

Surveillance Report

Report Details

Surveillance generated by nf-ncov-voc for lineage/clade: Unknown

This report is generated on 2024-12-03 using 20 number of genomes collected between 2024-07-26 and 2024-09-30

Additional Information

Organism: Severe acute respiratory syndrome coronavirus 2

Reference Accession: NC_045512.2

Reference Database Name: RefSeq

Table 1: Indicator Summary

This table contains key indicators identified

| Surveillance Indicator | Functional Categories | Mutations |
|----------------------------------|---|---|
| Transmissibility between humans | transmissibility | D614G, H655Y, H69del, K417N, N440K, N501Y, P681R, S373P, V70del |
| Infection Severity | ACE2 receptor binding affinity, viral load, outcome hazard ratio | D405N, D614G, D796Y, F486P, G339H, H655Y, H69del, K417N, N440K, N460K, N501Y, N679K, N764K, N969K, P681R, Q498R, Q954H, R408S, S371F, S373P, V70del, Y505H |
| Immunity after natural infection | convalescent plasma escape, reinfection, humoral response durability | D614G, H655Y, H69del, K147N, K417N, N440K, N450D, N501Y, P681R, V70del |
| Vaccines | vaccine neutralization efficacy | D405N, D614G, D796Y, H655Y, H69del, K417N, N440K, N501Y, N679K, N764K, N969K, P681R, Q498R, Q954H, R237K, R408S, S371F, S373P, V70del, Y505H |
| Monoclonal antibodies | monoclonal antibody serial passage escape, pharmaceutical effectiveness | D405N, D614G, D796Y, F486P, H655Y, H69del, K417N, L452W, N440K, N450D, N460K, N501Y, N679K, N764K, N969K, P681R, Q498R, Q954H, R408S, S371F, S373P, V70del, Y505H |
| Diagnostics | clinical indicators, antigenic test failure, symptom prevalence | D614G, H69del, K417N, N501Y, P681R, V70del |

Table 2: Mutation Details Summary

This table contains key functional impacts of mutations identified

| Mutations | Functional Category | Annotation Resource | Lineages | Sequence Depth | Reference Allele | Alternate Allele | Alternate Frequency |
|-----------|-------------------------------------|---------------------|----------|----------------|------------------|------------------|---------------------|
| M85del | immunosuppression variant emergence | Pokay | MC.2.1 | 19 | TATG | T | 0.053 |
| M85del | IFN activity | Pokay | MC.2.1 | 19 | TATG | T | 0.053 |
| H69del | convalescent plasma escape | Pokay | MC.2.1 | 19 | ATACATG | A | 1.0 |
| H69del | vaccine neutralization efficacy | Pokay | MC.2.1 | 19 | ATACATG | A | 1.0 |
| H69del | pharmaceutical effectiveness | Pokay | MC.2.1 | 19 | ATACATG | A | 1.0 |
| H69del | antibody epitope effects | Pokay | MC.2.1 | 19 | ATACATG | A | 1.0 |
| H69del | ACE2 receptor binding affinity | Pokay | MC.2.1 | 19 | ATACATG | A | 1.0 |
| H69del | vaccinee plasma binding | Pokay | MC.2.1 | 19 | ATACATG | A | 1.0 |
| H69del | immunosuppression variant emergence | Pokay | MC.2.1 | 19 | ATACATG | A | 1.0 |
| H69del | convalescent plasma binding | Pokay | MC.2.1 | 19 | ATACATG | A | 1.0 |
| H69del | anthropozoonotic events | Pokay | MC.2.1 | 19 | ATACATG | A | 1.0 |
| H69del | trafficking | Pokay | MC.2.1 | 19 | ATACATG | A | 1.0 |
| H69del | symptom prevalence | Pokay | MC.2.1 | 19 | ATACATG | A | 1.0 |
| H69del | virion structure | Pokay | MC.2.1 | 19 | ATACATG | A | 1.0 |

| Mutations | Functional Category | Annotation Resource | Lineages | Sequence Depth | Reference Allele | Alternate Allele | Alternate Frequency |
|-----------|-------------------------------------|---------------------|----------|----------------|------------------|------------------|---------------------|
| H69del | vaccine efficacy | Pokay | MC.2.1 | 19 | ATACATG | A | 1.0 |
| H69del | aerosolization | Pokay | MC.2.1 | 19 | ATACATG | A | 1.0 |
| H69del | environmental condition stability | Pokay | MC.2.1 | 19 | ATACATG | A | 1.0 |
| H69del | reinfection | Pokay | MC.2.1 | 19 | ATACATG | A | 1.0 |
| H69del | tissue specific neutralization | Pokay | MC.2.1 | 19 | ATACATG | A | 1.0 |
| H69del | clinical indicators | Pokay | MC.2.1 | 19 | ATACATG | A | 1.0 |
| H69del | tissue specific replication effects | Pokay | MC.2.1 | 19 | ATACATG | A | 1.0 |
| H69del | transmissibility | Pokay | MC.2.1 | 19 | ATACATG | A | 1.0 |
| H69del | outcome hazard ratio | Pokay | MC.2.1 | 19 | ATACATG | A | 1.0 |
| H69del | viral load | Pokay | MC.2.1 | 19 | ATACATG | A | 1.0 |
| V70del | convalescent plasma escape | Pokay | MC.2.1 | 19 | ATACATG | A | 1.0 |
| V70del | vaccine neutralization efficacy | Pokay | MC.2.1 | 19 | ATACATG | A | 1.0 |
| V70del | pharmaceutical effectiveness | Pokay | MC.2.1 | 19 | ATACATG | A | 1.0 |
| V70del | antibody epitope effects | Pokay | MC.2.1 | 19 | ATACATG | A | 1.0 |
| V70del | ACE2 receptor binding affinity | Pokay | MC.2.1 | 19 | ATACATG | A | 1.0 |
| V70del | vaccinee plasma binding | Pokay | MC.2.1 | 19 | ATACATG | A | 1.0 |

| Mutations | Functional Category | Annotation Resource | Lineages | Sequence Depth | Reference Allele | Alternate Allele | Alternate Frequency |
|-----------|-------------------------------------|---------------------|----------|----------------|------------------|------------------|---------------------|
| V70del | immunosuppression variant emergence | Pokay | MC.2.1 | 19 | ATACATG | A | 1.0 |
| V70del | convalescent plasma binding | Pokay | MC.2.1 | 19 | ATACATG | A | 1.0 |
| V70del | anthropozoonotic events | Pokay | MC.2.1 | 19 | ATACATG | A | 1.0 |
| V70del | trafficking | Pokay | MC.2.1 | 19 | ATACATG | A | 1.0 |
| V70del | symptom prevalence | Pokay | MC.2.1 | 19 | ATACATG | A | 1.0 |
| V70del | virion structure | Pokay | MC.2.1 | 19 | ATACATG | A | 1.0 |
| V70del | vaccine efficacy | Pokay | MC.2.1 | 19 | ATACATG | A | 1.0 |
| V70del | aerosolization | Pokay | MC.2.1 | 19 | ATACATG | A | 1.0 |
| V70del | environmental condition stability | Pokay | MC.2.1 | 19 | ATACATG | A | 1.0 |
| V70del | reinfection | Pokay | MC.2.1 | 19 | ATACATG | A | 1.0 |
| V70del | tissue specific neutralization | Pokay | MC.2.1 | 19 | ATACATG | A | 1.0 |
| V70del | clinical indicators | Pokay | MC.2.1 | 19 | ATACATG | A | 1.0 |
| V70del | tissue specific replication effects | Pokay | MC.2.1 | 19 | ATACATG | A | 1.0 |
| V70del | transmissibility | Pokay | MC.2.1 | 19 | ATACATG | A | 1.0 |
| V70del | outcome hazard ratio | Pokay | MC.2.1 | 19 | ATACATG | A | 1.0 |
| V70del | viral load | Pokay | MC.2.1 | 19 | ATACATG | A | 1.0 |
| K147N | convalescent plasma escape | Pokay | MC.2.1 | 20 | A | T | 0.05 |

| Mutations | Functional Category | Annotation Resource | Lineages | Sequence Depth | Reference Allele | Alternate Allele | Alternate Frequency |
|-----------|---|---------------------|----------|----------------|------------------|------------------|---------------------|
| R237K | vaccine neutralization efficacy | Pokay | MC.2.1 | 20 | G | A | 1.0 |
| G339H | gene expression increase | Pokay | MC.2.1 | 20 | GG | CA | 1.0 |
| G339H | ACE2 receptor binding affinity | Pokay | MC.2.1 | 20 | GG | CA | 1.0 |
| K356T | gene expression increase | Pokay | MC.2.1 | 20 | A | C | 1.0 |
| S371F | pharmaceutical effectiveness | Pokay | MC.2.1 | 20 | C | T | 1.0 |
| S371F | antibody epitope effects | Pokay | MC.2.1 | 20 | C | T | 1.0 |
| S371F | vaccine neutralization efficacy | Pokay | MC.2.1 | 20 | C | T | 1.0 |
| S371F | vaccinee plasma binding | Pokay | MC.2.1 | 20 | C | T | 1.0 |
| S371F | ACE2 receptor binding affinity | Pokay | MC.2.1 | 20 | C | T | 1.0 |
| S373P | pharmaceutical effectiveness | Pokay | MC.2.1 | 20 | T | C | 1.0 |
| S373P | antibody epitope effects | Pokay | MC.2.1 | 20 | T | C | 1.0 |
| S373P | vaccine neutralization efficacy | Pokay | MC.2.1 | 20 | T | C | 1.0 |
| S373P | vaccinee plasma binding | Pokay | MC.2.1 | 20 | T | C | 1.0 |
| S373P | ACE2 receptor binding affinity | Pokay | MC.2.1 | 20 | T | C | 1.0 |
| S373P | monoclonal antibody serial passage escape | Pokay | MC.2.1 | 20 | T | C | 1.0 |

| Mutations | Functional Category | Annotation Resource | Lineages | Sequence Depth | Reference Allele | Alternate Allele | Alternate Frequency |
|-----------|---------------------------------|---------------------|----------|----------------|------------------|------------------|---------------------|
| S373P | transmissibility | Pokay | MC.2.1 | 20 | T | C | 1.0 |
| D405N | pharmaceutical effectiveness | Pokay | MC.2.1 | 20 | G | A | 1.0 |
| D405N | antibody epitope effects | Pokay | MC.2.1 | 20 | G | A | 1.0 |
| D405N | vaccine neutralization efficacy | Pokay | MC.2.1 | 20 | G | A | 1.0 |
| D405N | vaccinee plasma binding | Pokay | MC.2.1 | 20 | G | A | 1.0 |
| D405N | ACE2 receptor binding affinity | Pokay | MC.2.1 | 20 | G | A | 1.0 |
| R408S | pharmaceutical effectiveness | Pokay | MC.2.1 | 20 | A | C | 1.0 |
| R408S | antibody epitope effects | Pokay | MC.2.1 | 20 | A | C | 1.0 |
| R408S | vaccine neutralization efficacy | Pokay | MC.2.1 | 20 | A | C | 1.0 |
| R408S | vaccinee plasma binding | Pokay | MC.2.1 | 20 | A | C | 1.0 |
| R408S | ACE2 receptor binding affinity | Pokay | MC.2.1 | 20 | A | C | 1.0 |
| R408S | gene expression increase | Pokay | MC.2.1 | 20 | A | C | 1.0 |
| R408S | vaccine efficacy | Pokay | MC.2.1 | 20 | A | C | 1.0 |
| K417N | pharmaceutical effectiveness | Pokay | MC.2.1 | 20 | G | T | 1.0 |
| K417N | antibody epitope effects | Pokay | MC.2.1 | 20 | G | T | 1.0 |
| K417N | vaccine neutralization efficacy | Pokay | MC.2.1 | 20 | G | T | 1.0 |

| Mutations | Functional Category | Annotation Resource | Lineages | Sequence Depth | Reference Allele | Alternate Allele | Alternate Frequency |
|-----------|---|---------------------|----------|----------------|------------------|------------------|---------------------|
| K417N | convalescent plasma escape | Pokay | MC.2.1 | 20 | G | T | 1.0 |
| K417N | convalescent plasma binding | Pokay | MC.2.1 | 20 | G | T | 1.0 |
| K417N | vaccinee plasma binding | Pokay | MC.2.1 | 20 | G | T | 1.0 |
| K417N | ACE2 receptor binding affinity | Pokay | MC.2.1 | 20 | G | T | 1.0 |
| K417N | T cell evasion | Pokay | MC.2.1 | 20 | G | T | 1.0 |
| K417N | tissue specific neutralization | Pokay | MC.2.1 | 20 | G | T | 1.0 |
| K417N | trafficking | Pokay | MC.2.1 | 20 | G | T | 1.0 |
| K417N | environmental condition stability | Pokay | MC.2.1 | 20 | G | T | 1.0 |
| K417N | outcome hazard ratio | Pokay | MC.2.1 | 20 | G | T | 1.0 |
| K417N | humoral response durability | Pokay | MC.2.1 | 20 | G | T | 1.0 |
| K417N | anthropozoonotic events | Pokay | MC.2.1 | 20 | G | T | 1.0 |
| K417N | reinfection | Pokay | MC.2.1 | 20 | G | T | 1.0 |
| K417N | symptom prevalence | Pokay | MC.2.1 | 20 | G | T | 1.0 |
| K417N | monoclonal antibody serial passage escape | Pokay | MC.2.1 | 20 | G | T | 1.0 |
| K417N | gene expression increase | Pokay | MC.2.1 | 20 | G | T | 1.0 |
| K417N | virion structure | Pokay | MC.2.1 | 20 | G | T | 1.0 |

| Mutations | Functional Category | Annotation Resource | Lineages | Sequence Depth | Reference Allele | Alternate Allele | Alternate Frequency |
|-----------|---|---------------------|----------|----------------|------------------|------------------|---------------------|
| K417N | viral load | Pokay | MC.2.1 | 20 | G | T | 1.0 |
| K417N | transmissibility | Pokay | MC.2.1 | 20 | G | T | 1.0 |
| N440K | pharmaceutical effectiveness | Pokay | MC.2.1 | 19 | T | G | 1.0 |
| N440K | antibody epitope effects | Pokay | MC.2.1 | 19 | T | G | 1.0 |
| N440K | vaccine neutralization efficacy | Pokay | MC.2.1 | 19 | T | G | 1.0 |
| N440K | convalescent plasma escape | Pokay | MC.2.1 | 19 | T | G | 1.0 |
| N440K | vaccinee plasma binding | Pokay | MC.2.1 | 19 | T | G | 1.0 |
| N440K | ACE2 receptor binding affinity | Pokay | MC.2.1 | 19 | T | G | 1.0 |
| N440K | monoclonal antibody serial passage escape | Pokay | MC.2.1 | 19 | T | G | 1.0 |
| N440K | transmissibility | Pokay | MC.2.1 | 19 | T | G | 1.0 |
| N440K | reinfection | Pokay | MC.2.1 | 19 | T | G | 1.0 |
| N450D | convalescent plasma escape | Pokay | MC.2.1 | 19 | A | G | 1.0 |
| N450D | monoclonal antibody serial passage escape | Pokay | MC.2.1 | 19 | A | G | 1.0 |
| N450D | antibody epitope effects | Pokay | MC.2.1 | 19 | A | G | 1.0 |
| L452W | monoclonal antibody serial passage escape | Pokay | MC.2.1 | 19 | CT | TG | 1.0 |

| Mutations | Functional Category | Annotation Resource | Lineages | Sequence Depth | Reference Allele | Alternate Allele | Alternate Frequency |
|-----------|---|---------------------|----------|----------------|------------------|------------------|---------------------|
| N460K | ACE2 receptor binding affinity | Pokay | MC.2.1 | 19 | T | A | 1.0 |
| N460K | pharmaceutical effectiveness | Pokay | MC.2.1 | 19 | T | A | 1.0 |
| N460K | gene expression increase | Pokay | MC.2.1 | 19 | T | A | 1.0 |
| N460K | monoclonal antibody serial passage escape | Pokay | MC.2.1 | 19 | T | A | 1.0 |
| F486P | ACE2 receptor binding affinity | Pokay | MC.2.1 | 20 | TT | CC | 1.0 |
| F486P | gene expression increase | Pokay | MC.2.1 | 20 | TT | CC | 1.0 |
| F486P | monoclonal antibody serial passage escape | Pokay | MC.2.1 | 20 | TT | CC | 1.0 |
| Q498R | pharmaceutical effectiveness | Pokay | MC.2.1 | 20 | A | G | 1.0 |
| Q498R | antibody epitope effects | Pokay | MC.2.1 | 20 | A | G | 1.0 |
| Q498R | vaccine neutralization efficacy | Pokay | MC.2.1 | 20 | A | G | 1.0 |
| Q498R | vaccinee plasma binding | Pokay | MC.2.1 | 20 | A | G | 1.0 |
| Q498R | ACE2 receptor binding affinity | Pokay | MC.2.1 | 20 | A | G | 1.0 |
| N501Y | vaccinee plasma binding | Pokay | MC.2.1 | 20 | A | T | 1.0 |
| N501Y | pharmaceutical effectiveness | Pokay | MC.2.1 | 20 | A | T | 1.0 |

| Mutations | Functional Category | Annotation Resource | Lineages | Sequence Depth | Reference Allele | Alternate Allele | Alternate Frequency |
|-----------|-----------------------------------|---------------------|----------|----------------|------------------|------------------|---------------------|
| N501Y | antibody epitope effects | Pokay | MC.2.1 | 20 | A | T | 1.0 |
| N501Y | vaccine neutralization efficacy | Pokay | MC.2.1 | 20 | A | T | 1.0 |
| N501Y | virion structure | Pokay | MC.2.1 | 20 | A | T | 1.0 |
| N501Y | convalescent plasma escape | Pokay | MC.2.1 | 20 | A | T | 1.0 |
| N501Y | reinfection | Pokay | MC.2.1 | 20 | A | T | 1.0 |
| N501Y | vaccine efficacy | Pokay | MC.2.1 | 20 | A | T | 1.0 |
| N501Y | trafficking | Pokay | MC.2.1 | 20 | A | T | 1.0 |
| N501Y | anthropozoonotic events | Pokay | MC.2.1 | 20 | A | T | 1.0 |
| N501Y | convalescent plasma binding | Pokay | MC.2.1 | 20 | A | T | 1.0 |
| N501Y | T cell evasion | Pokay | MC.2.1 | 20 | A | T | 1.0 |
| N501Y | transmissibility | Pokay | MC.2.1 | 20 | A | T | 1.0 |
| N501Y | ACE2 receptor binding affinity | Pokay | MC.2.1 | 20 | A | T | 1.0 |
| N501Y | tissue specific neutralization | Pokay | MC.2.1 | 20 | A | T | 1.0 |
| N501Y | environmental condition stability | Pokay | MC.2.1 | 20 | A | T | 1.0 |
| N501Y | outcome hazard ratio | Pokay | MC.2.1 | 20 | A | T | 1.0 |
| N501Y | symptom prevalence | Pokay | MC.2.1 | 20 | A | T | 1.0 |
| N501Y | aerosolization | Pokay | MC.2.1 | 20 | A | T | 1.0 |

| Mutations | Functional Category | Annotation Resource | Lineages | Sequence Depth | Reference Allele | Alternate Allele | Alternate Frequency |
|-----------|---|---------------------|----------|----------------|------------------|------------------|---------------------|
| N501Y | clinical indicators | Pokay | MC.2.1 | 20 | A | T | 1.0 |
| N501Y | tissue specific replication effects | Pokay | MC.2.1 | 20 | A | T | 1.0 |
| N501Y | viral load | Pokay | MC.2.1 | 20 | A | T | 1.0 |
| N501Y | humoral response durability | Pokay | MC.2.1 | 20 | A | T | 1.0 |
| N501Y | syncytium formation | Pokay | MC.2.1 | 20 | A | T | 1.0 |
| N501Y | immunosuppression variant emergence | Pokay | MC.2.1 | 20 | A | T | 1.0 |
| N501Y | homoplasmy | Pokay | MC.2.1 | 20 | A | T | 1.0 |
| N501Y | monoclonal antibody serial passage escape | Pokay | MC.2.1 | 20 | A | T | 1.0 |
| Y505H | pharmaceutical effectiveness | Pokay | MC.2.1 | 20 | T | C | 1.0 |
| Y505H | antibody epitope effects | Pokay | MC.2.1 | 20 | T | C | 1.0 |
| Y505H | vaccine neutralization efficacy | Pokay | MC.2.1 | 20 | T | C | 1.0 |
| Y505H | vaccinee plasma binding | Pokay | MC.2.1 | 20 | T | C | 1.0 |
| Y505H | ACE2 receptor binding affinity | Pokay | MC.2.1 | 20 | T | C | 1.0 |
| Y505H | gene expression increase | Pokay | MC.2.1 | 20 | T | C | 1.0 |
| Y505H | anthropozoonotic events | Pokay | MC.2.1 | 20 | T | C | 1.0 |

| Mutations | Functional Category | Annotation Resource | Lineages | Sequence Depth | Reference Allele | Alternate Allele | Alternate Frequency |
|-----------|-----------------------------------|---------------------|----------|----------------|------------------|------------------|---------------------|
| D614G | vaccine neutralization efficacy | Pokay | MC.2.1 | 20 | A | G | 1.0 |
| D614G | convalescent plasma binding | Pokay | MC.2.1 | 20 | A | G | 1.0 |
| D614G | vaccinee plasma binding | Pokay | MC.2.1 | 20 | A | G | 1.0 |
| D614G | pharmaceutical effectiveness | Pokay | MC.2.1 | 20 | A | G | 1.0 |
| D614G | antibody epitope effects | Pokay | MC.2.1 | 20 | A | G | 1.0 |
| D614G | convalescent plasma escape | Pokay | MC.2.1 | 20 | A | G | 1.0 |
| D614G | virion structure | Pokay | MC.2.1 | 20 | A | G | 1.0 |
| D614G | reinfection | Pokay | MC.2.1 | 20 | A | G | 1.0 |
| D614G | vaccine efficacy | Pokay | MC.2.1 | 20 | A | G | 1.0 |
| D614G | trafficking | Pokay | MC.2.1 | 20 | A | G | 1.0 |
| D614G | anthropozoonotic events | Pokay | MC.2.1 | 20 | A | G | 1.0 |
| D614G | T cell evasion | Pokay | MC.2.1 | 20 | A | G | 1.0 |
| D614G | transmissibility | Pokay | MC.2.1 | 20 | A | G | 1.0 |
| D614G | ACE2 receptor binding affinity | Pokay | MC.2.1 | 20 | A | G | 1.0 |
| D614G | tissue specific neutralization | Pokay | MC.2.1 | 20 | A | G | 1.0 |
| D614G | environmental condition stability | Pokay | MC.2.1 | 20 | A | G | 1.0 |
| D614G | aerosolization | Pokay | MC.2.1 | 20 | A | G | 1.0 |

| Mutations | Functional Category | Annotation Resource | Lineages | Sequence Depth | Reference Allele | Alternate Allele | Alternate Frequency |
|-----------|-------------------------------------|---------------------|----------|----------------|------------------|------------------|---------------------|
| D614G | clinical indicators | Pokay | MC.2.1 | 20 | A | G | 1.0 |
| D614G | tissue specific replication effects | Pokay | MC.2.1 | 20 | A | G | 1.0 |
| D614G | humoral response durability | Pokay | MC.2.1 | 20 | A | G | 1.0 |
| D614G | outcome hazard ratio | Pokay | MC.2.1 | 20 | A | G | 1.0 |
| D614G | syncytium formation | Pokay | MC.2.1 | 20 | A | G | 1.0 |
| D614G | immunosuppression variant emergence | Pokay | MC.2.1 | 20 | A | G | 1.0 |
| D614G | symptom prevalence | Pokay | MC.2.1 | 20 | A | G | 1.0 |
| D614G | viral load | Pokay | MC.2.1 | 20 | A | G | 1.0 |
| H655Y | pharmaceutical effectiveness | Pokay | MC.2.1 | 20 | C | T | 1.0 |
| H655Y | antibody epitope effects | Pokay | MC.2.1 | 20 | C | T | 1.0 |
| H655Y | vaccine neutralization efficacy | Pokay | MC.2.1 | 20 | C | T | 1.0 |
| H655Y | virion structure | Pokay | MC.2.1 | 20 | C | T | 1.0 |
| H655Y | convalescent plasma escape | Pokay | MC.2.1 | 20 | C | T | 1.0 |
| H655Y | reinfection | Pokay | MC.2.1 | 20 | C | T | 1.0 |
| H655Y | vaccine efficacy | Pokay | MC.2.1 | 20 | C | T | 1.0 |
| H655Y | trafficking | Pokay | MC.2.1 | 20 | C | T | 1.0 |

| Mutations | Functional Category | Annotation Resource | Lineages | Sequence Depth | Reference Allele | Alternate Allele | Alternate Frequency |
|-----------|---------------------------------|---------------------|----------|----------------|------------------|------------------|---------------------|
| H655Y | anthropozoonotic events | Pokay | MC.2.1 | 20 | C | T | 1.0 |
| H655Y | convalescent plasma binding | Pokay | MC.2.1 | 20 | C | T | 1.0 |
| H655Y | T cell evasion | Pokay | MC.2.1 | 20 | C | T | 1.0 |
| H655Y | transmissibility | Pokay | MC.2.1 | 20 | C | T | 1.0 |
| H655Y | outcome hazard ratio | Pokay | MC.2.1 | 20 | C | T | 1.0 |
| H655Y | vaccinee plasma binding | Pokay | MC.2.1 | 20 | C | T | 1.0 |
| H655Y | ACE2 receptor binding affinity | Pokay | MC.2.1 | 20 | C | T | 1.0 |
| H655Y | homoplasy | Pokay | MC.2.1 | 20 | C | T | 1.0 |
| N679K | pharmaceutical effectiveness | Pokay | MC.2.1 | 19 | T | G | 1.0 |
| N679K | antibody epitope effects | Pokay | MC.2.1 | 19 | T | G | 1.0 |
| N679K | vaccine neutralization efficacy | Pokay | MC.2.1 | 19 | T | G | 1.0 |
| N679K | vaccinee plasma binding | Pokay | MC.2.1 | 19 | T | G | 1.0 |
| N679K | ACE2 receptor binding affinity | Pokay | MC.2.1 | 19 | T | G | 1.0 |
| P681R | pharmaceutical effectiveness | Pokay | MC.2.1 | 19 | C | G | 1.0 |
| P681R | trafficking | Pokay | MC.2.1 | 19 | C | G | 1.0 |
| P681R | convalescent plasma escape | Pokay | MC.2.1 | 19 | C | G | 1.0 |

| Mutations | Functional Category | Annotation Resource | Lineages | Sequence Depth | Reference Allele | Alternate Allele | Alternate Frequency |
|-----------|---------------------------------|---------------------|----------|----------------|------------------|------------------|---------------------|
| P681R | antibody epitope effects | Pokay | MC.2.1 | 19 | C | G | 1.0 |
| P681R | vaccine neutralization efficacy | Pokay | MC.2.1 | 19 | C | G | 1.0 |
| P681R | convalescent plasma binding | Pokay | MC.2.1 | 19 | C | G | 1.0 |
| P681R | vaccinee plasma binding | Pokay | MC.2.1 | 19 | C | G | 1.0 |
| P681R | ACE2 receptor binding affinity | Pokay | MC.2.1 | 19 | C | G | 1.0 |
| P681R | outcome hazard ratio | Pokay | MC.2.1 | 19 | C | G | 1.0 |
| P681R | vaccine efficacy | Pokay | MC.2.1 | 19 | C | G | 1.0 |
| P681R | viral load | Pokay | MC.2.1 | 19 | C | G | 1.0 |
| P681R | symptom prevalence | Pokay | MC.2.1 | 19 | C | G | 1.0 |
| P681R | transmissibility | Pokay | MC.2.1 | 19 | C | G | 1.0 |
| P681R | virion structure | Pokay | MC.2.1 | 19 | C | G | 1.0 |
| N764K | pharmaceutical effectiveness | Pokay | MC.2.1 | 19 | C | A | 1.0 |
| N764K | antibody epitope effects | Pokay | MC.2.1 | 19 | C | A | 1.0 |
| N764K | vaccine neutralization efficacy | Pokay | MC.2.1 | 19 | C | A | 1.0 |
| N764K | vaccinee plasma binding | Pokay | MC.2.1 | 19 | C | A | 1.0 |
| N764K | ACE2 receptor binding affinity | Pokay | MC.2.1 | 19 | C | A | 1.0 |

| Mutations | Functional Category | Annotation Resource | Lineages | Sequence Depth | Reference Allele | Alternate Allele | Alternate Frequency |
|-----------|---------------------------------|---------------------|----------|----------------|------------------|------------------|---------------------|
| D796Y | pharmaceutical effectiveness | Pokay | MC.2.1 | 19 | G | T | 1.0 |
| D796Y | antibody epitope effects | Pokay | MC.2.1 | 19 | G | T | 1.0 |
| D796Y | vaccine neutralization efficacy | Pokay | MC.2.1 | 19 | G | T | 1.0 |
| D796Y | vaccinee plasma binding | Pokay | MC.2.1 | 19 | G | T | 1.0 |
| D796Y | ACE2 receptor binding affinity | Pokay | MC.2.1 | 19 | G | T | 1.0 |
| S939F | anthropozoonotic events | Pokay | MC.2.1 | 18 | C | T | 1.0 |
| Q954H | pharmaceutical effectiveness | Pokay | MC.2.1 | 17 | A | T | 1.0 |
| Q954H | antibody epitope effects | Pokay | MC.2.1 | 17 | A | T | 1.0 |
| Q954H | vaccine neutralization efficacy | Pokay | MC.2.1 | 17 | A | T | 1.0 |
| Q954H | vaccinee plasma binding | Pokay | MC.2.1 | 17 | A | T | 1.0 |
| Q954H | ACE2 receptor binding affinity | Pokay | MC.2.1 | 17 | A | T | 1.0 |
| N969K | pharmaceutical effectiveness | Pokay | MC.2.1 | 19 | T | A | 1.0 |
| N969K | antibody epitope effects | Pokay | MC.2.1 | 19 | T | A | 1.0 |
| N969K | vaccine neutralization efficacy | Pokay | MC.2.1 | 19 | T | A | 1.0 |
| N969K | vaccinee plasma binding | Pokay | MC.2.1 | 19 | T | A | 1.0 |

| Mutations | Functional Category | Annotation Resource | Lineages | Sequence Depth | Reference Allele | Alternate Allele | Alternate Frequency |
|-----------|--------------------------------|---------------------|----------|----------------|------------------|------------------|---------------------|
| N969K | ACE2 receptor binding affinity | Pokay | MC.2.1 | 19 | T | A | 1.0 |
| T9I | homoplasy | Pokay | MC.2.1 | 20 | C | T | 1.0 |
| T9I | frequency based fitness | Pokay | MC.2.1 | 20 | C | T | 1.0 |
| D3H | frequency based fitness | Pokay | MC.2.1 | 20 | G | C | 1.0 |
| Q19E | frequency based fitness | Pokay | MC.2.1 | 20 | C | G | 1.0 |
| F53F | frequency based fitness | Pokay | MC.2.1 | 20 | C | T | 1.0 |
| L93L | frequency based fitness | Pokay | MC.2.1 | 20 | C | T | 0.05 |
| F112F | frequency based fitness | Pokay | MC.2.1 | 20 | C | T | 1.0 |
| L120L | frequency based fitness | Pokay | MC.2.1 | 20 | C | T | 0.15 |
| P13L | homoplasy | Pokay | MC.2.1 | 20 | C | T | 1.0 |
| P13L | T cell evasion | Pokay | MC.2.1 | 20 | C | T | 1.0 |

Table 3: Functional Effect Summary

This table contains detailed functional descriptions of each functional category

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|--|---------------------|--|------------------|--|
| M85del | immunosuppression variant emergence | Pokay | Emergent as 22% variant by day 70 post-infection of female immunocompromised individual with chronic lymphocytic leukemia and acquired hypogammaglobulinemia. Variant became 100% in day 70 culture. Variant disappeared after convalescent plasma treatment (day 71) in subsequent patient sample sequencing. | 2020 | Avanzato et al. (2020) |
| M85del | IFN activity | Pokay | Deletions in the genomic nucleotide 500-523 range are shown in vitro culture to downregulated interferon A1/2 & B1 expression, and are associated with lower clinical severity of disease (Jan-Mar 2020 in China). variations of deletion in this region are found in separate lineages throughout the globe. This specific deletion (genomic 500-523) was tested in vitro for IFN response. | 2021 | Lin et al. (2021) |
| M85del | IFN activity | Pokay | Deletions in the genomic nucleotide 500-523 range are shown in vitro culture to downregulated interferon A1/2 & B1 expression, and are associated with lower clinical severity of disease (Jan-Mar 2020 in China). variations of deletion in this region are found in separate lineages throughout the globe. This specific deletion (genomic 509-523) was tested in vitro for IFN response. | 2021 | Lin et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|--|
| M85del | IFN activity | Pokay | Deletions in the genomic nucleotide 500-523 range are shown in vitro culture to downregulated interferon A1/2 & B1 expression, and are associated with lower clinical severity of disease (Jan-Mar 2020 in China). variations of deletion in this region are found in separate lineages throughout the globe. This specific deletion (genomic 509-517) was tested in vitro for IFN response. | 2021 | Lin et al. (2021) |
| H69del | convalescent plasma escape | Pokay | Artificially constructed HIV-1 pseudovirus with set of mutations drawn from plasma passage escape experiments and mutations from variants of concern completely ablates neutralization in 19 of 21 convalescents plasma collected mean 1.3 months post infection. [actual Y145del from manuscript substituted with more common Y144del description] | 2021 | Schmidt et al. (2021) |
| H69del | vaccine neutralization efficacy | Pokay | Neutralization efficiency (ID50) against B.1.525 reduced 4.2x relative to D614G wildtype using pseudotyped VSV assay on 8 Moderna vaccinee sera one week post-booster. | 2021 | Choi et al. (2021) |
| H69del | pharmaceutical effectiveness | Pokay | Omicron (a.k.a. B.1.1.529) Spike pseudotyped VSV and Vero E6 cells has somewhat reduced neutralization (2.7x) vs wild type with monoclonal antibody Sotrovimab (a.k.a. VIR-7831). [delins at 214 omitted for syntax compatibility] | 2021 | Cathcart et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|--|
| H69del | vaccine neutralization efficacy | Pokay | Omicron breakthrough infection after 3-dose vaccination resulted in a further 3.5-fold and 2.9-fold increase of Omicron BA.1 and BA.2 neutralizing titers. Omicron BA.4/5 showed the highest neutralization resistance of all variants tested, resulting in low geometric mean neutralizing titers in plasma samples obtained after the second vaccine dose (NT50 | 2022 | Wang et al. (2022) |
| H69del | antibody epitope effects | Pokay | Neutralization of the bsAbs Bi-Nab47D10-35B5. Omicron BA.1 has an IC50 fold change of 0.08x. | 2022 | Yuan et al. (2022) |
| H69del | vaccine neutralization efficacy | Pokay | Omicron B.1.1.529 (BA.1) neutralization of the Omicron variants by antibodies induced by three doses of Pfizer/BNT162b2 mRNA vaccine was 7-8-fold less potent than the D614G, and the Omicron variants still evade neutralization more efficiently. | 2022 | Neerukonda et al. (2022) |
| H69del | pharmaceutical effectiveness | Pokay | Omicron (B.1.1.529 [BA.1]) have higher sensitivity to inhibition by soluble angiotensin converting enzyme 2 (ACE2) and the endosomal inhibitor chloroquine compared to D614G | 2022 | Neerukonda et al. (2022) |
| H69del | antibody epitope effects | Pokay | Neutralization of the bsAbs Bi-Nab35B5-47D10. Omicron BA.1 has an IC50 fold change of 0.30x. | 2022 | Yuan et al. (2022) |
| H69del | vaccine neutralization efficacy | Pokay | Paradigms' ACE-2 variant LVE/STR chimera binds to SARS-2 Omicron variant B.1.1.529 spike protein trimer with high affinity. Determined using Surrogate Viral Neutralization Tests. | 2022 | Uhal B et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|--------------------------------|---------------------|--|------------------|--------------------------------------|
| H69del | ACE2 receptor binding affinity | Pokay | L27, V34 and E90 mutation resulted in ultrahigh affinity binding of the LVE-ACE-2 domain to the widest variety of VOCs, with KDs of 73 pM for binding to the Omicron B.1.1.529. Values were obtained with LVE-ACE-2/mAB chimeras containing the Y-T-E sequence that enhances binding to the FcRn receptor, which in turn is expected to extend biological half-life 3-4-fold. | 2022 | Uhal B et al. (2022) |
| H69del | antibody epitope effects | Pokay | Neutralization of the bsAbs 35B5. Omicron BA.1 has an IC50 fold change of 0.38x. | 2022 | Yuan et al. (2022) |
| H69del | vaccinee plasma binding | Pokay | All 10 individuals with 2 doses of the BNT162b2/BNT162b2 vaccine had a neutralizing titer in B.1 variant at an average of 729 NT50. | 2022 | Arora et al. (2022) |
| H69del | antibody epitope effects | Pokay | Plaque reduction neutralization test (PRNT) was used uring primary infection, post sixty daysof second dose vaccination, pre-reinfection and reinfection against Delta variant and was used to determine neutralizing antibodytitres. There was a 24.63x fold increase in antibody response from first infection to recovered and vaccinated with 2 doses (60 days). There was a 4.21x fold increase in antibody response pre-reinfection. There was a 39.27x fold increase in antibody response during reinfection. | 2022 | Shete et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|--------------------------|---------------------|--|------------------|-------------------------------------|
| H69del | antibody epitope effects | Pokay | Plaque reduction neutralization test (PRNT) was used uring primary infection, post sixty daysof second dose vaccination, pre-reinfection and reinfection against B.1 variant and was used to determine neutralizing antibodytitres. There was a 6.76x fold increase in antibody response from first infection to recovered and vaccinated with 2 doses (60 days). There was a 2.06x fold increase in antibody response pre-reinfection. There was a 8.18x fold increase in antibody response during reinfection. | 2022 | Shete et al. (2022) |
| H69del | vaccinee plasma binding | Pokay | All 10 individuals with 3 doses of the BNT162b2/BNT162b2 vaccine had a neutralizing titer in B.1 variant at an average of 3319 NT50. | 2022 | Arora et al. (2022) |
| H69del | antibody epitope effects | Pokay | Plaque reduction neutralization test (PRNT) was used uring primary infection, post sixty daysof second dose vaccination, pre-reinfection and reinfection against Omicron variant and was used to determine neutralizing antibodytitres. There was a 114.84x fold increase in antibody response from first infection to recovered and vaccinated with 2 doses (60 days). There was a 6.61x fold increase in antibody response pre-reinfection. There was a 1194.9x fold increase in antibody response during reinfection. | 2022 | Shete et al. (2022) |
| H69del | antibody epitope effects | Pokay | BnAb 002-S21F2 IC50 on the Omicron BA.1 variant is 1.0x fold the wildtype. | 2022 | Kumar et al. (2022) |
| H69del | antibody epitope effects | Pokay | Neutralization of the bsAbs 47D10. Omicron BA.1 has an IC50 fold change of 1.26x. | 2022 | Yuan et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|--|
| H69del | pharmaceutical effectiveness | Pokay | Omicron BA.3 have higher sensitivity to inhibition by soluble angiotensin converting enzyme 2 (ACE2) and the endosomal inhibitor chloroquine compared to D614G | 2022 | Neerukonda et al. (2022) |
| H69del | vaccine neutralization efficacy | Pokay | Omicron BA.3 neutralization of the Omicron variants by antibodies induced by three doses of Pfizer/BNT162b2 mRNA vaccine was 7-8-fold less potent than the D614G, and the Omicron variants still evade neutralization more efficiently. | 2022 | Neerukonda et al. (2022) |
| H69del | vaccinee plasma binding | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.3 (from South Africa/NICD-N22404/2021) were 4.2x-fold lower (95% CI: 0.15x-0.20x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| H69del | vaccine neutralization efficacy | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.3 (from South Africa/NICD-N22404/2021) were 6.2-fold lower (95% CI: 11.8x-14.3x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| H69del | vaccine neutralization efficacy | Pokay | paired testing of vaccine sera against ancestral virus compared to Omicron BA.1 shows that 3-dose vaccine regimen provides over 50x fold increase in protection against Omicron(B.1.1.529 [BA.1]) compared to a 2-dose regimen. | 2022 | Hao et al. (2022) |
| H69del | pharmaceutical effectiveness | Pokay | 4th antigenic exposure with Omicron (B.1.1.529 [BA.1])(n | 2022 | Wang et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|-------------------------------------|---------------------|---|------------------|--|
| H69del | vaccine neutralization efficacy | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.1 (from Botswana/R40B59_BHP_3321 001248/2021) were 3.4-fold lower (95% CI: 3.2x-3.6x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| H69del | vaccinee plasma binding | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.1 (from Botswana/R40B59_BHP_3321 001248/2021) were 28.7x-fold lower (95% CI: 0.03x-0.05) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| H69del | vaccinee plasma binding | Pokay | Neutralization activity of almost all Moderna Phase 1 sera tested actually *increased*. | 2021 | Shen et al. (2021) |
| H69del | immunosuppression variant emergence | Pokay | The delH69/V70 enhances viral infectivity, indicating its effect on virus fitness is independent to the N501Y RBM change [with which it is found in lineage B.1.1.7] Possibly arisen as a result of the virus evolving from immune selection pressure in infected individuals and possibly only one chronic infection in the case of lineage B.1.1.7. | 2020 | Kemp et al. (2020) |
| H69del | convalescent plasma escape | Pokay | One convalescent sera tested showed 4-fold or greater reduction in neutralization efficiency. | 2021 | Alenquer et al. (2021) |
| H69del | convalescent plasma escape | Pokay | Neutralization activity of almost all convalescent sera tested decreased ~2x. | 2021 | Shen et al. (2021) |
| H69del | convalescent plasma escape | Pokay | Neutralization activity of convalescent sera tested decreased ~2x with this B.1.1.7 pseudotyped virus. | 2021 | Shen et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|--|
| H69del | antibody epitope effects | Pokay | Reduces neutralization by structurally unmapped mAb COVA1-21 (cluster XI). | 2021 | Rees-Spear et al. (2021) |
| H69del | convalescent plasma binding | Pokay | Viruses containing the point mutations of B.1.1.7 showed that the single point mutations (Δ 69-70 and N501Y) were neutralized as efficiently as D614G across 10 convalescent sera from April 2020 infectees. | 2021 | Tada et al. (2021) |
| H69del | anthropozoonotic events | Pokay | This deletion outside the receptor binding domain in pseudotyped VSV promoted the capacity of pseudotyped VSV to transduce black flying fox (<i>Pteropus alecto</i>) kidney PabKi.1 cells (17.8%) to a level twice that of human epithelial-like Huh-7 cells (9.8%) | 2023 | Li et al. (2023) |
| H69del | convalescent plasma binding | Pokay | No notable change in neutralization efficiency, despite N439K by itself showing a ~2x decrease on average in 16 health workers' convalescent sera. | 2021 | Alenquer et al. (2021) |
| H69del | vaccine neutralization efficacy | Pokay | The neutralizing activity of vaccine was somewhat lower against B.1.1.7 in sera tested from most of the 24 patients with the BNT162b2 mRNA vaccine. (Fig. 4) | 2021 | Chen et al. (2021) |
| H69del | antibody epitope effects | Pokay | B.1.1.7 variant constellation ablates Class 3 N-terminal domain targeting antibody COV2-2489. | 2021 | Chen et al. (2021) |
| H69del | vaccine neutralization efficacy | Pokay | Observed 8.8-fold reduction in neutralization efficiency of Pfizer vaccinee sera (collected 14 days after second dose) against cultured B.1.1.7 sample. Contrast this with 1.3-fold reduction for just the pseudovirus combination of 'key' B.1.1.7 mutation N501Y. | 2021 | Bates et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|--|
| H69del | trafficking | Pokay | Lentiviral pseudotyped with this mutation set from Mink Cluster 5 lineage, was tested on ACE2.293T cells. Luciferase activity was measured two days postinfection, showing slight decrease in infection rate amongst the cells, much closer to D614G activity level than Y453F alone, suggesting compensatory effects between the deletion and the mutation in human cell entry fitness. | 2021 | Tada et al. (2021) |
| H69del | trafficking | Pokay | Lentiviral pseudotyped with this mutation set from Mink Cluster 5 lineage, was tested on ACE2.293T cells. Luciferase activity was measured two days postinfection, showing moderate decrease in infection rate amongst the cells, significantly lower than the deletion or Y453F alone, or their combination, suggesting a synergistic effect on poorer human cell entry fitness. | 2021 | Tada et al. (2021) |
| H69del | vaccine neutralization efficacy | Pokay | Pseudotyped B.1.1.298 virus has reduced neutralization activity vs wild type: 1.4x (30 sera Pfizer median 9 days post 2nd dose) and 1.3x (35 sera Moderna median 18 days post 2nd dose). This was NOT significant by ANOVA. | 2021 | Garcia-Beltran et al. (2021) |
| H69del | trafficking | Pokay | Lentiviral pseudotyped with this mutation set from Mink Cluster 5 lineage, was tested on ACE2.293T cells. Luciferase activity was measured two days postinfection, showing mild to modest decrease in infection rate amongst the cells, suggesting a net mild negative effect on human cell entry fitness. | 2021 | Tada et al. (2021) |
| H69del | convalescent plasma binding | Pokay | Lentiviral pseudotyped with the key mutations from Mink Cluster 5 was neutralized more easily than D614G in 10 convalescent sera from April 2020 infectees. | 2021 | Tada et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|---------------------------------------|
| H69del | trafficking | Pokay | Lentiviral pseudotyped with this mutation set from Mink Cluster 5 lineage, was tested on ACE2.293T cells. Luciferase activity was measured two days postinfection, showing no change in infection rate amongst the cells, markedly higher infectivity than either mutation alone, suggesting a synergistic net neutral effect on human cell entry fitness. | 2021 | Tada et al. (2021) |
| H69del | trafficking | Pokay | Lentiviral pseudotyped with all key mutations from Mink Cluster 5 lineage, was tested on ACE2.293T cells. Luciferase activity was measured two days postinfection, showing major (~50%) decrease in infection rate amongst the cells, suggesting that this anthropozoonotic event is driven by other factors at the expense of human cell entry fitness. | 2021 | Tada et al. (2021) |
| H69del | vaccine neutralization efficacy | Pokay | Neutralization efficiency (ID50) against B.1.1.7+E484K reduced 2.8x relative to D614G wildtype using pseudotyped VSV assay on 8 Moderna vaccinee sera one week post-booster. Compare with 1.2x reduction for B.1.1.7 without E484K. | 2021 | Choi et al. (2021) |
| H69del | vaccine neutralization efficacy | Pokay | Sera after the second dose of Pfizer showed an average reduction in neutralization titres against the B.1.1.7 + E484K variant of ~6.7x, markedly higher than B.1.1.7 alone. For first dose sera, a 9.7x drop was observed. | 2021 | Collier et al. (2021) |
| H69del | convalescent plasma escape | Pokay | Neutralization capacity GMT of 27 subjects' sera post-infection was markedly worse against B.1.1.7 + E484K than the lineage alone, with a 11.4x drop. | 2021 | Collier et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|--------------------------------|---------------------|--|------------------|--|
| H69del | antibody epitope effects | Pokay | Ablates Class 3 N-terminal domain targeting antibody COV2-2489, diminishes COV2-2676. | 2021 | Chen et al. (2021) |
| H69del | trafficking | Pokay | Lentiviral pseudotyped with this mutation set from B.1.1.7 was tested on ACE2.293T cells. Luciferase activity was measured two days postinfection, showing significant (40%) increase in infection rate amongst the cells, much more than the effect of either the deletion or the point mutation alone, suggesting that this combination has a synergistic effect contributing to cell entry fitness, more so than this combination with the addition of P681H. | 2021 | Tada et al. (2021) |
| H69del | symptom prevalence | Pokay | In comparison of B.1.1.7 lineage (193 cases) vs. 'wildtype' (125) in Berlin Jan 18 to March 29 2021, significant symptom changes are absent loss of smell/taste (P | 2021 | van Loon et al. (2021) |
| H69del | ACE2 receptor binding affinity | Pokay | This mutation combination causes major increase in binding affinity vs. wild type as measured by IC50 vs pseudotyped lentivirus, but combined with the complete set of B.1.1.7 lineage variants no major change vs wild type affinity is observed. | 2021 | Tada et al. (2021) |
| H69del | antibody epitope effects | Pokay | Reduction in neutralization by mAbs COVA1-18 (~4x), COVA2-15 (~9x). PG: these effects are largely missing in the deletion-alone data | 2021 | Shen et al. (2021) |
| H69del | symptom prevalence | Pokay | A higher proportion of cases infected with the B.1.1.7 variant were hypoxic on admission compared to other variants (70.0% vs 62.5%, p | 2021 | Snell et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|--|
| H69del | virion structure | Pokay | The Ratio of S2 (processed Spike) to full length Spike is higher for this mutation combination, due to a drop in the full length Spike measured, suggesting that this mutation compensates for decreased Spike production by improved proteolytic processing. | 2021 | Tada et al. (2021) |
| H69del | vaccine neutralization efficacy | Pokay | After one dose, individuals with prior infection showed enhanced T cell immunity, antibody secreting memory B cell response to spike and neutralizing antibodies effective against B.1.1.7 (authentic cell culture supernatants). By comparison, HCW receiving one vaccine dose without prior infection showed reduced immunity against variants. B.1.1.7 spike mutations resulted in increased, abrogated or unchanged T cell responses depending on human leukocyte antigen (HLA) polymorphisms. Study was 26 each post-infection and post first dose HCWs. | 2021 | Reynolds et al. (2021) |
| H69del | convalescent plasma escape | Pokay | Mean 2.6x reduction of NT50 value B.1.1.7 (Alpha) relative to wild type in 8 sera from older convalescent patients (52-92yo) collected 1-3m post symptom onset. | 2021 | Uriu et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|------------------------------------|
| H69del | vaccine neutralization efficacy | Pokay | Detectable antibodies against B.1.1.7 at various time points using pseudotyped lentivirus neutralization in Moderna vaccinee cohort: Day 29 33%, Day 43 100%, Day 119 100%, Day 209 96%. Detectable antibodies against B.1.1.7 at various time points using live virus FRNT neutralization in Moderna vaccinee cohort: Day 29 54%, Day 43 100%, Day 119 100%, Day 209 88%. Detectable antibodies against B.1.1.7 at various time points using ACE2 blocking assay in Moderna vaccinee cohort: Day 29 83%, Days 43,119,209 100%. | 2021 | Pegu et al. (2021) |
| H69del | vaccine neutralization efficacy | Pokay | Using national surveillance data from Israel, using Pfizer vaccine and an estimated prevalence of the B.1.1.7 variant of 94.5% among SARS-CoV-2 infections: Adjusted estimates of vaccine effectiveness 7+ days after second dose were 95.3% (95% CI 94.9–95.7): 91.5% against asymptomatic SARS-CoV-2 infection (90.7–92.2: 40.9 vs 1.8 per 100 000 person-days), 97.0% against symptomatic COVID-19 (96.7–97.2%), 97.2% against COVID-19-related hospitalisation (96.8–97.5%), 97.5% against severe or critical COVID-19-related hospitalisation (97.1–97.8%), and 96.7% against COVID-19-related death (96.0–97.3%). In all age groups, as vaccine coverage increased, the incidence of SARS-CoV-2 outcomes declined | 2021 | Haas et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|---|
| H69del | vaccine neutralization efficacy | Pokay | In sera 1-2 weeks after BNT162b2 first dose, from six patients previously infected with B.1, antibody titer in a microneutralization assay was on average 8192 for B.1.351 virus. This compares favorably (stronger) to post-infection neutralization titer against all variants tested in the same sera (wild type, B.1.1.7, B.1.351, and P.1). | 2021 | Luftig et al. (2021) |
| H69del | virion structure | Pokay | CryoEM analysis of B.1.1.7 demonstrates an increased propensity for 'up', receptor accessible conformation of the Spike protein trimer. | 2021 | Cai et al. (2021) |
| H69del | vaccine neutralization efficacy | Pokay | SARS-CoV-2 infection was confirmed in three HCWs working a single shift: all presented with mild symptoms of COVID-19. The two physicians were fully vaccinated with BNT162b2 vaccine, with the second dose administered 1 month before symptom onset. Both had high titres of IgG anti-spike antibodies at the time of diagnosis. WGS confirmed that all virus strains were VOC 202012/01-lineage B.1.1.7, suggesting a common source of exposure. Epidemiological investigation revealed that the suspected source was a SARS-CoV-2-positive patient who required endotracheal intubation due to severe COVID-19. All procedures were carried out using a full suite of personal protective equipment (PPE). | 2021 | Loconsole et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|----------------------------|---------------------|---|------------------|---|
| H69del | vaccine efficacy | Pokay | In a 1:5 test-negative matched control study of 8153 individuals who received the Moderna mRNA-1273 vaccine, 1422 test-positive were Alpha. Two dose vaccine efficacy against Alpha was 98.4% [96.9-99.1%], one dose VE was 90.1% (82.9-94.2%). | 2021 | Bruxvoort et al. (2021) |
| H69del | convalescent plasma escape | Pokay | Using a new rapid neutralization assay, based on reporter cells that become positive for GFP after overnight infection, sera from 58 convalescent individuals collected up to 9 months after symptoms, similarly neutralized B.1.1.7 and D614G. | 2021 | Planas et al. (2021) |
| H69del | antibody epitope effects | Pokay | Neutralization of the bsAbs Bi-Nab35B5-47D10. Alpha (B.1.1.7) has an IC50 fold change of 1.19x. | 2022 | Yuan et al. (2022) |
| H69del | antibody epitope effects | Pokay | B.1.1.7 pseudotyped virus model impairs binding by RBD-directed mAb 910-30. B.1.1.7 pseudotyped virus model abolishes N-terminal-domain-directed mAbs 5-24, 4-8, and 4A8. B.1.1.7 pseudotyped virus model impairs binding by N-terminal-domain-directed mAbs 2-17, 4-19, 5-7. | 2021 | Wang et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|--|
| H69del | vaccine neutralization efficacy | Pokay | 1.4x improvement in neutralization by serum collected 2 to 3 weeks after the second dose from vaccinees who had received BBIBP-CorV (pVNT50 against VSV pseudotyped as B.1.1.7). Convalescent plasma had similar titer against wild type as the BBIBP-CorV vaccinee sera. 2x reduction in neutralization by serum collected 2 to 3 weeks after the second dose from vaccinees who had received CoronaVac (pVNT50 against VSV pseudotyped as B.1.1.7). Convalescent plasma had similar titer against wild type as the CoronaVac vaccinee sera. | 2021 | Wang et al. (2021) |
| H69del | aerosolization | Pokay | Alpha variant cases in a large campus study showed fine-aerosol shedding amongst unmasked participants remained significantly greater for alpha variant infections (18-fold, 95% CI, 3.4 to 92-fold) after adjusting for the increased viral RNA in MTS and saliva, the number of coughs during sampling sessions, and symptom. After controlling for the effect of masks and numbers of coughs during sampling, alpha variant infection was associated with a 100-fold (95% CI, 16 to 650-fold) increase in coarse- and a 73-fold (95% CI, 15 to 350-fold) increase in fine-aerosol RNA shedding. | 2021 | Adenaiye et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|-----------------------------------|---------------------|--|------------------|---|
| H69del | environmental condition stability | Pokay | No differences in the stability of B.1.1.7 observed in the absence of simulated sunlight at either 20°C or 40°C (with a mean time for a 90% loss of viral infectivity across all dark conditions of 6.2 hours). However, a small but statistically significant difference in the stability was observed in simulated sunlight at 20°C and 20% relative humidity, with B.1.1.7 restoring wild type 90% loss time of 11 minutes vs. 7 and 8 minutes for B.1.319 (D614G) and B.28 (V367F) early 2020 viruses respectively. | 2021 | Schuit et al. (2021) |
| H69del | trafficking | Pokay | Modelling the Alpha variant in primary human airway epithelial (HAE) cultures, S1 to full length Spike ratio (measuring Spike furin cleavage processivity) increase 3.9x relative to wild type (5.4 vs 1.4). This is less efficient than Delta (11x vs wildtype using a P681R mutation instead). [del ~144 changed due to ambiguity] Furthermore the RNA ratio of Delta versus Alpha-spike/Delta-backbone continuously increased from 2.8 on day 1 to 9.8 on day 5 post infection in a co-infection model in HAEs, suggesting the spike gene drives the improved replication of Delta variant. | 2021 | Liu et al. (2021) |
| H69del | vaccine neutralization efficacy | Pokay | No significant difference in T-cell response to B.1.1.7 was observed (vs. ancestral) in blood drawn from 28 participants received the Pfizer-BioNTech vaccine and 2 received the Moderna vaccine. This is despite three mutations (Y144del, D614G, and P681H) overlapping T-cell epitope hotspots. | 2021 | Woldemeskel et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|-----------------------------------|---------------------|---|------------------|---------------------------------------|
| H69del | environmental condition stability | Pokay | Treatment with heat, soap and ethanol revealed similar inactivation profiles indicative of a comparable susceptibility towards disinfection. Furthermore, we observed comparable surface stability on steel, silver, copper and face masks. | 2021 | Meister et al. (2021) |
| H69del | vaccine neutralization efficacy | Pokay | The NAb titers (PRNT50) of sera collected from 38 vaccine recipients four-weeks after the second dose of inactivated whole-virion SARS-CoV-2 BBV152/COVAXIN vaccine [which contains D614G] were not significantly different between B.1.1.7 virus and ancestral D614G virus. | 2021 | Sapkal et al. (2021) |
| H69del | vaccine neutralization efficacy | Pokay | PBMCs of Pfizer/BioNTech BNT162b2 (n | 2021 | Tarke et al. (2021) |
| H69del | vaccine neutralization efficacy | Pokay | A single dose of BNT162b2 vaccine demonstrated vaccine effectiveness [symptomatic or asymptomatic in cohort of routinely NAAT-monitored UK HCWs] of 72% (95% CI 58-86) 21 days after first dose and 86% (95% CI 76-97) seven days after two doses in the antibody negative cohort. This cohort was vaccinated when the dominant variant in circulation was B.1.1.7 and demonstrates effectiveness against this variant. | 2021 | Hall et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|--|
| H69del | vaccine neutralization efficacy | Pokay | Between December 19, 2020 and Jan 24, 2021, 7214 of 9109 eligible HCWs at Sheba Medical Center in Israel had received one or more doses of BNT162b2 (Pfizer) vaccine. Adjusted rate reduction in SARS-CoV-2 NAAT positivity infection compared with unvaccinated workers 1-14 days after 1st dose was 30% (95% CI: 2-50), and 75% (95% CI: 72-84) after 15-28 days. Adjusted rate reduction in symptomatic COVID-19 compared with unvaccinated workers 1-14 days after 1st dose was 47% (95% CI: 17-66), and 85% (95% CI: 71-92) after 15-28 days. [Though often cited as an indicator of VE for B.1.1.7, during this time period in Israel, the prevalence of the B.1.1.7 variant increased from ~20% to 50% of cases (covariants.org), therefore these VE numbers likely represent a mix of B.1.1.7 and other lineage effects.] | 2021 | Amit et al. (2021) |
| H69del | vaccine neutralization efficacy | Pokay | We found that a single dose of the BNT162b2 vaccine is about 60-70% effective at preventing symptomatic disease in adults aged 70 years and older in England and that two doses are about 85-90% effective. Those who were vaccinated and went on to have symptoms had a 44% lower risk of being admitted hospital and a 51% lower risk of death compared with people who were unvaccinated. We also found that a single dose of the ChAdOx1-S vaccine was about 60-75% effective against symptomatic disease and provided an additional protective effect against hospital admission—it is too early to assess the effect on mortality. The B.1.1.7 variant now dominates in the UK and these results will largely reflect vaccine effectiveness against this variant. | 2021 | Lopez Bernal et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|--|
| H69del | antibody epitope effects | Pokay | Neutralization of the 47D10. Alpha (B.1.1.7) has an IC50 fold change of 0.40x. | 2022 | Yuan et al. (2022) |
| H69del | anthropozoonotic events | Pokay | First documented cases of domestic cat and dog infections with the B.1.1.7 strain. | 2021 | Hamer et al. (2021) |
| H69del | vaccine efficacy | Pokay | Effectiveness after one dose of vaccine (BNT162b2 or ChAdOx1 nCoV-19) with the delta variant was (48.7%: 95% confidence interval [CI], 45.5 to 51.7): the results were similar for both vaccines. With the BNT162b2 vaccine, the effectiveness of two doses was 93.7% (95% CI, 91.6 to 95.3) among those with the alpha variant. With the ChAdOx1 nCoV-19 vaccine, the effectiveness of two doses was 74.5% (95% CI, 68.4 to 79.4) among those with the alpha variant. | 2021 | Lopez Bernal et al. (2021) |
| H69del | antibody epitope effects | Pokay | Reduction in neutralization by mAbs COVA2-15 (~9x), B38 (~14x), S309 (~190x) by this B.1.1.7 pseudotyped virus model. | 2021 | Shen et al. (2021) |
| H69del | vaccine neutralization efficacy | Pokay | We observed a sharp decline in cases when ~50% of the elderly population was 2 weeks beyond their first vaccination dose and at a time point during which the B.1.1.7 variant gained transmission dominance. In support of this finding, it was suggested that, after the first vaccination dose, more than 70% of patients develop neutralization antibodies, ¹⁵ and the vaccine efficiency can reach 85%. | 2021 | Munitz et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|--|
| H69del | convalescent plasma escape | Pokay | Neutralizing antibody titers of 2/20 (10%) samples showed >10x reduction (sera collected ~1mo post Jan 2020 first wave in China). Neutralizing antibody titers of 8/20 samples (40%) decreased below an ID50 threshold of 40 (sera collected ~8mo post Jan 2020 first wave in China). | 2021 | Hu et al. (2021) |
| H69del | antibody epitope effects | Pokay | Lessens the potency of mAbs COVA2-17 (~5x, similar to N501Y alone), COVA1-12 (~11x) and COVA1-21 (>100x), which do not compete allosterically. | 2021 | Rees-Spear et al. (2021) |
| H69del | reinfection | Pokay | 36920 COVID Symptom Study app users reported SARS-CoV-2 test positivity in late 2020. Possible reinfections were identified in 249 (0.7% [95% CI 0.6-0.8]) of 36509 app users who reported a positive swab test before Oct 1, 2020, but there was no evidence that the frequency of reinfections was higher for the B.1.1.7 variant than for pre-existing variants. | 2021 | Graham et al. (2021) |
| H69del | vaccine neutralization efficacy | Pokay | Pseudotyped B.1.1.7 virus has reduced neutralization activity vs wild type: 2.1x (30 sera Pfizer median 9 days post 2nd dose) and 2.3x (35 sera Moderna median 18 days post 2nd dose). This was NOT significant by ANOVA. Note that Y145del was actually noted in the paper as the effect of their DNA construct, but this is equivalent at the protein level to the more commonly annotated Y144del. | 2021 | Garcia-Beltran et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|---------------------------------------|
| H69del | vaccine neutralization efficacy | Pokay | The sera of 16 individuals with time course collection was evaluated against VSV pseudotypes: neutralized D614G at week 2, whereas B.1.1.7 started to be neutralized at week 3, although less efficiently than D614G. B.1.1.7 and D614G strains were similarly neutralized at week 4 (1 week after booster dose). | 2021 | Planas et al. (2021) |
| H69del | vaccine neutralization efficacy | Pokay | Neutralization assays of B.1.1.7 virus showed a reduction of 2.5-fold (14 days post 2nd dose AstraZeneca, n | 2021 | Supasa et al. (2021) |
| H69del | antibody epitope effects | Pokay | Neutralization of the bsAbs 35B5. Alpha (B.1.1.7) has an IC50 fold change of 1.39x. | 2022 | Yuan et al. (2022) |
| H69del | vaccine efficacy | Pokay | In Minnesota in early 2021 when Alpha was prevalent, vaccine efficacy was estimated as: mRNA-1273 86% (95%CI: 81-90.6%) and BNT162b2: 76% (95%CI: 69-81%) using age, sex, race, PCR testing and vaccination date matched cohorts of unvaccinated, Pfizer and Moderna vaccinees. [variant list included is ancestral Alpha, as this was an observational study no variant list was given] | 2021 | Puranik et al. (2021) |
| H69del | antibody epitope effects | Pokay | ~20x resistance to mAb CQ038 by B.1.1.7 pseudotyped virus | 2021 | Hu et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|---------------------------------------|
| H69del | reinfection | Pokay | Reinfection with Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) B.1.1.7 variant in an immunocompromised 16yo female with end stage renal disease 94 days after initial infection with a B.1.2 lineage virus. Both lineages were the prevalent one at the time of 1st and 2nd infections respectively in Texas, where the patient was located (suggesting exposure risk rather than lineage immune evasion). | 2021 | Marquez et al. (2021) |
| H69del | vaccine neutralization efficacy | Pokay | Paradigm's ACE-2 variant LVE/STR chimera neutralizes Alpha Variant B.1.1.7 RBD significantly better than GenScript IgG FL18-740 w.t. ACE-2 mAB. Determined using Surrogate Viral Neutralization Tests. | 2022 | Uhal B et al. (2022) |
| H69del | antibody epitope effects | Pokay | Neutralization of the bsAbs Bi-Nab47D10-35B5. Alpha (B.1.1.7) has an IC50 fold change of 1.44x. | 2022 | Yuan et al. (2022) |
| H69del | vaccine neutralization efficacy | Pokay | A single dose of BNT162b2 (Pfizer) vaccine showed vaccine effectiveness of 70% (95% CI 55-85) 21 days after first dose and 85% (74-96) 7 days after two doses in the study population. Our findings show that the BNT162b2 vaccine can prevent both symptomatic and asymptomatic infection in working-age adults. This cohort (8203 treatment, 15121 control) was vaccinated when the dominant variant in circulation was B.1.1.7 and shows effectiveness against this variant. | 2021 | Hall et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|---------------------------------------|
| H69del | convalescent plasma escape | Pokay | NTD-specific nAbs showed a substantial (3-450x) decrease in neutralization potency against the recently reported highly transmissible B.1.1.7 variant of concern, whereas RBD-specific nAbs were either unaffected or showed lower decreases in potency. | 2021 | Graham et al. (2021) |
| H69del | tissue specific neutralization | Pokay | The nasal mucosa of Pfizer vaccinees with time course collection was evaluated against VSV pseudotypes: results (only one nasal swab from different previously infected vaccinee neutralizing at weeks 3 and 6 against B.1.1.7 and D614G) suggest that vaccinees probably do not elicit an early humoral response detectable at mucosal surfaces even though sera neutralization was observed. They strengthen the hypothesis that some vaccines may not protect against viral acquisition and infection of the oral–nasal region, but may prevent severe disease associated with viral dissemination in the lower respiratory tract. | 2021 | Planas et al. (2021) |
| H69del | pharmaceutical effectiveness | Pokay | Infectious viral titers in lung tissue determined using a tissue culture infectious dose (TCID) assay in 10 hamsters showed that Alpha Molnupiravir (MK-4482) had ~2.75x fold drop. | 2022 | Rosenke et al. (2022) |
| H69del | vaccine neutralization efficacy | Pokay | Neutralization efficiency (ID50) against B.1.1.7 reduced 1.2x relative to D614G wildtype using pseudotyped VSV assay on 8 Moderna vaccinee sera one week post-booster. | 2021 | Choi et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|--|
| H69del | reinfection | Pokay | Second infection in December 2020 with B.1.1.7 after April 2020 initial infection with B.2 in a 78-year-old man with a history of Type 2 diabetes mellitus, diabetic nephropathy on hemodialysis, chronic obstructive pulmonary disease (COPD), mixed central and obstructive sleep apnea, ischemic heart disease, with no history of immunosuppression. | 2021 | Harrington et al. (2021) |
| H69del | trafficking | Pokay | The entry efficiencies of Spike pseudotyped viruses bearing N501Y Variant 1 (B.1.1.7) mutant were about 3 to 4.4 times higher than that of the WT pseudovirus when viral input was normalized, suggesting that these spike variants promote the infectivity of SARS-CoV-2. | 2021 | Hu et al. (2021) |
| H69del | trafficking | Pokay | ~2.5x cleavage of S2 relative to WA1 (D614G) wildtype by Alpha variant variant as measured by mass spectrometry of Vero-TMPRSS culture. | 2021 | Esclera et al. (2021) |
| H69del | vaccine neutralization efficacy | Pokay | Virus neutralisation activity (using a live SARS-CoV-2 microneutralisation assay (ND50)) by vaccine induced antibodies was 9-fold lower against the B.1.1.7 variant than against a canonical non B.1.1.7 lineage. Vaccine efficacy against symptomatic NAAT positive infection was similar for B.1.1.7 and non-B.1.1.7 lineages (74.6% [95%CI 41.6-88.9] and 84% [95% CI 70.7-91.4] respectively). Furthermore, vaccination with ChAdOx1 nCoV-19 results in a reduction in the duration of shedding and viral load, which may translate into a material impact on transmission of disease. | 2021 | Emary et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|---|
| H69del | antibody epitope effects | Pokay | BnAb 002-S21F2 IC50 on the Alpha (B.1.1.7) variant is 1.0x fold the wildtype in 42 COVI. | 2022 | Kumar et al. (2022) |
| H69del | vaccine neutralization efficacy | Pokay | ELISpot assays show T cell neutralization reduced by 15.4% in this B.1.1.7 pseudotype relative to wild type in 18-20 pooled patient samples post second mRNA vaccine dose, with no significant difference between Pfizer and Moderna cohorts. Reduction was stronger in the S1 subunit than S2 (separate peptide pools were used). | 2021 | Gallagher et al. (2021) |
| H69del | vaccine neutralization efficacy | Pokay | 2.1x drop in neutralization using sera collected from 14 healthy adult participants that received two injections of the mRNA-1273 (Moderna) vaccine at a dose of 100 µg (18-55 years: day 1 (n | 2021 | Edara et al. (2021) |
| H69del | vaccine neutralization efficacy | Pokay | B.1.1.7 pseudotyped VSV was tested for neutralization in a clonal HEK-293T ACE2 TMPRSS2 cell line optimized for highly efficient S-mediated infection. A cohort of 12 Argentinian recipients of the Gamaleya Sputnik V Ad26 / Ad5 vaccine showed no statistically significant change in neutralization efficacy. | 2021 | Ikegame et al. (2021) |
| H69del | vaccine neutralization efficacy | Pokay | NVX-CoV2373 [Novavax] vaccine in phase 3 trial was 89.7% (95% CI, 80.2-94.6) effective in preventing COVID-19, with no hospitalizations or deaths reported. There were five cases of severe Covid-19, all in the placebo group. Post hoc analysis revealed efficacies of 96.4% (73.8-99.5) and 86.3% (71.3-93.5) against the prototype strain and B.1.1.7 variant, respectively. | 2021 | Heath et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|---------------------------------------|
| H69del | vaccine neutralization efficacy | Pokay | Pseudotyped B.1.1.7 Spike variants lentivirus. 3.5x reduction in neutralization with Moderna vaccinated patient sera after 29 days (1st dose). 2.0x reduction in neutralization with Moderna vaccinated patient sera after 57 days (2nd dose). 2.1x reduction in neutralization with Novavax Phase 1 post-vaccination sera. | 2021 | Shen et al. (2021) |
| H69del | clinical indicators | Pokay | After adjusting for the age factor, in a prospective Chinese cohort study B.1.1.7 variant infection (compared to B.1.140) was the risk factor for C-reactive protein (P | 2021 | Song et al. (2021) |
| H69del | vaccine efficacy | Pokay | Using a test-negative design using Ontario data between Dec 14, 2020 and May 30, 2021, 421,073 symptomatic community-dwelling individuals were tested. Against symptomatic infection caused by Alpha, vaccine effectiveness with partial vaccination (≥ 14 days after dose 1) was higher for mRNA-1273 (83%) than BNT162b2 (66%) and ChAdOx1 (64%), and full vaccination (≥ 7 days after dose 2) increased vaccine effectiveness for BNT162b2 (89%) and mRNA-1273 (92%). | 2021 | Nasreen et al. (2021) |
| H69del | trafficking | Pokay | Live virus was tested ex vivo in reconstituted bronchial epithelium, and out competed wild type. | 2021 | Touret et al. (2021) |
| H69del | vaccine neutralization efficacy | Pokay | Mean 1.7x reduction of NT50 value B.1.1.7 (Alpha) relative to wild type in 8 sera from adult BNT162b2 vaccinees (28-47yo) collected ~1m post booster. | 2021 | Uriu et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|--------------------------------------|
| H69del | ACE2 receptor binding affinity | Pokay | Flow cytometry was used on recombinant VSV proteins and yeast surface display to assess the binding of a labeled soluble ACE2 protein to cells expressing B.1.1.7. We observed a dramatic increase (relative to D614G) in binding of soluble ACE2 to B.1.1.7, and to a lesser extent to B.1.351, which both carry the N501Y mutation (see Fig 3). | 2021 | Planas et al. (2021) |
| H69del | ACE2 receptor binding affinity | Pokay | L27, V34 and E90 mutation resulted in ultrahigh affinity binding of the LVE-ACE-2 domain to the widest variety of VOCs, with KDs of 93 pM for binding to the Alpha B1.1.7. Values were obtained with LVE-ACE-2/mAB chimeras containing the Y-T-E sequence that enhances binding to the FcRn receptor, which in turn is expected to extend biological half-life 3-4-fold. | 2022 | Uhal B et al. (2022) |
| H69del | vaccine neutralization efficacy | Pokay | 1.5x reduction in neutralization (ID50) in sera 3 weeks after one dose of Pfizer/BioNTech BNT162b2 (up to 5 naive and post infection vaccinees) | 2021 | Gong et al. (2021) |
| H69del | vaccine neutralization efficacy | Pokay | nan | | UNKNOWN et al. () |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|-------------------------------------|---------------------|---|------------------|---|
| H69del | vaccine neutralization efficacy | Pokay | In Qatar, where Pfizer vaccine use is prevalent (<10% of the population covered in the time period of the study ending Mar 31, 2021), any time after one dose (including the 2 weeks where no major effect is expected) B.1.1.7 lineage effectiveness was observed as 29.5% (95% CI [22.9,35.5]) against infection, and 54.1% against severe/critical/fatal disease (95% CI [26.1-71.9]). Two weeks or more after 2nd dose, effectiveness climbed to 89.5% [85.9,92.3] against infection, and 100% against severe/critical/fatal disease (95% CI [81.7,100]). | | UNKNOWN et al. () |
| H69del | pharmaceutical effectiveness | Pokay | Lilly's LY-CoV16 showed marked reduction in neutralization of B.1.1.7. | 2021 | Dejnirattisai et al. (2021) |
| H69del | convalescent plasma escape | Pokay | Sera neutralized the B1.1.7 isolate with a lower potency (2-fold: 95% CL: 1.5 – 3-fold), and those with the lowest homotypic neutralizing potency had undetectable heterotypic potency (2/25). | 2021 | Skelly et al. (2021) |
| H69del | tissue specific replication effects | Pokay | In this report, by using a lower infectious dose, we demonstrate that B.1.1.7 (cultured sample Hong Kong/HKPU-00015/2021) exhibits higher infectivity and/or replication efficiency in the nasal epithelium. (Hamster model of infection) | 2021 | Mok et al. (2021) |
| H69del | convalescent plasma escape | Pokay | Neutralization capacity GMT of 27 subjects' sera post-infection was considerably higher (stronger) than after the second Pfizer dose, and 4.5x drop in B.1.1.7 neutralization was observed. | 2021 | Collier et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|--|
| H69del | vaccine neutralization efficacy | Pokay | 20/29 sera after the first dose of Pfizer showed an average reduction in neutralization titres against the B.1.1.7 variant of 3.2 ± 5.7 . After the second dose, the GMT was markedly increased compared with the first-dose titres, with a fold change of 1.9 ± 0.9 (mean \pm s.d.). Neutralization GMT of 27 subjects post-infection was considerably higher (stronger) than after the second Pfizer dose, and 4.5x drop in B.1.1.7 neutralization was observed. | 2021 | Collier et al. (2021) |
| H69del | transmissibility | Pokay | We estimate that this [B.1.1.17] variant has a 43–90% (range of 95% credible intervals 38–130%) higher reproduction number than preexisting variants. Data from other countries yield similar results: we estimate that R for VOC 202012/01 relative to other lineages is 55% (45–66%) higher in Denmark, 74% (66–82%) higher in Switzerland, and 59% (56–63%) higher in the United States, with consistent rates of displacement across regions within each country. | 2021 | Davies et al. (2021) |
| H69del | vaccine neutralization efficacy | Pokay | Lineage B.1.1.7 spike–pseudotyped VSV was tested for neutralization vs Wuhan reference genome pseudotype in 40 sera collected 7 or 21 days post-booster dose. Statistically significant change (22%) in neutralization was observed among the 26 sera from those < | 2021 | Muik et al. (2021) |
| H69del | transmissibility | Pokay | At the national level (Italy), we estimated a mean relative transmissibility of B.1.1.7 (compared to historical lineages) ranging between 1.55 and 1.57 (with confidence intervals between 1.45 and 1.66). | 2021 | Stefanelli et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|---|
| H69del | outcome hazard ratio | Pokay | On average across 7 European countries studied, using B.1.1.7 defining mutations: Significant shift to asymptomatic cases (27.4% vs 18.6% for non-VOC cases). Significant shift to infection in those without pre-existing conditions (44.8% vs 89% for non-VOC cases). Significant increase in hospitalization rate (11% vs 7.5% for non-VOC cases). Significant increase in ICU rate (1.4% vs 0.6% for non-VOC cases). Significant decrease in death rate (2.0% vs vs 4.0% for non-VOC cases). | 2021 | Funk et al. (2021) |
| H69del | vaccine neutralization efficacy | Pokay | Vaccine elicited antibodies neutralized virus with the B.1.1.7 spike protein with titers similar to D614G virus. Serum specimens from individuals vaccinated with the BNT162b2 mRNA vaccine neutralized D614G virus with titers that were on average 7-fold greater than convalescent sera. | 2021 | Tada et al. (2021) |
| H69del | transmissibility | Pokay | Oslo, Norway: Within households, we find an increase in the secondary attack rate by 60% (20% - 114%) compared to other variants. In general, we find a significant increase in the estimated reproduction number of 24% (95% CI 0% - 52%), or an absolute increase of 0.19 compared to other variants. | 2021 | Lindstrøm et al. (2021) |
| H69del | transmissibility | Pokay | Based on ~300,000 RT-PCR samples collected from December 6th 2020 to February 10th 2021 in Israel, the B.1.1.7 is 45% (95% CI:20-60%) more transmissible than the wild-type strain, and become dominant in Israel within 3.5 weeks. | 2021 | Munitz et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|----------------------|---------------------|--|------------------|---|
| H69del | outcome hazard ratio | Pokay | The matching-adjusted conditional odds ratio of hospitalisation was 1.58 (95% confidence interval 1.50 to 1.67) for COVID-19 patients infected with a SGTF-associated variant [primarily B.1.1.7], compared to those infected with non-SGTF-associated variants. The effect was modified by age ($p < 0.001$), with ORs of 0.96-1.13 below age 20 years and 1.57-1.67 in age groups 40 years or older. | 2021 | Nyberg et al. (2021) |
| H69del | outcome hazard ratio | Pokay | Using UK data 1 November 2020 to 14 February 2021, while correcting for misclassification of PCR test Spike Gene Target Failure (SGTF) and missingness in SGTF status, we estimate that the hazard of death associated with B.1.1.7 is 61% (42–82%) higher than with pre-existing variants after adjustment for age, sex, ethnicity, deprivation, residence in a care home, the local authority of residence and test date. This corresponds to the absolute risk of death for a 55–69-year-old man increasing from 0.6% to 0.9% (95% confidence interval, 0.8–1.0%) within 28 days of a positive test in the community. | 2021 | Davies et al. (2021) |
| H69del | viral load | Pokay | B.1.1.7 samples showed average Ct cycle threshold of 21.9 vs 23 for wildtype (i.e. ~2x higher viral load) comparing 37758 and 22535 samples respectively. | 2021 | Roquebert et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|----------------------|---------------------|---|------------------|--|
| H69del | transmissibility | Pokay | Based on 36920 COVID Symptom Study app users reported SARS-CoV-2 test positivity in late 2020, Rt of B.1.1.7 was 1.35x (95% CI 1.02-1.69) relative to pre-existing variants. However, Rt fell below 1 during regional and national lockdowns, even in regions with high proportions of infections with the B.1.1.7 variant. | 2021 | Graham et al. (2021) |
| H69del | outcome hazard ratio | Pokay | 341 samples collected Nov 9 to Dec 20, 2020 were sequenced from two London (UK) hospitals. 198 (58%) of 341 had B.1.1.7 infection and 143 (42%) had non-B.1.1.7 infection. No evidence was found of an association between severe disease and death and lineage (B.1.1.7 vs non-B.1.1.7) in unadjusted analyses (prevalence ratio [PR] 0.97 [95% CI 0.72-1.31]), or in analyses adjusted for hospital, sex, age, comorbidities, and ethnicity (adjusted PR 1.02 [0.76-1.38]). | 2021 | Frampton et al. (2021) |
| H69del | outcome hazard ratio | Pokay | From Sept 28 to Dec 27, 2020, positive COVID-19 tests were reported by 36 920 COVID Symptom Study app users whose region was known and who reported as healthy on app sign-up. We found no changes in reported symptoms or disease duration associated with B.1.1.7. | 2021 | Graham et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|----------------------|---------------------|--|------------------|---------------------------------------|
| H69del | viral load | Pokay | The 249 B.1.1.7 (a.k.a. N501Y.V1) variant cases in three Paris hospital labs had a ~10-fold viral load increase (~3.3 Ct drop in N gene probe) compared to 332 ancestral lineage cases from the same time frame (2020-12-20 to 2021-02-26). PG: BUT there is a discrepancy in drop between the ORF1ab and N probes, with the former suggesting only a 2-fold drop, consistent with the drop observed in B.1.351. This might indicate higher subgenomic RNA content in B.1.1.7 skewing the change. | 2021 | Teyssou et al. (2021) |
| H69del | viral load | Pokay | Using lack of S probe detection as a proxy for B.1.1.7 status, 275 putative B.1.1.7 samples and 390 'wild type' SARS-CoV-2 positive samples in Wales were compared for Ct values, suggesting ~12-fold increase (~3.5 Ct decrease) in viral load for B.1.1.7 samples. | 2021 | Couzens et al. (2021) |
| H69del | outcome hazard ratio | Pokay | The mortality hazard ratio associated with infection with [B.1.1.7] compared with infection with previously circulating variants was 1.64 (95% confidence interval 1.32 to 2.04) in patients who tested positive for covid-19 in the community (54906 matched pairs of participants who tested positive for SARS-CoV-2 in pillar 2 between 1 October 2020 and 29 January 2021). In this comparatively low risk group, this represents an increase in deaths from 2.5 to 4.1 per 1000 detected cases. | 2021 | Challen et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|--------------------------------|---------------------|---|------------------|--|
| H69del | viral load | Pokay | In a study of 1260 ICU subjects, viral load distributions (collected within 48h of admission) were elevated in both seropositive and seronegative subjects infected with B.1.1.7 ('UK variant'). PG: The PANGO tool defining Spike variants for B.1.1.7 are listed here, whereas the paper only used a test for D1118H. | 2021 | Ratcliff et al. (2021) |
| H69del | viral load | Pokay | This study reveals that B.1.1.7 SARS-CoV-2 variant is a slower-growing virus than parental B.1. Further, a higher replication along with reduced infectious viral titer was hypothesized to be linked to higher transmission with reduced pathogenicity. | 2021 | Nyayanit et al. (2021) |
| H69del | viral load | Pokay | We found that the British variant (clade B.1.1.7), compared to an ancestral SARS-CoV-2 clade B virus, produced higher levels of infectious virus late in infection and had a higher replicative fitness in human airway, alveolar and intestinal organoid models. | 2021 | Lamers et al. (2021) |
| H69del | outcome hazard ratio | Pokay | Danish study of the B.1.1.7 lineage shows hospital admission odds ratio of 1.63 vs other lineages. The adjusted OR was increased in all strata of age. | 2021 | Bager et al. (2021) |
| H69del | ACE2 receptor binding affinity | Pokay | This mutation causes major decrease in binding affinity vs. wild type as measured by IC50 vs pseudotyped lentivirus. | 2021 | Tada et al. (2021) |
| H69del | transmissibility | Pokay | Ontario, Feb 2021: The secondary attack rate for VOC index cases in this matched cohort was 1.31 times higher than non-VOC index cases (RR | 2021 | Buchan et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|---------------------------------------|
| H69del | viral load | Pokay | The median Ct value of RT-qPCR tests of the N-gene target in the Daxing B.1.1.7 group was significantly lower than the Shunyi B.1.470 group (P | 2021 | Song et al. (2021) |
| H69del | transmissibility | Pokay | Primary cases infected with B.1.1.7 had an increased transmissibility of 1.5-1.7 times that of primary cases infected with other lineages. The increased transmissibility of B.1.1.7 was multiplicative across age and viral load. | 2021 | Lyngse et al. (2021) |
| H69del | vaccine neutralization efficacy | Pokay | VSV pseudotype B.1.1.7 showed 1.77-fold reduction in neutralization efficiency vs wild type in 15 Pfizer BNT162b2 vaccinee sera 13-15 days post second dose. Cell fusion proficiency was unchanged. | 2021 | Hoffman et al. (2021) |
| H69del | vaccine neutralization efficacy | Pokay | Neutralizing antibody titers increased in previously infected vaccinees relative to uninfected vaccinees 5.2-fold against B.1.1.7 (contrast with 3.4 fold against original SARS-CoV-2). | 2021 | Leier et al. (2021) |
| H69del | outcome hazard ratio | Pokay | Using primarily S-defining mutations for lineage B.1.1.7, most models of hospitalization and fatality risk ratios from consortium members show elevated ratios (~1.3-1.7x). | 2021 | UNKNOWN et al. (2021) |
| H69del | trafficking | Pokay | VSV pseudotype B.1.1.7 showed no significant difference in cell entry relative to wild type in 6 cell lines. Cell fusion proficiency was unchanged. | 2021 | Hoffman et al. (2021) |
| H69del | ACE2 receptor binding affinity | Pokay | Six fold increase in affinity for ACE2 by the B.1.1.7 lineage vs wild type is driven by a drop in observed dissociation rate constant. | 2021 | Collier et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|-----------------------------------|---------------------|---|------------------|--|
| H69del | environmental condition stability | Pokay | Relative to D614G, this mutation demonstrated significant increase in infectivity (i.e. heat stability) after incubation at 50C after 1 hour. | 2021 | Tada et al. (2021) |
| H69del | trafficking | Pokay | Lentiviral pseudotyped with this mutation set from B.1.1.7 was tested on ACE2.293T cells. Luciferase activity was measured two days postinfection, showing significant (40%) increase in infection rate amongst the cells, much more than the effect of either the deletion or the point mutation alone, suggesting that this combination has a synergistic effect contributing to cell entry fitness, but to a smaller extent than N501Y and the deletion alone. | 2021 | Tada et al. (2021) |
| H69del | convalescent plasma binding | Pokay | These key B.1.1.7 mutations as a combination neutralized slightly less well than D614G and this was noticeable in the lack of sera with high neutralizing titer for the viruses across 10 convalescent sera from April 2020 infectees. | 2021 | Tada et al. (2021) |
| H69del | convalescent plasma binding | Pokay | Slight neutralization improvement on average in 16 health workers' convalescent sera. | 2021 | Alenquer et al. (2021) |
| H69del | vaccinee plasma binding | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.4/5 (from) were 17.2x-fold lower (95% CI: 0.6x-0.7x) than against 208-428 972-1834 4.3-4.7 US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|-------------------------------------|---------------------|---|------------------|---------------------------------------|
| H69del | vaccine neutralization efficacy | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.4/5 (from) were 13.0-fold lower (95% CI: 4.2x-4.6x) than against 208-428 972-1834 4.3-4.7 US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| H69del | outcome hazard ratio | Pokay | In Ontario, using a retrospective matched case (age, gender and onset date) study of 6,312 Omicron cases vs 8,875 Delta, the adjusted risk of hospitalization or death was 54% lower (HR | 2021 | Ulloa et al. (2021) |
| H69del | reinfection | Pokay | Population-level evidence suggests that the Omicron variant is associated with substantial ability to evade immunity from prior infection, evidenced by a reinfection hazard ratio of 2.39 (CI95: 1.88-3.11) relative to primary infection in the initial part of South Africa's 4th covid-19 wave (November 2021). In contrast, there is no population-wide epidemiological evidence of immune escape associated with the Beta or Delta variants. [minimal variant signature for Omicron (B.1.1.529) used based on H69del PCR dropout observed in November 2021 coincident with the rise of Omicron] | 2021 | Pulliam et al. (2021) |
| H69del | immunosuppression variant emergence | Pokay | The so-called 'delta F' variant combination previously observed in mink spillover events also emerged in a lymphoma patient (non-Hodgkin diffuse B-cell lymphoma IV stage B) with a long-term COVID-19 infection (4 months) where 18 de novo mutation occurred overall. Patient was taking rituximab, the B-cell-depleting agent, and had no detectable neutralizing antibody response. | 2021 | Bazykin et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|--------------------------------|---------------------|--|------------------|------------------------------------|
| H69del | vaccinee plasma binding | Pokay | 1.14x increase in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in previously non-seroconverted subjects. 1.09x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in post-infection vaccinees. | 2021 | Gong et al. (2021) |
| H69del | ACE2 receptor binding affinity | Pokay | Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant showed a 1.51x increase in binding (KD) relative to D614G, mostly due to decreased in 'off-rate' a.k.a. dissociation rate (Kdis). | 2021 | Gong et al. (2021) |
| H69del | convalescent plasma binding | Pokay | 1.33x increase in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset. | 2021 | Gong et al. (2021) |
| H69del | ACE2 receptor binding affinity | Pokay | Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant combination (representing B.1.1.7 aka Alpha) had 5.43x increased binding relative to D614G alone. | 2021 | Gong et al. (2021) |
| H69del | convalescent plasma binding | Pokay | This variant combination (representing B.1.1.7 aka Alpha) showed a 1.15x increase in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset. | 2021 | Gong et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|--|
| H69del | vaccinee plasma binding | Pokay | This variant combination (representing B.1.1.7 aka Alpha) showed no change in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in previously non-seroconverted subjects. 1.28x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in post-infection vaccinees. | 2021 | Gong et al. (2021) |
| V70del | convalescent plasma escape | Pokay | Artificially constructed HIV-1 pseudovirus with set of mutations drawn from plasma passage escape experiments and mutations from variants of concern completely ablates neutralization in 19 of 21 convalescents plasma collected mean 1.3 months post infection. [actual Y145del from manuscript substituted with more common Y144del description] | 2021 | Schmidt et al. (2021) |
| V70del | vaccine neutralization efficacy | Pokay | Neutralization efficiency (ID50) against B.1.525 reduced 4.2x relative to D614G wildtype using pseudotyped VSV assay on 8 Moderna vaccinee sera one week post-booster. | 2021 | Choi et al. (2021) |
| V70del | pharmaceutical effectiveness | Pokay | Omicron (a.k.a. B.1.1.529) Spike pseudotyped VSV and Vero E6 cells has somewhat reduced neutralization (2.7x) vs wild type with monoclonal antibody Sotrovimab (a.k.a. VIR-7831). [delins at 214 omitted for syntax compatibility] | 2021 | Cathcart et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|--|
| V70del | vaccine neutralization efficacy | Pokay | Omicron breakthrough infection after 3-dose vaccination resulted in a further 3.5-fold and 2.9-fold increase of Omicron BA.1 and BA.2 neutralizing titers. Omicron BA.4/5 showed the highest neutralization resistance of all variants tested, resulting in low geometric mean neutralizing titers in plasma samples obtained after the second vaccine dose (NT50 | 2022 | Wang et al. (2022) |
| V70del | antibody epitope effects | Pokay | Neutralization of the bsAbs Bi-Nab47D10-35B5. Omicron BA.1 has an IC50 fold change of 0.08x. | 2022 | Yuan et al. (2022) |
| V70del | vaccine neutralization efficacy | Pokay | Omicron B.1.1.529 (BA.1) neutralization of the Omicron variants by antibodies induced by three doses of Pfizer/BNT162b2 mRNA vaccine was 7-8-fold less potent than the D614G, and the Omicron variants still evade neutralization more efficiently. | 2022 | Neerukonda et al. (2022) |
| V70del | pharmaceutical effectiveness | Pokay | Omicron (B.1.1.529 [BA.1]) have higher sensitivity to inhibition by soluble angiotensin converting enzyme 2 (ACE2) and the endosomal inhibitor chloroquine compared to D614G | 2022 | Neerukonda et al. (2022) |
| V70del | antibody epitope effects | Pokay | Neutralization of the bsAbs Bi-Nab35B5-47D10. Omicron BA.1 has an IC50 fold change of 0.30x. | 2022 | Yuan et al. (2022) |
| V70del | vaccine neutralization efficacy | Pokay | Paradigms' ACE-2 variant LVE/STR chimera binds to SARS-2 Omicron variant B.1.1.529 spike protein trimer with high affinity. Determined using Surrogate Viral Neutralization Tests. | 2022 | Uhal B et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|--------------------------------|---------------------|--|------------------|--------------------------------------|
| V70del | ACE2 receptor binding affinity | Pokay | L27, V34 and E90 mutation resulted in ultrahigh affinity binding of the LVE-ACE-2 domain to the widest variety of VOCs, with KDs of 73 pM for binding to the Omicron B.1.1.529. Values were obtained with LVE-ACE-2/mAB chimeras containing the Y-T-E sequence that enhances binding to the FcRn receptor, which in turn is expected to extend biological half-life 3-4-fold. | 2022 | Uhal B et al. (2022) |
| V70del | antibody epitope effects | Pokay | Neutralization of the bsAbs 35B5. Omicron BA.1 has an IC50 fold change of 0.38x. | 2022 | Yuan et al. (2022) |
| V70del | vaccinee plasma binding | Pokay | All 10 individuals with 2 doses of the BNT162b2/BNT162b2 vaccine had a neutralizing titer in B.1 variant at an average of 729 NT50. | 2022 | Arora et al. (2022) |
| V70del | antibody epitope effects | Pokay | Plaque reduction neutralization test (PRNT) was used uring primary infection, post sixty daysof second dose vaccination, pre-reinfection and reinfection against Delta variant and was used to determine neutralizing antibodytitres. There was a 24.63x fold increase in antibody response from first infection to recovered and vaccinated with 2 doses (60 days). There was a 4.21x fold increase in antibody response pre-reinfection. There was a 39.27x fold increase in antibody response during reinfection. | 2022 | Shete et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|--------------------------|---------------------|--|------------------|-------------------------------------|
| V70del | antibody epitope effects | Pokay | Plaque reduction neutralization test (PRNT) was used uring primary infection, post sixty daysof second dose vaccination, pre-reinfection and reinfection against B.1 variant and was used to determine neutralizing antibodytitres. There was a 6.76x fold increase in antibody response from first infection to recovered and vaccinated with 2 doses (60 days). There was a 2.06x fold increase in antibody response pre-reinfection. There was a 8.18x fold increase in antibody response during reinfection. | 2022 | Shete et al. (2022) |
| V70del | vaccinee plasma binding | Pokay | All 10 individuals with 3 doses of the BNT162b2/BNT162b2 vaccine had a neutralizing titer in B.1 variant at an average of 3319 NT50. | 2022 | Arora et al. (2022) |
| V70del | antibody epitope effects | Pokay | Plaque reduction neutralization test (PRNT) was used uring primary infection, post sixty daysof second dose vaccination, pre-reinfection and reinfection against Omicron variant and was used to determine neutralizing antibodytitres. There was a 114.84x fold increase in antibody response from first infection to recovered and vaccinated with 2 doses (60 days). There was a 6.61x fold increase in antibody response pre-reinfection. There was a 1194.9x fold increase in antibody response during reinfection. | 2022 | Shete et al. (2022) |
| V70del | antibody epitope effects | Pokay | BnAb 002-S21F2 IC50 on the Omicron BA.1 variant is 1.0x fold the wildtype. | 2022 | Kumar et al. (2022) |
| V70del | antibody epitope effects | Pokay | Neutralization of the bsAbs 47D10. Omicron BA.1 has an IC50 fold change of 1.26x. | 2022 | Yuan et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|--|
| V70del | pharmaceutical effectiveness | Pokay | Omicron BA.3 have higher sensitivity to inhibition by soluble angiotensin converting enzyme 2 (ACE2) and the endosomal inhibitor chloroquine compared to D614G | 2022 | Neerukonda et al. (2022) |
| V70del | vaccine neutralization efficacy | Pokay | Omicron BA.3 neutralization of the Omicron variants by antibodies induced by three doses of Pfizer/BNT162b2 mRNA vaccine was 7-8-fold less potent than the D614G, and the Omicron variants still evade neutralization more efficiently. | 2022 | Neerukonda et al. (2022) |
| V70del | vaccinee plasma binding | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.3 (from South Africa/NICD-N22404/2021) were 4.2x-fold lower (95% CI: 0.15x-0.20x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| V70del | vaccine neutralization efficacy | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.3 (from South Africa/NICD-N22404/2021) were 6.2-fold lower (95% CI: 11.8x-14.3x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| V70del | vaccine neutralization efficacy | Pokay | paired testing of vaccine sera against ancestral virus compared to Omicron BA.1 shows that 3-dose vaccine regimen provides over 50x fold increase in protection against Omicron(B.1.1.529 [BA.1]) compared to a 2-dose regimen. | 2022 | Hao et al. (2022) |
| V70del | pharmaceutical effectiveness | Pokay | 4th antigenic exposure with Omicron (B.1.1.529 [BA.1])(n | 2022 | Wang et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|-------------------------------------|---------------------|---|------------------|--|
| V70del | vaccine neutralization efficacy | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.1 (from Botswana/R40B59_BHP_3321 001248/2021) were 3.4-fold lower (95% CI: 3.2x-3.6x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| V70del | vaccinee plasma binding | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.1 (from Botswana/R40B59_BHP_3321 001248/2021) were 28.7x-fold lower (95% CI: 0.03x-0.05) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| V70del | vaccinee plasma binding | Pokay | Neutralization activity of almost all Moderna Phase 1 sera tested actually *increased*. | 2021 | Shen et al. (2021) |
| V70del | immunosuppression variant emergence | Pokay | The delH69/V70 enhances viral infectivity, indicating its effect on virus fitness is independent to the N501Y RBM change [with which it is found in lineage B.1.1.7] Possibly arisen as a result of the virus evolving from immune selection pressure in infected individuals and possibly only one chronic infection in the case of lineage B.1.1.7. | 2020 | Kemp et al. (2020) |
| V70del | convalescent plasma escape | Pokay | One convalescent sera tested showed 4-fold or greater reduction in neutralization efficiency. | 2021 | Alenquer et al. (2021) |
| V70del | convalescent plasma escape | Pokay | Neutralization activity of almost all convalescent sera tested decreased ~2x. | 2021 | Shen et al. (2021) |
| V70del | convalescent plasma escape | Pokay | Neutralization activity of convalescent sera tested decreased ~2x with this B.1.1.7 pseudotyped virus. | 2021 | Shen et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|--|
| V70del | antibody epitope effects | Pokay | Reduces neutralization by structurally unmapped mAb COVA1-21 (cluster XI). | 2021 | Rees-Spear et al. (2021) |
| V70del | convalescent plasma binding | Pokay | Viruses containing the point mutations of B.1.1.7 showed that the single point mutations (Δ 69-70 and N501Y) were neutralized as efficiently as D614G across 10 convalescent sera from April 2020 infectees. | 2021 | Tada et al. (2021) |
| V70del | anthropozoonotic events | Pokay | This deletion outside the receptor binding domain in pseudotyped VSV promoted the capacity of pseudotyped VSV to transduce black flying fox (<i>Pteropus alecto</i>) kidney PabKi.1 cells (17.8%) to a level twice that of human epithelial-like Huh-7 cells (9.8%) | 2023 | Li et al. (2023) |
| V70del | convalescent plasma binding | Pokay | No notable change in neutralization efficiency, despite N439K by itself showing a ~2x decrease on average in 16 health workers' convalescent sera. | 2021 | Alenquer et al. (2021) |
| V70del | vaccine neutralization efficacy | Pokay | The neutralizing activity of vaccine was somewhat lower against B.1.1.7 in sera tested from most of the 24 patients with the BNT162b2 mRNA vaccine. (Fig. 4) | 2021 | Chen et al. (2021) |
| V70del | antibody epitope effects | Pokay | B.1.1.7 variant constellation ablates Class 3 N-terminal domain targeting antibody COV2-2489. | 2021 | Chen et al. (2021) |
| V70del | vaccine neutralization efficacy | Pokay | Observed 8.8-fold reduction in neutralization efficiency of Pfizer vaccinee sera (collected 14 days after second dose) against cultured B.1.1.7 sample. Contrast this with 1.3-fold reduction for just the pseudovirus combination of 'key' B.1.1.7 mutation N501Y. | 2021 | Bates et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|--|
| V70del | trafficking | Pokay | Lentiviral pseudotyped with this mutation set from Mink Cluster 5 lineage, was tested on ACE2.293T cells. Luciferase activity was measured two days postinfection, showing slight decrease in infection rate amongst the cells, much closer to D614G activity level than Y453F alone, suggesting compensatory effects between the deletion and the mutation in human cell entry fitness. | 2021 | Tada et al. (2021) |
| V70del | trafficking | Pokay | Lentiviral pseudotyped with this mutation set from Mink Cluster 5 lineage, was tested on ACE2.293T cells. Luciferase activity was measured two days postinfection, showing moderate decrease in infection rate amongst the cells, significantly lower than the deletion or Y453F alone, or their combination, suggesting a synergistic effect on poorer human cell entry fitness. | 2021 | Tada et al. (2021) |
| V70del | vaccine neutralization efficacy | Pokay | Pseudotyped B.1.1.298 virus has reduced neutralization activity vs wild type: 1.4x (30 sera Pfizer median 9 days post 2nd dose) and 1.3x (35 sera Moderna median 18 days post 2nd dose). This was NOT significant by ANOVA. | 2021 | Garcia-Beltran et al. (2021) |
| V70del | trafficking | Pokay | Lentiviral pseudotyped with this mutation set from Mink Cluster 5 lineage, was tested on ACE2.293T cells. Luciferase activity was measured two days postinfection, showing mild to modest decrease in infection rate amongst the cells, suggesting a net mild negative effect on human cell entry fitness. | 2021 | Tada et al. (2021) |
| V70del | convalescent plasma binding | Pokay | Lentiviral pseudotyped with the key mutations from Mink Cluster 5 was neutralized more easily than D614G in 10 convalescent sera from April 2020 infectees. | 2021 | Tada et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|---------------------------------------|
| V70del | trafficking | Pokay | Lentiviral pseudotyped with this mutation set from Mink Cluster 5 lineage, was tested on ACE2.293T cells. Luciferase activity was measured two days postinfection, showing no change in infection rate amongst the cells, markedly higher infectivity than either mutation alone, suggesting a synergistic net neutral effect on human cell entry fitness. | 2021 | Tada et al. (2021) |
| V70del | trafficking | Pokay | Lentiviral pseudotyped with all key mutations from Mink Cluster 5 lineage, was tested on ACE2.293T cells. Luciferase activity was measured two days postinfection, showing major (~50%) decrease in infection rate amongst the cells, suggesting that this anthropozoonotic event is driven by other factors at the expense of human cell entry fitness. | 2021 | Tada et al. (2021) |
| V70del | vaccine neutralization efficacy | Pokay | Neutralization efficiency (ID50) against B.1.1.7+E484K reduced 2.8x relative to D614G wildtype using pseudotyped VSV assay on 8 Moderna vaccinee sera one week post-booster. Compare with 1.2x reduction for B.1.1.7 without E484K. | 2021 | Choi et al. (2021) |
| V70del | vaccine neutralization efficacy | Pokay | Sera after the second dose of Pfizer showed an average reduction in neutralization titres against the B.1.1.7 + E484K variant of ~6.7x, markedly higher than B.1.1.7 alone. For first dose sera, a 9.7x drop was observed. | 2021 | Collier et al. (2021) |
| V70del | convalescent plasma escape | Pokay | Neutralization capacity GMT of 27 subjects' sera post-infection was markedly worse against B.1.1.7 + E484K than the lineage alone, with a 11.4x drop. | 2021 | Collier et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|--------------------------------|---------------------|--|------------------|--|
| V70del | antibody epitope effects | Pokay | Ablates Class 3 N-terminal domain targeting antibody COV2-2489, diminishes COV2-2676. | 2021 | Chen et al. (2021) |
| V70del | trafficking | Pokay | Lentiviral pseudotyped with this mutation set from B.1.1.7 was tested on ACE2.293T cells. Luciferase activity was measured two days postinfection, showing significant (40%) increase in infection rate amongst the cells, much more than the effect of either the deletion or the point mutation alone, suggesting that this combination has a synergistic effect contributing to cell entry fitness, more so than this combination with the addition of P681H. | 2021 | Tada et al. (2021) |
| V70del | symptom prevalence | Pokay | In comparison of B.1.1.7 lineage (193 cases) vs. 'wildtype' (125) in Berlin Jan 18 to March 29 2021, significant symptom changes are absent loss of smell/taste (P | 2021 | van Loon et al. (2021) |
| V70del | ACE2 receptor binding affinity | Pokay | This mutation combination causes major increase in binding affinity vs. wild type as measured by IC50 vs pseudotyped lentivirus, but combined with the complete set of B.1.1.7 lineage variants no major change vs wild type affinity is observed. | 2021 | Tada et al. (2021) |
| V70del | antibody epitope effects | Pokay | Reduction in neutralization by mAbs COVA1-18 (~4x), COVA2-15 (~9x). PG: these effects are largely missing in the deletion-alone data | 2021 | Shen et al. (2021) |
| V70del | symptom prevalence | Pokay | A higher proportion of cases infected with the B.1.1.7 variant were hypoxic on admission compared to other variants (70.0% vs 62.5%, p | 2021 | Snell et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|--|
| V70del | virion structure | Pokay | The Ratio of S2 (processed Spike) to full length Spike is higher for this mutation combination, due to a drop in the full length Spike measured, suggesting that this mutation compensates for decreased Spike production by improved proteolytic processing. | 2021 | Tada et al. (2021) |
| V70del | vaccine neutralization efficacy | Pokay | After one dose, individuals with prior infection showed enhanced T cell immunity, antibody secreting memory B cell response to spike and neutralizing antibodies effective against B.1.1.7 (authentic cell culture supernatants). By comparison, HCW receiving one vaccine dose without prior infection showed reduced immunity against variants. B.1.1.7 spike mutations resulted in increased, abrogated or unchanged T cell responses depending on human leukocyte antigen (HLA) polymorphisms. Study was 26 each post-infection and post first dose HCWs. | 2021 | Reynolds et al. (2021) |
| V70del | convalescent plasma escape | Pokay | Mean 2.6x reduction of NT50 value B.1.1.7 (Alpha) relative to wild type in 8 sera from older convalescent patients (52-92yo) collected 1-3m post symptom onset. | 2021 | Uriu et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|------------------------------------|
| V70del | vaccine neutralization efficacy | Pokay | Detectable antibodies against B.1.1.7 at various time points using pseudotyped lentivirus neutralization in Moderna vaccinee cohort: Day 29 33%, Day 43 100%, Day 119 100%, Day 209 96%. Detectable antibodies against B.1.1.7 at various time points using live virus FRNT neutralization in Moderna vaccinee cohort: Day 29 54%, Day 43 100%, Day 119 100%, Day 209 88%. Detectable antibodies against B.1.1.7 at various time points using ACE2 blocking assay in Moderna vaccinee cohort: Day 29 83%, Days 43,119,209 100%. | 2021 | Pegu et al. (2021) |
| V70del | vaccine neutralization efficacy | Pokay | Using national surveillance data from Israel, using Pfizer vaccine and an estimated prevalence of the B.1.1.7 variant of 94.5% among SARS-CoV-2 infections: Adjusted estimates of vaccine effectiveness 7+ days after second dose were 95.3% (95% CI 94.9–95.7): 91.5% against asymptomatic SARS-CoV-2 infection (90.7–92.2: 40.9 vs 1.8 per 100 000 person-days), 97.0% against symptomatic COVID-19 (96.7–97.2%), 97.2% against COVID-19-related hospitalisation (96.8–97.5%), 97.5% against severe or critical COVID-19-related hospitalisation (97.1–97.8%), and 96.7% against COVID-19-related death (96.0–97.3%). In all age groups, as vaccine coverage increased, the incidence of SARS-CoV-2 outcomes declined | 2021 | Haas et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|---|
| V70del | vaccine neutralization efficacy | Pokay | In sera 1-2 weeks after BNT162b2 first dose, from six patients previously infected with B.1, antibody titer in a microneutralization assay was on average 8192 for B.1.351 virus. This compares favorably (stronger) to post-infection neutralization titer against all variants tested in the same sera (wild type, B.1.1.7, B.1.351, and P.1). | 2021 | Luftig et al. (2021) |
| V70del | virion structure | Pokay | CryoEM analysis of B.1.1.7 demonstrates an increased propensity for 'up', receptor accessible conformation of the Spike protein trimer. | 2021 | Cai et al. (2021) |
| V70del | vaccine neutralization efficacy | Pokay | SARS-CoV-2 infection was confirmed in three HCWs working a single shift: all presented with mild symptoms of COVID-19. The two physicians were fully vaccinated with BNT162b2 vaccine, with the second dose administered 1 month before symptom onset. Both had high titres of IgG anti-spike antibodies at the time of diagnosis. WGS confirmed that all virus strains were VOC 202012/01-lineage B.1.1.7, suggesting a common source of exposure. Epidemiological investigation revealed that the suspected source was a SARS-CoV-2-positive patient who required endotracheal intubation due to severe COVID-19. All procedures were carried out using a full suite of personal protective equipment (PPE). | 2021 | Loconsole et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|----------------------------|---------------------|---|------------------|---|
| V70del | vaccine efficacy | Pokay | In a 1:5 test-negative matched control study of 8153 individuals who received the Moderna mRNA-1273 vaccine, 1422 test-positive were Alpha. Two dose vaccine efficacy against Alpha was 98.4% [96.9-99.1%], one dose VE was 90.1% (82.9-94.2%). | 2021 | Bruxvoort et al. (2021) |
| V70del | convalescent plasma escape | Pokay | Using a new rapid neutralization assay, based on reporter cells that become positive for GFP after overnight infection, sera from 58 convalescent individuals collected up to 9 months after symptoms, similarly neutralized B.1.1.7 and D614G. | 2021 | Planas et al. (2021) |
| V70del | antibody epitope effects | Pokay | Neutralization of the bsAbs Bi-Nab35B5-47D10. Alpha (B.1.1.7) has an IC50 fold change of 1.19x. | 2022 | Yuan et al. (2022) |
| V70del | antibody epitope effects | Pokay | B.1.1.7 pseudotyped virus model impairs binding by RBD-directed mAb 910-30. B.1.1.7 pseudotyped virus model abolishes N-terminal-domain-directed mAbs 5-24, 4-8, and 4A8. B.1.1.7 pseudotyped virus model impairs binding by N-terminal-domain-directed mAbs 2-17, 4-19, 5-7. | 2021 | Wang et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|--|
| V70del | vaccine neutralization efficacy | Pokay | 1.4x improvement in neutralization by serum collected 2 to 3 weeks after the second dose from vaccinees who had received BBIBP-CorV (pVNT50 against VSV pseudotyped as B.1.1.7). Convalescent plasma had similar titer against wild type as the BBIBP-CorV vaccinee sera. 2x reduction in neutralization by serum collected 2 to 3 weeks after the second dose from vaccinees who had received CoronaVac (pVNT50 against VSV pseudotyped as B.1.1.7). Convalescent plasma had similar titer against wild type as the CoronaVac vaccinee sera. | 2021 | Wang et al. (2021) |
| V70del | aerosolization | Pokay | Alpha variant cases in a large campus study showed fine-aerosol shedding amongst unmasked participants remained significantly greater for alpha variant infections (18-fold, 95% CI, 3.4 to 92-fold) after adjusting for the increased viral RNA in MTS and saliva, the number of coughs during sampling sessions, and symptom. After controlling for the effect of masks and numbers of coughs during sampling, alpha variant infection was associated with a 100-fold (95% CI, 16 to 650-fold) increase in coarse- and a 73-fold (95% CI, 15 to 350-fold) increase in fine-aerosol RNA shedding. | 2021 | Adenaiye et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|-----------------------------------|---------------------|--|------------------|---|
| V70del | environmental condition stability | Pokay | No differences in the stability of B.1.1.7 observed in the absence of simulated sunlight at either 20°C or 40°C (with a mean time for a 90% loss of viral infectivity across all dark conditions of 6.2 hours). However, a small but statistically significant difference in the stability was observed in simulated sunlight at 20°C and 20% relative humidity, with B.1.1.7 restoring wild type 90% loss time of 11 minutes vs. 7 and 8 minutes for B.1.319 (D614G) and B.28 (V367F) early 2020 viruses respectively. | 2021 | Schuit et al. (2021) |
| V70del | trafficking | Pokay | Modelling the Alpha variant in primary human airway epithelial (HAE) cultures, S1 to full length Spike ratio (measuring Spike furin cleavage processivity) increase 3.9x relative to wild type (5.4 vs 1.4). This is less efficient than Delta (11x vs wildtype using a P681R mutation instead). [del ~144 changed due to ambiguity] Furthermore the RNA ratio of Delta versus Alpha-spike/Delta-backbone continuously increased from 2.8 on day 1 to 9.8 on day 5 post infection in a co-infection model in HAEs, suggesting the spike gene drives the improved replication of Delta variant. | 2021 | Liu et al. (2021) |
| V70del | vaccine neutralization efficacy | Pokay | No significant difference in T-cell response to B.1.1.7 was observed (vs. ancestral) in blood drawn from 28 participants received the Pfizer-BioNTech vaccine and 2 received the Moderna vaccine. This is despite three mutations (Y144del, D614G, and P681H) overlapping T-cell epitope hotspots. | 2021 | Woldemeskel et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|-----------------------------------|---------------------|---|------------------|---------------------------------------|
| V70del | environmental condition stability | Pokay | Treatment with heat, soap and ethanol revealed similar inactivation profiles indicative of a comparable susceptibility towards disinfection. Furthermore, we observed comparable surface stability on steel, silver, copper and face masks. | 2021 | Meister et al. (2021) |
| V70del | vaccine neutralization efficacy | Pokay | The NAb titers (PRNT50) of sera collected from 38 vaccine recipients four-weeks after the second dose of inactivated whole-virion SARS-CoV-2 BBV152/COVAXIN vaccine [which contains D614G] were not significantly different between B.1.1.7 virus and ancestral D614G virus. | 2021 | Sapkal et al. (2021) |
| V70del | vaccine neutralization efficacy | Pokay | PBMCs of Pfizer/BioNTech BNT162b2 (n | 2021 | Tarke et al. (2021) |
| V70del | vaccine neutralization efficacy | Pokay | A single dose of BNT162b2 vaccine demonstrated vaccine effectiveness [symptomatic or asymptomatic in cohort of routinely NAAT-monitored UK HCWs] of 72% (95% CI 58-86) 21 days after first dose and 86% (95% CI 76-97) seven days after two doses in the antibody negative cohort. This cohort was vaccinated when the dominant variant in circulation was B.1.1.7 and demonstrates effectiveness against this variant. | 2021 | Hall et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|--|
| V70del | vaccine neutralization efficacy | Pokay | Between December 19, 2020 and Jan 24, 2021, 7214 of 9109 eligible HCWs at Sheba Medical Center in Israel had received one or more doses of BNT162b2 (Pfizer) vaccine. Adjusted rate reduction in SARS-CoV-2 NAAT positivity infection compared with unvaccinated workers 1-14 days after 1st dose was 30% (95% CI: 2-50), and 75% (95% CI: 72-84) after 15-28 days. Adjusted rate reduction in symptomatic COVID-19 compared with unvaccinated workers 1-14 days after 1st dose was 47% (95% CI: 17-66), and 85% (95% CI: 71-92) after 15-28 days. [Though often cited as an indicator of VE for B.1.1.7, during this time period in Israel, the prevalence of the B.1.1.7 variant increased from ~20% to 50% of cases (covariants.org), therefore these VE numbers likely represent a mix of B.1.1.7 and other lineage effects.] | 2021 | Amit et al. (2021) |
| V70del | vaccine neutralization efficacy | Pokay | We found that a single dose of the BNT162b2 vaccine is about 60-70% effective at preventing symptomatic disease in adults aged 70 years and older in England and that two doses are about 85-90% effective. Those who were vaccinated and went on to have symptoms had a 44% lower risk of being admitted hospital and a 51% lower risk of death compared with people who were unvaccinated. We also found that a single dose of the ChAdOx1-S vaccine was about 60-75% effective against symptomatic disease and provided an additional protective effect against hospital admission—it is too early to assess the effect on mortality. The B.1.1.7 variant now dominates in the UK and these results will largely reflect vaccine effectiveness against this variant. | 2021 | Lopez Bernal et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|--|
| V70del | antibody epitope effects | Pokay | Neutralization of the 47D10. Alpha (B.1.1.7) has an IC50 fold change of 0.40x. | 2022 | Yuan et al. (2022) |
| V70del | anthropozoonotic events | Pokay | First documented cases of domestic cat and dog infections with the B.1.1.7 strain. | 2021 | Hamer et al. (2021) |
| V70del | vaccine efficacy | Pokay | Effectiveness after one dose of vaccine (BNT162b2 or ChAdOx1 nCoV-19) with the delta variant was (48.7%: 95% confidence interval [CI], 45.5 to 51.7): the results were similar for both vaccines. With the BNT162b2 vaccine, the effectiveness of two doses was 93.7% (95% CI, 91.6 to 95.3) among those with the alpha variant. With the ChAdOx1 nCoV-19 vaccine, the effectiveness of two doses was 74.5% (95% CI, 68.4 to 79.4) among those with the alpha variant. | 2021 | Lopez Bernal et al. (2021) |
| V70del | antibody epitope effects | Pokay | Reduction in neutralization by mAbs COVA2-15 (~9x), B38 (~14x), S309 (~190x) by this B.1.1.7 pseudotyped virus model. | 2021 | Shen et al. (2021) |
| V70del | vaccine neutralization efficacy | Pokay | We observed a sharp decline in cases when ~50% of the elderly population was 2 weeks beyond their first vaccination dose and at a time point during which the B.1.1.7 variant gained transmission dominance. In support of this finding, it was suggested that, after the first vaccination dose, more than 70% of patients develop neutralization antibodies, ¹⁵ and the vaccine efficiency can reach 85%. | 2021 | Munitz et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|--|
| V70del | convalescent plasma escape | Pokay | Neutralizing antibody titers of 2/20 (10%) samples showed >10x reduction (sera collected ~1mo post Jan 2020 first wave in China). Neutralizing antibody titers of 8/20 samples (40%) decreased below an ID50 threshold of 40 (sera collected ~8mo post Jan 2020 first wave in China). | 2021 | Hu et al. (2021) |
| V70del | antibody epitope effects | Pokay | Lessens the potency of mAbs COVA2-17 (~5x, similar to N501Y alone), COVA1-12 (~11x) and COVA1-21 (>100x), which do not compete allosterically. | 2021 | Rees-Spear et al. (2021) |
| V70del | reinfection | Pokay | 36920 COVID Symptom Study app users reported SARS-CoV-2 test positivity in late 2020. Possible reinfections were identified in 249 (0.7% [95% CI 0.6-0.8]) of 36509 app users who reported a positive swab test before Oct 1, 2020, but there was no evidence that the frequency of reinfections was higher for the B.1.1.7 variant than for pre-existing variants. | 2021 | Graham et al. (2021) |
| V70del | vaccine neutralization efficacy | Pokay | Pseudotyped B.1.1.7 virus has reduced neutralization activity vs wild type: 2.1x (30 sera Pfizer median 9 days post 2nd dose) and 2.3x (35 sera Moderna median 18 days post 2nd dose). This was NOT significant by ANOVA. Note that Y145del was actually noted in the paper as the effect of their DNA construct, but this is equivalent at the protein level to the more commonly annotated Y144del. | 2021 | Garcia-Beltran et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|---------------------------------------|
| V70del | vaccine neutralization efficacy | Pokay | The sera of 16 individuals with time course collection was evaluated against VSV pseudotypes: neutralized D614G at week 2, whereas B.1.1.7 started to be neutralized at week 3, although less efficiently than D614G. B.1.1.7 and D614G strains were similarly neutralized at week 4 (1 week after booster dose). | 2021 | Planas et al. (2021) |
| V70del | vaccine neutralization efficacy | Pokay | Neutralization assays of B.1.1.7 virus showed a reduction of 2.5-fold (14 days post 2nd dose AstraZeneca, n | 2021 | Supasa et al. (2021) |
| V70del | antibody epitope effects | Pokay | Neutralization of the bsAbs 35B5. Alpha (B.1.1.7) has an IC50 fold change of 1.39x. | 2022 | Yuan et al. (2022) |
| V70del | vaccine efficacy | Pokay | In Minnesota in early 2021 when Alpha was prevalent, vaccine efficacy was estimated as: mRNA-1273 86% (95%CI: 81-90.6%) and BNT162b2: 76% (95%CI: 69-81%) using age, sex, race, PCR testing and vaccination date matched cohorts of unvaccinated, Pfizer and Moderna vaccinees. [variant list included is ancestral Alpha, as this was an observational study no variant list was given] | 2021 | Puranik et al. (2021) |
| V70del | antibody epitope effects | Pokay | ~20x resistance to mAb CQ038 by B.1.1.7 pseudotyped virus | 2021 | Hu et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|---------------------------------------|
| V70del | reinfection | Pokay | Reinfection with Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) B.1.1.7 variant in an immunocompromised 16yo female with end stage renal disease 94 days after initial infection with a B.1.2 lineage virus. Both lineages were the prevalent one at the time of 1st and 2nd infections respectively in Texas, where the patient was located (suggesting exposure risk rather than lineage immune evasion). | 2021 | Marquez et al. (2021) |
| V70del | vaccine neutralization efficacy | Pokay | Paradigm's ACE-2 variant LVE/STR chimera neutralizes Alpha Variant B.1.1.7 RBD significantly better than GenScript IgG FL18-740 w.t. ACE-2 mAB. Determined using Surrogate Viral Neutralization Tests. | 2022 | Uhal B et al. (2022) |
| V70del | antibody epitope effects | Pokay | Neutralization of the bsAbs Bi-Nab47D10-35B5. Alpha (B.1.1.7) has an IC50 fold change of 1.44x. | 2022 | Yuan et al. (2022) |
| V70del | vaccine neutralization efficacy | Pokay | A single dose of BNT162b2 (Pfizer) vaccine showed vaccine effectiveness of 70% (95% CI 55-85) 21 days after first dose and 85% (74-96) 7 days after two doses in the study population. Our findings show that the BNT162b2 vaccine can prevent both symptomatic and asymptomatic infection in working-age adults. This cohort (8203 treatment, 15121 control) was vaccinated when the dominant variant in circulation was B.1.1.7 and shows effectiveness against this variant. | 2021 | Hall et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|---------------------------------------|
| V70del | convalescent plasma escape | Pokay | NTD-specific nAbs showed a substantial (3-450x) decrease in neutralization potency against the recently reported highly transmissible B.1.1.7 variant of concern, whereas RBD-specific nAbs were either unaffected or showed lower decreases in potency. | 2021 | Graham et al. (2021) |
| V70del | tissue specific neutralization | Pokay | The nasal mucosa of Pfizer vaccinees with time course collection was evaluated against VSV pseudotypes: results (only one nasal swab from different previously infected vaccinee neutralizing at weeks 3 and 6 against B.1.1.7 and D614G) suggest that vaccinees probably do not elicit an early humoral response detectable at mucosal surfaces even though sera neutralization was observed. They strengthen the hypothesis that some vaccines may not protect against viral acquisition and infection of the oral–nasal region, but may prevent severe disease associated with viral dissemination in the lower respiratory tract. | 2021 | Planas et al. (2021) |
| V70del | pharmaceutical effectiveness | Pokay | Infectious viral titers in lung tissue determined using a tissue culture infectious dose (TCID) assay in 10 hamsters showed that Alpha Molnupiravir (MK-4482) had ~2.75x fold drop. | 2022 | Rosenke et al. (2022) |
| V70del | vaccine neutralization efficacy | Pokay | Neutralization efficiency (ID50) against B.1.1.7 reduced 1.2x relative to D614G wildtype using pseudotyped VSV assay on 8 Moderna vaccinee sera one week post-booster. | 2021 | Choi et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|--|
| V70del | reinfection | Pokay | Second infection in December 2020 with B.1.1.7 after April 2020 initial infection with B.2 in a 78-year-old man with a history of Type 2 diabetes mellitus, diabetic nephropathy on hemodialysis, chronic obstructive pulmonary disease (COPD), mixed central and obstructive sleep apnea, ischemic heart disease, with no history of immunosuppression. | 2021 | Harrington et al. (2021) |
| V70del | trafficking | Pokay | The entry efficiencies of Spike pseudotyped viruses bearing N501Y Variant 1 (B.1.1.7) mutant were about 3 to 4.4 times higher than that of the WT pseudovirus when viral input was normalized, suggesting that these spike variants promote the infectivity of SARS-CoV-2. | 2021 | Hu et al. (2021) |
| V70del | trafficking | Pokay | ~2.5x cleavage of S2 relative to WA1 (D614G) wildtype by Alpha variant variant as measured by mass spectrometry of Vero-TMPRSS culture. | 2021 | Esclera et al. (2021) |
| V70del | vaccine neutralization efficacy | Pokay | Virus neutralisation activity (using a live SARS-CoV-2 microneutralisation assay (ND50)) by vaccine induced antibodies was 9-fold lower against the B.1.1.7 variant than against a canonical non B.1.1.7 lineage. Vaccine efficacy against symptomatic NAAT positive infection was similar for B.1.1.7 and non-B.1.1.7 lineages (74.6% [95%CI 41.6-88.9] and 84% [95% CI 70.7-91.4] respectively). Furthermore, vaccination with ChAdOx1 nCoV-19 results in a reduction in the duration of shedding and viral load, which may translate into a material impact on transmission of disease. | 2021 | Emary et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|---|
| V70del | antibody epitope effects | Pokay | BnAb 002-S21F2 IC50 on the Alpha (B.1.1.7) variant is 1.0x fold the wildtype in 42 COVI. | 2022 | Kumar et al. (2022) |
| V70del | vaccine neutralization efficacy | Pokay | ELISpot assays show T cell neutralization reduced by 15.4% in this B.1.1.7 pseudotype relative to wild type in 18-20 pooled patient samples post second mRNA vaccine dose, with no significant difference between Pfizer and Moderna cohorts. Reduction was stronger in the S1 subunit than S2 (separate peptide pools were used). | 2021 | Gallagher et al. (2021) |
| V70del | vaccine neutralization efficacy | Pokay | 2.1x drop in neutralization using sera collected from 14 healthy adult participants that received two injections of the mRNA-1273 (Moderna) vaccine at a dose of 100 µg (18-55 years: day 1 (n | 2021 | Edara et al. (2021) |
| V70del | vaccine neutralization efficacy | Pokay | B.1.1.7 pseudotyped VSV was tested for neutralization in a clonal HEK-293T ACE2 TMPRSS2 cell line optimized for highly efficient S-mediated infection. A cohort of 12 Argentinian recipients of the Gamaleya Sputnik V Ad26 / Ad5 vaccine showed no statistically significant change in neutralization efficacy. | 2021 | Ikegame et al. (2021) |
| V70del | vaccine neutralization efficacy | Pokay | NVX-CoV2373 [Novavax] vaccine in phase 3 trial was 89.7% (95% CI, 80.2-94.6) effective in preventing COVID-19, with no hospitalizations or deaths reported. There were five cases of severe Covid-19, all in the placebo group. Post hoc analysis revealed efficacies of 96.4% (73.8-99.5) and 86.3% (71.3-93.5) against the prototype strain and B.1.1.7 variant, respectively. | 2021 | Heath et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|---------------------------------------|
| V70del | vaccine neutralization efficacy | Pokay | Pseudotyped B.1.1.7 Spike variants lentivirus. 3.5x reduction in neutralization with Moderna vaccinated patient sera after 29 days (1st dose). 2.0x reduction in neutralization with Moderna vaccinated patient sera after 57 days (2nd dose). 2.1x reduction in neutralization with Novavax Phase 1 post-vaccination sera. | 2021 | Shen et al. (2021) |
| V70del | clinical indicators | Pokay | After adjusting for the age factor, in a prospective Chinese cohort study B.1.1.7 variant infection (compared to B.1.140) was the risk factor for C-reactive protein (P | 2021 | Song et al. (2021) |
| V70del | vaccine efficacy | Pokay | Using a test-negative design using Ontario data between Dec 14, 2020 and May 30, 2021, 421,073 symptomatic community-dwelling individuals were tested. Against symptomatic infection caused by Alpha, vaccine effectiveness with partial vaccination (≥ 14 days after dose 1) was higher for mRNA-1273 (83%) than BNT162b2 (66%) and ChAdOx1 (64%), and full vaccination (≥ 7 days after dose 2) increased vaccine effectiveness for BNT162b2 (89%) and mRNA-1273 (92%). | 2021 | Nasreen et al. (2021) |
| V70del | trafficking | Pokay | Live virus was tested ex vivo in reconstituted bronchial epithelium, and out competed wild type. | 2021 | Touret et al. (2021) |
| V70del | vaccine neutralization efficacy | Pokay | Mean 1.7x reduction of NT50 value B.1.1.7 (Alpha) relative to wild type in 8 sera from adult BNT162b2 vaccinees (28-47yo) collected ~1m post booster. | 2021 | Uriu et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|--------------------------------------|
| V70del | ACE2 receptor binding affinity | Pokay | Flow cytometry was used on recombinant VSV proteins and yeast surface display to assess the binding of a labeled soluble ACE2 protein to cells expressing B.1.1.7. We observed a dramatic increase (relative to D614G) in binding of soluble ACE2 to B.1.1.7, and to a lesser extent to B.1.351, which both carry the N501Y mutation (see Fig 3). | 2021 | Planas et al. (2021) |
| V70del | ACE2 receptor binding affinity | Pokay | L27, V34 and E90 mutation resulted in ultrahigh affinity binding of the LVE-ACE-2 domain to the widest variety of VOCs, with KDs of 93 pM for binding to the Alpha B1.1.7. Values were obtained with LVE-ACE-2/mAB chimeras containing the Y-T-E sequence that enhances binding to the FcRn receptor, which in turn is expected to extend biological half-life 3-4-fold. | 2022 | Uhal B et al. (2022) |
| V70del | vaccine neutralization efficacy | Pokay | 1.5x reduction in neutralization (ID50) in sera 3 weeks after one dose of Pfizer/BioNTech BNT162b2 (up to 5 naive and post infection vaccinees) | 2021 | Gong et al. (2021) |
| V70del | vaccine neutralization efficacy | Pokay | nan | | UNKNOWN et al. () |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|-------------------------------------|---------------------|---|------------------|---|
| V70del | vaccine neutralization efficacy | Pokay | In Qatar, where Pfizer vaccine use is prevalent (<10% of the population covered in the time period of the study ending Mar 31, 2021), any time after one dose (including the 2 weeks where no major effect is expected) B.1.1.7 lineage effectiveness was observed as 29.5% (95% CI [22.9,35.5]) against infection, and 54.1% against severe/critical/fatal disease (95% CI [26.1-71.9]). Two weeks or more after 2nd dose, effectiveness climbed to 89.5% [85.9,92.3] against infection, and 100% against severe/critical/fatal disease (95% CI [81.7,100]). | | UNKNOWN et al. () |
| V70del | pharmaceutical effectiveness | Pokay | Lilly's LY-CoV16 showed marked reduction in neutralization of B.1.1.7. | 2021 | Dejnirattisai et al. (2021) |
| V70del | convalescent plasma escape | Pokay | Sera neutralized the B1.1.7 isolate with a lower potency (2-fold: 95% CL: 1.5 – 3-fold), and those with the lowest homotypic neutralizing potency had undetectable heterotypic potency (2/25). | 2021 | Skelly et al. (2021) |
| V70del | tissue specific replication effects | Pokay | In this report, by using a lower infectious dose, we demonstrate that B.1.1.7 (cultured sample Hong Kong/HKPU-00015/2021) exhibits higher infectivity and/or replication efficiency in the nasal epithelium. (Hamster model of infection) | 2021 | Mok et al. (2021) |
| V70del | convalescent plasma escape | Pokay | Neutralization capacity GMT of 27 subjects' sera post-infection was considerably higher (stronger) than after the second Pfizer dose, and 4.5x drop in B.1.1.7 neutralization was observed. | 2021 | Collier et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|--|
| V70del | vaccine neutralization efficacy | Pokay | 20/29 sera after the first dose of Pfizer showed an average reduction in neutralization titres against the B.1.1.7 variant of 3.2 ± 5.7 . After the second dose, the GMT was markedly increased compared with the first-dose titres, with a fold change of 1.9 ± 0.9 (mean \pm s.d.). Neutralization GMT of 27 subjects post-infection was considerably higher (stronger) than after the second Pfizer dose, and 4.5x drop in B.1.1.7 neutralization was observed. | 2021 | Collier et al. (2021) |
| V70del | transmissibility | Pokay | We estimate that this [B.1.1.17] variant has a 43–90% (range of 95% credible intervals 38–130%) higher reproduction number than preexisting variants. Data from other countries yield similar results: we estimate that R for VOC 202012/01 relative to other lineages is 55% (45–66%) higher in Denmark, 74% (66–82%) higher in Switzerland, and 59% (56–63%) higher in the United States, with consistent rates of displacement across regions within each country. | 2021 | Davies et al. (2021) |
| V70del | vaccine neutralization efficacy | Pokay | Lineage B.1.1.7 spike–pseudotyped VSV was tested for neutralization vs Wuhan reference genome pseudotype in 40 sera collected 7 or 21 days post-booster dose. Statistically significant change (22%) in neutralization was observed among the 26 sera from those < | 2021 | Muik et al. (2021) |
| V70del | transmissibility | Pokay | At the national level (Italy), we estimated a mean relative transmissibility of B.1.1.7 (compared to historical lineages) ranging between 1.55 and 1.57 (with confidence intervals between 1.45 and 1.66). | 2021 | Stefanelli et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|---|
| V70del | outcome hazard ratio | Pokay | On average across 7 European countries studied, using B.1.1.7 defining mutations: Significant shift to asymptomatic cases (27.4% vs 18.6% for non-VOC cases). Significant shift to infection in those without pre-existing conditions (44.8% vs 89% for non-VOC cases). Significant increase in hospitalization rate (11% vs 7.5% for non-VOC cases). Significant increase in ICU rate (1.4% vs 0.6% for non-VOC cases). Significant decrease in death rate (2.0% vs vs 4.0% for non-VOC cases). | 2021 | Funk et al. (2021) |
| V70del | vaccine neutralization efficacy | Pokay | Vaccine elicited antibodies neutralized virus with the B.1.1.7 spike protein with titers similar to D614G virus. Serum specimens from individuals vaccinated with the BNT162b2 mRNA vaccine neutralized D614G virus with titers that were on average 7-fold greater than convalescent sera. | 2021 | Tada et al. (2021) |
| V70del | transmissibility | Pokay | Oslo, Norway: Within households, we find an increase in the secondary attack rate by 60% (20% - 114%) compared to other variants. In general, we find a significant increase in the estimated reproduction number of 24% (95% CI 0% - 52%), or an absolute increase of 0.19 compared to other variants. | 2021 | Lindstrøm et al. (2021) |
| V70del | transmissibility | Pokay | Based on ~300,000 RT-PCR samples collected from December 6th 2020 to February 10th 2021 in Israel, the B.1.1.7 is 45% (95% CI:20-60%) more transmissible than the wild-type strain, and become dominant in Israel within 3.5 weeks. | 2021 | Munitz et al. (2021) |

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|-----------|----------------------|---------------------|--|------------------|---|
| V70del | outcome hazard ratio | Pokay | The matching-adjusted conditional odds ratio of hospitalisation was 1.58 (95% confidence interval 1.50 to 1.67) for COVID-19 patients infected with a SGTF-associated variant [primarily B.1.1.7], compared to those infected with non-SGTF-associated variants. The effect was modified by age ($p < 0.001$), with ORs of 0.96-1.13 below age 20 years and 1.57-1.67 in age groups 40 years or older. | 2021 | Nyberg et al. (2021) |
| V70del | outcome hazard ratio | Pokay | Using UK data 1 November 2020 to 14 February 2021, while correcting for misclassification of PCR test Spike Gene Target Failure (SGTF) and missingness in SGTF status, we estimate that the hazard of death associated with B.1.1.7 is 61% (42–82%) higher than with pre-existing variants after adjustment for age, sex, ethnicity, deprivation, residence in a care home, the local authority of residence and test date. This corresponds to the absolute risk of death for a 55–69-year-old man increasing from 0.6% to 0.9% (95% confidence interval, 0.8–1.0%) within 28 days of a positive test in the community. | 2021 | Davies et al. (2021) |
| V70del | viral load | Pokay | B.1.1.7 samples showed average Ct cycle threshold of 21.9 vs 23 for wildtype (i.e. ~2x higher viral load) comparing 37758 and 22535 samples respectively. | 2021 | Roquebert et al. (2021) |

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|-----------|----------------------|---------------------|---|------------------|--|
| V70del | transmissibility | Pokay | Based on 36920 COVID Symptom Study app users reported SARS-CoV-2 test positivity in late 2020, Rt of B.1.1.7 was 1.35x (95% CI 1.02-1.69) relative to pre-existing variants. However, Rt fell below 1 during regional and national lockdowns, even in regions with high proportions of infections with the B.1.1.7 variant. | 2021 | Graham et al. (2021) |
| V70del | outcome hazard ratio | Pokay | 341 samples collected Nov 9 to Dec 20, 2020 were sequenced from two London (UK) hospitals. 198 (58%) of 341 had B.1.1.7 infection and 143 (42%) had non-B.1.1.7 infection. No evidence was found of an association between severe disease and death and lineage (B.1.1.7 vs non-B.1.1.7) in unadjusted analyses (prevalence ratio [PR] 0.97 [95% CI 0.72-1.31]), or in analyses adjusted for hospital, sex, age, comorbidities, and ethnicity (adjusted PR 1.02 [0.76-1.38]). | 2021 | Frampton et al. (2021) |
| V70del | outcome hazard ratio | Pokay | From Sept 28 to Dec 27, 2020, positive COVID-19 tests were reported by 36 920 COVID Symptom Study app users whose region was known and who reported as healthy on app sign-up. We found no changes in reported symptoms or disease duration associated with B.1.1.7. | 2021 | Graham et al. (2021) |

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|-----------|----------------------|---------------------|--|------------------|---------------------------------------|
| V70del | viral load | Pokay | The 249 B.1.1.7 (a.k.a. N501Y.V1) variant cases in three Paris hospital labs had a ~10-fold viral load increase (~3.3 Ct drop in N gene probe) compared to 332 ancestral lineage cases from the same time frame (2020-12-20 to 2021-02-26). PG: BUT there is a discrepancy in drop between the ORF1ab and N probes, with the former suggesting only a 2-fold drop, consistent with the drop observed in B.1.351. This might indicate higher subgenomic RNA content in B.1.1.7 skewing the change. | 2021 | Teyssou et al. (2021) |
| V70del | viral load | Pokay | Using lack of S probe detection as a proxy for B.1.1.7 status, 275 putative B.1.1.7 samples and 390 'wild type' SARS-CoV-2 positive samples in Wales were compared for Ct values, suggesting ~12-fold increase (~3.5 Ct decrease) in viral load for B.1.1.7 samples. | 2021 | Couzens et al. (2021) |
| V70del | outcome hazard ratio | Pokay | The mortality hazard ratio associated with infection with [B.1.1.7] compared with infection with previously circulating variants was 1.64 (95% confidence interval 1.32 to 2.04) in patients who tested positive for covid-19 in the community (54906 matched pairs of participants who tested positive for SARS-CoV-2 in pillar 2 between 1 October 2020 and 29 January 2021). In this comparatively low risk group, this represents an increase in deaths from 2.5 to 4.1 per 1000 detected cases. | 2021 | Challen et al. (2021) |

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|-----------|--------------------------------|---------------------|---|------------------|--|
| V70del | viral load | Pokay | In a study of 1260 ICU subjects, viral load distributions (collected within 48h of admission) were elevated in both seropositive and seronegative subjects infected with B.1.1.7 ('UK variant'). PG: The PANGO tool defining Spike variants for B.1.1.7 are listed here, whereas the paper only used a test for D1118H. | 2021 | Ratcliff et al. (2021) |
| V70del | viral load | Pokay | This study reveals that B.1.1.7 SARS-CoV-2 variant is a slower-growing virus than parental B.1. Further, a higher replication along with reduced infectious viral titer was hypothesized to be linked to higher transmission with reduced pathogenicity. | 2021 | Nyayanit et al. (2021) |
| V70del | viral load | Pokay | We found that the British variant (clade B.1.1.7), compared to an ancestral SARS-CoV-2 clade B virus, produced higher levels of infectious virus late in infection and had a higher replicative fitness in human airway, alveolar and intestinal organoid models. | 2021 | Lamers et al. (2021) |
| V70del | outcome hazard ratio | Pokay | Danish study of the B.1.1.7 lineage shows hospital admission odds ratio of 1.63 vs other lineages. The adjusted OR was increased in all strata of age. | 2021 | Bager et al. (2021) |
| V70del | ACE2 receptor binding affinity | Pokay | This mutation causes major decrease in binding affinity vs. wild type as measured by IC50 vs pseudotyped lentivirus. | 2021 | Tada et al. (2021) |
| V70del | transmissibility | Pokay | Ontario, Feb 2021: The secondary attack rate for VOC index cases in this matched cohort was 1.31 times higher than non-VOC index cases (RR | 2021 | Buchan et al. (2021) |

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|-----------|---------------------------------|---------------------|--|------------------|---------------------------------------|
| V70del | viral load | Pokay | The median Ct value of RT-qPCR tests of the N-gene target in the Daxing B.1.1.7 group was significantly lower than the Shunyi B.1.470 group (P | 2021 | Song et al. (2021) |
| V70del | transmissibility | Pokay | Primary cases infected with B.1.1.7 had an increased transmissibility of 1.5-1.7 times that of primary cases infected with other lineages. The increased transmissibility of B.1.1.7 was multiplicative across age and viral load. | 2021 | Lyngse et al. (2021) |
| V70del | vaccine neutralization efficacy | Pokay | VSV pseudotype B.1.1.7 showed 1.77-fold reduction in neutralization efficiency vs wild type in 15 Pfizer BNT162b2 vaccinee sera 13-15 days post second dose. Cell fusion proficiency was unchanged. | 2021 | Hoffman et al. (2021) |
| V70del | vaccine neutralization efficacy | Pokay | Neutralizing antibody titers increased in previously infected vaccinees relative to uninfected vaccinees 5.2-fold against B.1.1.7 (contrast with 3.4 fold against original SARS-CoV-2). | 2021 | Leier et al. (2021) |
| V70del | outcome hazard ratio | Pokay | Using primarily S-defining mutations for lineage B.1.1.7, most models of hospitalization and fatality risk ratios from consortium members show elevated ratios (~1.3-1.7x). | 2021 | UNKNOWN et al. (2021) |
| V70del | trafficking | Pokay | VSV pseudotype B.1.1.7 showed no significant difference in cell entry relative to wild type in 6 cell lines. Cell fusion proficiency was unchanged. | 2021 | Hoffman et al. (2021) |
| V70del | ACE2 receptor binding affinity | Pokay | Six fold increase in affinity for ACE2 by the B.1.1.7 lineage vs wild type is driven by a drop in observed dissociation rate constant. | 2021 | Collier et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|-----------------------------------|---------------------|---|------------------|--|
| V70del | environmental condition stability | Pokay | Relative to D614G, this mutation demonstrated significant increase in infectivity (i.e. heat stability) after incubation at 50C after 1 hour. | 2021 | Tada et al. (2021) |
| V70del | trafficking | Pokay | Lentiviral pseudotyped with this mutation set from B.1.1.7 was tested on ACE2.293T cells. Luciferase activity was measured two days postinfection, showing significant (40%) increase in infection rate amongst the cells, much more than the effect of either the deletion or the point mutation alone, suggesting that this combination has a synergistic effect contributing to cell entry fitness, but to a smaller extent than N501Y and the deletion alone. | 2021 | Tada et al. (2021) |
| V70del | convalescent plasma binding | Pokay | These key B.1.1.7 mutations as a combination neutralized slightly less well than D614G and this was noticeable in the lack of sera with high neutralizing titer for the viruses across 10 convalescent sera from April 2020 infectees. | 2021 | Tada et al. (2021) |
| V70del | convalescent plasma binding | Pokay | Slight neutralization improvement on average in 16 health workers' convalescent sera. | 2021 | Alenquer et al. (2021) |
| V70del | vaccinee plasma binding | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.4/5 (from) were 17.2x-fold lower (95% CI: 0.6x-0.7x) than against 208-428 972-1834 4.3-4.7 US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|-------------------------------------|---------------------|---|------------------|--|
| V70del | vaccine neutralization efficacy | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.4/5 (from) were 13.0-fold lower (95% CI: 4.2x-4.6x) than against 208-428 972-1834 4.3-4.7 US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahade et al. (2022) |
| V70del | immunosuppression variant emergence | Pokay | The so-called 'delta F' variant combination previously observed in mink spillover events also emerged in a lymphoma patient (non-Hodgkin diffuse B-cell lymphoma IV stage B) with a long-term COVID-19 infection (4 months) where 18 de novo mutation occurred overall. Patient was taking rituximab, the B-cell-depleting agent, and had no detectable neutralizing antibody response. | 2021 | Bazykin et al. (2021) |
| V70del | vaccinee plasma binding | Pokay | 1.14x increase in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in previously non-seroconverted subjects. 1.09x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in post-infection vaccinees. | 2021 | Gong et al. (2021) |
| V70del | ACE2 receptor binding affinity | Pokay | Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant showed a 1.51x increase in binding (KD) relative to D614G, mostly due to decreased in 'off-rate' a.k.a. dissociation rate (Kdis). | 2021 | Gong et al. (2021) |
| V70del | convalescent plasma binding | Pokay | 1.33x increase in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset. | 2021 | Gong et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|--|
| V70del | ACE2 receptor binding affinity | Pokay | Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant combination (representing B.1.1.7 aka Alpha) had 5.43x increased binding relative to D614G alone. | 2021 | Gong et al. (2021) |
| V70del | convalescent plasma binding | Pokay | This variant combination (representing B.1.1.7 aka Alpha) showed a 1.15x increase in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset. | 2021 | Gong et al. (2021) |
| V70del | vaccinee plasma binding | Pokay | This variant combination (representing B.1.1.7 aka Alpha) showed no change in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in previously non-seroconverted subjects. 1.28x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in post-infection vaccinees. | 2021 | Gong et al. (2021) |
| K147N | convalescent plasma escape | Pokay | Escape mutant found after in passage in plasma pool of 26 convalescents obtained mean 1.3 months post infection. | 2021 | Schmidt et al. (2021) |
| R237K | vaccine neutralization efficacy | Pokay | 65yo female with no severe Covid-19 risk factors tested positive 36 days after second dose of BNT162b2 (Pfizer) vaccine. Presented with fatigue, sinus congestion, and a headache developed: her symptoms plateaued and began to resolve six days later. [Missing genome coverage in regions of Spike covering clinically relevant mutations K417T, L452R, E484K, A701V, D796H, N501Y] | 2021 | Hacisuleyman et al. (2021) |
| G339H | gene expression increase | Pokay | Experimentally, Spike gene expression increased 0.15 fold | 2020 | Starr et al. (2020) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|--|
| G339H | ACE2 receptor binding affinity | Pokay | The hACE2-binding affinity of XBB.1.5 RBD has a dissociation constant KD of 3.4 nM, where S486P is the distinguishing Spike mutation vs parent XBB.1 RBD with a much weaker KD (19 nM), as measured by surface plasmon resonance (SPR) assays. | 2023 | Yue et al. (2023) |
| K356T | gene expression increase | Pokay | Experimentally, Spike gene expression increased 0.14 fold | 2020 | Starr et al. (2020) |
| S371F | pharmaceutical effectiveness | Pokay | Omicron BA.2 have higher sensitivity to inhibition by soluble angiotensin converting enzyme 2 (ACE2) and the endosomal inhibitor chloroquine compared to D614G | 2022 | Neerukonda et al. (2022) |
| S371F | antibody epitope effects | Pokay | Neutralization of the bsAbs Bi-Nab35B5-47D10. Omicron BA.2 has an IC50 fold change of 0.07x. | 2022 | Yuan et al. (2022) |
| S371F | antibody epitope effects | Pokay | Neutralization of the bsAbs 35B5. Omicron BA.2 has an IC50 fold change of 0.09x. | 2022 | Yuan et al. (2022) |
| S371F | antibody epitope effects | Pokay | Neutralization of the bsAbs 47D10. Omicron BA.2 has an IC50 fold change of 0.08x. | 2022 | Yuan et al. (2022) |
| S371F | antibody epitope effects | Pokay | Neutralization of the bsAbs Bi-Nab47D10-35B5. Omicron BA.2 has an IC50 fold change of 0.04x. | 2022 | Yuan et al. (2022) |
| S371F | vaccine neutralization efficacy | Pokay | Omicron BA.2 neutralization of the Omicron variants by antibodies induced by three doses of Pfizer/BNT162b2 mRNA vaccine was 7-8-fold less potent than the D614G, and the Omicron variants still evade neutralization more efficiently. | 2022 | Neerukonda et al. (2022) |
| S371F | antibody epitope effects | Pokay | BnAb 002-S21F2 IC50 on the Omicron BA.2 variant is 0.8x fold the wildtype. | 2022 | Kumar et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|---------------------------------------|
| S371F | vaccinee plasma binding | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.2 (from South Africa/CERI-KRISP-K03 2307/2021) were 3.9x-fold lower (95% CI: 0.14x-0.17x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| S371F | ACE2 receptor binding affinity | Pokay | L27, V34 and E90 mutation resulted in ultrahigh affinity binding of the LVE-ACE-2 domain to the widest variety of VOCs, with KDs of 78fM for binding to the Omicron BA.2. Values were obtained with LVE-ACE-2/mAB chimeras containing the Y-T-E sequence that enhances binding to the FcRn receptor, which in turn is expected to extend biological half-life 3-4-fold. | 2022 | Uhal B et al. (2022) |
| S371F | vaccine neutralization efficacy | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.2 (from South Africa/CERI-KRISP-K03 2307/2021) were 4.5-fold lower (95% CI: 4.3x-4.7x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| S371F | vaccine neutralization efficacy | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.2.12.1 (from USA/NY-CDC-ASC2 10722700/2022) were 4.2-fold lower (95% CI: 5.8x-6.6x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |

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|-----------|---------------------------------|---------------------|--|------------------|--|
| S371F | vaccinee plasma binding | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.2.12.1 (from USA/NY-CDC-ASC2 10722700/2022) were 3.9x-fold lower (95% CI: 0.14x-0.18x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahade et al. (2022) |
| S371F | pharmaceutical effectiveness | Pokay | Omicron BA.3 have higher sensitivity to inhibition by soluble angiotensin converting enzyme 2 (ACE2) and the endosomal inhibitor chloroquine compared to D614G | 2022 | Neerukonda et al. (2022) |
| S371F | vaccine neutralization efficacy | Pokay | Omicron BA.3 neutralization of the Omicron variants by antibodies induced by three doses of Pfizer/BNT162b2 mRNA vaccine was 7-8-fold less potent than the D614G, and the Omicron variants still evade neutralization more efficiently. | 2022 | Neerukonda et al. (2022) |
| S371F | vaccinee plasma binding | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.3 (from South Africa/NICD-N22404/2021) were 4.2x-fold lower (95% CI: 0.15x-0.20x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahade et al. (2022) |
| S371F | vaccine neutralization efficacy | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.3 (from South Africa/NICD-N22404/2021) were 6.2-fold lower (95% CI: 11.8x-14.3x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahade et al. (2022) |

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| S371F | vaccinee plasma binding | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.4/5 (from) were 17.2x-fold lower (95% CI: 0.6x-0.7x) than against 208-428 972-1834 4.3-4.7 US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahade et al. (2022) |
| S371F | vaccine neutralization efficacy | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.4/5 (from) were 13.0-fold lower (95% CI: 4.2x-4.6x) than against 208-428 972-1834 4.3-4.7 US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahade et al. (2022) |
| S371F | ACE2 receptor binding affinity | Pokay | The hACE2-binding affinity of XBB.1.5 RBD has a dissociation constant KD of 3.4 nM, where S486P is the distinguishing Spike mutation vs parent XBB.1 RBD with a much weaker KD (19 nM), as measured by surface plasmon resonance (SPR) assays. | 2023 | Yue et al. (2023) |
| S373P | pharmaceutical effectiveness | Pokay | Omicron BA.2 have higher sensitivity to inhibition by soluble angiotensin converting enzyme 2 (ACE2) and the endosomal inhibitor chloroquine compared to D614G | 2022 | Neerukonda et al. (2022) |
| S373P | antibody epitope effects | Pokay | Neutralization of the bsAbs Bi-Nab35B5-47D10. Omicron BA.2 has an IC50 fold change of 0.07x. | 2022 | Yuan et al. (2022) |
| S373P | antibody epitope effects | Pokay | Neutralization of the bsAbs 35B5. Omicron BA.2 has an IC50 fold change of 0.09x. | 2022 | Yuan et al. (2022) |
| S373P | antibody epitope effects | Pokay | Neutralization of the bsAbs 47D10. Omicron BA.2 has an IC50 fold change of 0.08x. | 2022 | Yuan et al. (2022) |

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|-----------|---------------------------------|---------------------|---|------------------|--|
| S373P | antibody epitope effects | Pokay | Neutralization of the bsAbs Bi-Nab47D10-35B5. Omicron BA.2 has an IC50 fold change of 0.04x. | 2022 | Yuan et al. (2022) |
| S373P | vaccine neutralization efficacy | Pokay | Omicron BA.2 neutralization of the Omicron variants by antibodies induced by three doses of Pfizer/BNT162b2 mRNA vaccine was 7-8-fold less potent than the D614G, and the Omicron variants still evade neutralization more efficiently. | 2022 | Neerukonda et al. (2022) |
| S373P | antibody epitope effects | Pokay | BnAb 002-S21F2 IC50 on the Omicron BA.2 variant is 0.8x fold the wildtype. | 2022 | Kumar et al. (2022) |
| S373P | vaccinee plasma binding | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.2 (from South Africa/CERI-KRISP-K03 2307/2021) were 3.9x-fold lower (95% CI: 0.14x-0.17x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| S373P | ACE2 receptor binding affinity | Pokay | L27, V34 and E90 mutation resulted in ultrahigh affinity binding of the LVE-ACE-2 domain to the widest variety of VOCs, with KDs of 78fM for binding to the Omicron BA.2. Values were obtained with LVE-ACE-2/mAB chimeras containing the Y-T-E sequence that enhances binding to the FcRn receptor, which in turn is expected to extend biological half-life 3-4-fold. | 2022 | Uhal B et al. (2022) |
| S373P | vaccine neutralization efficacy | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.2 (from South Africa/CERI-KRISP-K03 2307/2021) were 4.5-fold lower (95% CI: 4.3x-4.7x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |

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| S373P | vaccinee plasma binding | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.2.12.1 (from USA/NY-CDC-ASC2 10722700/2022) were 3.9x-fold lower (95% CI: 0.14x-0.18x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| S373P | antibody epitope effects | Pokay | Neutralization of the bsAbs Bi-Nab47D10-35B5. Omicron BA.1 has an IC50 fold change of 0.08x. | 2022 | Yuan et al. (2022) |
| S373P | vaccine neutralization efficacy | Pokay | Omicron B.1.1.529 (BA.1) neutralization of the Omicron variants by antibodies induced by three doses of Pfizer/BNT162b2 mRNA vaccine was 7-8-fold less potent than the D614G, and the Omicron variants still evade neutralization more efficiently. | 2022 | Neerukonda et al. (2022) |
| S373P | pharmaceutical effectiveness | Pokay | Omicron (B.1.1.529 [BA.1]) have higher sensitivity to inhibition by soluble angiotensin converting enzyme 2 (ACE2) and the endosomal inhibitor chloroquine compared to D614G | 2022 | Neerukonda et al. (2022) |
| S373P | antibody epitope effects | Pokay | Neutralization of the bsAbs Bi-Nab35B5-47D10. Omicron BA.1 has an IC50 fold change of 0.30x. | 2022 | Yuan et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|--------------------------------------|
| S373P | vaccine neutralization efficacy | Pokay | Paradigms' ACE-2 variant LVE/STR chimera binds to SARS-2 Omicron variant B.1.1.529 spike protein trimer with high affinity. Determined using Surrogate Viral Neutralization Tests. | 2022 | Uhal B et al. (2022) |
| S373P | ACE2 receptor binding affinity | Pokay | L27, V34 and E90 mutation resulted in ultrahigh affinity binding of the LVE-ACE-2 domain to the widest variety of VOCs, with KDs of 73 pM for binding to the Omicron B.1.1.529. Values were obtained with LVE-ACE-2/mAB chimeras containing the Y-T-E sequence that enhances binding to the FcRn receptor, which in turn is expected to extend biological half-life 3-4-fold. | 2022 | Uhal B et al. (2022) |
| S373P | antibody epitope effects | Pokay | Neutralization of the bsAbs 35B5. Omicron BA.1 has an IC50 fold change of 0.38x. | 2022 | Yuan et al. (2022) |
| S373P | vaccinee plasma binding | Pokay | All 10 individuals with 2 doses of the BNT162b2/BNT162b2 vaccine had a neutralizing titer in B.1 variant at an average of 729 NT50. | 2022 | Arora et al. (2022) |
| S373P | antibody epitope effects | Pokay | Plaque reduction neutralization test (PRNT) was used uring primary infection, post sixty daysof second dose vaccination, pre-reinfection and reinfection against Delta variant and was used to determine neutralizing antibodytitres. There was a 24.63x fold increase in antibody response from first infection to recovered and vaccinated with 2 doses (60 days). There was a 4.21x fold increase in antibody response pre-reinfection. There was a 39.27x fold increase in antibody response during reinfection. | 2022 | Shete et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|--------------------------|---------------------|--|------------------|-------------------------------------|
| S373P | antibody epitope effects | Pokay | Plaque reduction neutralization test (PRNT) was used uring primary infection, post sixty daysof second dose vaccination, pre-reinfection and reinfection against B.1 variant and was used to determine neutralizing antibodytitres. There was a 6.76x fold increase in antibody response from first infection to recovered and vaccinated with 2 doses (60 days). There was a 2.06x fold increase in antibody response pre-reinfection. There was a 8.18x fold increase in antibody response during reinfection. | 2022 | Shete et al. (2022) |
| S373P | vaccinee plasma binding | Pokay | All 10 individuals with 3 doses of the BNT162b2/BNT162b2 vaccine had a neutralizing titer in B.1 variant at an average of 3319 NT50. | 2022 | Arora et al. (2022) |
| S373P | antibody epitope effects | Pokay | Plaque reduction neutralization test (PRNT) was used uring primary infection, post sixty daysof second dose vaccination, pre-reinfection and reinfection against Omicron variant and was used to determine neutralizing antibodytitres. There was a 114.84x fold increase in antibody response from first infection to recovered and vaccinated with 2 doses (60 days). There was a 6.61x fold increase in antibody response pre-reinfection. There was a 1194.9x fold increase in antibody response during reinfection. | 2022 | Shete et al. (2022) |
| S373P | antibody epitope effects | Pokay | BnAb 002-S21F2 IC50 on the Omicron BA.1 variant is 1.0x fold the wildtype. | 2022 | Kumar et al. (2022) |
| S373P | antibody epitope effects | Pokay | Neutralization of the bsAbs 47D10. Omicron BA.1 has an IC50 fold change of 1.26x. | 2022 | Yuan et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|--|
| S373P | pharmaceutical effectiveness | Pokay | Omicron BA.3 have higher sensitivity to inhibition by soluble angiotensin converting enzyme 2 (ACE2) and the endosomal inhibitor chloroquine compared to D614G | 2022 | Neerukonda et al. (2022) |
| S373P | vaccine neutralization efficacy | Pokay | Omicron BA.3 neutralization of the Omicron variants by antibodies induced by three doses of Pfizer/BNT162b2 mRNA vaccine was 7-8-fold less potent than the D614G, and the Omicron variants still evade neutralization more efficiently. | 2022 | Neerukonda et al. (2022) |
| S373P | vaccinee plasma binding | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.3 (from South Africa/NICD-N22404/2021) were 4.2x-fold lower (95% CI: 0.15x-0.20x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| S373P | vaccine neutralization efficacy | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.3 (from South Africa/NICD-N22404/2021) were 6.2-fold lower (95% CI: 11.8x-14.3x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| S373P | vaccine neutralization efficacy | Pokay | paired testing of vaccine sera against ancestral virus compared to Omicron BA.1 shows that 3-dose vaccine regimen provides over 50x fold increase in protection against Omicron(B.1.1.529 [BA.1]) compared to a 2-dose regimen. | 2022 | Hao et al. (2022) |
| S373P | pharmaceutical effectiveness | Pokay | 4th antigenic exposure with Omicron (B.1.1.529 [BA.1])(n | 2022 | Wang et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|---------------------------------------|
| S373P | vaccine neutralization efficacy | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.1 (from Botswana/R40B59_BHP_3321 001248/2021) were 3.4-fold lower (95% CI: 3.2x-3.6x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| S373P | vaccinee plasma binding | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.1 (from Botswana/R40B59_BHP_3321 001248/2021) were 28.7x-fold lower (95% CI: 0.03x-0.05) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| S373P | vaccinee plasma binding | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.4/5 (from) were 17.2x-fold lower (95% CI: 0.6x-0.7x) than against 208-428 972-1834 4.3-4.7 US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| S373P | vaccine neutralization efficacy | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.4/5 (from) were 13.0-fold lower (95% CI: 4.2x-4.6x) than against 208-428 972-1834 4.3-4.7 US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---|---------------------|---|------------------|--|
| S373P | vaccinee plasma binding | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, XD (from) were 1.5x-fold lower (95% CI: 0.05x-0.07x) than against 208-428 972-1834 4.3-4.7 US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| S373P | vaccine neutralization efficacy | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, XD (from) were 4.4-fold lower (95% CI: 4.3x-4.7x) than against 208-428 972-1834 4.3-4.7 US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| S373P | ACE2 receptor binding affinity | Pokay | The hACE2-binding affinity of XBB.1.5 RBD has a dissociation constant KD of 3.4 nM, where S486P is the distinguishing Spike mutation vs parent XBB.1 RBD with a much weaker KD (19 nM), as measured by surface plasmon resonance (SPR) assays. | 2023 | Yue et al. (2023) |
| S373P | monoclonal antibody serial passage escape | Pokay | Reduce affinity for mildly cross-reactive CR3022 (2003 pandemic SARS monoclonal antibody cross-reactive to SARS-CoV-2) | 2020 | Long et al. (2020) |
| S373P | transmissibility | Pokay | On December 7, 2021 the estimate of Omicron effective reproduction rate (Rt) is 3.12 [presumably R0 is higher], compared to 1.12 for the dominant Delta VOC at that time. [shorthand of variant list shared by all contemporary BA lineage used here] | 2021 | UNKNOWN et al. (2021) |
| D405N | pharmaceutical effectiveness | Pokay | Omicron BA.2 have higher sensitivity to inhibition by soluble angiotensin converting enzyme 2 (ACE2) and the endosomal inhibitor chloroquine compared to D614G | 2022 | Neerukonda et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|--|
| D405N | antibody epitope effects | Pokay | Neutralization of the bsAbs Bi-Nab35B5-47D10. Omicron BA.2 has an IC50 fold change of 0.07x. | 2022 | Yuan et al. (2022) |
| D405N | antibody epitope effects | Pokay | Neutralization of the bsAbs 35B5. Omicron BA.2 has an IC50 fold change of 0.09x. | 2022 | Yuan et al. (2022) |
| D405N | antibody epitope effects | Pokay | Neutralization of the bsAbs 47D10. Omicron BA.2 has an IC50 fold change of 0.08x. | 2022 | Yuan et al. (2022) |
| D405N | antibody epitope effects | Pokay | Neutralization of the bsAbs Bi-Nab47D10-35B5. Omicron BA.2 has an IC50 fold change of 0.04x. | 2022 | Yuan et al. (2022) |
| D405N | vaccine neutralization efficacy | Pokay | Omicron BA.2 neutralization of the Omicron variants by antibodies induced by three doses of Pfizer/BNT162b2 mRNA vaccine was 7-8-fold less potent than the D614G, and the Omicron variants still evade neutralization more efficiently. | 2022 | Neerukonda et al. (2022) |
| D405N | antibody epitope effects | Pokay | BnAb 002-S21F2 IC50 on the Omicron BA.2 variant is 0.8x fold the wildtype. | 2022 | Kumar et al. (2022) |
| D405N | vaccinee plasma binding | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.2 (from South Africa/CERI-KRISP-K03 2307/2021) were 3.9x-fold lower (95% CI: 0.14x-0.17x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|--|
| D405N | ACE2 receptor binding affinity | Pokay | L27, V34 and E90 mutation resulted in ultrahigh affinity binding of the LVE-ACE-2 domain to the widest variety of VOCs, with KDs of 78fM for binding to the Omicron BA.2. Values were obtained with LVE-ACE-2/mAB chimeras containing the Y-T-E sequence that enhances binding to the FcRn receptor, which in turn is expected to extend biological half-life 3-4-fold. | 2022 | Uhal B et al. (2022) |
| D405N | vaccine neutralization efficacy | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.2 (from South Africa/CERI-KRISP-K03 2307/2021) were 4.5-fold lower (95% CI: 4.3x-4.7x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| D405N | vaccine neutralization efficacy | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.2.12.1 (from USA/NY-CDC-ASC2 10722700/2022) were 4.2-fold lower (95% CI: 5.8x-6.6x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| D405N | vaccinee plasma binding | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.2.12.1 (from USA/NY-CDC-ASC2 10722700/2022) were 3.9x-fold lower (95% CI: 0.14x-0.18x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| D405N | pharmaceutical effectiveness | Pokay | Omicron BA.3 have higher sensitivity to inhibition by soluble angiotensin converting enzyme 2 (ACE2) and the endosomal inhibitor chloroquine compared to D614G | 2022 | Neerukonda et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|--|
| D405N | vaccine neutralization efficacy | Pokay | Omicron BA.3 neutralization of the Omicron variants by antibodies induced by three doses of Pfizer/BNT162b2 mRNA vaccine was 7-8-fold less potent than the D614G, and the Omicron variants still evade neutralization more efficiently. | 2022 | Neerukonda et al. (2022) |
| D405N | vaccinee plasma binding | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.3 (from South Africa/NICD-N22404/2021) were 4.2x-fold lower (95% CI: 0.15x-0.20x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| D405N | vaccine neutralization efficacy | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.3 (from South Africa/NICD-N22404/2021) were 6.2-fold lower (95% CI: 11.8x-14.3x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| D405N | vaccinee plasma binding | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.4/5 (from) were 17.2x-fold lower (95% CI: 0.6x-0.7x) than against 208-428 972-1834 4.3-4.7 US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| D405N | vaccine neutralization efficacy | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.4/5 (from) were 13.0-fold lower (95% CI: 4.2x-4.6x) than against 208-428 972-1834 4.3-4.7 US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|--|
| D405N | ACE2 receptor binding affinity | Pokay | The hACE2-binding affinity of XBB.1.5 RBD has a dissociation constant KD of 3.4 nM, where S486P is the distinguishing Spike mutation vs parent XBB.1 RBD with a much weaker KD (19 nM), as measured by surface plasmon resonance (SPR) assays. | 2023 | Yue et al. (2023) |
| R408S | pharmaceutical effectiveness | Pokay | Omicron BA.2 have higher sensitivity to inhibition by soluble angiotensin converting enzyme 2 (ACE2) and the endosomal inhibitor chloroquine compared to D614G | 2022 | Neerukonda et al. (2022) |
| R408S | antibody epitope effects | Pokay | Neutralization of the bsAbs Bi-Nab35B5-47D10. Omicron BA.2 has an IC50 fold change of 0.07x. | 2022 | Yuan et al. (2022) |
| R408S | antibody epitope effects | Pokay | Neutralization of the bsAbs 35B5. Omicron BA.2 has an IC50 fold change of 0.09x. | 2022 | Yuan et al. (2022) |
| R408S | antibody epitope effects | Pokay | Neutralization of the bsAbs 47D10. Omicron BA.2 has an IC50 fold change of 0.08x. | 2022 | Yuan et al. (2022) |
| R408S | antibody epitope effects | Pokay | Neutralization of the bsAbs Bi-Nab47D10-35B5. Omicron BA.2 has an IC50 fold change of 0.04x. | 2022 | Yuan et al. (2022) |
| R408S | vaccine neutralization efficacy | Pokay | Omicron BA.2 neutralization of the Omicron variants by antibodies induced by three doses of Pfizer/BNT162b2 mRNA vaccine was 7-8-fold less potent than the D614G, and the Omicron variants still evade neutralization more efficiently. | 2022 | Neerukonda et al. (2022) |
| R408S | antibody epitope effects | Pokay | BnAb 002-S21F2 IC50 on the Omicron BA.2 variant is 0.8x fold the wildtype. | 2022 | Kumar et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|--|
| R408S | vaccinee plasma binding | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.2 (from South Africa/CERI-KRISP-K03 2307/2021) were 3.9x-fold lower (95% CI: 0.14x-0.17x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahade et al. (2022) |
| R408S | ACE2 receptor binding affinity | Pokay | L27, V34 and E90 mutation resulted in ultrahigh affinity binding of the LVE-ACE-2 domain to the widest variety of VOCs, with KDs of 78fM for binding to the Omicron BA.2. Values were obtained with LVE-ACE-2/mAB chimeras containing the Y-T-E sequence that enhances binding to the FcRn receptor, which in turn is expected to extend biological half-life 3-4-fold. | 2022 | Uhal B et al. (2022) |
| R408S | vaccine neutralization efficacy | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.2 (from South Africa/CERI-KRISP-K03 2307/2021) were 4.5-fold lower (95% CI: 4.3x-4.7x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahade et al. (2022) |
| R408S | vaccine neutralization efficacy | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.2.12.1 (from USA/NY-CDC-ASC2 10722700/2022) were 4.2-fold lower (95% CI: 5.8x-6.6x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahade et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|--|
| R408S | vaccinee plasma binding | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.2.12.1 (from USA/NY-CDC-ASC2 10722700/2022) were 3.9x-fold lower (95% CI: 0.14x-0.18x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahade et al. (2022) |
| R408S | vaccinee plasma binding | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.4/5 (from) were 17.2x-fold lower (95% CI: 0.6x-0.7x) than against 208-428 972-1834 4.3-4.7 US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahade et al. (2022) |
| R408S | vaccine neutralization efficacy | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.4/5 (from) were 13.0-fold lower (95% CI: 4.2x-4.6x) than against 208-428 972-1834 4.3-4.7 US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahade et al. (2022) |
| R408S | ACE2 receptor binding affinity | Pokay | The hACE2-binding affinity of XBB.1.5 RBD has a dissociation constant KD of 3.4 nM, where S486P is the distinguishing Spike mutation vs parent XBB.1 RBD with a much weaker KD (19 nM), as measured by surface plasmon resonance (SPR) assays. | 2023 | Yue et al. (2023) |
| R408S | gene expression increase | Pokay | Experimentally, Spike gene expression increased 0.21 fold | 2020 | Starr et al. (2020) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|--|
| R408S | vaccine efficacy | Pokay | In a study of 481 vaccinees going from lowest to highest infection rate, 2 doses of CoronaVac and 1 dose of BNT162b2 had the lowest infection rate at 6.3%, then it was 3 doses of BNT162b2 having a infection rate of 16.6%. 2 and 3 doses of CoronaVac had 48.6% and 20.6% infection rate respectively. 2 doses of BNT162b2 has the highest infection rate at 49.2%. | 2022 | Zhou et al. (2022) |
| K417N | pharmaceutical effectiveness | Pokay | Omicron BA.2 have higher sensitivity to inhibition by soluble angiotensin converting enzyme 2 (ACE2) and the endosomal inhibitor chloroquine compared to D614G | 2022 | Neerukonda et al. (2022) |
| K417N | antibody epitope effects | Pokay | Neutralization of the bsAbs Bi-Nab35B5-47D10. Omicron BA.2 has an IC50 fold change of 0.07x. | 2022 | Yuan et al. (2022) |
| K417N | antibody epitope effects | Pokay | Neutralization of the bsAbs 35B5. Omicron BA.2 has an IC50 fold change of 0.09x. | 2022 | Yuan et al. (2022) |
| K417N | antibody epitope effects | Pokay | Neutralization of the bsAbs 47D10. Omicron BA.2 has an IC50 fold change of 0.08x. | 2022 | Yuan et al. (2022) |
| K417N | antibody epitope effects | Pokay | Neutralization of the bsAbs Bi-Nab47D10-35B5. Omicron BA.2 has an IC50 fold change of 0.04x. | 2022 | Yuan et al. (2022) |
| K417N | vaccine neutralization efficacy | Pokay | Omicron BA.2 neutralization of the Omicron variants by antibodies induced by three doses of Pfizer/BNT162b2 mRNA vaccine was 7-8-fold less potent than the D614G, and the Omicron variants still evade neutralization more efficiently. | 2022 | Neerukonda et al. (2022) |
| K417N | antibody epitope effects | Pokay | BnAb 002-S21F2 IC50 on the Omicron BA.2 variant is 0.8x fold the wildtype. | 2022 | Kumar et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|---------------------------------------|
| K417N | convalescent plasma escape | Pokay | Artificially constructed HIV-1 pseudovirus with set of mutations drawn from plasma passage escape experiments and mutations from variants of concern completely ablates neutralization in 19 of 21 convalescents plasma collected mean 1.3 months post infection. [actual Y145del from manuscript substituted with more common Y144del description] | 2021 | Schmidt et al. (2021) |
| K417N | convalescent plasma escape | Pokay | 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 | 2021 | Cele et al. (2021) |
| K417N | vaccine neutralization efficacy | Pokay | In human sera 8 weeks post-vaccination with INO-4800, a ~7-fold reduction in B.1.351 neutralization was observed. | 2021 | Andrade et al. (2021) |
| K417N | vaccine neutralization efficacy | Pokay | Four fold reduction in neutralization efficiency was observed in sera of ferrets post-vaccination with INO-4800 (DNA plasmid pGX9501 encoding full length Spike). | 2021 | Riddell et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|--------------------------------------|
| K417N | vaccine neutralization efficacy | Pokay | Monovalent mRNA-1273.351 encodes for the S protein found in the B.1.351 lineage and (2) mRNA-1273.211 comprising a 1:1 mix of mRNA-1273 and mRNA-1273.351. In a mouse study, primary vaccination series of mRNA-1273.351 was effective at increasing neutralizing antibody titers against the B.1.351 lineage, while mRNA-1273.211 was most effective at providing broad cross-variant neutralization. In addition, these results demonstrated a third dose of mRNA-1273.351 significantly increased both wild-type and B.1.351-specific neutralization titers. | 2021 | Wu et al. (2021) |
| K417N | vaccine neutralization efficacy | Pokay | Pzifer vaccinees that tested positive at least a week after the second dose were indeed disproportionately infected with B.1.351, as compared with unvaccinated individuals (odds ratio of 8:1), but were all infected before 14 days post second vaccination. | 2021 | Kustin et al. (2021) |
| K417N | convalescent plasma escape | Pokay | Mean 8.2x reduction of NT50 value B.1.351 (Beta) relative to wild type in 8 sera from older convalescent patients (52-92yo) collected 1-3m post symptom onset. | 2021 | Uriu et al. (2021) |
| K417N | vaccine neutralization efficacy | Pokay | Mean 6.3x reduction of NT50 value B.1.351 (Beta) relative to wild type in 8 sera from adult BNT162b2 vaccinees (28-47yo) collected ~1m post booster. | 2021 | Uriu et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|---------------------------------------|
| K417N | convalescent plasma escape | Pokay | 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. | 2021 | Skelly et al. (2021) |
| K417N | convalescent plasma binding | Pokay | In sera from six patients collected 1 to 12 weeks post-infection with B.1, antibody titer in a microneutralization assay was on average 8 for B.1.351 virus. Compare to much stronger neutralization titers for B.1.1.7 (256) and wild type (456.1) in the same sera. | 2021 | Luftig et al. (2021) |
| K417N | vaccine neutralization efficacy | Pokay | 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 potentially neutralizing WA1 while having FRNT50 for B.1.351 below the assay limit of detection (1:20). | 2021 | Bates et al. (2021) |
| K417N | convalescent plasma binding | Pokay | Sera from individuals who have been infected with Delta does not have strong neutralising activity against Beta. | 2021 | UNKNOWN et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|--|
| K417N | convalescent plasma escape | Pokay | 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 ~6x reduction in neutralizing titers, and 40% of the samples lacked any activity against B.1.351. | 2021 | Planas et al. (2021) |
| K417N | vaccinee plasma binding | Pokay | Sera from individuals who have been vaccinated and have had subsequent recent Delta infection have a high level of neutralising activity against Beta. | 2021 | UNKNOWN et al. (2021) |
| K417N | vaccine neutralization efficacy | Pokay | Paradigm's ACE-2 variant LVE/STR chimera neutralizes Beta Variant B.1.351 RBD significantly better than w.t. SARS-CoV-2 RBD. Determined using Surrogate Viral Neutralization Tests. | 2022 | Uhal B et al. (2022) |
| K417N | vaccine neutralization efficacy | Pokay | 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. | 2021 | Garcia-Beltran et al. (2021) |
| K417N | ACE2 receptor binding affinity | Pokay | Pseudotype lentivirus for the full B.1.351 Spike variant list shows increase affinity for ACE2 as measured by IC50. This is in contrast to B.1.1.7 which showed no major change, indicating that the shared N501Y mutation is the driver of affinity change, attenuated in the B.1.1.7 mutatioon set, but maintained in the B.1.351 lineage. | 2021 | Tada et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|--------------------------------------|
| K417N | vaccine neutralization efficacy | Pokay | [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.] | 2021 | Voysey et al. (2021) |
| K417N | ACE2 receptor binding affinity | Pokay | 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 greater extent to B.1.1.7, which both carry the N501Y mutation (see Fig 3). | 2021 | Planas et al. (2021) |
| K417N | vaccine neutralization efficacy | Pokay | PBMCs of Pfizer/BioNTech BNT162b2 (n | 2021 | Tarke et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|--|
| K417N | vaccine neutralization efficacy | Pokay | Relative to B.1.1.117, PRNT50 line virus neutralizing antibody activity assay of B.1.351 showed ~11x reduction in 13 vaccinees's sera collected through 41 days after vaccination. Neutralization by a placebo control group of 6 naturally infected patients showed a smaller ~8x drop (starting from a ~50% higher PRNT50 value than vaccinees 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 ~4x 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). | 2021 | Madhi et al. (2021) |
| K417N | vaccine neutralization efficacy | Pokay | Log10ID50 of Beta neutralizing antibodies is 0.899x the WT 1 month post-third dose of pfizer-BioNTech BNT162b2 in 13 Kidney transplant recipients (KTR) with median age of 55.5. | 2022 | McEvoy C et al. (2022) |
| K417N | convalescent plasma escape | Pokay | A 1.8-fold drop in FRNT50 for B.1.351 was observed in 44 sera collected between 1 and 301 post-infection. | 2021 | Bates et al. (2021) |
| K417N | vaccine neutralization efficacy | Pokay | 3.2x reduction in neutralization (ID50) in sera 3 weeks after one dose of Pfizer/BioNTech BNT162b2 (up to 5 naive and post infection vaccinees) | 2021 | Gong et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|--|
| K417N | vaccine neutralization efficacy | Pokay | Neutralization efficiency (ID50) against B.1.1.351-v1 reduced 6.9x relative to D614G wildtype using pseudotyped VSV assay on 8 Moderna vaccinee sera one week post-booster. | 2021 | Choi et al. (2021) |
| K417N | T cell evasion | Pokay | 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. | 2021 | Skelly et al. (2021) |
| K417N | convalescent plasma escape | Pokay | The neutralizing activity of 16/20 convalescent sera was significantly lower against this pseudotyped virus model of B.1.351, with similar results for the live virus. | 2021 | Wang et al. (2021) |
| K417N | vaccine neutralization efficacy | Pokay | Log10ID50 of Beta neutralizing antibodies is 0.803x the WT pre-third dose of pfizer-BioNTech BNT162b2 in 13 Kidney transplant recipients (KTR) with median age of 55.5. | 2022 | McEvoy C et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|------------------------------------|
| K417N | antibody epitope effects | Pokay | B.1.351 pseudotyped virus model ablates neutralization by RBD-directed mAbs CB6, 4-20, 2-4, 2-43, 910-30, 2-302-15, LY-Cov555, C121. B.1.351 pseudotyped virus model severely impairs neutralization by RBD-directed mAb 1-20. B.1.351 pseudotyped virus model impairs neutralization by RBD-directed mAb REGN10933. B.1.351 pseudotyped virus model ablates neutralization by N-terminal-domain-directed mAbs 5-24, 4-8, 4A8, 4-19. B.1.351 pseudotyped virus model severely impairs neutralization by N-terminal-domain-directed mAb 2-17. B.1.351 pseudotyped virus model impairs neutralization by N-terminal-domain-directed mAb 5-7. PG: Live virus data for the same mAbs is similar, but 1-20 becomes severally impaired, REGN10933 activity is ablated, and Brii-196 becomes impaired. | 2021 | Wang et al. (2021) |
| K417N | vaccine neutralization efficacy | Pokay | The neutralizing activity of vaccine was significantly lower against B.1.351 (12.4x in twelve Moderna-recipient sera: 10.3x in ten Pfizer-recipient sera). [this is a larger list of B.1.351 than modeled by Wang et al. (2021) by including L18F and R246I, less effective at neutralizing] | 2021 | Wang et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|---|
| K417N | vaccine neutralization efficacy | Pokay | 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 (~10x vs D614G) through week 6, the last timepoint measured. Three vaccinees never showed detectable neutralization to B.1.351 even after second dose. | 2021 | Planas et al. (2021) |
| K417N | pharmaceutical effectiveness | Pokay | DARPin SR16m molecule had a 0.036x fold change in IC50 in B.1.351 Beta | 2022 | Chonira et al. (2022) |
| K417N | tissue specific neutralization | Pokay | 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 vaccinee neutralizing at weeks 3 and 6, B.1.351 showed zero neutralization at either time point in any sample (and relatively impaired serum neutralization). | 2021 | Planas et al. (2021) |
| K417N | vaccine neutralization efficacy | Pokay | 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. | 2021 | Choi et al. (2021) |
| K417N | vaccine neutralization efficacy | Pokay | 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. | 2021 | Woldemeskel et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|---------------------------------------|
| K417N | vaccine neutralization efficacy | Pokay | 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 relative decrease was 6.1x vs wild type). | 2021 | Ikegame et al. (2021) |
| K417N | pharmaceutical effectiveness | Pokay | Trimeric proteins FSR22 had a 0.07x fold change in IC50 in B.1.351 Beta | 2022 | Chonira et al. (2022) |
| K417N | vaccine neutralization efficacy | Pokay | 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. | 2021 | Shinde et al. (2021) |
| K417N | pharmaceutical effectiveness | Pokay | DARPin SR22 molecule had a 1.57x fold change in IC50 in B.1.351 Beta | 2022 | Chonira et al. (2022) |
| K417N | pharmaceutical effectiveness | Pokay | Trimeric proteins FSR16m had a 0.054x fold change in IC50 in B.1.351 Beta | 2022 | Chonira et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|------------------------------|---------------------|---|------------------|---|
| K417N | pharmaceutical effectiveness | Pokay | B.1.351 virus neutralization (as tested using biolayer interferometry) of both Lilly antibodies was severely impacted, with LY-CoV16 and LY-CoV555 (due to mutations at 416 and 484 respectively) shows almost complete loss of neutralization of B.1.351. There was also escape from neutralization of B.1.351 by REGN10933 and a modest reduction in neutralization of B.1.351 by AZD8895 (while AZD1061 and AZD7442 showed equal neutralization of all SARS-CoV-2 variants tested). The three Adagio antibodies neutralized B.1.351. | 2021 | Dejnirattisai et al. (2021) |
| K417N | pharmaceutical effectiveness | Pokay | DARPin SR16m molecule had a 6.7x fold change in IC50 in B.1.617.2 Delta | 2022 | Chonira et al. (2022) |
| K417N | pharmaceutical effectiveness | Pokay | DARPin SR16m molecule had a 99.7x fold change in IC50 in B.1.617.2 Delta | 2022 | Chonira et al. (2022) |
| K417N | trafficking | Pokay | Lentiviral pseudotyped with all key mutations from B.1.351 lineage was tested on ACE2.293T cells. Luciferase activity was measured two days postinfection, showing modest decrease in infection rate amongst the cells, suggesting some synergy between the mutations to decrease cell entry fitness (i.e. cell entry is likely not the driver of this lineage's dominance). | 2021 | Tada et al. (2021) |
| K417N | convalescent plasma escape | Pokay | The most significant loss of neutralizing activity (PsVNA50 assay) using 6 hyperimmune immunoglobulin preparations from convalescent plasma was seen against authentic B.1.351 lineage virus (9.2-fold). Neutralization against 10 convalescent plasma was poorer (18.7x). | 2021 | Tang et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|-----------------------------------|---------------------|---|------------------|---------------------------------------|
| K417N | environmental condition stability | Pokay | Treatment with heat, soap and ethanol revealed similar inactivation profiles indicative of a comparable susceptibility towards disinfection. Furthermore, we observed comparable surface stability on steel, silver, copper and face masks. | 2021 | Meister et al. (2021) |
| K417N | environmental condition stability | Pokay | Relative to D614G, this mutation set (B.1.351+) demonstrated significant increase in infectivity (i.e. heat stability) after incubation at 50C after 1 hour. | 2021 | Tada et al. (2021) |
| K417N | vaccinee plasma binding | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.2 (from South Africa/CERI-KRISP-K03 2307/2021) were 3.9x-fold lower (95% CI: 0.14x-0.17x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| K417N | ACE2 receptor binding affinity | Pokay | L27, V34 and E90 mutation resulted in ultrahigh affinity binding of the LVE-ACE-2 domain to the widest variety of VOCs, with KDs of 78fM for binding to the Omicron BA.2. Values were obtained with LVE-ACE-2/mAB chimeras containing the Y-T-E sequence that enhances binding to the FcRn receptor, which in turn is expected to extend biological half-life 3-4-fold. | 2022 | Uhal B et al. (2022) |
| K417N | vaccine neutralization efficacy | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.2 (from South Africa/CERI-KRISP-K03 2307/2021) were 4.5-fold lower (95% CI: 4.3x-4.7x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|--|
| K417N | vaccine neutralization efficacy | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.2.12.1 (from USA/NY-CDC-ASC2 10722700/2022) were 4.2-fold lower (95% CI: 5.8x-6.6x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| K417N | vaccinee plasma binding | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.2.12.1 (from USA/NY-CDC-ASC2 10722700/2022) were 3.9x-fold lower (95% CI: 0.14x-0.18x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| K417N | pharmaceutical effectiveness | Pokay | Omicron (a.k.a. B.1.1.529) Spike pseudotyped VSV and Vero E6 cells has somewhat reduced neutralization (2.7x) vs wild type with monoclonal antibody Sotrovimab (a.k.a. VIR-7831). [delins at 214 omitted for syntax compatibility] | 2021 | Cathcart et al. (2021) |
| K417N | vaccine neutralization efficacy | Pokay | Omicron breakthrough infection after 3-dose vaccination resulted in a further 3.5-fold and 2.9-fold increase of Omicron BA.1 and BA.2 neutralizing titers. Omicron BA.4/5 showed the highest neutralization resistance of all variants tested, resulting in low geometric mean neutralizing titers in plasma samples obtained after the second vaccine dose (NT50 | 2022 | Wang et al. (2022) |
| K417N | antibody epitope effects | Pokay | Neutralization of the bsAbs Bi-Nab47D10-35B5. Omicron BA.1 has an IC50 fold change of 0.08x. | 2022 | Yuan et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|--|
| K417N | vaccine neutralization efficacy | Pokay | Omicron B.1.1.529 (BA.1) neutralization of the Omicron variants by antibodies induced by three doses of Pfizer/BNT162b2 mRNA vaccine was 7-8-fold less potent than the D614G, and the Omicron variants still evade neutralization more efficiently. | 2022 | Neerukonda et al. (2022) |
| K417N | pharmaceutical effectiveness | Pokay | Omicron (B.1.1.529 [BA.1]) have higher sensitivity to inhibition by soluble angiotensin converting enzyme 2 (ACE2) and the endosomal inhibitor chloroquine compared to D614G | 2022 | Neerukonda et al. (2022) |
| K417N | antibody epitope effects | Pokay | Neutralization of the bsAbs Bi-Nab35B5-47D10. Omicron BA.1 has an IC50 fold change of 0.30x. | 2022 | Yuan et al. (2022) |
| K417N | vaccine neutralization efficacy | Pokay | Paradigms' ACE-2 variant LVE/STR chimera binds to SARS-2 Omicron variant B.1.1.529 spike protein trimer with high affinity. Determined using Surrogate Viral Neutralization Tests. | 2022 | Uhal B et al. (2022) |
| K417N | ACE2 receptor binding affinity | Pokay | L27, V34 and E90 mutation resulted in ultrahigh affinity binding of the LVE-ACE-2 domain to the widest variety of VOCs, with KDs of 73 pM for binding to the Omicron B.1.1.529. Values were obtained with LVE-ACE-2/mAB chimeras containing the Y-T-E sequence that enhances binding to the FcRn receptor, which in turn is expected to extend biological half-life 3-4-fold. | 2022 | Uhal B et al. (2022) |
| K417N | antibody epitope effects | Pokay | Neutralization of the bsAbs 35B5. Omicron BA.1 has an IC50 fold change of 0.38x. | 2022 | Yuan et al. (2022) |
| K417N | vaccinee plasma binding | Pokay | All 10 individuals with 2 doses of the BNT162b2/BNT162b2 vaccine had a neutralizing titer in B.1 variant at an average of 729 NT50. | 2022 | Arora et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|--------------------------|---------------------|--|------------------|-------------------------------------|
| K417N | antibody epitope effects | Pokay | Plaque reduction neutralization test (PRNT) was used uring primary infection, post sixty daysof second dose vaccination, pre-reinfection and reinfection against Delta variant and was used to determine neutralizing antibodytitres. There was a 24.63x fold increase in antibody response from first infection to recovered and vaccinated with 2 doses (60 days). There was a 4.21x fold increase in antibody response pre-reinfection. There was a 39.27x fold increase in antibody response during reinfection. | 2022 | Shete et al. (2022) |
| K417N | antibody epitope effects | Pokay | Plaque reduction neutralization test (PRNT) was used uring primary infection, post sixty daysof second dose vaccination, pre-reinfection and reinfection against B.1 variant and was used to determine neutralizing antibodytitres. There was a 6.76x fold increase in antibody response from first infection to recovered and vaccinated with 2 doses (60 days). There was a 2.06x fold increase in antibody response pre-reinfection. There was a 8.18x fold increase in antibody response during reinfection. | 2022 | Shete et al. (2022) |
| K417N | vaccinee plasma binding | Pokay | All 10 individuals with 3 doses of the BNT162b2/BNT162b2 vaccine had a neutralizing titer in B.1 variant at an average of 3319 NT50. | 2022 | Arora et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|--|
| K417N | antibody epitope effects | Pokay | Plaque reduction neutralization test (PRNT) was used using primary infection, post sixty days of second dose vaccination, pre-reinfection and reinfection against Omicron variant and was used to determine neutralizing antibody titres. There was a 114.84x fold increase in antibody response from first infection to recovered and vaccinated with 2 doses (60 days). There was a 6.61x fold increase in antibody response pre-reinfection. There was a 1194.9x fold increase in antibody response during reinfection. | 2022 | Shete et al. (2022) |
| K417N | antibody epitope effects | Pokay | BnAb 002-S21F2 IC50 on the Omicron BA.1 variant is 1.0x fold the wildtype. | 2022 | Kumar et al. (2022) |
| K417N | antibody epitope effects | Pokay | Neutralization of the bsAbs 47D10. Omicron BA.1 has an IC50 fold change of 1.26x. | 2022 | Yuan et al. (2022) |
| K417N | pharmaceutical effectiveness | Pokay | Omicron BA.3 have higher sensitivity to inhibition by soluble angiotensin converting enzyme 2 (ACE2) and the endosomal inhibitor chloroquine compared to D614G | 2022 | Neerukonda et al. (2022) |
| K417N | vaccine neutralization efficacy | Pokay | Omicron BA.3 neutralization of the Omicron variants by antibodies induced by three doses of Pfizer/BNT162b2 mRNA vaccine was 7-8-fold less potent than the D614G, and the Omicron variants still evade neutralization more efficiently. | 2022 | Neerukonda et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|---------------------------------------|
| K417N | vaccinee plasma binding | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.3 (from South Africa/NICD-N22404/2021) were 4.2x-fold lower (95% CI: 0.15x-0.20x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| K417N | vaccine neutralization efficacy | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.3 (from South Africa/NICD-N22404/2021) were 6.2-fold lower (95% CI: 11.8x-14.3x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| K417N | vaccine neutralization efficacy | Pokay | paired testing of vaccine sera against ancestral virus compared to Omicron BA.1 shows that 3-dose vaccine regimen provides over 50x fold increase in protection against Omicron(B.1.1.529 [BA.1]) compared to a 2-dose regimen. | 2022 | Hao et al. (2022) |
| K417N | pharmaceutical effectiveness | Pokay | 4th antigenic exposure with Omicron (B.1.1.529 [BA.1])(n | 2022 | Wang et al. (2022) |
| K417N | vaccine neutralization efficacy | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.1 (from Botswana/R40B59_BHP_3321 001248/2021) were 3.4-fold lower (95% CI: 3.2x-3.6x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|---------------------------------------|
| K417N | vaccinee plasma binding | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.1 (from Botswana/R40B59_BHP_3321 001248/2021) were 28.7x-fold lower (95% CI: 0.03x-0.05) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| K417N | vaccinee plasma binding | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.4/5 (from) were 17.2x-fold lower (95% CI: 0.6x-0.7x) than against 208-428 972-1834 4.3-4.7 US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| K417N | vaccine neutralization efficacy | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.4/5 (from) were 13.0-fold lower (95% CI: 4.2x-4.6x) than against 208-428 972-1834 4.3-4.7 US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| K417N | outcome hazard ratio | Pokay | In Ontario, using a retrospective matched case (age, gender and onset date) study of 6,312 Omicron cases vs 8,875 Delta, the adjusted risk of hospitalization or death was 54% lower (HR | 2021 | Ulloa et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|--|
| K417N | vaccine neutralization efficacy | Pokay | 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 ~10-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 ~3 fold without the deletion] ID50 titres in non-infected mRNA vaccines more than two weeks post-booster were significant, but ~500x weaker than in previously infected patients after first dose. | 2021 | Stamatatos et al. (2021) |
| K417N | vaccine neutralization efficacy | Pokay | 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+. | 2021 | Pegu et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|--|
| K417N | vaccine neutralization efficacy | Pokay | 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 ~2 better neutralization than BNT162b2. [common defining B.1.351 mutations noted, as the manuscript does not provide details] | 2021 | Abe et al. (2021) |
| K417N | antibody epitope effects | Pokay | 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 ~10-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. | 2021 | Stamatatos et al. (2021) |
| K417N | convalescent plasma escape | Pokay | 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] | 2021 | Stamatatos et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|---------------------------------------|
| K417N | vaccine neutralization efficacy | Pokay | 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] | 2021 | Tada et al. (2021) |
| K417N | antibody epitope effects | Pokay | Neutralization of the bsAbs Bi-Nab35B5-47D10. Beta (B.1.351) has an IC50 fold change of 0.13x. | 2022 | Yuan et al. (2022) |
| K417N | pharmaceutical effectiveness | Pokay | Infectious viral titers in lung tissue determined using a tissue culture infectious dose (TCID) assay in 10 hamsters showed that Beta Molnupiravir (MK-4482) had ~1.75x fold drop. | 2022 | Rosenke et al. (2022) |
| K417N | ACE2 receptor binding affinity | Pokay | The B.1.351 variant constellation causes an ~20-fold increase in affinity for ACE2 compared with Wuhan RBD, which may influence transmissibility. | 2021 | Zhou et al. (2021) |
| K417N | humoral response durability | Pokay | 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. | 2020 | Betton et al. (2020) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|----------------------------|---------------------|---|------------------|--|
| K417N | trafficking | Pokay | ~6x cleavage of S2 relative to WA1 (D614G) wildtype by Beta variant as measured by mass spectrometry of Vero-TMPRSS culture [no mutations directly at furin cleavage site, but A701V is downstream] Compare to 4.5x or less for variants of concern with direct furin cleavage site mutations. | 2021 | Esclera et al. (2021) |
| K417N | outcome hazard ratio | Pokay | Compared to Alpha (B.1.1.7) variant, odds of progressing to severe disease were 1.24-fold (95% CI: 1.11-1.39) higher for Beta. Odds of progressing to critical disease were 1.49-fold (95% CI: 1.13-1.97) higher. Odds of COVID-19 death were 1.57-fold (95% CI: 1.03-2.43) higher. | 2021 | Abu-Raddad et al. (2021) |
| K417N | antibody epitope effects | Pokay | BnAb 002-S21F2 IC50 on the Beta (B.1.351) variant is 0.4x fold the wildtype. | 2022 | Kumar et al. (2022) |
| K417N | convalescent plasma escape | Pokay | In 34 convalescent cases 4–9 weeks following infection in June 2020, before the emergence of B.1.1.7, neutralization titers against B.1.351 were, on average, 13.3-fold reduced compared with an early Victoria sample ($p < 0.0001$). Significantly, 18 of 34 samples failed to reach 50% neutralization at a plasma dilution of 1:20, with a number showing a near total reduction of neutralization activity. In 13 convalescent cases 4–9 weeks following infection with B.1.1.7, neutralization titers against B.1.351 were, on average, 3.1-fold reduced compared with an early Victoria sample ($p < 0.0001$). | 2021 | Zhou et al. (2021) |
| K417N | antibody epitope effects | Pokay | Neutralization of the bsAbs Bi-Nab47D10-35B5. Beta (B.1.351) has an IC50 fold change of 0.15x. | 2022 | Yuan et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|-------------------------------------|
| K417N | vaccine neutralization efficacy | Pokay | Vaccine plasma neutralization of B.1.351-spike virus was nominally robust but lower (~3x) than other variants of concern. | 2021 | Liu et al. (2021) |
| K417N | vaccine neutralization efficacy | Pokay | 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. | 2021 | Choi et al. (2021) |
| K417N | antibody epitope effects | Pokay | Testing against B.1.351 the 20 most effective mAbs (19 anti-RBD, 1 anti-NTD) from a screen of 377 against wild type, 4 of 20 antibodies had >10-fold fall in neutralization titers, with most of these showing a complete knockout of activity. This is in line with the key roles of K417, E484, and N501, in particular E484, in antibody recognition of the ACE2 interaction surface of the RBD. Regeneron mAb cocktail: The neutralization of REGN10987 was unaffected by B.1.351, while REGN10933 was severely impaired (773-fold). AstraZeneca mAb cocktail: Neutralization by the AZ pair of antibodies was little affected on B.1.351 compared with Victoria. | 2021 | Zhou et al. (2021) |
| K417N | vaccine neutralization efficacy | Pokay | 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. | 2021 | Madhi et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|--|
| K417N | vaccine neutralization efficacy | Pokay | 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. | | UNKNOWN et al. () |
| K417N | anthropozoonotic events | Pokay | Unlike wild type or B.1.1.7, B.1.351 lineage virus was able to infect and replicate in common lab mouse strains, with high titer. PG: The virus used in these experiments has a non-typical deletion+sub in the 242 region. | 2021 | Montagutelli et al. (2021) |
| K417N | antibody epitope effects | Pokay | Neutralization of the bsAbs 35B5. Beta (B.1.351) has an IC50 fold change of 0.13x. | 2022 | Yuan et al. (2022) |
| K417N | vaccine neutralization efficacy | Pokay | Sera from healthcare workers (n | 2021 | Zhou et al. (2021) |
| K417N | antibody epitope effects | Pokay | Neutralization of the bsAbs 47D10. Beta (B.1.351) has an IC50 fold change of 0.88x. | 2022 | Yuan et al. (2022) |
| K417N | outcome hazard ratio | Pokay | 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. | 2021 | Funk et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|--|
| K417N | vaccine neutralization efficacy | Pokay | 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. | 2021 | Garcia-Beltran et al. (2021) |
| K417N | vaccine neutralization efficacy | Pokay | 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). | 2021 | Gallagher et al. (2021) |
| K417N | vaccine neutralization efficacy | Pokay | 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. | 2021 | Alenquer et al. (2021) |
| K417N | convalescent plasma escape | Pokay | 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. | 2021 | Stamatatos et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|--|
| K417N | vaccine neutralization efficacy | Pokay | 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 ~3-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 ~10 fold with L242del] ID50 titres in non-infected mRNA vaccines more than two weeks post-booster were significant, but >100x weaker than in previously infected patients after first dose. | 2021 | Stamatatos et al. (2021) |
| K417N | reinfection | Pokay | 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 February 2021 hospital outbreak in Luxembourg. Symptoms were mostly mild on first infection, and milder on second infection. | 2021 | Staub et al. (2021) |
| K417N | reinfection | Pokay | Hamsters re-infected with B.1.351 virus after seroconversion 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. | 2021 | Yinda et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|--|
| K417N | symptom prevalence | Pokay | 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. | 2021 | Munster et al. (2021) |
| K417N | vaccine neutralization efficacy | Pokay | Pseudotyped B.1.351 v3 virus has reduced neutralization activity vs wild type: 42.4x (30 sera Pfizer median 9 days post 2nd dose) and 19.2x (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. | 2021 | Garcia-Beltran et al. (2021) |
| K417N | vaccine neutralization efficacy | Pokay | The neutralization activities of two vaccines developed in China were tested against 501Y.V2 authentic virus: inactivated BBIBP-CorV (no significant change) and recombinant dimeric RBD vaccine ZF2001 (~1.6x reduction vs wildtype, p | 2021 | Huang et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|---------------------------------------|
| K417N | vaccine neutralization efficacy | Pokay | Most of the plasma from 55 Pfizer vaccinees developed high percentages of Wuhan-Hu-1 S-ACE2 blocking activity, peaking at day 28 (7 days post-boost). A strikingly consistent hierarchy of reduction in plasma antibody binding by variant S and RBD antigens was observed among study participants, with progressively decreased binding for B.1.1.7 (not significant), P.1 (significant) and B.1.351 (significant) compared to Wuhan-Hu-1 antigens. | 2021 | Röltgen et al. (2021) |
| K417N | vaccine neutralization efficacy | Pokay | During an outbreak of SARS-CoV-2 501Y.V2 in a nursing home, all non-vaccinated residents (5/5) versus half of those fully vaccinated 2-5 weeks prior with BNT162b2 (13/26) were infected. Two of 13 vaccinated versus 4 of 5 non-vaccinated residents presented severe disease. BNT162b2 did not prevent the outbreak, but reduced transmission and disease severity. Among the 13 fully vaccinated residents who were infected, 2 (15.4%) presented with an asymptomatic disease, 9 (69.2%) developed mild to moderate symptoms, and 2 (15.4%) progressed to severe disease with fatal evolution secondary to acute respiratory distress syndrome (ARDS). There was no relationship between anti-S antibody levels at diagnosis and disease severity. Overall, the proportion of residents with severe disease in the non-vaccinated group (4/5) was higher than that in the vaccinated group (2/13). Only 1 vaccinated staff, but 10 unvaccinated were infected in the outbreak (no severe disease). | 2021 | Bailey et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|--------------------------------------|
| K417N | vaccine neutralization efficacy | Pokay | The neutralizing activity of vaccine was significantly lower against B.1.351 in sera from all 24 patients with the BNT162b2 mRNA vaccine. (Fig. 4) | 2021 | Chen et al. (2021) |
| K417N | vaccine neutralization efficacy | Pokay | In sera 1-2 weeks after BNT162b2 first dose, from six patients previously infected with B.1, antibody titer in a microneutralization assay was on average 1625 for B.1.351 virus. This compares favorably (stronger) to most post-infection neutralization titer against all variants tested in the same sera (wild type, B.1.1.7, B.1.351, and P.1). | 2021 | Luftig et al. (2021) |
| K417N | vaccine neutralization efficacy | Pokay | 2.5x reduction in neutralization by serum collected 2 to 3 weeks after the second dose from vaccinees who had received BBIBP-CorV (pVNT50 against VSV pseudotyped as B.1.351). Convalescent plasma had similar titer against wild type as the BBIBP-CorV vaccinee sera. >3x reduction in neutralization by serum collected 2 to 3 weeks after the second dose from vaccinees who had received CoronaVac (pVNT50 against VSV pseudotyped as B.1.351). Convalescent plasma had similar titer against wild type as the CoronaVac vaccinee sera. | 2021 | Wang et al. (2021) |
| K417N | convalescent plasma escape | Pokay | B.1.1.351 variant constellation two-tailed Wilcoxon matched-pairs signed-rank test against 10 convalescent sera P | 2021 | Chen et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|--|
| K417N | vaccine neutralization efficacy | Pokay | Study 3001 on Ad26.COV2.S (Janssen vaccine) conducted September 21, 2020 through January 22, 2021 overlaps the emergence and dominance of the B.1.351 lineage of SARS-CoV-2 in South Africa. The SA arms of the Phase 3 double blind study showed severe/critical disease VE of 73.1% (95% CI: 40.0-89.4), and moderate to severe/critical disease VE of 52.0% (95% CI: 30.3-67.4). Compare to 78.0% and 74.4% for North American arm of the study during the same period (with low B.1.351 prevalence). Of the 66.9% of SA severe infections that have been sequenced as of this report, 94.5% are B.1.351. | 2021 | UNKNOWN et al. (2021) |
| K417N | vaccine neutralization efficacy | Pokay | The dominant circulating B.1.351 spike variant originating in RSA, which harbors E484K and additional substitutions in the RBD, NTD, and S2 and deletions in the NTD (amino acids 242–244), was neutralized with a 5.02-fold reduced titer | 2021 | Solfrosi et al. (2021) |
| K417N | convalescent plasma escape | Pokay | B.1.1.351 in 19 convalescent human sera ~1mo post infection had mild to moderate resistance against all samples | 2021 | Chen et al. (2021) |
| K417N | antibody epitope effects | Pokay | B.1.1.351 variant constellation ablates Class 1 receptor-binding-mot if targeting antibodies COV2-2050, 1B07, COVOX-384, and S2H58. B.1.1.351 variant constellation ablates Class 3 N-terminal domain targeting antibodies COV2-2489 and COV2-2676 (the only two tested). | 2021 | Chen et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|-----------------------------|---------------------|--|------------------|--|
| K417N | convalescent plasma escape | Pokay | In a Syrian hamster model, B.1.351 variant virus had >4x reduction in YRNT90 (measure of neutralization) using wild type convalescent sera. PG: Note that exact sequence for B.1.351 used was not disclosed. | 2021 | Cochin et al. (2021) |
| K417N | convalescent plasma escape | Pokay | In 13 plasma collected ~1mo after B.1.1.7 infection (nursing home in Ticino, Switzerland), neutralization reduced to undetectable levels in many plasma for B.1.351 pseudotyped virus, as well as WT and other VOCs. [paper does not detail the B.1.351 variants used, using the most popular as a stand in] | 2021 | McCallum et al. (2021) |
| K417N | convalescent plasma binding | Pokay | VSV pseudotype B.1.351 showed 7.86-fold decrease in NT50 vs wild type in sera from 9 ICU patients undergoing treatment in Germany (pre-variant infections). | 2021 | Hoffman et al. (2021) |
| K417N | antibody epitope effects | Pokay | Abrogates Bamlanivimab, Etesevimab, or their combined use neutralization as quantified by measuring virus-encoded luciferase activity in cell lysates at 16-18 h post transduction. | 2021 | Hoffman et al. (2021) |
| K417N | convalescent plasma escape | Pokay | Approximately 6-fold reduction in 15 ICU patient convalescent plasma neutralization as quantified by measuring virus-encoded luciferase activity in cell lysates at 16-18 h post transduction. | 2021 | Hoffman et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|---------------------------------------|
| K417N | vaccine neutralization efficacy | Pokay | Vaccine elicited antibodies neutralized virus with the B.1.351 spike protein had an average 3-fold reduction in titer (1:500), a titer that was still higher than the average titer with which convalescent sera neutralized D614G (1:139). Serum specimens from individuals vaccinated with the BNT162b2 mRNA vaccine neutralized D614G virus with titers that were on average 7-fold greater than convalescent sera. | 2021 | Tada et al. (2021) |
| K417N | trafficking | Pokay | In one of eight cell lines tested (293T lung cells), a modest increase in cell entry was observed. | 2021 | Hoffman et al. (2021) |
| K417N | vaccine neutralization efficacy | Pokay | Neutralizing antibody titers increased in previously infected vaccinees relative to uninfected vaccinees 6.5-fold against B.1.351 (contrast with 3.4 fold against original SARS-CoV-2). | 2021 | Leier et al. (2021) |
| K417N | pharmaceutical effectiveness | Pokay | VSV pseudotype B.1.351 entry mediated by the S proteins of the B.1.351 variant was completely resistant to blocking by REGN10989 and Bamlanivimab. Entry driven by the S proteins of the B.1.351 was partially resistant against Casirivimab. | 2021 | Hoffman et al. (2021) |
| K417N | vaccine neutralization efficacy | Pokay | B.1.351 pseudotyped lentivirus showed 3.4 and 3.8x reduction in IC50 serum dilution concentration for sera from BNT162b2 (Pfizer) or mRNA1273 (Moderna) vaccinees collected 28 days following booster dose. | 2021 | Zhou et al. (2021) |
| K417N | vaccine neutralization efficacy | Pokay | VSV pseudotype B.1.351 showed 7.85-fold reduction in neutralization efficiency vs wild type in 15 Pfizer BNT162b2 vaccinee sera 13-15 days post second dose. Cell fusion proficiency was slight impaired. | 2021 | Hoffman et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|--|
| K417N | vaccine neutralization efficacy | Pokay | After one dose, individuals with prior infection showed enhanced T cell immunity, antibody secreting memory B cell response to spike and neutralizing antibodies effective against B.1.351 (authentic cell culture supernatants). By comparison, HCW receiving one vaccine dose without prior infection showed reduced immunity against variants. B.1.351 spike mutations resulted in increased, abrogated or unchanged T cell responses depending on human leukocyte antigen (HLA) polymorphisms. Study was 26 each post-infection and post first dose HCWs. | 2021 | Reynolds et al. (2021) |
| K417N | trafficking | Pokay | VSV pseudotype B.1.351 showed slight decrease in cell entry relative to wild type in 263T-ACE2 (kidney) cell line, and slight increase in Calu-3 (lung). Cell fusion proficiency was slight impaired. | 2021 | Hoffman et al. (2021) |
| K417N | convalescent plasma binding | Pokay | We analyzed 34 convalescent samples including the WHONIBSC 20/130 reference serum, and, although a few sera showed near identical FRNT 50 values, the FRNT50 dilutions for the B.1.1.7 strain were 2.9-fold lower (geometric mean) than those for the Victoria strain ($p < 0.0001$). Sera from 13 subjects post-B.1.1.7 infection showed no significant change in neutralization against Victoria (~wild type), suggesting that B.1.1.7 infection also protects against ancestral virus. [Note that D1119H was included in the original paper, assuming typographical error and correcting to D1118H] | 2021 | Supasa et al. (2021) |
| K417N | vaccine neutralization efficacy | Pokay | nan | | UNKNOWN et al. () |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|--|
| K417N | vaccine neutralization efficacy | Pokay | In 15 Pfizer non-senior vaccinee sera collected 3-4 weeks post-booster [using Table S1, not the text that says 2-3 weeks], neutralization was reduced ~11x. | 2021 | Hoffman et al. (2021) |
| K417N | vaccine neutralization efficacy | Pokay | In Qatar, where Pfizer vaccine use is prevalent (<10% of the population covered in the time period of the study ending Mar 31, 2021), any time after one dose (including the 2 weeks where no major effect is expected) B.1.351 lineage effectiveness was observed as 16.9% (95% CI [10.4,23.0]) against infection, and 0% against severe/critical/fatal disease (95% CI [0-19.0]). Two weeks or more after 2nd dose, effectiveness climbed to 75.0% [70.5,78.9] against infection, and 100% against severe/critical/fatal disease (95% CI [73.7,100]). | | UNKNOWN et al. () |
| K417N | vaccinee plasma binding | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, XD (from) were 1.5x-fold lower (95% CI: 0.05x-0.07x) than against 208-428 972-1834 4.3-4.7 US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahade et al. (2022) |
| K417N | vaccine neutralization efficacy | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, XD (from) were 4.4-fold lower (95% CI: 4.3x-4.7x) than against 208-428 972-1834 4.3-4.7 US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahade et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---|---------------------|--|------------------|--------------------------------------|
| K417N | ACE2 receptor binding affinity | Pokay | The hACE2-binding affinity of XBB.1.5 RBD has a dissociation constant KD of 3.4 nM, where S486P is the distinguishing Spike mutation vs parent XBB.1 RBD with a much weaker KD (19 nM), as measured by surface plasmon resonance (SPR) assays. | 2023 | Yue et al. (2023) |
| K417N | antibody epitope effects | Pokay | >20% (ELISA significance threshold) drop in antibody binding (ELISA) by this variant against IgG1 monoclonal antibody ab1. | 2021 | Sun et al. (2021) |
| K417N | ACE2 receptor binding affinity | Pokay | Causes no detectable change in KD value for antibody binding of P5A-1D2. | 2021 | Zhang et al. (2021) |
| K417N | ACE2 receptor binding affinity | Pokay | Reported 3-fold decrease in affinity compared to wild-type RBD on the cell surface (Kd | 2021 | Tian et al. (2021) |
| K417N | ACE2 receptor binding affinity | Pokay | Causes no detectable change in KD value for antibody binding of P22A-1D1. | 2021 | Zhang et al. (2021) |
| K417N | ACE2 receptor binding affinity | Pokay | The K417N mutation decreased the affinity ~4 fold, mainly by decreasing the k(on) but also by increasing the k(off) as measured by surface plasmon resonance. | 2021 | Barton et al. (2021) |
| K417N | monoclonal antibody serial passage escape | Pokay | Escape mutation against monoclonal antibody LY-CoV016 | 2021 | Starr et al. (2021) |
| K417N | antibody epitope effects | Pokay | No detectable fold drop in IC50 of P5A-3C8. | 2021 | Zhang et al. (2021) |
| K417N | monoclonal antibody serial passage escape | Pokay | In vitro selection against class 1 (Spike 'up' conformation) monoclonal antibody C682, and to a lesser extent C614 and C660 | 2021 | Wang et al. (2021) |
| K417N | ACE2 receptor binding affinity | Pokay | Causes 7.5 fold decrease in KD value for antibody binding of P2C-1F11. | 2021 | Zhang et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|--------------------------------|---------------------|---|------------------|---|
| K417N | ACE2 receptor binding affinity | Pokay | Causes 1.5 fold decrease in KD value of antibody binding of ACE2. | 2021 | Zhang et al. (2021) |
| K417N | convalescent plasma escape | Pokay | In 19 convalescent human sera ~1mo post infection, Two-tailed Wilcoxon matched-pairs signed-rank test shows mild resistance P | 2021 | Chen et al. (2021) |
| K417N | antibody epitope effects | Pokay | No detectable fold drop in IC50 of P5A-1D2. | 2021 | Zhang et al. (2021) |
| K417N | ACE2 receptor binding affinity | Pokay | Causes 36.9 fold decrease in KD value for antibody binding of P5A-3C8. | 2021 | Zhang et al. (2021) |
| K417N | trafficking | Pokay | 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. | 2021 | Tada et al. (2021) |
| K417N | pharmaceutical effectiveness | Pokay | COR-101 lost ~6x binding against this isolated mutation. Estesevimab lost ~100x binding against this isolated mutation. | 2021 | Engelhart et al. (2021) |
| K417N | gene expression increase | Pokay | Experimentally, Spike gene expression increased 0.1 fold | 2020 | Starr et al. (2020) |
| K417N | antibody epitope effects | Pokay | 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. | 2021 | Wang et al. (2021) |
| K417N | antibody epitope effects | Pokay | 5 antibodies tested were less potent against K417N by ten-fold or more (class 1 mAbs) | 2021 | Wang et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|---|
| K417N | virion structure | Pokay | Estimated free energy change (ddG) for this variant is -0.86 kcal/mol (i.e. destabilizing relative to wild type) | 2021 | Spratt et al. (2021) |
| K417N | antibody epitope effects | Pokay | 1.1 fold drop in IC50 of P2C-1F11. | 2021 | Zhang et al. (2021) |
| K417N | antibody epitope effects | Pokay | No detectable fold drop in IC50 of P22A-1D1. | 2021 | Zhang et al. (2021) |
| K417N | vaccine neutralization efficacy | Pokay | 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 ~1/300. | 2021 | Wu et al. (2021) |
| K417N | convalescent plasma escape | Pokay | 27% of 44 early pandemic exposure convalescent plasma/sera lose all activity against a RBD triple mutant pseudovirus (RBD mutants of the 501Y.V2 'South African' lineage), while only 23% retained high titres | 2021 | Wibmer et al. (2021) |
| K417N | viral load | Pokay | B.1.351 and P.1 samples showed average Ct cycle threshold of 22.2 vs 23 for wildtype (i.e. ~60% higher viral load) comparing 3360 and 22535 samples respectively. | 2021 | Roquebert et al. (2021) |
| K417N | pharmaceutical effectiveness | Pokay | This mutated version of RBD completely abolishes the binding to a therapeutic antibody, Bamlanivimab, in vitro. | 2021 | Liu et al. (2021) |
| K417N | antibody epitope effects | Pokay | Ablates Class 1 receptor-binding-mot if targeting antibodies COV2-2050, 1B07, COVOX-384, and S2H58. | 2021 | Chen et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|--------------------------------------|
| K417N | vaccine neutralization efficacy | Pokay | 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 ~2x) decrease in neutralization by vaccine plasma was observed. | 2021 | Wang et al. (2021) |
| K417N | ACE2 receptor binding affinity | Pokay | 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. | 2021 | Barton et al. (2021) |
| K417N | antibody epitope effects | Pokay | 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 | 2021 | Wibmer et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|---|
| K417N | convalescent plasma escape | Pokay | In 19 convalescent human sera ~1mo post infection had mild to moderate resistance against most samples | 2021 | Chen et al. (2021) |
| K417N | pharmaceutical effectiveness | Pokay | Tixagevimab, Regdanvimab and COR-101 display reduced binding affinity to virus pseudotyped as RBD from B.1.351. | 2021 | Engelhart et al. (2021) |
| K417N | ACE2 receptor binding affinity | Pokay | This combination showed ~3x 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 | 2021 | Collier et al. (2021) |
| K417N | vaccine neutralization efficacy | Pokay | 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. | 2021 | Bates et al. (2021) |
| K417N | antibody epitope effects | Pokay | 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. | 2021 | Sun et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|--------------------------------|---------------------|---|------------------|--|
| K417N | ACE2 receptor binding affinity | Pokay | Using Microscale Thermophoresis, 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). | 2021 | Ramanathan et al. (2021) |
| K417N | ACE2 receptor binding affinity | Pokay | 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. | 2021 | Laffeber et al. (2021) |
| K417N | viral load | Pokay | The 62 B.1.351 (a.k.a. N501Y.V2) variant cases in three Paris hospital labs had a ~2-fold viral load increase (~1 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). | 2021 | Teyssou et al. (2021) |
| K417N | ACE2 receptor binding affinity | Pokay | Reported slight increase in affinity compared to wild-type RBD on the cell surface (Kd | 2021 | Tian et al. (2021) |
| K417N | ACE2 receptor binding affinity | Pokay | 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. | 2021 | Liu et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|--------------------------------|---------------------|--|------------------|---|
| K417N | ACE2 receptor binding affinity | Pokay | 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. | 2021 | Vogel et al. (2021) |
| K417N | trafficking | Pokay | 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. | 2021 | Hu et al. (2021) |
| K417N | transmissibility | Pokay | 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. | 2021 | Roquebert et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|--|
| K417N | transmissibility | Pokay | 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. | 2021 | Pearson et al. (2021) |
| K417N | convalescent plasma escape | Pokay | Average ~10-fold reduction in neutralization efficacy in convalescent sera of 16 health workers infected in Spring 2020. | 2021 | Alenquer et al. (2021) |
| K417N | vaccine neutralization efficacy | Pokay | 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 ~2000 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). | 2021 | Madhi et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|---------------------------------------|
| K417N | convalescent plasma escape | Pokay | Neutralizing antibody titers of 18 samples (90%) decreased against this B.1.351 pseudotyped virus below an ID50 threshold of 40 (sera collected ~8mo post Jan 2020 first wave in China). | 2021 | Hu et al. (2021) |
| K417N | antibody epitope effects | Pokay | Abolished neutralization by mAbs CQ026 and CQ038, greatly diminished neutralization by CQ012 and CQ046. | 2021 | Hu et al. (2021) |
| K417N | vaccine neutralization efficacy | Pokay | This variant of key B.1.351 lineage mutations showed ~10x decrease in Pfizer sera (3 weeks post-first dose: n | 2021 | Kuzmina et al. (2021) |
| K417N | vaccine neutralization efficacy | Pokay | This variant showed ~10x decrease in Pfizer sera (3 weeks post-first dose: n | 2021 | Kuzmina et al. (2021) |
| K417N | pharmaceutical effectiveness | Pokay | Trachea viral loads were tested by qRT-PCR and RNA scope at 3 dpi on 5 8-month-old male mice and there was a ~750x fold drop in the R3P1-E4 antibody in comparison to the IgG control. | 2022 | Li et al. (2022) |
| K417N | pharmaceutical effectiveness | Pokay | Lung viral loads were tested by qRT-PCR and RNA scope at 3 dpi on 5 8-month-old male mice and there was a ~2266x fold drop in the R3P1-E4 antibody in comparison to the IgG control. | 2022 | Li et al. (2022) |
| K417N | pharmaceutical effectiveness | Pokay | 100% of the 5 8-month-old male R3P1-E4 antibody treated mice survived 14 days after infection while only 60% the control group mice survived 5 days post infection. | 2022 | Li et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|---|
| K417N | trafficking | Pokay | ~5x 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] | 2021 | Kim et al. (2021) |
| K417N | vaccine neutralization efficacy | Pokay | This variant showed >5x decrease in Pfizer sera (3 weeks post-first dose: n | 2021 | Kuzmina et al. (2021) |
| K417N | trafficking | Pokay | ~9x more infectivity than D614G alone in HEK293T-ACE2 cells 48h post-transduction (no synergy as level approx. that of N501Y alone). | 2021 | Kuzmina et al. (2021) |
| K417N | vaccine neutralization efficacy | Pokay | This variant showed only minor in Pfizer sera (one or two dose) neutralization efficiency vs D614G (using lentivirus pseudotype). | 2021 | Kuzmina et al. (2021) |
| K417N | trafficking | Pokay | ~2x more infectivity than D614G alone in HEK293T-ACE2 cells 48h post-transduction. | 2021 | Kuzmina et al. (2021) |
| K417N | pharmaceutical effectiveness | Pokay | Bamlanivimab (LY-CoV555) lost ~32x binding against this double mutation. COR-101 lost ~160x binding against this double mutation. Casirivimab lost ~16x binding against this double mutation. Estesevimab lost ~32x binding against this double mutation. Regdanvimab lost ~4x binding against this double mutation. Tixagevimab lost ~12x binding against this double mutation. | 2021 | Engelhart et al. (2021) |
| K417N | trafficking | Pokay | ~13x more infective as D614G alone in HEK293T-ACE2 cells 48h post-transduction. | 2021 | Kuzmina et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|---|
| K417N | trafficking | Pokay | Approximately as infective as D614G alone in HEK293T-ACE2 cells 48h post-transduction (~additive effects of the individual variants). | 2021 | Kuzmina et al. (2021) |
| K417N | pharmaceutical effectiveness | Pokay | COR-101 lost ~20x binding against this double mutation. Estesevimab lost ~16x binding against this double mutation. Regdanvimab lost ~6x binding against this double mutation. M396 lost ~10x binding against this double mutation. | 2021 | Engelhart et al. (2021) |
| K417N | vaccine neutralization efficacy | Pokay | In post-vaccination sera from individuals who received one (3 weeks post-first dose: n | 2021 | Kuzmina et al. (2021) |
| K417N | convalescent plasma escape | Pokay | ~7x 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. | 2021 | Kuzmina et al. (2021) |
| K417N | convalescent plasma binding | Pokay | This variant combination (representing B.1.351 aka Beta) showed a 1.04x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset, in contrast to the largely positive binding values for each individual mutation that comprises the set. | 2021 | Gong et al. (2021) |
| K417N | ACE2 receptor binding affinity | Pokay | Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant combination (representing B.1.351 aka Beta) showed a 3.56x increase in binding (KD) relative to D614G. | 2021 | Gong et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|--------------------------------|---------------------|---|------------------|--|
| K417N | vaccinee plasma binding | Pokay | This variant combination (representing B.1.351 aka Beta) showed a 1.28x 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. It shows a 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 post-infection vaccinees. | 2021 | Gong et al. (2021) |
| K417N | ACE2 receptor binding affinity | Pokay | Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant showed a 1.5x decrease in binding (KD) relative to D614G. | 2021 | Gong et al. (2021) |
| K417N | convalescent plasma binding | Pokay | 2.16x increase in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset. | 2021 | Gong et al. (2021) |
| K417N | vaccinee plasma binding | Pokay | 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. | 2021 | Gong et al. (2021) |
| N440K | pharmaceutical effectiveness | Pokay | Omicron BA.2 have higher sensitivity to inhibition by soluble angiotensin converting enzyme 2 (ACE2) and the endosomal inhibitor chloroquine compared to D614G | 2022 | Neerukonda et al. (2022) |
| N440K | antibody epitope effects | Pokay | Neutralization of the bsAbs Bi-Nab35B5-47D10. Omicron BA.2 has an IC50 fold change of 0.07x. | 2022 | Yuan et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|--|
| N440K | antibody epitope effects | Pokay | Neutralization of the bsAbs 35B5. Omicron BA.2 has an IC50 fold change of 0.09x. | 2022 | Yuan et al. (2022) |
| N440K | antibody epitope effects | Pokay | Neutralization of the bsAbs 47D10. Omicron BA.2 has an IC50 fold change of 0.08x. | 2022 | Yuan et al. (2022) |
| N440K | antibody epitope effects | Pokay | Neutralization of the bsAbs Bi-Nab47D10-35B5. Omicron BA.2 has an IC50 fold change of 0.04x. | 2022 | Yuan et al. (2022) |
| N440K | vaccine neutralization efficacy | Pokay | Omicron BA.2 neutralization of the Omicron variants by antibodies induced by three doses of Pfizer/BNT162b2 mRNA vaccine was 7-8-fold less potent than the D614G, and the Omicron variants still evade neutralization more efficiently. | 2022 | Neerukonda et al. (2022) |
| N440K | antibody epitope effects | Pokay | BnAb 002-S21F2 IC50 on the Omicron BA.2 variant is 0.8x fold the wildtype. | 2022 | Kumar et al. (2022) |
| N440K | convalescent plasma escape | Pokay | Artificially constructed HIV-1 pseudovirus with set of mutations drawn from plasma passage escape experiments and mutations from variants of concern completely ablates neutralization in 19 of 21 convalescents plasma collected mean 1.3 months post infection. [actual Y145del from manuscript substituted with more common Y144del description] | 2021 | Schmidt et al. (2021) |
| N440K | vaccinee plasma binding | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.2 (from South Africa/CERI-KRISP-K03 2307/2021) were 3.9x-fold lower (95% CI: 0.14x-0.17x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|---------------------------------------|
| N440K | ACE2 receptor binding affinity | Pokay | L27, V34 and E90 mutation resulted in ultrahigh affinity binding of the LVE-ACE-2 domain to the widest variety of VOCs, with KDs of 78fM for binding to the Omicron BA.2. Values were obtained with LVE-ACE-2/mAB chimeras containing the Y-T-E sequence that enhances binding to the FcRn receptor, which in turn is expected to extend biological half-life 3-4-fold. | 2022 | Uhal B et al. (2022) |
| N440K | vaccine neutralization efficacy | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.2 (from South Africa/CERI-KRISP-K03 2307/2021) were 4.5-fold lower (95% CI: 4.3x-4.7x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| N440K | vaccine neutralization efficacy | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.2.12.1 (from USA/NY-CDC-ASC2 10722700/2022) were 4.2-fold lower (95% CI: 5.8x-6.6x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| N440K | vaccinee plasma binding | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.2.12.1 (from USA/NY-CDC-ASC2 10722700/2022) were 3.9x-fold lower (95% CI: 0.14x-0.18x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|--|
| N440K | pharmaceutical effectiveness | Pokay | Omicron (a.k.a. B.1.1.529) Spike pseudotyped VSV and Vero E6 cells has somewhat reduced neutralization (2.7x) vs wild type with monoclonal antibody Sotrovimab (a.k.a. VIR-7831). [delins at 214 omitted for syntax compatibility] | 2021 | Cathcart et al. (2021) |
| N440K | vaccine neutralization efficacy | Pokay | Omicron breakthrough infection after 3-dose vaccination resulted in a further 3.5-fold and 2.9-fold increase of Omicron BA.1 and BA.2 neutralizing titers. Omicron BA.4/5 showed the highest neutralization resistance of all variants tested, resulting in low geometric mean neutralizing titers in plasma samples obtained after the second vaccine dose (NT50) | 2022 | Wang et al. (2022) |
| N440K | antibody epitope effects | Pokay | Neutralization of the bsAbs Bi-Nab47D10-35B5. Omicron BA.1 has an IC50 fold change of 0.08x. | 2022 | Yuan et al. (2022) |
| N440K | vaccine neutralization efficacy | Pokay | Omicron B.1.1.529 (BA.1) neutralization of the Omicron variants by antibodies induced by three doses of Pfizer/BNT162b2 mRNA vaccine was 7-8-fold less potent than the D614G, and the Omicron variants still evade neutralization more efficiently. | 2022 | Neerukonda et al. (2022) |
| N440K | pharmaceutical effectiveness | Pokay | Omicron (B.1.1.529 [BA.1]) have higher sensitivity to inhibition by soluble angiotensin converting enzyme 2 (ACE2) and the endosomal inhibitor chloroquine compared to D614G | 2022 | Neerukonda et al. (2022) |
| N440K | antibody epitope effects | Pokay | Neutralization of the bsAbs Bi-Nab35B5-47D10. Omicron BA.1 has an IC50 fold change of 0.30x. | 2022 | Yuan et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|--------------------------------------|
| N440K | vaccine neutralization efficacy | Pokay | Paradigms' ACE-2 variant LVE/STR chimera binds to SARS-2 Omicron variant B.1.1.529 spike protein trimer with high affinity. Determined using Surrogate Viral Neutralization Tests. | 2022 | Uhal B et al. (2022) |
| N440K | ACE2 receptor binding affinity | Pokay | L27, V34 and E90 mutation resulted in ultrahigh affinity binding of the LVE-ACE-2 domain to the widest variety of VOCs, with KDs of 73 pM for binding to the Omicron B.1.1.529. Values were obtained with LVE-ACE-2/mAB chimeras containing the Y-T-E sequence that enhances binding to the FcRn receptor, which in turn is expected to extend biological half-life 3-4-fold. | 2022 | Uhal B et al. (2022) |
| N440K | antibody epitope effects | Pokay | Neutralization of the bsAbs 35B5. Omicron BA.1 has an IC50 fold change of 0.38x. | 2022 | Yuan et al. (2022) |
| N440K | vaccinee plasma binding | Pokay | All 10 individuals with 2 doses of the BNT162b2/BNT162b2 vaccine had a neutralizing titer in B.1 variant at an average of 729 NT50. | 2022 | Arora et al. (2022) |
| N440K | antibody epitope effects | Pokay | Plaque reduction neutralization test (PRNT) was used uring primary infection, post sixty daysof second dose vaccination, pre-reinfection and reinfection against Delta variant and was used to determine neutralizing antibodytitres. There was a 24.63x fold increase in antibody response from first infection to recovered and vaccinated with 2 doses (60 days). There was a 4.21x fold increase in antibody response pre-reinfection. There was a 39.27x fold increase in antibody response during reinfection. | 2022 | Shete et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|--------------------------|---------------------|--|------------------|-------------------------------------|
| N440K | antibody epitope effects | Pokay | Plaque reduction neutralization test (PRNT) was used uring primary infection, post sixty daysof second dose vaccination, pre-reinfection and reinfection against B.1 variant and was used to determine neutralizing antibodytitres. There was a 6.76x fold increase in antibody response from first infection to recovered and vaccinated with 2 doses (60 days). There was a 2.06x fold increase in antibody response pre-reinfection. There was a 8.18x fold increase in antibody response during reinfection. | 2022 | Shete et al. (2022) |
| N440K | vaccinee plasma binding | Pokay | All 10 individuals with 3 doses of the BNT162b2/BNT162b2 vaccine had a neutralizing titer in B.1 variant at an average of 3319 NT50. | 2022 | Arora et al. (2022) |
| N440K | antibody epitope effects | Pokay | Plaque reduction neutralization test (PRNT) was used uring primary infection, post sixty daysof second dose vaccination, pre-reinfection and reinfection against Omicron variant and was used to determine neutralizing antibodytitres. There was a 114.84x fold increase in antibody response from first infection to recovered and vaccinated with 2 doses (60 days). There was a 6.61x fold increase in antibody response pre-reinfection. There was a 1194.9x fold increase in antibody response during reinfection. | 2022 | Shete et al. (2022) |
| N440K | antibody epitope effects | Pokay | BnAb 002-S21F2 IC50 on the Omicron BA.1 variant is 1.0x fold the wildtype. | 2022 | Kumar et al. (2022) |
| N440K | antibody epitope effects | Pokay | Neutralization of the bsAbs 47D10. Omicron BA.1 has an IC50 fold change of 1.26x. | 2022 | Yuan et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|--|
| N440K | pharmaceutical effectiveness | Pokay | Omicron BA.3 have higher sensitivity to inhibition by soluble angiotensin converting enzyme 2 (ACE2) and the endosomal inhibitor chloroquine compared to D614G | 2022 | Neerukonda et al. (2022) |
| N440K | vaccine neutralization efficacy | Pokay | Omicron BA.3 neutralization of the Omicron variants by antibodies induced by three doses of Pfizer/BNT162b2 mRNA vaccine was 7-8-fold less potent than the D614G, and the Omicron variants still evade neutralization more efficiently. | 2022 | Neerukonda et al. (2022) |
| N440K | vaccinee plasma binding | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.3 (from South Africa/NICD-N22404/2021) were 4.2x-fold lower (95% CI: 0.15x-0.20x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| N440K | vaccine neutralization efficacy | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.3 (from South Africa/NICD-N22404/2021) were 6.2-fold lower (95% CI: 11.8x-14.3x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| N440K | vaccine neutralization efficacy | Pokay | paired testing of vaccine sera against ancestral virus compared to Omicron BA.1 shows that 3-dose vaccine regimen provides over 50x fold increase in protection against Omicron(B.1.1.529 [BA.1]) compared to a 2-dose regimen. | 2022 | Hao et al. (2022) |
| N440K | pharmaceutical effectiveness | Pokay | 4th antigenic exposure with Omicron (B.1.1.529 [BA.1])(n | 2022 | Wang et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|---------------------------------------|
| N440K | vaccine neutralization efficacy | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.1 (from Botswana/R40B59_BHP_3321 001248/2021) were 3.4-fold lower (95% CI: 3.2x-3.6x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurhade et al. (2022) |
| N440K | vaccinee plasma binding | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.1 (from Botswana/R40B59_BHP_3321 001248/2021) were 28.7x-fold lower (95% CI: 0.03x-0.05) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurhade et al. (2022) |
| N440K | vaccinee plasma binding | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.4/5 (from) were 17.2x-fold lower (95% CI: 0.6x-0.7x) than against 208-428 972-1834 4.3-4.7 US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurhade et al. (2022) |
| N440K | vaccine neutralization efficacy | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.4/5 (from) were 13.0-fold lower (95% CI: 4.2x-4.6x) than against 208-428 972-1834 4.3-4.7 US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurhade et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---|---------------------|--|------------------|--|
| N440K | vaccinee plasma binding | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, XD (from) were 1.5x-fold lower (95% CI: 0.05x-0.07x) than against 208-428 972-1834 4.3-4.7 US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| N440K | vaccine neutralization efficacy | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, XD (from) were 4.4-fold lower (95% CI: 4.3x-4.7x) than against 208-428 972-1834 4.3-4.7 US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| N440K | convalescent plasma escape | Pokay | Artificially constructed HIV-1 pseudovirus with set of mutations drawn from plasma passage escape experiments shows ablated neutralization efficacy (NT50 ~ 0) in two of 21 convalescents plasma collected mean 1.3 months post infection. Greater than 4-fold reduction was observed in most of the other plasma. 14 vaccinee plasma showed a slightly lower reduction in efficacy, albeit from a higher average starting point titre than convalescents. | 2021 | Schmidt et al. (2021) |
| N440K | ACE2 receptor binding affinity | Pokay | The hACE2-binding affinity of XBB.1.5 RBD has a dissociation constant KD of 3.4 nM, where S486P is the distinguishing Spike mutation vs parent XBB.1 RBD with a much weaker KD (19 nM), as measured by surface plasmon resonance (SPR) assays. | 2023 | Yue et al. (2023) |
| N440K | monoclonal antibody serial passage escape | Pokay | Positive selection (up to 45% of supernatant sequences) under two rounds of C135 monoclonal antibody passage, eliminated in subsequent passages | 2020 | Weisblum et al. (2020) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---|---------------------|--|------------------|--|
| N440K | transmissibility | Pokay | The N440K variant produced ten times higher infectious viral titers than a prevalent A2a strain, and over 1000 folds higher titers than a much less prevalent A3i strain prototype in Caco2 cells. Interestingly, A3i strain showed the highest viral RNA levels, but the lowest infectious titers in the culture supernatants, indicating the absence of correlation between the RNA content and the infectivity of the sample. | 2021 | Tandel et al. (2021) |
| N440K | pharmaceutical effectiveness | Pokay | This individual mutation found in the epitope from Sotrovimab causes a 0.7x reduction in neutralization efficacy using a VSV model on Vero E6 cells. | 2021 | Cathcart et al. (2021) |
| N440K | monoclonal antibody serial passage escape | Pokay | Class 3 antibody C669 mildly selected for the emergence of the N440K mutation in vitro (in contrast to N440H which caused mild escape in Class 1/2 mAb C653). | 2021 | Wang et al. (2021) |
| N440K | antibody epitope effects | Pokay | Greater than 10-fold reduction of binding efficiency vs wild type for mAb LY-CoV555. Abolishes binding of mAb ADG-1. | 2021 | Rappazzo et al. (2021) |
| N440K | antibody epitope effects | Pokay | Resistant to class 3 antibodies (i.e. Abs that do not directly interfere with ACE2 binding). | 2021 | Wang et al. (2021) |
| N440K | ACE2 receptor binding affinity | Pokay | Experimentally, ACE2 binding affinity increased 0.07 fold | 2020 | Starr et al. (2020) |
| N440K | antibody epitope effects | Pokay | Ablates binding by class 3 mAbs such as C135 that do not directly interfere with ACE2 binding, but clonal somatic mutations of memory B cells at 6.2 months (evolving humoral immune response) show pronounced increase in binding to the variant. | 2021 | Gaebler et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---|---------------------|--|------------------|---------------------------------------|
| N440K | antibody epitope effects | Pokay | N501Y substitution decreased the neutralizing and binding activities of CB6 and increased that of BD-23 | 2021 | Cheng et al. (2021) |
| N440K | reinfection | Pokay | A 47yo Indian male was reinfected with B.1.36 lineage virus in September 2020 after infection with genetically distinct B.1.36 virus in July, with negative PCR tests in between. While the first episode was asymptomatic, the second included fever, cough, and malaise. The second case additionally contained stopgain ORF3a:E261* | 2021 | Rani et al. (2021) |
| N450D | convalescent plasma escape | Pokay | Artificially constructed HIV-1 pseudovirus with set of mutations drawn from plasma passage escape experiments shows ablated neutralization efficacy (NT50 ~ 0) in two of 21 convalescents plasma collected mean 1.3 months post infection. Greater than 4-fold reduction was observed in most of the other plasma. 14 vaccinee plasma showed a slightly lower reduction in efficacy, albeit from a higher average starting point titre than convalescents. | 2021 | Schmidt et al. (2021) |
| N450D | convalescent plasma escape | Pokay | Strong reduction in neutralization capability of all 4 convalescent sera tested (2 ablations). | 2021 | Liu et al. (2021) |
| N450D | convalescent plasma escape | Pokay | Escape mutant found after in passage in plasma pool of 26 convalescents obtained mean 1.3 months post infection. | 2021 | Schmidt et al. (2021) |
| N450D | monoclonal antibody serial passage escape | Pokay | Escape variant 95% appearance in 2 passages against Regeneron monoclonal antibody RGN10934 @ 50ug/mL | 2020 | Baum et al. (2020) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---|---------------------|--|------------------|---|
| N450D | antibody epitope effects | Pokay | Mutant screen in neutralization assay with a broad range of monoclonal antibodies shows resistance to more than one antibody. | 2021 | Liu et al. (2021) |
| N450D | antibody epitope effects | Pokay | Highly resistant to mAb SARS2-07 and moderately resistant to SARS2-16 of 10 antibodies tested. | 2020 | Liu et al. (2020) |
| N450D | convalescent plasma escape | Pokay | No effective neutralization in 2 out of the 4 sera tested. | 2021 | Liu et al. (2021) |
| L452W | monoclonal antibody serial passage escape | Pokay | Ranked effective mutant against this position in the RBD for highly neutralizing COV2-2096 | 2020 | Greaney et al. (2020) |
| N460K | ACE2 receptor binding affinity | Pokay | The hACE2-binding affinity of XBB.1.5 RBD has a dissociation constant KD of 3.4 nM, where S486P is the distinguishing Spike mutation vs parent XBB.1 RBD with a much weaker KD (19 nM), as measured by surface plasmon resonance (SPR) assays. | 2023 | Yue et al. (2023) |
| N460K | ACE2 receptor binding affinity | Pokay | Experimentally, ACE2 binding affinity increased 0.09 fold | 2020 | Starr et al. (2020) |
| N460K | pharmaceutical effectiveness | Pokay | Inhibition of Omicron BA.2 RBD point mutant pseudotypes due to 3 mRNA vaccine doses results in high relative infection for this mutation, for individuals previously infected. | 2022 | Witte et al. (2022) |
| N460K | gene expression increase | Pokay | Experimentally, Spike gene expression increased 0.16 fold | 2020 | Starr et al. (2020) |
| N460K | ACE2 receptor binding affinity | Pokay | Selected with increasing proportion during in vitro evolution of Spike against ACE2 receptor | 2021 | Zahradnik et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---|---------------------|--|------------------|--|
| N460K | pharmaceutical effectiveness | Pokay | Inhibition of Omicron (B.1.1.529 [BA.1]) RBD point mutant pseudotypes under no vaccination results in high relative infection for this mutation, for individuals previously infected. | 2022 | Witte et al. (2022) |
| N460K | pharmaceutical effectiveness | Pokay | Inhibition of Omicron BA.2 RBD point mutant pseudotypes due to 1/2 mRNA vaccines results in high relative infection for this mutation, for individuals previously infected. | 2022 | Witte et al. (2022) |
| N460K | monoclonal antibody serial passage escape | Pokay | Escape mutation against monoclonal antibody LY-CoV016 | 2021 | Starr et al. (2021) |
| F486P | ACE2 receptor binding affinity | Pokay | The hACE2-binding affinity of XBB.1.5 RBD has a dissociation constant KD of 3.4 nM, where S486P is the distinguishing Spike mutation vs parent XBB.1 RBD with a much weaker KD (19 nM), as measured by surface plasmon resonance (SPR) assays. | 2023 | Yue et al. (2023) |
| F486P | gene expression increase | Pokay | Experimentally, Spike gene expression increased 0.22 fold | 2020 | Starr et al. (2020) |
| F486P | monoclonal antibody serial passage escape | Pokay | Ranked modestly effective mutant against this position in the RBD for highly neutralizing COV2-2832 monoclonal antibody | 2020 | Greaney et al. (2020) |
| F486P | monoclonal antibody serial passage escape | Pokay | Escape mutation against monoclonal antibody LY-CoV555 (antibody that forms the basis for Eli Lilly's bamlanivimab) | 2021 | Starr et al. (2021) |
| Q498R | pharmaceutical effectiveness | Pokay | Omicron BA.2 have higher sensitivity to inhibition by soluble angiotensin converting enzyme 2 (ACE2) and the endosomal inhibitor chloroquine compared to D614G | 2022 | Neerukonda et al. (2022) |
| Q498R | antibody epitope effects | Pokay | Neutralization of the bsAbs Bi-Nab35B5-47D10. Omicron BA.2 has an IC50 fold change of 0.07x. | 2022 | Yuan et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|--|
| Q498R | antibody epitope effects | Pokay | Neutralization of the bsAbs 35B5. Omicron BA.2 has an IC50 fold change of 0.09x. | 2022 | Yuan et al. (2022) |
| Q498R | antibody epitope effects | Pokay | Neutralization of the bsAbs 47D10. Omicron BA.2 has an IC50 fold change of 0.08x. | 2022 | Yuan et al. (2022) |
| Q498R | antibody epitope effects | Pokay | Neutralization of the bsAbs Bi-Nab47D10-35B5. Omicron BA.2 has an IC50 fold change of 0.04x. | 2022 | Yuan et al. (2022) |
| Q498R | vaccine neutralization efficacy | Pokay | Omicron BA.2 neutralization of the Omicron variants by antibodies induced by three doses of Pfizer/BNT162b2 mRNA vaccine was 7-8-fold less potent than the D614G, and the Omicron variants still evade neutralization more efficiently. | 2022 | Neerukonda et al. (2022) |
| Q498R | antibody epitope effects | Pokay | BnAb 002-S21F2 IC50 on the Omicron BA.2 variant is 0.8x fold the wildtype. | 2022 | Kumar et al. (2022) |
| Q498R | vaccinee plasma binding | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.2 (from South Africa/CERI-KRISP-K03 2307/2021) were 3.9x-fold lower (95% CI: 0.14x-0.17x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahade et al. (2022) |
| Q498R | ACE2 receptor binding affinity | Pokay | L27, V34 and E90 mutation resulted in ultrahigh affinity binding of the LVE-ACE-2 domain to the widest variety of VOCs, with KDs of 78fM for binding to the Omicron BA.2. Values were obtained with LVE-ACE-2/mAB chimeras containing the Y-T-E sequence that enhances binding to the FcRn receptor, which in turn is expected to extend biological half-life 3-4-fold. | 2022 | Uhal B et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|--|
| Q498R | vaccine neutralization efficacy | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.2 (from South Africa/CERI-KRISP-K03 2307/2021) were 4.5-fold lower (95% CI: 4.3x-4.7x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| Q498R | vaccine neutralization efficacy | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.2.12.1 (from USA/NY-CDC-ASC2 10722700/2022) were 4.2-fold lower (95% CI: 5.8x-6.6x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| Q498R | vaccinee plasma binding | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.2.12.1 (from USA/NY-CDC-ASC2 10722700/2022) were 3.9x-fold lower (95% CI: 0.14x-0.18x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| Q498R | antibody epitope effects | Pokay | Neutralization of the bsAbs Bi-Nab47D10-35B5. Omicron BA.1 has an IC50 fold change of 0.08x. | 2022 | Yuan et al. (2022) |
| Q498R | vaccine neutralization efficacy | Pokay | Omicron B.1.1.529 (BA.1) neutralization of the Omicron variants by antibodies induced by three doses of Pfizer/BNT162b2 mRNA vaccine was 7-8-fold less potent than the D614G, and the Omicron variants still evade neutralization more efficiently. | 2022 | Neerukonda et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|--|
| Q498R | pharmaceutical effectiveness | Pokay | Omicron (B.1.1.529 [BA.1]) have higher sensitivity to inhibition by soluble angiotensin converting enzyme 2 (ACE2) and the endosomal inhibitor chloroquine compared to D614G | 2022 | Neerukonda et al. (2022) |
| Q498R | antibody epitope effects | Pokay | Neutralization of the bsAbs Bi-Nab35B5-47D10. Omicron BA.1 has an IC50 fold change of 0.30x. | 2022 | Yuan et al. (2022) |
| Q498R | vaccine neutralization efficacy | Pokay | Paradigms' ACE-2 variant LVE/STR chimera binds to SARS-2 Omicron variant B.1.1.529 spike protein trimer with high affinity. Determined using Surrogate Viral Neutralization Tests. | 2022 | Uhal B et al. (2022) |
| Q498R | ACE2 receptor binding affinity | Pokay | L27, V34 and E90 mutation resulted in ultrahigh affinity binding of the LVE-ACE-2 domain to the widest variety of VOCs, with KDs of 73 pM for binding to the Omicron B.1.1.529. Values were obtained with LVE-ACE-2/mAB chimeras containing the Y-T-E sequence that enhances binding to the FcRn receptor, which in turn is expected to extend biological half-life 3-4-fold. | 2022 | Uhal B et al. (2022) |
| Q498R | antibody epitope effects | Pokay | Neutralization of the bsAbs 35B5. Omicron BA.1 has an IC50 fold change of 0.38x. | 2022 | Yuan et al. (2022) |
| Q498R | vaccinee plasma binding | Pokay | All 10 individuals with 2 doses of the BNT162b2/BNT162b2 vaccine had a neutralizing titer in B.1 variant at an average of 729 NT50. | 2022 | Arora et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|--------------------------|---------------------|--|------------------|-------------------------------------|
| Q498R | antibody epitope effects | Pokay | Plaque reduction neutralization test (PRNT) was used uring primary infection, post sixty daysof second dose vaccination, pre-reinfection and reinfection against Delta variant and was used to determine neutralizing antibodytitres. There was a 24.63x fold increase in antibody response from first infection to recovered and vaccinated with 2 doses (60 days). There was a 4.21x fold increase in antibody response pre-reinfection. There was a 39.27x fold increase in antibody response during reinfection. | 2022 | Shete et al. (2022) |
| Q498R | antibody epitope effects | Pokay | Plaque reduction neutralization test (PRNT) was used uring primary infection, post sixty daysof second dose vaccination, pre-reinfection and reinfection against B.1 variant and was used to determine neutralizing antibodytitres. There was a 6.76x fold increase in antibody response from first infection to recovered and vaccinated with 2 doses (60 days). There was a 2.06x fold increase in antibody response pre-reinfection. There was a 8.18x fold increase in antibody response during reinfection. | 2022 | Shete et al. (2022) |
| Q498R | vaccinee plasma binding | Pokay | All 10 individuals with 3 doses of the BNT162b2/BNT162b2 vaccine had a neutralizing titer in B.1 variant at an average of 3319 NT50. | 2022 | Arora et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|--|
| Q498R | antibody epitope effects | Pokay | Plaque reduction neutralization test (PRNT) was used using primary infection, post sixty days of second dose vaccination, pre-reinfection and reinfection against Omicron variant and was used to determine neutralizing antibody titres. There was a 114.84x fold increase in antibody response from first infection to recovered and vaccinated with 2 doses (60 days). There was a 6.61x fold increase in antibody response pre-reinfection. There was a 1194.9x fold increase in antibody response during reinfection. | 2022 | Shete et al. (2022) |
| Q498R | antibody epitope effects | Pokay | BnAb 002-S21F2 IC50 on the Omicron BA.1 variant is 1.0x fold the wildtype. | 2022 | Kumar et al. (2022) |
| Q498R | antibody epitope effects | Pokay | Neutralization of the bsAbs 47D10. Omicron BA.1 has an IC50 fold change of 1.26x. | 2022 | Yuan et al. (2022) |
| Q498R | pharmaceutical effectiveness | Pokay | Omicron BA.3 have higher sensitivity to inhibition by soluble angiotensin converting enzyme 2 (ACE2) and the endosomal inhibitor chloroquine compared to D614G | 2022 | Neerukonda et al. (2022) |
| Q498R | vaccine neutralization efficacy | Pokay | Omicron BA.3 neutralization of the Omicron variants by antibodies induced by three doses of Pfizer/BNT162b2 mRNA vaccine was 7-8-fold less potent than the D614G, and the Omicron variants still evade neutralization more efficiently. | 2022 | Neerukonda et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|---------------------------------------|
| Q498R | vaccinee plasma binding | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.3 (from South Africa/NICD-N22404/2021) were 4.2x-fold lower (95% CI: 0.15x-0.20x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| Q498R | vaccine neutralization efficacy | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.3 (from South Africa/NICD-N22404/2021) were 6.2-fold lower (95% CI: 11.8x-14.3x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| Q498R | vaccine neutralization efficacy | Pokay | paired testing of vaccine sera against ancestral virus compared to Omicron BA.1 shows that 3-dose vaccine regimen provides over 50x fold increase in protection against Omicron(B.1.1.529 [BA.1]) compared to a 2-dose regimen. | 2022 | Hao et al. (2022) |
| Q498R | pharmaceutical effectiveness | Pokay | 4th antigenic exposure with Omicron (B.1.1.529 [BA.1])(n | 2022 | Wang et al. (2022) |
| Q498R | vaccine neutralization efficacy | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.1 (from Botswana/R40B59_BHP_3321 001248/2021) were 3.4-fold lower (95% CI: 3.2x-3.6x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|---------------------------------------|
| Q498R | vaccinee plasma binding | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.1 (from Botswana/R40B59_BHP_3321 001248/2021) were 28.7x-fold lower (95% CI: 0.03x-0.05) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| Q498R | vaccinee plasma binding | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.4/5 (from) were 17.2x-fold lower (95% CI: 0.6x-0.7x) than against 208-428 972-1834 4.3-4.7 US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| Q498R | vaccine neutralization efficacy | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.4/5 (from) were 13.0-fold lower (95% CI: 4.2x-4.6x) than against 208-428 972-1834 4.3-4.7 US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| Q498R | vaccinee plasma binding | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, XD (from) were 1.5x-fold lower (95% CI: 0.05x-0.07x) than against 208-428 972-1834 4.3-4.7 US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| Q498R | vaccine neutralization efficacy | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, XD (from) were 4.4-fold lower (95% CI: 4.3x-4.7x) than against 208-428 972-1834 4.3-4.7 US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|--------------------------------|---------------------|---|------------------|---|
| Q498R | ACE2 receptor binding affinity | Pokay | The hACE2-binding affinity of XBB.1.5 RBD has a dissociation constant KD of 3.4 nM, where S486P is the distinguishing Spike mutation vs parent XBB.1 RBD with a much weaker KD (19 nM), as measured by surface plasmon resonance (SPR) assays. | 2023 | Yue et al. (2023) |
| Q498R | ACE2 receptor binding affinity | Pokay | Y501 makes a pi interaction with Y41 and places R498 to make a hydrogen bond and salt bridge to Q42 and D38 of ACE2, forming a strong network of new interactions supporting the impact of these residues on affinity. Q498R alone appears to decrease ACE2 binding. The synergism of Q498R with N501Y (and E484K) increases ACE2 binding by ~50- fold relative to WT. | 2021 | Zahradnik et al. (2021) |
| Q498R | ACE2 receptor binding affinity | Pokay | Y501 makes a pi interaction with Y41 and places R498 to make a hydrogen bond and salt bridge to Q42 and D38 of ACE2, forming a strong network of new interactions supporting the impact of these residues on affinity. Q498R alone appears to decrease ACE2 binding. The synergism of Q498R with N501Y (and E484K) increases ACE2 binding by ~50- fold relative to WT. The extent of affinity increase with Q498R and N501Y is not exactly quantified, as E484K always emerged with this duo during in vitro evolution. | 2021 | Zahradnik et al. (2021) |
| N501Y | vaccinee plasma binding | Pokay | Out of 10 individuals with 3 doses of the BNT162b2/BNT162b2/BNT162b2 vaccine had a neutralizing titer in B.1.640.2 variant was ~5.6x folds more significant in 9 individuals. | 2022 | Arora et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|--|
| N501Y | vaccinee plasma binding | Pokay | Out of 10 individuals with 2 doses of the BNT162b2/BNT162b2 vaccine, neutralizing titer in B.1.640.2 variant was ~1000x folds more significant in 8 individuals. | 2022 | Arora et al. (2022) |
| N501Y | pharmaceutical effectiveness | Pokay | Omicron BA.2 have higher sensitivity to inhibition by soluble angiotensin converting enzyme 2 (ACE2) and the endosomal inhibitor chloroquine compared to D614G | 2022 | Neerukonda et al. (2022) |
| N501Y | antibody epitope effects | Pokay | Neutralization of the bsAbs Bi-Nab35B5-47D10. Omicron BA.2 has an IC50 fold change of 0.07x. | 2022 | Yuan et al. (2022) |
| N501Y | antibody epitope effects | Pokay | Neutralization of the bsAbs 35B5. Omicron BA.2 has an IC50 fold change of 0.09x. | 2022 | Yuan et al. (2022) |
| N501Y | antibody epitope effects | Pokay | Neutralization of the bsAbs 47D10. Omicron BA.2 has an IC50 fold change of 0.08x. | 2022 | Yuan et al. (2022) |
| N501Y | antibody epitope effects | Pokay | Neutralization of the bsAbs Bi-Nab47D10-35B5. Omicron BA.2 has an IC50 fold change of 0.04x. | 2022 | Yuan et al. (2022) |
| N501Y | vaccine neutralization efficacy | Pokay | Omicron BA.2 neutralization of the Omicron variants by antibodies induced by three doses of Pfizer/BNT162b2 mRNA vaccine was 7-8-fold less potent than the D614G, and the Omicron variants still evade neutralization more efficiently. | 2022 | Neerukonda et al. (2022) |
| N501Y | antibody epitope effects | Pokay | BnAb 002-S21F2 IC50 on the Omicron BA.2 variant is 0.8x fold the wildtype. | 2022 | Kumar et al. (2022) |
| N501Y | virion structure | Pokay | CryoEM reveals the P.1 trimer to adopt exclusively a conformation in which one of the receptor-binding domains is in the “up” position. | 2021 | Wang et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|------------------------------------|
| N501Y | vaccine neutralization efficacy | Pokay | In 12 Moderna vaccinee sera 15 days post second dose (43 days since first vaccination), an average 2.8x decrease in reciprocal ID50 value was observed ten key point mutations in Spike in the P.1 lineage vs wildtype. A 4.8x decrease against the full P.1 type vs WA-1 was observed, though overall with a higher ID50 reciprocal value. In 10 Pfizer vaccinee sera 7 days or more post second dose (28 days or more since first vaccination), an average 2.2x decrease in reciprocal ID50 value was observed ten key point mutations in Spike in the P.1 lineage vs wildtype. A 3.8x decrease against the full P.1 type vs WA-1 was observed, with similar variant ID50 reciprocal value. | 2021 | Wang et al. (2021) |
| N501Y | convalescent plasma escape | Pokay | In convalescent sera one month or more post-infection in Spring 2020, an average 6.5x decrease in reciprocal ID50 value was observed ten key point mutations in Spike in the P.1 lineage vs wildtype. A 3.4x decrease against the full P.1 type vs WA-1 was observed, with better full P.1 ID50 reciprocal value compared to the 10-mutation model. | 2021 | Wang et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|--------------------------|---------------------|---|------------------|--|
| N501Y | antibody epitope effects | Pokay | Amongst RBD-targeting Emergency Use Authorized monoclonal antibody treatments CB6, LY-CoV555 and REGN10933 show abrogated neutralization activity against the ten key point mutations in Spike in the P.1 lineage vs wildtype or WA-1, but REGN10987 activity remains strong. RBD-targeting monoclonal antibodies 2-15 and C121 show abrogated neutralization activity against the ten key point mutations in Spike in the P.1 lineage vs wildtype or WA-1. N terminal domain targeting monoclonal antibodies 5-7, 4-8, 4-18 and 2-17 have abrogated neutralization activity against the ten key point mutations in Spike in the P.1 lineage vs wildtype or WA-1. | 2021 | Wang et al. (2021) |
| N501Y | reinfection | Pokay | After a 128 day interval, a patient in Sao Paulo State, Brazil reinfected with P.1 (first episode likely predates P.1 emergence). Both cases were fairly mild (difficulty breathing, tiredness, dizziness and fatigue). | 2021 | Malta Romano et al. (2021) |
| N501Y | vaccine efficacy | Pokay | In a 1:5 test-negative matched control study of 8153 individuals who received the Moderna mRNA-1273 vaccine, 349 test-positive were Gamma. Two dose vaccine efficacy against Gamma was 95.5 (90.9-97.8%), one dose VE was 74.2 (43.8-88.1%). | 2021 | Bruxvoort et al. (2021) |
| N501Y | trafficking | Pokay | ~6x cleavage of S2 relative to WA1 (D614G) wildtype by Gamma variant as measured by mass spectrometry of Vero-TMPRSS culture [no mutations directly at furin cleavage site, but H655Y is upstream] Compare to 4.5x or less for variants of concern with direct furin cleavage site mutations. | 2021 | Esclera et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|---|
| N501Y | reinfection | Pokay | Three healthcare workers (29-50yo) had confirmed P.1 [Gamma] re-infection in the Amazonas region of Brazil 3-9 months after initial infection from viruses with distinct lineage from P.1, but mild symptoms upon re-infection and evidence for infectiousness during re-infection. | 2021 | Naveca et al. (2021) |
| N501Y | vaccine neutralization efficacy | Pokay | Mean 3.0x reduction of NT50 value P.1 (Gamma) relative to wild type in 8 sera from adult BNT162b2 vaccinees (28-47yo) collected ~1m post booster. | 2021 | Uriu et al. (2021) |
| N501Y | convalescent plasma escape | Pokay | Mean 4.1x reduction of NT50 value P.1 (Gamma) relative to wild type in 8 sera from older convalescent patients (52-92yo) collected 1-3m post symptom onset. | 2021 | Uriu et al. (2021) |
| N501Y | antibody epitope effects | Pokay | BnAb 002-S21F2 IC50 on the Gamma (P.1) variant is 0.6x fold the wildtype. | 2022 | Kumar et al. (2022) |
| N501Y | vaccine neutralization efficacy | Pokay | The neutralizing activity of vaccine was slightly lower against B.1.1.248 variant constellation in sera tested from most of the 15 patients with the BNT162b2 mRNA vaccine. (Fig. 4) | 2021 | Chen et al. (2021) |
| N501Y | vaccine neutralization efficacy | Pokay | ELISpot assays show T cell neutralization reduced by 16.6% in this B.1.1.248 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). | 2021 | Gallagher et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|--|
| N501Y | antibody epitope effects | Pokay | B.1.1.248 variant constellation ablates Class 1 receptor-binding-mot if targeting antibodies COV2-2050, 1B07. B.1.1.248 variant constellation ablates Class 3 N-terminal domain targeting antibody COV2-2676. | 2021 | Chen et al. (2021) |
| N501Y | convalescent plasma escape | Pokay | B.1.1.7 variant constellation two-tailed Wilcoxon matched-pairs signed-rank test against 10 convalescent sera P | 2021 | Chen et al. (2021) |
| N501Y | anthropozoonotic events | Pokay | Unlike wild type or B.1.1.7, P.1 lineage virus was able to infect and replicate in common lab mouse strains, with high titer. | 2021 | Montagutelli et al. (2021) |
| N501Y | convalescent plasma escape | Pokay | B.1.1.248 variant constellation in 10 convalescent human sera ~1mo post infection had mild to moderate resistance against most samples, P | 2021 | Chen et al. (2021) |
| N501Y | vaccine neutralization efficacy | Pokay | Neutralizing antibody titers increased in previously infected vaccinees relative to uninfected vaccinees 4.3-fold against P.1 (contrast with 3.4 fold against original SARS-CoV-2). | 2021 | Leier et al. (2021) |
| N501Y | vaccine neutralization efficacy | Pokay | Pseudotyped P.1 virus has reduced neutralization activity vs wild type: 6.7x (30 sera Pfizer median 9 days post 2nd dose) and 4.5x (35 sera Moderna median 18 days post 2nd dose). This was significant by ANOVA. | 2021 | Garcia-Beltran et al. (2021) |
| N501Y | vaccine neutralization efficacy | Pokay | Using P.1 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. | 2021 | Alenquer et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|--|
| N501Y | vaccine neutralization efficacy | Pokay | In human sera 8 weeks post-vaccination with INO-4800, a ~2-fold reduction in P.1 neutralization was observed. | 2021 | Andrade et al. (2021) |
| N501Y | vaccine neutralization efficacy | Pokay | Among 46,884 HCWs in Manaus, Brazil vaccinated with at least one dose of CoronaVac, a 0.50-fold reduction (adjusted vaccine effectiveness, 49.6%: 95% CI, 11.3 - 71.4) in the odds of symptomatic SARS-CoV-2 infection was observed during the period 14 days or more after receiving the first dose. Estimated vaccine effectiveness of at least one dose against any SARS-CoV-2 infection was 35.1% (95% CI, -6.6 - 60.5) in the same time period. | 2021 | Hitchlings et al. (2021) |
| N501Y | pharmaceutical effectiveness | Pokay | VSV pseudotype P.1 entry mediated by the S proteins of the P.1 variant was completely resistant to blocking by REGN10989 and Bamlanivimab. Cell fusion proficiency was slight impaired. Entry driven by the S proteins of the B.1.351 was partially resistant against Casirivimab. | 2021 | Hoffman et al. (2021) |
| N501Y | convalescent plasma binding | Pokay | VSV pseudotype P.1 showed 4.8-fold decrease in NT50 vs wild type in sera from 9 ICU patients undergoing treatment in Germany (pre-variant infections). | 2021 | Hoffman et al. (2021) |
| N501Y | vaccine neutralization efficacy | Pokay | VSV pseudotype P.1 showed 5.12-fold reduction in neutralization efficiency vs wild type in 15 Pfizer BNT162b2 vaccinee sera 13-15 days post second dose. Cell fusion proficiency was slight impaired. | 2021 | Hoffman et al. (2021) |
| N501Y | trafficking | Pokay | VSV pseudotype P.1 showed slight decrease in cell entry relative to wild type in 262T and 263T-ACE2 (kidney) cell lines. Cell fusion proficiency was slight impaired. | 2021 | Hoffman et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|---|
| N501Y | convalescent plasma binding | Pokay | Neutralizing antibodies that were generated following a mild infection with SARS-CoV-2 B.1.128 were effective in vitro, and likely protective, against the SARS-CoV-2 P.1. variant in the majority of individuals based on 60 convalescent sera tested. | 2021 | Mendes-Correa et al. (2021) |
| N501Y | vaccine neutralization efficacy | Pokay | PBMCs of Pfizer/BioNTech BNT162b2 (n | 2021 | Tarke et al. (2021) |
| N501Y | convalescent plasma escape | Pokay | In 13 plasma collected ~1mo after B.1.1.7 infection (nursing home in Ticino, Switzerland), neutralization reduced to undetectable levels in many plasma for P.1 pseudotyped virus, as well as WT and other VOCs. [paper does not detail the P.1 variants used, using the most popular as a stand in] | 2021 | McCallum et al. (2021) |
| N501Y | vaccine neutralization efficacy | Pokay | 1.15x *increase* in neutralization (ID50) in sera 3 weeks after one dose of Pfizer/BioNTech BNT162b2 (up to 5 naive and post infection vaccinees) | 2021 | Gong et al. (2021) |
| N501Y | vaccine neutralization efficacy | Pokay | Neutralization efficiency (ID50) against P.1 reduced 3.2x relative to D614G wildtype using pseudotyped VSV assay on 8 Moderna vaccinee sera one week post-booster. | 2021 | Choi et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|---|
| N501Y | pharmaceutical effectiveness | Pokay | P.1 virus neutralization (as tested using biolayer interferometry) of both Lilly antibodies was severely impacted, with Lilly mAb combination LY-CoV16 and LY-CoV555 (due to mutations at 416 and 484 respectively) shows almost complete loss of neutralization of P.1. There was also escape from neutralization of P.1 by REGN10933 (one of 2 in Regeneron's mAb cocktail) and a modest reduction in neutralization of P.1 by AstraZeneca's AZD8895 (while AZD1061 and AZD7442 showed equal neutralization of all SARS-CoV-2 variants tested). The three Adagio antibodies neutralized P.1 with all reaching a plateau at 100% neutralization: interestingly, ADG30 showed a slight increase of neutralization of P.1. S309 Vir was largely unaffected, although for several viruses, including P.1, the antibody failed to completely neutralize, conceivably reflecting incomplete glycosylation at N343, since the sugar interaction is key to binding of this antibody. | 2021 | Dejnirattisai et al. (2021) |
| N501Y | vaccine neutralization efficacy | Pokay | P.1 lineage titers were reduced 7.6-fold and 9-fold for the BNT162b2 Pfizer (sera collected 4-14 days post-booster) and ChAdOx1 nCoV-19 AstraZeneca (sera collected 14 or 28 days post-booster) vaccines respectively. | 2021 | Dejnirattisai et al. (2021) |
| N501Y | vaccine neutralization efficacy | Pokay | In sera 1-2 weeks after BNT162b2 first dose, from six patients previously infected with B.1, antibody titer in a microneutralization assay was on average 2896 for P.1 virus. This compares favorably (stronger) to post-infection neutralization titer against all variants tested in the same sera (wild type, B.1.1.7, B.1.351, and P.1). | 2021 | Luftig et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|--|
| N501Y | convalescent plasma binding | Pokay | In sera from six patients collected 1 to 12 weeks post-infection with B.1, antibody titer in a microneutralization assay was on average 256 for B.1.1.7 virus. Compare to somewhat stronger neutralization titer for wild type (456.1) in the same sera. | 2021 | Luftig et al. (2021) |
| N501Y | vaccine neutralization efficacy | Pokay | Detectable antibodies against P.1 at various time points using pseudovirus neutralization in Moderna vaccinee cohort: Day 43 100%, Day 209 85%. | 2021 | Pegu et al. (2021) |
| N501Y | T cell evasion | Pokay | PBMCs of 11 mild COVID-19 patients collected 38-80 days after symptom onset were stimulated with the 15-mer peptide pools (w/ 10 residue overlaps) from the whole viral proteome, showing no significant CD4+ cell count effect for P.1, and a slight increase in CD8+ percentage (p | 2021 | Tarke et al. (2021) |
| N501Y | transmissibility | Pokay | The relative transmissibility of P.1 estimated at the national level (Italy) varied according to the assumed degree of cross-protection granted by infection with other lineages and ranged from 1.12 (95%CI 1.03-1.23) in the case of complete immune evasion by P.1 to 1.39 (95%CI 1.26-1.56) in the case of complete cross-protection. PG: variant list has been abbreviated due to mixed K417 bases in this lineage, potential miscalls of deletions | 2021 | Stefanelli et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|---------------------------------------|
| N501Y | convalescent plasma escape | Pokay | Artificially constructed HIV-1 pseudovirus with set of mutations drawn from plasma passage escape experiments and mutations from variants of concern completely ablates neutralization in 19 of 21 convalescents plasma collected mean 1.3 months post infection. [actual Y145del from manuscript substituted with more common Y144del description] | 2021 | Schmidt et al. (2021) |
| N501Y | convalescent plasma escape | Pokay | 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 | 2021 | Cele et al. (2021) |
| N501Y | vaccine neutralization efficacy | Pokay | In human sera 8 weeks post-vaccination with INO-4800, a ~7-fold reduction in B.1.351 neutralization was observed. | 2021 | Andrade et al. (2021) |
| N501Y | vaccine neutralization efficacy | Pokay | Four fold reduction in neutralization efficiency was observed in sera of ferrets post-vaccination with INO-4800 (DNA plasmid pGX9501 encoding full length Spike). | 2021 | Riddell et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|--------------------------------------|
| N501Y | vaccine neutralization efficacy | Pokay | Monovalent mRNA-1273.351 encodes for the S protein found in the B.1.351 lineage and (2) mRNA-1273.211 comprising a 1:1 mix of mRNA-1273 and mRNA-1273.351. In a mouse study, primary vaccination series of mRNA-1273.351 was effective at increasing neutralizing antibody titers against the B.1.351 lineage, while mRNA-1273.211 was most effective at providing broad cross-variant neutralization. In addition, these results demonstrated a third dose of mRNA-1273.351 significantly increased both wild-type and B.1.351-specific neutralization titers. | 2021 | Wu et al. (2021) |
| N501Y | vaccine neutralization efficacy | Pokay | Pzifer vaccinees that tested positive at least a week after the second dose were indeed disproportionately infected with B.1.351, as compared with unvaccinated individuals (odds ratio of 8:1), but were all infected before 14 days post second vaccination. | 2021 | Kustin et al. (2021) |
| N501Y | convalescent plasma escape | Pokay | Mean 8.2x reduction of NT50 value B.1.351 (Beta) relative to wild type in 8 sera from older convalescent patients (52-92yo) collected 1-3m post symptom onset. | 2021 | Uriu et al. (2021) |
| N501Y | vaccine neutralization efficacy | Pokay | Mean 6.3x reduction of NT50 value B.1.351 (Beta) relative to wild type in 8 sera from adult BNT162b2 vaccinees (28-47yo) collected ~1m post booster. | 2021 | Uriu et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|---------------------------------------|
| N501Y | convalescent plasma escape | Pokay | 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. | 2021 | Skelly et al. (2021) |
| N501Y | convalescent plasma binding | Pokay | In sera from six patients collected 1 to 12 weeks post-infection with B.1, antibody titer in a microneutralization assay was on average 8 for B.1.351 virus. Compare to much stronger neutralization titers for B.1.1.7 (256) and wild type (456.1) in the same sera. | 2021 | Luftig et al. (2021) |
| N501Y | vaccine neutralization efficacy | Pokay | 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 potentially neutralizing WA1 while having FRNT50 for B.1.351 below the assay limit of detection (1:20). | 2021 | Bates et al. (2021) |
| N501Y | convalescent plasma binding | Pokay | Sera from individuals who have been infected with Delta does not have strong neutralising activity against Beta. | 2021 | UNKNOWN et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|--|
| N501Y | convalescent plasma escape | Pokay | 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 ~6x reduction in neutralizing titers, and 40% of the samples lacked any activity against B.1.351. | 2021 | Planas et al. (2021) |
| N501Y | vaccinee plasma binding | Pokay | Sera from individuals who have been vaccinated and have had subsequent recent Delta infection have a high level of neutralising activity against Beta. | 2021 | UNKNOWN et al. (2021) |
| N501Y | vaccine neutralization efficacy | Pokay | Paradigm's ACE-2 variant LVE/STR chimera neutralizes Beta Variant B.1.351 RBD significantly better than w.t. SARS-CoV-2 RBD. Determined using Surrogate Viral Neutralization Tests. | 2022 | Uhal B et al. (2022) |
| N501Y | vaccine neutralization efficacy | Pokay | 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. | 2021 | Garcia-Beltran et al. (2021) |
| N501Y | ACE2 receptor binding affinity | Pokay | Pseudotype lentivirus for the full B.1.351 Spike variant list shows increase affinity for ACE2 as measured by IC50. This is in contrast to B.1.1.7 which showed no major change, indicating that the shared N501Y mutation is the driver of affinity change, attenuated in the B.1.1.7 mutatioon set, but maintained in the B.1.351 lineage. | 2021 | Tada et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|--------------------------------------|
| N501Y | vaccine neutralization efficacy | Pokay | [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.] | 2021 | Voysey et al. (2021) |
| N501Y | ACE2 receptor binding affinity | Pokay | 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 greater extent to B.1.1.7, which both carry the N501Y mutation (see Fig 3). | 2021 | Planas et al. (2021) |
| N501Y | vaccine neutralization efficacy | Pokay | PBMCs of Pfizer/BioNTech BNT162b2 (n | 2021 | Tarke et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|--|
| N501Y | vaccine neutralization efficacy | Pokay | Relative to B.1.1.117, PRNT50 line virus neutralizing antibody activity assay of B.1.351 showed ~11x reduction in 13 vaccinees's sera collected through 41 days after vaccination. Neutralization by a placebo control group of 6 naturally infected patients showed a smaller ~8x drop (starting from a ~50% higher PRNT50 value than vaccinees 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 ~4x 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). | 2021 | Madhi et al. (2021) |
| N501Y | vaccine neutralization efficacy | Pokay | Log10ID50 of Beta neutralizing antibodies is 0.899x the WT 1 month post-third dose of pfizer-BioNTech BNT162b2 in 13 Kidney transplant recipients (KTR) with median age of 55.5. | 2022 | McEvoy C et al. (2022) |
| N501Y | convalescent plasma escape | Pokay | A 1.8-fold drop in FRNT50 for B.1.351 was observed in 44 sera collected between 1 and 301 post-infection. | 2021 | Bates et al. (2021) |
| N501Y | vaccine neutralization efficacy | Pokay | 3.2x reduction in neutralization (ID50) in sera 3 weeks after one dose of Pfizer/BioNTech BNT162b2 (up to 5 naive and post infection vaccinees) | 2021 | Gong et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|--|
| N501Y | vaccine neutralization efficacy | Pokay | Neutralization efficiency (ID50) against B.1.1.351-v1 reduced 6.9x relative to D614G wildtype using pseudotyped VSV assay on 8 Moderna vaccinee sera one week post-booster. | 2021 | Choi et al. (2021) |
| N501Y | T cell evasion | Pokay | 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. | 2021 | Skelly et al. (2021) |
| N501Y | convalescent plasma escape | Pokay | The neutralizing activity of 16/20 convalescent sera was significantly lower against this pseudotyped virus model of B.1.351, with similar results for the live virus. | 2021 | Wang et al. (2021) |
| N501Y | vaccine neutralization efficacy | Pokay | Log10ID50 of Beta neutralizing antibodies is 0.803x the WT pre-third dose of pfizer-BioNTech BNT162b2 in 13 Kidney transplant recipients (KTR) with median age of 55.5. | 2022 | McEvoy C et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|------------------------------------|
| N501Y | antibody epitope effects | Pokay | B.1.351 pseudotyped virus model ablates neutralization by RBD-directed mAbs CB6, 4-20, 2-4, 2-43, 910-30, 2-302-15, LY-Cov555, C121. B.1.351 pseudotyped virus model severely impairs neutralization by RBD-directed mAb 1-20. B.1.351 pseudotyped virus model impairs neutralization by RBD-directed mAb REGN10933. B.1.351 pseudotyped virus model ablates neutralization by N-terminal-domain-directed mAbs 5-24, 4-8, 4A8, 4-19. B.1.351 pseudotyped virus model severely impairs neutralization by N-terminal-domain-directed mAb 2-17. B.1.351 pseudotyped virus model impairs neutralization by N-terminal-domain-directed mAb 5-7. PG: Live virus data for the same mAbs is similar, but 1-20 becomes severally impaired, REGN10933 activity is ablated, and Brii-196 becomes impaired. | 2021 | Wang et al. (2021) |
| N501Y | vaccine neutralization efficacy | Pokay | The neutralizing activity of vaccine was significantly lower against B.1.351 (12.4x in twelve Moderna-recipient sera: 10.3x in ten Pfizer-recipient sera). [this is a larger list of B.1.351 than modeled by Wang et al. (2021) by including L18F and R246I, less effective at neutralizing] | 2021 | Wang et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|---|
| N501Y | vaccine neutralization efficacy | Pokay | 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 (~10x vs D614G) through week 6, the last timepoint measured. Three vaccinees never showed detectable neutralization to B.1.351 even after second dose. | 2021 | Planas et al. (2021) |
| N501Y | pharmaceutical effectiveness | Pokay | DARPin SR16m molecule had a 0.036x fold change in IC50 in B.1.351 Beta | 2022 | Chonira et al. (2022) |
| N501Y | tissue specific neutralization | Pokay | 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 vaccinee neutralizing at weeks 3 and 6, B.1.351 showed zero neutralization at either time point in any sample (and relatively impaired serum neutralization). | 2021 | Planas et al. (2021) |
| N501Y | vaccine neutralization efficacy | Pokay | 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. | 2021 | Choi et al. (2021) |
| N501Y | vaccine neutralization efficacy | Pokay | 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. | 2021 | Woldemeskel et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|---------------------------------------|
| N501Y | vaccine neutralization efficacy | Pokay | 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 relative decrease was 6.1x vs wild type). | 2021 | Ikegame et al. (2021) |
| N501Y | pharmaceutical effectiveness | Pokay | Trimeric proteins FSR22 had a 0.07x fold change in IC50 in B.1.351 Beta | 2022 | Chonira et al. (2022) |
| N501Y | vaccine neutralization efficacy | Pokay | 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. | 2021 | Shinde et al. (2021) |
| N501Y | pharmaceutical effectiveness | Pokay | DARPin SR22 molecule had a 1.57x fold change in IC50 in B.1.351 Beta | 2022 | Chonira et al. (2022) |
| N501Y | pharmaceutical effectiveness | Pokay | Trimeric proteins FSR16m had a 0.054x fold change in IC50 in B.1.351 Beta | 2022 | Chonira et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|------------------------------|---------------------|---|------------------|---|
| N501Y | pharmaceutical effectiveness | Pokay | B.1.351 virus neutralization (as tested using biolayer interferometry) of both Lilly antibodies was severely impacted, with LY-CoV16 and LY-CoV555 (due to mutations at 416 and 484 respectively) shows almost complete loss of neutralization of B.1.351. There was also escape from neutralization of B.1.351 by REGN10933 and a modest reduction in neutralization of B.1.351 by AZD8895 (while AZD1061 and AZD7442 showed equal neutralization of all SARS-CoV-2 variants tested). The three Adagio antibodies neutralized B.1.351. | 2021 | Dejnirattisai et al. (2021) |
| N501Y | pharmaceutical effectiveness | Pokay | DARPin SR16m molecule had a 6.7x fold change in IC50 in B.1.617.2 Delta | 2022 | Chonira et al. (2022) |
| N501Y | pharmaceutical effectiveness | Pokay | DARPin SR16m molecule had a 99.7x fold change in IC50 in B.1.617.2 Delta | 2022 | Chonira et al. (2022) |
| N501Y | trafficking | Pokay | Lentiviral pseudotyped with all key mutations from B.1.351 lineage was tested on ACE2.293T cells. Luciferase activity was measured two days postinfection, showing modest decrease in infection rate amongst the cells, suggesting some synergy between the mutations to decrease cell entry fitness (i.e. cell entry is likely not the driver of this lineage's dominance). | 2021 | Tada et al. (2021) |
| N501Y | convalescent plasma escape | Pokay | The most significant loss of neutralizing activity (PsVNA50 assay) using 6 hyperimmune immunoglobulin preparations from convalescent plasma was seen against authentic B.1.351 lineage virus (9.2-fold). Neutralization against 10 convalescent plasma was poorer (18.7x). | 2021 | Tang et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|-----------------------------------|---------------------|---|------------------|--|
| N501Y | environmental condition stability | Pokay | Treatment with heat, soap and ethanol revealed similar inactivation profiles indicative of a comparable susceptibility towards disinfection. Furthermore, we observed comparable surface stability on steel, silver, copper and face masks. | 2021 | Meister et al. (2021) |
| N501Y | environmental condition stability | Pokay | Relative to D614G, this mutation set (B.1.351+) demonstrated significant increase in infectivity (i.e. heat stability) after incubation at 50C after 1 hour. | 2021 | Tada et al. (2021) |
| N501Y | outcome hazard ratio | Pokay | In the Parana state of Brazil, patients aged 20-29 years experienced a tripling of their case fatality rate (CFR), from 0.04% to 0.13%, while those aged 30-39, 40-49, 50-59 experienced approximate CFR doubling comparing February to January in 2021. Notably, the observed CFR increase coincided with the second consecutive month of declining number of diagnosed SARS-CoV-2 cases. Taken together, these preliminary findings suggest significant increases in CFR in young and middle-aged adults after identification of a novel SARS-CoV-2 strain circulating in Brazil. [this is somewhat indirect evidence that assume greatly increasing proportion of P.1 cases in March (70%) compared to February, but the first official ID of P.1 in Parana state (Feb 16th) may be due to testing procedures rather than actual prevalence] | 2021 | Santos de Oliveira et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|---|
| N501Y | outcome hazard ratio | Pokay | In the Southern Brazilian stats of Rio Grande do Sul, comparing pre-P.1 and post-P.1 waves: The increase in Case Fatality Rate occurred in a greatest intensity in the population between 20 and 59 years old and among patients without pre-existing risk conditions. Female 20 to 39 years old, with no pre-existing risk conditions, were at risk of death 5.65 times higher in February (95%CI | 2021 | Ribas Freitas et al. (2021) |
| N501Y | outcome hazard ratio | Pokay | On average across 7 European countries studied, using P.1 defining mutations: Significant shift to infection in those without pre-existing conditions (27.8% vs 89% for non-VOC cases). Significant increase in hospitalization rate (20% vs 7.5% for non-VOC cases). Significant increase in ICU rate (2.1% vs 0.6% for non-VOC cases). Significant increase in health care worker rate (19.8% vs 8.0% for non-VOC cases). | 2021 | Funk et al. (2021) |
| N501Y | vaccine neutralization efficacy | Pokay | This variant was designated A.27.RN according to its phylogenetic clade classification. It emerged in parallel with the B.1.1.7 variant, increased to >50% of all SARS-CoV-2 variants by week five. Subsequently it decreased to <10% of all variants by calendar week eight when B.1.1.7 had become the dominant strain. Antibodies induced by BNT162b2 (Pfizer) vaccination neutralized A.27.RN but with a two-to-threefold reduced efficacy as compared to the wild-type and B.1.1.7 strains. | 2021 | Mallm et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|---------------------------------------|
| N501Y | vaccinee plasma binding | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.2 (from South Africa/CERI-KRISP-K03 2307/2021) were 3.9x-fold lower (95% CI: 0.14x-0.17x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| N501Y | ACE2 receptor binding affinity | Pokay | L27, V34 and E90 mutation resulted in ultrahigh affinity binding of the LVE-ACE-2 domain to the widest variety of VOCs, with KDs of 78fM for binding to the Omicron BA.2. Values were obtained with LVE-ACE-2/mAB chimeras containing the Y-T-E sequence that enhances binding to the FcRn receptor, which in turn is expected to extend biological half-life 3-4-fold. | 2022 | Uhal B et al. (2022) |
| N501Y | vaccine neutralization efficacy | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.2 (from South Africa/CERI-KRISP-K03 2307/2021) were 4.5-fold lower (95% CI: 4.3x-4.7x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| N501Y | vaccine neutralization efficacy | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.2.12.1 (from USA/NY-CDC-ASC2 10722700/2022) were 4.2-fold lower (95% CI: 5.8x-6.6x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|--|
| N501Y | vaccinee plasma binding | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.2.12.1 (from USA/NY-CDC-ASC2 10722700/2022) were 3.9x-fold lower (95% CI: 0.14x-0.18x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| N501Y | pharmaceutical effectiveness | Pokay | Omicron (a.k.a. B.1.1.529) Spike pseudotyped VSV and Vero E6 cells has somewhat reduced neutralization (2.7x) vs wild type with monoclonal antibody Sotrovimab (a.k.a. VIR-7831). [delins at 214 omitted for syntax compatibility] | 2021 | Cathcart et al. (2021) |
| N501Y | vaccine neutralization efficacy | Pokay | Omicron breakthrough infection after 3-dose vaccination resulted in a further 3.5-fold and 2.9-fold increase of Omicron BA.1 and BA.2 neutralizing titers. Omicron BA.4/5 showed the highest neutralization resistance of all variants tested, resulting in low geometric mean neutralizing titers in plasma samples obtained after the second vaccine dose (NT50) | 2022 | Wang et al. (2022) |
| N501Y | antibody epitope effects | Pokay | Neutralization of the bsAbs Bi-Nab47D10-35B5. Omicron BA.1 has an IC50 fold change of 0.08x. | 2022 | Yuan et al. (2022) |
| N501Y | vaccine neutralization efficacy | Pokay | Omicron B.1.1.529 (BA.1) neutralization of the Omicron variants by antibodies induced by three doses of Pfizer/BNT162b2 mRNA vaccine was 7-8-fold less potent than the D614G, and the Omicron variants still evade neutralization more efficiently. | 2022 | Neerukonda et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|--|
| N501Y | pharmaceutical effectiveness | Pokay | Omicron (B.1.1.529 [BA.1]) have higher sensitivity to inhibition by soluble angiotensin converting enzyme 2 (ACE2) and the endosomal inhibitor chloroquine compared to D614G | 2022 | Neerukonda et al. (2022) |
| N501Y | antibody epitope effects | Pokay | Neutralization of the bsAbs Bi-Nab35B5-47D10. Omicron BA.1 has an IC50 fold change of 0.30x. | 2022 | Yuan et al. (2022) |
| N501Y | vaccine neutralization efficacy | Pokay | Paradigms' ACE-2 variant LVE/STR chimera binds to SARS-2 Omicron variant B.1.1.529 spike protein trimer with high affinity. Determined using Surrogate Viral Neutralization Tests. | 2022 | Uhal B et al. (2022) |
| N501Y | ACE2 receptor binding affinity | Pokay | L27, V34 and E90 mutation resulted in ultrahigh affinity binding of the LVE-ACE-2 domain to the widest variety of VOCs, with KDs of 73 pM for binding to the Omicron B.1.1.529. Values were obtained with LVE-ACE-2/mAB chimeras containing the Y-T-E sequence that enhances binding to the FcRn receptor, which in turn is expected to extend biological half-life 3-4-fold. | 2022 | Uhal B et al. (2022) |
| N501Y | antibody epitope effects | Pokay | Neutralization of the bsAbs 35B5. Omicron BA.1 has an IC50 fold change of 0.38x. | 2022 | Yuan et al. (2022) |
| N501Y | vaccinee plasma binding | Pokay | All 10 individuals with 2 doses of the BNT162b2/BNT162b2 vaccine had a neutralizing titer in B.1 variant at an average of 729 NT50. | 2022 | Arora et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|--------------------------|---------------------|--|------------------|-------------------------------------|
| N501Y | antibody epitope effects | Pokay | Plaque reduction neutralization test (PRNT) was used uring primary infection, post sixty daysof second dose vaccination, pre-reinfection and reinfection against Delta variant and was used to determine neutralizing antibodytitres. There was a 24.63x fold increase in antibody response from first infection to recovered and vaccinated with 2 doses (60 days). There was a 4.21x fold increase in antibody response pre-reinfection. There was a 39.27x fold increase in antibody response during reinfection. | 2022 | Shete et al. (2022) |
| N501Y | antibody epitope effects | Pokay | Plaque reduction neutralization test (PRNT) was used uring primary infection, post sixty daysof second dose vaccination, pre-reinfection and reinfection against B.1 variant and was used to determine neutralizing antibodytitres. There was a 6.76x fold increase in antibody response from first infection to recovered and vaccinated with 2 doses (60 days). There was a 2.06x fold increase in antibody response pre-reinfection. There was a 8.18x fold increase in antibody response during reinfection. | 2022 | Shete et al. (2022) |
| N501Y | vaccinee plasma binding | Pokay | All 10 individuals with 3 doses of the BNT162b2/BNT162b2 vaccine had a neutralizing titer in B.1 variant at an average of 3319 NT50. | 2022 | Arora et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|--|
| N501Y | antibody epitope effects | Pokay | Plaque reduction neutralization test (PRNT) was used using primary infection, post sixty days of second dose vaccination, pre-reinfection and reinfection against Omicron variant and was used to determine neutralizing antibody titres. There was a 114.84x fold increase in antibody response from first infection to recovered and vaccinated with 2 doses (60 days). There was a 6.61x fold increase in antibody response pre-reinfection. There was a 1194.9x fold increase in antibody response during reinfection. | 2022 | Shete et al. (2022) |
| N501Y | antibody epitope effects | Pokay | BnAb 002-S21F2 IC50 on the Omicron BA.1 variant is 1.0x fold the wildtype. | 2022 | Kumar et al. (2022) |
| N501Y | antibody epitope effects | Pokay | Neutralization of the bsAbs 47D10. Omicron BA.1 has an IC50 fold change of 1.26x. | 2022 | Yuan et al. (2022) |
| N501Y | pharmaceutical effectiveness | Pokay | Omicron BA.3 have higher sensitivity to inhibition by soluble angiotensin converting enzyme 2 (ACE2) and the endosomal inhibitor chloroquine compared to D614G | 2022 | Neerukonda et al. (2022) |
| N501Y | vaccine neutralization efficacy | Pokay | Omicron BA.3 neutralization of the Omicron variants by antibodies induced by three doses of Pfizer/BNT162b2 mRNA vaccine was 7-8-fold less potent than the D614G, and the Omicron variants still evade neutralization more efficiently. | 2022 | Neerukonda et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|---------------------------------------|
| N501Y | vaccinee plasma binding | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.3 (from South Africa/NICD-N22404/2021) were 4.2x-fold lower (95% CI: 0.15x-0.20x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| N501Y | vaccine neutralization efficacy | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.3 (from South Africa/NICD-N22404/2021) were 6.2-fold lower (95% CI: 11.8x-14.3x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| N501Y | vaccine neutralization efficacy | Pokay | paired testing of vaccine sera against ancestral virus compared to Omicron BA.1 shows that 3-dose vaccine regimen provides over 50x fold increase in protection against Omicron(B.1.1.529 [BA.1]) compared to a 2-dose regimen. | 2022 | Hao et al. (2022) |
| N501Y | pharmaceutical effectiveness | Pokay | 4th antigenic exposure with Omicron (B.1.1.529 [BA.1])(n | 2022 | Wang et al. (2022) |
| N501Y | vaccine neutralization efficacy | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.1 (from Botswana/R40B59_BHP_3321 001248/2021) were 3.4-fold lower (95% CI: 3.2x-3.6x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|---------------------------------------|
| N501Y | vaccinee plasma binding | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.1 (from Botswana/R40B59_BHP_3321 001248/2021) were 28.7x-fold lower (95% CI: 0.03x-0.05) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| N501Y | vaccine neutralization efficacy | Pokay | The neutralizing activity of vaccine was somewhat lower against B.1.1.7 in sera tested from most of the 24 patients with the BNT162b2 mRNA vaccine. (Fig. 4) | 2021 | Chen et al. (2021) |
| N501Y | antibody epitope effects | Pokay | B.1.1.7 variant constellation ablates Class 3 N-terminal domain targeting antibody COV2-2489. | 2021 | Chen et al. (2021) |
| N501Y | vaccine neutralization efficacy | Pokay | Observed 8.8-fold reduction in neutralization efficiency of Pfizer vaccinee sera (collected 14 days after second dose) against cultured B.1.1.7 sample. Contrast this with 1.3-fold reduction for just the pseudovirus combination of 'key' B.1.1.7 mutation N501Y. | 2021 | Bates et al. (2021) |
| N501Y | vaccine neutralization efficacy | Pokay | Neutralization efficiency (ID50) against B.1.1.7+E484K reduced 2.8x relative to D614G wildtype using pseudotyped VSV assay on 8 Moderna vaccinee sera one week post-booster. Compare with 1.2x reduction for B.1.1.7 without E484K. | 2021 | Choi et al. (2021) |
| N501Y | vaccine neutralization efficacy | Pokay | Sera after the second dose of Pfizer showed an average reduction in neutralization titres against the B.1.1.7 + E484K variant of ~6.7x, markedly higher than B.1.1.7 alone. For first dose sera, a 9.7x drop was observed. | 2021 | Collier et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|--------------------------------|---------------------|--|------------------|--|
| N501Y | convalescent plasma escape | Pokay | Neutralization capacity GMT of 27 subjects' sera post-infection was markedly worse against B.1.1.7 + E484K than the lineage alone, with a 11.4x drop. | 2021 | Collier et al. (2021) |
| N501Y | antibody epitope effects | Pokay | Ablates Class 3 N-terminal domain targeting antibody COV2-2489, diminishes COV2-2676. | 2021 | Chen et al. (2021) |
| N501Y | trafficking | Pokay | Lentiviral pseudotyped with this mutation set from B.1.1.7 was tested on ACE2.293T cells. Luciferase activity was measured two days postinfection, showing significant (40%) increase in infection rate amongst the cells, much more than the effect of either the deletion or the point mutation alone, suggesting that this combination has a synergistic effect contributing to cell entry fitness, more so than this combination with the addition of P681H. | 2021 | Tada et al. (2021) |
| N501Y | symptom prevalence | Pokay | In comparison of B.1.1.7 lineage (193 cases) vs. 'wildtype' (125) in Berlin Jan 18 to March 29 2021, significant symptom changes are absent loss of smell/taste (P | 2021 | van Loon et al. (2021) |
| N501Y | ACE2 receptor binding affinity | Pokay | This mutation combination causes major increase in binding affinity vs. wild type as measured by IC50 vs pseudotyped lentivirus, but combined with the complete set of B.1.1.7 lineage variants no major change vs wild type affinity is observed. | 2021 | Tada et al. (2021) |
| N501Y | antibody epitope effects | Pokay | Reduction in neutralization by mAbs COVA1-18 (~4x), COVA2-15 (~9x). PG: these effects are largely missing in the deletion-alone data | 2021 | Shen et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|--|
| N501Y | symptom prevalence | Pokay | A higher proportion of cases infected with the B.1.1.7 variant were hypoxic on admission compared to other variants (70.0% vs 62.5%, p | 2021 | Snell et al. (2021) |
| N501Y | virion structure | Pokay | The Ratio of S2 (processed Spike) to full length Spike is higher for this mutation combination, due to a drop in the full length Spike measured, suggesting that this mutation compensates for decreased Spike production by improved proteolytic processing. | 2021 | Tada et al. (2021) |
| N501Y | vaccine neutralization efficacy | Pokay | After one dose, individuals with prior infection showed enhanced T cell immunity, antibody secreting memory B cell response to spike and neutralizing antibodies effective against B.1.1.7 (authentic cell culture supernatants). By comparison, HCW receiving one vaccine dose without prior infection showed reduced immunity against variants. B.1.1.7 spike mutations resulted in increased, abrogated or unchanged T cell responses depending on human leukocyte antigen (HLA) polymorphisms. Study was 26 each post-infection and post first dose HCWs. | 2021 | Reynolds et al. (2021) |
| N501Y | convalescent plasma escape | Pokay | Mean 2.6x reduction of NT50 value B.1.1.7 (Alpha) relative to wild type in 8 sera from older convalescent patients (52-92yo) collected 1-3m post symptom onset. | 2021 | Uriu et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|------------------------------------|
| N501Y | vaccine neutralization efficacy | Pokay | Detectable antibodies against B.1.1.7 at various time points using pseudotyped lentivirus neutralization in Moderna vaccinee cohort: Day 29 33%, Day 43 100%, Day 119 100%, Day 209 96%. Detectable antibodies against B.1.1.7 at various time points using live virus FRNT neutralization in Moderna vaccinee cohort: Day 29 54%, Day 43 100%, Day 119 100%, Day 209 88%. Detectable antibodies against B.1.1.7 at various time points using ACE2 blocking assay in Moderna vaccinee cohort: Day 29 83%, Days 43,119,209 100%. | 2021 | Pegu et al. (2021) |
| N501Y | vaccine neutralization efficacy | Pokay | Using national surveillance data from Israel, using Pfizer vaccine and an estimated prevalence of the B.1.1.7 variant of 94.5% among SARS-CoV-2 infections: Adjusted estimates of vaccine effectiveness 7+ days after second dose were 95.3% (95% CI 94.9–95.7): 91.5% against asymptomatic SARS-CoV-2 infection (90.7–92.2: 40.9 vs 1.8 per 100 000 person-days), 97.0% against symptomatic COVID-19 (96.7–97.2%), 97.2% against COVID-19-related hospitalisation (96.8–97.5%), 97.5% against severe or critical COVID-19-related hospitalisation (97.1–97.8%), and 96.7% against COVID-19-related death (96.0–97.3%). In all age groups, as vaccine coverage increased, the incidence of SARS-CoV-2 outcomes declined | 2021 | Haas et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|---|
| N501Y | vaccine neutralization efficacy | Pokay | In sera 1-2 weeks after BNT162b2 first dose, from six patients previously infected with B.1, antibody titer in a microneutralization assay was on average 8192 for B.1.351 virus. This compares favorably (stronger) to post-infection neutralization titer against all variants tested in the same sera (wild type, B.1.1.7, B.1.351, and P.1). | 2021 | Luftig et al. (2021) |
| N501Y | virion structure | Pokay | CryoEM analysis of B.1.1.7 demonstrates an increased propensity for 'up', receptor accessible conformation of the Spike protein trimer. | 2021 | Cai et al. (2021) |
| N501Y | vaccine neutralization efficacy | Pokay | SARS-CoV-2 infection was confirmed in three HCWs working a single shift: all presented with mild symptoms of COVID-19. The two physicians were fully vaccinated with BNT162b2 vaccine, with the second dose administered 1 month before symptom onset. Both had high titres of IgG anti-spike antibodies at the time of diagnosis. WGS confirmed that all virus strains were VOC 202012/01-lineage B.1.1.7, suggesting a common source of exposure. Epidemiological investigation revealed that the suspected source was a SARS-CoV-2-positive patient who required endotracheal intubation due to severe COVID-19. All procedures were carried out using a full suite of personal protective equipment (PPE). | 2021 | Loconsole et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|----------------------------|---------------------|---|------------------|---|
| N501Y | vaccine efficacy | Pokay | In a 1:5 test-negative matched control study of 8153 individuals who received the Moderna mRNA-1273 vaccine, 1422 test-positive were Alpha. Two dose vaccine efficacy against Alpha was 98.4% [96.9-99.1%], one dose VE was 90.1% (82.9-94.2%). | 2021 | Bruxvoort et al. (2021) |
| N501Y | convalescent plasma escape | Pokay | Using a new rapid neutralization assay, based on reporter cells that become positive for GFP after overnight infection, sera from 58 convalescent individuals collected up to 9 months after symptoms, similarly neutralized B.1.1.7 and D614G. | 2021 | Planas et al. (2021) |
| N501Y | antibody epitope effects | Pokay | Neutralization of the bsAbs Bi-Nab35B5-47D10. Alpha (B.1.1.7) has an IC50 fold change of 1.19x. | 2022 | Yuan et al. (2022) |
| N501Y | antibody epitope effects | Pokay | B.1.1.7 pseudotyped virus model impairs binding by RBD-directed mAb 910-30. B.1.1.7 pseudotyped virus model abolishes N-terminal-domain-directed mAbs 5-24, 4-8, and 4A8. B.1.1.7 pseudotyped virus model impairs binding by N-terminal-domain-directed mAbs 2-17, 4-19, 5-7. | 2021 | Wang et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|--|
| N501Y | vaccine neutralization efficacy | Pokay | 1.4x improvement in neutralization by serum collected 2 to 3 weeks after the second dose from vaccinees who had received BBIBP-CorV (pVNT50 against VSV pseudotyped as B.1.1.7). Convalescent plasma had similar titer against wild type as the BBIBP-CorV vaccinee sera. 2x reduction in neutralization by serum collected 2 to 3 weeks after the second dose from vaccinees who had received CoronaVac (pVNT50 against VSV pseudotyped as B.1.1.7). Convalescent plasma had similar titer against wild type as the CoronaVac vaccinee sera. | 2021 | Wang et al. (2021) |
| N501Y | aerosolization | Pokay | Alpha variant cases in a large campus study showed fine-aerosol shedding amongst unmasked participants remained significantly greater for alpha variant infections (18-fold, 95% CI, 3.4 to 92-fold) after adjusting for the increased viral RNA in MTS and saliva, the number of coughs during sampling sessions, and symptom. After controlling for the effect of masks and numbers of coughs during sampling, alpha variant infection was associated with a 100-fold (95% CI, 16 to 650-fold) increase in coarse- and a 73-fold (95% CI, 15 to 350-fold) increase in fine-aerosol RNA shedding. | 2021 | Adenaiye et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|-----------------------------------|---------------------|--|------------------|---|
| N501Y | environmental condition stability | Pokay | No differences in the stability of B.1.1.7 observed in the absence of simulated sunlight at either 20°C or 40°C (with a mean time for a 90% loss of viral infectivity across all dark conditions of 6.2 hours). However, a small but statistically significant difference in the stability was observed in simulated sunlight at 20°C and 20% relative humidity, with B.1.1.7 restoring wild type 90% loss time of 11 minutes vs. 7 and 8 minutes for B.1.319 (D614G) and B.28 (V367F) early 2020 viruses respectively. | 2021 | Schuit et al. (2021) |
| N501Y | trafficking | Pokay | Modelling the Alpha variant in primary human airway epithelial (HAE) cultures, S1 to full length Spike ratio (measuring Spike furin cleavage processivity) increase 3.9x relative to wild type (5.4 vs 1.4). This is less efficient than Delta (11x vs wildtype using a P681R mutation instead). [del ~144 changed due to ambiguity] Furthermore the RNA ratio of Delta versus Alpha-spike/Delta-backbone continuously increased from 2.8 on day 1 to 9.8 on day 5 post infection in a co-infection model in HAEs, suggesting the spike gene drives the improved replication of Delta variant. | 2021 | Liu et al. (2021) |
| N501Y | vaccine neutralization efficacy | Pokay | No significant difference in T-cell response to B.1.1.7 was observed (vs. ancestral) in blood drawn from 28 participants received the Pfizer-BioNTech vaccine and 2 received the Moderna vaccine. This is despite three mutations (Y144del, D614G, and P681H) overlapping T-cell epitope hotspots. | 2021 | Woldemeskel et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|--------------------------------------|
| N501Y | vaccine neutralization efficacy | Pokay | The NAb titers (PRNT50) of sera collected from 38 vaccine recipients four-weeks after the second dose of inactivated whole-virion SARS-CoV-2 BBV152/COVAXIN vaccine [which contains D614G] were not significantly different between B.1.1.7 virus and ancestral D614G virus. | 2021 | Sapkal et al. (2021) |
| N501Y | vaccine neutralization efficacy | Pokay | PBMCs of Pfizer/BioNTech BNT162b2 (n | 2021 | Tarke et al. (2021) |
| N501Y | vaccine neutralization efficacy | Pokay | A single dose of BNT162b2 vaccine demonstrated vaccine effectiveness [symptomatic or asymptomatic in cohort of routinely NAAT-monitored UK HCWs] of 72% (95% CI 58-86) 21 days after first dose and 86% (95% CI 76-97) seven days after two doses in the antibody negative cohort. This cohort was vaccinated when the dominant variant in circulation was B.1.1.7 and demonstrates effectiveness against this variant. | 2021 | Hall et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|--|
| N501Y | vaccine neutralization efficacy | Pokay | Between December 19, 2020 and Jan 24, 2021, 7214 of 9109 eligible HCWs at Sheba Medical Center in Israel had received one or more doses of BNT162b2 (Pfizer) vaccine. Adjusted rate reduction in SARS-CoV-2 NAAT positivity infection compared with unvaccinated workers 1-14 days after 1st dose was 30% (95% CI: 2-50), and 75% (95% CI: 72-84) after 15-28 days. Adjusted rate reduction in symptomatic COVID-19 compared with unvaccinated workers 1-14 days after 1st dose was 47% (95% CI: 17-66), and 85% (95% CI: 71-92) after 15-28 days. [Though often cited as an indicator of VE for B.1.1.7, during this time period in Israel, the prevalence of the B.1.1.7 variant increased from ~20% to 50% of cases (covariants.org), therefore these VE numbers likely represent a mix of B.1.1.7 and other lineage effects.] | 2021 | Amit et al. (2021) |
| N501Y | vaccine neutralization efficacy | Pokay | We found that a single dose of the BNT162b2 vaccine is about 60-70% effective at preventing symptomatic disease in adults aged 70 years and older in England and that two doses are about 85-90% effective. Those who were vaccinated and went on to have symptoms had a 44% lower risk of being admitted hospital and a 51% lower risk of death compared with people who were unvaccinated. We also found that a single dose of the ChAdOx1-S vaccine was about 60-75% effective against symptomatic disease and provided an additional protective effect against hospital admission—it is too early to assess the effect on mortality. The B.1.1.7 variant now dominates in the UK and these results will largely reflect vaccine effectiveness against this variant. | 2021 | Lopez Bernal et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|--|
| N501Y | antibody epitope effects | Pokay | Neutralization of the 47D10. Alpha (B.1.1.7) has an IC50 fold change of 0.40x. | 2022 | Yuan et al. (2022) |
| N501Y | anthropozoonotic events | Pokay | First documented cases of domestic cat and dog infections with the B.1.1.7 strain. | 2021 | Hamer et al. (2021) |
| N501Y | vaccine efficacy | Pokay | Effectiveness after one dose of vaccine (BNT162b2 or ChAdOx1 nCoV-19) with the delta variant was (48.7%: 95% confidence interval [CI], 45.5 to 51.7): the results were similar for both vaccines. With the BNT162b2 vaccine, the effectiveness of two doses was 93.7% (95% CI, 91.6 to 95.3) among those with the alpha variant. With the ChAdOx1 nCoV-19 vaccine, the effectiveness of two doses was 74.5% (95% CI, 68.4 to 79.4) among those with the alpha variant. | 2021 | Lopez Bernal et al. (2021) |
| N501Y | antibody epitope effects | Pokay | Reduction in neutralization by mAbs COVA2-15 (~9x), B38 (~14x), S309 (~190x) by this B.1.1.7 pseudotyped virus model. | 2021 | Shen et al. (2021) |
| N501Y | vaccine neutralization efficacy | Pokay | We observed a sharp decline in cases when ~50% of the elderly population was 2 weeks beyond their first vaccination dose and at a time point during which the B.1.1.7 variant gained transmission dominance. In support of this finding, it was suggested that, after the first vaccination dose, more than 70% of patients develop neutralization antibodies, ¹⁵ and the vaccine efficiency can reach 85%. | 2021 | Munitz et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|--|
| N501Y | convalescent plasma escape | Pokay | Neutralizing antibody titers of 2/20 (10%) samples showed >10x reduction (sera collected ~1mo post Jan 2020 first wave in China). Neutralizing antibody titers of 8/20 samples (40%) decreased below an ID50 threshold of 40 (sera collected ~8mo post Jan 2020 first wave in China). | 2021 | Hu et al. (2021) |
| N501Y | antibody epitope effects | Pokay | Lessens the potency of mAbs COVA2-17 (~5x, similar to N501Y alone), COVA1-12 (~11x) and COVA1-21 (>100x), which do not compete allosterically. | 2021 | Rees-Spear et al. (2021) |
| N501Y | reinfection | Pokay | 36920 COVID Symptom Study app users reported SARS-CoV-2 test positivity in late 2020. Possible reinfections were identified in 249 (0.7% [95% CI 0.6-0.8]) of 36509 app users who reported a positive swab test before Oct 1, 2020, but there was no evidence that the frequency of reinfections was higher for the B.1.1.7 variant than for pre-existing variants. | 2021 | Graham et al. (2021) |
| N501Y | vaccine neutralization efficacy | Pokay | Pseudotyped B.1.1.7 virus has reduced neutralization activity vs wild type: 2.1x (30 sera Pfizer median 9 days post 2nd dose) and 2.3x (35 sera Moderna median 18 days post 2nd dose). This was NOT significant by ANOVA. Note that Y145del was actually noted in the paper as the effect of their DNA construct, but this is equivalent at the protein level to the more commonly annotated Y144del. | 2021 | Garcia-Beltran et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|---------------------------------------|
| N501Y | vaccine neutralization efficacy | Pokay | The sera of 16 individuals with time course collection was evaluated against VSV pseudotypes: neutralized D614G at week 2, whereas B.1.1.7 started to be neutralized at week 3, although less efficiently than D614G. B.1.1.7 and D614G strains were similarly neutralized at week 4 (1 week after booster dose). | 2021 | Planas et al. (2021) |
| N501Y | vaccine neutralization efficacy | Pokay | Neutralization assays of B.1.1.7 virus showed a reduction of 2.5-fold (14 days post 2nd dose AstraZeneca, n | 2021 | Supasa et al. (2021) |
| N501Y | antibody epitope effects | Pokay | Neutralization of the bsAbs 35B5. Alpha (B.1.1.7) has an IC50 fold change of 1.39x. | 2022 | Yuan et al. (2022) |
| N501Y | vaccine efficacy | Pokay | In Minnesota in early 2021 when Alpha was prevalent, vaccine efficacy was estimated as: mRNA-1273 86% (95%CI: 81-90.6%) and BNT162b2: 76% (95%CI: 69-81%) using age, sex, race, PCR testing and vaccination date matched cohorts of unvaccinated, Pfizer and Moderna vaccinees. [variant list included is ancestral Alpha, as this was an observational study no variant list was given] | 2021 | Puranik et al. (2021) |
| N501Y | antibody epitope effects | Pokay | ~20x resistance to mAb CQ038 by B.1.1.7 pseudotyped virus | 2021 | Hu et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|---------------------------------------|
| N501Y | reinfection | Pokay | Reinfection with Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) B.1.1.7 variant in an immunocompromised 16yo female with end stage renal disease 94 days after initial infection with a B.1.2 lineage virus. Both lineages were the prevalent one at the time of 1st and 2nd infections respectively in Texas, where the patient was located (suggesting exposure risk rather than lineage immune evasion). | 2021 | Marquez et al. (2021) |
| N501Y | vaccine neutralization efficacy | Pokay | Paradigm's ACE-2 variant LVE/STR chimera neutralizes Alpha Variant B.1.1.7 RBD significantly better than GenScript IgG FL18-740 w.t. ACE-2 mAB. Determined using Surrogate Viral Neutralization Tests. | 2022 | Uhal B et al. (2022) |
| N501Y | antibody epitope effects | Pokay | Neutralization of the bsAbs Bi-Nab47D10-35B5. Alpha (B.1.1.7) has an IC50 fold change of 1.44x. | 2022 | Yuan et al. (2022) |
| N501Y | vaccine neutralization efficacy | Pokay | A single dose of BNT162b2 (Pfizer) vaccine showed vaccine effectiveness of 70% (95% CI 55-85) 21 days after first dose and 85% (74-96) 7 days after two doses in the study population. Our findings show that the BNT162b2 vaccine can prevent both symptomatic and asymptomatic infection in working-age adults. This cohort (8203 treatment, 15121 control) was vaccinated when the dominant variant in circulation was B.1.1.7 and shows effectiveness against this variant. | 2021 | Hall et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|---------------------------------------|
| N501Y | convalescent plasma escape | Pokay | NTD-specific nAbs showed a substantial (3-450x) decrease in neutralization potency against the recently reported highly transmissible B.1.1.7 variant of concern, whereas RBD-specific nAbs were either unaffected or showed lower decreases in potency. | 2021 | Graham et al. (2021) |
| N501Y | tissue specific neutralization | Pokay | The nasal mucosa of Pfizer vaccinees with time course collection was evaluated against VSV pseudotypes: results (only one nasal swab from different previously infected vaccinee neutralizing at weeks 3 and 6 against B.1.1.7 and D614G) suggest that vaccinees probably do not elicit an early humoral response detectable at mucosal surfaces even though sera neutralization was observed. They strengthen the hypothesis that some vaccines may not protect against viral acquisition and infection of the oral–nasal region, but may prevent severe disease associated with viral dissemination in the lower respiratory tract. | 2021 | Planas et al. (2021) |
| N501Y | pharmaceutical effectiveness | Pokay | Infectious viral titers in lung tissue determined using a tissue culture infectious dose (TCID) assay in 10 hamsters showed that Alpha Molnupiravir (MK-4482) had ~2.75x fold drop. | 2022 | Rosenke et al. (2022) |
| N501Y | vaccine neutralization efficacy | Pokay | Neutralization efficiency (ID50) against B.1.1.7 reduced 1.2x relative to D614G wildtype using pseudotyped VSV assay on 8 Moderna vaccinee sera one week post-booster. | 2021 | Choi et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|--|
| N501Y | reinfection | Pokay | Second infection in December 2020 with B.1.1.7 after April 2020 initial infection with B.2 in a 78-year-old man with a history of Type 2 diabetes mellitus, diabetic nephropathy on hemodialysis, chronic obstructive pulmonary disease (COPD), mixed central and obstructive sleep apnea, ischemic heart disease, with no history of immunosuppression. | 2021 | Harrington et al. (2021) |
| N501Y | trafficking | Pokay | The entry efficiencies of Spike pseudotyped viruses bearing N501Y Variant 1 (B.1.1.7) mutant were about 3 to 4.4 times higher than that of the WT pseudovirus when viral input was normalized, suggesting that these spike variants promote the infectivity of SARS-CoV-2. | 2021 | Hu et al. (2021) |
| N501Y | trafficking | Pokay | ~2.5x cleavage of S2 relative to WA1 (D614G) wildtype by Alpha variant variant as measured by mass spectrometry of Vero-TMPRSS culture. | 2021 | Esclera et al. (2021) |
| N501Y | vaccine neutralization efficacy | Pokay | Virus neutralisation activity (using a live SARS-CoV-2 microneutralisation assay (ND50)) by vaccine induced antibodies was 9-fold lower against the B.1.1.7 variant than against a canonical non B.1.1.7 lineage. Vaccine efficacy against symptomatic NAAT positive infection was similar for B.1.1.7 and non-B.1.1.7 lineages (74.6% [95%CI 41.6-88.9] and 84% [95% CI 70.7-91.4] respectively). Furthermore, vaccination with ChAdOx1 nCoV-19 results in a reduction in the duration of shedding and viral load, which may translate into a material impact on transmission of disease. | 2021 | Emery et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|---|
| N501Y | antibody epitope effects | Pokay | BnAb 002-S21F2 IC50 on the Alpha (B.1.1.7) variant is 1.0x fold the wildtype in 42 COVI. | 2022 | Kumar et al. (2022) |
| N501Y | vaccine neutralization efficacy | Pokay | ELISpot assays show T cell neutralization reduced by 15.4% in this B.1.1.7 pseudotype relative to wild type in 18-20 pooled patient samples post second mRNA vaccine dose, with no significant difference between Pfizer and Moderna cohorts. Reduction was stronger in the S1 subunit than S2 (separate peptide pools were used). | 2021 | Gallagher et al. (2021) |
| N501Y | vaccine neutralization efficacy | Pokay | 2.1x drop in neutralization using sera collected from 14 healthy adult participants that received two injections of the mRNA-1273 (Moderna) vaccine at a dose of 100 µg (18-55 years: day 1 (n | 2021 | Edara et al. (2021) |
| N501Y | vaccine neutralization efficacy | Pokay | B.1.1.7 pseudotyped VSV was tested for neutralization in a clonal HEK-293T ACE2 TMPRSS2 cell line optimized for highly efficient S-mediated infection. A cohort of 12 Argentinian recipients of the Gamaleya Sputnik V Ad26 / Ad5 vaccine showed no statistically significant change in neutralization efficacy. | 2021 | Ikegame et al. (2021) |
| N501Y | vaccine neutralization efficacy | Pokay | NVX-CoV2373 [Novavax] vaccine in phase 3 trial was 89.7% (95% CI, 80.2-94.6) effective in preventing COVID-19, with no hospitalizations or deaths reported. There were five cases of severe Covid-19, all in the placebo group. Post hoc analysis revealed efficacies of 96.4% (73.8-99.5) and 86.3% (71.3-93.5) against the prototype strain and B.1.1.7 variant, respectively. | 2021 | Heath et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|---------------------------------------|
| N501Y | vaccine neutralization efficacy | Pokay | Pseudotyped B.1.1.7 Spike variants lentivirus. 3.5x reduction in neutralization with Moderna vaccinated patient sera after 29 days (1st dose). 2.0x reduction in neutralization with Moderna vaccinated patient sera after 57 days (2nd dose). 2.1x reduction in neutralization with Novavax Phase 1 post-vaccination sera. | 2021 | Shen et al. (2021) |
| N501Y | clinical indicators | Pokay | After adjusting for the age factor, in a prospective Chinese cohort study B.1.1.7 variant infection (compared to B.1.140) was the risk factor for C-reactive protein (P | 2021 | Song et al. (2021) |
| N501Y | vaccine efficacy | Pokay | Using a test-negative design using Ontario data between Dec 14, 2020 and May 30, 2021, 421,073 symptomatic community-dwelling individuals were tested. Against symptomatic infection caused by Alpha, vaccine effectiveness with partial vaccination (≥ 14 days after dose 1) was higher for mRNA-1273 (83%) than BNT162b2 (66%) and ChAdOx1 (64%), and full vaccination (≥ 7 days after dose 2) increased vaccine effectiveness for BNT162b2 (89%) and mRNA-1273 (92%). | 2021 | Nasreen et al. (2021) |
| N501Y | trafficking | Pokay | Live virus was tested ex vivo in reconstituted bronchial epithelium, and out competed wild type. | 2021 | Touret et al. (2021) |
| N501Y | vaccine neutralization efficacy | Pokay | Mean 1.7x reduction of NT50 value B.1.1.7 (Alpha) relative to wild type in 8 sera from adult BNT162b2 vaccinees (28-47yo) collected ~1m post booster. | 2021 | Uriu et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|--------------------------------------|
| N501Y | ACE2 receptor binding affinity | Pokay | Flow cytometry was used on recombinant VSV proteins and yeast surface display to assess the binding of a labeled soluble ACE2 protein to cells expressing B.1.1.7. We observed a dramatic increase (relative to D614G) in binding of soluble ACE2 to B.1.1.7, and to a lesser extent to B.1.351, which both carry the N501Y mutation (see Fig 3). | 2021 | Planas et al. (2021) |
| N501Y | ACE2 receptor binding affinity | Pokay | L27, V34 and E90 mutation resulted in ultrahigh affinity binding of the LVE-ACE-2 domain to the widest variety of VOCs, with KDs of 93 pM for binding to the Alpha B1.1.7. Values were obtained with LVE-ACE-2/mAB chimeras containing the Y-T-E sequence that enhances binding to the FcRn receptor, which in turn is expected to extend biological half-life 3-4-fold. | 2022 | Uhal B et al. (2022) |
| N501Y | vaccine neutralization efficacy | Pokay | 1.5x reduction in neutralization (ID50) in sera 3 weeks after one dose of Pfizer/BioNTech BNT162b2 (up to 5 naive and post infection vaccinees) | 2021 | Gong et al. (2021) |
| N501Y | vaccine neutralization efficacy | Pokay | nan | | UNKNOWN et al. () |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|-------------------------------------|---------------------|---|------------------|---|
| N501Y | vaccine neutralization efficacy | Pokay | In Qatar, where Pfizer vaccine use is prevalent (<10% of the population covered in the time period of the study ending Mar 31, 2021), any time after one dose (including the 2 weeks where no major effect is expected) B.1.1.7 lineage effectiveness was observed as 29.5% (95% CI [22.9,35.5]) against infection, and 54.1% against severe/critical/fatal disease (95% CI [26.1-71.9]). Two weeks or more after 2nd dose, effectiveness climbed to 89.5% [85.9,92.3] against infection, and 100% against severe/critical/fatal disease (95% CI [81.7,100]). | | UNKNOWN et al. () |
| N501Y | pharmaceutical effectiveness | Pokay | Lilly's LY-CoV16 showed marked reduction in neutralization of B.1.1.7. | 2021 | Dejnirattisai et al. (2021) |
| N501Y | convalescent plasma escape | Pokay | Sera neutralized the B1.1.7 isolate with a lower potency (2-fold: 95% CL: 1.5 – 3-fold), and those with the lowest homotypic neutralizing potency had undetectable heterotypic potency (2/25). | 2021 | Skelly et al. (2021) |
| N501Y | tissue specific replication effects | Pokay | In this report, by using a lower infectious dose, we demonstrate that B.1.1.7 (cultured sample Hong Kong/HKPU-00015/2021) exhibits higher infectivity and/or replication efficiency in the nasal epithelium. (Hamster model of infection) | 2021 | Mok et al. (2021) |
| N501Y | convalescent plasma escape | Pokay | Neutralization capacity GMT of 27 subjects' sera post-infection was considerably higher (stronger) than after the second Pfizer dose, and 4.5x drop in B.1.1.7 neutralization was observed. | 2021 | Collier et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|--|
| N501Y | vaccine neutralization efficacy | Pokay | 20/29 sera after the first dose of Pfizer showed an average reduction in neutralization titres against the B.1.1.7 variant of 3.2 ± 5.7 . After the second dose, the GMT was markedly increased compared with the first-dose titres, with a fold change of 1.9 ± 0.9 (mean \pm s.d.). Neutralization GMT of 27 subjects post-infection was considerably higher (stronger) than after the second Pfizer dose, and 4.5x drop in B.1.1.7 neutralization was observed. | 2021 | Collier et al. (2021) |
| N501Y | transmissibility | Pokay | We estimate that this [B.1.1.17] variant has a 43–90% (range of 95% credible intervals 38–130%) higher reproduction number than preexisting variants. Data from other countries yield similar results: we estimate that R for VOC 202012/01 relative to other lineages is 55% (45–66%) higher in Denmark, 74% (66–82%) higher in Switzerland, and 59% (56–63%) higher in the United States, with consistent rates of displacement across regions within each country. | 2021 | Davies et al. (2021) |
| N501Y | vaccine neutralization efficacy | Pokay | Lineage B.1.1.7 spike–pseudotyped VSV was tested for neutralization vs Wuhan reference genome pseudotype in 40 sera collected 7 or 21 days post-booster dose. Statistically significant change (22%) in neutralization was observed among the 26 sera from those < | 2021 | Muik et al. (2021) |
| N501Y | transmissibility | Pokay | At the national level (Italy), we estimated a mean relative transmissibility of B.1.1.7 (compared to historical lineages) ranging between 1.55 and 1.57 (with confidence intervals between 1.45 and 1.66). | 2021 | Stefanelli et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|---|
| N501Y | outcome hazard ratio | Pokay | On average across 7 European countries studied, using B.1.1.7 defining mutations: Significant shift to asymptomatic cases (27.4% vs 18.6% for non-VOC cases). Significant shift to infection in those without pre-existing conditions (44.8% vs 89% for non-VOC cases). Significant increase in hospitalization rate (11% vs 7.5% for non-VOC cases). Significant increase in ICU rate (1.4% vs 0.6% for non-VOC cases). Significant decrease in death rate (2.0% vs vs 4.0% for non-VOC cases). | 2021 | Funk et al. (2021) |
| N501Y | vaccine neutralization efficacy | Pokay | Vaccine elicited antibodies neutralized virus with the B.1.1.7 spike protein with titers similar to D614G virus. Serum specimens from individuals vaccinated with the BNT162b2 mRNA vaccine neutralized D614G virus with titers that were on average 7-fold greater than convalescent sera. | 2021 | Tada et al. (2021) |
| N501Y | transmissibility | Pokay | Oslo, Norway: Within households, we find an increase in the secondary attack rate by 60% (20% - 114%) compared to other variants. In general, we find a significant increase in the estimated reproduction number of 24% (95% CI 0% - 52%), or an absolute increase of 0.19 compared to other variants. | 2021 | Lindstrøm et al. (2021) |
| N501Y | transmissibility | Pokay | Based on ~300,000 RT-PCR samples collected from December 6th 2020 to February 10th 2021 in Israel, the B.1.1.7 is 45% (95% CI:20-60%) more transmissible than the wild-type strain, and become dominant in Israel within 3.5 weeks. | 2021 | Munitz et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|----------------------|---------------------|--|------------------|---|
| N501Y | outcome hazard ratio | Pokay | The matching-adjusted conditional odds ratio of hospitalisation was 1.58 (95% confidence interval 1.50 to 1.67) for COVID-19 patients infected with a SGTF-associated variant [primarily B.1.1.7], compared to those infected with non-SGTF-associated variants. The effect was modified by age ($p < 0.001$), with ORs of 0.96-1.13 below age 20 years and 1.57-1.67 in age groups 40 years or older. | 2021 | Nyberg et al. (2021) |
| N501Y | outcome hazard ratio | Pokay | Using UK data 1 November 2020 to 14 February 2021, while correcting for misclassification of PCR test Spike Gene Target Failure (SGTF) and missingness in SGTF status, we estimate that the hazard of death associated with B.1.1.7 is 61% (42–82%) higher than with pre-existing variants after adjustment for age, sex, ethnicity, deprivation, residence in a care home, the local authority of residence and test date. This corresponds to the absolute risk of death for a 55–69-year-old man increasing from 0.6% to 0.9% (95% confidence interval, 0.8–1.0%) within 28 days of a positive test in the community. | 2021 | Davies et al. (2021) |
| N501Y | viral load | Pokay | B.1.1.7 samples showed average Ct cycle threshold of 21.9 vs 23 for wildtype (i.e. ~2x higher viral load) comparing 37758 and 22535 samples respectively. | 2021 | Roquebert et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|----------------------|---------------------|---|------------------|--|
| N501Y | transmissibility | Pokay | Based on 36920 COVID Symptom Study app users reported SARS-CoV-2 test positivity in late 2020, Rt of B.1.1.7 was 1.35x (95% CI 1.02-1.69) relative to pre-existing variants. However, Rt fell below 1 during regional and national lockdowns, even in regions with high proportions of infections with the B.1.1.7 variant. | 2021 | Graham et al. (2021) |
| N501Y | outcome hazard ratio | Pokay | 341 samples collected Nov 9 to Dec 20, 2020 were sequenced from two London (UK) hospitals. 198 (58%) of 341 had B.1.1.7 infection and 143 (42%) had non-B.1.1.7 infection. No evidence was found of an association between severe disease and death and lineage (B.1.1.7 vs non-B.1.1.7) in unadjusted analyses (prevalence ratio [PR] 0.97 [95% CI 0.72-1.31]), or in analyses adjusted for hospital, sex, age, comorbidities, and ethnicity (adjusted PR 1.02 [0.76-1.38]). | 2021 | Frampton et al. (2021) |
| N501Y | outcome hazard ratio | Pokay | From Sept 28 to Dec 27, 2020, positive COVID-19 tests were reported by 36 920 COVID Symptom Study app users whose region was known and who reported as healthy on app sign-up. We found no changes in reported symptoms or disease duration associated with B.1.1.7. | 2021 | Graham et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|----------------------|---------------------|--|------------------|---------------------------------------|
| N501Y | viral load | Pokay | The 249 B.1.1.7 (a.k.a. N501Y.V1) variant cases in three Paris hospital labs had a ~10-fold viral load increase (~3.3 Ct drop in N gene probe) compared to 332 ancestral lineage cases from the same time frame (2020-12-20 to 2021-02-26). PG: BUT there is a discrepancy in drop between the ORF1ab and N probes, with the former suggesting only a 2-fold drop, consistent with the drop observed in B.1.351. This might indicate higher subgenomic RNA content in B.1.1.7 skewing the change. | 2021 | Teyssou et al. (2021) |
| N501Y | viral load | Pokay | Using lack of S probe detection as a proxy for B.1.1.7 status, 275 putative B.1.1.7 samples and 390 'wild type' SARS-CoV-2 positive samples in Wales were compared for Ct values, suggesting ~12-fold increase (~3.5 Ct decrease) in viral load for B.1.1.7 samples. | 2021 | Couzens et al. (2021) |
| N501Y | outcome hazard ratio | Pokay | The mortality hazard ratio associated with infection with [B.1.1.7] compared with infection with previously circulating variants was 1.64 (95% confidence interval 1.32 to 2.04) in patients who tested positive for covid-19 in the community (54906 matched pairs of participants who tested positive for SARS-CoV-2 in pillar 2 between 1 October 2020 and 29 January 2021). In this comparatively low risk group, this represents an increase in deaths from 2.5 to 4.1 per 1000 detected cases. | 2021 | Challen et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|--------------------------------|---------------------|---|------------------|--|
| N501Y | viral load | Pokay | In a study of 1260 ICU subjects, viral load distributions (collected within 48h of admission) were elevated in both seropositive and seronegative subjects infected with B.1.1.7 ('UK variant'). PG: The PANGO tool defining Spike variants for B.1.1.7 are listed here, whereas the paper only used a test for D1118H. | 2021 | Ratcliff et al. (2021) |
| N501Y | viral load | Pokay | This study reveals that B.1.1.7 SARS-CoV-2 variant is a slower-growing virus than parental B.1. Further, a higher replication along with reduced infectious viral titer was hypothesized to be linked to higher transmission with reduced pathogenicity. | 2021 | Nyayanit et al. (2021) |
| N501Y | viral load | Pokay | We found that the British variant (clade B.1.1.7), compared to an ancestral SARS-CoV-2 clade B virus, produced higher levels of infectious virus late in infection and had a higher replicative fitness in human airway, alveolar and intestinal organoid models. | 2021 | Lamers et al. (2021) |
| N501Y | outcome hazard ratio | Pokay | Danish study of the B.1.1.7 lineage shows hospital admission odds ratio of 1.63 vs other lineages. The adjusted OR was increased in all strata of age. | 2021 | Bager et al. (2021) |
| N501Y | ACE2 receptor binding affinity | Pokay | This mutation causes major decrease in binding affinity vs. wild type as measured by IC50 vs pseudotyped lentivirus. | 2021 | Tada et al. (2021) |
| N501Y | transmissibility | Pokay | Ontario, Feb 2021: The secondary attack rate for VOC index cases in this matched cohort was 1.31 times higher than non-VOC index cases (RR | 2021 | Buchan et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|---------------------------------------|
| N501Y | viral load | Pokay | The median Ct value of RT-qPCR tests of the N-gene target in the Daxing B.1.1.7 group was significantly lower than the Shunyi B.1.470 group (P | 2021 | Song et al. (2021) |
| N501Y | transmissibility | Pokay | Primary cases infected with B.1.1.7 had an increased transmissibility of 1.5-1.7 times that of primary cases infected with other lineages. The increased transmissibility of B.1.1.7 was multiplicative across age and viral load. | 2021 | Lyngse et al. (2021) |
| N501Y | vaccine neutralization efficacy | Pokay | VSV pseudotype B.1.1.7 showed 1.77-fold reduction in neutralization efficiency vs wild type in 15 Pfizer BNT162b2 vaccinee sera 13-15 days post second dose. Cell fusion proficiency was unchanged. | 2021 | Hoffman et al. (2021) |
| N501Y | vaccine neutralization efficacy | Pokay | Neutralizing antibody titers increased in previously infected vaccinees relative to uninfected vaccinees 5.2-fold against B.1.1.7 (contrast with 3.4 fold against original SARS-CoV-2). | 2021 | Leier et al. (2021) |
| N501Y | outcome hazard ratio | Pokay | Using primarily S-defining mutations for lineage B.1.1.7, most models of hospitalization and fatality risk ratios from consortium members show elevated ratios (~1.3-1.7x). | 2021 | UNKNOWN et al. (2021) |
| N501Y | trafficking | Pokay | VSV pseudotype B.1.1.7 showed no significant difference in cell entry relative to wild type in 6 cell lines. Cell fusion proficiency was unchanged. | 2021 | Hoffman et al. (2021) |
| N501Y | ACE2 receptor binding affinity | Pokay | Six fold increase in affinity for ACE2 by the B.1.1.7 lineage vs wild type is driven by a drop in observed dissociation rate constant. | 2021 | Collier et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|-----------------------------------|---------------------|---|------------------|--|
| N501Y | environmental condition stability | Pokay | Relative to D614G, this mutation demonstrated significant increase in infectivity (i.e. heat stability) after incubation at 50C after 1 hour. | 2021 | Tada et al. (2021) |
| N501Y | trafficking | Pokay | Lentiviral pseudotyped with this mutation set from B.1.1.7 was tested on ACE2.293T cells. Luciferase activity was measured two days postinfection, showing significant (40%) increase in infection rate amongst the cells, much more than the effect of either the deletion or the point mutation alone, suggesting that this combination has a synergistic effect contributing to cell entry fitness, but to a smaller extent than N501Y and the deletion alone. | 2021 | Tada et al. (2021) |
| N501Y | convalescent plasma binding | Pokay | These key B.1.1.7 mutations as a combination neutralized slightly less well than D614G and this was noticeable in the lack of sera with high neutralizing titer for the viruses across 10 convalescent sera from April 2020 infectees. | 2021 | Tada et al. (2021) |
| N501Y | convalescent plasma binding | Pokay | Slight neutralization improvement on average in 16 health workers' convalescent sera. | 2021 | Alenquer et al. (2021) |
| N501Y | convalescent plasma escape | Pokay | One convalescent sera tested showed 4-fold or greater reduction in neutralization efficiency. | 2021 | Alenquer et al. (2021) |
| N501Y | vaccinee plasma binding | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.4/5 (from) were 17.2x-fold lower (95% CI: 0.6x-0.7x) than against 208-428 972-1834 4.3-4.7 US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|--|
| N501Y | vaccine neutralization efficacy | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.4/5 (from) were 13.0-fold lower (95% CI: 4.2x-4.6x) than against 208-428 972-1834 4.3-4.7 US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahade et al. (2022) |
| N501Y | vaccine neutralization efficacy | Pokay | 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 ~10-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 ~3 fold without the deletion] ID50 titres in non-infected mRNA vaccines more than two weeks post-booster were significant, but ~500x weaker than in previously infected patients after first dose. | 2021 | Stamatatos et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|------------------------------------|
| N501Y | vaccine neutralization efficacy | Pokay | 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+. | 2021 | Pegu et al. (2021) |
| N501Y | vaccine neutralization efficacy | Pokay | 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 ~2 better neutralization than BNT162b2. [common defining B.1.351 mutations noted, as the manuscript does not provide details] | 2021 | Abe et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|--|
| N501Y | antibody epitope effects | Pokay | 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 ~10-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. | 2021 | Stamatatos et al. (2021) |
| N501Y | convalescent plasma escape | Pokay | 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] | 2021 | Stamatatos et al. (2021) |
| N501Y | vaccine neutralization efficacy | Pokay | 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] | 2021 | Tada et al. (2021) |
| N501Y | antibody epitope effects | Pokay | Neutralization of the bsAbs Bi-Nab35B5-47D10. Beta (B.1.351) has an IC50 fold change of 0.13x. | 2022 | Yuan et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|--------------------------------|---------------------|---|------------------|--|
| N501Y | pharmaceutical effectiveness | Pokay | Infectious viral titers in lung tissue determined using a tissue culture infectious dose (TCID) assay in 10 hamsters showed that Beta Molnupiravir (MK-4482) had ~1.75x fold drop. | 2022 | Rosenke et al. (2022) |
| N501Y | ACE2 receptor binding affinity | Pokay | The B.1.351 variant constellation causes an ~20-fold increase in affinity for ACE2 compared with Wuhan RBD, which may influence transmissibility. | 2021 | Zhou et al. (2021) |
| N501Y | humoral response durability | Pokay | 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. | 2020 | Betton et al. (2020) |
| N501Y | trafficking | Pokay | ~6x cleavage of S2 relative to WA1 (D614G) wildtype by Beta variant as measured by mass spectrometry of Vero-TMPRSS culture [no mutations directly at furin cleavage site, but A701V is downstream] Compare to 4.5x or less for variants of concern with direct furin cleavage site mutations. | 2021 | Esclera et al. (2021) |
| N501Y | outcome hazard ratio | Pokay | Compared to Alpha (B.1.1.7) variant, odds of progressing to severe disease were 1.24-fold (95% CI: 1.11-1.39) higher for Beta. Odds of progressing to critical disease were 1.49-fold (95% CI: 1.13-1.97) higher. Odds of COVID-19 death were 1.57-fold (95% CI: 1.03-2.43) higher. | 2021 | Abu-Raddad et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|-------------------------------------|
| N501Y | antibody epitope effects | Pokay | BnAb 002-S21F2 IC50 on the Beta (B.1.351) variant is 0.4x fold the wildtype. | 2022 | Kumar et al. (2022) |
| N501Y | convalescent plasma escape | Pokay | In 34 convalescent cases 4–9 weeks following infection in June 2020, before the emergence of B.1.1.7, neutralization titers against B.1.351 were, on average, 13.3-fold reduced compared with an early Victoria sample ($p < 0.0001$). Significantly, 18 of 34 samples failed to reach 50% neutralization at a plasma dilution of 1:20, with a number showing a near total reduction of neutralization activity. In 13 convalescent cases 4–9 weeks following infection with B.1.1.7, neutralization titers against B.1.351 were, on average, 3.1-fold reduced compared with an early Victoria sample ($p < 0.0001$). | 2021 | Zhou et al. (2021) |
| N501Y | antibody epitope effects | Pokay | Neutralization of the bsAbs Bi-Nab47D10-35B5. Beta (B.1.351) has an IC50 fold change of 0.15x. | 2022 | Yuan et al. (2022) |
| N501Y | vaccine neutralization efficacy | Pokay | Vaccine plasma neutralization of B.1.351-spike virus was nominally robust but lower (~3x) than other variants of concern. | 2021 | Liu et al. (2021) |
| N501Y | vaccine neutralization efficacy | Pokay | 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. | 2021 | Choi et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|--|
| N501Y | antibody epitope effects | Pokay | Testing against B.1.351 the 20 most effective mAbs (19 anti-RBD, 1 anti-NTD) from a screen of 377 against wild type, 4 of 20 antibodies had >10-fold fall in neutralization titers, with most of these showing a complete knockout of activity. This is in line with the key roles of K417, E484, and N501, in particular E484, in antibody recognition of the ACE2 interaction surface of the RBD. Regeneron mAb cocktail: The neutralization of REGN10987 was unaffected by B.1.351, while REGN10933 was severely impaired (773-fold). AstraZeneca mAb cocktail: Neutralization by the AZ pair of antibodies was little affected on B.1.351 compared with Victoria. | 2021 | Zhou et al. (2021) |
| N501Y | vaccine neutralization efficacy | Pokay | 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. | 2021 | Madhi et al. (2021) |
| N501Y | vaccine neutralization efficacy | Pokay | 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. | | UNKNOWN et al. () |
| N501Y | anthropozoonotic events | Pokay | Unlike wild type or B.1.1.7, B.1.351 lineage virus was able to infect and replicate in common lab mouse strains, with high titer. PG: The virus used in these experiments has a non-typical deletion+sub in the 242 region. | 2021 | Montagutelli et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|--|
| N501Y | antibody epitope effects | Pokay | Neutralization of the bsAbs 35B5. Beta (B.1.351) has an IC50 fold change of 0.13x. | 2022 | Yuan et al. (2022) |
| N501Y | vaccine neutralization efficacy | Pokay | Sera from healthcare workers (n | 2021 | Zhou et al. (2021) |
| N501Y | antibody epitope effects | Pokay | Neutralization of the bsAbs 47D10. Beta (B.1.351) has an IC50 fold change of 0.88x. | 2022 | Yuan et al. (2022) |
| N501Y | outcome hazard ratio | Pokay | 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. | 2021 | Funk et al. (2021) |
| N501Y | vaccine neutralization efficacy | Pokay | 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. | 2021 | Garcia-Beltran et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|--|
| N501Y | vaccine neutralization efficacy | Pokay | 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). | 2021 | Gallagher et al. (2021) |
| N501Y | vaccine neutralization efficacy | Pokay | 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. | 2021 | Alenquer et al. (2021) |
| N501Y | convalescent plasma escape | Pokay | 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. | 2021 | Stamatatos et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|--|
| N501Y | vaccine neutralization efficacy | Pokay | 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 ~3-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 ~10 fold with L242del] ID50 titres in non-infected mRNA vaccines more than two weeks post-booster were significant, but >100x weaker than in previously infected patients after first dose. | 2021 | Stamatatos et al. (2021) |
| N501Y | reinfection | Pokay | 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 February 2021 hospital outbreak in Luxembourg. Symptoms were mostly mild on first infection, and milder on second infection. | 2021 | Staub et al. (2021) |
| N501Y | reinfection | Pokay | Hamsters re-infected with B.1.351 virus after seroconversion 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. | 2021 | Yinda et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|--|
| N501Y | symptom prevalence | Pokay | 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. | 2021 | Munster et al. (2021) |
| N501Y | vaccine neutralization efficacy | Pokay | Pseudotyped B.1.351 v3 virus has reduced neutralization activity vs wild type: 42.4x (30 sera Pfizer median 9 days post 2nd dose) and 19.2x (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. | 2021 | Garcia-Beltran et al. (2021) |
| N501Y | vaccine neutralization efficacy | Pokay | The neutralization activities of two vaccines developed in China were tested against 501Y.V2 authentic virus: inactivated BBIBP-CorV (no significant change) and recombinant dimeric RBD vaccine ZF2001 (~1.6x reduction vs wildtype, p | 2021 | Huang et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|---------------------------------------|
| N501Y | vaccine neutralization efficacy | Pokay | Most of the plasma from 55 Pfizer vaccinees developed high percentages of Wuhan-Hu-1 S-ACE2 blocking activity, peaking at day 28 (7 days post-boost). A strikingly consistent hierarchy of reduction in plasma antibody binding by variant S and RBD antigens was observed among study participants, with progressively decreased binding for B.1.1.7 (not significant), P.1 (significant) and B.1.351 (significant) compared to Wuhan-Hu-1 antigens. | 2021 | Röltgen et al. (2021) |
| N501Y | vaccine neutralization efficacy | Pokay | During an outbreak of SARS-CoV-2 501Y.V2 in a nursing home, all non-vaccinated residents (5/5) versus half of those fully vaccinated 2-5 weeks prior with BNT162b2 (13/26) were infected. Two of 13 vaccinated versus 4 of 5 non-vaccinated residents presented severe disease. BNT162b2 did not prevent the outbreak, but reduced transmission and disease severity. Among the 13 fully vaccinated residents who were infected, 2 (15.4%) presented with an asymptomatic disease, 9 (69.2%) developed mild to moderate symptoms, and 2 (15.4%) progressed to severe disease with fatal evolution secondary to acute respiratory distress syndrome (ARDS). There was no relationship between anti-S antibody levels at diagnosis and disease severity. Overall, the proportion of residents with severe disease in the non-vaccinated group (4/5) was higher than that in the vaccinated group (2/13). Only 1 vaccinated staff, but 10 unvaccinated were infected in the outbreak (no severe disease). | 2021 | Bailey et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|--------------------------------------|
| N501Y | vaccine neutralization efficacy | Pokay | The neutralizing activity of vaccine was significantly lower against B.1.351 in sera from all 24 patients with the BNT162b2 mRNA vaccine. (Fig. 4) | 2021 | Chen et al. (2021) |
| N501Y | vaccine neutralization efficacy | Pokay | In sera 1-2 weeks after BNT162b2 first dose, from six patients previously infected with B.1, antibody titer in a microneutralization assay was on average 1625 for B.1.351 virus. This compares favorably (stronger) to most post-infection neutralization titer against all variants tested in the same sera (wild type, B.1.1.7, B.1.351, and P.1). | 2021 | Luftig et al. (2021) |
| N501Y | vaccine neutralization efficacy | Pokay | 2.5x reduction in neutralization by serum collected 2 to 3 weeks after the second dose from vaccinees who had received BBIBP-CorV (pVNT50 against VSV pseudotyped as B.1.351). Convalescent plasma had similar titer against wild type as the BBIBP-CorV vaccinee sera. >3x reduction in neutralization by serum collected 2 to 3 weeks after the second dose from vaccinees who had received CoronaVac (pVNT50 against VSV pseudotyped as B.1.351). Convalescent plasma had similar titer against wild type as the CoronaVac vaccinee sera. | 2021 | Wang et al. (2021) |
| N501Y | convalescent plasma escape | Pokay | B.1.1.351 variant constellation two-tailed Wilcoxon matched-pairs signed-rank test against 10 convalescent sera P | 2021 | Chen et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|--|
| N501Y | vaccine neutralization efficacy | Pokay | Study 3001 on Ad26.COV2.S (Janssen vaccine) conducted September 21, 2020 through January 22, 2021 overlaps the emergence and dominance of the B.1.351 lineage of SARS-CoV-2 in South Africa. The SA arms of the Phase 3 double blind study showed severe/critical disease VE of 73.1% (95% CI: 40.0-89.4), and moderate to severe/critical disease VE of 52.0% (95% CI: 30.3-67.4). Compare to 78.0% and 74.4% for North American arm of the study during the same period (with low B.1.351 prevalence). Of the 66.9% of SA severe infections that have been sequenced as of this report, 94.5% are B.1.351. | 2021 | UNKNOWN et al. (2021) |
| N501Y | vaccine neutralization efficacy | Pokay | The dominant circulating B.1.351 spike variant originating in RSA, which harbors E484K and additional substitutions in the RBD, NTD, and S2 and deletions in the NTD (amino acids 242–244), was neutralized with a 5.02-fold reduced titer | 2021 | Solfrosi et al. (2021) |
| N501Y | convalescent plasma escape | Pokay | B.1.1.351 in 19 convalescent human sera ~1mo post infection had mild to moderate resistance against all samples | 2021 | Chen et al. (2021) |
| N501Y | antibody epitope effects | Pokay | B.1.1.351 variant constellation ablates Class 1 receptor-binding-mot if targeting antibodies COV2-2050, 1B07, COVOX-384, and S2H58. B.1.1.351 variant constellation ablates Class 3 N-terminal domain targeting antibodies COV2-2489 and COV2-2676 (the only two tested). | 2021 | Chen et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|-----------------------------|---------------------|--|------------------|--|
| N501Y | convalescent plasma escape | Pokay | In a Syrian hamster model, B.1.351 variant virus had >4x reduction in YRNT90 (measure of neutralization) using wild type convalescent sera. PG: Note that exact sequence for B.1.351 used was not disclosed. | 2021 | Cochin et al. (2021) |
| N501Y | convalescent plasma escape | Pokay | In 13 plasma collected ~1mo after B.1.1.7 infection (nursing home in Ticino, Switzerland), neutralization reduced to undetectable levels in many plasma for B.1.351 pseudotyped virus, as well as WT and other VOCs. [paper does not detail the B.1.351 variants used, using the most popular as a stand in] | 2021 | McCallum et al. (2021) |
| N501Y | convalescent plasma binding | Pokay | VSV pseudotype B.1.351 showed 7.86-fold decrease in NT50 vs wild type in sera from 9 ICU patients undergoing treatment in Germany (pre-variant infections). | 2021 | Hoffman et al. (2021) |
| N501Y | antibody epitope effects | Pokay | Abrogates Bamlanivimab, Etesevimab, or their combined use neutralization as quantified by measuring virus-encoded luciferase activity in cell lysates at 16-18 h post transduction. | 2021 | Hoffman et al. (2021) |
| N501Y | convalescent plasma escape | Pokay | Approximately 6-fold reduction in 15 ICU patient convalescent plasma neutralization as quantified by measuring virus-encoded luciferase activity in cell lysates at 16-18 h post transduction. | 2021 | Hoffman et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|---------------------------------------|
| N501Y | vaccine neutralization efficacy | Pokay | Vaccine elicited antibodies neutralized virus with the B.1.351 spike protein had an average 3-fold reduction in titer (1:500), a titer that was still higher than the average titer with which convalescent sera neutralized D614G (1:139). Serum specimens from individuals vaccinated with the BNT162b2 mRNA vaccine neutralized D614G virus with titers that were on average 7-fold greater than convalescent sera. | 2021 | Tada et al. (2021) |
| N501Y | trafficking | Pokay | In one of eight cell lines tested (293T lung cells), a modest increase in cell entry was observed. | 2021 | Hoffman et al. (2021) |
| N501Y | vaccine neutralization efficacy | Pokay | Neutralizing antibody titers increased in previously infected vaccinees relative to uninfected vaccinees 6.5-fold against B.1.351 (contrast with 3.4 fold against original SARS-CoV-2). | 2021 | Leier et al. (2021) |
| N501Y | pharmaceutical effectiveness | Pokay | VSV pseudotype B.1.351 entry mediated by the S proteins of the B.1.351 variant was completely resistant to blocking by REGN10989 and Bamlanivimab. Entry driven by the S proteins of the B.1.351 was partially resistant against Casirivimab. | 2021 | Hoffman et al. (2021) |
| N501Y | vaccine neutralization efficacy | Pokay | B.1.351 pseudotyped lentivirus showed 3.4 and 3.8x reduction in IC50 serum dilution concentration for sera from BNT162b2 (Pfizer) or mRNA1273 (Moderna) vaccinees collected 28 days following booster dose. | 2021 | Zhou et al. (2021) |
| N501Y | vaccine neutralization efficacy | Pokay | VSV pseudotype B.1.351 showed 7.85-fold reduction in neutralization efficiency vs wild type in 15 Pfizer BNT162b2 vaccinee sera 13-15 days post second dose. Cell fusion proficiency was slight impaired. | 2021 | Hoffman et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|--|
| N501Y | vaccine neutralization efficacy | Pokay | After one dose, individuals with prior infection showed enhanced T cell immunity, antibody secreting memory B cell response to spike and neutralizing antibodies effective against B.1.351 (authentic cell culture supernatants). By comparison, HCW receiving one vaccine dose without prior infection showed reduced immunity against variants. B.1.351 spike mutations resulted in increased, abrogated or unchanged T cell responses depending on human leukocyte antigen (HLA) polymorphisms. Study was 26 each post-infection and post first dose HCWs. | 2021 | Reynolds et al. (2021) |
| N501Y | trafficking | Pokay | VSV pseudotype B.1.351 showed slight decrease in cell entry relative to wild type in 263T-ACE2 (kidney) cell line, and slight increase in Calu-3 (lung). Cell fusion proficiency was slight impaired. | 2021 | Hoffman et al. (2021) |
| N501Y | convalescent plasma binding | Pokay | We analyzed 34 convalescent samples including the WHONIBSC 20/130 reference serum, and, although a few sera showed near identical FRNT 50 values, the FRNT50 dilutions for the B.1.1.7 strain were 2.9-fold lower (geometric mean) than those for the Victoria strain ($p < 0.0001$). Sera from 13 subjects post-B.1.1.7 infection showed no significant change in neutralization against Victoria (~wild type), suggesting that B.1.1.7 infection also protects against ancestral virus. [Note that D1119H was included in the original paper, assuming typographical error and correcting to D1118H] | 2021 | Supasa et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|---|
| N501Y | vaccine neutralization efficacy | Pokay | In 15 Pfizer non-senior vaccinee sera collected 3-4 weeks post-booster [using Table S1, not the text that says 2-3 weeks], neutralization was reduced ~11x. | 2021 | Hoffman et al. (2021) |
| N501Y | vaccine neutralization efficacy | Pokay | In Qatar, where Pfizer vaccine use is prevalent (<10% of the population covered in the time period of the study ending Mar 31, 2021), any time after one dose (including the 2 weeks where no major effect is expected) B.1.351 lineage effectiveness was observed as 16.9% (95% CI [10.4,23.0]) against infection, and 0% against severe/critical/fatal disease (95% CI [0-19.0]). Two weeks or more after 2nd dose, effectiveness climbed to 75.0% [70.5,78.9] against infection, and 100% against severe/critical/fatal disease (95% CI [73.7,100]). | | UNKNOWN et al. () |
| N501Y | vaccine neutralization efficacy | Pokay | Sera from vaccinees [ChAdOx1 and BNT162b2 primarily used in UK] shows decreased ability to neutralize B.1.621 compared to first wave virus and Alpha, with a magnitude of change similar to Beta. | 2021 | UNKNOWN et al. (2021) |
| N501Y | vaccine efficacy | Pokay | In a 1:5 test-negative matched control study of 8153 individuals who received the Moderna mRNA-1273 vaccine, 69 test-positive were Mu. Two dose vaccine efficacy against Mu was 90.4% (73.9-96.5%), one dose VE was 45.8% (0.0-88.9%). | 2021 | Bruxvoort et al. (2021) |
| N501Y | vaccinee plasma binding | Pokay | Sera from individuals who have been vaccinated and have had subsequent recent Delta infection have a high level of neutralising activity against B.1.621. | 2021 | UNKNOWN et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|---------------------------------------|
| N501Y | convalescent plasma binding | Pokay | Sera from individuals who have been infected with Delta does not have strong neutralising activity against B.1.621 | 2021 | UNKNOWN et al. (2021) |
| N501Y | convalescent plasma binding | Pokay | In sera from six patients collected 1 to 12 weeks post-infection with B.1, antibody titer in a microneutralization assay was on average 71.46 for P.1 virus. Compare to much stronger neutralization titers for B.1.1.7 (256) and wild type (456.1) in the same sera. | 2021 | Luftig et al. (2021) |
| N501Y | vaccine neutralization efficacy | Pokay | Mean 7.6x reduction of NT50 value B.1.621 (Mu) relative to wild type in 8 sera from adult BNT162b2 vaccinees (28-47yo) collected ~1m post booster. [This is a greater reduction than Beta @ 6.3x] | 2021 | Uriu et al. (2021) |
| N501Y | vaccine neutralization efficacy | Pokay | Using live B.1.621 virus and a cytopathic effect-based assay, sera from 37 Pfizer/BioNTech BNT162b2 vaccinees collected 10-20 days post-booster showed significantly lower (95) but still 'robust' neutralization than against ancestral B.1 virus (107). | 2021 | Messali et al. (2021) |
| N501Y | convalescent plasma escape | Pokay | Mean 12.4x reduction of NT50 value B.1.621 (Mu) relative to wild type in 8 sera from older convalescent patients (52-92yo) collected 1-3m post symptom onset. [This is a greater reduction than Beta @ 8.2x] | 2021 | Uriu et al. (2021) |
| N501Y | vaccinee plasma binding | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, XD (from) were 1.5x-fold lower (95% CI: 0.05x-0.07x) than against 208-428 972-1834 4.3-4.7 US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|---------------------------------------|
| N501Y | vaccine neutralization efficacy | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, XD (from) were 4.4-fold lower (95% CI: 4.3x-4.7x) than against 208-428 972-1834 4.3-4.7 US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| N501Y | ACE2 receptor binding affinity | Pokay | The hACE2-binding affinity of XBB.1.5 RBD has a dissociation constant KD of 3.4 nM, where S486P is the distinguishing Spike mutation vs parent XBB.1 RBD with a much weaker KD (19 nM), as measured by surface plasmon resonance (SPR) assays. | 2023 | Yue et al. (2023) |
| N501Y | vaccine efficacy | Pokay | In a study of 481 vaccinees going from lowest to highest infection rate, 2 doses of CoronaVac and 1 dose of BNT162b2 had the lowest infection rate at 6.3%, then it was 3 doses of BNT162b2 having a infection rate of 16.6%. 2 and 3 doses of CoronaVac had 48.6% and 20.6% infection rate respectively. 2 doses of BNT162b2 has the highest infection rate at 49.2%. | 2022 | Zhou et al. (2022) |
| N501Y | vaccine neutralization efficacy | Pokay | 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 ~1/300. | 2021 | Wu et al. (2021) |
| N501Y | convalescent plasma escape | Pokay | 27% of 44 early pandemic exposure convalescent plasma/sera lose all activity against a RBD triple mutant pseudovirus (RBD mutants of the 501Y.V2 'South African' lineage), while only 23% retained high titres | 2021 | Wibmer et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|---|
| N501Y | viral load | Pokay | B.1.351 and P.1 samples showed average Ct cycle threshold of 22.2 vs 23 for wildtype (i.e. ~60% higher viral load) comparing 3360 and 22535 samples respectively. | 2021 | Roquebert et al. (2021) |
| N501Y | pharmaceutical effectiveness | Pokay | This mutated version of RBD completely abolishes the binding to a therapeutic antibody, Bamlanivimab, in vitro. | 2021 | Liu et al. (2021) |
| N501Y | antibody epitope effects | Pokay | Ablates Class 1 receptor-binding-mot if targeting antibodies COV2-2050, 1B07, COVOX-384, and S2H58. | 2021 | Chen et al. (2021) |
| N501Y | vaccine neutralization efficacy | Pokay | 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 ~2x) decrease in neutralization by vaccine plasma was observed. | 2021 | Wang et al. (2021) |
| N501Y | ACE2 receptor binding affinity | Pokay | 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. | 2021 | Barton et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|------------------------------|---------------------|--|------------------|---|
| N501Y | antibody epitope effects | Pokay | 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 | 2021 | Wibmer et al. (2021) |
| N501Y | convalescent plasma escape | Pokay | In 19 convalescent human sera ~1mo post infection had mild to moderate resistance against most samples | 2021 | Chen et al. (2021) |
| N501Y | pharmaceutical effectiveness | Pokay | Tixagevimab, Regdanvimab and COR-101 display reduced binding affinity to virus pseudotyped as RBD from B.1.351. | 2021 | Engelhart et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|--|
| N501Y | ACE2 receptor binding affinity | Pokay | This combination showed ~3x 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 | 2021 | Collier et al. (2021) |
| N501Y | vaccine neutralization efficacy | Pokay | 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. | 2021 | Bates et al. (2021) |
| N501Y | antibody epitope effects | Pokay | 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. | 2021 | Sun et al. (2021) |
| N501Y | ACE2 receptor binding affinity | Pokay | Using Microscale Thermophoresis, 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). | 2021 | Ramanathan et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|--------------------------------|---------------------|---|------------------|--|
| N501Y | ACE2 receptor binding affinity | Pokay | 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. | 2021 | Laffeber et al. (2021) |
| N501Y | viral load | Pokay | The 62 B.1.351 (a.k.a. N501Y.V2) variant cases in three Paris hospital labs had a ~2-fold viral load increase (~1 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). | 2021 | Teyssou et al. (2021) |
| N501Y | ACE2 receptor binding affinity | Pokay | Reported slight increase in affinity compared to wild-type RBD on the cell surface (Kd | 2021 | Tian et al. (2021) |
| N501Y | ACE2 receptor binding affinity | Pokay | 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. | 2021 | Liu et al. (2021) |
| N501Y | ACE2 receptor binding affinity | Pokay | 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. | 2021 | Vogel et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|----------------------------|---------------------|--|------------------|---|
| N501Y | trafficking | Pokay | 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. | 2021 | Hu et al. (2021) |
| N501Y | transmissibility | Pokay | 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. | 2021 | Roquebert et al. (2021) |
| N501Y | transmissibility | Pokay | 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. | 2021 | Pearson et al. (2021) |
| N501Y | convalescent plasma escape | Pokay | Average ~10-fold reduction in neutralization efficacy in convalescent sera of 16 health workers infected in Spring 2020. | 2021 | Alenquer et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|---------------------------------------|
| N501Y | vaccine neutralization efficacy | Pokay | 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 ~2000 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). | 2021 | Madhi et al. (2021) |
| N501Y | convalescent plasma escape | Pokay | Neutralizing antibody titers of 18 samples (90%) decreased against this B.1.351 pseudotyped virus below an ID50 threshold of 40 (sera collected ~8mo post Jan 2020 first wave in China). | 2021 | Hu et al. (2021) |
| N501Y | antibody epitope effects | Pokay | Abolished neutralization by mAbs CQ026 and CQ038, greatly diminished neutralization by CQ012 and CQ046. | 2021 | Hu et al. (2021) |
| N501Y | vaccine neutralization efficacy | Pokay | This variant of key B.1.351 lineage mutations showed ~10x decrease in Pfizer sera (3 weeks post-first dose: n | 2021 | Kuzmina et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|---|
| N501Y | pharmaceutical effectiveness | Pokay | Trachea viral loads were tested by qRT-PCR and RNA scope at 3 dpi on 5 8-month-old male mice and there was a ~750x fold drop in the R3P1-E4 antibody in comparison to the IgG control. | 2022 | Li et al. (2022) |
| N501Y | pharmaceutical effectiveness | Pokay | Lung viral loads were tested by qRT-PCR and RNA scope at 3 dpi on 5 8-month-old male mice and there was a ~2266x fold drop in the R3P1-E4 antibody in comparison to the IgG control. | 2022 | Li et al. (2022) |
| N501Y | pharmaceutical effectiveness | Pokay | 100% of the 5 8-month-old male R3P1-E4 antibody treated mice survived 14 days after infection while only 60% the control group mice survived 5 days post infection. | 2022 | Li et al. (2022) |
| N501Y | trafficking | Pokay | ~5x 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] | 2021 | Kim et al. (2021) |
| N501Y | vaccine neutralization efficacy | Pokay | This variant showed >5x decrease in Pfizer sera (3 weeks post-first dose: n | 2021 | Kuzmina et al. (2021) |
| N501Y | trafficking | Pokay | ~9x more infectivity than D614G alone in HEK293T-ACE2 cells 48h post-transduction (no synergy as level approx. that of N501Y alone). | 2021 | Kuzmina et al. (2021) |
| N501Y | pharmaceutical effectiveness | Pokay | Tixagevimab, Regdanvimab and COR-101 display reduced binding affinity to virus pseudotyped as RBD from P.1. | 2021 | Engelhart et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|---|
| N501Y | ACE2 receptor binding affinity | Pokay | The affinity of the P.1 RBD variants for ACE2 increased by 5.3 fold as measured by surface plasmon resonance relative to wild type RBD by increasing the k(on) and decreasing the k(off) rate constants. | 2021 | Barton et al. (2021) |
| N501Y | ACE2 receptor binding affinity | Pokay | The KD for the pseudotyped P.1-ACE2 interaction is 4.8 nM, showing that binding to P.1 is essentially indistinguishable from B.1.351 (4.0 nM), which binds with ~19x greater affinity than wild type. | 2021 | Dejnirattisai et al. (2021) |
| N501Y | vaccine neutralization efficacy | Pokay | The presence of these B.1.417/B.1.429 defining variants in 189 post-mRNA-vaccination COVID-19 cases was proportionally in line with lineage prevalence in Northern California during the study period, suggesting no effect of these variants on immune escape. | 2021 | Jacobson et al. (2021) |
| N501Y | antibody epitope effects | Pokay | Pseudotype for Day 152 virus from a chronically infected patient, neutralizing activity of purified IgG from 3 donors was mostly unaffected by the single mutations (Q493K/R or N439K), but the day 152 S pseudotype was resistant to neutralization. | 2021 | Clark et al. (2021) |
| N501Y | pharmaceutical effectiveness | Pokay | This Spike pseudotype for Day 152 virus from a chronically infected patient was completely resistant to REGN10933. | 2021 | Clark et al. (2021) |
| N501Y | antibody epitope effects | Pokay | Pseudotype for Day 152 virus from a chronically infected patient: although mAb C1A-B12 had no activity against this pseudotype, all three affinity optimized versions were active: the antibody containing the most mutations, C1A-B12.3, was the most potent (IC50 <0.5 µg/mL). | 2021 | Clark et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|--------------------------------|---------------------|--|------------------|---------------------------------------|
| N501Y | pharmaceutical effectiveness | Pokay | 3rd exposure to antigen by Delta (B.1.617.2) (n | 2022 | Wang et al. (2022) |
| N501Y | vaccine efficacy | Pokay | In sera from 17 sero-positive blood donors, and 18 months post-infection (May 2020) sera from 17 health care workers in Sweden, a 40x drop in neutralization by Omicron (B.1.1.529) pseudotyped lentivirus was observed in HEK293T cells using the First WHO International Standard (20/136). Median IC50 reduction was ~6x for the blood donors, and ~4.5x for the health care workers. | 2021 | Sheward et al. (2021) |
| N501Y | vaccine efficacy | Pokay | In a Belgian study including 1,433,135 persons (vaccinated between July 2021 to April 2022) infection-acquired immunity offered additional protection against symptomatic infection with Omicron in vaccinated persons compared to those without previous infection, when the infection was up to one year previous. | 2022 | Braeye et al. (2022) |
| N501Y | vaccine efficacy | Pokay | Pseudotyped virus neutralization demonstrated that Bi-Nab35B5-47D1 0 can efficiently neutralize VBMs including Alpha (B.1.1.7), Beta (B.1.351) and Kappa (B.1.617.1) and VOCs including Delta (B.1.617.2). | 2022 | Yuan et al. (2022) |
| N501Y | ACE2 receptor binding affinity | Pokay | Using molecular dynamics simulation, ACE2-RBD (Omicron) complex is destabilized by the E484A and Y505H mutations and stabilized by S477N and N501Y mutations. | 2022 | Zhang et al. (2022) |
| N501Y | trafficking | Pokay | ~13x more infective as D614G alone in HEK293T-ACE2 cells 48h post-transduction. | 2021 | Kuzmina et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|--|
| N501Y | ACE2 receptor binding affinity | Pokay | Y501 makes a pi interaction with Y41 and places R498 to make a hydrogen bond and salt bridge to Q42 and D38 of ACE2, forming a strong network of new interactions supporting the impact of these residues on affinity. Q498R alone appears to decrease ACE2 binding. The synergism of Q498R with N501Y (and E484K) increases ACE2 binding by ~50- fold relative to WT. | 2021 | Zahradnik et al. (2021) |
| N501Y | vaccine neutralization efficacy | Pokay | Log10ID50 of Omicron neutralizing antibodies is 0.686x the WT 1 month post-third dose of pfizer-BioNTech BNT162b2 in 13 Kidney transplant recipients (KTR) with median age of 55.5. | 2022 | McEvoy C et al. (2022) |
| N501Y | pharmaceutical effectiveness | Pokay | Omicron BA.4 have higher sensitivity to inhibition by soluble angiotensin converting enzyme 2 (ACE2) and the endosomal inhibitor chloroquine compared to D614G | 2022 | Neerukonda et al. (2022) |
| N501Y | viral load | Pokay | Viral load from lung tissue from 11 hamsters in 10 treatments for Omicron MK-4482 had the greatest drop 3 days post-infection determined by quantitative RT-PCR targeting sgE in comparison to Alpha MK-4482, Beta MK-4482 and Delta MK-4482. | 2022 | Rosenke et al. (2022) |
| N501Y | antibody epitope effects | Pokay | Ablates Class 1 receptor-binding-mot if targeting antibodies COV2-2050, 1B07, COVOX-384, and S2H58. Ablates Class 3 N-terminal domain targeting antibody COV2-2489, diminishes COV2-2676. | 2021 | Chen et al. (2021) |
| N501Y | pharmaceutical effectiveness | Pokay | Trimeric proteins FSR22 had a 0.0015x fold change in IC50 in B.1.1.529 Omicron | 2022 | Chonira et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|--|
| N501Y | pharmaceutical effectiveness | Pokay | Omicron BA.5 have higher sensitivity to inhibition by soluble angiotensin converting enzyme 2 (ACE2) and the endosomal inhibitor chloroquine compared to D614G | 2022 | Neerukonda et al. (2022) |
| N501Y | vaccine neutralization efficacy | Pokay | 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. | 2021 | Xie et al. (2021) |
| N501Y | vaccine neutralization efficacy | Pokay | 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 | 2021 | Chen et al. (2021) |
| N501Y | vaccinee plasma binding | Pokay | Out of 10 individuals with 2 doses of the BNT162b2/BNT162b2 vaccine, neutralizing titer in Omicron was ~100x folds more significant in 3 individuals. | 2022 | Arora et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|--|
| N501Y | vaccine neutralization efficacy | Pokay | Values taken 28 days after booster dose was given for BBIBP-CorV vaccine to 390 participants with 130 participants in the 0-14d-10m, 0-21d-10m and 0-28d-10m group. The geometric mean titers (GMT) of neutralizing antibody in 0-28d-10m and 0-21d-10m group were significantly higher than 0-14d-10m group at month 3, month 6 and month 10 after the second dose. A sharply decrease by 4.85-fold (GMT: 94.4-20.3), 4.67-fold (GMT: 134.4-28.8) and 4.49-fold (GMT: 145.5-32.4) was observed from day 28 to month 10 after the second dose in 0-14d-10m, 0-21d-10m and 0-28d-10m group, respectively, and they had similar decline kinetics. | 2022 | Yao T et al. (2022) |
| N501Y | vaccinee plasma binding | Pokay | Out of 10 individuals with 3 doses of the BNT162b2/BNT162b2/BNT162b2 vaccine, neutralizing titer in Omicron was ~17.5x folds more significant in 9 individuals. | 2022 | Arora et al. (2022) |
| N501Y | vaccine neutralization efficacy | Pokay | Omicron BA.4 neutralization of the Omicron variants by antibodies induced by three doses of Pfizer/BNT162b2 mRNA vaccine was 7-8-fold less potent than the D614G, and the Omicron variants still evade neutralization more efficiently. | 2022 | Neerukonda et al. (2022) |
| N501Y | vaccine neutralization efficacy | Pokay | Omicron BA.5 neutralization of the Omicron variants by antibodies induced by three doses of Pfizer/BNT162b2 mRNA vaccine was 7-8-fold less potent than the D614G, and the Omicron variants still evade neutralization more efficiently. | 2022 | Neerukonda et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|--|
| N501Y | vaccine efficacy | Pokay | Protection against symptomatic infection caused by Beta/Gamma (assumed by combined presence of N501Y and E484K) was also higher with partial vaccination for mRNA-1273 (77%) than BNT162b2 (60%) and ChAdOx1 (48%), and full vaccination increased effectiveness for BNT162b2 (84%). | 2021 | Nasreen et al. (2021) |
| N501Y | pharmaceutical effectiveness | Pokay | Infectious viral titers in lung tissue determined using a tissue culture infectious dose (TCID) assay in 10 hamsters showed that Omicron Molnupiravir (MK-4482) had no statistically significant change. | 2022 | Rosenke et al. (2022) |
| N501Y | vaccine neutralization efficacy | Pokay | Log10ID50 of Omicron neutralizing antibodies is 0.722x the WT pre-third dose of pfizer-BioNTech BNT162b2 in 13 Kidney transplant recipients (KTR) with median age of 55.5. | 2022 | McEvoy C et al. (2022) |
| N501Y | viral load | Pokay | Viral load from oral swabs from 11 hamsters in 10 treatments for Omicron MK-4482 had the greatest drop 3 days post-infection determined by quantitative RT-PCR targeting sgE in comparison to Alpha MK-4482, Beta MK-4482 and Delta MK-4482. | 2022 | Rosenke et al. (2022) |
| N501Y | pharmaceutical effectiveness | Pokay | Trimeric proteins FSR16m had a 0.025x fold change in IC50 in B.1.1.529 Omicron | 2022 | Chonira et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|--------------------------------|---------------------|--|------------------|---------------------------------------|
| N501Y | ACE2 receptor binding affinity | Pokay | In the case of VOC B.1.1.7+E484K, the addition of the E484K mutation to N501Y further increased the affinity, to ~15 fold higher than WT RBD (KD ~5 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. | 2021 | Barton et al. (2021) |
| N501Y | convalescent plasma escape | Pokay | In 19 convalescent human sera ~1mo post infection had mild to moderate resistance against all samples. | 2021 | Chen et al. (2021) |
| N501Y | syncytium formation | Pokay | ~50% Vero cell-cell membrane fusion assay under infection with VSV pseudotyped virus relative to wild type, significantly higher than D614G. | 2021 | Kim et al. (2021) |
| N501Y | trafficking | Pokay | ~12x more infectivity than D614G alone in HEK293T-ACE2 cells 48h post-transduction (~additive effects of 501 and 484). | 2021 | Kuzmina et al. (2021) |
| N501Y | trafficking | Pokay | ~6x 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] | 2021 | Kim et al. (2021) |
| N501Y | trafficking | Pokay | More efficient infectivity (24h) compared to wild type, in Caco-2 cells ~11x, Vero ~10x, and Calu-3 ~11x. Compare to wild type at ~5x across cell types. | 2021 | Kim et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|--------------------------------|---------------------|---|------------------|--|
| N501Y | antibody epitope effects | Pokay | Pseudotype for Day 146 virus from a chronically infected patient, neutralizing activity of purified IgG from 3 donors was mostly unaffected by the single mutations (Q493K/R or N439K), but the day 146 S pseudotype was resistant to neutralization. | 2021 | Clark et al. (2021) |
| N501Y | antibody epitope effects | Pokay | Pseudotype for Day 146 virus from a chronically infected patient: resistant to neutralization by mAb C1A-B12, and was still resistant to the affinity enhanced antibodies derived from it (i.e. no affinity maturation effect on neutralization). | 2021 | Clark et al. (2021) |
| N501Y | pharmaceutical effectiveness | Pokay | This Spike pseudotype for Day 146 virus from a chronically infected patient was completely resistant to REGN10933. The variant had a 4-fold decrease in REGN10987 neutralization sensitivity (2nd component of the Regeneron mAb cocktail). | 2021 | Clark et al. (2021) |
| N501Y | ACE2 receptor binding affinity | Pokay | Y501 makes a pi interaction with Y41 and places R498 to make a hydrogen bond and salt bridge to Q42 and D38 of ACE2, forming a strong network of new interactions supporting the impact of these residues on affinity. Q498R alone appears to decrease ACE2 binding. The synergism of Q498R with N501Y (and E484K) increases ACE2 binding by ~50- fold relative to WT. The extent of affinity increase with Q498R and N501Y is not exactly quantified, as E484K always emerged with this duo during in vitro evolution. | 2021 | Zahradnik et al. (2021) |
| N501Y | ACE2 receptor binding affinity | Pokay | Using Microscale Thermophoresis, this variant binds ACE2 at nearly two-fold greater affinity than the original SARS-COV-2 RBD (203.7 nM vs 402.5 nM). | 2021 | Ramanathan et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|-----------------------------------|---------------------|---|------------------|--|
| N501Y | trafficking | Pokay | Decreased stability of RBD expression in yeast, suggesting decreased Spike protein stability. | 2021 | Motozono et al. (2021) |
| N501Y | ACE2 receptor binding affinity | Pokay | 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. | 2021 | Zhu et al. (2021) |
| N501Y | virion structure | Pokay | Estimated free energy change (ddG) for this variant is 0.69 kcal/mol (i.e. stabilizing relative to wild type) | 2021 | Spratt et al. (2021) |
| N501Y | ACE2 receptor binding affinity | Pokay | Reported 4-fold increase in affinity compared to wild-type RBD on the cell surface (Kd | 2021 | Tian et al. (2021) |
| N501Y | environmental condition stability | Pokay | Relative to D614G, this mutation demonstrated significant increase in infectivity (i.e. heat stability) after incubation at 50C after 30 minutes or 1 hour | 2021 | Tada et al. (2021) |
| N501Y | ACE2 receptor binding affinity | Pokay | Experimentally, ACE2 binding affinity increased 0.24 fold | 2020 | Starr et al. (2020) |
| N501Y | antibody epitope effects | Pokay | Utilizing shark derived vnarodies, S375F mutation on Omicron RBD disrupts the structure of β -strand, which inhibits binding with 20G6. 20G6 binds to a hidden epitope on RBD which is highly conserved in sarbecoviruses. | 2022 | Feng et al. (2022) |
| N501Y | ACE2 receptor binding affinity | Pokay | 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 affinity is observed. | 2021 | Tada et al. (2021) |
| N501Y | ACE2 receptor binding affinity | Pokay | ~4-fold increase in binding affinity vs wild type. | 2021 | Motozono et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|--------------------------------|---------------------|--|------------------|---|
| N501Y | ACE2 receptor binding affinity | Pokay | 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. | 2021 | UNKNOWN et al. (2021) |
| N501Y | ACE2 receptor binding affinity | Pokay | Reported 10-fold increase in ACE2 binding vs wildtype (Kd | 2021 | Liu et al. (2021) |
| N501Y | ACE2 receptor binding affinity | Pokay | 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 | 2021 | Zahradnik et al. (2021) |
| N501Y | ACE2 receptor binding affinity | Pokay | 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. | 2021 | Gamez et al. (2021) |
| N501Y | convalescent plasma binding | Pokay | Viruses containing the point mutations of B.1.1.7 showed that the single point mutations (Δ 69-70 and N501Y) were neutralized as efficiently as D614G across 10 convalescent sera from April 2020 infectees. | 2021 | Tada et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|------------------------------|---------------------|---|------------------|--|
| N501Y | convalescent plasma binding | Pokay | In 30 samples collected 111 to 260 days post onset of symptoms, the convalescent plasma can neutralize both the reference USA-WA1/2020 strain and the mouse adapted strain that contains the N501Y spike mutation with similar efficiency. | 2021 | Rathnasinghe et al. (2021) |
| N501Y | pharmaceutical effectiveness | Pokay | COR-101 lost ~8x binding against this isolated mutation. Regdanvimab lost ~6x binding against this isolated mutation. | 2021 | Engelhart et al. (2021) |
| N501Y | antibody epitope effects | Pokay | 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. | 2021 | Haynes et al. (2021) |
| N501Y | antibody epitope effects | Pokay | 4 antibodies tested were less potent against K417N by ten-fold or more, in both mAb classes 1 and 3 | 2021 | Wang et al. (2021) |
| N501Y | antibody epitope effects | Pokay | Reduction in neutralization by mAbs COVA1-18 (~4x), COVA2-15 (~9x), S309 (~3x) | 2021 | Shen et al. (2021) |
| N501Y | antibody epitope effects | Pokay | 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. | 2021 | Rees-Spear et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|-------------------------------------|---------------------|--|------------------|---------------------------------------|
| N501Y | immunosuppression variant emergence | Pokay | Appeared (day 128) and persisted in chronic (152 day) SARS-CoV-2 infection of immunocompromised patient with severe antiphospholipid syndrome | 2020 | Choi et al. (2020) |
| N501Y | convalescent plasma escape | Pokay | 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. | 2021 | Kuzmina et al. (2021) |
| N501Y | trafficking | Pokay | This mutation alone accounts for most of the increased infectivity of the Alpha variant, as determined by modelling the infectivity of each Spike mutation independently in a competitive infection model of hamsters, and Vero E6 (NHP) and Calu-3 (human) cell lines. | 2021 | Liu et al. (2021) |
| N501Y | convalescent plasma escape | Pokay | 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. | 2021 | Tang et al. (2021) |
| N501Y | ACE2 receptor binding affinity | Pokay | The N501Y mutation had the biggest effect on ACE2 affinity of any VOC mutation tested, increasing the affinity ~10 fold to KD ~7 nM, by increasing the k(on) ~1.8 fold and decreasing the k(off) by ~ 7 fold as measured by surface plasmon resonance. | 2021 | Barton et al. (2021) |
| N501Y | vaccine efficacy | Pokay | In this Canadian test-negative study of 324033 individuals, two doses of either mRNA vaccine (BNT162b2 (Pfizer-BioNTech) or mRNA-1273 (Moderna)) was not associated with appreciable vaccine escape by lineage Alpha [defined here as N501Y positive, but E484K negative]. | 2021 | Chung et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|--|
| N501Y | T cell evasion | Pokay | 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 | 2021 | Reynolds et al. (2021) |
| N501Y | vaccine neutralization efficacy | Pokay | 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. | 2021 | Edara et al. (2021) |
| N501Y | vaccine neutralization efficacy | Pokay | 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. | 2021 | Wang et al. (2021) |
| N501Y | vaccine neutralization efficacy | Pokay | The presence of this variant in 189 post-mRNA-vaccination COVID-19 cases was proportionally in line with lineage prevalence in Northern California during the study period, suggesting no effect of these variants on immune escape. | 2021 | Jacobson et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|--|
| N501Y | vaccine neutralization efficacy | Pokay | 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. | 2021 | Rathnasinghe et al. (2021) |
| N501Y | antibody epitope effects | Pokay | 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. | 2021 | Klegerman et al. (2021) |
| N501Y | trafficking | Pokay | 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 independently evaluated and N501 is in both lineages, a significant decrease was observed, therefore the error bars described in this paper should be interpreted carefully] | 2021 | Tada et al. (2021) |
| N501Y | vaccine neutralization efficacy | Pokay | 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. | 2021 | Bates et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---|---------------------|---|------------------|---|
| N501Y | homoplasy | Pokay | 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). | 2021 | Flores-Alanis et al. (2021) |
| N501Y | monoclonal antibody serial passage escape | Pokay | In vitro selection against class 1 (Spike 'up' conformation) monoclonal antibody C663, and to a lesser extent C613. | 2021 | Wang et al. (2021) |
| N501Y | antibody epitope effects | Pokay | Of 50 mAbs tested, major loss of neutralization observed for S2X128, S2D8, S2X192, S2D19, S2H14, S2H19. | 2021 | Collier et al. (2021) |
| N501Y | pharmaceutical effectiveness | Pokay | COR-101 lost ~20x binding against this double mutation. Estesevimab lost ~16x binding against this double mutation. Regdanvimab lost ~6x binding against this double mutation. M396 lost ~10x binding against this double mutation. | 2021 | Engelhart et al. (2021) |
| N501Y | vaccine neutralization efficacy | Pokay | In post-vaccination sera from individuals who received one (3 weeks post-first dose: n | 2021 | Kuzmina et al. (2021) |
| N501Y | convalescent plasma escape | Pokay | ~7x 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. | 2021 | Kuzmina et al. (2021) |
| N501Y | pharmaceutical effectiveness | Pokay | Bamlanivimab (LY-CoV555) lost ~64x binding against this double mutation. COR-101 lost ~50x binding against this double mutation. Casirivimab lost ~250x binding against this double mutation. Estesevimab lost ~16x binding against this double mutation. Regdanvimab lost ~32x binding against this double mutation. Tixagevimab lost ~10x binding against this double mutation. | 2021 | Engelhart et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|---------------------------------------|
| N501Y | reinfection | Pokay | Partial sequencing of S gene reveals two cases of probable early 2021 B.1.1.7 lineage reinfection from non-B.1.1.7 original cases in Lombardy, with 45 to 90 days between infections (less than the typical 90 day guideline for this call). Patients were 56 and 58yo, immunocompetent, with one a former smoker with obesity and dyslipidemia. One case required intubation during first infection, but presented with mild symptoms upon reinfection. The other case convalesced at home during the first episode, but required CPAP support in the subacute clinical unit upon reinfection. | 2021 | Novazzi et al. (2021) |
| N501Y | vaccine neutralization efficacy | Pokay | This variant showed no change in Pfizer sera (one or two dose) neutralization efficiency vs D614G (using lentivirus pseudotype). | 2021 | Kuzmina et al. (2021) |
| N501Y | syncytium formation | Pokay | Slight increase in Vero cell-cell membrane fusion assay under infection with VSV pseudotyped virus relative to wild type, no change relative to D614G. | 2021 | Kim et al. (2021) |
| N501Y | trafficking | Pokay | More efficient infectivity (24h) compared to wild type, in Caco-2 cells ~13x, Vero ~10x, and Calu-3 ~10x. Compare to wild type at ~5x across cell types. | 2021 | Kim et al. (2021) |
| N501Y | trafficking | Pokay | ~4x 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). | 2021 | Kim et al. (2021) |
| N501Y | trafficking | Pokay | 9x more infectivity than D614G alone in HEK293T-ACE2 cells 48h post-transduction. | 2021 | Kuzmina et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|--------------------------------|---------------------|---|------------------|--|
| N501Y | trafficking | Pokay | More efficient infectivity (24h) compared to wild type, in Caco-2 cells ~9x, Vero ~8x, and Calu-3 ~8x. Compare to wild type at ~5x across cell types. | 2021 | Kim et al. (2021) |
| N501Y | trafficking | Pokay | Lentiviral pseudotyped with the key mutations from COH.20G/677H lineage was tested on ACE2.293T cells. Luciferase activity was measured two days postinfection, showing no significant change in infection rate amongst the cells, suggesting that this mutation does not contributing to cell entry fitness. | 2021 | Tada et al. (2021) |
| N501Y | convalescent plasma binding | Pokay | Lentiviral pseudotyped with the key mutations from COH.20G/677H ('Ohio') lineage was neutralized similarly to D614G in 10 convalescent sera from April 2020 infectees. | 2021 | Tada et al. (2021) |
| N501Y | ACE2 receptor binding affinity | Pokay | Lentiviral pseudotyped with the key mutations from COH.20G/677H lineage was tested on ACE2.293T cells for ACE2 affinity changes vs D614G alone, showing a ~70% drop in IC50 (i.e. increased affinity). | 2021 | Tada et al. (2021) |
| N501Y | anthropozoonotic events | Pokay | Mouse-adapted SARS-CoV-2 mutations after 11 serial passages in various immunocompromised mice strains. | 2021 | Rathnasinghe et al. (2021) |
| N501Y | convalescent plasma binding | Pokay | This variant combination (representing P.1 aka Gamma) showed a 1.3x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset. | 2021 | Gong et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|--------------------------------|---------------------|---|------------------|------------------------------------|
| N501Y | vaccinee plasma binding | Pokay | This variant combination (representing P.1 aka Gamma) showed a 1.14x decrease in Spike binding (relative to D614G alone) by 5 plasma 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in previously non-seroconverted subjects. 1.27x 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. | 2021 | Gong et al. (2021) |
| N501Y | ACE2 receptor binding affinity | Pokay | Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant combination (representing P.1 aka Gamma) showed a 4.24x increase in binding (KD) relative to D614G. | 2021 | Gong et al. (2021) |
| N501Y | convalescent plasma binding | Pokay | This variant combination (representing B.1.351 aka Beta) showed a 1.04x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset, in contrast to the largely positive binding values for each individual mutation that comprises the set. | 2021 | Gong et al. (2021) |
| N501Y | ACE2 receptor binding affinity | Pokay | Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant combination (representing B.1.351 aka Beta) showed a 3.56x increase in binding (KD) relative to D614G. | 2021 | Gong et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|--------------------------------|---------------------|---|------------------|------------------------------------|
| N501Y | vaccinee plasma binding | Pokay | This variant combination (representing B.1.351 aka Beta) showed a 1.28x 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. It shows a 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 post-infection vaccinees. | 2021 | Gong et al. (2021) |
| N501Y | ACE2 receptor binding affinity | Pokay | Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant combination (representing B.1.1.7 aka Alpha) had 5.43x increased binding relative to D614G alone. | 2021 | Gong et al. (2021) |
| N501Y | convalescent plasma binding | Pokay | This variant combination (representing B.1.1.7 aka Alpha) showed a 1.15x increase in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset. | 2021 | Gong et al. (2021) |
| N501Y | vaccinee plasma binding | Pokay | This variant combination (representing B.1.1.7 aka Alpha) showed no change in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in previously non-seroconverted subjects. 1.28x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in post-infection vaccinees. | 2021 | Gong et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|--------------------------------|---------------------|---|------------------|--|
| N501Y | ACE2 receptor binding affinity | Pokay | 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). | 2021 | Gong et al. (2021) |
| N501Y | convalescent plasma binding | Pokay | 1.65x increase in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset. | 2021 | Gong et al. (2021) |
| N501Y | vaccinee plasma binding | Pokay | 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. | 2021 | Gong et al. (2021) |
| Y505H | pharmaceutical effectiveness | Pokay | Omicron BA.2 have higher sensitivity to inhibition by soluble angiotensin converting enzyme 2 (ACE2) and the endosomal inhibitor chloroquine compared to D614G | 2022 | Neerukonda et al. (2022) |
| Y505H | antibody epitope effects | Pokay | Neutralization of the bsAbs Bi-Nab35B5-47D10. Omicron BA.2 has an IC50 fold change of 0.07x. | 2022 | Yuan et al. (2022) |
| Y505H | antibody epitope effects | Pokay | Neutralization of the bsAbs 35B5. Omicron BA.2 has an IC50 fold change of 0.09x. | 2022 | Yuan et al. (2022) |
| Y505H | antibody epitope effects | Pokay | Neutralization of the bsAbs 47D10. Omicron BA.2 has an IC50 fold change of 0.08x. | 2022 | Yuan et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|--|
| Y505H | antibody epitope effects | Pokay | Neutralization of the bsAbs Bi-Nab47D10-35B5. Omicron BA.2 has an IC50 fold change of 0.04x. | 2022 | Yuan et al. (2022) |
| Y505H | vaccine neutralization efficacy | Pokay | Omicron BA.2 neutralization of the Omicron variants by antibodies induced by three doses of Pfizer/BNT162b2 mRNA vaccine was 7-8-fold less potent than the D614G, and the Omicron variants still evade neutralization more efficiently. | 2022 | Neerukonda et al. (2022) |
| Y505H | antibody epitope effects | Pokay | BnAb 002-S21F2 IC50 on the Omicron BA.2 variant is 0.8x fold the wildtype. | 2022 | Kumar et al. (2022) |
| Y505H | vaccinee plasma binding | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.2 (from South Africa/CERI-KRISP-K03 2307/2021) were 3.9x-fold lower (95% CI: 0.14x-0.17x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| Y505H | ACE2 receptor binding affinity | Pokay | L27, V34 and E90 mutation resulted in ultrahigh affinity binding of the LVE-ACE-2 domain to the widest variety of VOCs, with KDs of 78fM for binding to the Omicron BA.2. Values were obtained with LVE-ACE-2/mAB chimeras containing the Y-T-E sequence that enhances binding to the FcRn receptor, which in turn is expected to extend biological half-life 3-4-fold. | 2022 | Uhal B et al. (2022) |
| Y505H | vaccine neutralization efficacy | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.2 (from South Africa/CERI-KRISP-K03 2307/2021) were 4.5-fold lower (95% CI: 4.3x-4.7x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|--|
| Y505H | vaccine neutralization efficacy | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.2.12.1 (from USA/NY-CDC-ASC2 10722700/2022) were 4.2-fold lower (95% CI: 5.8x-6.6x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| Y505H | vaccinee plasma binding | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.2.12.1 (from USA/NY-CDC-ASC2 10722700/2022) were 3.9x-fold lower (95% CI: 0.14x-0.18x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| Y505H | pharmaceutical effectiveness | Pokay | Omicron (a.k.a. B.1.1.529) Spike pseudotyped VSV and Vero E6 cells has somewhat reduced neutralization (2.7x) vs wild type with monoclonal antibody Sotrovimab (a.k.a. VIR-7831). [delins at 214 omitted for syntax compatibility] | 2021 | Cathcart et al. (2021) |
| Y505H | vaccine neutralization efficacy | Pokay | Omicron breakthrough infection after 3-dose vaccination resulted in a further 3.5-fold and 2.9-fold increase of Omicron BA.1 and BA.2 neutralizing titers. Omicron BA.4/5 showed the highest neutralization resistance of all variants tested, resulting in low geometric mean neutralizing titers in plasma samples obtained after the second vaccine dose (NT50 | 2022 | Wang et al. (2022) |
| Y505H | antibody epitope effects | Pokay | Neutralization of the bsAbs Bi-Nab47D10-35B5. Omicron BA.1 has an IC50 fold change of 0.08x. | 2022 | Yuan et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|--|
| Y505H | vaccine neutralization efficacy | Pokay | Omicron B.1.1.529 (BA.1) neutralization of the Omicron variants by antibodies induced by three doses of Pfizer/BNT162b2 mRNA vaccine was 7-8-fold less potent than the D614G, and the Omicron variants still evade neutralization more efficiently. | 2022 | Neerukonda et al. (2022) |
| Y505H | pharmaceutical effectiveness | Pokay | Omicron (B.1.1.529 [BA.1]) have higher sensitivity to inhibition by soluble angiotensin converting enzyme 2 (ACE2) and the endosomal inhibitor chloroquine compared to D614G | 2022 | Neerukonda et al. (2022) |
| Y505H | antibody epitope effects | Pokay | Neutralization of the bsAbs Bi-Nab35B5-47D10. Omicron BA.1 has an IC50 fold change of 0.30x. | 2022 | Yuan et al. (2022) |
| Y505H | vaccine neutralization efficacy | Pokay | Paradigms' ACE-2 variant LVE/STR chimera binds to SARS-2 Omicron variant B.1.1.529 spike protein trimer with high affinity. Determined using Surrogate Viral Neutralization Tests. | 2022 | Uhal B et al. (2022) |
| Y505H | ACE2 receptor binding affinity | Pokay | L27, V34 and E90 mutation resulted in ultrahigh affinity binding of the LVE-ACE-2 domain to the widest variety of VOCs, with KDs of 73 pM for binding to the Omicron B.1.1.529. Values were obtained with LVE-ACE-2/mAB chimeras containing the Y-T-E sequence that enhances binding to the FcRn receptor, which in turn is expected to extend biological half-life 3-4-fold. | 2022 | Uhal B et al. (2022) |
| Y505H | antibody epitope effects | Pokay | Neutralization of the bsAbs 35B5. Omicron BA.1 has an IC50 fold change of 0.38x. | 2022 | Yuan et al. (2022) |
| Y505H | vaccinee plasma binding | Pokay | All 10 individuals with 2 doses of the BNT162b2/BNT162b2 vaccine had a neutralizing titer in B.1 variant at an average of 729 NT50. | 2022 | Arora et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|--------------------------|---------------------|--|------------------|-------------------------------------|
| Y505H | antibody epitope effects | Pokay | Plaque reduction neutralization test (PRNT) was used uring primary infection, post sixty daysof second dose vaccination, pre-reinfection and reinfection against Delta variant and was used to determine neutralizing antibodytitres. There was a 24.63x fold increase in antibody response from first infection to recovered and vaccinated with 2 doses (60 days). There was a 4.21x fold increase in antibody response pre-reinfection. There was a 39.27x fold increase in antibody response during reinfection. | 2022 | Shete et al. (2022) |
| Y505H | antibody epitope effects | Pokay | Plaque reduction neutralization test (PRNT) was used uring primary infection, post sixty daysof second dose vaccination, pre-reinfection and reinfection against B.1 variant and was used to determine neutralizing antibodytitres. There was a 6.76x fold increase in antibody response from first infection to recovered and vaccinated with 2 doses (60 days). There was a 2.06x fold increase in antibody response pre-reinfection. There was a 8.18x fold increase in antibody response during reinfection. | 2022 | Shete et al. (2022) |
| Y505H | vaccinee plasma binding | Pokay | All 10 individuals with 3 doses of the BNT162b2/BNT162b2 vaccine had a neutralizing titer in B.1 variant at an average of 3319 NT50. | 2022 | Arora et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|--|
| Y505H | antibody epitope effects | Pokay | Plaque reduction neutralization test (PRNT) was used using primary infection, post sixty days of second dose vaccination, pre-reinfection and reinfection against Omicron variant and was used to determine neutralizing antibody titres. There was a 114.84x fold increase in antibody response from first infection to recovered and vaccinated with 2 doses (60 days). There was a 6.61x fold increase in antibody response pre-reinfection. There was a 1194.9x fold increase in antibody response during reinfection. | 2022 | Shete et al. (2022) |
| Y505H | antibody epitope effects | Pokay | BnAb 002-S21F2 IC50 on the Omicron BA.1 variant is 1.0x fold the wildtype. | 2022 | Kumar et al. (2022) |
| Y505H | antibody epitope effects | Pokay | Neutralization of the bsAbs 47D10. Omicron BA.1 has an IC50 fold change of 1.26x. | 2022 | Yuan et al. (2022) |
| Y505H | pharmaceutical effectiveness | Pokay | Omicron BA.3 have higher sensitivity to inhibition by soluble angiotensin converting enzyme 2 (ACE2) and the endosomal inhibitor chloroquine compared to D614G | 2022 | Neerukonda et al. (2022) |
| Y505H | vaccine neutralization efficacy | Pokay | Omicron BA.3 neutralization of the Omicron variants by antibodies induced by three doses of Pfizer/BNT162b2 mRNA vaccine was 7-8-fold less potent than the D614G, and the Omicron variants still evade neutralization more efficiently. | 2022 | Neerukonda et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|---------------------------------------|
| Y505H | vaccinee plasma binding | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.3 (from South Africa/NICD-N22404/2021) were 4.2x-fold lower (95% CI: 0.15x-0.20x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| Y505H | vaccine neutralization efficacy | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.3 (from South Africa/NICD-N22404/2021) were 6.2-fold lower (95% CI: 11.8x-14.3x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| Y505H | vaccine neutralization efficacy | Pokay | paired testing of vaccine sera against ancestral virus compared to Omicron BA.1 shows that 3-dose vaccine regimen provides over 50x fold increase in protection against Omicron(B.1.1.529 [BA.1]) compared to a 2-dose regimen. | 2022 | Hao et al. (2022) |
| Y505H | pharmaceutical effectiveness | Pokay | 4th antigenic exposure with Omicron (B.1.1.529 [BA.1])(n | 2022 | Wang et al. (2022) |
| Y505H | vaccine neutralization efficacy | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.1 (from Botswana/R40B59_BHP_3321 001248/2021) were 3.4-fold lower (95% CI: 3.2x-3.6x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|---------------------------------------|
| Y505H | vaccinee plasma binding | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.1 (from Botswana/R40B59_BHP_3321 001248/2021) were 28.7x-fold lower (95% CI: 0.03x-0.05) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| Y505H | vaccinee plasma binding | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.4/5 (from) were 17.2x-fold lower (95% CI: 0.6x-0.7x) than against 208-428 972-1834 4.3-4.7 US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| Y505H | vaccine neutralization efficacy | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.4/5 (from) were 13.0-fold lower (95% CI: 4.2x-4.6x) than against 208-428 972-1834 4.3-4.7 US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| Y505H | vaccinee plasma binding | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, XD (from) were 1.5x-fold lower (95% CI: 0.05x-0.07x) than against 208-428 972-1834 4.3-4.7 US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| Y505H | vaccine neutralization efficacy | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, XD (from) were 4.4-fold lower (95% CI: 4.3x-4.7x) than against 208-428 972-1834 4.3-4.7 US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|--|
| Y505H | ACE2 receptor binding affinity | Pokay | The hACE2-binding affinity of XBB.1.5 RBD has a dissociation constant KD of 3.4 nM, where S486P is the distinguishing Spike mutation vs parent XBB.1 RBD with a much weaker KD (19 nM), as measured by surface plasmon resonance (SPR) assays. | 2023 | Yue et al. (2023) |
| Y505H | ACE2 receptor binding affinity | Pokay | Using molecular dynamics simulation, ACE2-RBD (Omicron) complex is destabilized by the E484A and Y505H mutations and stabilized by S477N and N501Y mutations. | 2022 | Zhang et al. (2022) |
| Y505H | gene expression increase | Pokay | Experimentally, Spike gene expression increased 0.16 fold | 2020 | Starr et al. (2020) |
| Y505H | anthropozoonotic events | Pokay | Observed first in a single tiger (cohort of 5), potential adaptation. | 2020 | McAloose et al. (2020) |
| D614G | vaccine neutralization efficacy | Pokay | Subtype of the B.1.526 'New York' lineage, lentivirus pseudotyped with this mutation combination in showed no significant change in IC50 serum dilution concentration for sera from BNT162b2 (Pfizer) or mRNA1273 (Moderna) vaccinees collected 28 days following booster dose. | 2021 | Zhou et al. (2021) |
| D614G | vaccine neutralization efficacy | Pokay | Neutralization efficiency (ID50) against B.1.526 reduced 2.3x relative to D614G wildtype using pseudotyped VSV assay on 8 Moderna vaccinee sera one week post-booster. | 2021 | Choi et al. (2021) |
| D614G | convalescent plasma binding | Pokay | Subtype of the B.1.526 'New York' lineage, lentivirus pseudotyped with this mutation combination in showed no significant change in IC50 serum dilution concentration for 6 convalescent sera. | 2021 | Zhou et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|--|
| D614G | vaccine neutralization efficacy | Pokay | Subtype of the B.1.526 'New York' lineage, lentivirus pseudotyped with this mutation combination in showed 3.6x reduction in both IC50 serum dilution concentration for sera from 5 BNT162b2 (Pfizer) or 3 mRNA1273 (Moderna) vaccinees collected 28 days following booster dose. | 2021 | Zhou et al. (2021) |
| D614G | vaccine neutralization efficacy | Pokay | Detectable antibodies against B.1.526+E484K at various time points using pseudotyped lentivirus neutralization in Moderna vaccinee cohort: Day 43 100%, Day 209 88%. | 2021 | Pegu et al. (2021) |
| D614G | vaccine neutralization efficacy | Pokay | 2.3x reduction in neutralization (ID50) in sera 3 weeks after one dose of Pfizer/BioNTech BNT162b2 (up to 5 naive and post infection vaccinees) | 2021 | Gong et al. (2021) |
| D614G | convalescent plasma binding | Pokay | Subtype of the B.1.526 'New York' lineage, lentivirus pseudotyped with this mutation combination in showed 3.8x reduction in IC50 serum dilution concentration for 6 convalescent sera. | 2021 | Zhou et al. (2021) |
| D614G | vaccinee plasma binding | Pokay | Out of 10 individuals with 3 doses of the BNT162b2/BNT162b2/BNT162b2 vaccine had a neutralizing titer in B.1.640.2 variant was ~5.6x folds more significant in 9 individuals. | 2022 | Arora et al. (2022) |
| D614G | vaccinee plasma binding | Pokay | Out of 10 individuals with 2 doses of the BNT162b2/BNT162b2 vaccine, neutralizing titer in B.1.640.2 variant was ~1000x folds more significant in 8 individuals. | 2022 | Arora et al. (2022) |
| D614G | pharmaceutical effectiveness | Pokay | Omicron BA.2 have higher sensitivity to inhibition by soluble angiotensin converting enzyme 2 (ACE2) and the endosomal inhibitor chloroquine compared to D614G | 2022 | Neerukonda et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|--|
| D614G | antibody epitope effects | Pokay | Neutralization of the bsAbs Bi-Nab35B5-47D10. Omicron BA.2 has an IC50 fold change of 0.07x. | 2022 | Yuan et al. (2022) |
| D614G | antibody epitope effects | Pokay | Neutralization of the bsAbs 35B5. Omicron BA.2 has an IC50 fold change of 0.09x. | 2022 | Yuan et al. (2022) |
| D614G | antibody epitope effects | Pokay | Neutralization of the bsAbs 47D10. Omicron BA.2 has an IC50 fold change of 0.08x. | 2022 | Yuan et al. (2022) |
| D614G | antibody epitope effects | Pokay | Neutralization of the bsAbs Bi-Nab47D10-35B5. Omicron BA.2 has an IC50 fold change of 0.04x. | 2022 | Yuan et al. (2022) |
| D614G | vaccine neutralization efficacy | Pokay | Omicron BA.2 neutralization of the Omicron variants by antibodies induced by three doses of Pfizer/BNT162b2 mRNA vaccine was 7-8-fold less potent than the D614G, and the Omicron variants still evade neutralization more efficiently. | 2022 | Neerukonda et al. (2022) |
| D614G | antibody epitope effects | Pokay | BnAb 002-S21F2 IC50 on the Omicron BA.2 variant is 0.8x fold the wildtype. | 2022 | Kumar et al. (2022) |
| D614G | vaccine neutralization efficacy | Pokay | Neutralization efficiency (ID50) against B.1.1.427/429 reduced 2.1x relative to D614G wildtype using pseudotyped VSV assay on 8 Moderna vaccinee sera one week post-booster. | 2021 | Choi et al. (2021) |
| D614G | vaccine neutralization efficacy | Pokay | Detectable antibodies against B.1.1.7 in all samples at Day 43 and Day 209 using pseudotyped lentivirus neutralization in Moderna vaccinee cohort. | 2021 | Pegu et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|--|
| D614G | vaccine neutralization efficacy | Pokay | Pseudotyped B.1.1.429 virus has reduced neutralization activity vs wild type: 2.0x (30 sera Pfizer median 9 days post 2nd dose, 35 sera Moderna median 18 days post 2nd dose). This was NOT significant by ANOVA. | 2021 | Garcia-Beltran et al. (2021) |
| D614G | convalescent plasma escape | Pokay | Mean 2.7x reduction of NT50 value B.1.427 (Epsilon) relative to wild type in 8 sera from older convalescent patients (52-92yo) collected 1-3m post symptom onset. | 2021 | Uriu et al. (2021) |
| D614G | vaccine neutralization efficacy | Pokay | 6 of 11 (55%) vaccine recipients (Moderna or Pfizer), showed 2x reduction in neutralization to a B.1.429 lineage virus. | 2021 | Deng et al. (2021) |
| D614G | vaccine neutralization efficacy | Pokay | Mean 2.3x reduction of NT50 value B.1.427 (Epsilon) relative to wild type in 8 sera from adult BNT162b2 vaccinees (28-47yo) collected ~1m post booster. | 2021 | Uriu et al. (2021) |
| D614G | vaccine neutralization efficacy | Pokay | PBMCs of Pfizer/BioNTech BNT162b2 (n | 2021 | Tarke et al. (2021) |
| D614G | virion structure | Pokay | CryoEM reveals the P.1 trimer to adopt exclusively a conformation in which one of the receptor-binding domains is in the “up” position. | 2021 | Wang et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|------------------------------------|
| D614G | vaccine neutralization efficacy | Pokay | In 12 Moderna vaccinee sera 15 days post second dose (43 days since first vaccination), an average 2.8x decrease in reciprocal ID50 value was observed ten key point mutations in Spike in the P.1 lineage vs wildtype. A 4.8x decrease against the full P.1 type vs WA-1 was observed, though overall with a higher ID50 reciprocal value. In 10 Pfizer vaccinee sera 7 days or more post second dose (28 days or more since first vaccination), an average 2.2x decrease in reciprocal ID50 value was observed ten key point mutations in Spike in the P.1 lineage vs wildtype. A 3.8x decrease against the full P.1 type vs WA-1 was observed, with similar variant ID50 reciprocal value. | 2021 | Wang et al. (2021) |
| D614G | convalescent plasma escape | Pokay | In convalescent sera one month or more post-infection in Spring 2020, an average 6.5x decrease in reciprocal ID50 value was observed ten key point mutations in Spike in the P.1 lineage vs wildtype. A 3.4x decrease against the full P.1 type vs WA-1 was observed, with better full P.1 ID50 reciprocal value compared to the 10-mutation model. | 2021 | Wang et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|--------------------------|---------------------|---|------------------|--|
| D614G | antibody epitope effects | Pokay | Amongst RBD-targeting Emergency Use Authorized monoclonal antibody treatments CB6, LY-CoV555 and REGN10933 show abrogated neutralization activity against the ten key point mutations in Spike in the P.1 lineage vs wildtype or WA-1, but REGN10987 activity remains strong. RBD-targeting monoclonal antibodies 2-15 and C121 show abrogated neutralization activity against the ten key point mutations in Spike in the P.1 lineage vs wildtype or WA-1. N terminal domain targeting monoclonal antibodies 5-7, 4-8, 4-18 and 2-17 have abrogated neutralization activity against the ten key point mutations in Spike in the P.1 lineage vs wildtype or WA-1. | 2021 | Wang et al. (2021) |
| D614G | reinfection | Pokay | After a 128 day interval, a patient in Sao Paulo State, Brazil reinfected with P.1 (first episode likely predates P.1 emergence). Both cases were fairly mild (difficulty breathing, tiredness, dizziness and fatigue). | 2021 | Malta Romano et al. (2021) |
| D614G | vaccine efficacy | Pokay | In a 1:5 test-negative matched control study of 8153 individuals who received the Moderna mRNA-1273 vaccine, 349 test-positive were Gamma. Two dose vaccine efficacy against Gamma was 95.5 (90.9-97.8%), one dose VE was 74.2 (43.8-88.1%). | 2021 | Bruxvoort et al. (2021) |
| D614G | trafficking | Pokay | ~6x cleavage of S2 relative to WA1 (D614G) wildtype by Gamma variant as measured by mass spectrometry of Vero-TMPRSS culture [no mutations directly at furin cleavage site, but H655Y is upstream] Compare to 4.5x or less for variants of concern with direct furin cleavage site mutations. | 2021 | Esclera et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|---|
| D614G | reinfection | Pokay | Three healthcare workers (29-50yo) had confirmed P.1 [Gamma] re-infection in the Amazonas region of Brazil 3-9 months after initial infection from viruses with distinct lineage from P.1, but mild symptoms upon re-infection and evidence for infectiousness during re-infection. | 2021 | Naveca et al. (2021) |
| D614G | vaccine neutralization efficacy | Pokay | Mean 3.0x reduction of NT50 value P.1 (Gamma) relative to wild type in 8 sera from adult BNT162b2 vaccinees (28-47yo) collected ~1m post booster. | 2021 | Uriu et al. (2021) |
| D614G | convalescent plasma escape | Pokay | Mean 4.1x reduction of NT50 value P.1 (Gamma) relative to wild type in 8 sera from older convalescent patients (52-92yo) collected 1-3m post symptom onset. | 2021 | Uriu et al. (2021) |
| D614G | antibody epitope effects | Pokay | BnAb 002-S21F2 IC50 on the Gamma (P.1) variant is 0.6x fold the wildtype. | 2022 | Kumar et al. (2022) |
| D614G | vaccine neutralization efficacy | Pokay | The neutralizing activity of vaccine was slightly lower against B.1.1.248 variant constellation in sera tested from most of the 15 patients with the BNT162b2 mRNA vaccine. (Fig. 4) | 2021 | Chen et al. (2021) |
| D614G | vaccine neutralization efficacy | Pokay | ELISpot assays show T cell neutralization reduced by 16.6% in this B.1.1.248 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). | 2021 | Gallagher et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|--|
| D614G | antibody epitope effects | Pokay | B.1.1.248 variant constellation ablates Class 1 receptor-binding-mot if targeting antibodies COV2-2050, 1B07. B.1.1.248 variant constellation ablates Class 3 N-terminal domain targeting antibody COV2-2676. | 2021 | Chen et al. (2021) |
| D614G | convalescent plasma escape | Pokay | B.1.1.7 variant constellation two-tailed Wilcoxon matched-pairs signed-rank test against 10 convalescent sera P | 2021 | Chen et al. (2021) |
| D614G | anthropozoonotic events | Pokay | Unlike wild type or B.1.1.7, P.1 lineage virus was able to infect and replicate in common lab mouse strains, with high titer. | 2021 | Montagutelli et al. (2021) |
| D614G | convalescent plasma escape | Pokay | B.1.1.248 variant constellation in 10 convalescent human sera ~1mo post infection had mild to moderate resistance against most samples, P | 2021 | Chen et al. (2021) |
| D614G | vaccine neutralization efficacy | Pokay | Neutralizing antibody titers increased in previously infected vaccinees relative to uninfected vaccinees 4.3-fold against P.1 (contrast with 3.4 fold against original SARS-CoV-2). | 2021 | Leier et al. (2021) |
| D614G | vaccine neutralization efficacy | Pokay | Pseudotyped P.1 virus has reduced neutralization activity vs wild type: 6.7x (30 sera Pfizer median 9 days post 2nd dose) and 4.5x (35 sera Moderna median 18 days post 2nd dose). This was significant by ANOVA. | 2021 | Garcia-Beltran et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|---|
| D614G | pharmaceutical effectiveness | Pokay | P.1 virus neutralization (as tested using biolayer interferometry) of both Lilly antibodies was severely impacted, with Lilly mAb combination LY-CoV16 and LY-CoV555 (due to mutations at 416 and 484 respectively) shows almost complete loss of neutralization of P.1. There was also escape from neutralization of P.1 by REGN10933 (one of 2 in Regeneron's mAb cocktail) and a modest reduction in neutralization of P.1 by AstraZeneca's AZD8895 (while AZD1061 and AZD7442 showed equal neutralization of all SARS-CoV-2 variants tested). The three Adagio antibodies neutralized P.1 with all reaching a plateau at 100% neutralization: interestingly, ADG30 showed a slight increase of neutralization of P.1. S309 Vir was largely unaffected, although for several viruses, including P.1, the antibody failed to completely neutralize, conceivably reflecting incomplete glycosylation at N343, since the sugar interaction is key to binding of this antibody. | 2021 | Dejnirattisai et al. (2021) |
| D614G | vaccine neutralization efficacy | Pokay | P.1 lineage titers were reduced 7.6-fold and 9-fold for the BNT162b2 Pfizer (sera collected 4-14 days post-booster) and ChAdOx1 nCoV-19 AstraZeneca (sera collected 14 or 28 days post-booster) vaccines respectively. | 2021 | Dejnirattisai et al. (2021) |
| D614G | vaccine neutralization efficacy | Pokay | In sera 1-2 weeks after BNT162b2 first dose, from six patients previously infected with B.1, antibody titer in a microneutralization assay was on average 2896 for P.1 virus. This compares favorably (stronger) to post-infection neutralization titer against all variants tested in the same sera (wild type, B.1.1.7, B.1.351, and P.1). | 2021 | Luftig et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|--|
| D614G | convalescent plasma binding | Pokay | In sera from six patients collected 1 to 12 weeks post-infection with B.1, antibody titer in a microneutralization assay was on average 256 for B.1.1.7 virus. Compare to somewhat stronger neutralization titer for wild type (456.1) in the same sera. | 2021 | Luftig et al. (2021) |
| D614G | vaccine neutralization efficacy | Pokay | Detectable antibodies against P.1 at various time points using pseudovirus neutralization in Moderna vaccinee cohort: Day 43 100%, Day 209 85%. | 2021 | Pegu et al. (2021) |
| D614G | T cell evasion | Pokay | PBMCs of 11 mild COVID-19 patients collected 38-80 days after symptom onset were stimulated with the 15-mer peptide pools (w/ 10 residue overlaps) from the whole viral proteome, showing no significant CD4+ cell count effect for P.1, and a slight increase in CD8+ percentage (p | 2021 | Tarke et al. (2021) |
| D614G | transmissibility | Pokay | The relative transmissibility of P.1 estimated at the national level (Italy) varied according to the assumed degree of cross-protection granted by infection with other lineages and ranged from 1.12 (95%CI 1.03-1.23) in the case of complete immune evasion by P.1 to 1.39 (95%CI 1.26-1.56) in the case of complete cross-protection. PG: variant list has been abbreviated due to mixed K417 bases in this lineage, potential miscalls of deletions | 2021 | Stefanelli et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|---------------------------------------|
| D614G | convalescent plasma escape | Pokay | Artificially constructed HIV-1 pseudovirus with set of mutations drawn from plasma passage escape experiments and mutations from variants of concern completely ablates neutralization in 19 of 21 convalescents plasma collected mean 1.3 months post infection. [actual Y145del from manuscript substituted with more common Y144del description] | 2021 | Schmidt et al. (2021) |
| D614G | vaccine neutralization efficacy | Pokay | In human sera 8 weeks post-vaccination with INO-4800, a ~7-fold reduction in B.1.351 neutralization was observed. | 2021 | Andrade et al. (2021) |
| D614G | vaccine neutralization efficacy | Pokay | Four fold reduction in neutralization efficiency was observed in sera of ferrets post-vaccination with INO-4800 (DNA plasmid pGX9501 encoding full length Spike). | 2021 | Riddell et al. (2021) |
| D614G | vaccine neutralization efficacy | Pokay | Monovalent mRNA-1273.351 encodes for the S protein found in the B.1.351 lineage and (2) mRNA-1273.211 comprising a 1:1 mix of mRNA-1273 and mRNA-1273.351. In a mouse study, primary vaccination series of mRNA-1273.351 was effective at increasing neutralizing antibody titers against the B.1.351 lineage, while mRNA-1273.211 was most effective at providing broad cross-variant neutralization. In addition, these results demonstrated a third dose of mRNA-1273.351 significantly increased both wild-type and B.1.351-specific neutralization titers. | 2021 | Wu et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|--------------------------------------|
| D614G | vaccine neutralization efficacy | Pokay | Pzifer vaccinees that tested positive at least a week after the second dose were indeed disproportionately infected with B.1.351, as compared with unvaccinated individuals (odds ratio of 8:1), but were all infected before 14 days post second vaccination. | 2021 | Kustin et al. (2021) |
| D614G | convalescent plasma escape | Pokay | Mean 8.2x reduction of NT50 value B.1.351 (Beta) relative to wild type in 8 sera from older convalescent patients (52-92yo) collected 1-3m post symptom onset. | 2021 | Uriu et al. (2021) |
| D614G | vaccine neutralization efficacy | Pokay | Mean 6.3x reduction of NT50 value B.1.351 (Beta) relative to wild type in 8 sera from adult BNT162b2 vaccinees (28-47yo) collected ~1m post booster. | 2021 | Uriu et al. (2021) |
| D614G | convalescent plasma escape | Pokay | 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. | 2021 | Skelly et al. (2021) |
| D614G | convalescent plasma binding | Pokay | In sera from six patients collected 1 to 12 weeks post-infection with B.1, antibody titer in a microneutralization assay was on average 8 for B.1.351 virus. Compare to much stronger neutralization titers for B.1.1.7 (256) and wild type (456.1) in the same sera. | 2021 | Luftig et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|---------------------------------------|
| D614G | vaccine neutralization efficacy | Pokay | 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 potentially neutralizing WA1 while having FRNT50 for B.1.351 below the assay limit of detection (1:20). | 2021 | Bates et al. (2021) |
| D614G | convalescent plasma binding | Pokay | Sera from individuals who have been infected with Delta does not have strong neutralising activity against Beta. | 2021 | UNKNOWN et al. (2021) |
| D614G | convalescent plasma escape | Pokay | 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 ~6x reduction in neutralizing titers, and 40% of the samples lacked any activity against B.1.351. | 2021 | Planas et al. (2021) |
| D614G | vaccinee plasma binding | Pokay | Sera from individuals who have been vaccinated and have had subsequent recent Delta infection have a high level of neutralising activity against Beta. | 2021 | UNKNOWN et al. (2021) |
| D614G | vaccine neutralization efficacy | Pokay | Paradigm's ACE-2 variant LVE/STR chimera neutralizes Beta Variant B.1.351 RBD significantly better than w.t. SARS-CoV-2 RBD. Determined using Surrogate Viral Neutralization Tests. | 2022 | Uhal B et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|--|
| D614G | vaccine neutralization efficacy | Pokay | 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. | 2021 | Garcia-Beltran et al. (2021) |
| D614G | ACE2 receptor binding affinity | Pokay | Pseudotype lentivirus for the full B.1.351 Spike variant list shows increase affinity for ACE2 as measured by IC50. This is in contrast to B.1.1.7 which showed no major change, indicating that the shared N501Y mutation is the driver of affinity change, attenuated in the B.1.1.7 mutatioon set, but maintained in the B.1.351 lineage. | 2021 | Tada et al. (2021) |
| D614G | vaccine neutralization efficacy | Pokay | [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.] | 2021 | Voysey et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|--|
| D614G | ACE2 receptor binding affinity | Pokay | 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 greater extent to B.1.1.7, which both carry the N501Y mutation (see Fig 3). | 2021 | Planas et al. (2021) |
| D614G | vaccine neutralization efficacy | Pokay | PBMCs of Pfizer/BioNTech BNT162b2 (n | 2021 | Tarke et al. (2021) |
| D614G | vaccine neutralization efficacy | Pokay | Relative to B.1.1.117, PRNT50 line virus neutralizing antibody activity assay of B.1.351 showed ~11x reduction in 13 vaccinees's sera collected through 41 days after vaccination. Neutralization by a placebo control group of 6 naturally infected patients showed a smaller ~8x drop (starting from a ~50% higher PRNT50 value than vaccinees 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 ~4x 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). | 2021 | Madhi et al. (2021) |
| D614G | vaccine neutralization efficacy | Pokay | Log10ID50 of Beta neutralizing antibodies is 0.899x the WT 1 month post-third dose of pfizer-BioNTech BNT162b2 in 13 Kidney transplant recipients (KTR) with median age of 55.5. | 2022 | McEvoy C et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|--------------------------------------|
| D614G | convalescent plasma escape | Pokay | A 1.8-fold drop in FRNT50 for B.1.351 was observed in 44 sera collected between 1 and 301 post-infection. | 2021 | Bates et al. (2021) |
| D614G | vaccine neutralization efficacy | Pokay | 3.2x reduction in neutralization (ID50) in sera 3 weeks after one dose of Pfizer/BioNTech BNT162b2 (up to 5 naive and post infection vaccinees) | 2021 | Gong et al. (2021) |
| D614G | vaccine neutralization efficacy | Pokay | Neutralization efficiency (ID50) against B.1.1.351-v1 reduced 6.9x relative to D614G wildtype using pseudotyped VSV assay on 8 Moderna vaccinee sera one week post-booster. | 2021 | Choi et al. (2021) |
| D614G | T cell evasion | Pokay | 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. | 2021 | Skelly et al. (2021) |
| D614G | convalescent plasma escape | Pokay | The neutralizing activity of 16/20 convalescent sera was significantly lower against this pseudotyped virus model of B.1.351, with similar results for the live virus. | 2021 | Wang et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|--|
| D614G | vaccine neutralization efficacy | Pokay | Log10ID50 of Beta neutralizing antibodies is 0.803x the WT pre-third dose of pfizer-BioNTech BNT162b2 in 13 Kidney transplant recipients (KTR) with median age of 55.5. | 2022 | McEvoy C et al. (2022) |
| D614G | antibody epitope effects | Pokay | B.1.351 pseudotyped virus model ablates neutralization by RBD-directed mAbs CB6, 4-20, 2-4, 2-43, 910-30, 2-302-15, LY-Cov555, C121. B.1.351 pseudotyped virus model severely impairs neutralization by RBD-directed mAb 1-20. B.1.351 pseudotyped virus model impairs neutralization by RBD-directed mAb REGN10933. B.1.351 pseudotyped virus model ablates neutralization by N-terminal-domain-directed mAbs 5-24, 4-8, 4A8, 4-19. B.1.351 pseudotyped virus model severely impairs neutralization by N-terminal-domain-directed mAb 2-17. B.1.351 pseudotyped virus model impairs neutralization by N-terminal-domain-directed mAb 5-7. PG: Live virus data for the same mAbs is similar, but 1-20 becomes severally impaired, REGN10933 activity is ablated, and Brii-196 becomes impaired. | 2021 | Wang et al. (2021) |
| D614G | vaccine neutralization efficacy | Pokay | The neutralizing activity of vaccine was significantly lower against B.1.351 (12.4x in twelve Moderna-recipient sera: 10.3x in ten Pfizer-recipient sera). [this is a larger list of B.1.351 than modeled by Wang et al. (2021) by including L18F and R246I, less effective at neutralizing] | 2021 | Wang et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|---|
| D614G | vaccine neutralization efficacy | Pokay | 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 (~10x vs D614G) through week 6, the last timepoint measured. Three vaccinees never showed detectable neutralization to B.1.351 even after second dose. | 2021 | Planas et al. (2021) |
| D614G | pharmaceutical effectiveness | Pokay | DARPin SR16m molecule had a 0.036x fold change in IC50 in B.1.351 Beta | 2022 | Chonira et al. (2022) |
| D614G | tissue specific neutralization | Pokay | 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 vaccinee neutralizing at weeks 3 and 6, B.1.351 showed zero neutralization at either time point in any sample (and relatively impaired serum neutralization). | 2021 | Planas et al. (2021) |
| D614G | vaccine neutralization efficacy | Pokay | 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. | 2021 | Choi et al. (2021) |
| D614G | vaccine neutralization efficacy | Pokay | 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. | 2021 | Woldemeskel et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|---------------------------------------|
| D614G | vaccine neutralization efficacy | Pokay | 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 relative decrease was 6.1x vs wild type). | 2021 | Ikegame et al. (2021) |
| D614G | pharmaceutical effectiveness | Pokay | Trimeric proteins FSR22 had a 0.07x fold change in IC50 in B.1.351 Beta | 2022 | Chonira et al. (2022) |
| D614G | vaccine neutralization efficacy | Pokay | 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. | 2021 | Shinde et al. (2021) |
| D614G | pharmaceutical effectiveness | Pokay | DARPin SR22 molecule had a 1.57x fold change in IC50 in B.1.351 Beta | 2022 | Chonira et al. (2022) |
| D614G | pharmaceutical effectiveness | Pokay | Trimeric proteins FSR16m had a 0.054x fold change in IC50 in B.1.351 Beta | 2022 | Chonira et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|-----------------------------------|---------------------|---|------------------|---|
| D614G | pharmaceutical effectiveness | Pokay | B.1.351 virus neutralization (as tested using biolayer interferometry) of both Lilly antibodies was severely impacted, with LY-CoV16 and LY-CoV555 (due to mutations at 416 and 484 respectively) shows almost complete loss of neutralization of B.1.351. There was also escape from neutralization of B.1.351 by REGN10933 and a modest reduction in neutralization of B.1.351 by AZD8895 (while AZD1061 and AZD7442 showed equal neutralization of all SARS-CoV-2 variants tested). The three Adagio antibodies neutralized B.1.351. | 2021 | Dejnirattisai et al. (2021) |
| D614G | pharmaceutical effectiveness | Pokay | DARPin SR16m molecule had a 6.7x fold change in IC50 in B.1.617.2 Delta | 2022 | Chonira et al. (2022) |
| D614G | pharmaceutical effectiveness | Pokay | DARPin SR16m molecule had a 99.7x fold change in IC50 in B.1.617.2 Delta | 2022 | Chonira et al. (2022) |
| D614G | convalescent plasma escape | Pokay | The most significant loss of neutralizing activity (PsVNA50 assay) using 6 hyperimmune immunoglobulin preparations from convalescent plasma was seen against authentic B.1.351 lineage virus (9.2-fold). Neutralization against 10 convalescent plasma was poorer (18.7x). | 2021 | Tang et al. (2021) |
| D614G | environmental condition stability | Pokay | Treatment with heat, soap and ethanol revealed similar inactivation profiles indicative of a comparable susceptibility towards disinfection. Furthermore, we observed comparable surface stability on steel, silver, copper and face masks. | 2021 | Meister et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|-----------------------------------|---------------------|---|------------------|---------------------------------------|
| D614G | environmental condition stability | Pokay | Relative to D614G, this mutation set (B.1.351+) demonstrated significant increase in infectivity (i.e. heat stability) after incubation at 50C after 1 hour. | 2021 | Tada et al. (2021) |
| D614G | trafficking | Pokay | In two of eight cell lines tested (Caco-2 intestinal and Calu-3 lung), a modest increase in cell entry was observed. This increase was not observed in a Calu-3 cell line with overexpressed ACE2. [the virus tested as B.1.617 overlaps only partially with the Spike mutation lists used by PANGO, CDC, etc. for this lineage therefore the results should be interpreted carefully as transferable to B.1.617 generally] | 2021 | Hoffman et al. (2021) |
| D614G | convalescent plasma escape | Pokay | Approximately 2-fold reduction in 15 ICU patient convalescent plasma neutralization as quantified by measuring virus-encoded luciferase activity in cell lysates at 16-18 h post transduction. [PG: note that the virus tested as B.1.617 overlaps only partially with the Spike mutation lists used by PANGO, CDC, etc. for this lineage therefore the results should be interpreted carefully as transferable to B.1.617 generally] | 2021 | Hoffman et al. (2021) |
| D614G | antibody epitope effects | Pokay | Abrogates Bamlanivimab neutralization as quantified by measuring virus-encoded luciferase activity in cell lysates at 16-18 h post transduction. Significant decrease in combined Etesevimab+Bamlanivimab neutralization except at the highest concentration measured. [PG: note that the virus tested as B.1.617 overlaps only partially with the Spike mutation lists used by PANGO, CDC, etc. for this lineage therefore the results should be interpreted carefully as transferable to B.1.617 generally] | 2021 | Hoffman et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|---------------------------------------|
| D614G | vaccine neutralization efficacy | Pokay | In 15 Pfizer non-senior vaccinee sera collected 3-4 weeks post-booster [using Table S1, not the text that says 2-3 weeks], neutralization was reduced ~3x (compared to ~11x for B.1.351). [the virus tested as B.1.617 overlaps only partially with the Spike mutation lists used by PANGO, CDC, etc. for this lineage therefore the results should be interpreted carefully as transferable to B.1.617 generally] | 2021 | Hoffman et al. (2021) |
| D614G | vaccinee plasma binding | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.2 (from South Africa/CERI-KRISP-K03 2307/2021) were 3.9x-fold lower (95% CI: 0.14x-0.17x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| D614G | ACE2 receptor binding affinity | Pokay | L27, V34 and E90 mutation resulted in ultrahigh affinity binding of the LVE-ACE-2 domain to the widest variety of VOCs, with KDs of 78fM for binding to the Omicron BA.2. Values were obtained with LVE-ACE-2/mAB chimeras containing the Y-T-E sequence that enhances binding to the FcRn receptor, which in turn is expected to extend biological half-life 3-4-fold. | 2022 | Uhal B et al. (2022) |
| D614G | vaccine neutralization efficacy | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.2 (from South Africa/CERI-KRISP-K03 2307/2021) were 4.5-fold lower (95% CI: 4.3x-4.7x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|--|
| D614G | vaccine neutralization efficacy | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.2.12.1 (from USA/NY-CDC-ASC2 10722700/2022) were 4.2-fold lower (95% CI: 5.8x-6.6x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| D614G | vaccinee plasma binding | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.2.12.1 (from USA/NY-CDC-ASC2 10722700/2022) were 3.9x-fold lower (95% CI: 0.14x-0.18x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| D614G | vaccine neutralization efficacy | Pokay | Neutralization efficiency (ID50) against B.1.525 reduced 4.2x relative to D614G wildtype using pseudotyped VSV assay on 8 Moderna vaccinee sera one week post-booster. | 2021 | Choi et al. (2021) |
| D614G | pharmaceutical effectiveness | Pokay | Omicron (a.k.a. B.1.1.529) Spike pseudotyped VSV and Vero E6 cells has somewhat reduced neutralization (2.7x) vs wild type with monoclonal antibody Sotrovimab (a.k.a. VIR-7831). [delins at 214 omitted for syntax compatibility] | 2021 | Cathcart et al. (2021) |
| D614G | vaccine neutralization efficacy | Pokay | Omicron breakthrough infection after 3-dose vaccination resulted in a further 3.5-fold and 2.9-fold increase of Omicron BA.1 and BA.2 neutralizing titers. Omicron BA.4/5 showed the highest neutralization resistance of all variants tested, resulting in low geometric mean neutralizing titers in plasma samples obtained after the second vaccine dose (NT50 | 2022 | Wang et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|--|
| D614G | antibody epitope effects | Pokay | Neutralization of the bsAbs Bi-Nab47D10-35B5. Omicron BA.1 has an IC50 fold change of 0.08x. | 2022 | Yuan et al. (2022) |
| D614G | vaccine neutralization efficacy | Pokay | Omicron B.1.1.529 (BA.1) neutralization of the Omicron variants by antibodies induced by three doses of Pfizer/BNT162b2 mRNA vaccine was 7-8-fold less potent than the D614G, and the Omicron variants still evade neutralization more efficiently. | 2022 | Neerukonda et al. (2022) |
| D614G | pharmaceutical effectiveness | Pokay | Omicron (B.1.1.529 [BA.1]) have higher sensitivity to inhibition by soluble angiotensin converting enzyme 2 (ACE2) and the endosomal inhibitor chloroquine compared to D614G | 2022 | Neerukonda et al. (2022) |
| D614G | antibody epitope effects | Pokay | Neutralization of the bsAbs Bi-Nab35B5-47D10. Omicron BA.1 has an IC50 fold change of 0.30x. | 2022 | Yuan et al. (2022) |
| D614G | vaccine neutralization efficacy | Pokay | Paradigms' ACE-2 variant LVE/STR chimera binds to SARS-2 Omicron variant B.1.1.529 spike protein trimer with high affinity. Determined using Surrogate Viral Neutralization Tests. | 2022 | Uhal B et al. (2022) |
| D614G | ACE2 receptor binding affinity | Pokay | L27, V34 and E90 mutation resulted in ultrahigh affinity binding of the LVE-ACE-2 domain to the widest variety of VOCs, with KDs of 73 pM for binding to the Omicron B.1.1.529. Values were obtained with LVE-ACE-2/mAB chimeras containing the Y-T-E sequence that enhances binding to the FcRn receptor, which in turn is expected to extend biological half-life 3-4-fold. | 2022 | Uhal B et al. (2022) |
| D614G | antibody epitope effects | Pokay | Neutralization of the bsAbs 35B5. Omicron BA.1 has an IC50 fold change of 0.38x. | 2022 | Yuan et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|--------------------------|---------------------|--|------------------|-------------------------------------|
| D614G | vaccinee plasma binding | Pokay | All 10 individuals with 2 doses of the BNT162b2/BNT162b2 vaccine had a neutralizing titer in B.1 variant at an average of 729 NT50. | 2022 | Arora et al. (2022) |
| D614G | antibody epitope effects | Pokay | Plaque reduction neutralization test (PRNT) was used uring primary infection, post sixty daysof second dose vaccination, pre-reinfection and reinfection against Delta variant and was used to determine neutralizing antibodytitres. There was a 24.63x fold increase in antibody response from first infection to recovered and vaccinated with 2 doses (60 days). There was a 4.21x fold increase in antibody response pre-reinfection. There was a 39.27x fold increase in antibody response during reinfection. | 2022 | Shete et al. (2022) |
| D614G | antibody epitope effects | Pokay | Plaque reduction neutralization test (PRNT) was used uring primary infection, post sixty daysof second dose vaccination, pre-reinfection and reinfection against B.1 variant and was used to determine neutralizing antibodytitres. There was a 6.76x fold increase in antibody response from first infection to recovered and vaccinated with 2 doses (60 days). There was a 2.06x fold increase in antibody response pre-reinfection. There was a 8.18x fold increase in antibody response during reinfection. | 2022 | Shete et al. (2022) |
| D614G | vaccinee plasma binding | Pokay | All 10 individuals with 3 doses of the BNT162b2/BNT162b2 vaccine had a neutralizing titer in B.1 variant at an average of 3319 NT50. | 2022 | Arora et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|--|
| D614G | antibody epitope effects | Pokay | Plaque reduction neutralization test (PRNT) was used using primary infection, post sixty days of second dose vaccination, pre-reinfection and reinfection against Omicron variant and was used to determine neutralizing antibody titres. There was a 114.84x fold increase in antibody response from first infection to recovered and vaccinated with 2 doses (60 days). There was a 6.61x fold increase in antibody response pre-reinfection. There was a 1194.9x fold increase in antibody response during reinfection. | 2022 | Shete et al. (2022) |
| D614G | antibody epitope effects | Pokay | BnAb 002-S21F2 IC50 on the Omicron BA.1 variant is 1.0x fold the wildtype. | 2022 | Kumar et al. (2022) |
| D614G | antibody epitope effects | Pokay | Neutralization of the bsAbs 47D10. Omicron BA.1 has an IC50 fold change of 1.26x. | 2022 | Yuan et al. (2022) |
| D614G | pharmaceutical effectiveness | Pokay | Omicron BA.3 have higher sensitivity to inhibition by soluble angiotensin converting enzyme 2 (ACE2) and the endosomal inhibitor chloroquine compared to D614G | 2022 | Neerukonda et al. (2022) |
| D614G | vaccine neutralization efficacy | Pokay | Omicron BA.3 neutralization of the Omicron variants by antibodies induced by three doses of Pfizer/BNT162b2 mRNA vaccine was 7-8-fold less potent than the D614G, and the Omicron variants still evade neutralization more efficiently. | 2022 | Neerukonda et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|---------------------------------------|
| D614G | vaccinee plasma binding | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.3 (from South Africa/NICD-N22404/2021) were 4.2x-fold lower (95% CI: 0.15x-0.20x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| D614G | vaccine neutralization efficacy | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.3 (from South Africa/NICD-N22404/2021) were 6.2-fold lower (95% CI: 11.8x-14.3x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| D614G | vaccine neutralization efficacy | Pokay | paired testing of vaccine sera against ancestral virus compared to Omicron BA.1 shows that 3-dose vaccine regimen provides over 50x fold increase in protection against Omicron(B.1.1.529 [BA.1]) compared to a 2-dose regimen. | 2022 | Hao et al. (2022) |
| D614G | pharmaceutical effectiveness | Pokay | 4th antigenic exposure with Omicron (B.1.1.529 [BA.1])(n | 2022 | Wang et al. (2022) |
| D614G | vaccine neutralization efficacy | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.1 (from Botswana/R40B59_BHP_3321 001248/2021) were 3.4-fold lower (95% CI: 3.2x-3.6x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|--|
| D614G | vaccinee plasma binding | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.1 (from Botswana/R40B59_BHP_3321 001248/2021) were 28.7x-fold lower (95% CI: 0.03x-0.05) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| D614G | vaccine neutralization efficacy | Pokay | The neutralizing activity of vaccine was somewhat lower against B.1.1.7 in sera tested from most of the 24 patients with the BNT162b2 mRNA vaccine. (Fig. 4) | 2021 | Chen et al. (2021) |
| D614G | antibody epitope effects | Pokay | B.1.1.7 variant constellation ablates Class 3 N-terminal domain targeting antibody COV2-2489. | 2021 | Chen et al. (2021) |
| D614G | vaccine neutralization efficacy | Pokay | Observed 8.8-fold reduction in neutralization efficiency of Pfizer vaccinee sera (collected 14 days after second dose) against cultured B.1.1.7 sample. Contrast this with 1.3-fold reduction for just the pseudovirus combination of 'key' B.1.1.7 mutation N501Y. | 2021 | Bates et al. (2021) |
| D614G | vaccine neutralization efficacy | Pokay | Pseudotyped B.1.1.298 virus has reduced neutralization activity vs wild type: 1.4x (30 sera Pfizer median 9 days post 2nd dose) and 1.3x (35 sera Moderna median 18 days post 2nd dose). This was NOT significant by ANOVA. | 2021 | Garcia-Beltran et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|--|
| D614G | vaccine neutralization efficacy | Pokay | After one dose, individuals with prior infection showed enhanced T cell immunity, antibody secreting memory B cell response to spike and neutralizing antibodies effective against B.1.1.7 (authentic cell culture supernatants). By comparison, HCW receiving one vaccine dose without prior infection showed reduced immunity against variants. B.1.1.7 spike mutations resulted in increased, abrogated or unchanged T cell responses depending on human leukocyte antigen (HLA) polymorphisms. Study was 26 each post-infection and post first dose HCWs. | 2021 | Reynolds et al. (2021) |
| D614G | convalescent plasma escape | Pokay | Mean 2.6x reduction of NT50 value B.1.1.7 (Alpha) relative to wild type in 8 sera from older convalescent patients (52-92yo) collected 1-3m post symptom onset. | 2021 | Uriu et al. (2021) |
| D614G | vaccine neutralization efficacy | Pokay | Detectable antibodies against B.1.1.7 at various time points using pseudotyped lentivirus neutralization in Moderna vaccinee cohort: Day 29 33%, Day 43 100%, Day 119 100%, Day 209 96%. Detectable antibodies against B.1.1.7 at various time points using live virus FRNT neutralization in Moderna vaccinee cohort: Day 29 54%, Day 43 100%, Day 119 100%, Day 209 88%. Detectable antibodies against B.1.1.7 at various time points using ACE2 blocking assay in Moderna vaccinee cohort: Day 29 83%, Days 43,119,209 100%. | 2021 | Pegu et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|--------------------------------------|
| D614G | vaccine neutralization efficacy | Pokay | Using national surveillance data from Israel, using Pfizer vaccine and an estimated prevalence of the B.1.1.7 variant of 94.5% among SARS-CoV-2 infections: Adjusted estimates of vaccine effectiveness 7+ days after second dose were 95.3% (95% CI 94.9–95.7): 91.5% against asymptomatic SARS-CoV-2 infection (90.7–92.2: 40.9 vs 1.8 per 100 000 person-days), 97.0% against symptomatic COVID-19 (96.7–97.2%), 97.2% against COVID-19-related hospitalisation (96.8–97.5%), 97.5% against severe or critical COVID-19-related hospitalisation (97.1–97.8%), and 96.7% against COVID-19-related death (96.0–97.3%). In all age groups, as vaccine coverage increased, the incidence of SARS-CoV-2 outcomes declined | 2021 | Haas et al. (2021) |
| D614G | vaccine neutralization efficacy | Pokay | In sera 1-2 weeks after BNT162b2 first dose, from six patients previously infected with B.1, antibody titer in a microneutralization assay was on average 8192 for B.1.351 virus. This compares favorably (stronger) to post-infection neutralization titer against all variants tested in the same sera (wild type, B.1.1.7, B.1.351, and P.1). | 2021 | Luftig et al. (2021) |
| D614G | virion structure | Pokay | CryoEM analysis of B.1.1.7 demonstrates an increased propensity for 'up', receptor accessible conformation of the Spike protein trimer. | 2021 | Cai et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|---|
| D614G | vaccine neutralization efficacy | Pokay | SARS-CoV-2 infection was confirmed in three HCWs working a single shift: all presented with mild symptoms of COVID-19. The two physicians were fully vaccinated with BNT162b2 vaccine, with the second dose administered 1 month before symptom onset. Both had high titres of IgG anti-spike antibodies at the time of diagnosis. WGS confirmed that all virus strains were VOC 202012/01-lineage B.1.1.7, suggesting a common source of exposure. Epidemiological investigation revealed that the suspected source was a SARS-CoV-2-positive patient who required endotracheal intubation due to severe COVID-19. All procedures were carried out using a full suite of personal protective equipment (PPE). | 2021 | Loconsole et al. (2021) |
| D614G | vaccine efficacy | Pokay | In a 1:5 test-negative matched control study of 8153 individuals who received the Moderna mRNA-1273 vaccine, 1422 test-positive were Alpha. Two dose vaccine efficacy against Alpha was 98.4% [96.9-99.1%], one dose VE was 90.1% (82.9-94.2%). | 2021 | Bruxvoort et al. (2021) |
| D614G | convalescent plasma escape | Pokay | Using a new rapid neutralization assay, based on reporter cells that become positive for GFP after overnight infection, sera from 58 convalescent individuals collected up to 9 months after symptoms, similarly neutralized B.1.1.7 and D614G. | 2021 | Planas et al. (2021) |
| D614G | antibody epitope effects | Pokay | Neutralization of the bsAbs Bi-Nab35B5-47D10. Alpha (B.1.1.7) has an IC50 fold change of 1.19x. | 2022 | Yuan et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|--|
| D614G | antibody epitope effects | Pokay | B.1.1.7 pseudotyped virus model impairs binding by RBD-directed mAb 910-30. B.1.1.7 pseudotyped virus model abolishes N-terminal-domain-directed mAbs 5-24, 4-8, and 4A8. B.1.1.7 pseudotyped virus model impairs binding by N-terminal-domain-directed mAbs 2-17, 4-19, 5-7. | 2021 | Wang et al. (2021) |
| D614G | vaccine neutralization efficacy | Pokay | 1.4x improvement in neutralization by serum collected 2 to 3 weeks after the second dose from vaccinees who had received BBIBP-CorV (pVNT50 against VSV pseudotyped as B.1.1.7). Convalescent plasma had similar titer against wild type as the BBIBP-CorV vaccinee sera. 2x reduction in neutralization by serum collected 2 to 3 weeks after the second dose from vaccinees who had received CoronaVac (pVNT50 against VSV pseudotyped as B.1.1.7). Convalescent plasma had similar titer against wild type as the CoronaVac vaccinee sera. | 2021 | Wang et al. (2021) |
| D614G | aerosolization | Pokay | Alpha variant cases in a large campus study showed fine-aerosol shedding amongst unmasked participants remained significantly greater for alpha variant infections (18-fold, 95% CI, 3.4 to 92-fold) after adjusting for the increased viral RNA in MTS and saliva, the number of coughs during sampling sessions, and symptom. After controlling for the effect of masks and numbers of coughs during sampling, alpha variant infection was associated with a 100-fold (95% CI, 16 to 650-fold) increase in coarse- and a 73-fold (95% CI, 15 to 350-fold) increase in fine-aerosol RNA shedding. | 2021 | Adenaiye et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|-----------------------------------|---------------------|--|------------------|---|
| D614G | environmental condition stability | Pokay | No differences in the stability of B.1.1.7 observed in the absence of simulated sunlight at either 20°C or 40°C (with a mean time for a 90% loss of viral infectivity across all dark conditions of 6.2 hours). However, a small but statistically significant difference in the stability was observed in simulated sunlight at 20°C and 20% relative humidity, with B.1.1.7 restoring wild type 90% loss time of 11 minutes vs. 7 and 8 minutes for B.1.319 (D614G) and B.28 (V367F) early 2020 viruses respectively. | 2021 | Schuit et al. (2021) |
| D614G | trafficking | Pokay | Modelling the Alpha variant in primary human airway epithelial (HAE) cultures, S1 to full length Spike ratio (measuring Spike furin cleavage processivity) increase 3.9x relative to wild type (5.4 vs 1.4). This is less efficient than Delta (11x vs wildtype using a P681R mutation instead). [del ~144 changed due to ambiguity] Furthermore the RNA ratio of Delta versus Alpha-spike/Delta-backbone continuously increased from 2.8 on day 1 to 9.8 on day 5 post infection in a co-infection model in HAEs, suggesting the spike gene drives the improved replication of Delta variant. | 2021 | Liu et al. (2021) |
| D614G | vaccine neutralization efficacy | Pokay | No significant difference in T-cell response to B.1.1.7 was observed (vs. ancestral) in blood drawn from 28 participants received the Pfizer-BioNTech vaccine and 2 received the Moderna vaccine. This is despite three mutations (Y144del, D614G, and P681H) overlapping T-cell epitope hotspots. | 2021 | Woldemeskel et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|--------------------------------------|
| D614G | vaccine neutralization efficacy | Pokay | The NAb titers (PRNT50) of sera collected from 38 vaccine recipients four-weeks after the second dose of inactivated whole-virion SARS-CoV-2 BBV152/COVAXIN vaccine [which contains D614G] were not significantly different between B.1.1.7 virus and ancestral D614G virus. | 2021 | Sapkal et al. (2021) |
| D614G | vaccine neutralization efficacy | Pokay | PBMCs of Pfizer/BioNTech BNT162b2 (n | 2021 | Tarke et al. (2021) |
| D614G | vaccine neutralization efficacy | Pokay | A single dose of BNT162b2 vaccine demonstrated vaccine effectiveness [symptomatic or asymptomatic in cohort of routinely NAAT-monitored UK HCWs] of 72% (95% CI 58-86) 21 days after first dose and 86% (95% CI 76-97) seven days after two doses in the antibody negative cohort. This cohort was vaccinated when the dominant variant in circulation was B.1.1.7 and demonstrates effectiveness against this variant. | 2021 | Hall et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|--|
| D614G | vaccine neutralization efficacy | Pokay | Between December 19, 2020 and Jan 24, 2021, 7214 of 9109 eligible HCWs at Sheba Medical Center in Israel had received one or more doses of BNT162b2 (Pfizer) vaccine. Adjusted rate reduction in SARS-CoV-2 NAAT positivity infection compared with unvaccinated workers 1-14 days after 1st dose was 30% (95% CI: 2-50), and 75% (95% CI: 72-84) after 15-28 days. Adjusted rate reduction in symptomatic COVID-19 compared with unvaccinated workers 1-14 days after 1st dose was 47% (95% CI: 17-66), and 85% (95% CI: 71-92) after 15-28 days. [Though often cited as an indicator of VE for B.1.1.7, during this time period in Israel, the prevalence of the B.1.1.7 variant increased from ~20% to 50% of cases (covariants.org), therefore these VE numbers likely represent a mix of B.1.1.7 and other lineage effects.] | 2021 | Amit et al. (2021) |
| D614G | vaccine neutralization efficacy | Pokay | We found that a single dose of the BNT162b2 vaccine is about 60-70% effective at preventing symptomatic disease in adults aged 70 years and older in England and that two doses are about 85-90% effective. Those who were vaccinated and went on to have symptoms had a 44% lower risk of being admitted hospital and a 51% lower risk of death compared with people who were unvaccinated. We also found that a single dose of the ChAdOx1-S vaccine was about 60-75% effective against symptomatic disease and provided an additional protective effect against hospital admission—it is too early to assess the effect on mortality. The B.1.1.7 variant now dominates in the UK and these results will largely reflect vaccine effectiveness against this variant. | 2021 | Lopez Bernal et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|--|
| D614G | antibody epitope effects | Pokay | Neutralization of the 47D10. Alpha (B.1.1.7) has an IC50 fold change of 0.40x. | 2022 | Yuan et al. (2022) |
| D614G | anthropozoonotic events | Pokay | First documented cases of domestic cat and dog infections with the B.1.1.7 strain. | 2021 | Hamer et al. (2021) |
| D614G | vaccine efficacy | Pokay | Effectiveness after one dose of vaccine (BNT162b2 or ChAdOx1 nCoV-19) with the delta variant was (48.7%: 95% confidence interval [CI], 45.5 to 51.7): the results were similar for both vaccines. With the BNT162b2 vaccine, the effectiveness of two doses was 93.7% (95% CI, 91.6 to 95.3) among those with the alpha variant. With the ChAdOx1 nCoV-19 vaccine, the effectiveness of two doses was 74.5% (95% CI, 68.4 to 79.4) among those with the alpha variant. | 2021 | Lopez Bernal et al. (2021) |
| D614G | antibody epitope effects | Pokay | Reduction in neutralization by mAbs COVA2-15 (~9x), B38 (~14x), S309 (~190x) by this B.1.1.7 pseudotyped virus model. | 2021 | Shen et al. (2021) |
| D614G | vaccine neutralization efficacy | Pokay | We observed a sharp decline in cases when ~50% of the elderly population was 2 weeks beyond their first vaccination dose and at a time point during which the B.1.1.7 variant gained transmission dominance. In support of this finding, it was suggested that, after the first vaccination dose, more than 70% of patients develop neutralization antibodies, ¹⁵ and the vaccine efficiency can reach 85%. | 2021 | Munitz et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|--|
| D614G | convalescent plasma escape | Pokay | Neutralizing antibody titers of 2/20 (10%) samples showed >10x reduction (sera collected ~1mo post Jan 2020 first wave in China). Neutralizing antibody titers of 8/20 samples (40%) decreased below an ID50 threshold of 40 (sera collected ~8mo post Jan 2020 first wave in China). | 2021 | Hu et al. (2021) |
| D614G | antibody epitope effects | Pokay | Lessens the potency of mAbs COVA2-17 (~5x, similar to N501Y alone), COVA1-12 (~11x) and COVA1-21 (>100x), which do not compete allosterically. | 2021 | Rees-Spear et al. (2021) |
| D614G | reinfection | Pokay | 36920 COVID Symptom Study app users reported SARS-CoV-2 test positivity in late 2020. Possible reinfections were identified in 249 (0.7% [95% CI 0.6-0.8]) of 36509 app users who reported a positive swab test before Oct 1, 2020, but there was no evidence that the frequency of reinfections was higher for the B.1.1.7 variant than for pre-existing variants. | 2021 | Graham et al. (2021) |
| D614G | vaccine neutralization efficacy | Pokay | Pseudotyped B.1.1.7 virus has reduced neutralization activity vs wild type: 2.1x (30 sera Pfizer median 9 days post 2nd dose) and 2.3x (35 sera Moderna median 18 days post 2nd dose). This was NOT significant by ANOVA. Note that Y145del was actually noted in the paper as the effect of their DNA construct, but this is equivalent at the protein level to the more commonly annotated Y144del. | 2021 | Garcia-Beltran et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|---------------------------------------|
| D614G | vaccine neutralization efficacy | Pokay | The sera of 16 individuals with time course collection was evaluated against VSV pseudotypes: neutralized D614G at week 2, whereas B.1.1.7 started to be neutralized at week 3, although less efficiently than D614G. B.1.1.7 and D614G strains were similarly neutralized at week 4 (1 week after booster dose). | 2021 | Planas et al. (2021) |
| D614G | vaccine neutralization efficacy | Pokay | Neutralization assays of B.1.1.7 virus showed a reduction of 2.5-fold (14 days post 2nd dose AstraZeneca, n | 2021 | Supasa et al. (2021) |
| D614G | antibody epitope effects | Pokay | Neutralization of the bsAbs 35B5. Alpha (B.1.1.7) has an IC50 fold change of 1.39x. | 2022 | Yuan et al. (2022) |
| D614G | vaccine efficacy | Pokay | In Minnesota in early 2021 when Alpha was prevalent, vaccine efficacy was estimated as: mRNA-1273 86% (95%CI: 81-90.6%) and BNT162b2: 76% (95%CI: 69-81%) using age, sex, race, PCR testing and vaccination date matched cohorts of unvaccinated, Pfizer and Moderna vaccinees. [variant list included is ancestral Alpha, as this was an observational study no variant list was given] | 2021 | Puranik et al. (2021) |
| D614G | antibody epitope effects | Pokay | ~20x resistance to mAb CQ038 by B.1.1.7 pseudotyped virus | 2021 | Hu et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|---------------------------------------|
| D614G | reinfection | Pokay | Reinfection with Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) B.1.1.7 variant in an immunocompromised 16yo female with end stage renal disease 94 days after initial infection with a B.1.2 lineage virus. Both lineages were the prevalent one at the time of 1st and 2nd infections respectively in Texas, where the patient was located (suggesting exposure risk rather than lineage immune evasion). | 2021 | Marquez et al. (2021) |
| D614G | vaccine neutralization efficacy | Pokay | Paradigm's ACE-2 variant LVE/STR chimera neutralizes Alpha Variant B.1.1.7 RBD significantly better than GenScript IgG FL18-740 w.t. ACE-2 mAB. Determined using Surrogate Viral Neutralization Tests. | 2022 | Uhal B et al. (2022) |
| D614G | antibody epitope effects | Pokay | Neutralization of the bsAbs Bi-Nab47D10-35B5. Alpha (B.1.1.7) has an IC50 fold change of 1.44x. | 2022 | Yuan et al. (2022) |
| D614G | vaccine neutralization efficacy | Pokay | A single dose of BNT162b2 (Pfizer) vaccine showed vaccine effectiveness of 70% (95% CI 55-85) 21 days after first dose and 85% (74-96) 7 days after two doses in the study population. Our findings show that the BNT162b2 vaccine can prevent both symptomatic and asymptomatic infection in working-age adults. This cohort (8203 treatment, 15121 control) was vaccinated when the dominant variant in circulation was B.1.1.7 and shows effectiveness against this variant. | 2021 | Hall et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|---------------------------------------|
| D614G | convalescent plasma escape | Pokay | NTD-specific nAbs showed a substantial (3-450x) decrease in neutralization potency against the recently reported highly transmissible B.1.1.7 variant of concern, whereas RBD-specific nAbs were either unaffected or showed lower decreases in potency. | 2021 | Graham et al. (2021) |
| D614G | tissue specific neutralization | Pokay | The nasal mucosa of Pfizer vaccinees with time course collection was evaluated against VSV pseudotypes: results (only one nasal swab from different previously infected vaccinee neutralizing at weeks 3 and 6 against B.1.1.7 and D614G) suggest that vaccinees probably do not elicit an early humoral response detectable at mucosal surfaces even though sera neutralization was observed. They strengthen the hypothesis that some vaccines may not protect against viral acquisition and infection of the oral–nasal region, but may prevent severe disease associated with viral dissemination in the lower respiratory tract. | 2021 | Planas et al. (2021) |
| D614G | pharmaceutical effectiveness | Pokay | Infectious viral titers in lung tissue determined using a tissue culture infectious dose (TCID) assay in 10 hamsters showed that Alpha Molnupiravir (MK-4482) had ~2.75x fold drop. | 2022 | Rosenke et al. (2022) |
| D614G | vaccine neutralization efficacy | Pokay | Neutralization efficiency (ID50) against B.1.1.7 reduced 1.2x relative to D614G wildtype using pseudotyped VSV assay on 8 Moderna vaccinee sera one week post-booster. | 2021 | Choi et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|--|
| D614G | reinfection | Pokay | Second infection in December 2020 with B.1.1.7 after April 2020 initial infection with B.2 in a 78-year-old man with a history of Type 2 diabetes mellitus, diabetic nephropathy on hemodialysis, chronic obstructive pulmonary disease (COPD), mixed central and obstructive sleep apnea, ischemic heart disease, with no history of immunosuppression. | 2021 | Harrington et al. (2021) |
| D614G | trafficking | Pokay | The entry efficiencies of Spike pseudotyped viruses bearing N501Y Variant 1 (B.1.1.7) mutant were about 3 to 4.4 times higher than that of the WT pseudovirus when viral input was normalized, suggesting that these spike variants promote the infectivity of SARS-CoV-2. | 2021 | Hu et al. (2021) |
| D614G | trafficking | Pokay | ~2.5x cleavage of S2 relative to WA1 (D614G) wildtype by Alpha variant variant as measured by mass spectrometry of Vero-TMPRSS culture. | 2021 | Esclera et al. (2021) |
| D614G | vaccine neutralization efficacy | Pokay | Virus neutralisation activity (using a live SARS-CoV-2 microneutralisation assay (ND50)) by vaccine induced antibodies was 9-fold lower against the B.1.1.7 variant than against a canonical non B.1.1.7 lineage. Vaccine efficacy against symptomatic NAAT positive infection was similar for B.1.1.7 and non-B.1.1.7 lineages (74.6% [95%CI 41.6-88.9] and 84% [95% CI 70.7-91.4] respectively). Furthermore, vaccination with ChAdOx1 nCoV-19 results in a reduction in the duration of shedding and viral load, which may translate into a material impact on transmission of disease. | 2021 | Emary et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|---|
| D614G | antibody epitope effects | Pokay | BnAb 002-S21F2 IC50 on the Alpha (B.1.1.7) variant is 1.0x fold the wildtype in 42 COVI. | 2022 | Kumar et al. (2022) |
| D614G | vaccine neutralization efficacy | Pokay | ELISpot assays show T cell neutralization reduced by 15.4% in this B.1.1.7 pseudotype relative to wild type in 18-20 pooled patient samples post second mRNA vaccine dose, with no significant difference between Pfizer and Moderna cohorts. Reduction was stronger in the S1 subunit than S2 (separate peptide pools were used). | 2021 | Gallagher et al. (2021) |
| D614G | vaccine neutralization efficacy | Pokay | 2.1x drop in neutralization using sera collected from 14 healthy adult participants that received two injections of the mRNA-1273 (Moderna) vaccine at a dose of 100 µg (18-55 years: day 1 (n | 2021 | Edara et al. (2021) |
| D614G | vaccine neutralization efficacy | Pokay | B.1.1.7 pseudotyped VSV was tested for neutralization in a clonal HEK-293T ACE2 TMPRSS2 cell line optimized for highly efficient S-mediated infection. A cohort of 12 Argentinian recipients of the Gamaleya Sputnik V Ad26 / Ad5 vaccine showed no statistically significant change in neutralization efficacy. | 2021 | Ikegame et al. (2021) |
| D614G | vaccine neutralization efficacy | Pokay | NVX-CoV2373 [Novavax] vaccine in phase 3 trial was 89.7% (95% CI, 80.2-94.6) effective in preventing COVID-19, with no hospitalizations or deaths reported. There were five cases of severe Covid-19, all in the placebo group. Post hoc analysis revealed efficacies of 96.4% (73.8-99.5) and 86.3% (71.3-93.5) against the prototype strain and B.1.1.7 variant, respectively. | 2021 | Heath et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|---------------------------------------|
| D614G | vaccine neutralization efficacy | Pokay | Pseudotyped B.1.1.7 Spike variants lentivirus. 3.5x reduction in neutralization with Moderna vaccinated patient sera after 29 days (1st dose). 2.0x reduction in neutralization with Moderna vaccinated patient sera after 57 days (2nd dose). 2.1x reduction in neutralization with Novavax Phase 1 post-vaccination sera. | 2021 | Shen et al. (2021) |
| D614G | clinical indicators | Pokay | After adjusting for the age factor, in a prospective Chinese cohort study B.1.1.7 variant infection (compared to B.1.140) was the risk factor for C-reactive protein (P | 2021 | Song et al. (2021) |
| D614G | vaccine efficacy | Pokay | Using a test-negative design using Ontario data between Dec 14, 2020 and May 30, 2021, 421,073 symptomatic community-dwelling individuals were tested. Against symptomatic infection caused by Alpha, vaccine effectiveness with partial vaccination (≥ 14 days after dose 1) was higher for mRNA-1273 (83%) than BNT162b2 (66%) and ChAdOx1 (64%), and full vaccination (≥ 7 days after dose 2) increased vaccine effectiveness for BNT162b2 (89%) and mRNA-1273 (92%). | 2021 | Nasreen et al. (2021) |
| D614G | trafficking | Pokay | Live virus was tested ex vivo in reconstituted bronchial epithelium, and out competed wild type. | 2021 | Touret et al. (2021) |
| D614G | vaccine neutralization efficacy | Pokay | Mean 1.7x reduction of NT50 value B.1.1.7 (Alpha) relative to wild type in 8 sera from adult BNT162b2 vaccinees (28-47yo) collected ~1m post booster. | 2021 | Uriu et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|--------------------------------------|
| D614G | ACE2 receptor binding affinity | Pokay | Flow cytometry was used on recombinant VSV proteins and yeast surface display to assess the binding of a labeled soluble ACE2 protein to cells expressing B.1.1.7. We observed a dramatic increase (relative to D614G) in binding of soluble ACE2 to B.1.1.7, and to a lesser extent to B.1.351, which both carry the N501Y mutation (see Fig 3). | 2021 | Planas et al. (2021) |
| D614G | ACE2 receptor binding affinity | Pokay | L27, V34 and E90 mutation resulted in ultrahigh affinity binding of the LVE-ACE-2 domain to the widest variety of VOCs, with KDs of 93 pM for binding to the Alpha B1.1.7. Values were obtained with LVE-ACE-2/mAB chimeras containing the Y-T-E sequence that enhances binding to the FcRn receptor, which in turn is expected to extend biological half-life 3-4-fold. | 2022 | Uhal B et al. (2022) |
| D614G | vaccine neutralization efficacy | Pokay | 1.5x reduction in neutralization (ID50) in sera 3 weeks after one dose of Pfizer/BioNTech BNT162b2 (up to 5 naive and post infection vaccinees) | 2021 | Gong et al. (2021) |
| D614G | vaccine neutralization efficacy | Pokay | nan | | UNKNOWN et al. () |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|-------------------------------------|---------------------|---|------------------|---|
| D614G | vaccine neutralization efficacy | Pokay | In Qatar, where Pfizer vaccine use is prevalent (<10% of the population covered in the time period of the study ending Mar 31, 2021), any time after one dose (including the 2 weeks where no major effect is expected) B.1.1.7 lineage effectiveness was observed as 29.5% (95% CI [22.9,35.5]) against infection, and 54.1% against severe/critical/fatal disease (95% CI [26.1-71.9]). Two weeks or more after 2nd dose, effectiveness climbed to 89.5% [85.9,92.3] against infection, and 100% against severe/critical/fatal disease (95% CI [81.7,100]). | | UNKNOWN et al. () |
| D614G | pharmaceutical effectiveness | Pokay | Lilly's LY-CoV16 showed marked reduction in neutralization of B.1.1.7. | 2021 | Dejnirattisai et al. (2021) |
| D614G | convalescent plasma escape | Pokay | Sera neutralized the B.1.1.7 isolate with a lower potency (2-fold: 95% CL: 1.5 – 3-fold), and those with the lowest homotypic neutralizing potency had undetectable heterotypic potency (2/25). | 2021 | Skelly et al. (2021) |
| D614G | tissue specific replication effects | Pokay | In this report, by using a lower infectious dose, we demonstrate that B.1.1.7 (cultured sample Hong Kong/HKPU-00015/2021) exhibits higher infectivity and/or replication efficiency in the nasal epithelium. (Hamster model of infection) | 2021 | Mok et al. (2021) |
| D614G | vaccinee plasma binding | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.4/5 (from) were 17.2x-fold lower (95% CI: 0.6x-0.7x) than against 208-428 972-1834 4.3-4.7 US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahade et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|--|
| D614G | vaccine neutralization efficacy | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.4/5 (from) were 13.0-fold lower (95% CI: 4.2x-4.6x) than against 208-428 972-1834 4.3-4.7 US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahade et al. (2022) |
| D614G | vaccine neutralization efficacy | Pokay | Mean 1.7x reduction of NT50 value for C.37 (Lambda) relative to wild type in 8 sera from adult BNT162b2 vaccinees (28-47yo) collected ~1m post booster. | 2021 | Uriu et al. (2021) |
| D614G | convalescent plasma escape | Pokay | Mean 3.4x reduction of NT50 value for C.37 (Lambda) relative to wild type in 8 sera from older convalescent patients (52-92yo) collected 1-3m post symptom onset. | 2021 | Uriu et al. (2021) |
| D614G | pharmaceutical effectiveness | Pokay | Trimeric proteins FSR22 had a 0.048x fold change in IC50 in C.37 Lambda | 2022 | Chonira et al. (2022) |
| D614G | pharmaceutical effectiveness | Pokay | Trimeric proteins FSR16m had a 0.038x fold change in IC50 in C.37 Lambda | 2022 | Chonira et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|--|
| D614G | vaccine neutralization efficacy | Pokay | 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 ~10-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 ~3 fold without the deletion] ID50 titres in non-infected mRNA vaccines more than two weeks post-booster were significant, but ~500x weaker than in previously infected patients after first dose. | 2021 | Stamatatos et al. (2021) |
| D614G | vaccine neutralization efficacy | Pokay | 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+. | 2021 | Pegu et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|--|
| D614G | vaccine neutralization efficacy | Pokay | 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 ~2 better neutralization than BNT162b2. [common defining B.1.351 mutations noted, as the manuscript does not provide details] | 2021 | Abe et al. (2021) |
| D614G | antibody epitope effects | Pokay | 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 ~10-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. | 2021 | Stamatatos et al. (2021) |
| D614G | convalescent plasma escape | Pokay | 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] | 2021 | Stamatatos et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|---------------------------------------|
| D614G | vaccine neutralization efficacy | Pokay | 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] | 2021 | Tada et al. (2021) |
| D614G | antibody epitope effects | Pokay | Neutralization of the bsAbs Bi-Nab35B5-47D10. Beta (B.1.351) has an IC50 fold change of 0.13x. | 2022 | Yuan et al. (2022) |
| D614G | pharmaceutical effectiveness | Pokay | Infectious viral titers in lung tissue determined using a tissue culture infectious dose (TCID) assay in 10 hamsters showed that Beta Molnupiravir (MK-4482) had ~1.75x fold drop. | 2022 | Rosenke et al. (2022) |
| D614G | ACE2 receptor binding affinity | Pokay | The B.1.351 variant constellation causes an ~20-fold increase in affinity for ACE2 compared with Wuhan RBD, which may influence transmissibility. | 2021 | Zhou et al. (2021) |
| D614G | humoral response durability | Pokay | 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. | 2020 | Betton et al. (2020) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|----------------------------|---------------------|---|------------------|--|
| D614G | trafficking | Pokay | ~6x cleavage of S2 relative to WA1 (D614G) wildtype by Beta variant as measured by mass spectrometry of Vero-TMPRSS culture [no mutations directly at furin cleavage site, but A701V is downstream] Compare to 4.5x or less for variants of concern with direct furin cleavage site mutations. | 2021 | Esclera et al. (2021) |
| D614G | outcome hazard ratio | Pokay | Compared to Alpha (B.1.1.7) variant, odds of progressing to severe disease were 1.24-fold (95% CI: 1.11-1.39) higher for Beta. Odds of progressing to critical disease were 1.49-fold (95% CI: 1.13-1.97) higher. Odds of COVID-19 death were 1.57-fold (95% CI: 1.03-2.43) higher. | 2021 | Abu-Raddad et al. (2021) |
| D614G | antibody epitope effects | Pokay | BnAb 002-S21F2 IC50 on the Beta (B.1.351) variant is 0.4x fold the wildtype. | 2022 | Kumar et al. (2022) |
| D614G | convalescent plasma escape | Pokay | In 34 convalescent cases 4–9 weeks following infection in June 2020, before the emergence of B.1.1.7, neutralization titers against B.1.351 were, on average, 13.3-fold reduced compared with an early Victoria sample ($p < 0.0001$). Significantly, 18 of 34 samples failed to reach 50% neutralization at a plasma dilution of 1:20, with a number showing a near total reduction of neutralization activity. In 13 convalescent cases 4–9 weeks following infection with B.1.1.7, neutralization titers against B.1.351 were, on average, 3.1-fold reduced compared with an early Victoria sample ($p < 0.0001$). | 2021 | Zhou et al. (2021) |
| D614G | antibody epitope effects | Pokay | Neutralization of the bsAbs Bi-Nab47D10-35B5. Beta (B.1.351) has an IC50 fold change of 0.15x. | 2022 | Yuan et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|-------------------------------------|
| D614G | vaccine neutralization efficacy | Pokay | Vaccine plasma neutralization of B.1.351-spike virus was nominally robust but lower (~3x) than other variants of concern. | 2021 | Liu et al. (2021) |
| D614G | vaccine neutralization efficacy | Pokay | 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. | 2021 | Choi et al. (2021) |
| D614G | antibody epitope effects | Pokay | Testing against B.1.351 the 20 most effective mAbs (19 anti-RBD, 1 anti-NTD) from a screen of 377 against wild type, 4 of 20 antibodies had >10-fold fall in neutralization titers, with most of these showing a complete knockout of activity. This is in line with the key roles of K417, E484, and N501, in particular E484, in antibody recognition of the ACE2 interaction surface of the RBD. Regeneron mAb cocktail: The neutralization of REGN10987 was unaffected by B.1.351, while REGN10933 was severely impaired (773-fold). AstraZeneca mAb cocktail: Neutralization by the AZ pair of antibodies was little affected on B.1.351 compared with Victoria. | 2021 | Zhou et al. (2021) |
| D614G | vaccine neutralization efficacy | Pokay | 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. | 2021 | Madhi et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|--|
| D614G | vaccine neutralization efficacy | Pokay | 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. | | UNKNOWN et al. () |
| D614G | anthropozoonotic events | Pokay | Unlike wild type or B.1.1.7, B.1.351 lineage virus was able to infect and replicate in common lab mouse strains, with high titer. PG: The virus used in these experiments has a non-typical deletion+sub in the 242 region. | 2021 | Montagutelli et al. (2021) |
| D614G | antibody epitope effects | Pokay | Neutralization of the bsAbs 35B5. Beta (B.1.351) has an IC50 fold change of 0.13x. | 2022 | Yuan et al. (2022) |
| D614G | vaccine neutralization efficacy | Pokay | Sera from healthcare workers (n | 2021 | Zhou et al. (2021) |
| D614G | antibody epitope effects | Pokay | Neutralization of the bsAbs 47D10. Beta (B.1.351) has an IC50 fold change of 0.88x. | 2022 | Yuan et al. (2022) |
| D614G | outcome hazard ratio | Pokay | 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. | 2021 | Funk et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|--|
| D614G | vaccine neutralization efficacy | Pokay | 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. | 2021 | Garcia-Beltran et al. (2021) |
| D614G | vaccine neutralization efficacy | Pokay | 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). | 2021 | Gallagher et al. (2021) |
| D614G | convalescent plasma escape | Pokay | 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. | 2021 | Stamatatos et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|--|
| D614G | vaccine neutralization efficacy | Pokay | 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 ~3-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 ~10 fold with L242del] ID50 titres in non-infected mRNA vaccines more than two weeks post-booster were significant, but >100x weaker than in previously infected patients after first dose. | 2021 | Stamatatos et al. (2021) |
| D614G | vaccine neutralization efficacy | Pokay | Pseudotyped B.1.351 v3 virus has reduced neutralization activity vs wild type: 42.4x (30 sera Pfizer median 9 days post 2nd dose) and 19.2x (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. | 2021 | Garcia-Beltran et al. (2021) |
| D614G | vaccine neutralization efficacy | Pokay | The neutralization activities of two vaccines developed in China were tested against 501Y.V2 authentic virus: inactivated BBIBP-CorV (no significant change) and recombinant dimeric RBD vaccine ZF2001 (~1.6x reduction vs wildtype, p | 2021 | Huang et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|---------------------------------------|
| D614G | vaccine neutralization efficacy | Pokay | Most of the plasma from 55 Pfizer vaccinees developed high percentages of Wuhan-Hu-1 S-ACE2 blocking activity, peaking at day 28 (7 days post-boost). A strikingly consistent hierarchy of reduction in plasma antibody binding by variant S and RBD antigens was observed among study participants, with progressively decreased binding for B.1.1.7 (not significant), P.1 (significant) and B.1.351 (significant) compared to Wuhan-Hu-1 antigens. | 2021 | Röltgen et al. (2021) |
| D614G | vaccine neutralization efficacy | Pokay | During an outbreak of SARS-CoV-2 501Y.V2 in a nursing home, all non-vaccinated residents (5/5) versus half of those fully vaccinated 2-5 weeks prior with BNT162b2 (13/26) were infected. Two of 13 vaccinated versus 4 of 5 non-vaccinated residents presented severe disease. BNT162b2 did not prevent the outbreak, but reduced transmission and disease severity. Among the 13 fully vaccinated residents who were infected, 2 (15.4%) presented with an asymptomatic disease, 9 (69.2%) developed mild to moderate symptoms, and 2 (15.4%) progressed to severe disease with fatal evolution secondary to acute respiratory distress syndrome (ARDS). There was no relationship between anti-S antibody levels at diagnosis and disease severity. Overall, the proportion of residents with severe disease in the non-vaccinated group (4/5) was higher than that in the vaccinated group (2/13). Only 1 vaccinated staff, but 10 unvaccinated were infected in the outbreak (no severe disease). | 2021 | Bailey et al. (2021) |

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|-----------|---------------------------------|---------------------|--|------------------|--------------------------------------|
| D614G | vaccine neutralization efficacy | Pokay | The neutralizing activity of vaccine was significantly lower against B.1.351 in sera from all 24 patients with the BNT162b2 mRNA vaccine. (Fig. 4) | 2021 | Chen et al. (2021) |
| D614G | vaccine neutralization efficacy | Pokay | In sera 1-2 weeks after BNT162b2 first dose, from six patients previously infected with B.1, antibody titer in a microneutralization assay was on average 1625 for B.1.351 virus. This compares favorably (stronger) to most post-infection neutralization titer against all variants tested in the same sera (wild type, B.1.1.7, B.1.351, and P.1). | 2021 | Luftig et al. (2021) |
| D614G | vaccine neutralization efficacy | Pokay | 2.5x reduction in neutralization by serum collected 2 to 3 weeks after the second dose from vaccinees who had received BBIBP-CorV (pVNT50 against VSV pseudotyped as B.1.351). Convalescent plasma had similar titer against wild type as the BBIBP-CorV vaccinee sera. >3x reduction in neutralization by serum collected 2 to 3 weeks after the second dose from vaccinees who had received CoronaVac (pVNT50 against VSV pseudotyped as B.1.351). Convalescent plasma had similar titer against wild type as the CoronaVac vaccinee sera. | 2021 | Wang et al. (2021) |
| D614G | convalescent plasma escape | Pokay | B.1.1.351 variant constellation two-tailed Wilcoxon matched-pairs signed-rank test against 10 convalescent sera P | 2021 | Chen et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|--|
| D614G | vaccine neutralization efficacy | Pokay | Study 3001 on Ad26.COV2.S (Janssen vaccine) conducted September 21, 2020 through January 22, 2021 overlaps the emergence and dominance of the B.1.351 lineage of SARS-CoV-2 in South Africa. The SA arms of the Phase 3 double blind study showed severe/critical disease VE of 73.1% (95% CI: 40.0-89.4), and moderate to severe/critical disease VE of 52.0% (95% CI: 30.3-67.4). Compare to 78.0% and 74.4% for North American arm of the study during the same period (with low B.1.351 prevalence). Of the 66.9% of SA severe infections that have been sequenced as of this report, 94.5% are B.1.351. | 2021 | UNKNOWN et al. (2021) |
| D614G | vaccine neutralization efficacy | Pokay | The dominant circulating B.1.351 spike variant originating in RSA, which harbors E484K and additional substitutions in the RBD, NTD, and S2 and deletions in the NTD (amino acids 242–244), was neutralized with a 5.02-fold reduced titer | 2021 | Solfrosi et al. (2021) |
| D614G | convalescent plasma escape | Pokay | B.1.1.351 in 19 convalescent human sera ~1mo post infection had mild to moderate resistance against all samples | 2021 | Chen et al. (2021) |
| D614G | antibody epitope effects | Pokay | B.1.1.351 variant constellation ablates Class 1 receptor-binding-mot if targeting antibodies COV2-2050, 1B07, COVOX-384, and S2H58. B.1.1.351 variant constellation ablates Class 3 N-terminal domain targeting antibodies COV2-2489 and COV2-2676 (the only two tested). | 2021 | Chen et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|--|
| D614G | convalescent plasma escape | Pokay | In a Syrian hamster model, B.1.351 variant virus had >4x reduction in YRNT90 (measure of neutralization) using wild type convalescent sera. PG: Note that exact sequence for B.1.351 used was not disclosed. | 2021 | Cochin et al. (2021) |
| D614G | convalescent plasma escape | Pokay | In 13 plasma collected ~1mo after B.1.1.7 infection (nursing home in Ticino, Switzerland), neutralization reduced to undetectable levels in many plasma for B.1.351 pseudotyped virus, as well as WT and other VOCs. [paper does not detail the B.1.351 variants used, using the most popular as a stand in] | 2021 | McCallum et al. (2021) |
| D614G | vaccine neutralization efficacy | Pokay | Neutralization efficiency (ID50) against B.1.617.1-v1 ('Kappa') reduced 3.4x relative to D614G wildtype using pseudotyped VSV assay on 8 Moderna vaccinee sera one week post-booster. | 2021 | Choi et al. (2021) |
| D614G | vaccine neutralization efficacy | Pokay | Relative to B.1, Delta (B.1.617.2) shows mean 2.1x decrease in neutralization efficiency by 18 vaccinee sera (BNT162b2 and mRNA1273). | 2021 | Wilhelm et al. (2021) |
| D614G | convalescent plasma escape | Pokay | Relative to B.1, Delta (B.1.617.2) shows 3.64x decrease in neutralization efficiency by convalescent plasma [no cohort details provided] | 2021 | Wilhelm et al. (2021) |
| D614G | outcome hazard ratio | Pokay | B.1.526 (Iota) substantially increased IFR in older adults: by 46% (95% CI: 7.4 – 84%) among 45-64 year-olds, 82% (95% CI: 20 – 140%) among 65-74 year-olds, and 62% (95% CI: 45 – 80%) among 75+ during Nov 2020 – Apr 2021, compared to baseline IFR estimated for preexisting variants. [minimum clade defining mutations listed] | 2021 | Yang et al. (2021) |

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|-----------|---------------------------------|---------------------|---|------------------|---|
| D614G | vaccine neutralization efficacy | Pokay | Sera from vaccinees [ChAdOx1 and BNT162b2 primarily used in UK] shows decreased ability to neutralize B.1.621 compared to first wave virus and Alpha, with a magnitude of change similar to Beta. | 2021 | UNKNOWN et al. (2021) |
| D614G | vaccine efficacy | Pokay | In a 1:5 test-negative matched control study of 8153 individuals who received the Moderna mRNA-1273 vaccine, 69 test-positive were Mu. Two dose vaccine efficacy against Mu was 90.4% (73.9-96.5%), one dose VE was 45.8% (0.0-88.9%). | 2021 | Bruxvoort et al. (2021) |
| D614G | vaccinee plasma binding | Pokay | Sera from individuals who have been vaccinated and have had subsequent recent Delta infection have a high level of neutralising activity against B.1.621. | 2021 | UNKNOWN et al. (2021) |
| D614G | convalescent plasma binding | Pokay | Sera from individuals who have been infected with Delta does not have strong neutralising activity against B.1.621 | 2021 | UNKNOWN et al. (2021) |
| D614G | convalescent plasma binding | Pokay | In sera from six patients collected 1 to 12 weeks post-infection with B.1, antibody titer in a microneutralization assay was on average 71.46 for P.1 virus. Compare to much stronger neutralization titers for B.1.1.7 (256) and wild type (456.1) in the same sera. | 2021 | Luftig et al. (2021) |
| D614G | vaccine neutralization efficacy | Pokay | Mean 7.6x reduction of NT50 value B.1.621 (Mu) relative to wild type in 8 sera from adult BNT162b2 vaccinees (28-47yo) collected ~1m post booster. [This is a greater reduction than Beta @ 6.3x] | 2021 | Uriu et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|---------------------------------------|
| D614G | vaccine neutralization efficacy | Pokay | Using live B.1.621 virus and a cytopathic effect-based assay, sera from 37 Pfizer/BioNTech BNT162b2 vaccinees collected 10-20 days post-booster showed significantly lower (95) but still 'robust' neutralization than against ancestral B.1 virus (107). | 2021 | Messali et al. (2021) |
| D614G | convalescent plasma escape | Pokay | Mean 12.4x reduction of NT50 value B.1.621 (Mu) relative to wild type in 8 sera from older convalescent patients (52-92yo) collected 1-3m post symptom onset. [This is a greater reduction than Beta @ 8.2x] | 2021 | Uriu et al. (2021) |
| D614G | vaccinee plasma binding | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, XD (from) were 1.5x-fold lower (95% CI: 0.05x-0.07x) than against 208-428 972-1834 4.3-4.7 US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| D614G | vaccine neutralization efficacy | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, XD (from) were 4.4-fold lower (95% CI: 4.3x-4.7x) than against 208-428 972-1834 4.3-4.7 US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| D614G | vaccine neutralization efficacy | Pokay | Using a pseudovirus assay and 6 ChAdOx1 vaccinee sera, this lineage defining mutation combination from B.1.617.3 conferred a ~11.8x drop in neutralization (NT50) [suggesting role for T19R and T95I in half the sera]. | 2021 | Mishra et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|--|
| D614G | syncytium formation | Pokay | Using ACE2-GFP+Spike-RFP fluorescence assay, this lineage defining mutation combination from B.1.617.3 increased syncytium formation ~2.3x. | 2021 | Mishra et al. (2021) |
| D614G | transmissibility | Pokay | Using a pseudovirus assay, this lineage defining mutation combination from B.1.617.3 conferred a ~4.5x infectivity advantage to the spike particles. | 2021 | Mishra et al. (2021) |
| D614G | vaccine neutralization efficacy | Pokay | 51yo female with no severe COVID-19 risk factors tested positive 19 days after second dose of mRNA-1273 (Moderna) vaccine. Presented with sore throat, congestion, and headache developed: the next day she lost her sense of smell. Symptoms resolved over a one week period. Serum obtained 4 days after symptom onset was tested for neutralization against wild-type virus, the E484K mutant, and the B.1.526 variant. It was equally effective against each. These data suggest that the antibody response recognized these variants but was nonetheless insufficient to prevent a breakthrough infection. The virus detected matched neither B.1.1.7 nor B.1.526 VOC strains in wide circulation in New York at the time of infection, though shared some mutations. | 2021 | Hacisuleyman et al. (2021) |
| D614G | transmissibility | Pokay | Using a pseudovirus assay, this NTD mutation combination from B.1.617.3 did not confer an infectivity advantage to the spike particles. | 2021 | Mishra et al. (2021) |
| D614G | transmissibility | Pokay | Using a pseudovirus assay, this NTD mutation from B.1.617.3 did not confer an infectivity advantage to the spike particles. | 2021 | Mishra et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|---------------------------------------|
| D614G | trafficking | Pokay | ~3.5x cleavage of S2 relative to WA1 (D614G) wildtype by Kappa (B.1.617.1) variant as measured by mass spectrometry of Vero-TMPRSS culture (compare to ~4.5x for closely related Delta B.1.617.2 also with P681R at the cleavage site). | 2021 | Esclera et al. (2021) |
| D614G | vaccine neutralization efficacy | Pokay | 1.5x reduction in neutralization (ID50) in sera 3 weeks after one dose of Pfizer/BioNTech BNT162b2 (up to 5 naive and post infection vaccinees) [exact set of variants used is not listed in the manuscript] | 2021 | Gong et al. (2021) |
| D614G | vaccine neutralization efficacy | Pokay | Inferring from two B.1.617.1 variants tested, estimate baseline 3.3x reduction in ID50 relative to D614G wildtype using pseudotyped VSV assay on 8 Moderna vaccinee sera one week post-booster. | 2021 | Choi et al. (2021) |
| D614G | convalescent plasma binding | Pokay | This variant combination (representing lineage B.1.617.1) showed a 2x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset. [exact variant list not provided in manuscript, is inferred and represents minimal set agreed upon commonly] | 2021 | Gong et al. (2021) |
| D614G | vaccine neutralization efficacy | Pokay | Average 2x neutralization efficiency decrease against sera from 26 Phase II trial Covaxin (BBV152) vaccine recipients. Very similar to B.1.1.7 (~2x) in the same study, and the neutralization from 17 sera of natural infections across B1 lineages. | 2021 | Yadav et al. (2021) |
| D614G | convalescent plasma escape | Pokay | Relative to B.1, Kappa (B.1.617.1) shows 5.71x decrease in neutralization efficiency by convalescent plasma [no cohort details provided] | 2021 | Wilhelm et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|---------------------------------------|
| D614G | vaccine neutralization efficacy | Pokay | Relative to B.1, Kappa (B.1.617.1) shows mean 1.97x decrease in neutralization efficiency by 18 vaccinee sera (BNT162b2 and mRNA1273). | 2021 | Wilhelm et al. (2021) |
| D614G | vaccinee plasma binding | Pokay | This variant combination (representing lineage B.1.617.1) showed a 1.79x 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. 1.64x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in post-infection vaccinees. [exact variant list not provided in manuscript, is inferred and represents minimal set agreed upon commonly] | 2021 | Gong et al. (2021) |
| D614G | ACE2 receptor binding affinity | Pokay | Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant combination (representing lineage B.1.617.1) showed a 1.12x increase in binding (KD) relative to D614G, but described as 'not significant'. [exact variant list not provided in manuscript, is inferred and represents minimal set agreed upon commonly] | 2021 | Gong et al. (2021) |
| D614G | antibody epitope effects | Pokay | Neutralization of the bsAbs 47D10. Kappa (B.1.617.1) has an IC50 fold change of 80.2x. | 2022 | Yuan et al. (2022) |
| D614G | antibody epitope effects | Pokay | Neutralization of the bsAbs Bi-Nab47D10-35B5. Kappa (B.1.617.1) has an IC50 fold change of 2.3x. | 2022 | Yuan et al. (2022) |
| D614G | antibody epitope effects | Pokay | Neutralization of the bsAbs 35B5. Kappa (B.1.617.1) has an IC50 fold change of 0.68x. | 2022 | Yuan et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|--|
| D614G | antibody epitope effects | Pokay | Neutralization of the bsAbs Bi-Nab35B5-47D10. Kappa (B.1.617.1) has an IC50 fold change of 0.13x. | 2022 | Yuan et al. (2022) |
| D614G | vaccine neutralization efficacy | Pokay | Neutralization efficiency (ID50) against B.1.617.1-v1 ('Kappa') reduced 3.3x relative to D614G wildtype using pseudotyped VSV assay on 8 Moderna vaccinee sera one week post-booster. | 2021 | Choi et al. (2021) |
| D614G | vaccine neutralization efficacy | Pokay | In a cluster of B.1.617[.1] infections related to travel from India to USA, one patient with mild symptoms had received their second dose of Pfizer vaccine more than two weeks before the infection [i.e. vaccine breakthrough]. | 2021 | Verghese et al. (2021) |
| D614G | trafficking | Pokay | ~4.5x cleavage of S2 relative to WA1 (D614G) wildtype by Delta (B.1.617.2) variant as measured by mass spectrometry of Vero-TMPRSS culture (compare to ~3.5x for closely related Kappa B.1.617.1 also with P681R at the cleavage site). | 2021 | Esclera et al. (2021) |
| D614G | vaccine neutralization efficacy | Pokay | Neutralization efficiency (ID50) against B.1.617.1-v1 ('Kappa') reduced 3.3x relative to D614G wildtype using pseudotyped VSV assay on 8 Moderna vaccinee sera one week post-booster. [Mutation list in publication appears to contain a typo with R158del instead of R158G] | 2021 | Choi et al. (2021) |
| D614G | vaccine neutralization efficacy | Pokay | Mean 2.6x reduction of NT50 value B.1.617.2 (Delta) relative to wild type in 8 sera from adult BNT162b2 vaccinees (28-47yo) collected ~1m post booster. | 2021 | Uriu et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|-------------------------------------|---------------------|--|------------------|---------------------------------------|
| D614G | convalescent plasma escape | Pokay | Mean 4.0x reduction of NT50 value B.1.617.2 (Delta) relative to wild type in 8 sera from older convalescent patients (52-92yo) collected 1-3m post symptom onset. | 2021 | Uriu et al. (2021) |
| D614G | trafficking | Pokay | Modelling the Delta variant in primary human airway epithelial (HAE) cultures, S1 to full length Spike ratio (measuring Spike furin cleavage processivity) increased 11x relative to wild type (15.3 vs 1.4). [del ~157 truncated due to ambiguity] Furthermore the RNA ratio of Delta versus Alpha-spike/Delta-backbone continuously increased from 2.8 on day 1 to 9.8 on day 5 post infection in a coinfection model in HAEs, suggesting the spike gene drives the improved replication of Delta variant. | 2021 | Liu et al. (2021) |
| D614G | pharmaceutical effectiveness | Pokay | Trimeric proteins FSR22 had a 0.10x fold change in IC50 in B.1.617.2 Delta | 2022 | Chonira et al. (2022) |
| D614G | pharmaceutical effectiveness | Pokay | Trimeric proteins FSR16m had a 0.020x fold change in IC50 in B.1.617.2 Delta | 2022 | Chonira et al. (2022) |
| D614G | trafficking | Pokay | In primary human airway epithelial cultures, S1 to full length Spike ratio (measuring Spike furin cleavage processivity) increase 1.9x relative to wild type (2.7 vs 1.4). This is the Delta variant with the P681R furin cleavage site mutation absent. [del ~157 truncated due to ambiguity] | 2021 | Liu et al. (2021) |
| D614G | immunosuppression variant emergence | Pokay | 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. | 2021 | Landis et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|---|
| D614G | transmissibility | Pokay | Normalized for particle number, on ACE2.293T cells showed that the B.1.618 spike protein was about as infective as D614G wild type. | 2021 | Tada et al. (2021) |
| D614G | vaccine neutralization efficacy | Pokay | The estimated vaccine effectiveness against R.1 strain SARS-CoV-2 infection among residents in a Kentucky skilled nursing facility was 66.2% (95% CI | 2021 | Cavanaugh et al. (2021) |
| D614G | vaccine neutralization efficacy | Pokay | Plasma neutralizing activity was also assessed against SARS-CoV-2 Delta, Omicron BA.1, BA.2 and BA.4/5 variants using viruses pseudotyped with appropriate variant spikeproteins. Delta breakthrough infection resulted in 15-fold increased neutralizing titers. | 2022 | Wang et al. (2022) |
| D614G | ACE2 receptor binding affinity | Pokay | L27, V34 and E90 mutation resulted in ultrahigh affinity binding of the LVE-ACE-2 domain to the widest variety of VOCs, with KDs of 507 pM for binding to the Delta B.1.617.2. Values were obtained with LVE-ACE-2/mAB chimeras containing the Y-T-E sequence that enhances binding to the FcRn receptor, which in turn is expected to extend biological half-life 3-4-fold. | 2022 | Uhal B et al. (2022) |
| D614G | vaccine neutralization efficacy | Pokay | Plasma neutralizing activity in 49 participants was measured using HIV-1 pseudotyped with the 100 WT SARS-CoV-2 spike protein. Delta breakthrough infection resulted in 11-fold increased geometric mean half-maximal neutralizing titer (NT50). | 2022 | Wang et al. (2022) |
| D614G | vaccine neutralization efficacy | Pokay | Log10ID50 of Delta neutralizing antibodies is 0.872x the WT pre-third dose of pfizer-BioNTech BNT162b2 in 13 Kidney transplant recipients (KTR) with median age of 55.5. | 2022 | McEvoy C et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|--|
| D614G | vaccine neutralization efficacy | Pokay | Paradigm's ACE-2 variant LVE/STR chimera neutralizes Delta Variant B.1.617.2 RBD or w.t. SARS-CoV-2 RBD with nearly equal potency determined using Surrogate Viral Neutralization Tests. | 2022 | Uhal B et al. (2022) |
| D614G | vaccine neutralization efficacy | Pokay | Log10ID50 of Delta neutralizing antibodies is 0.952x the WT 1 month post-third dose of pfizer-BioNTech BNT162b2 in 13 Kidney transplant recipients (KTR) with median age of 55.5. | 2022 | McEvoy C et al. (2022) |
| D614G | outcome hazard ratio | Pokay | In the UK, of 43338 COVID-19-positive patients, 8682 had the Delta variant (median age 31 years [IQR 17–43]) and 196 were admitted to hospital within 14 days after the specimen was taken (adjusted hazard ratio [HR] 2.26 [95% CI 1.32–3.89] relative to Alpha cases). Being admitted to hospital or attending emergency care within 14 days for Delta cases had an adjusted HR 1.45 [95% CI 1.08–1.95] relative to Alpha. Most patients were unvaccinated (32 078 [74.0%] across both groups). The HRs for vaccinated patients were similar: 1.94 [95% CI 0.47–8.05] for hospitalization and 1.58 [0.69–3.61] for hospital admission or emergency care attendance. | 2021 | Twohig et al. (2021) |
| D614G | vaccine efficacy | Pokay | During December 14, 2020–August 14, 2021, frontline worker without previous documented SARS-CoV-2 infection were monitored regularly. Of 4,217 participants, 3,483 (83%) were vaccinated: 2,278 (65%) received Pfizer-BioNTech, 1,138 (33%) Moderna, and 67 (2%) Janssen (Johnson & Johnson) COVID-19 vaccines. Adjusted VE during this Delta predominant period was 66% (95% CI | 2021 | Fowlkes et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|---------------------------------------|
| D614G | vaccine neutralization efficacy | Pokay | Case 62541 cluster in Singapore included a fully vaccinated nurse 2 months post-vaccine [likely Pfizer based on dates and supply], and a doctor of unknown vaccine status. This cluster was caused by a B.1.617.2 virus [via crossreference to | | UNKNOWN et al. () |
| D614G | vaccinee plasma binding | Pokay | This variant combination (representing lineage B.1.617.2 aka Delta) showed a 1.64x 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. 1.89x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in post-infection vaccinees. [exact variant list not provided in manuscript, is inferred and represents minimal set agreed upon commonly] | 2021 | Gong et al. (2021) |
| D614G | vaccine neutralization efficacy | Pokay | nan | | UNKNOWN et al. () |
| D614G | vaccine efficacy | Pokay | 136,160 reports from 14,997 nursing care facilities were broken into pre-Delta (Mar 1-May 9, 2021), intermediate (May 10-Jun 20, 2021) and Delta (Jun 21-Aug 1, 2021). Two doses of mRNA vaccines were 74.7% effective against infection among nursing home residents early in the vaccination program (March–May 2021). During June–July 2021, when B.1.617.2 (Delta) variant circulation predominated, effectiveness declined significantly to 53.1%. | 2021 | Nanduri et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|----------------------|---------------------|---|------------------|-------------------------------------|
| D614G | vaccine efficacy | Pokay | Using a matched test-negative, case- control study design in Qatar, BNT162b2 effectiveness against any Delta infection, symptomatic or asymptomatic, was 64.2% (95% CI: 38.1-80.1%) ≥ 14 days after the first dose and before the second dose, but was only 53.5% (95% CI: 43.9-61.4%) ≥ 14 days after the second dose, in a population in which a large proportion of fully vaccinated persons received their second dose several months earlier. Corresponding effectiveness measures for mRNA-1273 were 79.0% (95% CI: 58.9-90.1%) and 84.8% (95% CI: 75.9-90.8%), respectively. Effectiveness against any severe, critical, or fatal COVID-19 disease due to Delta was 89.7% (95% CI: 61.0-98.1%) for BNT162b2 and 100.0% (95% CI: 41.2-100.0%) for mRNA-1273, ≥ 14 days after the second dose. The lower VE in Qatar relative to those reported in some other jurisdictions such as the UK and Canada (75%+) may reflect waning of vaccine protection for those who received their second dose by end of 2020 or early 2021. Risk perception and behaviour amongst vaccinated individuals over time may also play a role. | 2021 | Tang et al. (2021) |
| D614G | outcome hazard ratio | Pokay | In Denmark, for the period Jan 1 to Jun 27, 2021, Delta variant was associated with increased an risk ratio of 2.83 [95% CI 2.02–3.98] for hospitalization. | 2021 | Bager et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|---------------------------------------|
| D614G | vaccine efficacy | Pokay | Of 218 individuals with B.1.617.2 infection in Singapore, 84 had received a mRNA vaccine of which 71 were fully vaccinated, 130 were unvaccinated and 4 received a non-mRNA. Despite significantly older age in the vaccine breakthrough group, the odds of severe COVID-19 requiring oxygen supplementation was significantly lower following vaccination (adjusted odds ratio 0.07 95%CI: 0.015-0.335, p | 2021 | Chia et al. (2021) |
| D614G | vaccine efficacy | Pokay | The incidence rate of Covid-19 during the Delta-dominant period (Jul-Aug 2021) was lower for late vaccinated (49.0/1000 person-years) [formerly placebo] versus early vaccinated (77.1/1000 person-years) participants in the Moderna mRNA-1273 Phase 3 trials, representing a 36.4% VE reduction (95% CI 17.1%-51.5%). There were fewer severe Covid-19 cases in the late group (6: 6.2/1000 person-years) than early (13: 3.3/1000 person-years), representing a 46.0% reduction (95% CI -52.4%-83.2%). Three Covid-19 related hospitalizations occurred with two resulting deaths in the early group. | 2021 | Baden et al. (2021) |
| D614G | vaccine neutralization efficacy | Pokay | 2.3x reduction in neutralization (ID50) in sera 3 weeks after one dose of Pfizer/BioNTech BNT162b2 (up to 5 naive and post infection vaccinees) [exact set of variants used is not listed in the manuscript] | 2021 | Gong et al. (2021) |
| D614G | pharmaceutical effectiveness | Pokay | Infectious viral titers in lung tissue determined using a tissue culture infectious dose (TCID) assay in 10 hamsters showed that Delta Molnupiravir (MK-4482) had ~4x fold drop. | 2022 | Rosenke et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|--|
| D614G | vaccine efficacy | Pokay | Using a test-negative design using Ontario data between Dec 14, 2020 and May 30, 2021, 421,073 symptomatic community-dwelling individuals were tested. Against Delta, vaccine effectiveness after partial vaccination tended to be lower compared to Alpha for mRNA-1273 (72% vs. 83%) and BNT162b2 (56% vs. 66%), but was similar to Alpha for ChAdOx1 (67% vs. 64%). Full vaccination with BNT162b2 increased protection against Delta (87%) to levels comparable to Alpha (89%) and Beta/Gamma (84%). Delta-positive cases were biased towards young male residents of the Peel region. | 2021 | Nasreen et al. (2021) |
| D614G | outcome hazard ratio | Pokay | In Ontario between Feb 7 and Jun 27, 2021, increased risk with the Delta variant was 108% (95% CI 78%–140%) for hospitalization, 235% (95% CI 160%–331%) for ICU admission and 133% (95% CI 54%–231%) for death. | 2021 | UNKNOWN et al. (2021) |
| D614G | vaccine neutralization efficacy | Pokay | Vaccination of health care workers in Delhi was started in early 2021, with the ChdOx-1 (Astra Zeneca) vaccine. Surveillance has suggested B.1.1.7 dominance in the Delhi area during early 2021, with growth of B.1.617 since March 2021. During the wave of infections during March and April an outbreak of SARS-CoV-2 was confirmed in 33 vaccinated staff members at a single tertiary centre (age 27-77 years). Sequencing revealed that 16/33 were B.1.617.2, with a range of other B lineage viruses including B.1.1.7 for the rest except one A lineage case. Importantly no severe cases were documented in this event. | 2021 | Ferreira et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|--------------------------------|---------------------|--|------------------|--|
| D614G | vaccine efficacy | Pokay | Effectiveness after one dose of vaccine (BNT162b2 or ChAdOx1 nCoV-19) with the delta variant was (30.7%: 95% confidence interval [CI], 25.2 to 35.7): the results were similar for both vaccines. With the BNT162b2 vaccine, the effectiveness of two doses was 88.0% (95% CI, 85.3 to 90.1) among those with the delta variant. With the ChAdOx1 nCoV-19 vaccine, the effectiveness of two doses was 67.0% (95% CI, 61.3 to 71.8) among those with the delta variant. | 2021 | Lopez Bernal et al. (2021) |
| D614G | convalescent plasma binding | Pokay | This variant combination (representing lineage B.1.617.2 aka Delta) showed a 1.92x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset. [exact variant list not provided in manuscript, is inferred and represents minimal set agreed upon commonly] | 2021 | Gong et al. (2021) |
| D614G | ACE2 receptor binding affinity | Pokay | Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant combination (representing lineage B.1.617.2 aka Delta) showed a 2.34x increase in binding (KD) relative to D614G. [exact variant list not provided in manuscript, is inferred and represents minimal set agreed upon commonly] | 2021 | Gong et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|--------------------------|---------------------|---|------------------|---|
| D614G | vaccine efficacy | Pokay | In Minnesota in July 2020 (when Delta variant prevalence was >70%), the effectiveness against infection for mRNA-1273 was estimated at 76% (95% CI: 58-87%) using age, sex, race, PCR testing and vaccination date matched cohorts of unvaccinated, Pfizer and Moderna vaccinees. An even more pronounced reduction in effectiveness was observed for BNT162b2 of 42% (95% CI: 13-62%). mRNA-1273 conferred a two-fold risk reduction against breakthrough infection compared to BNT162b2 (IRR | 2021 | Puranik et al. (2021) |
| D614G | vaccine efficacy | Pokay | In a 1:5 test-negative matched control study of 8153 individuals who received the Moderna mRNA-1273 vaccine, 2027 test-positive cases were Delta. Two dose vaccine efficacy against Delta decreased from 94.1% (90.5-96.3%) 14-60 days after vaccination to 80.0% (70.2-86.6%) 151-180 days after vaccination. Waning was less pronounced for non-Delta variants. VE against Delta was lower among individuals aged ≥65 years (75.2% [59.6-84.8%]) than those aged 18-64 years (87.9% [85.5-89.9%]). VE against Delta hospitalization was 97.6% (92.8-99.2%). One-dose VE was 77.0% (60.7-86.5%) against Delta infection. | 2021 | Bruxvoort et al. (2021) |
| D614G | antibody epitope effects | Pokay | Neutralization of the bsAbs 47D10. Delta (B.1.617.2) has an IC50 fold change of 46.5x. | 2022 | Yuan et al. (2022) |
| D614G | antibody epitope effects | Pokay | Neutralization of the bsAbs Bi-Nab35B5-47D10. Delta (B.1.617.2) has an IC50 fold change of 0.57x. | 2022 | Yuan et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|--------------------------|---------------------|---|------------------|---|
| D614G | antibody epitope effects | Pokay | Neutralization of the bsAbs Bi-Nab47D10-35B5. Delta (B.1.617.2) has an IC50 fold change of 0.15x. | 2022 | Yuan et al. (2022) |
| D614G | antibody epitope effects | Pokay | Neutralization of the bsAbs 35B5. Delta (B.1.617.2) has an IC50 fold change of 0.87x. | 2022 | Yuan et al. (2022) |
| D614G | antibody epitope effects | Pokay | BnAb 002-S21F2 IC50 on the Delta (B.1.617.2) variant is 0.6x fold the wildtype. | 2022 | Kumar et al. (2022) |
| D614G | reinfection | Pokay | A 42yo Iranian male was reinfected with B.1.36 lineage virus 128 days after infection with genetically distinct B.1.36 virus, with negative PCR tests in between. In the first instance patient presented with cough, headache, severe diarrhea. In the second instance symptoms were more severe: body pain, shortness of breath, headache and anosmia. Anti-SARS-CoV-2 IgG and IgM tests were negative after both episodes. [Non-seroconversion may be associated with elevated risk of re-infection] [I210del is a homoplasy that has appeared in several disparate parts of the global phylogenetic tree, including A and B lineages, primarily in LMICs] | 2021 | Salehi-Vaziri et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|-----------------------------|---------------------|--|------------------|-------------------------------------|
| D614G | humoral response durability | Pokay | 27yo female nurse reinfectd in December 2020 (B.1.177) after initial infection in March 2020 (B.3), i.e. with a 9 month interval. Both cases were mild. No significant differences in the neutralizing capacity of the two lineages were observed in 4 sera taken (1 pre-reinfection, three post-reinfection). Neutralizing antibody titres (IC50) before and immediately after re-infection were <300 against both strains, and jumped >7x upon re-infection. Viral titres were also higher in the second case. Second case also includes N:p.A220V | 2021 | Brehm et al. (2021) |
| D614G | reinfection | Pokay | 27yo female nurse reinfectd in December 2020 (B.1.177) after initial infection in March 2020 (B.3). Both cases were mild. Second case also includes N:p.A220V | 2021 | Brehm et al. (2021) |
| D614G | syncytium formation | Pokay | Slight increase in Vero cell-cell membrane fusion assay under infection with VSV pseudotyped virus relative to wild type, no change relative to D614G. | 2021 | Kim et al. (2021) |
| D614G | trafficking | Pokay | ~4x 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). | 2021 | Kim et al. (2021) |
| D614G | trafficking | Pokay | No change in infectivity (24h) relative to D614G alone in Caco-2 cells, Vero or Calu-3. | 2021 | Kim et al. (2021) |
| D614G | trafficking | Pokay | 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. | 2021 | Hu et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|----------------------------|---------------------|--|------------------|---|
| D614G | transmissibility | Pokay | 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. | 2021 | Roquebert et al. (2021) |
| D614G | transmissibility | Pokay | 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. | 2021 | Pearson et al. (2021) |
| D614G | convalescent plasma escape | Pokay | Average ~10-fold reduction in neutralization efficacy in convalescent sera of 16 health workers infected in Spring 2020. | 2021 | Alenquer et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|---------------------------------------|
| D614G | vaccine neutralization efficacy | Pokay | 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 ~2000 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). | 2021 | Madhi et al. (2021) |
| D614G | convalescent plasma escape | Pokay | Neutralizing antibody titers of 18 samples (90%) decreased against this B.1.351 pseudotyped virus below an ID50 threshold of 40 (sera collected ~8mo post Jan 2020 first wave in China). | 2021 | Hu et al. (2021) |
| D614G | antibody epitope effects | Pokay | Abolished neutralization by mAbs CQ026 and CQ038, greatly diminished neutralization by CQ012 and CQ046. | 2021 | Hu et al. (2021) |
| D614G | vaccine neutralization efficacy | Pokay | This variant of key B.1.351 lineage mutations showed ~10x decrease in Pfizer sera (3 weeks post-first dose: n | 2021 | Kuzmina et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|---|
| D614G | vaccine neutralization efficacy | Pokay | This variant showed ~10x decrease in Pfizer sera (3 weeks post-first dose: n | 2021 | Kuzmina et al. (2021) |
| D614G | trafficking | Pokay | ~5x 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] | 2021 | Kim et al. (2021) |
| D614G | vaccine neutralization efficacy | Pokay | This variant showed >5x decrease in Pfizer sera (3 weeks post-first dose: n | 2021 | Kuzmina et al. (2021) |
| D614G | trafficking | Pokay | ~9x more infectivity than D614G alone in HEK293T-ACE2 cells 48h post-transduction (no synergy as level approx. that of N501Y alone). | 2021 | Kuzmina et al. (2021) |
| D614G | vaccine neutralization efficacy | Pokay | This variant showed only minor in Pfizer sera (one or two dose) neutralization efficiency vs D614G (using lentivirus pseudotype). | 2021 | Kuzmina et al. (2021) |
| D614G | trafficking | Pokay | ~2x more infectivity than D614G alone in HEK293T-ACE2 cells 48h post-transduction. | 2021 | Kuzmina et al. (2021) |
| D614G | ACE2 receptor binding affinity | Pokay | The KD for the pseudotyped P.1-ACE2 interaction is 4.8 nM, showing that binding to P.1 is essentially indistinguishable from B.1.351 (4.0 nM), which binds with ~19x greater affinity than wild type. | 2021 | Dejnirattisai et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|--------------------------------------|
| D614G | reinfection | Pokay | A 47yo Indian male was reinfected with B.1.36 lineage virus in September 2020 after infection with genetically distinct B.1.36 virus in July, with negative PCR tests in between. While the first episode was asymptomatic, the second included fever, cough, and malaise. The second case additionally contained stopgain ORF3a:E261* | 2021 | Rani et al. (2021) |
| D614G | transmissibility | Pokay | Using a pseudovirus assay, this NTD+RBD mutation combination from B.1.617.3 conferred a ~3x infectivity advantage to the spike particles [less than L452R or E484Q alone working with the delins]. | 2021 | Mishra et al. (2021) |
| D614G | ACE2 receptor binding affinity | Pokay | Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant combination (representing lineage B.1.617) showed a 1.85x increase in binding (KD) relative to D614G. [exact variant list not provided in manuscript, is inferred from common knowledge] | 2021 | Gong et al. (2021) |
| D614G | vaccine neutralization efficacy | Pokay | 1.4x reduction in neutralization (ID50) in sera 3 weeks after one dose of Pfizer/BioNTech BNT162b2 (up to 5 naive and post infection vaccinees) | 2021 | Gong et al. (2021) |
| D614G | transmissibility | Pokay | The combination caused a 3-fold increase in infectivity relative to D614G wild type. [compare to 3.5x for L452R alone] | 2021 | Tada et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|--------------------------------------|
| D614G | convalescent plasma escape | Pokay | Pseudotyped viruses for B.1.617 was 2.3-fold resistant to neutralization by convalescent sera compared to wild type - a finding that was similar to that of the 3-fold resistance of the South Africa B.1.351 variant using the same assay. The resistance of B.1.617 was caused by the L452R and E484Q mutation, based on results from viruses pseudotyped for individual variants within B.1.617. [details on the convalescent patient sera collection are not abundantly clear in the preprint] | 2021 | Tada et al. (2021) |
| D614G | vaccine neutralization efficacy | Pokay | Using a pseudovirus assay and 6 ChAdOx1 vaccinee sera, this NTD+RBD mutation combination from B.1.617.3 conferred a ~3x drop in neutralization (NT50) [working with the delins, less than just L452R but more than just E484Q]. | 2021 | Mishra et al. (2021) |
| D614G | vaccinee plasma binding | Pokay | This variant combination (representing lineage B.1.617) showed a 1.30x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in previously non-seroconverted subjects. 1.18x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in post-infection vaccinees. [exact variant list not provided in manuscript, is inferred from common knowledge] | 2021 | Gong et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|--------------------------------------|
| D614G | vaccine neutralization efficacy | Pokay | Pseudotyped viruses for B.1.617 was 4-fold resistant to neutralization by 6 BNT162b2 vaccine sera 28 days post-booster compared to wild type - a finding that was similar to that of the 3.4-fold resistance of the South Africa B.1.351 variant using the same assay. Neutralization by 3 Moderna vaccine sera 28 days post-booster was 5-fold resistant (vs. 2.2-fold for B.1.351). The resistance of B.1.617 was caused by the L452R and E484Q mutation, based on results from viruses pseudotyped for individual variants within B.1.617. | 2021 | Tada et al. (2021) |
| D614G | convalescent plasma binding | Pokay | This variant combination (representing lineage B.1.617) showed a 1.22x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset. [exact variant list not provided in manuscript, is inferred from common knowledge] | 2021 | Gong et al. (2021) |
| D614G | syncytium formation | Pokay | Using ACE2-GFP+Spike-RFP fluorescence assay, this NTD+RBD mutation combination from B.1.617.3 increased syncytium formation ~2.5x. | 2021 | Mishra et al. (2021) |
| D614G | transmissibility | Pokay | Normalized for particle number, on ACE2.293T cells showed that the B.1.617 spike protein was >2-fold increase in infectivity relative to D614G wild type. | 2021 | Tada et al. (2021) |
| D614G | vaccine neutralization efficacy | Pokay | Using a pseudovirus assay and 6 ChAdOx1 vaccinee sera, this NTD+RBD mutation combination from B.1.617.3 conferred a 7.42x drop in neutralization (NT50) [mostly from 3 of the sera]. | 2021 | Mishra et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|---|
| D614G | vaccine efficacy | Pokay | In a 1:5 test-negative matched control study of 8153 individuals who received the Moderna mRNA-1273 vaccine, 583 test-positive were Epsilon. Two dose vaccine efficacy against Epsilon was 97.6 (90.2-99.4%), one dose VE was 76.3 (48.1-89.1%). | 2021 | Bruxvoort et al. (2021) |
| D614G | vaccine neutralization efficacy | Pokay | Using a pseudovirus assay and 6 ChAdOx1 vaccinee sera, this RBD mutation conferred a 2.36x drop in neutralization (NT50). | 2021 | Mishra et al. (2021) |
| D614G | transmissibility | Pokay | Increased infectivity of the B.1.617 spike was attributed to L452R, which itself caused a 3.5-fold increase in infectivity relative to D614G wild type. [In combination with E484Q caused a somewhat less 3-fold increase] | 2021 | Tada et al. (2021) |
| D614G | transmissibility | Pokay | The L452R mutation increased the infectivity more than two-fold in these conditions. | 2021 | Mishra et al. (2021) |
| D614G | transmissibility | Pokay | Using a pseudovirus assay, this NTD+RBD mutation combination from B.1.617.3 conferred a ~2x infectivity advantage to the spike particles. | 2021 | Mishra et al. (2021) |
| D614G | syncytium formation | Pokay | Using ACE2-GFP+Spike-RFP fluorescence assay, this NTD+RBD mutation combination from B.1.617.3 increased syncytium formation ~2x. | 2021 | Mishra et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|-----------------------------|---------------------|---|------------------|--|
| D614G | symptom prevalence | Pokay | Compared to the clade 20A strains that predominated during phase 1 between March and May 2020, the Marseille-4 variant (characterized by this mutation plus N:p.M234I:A376T) was associated with a lower frequency of cough, rhinitis, and olfactory and gustatory disorders. By contrast, hypoxemia was more frequent in patients infected with the Marseille-4 variant. | 2021 | Fournier et al. (2021) |
| D614G | reinfection | Pokay | 11 cases of re-infection with the 'Marseille-4' variant found within 1028 positive tests, where all of the earlier infections were from different strains. This lineage is also characterized by N:p.M234I:A376T | 2021 | Fournier et al. (2021) |
| D614G | convalescent plasma binding | Pokay | Lentiviral pseudotyped with the key mutations from 20A.EU2 lineage was neutralized slightly less than D614G in 10 convalescent sera from April 2020 infectees. | 2021 | Tada et al. (2021) |
| D614G | trafficking | Pokay | Lentiviral pseudotyped with the key mutations from 20A.EU2 lineage was tested on ACE2.293T cells. Luciferase activity was measured two days postinfection, showing no significant change in infection rate amongst the cells, suggesting that this mutation does not contributing to cell entry fitness. | 2021 | Tada et al. (2021) |
| D614G | trafficking | Pokay | ~13x more infective as D614G alone in HEK293T-ACE2 cells 48h post-transduction. | 2021 | Kuzmina et al. (2021) |
| D614G | trafficking | Pokay | Approximately as infective as D614G alone in HEK293T-ACE2 cells 48h post-transduction (~additive effects of the individual variants). | 2021 | Kuzmina et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|---------------------------------------|
| D614G | syncytium formation | Pokay | ~50% Vero cell-cell membrane fusion assay under infection with VSV pseudotyped virus relative to wild type, significantly higher than D614G. | 2021 | Kim et al. (2021) |
| D614G | trafficking | Pokay | ~12x more infectivity than D614G alone in HEK293T-ACE2 cells 48h post-transduction (~additive effects of 501 and 484). | 2021 | Kuzmina et al. (2021) |
| D614G | trafficking | Pokay | ~6x 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] | 2021 | Kim et al. (2021) |
| D614G | trafficking | Pokay | More efficient infectivity (24h) compared to wild type, in Caco-2 cells ~11x, Vero ~10x, and Calu-3 ~11x. Compare to wild type at ~5x across cell types. | 2021 | Kim et al. (2021) |
| D614G | vaccine neutralization efficacy | Pokay | The study demonstrated 1.92 and 1.09 fold reductions (ELISA) in the neutralizing titer against B.1.1.28.2 (P2) variant (n | 2021 | Sapkai et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|---------------------------------------|
| D614G | vaccine neutralization efficacy | Pokay | Study 3001 on Ad26.COV2.S (Janssen vaccine) conducted September 21, 2020 through January 22, 2021 overlaps the emergence and dominance of the P.1 & P.2 lineages of SARS-CoV-2 in Brazil. The Brazilian arm of the Phase 3 double blind study showed severe/critical disease VE of 81.9% (95% CI: 17.0-98.1), and moderate to severe/critical disease VE of 66.2% (95% CI: 51.0-77.1). Compare to 78.0% and 74.4% for North American arm of the study during the same period (with low B.1.351 prevalence). Of the 69.3% of mostly severe infections sequenced as of this report, 69.4% were of P.2 lineage [defining lineage SNPs reported here]. | 2021 | UNKNOWN et al. (2021) |
| D614G | vaccine neutralization efficacy | Pokay | 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. | 2021 | Tada et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|--|
| D614G | convalescent plasma escape | Pokay | 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] | 2021 | Tada et al. (2021) |
| D614G | vaccine neutralization efficacy | Pokay | Pseudotyped P.2 virus has reduced neutralization activity vs wild type: 5.8x (30 sera Pfizer median 9 days post 2nd dose) and 2.9x (35 sera Moderna median 18 days post 2nd dose). This was significant by ANOVA. | 2021 | Garcia-Beltran et al. (2021) |
| D614G | vaccine neutralization efficacy | Pokay | Using a pseudovirus assay and 6 ChAdOx1 vaccinee sera, this NTD+RBD mutation combination from B.1.617.3 conferred a 1.34x drop in neutralization (NT50) [mostly from a single serum]. | 2021 | Mishra et al. (2021) |
| D614G | transmissibility | Pokay | Using a pseudovirus assay, this NTD+RBD mutation combination from B.1.617.3 conferred a ~4x infectivity advantage to the spike particles. | 2021 | Mishra et al. (2021) |
| D614G | transmissibility | Pokay | Using a pseudovirus assay, RBD-specific mutation E484Q did not significantly confer infectivity advantage to the spike particles. | 2021 | Mishra et al. (2021) |
| D614G | syncytium formation | Pokay | Using ACE2-GFP+Spike-RFP fluorescence assay, this NTD+RBD mutation combination from B.1.617.3 did not affect syncytium formation. | 2021 | Mishra et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|---------------------------------------|
| D614G | vaccine neutralization efficacy | Pokay | This variant showed no change in Pfizer sera (one or two dose) neutralization efficiency vs D614G (using lentivirus pseudotype). | 2021 | Kuzmina et al. (2021) |
| D614G | trafficking | Pokay | More efficient infectivity (24h) compared to wild type, in Caco-2 cells ~13x, Vero ~10x, and Calu-3 ~10x. Compare to wild type at ~5x across cell types. | 2021 | Kim et al. (2021) |
| D614G | trafficking | Pokay | 9x more infectivity than D614G alone in HEK293T-ACE2 cells 48h post-transduction. | 2021 | Kuzmina et al. (2021) |
| D614G | trafficking | Pokay | More efficient infectivity (24h) compared to wild type, in Caco-2 cells ~9x, Vero ~8x, and Calu-3 ~8x. Compare to wild type at ~5x across cell types. | 2021 | Kim et al. (2021) |
| D614G | trafficking | Pokay | Lentiviral pseudotyped with the key mutations from COH.20G/677H lineage was tested on ACE2.293T cells. Luciferase activity was measured two days postinfection, showing no significant change in infection rate amongst the cells, suggesting that this mutation does not contributing to cell entry fitness. | 2021 | Tada et al. (2021) |
| D614G | convalescent plasma binding | Pokay | Lentiviral pseudotyped with the key mutations from COH.20G/677H ('Ohio') lineage was neutralized similarly to D614G in 10 convalescent sera from April 2020 infectees. | 2021 | Tada et al. (2021) |
| D614G | ACE2 receptor binding affinity | Pokay | Lentiviral pseudotyped with the key mutations from COH.20G/677H lineage was tested on ACE2.293T cells for ACE2 affinity changes vs D614G alone, showing a ~70% drop in IC50 (i.e. increased affinity). | 2021 | Tada et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|-----------------------------|---------------------|--|------------------|---|
| D614G | anthropozoonotic events | Pokay | This mutation (a.k.a. 'Doug') outside the receptor binding domain, while highly favorable to improved human-human transmission, decreases transduction in naked mole-rat (<i>Heterocephalus glaber</i>) fibroblast and Japanese pipistrelle bat (<i>Pipistrellus abramus</i>) cell cultures using a pseudotyped VSV assay. | 2023 | Li et al. (2023) |
| D614G | trafficking | Pokay | 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. | 2021 | Daniloski et al. (2021) |
| D614G | trafficking | Pokay | ~4x more efficient S2 domain cleavage compared to wild type in Caco-2 cells, mid-range of three cell line tested (Vero and Calu-3). | 2021 | Kim et al. (2021) |
| D614G | convalescent plasma binding | Pokay | 1.14x increase in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset. | 2021 | Gong et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|---------------------------------------|
| D614G | vaccine neutralization efficacy | Pokay | 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. | 2021 | Kuzmina et al. (2021) |
| D614G | vaccinee plasma binding | Pokay | 1.08x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in previously non-seroconverted subjects. 1.11x increase in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in post-infection vaccinees. | 2021 | Gong et al. (2021) |
| D614G | ACE2 receptor binding affinity | Pokay | In four cell lines (including 293T-hACE2 cells), this mutation combination increases infectivity vs D614G alone | 2020 | Li et al. (2020) |
| D614G | vaccine neutralization efficacy | Pokay | Using a pseudovirus assay and 6 ChAdOx1 vaccinee sera, this NTD mutation conferred a 4.85x drop in neutralization (NT50). | 2021 | Mishra et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|--|
| D614G | vaccine neutralization efficacy | Pokay | 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. | 2021 | Garcia-Beltran et al. (2021) |
| D614G | virion structure | Pokay | 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. | 2020 | Yurkovetskiy et al. (2020) |
| D614G | pharmaceutical effectiveness | Pokay | This individual mutation found in the epitope from Sotrovimab causes a 1.0x reduction in neutralization efficacy using a VSV model on Vero E6 cells. | 2021 | Cathcart et al. (2021) |
| D614G | virion structure | Pokay | Based on pseudotyped virus experiments, D614G may increase infectivity by assembling more functional S protein into the virion. | 2020 | Zhang et al. (2020) |
| D614G | vaccinee plasma binding | Pokay | 1.43x 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. 1.37x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in post-infection vaccinees. | 2021 | Gong et al. (2021) |
| D614G | transmissibility | Pokay | Using a pseudovirus assay, this NTD mutation combination from B.1.617.3 conferred a nearly two-fold infectivity advantage to the spike particles. | 2021 | Mishra et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|-----------------------------------|---------------------|--|------------------|---------------------------------------|
| D614G | trafficking | Pokay | Among S variants tested, the D614G mutant shows the highest cell entry (~3.5x wild type), as supported by structural and binding analyses. | 2020 | Ozono et al. (2020) |
| D614G | trafficking | Pokay | We report here pseudoviruses carrying SG614 enter ACE2-expressing cells more efficiently than wild type (~9-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. | 2020 | UNKNOWN et al. (2020) |
| D614G | trafficking | Pokay | 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) | 2021 | Barrett et al. (2021) |
| D614G | environmental condition stability | Pokay | Relative to wild type, D614G showed increased infectivity (ie. cold stability) after storage at -20°C for up to 30 days. | 2021 | Huang et al. (2021) |
| D614G | convalescent plasma binding | Pokay | 1.53x increase in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset. | 2021 | Gong et al. (2021) |
| D614G | ACE2 receptor binding affinity | Pokay | Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant showed a slight decrease in binding (KD) relative to D614G. | 2021 | Gong et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|--------------------------------|---------------------|--|------------------|--------------------------------------|
| D614G | viral load | Pokay | 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. | 2020 | Plante et al. (2020) |
| D614G | virion structure | Pokay | Estimated free energy change (ddG) for this variant is 2.5 kcal/mol (i.e. stabilizing relative to wild type) | 2021 | Spratt et al. (2021) |
| D614G | syncytium formation | Pokay | Slight increase in Vero cell-cell membrane fusion assay under infection with VSV pseudotyped virus. | 2021 | Kim et al. (2021) |
| D614G | ACE2 receptor binding affinity | Pokay | Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant showed a 1.35x decrease in binding (KD) relative to D614G. | 2021 | Gong et al. (2021) |
| D614G | vaccinee plasma binding | Pokay | 1.05x 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. 1.45x 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. | 2021 | Gong et al. (2021) |
| D614G | convalescent plasma binding | Pokay | 1.97x increase in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset. | 2021 | Gong et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|--------------------------------|---------------------|---|------------------|--|
| D614G | ACE2 receptor binding affinity | Pokay | Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant showed a 1.5x decrease in binding (KD) relative to D614G. | 2021 | Gong et al. (2021) |
| D614G | virion structure | Pokay | 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. | 2020 | Weissman et al. (2020) |
| D614G | vaccinee plasma binding | Pokay | 1.23x increase in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in previously non-seroconverted subjects. 1.1x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in post-infection vaccinees. | 2021 | Gong et al. (2021) |
| D614G | convalescent plasma binding | Pokay | No change in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset. | 2021 | Gong et al. (2021) |
| D614G | ACE2 receptor binding affinity | Pokay | Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant showed a 1.1x decrease in binding (KD) relative to D614G. | 2021 | Gong et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|--------------------------------|---------------------|---|------------------|------------------------------------|
| D614G | vaccinee plasma binding | Pokay | This variant combination (representing lineage B.1.526) showed a 1.34x 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. 1.19x 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. | 2021 | Gong et al. (2021) |
| D614G | convalescent plasma binding | Pokay | This variant combination (representing lineage B.1.526) showed a 1.02x increase in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset. | 2021 | Gong et al. (2021) |
| D614G | ACE2 receptor binding affinity | Pokay | Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant combination (representing lineage B.1.526) showed a 1.78x increase in binding (KD) relative to D614G, even though each variant independently decreases binding. | 2021 | Gong et al. (2021) |
| D614G | ACE2 receptor binding affinity | Pokay | Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant showed a 1.42x increase in binding (KD) relative to D614G. | 2021 | Gong et al. (2021) |
| D614G | vaccinee plasma binding | Pokay | 1.08x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in previously non-seroconverted subjects. 1.27x 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. | 2021 | Gong et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|--------------------------------|---------------------|---|------------------|------------------------------------|
| D614G | convalescent plasma binding | Pokay | 1.19x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset. | 2021 | Gong et al. (2021) |
| D614G | ACE2 receptor binding affinity | Pokay | Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant combination (representing lineage B.1.429 aka Epsilon) showed a 2.82x increase in binding (KD) relative to D614G, indicating a strong marginal effect for L452R. | 2021 | Gong et al. (2021) |
| D614G | vaccinee plasma binding | Pokay | This variant combination (representing lineage B.1.429 aka Epsilon) showed a 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 previously non-seroconverted subjects. [Stark contrast to 2.15x increase in binding by convalescent plasma 8 months post infection, presumably via memory B cell affinity maturation against L452R effects] 1.12x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in post-infection vaccinees. | 2021 | Gong et al. (2021) |
| D614G | convalescent plasma binding | Pokay | This variant combination (representing lineage B.1.429 aka Epsilon) showed a 1.1x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset, indicating ablated marginal effect from L452R. | 2021 | Gong et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|--------------------------------|---------------------|--|------------------|------------------------------------|
| D614G | vaccinee plasma binding | Pokay | 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). | 2021 | Gong et al. (2021) |
| D614G | ACE2 receptor binding affinity | Pokay | 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). | 2021 | Gong et al. (2021) |
| D614G | convalescent plasma binding | Pokay | 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). | 2021 | Gong et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|--------------------------------|---------------------|---|------------------|------------------------------------|
| D614G | convalescent plasma binding | Pokay | This variant combination (representing P.1 aka Gamma) showed a 1.3x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset. | 2021 | Gong et al. (2021) |
| D614G | vaccinee plasma binding | Pokay | This variant combination (representing P.1 aka Gamma) showed a 1.14x decrease in Spike binding (relative to D614G alone) by 5 plasma 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in previously non-seroconverted subjects. 1.27x 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. | 2021 | Gong et al. (2021) |
| D614G | ACE2 receptor binding affinity | Pokay | Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant combination (representing P.1 aka Gamma) showed a 4.24x increase in binding (KD) relative to D614G. | 2021 | Gong et al. (2021) |
| D614G | convalescent plasma binding | Pokay | This variant combination (representing B.1.351 aka Beta) showed a 1.04x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset, in contrast to the largely positive binding values for each individual mutation that comprises the set. | 2021 | Gong et al. (2021) |
| D614G | ACE2 receptor binding affinity | Pokay | Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant combination (representing B.1.351 aka Beta) showed a 3.56x increase in binding (KD) relative to D614G. | 2021 | Gong et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|--------------------------------|---------------------|---|------------------|------------------------------------|
| D614G | vaccinee plasma binding | Pokay | This variant combination (representing B.1.351 aka Beta) showed a 1.28x 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. It shows a 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 post-infection vaccinees. | 2021 | Gong et al. (2021) |
| D614G | vaccinee plasma binding | Pokay | 1.29x 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. 1.39x 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. | 2021 | Gong et al. (2021) |
| D614G | ACE2 receptor binding affinity | Pokay | Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant showed a 1.96x increase in binding (KD) relative to D614G. | 2021 | Gong et al. (2021) |
| D614G | convalescent plasma binding | Pokay | 1.65x increase in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset. | 2021 | Gong et al. (2021) |
| D614G | convalescent plasma binding | Pokay | 1.08x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset. | 2021 | Gong et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|--------------------------------|---------------------|--|------------------|------------------------------------|
| D614G | vaccinee plasma binding | Pokay | 1.23x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in previously non-seroconverted subjects. 1.37x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in post-infection vaccinees. | 2021 | Gong et al. (2021) |
| D614G | ACE2 receptor binding affinity | Pokay | Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant showed a 1.58x increase in binding (KD) relative to D614G. | 2021 | Gong et al. (2021) |
| D614G | vaccinee plasma binding | Pokay | 1.14x increase in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in previously non-seroconverted subjects. 1.09x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in post-infection vaccinees. | 2021 | Gong et al. (2021) |
| D614G | ACE2 receptor binding affinity | Pokay | Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant showed a 1.51x increase in binding (KD) relative to D614G, mostly due to decreased in 'off-rate' a.k.a. dissociation rate (Kdis). | 2021 | Gong et al. (2021) |
| D614G | convalescent plasma binding | Pokay | 1.33x increase in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset. | 2021 | Gong et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|--------------------------------|---------------------|--|------------------|------------------------------------|
| D614G | ACE2 receptor binding affinity | Pokay | Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant combination (representing B.1.1.7 aka Alpha) had 5.43x increased binding relative to D614G alone. | 2021 | Gong et al. (2021) |
| D614G | convalescent plasma binding | Pokay | This variant combination (representing B.1.1.7 aka Alpha) showed a 1.15x increase in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset. | 2021 | Gong et al. (2021) |
| D614G | vaccinee plasma binding | Pokay | This variant combination (representing B.1.1.7 aka Alpha) showed no change in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in previously non-seroconverted subjects. 1.28x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in post-infection vaccinees. | 2021 | Gong et al. (2021) |
| D614G | ACE2 receptor binding affinity | Pokay | Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant combination showed no change relative to D614G. | 2021 | Gong et al. (2021) |
| D614G | vaccinee plasma binding | Pokay | 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. | 2021 | Gong et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|--------------------------------|---------------------|--|------------------|------------------------------------|
| D614G | convalescent plasma binding | Pokay | 2.11x increase in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset. | 2021 | Gong et al. (2021) |
| D614G | ACE2 receptor binding affinity | Pokay | Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant showed a 1.33x decrease in binding (KD) relative to D614G. | 2021 | Gong et al. (2021) |
| D614G | vaccinee plasma binding | Pokay | 1.16x increase in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in previously non-seroconverted subjects. 1.02x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in post-infection vaccinees. | 2021 | Gong et al. (2021) |
| D614G | convalescent plasma binding | Pokay | 1.56x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset. | 2021 | Gong et al. (2021) |
| D614G | ACE2 receptor binding affinity | Pokay | Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant showed a 1.32x increase in binding (KD) relative to D614G. | 2021 | Gong et al. (2021) |
| D614G | vaccinee plasma binding | Pokay | 1.37x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in previously non-seroconverted subjects. 1.56x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in post-infection vaccinees. | 2021 | Gong et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|--------------------------------|---------------------|--|------------------|------------------------------------|
| D614G | ACE2 receptor binding affinity | Pokay | Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant showed a 1.33x increase in binding (KD) relative to D614G. | 2021 | Gong et al. (2021) |
| D614G | convalescent plasma binding | Pokay | 1.15x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset. | 2021 | Gong et al. (2021) |
| D614G | vaccinee plasma binding | Pokay | 1.03x 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. 1.32x 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. | 2021 | Gong et al. (2021) |
| D614G | convalescent plasma binding | Pokay | 1.09x increase in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset. | 2021 | Gong et al. (2021) |
| D614G | vaccinee plasma binding | Pokay | 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. 1.59x 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. | 2021 | Gong et al. (2021) |
| D614G | ACE2 receptor binding affinity | Pokay | Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant showed a 1.82x increase in binding (KD) relative to D614G. | 2021 | Gong et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|--------------------------------|---------------------|---|------------------|------------------------------------|
| D614G | ACE2 receptor binding affinity | Pokay | Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant showed a 1.19x increase in binding (KD) relative to D614G. | 2021 | Gong et al. (2021) |
| D614G | convalescent plasma binding | Pokay | 2.29x increase in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset. | 2021 | Gong et al. (2021) |
| D614G | vaccinee plasma binding | Pokay | 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. | 2021 | Gong et al. (2021) |
| D614G | ACE2 receptor binding affinity | Pokay | Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant showed a 1.08x decrease in binding (KD) relative to D614G. | 2021 | Gong et al. (2021) |
| D614G | vaccinee plasma binding | Pokay | No significant change in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in previously non-seroconverted subjects. 1.19x 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. | 2021 | Gong et al. (2021) |
| D614G | convalescent plasma binding | Pokay | 2.16x increase in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset. | 2021 | Gong et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|---------------------------------------|
| D614G | vaccinee plasma binding | Pokay | 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. | 2021 | Gong et al. (2021) |
| D614G | vaccinee plasma binding | Pokay | 1.04x increase in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in 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. | 2021 | Gong et al. (2021) |
| D614G | ACE2 receptor binding affinity | Pokay | Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant showed a 1.28x increase in binding (KD) relative to D614G. | 2021 | Gong et al. (2021) |
| D614G | convalescent plasma escape | Pokay | Relative to B.1, Epsilon (B.1.417/429) shows 1.74x-2.35x decrease in neutralization efficiency by convalescent plasma [no cohort details provided] | 2021 | Wilhelm et al. (2021) |
| D614G | vaccine neutralization efficacy | Pokay | Relative to B.1, Epsilon (B.1.417/429) shows 1.74x-2.35x decrease in neutralization efficiency by 18 vaccinee sera (BNT162b2 and mRNA1273). | 2021 | Wilhelm et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|--------------------------------|---------------------|--|------------------|------------------------------------|
| D614G | vaccinee plasma binding | Pokay | 1.05x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in previously non-seroconverted subjects. 1.16x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in post-infection vaccinees. | 2021 | Gong et al. (2021) |
| D614G | convalescent plasma binding | Pokay | 2.15x increase in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset. | 2021 | Gong et al. (2021) |
| D614G | ACE2 receptor binding affinity | Pokay | Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant showed a 2.66x increase in binding (KD) relative to D614G. | 2021 | Gong et al. (2021) |
| D614G | convalescent plasma binding | Pokay | 1.42x increase in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset. | 2021 | Gong et al. (2021) |
| D614G | ACE2 receptor binding affinity | Pokay | This variant appears twice in the experiments, with slightly different affinities (both ~1.2x decrease in binding relative to D614G) using flow cytometry and ACE2 ectodomains-Fc portion IgG complex. | 2021 | Gong et al. (2021) |
| D614G | vaccinee plasma binding | Pokay | 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. | 2021 | Gong et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|--------------------------------|---------------------|---|------------------|------------------------------------|
| D614G | ACE2 receptor binding affinity | Pokay | 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). | 2021 | Gong et al. (2021) |
| D614G | vaccinee plasma binding | Pokay | 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. | 2021 | Gong et al. (2021) |
| D614G | convalescent plasma binding | Pokay | 1.29x increase in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset. | 2021 | Gong et al. (2021) |
| D614G | ACE2 receptor binding affinity | Pokay | Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant showed a 1.18x increase in binding (KD) relative to D614G, mostly due to decreased in 'off-rate' a.k.a. dissociation rate (Kdis). | 2021 | Gong et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|---|
| D614G | vaccinee plasma binding | Pokay | No significant change in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in previously non-seroconverted subjects. 1.04x increase in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in post-infection vaccinees. | 2021 | Gong et al. (2021) |
| D614G | convalescent plasma binding | Pokay | 1.48x increase in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset. | 2021 | Gong et al. (2021) |
| D614G | ACE2 receptor binding affinity | Pokay | Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant showed a 1.21x increase in binding (KD) relative to D614G. | 2021 | Gong et al. (2021) |
| D614G | vaccinee plasma binding | Pokay | 1.04x increase in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in previously non-seroconverted subjects. 1.09x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in post-infection vaccinees. | 2021 | Gong et al. (2021) |
| D614G | vaccine neutralization efficacy | Pokay | No significant change in virus neutralization by 18 Pfizer two dose vaccinee sera compared to B.1.1.7. [results without including the used mutation A27S likely generalizable, as this is not a lineage defining mutation] | 2021 | Zuckerman et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|--------------------------------|---------------------|--|------------------|------------------------------------|
| D614G | vaccinee plasma binding | Pokay | 1.14x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in previously non-seroconverted subjects. 1.11x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in post-infection vaccinees. | 2021 | Gong et al. (2021) |
| D614G | ACE2 receptor binding affinity | Pokay | Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant showed a 1.23x decrease in binding (KD) relative to D614G. | 2021 | Gong et al. (2021) |
| D614G | convalescent plasma binding | Pokay | 1.26x increase in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset. | 2021 | Gong et al. (2021) |
| D614G | convalescent plasma binding | Pokay | 1.11x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset. | 2021 | Gong et al. (2021) |
| D614G | vaccinee plasma binding | Pokay | 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. | 2021 | Gong et al. (2021) |
| D614G | ACE2 receptor binding affinity | Pokay | Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant showed essentially no change in binding (KD) relative to D614G. | 2021 | Gong et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|--------------------------------|---------------------|--|------------------|------------------------------------|
| D614G | ACE2 receptor binding affinity | Pokay | Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant showed a 1.12x decrease in binding (KD) relative to D614G. | 2021 | Gong et al. (2021) |
| D614G | convalescent plasma binding | Pokay | 1.58x increase in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset. | 2021 | Gong et al. (2021) |
| D614G | vaccinee plasma binding | Pokay | 1.02x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in previously non-seroconverted subjects. 1.47x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in post-infection vaccinees. | 2021 | Gong et al. (2021) |
| D614G | convalescent plasma binding | Pokay | 1.06x increase in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset. | 2021 | Gong et al. (2021) |
| D614G | vaccinee plasma binding | Pokay | 2x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in previously non-seroconverted subjects. 1.12x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in post-infection vaccinees. | 2021 | Gong et al. (2021) |
| D614G | ACE2 receptor binding affinity | Pokay | Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant showed a 1.3x decrease in binding (KD) relative to D614G. | 2021 | Gong et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|--------------------------------|---------------------|--|------------------|------------------------------------|
| D614G | vaccinee plasma binding | Pokay | 1.32x 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. 1.22x 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. | 2021 | Gong et al. (2021) |
| D614G | convalescent plasma binding | Pokay | 1.56x increase in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset. | 2021 | Gong et al. (2021) |
| D614G | ACE2 receptor binding affinity | Pokay | Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant showed a 1.69x decrease in binding (KD) relative to D614G. | 2021 | Gong et al. (2021) |
| D614G | convalescent plasma binding | Pokay | 1.96x increase in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset. | 2021 | Gong et al. (2021) |
| D614G | ACE2 receptor binding affinity | Pokay | Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant showed a 1.23x increase in binding (KD) relative to D614G, mostly due to decreased in 'off-rate' a.k.a. dissociation rate (Kdis). | 2021 | Gong et al. (2021) |
| D614G | vaccinee plasma binding | Pokay | 1.09x increase in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in previously non-seroconverted subjects. 1.08x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in post-infection vaccinees. | 2021 | Gong et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|--|
| D614G | trafficking | Pokay | Quantification of the band intensities showed that the P681R mutation, which lies near the proteolytic processing site, caused a small increase in proteolytic processing as measured by a 2-fold decrease in the ratio of S/S2. | 2021 | Tada et al. (2021) |
| H655Y | pharmaceutical effectiveness | Pokay | Omicron BA.2 have higher sensitivity to inhibition by soluble angiotensin converting enzyme 2 (ACE2) and the endosomal inhibitor chloroquine compared to D614G | 2022 | Neerukonda et al. (2022) |
| H655Y | antibody epitope effects | Pokay | Neutralization of the bsAbs Bi-Nab35B5-47D10. Omicron BA.2 has an IC50 fold change of 0.07x. | 2022 | Yuan et al. (2022) |
| H655Y | antibody epitope effects | Pokay | Neutralization of the bsAbs 35B5. Omicron BA.2 has an IC50 fold change of 0.09x. | 2022 | Yuan et al. (2022) |
| H655Y | antibody epitope effects | Pokay | Neutralization of the bsAbs 47D10. Omicron BA.2 has an IC50 fold change of 0.08x. | 2022 | Yuan et al. (2022) |
| H655Y | antibody epitope effects | Pokay | Neutralization of the bsAbs Bi-Nab47D10-35B5. Omicron BA.2 has an IC50 fold change of 0.04x. | 2022 | Yuan et al. (2022) |
| H655Y | vaccine neutralization efficacy | Pokay | Omicron BA.2 neutralization of the Omicron variants by antibodies induced by three doses of Pfizer/BNT162b2 mRNA vaccine was 7-8-fold less potent than the D614G, and the Omicron variants still evade neutralization more efficiently. | 2022 | Neerukonda et al. (2022) |
| H655Y | antibody epitope effects | Pokay | BnAb 002-S21F2 IC50 on the Omicron BA.2 variant is 0.8x fold the wildtype. | 2022 | Kumar et al. (2022) |
| H655Y | virion structure | Pokay | CryoEM reveals the P.1 trimer to adopt exclusively a conformation in which one of the receptor-binding domains is in the "up" position. | 2021 | Wang et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|------------------------------------|
| H655Y | vaccine neutralization efficacy | Pokay | In 12 Moderna vaccinee sera 15 days post second dose (43 days since first vaccination), an average 2.8x decrease in reciprocal ID50 value was observed ten key point mutations in Spike in the P.1 lineage vs wildtype. A 4.8x decrease against the full P.1 type vs WA-1 was observed, though overall with a higher ID50 reciprocal value. In 10 Pfizer vaccinee sera 7 days or more post second dose (28 days or more since first vaccination), an average 2.2x decrease in reciprocal ID50 value was observed ten key point mutations in Spike in the P.1 lineage vs wildtype. A 3.8x decrease against the full P.1 type vs WA-1 was observed, with similar variant ID50 reciprocal value. | 2021 | Wang et al. (2021) |
| H655Y | convalescent plasma escape | Pokay | In convalescent sera one month or more post-infection in Spring 2020, an average 6.5x decrease in reciprocal ID50 value was observed ten key point mutations in Spike in the P.1 lineage vs wildtype. A 3.4x decrease against the full P.1 type vs WA-1 was observed, with better full P.1 ID50 reciprocal value compared to the 10-mutation model. | 2021 | Wang et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|--------------------------|---------------------|---|------------------|--|
| H655Y | antibody epitope effects | Pokay | Amongst RBD-targeting Emergency Use Authorized monoclonal antibody treatments CB6, LY-CoV555 and REGN10933 show abrogated neutralization activity against the ten key point mutations in Spike in the P.1 lineage vs wildtype or WA-1, but REGN10987 activity remains strong. RBD-targeting monoclonal antibodies 2-15 and C121 show abrogated neutralization activity against the ten key point mutations in Spike in the P.1 lineage vs wildtype or WA-1. N terminal domain targeting monoclonal antibodies 5-7, 4-8, 4-18 and 2-17 have abrogated neutralization activity against the ten key point mutations in Spike in the P.1 lineage vs wildtype or WA-1. | 2021 | Wang et al. (2021) |
| H655Y | reinfection | Pokay | After a 128 day interval, a patient in Sao Paulo State, Brazil reinfected with P.1 (first episode likely predates P.1 emergence). Both cases were fairly mild (difficulty breathing, tiredness, dizziness and fatigue). | 2021 | Malta Romano et al. (2021) |
| H655Y | vaccine efficacy | Pokay | In a 1:5 test-negative matched control study of 8153 individuals who received the Moderna mRNA-1273 vaccine, 349 test-positive were Gamma. Two dose vaccine efficacy against Gamma was 95.5 (90.9-97.8%), one dose VE was 74.2 (43.8-88.1%). | 2021 | Bruxvoort et al. (2021) |
| H655Y | trafficking | Pokay | ~6x cleavage of S2 relative to WA1 (D614G) wildtype by Gamma variant as measured by mass spectrometry of Vero-TMPRSS culture [no mutations directly at furin cleavage site, but H655Y is upstream] Compare to 4.5x or less for variants of concern with direct furin cleavage site mutations. | 2021 | Esclera et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|---|
| H655Y | reinfection | Pokay | Three healthcare workers (29-50yo) had confirmed P.1 [Gamma] re-infection in the Amazonas region of Brazil 3-9 months after initial infection from viruses with distinct lineage from P.1, but mild symptoms upon re-infection and evidence for infectiousness during re-infection. | 2021 | Naveca et al. (2021) |
| H655Y | vaccine neutralization efficacy | Pokay | Mean 3.0x reduction of NT50 value P.1 (Gamma) relative to wild type in 8 sera from adult BNT162b2 vaccinees (28-47yo) collected ~1m post booster. | 2021 | Uriu et al. (2021) |
| H655Y | convalescent plasma escape | Pokay | Mean 4.1x reduction of NT50 value P.1 (Gamma) relative to wild type in 8 sera from older convalescent patients (52-92yo) collected 1-3m post symptom onset. | 2021 | Uriu et al. (2021) |
| H655Y | antibody epitope effects | Pokay | BnAb 002-S21F2 IC50 on the Gamma (P.1) variant is 0.6x fold the wildtype. | 2022 | Kumar et al. (2022) |
| H655Y | vaccine neutralization efficacy | Pokay | The neutralizing activity of vaccine was slightly lower against B.1.1.248 variant constellation in sera tested from most of the 15 patients with the BNT162b2 mRNA vaccine. (Fig. 4) | 2021 | Chen et al. (2021) |
| H655Y | vaccine neutralization efficacy | Pokay | ELISpot assays show T cell neutralization reduced by 16.6% in this B.1.1.248 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). | 2021 | Gallagher et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|--|
| H655Y | antibody epitope effects | Pokay | B.1.1.248 variant constellation ablates Class 1 receptor-binding-mot if targeting antibodies COV2-2050, 1B07. B.1.1.248 variant constellation ablates Class 3 N-terminal domain targeting antibody COV2-2676. | 2021 | Chen et al. (2021) |
| H655Y | convalescent plasma escape | Pokay | B.1.1.7 variant constellation two-tailed Wilcoxon matched-pairs signed-rank test against 10 convalescent sera P | 2021 | Chen et al. (2021) |
| H655Y | anthropozoonotic events | Pokay | Unlike wild type or B.1.1.7, P.1 lineage virus was able to infect and replicate in common lab mouse strains, with high titer. | 2021 | Montagutelli et al. (2021) |
| H655Y | convalescent plasma escape | Pokay | B.1.1.248 variant constellation in 10 convalescent human sera ~1mo post infection had mild to moderate resistance against most samples, P | 2021 | Chen et al. (2021) |
| H655Y | vaccine neutralization efficacy | Pokay | Neutralizing antibody titers increased in previously infected vaccinees relative to uninfected vaccinees 4.3-fold against P.1 (contrast with 3.4 fold against original SARS-CoV-2). | 2021 | Leier et al. (2021) |
| H655Y | vaccine neutralization efficacy | Pokay | Pseudotyped P.1 virus has reduced neutralization activity vs wild type: 6.7x (30 sera Pfizer median 9 days post 2nd dose) and 4.5x (35 sera Moderna median 18 days post 2nd dose). This was significant by ANOVA. | 2021 | Garcia-Beltran et al. (2021) |
| H655Y | vaccine neutralization efficacy | Pokay | Using P.1 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. | 2021 | Alenquer et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|--|
| H655Y | vaccine neutralization efficacy | Pokay | In human sera 8 weeks post-vaccination with INO-4800, a ~2-fold reduction in P.1 neutralization was observed. | 2021 | Andrade et al. (2021) |
| H655Y | vaccine neutralization efficacy | Pokay | Among 46,884 HCWs in Manaus, Brazil vaccinated with at least one dose of CoronaVac, a 0.50-fold reduction (adjusted vaccine effectiveness, 49.6%: 95% CI, 11.3 - 71.4) in the odds of symptomatic SARS-CoV-2 infection was observed during the period 14 days or more after receiving the first dose. Estimated vaccine effectiveness of at least one dose against any SARS-CoV-2 infection was 35.1% (95% CI, -6.6 - 60.5) in the same time period. | 2021 | Hitchlings et al. (2021) |
| H655Y | pharmaceutical effectiveness | Pokay | VSV pseudotype P.1 entry mediated by the S proteins of the P.1 variant was completely resistant to blocking by REGN10989 and Bamlanivimab. Cell fusion proficiency was slight impaired. Entry driven by the S proteins of the B.1.351 was partially resistant against Casirivimab. | 2021 | Hoffman et al. (2021) |
| H655Y | convalescent plasma binding | Pokay | VSV pseudotype P.1 showed 4.8-fold decrease in NT50 vs wild type in sera from 9 ICU patients undergoing treatment in Germany (pre-variant infections). | 2021 | Hoffman et al. (2021) |
| H655Y | vaccine neutralization efficacy | Pokay | VSV pseudotype P.1 showed 5.12-fold reduction in neutralization efficiency vs wild type in 15 Pfizer BNT162b2 vaccinee sera 13-15 days post second dose. Cell fusion proficiency was slight impaired. | 2021 | Hoffman et al. (2021) |
| H655Y | trafficking | Pokay | VSV pseudotype P.1 showed slight decrease in cell entry relative to wild type in 262T and 263T-ACE2 (kidney) cell lines. Cell fusion proficiency was slight impaired. | 2021 | Hoffman et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|---|
| H655Y | convalescent plasma binding | Pokay | Neutralizing antibodies that were generated following a mild infection with SARS-CoV-2 B.1.128 were effective in vitro, and likely protective, against the SARS-CoV-2 P.1. variant in the majority of individuals based on 60 convalescent sera tested. | 2021 | Mendes-Correa et al. (2021) |
| H655Y | vaccine neutralization efficacy | Pokay | PBMCs of Pfizer/BioNTech BNT162b2 (n | 2021 | Tarke et al. (2021) |
| H655Y | convalescent plasma escape | Pokay | In 13 plasma collected ~1mo after B.1.1.7 infection (nursing home in Ticino, Switzerland), neutralization reduced to undetectable levels in many plasma for P.1 pseudotyped virus, as well as WT and other VOCs. [paper does not detail the P.1 variants used, using the most popular as a stand in] | 2021 | McCallum et al. (2021) |
| H655Y | vaccine neutralization efficacy | Pokay | 1.15x *increase* in neutralization (ID50) in sera 3 weeks after one dose of Pfizer/BioNTech BNT162b2 (up to 5 naive and post infection vaccinees) | 2021 | Gong et al. (2021) |
| H655Y | vaccine neutralization efficacy | Pokay | Neutralization efficiency (ID50) against P.1 reduced 3.2x relative to D614G wildtype using pseudotyped VSV assay on 8 Moderna vaccinee sera one week post-booster. | 2021 | Choi et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|---|
| H655Y | pharmaceutical effectiveness | Pokay | P.1 virus neutralization (as tested using biolayer interferometry) of both Lilly antibodies was severely impacted, with Lilly mAb combination LY-CoV16 and LY-CoV555 (due to mutations at 416 and 484 respectively) shows almost complete loss of neutralization of P.1. There was also escape from neutralization of P.1 by REGN10933 (one of 2 in Regeneron's mAb cocktail) and a modest reduction in neutralization of P.1 by AstraZeneca's AZD8895 (while AZD1061 and AZD7442 showed equal neutralization of all SARS-CoV-2 variants tested). The three Adagio antibodies neutralized P.1 with all reaching a plateau at 100% neutralization: interestingly, ADG30 showed a slight increase of neutralization of P.1. S309 Vir was largely unaffected, although for several viruses, including P.1, the antibody failed to completely neutralize, conceivably reflecting incomplete glycosylation at N343, since the sugar interaction is key to binding of this antibody. | 2021 | Dejnirattisai et al. (2021) |
| H655Y | vaccine neutralization efficacy | Pokay | P.1 lineage titers were reduced 7.6-fold and 9-fold for the BNT162b2 Pfizer (sera collected 4-14 days post-booster) and ChAdOx1 nCoV-19 AstraZeneca (sera collected 14 or 28 days post-booster) vaccines respectively. | 2021 | Dejnirattisai et al. (2021) |
| H655Y | vaccine neutralization efficacy | Pokay | In sera 1-2 weeks after BNT162b2 first dose, from six patients previously infected with B.1, antibody titer in a microneutralization assay was on average 2896 for P.1 virus. This compares favorably (stronger) to post-infection neutralization titer against all variants tested in the same sera (wild type, B.1.1.7, B.1.351, and P.1). | 2021 | Luftig et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|--|
| H655Y | convalescent plasma binding | Pokay | In sera from six patients collected 1 to 12 weeks post-infection with B.1, antibody titer in a microneutralization assay was on average 256 for B.1.1.7 virus. Compare to somewhat stronger neutralization titer for wild type (456.1) in the same sera. | 2021 | Luftig et al. (2021) |
| H655Y | vaccine neutralization efficacy | Pokay | Detectable antibodies against P.1 at various time points using pseudovirus neutralization in Moderna vaccinee cohort: Day 43 100%, Day 209 85%. | 2021 | Pegu et al. (2021) |
| H655Y | T cell evasion | Pokay | PBMCs of 11 mild COVID-19 patients collected 38-80 days after symptom onset were stimulated with the 15-mer peptide pools (w/ 10 residue overlaps) from the whole viral proteome, showing no significant CD4+ cell count effect for P.1, and a slight increase in CD8+ percentage (p | 2021 | Tarke et al. (2021) |
| H655Y | transmissibility | Pokay | The relative transmissibility of P.1 estimated at the national level (Italy) varied according to the assumed degree of cross-protection granted by infection with other lineages and ranged from 1.12 (95%CI 1.03-1.23) in the case of complete immune evasion by P.1 to 1.39 (95%CI 1.26-1.56) in the case of complete cross-protection. PG: variant list has been abbreviated due to mixed K417 bases in this lineage, potential miscalls of deletions | 2021 | Stefanelli et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|----------------------|---------------------|---|------------------|--|
| H655Y | outcome hazard ratio | Pokay | In the Parana state of Brazil, patients aged 20-29 years experienced a tripling of their case fatality rate (CFR), from 0.04% to 0.13%, while those aged 30-39, 40-49, 50-59 experienced approximate CFR doubling comparing February to January in 2021. Notably, the observed CFR increase coincided with the second consecutive month of declining number of diagnosed SARS-CoV-2 cases. Taken together, these preliminary findings suggest significant increases in CFR in young and middle-aged adults after identification of a novel SARS-CoV-2 strain circulating in Brazil. [this is somewhat indirect evidence that assume greatly increasing proportion of P.1 cases in March (70%) compared to February, but the first official ID of P.1 in Parana state (Feb 16th) may be due to testing procedures rather than actual prevalence] | 2021 | Santos de Oliveira et al. (2021) |
| H655Y | outcome hazard ratio | Pokay | In the Southern Brazilian states of Rio Grande do Sul, comparing pre-P.1 and post-P.1 waves: The increase in Case Fatality Rate occurred in a greatest intensity in the population between 20 and 59 years old and among patients without pre-existing risk conditions. Female 20 to 39 years old, with no pre-existing risk conditions, were at risk of death 5.65 times higher in February (95%CI | 2021 | Ribas Freitas et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|---------------------------------------|
| H655Y | outcome hazard ratio | Pokay | On average across 7 European countries studied, using P.1 defining mutations: Significant shift to infection in those without pre-existing conditions (27.8% vs 89% for non-VOC cases). Significant increase in hospitalization rate (20% vs 7.5% for non-VOC cases). Significant increase in ICU rate (2.1% vs 0.6% for non-VOC cases). Significant increase in health care worker rate (19.8% vs 8.0% for non-VOC cases). | 2021 | Funk et al. (2021) |
| H655Y | vaccine neutralization efficacy | Pokay | This variant was designated A.27.RN according to its phylogenetic clade classification. It emerged in parallel with the B.1.1.7 variant, increased to >50% of all SARS-CoV-2 variants by week five. Subsequently it decreased to <10% of all variants by calendar week eight when B.1.1.7 had become the dominant strain. Antibodies induced by BNT162b2 (Pfizer) vaccination neutralized A.27.RN but with a two-to-threefold reduced efficacy as compared to the wild-type and B.1.1.7 strains. | 2021 | Mallm et al. (2021) |
| H655Y | vaccinee plasma binding | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.2 (from South Africa/CERI-KRISP-K03 2307/2021) were 3.9x-fold lower (95% CI: 0.14x-0.17x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|---------------------------------------|
| H655Y | ACE2 receptor binding affinity | Pokay | L27, V34 and E90 mutation resulted in ultrahigh affinity binding of the LVE-ACE-2 domain to the widest variety of VOCs, with KDs of 78fM for binding to the Omicron BA.2. Values were obtained with LVE-ACE-2/mAB chimeras containing the Y-T-E sequence that enhances binding to the FcRn receptor, which in turn is expected to extend biological half-life 3-4-fold. | 2022 | Uhal B et al. (2022) |
| H655Y | vaccine neutralization efficacy | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.2 (from South Africa/CERI-KRISP-K03 2307/2021) were 4.5-fold lower (95% CI: 4.3x-4.7x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| H655Y | vaccine neutralization efficacy | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.2.12.1 (from USA/NY-CDC-ASC2 10722700/2022) were 4.2-fold lower (95% CI: 5.8x-6.6x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| H655Y | vaccinee plasma binding | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.2.12.1 (from USA/NY-CDC-ASC2 10722700/2022) were 3.9x-fold lower (95% CI: 0.14x-0.18x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|--|
| H655Y | pharmaceutical effectiveness | Pokay | Omicron (a.k.a. B.1.1.529) Spike pseudotyped VSV and Vero E6 cells has somewhat reduced neutralization (2.7x) vs wild type with monoclonal antibody Sotrovimab (a.k.a. VIR-7831). [delins at 214 omitted for syntax compatibility] | 2021 | Cathcart et al. (2021) |
| H655Y | vaccine neutralization efficacy | Pokay | Omicron breakthrough infection after 3-dose vaccination resulted in a further 3.5-fold and 2.9-fold increase of Omicron BA.1 and BA.2 neutralizing titers. Omicron BA.4/5 showed the highest neutralization resistance of all variants tested, resulting in low geometric mean neutralizing titers in plasma samples obtained after the second vaccine dose (NT50 | 2022 | Wang et al. (2022) |
| H655Y | antibody epitope effects | Pokay | Neutralization of the bsAbs Bi-Nab47D10-35B5. Omicron BA.1 has an IC50 fold change of 0.08x. | 2022 | Yuan et al. (2022) |
| H655Y | vaccine neutralization efficacy | Pokay | Omicron B.1.1.529 (BA.1) neutralization of the Omicron variants by antibodies induced by three doses of Pfizer/BNT162b2 mRNA vaccine was 7-8-fold less potent than the D614G, and the Omicron variants still evade neutralization more efficiently. | 2022 | Neerukonda et al. (2022) |
| H655Y | pharmaceutical effectiveness | Pokay | Omicron (B.1.1.529 [BA.1]) have higher sensitivity to inhibition by soluble angiotensin converting enzyme 2 (ACE2) and the endosomal inhibitor chloroquine compared to D614G | 2022 | Neerukonda et al. (2022) |
| H655Y | antibody epitope effects | Pokay | Neutralization of the bsAbs Bi-Nab35B5-47D10. Omicron BA.1 has an IC50 fold change of 0.30x. | 2022 | Yuan et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|--------------------------------------|
| H655Y | vaccine neutralization efficacy | Pokay | Paradigms' ACE-2 variant LVE/STR chimera binds to SARS-2 Omicron variant B.1.1.529 spike protein trimer with high affinity. Determined using Surrogate Viral Neutralization Tests. | 2022 | Uhal B et al. (2022) |
| H655Y | ACE2 receptor binding affinity | Pokay | L27, V34 and E90 mutation resulted in ultrahigh affinity binding of the LVE-ACE-2 domain to the widest variety of VOCs, with KDs of 73 pM for binding to the Omicron B.1.1.529. Values were obtained with LVE-ACE-2/mAB chimeras containing the Y-T-E sequence that enhances binding to the FcRn receptor, which in turn is expected to extend biological half-life 3-4-fold. | 2022 | Uhal B et al. (2022) |
| H655Y | antibody epitope effects | Pokay | Neutralization of the bsAbs 35B5. Omicron BA.1 has an IC50 fold change of 0.38x. | 2022 | Yuan et al. (2022) |
| H655Y | vaccinee plasma binding | Pokay | All 10 individuals with 2 doses of the BNT162b2/BNT162b2 vaccine had a neutralizing titer in B.1 variant at an average of 729 NT50. | 2022 | Arora et al. (2022) |
| H655Y | antibody epitope effects | Pokay | Plaque reduction neutralization test (PRNT) was used uring primary infection, post sixty daysof second dose vaccination, pre-reinfection and reinfection against Delta variant and was used to determine neutralizing antibodytitres. There was a 24.63x fold increase in antibody response from first infection to recovered and vaccinated with 2 doses (60 days). There was a 4.21x fold increase in antibody response pre-reinfection. There was a 39.27x fold increase in antibody response during reinfection. | 2022 | Shete et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|--------------------------|---------------------|--|------------------|-------------------------------------|
| H655Y | antibody epitope effects | Pokay | Plaque reduction neutralization test (PRNT) was used uring primary infection, post sixty daysof second dose vaccination, pre-reinfection and reinfection against B.1 variant and was used to determine neutralizing antibodytitres. There was a 6.76x fold increase in antibody response from first infection to recovered and vaccinated with 2 doses (60 days). There was a 2.06x fold increase in antibody response pre-reinfection. There was a 8.18x fold increase in antibody response during reinfection. | 2022 | Shete et al. (2022) |
| H655Y | vaccinee plasma binding | Pokay | All 10 individuals with 3 doses of the BNT162b2/BNT162b2 vaccine had a neutralizing titer in B.1 variant at an average of 3319 NT50. | 2022 | Arora et al. (2022) |
| H655Y | antibody epitope effects | Pokay | Plaque reduction neutralization test (PRNT) was used uring primary infection, post sixty daysof second dose vaccination, pre-reinfection and reinfection against Omicron variant and was used to determine neutralizing antibodytitres. There was a 114.84x fold increase in antibody response from first infection to recovered and vaccinated with 2 doses (60 days). There was a 6.61x fold increase in antibody response pre-reinfection. There was a 1194.9x fold increase in antibody response during reinfection. | 2022 | Shete et al. (2022) |
| H655Y | antibody epitope effects | Pokay | BnAb 002-S21F2 IC50 on the Omicron BA.1 variant is 1.0x fold the wildtype. | 2022 | Kumar et al. (2022) |
| H655Y | antibody epitope effects | Pokay | Neutralization of the bsAbs 47D10. Omicron BA.1 has an IC50 fold change of 1.26x. | 2022 | Yuan et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|--|
| H655Y | pharmaceutical effectiveness | Pokay | Omicron BA.3 have higher sensitivity to inhibition by soluble angiotensin converting enzyme 2 (ACE2) and the endosomal inhibitor chloroquine compared to D614G | 2022 | Neerukonda et al. (2022) |
| H655Y | vaccine neutralization efficacy | Pokay | Omicron BA.3 neutralization of the Omicron variants by antibodies induced by three doses of Pfizer/BNT162b2 mRNA vaccine was 7-8-fold less potent than the D614G, and the Omicron variants still evade neutralization more efficiently. | 2022 | Neerukonda et al. (2022) |
| H655Y | vaccinee plasma binding | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.3 (from South Africa/NICD-N22404/2021) were 4.2x-fold lower (95% CI: 0.15x-0.20x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| H655Y | vaccine neutralization efficacy | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.3 (from South Africa/NICD-N22404/2021) were 6.2-fold lower (95% CI: 11.8x-14.3x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| H655Y | vaccine neutralization efficacy | Pokay | paired testing of vaccine sera against ancestral virus compared to Omicron BA.1 shows that 3-dose vaccine regimen provides over 50x fold increase in protection against Omicron(B.1.1.529 [BA.1]) compared to a 2-dose regimen. | 2022 | Hao et al. (2022) |
| H655Y | pharmaceutical effectiveness | Pokay | 4th antigenic exposure with Omicron (B.1.1.529 [BA.1])(n | 2022 | Wang et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|---------------------------------------|
| H655Y | vaccine neutralization efficacy | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.1 (from Botswana/R40B59_BHP_3321 001248/2021) were 3.4-fold lower (95% CI: 3.2x-3.6x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| H655Y | vaccinee plasma binding | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.1 (from Botswana/R40B59_BHP_3321 001248/2021) were 28.7x-fold lower (95% CI: 0.03x-0.05) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| H655Y | vaccinee plasma binding | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.4/5 (from) were 17.2x-fold lower (95% CI: 0.6x-0.7x) than against 208-428 972-1834 4.3-4.7 US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| H655Y | vaccine neutralization efficacy | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.4/5 (from) were 13.0-fold lower (95% CI: 4.2x-4.6x) than against 208-428 972-1834 4.3-4.7 US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| H655Y | vaccine neutralization efficacy | Pokay | Neutralization efficiency (ID50) against A.VOI.V2 (first identified in Angola) reduced 8.0x relative to D614G wildtype using pseudotyped VSV assay on 8 Moderna vaccinee sera one week post-booster. | 2021 | Choi et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|--|
| H655Y | vaccinee plasma binding | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, XD (from) were 1.5x-fold lower (95% CI: 0.05x-0.07x) than against 208-428 972-1834 4.3-4.7 US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| H655Y | vaccine neutralization efficacy | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, XD (from) were 4.4-fold lower (95% CI: 4.3x-4.7x) than against 208-428 972-1834 4.3-4.7 US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| H655Y | anthropozoonotic events | Pokay | Mouse-adapted SARS-CoV-2 mutations after 11 serial passages in various immunocompromised mice strains. | 2021 | Rathnasinghe et al. (2021) |
| H655Y | convalescent plasma binding | Pokay | This variant combination (representing P.1 aka Gamma) showed a 1.3x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset. | 2021 | Gong et al. (2021) |
| H655Y | vaccinee plasma binding | Pokay | This variant combination (representing P.1 aka Gamma) showed a 1.14x decrease in Spike binding (relative to D614G alone) by 5 plasma 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in previously non-seroconverted subjects. 1.27x 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. | 2021 | Gong et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|--------------------------------|---------------------|--|------------------|---------------------------------------|
| H655Y | ACE2 receptor binding affinity | Pokay | Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant combination (representing P.1 aka Gamma) showed a 4.24x increase in binding (KD) relative to D614G. | 2021 | Gong et al. (2021) |
| H655Y | convalescent plasma binding | Pokay | 1.48x increase in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset. | 2021 | Gong et al. (2021) |
| H655Y | ACE2 receptor binding affinity | Pokay | Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant showed a 1.21x increase in binding (KD) relative to D614G. | 2021 | Gong et al. (2021) |
| H655Y | vaccinee plasma binding | Pokay | 1.04x increase in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in previously non-seroconverted subjects. 1.09x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in post-infection vaccinees. | 2021 | Gong et al. (2021) |
| H655Y | homoplasy | Pokay | In experimental models of SARS-CoV-2 mutational evolution (without immune pressure), this mutation in the N terminal domain appears convergent. | 2021 | Borges et al. (2021) |
| H655Y | anthropozoonotic events | Pokay | Six minks were intranasally infected with WA1 isolate, all developed this mutation during infection. | 2021 | Esclera et al. (2021) |
| H655Y | anthropozoonotic events | Pokay | This mutation outside the receptor binding domain increases the virus transduction rate in tree shrew (<i>Tupaia belangeri</i>), (as it does in humans) according to pseudotyped VSV experiments. | 2023 | Li et al. (2023) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|--|
| H655Y | virion structure | Pokay | Estimated free energy change (ddG) for this variant is 0.87 kcal/mol (i.e. stabilizing relative to wild type) | 2021 | Spratt et al. (2021) |
| N679K | pharmaceutical effectiveness | Pokay | Omicron BA.2 have higher sensitivity to inhibition by soluble angiotensin converting enzyme 2 (ACE2) and the endosomal inhibitor chloroquine compared to D614G | 2022 | Neerukonda et al. (2022) |
| N679K | antibody epitope effects | Pokay | Neutralization of the bsAbs Bi-Nab35B5-47D10. Omicron BA.2 has an IC50 fold change of 0.07x. | 2022 | Yuan et al. (2022) |
| N679K | antibody epitope effects | Pokay | Neutralization of the bsAbs 35B5. Omicron BA.2 has an IC50 fold change of 0.09x. | 2022 | Yuan et al. (2022) |
| N679K | antibody epitope effects | Pokay | Neutralization of the bsAbs 47D10. Omicron BA.2 has an IC50 fold change of 0.08x. | 2022 | Yuan et al. (2022) |
| N679K | antibody epitope effects | Pokay | Neutralization of the bsAbs Bi-Nab47D10-35B5. Omicron BA.2 has an IC50 fold change of 0.04x. | 2022 | Yuan et al. (2022) |
| N679K | vaccine neutralization efficacy | Pokay | Omicron BA.2 neutralization of the Omicron variants by antibodies induced by three doses of Pfizer/BNT162b2 mRNA vaccine was 7-8-fold less potent than the D614G, and the Omicron variants still evade neutralization more efficiently. | 2022 | Neerukonda et al. (2022) |
| N679K | antibody epitope effects | Pokay | BnAb 002-S21F2 IC50 on the Omicron BA.2 variant is 0.8x fold the wildtype. | 2022 | Kumar et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|---------------------------------------|
| N679K | vaccinee plasma binding | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.2 (from South Africa/CERI-KRISP-K03 2307/2021) were 3.9x-fold lower (95% CI: 0.14x-0.17x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| N679K | ACE2 receptor binding affinity | Pokay | L27, V34 and E90 mutation resulted in ultrahigh affinity binding of the LVE-ACE-2 domain to the widest variety of VOCs, with KDs of 78fM for binding to the Omicron BA.2. Values were obtained with LVE-ACE-2/mAB chimeras containing the Y-T-E sequence that enhances binding to the FcRn receptor, which in turn is expected to extend biological half-life 3-4-fold. | 2022 | Uhal B et al. (2022) |
| N679K | vaccine neutralization efficacy | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.2 (from South Africa/CERI-KRISP-K03 2307/2021) were 4.5-fold lower (95% CI: 4.3x-4.7x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| N679K | vaccine neutralization efficacy | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.2.12.1 (from USA/NY-CDC-ASC2 10722700/2022) were 4.2-fold lower (95% CI: 5.8x-6.6x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|--|
| N679K | vaccinee plasma binding | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.2.12.1 (from USA/NY-CDC-ASC2 10722700/2022) were 3.9x-fold lower (95% CI: 0.14x-0.18x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahade et al. (2022) |
| N679K | pharmaceutical effectiveness | Pokay | Omicron (a.k.a. B.1.1.529) Spike pseudotyped VSV and Vero E6 cells has somewhat reduced neutralization (2.7x) vs wild type with monoclonal antibody Sotrovimab (a.k.a. VIR-7831). [delins at 214 omitted for syntax compatibility] | 2021 | Cathcart et al. (2021) |
| N679K | vaccine neutralization efficacy | Pokay | Omicron breakthrough infection after 3-dose vaccination resulted in a further 3.5-fold and 2.9-fold increase of Omicron BA.1 and BA.2 neutralizing titers. Omicron BA.4/5 showed the highest neutralization resistance of all variants tested, resulting in low geometric mean neutralizing titers in plasma samples obtained after the second vaccine dose (NT50) | 2022 | Wang et al. (2022) |
| N679K | antibody epitope effects | Pokay | Neutralization of the bsAbs Bi-Nab47D10-35B5. Omicron BA.1 has an IC50 fold change of 0.08x. | 2022 | Yuan et al. (2022) |
| N679K | vaccine neutralization efficacy | Pokay | Omicron B.1.1.529 (BA.1) neutralization of the Omicron variants by antibodies induced by three doses of Pfizer/BNT162b2 mRNA vaccine was 7-8-fold less potent than the D614G, and the Omicron variants still evade neutralization more efficiently. | 2022 | Neerukonda et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|--|
| N679K | pharmaceutical effectiveness | Pokay | Omicron (B.1.1.529 [BA.1]) have higher sensitivity to inhibition by soluble angiotensin converting enzyme 2 (ACE2) and the endosomal inhibitor chloroquine compared to D614G | 2022 | Neerukonda et al. (2022) |
| N679K | antibody epitope effects | Pokay | Neutralization of the bsAbs Bi-Nab35B5-47D10. Omicron BA.1 has an IC50 fold change of 0.30x. | 2022 | Yuan et al. (2022) |
| N679K | vaccine neutralization efficacy | Pokay | Paradigms' ACE-2 variant LVE/STR chimera binds to SARS-2 Omicron variant B.1.1.529 spike protein trimer with high affinity. Determined using Surrogate Viral Neutralization Tests. | 2022 | Uhal B et al. (2022) |
| N679K | ACE2 receptor binding affinity | Pokay | L27, V34 and E90 mutation resulted in ultrahigh affinity binding of the LVE-ACE-2 domain to the widest variety of VOCs, with KDs of 73 pM for binding to the Omicron B.1.1.529. Values were obtained with LVE-ACE-2/mAB chimeras containing the Y-T-E sequence that enhances binding to the FcRn receptor, which in turn is expected to extend biological half-life 3-4-fold. | 2022 | Uhal B et al. (2022) |
| N679K | antibody epitope effects | Pokay | Neutralization of the bsAbs 35B5. Omicron BA.1 has an IC50 fold change of 0.38x. | 2022 | Yuan et al. (2022) |
| N679K | vaccinee plasma binding | Pokay | All 10 individuals with 2 doses of the BNT162b2/BNT162b2 vaccine had a neutralizing titer in B.1 variant at an average of 729 NT50. | 2022 | Arora et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|--------------------------|---------------------|--|------------------|-------------------------------------|
| N679K | antibody epitope effects | Pokay | Plaque reduction neutralization test (PRNT) was used uring primary infection, post sixty daysof second dose vaccination, pre-reinfection and reinfection against Delta variant and was used to determine neutralizing antibodytitres. There was a 24.63x fold increase in antibody response from first infection to recovered and vaccinated with 2 doses (60 days). There was a 4.21x fold increase in antibody response pre-reinfection. There was a 39.27x fold increase in antibody response during reinfection. | 2022 | Shete et al. (2022) |
| N679K | antibody epitope effects | Pokay | Plaque reduction neutralization test (PRNT) was used uring primary infection, post sixty daysof second dose vaccination, pre-reinfection and reinfection against B.1 variant and was used to determine neutralizing antibodytitres. There was a 6.76x fold increase in antibody response from first infection to recovered and vaccinated with 2 doses (60 days). There was a 2.06x fold increase in antibody response pre-reinfection. There was a 8.18x fold increase in antibody response during reinfection. | 2022 | Shete et al. (2022) |
| N679K | vaccinee plasma binding | Pokay | All 10 individuals with 3 doses of the BNT162b2/BNT162b2 vaccine had a neutralizing titer in B.1 variant at an average of 3319 NT50. | 2022 | Arora et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|--|
| N679K | antibody epitope effects | Pokay | Plaque reduction neutralization test (PRNT) was used using primary infection, post sixty days of second dose vaccination, pre-reinfection and reinfection against Omicron variant and was used to determine neutralizing antibody titres. There was a 114.84x fold increase in antibody response from first infection to recovered and vaccinated with 2 doses (60 days). There was a 6.61x fold increase in antibody response pre-reinfection. There was a 1194.9x fold increase in antibody response during reinfection. | 2022 | Shete et al. (2022) |
| N679K | antibody epitope effects | Pokay | BnAb 002-S21F2 IC50 on the Omicron BA.1 variant is 1.0x fold the wildtype. | 2022 | Kumar et al. (2022) |
| N679K | antibody epitope effects | Pokay | Neutralization of the bsAbs 47D10. Omicron BA.1 has an IC50 fold change of 1.26x. | 2022 | Yuan et al. (2022) |
| N679K | pharmaceutical effectiveness | Pokay | Omicron BA.3 have higher sensitivity to inhibition by soluble angiotensin converting enzyme 2 (ACE2) and the endosomal inhibitor chloroquine compared to D614G | 2022 | Neerukonda et al. (2022) |
| N679K | vaccine neutralization efficacy | Pokay | Omicron BA.3 neutralization of the Omicron variants by antibodies induced by three doses of Pfizer/BNT162b2 mRNA vaccine was 7-8-fold less potent than the D614G, and the Omicron variants still evade neutralization more efficiently. | 2022 | Neerukonda et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|---------------------------------------|
| N679K | vaccinee plasma binding | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.3 (from South Africa/NICD-N22404/2021) were 4.2x-fold lower (95% CI: 0.15x-0.20x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| N679K | vaccine neutralization efficacy | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.3 (from South Africa/NICD-N22404/2021) were 6.2-fold lower (95% CI: 11.8x-14.3x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| N679K | vaccine neutralization efficacy | Pokay | paired testing of vaccine sera against ancestral virus compared to Omicron BA.1 shows that 3-dose vaccine regimen provides over 50x fold increase in protection against Omicron(B.1.1.529 [BA.1]) compared to a 2-dose regimen. | 2022 | Hao et al. (2022) |
| N679K | pharmaceutical effectiveness | Pokay | 4th antigenic exposure with Omicron (B.1.1.529 [BA.1])(n | 2022 | Wang et al. (2022) |
| N679K | vaccine neutralization efficacy | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.1 (from Botswana/R40B59_BHP_3321 001248/2021) were 3.4-fold lower (95% CI: 3.2x-3.6x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|---------------------------------------|
| N679K | vaccinee plasma binding | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.1 (from Botswana/R40B59_BHP_3321 001248/2021) were 28.7x-fold lower (95% CI: 0.03x-0.05) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurhade et al. (2022) |
| N679K | vaccinee plasma binding | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.4/5 (from) were 17.2x-fold lower (95% CI: 0.6x-0.7x) than against 208-428 972-1834 4.3-4.7 US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurhade et al. (2022) |
| N679K | vaccine neutralization efficacy | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.4/5 (from) were 13.0-fold lower (95% CI: 4.2x-4.6x) than against 208-428 972-1834 4.3-4.7 US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurhade et al. (2022) |
| N679K | vaccinee plasma binding | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, XD (from) were 1.5x-fold lower (95% CI: 0.05x-0.07x) than against 208-428 972-1834 4.3-4.7 US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurhade et al. (2022) |
| N679K | vaccine neutralization efficacy | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, XD (from) were 4.4-fold lower (95% CI: 4.3x-4.7x) than against 208-428 972-1834 4.3-4.7 US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurhade et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|------------------------------|---------------------|---|------------------|---------------------------------------|
| P681R | pharmaceutical effectiveness | Pokay | DARPin SR16m molecule had a 6.7x fold change in IC50 in B.1.617.2 Delta | 2022 | Chonira et al. (2022) |
| P681R | pharmaceutical effectiveness | Pokay | DARPin SR16m molecule had a 99.7x fold change in IC50 in B.1.617.2 Delta | 2022 | Chonira et al. (2022) |
| P681R | trafficking | Pokay | In two of eight cell lines tested (Caco-2 intestinal and Calu-3 lung), a modest increase in cell entry was observed. This increase was not observed in a Calu-3 cell line with overexpressed ACE2. [the virus tested as B.1.617 overlaps only partially with the Spike mutation lists used by PANGO, CDC, etc. for this lineage therefore the results should be interpreted carefully as transferable to B.1.617 generally] | 2021 | Hoffman et al. (2021) |
| P681R | convalescent plasma escape | Pokay | Approximately 2-fold reduction in 15 ICU patient convalescent plasma neutralization as quantified by measuring virus-encoded luciferase activity in cell lysates at 16-18 h post transduction. [PG: note that the virus tested as B.1.617 overlaps only partially with the Spike mutation lists used by PANGO, CDC, etc. for this lineage therefore the results should be interpreted carefully as transferable to B.1.617 generally] | 2021 | Hoffman et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|---------------------------------------|
| P681R | antibody epitope effects | Pokay | Abrogates Bamlanivimab neutralization as quantified by measuring virus-encoded luciferase activity in cell lysates at 16-18 h post transduction. Significant decrease in combined Etesevimab+Bamlanivimab neutralization except at the highest concentration measured. [PG: note that the virus tested as B.1.617 overlaps only partially with the Spike mutation lists used by PANGO, CDC, etc. for this lineage therefore the results should be interpreted carefully as transferable to B.1.617 generally] | 2021 | Hoffman et al. (2021) |
| P681R | vaccine neutralization efficacy | Pokay | In 15 Pfizer non-senior vaccinee sera collected 3-4 weeks post-booster [using Table S1, not the text that says 2-3 weeks], neutralization was reduced ~3x (compared to ~11x for B.1.351). [the virus tested as B.1.617 overlaps only partially with the Spike mutation lists used by PANGO, CDC, etc. for this lineage therefore the results should be interpreted carefully as transferable to B.1.617 generally] | 2021 | Hoffman et al. (2021) |
| P681R | vaccine neutralization efficacy | Pokay | Neutralization efficiency (ID50) against B.1.617.1-v1 ('Kappa') reduced 3.4x relative to D614G wildtype using pseudotyped VSV assay on 8 Moderna vaccinee sera one week post-booster. | 2021 | Choi et al. (2021) |
| P681R | vaccine neutralization efficacy | Pokay | Relative to B.1, Delta (B.1.617.2) shows mean 2.1x decrease in neutralization efficiency by 18 vaccinee sera (BNT162b2 and mRNA1273). | 2021 | Wilhelm et al. (2021) |
| P681R | convalescent plasma escape | Pokay | Relative to B.1, Delta (B.1.617.2) shows 3.64x decrease in neutralization efficiency by convalescent plasma [no cohort details provided] | 2021 | Wilhelm et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|---------------------------------------|
| P681R | trafficking | Pokay | ~3.5x cleavage of S2 relative to WA1 (D614G) wildtype by Kappa (B.1.617.1) variant as measured by mass spectrometry of Vero-TMPRSS culture (compare to ~4.5x for closely related Delta B.1.617.2 also with P681R at the cleavage site). | 2021 | Esclera et al. (2021) |
| P681R | vaccine neutralization efficacy | Pokay | 1.5x reduction in neutralization (ID50) in sera 3 weeks after one dose of Pfizer/BioNTech BNT162b2 (up to 5 naive and post infection vaccinees) [exact set of variants used is not listed in the manuscript] | 2021 | Gong et al. (2021) |
| P681R | vaccine neutralization efficacy | Pokay | Inferring from two B.1.617.1 variants tested, estimate baseline 3.3x reduction in ID50 relative to D614G wildtype using pseudotyped VSV assay on 8 Moderna vaccinee sera one week post-booster. | 2021 | Choi et al. (2021) |
| P681R | convalescent plasma binding | Pokay | This variant combination (representing lineage B.1.617.1) showed a 2x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset. [exact variant list not provided in manuscript, is inferred and represents minimal set agreed upon commonly] | 2021 | Gong et al. (2021) |
| P681R | vaccine neutralization efficacy | Pokay | Average 2x neutralization efficiency decrease against sera from 26 Phase II trial Covaxin (BBV152) vaccine recipients. Very similar to B.1.1.7 (~2x) in the same study, and the neutralization from 17 sera of natural infections across B1 lineages. | 2021 | Yadav et al. (2021) |
| P681R | convalescent plasma escape | Pokay | Relative to B.1, Kappa (B.1.617.1) shows 5.71x decrease in neutralization efficiency by convalescent plasma [no cohort details provided] | 2021 | Wilhelm et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|---------------------------------------|
| P681R | vaccine neutralization efficacy | Pokay | Relative to B.1, Kappa (B.1.617.1) shows mean 1.97x decrease in neutralization efficiency by 18 vaccinee sera (BNT162b2 and mRNA1273). | 2021 | Wilhelm et al. (2021) |
| P681R | vaccinee plasma binding | Pokay | This variant combination (representing lineage B.1.617.1) showed a 1.79x 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. 1.64x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in post-infection vaccinees. [exact variant list not provided in manuscript, is inferred and represents minimal set agreed upon commonly] | 2021 | Gong et al. (2021) |
| P681R | ACE2 receptor binding affinity | Pokay | Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant combination (representing lineage B.1.617.1) showed a 1.12x increase in binding (KD) relative to D614G, but described as 'not significant'. [exact variant list not provided in manuscript, is inferred and represents minimal set agreed upon commonly] | 2021 | Gong et al. (2021) |
| P681R | antibody epitope effects | Pokay | Neutralization of the bsAbs 47D10. Kappa (B.1.617.1) has an IC50 fold change of 80.2x. | 2022 | Yuan et al. (2022) |
| P681R | antibody epitope effects | Pokay | Neutralization of the bsAbs Bi-Nab47D10-35B5. Kappa (B.1.617.1) has an IC50 fold change of 2.3x. | 2022 | Yuan et al. (2022) |
| P681R | antibody epitope effects | Pokay | Neutralization of the bsAbs 35B5. Kappa (B.1.617.1) has an IC50 fold change of 0.68x. | 2022 | Yuan et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|--|
| P681R | antibody epitope effects | Pokay | Neutralization of the bsAbs Bi-Nab35B5-47D10. Kappa (B.1.617.1) has an IC50 fold change of 0.13x. | 2022 | Yuan et al. (2022) |
| P681R | vaccine neutralization efficacy | Pokay | Neutralization efficiency (ID50) against B.1.617.1-v1 ('Kappa') reduced 3.3x relative to D614G wildtype using pseudotyped VSV assay on 8 Moderna vaccinee sera one week post-booster. | 2021 | Choi et al. (2021) |
| P681R | vaccine neutralization efficacy | Pokay | In a cluster of B.1.617[.1] infections related to travel from India to USA, one patient with mild symptoms had received their second dose of Pfizer vaccine more than two weeks before the infection [i.e. vaccine breakthrough]. | 2021 | Verghese et al. (2021) |
| P681R | trafficking | Pokay | ~4.5x cleavage of S2 relative to WA1 (D614G) wildtype by Delta (B.1.617.2) variant as measured by mass spectrometry of Vero-TMPRSS culture (compare to ~3.5x for closely related Kappa B.1.617.1 also with P681R at the cleavage site). | 2021 | Esclera et al. (2021) |
| P681R | vaccine neutralization efficacy | Pokay | Neutralization efficiency (ID50) against B.1.617.1-v1 ('Kappa') reduced 3.3x relative to D614G wildtype using pseudotyped VSV assay on 8 Moderna vaccinee sera one week post-booster. [Mutation list in publication appears to contain a typo with R158del instead of R158G] | 2021 | Choi et al. (2021) |
| P681R | vaccine neutralization efficacy | Pokay | Mean 2.6x reduction of NT50 value B.1.617.2 (Delta) relative to wild type in 8 sera from adult BNT162b2 vaccinees (28-47yo) collected ~1m post booster. | 2021 | Uriu et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|---------------------------------------|
| P681R | convalescent plasma escape | Pokay | Mean 4.0x reduction of NT50 value B.1.617.2 (Delta) relative to wild type in 8 sera from older convalescent patients (52-92yo) collected 1-3m post symptom onset. | 2021 | Uriu et al. (2021) |
| P681R | trafficking | Pokay | Modelling the Delta variant in primary human airway epithelial (HAE) cultures, S1 to full length Spike ratio (measuring Spike furin cleavage processivity) increased 11x relative to wild type (15.3 vs 1.4). [del ~157 truncated due to ambiguity] Furthermore the RNA ratio of Delta versus Alpha-spike/Delta-backbone continuously increased from 2.8 on day 1 to 9.8 on day 5 post infection in a coinfection model in HAEs, suggesting the spike gene drives the improved replication of Delta variant. | 2021 | Liu et al. (2021) |
| P681R | pharmaceutical effectiveness | Pokay | Trimeric proteins FSR22 had a 0.10x fold change in IC50 in B.1.617.2 Delta | 2022 | Chonira et al. (2022) |
| P681R | pharmaceutical effectiveness | Pokay | Trimeric proteins FSR16m had a 0.020x fold change in IC50 in B.1.617.2 Delta | 2022 | Chonira et al. (2022) |
| P681R | vaccine neutralization efficacy | Pokay | Plasma neutralizing activity was also assessed against SARS-CoV-2 Delta, Omicron BA.1, BA.2 and BA.4/5 variants using viruses pseudotyped with appropriate variant spikeproteins. Delta breakthrough infection resulted in 15-fold increased neutralizing titers. | 2022 | Wang et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|--|
| P681R | ACE2 receptor binding affinity | Pokay | L27, V34 and E90 mutation resulted in ultrahigh affinity binding of the LVE-ACE-2 domain to the widest variety of VOCs, with KDs of 507 pM for binding to the Delta B.1.617.2. Values were obtained with LVE-ACE-2/mAB chimeras containing the Y-T-E sequence that enhances binding to the FcRn receptor, which in turn is expected to extend biological half-life 3-4-fold. | 2022 | Uhal B et al. (2022) |
| P681R | vaccine neutralization efficacy | Pokay | Plasma neutralizing activity in 49 participants was measured using HIV-1 pseudotyped with the 100 WT SARS-CoV-2 spike protein. Delta breakthrough infection resulted in 11-fold increased geometric mean half-maximal neutralizing titer (NT50). | 2022 | Wang et al. (2022) |
| P681R | vaccine neutralization efficacy | Pokay | Log10ID50 of Delta neutralizing antibodies is 0.872x the WT pre-third dose of pfizer-BioNTech BNT162b2 in 13 Kidney transplant recipients (KTR) with median age of 55.5. | 2022 | McEvoy C et al. (2022) |
| P681R | vaccine neutralization efficacy | Pokay | Paradigm's ACE-2 variant LVE/STR chimera neutralizes Delta Variant B.1.617.2 RBD or w.t. SARS-CoV-2 RBD with nearly equal potency determined using Surrogate Viral Neutralization Tests. | 2022 | Uhal B et al. (2022) |
| P681R | vaccine neutralization efficacy | Pokay | Log10ID50 of Delta neutralizing antibodies is 0.952x the WT 1 month post-third dose of pfizer-BioNTech BNT162b2 in 13 Kidney transplant recipients (KTR) with median age of 55.5. | 2022 | McEvoy C et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|---------------------------------------|
| P681R | outcome hazard ratio | Pokay | In the UK, of 43338 COVID-19-positive patients, 8682 had the Delta variant (median age 31 years [IQR 17–43]) and 196 were admitted to hospital within 14 days after the specimen was taken (adjusted hazard ratio [HR] 2.26 [95% CI 1.32–3.89] relative to Alpha cases). Being admitted to hospital or attending emergency care within 14 days for Delta cases had an adjusted HR 1.45 [95% CI 1.08–1.95] relative to Alpha. Most patients were unvaccinated (32 078 [74.0%] across both groups). The HRs for vaccinated patients were similar: 1.94 [95% CI 0.47–8.05] for hospitalization and 1.58 [0.69–3.61] for hospital admission or emergency care attendance. | 2021 | Twohig et al. (2021) |
| P681R | vaccine efficacy | Pokay | During December 14, 2020–August 14, 2021, frontline worker without previous documented SARS-CoV-2 infection were monitored regularly. Of 4,217 participants, 3,483 (83%) were vaccinated: 2,278 (65%) received Pfizer-BioNTech, 1,138 (33%) Moderna, and 67 (2%) Janssen (Johnson & Johnson) COVID-19 vaccines. Adjusted VE during this Delta predominant period was 66% (95% CI | 2021 | Fowlkes et al. (2021) |
| P681R | vaccine neutralization efficacy | Pokay | Case 62541 cluster in Singapore included a fully vaccinated nurse 2 months post-vaccine [likely Pfizer based on dates and supply], and a doctor of unknown vaccine status. This cluster was caused by a B.1.617.2 virus [via crossreference to | | UNKNOWN et al. () |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|---------------------------------------|
| P681R | vaccinee plasma binding | Pokay | This variant combination (representing lineage B.1.617.2 aka Delta) showed a 1.64x 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. 1.89x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in post-infection vaccinees. [exact variant list not provided in manuscript, is inferred and represents minimal set agreed upon commonly] | 2021 | Gong et al. (2021) |
| P681R | vaccine neutralization efficacy | Pokay | nan | | UNKNOWN et al. () |
| P681R | vaccine efficacy | Pokay | 136,160 reports from 14,997 nursing care facilities were broken into pre-Delta (Mar 1-May 9, 2021), intermediate (May 10-Jun 20, 2021) and Delta (Jun 21-Aug 1, 2021). Two doses of mRNA vaccines were 74.7% effective against infection among nursing home residents early in the vaccination program (March–May 2021). During June–July 2021, when B.1.617.2 (Delta) variant circulation predominated, effectiveness declined significantly to 53.1%. | 2021 | Nanduri et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|----------------------|---------------------|---|------------------|-------------------------------------|
| P681R | vaccine efficacy | Pokay | Using a matched test-negative, case- control study design in Qatar, BNT162b2 effectiveness against any Delta infection, symptomatic or asymptomatic, was 64.2% (95% CI: 38.1-80.1%) ≥ 14 days after the first dose and before the second dose, but was only 53.5% (95% CI: 43.9-61.4%) ≥ 14 days after the second dose, in a population in which a large proportion of fully vaccinated persons received their second dose several months earlier. Corresponding effectiveness measures for mRNA-1273 were 79.0% (95% CI: 58.9-90.1%) and 84.8% (95% CI: 75.9-90.8%), respectively. Effectiveness against any severe, critical, or fatal COVID-19 disease due to Delta was 89.7% (95% CI: 61.0-98.1%) for BNT162b2 and 100.0% (95% CI: 41.2-100.0%) for mRNA-1273, ≥ 14 days after the second dose. The lower VE in Qatar relative to those reported in some other jurisdictions such as the UK and Canada (75%+) may reflect waning of vaccine protection for those who received their second dose by end of 2020 or early 2021. Risk perception and behaviour amongst vaccinated individuals over time may also play a role. | 2021 | Tang et al. (2021) |
| P681R | outcome hazard ratio | Pokay | In Denmark, for the period Jan 1 to Jun 27, 2021, Delta variant was associated with increased an risk ratio of 2.83 [95% CI 2.02–3.98] for hospitalization. | 2021 | Bager et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|---------------------------------------|
| P681R | vaccine efficacy | Pokay | Of 218 individuals with B.1.617.2 infection in Singapore, 84 had received a mRNA vaccine of which 71 were fully vaccinated, 130 were unvaccinated and 4 received a non-mRNA. Despite significantly older age in the vaccine breakthrough group, the odds of severe COVID-19 requiring oxygen supplementation was significantly lower following vaccination (adjusted odds ratio 0.07 95%CI: 0.015-0.335, p | 2021 | Chia et al. (2021) |
| P681R | vaccine efficacy | Pokay | The incidence rate of Covid-19 during the Delta-dominant period (Jul-Aug 2021) was lower for late vaccinated (49.0/1000 person-years) [formerly placebo] versus early vaccinated (77.1/1000 person-years) participants in the Moderna mRNA-1273 Phase 3 trials, representing a 36.4% VE reduction (95% CI 17.1%-51.5%). There were fewer severe Covid-19 cases in the late group (6: 6.2/1000 person-years) than early (13: 3.3/1000 person-years), representing a 46.0% reduction (95% CI -52.4%-83.2%). Three Covid-19 related hospitalizations occurred with two resulting deaths in the early group. | 2021 | Baden et al. (2021) |
| P681R | vaccine neutralization efficacy | Pokay | 2.3x reduction in neutralization (ID50) in sera 3 weeks after one dose of Pfizer/BioNTech BNT162b2 (up to 5 naive and post infection vaccinees) [exact set of variants used is not listed in the manuscript] | 2021 | Gong et al. (2021) |
| P681R | pharmaceutical effectiveness | Pokay | Infectious viral titers in lung tissue determined using a tissue culture infectious dose (TCID) assay in 10 hamsters showed that Delta Molnupiravir (MK-4482) had ~4x fold drop. | 2022 | Rosenke et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|--|
| P681R | vaccine efficacy | Pokay | Using a test-negative design using Ontario data between Dec 14, 2020 and May 30, 2021, 421,073 symptomatic community-dwelling individuals were tested. Against Delta, vaccine effectiveness after partial vaccination tended to be lower compared to Alpha for mRNA-1273 (72% vs. 83%) and BNT162b2 (56% vs. 66%), but was similar to Alpha for ChAdOx1 (67% vs. 64%). Full vaccination with BNT162b2 increased protection against Delta (87%) to levels comparable to Alpha (89%) and Beta/Gamma (84%). Delta-positive cases were biased towards young male residents of the Peel region. | 2021 | Nasreen et al. (2021) |
| P681R | outcome hazard ratio | Pokay | In Ontario between Feb 7 and Jun 27, 2021, increased risk with the Delta variant was 108% (95% CI 78%–140%) for hospitalization, 235% (95% CI 160%–331%) for ICU admission and 133% (95% CI 54%–231%) for death. | 2021 | UNKNOWN et al. (2021) |
| P681R | vaccine neutralization efficacy | Pokay | Vaccination of health care workers in Delhi was started in early 2021, with the ChdOx-1 (Astra Zeneca) vaccine. Surveillance has suggested B.1.1.7 dominance in the Delhi area during early 2021, with growth of B.1.617 since March 2021. During the wave of infections during March and April an outbreak of SARS-CoV-2 was confirmed in 33 vaccinated staff members at a single tertiary centre (age 27-77 years). Sequencing revealed that 16/33 were B.1.617.2, with a range of other B lineage viruses including B.1.1.7 for the rest except one A lineage case. Importantly no severe cases were documented in this event. | 2021 | Ferreira et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|--------------------------------|---------------------|--|------------------|--|
| P681R | vaccine efficacy | Pokay | Effectiveness after one dose of vaccine (BNT162b2 or ChAdOx1 nCoV-19) with the delta variant was (30.7%: 95% confidence interval [CI], 25.2 to 35.7): the results were similar for both vaccines. With the BNT162b2 vaccine, the effectiveness of two doses was 88.0% (95% CI, 85.3 to 90.1) among those with the delta variant. With the ChAdOx1 nCoV-19 vaccine, the effectiveness of two doses was 67.0% (95% CI, 61.3 to 71.8) among those with the delta variant. | 2021 | Lopez Bernal et al. (2021) |
| P681R | convalescent plasma binding | Pokay | This variant combination (representing lineage B.1.617.2 aka Delta) showed a 1.92x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom-onset. [exact variant list not provided in manuscript, is inferred and represents minimal set agreed upon commonly] | 2021 | Gong et al. (2021) |
| P681R | ACE2 receptor binding affinity | Pokay | Using flow cytometry and ACE2 ectodomains-Fc portion IgG complex, this variant combination (representing lineage B.1.617.2 aka Delta) showed a 2.34x increase in binding (KD) relative to D614G. [exact variant list not provided in manuscript, is inferred and represents minimal set agreed upon commonly] | 2021 | Gong et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|--------------------------|---------------------|---|------------------|---|
| P681R | vaccine efficacy | Pokay | In Minnesota in July 2020 (when Delta variant prevalence was >70%), the effectiveness against infection for mRNA-1273 was estimated at 76% (95% CI: 58-87%) using age, sex, race, PCR testing and vaccination date matched cohorts of unvaccinated, Pfizer and Moderna vaccinees. An even more pronounced reduction in effectiveness was observed for BNT162b2 of 42% (95% CI: 13-62%). mRNA-1273 conferred a two-fold risk reduction against breakthrough infection compared to BNT162b2 (IRR | 2021 | Puranik et al. (2021) |
| P681R | vaccine efficacy | Pokay | In a 1:5 test-negative matched control study of 8153 individuals who received the Moderna mRNA-1273 vaccine, 2027 test-positive cases were Delta. Two dose vaccine efficacy against Delta decreased from 94.1% (90.5-96.3%) 14-60 days after vaccination to 80.0% (70.2-86.6%) 151-180 days after vaccination. Waning was less pronounced for non-Delta variants. VE against Delta was lower among individuals aged ≥65 years (75.2% [59.6-84.8%]) than those aged 18-64 years (87.9% [85.5-89.9%]). VE against Delta hospitalization was 97.6% (92.8-99.2%). One-dose VE was 77.0% (60.7-86.5%) against Delta infection. | 2021 | Bruxvoort et al. (2021) |
| P681R | antibody epitope effects | Pokay | Neutralization of the bsAbs 47D10. Delta (B.1.617.2) has an IC50 fold change of 46.5x. | 2022 | Yuan et al. (2022) |
| P681R | antibody epitope effects | Pokay | Neutralization of the bsAbs Bi-Nab35B5-47D10. Delta (B.1.617.2) has an IC50 fold change of 0.57x. | 2022 | Yuan et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|--|
| P681R | antibody epitope effects | Pokay | Neutralization of the bsAbs Bi-Nab47D10-35B5. Delta (B.1.617.2) has an IC50 fold change of 0.15x. | 2022 | Yuan et al. (2022) |
| P681R | antibody epitope effects | Pokay | Neutralization of the bsAbs 35B5. Delta (B.1.617.2) has an IC50 fold change of 0.87x. | 2022 | Yuan et al. (2022) |
| P681R | antibody epitope effects | Pokay | BnAb 002-S21F2 IC50 on the Delta (B.1.617.2) variant is 0.6x fold the wildtype. | 2022 | Kumar et al. (2022) |
| P681R | vaccine neutralization efficacy | Pokay | Neutralization efficiency (ID50) against A.23.1-v2 reduced 2.3x relative to D614G wildtype using pseudotyped VSV assay on 8 Moderna vaccinee sera one week post-booster. | 2021 | Choi et al. (2021) |
| P681R | vaccine neutralization efficacy | Pokay | Neutralization efficiency (ID50) against A.23.1-v1 reduced 1.1x relative to D614G wildtype using pseudotyped VSV assay on 8 Moderna vaccinee sera one week post-booster. | 2021 | Choi et al. (2021) |
| P681R | trafficking | Pokay | This variant combination shows a ~3x decrease in cell entry efficiency (RLU measurement in 293T cells) compared to D614G, significantly less of a decrease than any B.1.617 lineage variants alone, suggesting a synergistic effect on cell entry while maintaining known immunity escape mutants. | 2021 | Ferreira et al. (2021) |
| P681R | viral load | Pokay | In 9 infected hamsters each for B.1 and B.1.617.1, no significant change in viral load or subgenomic RNA levels were detected. | 2021 | Yadav et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------|---------------------|--|------------------|---------------------------------------|
| P681R | symptom prevalence | Pokay | Gross examination of 3+3 hamster lung specimens showed pronounced congestion and hemorrhages on days 5 and 7 post-infection in the case of the B.1.617.1 as compared with the B.1. The lung lesions with the B.1 variant were minimal to mild whereas with B.1.617.1 they were moderate. For B.1 pneumonic changes were minimal to mild (inflammatory cell infiltration, focal consolidation and mild congestion). The pronounced changes (moderate to severe) with mononuclear infiltration in the alveolar interstitial space, interstitial septal thickening, consolidation and pneumocyte hyperplasia were observed with B.1.617.1 variant consistently. | 2021 | Yadav et al. (2021) |
| P681R | transmissibility | Pokay | Normalized for particle number, on ACE2.293T cells showed that the B.1.617 spike protein was >2-fold increase in infectivity relative to D614G wild type. | 2021 | Tada et al. (2021) |
| P681R | trafficking | Pokay | This mutation in the first base of the furin cleavage site maintains the RXXR recognition motif, and is presumed to enhance cleavage based on the removal of a proline-directed phosphatase recognition site at S680. In a homologous site in Infectious Bronchitis Virus (IBV, Gammacoronaviruses), abolition of S680 phosphorylation improves furin cleavage (and presumably cell entry). [Inference from similar positively charged substitution P681H actually described in the work] | 2021 | UNKNOWN et al. (2021) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|--|
| P681R | virion structure | Pokay | The Ratio of S2 (processed Spike) to full length Spike is higher for this mutation, due to a drop in the full length Spike measured, suggesting that this mutation compensates for decreased Spike production by improved proteolytic processing. [PG: Inferred by conservative AA substitution of described P681H] | 2021 | Tada et al. (2021) |
| P681R | trafficking | Pokay | Quantification of the band intensities showed that the P681R mutation, which lies near the proteolytic processing site, caused a small increase in proteolytic processing as measured by a 2-fold decrease in the ratio of S/S2. | 2021 | Tada et al. (2021) |
| N764K | pharmaceutical effectiveness | Pokay | Omicron BA.2 have higher sensitivity to inhibition by soluble angiotensin converting enzyme 2 (ACE2) and the endosomal inhibitor chloroquine compared to D614G | 2022 | Neerukonda et al. (2022) |
| N764K | antibody epitope effects | Pokay | Neutralization of the bsAbs Bi-Nab35B5-47D10. Omicron BA.2 has an IC50 fold change of 0.07x. | 2022 | Yuan et al. (2022) |
| N764K | antibody epitope effects | Pokay | Neutralization of the bsAbs 35B5. Omicron BA.2 has an IC50 fold change of 0.09x. | 2022 | Yuan et al. (2022) |
| N764K | antibody epitope effects | Pokay | Neutralization of the bsAbs 47D10. Omicron BA.2 has an IC50 fold change of 0.08x. | 2022 | Yuan et al. (2022) |
| N764K | antibody epitope effects | Pokay | Neutralization of the bsAbs Bi-Nab47D10-35B5. Omicron BA.2 has an IC50 fold change of 0.04x. | 2022 | Yuan et al. (2022) |
| N764K | vaccine neutralization efficacy | Pokay | Omicron BA.2 neutralization of the Omicron variants by antibodies induced by three doses of Pfizer/BNT162b2 mRNA vaccine was 7-8-fold less potent than the D614G, and the Omicron variants still evade neutralization more efficiently. | 2022 | Neerukonda et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|---------------------------------------|
| N764K | antibody epitope effects | Pokay | BnAb 002-S21F2 IC50 on the Omicron BA.2 variant is 0.8x fold the wildtype. | 2022 | Kumar et al. (2022) |
| N764K | vaccinee plasma binding | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.2 (from South Africa/CERI-KRISP-K03 2307/2021) were 3.9x-fold lower (95% CI: 0.14x-0.17x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| N764K | ACE2 receptor binding affinity | Pokay | L27, V34 and E90 mutation resulted in ultrahigh affinity binding of the LVE-ACE-2 domain to the widest variety of VOCs, with KDs of 78fM for binding to the Omicron BA.2. Values were obtained with LVE-ACE-2/mAB chimeras containing the Y-T-E sequence that enhances binding to the FcRn receptor, which in turn is expected to extend biological half-life 3-4-fold. | 2022 | Uhal B et al. (2022) |
| N764K | vaccine neutralization efficacy | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.2 (from South Africa/CERI-KRISP-K03 2307/2021) were 4.5-fold lower (95% CI: 4.3x-4.7x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| N764K | vaccine neutralization efficacy | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.2.12.1 (from USA/NY-CDC-ASC2 10722700/2022) were 4.2-fold lower (95% CI: 5.8x-6.6x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|--|
| N764K | vaccinee plasma binding | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.2.12.1 (from USA/NY-CDC-ASC2 10722700/2022) were 3.9x-fold lower (95% CI: 0.14x-0.18x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| N764K | pharmaceutical effectiveness | Pokay | Omicron (a.k.a. B.1.1.529) Spike pseudotyped VSV and Vero E6 cells has somewhat reduced neutralization (2.7x) vs wild type with monoclonal antibody Sotrovimab (a.k.a. VIR-7831). [delins at 214 omitted for syntax compatibility] | 2021 | Cathcart et al. (2021) |
| N764K | vaccine neutralization efficacy | Pokay | Omicron breakthrough infection after 3-dose vaccination resulted in a further 3.5-fold and 2.9-fold increase of Omicron BA.1 and BA.2 neutralizing titers. Omicron BA.4/5 showed the highest neutralization resistance of all variants tested, resulting in low geometric mean neutralizing titers in plasma samples obtained after the second vaccine dose (NT50) | 2022 | Wang et al. (2022) |
| N764K | antibody epitope effects | Pokay | Neutralization of the bsAbs Bi-Nab47D10-35B5. Omicron BA.1 has an IC50 fold change of 0.08x. | 2022 | Yuan et al. (2022) |
| N764K | vaccine neutralization efficacy | Pokay | Omicron B.1.1.529 (BA.1) neutralization of the Omicron variants by antibodies induced by three doses of Pfizer/BNT162b2 mRNA vaccine was 7-8-fold less potent than the D614G, and the Omicron variants still evade neutralization more efficiently. | 2022 | Neerukonda et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|--|
| N764K | pharmaceutical effectiveness | Pokay | Omicron (B.1.1.529 [BA.1]) have higher sensitivity to inhibition by soluble angiotensin converting enzyme 2 (ACE2) and the endosomal inhibitor chloroquine compared to D614G | 2022 | Neerukonda et al. (2022) |
| N764K | antibody epitope effects | Pokay | Neutralization of the bsAbs Bi-Nab35B5-47D10. Omicron BA.1 has an IC50 fold change of 0.30x. | 2022 | Yuan et al. (2022) |
| N764K | vaccine neutralization efficacy | Pokay | Paradigms' ACE-2 variant LVE/STR chimera binds to SARS-2 Omicron variant B.1.1.529 spike protein trimer with high affinity. Determined using Surrogate Viral Neutralization Tests. | 2022 | Uhal B et al. (2022) |
| N764K | ACE2 receptor binding affinity | Pokay | L27, V34 and E90 mutation resulted in ultrahigh affinity binding of the LVE-ACE-2 domain to the widest variety of VOCs, with KDs of 73 pM for binding to the Omicron B.1.1.529. Values were obtained with LVE-ACE-2/mAB chimeras containing the Y-T-E sequence that enhances binding to the FcRn receptor, which in turn is expected to extend biological half-life 3-4-fold. | 2022 | Uhal B et al. (2022) |
| N764K | antibody epitope effects | Pokay | Neutralization of the bsAbs 35B5. Omicron BA.1 has an IC50 fold change of 0.38x. | 2022 | Yuan et al. (2022) |
| N764K | vaccinee plasma binding | Pokay | All 10 individuals with 2 doses of the BNT162b2/BNT162b2 vaccine had a neutralizing titer in B.1 variant at an average of 729 NT50. | 2022 | Arora et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|--------------------------|---------------------|--|------------------|-------------------------------------|
| N764K | antibody epitope effects | Pokay | Plaque reduction neutralization test (PRNT) was used uring primary infection, post sixty daysof second dose vaccination, pre-reinfection and reinfection against Delta variant and was used to determine neutralizing antibodytitres. There was a 24.63x fold increase in antibody response from first infection to recovered and vaccinated with 2 doses (60 days). There was a 4.21x fold increase in antibody response pre-reinfection. There was a 39.27x fold increase in antibody response during reinfection. | 2022 | Shete et al. (2022) |
| N764K | antibody epitope effects | Pokay | Plaque reduction neutralization test (PRNT) was used uring primary infection, post sixty daysof second dose vaccination, pre-reinfection and reinfection against B.1 variant and was used to determine neutralizing antibodytitres. There was a 6.76x fold increase in antibody response from first infection to recovered and vaccinated with 2 doses (60 days). There was a 2.06x fold increase in antibody response pre-reinfection. There was a 8.18x fold increase in antibody response during reinfection. | 2022 | Shete et al. (2022) |
| N764K | vaccinee plasma binding | Pokay | All 10 individuals with 3 doses of the BNT162b2/BNT162b2 vaccine had a neutralizing titer in B.1 variant at an average of 3319 NT50. | 2022 | Arora et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|--|
| N764K | antibody epitope effects | Pokay | Plaque reduction neutralization test (PRNT) was used using primary infection, post sixty days of second dose vaccination, pre-reinfection and reinfection against Omicron variant and was used to determine neutralizing antibody titres. There was a 114.84x fold increase in antibody response from first infection to recovered and vaccinated with 2 doses (60 days). There was a 6.61x fold increase in antibody response pre-reinfection. There was a 1194.9x fold increase in antibody response during reinfection. | 2022 | Shete et al. (2022) |
| N764K | antibody epitope effects | Pokay | BnAb 002-S21F2 IC50 on the Omicron BA.1 variant is 1.0x fold the wildtype. | 2022 | Kumar et al. (2022) |
| N764K | antibody epitope effects | Pokay | Neutralization of the bsAbs 47D10. Omicron BA.1 has an IC50 fold change of 1.26x. | 2022 | Yuan et al. (2022) |
| N764K | pharmaceutical effectiveness | Pokay | Omicron BA.3 have higher sensitivity to inhibition by soluble angiotensin converting enzyme 2 (ACE2) and the endosomal inhibitor chloroquine compared to D614G | 2022 | Neerukonda et al. (2022) |
| N764K | vaccine neutralization efficacy | Pokay | Omicron BA.3 neutralization of the Omicron variants by antibodies induced by three doses of Pfizer/BNT162b2 mRNA vaccine was 7-8-fold less potent than the D614G, and the Omicron variants still evade neutralization more efficiently. | 2022 | Neerukonda et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|---------------------------------------|
| N764K | vaccinee plasma binding | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.3 (from South Africa/NICD-N22404/2021) were 4.2x-fold lower (95% CI: 0.15x-0.20x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| N764K | vaccine neutralization efficacy | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.3 (from South Africa/NICD-N22404/2021) were 6.2-fold lower (95% CI: 11.8x-14.3x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| N764K | vaccine neutralization efficacy | Pokay | paired testing of vaccine sera against ancestral virus compared to Omicron BA.1 shows that 3-dose vaccine regimen provides over 50x fold increase in protection against Omicron(B.1.1.529 [BA.1]) compared to a 2-dose regimen. | 2022 | Hao et al. (2022) |
| N764K | pharmaceutical effectiveness | Pokay | 4th antigenic exposure with Omicron (B.1.1.529 [BA.1])(n | 2022 | Wang et al. (2022) |
| N764K | vaccine neutralization efficacy | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.1 (from Botswana/R40B59_BHP_3321 001248/2021) were 3.4-fold lower (95% CI: 3.2x-3.6x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|---------------------------------------|
| N764K | vaccinee plasma binding | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.1 (from Botswana/R40B59_BHP_3321 001248/2021) were 28.7x-fold lower (95% CI: 0.03x-0.05) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurhade et al. (2022) |
| N764K | vaccinee plasma binding | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.4/5 (from) were 17.2x-fold lower (95% CI: 0.6x-0.7x) than against 208-428 972-1834 4.3-4.7 US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurhade et al. (2022) |
| N764K | vaccine neutralization efficacy | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.4/5 (from) were 13.0-fold lower (95% CI: 4.2x-4.6x) than against 208-428 972-1834 4.3-4.7 US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurhade et al. (2022) |
| N764K | vaccinee plasma binding | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, XD (from) were 1.5x-fold lower (95% CI: 0.05x-0.07x) than against 208-428 972-1834 4.3-4.7 US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurhade et al. (2022) |
| N764K | vaccine neutralization efficacy | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, XD (from) were 4.4-fold lower (95% CI: 4.3x-4.7x) than against 208-428 972-1834 4.3-4.7 US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurhade et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|--|
| D796Y | pharmaceutical effectiveness | Pokay | Omicron BA.2 have higher sensitivity to inhibition by soluble angiotensin converting enzyme 2 (ACE2) and the endosomal inhibitor chloroquine compared to D614G | 2022 | Neerukonda et al. (2022) |
| D796Y | antibody epitope effects | Pokay | Neutralization of the bsAbs Bi-Nab35B5-47D10. Omicron BA.2 has an IC50 fold change of 0.07x. | 2022 | Yuan et al. (2022) |
| D796Y | antibody epitope effects | Pokay | Neutralization of the bsAbs 35B5. Omicron BA.2 has an IC50 fold change of 0.09x. | 2022 | Yuan et al. (2022) |
| D796Y | antibody epitope effects | Pokay | Neutralization of the bsAbs 47D10. Omicron BA.2 has an IC50 fold change of 0.08x. | 2022 | Yuan et al. (2022) |
| D796Y | antibody epitope effects | Pokay | Neutralization of the bsAbs Bi-Nab47D10-35B5. Omicron BA.2 has an IC50 fold change of 0.04x. | 2022 | Yuan et al. (2022) |
| D796Y | vaccine neutralization efficacy | Pokay | Omicron BA.2 neutralization of the Omicron variants by antibodies induced by three doses of Pfizer/BNT162b2 mRNA vaccine was 7-8-fold less potent than the D614G, and the Omicron variants still evade neutralization more efficiently. | 2022 | Neerukonda et al. (2022) |
| D796Y | antibody epitope effects | Pokay | BnAb 002-S21F2 IC50 on the Omicron BA.2 variant is 0.8x fold the wildtype. | 2022 | Kumar et al. (2022) |

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|-----------|---------------------------------|---------------------|--|------------------|---------------------------------------|
| D796Y | vaccine neutralization efficacy | Pokay | This variant was designated A.27.RN according to its phylogenetic clade classification. It emerged in parallel with the B.1.1.7 variant, increased to >50% of all SARS-CoV-2 variants by week five. Subsequently it decreased to <10% of all variants by calendar week eight when B.1.1.7 had become the dominant strain. Antibodies induced by BNT162b2 (Pfizer) vaccination neutralized A.27.RN but with a two-to-threefold reduced efficacy as compared to the wild-type and B.1.1.7 strains. | 2021 | Mallm et al. (2021) |
| D796Y | vaccinee plasma binding | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.2 (from South Africa/CERI-KRISP-K03 2307/2021) were 3.9x-fold lower (95% CI: 0.14x-0.17x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| D796Y | ACE2 receptor binding affinity | Pokay | L27, V34 and E90 mutation resulted in ultrahigh affinity binding of the LVE-ACE-2 domain to the widest variety of VOCs, with KDs of 78fM for binding to the Omicron BA.2. Values were obtained with LVE-ACE-2/mAB chimeras containing the Y-T-E sequence that enhances binding to the FcRn receptor, which in turn is expected to extend biological half-life 3-4-fold. | 2022 | Uhal B et al. (2022) |
| D796Y | vaccine neutralization efficacy | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.2 (from South Africa/CERI-KRISP-K03 2307/2021) were 4.5-fold lower (95% CI: 4.3x-4.7x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |

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|-----------|---------------------------------|---------------------|---|------------------|--|
| D796Y | vaccine neutralization efficacy | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.2.12.1 (from USA/NY-CDC-ASC2 10722700/2022) were 4.2-fold lower (95% CI: 5.8x-6.6x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| D796Y | vaccinee plasma binding | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.2.12.1 (from USA/NY-CDC-ASC2 10722700/2022) were 3.9x-fold lower (95% CI: 0.14x-0.18x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| D796Y | pharmaceutical effectiveness | Pokay | Omicron (a.k.a. B.1.1.529) Spike pseudotyped VSV and Vero E6 cells has somewhat reduced neutralization (2.7x) vs wild type with monoclonal antibody Sotrovimab (a.k.a. VIR-7831). [delins at 214 omitted for syntax compatibility] | 2021 | Cathcart et al. (2021) |
| D796Y | vaccine neutralization efficacy | Pokay | Omicron breakthrough infection after 3-dose vaccination resulted in a further 3.5-fold and 2.9-fold increase of Omicron BA.1 and BA.2 neutralizing titers. Omicron BA.4/5 showed the highest neutralization resistance of all variants tested, resulting in low geometric mean neutralizing titers in plasma samples obtained after the second vaccine dose (NT50 | 2022 | Wang et al. (2022) |
| D796Y | antibody epitope effects | Pokay | Neutralization of the bsAbs Bi-Nab47D10-35B5. Omicron BA.1 has an IC50 fold change of 0.08x. | 2022 | Yuan et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|--|
| D796Y | vaccine neutralization efficacy | Pokay | Omicron B.1.1.529 (BA.1) neutralization of the Omicron variants by antibodies induced by three doses of Pfizer/BNT162b2 mRNA vaccine was 7-8-fold less potent than the D614G, and the Omicron variants still evade neutralization more efficiently. | 2022 | Neerukonda et al. (2022) |
| D796Y | pharmaceutical effectiveness | Pokay | Omicron (B.1.1.529 [BA.1]) have higher sensitivity to inhibition by soluble angiotensin converting enzyme 2 (ACE2) and the endosomal inhibitor chloroquine compared to D614G | 2022 | Neerukonda et al. (2022) |
| D796Y | antibody epitope effects | Pokay | Neutralization of the bsAbs Bi-Nab35B5-47D10. Omicron BA.1 has an IC50 fold change of 0.30x. | 2022 | Yuan et al. (2022) |
| D796Y | vaccine neutralization efficacy | Pokay | Paradigms' ACE-2 variant LVE/STR chimera binds to SARS-2 Omicron variant B.1.1.529 spike protein trimer with high affinity. Determined using Surrogate Viral Neutralization Tests. | 2022 | Uhal B et al. (2022) |
| D796Y | ACE2 receptor binding affinity | Pokay | L27, V34 and E90 mutation resulted in ultrahigh affinity binding of the LVE-ACE-2 domain to the widest variety of VOCs, with KDs of 73 pM for binding to the Omicron B.1.1.529. Values were obtained with LVE-ACE-2/mAB chimeras containing the Y-T-E sequence that enhances binding to the FcRn receptor, which in turn is expected to extend biological half-life 3-4-fold. | 2022 | Uhal B et al. (2022) |
| D796Y | antibody epitope effects | Pokay | Neutralization of the bsAbs 35B5. Omicron BA.1 has an IC50 fold change of 0.38x. | 2022 | Yuan et al. (2022) |
| D796Y | vaccinee plasma binding | Pokay | All 10 individuals with 2 doses of the BNT162b2/BNT162b2 vaccine had a neutralizing titer in B.1 variant at an average of 729 NT50. | 2022 | Arora et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|--------------------------|---------------------|--|------------------|-------------------------------------|
| D796Y | antibody epitope effects | Pokay | Plaque reduction neutralization test (PRNT) was used uring primary infection, post sixty daysof second dose vaccination, pre-reinfection and reinfection against Delta variant and was used to determine neutralizing antibodytitres. There was a 24.63x fold increase in antibody response from first infection to recovered and vaccinated with 2 doses (60 days). There was a 4.21x fold increase in antibody response pre-reinfection. There was a 39.27x fold increase in antibody response during reinfection. | 2022 | Shete et al. (2022) |
| D796Y | antibody epitope effects | Pokay | Plaque reduction neutralization test (PRNT) was used uring primary infection, post sixty daysof second dose vaccination, pre-reinfection and reinfection against B.1 variant and was used to determine neutralizing antibodytitres. There was a 6.76x fold increase in antibody response from first infection to recovered and vaccinated with 2 doses (60 days). There was a 2.06x fold increase in antibody response pre-reinfection. There was a 8.18x fold increase in antibody response during reinfection. | 2022 | Shete et al. (2022) |
| D796Y | vaccinee plasma binding | Pokay | All 10 individuals with 3 doses of the BNT162b2/BNT162b2 vaccine had a neutralizing titer in B.1 variant at an average of 3319 NT50. | 2022 | Arora et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|--|
| D796Y | antibody epitope effects | Pokay | Plaque reduction neutralization test (PRNT) was used using primary infection, post sixty days of second dose vaccination, pre-reinfection and reinfection against Omicron variant and was used to determine neutralizing antibody titres. There was a 114.84x fold increase in antibody response from first infection to recovered and vaccinated with 2 doses (60 days). There was a 6.61x fold increase in antibody response pre-reinfection. There was a 1194.9x fold increase in antibody response during reinfection. | 2022 | Shete et al. (2022) |
| D796Y | antibody epitope effects | Pokay | BnAb 002-S21F2 IC50 on the Omicron BA.1 variant is 1.0x fold the wildtype. | 2022 | Kumar et al. (2022) |
| D796Y | antibody epitope effects | Pokay | Neutralization of the bsAbs 47D10. Omicron BA.1 has an IC50 fold change of 1.26x. | 2022 | Yuan et al. (2022) |
| D796Y | pharmaceutical effectiveness | Pokay | Omicron BA.3 have higher sensitivity to inhibition by soluble angiotensin converting enzyme 2 (ACE2) and the endosomal inhibitor chloroquine compared to D614G | 2022 | Neerukonda et al. (2022) |
| D796Y | vaccine neutralization efficacy | Pokay | Omicron BA.3 neutralization of the Omicron variants by antibodies induced by three doses of Pfizer/BNT162b2 mRNA vaccine was 7-8-fold less potent than the D614G, and the Omicron variants still evade neutralization more efficiently. | 2022 | Neerukonda et al. (2022) |

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|-----------|---------------------------------|---------------------|---|------------------|---------------------------------------|
| D796Y | vaccinee plasma binding | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.3 (from South Africa/NICD-N22404/2021) were 4.2x-fold lower (95% CI: 0.15x-0.20x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| D796Y | vaccine neutralization efficacy | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.3 (from South Africa/NICD-N22404/2021) were 6.2-fold lower (95% CI: 11.8x-14.3x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| D796Y | vaccine neutralization efficacy | Pokay | paired testing of vaccine sera against ancestral virus compared to Omicron BA.1 shows that 3-dose vaccine regimen provides over 50x fold increase in protection against Omicron(B.1.1.529 [BA.1]) compared to a 2-dose regimen. | 2022 | Hao et al. (2022) |
| D796Y | pharmaceutical effectiveness | Pokay | 4th antigenic exposure with Omicron (B.1.1.529 [BA.1])(n | 2022 | Wang et al. (2022) |
| D796Y | vaccine neutralization efficacy | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.1 (from Botswana/R40B59_BHP_3321 001248/2021) were 3.4-fold lower (95% CI: 3.2x-3.6x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|---------------------------------------|
| D796Y | vaccinee plasma binding | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.1 (from Botswana/R40B59_BHP_3321 001248/2021) were 28.7x-fold lower (95% CI: 0.03x-0.05) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| D796Y | vaccinee plasma binding | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.4/5 (from) were 17.2x-fold lower (95% CI: 0.6x-0.7x) than against 208-428 972-1834 4.3-4.7 US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| D796Y | vaccine neutralization efficacy | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.4/5 (from) were 13.0-fold lower (95% CI: 4.2x-4.6x) than against 208-428 972-1834 4.3-4.7 US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| D796Y | vaccinee plasma binding | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, XD (from) were 1.5x-fold lower (95% CI: 0.05x-0.07x) than against 208-428 972-1834 4.3-4.7 US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| D796Y | vaccine neutralization efficacy | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, XD (from) were 4.4-fold lower (95% CI: 4.3x-4.7x) than against 208-428 972-1834 4.3-4.7 US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |

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|-----------|---------------------------------|---------------------|---|------------------|--|
| S939F | anthropozoonotic events | Pokay | This mutation outside the receptor binding domain significantly reduced the tropism of SARS-CoV-2 to MfuKi (eastern bent-wing bat kidney cell, <i>Miniopterus fuliginosus</i>) cell cultures using a pseudotyped VSV assay. | 2023 | Li et al. (2023) |
| Q954H | pharmaceutical effectiveness | Pokay | Omicron BA.2 have higher sensitivity to inhibition by soluble angiotensin converting enzyme 2 (ACE2) and the endosomal inhibitor chloroquine compared to D614G | 2022 | Neerukonda et al. (2022) |
| Q954H | antibody epitope effects | Pokay | Neutralization of the bsAbs Bi-Nab35B5-47D10. Omicron BA.2 has an IC50 fold change of 0.07x. | 2022 | Yuan et al. (2022) |
| Q954H | antibody epitope effects | Pokay | Neutralization of the bsAbs 35B5. Omicron BA.2 has an IC50 fold change of 0.09x. | 2022 | Yuan et al. (2022) |
| Q954H | antibody epitope effects | Pokay | Neutralization of the bsAbs 47D10. Omicron BA.2 has an IC50 fold change of 0.08x. | 2022 | Yuan et al. (2022) |
| Q954H | antibody epitope effects | Pokay | Neutralization of the bsAbs Bi-Nab47D10-35B5. Omicron BA.2 has an IC50 fold change of 0.04x. | 2022 | Yuan et al. (2022) |
| Q954H | vaccine neutralization efficacy | Pokay | Omicron BA.2 neutralization of the Omicron variants by antibodies induced by three doses of Pfizer/BNT162b2 mRNA vaccine was 7-8-fold less potent than the D614G, and the Omicron variants still evade neutralization more efficiently. | 2022 | Neerukonda et al. (2022) |
| Q954H | antibody epitope effects | Pokay | BnAb 002-S21F2 IC50 on the Omicron BA.2 variant is 0.8x fold the wildtype. | 2022 | Kumar et al. (2022) |

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| Q954H | ACE2 receptor binding affinity | Pokay | L27, V34 and E90 mutation resulted in ultrahigh affinity binding of the LVE-ACE-2 domain to the widest variety of VOCs, with KDs of 78fM for binding to the Omicron BA.2. Values were obtained with LVE-ACE-2/mAB chimeras containing the Y-T-E sequence that enhances binding to the FcRn receptor, which in turn is expected to extend biological half-life 3-4-fold. | 2022 | Uhal B et al. (2022) |
| Q954H | vaccine neutralization efficacy | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.2 (from South Africa/CERI-KRISP-K03 2307/2021) were 4.5-fold lower (95% CI: 4.3x-4.7x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
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| Q954H | pharmaceutical effectiveness | Pokay | Omicron (a.k.a. B.1.1.529) Spike pseudotyped VSV and Vero E6 cells has somewhat reduced neutralization (2.7x) vs wild type with monoclonal antibody Sotrovimab (a.k.a. VIR-7831). [delins at 214 omitted for syntax compatibility] | 2021 | Cathcart et al. (2021) |
| Q954H | vaccine neutralization efficacy | Pokay | Omicron breakthrough infection after 3-dose vaccination resulted in a further 3.5-fold and 2.9-fold increase of Omicron BA.1 and BA.2 neutralizing titers. Omicron BA.4/5 showed the highest neutralization resistance of all variants tested, resulting in low geometric mean neutralizing titers in plasma samples obtained after the second vaccine dose (NT50) | 2022 | Wang et al. (2022) |
| Q954H | antibody epitope effects | Pokay | Neutralization of the bsAbs Bi-Nab47D10-35B5. Omicron BA.1 has an IC50 fold change of 0.08x. | 2022 | Yuan et al. (2022) |
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| Q954H | vaccine neutralization efficacy | Pokay | Paradigms' ACE-2 variant LVE/STR chimera binds to SARS-2 Omicron variant B.1.1.529 spike protein trimer with high affinity. Determined using Surrogate Viral Neutralization Tests. | 2022 | Uhal B et al. (2022) |
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| Q954H | antibody epitope effects | Pokay | Plaque reduction neutralization test (PRNT) was used uring primary infection, post sixty daysof second dose vaccination, pre-reinfection and reinfection against Delta variant and was used to determine neutralizing antibodytitres. There was a 24.63x fold increase in antibody response from first infection to recovered and vaccinated with 2 doses (60 days). There was a 4.21x fold increase in antibody response pre-reinfection. There was a 39.27x fold increase in antibody response during reinfection. | 2022 | Shete et al. (2022) |
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| Q954H | vaccinee plasma binding | Pokay | All 10 individuals with 3 doses of the BNT162b2/BNT162b2 vaccine had a neutralizing titer in B.1 variant at an average of 3319 NT50. | 2022 | Arora et al. (2022) |

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| Q954H | antibody epitope effects | Pokay | Plaque reduction neutralization test (PRNT) was used using primary infection, post sixty days of second dose vaccination, pre-reinfection and reinfection against Omicron variant and was used to determine neutralizing antibody titres. There was a 114.84x fold increase in antibody response from first infection to recovered and vaccinated with 2 doses (60 days). There was a 6.61x fold increase in antibody response pre-reinfection. There was a 1194.9x fold increase in antibody response during reinfection. | 2022 | Shete et al. (2022) |
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| Q954H | vaccine neutralization efficacy | Pokay | paired testing of vaccine sera against ancestral virus compared to Omicron BA.1 shows that 3-dose vaccine regimen provides over 50x fold increase in protection against Omicron(B.1.1.529 [BA.1]) compared to a 2-dose regimen. | 2022 | Hao et al. (2022) |
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| Q954H | vaccinee plasma binding | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.4/5 (from) were 17.2x-fold lower (95% CI: 0.6x-0.7x) than against 208-428 972-1834 4.3-4.7 US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| Q954H | vaccine neutralization efficacy | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.4/5 (from) were 13.0-fold lower (95% CI: 4.2x-4.6x) than against 208-428 972-1834 4.3-4.7 US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| Q954H | vaccinee plasma binding | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, XD (from) were 1.5x-fold lower (95% CI: 0.05x-0.07x) than against 208-428 972-1834 4.3-4.7 US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| Q954H | vaccine neutralization efficacy | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, XD (from) were 4.4-fold lower (95% CI: 4.3x-4.7x) than against 208-428 972-1834 4.3-4.7 US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|--|
| N969K | pharmaceutical effectiveness | Pokay | Omicron BA.2 have higher sensitivity to inhibition by soluble angiotensin converting enzyme 2 (ACE2) and the endosomal inhibitor chloroquine compared to D614G | 2022 | Neerukonda et al. (2022) |
| N969K | antibody epitope effects | Pokay | Neutralization of the bsAbs Bi-Nab35B5-47D10. Omicron BA.2 has an IC50 fold change of 0.07x. | 2022 | Yuan et al. (2022) |
| N969K | antibody epitope effects | Pokay | Neutralization of the bsAbs 35B5. Omicron BA.2 has an IC50 fold change of 0.09x. | 2022 | Yuan et al. (2022) |
| N969K | antibody epitope effects | Pokay | Neutralization of the bsAbs 47D10. Omicron BA.2 has an IC50 fold change of 0.08x. | 2022 | Yuan et al. (2022) |
| N969K | antibody epitope effects | Pokay | Neutralization of the bsAbs Bi-Nab47D10-35B5. Omicron BA.2 has an IC50 fold change of 0.04x. | 2022 | Yuan et al. (2022) |
| N969K | vaccine neutralization efficacy | Pokay | Omicron BA.2 neutralization of the Omicron variants by antibodies induced by three doses of Pfizer/BNT162b2 mRNA vaccine was 7-8-fold less potent than the D614G, and the Omicron variants still evade neutralization more efficiently. | 2022 | Neerukonda et al. (2022) |
| N969K | antibody epitope effects | Pokay | BnAb 002-S21F2 IC50 on the Omicron BA.2 variant is 0.8x fold the wildtype. | 2022 | Kumar et al. (2022) |
| N969K | vaccinee plasma binding | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.2 (from South Africa/CERI-KRISP-K03 2307/2021) were 3.9x-fold lower (95% CI: 0.14x-0.17x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|---------------------------------------|
| N969K | ACE2 receptor binding affinity | Pokay | L27, V34 and E90 mutation resulted in ultrahigh affinity binding of the LVE-ACE-2 domain to the widest variety of VOCs, with KDs of 78fM for binding to the Omicron BA.2. Values were obtained with LVE-ACE-2/mAB chimeras containing the Y-T-E sequence that enhances binding to the FcRn receptor, which in turn is expected to extend biological half-life 3-4-fold. | 2022 | Uhal B et al. (2022) |
| N969K | vaccine neutralization efficacy | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.2 (from South Africa/CERI-KRISP-K03 2307/2021) were 4.5-fold lower (95% CI: 4.3x-4.7x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| N969K | vaccine neutralization efficacy | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.2.12.1 (from USA/NY-CDC-ASC2 10722700/2022) were 4.2-fold lower (95% CI: 5.8x-6.6x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| N969K | vaccinee plasma binding | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.2.12.1 (from USA/NY-CDC-ASC2 10722700/2022) were 3.9x-fold lower (95% CI: 0.14x-0.18x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|--|
| N969K | pharmaceutical effectiveness | Pokay | Omicron (a.k.a. B.1.1.529) Spike pseudotyped VSV and Vero E6 cells has somewhat reduced neutralization (2.7x) vs wild type with monoclonal antibody Sotrovimab (a.k.a. VIR-7831). [delins at 214 omitted for syntax compatibility] | 2021 | Cathcart et al. (2021) |
| N969K | vaccine neutralization efficacy | Pokay | Omicron breakthrough infection after 3-dose vaccination resulted in a further 3.5-fold and 2.9-fold increase of Omicron BA.1 and BA.2 neutralizing titers. Omicron BA.4/5 showed the highest neutralization resistance of all variants tested, resulting in low geometric mean neutralizing titers in plasma samples obtained after the second vaccine dose (NT50 | 2022 | Wang et al. (2022) |
| N969K | antibody epitope effects | Pokay | Neutralization of the bsAbs Bi-Nab47D10-35B5. Omicron BA.1 has an IC50 fold change of 0.08x. | 2022 | Yuan et al. (2022) |
| N969K | vaccine neutralization efficacy | Pokay | Omicron B.1.1.529 (BA.1) neutralization of the Omicron variants by antibodies induced by three doses of Pfizer/BNT162b2 mRNA vaccine was 7-8-fold less potent than the D614G, and the Omicron variants still evade neutralization more efficiently. | 2022 | Neerukonda et al. (2022) |
| N969K | pharmaceutical effectiveness | Pokay | Omicron (B.1.1.529 [BA.1]) have higher sensitivity to inhibition by soluble angiotensin converting enzyme 2 (ACE2) and the endosomal inhibitor chloroquine compared to D614G | 2022 | Neerukonda et al. (2022) |
| N969K | antibody epitope effects | Pokay | Neutralization of the bsAbs Bi-Nab35B5-47D10. Omicron BA.1 has an IC50 fold change of 0.30x. | 2022 | Yuan et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|--------------------------------------|
| N969K | vaccine neutralization efficacy | Pokay | Paradigms' ACE-2 variant LVE/STR chimera binds to SARS-2 Omicron variant B.1.1.529 spike protein trimer with high affinity. Determined using Surrogate Viral Neutralization Tests. | 2022 | Uhal B et al. (2022) |
| N969K | ACE2 receptor binding affinity | Pokay | L27, V34 and E90 mutation resulted in ultrahigh affinity binding of the LVE-ACE-2 domain to the widest variety of VOCs, with KDs of 73 pM for binding to the Omicron B.1.1.529. Values were obtained with LVE-ACE-2/mAB chimeras containing the Y-T-E sequence that enhances binding to the FcRn receptor, which in turn is expected to extend biological half-life 3-4-fold. | 2022 | Uhal B et al. (2022) |
| N969K | antibody epitope effects | Pokay | Neutralization of the bsAbs 35B5. Omicron BA.1 has an IC50 fold change of 0.38x. | 2022 | Yuan et al. (2022) |
| N969K | vaccinee plasma binding | Pokay | All 10 individuals with 2 doses of the BNT162b2/BNT162b2 vaccine had a neutralizing titer in B.1 variant at an average of 729 NT50. | 2022 | Arora et al. (2022) |
| N969K | antibody epitope effects | Pokay | Plaque reduction neutralization test (PRNT) was used uring primary infection, post sixty daysof second dose vaccination, pre-reinfection and reinfection against Delta variant and was used to determine neutralizing antibodytitres. There was a 24.63x fold increase in antibody response from first infection to recovered and vaccinated with 2 doses (60 days). There was a 4.21x fold increase in antibody response pre-reinfection. There was a 39.27x fold increase in antibody response during reinfection. | 2022 | Shete et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|--------------------------|---------------------|--|------------------|-------------------------------------|
| N969K | antibody epitope effects | Pokay | Plaque reduction neutralization test (PRNT) was used uring primary infection, post sixty daysof second dose vaccination, pre-reinfection and reinfection against B.1 variant and was used to determine neutralizing antibodytitres. There was a 6.76x fold increase in antibody response from first infection to recovered and vaccinated with 2 doses (60 days). There was a 2.06x fold increase in antibody response pre-reinfection. There was a 8.18x fold increase in antibody response during reinfection. | 2022 | Shete et al. (2022) |
| N969K | vaccinee plasma binding | Pokay | All 10 individuals with 3 doses of the BNT162b2/BNT162b2 vaccine had a neutralizing titer in B.1 variant at an average of 3319 NT50. | 2022 | Arora et al. (2022) |
| N969K | antibody epitope effects | Pokay | Plaque reduction neutralization test (PRNT) was used uring primary infection, post sixty daysof second dose vaccination, pre-reinfection and reinfection against Omicron variant and was used to determine neutralizing antibodytitres. There was a 114.84x fold increase in antibody response from first infection to recovered and vaccinated with 2 doses (60 days). There was a 6.61x fold increase in antibody response pre-reinfection. There was a 1194.9x fold increase in antibody response during reinfection. | 2022 | Shete et al. (2022) |
| N969K | antibody epitope effects | Pokay | BnAb 002-S21F2 IC50 on the Omicron BA.1 variant is 1.0x fold the wildtype. | 2022 | Kumar et al. (2022) |
| N969K | antibody epitope effects | Pokay | Neutralization of the bsAbs 47D10. Omicron BA.1 has an IC50 fold change of 1.26x. | 2022 | Yuan et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|--|
| N969K | pharmaceutical effectiveness | Pokay | Omicron BA.3 have higher sensitivity to inhibition by soluble angiotensin converting enzyme 2 (ACE2) and the endosomal inhibitor chloroquine compared to D614G | 2022 | Neerukonda et al. (2022) |
| N969K | vaccine neutralization efficacy | Pokay | Omicron BA.3 neutralization of the Omicron variants by antibodies induced by three doses of Pfizer/BNT162b2 mRNA vaccine was 7-8-fold less potent than the D614G, and the Omicron variants still evade neutralization more efficiently. | 2022 | Neerukonda et al. (2022) |
| N969K | vaccinee plasma binding | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.3 (from South Africa/NICD-N22404/2021) were 4.2x-fold lower (95% CI: 0.15x-0.20x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| N969K | vaccine neutralization efficacy | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.3 (from South Africa/NICD-N22404/2021) were 6.2-fold lower (95% CI: 11.8x-14.3x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| N969K | vaccine neutralization efficacy | Pokay | paired testing of vaccine sera against ancestral virus compared to Omicron BA.1 shows that 3-dose vaccine regimen provides over 50x fold increase in protection against Omicron(B.1.1.529 [BA.1]) compared to a 2-dose regimen. | 2022 | Hao et al. (2022) |
| N969K | pharmaceutical effectiveness | Pokay | 4th antigenic exposure with Omicron (B.1.1.529 [BA.1])(n | 2022 | Wang et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|--|------------------|---------------------------------------|
| N969K | vaccine neutralization efficacy | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.1 (from Botswana/R40B59_BHP_3321 001248/2021) were 3.4-fold lower (95% CI: 3.2x-3.6x) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| N969K | vaccinee plasma binding | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.1 (from Botswana/R40B59_BHP_3321 001248/2021) were 28.7x-fold lower (95% CI: 0.03x-0.05) than against US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| N969K | vaccinee plasma binding | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.4/5 (from) were 17.2x-fold lower (95% CI: 0.6x-0.7x) than against 208-428 972-1834 4.3-4.7 US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| N969K | vaccine neutralization efficacy | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, BA.4/5 (from) were 13.0-fold lower (95% CI: 4.2x-4.6x) than against 208-428 972-1834 4.3-4.7 US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|---------------------------------|---------------------|---|------------------|---------------------------------------|
| N969K | vaccinee plasma binding | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, XD (from) were 1.5x-fold lower (95% CI: 0.05x-0.07x) than against 208-428 972-1834 4.3-4.7 US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| N969K | vaccine neutralization efficacy | Pokay | In 22 Pfizer/BNT162b2-vaccinated sera (ages 26-74, median 65) collected 1 month after dose 3, XD (from) were 4.4-fold lower (95% CI: 4.3x-4.7x) than against 208-428 972-1834 4.3-4.7 US-WA1/2020 using an infectious cDNA clone of mNG USA-WA1/2020. | 2022 | Kurahde et al. (2022) |
| T9I | homoplasmy | Pokay | In experimental models of SARS-CoV-2 mutational evolution (without immune pressure), this mutation appears convergent. | 2021 | Borges et al. (2021) |
| T9I | frequency based fitness | Pokay | Calculated to have an increased fitness (11x overrepresentation vs expected count of ~300 in public genome datasets), analysis as of 2023-05-11 | 2023 | UNKNOWN et al. (2023) |
| D3H | frequency based fitness | Pokay | Calculated to have an increased fitness (227x overrepresentation vs expected count of ~14 in public genome datasets), analysis as of 2023-05-11 | 2023 | UNKNOWN et al. (2023) |
| Q19E | frequency based fitness | Pokay | Calculated to have an increased fitness (16x overrepresentation vs expected count of ~8 in public genome datasets), analysis as of 2023-05-11 | 2023 | UNKNOWN et al. (2023) |
| F53F | frequency based fitness | Pokay | Calculated to have an increased fitness (163x overrepresentation vs expected count of ~567 in public genome datasets), analysis as of 2023-05-11 | 2023 | UNKNOWN et al. (2023) |

| Mutations | Functional Category | Annotation Resource | Functional Effect | Publication Year | Citation |
|-----------|-------------------------|---------------------|---|------------------|--|
| L93L | frequency based fitness | Pokay | Calculated to have an increased fitness (29x overrepresentation vs expected count of ~628 in public genome datasets), analysis as of 2023-05-11 | 2023 | UNKNOWN et al. (2023) |
| F112F | frequency based fitness | Pokay | Calculated to have an increased fitness (11x overrepresentation vs expected count of ~463 in public genome datasets), analysis as of 2023-05-11 | 2023 | UNKNOWN et al. (2023) |
| L120L | frequency based fitness | Pokay | Calculated to have an increased fitness (12x overrepresentation vs expected count of ~622 in public genome datasets), analysis as of 2023-05-11 | 2023 | UNKNOWN et al. (2023) |
| P13L | homoplasy | Pokay | In experimental models of SARS-CoV-2 mutational evolution (without immune pressure), this mutation appears convergent. | 2021 | Borges et al. (2021) |
| P13L | T cell evasion | Pokay | Variant causes complete loss of T cell line responsiveness to B*27:05-restricted CD8+ N epitope QRNAPRITF 1-17(2,13). | 2021 | de Silva et al. (2021) |

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