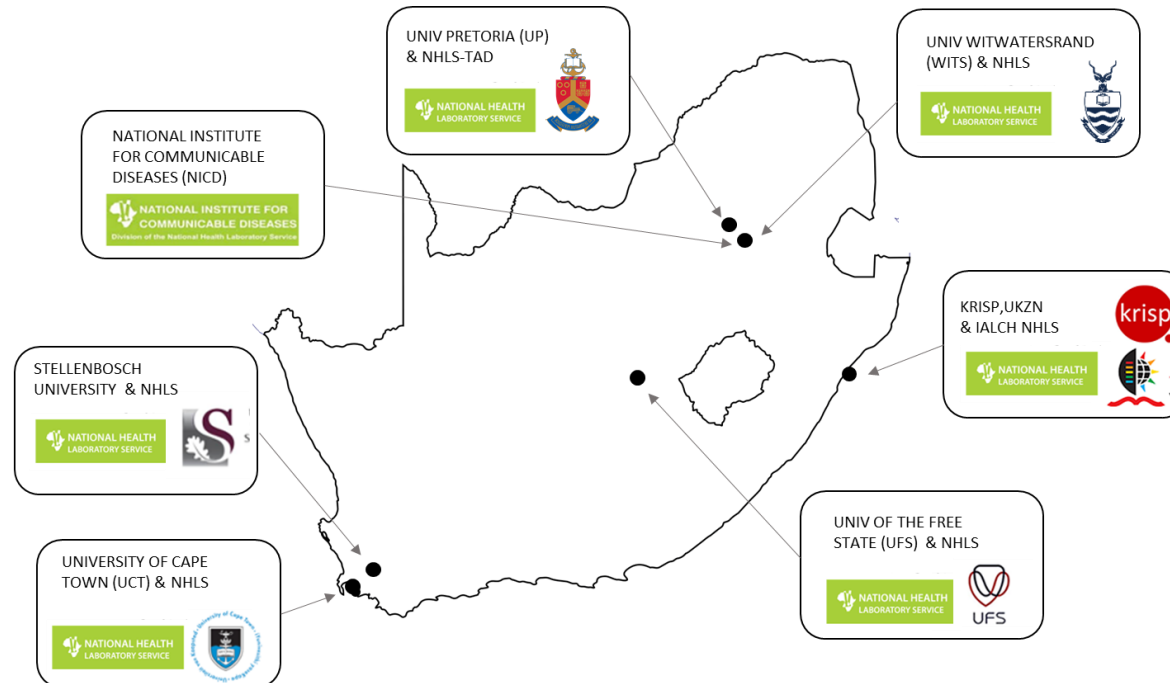


## SARS-CoV-2 Sequencing Update 16 September 2022



Supported by the DSI and the SA MRC

Msomi N, Mlisana K, et al. Lancet Microbe 2020

The genomic data presented here are based on South African SARS-CoV-2 sequence data downloaded from GISAID ([www.gisaid.org](http://www.gisaid.org)) on 16 September 2022 at 11h10



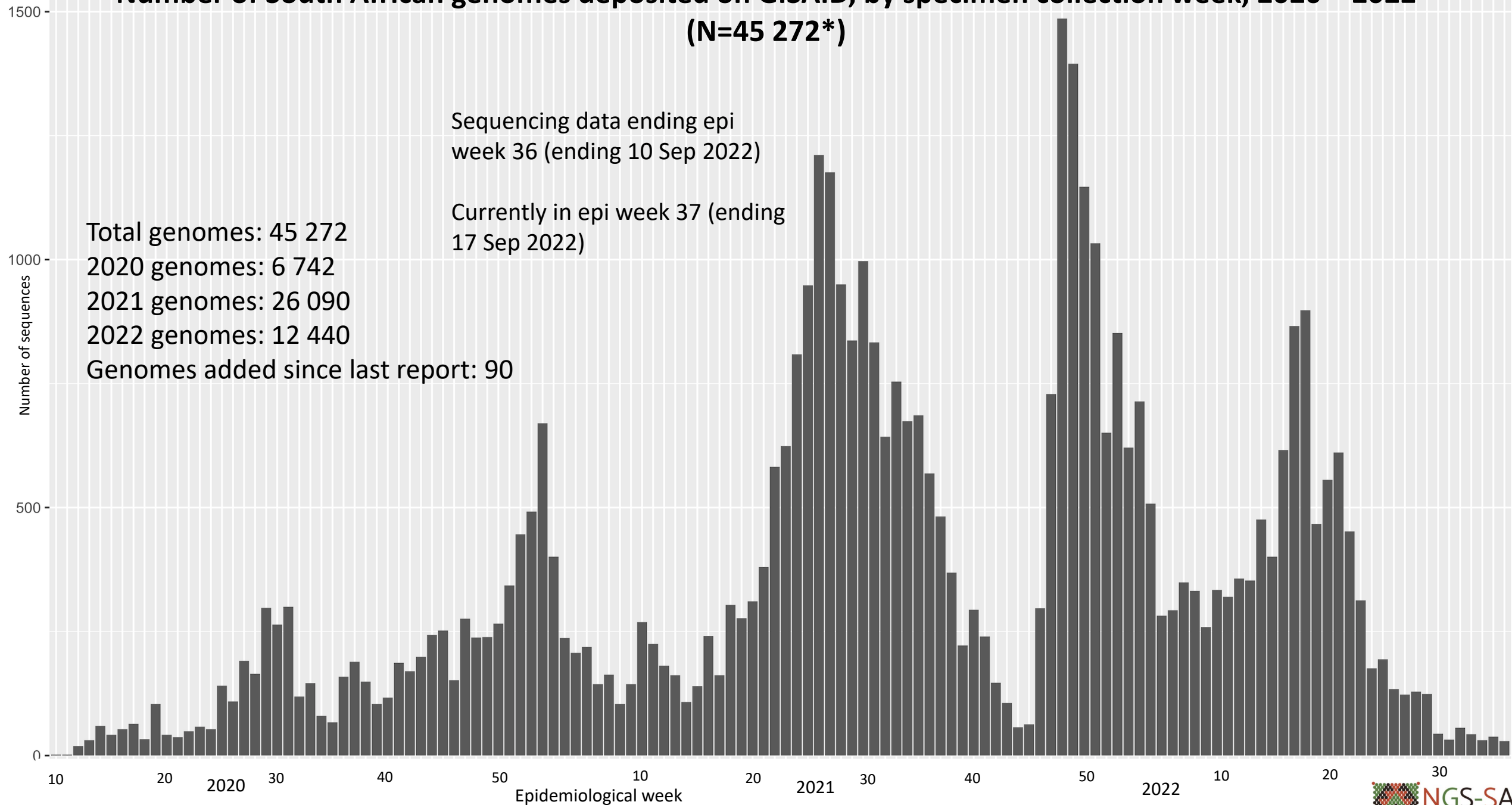
Data license: <https://www.gisaid.org/registration/terms-of-use/>

Elbe, S., and Buckland-Merrett, G. (2017) Data, disease and diplomacy: GISAID's innovative contribution to global health. *Global Challenges*, 1:33-46. DOI: 10.1002/gch2.1018 PMID: 31565258

Shu, Y., McCauley, J. (2017) GISAID: Global initiative on sharing all influenza data – from vision to reality. *EuroSurveillance*, 22(13) DOI: 10.2807/1560-7917.ES.2017.22.13.30494 PMID: PMC5388101

# Number of South African genomes deposited on GISAID, by specimen collection week, 2020 – 2022

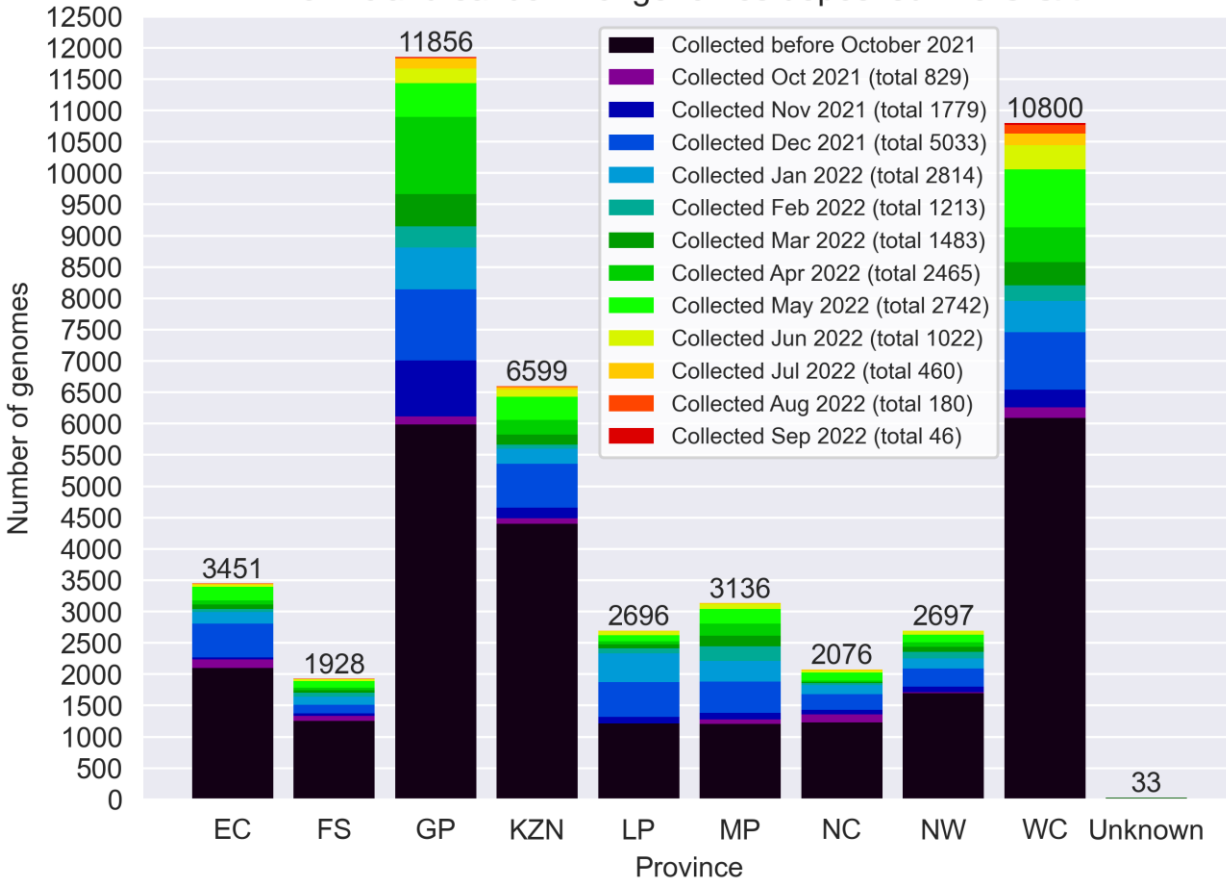
(N=45 272\*)



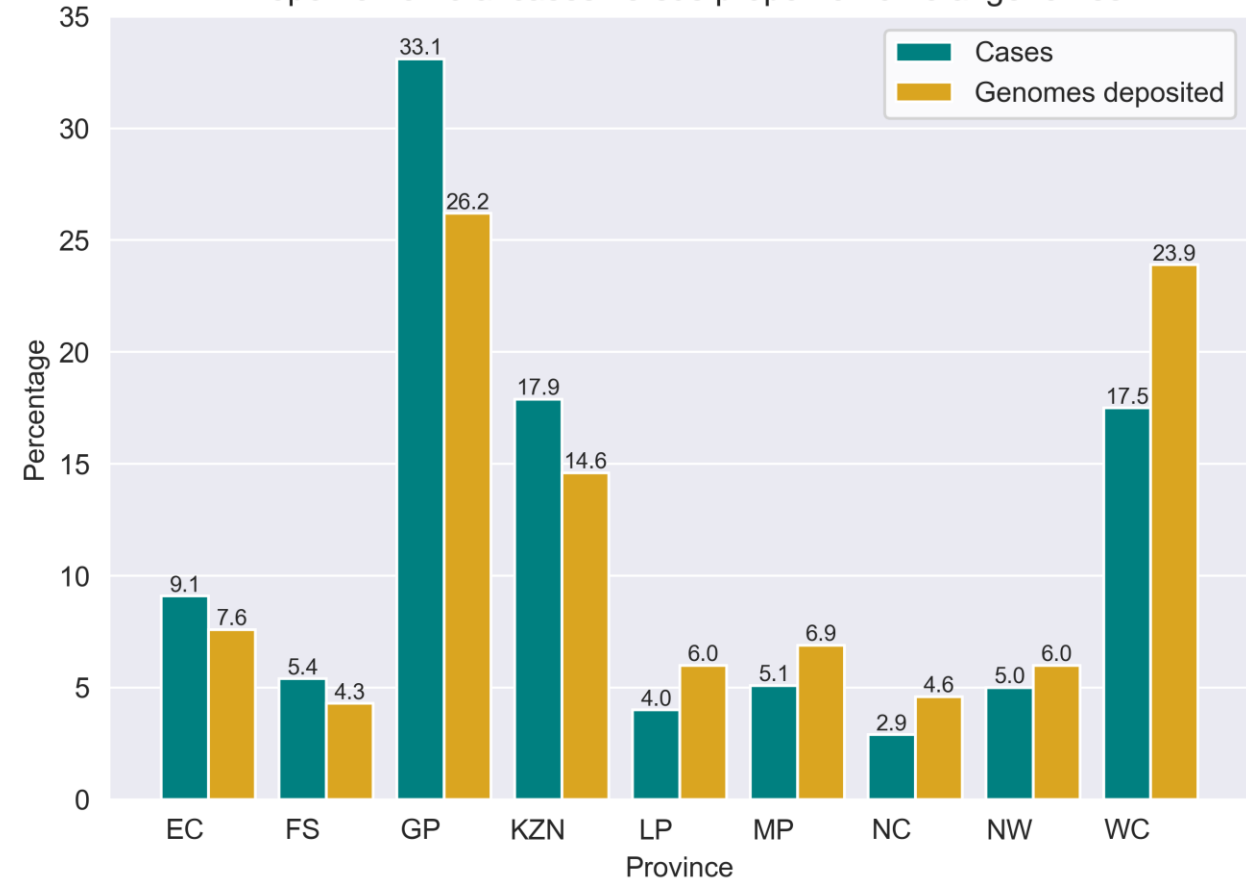
\*This represents the cleaned, de-duplicated dataset of unique **National and Pneumonia Surveillance** sequences. This dataset will be used for all further figures.

# GISAID genomes vs total cases, 2020 – 2022 (N=45 272)

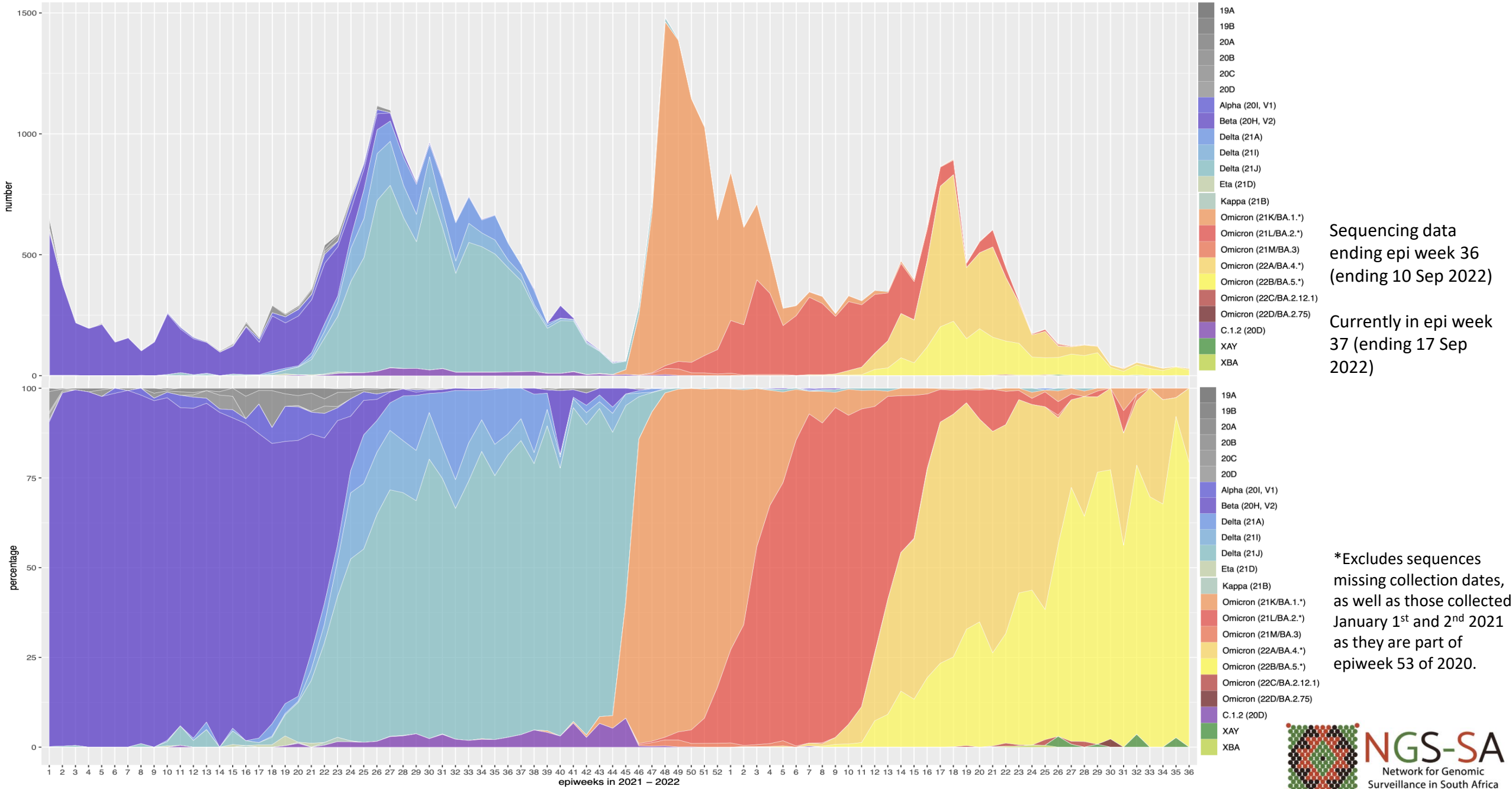
Provincial breakdown of genomes deposited into GISAID



Proportion of total cases versus proportion of total genomes

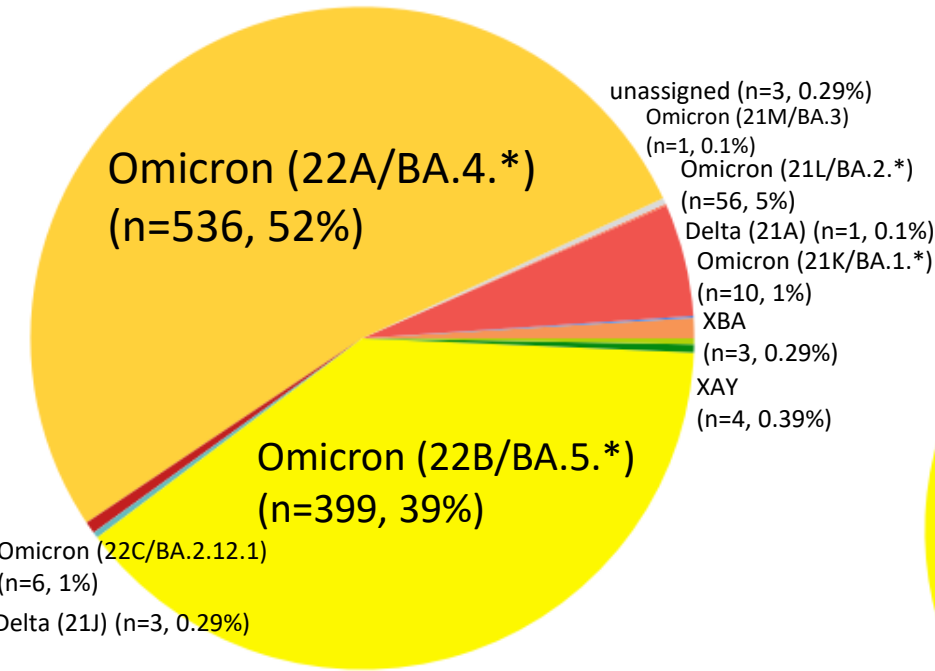


# Number and percentage of clades by epiweek in South Africa, 2021 – 2022 (38 443\*)



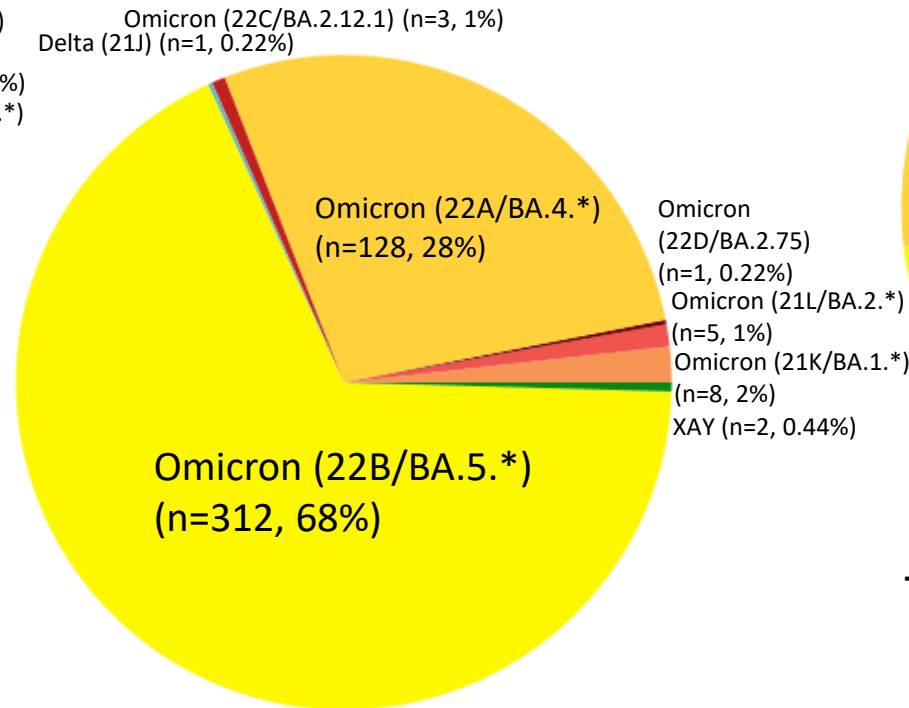
# Prevalence of Variants of Concern (VOC) and Variants of Interest (VOI) in June – August 2022

June (N=1022)



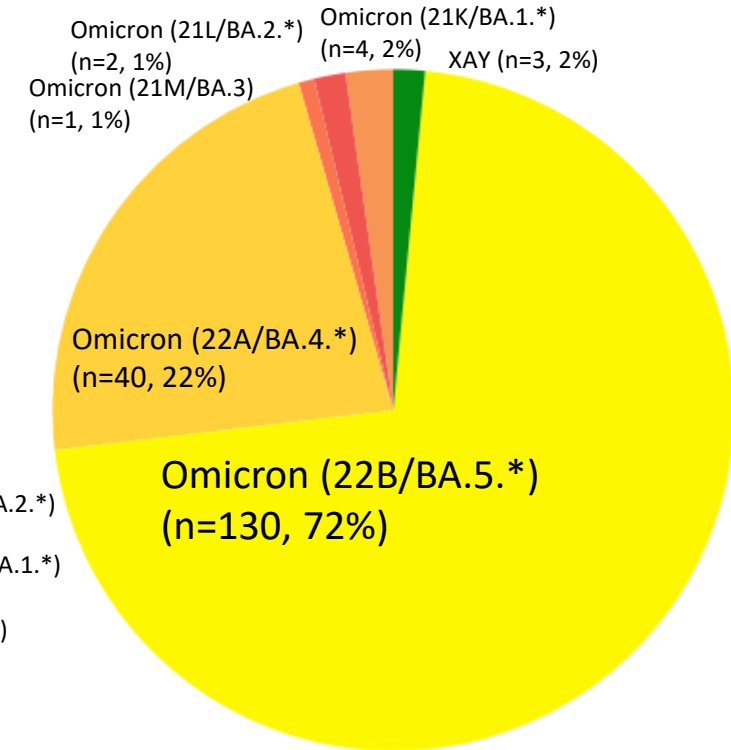
Total Omicron in June: 1008 (98.6%)

July (N=460)

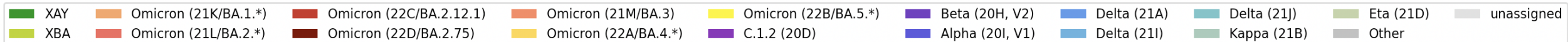


Total Omicron in July: 457 (99.3%)

August (N=180)

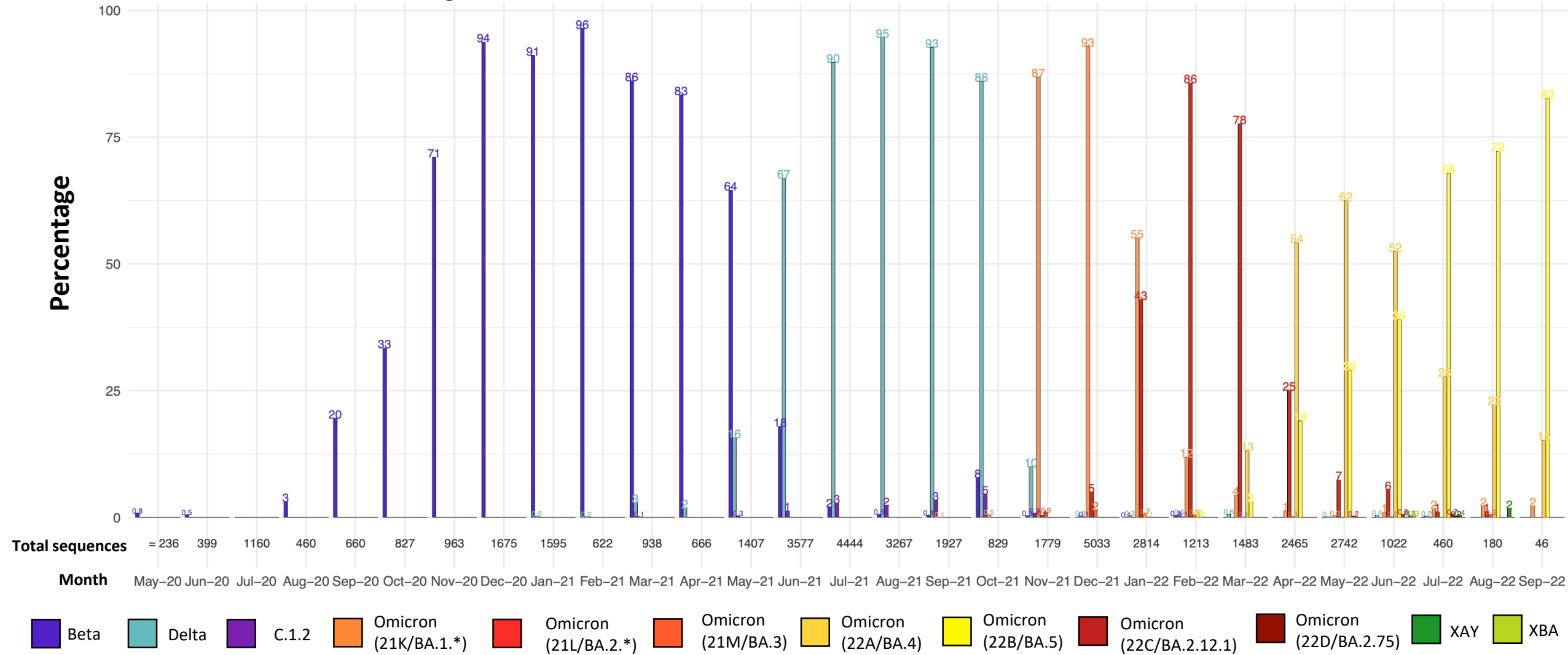


Total Omicron in August: 177 (98.3%)



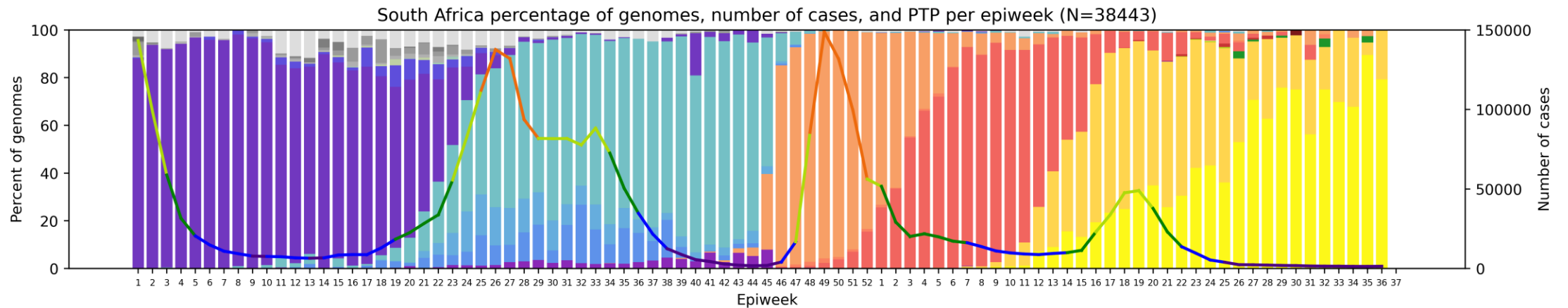
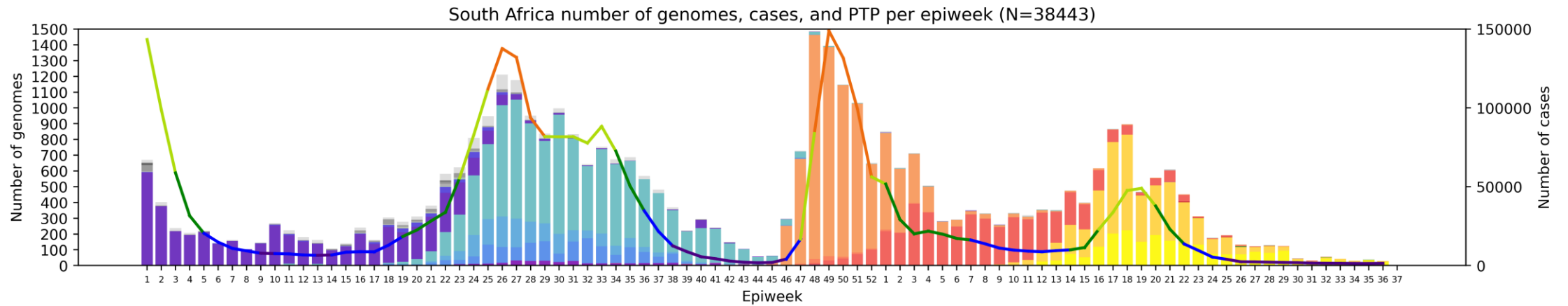
# Detection Rates: Beta, Delta, C.1.2 and Omicron

Detection rates of variants being monitored in South Africa

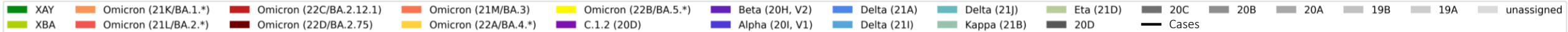


\*Bars represent percentage prevalence of variant for the month; total number sequences collected for the month are given below the bar

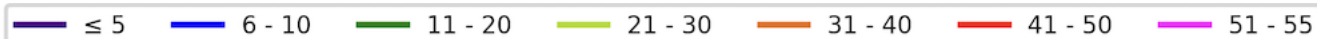
# South Africa, 2021-2022, n = 38 443\*



## Clade key (bar graph)



## Weekly percentage testing positive key (line graph)

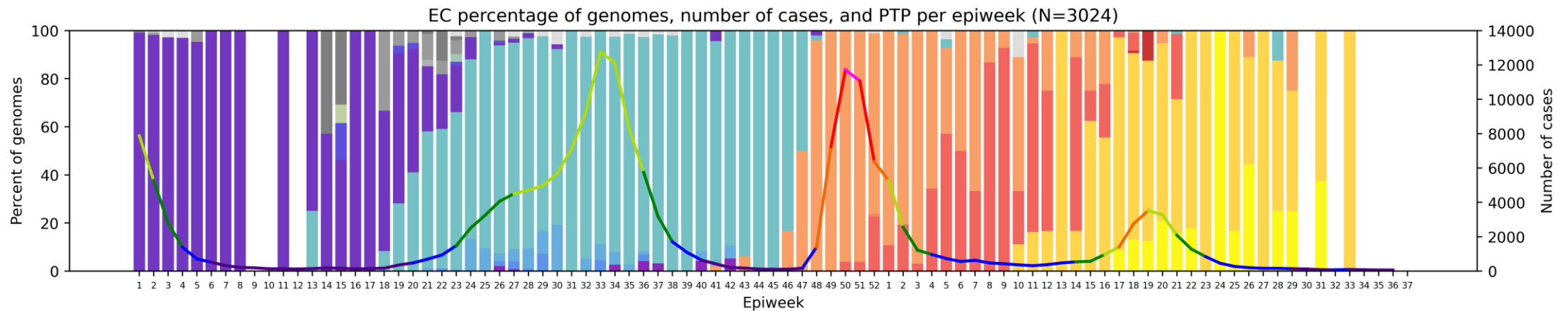
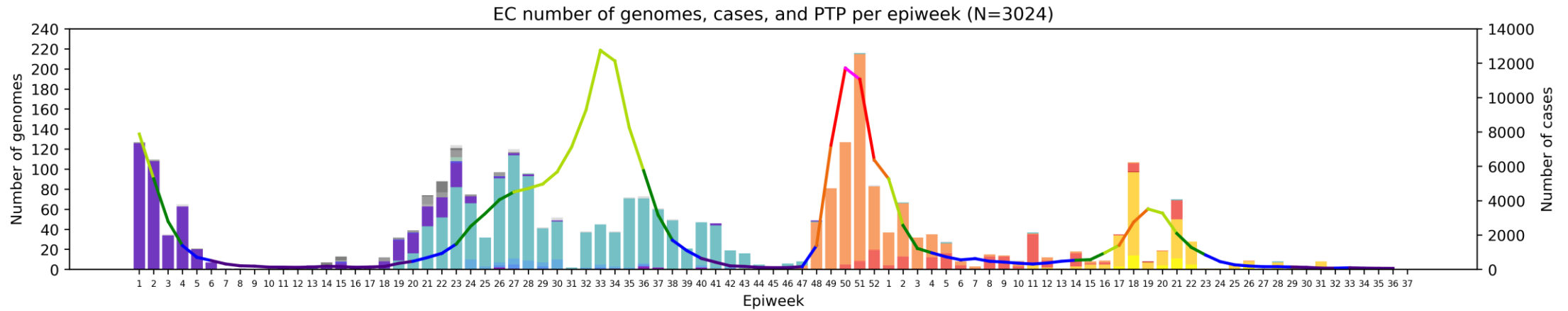


\*Excludes sequences missing collection dates, as well as those collected January 1<sup>st</sup> and 2<sup>nd</sup> 2021 as they are part of epiweek 53 of 2020.

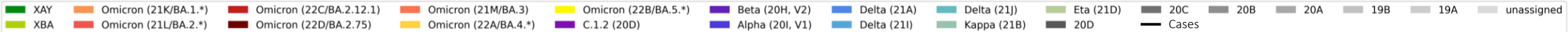


# Eastern Cape Province, 2021-2022, n = 3024

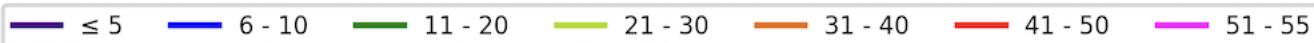
Genomes added since last report: 1\*



## Clade key (bar graph)



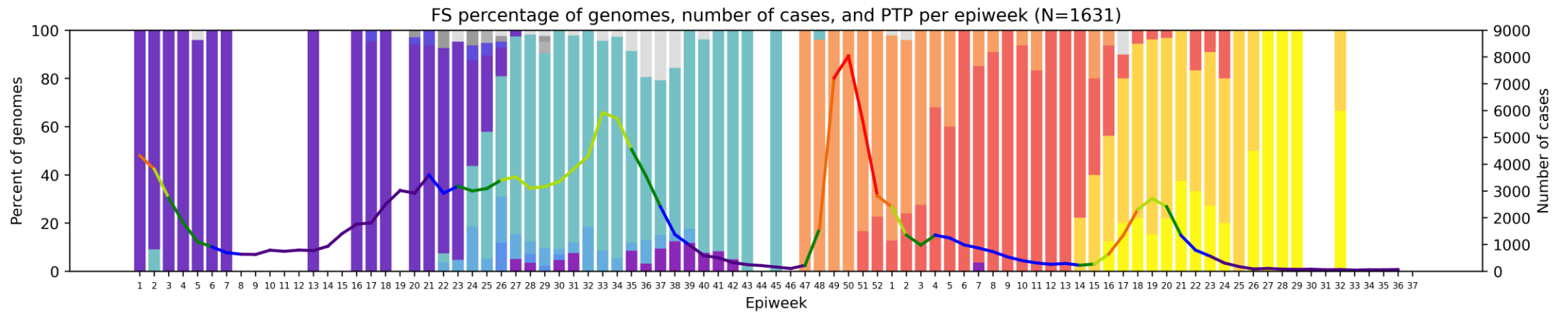
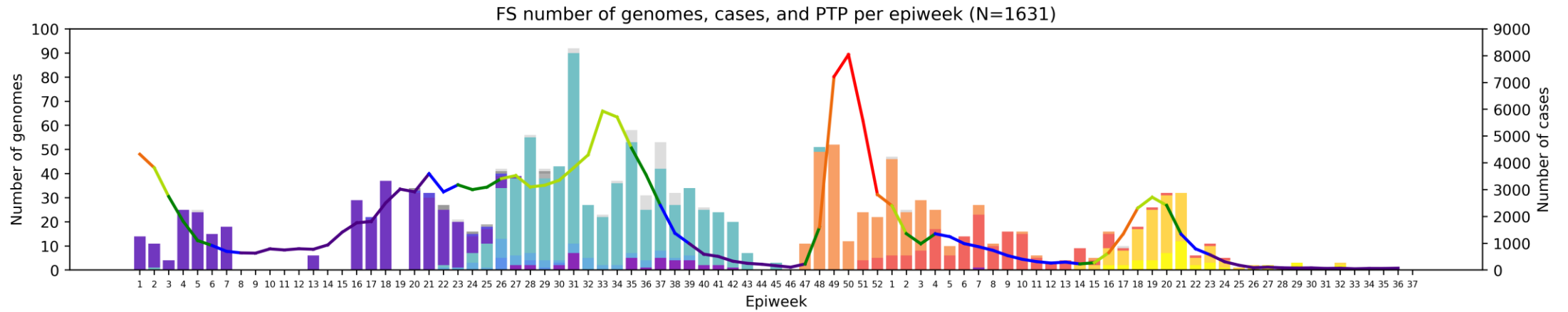
## Weekly percentage testing positive key (line graph)



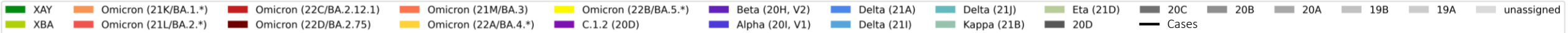
\*May include genomes from 2020 which are not pictured here and are not included in the slide total.

# Free State Province, 2021-2022, n = 1631

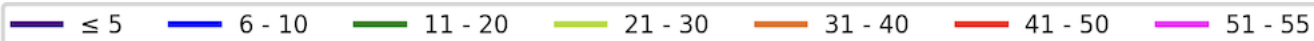
Genomes added since last report: 0\*



## Clade key (bar graph)



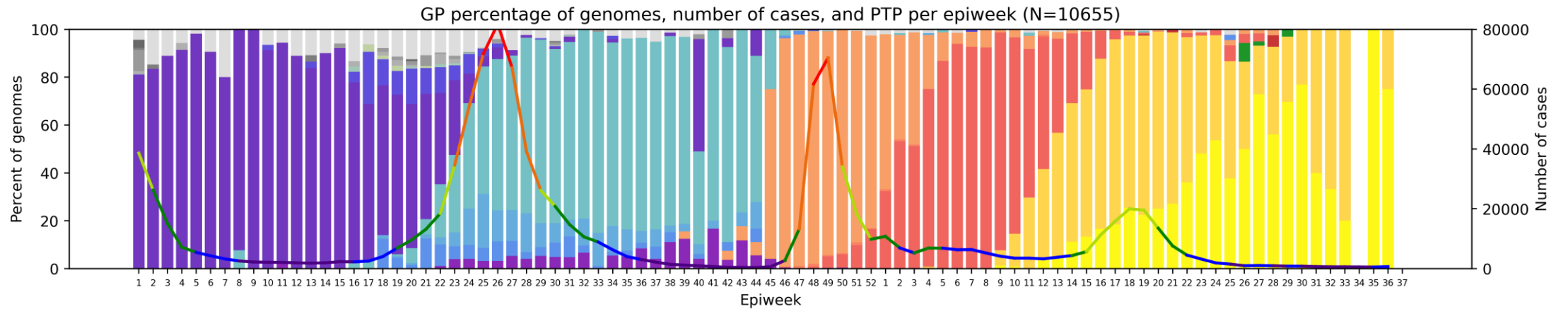
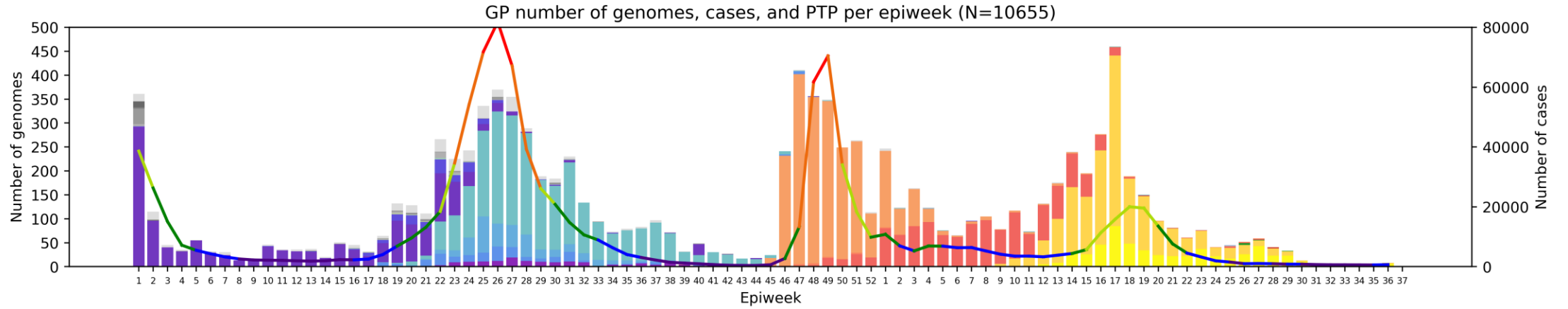
## Weekly percentage testing positive key (line graph)



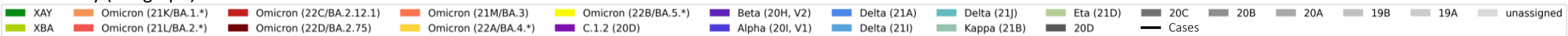
\*May include genomes from 2020 which are not pictured here and are not included in the slide total.

# Gauteng Province, 2021-2022, n = 10 655

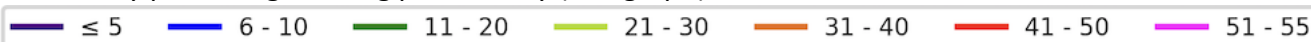
Genomes added since last report: 17\*



## Clade key (bar graph)



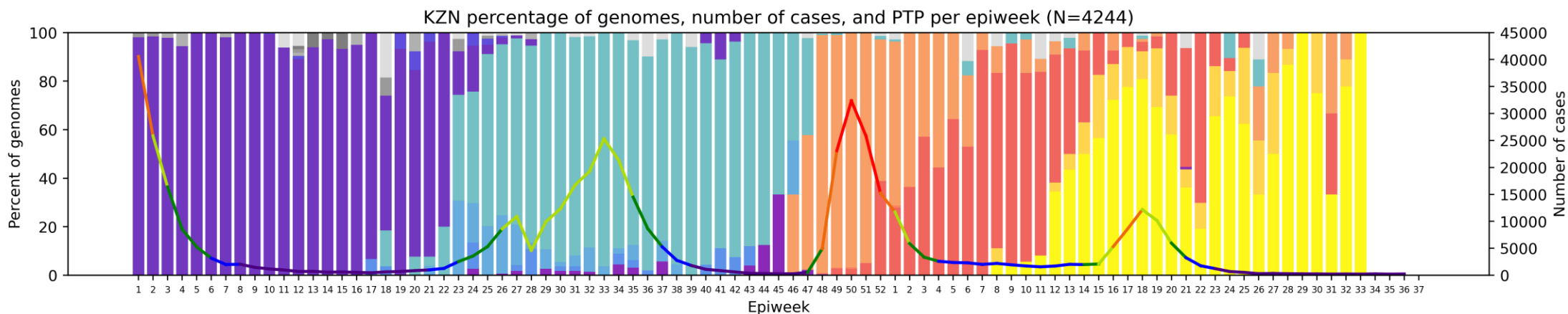
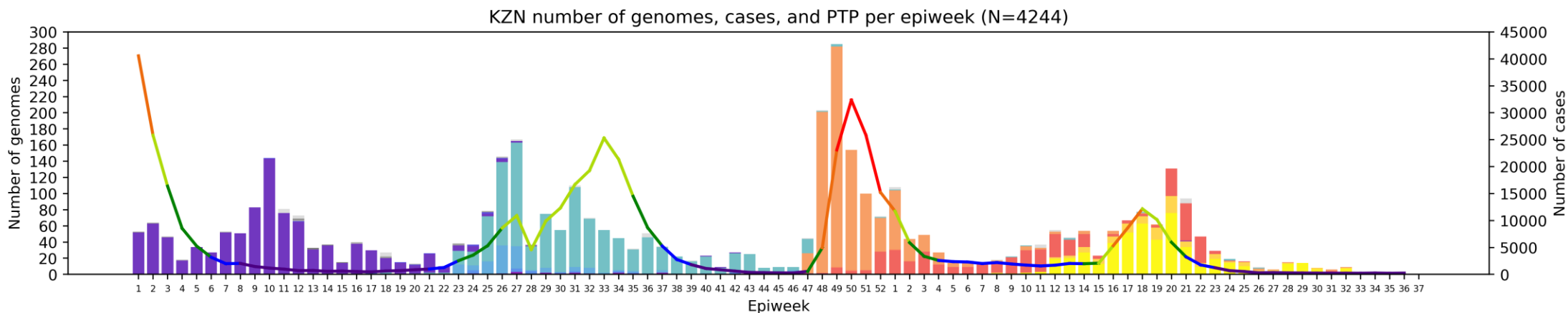
## Weekly percentage testing positive key (line graph)



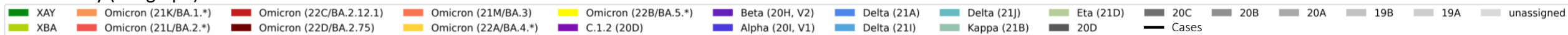
\*May include genomes from 2020 which are not pictured here and are not included in the slide total.

# KwaZulu-Natal Province, 2021-2022, n = 4244

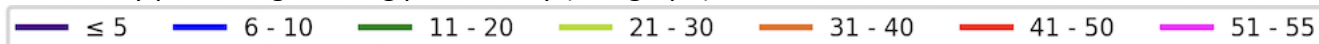
Genomes added since last report: 1\*



## Clade key (bar graph)



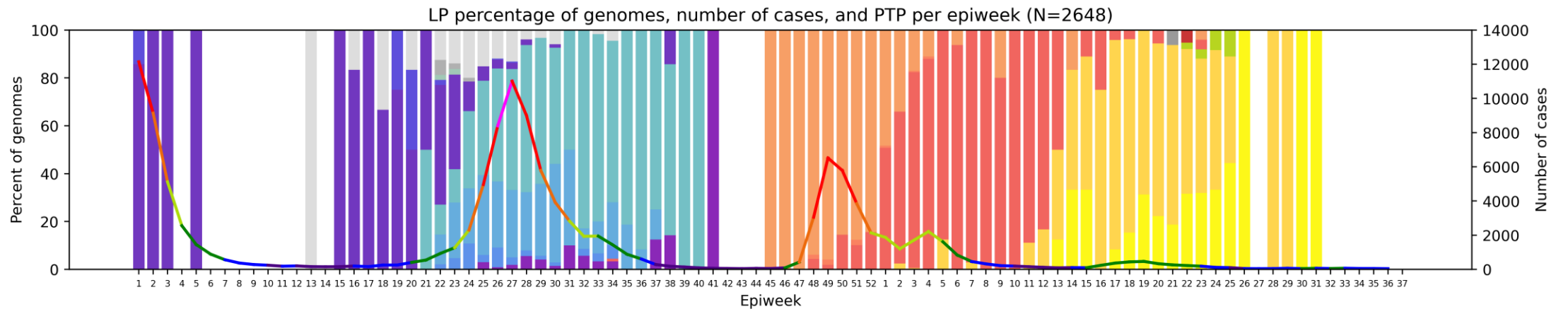
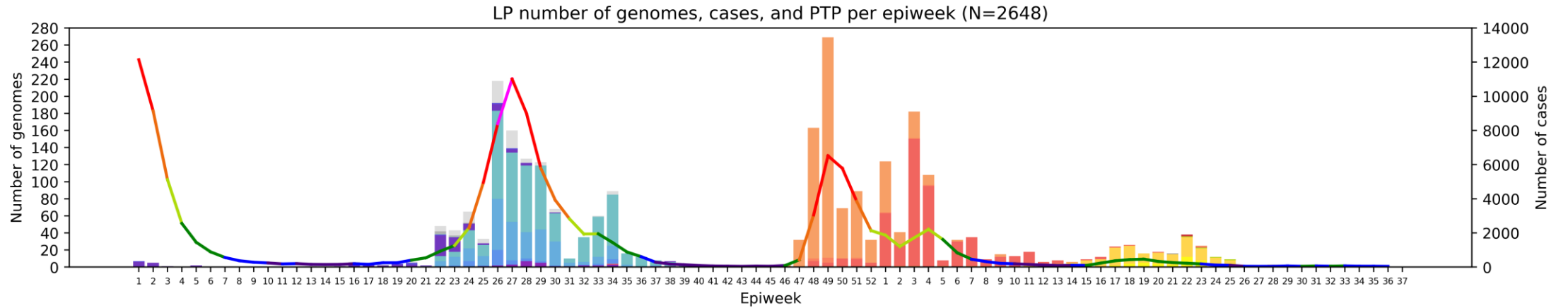
## Weekly percentage testing positive key (line graph)



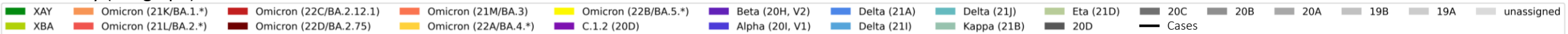
\*May include genomes from 2020 which are not pictured here and are not included in the slide total.

# Limpopo Province, 2021-2022, n = 2648

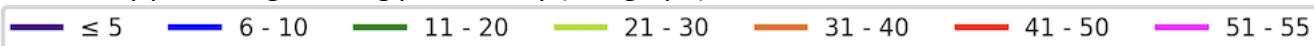
Genomes added since last report: 0\*



## Clade key (bar graph)



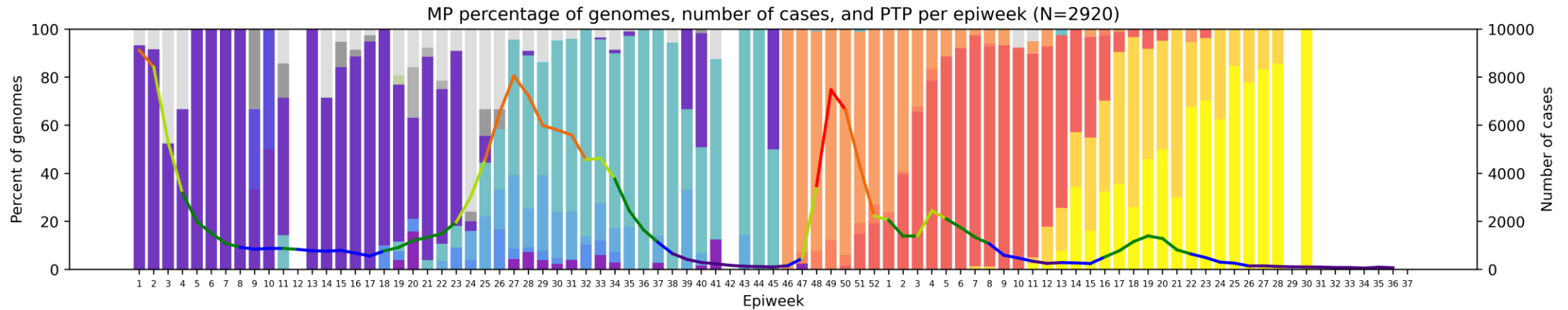
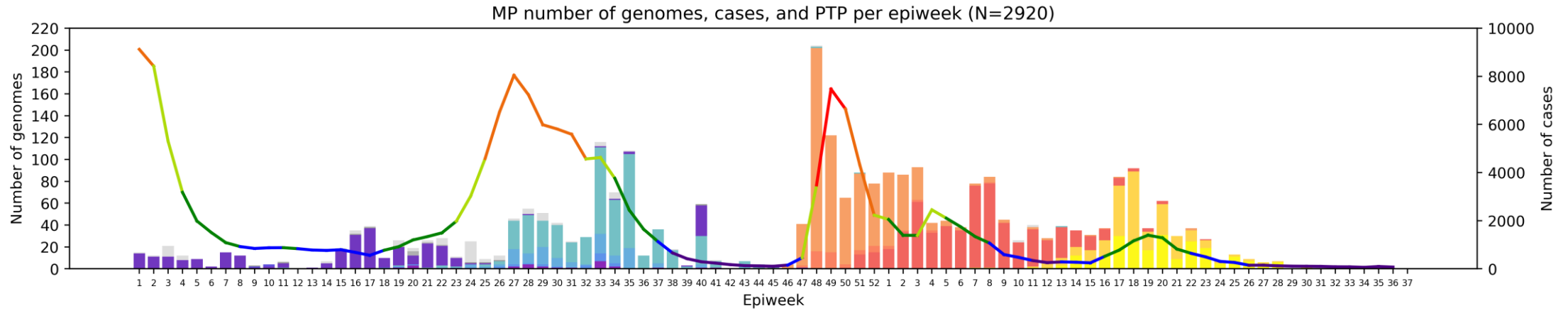
## Weekly percentage testing positive key (line graph)



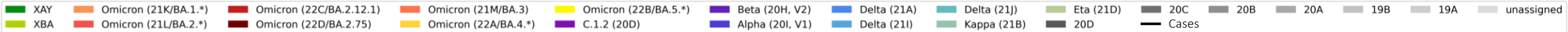
\*May include genomes from 2020 which are not pictured here and are not included in the slide total.

# Mpumalanga Province, 2021-2022, n = 2920

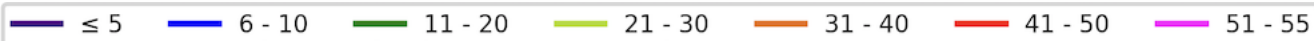
Genomes added since last report: 0\*



## Clade key (bar graph)



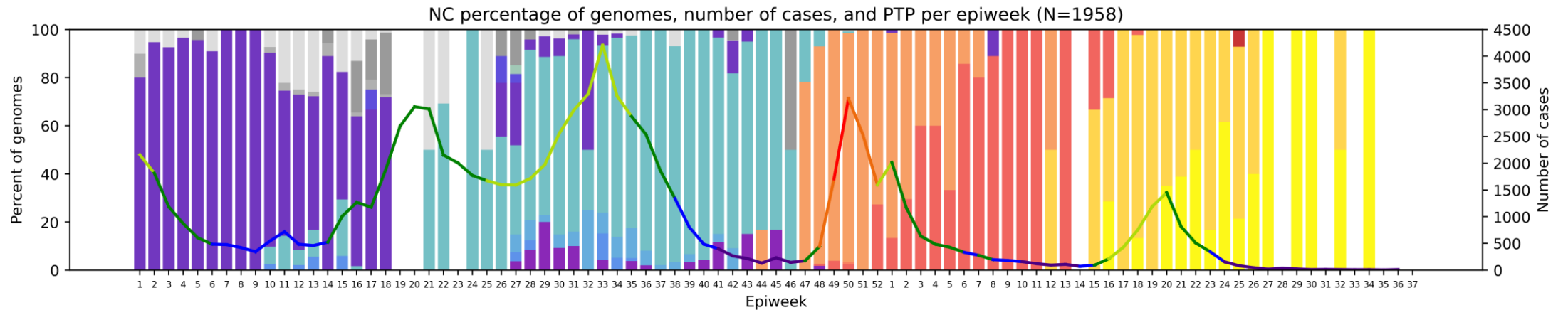
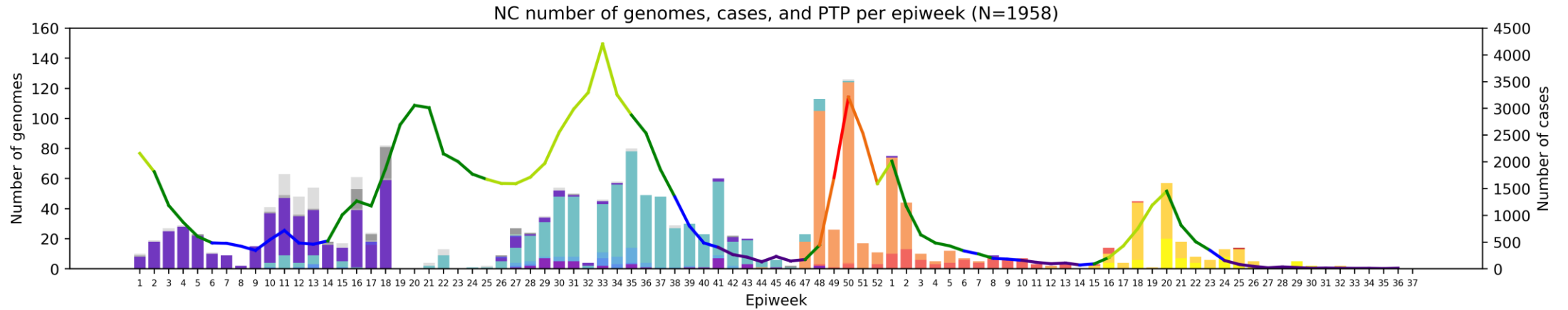
## Weekly percentage testing positive key (line graph)



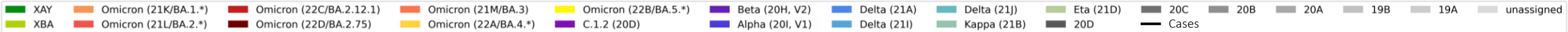
\*May include genomes from 2020 which are not pictured here and are not included in the slide total.

# Northern Cape Province, 2021-2022, n = 1958

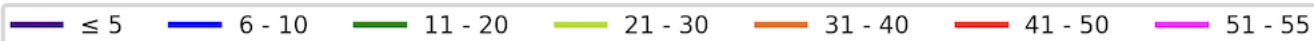
Genomes added since last report: 1\*



## Clade key (bar graph)



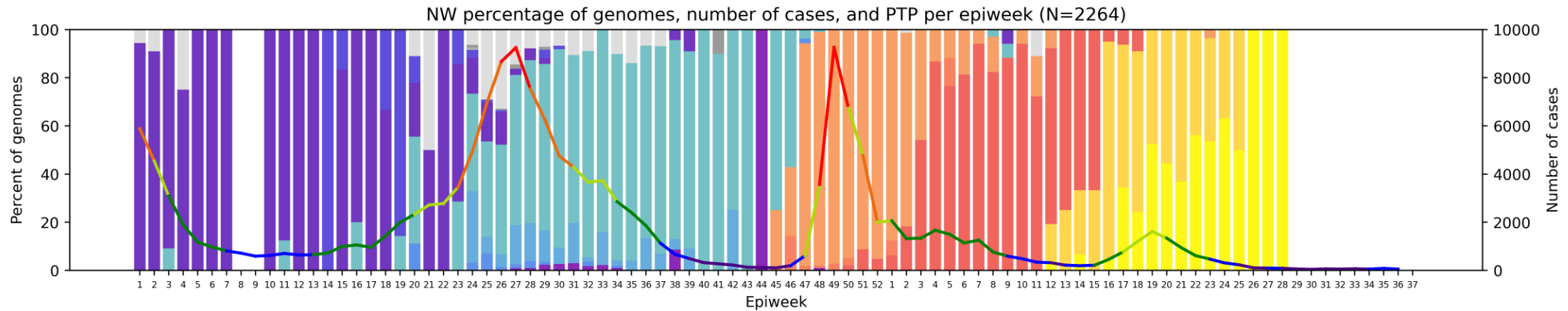
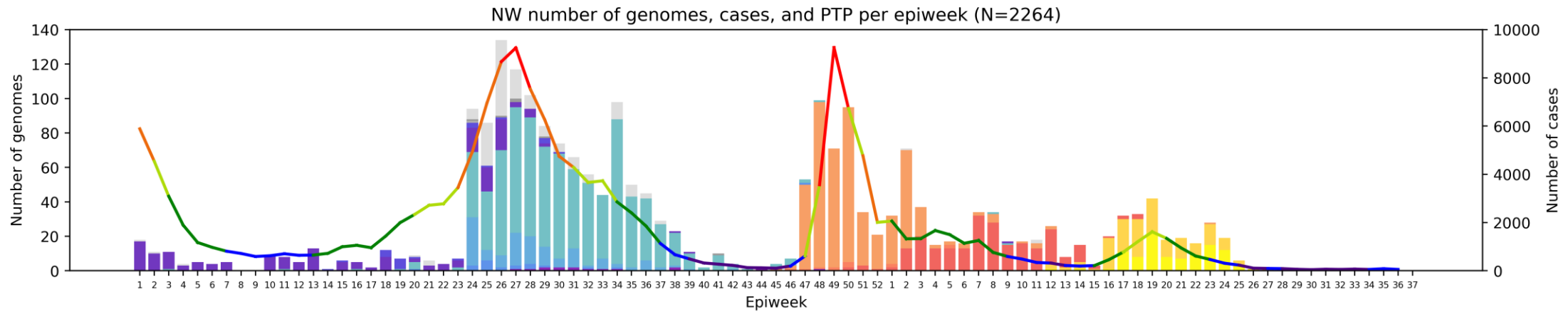
## Weekly percentage testing positive key (line graph)



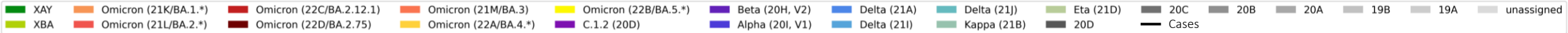
\*May include genomes from 2020 which are not pictured here and are not included in the slide total.

# North West Province, 2021-2022, n = 2264

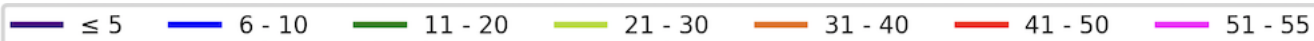
Genomes added since last report: 0\*



## Clade key (bar graph)



## Weekly percentage testing positive key (line graph)

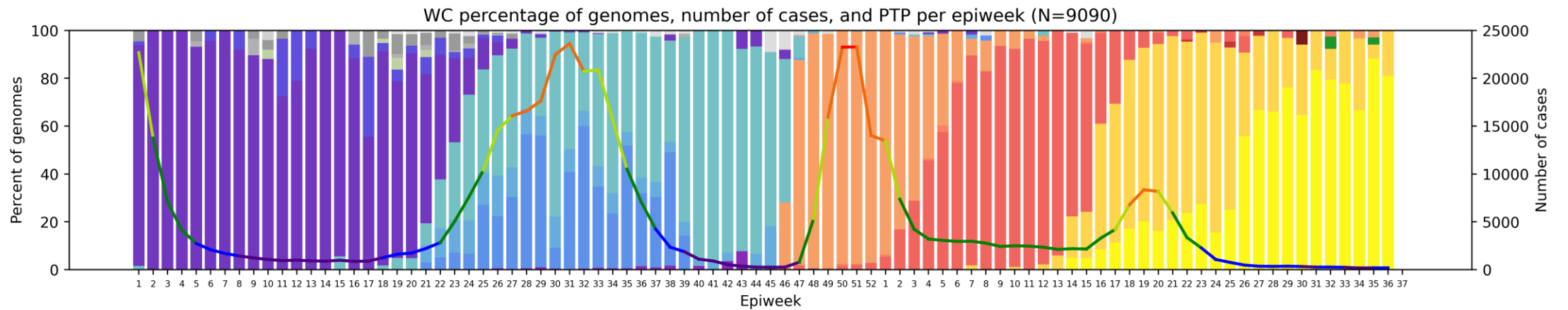
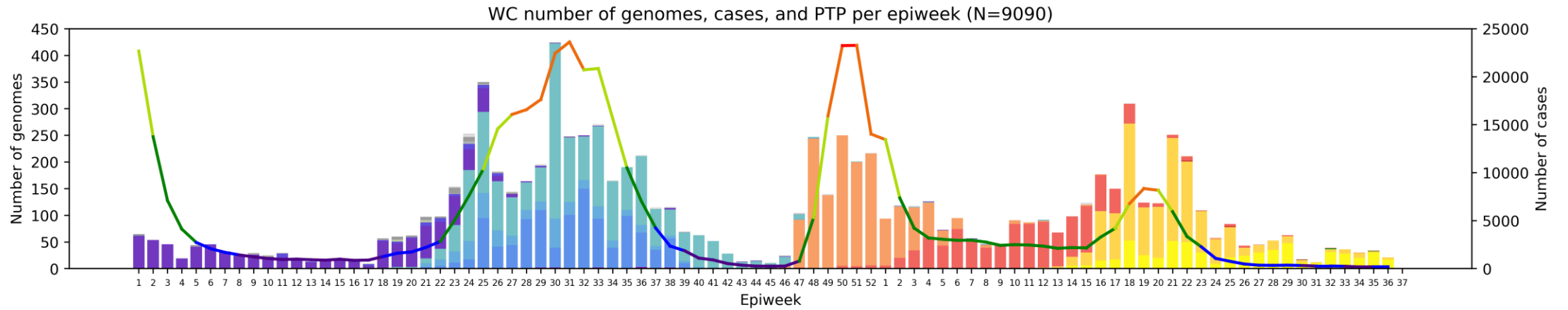


\*May include genomes from 2020 which are not pictured here and are not included in the slide total.

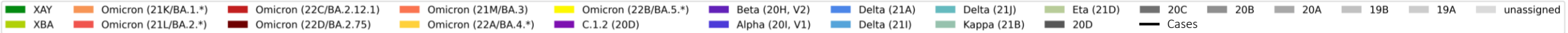


# Western Cape Province, 2021-2022, n = 9090

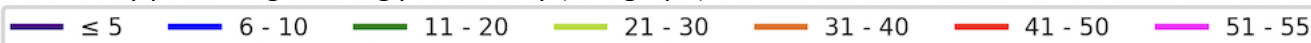
Genomes added since last report: 70\*



## Clade key (bar graph)



## Weekly percentage testing positive key (line graph)



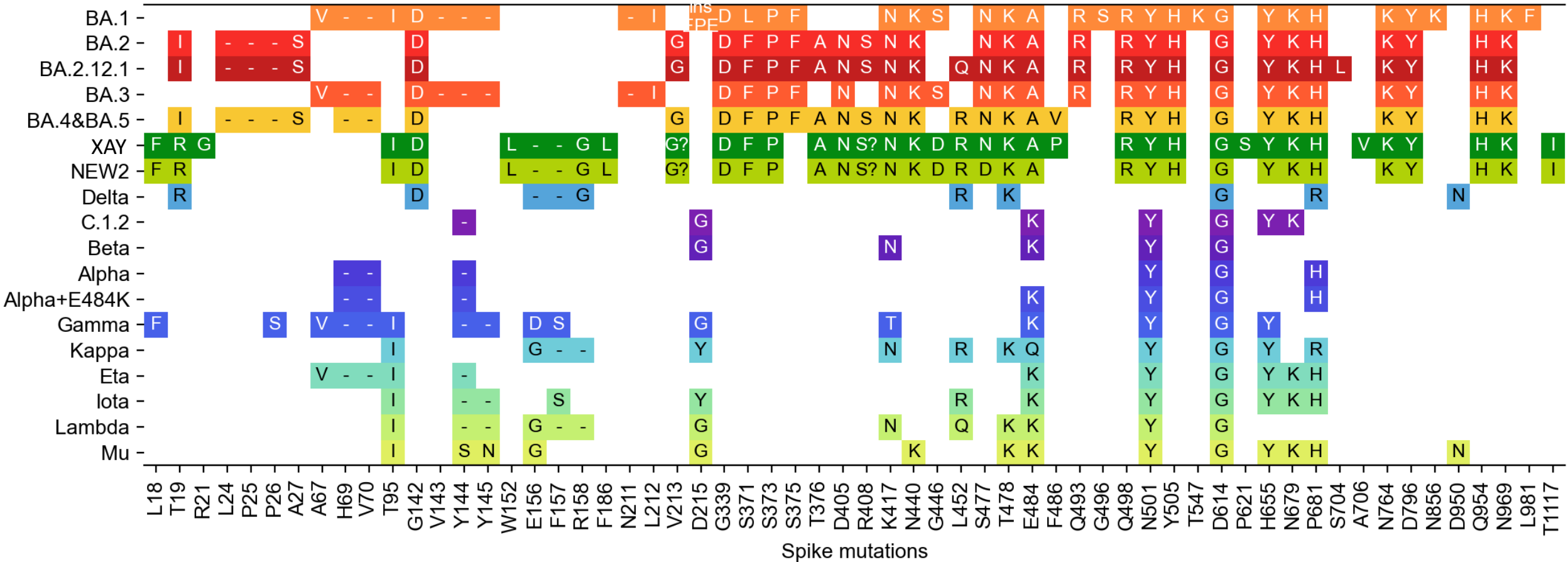
\*May include genomes from 2020 which are not pictured here and are not included in the slide total.

# Summary

- **Sequencing update**
  - All provinces have sequences for June and July. Only the North West does not have August data. Gauteng and the Western Cape have September data.
- **Variant of Concern Omicron in South Africa**
  - Omicron continued to dominate in June (99%), July (99%), August (98%), and currently makes up 100% of September sequences although numbers are small.
  - Omicron BA.5 was dominant in July (68%) and August (72%), and makes up 83% of September data.
  - BA.2.12.1 was detected in South Africa at low prevalence in May, June and July (<1%)
  - BA.2.75 has only been detected once in South Africa in July (n=1).
- **N=13 sequences with novel mutational profile**
  - The New1 cluster (n = 9, predominantly from Gauteng) has been designated “XAY”, and the New2 cluster (n = 4, Limpopo) has been designated XBA<sup>1</sup>.
  - N=1 new XAY has been detected since the previous report, collected 31 August in the Western Cape.
- Low frequency of previously circulating variants such as Delta not detected since July.

<sup>1</sup> <https://github.com/cov-lineages/pango-designation/issues/844>

# Spike protein mutation\* profile of Variants of Interest and Concern



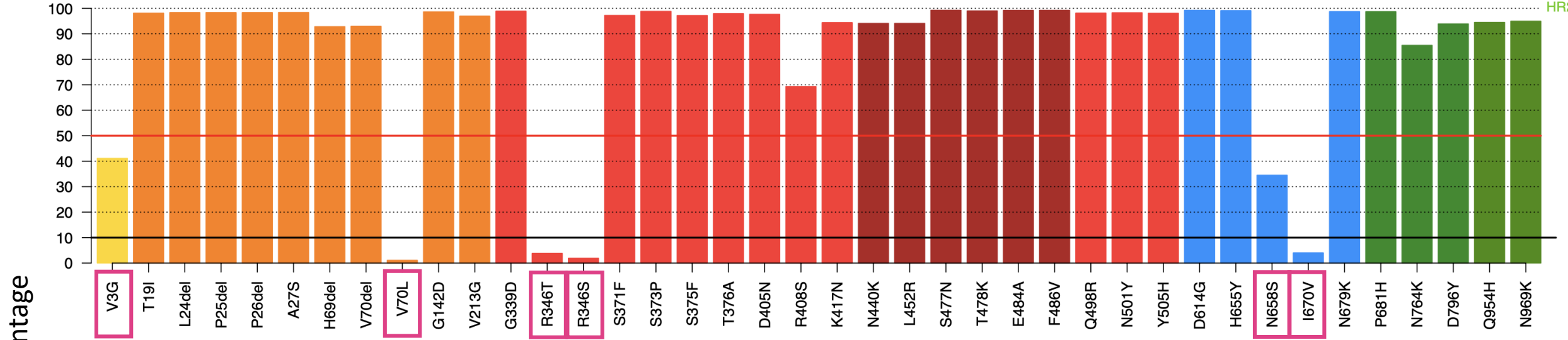
- Multiple changes within the two immunogenic regions in S1 (NTD and RBD)
  - Including a three amino acid insertion
- Accumulation of mutations surrounding the furin cleavage site
  - Including combination of N679K and P681H
- Effect of most spike S2 subunit changes have not been defined, but may be linked to immune escape

\*Only mutations present in Omicron, Delta, or the new SGTP sequences are pictured

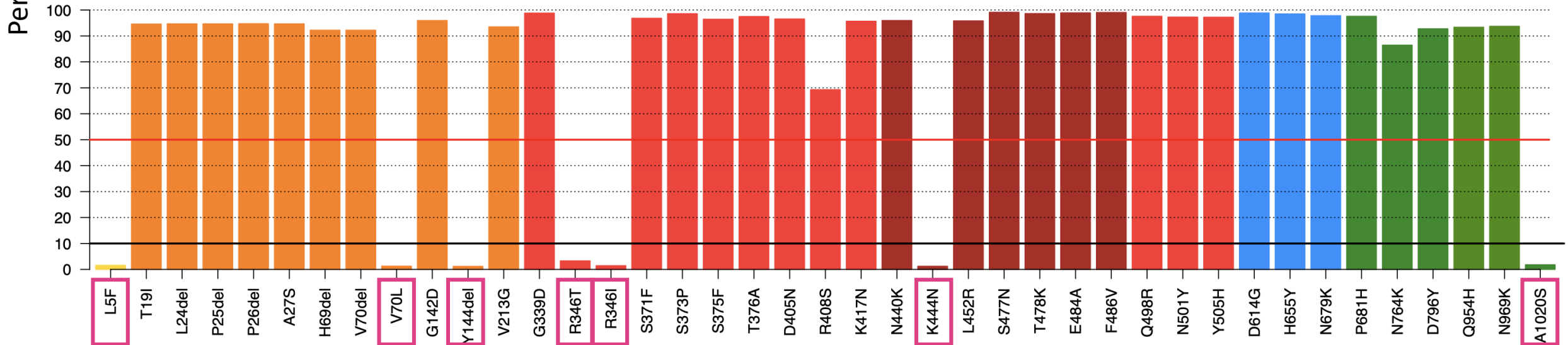
# BA.4 and BA.5 spike mutations

SP  
NTD  
RBD  
RBM  
S1  
S2  
HR1  
HR2

Frequency of spike SNVs for Omicron (22A/BA.4.\*) (n = 3953)

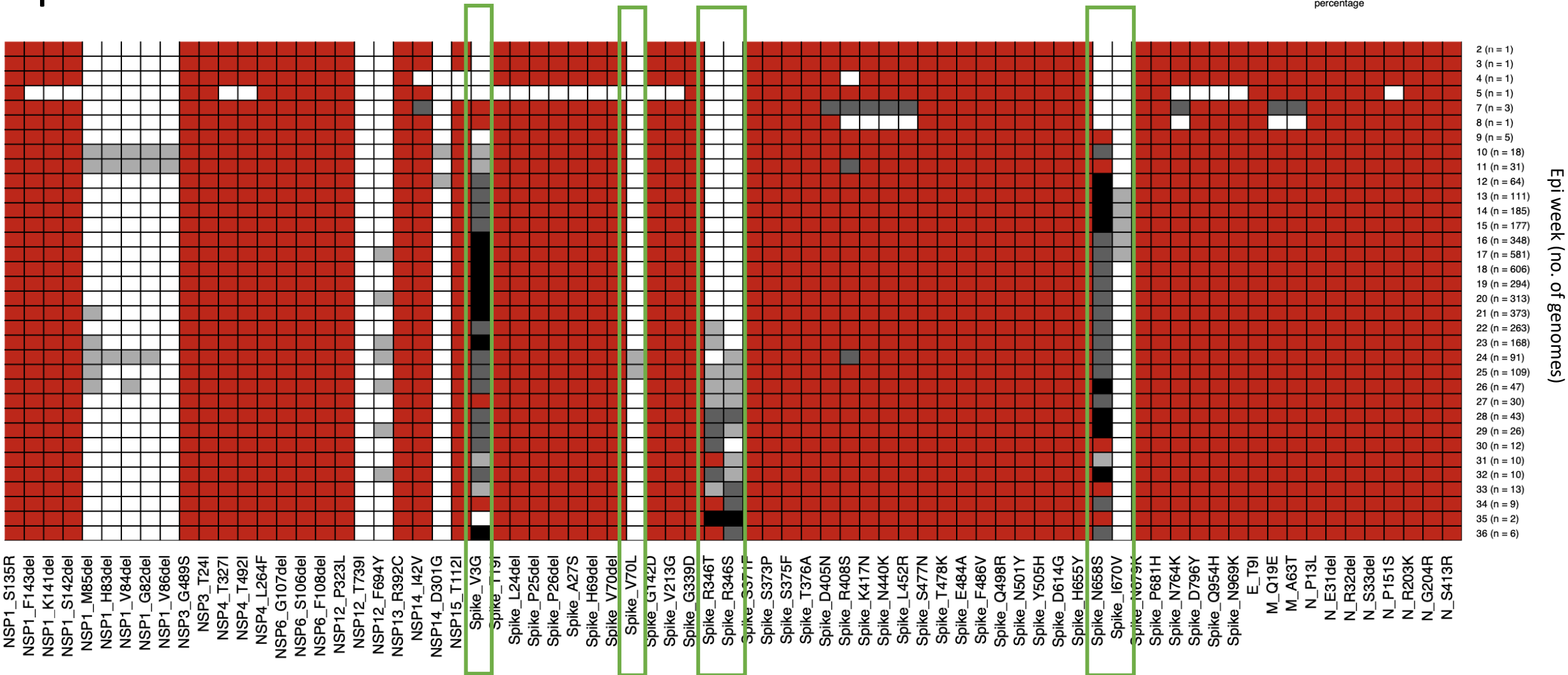
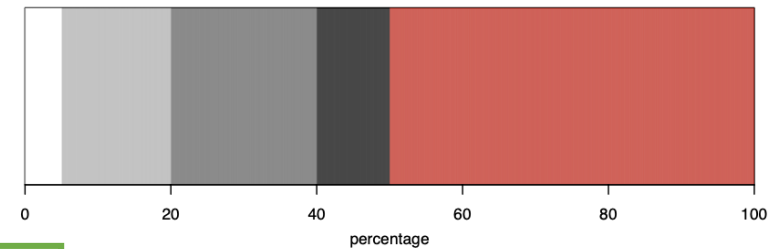


Frequency of spike SNVs for Omicron (22B/BA.5.\*) (n = 2202)



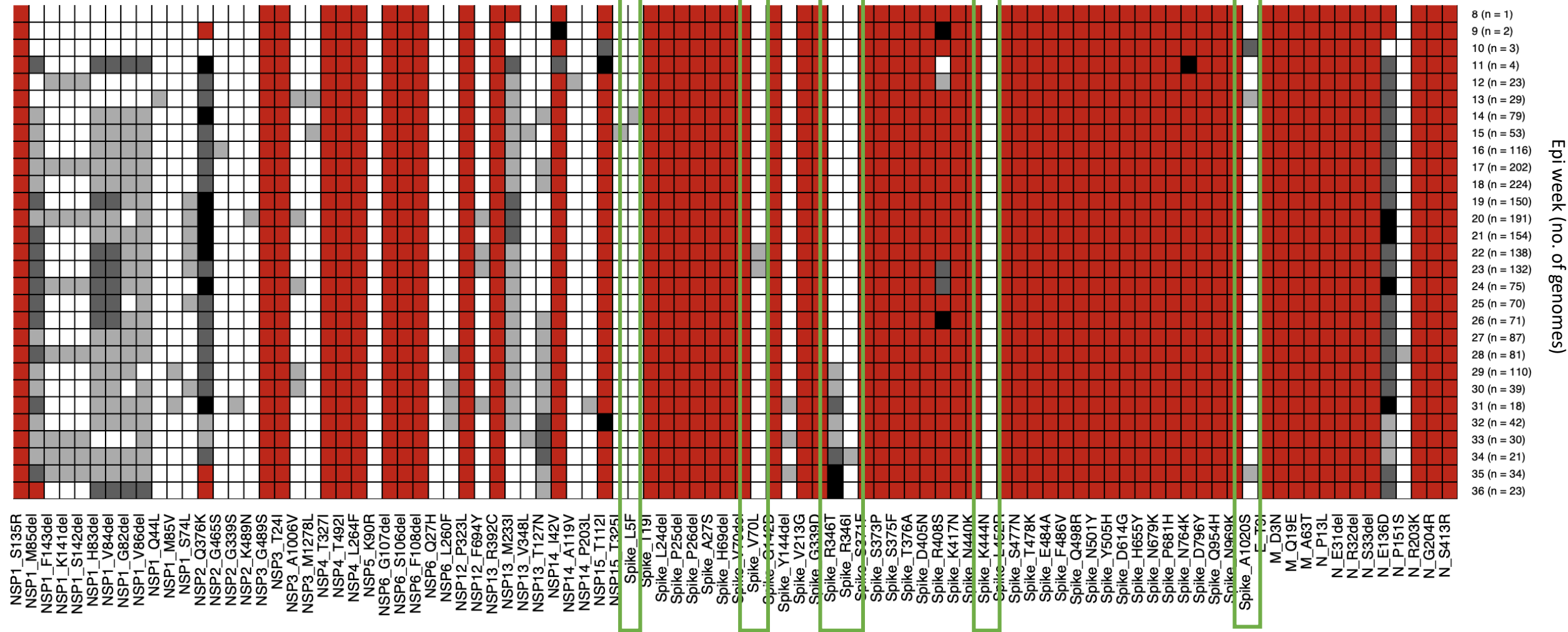
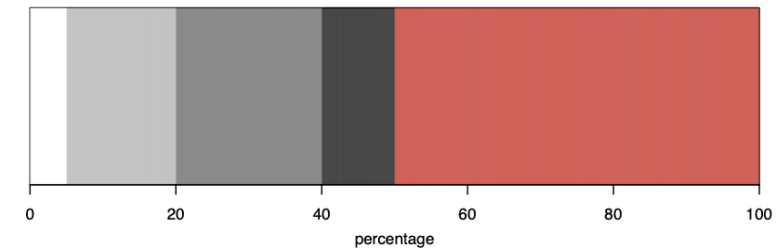
Mutation

# BA.4 whole genome mutation prevalence over time



NSP1\_S135R  
 NSP1\_F143del  
 NSP1\_K141del  
 NSP1\_S142del  
 NSP1\_M85del  
 NSP1\_H83del  
 NSP1\_V84del  
 NSP1\_G82del  
 NSP1\_V86del  
 NSP3\_G489S  
 NSP3\_T24I  
 NSP4\_T327I  
 NSP4\_T492I  
 NSP4\_L264F  
 NSP6\_G107del  
 NSP6\_S106del  
 NSP6\_F108del  
 NSP12\_P323L  
 NSP12\_T739I  
 NSP12\_F694Y  
 NSP13\_R392C  
 NSP14\_I42V  
 NSP14\_D301G  
 NSP15\_T112I  
 Spike\_V3G  
 Spike\_I19I  
 Spike\_L24del  
 Spike\_P25del  
 Spike\_P26del  
 Spike\_A27S  
 Spike\_H69del  
 Spike\_V70del  
 Spike\_V70L  
 Spike\_G142D  
 Spike\_V213G  
 Spike\_G339D  
 Spike\_R346T  
 Spike\_R346S  
 Spike\_S371F  
 Spike\_S373P  
 Spike\_S375F  
 Spike\_T376A  
 Spike\_D405N  
 Spike\_R408S  
 Spike\_K417N  
 Spike\_N440K  
 Spike\_L452R  
 Spike\_S477N  
 Spike\_T478K  
 Spike\_E484A  
 Spike\_F486V  
 Spike\_Q498R  
 Spike\_N501Y  
 Spike\_Y505H  
 Spike\_D614G  
 Spike\_H655Y  
 Spike\_N658S  
 Spike\_I670V  
 Spike\_V679K  
 Spike\_P681H  
 Spike\_N764K  
 Spike\_D796Y  
 Spike\_Q954H  
 Spike\_N969K  
 E\_T9I  
 M\_Q19E  
 M\_A63T  
 N\_P13L  
 N\_E31del  
 N\_R32del  
 N\_S33del  
 N\_P151S  
 N\_R203K  
 N\_G204R  
 N\_S413R

# BA.5 whole genome mutation prevalence over time





# NGS-SA

Network for Genomic Surveillance in South Africa



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INYUVESI  
YAKWAZULU-NATALI



EDCTP

This project (RIA2020EF-3030) is part of the EDCTP2 programme supported by the European Union"



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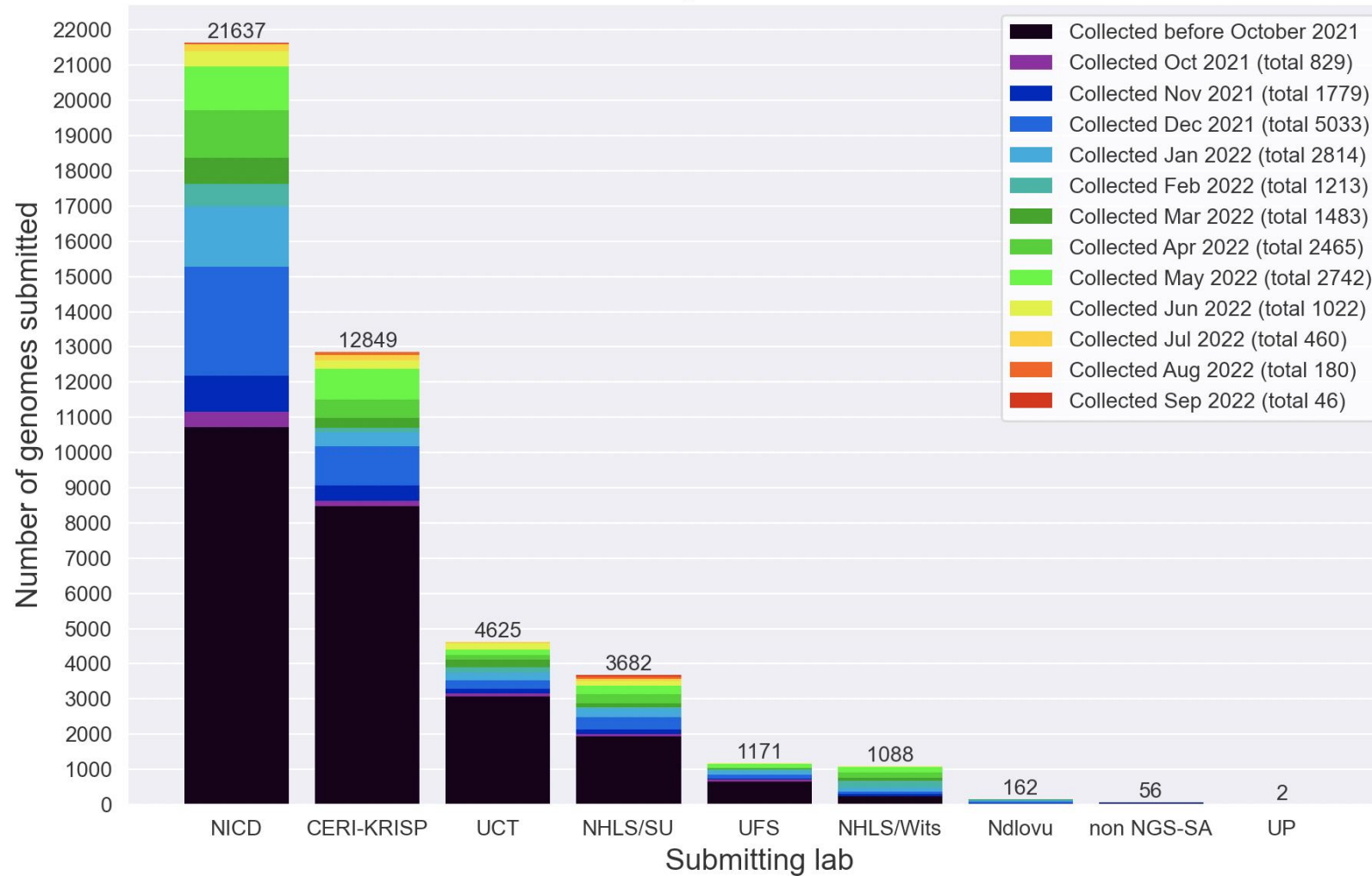
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# South African genomes submitted per submitting lab, 2020 - 2022 (N=45 272)

Submitting labs in South Africa



## NGS-SA Labs

- CERI:** Centre for Epidemic Response and Innovation
- KRISP:** KZN Research Innovation and Sequencing Platform
- NDLOVU:** Ndlovu Research Laboratories
- NICD:** National Institute for Communicable Diseases
- NHLS:** National Health Laboratory Service
- SU:** Stellenbosch University
- UCT:** University of Cape Town
- UFS:** University of the Free State
- UP:** University of Pretoria

Multiple labs from NGS-SA and collaborating public and private laboratories are contributing to sequencing, both as originating and as submitting (pictured here) laboratories.

# Currently circulating Variants of Concern (VOC)

WHO label	Pango lineage <sup>•</sup>	GISAID clade	Nextstrain clade	Additional amino acid changes monitored <sup>°</sup>	Earliest documented samples	Date of designation
Omicron*	B.1.1.529	GR/484A	21K, 21L, 21M, 22A, 22B, 22C, 22D	+S:R346K +S:L452X +S:F486V	Multiple countries, Nov-2021	VUM: 24-Nov-2021 VOC: 26-Nov-2021

\* Includes BA.1, BA.2, BA.3, BA.4, BA.5 and descendent lineages. It also includes BA.1/BA.2 circulating recombinant forms such as XE. WHO emphasizes that these descendant lineages should be monitored as distinct lineages by public health authorities and comparative assessments of their virus characteristics should be undertaken.

<sup>•</sup> Only found in a subset of sequences

# Previously circulating Variants of Concern

WHO label	Pango lineage•	GISAID clade	Nextstrain clade	Earliest documented samples	Date of designation
Alpha	B.1.1.7	GRY	20I (V1)	United Kingdom, Sep-2020	VOC: 18-Dec-2020 Previous VOC: 09-Mar-2022
Beta	B.1.351	GH/501Y.V2	20H (V2)	South Africa, May-2020	VOC: 18-Dec-2020 Previous VOC: 09-Mar-2022
Gamma	P.1	GR/501Y.V3	20J (V3)	Brazil, Nov-2020	VOC: 11-Jan-2021 Previous VOC: 09-Mar-2022
Delta	B.1.617.2	G/478K.V1	21A, 21I, 21J	India, Oct-2020	VOI: 4-Apr-2021 VOC: 11-May-2021 Previous VOC: 7-Jun-2022

• Includes all descendant lineages. See the [cov-lineages.org](https://cov-lineages.org) and the Pango network websites for further details.

<https://www.who.int/en/activities/tracking-SARS-CoV-2-variants/> accessed 12 August 2022

# Submission of routine specimens for sequencing

- representative of multiple geographic regions (provinces/districts/health facilities) from individuals of
  - all ages
  - over as many time periods during the SARS-CoV-2 epidemic in South Africa
- requested that testing laboratories in both the private and public sectors, submit respiratory samples to their closest NGS-SA sequencing laboratory on a routine basis (ideally every week) as follows, depending on the capacity of the testing laboratory:
  - All positives samples should be sent every week (NGS-SA laboratory will perform random sampling as described below) **OR**
  - A weekly selection of approximately 10%-20% of randomly selected positive samples should be sent every week. Number of selected samples will depend on the size of laboratory and how many other laboratories are drained by the submitting laboratory.

# Submission of special interest specimens for sequencing

In addition to routine samples mentioned above, please send specimens separately to above and clearly marked if:

- Suspected vaccine breakthrough ( $\geq 14$  days after vaccine), especially if hospitalised and clinically severe
- Suspected re-infection ( $\geq 90$  days after previous episode), especially if hospitalised and clinically severe
- Prolonged shedding with high SARS-CoV-2 viral loads (i.e. Ct values less than 30 for more than 1 month post-primary diagnosis) in immunocompromised individuals
- Possible animal-to-human transmission
- Suspected cases of importation from another country, especially countries known to harbour SARS-CoV-2 variants of concern or countries with little available information
- Clusters of “unusual” cases (e.g., in terms of disease presentation, patient groups affected, etc.)