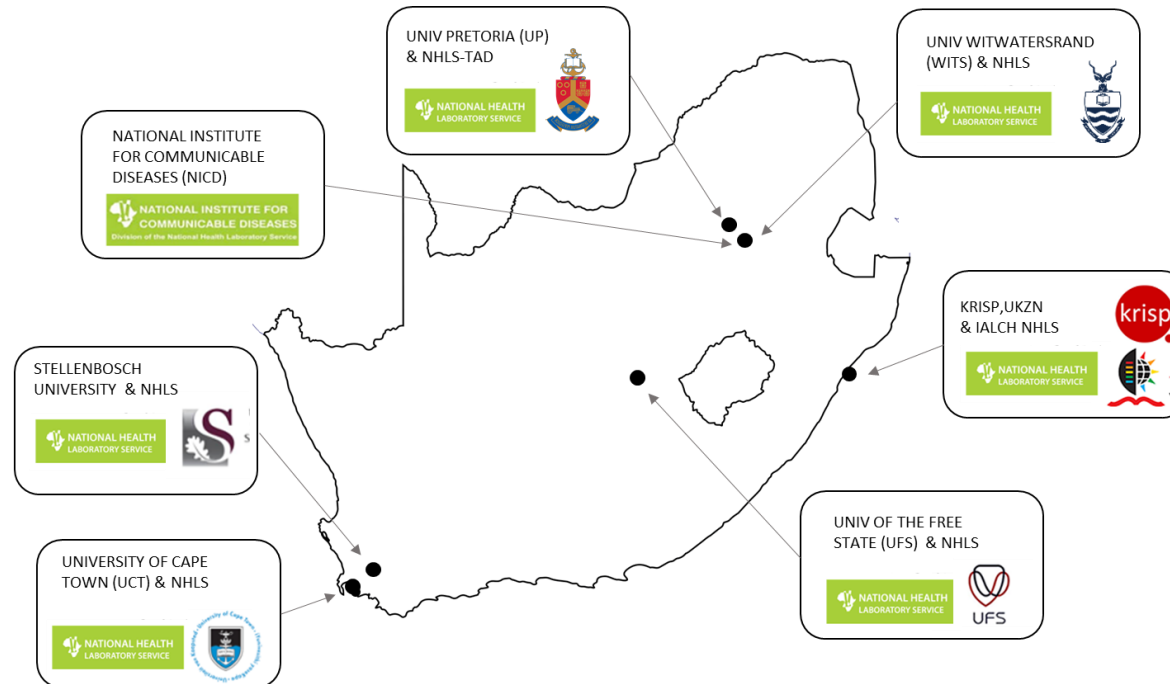


## SARS-CoV-2 Sequencing Update 05 April 2024



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 05 April 2024 at 08h00



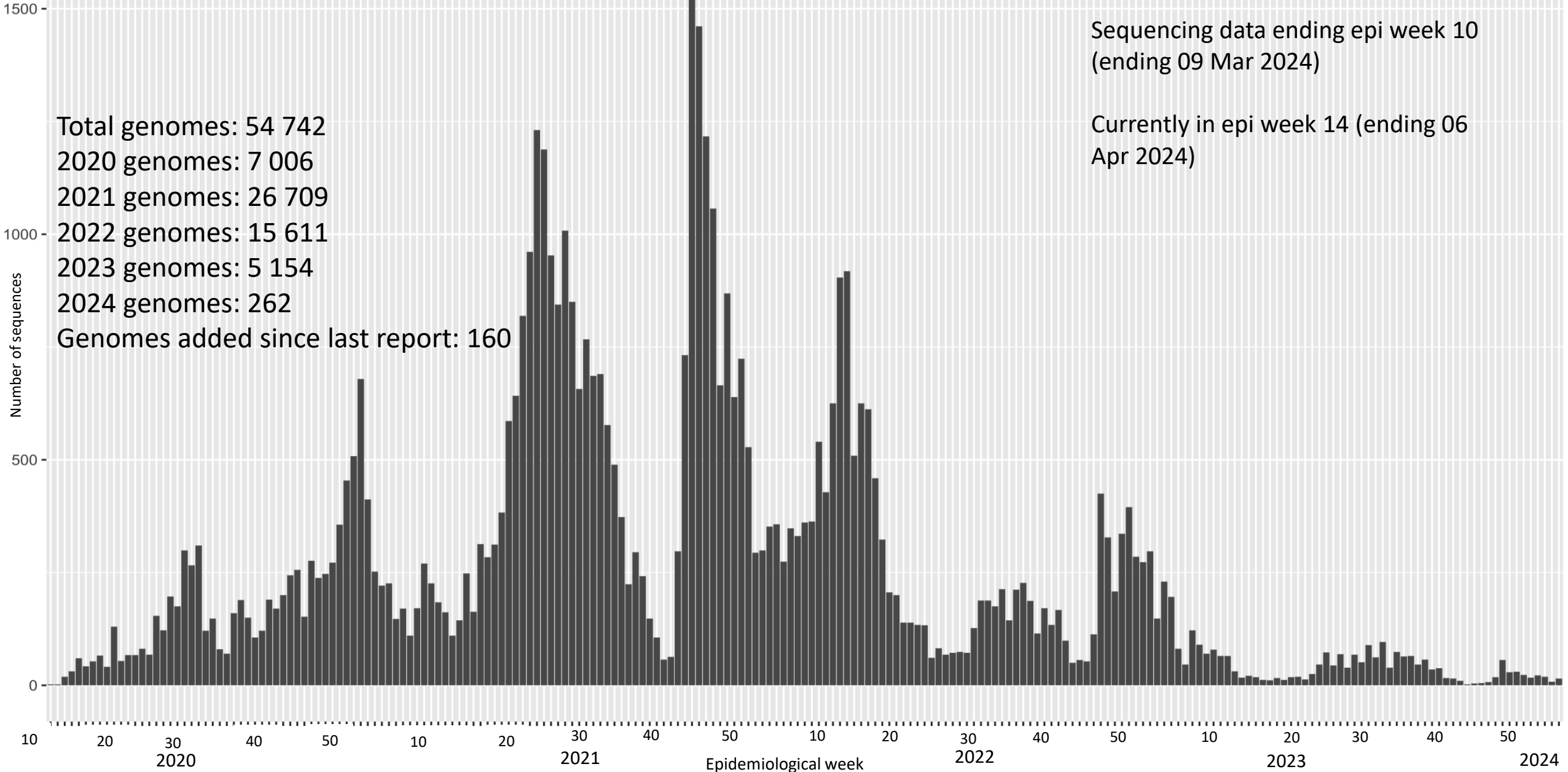
Data license: <https://www.gisaid.org/registration/terms-of-use/>

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 – 2024

(N=54 742\*)



Total genomes: 54 742

2020 genomes: 7 006

2021 genomes: 26 709

2022 genomes: 15 611

2023 genomes: 5 154

2024 genomes: 262

Genomes added since last report: 160

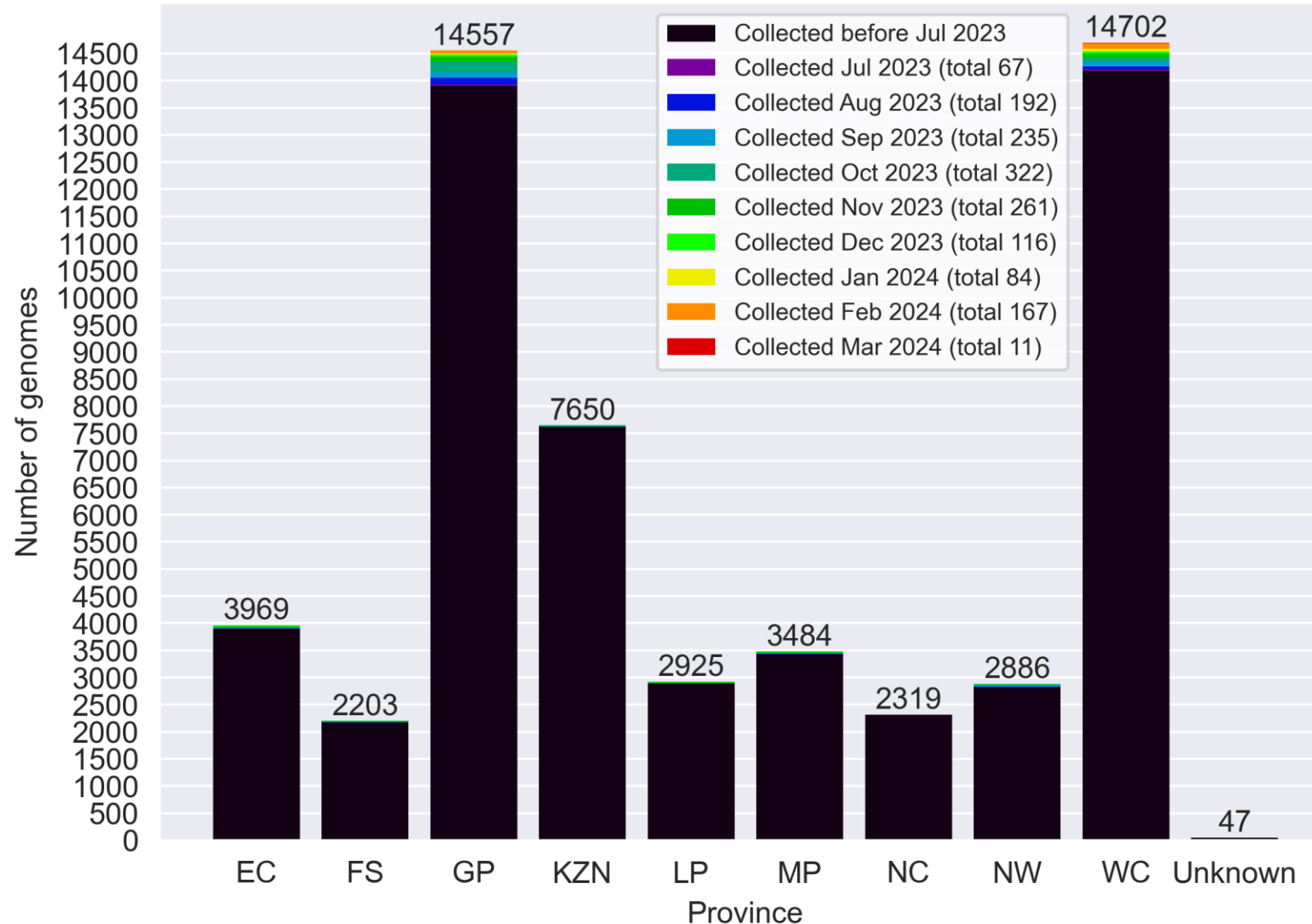
Sequencing data ending epi week 10  
(ending 09 Mar 2024)

Currently in epi week 14 (ending 06  
Apr 2024)

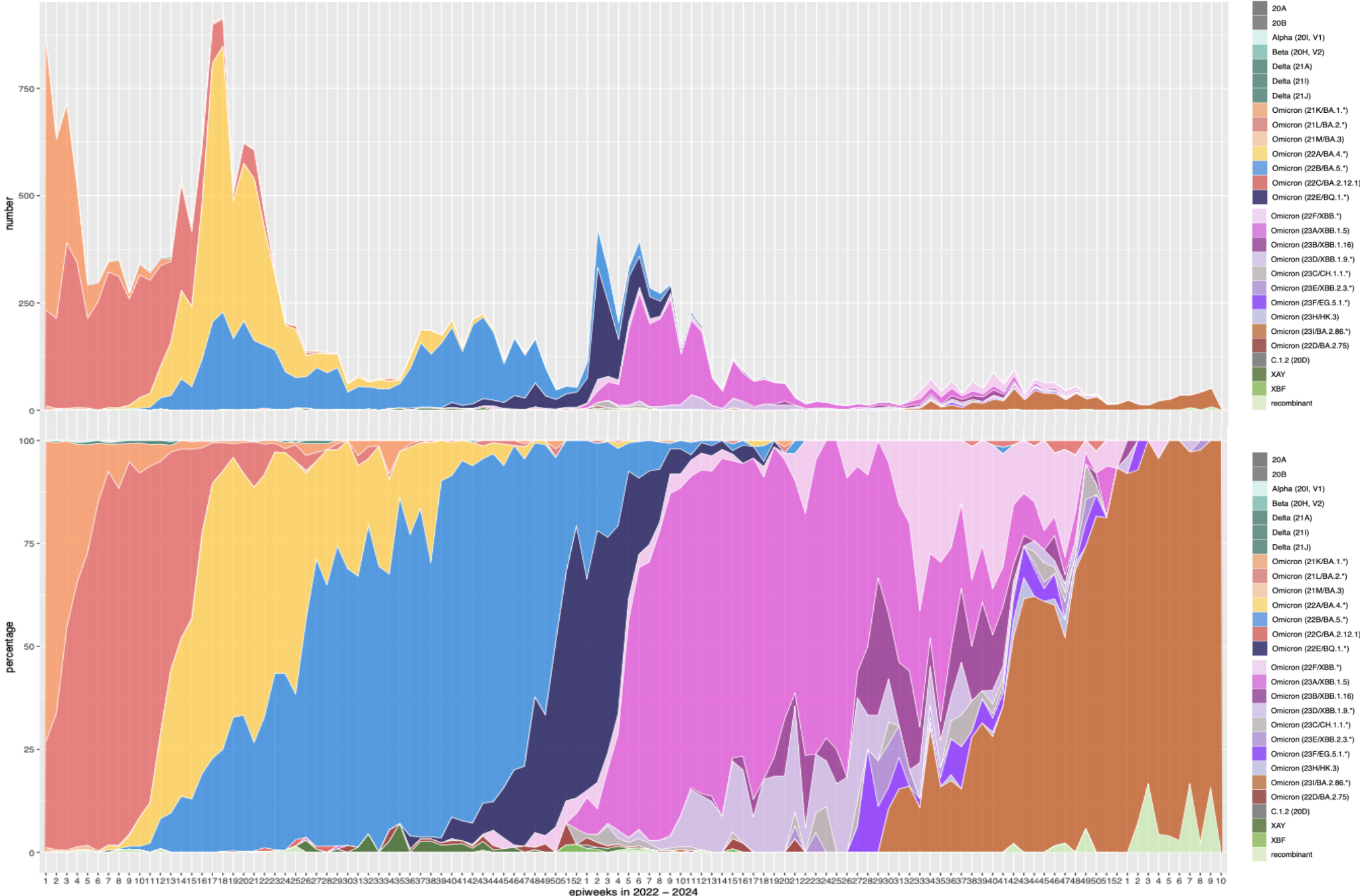
\*This represents the cleaned, de-duplicated dataset of unique National and Pneumonia Surveillance sequences. This dataset will be used for all further figures.

# GISAID genomes vs total cases, 2020 – 2024 (N= 54 742)

Provincial breakdown of genomes deposited into GISAID



# Number and percentage of clades by epiweek in South Africa, 2022-2024 (20 984\*)

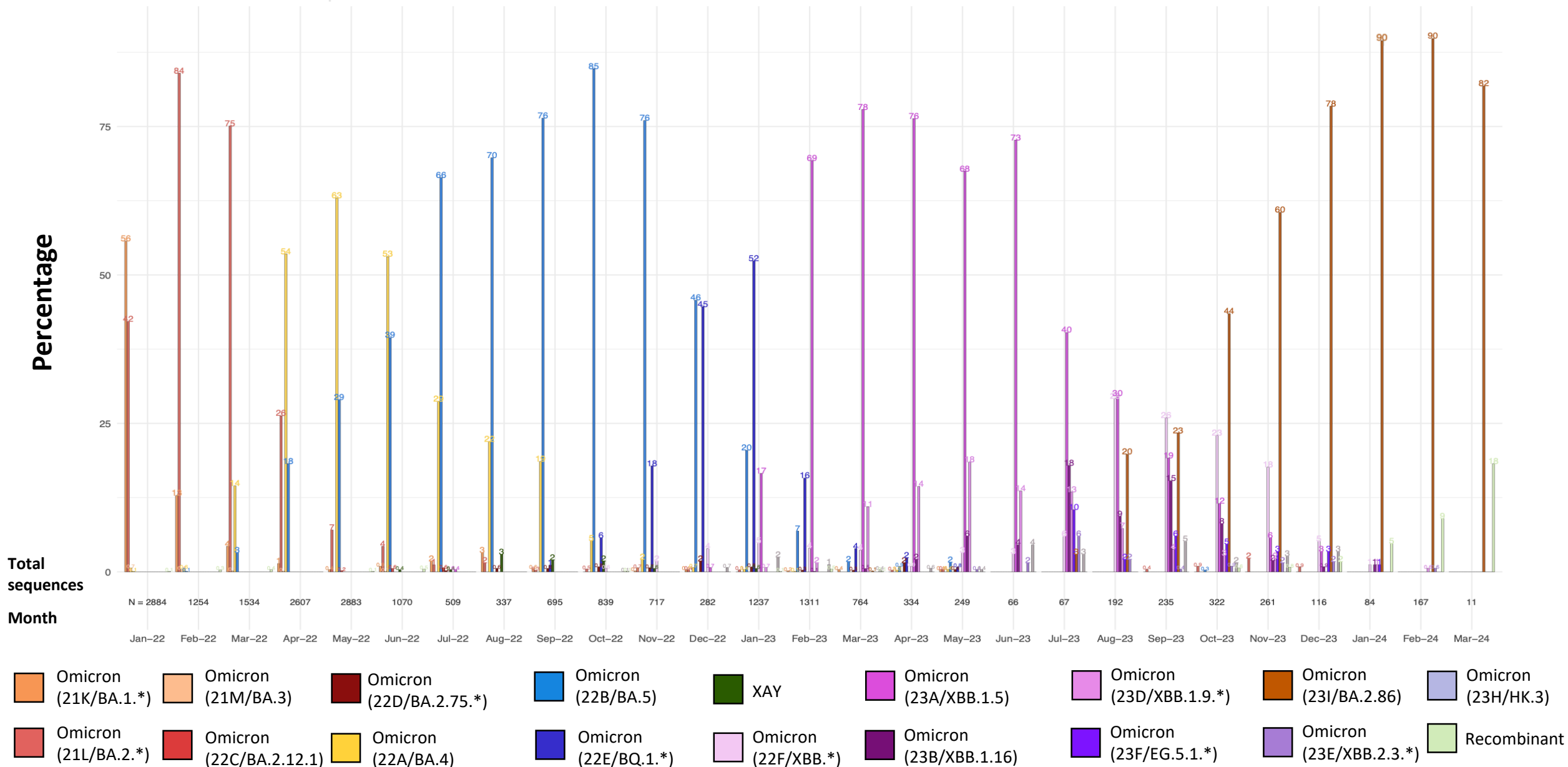


Sequencing data  
ending epi week 10  
(ending 09 Mar 2024)

Currently in epi week  
14 (ending 06 Apr  
2024)

\*Excludes sequences  
missing collection dates,  
as well as those collected  
January 1<sup>st</sup> 2022 as they  
are part of epiweek 52 of  
2021.

# Detection Rates: Omicron and recombinants



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

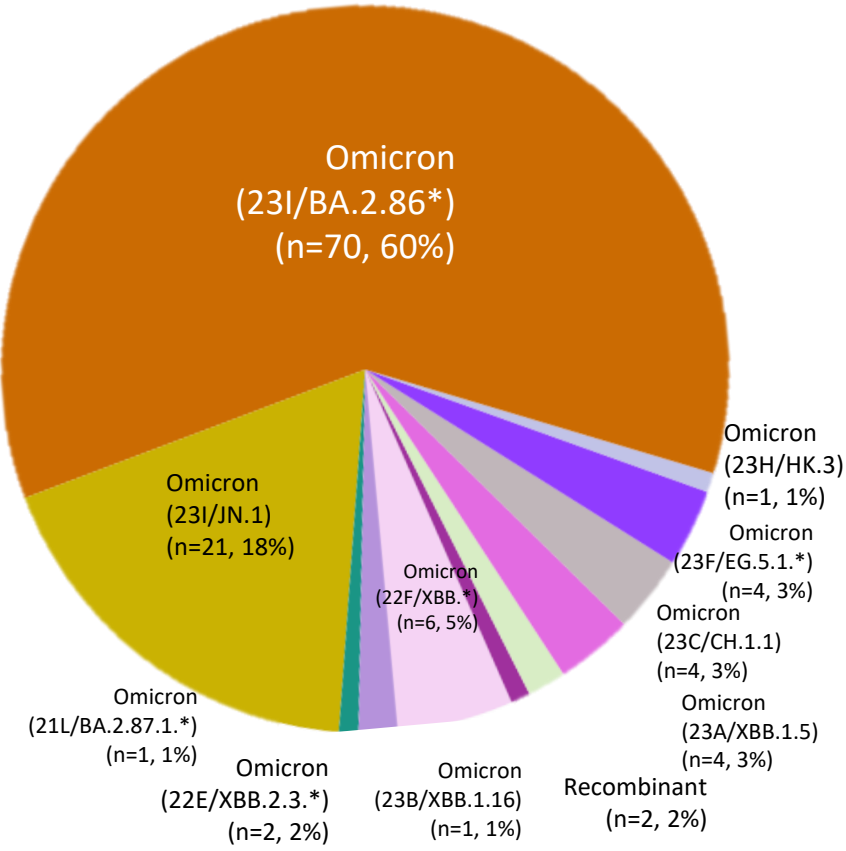
# Prevalence of Variants of Concern (VOC) and Variants of Interest (VOI) in

December (N=116)

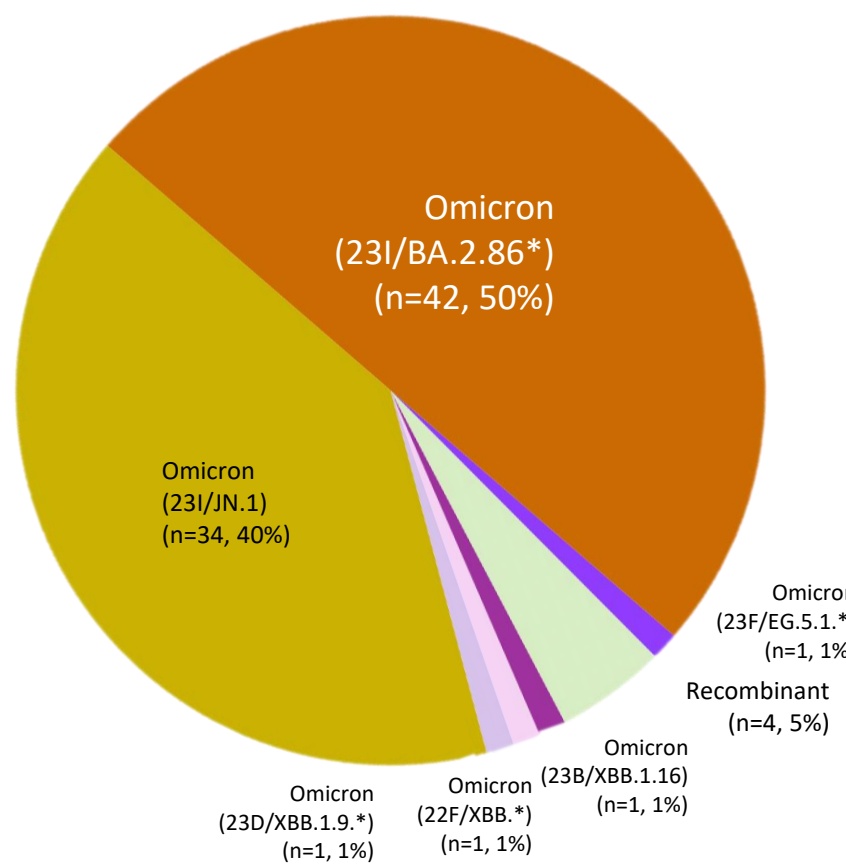
**December 2023 – February 2024**

February (N=167)

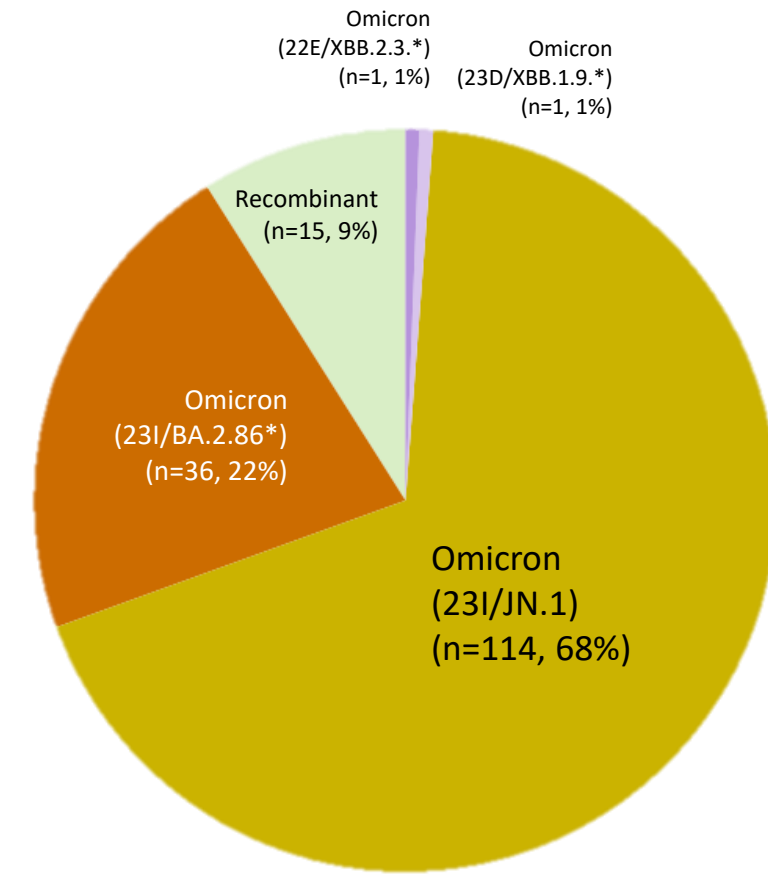
January (N=84)



**Total Omicron in December: 116 (100%)**

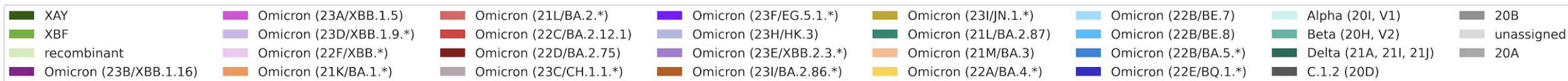


**Total Omicron in January: 84 (100%)**



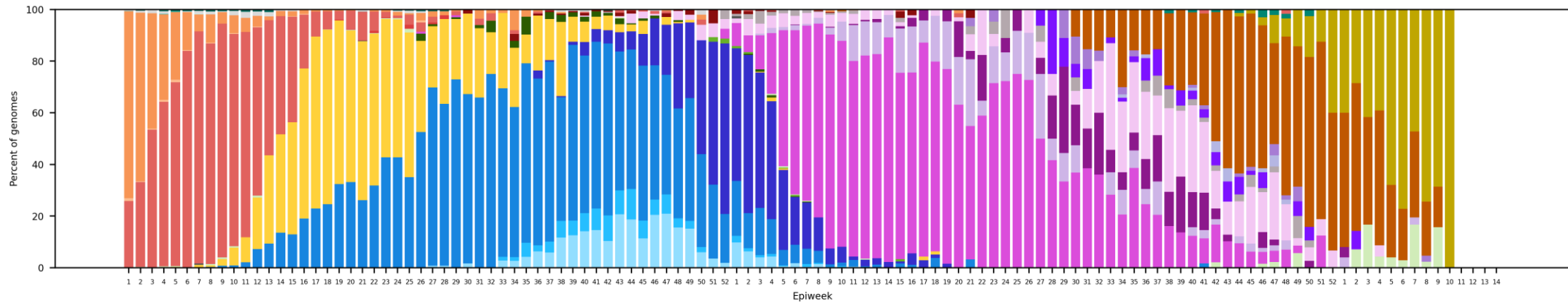
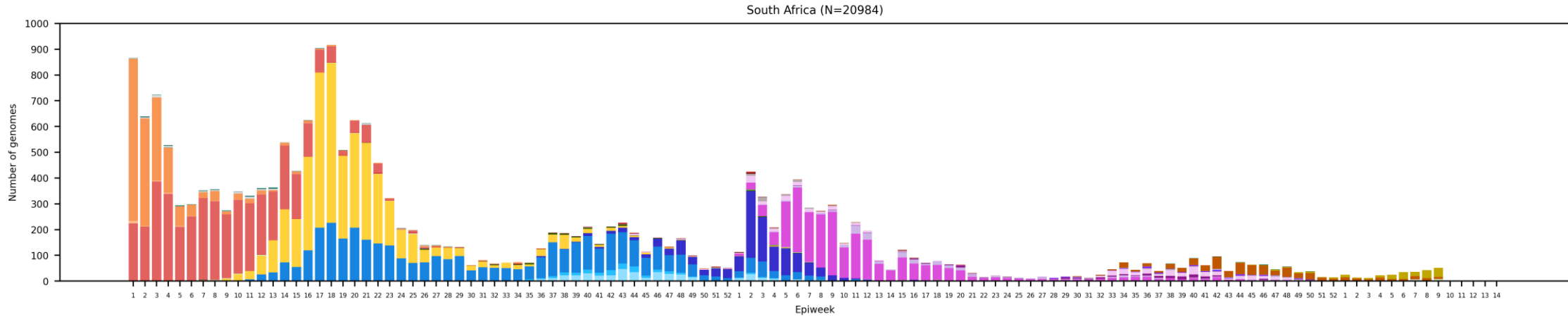
**Total Omicron in February: 167 (100%)**

Clade key (bar graph)

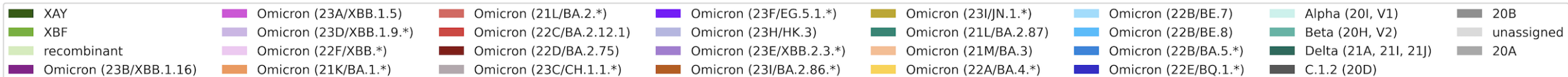




# South Africa, 2022-2024, n = 20 984\*



## Clade key (bar graph)



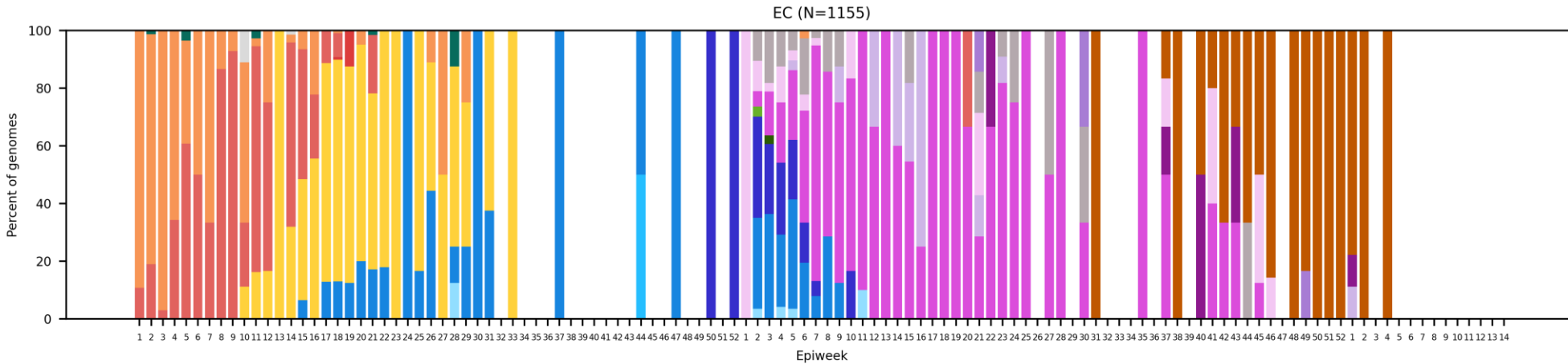
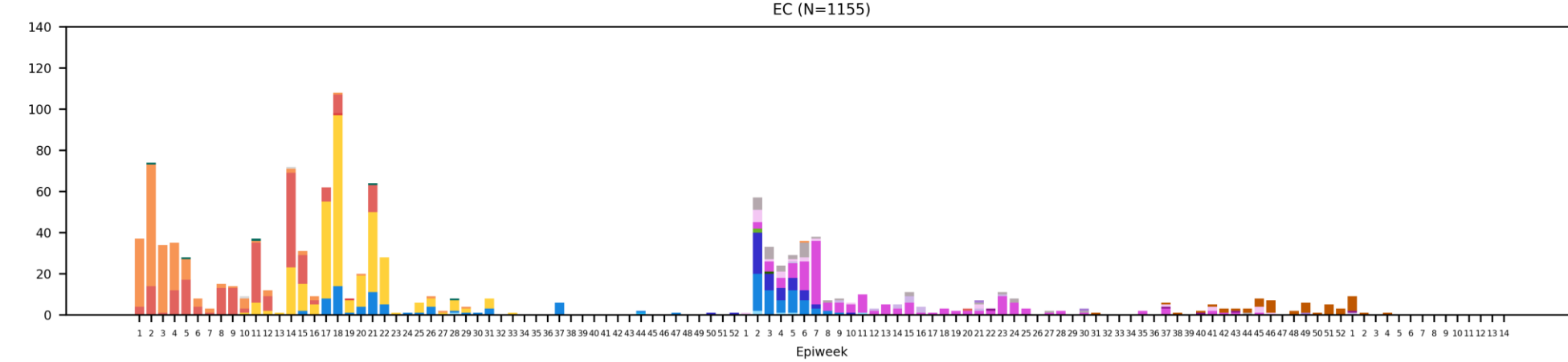
\*Excludes sequences missing collection dates. Lineages of particular interest (mainly WHO Omicron subvariants under monitoring) are separate from the main clade groupings.

#Recombinants include all recombinant lineages (viruses consisting of segments of two different lineages) detected in South Africa at low levels. Currently it consists of XT, XAS, XAZ, XBA, XBF.

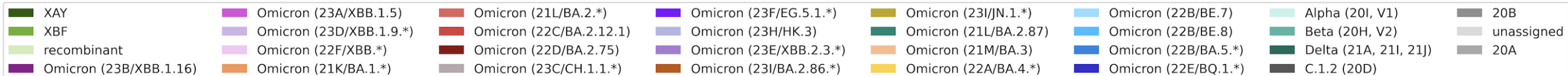


# Eastern Cape Province, 2022-2024, n = 1155

Genomes added since last report: 0\*



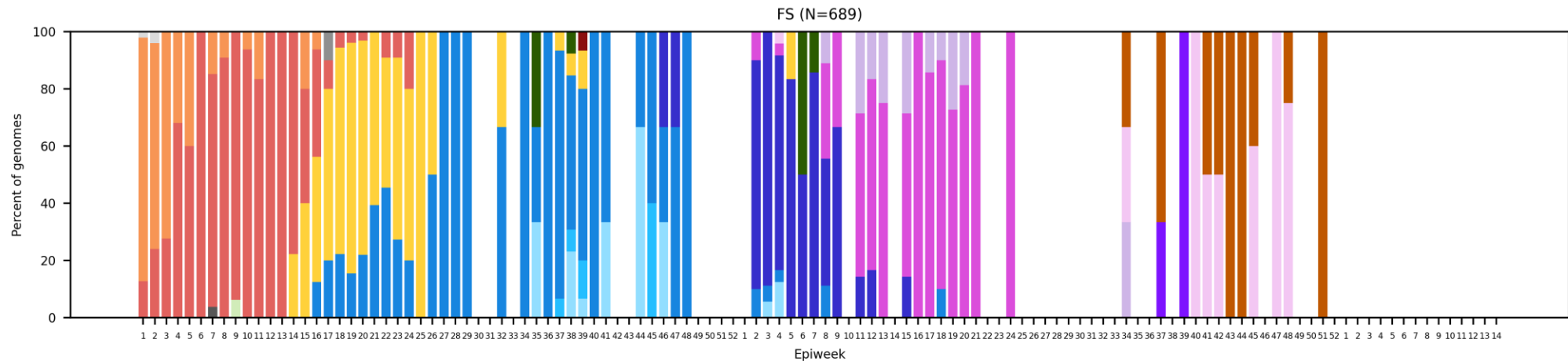
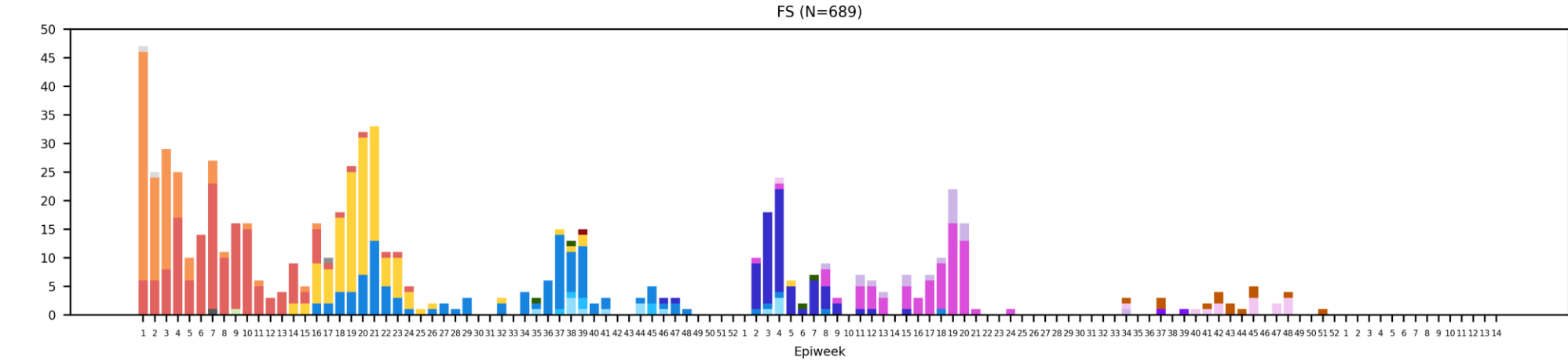
## Clade key (bar graph)



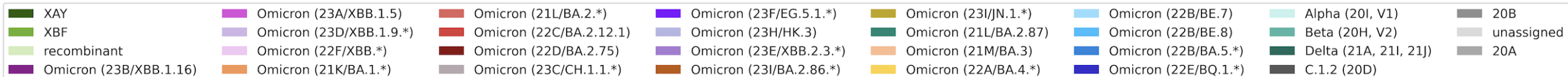
\*May include genomes from 2020 and 2021 which are not pictured here and are not included in the slide total.

# Free State Province, 2022-2024, n = 689

Genomes added since last report: 0\*



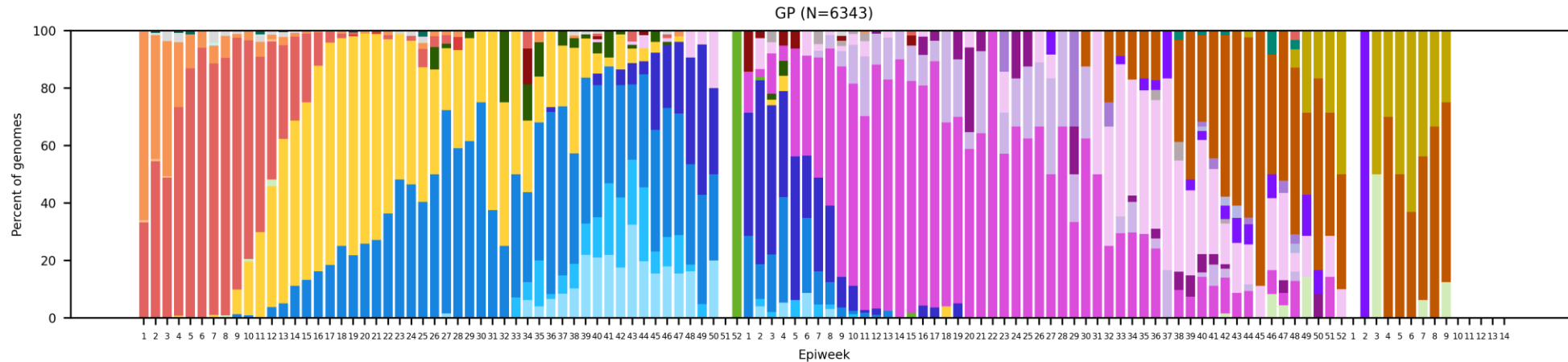
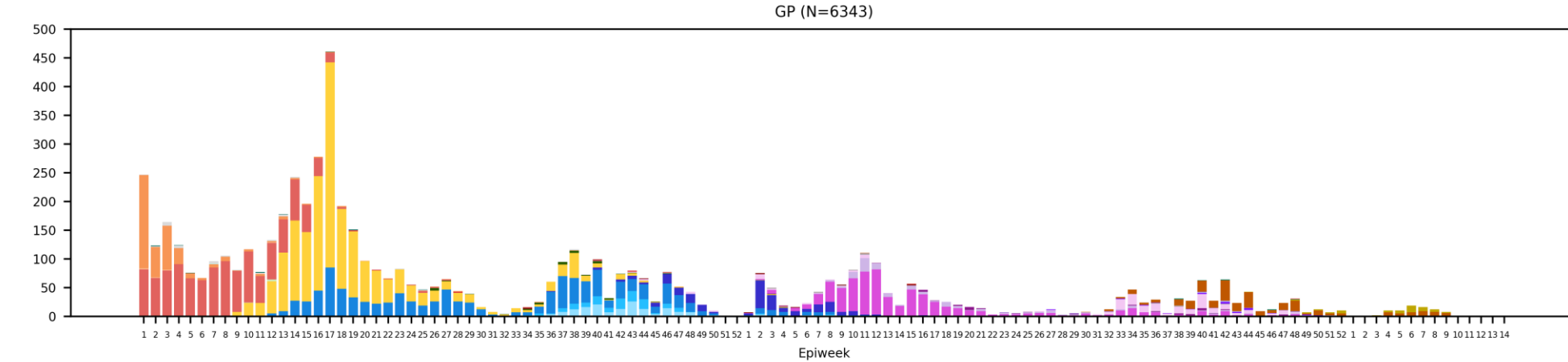
## Clade key (bar graph)



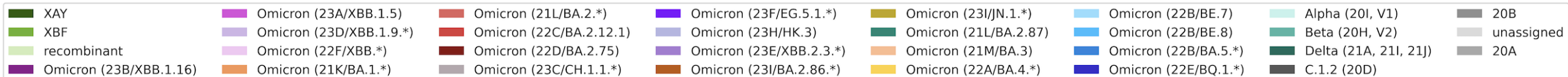
\*May include genomes from 2020 and 2021 which are not pictured here and are not included in the slide total.

# Gauteng Province, 2022-2024, n = 6343

Genomes added since last report: 60\*

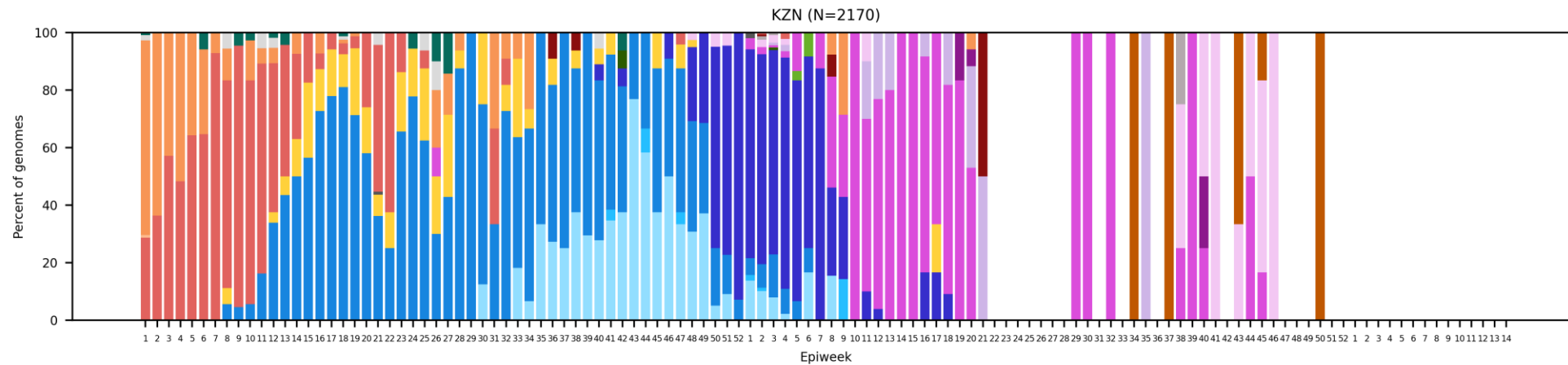
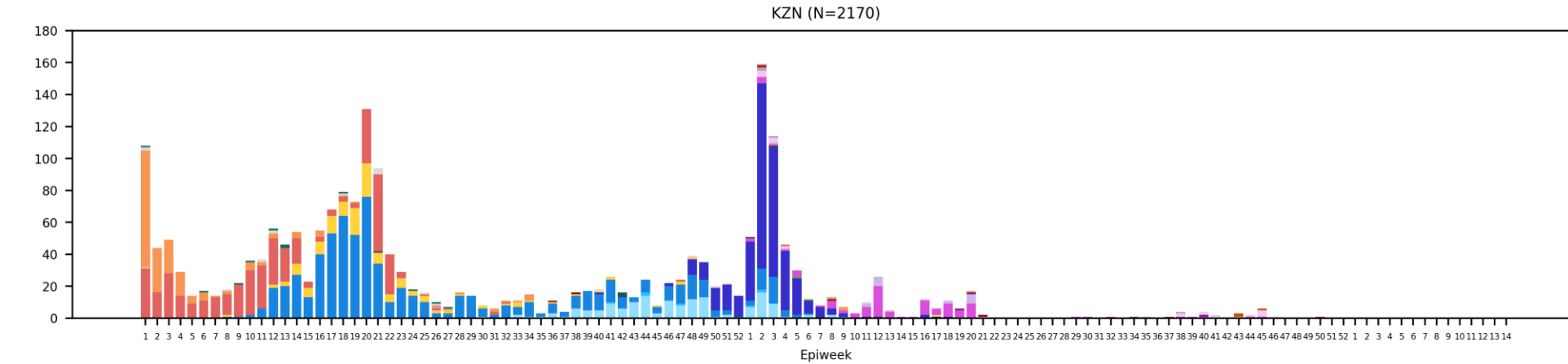


## Clade key (bar graph)

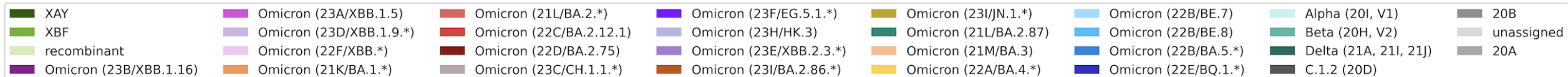


# KwaZulu-Natal Province, 2022-2024, n = 2170

Genomes added since last report: 0\*



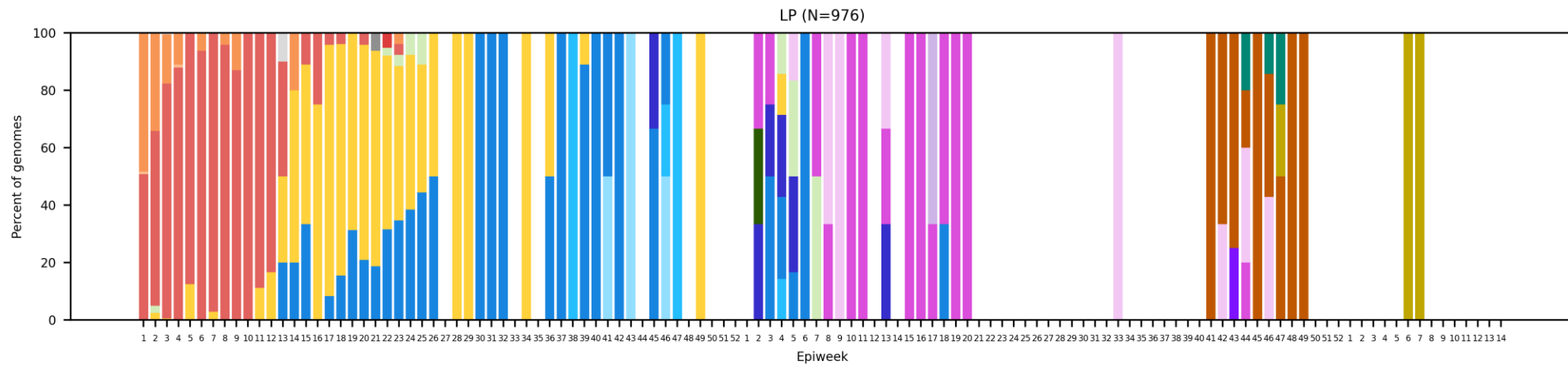
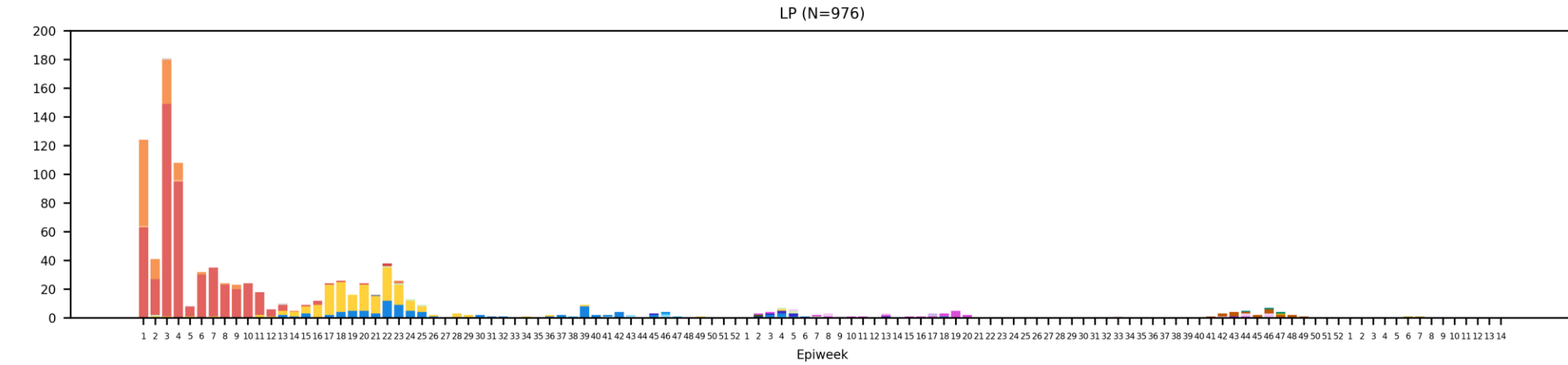
## Clade key (bar graph)



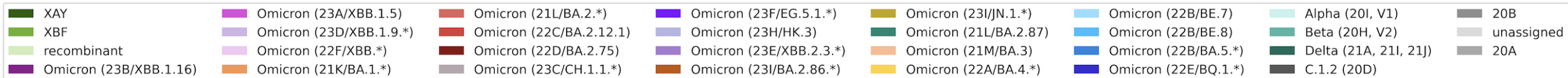
\*May include genomes from 2020 and 2021 which are not pictured here and are not included in the slide total.

# Limpopo Province, 2022-2024, n = 976

Genomes added since last report: 4\*

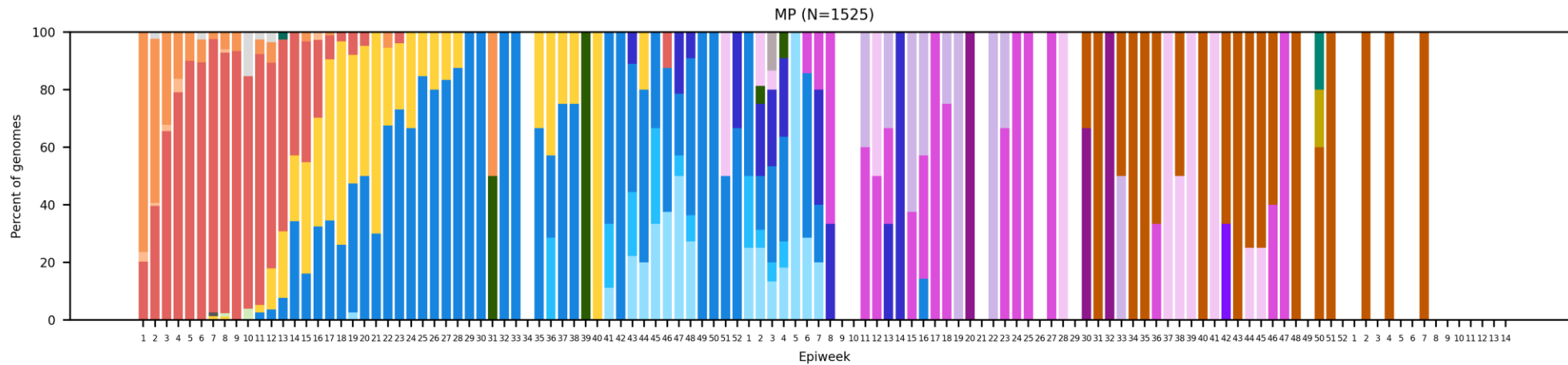
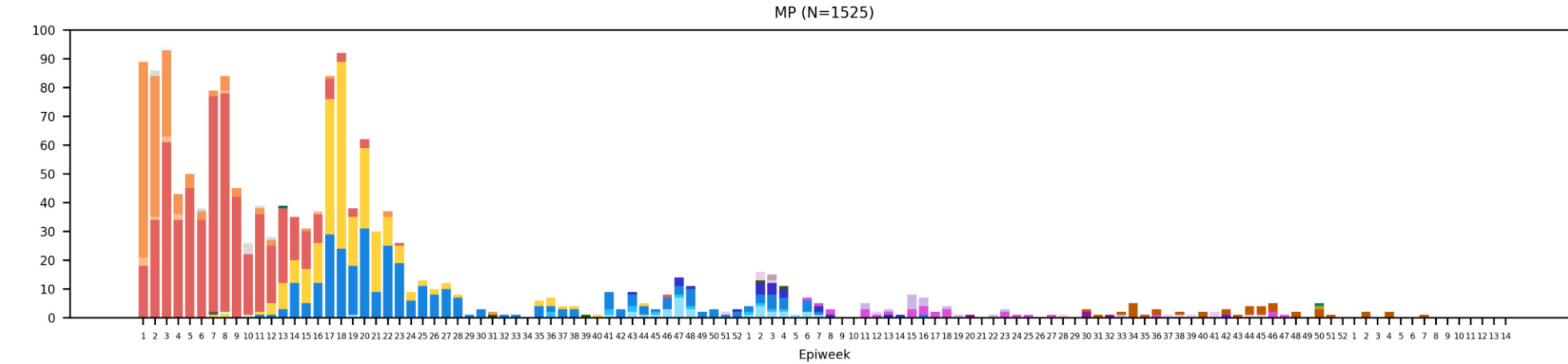


## Clade key (bar graph)

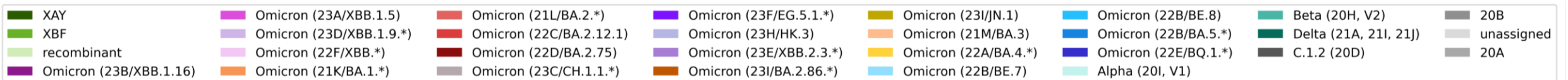


# Mpumalanga Province, 2022-2024, n = 1525

Genomes added since last report: 1\*



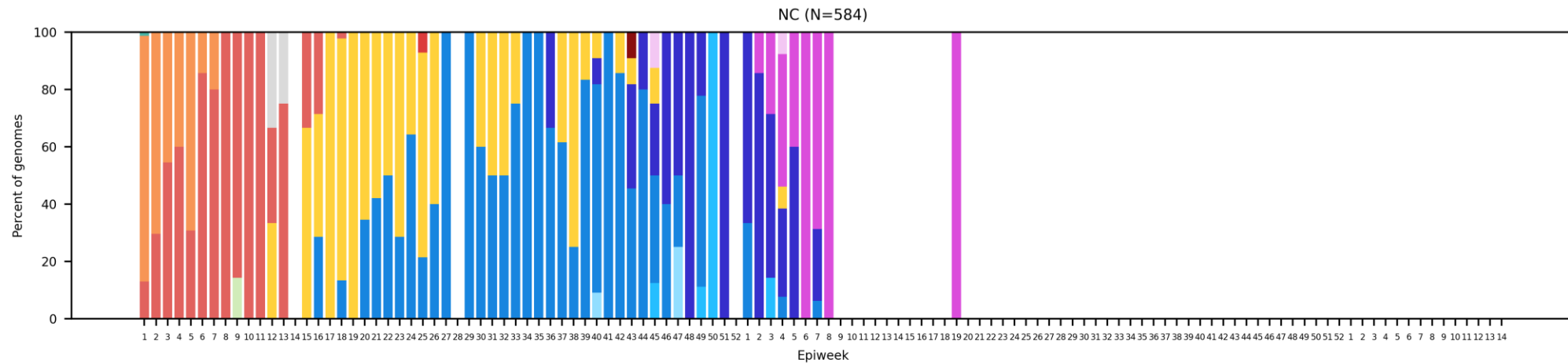
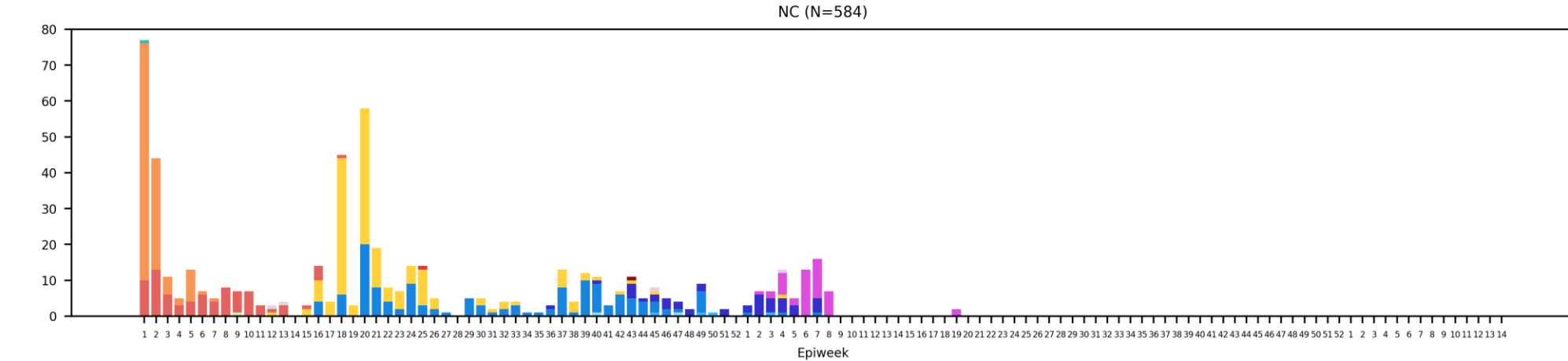
## Clade key (bar graph)



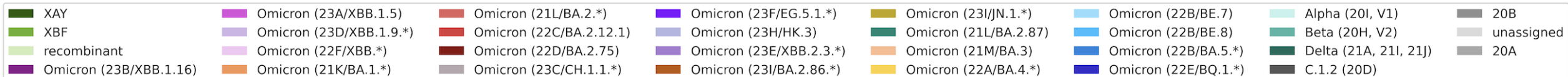
\*May include genomes from 2020 and 2021 which are not pictured here and are not included in the slide total.

# Northern Cape Province, 2022-2025, n = 584

Genomes added since last report: 0\*



## Clade key (bar graph)



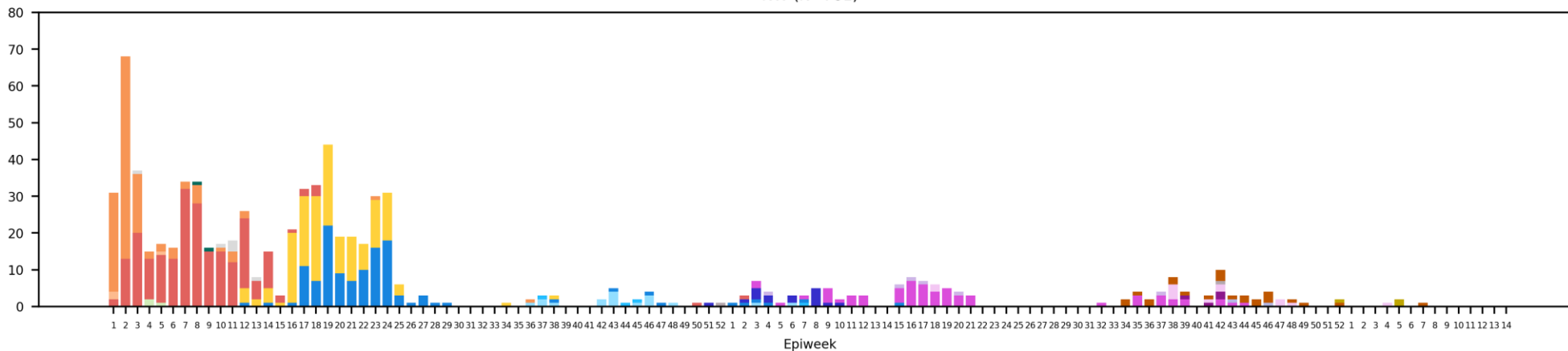
\*May include genomes from 2020 and 2021 which are not pictured here and are not included in the slide total.



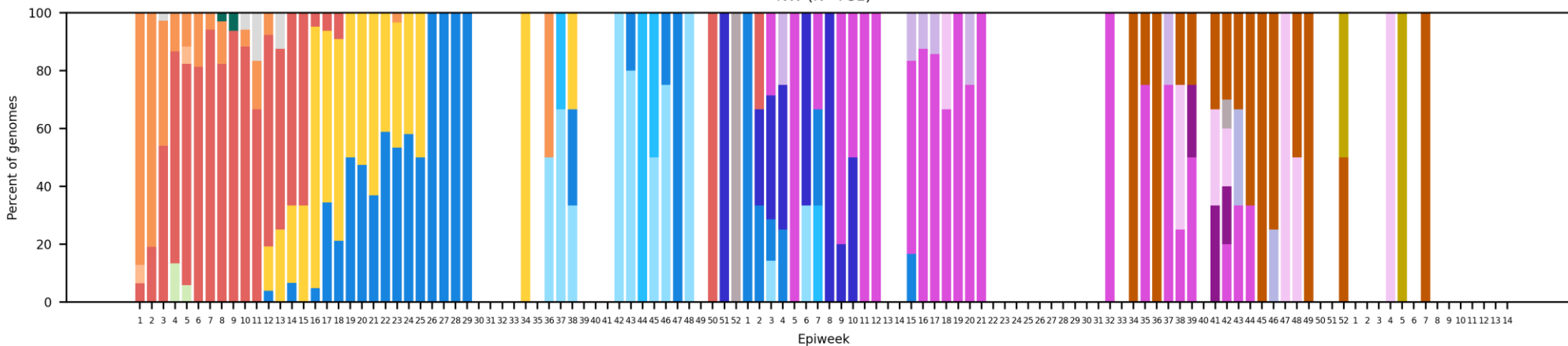
# North West Province, 2022-2024, n = 781

Genomes added since last report: 3\*

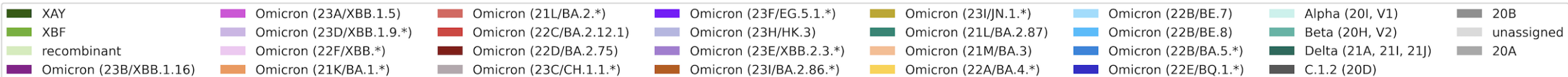
NW (N=781)



NW (N=781)



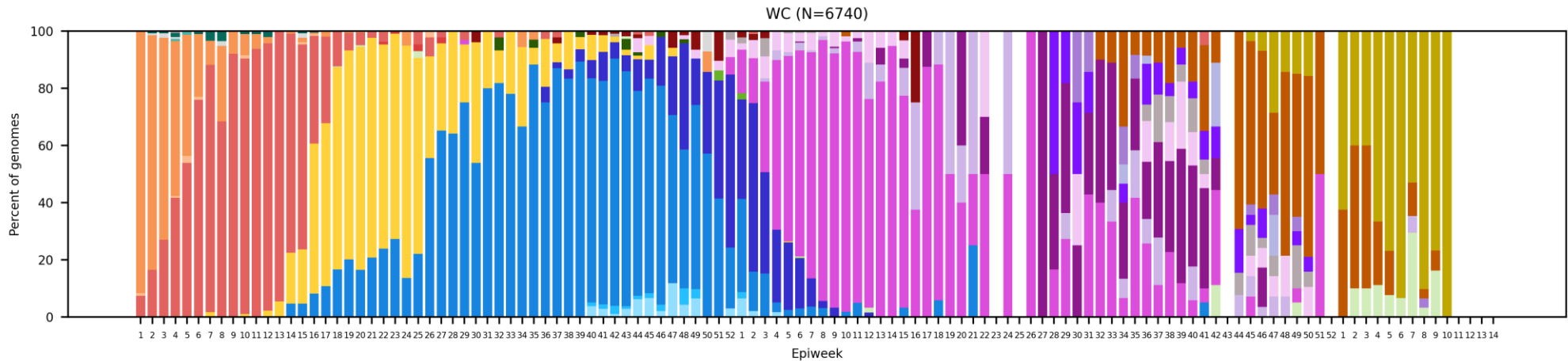
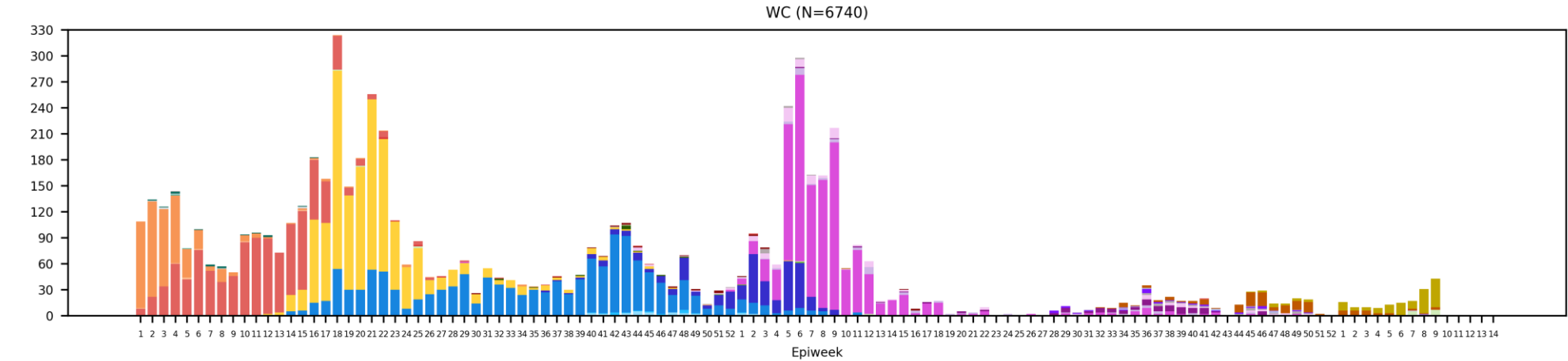
## Clade key (bar graph)



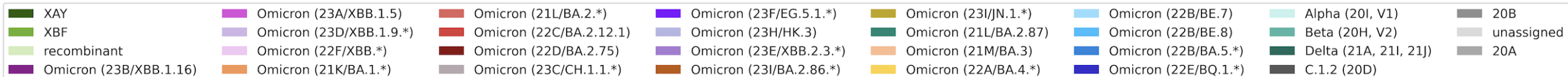
\*May include genomes from 2020 and 2021 which are not pictured here and are not included in the slide total.

# Western Cape Province, 2022-2024, n = 6740

Genomes added since last report: 92\*



## Clade key (bar graph)



\*May include genomes from 2020 and 2021 which are not pictured here and are not included in the slide total.

# Summary

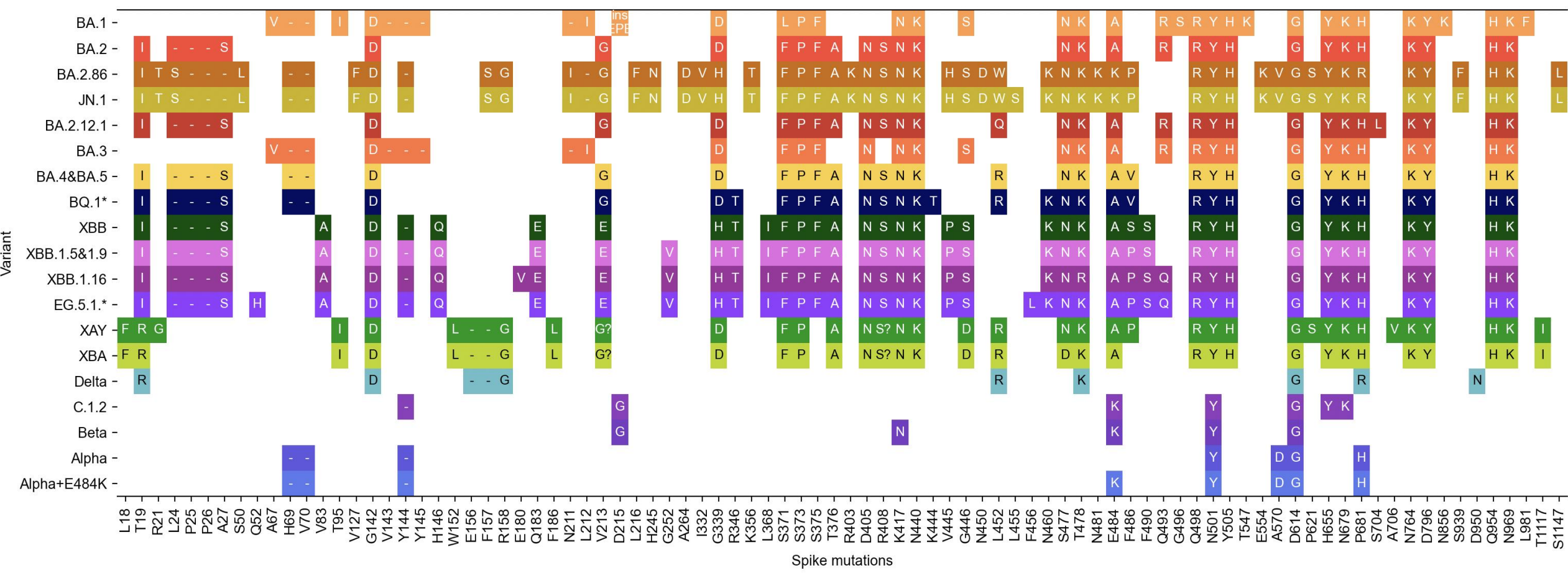
- **Sequencing update**

- December sequences (n=116) are from all provinces except the Northern Cape. January sequences (n=84) are from the Western Cape, Mpumalanga, Eastern Cape, North West and Gauteng, and February sequences (n=167) are from the Western Cape, Mpumalanga, Eastern Cape, North West and Gauteng. March sequences (n=11) are from the Western Cape

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

- BA.2.86 was dominant at 60% of sequences in December, but decreased to 50% in January, 22% in February, and 9% in March (based on low numbers in March)
- JN.1 constituted 18% of December sequences, 40% of January sequences, 68% of February sequences, and 73% of March sequences
- Nine sequences of newly designated BA.2.87.1 lineage were detected in SA in September-December 2023 – no new sequences have been detected since December 2023
- Recombinant XDD.1.1 (EG.5.1.1 and JN.1.1) has been detected in Gauteng (n=1) and the Western Cape (n=17). It has a cumulative prevalence of <0.5% worldwide

# 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

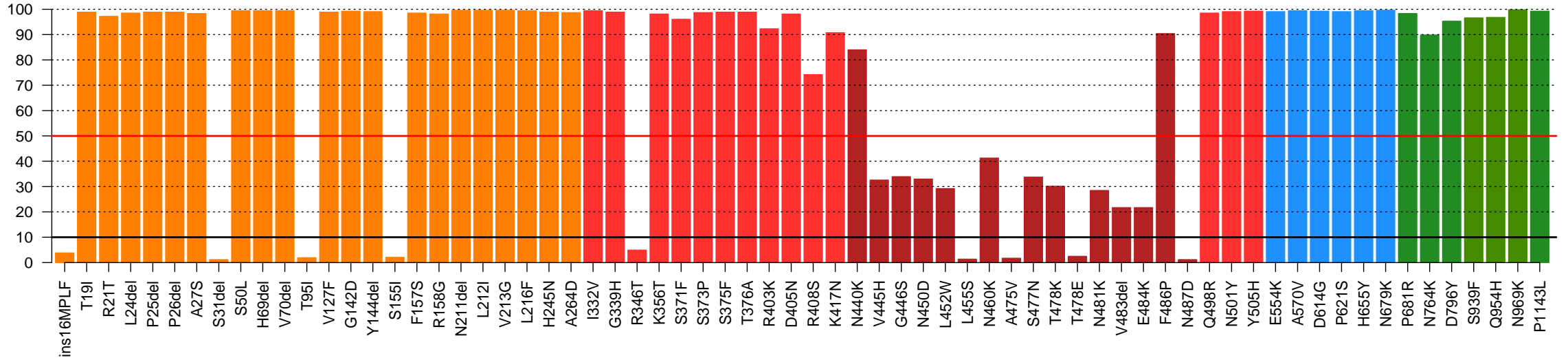
\*Only mutations present in Omicron, Delta, or recombinant sequences are pictured

# BA.2.86.\* and JN.1.\* spike mutations\*

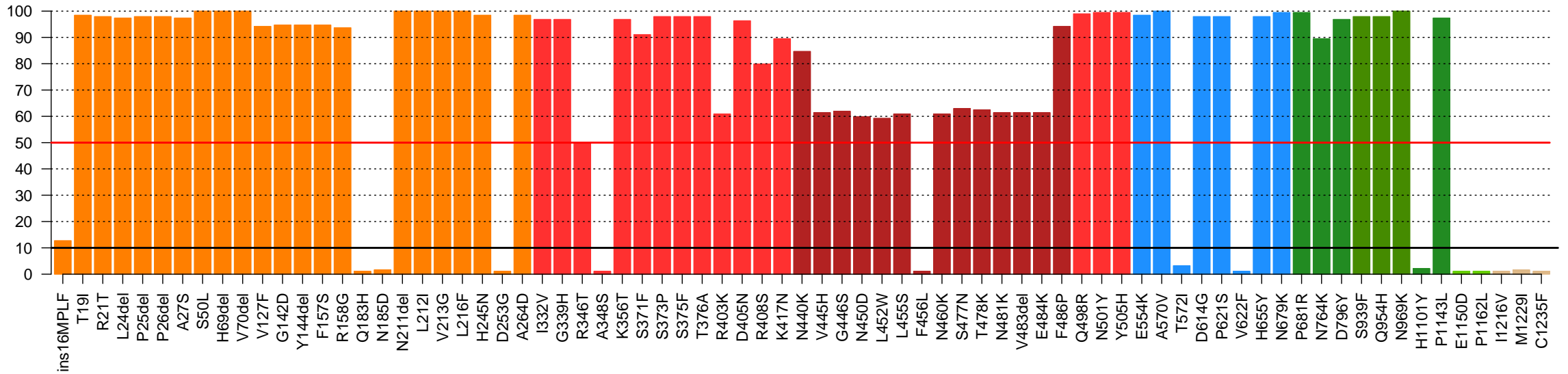
SP  
NTD  
RBD  
RBM  
S1  
S2  
HR1  
HR2

Percentage

Frequency of spike SNVs for Omicron (23I/BA.2.86.\*) (n = 531)



Frequency of spike SNVs for Omicron (23I/JN.1.\*) (n = 189)



Mutation

\*Only mutations present in ≥1% of sequences are shown.



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NICD COVID-19 response team  
NICD SARS-CoV-2 Sequencing Group



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REPUBLIC OF SOUTH AFRICA



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Network for Genomic Surveillance in South Africa



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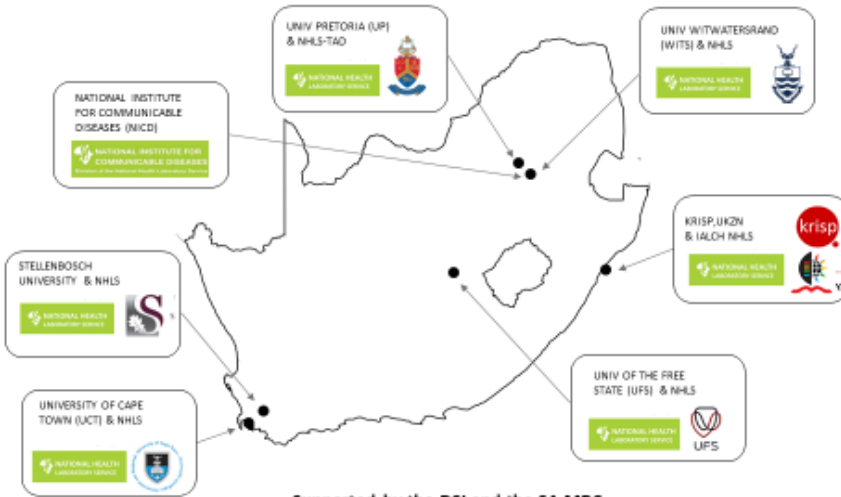






# NGS-SA

Network for Genomic Surveillance in South Africa



UNIVERSITEIT VAN PRETORIA  
UNIVERSITY OF PRETORIA  
YUNIBESITHI YA PRETORIA



UNIVERSITY OF CAPE TOWN  
IYUNIVESITHI YASEKAPA • UNIVERSITEIT VAN KAAPSTAD



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UNIVERSITY



UNIVERSITY OF  
KWAZULU-NATAL™  
INYUVESI  
YAKWAZULU-NATALI

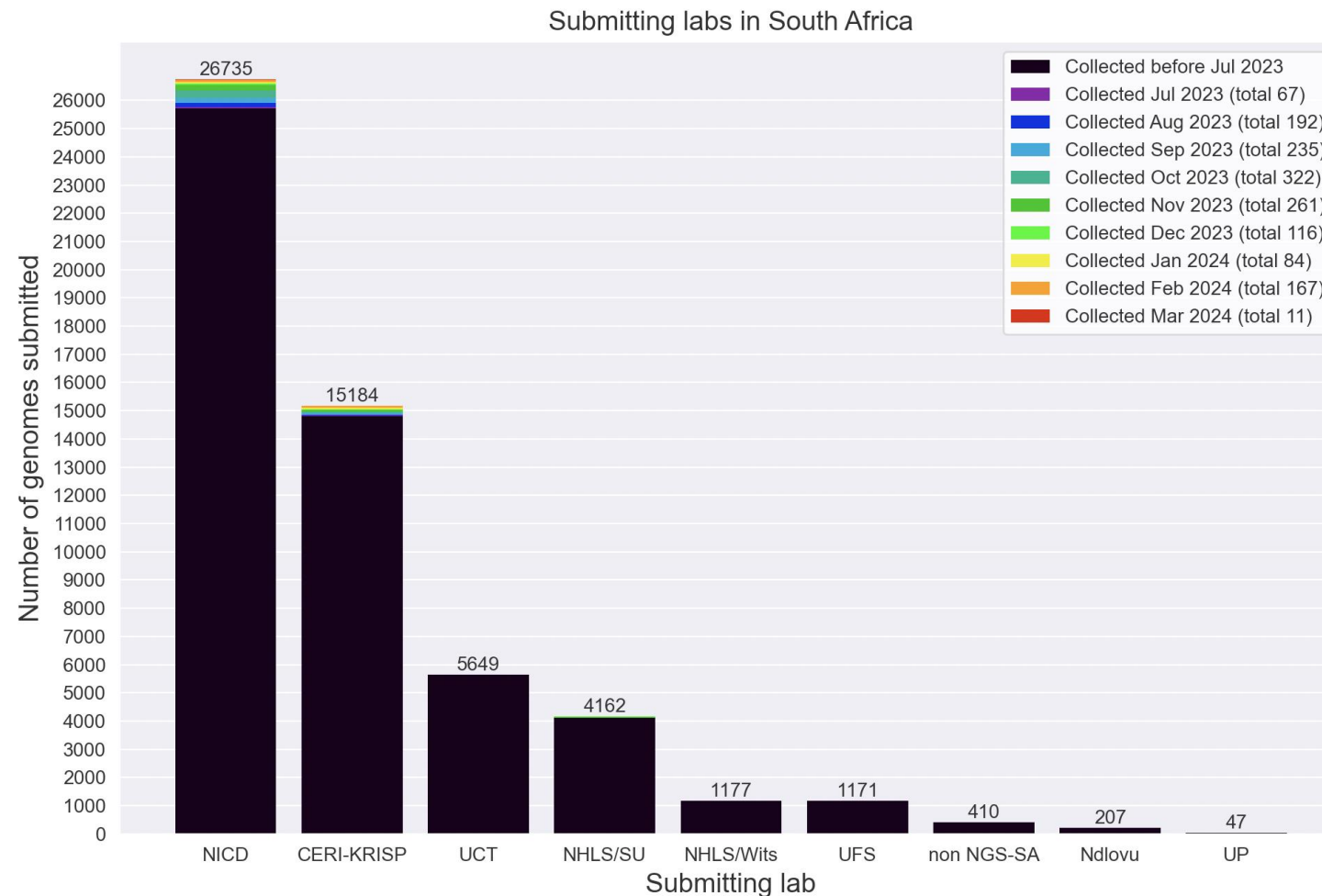


EDCTP

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



# South African genomes submitted per submitting lab, 2020 - 2024 (N= 54 742)



## 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 Interest (VOI) as of 09 February 2024

Pango lineage	Nextstrain clade	Genetic features	Earliest documented samples	Date of designation and risk assessments
XBB.1.5	23A	<p>Recombinant of BA.2.10.1 and BA.2.75 sublineages, i.e. BJ.1 and BM.1.1.1, with a breakpoint in S1.</p> <p>XBB.1 + S:F486P (similar Spike genetic profile as XBB.1.9.1)</p> <p>Includes XBB.1.5.70 (23G): XBB.1.5 + S:L455F and S:F456L</p>	21-10-2022	<p>11-01-2023</p> <p><a href="#">XBB.1.5 Rapid Risk Assessment, 11 January 2023</a></p> <p><a href="#">XBB.1.5 Updated Rapid Risk Assessment, 25 January 2023</a></p> <p><a href="#">XBB.1.5 Updated Risk Assessment, 24 February 2023</a></p> <p><a href="#">XBB.1.5 Updated Risk Assessment, 20 June 2023</a></p>
XBB.1.16	23B	<p>Recombinant of BA.2.10.1 and BA.2.75 sublineages, i.e. BJ.1 and BM.1.1.1</p> <p>XBB.1 + S:E180V, S:K478R and S:F486P</p>	09-01-2023	<p>17-04-2023</p> <p><a href="#">XBB.1.16 Initial Risk Assessment, 17 April 2023</a></p> <p><a href="#">XBB.1.16 Updated Risk Assessment, 05 June 2023</a></p>
EG.5	Not assigned	<p>XBB.1.9.2 + S:F456L</p> <p>Includes</p> <p>EG.5.1 (23F): EG.5 + S:Q52H</p> <p>HK.3 (23H): EG.5 + S:Q52H, S:L455F</p> <p>HV.1: EG.5 + S:Q52H, S:F157L, S:L452R</p>	17-02-2023	<p>09-08-2023</p> <p><a href="#">EG.5 Initial Risk Evaluation, 09 August 2023</a></p> <p><a href="#">EG.5 Updated Risk Evaluation, 21 September 2023</a></p> <p><a href="#">EG.5 Updated Risk Evaluation, 21 November 2023</a></p>
BA.2.86 <sup>s</sup>	23I	<a href="#">Mutations relative to BA.2</a>	24-07-2023	<p>21-11-2023</p> <p><a href="#">BA.2.86 Initial Risk Evaluation, 21 November 2023</a></p>
JN.1	Not assigned	BA.2.86 + S:L455S	25-08-2023	<p>09-02-2024</p> <p><a href="#">JN.1 Initial Risk Evaluation 18 December 2023</a></p> <p><a href="#">JN.1 Updated Risk Evaluation 9 February 2024</a></p>

# Currently circulating variants under monitoring (VUMs) as of 29 January 2024

Pango lineage	Nextstrain clade	Genetic features	Earliest documented samples	Date of designation and risk assessments
XBB*	22F	BA.2+ S:V83A, S:Y144-, S:H146Q, S:Q183E, S:V213E, S:G252V, S:G339H, S:R346T, S:L368I, S:V445P, S:G446S, S:N460K, S:F486S, S:F490S	19-08-2022	12-10-2022
XBB.1.9.1	23D	Recombinant of BA.2.10.1 and BA.2.75 sublineages, i.e. BJ.1 and BM.1.1.1 XBB.1 + S:F486P (similar Spike genetic profile as XBB.1.5)	05-12-2022	30-03-2023
XBB.2.3	23E	Recombinant of BA.2.10.1 and BA.2.75 sublineages, i.e. BJ.1 and BM.1.1.1 XBB + S:D253G, S:F486P, S:P521S	09-12-2022	17-05-2023

\* Excludes XBB sublineages listed here as VOIs and VUMs

# 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.)