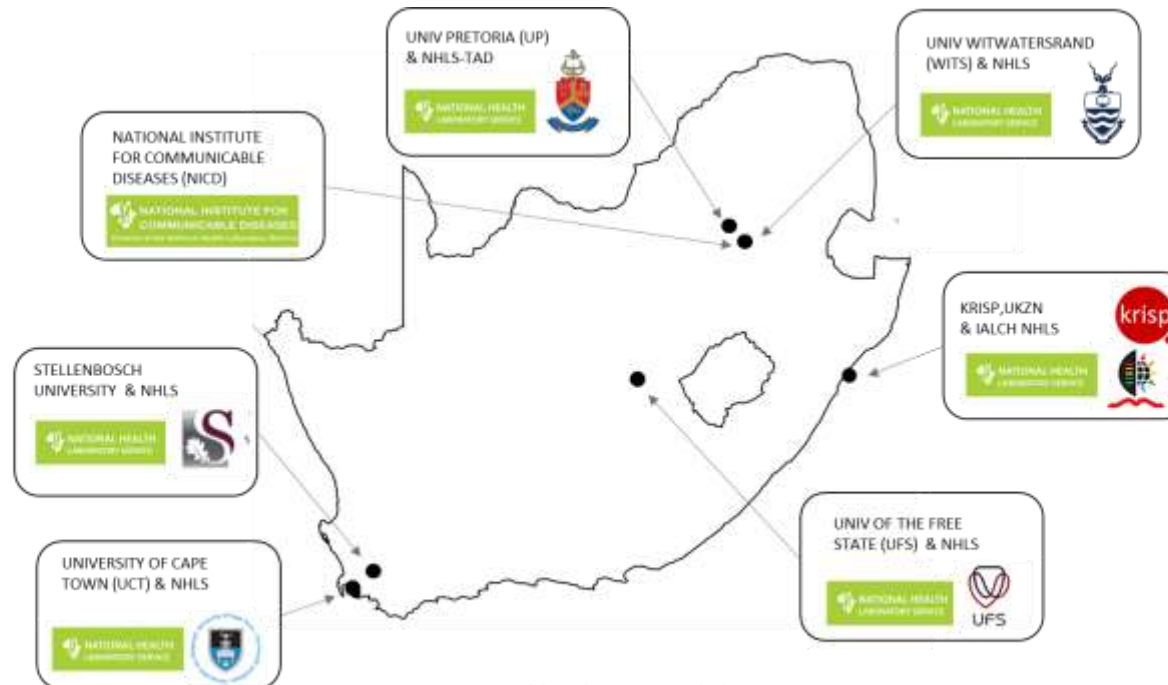


## SARS-CoV-2 Sequencing Update 02 September 2022



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 01 September 2022 at 08h37

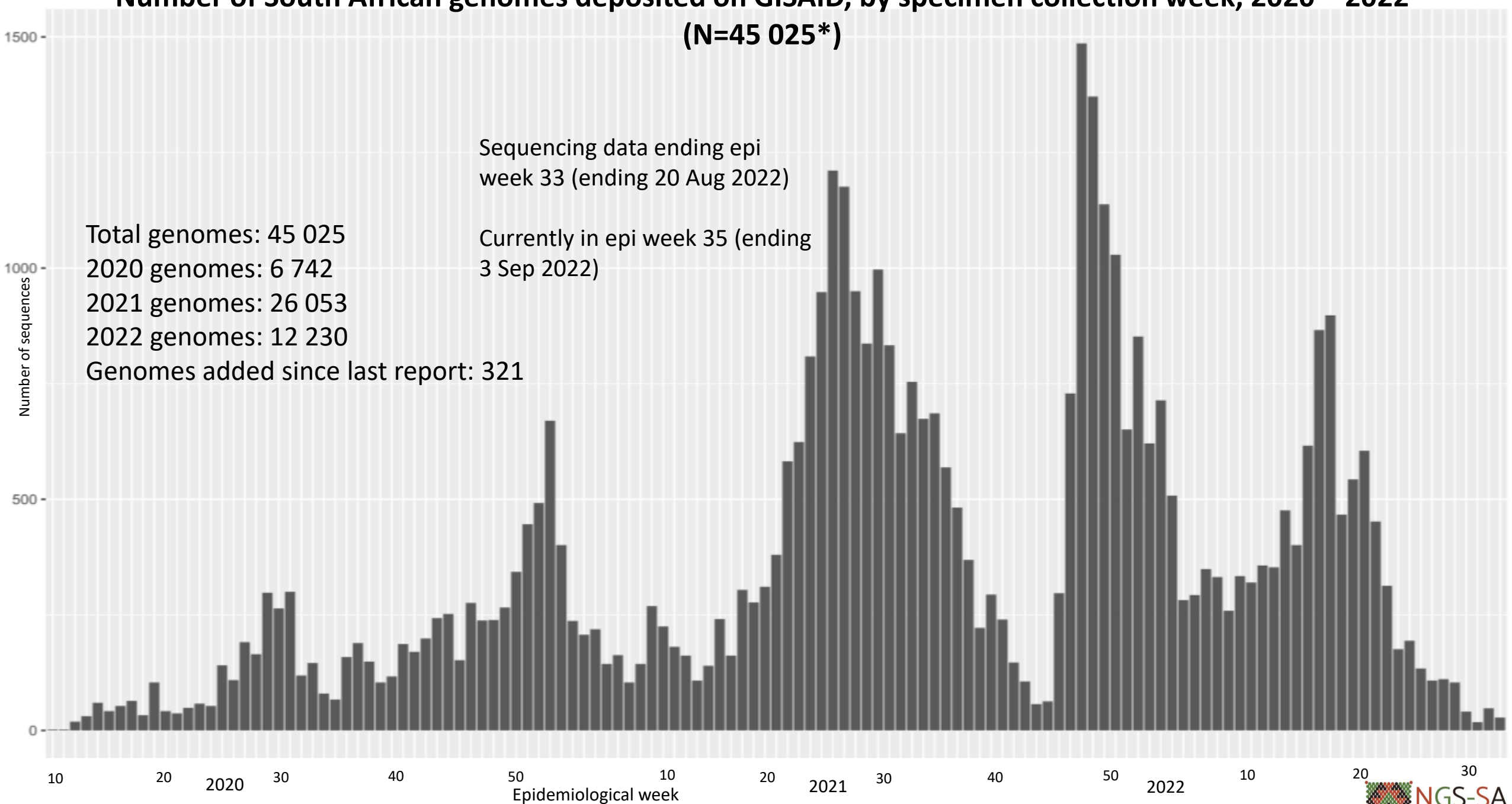


Data license: <https://www.gisaid.org/registration/terms-of-use/>

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 PMCID: 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 PMCID: PMC5388101

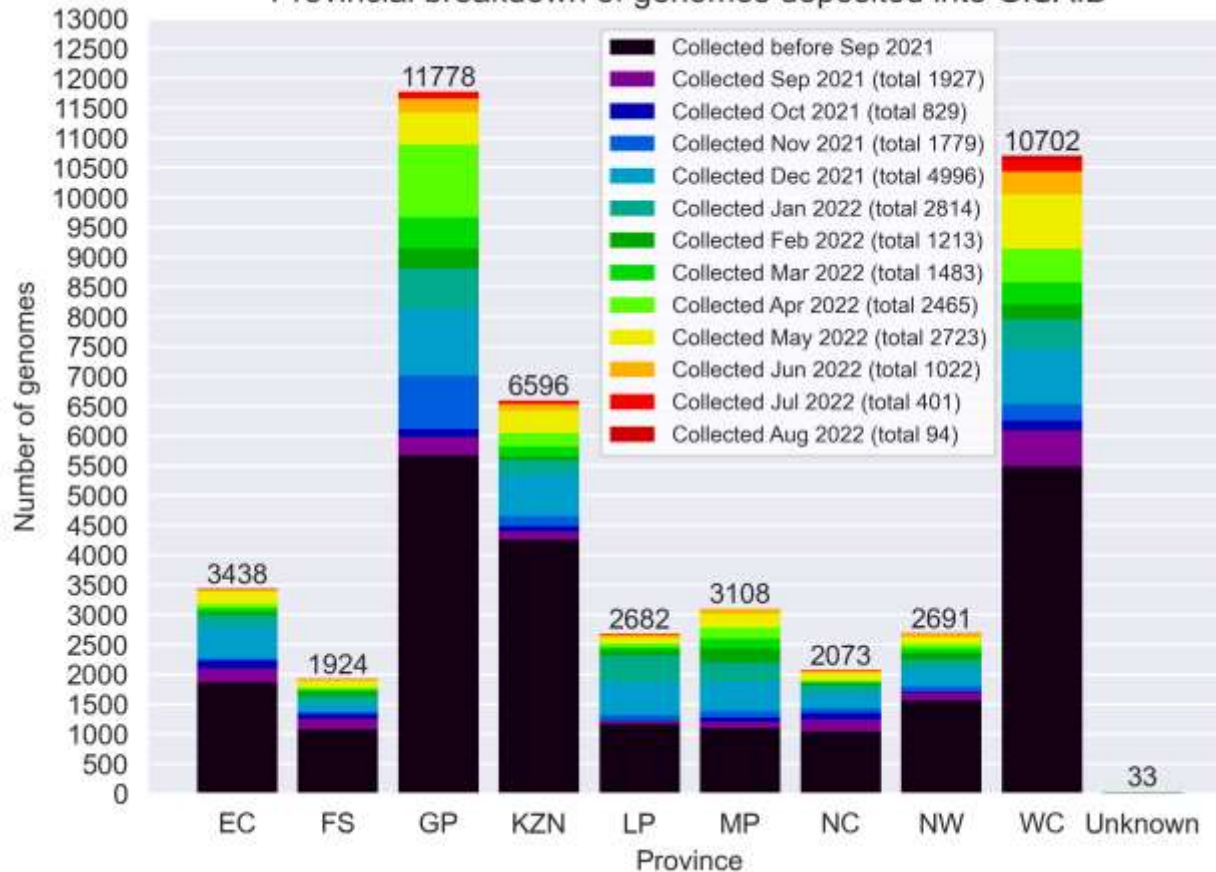
# Number of South African genomes deposited on GISAID, by specimen collection week, 2020 – 2022 (N=45 025\*)



\*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=45 025)

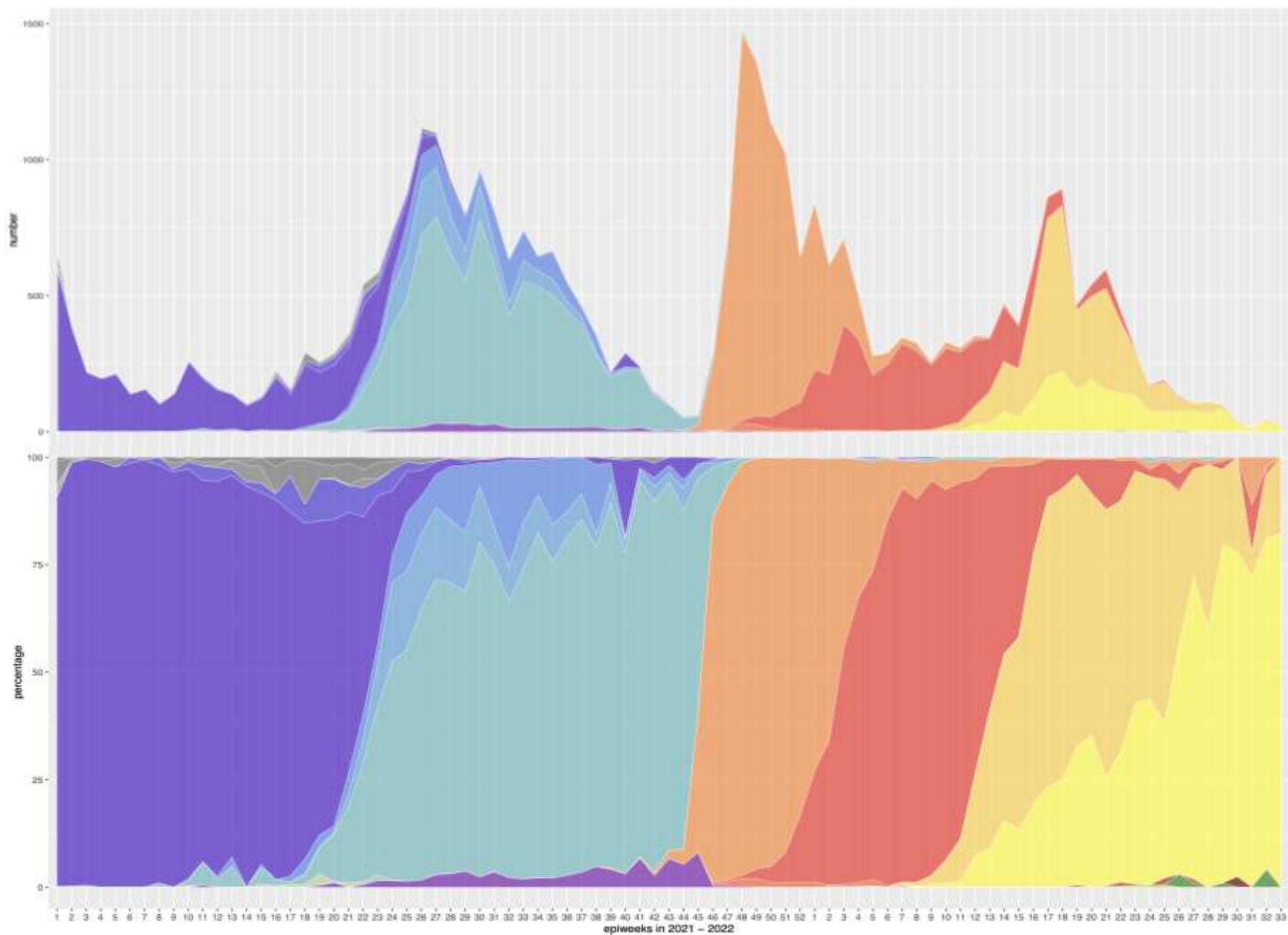
Provincial breakdown of genomes deposited into GISAID



Proportion of total cases versus proportion of total genomes



# Number and percentage of clades by epiweek in South Africa, 2021 – 2022 (38 196\*)



Nextclade clades

- 19A
- 19B
- 20A
- 20B
- 20C
- 20D
- Alpha (20I, V1)
- Beta (20H, V2)
- Delta (21A)
- Delta (21I)
- Delta (21J)
- Eta (21D)
- Kappa (21B)
- Omicron (21K/BA.1.\*)
- Omicron (21L/BA.2.\*)
- Omicron (21M/BA.3)
- Omicron (22A/BA.4.\*)
- Omicron (22B/BA.5.\*)
- Omicron (22C/BA.2.12.1)
- Omicron (22D/BA.2.75)
- C.1.2 (20C)
- XAY
- New2

Sequencing data  
ending epi week 33  
(ending 20 Aug 2022)

Currently in epi week  
35 (ending 3 Sep 2022)

Nextclade clades

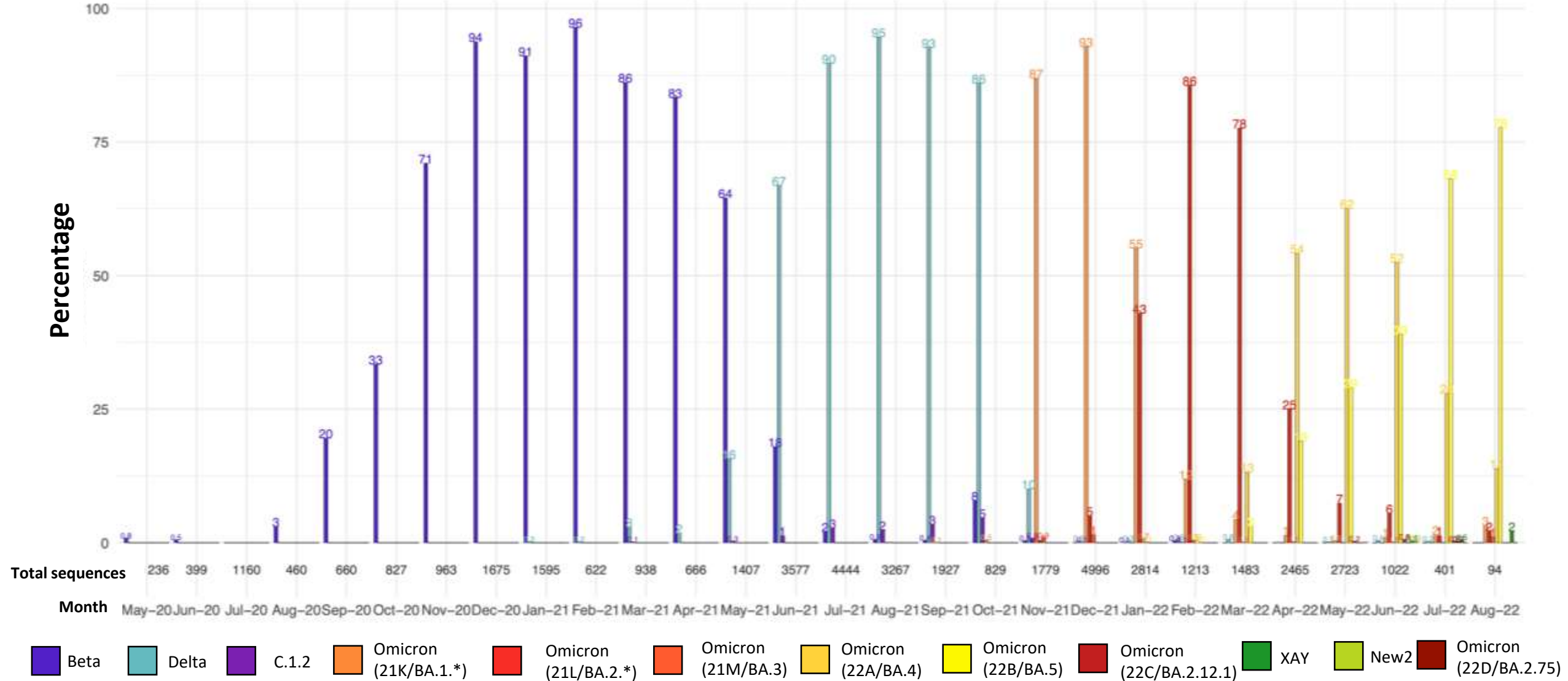
- 19A
- 19B
- 20A
- 20B
- 20C
- 20D
- Alpha (20I, V1)
- Beta (20H, V2)
- Delta (21A)
- Delta (21I)
- Delta (21J)
- Eta (21D)
- Kappa (21B)
- Omicron (21K/BA.1.\*)
- Omicron (21L/BA.2.\*)
- Omicron (21M/BA.3)
- Omicron (22A/BA.4.\*)
- Omicron (22B/BA.5.\*)
- Omicron (22C/BA.2.12.1)
- Omicron (22D/BA.2.75)
- C.1.2 (20C)
- XAY
- New2

\*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.



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

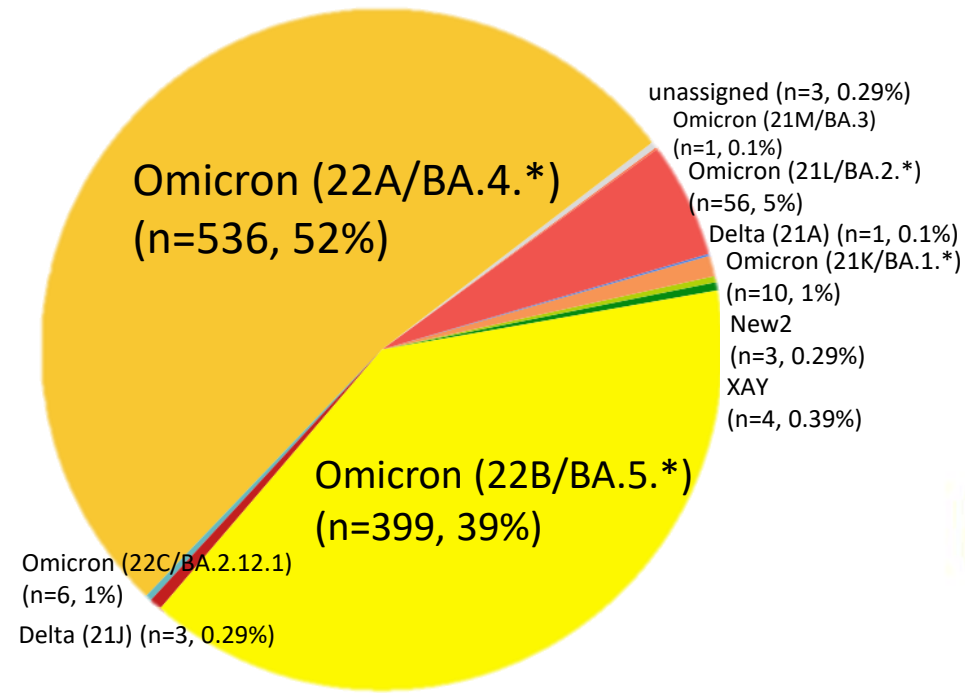
Detection rates of variants being monitored in South Africa



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

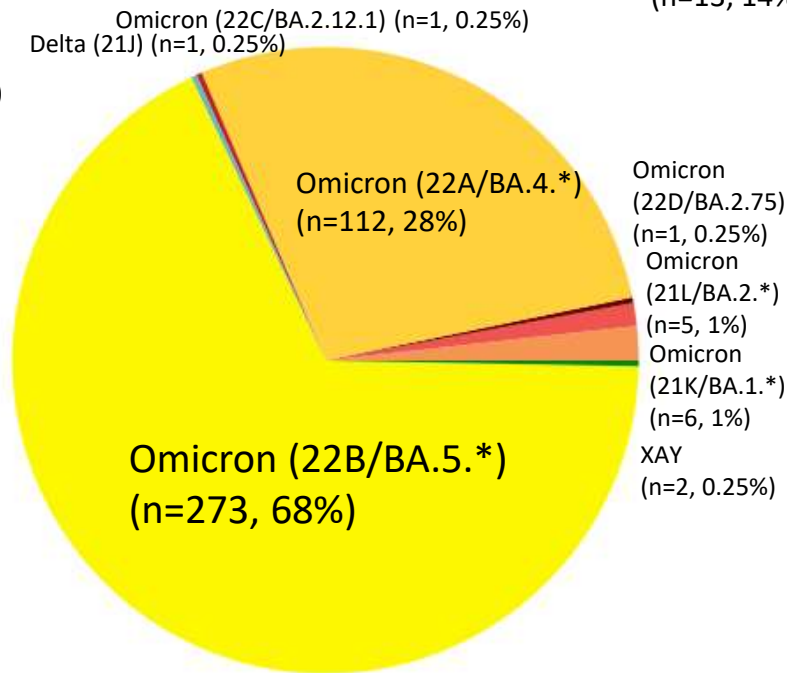
# Prevalence of Variants of Concern (VOC) and Variants of Interest (VOI) in June – August 2022

June (N=1022)



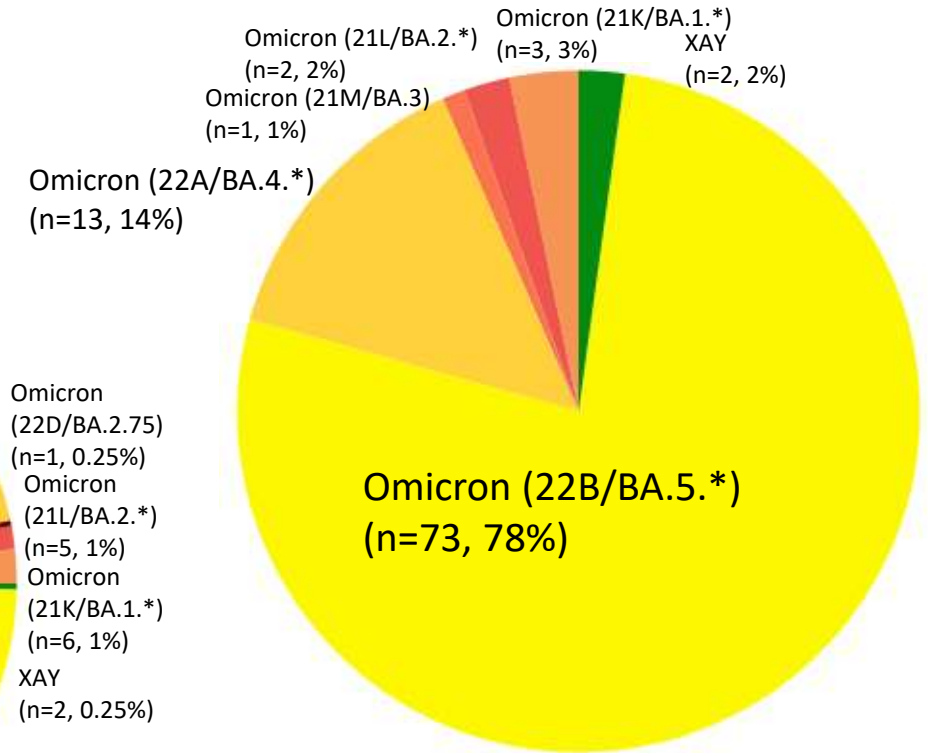
Total Omicron in June: 1008 (98.6%)

July (N=401)



Total Omicron in July: 398 (99.3%)

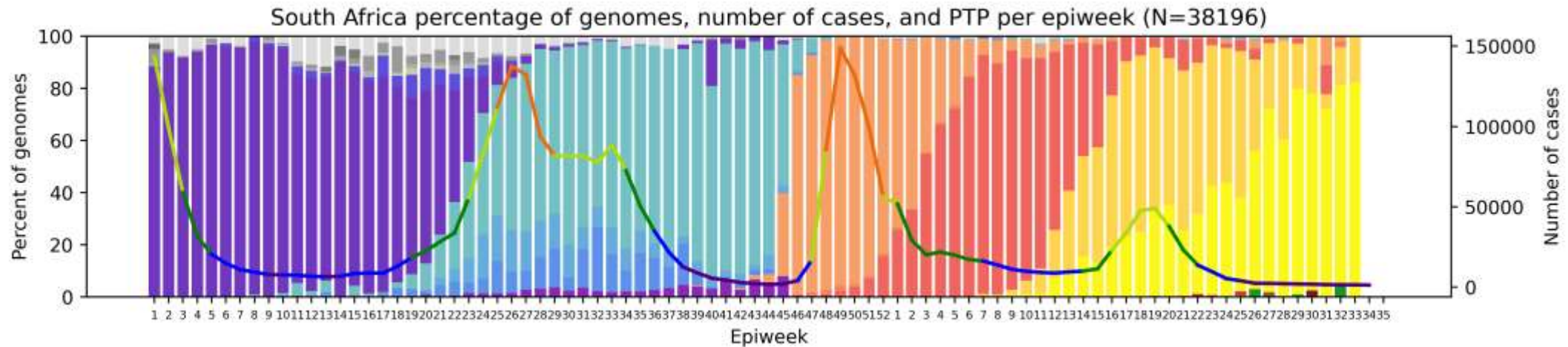
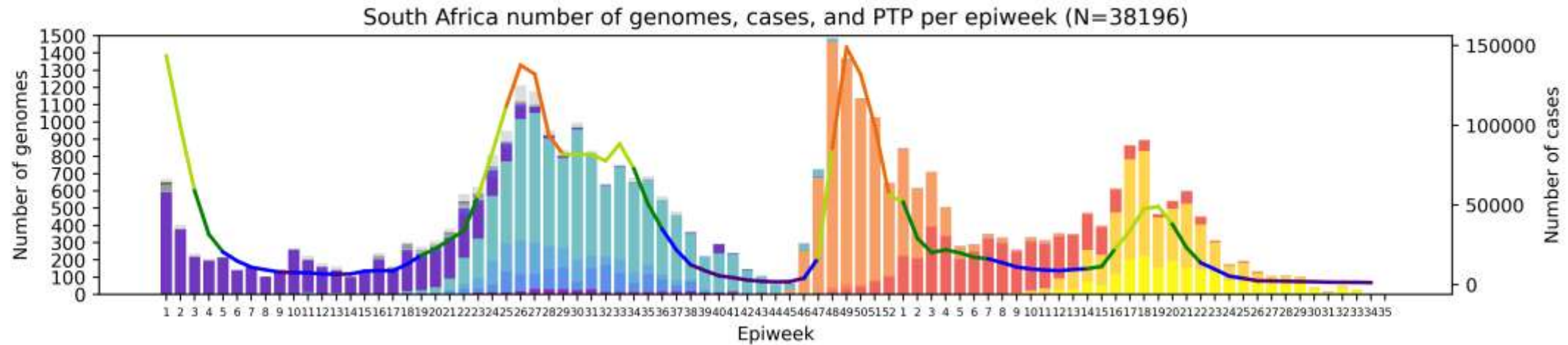
August (N=94)



Total Omicron in August: 92 (97.9%)



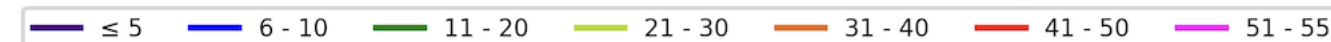
# South Africa, 2021-2022, n = 38 196\*



Clade key (bar graph)



Weekly percentage testing positive key (line graph)

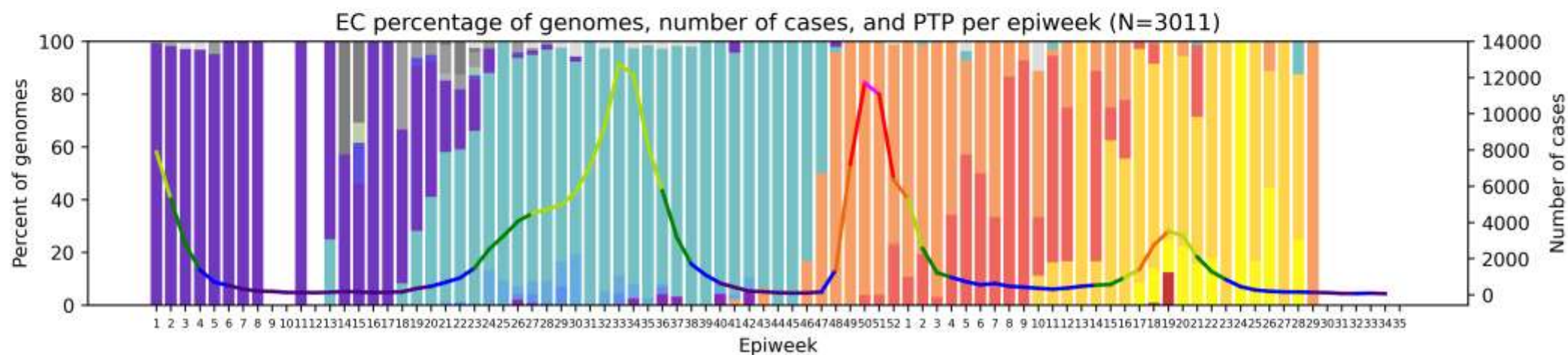
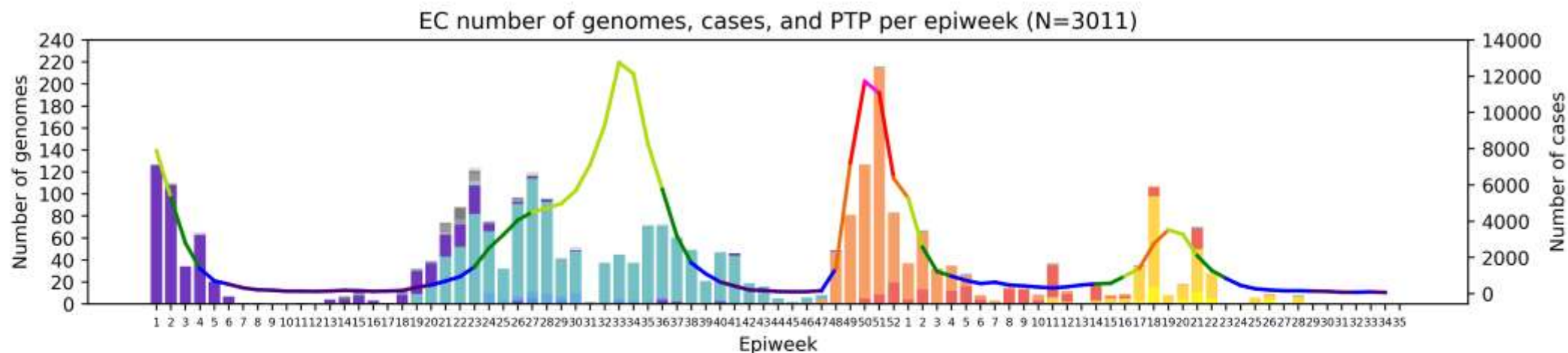


\*Excludes sequences missing collection dates, as well as those collected January 1<sup>st</sup> and 2<sup>nd</sup> 2021 as they are part of epiweek 53 of 2020.



# Eastern Cape Province, 2021-2022, n = 3011

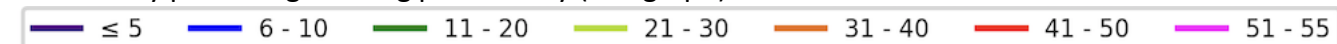
Genomes added since last report: 7\*



Clade key (bar graph)



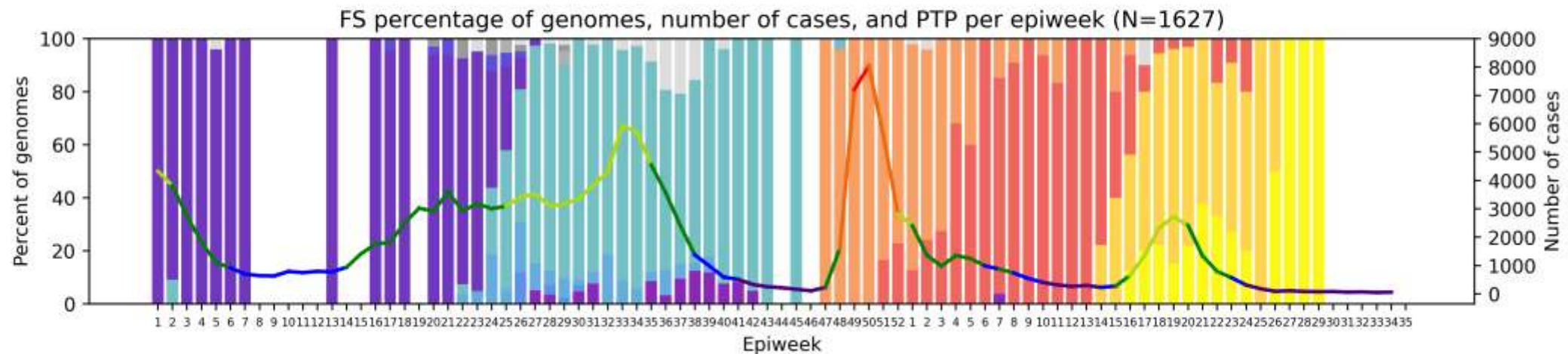
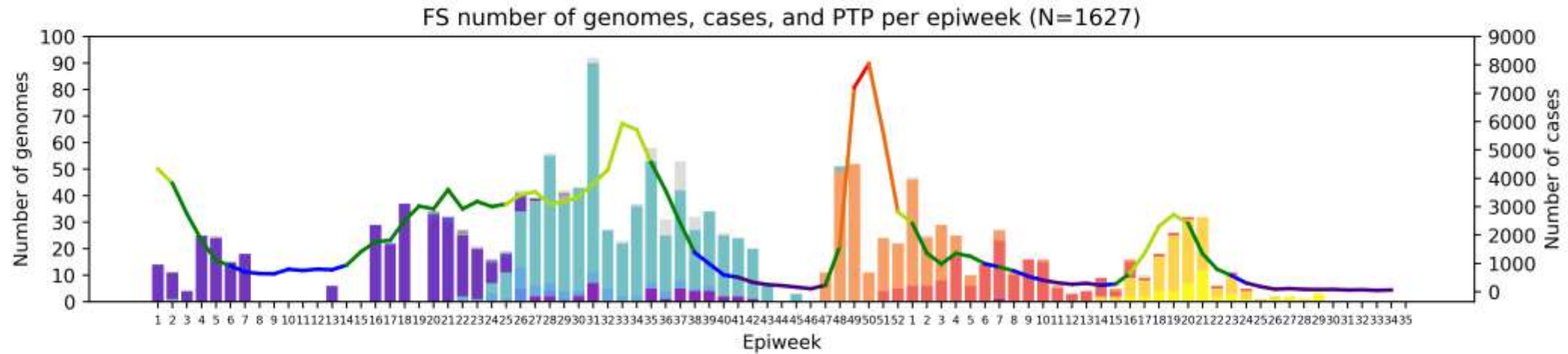
Weekly percentage testing positive key (line graph)



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

# Free State Province, 2021-2022, n = 1627

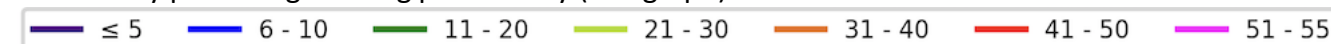
Genomes added since last report: 4\*



Clade key (bar graph)



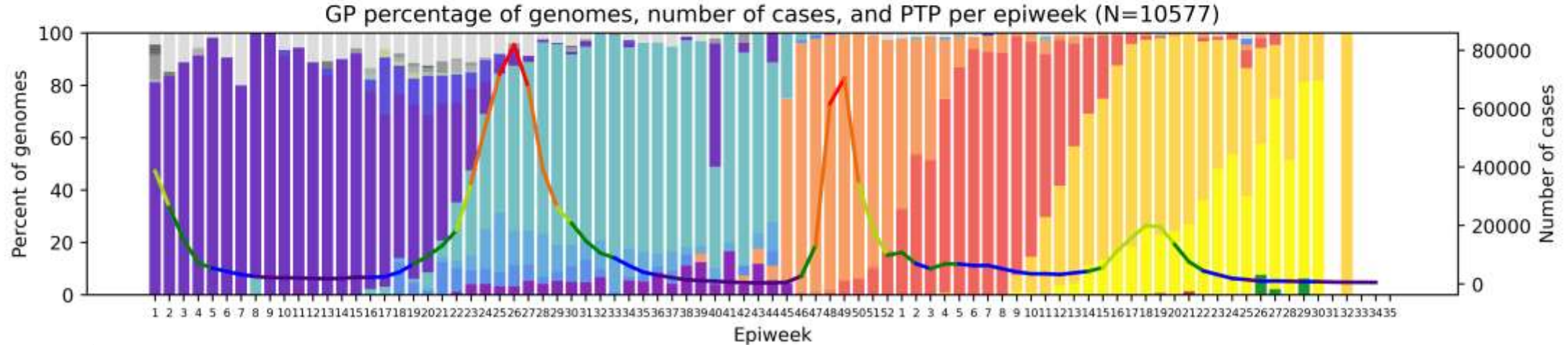
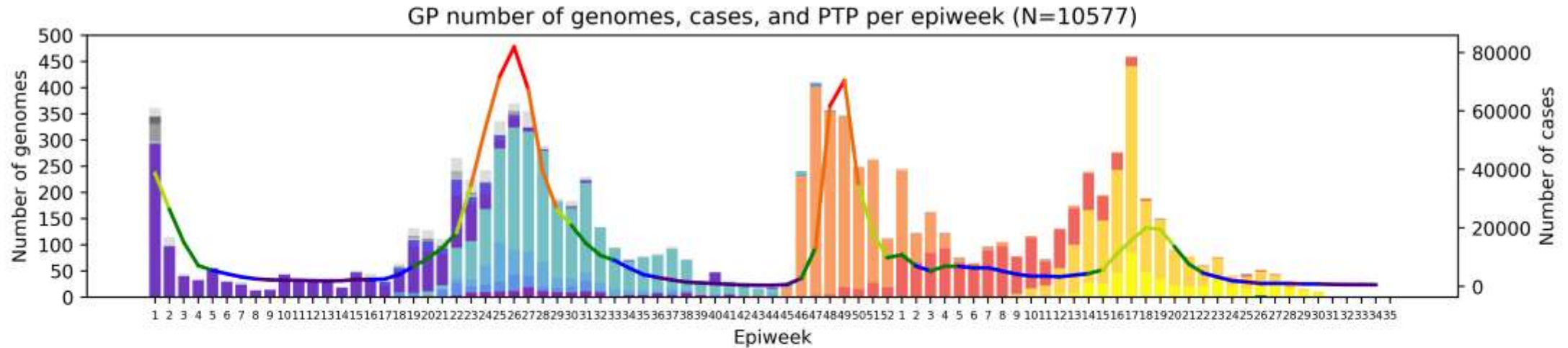
Weekly percentage testing positive key (line graph)



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

# Gauteng Province, 2021-2022, n = 10 577

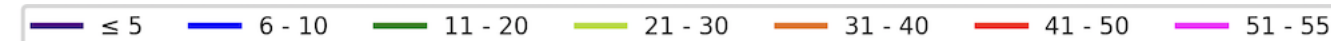
Genomes added since last report: 85\*



Clade key (bar graph)



Weekly percentage testing positive key (line graph)

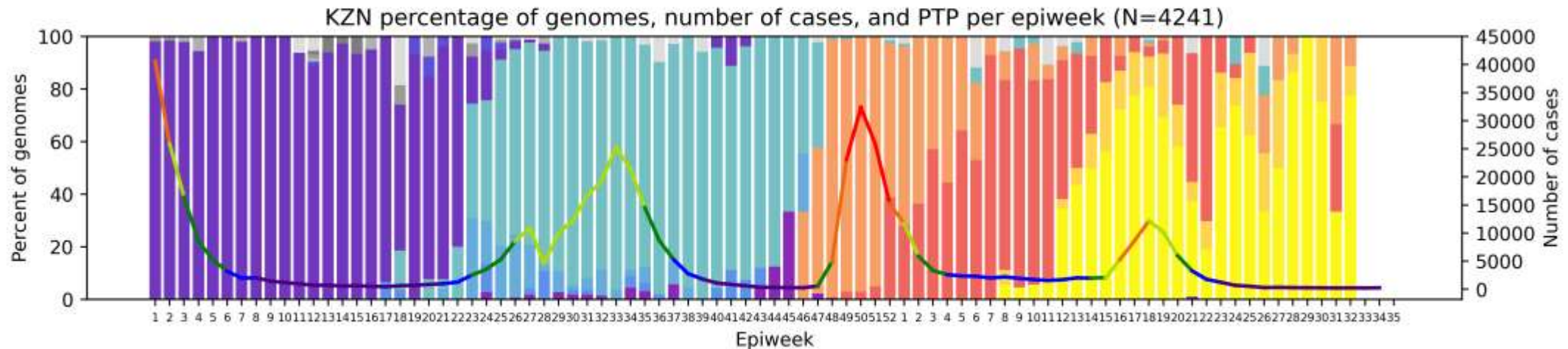
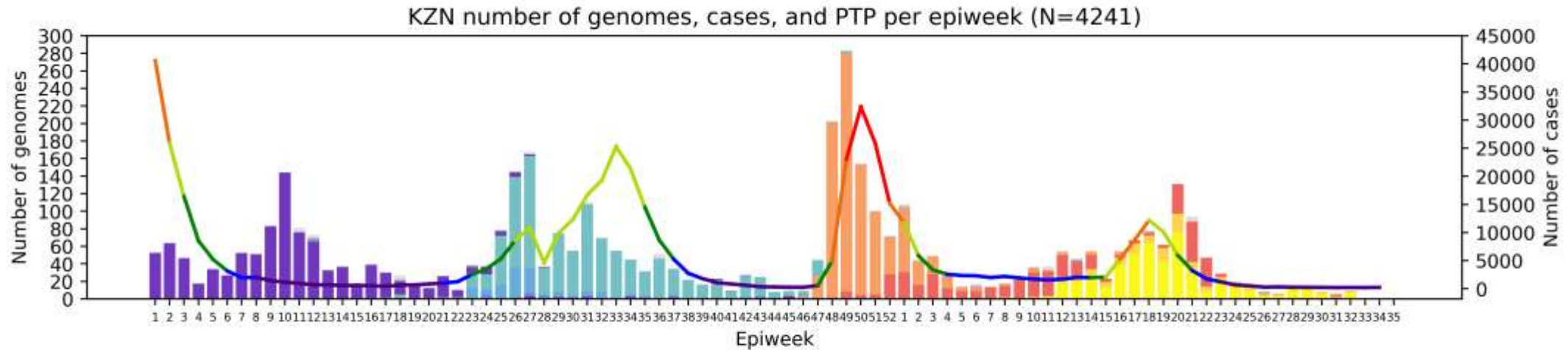


\*May include genomes from 2020 which are not pictured here and are not included in the slide total.



# KwaZulu-Natal Province, 2021-2022, n = 4241

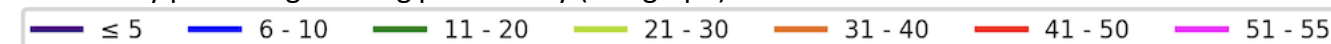
Genomes added since last report: 89\*



Clade key (bar graph)



Weekly percentage testing positive key (line graph)

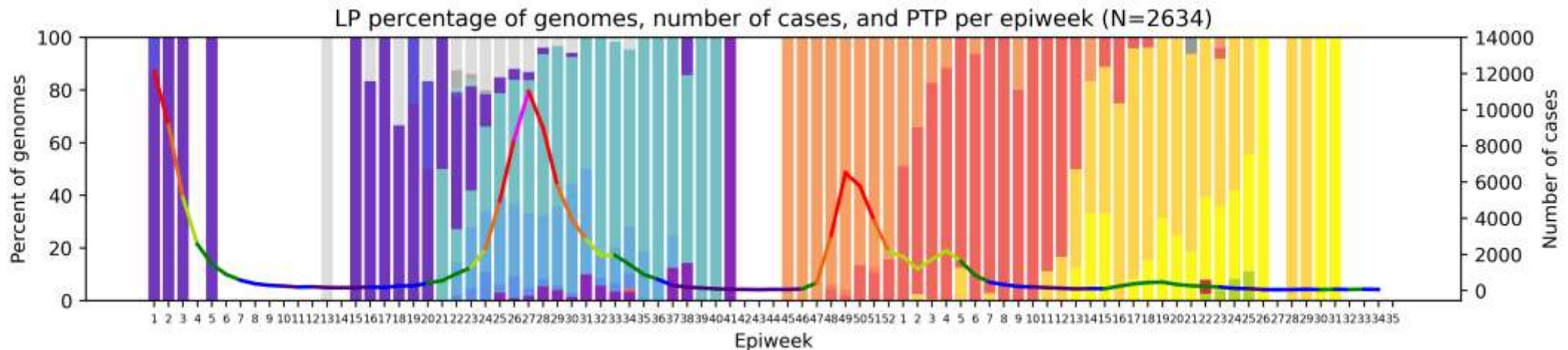
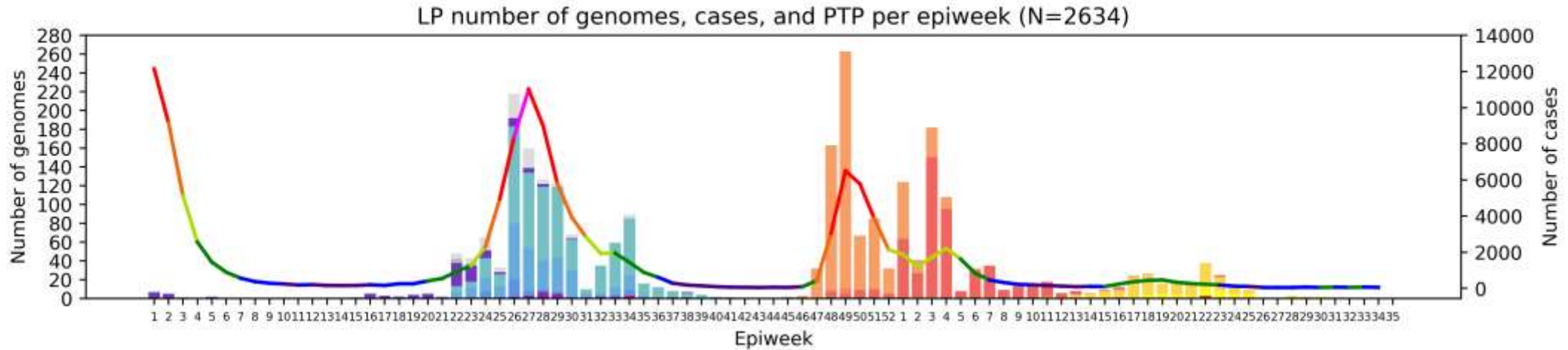


\*May include genomes from 2020 which are not pictured here and are not included in the slide total.



# Limpopo Province, 2021-2022, n = 2634

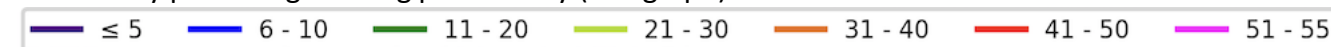
Genomes added since last report: 24\*



Clade key (bar graph)



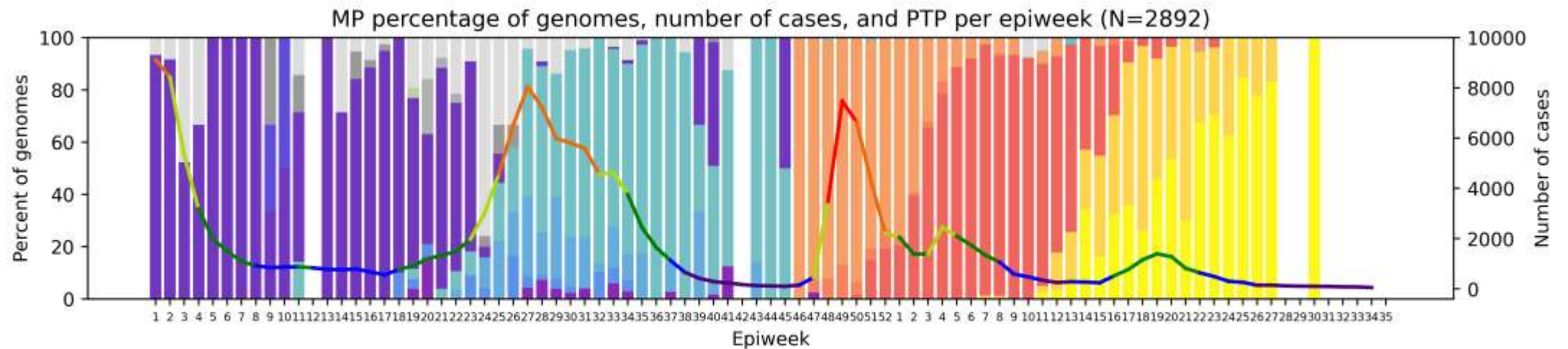
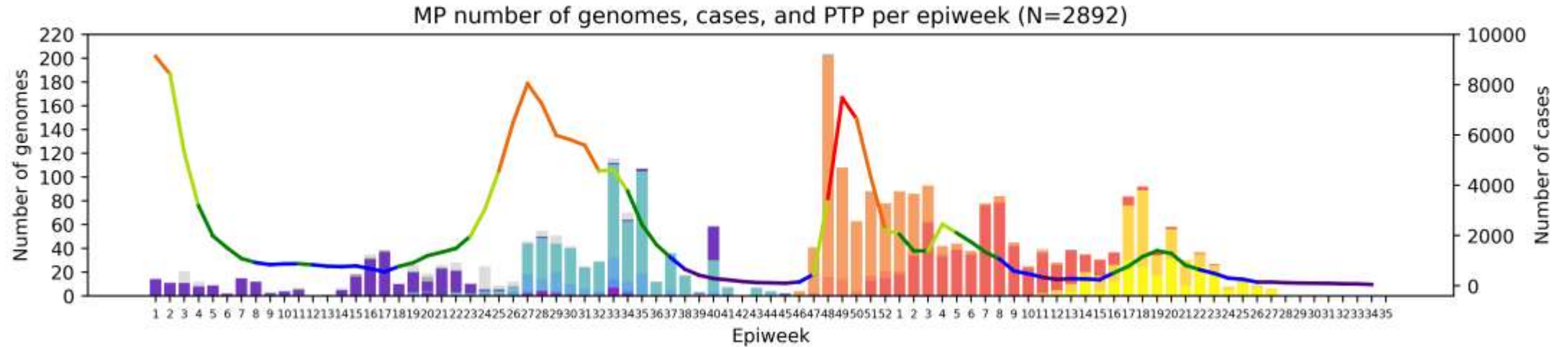
Weekly percentage testing positive key (line graph)



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

# Mpumalanga Province, 2021-2022, n = 2892

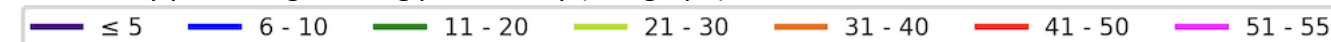
Genomes added since last report: 56\*



Clade key (bar graph)



Weekly percentage testing positive key (line graph)

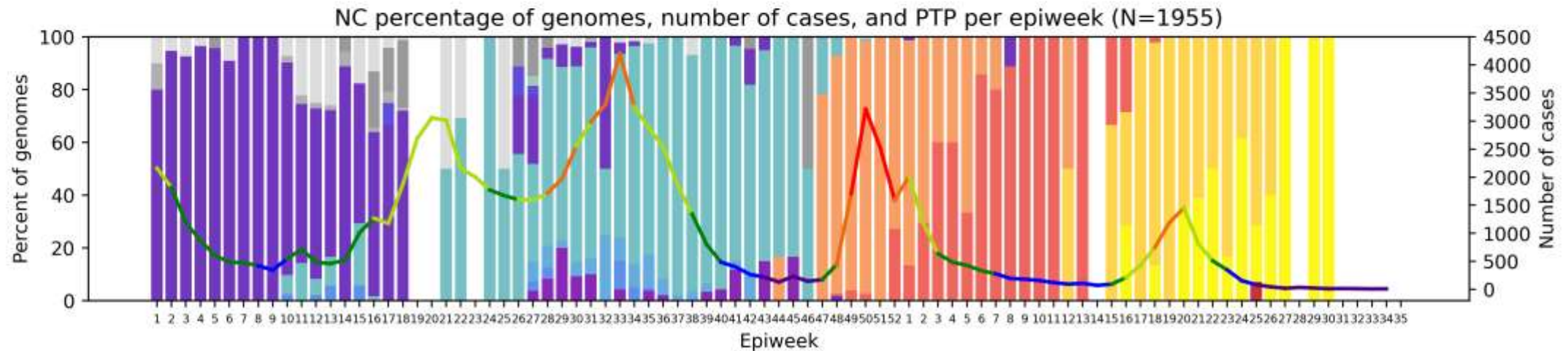
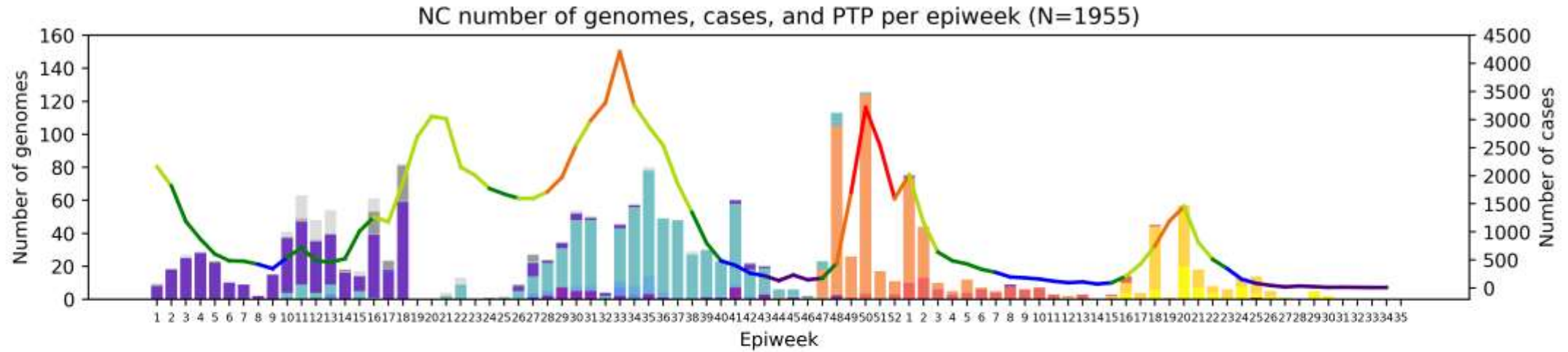


\*May include genomes from 2020 which are not pictured here and are not included in the slide total.



# Northern Cape Province, 2021-2022, n = 1955

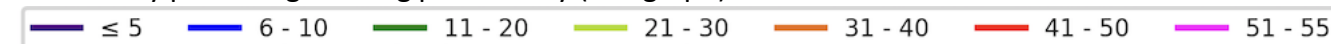
Genomes added since last report: 13\*



Clade key (bar graph)



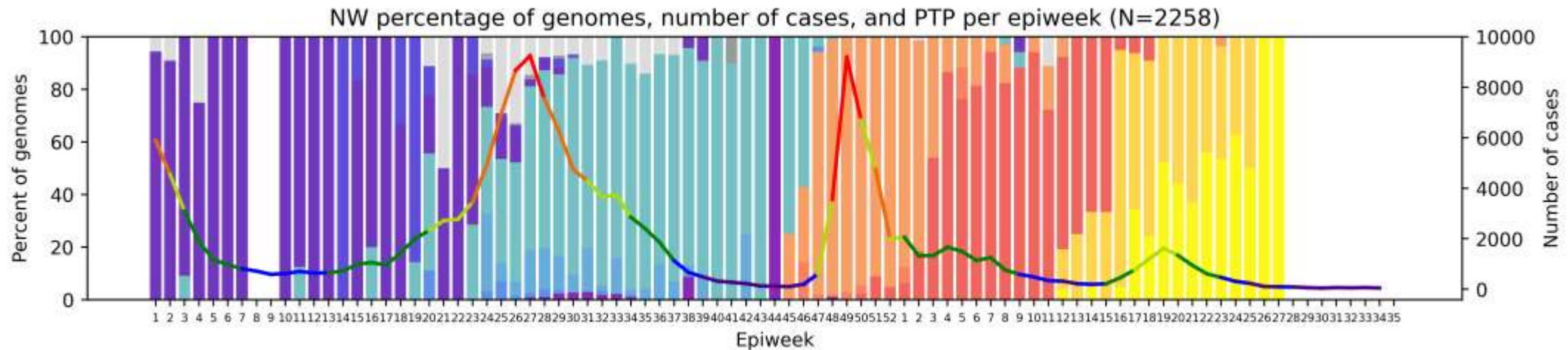
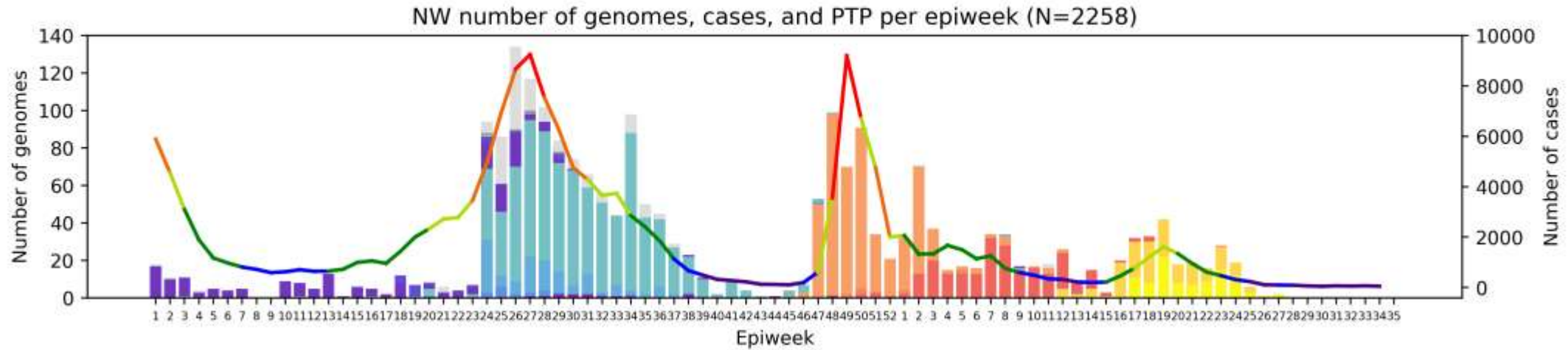
Weekly percentage testing positive key (line graph)



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

# North West Province, 2021-2022, n = 2258

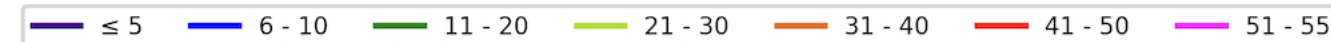
Genomes added since last report: 10\*



Clade key (bar graph)



Weekly percentage testing positive key (line graph)

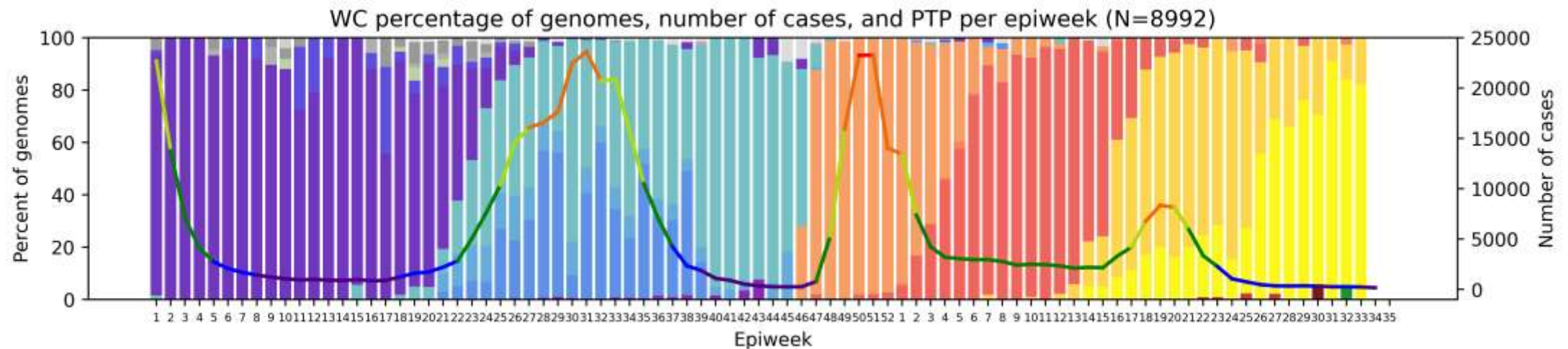
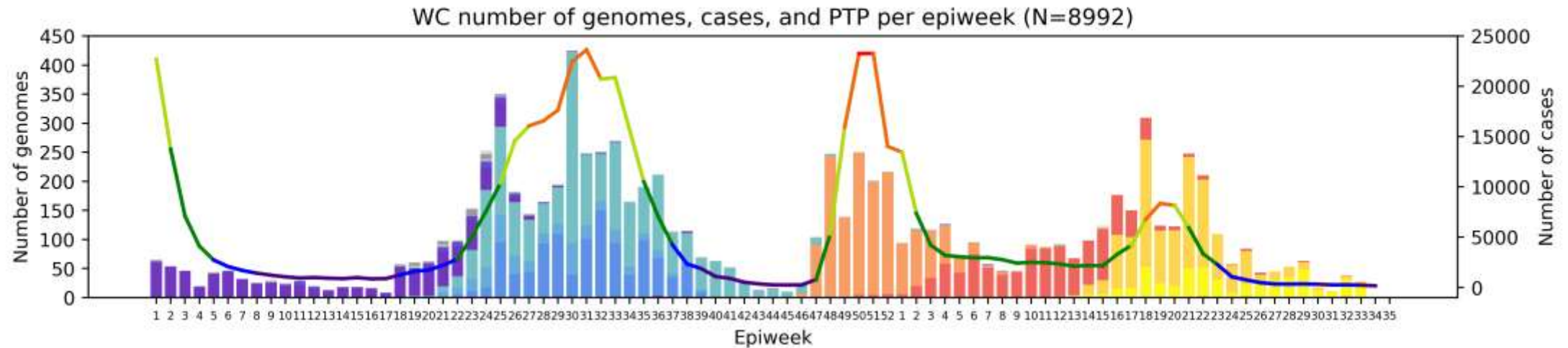


\*May include genomes from 2020 which are not pictured here and are not included in the slide total.



# Western Cape Province, 2021-2022, n = 8992

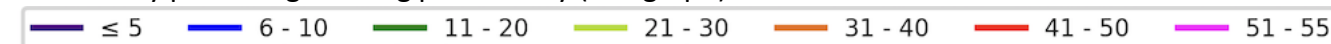
Genomes added since last report: 33\*



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 May, June and July. August sequences are from GP, KZN, LP and WC.
- Omicron dominated in June (98.6%), July (99.3%) and August (97.9%).

- **N=12 sequences with novel mutational profile**

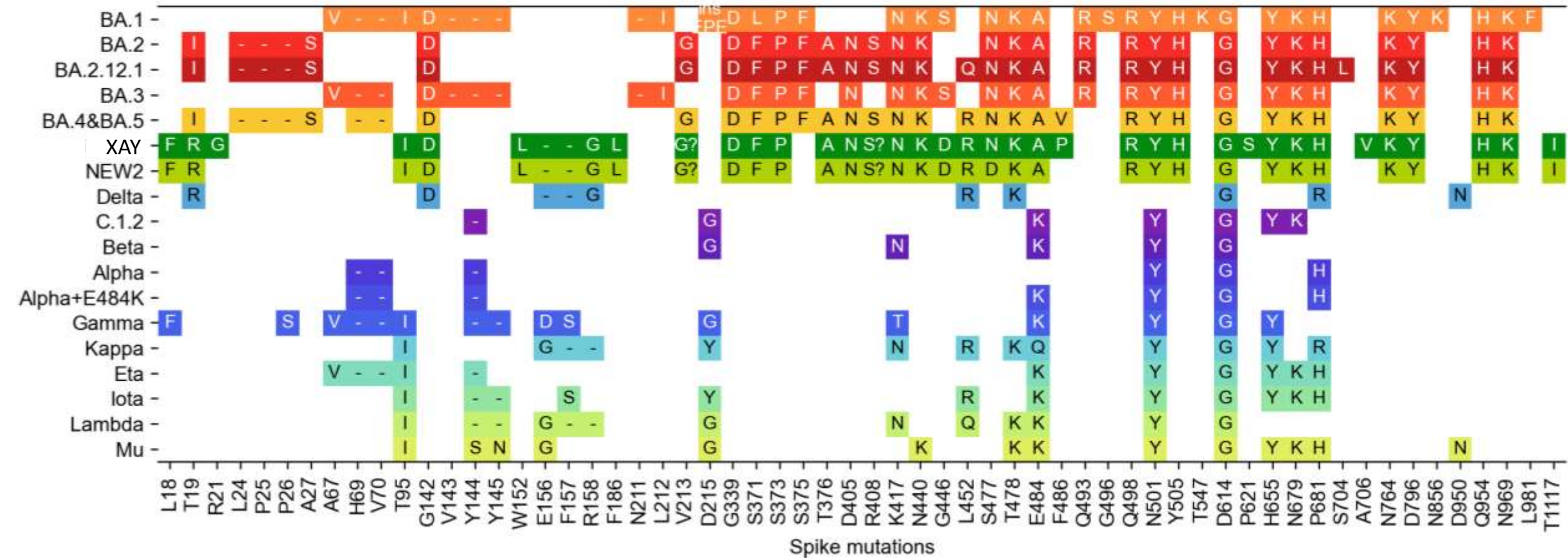
- The designation of XAY has changed since the previous update. The New1 cluster (n = 8, predominantly from Gauteng) has been designated “XAY” while New2 cluster’s numbers (n = 4) are still too low for designation<sup>1</sup>.
- One new XAY sequence has been detected since our last report, collected 18 July 2022 in Gauteng.

- **Variant of Concern Omicron in South Africa**

- Dominates 2022 sequencing data at >98% of genomes.
  - While BA.1 was the predominant lineage in January (55%), BA.2 dominated in February (86%) and March (78%).
  - Omicron lineages BA.4 and BA.5 increased in prevalence in March (16%), and together are dominant in April (73%), May (91%), June (91%), July (96%) and August (92%).
  - BA.2.12.1 was detected in South Africa at low prevalence in May, June and July (<1%)
  - BA.2.75 was detected for the first time in South Africa in July (n=1).
- Low frequency of previously circulating variants such as Delta still detected in recent data.

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

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

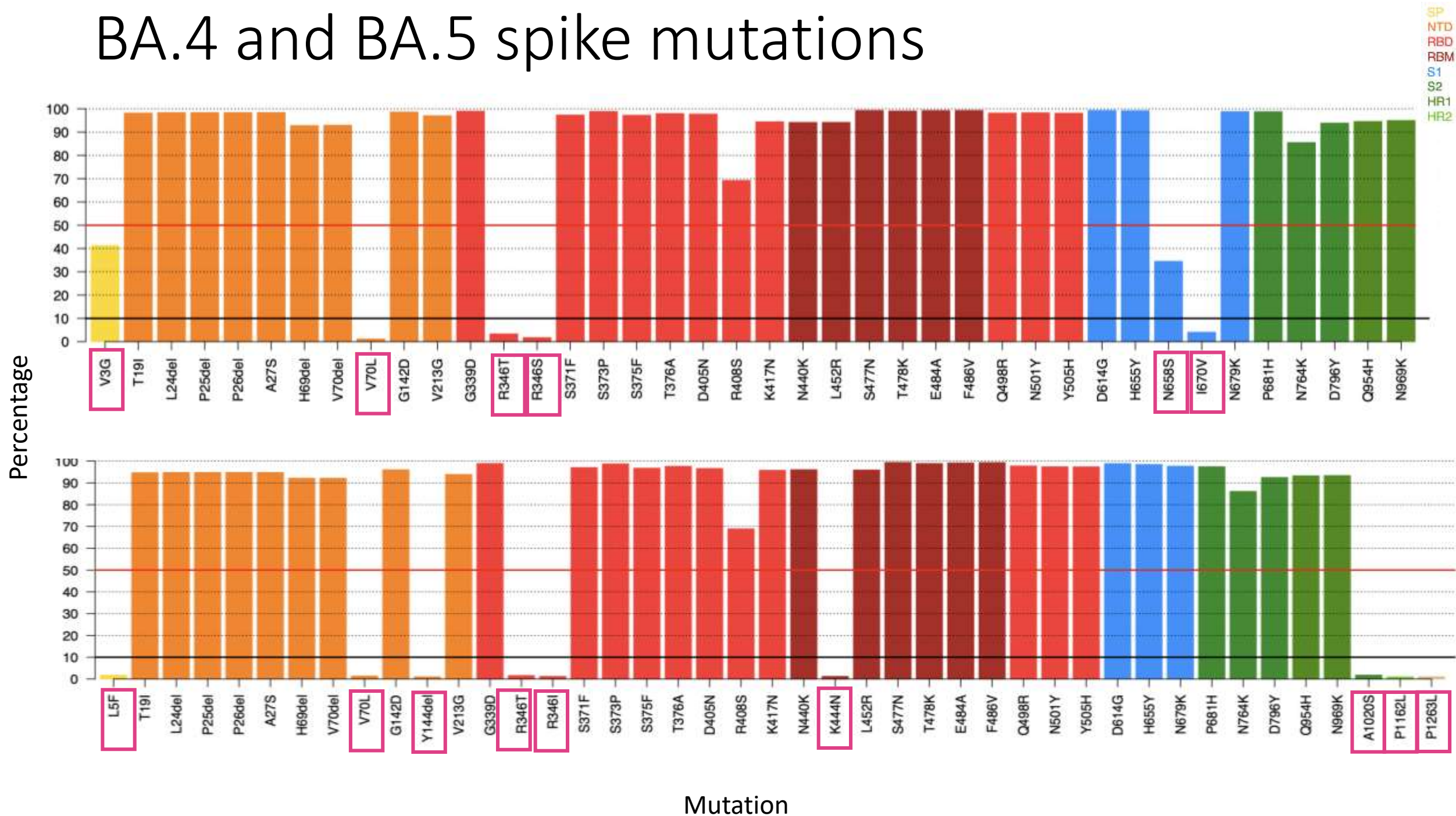


- Multiple changes within the two immunogenic regions in S1 (NTD and RBD)
  - Including a three amino acid insertion
- Accumulation of mutations surrounding the furin cleavage site
  - Including combination of N679K and P681H
- Effect of most spike S2 subunit changes have not been defined, but may be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

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

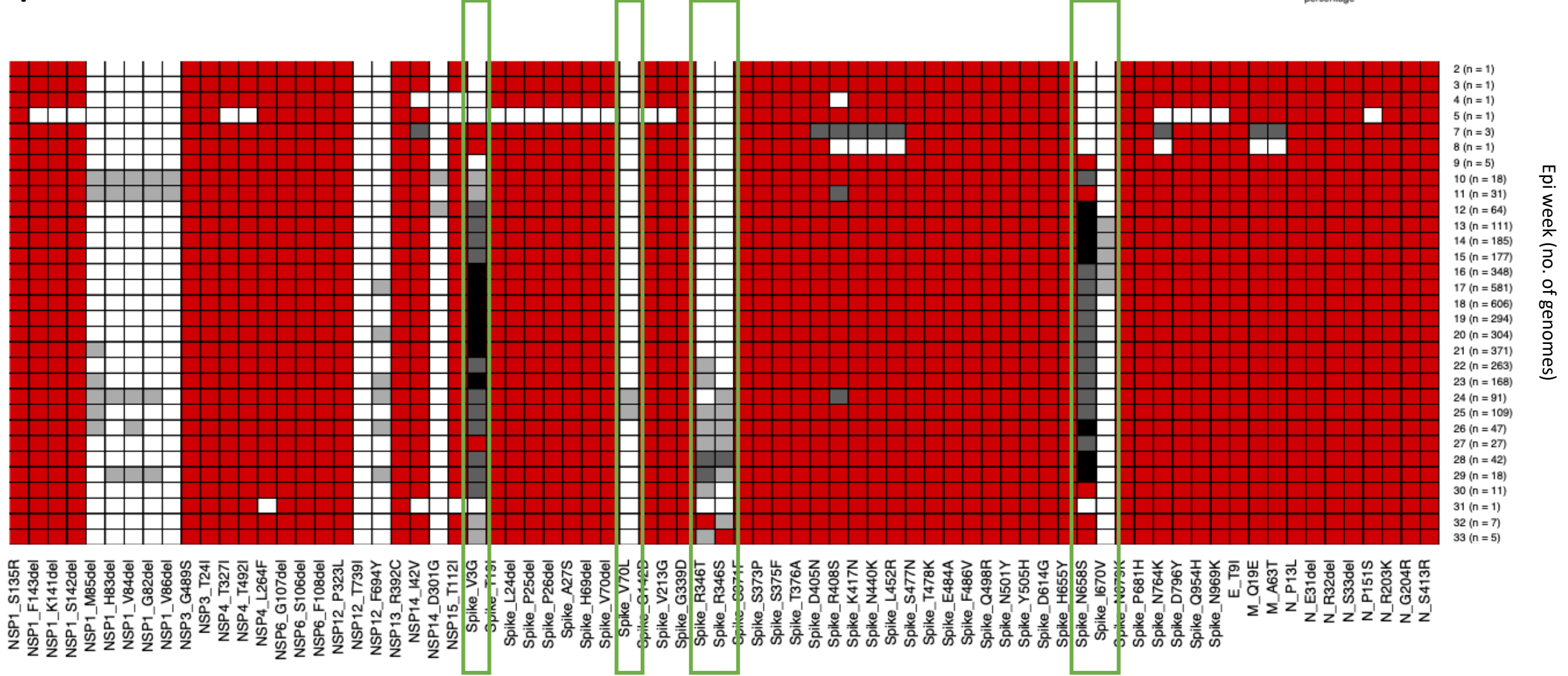


# BA.4 and BA.5 spike mutations

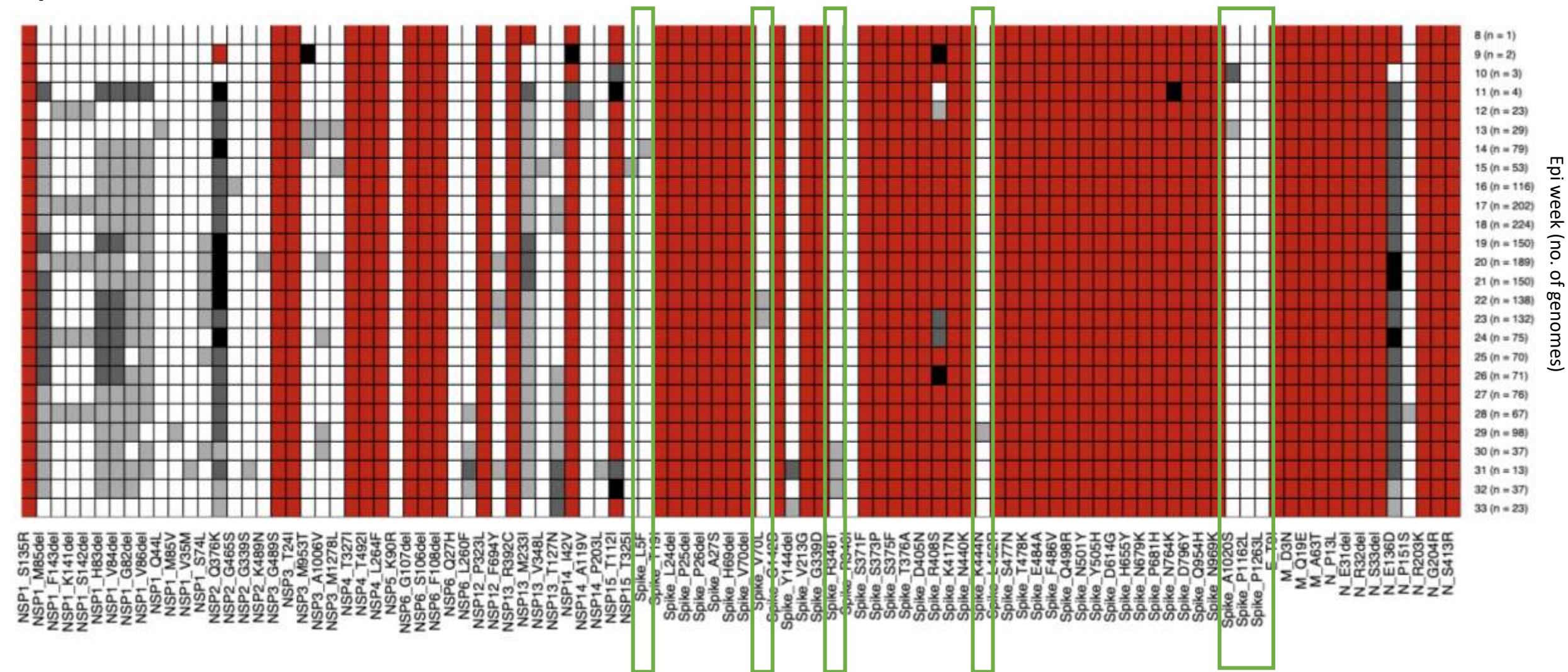
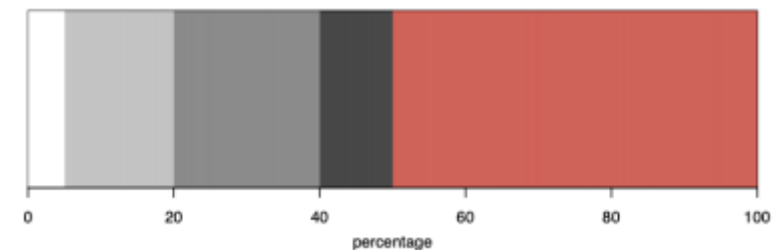




# BA.4 whole genome mutation prevalence over time



# BA.5 whole genome mutation prevalence over time







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EDCTP

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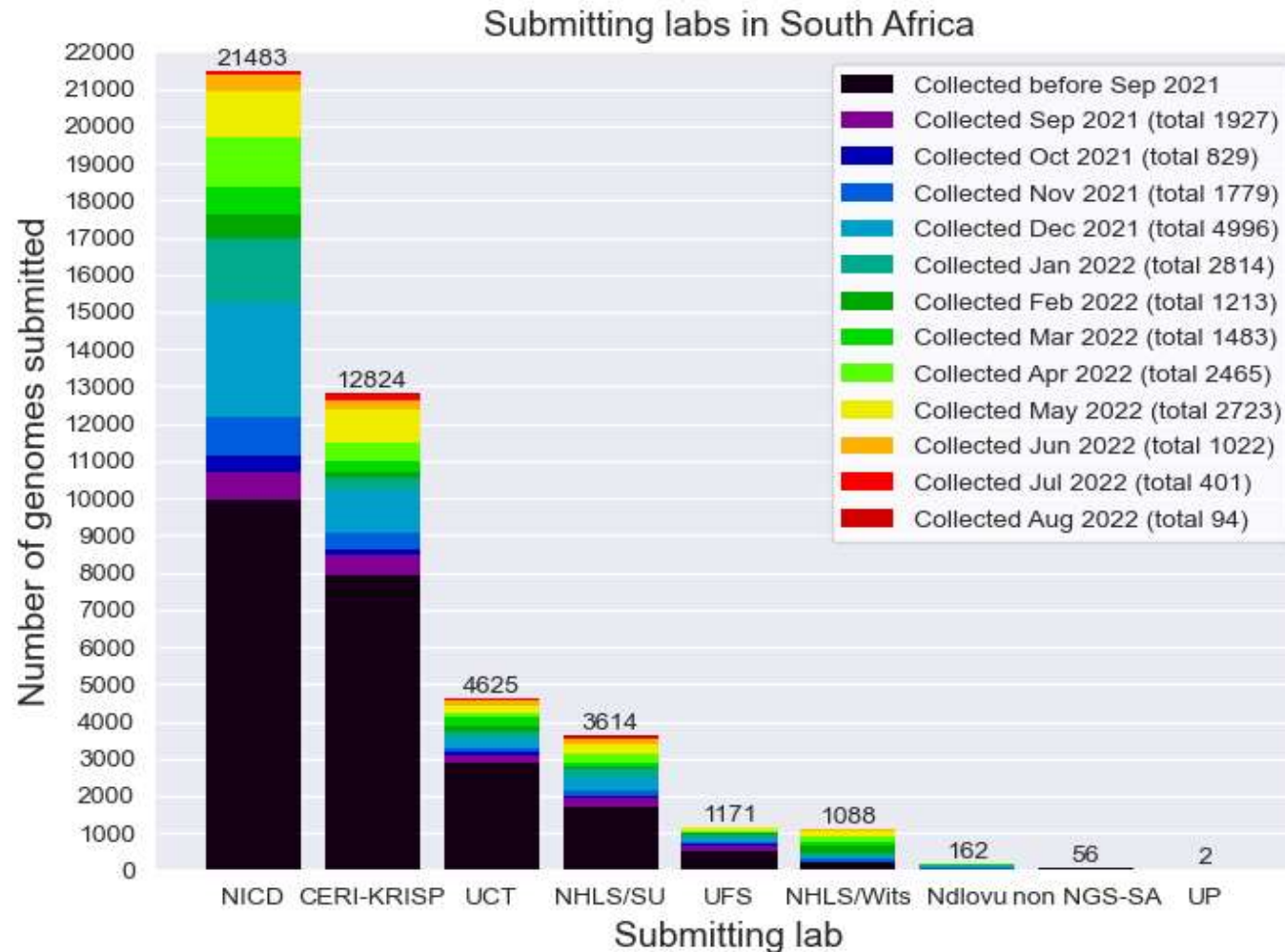
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Glenda Gray



# South African genomes submitted per submitting lab, 2020 - 2022 (N=45 025)



## 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 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.)