

# NETEC COVID-19 Webinar Series:

## SARS-CoV-2: Mutations and Variants and Strains (Oh My!)



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# Welcome

**Radu Postelnicu, MD**

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➤ **Welcome:** Radu Postelnicu, MD

➤ **Introduction to SARS-CoV-2 Variants and Mutations:**

Anne Piantadosi, MD, PhD,  
Assistant Professor, Emory School of Medicine Department of Pathology

➤ **COVID Variants:** James V. Lawler, MD, MPH, FIDSA

➤ **Questions and Answers with NETEC**

➤ **NETEC Resources:** Radu Postelnicu, MD

## National Emerging Special Pathogens Training and Education Center

### Mission Statement

To increase the capability of the United States public health and health care systems to safely and effectively manage individuals with suspected and confirmed special pathogens

For more information

Please visit us at [www.netec.org](http://www.netec.org)  
or email us at [info@netec.org](mailto:info@netec.org)



## Assessment

Empower hospitals to gauge their readiness using  
**Self-Assessment**

Measure facility and healthcare worker readiness using  
**Metrics**

Provide direct feedback to hospitals via  
**On-Site Assessment**

## Education

Provide self-paced education through  
**Online Trainings**

Deliver didactic and hands-on simulation training via  
**In-Person Courses**

COVID-19 focused  
**Webinars**

## Technical Assistance

**Onsite & Remote Guidance**

Compile  
**Online Repository** of tools and resources

Develop customizable  
**Exercise Templates** based on the HSEEP model

Provide  
**Emergency On-Call Mobilization**

## Research Network

**Online Repository**  
Built for rapid implementation of clinical research protocols

**Develop Policies, Procedures and Data Capture Tools** to facilitate research

Create infrastructure for a  
**Specimen Biorepository**



Cross-Cutting, Supportive Activities



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# **Introduction to SARS-CoV-2 Variants and Mutations**

**Anne Piantadosi, MD, PhD**

**Assistant Professor, Emory School of Medicine Department of Pathology**

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## Definitions

### Mutation:

**A change in the virus genome, e.g. point mutation, deletion**

### Variant:

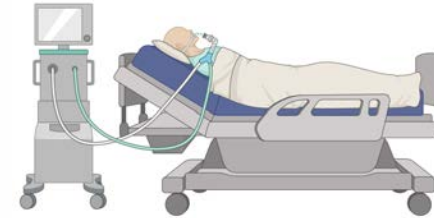
**A virus that contains multiple mutations in a distinct pattern**

- The mutations are shared by other viruses that came from a common ancestor
- The variant is easy to distinguish from other viruses by genome sequencing

## When do We Care About Mutations and Variants?

When they

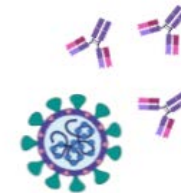
➔ Increase pathogenicity



➔ Increase transmissibility



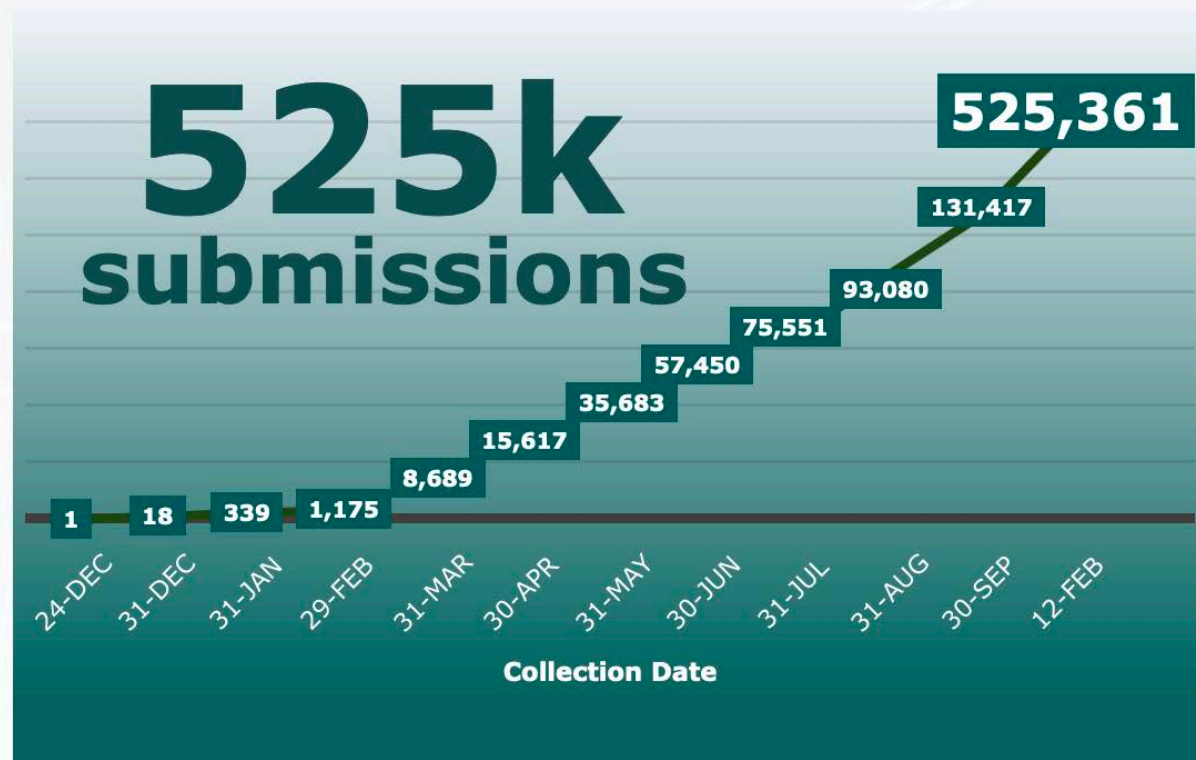
➔ Allow escape from the immune response




# hCoV-19 Data Sharing via GISAID – 2.12.2021

SARS-CoV-2 mutations and variants are identified by *massive* global efforts in viral genome sequencing

## hCoV-19 Data Sharing via GISAID



# SARS-CoV-2 Sequencing for Public Health Emergency Response, Epidemiology, and Surveillance (SPHERES)



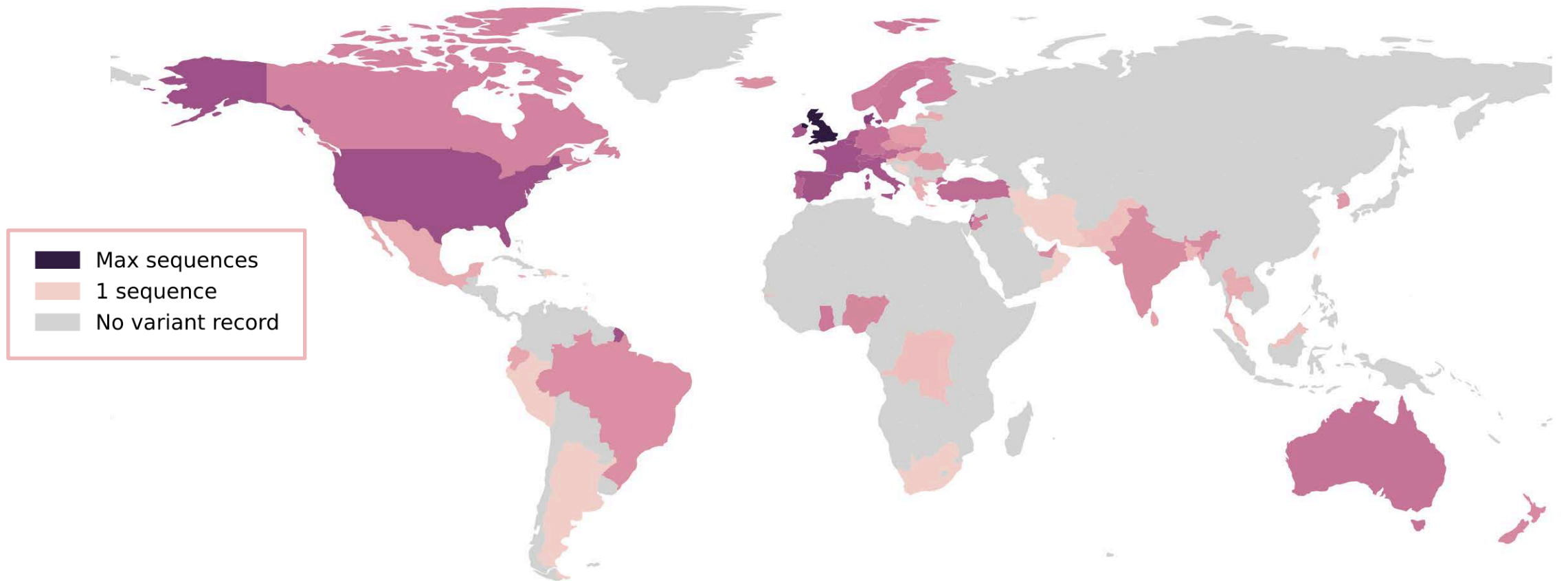
**SARS-CoV-2 genomic surveillance in the U.S. is performed by state health departments, the CDC, academic institutions, nonprofit organizations, and companies**

# Variant B.1.1.7

AKA “UK variant”; “501Y.V1”

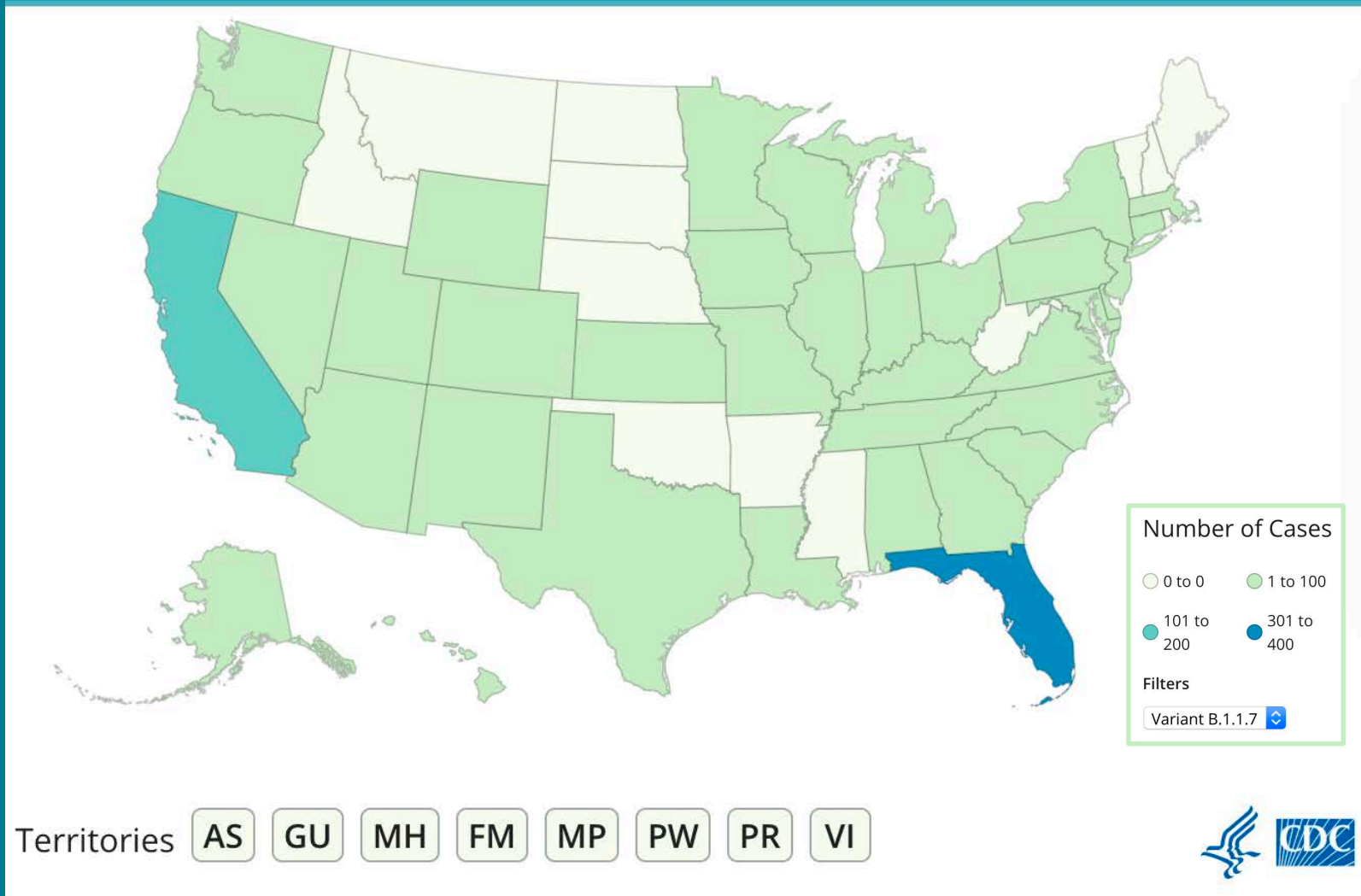
**Figure 3 – Map of B.1.1.7 sequence counts**

Map showing the logged number of sequences of the variant in each country. Countries with more sequences are shown in darker colours



# Variant B.1.1.7 in the United States

## Emerging Variant Cases in the United States\*†



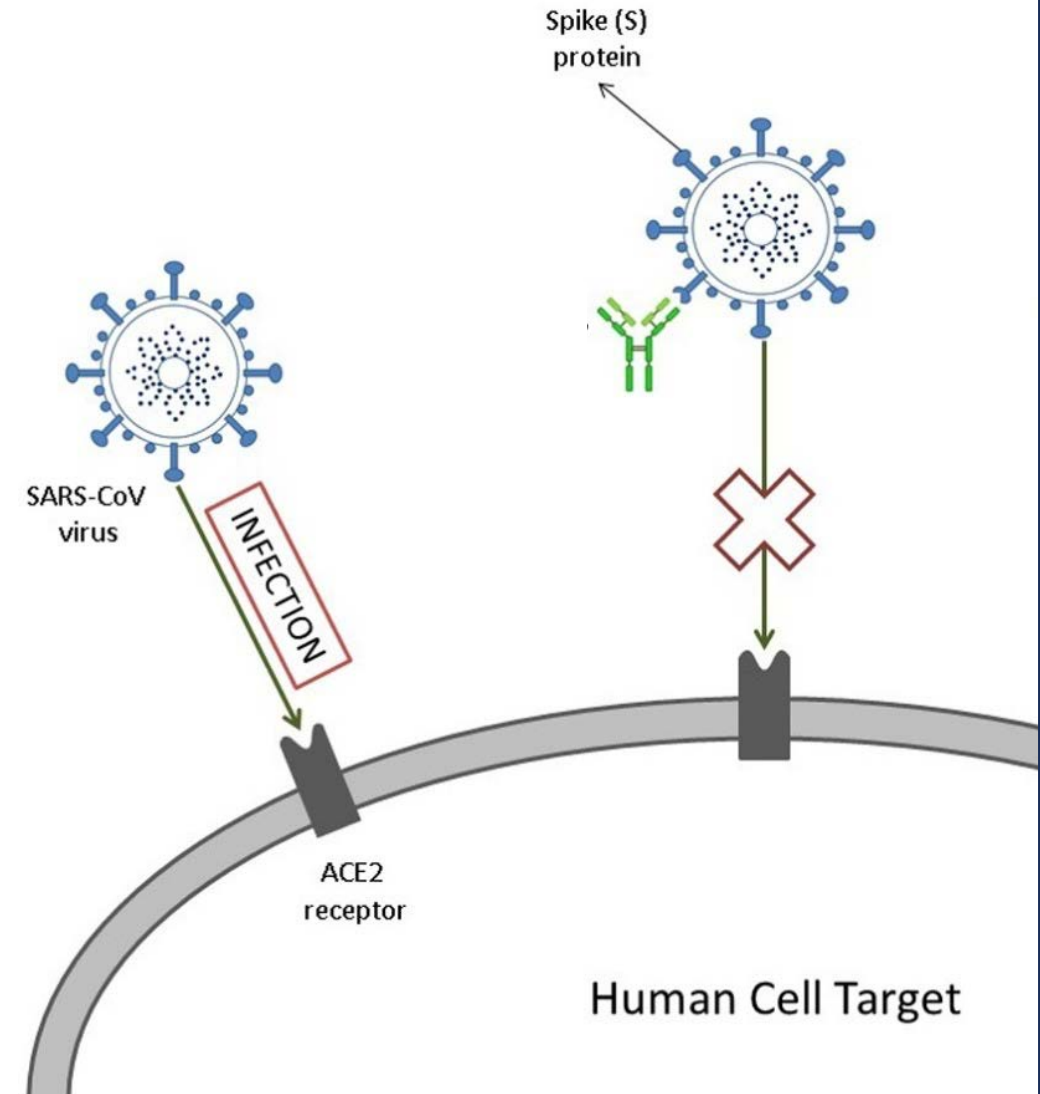
Data Table	
Location	B.1.1.7 Variant
Florida	347
California	159
New York	59
Colorado	41
Georgia	37
Texas	35
New Jersey	31
Michigan	29
Pennsylva...	25
Illinois	23
Maryland	22
North Caroli	21
Connecticut	20
Minnesota	18
Washington	15
Louisiana	14
Indiana	12
Massachuse	10
Iowa	8
Alabama	7
Nevada	6

## Variant B.1.1.7

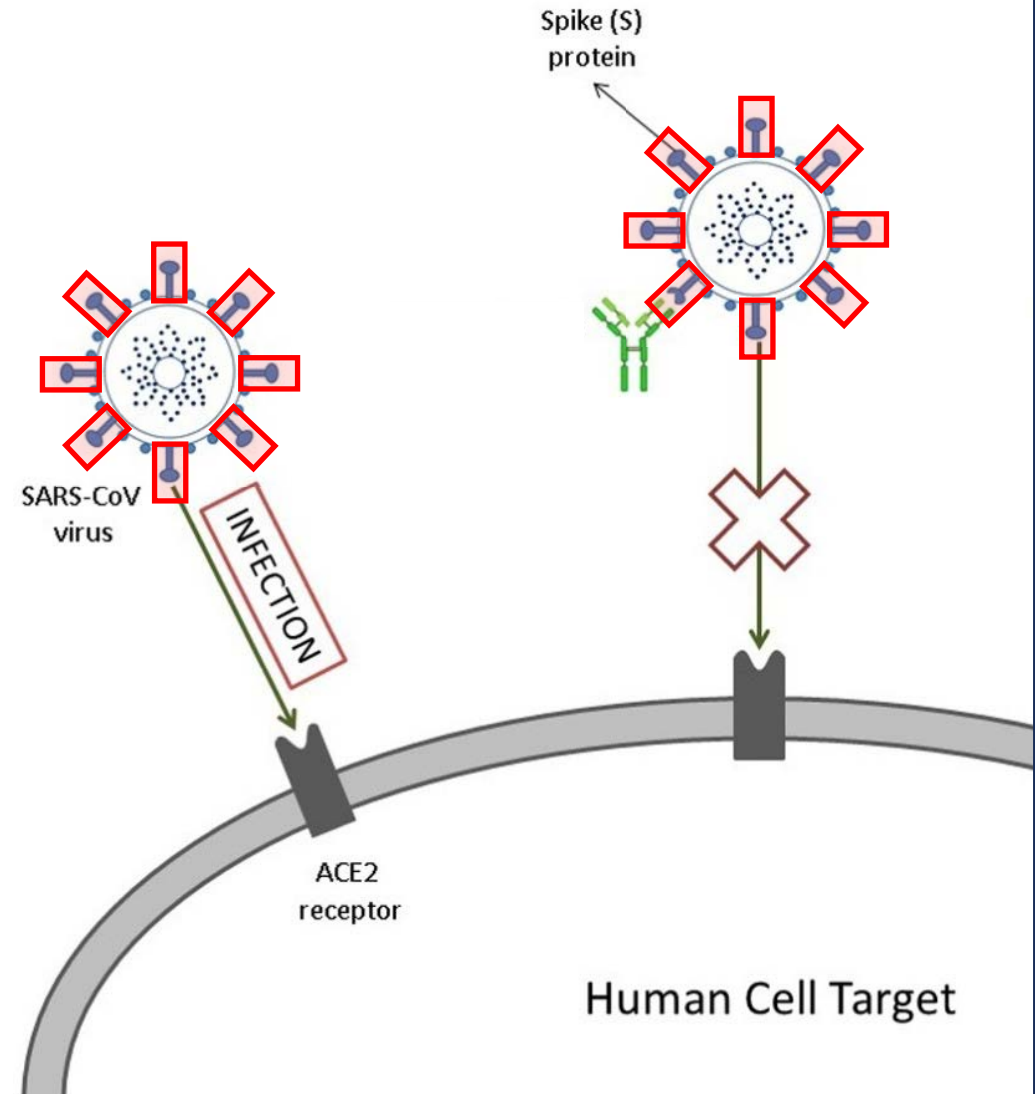
---

- ✓ Is increasing in frequency
  - ✓ Is more transmissible
  - ✓ Is associated with higher viral loads
  - ✓ Contains 23 mutations
-

➔ **Mutations in the receptor binding domain (RBD) of the spike protein can affect both infection and susceptibility to antibodies**



➔ **Mutations in the receptor binding domain (RBD) of the spike protein can affect both infection and susceptibility to antibodies**



## Mutation N501Y

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**Increases binding to ACE2 receptor**



**Does not seem to be associated with reduced neutralization**



**Is found in other rapidly-spreading variants**

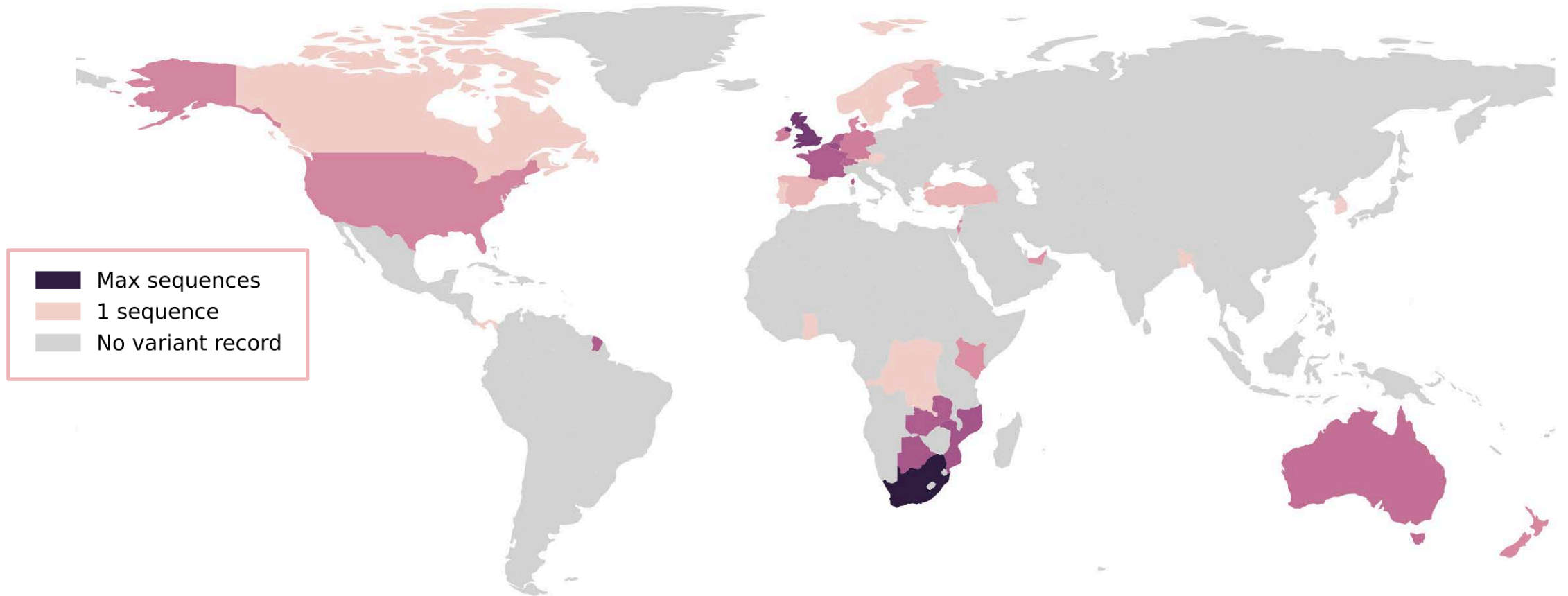
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# Variant B.1.351

AKA “South Africa variant”; “501Y.V2”

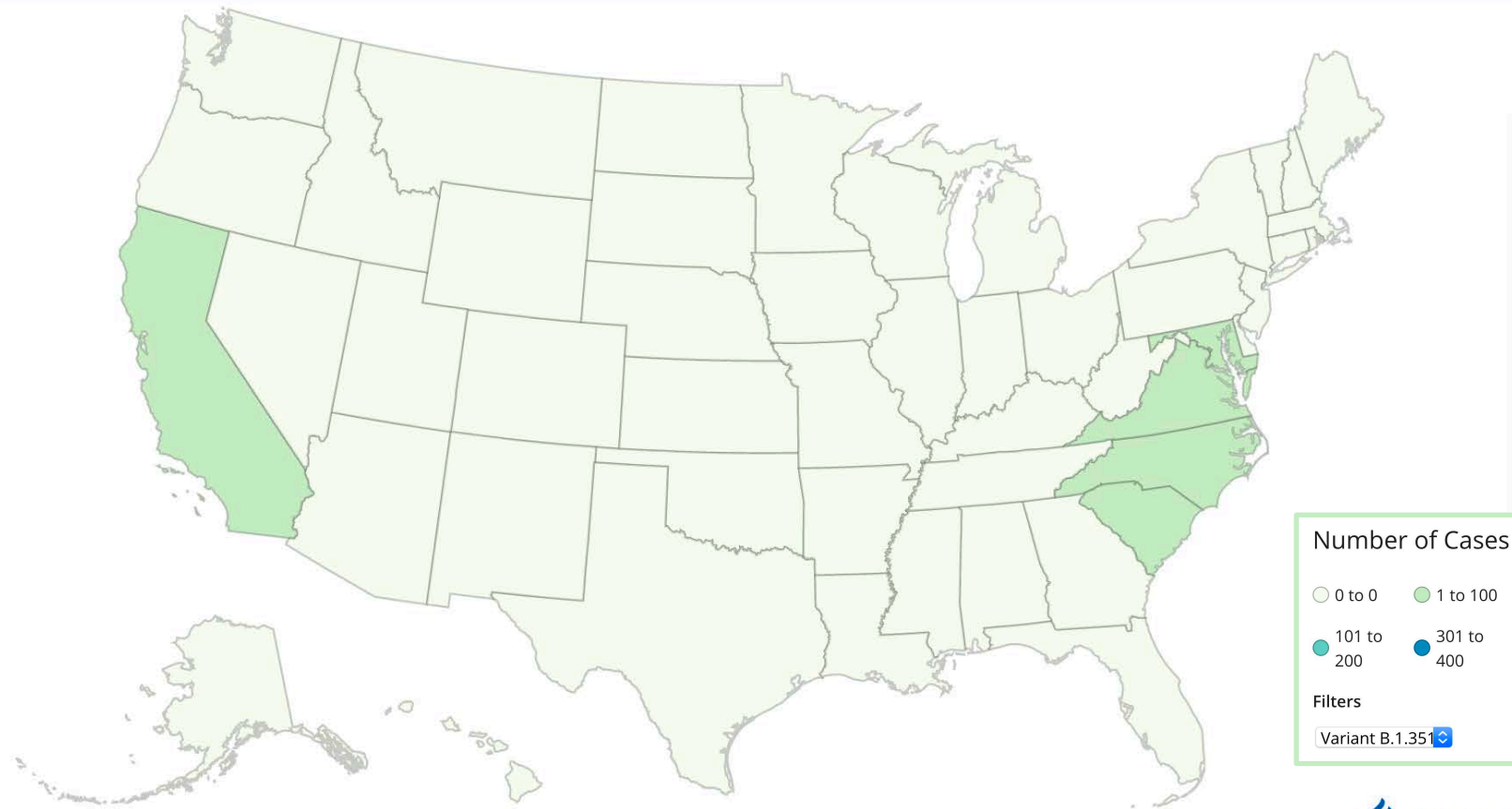
**Figure 3 – Map of B.1.351 sequence counts**

Map showing the logged number of sequences of the variant in each country. Countries with more sequences are shown in darker colours



# Variant B.1.351 in the United States

## Emerging Variant Cases in the United States\*†



Territories

AS

GU

MH

FM

MP

PW

PR

VI



### Data Table

Location	B.1.351 Variant
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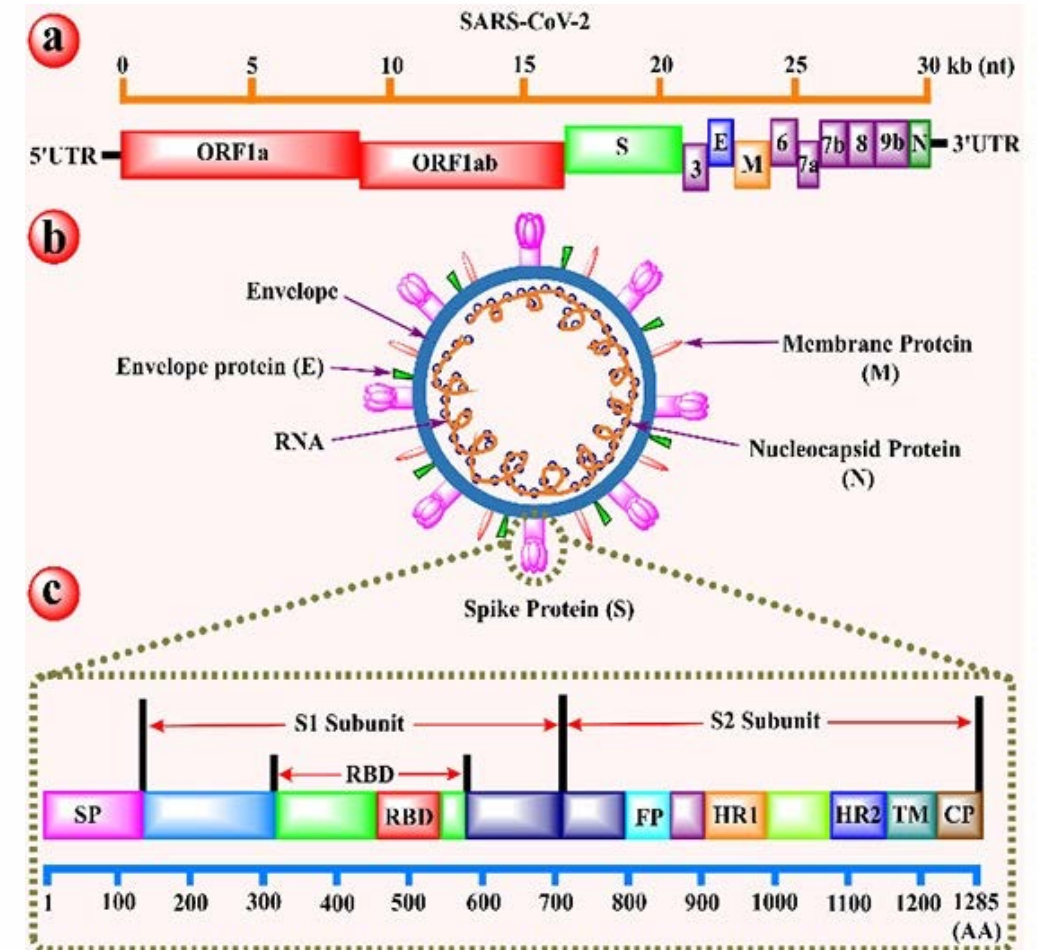
Maryland	7
South Caroli...	2
California	2
Virginia	1
North Caroli...	1
Wyoming	0
Wisconsin	0
West Virgi...	0
Washington	0
Virgin Islan...	0

## Variant B.1.351

- 
- ✓ Is increasing in frequency
  - ✓ Is more transmissible
  - ✓ Is less susceptible to antibodies from previously-infected individuals and vaccinated individuals
  - ✓ Contains a different set of mutations
-

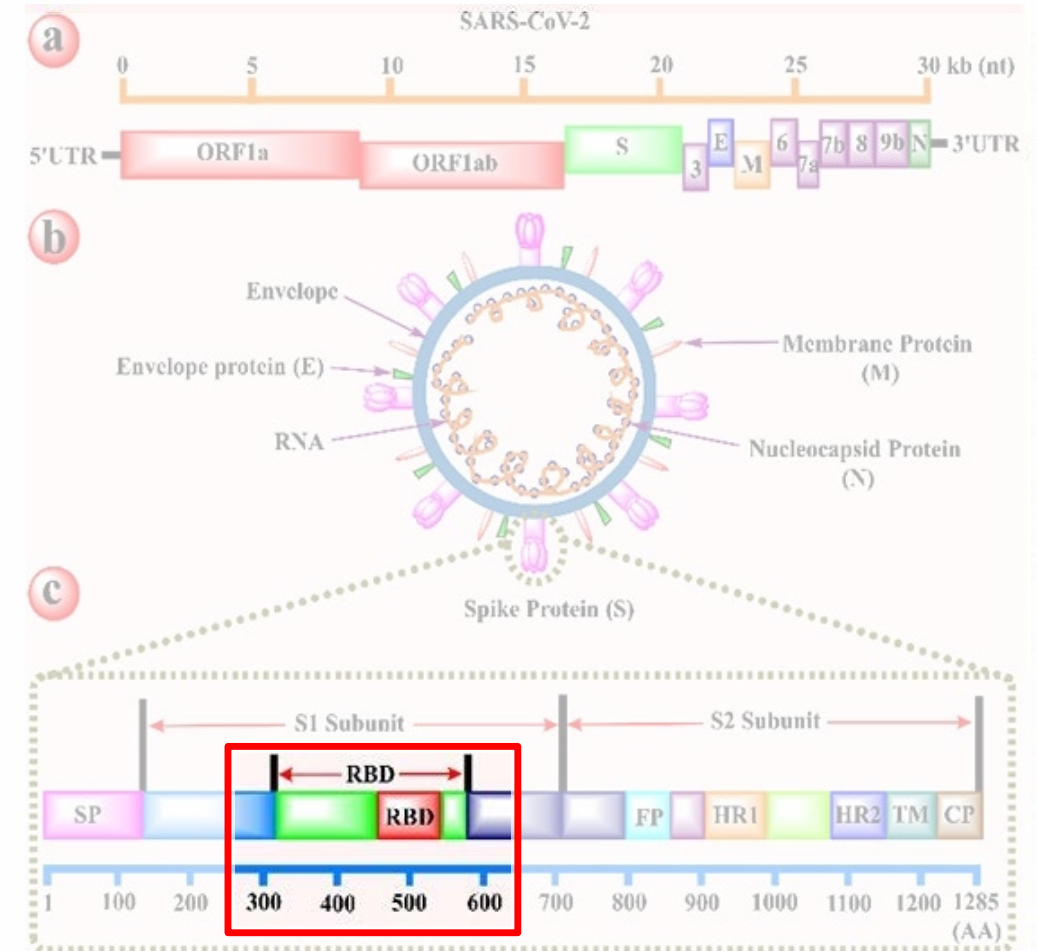
## Variant B.1.351 Contains Multiple RBD Mutations

➔ Mutations N501Y, E484K, and K417N are in the receptor binding domain (RBD) of the Spike protein



## Variant B.1.351 Contains Multiple RBD Mutations

➔ Mutations N501Y, E484K, and K417N are in the receptor binding domain (RBD) of the Spike protein



## Mutation E484K

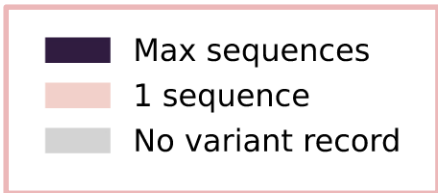
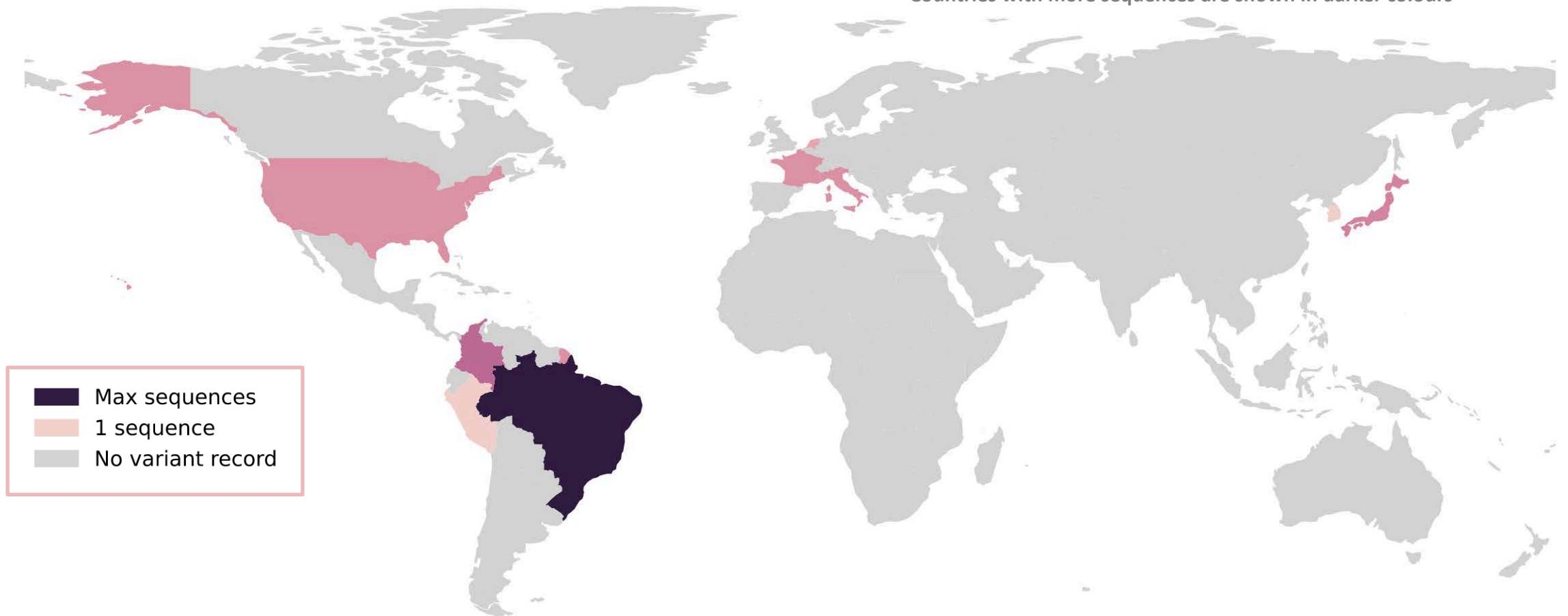
- 
- ✓ **Increases binding to ACE2 receptor**
  - ✓ **Is not neutralized as easily by convalescent sera from previously-infected patients**
  - ✓ **Is found in other variants, which evolved independently**
-

# Variant P.1

AKA “Brazil variant”

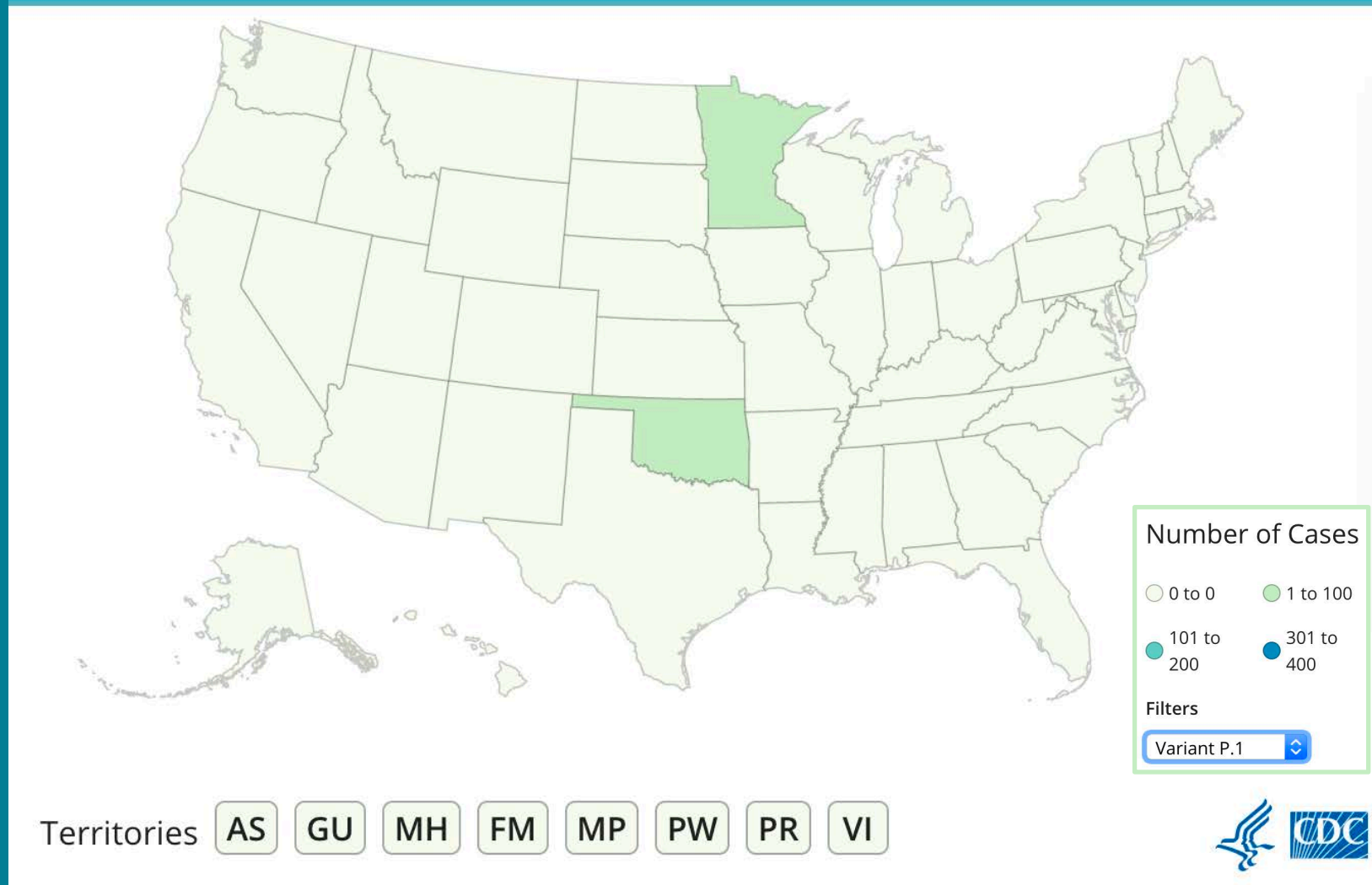
## Figure 3 – Map of P.1 sequence counts

Map showing the logged number of sequences of the variant in each country. Countries with more sequences are shown in darker colours



# Variant P.1 in the United States

Emerging Variant Cases in the United States\*†



Data Table	
Location	P.1 Variant
● Minnesota	2
● Oklahoma	1
● Wyoming	0
● Wisconsin	0
● West Virginia	0
● Washington	0
● Virginia	0
● Virgin Islands	0
● Vermont	0
● Utah	0

## Variant P.1

- ✓ **Caused a surge of cases in Brazil, in a population that had already experienced a rate of infection**
- ✓ **Is associated with reinfection**
- ✓ **Contains mutations N501Y, E484K, and K417N**

## Summary of Variants and Mutations

➔ Variants noted to be **increasing in frequency**:

**B.1.1.7**

**B.1.135**

**P.1**

➔ Mutations:

**N501Y**

**E484K**

**K417N**

## Summary of Variants and Mutations

➔ Variants noted to be **less susceptible to antibodies:**

**B.1.1.7**

**B.1.135**

**P.1**

➔ Mutations:

**N501Y**

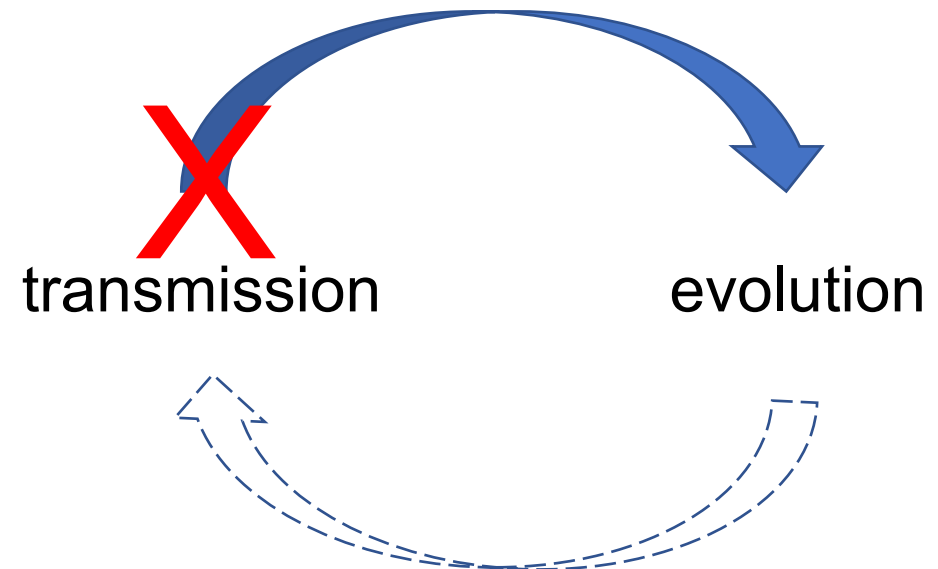
**E484K**

**K417N**

## Summary

- It is crucial to identify and respond to changes in SARS-CoV-2 that make it more transmissible, more pathogenic, and less susceptible to the immune response
- Identifying and monitoring important SARS-CoV-2 mutations and variants within an actionable timeframe requires substantial coordinated effort among hospitals, public health organizations, and researchers

➤ Preventing transmission is key to slowing evolution



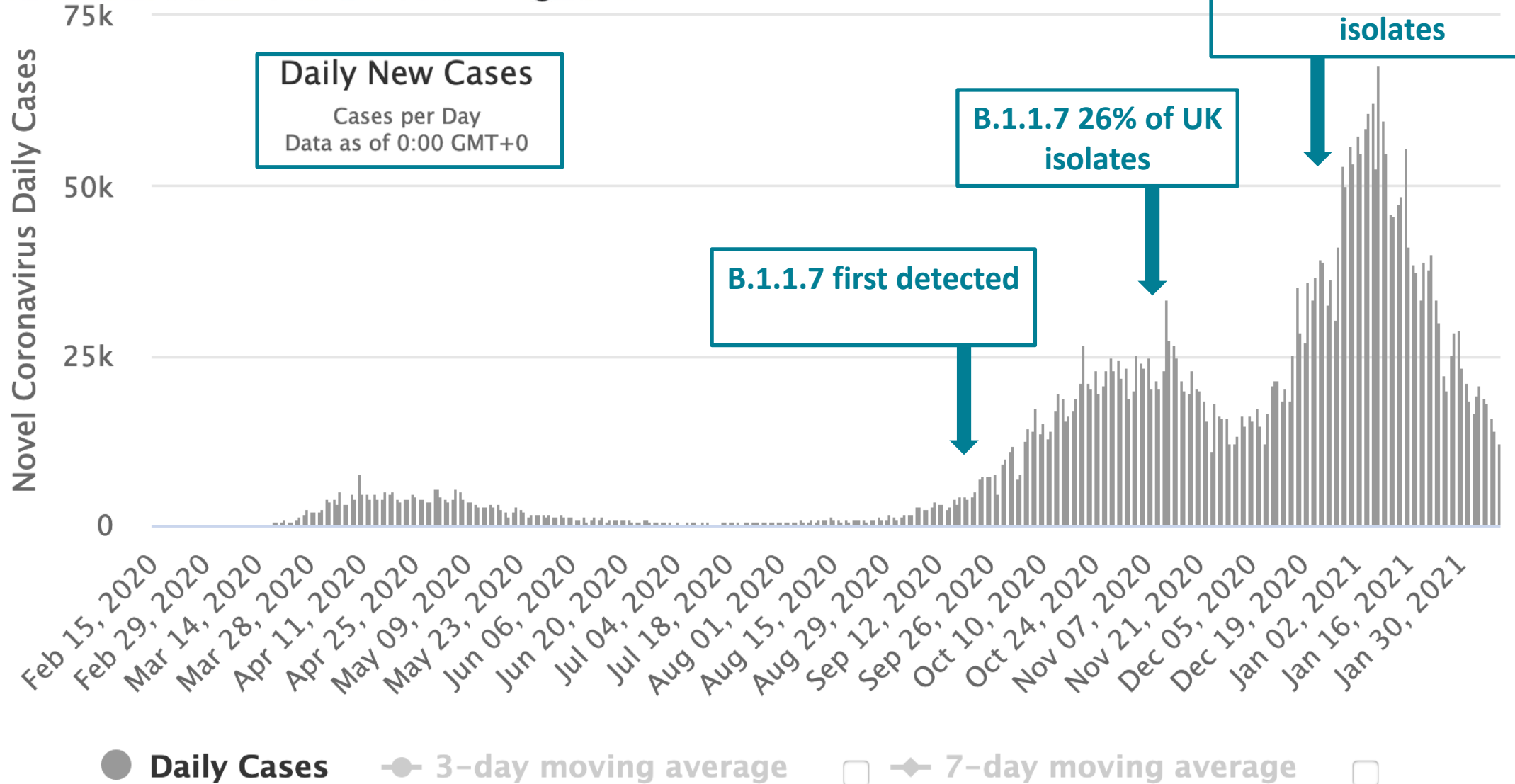
# COVID Variants

**James V. Lawler, MD, MPH, FIDSA**



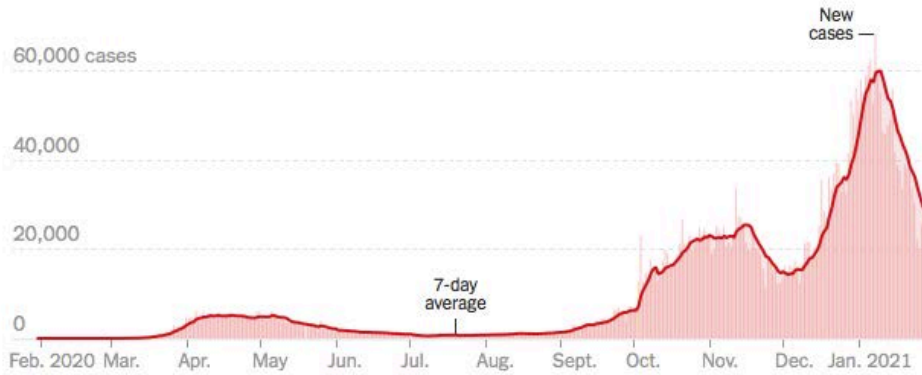
# B.1.1.7 in United Kingdom

## Daily New Cases in the United Kingdom



# U.K. B.1.1.7 Variant Surge

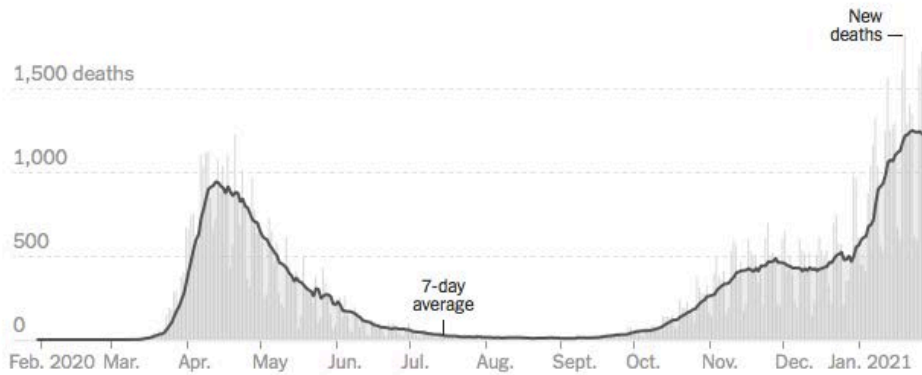
## New reported cases by day



These are days with a reporting anomaly. Read more [here](#).

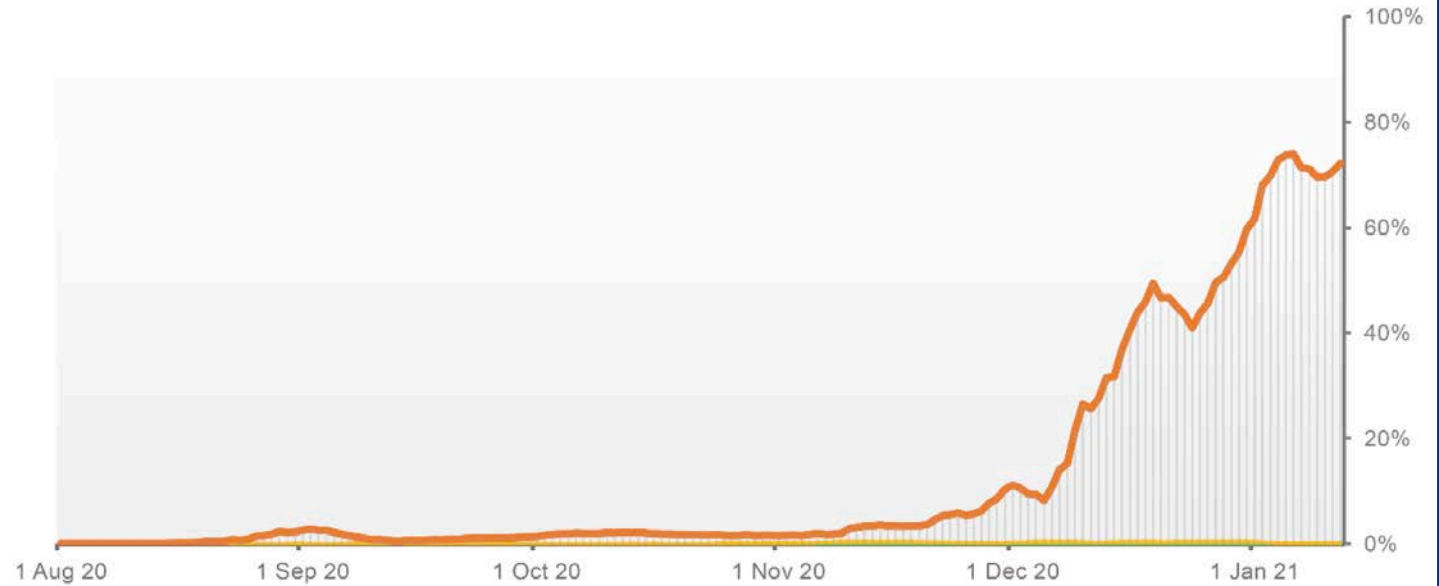
Note: The seven-day average is the average of a day and the previous six days of data.

## New reported deaths by day



## SARS-CoV-2 targets in strong positive test results

Five-day rolling rate per total number of strong positives by date of test result



Lighthouse Lab, Alderley Park  
12<sup>th</sup> Jan 2021

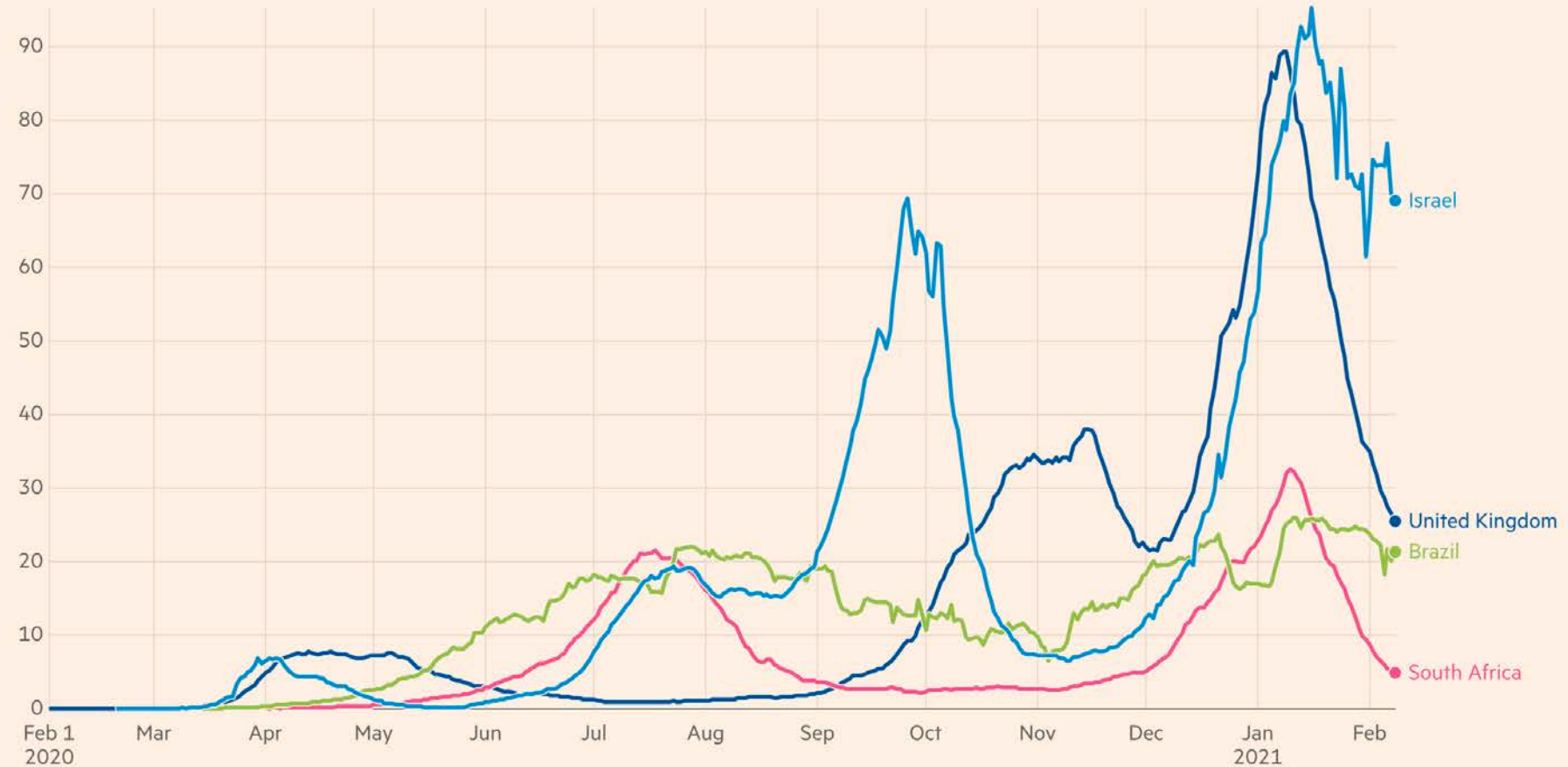
- ORF1ab target failure (N and S-genes targets strong positives)
- N-gene target failure (ORF1ab and S-gene targets strong positives)
- S-gene target failure (ORF1ab and N-gene targets strong positives)

Figure 1. TaqPath™ COVID 19 Assay, S-gene detection in comparison to ORF1ab and N-gene.

# COVID-19 in United Kingdom, South Africa, Brazil and Israel

New confirmed cases of Covid-19 in United Kingdom, South Africa, Brazil and Israel

Seven-day rolling average of new cases (per 100k)



Source: Financial Times analysis of data from the Johns Hopkins CSSE, the Covid Tracking Project, the World Health Organization, the UK Government coronavirus dashboard and the Swedish Public Health Agency. **FINANCIAL TIMES**  
Data updated February 10 2021 2.30pm GMT. Interactive version: [ft.com/covid19](https://ft.com/covid19)

## CORONAVIRUS

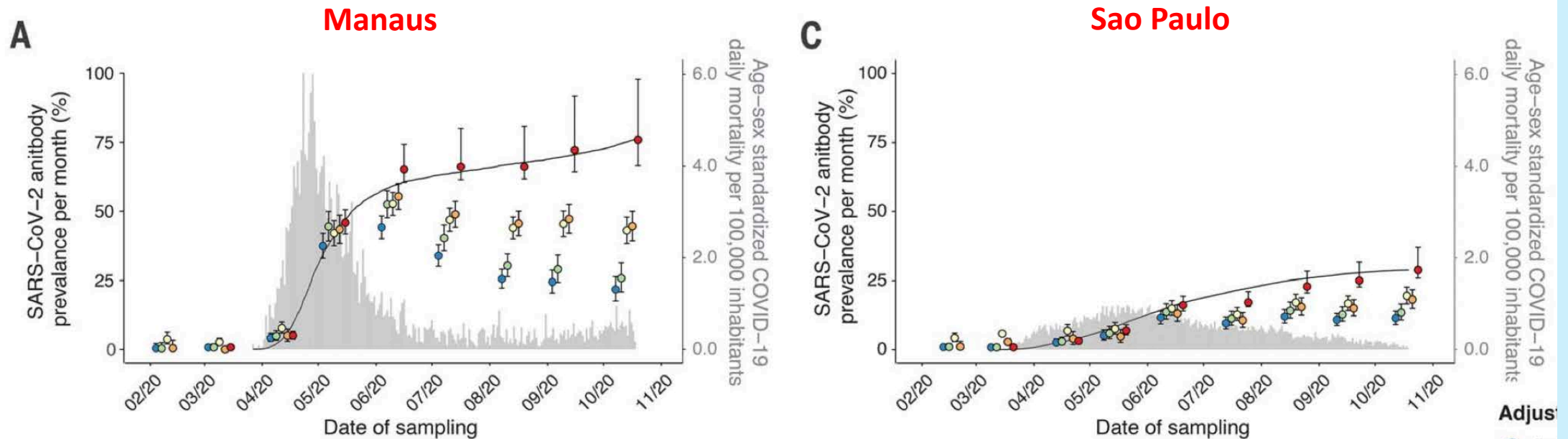
# Three-quarters attack rate of SARS-CoV-2 in the Brazilian Amazon during a largely unmitigated epidemic

Lewis F. Buss<sup>1\*</sup>, Carlos A. Prete Jr.<sup>2\*</sup>, Claudia M. M. Abraham<sup>3\*</sup>, Alfredo Mendrone Jr.<sup>4,5\*</sup>, Tassila Salomon<sup>6,7\*</sup>, Cesar de Almeida-Neto<sup>4,5</sup>, Rafael F. O. França<sup>8</sup>, Maria C. Belotti<sup>2</sup>, Maria P. S. S. Carvalho<sup>3</sup>, Allyson G. Costa<sup>3</sup>, Myuki A. E. Crispim<sup>3</sup>, Suzete C. Ferreira<sup>4,5</sup>, Nelson A. Fraiji<sup>3</sup>, Susie Gurzenda<sup>9</sup>, Charles Whittaker<sup>10</sup>, Leonardo T. Kamaura<sup>11</sup>, Pedro L. Takecian<sup>11</sup>, Pedro da Silva Peixoto<sup>11</sup>, Marcio K. Oikawa<sup>12</sup>, Anna S. Nishiya<sup>4,5</sup>, Vanderson Rocha<sup>4,5</sup>, Nanci A. Salles<sup>4</sup>, Andreza Aruska de Souza Santos<sup>13</sup>, Martirene A. da Silva<sup>3</sup>, Brian Custer<sup>14,15</sup>, Kris V. Parag<sup>16</sup>, Manoel Barral-Netto<sup>17</sup>, Moritz U. G. Kraemer<sup>18</sup>, Rafael H. M. Pereira<sup>19</sup>, Oliver G. Pybus<sup>18</sup>, Michael P. Busch<sup>14,15</sup>, Márcia C. Castro<sup>9</sup>, Christopher Dye<sup>18</sup>, Vítor H. Nascimento<sup>2</sup>, Nuno R. Faria<sup>1,16,18†</sup>, Ester C. Sabino<sup>1†</sup>

Buss *et al.*, *Science* **371**, 288–292 (2021) 15 January 2021



Evidence of 76% community attack rate in Manaus, Brazil by late October, vs 29% in Sao Paulo





ABOUT US

WHAT WE DO

WHERE WE WORK

RESOURCES

LATEST

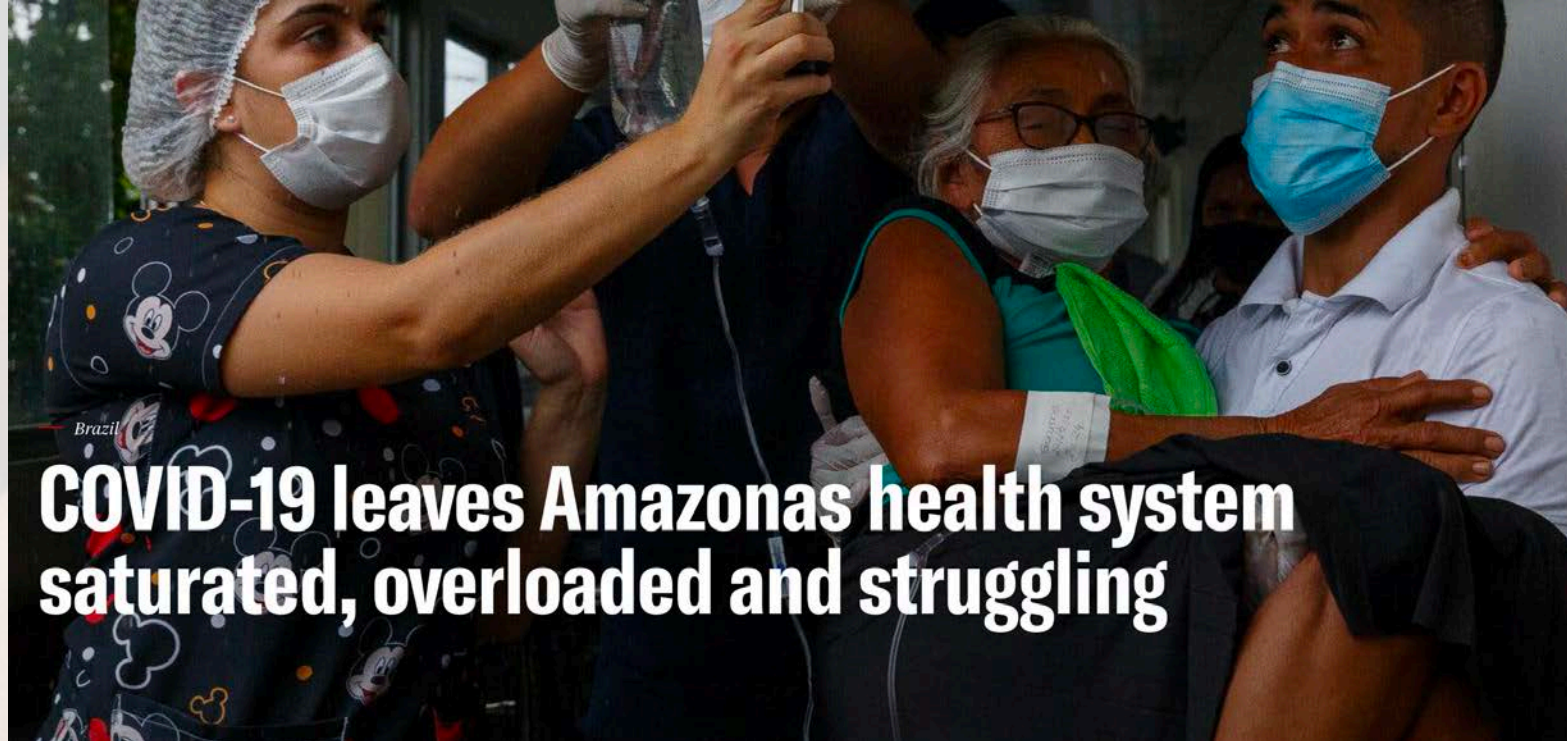


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## Brazil COVID-19 leaves Amazonas health system saturated, overloaded and struggling

Project Update | 21 January 2021

The health system in Manaus, the capital of Amazonas state, in northwestern Brazil, has collapsed for the second time. Although hospitals have been adding COVID-19 bed capacity at an astonishing rate, the numbers of new patients with the coronavirus have continued to grow even faster, meaning the entire health system is saturated and overloaded.

More seriously, the city's capacity to produce oxygen is running at less than a third of the current needs, leaving some hospitals unable to ventilate patients and reportedly resulting in people dying of asphyxiation. The knock-on effect on towns upriver, in the rural Amazon region, are starting to show, and could be just as devastating.

**Patients and hospitals upriver seriously struggling**

<https://www.msf.org/coronavirus-covid-19-collapses-health-system-manaus-brazil>

# Mutation Mapping and Binding of Antibodies

bioRxiv preprint doi: <https://doi.org/10.1101/2020.12.31.425021>; this version posted January 4, 2021. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under a [CC-BY 4.0 International license](#).

## Comprehensive mapping of mutations to the SARS-CoV-2 receptor-binding domain that affect recognition by polyclonal human serum antibodies

Allison J. Greaney<sup>1,2</sup>, Andrea N. Loes<sup>1,3</sup>, Katharine H.D. Crawford<sup>1,2</sup>, Tyler N. Starr<sup>1,3</sup>, Keara D. Malone<sup>1</sup>, Helen Y. Chu<sup>4</sup>, Jesse D. Bloom<sup>1,3,#</sup>

<sup>1</sup>Basic Sciences Division and Computational Biology Program, Fred Hutchinson Cancer Research Center, Seattle, WA 98109, USA

<sup>2</sup>Department of Genome Sciences & Medical Scientist Training Program, University of Washington, Seattle, WA 98195, USA

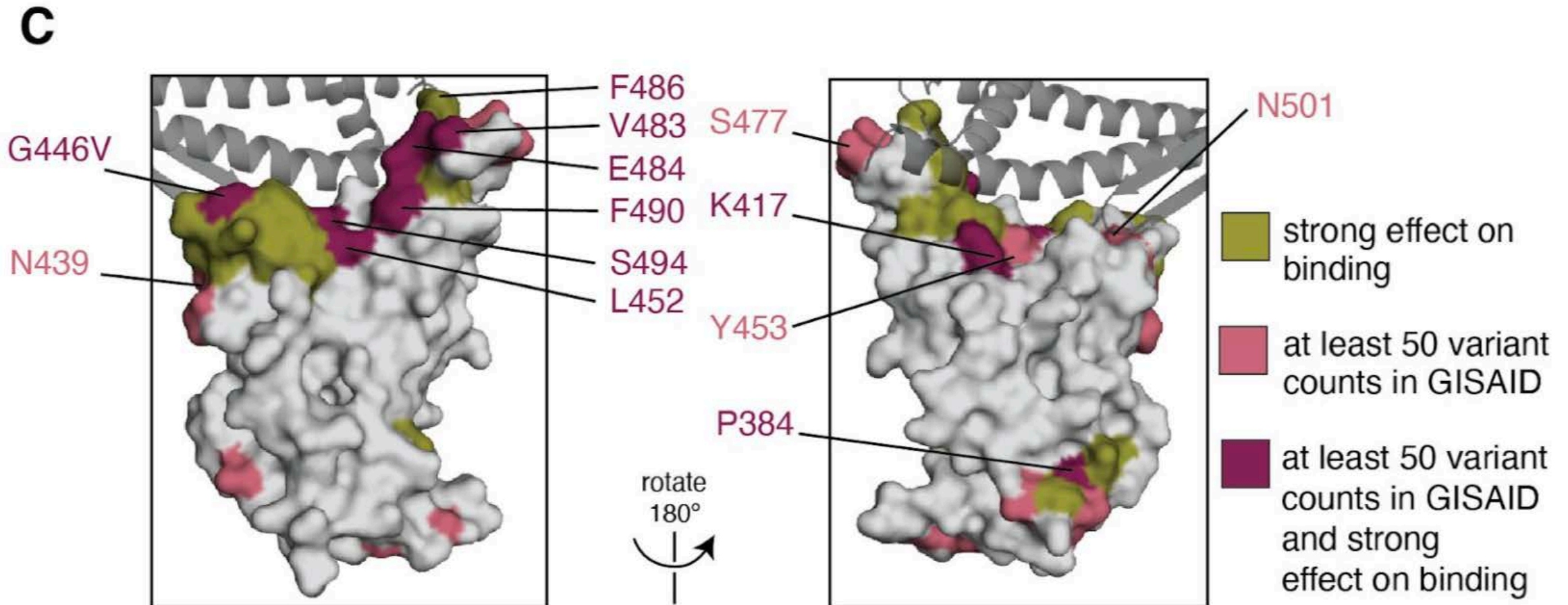
<sup>3</sup>Howard Hughes Medical Institute, Seattle, WA 98109, USA

<sup>4</sup>Division of Allergy and Infectious Diseases, University of Washington, Seattle, Washington, USA

#correspondence to [jbloom@fredhutch.org](mailto:jbloom@fredhutch.org)

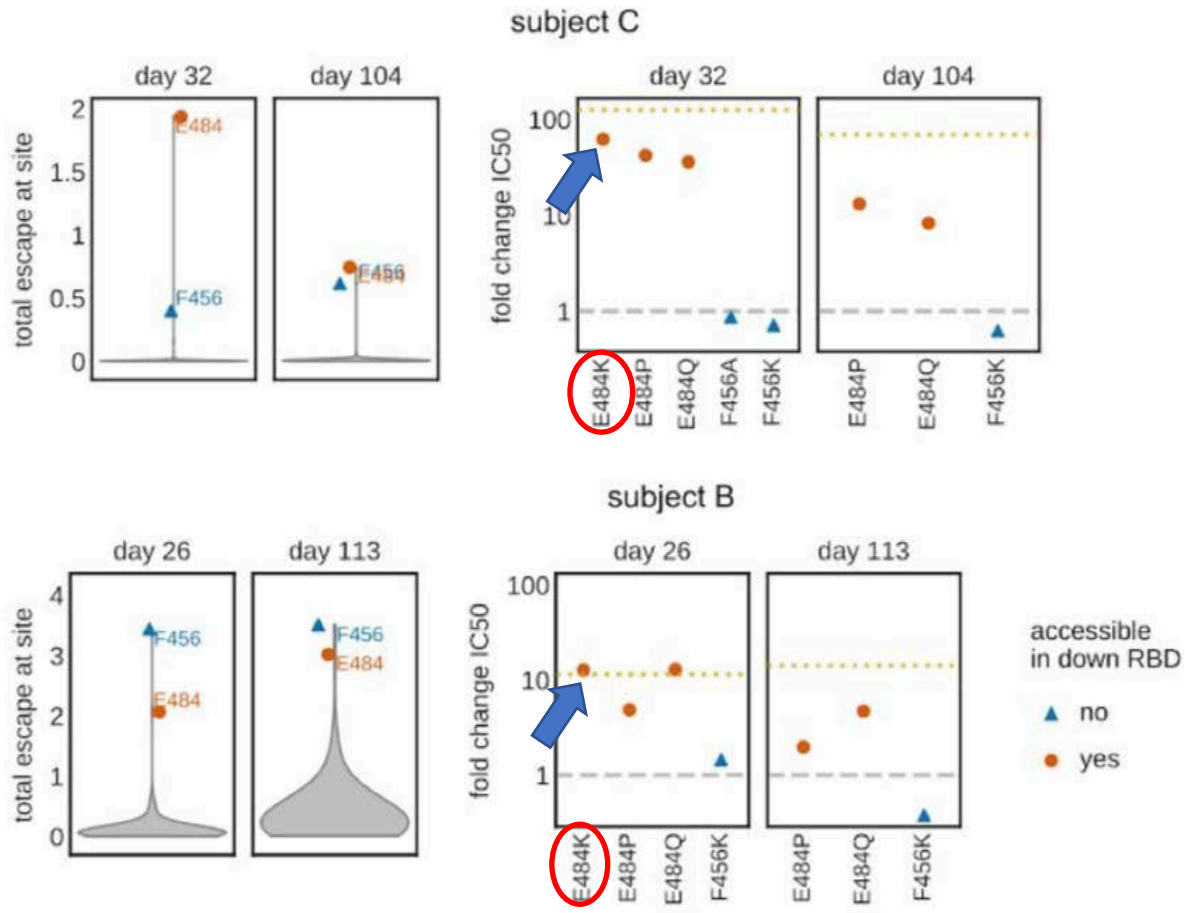
“In particular, binding by all 11 samples was reduced by mutations at site F456, and binding by most samples (9 of 11) was reduced by mutations at site E484 (**Figure 2A**). Both of these sites are within the receptor-binding ridge epitope. Notably, E484 is a site at which mutations have recently been demonstrated to reduce neutralization by several monoclonal antibodies and sera”

# Frequency of Mutations that Affect Serum Antibody Binding Among Circulating SARS-CoV-2 Isolates

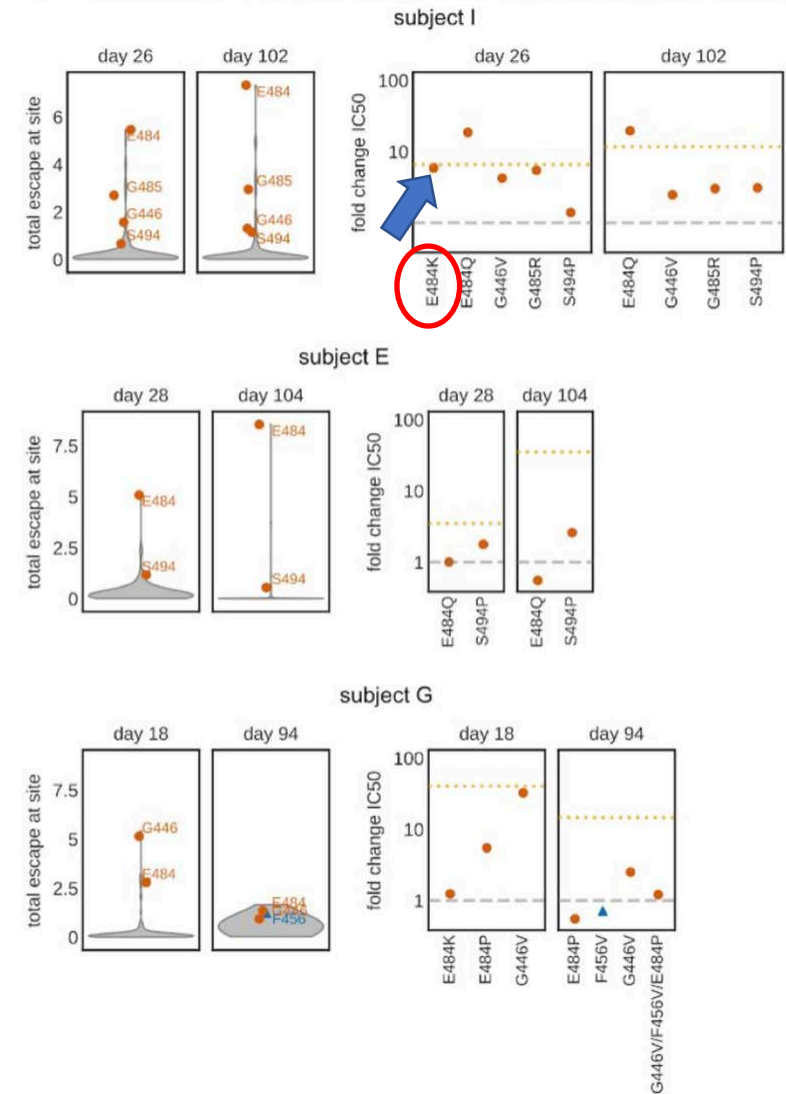


# Mutations Mapped to Reduce Serum Antibody Binding Often Reduce Viral Neutralization

## A Mutations at 484 can have large effects on neutralization.



## B Mutations at 446, 485, and 494 can also affect neutralization.



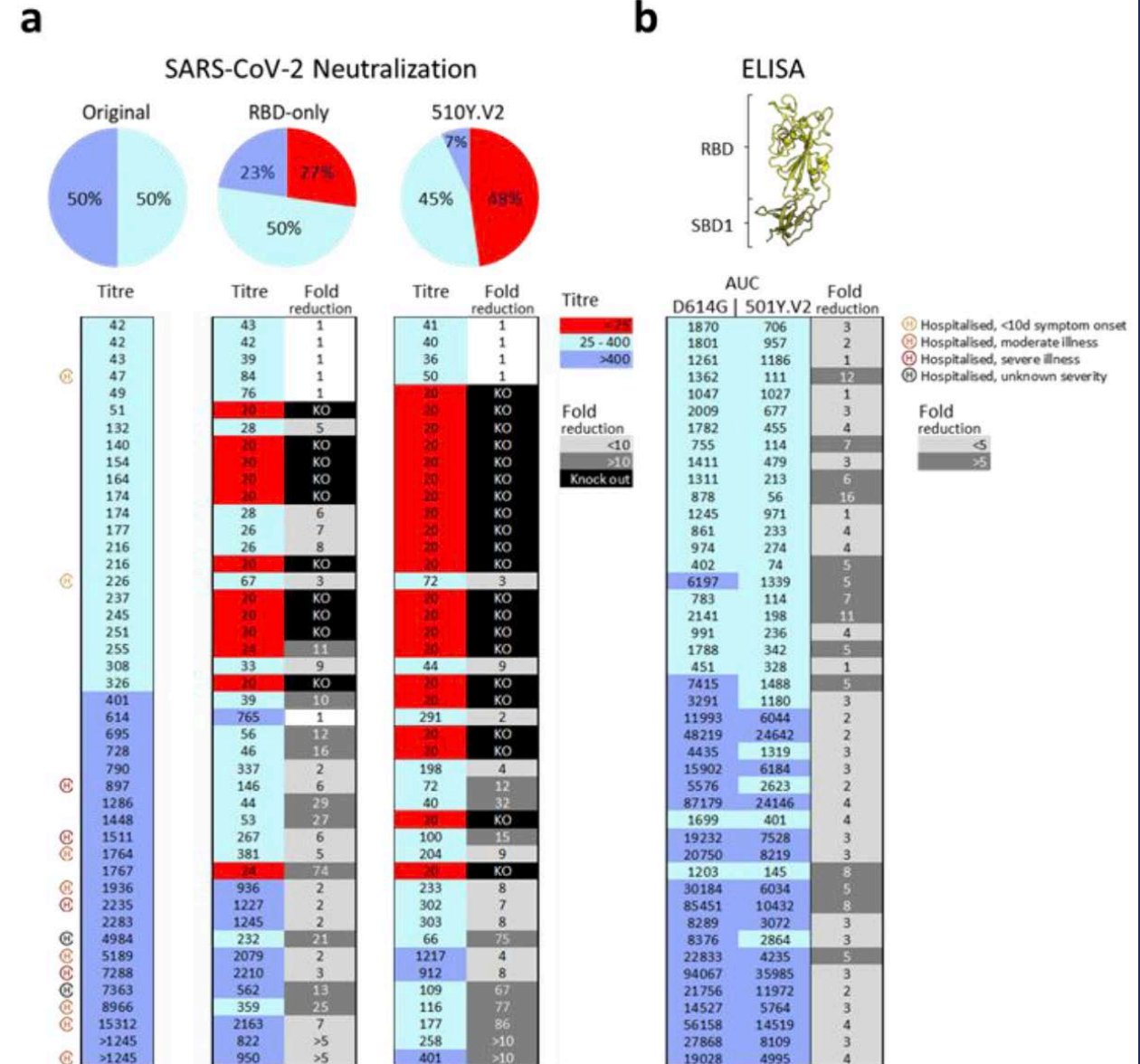
# SARS-CoV-2 501Y.V2

bioRxiv preprint doi: <https://doi.org/10.1101/2021.01.18.427166>; this version posted January 19, 2021. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY-ND 4.0 International license.

## SARS-CoV-2 501Y.V2 escapes neutralization by South African COVID-19 donor plasma

Constantinos Kurt Wibmer<sup>1</sup>, Frances Ayres<sup>1</sup>, Tandile Hermanus<sup>1</sup>, Mashudu Madzivhandila<sup>1</sup>, Prudence Kgagudi<sup>1</sup>, Bronwen E. Lambson<sup>1,2</sup>, Marion Vermeulen<sup>3</sup>, Karin van den Berg<sup>3,4</sup>, Theresa Rossouw<sup>5</sup>, Michael Boswell<sup>6</sup>, Veronica Ueckermann<sup>6</sup>, Susan Meiring<sup>1</sup>, Anne von Gottberg<sup>1,2</sup>, Cheryl Cohen<sup>1,7</sup>, Lynn Morris<sup>1,2</sup>, Jinal N. Bhiman<sup>1,2\*</sup>, Penny L. Moore<sup>1,2\*</sup>

**Fig.2 | SARS-CoV-2 501Y.V2 increased resistance to neutralization by convalescent plasma/serum. a.** Plasma/serum samples collected from SARS-CoV-2 infected individuals who were (n=14) or were not (n=30) hospitalized with COVID-19, ranked by titre against the original SARS-CoV-2 D614G lineage (left pie chart / column 1). Neutralization titre is coloured according to magnitude, where titres greater or lesser than 1:400 are coloured dark or light blue, respectively. Neutralization titre and fold decrease relative to the original lineage are shown for an RBD-only chimeric virus containing the K417N, E484K, and N501Y substitutions (middle pie chart / columns 2 and 3), and the 501Y.V2 lineage virus (right pie chart / column 4 and 5). Neutralization titres <1:25 are coloured red, while a complete knock out of neutralization activity is highlighted in black. **b.** Binding of plasma samples (from Fig.2a) against RBD+SBD1 (shown in yellow and olive cartoon view) from the original virus (column 1) or the 501Y.V2 lineage (column 2) and plotted as area under the curve. The fold reduction in AUC is shown in column 3.



# Moderna Vaccine Neutralizing Antibodies vs UK and South Africa Variants

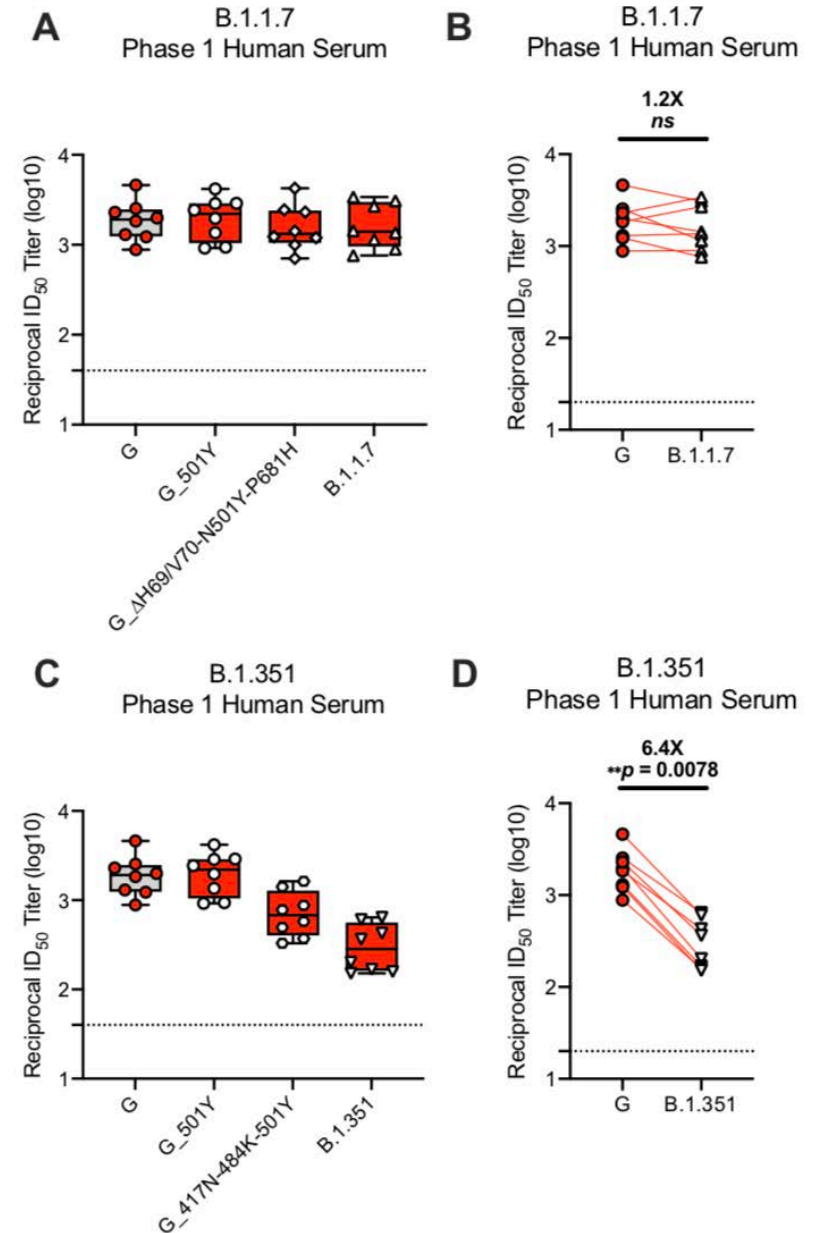
bioRxiv preprint doi: <https://doi.org/10.1101/2021.01.25.427948>; this version posted January 25, 2021. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.

## mRNA-1273 vaccine induces neutralizing antibodies against spike mutants from global SARS-CoV-2 variants

Kai Wu<sup>1\*</sup>, Anne P. Werner<sup>2\*</sup>, Juan I. Moliva<sup>2</sup>, Matthew Koch<sup>1</sup>, Angela Choi<sup>1</sup>, Guillaume B. E. Stewart-Jones<sup>1</sup>, Hamilton Bennett<sup>1</sup>, Seyhan Boyoglu-Barnum<sup>2</sup>, Wei Shi<sup>2</sup>, Barney S. Graham<sup>2</sup>, Andrea Carfi<sup>1#</sup>, Kizzmekia S. Corbett<sup>2#</sup>, Robert A. Seder<sup>2#</sup>, Darin K. Edwards<sup>1#</sup>

<sup>1</sup>Moderna Inc., Cambridge, MA, USA

<sup>2</sup>National Institutes of Health, National Institute of Allergy and Infectious Diseases, Vaccine Research Center, Bethesda, MD, USA



# Pfizer/BioNTech Neutralizing Antibodies vs Variants

Brief Communication | Published: 08 February 2021

## Neutralization of SARS-CoV-2 spike 69/70 deletion, E484K and N501Y variants by BNT162b2 vaccine-elicited sera

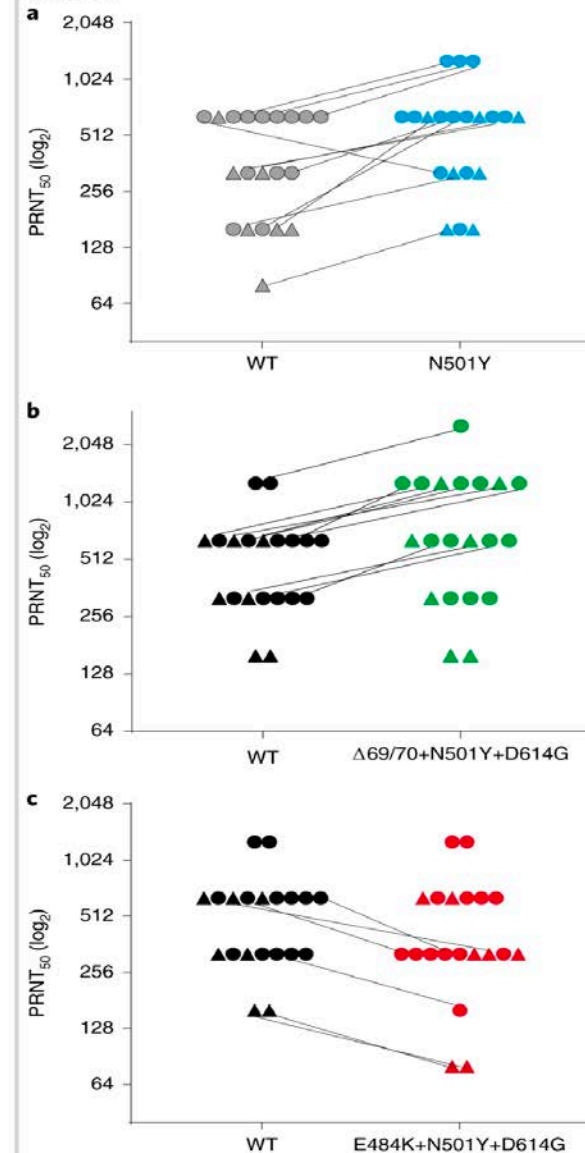
Xuping Xie, Yang Liu, Jianying Liu, Xianwen Zhang, Jing Zou, Camila R. Fontes-Garfias, Hongjie Xia, Kena A. Swanson, Mark Cutler, David Cooper, Vineet D. Menachery, Scott C. Weaver, Philip R. Dormitzer ✉ & Pei-Yong Shi ✉

*Nature Medicine* (2021) | Cite this article

14k Accesses | 2089 Altmetric | Metrics

**a**, WT (USA-WA1/2020) and mutant N501Y. **b**, WT and  $\Delta 69/70 + N501Y + D614G$ . **c**, WT and E484K + N501Y + D614G. Seven (triangles) and 13 (circles) sera were drawn 2 and 4 weeks after the second dose of vaccination, respectively. Sera with different PRNT<sub>50</sub>s against WT and mutant viruses are connected by lines. Results in **a** were from one experiment; results in **b** and **c** were from another set of experiments. Each data point is the average of duplicate assay results.

Fig. 1: PRNT<sub>50</sub>s of 20 BNT162b2-vaccinated human sera against WT and mutant SARS-CoV-2.



# Impact of Pfizer Vaccine on Epidemic

medRxiv preprint doi: <https://doi.org/10.1101/2021.02.08.21251325>; this version posted February 9, 2021. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted medRxiv a license to display the preprint in perpetuity. It is made available under a [CC-BY-NC-ND 4.0 International license](#) .

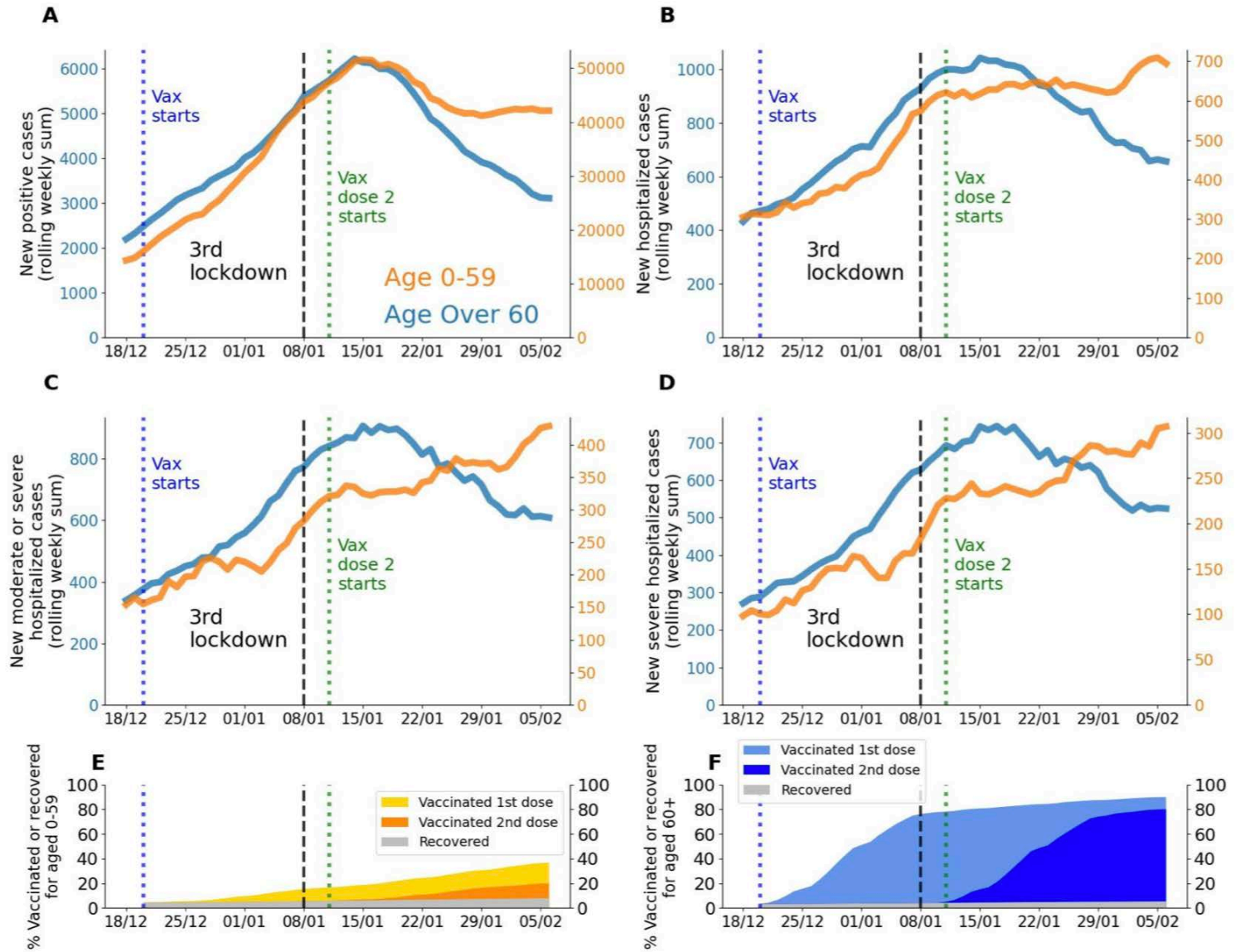
## **Patterns of COVID-19 pandemic dynamics following deployment of a broad national immunization program**

Hagai Rossman<sup>1,2</sup>, Smadar Shilo<sup>1,2,3</sup>, Tomer Meir<sup>1,2</sup>, Malka Gorfine<sup>†4\*</sup>, Uri Shalit<sup>†5\*</sup>, Eran Segal<sup>†1,2\*</sup>

1. Department of Computer Science and Applied Mathematics, Weizmann Institute of Science, Rehovot, Israel
2. Department of Molecular Cell Biology, Weizmann Institute of Science, Rehovot, Israel
3. Pediatric Diabetes Clinic, Institute of Diabetes, Endocrinology and Metabolism, Rambam Health Care Campus, Haifa, Israel.
4. Department of Statistics and Operations Research, Tel Aviv University, Ramat Aviv, Israel
5. Technion - Israel Institute of Technology, Haifa, Israel

# Pfizer/BioNTech Efficacy in Israel

B.1.1.7 variant was >40% of Israel SARS-CoV-2 isolates as of Jan 20th



## Novavax Clinical Trial Results Against Variants

➤ **UK Phase 3 and South Africa Phase 2b-- >20,000 subjects**

➤ **UK: > 15,000 subjects; B117 was >50% of viruses**

- Overall efficacy 89%
- Subgroup: efficacy 95.6% vs wild-type strain; 85.2% vs B117

➤ **South Africa: 4,400 enrollees overall; *93% of infections due to South African variant (B.1.351)***

- Overall efficacy 49.4%
- Subgroup analysis: 60% efficacy in HIV neg

## Johnson and Johnson vs South Africa Variant

➔ **The vaccine's efficacy dropped from 72% in the United States to 57% in South Africa, where B.1.351 comprised most cases**

- **15% (N=6,576) enrolled in South Africa**

➔ **Vaccine was 85% effective in preventing severe disease in all three regions where the trial was run: the United States, Latin America, and South Africa. After 28 days, none of the vaccinated participants who developed Covid-19 had to be hospitalized**

<https://www.nytimes.com/2021/01/29/health/covid-vaccine-johnson-and-johnson-variants.html>

<https://www.jnj.com/johnson-johnson-announces-single-shot-janssen-covid-19-vaccine-candidate-met-primary-endpoints-in-interim-analysis-of-its-phase-3-ensemble-trial>

## AstraZeneca/Oxford Vaccine vs South African Variant

### ➔ 7 Feb News – AstraZeneca/Oxford Vaccine Ineffective against South African variant

- New data involving over 1,700 participants showed it has only 22% efficacy against the new [coronavirus](#) variant B.1.351, also known as 501Y.V2, currently dominant in the country
- This is a significant drop from the 75% reported efficacy of the vaccine in reducing mild to moderate COVID-19 before B.1.351 became the dominant variant in South Africa

## Effect on Monoclonal Antibody Therapeutics

➔ Significant reduction in neutralizing antibodies from mutations associated with South African and Brazil variants (particularly E484K mutation in spike protein) raises serious concern about efficacy of monoclonal antibody therapeutics



# The Coming Storm

## Genomic epidemiology identifies emergence and rapid transmission of SARS-CoV-2 B.1.1.7 in the United States

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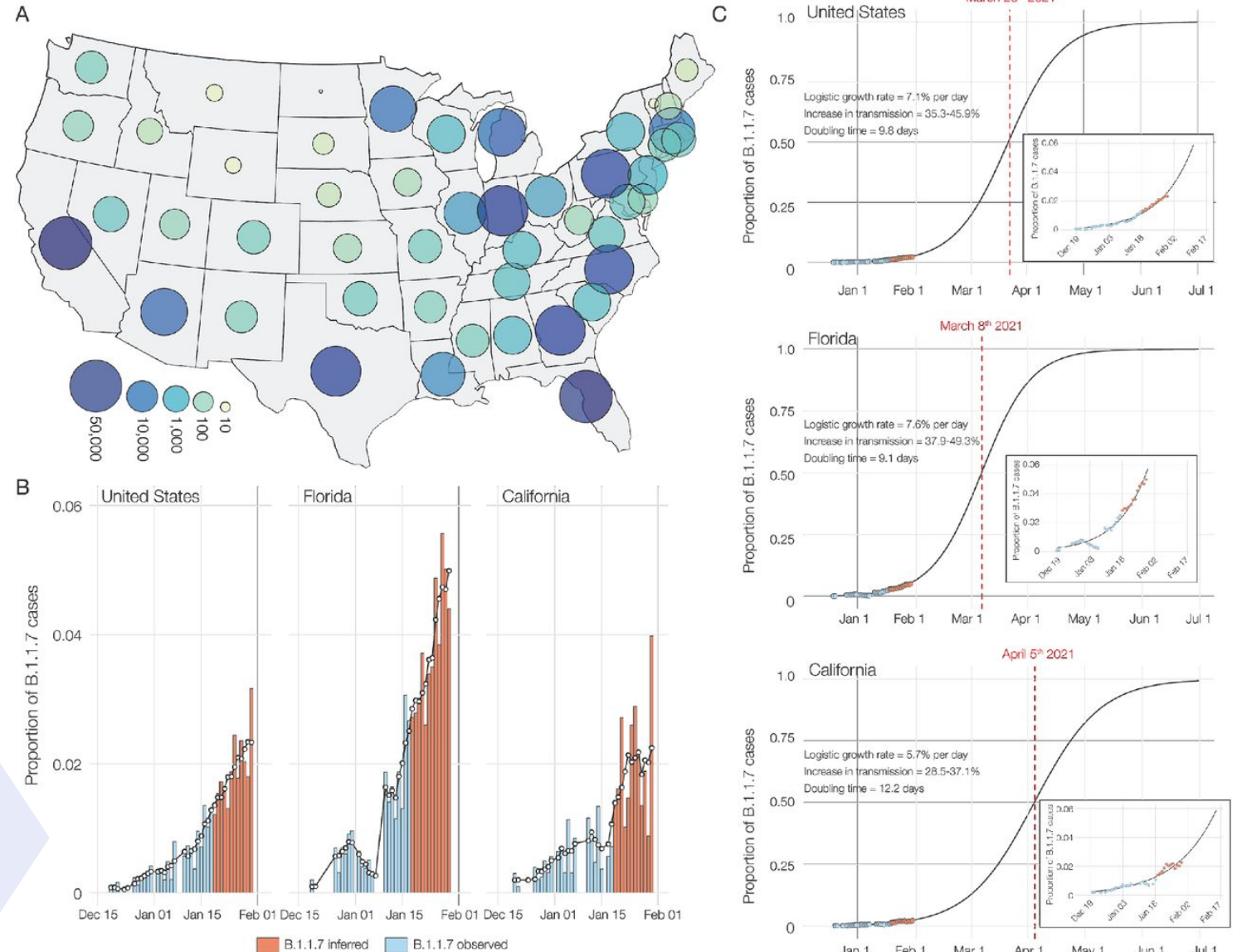
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Figure 1.

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SGTF and B.1.1.7 in SARS-CoV-2 tests at Helix since December 15, 2020.

(A) Map of contiguous states in the USA with each bubble representing the number of positive tests from each state. (B) Estimated proportion of B.1.1.7 in total number of positive tests with Cq(N gene) < 27, in the U.S., California and Florida from December 15th, 2020 to January 30th, 2021. The proportion of B.1.1.7 samples was estimated using: (Observed B.1.1.7 sequences/Sequenced SGTF samples) \* (Positive tests with SGTF/Total positive tests). Due to the lag in sequencing, the average proportion of B.1.1.7 sequences in sequenced samples with SGTF from the last five days (January 13-18) was used to infer the proportion of B.1.1.7 cases in total positive tests for the January 19-30 time period between. The black line shows the 5-day rolling average of the estimated proportion of B.1.1.7 in total positives. (C) Logistic growth curves fit to the rolling average of the estimated proportion of B.1.1.7 in total positives for the U.S., Florida and California. The predicted time when the estimated proportion of B.1.1.7 cases crosses 0.5 is indicated in red.



# Questions and Answers



A person wearing full personal protective equipment (PPE) including a face shield, a surgical mask, and blue gloves, standing in a clinical or hospital setting. The background is a light blue wall with a door and some equipment.

# **NETEC Resources**

**Radu Postelnicu, MD**



## New York Times New Variants Tracker

[Click here to access The New York Times New Variants Tracker](#)

## NETEC is Here to Help

**NETEC** will continue to build resources, develop online education, and deliver technical training to meet the needs of our partners

### Ask for help!

- Send questions to [info@netec.org](mailto:info@netec.org) - they will be answered by NETEC SMEs
- Submit a Technical Assistance request at [NETEC.org](https://www.netec.org)

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