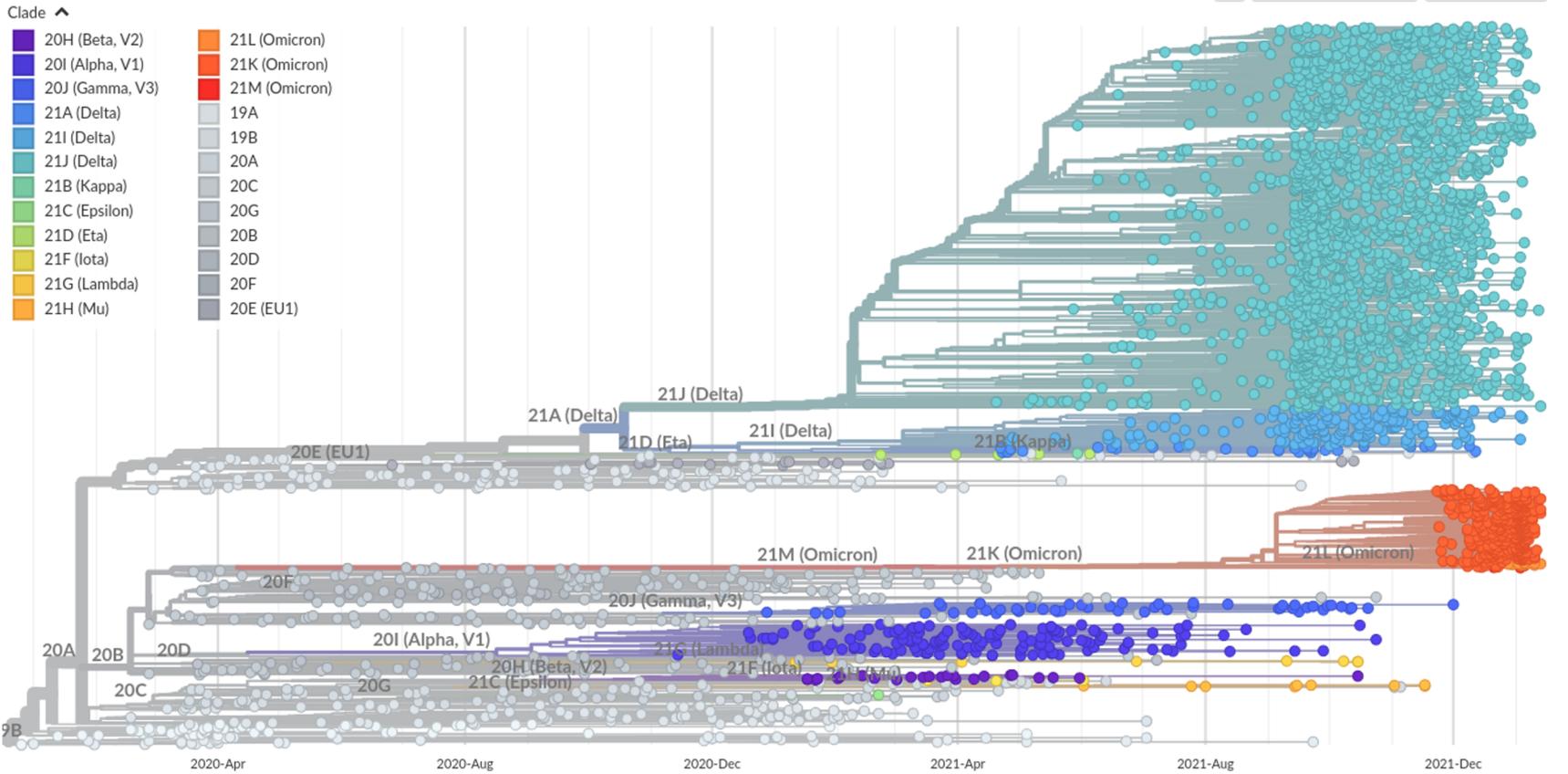


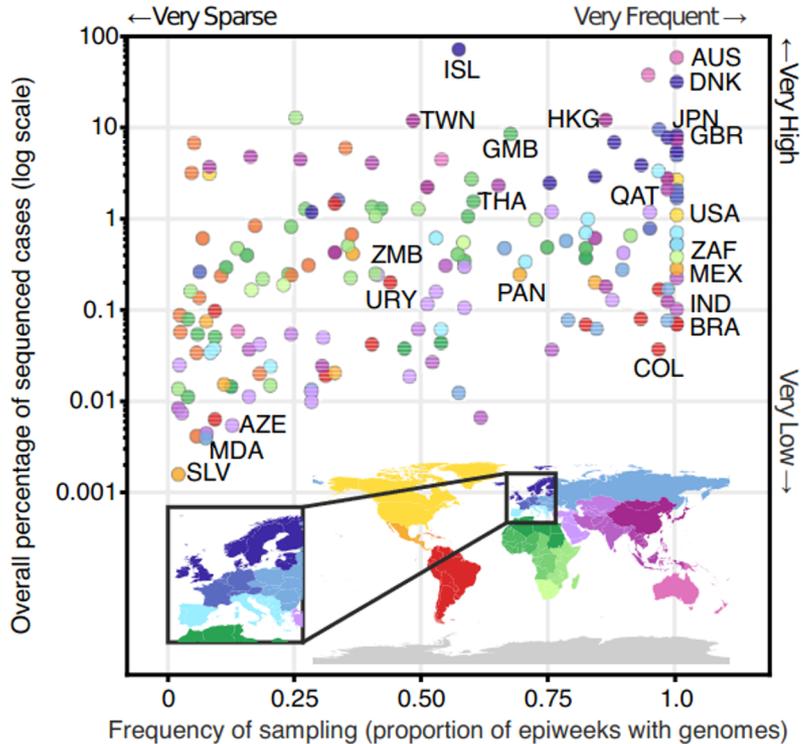
Wastewater sequencing (+Freyja) uncovers  
early, cryptic SARS-CoV-2 variant spread

February 28, 2022

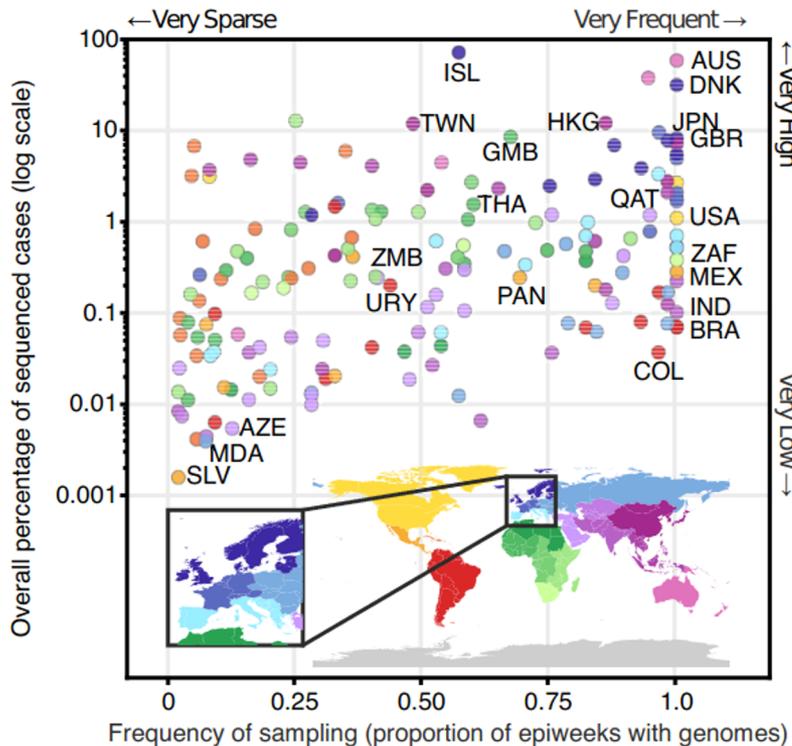
# SARS-CoV-2 continues to evolve



# Clinical sampling blind spots

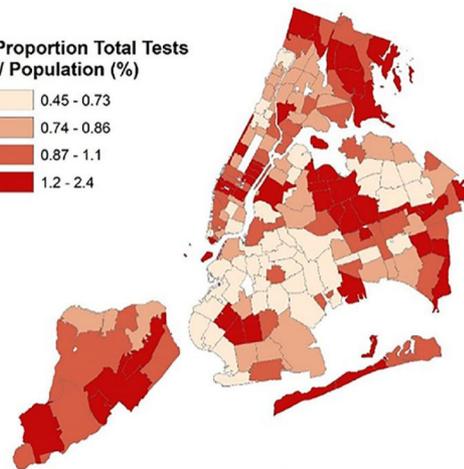
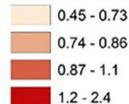


# Clinical sampling blind spots

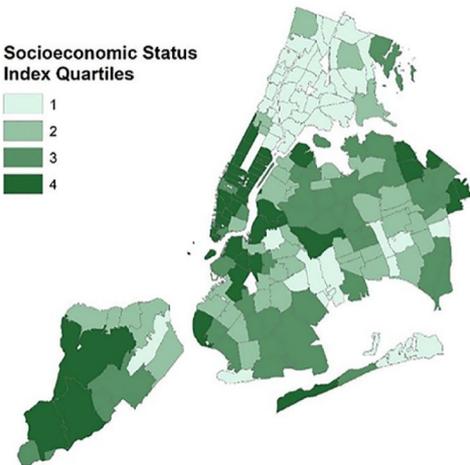
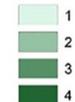


Brito, Semenova, Dudas et al., 2021

Proportion Total Tests / Population (%)

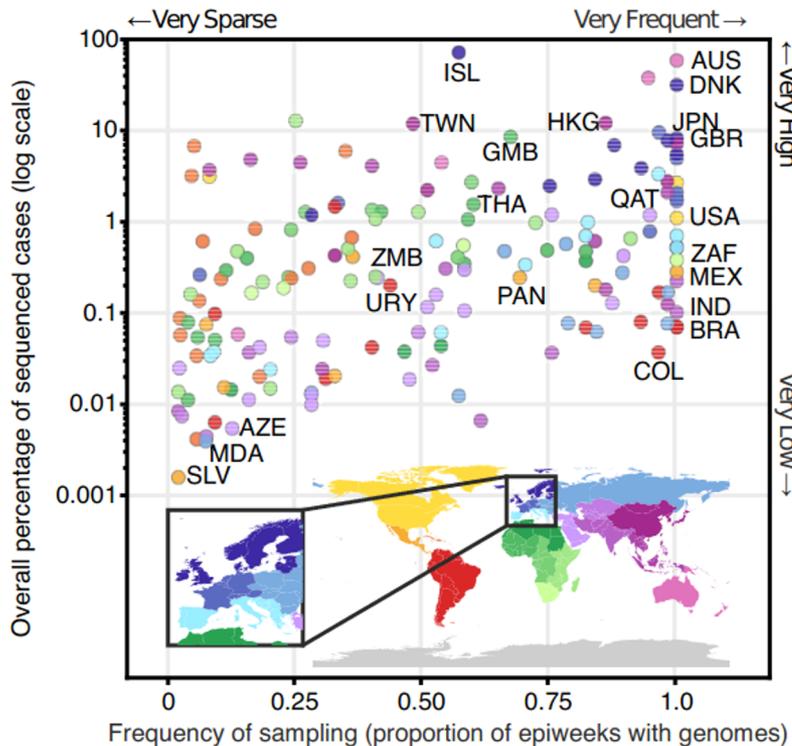


Socioeconomic Status Index Quartiles



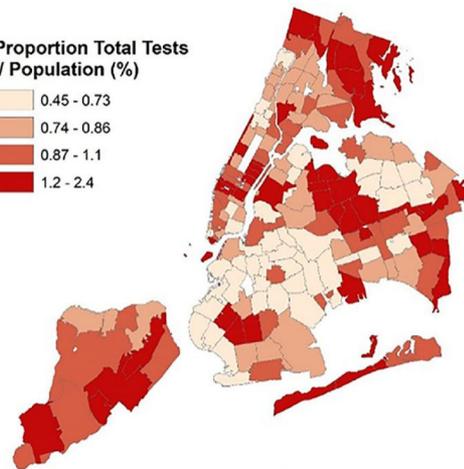
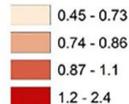
Lieberman-Cribbin et al., 2020

# Clinical sampling blind spots

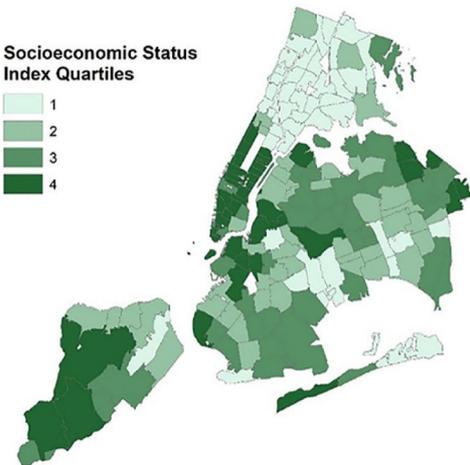
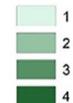


Brito, Semenova, Dudas et al., 2021

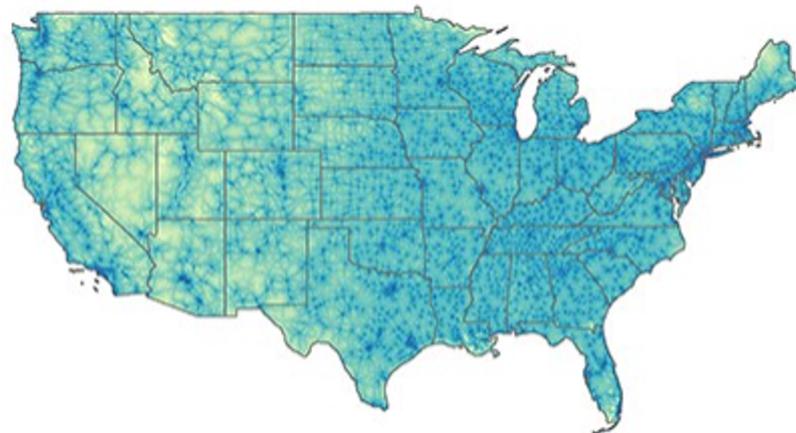
Proportion Total Tests / Population (%)



Socioeconomic Status Index Quartiles



Lieberman-Cribbin et al., 2020

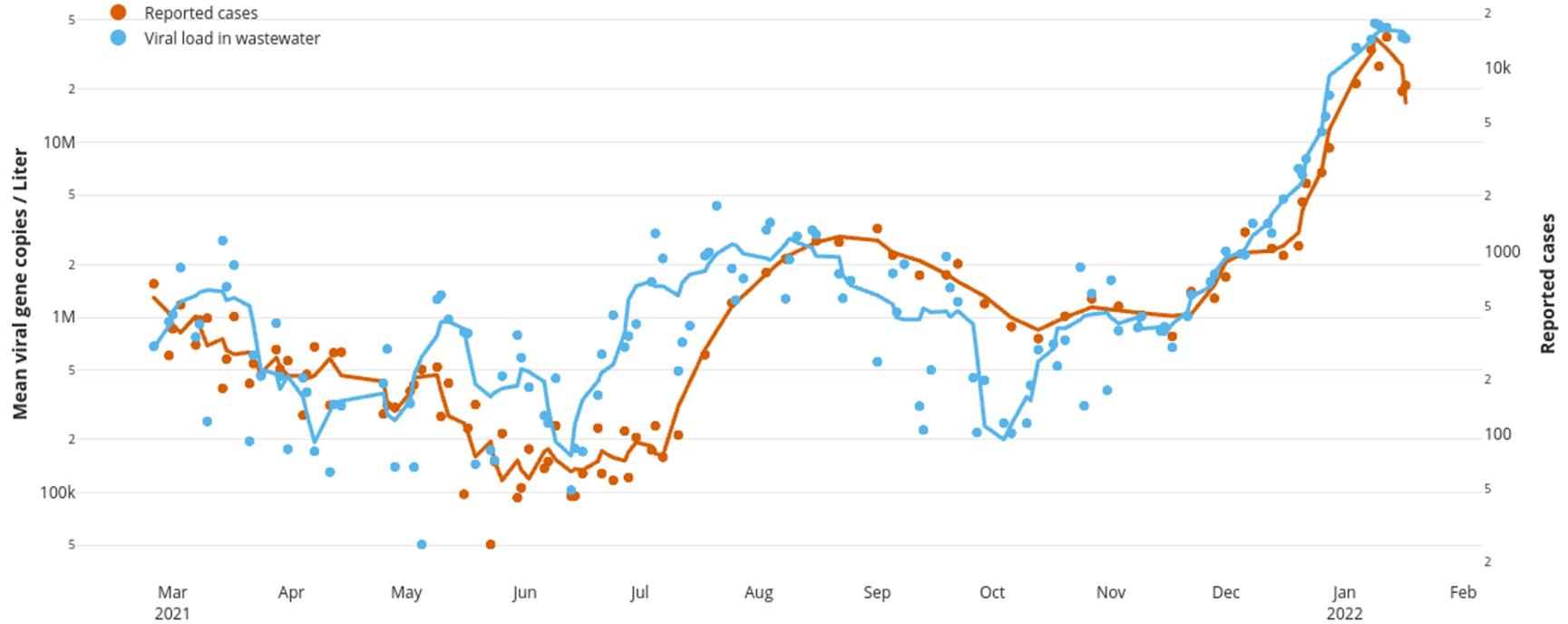


Minutes to Testing Site

2 20 60 120 360

Rader, Astley et al., 2020

# Wastewater surveillance is a promising alternative



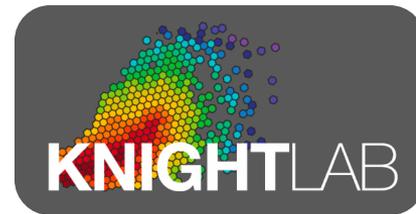
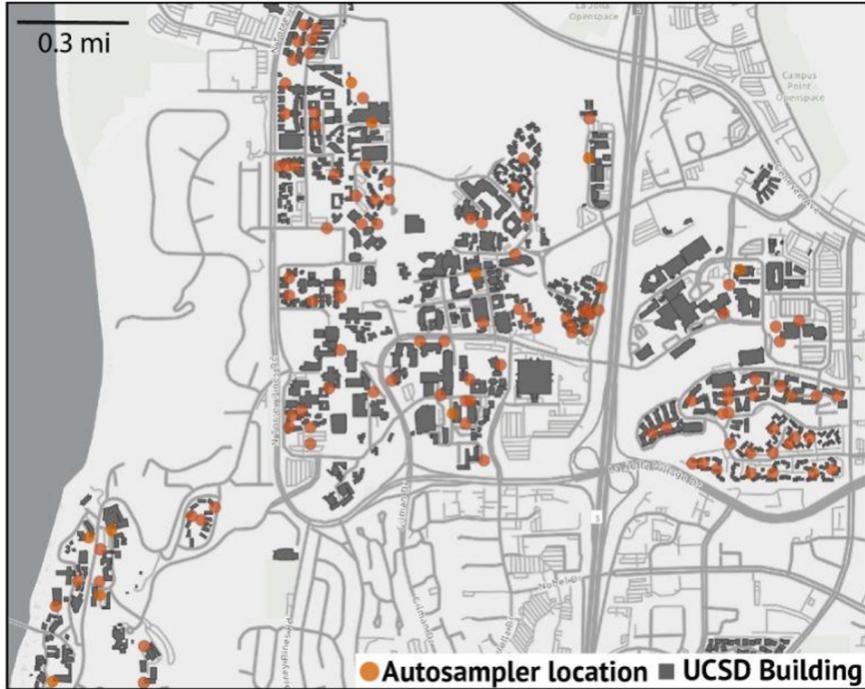


Image credit: Erik Jepsen, Caroline Sheikhzadeh, UCSD

## UCSD Campus



### Sampler Types

**Residential: 72**

**Isolation dorms: 4**

**Non-residential: 58**

Fall 2021: 18,000 residents in campus housing

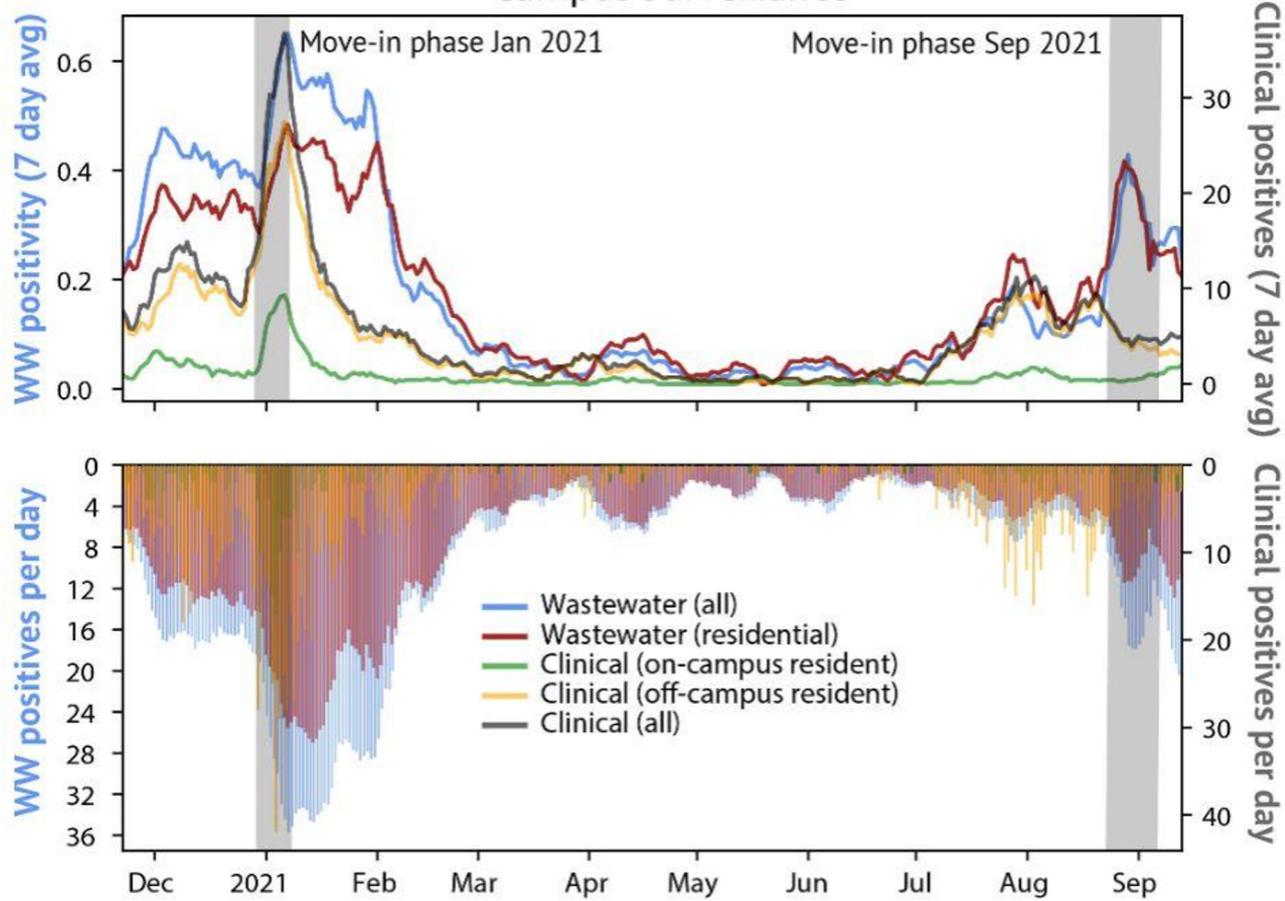
## Point Loma



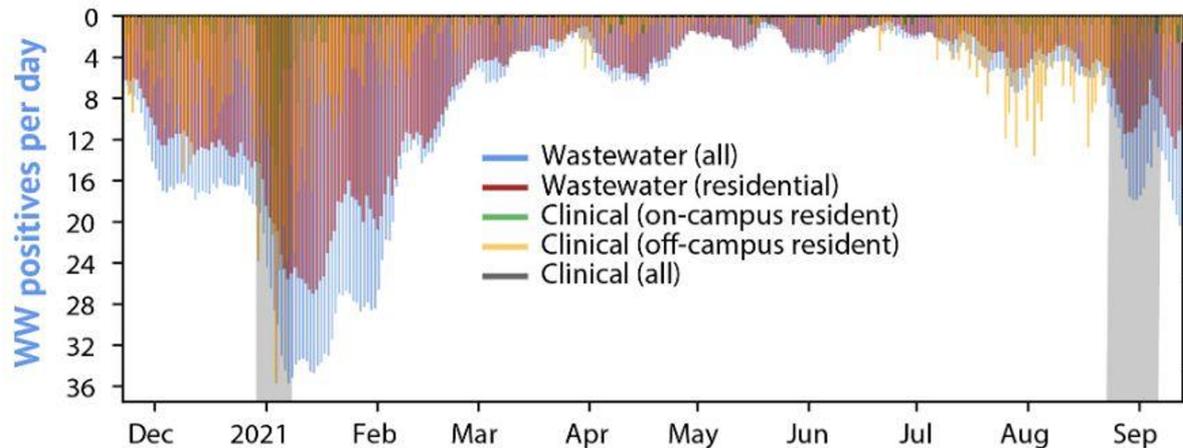
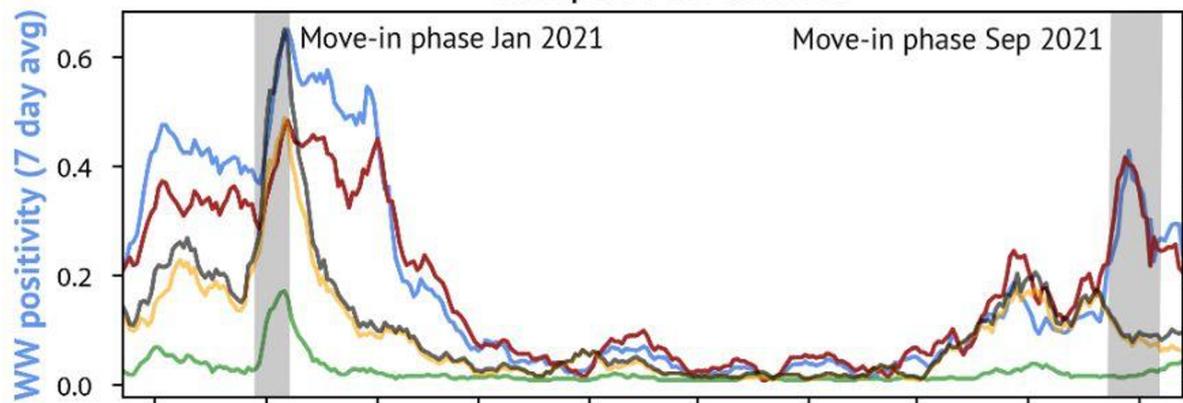
Primary wastewater treatment plant serving the greater SD area

Serves ~2.3 million residents

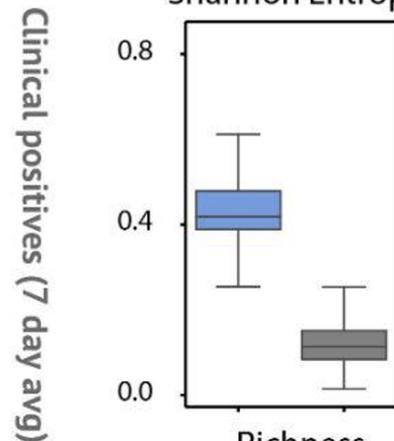
# Campus Surveillance



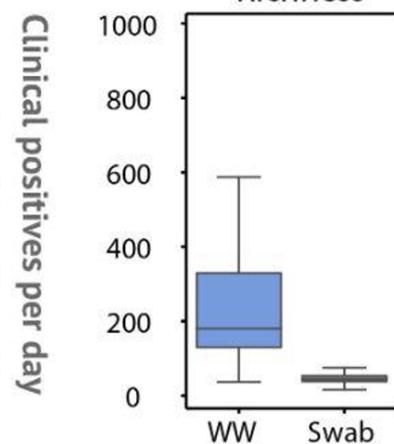
# Campus Surveillance



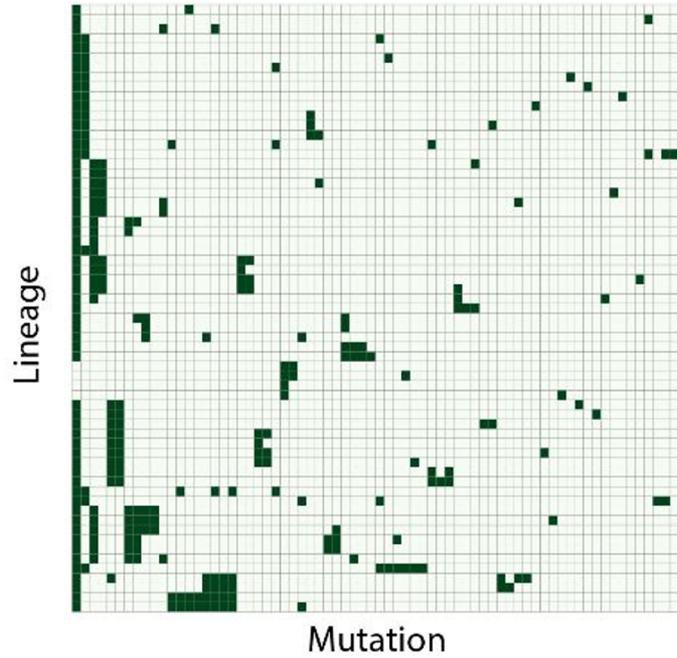
# Shannon Entropy



# Richness

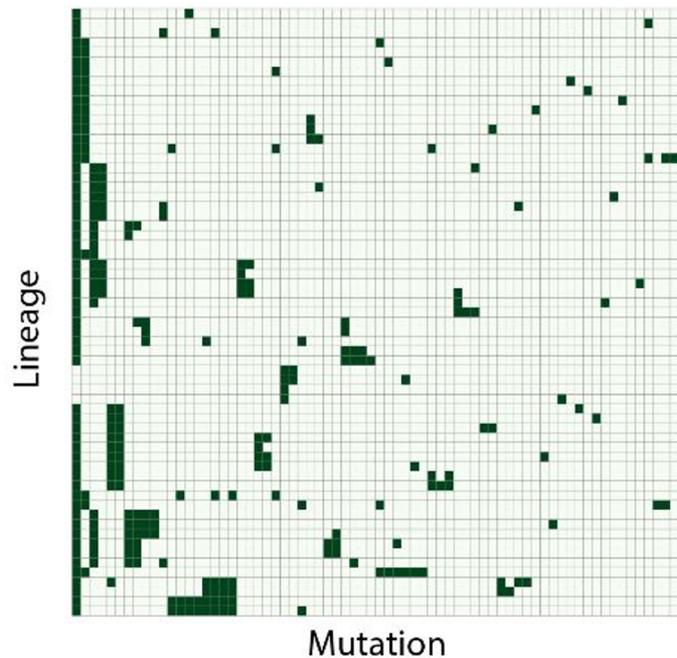


## Lineage Barcoding

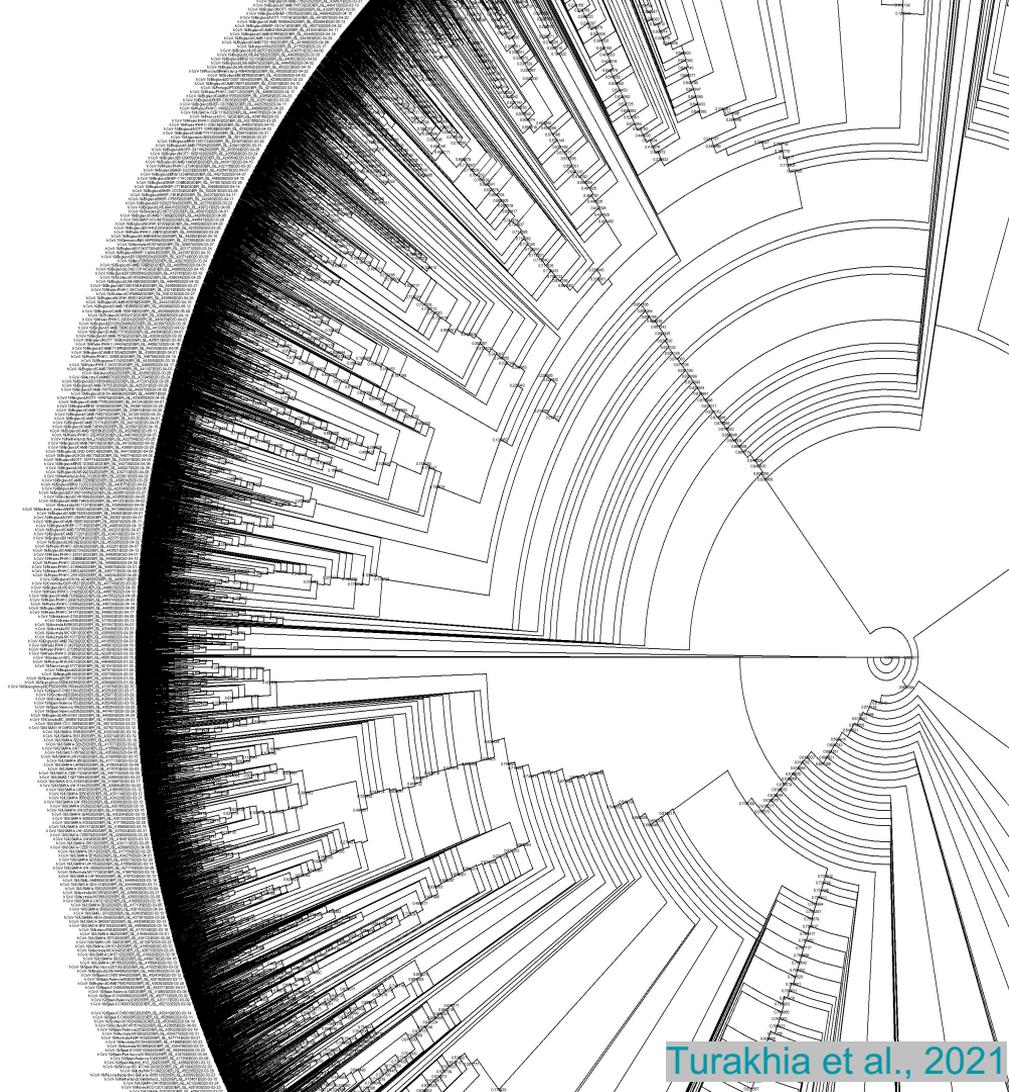


>1200 SARS-CoV-2 lineages

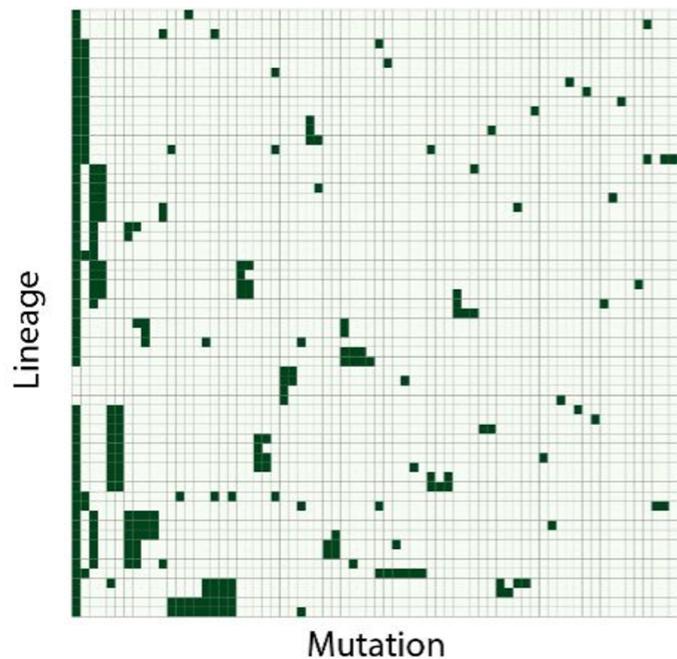
## Lineage Barcoding



>1200 SARS-CoV-2 lineages

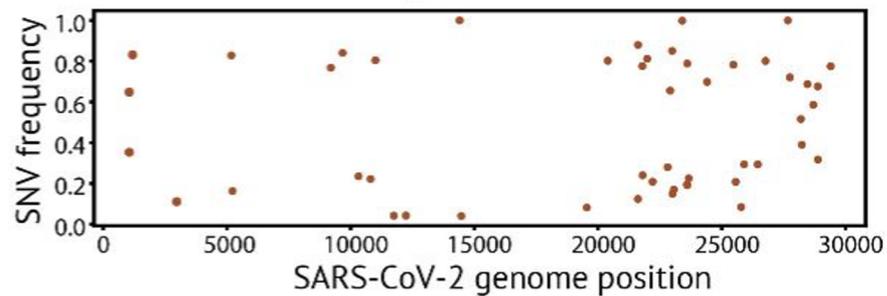


## Lineage Barcoding

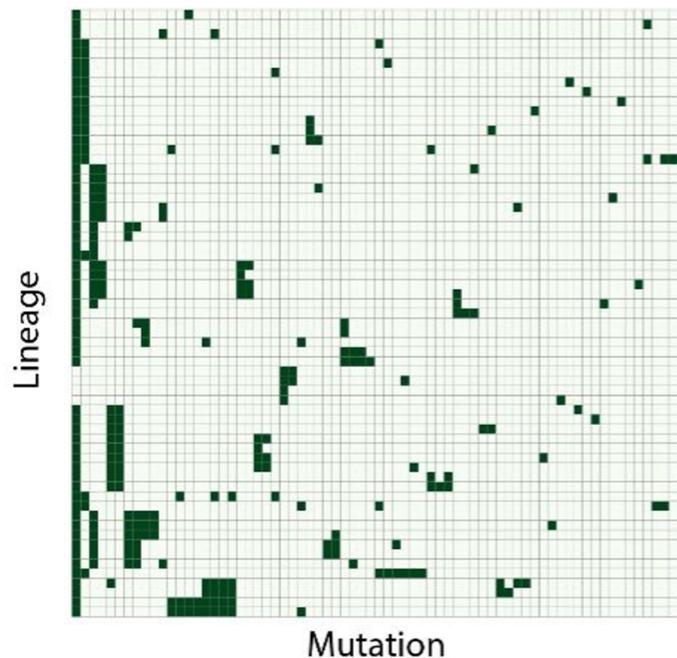


>1200 SARS-CoV-2 lineages

## Detection of Single Nucleotide Variants

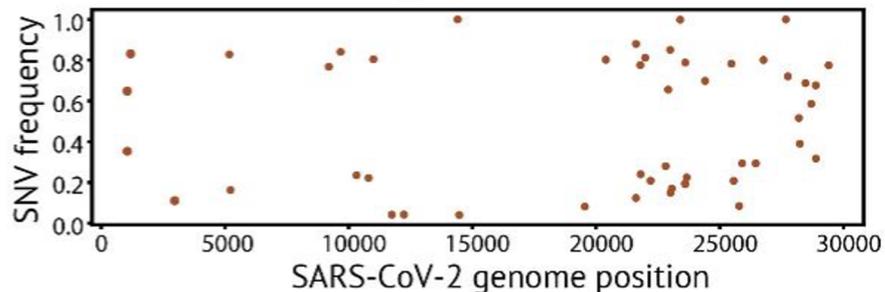


## Lineage Barcoding



>1200 SARS-CoV-2 lineages

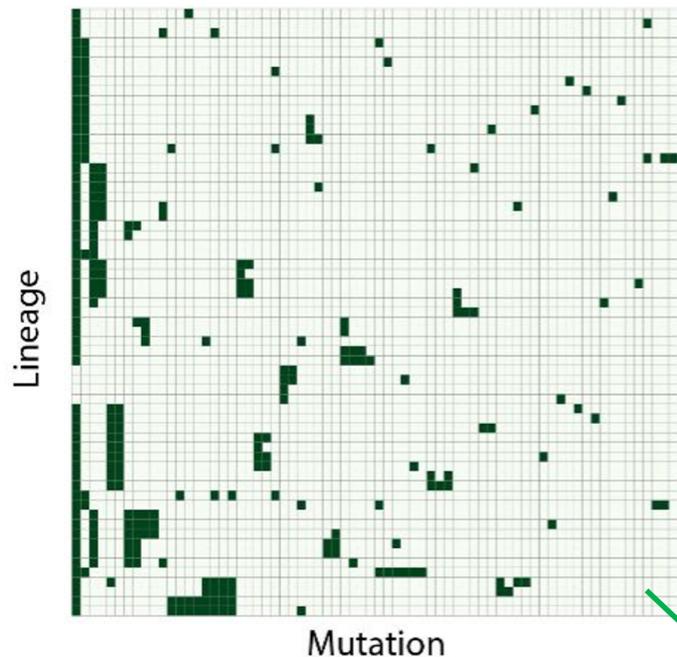
## Detection of Single Nucleotide Variants



## Depth-weighted de-mixing

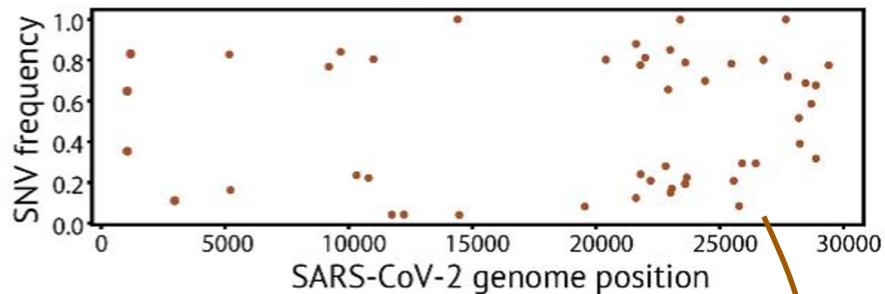
$$\hat{x} = \underset{\substack{x \geq 0 \\ \sum x = 1}}{\operatorname{argmin}} \|A^T x - b\|_{1W}$$

## Lineage Barcoding



>1200 SARS-CoV-2 lineages

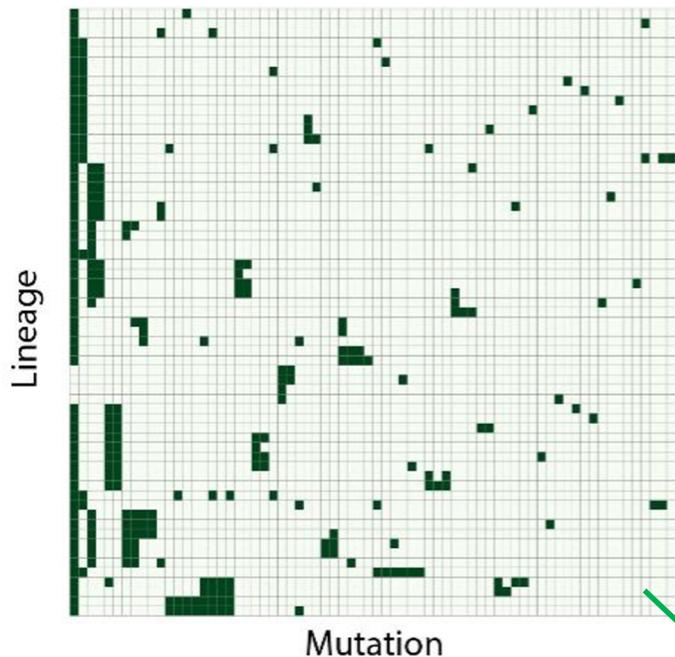
## Detection of Single Nucleotide Variants



Depth-weighted de-mixing

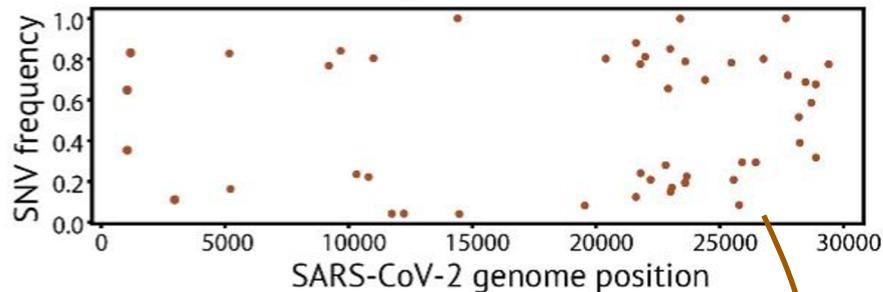
$$\hat{x} = \underset{\substack{x \geq 0 \\ \sum x = 1}}{\operatorname{argmin}} \|A^T x - b\|_{1W}$$

## Lineage Barcoding



>1200 SARS-CoV-2 lineages

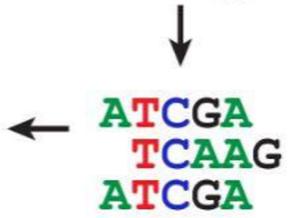
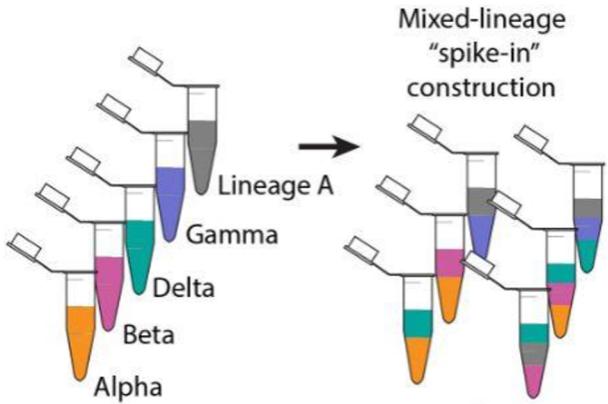
## Detection of Single Nucleotide Variants



Depth-weighted de-mixing

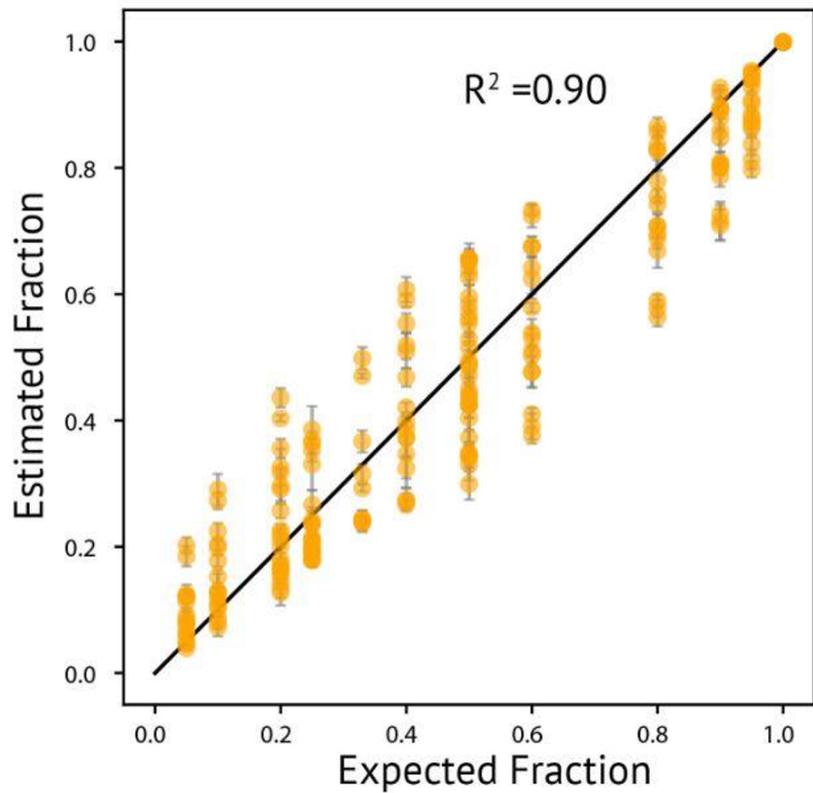
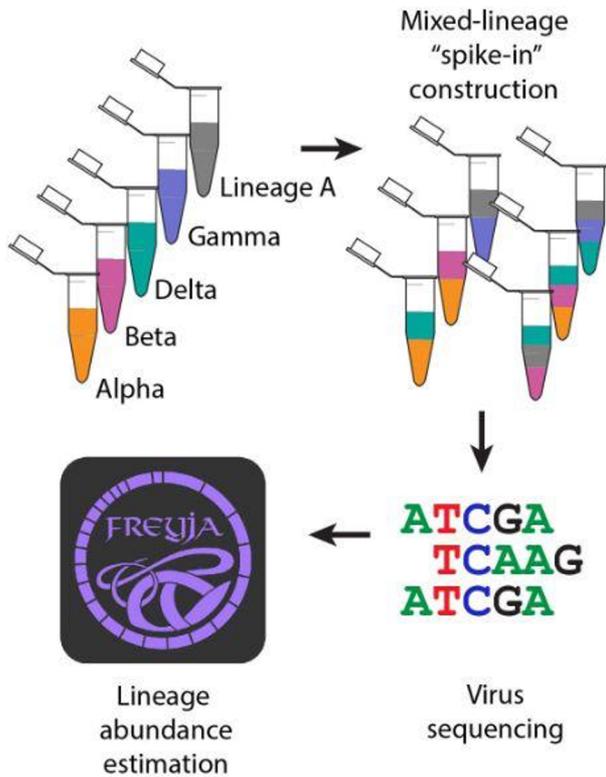
$$\hat{x} = \underset{\substack{x \geq 0 \\ \sum x = 1}}{\operatorname{argmin}} \|A^T x - b\|_{1W}$$

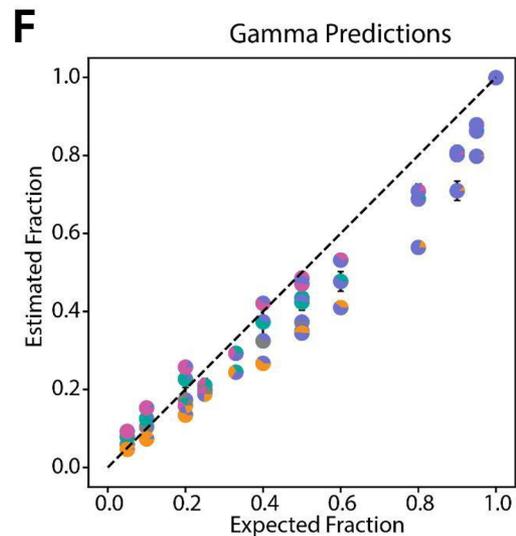
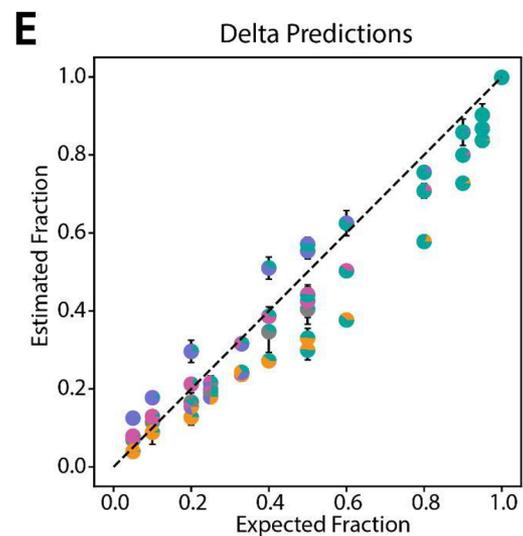
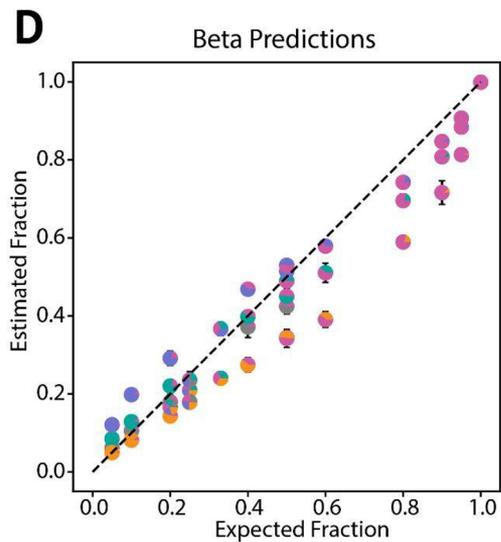
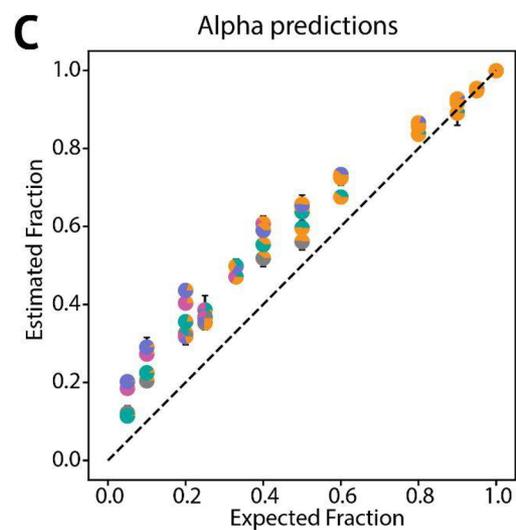
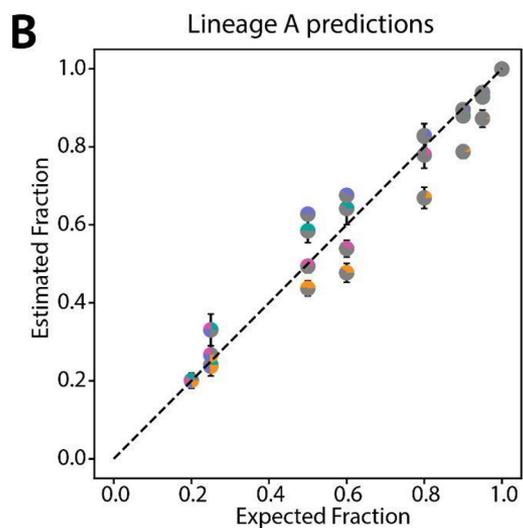
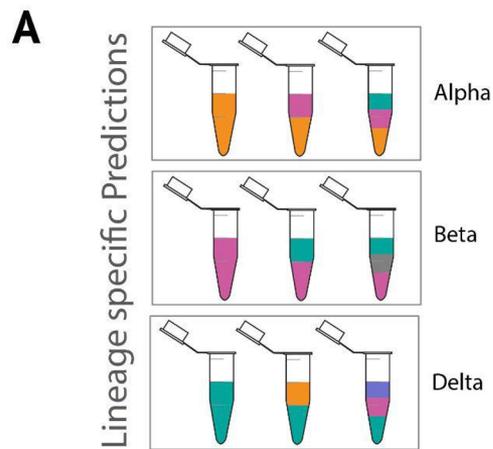




Lineage  
abundance  
estimation

Virus  
sequencing

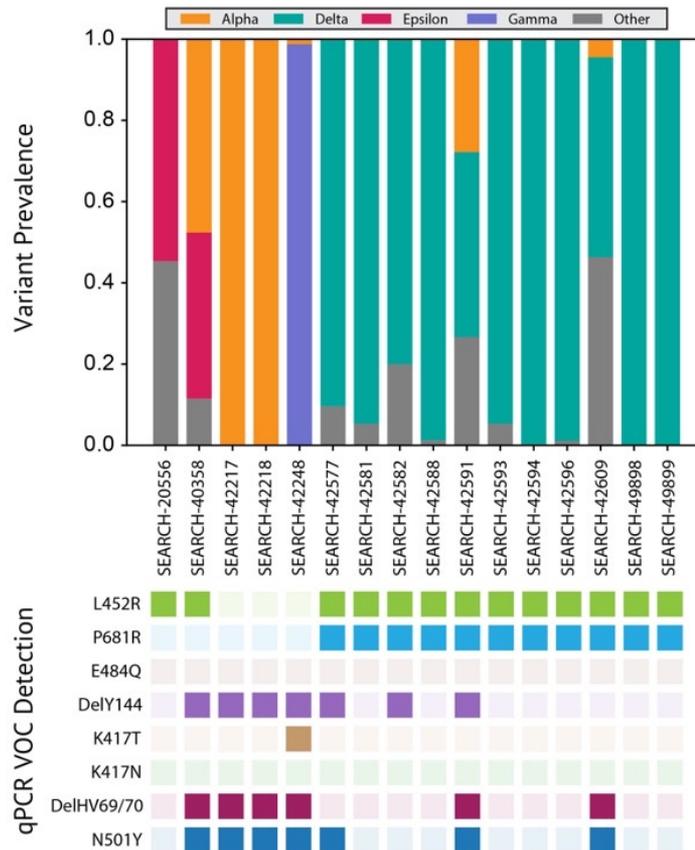




Does this work on wastewater?

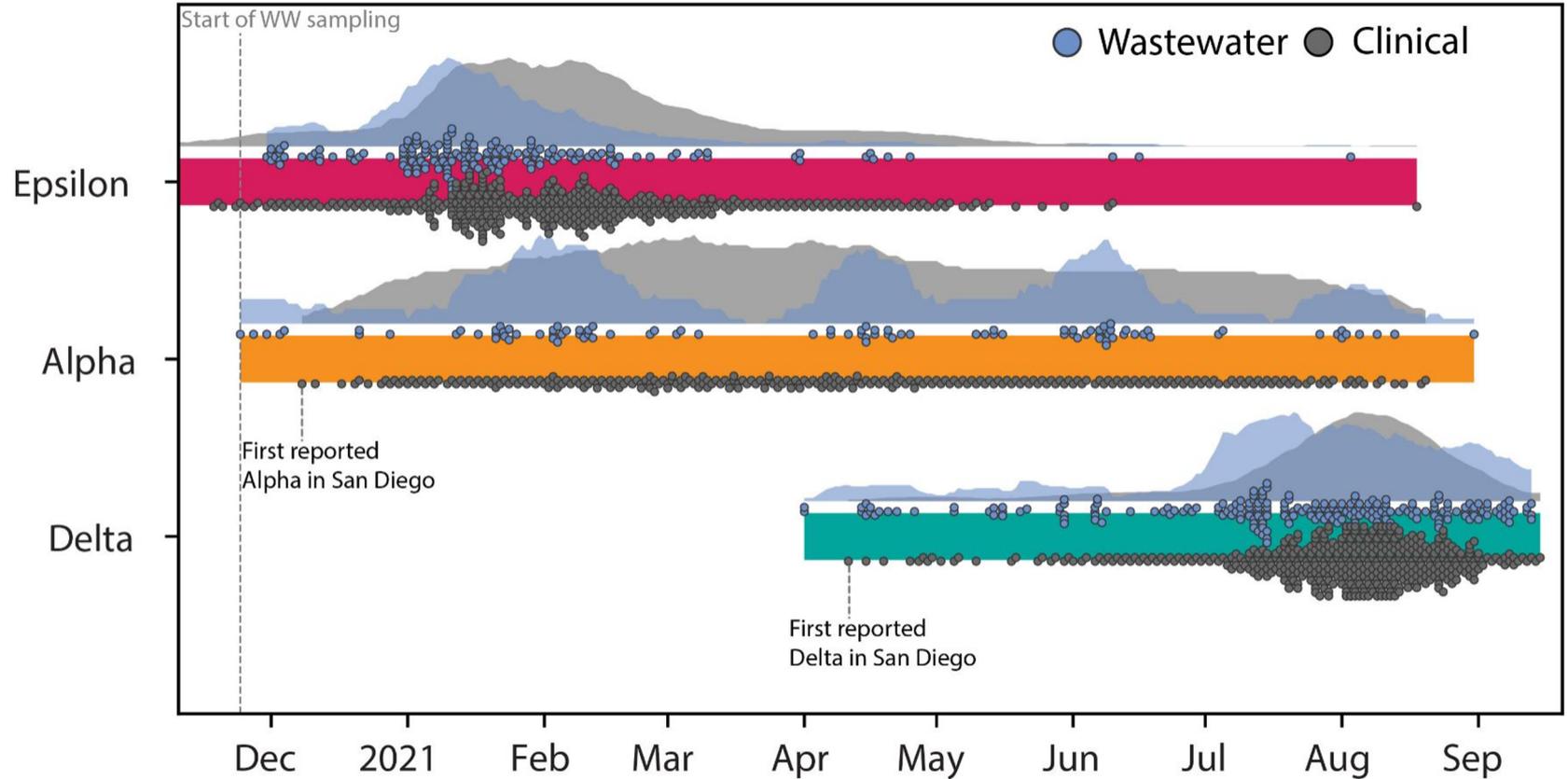


# Does this work on wastewater?

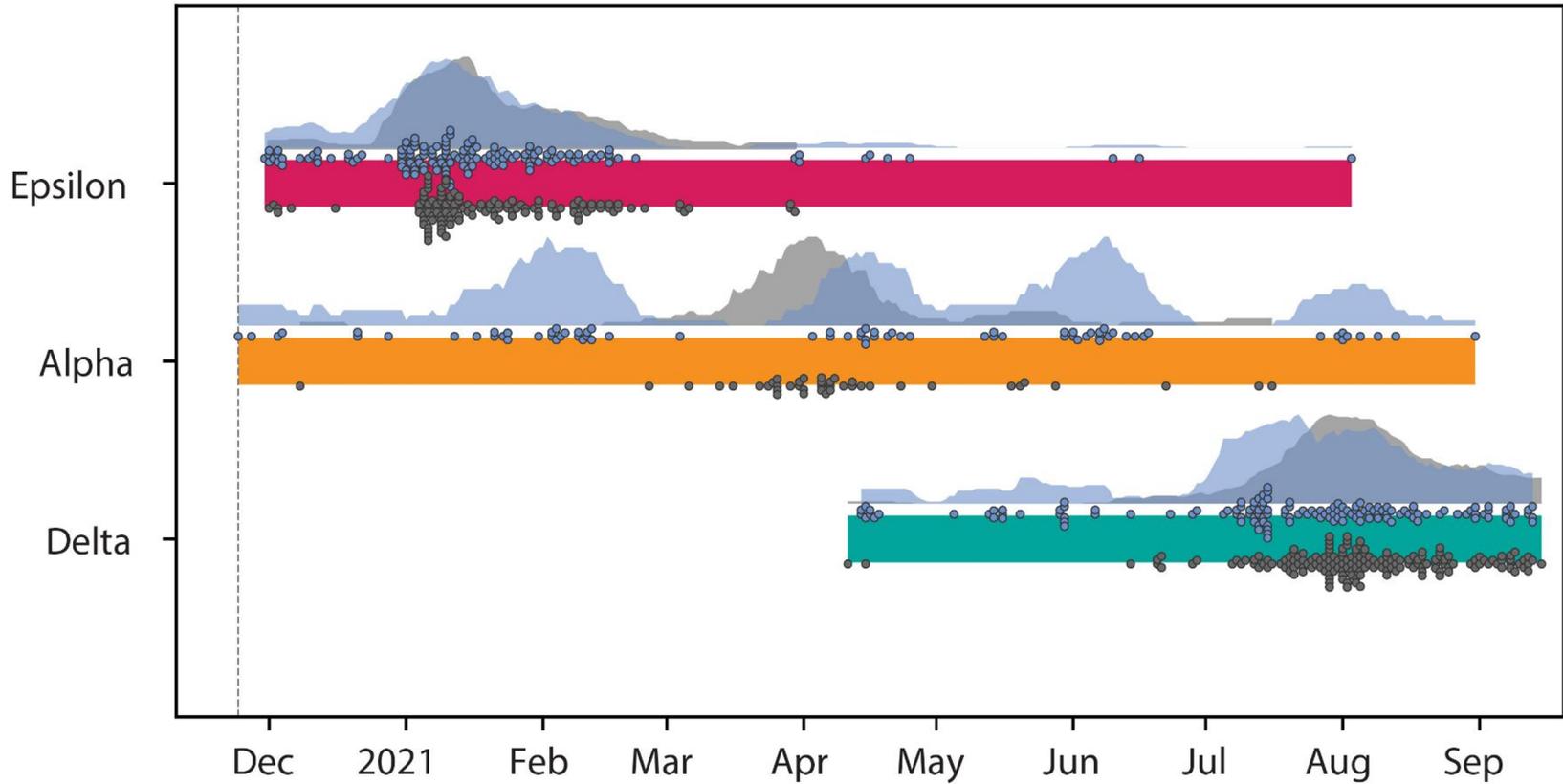


Mutation	Variants	Mutation	Variants
L452R	Delta, Epsilon, Kappa	K417T	Gamma
P681R	Delta, Kappa	K417N	Beta
E484Q	Kappa	DelHV69/70	Alpha
DelY144	Alpha	N501Y	Alpha, Beta, Gamma

# San Diego County Surveillance

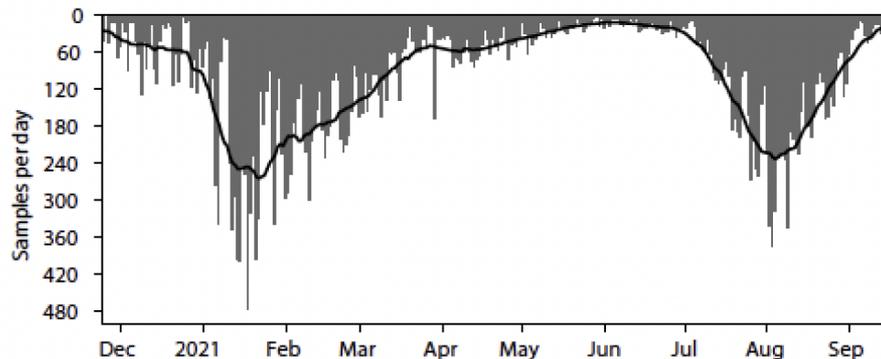
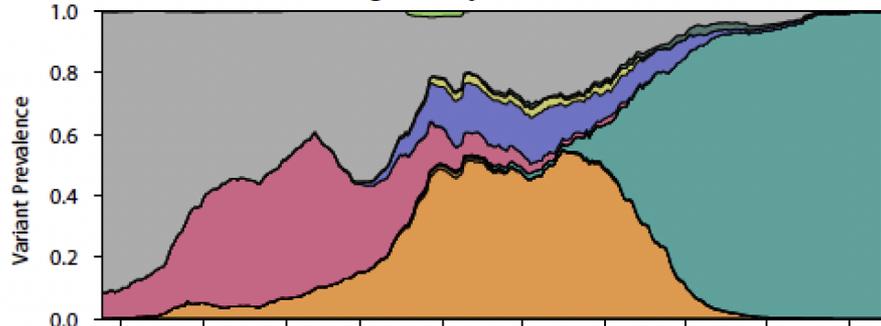


# UCSD Campus Surveillance

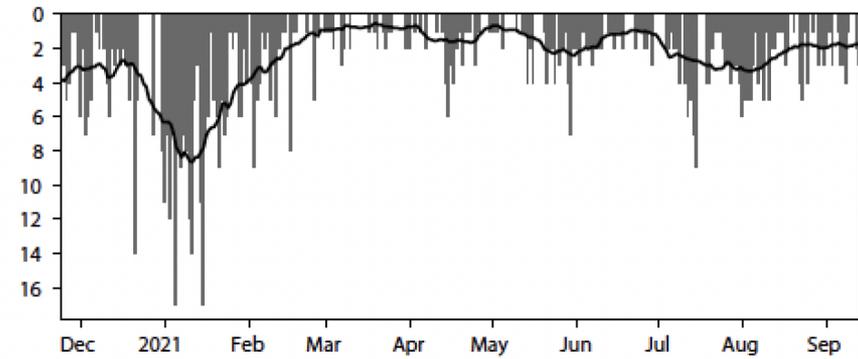
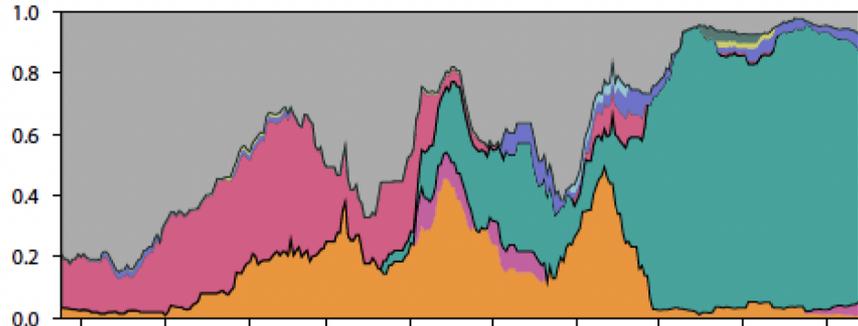


■ Alpha 
 ■ B.1.1.318-like 
 ■ B.1.617.1-like 
 ■ Beta 
 ■ Delta 
 ■ Epsilon 
 ■ Gamma 
 ■ Iota 
 ■ Mu 
 ■ Other 
 ■ Zeta 
 ■ B.1.1.7-like+E484K 
 ■ Lambda 
 ■ Theta 
 ■ Eta

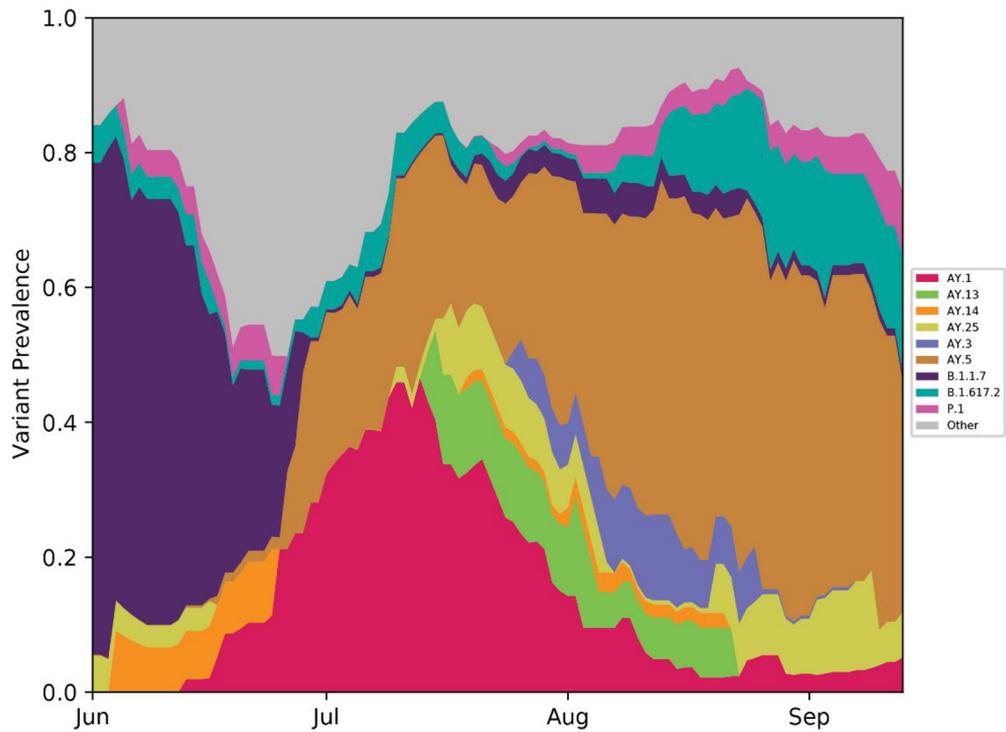
San Diego County clinical surveillance



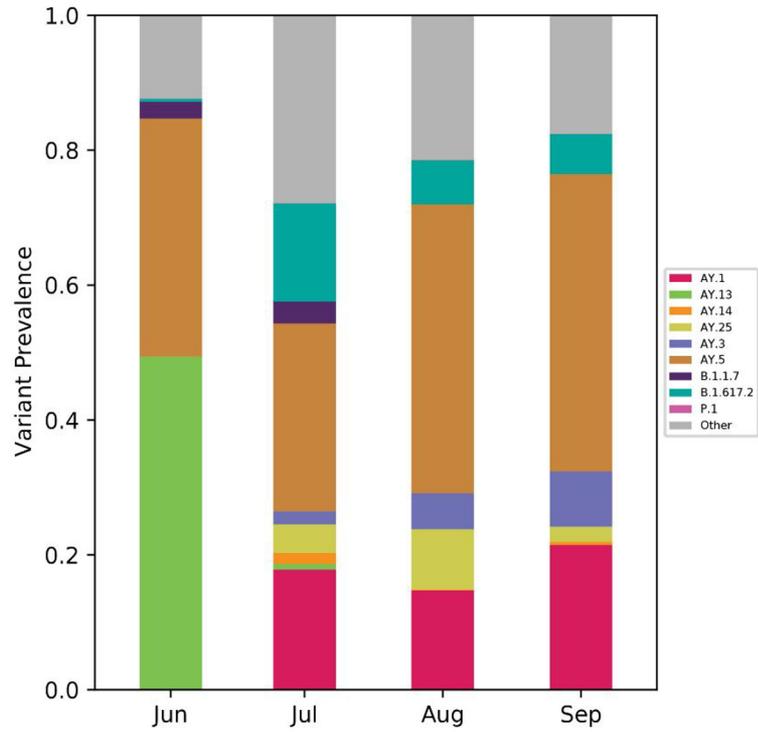
Campus and San Diego County wastewater surveillance



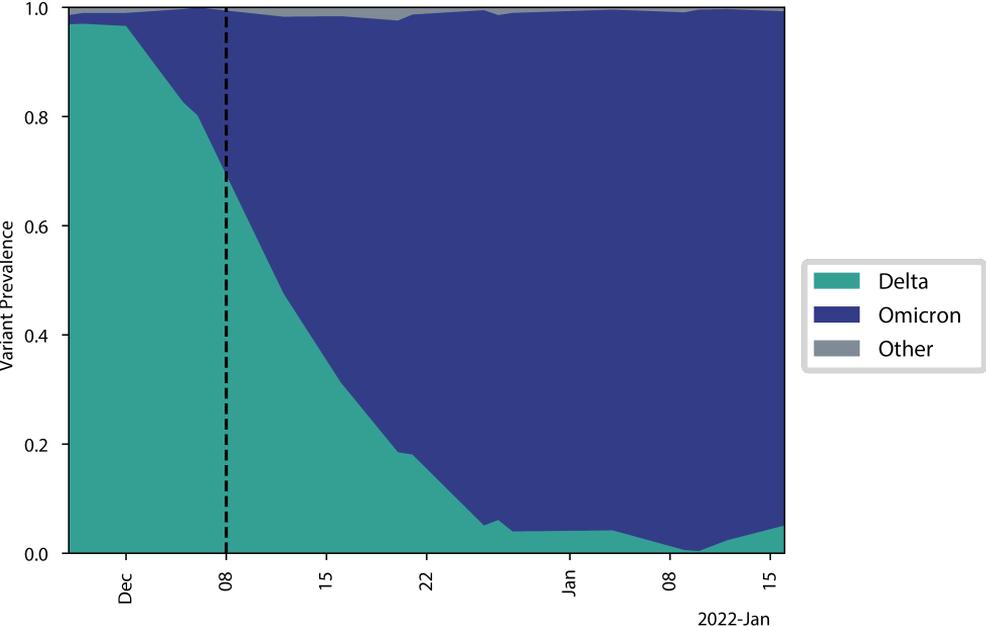
## RTL (Campus)



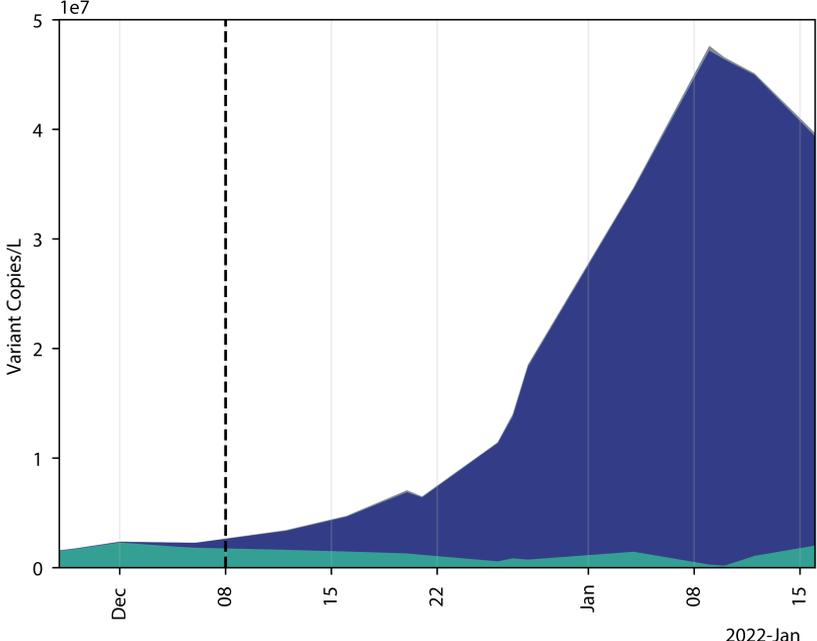
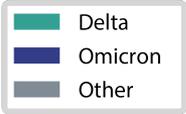
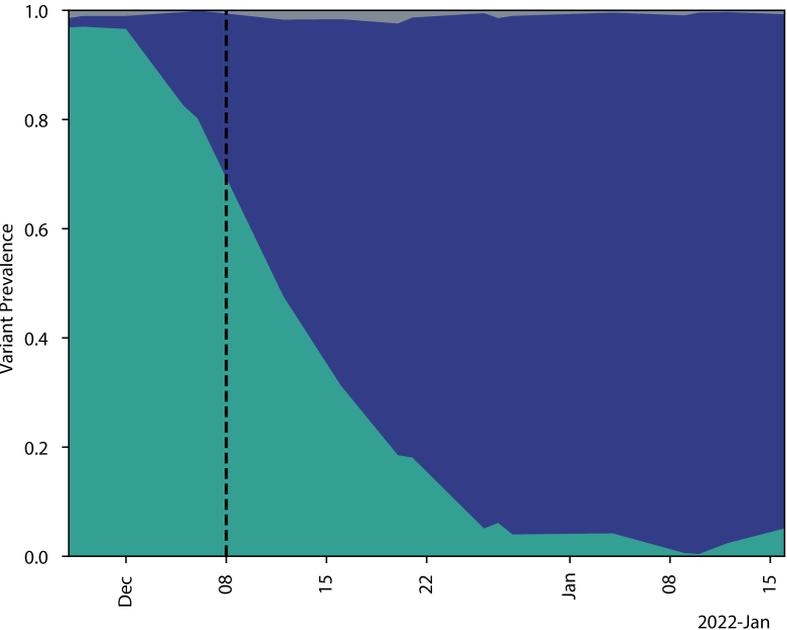
## Point Loma



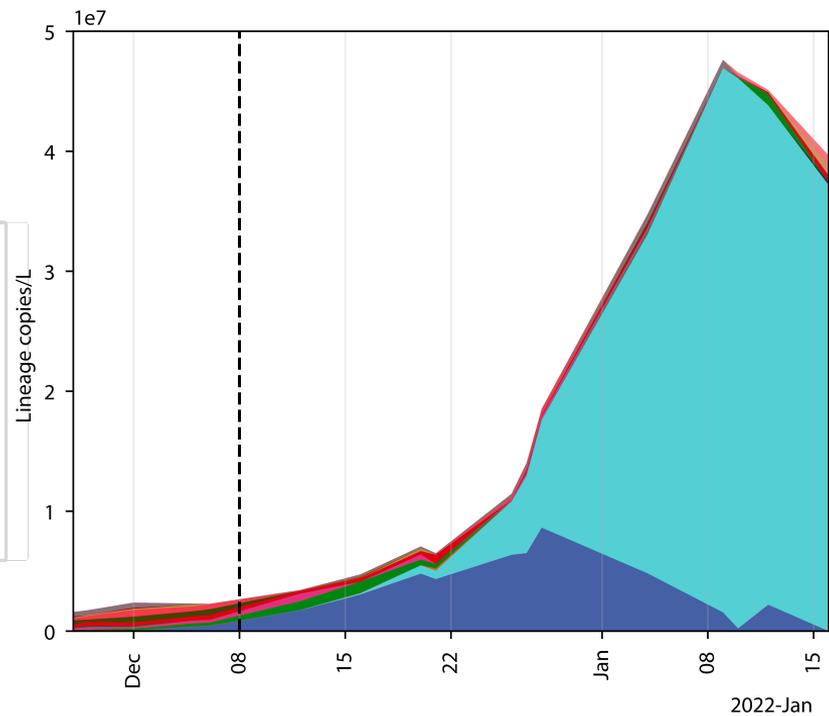
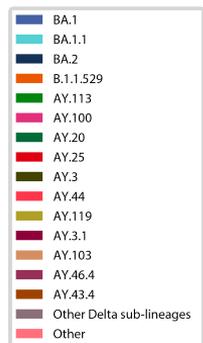
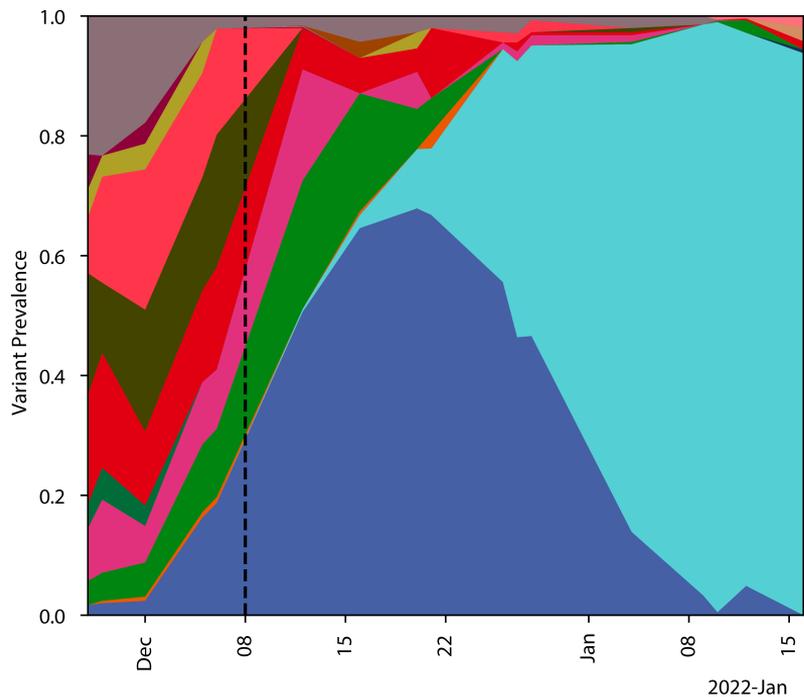
# The Omicron wave in San Diego



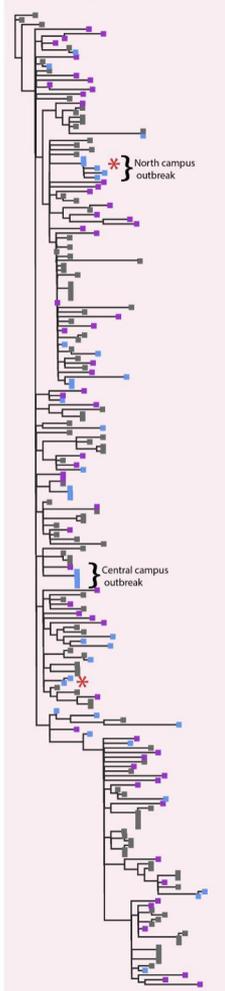
# The Omicron wave in San Diego



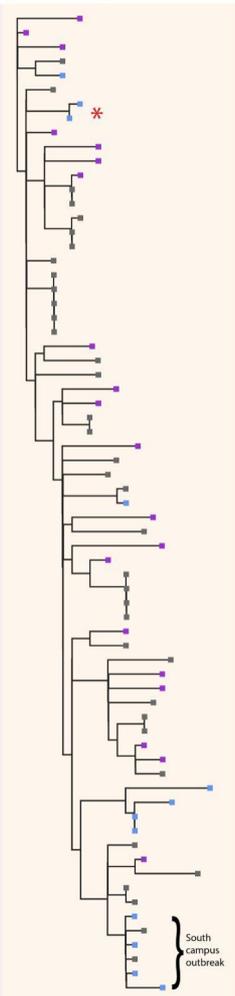
# The Omicron wave in San Diego



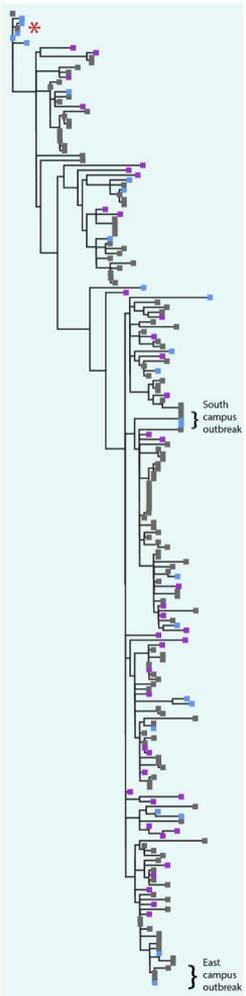
Epsilon



Alpha



Delta

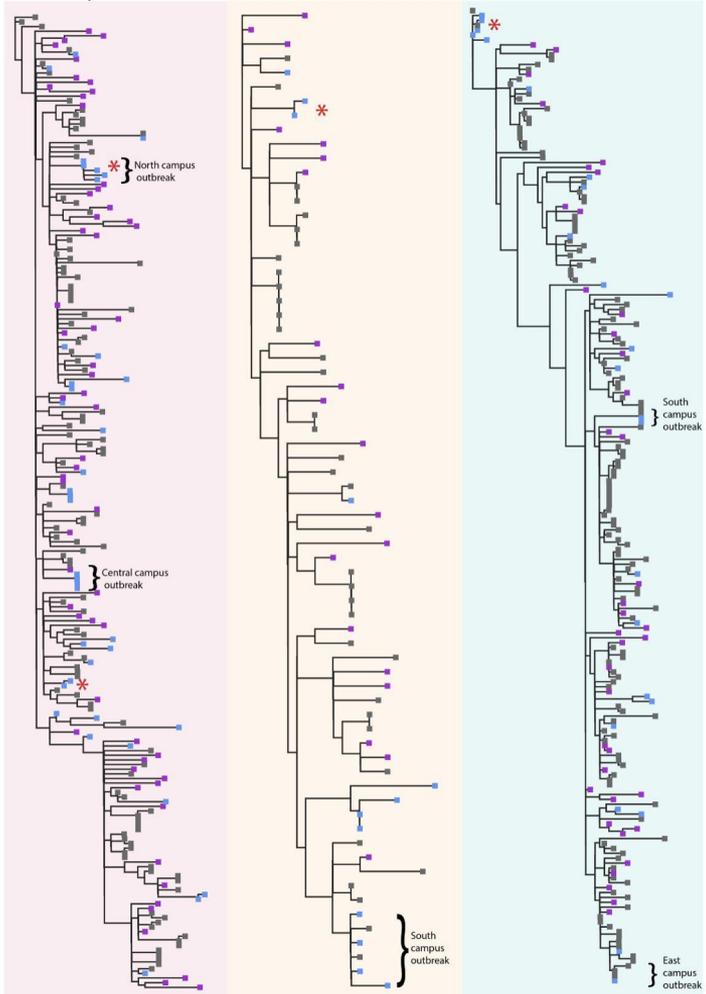


■ UCSD Wastewater ■ UCSD Clinical ■ United States

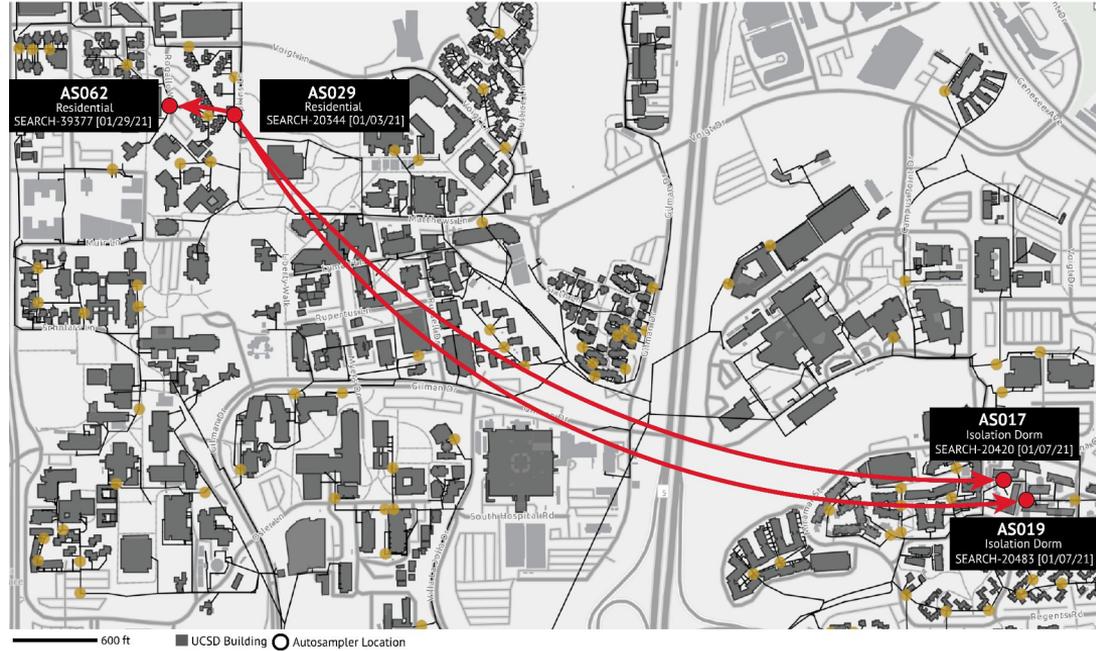
Epsilon

Alpha

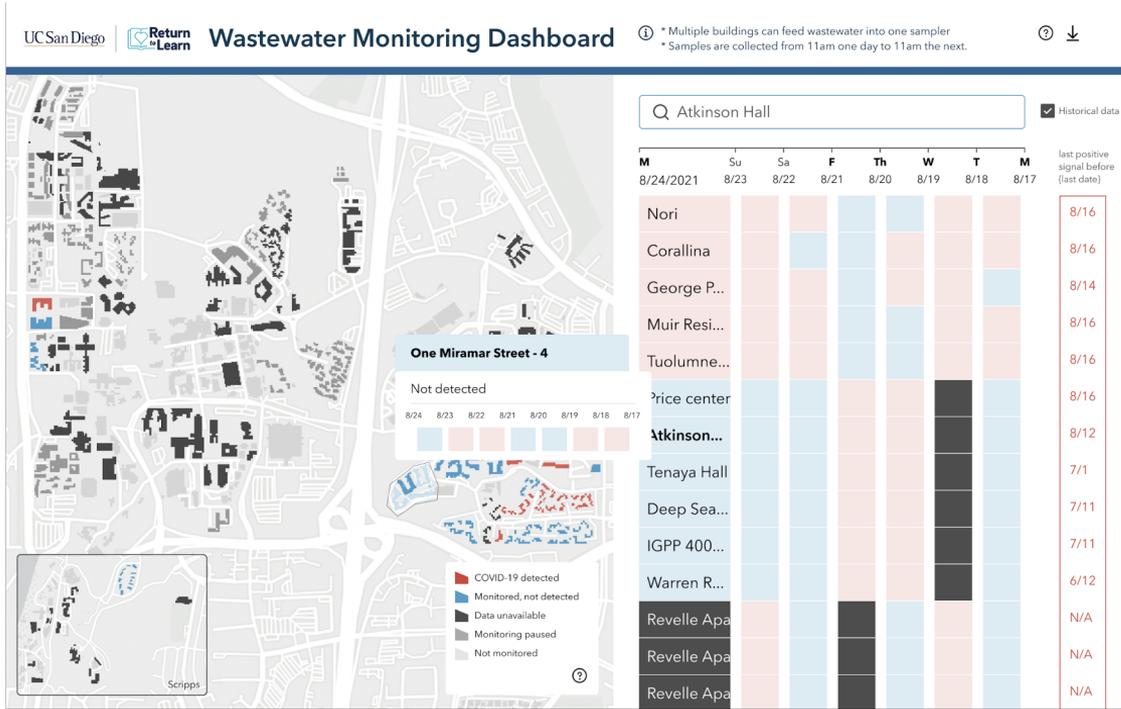
Delta



■ UCSD Wastewater 
 ■ UCSD Clinical 
 ■ United States



# Public health use of wastewater surveillance



UC San Diego CAMPUS NOTICE

OFFICE OF THE CHANCELLOR

January 24, 2022



ALL STUDENTS, ACADEMICS AND CAMPUS STAFF AT UC SAN DIEGO

## Return to In-Person Instruction [Jan. 31](#)

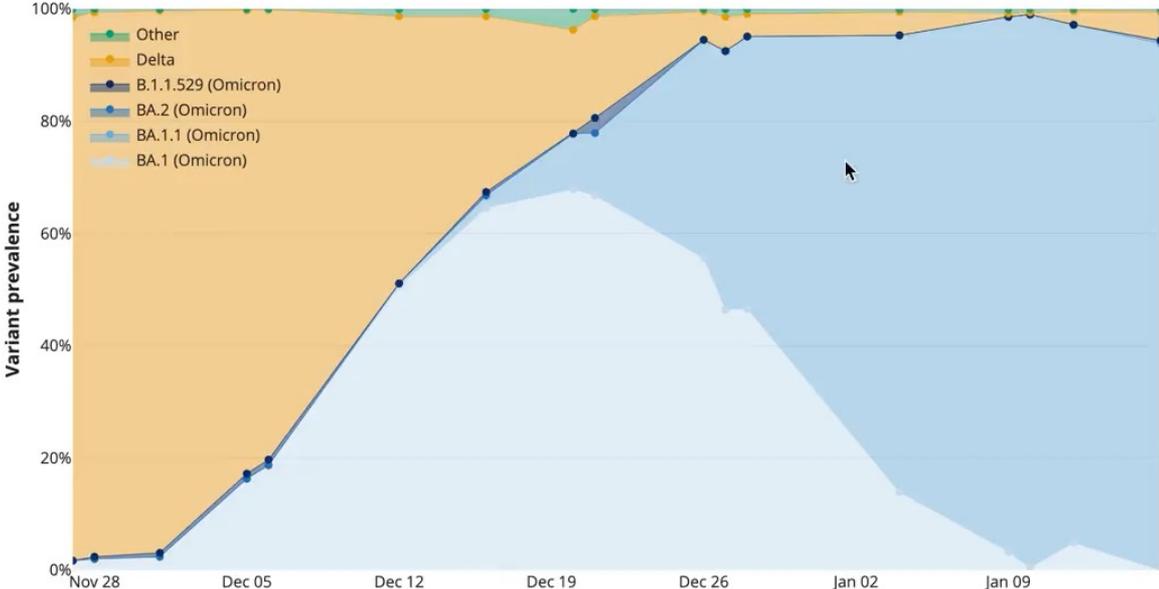
I am happy to report that UC San Diego is on schedule to return to in-person instruction [beginning Monday, Jan. 31](#). As of today, [viral levels in wastewater reported from the Point Loma treatment facility are dropping, student positivity rates on and off campus are falling](#), and our proactive use of rapid antigen tests has greatly reduced the need for isolation housing for returning students.

Reply to All

# Public health use of wastewater surveillance

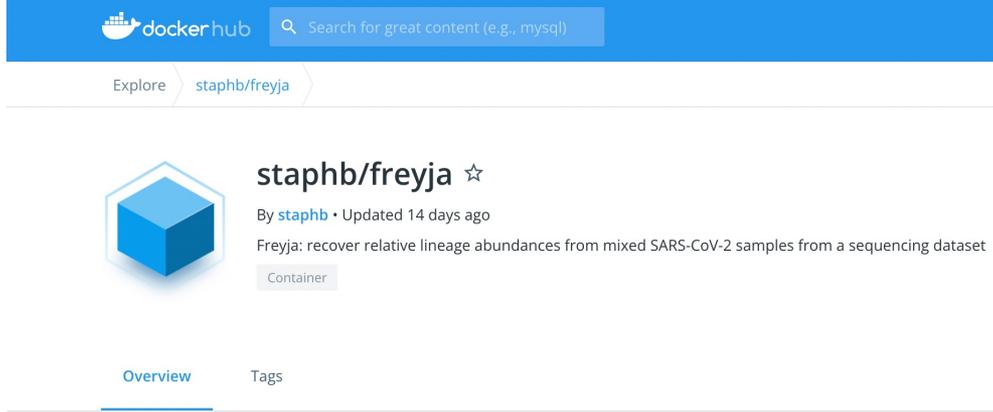
## Wastewater lineages

Prevalence | Scale by viral load | Scale by cases

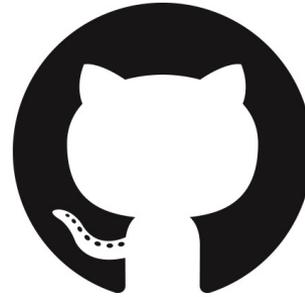


# Code deployment and usage

# BIOCONDA<sup>®</sup>



The screenshot shows the Docker Hub interface for the container 'staphb/freyja'. At the top, there is a blue navigation bar with the Docker Hub logo and a search bar containing the text 'Search for great content (e.g., mysql)'. Below the navigation bar, there are breadcrumb links: 'Explore' and 'staphb/freyja'. The main content area features a blue cube icon representing the container. To the right of the icon, the text reads 'staphb/freyja ☆', followed by 'By staphb • Updated 14 days ago' and a description: 'Freyja: recover relative lineage abundances from mixed SARS-CoV-2 samples from a sequencing dataset'. A 'Container' tag is visible below the description. At the bottom of the interface, there are two tabs: 'Overview' (which is selected and underlined) and 'Tags'.



[← Back to list](#)

## Freyja\_FASTQ

Version:

Source: [github.com/theiagen/public\\_health\\_viral\\_genomics/Freyja\\_FASTQ:v2.0.0](https://github.com/theiagen/public_health_viral_genomics/Freyja_FASTQ:v2.0.0)

Synopsis:

*No documentation provided*

- Run workflow with inputs defined by file paths
- Run workflow(s) with inputs defined by data table

### Step 1

Select root entity type:

### Step 2

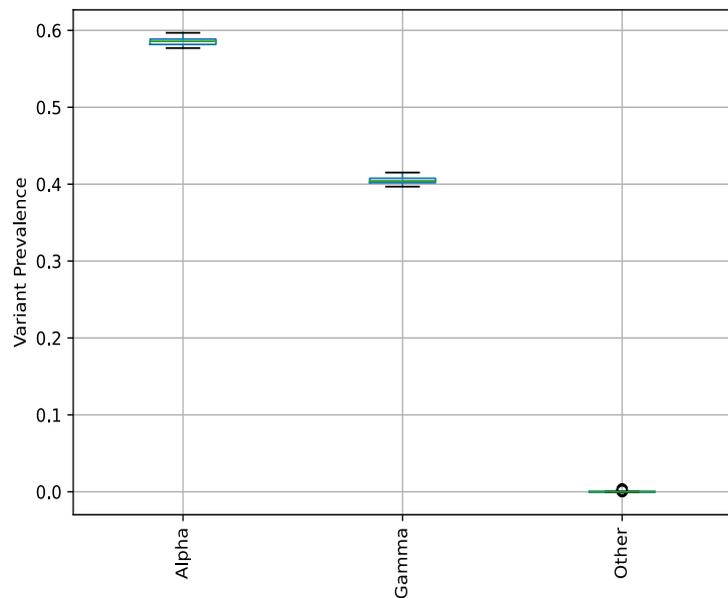
No data selected

- Use call caching
- Delete intermediate outputs 
- Use reference disks 
- Retry with more memory 



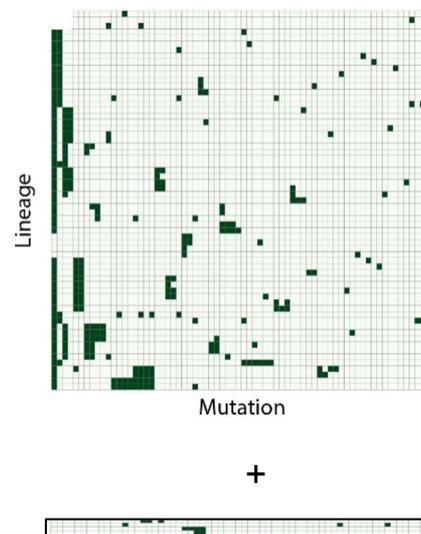
# Ongoing development of Freyja

## Fast bootstrapping



**Now available**

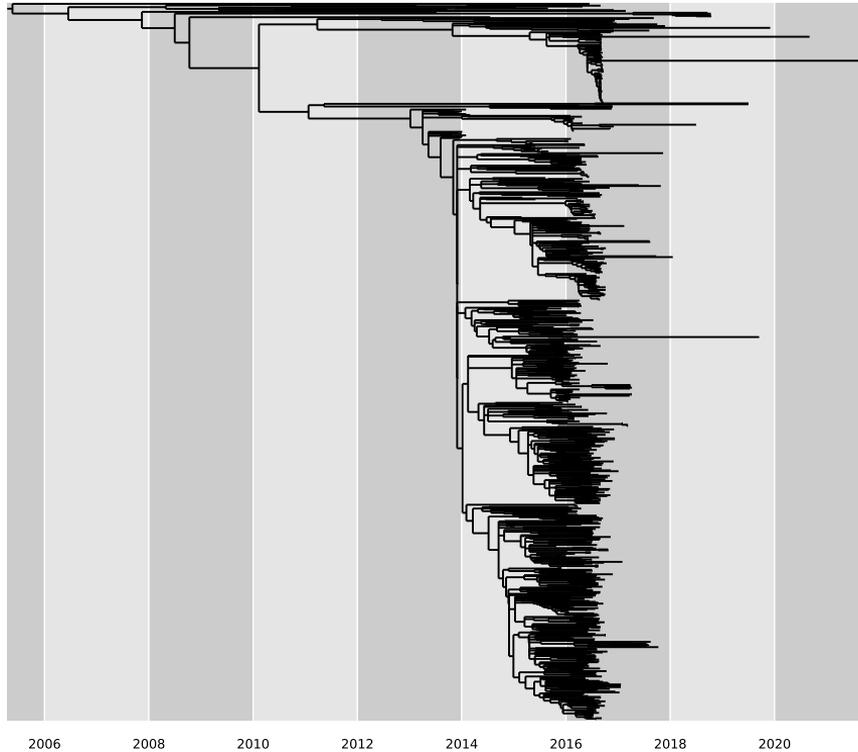
## Novel lineage detection



**Coming soon**

# Ongoing: Extending to other viruses

Zika (2013-2019)



Coming soon

# Thanks!!

Smruthi Karthikeyan

Peter DeHoff

Andersen Lab

Knight Lab

Kevin Libuit (Theiagen)



NIH T32 Training grant 5T32AI007244-38