AY.46.2, AY.45, AY.108, AY.11, AY.113, AY.118, AY.13, AY.3.1, AY.53, AY.73, AY.103, AY.43.4, AY.124, AY.109, AY.84, AY.23, AY.89, AY.36, AY.44, AY.34.1, AY.46.1, AY.119.1, AY.77, AY.27, AY.75, AY.4, AY.66, AY.125, AY.59, B.1.617.2, AY.86, AY.19, AY.116.1, AY.117, AY.102, AY.15, AY.32, AY.34, AY.116, AY.9, AY.70, AY.9.2.1, AY.37, AY.121.1, AY.43.3, AY.2, AY.4.4, AY.47, AY.25, AY.120.1, AY.42, AY.74, AY.105, AY.120, AY.104, AY.126, AY.106, AY.51, AY.46.4, AY.43, AY.64, AY.78, AY.3, AY.107, AY.6, AY.7.1, AY.99, AY.26, AY.68, AY.38, AY.46.6, AY.41, AY.99.2, AY.46, AY.67, AY.39, AY.4.2.1, AY.4.3, AY.35, AY.20, AY.110, AY.111, AY.33, AY.49, AY.57, AY.92, AY.14, AY.4.2, AY.40, AY.72, AY.85, AY.39.1, AY.21, AY.94, AY.17, AY.98, AY.60, AY.25.1, AY.1, AY.119, AY.4.5, AY.61, AY.82, AY.121, AY.16.1, AY.56, AY.18, AY.4.2.2, AY.28, AY.93, AY.10, AY.5.3, AY.24, AY.16, AY.62, AY.122, AY.29, AY.83, AY.98.1, AY.9.2, AY.48, AY.4.6, AY.122.1, AY.55, AY.87, AY.101,	Tada et al. (2021)	59202	G,GTCGT,GTCGG	0.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Alternate Allele	Alternate Frequency
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	Gong et al. (2021)	1	T	1.0
p.P26S	convalescent plasma binding	1.08x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset.	AY.4.3	Gong et al. (2021)	1	T	1.0
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	Gong et al. (2021)	1	T	1.0
p.P681H	ACE2 receptor binding affinity	Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant showed a 1.23x decrease in binding (KD) relative to D614G.	AY.5	Gong et al. (2021)	18	GTCGT,ATCGG,G	1.0,GTCGG
p.P681H	antibody epitope effects	Ablates Class 3 N-terminal domain targeting antibody COV2-2489, diminishes COV2-2676.	AY.5	Chen et al. (2021)	18	GTCGT,ATCGG,G	1.0,GTCGG
p.P681H	antibody epitope effects	Wildtype elicits immune response, COVID-19 cohort epitope score > 99th percentile of the 497 pre-pandemic controls, mutant drops PIWAS epitope score from 7.8% to 1.2% (significantly poorer immune recognition) Together with other B1.1.7 lineage mutational changes (Spike: Y144del,N501Y, A570D Nucleoprotein: D3L, S235F) resulted in only 2 of 579 individuals (0.3% of the population) having a dramatic reduction in PIWAS antigen scores, which reflects the peak epitope signal along the entire antigen.	AY.5	Haynes et al. (2021)	18	GTCGT,ATCGG,G	1.0,GTCGG
p.P681H	antibody epitope effects	This variant is adjacent to the Spike protein furin cleavage site (cleavage of S into S1 and S2 subunits is required for viral membrane fusion and subsequent entry into host cells), a site shown to be highly immunogenic.	AY.5	Johnson et al. (2020)	18	GTCGT,ATCGG,G	1.0,GTCGG
p.P681H	convalescent plasma binding	1.26x increase in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset.	AY.5	Gong et al. (2021)	18	GTCGT,ATCGG,G	1.0,GTCGG

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Alternate Allele	Alternate Frequency
p.P681H	trafficking	While the introduction of P681H in the SARS-CoV-2 B.1.1.7 variant may increase spike cleavage by furin-like proteases, this does not significantly impact viral entry or cell-cell spread. We consider that other factors are at play to account for the increased in transmission and disease severity attributed to this variant of concern (VOC).	AY.5	Lubinski et al. (2021)	18	GTCGT,ATCGG,G	1.0,GTCGG
p.P681H	trafficking	This mutation in the first base of the furin clevage site maintains the RXXR recognition motif, and is presumed to enhance cleavage based on the removal of a proline-directed phosphotase recognition site at S680. In a homologuous site in Infectious Bronchitis Virus (IBV, Gammacoronaviruses), abolition of S680 phosphorylation improves furin cleavage (and presumably cell entry).	AY.5	Maaroufi (2021)	18	GTCGT,ATCGG,G	1.0,GTCGG
p.P681H	trafficking	Lentiviral pseudotyped with this individual mutation from B.1.1.7 was tested on ACE2.293T cells. Luciferase activity was measured two days postinfection, showing NO statistically significant infection rate change amongst the cells, suggesting that furin cleavage typically used for cell entry is not affected by this change one amino acid upstream of the RXXR recognition pattern.	AY.5	Tada et al. (2021)	18	GTCGT,ATCGG,G	1.0,GTCGG
p.P681H	vaccine neutralization efficacy	No significant change in virus neutralzation by 18 Pfizer two dose vaccinee sera compared to B.1.1.7. [results without including the used mutation A27S likely generalizable, as this is not a lineage defining mutation]	AY.5	Zuckerman et al. (2021)	18	GTCGT,ATCGG,G	1.0,GTCGG
p.P681H	vaccinee plasma binding	1.14x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in previously non-seroconverted subjects. 1.11x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in post-infection vaccinees.	AY.5	Gong et al. (2021)	18	GTCGT,ATCGG,G	1.0,GTCGG
p.P681H	virion structure	The Ratio of S2 (processed Spike) to full length Spike is higher for this mutation, due to a drop in the full length Spike measured, suggesting that this mutation compensates for decreased Spike production by improved proteolytic processing.	AY.5	Tada et al. (2021)	18	GTCGT,ATCGG,G	1.0,GTCGG

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Alternate Allele	Alternate Frequency
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.106, AY.114, AY.119.1, AY.77, AY.78, AY.107, AY.4, AY.1, AY.119, AY.4.5, AY.125, B.1.617.2, AY.121, AY.88, AY.4.2.2, AY.116.1, AY.117, AY.108, AY.5.3, AY.102, AY.113, AY.118, AY.34, AY.116, AY.39, AY.4.2.1, AY.4.3, AY.121.1, AY.29, AY.124, AY.4.4, AY.20, AY.43.4, AY.109, AY.110, AY.111, AY.127, AY.89, AY.36, AY.34.1, AY.4.6, AY.92, AY.120.1, AY.4.2, AY.42, AY.120, AY.85, AY.104, AY.39.1, AY.101, AY.126, AY.100	Gong et al. (2021)	4187	T	0.67

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	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-symptom-onset.	AY.106, AY.114, AY.119.1, AY.77, AY.78, AY.107, AY.4, AY.1, AY.119, AY.4.5, AY.125, B.1.617.2, AY.121, AY.88, AY.4.2.2, AY.116.1, AY.117, AY.108, AY.5.3, AY.102, AY.113, AY.118, AY.34, AY.116, AY.39, AY.4.2.1, AY.4.3, AY.121.1, AY.29, AY.124, AY.4.4, AY.20, AY.43.4, AY.109, AY.110, AY.111, AY.127, AY.89, AY.36, AY.34.1, AY.4.6, AY.92, AY.120.1, AY.4.2, AY.42, AY.120, AY.85, AY.104, AY.39.1, AY.101, AY.126, AY.100	Gong et al. (2021)	4187	T	0.67

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Alternate Allele	Alternate Frequency
p.T95I	vaccinee plasma binding	1.16x increase in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in previously non-seroconverted subjects. 1.02x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in post-infection vaccinees.	AY.106, AY.114, AY.119.1, AY.77, AY.78, AY.107, AY.4, AY.1, AY.119, AY.4.5, AY.125, B.1.617.2, AY.121, AY.88, AY.4.2.2, AY.116.1, AY.117, AY.108, AY.5.3, AY.102, AY.113, AY.118, AY.34, AY.116, AY.39, AY.4.2.1, AY.4.3, AY.121.1, AY.29, AY.124, AY.4.4, AY.20, AY.43.4, AY.109, AY.110, AY.111, AY.127, AY.89, AY.36, AY.34.1, AY.4.6, AY.92, AY.120.1, AY.4.2, AY.42, AY.120, AY.85, AY.104, AY.39.1, AY.101, AY.126, AY.100	Gong et al. (2021)	4187	T	0.67
p.K417N	ACE2 receptor binding affinity	The K417N mutation decreased the affinity extasciitilde4 fold, mainly by decreasing the k(on) but also by increasing the k(off) as measured by surface plasmon resonance.	AY.2, AY.1	Barton et al. (2021)	10	T	1.0
p.K417N	ACE2 receptor binding affinity	This combination showed extasciitilde3x increase binding to ACE2 vs wild type, about half that of the B.1.1.7 lineage, suggesting that the K417N mutation is slightly detrimental to ACE2 binding, probably as a result of disrupting the salt bridge formed with ACE2 residue D30	AY.2, AY.1	Collier et al. (2021)	10	T	1.0
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.2, AY.1	Gong et al. (2021)	10	T	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Alternate Allele	Alternate Frequency
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.2, AY.1	Laffeber et al. (2021)	10	T	1.0
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.2, AY.1	Liu et al. (2021)	10	T	1.0
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.2, AY.1	Ramanathan et al. (2021)	10	T	1.0
p.K417N	ACE2 receptor binding affinity	Reported 3-fold decrease in affinity compared to wild-type RBD on the cell surface (Kd	AY.2, AY.1	Tian et al. (2021)	10	T	1.0
p.K417N	ACE2 receptor binding affinity	Reported slight increase in affinity compared to wild-type RBD on the cell surface (Kd	AY.2, AY.1	Tian et al. (2021)	10	T	1.0
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.2, AY.1	Vogel et al. (2021)	10	T	1.0
p.K417N	antibody epitope effects	>20% (ELISA significance threshold) drop in antibody binding (ELISA) by this variant against IgG1 monoclonal antibody ab1.	AY.2, AY.1	Sun et al. (2021)	10	T	1.0
p.K417N	antibody epitope effects	5 antibodies tested were less potent against K417N by ten-fold or more (class 1 mAbs)	AY.2, AY.1	Wang et al. (2021)	10	T	1.0
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.2, AY.1	Wang et al. (2021)	10	T	1.0
p.K417N	convalescent plasma binding	2.16x increase in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset.	AY.2, AY.1	Gong et al. (2021)	10	T	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Alternate Allele	Alternate Frequency
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.2, AY.1	Cele et al. (2021)	10	T	1.0
p.K417N	convalescent plasma escape	In 19 convalescent human sera extasciitilde1mo post infection, Two-tailed Wilcoxon matched-pairs signed-rank test shows mild resistence P	AY.2, AY.1	Chen et al. (2021)	10	T	1.0
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% retained high titres	AY.2, AY.1	Wibmer et al. (2021)	10	T	1.0
p.K417N	convalescent plasma escape	Nearly half (21 of 44, 48%) of early pandemic exposure convalescent plasma/sera failed to neutralize the 501Y.V2 ("South African") lineage pseudovirus construct Only 3 of 44 convascent sera (those with the highest titer, which correlated direectly with initial infection severity) had high neutralization against this 501Y.V2 PG: note that lineage variant R246I was excluded from the text in reference to these sera assays, not sure if that was an oversight.	AY.2, AY.1	Wibmer et al. (2021)	10	T	1.0
p.K417N	gene expression increase	Experimentally, Spike gene expression increased 0.1 fold	AY.2, AY.1	Starr et al. (2020)	10	T	1.0
p.K417N	monoclonal antibody serial passage escape	Escape mutation against monoclonal antibody LY-CoV016	AY.2, AY.1	Starr et al. (2021)	10	T	1.0
p.K417N	monoclonal antibody serial passage escape	In vitro selection against class 1 (Spike 'up' conformation) monoclonal antibody C682, and to a lesser extent C614 and C660	AY.2, AY.1	Wang et al. (2021)	10	T	1.0
p.K417N	pharmaceutical effectiveness	COR-101 lost extasciitilde6x binding against this isolated mutation. Estesevimab lost extasciitilde100x binding against this isolated mutation.	AY.2, AY.1	Engelhart et al. (2021)	10	T	1.0
p.K417N	pharmaceutical effectiveness	Tixagevimab, Regdanvimab and COR-101 display reduced binding affinity to virus pseudotyped as RBD from B.1.351.	AY.2, AY.1	Engelhart et al. (2021)	10	T	1.0
p.K417N	pharmaceutical effectiveness	This mutated version of RBD completely abolishes the binding to a therapeutic antibody, Bamlanivimab, in vitro.	AY.2, AY.1	Liu et al. (2021)	10	T	1.0
p.K417N	trafficking	extasciitilde2x more infectivity than D614G alone in HEK293T-ACE2 cells 48h post-transduction.	AY.2, AY.1	Kuzmina et al. (2021)	10	T	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Alternate Allele	Alternate Frequency
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.2, AY.1	Tada et al. (2021)	10	T	1.0
p.K417N	vaccine neutralization efficacy	This variant showed only minor in Pfizer sera (one or two dose) neutralization efficiency vs D614G (using lentivirus pseudotype).	AY.2, AY.1	Kuzmina et al. (2021)	10	T	1.0
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.2, AY.1	Gong et al. (2021)	10	T	1.0
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.2, AY.1	Spratt et al. (2021)	10	T	1.0

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