

# SARS-CoV-2 | Variants and mutations

As SARS-CoV-2 continues to mutate, there are numerous variants popping up around the world. As new variants arise, stay up to date through our **Notable Variants** blog. Did you know you can identify each of these key mutations using our TaqMan SARS-CoV-2 Mutation Panel? **Create your custom panel**

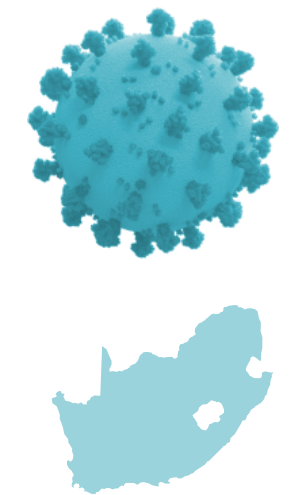


## Alpha (B.1.1.7) B.1.177, B.1.258

**First detected:** United Kingdom

**Key mutations:**

- A1708D** Defining SNP associated with B.1.1.7 lineage in PANGO International Lineage Report
- A570D** Defining SNP associated with B.1.1.7 lineage in PANGO International Lineage Report
- D3L** Defining SNP associated with B.1.1.7 lineage
- D614G** Thought to make the coronavirus **more infectious**
- delH69V70** Alters the shape of the spike and may help it **evade some antibodies**
- delY144** Alters the shape of the spike and may help it **evade some antibodies**
- N439K** Impacts ability to evade **antibody-mediated immunity**
- N501Y** Helps the virus latch on more tightly to human cells
- P681H** Predicted to **enhance systemic infection** and associated with **increased transmissibility**
- Q27ST** Defining SNP associated with B.1.1.7 lineage in PANGO International Lineage Report
- S982A** Defining SNP associated with B.1.1.7 lineage in PANGO International Lineage Report
- T16176C** Mutation associated with B.1.1.7 lineage
- T7161** Defining SNP associated with B.1.1.7 lineage in PANGO International Lineage Report



## Beta (B.1.351) B.1.1.33

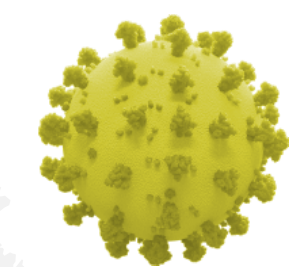
**First detected:** South Africa

**Key mutations:**

- A701V** Defining SNP associated with B.1.351 lineage in PANGO International Lineage Report
- D215G** May help the virus latch on tighter
- D614G** Thought to make the coronavirus **more infectious**
- D80A** Contributes to antibody neutralization escape together with L18F, D215G and delL242\_L244
- delL242** Associated with reduced capacity for binding certain antibodies
- E484K** **Reduces antibody recognition;** Associated with **vaccine resistance**
- K417N** Helps the virus bind more tightly to human cells
- L18F** May help the virus latch on tighter
- L242\_244L** Deletion associated with the B.1.351
- N501Y** Helps the virus latch on more tightly to human cells
- R246I** Contributes to antibody neutralization escape

We closely track literature and trends to design assays for detecting emerging SARS-CoV-2 mutations. Find the most up-to-date list of available assays at [thermofisher.com/mutationpanel](https://thermofisher.com/mutationpanel)

This graphic represents the most up-to-date information as of June 2nd, 2022.

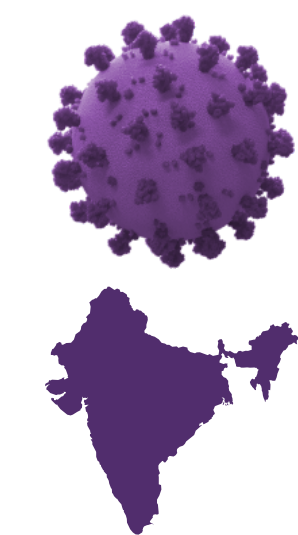


## Gamma (P.1)

**First detected:** Brazil (and in Japan, detected in travelers from Brazil)

**Key mutations:**

- D614G** Thought to make the coronavirus **more infectious**
- E484K** **Reduces antibody recognition;** Associated with **vaccine resistance**
- K417T** May help the virus latch on tighter
- L18F** May help the virus latch on tighter
- N501Y** Helps the virus latch on more tightly to human cells
- T20N** May help the virus latch on tighter



## Delta (B.1.617.2) Kappa (B.1.617.1) B.1.617.3

**First detected:** India

**Key mutations:**

- E484Q\*** May be associated with **increased transmissibility;** Appears to be very similar to E484K and may be associated with immune escape
- EFR156-158G** Defining SNP associated with Delta variant
- L452R** May give an advantage at spreading over other variants
- P681R** May help the virus latch on tighter and may result in **increased transmissibility**
- T19R** associated with increased transmissibility, potential reduction in neutralization by some monoclonal antibody treatments, and potential reduction in neutralization by post-vaccination sera
- T478K** associated with increased transmissibility, potential reduction in neutralization by some monoclonal antibody treatments, and potential reduction in neutralization by post-vaccination sera

\*Absence of this mutation in the Delta variant



## Delta + (AY.4.2)

**First detected:** India

**Key mutation:**

- Y145H** Defining SNP associated with Delta Plus variant. Mutation located in the spike protein. Selective advantage of mutation still under investigation, but may lead to increased immune evasion.

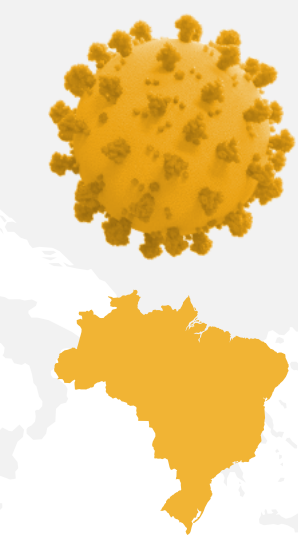


## Epsilon (B.1.427/B.1.429)

**First detected:** California (USA)

**Key mutations:**

- L452R** Reduces antibody recognition; Associated with **vaccine resistance**
- S13I** Associated with variant that causes **increased transmissibility**
- W152C** SNP associated with B.1.427 and B.1.429 lineages



## Zeta (P.2)

**First detected:** Brazil

**Key mutation:**

- V1176F** Potential **reduction in neutralization** by some antibody treatments

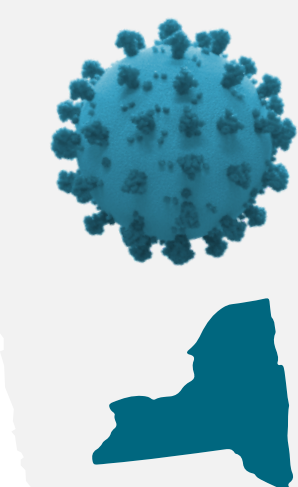


## Eta (B.1.525) B.1.1.207

**First detected:** United Kingdom/Nigeria

**Key mutations:**

- E484K** **Reduces antibody recognition;** Associated with **vaccine resistance**
- F888L** Potential **reduction in neutralization** by some antibody treatments
- Q52R** Mutation associated with Eta variant that causes potential reduction in neutralization by some monoclonal antibody treatments, and potential reduction in neutralization by convalescent and post-vaccination sera
- Q677H.CAG.CAC**
- Q677H.CAG.CAT**

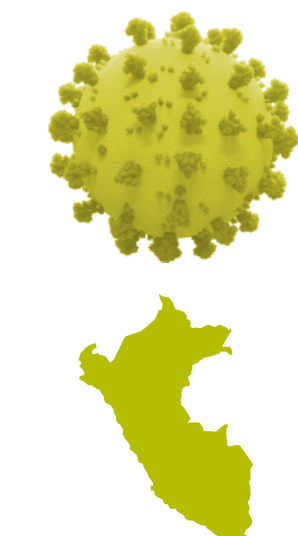


## Iota (B.1.526)

**First detected:** New York (USA)

**Key mutations:**

- F157S** Associated with reduced susceptibility; reduced neutralization by convalescent and post-vaccination sera
- Q5412H** SNP associated with B.1.526 lineage
- S477N** Associated with reduced susceptibility
- T95I** Associated with reduced susceptibility; reduced neutralization by convalescent and post-vaccination sera

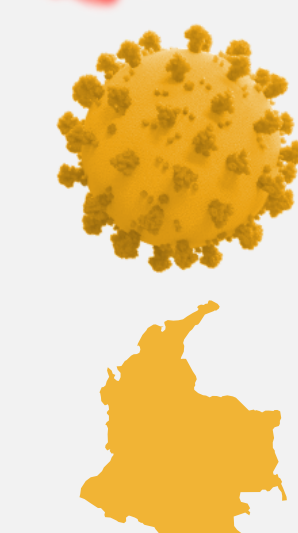


## Lambda (C.37)

**First detected:** Peru

**Key mutations:**

- F2387V** Mutation associated with C.37 WHO Variant of Interest
- L452Q** Mutation associated with C.37 WHO Variant of Interest

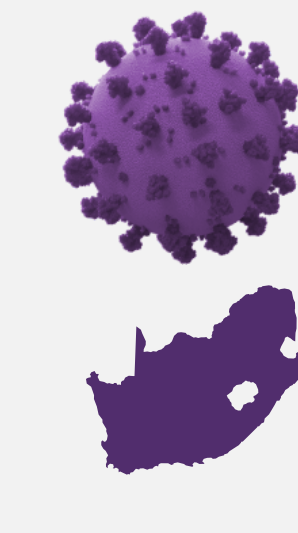


## Mu (B.1.621)

**First detected:** Colombia

**Key mutations:**

- A13057T** SNP associated with Mu VOI according to WHO
- A28272T** SNP associated with Mu VOI according to WHO
- R346K** SNP associated with Mu VOI according to WHO
- T1055A** SNP associated with Mu VOI according to WHO
- T95I** Associated with reduced susceptibility; reduced neutralization by convalescent and post-vaccination sera

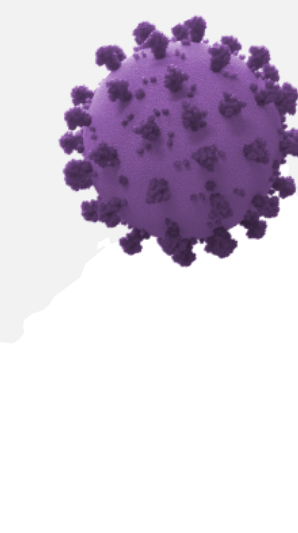


## Omicron (B.1.1.529)

**First detected:** South Africa

**Key mutations:**

- G339D** May be associated with **increased transmissibility, vaccine resistance** and risk for **reinfections**
- Q493R** May be associated with **increased transmissibility, vaccine resistance** and risk for **reinfections**

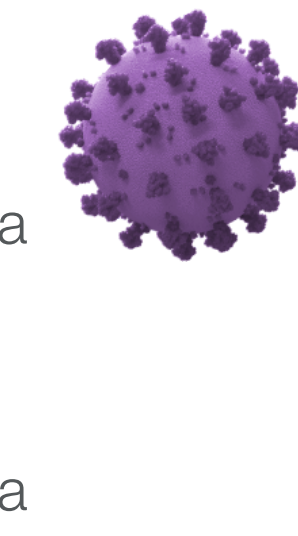


## Omicron (BA.1, BA.1.1, BA.2, BA.3)

**First detected:** Various Countries

**Key mutations:**

- A2710T** SNP associated with high percentage of BA.1 and BA.1.1 Omicron Variant of Concern
- Q954H** SNP associated with Omicron Variant of Concern
- R346K** SNP associated with Mu Variant of Interest and Omicron Variant of Concern according to WHO
- T13195C** SNP associated with high percentage of BA.1 and BA.1.1 Omicron Variant of Concern
- T547K** SNP associated with high percentage of BA.1 and BA.1.1 Omicron Variant of Concern
- T376A** Defining SNP associated with BA.2 sub lineage of the Omicron variant, considered a Variant of Concern by the WHO
- V213G** Defining SNP associated with BA.2 sub lineage of the Omicron variant, considered a Variant of Concern by the WHO

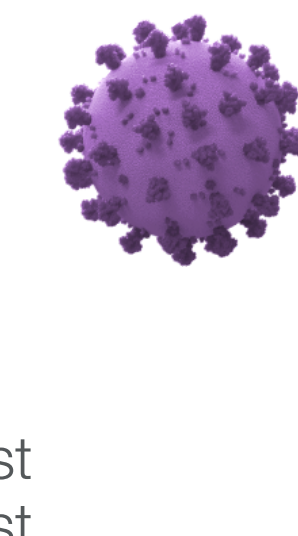


## Omicron (BA.4)

**First detected:** Various Countries

**Key mutations:**

- L11F** Defining SNP associated with BA.4 sub lineage of the Omicron variant



## Omicron (BA.5)

**First detected:** Various Countries

**Key mutations:**

- D3N** Defining SNP associated with BA.5 sub lineage of the Omicron variant