Surveillance report

Surveillance generated by nf-ncov-voc for Alpha variant

Date

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

Pango Lineages

Pango Lineages in this report ['B.1.1.7', 'B.1.1.70', 'B.1.1.71', 'Q.1', 'Q.3', 'Q.4', 'Q.8']

Indicator

This table contains key indicators identified

Indicator	Sub-categories from POKAY	Mutations
Transmissibility between humans	transmissibility	p.A570D, p.D1118H, p.H69del, p.N501Y, p.P681H, p.S982A, p.T716I, p.V70del, p.Y144del
Infection Severity	ACE2 receptor binding affinity, viral load, outcome hazard ratio	p.A570D, p.D1118H, p.D614G, p.H69del, p.L5F, p.N501Y, p.P681H, p.S982A, p.T716I, p.V70del, p.Y144del
Immunity after natural infection	convalescent plasma escape, reinfection, humoral response durability	p.A570D, p.D1118H, p.D614G, p.H69del, p.N501Y, p.P681H, p.S982A, p.T716I, p.V70del, p.Y144del
Vaccines	vaccine neutralization efficacy	p.A570D, p.D1118H, p.D614G, p.H69del, p.N501Y, p.P681H, p.S982A, p.T716I, p.V70del, p.Y144del
Monoclonal antibodies	monoclonal antibody serial passage escape, pharmaceutical effectiveness	p.N501Y
Diagnostics	clinical indicators, antigenic test failure, symptom prevalence	p.A570D, p.D1118H, p.D614G, p.H69del, p.N501Y, p.P681H, p.S982A, p.T716I, p.V70del, p.Y144del

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
p.V70del	ACE2 receptor binding affinity	Six fold increase in affinity for ACE2 by the B.1.1.7 lineage vs wild type is driven by a drop in observed dissociation rate constant.	B.1.1.7, Q.3, Q.1	Collier et al. (2021)	36460	ATACATG	A	nan
p.V70del	ACE2 receptor binding affinity	Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant showed a 1.51x increase in binding (KD) relative to D614G, mostly due to decreased in "off-rate" a.k.a. dissociation rate (Kdis).	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Gong et al. (2021)	36470	ATACATG	A	nan
p.V70del	ACE2 receptor binding affinity	Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant combination (representing B.1.1.7 aka Alpha) had 5.43x increased binding relative to D614G alone.	B.1.1.7, Q.3, Q.1	Gong et al. (2021)	36460	ATACATG	A	nan
p.V70del	ACE2 receptor binding affinity	Flow cytometry was used on recombinant VSV proteins and yeast surface display to assess the binding of a labeled soluble ACE2 protein to cells expressing B.1.1.7. We observed a dramatic increase (relative to D614G) in binding of soluble ACE2 to B.1.1.7, and to a lesser extent to B.1.351, which both carry the N501Y mutation (see Fig 3).	B.1.1.7, Q.3, Q.1	Planas et al. (2021)	36460	ATACATG	A	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.V70del	ACE2 receptor binding affinity	This mutation combination causes major increase in binding affinity vs. wild type as measured by IC50 vs pseudotyped lentivirus, but combined with the complete set of B.1.1.7 lineage variants no major change vs wild type affnity is observed.	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Tada et al. (2021)	36470	ATACATG	A	nan
p.V70del	ACE2 receptor binding affinity	This mutation causes major decrease in binding affinity vs. wild type as measured by IC50 vs pseudotyped lentivirus.	B.1.1.7, Q.3, Q.1	Tada et al. (2021)	36460	ATACATG	A	nan
p.V70del	anthropozoonotic events	First documented cases of domestic cat and dog infections with the B.1.1.7 strain.	B.1.1.7, Q.3, Q.1	Hamer et al. (2021)	36460	ATACATG	A	nan
p.V70del	antibody epitope effects	Ablates Class 3 N-terminal domain targeting antibody COV2-2489, diminishes COV2-2676.	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Chen et al. (2021)	36470	ATACATG	A	nan
p.V70del	antibody epitope effects	extasciitilde20x resistence to mAb CQ038 by B.1.1.7 pseudotyped virus	B.1.1.7, Q.3, Q.1	Hu et al. (2021)	36460	ATACATG	A	nan
p.V70del	antibody epitope effects	Reduces neutralization by structurally unmapped mAb COVA1-21 (cluster XI).	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Rees-Spear et al. (2021)	36470	ATACATG	A	nan
p.V70del	antibody epitope effects	Lessens the potency of mAbs COVA2-17 (extasciitilde5x, similar to N501Y alone), COVA1-12 (extasciitilde11x) and COVA1-21 (>100x), which do not compete allosterically.	B.1.1.7, Q.3, Q.1	Rees-Spear et al. (2021)	36460	ATACATG	A	nan
p.V70del	antibody epitope effects	Reduction in neutralization by mAbs COVA1-18 (extasciitilde4x), COVA2-15 (extasciitilde9x). PG: these effects are laregly missing in the deletion-alone data	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Shen et al. (2021)	36470	ATACATG	A	nan
p.V70del	antibody epitope effects	Reduction in neutralization by mAbs COVA2-15 (extasciitilde9x), B38 (extasciitilde14x), S309 (extasciitilde190x) by this B.1.1.7 pseudotyped virus model.	B.1.1.7, Q.3, Q.1	Shen et al. (2021)	36460	ATACATG	A	nan
p.V70del	antibody epitope effects	B.1.1.7 pseudotyped virus model impairs binding by RBD-directed mAb 910-30. B.1.1.7 pseudotyped virus model abolishes N-terminal-domain-directed mAbs 5-24, 4-8, and 4A8. B.1.1.7 pseudotyped virus model impairs binding by N-terminal-domain-directed mAbs 2-17, 4-19, 5-7.	B.1.1.7, Q.3, Q.1	Wang et al. (2021)	36460	ATACATG	A	nan
p.V70del	clinical indicators	After adjusting for the age factor, in a prospective Chinese cohort study B.1.1.7 variant infection (compared to B.1.140) was the risk factor for C-reactive protein (P	B.1.1.7, Q.3, Q.1	Song et al. (2021)	36460	ATACATG	A	nan
p.V70del	convalescent plasma binding	1.33x increase in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset.	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Gong et al. (2021)	36470	ATACATG	A	nan
p.V70del	convalescent plasma binding	This variant combination (representing B.1.1.7 aka Alpha) showed a 1.15x increase in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset.	B.1.1.7, Q.3, Q.1	Gong et al. (2021)	36460	ATACATG	A	nan
p.V70del	convalescent plasma escape	One convalescent sera tested showed 4-fold or greater reduction in neutralization efficiency.	Q.8, Q.3, Q.1, B.1.1.7	Alenquer et al. (2021)	36468	ATACATG	A	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.V70del	convalescent plasma escape	Slight neutralization improvement on average in 16 health workers' convalescent sera.	Q.8, Q.3, Q.1, B.1.1.7	Alenquer et al. (2021)	36468	ATACATG	A	nan
p.V70del	convalescent plasma escape	Neutralization capacity GMT of 27 subjects' sera post-infection was considerably higher (stronger) than after the second Pfizer dose, and 4.5x drop in B.1.1.7 neutralization was observed.	B.1.1.7, Q.3, Q.1	Collier et al. (2021)	36460	ATACATG	A	nan
p.V70del	convalescent plasma escape	NTD-specific nAbs showed a substantial (3-450x) decrease in neutralization potency against the recently reported highly transmissible B.1.1.7 variant of concern, whereas RBD-specific nAbs were either unaffected or showed lower decreases in potency.	B.1.1.7, Q.3, Q.1	Graham et al. (2021)	36460	ATACATG	A	nan
p.V70del	convalescent plasma escape	Neutralizing antibody titers of 2/20 (10%) samples showed >10x reduction (sera collected extasciitilde1mo post Jan 2020 first wave in China). Neutralizing antibody titers of 8/20 samples (40%) decreased below an ID50 threshold of 40 (sera collected extasciitilde8mo post Jan 2020 first wave in China).	B.1.1.7, Q.3, Q.1	Hu et al. (2021)	36460	ATACATG	A	nan
p.V70del	convalescent plasma escape	Fatal COVID-19 complications in immunocomprimised patient after immune escape from convalescent plasma	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Kemp et al. (2020)	36470	ATACATG	A	nan
p.V70del	convalescent plasma escape	Using a new rapid neutralization assay, based on reporter cells that become positive for GFP after overnight infection, sera from 58 convalescent individuals collected up to 9 months after symptoms, similarly neutralized B.1.1.7 and D614G.	B.1.1.7, Q.3, Q.1	Planas et al. (2021)	36460	ATACATG	A	nan
p.V70del	convalescent plasma escape	Maximum fold-decrease in potency for the serum samples from mild illness was 8.2 but the majority of samples showed less than a 3-fold change. Similarly, the maximum decrease seen for samples from hospitalized patients was a 9.1-fold change, but most of the samples showed minimal change in the potency of their neutralization. Overall, three samples from each cohort (8%) showed a 5–10-fold reduction, but as they were potently neutralizing sera, the reduced ID50 values were still >1:100.	B.1.1.7, Q.3, Q.1	Rees-Spear et al. (2021)	36460	ATACATG	A	nan
p.V70del	convalescent plasma escape	Neutralization activity of almost all Moderna Phase 1 sera tested actually *increased*.	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Shen et al. (2021)	36470	ATACATG	A	nan
p.V70del	convalescent plasma escape	Neutralization activity of convalescent sera tested decreased <2x with this B.1.1.7 pseudotyped virus.	B.1.1.7, Q.3, Q.1	Shen et al. (2021)	36460	ATACATG	A	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.V70del	convalescent plasma escape	We analyzed 34 convalescent samples including the WHONIBSC 20/130 reference serum, and, although a few sera showed near identical FRNT 50 values, the FRNT50 dilutions for the B.1.1.7 strain were 2.9-fold lower (geometric mean) than those for the Victoria strain ($p < 0.0001$). Sera from 13 subjects post-B.1.1.7 infection showed no significant change in neutralization against Victoria (extasciitildewild type), suggesting that B.1.1.7 infection also protects against ancestral virus. [Note that D1119H was included in the original paper, assuming typographical error and correcting to D1118H]	B.1.1.7, Q.3, Q.1	Supasa et al. (2021)	36460	ATACATG	A	nan
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.	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Tada et al. (2021)	36470	ATACATG	A	nan
p.V70del	convalescent plasma escape	These key B.1.1.7 mutations as a combination neutralized slightly less well than D614G and this was noticeable in the lack of sera with high neutralizing titer for the viruses across 10 convalescent sera from April 2020 infectees.	Q.8, Q.3, Q.1, B.1.1.7	Tada et al. (2021)	36468	ATACATG	A	nan
p.V70del	convalescent plasma escape	Loss of neutralizing activity using 6 hyperimmune immunoglobulin preparations from convalescent plasma was minimal against B.1.1.7 (1.9-fold). Neutralization against 10 convalescent plasma was poorer.	B.1.1.7, Q.3, Q.1	Tang et al. (2021)	36460	ATACATG	A	nan
p.V70del	convalescent plasma escape	The neutralizing activity of 8/20 convalescent sera was significantly lower against this pseudotyped virus model of B.1.1.7, yet almost no effect was detected using the live B.1.1.7 virus.	B.1.1.7, Q.3, Q.1	Wang et al. (2021)	36460	ATACATG	A	nan
p.V70del	environmental condition stability	Treatment with heat, soap and ethanol revealed similar inactivation profiles indicative of a comparable susceptibility towards disinfection. Furthermore, we observed comparable surface stability on steel, silver, copper and face masks.	B.1.1.7, Q.3, Q.1	Meister et al. (2021)	36460	ATACATG	A	nan
p.V70del	environmental condition stability	No differences in the stability of B.1.1.7 observed in the absence of simulated sunlight at either 20°C or 40°C (with a mean time for a 90% loss of viral infectivity across all dark conditions of 6.2 hours). However, a small but statistically significant difference in the stability was observed in simulated sunlight at 20°C and 20% relative humidity, with B.1.1.7 restoring wild type 90% loss time of 11 minutes vs. 7 and 8 minutes for B.1.319 (D614G) and B.28 (V367F) early 2020 viruses respectively.	B.1.1.7, Q.3, Q.1	Schuit et al. (2021)	36460	ATACATG	A	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.V70del	environmental condition stability	Relative to D614G, this mutation demonstrated significant increase in infectivity (i.e. heat stability) after incubation at 50C after 1 hour.	Q.8, Q.3, Q.1, B.1.1.7	Tada et al. (2021)	36468	ATACATG	A	nan
p.V70del	immunosuppression variant emergence	The delH69/V70 enhances viral infectivity, indicating its effect on virus fitness is independent to the N501Y RBM change [with which it is found in lineage B.1.1.7] Possibly arisen as a result of the virus evolving from immune selection pressure in infected individuals and possibly only one chronic infection in the case of lineage B.1.1.7.	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Kemp et al. (2020)	36470	ATACATG	A	nan
p.V70del	outcome hazard ratio	Danish study of the B.1.1.7 lineage shows hospital admission odds ratio of 1.63 vs other lineages. The adjusted OR was increased in all strata of age.	B.1.1.7, Q.3, Q.1	Bager et al. (2021)	36460	ATACATG	A	nan
p.V70del	outcome hazard ratio	The mortality hazard ratio associated with infection with [B.1.1.7] compared with infection with previously circulating variants was 1.64 (95% confidence interval 1.32 to 2.04) in patients who tested positive for covid-19 in the community (54906 matched pairs of participants who tested positive for SARS-CoV-2 in pillar 2 between 1 October 2020 and 29 January 2021). In this comparatively low risk group, this represents an increase in deaths from 2.5 to 4.1 per 1000 detected cases.	B.1.1.7, Q.3, Q.1	Challen et al. (2021)	36460	ATACATG	A	nan
p.V70del	outcome hazard ratio	Using UK data 1 November 2020 to 14 February 2021, while correcting for misclassification of PCR test Spike Gene Target Failure (SGTF) and missingness in SGTF status, we estimate that the hazard of death associated with B.1.1.7 is 61% (42–82%) higher than with pre-existing variants after adjustment for age, sex, ethnicity, deprivation, residence in a care home, the local authority of residence and test date. This corresponds to the absolute risk of death for a 55–69-year-old man increasing from 0.6% to 0.9% (95% confidence interval, 0.8–1.0%) within 28 days of a positive test in the community.	B.1.1.7, Q.3, Q.1	Davies et al. (2021)	36460	ATACATG	A	nan
p.V70del	outcome hazard ratio	341 samples collected Nov 9 to Dec 20, 2020 were sequenced from two London (UK) hospitals. 198 (58%) of 341 had B.1.1.7 infection and 143 (42%) had non-B.1.1.7 infection. No evidence was found of an association between severe disease and death and lineage (B.1.1.7 vs non-B.1.1.7) in unadjusted analyses (prevalence ratio [PR] 0 · 97 [95% CI 0 · 72-1 · 31]), or in analyses adjusted for hospital, sex, age, comorbidities, and ethnicity (adjusted PR 1 · 02 [0 · 76-1 · 38]).	B.1.1.7, Q.3, Q.1	Frampton et al. (2021)	36460	ATACATG	A	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.V70del	outcome hazard ratio	On average across 7 European countries studied, using B.1.1.7 defining mutations: Significant shift to asymptomatic cases (27.4% vs 18.6% for non-VOC cases). Significant shift to infection in those without pre-existing conditions (44.8% vs 89% for non-VOC cases). Significant increase in hospitalization rate (11% vs 7.5% for non-VOC cases). Significant increase in ICU rate (1.4% vs 0.6% for non-VOC cases). Significant decrease in death rate (2.0% vs vs 4.0% for non-VOC cases).	B.1.1.7, Q.3, Q.1	Funk et al. (2021)	36460	ATACATG	A	nan
p.V70del	outcome hazard ratio	From Sept 28 to Dec 27, 2020, positive COVID-19 tests were reported by 36 920 COVID Symptom Study app users whose region was known and who reported as healthy on app sign-up. We found no changes in reported symptoms or disease duration associated with B.1.1.7.	B.1.1.7, Q.3, Q.1	Graham et al. (2021)	36460	ATACATG	A	nan
p.V70del	outcome hazard ratio	Using primarily S-defining mutations for lineage B.1.1.7, most models of hospitalization and fatality risk ratios from consortium members show elevated ratios (extasciitilde1.3-1.7x).	B.1.1.7, Q.3, Q.1	NERVTAG Consortium (2021)	36460	ATACATG	A	nan
p.V70del	outcome hazard ratio	The matching-adjusted conditional odds ratio of hospitalisation was 1.58 (95% confidence interval 1.50 to 1.67) for COVID-19 patients infected with a SGTF-associated variant [primarily B.1.1.7], compared to those infected with non-SGTF-associated variants. The effect was modified by age ($p<0.001$), with ORs of 0.96-1.13 below age 20 years and 1.57-1.67 in age groups 40 years or older.	B.1.1.7, Q.3, Q.1	Nyberg et al. (2021)	36460	ATACATG	A	nan
p.V70del	reinfection	36920 COVID Symptom Study app users reported SARS-CoV-2 test positivity in late 2020. Possible reinfections were identified in 249 (0.7% [95% CI 0.6-0.8]) of 36509 app users who reported a positive swab test before Oct 1, 2020, but there was no evidence that the frequency of reinfections was higher for the B.1.1.7 variant than for pre-existing variants.	B.1.1.7, Q.3, Q.1	Graham et al. (2021)	36460	ATACATG	A	nan
p.V70del	reinfection	Second infection in December 2020 with B.1.1.7 after April 2020 initial infection with B.2 in a 78-year-old man with a history of Type 2 diabetes mellitus, diabetic nephropathy on hemodialysis, chronic obstructive pulmonary disease (COPD), mixed central and obstructive sleep apnea, ischemic heart disease, with no history of immunosuppression.	B.1.1.7, Q.3, Q.1	Harrington et al. (2021)	36460	ATACATG	A	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.V70del	reinfection	Reinfection with Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) B.1.1.7 variant in an immunocompromised 16yo female with end stage renal disease 94 days after initial infection with a B.1.2 lineage virus. Both lineages were the prevalent one at the time of 1st and 2nd infections respectively in Texas, where the patient was located (suggesting exposure risk rather than lineage immune evasion).	B.1.1.7, Q.3, Q.1	Marquez et al. (2021)	36460	ATACATG	A	nan
p.V70del	symptom prevalence	A higher proportion of cases infected with the B.1.1.7 variant were hypoxic on admission compared to other variants (70.0% vs 62.5%, p	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Snell et al. (2021)	36470	ATACATG	A	nan
p.V70del	symptom prevalence	In comparison of B.1.1.7 lineage (193 cases) vs. "wildtype" (125) in Berlin Jan 18 to March 29 2021, significant symptom changes are absent loss of smell/taste (P	B.1.1.7, Q.8, Q.3, Q.4, Q.1	van Loon et al. (2021)	36470	ATACATG	A	nan
p.V70del	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.1.1.7, Q.3, Q.1	Planas et al. (2021)	36460	ATACATG	A	nan
p.V70del	trafficking	extasciitilde2.5x cleavage of S2 relative to WA1 (D614G) wildtype by Alpha variant variant as measured by mass spectrometry of Vero-TMPRSS culture.	B.1.1.7, Q.3, Q.1	Esclera et al. (2021)	36460	ATACATG	A	nan
p.V70del	trafficking	VSV pseudotype B.1.1.7 showed no significant difference in cell entry relative to wild type in 6 cell lines. Cell fusion proficiency was unchanged.	B.1.1.7, Q.3, Q.1	Hoffman et al. (2021)	36460	ATACATG	A	nan
p.V70del	trafficking	The entry efficiencies of Spike pseudotyped viruses bearing N501Y Variant 1 (B.1.1.7) mutant were about 3 to 4.4 times higher than that of the WT pseudovirus when viral input was normalized, suggesting that these spike variants promote the infectivity of SARS-CoV-2.	B.1.1.7, Q.3, Q.1	Hu et al. (2021)	36460	ATACATG	A	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.V70del	trafficking	Lentiviral pseudotyped with this mutation set from B.1.1.7 was tested on ACE2.293T cells. Luciferase activity was measured two days postinfection, showing significant (40%) increase in infection rate amongst the cells, much more than the effect of either the deletion or the point mutation alone, suggetsing that this combination has a synergistic effect contributing to cell entry fitness, moreso than this combination with the addition of P681H.	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Tada et al. (2021)	36470	ATACATG	A	nan
p.V70del	trafficking	Lentiviral pseudotyped with this mutation set from B.1.1.7 was tested on ACE2.293T cells. Luciferase activity was measured two days postinfection, showing significant (40%) increase in infection rate amongst the cells, much more than the effect of either the deletion or the point mutation alone, suggetsing that this combination has a synergistic effect contributing to cell entry fitness, but to a smaller extent than N501Y and the deletion alone.	Q.8, Q.3, Q.1, B.1.1.7	Tada et al. (2021)	36468	ATACATG	A	nan
p.V70del	trafficking	Live virus was tested ex vivo in reconstituted brochial epithelium, and out competed wild type.	B.1.1.7, Q.3, Q.1	Touret et al. (2021)	36460	ATACATG	A	nan
p.V70del	transmissibility	We estimate that this [B.1.1.17] variant has a 43–90% (range of 95% credible intervals 38–130%) higher reproduction number than preexisting variants. Data from other countries yield similar results: we estimate that R for VOC 202012/01 relative to other lineages is 55% (45–66%) higher in Denmark, 74% (66–82%) higher in Switzerland, and 59% (56–63%) higher in the United States, with consistent rates of displacement across regions within each country.	B.1.1.7, Q.3, Q.1	Davies et al. (2021)	36460	ATACATG	A	nan
p.V70del	transmissibility	Based on 36920 COVID Symptom Study app users reported SARS-CoV-2 test positivity in late 2020, Rt of B.1.1.7 was 1.35x (95% CI 1.02-1.69) relative to pre-existing variants. However, Rt fell below 1 during regional and national lockdowns, even in regions with high proportions of infections with the B.1.1.7 variant.	B.1.1.7, Q.3, Q.1	Graham et al. (2021)	36460	ATACATG	A	nan
p.V70del	transmissibility	Ontario, Feb 2021: The secondary attack rate for VOC index cases in this matched cohort was 1.31 times higher than non-VOC index cases (RR	B.1.1.7, Q.3, Q.1	Lindstrøm et al. (2021)	36460	ATACATG	A	nan
p.V70del	transmissibility	Primary cases infected with B.1.1.7 had an increased transmissibility of 1.5-1.7 times that of primary cases infected with other lineages. The increased transmissibility of B.1.1.7 was multiplicative across age and viral load.	B.1.1.7, Q.3, Q.1	Lyngse et al. (2021)	36460	ATACATG	A	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.V70del	transmissibility	Based on 300,000 RT-PCR samples collected from December 6th 2020 to February 10th 2021 in Israel, the B.1.1.7 is 45% (95% CI:20-60%) more transmissible than the wild-type strain, and become dominant in Israel within 3.5 weeks.	B.1.1.7, Q.3, Q.1	Munitz et al. (2021)	36460	ATACATG	A	nan
p.V70del	transmissibility	At the national level (Italy), we estimated a mean relative transmissibility of B.1.1.7 (compared to historical lineages) ranging between 1.55 and 1.57 (with confidence intervals between 1.45 and 1.66).	B.1.1.7, Q.3, Q.1	Stefanelli et al. (2021)	36460	ATACATG	A	nan
p.V70del	vaccine efficacy	In Minnesota in early 2021 when Alpha was prevalent, vaccine efficacy was estimated as: mRNA-1273 86% (95%CI: 81-90.6%) and BNT162b2: 76% (95%CI: 69-81%) using age, sex, race, PCR testing and vaccination date matched cohorts of unvaccinated, Pfizer and Moderna vaccinees. [variant list included is ancestral Alpha, as this was an observational study no variant list was given]	B.1.1.7, Q.3, Q.1	Puranik et al. (2021)	36460	ATACATG	A	nan
p.V70del	vaccine neutralization efficacy	nan	B.1.1.7, Q.3, Q.1	All vaccinees were on a strict 3 week interval for second dose (	36460	ATACATG	A	nan
p.V70del	vaccine neutralization efficacy	Between December 19, 2020 and Jan 24, 2021, 7214 of 9109 eligible HCWs at Sheba Medical Center in Israel had received one or more doses of BNT162b2 (Pfizer) vaccine. Adjusted rate reduction in SARS-CoV-2 NAAT positivity infection compared with unvaccinated workers 1-14 days after 1st dose was 30% (95% CI: 2-50), and 75% (95% CI: 72-84) after 15-28 days. Adjusted rate reduction in symptomatic COVID-19 compared with unvaccinated workers 1-14 days after 1st dose was 47% (95% CI: 17-66), and 85% (95% CI: 71-92) after 15-28 days. [Though often cited as an indicator of VE for B.1.1.7, during this time period in Israel, the prevalence of the B.1.1.7 variant increased from extasciitilde20% to 50% of cases (covariants.org), therefore these VE numbers likely represent a mix of B.1.1.7 and other lineage effects.]	B.1.1.7, Q.3, Q.1	Amit et al. (2021)	36460	ATACATG	A	nan
p.V70del	vaccine neutralization efficacy	Neutralization efficiency (ID50) against B.1.1.7 reduced 1.2x relative to D614G wildtype using pseudotyped VSV assay on 8 Moderna vaccinee sera one week post-booster.	B.1.1.7, Q.3, Q.1	Choi et al. (2021)	36460	ATACATG	A	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.V70del	vaccine neutralization efficacy	20/29 sera after the first dose of Pfizer showed an average reduction in neutralization titres against the B.1.1.7 variant of 3.2 ± 5.7. After the second dose, the GMT was markedly increased compared with the first-dose titres, with a fold change of 1.9 ± 0.9 (mean ± s.d.). Neutralization GMT of 27 subjects post-infection was considerably higher (stronger) than after the second Pfizer dose, and 4.5x drop in B.1.1.7 neutralization was observed.	B.1.1.7, Q.3, Q.1	Collier et al. (2021)	36460	ATACATG	A	nan
p.V70del	vaccine neutralization efficacy	2.1x drop in neutralization using sera collected from 14 healthy adult participants that received two injections of the mRNA-1273 (Moderna) vaccine at a dose of 100 µg (18-55 years: day 1 (n	B.1.1.7, Q.3, Q.1	Edara et al. (2021)	36460	ATACATG	A	nan
p.V70del	vaccine neutralization efficacy	Virus neutralisation activity (using a live SARS-CoV-2 microneutralisation assay (ND50)) by vaccine induced antibodies was 9-fold lower against the B.1.1.7 variant than against a canonical non B.1.1.7 lineage. Vaccine efficacy against symptomatic NAAT positive infection was similar for B.1.1.7 and non-B.1.1.7 lineages (74.6% [95%CI 41.6-88.9] and 84% [95% CI 70.7-91.4] respectively). Furthermore, vaccination with ChAdOx1 nCoV-19 results in a reduction in the duration of shedding and viral load, which may translate into a material impact on transmission of disease.	B.1.1.7, Q.3, Q.1	Emary et al. (2021)	36460	ATACATG	A	nan
p.V70del	vaccine neutralization efficacy	ELISpot assays show T cell neutralization reduced by 15.4% in this B.1.1.7 pseudotype relative to wild type in 18-20 pooled patient samples post second mRNA vaccine dose, with no significant difference between Pfizer and Moderna cohorts. Reduction was stronger in the S1 subunit than S2 (separate peptide pools were used).	B.1.1.7, Q.3, Q.1	Gallagher et al. (2021)	36460	ATACATG	A	nan
p.V70del	vaccine neutralization efficacy	Pseudotyped B.1.1.7 virus has reduced neutralization activity vs wild type: 2.1x (30 sera Pfizer median 9 days post 2nd dose) and 2.3x (35 sera Moderna median 18 days post 2nd dose). This was NOT significant by ANOVA. Note that Y145del was actually noted in the paper as the effect of their DNA construct, but this is equivalent at the protein level to the more commonly annotated Y144del.	B.1.1.7, Q.3, Q.1	Garcia-Beltran et al. (2021)	36460	ATACATG	A	nan
p.V70del	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)	B.1.1.7, Q.3, Q.1	Gong et al. (2021)	36460	ATACATG	A	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.V70del	vaccine neutralization efficacy	Using national surveillance data from Israel, using Pfizer vaccine and an estimated prevalence of the B.1.1.7 variant of 94.5% among SARS-CoV-2 infections: Adjusted estimates of vaccine effectiveness 7+ days after second dose were 95 · 3% (95% CI 94.9–95.7): 91.5% against asymptomatic SARS-CoV-2 infection (90 · 7–92 · 2: 40.9 vs 1.8 per 100 000 person-days), 97 · 0% against symptomatic COVID-19 (96.7–97.2%), 97.2% against COVID-19-related hospitalisation (96.8–97.5%), 97.5% against severe or critical COVID-19-related hospitalisation (97.1–97.8%), and 96.7% against COVID-19-related death (96.0–97.3%). In all age groups, as vaccine coverage increased, the incidence of SARS-CoV-2 outcomes declined	B.1.1.7, Q.3, Q.1	Haas et al. (2021)	36460	ATACATG	A	nan
p.V70del	vaccine neutralization efficacy	A single dose of BNT162b2 (Pfizer) vaccine showed vaccine effectiveness of 70% (95% CI 55-85) 21 days after first dose and 85% (74-96) 7 days after two doses in the study population. Our findings show that the BNT162b2 vaccine can prevent both symptomatic and asymptomatic infection in working-age adults. This cohort (8203 treatment, 15121 control) was vaccinated when the dominant variant in circulation was B.1.1.7 and shows effectiveness against this variant.	B.1.1.7, Q.3, Q.1	Hall et al. (2021)	36460	ATACATG	A	nan
p.V70del	vaccine neutralization efficacy	A single dose of BNT162b2 vaccine demonstrated vaccine effectiveness [symptomatic or asymptomatic in cohort opf routinely NAAT-monitored UK HCWs] of 72% (95% CI 58-86) 21 days after first dose and 86% (95% CI 76-97) seven days after two doses in the antibody negative cohort. This cohort was vaccinated when the dominant variant in circulation was B.1.1.7 and demonstrates effectiveness against this variant.	B.1.1.7, Q.3, Q.1	Hall et al. (2021)	36460	ATACATG	A	nan
p.V70del	vaccine neutralization efficacy	NVX-CoV2373 [Novavax] vaccine in phase 3 trial was 89.7% (95% CI, 80.2-94.6) effective in preventing COVID-19, with no hospitalizations or deaths reported. There were five cases of severe Covid-19, all in the placebo group. Post hoc analysis revealed efficacies of 96.4% (73.8-99.5) and 86.3% (71.3-93.5) against the prototype strain and B.1.1.7 variant, respectively.	B.1.1.7, Q.3, Q.1	Heath et al. (2021)	36460	ATACATG	A	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.V70del	vaccine neutralization efficacy	VSV pseudotype B.1.1.7 showed 1.77-fold reduction in neutralization efficiency vs wild type in 15 Pfizer BNT162b2 vaccinee sera 13-15 days post second dose. Cell fusion proficiency was unchanged.	B.1.1.7, Q.3, Q.1	Hoffman et al. (2021)	36460	ATACATG	A	nan
p.V70del	vaccine neutralization efficacy	B.1.1.7 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 no statistically sognificant change in neutralization effiacacy.	B.1.1.7, Q.3, Q.1	Ikegame et al. (2021)	36460	ATACATG	A	nan
p.V70del	vaccine neutralization efficacy	Neutralizing antibody titers increased in previously infected vaccinees relative to uninfected vaccinees 5.2-fold against B.1.1.7 (contrast with 3.4 fold against original SARS-CoV-2).	B.1.1.7, Q.3, Q.1	Leier et al. (2021)	36460	ATACATG	A	nan
p.V70del	vaccine neutralization efficacy	SARS-CoV-2 infection was confirmed in three HCWs working a single shift: all presented with mild symptoms of COVID-19. The two physicians were fully vaccinated with BNT162b2 vaccine, with the second dose administered 1 month before symptom onset. Both had high titres of IgG anti-spike antibodies at the time of diagnosis. WGS confirmed that all virus strains were VOC 202012/01-lineage B.1.1.7, suggesting a common source of exposure. Epidemiological investigation revealed that the suspected source was a SARS-CoV-2-positive patient who required endotracheal intubation due to severe COVID-19. All procedures were carried out using a full suite of personal protective equipment (PPE).	B.1.1.7, Q.3, Q.1	Loconsole et al. (2021)	36460	ATACATG	A	nan
p.V70del	vaccine neutralization efficacy	We found that a single dose of the BNT162b2 vaccine is about 60-70% effective at preventing symptomatic disease in adults aged 70 years and older in England and that two doses are about 85-90% effective. Those who were vaccinated and went on to have symptoms had a 44% lower risk of being admitted hospital and a 51% lower risk of death compared with people who were unvaccinated. We also found that a single dose of the ChAdOx1-S vaccine was about 60-75% effective against symptomatic disease and provided an additional protective effect against hospital admission—it is too early to assess the effect on mortality. The B.1.1.7 variant now dominates in the UK and these results will largely reflect vaccine effectiveness against this variant.	B.1.1.7, Q.3, Q.1	Lopez Bernal et al. (2021)	36460	ATACATG	A	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.V70del	vaccine neutralization efficacy	In sera 1-2 weeks after BNT162b2 first dose, from six patients previously infected with B.1, antibody titer in a microneutralization assay was on average 8192 for B.1.351 virus. This compares favorably (stronger) to post-infection neutralization titer against all variants tested in the same sera (wild type, B.1.1.7, B.1.351, and P.1).	B.1.1.7, Q.3, Q.1	Luftig et al. (2021)	36460	ATACATG	A	nan
p.V70del	vaccine neutralization efficacy	Lineage B.1.1.7 spike–pseudotyped VSV was tested for neutralization vs Wuhan reference genome pseudotype in 40 sera collected 7 or 21 days post-booster dose. Statistically significant change (22%) in neutralization was observed among the 26 sera from those <	B.1.1.7, Q.3, Q.1	Muik et al. (2021)	36460	ATACATG	A	nan
p.V70del	vaccine neutralization efficacy	We observed a sharp decline in cases when 50% of the elderly population was 2 weeks beyond their first vaccination dose and at a time point during which the B.1.1.7 variant gained transmission dominance. In support of this finding, it was suggested that, after the first vaccination dose, more than 70% of patients develop neutralization antibodies,15 and the vaccine efficiency can reach 85%.	B.1.1.7, Q.3, Q.1	Munitz et al. (2021)	36460	ATACATG	A	nan
p.V70del	vaccine neutralization efficacy	Detectable antibodies against B.1.1.7 at various time points using pseudotyped lentivirus neutralization in Moderna vaccinee cohort: Day 29 33%, Day 43 100%, Day 119 100%, Day 209 96%. Detectable antibodies against B.1.1.7 at various time points using live virus FRNT neutralization in Moderna vaccinee cohort: Day 29 54%, Day 43 100%, Day 119 100%, Day 209 88%. Detectable antibodies against B.1.1.7 at various time points using ACE2 blocking assay in Moderna vaccinee cohort: Day 29 83%, Days 43,119,209 100%.	B.1.1.7, Q.3, Q.1	Pegu et al (2021)	36460	ATACATG	A	nan
p.V70del	vaccine neutralization efficacy	The sera of 16 individuals with time course collection was evaulated against VSV pseudotypes: neutralized D614G at week 2, whereas B.1.1.7 started to be neutralized at week 3, although less efficiently than D614G. B.1.1.7 and D614G strains were similarly neutralized at week 4 (1 week after booster dose).	B.1.1.7, Q.3, Q.1	Planas et al. (2021)	36460	ATACATG	A	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.V70del	vaccine neutralization efficacy	After one dose, individuals with prior infection showed enhanced T cell immunity, antibody secreting memory B cell response to spike and neutralizing antibodies effective against B.1.1.7 (authentic cell culture supernatants). By comparison, HCW receiving one vaccine dose without prior infection showed reduced immunity against variants. B.1.1.7 spike mutations resulted in increased, abrogated or unchanged T cell responses depending on human leukocyte antigen (HLA) polymorphisms. Study was 26 each post-infection and post first dose HCWs.	B.1.1.7, Q.3, Q.1	Reynolds et al. (2021)	36460	ATACATG	A	nan
p.V70del	vaccine neutralization efficacy	The NAb titers (PRNT50) of sera collected from 38 vaccine recipients four-weeks after the second dose of inactivated whole-virion SARS-CoV-2 BBV152/COVAXIN vaccine [which contains D614G] were not significantly different between B.1.1.7 virus and ancestral D614G virus.	B.1.1.7, Q.3, Q.1	Sapkal et al. (2021)	36460	ATACATG	A	nan
p.V70del	vaccine neutralization efficacy	Pseudotyped B.1.1.7 Spike variants lentivirus. 3.5x reduction in neutralization with Moderna vaccinated patient sera after 29 days (1st dose). 2.0x reduction in neutralization with Moderna vaccinated patient sera after 57 days (2nd dose). 2.1x reduction in neutralization with Novavax Phase 1 post-vaccination sera.	B.1.1.7, Q.3, Q.1	Shen et al. (2021)	36460	ATACATG	A	nan
p.V70del	vaccine neutralization efficacy	Neutralization assays of B.1.1.7 virus showed a reduction of 2.5-fold (14 days post 2nd dose AstraZeneca, n	B.1.1.7, Q.3, Q.1	Supasa et al. (2021)	36460	ATACATG	A	nan
p.V70del	vaccine neutralization efficacy	Vaccine elicited antibodies neutralized virus with the B.1.1.7 spike protein with titers similar to D614G virus. Serum specimens from individuals vaccinated with the BNT162b2 mRNA vaccine neutralized D614G virus with titers that were on average 7-fold greater than convalescent sera.	B.1.1.7, Q.3, Q.1	Tada et al. (2021)	36460	ATACATG	A	nan
p.V70del	vaccine neutralization efficacy	PBMCs of Pfizer/BioNTech BNT162b2 (n	B.1.1.7, Q.3, Q.1	Tarke et al. (2021)	36460	ATACATG	A	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.V70del	vaccine neutralization efficacy	1.4x improvement in neutralization by serum collected 2 to 3 weeks after the second dose from vaccinees who had received BBIBP-CorV (pVNT50 against VSV pseudotyped as B.1.1.7). Convalescent plasma had similar titer against wild type as the BBIBP-CorV vaccinee sera. 2x reduction in neutralization by serum collected 2 to 3 weeks after the second dose from vaccinees who had received CoronaVac (pVNT50 against VSV pseudotyped as B.1.1.7). Convalescent plasma had similar titer against wild type as the CoronaVac vaccinee sera.	B.1.1.7, Q.3, Q.1	Wang et al. (2021)	36460	ATACATG	A	nan
p.V70del	vaccine neutralization efficacy	No significant difference in T-cell response to B.1.1.7 was observed (vs. ancestral) in blood drawn from 28 participants received the Pfizer-BioNTech vaccine and 2 received the Moderna vaccine. This is despite three mutations (Y144del, D614G, and P681H) overlapping T-cell epitope hotspots.	B.1.1.7, Q.3, Q.1	Woldemeskel et al. (2021)	36460	ATACATG	A	nan
p.V70del	vaccinee plasma binding	1.14x increase in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in previously non-seroconverted subjects. 1.09x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in post-infection vaccinees.	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Gong et al. (2021)	36470	ATACATG	A	nan
p.V70del	vaccinee plasma binding	This variant combination (representing B.1.1.7 aka Alpha) showed no change in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in previously non-seroconverted subjects. 1.28x 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.1.1.7, Q.3, Q.1	Gong et al. (2021)	36460	ATACATG	A	nan
p.V70del	viral load	Using lack of S probe detection as a proxy for B.1.1.7 status, 275 putative B.1.1.7 samples and 390 "wild type" SARS-CoV-2 positive samples in Wales were compared for Ct values, suggesting extasciitilde12-fold increase (extasciitilde3.5 Ct decrease) in viral load for B.1.1.7 samples.	B.1.1.7, Q.3, Q.1	Couzens et al. (2021)	36460	ATACATG	A	nan
p.V70del	viral load	We found that the British variant (clade B.1.1.7), compared to an ancestral SARS-CoV-2 clade B virus, produced higher levels of infectious virus late in infection and had a higher replicative fitness in human airway, alveolar and intestinal organoid models.	B.1.1.7, Q.3, Q.1	Lamers et al. (2021)	36460	ATACATG	A	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.V70del	viral load	This study reveals that B.1.1.7 SARS-CoV-2 variant is a slower-growing virus than parental B.1. Further, a higher replication along with reduced infectious viral titer was hypothesized to be linked to higher transmission with reduced pathogenicity.	B.1.1.7, Q.3, Q.1	Nyayanit et al. (2021)	36460	ATACATG	A	nan
p.V70del	viral load	In a study of 1260 ICU subjects, viral load distributions (collected within 48h of admission) were elevated in both seropositive and seronegative subjects infected with B.1.1.7 ("UK variant"). PG: The PANGO tool defining Spike variants for B.1.1.7 are listed here, whereas the paper only used a test for D1118H.	B.1.1.7, Q.3, Q.1	Ratcliff et al. (2021)	36460	ATACATG	A	nan
p.V70del	viral load	B.1.1.7 samples showed average Ct cycle threshold of 21.9 vs 23 for wildtype (i.e. extasciitilde2x higher viral load) comparing 37758 and 22535 samples respectively.	B.1.1.7, Q.3, Q.1	Roquebert et al. (2021)	36460	ATACATG	A	nan
p.V70del	viral load	The median Ct value of RT-qPCR tests of the N-gene target in the Daxing B.1.1.7 group was significantly lower than the Shunyi B.1.470 group (P	B.1.1.7, Q.3, Q.1	Song et al. (2021)	36460	ATACATG	A	nan
p.V70del	viral load	The 249 B.1.1.7 (a.k.a. N501Y.V1) variant cases in three Paris hospital labs had a extasciitilde10-fold viral load increase (extasciitilde3.3 Ct drop in N gene probe) compared to 332 ancestral lineage cases from the same time frame (2020-12-20 to 2021-02-26). PG: BUT there is a discrepancy in drop between the ORF1ab and N probes, with the former suggesting only a 2-fold drop, consistent with the drop observed in B.1.351. This might indicate higher subgenomic RNA content in B.1.1.7 skewing the change.	B.1.1.7, Q.3, Q.1	Teyssou et al. (2021)	36460	ATACATG	A	nan
p.V70del	virion structure	CryoEM analysis of B.1.1.7 demonstrates an increased propensity for 'up', receptor accessible conformation of the Spike protein trimer.	B.1.1.7, Q.3, Q.1	Cai et al. (2021)	36460	ATACATG	A	nan
p.V70del	virion structure	The Ratio of S2 (processed Spike) to full length Spike is higher for this mutation combination, due to a drop in the full length Spike measured, suggesting that this mutation compensates for decreased Spike production by improved proteolytic processing.	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Tada et al. (2021)	36470	ATACATG	A	nan
p.V70del	virion structure	The Ratio of S2 (processed Spike) to full length Spike is higher for this mutation combination, due to a drop in the full length Spike measured, suggesting that this mutation compensates for decreased Spike production by improved proteolytic processing.	Q.8, Q.3, Q.1, B.1.1.7	Tada et al. (2021)	36468	ATACATG	A	nan
p.S982A	ACE2 receptor binding affinity	Six fold increase in affinity for ACE2 by the B.1.1.7 lineage vs wild type is driven by a drop in observed dissociation rate constant.	B.1.1.7, Q.3, Q.1	Collier et al. (2021)	37121	T	G	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.S982A	ACE2 receptor binding affinity	Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant showed a 1.3x decrease in binding (KD) relative to D614G.	Q.1, B.1.1.7, Q.3, Q.4	Gong et al. (2021)	37123	T	G	nan
p.S982A	ACE2 receptor binding affinity	Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant combination (representing B.1.1.7 aka Alpha) had 5.43x increased binding relative to D614G alone.	B.1.1.7, Q.3, Q.1	Gong et al. (2021)	37121	T	G	nan
p.S982A	ACE2 receptor binding affinity	Flow cytometry was used on recombinant VSV proteins and yeast surface display to assess the binding of a labeled soluble ACE2 protein to cells expressing B.1.1.7. We observed a dramatic increase (relative to D614G) in binding of soluble ACE2 to B.1.1.7, and to a lesser extent to B.1.351, which both carry the N501Y mutation (see Fig 3).	B.1.1.7, Q.3, Q.1	Planas et al. (2021)	37121	T	G	nan
p.S982A	ACE2 receptor binding affinity	This mutation causes major decrease in binding affinity vs. wild type as measured by IC50 vs pseudotyped lentivirus.	Q.1, B.1.1.7, Q.3, Q.4	Tada et al. (2021)	37123	T	G	nan
p.S982A	ACE2 receptor binding affinity	This mutation causes major decrease in binding affinity vs. wild type as measured by IC50 vs pseudotyped lentivirus.	B.1.1.7, Q.3, Q.1	Tada et al. (2021)	37121	T	G	nan
p.S982A	anthropozoonotic events	First documented cases of domestic cat and dog infections with the B.1.1.7 strain.	B.1.1.7, Q.3, Q.1	Hamer et al. (2021)	37121	T	G	nan
p.S982A	antibody epitope effects	Not in a major wildtype epitope, mutant has no significant effect on PIWAS epitope score Found in B.1.1.7 lineage, but assumed to not pay a major role in antigenicity.	Q.1, B.1.1.7, Q.3, Q.4	Haynes et al. (2021)	37123	T	G	nan
p.S982A	antibody epitope effects	extasciitilde20x resistence to mAb CQ038 by B.1.1.7 pseudotyped virus	B.1.1.7, Q.3, Q.1	Hu et al. (2021)	37121	T	G	nan
p.S982A	antibody epitope effects	Lessens the potency of mAbs COVA2-17 (extasciitilde5x, similar to N501Y alone), COVA1-12 (extasciitilde11x) and COVA1-21 (>100x), which do not compete allosterically.	B.1.1.7, Q.3, Q.1	Rees-Spear et al. (2021)	37121	T	G	nan
p.S982A	antibody epitope effects	Reduction in neutralization by mAbs COVA2-15 (extasciitilde9x), B38 (extasciitilde14x), S309 (extasciitilde190x) by this B.1.1.7 pseudotyped virus model.	B.1.1.7, Q.3, Q.1	Shen et al. (2021)	37121	T	G	nan
p.S982A	antibody epitope effects	B.1.1.7 pseudotyped virus model impairs binding by RBD-directed mAb 910-30. B.1.1.7 pseudotyped virus model abolishes N-terminal-domain-directed mAbs 5-24, 4-8, and 4A8. B.1.1.7 pseudotyped virus model impairs binding by N-terminal-domain-directed mAbs 2-17, 4-19, 5-7.	B.1.1.7, Q.3, Q.1	Wang et al. (2021)	37121	T	G	nan
p.S982A	clinical indicators	After adjusting for the age factor, in a prospective Chinese cohort study B.1.1.7 variant infection (compared to B.1.140) was the risk factor for C-reactive protein (P	B.1.1.7, Q.3, Q.1	Song et al. (2021)	37121	T	G	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.S982A	convalescent plasma binding	1.06x increase in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset.	Q.1, B.1.1.7, Q.3, Q.4	Gong et al. (2021)	37123	T	G	nan
p.S982A	convalescent plasma binding	This variant combination (representing B.1.1.7 aka Alpha) showed a 1.15x increase in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset.	B.1.1.7, Q.3, Q.1	Gong et al. (2021)	37121	T	G	nan
p.S982A	convalescent plasma escape	Neutralization capacity GMT of 27 subjects' sera post-infection was considerably higher (stronger) than after the second Pfizer dose, and 4.5x drop in B.1.1.7 neutralization was observed.	B.1.1.7, Q.3, Q.1	Collier et al. (2021)	37121	T	G	nan
p.S982A	convalescent plasma escape	NTD-specific nAbs showed a substantial (3-450x) decrease in neutralization potency against the recently reported highly transmissible B.1.1.7 variant of concern, whereas RBD-specific nAbs were either unaffected or showed lower decreases in potency.	B.1.1.7, Q.3, Q.1	Graham et al. (2021)	37121	T	G	nan
p.S982A	convalescent plasma escape	Neutralizing antibody titers of 2/20 (10%) samples showed >10x reduction (sera collected extasciitilde1mo post Jan 2020 first wave in China). Neutralizing antibody titers of 8/20 samples (40%) decreased below an ID50 threshold of 40 (sera collected extasciitilde8mo post Jan 2020 first wave in China).	B.1.1.7, Q.3, Q.1	Hu et al. (2021)	37121	T	G	nan
p.S982A	convalescent plasma escape	Using a new rapid neutralization assay, based on reporter cells that become positive for GFP after overnight infection, sera from 58 convalescent individuals collected up to 9 months after symptoms, similarly neutralized B.1.1.7 and D614G.	B.1.1.7, Q.3, Q.1	Planas et al. (2021)	37121	T	G	nan
p.S982A	convalescent plasma escape	Maximum fold-decrease in potency for the serum samples from mild illness was 8.2 but the majority of samples showed less than a 3-fold change. Similarly, the maximum decrease seen for samples from hospitalized patients was a 9.1-fold change, but most of the samples showed minimal change in the potency of their neutralization. Overall, three samples from each cohort (8%) showed a 5–10-fold reduction, but as they were potently neutralizing sera, the reduced ID50 values were still >1:100.	B.1.1.7, Q.3, Q.1	Rees-Spear et al. (2021)	37121	T	G	nan
p.S982A	convalescent plasma escape	Neutralization activity of convalescent sera tested decreased <2x with this B.1.1.7 pseudotyped virus.	B.1.1.7, Q.3, Q.1	Shen et al. (2021)	37121	T	G	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.S982A	convalescent plasma escape	We analyzed 34 convalescent samples including the WHONIBSC 20/130 reference serum, and, although a few sera showed near identical FRNT 50 values, the FRNT50 dilutions for the B.1.1.7 strain were 2.9-fold lower (geometric mean) than those for the Victoria strain ($p < 0.0001$). Sera from 13 subjects post-B.1.1.7 infection showed no significant change in neutralization against Victoria (extasciitildewild type), suggesting that B.1.1.7 infection also protects against ancestral virus. [Note that D1119H was included in the original paper, assuming typographical error and correcting to D1118H]	B.1.1.7, Q.3, Q.1	Supasa et al. (2021)	37121	T	G	nan
p.S982A	convalescent plasma escape	Loss of neutralizing activity using 6 hyperimmune immunoglobulin preparations from convalescent plasma was minimal against B.1.1.7 (1.9-fold). Neutralization against 10 convalescent plasma was poorer.	B.1.1.7, Q.3, Q.1	Tang et al. (2021)	37121	T	G	nan
p.S982A	convalescent plasma escape	The neutralizing activity of 6/20 convalescent sera was significantly lower against this single variant pseudotyped virus model, showing similar patterns to the pseudotyped virus model of B.1.1.7.	Q.1, B.1.1.7, Q.3, Q.4	Wang et al. (2021)	37123	T	G	nan
p.S982A	convalescent plasma escape	The neutralizing activity of 8/20 convalescent sera was significantly lower against this pseudotyped virus model of B.1.1.7, yet almost no effect was detected using the live B.1.1.7 virus.	B.1.1.7, Q.3, Q.1	Wang et al. (2021)	37121	T	G	nan
p.S982A	environmental condition stability	Treatment with heat, soap and ethanol revealed similar inactivation profiles indicative of a comparable susceptibility towards disinfection. Furthermore, we observed comparable surface stability on steel, silver, copper and face masks.	B.1.1.7, Q.3, Q.1	Meister et al. (2021)	37121	T	G	nan
p.S982A	environmental condition stability	No differences in the stability of B.1.1.7 observed in the absence of simulated sunlight at either 20°C or 40°C (with a mean time for a 90% loss of viral infectivity across all dark conditions of 6.2 hours). However, a small but statistically significant difference in the stability was observed in simulated sunlight at 20°C and 20% relative humidity, with B.1.1.7 restoring wild type 90% loss time of 11 minutes vs. 7 and 8 minutes for B.1.319 (D614G) and B.28 (V367F) early 2020 viruses respectively.	B.1.1.7, Q.3, Q.1	Schuit et al. (2021)	37121	T	G	nan
p.S982A	environmental condition stability	Relative to D614G, this mutation demonstrated significant increase in infectivity (i.e. heat stability) after incubation at 50C after 30 minutes or 1 hour	Q.1, B.1.1.7, Q.3, Q.4	Tada et al. (2021)	37123	T	G	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.S982A	outcome hazard ratio	Danish study of the B.1.1.7 lineage shows hospital admission odds ratio of 1.63 vs other lineages. The adjusted OR was increased in all strata of age.	B.1.1.7, Q.3, Q.1	Bager et al. (2021)	37121	T	G	nan
p.S982A	outcome hazard ratio	The mortality hazard ratio associated with infection with [B.1.1.7] compared with infection with previously circulating variants was 1.64 (95% confidence interval 1.32 to 2.04) in patients who tested positive for covid-19 in the community (54906 matched pairs of participants who tested positive for SARS-CoV-2 in pillar 2 between 1 October 2020 and 29 January 2021). In this comparatively low risk group, this represents an increase in deaths from 2.5 to 4.1 per 1000 detected cases.	B.1.1.7, Q.3, Q.1	Challen et al. (2021)	37121	T	G	nan
p.S982A	outcome hazard ratio	Using UK data 1 November 2020 to 14 February 2021, while correcting for misclassification of PCR test Spike Gene Target Failure (SGTF) and missingness in SGTF status, we estimate that the hazard of death associated with B.1.1.7 is 61% (42–82%) higher than with pre-existing variants after adjustment for age, sex, ethnicity, deprivation, residence in a care home, the local authority of residence and test date. This corresponds to the absolute risk of death for a 55–69-year-old man increasing from 0.6% to 0.9% (95% confidence interval, 0.8–1.0%) within 28 days of a positive test in the community.	B.1.1.7, Q.3, Q.1	Davies et al. (2021)	37121	T	G	nan
p.S982A	outcome hazard ratio	341 samples collected Nov 9 to Dec 20, 2020 were sequenced from two London (UK) hospitals. 198 (58%) of 341 had B.1.1.7 infection and 143 (42%) had non-B.1.1.7 infection. No evidence was found of an association between severe disease and death and lineage (B.1.1.7 vs non-B.1.1.7) in unadjusted analyses (prevalence ratio [PR] 0 · 97 [95% CI 0 · 72-1 · 31]), or in analyses adjusted for hospital, sex, age, comorbidities, and ethnicity (adjusted PR 1 · 02 [0 · 76-1 · 38]).	B.1.1.7, Q.3, Q.1	Frampton et al. (2021)	37121	T	G	nan
p.S982A	outcome hazard ratio	On average across 7 European countries studied, using B.1.1.7 defining mutations: Significant shift to asymptomatic cases (27.4% vs 18.6% for non-VOC cases). Significant shift to infection in those without pre-existing conditions (44.8% vs 89% for non-VOC cases). Significant increase in hospitalization rate (11% vs 7.5% for non-VOC cases). Significant increase in ICU rate (1.4% vs 0.6% for non-VOC cases). Significant decrease in death rate (2.0% vs vs 4.0% for non-VOC cases).	B.1.1.7, Q.3, Q.1	Funk et al. (2021)	37121	T	G	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.S982A	outcome hazard ratio	From Sept 28 to Dec 27, 2020, positive COVID-19 tests were reported by 36 920 COVID Symptom Study app users whose region was known and who reported as healthy on app sign-up. We found no changes in reported symptoms or disease duration associated with B.1.1.7.	B.1.1.7, Q.3, Q.1	Graham et al. (2021)	37121	T	G	nan
p.S982A	outcome hazard ratio	Using primarily S-defining mutations for lineage B.1.1.7, most models of hospitalization and fatality risk ratios from consortium members show elevated ratios (extasciitilde1.3-1.7x).	B.1.1.7, Q.3, Q.1	NERVTAG Consortium (2021)	37121	T	G	nan
p.S982A	outcome hazard ratio	The matching-adjusted conditional odds ratio of hospitalisation was 1.58 (95% confidence interval 1.50 to 1.67) for COVID-19 patients infected with a SGTF-associated variant [primarily B.1.1.7], compared to those infected with non-SGTF-associated variants. The effect was modified by age (p<0.001), with ORs of 0.96-1.13 below age 20 years and 1.57-1.67 in age groups 40 years or older.	B.1.1.7, Q.3, Q.1	Nyberg et al. (2021)	37121	T	G	nan
p.S982A	reinfection	36920 COVID Symptom Study app users reported SARS-CoV-2 test positivity in late 2020. Possible reinfections were identified in 249 (0.7% [95% CI 0.6-0.8]) of 36509 app users who reported a positive swab test before Oct 1, 2020, but there was no evidence that the frequency of reinfections was higher for the B.1.1.7 variant than for pre-existing variants.	B.1.1.7, Q.3, Q.1	Graham et al. (2021)	37121	T	G	nan
p.S982A	reinfection	Second infection in December 2020 with B.1.1.7 after April 2020 initial infection with B.2 in a 78-year-old man with a history of Type 2 diabetes mellitus, diabetic nephropathy on hemodialysis, chronic obstructive pulmonary disease (COPD), mixed central and obstructive sleep apnea, ischemic heart disease, with no history of immunosuppression.	B.1.1.7, Q.3, Q.1	Harrington et al. (2021)	37121	T	G	nan
p.S982A	reinfection	Reinfection with Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) B.1.1.7 variant in an immunocompromised 16yo female with end stage renal disease 94 days after initial infection with a B.1.2 lineage virus. Both lineages were the prevalent one at the time of 1st and 2nd infections respectively in Texas, where the patient was located (suggesting exposure risk rather than lineage immune evasion).	B.1.1.7, Q.3, Q.1	Marquez et al. (2021)	37121	T	G	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.S982A	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.1.1.7, Q.3, Q.1	Planas et al. (2021)	37121	T	G	nan
p.S982A	trafficking	extasciitilde2.5x cleavage of S2 relative to WA1 (D614G) wildtype by Alpha variant variant as measured by mass spectrometry of Vero-TMPRSS culture.	B.1.1.7, Q.3, Q.1	Esclera et al. (2021)	37121	T	G	nan
p.S982A	trafficking	VSV pseudotype B.1.1.7 showed no significant difference in cell entry relative to wild type in 6 cell lines. Cell fusion proficiency was unchanged.	B.1.1.7, Q.3, Q.1	Hoffman et al. (2021)	37121	T	G	nan
p.S982A	trafficking	The entry efficiencies of Spike pseudotyped viruses bearing N501Y Variant 1 (B.1.1.7) mutant were about 3 to 4.4 times higher than that of the WT pseudovirus when viral input was normalized, suggesting that these spike variants promote the infectivity of SARS-CoV-2.	B.1.1.7, Q.3, Q.1	Hu et al. (2021)	37121	T	G	nan
p.S982A	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 major (70%) increase in infection rate amongst the cells, hence this individual variant is likely to significantly contribute to cell entry fitness.	Q.1, B.1.1.7, Q.3, Q.4	Tada et al. (2021)	37123	T	G	nan
p.S982A	trafficking	Live virus was tested ex vivo in reconstituted brochial epithelium, and out competed wild type.	B.1.1.7, Q.3, Q.1	Touret et al. (2021)	37121	T	G	nan
p.S982A	transmissibility	We estimate that this [B.1.1.17] variant has a 43–90% (range of 95% credible intervals 38–130%) higher reproduction number than preexisting variants. Data from other countries yield similar results: we estimate that R for VOC 202012/01 relative to other lineages is 55% (45–66%) higher in Denmark, 74% (66–82%) higher in Switzerland, and 59% (56–63%) higher in the United States, with consistent rates of displacement across regions within each country.	B.1.1.7, Q.3, Q.1	Davies et al. (2021)	37121	T	G	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.S982A	transmissibility	Based on 36920 COVID Symptom Study app users reported SARS-CoV-2 test positivity in late 2020, Rt of B.1.1.7 was 1.35x (95% CI 1.02-1.69) relative to pre-existing variants. However, Rt fell below 1 during regional and national lockdowns, even in regions with high proportions of infections with the B.1.1.7 variant.	B.1.1.7, Q.3, Q.1	Graham et al. (2021)	37121	T	G	nan
p.S982A	transmissibility	Ontario, Feb 2021: The secondary attack rate for VOC index cases in this matched cohort was 1.31 times higher than non-VOC index cases (RR	B.1.1.7, Q.3, Q.1	Lindstrøm et al. (2021)	37121	T	G	nan
p.S982A	transmissibility	Primary cases infected with B.1.1.7 had an increased transmissibility of 1.5-1.7 times that of primary cases infected with other lineages. The increased transmissibility of B.1.1.7 was multiplicative across age and viral load.	B.1.1.7, Q.3, Q.1	Lyngse et al. (2021)	37121	T	G	nan
p.S982A	transmissibility	Based on 300,000 RT-PCR samples collected from December 6th 2020 to February 10th 2021 in Israel, the B.1.1.7 is 45% (95% CI:20-60%) more transmissible than the wild-type strain, and become dominant in Israel within 3.5 weeks.	B.1.1.7, Q.3, Q.1	Munitz et al. (2021)	37121	T	G	nan
p.S982A	transmissibility	At the national level (Italy), we estimated a mean relative transmissibility of B.1.1.7 (compared to historical lineages) ranging between 1.55 and 1.57 (with confidence intervals between 1.45 and 1.66).	B.1.1.7, Q.3, Q.1	Stefanelli et al. (2021)	37121	T	G	nan
p.S982A	vaccine efficacy	In Minnesota in early 2021 when Alpha was prevalent, vaccine efficacy was estimated as: mRNA-1273 86% (95%CI: 81-90.6%) and BNT162b2: 76% (95%CI: 69-81%) using age, sex, race, PCR testing and vaccination date matched cohorts of unvaccinated, Pfizer and Moderna vaccinees. [variant list included is ancestral Alpha, as this was an observational study no variant list was given]	B.1.1.7, Q.3, Q.1	Puranik et al. (2021)	37121	T	G	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.S982A	vaccine neutralization efficacy	Between December 19, 2020 and Jan 24, 2021, 7214 of 9109 eligible HCWs at Sheba Medical Center in Israel had received one or more doses of BNT162b2 (Pfizer) vaccine. Adjusted rate reduction in SARS-CoV-2 NAAT positivity infection compared with unvaccinated workers 1-14 days after 1st dose was 30% (95% CI: 2-50), and 75% (95% CI: 72-84) after 15-28 days. Adjusted rate reduction in symptomatic COVID-19 compared with unvaccinated workers 1-14 days after 1st dose was 47% (95% CI: 17-66), and 85% (95% CI: 71-92) after 15-28 days. [Though often cited as an indicator of VE for B.1.1.7, during this time period in Israel, the prevalence of the B.1.1.7 variant increased from extasciitilde20% to 50% of cases (covariants.org), therefore these VE numbers likely represent a mix of B.1.1.7 and other lineage effects.]	B.1.1.7, Q.3, Q.1	Amit et al. (2021)	37121	T	G	nan
p.S982A	vaccine neutralization efficacy	Neutralization efficiency (ID50) against B.1.1.7 reduced 1.2x relative to D614G wildtype using pseudotyped VSV assay on 8 Moderna vaccinee sera one week post-booster.	B.1.1.7, Q.3, Q.1	Choi et al. (2021)	37121	T	G	nan
p.S982A	vaccine neutralization efficacy	20/29 sera after the first dose of Pfizer showed an average reduction in neutralization titres against the B.1.1.7 variant of 3.2 ± 5.7. After the second dose, the GMT was markedly increased compared with the first-dose titres, with a fold change of 1.9 ± 0.9 (mean ± s.d.). Neutralization GMT of 27 subjects post-infection was considerably higher (stronger) than after the second Pfizer dose, and 4.5x drop in B.1.1.7 neutralization was observed.	B.1.1.7, Q.3, Q.1	Collier et al. (2021)	37121	T	G	nan
p.S982A	vaccine neutralization efficacy	2.1x drop in neutralization using sera collected from 14 healthy adult participants that received two injections of the mRNA-1273 (Moderna) vaccine at a dose of 100 µg (18-55 years: day 1 (n	B.1.1.7, Q.3, Q.1	Edara et al. (2021)	37121	T	G	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.S982A	vaccine neutralization efficacy	Virus neutralisation activity (using a live SARS-CoV-2 microneutralisation assay (ND50)) by vaccine induced antibodies was 9-fold lower against the B.1.1.7 variant than against a canonical non B.1.1.7 lineage. Vaccine efficacy against symptomatic NAAT positive infection was similar for B.1.1.7 and non-B.1.1.7 lineages (74.6% [95%CI 41.6-88.9] and 84% [95% CI 70.7-91.4] respectively). Furthermore, vaccination with ChAdOx1 nCoV-19 results in a reduction in the duration of shedding and viral load, which may translate into a material impact on transmission of disease.	B.1.1.7, Q.3, Q.1	Emary et al. (2021)	37121	T	G	nan
p.S982A	vaccine neutralization efficacy	ELISpot assays show T cell neutralization reduced by 15.4% in this B.1.1.7 pseudotype relative to wild type in 18-20 pooled patient samples post second mRNA vaccine dose, with no significant difference between Pfizer and Moderna cohorts. Reduction was stronger in the S1 subunit than S2 (separate peptide pools were used).	B.1.1.7, Q.3, Q.1	Gallagher et al. (2021)	37121	T	G	nan
p.S982A	vaccine neutralization efficacy	Pseudotyped B.1.1.7 virus has reduced neutralization activity vs wild type: 2.1x (30 sera Pfizer median 9 days post 2nd dose) and 2.3x (35 sera Moderna median 18 days post 2nd dose). This was NOT significant by ANOVA. Note that Y145del was actually noted in the paper as the effect of their DNA construct, but this is equivalent at the protein level to the more commonly annotated Y144del.	B.1.1.7, Q.3, Q.1	Garcia-Beltran et al. (2021)	37121	T	G	nan
p.S982A	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)	B.1.1.7, Q.3, Q.1	Gong et al. (2021)	37121	T	G	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.S982A	vaccine neutralization efficacy	Using national surveillance data from Israel, using Pfizer vaccine and an estimated prevalence of the B.1.1.7 variant of 94.5% among SARS-CoV-2 infections: Adjusted estimates of vaccine effectiveness 7+ days after second dose were 95 · 3% (95% CI 94.9–95.7): 91.5% against asymptomatic SARS-CoV-2 infection (90 · 7–92 · 2: 40.9 vs 1.8 per 100 000 person-days), 97 · 0% against symptomatic COVID-19 (96.7–97.2%), 97.2% against COVID-19-related hospitalisation (96.8–97.5%), 97.5% against severe or critical COVID-19-related hospitalisation (97.1–97.8%), and 96.7% against COVID-19-related death (96.0–97.3%). In all age groups, as vaccine coverage increased, the incidence of SARS-CoV-2 outcomes declined	B.1.1.7, Q.3, Q.1	Haas et al. (2021)	37121	T	G	nan
p.S982A	vaccine neutralization efficacy	A single dose of BNT162b2 (Pfizer) vaccine showed vaccine effectiveness of 70% (95% CI 55-85) 21 days after first dose and 85% (74-96) 7 days after two doses in the study population. Our findings show that the BNT162b2 vaccine can prevent both symptomatic and asymptomatic infection in working-age adults. This cohort (8203 treatment, 15121 control) was vaccinated when the dominant variant in circulation was B.1.1.7 and shows effectiveness against this variant.	B.1.1.7, Q.3, Q.1	Hall et al. (2021)	37121	T	G	nan
p.S982A	vaccine neutralization efficacy	A single dose of BNT162b2 vaccine demonstrated vaccine effectiveness [symptomatic or asymptomatic in cohort opf routinely NAAT-monitored UK HCWs] of 72% (95% CI 58-86) 21 days after first dose and 86% (95% CI 76-97) seven days after two doses in the antibody negative cohort. This cohort was vaccinated when the dominant variant in circulation was B.1.1.7 and demonstrates effectiveness against this variant.	B.1.1.7, Q.3, Q.1	Hall et al. (2021)	37121	T	G	nan
p.S982A	vaccine neutralization efficacy	NVX-CoV2373 [Novavax] vaccine in phase 3 trial was 89.7% (95% CI, 80.2-94.6) effective in preventing COVID-19, with no hospitalizations or deaths reported. There were five cases of severe Covid-19, all in the placebo group. Post hoc analysis revealed efficacies of 96.4% (73.8-99.5) and 86.3% (71.3-93.5) against the prototype strain and B.1.1.7 variant, respectively.	B.1.1.7, Q.3, Q.1	Heath et al. (2021)	37121	T	G	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.S982A	vaccine neutralization efficacy	VSV pseudotype B.1.1.7 showed 1.77-fold reduction in neutralization efficiency vs wild type in 15 Pfizer BNT162b2 vaccinee sera 13-15 days post second dose. Cell fusion proficiency was unchanged.	B.1.1.7, Q.3, Q.1	Hoffman et al. (2021)	37121	T	G	nan
p.S982A	vaccine neutralization efficacy	B.1.1.7 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 no statistically sognificant change in neutralization effiacacy.	B.1.1.7, Q.3, Q.1	Ikegame et al. (2021)	37121	T	G	nan
p.S982A	vaccine neutralization efficacy	Neutralizing antibody titers increased in previously infected vaccinees relative to uninfected vaccinees 5.2-fold against B.1.1.7 (contrast with 3.4 fold against original SARS-CoV-2).	B.1.1.7, Q.3, Q.1	Leier et al. (2021)	37121	T	G	nan
p.S982A	vaccine neutralization efficacy	SARS-CoV-2 infection was confirmed in three HCWs working a single shift: all presented with mild symptoms of COVID-19. The two physicians were fully vaccinated with BNT162b2 vaccine, with the second dose administered 1 month before symptom onset. Both had high titres of IgG anti-spike antibodies at the time of diagnosis. WGS confirmed that all virus strains were VOC 202012/01-lineage B.1.1.7, suggesting a common source of exposure. Epidemiological investigation revealed that the suspected source was a SARS-CoV-2-positive patient who required endotracheal intubation due to severe COVID-19. All procedures were carried out using a full suite of personal protective equipment (PPE).	B.1.1.7, Q.3, Q.1	Loconsole et al. (2021)	37121	T	G	nan
p.S982A	vaccine neutralization efficacy	We found that a single dose of the BNT162b2 vaccine is about 60-70% effective at preventing symptomatic disease in adults aged 70 years and older in England and that two doses are about 85-90% effective. Those who were vaccinated and went on to have symptoms had a 44% lower risk of being admitted hospital and a 51% lower risk of death compared with people who were unvaccinated. We also found that a single dose of the ChAdOx1-S vaccine was about 60-75% effective against symptomatic disease and provided an additional protective effect against hospital admission—it is too early to assess the effect on mortality. The B.1.1.7 variant now dominates in the UK and these results will largely reflect vaccine effectiveness against this variant.	B.1.1.7, Q.3, Q.1	Lopez Bernal et al. (2021)	37121	T	G	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.S982A	vaccine neutralization efficacy	In sera 1-2 weeks after BNT162b2 first dose, from six patients previously infected with B.1, antibody titer in a microneutralization assay was on average 8192 for B.1.351 virus. This compares favorably (stronger) to post-infection neutralization titer against all variants tested in the same sera (wild type, B.1.1.7, B.1.351, and P.1).	B.1.1.7, Q.3, Q.1	Luftig et al. (2021)	37121	T	G	nan
p.S982A	vaccine neutralization efficacy	Lineage B.1.1.7 spike–pseudotyped VSV was tested for neutralization vs Wuhan reference genome pseudotype in 40 sera collected 7 or 21 days post-booster dose. Statistically significant change (22%) in neutralization was observed among the 26 sera from those <	B.1.1.7, Q.3, Q.1	Muik et al. (2021)	37121	T	G	nan
p.S982A	vaccine neutralization efficacy	We observed a sharp decline in cases when 50% of the elderly population was 2 weeks beyond their first vaccination dose and at a time point during which the B.1.1.7 variant gained transmission dominance. In support of this finding, it was suggested that, after the first vaccination dose, more than 70% of patients develop neutralization antibodies,15 and the vaccine efficiency can reach 85%.	B.1.1.7, Q.3, Q.1	Munitz et al. (2021)	37121	T	G	nan
p.S982A	vaccine neutralization efficacy	Detectable antibodies against B.1.1.7 at various time points using pseudotyped lentivirus neutralization in Moderna vaccinee cohort: Day 29 33%, Day 43 100%, Day 119 100%, Day 209 96%. Detectable antibodies against B.1.1.7 at various time points using live virus FRNT neutralization in Moderna vaccinee cohort: Day 29 54%, Day 43 100%, Day 119 100%, Day 209 88%. Detectable antibodies against B.1.1.7 at various time points using ACE2 blocking assay in Moderna vaccinee cohort: Day 29 83%, Days 43,119,209 100%.	B.1.1.7, Q.3, Q.1	Pegu et al (2021)	37121	T	G	nan
p.S982A	vaccine neutralization efficacy	The sera of 16 individuals with time course collection was evaulated against VSV pseudotypes: neutralized D614G at week 2, whereas B.1.1.7 started to be neutralized at week 3, although less efficiently than D614G. B.1.1.7 and D614G strains were similarly neutralized at week 4 (1 week after booster dose).	B.1.1.7, Q.3, Q.1	Planas et al. (2021)	37121	T	G	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.S982A	vaccine neutralization efficacy	After one dose, individuals with prior infection showed enhanced T cell immunity, antibody secreting memory B cell response to spike and neutralizing antibodies effective against B.1.1.7 (authentic cell culture supernatants). By comparison, HCW receiving one vaccine dose without prior infection showed reduced immunity against variants. B.1.1.7 spike mutations resulted in increased, abrogated or unchanged T cell responses depending on human leukocyte antigen (HLA) polymorphisms. Study was 26 each post-infection and post first dose HCWs.	B.1.1.7, Q.3, Q.1	Reynolds et al. (2021)	37121	T	G	nan
p.S982A	vaccine neutralization efficacy	The NAb titers (PRNT50) of sera collected from 38 vaccine recipients four-weeks after the second dose of inactivated whole-virion SARS-CoV-2 BBV152/COVAXIN vaccine [which contains D614G] were not significantly different between B.1.1.7 virus and ancestral D614G virus.	B.1.1.7, Q.3, Q.1	Sapkal et al. (2021)	37121	T	G	nan
p.S982A	vaccine neutralization efficacy	Pseudotyped B.1.1.7 Spike variants lentivirus. 3.5x reduction in neutralization with Moderna vaccinated patient sera after 29 days (1st dose). 2.0x reduction in neutralization with Moderna vaccinated patient sera after 57 days (2nd dose). 2.1x reduction in neutralization with Novavax Phase 1 post-vaccination sera.	B.1.1.7, Q.3, Q.1	Shen et al. (2021)	37121	T	G	nan
p.S982A	vaccine neutralization efficacy	Neutralization assays of B.1.1.7 virus showed a reduction of 2.5-fold (14 days post 2nd dose AstraZeneca, n	B.1.1.7, Q.3, Q.1	Supasa et al. (2021)	37121	T	G	nan
p.S982A	vaccine neutralization efficacy	Vaccine elicited antibodies neutralized virus with the B.1.1.7 spike protein with titers similar to D614G virus. Serum specimens from individuals vaccinated with the BNT162b2 mRNA vaccine neutralized D614G virus with titers that were on average 7-fold greater than convalescent sera.	B.1.1.7, Q.3, Q.1	Tada et al. (2021)	37121	T	G	nan
p.S982A	vaccine neutralization efficacy	PBMCs of Pfizer/BioNTech BNT162b2 (n	B.1.1.7, Q.3, Q.1	Tarke et al. (2021)	37121	T	G	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.S982A	vaccine neutralization efficacy	1.4x improvement in neutralization by serum collected 2 to 3 weeks after the second dose from vaccinees who had received BBIBP-CorV (pVNT50 against VSV pseudotyped as B.1.1.7). Convalescent plasma had similar titer against wild type as the BBIBP-CorV vaccinee sera. 2x reduction in neutralization by serum collected 2 to 3 weeks after the second dose from vaccinees who had received CoronaVac (pVNT50 against VSV pseudotyped as B.1.1.7). Convalescent plasma had similar titer against wild type as the CoronaVac vaccinee sera.	B.1.1.7, Q.3, Q.1	Wang et al. (2021)	37121	T	G	nan
p.S982A	vaccine neutralization efficacy	No significant difference in T-cell response to B.1.1.7 was observed (vs. ancestral) in blood drawn from 28 participants received the Pfizer-BioNTech vaccine and 2 received the Moderna vaccine. This is despite three mutations (Y144del, D614G, and P681H) overlapping T-cell epitope hotspots.	B.1.1.7, Q.3, Q.1	Woldemeskel et al. (2021)	37121	T	G	nan
p.S982A	vaccinee plasma binding	2x 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. 1.12x 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.	Q.1, B.1.1.7, Q.3, Q.4	Gong et al. (2021)	37123	T	G	nan
p.S982A	vaccinee plasma binding	This variant combination (representing B.1.1.7 aka Alpha) showed no change in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in previously non-seroconverted subjects. 1.28x 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.1.1.7, Q.3, Q.1	Gong et al. (2021)	37121	T	G	nan
p.S982A	viral load	Using lack of S probe detection as a proxy for B.1.1.7 status, 275 putative B.1.1.7 samples and 390 "wild type" SARS-CoV-2 positive samples in Wales were compared for Ct values, suggesting extasciitilde12-fold increase (extasciitilde3.5 Ct decrease) in viral load for B.1.1.7 samples.	B.1.1.7, Q.3, Q.1	Couzens et al. (2021)	37121	T	G	nan
p.S982A	viral load	We found that the British variant (clade B.1.1.7), compared to an ancestral SARS-CoV-2 clade B virus, produced higher levels of infectious virus late in infection and had a higher replicative fitness in human airway, alveolar and intestinal organoid models.	B.1.1.7, Q.3, Q.1	Lamers et al. (2021)	37121	T	G	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.S982A	viral load	This study reveals that B.1.1.7 SARS-CoV-2 variant is a slower-growing virus than parental B.1. Further, a higher replication along with reduced infectious viral titer was hypothesized to be linked to higher transmission with reduced pathogenicity.	B.1.1.7, Q.3, Q.1	Nyayanit et al. (2021)	37121	T	G	nan
p.S982A	viral load	In a study of 1260 ICU subjects, viral load distributions (collected within 48h of admission) were elevated in both seropositive and seronegative subjects infected with B.1.1.7 ("UK variant"). PG: The PANGO tool defining Spike variants for B.1.1.7 are listed here, whereas the paper only used a test for D1118H.	B.1.1.7, Q.3, Q.1	Ratcliff et al. (2021)	37121	T	G	nan
p.S982A	viral load	B.1.1.7 samples showed average Ct cycle threshold of 21.9 vs 23 for wildtype (i.e. extasciitilde2x higher viral load) comparing 37758 and 22535 samples respectively.	B.1.1.7, Q.3, Q.1	Roquebert et al. (2021)	37121	T	G	nan
p.S982A	viral load	The median Ct value of RT-qPCR tests of the N-gene target in the Daxing B.1.1.7 group was significantly lower than the Shunyi B.1.470 group (P	B.1.1.7, Q.3, Q.1	Song et al. (2021)	37121	T	G	nan
p.S982A	viral load	The 249 B.1.1.7 (a.k.a. N501Y.V1) variant cases in three Paris hospital labs had a extasciitilde10-fold viral load increase (extasciitilde3.3 Ct drop in N gene probe) compared to 332 ancestral lineage cases from the same time frame (2020-12-20 to 2021-02-26). PG: BUT there is a discrepancy in drop between the ORF1ab and N probes, with the former suggesting only a 2-fold drop, consistent with the drop observed in B.1.351. This might indicate higher subgenomic RNA content in B.1.1.7 skewing the change.	B.1.1.7, Q.3, Q.1	Teyssou et al. (2021)	37121	T	G	nan
p.S982A	virion structure	CryoEM analysis of B.1.1.7 demonstrates an increased propensity for 'up', receptor accessible conformation of the Spike protein trimer.	B.1.1.7, Q.3, Q.1	Cai et al. (2021)	37121	T	G	nan
p.L5F	ACE2 receptor binding affinity	Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant showed a 1.1x decrease in binding (KD) relative to D614G.	Q.1	Gong et al. (2021)	44	C	T	nan
p.L5F	convalescent plasma binding	No change in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset.	Q.1	Gong et al. (2021)	44	C	T	nan
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.	Q.1	Gong et al. (2021)	44	C	T	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.Y144del	ACE2 receptor binding affinity	Six fold increase in affinity for ACE2 by the B.1.1.7 lineage vs wild type is driven by a drop in observed dissociation rate constant.	B.1.1.7, Q.3, Q.1	Collier et al. (2021)	70911	TTTA	T	nan
p.Y144del	ACE2 receptor binding affinity	Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant showed a slight decrease in binding (KD) relative to D614G.	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Gong et al. (2021)	70921	TTTA	T	nan
p.Y144del	ACE2 receptor binding affinity	Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant combination (representing B.1.1.7 aka Alpha) had 5.43x increased binding relative to D614G alone.	B.1.1.7, Q.3, Q.1	Gong et al. (2021)	70911	TTTA	T	nan
p.Y144del	ACE2 receptor binding affinity	Flow cytometry was used on recombinant VSV proteins and yeast surface display to assess the binding of a labeled soluble ACE2 protein to cells expressing B.1.1.7. We observed a dramatic increase (relative to D614G) in binding of soluble ACE2 to B.1.1.7, and to a lesser extent to B.1.351, which both carry the N501Y mutation (see Fig 3).	B.1.1.7, Q.3, Q.1	Planas et al. (2021)	70911	TTTA	T	nan
p.Y144del	ACE2 receptor binding affinity	This mutation causes major decrease in binding affinity vs. wild type as measured by IC50 vs pseudotyped lentivirus.	B.1.1.7, Q.3, Q.1	Tada et al. (2021)	70911	TTTA	T	nan
p.Y144del	anthropozoonotic events	First documented cases of domestic cat and dog infections with the B.1.1.7 strain.	B.1.1.7, Q.3, Q.1	Hamer et al. (2021)	70911	TTTA	T	nan
p.Y144del	antibody epitope effects	Wildtype elicits immune response, COVID-19 cohort epitope score > 99th percentile of the 497 prepandemic controls, mutant drops PIWAS epitope score from 1% to 0.17% (poorer immune recognition) Together with other B1.1.7 lineage mutational changes (Spike: N501Y, A570D, P681H, 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.	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Haynes et al. (2021)	70921	TTTA	T	nan
p.Y144del	antibody epitope effects	extasciitilde20x resistence to mAb CQ038 by B.1.1.7 pseudotyped virus	B.1.1.7, Q.3, Q.1	Hu et al. (2021)	70911	TTTA	T	nan
p.Y144del	antibody epitope effects	Massive reduction in S2M28 monoclonal antibody EC50 (i.e. ablated recognition), within antigenic supersite "i" Massive reduction in S2X28 monoclonal antibody EC50 (i.e. ablated recognition), within antigenic supersite "i" Massive reduction in S2X333 monoclonal antibody EC50 (i.e. ablated recognition), within antigenic supersite "i" Massive reduction in 4A8 monoclonal antibody EC50 (i.e. ablated recognition)	B.1.1.7, Q.8, Q.3, Q.4, Q.1	McCallum et al. (2021)	70921	TTTA	T	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.Y144del	antibody epitope effects	Lessens the potency of mAbs COVA2-17 (extasciitilde5x, similar to N501Y alone), COVA1-12 (extasciitilde11x) and COVA1-21 (>100x), which do not compete allosterically.	B.1.1.7, Q.3, Q.1	Rees-Spear et al. (2021)	70911	TTTA	T	nan
p.Y144del	antibody epitope effects	Reduction in neutralization by mAbs COVA2-15 (extasciitilde9x), B38 (extasciitilde14x), S309 (extasciitilde190x) by this B.1.1.7 pseudotyped virus model.	B.1.1.7, Q.3, Q.1	Shen et al. (2021)	70911	TTTA	T	nan
p.Y144del	antibody epitope effects	Abolishes neutralization by N-terminal-domain-directed mAbs 5-24, 4-8, and 4A8.	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Wang et al. (2021)	70921	TTTA	T	nan
p.Y144del	antibody epitope effects	B.1.1.7 pseudotyped virus model impairs binding by RBD-directed mAb 910-30. B.1.1.7 pseudotyped virus model abolishes N-terminal-domain-directed mAbs 5-24, 4-8, and 4A8. B.1.1.7 pseudotyped virus model impairs binding by N-terminal-domain-directed mAbs 2-17, 4-19, 5-7.	B.1.1.7, Q.3, Q.1	Wang et al. (2021)	70911	TTTA	T	nan
p.Y144del	clinical indicators	After adjusting for the age factor, in a prospective Chinese cohort study B.1.1.7 variant infection (compared to B.1.140) was the risk factor for C-reactive protein (P	B.1.1.7, Q.3, Q.1	Song et al. (2021)	70911	TTTA	T	nan
p.Y144del	convalescent plasma binding	1.14x increase in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset.	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Gong et al. (2021)	70921	TTTA	T	nan
p.Y144del	convalescent plasma binding	This variant combination (representing B.1.1.7 aka Alpha) showed a 1.15x increase in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset.	B.1.1.7, Q.3, Q.1	Gong et al. (2021)	70911	TTTA	T	nan
p.Y144del	convalescent plasma escape	Neutralization capacity GMT of 27 subjects' sera post-infection was considerably higher (stronger) than after the second Pfizer dose, and 4.5x drop in B.1.1.7 neutralization was observed.	B.1.1.7, Q.3, Q.1	Collier et al. (2021)	70911	TTTA	T	nan
p.Y144del	convalescent plasma escape	NTD-specific nAbs showed a substantial (3-450x) decrease in neutralization potency against the recently reported highly transmissible B.1.1.7 variant of concern, whereas RBD-specific nAbs were either unaffected or showed lower decreases in potency.	B.1.1.7, Q.3, Q.1	Graham et al. (2021)	70911	TTTA	T	nan
p.Y144del	convalescent plasma escape	Neutralizing antibody titers of 2/20 (10%) samples showed >10x reduction (sera collected extasciitilde1mo post Jan 2020 first wave in China). Neutralizing antibody titers of 8/20 samples (40%) decreased below an ID50 threshold of 40 (sera collected extasciitilde8mo post Jan 2020 first wave in China).	B.1.1.7, Q.3, Q.1	Hu et al. (2021)	70911	TTTA	T	nan
p.Y144del	convalescent plasma escape	Virus evolution data in 9 immunocomprised patients with long active COVID-19 infections was gathered, showing sequence deletion hotspots. This variant was present in 4 patients.	B.1.1.7, Q.8, Q.3, Q.4, Q.1	McCarthy et al. (2021)	70921	TTTA	T	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.Y144del	convalescent plasma escape	Using a new rapid neutralization assay, based on reporter cells that become positive for GFP after overnight infection, sera from 58 convalescent individuals collected up to 9 months after symptoms, similarly neutralized B.1.1.7 and D614G.	B.1.1.7, Q.3, Q.1	Planas et al. (2021)	70911	TTTA	T	nan
p.Y144del	convalescent plasma escape	Maximum fold-decrease in potency for the serum samples from mild illness was 8.2 but the majority of samples showed less than a 3-fold change. Similarly, the maximum decrease seen for samples from hospitalized patients was a 9.1-fold change, but most of the samples showed minimal change in the potency of their neutralization. Overall, three samples from each cohort (8%) showed a 5–10-fold reduction, but as they were potently neutralizing sera, the reduced ID50 values were still >1:100.	B.1.1.7, Q.3, Q.1	Rees-Spear et al. (2021)	70911	TTTA	T	nan
p.Y144del	convalescent plasma escape	Neutralization activity of convalescent sera tested decreased <2x with this B.1.1.7 pseudotyped virus.	B.1.1.7, Q.3, Q.1	Shen et al. (2021)	70911	TTTA	T	nan
p.Y144del	convalescent plasma escape	We analyzed 34 convalescent samples including the WHONIBSC 20/130 reference serum, and, although a few sera showed near identical FRNT 50 values, the FRNT50 dilutions for the B.1.1.7 strain were 2.9-fold lower (geometric mean) than those for the Victoria strain ($p < 0.0001$). Sera from 13 subjects post-B.1.1.7 infection showed no significant change in neutralization against Victoria (extasciitildewild type), suggesting that B.1.1.7 infection also protects against ancestral virus. [Note that D1119H was included in the original paper, assuming typographical error and correcting to D1118H]	B.1.1.7, Q.3, Q.1	Supasa et al. (2021)	70911	TTTA	T	nan
p.Y144del	convalescent plasma escape	Loss of neutralizing activity using 6 hyperimmune immunoglobulin preparations from convalescent plasma was minimal against B.1.1.7 (1.9-fold). Neutralization against 10 convalescent plasma was poorer.	B.1.1.7, Q.3, Q.1	Tang et al. (2021)	70911	TTTA	T	nan
p.Y144del	convalescent plasma escape	The neutralizing activity of 8/20 convalescent sera was significantly lower against this pseudotyped virus model of B.1.1.7, yet almost no effect was detected using the live B.1.1.7 virus.	B.1.1.7, Q.3, Q.1	Wang et al. (2021)	70911	TTTA	T	nan
p.Y144del	environmental condition stability	Treatment with heat, soap and ethanol revealed similar inactivation profiles indicative of a comparable susceptibility towards disinfection. Furthermore, we observed comparable surface stability on steel, silver, copper and face masks.	B.1.1.7, Q.3, Q.1	Meister et al. (2021)	70911	TTTA	T	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.Y144del	environmental condition stability	No differences in the stability of B.1.1.7 observed in the absence of simulated sunlight at either 20°C or 40°C (with a mean time for a 90% loss of viral infectivity across all dark conditions of 6.2 hours). However, a small but statistically significant difference in the stability was observed in simulated sunlight at 20°C and 20% relative humidity, with B.1.1.7 restoring wild type 90% loss time of 11 minutes vs. 7 and 8 minutes for B.1.319 (D614G) and B.28 (V367F) early 2020 viruses respectively.	B.1.1.7, Q.3, Q.1	Schuit et al. (2021)	70911	TTTA	T	nan
p.Y144del	immunosuppression variant emergence	Emergent as 100% variant from larger minor (1% allele frequency) deletion by day 70 post-infection of female immunocompromised individual with chronic lymphocytic leukemia and acquired hypogammaglobulinemia. Variant disappeared after convalescent plasma treatment (day 71) in subsequent sample sequencing.	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Avanzato et al. (2020)	70921	TTTA	T	nan
p.Y144del	outcome hazard ratio	Danish study of the B.1.1.7 lineage shows hospital admission odds ratio of 1.63 vs other lineages. The adjusted OR was increased in all strata of age.	B.1.1.7, Q.3, Q.1	Bager et al. (2021)	70911	TTTA	T	nan
p.Y144del	outcome hazard ratio	The mortality hazard ratio associated with infection with [B.1.1.7] compared with infection with previously circulating variants was 1.64 (95% confidence interval 1.32 to 2.04) in patients who tested positive for covid-19 in the community (54906 matched pairs of participants who tested positive for SARS-CoV-2 in pillar 2 between 1 October 2020 and 29 January 2021). In this comparatively low risk group, this represents an increase in deaths from 2.5 to 4.1 per 1000 detected cases.	B.1.1.7, Q.3, Q.1	Challen et al. (2021)	70911	TTTA	T	nan
p.Y144del	outcome hazard ratio	Using UK data 1 November 2020 to 14 February 2021, while correcting for misclassification of PCR test Spike Gene Target Failure (SGTF) and missingness in SGTF status, we estimate that the hazard of death associated with B.1.1.7 is 61% (42–82%) higher than with pre-existing variants after adjustment for age, sex, ethnicity, deprivation, residence in a care home, the local authority of residence and test date. This corresponds to the absolute risk of death for a 55–69-year-old man increasing from 0.6% to 0.9% (95% confidence interval, 0.8–1.0%) within 28 days of a positive test in the community.	B.1.1.7, Q.3, Q.1	Davies et al. (2021)	70911	TTTA	T	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.Y144del	outcome hazard ratio	341 samples collected Nov 9 to Dec 20, 2020 were sequenced from two London (UK) hospitals. 198 (58%) of 341 had B.1.1.7 infection and 143 (42%) had non-B.1.1.7 infection. No evidence was found of an association between severe disease and death and lineage (B.1.1.7 vs non-B.1.1.7) in unadjusted analyses (prevalence ratio [PR] 0 · 97 [95% CI 0 · 72-1 · 31]), or in analyses adjusted for hospital, sex, age, comorbidities, and ethnicity (adjusted PR 1 · 02 [0 · 76-1 · 38]).	B.1.1.7, Q.3, Q.1	Frampton et al. (2021)	70911	TTTA	T	nan
p.Y144del	outcome hazard ratio	On average across 7 European countries studied, using B.1.1.7 defining mutations: Significant shift to asymptomatic cases (27.4% vs 18.6% for non-VOC cases). Significant shift to infection in those without pre-existing conditions (44.8% vs 89% for non-VOC cases). Significant increase in hospitalization rate (11% vs 7.5% for non-VOC cases). Significant increase in ICU rate (1.4% vs 0.6% for non-VOC cases). Significant decrease in death rate (2.0% vs vs 4.0% for non-VOC cases).	B.1.1.7, Q.3, Q.1	Funk et al. (2021)	70911	TTTA	T	nan
p.Y144del	outcome hazard ratio	From Sept 28 to Dec 27, 2020, positive COVID-19 tests were reported by 36 920 COVID Symptom Study app users whose region was known and who reported as healthy on app sign-up. We found no changes in reported symptoms or disease duration associated with B.1.1.7.	B.1.1.7, Q.3, Q.1	Graham et al. (2021)	70911	TTTA	T	nan
p.Y144del	outcome hazard ratio	Using primarily S-defining mutations for lineage B.1.1.7, most models of hospitalization and fatality risk ratios from consortium members show elevated ratios (extasciitilde1.3-1.7x).	B.1.1.7, Q.3, Q.1	NERVTAG Consortium (2021)	70911	TTTA	T	nan
p.Y144del	outcome hazard ratio	The matching-adjusted conditional odds ratio of hospitalisation was 1.58 (95% confidence interval 1.50 to 1.67) for COVID-19 patients infected with a SGTF-associated variant [primarily B.1.1.7], compared to those infected with non-SGTF-associated variants. The effect was modified by age (p<0.001), with ORs of 0.96-1.13 below age 20 years and 1.57-1.67 in age groups 40 years or older.	B.1.1.7, Q.3, Q.1	Nyberg et al. (2021)	70911	TTTA	T	nan
p.Y144del	reinfection	36920 COVID Symptom Study app users reported SARS-CoV-2 test positivity in late 2020. Possible reinfections were identified in 249 (0.7% [95% CI 0.6-0.8]) of 36509 app users who reported a positive swab test before Oct 1, 2020, but there was no evidence that the frequency of reinfections was higher for the B.1.1.7 variant than for pre-existing variants.	B.1.1.7, Q.3, Q.1	Graham et al. (2021)	70911	TTTA	T	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.Y144del	reinfection	Second infection in December 2020 with B.1.1.7 after April 2020 initial infection with B.2 in a 78-year-old man with a history of Type 2 diabetes mellitus, diabetic nephropathy on hemodialysis, chronic obstructive pulmonary disease (COPD), mixed central and obstructive sleep apnea, ischemic heart disease, with no history of immunosuppression.	B.1.1.7, Q.3, Q.1	Harrington et al. (2021)	70911	TTTA	T	nan
p.Y144del	reinfection	Reinfection with Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) B.1.1.7 variant in an immunocompromised 16yo female with end stage renal disease 94 days after initial infection with a B.1.2 lineage virus. Both lineages were the prevalent one at the time of 1st and 2nd infections respectively in Texas, where the patient was located (suggesting exposure risk rather than lineage immune evasion).	B.1.1.7, Q.3, Q.1	Marquez et al. (2021)	70911	TTTA	T	nan
p.Y144del	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.1.1.7, Q.3, Q.1	Planas et al. (2021)	70911	TTTA	T	nan
p.Y144del	trafficking	extasciitilde2.5x cleavage of S2 relative to WA1 (D614G) wildtype by Alpha variant variant as measured by mass spectrometry of Vero-TMPRSS culture.	B.1.1.7, Q.3, Q.1	Esclera et al. (2021)	70911	TTTA	T	nan
p.Y144del	trafficking	VSV pseudotype B.1.1.7 showed no significant difference in cell entry relative to wild type in 6 cell lines. Cell fusion proficiency was unchanged.	B.1.1.7, Q.3, Q.1	Hoffman et al. (2021)	70911	TTTA	T	nan
p.Y144del	trafficking	The entry efficiencies of Spike pseudotyped viruses bearing N501Y Variant 1 (B.1.1.7) mutant were about 3 to 4.4 times higher than that of the WT pseudovirus when viral input was normalized, suggesting that these spike variants promote the infectivity of SARS-CoV-2.	B.1.1.7, Q.3, Q.1	Hu et al. (2021)	70911	TTTA	T	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.Y144del	trafficking	Lentiviral pseudotyped with this individual mutation from B.1.1.7 was tested on ACE2.293T cells. Luciferase activity was measured two days postinfection, showing slightly increased infection rate amongst the cells.	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Tada et al. (2021)	70921	TTTA	T	nan
p.Y144del	trafficking	Live virus was tested ex vivo in reconstituted brochial epithelium, and out competed wild type.	B.1.1.7, Q.3, Q.1	Touret et al. (2021)	70911	TTTA	T	nan
p.Y144del	transmissibility	We estimate that this [B.1.1.17] variant has a 43–90% (range of 95% credible intervals 38–130%) higher reproduction number than preexisting variants. Data from other countries yield similar results: we estimate that R for VOC 202012/01 relative to other lineages is 55% (45–66%) higher in Denmark, 74% (66–82%) higher in Switzerland, and 59% (56–63%) higher in the United States, with consistent rates of displacement across regions within each country.	B.1.1.7, Q.3, Q.1	Davies et al. (2021)	70911	TTTA	T	nan
p.Y144del	transmissibility	Based on 36920 COVID Symptom Study app users reported SARS-CoV-2 test positivity in late 2020, Rt of B.1.1.7 was 1.35x (95% CI 1.02-1.69) relative to pre-existing variants. However, Rt fell below 1 during regional and national lockdowns, even in regions with high proportions of infections with the B.1.1.7 variant.	B.1.1.7, Q.3, Q.1	Graham et al. (2021)	70911	TTTA	T	nan
p.Y144del	transmissibility	Ontario, Feb 2021: The secondary attack rate for VOC index cases in this matched cohort was 1.31 times higher than non-VOC index cases (RR	B.1.1.7, Q.3, Q.1	Lindstrøm et al. (2021)	70911	TTTA	T	nan
p.Y144del	transmissibility	Primary cases infected with B.1.1.7 had an increased transmissibility of 1.5-1.7 times that of primary cases infected with other lineages. The increased transmissibility of B.1.1.7 was multiplicative across age and viral load.	B.1.1.7, Q.3, Q.1	Lyngse et al. (2021)	70911	TTTA	T	nan
p.Y144del	transmissibility	Based on 300,000 RT-PCR samples collected from December 6th 2020 to February 10th 2021 in Israel, the B.1.1.7 is 45% (95% CI:20-60%) more transmissible than the wild-type strain, and become dominant in Israel within 3.5 weeks.	B.1.1.7, Q.3, Q.1	Munitz et al. (2021)	70911	TTTA	T	nan
p.Y144del	transmissibility	At the national level (Italy), we estimated a mean relative transmissibility of B.1.1.7 (compared to historical lineages) ranging between 1.55 and 1.57 (with confidence intervals between 1.45 and 1.66).	B.1.1.7, Q.3, Q.1	Stefanelli et al. (2021)	70911	TTTA	T	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.Y144del	vaccine efficacy	In Minnesota in early 2021 when Alpha was prevalent, vaccine efficacy was estimated as: mRNA-1273 86% (95%CI: 81-90.6%) and BNT162b2: 76% (95%CI: 69-81%) using age, sex, race, PCR testing and vaccination date matched cohorts of unvaccinated, Pfizer and Moderna vaccinees. [variant list included is ancestral Alpha, as this was an observational study no variant list was given]	B.1.1.7, Q.3, Q.1	Puranik et al. (2021)	70911	TTTA	T	nan
p.Y144del	vaccine neutralization efficacy	nan	B.1.1.7, Q.3, Q.1	All vaccinees were on a strict 3 week interval for second dose (	70911	TTTA	T	nan
p.Y144del	vaccine neutralization efficacy	Between December 19, 2020 and Jan 24, 2021, 7214 of 9109 eligible HCWs at Sheba Medical Center in Israel had received one or more doses of BNT162b2 (Pfizer) vaccine. Adjusted rate reduction in SARS-CoV-2 NAAT positivity infection compared with unvaccinated workers 1-14 days after 1st dose was 30% (95% CI: 2-50), and 75% (95% CI: 72-84) after 15-28 days. Adjusted rate reduction in symptomatic COVID-19 compared with unvaccinated workers 1-14 days after 1st dose was 47% (95% CI: 17-66), and 85% (95% CI: 71-92) after 15-28 days. [Though often cited as an indicator of VE for B.1.1.7, during this time period in Israel, the prevalence of the B.1.1.7 variant increased from extasciitilde20% to 50% of cases (covariants.org), therefore these VE numbers likely represent a mix of B.1.1.7 and other lineage effects.]	B.1.1.7, Q.3, Q.1	Amit et al. (2021)	70911	TTTA	T	nan
p.Y144del	vaccine neutralization efficacy	Neutralization efficiency (ID50) against B.1.1.7 reduced 1.2x relative to D614G wildtype using pseudotyped VSV assay on 8 Moderna vaccinee sera one week post-booster.	B.1.1.7, Q.3, Q.1	Choi et al. (2021)	70911	TTTA	T	nan
p.Y144del	vaccine neutralization efficacy	20/29 sera after the first dose of Pfizer showed an average reduction in neutralization titres against the B.1.1.7 variant of 3.2 ± 5.7. After the second dose, the GMT was markedly increased compared with the first-dose titres, with a fold change of 1.9 ± 0.9 (mean ± s.d.). Neutralization GMT of 27 subjects post-infection was considerably higher (stronger) than after the second Pfizer dose, and 4.5x drop in B.1.1.7 neutralization was observed.	B.1.1.7, Q.3, Q.1	Collier et al. (2021)	70911	TTTA	T	nan
p.Y144del	vaccine neutralization efficacy	2.1x drop in neutralization using sera collected from 14 healthy adult participants that received two injections of the mRNA-1273 (Moderna) vaccine at a dose of 100 µg (18-55 years: day 1 (n	B.1.1.7, Q.3, Q.1	Edara et al. (2021)	70911	TTTA	T	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.Y144del	vaccine neutralization efficacy	Virus neutralisation activity (using a live SARS-CoV-2 microneutralisation assay (ND50)) by vaccine induced antibodies was 9-fold lower against the B.1.1.7 variant than against a canonical non B.1.1.7 lineage. Vaccine efficacy against symptomatic NAAT positive infection was similar for B.1.1.7 and non-B.1.1.7 lineages (74.6% [95%CI 41.6-88.9] and 84% [95% CI 70.7-91.4] respectively). Furthermore, vaccination with ChAdOx1 nCoV-19 results in a reduction in the duration of shedding and viral load, which may translate into a material impact on transmission of disease.	B.1.1.7, Q.3, Q.1	Emary et al. (2021)	70911	TTTA	T	nan
p.Y144del	vaccine neutralization efficacy	ELISpot assays show T cell neutralization reduced by 15.4% in this B.1.1.7 pseudotype relative to wild type in 18-20 pooled patient samples post second mRNA vaccine dose, with no significant difference between Pfizer and Moderna cohorts. Reduction was stronger in the S1 subunit than S2 (separate peptide pools were used).	B.1.1.7, Q.3, Q.1	Gallagher et al. (2021)	70911	TTTA	T	nan
p.Y144del	vaccine neutralization efficacy	Pseudotyped B.1.1.7 virus has reduced neutralization activity vs wild type: 2.1x (30 sera Pfizer median 9 days post 2nd dose) and 2.3x (35 sera Moderna median 18 days post 2nd dose). This was NOT significant by ANOVA. Note that Y145del was actually noted in the paper as the effect of their DNA construct, but this is equivalent at the protein level to the more commonly annotated Y144del.	B.1.1.7, Q.3, Q.1	Garcia-Beltran et al. (2021)	70911	TTTA	T	nan
p.Y144del	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)	B.1.1.7, Q.3, Q.1	Gong et al. (2021)	70911	TTTA	T	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.Y144del	vaccine neutralization efficacy	Using national surveillance data from Israel, using Pfizer vaccine and an estimated prevalence of the B.1.1.7 variant of 94.5% among SARS-CoV-2 infections: Adjusted estimates of vaccine effectiveness 7+ days after second dose were 95 · 3% (95% CI 94.9–95.7): 91.5% against asymptomatic SARS-CoV-2 infection (90 · 7–92 · 2: 40.9 vs 1.8 per 100 000 person-days), 97 · 0% against symptomatic COVID-19 (96.7–97.2%), 97.2% against COVID-19-related hospitalisation (96.8–97.5%), 97.5% against severe or critical COVID-19-related hospitalisation (97.1–97.8%), and 96.7% against COVID-19-related death (96.0–97.3%). In all age groups, as vaccine coverage increased, the incidence of SARS-CoV-2 outcomes declined	B.1.1.7, Q.3, Q.1	Haas et al. (2021)	70911	TTTA	T	nan
p.Y144del	vaccine neutralization efficacy	A single dose of BNT162b2 (Pfizer) vaccine showed vaccine effectiveness of 70% (95% CI 55-85) 21 days after first dose and 85% (74-96) 7 days after two doses in the study population. Our findings show that the BNT162b2 vaccine can prevent both symptomatic and asymptomatic infection in working-age adults. This cohort (8203 treatment, 15121 control) was vaccinated when the dominant variant in circulation was B.1.1.7 and shows effectiveness against this variant.	B.1.1.7, Q.3, Q.1	Hall et al. (2021)	70911	TTTA	T	nan
p.Y144del	vaccine neutralization efficacy	A single dose of BNT162b2 vaccine demonstrated vaccine effectiveness [symptomatic or asymptomatic in cohort opf routinely NAAT-monitored UK HCWs] of 72% (95% CI 58-86) 21 days after first dose and 86% (95% CI 76-97) seven days after two doses in the antibody negative cohort. This cohort was vaccinated when the dominant variant in circulation was B.1.1.7 and demonstrates effectiveness against this variant.	B.1.1.7, Q.3, Q.1	Hall et al. (2021)	70911	TTTA	T	nan
p.Y144del	vaccine neutralization efficacy	NVX-CoV2373 [Novavax] vaccine in phase 3 trial was 89.7% (95% CI, 80.2-94.6) effective in preventing COVID-19, with no hospitalizations or deaths reported. There were five cases of severe Covid-19, all in the placebo group. Post hoc analysis revealed efficacies of 96.4% (73.8-99.5) and 86.3% (71.3-93.5) against the prototype strain and B.1.1.7 variant, respectively.	B.1.1.7, Q.3, Q.1	Heath et al. (2021)	70911	TTTA	T	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.Y144del	vaccine neutralization efficacy	VSV pseudotype B.1.1.7 showed 1.77-fold reduction in neutralization efficiency vs wild type in 15 Pfizer BNT162b2 vaccinee sera 13-15 days post second dose. Cell fusion proficiency was unchanged.	B.1.1.7, Q.3, Q.1	Hoffman et al. (2021)	70911	TTTA	T	nan
p.Y144del	vaccine neutralization efficacy	B.1.1.7 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 no statistically sognificant change in neutralization effiacacy.	B.1.1.7, Q.3, Q.1	Ikegame et al. (2021)	70911	TTTA	T	nan
p.Y144del	vaccine neutralization efficacy	Neutralizing antibody titers increased in previously infected vaccinees relative to uninfected vaccinees 5.2-fold against B.1.1.7 (contrast with 3.4 fold against original SARS-CoV-2).	B.1.1.7, Q.3, Q.1	Leier et al. (2021)	70911	TTTA	T	nan
p.Y144del	vaccine neutralization efficacy	SARS-CoV-2 infection was confirmed in three HCWs working a single shift: all presented with mild symptoms of COVID-19. The two physicians were fully vaccinated with BNT162b2 vaccine, with the second dose administered 1 month before symptom onset. Both had high titres of IgG anti-spike antibodies at the time of diagnosis. WGS confirmed that all virus strains were VOC 202012/01-lineage B.1.1.7, suggesting a common source of exposure. Epidemiological investigation revealed that the suspected source was a SARS-CoV-2-positive patient who required endotracheal intubation due to severe COVID-19. All procedures were carried out using a full suite of personal protective equipment (PPE).	B.1.1.7, Q.3, Q.1	Loconsole et al. (2021)	70911	TTTA	T	nan
p.Y144del	vaccine neutralization efficacy	We found that a single dose of the BNT162b2 vaccine is about 60-70% effective at preventing symptomatic disease in adults aged 70 years and older in England and that two doses are about 85-90% effective. Those who were vaccinated and went on to have symptoms had a 44% lower risk of being admitted hospital and a 51% lower risk of death compared with people who were unvaccinated. We also found that a single dose of the ChAdOx1-S vaccine was about 60-75% effective against symptomatic disease and provided an additional protective effect against hospital admission—it is too early to assess the effect on mortality. The B.1.1.7 variant now dominates in the UK and these results will largely reflect vaccine effectiveness against this variant.	B.1.1.7, Q.3, Q.1	Lopez Bernal et al. (2021)	70911	TTTA	T	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.Y144del	vaccine neutralization efficacy	In sera 1-2 weeks after BNT162b2 first dose, from six patients previously infected with B.1, antibody titer in a microneutralization assay was on average 8192 for B.1.351 virus. This compares favorably (stronger) to post-infection neutralization titer against all variants tested in the same sera (wild type, B.1.1.7, B.1.351, and P.1).	B.1.1.7, Q.3, Q.1	Luftig et al. (2021)	70911	TTTA	T	nan
p.Y144del	vaccine neutralization efficacy	Lineage B.1.1.7 spike–pseudotyped VSV was tested for neutralization vs Wuhan reference genome pseudotype in 40 sera collected 7 or 21 days post-booster dose. Statistically significant change (22%) in neutralization was observed among the 26 sera from those <	B.1.1.7, Q.3, Q.1	Muik et al. (2021)	70911	TTTA	T	nan
p.Y144del	vaccine neutralization efficacy	We observed a sharp decline in cases when 50% of the elderly population was 2 weeks beyond their first vaccination dose and at a time point during which the B.1.1.7 variant gained transmission dominance. In support of this finding, it was suggested that, after the first vaccination dose, more than 70% of patients develop neutralization antibodies,15 and the vaccine efficiency can reach 85%.	B.1.1.7, Q.3, Q.1	Munitz et al. (2021)	70911	TTTA	T	nan
p.Y144del	vaccine neutralization efficacy	Detectable antibodies against B.1.1.7 at various time points using pseudotyped lentivirus neutralization in Moderna vaccinee cohort: Day 29 33%, Day 43 100%, Day 119 100%, Day 209 96%. Detectable antibodies against B.1.1.7 at various time points using live virus FRNT neutralization in Moderna vaccinee cohort: Day 29 54%, Day 43 100%, Day 119 100%, Day 209 88%. Detectable antibodies against B.1.1.7 at various time points using ACE2 blocking assay in Moderna vaccinee cohort: Day 29 83%, Days 43,119,209 100%.	B.1.1.7, Q.3, Q.1	Pegu et al (2021)	70911	TTTA	T	nan
p.Y144del	vaccine neutralization efficacy	The sera of 16 individuals with time course collection was evaulated against VSV pseudotypes: neutralized D614G at week 2, whereas B.1.1.7 started to be neutralized at week 3, although less efficiently than D614G. B.1.1.7 and D614G strains were similarly neutralized at week 4 (1 week after booster dose).	B.1.1.7, Q.3, Q.1	Planas et al. (2021)	70911	TTTA	T	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.Y144del	vaccine neutralization efficacy	After one dose, individuals with prior infection showed enhanced T cell immunity, antibody secreting memory B cell response to spike and neutralizing antibodies effective against B.1.1.7 (authentic cell culture supernatants). By comparison, HCW receiving one vaccine dose without prior infection showed reduced immunity against variants. B.1.1.7 spike mutations resulted in increased, abrogated or unchanged T cell responses depending on human leukocyte antigen (HLA) polymorphisms. Study was 26 each post-infection and post first dose HCWs.	B.1.1.7, Q.3, Q.1	Reynolds et al. (2021)	70911	TTTA	T	nan
p.Y144del	vaccine neutralization efficacy	The NAb titers (PRNT50) of sera collected from 38 vaccine recipients four-weeks after the second dose of inactivated whole-virion SARS-CoV-2 BBV152/COVAXIN vaccine [which contains D614G] were not significantly different between B.1.1.7 virus and ancestral D614G virus.	B.1.1.7, Q.3, Q.1	Sapkal et al. (2021)	70911	TTTA	T	nan
p.Y144del	vaccine neutralization efficacy	Pseudotyped B.1.1.7 Spike variants lentivirus. 3.5x reduction in neutralization with Moderna vaccinated patient sera after 29 days (1st dose). 2.0x reduction in neutralization with Moderna vaccinated patient sera after 57 days (2nd dose). 2.1x reduction in neutralization with Novavax Phase 1 post-vaccination sera.	B.1.1.7, Q.3, Q.1	Shen et al. (2021)	70911	TTTA	T	nan
p.Y144del	vaccine neutralization efficacy	Neutralization assays of B.1.1.7 virus showed a reduction of 2.5-fold (14 days post 2nd dose AstraZeneca, n	B.1.1.7, Q.3, Q.1	Supasa et al. (2021)	70911	TTTA	T	nan
p.Y144del	vaccine neutralization efficacy	Vaccine elicited antibodies neutralized virus with the B.1.1.7 spike protein with titers similar to D614G virus. Serum specimens from individuals vaccinated with the BNT162b2 mRNA vaccine neutralized D614G virus with titers that were on average 7-fold greater than convalescent sera.	B.1.1.7, Q.3, Q.1	Tada et al. (2021)	70911	TTTA	T	nan
p.Y144del	vaccine neutralization efficacy	PBMCs of Pfizer/BioNTech BNT162b2 (n	B.1.1.7, Q.3, Q.1	Tarke et al. (2021)	70911	TTTA	T	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.Y144del	vaccine neutralization efficacy	1.4x improvement in neutralization by serum collected 2 to 3 weeks after the second dose from vaccinees who had received BBIBP-CorV (pVNT50 against VSV pseudotyped as B.1.1.7). Convalescent plasma had similar titer against wild type as the BBIBP-CorV vaccinee sera. 2x reduction in neutralization by serum collected 2 to 3 weeks after the second dose from vaccinees who had received CoronaVac (pVNT50 against VSV pseudotyped as B.1.1.7). Convalescent plasma had similar titer against wild type as the CoronaVac vaccinee sera.	B.1.1.7, Q.3, Q.1	Wang et al. (2021)	70911	TTTA	T	nan
p.Y144del	vaccine neutralization efficacy	No significant difference in T-cell response to B.1.1.7 was observed (vs. ancestral) in blood drawn from 28 participants received the Pfizer-BioNTech vaccine and 2 received the Moderna vaccine. This is despite three mutations (Y144del, D614G, and P681H) overlapping T-cell epitope hotspots.	B.1.1.7, Q.3, Q.1	Woldemeskel et al. (2021)	70911	TTTA	T	nan
p.Y144del	vaccinee plasma binding	1.08x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in previously non-seroconverted subjects. 1.11x 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.	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Gong et al. (2021)	70921	TTTA	T	nan
p.Y144del	vaccinee plasma binding	This variant combination (representing B.1.1.7 aka Alpha) showed no change in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in previously non-seroconverted subjects. 1.28x 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.1.1.7, Q.3, Q.1	Gong et al. (2021)	70911	TTTA	T	nan
p.Y144del	viral load	Using lack of S probe detection as a proxy for B.1.1.7 status, 275 putative B.1.1.7 samples and 390 "wild type" SARS-CoV-2 positive samples in Wales were compared for Ct values, suggesting extasciitilde12-fold increase (extasciitilde3.5 Ct decrease) in viral load for B.1.1.7 samples.	B.1.1.7, Q.3, Q.1	Couzens et al. (2021)	70911	TTTA	T	nan
p.Y144del	viral load	We found that the British variant (clade B.1.1.7), compared to an ancestral SARS-CoV-2 clade B virus, produced higher levels of infectious virus late in infection and had a higher replicative fitness in human airway, alveolar and intestinal organoid models.	B.1.1.7, Q.3, Q.1	Lamers et al. (2021)	70911	TTTA	T	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.Y144del	viral load	This study reveals that B.1.1.7 SARS-CoV-2 variant is a slower-growing virus than parental B.1. Further, a higher replication along with reduced infectious viral titer was hypothesized to be linked to higher transmission with reduced pathogenicity.	B.1.1.7, Q.3, Q.1	Nyayanit et al. (2021)	70911	TTTA	T	nan
p.Y144del	viral load	In a study of 1260 ICU subjects, viral load distributions (collected within 48h of admission) were elevated in both seropositive and seronegative subjects infected with B.1.1.7 ("UK variant"). PG: The PANGO tool defining Spike variants for B.1.1.7 are listed here, whereas the paper only used a test for D1118H.	B.1.1.7, Q.3, Q.1	Ratcliff et al. (2021)	70911	TTTA	T	nan
p.Y144del	viral load	B.1.1.7 samples showed average Ct cycle threshold of 21.9 vs 23 for wildtype (i.e. extasciitilde2x higher viral load) comparing 37758 and 22535 samples respectively.	B.1.1.7, Q.3, Q.1	Roquebert et al. (2021)	70911	TTTA	T	nan
p.Y144del	viral load	The median Ct value of RT-qPCR tests of the N-gene target in the Daxing B.1.1.7 group was significantly lower than the Shunyi B.1.470 group (P	B.1.1.7, Q.3, Q.1	Song et al. (2021)	70911	TTTA	T	nan
p.Y144del	viral load	The 249 B.1.1.7 (a.k.a. N501Y.V1) variant cases in three Paris hospital labs had a extasciitilde10-fold viral load increase (extasciitilde3.3 Ct drop in N gene probe) compared to 332 ancestral lineage cases from the same time frame (2020-12-20 to 2021-02-26). PG: BUT there is a discrepancy in drop between the ORF1ab and N probes, with the former suggesting only a 2-fold drop, consistent with the drop observed in B.1.351. This might indicate higher subgenomic RNA content in B.1.1.7 skewing the change.	B.1.1.7, Q.3, Q.1	Teyssou et al. (2021)	70911	TTTA	T	nan
p.Y144del	virion structure	CryoEM analysis of B.1.1.7 demonstrates an increased propensity for 'up', receptor accessible conformation of the Spike protein trimer.	B.1.1.7, Q.3, Q.1	Cai et al. (2021)	70911	TTTA	T	nan
p.H69del	ACE2 receptor binding affinity	Six fold increase in affinity for ACE2 by the B.1.1.7 lineage vs wild type is driven by a drop in observed dissociation rate constant.	B.1.1.7, Q.3, Q.1	Collier et al. (2021)	36460	ATACATG	A	nan
p.H69del	ACE2 receptor binding affinity	Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant showed a 1.51x increase in binding (KD) relative to D614G, mostly due to decreased in "off-rate" a.k.a. dissociation rate (Kdis).	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Gong et al. (2021)	36470	ATACATG	A	nan
p.H69del	ACE2 receptor binding affinity	Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant combination (representing B.1.1.7 aka Alpha) had 5.43x increased binding relative to D614G alone.	B.1.1.7, Q.3, Q.1	Gong et al. (2021)	36460	ATACATG	A	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.H69del	ACE2 receptor binding affinity	Flow cytometry was used on recombinant VSV proteins and yeast surface display to assess the binding of a labeled soluble ACE2 protein to cells expressing B.1.1.7. We observed a dramatic increase (relative to D614G) in binding of soluble ACE2 to B.1.1.7, and to a lesser extent to B.1.351, which both carry the N501Y mutation (see Fig 3).	B.1.1.7, Q.3, Q.1	Planas et al. (2021)	36460	ATACATG	A	nan
p.H69del	ACE2 receptor binding affinity	This mutation combination causes major increase in binding affinity vs. wild type as measured by IC50 vs pseudotyped lentivirus, but combined with the complete set of B.1.1.7 lineage variants no major change vs wild type affnity is observed.	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Tada et al. (2021)	36470	ATACATG	A	nan
p.H69del	ACE2 receptor binding affinity	This mutation causes major decrease in binding affinity vs. wild type as measured by IC50 vs pseudotyped lentivirus.	B.1.1.7, Q.3, Q.1	Tada et al. (2021)	36460	ATACATG	A	nan
p.H69del	anthropozoonotic events	First documented cases of domestic cat and dog infections with the B.1.1.7 strain.	B.1.1.7, Q.3, Q.1	Hamer et al. (2021)	36460	ATACATG	A	nan
p.H69del	antibody epitope effects	Ablates Class 3 N-terminal domain targeting antibody COV2-2489, diminishes COV2-2676.	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Chen et al. (2021)	36470	ATACATG	A	nan
p.H69del	antibody epitope effects	extasciitilde20x resistence to mAb CQ038 by B.1.1.7 pseudotyped virus	B.1.1.7, Q.3, Q.1	Hu et al. (2021)	36460	ATACATG	A	nan
p.H69del	antibody epitope effects	Reduces neutralization by structurally unmapped mAb COVA1-21 (cluster XI).	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Rees-Spear et al. (2021)	36470	ATACATG	A	nan
p.H69del	antibody epitope effects	Lessens the potency of mAbs COVA2-17 (extasciitilde5x, similar to N501Y alone), COVA1-12 (extasciitilde11x) and COVA1-21 (>100x), which do not compete allosterically.	B.1.1.7, Q.3, Q.1	Rees-Spear et al. (2021)	36460	ATACATG	A	nan
p.H69del	antibody epitope effects	Reduction in neutralization by mAbs COVA1-18 (extasciitilde4x), COVA2-15 (extasciitilde9x). PG: these effects are laregly missing in the deletion-alone data	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Shen et al. (2021)	36470	ATACATG	A	nan
p.H69del	antibody epitope effects	Reduction in neutralization by mAbs COVA2-15 (extasciitilde9x), B38 (extasciitilde14x), S309 (extasciitilde190x) by this B.1.1.7 pseudotyped virus model.	B.1.1.7, Q.3, Q.1	Shen et al. (2021)	36460	ATACATG	A	nan
p.H69del	antibody epitope effects	B.1.1.7 pseudotyped virus model impairs binding by RBD-directed mAb 910-30. B.1.1.7 pseudotyped virus model abolishes N-terminal-domain-directed mAbs 5-24, 4-8, and 4A8. B.1.1.7 pseudotyped virus model impairs binding by N-terminal-domain-directed mAbs 2-17, 4-19, 5-7.	B.1.1.7, Q.3, Q.1	Wang et al. (2021)	36460	ATACATG	A	nan
p.H69del	clinical indicators	After adjusting for the age factor, in a prospective Chinese cohort study B.1.1.7 variant infection (compared to B.1.140) was the risk factor for C-reactive protein (P	B.1.1.7, Q.3, Q.1	Song et al. (2021)	36460	ATACATG	A	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.H69del	convalescent plasma binding	1.33x increase in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset.	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Gong et al. (2021)	36470	ATACATG	A	nan
p.H69del	convalescent plasma binding	This variant combination (representing B.1.1.7 aka Alpha) showed a 1.15x increase in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset.	B.1.1.7, Q.3, Q.1	Gong et al. (2021)	36460	ATACATG	A	nan
p.H69del	convalescent plasma escape	One convalescent sera tested showed 4-fold or greater reduction in neutralization efficiency.	Q.8, Q.3, Q.1, B.1.1.7	Alenquer et al. (2021)	36468	ATACATG	A	nan
p.H69del	convalescent plasma escape	Slight neutralization improvement on average in 16 health workers' convalescent sera.	Q.8, Q.3, Q.1, B.1.1.7	Alenquer et al. (2021)	36468	ATACATG	A	nan
p.H69del	convalescent plasma escape	Neutralization capacity GMT of 27 subjects' sera post-infection was considerably higher (stronger) than after the second Pfizer dose, and 4.5x drop in B.1.1.7 neutralization was observed.	B.1.1.7, Q.3, Q.1	Collier et al. (2021)	36460	ATACATG	A	nan
p.H69del	convalescent plasma escape	NTD-specific nAbs showed a substantial (3-450x) decrease in neutralization potency against the recently reported highly transmissible B.1.1.7 variant of concern, whereas RBD-specific nAbs were either unaffected or showed lower decreases in potency.	B.1.1.7, Q.3, Q.1	Graham et al. (2021)	36460	ATACATG	A	nan
p.H69del	convalescent plasma escape	Neutralizing antibody titers of 2/20 (10%) samples showed >10x reduction (sera collected extasciitilde1mo post Jan 2020 first wave in China). Neutralizing antibody titers of 8/20 samples (40%) decreased below an ID50 threshold of 40 (sera collected extasciitilde8mo post Jan 2020 first wave in China).	B.1.1.7, Q.3, Q.1	Hu et al. (2021)	36460	ATACATG	A	nan
p.H69del	convalescent plasma escape	Fatal COVID-19 complications in immunocomprimised patient after immune escape from convalescent plasma	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Kemp et al. (2020)	36470	ATACATG	A	nan
p.H69del	convalescent plasma escape	Using a new rapid neutralization assay, based on reporter cells that become positive for GFP after overnight infection, sera from 58 convalescent individuals collected up to 9 months after symptoms, similarly neutralized B.1.1.7 and D614G.	B.1.1.7, Q.3, Q.1	Planas et al. (2021)	36460	ATACATG	A	nan
p.H69del	convalescent plasma escape	Maximum fold-decrease in potency for the serum samples from mild illness was 8.2 but the majority of samples showed less than a 3-fold change. Similarly, the maximum decrease seen for samples from hospitalized patients was a 9.1-fold change, but most of the samples showed minimal change in the potency of their neutralization. Overall, three samples from each cohort (8%) showed a 5–10-fold reduction, but as they were potently neutralizing sera, the reduced ID50 values were still >1:100.	B.1.1.7, Q.3, Q.1	Rees-Spear et al. (2021)	36460	ATACATG	A	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.H69del	convalescent plasma escape	Neutralization activity of almost all Moderna Phase 1 sera tested actually *increased*.	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Shen et al. (2021)	36470	ATACATG	A	nan
p.H69del	convalescent plasma escape	Neutralization activity of convalescent sera tested decreased <2x with this B.1.1.7 pseudotyped virus.	B.1.1.7, Q.3, Q.1	Shen et al. (2021)	36460	ATACATG	A	nan
p.H69del	convalescent plasma escape	We analyzed 34 convalescent samples including the WHONIBSC 20/130 reference serum, and, although a few sera showed near identical FRNT 50 values, the FRNT50 dilutions for the B.1.1.7 strain were 2.9-fold lower (geometric mean) than those for the Victoria strain ($p < 0.0001$). Sera from 13 subjects post-B.1.1.7 infection showed no significant change in neutralization against Victoria (extasciitildewild type), suggesting that B.1.1.7 infection also protects against ancestral virus. [Note that D1119H was included in the original paper, assuming typographical error and correcting to D1118H]	B.1.1.7, Q.3, Q.1	Supasa et al. (2021)	36460	ATACATG	A	nan
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.	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Tada et al. (2021)	36470	ATACATG	A	nan
p.H69del	convalescent plasma escape	These key B.1.1.7 mutations as a combination neutralized slightly less well than D614G and this was noticeable in the lack of sera with high neutralizing titer for the viruses across 10 convalescent sera from April 2020 infectees.	Q.8, Q.3, Q.1, B.1.1.7	Tada et al. (2021)	36468	ATACATG	A	nan
p.H69del	convalescent plasma escape	Loss of neutralizing activity using 6 hyperimmune immunoglobulin preparations from convalescent plasma was minimal against B.1.1.7 (1.9-fold). Neutralization against 10 convalescent plasma was poorer.	B.1.1.7, Q.3, Q.1	Tang et al. (2021)	36460	ATACATG	A	nan
p.H69del	convalescent plasma escape	The neutralizing activity of 8/20 convalescent sera was significantly lower against this pseudotyped virus model of B.1.1.7, yet almost no effect was detected using the live B.1.1.7 virus.	B.1.1.7, Q.3, Q.1	Wang et al. (2021)	36460	ATACATG	A	nan
p.H69del	environmental condition stability	Treatment with heat, soap and ethanol revealed similar inactivation profiles indicative of a comparable susceptibility towards disinfection. Furthermore, we observed comparable surface stability on steel, silver, copper and face masks.	B.1.1.7, Q.3, Q.1	Meister et al. (2021)	36460	ATACATG	A	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.H69del	environmental condition stability	No differences in the stability of B.1.1.7 observed in the absence of simulated sunlight at either 20°C or 40°C (with a mean time for a 90% loss of viral infectivity across all dark conditions of 6.2 hours). However, a small but statistically significant difference in the stability was observed in simulated sunlight at 20°C and 20% relative humidity, with B.1.1.7 restoring wild type 90% loss time of 11 minutes vs. 7 and 8 minutes for B.1.319 (D614G) and B.28 (V367F) early 2020 viruses respectively.	B.1.1.7, Q.3, Q.1	Schuit et al. (2021)	36460	ATACATG	A	nan
p.H69del	environmental condition stability	Relative to D614G, this mutation demonstrated significant increase in infectivity (i.e. heat stability) after incubation at 50C after 1 hour.	Q.8, Q.3, Q.1, B.1.1.7	Tada et al. (2021)	36468	ATACATG	A	nan
p.H69del	immunosuppression variant emergence	The delH69/V70 enhances viral infectivity, indicating its effect on virus fitness is independent to the N501Y RBM change [with which it is found in lineage B.1.1.7] Possibly arisen as a result of the virus evolving from immune selection pressure in infected individuals and possibly only one chronic infection in the case of lineage B.1.1.7.	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Kemp et al. (2020)	36470	ATACATG	A	nan
p.H69del	outcome hazard ratio	Danish study of the B.1.1.7 lineage shows hospital admission odds ratio of 1.63 vs other lineages. The adjusted OR was increased in all strata of age.	B.1.1.7, Q.3, Q.1	Bager et al. (2021)	36460	ATACATG	A	nan
p.H69del	outcome hazard ratio	The mortality hazard ratio associated with infection with [B.1.1.7] compared with infection with previously circulating variants was 1.64 (95% confidence interval 1.32 to 2.04) in patients who tested positive for covid-19 in the community (54906 matched pairs of participants who tested positive for SARS-CoV-2 in pillar 2 between 1 October 2020 and 29 January 2021). In this comparatively low risk group, this represents an increase in deaths from 2.5 to 4.1 per 1000 detected cases.	B.1.1.7, Q.3, Q.1	Challen et al. (2021)	36460	ATACATG	A	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.H69del	outcome hazard ratio	Using UK data 1 November 2020 to 14 February 2021, while correcting for misclassification of PCR test Spike Gene Target Failure (SGTF) and missingness in SGTF status, we estimate that the hazard of death associated with B.1.1.7 is 61% (42–82%) higher than with pre-existing variants after adjustment for age, sex, ethnicity, deprivation, residence in a care home, the local authority of residence and test date. This corresponds to the absolute risk of death for a 55–69-year-old man increasing from 0.6% to 0.9% (95% confidence interval, 0.8–1.0%) within 28 days of a positive test in the community.	B.1.1.7, Q.3, Q.1	Davies et al. (2021)	36460	ATACATG	A	nan
p.H69del	outcome hazard ratio	341 samples collected Nov 9 to Dec 20, 2020 were sequenced from two London (UK) hospitals. 198 (58%) of 341 had B.1.1.7 infection and 143 (42%) had non-B.1.1.7 infection. No evidence was found of an association between severe disease and death and lineage (B.1.1.7 vs non-B.1.1.7) in unadjusted analyses (prevalence ratio [PR] 0 · 97 [95% CI 0 · 72-1 · 31]), or in analyses adjusted for hospital, sex, age, comorbidities, and ethnicity (adjusted PR 1 · 02 [0 · 76-1 · 38]).	B.1.1.7, Q.3, Q.1	Frampton et al. (2021)	36460	ATACATG	A	nan
p.H69del	outcome hazard ratio	On average across 7 European countries studied, using B.1.1.7 defining mutations: Significant shift to asymptomatic cases (27.4% vs 18.6% for non-VOC cases). Significant shift to infection in those without pre-existing conditions (44.8% vs 89% for non-VOC cases). Significant increase in hospitalization rate (11% vs 7.5% for non-VOC cases). Significant increase in ICU rate (1.4% vs 0.6% for non-VOC cases). Significant decrease in death rate (2.0% vs vs 4.0% for non-VOC cases).	B.1.1.7, Q.3, Q.1	Funk et al. (2021)	36460	ATACATG	A	nan
p.H69del	outcome hazard ratio	From Sept 28 to Dec 27, 2020, positive COVID-19 tests were reported by 36 920 COVID Symptom Study app users whose region was known and who reported as healthy on app sign-up. We found no changes in reported symptoms or disease duration associated with B.1.1.7.	B.1.1.7, Q.3, Q.1	Graham et al. (2021)	36460	ATACATG	A	nan
p.H69del	outcome hazard ratio	Using primarily S-defining mutations for lineage B.1.1.7, most models of hospitalization and fatality risk ratios from consortium members show elevated ratios (extasciitilde1.3-1.7x).	B.1.1.7, Q.3, Q.1	NERVTAG Consortium (2021)	36460	ATACATG	A	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.H69del	outcome hazard ratio	The matching-adjusted conditional odds ratio of hospitalisation was 1.58 (95% confidence interval 1.50 to 1.67) for COVID-19 patients infected with a SGTF-associated variant [primarily B.1.1.7], compared to those infected with non-SGTF-associated variants. The effect was modified by age (p<0.001), with ORs of 0.96-1.13 below age 20 years and 1.57-1.67 in age groups 40 years or older.	B.1.1.7, Q.3, Q.1	Nyberg et al. (2021)	36460	ATACATG	A	nan
p.H69del	reinfection	36920 COVID Symptom Study app users reported SARS-CoV-2 test positivity in late 2020. Possible reinfections were identified in 249 (0.7% [95% CI 0.6-0.8]) of 36509 app users who reported a positive swab test before Oct 1, 2020, but there was no evidence that the frequency of reinfections was higher for the B.1.1.7 variant than for pre-existing variants.	B.1.1.7, Q.3, Q.1	Graham et al. (2021)	36460	ATACATG	A	nan
p.H69del	reinfection	Second infection in December 2020 with B.1.1.7 after April 2020 initial infection with B.2 in a 78-year-old man with a history of Type 2 diabetes mellitus, diabetic nephropathy on hemodialysis, chronic obstructive pulmonary disease (COPD), mixed central and obstructive sleep apnea, ischemic heart disease, with no history of immunosuppression.	B.1.1.7, Q.3, Q.1	Harrington et al. (2021)	36460	ATACATG	A	nan
p.H69del	reinfection	Reinfection with Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) B.1.1.7 variant in an immunocompromised 16yo female with end stage renal disease 94 days after initial infection with a B.1.2 lineage virus. Both lineages were the prevalent one at the time of 1st and 2nd infections respectively in Texas, where the patient was located (suggesting exposure risk rather than lineage immune evasion).	B.1.1.7, Q.3, Q.1	Marquez et al. (2021)	36460	ATACATG	A	nan
p.H69del	symptom prevalence	A higher proportion of cases infected with the B.1.1.7 variant were hypoxic on admission compared to other variants (70.0% vs 62.5%, p	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Snell et al. (2021)	36470	ATACATG	A	nan
p.H69del	symptom prevalence	In comparison of B.1.1.7 lineage (193 cases) vs. "wildtype" (125) in Berlin Jan 18 to March 29 2021, significant symptom changes are absent loss of smell/taste (P	B.1.1.7, Q.8, Q.3, Q.4, Q.1	van Loon et al. (2021)	36470	ATACATG	A	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.H69del	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.1.1.7, Q.3, Q.1	Planas et al. (2021)	36460	ATACATG	A	nan
p.H69del	trafficking	extasciitilde2.5x cleavage of S2 relative to WA1 (D614G) wildtype by Alpha variant variant as measured by mass spectrometry of Vero-TMPRSS culture.	B.1.1.7, Q.3, Q.1	Esclera et al. (2021)	36460	ATACATG	A	nan
p.H69del	trafficking	VSV pseudotype B.1.1.7 showed no significant difference in cell entry relative to wild type in 6 cell lines. Cell fusion proficiency was unchanged.	B.1.1.7, Q.3, Q.1	Hoffman et al. (2021)	36460	ATACATG	A	nan
p.H69del	trafficking	The entry efficiencies of Spike pseudotyped viruses bearing N501Y Variant 1 (B.1.1.7) mutant were about 3 to 4.4 times higher than that of the WT pseudovirus when viral input was normalized, suggesting that these spike variants promote the infectivity of SARS-CoV-2.	B.1.1.7, Q.3, Q.1	Hu et al. (2021)	36460	ATACATG	A	nan
p.H69del	trafficking	Lentiviral pseudotyped with this mutation set from B.1.1.7 was tested on ACE2.293T cells. Luciferase activity was measured two days postinfection, showing significant (40%) increase in infection rate amongst the cells, much more than the effect of either the deletion or the point mutation alone, suggetsing that this combination has a synergistic effect contributing to cell entry fitness, moreso than this combination with the addition of P681H.	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Tada et al. (2021)	36470	ATACATG	A	nan
p.H69del	trafficking	Lentiviral pseudotyped with this mutation set from B.1.1.7 was tested on ACE2.293T cells. Luciferase activity was measured two days postinfection, showing significant (40%) increase in infection rate amongst the cells, much more than the effect of either the deletion or the point mutation alone, suggetsing that this combination has a synergistic effect contributing to cell entry fitness, but to a smaller extent than N501Y and the deletion alone.	Q.8, Q.3, Q.1, B.1.1.7	Tada et al. (2021)	36468	ATACATG	A	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.H69del	trafficking	Live virus was tested ex vivo in reconstituted brochial epithelium, and out competed wild type.	B.1.1.7, Q.3, Q.1	Touret et al. (2021)	36460	ATACATG	A	nan
p.H69del	transmissibility	We estimate that this [B.1.1.17] variant has a 43–90% (range of 95% credible intervals 38–130%) higher reproduction number than preexisting variants. Data from other countries yield similar results: we estimate that R for VOC 202012/01 relative to other lineages is 55% (45–66%) higher in Denmark, 74% (66–82%) higher in Switzerland, and 59% (56–63%) higher in the United States, with consistent rates of displacement across regions within each country.	B.1.1.7, Q.3, Q.1	Davies et al. (2021)	36460	ATACATG	A	nan
p.H69del	transmissibility	Based on 36920 COVID Symptom Study app users reported SARS-CoV-2 test positivity in late 2020, Rt of B.1.1.7 was 1.35x (95% CI 1.02-1.69) relative to pre-existing variants. However, Rt fell below 1 during regional and national lockdowns, even in regions with high proportions of infections with the B.1.1.7 variant.	B.1.1.7, Q.3, Q.1	Graham et al. (2021)	36460	ATACATG	A	nan
p.H69del	transmissibility	Ontario, Feb 2021: The secondary attack rate for VOC index cases in this matched cohort was 1.31 times higher than non-VOC index cases (RR	B.1.1.7, Q.3, Q.1	Lindstrøm et al. (2021)	36460	ATACATG	A	nan
p.H69del	transmissibility	Primary cases infected with B.1.1.7 had an increased transmissibility of 1.5-1.7 times that of primary cases infected with other lineages. The increased transmissibility of B.1.1.7 was multiplicative across age and viral load.	B.1.1.7, Q.3, Q.1	Lyngse et al. (2021)	36460	ATACATG	A	nan
p.H69del	transmissibility	Based on 300,000 RT-PCR samples collected from December 6th 2020 to February 10th 2021 in Israel, the B.1.1.7 is 45% (95% CI:20-60%) more transmissible than the wild-type strain, and become dominant in Israel within 3.5 weeks.	B.1.1.7, Q.3, Q.1	Munitz et al. (2021)	36460	ATACATG	A	nan
p.H69del	transmissibility	At the national level (Italy), we estimated a mean relative transmissibility of B.1.1.7 (compared to historical lineages) ranging between 1.55 and 1.57 (with confidence intervals between 1.45 and 1.66).	B.1.1.7, Q.3, Q.1	Stefanelli et al. (2021)	36460	ATACATG	A	nan
p.H69del	vaccine efficacy	In Minnesota in early 2021 when Alpha was prevalent, vaccine efficacy was estimated as: mRNA-1273 86% (95%CI: 81-90.6%) and BNT162b2: 76% (95%CI: 69-81%) using age, sex, race, PCR testing and vaccination date matched cohorts of unvaccinated, Pfizer and Moderna vaccinees. [variant list included is ancestral Alpha, as this was an observational study no variant list was given]	B.1.1.7, Q.3, Q.1	Puranik et al. (2021)	36460	ATACATG	A	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.H69del	vaccine neutralization efficacy	nan	B.1.1.7, Q.3, Q.1	All vaccinees were on a strict 3 week interval for second dose (	36460	ATACATG	A	nan
p.H69del	vaccine neutralization efficacy	Between December 19, 2020 and Jan 24, 2021, 7214 of 9109 eligible HCWs at Sheba Medical Center in Israel had received one or more doses of BNT162b2 (Pfizer) vaccine. Adjusted rate reduction in SARS-CoV-2 NAAT positivity infection compared with unvaccinated workers 1-14 days after 1st dose was 30% (95% CI: 2-50), and 75% (95% CI: 72-84) after 15-28 days. Adjusted rate reduction in symptomatic COVID-19 compared with unvaccinated workers 1-14 days after 1st dose was 47% (95% CI: 17-66), and 85% (95% CI: 71-92) after 15-28 days. [Though often cited as an indicator of VE for B.1.1.7, during this time period in Israel, the prevalence of the B.1.1.7 variant increased from extasciitilde20% to 50% of cases (covariants.org), therefore these VE numbers likely represent a mix of B.1.1.7 and other lineage effects.]	B.1.1.7, Q.3, Q.1	Amit et al. (2021)	36460	ATACATG	A	nan
p.H69del	vaccine neutralization efficacy	Neutralization efficiency (ID50) against B.1.1.7 reduced 1.2x relative to D614G wildtype using pseudotyped VSV assay on 8 Moderna vaccinee sera one week post-booster.	B.1.1.7, Q.3, Q.1	Choi et al. (2021)	36460	ATACATG	A	nan
p.H69del	vaccine neutralization efficacy	20/29 sera after the first dose of Pfizer showed an average reduction in neutralization titres against the B.1.1.7 variant of 3.2 ± 5.7. After the second dose, the GMT was markedly increased compared with the first-dose titres, with a fold change of 1.9 ± 0.9 (mean ± s.d.). Neutralization GMT of 27 subjects post-infection was considerably higher (stronger) than after the second Pfizer dose, and 4.5x drop in B.1.1.7 neutralization was observed.	B.1.1.7, Q.3, Q.1	Collier et al. (2021)	36460	ATACATG	A	nan
p.H69del	vaccine neutralization efficacy	2.1x drop in neutralization using sera collected from 14 healthy adult participants that received two injections of the mRNA-1273 (Moderna) vaccine at a dose of 100 µg (18-55 years: day 1 (n	B.1.1.7, Q.3, Q.1	Edara et al. (2021)	36460	ATACATG	A	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.H69del	vaccine neutralization efficacy	Virus neutralisation activity (using a live SARS-CoV-2 microneutralisation assay (ND50)) by vaccine induced antibodies was 9-fold lower against the B.1.1.7 variant than against a canonical non B.1.1.7 lineage. Vaccine efficacy against symptomatic NAAT positive infection was similar for B.1.1.7 and non-B.1.1.7 lineages (74.6% [95%CI 41.6-88.9] and 84% [95% CI 70.7-91.4] respectively). Furthermore, vaccination with ChAdOx1 nCoV-19 results in a reduction in the duration of shedding and viral load, which may translate into a material impact on transmission of disease.	B.1.1.7, Q.3, Q.1	Emary et al. (2021)	36460	ATACATG	A	nan
p.H69del	vaccine neutralization efficacy	ELISpot assays show T cell neutralization reduced by 15.4% in this B.1.1.7 pseudotype relative to wild type in 18-20 pooled patient samples post second mRNA vaccine dose, with no significant difference between Pfizer and Moderna cohorts. Reduction was stronger in the S1 subunit than S2 (separate peptide pools were used).	B.1.1.7, Q.3, Q.1	Gallagher et al. (2021)	36460	ATACATG	A	nan
p.H69del	vaccine neutralization efficacy	Pseudotyped B.1.1.7 virus has reduced neutralization activity vs wild type: 2.1x (30 sera Pfizer median 9 days post 2nd dose) and 2.3x (35 sera Moderna median 18 days post 2nd dose). This was NOT significant by ANOVA. Note that Y145del was actually noted in the paper as the effect of their DNA construct, but this is equivalent at the protein level to the more commonly annotated Y144del.	B.1.1.7, Q.3, Q.1	Garcia-Beltran et al. (2021)	36460	ATACATG	A	nan
p.H69del	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)	B.1.1.7, Q.3, Q.1	Gong et al. (2021)	36460	ATACATG	A	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.H69del	vaccine neutralization efficacy	Using national surveillance data from Israel, using Pfizer vaccine and an estimated prevalence of the B.1.1.7 variant of 94.5% among SARS-CoV-2 infections: Adjusted estimates of vaccine effectiveness 7+ days after second dose were 95 · 3% (95% CI 94.9–95.7): 91.5% against asymptomatic SARS-CoV-2 infection (90 · 7–92 · 2: 40.9 vs 1.8 per 100 000 person-days), 97 · 0% against symptomatic COVID-19 (96.7–97.2%), 97.2% against COVID-19-related hospitalisation (96.8–97.5%), 97.5% against severe or critical COVID-19-related hospitalisation (97.1–97.8%), and 96.7% against COVID-19-related death (96.0–97.3%). In all age groups, as vaccine coverage increased, the incidence of SARS-CoV-2 outcomes declined	B.1.1.7, Q.3, Q.1	Haas et al. (2021)	36460	ATACATG	A	nan
p.H69del	vaccine neutralization efficacy	A single dose of BNT162b2 (Pfizer) vaccine showed vaccine effectiveness of 70% (95% CI 55-85) 21 days after first dose and 85% (74-96) 7 days after two doses in the study population. Our findings show that the BNT162b2 vaccine can prevent both symptomatic and asymptomatic infection in working-age adults. This cohort (8203 treatment, 15121 control) was vaccinated when the dominant variant in circulation was B.1.1.7 and shows effectiveness against this variant.	B.1.1.7, Q.3, Q.1	Hall et al. (2021)	36460	ATACATG	A	nan
p.H69del	vaccine neutralization efficacy	A single dose of BNT162b2 vaccine demonstrated vaccine effectiveness [symptomatic or asymptomatic in cohort opf routinely NAAT-monitored UK HCWs] of 72% (95% CI 58-86) 21 days after first dose and 86% (95% CI 76-97) seven days after two doses in the antibody negative cohort. This cohort was vaccinated when the dominant variant in circulation was B.1.1.7 and demonstrates effectiveness against this variant.	B.1.1.7, Q.3, Q.1	Hall et al. (2021)	36460	ATACATG	A	nan
p.H69del	vaccine neutralization efficacy	NVX-CoV2373 [Novavax] vaccine in phase 3 trial was 89.7% (95% CI, 80.2-94.6) effective in preventing COVID-19, with no hospitalizations or deaths reported. There were five cases of severe Covid-19, all in the placebo group. Post hoc analysis revealed efficacies of 96.4% (73.8-99.5) and 86.3% (71.3-93.5) against the prototype strain and B.1.1.7 variant, respectively.	B.1.1.7, Q.3, Q.1	Heath et al. (2021)	36460	ATACATG	A	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.H69del	vaccine neutralization efficacy	VSV pseudotype B.1.1.7 showed 1.77-fold reduction in neutralization efficiency vs wild type in 15 Pfizer BNT162b2 vaccinee sera 13-15 days post second dose. Cell fusion proficiency was unchanged.	B.1.1.7, Q.3, Q.1	Hoffman et al. (2021)	36460	ATACATG	A	nan
p.H69del	vaccine neutralization efficacy	B.1.1.7 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 no statistically sognificant change in neutralization effiacacy.	B.1.1.7, Q.3, Q.1	Ikegame et al. (2021)	36460	ATACATG	A	nan
p.H69del	vaccine neutralization efficacy	Neutralizing antibody titers increased in previously infected vaccinees relative to uninfected vaccinees 5.2-fold against B.1.1.7 (contrast with 3.4 fold against original SARS-CoV-2).	B.1.1.7, Q.3, Q.1	Leier et al. (2021)	36460	ATACATG	A	nan
p.H69del	vaccine neutralization efficacy	SARS-CoV-2 infection was confirmed in three HCWs working a single shift: all presented with mild symptoms of COVID-19. The two physicians were fully vaccinated with BNT162b2 vaccine, with the second dose administered 1 month before symptom onset. Both had high titres of IgG anti-spike antibodies at the time of diagnosis. WGS confirmed that all virus strains were VOC 202012/01-lineage B.1.1.7, suggesting a common source of exposure. Epidemiological investigation revealed that the suspected source was a SARS-CoV-2-positive patient who required endotracheal intubation due to severe COVID-19. All procedures were carried out using a full suite of personal protective equipment (PPE).	B.1.1.7, Q.3, Q.1	Loconsole et al. (2021)	36460	ATACATG	A	nan
p.H69del	vaccine neutralization efficacy	We found that a single dose of the BNT162b2 vaccine is about 60-70% effective at preventing symptomatic disease in adults aged 70 years and older in England and that two doses are about 85-90% effective. Those who were vaccinated and went on to have symptoms had a 44% lower risk of being admitted hospital and a 51% lower risk of death compared with people who were unvaccinated. We also found that a single dose of the ChAdOx1-S vaccine was about 60-75% effective against symptomatic disease and provided an additional protective effect against hospital admission—it is too early to assess the effect on mortality. The B.1.1.7 variant now dominates in the UK and these results will largely reflect vaccine effectiveness against this variant.	B.1.1.7, Q.3, Q.1	Lopez Bernal et al. (2021)	36460	ATACATG	A	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.H69del	vaccine neutralization efficacy	In sera 1-2 weeks after BNT162b2 first dose, from six patients previously infected with B.1, antibody titer in a microneutralization assay was on average 8192 for B.1.351 virus. This compares favorably (stronger) to post-infection neutralization titer against all variants tested in the same sera (wild type, B.1.1.7, B.1.351, and P.1).	B.1.1.7, Q.3, Q.1	Luftig et al. (2021)	36460	ATACATG	A	nan
p.H69del	vaccine neutralization efficacy	Lineage B.1.1.7 spike–pseudotyped VSV was tested for neutralization vs Wuhan reference genome pseudotype in 40 sera collected 7 or 21 days post-booster dose. Statistically significant change (22%) in neutralization was observed among the 26 sera from those <	B.1.1.7, Q.3, Q.1	Muik et al. (2021)	36460	ATACATG	A	nan
p.H69del	vaccine neutralization efficacy	We observed a sharp decline in cases when 50% of the elderly population was 2 weeks beyond their first vaccination dose and at a time point during which the B.1.1.7 variant gained transmission dominance. In support of this finding, it was suggested that, after the first vaccination dose, more than 70% of patients develop neutralization antibodies,15 and the vaccine efficiency can reach 85%.	B.1.1.7, Q.3, Q.1	Munitz et al. (2021)	36460	ATACATG	A	nan
p.H69del	vaccine neutralization efficacy	Detectable antibodies against B.1.1.7 at various time points using pseudotyped lentivirus neutralization in Moderna vaccinee cohort: Day 29 33%, Day 43 100%, Day 119 100%, Day 209 96%. Detectable antibodies against B.1.1.7 at various time points using live virus FRNT neutralization in Moderna vaccinee cohort: Day 29 54%, Day 43 100%, Day 119 100%, Day 209 88%. Detectable antibodies against B.1.1.7 at various time points using ACE2 blocking assay in Moderna vaccinee cohort: Day 29 83%, Days 43,119,209 100%.	B.1.1.7, Q.3, Q.1	Pegu et al (2021)	36460	ATACATG	A	nan
p.H69del	vaccine neutralization efficacy	The sera of 16 individuals with time course collection was evaulated against VSV pseudotypes: neutralized D614G at week 2, whereas B.1.1.7 started to be neutralized at week 3, although less efficiently than D614G. B.1.1.7 and D614G strains were similarly neutralized at week 4 (1 week after booster dose).	B.1.1.7, Q.3, Q.1	Planas et al. (2021)	36460	ATACATG	A	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.H69del	vaccine neutralization efficacy	After one dose, individuals with prior infection showed enhanced T cell immunity, antibody secreting memory B cell response to spike and neutralizing antibodies effective against B.1.1.7 (authentic cell culture supernatants). By comparison, HCW receiving one vaccine dose without prior infection showed reduced immunity against variants. B.1.1.7 spike mutations resulted in increased, abrogated or unchanged T cell responses depending on human leukocyte antigen (HLA) polymorphisms. Study was 26 each post-infection and post first dose HCWs.	B.1.1.7, Q.3, Q.1	Reynolds et al. (2021)	36460	ATACATG	A	nan
p.H69del	vaccine neutralization efficacy	The NAb titers (PRNT50) of sera collected from 38 vaccine recipients four-weeks after the second dose of inactivated whole-virion SARS-CoV-2 BBV152/COVAXIN vaccine [which contains D614G] were not significantly different between B.1.1.7 virus and ancestral D614G virus.	B.1.1.7, Q.3, Q.1	Sapkal et al. (2021)	36460	ATACATG	A	nan
p.H69del	vaccine neutralization efficacy	Pseudotyped B.1.1.7 Spike variants lentivirus. 3.5x reduction in neutralization with Moderna vaccinated patient sera after 29 days (1st dose). 2.0x reduction in neutralization with Moderna vaccinated patient sera after 57 days (2nd dose). 2.1x reduction in neutralization with Novavax Phase 1 post-vaccination sera.	B.1.1.7, Q.3, Q.1	Shen et al. (2021)	36460	ATACATG	A	nan
p.H69del	vaccine neutralization efficacy	Neutralization assays of B.1.1.7 virus showed a reduction of 2.5-fold (14 days post 2nd dose AstraZeneca, n	B.1.1.7, Q.3, Q.1	Supasa et al. (2021)	36460	ATACATG	A	nan
p.H69del	vaccine neutralization efficacy	Vaccine elicited antibodies neutralized virus with the B.1.1.7 spike protein with titers similar to D614G virus. Serum specimens from individuals vaccinated with the BNT162b2 mRNA vaccine neutralized D614G virus with titers that were on average 7-fold greater than convalescent sera.	B.1.1.7, Q.3, Q.1	Tada et al. (2021)	36460	ATACATG	A	nan
p.H69del	vaccine neutralization efficacy	PBMCs of Pfizer/BioNTech BNT162b2 (n	B.1.1.7, Q.3, Q.1	Tarke et al. (2021)	36460	ATACATG	A	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.H69del	vaccine neutralization efficacy	1.4x improvement in neutralization by serum collected 2 to 3 weeks after the second dose from vaccinees who had received BBIBP-CorV (pVNT50 against VSV pseudotyped as B.1.1.7). Convalescent plasma had similar titer against wild type as the BBIBP-CorV vaccinee sera. 2x reduction in neutralization by serum collected 2 to 3 weeks after the second dose from vaccinees who had received CoronaVac (pVNT50 against VSV pseudotyped as B.1.1.7). Convalescent plasma had similar titer against wild type as the CoronaVac vaccinee sera.	B.1.1.7, Q.3, Q.1	Wang et al. (2021)	36460	ATACATG	A	nan
p.H69del	vaccine neutralization efficacy	No significant difference in T-cell response to B.1.1.7 was observed (vs. ancestral) in blood drawn from 28 participants received the Pfizer-BioNTech vaccine and 2 received the Moderna vaccine. This is despite three mutations (Y144del, D614G, and P681H) overlapping T-cell epitope hotspots.	B.1.1.7, Q.3, Q.1	Woldemeskel et al. (2021)	36460	ATACATG	A	nan
p.H69del	vaccinee plasma binding	1.14x increase in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in previously non-seroconverted subjects. 1.09x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in post-infection vaccinees.	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Gong et al. (2021)	36470	ATACATG	A	nan
p.H69del	vaccinee plasma binding	This variant combination (representing B.1.1.7 aka Alpha) showed no change in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in previously non-seroconverted subjects. 1.28x 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.1.1.7, Q.3, Q.1	Gong et al. (2021)	36460	ATACATG	A	nan
p.H69del	viral load	Using lack of S probe detection as a proxy for B.1.1.7 status, 275 putative B.1.1.7 samples and 390 "wild type" SARS-CoV-2 positive samples in Wales were compared for Ct values, suggesting extasciitilde12-fold increase (extasciitilde3.5 Ct decrease) in viral load for B.1.1.7 samples.	B.1.1.7, Q.3, Q.1	Couzens et al. (2021)	36460	ATACATG	A	nan
p.H69del	viral load	We found that the British variant (clade B.1.1.7), compared to an ancestral SARS-CoV-2 clade B virus, produced higher levels of infectious virus late in infection and had a higher replicative fitness in human airway, alveolar and intestinal organoid models.	B.1.1.7, Q.3, Q.1	Lamers et al. (2021)	36460	ATACATG	A	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.H69del	viral load	This study reveals that B.1.1.7 SARS-CoV-2 variant is a slower-growing virus than parental B.1. Further, a higher replication along with reduced infectious viral titer was hypothesized to be linked to higher transmission with reduced pathogenicity.	B.1.1.7, Q.3, Q.1	Nyayanit et al. (2021)	36460	ATACATG	A	nan
p.H69del	viral load	In a study of 1260 ICU subjects, viral load distributions (collected within 48h of admission) were elevated in both seropositive and seronegative subjects infected with B.1.1.7 ("UK variant"). PG: The PANGO tool defining Spike variants for B.1.1.7 are listed here, whereas the paper only used a test for D1118H.	B.1.1.7, Q.3, Q.1	Ratcliff et al. (2021)	36460	ATACATG	A	nan
p.H69del	viral load	B.1.1.7 samples showed average Ct cycle threshold of 21.9 vs 23 for wildtype (i.e. extasciitilde2x higher viral load) comparing 37758 and 22535 samples respectively.	B.1.1.7, Q.3, Q.1	Roquebert et al. (2021)	36460	ATACATG	A	nan
p.H69del	viral load	The median Ct value of RT-qPCR tests of the N-gene target in the Daxing B.1.1.7 group was significantly lower than the Shunyi B.1.470 group (P	B.1.1.7, Q.3, Q.1	Song et al. (2021)	36460	ATACATG	A	nan
p.H69del	viral load	The 249 B.1.1.7 (a.k.a. N501Y.V1) variant cases in three Paris hospital labs had a extasciitilde10-fold viral load increase (extasciitilde3.3 Ct drop in N gene probe) compared to 332 ancestral lineage cases from the same time frame (2020-12-20 to 2021-02-26). PG: BUT there is a discrepancy in drop between the ORF1ab and N probes, with the former suggesting only a 2-fold drop, consistent with the drop observed in B.1.351. This might indicate higher subgenomic RNA content in B.1.1.7 skewing the change.	B.1.1.7, Q.3, Q.1	Teyssou et al. (2021)	36460	ATACATG	A	nan
p.H69del	virion structure	CryoEM analysis of B.1.1.7 demonstrates an increased propensity for 'up', receptor accessible conformation of the Spike protein trimer.	B.1.1.7, Q.3, Q.1	Cai et al. (2021)	36460	ATACATG	A	nan
p.H69del	virion structure	The Ratio of S2 (processed Spike) to full length Spike is higher for this mutation combination, due to a drop in the full length Spike measured, suggesting that this mutation compensates for decreased Spike production by improved proteolytic processing.	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Tada et al. (2021)	36470	ATACATG	A	nan
p.H69del	virion structure	The Ratio of S2 (processed Spike) to full length Spike is higher for this mutation combination, due to a drop in the full length Spike measured, suggesting that this mutation compensates for decreased Spike production by improved proteolytic processing.	Q.8, Q.3, Q.1, B.1.1.7	Tada et al. (2021)	36468	ATACATG	A	nan
p.T716I	ACE2 receptor binding affinity	Six fold increase in affinity for ACE2 by the B.1.1.7 lineage vs wild type is driven by a drop in observed dissociation rate constant.	B.1.1.7, Q.3, Q.1	Collier et al. (2021)	37125	C	T	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.T716I	ACE2 receptor binding affinity	Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant showed a 1.12x decrease in binding (KD) relative to D614G.	Q.1, B.1.1.7, Q.3, Q.4	Gong et al. (2021)	37127	C	T	nan
p.T716I	ACE2 receptor binding affinity	Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant combination (representing B.1.1.7 aka Alpha) had 5.43x increased binding relative to D614G alone.	B.1.1.7, Q.3, Q.1	Gong et al. (2021)	37125	C	T	nan
p.T716I	ACE2 receptor binding affinity	Flow cytometry was used on recombinant VSV proteins and yeast surface display to assess the binding of a labeled soluble ACE2 protein to cells expressing B.1.1.7. We observed a dramatic increase (relative to D614G) in binding of soluble ACE2 to B.1.1.7, and to a lesser extent to B.1.351, which both carry the N501Y mutation (see Fig 3).	B.1.1.7, Q.3, Q.1	Planas et al. (2021)	37125	C	T	nan
p.T716I	ACE2 receptor binding affinity	This mutation causes major decrease in binding affinity vs. wild type as measured by IC50 vs pseudotyped lentivirus.	B.1.1.7, Q.3, Q.1	Tada et al. (2021)	37125	C	T	nan
p.T716I	anthropozoonotic events	First documented cases of domestic cat and dog infections with the B.1.1.7 strain.	B.1.1.7, Q.3, Q.1	Hamer et al. (2021)	37125	C	T	nan
p.T716I	anthropozoonotic events	Observed first in a single tiger (cohort of 5), potential adaptation.	Q.1, B.1.1.7, Q.3, Q.4	McAloose et al. (2020)	37127	C	T	nan
p.T716I	antibody epitope effects	Not in a major wildtype epitope, mutant increases PIWAS epitope score from 0.69% to 2.3% Found in B.1.1.7 lineage, but assumed to not pay a major role in antigenicity.	Q.1, B.1.1.7, Q.3, Q.4	Haynes et al. (2021)	37127	C	T	nan
p.T716I	antibody epitope effects	extasciitilde20x resistence to mAb CQ038 by B.1.1.7 pseudotyped virus	B.1.1.7, Q.3, Q.1	Hu et al. (2021)	37125	C	T	nan
p.T716I	antibody epitope effects	Lessens the potency of mAbs COVA2-17 (extasciitilde5x, similar to N501Y alone), COVA1-12 (extasciitilde11x) and COVA1-21 (>100x), which do not compete allosterically.	B.1.1.7, Q.3, Q.1	Rees-Spear et al. (2021)	37125	C	T	nan
p.T716I	antibody epitope effects	Reduction in neutralization by mAbs COVA2-15 (extasciitilde9x), B38 (extasciitilde14x), S309 (extasciitilde190x) by this B.1.1.7 pseudotyped virus model.	B.1.1.7, Q.3, Q.1	Shen et al. (2021)	37125	C	T	nan
p.T716I	antibody epitope effects	B.1.1.7 pseudotyped virus model impairs binding by RBD-directed mAb 910-30. B.1.1.7 pseudotyped virus model abolishes N-terminal-domain-directed mAbs 5-24, 4-8, and 4A8. B.1.1.7 pseudotyped virus model impairs binding by N-terminal-domain-directed mAbs 2-17, 4-19, 5-7.	B.1.1.7, Q.3, Q.1	Wang et al. (2021)	37125	C	T	nan
p.T716I	clinical indicators	After adjusting for the age factor, in a prospective Chinese cohort study B.1.1.7 variant infection (compared to B.1.140) was the risk factor for C-reactive protein (P	B.1.1.7, Q.3, Q.1	Song et al. (2021)	37125	C	T	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.T716I	convalescent plasma binding	1.58x increase in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset.	Q.1, B.1.1.7, Q.3, Q.4	Gong et al. (2021)	37127	C	T	nan
p.T716I	convalescent plasma binding	This variant combination (representing B.1.1.7 aka Alpha) showed a 1.15x increase in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset.	B.1.1.7, Q.3, Q.1	Gong et al. (2021)	37125	C	T	nan
p.T716I	convalescent plasma escape	Neutralization capacity GMT of 27 subjects' sera post-infection was considerably higher (stronger) than after the second Pfizer dose, and 4.5x drop in B.1.1.7 neutralization was observed.	B.1.1.7, Q.3, Q.1	Collier et al. (2021)	37125	C	T	nan
p.T716I	convalescent plasma escape	NTD-specific nAbs showed a substantial (3-450x) decrease in neutralization potency against the recently reported highly transmissible B.1.1.7 variant of concern, whereas RBD-specific nAbs were either unaffected or showed lower decreases in potency.	B.1.1.7, Q.3, Q.1	Graham et al. (2021)	37125	C	T	nan
p.T716I	convalescent plasma escape	Neutralizing antibody titers of 2/20 (10%) samples showed >10x reduction (sera collected extasciitilde1mo post Jan 2020 first wave in China). Neutralizing antibody titers of 8/20 samples (40%) decreased below an ID50 threshold of 40 (sera collected extasciitilde8mo post Jan 2020 first wave in China).	B.1.1.7, Q.3, Q.1	Hu et al. (2021)	37125	C	T	nan
p.T716I	convalescent plasma escape	Using a new rapid neutralization assay, based on reporter cells that become positive for GFP after overnight infection, sera from 58 convalescent individuals collected up to 9 months after symptoms, similarly neutralized B.1.1.7 and D614G.	B.1.1.7, Q.3, Q.1	Planas et al. (2021)	37125	C	T	nan
p.T716I	convalescent plasma escape	Maximum fold-decrease in potency for the serum samples from mild illness was 8.2 but the majority of samples showed less than a 3-fold change. Similarly, the maximum decrease seen for samples from hospitalized patients was a 9.1-fold change, but most of the samples showed minimal change in the potency of their neutralization. Overall, three samples from each cohort (8%) showed a 5–10-fold reduction, but as they were potently neutralizing sera, the reduced ID50 values were still >1:100.	B.1.1.7, Q.3, Q.1	Rees-Spear et al. (2021)	37125	C	T	nan
p.T716I	convalescent plasma escape	Neutralization activity of convalescent sera tested decreased <2x with this B.1.1.7 pseudotyped virus.	B.1.1.7, Q.3, Q.1	Shen et al. (2021)	37125	C	T	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.T716I	convalescent plasma escape	We analyzed 34 convalescent samples including the WHONIBSC 20/130 reference serum, and, although a few sera showed near identical FRNT 50 values, the FRNT50 dilutions for the B.1.1.7 strain were 2.9-fold lower (geometric mean) than those for the Victoria strain ($p < 0.0001$). Sera from 13 subjects post-B.1.1.7 infection showed no significant change in neutralization against Victoria (extasciitildewild type), suggesting that B.1.1.7 infection also protects against ancestral virus. [Note that D1119H was included in the original paper, assuming typographical error and correcting to D1118H]	B.1.1.7, Q.3, Q.1	Supasa et al. (2021)	37125	C	T	nan
p.T716I	convalescent plasma escape	Loss of neutralizing activity using 6 hyperimmune immunoglobulin preparations from convalescent plasma was minimal against B.1.1.7 (1.9-fold). Neutralization against 10 convalescent plasma was poorer.	B.1.1.7, Q.3, Q.1	Tang et al. (2021)	37125	C	T	nan
p.T716I	convalescent plasma escape	The neutralizing activity of 8/20 convalescent sera was significantly lower against this pseudotyped virus model of B.1.1.7, yet almost no effect was detected using the live B.1.1.7 virus.	B.1.1.7, Q.3, Q.1	Wang et al. (2021)	37125	C	T	nan
p.T716I	environmental condition stability	Treatment with heat, soap and ethanol revealed similar inactivation profiles indicative of a comparable susceptibility towards disinfection. Furthermore, we observed comparable surface stability on steel, silver, copper and face masks.	B.1.1.7, Q.3, Q.1	Meister et al. (2021)	37125	C	T	nan
p.T716I	environmental condition stability	No differences in the stability of B.1.1.7 observed in the absence of simulated sunlight at either 20°C or 40°C (with a mean time for a 90% loss of viral infectivity across all dark conditions of 6.2 hours). However, a small but statistically significant difference in the stability was observed in simulated sunlight at 20°C and 20% relative humidity, with B.1.1.7 restoring wild type 90% loss time of 11 minutes vs. 7 and 8 minutes for B.1.319 (D614G) and B.28 (V367F) early 2020 viruses respectively.	B.1.1.7, Q.3, Q.1	Schuit et al. (2021)	37125	C	T	nan
p.T716I	outcome hazard ratio	Danish study of the B.1.1.7 lineage shows hospital admission odds ratio of 1.63 vs other lineages. The adjusted OR was increased in all strata of age.	B.1.1.7, Q.3, Q.1	Bager et al. (2021)	37125	C	T	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.T716I	outcome hazard ratio	The mortality hazard ratio associated with infection with [B.1.1.7] compared with infection with previously circulating variants was 1.64 (95% confidence interval 1.32 to 2.04) in patients who tested positive for covid-19 in the community (54906 matched pairs of participants who tested positive for SARS-CoV-2 in pillar 2 between 1 October 2020 and 29 January 2021). In this comparatively low risk group, this represents an increase in deaths from 2.5 to 4.1 per 1000 detected cases.	B.1.1.7, Q.3, Q.1	Challen et al. (2021)	37125	C	T	nan
p.T716I	outcome hazard ratio	Using UK data 1 November 2020 to 14 February 2021, while correcting for misclassification of PCR test Spike Gene Target Failure (SGTF) and missingness in SGTF status, we estimate that the hazard of death associated with B.1.1.7 is 61% (42–82%) higher than with pre-existing variants after adjustment for age, sex, ethnicity, deprivation, residence in a care home, the local authority of residence and test date. This corresponds to the absolute risk of death for a 55–69-year-old man increasing from 0.6% to 0.9% (95% confidence interval, 0.8–1.0%) within 28 days of a positive test in the community.	B.1.1.7, Q.3, Q.1	Davies et al. (2021)	37125	C	T	nan
p.T716I	outcome hazard ratio	341 samples collected Nov 9 to Dec 20, 2020 were sequenced from two London (UK) hospitals. 198 (58%) of 341 had B.1.1.7 infection and 143 (42%) had non-B.1.1.7 infection. No evidence was found of an association between severe disease and death and lineage (B.1.1.7 vs non-B.1.1.7) in unadjusted analyses (prevalence ratio [PR] 0 · 97 [95% CI 0 · 72-1 · 31]), or in analyses adjusted for hospital, sex, age, comorbidities, and ethnicity (adjusted PR 1 · 02 [0 · 76-1 · 38]).	B.1.1.7, Q.3, Q.1	Frampton et al. (2021)	37125	C	T	nan
p.T716I	outcome hazard ratio	On average across 7 European countries studied, using B.1.1.7 defining mutations: Significant shift to asymptomatic cases (27.4% vs 18.6% for non-VOC cases). Significant shift to infection in those without pre-existing conditions (44.8% vs 89% for non-VOC cases). Significant increase in hospitalization rate (11% vs 7.5% for non-VOC cases). Significant increase in ICU rate (1.4% vs 0.6% for non-VOC cases). Significant decrease in death rate (2.0% vs vs 4.0% for non-VOC cases).	B.1.1.7, Q.3, Q.1	Funk et al. (2021)	37125	C	T	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.T716I	outcome hazard ratio	From Sept 28 to Dec 27, 2020, positive COVID-19 tests were reported by 36 920 COVID Symptom Study app users whose region was known and who reported as healthy on app sign-up. We found no changes in reported symptoms or disease duration associated with B.1.1.7.	B.1.1.7, Q.3, Q.1	Graham et al. (2021)	37125	C	T	nan
p.T716I	outcome hazard ratio	Using primarily S-defining mutations for lineage B.1.1.7, most models of hospitalization and fatality risk ratios from consortium members show elevated ratios (extasciitilde1.3-1.7x).	B.1.1.7, Q.3, Q.1	NERVTAG Consortium (2021)	37125	C	T	nan
p.T716I	outcome hazard ratio	The matching-adjusted conditional odds ratio of hospitalisation was 1.58 (95% confidence interval 1.50 to 1.67) for COVID-19 patients infected with a SGTF-associated variant [primarily B.1.1.7], compared to those infected with non-SGTF-associated variants. The effect was modified by age (p<0.001), with ORs of 0.96-1.13 below age 20 years and 1.57-1.67 in age groups 40 years or older.	B.1.1.7, Q.3, Q.1	Nyberg et al. (2021)	37125	C	T	nan
p.T716I	reinfection	36920 COVID Symptom Study app users reported SARS-CoV-2 test positivity in late 2020. Possible reinfections were identified in 249 (0.7% [95% CI 0.6-0.8]) of 36509 app users who reported a positive swab test before Oct 1, 2020, but there was no evidence that the frequency of reinfections was higher for the B.1.1.7 variant than for pre-existing variants.	B.1.1.7, Q.3, Q.1	Graham et al. (2021)	37125	C	T	nan
p.T716I	reinfection	Second infection in December 2020 with B.1.1.7 after April 2020 initial infection with B.2 in a 78-year-old man with a history of Type 2 diabetes mellitus, diabetic nephropathy on hemodialysis, chronic obstructive pulmonary disease (COPD), mixed central and obstructive sleep apnea, ischemic heart disease, with no history of immunosuppression.	B.1.1.7, Q.3, Q.1	Harrington et al. (2021)	37125	C	T	nan
p.T716I	reinfection	Reinfection with Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) B.1.1.7 variant in an immunocompromised 16yo female with end stage renal disease 94 days after initial infection with a B.1.2 lineage virus. Both lineages were the prevalent one at the time of 1st and 2nd infections respectively in Texas, where the patient was located (suggesting exposure risk rather than lineage immune evasion).	B.1.1.7, Q.3, Q.1	Marquez et al. (2021)	37125	C	T	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.T716I	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.1.1.7, Q.3, Q.1	Planas et al. (2021)	37125	C	T	nan
p.T716I	trafficking	extasciitilde2.5x cleavage of S2 relative to WA1 (D614G) wildtype by Alpha variant variant as measured by mass spectrometry of Vero-TMPRSS culture.	B.1.1.7, Q.3, Q.1	Esclera et al. (2021)	37125	C	T	nan
p.T716I	trafficking	VSV pseudotype B.1.1.7 showed no significant difference in cell entry relative to wild type in 6 cell lines. Cell fusion proficiency was unchanged.	B.1.1.7, Q.3, Q.1	Hoffman et al. (2021)	37125	C	T	nan
p.T716I	trafficking	The entry efficiencies of Spike pseudotyped viruses bearing N501Y Variant 1 (B.1.1.7) mutant were about 3 to 4.4 times higher than that of the WT pseudovirus when viral input was normalized, suggesting that these spike variants promote the infectivity of SARS-CoV-2.	B.1.1.7, Q.3, Q.1	Hu et al. (2021)	37125	C	T	nan
p.T716I	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 major decrease in infection rate amongst the cells, hence this individual variant is unlikely to contribute to cell entry fitness. T716I was expressed at significantly lower level, accounting for the decreased infectivity of this spike protein. This property may be specific to spike protein biosynthesis in 293T cells and is not likely to reflect the situation in vivo given the reported increase in infectivity of the B.1.1.7 virus.	Q.1, B.1.1.7, Q.3, Q.4	Tada et al. (2021)	37127	C	T	nan
p.T716I	trafficking	Live virus was tested ex vivo in reconstituted brochial epithelium, and out competed wild type.	B.1.1.7, Q.3, Q.1	Touret et al. (2021)	37125	C	T	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.T716I	transmissibility	We estimate that this [B.1.1.17] variant has a 43–90% (range of 95% credible intervals 38–130%) higher reproduction number than preexisting variants. Data from other countries yield similar results: we estimate that R for VOC 202012/01 relative to other lineages is 55% (45–66%) higher in Denmark, 74% (66–82%) higher in Switzerland, and 59% (56–63%) higher in the United States, with consistent rates of displacement across regions within each country.	B.1.1.7, Q.3, Q.1	Davies et al. (2021)	37125	C	T	nan
p.T716I	transmissibility	Based on 36920 COVID Symptom Study app users reported SARS-CoV-2 test positivity in late 2020, Rt of B.1.1.7 was 1.35x (95% CI 1.02-1.69) relative to pre-existing variants. However, Rt fell below 1 during regional and national lockdowns, even in regions with high proportions of infections with the B.1.1.7 variant.	B.1.1.7, Q.3, Q.1	Graham et al. (2021)	37125	C	T	nan
p.T716I	transmissibility	Ontario, Feb 2021: The secondary attack rate for VOC index cases in this matched cohort was 1.31 times higher than non-VOC index cases (RR	B.1.1.7, Q.3, Q.1	Lindstrøm et al. (2021)	37125	C	T	nan
p.T716I	transmissibility	Primary cases infected with B.1.1.7 had an increased transmissibility of 1.5-1.7 times that of primary cases infected with other lineages. The increased transmissibility of B.1.1.7 was multiplicative across age and viral load.	B.1.1.7, Q.3, Q.1	Lyngse et al. (2021)	37125	C	T	nan
p.T716I	transmissibility	Based on 300,000 RT-PCR samples collected from December 6th 2020 to February 10th 2021 in Israel, the B.1.1.7 is 45% (95% CI:20-60%) more transmissible than the wild-type strain, and become dominant in Israel within 3.5 weeks.	B.1.1.7, Q.3, Q.1	Munitz et al. (2021)	37125	C	T	nan
p.T716I	transmissibility	At the national level (Italy), we estimated a mean relative transmissibility of B.1.1.7 (compared to historical lineages) ranging between 1.55 and 1.57 (with confidence intervals between 1.45 and 1.66).	B.1.1.7, Q.3, Q.1	Stefanelli et al. (2021)	37125	C	T	nan
p.T716I	vaccine efficacy	In Minnesota in early 2021 when Alpha was prevalent, vaccine efficacy was estimated as: mRNA-1273 86% (95%CI: 81-90.6%) and BNT162b2: 76% (95%CI: 69-81%) using age, sex, race, PCR testing and vaccination date matched cohorts of unvaccinated, Pfizer and Moderna vaccinees. [variant list included is ancestral Alpha, as this was an observational study no variant list was given]	B.1.1.7, Q.3, Q.1	Puranik et al. (2021)	37125	C	T	nan
p.T716I	vaccine neutralization efficacy	nan	B.1.1.7, Q.3, Q.1	All vaccinees were on a strict 3 week interval for second dose (	37125	C	T	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.T716I	vaccine neutralization efficacy	Between December 19, 2020 and Jan 24, 2021, 7214 of 9109 eligible HCWs at Sheba Medical Center in Israel had received one or more doses of BNT162b2 (Pfizer) vaccine. Adjusted rate reduction in SARS-CoV-2 NAAT positivity infection compared with unvaccinated workers 1-14 days after 1st dose was 30% (95% CI: 2-50), and 75% (95% CI: 72-84) after 15-28 days. Adjusted rate reduction in symptomatic COVID-19 compared with unvaccinated workers 1-14 days after 1st dose was 47% (95% CI: 17-66), and 85% (95% CI: 71-92) after 15-28 days. [Though often cited as an indicator of VE for B.1.1.7, during this time period in Israel, the prevalence of the B.1.1.7 variant increased from extasciitilde20% to 50% of cases (covariants.org), therefore these VE numbers likely represent a mix of B.1.1.7 and other lineage effects.]	B.1.1.7, Q.3, Q.1	Amit et al. (2021)	37125	C	T	nan
p.T716I	vaccine neutralization efficacy	Neutralization efficiency (ID50) against B.1.1.7 reduced 1.2x relative to D614G wildtype using pseudotyped VSV assay on 8 Moderna vaccinee sera one week post-booster.	B.1.1.7, Q.3, Q.1	Choi et al. (2021)	37125	C	T	nan
p.T716I	vaccine neutralization efficacy	20/29 sera after the first dose of Pfizer showed an average reduction in neutralization titres against the B.1.1.7 variant of 3.2 ± 5.7. After the second dose, the GMT was markedly increased compared with the first-dose titres, with a fold change of 1.9 ± 0.9 (mean ± s.d.). Neutralization GMT of 27 subjects post-infection was considerably higher (stronger) than after the second Pfizer dose, and 4.5x drop in B.1.1.7 neutralization was observed.	B.1.1.7, Q.3, Q.1	Collier et al. (2021)	37125	C	T	nan
p.T716I	vaccine neutralization efficacy	2.1x drop in neutralization using sera collected from 14 healthy adult participants that received two injections of the mRNA-1273 (Moderna) vaccine at a dose of 100 µg (18-55 years: day 1 (n	B.1.1.7, Q.3, Q.1	Edara et al. (2021)	37125	C	T	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.T716I	vaccine neutralization efficacy	Virus neutralisation activity (using a live SARS-CoV-2 microneutralisation assay (ND50)) by vaccine induced antibodies was 9-fold lower against the B.1.1.7 variant than against a canonical non B.1.1.7 lineage. Vaccine efficacy against symptomatic NAAT positive infection was similar for B.1.1.7 and non-B.1.1.7 lineages (74.6% [95%CI 41.6-88.9] and 84% [95% CI 70.7-91.4] respectively). Furthermore, vaccination with ChAdOx1 nCoV-19 results in a reduction in the duration of shedding and viral load, which may translate into a material impact on transmission of disease.	B.1.1.7, Q.3, Q.1	Emary et al. (2021)	37125	C	T	nan
p.T716I	vaccine neutralization efficacy	ELISpot assays show T cell neutralization reduced by 15.4% in this B.1.1.7 pseudotype relative to wild type in 18-20 pooled patient samples post second mRNA vaccine dose, with no significant difference between Pfizer and Moderna cohorts. Reduction was stronger in the S1 subunit than S2 (separate peptide pools were used).	B.1.1.7, Q.3, Q.1	Gallagher et al. (2021)	37125	C	T	nan
p.T716I	vaccine neutralization efficacy	Pseudotyped B.1.1.7 virus has reduced neutralization activity vs wild type: 2.1x (30 sera Pfizer median 9 days post 2nd dose) and 2.3x (35 sera Moderna median 18 days post 2nd dose). This was NOT significant by ANOVA. Note that Y145del was actually noted in the paper as the effect of their DNA construct, but this is equivalent at the protein level to the more commonly annotated Y144del.	B.1.1.7, Q.3, Q.1	Garcia-Beltran et al. (2021)	37125	C	T	nan
p.T716I	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)	B.1.1.7, Q.3, Q.1	Gong et al. (2021)	37125	C	T	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.T716I	vaccine neutralization efficacy	Using national surveillance data from Israel, using Pfizer vaccine and an estimated prevalence of the B.1.1.7 variant of 94.5% among SARS-CoV-2 infections: Adjusted estimates of vaccine effectiveness 7+ days after second dose were 95 · 3% (95% CI 94.9–95.7): 91.5% against asymptomatic SARS-CoV-2 infection (90 · 7–92 · 2: 40.9 vs 1.8 per 100 000 person-days), 97 · 0% against symptomatic COVID-19 (96.7–97.2%), 97.2% against COVID-19-related hospitalisation (96.8–97.5%), 97.5% against severe or critical COVID-19-related hospitalisation (97.1–97.8%), and 96.7% against COVID-19-related death (96.0–97.3%). In all age groups, as vaccine coverage increased, the incidence of SARS-CoV-2 outcomes declined	B.1.1.7, Q.3, Q.1	Haas et al. (2021)	37125	C	T	nan
p.T716I	vaccine neutralization efficacy	A single dose of BNT162b2 (Pfizer) vaccine showed vaccine effectiveness of 70% (95% CI 55-85) 21 days after first dose and 85% (74-96) 7 days after two doses in the study population. Our findings show that the BNT162b2 vaccine can prevent both symptomatic and asymptomatic infection in working-age adults. This cohort (8203 treatment, 15121 control) was vaccinated when the dominant variant in circulation was B.1.1.7 and shows effectiveness against this variant.	B.1.1.7, Q.3, Q.1	Hall et al. (2021)	37125	C	T	nan
p.T716I	vaccine neutralization efficacy	A single dose of BNT162b2 vaccine demonstrated vaccine effectiveness [symptomatic or asymptomatic in cohort opf routinely NAAT-monitored UK HCWs] of 72% (95% CI 58-86) 21 days after first dose and 86% (95% CI 76-97) seven days after two doses in the antibody negative cohort. This cohort was vaccinated when the dominant variant in circulation was B.1.1.7 and demonstrates effectiveness against this variant.	B.1.1.7, Q.3, Q.1	Hall et al. (2021)	37125	C	T	nan
p.T716I	vaccine neutralization efficacy	NVX-CoV2373 [Novavax] vaccine in phase 3 trial was 89.7% (95% CI, 80.2-94.6) effective in preventing COVID-19, with no hospitalizations or deaths reported. There were five cases of severe Covid-19, all in the placebo group. Post hoc analysis revealed efficacies of 96.4% (73.8-99.5) and 86.3% (71.3-93.5) against the prototype strain and B.1.1.7 variant, respectively.	B.1.1.7, Q.3, Q.1	Heath et al. (2021)	37125	C	T	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.T716I	vaccine neutralization efficacy	VSV pseudotype B.1.1.7 showed 1.77-fold reduction in neutralization efficiency vs wild type in 15 Pfizer BNT162b2 vaccinee sera 13-15 days post second dose. Cell fusion proficiency was unchanged.	B.1.1.7, Q.3, Q.1	Hoffman et al. (2021)	37125	C	T	nan
p.T716I	vaccine neutralization efficacy	B.1.1.7 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 no statistically sognificant change in neutralization effiacacy.	B.1.1.7, Q.3, Q.1	Ikegame et al. (2021)	37125	C	T	nan
p.T716I	vaccine neutralization efficacy	Neutralizing antibody titers increased in previously infected vaccinees relative to uninfected vaccinees 5.2-fold against B.1.1.7 (contrast with 3.4 fold against original SARS-CoV-2).	B.1.1.7, Q.3, Q.1	Leier et al. (2021)	37125	C	T	nan
p.T716I	vaccine neutralization efficacy	SARS-CoV-2 infection was confirmed in three HCWs working a single shift: all presented with mild symptoms of COVID-19. The two physicians were fully vaccinated with BNT162b2 vaccine, with the second dose administered 1 month before symptom onset. Both had high titres of IgG anti-spike antibodies at the time of diagnosis. WGS confirmed that all virus strains were VOC 202012/01-lineage B.1.1.7, suggesting a common source of exposure. Epidemiological investigation revealed that the suspected source was a SARS-CoV-2-positive patient who required endotracheal intubation due to severe COVID-19. All procedures were carried out using a full suite of personal protective equipment (PPE).	B.1.1.7, Q.3, Q.1	Loconsole et al. (2021)	37125	C	T	nan
p.T716I	vaccine neutralization efficacy	We found that a single dose of the BNT162b2 vaccine is about 60-70% effective at preventing symptomatic disease in adults aged 70 years and older in England and that two doses are about 85-90% effective. Those who were vaccinated and went on to have symptoms had a 44% lower risk of being admitted hospital and a 51% lower risk of death compared with people who were unvaccinated. We also found that a single dose of the ChAdOx1-S vaccine was about 60-75% effective against symptomatic disease and provided an additional protective effect against hospital admission—it is too early to assess the effect on mortality. The B.1.1.7 variant now dominates in the UK and these results will largely reflect vaccine effectiveness against this variant.	B.1.1.7, Q.3, Q.1	Lopez Bernal et al. (2021)	37125	C	T	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.T716I	vaccine neutralization efficacy	In sera 1-2 weeks after BNT162b2 first dose, from six patients previously infected with B.1, antibody titer in a microneutralization assay was on average 8192 for B.1.351 virus. This compares favorably (stronger) to post-infection neutralization titer against all variants tested in the same sera (wild type, B.1.1.7, B.1.351, and P.1).	B.1.1.7, Q.3, Q.1	Luftig et al. (2021)	37125	C	T	nan
p.T716I	vaccine neutralization efficacy	Lineage B.1.1.7 spike–pseudotyped VSV was tested for neutralization vs Wuhan reference genome pseudotype in 40 sera collected 7 or 21 days post-booster dose. Statistically significant change (22%) in neutralization was observed among the 26 sera from those <	B.1.1.7, Q.3, Q.1	Muik et al. (2021)	37125	C	T	nan
p.T716I	vaccine neutralization efficacy	We observed a sharp decline in cases when 50% of the elderly population was 2 weeks beyond their first vaccination dose and at a time point during which the B.1.1.7 variant gained transmission dominance. In support of this finding, it was suggested that, after the first vaccination dose, more than 70% of patients develop neutralization antibodies,15 and the vaccine efficiency can reach 85%.	B.1.1.7, Q.3, Q.1	Munitz et al. (2021)	37125	C	T	nan
p.T716I	vaccine neutralization efficacy	Detectable antibodies against B.1.1.7 at various time points using pseudotyped lentivirus neutralization in Moderna vaccinee cohort: Day 29 33%, Day 43 100%, Day 119 100%, Day 209 96%. Detectable antibodies against B.1.1.7 at various time points using live virus FRNT neutralization in Moderna vaccinee cohort: Day 29 54%, Day 43 100%, Day 119 100%, Day 209 88%. Detectable antibodies against B.1.1.7 at various time points using ACE2 blocking assay in Moderna vaccinee cohort: Day 29 83%, Days 43,119,209 100%.	B.1.1.7, Q.3, Q.1	Pegu et al (2021)	37125	C	T	nan
p.T716I	vaccine neutralization efficacy	The sera of 16 individuals with time course collection was evaulated against VSV pseudotypes: neutralized D614G at week 2, whereas B.1.1.7 started to be neutralized at week 3, although less efficiently than D614G. B.1.1.7 and D614G strains were similarly neutralized at week 4 (1 week after booster dose).	B.1.1.7, Q.3, Q.1	Planas et al. (2021)	37125	C	T	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.T716I	vaccine neutralization efficacy	After one dose, individuals with prior infection showed enhanced T cell immunity, antibody secreting memory B cell response to spike and neutralizing antibodies effective against B.1.1.7 (authentic cell culture supernatants). By comparison, HCW receiving one vaccine dose without prior infection showed reduced immunity against variants. B.1.1.7 spike mutations resulted in increased, abrogated or unchanged T cell responses depending on human leukocyte antigen (HLA) polymorphisms. Study was 26 each post-infection and post first dose HCWs.	B.1.1.7, Q.3, Q.1	Reynolds et al. (2021)	37125	C	T	nan
p.T716I	vaccine neutralization efficacy	The NAb titers (PRNT50) of sera collected from 38 vaccine recipients four-weeks after the second dose of inactivated whole-virion SARS-CoV-2 BBV152/COVAXIN vaccine [which contains D614G] were not significantly different between B.1.1.7 virus and ancestral D614G virus.	B.1.1.7, Q.3, Q.1	Sapkal et al. (2021)	37125	C	T	nan
p.T716I	vaccine neutralization efficacy	Pseudotyped B.1.1.7 Spike variants lentivirus. 3.5x reduction in neutralization with Moderna vaccinated patient sera after 29 days (1st dose). 2.0x reduction in neutralization with Moderna vaccinated patient sera after 57 days (2nd dose). 2.1x reduction in neutralization with Novavax Phase 1 post-vaccination sera.	B.1.1.7, Q.3, Q.1	Shen et al. (2021)	37125	C	T	nan
p.T716I	vaccine neutralization efficacy	Neutralization assays of B.1.1.7 virus showed a reduction of 2.5-fold (14 days post 2nd dose AstraZeneca, n	B.1.1.7, Q.3, Q.1	Supasa et al. (2021)	37125	C	T	nan
p.T716I	vaccine neutralization efficacy	Vaccine elicited antibodies neutralized virus with the B.1.1.7 spike protein with titers similar to D614G virus. Serum specimens from individuals vaccinated with the BNT162b2 mRNA vaccine neutralized D614G virus with titers that were on average 7-fold greater than convalescent sera.	B.1.1.7, Q.3, Q.1	Tada et al. (2021)	37125	C	T	nan
p.T716I	vaccine neutralization efficacy	PBMCs of Pfizer/BioNTech BNT162b2 (n	B.1.1.7, Q.3, Q.1	Tarke et al. (2021)	37125	C	T	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.T716I	vaccine neutralization efficacy	1.4x improvement in neutralization by serum collected 2 to 3 weeks after the second dose from vaccinees who had received BBIBP-CorV (pVNT50 against VSV pseudotyped as B.1.1.7). Convalescent plasma had similar titer against wild type as the BBIBP-CorV vaccinee sera. 2x reduction in neutralization by serum collected 2 to 3 weeks after the second dose from vaccinees who had received CoronaVac (pVNT50 against VSV pseudotyped as B.1.1.7). Convalescent plasma had similar titer against wild type as the CoronaVac vaccinee sera.	B.1.1.7, Q.3, Q.1	Wang et al. (2021)	37125	C	T	nan
p.T716I	vaccine neutralization efficacy	No significant difference in T-cell response to B.1.1.7 was observed (vs. ancestral) in blood drawn from 28 participants received the Pfizer-BioNTech vaccine and 2 received the Moderna vaccine. This is despite three mutations (Y144del, D614G, and P681H) overlapping T-cell epitope hotspots.	B.1.1.7, Q.3, Q.1	Woldemeskel et al. (2021)	37125	C	T	nan
p.T716I	vaccinee plasma binding	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 previously non-seroconverted subjects. 1.47x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in post-infection vaccinees.	Q.1, B.1.1.7, Q.3, Q.4	Gong et al. (2021)	37127	C	T	nan
p.T716I	vaccinee plasma binding	This variant combination (representing B.1.1.7 aka Alpha) showed no change in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in previously non-seroconverted subjects. 1.28x 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.1.1.7, Q.3, Q.1	Gong et al. (2021)	37125	C	T	nan
p.T716I	viral load	Using lack of S probe detection as a proxy for B.1.1.7 status, 275 putative B.1.1.7 samples and 390 ”wild type” SARS-CoV-2 positive samples in Wales were compared for Ct values, suggesting extasciitilde12-fold increase (extasciitilde3.5 Ct decrease) in viral load for B.1.1.7 samples.	B.1.1.7, Q.3, Q.1	Couzens et al. (2021)	37125	C	T	nan
p.T716I	viral load	We found that the British variant (clade B.1.1.7), compared to an ancestral SARS-CoV-2 clade B virus, produced higher levels of infectious virus late in infection and had a higher replicative fitness in human airway, alveolar and intestinal organoid models.	B.1.1.7, Q.3, Q.1	Lamers et al. (2021)	37125	C	T	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.T716I	viral load	This study reveals that B.1.1.7 SARS-CoV-2 variant is a slower-growing virus than parental B.1. Further, a higher replication along with reduced infectious viral titer was hypothesized to be linked to higher transmission with reduced pathogenicity.	B.1.1.7, Q.3, Q.1	Nyayanit et al. (2021)	37125	C	T	nan
p.T716I	viral load	In a study of 1260 ICU subjects, viral load distributions (collected within 48h of admission) were elevated in both seropositive and seronegative subjects infected with B.1.1.7 ("UK variant"). PG: The PANGO tool defining Spike variants for B.1.1.7 are listed here, whereas the paper only used a test for D1118H.	B.1.1.7, Q.3, Q.1	Ratcliff et al. (2021)	37125	C	T	nan
p.T716I	viral load	B.1.1.7 samples showed average Ct cycle threshold of 21.9 vs 23 for wildtype (i.e. extasciitilde2x higher viral load) comparing 37758 and 22535 samples respectively.	B.1.1.7, Q.3, Q.1	Roquebert et al. (2021)	37125	C	T	nan
p.T716I	viral load	The median Ct value of RT-qPCR tests of the N-gene target in the Daxing B.1.1.7 group was significantly lower than the Shunyi B.1.470 group (P	B.1.1.7, Q.3, Q.1	Song et al. (2021)	37125	C	T	nan
p.T716I	viral load	The 249 B.1.1.7 (a.k.a. N501Y.V1) variant cases in three Paris hospital labs had a extasciitilde10-fold viral load increase (extasciitilde3.3 Ct drop in N gene probe) compared to 332 ancestral lineage cases from the same time frame (2020-12-20 to 2021-02-26). PG: BUT there is a discrepancy in drop between the ORF1ab and N probes, with the former suggesting only a 2-fold drop, consistent with the drop observed in B.1.351. This might indicate higher subgenomic RNA content in B.1.1.7 skewing the change.	B.1.1.7, Q.3, Q.1	Teyssou et al. (2021)	37125	C	T	nan
p.T716I	virion structure	CryoEM analysis of B.1.1.7 demonstrates an increased propensity for 'up', receptor accessible conformation of the Spike protein trimer.	B.1.1.7, Q.3, Q.1	Cai et al. (2021)	37125	C	T	nan
p.N501Y	ACE2 receptor binding affinity	The N501Y mutation had the biggest effect on ACE2 affinity of any VOC mutation tested, increasing the affinity extasciitilde10 fold to KD extasciitilde7 nM, by increasing the k(on) extasciitilde1.8 fold and decreasing the k(off) by extasciitilde 7 fold as measured by surface plasmon resonance.	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Barton et al. (2021)	37077	A	T	nan
p.N501Y	ACE2 receptor binding affinity	This combination showed extasciitilde3x increase binding to ACE2 vs wild type, about half that of the B.1.1.7 lineage, suggesting that the K417N mutation is slightly detrimental to ACE2 binding, probably as a result of disrupting the salt bridge formed with ACE2 residue D30	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Collier et al. (2021)	37077	A	T	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.N501Y	ACE2 receptor binding affinity	Six fold increase in affinity for ACE2 by the B.1.1.7 lineage vs wild type is driven by a drop in observed dissociation rate constant.	B.1.1.7, Q.3, Q.1	Collier et al. (2021)	37067	A	T	nan
p.N501Y	ACE2 receptor binding affinity	The most frequent RBM mutation N501Y (165,519 instances) makes defective the atypical N-glycosylation sequon NGV 501-503, becoming a key RBM position for the interaction with hACE2-binding hotspot 353.	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Gamez et al. (2021)	37077	A	T	nan
p.N501Y	ACE2 receptor binding affinity	Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant showed a 2.52x increase in binding (KD) relative to D614G, mostly due to decreased in "off-rate" a.k.a. dissociation rate (Kdis). Compare to full Spike variant complements for major lineages containing this variant subset: 5.43x (B.1.1.7 aka Alpha), 3.56x (B.1.351 aka Beta), 4.24x (P.1 aka Gamma).	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Gong et al. (2021)	37077	A	T	nan
p.N501Y	ACE2 receptor binding affinity	Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant combination (representing B.1.1.7 aka Alpha) had 5.43x increased binding relative to D614G alone.	B.1.1.7, Q.3, Q.1	Gong et al. (2021)	37067	A	T	nan
p.N501Y	ACE2 receptor binding affinity	RBD containing the N501Y mutation results in 9-fold stronger binding to the hACE2 receptor than wild type RBD. The E484K mutation does not significantly influence the affinity for the receptor, while K417N attenuates affinity. As a result, RBD from B.1.351 containing all three mutations binds 3-fold stronger to hACE2 than wild type RBD but 3-fold weaker than N501Y.	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Laffeber et al. (2021)	37077	A	T	nan
p.N501Y	ACE2 receptor binding affinity	Reported 10-fold increase in ACE2 binding vs wild-type (Kd	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Liu et al. (2021)	37077	A	T	nan
p.N501Y	ACE2 receptor binding affinity	Studying the key covariants in lineage of concern 501Y.V2, observed about 2-fold increase in ACE2 binding vs wildtype, but greatly decreased mAb binding, suggesting evolutionary optimum tension between immune evasion and ACE2 binding affinity as the N501Y variant alone has 10x increase in affinity but no effect on tested mAb binding.	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Liu et al. (2021)	37077	A	T	nan
p.N501Y	ACE2 receptor binding affinity	extasciitilde4-fold increase in binding affinity vs wild type.	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Motozono et al. (2021)	37077	A	T	nan
p.N501Y	ACE2 receptor binding affinity	Flow cytometry was used on recombinant VSV proteins and yeast surface display to assess the binding of a labeled soluble ACE2 protein to cells expressing B.1.1.7. We observed a dramatic increase (relative to D614G) in binding of soluble ACE2 to B.1.1.7, and to a lesser extent to B.1.351, which both carry the N501Y mutation (see Fig 3).	B.1.1.7, Q.3, Q.1	Planas et al. (2021)	37067	A	T	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.N501Y	ACE2 receptor binding affinity	Using Microscale Thermopheresis, this variant binds ACE2 at nearly two-fold greater affinity than the original SARS-COV-2 RBD (203.7 nM vs 402.5 nM).	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Ramanathan et al. (2021)	37077	A	T	nan
p.N501Y	ACE2 receptor binding affinity	Using Mircoscale Thermopheresis, the B.1.351 variant harboring three mutations, binds ACE2 at nearly five-fold greater affinity than the original SARS-COV-2 RBD (Kd 87.6, vs 402.5 nM).	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Ramanathan et al. (2021)	37077	A	T	nan
p.N501Y	ACE2 receptor binding affinity	In silico methods (PyMOL and PDBePISA) involving mutagenesis (N501Y mutation) and interface analysis focusing on the Spike RDB-ACE2 interaction showed that the SARS-CoV-2 N501Y mutant (lineage B.1.1.7) establishes a more significant number of interactions relating to the mutant residue Y501 (Spike RDB) with residues Y41 and K353 (ACE2). This finding shows that the increased infectivity of SARS-CoV-2 lineage B.1.1.7 is associated with the interaction force between the Spike RBD Y501 mutant residue with the ACE2 receptor, which in this strain is increased.	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Santos and Passos (2021)	37077	A	T	nan
p.N501Y	ACE2 receptor binding affinity	Experimentally, ACE2 binding affinity increased 0.24 fold	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Starr et al. (2020)	37077	A	T	nan
p.N501Y	ACE2 receptor binding affinity	This single mutation causes major increase in binding affinity vs. wild type as measured by IC50 vs pseudotyped lentivirus, but combined with the complete set of B.1.1.7 lineage variants no major change vs wild type affnity is observed.	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Tada et al. (2021)	37077	A	T	nan
p.N501Y	ACE2 receptor binding affinity	This mutation combination causes major increase in binding affinity vs. wild type as measured by IC50 vs pseudotyped lentivirus, but combined with the complete set of B.1.1.7 lineage variants no major change vs wild type affnity is observed.	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Tada et al. (2021)	37077	A	T	nan
p.N501Y	ACE2 receptor binding affinity	This mutation causes major decrease in binding affinity vs. wild type as measured by IC50 vs pseudotyped lentivirus.	B.1.1.7, Q.3, Q.1	Tada et al. (2021)	37067	A	T	nan
p.N501Y	ACE2 receptor binding affinity	Reported 4-fold increase in affinity compared to wild-type RBD on the cell surface (Kd	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Tian et al. (2021)	37077	A	T	nan
p.N501Y	ACE2 receptor binding affinity	Reported slight increase in affinity compared to wild-type RBD on the cell surface (Kd	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Tian et al. (2021)	37077	A	T	nan
p.N501Y	ACE2 receptor binding affinity	The affinity of ACE2 for this mutation combination was twice as high as for wild type. Having in mind that the affinity of SARS-CoV-2 for ACE2 is only 4-fold higher compared to SARS-CoV-1, this factor of 2 is expected to be biologically significant.	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Vogel et al. (2021)	37077	A	T	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.N501Y	ACE2 receptor binding affinity	Among the first selected and fixed variants in an in vitro evolution experiment for ACE2 binding. Calculated disassociation constant for this variant is nearly four fold lower than wild type (Kd	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Zahradnik et al. (2021)	37077	A	T	nan
p.N501Y	ACE2 receptor binding affinity	N501Y residue inserts into a cavity at the binding interface near Y41 of ACE2. The additional interactions result in increased affinity of ACE2 for the N501Y mutant, accounting for its increased infectivity.	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Zhu et al. (2021)	37077	A	T	nan
p.N501Y	T cell evasion	Vaccinated, but not post-infection sera, show decreased average T cell response to an N501Y peptide. When we primed transgenic mice expressing human HLA-DRB1*0401 with the Wuhan Hu-1 peptide pool, T cell responses to the B.1.1.7 variant peptide pool were significantly reduced (p	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Reynolds et al. (2021)	37077	A	T	nan
p.N501Y	anthropozoonotic events	First documented cases of domestic cat and dog infections with the B.1.1.7 strain.	B.1.1.7, Q.3, Q.1	Hamer et al. (2021)	37067	A	T	nan
p.N501Y	antibody epitope effects	Ablates Class 3 N-terminal domain targeting antibody COV2-2489, diminishes COV2-2676.	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Chen et al. (2021)	37077	A	T	nan
p.N501Y	antibody epitope effects	Ablates Class 3 N-terminal domain targeting antibody COV2-2489, diminishes COV2-2676.	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Chen et al. (2021)	37077	A	T	nan
p.N501Y	antibody epitope effects	Of 50 mAbs tested, major loss of neutralization observed for S2X128, S2D8, S2X192, S2D19, S2H14, S2H19.	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Collier et al. (2021)	37077	A	T	nan
p.N501Y	antibody epitope effects	Wildtype elicits immune response, COVID-19 cohort epitope score > 99th percentile of the 497 pre-pandemic controls, mutant drops PIWAS epitope score from 3% to 1.2% (poorer immune recognition) Together with other B1.1.7 lineage mutational changes (Spike: Y144del, A570D, P681H, Nucleoprotein: D3L, S235F) resulted in only 2 or 579 individuals (0.3% of the population) having a dramatic reduction in PIWAS antigen scores, which reflects the peak epitope signal along the entire antigen.	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Haynes et al. (2021)	37077	A	T	nan
p.N501Y	antibody epitope effects	extasciitilde20x resistence to mAb CQ038 by B.1.1.7 pseudotyped virus	B.1.1.7, Q.3, Q.1	Hu et al. (2021)	37067	A	T	nan
p.N501Y	antibody epitope effects	Contrary to other reports on N501Y containing lineages (i.e. with additional mutations), N501Y alone may have an even greater affinity for a human monoclonal antibody specific for wild type. These results suggest that the individual N501Y mutation does not contribute to altered viral properties by itself, but may contribute to a collective conformational shift produced by multiple mutations.	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Klegerman et al. (2021)	37077	A	T	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.N501Y	antibody epitope effects	Lowered the neutralization potency of mAb COVA1-12 to the limit of the assay. Decrease in potency was observed against the N501Y pseudotype for the cluster IX mAb COVA2-17.	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Rees-Spear et al. (2021)	37077	A	T	nan
p.N501Y	antibody epitope effects	Lessens the potency of mAbs COVA2-17 (extasciitilde5x, similar to N501Y alone), COVA1-12 (extasciitilde11x) and COVA1-21 (>100x), which do not compete allosterically.	B.1.1.7, Q.3, Q.1	Rees-Spear et al. (2021)	37067	A	T	nan
p.N501Y	antibody epitope effects	Reduction in neutralization by mAbs COVA1-18 (extasciitilde4x), COVA2-15 (extasciitilde9x), S309 (extasciitilde3x)	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Shen et al. (2021)	37077	A	T	nan
p.N501Y	antibody epitope effects	Reduction in neutralization by mAbs COVA1-18 (extasciitilde4x), COVA2-15 (extasciitilde9x). PG: these effects are laregly missing in the deletion-alone data	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Shen et al. (2021)	37077	A	T	nan
p.N501Y	antibody epitope effects	Reduction in neutralization by mAbs COVA2-15 (extasciitilde9x), B38 (extasciitilde14x), S309 (extasciitilde190x) by this B.1.1.7 pseudotyped virus model.	B.1.1.7, Q.3, Q.1	Shen et al. (2021)	37067	A	T	nan
p.N501Y	antibody epitope effects	4 antibodies tested were less potent against K417N by ten-fold or more, in both mAb classes 1 and 3	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Wang et al. (2021)	37077	A	T	nan
p.N501Y	antibody epitope effects	B.1.1.7 pseudotyped virus model impairs binding by RBD-directed mAb 910-30. B.1.1.7 pseudotyped virus model abolishes N-terminal-domain-directed mAbs 5-24, 4-8, and 4A8. B.1.1.7 pseudotyped virus model impairs binding by N-terminal-domain-directed mAbs 2-17, 4-19, 5-7.	B.1.1.7, Q.3, Q.1	Wang et al. (2021)	37067	A	T	nan
p.N501Y	clinical indicators	After adjusting for the age factor, in a prospective Chinese cohort study B.1.1.7 variant infection (compared to B.1.140) was the risk factor for C-reactive protein (P	B.1.1.7, Q.3, Q.1	Song et al. (2021)	37067	A	T	nan
p.N501Y	convalescent plasma binding	1.65x increase in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset.	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Gong et al. (2021)	37077	A	T	nan
p.N501Y	convalescent plasma binding	This variant combination (representing B.1.1.7 aka Alpha) showed a 1.15x increase in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset.	B.1.1.7, Q.3, Q.1	Gong et al. (2021)	37067	A	T	nan
p.N501Y	convalescent plasma escape	One convalescent sera tested showed 4-fold or greater reduction in neutralization efficiency.	Q.8, Q.3, Q.1, B.1.1.7	Alenquer et al. (2021)	37075	A	T	nan
p.N501Y	convalescent plasma escape	Slight neutralization improvement on average in 16 health workers' convalescent sera.	Q.8, Q.3, Q.1, B.1.1.7	Alenquer et al. (2021)	37075	A	T	nan
p.N501Y	convalescent plasma escape	The 501Y.V2 to first wave IC50 ratio ranged from 6 to 200-fold. Averaging across all 7 participant convalescent sera highlighted the dramatic decrease in sensitivity to neutralization of authentic 501Y.V2 variants. PG: I'm purposefully ignoring D614G and A701V as contributors	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Cele et al. (2021)	37077	A	T	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.N501Y	convalescent plasma escape	Neutralization capacity GMT of 27 subjects' sera post-infection was considerably higher (stronger) than after the second Pfizer dose, and 4.5x drop in B.1.1.7 neutralization was observed.	B.1.1.7, Q.3, Q.1	Collier et al. (2021)	37067	A	T	nan
p.N501Y	convalescent plasma escape	NTD-specific nAbs showed a substantial (3-450x) decrease in neutralization potency against the recently reported highly transmissible B.1.1.7 variant of concern, whereas RBD-specific nAbs were either unaffected or showed lower decreases in potency.	B.1.1.7, Q.3, Q.1	Graham et al. (2021)	37067	A	T	nan
p.N501Y	convalescent plasma escape	Neutralizing antibody titers of 2/20 (10%) samples showed >10x reduction (sera collected extasciitilde1mo post Jan 2020 first wave in China). Neutralizing antibody titers of 8/20 samples (40%) decreased below an ID50 threshold of 40 (sera collected extasciitilde8mo post Jan 2020 first wave in China).	B.1.1.7, Q.3, Q.1	Hu et al. (2021)	37067	A	T	nan
p.N501Y	convalescent plasma escape	0.7x reduction in neutralization by key variant in several variants of concern in sera collected from cohort of 10 with severe disease 21 to 63 days post-onset.	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Kuzmina et al. (2021)	37077	A	T	nan
p.N501Y	convalescent plasma escape	Using a new rapid neutralization assay, based on reporter cells that become positive for GFP after overnight infection, sera from 58 convalescent individuals collected up to 9 months after symptoms, similarly neutralized B.1.1.7 and D614G.	B.1.1.7, Q.3, Q.1	Planas et al. (2021)	37067	A	T	nan
p.N501Y	convalescent plasma escape	In 30 samples collected 111 to 260 days post onset of symptoms, the covalescent plasma can neutralize both the reference USA-WA1/2020 strain and the mouse adapted strain that contains the N501Y spike mutation with similar efficiency.	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Rathnasinghe et al. (2021)	37077	A	T	nan
p.N501Y	convalescent plasma escape	Maximum fold-decrease in potency for the serum samples from mild illness was 8.2 but the majority of samples showed less than a 3-fold change. Similarly, the maximum decrease seen for samples from hospitalized patients was a 9.1-fold change, but most of the samples showed minimal change in the potency of their neutralization. Overall, three samples from each cohort (8%) showed a 5–10-fold reduction, but as they were potently neutralizing sera, the reduced ID50 values were still >1:100.	B.1.1.7, Q.3, Q.1	Rees-Spear et al. (2021)	37067	A	T	nan
p.N501Y	convalescent plasma escape	Neutralization activity of convalescent sera tested decreased extasciitilde2x with this B.1.1.7 pseudotyped virus.	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Shen et al. (2021)	37077	A	T	nan
p.N501Y	convalescent plasma escape	Neutralization activity of convalescent sera tested decreased <2x with this B.1.1.7 pseudotyped virus.	B.1.1.7, Q.3, Q.1	Shen et al. (2021)	37067	A	T	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.N501Y	convalescent plasma escape	We analyzed 34 convalescent samples including the WHONIBSC 20/130 reference serum, and, although a few sera showed near identical FRNT 50 values, the FRNT50 dilutions for the B.1.1.7 strain were 2.9-fold lower (geometric mean) than those for the Victoria strain ($p < 0.0001$). Sera from 13 subjects post-B.1.1.7 infection showed no significant change in neutralization against Victoria (extasciitildewild type), suggesting that B.1.1.7 infection also protects against ancestral virus. [Note that D1119H was included in the original paper, assuming typographical error and correcting to D1118H]	B.1.1.7, Q.3, Q.1	Supasa et al. (2021)	37067	A	T	nan
p.N501Y	convalescent plasma escape	Viruses containing the point mutations of B.1.1.7 showed that the single point mutations (Δ69-70 and N501Y) were neutralized as efficiently as D614G across 10 convalescent sera from April 2020 infectees.	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Tada et al. (2021)	37077	A	T	nan
p.N501Y	convalescent plasma escape	These key B.1.1.7 mutations as a combination neutralized slightly less well than D614G and this was noticeable in the lack of sera with high neutralizing titer for the viruses across 10 convalescent sera from April 2020 infectees.	Q.8, Q.3, Q.1, B.1.1.7	Tada et al. (2021)	37075	A	T	nan
p.N501Y	convalescent plasma escape	As measured by surface plasmon resonance, RBD with the N501Y mutation alone showed a mean 2.1x decrease in binding affinity for six batches of hyperimmune immunoglobulin (hCoV-2IG) preparations generated from SARS-CoV-2 convalescent plasma.	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Tang et al. (2021)	37077	A	T	nan
p.N501Y	convalescent plasma escape	Loss of neutralizing activity using 6 hyperimmune immunoglobulin preparations from convalescent plasma was minimal against B.1.1.7 (1.9-fold). Neutralization against 10 convalescent plasma was poorer.	B.1.1.7, Q.3, Q.1	Tang et al. (2021)	37067	A	T	nan
p.N501Y	convalescent plasma escape	The neutralizing activity of 8/20 convalescent sera was significantly lower against this pseudotyped virus model of B.1.1.7, yet almost no effect was detected using the live B.1.1.7 virus.	B.1.1.7, Q.3, Q.1	Wang et al. (2021)	37067	A	T	nan
p.N501Y	convalescent plasma escape	27% of 44 early pandemic exposure convalescent plasma/sera lose all activity against a RBD triple mutant pseudovirus (RBD mutatants of the 501Y.V2 "South African" lineage), while only 23% retained high titres	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Wibmer et al. (2021)	37077	A	T	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.N501Y	convalescent plasma escape	Nearly half (21 of 44, 48%) of early pandemic exposure convalescent plasma/sera failed to neutralize the 501Y.V2 ("South African") lineage pseudovirus construct Only 3 of 44 convascent sera (those with the highest titer, which correlated direectly with initial infection severity) had high neutralization against this 501Y.V2 PG: note that lineage variant R246I was excluded from the text in reference to these sera assays, not sure if that was an oversight.	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Wibmer et al. (2021)	37077	A	T	nan
p.N501Y	environmental condition stability	Treatment with heat, soap and ethanol revealed similar inactivation profiles indicative of a comparable susceptibility towards disinfection. Furthermore, we observed comparable surface stability on steel, silver, copper and face masks.	B.1.1.7, Q.3, Q.1	Meister et al. (2021)	37067	A	T	nan
p.N501Y	environmental condition stability	No differences in the stability of B.1.1.7 observed in the absence of simulated sunlight at either 20°C or 40°C (with a mean time for a 90% loss of viral infectivity across all dark conditions of 6.2 hours). However, a small but statistically significant difference in the stability was observed in simulated sunlight at 20°C and 20% relative humidity, with B.1.1.7 restoring wild type 90% loss time of 11 minutes vs. 7 and 8 minutes for B.1.319 (D614G) and B.28 (V367F) early 2020 viruses respectively.	B.1.1.7, Q.3, Q.1	Schuit et al. (2021)	37067	A	T	nan
p.N501Y	environmental condition stability	Relative to D614G, this mutation demonstrated significant increase in infectivity (i.e. heat stability) after incubation at 50C after 30 minutes or 1 hour	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Tada et al. (2021)	37077	A	T	nan
p.N501Y	environmental condition stability	Relative to D614G, this mutation demonstrated significant increase in infectivity (i.e. heat stability) after incubation at 50C after 1 hour.	Q.8, Q.3, Q.1, B.1.1.7	Tada et al. (2021)	37075	A	T	nan
p.N501Y	homoplasy	Variant within the six key residues in the receptor binding domain (RBD). Independently reported in UK, Australia (same origin as UK), and South Africa (independent origin).	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Flores-Alanis et al. (2021)	37077	A	T	nan
p.N501Y	immunosuppression variant emergence	Appeared (day 128) and persisted in chronic (152 day) SARS-CoV-2 infection of immunocompromised patient with severe antiphospholipid syndrome	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Choi et al. (2020)	37077	A	T	nan
p.N501Y	monoclonal antibody serial passage escape	In vitro selection against class 1 (Spike 'up' conformation) monoclonal antibody C663, and to a lesser extent C613.	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Wang et al. (2021)	37077	A	T	nan
p.N501Y	outcome hazard ratio	Danish study of the B.1.1.7 lineage shows hospital admission odds ratio of 1.63 vs other lineages. The adjusted OR was increased in all strata of age.	B.1.1.7, Q.3, Q.1	Bager et al. (2021)	37067	A	T	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.N501Y	outcome hazard ratio	The mortality hazard ratio associated with infection with [B.1.1.7] compared with infection with previously circulating variants was 1.64 (95% confidence interval 1.32 to 2.04) in patients who tested positive for covid-19 in the community (54906 matched pairs of participants who tested positive for SARS-CoV-2 in pillar 2 between 1 October 2020 and 29 January 2021). In this comparatively low risk group, this represents an increase in deaths from 2.5 to 4.1 per 1000 detected cases.	B.1.1.7, Q.3, Q.1	Challen et al. (2021)	37067	A	T	nan
p.N501Y	outcome hazard ratio	Using UK data 1 November 2020 to 14 February 2021, while correcting for misclassification of PCR test Spike Gene Target Failure (SGTF) and missingness in SGTF status, we estimate that the hazard of death associated with B.1.1.7 is 61% (42–82%) higher than with pre-existing variants after adjustment for age, sex, ethnicity, deprivation, residence in a care home, the local authority of residence and test date. This corresponds to the absolute risk of death for a 55–69-year-old man increasing from 0.6% to 0.9% (95% confidence interval, 0.8–1.0%) within 28 days of a positive test in the community.	B.1.1.7, Q.3, Q.1	Davies et al. (2021)	37067	A	T	nan
p.N501Y	outcome hazard ratio	341 samples collected Nov 9 to Dec 20, 2020 were sequenced from two London (UK) hospitals. 198 (58%) of 341 had B.1.1.7 infection and 143 (42%) had non-B.1.1.7 infection. No evidence was found of an association between severe disease and death and lineage (B.1.1.7 vs non-B.1.1.7) in unadjusted analyses (prevalence ratio [PR] 0 · 97 [95% CI 0 · 72-1 · 31]), or in analyses adjusted for hospital, sex, age, comorbidities, and ethnicity (adjusted PR 1 · 02 [0 · 76-1 · 38]).	B.1.1.7, Q.3, Q.1	Frampton et al. (2021)	37067	A	T	nan
p.N501Y	outcome hazard ratio	On average across 7 European countries studied, using B.1.1.7 defining mutations: Significant shift to asymptomatic cases (27.4% vs 18.6% for non-VOC cases). Significant shift to infection in those without pre-existing conditions (44.8% vs 89% for non-VOC cases). Significant increase in hospitalization rate (11% vs 7.5% for non-VOC cases). Significant increase in ICU rate (1.4% vs 0.6% for non-VOC cases). Significant decrease in death rate (2.0% vs vs 4.0% for non-VOC cases).	B.1.1.7, Q.3, Q.1	Funk et al. (2021)	37067	A	T	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.N501Y	outcome hazard ratio	From Sept 28 to Dec 27, 2020, positive COVID-19 tests were reported by 36 920 COVID Symptom Study app users whose region was known and who reported as healthy on app sign-up. We found no changes in reported symptoms or disease duration associated with B.1.1.7.	B.1.1.7, Q.3, Q.1	Graham et al. (2021)	37067	A	T	nan
p.N501Y	outcome hazard ratio	Using primarily S-defining mutations for lineage B.1.1.7, most models of hospitalization and fatality risk ratios from consortium members show elevated ratios (extasciitilde1.3-1.7x).	B.1.1.7, Q.3, Q.1	NERVTAG Consortium (2021)	37067	A	T	nan
p.N501Y	outcome hazard ratio	The matching-adjusted conditional odds ratio of hospitalisation was 1.58 (95% confidence interval 1.50 to 1.67) for COVID-19 patients infected with a SGTF-associated variant [primarily B.1.1.7], compared to those infected with non-SGTF-associated variants. The effect was modified by age (p<0.001), with ORs of 0.96-1.13 below age 20 years and 1.57-1.67 in age groups 40 years or older.	B.1.1.7, Q.3, Q.1	Nyberg et al. (2021)	37067	A	T	nan
p.N501Y	pharmaceutical effectiveness	COR-101 lost extasciitilde8x binding against this isolated mutation. Regdanvimab lost extasciitilde6x binding against this isolated mutation.	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Engelhart et al. (2021)	37077	A	T	nan
p.N501Y	pharmaceutical effectiveness	Tixagevimab, Regdanvimab and COR-101 display reduced binding affinity to virus pseudotyped as RBD from B.1.351.	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Engelhart et al. (2021)	37077	A	T	nan
p.N501Y	pharmaceutical effectiveness	This mutated version of RBD completely abolishes the binding to a therapeutic antibody, Bamlanivimab, in vitro.	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Liu et al. (2021)	37077	A	T	nan
p.N501Y	reinfection	36920 COVID Symptom Study app users reported SARS-CoV-2 test positivity in late 2020. Possible reinfections were identified in 249 (0.7% [95% CI 0.6-0.8]) of 36509 app users who reported a positive swab test before Oct 1, 2020, but there was no evidence that the frequency of reinfections was higher for the B.1.1.7 variant than for pre-existing variants.	B.1.1.7, Q.3, Q.1	Graham et al. (2021)	37067	A	T	nan
p.N501Y	reinfection	Second infection in December 2020 with B.1.1.7 after April 2020 initial infection with B.2 in a 78-year-old man with a history of Type 2 diabetes mellitus, diabetic nephropathy on hemodialysis, chronic obstructive pulmonary disease (COPD), mixed central and obstructive sleep apnea, ischemic heart disease, with no history of immunosuppression.	B.1.1.7, Q.3, Q.1	Harrington et al. (2021)	37067	A	T	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.N501Y	reinfection	Reinfection with Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) B.1.1.7 variant in an immunocompromised 16yo female with end stage renal disease 94 days after initial infection with a B.1.2 lineage virus. Both lineages were the prevalent one at the time of 1st and 2nd infections respectively in Texas, where the patient was located (suggesting exposure risk rather than lineage immune evasion).	B.1.1.7, Q.3, Q.1	Marquez et al. (2021)	37067	A	T	nan
p.N501Y	reinfection	Partial sequencing of S gene reveals two cases of probable early 2021 B.1.1.7 lineage reinfection from non-B.1.1.7 original cases in Lombardy, with 45 to 90 days between infections (less than the typical 90 day guideline for this call). Patients were 56 and 58yo, immunocompenent, with one a former smoker with obesity and dyslipidemia. One case required intubation during first infection, but presented with mild symptoms upon reinfection. The other case convalesced at home during the first episode, but required CPAP support in the subacute clinical unit upon reinfection.	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Novazzi et al. (2021)	37077	A	T	nan
p.N501Y	symptom prevalence	A higher proportion of cases infected with the B.1.1.7 variant were hypoxic on admission compared to other variants (70.0% vs 62.5%, p	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Snell et al. (2021)	37077	A	T	nan
p.N501Y	symptom prevalence	In comparison of B.1.1.7 lineage (193 cases) vs. "wildtype" (125) in Berlin Jan 18 to March 29 2021, significant symptom changes are absent loss of smell/taste (P	B.1.1.7, Q.8, Q.3, Q.4, Q.1	van Loon et al. (2021)	37077	A	T	nan
p.N501Y	syncytium formation	Slight increase in Vero cell-cell membrane fusion assay under infection with VSV pseudotyped virus relative to wild type, no change relative to D614G.	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Kim et al. (2021)	37077	A	T	nan
p.N501Y	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.1.1.7, Q.3, Q.1	Planas et al. (2021)	37067	A	T	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.N501Y	trafficking	extasciitilde2.5x cleavage of S2 relative to WA1 (D614G) wildtype by Alpha variant variant as measured by mass spectrometry of Vero-TMPRSS culture.	B.1.1.7, Q.3, Q.1	Esclera et al. (2021)	37067	A	T	nan
p.N501Y	trafficking	VSV pseudotype B.1.1.7 showed no significant difference in cell entry relative to wild type in 6 cell lines. Cell fusion proficiency was unchanged.	B.1.1.7, Q.3, Q.1	Hoffman et al. (2021)	37067	A	T	nan
p.N501Y	trafficking	The entry efficiencies of Spike pseudotyped viruses bearing N501Y Variant 1 (B.1.1.7) mutant were about 3 to 4.4 times higher than that of the WT pseudovirus when viral input was normalized, suggesting that these spike variants promote the infectivity of SARS-CoV-2.	B.1.1.7, Q.3, Q.1	Hu et al. (2021)	37067	A	T	nan
p.N501Y	trafficking	More efficient infectivity (24h) compared to wild type, in Caco-2 cells extasciitilde9x, Vero extasciitilde8x, and Calu-3 extasciitilde8x. Compare to wild type at extasciitilde5x across cell types.	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Kim et al. (2021)	37077	A	T	nan
p.N501Y	trafficking	extasciitilde4x more efficient S2 domain cleavage compared to wild type, no change relative to D614G alone in Caco-2 cells, mid-range of three cell line tested (Vero and Calu-3).	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Kim et al. (2021)	37077	A	T	nan
p.N501Y	trafficking	9x more infectivity than D614G alone in HEK293T-ACE2 cells 48h post-transduction.	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Kuzmina et al. (2021)	74091	A	T	nan
p.N501Y	trafficking	Decreased stability of RBD expression in yeast, suggesting decreased Spike protein stability.	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Motozono et al. (2021)	37077	A	T	nan
p.N501Y	trafficking	Lentiviral pseudotyped with this individual mutation from B.1.1.7 was tested on ACE2.293T cells. Luciferase activity was measured two days postinfection, showing slightly increased infection rate amongst the cells. [in what is essentially a replicate experiment in the same paper, because each B.1.351 lineage variant was independetly evaluated and N501 is in both lineages, a significant decrease was observed, therefore the error bars described in this paper should be interpreted carefully]	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Tada et al. (2021)	37077	A	T	nan
p.N501Y	trafficking	Lentiviral pseudotyped with this mutation set from B.1.1.7 was tested on ACE2.293T cells. Luciferase activity was measured two days postinfection, showing significant (40%) increase in infection rate amongst the cells, much more than the effect of either the deletion or the point mutation alone, suggetsing that this combination has a synergistic effect contributing to cell entry fitness, moreso than this combination with the addition of P681H.	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Tada et al. (2021)	37077	A	T	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.N501Y	trafficking	Lentiviral pseudotyped with this mutation set from B.1.1.7 was tested on ACE2.293T cells. Luciferase activity was measured two days postinfection, showing significant (40%) increase in infection rate amongst the cells, much more than the effect of either the deletion or the point mutation alone, suggetsing that this combination has a synergistic effect contributing to cell entry fitness, but to a smaller extent than N501Y and the deletion alone.	Q.8, Q.3, Q.1, B.1.1.7	Tada et al. (2021)	37075	A	T	nan
p.N501Y	trafficking	Live virus was tested ex vivo in reconstituted brochial epithelium, and out competed wild type.	B.1.1.7, Q.3, Q.1	Touret et al. (2021)	37067	A	T	nan
p.N501Y	transmissibility	We estimate that this [B.1.1.17] variant has a 43–90% (range of 95% credible intervals 38–130%) higher reproduction number than preexisting variants. Data from other countries yield similar results: we estimate that R for VOC 202012/01 relative to other lineages is 55% (45–66%) higher in Denmark, 74% (66–82%) higher in Switzerland, and 59% (56–63%) higher in the United States, with consistent rates of displacement across regions within each country.	B.1.1.7, Q.3, Q.1	Davies et al. (2021)	37067	A	T	nan
p.N501Y	transmissibility	Based on 36920 COVID Symptom Study app users reported SARS-CoV-2 test positivity in late 2020, Rt of B.1.1.7 was 1.35x (95% CI 1.02-1.69) relative to pre-existing variants. However, Rt fell below 1 during regional and national lockdowns, even in regions with high proportions of infections with the B.1.1.7 variant.	B.1.1.7, Q.3, Q.1	Graham et al. (2021)	37067	A	T	nan
p.N501Y	transmissibility	Ontario, Feb 2021: The secondary attack rate for VOC index cases in this matched cohort was 1.31 times higher than non-VOC index cases (RR	B.1.1.7, Q.3, Q.1	Lindstrøm et al. (2021)	37067	A	T	nan
p.N501Y	transmissibility	Primary cases infected with B.1.1.7 had an increased transmissibility of 1.5-1.7 times that of primary cases infected with other lineages. The increased transmissibility of B.1.1.7 was multiplicative across age and viral load.	B.1.1.7, Q.3, Q.1	Lyngse et al. (2021)	37067	A	T	nan
p.N501Y	transmissibility	Based on 300,000 RT-PCR samples collected from December 6th 2020 to February 10th 2021 in Israel, the B.1.1.7 is 45% (95% CI:20-60%) more transmissible than the wild-type strain, and become dominant in Israel within 3.5 weeks.	B.1.1.7, Q.3, Q.1	Munitz et al. (2021)	37067	A	T	nan
p.N501Y	transmissibility	At the national level (Italy), we estimated a mean relative transmissibility of B.1.1.7 (compared to historical lineages) ranging between 1.55 and 1.57 (with confidence intervals between 1.45 and 1.66).	B.1.1.7, Q.3, Q.1	Stefanelli et al. (2021)	37067	A	T	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.N501Y	vaccine efficacy	In Minnesota in early 2021 when Alpha was prevalent, vaccine efficacy was estimated as: mRNA-1273 86% (95%CI: 81-90.6%) and BNT162b2: 76% (95%CI: 69-81%) using age, sex, race, PCR testing and vaccination date matched cohorts of unvaccinated, Pfizer and Moderna vaccinees. [variant list included is ancestral Alpha, as this was an observational study no variant list was given]	B.1.1.7, Q.3, Q.1	Puranik et al. (2021)	37067	A	T	nan
p.N501Y	vaccine neutralization efficacy	nan	B.1.1.7, Q.3, Q.1	All vaccinees were on a strict 3 week interval for second dose (	37067	A	T	nan
p.N501Y	vaccine neutralization efficacy	Between December 19, 2020 and Jan 24, 2021, 7214 of 9109 eligible HCWs at Sheba Medical Center in Israel had received one or more doses of BNT162b2 (Pfizer) vaccine. Adjusted rate reduction in SARS-CoV-2 NAAT positivity infection compared with unvaccinated workers 1-14 days after 1st dose was 30% (95% CI: 2-50), and 75% (95% CI: 72-84) after 15-28 days. Adjusted rate reduction in symptomatic COVID-19 compared with unvaccinated workers 1-14 days after 1st dose was 47% (95% CI: 17-66), and 85% (95% CI: 71-92) after 15-28 days. [Though often cited as an indicator of VE for B.1.1.7, during this time period in Israel, the prevalence of the B.1.1.7 variant increased from extasciitilde20% to 50% of cases (covariants.org), therefore these VE numbers likely represent a mix of B.1.1.7 and other lineage effects.]	B.1.1.7, Q.3, Q.1	Amit et al. (2021)	37067	A	T	nan
p.N501Y	vaccine neutralization efficacy	Observed 1.3-fold reduction in neutralization efficiency of Pfizer vaccinee sera (collected 14 days after second dose) against pseudotype B.1.1.7 key variant lentivirus. Compare to 2.6-fold reduction against cultured B.1.1.7 virus.	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Bates et al. (2021)	37077	A	T	nan
p.N501Y	vaccine neutralization efficacy	Neutralization efficiency (ID50) against B.1.1.7 reduced 1.2x relative to D614G wildtype using pseudotyped VSV assay on 8 Moderna vaccinee sera one week post-booster.	B.1.1.7, Q.3, Q.1	Choi et al. (2021)	37067	A	T	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.N501Y	vaccine neutralization efficacy	20/29 sera after the first dose of Pfizer showed an average reduction in neutralization titres against the B.1.1.7 variant of 3.2 ± 5.7. After the second dose, the GMT was markedly increased compared with the first-dose titres, with a fold change of 1.9 ± 0.9 (mean ± s.d.). Neutralization GMT of 27 subjects post-infection was considerably higher (stronger) than after the second Pfizer dose, and 4.5x drop in B.1.1.7 neutralization was observed.	B.1.1.7, Q.3, Q.1	Collier et al. (2021)	37067	A	T	nan
p.N501Y	vaccine neutralization efficacy	1.2x drop in neutralization using sera collected from 14 healthy adult participants that received two injections of the mRNA-1273 (Moderna) vaccine at a dose of 100 µg (18-55 years: day 1 and day 14 post-2nd dose) against a recombinant single variant virus (modified replicating WA-1 cDNA clone) relative to contemporary circulating D614G variant (USA/GA-EHC-083E/2020) using a live-virus Focus Reduction Neutralization Test (FRNT) assay.	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Edara et al. (2021)	37077	A	T	nan
p.N501Y	vaccine neutralization efficacy	2.1x drop in neutralization using sera collected from 14 healthy adult participants that received two injections of the mRNA-1273 (Moderna) vaccine at a dose of 100 µg (18-55 years: day 1 (n	B.1.1.7, Q.3, Q.1	Edara et al. (2021)	37067	A	T	nan
p.N501Y	vaccine neutralization efficacy	Virus neutralisation activity (using a live SARS-CoV-2 microneutralisation assay (ND50)) by vaccine induced antibodies was 9-fold lower against the B.1.1.7 variant than against a canonical non B.1.1.7 lineage. Vaccine efficacy against symptomatic NAAT positive infection was similar for B.1.1.7 and non-B.1.1.7 lineages (74.6% [95%CI 41.6-88.9] and 84% [95% CI 70.7-91.4] respectively). Furthermore, vaccination with ChAdOx1 nCoV-19 results in a reduction in the duration of shedding and viral load, which may translate into a material impact on transmission of disease.	B.1.1.7, Q.3, Q.1	Emary et al. (2021)	37067	A	T	nan
p.N501Y	vaccine neutralization efficacy	ELISpot assays show T cell neutralization reduced by 15.4% in this B.1.1.7 pseudotype relative to wild type in 18-20 pooled patient samples post second mRNA vaccine dose, with no significant difference between Pfizer and Moderna cohorts. Reduction was stronger in the S1 subunit than S2 (separate peptide pools were used).	B.1.1.7, Q.3, Q.1	Gallagher et al. (2021)	37067	A	T	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.N501Y	vaccine neutralization efficacy	Pseudotyped B.1.1.7 virus has reduced neutralization activity vs wild type: 2.1x (30 sera Pfizer median 9 days post 2nd dose) and 2.3x (35 sera Moderna median 18 days post 2nd dose). This was NOT significant by ANOVA. Note that Y145del was actually noted in the paper as the effect of their DNA construct, but this is equivalent at the protein level to the more commonly annotated Y144del.	B.1.1.7, Q.3, Q.1	Garcia-Beltran et al. (2021)	37067	A	T	nan
p.N501Y	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)	B.1.1.7, Q.3, Q.1	Gong et al. (2021)	37067	A	T	nan
p.N501Y	vaccine neutralization efficacy	Using national surveillance data from Israel, using Pfizer vaccine and an estimated prevalence of the B.1.1.7 variant of 94.5% among SARS-CoV-2 infections: Adjusted estimates of vaccine effectiveness 7+ days after second dose were 95 · 3% (95% CI 94.9–95.7): 91.5% against asymptomatic SARS-CoV-2 infection (90 · 7–92 · 2: 40.9 vs 1.8 per 100 000 person-days), 97 · 0% against symptomatic COVID-19 (96.7–97.2%), 97.2% against COVID-19-related hospitalisation (96.8–97.5%), 97.5% against severe or critical COVID-19-related hospitalisation (97.1–97.8%), and 96.7% against COVID-19-related death (96.0–97.3%). In all age groups, as vaccine coverage increased, the incidence of SARS-CoV-2 outcomes declined	B.1.1.7, Q.3, Q.1	Haas et al. (2021)	37067	A	T	nan
p.N501Y	vaccine neutralization efficacy	A single dose of BNT162b2 (Pfizer) vaccine showed vaccine effectiveness of 70% (95% CI 55-85) 21 days after first dose and 85% (74-96) 7 days after two doses in the study population. Our findings show that the BNT162b2 vaccine can prevent both symptomatic and asymptomatic infection in working-age adults. This cohort (8203 treatment, 15121 control) was vaccinated when the dominant variant in circulation was B.1.1.7 and shows effectiveness against this variant.	B.1.1.7, Q.3, Q.1	Hall et al. (2021)	37067	A	T	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.N501Y	vaccine neutralization efficacy	A single dose of BNT162b2 vaccine demonstrated vaccine effectiveness [symptomatic or asymptomatic in cohort opf routinely NAAT-monitored UK HCWs] of 72% (95% CI 58-86) 21 days after first dose and 86% (95% CI 76-97) seven days after two doses in the antibody negative cohort. This cohort was vaccinated when the dominant variant in circulation was B.1.1.7 and demonstrates effectiveness against this variant.	B.1.1.7, Q.3, Q.1	Hall et al. (2021)	37067	A	T	nan
p.N501Y	vaccine neutralization efficacy	NVX-CoV2373 [Novavax] vaccine in phase 3 trial was 89.7% (95% CI, 80.2-94.6) effective in preventing COVID-19, with no hospitalizations or deaths reported. There were five cases of severe Covid-19, all in the placebo group. Post hoc analysis revealed efficacies of 96.4% (73.8-99.5) and 86.3% (71.3-93.5) against the prototype strain and B.1.1.7 variant, respectively.	B.1.1.7, Q.3, Q.1	Heath et al. (2021)	37067	A	T	nan
p.N501Y	vaccine neutralization efficacy	VSV pseudotype B.1.1.7 showed 1.77-fold reduction in neutralization efficiency vs wild type in 15 Pfizer BNT162b2 vaccinee sera 13-15 days post second dose. Cell fusion proficiency was unchanged.	B.1.1.7, Q.3, Q.1	Hoffman et al. (2021)	37067	A	T	nan
p.N501Y	vaccine neutralization efficacy	B.1.1.7 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 no statistically sognificant change in neutralization effiacacy.	B.1.1.7, Q.3, Q.1	Ikegame et al. (2021)	37067	A	T	nan
p.N501Y	vaccine neutralization efficacy	The presence of this variant in 189 post-mRNA-vaccination COVID-19 cases was proportionally in line with lineage prevalence in Northen California during the study period, suggesting no effect of these variants on immune escape.	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Jacobson et al. (2021)	37077	A	T	nan
p.N501Y	vaccine neutralization efficacy	This variant showed no change in Pfizer sera (one or two dose) neutralization efficiency vs D614G (using lentivirus pseudotype).	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Kuzmina et al. (2021)	37077	A	T	nan
p.N501Y	vaccine neutralization efficacy	Neutralizing antibody titers increased in previously infected vaccinees relative to uninfected vaccinees 5.2-fold against B.1.1.7 (contrast with 3.4 fold against original SARS-CoV-2).	B.1.1.7, Q.3, Q.1	Leier et al. (2021)	37067	A	T	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.N501Y	vaccine neutralization efficacy	SARS-CoV-2 infection was confirmed in three HCWs working a single shift: all presented with mild symptoms of COVID-19. The two physicians were fully vaccinated with BNT162b2 vaccine, with the second dose administered 1 month before symptom onset. Both had high titres of IgG anti-spike antibodies at the time of diagnosis. WGS confirmed that all virus strains were VOC 202012/01-lineage B.1.1.7, suggesting a common source of exposure. Epidemiological investigation revealed that the suspected source was a SARS-CoV-2-positive patient who required endotracheal intubation due to severe COVID-19. All procedures were carried out using a full suite of personal protective equipment (PPE).	B.1.1.7, Q.3, Q.1	Loconsole et al. (2021)	37067	A	T	nan
p.N501Y	vaccine neutralization efficacy	We found that a single dose of the BNT162b2 vaccine is about 60-70% effective at preventing symptomatic disease in adults aged 70 years and older in England and that two doses are about 85-90% effective. Those who were vaccinated and went on to have symptoms had a 44% lower risk of being admitted hospital and a 51% lower risk of death compared with people who were unvaccinated. We also found that a single dose of the ChAdOx1-S vaccine was about 60-75% effective against symptomatic disease and provided an additional protective effect against hospital admission—it is too early to assess the effect on mortality. The B.1.1.7 variant now dominates in the UK and these results will largely reflect vaccine effectiveness against this variant.	B.1.1.7, Q.3, Q.1	Lopez Bernal et al. (2021)	37067	A	T	nan
p.N501Y	vaccine neutralization efficacy	In sera 1-2 weeks after BNT162b2 first dose, from six patients previously infected with B.1, antibody titer in a microneutralization assay was on average 8192 for B.1.351 virus. This compares favorably (stronger) to post-infection neutralization titer against all variants tested in the same sera (wild type, B.1.1.7, B.1.351, and P.1).	B.1.1.7, Q.3, Q.1	Luftig et al. (2021)	37067	A	T	nan
p.N501Y	vaccine neutralization efficacy	Lineage B.1.1.7 spike–pseudotyped VSV was tested for neutralization vs Wuhan reference genome pseudotype in 40 sera collected 7 or 21 days post-booster dose. Statistically significant change (22%) in neutralization was observed among the 26 sera from those <	B.1.1.7, Q.3, Q.1	Muik et al. (2021)	37067	A	T	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.N501Y	vaccine neutralization efficacy	We observed a sharp decline in cases when 50% of the elderly population was 2 weeks beyond their first vaccination dose and at a time point during which the B.1.1.7 variant gained transmission dominance. In support of this finding, it was suggested that, after the first vaccination dose, more than 70% of patients develop neutralization antibodies,15 and the vaccine efficiency can reach 85%.	B.1.1.7, Q.3, Q.1	Munitz et al. (2021)	37067	A	T	nan
p.N501Y	vaccine neutralization efficacy	Detectable antibodies against B.1.1.7 at various time points using pseudotyped lentivirus neutralization in Moderna vaccinee cohort: Day 29 33%, Day 43 100%, Day 119 100%, Day 209 96%. Detectable antibodies against B.1.1.7 at various time points using live virus FRNT neutralization in Moderna vaccinee cohort: Day 29 54%, Day 43 100%, Day 119 100%, Day 209 88%. Detectable antibodies against B.1.1.7 at various time points using ACE2 blocking assay in Moderna vaccinee cohort: Day 29 83%, Days 43,119,209 100%.	B.1.1.7, Q.3, Q.1	Pegu et al (2021)	37067	A	T	nan
p.N501Y	vaccine neutralization efficacy	The sera of 16 individuals with time course collection was evaulated against VSV pseudotypes: neutralized D614G at week 2, whereas B.1.1.7 started to be neutralized at week 3, although less efficiently than D614G. B.1.1.7 and D614G strains were similarly neutralized at week 4 (1 week after booster dose).	B.1.1.7, Q.3, Q.1	Planas et al. (2021)	37067	A	T	nan
p.N501Y	vaccine neutralization efficacy	Human sera from 6 two-dose Pfizer vaccinated individuals (47-68 days post 1st-dose) can neutralize both the reference USA-WA1/2020 strain and the mouse adapted SARS-CoV-2 strain that contains the N501Y spike mutation with similar efficiency.	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Rathnasinghe et al. (2021)	37077	A	T	nan
p.N501Y	vaccine neutralization efficacy	After one dose, individuals with prior infection showed enhanced T cell immunity, antibody secreting memory B cell response to spike and neutralizing antibodies effective against B.1.1.7 (authentic cell culture supernatants). By comparison, HCW receiving one vaccine dose without prior infection showed reduced immunity against variants. B.1.1.7 spike mutations resulted in increased, abrogated or unchanged T cell responses depending on human leukocyte antigen (HLA) polymorphisms. Study was 26 each post-infection and post first dose HCWs.	B.1.1.7, Q.3, Q.1	Reynolds et al. (2021)	37067	A	T	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.N501Y	vaccine neutralization efficacy	The NAb titers (PRNT50) of sera collected from 38 vaccine recipients four-weeks after the second dose of inactivated whole-virion SARS-CoV-2 BBV152/COVAXIN vaccine [which contains D614G] were not significantly different between B.1.1.7 virus and ancestral D614G virus.	B.1.1.7, Q.3, Q.1	Sapkal et al. (2021)	37067	A	T	nan
p.N501Y	vaccine neutralization efficacy	Pseudotyped B.1.1.7 Spike variants lentivirus. 3.5x reduction in neutralization with Moderna vaccinated patient sera after 29 days (1st dose). 2.0x reduction in neutralization with Moderna vaccinated patient sera after 57 days (2nd dose). 2.1x reduction in neutralization with Novavax Phase 1 post-vaccination sera.	B.1.1.7, Q.3, Q.1	Shen et al. (2021)	37067	A	T	nan
p.N501Y	vaccine neutralization efficacy	Neutralization assays of B.1.1.7 virus showed a reduction of 2.5-fold (14 days post 2nd dose AstraZeneca, n	B.1.1.7, Q.3, Q.1	Supasa et al. (2021)	37067	A	T	nan
p.N501Y	vaccine neutralization efficacy	Vaccine elicited antibodies neutralized virus with the B.1.1.7 spike protein with titers similar to D614G virus. Serum specimens from individuals vaccinated with the BNT162b2 mRNA vaccine neutralized D614G virus with titers that were on average 7-fold greater than convalescent sera.	B.1.1.7, Q.3, Q.1	Tada et al. (2021)	37067	A	T	nan
p.N501Y	vaccine neutralization efficacy	PBMCs of Pfizer/BioNTech BNT162b2 (n	B.1.1.7, Q.3, Q.1	Tarke et al. (2021)	37067	A	T	nan
p.N501Y	vaccine neutralization efficacy	In a cohort of 20 patients 8+ weeks after second vaccine dose of Moderna (mRNA-1273) or Pfizer-BioNTech (BNT162b2) vaccines, a modest decrease in neutralization by vaccine plasma was observed.	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Wang et al. (2021)	37077	A	T	nan
p.N501Y	vaccine neutralization efficacy	1.4x improvement in neutralization by serum collected 2 to 3 weeks after the second dose from vaccinees who had received BBIBP-CorV (pVNT50 against VSV pseudotyped as B.1.1.7). Convalescent plasma had similar titer against wild type as the BBIBP-CorV vaccinee sera. 2x reduction in neutralization by serum collected 2 to 3 weeks after the second dose from vaccinees who had received CoronaVac (pVNT50 against VSV pseudotyped as B.1.1.7). Convalescent plasma had similar titer against wild type as the CoronaVac vaccinee sera.	B.1.1.7, Q.3, Q.1	Wang et al. (2021)	37067	A	T	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.N501Y	vaccine neutralization efficacy	No significant difference in T-cell response to B.1.1.7 was observed (vs. ancestral) in blood drawn from 28 participants received the Pfizer-BioNTech vaccine and 2 received the Moderna vaccine. This is despite three mutations (Y144del, D614G, and P681H) overlapping T-cell epitope hotspots.	B.1.1.7, Q.3, Q.1	Woldemeskel et al. (2021)	37067	A	T	nan
p.N501Y	vaccinee plasma binding	1.17x increase in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in previously non-seroconverted subjects. 1.09x increase in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in post-infection vaccinees.	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Gong et al. (2021)	37077	A	T	nan
p.N501Y	vaccinee plasma binding	This variant combination (representing B.1.1.7 aka Alpha) showed no change in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in previously non-seroconverted subjects. 1.28x 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.1.1.7, Q.3, Q.1	Gong et al. (2021)	37067	A	T	nan
p.N501Y	viral load	Using lack of S probe detection as a proxy for B.1.1.7 status, 275 putative B.1.1.7 samples and 390 "wild type" SARS-CoV-2 positive samples in Wales were compared for Ct values, suggesting extasciitilde12-fold increase (extasciitilde3.5 Ct decrease) in viral load for B.1.1.7 samples.	B.1.1.7, Q.3, Q.1	Couzens et al. (2021)	37067	A	T	nan
p.N501Y	viral load	We found that the British variant (clade B.1.1.7), compared to an ancestral SARS-CoV-2 clade B virus, produced higher levels of infectious virus late in infection and had a higher replicative fitness in human airway, alveolar and intestinal organoid models.	B.1.1.7, Q.3, Q.1	Lamers et al. (2021)	37067	A	T	nan
p.N501Y	viral load	This study reveals that B.1.1.7 SARS-CoV-2 variant is a slower-growing virus than parental B.1. Further, a higher replication along with reduced infectious viral titer was hypothesized to be linked to higher transmission with reduced pathogenicity.	B.1.1.7, Q.3, Q.1	Nyayanit et al. (2021)	37067	A	T	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.N501Y	viral load	In a study of 1260 ICU subjects, viral load distributions (collected within 48h of admission) were elevated in both seropositive and seronegative subjects infected with B.1.1.7 ("UK variant"). PG: The PANGO tool defining Spike variants for B.1.1.7 are listed here, whereas the paper only used a test for D1118H.	B.1.1.7, Q.3, Q.1	Ratcliff et al. (2021)	37067	A	T	nan
p.N501Y	viral load	B.1.1.7 samples showed average Ct cycle threshold of 21.9 vs 23 for wildtype (i.e. extasciitilde2x higher viral load) comparing 37758 and 22535 samples respectively.	B.1.1.7, Q.3, Q.1	Roquebert et al. (2021)	37067	A	T	nan
p.N501Y	viral load	The median Ct value of RT-qPCR tests of the N-gene target in the Daxing B.1.1.7 group was significantly lower than the Shunyi B.1.470 group (P	B.1.1.7, Q.3, Q.1	Song et al. (2021)	37067	A	T	nan
p.N501Y	viral load	The 249 B.1.1.7 (a.k.a. N501Y.V1) variant cases in three Paris hospital labs had a extasciitilde10-fold viral load increase (extasciitilde3.3 Ct drop in N gene probe) compared to 332 ancestral lineage cases from the same time frame (2020-12-20 to 2021-02-26). PG: BUT there is a discrepancy in drop between the ORF1ab and N probes, with the former suggesting only a 2-fold drop, consistent with the drop observed in B.1.351. This might indicate higher subgenomic RNA content in B.1.1.7 skewing the change.	B.1.1.7, Q.3, Q.1	Teyssou et al. (2021)	37067	A	T	nan
p.N501Y	virion structure	CryoEM analysis of B.1.1.7 demonstrates an increased propensity for 'up', receptor accessible conformation of the Spike protein trimer.	B.1.1.7, Q.3, Q.1	Cai et al. (2021)	37067	A	T	nan
p.N501Y	virion structure	Estimated free energy change (ddG) for this variant is 0.69 kcal/mol (i.e. stabilizing relative to wild type)	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Spratt et al. (2021)	37077	A	T	nan
p.N501Y	virion structure	The Ratio of S2 (processed Spike) to full length Spike is higher for this mutation combination, due to a drop in the full length Spike measured, suggesting that this mutation compensates for decreased Spike production by improved proteolytic processing.	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Tada et al. (2021)	37077	A	T	nan
p.N501Y	virion structure	The Ratio of S2 (processed Spike) to full length Spike is higher for this mutation combination, due to a drop in the full length Spike measured, suggesting that this mutation compensates for decreased Spike production by improved proteolytic processing.	Q.8, Q.3, Q.1, B.1.1.7	Tada et al. (2021)	37075	A	T	nan
p.A570D	ACE2 receptor binding affinity	Six fold increase in affinity for ACE2 by the B.1.1.7 lineage vs wild type is driven by a drop in observed dissociation rate constant.	B.1.1.7, Q.3, Q.1	Collier et al. (2021)	37140	C	A	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.A570D	ACE2 receptor binding affinity	Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant showed a 1.18x increase in binding (KD) relative to D614G, mostly due to decreased in "off-rate" a.k.a. dissociation rate (Kdis).	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Gong et al. (2021)	37150	C	A	nan
p.A570D	ACE2 receptor binding affinity	Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant combination (representing B.1.1.7 aka Alpha) had 5.43x increased binding relative to D614G alone.	B.1.1.7, Q.3, Q.1	Gong et al. (2021)	37140	C	A	nan
p.A570D	ACE2 receptor binding affinity	Flow cytometry was used on recombinant VSV proteins and yeast surface display to assess the binding of a labeled soluble ACE2 protein to cells expressing B.1.1.7. We observed a dramatic increase (relative to D614G) in binding of soluble ACE2 to B.1.1.7, and to a lesser extent to B.1.351, which both carry the N501Y mutation (see Fig 3).	B.1.1.7, Q.3, Q.1	Planas et al. (2021)	37140	C	A	nan
p.A570D	ACE2 receptor binding affinity	This mutation causes major decrease in binding affinity vs. wild type as measured by IC50 vs pseudotyped lentivirus.	B.1.1.7, Q.3, Q.1	Tada et al. (2021)	37140	C	A	nan
p.A570D	anthropozoonotic events	First documented cases of domestic cat and dog infections with the B.1.1.7 strain.	B.1.1.7, Q.3, Q.1	Hamer et al. (2021)	37140	C	A	nan
p.A570D	antibody epitope effects	Wildtype elicits immune response, COVID-19 cohort epitope score > 99th percentile of the 497 prepandemic controls, mutant raises PIWAS epitope score from 3.6% to 6.2% (improved immune recognition) Together with other B1.1.7 lineage mutational changes (Spike: Y144del,N501Y, P681H, 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.	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Haynes et al. (2021)	37150	C	A	nan
p.A570D	antibody epitope effects	extasciitilde20x resistence to mAb CQ038 by B.1.1.7 pseudotyped virus	B.1.1.7, Q.3, Q.1	Hu et al. (2021)	37140	C	A	nan
p.A570D	antibody epitope effects	Lessens the potency of mAbs COVA2-17 (extasciitilde5x, similar to N501Y alone), COVA1-12 (extasciitilde11x) and COVA1-21 (>100x), which do not compete allosterically.	B.1.1.7, Q.3, Q.1	Rees-Spear et al. (2021)	37140	C	A	nan
p.A570D	antibody epitope effects	Reduction in neutralization by mAbs COVA2-15 (extasciitilde9x), B38 (extasciitilde14x), S309 (extasciitilde190x) by this B.1.1.7 pseudotyped virus model.	B.1.1.7, Q.3, Q.1	Shen et al. (2021)	37140	C	A	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.A570D	antibody epitope effects	B.1.1.7 pseudotyped virus model impairs binding by RBD-directed mAb 910-30. B.1.1.7 pseudotyped virus model abolishes N-terminal-domain-directed mAbs 5-24, 4-8, and 4A8. B.1.1.7 pseudotyped virus model impairs binding by N-terminal-domain-directed mAbs 2-17, 4-19, 5-7.	B.1.1.7, Q.3, Q.1	Wang et al. (2021)	37140	C	A	nan
p.A570D	clinical indicators	After adjusting for the age factor, in a prospective Chinese cohort study B.1.1.7 variant infection (compared to B.1.140) was the risk factor for C-reactive protein (P	B.1.1.7, Q.3, Q.1	Song et al. (2021)	37140	C	A	nan
p.A570D	convalescent plasma binding	1.29x increase in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset.	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Gong et al. (2021)	37150	C	A	nan
p.A570D	convalescent plasma binding	This variant combination (representing B.1.1.7 aka Alpha) showed a 1.15x increase in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset.	B.1.1.7, Q.3, Q.1	Gong et al. (2021)	37140	C	A	nan
p.A570D	convalescent plasma escape	Neutralization capacity GMT of 27 subjects' sera post-infection was considerably higher (stronger) than after the second Pfizer dose, and 4.5x drop in B.1.1.7 neutralization was observed.	B.1.1.7, Q.3, Q.1	Collier et al. (2021)	37140	C	A	nan
p.A570D	convalescent plasma escape	NTD-specific nAbs showed a substantial (3-450x) decrease in neutralization potency against the recently reported highly transmissible B.1.1.7 variant of concern, whereas RBD-specific nAbs were either unaffected or showed lower decreases in potency.	B.1.1.7, Q.3, Q.1	Graham et al. (2021)	37140	C	A	nan
p.A570D	convalescent plasma escape	Neutralizing antibody titers of 2/20 (10%) samples showed >10x reduction (sera collected extasciitilde1mo post Jan 2020 first wave in China). Neutralizing antibody titers of 8/20 samples (40%) decreased below an ID50 threshold of 40 (sera collected extasciitilde8mo post Jan 2020 first wave in China).	B.1.1.7, Q.3, Q.1	Hu et al. (2021)	37140	C	A	nan
p.A570D	convalescent plasma escape	Using a new rapid neutralization assay, based on reporter cells that become positive for GFP after overnight infection, sera from 58 convalescent individuals collected up to 9 months after symptoms, similarly neutralized B.1.1.7 and D614G.	B.1.1.7, Q.3, Q.1	Planas et al. (2021)	37140	C	A	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.A570D	convalescent plasma escape	Maximum fold-decrease in potency for the serum samples from mild illness was 8.2 but the majority of samples showed less than a 3-fold change. Similarly, the maximum decrease seen for samples from hospitalized patients was a 9.1-fold change, but most of the samples showed minimal change in the potency of their neutralization. Overall, three samples from each cohort (8%) showed a 5–10-fold reduction, but as they were potently neutralizing sera, the reduced ID50 values were still >1:100.	B.1.1.7, Q.3, Q.1	Rees-Spear et al. (2021)	37140	C	A	nan
p.A570D	convalescent plasma escape	Neutralization activity of convalescent sera tested decreased <2x with this B.1.1.7 pseudotyped virus.	B.1.1.7, Q.3, Q.1	Shen et al. (2021)	37140	C	A	nan
p.A570D	convalescent plasma escape	We analyzed 34 convalescent samples including the WHONIBSC 20/130 reference serum, and, although a few sera showed near identical FRNT 50 values, the FRNT50 dilutions for the B.1.1.7 strain were 2.9-fold lower (geometric mean) than those for the Victoria strain ($p < 0.0001$). Sera from 13 subjects post-B.1.1.7 infection showed no significant change in neutralization against Victoria (extasciitildewild type), suggesting that B.1.1.7 infection also protects against ancestral virus. [Note that D1119H was included in the original paper, assuming typographical error and correcting to D1118H]	B.1.1.7, Q.3, Q.1	Supasa et al. (2021)	37140	C	A	nan
p.A570D	convalescent plasma escape	Loss of neutralizing activity using 6 hyperimmune immunoglobulin preparations from convalescent plasma was minimal against B.1.1.7 (1.9-fold). Neutralization against 10 convalescent plasma was poorer.	B.1.1.7, Q.3, Q.1	Tang et al. (2021)	37140	C	A	nan
p.A570D	convalescent plasma escape	The neutralizing activity of 8/20 convalescent sera was significantly lower against this pseudotyped virus model of B.1.1.7, yet almost no effect was detected using the live B.1.1.7 virus.	B.1.1.7, Q.3, Q.1	Wang et al. (2021)	37140	C	A	nan
p.A570D	environmental condition stability	Treatment with heat, soap and ethanol revealed similar inactivation profiles indicative of a comparable susceptibility towards disinfection. Furthermore, we observed comparable surface stability on steel, silver, copper and face masks.	B.1.1.7, Q.3, Q.1	Meister et al. (2021)	37140	C	A	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.A570D	environmental condition stability	No differences in the stability of B.1.1.7 observed in the absence of simulated sunlight at either 20°C or 40°C (with a mean time for a 90% loss of viral infectivity across all dark conditions of 6.2 hours). However, a small but statistically significant difference in the stability was observed in simulated sunlight at 20°C and 20% relative humidity, with B.1.1.7 restoring wild type 90% loss time of 11 minutes vs. 7 and 8 minutes for B.1.319 (D614G) and B.28 (V367F) early 2020 viruses respectively.	B.1.1.7, Q.3, Q.1	Schuit et al. (2021)	37140	C	A	nan
p.A570D	outcome hazard ratio	Danish study of the B.1.1.7 lineage shows hospital admission odds ratio of 1.63 vs other lineages. The adjusted OR was increased in all strata of age.	B.1.1.7, Q.3, Q.1	Bager et al. (2021)	37140	C	A	nan
p.A570D	outcome hazard ratio	The mortality hazard ratio associated with infection with [B.1.1.7] compared with infection with previously circulating variants was 1.64 (95% confidence interval 1.32 to 2.04) in patients who tested positive for covid-19 in the community (54906 matched pairs of participants who tested positive for SARS-CoV-2 in pillar 2 between 1 October 2020 and 29 January 2021). In this comparatively low risk group, this represents an increase in deaths from 2.5 to 4.1 per 1000 detected cases.	B.1.1.7, Q.3, Q.1	Challen et al. (2021)	37140	C	A	nan
p.A570D	outcome hazard ratio	Using UK data 1 November 2020 to 14 February 2021, while correcting for misclassification of PCR test Spike Gene Target Failure (SGTF) and missingness in SGTF status, we estimate that the hazard of death associated with B.1.1.7 is 61% (42–82%) higher than with pre-existing variants after adjustment for age, sex, ethnicity, deprivation, residence in a care home, the local authority of residence and test date. This corresponds to the absolute risk of death for a 55–69-year-old man increasing from 0.6% to 0.9% (95% confidence interval, 0.8–1.0%) within 28 days of a positive test in the community.	B.1.1.7, Q.3, Q.1	Davies et al. (2021)	37140	C	A	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.A570D	outcome hazard ratio	341 samples collected Nov 9 to Dec 20, 2020 were sequenced from two London (UK) hospitals. 198 (58%) of 341 had B.1.1.7 infection and 143 (42%) had non-B.1.1.7 infection. No evidence was found of an association between severe disease and death and lineage (B.1.1.7 vs non-B.1.1.7) in unadjusted analyses (prevalence ratio [PR] 0 · 97 [95% CI 0 · 72-1 · 31]), or in analyses adjusted for hospital, sex, age, comorbidities, and ethnicity (adjusted PR 1 · 02 [0 · 76-1 · 38]).	B.1.1.7, Q.3, Q.1	Frampton et al. (2021)	37140	C	A	nan
p.A570D	outcome hazard ratio	On average across 7 European countries studied, using B.1.1.7 defining mutations: Significant shift to asymptomatic cases (27.4% vs 18.6% for non-VOC cases). Significant shift to infection in those without pre-existing conditions (44.8% vs 89% for non-VOC cases). Significant increase in hospitalization rate (11% vs 7.5% for non-VOC cases). Significant increase in ICU rate (1.4% vs 0.6% for non-VOC cases). Significant decrease in death rate (2.0% vs vs 4.0% for non-VOC cases).	B.1.1.7, Q.3, Q.1	Funk et al. (2021)	37140	C	A	nan
p.A570D	outcome hazard ratio	From Sept 28 to Dec 27, 2020, positive COVID-19 tests were reported by 36 920 COVID Symptom Study app users whose region was known and who reported as healthy on app sign-up. We found no changes in reported symptoms or disease duration associated with B.1.1.7.	B.1.1.7, Q.3, Q.1	Graham et al. (2021)	37140	C	A	nan
p.A570D	outcome hazard ratio	Using primarily S-defining mutations for lineage B.1.1.7, most models of hospitalization and fatality risk ratios from consortium members show elevated ratios (extasciitilde1.3-1.7x).	B.1.1.7, Q.3, Q.1	NERVTAG Consortium (2021)	37140	C	A	nan
p.A570D	outcome hazard ratio	The matching-adjusted conditional odds ratio of hospitalisation was 1.58 (95% confidence interval 1.50 to 1.67) for COVID-19 patients infected with a SGTF-associated variant [primarily B.1.1.7], compared to those infected with non-SGTF-associated variants. The effect was modified by age (p<0.001), with ORs of 0.96-1.13 below age 20 years and 1.57-1.67 in age groups 40 years or older.	B.1.1.7, Q.3, Q.1	Nyberg et al. (2021)	37140	C	A	nan
p.A570D	reinfection	36920 COVID Symptom Study app users reported SARS-CoV-2 test positivity in late 2020. Possible reinfections were identified in 249 (0.7% [95% CI 0.6-0.8]) of 36509 app users who reported a positive swab test before Oct 1, 2020, but there was no evidence that the frequency of reinfections was higher for the B.1.1.7 variant than for pre-existing variants.	B.1.1.7, Q.3, Q.1	Graham et al. (2021)	37140	C	A	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.A570D	reinfection	Second infection in December 2020 with B.1.1.7 after April 2020 initial infection with B.2 in a 78-year-old man with a history of Type 2 diabetes mellitus, diabetic nephropathy on hemodialysis, chronic obstructive pulmonary disease (COPD), mixed central and obstructive sleep apnea, ischemic heart disease, with no history of immunosuppression.	B.1.1.7, Q.3, Q.1	Harrington et al. (2021)	37140	C	A	nan
p.A570D	reinfection	Reinfection with Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) B.1.1.7 variant in an immunocompromised 16yo female with end stage renal disease 94 days after initial infection with a B.1.2 lineage virus. Both lineages were the prevalent one at the time of 1st and 2nd infections respectively in Texas, where the patient was located (suggesting exposure risk rather than lineage immune evasion).	B.1.1.7, Q.3, Q.1	Marquez et al. (2021)	37140	C	A	nan
p.A570D	reinfection	Partial sequencing of S gene reveals two cases of probable early 2021 B.1.1.7 lineage reinfection from non-B.1.1.7 original cases in Lombardy, with 45 to 90 days between infections (less than the typical 90 day guideline for this call). Patients were 56 and 58yo, immunocompenent, with one a former smoker with obesity and dyslipidemia. One case required intubation during first infection, but presented with mild symptoms upon reinfection. The other case convalesced at home during the first episode, but required CPAP support in the subacute clinical unit upon reinfection.	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Novazzi et al. (2021)	37150	C	A	nan
p.A570D	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.1.1.7, Q.3, Q.1	Planas et al. (2021)	37140	C	A	nan
p.A570D	trafficking	extasciitilde2.5x cleavage of S2 relative to WA1 (D614G) wildtype by Alpha variant variant as measured by mass spectrometry of Vero-TMPRSS culture.	B.1.1.7, Q.3, Q.1	Esclera et al. (2021)	37140	C	A	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.A570D	trafficking	VSV pseudotype B.1.1.7 showed no significant difference in cell entry relative to wild type in 6 cell lines. Cell fusion proficiency was unchanged.	B.1.1.7, Q.3, Q.1	Hoffman et al. (2021)	37140	C	A	nan
p.A570D	trafficking	The entry efficiencies of Spike pseudotyped viruses bearing N501Y Variant 1 (B.1.1.7) mutant were about 3 to 4.4 times higher than that of the WT pseudovirus when viral input was normalized, suggesting that these spike variants promote the infectivity of SARS-CoV-2.	B.1.1.7, Q.3, Q.1	Hu et al. (2021)	37140	C	A	nan
p.A570D	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 statistically significant increased infection rate amongst the cells.	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Tada et al. (2021)	37150	C	A	nan
p.A570D	trafficking	Live virus was tested ex vivo in reconstituted brochial epithelium, and out competed wild type.	B.1.1.7, Q.3, Q.1	Touret et al. (2021)	37140	C	A	nan
p.A570D	transmissibility	We estimate that this [B.1.1.17] variant has a 43–90% (range of 95% credible intervals 38–130%) higher reproduction number than preexisting variants. Data from other countries yield similar results: we estimate that R for VOC 202012/01 relative to other lineages is 55% (45–66%) higher in Denmark, 74% (66–82%) higher in Switzerland, and 59% (56–63%) higher in the United States, with consistent rates of displacement across regions within each country.	B.1.1.7, Q.3, Q.1	Davies et al. (2021)	37140	C	A	nan
p.A570D	transmissibility	Based on 36920 COVID Symptom Study app users reported SARS-CoV-2 test positivity in late 2020, Rt of B.1.1.7 was 1.35x (95% CI 1.02-1.69) relative to pre-existing variants. However, Rt fell below 1 during regional and national lockdowns, even in regions with high proportions of infections with the B.1.1.7 variant.	B.1.1.7, Q.3, Q.1	Graham et al. (2021)	37140	C	A	nan
p.A570D	transmissibility	Ontario, Feb 2021: The secondary attack rate for VOC index cases in this matched cohort was 1.31 times higher than non-VOC index cases (RR	B.1.1.7, Q.3, Q.1	Lindstrøm et al. (2021)	37140	C	A	nan
p.A570D	transmissibility	Primary cases infected with B.1.1.7 had an increased transmissibility of 1.5-1.7 times that of primary cases infected with other lineages. The increased transmissibility of B.1.1.7 was multiplicative across age and viral load.	B.1.1.7, Q.3, Q.1	Lyngse et al. (2021)	37140	C	A	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.A570D	transmissibility	Based on 300,000 RT-PCR samples collected from December 6th 2020 to February 10th 2021 in Israel, the B.1.1.7 is 45% (95% CI:20-60%) more transmissible than the wild-type strain, and become dominant in Israel within 3.5 weeks.	B.1.1.7, Q.3, Q.1	Munitz et al. (2021)	37140	C	A	nan
p.A570D	transmissibility	At the national level (Italy), we estimated a mean relative transmissibility of B.1.1.7 (compared to historical lineages) ranging between 1.55 and 1.57 (with confidence intervals between 1.45 and 1.66).	B.1.1.7, Q.3, Q.1	Stefanelli et al. (2021)	37140	C	A	nan
p.A570D	vaccine efficacy	In Minnesota in early 2021 when Alpha was prevalent, vaccine efficacy was estimated as: mRNA-1273 86% (95%CI: 81-90.6%) and BNT162b2: 76% (95%CI: 69-81%) using age, sex, race, PCR testing and vaccination date matched cohorts of unvaccinated, Pfizer and Moderna vaccinees. [variant list included is ancestral Alpha, as this was an observational study no variant list was given]	B.1.1.7, Q.3, Q.1	Puranik et al. (2021)	37140	C	A	nan
p.A570D	vaccine neutralization efficacy	nan	B.1.1.7, Q.3, Q.1	All vaccinees were on a strict 3 week interval for second dose (	37140	C	A	nan
p.A570D	vaccine neutralization efficacy	Between December 19, 2020 and Jan 24, 2021, 7214 of 9109 eligible HCWs at Sheba Medical Center in Israel had received one or more doses of BNT162b2 (Pfizer) vaccine. Adjusted rate reduction in SARS-CoV-2 NAAT positivity infection compared with unvaccinated workers 1-14 days after 1st dose was 30% (95% CI: 2-50), and 75% (95% CI: 72-84) after 15-28 days. Adjusted rate reduction in symptomatic COVID-19 compared with unvaccinated workers 1-14 days after 1st dose was 47% (95% CI: 17-66), and 85% (95% CI: 71-92) after 15-28 days. [Though often cited as an indicator of VE for B.1.1.7, during this time period in Israel, the prevalence of the B.1.1.7 variant increased from extasciitilde20% to 50% of cases (covariants.org), therefore these VE numbers likely represent a mix of B.1.1.7 and other lineage effects.]	B.1.1.7, Q.3, Q.1	Amit et al. (2021)	37140	C	A	nan
p.A570D	vaccine neutralization efficacy	Neutralization efficiency (ID50) against B.1.1.7 reduced 1.2x relative to D614G wildtype using pseudotyped VSV assay on 8 Moderna vaccinee sera one week post-booster.	B.1.1.7, Q.3, Q.1	Choi et al. (2021)	37140	C	A	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.A570D	vaccine neutralization efficacy	20/29 sera after the first dose of Pfizer showed an average reduction in neutralization titres against the B.1.1.7 variant of 3.2 ± 5.7. After the second dose, the GMT was markedly increased compared with the first-dose titres, with a fold change of 1.9 ± 0.9 (mean ± s.d.). Neutralization GMT of 27 subjects post-infection was considerably higher (stronger) than after the second Pfizer dose, and 4.5x drop in B.1.1.7 neutralization was observed.	B.1.1.7, Q.3, Q.1	Collier et al. (2021)	37140	C	A	nan
p.A570D	vaccine neutralization efficacy	2.1x drop in neutralization using sera collected from 14 healthy adult participants that received two injections of the mRNA-1273 (Moderna) vaccine at a dose of 100 µg (18-55 years: day 1 (n	B.1.1.7, Q.3, Q.1	Edara et al. (2021)	37140	C	A	nan
p.A570D	vaccine neutralization efficacy	Virus neutralisation activity (using a live SARS-CoV-2 microneutralisation assay (ND50)) by vaccine induced antibodies was 9-fold lower against the B.1.1.7 variant than against a canonical non B.1.1.7 lineage. Vaccine efficacy against symptomatic NAAT positive infection was similar for B.1.1.7 and non-B.1.1.7 lineages (74.6% [95%CI 41.6-88.9] and 84% [95% CI 70.7-91.4] respectively). Furthermore, vaccination with ChAdOx1 nCoV-19 results in a reduction in the duration of shedding and viral load, which may translate into a material impact on transmission of disease.	B.1.1.7, Q.3, Q.1	Emary et al. (2021)	37140	C	A	nan
p.A570D	vaccine neutralization efficacy	ELISpot assays show T cell neutralization reduced by 15.4% in this B.1.1.7 pseudotype relative to wild type in 18-20 pooled patient samples post second mRNA vaccine dose, with no significant difference between Pfizer and Moderna cohorts. Reduction was stronger in the S1 subunit than S2 (separate peptide pools were used).	B.1.1.7, Q.3, Q.1	Gallagher et al. (2021)	37140	C	A	nan
p.A570D	vaccine neutralization efficacy	Pseudotyped B.1.1.7 virus has reduced neutralization activity vs wild type: 2.1x (30 sera Pfizer median 9 days post 2nd dose) and 2.3x (35 sera Moderna median 18 days post 2nd dose). This was NOT significant by ANOVA. Note that Y145del was actually noted in the paper as the effect of their DNA construct, but this is equivalent at the protein level to the more commonly annotated Y144del.	B.1.1.7, Q.3, Q.1	Garcia-Beltran et al. (2021)	37140	C	A	nan
p.A570D	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)	B.1.1.7, Q.3, Q.1	Gong et al. (2021)	37140	C	A	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.A570D	vaccine neutralization efficacy	Using national surveillance data from Israel, using Pfizer vaccine and an estimated prevalence of the B.1.1.7 variant of 94.5% among SARS-CoV-2 infections: Adjusted estimates of vaccine effectiveness 7+ days after second dose were 95 · 3% (95% CI 94.9–95.7): 91.5% against asymptomatic SARS-CoV-2 infection (90 · 7–92 · 2: 40.9 vs 1.8 per 100 000 person-days), 97 · 0% against symptomatic COVID-19 (96.7–97.2%), 97.2% against COVID-19-related hospitalisation (96.8–97.5%), 97.5% against severe or critical COVID-19-related hospitalisation (97.1–97.8%), and 96.7% against COVID-19-related death (96.0–97.3%). In all age groups, as vaccine coverage increased, the incidence of SARS-CoV-2 outcomes declined	B.1.1.7, Q.3, Q.1	Haas et al. (2021)	37140	C	A	nan
p.A570D	vaccine neutralization efficacy	A single dose of BNT162b2 (Pfizer) vaccine showed vaccine effectiveness of 70% (95% CI 55-85) 21 days after first dose and 85% (74-96) 7 days after two doses in the study population. Our findings show that the BNT162b2 vaccine can prevent both symptomatic and asymptomatic infection in working-age adults. This cohort (8203 treatment, 15121 control) was vaccinated when the dominant variant in circulation was B.1.1.7 and shows effectiveness against this variant.	B.1.1.7, Q.3, Q.1	Hall et al. (2021)	37140	C	A	nan
p.A570D	vaccine neutralization efficacy	A single dose of BNT162b2 vaccine demonstrated vaccine effectiveness [symptomatic or asymptomatic in cohort opf routinely NAAT-monitored UK HCWs] of 72% (95% CI 58-86) 21 days after first dose and 86% (95% CI 76-97) seven days after two doses in the antibody negative cohort. This cohort was vaccinated when the dominant variant in circulation was B.1.1.7 and demonstrates effectiveness against this variant.	B.1.1.7, Q.3, Q.1	Hall et al. (2021)	37140	C	A	nan
p.A570D	vaccine neutralization efficacy	NVX-CoV2373 [Novavax] vaccine in phase 3 trial was 89.7% (95% CI, 80.2-94.6) effective in preventing COVID-19, with no hospitalizations or deaths reported. There were five cases of severe Covid-19, all in the placebo group. Post hoc analysis revealed efficacies of 96.4% (73.8-99.5) and 86.3% (71.3-93.5) against the prototype strain and B.1.1.7 variant, respectively.	B.1.1.7, Q.3, Q.1	Heath et al. (2021)	37140	C	A	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.A570D	vaccine neutralization efficacy	VSV pseudotype B.1.1.7 showed 1.77-fold reduction in neutralization efficiency vs wild type in 15 Pfizer BNT162b2 vaccinee sera 13-15 days post second dose. Cell fusion proficiency was unchanged.	B.1.1.7, Q.3, Q.1	Hoffman et al. (2021)	37140	C	A	nan
p.A570D	vaccine neutralization efficacy	B.1.1.7 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 no statistically sognificant change in neutralization effiacacy.	B.1.1.7, Q.3, Q.1	Ikegame et al. (2021)	37140	C	A	nan
p.A570D	vaccine neutralization efficacy	Neutralizing antibody titers increased in previously infected vaccinees relative to uninfected vaccinees 5.2-fold against B.1.1.7 (contrast with 3.4 fold against original SARS-CoV-2).	B.1.1.7, Q.3, Q.1	Leier et al. (2021)	37140	C	A	nan
p.A570D	vaccine neutralization efficacy	SARS-CoV-2 infection was confirmed in three HCWs working a single shift: all presented with mild symptoms of COVID-19. The two physicians were fully vaccinated with BNT162b2 vaccine, with the second dose administered 1 month before symptom onset. Both had high titres of IgG anti-spike antibodies at the time of diagnosis. WGS confirmed that all virus strains were VOC 202012/01-lineage B.1.1.7, suggesting a common source of exposure. Epidemiological investigation revealed that the suspected source was a SARS-CoV-2-positive patient who required endotracheal intubation due to severe COVID-19. All procedures were carried out using a full suite of personal protective equipment (PPE).	B.1.1.7, Q.3, Q.1	Loconsole et al. (2021)	37140	C	A	nan
p.A570D	vaccine neutralization efficacy	We found that a single dose of the BNT162b2 vaccine is about 60-70% effective at preventing symptomatic disease in adults aged 70 years and older in England and that two doses are about 85-90% effective. Those who were vaccinated and went on to have symptoms had a 44% lower risk of being admitted hospital and a 51% lower risk of death compared with people who were unvaccinated. We also found that a single dose of the ChAdOx1-S vaccine was about 60-75% effective against symptomatic disease and provided an additional protective effect against hospital admission—it is too early to assess the effect on mortality. The B.1.1.7 variant now dominates in the UK and these results will largely reflect vaccine effectiveness against this variant.	B.1.1.7, Q.3, Q.1	Lopez Bernal et al. (2021)	37140	C	A	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.A570D	vaccine neutralization efficacy	In sera 1-2 weeks after BNT162b2 first dose, from six patients previously infected with B.1, antibody titer in a microneutralization assay was on average 8192 for B.1.351 virus. This compares favorably (stronger) to post-infection neutralization titer against all variants tested in the same sera (wild type, B.1.1.7, B.1.351, and P.1).	B.1.1.7, Q.3, Q.1	Luftig et al. (2021)	37140	C	A	nan
p.A570D	vaccine neutralization efficacy	Lineage B.1.1.7 spike–pseudotyped VSV was tested for neutralization vs Wuhan reference genome pseudotype in 40 sera collected 7 or 21 days post-booster dose. Statistically significant change (22%) in neutralization was observed among the 26 sera from those <	B.1.1.7, Q.3, Q.1	Muik et al. (2021)	37140	C	A	nan
p.A570D	vaccine neutralization efficacy	We observed a sharp decline in cases when 50% of the elderly population was 2 weeks beyond their first vaccination dose and at a time point during which the B.1.1.7 variant gained transmission dominance. In support of this finding, it was suggested that, after the first vaccination dose, more than 70% of patients develop neutralization antibodies,15 and the vaccine efficiency can reach 85%.	B.1.1.7, Q.3, Q.1	Munitz et al. (2021)	37140	C	A	nan
p.A570D	vaccine neutralization efficacy	Detectable antibodies against B.1.1.7 at various time points using pseudotyped lentivirus neutralization in Moderna vaccinee cohort: Day 29 33%, Day 43 100%, Day 119 100%, Day 209 96%. Detectable antibodies against B.1.1.7 at various time points using live virus FRNT neutralization in Moderna vaccinee cohort: Day 29 54%, Day 43 100%, Day 119 100%, Day 209 88%. Detectable antibodies against B.1.1.7 at various time points using ACE2 blocking assay in Moderna vaccinee cohort: Day 29 83%, Days 43,119,209 100%.	B.1.1.7, Q.3, Q.1	Pegu et al (2021)	37140	C	A	nan
p.A570D	vaccine neutralization efficacy	The sera of 16 individuals with time course collection was evaulated against VSV pseudotypes: neutralized D614G at week 2, whereas B.1.1.7 started to be neutralized at week 3, although less efficiently than D614G. B.1.1.7 and D614G strains were similarly neutralized at week 4 (1 week after booster dose).	B.1.1.7, Q.3, Q.1	Planas et al. (2021)	37140	C	A	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.A570D	vaccine neutralization efficacy	After one dose, individuals with prior infection showed enhanced T cell immunity, antibody secreting memory B cell response to spike and neutralizing antibodies effective against B.1.1.7 (authentic cell culture supernatants). By comparison, HCW receiving one vaccine dose without prior infection showed reduced immunity against variants. B.1.1.7 spike mutations resulted in increased, abrogated or unchanged T cell responses depending on human leukocyte antigen (HLA) polymorphisms. Study was 26 each post-infection and post first dose HCWs.	B.1.1.7, Q.3, Q.1	Reynolds et al. (2021)	37140	C	A	nan
p.A570D	vaccine neutralization efficacy	The NAb titers (PRNT50) of sera collected from 38 vaccine recipients four-weeks after the second dose of inactivated whole-virion SARS-CoV-2 BBV152/COVAXIN vaccine [which contains D614G] were not significantly different between B.1.1.7 virus and ancestral D614G virus.	B.1.1.7, Q.3, Q.1	Sapkal et al. (2021)	37140	C	A	nan
p.A570D	vaccine neutralization efficacy	Pseudotyped B.1.1.7 Spike variants lentivirus. 3.5x reduction in neutralization with Moderna vaccinated patient sera after 29 days (1st dose). 2.0x reduction in neutralization with Moderna vaccinated patient sera after 57 days (2nd dose). 2.1x reduction in neutralization with Novavax Phase 1 post-vaccination sera.	B.1.1.7, Q.3, Q.1	Shen et al. (2021)	37140	C	A	nan
p.A570D	vaccine neutralization efficacy	Neutralization assays of B.1.1.7 virus showed a reduction of 2.5-fold (14 days post 2nd dose AstraZeneca, n	B.1.1.7, Q.3, Q.1	Supasa et al. (2021)	37140	C	A	nan
p.A570D	vaccine neutralization efficacy	Vaccine elicited antibodies neutralized virus with the B.1.1.7 spike protein with titers similar to D614G virus. Serum specimens from individuals vaccinated with the BNT162b2 mRNA vaccine neutralized D614G virus with titers that were on average 7-fold greater than convalescent sera.	B.1.1.7, Q.3, Q.1	Tada et al. (2021)	37140	C	A	nan
p.A570D	vaccine neutralization efficacy	PBMCs of Pfizer/BioNTech BNT162b2 (n	B.1.1.7, Q.3, Q.1	Tarke et al. (2021)	37140	C	A	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.A570D	vaccine neutralization efficacy	1.4x improvement in neutralization by serum collected 2 to 3 weeks after the second dose from vaccinees who had received BBIBP-CorV (pVNT50 against VSV pseudotyped as B.1.1.7). Convalescent plasma had similar titer against wild type as the BBIBP-CorV vaccinee sera. 2x reduction in neutralization by serum collected 2 to 3 weeks after the second dose from vaccinees who had received CoronaVac (pVNT50 against VSV pseudotyped as B.1.1.7). Convalescent plasma had similar titer against wild type as the CoronaVac vaccinee sera.	B.1.1.7, Q.3, Q.1	Wang et al. (2021)	37140	C	A	nan
p.A570D	vaccine neutralization efficacy	No significant difference in T-cell response to B.1.1.7 was observed (vs. ancestral) in blood drawn from 28 participants received the Pfizer-BioNTech vaccine and 2 received the Moderna vaccine. This is despite three mutations (Y144del, D614G, and P681H) overlapping T-cell epitope hotspots.	B.1.1.7, Q.3, Q.1	Woldemeskel et al. (2021)	37140	C	A	nan
p.A570D	vaccinee plasma binding	No significant change in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in previously non-seroconverted subjects. 1.04x 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.	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Gong et al. (2021)	37150	C	A	nan
p.A570D	vaccinee plasma binding	This variant combination (representing B.1.1.7 aka Alpha) showed no change in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in previously non-seroconverted subjects. 1.28x 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.1.1.7, Q.3, Q.1	Gong et al. (2021)	37140	C	A	nan
p.A570D	viral load	Using lack of S probe detection as a proxy for B.1.1.7 status, 275 putative B.1.1.7 samples and 390 "wild type" SARS-CoV-2 positive samples in Wales were compared for Ct values, suggesting extasciitilde12-fold increase (extasciitilde3.5 Ct decrease) in viral load for B.1.1.7 samples.	B.1.1.7, Q.3, Q.1	Couzens et al. (2021)	37140	C	A	nan
p.A570D	viral load	We found that the British variant (clade B.1.1.7), compared to an ancestral SARS-CoV-2 clade B virus, produced higher levels of infectious virus late in infection and had a higher replicative fitness in human airway, alveolar and intestinal organoid models.	B.1.1.7, Q.3, Q.1	Lamers et al. (2021)	37140	C	A	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.A570D	viral load	This study reveals that B.1.1.7 SARS-CoV-2 variant is a slower-growing virus than parental B.1. Further, a higher replication along with reduced infectious viral titer was hypothesized to be linked to higher transmission with reduced pathogenicity.	B.1.1.7, Q.3, Q.1	Nyayanit et al. (2021)	37140	C	A	nan
p.A570D	viral load	In a study of 1260 ICU subjects, viral load distributions (collected within 48h of admission) were elevated in both seropositive and seronegative subjects infected with B.1.1.7 ("UK variant"). PG: The PANGO tool defining Spike variants for B.1.1.7 are listed here, whereas the paper only used a test for D1118H.	B.1.1.7, Q.3, Q.1	Ratcliff et al. (2021)	37140	C	A	nan
p.A570D	viral load	B.1.1.7 samples showed average Ct cycle threshold of 21.9 vs 23 for wildtype (i.e. extasciitilde2x higher viral load) comparing 37758 and 22535 samples respectively.	B.1.1.7, Q.3, Q.1	Roquebert et al. (2021)	37140	C	A	nan
p.A570D	viral load	The median Ct value of RT-qPCR tests of the N-gene target in the Daxing B.1.1.7 group was significantly lower than the Shunyi B.1.470 group (P	B.1.1.7, Q.3, Q.1	Song et al. (2021)	37140	C	A	nan
p.A570D	viral load	The 249 B.1.1.7 (a.k.a. N501Y.V1) variant cases in three Paris hospital labs had a extasciitilde10-fold viral load increase (extasciitilde3.3 Ct drop in N gene probe) compared to 332 ancestral lineage cases from the same time frame (2020-12-20 to 2021-02-26). PG: BUT there is a discrepancy in drop between the ORF1ab and N probes, with the former suggesting only a 2-fold drop, consistent with the drop observed in B.1.351. This might indicate higher subgenomic RNA content in B.1.1.7 skewing the change.	B.1.1.7, Q.3, Q.1	Teyssou et al. (2021)	37140	C	A	nan
p.A570D	virion structure	CryoEM analysis of B.1.1.7 demonstrates an increased propensity for 'up', receptor accessible conformation of the Spike protein trimer.	B.1.1.7, Q.3, Q.1	Cai et al. (2021)	37140	C	A	nan
p.A570D	virion structure	Estimated that there is very little free energy change (ddG. -0.02 kcal/mol) for this variant (i.e. approx. same stability as wild type)	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Spratt et al. (2021)	37150	C	A	nan
p.A570D	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.	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Tada et al. (2021)	37150	C	A	nan
p.D1118H	ACE2 receptor binding affinity	Six fold increase in affinity for ACE2 by the B.1.1.7 lineage vs wild type is driven by a drop in observed dissociation rate constant.	B.1.1.7, Q.3, Q.1	Collier et al. (2021)	37143	G	C	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.D1118H	ACE2 receptor binding affinity	Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant showed a 1.23x increase in binding (KD) relative to D614G, mostly due to decreased in "off-rate" a.k.a. dissociation rate (Kdis).	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Gong et al. (2021)	37153	G	C	nan
p.D1118H	ACE2 receptor binding affinity	Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant combination (representing B.1.1.7 aka Alpha) had 5.43x increased binding relative to D614G alone.	B.1.1.7, Q.3, Q.1	Gong et al. (2021)	37143	G	C	nan
p.D1118H	ACE2 receptor binding affinity	Flow cytometry was used on recombinant VSV proteins and yeast surface display to assess the binding of a labeled soluble ACE2 protein to cells expressing B.1.1.7. We observed a dramatic increase (relative to D614G) in binding of soluble ACE2 to B.1.1.7, and to a lesser extent to B.1.351, which both carry the N501Y mutation (see Fig 3).	B.1.1.7, Q.3, Q.1	Planas et al. (2021)	37143	G	C	nan
p.D1118H	ACE2 receptor binding affinity	This mutation causes major decrease in binding affinity vs. wild type as measured by IC50 vs pseudotyped lentivirus.	B.1.1.7, Q.3, Q.1	Tada et al. (2021)	37143	G	C	nan
p.D1118H	T cell evasion	Mutation is predicted to lose the T cell epitope for people carrying DRB1*0301 and DRB1*0401, but not for example in those who are DRB1*0701 or DRB1*1501 who would be predicted to show an enhanced response. This is also observed in a study of 26 each post-infection and post first dose HCWs.	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Reynolds et al. (2021)	37153	G	C	nan
p.D1118H	anthropozoonotic events	First documented cases of domestic cat and dog infections with the B.1.1.7 strain.	B.1.1.7, Q.3, Q.1	Hamer et al. (2021)	37143	G	C	nan
p.D1118H	antibody epitope effects	Not in a major wildtype epitope, mutant has no significant effect on PIWAS epitope score Found in B.1.1.7 lineage, but assumed to not pay a major role in antigenicity.	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Haynes et al. (2021)	37153	G	C	nan
p.D1118H	antibody epitope effects	extasciitilde20x resistence to mAb CQ038 by B.1.1.7 pseudotyped virus	B.1.1.7, Q.3, Q.1	Hu et al. (2021)	37143	G	C	nan
p.D1118H	antibody epitope effects	Lessens the potency of mAbs COVA2-17 (extasciitilde5x, similar to N501Y alone), COVA1-12 (extasciitilde11x) and COVA1-21 (>100x), which do not compete allosterically.	B.1.1.7, Q.3, Q.1	Rees-Spear et al. (2021)	37143	G	C	nan
p.D1118H	antibody epitope effects	Reduction in neutralization by mAbs COVA2-15 (extasciitilde9x), B38 (extasciitilde14x), S309 (extasciitilde190x) by this B.1.1.7 pseudotyped virus model.	B.1.1.7, Q.3, Q.1	Shen et al. (2021)	37143	G	C	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.D1118H	antibody epitope effects	B.1.1.7 pseudotyped virus model impairs binding by RBD-directed mAb 910-30. B.1.1.7 pseudotyped virus model abolishes N-terminal-domain-directed mAbs 5-24, 4-8, and 4A8. B.1.1.7 pseudotyped virus model impairs binding by N-terminal-domain-directed mAbs 2-17, 4-19, 5-7.	B.1.1.7, Q.3, Q.1	Wang et al. (2021)	37143	G	C	nan
p.D1118H	clinical indicators	After adjusting for the age factor, in a prospective Chinese cohort study B.1.1.7 variant infection (compared to B.1.140) was the risk factor for C-reactive protein (P	B.1.1.7, Q.3, Q.1	Song et al. (2021)	37143	G	C	nan
p.D1118H	convalescent plasma binding	1.96x increase in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset.	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Gong et al. (2021)	37153	G	C	nan
p.D1118H	convalescent plasma binding	This variant combination (representing B.1.1.7 aka Alpha) showed a 1.15x increase in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset.	B.1.1.7, Q.3, Q.1	Gong et al. (2021)	37143	G	C	nan
p.D1118H	convalescent plasma escape	Neutralization capacity GMT of 27 subjects' sera post-infection was considerably higher (stronger) than after the second Pfizer dose, and 4.5x drop in B.1.1.7 neutralization was observed.	B.1.1.7, Q.3, Q.1	Collier et al. (2021)	37143	G	C	nan
p.D1118H	convalescent plasma escape	NTD-specific nAbs showed a substantial (3-450x) decrease in neutralization potency against the recently reported highly transmissible B.1.1.7 variant of concern, whereas RBD-specific nAbs were either unaffected or showed lower decreases in potency.	B.1.1.7, Q.3, Q.1	Graham et al. (2021)	37143	G	C	nan
p.D1118H	convalescent plasma escape	Neutralizing antibody titers of 2/20 (10%) samples showed >10x reduction (sera collected extasciitilde1mo post Jan 2020 first wave in China). Neutralizing antibody titers of 8/20 samples (40%) decreased below an ID50 threshold of 40 (sera collected extasciitilde8mo post Jan 2020 first wave in China).	B.1.1.7, Q.3, Q.1	Hu et al. (2021)	37143	G	C	nan
p.D1118H	convalescent plasma escape	Using a new rapid neutralization assay, based on reporter cells that become positive for GFP after overnight infection, sera from 58 convalescent individuals collected up to 9 months after symptoms, similarly neutralized B.1.1.7 and D614G.	B.1.1.7, Q.3, Q.1	Planas et al. (2021)	37143	G	C	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.D1118H	convalescent plasma escape	Maximum fold-decrease in potency for the serum samples from mild illness was 8.2 but the majority of samples showed less than a 3-fold change. Similarly, the maximum decrease seen for samples from hospitalized patients was a 9.1-fold change, but most of the samples showed minimal change in the potency of their neutralization. Overall, three samples from each cohort (8%) showed a 5–10-fold reduction, but as they were potently neutralizing sera, the reduced ID50 values were still >1:100.	B.1.1.7, Q.3, Q.1	Rees-Spear et al. (2021)	37143	G	C	nan
p.D1118H	convalescent plasma escape	Neutralization activity of convalescent sera tested decreased <2x with this B.1.1.7 pseudotyped virus.	B.1.1.7, Q.3, Q.1	Shen et al. (2021)	37143	G	C	nan
p.D1118H	convalescent plasma escape	We analyzed 34 convalescent samples including the WHONIBSC 20/130 reference serum, and, although a few sera showed near identical FRNT 50 values, the FRNT50 dilutions for the B.1.1.7 strain were 2.9-fold lower (geometric mean) than those for the Victoria strain ($p < 0.0001$). Sera from 13 subjects post-B.1.1.7 infection showed no significant change in neutralization against Victoria (extasciitildewild type), suggesting that B.1.1.7 infection also protects against ancestral virus. [Note that D1119H was included in the original paper, assuming typographical error and correcting to D1118H]	B.1.1.7, Q.3, Q.1	Supasa et al. (2021)	37143	G	C	nan
p.D1118H	convalescent plasma escape	Loss of neutralizing activity using 6 hyperimmune immunoglobulin preparations from convalescent plasma was minimal against B.1.1.7 (1.9-fold). Neutralization against 10 convalescent plasma was poorer.	B.1.1.7, Q.3, Q.1	Tang et al. (2021)	37143	G	C	nan
p.D1118H	convalescent plasma escape	The neutralizing activity of 8/20 convalescent sera was significantly lower against this pseudotyped virus model of B.1.1.7, yet almost no effect was detected using the live B.1.1.7 virus.	B.1.1.7, Q.3, Q.1	Wang et al. (2021)	37143	G	C	nan
p.D1118H	environmental condition stability	Treatment with heat, soap and ethanol revealed similar inactivation profiles indicative of a comparable susceptibility towards disinfection. Furthermore, we observed comparable surface stability on steel, silver, copper and face masks.	B.1.1.7, Q.3, Q.1	Meister et al. (2021)	37143	G	C	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.D1118H	environmental condition stability	No differences in the stability of B.1.1.7 observed in the absence of simulated sunlight at either 20°C or 40°C (with a mean time for a 90% loss of viral infectivity across all dark conditions of 6.2 hours). However, a small but statistically significant difference in the stability was observed in simulated sunlight at 20°C and 20% relative humidity, with B.1.1.7 restoring wild type 90% loss time of 11 minutes vs. 7 and 8 minutes for B.1.319 (D614G) and B.28 (V367F) early 2020 viruses respectively.	B.1.1.7, Q.3, Q.1	Schuit et al. (2021)	37143	G	C	nan
p.D1118H	outcome hazard ratio	Danish study of the B.1.1.7 lineage shows hospital admission odds ratio of 1.63 vs other lineages. The adjusted OR was increased in all strata of age.	B.1.1.7, Q.3, Q.1	Bager et al. (2021)	37143	G	C	nan
p.D1118H	outcome hazard ratio	The mortality hazard ratio associated with infection with [B.1.1.7] compared with infection with previously circulating variants was 1.64 (95% confidence interval 1.32 to 2.04) in patients who tested positive for covid-19 in the community (54906 matched pairs of participants who tested positive for SARS-CoV-2 in pillar 2 between 1 October 2020 and 29 January 2021). In this comparatively low risk group, this represents an increase in deaths from 2.5 to 4.1 per 1000 detected cases.	B.1.1.7, Q.3, Q.1	Challen et al. (2021)	37143	G	C	nan
p.D1118H	outcome hazard ratio	Using UK data 1 November 2020 to 14 February 2021, while correcting for misclassification of PCR test Spike Gene Target Failure (SGTF) and missingness in SGTF status, we estimate that the hazard of death associated with B.1.1.7 is 61% (42–82%) higher than with pre-existing variants after adjustment for age, sex, ethnicity, deprivation, residence in a care home, the local authority of residence and test date. This corresponds to the absolute risk of death for a 55–69-year-old man increasing from 0.6% to 0.9% (95% confidence interval, 0.8–1.0%) within 28 days of a positive test in the community.	B.1.1.7, Q.3, Q.1	Davies et al. (2021)	37143	G	C	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.D1118H	outcome hazard ratio	341 samples collected Nov 9 to Dec 20, 2020 were sequenced from two London (UK) hospitals. 198 (58%) of 341 had B.1.1.7 infection and 143 (42%) had non-B.1.1.7 infection. No evidence was found of an association between severe disease and death and lineage (B.1.1.7 vs non-B.1.1.7) in unadjusted analyses (prevalence ratio [PR] 0 · 97 [95% CI 0 · 72-1 · 31]), or in analyses adjusted for hospital, sex, age, comorbidities, and ethnicity (adjusted PR 1 · 02 [0 · 76-1 · 38]).	B.1.1.7, Q.3, Q.1	Frampton et al. (2021)	37143	G	C	nan
p.D1118H	outcome hazard ratio	On average across 7 European countries studied, using B.1.1.7 defining mutations: Significant shift to asymptomatic cases (27.4% vs 18.6% for non-VOC cases). Significant shift to infection in those without pre-existing conditions (44.8% vs 89% for non-VOC cases). Significant increase in hospitalization rate (11% vs 7.5% for non-VOC cases). Significant increase in ICU rate (1.4% vs 0.6% for non-VOC cases). Significant decrease in death rate (2.0% vs vs 4.0% for non-VOC cases).	B.1.1.7, Q.3, Q.1	Funk et al. (2021)	37143	G	C	nan
p.D1118H	outcome hazard ratio	From Sept 28 to Dec 27, 2020, positive COVID-19 tests were reported by 36 920 COVID Symptom Study app users whose region was known and who reported as healthy on app sign-up. We found no changes in reported symptoms or disease duration associated with B.1.1.7.	B.1.1.7, Q.3, Q.1	Graham et al. (2021)	37143	G	C	nan
p.D1118H	outcome hazard ratio	Using primarily S-defining mutations for lineage B.1.1.7, most models of hospitalization and fatality risk ratios from consortium members show elevated ratios (extasciitilde1.3-1.7x).	B.1.1.7, Q.3, Q.1	NERVTAG Consortium (2021)	37143	G	C	nan
p.D1118H	outcome hazard ratio	The matching-adjusted conditional odds ratio of hospitalisation was 1.58 (95% confidence interval 1.50 to 1.67) for COVID-19 patients infected with a SGTF-associated variant [primarily B.1.1.7], compared to those infected with non-SGTF-associated variants. The effect was modified by age (p<0.001), with ORs of 0.96-1.13 below age 20 years and 1.57-1.67 in age groups 40 years or older.	B.1.1.7, Q.3, Q.1	Nyberg et al. (2021)	37143	G	C	nan
p.D1118H	reinfection	36920 COVID Symptom Study app users reported SARS-CoV-2 test positivity in late 2020. Possible reinfections were identified in 249 (0.7% [95% CI 0.6-0.8]) of 36509 app users who reported a positive swab test before Oct 1, 2020, but there was no evidence that the frequency of reinfections was higher for the B.1.1.7 variant than for pre-existing variants.	B.1.1.7, Q.3, Q.1	Graham et al. (2021)	37143	G	C	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.D1118H	reinfection	Second infection in December 2020 with B.1.1.7 after April 2020 initial infection with B.2 in a 78-year-old man with a history of Type 2 diabetes mellitus, diabetic nephropathy on hemodialysis, chronic obstructive pulmonary disease (COPD), mixed central and obstructive sleep apnea, ischemic heart disease, with no history of immunosuppression.	B.1.1.7, Q.3, Q.1	Harrington et al. (2021)	37143	G	C	nan
p.D1118H	reinfection	Reinfection with Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) B.1.1.7 variant in an immunocompromised 16yo female with end stage renal disease 94 days after initial infection with a B.1.2 lineage virus. Both lineages were the prevalent one at the time of 1st and 2nd infections respectively in Texas, where the patient was located (suggesting exposure risk rather than lineage immune evasion).	B.1.1.7, Q.3, Q.1	Marquez et al. (2021)	37143	G	C	nan
p.D1118H	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.1.1.7, Q.3, Q.1	Planas et al. (2021)	37143	G	C	nan
p.D1118H	trafficking	extasciitilde2.5x cleavage of S2 relative to WA1 (D614G) wildtype by Alpha variant variant as measured by mass spectrometry of Vero-TMPRSS culture.	B.1.1.7, Q.3, Q.1	Esclera et al. (2021)	37143	G	C	nan
p.D1118H	trafficking	VSV pseudotype B.1.1.7 showed no significant difference in cell entry relative to wild type in 6 cell lines. Cell fusion proficiency was unchanged.	B.1.1.7, Q.3, Q.1	Hoffman et al. (2021)	37143	G	C	nan
p.D1118H	trafficking	The entry efficiencies of Spike pseudotyped viruses bearing N501Y Variant 1 (B.1.1.7) mutant were about 3 to 4.4 times higher than that of the WT pseudovirus when viral input was normalized, suggesting that these spike variants promote the infectivity of SARS-CoV-2.	B.1.1.7, Q.3, Q.1	Hu et al. (2021)	37143	G	C	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.D1118H	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 mild decrease in infection rate amongst the cells, hence this individual variant is unlikely to contribute to cell entry fitness.	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Tada et al. (2021)	37153	G	C	nan
p.D1118H	trafficking	Live virus was tested ex vivo in reconstituted brochial epithelium, and out competed wild type.	B.1.1.7, Q.3, Q.1	Touret et al. (2021)	37143	G	C	nan
p.D1118H	transmissibility	We estimate that this [B.1.1.17] variant has a 43–90% (range of 95% credible intervals 38–130%) higher reproduction number than preexisting variants. Data from other countries yield similar results: we estimate that R for VOC 202012/01 relative to other lineages is 55% (45–66%) higher in Denmark, 74% (66–82%) higher in Switzerland, and 59% (56–63%) higher in the United States, with consistent rates of displacement across regions within each country.	B.1.1.7, Q.3, Q.1	Davies et al. (2021)	37143	G	C	nan
p.D1118H	transmissibility	Based on 36920 COVID Symptom Study app users reported SARS-CoV-2 test positivity in late 2020, Rt of B.1.1.7 was 1.35x (95% CI 1.02-1.69) relative to pre-existing variants. However, Rt fell below 1 during regional and national lockdowns, even in regions with high proportions of infections with the B.1.1.7 variant.	B.1.1.7, Q.3, Q.1	Graham et al. (2021)	37143	G	C	nan
p.D1118H	transmissibility	Ontario, Feb 2021: The secondary attack rate for VOC index cases in this matched cohort was 1.31 times higher than non-VOC index cases (RR	B.1.1.7, Q.3, Q.1	Lindstrøm et al. (2021)	37143	G	C	nan
p.D1118H	transmissibility	Primary cases infected with B.1.1.7 had an increased transmissibility of 1.5-1.7 times that of primary cases infected with other lineages. The increased transmissibility of B.1.1.7 was multiplicative across age and viral load.	B.1.1.7, Q.3, Q.1	Lyngse et al. (2021)	37143	G	C	nan
p.D1118H	transmissibility	Based on 300,000 RT-PCR samples collected from December 6th 2020 to February 10th 2021 in Israel, the B.1.1.7 is 45% (95% CI:20-60%) more transmissible than the wild-type strain, and become dominant in Israel within 3.5 weeks.	B.1.1.7, Q.3, Q.1	Munitz et al. (2021)	37143	G	C	nan
p.D1118H	transmissibility	At the national level (Italy), we estimated a mean relative transmissibility of B.1.1.7 (compared to historical lineages) ranging between 1.55 and 1.57 (with confidence intervals between 1.45 and 1.66).	B.1.1.7, Q.3, Q.1	Stefanelli et al. (2021)	37143	G	C	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.D1118H	vaccine efficacy	In Minnesota in early 2021 when Alpha was prevalent, vaccine efficacy was estimated as: mRNA-1273 86% (95%CI: 81-90.6%) and BNT162b2: 76% (95%CI: 69-81%) using age, sex, race, PCR testing and vaccination date matched cohorts of unvaccinated, Pfizer and Moderna vaccinees. [variant list included is ancestral Alpha, as this was an observational study no variant list was given]	B.1.1.7, Q.3, Q.1	Puranik et al. (2021)	37143	G	C	nan
p.D1118H	vaccine neutralization efficacy	nan	B.1.1.7, Q.3, Q.1	All vaccinees were on a strict 3 week interval for second dose (	37143	G	C	nan
p.D1118H	vaccine neutralization efficacy	Between December 19, 2020 and Jan 24, 2021, 7214 of 9109 eligible HCWs at Sheba Medical Center in Israel had received one or more doses of BNT162b2 (Pfizer) vaccine. Adjusted rate reduction in SARS-CoV-2 NAAT positivity infection compared with unvaccinated workers 1-14 days after 1st dose was 30% (95% CI: 2-50), and 75% (95% CI: 72-84) after 15-28 days. Adjusted rate reduction in symptomatic COVID-19 compared with unvaccinated workers 1-14 days after 1st dose was 47% (95% CI: 17-66), and 85% (95% CI: 71-92) after 15-28 days. [Though often cited as an indicator of VE for B.1.1.7, during this time period in Israel, the prevalence of the B.1.1.7 variant increased from extasciitilde20% to 50% of cases (covariants.org), therefore these VE numbers likely represent a mix of B.1.1.7 and other lineage effects.]	B.1.1.7, Q.3, Q.1	Amit et al. (2021)	37143	G	C	nan
p.D1118H	vaccine neutralization efficacy	Neutralization efficiency (ID50) against B.1.1.7 reduced 1.2x relative to D614G wildtype using pseudotyped VSV assay on 8 Moderna vaccinee sera one week post-booster.	B.1.1.7, Q.3, Q.1	Choi et al. (2021)	37143	G	C	nan
p.D1118H	vaccine neutralization efficacy	20/29 sera after the first dose of Pfizer showed an average reduction in neutralization titres against the B.1.1.7 variant of 3.2 ± 5.7. After the second dose, the GMT was markedly increased compared with the first-dose titres, with a fold change of 1.9 ± 0.9 (mean ± s.d.). Neutralization GMT of 27 subjects post-infection was considerably higher (stronger) than after the second Pfizer dose, and 4.5x drop in B.1.1.7 neutralization was observed.	B.1.1.7, Q.3, Q.1	Collier et al. (2021)	37143	G	C	nan
p.D1118H	vaccine neutralization efficacy	2.1x drop in neutralization using sera collected from 14 healthy adult participants that received two injections of the mRNA-1273 (Moderna) vaccine at a dose of 100 µg (18-55 years: day 1 (n	B.1.1.7, Q.3, Q.1	Edara et al. (2021)	37143	G	C	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.D1118H	vaccine neutralization efficacy	Virus neutralisation activity (using a live SARS-CoV-2 microneutralisation assay (ND50)) by vaccine induced antibodies was 9-fold lower against the B.1.1.7 variant than against a canonical non B.1.1.7 lineage. Vaccine efficacy against symptomatic NAAT positive infection was similar for B.1.1.7 and non-B.1.1.7 lineages (74.6% [95%CI 41.6-88.9] and 84% [95% CI 70.7-91.4] respectively). Furthermore, vaccination with ChAdOx1 nCoV-19 results in a reduction in the duration of shedding and viral load, which may translate into a material impact on transmission of disease.	B.1.1.7, Q.3, Q.1	Emary et al. (2021)	37143	G	C	nan
p.D1118H	vaccine neutralization efficacy	ELISpot assays show T cell neutralization reduced by 15.4% in this B.1.1.7 pseudotype relative to wild type in 18-20 pooled patient samples post second mRNA vaccine dose, with no significant difference between Pfizer and Moderna cohorts. Reduction was stronger in the S1 subunit than S2 (separate peptide pools were used).	B.1.1.7, Q.3, Q.1	Gallagher et al. (2021)	37143	G	C	nan
p.D1118H	vaccine neutralization efficacy	Pseudotyped B.1.1.7 virus has reduced neutralization activity vs wild type: 2.1x (30 sera Pfizer median 9 days post 2nd dose) and 2.3x (35 sera Moderna median 18 days post 2nd dose). This was NOT significant by ANOVA. Note that Y145del was actually noted in the paper as the effect of their DNA construct, but this is equivalent at the protein level to the more commonly annotated Y144del.	B.1.1.7, Q.3, Q.1	Garcia-Beltran et al. (2021)	37143	G	C	nan
p.D1118H	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)	B.1.1.7, Q.3, Q.1	Gong et al. (2021)	37143	G	C	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.D1118H	vaccine neutralization efficacy	Using national surveillance data from Israel, using Pfizer vaccine and an estimated prevalence of the B.1.1.7 variant of 94.5% among SARS-CoV-2 infections: Adjusted estimates of vaccine effectiveness 7+ days after second dose were 95 · 3% (95% CI 94.9–95.7): 91.5% against asymptomatic SARS-CoV-2 infection (90 · 7–92 · 2: 40.9 vs 1.8 per 100 000 person-days), 97 · 0% against symptomatic COVID-19 (96.7–97.2%), 97.2% against COVID-19-related hospitalisation (96.8–97.5%), 97.5% against severe or critical COVID-19-related hospitalisation (97.1–97.8%), and 96.7% against COVID-19-related death (96.0–97.3%). In all age groups, as vaccine coverage increased, the incidence of SARS-CoV-2 outcomes declined	B.1.1.7, Q.3, Q.1	Haas et al. (2021)	37143	G	C	nan
p.D1118H	vaccine neutralization efficacy	A single dose of BNT162b2 (Pfizer) vaccine showed vaccine effectiveness of 70% (95% CI 55-85) 21 days after first dose and 85% (74-96) 7 days after two doses in the study population. Our findings show that the BNT162b2 vaccine can prevent both symptomatic and asymptomatic infection in working-age adults. This cohort (8203 treatment, 15121 control) was vaccinated when the dominant variant in circulation was B.1.1.7 and shows effectiveness against this variant.	B.1.1.7, Q.3, Q.1	Hall et al. (2021)	37143	G	C	nan
p.D1118H	vaccine neutralization efficacy	A single dose of BNT162b2 vaccine demonstrated vaccine effectiveness [symptomatic or asymptomatic in cohort opf routinely NAAT-monitored UK HCWs] of 72% (95% CI 58-86) 21 days after first dose and 86% (95% CI 76-97) seven days after two doses in the antibody negative cohort. This cohort was vaccinated when the dominant variant in circulation was B.1.1.7 and demonstrates effectiveness against this variant.	B.1.1.7, Q.3, Q.1	Hall et al. (2021)	37143	G	C	nan
p.D1118H	vaccine neutralization efficacy	NVX-CoV2373 [Novavax] vaccine in phase 3 trial was 89.7% (95% CI, 80.2-94.6) effective in preventing COVID-19, with no hospitalizations or deaths reported. There were five cases of severe Covid-19, all in the placebo group. Post hoc analysis revealed efficacies of 96.4% (73.8-99.5) and 86.3% (71.3-93.5) against the prototype strain and B.1.1.7 variant, respectively.	B.1.1.7, Q.3, Q.1	Heath et al. (2021)	37143	G	C	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.D1118H	vaccine neutralization efficacy	VSV pseudotype B.1.1.7 showed 1.77-fold reduction in neutralization efficiency vs wild type in 15 Pfizer BNT162b2 vaccinee sera 13-15 days post second dose. Cell fusion proficiency was unchanged.	B.1.1.7, Q.3, Q.1	Hoffman et al. (2021)	37143	G	C	nan
p.D1118H	vaccine neutralization efficacy	B.1.1.7 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 no statistically sognificant change in neutralization effiacacy.	B.1.1.7, Q.3, Q.1	Ikegame et al. (2021)	37143	G	C	nan
p.D1118H	vaccine neutralization efficacy	Neutralizing antibody titers increased in previously infected vaccinees relative to uninfected vaccinees 5.2-fold against B.1.1.7 (contrast with 3.4 fold against original SARS-CoV-2).	B.1.1.7, Q.3, Q.1	Leier et al. (2021)	37143	G	C	nan
p.D1118H	vaccine neutralization efficacy	SARS-CoV-2 infection was confirmed in three HCWs working a single shift: all presented with mild symptoms of COVID-19. The two physicians were fully vaccinated with BNT162b2 vaccine, with the second dose administered 1 month before symptom onset. Both had high titres of IgG anti-spike antibodies at the time of diagnosis. WGS confirmed that all virus strains were VOC 202012/01-lineage B.1.1.7, suggesting a common source of exposure. Epidemiological investigation revealed that the suspected source was a SARS-CoV-2-positive patient who required endotracheal intubation due to severe COVID-19. All procedures were carried out using a full suite of personal protective equipment (PPE).	B.1.1.7, Q.3, Q.1	Loconsole et al. (2021)	37143	G	C	nan
p.D1118H	vaccine neutralization efficacy	We found that a single dose of the BNT162b2 vaccine is about 60-70% effective at preventing symptomatic disease in adults aged 70 years and older in England and that two doses are about 85-90% effective. Those who were vaccinated and went on to have symptoms had a 44% lower risk of being admitted hospital and a 51% lower risk of death compared with people who were unvaccinated. We also found that a single dose of the ChAdOx1-S vaccine was about 60-75% effective against symptomatic disease and provided an additional protective effect against hospital admission—it is too early to assess the effect on mortality. The B.1.1.7 variant now dominates in the UK and these results will largely reflect vaccine effectiveness against this variant.	B.1.1.7, Q.3, Q.1	Lopez Bernal et al. (2021)	37143	G	C	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.D1118H	vaccine neutralization efficacy	In sera 1-2 weeks after BNT162b2 first dose, from six patients previously infected with B.1, antibody titer in a microneutralization assay was on average 8192 for B.1.351 virus. This compares favorably (stronger) to post-infection neutralization titer against all variants tested in the same sera (wild type, B.1.1.7, B.1.351, and P.1).	B.1.1.7, Q.3, Q.1	Luftig et al. (2021)	37143	G	C	nan
p.D1118H	vaccine neutralization efficacy	Lineage B.1.1.7 spike–pseudotyped VSV was tested for neutralization vs Wuhan reference genome pseudotype in 40 sera collected 7 or 21 days post-booster dose. Statistically significant change (22%) in neutralization was observed among the 26 sera from those <	B.1.1.7, Q.3, Q.1	Muik et al. (2021)	37143	G	C	nan
p.D1118H	vaccine neutralization efficacy	We observed a sharp decline in cases when 50% of the elderly population was 2 weeks beyond their first vaccination dose and at a time point during which the B.1.1.7 variant gained transmission dominance. In support of this finding, it was suggested that, after the first vaccination dose, more than 70% of patients develop neutralization antibodies,15 and the vaccine efficiency can reach 85%.	B.1.1.7, Q.3, Q.1	Munitz et al. (2021)	37143	G	C	nan
p.D1118H	vaccine neutralization efficacy	Detectable antibodies against B.1.1.7 at various time points using pseudotyped lentivirus neutralization in Moderna vaccinee cohort: Day 29 33%, Day 43 100%, Day 119 100%, Day 209 96%. Detectable antibodies against B.1.1.7 at various time points using live virus FRNT neutralization in Moderna vaccinee cohort: Day 29 54%, Day 43 100%, Day 119 100%, Day 209 88%. Detectable antibodies against B.1.1.7 at various time points using ACE2 blocking assay in Moderna vaccinee cohort: Day 29 83%, Days 43,119,209 100%.	B.1.1.7, Q.3, Q.1	Pegu et al (2021)	37143	G	C	nan
p.D1118H	vaccine neutralization efficacy	The sera of 16 individuals with time course collection was evaulated against VSV pseudotypes: neutralized D614G at week 2, whereas B.1.1.7 started to be neutralized at week 3, although less efficiently than D614G. B.1.1.7 and D614G strains were similarly neutralized at week 4 (1 week after booster dose).	B.1.1.7, Q.3, Q.1	Planas et al. (2021)	37143	G	C	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.D1118H	vaccine neutralization efficacy	After one dose, individuals with prior infection showed enhanced T cell immunity, antibody secreting memory B cell response to spike and neutralizing antibodies effective against B.1.1.7 (authentic cell culture supernatants). By comparison, HCW receiving one vaccine dose without prior infection showed reduced immunity against variants. B.1.1.7 spike mutations resulted in increased, abrogated or unchanged T cell responses depending on human leukocyte antigen (HLA) polymorphisms. Study was 26 each post-infection and post first dose HCWs.	B.1.1.7, Q.3, Q.1	Reynolds et al. (2021)	37143	G	C	nan
p.D1118H	vaccine neutralization efficacy	The NAb titers (PRNT50) of sera collected from 38 vaccine recipients four-weeks after the second dose of inactivated whole-virion SARS-CoV-2 BBV152/COVAXIN vaccine [which contains D614G] were not significantly different between B.1.1.7 virus and ancestral D614G virus.	B.1.1.7, Q.3, Q.1	Sapkal et al. (2021)	37143	G	C	nan
p.D1118H	vaccine neutralization efficacy	Pseudotyped B.1.1.7 Spike variants lentivirus. 3.5x reduction in neutralization with Moderna vaccinated patient sera after 29 days (1st dose). 2.0x reduction in neutralization with Moderna vaccinated patient sera after 57 days (2nd dose). 2.1x reduction in neutralization with Novavax Phase 1 post-vaccination sera.	B.1.1.7, Q.3, Q.1	Shen et al. (2021)	37143	G	C	nan
p.D1118H	vaccine neutralization efficacy	Neutralization assays of B.1.1.7 virus showed a reduction of 2.5-fold (14 days post 2nd dose AstraZeneca, n	B.1.1.7, Q.3, Q.1	Supasa et al. (2021)	37143	G	C	nan
p.D1118H	vaccine neutralization efficacy	Vaccine elicited antibodies neutralized virus with the B.1.1.7 spike protein with titers similar to D614G virus. Serum specimens from individuals vaccinated with the BNT162b2 mRNA vaccine neutralized D614G virus with titers that were on average 7-fold greater than convalescent sera.	B.1.1.7, Q.3, Q.1	Tada et al. (2021)	37143	G	C	nan
p.D1118H	vaccine neutralization efficacy	PBMCs of Pfizer/BioNTech BNT162b2 (n	B.1.1.7, Q.3, Q.1	Tarke et al. (2021)	37143	G	C	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.D1118H	vaccine neutralization efficacy	1.4x improvement in neutralization by serum collected 2 to 3 weeks after the second dose from vaccinees who had received BBIBP-CorV (pVNT50 against VSV pseudotyped as B.1.1.7). Convalescent plasma had similar titer against wild type as the BBIBP-CorV vaccinee sera. 2x reduction in neutralization by serum collected 2 to 3 weeks after the second dose from vaccinees who had received CoronaVac (pVNT50 against VSV pseudotyped as B.1.1.7). Convalescent plasma had similar titer against wild type as the CoronaVac vaccinee sera.	B.1.1.7, Q.3, Q.1	Wang et al. (2021)	37143	G	C	nan
p.D1118H	vaccine neutralization efficacy	No significant difference in T-cell response to B.1.1.7 was observed (vs. ancestral) in blood drawn from 28 participants received the Pfizer-BioNTech vaccine and 2 received the Moderna vaccine. This is despite three mutations (Y144del, D614G, and P681H) overlapping T-cell epitope hotspots.	B.1.1.7, Q.3, Q.1	Woldemeskel et al. (2021)	37143	G	C	nan
p.D1118H	vaccinee plasma binding	1.09x increase in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in previously non-seroconverted subjects. 1.08x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in post-infection vaccinees.	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Gong et al. (2021)	37153	G	C	nan
p.D1118H	vaccinee plasma binding	This variant combination (representing B.1.1.7 aka Alpha) showed no change in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in previously non-seroconverted subjects. 1.28x 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.1.1.7, Q.3, Q.1	Gong et al. (2021)	37143	G	C	nan
p.D1118H	viral load	Using lack of S probe detection as a proxy for B.1.1.7 status, 275 putative B.1.1.7 samples and 390 ”wild type” SARS-CoV-2 positive samples in Wales were compared for Ct values, suggesting extasciitilde12-fold increase (extasciitilde3.5 Ct decrease) in viral load for B.1.1.7 samples.	B.1.1.7, Q.3, Q.1	Couzens et al. (2021)	37143	G	C	nan
p.D1118H	viral load	We found that the British variant (clade B.1.1.7), compared to an ancestral SARS-CoV-2 clade B virus, produced higher levels of infectious virus late in infection and had a higher replicative fitness in human airway, alveolar and intestinal organoid models.	B.1.1.7, Q.3, Q.1	Lamers et al. (2021)	37143	G	C	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.D1118H	viral load	This study reveals that B.1.1.7 SARS-CoV-2 variant is a slower-growing virus than parental B.1. Further, a higher replication along with reduced infectious viral titer was hypothesized to be linked to higher transmission with reduced pathogenicity.	B.1.1.7, Q.3, Q.1	Nyayanit et al. (2021)	37143	G	C	nan
p.D1118H	viral load	In a study of 1260 ICU subjects, viral load distributions (collected within 48h of admission) were elevated in both seropositive and seronegative subjects infected with B.1.1.7 ("UK variant"). PG: The PANGO tool defining Spike variants for B.1.1.7 are listed here, whereas the paper only used a test for D1118H.	B.1.1.7, Q.3, Q.1	Ratcliff et al. (2021)	37143	G	C	nan
p.D1118H	viral load	B.1.1.7 samples showed average Ct cycle threshold of 21.9 vs 23 for wildtype (i.e. extasciitilde2x higher viral load) comparing 37758 and 22535 samples respectively.	B.1.1.7, Q.3, Q.1	Roquebert et al. (2021)	37143	G	C	nan
p.D1118H	viral load	The median Ct value of RT-qPCR tests of the N-gene target in the Daxing B.1.1.7 group was significantly lower than the Shunyi B.1.470 group (P	B.1.1.7, Q.3, Q.1	Song et al. (2021)	37143	G	C	nan
p.D1118H	viral load	The 249 B.1.1.7 (a.k.a. N501Y.V1) variant cases in three Paris hospital labs had a extasciitilde10-fold viral load increase (extasciitilde3.3 Ct drop in N gene probe) compared to 332 ancestral lineage cases from the same time frame (2020-12-20 to 2021-02-26). PG: BUT there is a discrepancy in drop between the ORF1ab and N probes, with the former suggesting only a 2-fold drop, consistent with the drop observed in B.1.351. This might indicate higher subgenomic RNA content in B.1.1.7 skewing the change.	B.1.1.7, Q.3, Q.1	Teyssou et al. (2021)	37143	G	C	nan
p.D1118H	virion structure	CryoEM analysis of B.1.1.7 demonstrates an increased propensity for 'up', receptor accessible conformation of the Spike protein trimer.	B.1.1.7, Q.3, Q.1	Cai et al. (2021)	37143	G	C	nan
p.D614G	ACE2 receptor binding affinity	Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant showed a 1.18x increase in binding (KD) relative to D614G, mostly due to decreased in "off-rate" a.k.a. dissociation rate (Kdis).	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Gong et al. (2021)	37152	A	G	nan
p.D614G	ACE2 receptor binding affinity	Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant showed a 1.23x increase in binding (KD) relative to D614G, mostly due to decreased in "off-rate" a.k.a. dissociation rate (Kdis).	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Gong et al. (2021)	37152	A	G	nan
p.D614G	ACE2 receptor binding affinity	Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant showed a 1.51x increase in binding (KD) relative to D614G, mostly due to decreased in "off-rate" a.k.a. dissociation rate (Kdis).	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Gong et al. (2021)	37152	A	G	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.D614G	ACE2 receptor binding affinity	Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant combination (representing B.1.1.7 aka Alpha) had 5.43x increased binding relative to D614G alone.	B.1.1.7, Q.3, Q.1	Gong et al. (2021)	37142	A	G	nan
p.D614G	ACE2 receptor binding affinity	Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant showed a 1.1x decrease in binding (KD) relative to D614G.	Q.1	Gong et al. (2021)	44	A	G	nan
p.D614G	ACE2 receptor binding affinity	Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant showed a 2.52x increase in binding (KD) relative to D614G, mostly due to decreased in "off-rate" a.k.a. dissociation rate (Kdis). Compare to full Spike variant complements for major lineages containing this variant subset: 5.43x (B.1.1.7 aka Alpha), 3.56x (B.1.351 aka Beta), 4.24x (P.1 aka Gamma).	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Gong et al. (2021)	37152	A	G	nan
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.	Q.8, Q.3, Q.1, B.1.1.7	Gong et al. (2021)	37150	A	G	nan
p.D614G	ACE2 receptor binding affinity	Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant showed a 1.3x decrease in binding (KD) relative to D614G.	Q.1, B.1.1.7, Q.3, Q.4	Gong et al. (2021)	37144	A	G	nan
p.D614G	ACE2 receptor binding affinity	Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant showed a 1.12x decrease in binding (KD) relative to D614G.	Q.1, B.1.1.7, Q.3, Q.4	Gong et al. (2021)	37144	A	G	nan
p.D614G	ACE2 receptor binding affinity	Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant showed a slight decrease in binding (KD) relative to D614G.	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Gong et al. (2021)	37152	A	G	nan
p.D614G	ACE2 receptor binding affinity	In four cell lines (including 293T-hACE2 cells), this mutation combination increases infectivity vs D614G alone	B.1.1.7, Q.8, Q.3, Q.4, B.1.1.70, B.1.1.71, Q.1	Li et al. (2020)	37157	A	G	nan
p.D614G	ACE2 receptor binding affinity	Flow cytometry was used on recombinant VSV proteins and yeast surface display to assess the binding of a labeled soluble ACE2 protein to cells expressing B.1.1.7. We observed a dramatic increase (relative to D614G) in binding of soluble ACE2 to B.1.1.7, and to a lesser extent to B.1.351, which both carry the N501Y mutation (see Fig 3).	B.1.1.7, Q.3, Q.1	Planas et al. (2021)	37142	A	G	nan
p.D614G	anthropozoonotic events	First documented cases of domestic cat and dog infections with the B.1.1.7 strain.	B.1.1.7, Q.3, Q.1	Hamer et al. (2021)	37142	A	G	nan
p.D614G	antibody epitope effects	extasciitilde20x resistence to mAb CQ038 by B.1.1.7 pseudotyped virus	B.1.1.7, Q.3, Q.1	Hu et al. (2021)	37142	A	G	nan
p.D614G	antibody epitope effects	Lessens the potency of mAbs COVA2-17 (extasciitilde5x, similar to N501Y alone), COVA1-12 (extasciitilde11x) and COVA1-21 (>100x), which do not compete allosterically.	B.1.1.7, Q.3, Q.1	Rees-Spear et al. (2021)	37142	A	G	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.D614G	antibody epitope effects	Reduction in neutralization by mAbs COVA2-15 (extasciitilde9x), B38 (extasciitilde14x), S309 (extasciitilde190x) by this B.1.1.7 pseudotyped virus model.	B.1.1.7, Q.3, Q.1	Shen et al. (2021)	37142	A	G	nan
p.D614G	antibody epitope effects	B.1.1.7 pseudotyped virus model impairs binding by RBD-directed mAb 910-30. B.1.1.7 pseudotyped virus model abolishes N-terminal-domain-directed mAbs 5-24, 4-8, and 4A8. B.1.1.7 pseudotyped virus model impairs binding by N-terminal-domain-directed mAbs 2-17, 4-19, 5-7.	B.1.1.7, Q.3, Q.1	Wang et al. (2021)	37142	A	G	nan
p.D614G	clinical indicators	After adjusting for the age factor, in a prospective Chinese cohort study B.1.1.7 variant infection (compared to B.1.140) was the risk factor for C-reactive protein (P	B.1.1.7, Q.3, Q.1	Song et al. (2021)	37142	A	G	nan
p.D614G	convalescent plasma binding	1.29x increase in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset.	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Gong et al. (2021)	37152	A	G	nan
p.D614G	convalescent plasma binding	1.96x increase in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset.	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Gong et al. (2021)	37152	A	G	nan
p.D614G	convalescent plasma binding	1.33x increase in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset.	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Gong et al. (2021)	37152	A	G	nan
p.D614G	convalescent plasma binding	This variant combination (representing B.1.1.7 aka Alpha) showed a 1.15x increase in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset.	B.1.1.7, Q.3, Q.1	Gong et al. (2021)	37142	A	G	nan
p.D614G	convalescent plasma binding	No change in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset.	Q.1	Gong et al. (2021)	44	A	G	nan
p.D614G	convalescent plasma binding	1.65x increase in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset.	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Gong et al. (2021)	37152	A	G	nan
p.D614G	convalescent plasma binding	1.26x increase in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset.	Q.8, Q.3, Q.1, B.1.1.7	Gong et al. (2021)	37150	A	G	nan
p.D614G	convalescent plasma binding	1.06x increase in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset.	Q.1, B.1.1.7, Q.3, Q.4	Gong et al. (2021)	37144	A	G	nan
p.D614G	convalescent plasma binding	1.58x increase in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset.	Q.1, B.1.1.7, Q.3, Q.4	Gong et al. (2021)	37144	A	G	nan
p.D614G	convalescent plasma binding	1.14x increase in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset.	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Gong et al. (2021)	37152	A	G	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.D614G	convalescent plasma escape	NTD-specific nAbs showed a substantial (3-450x) decrease in neutralization potency against the recently reported highly transmissible B.1.1.7 variant of concern, whereas RBD-specific nAbs were either unaffected or showed lower decreases in potency.	B.1.1.7, Q.3, Q.1	Graham et al. (2021)	37142	A	G	nan
p.D614G	convalescent plasma escape	Neutralizing antibody titers of 2/20 (10%) samples showed >10x reduction (sera collected extasciitilde1mo post Jan 2020 first wave in China). Neutralizing antibody titers of 8/20 samples (40%) decreased below an ID50 threshold of 40 (sera collected extasciitilde8mo post Jan 2020 first wave in China).	B.1.1.7, Q.3, Q.1	Hu et al. (2021)	37142	A	G	nan
p.D614G	convalescent plasma escape	Using a new rapid neutralization assay, based on reporter cells that become positive for GFP after overnight infection, sera from 58 convalescent individuals collected up to 9 months after symptoms, similarly neutralized B.1.1.7 and D614G.	B.1.1.7, Q.3, Q.1	Planas et al. (2021)	37142	A	G	nan
p.D614G	convalescent plasma escape	Maximum fold-decrease in potency for the serum samples from mild illness was 8.2 but the majority of samples showed less than a 3-fold change. Similarly, the maximum decrease seen for samples from hospitalized patients was a 9.1-fold change, but most of the samples showed minimal change in the potency of their neutralization. Overall, three samples from each cohort (8%) showed a 5–10-fold reduction, but as they were potently neutralizing sera, the reduced ID50 values were still >1:100.	B.1.1.7, Q.3, Q.1	Rees-Spear et al. (2021)	37142	A	G	nan
p.D614G	convalescent plasma escape	Neutralization activity of convalescent sera tested decreased <2x with this B.1.1.7 pseudotyped virus.	B.1.1.7, Q.3, Q.1	Shen et al. (2021)	37142	A	G	nan
p.D614G	convalescent plasma escape	We analyzed 34 convalescent samples including the WHONIBSC 20/130 reference serum, and, although a few sera showed near identical FRNT 50 values, the FRNT50 dilutions for the B.1.1.7 strain were 2.9-fold lower (geometric mean) than those for the Victoria strain ($p < 0.0001$). Sera from 13 subjects post-B.1.1.7 infection showed no significant change in neutralization against Victoria (extasciitildewild type), suggesting that B.1.1.7 infection also protects against ancestral virus. [Note that D1119H was included in the original paper, assuming typographical error and correcting to D1118H]	B.1.1.7, Q.3, Q.1	Supasa et al. (2021)	37142	A	G	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.D614G	convalescent plasma escape	Loss of neutralizing activity using 6 hyperimmune immunoglobulin preparations from convalescent plasma was minimal against B.1.1.7 (1.9-fold). Neutralization against 10 convalescent plasma was poorer.	B.1.1.7, Q.3, Q.1	Tang et al. (2021)	37142	A	G	nan
p.D614G	convalescent plasma escape	The neutralizing activity of 8/20 convalescent sera was significantly lower against this pseudotyped virus model of B.1.1.7, yet almost no effect was detected using the live B.1.1.7 virus.	B.1.1.7, Q.3, Q.1	Wang et al. (2021)	37142	A	G	nan
p.D614G	environmental condition stability	Treatment with heat, soap and ethanol revealed similar inactivation profiles indicative of a comparable susceptibility towards disinfection. Furthermore, we observed comparable surface stability on steel, silver, copper and face masks.	B.1.1.7, Q.3, Q.1	Meister et al. (2021)	37142	A	G	nan
p.D614G	environmental condition stability	No differences in the stability of B.1.1.7 observed in the absence of simulated sunlight at either 20°C or 40°C (with a mean time for a 90% loss of viral infectivity across all dark conditions of 6.2 hours). However, a small but statistically significant difference in the stability was observed in simulated sunlight at 20°C and 20% relative humidity, with B.1.1.7 restoring wild type 90% loss time of 11 minutes vs. 7 and 8 minutes for B.1.319 (D614G) and B.28 (V367F) early 2020 viruses respectively.	B.1.1.7, Q.3, Q.1	Schuit et al. (2021)	37142	A	G	nan
p.D614G	immunosuppression variant emergence	Studying 94 COVID-19 extended infection cases with genomics April 1 to October 17, 2020, one case developed 23 mutations in a 19 day period, including this combination in Spike.	B.1.1.7, Q.8, Q.3, Q.4, B.1.1.70, B.1.1.71, Q.1	Landis et al. (2021)	37157	A	G	nan
p.D614G	reinfection	36920 COVID Symptom Study app users reported SARS-CoV-2 test positivity in late 2020. Possible reinfections were identified in 249 (0.7% [95% CI 0.6-0.8]) of 36509 app users who reported a positive swab test before Oct 1, 2020, but there was no evidence that the frequency of reinfections was higher for the B.1.1.7 variant than for pre-existing variants.	B.1.1.7, Q.3, Q.1	Graham et al. (2021)	37142	A	G	nan
p.D614G	reinfection	Second infection in December 2020 with B.1.1.7 after April 2020 initial infection with B.2 in a 78-year-old man with a history of Type 2 diabetes mellitus, diabetic nephropathy on hemodialysis, chronic obstructive pulmonary disease (COPD), mixed central and obstructive sleep apnea, ischemic heart disease, with no history of immunosuppression.	B.1.1.7, Q.3, Q.1	Harrington et al. (2021)	37142	A	G	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.D614G	reinfection	Reinfection with Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) B.1.1.7 variant in an immunocompromised 16yo female with end stage renal disease 94 days after initial infection with a B.1.2 lineage virus. Both lineages were the prevalent one at the time of 1st and 2nd infections respectively in Texas, where the patient was located (suggesting exposure risk rather than lineage immune evasion).	B.1.1.7, Q.3, Q.1	Marquez et al. (2021)	37142	A	G	nan
p.D614G	syncytium formation	Slight increase in Vero cell-cell membrane fusion assay under infection with VSV pseudotyped virus.	B.1.1.7, Q.8, Q.3, Q.4, B.1.1.70, B.1.1.71, Q.1	Kim et al. (2021)	37157	A	G	nan
p.D614G	syncytium formation	Slight increase in Vero cell-cell membrane fusion assay under infection with VSV pseudotyped virus relative to wild type, no change relative to D614G.	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Kim et al. (2021)	37152	A	G	nan
p.D614G	tissue specific neutralization	The nasal mucosa of Pfizer vaccinees with time course collection was evaluated against VSV pseudotypes: results (only one nasal swab from different previously infected vacinee neutralizing at weeks 3 and 6 against B.1.1.7 and D614G) suggest that vaccinees probably do not elicit an early humoral response detectable at mucosal surfaces even though sera neutralization was observed. They strengthen the hypothesis that some vaccines may not protect against viral acquisition and infection of the oral–nasal region, but may prevent severe disease associated with viral dissemination in the lower respiratory tract.	B.1.1.7, Q.8, Q.3, Q.4, B.1.1.70, B.1.1.71, Q.1	Planas et al. (2021)	37157	A	G	nan
p.D614G	tissue specific neutralization	The nasal mucosa of Pfizer vaccinees with time course collection was evaluated against VSV pseudotypes: results (only one nasal swab from different previously infected vacinee neutralizing at weeks 3 and 6 against B.1.1.7 and D614G) suggest that vaccinees probably do not elicit an early humoral response detectable at mucosal surfaces even though sera neutralization was observed. They strengthen the hypothesis that some vaccines may not protect against viral acquisition and infection of the oral–nasal region, but may prevent severe disease associated with viral dissemination in the lower respiratory tract.	B.1.1.7, Q.3, Q.1	Planas et al. (2021)	37142	A	G	nan
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)	B.1.1.7, Q.8, Q.3, Q.4, B.1.1.70, B.1.1.71, Q.1	Barrett et al. (2021)	37157	A	G	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.D614G	trafficking	The increased transduction with Spike D614G ranged from 1.3- to 2.4-fold in Caco-2 and Calu-3 cells expressing endogenous ACE2 and from 1.5- to 7.7-fold in A549ACE2 and Huh7.5ACE2 overexpressing ACE2. Although there is minimal difference in ACE2 receptor binding between the D614 and G614 Spike variants, the G614 variant is more resistant to proteolytic cleavage, suggesting a possible mechanism for the increased transduction.	B.1.1.7, Q.8, Q.3, Q.4, B.1.1.70, B.1.1.71, Q.1	Daniloski et al. (2021)	37157	A	G	nan
p.D614G	trafficking	extasciitilde2.5x cleavage of S2 relative to WA1 (D614G) wildtype by Alpha variant variant as measured by mass spectrometry of Vero-TMPRSS culture.	B.1.1.7, Q.3, Q.1	Esclera et al. (2021)	37142	A	G	nan
p.D614G	trafficking	The entry efficiencies of Spike pseudotyped viruses bearing N501Y Variant 1 (B.1.1.7) mutant were about 3 to 4.4 times higher than that of the WT pseudovirus when viral input was normalized, suggesting that these spike variants promote the infectivity of SARS-CoV-2.	B.1.1.7, Q.3, Q.1	Hu et al. (2021)	37142	A	G	nan
p.D614G	trafficking	No change in infectivity (24h) relative to D614G alone in Caco-2 cells, Vero or Calu-3.	B.1.1.7, Q.8, Q.3, Q.4, B.1.1.70, B.1.1.71, Q.1	Kim et al. (2021)	37157	A	G	nan
p.D614G	trafficking	extasciitilde4x more efficient S2 domain cleavage compared to wild type in Caco-2 cells, mid-range of three cell line tested (Vero and Calu-3).	B.1.1.7, Q.8, Q.3, Q.4, B.1.1.70, B.1.1.71, Q.1	Kim et al. (2021)	37157	A	G	nan
p.D614G	trafficking	More efficient infectivity (24h) compared to wild type, in Caco-2 cells extasciitilde9x, Vero extasciitilde8x, and Calu-3 extasciitilde8x. Compare to wild type at extasciitilde5x across cell types.	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Kim et al. (2021)	37152	A	G	nan
p.D614G	trafficking	extasciitilde4x more efficient S2 domain cleavage compared to wild type, no change relative to D614G alone in Caco-2 cells, mid-range of three cell line tested (Vero and Calu-3).	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Kim et al. (2021)	37152	A	G	nan
p.D614G	trafficking	9x more infectivity than D614G alone in HEK293T-ACE2 cells 48h post-transduction.	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Kuzmina et al. (2021)	74241	A	G	nan
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.	B.1.1.7, Q.8, Q.3, Q.4, B.1.1.70, B.1.1.71, Q.1	Ozono et al. (2020)	37157	A	G	nan
p.D614G	trafficking	Quantification of the band intensities showed that the P681R mutation, which lies near the proteolytic processing site, caused a small increase in proteolytic processing as measured by a 2-fold decrease in the ratio of S/S2.	Q.4	Tada et al. (2021)	2	A	G	nan
p.D614G	trafficking	Live virus was tested ex vivo in reconstituted brochial epithelium, and out competed wild type.	B.1.1.7, Q.3, Q.1	Touret et al. (2021)	37142	A	G	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.D614G	trafficking	We report here pseudoviruses carrying SG614 enter ACE2-expressing cells more efficiently than wild type (extasciitilde9-fold). This increased entry correlates with less S1-domain shedding and higher S-protein incorporation into the virion. D614G does not alter S-protein binding to ACE2 or neutralization sensitivity of pseudoviruses. Thus, D614G may increase infectivity by assembling more functional S protein into the virion.	B.1.1.7, Q.8, Q.3, Q.4, B.1.1.70, B.1.1.71, Q.1	Zhang et l. (2020)	37157	A	G	nan
p.D614G	vaccine efficacy	In Minnesota in early 2021 when Alpha was prevalent, vaccine efficacy was estimated as: mRNA-1273 86% (95%CI: 81-90.6%) and BNT162b2: 76% (95%CI: 69-81%) using age, sex, race, PCR testing and vaccination date matched cohorts of unvaccinated, Pfizer and Moderna vaccinees. [variant list included is ancestral Alpha, as this was an observational study no variant list was given]	B.1.1.7, Q.3, Q.1	Puranik et al. (2021)	37142	A	G	nan
p.D614G	vaccine neutralization efficacy	nan	B.1.1.7, Q.3, Q.1	All vaccinees were on a strict 3 week interval for second dose (	37142	A	G	nan
p.D614G	vaccine neutralization efficacy	Between December 19, 2020 and Jan 24, 2021, 7214 of 9109 eligible HCWs at Sheba Medical Center in Israel had received one or more doses of BNT162b2 (Pfizer) vaccine. Adjusted rate reduction in SARS-CoV-2 NAAT positivity infection compared with unvaccinated workers 1-14 days after 1st dose was 30% (95% CI: 2-50), and 75% (95% CI: 72-84) after 15-28 days. Adjusted rate reduction in symptomatic COVID-19 compared with unvaccinated workers 1-14 days after 1st dose was 47% (95% CI: 17-66), and 85% (95% CI: 71-92) after 15-28 days. [Though often cited as an indicator of VE for B.1.1.7, during this time period in Israel, the prevalence of the B.1.1.7 variant increased from extasciitilde20% to 50% of cases (covariants.org), therefore these VE numbers likely represent a mix of B.1.1.7 and other lineage effects.]	B.1.1.7, Q.3, Q.1	Amit et al. (2021)	37142	A	G	nan
p.D614G	vaccine neutralization efficacy	Neutralization efficiency (ID50) against B.1.1.7 reduced 1.2x relative to D614G wildtype using pseudotyped VSV assay on 8 Moderna vaccinee sera one week post-booster.	B.1.1.7, Q.3, Q.1	Choi et al. (2021)	37142	A	G	nan
p.D614G	vaccine neutralization efficacy	2.1x drop in neutralization using sera collected from 14 healthy adult participants that received two injections of the mRNA-1273 (Moderna) vaccine at a dose of 100 µg (18-55 years: day 1 (n	B.1.1.7, Q.3, Q.1	Edara et al. (2021)	37142	A	G	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.D614G	vaccine neutralization efficacy	Virus neutralisation activity (using a live SARS-CoV-2 microneutralisation assay (ND50)) by vaccine induced antibodies was 9-fold lower against the B.1.1.7 variant than against a canonical non B.1.1.7 lineage. Vaccine efficacy against symptomatic NAAT positive infection was similar for B.1.1.7 and non-B.1.1.7 lineages (74.6% [95%CI 41.6-88.9] and 84% [95% CI 70.7-91.4] respectively). Furthermore, vaccination with ChAdOx1 nCoV-19 results in a reduction in the duration of shedding and viral load, which may translate into a material impact on transmission of disease.	B.1.1.7, Q.3, Q.1	Emary et al. (2021)	37142	A	G	nan
p.D614G	vaccine neutralization efficacy	ELISpot assays show T cell neutralization reduced by 15.4% in this B.1.1.7 pseudotype relative to wild type in 18-20 pooled patient samples post second mRNA vaccine dose, with no significant difference between Pfizer and Moderna cohorts. Reduction was stronger in the S1 subunit than S2 (separate peptide pools were used).	B.1.1.7, Q.3, Q.1	Gallagher et al. (2021)	37142	A	G	nan
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.	B.1.1.7, Q.8, Q.3, Q.4, B.1.1.70, B.1.1.71, Q.1	Garcia-Beltran et al. (2021)	37157	A	G	nan
p.D614G	vaccine neutralization efficacy	Pseudotyped B.1.1.7 virus has reduced neutralization activity vs wild type: 2.1x (30 sera Pfizer median 9 days post 2nd dose) and 2.3x (35 sera Moderna median 18 days post 2nd dose). This was NOT significant by ANOVA. Note that Y145del was actually noted in the paper as the effect of their DNA construct, but this is equivalent at the protein level to the more commonly annotated Y144del.	B.1.1.7, Q.3, Q.1	Garcia-Beltran et al. (2021)	37142	A	G	nan
p.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)	B.1.1.7, Q.3, Q.1	Gong et al. (2021)	37142	A	G	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.D614G	vaccine neutralization efficacy	Using national surveillance data from Israel, using Pfizer vaccine and an estimated prevalence of the B.1.1.7 variant of 94.5% among SARS-CoV-2 infections: Adjusted estimates of vaccine effectiveness 7+ days after second dose were 95 · 3% (95% CI 94.9–95.7): 91.5% against asymptomatic SARS-CoV-2 infection (90 · 7–92 · 2: 40.9 vs 1.8 per 100 000 person-days), 97 · 0% against symptomatic COVID-19 (96.7–97.2%), 97.2% against COVID-19-related hospitalisation (96.8–97.5%), 97.5% against severe or critical COVID-19-related hospitalisation (97.1–97.8%), and 96.7% against COVID-19-related death (96.0–97.3%). In all age groups, as vaccine coverage increased, the incidence of SARS-CoV-2 outcomes declined	B.1.1.7, Q.3, Q.1	Haas et al. (2021)	37142	A	G	nan
p.D614G	vaccine neutralization efficacy	A single dose of BNT162b2 (Pfizer) vaccine showed vaccine effectiveness of 70% (95% CI 55-85) 21 days after first dose and 85% (74-96) 7 days after two doses in the study population. Our findings show that the BNT162b2 vaccine can prevent both symptomatic and asymptomatic infection in working-age adults. This cohort (8203 treatment, 15121 control) was vaccinated when the dominant variant in circulation was B.1.1.7 and shows effectiveness against this variant.	B.1.1.7, Q.3, Q.1	Hall et al. (2021)	37142	A	G	nan
p.D614G	vaccine neutralization efficacy	A single dose of BNT162b2 vaccine demonstrated vaccine effectiveness [symptomatic or asymptomatic in cohort opf routinely NAAT-monitored UK HCWs] of 72% (95% CI 58-86) 21 days after first dose and 86% (95% CI 76-97) seven days after two doses in the antibody negative cohort. This cohort was vaccinated when the dominant variant in circulation was B.1.1.7 and demonstrates effectiveness against this variant.	B.1.1.7, Q.3, Q.1	Hall et al. (2021)	37142	A	G	nan
p.D614G	vaccine neutralization efficacy	NVX-CoV2373 [Novavax] vaccine in phase 3 trial was 89.7% (95% CI, 80.2-94.6) effective in preventing COVID-19, with no hospitalizations or deaths reported. There were five cases of severe Covid-19, all in the placebo group. Post hoc analysis revealed efficacies of 96.4% (73.8-99.5) and 86.3% (71.3-93.5) against the prototype strain and B.1.1.7 variant, respectively.	B.1.1.7, Q.3, Q.1	Heath et al. (2021)	37142	A	G	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.D614G	vaccine neutralization efficacy	B.1.1.7 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 no statistically sognificant change in neutralization effiacacy.	B.1.1.7, Q.3, Q.1	Ikegame et al. (2021)	37142	A	G	nan
p.D614G	vaccine neutralization efficacy	Using a lentivirus virus pseudotyped with D614G Spike, sera from vaccinated individuals who received the second dose (9–11 days post-second dose of Pfizer) exhibited a robust neutralizing potential, with a mean NT50 value of 99,000. This was an average of a 2-fold increase, relative to sera drawn from the individuals who received one dose of vaccination—mean NT50 dilution of 51,300. Importantly, a 6-fold increase in mean NT50 dilution was obtained when sera from the first vaccination dose was compared to convalescent sera from cohort with severe disease (NT50 51,000 vs 8,700) 21 to 63 days post-onset.	B.1.1.7, Q.8, Q.3, Q.4, B.1.1.70, B.1.1.71, Q.1	Kuzmina et al. (2021)	37157	A	G	nan
p.D614G	vaccine neutralization efficacy	This variant showed no change in Pfizer sera (one or two dose) neutralization efficiency vs D614G (using lentivirus pseudotype).	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Kuzmina et al. (2021)	37152	A	G	nan
p.D614G	vaccine neutralization efficacy	SARS-CoV-2 infection was confirmed in three HCWs working a single shift: all presented with mild symptoms of COVID-19. The two physicians were fully vaccinated with BNT162b2 vaccine, with the second dose administered 1 month before symptom onset. Both had high titres of IgG anti-spike antibodies at the time of diagnosis. WGS confirmed that all virus strains were VOC 202012/01-lineage B.1.1.7, suggesting a common source of exposure. Epidemiological investigation revealed that the suspected source was a SARS-CoV-2-positive patient who required endotracheal intubation due to severe COVID-19. All procedures were carried out using a full suite of personal protective equipment (PPE).	B.1.1.7, Q.3, Q.1	Loconsole et al. (2021)	37142	A	G	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.D614G	vaccine neutralization efficacy	We found that a single dose of the BNT162b2 vaccine is about 60-70% effective at preventing symptomatic disease in adults aged 70 years and older in England and that two doses are about 85-90% effective. Those who were vaccinated and went on to have symptoms had a 44% lower risk of being admitted hospital and a 51% lower risk of death compared with people who were unvaccinated. We also found that a single dose of the ChAdOx1-S vaccine was about 60-75% effective against symptomatic disease and provided an additional protective effect against hospital admission—it is too early to assess the effect on mortality. The B.1.1.7 variant now dominates in the UK and these results will largely reflect vaccine effectiveness against this variant.	B.1.1.7, Q.3, Q.1	Lopez Bernal et al. (2021)	37142	A	G	nan
p.D614G	vaccine neutralization efficacy	In sera 1-2 weeks after BNT162b2 first dose, from six patients previously infected with B.1, antibody titer in a microneutralization assay was on average 8192 for B.1.351 virus. This compares favorably (stronger) to post-infection neutralization titer against all variants tested in the same sera (wild type, B.1.1.7, B.1.351, and P.1).	B.1.1.7, Q.3, Q.1	Luftig et al. (2021)	37142	A	G	nan
p.D614G	vaccine neutralization efficacy	We observed a sharp decline in cases when 50% of the elderly population was 2 weeks beyond their first vaccination dose and at a time point during which the B.1.1.7 variant gained transmission dominance. In support of this finding, it was suggested that, after the first vaccination dose, more than 70% of patients develop neutralization antibodies,15 and the vaccine efficiency can reach 85%.	B.1.1.7, Q.3, Q.1	Munitz et al. (2021)	37142	A	G	nan
p.D614G	vaccine neutralization efficacy	Detectable antibodies against B.1.1.7 at various time points using pseudotyped lentivirus neutralization in Moderna vaccinee cohort: Day 29 33%, Day 43 100%, Day 119 100%, Day 209 96%. Detectable antibodies against B.1.1.7 at various time points using live virus FRNT neutralization in Moderna vaccinee cohort: Day 29 54%, Day 43 100%, Day 119 100%, Day 209 88%. Detectable antibodies against B.1.1.7 at various time points using ACE2 blocking assay in Moderna vaccinee cohort: Day 29 83%, Days 43,119,209 100%.	B.1.1.7, Q.3, Q.1	Pegu et al (2021)	37142	A	G	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.D614G	vaccine neutralization efficacy	The sera of 16 individuals with time course collection was evaulated against VSV pseudotypes: neutralized D614G at week 2, whereas B.1.1.7 started to be neutralized at week 3, although less efficiently than D614G. B.1.1.7 and D614G strains were similarly neutralized at week 4 (1 week after booster dose).	B.1.1.7, Q.3, Q.1	Planas et al. (2021)	37142	A	G	nan
p.D614G	vaccine neutralization efficacy	After one dose, individuals with prior infection showed enhanced T cell immunity, antibody secreting memory B cell response to spike and neutralizing antibodies effective against B.1.1.7 (authentic cell culture supernatants). By comparison, HCW receiving one vaccine dose without prior infection showed reduced immunity against variants. B.1.1.7 spike mutations resulted in increased, abrogated or unchanged T cell responses depending on human leukocyte antigen (HLA) polymorphisms. Study was 26 each post-infection and post first dose HCWs.	B.1.1.7, Q.3, Q.1	Reynolds et al. (2021)	37142	A	G	nan
p.D614G	vaccine neutralization efficacy	The NAb titers (PRNT50) of sera collected from 38 vaccine recipients four-weeks after the second dose of inactivated whole-virion SARS-CoV-2 BBV152/COVAXIN vaccine [which contains D614G] were not significantly different between B.1.1.7 virus and ancestral D614G virus.	B.1.1.7, Q.3, Q.1	Sapkal et al. (2021)	37142	A	G	nan
p.D614G	vaccine neutralization efficacy	Pseudotyped B.1.1.7 Spike variants lentivirus. 3.5x reduction in neutralization with Moderna vaccinated patient sera after 29 days (1st dose). 2.0x reduction in neutralization with Moderna vaccinated patient sera after 57 days (2nd dose). 2.1x reduction in neutralization with Novavax Phase 1 post-vaccination sera.	B.1.1.7, Q.3, Q.1	Shen et al. (2021)	37142	A	G	nan
p.D614G	vaccine neutralization efficacy	Neutralization assays of B.1.1.7 virus showed a reduction of 2.5-fold (14 days post 2nd dose AstraZeneca, n	B.1.1.7, Q.3, Q.1	Supasa et al. (2021)	37142	A	G	nan
p.D614G	vaccine neutralization efficacy	PBMCs of Pfizer/BioNTech BNT162b2 (n	B.1.1.7, Q.3, Q.1	Tarke et al. (2021)	37142	A	G	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.D614G	vaccine neutralization efficacy	1.4x improvement in neutralization by serum collected 2 to 3 weeks after the second dose from vaccinees who had received BBIBP-CorV (pVNT50 against VSV pseudotyped as B.1.1.7). Convalescent plasma had similar titer against wild type as the BBIBP-CorV vaccinee sera. 2x reduction in neutralization by serum collected 2 to 3 weeks after the second dose from vaccinees who had received CoronaVac (pVNT50 against VSV pseudotyped as B.1.1.7). Convalescent plasma had similar titer against wild type as the CoronaVac vaccinee sera.	B.1.1.7, Q.3, Q.1	Wang et al. (2021)	37142	A	G	nan
p.D614G	vaccine neutralization efficacy	No significant difference in T-cell response to B.1.1.7 was observed (vs. ancestral) in blood drawn from 28 participants received the Pfizer-BioNTech vaccine and 2 received the Moderna vaccine. This is despite three mutations (Y144del, D614G, and P681H) overlapping T-cell epitope hotspots.	B.1.1.7, Q.3, Q.1	Woldemeskel et al. (2021)	37142	A	G	nan
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]	Q.8, Q.3, Q.1, B.1.1.7	Zuckerman et al. (2021)	37150	A	G	nan
p.D614G	vaccinee plasma binding	No significant change in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in previously non-seroconverted subjects. 1.04x 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.	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Gong et al. (2021)	37152	A	G	nan
p.D614G	vaccinee plasma binding	1.09x increase in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in previously non-seroconverted subjects. 1.08x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in post-infection vaccinees.	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Gong et al. (2021)	37152	A	G	nan
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.	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Gong et al. (2021)	37152	A	G	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.D614G	vaccinee plasma binding	This variant combination (representing B.1.1.7 aka Alpha) showed no change in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in previously non-seroconverted subjects. 1.28x 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.1.1.7, Q.3, Q.1	Gong et al. (2021)	37142	A	G	nan
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.	Q.1	Gong et al. (2021)	44	A	G	nan
p.D614G	vaccinee plasma binding	1.17x increase in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in previously non-seroconverted subjects. 1.09x increase in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in post-infection vaccinees.	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Gong et al. (2021)	37152	A	G	nan
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.	Q.8, Q.3, Q.1, B.1.1.7	Gong et al. (2021)	37150	A	G	nan
p.D614G	vaccinee plasma binding	2x 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. 1.12x 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.	Q.1, B.1.1.7, Q.3, Q.4	Gong et al. (2021)	37144	A	G	nan
p.D614G	vaccinee plasma binding	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 previously non-seroconverted subjects. 1.47x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in post-infection vaccinees.	Q.1, B.1.1.7, Q.3, Q.4	Gong et al. (2021)	37144	A	G	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.D614G	vaccinee plasma binding	1.08x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in previously non-seroconverted subjects. 1.11x 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.	B.1.1.7, Q.8, Q.3, Q.4, Q.1	Gong et al. (2021)	37152	A	G	nan
p.D614G	viral load	Hamsters infected with SARS-CoV-2 expressing spike(D614G) (G614 virus) produced higher infectious titres in nasal washes and the trachea, but not in the lungs, supporting clinical evidence showing that the mutation enhances viral loads in the upper respiratory tract of COVID-19 patients and may increase transmission.	B.1.1.7, Q.8, Q.3, Q.4, B.1.1.70, B.1.1.71, Q.1	Plante et al. (2020)	37157	A	G	nan
p.D614G	virion structure	CryoEM analysis of B.1.1.7 demonstrates an increased propensity for 'up', receptor accessible conformation of the Spike protein trimer.	B.1.1.7, Q.3, Q.1	Cai et al. (2021)	37142	A	G	nan
p.D614G	virion structure	Estimated free energy change (ddG) for this variant is 2.5 kcal/mol (i.e. stabilizing relative to wild type)	B.1.1.7, Q.8, Q.3, Q.4, B.1.1.70, B.1.1.71, Q.1	Spratt et al. (2021)	37157	A	G	nan
p.D614G	virion structure	Negative stain EM shows increased proportion of "one-up" trimer conformation of Spike proteins on the surface of virions, where the up conformation is presumed to be more likely to bind ACE2.	B.1.1.7, Q.8, Q.3, Q.4, B.1.1.70, B.1.1.71, Q.1	Weissman et al. (2020)	37157	A	G	nan
p.D614G	virion structure	CryoEM shows increased proportion of "one-up" trimer conformation of Spike proteins on the surface of virions, where the up conformation is presumed to be more likely to bind ACE2.	B.1.1.7, Q.8, Q.3, Q.4, B.1.1.70, B.1.1.71, Q.1	Yurkovetskiy et al. (2020)	37157	A	G	nan
p.D614G	virion structure	Based on pseudotyped virus experiments, D614G may increase infectivity by assembling more functional S protein into the virion.	B.1.1.7, Q.8, Q.3, Q.4, B.1.1.70, B.1.1.71, Q.1	Zhang et al. (2020)	37157	A	G	nan
p.P681H	ACE2 receptor binding affinity	Six fold increase in affinity for ACE2 by the B.1.1.7 lineage vs wild type is driven by a drop in observed dissociation rate constant.	B.1.1.7, Q.3, Q.1	Collier et al. (2021)	37134	C	A	nan
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.	Q.8, Q.3, Q.1, B.1.1.7	Gong et al. (2021)	37142	C	A	nan
p.P681H	ACE2 receptor binding affinity	Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant combination (representing B.1.1.7 aka Alpha) had 5.43x increased binding relative to D614G alone.	B.1.1.7, Q.3, Q.1	Gong et al. (2021)	37134	C	A	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.P681H	ACE2 receptor binding affinity	Flow cytometry was used on recombinant VSV proteins and yeast surface display to assess the binding of a labeled soluble ACE2 protein to cells expressing B.1.1.7. We observed a dramatic increase (relative to D614G) in binding of soluble ACE2 to B.1.1.7, and to a lesser extent to B.1.351, which both carry the N501Y mutation (see Fig 3).	B.1.1.7, Q.3, Q.1	Planas et al. (2021)	37134	C	A	nan
p.P681H	ACE2 receptor binding affinity	This mutation causes major decrease in binding affinity vs. wild type as measured by IC50 vs pseudotyped lentivirus.	B.1.1.7, Q.3, Q.1	Tada et al. (2021)	37134	C	A	nan
p.P681H	anthropozoonotic events	First documented cases of domestic cat and dog infections with the B.1.1.7 strain.	B.1.1.7, Q.3, Q.1	Hamer et al. (2021)	37134	C	A	nan
p.P681H	antibody epitope effects	Ablates Class 3 N-terminal domain targeting antibody COV2-2489, diminishes COV2-2676.	Q.8, Q.3, Q.1, B.1.1.7	Chen et al. (2021)	37142	C	A	nan
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.	Q.8, Q.3, Q.1, B.1.1.7	Haynes et al. (2021)	37142	C	A	nan
p.P681H	antibody epitope effects	extasciitilde20x resistence to mAb CQ038 by B.1.1.7 pseudotyped virus	B.1.1.7, Q.3, Q.1	Hu et al. (2021)	37134	C	A	nan
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.	Q.8, Q.3, Q.1, B.1.1.7	Johnson et al. (2020)	37142	C	A	nan
p.P681H	antibody epitope effects	Lessens the potency of mAbs COVA2-17 (extasciitilde5x, similar to N501Y alone), COVA1-12 (extasciitilde11x) and COVA1-21 (>100x), which do not compete allosterically.	B.1.1.7, Q.3, Q.1	Rees-Spear et al. (2021)	37134	C	A	nan
p.P681H	antibody epitope effects	Reduction in neutralization by mAbs COVA2-15 (extasciitilde9x), B38 (extasciitilde14x), S309 (extasciitilde190x) by this B.1.1.7 pseudotyped virus model.	B.1.1.7, Q.3, Q.1	Shen et al. (2021)	37134	C	A	nan
p.P681H	antibody epitope effects	B.1.1.7 pseudotyped virus model impairs binding by RBD-directed mAb 910-30. B.1.1.7 pseudotyped virus model abolishes N-terminal-domain-directed mAbs 5-24, 4-8, and 4A8. B.1.1.7 pseudotyped virus model impairs binding by N-terminal-domain-directed mAbs 2-17, 4-19, 5-7.	B.1.1.7, Q.3, Q.1	Wang et al. (2021)	37134	C	A	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.P681H	clinical indicators	After adjusting for the age factor, in a prospective Chinese cohort study B.1.1.7 variant infection (compared to B.1.140) was the risk factor for C-reactive protein (P	B.1.1.7, Q.3, Q.1	Song et al. (2021)	37134	C	A	nan
p.P681H	convalescent plasma binding	1.26x increase in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset.	Q.8, Q.3, Q.1, B.1.1.7	Gong et al. (2021)	37142	C	A	nan
p.P681H	convalescent plasma binding	This variant combination (representing B.1.1.7 aka Alpha) showed a 1.15x increase in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset.	B.1.1.7, Q.3, Q.1	Gong et al. (2021)	37134	C	A	nan
p.P681H	convalescent plasma escape	One convalescent sera tested showed 4-fold or greater reduction in neutralization efficiency.	Q.8, Q.3, Q.1, B.1.1.7	Alenquer et al. (2021)	37142	C	A	nan
p.P681H	convalescent plasma escape	Slight neutralization improvement on average in 16 health workers' convalescent sera.	Q.8, Q.3, Q.1, B.1.1.7	Alenquer et al. (2021)	37142	C	A	nan
p.P681H	convalescent plasma escape	Neutralization capacity GMT of 27 subjects' sera post-infection was considerably higher (stronger) than after the second Pfizer dose, and 4.5x drop in B.1.1.7 neutralization was observed.	B.1.1.7, Q.3, Q.1	Collier et al. (2021)	37134	C	A	nan
p.P681H	convalescent plasma escape	NTD-specific nAbs showed a substantial (3-450x) decrease in neutralization potency against the recently reported highly transmissible B.1.1.7 variant of concern, whereas RBD-specific nAbs were either unaffected or showed lower decreases in potency.	B.1.1.7, Q.3, Q.1	Graham et al. (2021)	37134	C	A	nan
p.P681H	convalescent plasma escape	Neutralizing antibody titers of 2/20 (10%) samples showed >10x reduction (sera collected extasciitilde1mo post Jan 2020 first wave in China). Neutralizing antibody titers of 8/20 samples (40%) decreased below an ID50 threshold of 40 (sera collected extasciitilde8mo post Jan 2020 first wave in China).	B.1.1.7, Q.3, Q.1	Hu et al. (2021)	37134	C	A	nan
p.P681H	convalescent plasma escape	Using a new rapid neutralization assay, based on reporter cells that become positive for GFP after overnight infection, sera from 58 convalescent individuals collected up to 9 months after symptoms, similarly neutralized B.1.1.7 and D614G.	B.1.1.7, Q.3, Q.1	Planas et al. (2021)	37134	C	A	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.P681H	convalescent plasma escape	Maximum fold-decrease in potency for the serum samples from mild illness was 8.2 but the majority of samples showed less than a 3-fold change. Similarly, the maximum decrease seen for samples from hospitalized patients was a 9.1-fold change, but most of the samples showed minimal change in the potency of their neutralization. Overall, three samples from each cohort (8%) showed a 5–10-fold reduction, but as they were potently neutralizing sera, the reduced ID50 values were still >1:100.	B.1.1.7, Q.3, Q.1	Rees-Spear et al. (2021)	37134	C	A	nan
p.P681H	convalescent plasma escape	Neutralization activity of convalescent sera tested decreased <2x with this B.1.1.7 pseudotyped virus.	B.1.1.7, Q.3, Q.1	Shen et al. (2021)	37134	C	A	nan
p.P681H	convalescent plasma escape	We analyzed 34 convalescent samples including the WHONIBSC 20/130 reference serum, and, although a few sera showed near identical FRNT 50 values, the FRNT50 dilutions for the B.1.1.7 strain were 2.9-fold lower (geometric mean) than those for the Victoria strain ($p < 0.0001$). Sera from 13 subjects post-B.1.1.7 infection showed no significant change in neutralization against Victoria (extasciitildewild type), suggesting that B.1.1.7 infection also protects against ancestral virus. [Note that D1119H was included in the original paper, assuming typographical error and correcting to D1118H]	B.1.1.7, Q.3, Q.1	Supasa et al. (2021)	37134	C	A	nan
p.P681H	convalescent plasma escape	These key B.1.1.7 mutations as a combination neutralized slightly less well than D614G and this was noticeable in the lack of sera with high neutralizing titer for the viruses across 10 convalescent sera from April 2020 infectees.	Q.8, Q.3, Q.1, B.1.1.7	Tada et al. (2021)	37142	C	A	nan
p.P681H	convalescent plasma escape	Loss of neutralizing activity using 6 hyperimmune immunoglobulin preparations from convalescent plasma was minimal against B.1.1.7 (1.9-fold). Neutralization against 10 convalescent plasma was poorer.	B.1.1.7, Q.3, Q.1	Tang et al. (2021)	37134	C	A	nan
p.P681H	convalescent plasma escape	The neutralizing activity of 8/20 convalescent sera was significantly lower against this pseudotyped virus model of B.1.1.7, yet almost no effect was detected using the live B.1.1.7 virus.	B.1.1.7, Q.3, Q.1	Wang et al. (2021)	37134	C	A	nan
p.P681H	environmental condition stability	Treatment with heat, soap and ethanol revealed similar inactivation profiles indicative of a comparable susceptibility towards disinfection. Furthermore, we observed comparable surface stability on steel, silver, copper and face masks.	B.1.1.7, Q.3, Q.1	Meister et al. (2021)	37134	C	A	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.P681H	environmental condition stability	No differences in the stability of B.1.1.7 observed in the absence of simulated sunlight at either 20°C or 40°C (with a mean time for a 90% loss of viral infectivity across all dark conditions of 6.2 hours). However, a small but statistically significant difference in the stability was observed in simulated sunlight at 20°C and 20% relative humidity, with B.1.1.7 restoring wild type 90% loss time of 11 minutes vs. 7 and 8 minutes for B.1.319 (D614G) and B.28 (V367F) early 2020 viruses respectively.	B.1.1.7, Q.3, Q.1	Schuit et al. (2021)	37134	C	A	nan
p.P681H	environmental condition stability	Relative to D614G, this mutation demonstrated significant increase in infectivity (i.e. heat stability) after incubation at 50C after 1 hour.	Q.8, Q.3, Q.1, B.1.1.7	Tada et al. (2021)	37142	C	A	nan
p.P681H	outcome hazard ratio	Danish study of the B.1.1.7 lineage shows hospital admission odds ratio of 1.63 vs other lineages. The adjusted OR was increased in all strata of age.	B.1.1.7, Q.3, Q.1	Bager et al. (2021)	37134	C	A	nan
p.P681H	outcome hazard ratio	The mortality hazard ratio associated with infection with [B.1.1.7] compared with infection with previously circulating variants was 1.64 (95% confidence interval 1.32 to 2.04) in patients who tested positive for covid-19 in the community (54906 matched pairs of participants who tested positive for SARS-CoV-2 in pillar 2 between 1 October 2020 and 29 January 2021). In this comparatively low risk group, this represents an increase in deaths from 2.5 to 4.1 per 1000 detected cases.	B.1.1.7, Q.3, Q.1	Challen et al. (2021)	37134	C	A	nan
p.P681H	outcome hazard ratio	Using UK data 1 November 2020 to 14 February 2021, while correcting for misclassification of PCR test Spike Gene Target Failure (SGTF) and missingness in SGTF status, we estimate that the hazard of death associated with B.1.1.7 is 61% (42–82%) higher than with pre-existing variants after adjustment for age, sex, ethnicity, deprivation, residence in a care home, the local authority of residence and test date. This corresponds to the absolute risk of death for a 55–69-year-old man increasing from 0.6% to 0.9% (95% confidence interval, 0.8–1.0%) within 28 days of a positive test in the community.	B.1.1.7, Q.3, Q.1	Davies et al. (2021)	37134	C	A	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.P681H	outcome hazard ratio	341 samples collected Nov 9 to Dec 20, 2020 were sequenced from two London (UK) hospitals. 198 (58%) of 341 had B.1.1.7 infection and 143 (42%) had non-B.1.1.7 infection. No evidence was found of an association between severe disease and death and lineage (B.1.1.7 vs non-B.1.1.7) in unadjusted analyses (prevalence ratio [PR] 0 · 97 [95% CI 0 · 72-1 · 31]), or in analyses adjusted for hospital, sex, age, comorbidities, and ethnicity (adjusted PR 1 · 02 [0 · 76-1 · 38]).	B.1.1.7, Q.3, Q.1	Frampton et al. (2021)	37134	C	A	nan
p.P681H	outcome hazard ratio	On average across 7 European countries studied, using B.1.1.7 defining mutations: Significant shift to asymptomatic cases (27.4% vs 18.6% for non-VOC cases). Significant shift to infection in those without pre-existing conditions (44.8% vs 89% for non-VOC cases). Significant increase in hospitalization rate (11% vs 7.5% for non-VOC cases). Significant increase in ICU rate (1.4% vs 0.6% for non-VOC cases). Significant decrease in death rate (2.0% vs vs 4.0% for non-VOC cases).	B.1.1.7, Q.3, Q.1	Funk et al. (2021)	37134	C	A	nan
p.P681H	outcome hazard ratio	From Sept 28 to Dec 27, 2020, positive COVID-19 tests were reported by 36 920 COVID Symptom Study app users whose region was known and who reported as healthy on app sign-up. We found no changes in reported symptoms or disease duration associated with B.1.1.7.	B.1.1.7, Q.3, Q.1	Graham et al. (2021)	37134	C	A	nan
p.P681H	outcome hazard ratio	Using primarily S-defining mutations for lineage B.1.1.7, most models of hospitalization and fatality risk ratios from consortium members show elevated ratios (extasciitilde1.3-1.7x).	B.1.1.7, Q.3, Q.1	NERVTAG Consortium (2021)	37134	C	A	nan
p.P681H	outcome hazard ratio	The matching-adjusted conditional odds ratio of hospitalisation was 1.58 (95% confidence interval 1.50 to 1.67) for COVID-19 patients infected with a SGTF-associated variant [primarily B.1.1.7], compared to those infected with non-SGTF-associated variants. The effect was modified by age (p<0.001), with ORs of 0.96-1.13 below age 20 years and 1.57-1.67 in age groups 40 years or older.	B.1.1.7, Q.3, Q.1	Nyberg et al. (2021)	37134	C	A	nan
p.P681H	reinfection	36920 COVID Symptom Study app users reported SARS-CoV-2 test positivity in late 2020. Possible reinfections were identified in 249 (0.7% [95% CI 0.6-0.8]) of 36509 app users who reported a positive swab test before Oct 1, 2020, but there was no evidence that the frequency of reinfections was higher for the B.1.1.7 variant than for pre-existing variants.	B.1.1.7, Q.3, Q.1	Graham et al. (2021)	37134	C	A	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.P681H	reinfection	Second infection in December 2020 with B.1.1.7 after April 2020 initial infection with B.2 in a 78-year-old man with a history of Type 2 diabetes mellitus, diabetic nephropathy on hemodialysis, chronic obstructive pulmonary disease (COPD), mixed central and obstructive sleep apnea, ischemic heart disease, with no history of immunosuppression.	B.1.1.7, Q.3, Q.1	Harrington et al. (2021)	37134	C	A	nan
p.P681H	reinfection	Reinfection with Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) B.1.1.7 variant in an immunocompromised 16yo female with end stage renal disease 94 days after initial infection with a B.1.2 lineage virus. Both lineages were the prevalent one at the time of 1st and 2nd infections respectively in Texas, where the patient was located (suggesting exposure risk rather than lineage immune evasion).	B.1.1.7, Q.3, Q.1	Marquez et al. (2021)	37134	C	A	nan
p.P681H	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.1.1.7, Q.3, Q.1	Planas et al. (2021)	37134	C	A	nan
p.P681H	trafficking	extasciitilde2.5x cleavage of S2 relative to WA1 (D614G) wildtype by Alpha variant variant as measured by mass spectrometry of Vero-TMPRSS culture.	B.1.1.7, Q.3, Q.1	Esclera et al. (2021)	37134	C	A	nan
p.P681H	trafficking	VSV pseudotype B.1.1.7 showed no significant difference in cell entry relative to wild type in 6 cell lines. Cell fusion proficiency was unchanged.	B.1.1.7, Q.3, Q.1	Hoffman et al. (2021)	37134	C	A	nan
p.P681H	trafficking	The entry efficiencies of Spike pseudotyped viruses bearing N501Y Variant 1 (B.1.1.7) mutant were about 3 to 4.4 times higher than that of the WT pseudovirus when viral input was normalized, suggesting that these spike variants promote the infectivity of SARS-CoV-2.	B.1.1.7, Q.3, Q.1	Hu et al. (2021)	37134	C	A	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	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).	Q.8, Q.3, Q.1, B.1.1.7	Lubinski et al. (2021)	37142	C	A	nan
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).	Q.8, Q.3, Q.1, B.1.1.7	Maaroufi (2021)	37142	C	A	nan
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.	Q.8, Q.3, Q.1, B.1.1.7	Tada et al. (2021)	37142	C	A	nan
p.P681H	trafficking	Lentiviral pseudotyped with this mutation set from B.1.1.7 was tested on ACE2.293T cells. Luciferase activity was measured two days postinfection, showing significant (40%) increase in infection rate amongst the cells, much more than the effect of either the deletion or the point mutation alone, suggetsing that this combination has a synergistic effect contributing to cell entry fitness, but to a smaller extent than N501Y and the deletion alone.	Q.8, Q.3, Q.1, B.1.1.7	Tada et al. (2021)	37142	C	A	nan
p.P681H	trafficking	Live virus was tested ex vivo in reconstituted brochial epithelium, and out competed wild type.	B.1.1.7, Q.3, Q.1	Touret et al. (2021)	37134	C	A	nan
p.P681H	transmissibility	We estimate that this [B.1.1.17] variant has a 43–90% (range of 95% credible intervals 38–130%) higher reproduction number than preexisting variants. Data from other countries yield similar results: we estimate that R for VOC 202012/01 relative to other lineages is 55% (45–66%) higher in Denmark, 74% (66–82%) higher in Switzerland, and 59% (56–63%) higher in the United States, with consistent rates of displacement across regions within each country.	B.1.1.7, Q.3, Q.1	Davies et al. (2021)	37134	C	A	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.P681H	transmissibility	Based on 36920 COVID Symptom Study app users reported SARS-CoV-2 test positivity in late 2020, Rt of B.1.1.7 was 1.35x (95% CI 1.02-1.69) relative to pre-existing variants. However, Rt fell below 1 during regional and national lockdowns, even in regions with high proportions of infections with the B.1.1.7 variant.	B.1.1.7, Q.3, Q.1	Graham et al. (2021)	37134	C	A	nan
p.P681H	transmissibility	Ontario, Feb 2021: The secondary attack rate for VOC index cases in this matched cohort was 1.31 times higher than non-VOC index cases (RR	B.1.1.7, Q.3, Q.1	Lindstrøm et al. (2021)	37134	C	A	nan
p.P681H	transmissibility	Primary cases infected with B.1.1.7 had an increased transmissibility of 1.5-1.7 times that of primary cases infected with other lineages. The increased transmissibility of B.1.1.7 was multiplicative across age and viral load.	B.1.1.7, Q.3, Q.1	Lyngse et al. (2021)	37134	C	A	nan
p.P681H	transmissibility	Based on 300,000 RT-PCR samples collected from December 6th 2020 to February 10th 2021 in Israel, the B.1.1.7 is 45% (95% CI:20-60%) more transmissible than the wild-type strain, and become dominant in Israel within 3.5 weeks.	B.1.1.7, Q.3, Q.1	Munitz et al. (2021)	37134	C	A	nan
p.P681H	transmissibility	At the national level (Italy), we estimated a mean relative transmissibility of B.1.1.7 (compared to historical lineages) ranging between 1.55 and 1.57 (with confidence intervals between 1.45 and 1.66).	B.1.1.7, Q.3, Q.1	Stefanelli et al. (2021)	37134	C	A	nan
p.P681H	vaccine efficacy	In Minnesota in early 2021 when Alpha was prevalent, vaccine efficacy was estimated as: mRNA-1273 86% (95%CI: 81-90.6%) and BNT162b2: 76% (95%CI: 69-81%) using age, sex, race, PCR testing and vaccination date matched cohorts of unvaccinated, Pfizer and Moderna vaccinees. [variant list included is ancestral Alpha, as this was an observational study no variant list was given]	B.1.1.7, Q.3, Q.1	Puranik et al. (2021)	37134	C	A	nan
p.P681H	vaccine neutralization efficacy	nan	B.1.1.7, Q.3, Q.1	All vaccinees were on a strict 3 week interval for second dose (	37134	C	A	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.P681H	vaccine neutralization efficacy	Between December 19, 2020 and Jan 24, 2021, 7214 of 9109 eligible HCWs at Sheba Medical Center in Israel had received one or more doses of BNT162b2 (Pfizer) vaccine. Adjusted rate reduction in SARS-CoV-2 NAAT positivity infection compared with unvaccinated workers 1-14 days after 1st dose was 30% (95% CI: 2-50), and 75% (95% CI: 72-84) after 15-28 days. Adjusted rate reduction in symptomatic COVID-19 compared with unvaccinated workers 1-14 days after 1st dose was 47% (95% CI: 17-66), and 85% (95% CI: 71-92) after 15-28 days. [Though often cited as an indicator of VE for B.1.1.7, during this time period in Israel, the prevalence of the B.1.1.7 variant increased from extasciitilde20% to 50% of cases (covariants.org), therefore these VE numbers likely represent a mix of B.1.1.7 and other lineage effects.]	B.1.1.7, Q.3, Q.1	Amit et al. (2021)	37134	C	A	nan
p.P681H	vaccine neutralization efficacy	Neutralization efficiency (ID50) against B.1.1.7 reduced 1.2x relative to D614G wildtype using pseudotyped VSV assay on 8 Moderna vaccinee sera one week post-booster.	B.1.1.7, Q.3, Q.1	Choi et al. (2021)	37134	C	A	nan
p.P681H	vaccine neutralization efficacy	20/29 sera after the first dose of Pfizer showed an average reduction in neutralization titres against the B.1.1.7 variant of 3.2 ± 5.7. After the second dose, the GMT was markedly increased compared with the first-dose titres, with a fold change of 1.9 ± 0.9 (mean ± s.d.). Neutralization GMT of 27 subjects post-infection was considerably higher (stronger) than after the second Pfizer dose, and 4.5x drop in B.1.1.7 neutralization was observed.	B.1.1.7, Q.3, Q.1	Collier et al. (2021)	37134	C	A	nan
p.P681H	vaccine neutralization efficacy	2.1x drop in neutralization using sera collected from 14 healthy adult participants that received two injections of the mRNA-1273 (Moderna) vaccine at a dose of 100 µg (18-55 years: day 1 (n	B.1.1.7, Q.3, Q.1	Edara et al. (2021)	37134	C	A	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.P681H	vaccine neutralization efficacy	Virus neutralisation activity (using a live SARS-CoV-2 microneutralisation assay (ND50)) by vaccine induced antibodies was 9-fold lower against the B.1.1.7 variant than against a canonical non B.1.1.7 lineage. Vaccine efficacy against symptomatic NAAT positive infection was similar for B.1.1.7 and non-B.1.1.7 lineages (74.6% [95%CI 41.6-88.9] and 84% [95% CI 70.7-91.4] respectively). Furthermore, vaccination with ChAdOx1 nCoV-19 results in a reduction in the duration of shedding and viral load, which may translate into a material impact on transmission of disease.	B.1.1.7, Q.3, Q.1	Emary et al. (2021)	37134	C	A	nan
p.P681H	vaccine neutralization efficacy	ELISpot assays show T cell neutralization reduced by 15.4% in this B.1.1.7 pseudotype relative to wild type in 18-20 pooled patient samples post second mRNA vaccine dose, with no significant difference between Pfizer and Moderna cohorts. Reduction was stronger in the S1 subunit than S2 (separate peptide pools were used).	B.1.1.7, Q.3, Q.1	Gallagher et al. (2021)	37134	C	A	nan
p.P681H	vaccine neutralization efficacy	Pseudotyped B.1.1.7 virus has reduced neutralization activity vs wild type: 2.1x (30 sera Pfizer median 9 days post 2nd dose) and 2.3x (35 sera Moderna median 18 days post 2nd dose). This was NOT significant by ANOVA. Note that Y145del was actually noted in the paper as the effect of their DNA construct, but this is equivalent at the protein level to the more commonly annotated Y144del.	B.1.1.7, Q.3, Q.1	Garcia-Beltran et al. (2021)	37134	C	A	nan
p.P681H	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)	B.1.1.7, Q.3, Q.1	Gong et al. (2021)	37134	C	A	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.P681H	vaccine neutralization efficacy	Using national surveillance data from Israel, using Pfizer vaccine and an estimated prevalence of the B.1.1.7 variant of 94.5% among SARS-CoV-2 infections: Adjusted estimates of vaccine effectiveness 7+ days after second dose were 95 · 3% (95% CI 94.9–95.7): 91.5% against asymptomatic SARS-CoV-2 infection (90 · 7–92 · 2: 40.9 vs 1.8 per 100 000 person-days), 97 · 0% against symptomatic COVID-19 (96.7–97.2%), 97.2% against COVID-19-related hospitalisation (96.8–97.5%), 97.5% against severe or critical COVID-19-related hospitalisation (97.1–97.8%), and 96.7% against COVID-19-related death (96.0–97.3%). In all age groups, as vaccine coverage increased, the incidence of SARS-CoV-2 outcomes declined	B.1.1.7, Q.3, Q.1	Haas et al. (2021)	37134	C	A	nan
p.P681H	vaccine neutralization efficacy	A single dose of BNT162b2 (Pfizer) vaccine showed vaccine effectiveness of 70% (95% CI 55-85) 21 days after first dose and 85% (74-96) 7 days after two doses in the study population. Our findings show that the BNT162b2 vaccine can prevent both symptomatic and asymptomatic infection in working-age adults. This cohort (8203 treatment, 15121 control) was vaccinated when the dominant variant in circulation was B.1.1.7 and shows effectiveness against this variant.	B.1.1.7, Q.3, Q.1	Hall et al. (2021)	37134	C	A	nan
p.P681H	vaccine neutralization efficacy	A single dose of BNT162b2 vaccine demonstrated vaccine effectiveness [symptomatic or asymptomatic in cohort opf routinely NAAT-monitored UK HCWs] of 72% (95% CI 58-86) 21 days after first dose and 86% (95% CI 76-97) seven days after two doses in the antibody negative cohort. This cohort was vaccinated when the dominant variant in circulation was B.1.1.7 and demonstrates effectiveness against this variant.	B.1.1.7, Q.3, Q.1	Hall et al. (2021)	37134	C	A	nan
p.P681H	vaccine neutralization efficacy	NVX-CoV2373 [Novavax] vaccine in phase 3 trial was 89.7% (95% CI, 80.2-94.6) effective in preventing COVID-19, with no hospitalizations or deaths reported. There were five cases of severe Covid-19, all in the placebo group. Post hoc analysis revealed efficacies of 96.4% (73.8-99.5) and 86.3% (71.3-93.5) against the prototype strain and B.1.1.7 variant, respectively.	B.1.1.7, Q.3, Q.1	Heath et al. (2021)	37134	C	A	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.P681H	vaccine neutralization efficacy	VSV pseudotype B.1.1.7 showed 1.77-fold reduction in neutralization efficiency vs wild type in 15 Pfizer BNT162b2 vaccinee sera 13-15 days post second dose. Cell fusion proficiency was unchanged.	B.1.1.7, Q.3, Q.1	Hoffman et al. (2021)	37134	C	A	nan
p.P681H	vaccine neutralization efficacy	B.1.1.7 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 no statistically sognificant change in neutralization effiacacy.	B.1.1.7, Q.3, Q.1	Ikegame et al. (2021)	37134	C	A	nan
p.P681H	vaccine neutralization efficacy	Neutralizing antibody titers increased in previously infected vaccinees relative to uninfected vaccinees 5.2-fold against B.1.1.7 (contrast with 3.4 fold against original SARS-CoV-2).	B.1.1.7, Q.3, Q.1	Leier et al. (2021)	37134	C	A	nan
p.P681H	vaccine neutralization efficacy	SARS-CoV-2 infection was confirmed in three HCWs working a single shift: all presented with mild symptoms of COVID-19. The two physicians were fully vaccinated with BNT162b2 vaccine, with the second dose administered 1 month before symptom onset. Both had high titres of IgG anti-spike antibodies at the time of diagnosis. WGS confirmed that all virus strains were VOC 202012/01-lineage B.1.1.7, suggesting a common source of exposure. Epidemiological investigation revealed that the suspected source was a SARS-CoV-2-positive patient who required endotracheal intubation due to severe COVID-19. All procedures were carried out using a full suite of personal protective equipment (PPE).	B.1.1.7, Q.3, Q.1	Loconsole et al. (2021)	37134	C	A	nan
p.P681H	vaccine neutralization efficacy	We found that a single dose of the BNT162b2 vaccine is about 60-70% effective at preventing symptomatic disease in adults aged 70 years and older in England and that two doses are about 85-90% effective. Those who were vaccinated and went on to have symptoms had a 44% lower risk of being admitted hospital and a 51% lower risk of death compared with people who were unvaccinated. We also found that a single dose of the ChAdOx1-S vaccine was about 60-75% effective against symptomatic disease and provided an additional protective effect against hospital admission—it is too early to assess the effect on mortality. The B.1.1.7 variant now dominates in the UK and these results will largely reflect vaccine effectiveness against this variant.	B.1.1.7, Q.3, Q.1	Lopez Bernal et al. (2021)	37134	C	A	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.P681H	vaccine neutralization efficacy	In sera 1-2 weeks after BNT162b2 first dose, from six patients previously infected with B.1, antibody titer in a microneutralization assay was on average 8192 for B.1.351 virus. This compares favorably (stronger) to post-infection neutralization titer against all variants tested in the same sera (wild type, B.1.1.7, B.1.351, and P.1).	B.1.1.7, Q.3, Q.1	Luftig et al. (2021)	37134	C	A	nan
p.P681H	vaccine neutralization efficacy	Lineage B.1.1.7 spike–pseudotyped VSV was tested for neutralization vs Wuhan reference genome pseudotype in 40 sera collected 7 or 21 days post-booster dose. Statistically significant change (22%) in neutralization was observed among the 26 sera from those <	B.1.1.7, Q.3, Q.1	Muik et al. (2021)	37134	C	A	nan
p.P681H	vaccine neutralization efficacy	We observed a sharp decline in cases when 50% of the elderly population was 2 weeks beyond their first vaccination dose and at a time point during which the B.1.1.7 variant gained transmission dominance. In support of this finding, it was suggested that, after the first vaccination dose, more than 70% of patients develop neutralization antibodies,15 and the vaccine efficiency can reach 85%.	B.1.1.7, Q.3, Q.1	Munitz et al. (2021)	37134	C	A	nan
p.P681H	vaccine neutralization efficacy	Detectable antibodies against B.1.1.7 at various time points using pseudotyped lentivirus neutralization in Moderna vaccinee cohort: Day 29 33%, Day 43 100%, Day 119 100%, Day 209 96%. Detectable antibodies against B.1.1.7 at various time points using live virus FRNT neutralization in Moderna vaccinee cohort: Day 29 54%, Day 43 100%, Day 119 100%, Day 209 88%. Detectable antibodies against B.1.1.7 at various time points using ACE2 blocking assay in Moderna vaccinee cohort: Day 29 83%, Days 43,119,209 100%.	B.1.1.7, Q.3, Q.1	Pegu et al (2021)	37134	C	A	nan
p.P681H	vaccine neutralization efficacy	The sera of 16 individuals with time course collection was evaulated against VSV pseudotypes: neutralized D614G at week 2, whereas B.1.1.7 started to be neutralized at week 3, although less efficiently than D614G. B.1.1.7 and D614G strains were similarly neutralized at week 4 (1 week after booster dose).	B.1.1.7, Q.3, Q.1	Planas et al. (2021)	37134	C	A	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.P681H	vaccine neutralization efficacy	After one dose, individuals with prior infection showed enhanced T cell immunity, antibody secreting memory B cell response to spike and neutralizing antibodies effective against B.1.1.7 (authentic cell culture supernatants). By comparison, HCW receiving one vaccine dose without prior infection showed reduced immunity against variants. B.1.1.7 spike mutations resulted in increased, abrogated or unchanged T cell responses depending on human leukocyte antigen (HLA) polymorphisms. Study was 26 each post-infection and post first dose HCWs.	B.1.1.7, Q.3, Q.1	Reynolds et al. (2021)	37134	C	A	nan
p.P681H	vaccine neutralization efficacy	The NAb titers (PRNT50) of sera collected from 38 vaccine recipients four-weeks after the second dose of inactivated whole-virion SARS-CoV-2 BBV152/COVAXIN vaccine [which contains D614G] were not significantly different between B.1.1.7 virus and ancestral D614G virus.	B.1.1.7, Q.3, Q.1	Sapkal et al. (2021)	37134	C	A	nan
p.P681H	vaccine neutralization efficacy	Pseudotyped B.1.1.7 Spike variants lentivirus. 3.5x reduction in neutralization with Moderna vaccinated patient sera after 29 days (1st dose). 2.0x reduction in neutralization with Moderna vaccinated patient sera after 57 days (2nd dose). 2.1x reduction in neutralization with Novavax Phase 1 post-vaccination sera.	B.1.1.7, Q.3, Q.1	Shen et al. (2021)	37134	C	A	nan
p.P681H	vaccine neutralization efficacy	Neutralization assays of B.1.1.7 virus showed a reduction of 2.5-fold (14 days post 2nd dose AstraZeneca, n	B.1.1.7, Q.3, Q.1	Supasa et al. (2021)	37134	C	A	nan
p.P681H	vaccine neutralization efficacy	Vaccine elicited antibodies neutralized virus with the B.1.1.7 spike protein with titers similar to D614G virus. Serum specimens from individuals vaccinated with the BNT162b2 mRNA vaccine neutralized D614G virus with titers that were on average 7-fold greater than convalescent sera.	B.1.1.7, Q.3, Q.1	Tada et al. (2021)	37134	C	A	nan
p.P681H	vaccine neutralization efficacy	PBMCs of Pfizer/BioNTech BNT162b2 (n	B.1.1.7, Q.3, Q.1	Tarke et al. (2021)	37134	C	A	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.P681H	vaccine neutralization efficacy	1.4x improvement in neutralization by serum collected 2 to 3 weeks after the second dose from vaccinees who had received BBIBP-CorV (pVNT50 against VSV pseudotyped as B.1.1.7). Convalescent plasma had similar titer against wild type as the BBIBP-CorV vaccinee sera. 2x reduction in neutralization by serum collected 2 to 3 weeks after the second dose from vaccinees who had received CoronaVac (pVNT50 against VSV pseudotyped as B.1.1.7). Convalescent plasma had similar titer against wild type as the CoronaVac vaccinee sera.	B.1.1.7, Q.3, Q.1	Wang et al. (2021)	37134	C	A	nan
p.P681H	vaccine neutralization efficacy	No significant difference in T-cell response to B.1.1.7 was observed (vs. ancestral) in blood drawn from 28 participants received the Pfizer-BioNTech vaccine and 2 received the Moderna vaccine. This is despite three mutations (Y144del, D614G, and P681H) overlapping T-cell epitope hotspots.	B.1.1.7, Q.3, Q.1	Woldemeskel et al. (2021)	37134	C	A	nan
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]	Q.8, Q.3, Q.1, B.1.1.7	Zuckerman et al. (2021)	37142	C	A	nan
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.	Q.8, Q.3, Q.1, B.1.1.7	Gong et al. (2021)	37142	C	A	nan
p.P681H	vaccinee plasma binding	This variant combination (representing B.1.1.7 aka Alpha) showed no change in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in previously non-seroconverted subjects. 1.28x 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.1.1.7, Q.3, Q.1	Gong et al. (2021)	37134	C	A	nan
p.P681H	viral load	Using lack of S probe detection as a proxy for B.1.1.7 status, 275 putative B.1.1.7 samples and 390 "wild type" SARS-CoV-2 positive samples in Wales were compared for Ct values, suggesting extasciitilde12-fold increase (extasciitilde3.5 Ct decrease) in viral load for B.1.1.7 samples.	B.1.1.7, Q.3, Q.1	Couzens et al. (2021)	37134	C	A	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.P681H	viral load	We found that the British variant (clade B.1.1.7), compared to an ancestral SARS-CoV-2 clade B virus, produced higher levels of infectious virus late in infection and had a higher replicative fitness in human airway, alveolar and intestinal organoid models.	B.1.1.7, Q.3, Q.1	Lamers et al. (2021)	37134	C	A	nan
p.P681H	viral load	This study reveals that B.1.1.7 SARS-CoV-2 variant is a slower-growing virus than parental B.1. Further, a higher replication along with reduced infectious viral titer was hypothesized to be linked to higher transmission with reduced pathogenicity.	B.1.1.7, Q.3, Q.1	Nyayanit et al. (2021)	37134	C	A	nan
p.P681H	viral load	In a study of 1260 ICU subjects, viral load distributions (collected within 48h of admission) were elevated in both seropositive and seronegative subjects infected with B.1.1.7 ("UK variant"). PG: The PANGO tool defining Spike variants for B.1.1.7 are listed here, whereas the paper only used a test for D1118H.	B.1.1.7, Q.3, Q.1	Ratcliff et al. (2021)	37134	C	A	nan
p.P681H	viral load	B.1.1.7 samples showed average Ct cycle threshold of 21.9 vs 23 for wildtype (i.e. extasciitilde2x higher viral load) comparing 37758 and 22535 samples respectively.	B.1.1.7, Q.3, Q.1	Roquebert et al. (2021)	37134	C	A	nan
p.P681H	viral load	The median Ct value of RT-qPCR tests of the N-gene target in the Daxing B.1.1.7 group was significantly lower than the Shunyi B.1.470 group (P	B.1.1.7, Q.3, Q.1	Song et al. (2021)	37134	C	A	nan
p.P681H	viral load	The 249 B.1.1.7 (a.k.a. N501Y.V1) variant cases in three Paris hospital labs had a extasciitilde10-fold viral load increase (extasciitilde3.3 Ct drop in N gene probe) compared to 332 ancestral lineage cases from the same time frame (2020-12-20 to 2021-02-26). PG: BUT there is a discrepancy in drop between the ORF1ab and N probes, with the former suggesting only a 2-fold drop, consistent with the drop observed in B.1.351. This might indicate higher subgenomic RNA content in B.1.1.7 skewing the change.	B.1.1.7, Q.3, Q.1	Teyssou et al. (2021)	37134	C	A	nan
p.P681H	virion structure	CryoEM analysis of B.1.1.7 demonstrates an increased propensity for 'up', receptor accessible conformation of the Spike protein trimer.	B.1.1.7, Q.3, Q.1	Cai et al. (2021)	37134	C	A	nan
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.	Q.8, Q.3, Q.1, B.1.1.7	Tada et al. (2021)	37142	C	A	nan

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.P681H	virion structure	The Ratio of S2 (processed Spike) to full length Spike is higher for this mutation combination, due to a drop in the full length Spike measured, suggesting that this mutation compensates for decreased Spike production by improved proteolytic processing.	Q.8, Q.3, Q.1, B.1.1.7	Tada et al. (2021)	37142	C	A	nan

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)