Surveillance report

Surveillance generated by nf-ncov-voc for Kappa variant

Date

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

Pango Lineages

Pango Lineages in this report ['B.1.617.1']

Indicator

This table contains key indicators identified

Indicator	Sub-categories from POKAY	Mutations
Transmissibility between humans	transmissibility	D614G, E484Q, L452R, P681R
Infection Severity	ACE2 receptor binding affinity, viral load, outcome hazard ratio	D614G, E154K, E484Q, G142D, L452R, P681R, Q1071H, T95I
Immunity after natural infection	convalescent plasma escape, reinfection, humoral response durability	D614G, E154K, E484Q, G142D, K444N, L452R, P681R, Q1071H
Vaccines	vaccine neutralization efficacy	D614G, E154K, E484Q, G142D, L452R, P681R, Q1071H, T95I
Monoclonal antibodies	monoclonal antibody serial passage escape, pharmaceutical effectiveness	E484Q, G142D, L452R
Diagnostics	clinical indicators, antigenic test failure, symptom prevalence	

Mutation Significance

This table contains key functional impacts of mutations identified

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
Q1071H	ACE2 receptor binding affinity	Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant combination (representing lineage B.1.617.1) showed a 1.12x increase in binding (KD) relative to D614G, but described as "not significant". [exact variant list not provided in manuscript, is inferred and represents minimal set agreed upon commonly]	B.1.617.1	Gong et al. (2021)	451	A	T	1.0
Q1071H	convalescent plasma escape	Relative to B.1, Kappa (B.1.617.1) shows 5.71x decrease in neutralization efficiency by convalescent plasma [no cohort details provided]	B.1.617.1	Wilhelm et al. (2021)	451	A	T	1.0
Q1071H	trafficking	extasciitilde3.5x cleavage of S2 relative to WA1 (D614G) wildtype by Kappa (B.1.617.1) variant as measured by mass spectrometry of Vero-TMPRSS culture (compare to extasciitilde4.5x for closely related Delta B.1.617.2 also with P681R at the cleavage site).	B.1.617.1	Esclera et al. (2021)	451	A	T	1.0
Q1071H	vaccine neutralization efficacy	Inferring from two B.1.617.1 variants tested, estimate baseline 3.3x reduction in ID50 relative to D614G wildtype using pseudotyped VSV assay on 8 Moderna vaccinee sera one week post-booster.	B.1.617.1	Choi et al. (2021)	451	A	T	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
Q1071H	vaccine neutralization efficacy	Neutralization efficiency (ID50) against B.1.617.1-v1 ("Kappa") reduced 3.4x relative to D614G wild-type using pseudotyped VSV assay on 8 Moderna vaccinee sera one week post-booster.	B.1.617.1	Choi et al. (2021)	451	A	T	1.0
Q1071H	vaccine neutralization efficacy	1.5x reduction in neutralization (ID50) in sera 3 weeks after one dose of Pfizer/BioNTech BNT162b2 (up to 5 naive and post infection vaccinees) [exact set of variants used is not listed in the manuscript]	B.1.617.1	Gong et al. (2021)	451	A	T	1.0
Q1071H	vaccine neutralization efficacy	Relative to B.1, Kappa (B.1.617.1) shows mean 1.97x decrease in neutralization efficiency by 18 vaccinee sera (BNT162b2 and mRNA1273).	B.1.617.1	Wilhelm et al. (2021)	451	A	T	1.0
Q1071H	vaccine neutralization efficacy	Average 2x neutralization efficiency decrease against sera from 26 Phase II trial Covaxin (BBV152) vaccine recipents. Very similar to B.1.1.7 (extasciitilde2x) in the same study, and the neutralization from 17 sera of natural infections across B1 lineages.	B.1.617.1	Yadav et al. (2021)	451	A	T	1.0
P681R	ACE2 receptor binding affinity	Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant combination (representing lineage B.1.617.1) showed a 1.12x increase in binding (KD) relative to D614G, but described as "not significant". [exact variant list not provided in manuscript, is inferred and represents minimal set agreed upon commonly]	B.1.617.1	Gong et al. (2021)	449	C	G	1.0
P681R	convalescent plasma escape	Relative to B.1, Kappa (B.1.617.1) shows 5.71x decrease in neutralization efficiency by convalescent plasma [no cohort details provided]	B.1.617.1	Wilhelm et al. (2021)	449	C	G	1.0
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.	B.1.617.1	Yadav et al. (2021)	449	C	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
P681R	trafficking	extasciitilde3.5x cleavage of S2 relative to WA1 (D614G) wildtype by Kappa (B.1.617.1) variant as measured by mass spectrometry of Vero-TMPRSS culture (compare to extasciitilde4.5x for closely related Delta B.1.617.2 also with P681R at the cleavage site).	B.1.617.1	Esclera et al. (2021)	449	C	G	1.0
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]	B.1.617.1	Maaroufi (2021)	449	C	G	1.0
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.	B.1.617.1	Tada et al. (2021)	449	C	G	1.0
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.	B.1.617.1	Tada et al. (2021)	449	C	G	1.0
P681R	vaccine neutralization efficacy	Inferring from two B.1.617.1 variants tested, estimate baseline 3.3x reduction in ID50 relative to D614G wildtype using pseudotyped VSV assay on 8 Moderna vaccinee sera one week post-booster.	B.1.617.1	Choi et al. (2021)	449	C	G	1.0
P681R	vaccine neutralization efficacy	Neutralization efficiency (ID50) against B.1.617.1-v1 ("Kappa") reduced 3.4x relative to D614G wildtype using pseudotyped VSV assay on 8 Moderna vaccinee sera one week post-booster.	B.1.617.1	Choi et al. (2021)	449	C	G	1.0
P681R	vaccine neutralization efficacy	1.5x reduction in neutralization (ID50) in sera 3 weeks after one dose of Pfizer/BioNTech BNT162b2 (up to 5 naive and post infection vaccinees) [exact set of variants used is not listed in the manuscript]	B.1.617.1	Gong et al. (2021)	449	C	G	1.0
P681R	vaccine neutralization efficacy	Relative to B.1, Kappa (B.1.617.1) shows mean 1.97x decrease in neutralization efficiency by 18 vaccinee sera (BNT162b2 and mRNA1273).	B.1.617.1	Wilhelm et al. (2021)	449	C	G	1.0
P681R	vaccine neutralization efficacy	Average 2x neutralization efficiency decrease against sera from 26 Phase II trial Covaxin (BBV152) vaccine recipents. Very similar to B.1.1.7 (extasciitilde2x) in the same study, and the neutralization from 17 sera of natural infections across B1 lineages.	B.1.617.1	Yadav et al. (2021)	449	C	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
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.	B.1.617.1	Yadav et al. (2021)	449	C	G	1.0
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]	B.1.617.1	Tada et al. (2021)	449	C	G	1.0
D614G	ACE2 receptor binding affinity	Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant combination (representing lineage B.1.617.1) showed a 1.12x increase in binding (KD) relative to D614G, but described as "not significant". [exact variant list not provided in manuscript, is inferred and represents minimal set agreed upon commonly]	B.1.617.1	Gong et al. (2021)	451	A	G	1.0
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.	B.1.617.1	Gong et al. (2021)	451	A	G	1.0
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]	B.1.617.1	Gong et al. (2021)	451	A	G	1.0
D614G	ACE2 receptor binding affinity	Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant showed a 1.33x decrease in binding (KD) relative to D614G.	B.1.617.1	Gong et al. (2021)	451	A	G	1.0
D614G	ACE2 receptor binding affinity	In four cell lines (including 293T-hACE2 cells), this mutation combination increases infectivity vs D614G alone	B.1.617.1	Li et al. (2020)	451	A	G	1.0
D614G	convalescent plasma binding	2.15x increase in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset.	B.1.617.1	Gong et al. (2021)	451	A	G	1.0
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]	B.1.617.1	Gong et al. (2021)	451	A	G	1.0
D614G	convalescent plasma binding	No change in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset.	B.1.617.1	Gong et al. (2021)	451	A	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
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]	B.1.617.1	Tada et al. (2021)	451	A	G	1.0
D614G	convalescent plasma escape	Relative to B.1, Kappa (B.1.617.1) shows 5.71x decrease in neutralization efficiency by convalescent plasma [no cohort details provided]	B.1.617.1	Wilhelm et al. (2021)	451	A	G	1.0
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]	B.1.617.1	Wilhelm et al. (2021)	451	A	G	1.0
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.	B.1.617.1	Landis et al. (2021)	451	A	G	1.0
D614G	syncytium formation	Slight increase in Vero cell-cell membrane fusion assay under infection with VSV pseudotyped virus.	B.1.617.1	Kim et al. (2021)	451	A	G	1.0
D614G	tissue specific neutralization	The nasal mucosa of Pfizer vaccinees with time course collection was evaluated against VSV pseudotypes: results (only one nasal swab from different previously infected vacinee neutralizing at weeks 3 and 6 against B.1.1.7 and D614G) suggest that vaccinees probably do not elicit an early humoral response detectable at mucosal surfaces even though sera neutralization was observed. They strengthen the hypothesis that some vaccines may not protect against viral acquisition and infection of the oral–nasal region, but may prevent severe disease associated with viral dissemination in the lower respiratory tract.	B.1.617.1	Planas et al. (2021)	451	A	G	1.0
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)	B.1.617.1	Barrett et al. (2021)	451	A	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
D614G	trafficking	The increased transduction with Spike D614G ranged from 1.3- to 2.4-fold in Caco-2 and Calu-3 cells expressing endogenous ACE2 and from 1.5- to 7.7-fold in A549ACE2 and Huh7.5ACE2 overexpressing ACE2. Although there is minimal difference in ACE2 receptor binding between the D614 and G614 Spike variants, the G614 variant is more resistant to proteolytic cleavage, suggesting a possible mechanism for the increased transduction.	B.1.617.1	Daniloski et al. (2021)	451	A	G	1.0
D614G	trafficking	extasciitilde3.5x cleavage of S2 relative to WA1 (D614G) wildtype by Kappa (B.1.617.1) variant as measured by mass spectrometry of Vero-TMPRSS culture (compare to extasciitilde4.5x for closely related Delta B.1.617.2 also with P681R at the cleavage site).	B.1.617.1	Esclera et al. (2021)	451	A	G	1.0
D614G	trafficking	No change in infectivity (24h) relative to D614G alone in Caco-2 cells, Vero or Calu-3.	B.1.617.1	Kim et al. (2021)	451	A	G	1.0
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).	B.1.617.1	Kim et al. (2021)	451	A	G	1.0
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.	B.1.617.1	Ozono et al. (2020)	451	A	G	1.0
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.	B.1.617.1	Tada et al. (2021)	451	A	G	1.0
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.	B.1.617.1	Zhang et l. (2020)	451	A	G	1.0
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]	B.1.617.1	Tada et al. (2021)	451	A	G	1.0
D614G	transmissibility	The combination caused a 3-fold increase in infectivity relative to D614G wild type. [compare to 3.5x for L452R alone]	B.1.617.1	Tada et al. (2021)	451	A	G	1.0

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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.	B.1.617.1	Tada et al. (2021)	451	A	G	1.0
D614G	vaccine neutralization efficacy	Inferring from two B.1.617.1 variants tested, estimate baseline 3.3x reduction in ID50 relative to D614G wildtype using pseudotyped VSV assay on 8 Moderna vaccinee sera one week post-booster.	B.1.617.1	Choi et al. (2021)	451	A	G	1.0
D614G	vaccine neutralization efficacy	Neutralization efficiency (ID50) against B.1.617.1-v1 ("Kappa") reduced 3.4x relative to D614G wildtype using pseudotyped VSV assay on 8 Moderna vaccinee sera one week post-booster.	B.1.617.1	Choi et al. (2021)	451	A	G	1.0
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.	B.1.617.1	Garcia-Beltran et al. (2021)	451	A	G	1.0
D614G	vaccine neutralization efficacy	1.5x reduction in neutralization (ID50) in sera 3 weeks after one dose of Pfizer/BioNTech BNT162b2 (up to 5 naive and post infection vaccinees) [exact set of variants used is not listed in the manuscript]	B.1.617.1	Gong et al. (2021)	451	A	G	1.0
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)	B.1.617.1	Gong et al. (2021)	451	A	G	1.0
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.	B.1.617.1	Kuzmina et al. (2021)	451	A	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
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.	B.1.617.1	Tada et al. (2021)	451	A	G	1.0
D614G	vaccine neutralization efficacy	Relative to B.1, Kappa (B.1.617.1) shows mean 1.97x decrease in neutralization efficiency by 18 vaccinee sera (BNT162b2 and mRNA1273).	B.1.617.1	Wilhelm et al. (2021)	451	A	G	1.0
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).	B.1.617.1	Wilhelm et al. (2021)	451	A	G	1.0
D614G	vaccine neutralization efficacy	Average 2x neutralization efficiency decrease against sera from 26 Phase II trial Covaxin (BBV152) vaccine recipents. Very similar to B.1.1.7 (extasciitilde2x) in the same study, and the neutralization from 17 sera of natural infections across B1 lineages.	B.1.617.1	Yadav et al. (2021)	451	A	G	1.0
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.	B.1.617.1	Gong et al. (2021)	451	A	G	1.0
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]	B.1.617.1	Gong et al. (2021)	451	A	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
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.	B.1.617.1	Gong et al. (2021)	451	A	G	1.0
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.	B.1.617.1	Plante et al. (2020)	451	A	G	1.0
D614G	virion structure	Estimated free energy change (ddG) for this variant is 2.5 kcal/mol (i.e. stabilizing relative to wild type)	B.1.617.1	Spratt et al. (2021)	451	A	G	1.0
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.	B.1.617.1	Weissman et al. (2020)	451	A	G	1.0
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.	B.1.617.1	Yurkovetskiy et al. (2020)	451	A	G	1.0
D614G	virion structure	Based on pseudotyped virus experiments, D614G may increase infectivity by assembling more functional S protein into the virion.	B.1.617.1	Zhang et al. (2020)	451	A	G	1.0
E154K	ACE2 receptor binding affinity	Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant combination (representing lineage B.1.617.1) showed a 1.12x increase in binding (KD) relative to D614G, but described as "not significant". [exact variant list not provided in manuscript, is inferred and represents minimal set agreed upon commonly]	B.1.617.1	Gong et al. (2021)	438	G	A	1.0
E154K	convalescent plasma escape	Escape mutant found after in passage in plasma pool of 26 convalescents mean 1.5 post symptom onset.	B.1.617.1	Schmidt et al. (2021)	438	G	A	1.0
E154K	convalescent plasma escape	Relative to B.1, Kappa (B.1.617.1) shows 5.71x decrease in neutralization efficiency by convalescent plasma [no cohort details provided]	B.1.617.1	Wilhelm et al. (2021)	438	G	A	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
E154K	trafficking	extasciitilde3.5x cleavage of S2 relative to WA1 (D614G) wildtype by Kappa (B.1.617.1) variant as measured by mass spectrometry of Vero-TMPRSS culture (compare to extasciitilde4.5x for closely related Delta B.1.617.2 also with P681R at the cleavage site).	B.1.617.1	Esclera et al. (2021)	438	G	A	1.0
E154K	vaccine neutralization efficacy	Inferring from two B.1.617.1 variants tested, estimate baseline 3.3x reduction in ID50 relative to D614G wildtype using pseudotyped VSV assay on 8 Moderna vaccinee sera one week post-booster.	B.1.617.1	Choi et al. (2021)	438	G	A	1.0
E154K	vaccine neutralization efficacy	Neutralization efficiency (ID50) against B.1.617.1-v1 ("Kappa") reduced 3.4x relative to D614G wildtype using pseudotyped VSV assay on 8 Moderna vaccinee sera one week post-booster.	B.1.617.1	Choi et al. (2021)	438	G	A	1.0
E154K	vaccine neutralization efficacy	1.5x reduction in neutralization (ID50) in sera 3 weeks after one dose of Pfizer/BioNTech BNT162b2 (up to 5 naive and post infection vaccinees) [exact set of variants used is not listed in the manuscript]	B.1.617.1	Gong et al. (2021)	438	G	A	1.0
E154K	vaccine neutralization efficacy	Relative to B.1, Kappa (B.1.617.1) shows mean 1.97x decrease in neutralization efficiency by 18 vaccinee sera (BNT162b2 and mRNA1273).	B.1.617.1	Wilhelm et al. (2021)	438	G	A	1.0
E154K	vaccine neutralization efficacy	Average 2x neutralization efficiency decrease against sera from 26 Phase II trial Covaxin (BBV152) vaccine recipents. Very similar to B.1.1.7 (extasciitilde2x) in the same study, and the neutralization from 17 sera of natural infections across B1 lineages.	B.1.617.1	Yadav et al. (2021)	438	G	A	1.0
L452R	ACE2 receptor binding affinity	Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant showed a 2.66x increase in binding (KD) relative to D614G.	B.1.617.1	Gong et al. (2021)	450	T	G	1.0
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]	B.1.617.1	Gong et al. (2021)	450	T	G	1.0
L452R	ACE2 receptor binding affinity	Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant combination (representing lineage B.1.617.1) showed a 1.12x increase in binding (KD) relative to D614G, but described as "not significant". [exact variant list not provided in manuscript, is inferred and represents minimal set agreed upon commonly]	B.1.617.1	Gong et al. (2021)	450	T	G	1.0
L452R	ACE2 receptor binding affinity	extasciitilde1.7-fold increase in binding affinity vs wild type.	B.1.617.1	Motozono et al. (2021)	450	T	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
L452R	T cell evasion	L452R derivative virus did not induce IFN-gamma expression even at the highest concentration tested (10 nM) in two different A*24:02 convalescent sera donor plasma (linear epitope NYNYLYRLF 448,456).	B.1.617.1	Motozono et al. (2021)	450	T	G	1.0
L452R	antibody epitope effects	Resistent to some neutralizing antibodies: mAbs X593 and P2B-2F6	B.1.617.1	Li et al. (2020)	450	T	G	1.0
L452R	antibody epitope effects	Mutant screen in neutralization assay with a broad range of monoclonal antibodies shows resistence to more than one antibody.	B.1.617.1	Liu et al. (2021)	450	T	G	1.0
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.	B.1.617.1	McCallum et al. (2021)	450	T	G	1.0
L452R	antibody epitope effects	extasciitilde20% (ELISA significance threshold) drop in antibody binding (ELISA) by this variant against monoclonal antibody VH ab6.	B.1.617.1	Sun et al. (2021)	450	T	G	1.0
L452R	convalescent plasma binding	2.15x increase in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset.	B.1.617.1	Gong et al. (2021)	450	T	G	1.0
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]	B.1.617.1	Gong et al. (2021)	450	T	G	1.0
L452R	convalescent plasma escape	Observed extasciitilde2x decrease on average in 16 health workers' convalescent sera.	B.1.617.1	Alenquer et al. (2021)	450	T	G	1.0
L452R	convalescent plasma escape	Ablation of neutralization capability of 3 of 4 convalescent sera tested, the other is significantly hindered.	B.1.617.1	Liu et al. (2021)	450	T	G	1.0
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]	B.1.617.1	Tada et al. (2021)	450	T	G	1.0
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]	B.1.617.1	Wilhelm et al. (2021)	450	T	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
L452R	convalescent plasma escape	Relative to B.1, Kappa (B.1.617.1) shows 5.71x decrease in neutralization efficiency by convalescent plasma [no cohort details provided]	B.1.617.1	Wilhelm et al. (2021)	450	T	G	1.0
L452R	gene expression increase	Experimentally, Spike gene expression increased 0.32 fold	B.1.617.1	Starr et al. (2020)	450	T	G	1.0
L452R	monoclonal antibody serial passage escape	Ranked effective mutant against this position in the RBD for highly neutralizing COV2-2096	B.1.617.1	Greaney et al. (2020)	450	T	G	1.0
L452R	monoclonal antibody serial passage escape	Escape mutation against monoclonal antibody LY-CoV555 (antibody that forms the basis for Eli Lilly's bamlanivimab)	B.1.617.1	Starr et al. (2021)	450	T	G	1.0
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.	B.1.617.1	Wang et al. (2021)	450	T	G	1.0
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.	B.1.617.1	Engelhart et al. (2021)	450	T	G	1.0
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.	B.1.617.1	McCallum et al. (2021)	450	T	G	1.0
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.	B.1.617.1	Yadav et al. (2021)	450	T	G	1.0
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.	B.1.617.1	Deng et al. (2021)	450	T	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
L452R	trafficking	extasciitilde3.5x cleavage of S2 relative to WA1 (D614G) wildtype by Kappa (B.1.617.1) variant as measured by mass spectrometry of Vero-TMPRSS culture (compare to extasciitilde4.5x for closely related Delta B.1.617.2 also with P681R at the cleavage site).	B.1.617.1	Esclera et al. (2021)	450	T	G	1.0
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]	B.1.617.1	Ferriera et al (2021)	450	T	G	1.0
L452R	trafficking	Increased stability of RBD expression in yeast, suggesting increased Spike protein stability.	B.1.617.1	Motozono et al. (2021)	450	T	G	1.0
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]	B.1.617.1	Tada et al. (2021)	450	T	G	1.0
L452R	transmissibility	The combination caused a 3-fold increase in infectivity relative to D614G wild type. [compare to 3.5x for L452R alone]	B.1.617.1	Tada et al. (2021)	450	T	G	1.0
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.	B.1.617.1	Tada et al. (2021)	450	T	G	1.0
L452R	vaccine neutralization efficacy	Inferring from two B.1.617.1 variants tested, estimate baseline 3.3x reduction in ID50 relative to D614G wildtype using pseudotyped VSV assay on 8 Moderna vaccinee sera one week post-booster.	B.1.617.1	Choi et al. (2021)	450	T	G	1.0
L452R	vaccine neutralization efficacy	Neutralization efficiency (ID50) against B.1.617.1-v1 (”Kappa”) reduced 3.4x relative to D614G wildtype using pseudotyped VSV assay on 8 Moderna vaccinee sera one week post-booster.	B.1.617.1	Choi et al. (2021)	450	T	G	1.0
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.	B.1.617.1	Ferreira et al. (2021)	450	T	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
L452R	vaccine neutralization efficacy	Nine stored sera from Pfizer BNT162b2 vaccinees were tested against a range of spike mutation bearing PV. 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].	B.1.617.1	Ferreira et al. (2021)	450	T	G	1.0
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)	B.1.617.1	Gong et al. (2021)	450	T	G	1.0
L452R	vaccine neutralization efficacy	1.5x reduction in neutralization (ID50) in sera 3 weeks after one dose of Pfizer/BioNTech BNT162b2 (up to 5 naive and post infection vaccinees) [exact set of variants used is not listed in the manuscript]	B.1.617.1	Gong et al. (2021)	450	T	G	1.0
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.	B.1.617.1	Jacobson et al. (2021)	450	T	G	1.0
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.	B.1.617.1	Tada et al. (2021)	450	T	G	1.0
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).	B.1.617.1	Wilhelm et al. (2021)	450	T	G	1.0
L452R	vaccine neutralization efficacy	Relative to B.1, Kappa (B.1.617.1) shows mean 1.97x decrease in neutralization efficiency by 18 vaccinee sera (BNT162b2 and mRNA1273).	B.1.617.1	Wilhelm et al. (2021)	450	T	G	1.0
L452R	vaccine neutralization efficacy	Average 2x neutralization efficiency decrease against sera from 26 Phase II trial Covaxin (BBV152) vaccine recipents. Very similar to B.1.1.7 (extasciitilde2x) in the same study, and the neutralization from 17 sera of natural infections across B1 lineages.	B.1.617.1	Yadav et al. (2021)	450	T	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
L452R	vaccinee plasma binding	1.05x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in previously non-seroconverted subjects. 1.16x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in post-infection vaccinees.	B.1.617.1	Gong et al. (2021)	450	T	G	1.0
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]	B.1.617.1	Gong et al. (2021)	450	T	G	1.0
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.	B.1.617.1	Yadav et al. (2021)	450	T	G	1.0
L452R	virion structure	Estimated free energy change (ddG) for this variant is -0.67 kcal/mol (i.e. destabilizing relative to wild type)	B.1.617.1	Spratt et al. (2021)	450	T	G	1.0
G142D	ACE2 receptor binding affinity	Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant combination (representing lineage B.1.617.1) showed a 1.12x increase in binding (KD) relative to D614G, but described as "not significant". [exact variant list not provided in manuscript, is inferred and represents minimal set agreed upon commonly]	B.1.617.1	Gong et al. (2021)	428	G	A	1.0
G142D	convalescent plasma escape	Relative to B.1, Kappa (B.1.617.1) shows 5.71x decrease in neutralization efficiency by convalescent plasma [no cohort details provided]	B.1.617.1	Wilhelm et al. (2021)	428	G	A	1.0
G142D	monoclonal antibody serial passage escape	Escape mutation against Spike N terminal domain antigenic supersite i mAbs S2M28, S2X28, S2X333	B.1.617.1	McCallum et al. (2021)	428	G	A	1.0
G142D	monoclonal antibody serial passage escape	Selected twice in passage with mAb COV2-2489.	B.1.617.1	Suryadevara et al. (2021)	428	G	A	1.0
G142D	trafficking	extasciitilde3.5x cleavage of S2 relative to WA1 (D614G) wildtype by Kappa (B.1.617.1) variant as measured by mass spectrometry of Vero-TMPRSS culture (compare to extasciitilde4.5x for closely related Delta B.1.617.2 also with P681R at the cleavage site).	B.1.617.1	Esclera et al. (2021)	428	G	A	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
G142D	vaccine neutralization efficacy	Inferring from two B.1.617.1 variants tested, estimate baseline 3.3x reduction in ID50 relative to D614G wildtype using pseudotyped VSV assay on 8 Moderna vaccinee sera one week post-booster.	B.1.617.1	Choi et al. (2021)	428	G	A	1.0
G142D	vaccine neutralization efficacy	Neutralization efficiency (ID50) against B.1.617.1-v1 ("Kappa") reduced 3.4x relative to D614G wildtype using pseudotyped VSV assay on 8 Moderna vaccinee sera one week post-booster.	B.1.617.1	Choi et al. (2021)	428	G	A	1.0
G142D	vaccine neutralization efficacy	1.5x reduction in neutralization (ID50) in sera 3 weeks after one dose of Pfizer/BioNTech BNT162b2 (up to 5 naive and post infection vaccinees) [exact set of variants used is not listed in the manuscript]	B.1.617.1	Gong et al. (2021)	428	G	A	1.0
G142D	vaccine neutralization efficacy	Relative to B.1, Kappa (B.1.617.1) shows mean 1.97x decrease in neutralization efficiency by 18 vaccinee sera (BNT162b2 and mRNA1273).	B.1.617.1	Wilhelm et al. (2021)	428	G	A	1.0
G142D	vaccine neutralization efficacy	Average 2x neutralization efficiency decrease against sera from 26 Phase II trial Covaxin (BBV152) vaccine recipents. Very similar to B.1.1.7 (extasciitilde2x) in the same study, and the neutralization from 17 sera of natural infections across B1 lineages.	B.1.617.1	Yadav et al. (2021)	428	G	A	1.0
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.	B.1.617.1	Gong et al. (2021)	437	C	T	1.0
T95I	convalescent plasma binding	No change in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset.	B.1.617.1	Gong et al. (2021)	437	C	T	1.0
T95I	vaccine neutralization efficacy	Neutralization efficiency (ID50) against B.1.617.1-v1 ("Kappa") reduced 3.4x relative to D614G wildtype using pseudotyped VSV assay on 8 Moderna vaccinee sera one week post-booster.	B.1.617.1	Choi et al. (2021)	437	C	T	1.0
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.	B.1.617.1	Gong et al. (2021)	437	C	T	1.0
E484Q	ACE2 receptor binding affinity	Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant combination (representing lineage B.1.617.1) showed a 1.12x increase in binding (KD) relative to D614G, but described as "not significant". [exact variant list not provided in manuscript, is inferred and represents minimal set agreed upon commonly]	B.1.617.1	Gong et al. (2021)	449	G	C	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
E484Q	ACE2 receptor binding affinity	Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant combination (representing lineage B.1.617) showed a 1.85x increase in binding (KD) relative to D614G. [exact variant list not provided in manuscript, is inferred fro common knowledge]	B.1.617.1	Gong et al. (2021)	449	G	C	1.0
E484Q	antibody epitope effects	>20% (ELISA significance threshold) drop in antibody binding by this variant against monoclonal antibody VH-Fc ab8.	B.1.617.1	Sun et al. (2021)	449	G	C	1.0
E484Q	convalescent plasma binding	This variant combination (representing lineage B.1.617) showed a 1.22x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset. [exact variant list not provided in manuscript, is inferred fro common knowledge]	B.1.617.1	Gong et al. (2021)	449	G	C	1.0
E484Q	convalescent plasma escape	In 3 of 11 subjects' convalescent sera in an early+late mutational landscape analysis of the RBD, E484Q shows a notably resistant profile, comparable to or even more resistant than E484K at later time points (i.e. more resistant to immune cell somatic mutation evolution), see Figure 5a,b. Subject C 32 days post-infection showed »10 fold reduction in neutralization, reducing to extasciitilde10-fold by day 104. Subject B 26 days post-infection showed extasciitilde10 fold reduction in neutralization, reducing to extasciitilde4x at day 113. Notably, Subject B also showed smaller than typical (extasciitilde10 vs 30+ fold) reduction in one-month neutralization by E484K at day 32, and no E484K immune escape at day 104. Subject I 26 days post-infection showed extasciitilde10 fold reduction in neutralization, with no reduction in escape at day 102. Notably, Subject I also showed smaller than typical (extasciitilde10 vs 30+ fold) reduction in one-month neutralization by E484K at day 26, and no E484K immune escape at day 102.	B.1.617.1	Greaney et al. (2021)	449	G	C	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
E484Q	convalescent plasma escape	Pseudotyped viruses for B.1.617 was 2.3-fold resistant to neutralization by convalescent sera compared to wild type - a finding that was similar to that of the 3-fold resistance of the South Africa B.1.351 variant using the same assay. The resistance of B.1.617 was caused by the L452R and E484Q mutation, based on results from viruses pseudotyped for individual variants within B.1.617. [details on the convalescent patient sera collection are not abundantly clear in the preprint]	B.1.617.1	Tada et al. (2021)	449	G	C	1.0
E484Q	convalescent plasma escape	Relative to B.1, Kappa (B.1.617.1) shows 5.71x decrease in neutralization efficiency by convalescent plasma [no cohort details provided]	B.1.617.1	Wilhelm et al. (2021)	449	G	C	1.0
E484Q	monoclonal antibody serial passage escape	Escape mutation against monoclonal antibody LY-CoV555 (antibody that forms the basis for Eli Lilly's bamlanivimab)	B.1.617.1	Starr et al. (2021)	449	G	C	1.0
E484Q	pharmaceutical effectiveness	Bamlanivimab (LY-CoV555) lost extasciitilde20x binding against this isolated mutation. Casirivimab lost extasciitilde4x binding against this isolated mutation.	B.1.617.1	Engelhart et al. (2021)	449	G	C	1.0
E484Q	symptom prevalence	Gross examination of 3+3 hamster lung specimens showed pronounced congestion and hemorrhages on days 5 and 7 post-infection in the case of the B.1.617.1 as compared with the B.1. The lung lesions with the B.1 variant were minimal to mild whereas with B.1.617.1 they were moderate. For B.1 pneumonic changes were minimal to mild (inflammatory cell infiltration, focal consolidation and mild congestion). The pronounced changes (moderate to severe) with mononuclear infiltration in the alveolar interstitial space, interstitial septal thickening, consolidation and pneumocyte hyperplasia were observed with B.1.617.1 variant consistently.	B.1.617.1	Yadav et al. (2021)	449	G	C	1.0
E484Q	trafficking	extasciitilde3.5x cleavage of S2 relative to WA1 (D614G) wildtype by Kappa (B.1.617.1) variant as measured by mass spectrometry of Vero-TMPRSS culture (compare to extasciitilde4.5x for closely related Delta B.1.617.2 also with P681R at the cleavage site).	B.1.617.1	Esclera et al. (2021)	449	G	C	1.0
E484Q	trafficking	This variant alone shows a 10x decrease in cell entry efficiency (RLU measurement in 293T cells) compared to D614G.	B.1.617.1	Ferriera et al (2021)	449	G	C	1.0
E484Q	transmissibility	The combination caused a 3-fold increase in infectivity relative to D614G wild type. [compare to 3.5x for L452R alone]	B.1.617.1	Tada et al. (2021)	449	G	C	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
E484Q	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.	B.1.617.1	Tada et al. (2021)	449	G	C	1.0
E484Q	vaccine neutralization efficacy	Inferring from two B.1.617.1 variants tested, estimate baseline 3.3x reduction in ID50 relative to D614G wildtype using pseudotyped VSV assay on 8 Moderna vaccinee sera one week post-booster.	B.1.617.1	Choi et al. (2021)	449	G	C	1.0
E484Q	vaccine neutralization efficacy	Neutralization efficiency (ID50) against B.1.617.1-v1 ("Kappa") reduced 3.4x relative to D614G wildtype using pseudotyped VSV assay on 8 Moderna vaccinee sera one week post-booster.	B.1.617.1	Choi et al. (2021)	449	G	C	1.0
E484Q	vaccine neutralization efficacy	Nine stored sera from Pfizer BNT162b2 vaccinees were tested against a range of spike mutation bearing PV. E484Q had a extasciitilde5x drop in neutralization (vs extasciitilde10x for E484K). When E484Q and L452R were combined, the fold change was significant, but similar to that of L452R alone (extasciitilde2x), suggesting no evidence for an additive effect [perhaps even E484Q effect dilution].	B.1.617.1	Ferreira et al. (2021)	449	G	C	1.0
E484Q	vaccine neutralization efficacy	1.5x reduction in neutralization (ID50) in sera 3 weeks after one dose of Pfizer/BioNTech BNT162b2 (up to 5 naive and post infection vaccinees) [exact set of variants used is not listed in the manuscript]	B.1.617.1	Gong et al. (2021)	449	G	C	1.0
E484Q	vaccine neutralization efficacy	1.4x reduction in neutralization (ID50) in sera 3 weeks after one dose of Pfizer/BioNTech BNT162b2 (up to 5 naive and post infection vaccinees)	B.1.617.1	Gong et al. (2021)	449	G	C	1.0
E484Q	vaccine neutralization efficacy	Pseudotyped viruses for B.1.617 was 4-fold resistant to neutralization by 6 BNT162b2 vaccine sera 28 days post-booster compared to wild type - a finding that was similar to that of the 3.4-fold resistance of the South Africa B.1.351 variant using the same assay. Neutralization by 3 Moderna vaccine sera 28 days post-booster was 5-fold resistant (vs. 2.2-fold for B.1.351). The resistance of B.1.617 was caused by the L452R and E484Q mutation, based on results from viruses pseudotyped for individual variants within B.1.617.	B.1.617.1	Tada et al. (2021)	449	G	C	1.0
E484Q	vaccine neutralization efficacy	Relative to B.1, Kappa (B.1.617.1) shows mean 1.97x decrease in neutralization efficiency by 18 vaccinee sera (BNT162b2 and mRNA1273).	B.1.617.1	Wilhelm et al. (2021)	449	G	C	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
E484Q	vaccine neutralization efficacy	Average 2x neutralization efficiency decrease against sera from 26 Phase II trial Covaxin (BBV152) vaccine recipents. Very similar to B.1.1.7 (extasciitilde2x) in the same study, and the neutralization from 17 sera of natural infections across B1 lineages.	B.1.617.1	Yadav et al. (2021)	449	G	C	1.0
E484Q	vaccinee plasma binding	This variant combination (representing lineage B.1.617) showed a 1.30x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in previously non-seroconverted subjects. 1.18x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in post-infection vaccinees. [exact variant list not provided in manuscript, is inferred fro common knowledge]	B.1.617.1	Gong et al. (2021)	449	G	C	1.0
E484Q	viral load	In 9 infected hamsters each for B.1 and B.1.617.1, no significant change in viral load or subgenomic RNA levels were detected.	B.1.617.1	Yadav et al. (2021)	449	G	C	1.0

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