Surveillance report

Surveillance generated by nf-ncov-voc for Beta variant

Date

This report is generated on 2022-05-06 using 272378 number of genomes collected between 2020-02-25 and 2022-04-06

Pango Lineages

Pango Lineages in this report ['B.1.351', 'B.1.351.2', 'B.1.351.3']

Indicator

This table contains key indicators identified

Indicator	Sub-categories from POKAY	Mutations
Transmissibility between humans	transmissibility	p.D614G, p.E484K, p.K417N, p.N501Y
Infection Severity	ACE2 receptor binding affinity, viral load, outcome hazard ratio	p.A701V, p.D215G, p.D614G, p.D80A, p.E484K, p.K417N, p.L18F, p.L242del, p.N501Y
Immunity after natural infection	convalescent plasma escape, reinfection, humoral response durability	p.A243del, p.A701V, p.D215G, p.D614G, p.D80A, p.E484K, p.K417N, p.L18F, p.L242del, p.N501Y
Vaccines	vaccine neutralization efficacy	p.A701V, p.D215G, p.D614G, p.D80A, p.E484K, p.K417N, p.L18F, p.L242del, p.N501Y
Monoclonal antibodies	monoclonal antibody serial passage escape, pharmaceutical effectiveness	p.E484K, p.K417N, p.N501Y
Diagnostics	clinical indicators, antigenic test failure, symptom prevalence	

Mutation Significance

This table contains key functional impacts of mutations identified

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.L242del	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.1.351. We observed an increase (relative to D614G) in binding of soluble ACE2 to B.1.351, and to a much gearter extent to B.1.1.7, which both carry the N501Y mutation (see Fig 3).	B.1.351.2, B.1.351, B.1.351.3	Planas et al. (2021)	807	ACTTTACTTG	A	0.99

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.L242del	CD8 plus T cell response	Encouragingly, we find that the majority of T cell responses in recipients of two doses of the BNT162b2 vaccine are generated by epitopes that are invariant between the [wildtype] and two of the current variants of concern (B.1.1.7 and B.1.351). In over 90% of two dose mRNA vaccinees, heterotypic neutralizing titres (NT50) against B.1.1.7 and B.1.351 remain comfortably above the level associated with immune protection in recent vaccine trials. However, in over 50% of convalescent COVID-19 individuals and recipients of a only a single dose of mRNA vaccine – heterotypic neutralization dropped to negligible levels, particularly against B.1.351.	B.1.351.2, B.1.351, B.1.351.3	Skelly et al. (2021)	807	ACTTTACTTG	A	0.99
p.L242del	antibody epitope effects	Anti-NTD CV1 mAb isolated from an early pandemic case was unable to neutralize either partial B.1.351 variant pseudovirus used (A701V or L242del). The neutralization potency of mAb CV30, which contacts K417 and N501 but not E484, was extasciitilde10-fold weaker toward both B.1.351 variants. The neutralization potency of anti-RBD mAb CV3-1 was 3-4-fold less potent against the B.1.351 variants, while anti-RBD mAb CV2-75 was modestly less effective.	B.1.351.2, B.1.351, B.1.351.3	Stamatatos et al. (2021)	807	ACTTTACTTG	A	0.99
p.L242del	antibody epitope effects	B.1.351 pseudotyped virus model ablates neutralization by N-terminal-domain-directed mAbs 5-24, 4-8, 4A8, 2-17, and 4-19 (independent of S:p.R246I).	B.1.351.2, B.1.351, B.1.351.3	Wang et al. (2021)	807	ACTTTACTTG	A	0.99
p.L242del	antibody epitope effects	Ablates binding of Spike N terminal domain targeting monoclonal antibody 4A8, by disruption of N5-loop/supersite loop, may work synergistically with 501Y.V2 ("South African") lineage background variant R246I to disrupt paratope binding. [PG: del extent simplified to accomodate minor position realignments]	B.1.351.2, B.1.351, B.1.351.3	Wibmer et al. (2021)	807	ACTTTACTTG	A	0.99
p.L242del	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.1.351.2, B.1.351, B.1.351.3	Cele et al. (2021)	807	ACTTTACTTG	A	0.99
p.L242del	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 1 patient.	B.1.351.2, B.1.351, B.1.351.3	McCarthy et al. (2021)	807	ACTTTACTTG	A	0.99

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.L242del	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 had mean extasciitilde6x reduction in neutralizing titers, and 40% of the samples lacked any activity against B.1.351.	B.1.351.2, B.1.351, B.1.351.3	Planas et al. (2021)	807	ACTTTACTTG	A	0.99
p.L242del	convalescent plasma escape	In over 90% of two dose mRNA vaccinees, heterotypic neutralizing titres (NT50) against B.1.1.7 and B.1.351 remain comfortably above the level associated with immune protection in recent vaccine trials. However, in over 50% of convalescent COVID-19 individuals (5/9) and recipients of a only a single dose of mRNA vaccine (10/11) – heterotypic neutralization dropped to negligible levels, particularly against B.1.351.	B.1.351.2, B.1.351, B.1.351.3	Skelly et al. (2021)	807	ACTTTACTTG	A	0.99
p.L242del	convalescent plasma escape	Using convalescent sera from 15 early pandemic patients (Seattle Flu Study), mean 220 days post symptom onset (IQR 125-269, and three asymptomatic cases) with 27% WHO disease severity scale 3, 7 of 15 neutralized this B.1.351 pseudotype that includes the L242del, and only one had titers above 100. Only one of the 15 sera achieved 80% neutralization. [compare to 5 and 1 for pseudotype without the deletion]	B.1.351.2, B.1.351, B.1.351.3	Stamatatos et al. (2021)	807	ACTTTACTTG	A	0.99
p.L242del	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.1.351.2, B.1.351, B.1.351.3	Wibmer et al. (2021)	807	ACTTTACTTG	A	0.99
p.L242del	humoral response durability	In a prospective study of 107 hospitalized patients, decrease of IgG rates and serological assays becoming negative did not imply loss of neutralizing capacity. Our results indicate a sustained humoral response against the ancestral strain and the D614G, B.1.1.7 and P.1 variants for at least 6 months (last of two samples taken) in patients previously hospitalized for COVID-19. A weaker protection was however observed for the B.1.351 variant.	B.1.351.2, B.1.351, B.1.351.3	Betton et al. (2020)	807	ACTTTACTTG	A	0.99

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.L242del	outcome hazard ratio	On average across 7 European countries studied, using B.1.351 defining mutations: Significant shift to infection in those without pre-existing conditions (79.6% vs 89% for non-VOC cases). Significant increase in hospitalization rate (19.3% vs 7.5% for non-VOC cases). Significant increase in ICU rate (2.3% vs 0.6% for non-VOC cases). PG: seems to be different notations around the LAL deletion, using the minimal shared definition to catch as many as possible.	B.1.351.2, B.1.351, B.1.351.3	Funk et al. (2021)	807	ACTTTACTTG	A	0.99
p.L242del	tissue specific neutralization	The nasal mucosa of Pfizer vaccinees with time course collection was evaluated against VSV pseudotypes: while B.1.1.7 and D614G showed neutralization by nasal swab from only one different previously infected vacinee neutralizing at weeks 3 and 6, B.1.351 showed zero neutralization at either time point in any sample (and relatively impaired serum neutralization).	B.1.351.2, B.1.351, B.1.351.3	Planas et al. (2021)	807	ACTTTACTTG	A	0.99
p.L242del	trafficking	Lentiviral pseudotyped with this individual mutation from B.1.351 was tested on ACE2.293T cells. Luciferase activity was measured two days postinfection, showing mild decrease in infection rate amongst the cells, suggesting that this deletion does not contributing to cell entry fitness.	B.1.351.2, B.1.351, B.1.351.3	Tada et al. (2021)	807	ACTTTACTTG	A	0.99
p.L242del	vaccine neutralization efficacy	The Janssen single dose vaccine showed 72% efficacy at preventing moderate and severe disease, which was reduced to 57% in South Africa, where 92.6% of infections are estimated to have been B.1.351. 100% reduction in hospitalization risk remains across variants after 28 days post-vaccination.	B.1.351.2, B.1.351, B.1.351.3	nan	807	ACTTTACTTG	A	0.99
p.L242del	vaccine neutralization efficacy	In an Ontario long term care facility, cumulatively, weaker BNT162b2 vaccine stimulation, age/comorbidities, produced a 130-fold reduction in apparent neutralization titers in mean 88yo LTCH residents against Beta (B.1.351), relative to staff vaccinees against D614G wild type. 37.9% of 116 two-dose-mRNA-vaccinated residents had undetectable neutralizing antibodies to B.1.351. mRNA-1273 vaccinee sera displayed extasciitilde2 better neutralization than BNT162b2. [common defining B.1.351 mutations noted, as the manuscript does not provide details]	B.1.351.2, B.1.351, B.1.351.3	Abe et al. (2021)	807	ACTTTACTTG	A	0.99

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.L242del	vaccine neutralization efficacy	Observed 8.8-fold reduction in neutralization efficiency of Pfizer vaccinee sera (collected 14 days after second dose) against cultured B.1.351 sample. Contrast this with 1.4-fold reduction for just the pseudovirus combination of "key" B.1.351 mutations K417N+E484K+N501Y. WA1 and B.1.351 FRNT50 titers correlated weakly at the individual level, with some individual's serum potently neutralizing WA1 while having FRNT50 for B.1.351 below the assay limit of detection (1:20).	B.1.351.2, B.1.351, B.1.351.3	Bates et al. (2021)	807	ACTTTACTTG	A	0.99
p.L242del	vaccine neutralization efficacy	Neutralization efficiency (ID50) against B.1.1.351-v3 reduced 8.4x relative to D614G wildtype using pseudotyped VSV assay on 8 Moderna vaccinee sera one week post-booster.	B.1.351.2, B.1.351, B.1.351.3	Choi et al. (2021)	807	ACTTTACTTG	A	0.99
p.L242del	vaccine neutralization efficacy	Neutralization efficiency (ID50) against B.1.1.351-v2 reduced 7.3x relative to D614G wildtype using pseudotyped VSV assay on 8 Moderna vaccinee sera one week post-booster.	B.1.351.2, B.1.351, B.1.351.3	Choi et al. (2021)	807	ACTTTACTTG	A	0.99
p.L242del	vaccine neutralization efficacy	ELISpot assays show T cell neutralization reduced by 29.8% in this B.1.351 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.1.351.2, B.1.351, B.1.351.3	Gallagher et al. (2021)	807	ACTTTACTTG	A	0.99
p.L242del	vaccine neutralization efficacy	Pseudotyped B.1.351 v1 virus has reduced neutralization activity vs wild type: 34.5x (30 sera Pfizer median 9 days post 2nd dose) and 27.7x (35 sera Moderna median 18 days post 2nd dose). This was significant by ANOVA. Notably, 36.7% (11/30) recipients of two-dose Pfizer and 42.9% (15/35) recipients of two-dose Moderna vaccines did not have detectable neutralization of at least one of the B.1.351 variants.	B.1.351.2, B.1.351, B.1.351.3	Garcia-Beltran et al. (2021)	807	ACTTTACTTG	A	0.99
p.L242del	vaccine neutralization efficacy	Pseudotyped B.1.351 v2 virus has reduced neutralization activity vs wild type: 41.2x (30 sera Pfizer median 9 days post 2nd dose) and 20.8x (35 sera Moderna median 18 days post 2nd dose). This was significant by ANOVA. Notably, 36.7% (11/30) recipients of two-dose Pfizer and 42.9% (15/35) recipients of two-dose Moderna vaccines did not have detectable neutralization of at least one of the B.1.351 variants.	B.1.351.2, B.1.351, B.1.351.3	Garcia-Beltran et al. (2021)	807	ACTTTACTTG	A	0.99

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.L242del	vaccine neutralization efficacy	B.1.351 pseudotyped VSV was tested for neutralization in a clonal HEK-293T ACE2 TMPRSS2 cell line optimized for highly efficient S-mediated infection. Only 1 out of 12 serum samples from a cohort of Argentinian recipients of the Gamaleya Sputnik V Ad26 / Ad5 vaccine showed effective neutralization (IC90) at full serum strength (average realtive decrease was 6.1x vs wild type).	B.1.351.2, B.1.351, B.1.351.3	Ikegame et al. (2021)	807	ACTTTACTTG	A	0.99
p.L242del	vaccine neutralization efficacy	Vaccine plasma neutralization of B.1.351-spike virus was nominally robust but lower (extasciitilde3x) than other variants of concern.	B.1.351.2, B.1.351, B.1.351.3	Liu et al. (2021)	807	ACTTTACTTG	A	0.99
p.L242del	vaccine neutralization efficacy	A two-dose regimen of (AstraZeneca) ChAdOx1-nCoV19 did not show protection against mild-moderate Covid-19 due to B.1.351 variant, however, vaccine efficacy against severe Covid-19 is undetermined.	B.1.351.2, B.1.351, B.1.351.3	Madhi et al. (2021)	807	ACTTTACTTG	A	0.99
p.L242del	vaccine neutralization efficacy	Relative to B.1.1.117, PRNT50 line virus neutralizating antibody activity assay of B.1.351 showed extasciitilde11x reduction in 13 vacinees's sera collected through 41 days after vaccination. Neutralization by a placebo control group of 6 naturally infected patients showed a smaller extasciitilde8x drop (starting from a extasciitilde50% higher PRNT50 value than vacinees for B.1.1.117 neutralization). Serum samples obtained from 13 ChAdOx1 nCoV-19 vaccine recipients without SARS-CoV-2 infection through 41 days after vaccination showed extasciitilde4x reduction in neutralization (ID50) for full B.1.351 pseudotype HIV-1 virus compared to D614G alone. This RBD variant combination's neutralization by a placebo control group of 6 naturally infected patients showed a slightly higher 4.6x drop (though with D614G starting at a 1.7x higher titre than vaccinee sera).	B.1.351.2, B.1.351, B.1.351.3	Madhi et al. (2021)	807	ACTTTACTTG	A	0.99
p.L242del	vaccine neutralization efficacy	The Novavax vaccine, which achieved 95.6% efficacy against previous SARS-CoV-2 strains, had reduced efficacy of 60% in South Africa, where 92.6% of infections are estimated to have been B.1.351.	B.1.351.2, B.1.351, B.1.351.3	Novavax (2021)	807	ACTTTACTTG	A	0.99

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.L242del	vaccine neutralization efficacy	Detectable antibodies against B.1.351 at various time points using pseudotyped lentivirus neutralization in Moderna vaccinee cohort: Day 29 8%, Day 43 100%, Day 119 71%, Day 209 54%. Detectable antibodies against B.1.351 at various time points using live virus FRNT neutralization in Moderna vaccinee cohort: Day 29 8%, Day 43 100%, Day 119 79%, Day 209 58%. Detectable antibodies against B.1.351 at various time points using ACE2 blocking assay in Moderna vaccinee cohort: Day 29 63%, Day 43 100%, Day 119 71%, Day 209 79%. Decreased neutralization on some assays was seen especially in those vaccinees tested that were 71+.	B.1.351.2, B.1.351, B.1.351.3	Pegu et al (2021)	807	ACTTTACTTG	A	0.99
p.L242del	vaccine neutralization efficacy	The sera of 16 individuals with time course collection was evaluated against VSV pseudotypes: while BD614G and B.1.1.7 were neutralized earlier, the anti-B.1.351 response was negative up to week 3, and became detectable at week 4 (1 week after booster dose), at a level lower than the two other viruses (extasciitilde10x vs D614G) through week 6, the last timepoint measured. Three vaccinees never showed detectable neutralization to B.1.351 even after second dose.	B.1.351.2, B.1.351, B.1.351.3	Planas et al. (2021)	807	ACTTTACTTG	A	0.99
p.L242del	vaccine neutralization efficacy	In a randomized phase 2a-b control trial of the Novavax (NVX-CoV2373) vaccine in South Africa, where B.1.351 virus dominates, efficacy was 60.1% (95% CI, 19.9 to 80.1) in HIV-negative and initially SARS-CoV-2 seronegative participants using the primary endpoint of laboratory-confirmed symptomatic Covid-19 at 7 days or more after the second dose among participants.	B.1.351.2, B.1.351, B.1.351.3	Shinde et al. (2021)	807	ACTTTACTTG	A	0.99
p.L242del	vaccine neutralization efficacy	In sera collected from 15 early pandemic patients (Seattle Flu Study), mean 16 days post first dose with either Pfizer/BioNTech or Moderna vaccines, the median ID50 titers were extasciitilde10-fold lower against this B.1.351 pseudotyped virus relative to wild type. A single asymptomatic patient, who had no detectable RBD-specific IgG memory before vaccination, also did not elicit nAbs against the B.1.351 variant. [compare to extasciitilde3 fold without the deletion] ID50 titres in non-infected mRNA vaccines more than two weeks post-booster were significant, but extasciitilde500x weaker than in previously infected patients after first dose.	B.1.351.2, B.1.351, B.1.351.3	Stamatatos et al. (2021)	807	ACTTTACTTG	A	0.99

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.L242del	vaccine neutralization efficacy	Pseudotyped viruses for B.1.351 was 3.4-fold resistant to neutralization by 6 BNT162b2 vaccine sera 28 days post-booster compared to wild type. Neutralization by 3 Moderna vaccine sera 28 days post-booster was 2.2-fold resistant. [Exact list of B.1.351 mutations used in these assays was not included in the preprint]	B.1.351.2, B.1.351, B.1.351.3	Tada et al. (2021)	807	ACTTTACTTG	A	0.99
p.L242del	vaccine neutralization efficacy	PBMCs of Pfizer/BioNTech BNT162b2 (n	B.1.351.2, B.1.351, B.1.351.3	Tarke et al. (2021)	807	ACTTTACTTG	A	0.99
p.L242del	vaccine neutralization efficacy	[Contrary to how this paper has been cited, Voysey et al. do NOT show evidence of decreased effectiveness of ChAdOx1 (AstraZeneca) against the South African B.1.351 lineage. Insufficient numbers reaching the primary study endpoint were available in that arm of the vaccine study to report any statistics from the South African participants. Additionally, the study period of the paper ended in November 2020, while the earliest reported case of this lineage is October (covariants.org), only becoming dominant by mid-November.]	B.1.351.2, B.1.351, B.1.351.3	Voysey et al. (2021)	807	ACTTTACTTG	A	0.99
p.L242del	vaccine neutralization efficacy	No significant difference in T-cell response to B.1.351 was observed (vs. ancestral) in blood drawn from 28 participants received the Pfizer-BioNTech vaccine and 2 received the Moderna vaccine.	B.1.351.2, B.1.351, B.1.351.3	Woldemeskel et al. (2021)	807	ACTTTACTTG	A	0.99
p.L242del	vaccine neutralization efficacy	Sera from healthcare workers (n	B.1.351.2, B.1.351, B.1.351.3	Zhou et al. (2021)	807	ACTTTACTTG	A	0.99
p.L242del	virion structure	The L18F and D80A of the B.1.351 lineage lead to reconfiguration of the N-terminal segment despite the disulfide between Cys16 and Cys136 that partly anchors the N-terminal peptide. The most consequential changes are probably from the triple residue deletion... which causes a shift of the nearby loop 144-155 and must also reconfigure the adjacent disorder loop (residues 246-260), both of which form part of the neutralizing epitopes...bringing large changes in the antigenic surface in this region.	B.1.351.2, B.1.351, B.1.351.3	Cai et al. (2021)	807	ACTTTACTTG	A	0.99
p.A701V	ACE2 receptor binding affinity	Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant showed essentially no change in binding (KD) relative to D614G.	B.1.351.2, B.1.351, B.1.351.3	Gong et al. (2021)	896	C	T	1.0

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p.A701V	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.1.351. We observed an increase (relative to D614G) in binding of soluble ACE2 to B.1.351, and to a much gearter extent to B.1.1.7, which both carry the N501Y mutation (see Fig 3).	B.1.351.2, B.1.351, B.1.351.3	Planas et al. (2021)	896	C	T	1.0
p.A701V	CD8 plus T cell response	Encouragingly, we find that the majority of T cell responses in recipients of two doses of the BNT162b2 vaccine are generated by epitopes that are invariant between the [wildtype] and two of the current variants of concern (B.1.1.7 and B.1.351). In over 90% of two dose mRNA vaccinees, heterotypic neutralizing titres (NT50) against B.1.1.7 and B.1.351 remain comfortably above the level associated with immune protection in recent vaccine trials. However, in over 50% of convalescent COVID-19 individuals and recipients of a only a single dose of mRNA vaccine – heterotypic neutralization dropped to negligible levels, particularly against B.1.351.	B.1.351.2, B.1.351, B.1.351.3	Skelly et al. (2021)	896	C	T	1.0
p.A701V	antibody epitope effects	Anti-NTD CV1 mAb isolated from an early pandemic case was unable to neutralize either partial B.1.351 variant pseudovirus used (A701V or L242del). The neutralization potency of mAb CV30, which contacts K417 and N501 but not E484, was extasciitilde10-fold weaker toward both B.1.351 variants. The neutralization potency of anti-RBD mAb CV3-1 was 3-4-fold less potent against the B.1.351 variants, while anti-RBD mAb CV2-75 was modestly less effective.	B.1.351.2, B.1.351, B.1.351.3	Stamatatos et al. (2021)	896	C	T	1.0
p.A701V	convalescent plasma binding	1.11x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset.	B.1.351.2, B.1.351, B.1.351.3	Gong et al. (2021)	896	C	T	1.0
p.A701V	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 had mean extasciitilde6x reduction in neutralizing titers, and 40% of the samples lacked any activity against B.1.351.	B.1.351.2, B.1.351, B.1.351.3	Planas et al. (2021)	896	C	T	1.0

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p.A701V	convalescent plasma escape	Using convalescent sera from 15 early pandemic patients (Seattle Flu Study), mean 220 days post symptom onset (IQR 125-269, and three asymptomatic cases) with 27% WHO disease severity scale 3, one third (5/15) of sera neutralized this B.1.351 pseudotype and only three had ID50 titers above 100. Only two of the 15 sera achieved 80% neutralization.	B.1.351.2, B.1.351, B.1.351.3	Stamatatos et al. (2021)	896	C	T	1.0
p.A701V	humoral response durability	In a prospective study of 107 hospitalized patients, decrease of IgG rates and serological assays becoming negative did not imply loss of neutralizing capacity. Our results indicate a sustained humoral response against the ancestral strain and the D614G, B.1.1.7 and P.1 variants for at least 6 months (last of two samples taken) in patients previously hospitalized for COVID-19. A weaker protection was however observed for the B.1.351 variant.	B.1.351.2, B.1.351, B.1.351.3	Betton et al. (2020)	896	C	T	1.0
p.A701V	outcome hazard ratio	On average across 7 European countries studied, using B.1.351 defining mutations: Significant shift to infection in those without pre-existing conditions (79.6% vs 89% for non-VOC cases). Significant increase in hospitalization rate (19.3% vs 7.5% for non-VOC cases). Significant increase in ICU rate (2.3% vs 0.6% for non-VOC cases). PG: seems to be different notations around the LAL deletion, using the minimal shared definition to catch as many as possible.	B.1.351.2, B.1.351, B.1.351.3	Funk et al. (2021)	896	C	T	1.0
p.A701V	reinfection	4 health care workers in the 20's and 30's with no underlying conditions and seropositivity or confirmed 2020 SARS-CoV-2 infections were confirmed to have B.1.351 infection during a Februrary 2021 hospital outbreak in Luxembourg. Symptoms were mostly mild on first infection, and milder on second infection.	B.1.351.2, B.1.351, B.1.351.3	Staub et al. (2021)	896	C	T	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.A701V	reinfection	Hamsters re-infected with B.1.351 virus after seroversion from previous infection with a lineage A virus did not transmit virus to naive sentinels via direct contact transmission, in contrast to the non-seroconverted animals. They had little infectious virus and no pathology in the lungs. Initial infection with SARS-CoV-2 lineage A does not prevent heterologous reinfection with B.1.351, but prevents disease and onward transmission.	B.1.351.2, B.1.351, B.1.351.3	Yinda et al. (2021)	896	C	T	1.0
p.A701V	symptom prevalence	Inoculation with the B.1.351 isolate resulted in lower clinical scores in 6 rhesus macaques that correlated with lower virus titers in the lungs, less severe histologic lung lesions and less viral antigen detected in the lungs. Our comparative pathogenicity study suggests that ongoing circulation under diverse evolutionary pressure favors transmissibility and immune evasion rather than an increase in intrinsic pathogenicity.	B.1.351.2, B.1.351, B.1.351.3	Munster et al. (2021)	896	C	T	1.0
p.A701V	tissue specific neutralization	The nasal mucosa of Pfizer vaccinees with time course collection was evaluated against VSV pseudotypes: while B.1.1.7 and D614G showed neutralization by nasal swab from only one different previously infected vacinee neutralizing at weeks 3 and 6, B.1.351 showed zero neutralization at either time point in any sample (and relatively impaired serum neutralization).	B.1.351.2, B.1.351, B.1.351.3	Planas et al. (2021)	896	C	T	1.0
p.A701V	trafficking	Lentiviral pseudotyped with this individual mutation from B.1.351 was tested on ACE2.293T cells. Luciferase activity was measured two days postinfection, showing mild decrease in infection rate amongst the cells, suggesting that this mutation does not contributing to cell entry fitness.	B.1.351.2, B.1.351, B.1.351.3	Tada et al. (2021)	896	C	T	1.0
p.A701V	vaccine neutralization efficacy	The Janssen single dose vaccine showed 72% efficacy at preventing moderate and severe disease, which was reduced to 57% in South Africa, where 92.6% of infections are estimated to have been B.1.351. 100% reduction in hospitalization risk remains across variants after 28 days post-vaccination.	B.1.351.2, B.1.351, B.1.351.3	nan	896	C	T	1.0
p.A701V	vaccine neutralization efficacy	Using B.1.351 defining mutations for Spike, observed 4x average decrease in neutralization efficiency (but still relevant titres) for sera from 10 BNT162b2 vaccinees 12 days after second dose, but only one relevant titre 12 days after first dose. Compares unfavorably to wild type or B.1.1.7 titres.	B.1.351.2, B.1.351, B.1.351.3	Alenquer et al. (2021)	896	C	T	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.A701V	vaccine neutralization efficacy	Observed 8.8-fold reduction in neutralization efficiency of Pfizer vaccinee sera (collected 14 days after second dose) against cultured B.1.351 sample. Contrast this with 1.4-fold reduction for just the pseudovirus combination of "key" B.1.351 mutations K417N+E484K+N501Y. WA1 and B.1.351 FRNT50 titers correlated weakly at the individual level, with some individual's serum potently neutralizing WA1 while having FRNT50 for B.1.351 below the assay limit of detection (1:20).	B.1.351.2, B.1.351, B.1.351.3	Bates et al. (2021)	896	C	T	1.0
p.A701V	vaccine neutralization efficacy	Neutralization efficiency (ID50) against B.1.1.351-v3 reduced 8.4x relative to D614G wildtype using pseudotyped VSV assay on 8 Moderna vaccinee sera one week post-booster.	B.1.351.2, B.1.351, B.1.351.3	Choi et al. (2021)	896	C	T	1.0
p.A701V	vaccine neutralization efficacy	Neutralization efficiency (ID50) against B.1.1.351-v2 reduced 7.3x relative to D614G wildtype using pseudotyped VSV assay on 8 Moderna vaccinee sera one week post-booster.	B.1.351.2, B.1.351, B.1.351.3	Choi et al. (2021)	896	C	T	1.0
p.A701V	vaccine neutralization efficacy	ELISpot assays show T cell neutralization reduced by 29.8% in this B.1.351 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.1.351.2, B.1.351, B.1.351.3	Gallagher et al. (2021)	896	C	T	1.0
p.A701V	vaccine neutralization efficacy	Pseudotyped B.1.351 v1 virus has reduced neutralization activity vs wild type: 34.5x (30 sera Pfizer median 9 days post 2nd dose) and 27.7x (35 sera Moderna median 18 days post 2nd dose). This was significant by ANOVA. Notably, 36.7% (11/30) recipients of two-dose Pfizer and 42.9% (15/35) recipients of two-dose Moderna vaccines did not have detectable neutralization of at least one of the B.1.351 variants.	B.1.351.2, B.1.351, B.1.351.3	Garcia-Beltran et al. (2021)	896	C	T	1.0
p.A701V	vaccine neutralization efficacy	Pseudotyped B.1.351 v2 virus has reduced neutralization activity vs wild type: 41.2x (30 sera Pfizer median 9 days post 2nd dose) and 20.8x (35 sera Moderna median 18 days post 2nd dose). This was significant by ANOVA. Notably, 36.7% (11/30) recipients of two-dose Pfizer and 42.9% (15/35) recipients of two-dose Moderna vaccines did not have detectable neutralization of at least one of the B.1.351 variants.	B.1.351.2, B.1.351, B.1.351.3	Garcia-Beltran et al. (2021)	896	C	T	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.A701V	vaccine neutralization efficacy	B.1.351 pseudotyped VSV was tested for neutralization in a clonal HEK-293T ACE2 TMPRSS2 cell line optimized for highly efficient S-mediated infection. Only 1 out of 12 serum samples from a cohort of Argentinian recipients of the Gamaleya Sputnik V Ad26 / Ad5 vaccine showed effective neutralization (IC90) at full serum strength (average realtive decrease was 6.1x vs wild type).	B.1.351.2, B.1.351, B.1.351.3	Ikegame et al. (2021)	896	C	T	1.0
p.A701V	vaccine neutralization efficacy	Vaccine plasma neutralization of B.1.351-spike virus was nominally robust but lower (extasciitilde3x) than other variants of concern.	B.1.351.2, B.1.351, B.1.351.3	Liu et al. (2021)	896	C	T	1.0
p.A701V	vaccine neutralization efficacy	A two-dose regimen of (AstraZeneca) ChAdOx1-nCoV19 did not show protection against mild-moderate Covid-19 due to B.1.351 variant, however, vaccine efficacy against severe Covid-19 is undetermined.	B.1.351.2, B.1.351, B.1.351.3	Madhi et al. (2021)	896	C	T	1.0
p.A701V	vaccine neutralization efficacy	Relative to B.1.1.117, PRNT50 line virus neutralizating antibody activity assay of B.1.351 showed extasciitilde11x reduction in 13 vacinees's sera collected through 41 days after vaccination. Neutralization by a placebo control group of 6 naturally infected patients showed a smaller extasciitilde8x drop (starting from a extasciitilde50% higher PRNT50 value than vacinees for B.1.1.117 neutralization). Serum samples obtained from 13 ChAdOx1 nCoV-19 vaccine recipients without SARS-CoV-2 infection through 41 days after vaccination showed extasciitilde4x reduction in neutralization (ID50) for full B.1.351 pseudotype HIV-1 virus compared to D614G alone. This RBD variant combination's neutralization by a placebo control group of 6 naturally infected patients showed a slightly higher 4.6x drop (though with D614G starting at a 1.7x higher titre than vaccinee sera).	B.1.351.2, B.1.351, B.1.351.3	Madhi et al. (2021)	896	C	T	1.0
p.A701V	vaccine neutralization efficacy	The Novavax vaccine, which achieved 95.6% efficacy against previous SARS-CoV-2 strains, had reduced efficacy of 60% in South Africa, where 92.6% of infections are estimated to have been B.1.351.	B.1.351.2, B.1.351, B.1.351.3	Novavax (2021)	896	C	T	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.A701V	vaccine neutralization efficacy	The sera of 16 individuals with time course collection was evaluated against VSV pseudotypes: while BD614G and B.1.1.7 were neutralized earlier, the anti-B.1.351 response was negative up to week 3, and became detectable at week 4 (1 week after booster dose), at a level lower than the two other viruses (extasciitilde10x vs D614G) through week 6, the last timepoint measured. Three vaccinees never showed detectable neutralization to B.1.351 even after second dose.	B.1.351.2, B.1.351, B.1.351.3	Planas et al. (2021)	896	C	T	1.0
p.A701V	vaccine neutralization efficacy	In a randomized phase 2a-b control trial of the Novavax (NVX-CoV2373) vaccine in South Africa, where B.1.351 virus dominates, efficacy was 60.1% (95% CI, 19.9 to 80.1) in HIV-negative and initially SARS-CoV-2 seronegative participants using the primary endpoint of laboratory-confirmed symptomatic Covid-19 at 7 days or more after the second dose among participants.	B.1.351.2, B.1.351, B.1.351.3	Shinde et al. (2021)	896	C	T	1.0
p.A701V	vaccine neutralization efficacy	In sera collected from 15 early pandemic patients (Seattle Flu Study), mean 16 days post first dose with either Pfizer/BioNTech or Moderna vaccines, the median ID50 titers were extasciitilde3-fold lower against this B.1.351 pseudotyped virus relative to wild type. A single asymptomatic patient, who had no detectable RBD-specific IgG memory before vaccination, also did not elicit nAbs against the B.1.351 variant. [compare to extasciitilde10 fold with L242del] ID50 titres in non-infected mRNA vaccines more than two weeks post-booster were signficiant, but >100x weaker than in previously infected patients after first dose.	B.1.351.2, B.1.351, B.1.351.3	Stamatatos et al. (2021)	896	C	T	1.0
p.A701V	vaccine neutralization efficacy	PBMCs of Pfizer/BioNTech BNT162b2 (n	B.1.351.2, B.1.351, B.1.351.3	Tarke et al. (2021)	896	C	T	1.0
p.A701V	vaccine neutralization efficacy	[Contrary to how this paper has been cited, Voysey et al. do NOT show evidence of decreased effectiveness of ChAdOx1 (AstraZeneca) against the South African B.1.351 lineage. Insufficient numbers reaching the primary study endpoint were available in that arm of the vaccine study to report any statistics from the South African participants. Additionally, the study period of the paper ended in November 2020, while the earliest reported case of this lineage is October (covariants.org), only becoming dominant by mid-November.]	B.1.351.2, B.1.351, B.1.351.3	Voysey et al. (2021)	896	C	T	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.A701V	vaccine neutralization efficacy	No significant difference in T-cell response to B.1.351 was observed (vs. ancestral) in blood drawn from 28 participants received the Pfizer-BioNTech vaccine and 2 received the Moderna vaccine.	B.1.351.2, B.1.351, B.1.351.3	Woldemeskel et al. (2021)	896	C	T	1.0
p.A701V	vaccine neutralization efficacy	Sera from healthcare workers (n	B.1.351.2, B.1.351, B.1.351.3	Zhou et al. (2021)	896	C	T	1.0
p.A701V	vaccinee plasma binding	1.19x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in previously non-seroconverted subjects. 1.1x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in post-infection vaccinees.	B.1.351.2, B.1.351, B.1.351.3	Gong et al. (2021)	896	C	T	1.0
p.A701V	virion structure	Estimated free energy change (ddG) for this variant is -0.33 kcal/mol (i.e. destabilizing relative to wild type)	B.1.351.2, B.1.351, B.1.351.3	Spratt et al. (2021)	896	C	T	1.0
p.A243del	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.1.351.2, B.1.351, B.1.351.3	Cele et al. (2021)	792	ACTTTACTTG	A	0.99
p.A243del	convalescent plasma escape	In over 90% of two dose mRNA vaccinees, heterotypic neutralizing titres (NT50) against B.1.1.7 and B.1.351 remain comfortably above the level associated with immune protection in recent vaccine trials. However, in over 50% of convalescent COVID-19 individuals (5/9) and recipients of a only a single dose of mRNA vaccine (10/11) – heterotypic neutralization dropped to negligible levels, particularly against B.1.351.	B.1.351.2, B.1.351, B.1.351.3	Skelly et al. (2021)	792	ACTTTACTTG	A	0.99
p.A243del	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.1.351.2, B.1.351, B.1.351.3	Wibmer et al. (2021)	792	ACTTTACTTG	A	0.99
p.D614G	ACE2 receptor binding affinity	Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant showed essentially no change in binding (KD) relative to D614G.	B.1.351.2, B.1.351, B.1.351.3	Gong et al. (2021)	896	A	G	1.0

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 showed a 1.19x increase in binding (KD) relative to D614G.	B.1.351.2, B.1.351, B.1.351.3	Gong et al. (2021)	896	A	G	1.0
p.D614G	ACE2 receptor binding affinity	Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant combination showed no change relative to D614G.	B.1.351.2, B.1.351, B.1.351.3	Gong et al. (2021)	896	A	G	1.0
p.D614G	ACE2 receptor binding affinity	This variant appears twice in the experiments, with slightly different affinities (both extasciitilde1.2x decrease in binding relative to D614G) using flow cytometry and ACE2 ectodomains-Fc portion IgG complex.	B.1.351.2, B.1.351, B.1.351.3	Gong et al. (2021)	896	A	G	1.0
p.D614G	ACE2 receptor binding affinity	Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant showed a 1.5x decrease in binding (KD) relative to D614G.	B.1.351.2, B.1.351, B.1.351.3	Gong et al. (2021)	896	A	G	1.0
p.D614G	ACE2 receptor binding affinity	Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant showed a 1.07x decrease in binding (KD) relative to D614G. Compare to increased binding in full Spike variant complements for major lineages containing this variant subset: 3.56x (B.1.351 aka Beta), 4.24x (P.1 aka Gamma).	B.1.351.2, B.1.351, B.1.351.3	Gong et al. (2021)	896	A	G	1.0
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.1.351.2, B.1.351, B.1.351.3	Gong et al. (2021)	896	A	G	1.0
p.D614G	ACE2 receptor binding affinity	In four cell lines (including 293T-hACE2 cells), this mutation combination increases infectivity vs D614G alone	B.1.351.2, B.1.351, B.1.351.3	Li et al. (2020)	896	A	G	1.0
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.1.351. We observed an increase (relative to D614G) in binding of soluble ACE2 to B.1.351, and to a much gearter extent to B.1.1.7, which both carry the N501Y mutation (see Fig 3).	B.1.351.2, B.1.351, B.1.351.3	Planas et al. (2021)	896	A	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.D614G	CD8 plus T cell response	Encouragingly, we find that the majority of T cell responses in recipients of two doses of the BNT162b2 vaccine are generated by epitopes that are invariant between the [wildtype] and two of the current variants of concern (B.1.1.7 and B.1.351). In over 90% of two dose mRNA vaccinees, heterotypic neutralizing titres (NT50) against B.1.1.7 and B.1.351 remain comfortably above the level associated with immune protection in recent vaccine trials. However, in over 50% of convalescent COVID-19 individuals and recipients of a only a single dose of mRNA vaccine – heterotypic neutralization dropped to negligible levels, particularly against B.1.351.	B.1.351.2, B.1.351, B.1.351.3	Skelly et al. (2021)	896	A	G	1.0
p.D614G	antibody epitope effects	Abolished neutralization by mAbs CQ026 and CQ038, greatly diminished neutralization by CQ012 and CQ046.	B.1.351.2, B.1.351, B.1.351.3	Hu et al. (2021)	896	A	G	1.0
p.D614G	antibody epitope effects	Anti-NTD CV1 mAb isolated from an early pandemic case was unable to neutralize either partial B.1.351 variant pseudovirus used (A701V or L242del). The neutralization potency of mAb CV30, which contacts K417 and N501 but not E484, was extasciitilde10-fold weaker toward both B.1.351 variants. The neutralization potency of anti-RBD mAb CV3-1 was 3-4-fold less potent against the B.1.351 variants, while anti-RBD mAb CV2-75 was modestly less effective.	B.1.351.2, B.1.351, B.1.351.3	Stamatatos et al. (2021)	896	A	G	1.0
p.D614G	antibody epitope effects	Anti-NTD CV1 mAb isolated from an early pandemic case was unable to neutralize either partial B.1.351 variant pseudovirus used (A701V or L242del). The neutralization potency of mAb CV30, which contacts K417 and N501 but not E484, was extasciitilde10-fold weaker toward both B.1.351 variants. The neutralization potency of anti-RBD mAb CV3-1 was 3-4-fold less potent against the B.1.351 variants, while anti-RBD mAb CV2-75 was modestly less effective.	B.1.351.2, B.1.351, B.1.351.3	Stamatatos et al. (2021)	896	A	G	1.0
p.D614G	convalescent plasma binding	1.11x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset.	B.1.351.2, B.1.351, B.1.351.3	Gong et al. (2021)	896	A	G	1.0
p.D614G	convalescent plasma binding	2.29x increase in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset.	B.1.351.2, B.1.351, B.1.351.3	Gong et al. (2021)	896	A	G	1.0
p.D614G	convalescent plasma binding	2.11x increase in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset.	B.1.351.2, B.1.351, B.1.351.3	Gong et al. (2021)	896	A	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.D614G	convalescent plasma binding	1.42x increase in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset.	B.1.351.2, B.1.351, B.1.351.3	Gong et al. (2021)	896	A	G	1.0
p.D614G	convalescent plasma binding	2.16x increase in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset.	B.1.351.2, B.1.351, B.1.351.3	Gong et al. (2021)	896	A	G	1.0
p.D614G	convalescent plasma binding	1.66x increase in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset. Compare to decreased binding in full Spike variant complements for major lineages containing this variant subset: 0.96x (B.1.351 aka Beta), 0.77x (P.1 aka Gamma).	B.1.351.2, B.1.351, B.1.351.3	Gong et al. (2021)	896	A	G	1.0
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.1.351.2, B.1.351, B.1.351.3	Gong et al. (2021)	896	A	G	1.0
p.D614G	convalescent plasma escape	Average extasciitilde10-fold reduction in neutralization efficacy in convalescent sera of 16 health workers infected in Spring 2020.	B.1.351.2, B.1.351, B.1.351.3	Alenquer et al. (2021)	896	A	G	1.0
p.D614G	convalescent plasma escape	Neutralizing antibody titers of 18 samples (90%) decreased against this B.1.351 pseudotyped virus below an ID50 threshold of 40 (sera collected extasciitilde8mo post Jan 2020 first wave in China).	B.1.351.2, B.1.351, B.1.351.3	Hu et al. (2021)	896	A	G	1.0
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 had mean extasciitilde6x reduction in neutralizing titers, and 40% of the samples lacked any activity against B.1.351.	B.1.351.2, B.1.351, B.1.351.3	Planas et al. (2021)	896	A	G	1.0
p.D614G	convalescent plasma escape	In over 90% of two dose mRNA vaccinees, heterotypic neutralizing titres (NT50) against B.1.1.7 and B.1.351 remain comfortably above the level associated with immune protection in recent vaccine trials. However, in over 50% of convalescent COVID-19 individuals (5/9) and recipients of a only a single dose of mRNA vaccine (10/11) – heterotypic neutralization dropped to negligible levels, particularly against B.1.351.	B.1.351.2, B.1.351, B.1.351.3	Skelly et al. (2021)	896	A	G	1.0
p.D614G	convalescent plasma escape	Using convalescent sera from 15 early pandemic patients (Seattle Flu Study), mean 220 days post symptom onset (IQR 125-269, and three asymptomatic cases) with 27% WHO disease severity scale 3, one third (5/15) of sera neutralized this B.1.351 pseudotype and only three had ID50 titers above 100. Only two of the 15 sera achieved 80% neutralization.	B.1.351.2, B.1.351, B.1.351.3	Stamatatos et al. (2021)	896	A	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.D614G	convalescent plasma escape	Using convalescent sera from 15 early pandemic patients (Seattle Flu Study), mean 220 days post symptom onset (IQR 125-269, and three asymptomatic cases) with 27% WHO disease severity scale 3, 7 of 15 neutralized this B.1.351 pseudotype that includes the L242del, and only one had titers above 100. Only one of the 15 sera achieved 80% neutralization. [compare to 5 and 1 for pseudotype without the deletion]	B.1.351.2, B.1.351, B.1.351.3	Stamatatos et al. (2021)	896	A	G	1.0
p.D614G	convalescent plasma escape	Pseudotyped viruses for B.1.618 was 2.5-fold resistant to neutralization by convalescent sera compared to wild type - a finding that was similar to that of the 3-fold resistance of the South Africa B.1.351 variant using the same assay. The resistance of B.1.618 was caused by the E484K mutation, based on results from viruses pseudotyped for individual variants within B.1.618. [details on the convalescent patient sera collection are not abundantly clear in the preprint]	B.1.351.2, B.1.351, B.1.351.3	Tada et al. (2021)	896	A	G	1.0
p.D614G	humoral response durability	In a prospective study of 107 hospitalized patients, decrease of IgG rates and serological assays becoming negative did not imply loss of neutralizing capacity. Our results indicate a sustained humoral response against the ancestral strain and the D614G, B.1.1.7 and P.1 variants for at least 6 months (last of two samples taken) in patients previously hospitalized for COVID-19. A weaker protection was however observed for the B.1.351 variant.	B.1.351.2, B.1.351, B.1.351.3	Betton et al. (2020)	896	A	G	1.0
p.D614G	immunosuppression variant emergence	Studying 94 COVID-19 extended infection cases with genomics April 1 to October 17, 2020, one case developed 23 mutations in a 19 day period, including this combination in Spike.	B.1.351.2, B.1.351, B.1.351.3	Landis et al. (2021)	896	A	G	1.0
p.D614G	outcome hazard ratio	On average across 7 European countries studied, using B.1.351 defining mutations: Significant shift to infection in those without pre-existing conditions (79.6% vs 89% for non-VOC cases). Significant increase in hospitalization rate (19.3% vs 7.5% for non-VOC cases). Significant increase in ICU rate (2.3% vs 0.6% for non-VOC cases). PG: seems to be different notations around the LAL deletion, using the minimal shared definition to catch as many as possible.	B.1.351.2, B.1.351, B.1.351.3	Funk et al. (2021)	896	A	G	1.0
p.D614G	syncytium formation	Slight increase in Vero cell-cell membrane fusion assay under infection with VSV pseudotyped virus.	B.1.351.2, B.1.351, B.1.351.3	Kim et al. (2021)	896	A	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.D614G	syncytium formation	extasciitilde50% Vero cell-cell membrane fusion assay under infection with VSV pseudotyped virus relative to wild type, signficantly higher than D614G.	B.1.351.2, B.1.351, B.1.351.3	Kim et al. (2021)	896	A	G	1.0
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.1.351.2, B.1.351, B.1.351.3	Kim et al. (2021)	896	A	G	1.0
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.1.351.2, B.1.351, B.1.351.3	Planas et al. (2021)	896	A	G	1.0
p.D614G	tissue specific neutralization	The nasal mucosa of Pfizer vaccinees with time course collection was evaluated against VSV pseudotypes: while B.1.1.7 and D614G showed neutralization by nasal swab from only one different previously infected vacinee neutralizing at weeks 3 and 6, B.1.351 showed zero neutralization at either time point in any sample (and relatively impaired serum neutralization).	B.1.351.2, B.1.351, B.1.351.3	Planas et al. (2021)	896	A	G	1.0
p.D614G	trafficking	Circulating variant shown in vitro to not have major defects or enhancement of cell surface protein trafficking (i.e. Spike cleavage or fusion required for cell entry)	B.1.351.2, B.1.351, B.1.351.3	Barrett et al. (2021)	896	A	G	1.0
p.D614G	trafficking	The increased transduction with Spike D614G ranged from 1.3- to 2.4-fold in Caco-2 and Calu-3 cells expressing endogenous ACE2 and from 1.5- to 7.7-fold in A549ACE2 and Huh7.5ACE2 overexpressing ACE2. Although there is minimal difference in ACE2 receptor binding between the D614 and G614 Spike variants, the G614 variant is more resistant to proteolytic cleavage, suggesting a possible mechanism for the increased transduction.	B.1.351.2, B.1.351, B.1.351.3	Daniloski et al. (2021)	896	A	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.D614G	trafficking	The entry efficiencies of Spike pseudotyped viruses bearing N501Y Variant 2 (B.1.351) 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.1.351.2, B.1.351, B.1.351.3	Hu et al. (2021)	896	A	G	1.0
p.D614G	trafficking	No change in infectivity (24h) relative to D614G alone in Caco-2 cells, Vero or Calu-3.	B.1.351.2, B.1.351, B.1.351.3	Kim et al. (2021)	896	A	G	1.0
p.D614G	trafficking	extasciitilde4x more efficient S2 domain cleavage compared to wild type in Caco-2 cells, mid-range of three cell line tested (Vero and Calu-3).	B.1.351.2, B.1.351, B.1.351.3	Kim et al. (2021)	896	A	G	1.0
p.D614G	trafficking	More efficient infectivity (24h) compared to wild type, in Caco-2 cells extasciitilde11x, Vero extasciitilde10x, and Calu-3 extasciitilde11x. Compare to wild type at extasciitilde5x across cell types.	B.1.351.2, B.1.351, B.1.351.3	Kim et al. (2021)	896	A	G	1.0
p.D614G	trafficking	extasciitilde6x more efficient S2 domain cleavage compared to wild type, compared to 4x by D614G alone in Caco-2 cells, mid-range of three cell line tested (Vero and Calu-3). [N501Y+D614G does not show an increase in cleavage, therefore a synergistic effect of the trio is implied]	B.1.351.2, B.1.351, B.1.351.3	Kim et al. (2021)	896	A	G	1.0
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.1.351.2, B.1.351, B.1.351.3	Kim et al. (2021)	896	A	G	1.0
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.1.351.2, B.1.351, B.1.351.3	Kim et al. (2021)	896	A	G	1.0
p.D614G	trafficking	extasciitilde2x more infectivity than D614G alone in HEK293T-ACE2 cells 48h post-transduction.	B.1.351.2, B.1.351, B.1.351.3	Kuzmina et al. (2021)	896	A	G	1.0
p.D614G	trafficking	Approximately as infective as D614G alone in HEK293T-ACE2 cells 48h post-transduction (extasciitildeadditive effects of the individual variants).	B.1.351.2, B.1.351, B.1.351.3	Kuzmina et al. (2021)	896	A	G	1.0
p.D614G	trafficking	extasciitilde13x more infective as D614G alone in HEK293T-ACE2 cells 48h post-transduction.	B.1.351.2, B.1.351, B.1.351.3	Kuzmina et al. (2021)	896	A	G	1.0
p.D614G	trafficking	extasciitilde12x more infectivity than D614G alone in HEK293T-ACE2 cells 48h post-transduction (extasciitildeadditive effects of 501 and 484).	B.1.351.2, B.1.351, B.1.351.3	Kuzmina et al. (2021)	896	A	G	1.0
p.D614G	trafficking	extasciitilde2x more infectivity than D614G alone in HEK293T-ACE2 cells 48h post-transduction.	B.1.351.2, B.1.351, B.1.351.3	Kuzmina et al. (2021)	896	A	G	1.0
p.D614G	trafficking	extasciitilde9x more infectivity than D614G alone in HEK293T-ACE2 cells 48h post-transduction (no synergy as level approx. that of N501Y alone).	B.1.351.2, B.1.351, B.1.351.3	Kuzmina et al. (2021)	896	A	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.D614G	trafficking	9x more infectivity than D614G alone in HEK293T-ACE2 cells 48h post-transduction.	B.1.351.2, B.1.351, B.1.351.3	Kuzmina et al. (2021)	916	A	G	1.0
p.D614G	trafficking	Among S variants tested, the D614G mutant shows the highest cell entry (extasciitilde3.5x wild type), as supported by structural and binding analyses.	B.1.351.2, B.1.351, B.1.351.3	Ozono et al. (2020)	896	A	G	1.0
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.1.351.2, B.1.351, B.1.351.3	Zhang et l. (2020)	896	A	G	1.0
p.D614G	transmissibility	Assuming complete cross-protection, we estimate 501Y.V2/B.1.351 was 1.50 (95% CrI: 1.20-2.13) times as transmissible than previously circulating variants. Assuming instead that 501Y.V2 is identically transmissible, the new variant evades 21% (95% CrI: 11-36%) of previously acquired immunity. Reality may lie between these extremes, with an intermediate increase in transmissibility and mildly imperfect cross-protection from past exposure.	B.1.351.2, B.1.351, B.1.351.3	Pearson et al. (2021)	896	A	G	1.0
p.D614G	transmissibility	36,590 variant-specific RT-PCR tests were performed on samples collected between April 12 and May 7, 2021 in France to compare variant spread. Compared to January to March 2021, B.1.351 variant had a significant transmission advantage over B.1.1.7 in some regions (15.1 to 16.1% in Île-de-France and 16.1 to 18.8% in Hauts-de-France). This shift in transmission advantage is consistent with the immune evasion abilities of B.1.351 and the high levels of immunization in these regions.	B.1.351.2, B.1.351, B.1.351.3	Roquebert et al. (2021)	896	A	G	1.0
p.D614G	vaccine neutralization efficacy	The Janssen single dose vaccine showed 72% efficacy at preventing moderate and severe disease, which was reduced to 57% in South Africa, where 92.6% of infections are estimated to have been B.1.351. 100% reduction in hospitalization risk remains across variants after 28 days post-vaccination.	B.1.351.2, B.1.351, B.1.351.3	nan	896	A	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.D614G	vaccine neutralization efficacy	In an Ontario long term care facility, cumulatively, weaker BNT162b2 vaccine stimulation, age/comorbidities, produced a 130-fold reduction in apparent neutralization titers in mean 88yo LTCH residents against Beta (B.1.351), relative to staff vaccinees against D614G wild type. 37.9% of 116 two-dose-mRNA-vaccinated residents had undetectable neutralizing antibodies to B.1.351. mRNA-1273 vaccinee sera displayed extasciitilde2 better neutralization than BNT162b2. [common defining B.1.351 mutations noted, as the manuscript does not provide details]	B.1.351.2, B.1.351, B.1.351.3	Abe et al. (2021)	896	A	G	1.0
p.D614G	vaccine neutralization efficacy	Observed 8.8-fold reduction in neutralization efficiency of Pfizer vaccinee sera (collected 14 days after second dose) against cultured B.1.351 sample. Contrast this with 1.4-fold reduction for just the pseudovirus combination of "key" B.1.351 mutations K417N+E484K+N501Y. WA1 and B.1.351 FRNT50 titers correlated weakly at the individual level, with some individual's serum potently neutralizing WA1 while having FRNT50 for B.1.351 below the assay limit of detection (1:20).	B.1.351.2, B.1.351, B.1.351.3	Bates et al. (2021)	896	A	G	1.0
p.D614G	vaccine neutralization efficacy	Neutralization efficiency (ID50) against B.1.1.351-v3 reduced 8.4x relative to D614G wildtype using pseudotyped VSV assay on 8 Moderna vaccinee sera one week post-booster.	B.1.351.2, B.1.351, B.1.351.3	Choi et al. (2021)	896	A	G	1.0
p.D614G	vaccine neutralization efficacy	Neutralization efficiency (ID50) against B.1.1.351-v2 reduced 7.3x relative to D614G wildtype using pseudotyped VSV assay on 8 Moderna vaccinee sera one week post-booster.	B.1.351.2, B.1.351, B.1.351.3	Choi et al. (2021)	896	A	G	1.0
p.D614G	vaccine neutralization efficacy	ELISpot assays show T cell neutralization reduced by 29.8% in this B.1.351 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.1.351.2, B.1.351, B.1.351.3	Gallagher et al. (2021)	896	A	G	1.0
p.D614G	vaccine neutralization efficacy	Pseudotyped D614G virus has reduced neutralization activity vs wild type: 1.2x (37 sera Pfizer median 9 days post 2nd dose, 37 sera Moderna median 18 days post 2nd dose). This was NOT significant by ANOVA.	B.1.351.2, B.1.351, B.1.351.3	Garcia-Beltran et al. (2021)	896	A	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.D614G	vaccine neutralization efficacy	Pseudotyped B.1.351 v1 virus has reduced neutralization activity vs wild type: 34.5x (30 sera Pfizer median 9 days post 2nd dose) and 27.7x (35 sera Moderna median 18 days post 2nd dose). This was significant by ANOVA. Notably, 36.7% (11/30) recipients of two-dose Pfizer and 42.9% (15/35) recipients of two-dose Moderna vaccines did not have detectable neutralization of at least one of the B.1.351 variants.	B.1.351.2, B.1.351, B.1.351.3	Garcia-Beltran et al. (2021)	896	A	G	1.0
p.D614G	vaccine neutralization efficacy	Pseudotyped B.1.351 v2 virus has reduced neutralization activity vs wild type: 41.2x (30 sera Pfizer median 9 days post 2nd dose) and 20.8x (35 sera Moderna median 18 days post 2nd dose). This was significant by ANOVA. Notably, 36.7% (11/30) recipients of two-dose Pfizer and 42.9% (15/35) recipients of two-dose Moderna vaccines did not have detectable neutralization of at least one of the B.1.351 variants.	B.1.351.2, B.1.351, B.1.351.3	Garcia-Beltran et al. (2021)	896	A	G	1.0
p.D614G	vaccine neutralization efficacy	B.1.351 pseudotyped VSV was tested for neutralization in a clonal HEK-293T ACE2 TMPRSS2 cell line optimized for highly efficient S-mediated infection. Only 1 out of 12 serum samples from a cohort of Argentinian recipients of the Gamaleya Sputnik V Ad26 / Ad5 vaccine showed effective neutralization (IC90) at full serum strength (average realtive decrease was 6.1x vs wild type).	B.1.351.2, B.1.351, B.1.351.3	Ikegame et al. (2021)	896	A	G	1.0
p.D614G	vaccine neutralization efficacy	Using a lentivirus virus pseudotyped with D614G Spike, sera from vaccinated individuals who received the second dose (9–11 days post-second dose of Pfizer) exhibited a robust neutralizing potential, with a mean NT50 value of 99,000. This was an average of a 2-fold increase, relative to sera drawn from the individuals who received one dose of vaccination—mean NT50 dilution of 51,300. Importantly, a 6-fold increase in mean NT50 dilution was obtained when sera from the first vaccination dose was compared to convalescent sera from cohort with severe disease (NT50 51,000 vs 8,700) 21 to 63 days post-onset.	B.1.351.2, B.1.351, B.1.351.3	Kuzmina et al. (2021)	896	A	G	1.0
p.D614G	vaccine neutralization efficacy	This variant showed only minor in Pfizer sera (one or two dose) neutralization efficiency vs D614G (using lentivirus pseudotype).	B.1.351.2, B.1.351, B.1.351.3	Kuzmina et al. (2021)	896	A	G	1.0
p.D614G	vaccine neutralization efficacy	This variant showed >5x decrease in Pfizer sera (3 weeks post-first dose: n	B.1.351.2, B.1.351, B.1.351.3	Kuzmina et al. (2021)	896	A	G	1.0
p.D614G	vaccine neutralization efficacy	This variant showed only minor in Pfizer sera (one or two dose) neutralization efficiency vs D614G (using lentivirus pseudotype).	B.1.351.2, B.1.351, B.1.351.3	Kuzmina et al. (2021)	896	A	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.D614G	vaccine neutralization efficacy	This variant showed extasciitilde10x decrease in Pfizer sera (3 weeks post-first dose: n	B.1.351.2, B.1.351, B.1.351.3	Kuzmina et al. (2021)	896	A	G	1.0
p.D614G	vaccine neutralization efficacy	This variant of key B.1.351 lineage mutations showed extasciitilde10x decrease in Pfizer sera (3 weeks post-first dose: n	B.1.351.2, B.1.351, B.1.351.3	Kuzmina et al. (2021)	896	A	G	1.0
p.D614G	vaccine neutralization efficacy	This variant showed >5x decrease in Pfizer sera (3 weeks post-first dose: n	B.1.351.2, B.1.351, B.1.351.3	Kuzmina et al. (2021)	896	A	G	1.0
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.1.351.2, B.1.351, B.1.351.3	Kuzmina et al. (2021)	896	A	G	1.0
p.D614G	vaccine neutralization efficacy	Vaccine plasma neutralization of B.1.351-spike virus was nominally robust but lower (extasciitilde3x) than other variants of concern.	B.1.351.2, B.1.351, B.1.351.3	Liu et al. (2021)	896	A	G	1.0
p.D614G	vaccine neutralization efficacy	A two-dose regimen of (AstraZeneca) ChAdOx1-nCoV19 did not show protection against mild-moderate Covid-19 due to B.1.351 variant, however, vaccine efficacy against severe Covid-19 is undetermined.	B.1.351.2, B.1.351, B.1.351.3	Madhi et al. (2021)	896	A	G	1.0
p.D614G	vaccine neutralization efficacy	In a multicenter, double-blind, randomized, controlled trial to assess the safety and efficacy of the ChAdOx1 nCoV-19 vaccine (AZD1222) with enrollment June 24 and November 9, 2020 from extasciitilde2000 HIV-negative 18-64 year olds (1:1 placebo to treatment), incidence of serious adverse events 14 or more days post- 2nd dose was balanced between the vaccine and placebo groups. A two-dose regimen of the ChAdOx1 nCoV-19 vaccine did not show protection against mild-to-moderate Covid-19 due to the B.1.351 variant. Serum samples obtained from 13 ChAdOx1 nCoV-19 vaccine recipients without SARS-CoV-2 infection through 41 days after vaccination showed 3.5x reduction in neutralization (ID50) for B.1.351 RBD pseudotype HIB-1 virus compared to D614G alone. This RBD variant combination's neutralization by a placebo control group of 6 naturally infected patients showed a similar 3.2x drop (though with D614G starting at a 1.7x higher titre than vaccinee sera).	B.1.351.2, B.1.351, B.1.351.3	Madhi et al. (2021)	896	A	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.D614G	vaccine neutralization efficacy	Relative to B.1.1.117, PRNT50 line virus neutralizating antibody activity assay of B.1.351 showed extasciitilde11x reduction in 13 vacinees's sera collected through 41 days after vaccination. Neutralization by a placebo control group of 6 naturally infected patients showed a smaller extasciitilde8x drop (starting from a extasciitilde50% higher PRNT50 value than vacinees for B.1.1.117 neutralization). Serum samples obtained from 13 ChAdOx1 nCoV-19 vaccine recipients without SARS-CoV-2 infection through 41 days after vaccination showed extasciitilde4x reduction in neutralization (ID50) for full B.1.351 pseudotype HIV-1 virus compared to D614G alone. This RBD variant combination's neutralization by a placebo control group of 6 naturally infected patients showed a slightly higher 4.6x drop (though with D614G starting at a 1.7x higher titre than vaccinee sera).	B.1.351.2, B.1.351, B.1.351.3	Madhi et al. (2021)	896	A	G	1.0
p.D614G	vaccine neutralization efficacy	The Novavax vaccine, which achieved 95.6% efficacy against previous SARS-CoV-2 strains, had reduced efficacy of 60% in South Africa, where 92.6% of infections are estimated to have been B.1.351.	B.1.351.2, B.1.351, B.1.351.3	Novavax (2021)	896	A	G	1.0
p.D614G	vaccine neutralization efficacy	Detectable antibodies against B.1.351 at various time points using pseudotyped lentivirus neutralization in Moderna vaccinee cohort: Day 29 8%, Day 43 100%, Day 119 71%, Day 209 54%. Detectable antibodies against B.1.351 at various time points using live virus FRNT neutralization in Moderna vaccinee cohort: Day 29 8%, Day 43 100%, Day 119 79%, Day 209 58%. Detectable antibodies against B.1.351 at various time points using ACE2 blocking assay in Moderna vaccinee cohort: Day 29 63%, Day 43 100%, Day 119 71%, Day 209 79%. Decreased neutralization on some assays was seen especially in those vaccinees tested that were 71+.	B.1.351.2, B.1.351, B.1.351.3	Pegu et al (2021)	896	A	G	1.0

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 evaluated against VSV pseudotypes: while BD614G and B.1.1.7 were neutralized earlier, the anti-B.1.351 response was negative up to week 3, and became detectable at week 4 (1 week after booster dose), at a level lower than the two other viruses (extasciitilde10x vs D614G) through week 6, the last timepoint measured. Three vaccinees never showed detectable neutralization to B.1.351 even after second dose.	B.1.351.2, B.1.351, B.1.351.3	Planas et al. (2021)	896	A	G	1.0
p.D614G	vaccine neutralization efficacy	In a randomized phase 2a-b control trial of the Novavax (NVX-CoV2373) vaccine in South Africa, where B.1.351 virus dominates, efficacy was 60.1% (95% CI, 19.9 to 80.1) in HIV-negative and initially SARS-CoV-2 seronegative participants using the primary endpoint of laboratory-confirmed symptomatic Covid-19 at 7 days or more after the second dose among participants.	B.1.351.2, B.1.351, B.1.351.3	Shinde et al. (2021)	896	A	G	1.0
p.D614G	vaccine neutralization efficacy	In sera collected from 15 early pandemic patients (Seattle Flu Study), mean 16 days post first dose with either Pfizer/BioNTech or Moderna vaccines, the median ID50 titers were extasciitilde3-fold lower against this B.1.351 pseudotyped virus relative to wild type. A single asymptomatic patient, who had no detectable RBD-specific IgG memory before vaccination, also did not elicit nAbs against the B.1.351 variant. [compare to extasciitilde10 fold with L242del] ID50 titres in non-infected mRNA vaccines more than two weeks post-booster were signficiant, but >100x weaker than in previously infected patients after first dose.	B.1.351.2, B.1.351, B.1.351.3	Stamatatos et al. (2021)	896	A	G	1.0
p.D614G	vaccine neutralization efficacy	In sera collected from 15 early pandemic patients (Seattle Flu Study), mean 16 days post first dose with either Pfizer/BioNTech or Moderna vaccines, the median ID50 titers were extasciitilde10-fold lower against this B.1.351 pseudotyped virus relative to wild type. A single asymptomatic patient, who had no detectable RBD-specific IgG memory before vaccination, also did not elicit nAbs against the B.1.351 variant. [compare to extasciitilde3 fold without the deletion] ID50 titres in non-infected mRNA vaccines more than two weeks post-booster were significant, but extasciitilde500x weaker than in previously infected patients after first dose.	B.1.351.2, B.1.351, B.1.351.3	Stamatatos et al. (2021)	896	A	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.D614G	vaccine neutralization efficacy	Pseudotyped viruses for B.1.351 was 3.4-fold resistant to neutralization by 6 BNT162b2 vaccine sera 28 days post-booster compared to wild type. Neutralization by 3 Moderna vaccine sera 28 days post-booster was 2.2-fold resistant. [Exact list of B.1.351 mutations used in these assays was not included in the preprint]	B.1.351.2, B.1.351, B.1.351.3	Tada et al. (2021)	896	A	G	1.0
p.D614G	vaccine neutralization efficacy	Pseudotyped viruses for B.1.618 was 2.7-fold resistant to neutralization by 6 BNT162b2 vaccine sera 28 days post-booster compared to wild type - a finding that was similar to that of the 3.4-fold resistance of the South Africa B.1.351 variant using the same assay. Neutralization by 3 Moderna vaccine sera 28 days post-booster was 3-fold resistant (vs. 2.2-fold for B.1.351). The resistance of B.1.618 was caused by the E484K mutation, based on results from viruses pseudotyped for individual variants within B.1.618.	B.1.351.2, B.1.351, B.1.351.3	Tada et al. (2021)	896	A	G	1.0
p.D614G	vaccine neutralization efficacy	PBMCs of Pfizer/BioNTech BNT162b2 (n	B.1.351.2, B.1.351, B.1.351.3	Tarke et al. (2021)	896	A	G	1.0
p.D614G	vaccine neutralization efficacy	[Contrary to how this paper has been cited, Voysey et al. do NOT show evidence of decreased effectiveness of ChAdOx1 (AstraZeneca) against the South African B.1.351 lineage. Insufficient numbers reaching the primary study endpoint were available in that arm of the vaccine study to report any statistics from the South African participants. Additionally, the study period of the paper ended in November 2020, while the earliest reported case of this lineage is October (covariants.org), only becoming dominant by mid-November.]	B.1.351.2, B.1.351, B.1.351.3	Voysey et al. (2021)	896	A	G	1.0
p.D614G	vaccine neutralization efficacy	No significant difference in T-cell response to B.1.351 was observed (vs. ancestral) in blood drawn from 28 participants received the Pfizer-BioNTech vaccine and 2 received the Moderna vaccine.	B.1.351.2, B.1.351, B.1.351.3	Woldemeskel et al. (2021)	896	A	G	1.0
p.D614G	vaccine neutralization efficacy	Sera from healthcare workers (n	B.1.351.2, B.1.351, B.1.351.3	Zhou et al. (2021)	896	A	G	1.0
p.D614G	vaccinee plasma binding	1.19x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in previously non-seroconverted subjects. 1.1x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in post-infection vaccinees.	B.1.351.2, B.1.351, B.1.351.3	Gong et al. (2021)	896	A	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.D614G	vaccinee plasma binding	1.79x increase in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in previously non-seroconverted subjects. 1.3x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in post-infection vaccinees.	B.1.351.2, B.1.351, B.1.351.3	Gong et al. (2021)	896	A	G	1.0
p.D614G	vaccinee plasma binding	1.64x 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. 1.35x 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.1.351.2, B.1.351, B.1.351.3	Gong et al. (2021)	896	A	G	1.0
p.D614G	vaccinee plasma binding	1.16x increase in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in previously non-seroconverted subjects. 1.06x increase in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in post-infection vaccinees.	B.1.351.2, B.1.351, B.1.351.3	Gong et al. (2021)	896	A	G	1.0
p.D614G	vaccinee plasma binding	1.76x increase in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in previously non-seroconverted subjects. 1.75x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in post-infection vaccinees.	B.1.351.2, B.1.351, B.1.351.3	Gong et al. (2021)	896	A	G	1.0
p.D614G	vaccinee plasma binding	1.30x increase in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in previously non-seroconverted subjects. Compare to varied binding in full Spike variant complements for major lineages containing this variant subset: 1.28x increase (B.1.351 aka Beta), and 1.14x decrease (P.1 aka Gamma). 1.47x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in post-infection vaccinees. Compare to varied binding in full Spike variant complements for major lineages containing this variant subset: 1.17x increase (B.1.351 aka Beta), and 1.47x decrease (P.1 aka Gamma).	B.1.351.2, B.1.351, B.1.351.3	Gong et al. (2021)	896	A	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
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.1.351.2, B.1.351, B.1.351.3	Gong et al. (2021)	896	A	G	1.0
p.D614G	viral load	Hamsters infected with SARS-CoV-2 expressing spike(D614G) (G614 virus) produced higher infectious titres in nasal washes and the trachea, but not in the lungs, supporting clinical evidence showing that the mutation enhances viral loads in the upper respiratory tract of COVID-19 patients and may increase transmission.	B.1.351.2, B.1.351, B.1.351.3	Plante et al. (2020)	896	A	G	1.0
p.D614G	virion structure	Estimated free energy change (ddG) for this variant is 2.5 kcal/mol (i.e. stabilizing relative to wild type)	B.1.351.2, B.1.351, B.1.351.3	Spratt et al. (2021)	896	A	G	1.0
p.D614G	virion structure	Negative stain EM shows increased proportion of "one-up" trimer conformation of Spike proteins on the surface of virions, where the up conformation is presumed to be more likely to bind ACE2.	B.1.351.2, B.1.351, B.1.351.3	Weissman et al. (2020)	896	A	G	1.0
p.D614G	virion structure	CryoEM shows increased proportion of "one-up" trimer conformation of Spike proteins on the surface of virions, where the up conformation is presumed to be more likely to bind ACE2.	B.1.351.2, B.1.351, B.1.351.3	Yurkovetskiy et al. (2020)	896	A	G	1.0
p.D614G	virion structure	Based on pseudotyped virus experiments, D614G may increase infectivity by assembling more functional S protein into the virion.	B.1.351.2, B.1.351, B.1.351.3	Zhang et al. (2020)	896	A	G	1.0
p.D215G	ACE2 receptor binding affinity	Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant showed a 1.19x increase in binding (KD) relative to D614G.	B.1.351.2, B.1.351, B.1.351.3	Gong et al. (2021)	895	A	G	1.0
p.D215G	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.1.351. We observed an increase (relative to D614G) in binding of soluble ACE2 to B.1.351, and to a much gearter extent to B.1.1.7, which both carry the N501Y mutation (see Fig 3).	B.1.351.2, B.1.351, B.1.351.3	Planas et al. (2021)	895	A	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.D215G	CD8 plus T cell response	Encouragingly, we find that the majority of T cell responses in recipients of two doses of the BNT162b2 vaccine are generated by epitopes that are invariant between the [wildtype] and two of the current variants of concern (B.1.1.7 and B.1.351). In over 90% of two dose mRNA vaccinees, heterotypic neutralizing titres (NT50) against B.1.1.7 and B.1.351 remain comfortably above the level associated with immune protection in recent vaccine trials. However, in over 50% of convalescent COVID-19 individuals and recipients of a only a single dose of mRNA vaccine – heterotypic neutralization dropped to negligible levels, particularly against B.1.351.	B.1.351.2, B.1.351, B.1.351.3	Skelly et al. (2021)	895	A	G	1.0
p.D215G	antibody epitope effects	Anti-NTD CV1 mAb isolated from an early pandemic case was unable to neutralize either partial B.1.351 variant pseudovirus used (A701V or L242del). The neutralization potency of mAb CV30, which contacts K417 and N501 but not E484, was extasciitilde10-fold weaker toward both B.1.351 variants. The neutralization potency of anti-RBD mAb CV3-1 was 3-4-fold less potent against the B.1.351 variants, while anti-RBD mAb CV2-75 was modestly less effective.	B.1.351.2, B.1.351, B.1.351.3	Stamatatos et al. (2021)	895	A	G	1.0
p.D215G	antibody epitope effects	Anti-NTD CV1 mAb isolated from an early pandemic case was unable to neutralize either partial B.1.351 variant pseudovirus used (A701V or L242del). The neutralization potency of mAb CV30, which contacts K417 and N501 but not E484, was extasciitilde10-fold weaker toward both B.1.351 variants. The neutralization potency of anti-RBD mAb CV3-1 was 3-4-fold less potent against the B.1.351 variants, while anti-RBD mAb CV2-75 was modestly less effective.	B.1.351.2, B.1.351, B.1.351.3	Stamatatos et al. (2021)	895	A	G	1.0
p.D215G	convalescent plasma binding	2.29x increase in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset.	B.1.351.2, B.1.351, B.1.351.3	Gong et al. (2021)	895	A	G	1.0
p.D215G	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.1.351.2, B.1.351, B.1.351.3	Cele et al. (2021)	895	A	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.D215G	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 had mean extasciitilde6x reduction in neutralizing titers, and 40% of the samples lacked any activity against B.1.351.	B.1.351.2, B.1.351, B.1.351.3	Planas et al. (2021)	895	A	G	1.0
p.D215G	convalescent plasma escape	In over 90% of two dose mRNA vaccinees, heterotypic neutralizing titres (NT50) against B.1.1.7 and B.1.351 remain comfortably above the level associated with immune protection in recent vaccine trials. However, in over 50% of convalescent COVID-19 individuals (5/9) and recipients of a only a single dose of mRNA vaccine (10/11) – heterotypic neutralization dropped to negligible levels, particularly against B.1.351.	B.1.351.2, B.1.351, B.1.351.3	Skelly et al. (2021)	895	A	G	1.0
p.D215G	convalescent plasma escape	Using convalescent sera from 15 early pandemic patients (Seattle Flu Study), mean 220 days post symptom onset (IQR 125-269, and three asymptomatic cases) with 27% WHO disease severity scale 3, one third (5/15) of sera neutralized this B.1.351 pseudotype and only three had ID50 titers above 100. Only two of the 15 sera achieved 80% neutralization.	B.1.351.2, B.1.351, B.1.351.3	Stamatatos et al. (2021)	895	A	G	1.0
p.D215G	convalescent plasma escape	Using convalescent sera from 15 early pandemic patients (Seattle Flu Study), mean 220 days post symptom onset (IQR 125-269, and three asymptomatic cases) with 27% WHO disease severity scale 3, 7 of 15 neutralized this B.1.351 pseudotype that includes the L242del, and only one had titers above 100. Only one of the 15 sera achieved 80% neutralization. [compare to 5 and 1 for pseudotype without the deletion]	B.1.351.2, B.1.351, B.1.351.3	Stamatatos et al. (2021)	895	A	G	1.0
p.D215G	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.1.351.2, B.1.351, B.1.351.3	Wibmer et al. (2021)	895	A	G	1.0
p.D215G	homoplasy	In experimental models of SARS-CoV-2 mutational evolution (without immune pressure), this mutation in the N terminal domain appears convergent.	B.1.351.2, B.1.351, B.1.351.3	Borges et al. (2021)	895	A	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.D215G	humoral response durability	In a prospective study of 107 hospitalized patients, decrease of IgG rates and serological assays becoming negative did not imply loss of neutralizing capacity. Our results indicate a sustained humoral response against the ancestral strain and the D614G, B.1.1.7 and P.1 variants for at least 6 months (last of two samples taken) in patients previously hospitalized for COVID-19. A weaker protection was however observed for the B.1.351 variant.	B.1.351.2, B.1.351, B.1.351.3	Betton et al. (2020)	895	A	G	1.0
p.D215G	outcome hazard ratio	On average across 7 European countries studied, using B.1.351 defining mutations: Significant shift to infection in those without pre-existing conditions (79.6% vs 89% for non-VOC cases). Significant increase in hospitalization rate (19.3% vs 7.5% for non-VOC cases). Significant increase in ICU rate (2.3% vs 0.6% for non-VOC cases). PG: seems to be different notations around the LAL deletion, using the minimal shared definition to catch as many as possible.	B.1.351.2, B.1.351, B.1.351.3	Funk et al. (2021)	895	A	G	1.0
p.D215G	reinfection	4 health care workers in the 20's and 30's with no underlying conditions and seropositivity or confirmed 2020 SARS-CoV-2 infections were confirmed to have B.1.351 infection during a Februrary 2021 hospital outbreak in Luxembourg. Symptoms were mostly mild on first infection, and milder on second infection.	B.1.351.2, B.1.351, B.1.351.3	Staub et al. (2021)	895	A	G	1.0
p.D215G	reinfection	Hamsters re-infected with B.1.351 virus after seroversion from previous infection with a lineage A virus did not transmit virus to naive sentinels via direct contact transmission, in contrast to the non-seroconverted animals. They had little infectious virus and no pathology in the lungs. Initial infection with SARS-CoV-2 lineage A does not prevent heterologous reinfection with B.1.351, but prevents disease and onward transmission.	B.1.351.2, B.1.351, B.1.351.3	Yinda et al. (2021)	895	A	G	1.0
p.D215G	symptom prevalence	Inoculation with the B.1.351 isolate resulted in lower clinical scores in 6 rhesus macaques that correlated with lower virus titers in the lungs, less severe histologic lung lesions and less viral antigen detected in the lungs. Our comparative pathogenicity study suggests that ongoing circulation under diverse evolutionary pressure favors transmissibility and immune evasion rather than an increase in intrinsic pathogenicity.	B.1.351.2, B.1.351, B.1.351.3	Munster et al. (2021)	895	A	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.D215G	tissue specific neutralization	The nasal mucosa of Pfizer vaccinees with time course collection was evaluated against VSV pseudotypes: while B.1.1.7 and D614G showed neutralization by nasal swab from only one different previously infected vacinee neutralizing at weeks 3 and 6, B.1.351 showed zero neutralization at either time point in any sample (and relatively impaired serum neutralization).	B.1.351.2, B.1.351, B.1.351.3	Planas et al. (2021)	895	A	G	1.0
p.D215G	trafficking	Lentiviral pseudotyped with this individual mutation from B.1.351 was tested on ACE2.293T cells. Luciferase activity was measured two days postinfection, showing mild decrease in infection rate amongst the cells, suggesting that this mutation does not contributing to cell entry fitness.	B.1.351.2, B.1.351, B.1.351.3	Tada et al. (2021)	895	A	G	1.0
p.D215G	vaccine neutralization efficacy	The Janssen single dose vaccine showed 72% efficacy at preventing moderate and severe disease, which was reduced to 57% in South Africa, where 92.6% of infections are estimated to have been B.1.351. 100% reduction in hospitalization risk remains across variants after 28 days post-vaccination.	B.1.351.2, B.1.351, B.1.351.3	nan	895	A	G	1.0
p.D215G	vaccine neutralization efficacy	In an Ontario long term care facility, cumulatively, weaker BNT162b2 vaccine stimulation, age/comorbidities, produced a 130-fold reduction in apparent neutralization titers in mean 88yo LTCH residents against Beta (B.1.351), relative to staff vaccinees against D614G wild type. 37.9% of 116 two-dose-mRNA-vaccinated residents had undetectable neutralizing antibodies to B.1.351. mRNA-1273 vaccinee sera displayed extasciitilde2 better neutralization than BNT162b2. [common defining B.1.351 mutations noted, as the manuscript does not provide details]	B.1.351.2, B.1.351, B.1.351.3	Abe et al. (2021)	895	A	G	1.0
p.D215G	vaccine neutralization efficacy	Using B.1.351 defining mutations for Spike, observed 4x average decrease in neutralization efficiency (but still relevant titres) for sera from 10 BNT162b2 vaccinees 12 days after second dose, but only one relevant titre 12 days after first dose. Compares unfavorably to wild type or B.1.1.7 titres.	B.1.351.2, B.1.351, B.1.351.3	Alenquer et al. (2021)	895	A	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.D215G	vaccine neutralization efficacy	Observed 8.8-fold reduction in neutralization efficiency of Pfizer vaccinee sera (collected 14 days after second dose) against cultured B.1.351 sample. Contrast this with 1.4-fold reduction for just the pseudovirus combination of "key" B.1.351 mutations K417N+E484K+N501Y. WA1 and B.1.351 FRNT50 titers correlated weakly at the individual level, with some individual's serum potently neutralizing WA1 while having FRNT50 for B.1.351 below the assay limit of detection (1:20).	B.1.351.2, B.1.351, B.1.351.3	Bates et al. (2021)	895	A	G	1.0
p.D215G	vaccine neutralization efficacy	Neutralization efficiency (ID50) against B.1.1.351-v3 reduced 8.4x relative to D614G wildtype using pseudotyped VSV assay on 8 Moderna vaccinee sera one week post-booster.	B.1.351.2, B.1.351, B.1.351.3	Choi et al. (2021)	895	A	G	1.0
p.D215G	vaccine neutralization efficacy	Neutralization efficiency (ID50) against B.1.1.351-v2 reduced 7.3x relative to D614G wildtype using pseudotyped VSV assay on 8 Moderna vaccinee sera one week post-booster.	B.1.351.2, B.1.351, B.1.351.3	Choi et al. (2021)	895	A	G	1.0
p.D215G	vaccine neutralization efficacy	ELISpot assays show T cell neutralization reduced by 29.8% in this B.1.351 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.1.351.2, B.1.351, B.1.351.3	Gallagher et al. (2021)	895	A	G	1.0
p.D215G	vaccine neutralization efficacy	Pseudotyped B.1.351 v1 virus has reduced neutralization activity vs wild type: 34.5x (30 sera Pfizer median 9 days post 2nd dose) and 27.7x (35 sera Moderna median 18 days post 2nd dose). This was significant by ANOVA. Notably, 36.7% (11/30) recipients of two-dose Pfizer and 42.9% (15/35) recipients of two-dose Moderna vaccines did not have detectable neutralization of at least one of the B.1.351 variants.	B.1.351.2, B.1.351, B.1.351.3	Garcia-Beltran et al. (2021)	895	A	G	1.0
p.D215G	vaccine neutralization efficacy	Pseudotyped B.1.351 v2 virus has reduced neutralization activity vs wild type: 41.2x (30 sera Pfizer median 9 days post 2nd dose) and 20.8x (35 sera Moderna median 18 days post 2nd dose). This was significant by ANOVA. Notably, 36.7% (11/30) recipients of two-dose Pfizer and 42.9% (15/35) recipients of two-dose Moderna vaccines did not have detectable neutralization of at least one of the B.1.351 variants.	B.1.351.2, B.1.351, B.1.351.3	Garcia-Beltran et al. (2021)	895	A	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.D215G	vaccine neutralization efficacy	B.1.351 pseudotyped VSV was tested for neutralization in a clonal HEK-293T ACE2 TMPRSS2 cell line optimized for highly efficient S-mediated infection. Only 1 out of 12 serum samples from a cohort of Argentinian recipients of the Gamaleya Sputnik V Ad26 / Ad5 vaccine showed effective neutralization (IC90) at full serum strength (average realtive decrease was 6.1x vs wild type).	B.1.351.2, B.1.351, B.1.351.3	Ikegame et al. (2021)	895	A	G	1.0
p.D215G	vaccine neutralization efficacy	Vaccine plasma neutralization of B.1.351-spike virus was nominally robust but lower (extasciitilde3x) than other variants of concern.	B.1.351.2, B.1.351, B.1.351.3	Liu et al. (2021)	895	A	G	1.0
p.D215G	vaccine neutralization efficacy	A two-dose regimen of (AstraZeneca) ChAdOx1-nCoV19 did not show protection against mild-moderate Covid-19 due to B.1.351 variant, however, vaccine efficacy against severe Covid-19 is undetermined.	B.1.351.2, B.1.351, B.1.351.3	Madhi et al. (2021)	895	A	G	1.0
p.D215G	vaccine neutralization efficacy	Relative to B.1.1.117, PRNT50 line virus neutralizating antibody activity assay of B.1.351 showed extasciitilde11x reduction in 13 vacinees's sera collected through 41 days after vaccination. Neutralization by a placebo control group of 6 naturally infected patients showed a smaller extasciitilde8x drop (starting from a extasciitilde50% higher PRNT50 value than vacinees for B.1.1.117 neutralization). Serum samples obtained from 13 ChAdOx1 nCoV-19 vaccine recipients without SARS-CoV-2 infection through 41 days after vaccination showed extasciitilde4x reduction in neutralization (ID50) for full B.1.351 pseudotype HIV-1 virus compared to D614G alone. This RBD variant combination's neutralization by a placebo control group of 6 naturally infected patients showed a slightly higher 4.6x drop (though with D614G starting at a 1.7x higher titre than vaccinee sera).	B.1.351.2, B.1.351, B.1.351.3	Madhi et al. (2021)	895	A	G	1.0
p.D215G	vaccine neutralization efficacy	The Novavax vaccine, which achieved 95.6% efficacy against previous SARS-CoV-2 strains, had reduced efficacy of 60% in South Africa, where 92.6% of infections are estimated to have been B.1.351.	B.1.351.2, B.1.351, B.1.351.3	Novavax (2021)	895	A	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.D215G	vaccine neutralization efficacy	Detectable antibodies against B.1.351 at various time points using pseudotyped lentivirus neutralization in Moderna vaccinee cohort: Day 29 8%, Day 43 100%, Day 119 71%, Day 209 54%. Detectable antibodies against B.1.351 at various time points using live virus FRNT neutralization in Moderna vaccinee cohort: Day 29 8%, Day 43 100%, Day 119 79%, Day 209 58%. Detectable antibodies against B.1.351 at various time points using ACE2 blocking assay in Moderna vaccinee cohort: Day 29 63%, Day 43 100%, Day 119 71%, Day 209 79%. Decreased neutralization on some assays was seen especially in those vaccinees tested that were 71+.	B.1.351.2, B.1.351, B.1.351.3	Pegu et al (2021)	895	A	G	1.0
p.D215G	vaccine neutralization efficacy	The sera of 16 individuals with time course collection was evaluated against VSV pseudotypes: while BD614G and B.1.1.7 were neutralized earlier, the anti-B.1.351 response was negative up to week 3, and became detectable at week 4 (1 week after booster dose), at a level lower than the two other viruses (extasciitilde10x vs D614G) through week 6, the last timepoint measured. Three vaccinees never showed detectable neutralization to B.1.351 even after second dose.	B.1.351.2, B.1.351, B.1.351.3	Planas et al. (2021)	895	A	G	1.0
p.D215G	vaccine neutralization efficacy	In a randomized phase 2a-b control trial of the Novavax (NVX-CoV2373) vaccine in South Africa, where B.1.351 virus dominates, efficacy was 60.1% (95% CI, 19.9 to 80.1) in HIV-negative and initially SARS-CoV-2 seronegative participants using the primary endpoint of laboratory-confirmed symptomatic Covid-19 at 7 days or more after the second dose among participants.	B.1.351.2, B.1.351, B.1.351.3	Shinde et al. (2021)	895	A	G	1.0
p.D215G	vaccine neutralization efficacy	In sera collected from 15 early pandemic patients (Seattle Flu Study), mean 16 days post first dose with either Pfizer/BioNTech or Moderna vaccines, the median ID50 titers were extasciitilde3-fold lower against this B.1.351 pseudotyped virus relative to wild type. A single asymptomatic patient, who had no detectable RBD-specific IgG memory before vaccination, also did not elicit nAbs against the B.1.351 variant. [compare to extasciitilde10 fold with L242del] ID50 titres in non-infected mRNA vaccines more than two weeks post-booster were signficiant, but >100x weaker than in previously infected patients after first dose.	B.1.351.2, B.1.351, B.1.351.3	Stamatatos et al. (2021)	895	A	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.D215G	vaccine neutralization efficacy	In sera collected from 15 early pandemic patients (Seattle Flu Study), mean 16 days post first dose with either Pfizer/BioNTech or Moderna vaccines, the median ID50 titers were extasciitilde10-fold lower against this B.1.351 pseudotyped virus relative to wild type. A single asymptomatic patient, who had no detectable RBD-specific IgG memory before vaccination, also did not elicit nAbs against the B.1.351 variant. [compare to extasciitilde3 fold without the deletion] ID50 titres in non-infected mRNA vaccines more than two weeks post-booster were significant, but extasciitilde500x weaker than in previously infected patients after first dose.	B.1.351.2, B.1.351, B.1.351.3	Stamatatos et al. (2021)	895	A	G	1.0
p.D215G	vaccine neutralization efficacy	Pseudotyped viruses for B.1.351 was 3.4-fold resistant to neutralization by 6 BNT162b2 vaccine sera 28 days post-booster compared to wild type. Neutralization by 3 Moderna vaccine sera 28 days post-booster was 2.2-fold resistant. [Exact list of B.1.351 mutations used in these assays was not included in the preprint]	B.1.351.2, B.1.351, B.1.351.3	Tada et al. (2021)	895	A	G	1.0
p.D215G	vaccine neutralization efficacy	PBMCs of Pfizer/BioNTech BNT162b2 (n	B.1.351.2, B.1.351, B.1.351.3	Tarke et al. (2021)	895	A	G	1.0
p.D215G	vaccine neutralization efficacy	[Contrary to how this paper has been cited, Voysey et al. do NOT show evidence of decreased effectiveness of ChAdOx1 (AstraZeneca) against the South African B.1.351 lineage. Insufficient numbers reaching the primary study endpoint were available in that arm of the vaccine study to report any statistics from the South African participants. Additionally, the study period of the paper ended in November 2020, while the earliest reported case of this lineage is October (covariants.org), only becoming dominant by mid-November.]	B.1.351.2, B.1.351, B.1.351.3	Voysey et al. (2021)	895	A	G	1.0
p.D215G	vaccine neutralization efficacy	No significant difference in T-cell response to B.1.351 was observed (vs. ancestral) in blood drawn from 28 participants received the Pfizer-BioNTech vaccine and 2 received the Moderna vaccine.	B.1.351.2, B.1.351, B.1.351.3	Woldemeskel et al. (2021)	895	A	G	1.0
p.D215G	vaccine neutralization efficacy	Sera from healthcare workers (n	B.1.351.2, B.1.351, B.1.351.3	Zhou et al. (2021)	895	A	G	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.D215G	vaccinee plasma binding	1.79x increase in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in previously non-seroconverted subjects. 1.3x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in post-infection vaccinees.	B.1.351.2, B.1.351, B.1.351.3	Gong et al. (2021)	895	A	G	1.0
p.D215G	virion structure	Estimated free energy change (ddG) for this variant is 0.98 kcal/mol (i.e. stabilizing relative to wild type)	B.1.351.2, B.1.351, B.1.351.3	Spratt et al. (2021)	895	A	G	1.0
p.E484K	ACE2 receptor binding affinity	The affinity of the B.1.351 RBD variants for ACE2 increased by 3.7 fold as measured by surface plasmon resonance relative to wild type RBD by increasing the k(on) and decreasing the k(off) rate constants.	B.1.351.2, B.1.351, B.1.351.3	Barton et al. (2021)	888	G	A	1.0
p.E484K	ACE2 receptor binding affinity	In the case of VOC B.1.1.7+E484K, the addition of the E484K mutation to N501Y further increased the affinity, to extasciitilde15 fold higher than WT RBD (KD extasciitilde5 nM), by further increasing the k(on) as measured by surface plasmon resonance. Because the higher k(on) could result in mass transfer limiting binding, we confirmed that the kinetic measurement for this variant was not substantially affected by varying levels of immobilization.	B.1.351.2, B.1.351, B.1.351.3	Barton et al. (2021)	888	G	A	1.0
p.E484K	ACE2 receptor binding affinity	This combination showed extasciitilde3x increase binding to ACE2 vs wild type, about half that of the B.1.1.7 lineage, suggesting that the K417N mutation is slightly detrimental to ACE2 binding, probably as a result of disrupting the salt bridge formed with ACE2 residue D30	B.1.351.2, B.1.351, B.1.351.3	Collier et al. (2021)	888	G	A	1.0
p.E484K	ACE2 receptor binding affinity	This variant appears twice in the experiments, with slightly different affinities (both extasciitilde1.2x decrease in binding relative to D614G) using flow cytometry and ACE2 ectodomains-Fc portion IgG complex.	B.1.351.2, B.1.351, B.1.351.3	Gong et al. (2021)	888	G	A	1.0
p.E484K	ACE2 receptor binding affinity	RBD containing the N501Y mutation results in 9-fold stronger binding to the hACE2 receptor than wild type RBD. The E484K mutation does not significantly influence the affinity for the receptor, while K417N attenuates affinity. As a result, RBD from B.1.351 containing all three mutations binds 3-fold stronger to hACE2 than wild type RBD but 3-fold weaker than N501Y.	B.1.351.2, B.1.351, B.1.351.3	Laffeber et al. (2021)	888	G	A	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.E484K	ACE2 receptor binding affinity	Studying the key covariants in lineage of concern 501Y.V2, observed about 2-fold increase in ACE2 binding vs wildtype, but greatly decreased mAb binding, suggesting evolutionary optimum tension between immune evasion and ACE2 binding affinity as the N501Y variant alone has 10x increase in affinity but no effect on tested mAb binding.	B.1.351.2, B.1.351, B.1.351.3	Liu et al. (2021)	888	G	A	1.0
p.E484K	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.1.351. We observed an increase (relative to D614G) in binding of soluble ACE2 to B.1.351, and to a much gearter extent to B.1.1.7, which both carry the N501Y mutation (see Fig 3).	B.1.351.2, B.1.351, B.1.351.3	Planas et al. (2021)	888	G	A	1.0
p.E484K	ACE2 receptor binding affinity	Using Mircoscale Thermopheresis, the B.1.351 variant harboring three mutations, binds ACE2 at nearly five-fold greater affinity than the original SARS-COV-2 RBD (Kd 87.6, vs 402.5 nM).	B.1.351.2, B.1.351, B.1.351.3	Ramanathan et al. (2021)	888	G	A	1.0
p.E484K	ACE2 receptor binding affinity	Experimentally, ACE2 binding affinity increased 0.06 fold	B.1.351.2, B.1.351, B.1.351.3	Starr et al. (2020)	888	G	A	1.0
p.E484K	ACE2 receptor binding affinity	Reported moderate increase in affinity compared to wild-type RBD on the cell surface (Kd	B.1.351.2, B.1.351, B.1.351.3	Tian et al. (2021)	888	G	A	1.0
p.E484K	ACE2 receptor binding affinity	Reported slight increase in affinity compared to wild-type RBD on the cell surface (Kd	B.1.351.2, B.1.351, B.1.351.3	Tian et al. (2021)	888	G	A	1.0
p.E484K	ACE2 receptor binding affinity	The affinity of ACE2 for this mutation combination was twice as high as for wild type. Having in mind that the affinity of SARS-CoV-2 for ACE2 is only 4-fold higher compared to SARS-CoV-1, this factor of 2 is expected to be biologically significant.	B.1.351.2, B.1.351, B.1.351.3	Vogel et al. (2021)	888	G	A	1.0
p.E484K	ACE2 receptor binding affinity	Among the first selected variants in an in vitro evolution experiment for ACE2 binding.	B.1.351.2, B.1.351, B.1.351.3	Zahradnik et al. (2021)	888	G	A	1.0
p.E484K	CD8 plus T cell response	Encouragingly, we find that the majority of T cell responses in recipients of two doses of the BNT162b2 vaccine are generated by epitopes that are invariant between the [wildtype] and two of the current variants of concern (B.1.1.7 and B.1.351). In over 90% of two dose mRNA vaccinees, heterotypic neutralizing titres (NT50) against B.1.1.7 and B.1.351 remain comfortably above the level associated with immune protection in recent vaccine trials. However, in over 50% of convalescent COVID-19 individuals and recipients of a only a single dose of mRNA vaccine – heterotypic neutralization dropped to negligible levels, particularly against B.1.351.	B.1.351.2, B.1.351, B.1.351.3	Skelly et al. (2021)	888	G	A	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.E484K	T cell evasion	Analyzing responses to the E484K mutation seen in B.1.351 and P.1 variants, we noted that it did not fall in a region predicted to bind the HLAII alleles tested (table S4). The mutation appeared to have no substantial or differential impact on T cell responses.	B.1.351.2, B.1.351, B.1.351.3	Reynolds et al. (2021)	888	G	A	1.0
p.E484K	antibody epitope effects	Ablates Class 1 receptor-binding-motif targeting antibodies COV2-2050, 1B07, COVOX-384 and S2H58.	B.1.351.2, B.1.351, B.1.351.3	Chen et al. (2021)	888	G	A	1.0
p.E484K	antibody epitope effects	Ablates Class 1 receptor-binding-motif targeting antibodies COV2-2050, 1B07, COVOX-384, and S2H58.	B.1.351.2, B.1.351, B.1.351.3	Chen et al. (2021)	888	G	A	1.0
p.E484K	antibody epitope effects	Ablates Class 1 receptor-binding-motif targeting antibodies COV2-2050, 1B07, COVOX-384, and S2H58. Ablates Class 3 N-terminal domain targeting antibody COV2-2489, diminishes COV2-2676.	B.1.351.2, B.1.351, B.1.351.3	Chen et al. (2021)	888	G	A	1.0
p.E484K	antibody epitope effects	Of 50 mAbs tested, major loss of neutralization observed for S2N28, S2X615, S2N12, S2X192, S2H7, S2X16, S2X58, S2H70, S2X613, S2D19, S2N22, S2D32, S2H58, S2M11, S2D106, S2X30.	B.1.351.2, B.1.351, B.1.351.3	Collier et al. (2021)	888	G	A	1.0
p.E484K	antibody epitope effects	Ablates binding by class 2 mAbs such as C144 that directly interfere with ACE2 binding, but clonal somatic mutations of memory B cells at 6.2 months (evolving humoral immune response) show pronounced increase in binding to the variant.	B.1.351.2, B.1.351, B.1.351.3	Gaebler et al. (2021)	888	G	A	1.0
p.E484K	antibody epitope effects	Abolished neutralization by mAbs CQ026 and CQ038, greatly diminished neutralization by CQ012 and CQ046.	B.1.351.2, B.1.351, B.1.351.3	Hu et al. (2021)	888	G	A	1.0
p.E484K	antibody epitope effects	Monoclonal antibodies 13G9 and 58G6 maintain fairly high neutralization potency, compared to others interfacing with E484K.	B.1.351.2, B.1.351, B.1.351.3	Li et al. (2021)	888	G	A	1.0
p.E484K	antibody epitope effects	Mutant screen in neutralization assay with a broad range of monoclonal antibodies shows high resistence to 4 antibodies, and broad low level resistence against much of the rest of the panel.	B.1.351.2, B.1.351, B.1.351.3	Liu et al. (2020)	888	G	A	1.0
p.E484K	antibody epitope effects	Massive reduction in binding efficiency vs wild type for mAb LY-CoV555.	B.1.351.2, B.1.351, B.1.351.3	Rappazzo et al. (2021)	888	G	A	1.0
p.E484K	antibody epitope effects	Anti-NTD CV1 mAb isolated from an early pandemic case was unable to neutralize either partial B.1.351 variant pseudovirus used (A701V or L242del). The neutralization potency of mAb CV30, which contacts K417 and N501 but not E484, was extasciitilde10-fold weaker toward both B.1.351 variants. The neutralization potency of anti-RBD mAb CV3-1 was 3-4-fold less potent against the B.1.351 variants, while anti-RBD mAb CV2-75 was modestly less effective.	B.1.351.2, B.1.351, B.1.351.3	Stamatatos et al. (2021)	888	G	A	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.E484K	antibody epitope effects	Anti-NTD CV1 mAb isolated from an early pandemic case was unable to neutralize either partial B.1.351 variant pseudovirus used (A701V or L242del). The neutralization potency of mAb CV30, which contacts K417 and N501 but not E484, was extasciitilde10-fold weaker toward both B.1.351 variants. The neutralization potency of anti-RBD mAb CV3-1 was 3-4-fold less potent against the B.1.351 variants, while anti-RBD mAb CV2-75 was modestly less effective.	B.1.351.2, B.1.351, B.1.351.3	Stamatatos et al. (2021)	888	G	A	1.0
p.E484K	antibody epitope effects	Complete loss of binding in ELISA by the variant against monoclonal antibody VH-Fc ab8	B.1.351.2, B.1.351, B.1.351.3	Sun et al. (2021)	888	G	A	1.0
p.E484K	antibody epitope effects	Complete loss of binding in ELISA by the variant against monoclonal antibodies ab8 and IgG1 ab1. Complete loss for the same antibodies was also observed against S1 pseudotyped and full Spike protein trimers with both B.1.351 and P.1 lineage variants, with slight binding signal for P.1 against IgG1 at the highest concentration tested (1uM). Complete loss of neutralization by these two antibodies was also observed.	B.1.351.2, B.1.351, B.1.351.3	Sun et al. (2021)	888	G	A	1.0
p.E484K	antibody epitope effects	Pseudotyped virus model ablates neutralization by RBD-directed mAbs 4-20, 2-4, 2-43, 2-30, 2-15, LY-Cov555, C121. Pseudotyped virus model impairs neutralization by RBD-directed mAb COV2-2196 (somewhat more than fully pseudotyped B.1.351 or live virus)	B.1.351.2, B.1.351, B.1.351.3	Wang et al. (2021)	888	G	A	1.0
p.E484K	antibody epitope effects	Resistent to all seven class 2 (Spike 'up' or 'down' conformation, RBD targeting) antibodies tested, with 10-fold or greater reduction in neutralization (plus notable reudction in two unclassfied mAbs).	B.1.351.2, B.1.351, B.1.351.3	Wang et al. (2021)	888	G	A	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.E484K	antibody epitope effects	Ablates ELISA test binding for class 1 (Spike 'up' conformation only, RBD targeting) monoclonal antibody CA1 on 501Y.V2 ("South African") lineage background Ablates ELISA test binding for class 1 (Spike 'up' conformation only, RBD targeting) monoclonal antibody LyCoV016 (also known as CB6 or JS016) on 501Y.V2 ("South African") lineage background Ablates ELISA test binding for class 1 (Spike 'up' conformation only, RBD targeting) monoclonal antibody CC12.1 on 501Y.V2 ("South African") lineage background Ablates ELISA test binding for class 2 (Spike 'up' or 'down' conformation, RBD targeting) monoclonal antibody BD23 on 501Y.V2 ("South African") lineage background Ablates ELISA test binding for class 2 (Spike 'up' or 'down' conformation, RBD targeting) monoclonal antibody C119 (also known as CB6 or JS016) on 501Y.V2 ("South African") lineage background Ablates ELISA test binding for class 2 (Spike 'up' or 'down' conformation, RBD targeting) monoclonal antibody P2B-2F6 on 501Y.V2 ("South African") lineage background	B.1.351.2, B.1.351, B.1.351.3	Wibmer et al. (2021)	888	G	A	1.0
p.E484K	convalescent plasma binding	1.42x increase in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset.	B.1.351.2, B.1.351, B.1.351.3	Gong et al. (2021)	888	G	A	1.0
p.E484K	convalescent plasma escape	Average extasciitilde5-fold reduction in neutralization efficacy in convalescent sera of 16 health workers infected in Spring 2020.	B.1.351.2, B.1.351, B.1.351.3	Alenquer et al. (2021)	888	G	A	1.0
p.E484K	convalescent plasma escape	Average extasciitilde10-fold reduction in neutralization efficacy in convalescent sera of 16 health workers infected in Spring 2020.	B.1.351.2, B.1.351, B.1.351.3	Alenquer et al. (2021)	888	G	A	1.0
p.E484K	convalescent plasma escape	This mutation occurred in 100% of sequenced virions after 12 passages and led to a 4-fold decrease in convalescent plasma neutralization activity	B.1.351.2, B.1.351, B.1.351.3	Andreano et al. (2020)	888	G	A	1.0
p.E484K	convalescent plasma escape	The 501Y.V2 to first wave IC50 ratio ranged from 6 to 200-fold. Averaging across all 7 participant convalescent sera highlighted the dramatic decrease in sensitivity to neutralization of authentic 501Y.V2 variants. PG: I'm purposefully ignoring D614G and A701V as contributors	B.1.351.2, B.1.351, B.1.351.3	Cele et al. (2021)	888	G	A	1.0
p.E484K	convalescent plasma escape	In 19 convalescent human sera extasciitilde1mo post infection had mild to moderate resistence against most samples	B.1.351.2, B.1.351, B.1.351.3	Chen et al. (2021)	888	G	A	1.0
p.E484K	convalescent plasma escape	In 19 convalescent human sera extasciitilde1mo post infection had mild to moderate resistence against all samples.	B.1.351.2, B.1.351, B.1.351.3	Chen et al. (2021)	888	G	A	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.E484K	convalescent plasma escape	Neutralizing antibody titers of 18 samples (90%) decreased against this B.1.351 pseudotyped virus below an ID50 threshold of 40 (sera collected extasciitilde8mo post Jan 2020 first wave in China).	B.1.351.2, B.1.351, B.1.351.3	Hu et al. (2021)	888	G	A	1.0
p.E484K	convalescent plasma escape	extasciitilde7x reduction in neutralization by key B.1.351 lineage RBD variant combination in sera collected from cohort of 10 with severe disease 21 to 63 days post-onset. Two of the cohort showed no neutralization against this variant.	B.1.351.2, B.1.351, B.1.351.3	Kuzmina et al. (2021)	888	G	A	1.0
p.E484K	convalescent plasma escape	Remarkably, several of the E484 escape mutants were resistant to neutralization at the highest concentration (1:80 initial dilution) of all 4 convalescent sera tested (triplicate experiments). Against a wider panel of 16 convalescent plasma (no replicates), all but one show major resistance.	B.1.351.2, B.1.351, B.1.351.3	Liu et al. (2021)	888	G	A	1.0
p.E484K	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 had mean extasciitilde6x reduction in neutralizing titers, and 40% of the samples lacked any activity against B.1.351.	B.1.351.2, B.1.351, B.1.351.3	Planas et al. (2021)	888	G	A	1.0
p.E484K	convalescent plasma escape	Escape mutant found after in passage in plasma pool of 26 convalescents mean 1.5 post symptom onset.	B.1.351.2, B.1.351, B.1.351.3	Schmidt et al. (2021)	888	G	A	1.0
p.E484K	convalescent plasma escape	In over 90% of two dose mRNA vaccinees, heterotypic neutralizing titres (NT50) against B.1.1.7 and B.1.351 remain comfortably above the level associated with immune protection in recent vaccine trials. However, in over 50% of convalescent COVID-19 individuals (5/9) and recipients of a only a single dose of mRNA vaccine (10/11) – heterotypic neutralization dropped to negligible levels, particularly against B.1.351.	B.1.351.2, B.1.351, B.1.351.3	Skelly et al. (2021)	888	G	A	1.0
p.E484K	convalescent plasma escape	Using convalescent sera from 15 early pandemic patients (Seattle Flu Study), mean 220 days post symptom onset (IQR 125-269, and three asymptomatic cases) with 27% WHO disease severity scale 3, one third (5/15) of sera neutralized this B.1.351 pseudotype and only three had ID50 titers above 100. Only two of the 15 sera achieved 80% neutralization.	B.1.351.2, B.1.351, B.1.351.3	Stamatatos et al. (2021)	888	G	A	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.E484K	convalescent plasma escape	Using convalescent sera from 15 early pandemic patients (Seattle Flu Study), mean 220 days post symptom onset (IQR 125-269, and three asymptomatic cases) with 27% WHO disease severity scale 3, 7 of 15 neutralized this B.1.351 pseudotype that includes the L242del, and only one had titers above 100. Only one of the 15 sera achieved 80% neutralization. [compare to 5 and 1 for pseudotype without the deletion]	B.1.351.2, B.1.351, B.1.351.3	Stamatatos et al. (2021)	888	G	A	1.0
p.E484K	convalescent plasma escape	The only mutation in the B.1.351 lineage that appears to contribute to neutralization reduction (extasciitilde1.7x across 10 convalescent sera from April 2020 infectees)	B.1.351.2, B.1.351, B.1.351.3	Tada et al. (2021)	888	G	A	1.0
p.E484K	convalescent plasma escape	Pseudotyped viruses for B.1.618 was 2.5-fold resistant to neutralization by convalescent sera compared to wild type - a finding that was similar to that of the 3-fold resistance of the South Africa B.1.351 variant using the same assay. The resistance of B.1.618 was caused by the E484K mutation, based on results from viruses pseudotyped for individual variants within B.1.618. [details on the convalescent patient sera collection are not abundantly clear in the preprint]	B.1.351.2, B.1.351, B.1.351.3	Tada et al. (2021)	888	G	A	1.0
p.E484K	convalescent plasma escape	As measured by surface plasmon resonance, RBD with the E484K mutation alone showed a mean 19.1x decrease in binding affinity for six batches of hyperimmune immunoglobulin (hCoV-2IG) preparations generated from SARS-CoV-2 convalescent plasma.	B.1.351.2, B.1.351, B.1.351.3	Tang et al. (2021)	888	G	A	1.0
p.E484K	convalescent plasma escape	Demonstrate (via competitive assays in human and mouse) immune escape from polyclonal antibodies induced by vaccination or infection, comparable to what was previously shown with monoclonal antibodies for N501Y and more importantly for E484K. Even though viral mutations may more strongly affect monoclonal antibodies than sera activity, the latter may also be reduced as confirmed here.	B.1.351.2, B.1.351, B.1.351.3	Vogel et al. (2021)	888	G	A	1.0
p.E484K	convalescent plasma escape	The neutralizing activity of 15/20 convalescent sera was significantly lower against this pseudotyped virus model	B.1.351.2, B.1.351, B.1.351.3	Wang et al. (2021)	888	G	A	1.0
p.E484K	convalescent plasma escape	27% of 44 early pandemic exposure convalescent plasma/sera lose all activity against a RBD triple mutant pseudovirus (RBD mutatants of the 501Y.V2 "South African" lineage), while only 23% retained high titres	B.1.351.2, B.1.351, B.1.351.3	Wibmer et al. (2021)	888	G	A	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.E484K	convalescent plasma escape	Nearly half (21 of 44, 48%) of early pandemic exposure convalescent plasma/sera failed to neutralize the 501Y.V2 (”South African”) lineage pseudovirus construct Only 3 of 44 convascent sera (those with the highest titer, which correlated direectly with initial infection severity) had high neutralization against this 501Y.V2 PG: note that lineage variant R246I was excluded from the text in reference to these sera assays, not sure if that was an oversight.	B.1.351.2, B.1.351, B.1.351.3	Wibmer et al. (2021)	888	G	A	1.0
p.E484K	convalescent plasma escape	Subtype of the B.1.526 ”New York” lineage, lentivirus pseudotyped with this mutation combination in showed 3.3x reduction in IC50 serum dilution concentration for 6 convalescent sera.	B.1.351.2, B.1.351, B.1.351.3	Zhou et al. (2021)	888	G	A	1.0
p.E484K	humoral response durability	In a prospective study of 107 hospitalized patients, decrease of IgG rates and serological assays becoming negative did not imply loss of neutralizing capacity. Our results indicate a sustained humoral response against the ancestral strain and the D614G, B.1.1.7 and P.1 variants for at least 6 months (last of two samples taken) in patients previously hospitalized for COVID-19. A weaker protection was however observed for the B.1.351 variant.	B.1.351.2, B.1.351, B.1.351.3	Betton et al. (2020)	888	G	A	1.0
p.E484K	monoclonal antibody serial passage escape	The engineered mutation cause 10-fold or more increase in the disassociation constant with many monoclonal antibodies (C144/C002/C121/C104/C110).	B.1.351.2, B.1.351, B.1.351.3	Barnes et al. (2020)	888	G	A	1.0
p.E484K	monoclonal antibody serial passage escape	Escape variant 100% appearance in 2 passages against Regeneron monoclonal antibody REGN10989 @ 50ug/mL (99% after one passage)	B.1.351.2, B.1.351, B.1.351.3	Baum et al. (2020)	888	G	A	1.0
p.E484K	monoclonal antibody serial passage escape	Mildly effective mutant against this position in the RBD for highly neutralizing COV2-2479 monoclonal antibody Effective mutant against this position in the RBD for highly neutralizing COV2-2050 monoclonal antibody	B.1.351.2, B.1.351, B.1.351.3	Greaney et al. (2020)	888	G	A	1.0
p.E484K	monoclonal antibody serial passage escape	Escape mutation against monoclonal antibody LY-CoV555 (antibody that forms the basis for Eli Lilly’s bamlanivimab)	B.1.351.2, B.1.351, B.1.351.3	Starr et al. (2021)	888	G	A	1.0
p.E484K	monoclonal antibody serial passage escape	Class 2 antibodies C627, C602, C671, C643, and class 2/3 antibody C603 selected for the emergence of the E484K mutation in vitro.	B.1.351.2, B.1.351, B.1.351.3	Wang et al. (2021)	888	G	A	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.E484K	monoclonal antibody serial passage escape	Strong positive selection (up to 50% of supernatant sequences) after C121 monoclonal antibody assay, decreasing in subsequent passages Strong positive selection (up to 44% of supernatant sequences) after after one round of C144 monoclonal antibody passage, then waning on subsequent passages	B.1.351.2, B.1.351, B.1.351.3	Weisblum et al. (2020)	888	G	A	1.0
p.E484K	outcome hazard ratio	On average across 7 European countries studied, using B.1.351 defining mutations: Significant shift to infection in those without pre-existing conditions (79.6% vs 89% for non-VOC cases). Significant increase in hospitalization rate (19.3% vs 7.5% for non-VOC cases). Significant increase in ICU rate (2.3% vs 0.6% for non-VOC cases). PG: seems to be different notations around the LAL deletion, using the minimal shared definition to catch as many as possible.	B.1.351.2, B.1.351, B.1.351.3	Funk et al. (2021)	888	G	A	1.0
p.E484K	pharmaceutical effectiveness	Bamlanivimab (LY-CoV555) lost extasciitilde16x binding against this isolated mutation. Casirivimab lost extasciitilde16x binding against this isolated mutation.	B.1.351.2, B.1.351, B.1.351.3	Engelhart et al. (2021)	888	G	A	1.0
p.E484K	pharmaceutical effectiveness	Tixagevimab, Regdanvimab and COR-101 display reduced binding affinity to virus pseudotyped as RBD from B.1.351.	B.1.351.2, B.1.351, B.1.351.3	Engelhart et al. (2021)	888	G	A	1.0
p.E484K	pharmaceutical effectiveness	Bamlanivimab (LY-CoV555) lost extasciitilde32x binding against this double mutation. COR-101 lost extasciitilde160x binding against this double mutation. Casirivimab lost extasciitilde16x binding against this double mutation. Estesevimab lost extasciitilde32x binding against this double mutation. Regdanvimab lost extasciitilde4x binding against this double mutation. Tixagevimab lost extasciitilde12x binding against this double mutation.	B.1.351.2, B.1.351, B.1.351.3	Engelhart et al. (2021)	888	G	A	1.0
p.E484K	pharmaceutical effectiveness	Bamlanivimab (LY-CoV555) lost extasciitilde64x binding against this double mutation. COR-101 lost extasciitilde50x binding against this double mutation. Casirivimab lost extasciitilde250x binding against this double mutation. Estesevimab lost extasciitilde16x binding against this double mutation. Regdanvimab lost extasciitilde32x binding against this double mutation. Tixagevimab lost extasciitilde10x binding against this double mutation.	B.1.351.2, B.1.351, B.1.351.3	Engelhart et al. (2021)	888	G	A	1.0
p.E484K	pharmaceutical effectiveness	This mutated version of RBD completely abolishes the binding to a therapeutic antibody, Bamlanivimab, in vitro.	B.1.351.2, B.1.351, B.1.351.3	Liu et al. (2021)	888	G	A	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.E484K	reinfection	4 health care workers in the 20's and 30's with no underlying conditions and seropositivity or confirmed 2020 SARS-CoV-2 infections were confirmed to have B.1.351 infection during a Februrary 2021 hospital outbreak in Luxembourg. Symptoms were mostly mild on first infection, and milder on second infection.	B.1.351.2, B.1.351, B.1.351.3	Staub et al. (2021)	888	G	A	1.0
p.E484K	reinfection	Hamsters re-infected with B.1.351 virus after seroversion from previous infection with a lineage A virus did not transmit virus to naive sentinels via direct contact transmission, in contrast to the non-seroconverted animals. They had little infectious virus and no pathology in the lungs. Initial infection with SARS-CoV-2 lineage A does not prevent heterologous reinfection with B.1.351, but prevents disease and onward transmission.	B.1.351.2, B.1.351, B.1.351.3	Yinda et al. (2021)	888	G	A	1.0
p.E484K	symptom prevalence	Inoculation with the B.1.351 isolate resulted in lower clinical scores in 6 rhesus macaques that correlated with lower virus titers in the lungs, less severe histologic lung lesions and less viral antigen detected in the lungs. Our comparative pathogenicity study suggests that ongoing circulation under diverse evolutionary pressure favors transmissibility and immune evasion rather than an increase in intrinsic pathogenicity.	B.1.351.2, B.1.351, B.1.351.3	Munster et al. (2021)	888	G	A	1.0
p.E484K	syncytium formation	extasciitilde50% Vero cell-cell membrane fusion assay under infection with VSV pseudotyped virus relative to wild type, signficantly higher than D614G.	B.1.351.2, B.1.351, B.1.351.3	Kim et al. (2021)	888	G	A	1.0
p.E484K	tissue specific neutralization	The nasal mucosa of Pfizer vaccinees with time course collection was evaluated against VSV pseudotypes: while B.1.1.7 and D614G showed neutralization by nasal swab from only one different previously infected vacinee neutralizing at weeks 3 and 6, B.1.351 showed zero neutralization at either time point in any sample (and relatively impaired serum neutralization).	B.1.351.2, B.1.351, B.1.351.3	Planas et al. (2021)	888	G	A	1.0
p.E484K	trafficking	This variant alone shows a extasciitilde5x decrease in cell entry efficiency (RLU measurement in 293T cells) compared to D614G.	B.1.351.2, B.1.351, B.1.351.3	Ferriera et al (2021)	888	G	A	1.0
p.E484K	trafficking	The entry efficiencies of Spike pseudotyped viruses bearing N501Y Variant 2 (B.1.351) 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.1.351.2, B.1.351, B.1.351.3	Hu et al. (2021)	888	G	A	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.E484K	trafficking	More efficient infectivity (24h) compared to wild type, in Caco-2 cells extasciitilde11x, Vero extasciitilde10x, and Calu-3 extasciitilde11x. Compare to wild type at extasciitilde5x across cell types.	B.1.351.2, B.1.351, B.1.351.3	Kim et al. (2021)	888	G	A	1.0
p.E484K	trafficking	extasciitilde6x more efficient S2 domain cleavage compared to wild type, compared to 4x by D614G alone in Caco-2 cells, mid-range of three cell line tested (Vero and Calu-3). [N501Y+D614G does not show an increase in cleavage, therefore a synergistic effect of the trio is implied]	B.1.351.2, B.1.351, B.1.351.3	Kim et al. (2021)	888	G	A	1.0
p.E484K	trafficking	extasciitilde2x more infectivity than D614G alone in HEK293T-ACE2 cells 48h post-transduction.	B.1.351.2, B.1.351, B.1.351.3	Kuzmina et al. (2021)	888	G	A	1.0
p.E484K	trafficking	Approximately as infective as D614G alone in HEK293T-ACE2 cells 48h post-transduction (extasciitildeadditive effects of the individual variants).	B.1.351.2, B.1.351, B.1.351.3	Kuzmina et al. (2021)	888	G	A	1.0
p.E484K	trafficking	extasciitilde13x more infective as D614G alone in HEK293T-ACE2 cells 48h post-transduction.	B.1.351.2, B.1.351, B.1.351.3	Kuzmina et al. (2021)	888	G	A	1.0
p.E484K	trafficking	extasciitilde12x more infectivity than D614G alone in HEK293T-ACE2 cells 48h post-transduction (extasciitildeadditive effects of 501 and 484).	B.1.351.2, B.1.351, B.1.351.3	Kuzmina et al. (2021)	888	G	A	1.0
p.E484K	trafficking	Lentiviral pseudotyped with this individual mutation from B.1.351 was tested on ACE2.293T cells. Luciferase activity was measured two days postinfection, showing no change in infection rate amongst the cells.	B.1.351.2, B.1.351, B.1.351.3	Tada et al. (2021)	888	G	A	1.0
p.E484K	transmissibility	Assuming complete cross-protection, we estimate 501Y.V2/B.1.351 was 1.50 (95% CrI: 1.20-2.13) times as transmissible than previously circulating variants. Assuming instead that 501Y.V2 is identically transmissible, the new variant evades 21% (95% CrI: 11-36%) of previously acquired immunity. Reality may lie between these extremes, with an intermediate increase in transmissibility and mildly imperfect cross-protection from past exposure.	B.1.351.2, B.1.351, B.1.351.3	Pearson et al. (2021)	888	G	A	1.0
p.E484K	transmissibility	36,590 variant-specific RT-PCR tests were performed on samples collected between April 12 and May 7, 2021 in France to compare variant spread. Compared to January to March 2021, B.1.351 variant had a significant transmission advantage over B.1.1.7 in some regions (15.1 to 16.1% in Île-de-France and 16.1 to 18.8% in Hauts-de-France). This shift in transmission advantage is consistent with the immune evasion abilities of B.1.351 and the high levels of immunization in these regions.	B.1.351.2, B.1.351, B.1.351.3	Roquebert et al. (2021)	888	G	A	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.E484K	vaccine neutralization efficacy	The Janssen single dose vaccine showed 72% efficacy at preventing moderate and severe disease, which was reduced to 57% in South Africa, where 92.6% of infections are estimated to have been B.1.351. 100% reduction in hospitalization risk remains across variants after 28 days post-vaccination.	B.1.351.2, B.1.351, B.1.351.3	nan	888	G	A	1.0
p.E484K	vaccine neutralization efficacy	In an Ontario long term care facility, cumulatively, weaker BNT162b2 vaccine stimulation, age/comorbidities, produced a 130-fold reduction in apparent neutralization titers in mean 88yo LTCH residents against Beta (B.1.351), relative to staff vaccinees against D614G wild type. 37.9% of 116 two-dose-mRNA-vaccinated residents had undetectable neutralizing antibodies to B.1.351. mRNA-1273 vaccinee sera displayed extasciitilde2 better neutralization than BNT162b2. [common defining B.1.351 mutations noted, as the manuscript does not provide details]	B.1.351.2, B.1.351, B.1.351.3	Abe et al. (2021)	888	G	A	1.0
p.E484K	vaccine neutralization efficacy	Using B.1.351 defining mutations for Spike, observed 4x average decrease in neutralization efficiency (but still relevant titres) for sera from 10 BNT162b2 vaccinees 12 days after second dose, but only one relevant titre 12 days after first dose. Compares unfavorably to wild type or B.1.1.7 titres.	B.1.351.2, B.1.351, B.1.351.3	Alenquer et al. (2021)	888	G	A	1.0
p.E484K	vaccine neutralization efficacy	Observed 1.4-fold reduction in neutralization efficiency of Pfizer vaccinee sera (collected 14 days after second dose) against pseudotype B.1.351 key variants lentivirus. Compare to 8.8-fold reduction against cultured B.1.351 virus.	B.1.351.2, B.1.351, B.1.351.3	Bates et al. (2021)	888	G	A	1.0
p.E484K	vaccine neutralization efficacy	Observed 8.8-fold reduction in neutralization efficiency of Pfizer vaccinee sera (collected 14 days after second dose) against cultured B.1.351 sample. Contrast this with 1.4-fold reduction for just the pseudovirus combination of "key" B.1.351 mutations K417N+E484K+N501Y. WA1 and B.1.351 FRNT50 titers correlated weakly at the individual level, with some individual's serum potently neutralizing WA1 while having FRNT50 for B.1.351 below the assay limit of detection (1:20).	B.1.351.2, B.1.351, B.1.351.3	Bates et al. (2021)	888	G	A	1.0
p.E484K	vaccine neutralization efficacy	The neutralizing activity of vaccine was slightly to significantly lower against this variant combination in sera from all 24 patients with the BNT162b2 mRNA vaccine. (Fig. 4) [In stark contrast to this combination plus K417N, which had no effect (P<0.0001 vs. P	B.1.351.2, B.1.351, B.1.351.3	Chen et al. (2021)	888	G	A	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.E484K	vaccine neutralization efficacy	Neutralization efficiency (ID50) against B.1.1.351-v3 reduced 8.4x relative to D614G wildtype using pseudotyped VSV assay on 8 Moderna vaccinee sera one week post-booster.	B.1.351.2, B.1.351, B.1.351.3	Choi et al. (2021)	888	G	A	1.0
p.E484K	vaccine neutralization efficacy	Neutralization efficiency (ID50) against B.1.1.351-v2 reduced 7.3x relative to D614G wildtype using pseudotyped VSV assay on 8 Moderna vaccinee sera one week post-booster.	B.1.351.2, B.1.351, B.1.351.3	Choi et al. (2021)	888	G	A	1.0
p.E484K	vaccine neutralization efficacy	Nine stored sera from Pfizer BNT162b2 vaccinees were tested against a range of spike mutation bearing PV. E484K conferred a ten-fold reduction in neutralisation by vaccine sera.	B.1.351.2, B.1.351, B.1.351.3	Ferreira et al. (2021)	888	G	A	1.0
p.E484K	vaccine neutralization efficacy	ELISpot assays show T cell neutralization reduced by 29.8% in this B.1.351 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.1.351.2, B.1.351, B.1.351.3	Gallagher et al. (2021)	888	G	A	1.0
p.E484K	vaccine neutralization efficacy	Pseudotyped B.1.351 v1 virus has reduced neutralization activity vs wild type: 34.5x (30 sera Pfizer median 9 days post 2nd dose) and 27.7x (35 sera Moderna median 18 days post 2nd dose). This was significant by ANOVA. Notably, 36.7% (11/30) recipients of two-dose Pfizer and 42.9% (15/35) recipients of two-dose Moderna vaccines did not have detectable neutralization of at least one of the B.1.351 variants.	B.1.351.2, B.1.351, B.1.351.3	Garcia-Beltran et al. (2021)	888	G	A	1.0
p.E484K	vaccine neutralization efficacy	Pseudotyped B.1.351 v2 virus has reduced neutralization activity vs wild type: 41.2x (30 sera Pfizer median 9 days post 2nd dose) and 20.8x (35 sera Moderna median 18 days post 2nd dose). This was significant by ANOVA. Notably, 36.7% (11/30) recipients of two-dose Pfizer and 42.9% (15/35) recipients of two-dose Moderna vaccines did not have detectable neutralization of at least one of the B.1.351 variants.	B.1.351.2, B.1.351, B.1.351.3	Garcia-Beltran et al. (2021)	888	G	A	1.0
p.E484K	vaccine neutralization efficacy	E484K pseudotyped VSV was tested for neutralization in a clonal HEK-293T ACE2 TMPRSS2 cell line optimized for highly efficient S-mediated infection. A cohort of 12 Argentinian recipients of the Gamaleya Sputnik V Ad26 / Ad5 vaccine showed a mean 2.8x decrease in neutralization effiacacy.	B.1.351.2, B.1.351, B.1.351.3	Ikegame et al. (2021)	888	G	A	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.E484K	vaccine neutralization efficacy	B.1.351 pseudotyped VSV was tested for neutralization in a clonal HEK-293T ACE2 TMPRSS2 cell line optimized for highly efficient S-mediated infection. Only 1 out of 12 serum samples from a cohort of Argentinian recipients of the Gamaleya Sputnik V Ad26 / Ad5 vaccine showed effective neutralization (IC90) at full serum strength (average realtive decrease was 6.1x vs wild type).	B.1.351.2, B.1.351, B.1.351.3	Ikegame et al. (2021)	888	G	A	1.0
p.E484K	vaccine neutralization efficacy	Human sera from 5 two-dose Pfizer vaccinated individuals (47-68 days post 1st-dose) neutralized this variant 3.4x less relative to reference USA-WA1/2020 strain. 8 convalescent plasma with weak IgG ELISA titre neutralized this variant 2.4x less relative to reference USA-WA1/2020 strain. One plasma failed to neutralize at all. 11 convalescent plasma with moderate IgG ELISA titre neutralized this variant 4.2x less relative to reference USA-WA1/2020 strain. 11 convalescent plasma with high IgG ELISA titre neutralized this variant 2.6x less relative to reference USA-WA1/2020 strain.	B.1.351.2, B.1.351, B.1.351.3	Jangra et al. (2021)	888	G	A	1.0
p.E484K	vaccine neutralization efficacy	This variant showed only minor in Pfizer sera (one or two dose) neutralization efficiency vs D614G (using lentivirus pseudotype).	B.1.351.2, B.1.351, B.1.351.3	Kuzmina et al. (2021)	888	G	A	1.0
p.E484K	vaccine neutralization efficacy	This variant showed extasciitilde10x decrease in Pfizer sera (3 weeks post-first dose: n	B.1.351.2, B.1.351, B.1.351.3	Kuzmina et al. (2021)	888	G	A	1.0
p.E484K	vaccine neutralization efficacy	This variant of key B.1.351 lineage mutations showed extasciitilde10x decrease in Pfizer sera (3 weeks post-first dose: n	B.1.351.2, B.1.351, B.1.351.3	Kuzmina et al. (2021)	888	G	A	1.0
p.E484K	vaccine neutralization efficacy	This variant showed >5x decrease in Pfizer sera (3 weeks post-first dose: n	B.1.351.2, B.1.351, B.1.351.3	Kuzmina et al. (2021)	888	G	A	1.0
p.E484K	vaccine neutralization efficacy	In post-vaccination sera from individuals who received one (3 weeks post-first dose: n	B.1.351.2, B.1.351, B.1.351.3	Kuzmina et al. (2021)	888	G	A	1.0
p.E484K	vaccine neutralization efficacy	Vaccine plasma neutralization of B.1.351-spike virus was nominally robust but lower (extasciitilde3x) than other variants of concern.	B.1.351.2, B.1.351, B.1.351.3	Liu et al. (2021)	888	G	A	1.0
p.E484K	vaccine neutralization efficacy	A two-dose regimen of (AstraZeneca) ChAdOx1-nCoV19 did not show protection against mild-moderate Covid-19 due to B.1.351 variant, however, vaccine efficacy against severe Covid-19 is undetermined.	B.1.351.2, B.1.351, B.1.351.3	Madhi et al. (2021)	888	G	A	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.E484K	vaccine neutralization efficacy	In a multicenter, double-blind, randomized, controlled trial to assess the safety and efficacy of the ChAdOx1 nCoV-19 vaccine (AZD1222) with enrollment June 24 and November 9, 2020 from extasciitilde2000 HIV-negative 18-64 year olds (1:1 placebo to treatment), incidence of serious adverse events 14 or more days post- 2nd dose was balanced between the vaccine and placebo groups. A two-dose regimen of the ChAdOx1 nCoV-19 vaccine did not show protection against mild-to-moderate Covid-19 due to the B.1.351 variant. Serum samples obtained from 13 ChAdOx1 nCoV-19 vaccine recipients without SARS-CoV-2 infection through 41 days after vaccination showed 3.5x reduction in neutralization (ID50) for B.1.351 RBD pseudotype HIB-1 virus compared to D614G alone. This RBD variant combination's neutralization by a placebo control group of 6 naturally infected patients showed a similar 3.2x drop (though with D614G starting at a 1.7x higher titre than vaccinee sera).	B.1.351.2, B.1.351, B.1.351.3	Madhi et al. (2021)	888	G	A	1.0
p.E484K	vaccine neutralization efficacy	Relative to B.1.1.117, PRNT50 line virus neutralizating antibody activity assay of B.1.351 showed extasciitilde11x reduction in 13 vacinees's sera collected through 41 days after vaccination. Neutralization by a placebo control group of 6 naturally infected patients showed a smaller extasciitilde8x drop (starting from a extasciitilde50% higher PRNT50 value than vacinees for B.1.1.117 neutralization). Serum samples obtained from 13 ChAdOx1 nCoV-19 vaccine recipients without SARS-CoV-2 infection through 41 days after vaccination showed extasciitilde4x reduction in neutralization (ID50) for full B.1.351 pseudotype HIV-1 virus compared to D614G alone. This RBD variant combination's neutralization by a placebo control group of 6 naturally infected patients showed a slightly higher 4.6x drop (though with D614G starting at a 1.7x higher titre than vaccinee sera).	B.1.351.2, B.1.351, B.1.351.3	Madhi et al. (2021)	888	G	A	1.0
p.E484K	vaccine neutralization efficacy	The Novavax vaccine, which achieved 95.6% efficacy against previous SARS-CoV-2 strains, had reduced efficacy of 60% in South Africa, where 92.6% of infections are estimated to have been B.1.351.	B.1.351.2, B.1.351, B.1.351.3	Novavax (2021)	888	G	A	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.E484K	vaccine neutralization efficacy	Detectable antibodies against B.1.351 at various time points using pseudotyped lentivirus neutralization in Moderna vaccinee cohort: Day 29 8%, Day 43 100%, Day 119 71%, Day 209 54%. Detectable antibodies against B.1.351 at various time points using live virus FRNT neutralization in Moderna vaccinee cohort: Day 29 8%, Day 43 100%, Day 119 79%, Day 209 58%. Detectable antibodies against B.1.351 at various time points using ACE2 blocking assay in Moderna vaccinee cohort: Day 29 63%, Day 43 100%, Day 119 71%, Day 209 79%. Decreased neutralization on some assays was seen especially in those vaccinees tested that were 71+.	B.1.351.2, B.1.351, B.1.351.3	Pegu et al (2021)	888	G	A	1.0
p.E484K	vaccine neutralization efficacy	The sera of 16 individuals with time course collection was evaluated against VSV pseudotypes: while BD614G and B.1.1.7 were neutralized earlier, the anti-B.1.351 response was negative up to week 3, and became detectable at week 4 (1 week after booster dose), at a level lower than the two other viruses (extasciitilde10x vs D614G) through week 6, the last timepoint measured. Three vaccinees never showed detectable neutralization to B.1.351 even after second dose.	B.1.351.2, B.1.351, B.1.351.3	Planas et al. (2021)	888	G	A	1.0
p.E484K	vaccine neutralization efficacy	In a randomized phase 2a-b control trial of the Novavax (NVX-CoV2373) vaccine in South Africa, where B.1.351 virus dominates, efficacy was 60.1% (95% CI, 19.9 to 80.1) in HIV-negative and initially SARS-CoV-2 seronegative participants using the primary endpoint of laboratory-confirmed symptomatic Covid-19 at 7 days or more after the second dose among participants.	B.1.351.2, B.1.351, B.1.351.3	Shinde et al. (2021)	888	G	A	1.0
p.E484K	vaccine neutralization efficacy	Neutralizing antibody titers of non-human primate sera after one or two doses of Ad26.COV2.S (Jannsen vaccine) against the variants containing the E484K substitution in the RBD were present but reduced (fold reduction between 3.35–7.78, 95% confidence interval all above twofold difference, one-sample t test).	B.1.351.2, B.1.351, B.1.351.3	Solfrosi et al. (2021)	888	G	A	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.E484K	vaccine neutralization efficacy	In sera collected from 15 early pandemic patients (Seattle Flu Study), mean 16 days post first dose with either Pfizer/BioNTech or Moderna vaccines, the median ID50 titers were extasciitilde3-fold lower against this B.1.351 pseudotyped virus relative to wild type. A single asymptomatic patient, who had no detectable RBD-specific IgG memory before vaccination, also did not elicit nAbs against the B.1.351 variant. [compare to extasciitilde10 fold with L242del] ID50 titres in non-infected mRNA vaccines more than two weeks post-booster were signficiant, but >100x weaker than in previously infected patients after first dose.	B.1.351.2, B.1.351, B.1.351.3	Stamatatos et al. (2021)	888	G	A	1.0
p.E484K	vaccine neutralization efficacy	In sera collected from 15 early pandemic patients (Seattle Flu Study), mean 16 days post first dose with either Pfizer/BioNTech or Moderna vaccines, the median ID50 titers were extasciitilde10-fold lower against this B.1.351 pseudotyped virus relative to wild type. A single asymptomatic patient, who had no detectable RBD-specific IgG memory before vaccination, also did not elicit nAbs against the B.1.351 variant. [compare to extasciitilde3 fold without the deletion] ID50 titres in non-infected mRNA vaccines more than two weeks post-booster were significant, but extasciitilde500x weaker than in previously infected patients after first dose.	B.1.351.2, B.1.351, B.1.351.3	Stamatatos et al. (2021)	888	G	A	1.0
p.E484K	vaccine neutralization efficacy	Pseudotyped viruses for B.1.618 was 2.7-fold resistant to neutralization by 6 BNT162b2 vaccine sera 28 days post-booster compared to wild type - a finding that was similar to that of the 3.4-fold resistance of the South Africa B.1.351 variant using the same assay. Neutralization by 3 Moderna vaccine sera 28 days post-booster was 3-fold resistant (vs. 2.2-fold for B.1.351). The resistance of B.1.618 was caused by the E484K mutation, based on results from viruses pseudotyped for individual variants within B.1.618.	B.1.351.2, B.1.351, B.1.351.3	Tada et al. (2021)	888	G	A	1.0
p.E484K	vaccine neutralization efficacy	Pseudotyped viruses for B.1.351 was 3.4-fold resistant to neutralization by 6 BNT162b2 vaccine sera 28 days post-booster compared to wild type. Neutralization by 3 Moderna vaccine sera 28 days post-booster was 2.2-fold resistant. [Exact list of B.1.351 mutations used in these assays was not included in the preprint]	B.1.351.2, B.1.351, B.1.351.3	Tada et al. (2021)	888	G	A	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.E484K	vaccine neutralization efficacy	PBMCs of Pfizer/BioNTech BNT162b2 (n	B.1.351.2, B.1.351, B.1.351.3	Tarke et al. (2021)	888	G	A	1.0
p.E484K	vaccine neutralization efficacy	[Contrary to how this paper has been cited, Voysey et al. do NOT show evidence of decreased effectiveness of ChAdOx1 (AstraZeneca) against the South African B.1.351 lineage. Insufficient numbers reaching the primary study endpoint were available in that arm of the vaccine study to report any statistics from the South African participants. Additionally, the study period of the paper ended in November 2020, while the earliest reported case of this lineage is October (covariants.org), only becoming dominant by mid-November.]	B.1.351.2, B.1.351, B.1.351.3	Voysey et al. (2021)	888	G	A	1.0
p.E484K	vaccine neutralization efficacy	In a cohort of 20 patients 8+ weeks after second vaccine dose of Moderna (mRNA-1273) or Pfizer-BioNTech (BNT162b2) vaccines, ELISA tests show 10x reduced efficacy of a majority of isolated antibodies, but only a modest decrease for vaccine plasma overall.	B.1.351.2, B.1.351, B.1.351.3	Wang et al. (2021)	888	G	A	1.0
p.E484K	vaccine neutralization efficacy	In a cohort of 20 patients 8+ weeks after second vaccine dose of Moderna (mRNA-1273) or Pfizer-BioNTech (BNT162b2) vaccines, a significant (0.5 to 20-fold, but average extasciitilde2x) decrease in neutralization by vaccine plasma was observed.	B.1.351.2, B.1.351, B.1.351.3	Wang et al. (2021)	888	G	A	1.0
p.E484K	vaccine neutralization efficacy	No significant difference in T-cell response to B.1.351 was observed (vs. ancestral) in blood drawn from 28 participants received the Pfizer-BioNTech vaccine and 2 received the Moderna vaccine.	B.1.351.2, B.1.351, B.1.351.3	Woldemeskel et al. (2021)	888	G	A	1.0
p.E484K	vaccine neutralization efficacy	In Moderna vaccinee sera, 2.7x reduction in neutralization, and 6.4 for the full B.1.351 Spike mutation complement, but despite the observed decreases, titers in human vaccinee sera against the B.1.351 variant remained at clinically significant level of extasciitilde1/300.	B.1.351.2, B.1.351, B.1.351.3	Wu et al. (2021)	888	G	A	1.0
p.E484K	vaccine neutralization efficacy	In 20 sera from BNT162b2 mRNA vaccine inoculated participants, 6 displayed mild (2x) reductions in neutralization. This variant combination showed the highest reduction, but the magnitude of the differences was small compared to the >4x differences in HA-inhibition titers that have been used to signal potential need for a strain change in influenza vaccines.	B.1.351.2, B.1.351, B.1.351.3	Xie et al. (2021)	888	G	A	1.0
p.E484K	vaccine neutralization efficacy	Sera from healthcare workers (n	B.1.351.2, B.1.351, B.1.351.3	Zhou et al. (2021)	888	G	A	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.E484K	vaccinee plasma binding	1.16x increase in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in previously non-seroconverted subjects. 1.06x increase in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in post-infection vaccinees.	B.1.351.2, B.1.351, B.1.351.3	Gong et al. (2021)	888	G	A	1.0
p.E484K	viral load	B.1.351 and P.1 samples showed average Ct cycle threshold of 22.2 vs 23 for wildtype (i.e. extasciitilde60% higher viral load) comparing 3360 and 22535 samples respectively.	B.1.351.2, B.1.351, B.1.351.3	Roquebert et al. (2021)	888	G	A	1.0
p.E484K	viral load	The 62 B.1.351 (a.k.a. N501Y.V2) variant cases in three Paris hospital labs had a extasciitilde2-fold viral load increase (extasciitilde1 Ct drop in both N and ORF1ab probes) compared to 332 ancestral lineage cases from the same time frame (2020-12-20 to 2021-02-26).	B.1.351.2, B.1.351, B.1.351.3	Teyssou et al. (2021)	888	G	A	1.0
p.E484K	virion structure	Estimated free energy change (ddG) for this variant is -0.6 kcal/mol (i.e. destabilizing relative to wild type)	B.1.351.2, B.1.351, B.1.351.3	Spratt et al. (2021)	888	G	A	1.0
p.L18F	ACE2 receptor binding affinity	Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant showed a 1.07x decrease in binding (KD) relative to D614G. Compare to increased binding in full Spike variant complements for major lineages containing this variant subset: 3.56x (B.1.351 aka Beta), 4.24x (P.1 aka Gamma).	B.1.351.2, B.1.351, B.1.351.3	Gong et al. (2021)	895	C	T	0.64
p.L18F	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.1.351. We observed an increase (relative to D614G) in binding of soluble ACE2 to B.1.351, and to a much gearter extent to B.1.1.7, which both carry the N501Y mutation (see Fig 3).	B.1.351.2, B.1.351, B.1.351.3	Planas et al. (2021)	895	C	T	0.64

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.L18F	CD8 plus T cell response	Encouragingly, we find that the majority of T cell responses in recipients of two doses of the BNT162b2 vaccine are generated by epitopes that are invariant between the [wildtype] and two of the current variants of concern (B.1.1.7 and B.1.351). In over 90% of two dose mRNA vaccinees, heterotypic neutralizing titres (NT50) against B.1.1.7 and B.1.351 remain comfortably above the level associated with immune protection in recent vaccine trials. However, in over 50% of convalescent COVID-19 individuals and recipients of a only a single dose of mRNA vaccine – heterotypic neutralization dropped to negligible levels, particularly against B.1.351.	B.1.351.2, B.1.351, B.1.351.3	Skelly et al. (2021)	895	C	T	0.64
p.L18F	antibody epitope effects	Massive reduction in S2L28 monoclonal antibody EC50 (i.e. ablated recognition), within antigenic supersite "i", but no effect on other mAbs within that supersite	B.1.351.2, B.1.351, B.1.351.3	McCallum et al. (2021)	895	C	T	0.64
p.L18F	antibody epitope effects	Ablates neutralization by N-terminal-domain-targeting mAbs 4-19. Impairs neutralization by N-terminal-domain-targeting mAbs 4A8 and 2-17.	B.1.351.2, B.1.351, B.1.351.3	Wang et al. (2021)	895	C	T	0.64
p.L18F	convalescent plasma binding	1.66x increase in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset. Compare to decreased binding in full Spike variant complements for major lineages containing this variant subset: 0.96x (B.1.351 aka Beta), 0.77x (P.1 aka Gamma).	B.1.351.2, B.1.351, B.1.351.3	Gong et al. (2021)	895	C	T	0.64
p.L18F	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.1.351.2, B.1.351, B.1.351.3	Cele et al. (2021)	895	C	T	0.64
p.L18F	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 had mean extasciitilde6x reduction in neutralizing titers, and 40% of the samples lacked any activity against B.1.351.	B.1.351.2, B.1.351, B.1.351.3	Planas et al. (2021)	895	C	T	0.64

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.L18F	convalescent plasma escape	In over 90% of two dose mRNA vaccinees, heterotypic neutralizing titres (NT50) against B.1.1.7 and B.1.351 remain comfortably above the level associated with immune protection in recent vaccine trials. However, in over 50% of convalescent COVID-19 individuals (5/9) and recipients of a only a single dose of mRNA vaccine (10/11) – heterotypic neutralization dropped to negligible levels, particularly against B.1.351.	B.1.351.2, B.1.351, B.1.351.3	Skelly et al. (2021)	895	C	T	0.64
p.L18F	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.1.351.2, B.1.351, B.1.351.3	Wibmer et al. (2021)	895	C	T	0.64
p.L18F	tissue specific neutralization	The nasal mucosa of Pfizer vaccinees with time course collection was evaluated against VSV pseudotypes: while B.1.1.7 and D614G showed neutralization by nasal swab from only one different previously infected vacinee neutralizing at weeks 3 and 6, B.1.351 showed zero neutralization at either time point in any sample (and relatively impaired serum neutralization).	B.1.351.2, B.1.351, B.1.351.3	Planas et al. (2021)	895	C	T	0.64
p.L18F	trafficking	Lentiviral pseudotyped with this individual mutation from B.1.351 was tested on ACE2.293T cells. Luciferase activity was measured two days postinfection, showing mild decrease in infection rate amongst the cells, suggetsing that this mutation does not contributing to cell entry fitness.	B.1.351.2, B.1.351, B.1.351.3	Tada et al. (2021)	895	C	T	0.64
p.L18F	vaccine neutralization efficacy	Observed 8.8-fold reduction in neutralization efficiency of Pfizer vaccinee sera (collected 14 days after second dose) against cultured B.1.351 sample. Contrast this with 1.4-fold reduction for just the pseudovirus combination of ”key” B.1.351 mutations K417N+E484K+N501Y. WA1 and B.1.351 FRNT50 titers correlated weakly at the individual level, with some individual’s serum potently neutralizing WA1 while having FRNT50 for B.1.351 below the assay limit of detection (1:20).	B.1.351.2, B.1.351, B.1.351.3	Bates et al. (2021)	895	C	T	0.64

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.L18F	vaccine neutralization efficacy	Neutralization efficiency (ID50) against B.1.1.351-v2 reduced 7.3x relative to D614G wildtype using pseudotyped VSV assay on 8 Moderna vaccinee sera one week post-booster.	B.1.351.2, B.1.351, B.1.351.3	Choi et al. (2021)	895	C	T	0.64
p.L18F	vaccine neutralization efficacy	Pseudotyped B.1.351 v2 virus has reduced neutralization activity vs wild type: 41.2x (30 sera Pfizer median 9 days post 2nd dose) and 20.8x (35 sera Moderna median 18 days post 2nd dose). This was significant by ANOVA. Notably, 36.7% (11/30) recipients of two-dose Pfizer and 42.9% (15/35) recipients of two-dose Moderna vaccines did not have detectable neutralization of at least one of the B.1.351 variants.	B.1.351.2, B.1.351, B.1.351.3	Garcia-Beltran et al. (2021)	895	C	T	0.64
p.L18F	vaccine neutralization efficacy	B.1.351 pseudotyped VSV was tested for neutralization in a clonal HEK-293T ACE2 TMPRSS2 cell line optimized for highly efficient S-mediated infection. Only 1 out of 12 serum samples from a cohort of Argentinian recipients of the Gamaleya Sputnik V Ad26 / Ad5 vaccine showed effective neutralization (IC90) at full serum strength (average realtive decrease was 6.1x vs wild type).	B.1.351.2, B.1.351, B.1.351.3	Ikegame et al. (2021)	895	C	T	0.64
p.L18F	vaccine neutralization efficacy	Relative to B.1.1.117, PRNT50 line virus neutralizating antibody activity assay of B.1.351 showed extasciitilde11x reduction in 13 vacinees's sera collected through 41 days after vaccination. Neutralization by a placebo control group of 6 naturally infected patients showed a smaller extasciitilde8x drop (starting from a extasciitilde50% higher PRNT50 value than vacinees for B.1.1.117 neutralization). Serum samples obtained from 13 ChAdOx1 nCoV-19 vaccine recipients without SARS-CoV-2 infection through 41 days after vaccination showed extasciitilde4x reduction in neutralization (ID50) for full B.1.351 pseudotype HIV-1 virus compared to D614G alone. This RBD variant combination's neutralization by a placebo control group of 6 naturally infected patients showed a slightly higher 4.6x drop (though with D614G starting at a 1.7x higher titre than vaccinee sera).	B.1.351.2, B.1.351, B.1.351.3	Madhi et al. (2021)	895	C	T	0.64

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.L18F	vaccine neutralization efficacy	The sera of 16 individuals with time course collection was evaluated against VSV pseudotypes: while BD614G and B.1.1.7 were neutralized earlier, the anti-B.1.351 response was negative up to week 3, and became detectable at week 4 (1 week after booster dose), at a level lower than the two other viruses (extasciitilde10x vs D614G) through week 6, the last timepoint measured. Three vaccinees never showed detectable neutralization to B.1.351 even after second dose.	B.1.351.2, B.1.351, B.1.351.3	Planas et al. (2021)	895	C	T	0.64
p.L18F	vaccine neutralization efficacy	In a randomized phase 2a-b control trial of the Novavax (NVX-CoV2373) vaccine in South Africa, where B.1.351 virus dominates, efficacy was 60.1% (95% CI, 19.9 to 80.1) in HIV-negative and initially SARS-CoV-2 seronegative participants using the primary endpoint of laboratory-confirmed symptomatic Covid-19 at 7 days or more after the second dose among participants.	B.1.351.2, B.1.351, B.1.351.3	Shinde et al. (2021)	895	C	T	0.64
p.L18F	vaccine neutralization efficacy	PBMCs of Pfizer/BioNTech BNT162b2 (n	B.1.351.2, B.1.351, B.1.351.3	Tarke et al. (2021)	895	C	T	0.64
p.L18F	vaccine neutralization efficacy	[Contrary to how this paper has been cited, Voysey et al. do NOT show evidence of decreased effectiveness of ChAdOx1 (AstraZeneca) against the South African B.1.351 lineage. Insufficient numbers reaching the primary study endpoint were available in that arm of the vaccine study to report any statistics from the South African participants. Additionally, the study period of the paper ended in November 2020, while the earliest reported case of this lineage is October (covariants.org), only becoming dominant by mid-November.]	B.1.351.2, B.1.351, B.1.351.3	Voysey et al. (2021)	895	C	T	0.64
p.L18F	vaccine neutralization efficacy	No significant difference in T-cell response to B.1.351 was observed (vs. ancestral) in blood drawn from 28 participants received the Pfizer-BioNTech vaccine and 2 received the Moderna vaccine.	B.1.351.2, B.1.351, B.1.351.3	Woldemeskel et al. (2021)	895	C	T	0.64

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.L18F	vaccinee plasma binding	1.30x increase in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in previously non-seroconverted subjects. Compare to varied binding in full Spike variant complements for major lineages containing this variant subset: 1.28x increase (B.1.351 aka Beta), and 1.14x decrease (P.1 aka Gamma). 1.47x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in post-infection vaccinees. Compare to varied binding in full Spike variant complements for major lineages containing this variant subset: 1.17x increase (B.1.351 aka Beta), and 1.47x decrease (P.1 aka Gamma).	B.1.351.2, B.1.351, B.1.351.3	Gong et al. (2021)	895	C	T	0.64
p.L18F	virion structure	The L18F and D80A of the B.1.351 lineage lead to reconfiguration of the N-terminal segment despite the disulfide between Cys16 and Cys136 that partly anchors the N-terminal peptide. The most consequential changes are probably from the triple residue deletion... which causes a shift of the nearby loop 144-155 and must also reconfigure the adjacent disorder loop (residues 246-260), both of which form part of the neutralizing epitopes...bringing large changes in the antigenic surface in this region.	B.1.351.2, B.1.351, B.1.351.3	Cai et al. (2021)	895	C	T	0.64
p.K417N	ACE2 receptor binding affinity	The K417N mutation decreased the affinity extasciitilde4 fold, mainly by decreasing the k(on) but also by increasing the k(off) as measured by surface plasmon resonance.	B.1.351.2, B.1.351, B.1.351.3	Barton et al. (2021)	912	G	T	1.0
p.K417N	ACE2 receptor binding affinity	The affinity of the B.1.351 RBD variants for ACE2 increased by 3.7 fold as measured by surface plasmon resonance relative to wild type RBD by increasing the k(on) and decreasing the k(off) rate constants.	B.1.351.2, B.1.351, B.1.351.3	Barton et al. (2021)	912	G	T	1.0
p.K417N	ACE2 receptor binding affinity	This combination showed extasciitilde3x increase binding to ACE2 vs wild type, about half that of the B.1.1.7 lineage, suggesting that the K417N mutation is slightly detrimental to ACE2 binding, probably as a result of disrupting the salt bridge formed with ACE2 residue D30	B.1.351.2, B.1.351, B.1.351.3	Collier et al. (2021)	912	G	T	1.0
p.K417N	ACE2 receptor binding affinity	Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant showed a 1.5x decrease in binding (KD) relative to D614G.	B.1.351.2, B.1.351, B.1.351.3	Gong et al. (2021)	912	G	T	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.K417N	ACE2 receptor binding affinity	RBD containing the N501Y mutation results in 9-fold stronger binding to the hACE2 receptor than wild type RBD. The E484K mutation does not significantly influence the affinity for the receptor, while K417N attenuates affinity. As a result, RBD from B.1.351 containing all three mutations binds 3-fold stronger to hACE2 than wild type RBD but 3-fold weaker than N501Y.	B.1.351.2, B.1.351, B.1.351.3	Laffeber et al. (2021)	912	G	T	1.0
p.K417N	ACE2 receptor binding affinity	Studying the key covariants in lineage of concern 501Y.V2, observed about 2-fold increase in ACE2 binding vs wildtype, but greatly decreased mAb binding, suggesting evolutionary optimum tension between immune evasion and ACE2 binding affinity as the N501Y variant alone has 10x increase in affinity but no effect on tested mAb binding.	B.1.351.2, B.1.351, B.1.351.3	Liu et al. (2021)	912	G	T	1.0
p.K417N	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.1.351. We observed an increase (relative to D614G) in binding of soluble ACE2 to B.1.351, and to a much gearter extent to B.1.1.7, which both carry the N501Y mutation (see Fig 3).	B.1.351.2, B.1.351, B.1.351.3	Planas et al. (2021)	912	G	T	1.0
p.K417N	ACE2 receptor binding affinity	Using Mircoscale Thermopheresis, the B.1.351 variant harboring three mutations, binds ACE2 at nearly five-fold greater affinity than the original SARS-COV-2 RBD (Kd 87.6, vs 402.5 nM).	B.1.351.2, B.1.351, B.1.351.3	Ramanathan et al. (2021)	912	G	T	1.0
p.K417N	ACE2 receptor binding affinity	Reported 3-fold decrease in affinity compared to wild-type RBD on the cell surface (Kd	B.1.351.2, B.1.351, B.1.351.3	Tian et al. (2021)	912	G	T	1.0
p.K417N	ACE2 receptor binding affinity	Reported slight increase in affinity compared to wild-type RBD on the cell surface (Kd	B.1.351.2, B.1.351, B.1.351.3	Tian et al. (2021)	912	G	T	1.0
p.K417N	ACE2 receptor binding affinity	The affinity of ACE2 for this mutation combination was twice as high as for wild type. Having in mind that the affinity of SARS-CoV-2 for ACE2 is only 4-fold higher compared to SARS-CoV-1, this factor of 2 is expected to be biologically significant.	B.1.351.2, B.1.351, B.1.351.3	Vogel et al. (2021)	912	G	T	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.K417N	CD8 plus T cell response	Encouragingly, we find that the majority of T cell responses in recipients of two doses of the BNT162b2 vaccine are generated by epitopes that are invariant between the [wildtype] and two of the current variants of concern (B.1.1.7 and B.1.351). In over 90% of two dose mRNA vaccinees, heterotypic neutralizing titres (NT50) against B.1.1.7 and B.1.351 remain comfortably above the level associated with immune protection in recent vaccine trials. However, in over 50% of convalescent COVID-19 individuals and recipients of a only a single dose of mRNA vaccine – heterotypic neutralization dropped to negligible levels, particularly against B.1.351.	B.1.351.2, B.1.351, B.1.351.3	Skelly et al. (2021)	912	G	T	1.0
p.K417N	antibody epitope effects	Ablates Class 1 receptor-binding-motif targeting antibodies COV2-2050, 1B07, COVOX-384, and S2H58.	B.1.351.2, B.1.351, B.1.351.3	Chen et al. (2021)	912	G	T	1.0
p.K417N	antibody epitope effects	Abolished neutralization by mAbs CQ026 and CQ038, greatly diminished neutralization by CQ012 and CQ046.	B.1.351.2, B.1.351, B.1.351.3	Hu et al. (2021)	912	G	T	1.0
p.K417N	antibody epitope effects	Anti-NTD CV1 mAb isolated from an early pandemic case was unable to neutralize either partial B.1.351 variant pseudovirus used (A701V or L242del). The neutralization potency of mAb CV30, which contacts K417 and N501 but not E484, was extasciitilde10-fold weaker toward both B.1.351 variants. The neutralization potency of anti-RBD mAb CV3-1 was 3-4-fold less potent against the B.1.351 variants, while anti-RBD mAb CV2-75 was modestly less effective.	B.1.351.2, B.1.351, B.1.351.3	Stamatatos et al. (2021)	912	G	T	1.0
p.K417N	antibody epitope effects	Anti-NTD CV1 mAb isolated from an early pandemic case was unable to neutralize either partial B.1.351 variant pseudovirus used (A701V or L242del). The neutralization potency of mAb CV30, which contacts K417 and N501 but not E484, was extasciitilde10-fold weaker toward both B.1.351 variants. The neutralization potency of anti-RBD mAb CV3-1 was 3-4-fold less potent against the B.1.351 variants, while anti-RBD mAb CV2-75 was modestly less effective.	B.1.351.2, B.1.351, B.1.351.3	Stamatatos et al. (2021)	912	G	T	1.0
p.K417N	antibody epitope effects	>20% (ELISA significance threshold) drop in antibody binding (ELISA) by this variant against IgG1 monoclonal antibody ab1.	B.1.351.2, B.1.351, B.1.351.3	Sun et al. (2021)	912	G	T	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.K417N	antibody epitope effects	Complete loss of binding in ELISA by the variant against monoclonal antibodies ab8 and IgG1 ab1. Complete loss for the same antibodies was also observed against S1 pseudotyped and full Spike protein trimers with both B.1.351 and P.1 lineage variants, with slight binding signal for P.1 against IgG1 at the highest concentration tested (1uM). Complete loss of neutralization by these two antibodies was also observed.	B.1.351.2, B.1.351, B.1.351.3	Sun et al. (2021)	912	G	T	1.0
p.K417N	antibody epitope effects	5 antibodies tested were less potent against K417N by ten-fold or more (class 1 mAbs)	B.1.351.2, B.1.351, B.1.351.3	Wang et al. (2021)	912	G	T	1.0
p.K417N	antibody epitope effects	Pseudotyped virus model ablates binding by RBD-directed mAbs CB6 and 910-30 (targeting the inner side of the RBD). Pseudotyped virus model impairs binding by RBD-directed mAbs 4-20 and REGN10933.	B.1.351.2, B.1.351, B.1.351.3	Wang et al. (2021)	912	G	T	1.0
p.K417N	antibody epitope effects	Ablates ELISA test binding for class 1 (Spike 'up' conformation only, RBD targeting) monoclonal antibody CA1 on 501Y.V2 ("South African") lineage background Ablates ELISA test binding for class 1 (Spike 'up' conformation only, RBD targeting) monoclonal antibody LyCoV016 (also known as CB6 or JS016) on 501Y.V2 ("South African") lineage background Ablates ELISA test binding for class 1 (Spike 'up' conformation only, RBD targeting) monoclonal antibody CC12.1 on 501Y.V2 ("South African") lineage background Ablates ELISA test binding for class 2 (Spike 'up' or 'down' conformation, RBD targeting) monoclonal antibody BD23 on 501Y.V2 ("South African") lineage background Ablates ELISA test binding for class 2 (Spike 'up' or 'down' conformation, RBD targeting) monoclonal antibody C119 (also known as CB6 or JS016) on 501Y.V2 ("South African") lineage background Ablates ELISA test binding for class 2 (Spike 'up' or 'down' conformation, RBD targeting) monoclonal antibody P2B-2F6 on 501Y.V2 ("South African") lineage background	B.1.351.2, B.1.351, B.1.351.3	Wibmer et al. (2021)	912	G	T	1.0
p.K417N	convalescent plasma binding	2.16x increase in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset.	B.1.351.2, B.1.351, B.1.351.3	Gong et al. (2021)	912	G	T	1.0
p.K417N	convalescent plasma escape	Average extasciitilde10-fold reduction in neutralization efficacy in convalescent sera of 16 health workers infected in Spring 2020.	B.1.351.2, B.1.351, B.1.351.3	Alenquer et al. (2021)	912	G	T	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.K417N	convalescent plasma escape	The 501Y.V2 to first wave IC50 ratio ranged from 6 to 200-fold. Averaging across all 7 participant convalescent sera highlighted the dramatic decrease in sensitivity to neutralization of authentic 501Y.V2 variants. PG: I'm purposefully ignoring D614G and A701V as contributors	B.1.351.2, B.1.351, B.1.351.3	Cele et al. (2021)	912	G	T	1.0
p.K417N	convalescent plasma escape	In 19 convalescent human sera extasciitilde1mo post infection, Two-tailed Wilcoxon matched-pairs signed-rank test shows mild resistence P	B.1.351.2, B.1.351, B.1.351.3	Chen et al. (2021)	912	G	T	1.0
p.K417N	convalescent plasma escape	In 19 convalescent human sera extasciitilde1mo post infection had mild to moderate resistence against most samples	B.1.351.2, B.1.351, B.1.351.3	Chen et al. (2021)	912	G	T	1.0
p.K417N	convalescent plasma escape	Neutralizing antibody titers of 18 samples (90%) decreased against this B.1.351 pseudotyped virus below an ID50 threshold of 40 (sera collected extasciitilde8mo post Jan 2020 first wave in China).	B.1.351.2, B.1.351, B.1.351.3	Hu et al. (2021)	912	G	T	1.0
p.K417N	convalescent plasma escape	extasciitilde7x reduction in neutralization by key B.1.351 lineage RBD variant combination in sera collected from cohort of 10 with severe disease 21 to 63 days post-onset. Two of the cohort showed no neutralization against this variant.	B.1.351.2, B.1.351, B.1.351.3	Kuzmina et al. (2021)	912	G	T	1.0
p.K417N	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 had mean extasciitilde6x reduction in neutralizing titers, and 40% of the samples lacked any activity against B.1.351.	B.1.351.2, B.1.351, B.1.351.3	Planas et al. (2021)	912	G	T	1.0
p.K417N	convalescent plasma escape	In over 90% of two dose mRNA vaccinees, heterotypic neutralizing titres (NT50) against B.1.1.7 and B.1.351 remain comfortably above the level associated with immune protection in recent vaccine trials. However, in over 50% of convalescent COVID-19 individuals (5/9) and recipients of a only a single dose of mRNA vaccine (10/11) – heterotypic neutralization dropped to negligible levels, particularly against B.1.351.	B.1.351.2, B.1.351, B.1.351.3	Skelly et al. (2021)	912	G	T	1.0
p.K417N	convalescent plasma escape	Using convalescent sera from 15 early pandemic patients (Seattle Flu Study), mean 220 days post symptom onset (IQR 125-269, and three asymptomatic cases) with 27% WHO disease severity scale 3, one third (5/15) of sera neutralized this B.1.351 pseudotype and only three had ID50 titers above 100. Only two of the 15 sera achieved 80% neutralization.	B.1.351.2, B.1.351, B.1.351.3	Stamatatos et al. (2021)	912	G	T	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.K417N	convalescent plasma escape	Using convalescent sera from 15 early pandemic patients (Seattle Flu Study), mean 220 days post symptom onset (IQR 125-269, and three asymptomatic cases) with 27% WHO disease severity scale 3, 7 of 15 neutralized this B.1.351 pseudotype that includes the L242del, and only one had titers above 100. Only one of the 15 sera achieved 80% neutralization. [compare to 5 and 1 for pseudotype without the deletion]	B.1.351.2, B.1.351, B.1.351.3	Stamatatos et al. (2021)	912	G	T	1.0
p.K417N	convalescent plasma escape	Demonstrate (via competitive assays in human and mouse) immune escape from polyclonal antibodies induced by vaccination or infection, comparable to what was previously shown with monoclonal antibodies for N501Y and more importantly for E484K. Even though viral mutations may more strongly affect monoclonal antibodies than sera activity, the latter may also be reduced as confirmed here.	B.1.351.2, B.1.351, B.1.351.3	Vogel et al. (2021)	912	G	T	1.0
p.K417N	convalescent plasma escape	27% of 44 early pandemic exposure convalescent plasma/sera lose all activity against a RBD triple mutant pseudovirus (RBD mutatants of the 501Y.V2 "South African" lineage), while only 23% retained high titres	B.1.351.2, B.1.351, B.1.351.3	Wibmer et al. (2021)	912	G	T	1.0
p.K417N	convalescent plasma escape	Nearly half (21 of 44, 48%) of early pandemic exposure convalescent plasma/sera failed to neutralize the 501Y.V2 ("South African") lineage pseudovirus construct Only 3 of 44 convascent sera (those with the highest titer, which correlated direectly with initial infection severity) had high neutralization against this 501Y.V2 PG: note that lineage variant R246I was excluded from the text in reference to these sera assays, not sure if that was an oversight.	B.1.351.2, B.1.351, B.1.351.3	Wibmer et al. (2021)	912	G	T	1.0
p.K417N	gene expression increase	Experimentally, Spike gene expression increased 0.1 fold	B.1.351.2, B.1.351, B.1.351.3	Starr et al. (2020)	912	G	T	1.0
p.K417N	humoral response durability	In a prospective study of 107 hospitalized patients, decrease of IgG rates and serological assays becoming negative did not imply loss of neutralizing capacity. Our results indicate a sustained humoral response against the ancestral strain and the D614G, B.1.1.7 and P.1 variants for at least 6 months (last of two samples taken) in patients previously hospitalized for COVID-19. A weaker protection was however observed for the B.1.351 variant.	B.1.351.2, B.1.351, B.1.351.3	Betton et al. (2020)	912	G	T	1.0
p.K417N	monoclonal antibody serial passage escape	Escape mutation against monoclonal antibody LY-CoV016	B.1.351.2, B.1.351, B.1.351.3	Starr et al. (2021)	912	G	T	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.K417N	monoclonal antibody serial passage escape	In vitro selection against class 1 (Spike 'up' conformation) monoclonal antibody C682, and to a lesser extent C614 and C660	B.1.351.2, B.1.351, B.1.351.3	Wang et al. (2021)	912	G	T	1.0
p.K417N	outcome hazard ratio	On average across 7 European countries studied, using B.1.351 defining mutations: Significant shift to infection in those without pre-existing conditions (79.6% vs 89% for non-VOC cases). Significant increase in hospitalization rate (19.3% vs 7.5% for non-VOC cases). Significant increase in ICU rate (2.3% vs 0.6% for non-VOC cases). PG: seems to be different notations around the LAL deletion, using the minimal shared definition to catch as many as possible.	B.1.351.2, B.1.351, B.1.351.3	Funk et al. (2021)	912	G	T	1.0
p.K417N	pharmaceutical effectiveness	COR-101 lost extasciitilde6x binding against this isolated mutation. Estesevimab lost extasciitilde100x binding against this isolated mutation.	B.1.351.2, B.1.351, B.1.351.3	Engelhart et al. (2021)	912	G	T	1.0
p.K417N	pharmaceutical effectiveness	Tixagevimab, Regdanvimab and COR-101 display reduced binding affinity to virus pseudotyped as RBD from B.1.351.	B.1.351.2, B.1.351, B.1.351.3	Engelhart et al. (2021)	912	G	T	1.0
p.K417N	pharmaceutical effectiveness	Bamlanivimab (LY-CoV555) lost extasciitilde32x binding against this double mutation. COR-101 lost extasciitilde160x binding against this double mutation. Casirivimab lost extasciitilde16x binding against this double mutation. Estesevimab lost extasciitilde32x binding against this double mutation. Regdanvimab lost extasciitilde4x binding against this double mutation. Tixagevimab lost extasciitilde12x binding against this double mutation.	B.1.351.2, B.1.351, B.1.351.3	Engelhart et al. (2021)	912	G	T	1.0
p.K417N	pharmaceutical effectiveness	COR-101 lost extasciitilde20x binding against this double mutation. Estesevimab lost extasciitilde16x binding against this double mutation. Regdanvimab lost extasciitilde6x binding against this double mutation. M396 lost extasciitilde10x binding against this double mutation.	B.1.351.2, B.1.351, B.1.351.3	Engelhart et al. (2021)	912	G	T	1.0
p.K417N	pharmaceutical effectiveness	This mutated version of RBD completely abolishes the binding to a therapeutic antibody, Bamlanivimab, in vitro.	B.1.351.2, B.1.351, B.1.351.3	Liu et al. (2021)	912	G	T	1.0
p.K417N	reinfection	4 health care workers in the 20's and 30's with no underlying conditions and seropositivity or confirmed 2020 SARS-CoV-2 infections were confirmed to have B.1.351 infection during a Februrary 2021 hospital outbreak in Luxembourg. Symptoms were mostly mild on first infection, and milder on second infection.	B.1.351.2, B.1.351, B.1.351.3	Staub et al. (2021)	912	G	T	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.K417N	reinfection	Hamsters re-infected with B.1.351 virus after seroversion from previous infection with a lineage A virus did not transmit virus to naive sentinels via direct contact transmission, in contrast to the non-seroconverted animals. They had little infectious virus and no pathology in the lungs. Initial infection with SARS-CoV-2 lineage A does not prevent heterologous reinfection with B.1.351, but prevents disease and onward transmission.	B.1.351.2, B.1.351, B.1.351.3	Yinda et al. (2021)	912	G	T	1.0
p.K417N	symptom prevalence	Inoculation with the B.1.351 isolate resulted in lower clinical scores in 6 rhesus macaques that correlated with lower virus titers in the lungs, less severe histologic lung lesions and less viral antigen detected in the lungs. Our comparative pathogenicity study suggests that ongoing circulation under diverse evolutionary pressure favors transmissibility and immune evasion rather than an increase in intrinsic pathogenicity.	B.1.351.2, B.1.351, B.1.351.3	Munster et al. (2021)	912	G	T	1.0
p.K417N	tissue specific neutralization	The nasal mucosa of Pfizer vaccinees with time course collection was evaluated against VSV pseudotypes: while B.1.1.7 and D614G showed neutralization by nasal swab from only one different previously infected vacinee neutralizing at weeks 3 and 6, B.1.351 showed zero neutralization at either time point in any sample (and relatively impaired serum neutralization).	B.1.351.2, B.1.351, B.1.351.3	Planas et al. (2021)	912	G	T	1.0
p.K417N	trafficking	The entry efficiencies of Spike pseudotyped viruses bearing N501Y Variant 2 (B.1.351) 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.1.351.2, B.1.351, B.1.351.3	Hu et al. (2021)	912	G	T	1.0
p.K417N	trafficking	extasciitilde2x more infectivity than D614G alone in HEK293T-ACE2 cells 48h post-transduction.	B.1.351.2, B.1.351, B.1.351.3	Kuzmina et al. (2021)	912	G	T	1.0
p.K417N	trafficking	Approximately as infective as D614G alone in HEK293T-ACE2 cells 48h post-transduction (extasciitildeadditive effects of the individual variants).	B.1.351.2, B.1.351, B.1.351.3	Kuzmina et al. (2021)	912	G	T	1.0
p.K417N	trafficking	extasciitilde13x more infective as D614G alone in HEK293T-ACE2 cells 48h post-transduction.	B.1.351.2, B.1.351, B.1.351.3	Kuzmina et al. (2021)	912	G	T	1.0
p.K417N	trafficking	extasciitilde9x more infectivity than D614G alone in HEK293T-ACE2 cells 48h post-transduction (no synergy as level approx. that of N501Y alone).	B.1.351.2, B.1.351, B.1.351.3	Kuzmina et al. (2021)	912	G	T	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.K417N	trafficking	Lentiviral pseudotyped with this individual mutation from B.1.351 was tested on ACE2.293T cells. Luciferase activity was measured two days postinfection, showing mild decrease in infection rate amongst the cells, suggesting that this mutation does not contributing to cell entry fitness.	B.1.351.2, B.1.351, B.1.351.3	Tada et al. (2021)	912	G	T	1.0
p.K417N	transmissibility	Assuming complete cross-protection, we estimate 501Y.V2/B.1.351 was 1.50 (95% CrI: 1.20-2.13) times as transmissible than previously circulating variants. Assuming instead that 501Y.V2 is identically transmissible, the new variant evades 21% (95% CrI: 11-36%) of previously acquired immunity. Reality may lie between these extremes, with an intermediate increase in transmissibility and mildly imperfect cross-protection from past exposure.	B.1.351.2, B.1.351, B.1.351.3	Pearson et al. (2021)	912	G	T	1.0
p.K417N	transmissibility	36,590 variant-specific RT-PCR tests were performed on samples collected between April 12 and May 7, 2021 in France to compare variant spread. Compared to January to March 2021, B.1.351 variant had a significant transmission advantage over B.1.1.7 in some regions (15.1 to 16.1% in Île-de-France and 16.1 to 18.8% in Hauts-de-France). This shift in transmission advantage is consistent with the immune evasion abilities of B.1.351 and the high levels of immunization in these regions.	B.1.351.2, B.1.351, B.1.351.3	Roquebert et al. (2021)	912	G	T	1.0
p.K417N	vaccine neutralization efficacy	The Janssen single dose vaccine showed 72% efficacy at preventing moderate and severe disease, which was reduced to 57% in South Africa, where 92.6% of infections are estimated to have been B.1.351. 100% reduction in hospitalization risk remains across variants after 28 days post-vaccination.	B.1.351.2, B.1.351, B.1.351.3	nan	912	G	T	1.0
p.K417N	vaccine neutralization efficacy	In an Ontario long term care facility, cumulatively, weaker BNT162b2 vaccine stimulation, age/comorbidities, produced a 130-fold reduction in apparent neutralization titers in mean 88yo LTCH residents against Beta (B.1.351), relative to staff vaccinees against D614G wild type. 37.9% of 116 two-dose-mRNA-vaccinated residents had undetectable neutralizing antibodies to B.1.351. mRNA-1273 vaccinee sera displayed extasciitilde2 better neutralization than BNT162b2. [common defining B.1.351 mutations noted, as the manuscript does not provide details]	B.1.351.2, B.1.351, B.1.351.3	Abe et al. (2021)	912	G	T	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.K417N	vaccine neutralization efficacy	Using B.1.351 defining mutations for Spike, observed 4x average decrease in neutralization efficiency (but still relevant titres) for sera from 10 BNT162b2 vaccinees 12 days after second dose, but only one relevant titre 12 days after first dose. Compares unfavorably to wild type or B.1.1.7 titres.	B.1.351.2, B.1.351, B.1.351.3	Alenquer et al. (2021)	912	G	T	1.0
p.K417N	vaccine neutralization efficacy	Observed 1.4-fold reduction in neutralization efficiency of Pfizer vaccinee sera (collected 14 days after second dose) against pseudotype B.1.351 key variants lentivirus. Compare to 8.8-fold reduction against cultured B.1.351 virus.	B.1.351.2, B.1.351, B.1.351.3	Bates et al. (2021)	912	G	T	1.0
p.K417N	vaccine neutralization efficacy	Observed 8.8-fold reduction in neutralization efficiency of Pfizer vaccinee sera (collected 14 days after second dose) against cultured B.1.351 sample. Contrast this with 1.4-fold reduction for just the pseudovirus combination of "key" B.1.351 mutations K417N+E484K+N501Y. WA1 and B.1.351 FRNT50 titers correlated weakly at the individual level, with some individual's serum potently neutralizing WA1 while having FRNT50 for B.1.351 below the assay limit of detection (1:20).	B.1.351.2, B.1.351, B.1.351.3	Bates et al. (2021)	912	G	T	1.0
p.K417N	vaccine neutralization efficacy	Neutralization efficiency (ID50) against B.1.1.351-v3 reduced 8.4x relative to D614G wildtype using pseudotyped VSV assay on 8 Moderna vaccinee sera one week post-booster.	B.1.351.2, B.1.351, B.1.351.3	Choi et al. (2021)	912	G	T	1.0
p.K417N	vaccine neutralization efficacy	Neutralization efficiency (ID50) against B.1.1.351-v2 reduced 7.3x relative to D614G wildtype using pseudotyped VSV assay on 8 Moderna vaccinee sera one week post-booster.	B.1.351.2, B.1.351, B.1.351.3	Choi et al. (2021)	912	G	T	1.0
p.K417N	vaccine neutralization efficacy	ELISpot assays show T cell neutralization reduced by 29.8% in this B.1.351 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.1.351.2, B.1.351, B.1.351.3	Gallagher et al. (2021)	912	G	T	1.0
p.K417N	vaccine neutralization efficacy	Pseudotyped B.1.351 v1 virus has reduced neutralization activity vs wild type: 34.5x (30 sera Pfizer median 9 days post 2nd dose) and 27.7x (35 sera Moderna median 18 days post 2nd dose). This was significant by ANOVA. Notably, 36.7% (11/30) recipients of two-dose Pfizer and 42.9% (15/35) recipients of two-dose Moderna vaccines did not have detectable neutralization of at least one of the B.1.351 variants.	B.1.351.2, B.1.351, B.1.351.3	Garcia-Beltran et al. (2021)	912	G	T	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.K417N	vaccine neutralization efficacy	Pseudotyped B.1.351 v2 virus has reduced neutralization activity vs wild type: 41.2x (30 sera Pfizer median 9 days post 2nd dose) and 20.8x (35 sera Moderna median 18 days post 2nd dose). This was significant by ANOVA. Notably, 36.7% (11/30) recipients of two-dose Pfizer and 42.9% (15/35) recipients of two-dose Moderna vaccines did not have detectable neutralization of at least one of the B.1.351 variants.	B.1.351.2, B.1.351, B.1.351.3	Garcia-Beltran et al. (2021)	912	G	T	1.0
p.K417N	vaccine neutralization efficacy	B.1.351 pseudotyped VSV was tested for neutralization in a clonal HEK-293T ACE2 TMPRSS2 cell line optimized for highly efficient S-mediated infection. Only 1 out of 12 serum samples from a cohort of Argentinian recipients of the Gamaleya Sputnik V Ad26 / Ad5 vaccine showed effective neutralization (IC90) at full serum strength (average realtive decrease was 6.1x vs wild type).	B.1.351.2, B.1.351, B.1.351.3	Ikegame et al. (2021)	912	G	T	1.0
p.K417N	vaccine neutralization efficacy	This variant showed only minor in Pfizer sera (one or two dose) neutralization efficiency vs D614G (using lentivirus pseudotype).	B.1.351.2, B.1.351, B.1.351.3	Kuzmina et al. (2021)	912	G	T	1.0
p.K417N	vaccine neutralization efficacy	This variant showed extasciitilde10x decrease in Pfizer sera (3 weeks post-first dose: n	B.1.351.2, B.1.351, B.1.351.3	Kuzmina et al. (2021)	912	G	T	1.0
p.K417N	vaccine neutralization efficacy	This variant of key B.1.351 lineage mutations showed extasciitilde10x decrease in Pfizer sera (3 weeks post-first dose: n	B.1.351.2, B.1.351, B.1.351.3	Kuzmina et al. (2021)	912	G	T	1.0
p.K417N	vaccine neutralization efficacy	This variant showed >5x decrease in Pfizer sera (3 weeks post-first dose: n	B.1.351.2, B.1.351, B.1.351.3	Kuzmina et al. (2021)	912	G	T	1.0
p.K417N	vaccine neutralization efficacy	In post-vaccination sera from individuals who received one (3 weeks post-first dose: n	B.1.351.2, B.1.351, B.1.351.3	Kuzmina et al. (2021)	912	G	T	1.0
p.K417N	vaccine neutralization efficacy	Vaccine plasma neutralization of B.1.351-spike virus was nominally robust but lower (extasciitilde3x) than other variants of concern.	B.1.351.2, B.1.351, B.1.351.3	Liu et al. (2021)	912	G	T	1.0
p.K417N	vaccine neutralization efficacy	A two-dose regimen of (AstraZeneca) ChAdOx1-nCoV19 did not show protection against mild-moderate Covid-19 due to B.1.351 variant, however, vaccine efficacy against severe Covid-19 is undetermined.	B.1.351.2, B.1.351, B.1.351.3	Madhi et al. (2021)	912	G	T	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.K417N	vaccine neutralization efficacy	In a multicenter, double-blind, randomized, controlled trial to assess the safety and efficacy of the ChAdOx1 nCoV-19 vaccine (AZD1222) with enrollment June 24 and November 9, 2020 from extasciitilde2000 HIV-negative 18-64 year olds (1:1 placebo to treatment), incidence of serious adverse events 14 or more days post- 2nd dose was balanced between the vaccine and placebo groups. A two-dose regimen of the ChAdOx1 nCoV-19 vaccine did not show protection against mild-to-moderate Covid-19 due to the B.1.351 variant. Serum samples obtained from 13 ChAdOx1 nCoV-19 vaccine recipients without SARS-CoV-2 infection through 41 days after vaccination showed 3.5x reduction in neutralization (ID50) for B.1.351 RBD pseudotype HIB-1 virus compared to D614G alone. This RBD variant combination's neutralization by a placebo control group of 6 naturally infected patients showed a similar 3.2x drop (though with D614G starting at a 1.7x higher titre than vaccinee sera).	B.1.351.2, B.1.351, B.1.351.3	Madhi et al. (2021)	912	G	T	1.0
p.K417N	vaccine neutralization efficacy	Relative to B.1.1.117, PRNT50 line virus neutralizating antibody activity assay of B.1.351 showed extasciitilde11x reduction in 13 vacinees's sera collected through 41 days after vaccination. Neutralization by a placebo control group of 6 naturally infected patients showed a smaller extasciitilde8x drop (starting from a extasciitilde50% higher PRNT50 value than vacinees for B.1.1.117 neutralization). Serum samples obtained from 13 ChAdOx1 nCoV-19 vaccine recipients without SARS-CoV-2 infection through 41 days after vaccination showed extasciitilde4x reduction in neutralization (ID50) for full B.1.351 pseudotype HIV-1 virus compared to D614G alone. This RBD variant combination's neutralization by a placebo control group of 6 naturally infected patients showed a slightly higher 4.6x drop (though with D614G starting at a 1.7x higher titre than vaccinee sera).	B.1.351.2, B.1.351, B.1.351.3	Madhi et al. (2021)	912	G	T	1.0
p.K417N	vaccine neutralization efficacy	The Novavax vaccine, which achieved 95.6% efficacy against previous SARS-CoV-2 strains, had reduced efficacy of 60% in South Africa, where 92.6% of infections are estimated to have been B.1.351.	B.1.351.2, B.1.351, B.1.351.3	Novavax (2021)	912	G	T	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.K417N	vaccine neutralization efficacy	Detectable antibodies against B.1.351 at various time points using pseudotyped lentivirus neutralization in Moderna vaccinee cohort: Day 29 8%, Day 43 100%, Day 119 71%, Day 209 54%. Detectable antibodies against B.1.351 at various time points using live virus FRNT neutralization in Moderna vaccinee cohort: Day 29 8%, Day 43 100%, Day 119 79%, Day 209 58%. Detectable antibodies against B.1.351 at various time points using ACE2 blocking assay in Moderna vaccinee cohort: Day 29 63%, Day 43 100%, Day 119 71%, Day 209 79%. Decreased neutralization on some assays was seen especially in those vaccinees tested that were 71+.	B.1.351.2, B.1.351, B.1.351.3	Pegu et al (2021)	912	G	T	1.0
p.K417N	vaccine neutralization efficacy	The sera of 16 individuals with time course collection was evaluated against VSV pseudotypes: while BD614G and B.1.1.7 were neutralized earlier, the anti-B.1.351 response was negative up to week 3, and became detectable at week 4 (1 week after booster dose), at a level lower than the two other viruses (extasciitilde10x vs D614G) through week 6, the last timepoint measured. Three vaccinees never showed detectable neutralization to B.1.351 even after second dose.	B.1.351.2, B.1.351, B.1.351.3	Planas et al. (2021)	912	G	T	1.0
p.K417N	vaccine neutralization efficacy	In a randomized phase 2a-b control trial of the Novavax (NVX-CoV2373) vaccine in South Africa, where B.1.351 virus dominates, efficacy was 60.1% (95% CI, 19.9 to 80.1) in HIV-negative and initially SARS-CoV-2 seronegative participants using the primary endpoint of laboratory-confirmed symptomatic Covid-19 at 7 days or more after the second dose among participants.	B.1.351.2, B.1.351, B.1.351.3	Shinde et al. (2021)	912	G	T	1.0
p.K417N	vaccine neutralization efficacy	In sera collected from 15 early pandemic patients (Seattle Flu Study), mean 16 days post first dose with either Pfizer/BioNTech or Moderna vaccines, the median ID50 titers were extasciitilde3-fold lower against this B.1.351 pseudotyped virus relative to wild type. A single asymptomatic patient, who had no detectable RBD-specific IgG memory before vaccination, also did not elicit nAbs against the B.1.351 variant. [compare to extasciitilde10 fold with L242del] ID50 titres in non-infected mRNA vaccines more than two weeks post-booster were signficiant, but >100x weaker than in previously infected patients after first dose.	B.1.351.2, B.1.351, B.1.351.3	Stamatatos et al. (2021)	912	G	T	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.K417N	vaccine neutralization efficacy	In sera collected from 15 early pandemic patients (Seattle Flu Study), mean 16 days post first dose with either Pfizer/BioNTech or Moderna vaccines, the median ID50 titers were extasciitilde10-fold lower against this B.1.351 pseudotyped virus relative to wild type. A single asymptomatic patient, who had no detectable RBD-specific IgG memory before vaccination, also did not elicit nAbs against the B.1.351 variant. [compare to extasciitilde3 fold without the deletion] ID50 titres in non-infected mRNA vaccines more than two weeks post-booster were significant, but extasciitilde500x weaker than in previously infected patients after first dose.	B.1.351.2, B.1.351, B.1.351.3	Stamatatos et al. (2021)	912	G	T	1.0
p.K417N	vaccine neutralization efficacy	Pseudotyped viruses for B.1.351 was 3.4-fold resistant to neutralization by 6 BNT162b2 vaccine sera 28 days post-booster compared to wild type. Neutralization by 3 Moderna vaccine sera 28 days post-booster was 2.2-fold resistant. [Exact list of B.1.351 mutations used in these assays was not included in the preprint]	B.1.351.2, B.1.351, B.1.351.3	Tada et al. (2021)	912	G	T	1.0
p.K417N	vaccine neutralization efficacy	PBMCs of Pfizer/BioNTech BNT162b2 (n	B.1.351.2, B.1.351, B.1.351.3	Tarke et al. (2021)	912	G	T	1.0
p.K417N	vaccine neutralization efficacy	[Contrary to how this paper has been cited, Voysey et al. do NOT show evidence of decreased effectiveness of ChAdOx1 (AstraZeneca) against the South African B.1.351 lineage. Insufficient numbers reaching the primary study endpoint were available in that arm of the vaccine study to report any statistics from the South African participants. Additionally, the study period of the paper ended in November 2020, while the earliest reported case of this lineage is October (covariants.org), only becoming dominant by mid-November.]	B.1.351.2, B.1.351, B.1.351.3	Voysey et al. (2021)	912	G	T	1.0
p.K417N	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 significant (0.5 to 20-fold, but average extasciitilde2x) decrease in neutralization by vaccine plasma was observed.	B.1.351.2, B.1.351, B.1.351.3	Wang et al. (2021)	912	G	T	1.0
p.K417N	vaccine neutralization efficacy	No significant difference in T-cell response to B.1.351 was observed (vs. ancestral) in blood drawn from 28 participants received the Pfizer-BioNTech vaccine and 2 received the Moderna vaccine.	B.1.351.2, B.1.351, B.1.351.3	Woldemeskel et al. (2021)	912	G	T	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.K417N	vaccine neutralization efficacy	In Moderna vaccinee sera, 2.7x reduction in neutralization, and 6.4 for the full B.1.351 Spike mutation complement, but despite the observed decreases, titers in human vaccinee sera against the B.1.351 variant remained at clinically significant level of extasciitilde1/300.	B.1.351.2, B.1.351, B.1.351.3	Wu et al. (2021)	912	G	T	1.0
p.K417N	vaccine neutralization efficacy	Sera from healthcare workers (n	B.1.351.2, B.1.351, B.1.351.3	Zhou et al. (2021)	912	G	T	1.0
p.K417N	vaccinee plasma binding	1.76x increase in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in previously non-seroconverted subjects. 1.75x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in post-infection vaccinees.	B.1.351.2, B.1.351, B.1.351.3	Gong et al. (2021)	912	G	T	1.0
p.K417N	viral load	B.1.351 and P.1 samples showed average Ct cycle threshold of 22.2 vs 23 for wildtype (i.e. extasciitilde60% higher viral load) comparing 3360 and 22535 samples respectively.	B.1.351.2, B.1.351, B.1.351.3	Roquebert et al. (2021)	912	G	T	1.0
p.K417N	viral load	The 62 B.1.351 (a.k.a. N501Y.V2) variant cases in three Paris hospital labs had a extasciitilde2-fold viral load increase (extasciitilde1 Ct drop in both N and ORF1ab probes) compared to 332 ancestral lineage cases from the same time frame (2020-12-20 to 2021-02-26).	B.1.351.2, B.1.351, B.1.351.3	Teyssou et al. (2021)	912	G	T	1.0
p.K417N	virion structure	Estimated free energy change (ddG) for this variant is -0.86 kcal/mol (i.e. destabilizing relative to wild type)	B.1.351.2, B.1.351, B.1.351.3	Spratt et al. (2021)	912	G	T	1.0
p.D80A	ACE2 receptor binding affinity	Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant combination showed no change relative to D614G.	B.1.351.2, B.1.351, B.1.351.3	Gong et al. (2021)	895	A	C	1.0
p.D80A	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.1.351. We observed an increase (relative to D614G) in binding of soluble ACE2 to B.1.351, and to a much gearter extent to B.1.1.7, which both carry the N501Y mutation (see Fig 3).	B.1.351.2, B.1.351, B.1.351.3	Planas et al. (2021)	895	A	C	1.0
p.D80A	CD8 plus T cell response	One individual of 30 in the study, with HLA supertype HLA*A24:02, had a linear epitope that overlaps this variant of concern.	B.1.351.2, B.1.351, B.1.351.3	Redd et al. (2021)	895	A	C	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.D80A	CD8 plus T cell response	Encouragingly, we find that the majority of T cell responses in recipients of two doses of the BNT162b2 vaccine are generated by epitopes that are invariant between the [wildtype] and two of the current variants of concern (B.1.1.7 and B.1.351). In over 90% of two dose mRNA vaccinees, heterotypic neutralizing titres (NT50) against B.1.1.7 and B.1.351 remain comfortably above the level associated with immune protection in recent vaccine trials. However, in over 50% of convalescent COVID-19 individuals and recipients of a only a single dose of mRNA vaccine – heterotypic neutralization dropped to negligible levels, particularly against B.1.351.	B.1.351.2, B.1.351, B.1.351.3	Skelly et al. (2021)	895	A	C	1.0
p.D80A	antibody epitope effects	Anti-NTD CV1 mAb isolated from an early pandemic case was unable to neutralize either partial B.1.351 variant pseudovirus used (A701V or L242del). The neutralization potency of mAb CV30, which contacts K417 and N501 but not E484, was extasciitilde10-fold weaker toward both B.1.351 variants. The neutralization potency of anti-RBD mAb CV3-1 was 3-4-fold less potent against the B.1.351 variants, while anti-RBD mAb CV2-75 was modestly less effective.	B.1.351.2, B.1.351, B.1.351.3	Stamatatos et al. (2021)	895	A	C	1.0
p.D80A	antibody epitope effects	Anti-NTD CV1 mAb isolated from an early pandemic case was unable to neutralize either partial B.1.351 variant pseudovirus used (A701V or L242del). The neutralization potency of mAb CV30, which contacts K417 and N501 but not E484, was extasciitilde10-fold weaker toward both B.1.351 variants. The neutralization potency of anti-RBD mAb CV3-1 was 3-4-fold less potent against the B.1.351 variants, while anti-RBD mAb CV2-75 was modestly less effective.	B.1.351.2, B.1.351, B.1.351.3	Stamatatos et al. (2021)	895	A	C	1.0
p.D80A	antibody epitope effects	Abolishes neutralizing activity of N-terminal-domain-directed mAb 4-19.	B.1.351.2, B.1.351, B.1.351.3	Wang et al. (2021)	895	A	C	1.0
p.D80A	convalescent plasma binding	2.11x increase in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset.	B.1.351.2, B.1.351, B.1.351.3	Gong et al. (2021)	895	A	C	1.0
p.D80A	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.1.351.2, B.1.351, B.1.351.3	Cele et al. (2021)	895	A	C	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.D80A	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 had mean extasciitilde6x reduction in neutralizing titers, and 40% of the samples lacked any activity against B.1.351.	B.1.351.2, B.1.351, B.1.351.3	Planas et al. (2021)	895	A	C	1.0
p.D80A	convalescent plasma escape	In over 90% of two dose mRNA vaccinees, heterotypic neutralizing titres (NT50) against B.1.1.7 and B.1.351 remain comfortably above the level associated with immune protection in recent vaccine trials. However, in over 50% of convalescent COVID-19 individuals (5/9) and recipients of a only a single dose of mRNA vaccine (10/11) – heterotypic neutralization dropped to negligible levels, particularly against B.1.351.	B.1.351.2, B.1.351, B.1.351.3	Skelly et al. (2021)	895	A	C	1.0
p.D80A	convalescent plasma escape	Using convalescent sera from 15 early pandemic patients (Seattle Flu Study), mean 220 days post symptom onset (IQR 125-269, and three asymptomatic cases) with 27% WHO disease severity scale 3, one third (5/15) of sera neutralized this B.1.351 pseudotype and only three had ID50 titers above 100. Only two of the 15 sera achieved 80% neutralization.	B.1.351.2, B.1.351, B.1.351.3	Stamatatos et al. (2021)	895	A	C	1.0
p.D80A	convalescent plasma escape	Using convalescent sera from 15 early pandemic patients (Seattle Flu Study), mean 220 days post symptom onset (IQR 125-269, and three asymptomatic cases) with 27% WHO disease severity scale 3, 7 of 15 neutralized this B.1.351 pseudotype that includes the L242del, and only one had titers above 100. Only one of the 15 sera achieved 80% neutralization. [compare to 5 and 1 for pseudotype without the deletion]	B.1.351.2, B.1.351, B.1.351.3	Stamatatos et al. (2021)	895	A	C	1.0
p.D80A	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.1.351.2, B.1.351, B.1.351.3	Wibmer et al. (2021)	895	A	C	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.D80A	humoral response durability	In a prospective study of 107 hospitalized patients, decrease of IgG rates and serological assays becoming negative did not imply loss of neutralizing capacity. Our results indicate a sustained humoral response against the ancestral strain and the D614G, B.1.1.7 and P.1 variants for at least 6 months (last of two samples taken) in patients previously hospitalized for COVID-19. A weaker protection was however observed for the B.1.351 variant.	B.1.351.2, B.1.351, B.1.351.3	Betton et al. (2020)	895	A	C	1.0
p.D80A	outcome hazard ratio	On average across 7 European countries studied, using B.1.351 defining mutations: Significant shift to infection in those without pre-existing conditions (79.6% vs 89% for non-VOC cases). Significant increase in hospitalization rate (19.3% vs 7.5% for non-VOC cases). Significant increase in ICU rate (2.3% vs 0.6% for non-VOC cases). PG: seems to be different notations around the LAL deletion, using the minimal shared definition to catch as many as possible.	B.1.351.2, B.1.351, B.1.351.3	Funk et al. (2021)	895	A	C	1.0
p.D80A	reinfection	4 health care workers in the 20's and 30's with no underlying conditions and seropositivity or confirmed 2020 SARS-CoV-2 infections were confirmed to have B.1.351 infection during a Februrary 2021 hospital outbreak in Luxembourg. Symptoms were mostly mild on first infection, and milder on second infection.	B.1.351.2, B.1.351, B.1.351.3	Staub et al. (2021)	895	A	C	1.0
p.D80A	reinfection	Hamsters re-infected with B.1.351 virus after seroversion from previous infection with a lineage A virus did not transmit virus to naive sentinels via direct contact transmission, in contrast to the non-seroconverted animals. They had little infectious virus and no pathology in the lungs. Initial infection with SARS-CoV-2 lineage A does not prevent heterologous reinfection with B.1.351, but prevents disease and onward transmission.	B.1.351.2, B.1.351, B.1.351.3	Yinda et al. (2021)	895	A	C	1.0
p.D80A	symptom prevalence	Inoculation with the B.1.351 isolate resulted in lower clinical scores in 6 rhesus macaques that correlated with lower virus titers in the lungs, less severe histologic lung lesions and less viral antigen detected in the lungs. Our comparative pathogenicity study suggests that ongoing circulation under diverse evolutionary pressure favors transmissibility and immune evasion rather than an increase in intrinsic pathogenicity.	B.1.351.2, B.1.351, B.1.351.3	Munster et al. (2021)	895	A	C	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.D80A	tissue specific neutralization	The nasal mucosa of Pfizer vaccinees with time course collection was evaluated against VSV pseudotypes: while B.1.1.7 and D614G showed neutralization by nasal swab from only one different previously infected vacinee neutralizing at weeks 3 and 6, B.1.351 showed zero neutralization at either time point in any sample (and relatively impaired serum neutralization).	B.1.351.2, B.1.351, B.1.351.3	Planas et al. (2021)	895	A	C	1.0
p.D80A	trafficking	Lentiviral pseudotyped with this individual mutation from B.1.351 was tested on ACE2.293T cells. Luciferase activity was measured two days postinfection, showing mild decrease in infection rate amongst the cells, suggesting that this mutation does not contributing to cell entry fitness.	B.1.351.2, B.1.351, B.1.351.3	Tada et al. (2021)	895	A	C	1.0
p.D80A	vaccine neutralization efficacy	The Janssen single dose vaccine showed 72% efficacy at preventing moderate and severe disease, which was reduced to 57% in South Africa, where 92.6% of infections are estimated to have been B.1.351. 100% reduction in hospitalization risk remains across variants after 28 days post-vaccination.	B.1.351.2, B.1.351, B.1.351.3	nan	895	A	C	1.0
p.D80A	vaccine neutralization efficacy	In an Ontario long term care facility, cumulatively, weaker BNT162b2 vaccine stimulation, age/comorbidities, produced a 130-fold reduction in apparent neutralization titers in mean 88yo LTCH residents against Beta (B.1.351), relative to staff vaccinees against D614G wild type. 37.9% of 116 two-dose-mRNA-vaccinated residents had undetectable neutralizing antibodies to B.1.351. mRNA-1273 vaccinee sera displayed extasciitilde2 better neutralization than BNT162b2. [common defining B.1.351 mutations noted, as the manuscript does not provide details]	B.1.351.2, B.1.351, B.1.351.3	Abe et al. (2021)	895	A	C	1.0
p.D80A	vaccine neutralization efficacy	Using B.1.351 defining mutations for Spike, observed 4x average decrease in neutralization efficiency (but still relevant titres) for sera from 10 BNT162b2 vaccinees 12 days after second dose, but only one relevant titre 12 days after first dose. Compares unfavorably to wild type or B.1.1.7 titres.	B.1.351.2, B.1.351, B.1.351.3	Alenquer et al. (2021)	895	A	C	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.D80A	vaccine neutralization efficacy	Observed 8.8-fold reduction in neutralization efficiency of Pfizer vaccinee sera (collected 14 days after second dose) against cultured B.1.351 sample. Contrast this with 1.4-fold reduction for just the pseudovirus combination of "key" B.1.351 mutations K417N+E484K+N501Y. WA1 and B.1.351 FRNT50 titers correlated weakly at the individual level, with some individual's serum potently neutralizing WA1 while having FRNT50 for B.1.351 below the assay limit of detection (1:20).	B.1.351.2, B.1.351, B.1.351.3	Bates et al. (2021)	895	A	C	1.0
p.D80A	vaccine neutralization efficacy	Neutralization efficiency (ID50) against B.1.1.351-v3 reduced 8.4x relative to D614G wildtype using pseudotyped VSV assay on 8 Moderna vaccinee sera one week post-booster.	B.1.351.2, B.1.351, B.1.351.3	Choi et al. (2021)	895	A	C	1.0
p.D80A	vaccine neutralization efficacy	Neutralization efficiency (ID50) against B.1.1.351-v2 reduced 7.3x relative to D614G wildtype using pseudotyped VSV assay on 8 Moderna vaccinee sera one week post-booster.	B.1.351.2, B.1.351, B.1.351.3	Choi et al. (2021)	895	A	C	1.0
p.D80A	vaccine neutralization efficacy	ELISpot assays show T cell neutralization reduced by 29.8% in this B.1.351 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.1.351.2, B.1.351, B.1.351.3	Gallagher et al. (2021)	895	A	C	1.0
p.D80A	vaccine neutralization efficacy	Pseudotyped B.1.351 v1 virus has reduced neutralization activity vs wild type: 34.5x (30 sera Pfizer median 9 days post 2nd dose) and 27.7x (35 sera Moderna median 18 days post 2nd dose). This was significant by ANOVA. Notably, 36.7% (11/30) recipients of two-dose Pfizer and 42.9% (15/35) recipients of two-dose Moderna vaccines did not have detectable neutralization of at least one of the B.1.351 variants.	B.1.351.2, B.1.351, B.1.351.3	Garcia-Beltran et al. (2021)	895	A	C	1.0
p.D80A	vaccine neutralization efficacy	Pseudotyped B.1.351 v2 virus has reduced neutralization activity vs wild type: 41.2x (30 sera Pfizer median 9 days post 2nd dose) and 20.8x (35 sera Moderna median 18 days post 2nd dose). This was significant by ANOVA. Notably, 36.7% (11/30) recipients of two-dose Pfizer and 42.9% (15/35) recipients of two-dose Moderna vaccines did not have detectable neutralization of at least one of the B.1.351 variants.	B.1.351.2, B.1.351, B.1.351.3	Garcia-Beltran et al. (2021)	895	A	C	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.D80A	vaccine neutralization efficacy	B.1.351 pseudotyped VSV was tested for neutralization in a clonal HEK-293T ACE2 TMPRSS2 cell line optimized for highly efficient S-mediated infection. Only 1 out of 12 serum samples from a cohort of Argentinian recipients of the Gamaleya Sputnik V Ad26 / Ad5 vaccine showed effective neutralization (IC90) at full serum strength (average realtive decrease was 6.1x vs wild type).	B.1.351.2, B.1.351, B.1.351.3	Ikegame et al. (2021)	895	A	C	1.0
p.D80A	vaccine neutralization efficacy	Vaccine plasma neutralization of B.1.351-spike virus was nominally robust but lower (extasciitilde3x) than other variants of concern.	B.1.351.2, B.1.351, B.1.351.3	Liu et al. (2021)	895	A	C	1.0
p.D80A	vaccine neutralization efficacy	A two-dose regimen of (AstraZeneca) ChAdOx1-nCoV19 did not show protection against mild-moderate Covid-19 due to B.1.351 variant, however, vaccine efficacy against severe Covid-19 is undetermined.	B.1.351.2, B.1.351, B.1.351.3	Madhi et al. (2021)	895	A	C	1.0
p.D80A	vaccine neutralization efficacy	Relative to B.1.1.117, PRNT50 line virus neutralizating antibody activity assay of B.1.351 showed extasciitilde11x reduction in 13 vacinees's sera collected through 41 days after vaccination. Neutralization by a placebo control group of 6 naturally infected patients showed a smaller extasciitilde8x drop (starting from a extasciitilde50% higher PRNT50 value than vacinees for B.1.1.117 neutralization). Serum samples obtained from 13 ChAdOx1 nCoV-19 vaccine recipients without SARS-CoV-2 infection through 41 days after vaccination showed extasciitilde4x reduction in neutralization (ID50) for full B.1.351 pseudotype HIV-1 virus compared to D614G alone. This RBD variant combination's neutralization by a placebo control group of 6 naturally infected patients showed a slightly higher 4.6x drop (though with D614G starting at a 1.7x higher titre than vaccinee sera).	B.1.351.2, B.1.351, B.1.351.3	Madhi et al. (2021)	895	A	C	1.0
p.D80A	vaccine neutralization efficacy	The Novavax vaccine, which achieved 95.6% efficacy against previous SARS-CoV-2 strains, had reduced efficacy of 60% in South Africa, where 92.6% of infections are estimated to have been B.1.351.	B.1.351.2, B.1.351, B.1.351.3	Novavax (2021)	895	A	C	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.D80A	vaccine neutralization efficacy	Detectable antibodies against B.1.351 at various time points using pseudotyped lentivirus neutralization in Moderna vaccinee cohort: Day 29 8%, Day 43 100%, Day 119 71%, Day 209 54%. Detectable antibodies against B.1.351 at various time points using live virus FRNT neutralization in Moderna vaccinee cohort: Day 29 8%, Day 43 100%, Day 119 79%, Day 209 58%. Detectable antibodies against B.1.351 at various time points using ACE2 blocking assay in Moderna vaccinee cohort: Day 29 63%, Day 43 100%, Day 119 71%, Day 209 79%. Decreased neutralization on some assays was seen especially in those vaccinees tested that were 71+.	B.1.351.2, B.1.351, B.1.351.3	Pegu et al (2021)	895	A	C	1.0
p.D80A	vaccine neutralization efficacy	The sera of 16 individuals with time course collection was evaluated against VSV pseudotypes: while BD614G and B.1.1.7 were neutralized earlier, the anti-B.1.351 response was negative up to week 3, and became detectable at week 4 (1 week after booster dose), at a level lower than the two other viruses (extasciitilde10x vs D614G) through week 6, the last timepoint measured. Three vaccinees never showed detectable neutralization to B.1.351 even after second dose.	B.1.351.2, B.1.351, B.1.351.3	Planas et al. (2021)	895	A	C	1.0
p.D80A	vaccine neutralization efficacy	In a randomized phase 2a-b control trial of the Novavax (NVX-CoV2373) vaccine in South Africa, where B.1.351 virus dominates, efficacy was 60.1% (95% CI, 19.9 to 80.1) in HIV-negative and initially SARS-CoV-2 seronegative participants using the primary endpoint of laboratory-confirmed symptomatic Covid-19 at 7 days or more after the second dose among participants.	B.1.351.2, B.1.351, B.1.351.3	Shinde et al. (2021)	895	A	C	1.0
p.D80A	vaccine neutralization efficacy	In sera collected from 15 early pandemic patients (Seattle Flu Study), mean 16 days post first dose with either Pfizer/BioNTech or Moderna vaccines, the median ID50 titers were extasciitilde3-fold lower against this B.1.351 pseudotyped virus relative to wild type. A single asymptomatic patient, who had no detectable RBD-specific IgG memory before vaccination, also did not elicit nAbs against the B.1.351 variant. [compare to extasciitilde10 fold with L242del] ID50 titres in non-infected mRNA vaccines more than two weeks post-booster were signficiant, but >100x weaker than in previously infected patients after first dose.	B.1.351.2, B.1.351, B.1.351.3	Stamatatos et al. (2021)	895	A	C	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.D80A	vaccine neutralization efficacy	In sera collected from 15 early pandemic patients (Seattle Flu Study), mean 16 days post first dose with either Pfizer/BioNTech or Moderna vaccines, the median ID50 titers were extasciitilde10-fold lower against this B.1.351 pseudotyped virus relative to wild type. A single asymptomatic patient, who had no detectable RBD-specific IgG memory before vaccination, also did not elicit nAbs against the B.1.351 variant. [compare to extasciitilde3 fold without the deletion] ID50 titres in non-infected mRNA vaccines more than two weeks post-booster were significant, but extasciitilde500x weaker than in previously infected patients after first dose.	B.1.351.2, B.1.351, B.1.351.3	Stamatatos et al. (2021)	895	A	C	1.0
p.D80A	vaccine neutralization efficacy	Pseudotyped viruses for B.1.351 was 3.4-fold resistant to neutralization by 6 BNT162b2 vaccine sera 28 days post-booster compared to wild type. Neutralization by 3 Moderna vaccine sera 28 days post-booster was 2.2-fold resistant. [Exact list of B.1.351 mutations used in these assays was not included in the preprint]	B.1.351.2, B.1.351, B.1.351.3	Tada et al. (2021)	895	A	C	1.0
p.D80A	vaccine neutralization efficacy	PBMCs of Pfizer/BioNTech BNT162b2 (n	B.1.351.2, B.1.351, B.1.351.3	Tarke et al. (2021)	895	A	C	1.0
p.D80A	vaccine neutralization efficacy	[Contrary to how this paper has been cited, Voysey et al. do NOT show evidence of decreased effectiveness of ChAdOx1 (AstraZeneca) against the South African B.1.351 lineage. Insufficient numbers reaching the primary study endpoint were available in that arm of the vaccine study to report any statistics from the South African participants. Additionally, the study period of the paper ended in November 2020, while the earliest reported case of this lineage is October (covariants.org), only becoming dominant by mid-November.]	B.1.351.2, B.1.351, B.1.351.3	Voysey et al. (2021)	895	A	C	1.0
p.D80A	vaccine neutralization efficacy	No significant difference in T-cell response to B.1.351 was observed (vs. ancestral) in blood drawn from 28 participants received the Pfizer-BioNTech vaccine and 2 received the Moderna vaccine.	B.1.351.2, B.1.351, B.1.351.3	Woldemeskel et al. (2021)	895	A	C	1.0
p.D80A	vaccine neutralization efficacy	Sera from healthcare workers (n	B.1.351.2, B.1.351, B.1.351.3	Zhou et al. (2021)	895	A	C	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.D80A	vaccinee plasma binding	1.64x 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. 1.35x 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.1.351.2, B.1.351, B.1.351.3	Gong et al. (2021)	895	A	C	1.0
p.D80A	virion structure	The L18F and D80A of the B.1.351 lineage lead to reconfiguration of the N-terminal segment despite the disulfide between Cys16 and Cys136 that partly anchors the N-terminal peptide. The most consequential changes are probably from the triple residue deletion... which causes a shift of the nearby loop 144-155 and must also reconfigure the adjacent disorder loop (residues 246-260), both of which form part of the neutralizing epitopes...bringing large changes in the antigenic surface in this region.	B.1.351.2, B.1.351, B.1.351.3	Cai et al. (2021)	895	A	C	1.0
p.D80A	virion structure	Estimated that there is no free energy change (ddG) for this variant (i.e. same stability as wild type)	B.1.351.2, B.1.351, B.1.351.3	Spratt et al. (2021)	895	A	C	1.0
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.1.351.2, B.1.351, B.1.351.3	Barton et al. (2021)	884	A	T	1.0
p.N501Y	ACE2 receptor binding affinity	In the case of VOC B.1.1.7+E484K, the addition of the E484K mutation to N501Y further increased the affinity, to extasciitilde15 fold higher than WT RBD (KD extasciitilde5 nM), by further increasing the k(on) as measured by surface plasmon resonance. Because the higher k(on) could result in mass transfer limiting binding, we confirmed that the kinetic measurement for this variant was not substantially affected by varying levels of immobilization.	B.1.351.2, B.1.351, B.1.351.3	Barton et al. (2021)	884	A	T	1.0
p.N501Y	ACE2 receptor binding affinity	The affinity of the B.1.351 RBD variants for ACE2 increased by 3.7 fold as measured by surface plasmon resonance relative to wild type RBD by increasing the k(on) and decreasing the k(off) rate constants.	B.1.351.2, B.1.351, B.1.351.3	Barton et al. (2021)	884	A	T	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
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.1.351.2, B.1.351, B.1.351.3	Collier et al. (2021)	884	A	T	1.0
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.1.351.2, B.1.351, B.1.351.3	Gamez et al. (2021)	884	A	T	1.0
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.1.351.2, B.1.351, B.1.351.3	Gong et al. (2021)	884	A	T	1.0
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.1.351.2, B.1.351, B.1.351.3	Laffeber et al. (2021)	884	A	T	1.0
p.N501Y	ACE2 receptor binding affinity	Reported 10-fold increase in ACE2 binding vs wild-type (Kd	B.1.351.2, B.1.351, B.1.351.3	Liu et al. (2021)	884	A	T	1.0
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.1.351.2, B.1.351, B.1.351.3	Liu et al. (2021)	884	A	T	1.0
p.N501Y	ACE2 receptor binding affinity	extasciitilde4-fold increase in binding affinity vs wild type.	B.1.351.2, B.1.351, B.1.351.3	Motozono et al. (2021)	884	A	T	1.0
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.1.351. We observed an increase (relative to D614G) in binding of soluble ACE2 to B.1.351, and to a much gearter extent to B.1.1.7, which both carry the N501Y mutation (see Fig 3).	B.1.351.2, B.1.351, B.1.351.3	Planas et al. (2021)	884	A	T	1.0

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.1.351.2, B.1.351, B.1.351.3	Ramanathan et al. (2021)	884	A	T	1.0
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.1.351.2, B.1.351, B.1.351.3	Ramanathan et al. (2021)	884	A	T	1.0
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.1.351.2, B.1.351, B.1.351.3	Santos and Passos (2021)	884	A	T	1.0
p.N501Y	ACE2 receptor binding affinity	Experimentally, ACE2 binding affinity increased 0.24 fold	B.1.351.2, B.1.351, B.1.351.3	Starr et al. (2020)	884	A	T	1.0
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.1.351.2, B.1.351, B.1.351.3	Tada et al. (2021)	884	A	T	1.0
p.N501Y	ACE2 receptor binding affinity	Reported 4-fold increase in affinity compared to wild-type RBD on the cell surface (Kd	B.1.351.2, B.1.351, B.1.351.3	Tian et al. (2021)	884	A	T	1.0
p.N501Y	ACE2 receptor binding affinity	Reported slight increase in affinity compared to wild-type RBD on the cell surface (Kd	B.1.351.2, B.1.351, B.1.351.3	Tian et al. (2021)	884	A	T	1.0
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.1.351.2, B.1.351, B.1.351.3	Vogel et al. (2021)	884	A	T	1.0
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.1.351.2, B.1.351, B.1.351.3	Zahradnik et al. (2021)	884	A	T	1.0
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.1.351.2, B.1.351, B.1.351.3	Zhu et al. (2021)	884	A	T	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.N501Y	CD8 plus T cell response	Encouragingly, we find that the majority of T cell responses in recipients of two doses of the BNT162b2 vaccine are generated by epitopes that are invariant between the [wildtype] and two of the current variants of concern (B.1.1.7 and B.1.351). In over 90% of two dose mRNA vaccinees, heterotypic neutralizing titres (NT50) against B.1.1.7 and B.1.351 remain comfortably above the level associated with immune protection in recent vaccine trials. However, in over 50% of convalescent COVID-19 individuals and recipients of a only a single dose of mRNA vaccine – heterotypic neutralization dropped to negligible levels, particularly against B.1.351.	B.1.351.2, B.1.351, B.1.351.3	Skelly et al. (2021)	884	A	T	1.0
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.1.351.2, B.1.351, B.1.351.3	Reynolds et al. (2021)	884	A	T	1.0
p.N501Y	antibody epitope effects	Ablates Class 3 N-terminal domain targeting antibody COV2-2489, diminishes COV2-2676.	B.1.351.2, B.1.351, B.1.351.3	Chen et al. (2021)	884	A	T	1.0
p.N501Y	antibody epitope effects	Ablates Class 1 receptor-binding-motif targeting antibodies COV2-2050, 1B07, COVOX-384, and S2H58. Ablates Class 3 N-terminal domain targeting antibody COV2-2489, diminishes COV2-2676.	B.1.351.2, B.1.351, B.1.351.3	Chen et al. (2021)	884	A	T	1.0
p.N501Y	antibody epitope effects	Ablates Class 1 receptor-binding-motif targeting antibodies COV2-2050, 1B07, COVOX-384, and S2H58.	B.1.351.2, B.1.351, B.1.351.3	Chen et al. (2021)	884	A	T	1.0
p.N501Y	antibody epitope effects	Of 50 mAbs tested, major loss of neutralization observed for S2X128, S2D8, S2X192, S2D19, S2H14, S2H19.	B.1.351.2, B.1.351, B.1.351.3	Collier et al. (2021)	884	A	T	1.0
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.1.351.2, B.1.351, B.1.351.3	Haynes et al. (2021)	884	A	T	1.0
p.N501Y	antibody epitope effects	Abolished neutralization by mAbs CQ026 and CQ038, greatly diminished neutralization by CQ012 and CQ046.	B.1.351.2, B.1.351, B.1.351.3	Hu et al. (2021)	884	A	T	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
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.1.351.2, B.1.351, B.1.351.3	Klegerman et al. (2021)	884	A	T	1.0
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.1.351.2, B.1.351, B.1.351.3	Rees-Spear et al. (2021)	884	A	T	1.0
p.N501Y	antibody epitope effects	Reduction in neutralization by mAbs COVA1-18 (extasciitilde4x), COVA2-15 (extasciitilde9x), S309 (extasciitilde3x)	B.1.351.2, B.1.351, B.1.351.3	Shen et al. (2021)	884	A	T	1.0
p.N501Y	antibody epitope effects	Anti-NTD CV1 mAb isolated from an early pandemic case was unable to neutralize either partial B.1.351 variant pseudovirus used (A701V or L242del). The neutralization potency of mAb CV30, which contacts K417 and N501 but not E484, was extasciitilde10-fold weaker toward both B.1.351 variants. The neutralization potency of anti-RBD mAb CV3-1 was 3-4-fold less potent against the B.1.351 variants, while anti-RBD mAb CV2-75 was modestly less effective.	B.1.351.2, B.1.351, B.1.351.3	Stamatatos et al. (2021)	884	A	T	1.0
p.N501Y	antibody epitope effects	Anti-NTD CV1 mAb isolated from an early pandemic case was unable to neutralize either partial B.1.351 variant pseudovirus used (A701V or L242del). The neutralization potency of mAb CV30, which contacts K417 and N501 but not E484, was extasciitilde10-fold weaker toward both B.1.351 variants. The neutralization potency of anti-RBD mAb CV3-1 was 3-4-fold less potent against the B.1.351 variants, while anti-RBD mAb CV2-75 was modestly less effective.	B.1.351.2, B.1.351, B.1.351.3	Stamatatos et al. (2021)	884	A	T	1.0
p.N501Y	antibody epitope effects	Complete loss of binding in ELISA by the variant against monoclonal antibodies ab8 and IgG1 ab1. Complete loss for the same antibodies was also observed against S1 pseudotyped and full Spike protein trimers with both B.1.351 and P.1 lineage variants, with slight binding signal for P.1 against IgG1 at the highest concentration tested (1uM). Complete loss of neutralization by these two antibodies was also observed.	B.1.351.2, B.1.351, B.1.351.3	Sun et al. (2021)	884	A	T	1.0
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.1.351.2, B.1.351, B.1.351.3	Wang et al. (2021)	884	A	T	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.N501Y	antibody epitope effects	Ablates ELISA test binding for class 1 (Spike 'up' conformation only, RBD targeting) monoclonal antibody CA1 on 501Y.V2 ("South African") lineage background Ablates ELISA test binding for class 1 (Spike 'up' conformation only, RBD targeting) monoclonal antibody LyCoV016 (also known as CB6 or JS016) on 501Y.V2 ("South African") lineage background Ablates ELISA test binding for class 1 (Spike 'up' conformation only, RBD targeting) monoclonal antibody CC12.1 on 501Y.V2 ("South African") lineage background Ablates ELISA test binding for class 2 (Spike 'up' or 'down' conformation, RBD targeting) monoclonal antibody BD23 on 501Y.V2 ("South African") lineage background Ablates ELISA test binding for class 2 (Spike 'up' or 'down' conformation, RBD targeting) monoclonal antibody C119 (also known as CB6 or JS016) on 501Y.V2 ("South African") lineage background Ablates ELISA test binding for class 2 (Spike 'up' or 'down' conformation, RBD targeting) monoclonal antibody P2B-2F6 on 501Y.V2 ("South African") lineage background	B.1.351.2, B.1.351, B.1.351.3	Wibmer et al. (2021)	884	A	T	1.0
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.1.351.2, B.1.351, B.1.351.3	Gong et al. (2021)	884	A	T	1.0
p.N501Y	convalescent plasma escape	Average extasciitilde10-fold reduction in neutralization efficacy in convalescent sera of 16 health workers infected in Spring 2020.	B.1.351.2, B.1.351, B.1.351.3	Alenquer et al. (2021)	884	A	T	1.0
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.1.351.2, B.1.351, B.1.351.3	Cele et al. (2021)	884	A	T	1.0
p.N501Y	convalescent plasma escape	In 19 convalescent human sera extasciitilde1mo post infection had mild to moderate resistence against all samples.	B.1.351.2, B.1.351, B.1.351.3	Chen et al. (2021)	884	A	T	1.0
p.N501Y	convalescent plasma escape	In 19 convalescent human sera extasciitilde1mo post infection had mild to moderate resistence against most samples	B.1.351.2, B.1.351, B.1.351.3	Chen et al. (2021)	884	A	T	1.0
p.N501Y	convalescent plasma escape	Neutralizing antibody titers of 18 samples (90%) decreased against this B.1.351 pseudotyped virus below an ID50 threshold of 40 (sera collected extasciitilde8mo post Jan 2020 first wave in China).	B.1.351.2, B.1.351, B.1.351.3	Hu et al. (2021)	884	A	T	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
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.1.351.2, B.1.351, B.1.351.3	Kuzmina et al. (2021)	884	A	T	1.0
p.N501Y	convalescent plasma escape	extasciitilde7x reduction in neutralization by key B.1.351 lineage RBD variant combination in sera collected from cohort of 10 with severe disease 21 to 63 days post-onset. Two of the cohort showed no neutralization against this variant.	B.1.351.2, B.1.351, B.1.351.3	Kuzmina et al. (2021)	884	A	T	1.0
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 had mean extasciitilde6x reduction in neutralizing titers, and 40% of the samples lacked any activity against B.1.351.	B.1.351.2, B.1.351, B.1.351.3	Planas et al. (2021)	884	A	T	1.0
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.1.351.2, B.1.351, B.1.351.3	Rathnasinghe et al. (2021)	884	A	T	1.0
p.N501Y	convalescent plasma escape	Neutralization activity of convalescent sera tested decreased extasciitilde2x with this B.1.1.7 pseudotyped virus.	B.1.351.2, B.1.351, B.1.351.3	Shen et al. (2021)	884	A	T	1.0
p.N501Y	convalescent plasma escape	In over 90% of two dose mRNA vaccinees, heterotypic neutralizing titres (NT50) against B.1.1.7 and B.1.351 remain comfortably above the level associated with immune protection in recent vaccine trials. However, in over 50% of convalescent COVID-19 individuals (5/9) and recipients of a only a single dose of mRNA vaccine (10/11) – heterotypic neutralization dropped to negligible levels, particularly against B.1.351.	B.1.351.2, B.1.351, B.1.351.3	Skelly et al. (2021)	884	A	T	1.0
p.N501Y	convalescent plasma escape	Using convalescent sera from 15 early pandemic patients (Seattle Flu Study), mean 220 days post symptom onset (IQR 125-269, and three asymptomatic cases) with 27% WHO disease severity scale 3, one third (5/15) of sera neutralized this B.1.351 pseudotype and only three had ID50 titers above 100. Only two of the 15 sera achieved 80% neutralization.	B.1.351.2, B.1.351, B.1.351.3	Stamatatos et al. (2021)	884	A	T	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.N501Y	convalescent plasma escape	Using convalescent sera from 15 early pandemic patients (Seattle Flu Study), mean 220 days post symptom onset (IQR 125-269, and three asymptomatic cases) with 27% WHO disease severity scale 3, 7 of 15 neutralized this B.1.351 pseudotype that includes the L242del, and only one had titers above 100. Only one of the 15 sera achieved 80% neutralization. [compare to 5 and 1 for pseudotype without the deletion]	B.1.351.2, B.1.351, B.1.351.3	Stamatatos et al. (2021)	884	A	T	1.0
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.1.351.2, B.1.351, B.1.351.3	Tada et al. (2021)	884	A	T	1.0
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.1.351.2, B.1.351, B.1.351.3	Tang et al. (2021)	884	A	T	1.0
p.N501Y	convalescent plasma escape	Demonstrate (via competitive assays in human and mouse) immune escape from polyclonal antibodies induced by vaccination or infection, comparable to what was previously shown with monoclonal antibodies for N501Y and more importantly for E484K. Even though viral mutations may more strongly affect monoclonal antibodies than sera activity, the latter may also be reduced as confirmed here.	B.1.351.2, B.1.351, B.1.351.3	Vogel et al. (2021)	884	A	T	1.0
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.1.351.2, B.1.351, B.1.351.3	Wibmer et al. (2021)	884	A	T	1.0
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.1.351.2, B.1.351, B.1.351.3	Wibmer et al. (2021)	884	A	T	1.0
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.1.351.2, B.1.351, B.1.351.3	Tada et al. (2021)	884	A	T	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
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.1.351.2, B.1.351, B.1.351.3	Flores-Alanis et al. (2021)	884	A	T	1.0
p.N501Y	humoral response durability	In a prospective study of 107 hospitalized patients, decrease of IgG rates and serological assays becoming negative did not imply loss of neutralizing capacity. Our results indicate a sustained humoral response against the ancestral strain and the D614G, B.1.1.7 and P.1 variants for at least 6 months (last of two samples taken) in patients previously hospitalized for COVID-19. A weaker protection was however observed for the B.1.351 variant.	B.1.351.2, B.1.351, B.1.351.3	Betton et al. (2020)	884	A	T	1.0
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.1.351.2, B.1.351, B.1.351.3	Choi et al. (2020)	884	A	T	1.0
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.1.351.2, B.1.351, B.1.351.3	Wang et al. (2021)	884	A	T	1.0
p.N501Y	outcome hazard ratio	On average across 7 European countries studied, using B.1.351 defining mutations: Significant shift to infection in those without pre-existing conditions (79.6% vs 89% for non-VOC cases). Significant increase in hospitalization rate (19.3% vs 7.5% for non-VOC cases). Significant increase in ICU rate (2.3% vs 0.6% for non-VOC cases). PG: seems to be different notations around the LAL deletion, using the minimal shared definition to catch as many as possible.	B.1.351.2, B.1.351, B.1.351.3	Funk et al. (2021)	884	A	T	1.0
p.N501Y	pharmaceutical effectiveness	COR-101 lost extasciitilde8x binding against this isolated mutation. Regdanvimab lost extasciitilde6x binding against this isolated mutation.	B.1.351.2, B.1.351, B.1.351.3	Engelhart et al. (2021)	884	A	T	1.0
p.N501Y	pharmaceutical effectiveness	Tixagevimab, Regdanvimab and COR-101 display reduced binding affinity to virus pseudotyped as RBD from B.1.351.	B.1.351.2, B.1.351, B.1.351.3	Engelhart et al. (2021)	884	A	T	1.0
p.N501Y	pharmaceutical effectiveness	Bamlanivimab (LY-CoV555) lost extasciitilde64x binding against this double mutation. COR-101 lost extasciitilde50x binding against this double mutation. Casirivimab lost extasciitilde250x binding against this double mutation. Estesevimab lost extasciitilde16x binding against this double mutation. Regdanvimab lost extasciitilde32x binding against this double mutation. Tixagevimab lost extasciitilde10x binding against this double mutation.	B.1.351.2, B.1.351, B.1.351.3	Engelhart et al. (2021)	884	A	T	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.N501Y	pharmaceutical effectiveness	COR-101 lost extasciitilde20x binding against this double mutation. Estesevimab lost extasciitilde16x binding against this double mutation. Regdanvimab lost extasciitilde6x binding against this double mutation. M396 lost extasciitilde10x binding against this double mutation.	B.1.351.2, B.1.351, B.1.351.3	Engelhart et al. (2021)	884	A	T	1.0
p.N501Y	pharmaceutical effectiveness	This mutated version of RBD completely abolishes the binding to a therapeutic antibody, Bamlanivimab, in vitro.	B.1.351.2, B.1.351, B.1.351.3	Liu et al. (2021)	884	A	T	1.0
p.N501Y	reinfection	4 health care workers in the 20's and 30's with no underlying conditions and seropositivity or confirmed 2020 SARS-CoV-2 infections were confirmed to have B.1.351 infection during a Februrary 2021 hospital outbreak in Luxembourg. Symptoms were mostly mild on first infection, and milder on second infection.	B.1.351.2, B.1.351, B.1.351.3	Staub et al. (2021)	884	A	T	1.0
p.N501Y	reinfection	Hamsters re-infected with B.1.351 virus after seroversion from previous infection with a lineage A virus did not transmit virus to naive sentinels via direct contact transmission, in contrast to the non-seroconverted animals. They had little infectious virus and no pathology in the lungs. Initial infection with SARS-CoV-2 lineage A does not prevent heterologous reinfection with B.1.351, but prevents disease and onward transmission.	B.1.351.2, B.1.351, B.1.351.3	Yinda et al. (2021)	884	A	T	1.0
p.N501Y	symptom prevalence	Inoculation with the B.1.351 isolate resulted in lower clinical scores in 6 rhesus macaques that correlated with lower virus titers in the lungs, less severe histologic lung lesions and less viral antigen detected in the lungs. Our comparative pathogenicity study suggests that ongoing circulation under diverse evolutionary pressure favors transmissibility and immune evasion rather than an increase in intrinsic pathogenicity.	B.1.351.2, B.1.351, B.1.351.3	Munster et al. (2021)	884	A	T	1.0
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.1.351.2, B.1.351, B.1.351.3	Kim et al. (2021)	884	A	T	1.0
p.N501Y	syncytium formation	extasciitilde50% Vero cell-cell membrane fusion assay under infection with VSV pseudotyped virus relative to wild type, signficantly higher than D614G.	B.1.351.2, B.1.351, B.1.351.3	Kim et al. (2021)	884	A	T	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.N501Y	tissue specific neutralization	The nasal mucosa of Pfizer vaccinees with time course collection was evaluated against VSV pseudotypes: while B.1.1.7 and D614G showed neutralization by nasal swab from only one different previously infected vacinee neutralizing at weeks 3 and 6, B.1.351 showed zero neutralization at either time point in any sample (and relatively impaired serum neutralization).	B.1.351.2, B.1.351, B.1.351.3	Planas et al. (2021)	884	A	T	1.0
p.N501Y	trafficking	The entry efficiencies of Spike pseudotyped viruses bearing N501Y Variant 2 (B.1.351) 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.1.351.2, B.1.351, B.1.351.3	Hu et al. (2021)	884	A	T	1.0
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.1.351.2, B.1.351, B.1.351.3	Kim et al. (2021)	884	A	T	1.0
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.1.351.2, B.1.351, B.1.351.3	Kim et al. (2021)	884	A	T	1.0
p.N501Y	trafficking	More efficient infectivity (24h) compared to wild type, in Caco-2 cells extasciitilde11x, Vero extasciitilde10x, and Calu-3 extasciitilde11x. Compare to wild type at extasciitilde5x across cell types.	B.1.351.2, B.1.351, B.1.351.3	Kim et al. (2021)	884	A	T	1.0
p.N501Y	trafficking	extasciitilde6x more efficient S2 domain cleavage compared to wild type, compared to 4x by D614G alone in Caco-2 cells, mid-range of three cell line tested (Vero and Calu-3). [N501Y+D614G does not show an increase in cleavage, therefore a synergistic effect of the trio is implied]	B.1.351.2, B.1.351, B.1.351.3	Kim et al. (2021)	884	A	T	1.0
p.N501Y	trafficking	9x more infectivity than D614G alone in HEK293T-ACE2 cells 48h post-transduction.	B.1.351.2, B.1.351, B.1.351.3	Kuzmina et al. (2021)	904	A	T	1.0
p.N501Y	trafficking	extasciitilde12x more infectivity than D614G alone in HEK293T-ACE2 cells 48h post-transduction (extasciitildeadditive effects of 501 and 484).	B.1.351.2, B.1.351, B.1.351.3	Kuzmina et al. (2021)	884	A	T	1.0
p.N501Y	trafficking	extasciitilde13x more infective as D614G alone in HEK293T-ACE2 cells 48h post-transduction.	B.1.351.2, B.1.351, B.1.351.3	Kuzmina et al. (2021)	884	A	T	1.0
p.N501Y	trafficking	extasciitilde9x more infectivity than D614G alone in HEK293T-ACE2 cells 48h post-transduction (no synergy as level approx. that of N501Y alone).	B.1.351.2, B.1.351, B.1.351.3	Kuzmina et al. (2021)	884	A	T	1.0
p.N501Y	trafficking	Decreased stability of RBD expression in yeast, suggesting decreased Spike protein stability.	B.1.351.2, B.1.351, B.1.351.3	Motozono et al. (2021)	884	A	T	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
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 indepedetly evaluated and N501 is in both lineages, a significant decrease was observed, therefore the error bars described in this paper should be interpreted carefully]	B.1.351.2, B.1.351, B.1.351.3	Tada et al. (2021)	884	A	T	1.0
p.N501Y	transmissibility	Assuming complete cross-protection, we estimate 501Y.V2/B.1.351 was 1.50 (95% CrI: 1.20-2.13) times as transmissible than previously circulating variants. Assuming instead that 501Y.V2 is identically transmissible, the new variant evades 21% (95% CrI: 11-36%) of previously acquired immunity. Reality may lie between these extremes, with an intermediate increase in transmissibility and mildly imperfect cross-protection from past exposure.	B.1.351.2, B.1.351, B.1.351.3	Pearson et al. (2021)	884	A	T	1.0
p.N501Y	transmissibility	36,590 variant-specific RT-PCR tests were performed on samples collected between April 12 and May 7, 2021 in France to compare variant spread. Compared to January to March 2021, B.1.351 variant had a significant transmission advantage over B.1.1.7 in some regions (15.1 to 16.1% in Île-de-France and 16.1 to 18.8% in Hauts-de-France). This shift in transmission advantage is consistent with the immune evasion abilities of B.1.351 and the high levels of immunization in these regions.	B.1.351.2, B.1.351, B.1.351.3	Roquebert et al. (2021)	884	A	T	1.0
p.N501Y	vaccine neutralization efficacy	The Janssen single dose vaccine showed 72% efficacy at preventing moderate and severe disease, which was reduced to 57% in South Africa, where 92.6% of infections are estimated to have been B.1.351. 100% reduction in hospitalization risk remains across variants after 28 days post-vaccination.	B.1.351.2, B.1.351, B.1.351.3	nan	884	A	T	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.N501Y	vaccine neutralization efficacy	In an Ontario long term care facility, cumulatively, weaker BNT162b2 vaccine stimulation, age/comorbidities, produced a 130-fold reduction in apparent neutralization titers in mean 88yo LTCH residents against Beta (B.1.351), relative to staff vaccinees against D614G wild type. 37.9% of 116 two-dose-mRNA-vaccinated residents had undetectable neutralizing antibodies to B.1.351. mRNA-1273 vaccinee sera displayed extasciitilde2 better neutralization than BNT162b2. [common defining B.1.351 mutations noted, as the manuscript does not provide details]	B.1.351.2, B.1.351, B.1.351.3	Abe et al. (2021)	884	A	T	1.0
p.N501Y	vaccine neutralization efficacy	Using B.1.351 defining mutations for Spike, observed 4x average decrease in neutralization efficiency (but still relevant titres) for sera from 10 BNT162b2 vaccinees 12 days after second dose, but only one relevant titre 12 days after first dose. Compares unfavorably to wild type or B.1.1.7 titres.	B.1.351.2, B.1.351, B.1.351.3	Alenquer et al. (2021)	884	A	T	1.0
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.1.351.2, B.1.351, B.1.351.3	Bates et al. (2021)	884	A	T	1.0
p.N501Y	vaccine neutralization efficacy	Observed 1.4-fold reduction in neutralization efficiency of Pfizer vaccinee sera (collected 14 days after second dose) against pseudotype B.1.351 key variants lentivirus. Compare to 8.8-fold reduction against cultured B.1.351 virus.	B.1.351.2, B.1.351, B.1.351.3	Bates et al. (2021)	884	A	T	1.0
p.N501Y	vaccine neutralization efficacy	Observed 8.8-fold reduction in neutralization efficiency of Pfizer vaccinee sera (collected 14 days after second dose) against cultured B.1.351 sample. Contrast this with 1.4-fold reduction for just the pseudovirus combination of "key" B.1.351 mutations K417N+E484K+N501Y. WA1 and B.1.351 FRNT50 titers correlated weakly at the individual level, with some individual's serum potently neutralizing WA1 while having FRNT50 for B.1.351 below the assay limit of detection (1:20).	B.1.351.2, B.1.351, B.1.351.3	Bates et al. (2021)	884	A	T	1.0
p.N501Y	vaccine neutralization efficacy	The neutralizing activity of vaccine was slightly to significantly lower against this variant combination in sera from all 24 patients with the BNT162b2 mRNA vaccine. (Fig. 4) [In stark contrast to this combination plus K417N, which had no effect (P<0.0001 vs. P	B.1.351.2, B.1.351, B.1.351.3	Chen et al. (2021)	884	A	T	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.N501Y	vaccine neutralization efficacy	Neutralization efficiency (ID50) against B.1.1.351-v3 reduced 8.4x relative to D614G wildtype using pseudotyped VSV assay on 8 Moderna vaccinee sera one week post-booster.	B.1.351.2, B.1.351, B.1.351.3	Choi et al. (2021)	884	A	T	1.0
p.N501Y	vaccine neutralization efficacy	Neutralization efficiency (ID50) against B.1.1.351-v2 reduced 7.3x relative to D614G wildtype using pseudotyped VSV assay on 8 Moderna vaccinee sera one week post-booster.	B.1.351.2, B.1.351, B.1.351.3	Choi et al. (2021)	884	A	T	1.0
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.1.351.2, B.1.351, B.1.351.3	Edara et al. (2021)	884	A	T	1.0
p.N501Y	vaccine neutralization efficacy	ELISpot assays show T cell neutralization reduced by 29.8% in this B.1.351 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.1.351.2, B.1.351, B.1.351.3	Gallagher et al. (2021)	884	A	T	1.0
p.N501Y	vaccine neutralization efficacy	Pseudotyped B.1.351 v1 virus has reduced neutralization activity vs wild type: 34.5x (30 sera Pfizer median 9 days post 2nd dose) and 27.7x (35 sera Moderna median 18 days post 2nd dose). This was significant by ANOVA. Notably, 36.7% (11/30) recipients of two-dose Pfizer and 42.9% (15/35) recipients of two-dose Moderna vaccines did not have detectable neutralization of at least one of the B.1.351 variants.	B.1.351.2, B.1.351, B.1.351.3	Garcia-Beltran et al. (2021)	884	A	T	1.0
p.N501Y	vaccine neutralization efficacy	Pseudotyped B.1.351 v2 virus has reduced neutralization activity vs wild type: 41.2x (30 sera Pfizer median 9 days post 2nd dose) and 20.8x (35 sera Moderna median 18 days post 2nd dose). This was significant by ANOVA. Notably, 36.7% (11/30) recipients of two-dose Pfizer and 42.9% (15/35) recipients of two-dose Moderna vaccines did not have detectable neutralization of at least one of the B.1.351 variants.	B.1.351.2, B.1.351, B.1.351.3	Garcia-Beltran et al. (2021)	884	A	T	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.N501Y	vaccine neutralization efficacy	B.1.351 pseudotyped VSV was tested for neutralization in a clonal HEK-293T ACE2 TMPRSS2 cell line optimized for highly efficient S-mediated infection. Only 1 out of 12 serum samples from a cohort of Argentinian recipients of the Gamaleya Sputnik V Ad26 / Ad5 vaccine showed effective neutralization (IC90) at full serum strength (average realtive decrease was 6.1x vs wild type).	B.1.351.2, B.1.351, B.1.351.3	Ikegame et al. (2021)	884	A	T	1.0
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.1.351.2, B.1.351, B.1.351.3	Jacobson et al. (2021)	884	A	T	1.0
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.1.351.2, B.1.351, B.1.351.3	Kuzmina et al. (2021)	884	A	T	1.0
p.N501Y	vaccine neutralization efficacy	This variant showed >5x decrease in Pfizer sera (3 weeks post-first dose: n	B.1.351.2, B.1.351, B.1.351.3	Kuzmina et al. (2021)	884	A	T	1.0
p.N501Y	vaccine neutralization efficacy	This variant showed >5x decrease in Pfizer sera (3 weeks post-first dose: n	B.1.351.2, B.1.351, B.1.351.3	Kuzmina et al. (2021)	884	A	T	1.0
p.N501Y	vaccine neutralization efficacy	In post-vaccination sera from individuals who received one (3 weeks post-first dose: n	B.1.351.2, B.1.351, B.1.351.3	Kuzmina et al. (2021)	884	A	T	1.0
p.N501Y	vaccine neutralization efficacy	This variant of key B.1.351 lineage mutations showed extasciitilde10x decrease in Pfizer sera (3 weeks post-first dose: n	B.1.351.2, B.1.351, B.1.351.3	Kuzmina et al. (2021)	884	A	T	1.0
p.N501Y	vaccine neutralization efficacy	Vaccine plasma neutralization of B.1.351-spike virus was nominally robust but lower (extasciitilde3x) than other variants of concern.	B.1.351.2, B.1.351, B.1.351.3	Liu et al. (2021)	884	A	T	1.0
p.N501Y	vaccine neutralization efficacy	A two-dose regimen of (AstraZeneca) ChAdOx1-nCoV19 did not show protection against mild-moderate Covid-19 due to B.1.351 variant, however, vaccine efficacy against severe Covid-19 is undetermined.	B.1.351.2, B.1.351, B.1.351.3	Madhi et al. (2021)	884	A	T	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.N501Y	vaccine neutralization efficacy	In a multicenter, double-blind, randomized, controlled trial to assess the safety and efficacy of the ChAdOx1 nCoV-19 vaccine (AZD1222) with enrollment June 24 and November 9, 2020 from extasciitilde2000 HIV-negative 18-64 year olds (1:1 placebo to treatment), incidence of serious adverse events 14 or more days post- 2nd dose was balanced between the vaccine and placebo groups. A two-dose regimen of the ChAdOx1 nCoV-19 vaccine did not show protection against mild-to-moderate Covid-19 due to the B.1.351 variant. Serum samples obtained from 13 ChAdOx1 nCoV-19 vaccine recipients without SARS-CoV-2 infection through 41 days after vaccination showed 3.5x reduction in neutralization (ID50) for B.1.351 RBD pseudotype HIB-1 virus compared to D614G alone. This RBD variant combination's neutralization by a placebo control group of 6 naturally infected patients showed a similar 3.2x drop (though with D614G starting at a 1.7x higher titre than vaccinee sera).	B.1.351.2, B.1.351, B.1.351.3	Madhi et al. (2021)	884	A	T	1.0
p.N501Y	vaccine neutralization efficacy	Relative to B.1.1.117, PRNT50 line virus neutralizating antibody activity assay of B.1.351 showed extasciitilde11x reduction in 13 vacinees's sera collected through 41 days after vaccination. Neutralization by a placebo control group of 6 naturally infected patients showed a smaller extasciitilde8x drop (starting from a extasciitilde50% higher PRNT50 value than vacinees for B.1.1.117 neutralization). Serum samples obtained from 13 ChAdOx1 nCoV-19 vaccine recipients without SARS-CoV-2 infection through 41 days after vaccination showed extasciitilde4x reduction in neutralization (ID50) for full B.1.351 pseudotype HIV-1 virus compared to D614G alone. This RBD variant combination's neutralization by a placebo control group of 6 naturally infected patients showed a slightly higher 4.6x drop (though with D614G starting at a 1.7x higher titre than vaccinee sera).	B.1.351.2, B.1.351, B.1.351.3	Madhi et al. (2021)	884	A	T	1.0
p.N501Y	vaccine neutralization efficacy	The Novavax vaccine, which achieved 95.6% efficacy against previous SARS-CoV-2 strains, had reduced efficacy of 60% in South Africa, where 92.6% of infections are estimated to have been B.1.351.	B.1.351.2, B.1.351, B.1.351.3	Novavax (2021)	884	A	T	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.N501Y	vaccine neutralization efficacy	Detectable antibodies against B.1.351 at various time points using pseudotyped lentivirus neutralization in Moderna vaccinee cohort: Day 29 8%, Day 43 100%, Day 119 71%, Day 209 54%. Detectable antibodies against B.1.351 at various time points using live virus FRNT neutralization in Moderna vaccinee cohort: Day 29 8%, Day 43 100%, Day 119 79%, Day 209 58%. Detectable antibodies against B.1.351 at various time points using ACE2 blocking assay in Moderna vaccinee cohort: Day 29 63%, Day 43 100%, Day 119 71%, Day 209 79%. Decreased neutralization on some assays was seen especially in those vaccinees tested that were 71+.	B.1.351.2, B.1.351, B.1.351.3	Pegu et al (2021)	884	A	T	1.0
p.N501Y	vaccine neutralization efficacy	The sera of 16 individuals with time course collection was evaluated against VSV pseudotypes: while BD614G and B.1.1.7 were neutralized earlier, the anti-B.1.351 response was negative up to week 3, and became detectable at week 4 (1 week after booster dose), at a level lower than the two other viruses (extasciitilde10x vs D614G) through week 6, the last timepoint measured. Three vaccinees never showed detectable neutralization to B.1.351 even after second dose.	B.1.351.2, B.1.351, B.1.351.3	Planas et al. (2021)	884	A	T	1.0
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.1.351.2, B.1.351, B.1.351.3	Rathnasinghe et al. (2021)	884	A	T	1.0
p.N501Y	vaccine neutralization efficacy	In a randomized phase 2a-b control trial of the Novavax (NVX-CoV2373) vaccine in South Africa, where B.1.351 virus dominates, efficacy was 60.1% (95% CI, 19.9 to 80.1) in HIV-negative and initially SARS-CoV-2 seronegative participants using the primary endpoint of laboratory-confirmed symptomatic Covid-19 at 7 days or more after the second dose among participants.	B.1.351.2, B.1.351, B.1.351.3	Shinde et al. (2021)	884	A	T	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.N501Y	vaccine neutralization efficacy	In sera collected from 15 early pandemic patients (Seattle Flu Study), mean 16 days post first dose with either Pfizer/BioNTech or Moderna vaccines, the median ID50 titers were extasciitilde3-fold lower against this B.1.351 pseudotyped virus relative to wild type. A single asymptomatic patient, who had no detectable RBD-specific IgG memory before vaccination, also did not elicit nAbs against the B.1.351 variant. [compare to extasciitilde10 fold with L242del] ID50 titres in non-infected mRNA vaccines more than two weeks post-booster were signficiant, but >100x weaker than in previously infected patients after first dose.	B.1.351.2, B.1.351, B.1.351.3	Stamatatos et al. (2021)	884	A	T	1.0
p.N501Y	vaccine neutralization efficacy	In sera collected from 15 early pandemic patients (Seattle Flu Study), mean 16 days post first dose with either Pfizer/BioNTech or Moderna vaccines, the median ID50 titers were extasciitilde10-fold lower against this B.1.351 pseudotyped virus relative to wild type. A single asymptomatic patient, who had no detectable RBD-specific IgG memory before vaccination, also did not elicit nAbs against the B.1.351 variant. [compare to extasciitilde3 fold without the deletion] ID50 titres in non-infected mRNA vaccines more than two weeks post-booster were significant, but extasciitilde500x weaker than in previously infected patients after first dose.	B.1.351.2, B.1.351, B.1.351.3	Stamatatos et al. (2021)	884	A	T	1.0
p.N501Y	vaccine neutralization efficacy	Pseudotyped viruses for B.1.351 was 3.4-fold resistant to neutralization by 6 BNT162b2 vaccine sera 28 days post-booster compared to wild type. Neutralization by 3 Moderna vaccine sera 28 days post-booster was 2.2-fold resistant. [Exact list of B.1.351 mutations used in these assays was not included in the preprint]	B.1.351.2, B.1.351, B.1.351.3	Tada et al. (2021)	884	A	T	1.0
p.N501Y	vaccine neutralization efficacy	PBMCs of Pfizer/BioNTech BNT162b2 (n	B.1.351.2, B.1.351, B.1.351.3	Tarke et al. (2021)	884	A	T	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
p.N501Y	vaccine neutralization efficacy	[Contrary to how this paper has been cited, Voysey et al. do NOT show evidence of decreased effectiveness of ChAdOx1 (AstraZeneca) against the South African B.1.351 lineage. Insufficient numbers reaching the primary study endpoint were available in that arm of the vaccine study to report any statistics from the South African participants. Additionally, the study period of the paper ended in November 2020, while the earliest reported case of this lineage is October (covariants.org), only becoming dominant by mid-November.]	B.1.351.2, B.1.351, B.1.351.3	Voysey et al. (2021)	884	A	T	1.0
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.1.351.2, B.1.351, B.1.351.3	Wang et al. (2021)	884	A	T	1.0
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 significant (0.5 to 20-fold, but average extasciitilde2x) decrease in neutralization by vaccine plasma was observed.	B.1.351.2, B.1.351, B.1.351.3	Wang et al. (2021)	884	A	T	1.0
p.N501Y	vaccine neutralization efficacy	No significant difference in T-cell response to B.1.351 was observed (vs. ancestral) in blood drawn from 28 participants received the Pfizer-BioNTech vaccine and 2 received the Moderna vaccine.	B.1.351.2, B.1.351, B.1.351.3	Woldemeskel et al. (2021)	884	A	T	1.0
p.N501Y	vaccine neutralization efficacy	In Moderna vaccinee sera, 2.7x reduction in neutralization, and 6.4 for the full B.1.351 Spike mutation complement, but despite the observed decreases, titers in human vaccinee sera against the B.1.351 variant remained at clinically significant level of extasciitilde1/300.	B.1.351.2, B.1.351, B.1.351.3	Wu et al. (2021)	884	A	T	1.0
p.N501Y	vaccine neutralization efficacy	In 20 sera from BNT162b2 mRNA vaccine inoculated participants, 6 displayed mild (2x) reductions in neutralization. This variant combination showed the highest reduction, but the magnitude of the differences was small compared to the >4x differences in HA-inhibition titers that have been used to signal potential need for a strain change in influenza vaccines.	B.1.351.2, B.1.351, B.1.351.3	Xie et al. (2021)	884	A	T	1.0
p.N501Y	vaccine neutralization efficacy	Sera from healthcare workers (n	B.1.351.2, B.1.351, B.1.351.3	Zhou et al. (2021)	884	A	T	1.0

Mutations	Sub-category	Function	Lineages	Citation	Sequence Depth	Reference Allele	Alternate Allele	Alternate Frequency
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.1.351.2, B.1.351, B.1.351.3	Gong et al. (2021)	884	A	T	1.0
p.N501Y	viral load	B.1.351 and P.1 samples showed average Ct cycle threshold of 22.2 vs 23 for wildtype (i.e. extasciitilde60% higher viral load) comparing 3360 and 22535 samples respectively.	B.1.351.2, B.1.351, B.1.351.3	Roquebert et al. (2021)	884	A	T	1.0
p.N501Y	viral load	The 62 B.1.351 (a.k.a. N501Y.V2) variant cases in three Paris hospital labs had a extasciitilde2-fold viral load increase (extasciitilde1 Ct drop in both N and ORF1ab probes) compared to 332 ancestral lineage cases from the same time frame (2020-12-20 to 2021-02-26).	B.1.351.2, B.1.351, B.1.351.3	Teyssou et al. (2021)	884	A	T	1.0
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.1.351.2, B.1.351, B.1.351.3	Spratt et al. (2021)	884	A	T	1.0

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