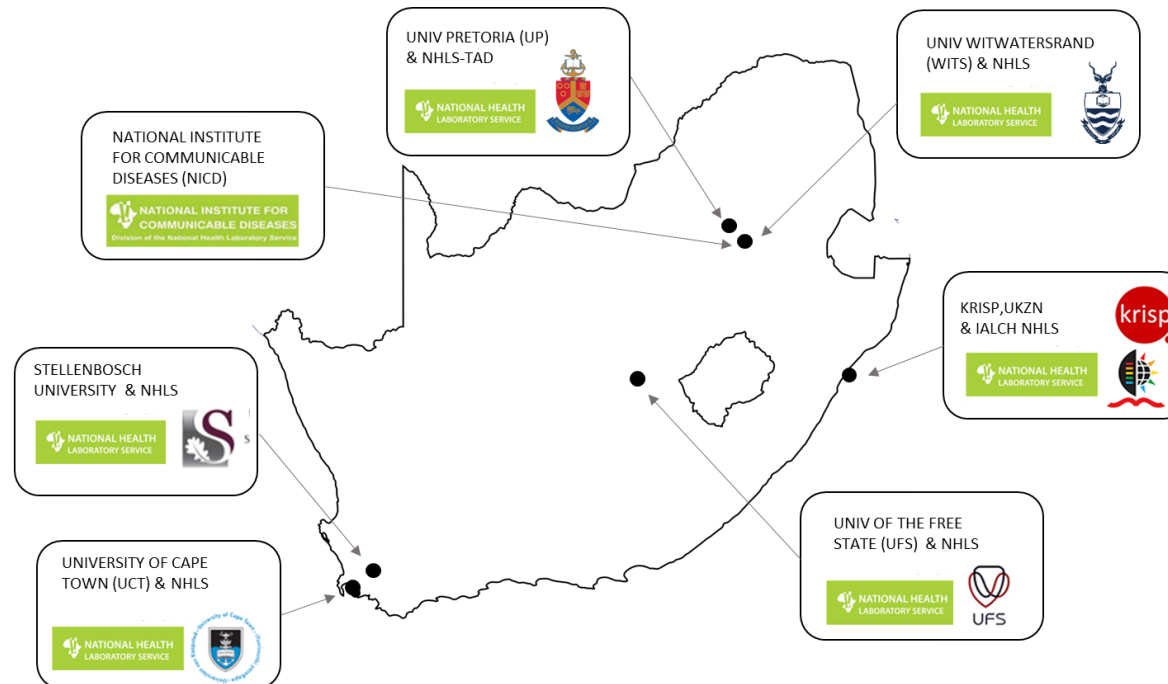


## SARS-CoV-2 Sequencing Update 21 April 2023



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 21 April 2023 at 08h44



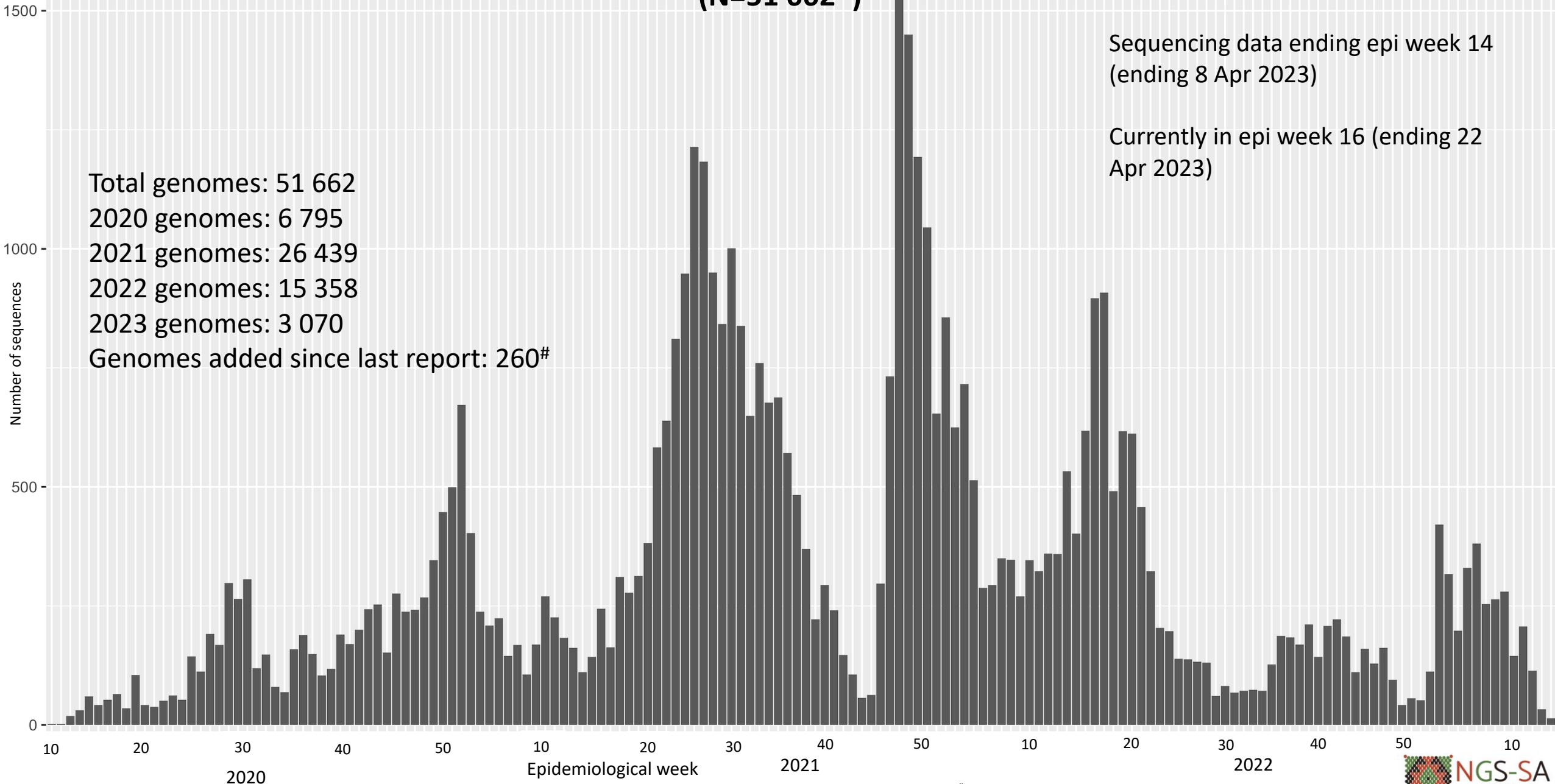
Data license: <https://www.gisaid.org/registration/terms-of-use/>

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

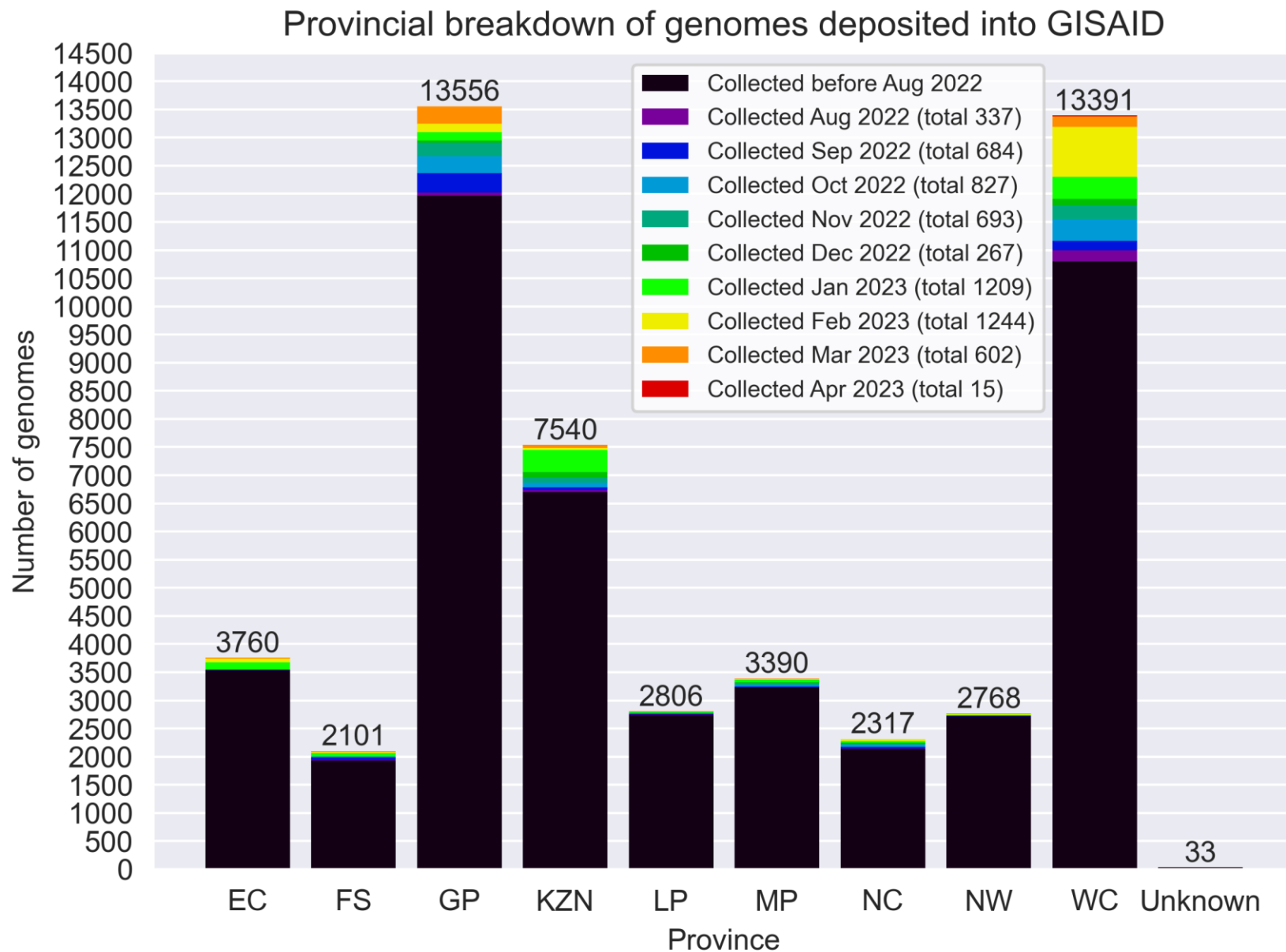
# Number of South African genomes deposited on GISAID, by specimen collection week, 2020 – 2023

(N=51 662\*)

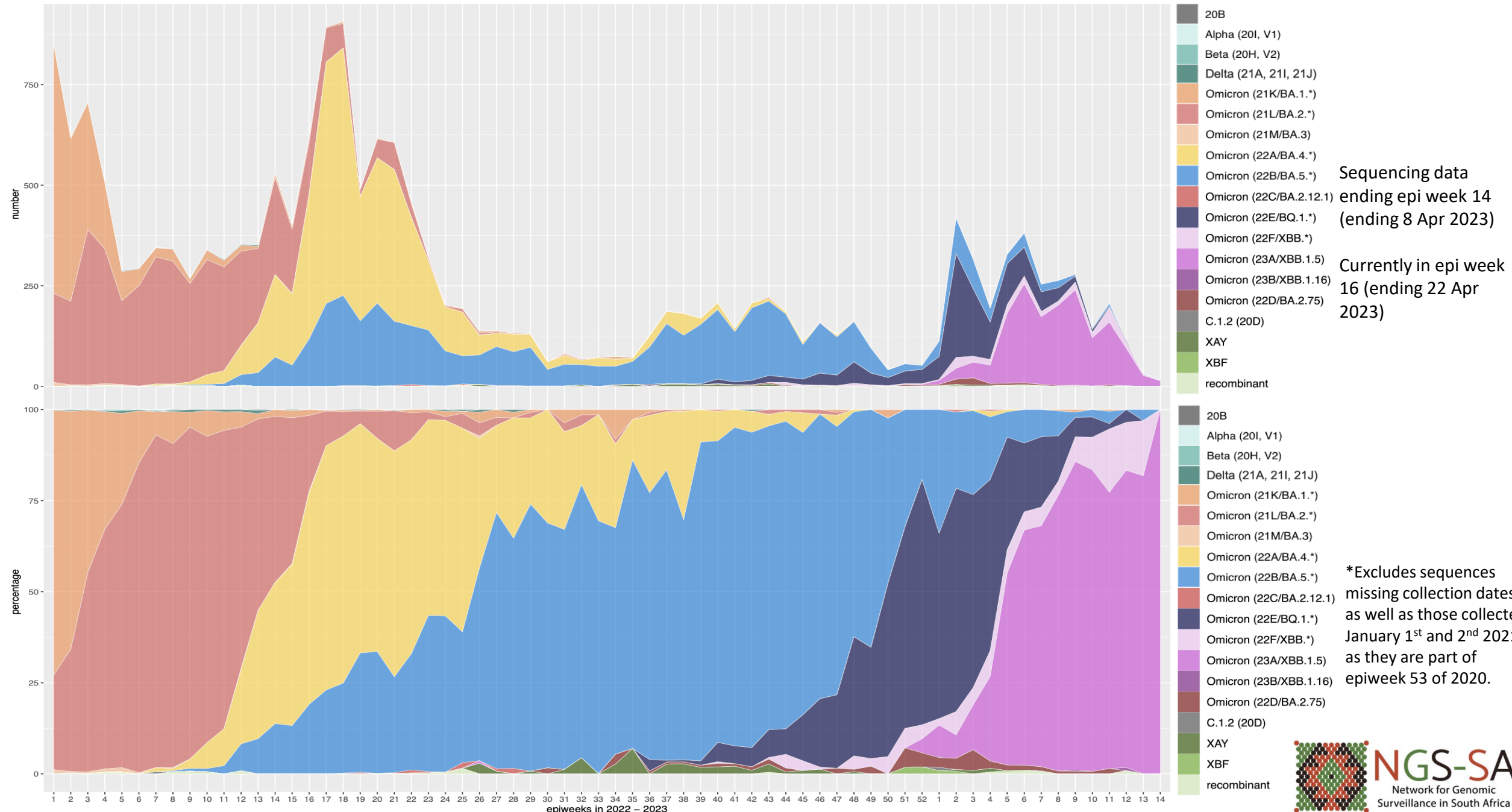


\*This represents the cleaned, de-duplicated dataset of unique **National and Pneumonia Surveillance** sequences. This dataset will be used for all further figures; <sup>#</sup>n=14 genomes from 2021 were removed due to duplication

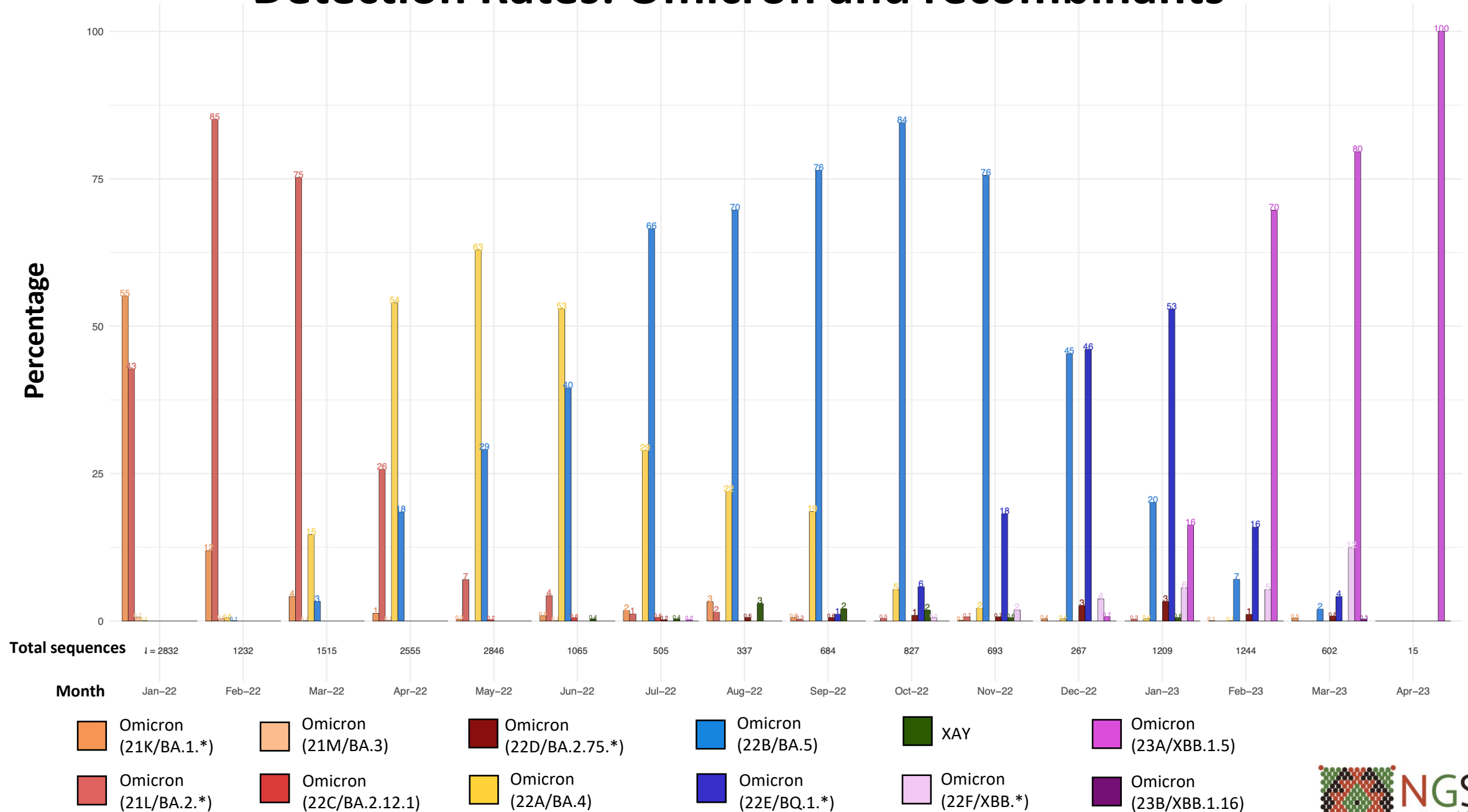
# GISAID genomes vs total cases, 2020 – 2023 (N= 51 662)



# Number and percentage of clades by epiweek in South Africa, 2022-2023 (18 385\*)



# 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

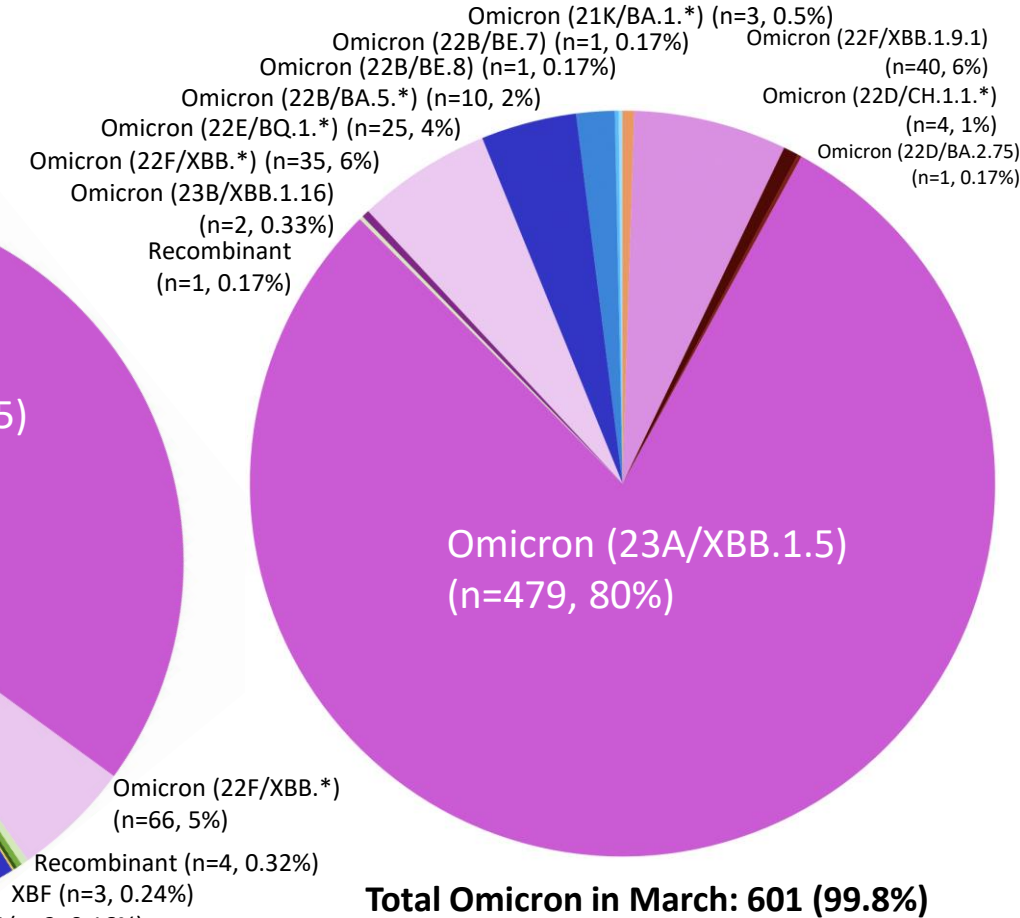
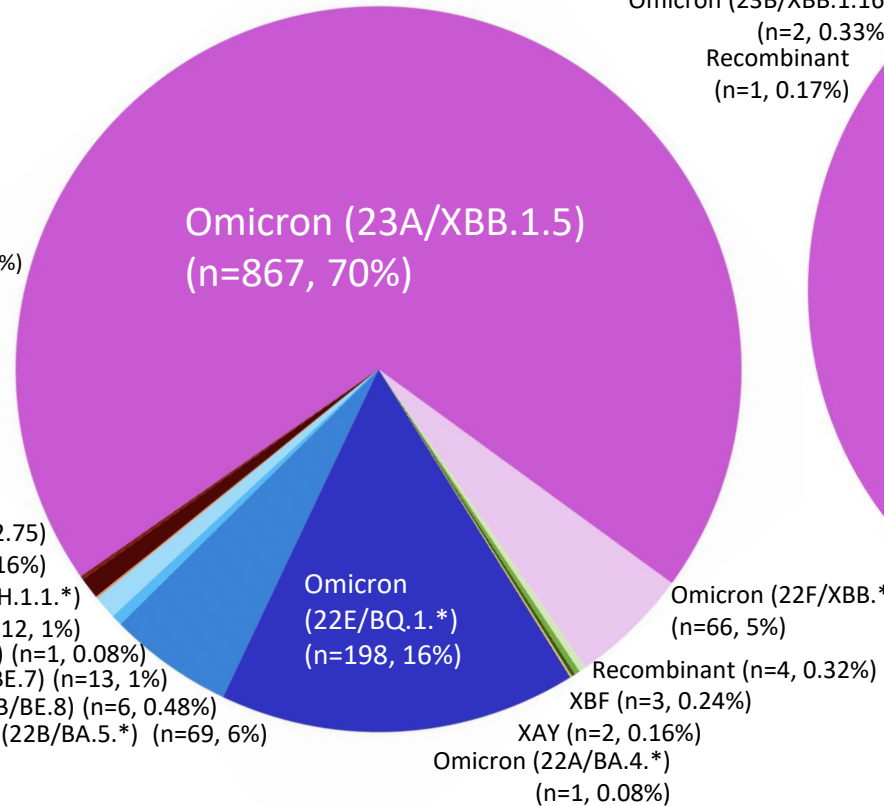
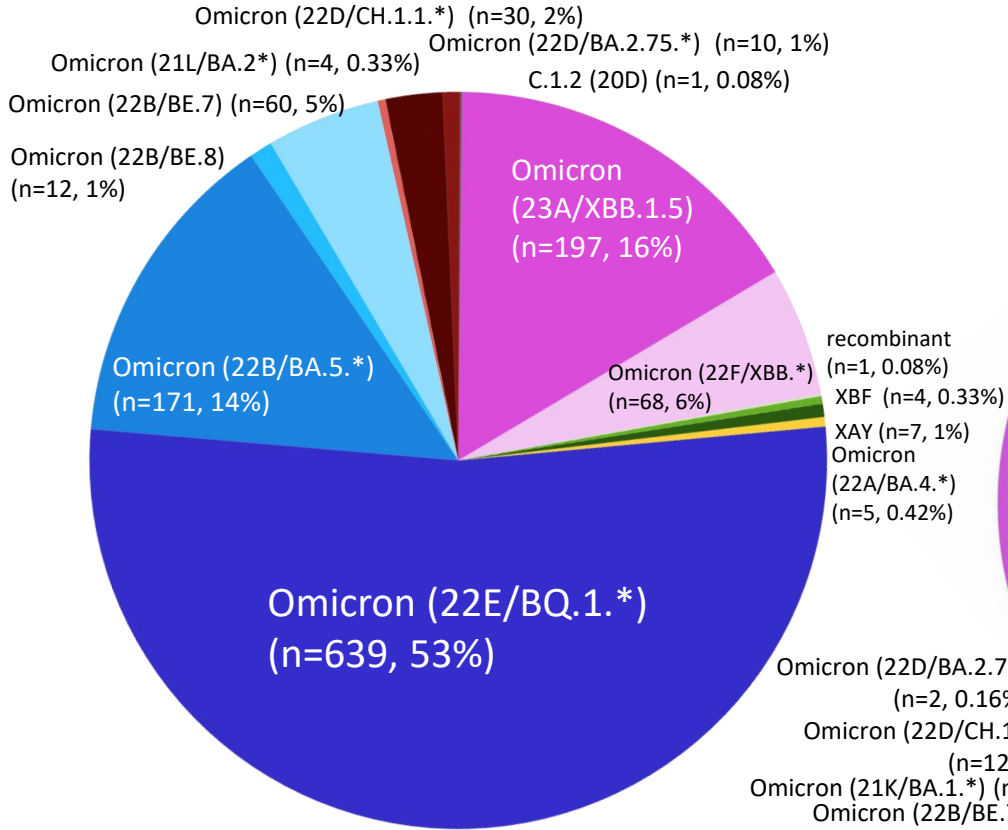
# Prevalence of Variants of Concern (VOC) and Variants of Interest (VOI) in

## Jan – Mar 2023

Jan (N=1209)

Mar (N=602)

Feb (N=1244)

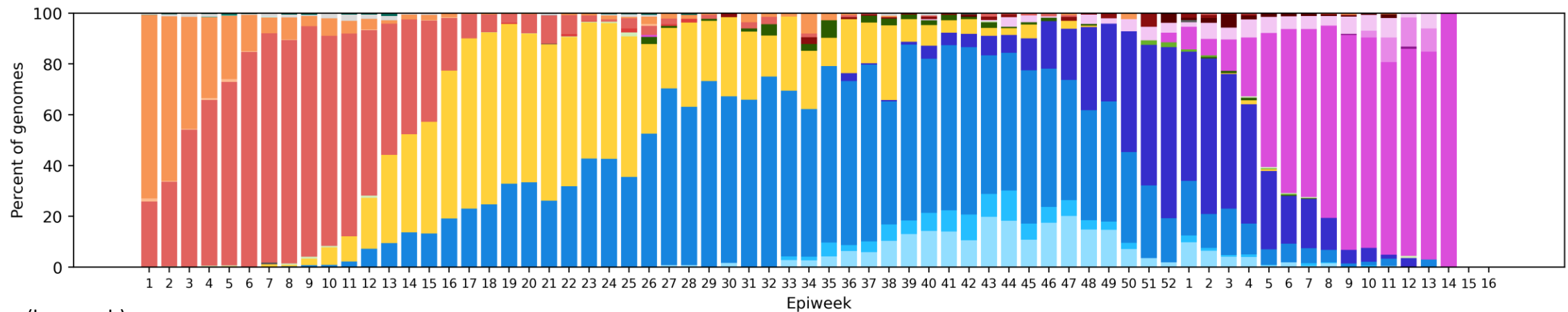
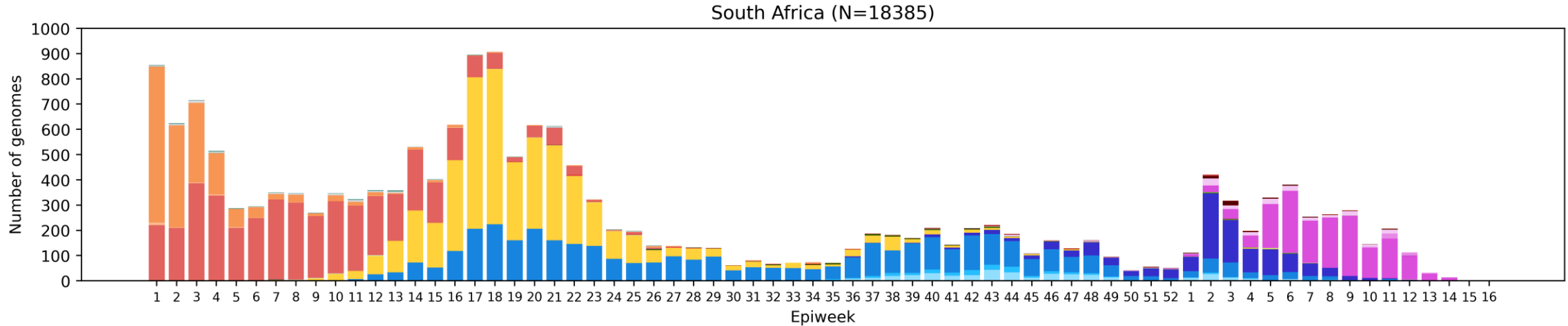


Clade key (bar graph)

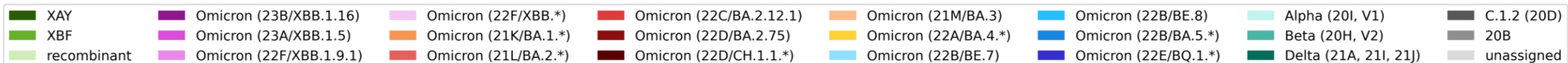
XAY	Omicron (23B/XBB.1.16)	Omicron (22F/XBB.*)	Omicron (22C/BA.2.12.1)	Omicron (21M/BA.3)	Omicron (22B/BE.8)	Alpha (20I, V1)	C.1.2 (20D)
XBF	Omicron (23A/XBB.1.5)	Omicron (21K/BA.1.*)	Omicron (22D/BA.2.75)	Omicron (22A/BA.4.*)	Omicron (22B/BA.5.*)	Beta (20H, V2)	20B
recombinant	Omicron (22F/XBB.1.9.1)	Omicron (21L/BA.2.*)	Omicron (22D/CH.1.1.*)	Omicron (22B/BE.7)	Omicron (22E/BQ.1.*)	Delta (21A, 21I, 21J)	unassigned

Note: XBF is an Omicron-Omicron recombinant and so is counted in the total number of Omicrons.

# South Africa, 2022-2023, n = 18 385\*



Clade key (bar graph)



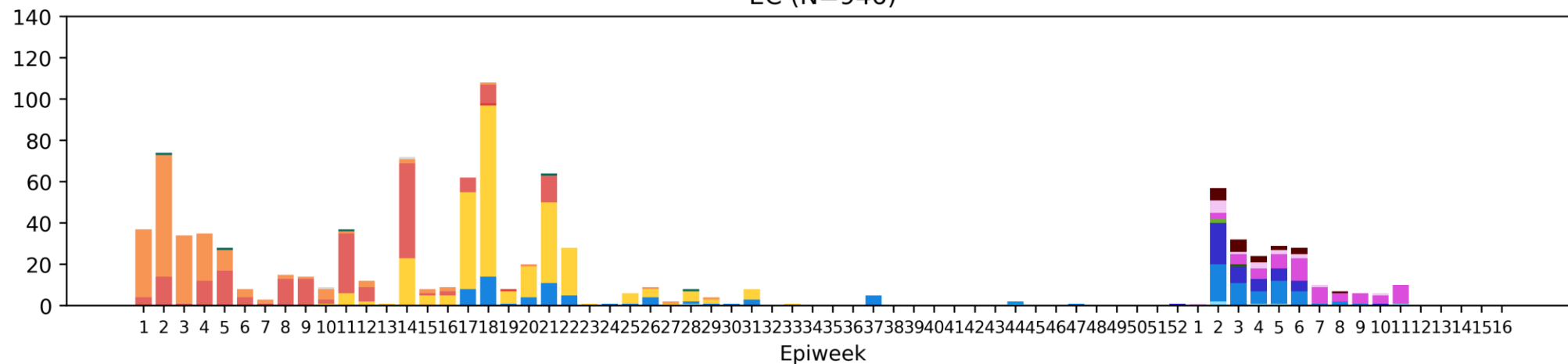
\*Excludes sequences missing collection dates. Lineages of particular interest (mainly WHO Omicron subvariants under monitoring) are separate from the main clade groupings.

#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.

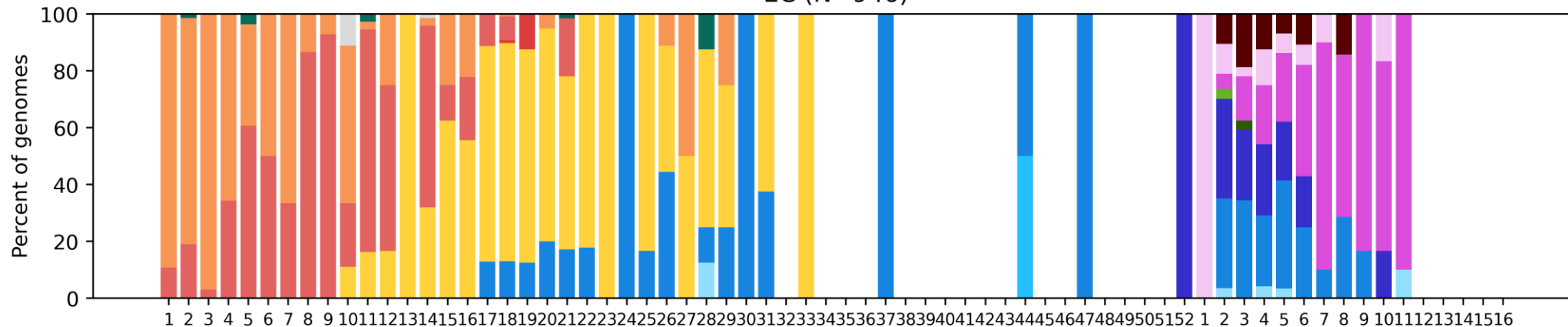
# Eastern Cape Province, 2022-2023, n = 946

Genomes added since last report: 13\*

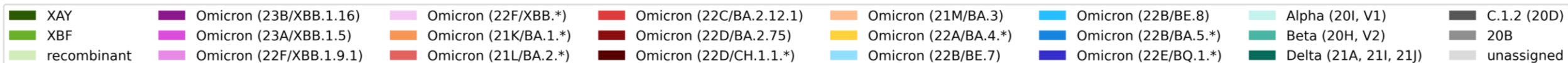
EC (N=946)



EC (N=946)



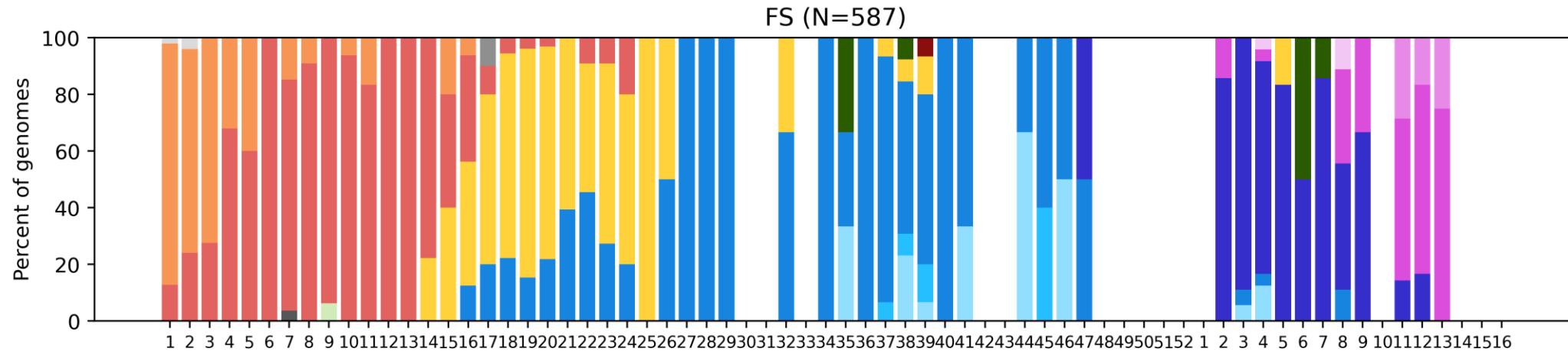
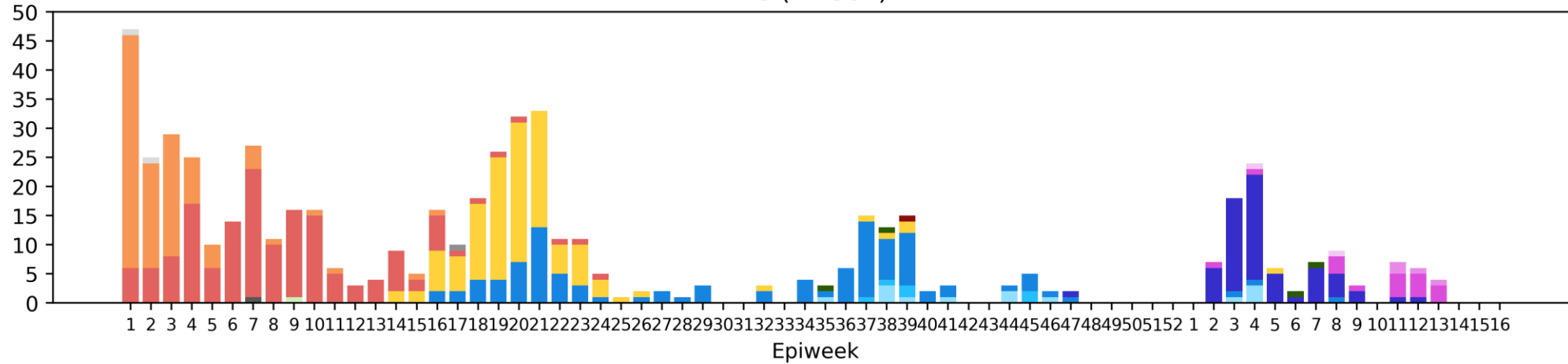
Clade key (bar graph)



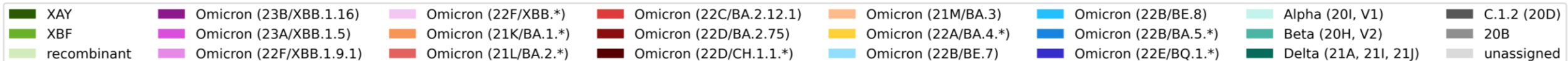
\*May include genomes from 2020 and 2021 which are not pictured here and are not included in the slide total.

# Free State Province, 2022-2023, n = 587

Genomes added since last report: 16\*  
FS (N=587)



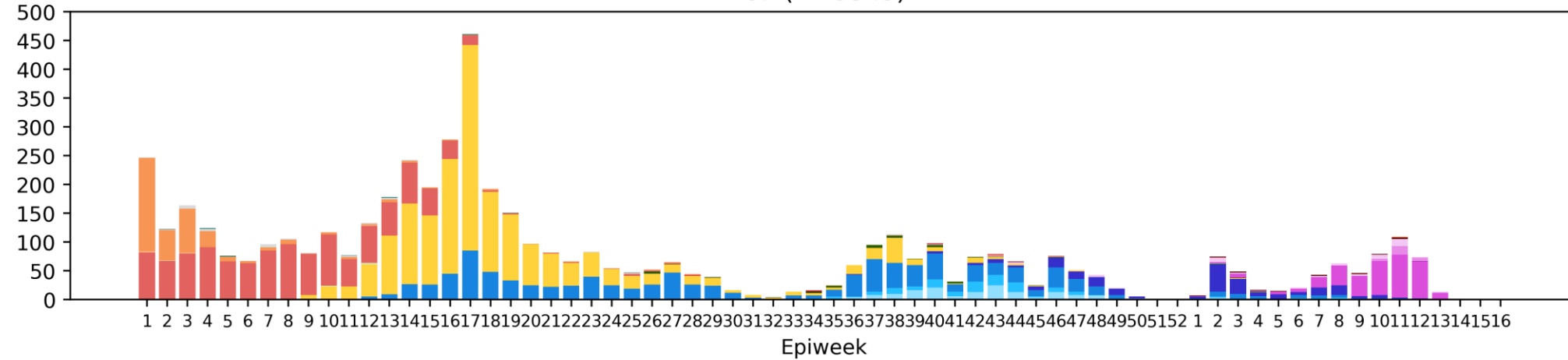
Clade key (bar graph)



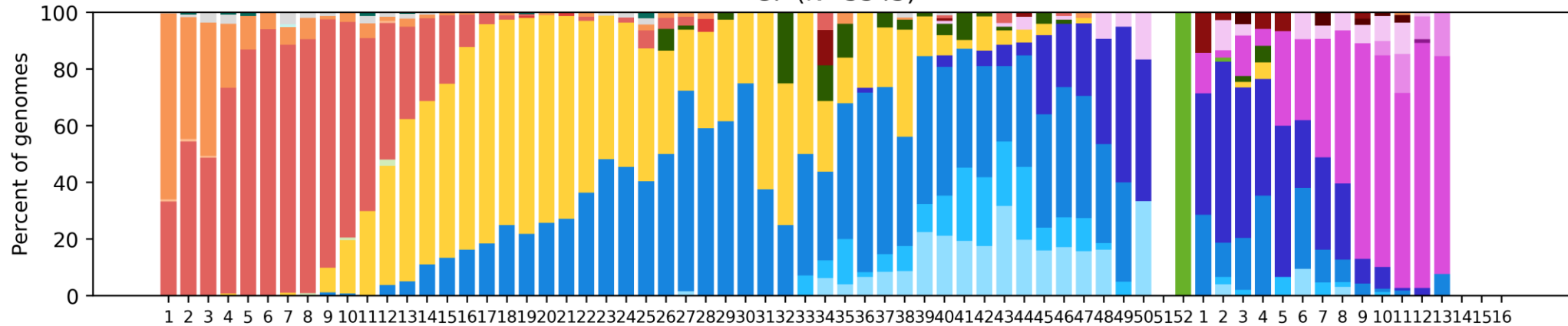
# Gauteng Province, 2022-2023, n = 5343

Genomes added since last report: 113\*

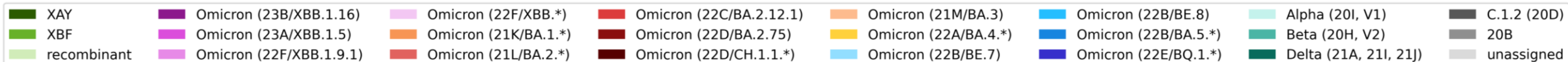
GP (N=5343)



GP (N=5343)



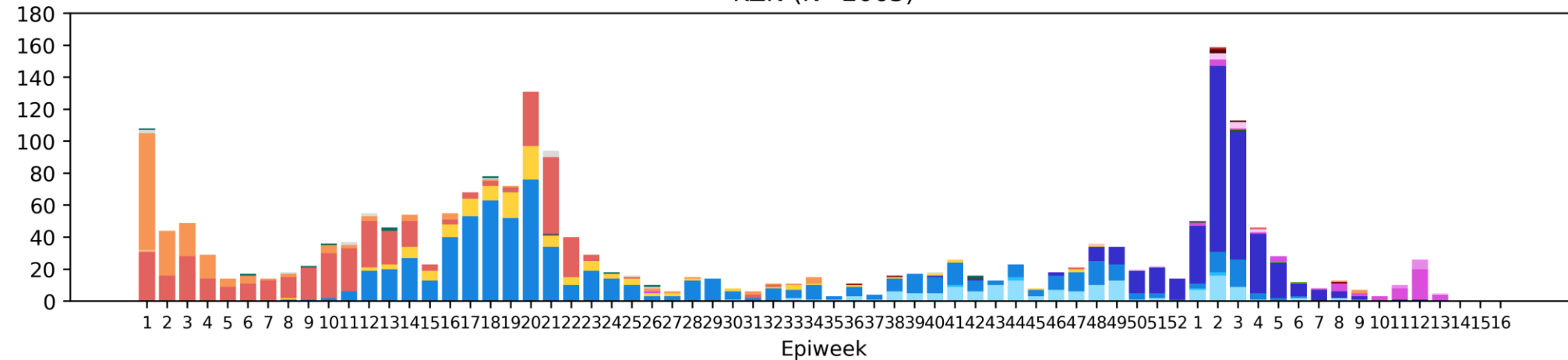
Clade key (bar graph)



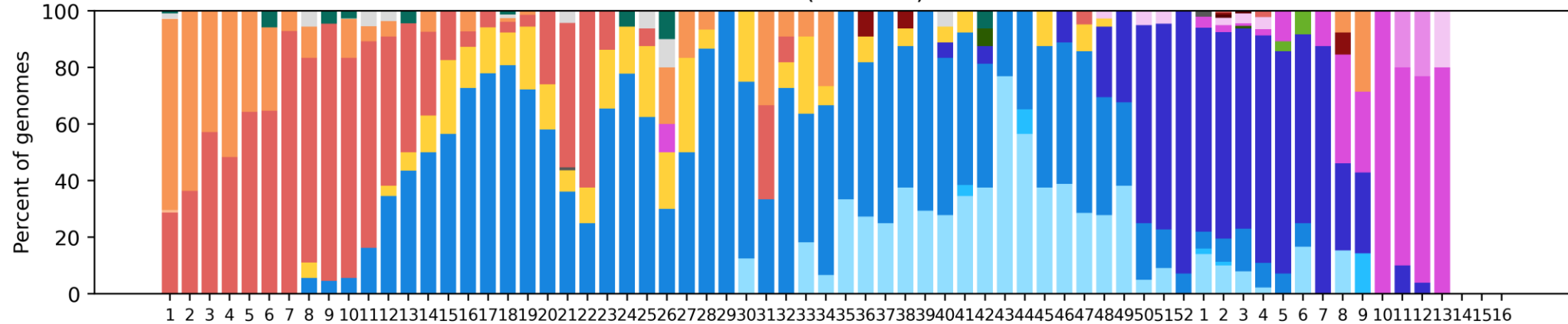
# KwaZulu-Natal Province, 2022-2023, n = 2063

Genomes added since last report: 50\*

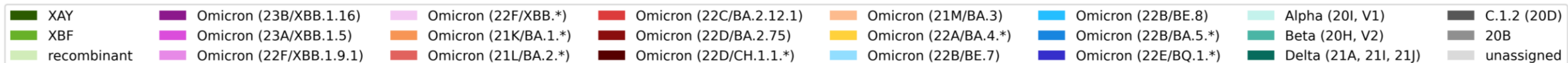
KZN (N=2063)



KZN (N=2063)

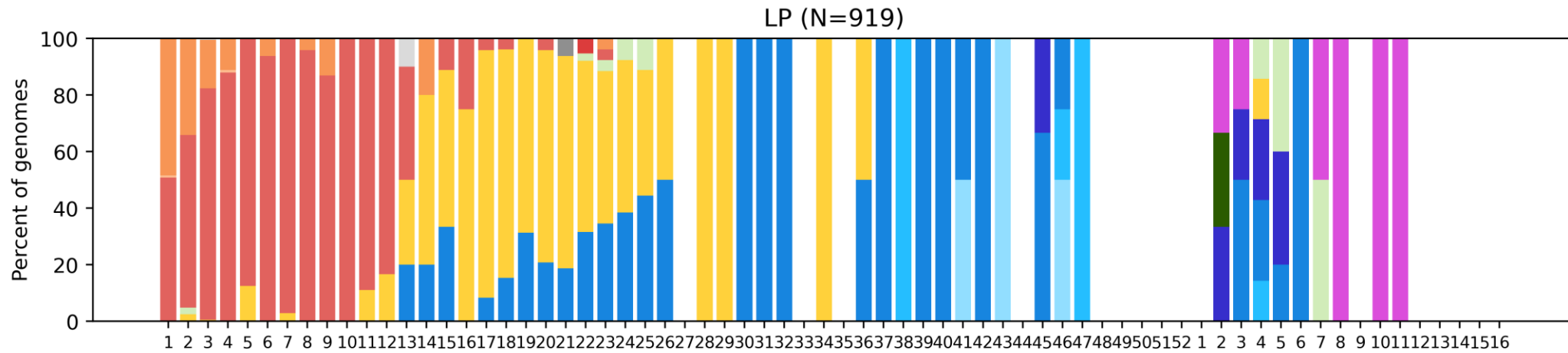
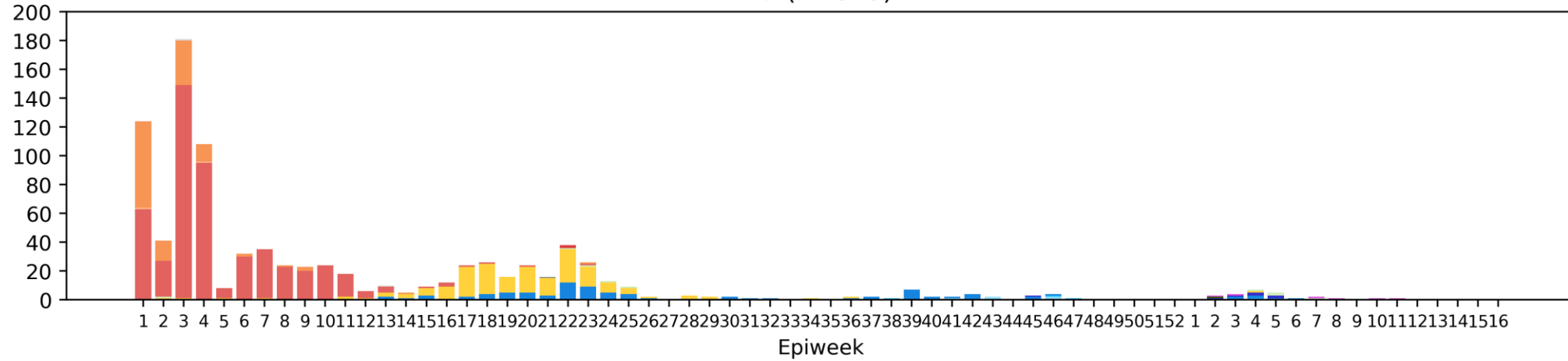


Clade key (bar graph)

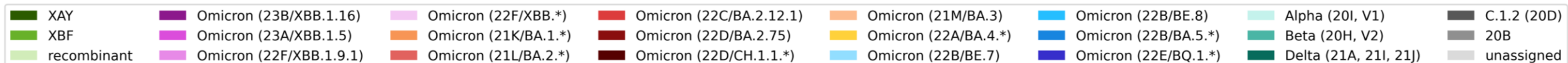


# Limpopo Province, 2022-2023, n = 919

Genomes added since last report: 1\*  
LP (N=919)



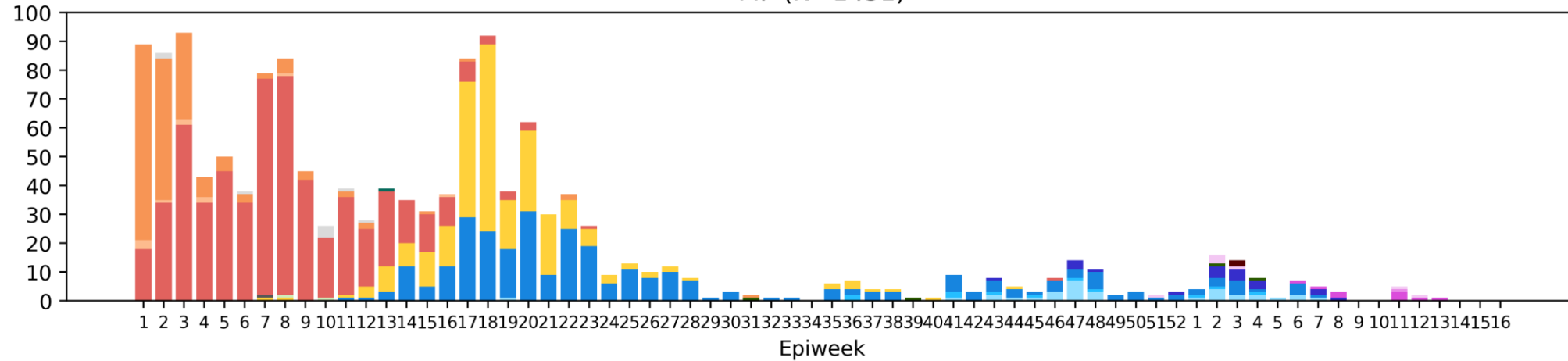
Clade key (bar graph)



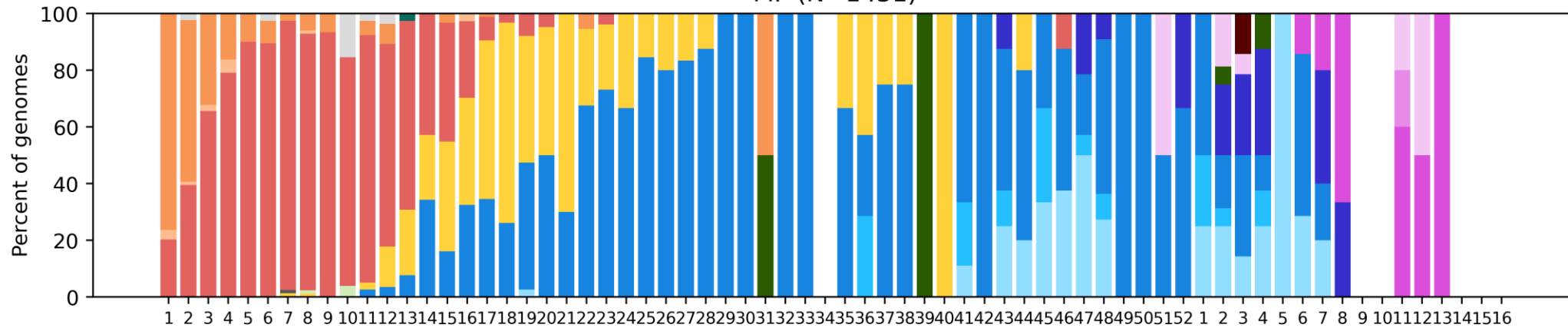
# Mpumalanga Province, 2022-2023, n = 1431

Genomes added since last report: 6\*

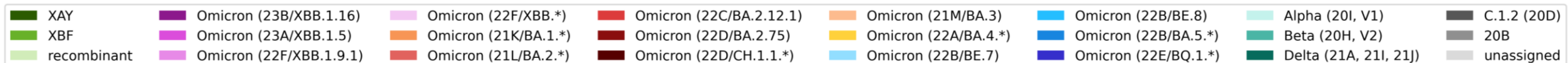
MP (N=1431)



MP (N=1431)



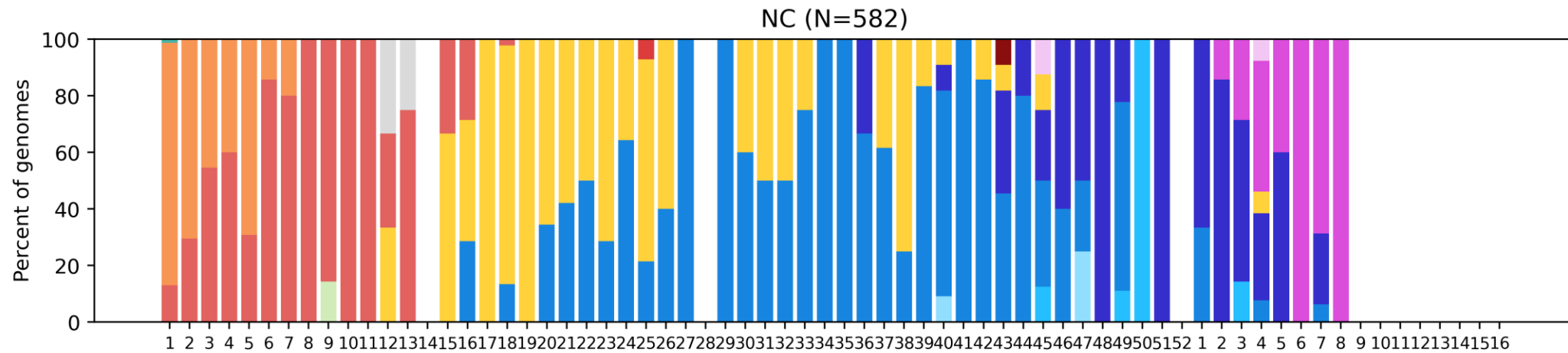
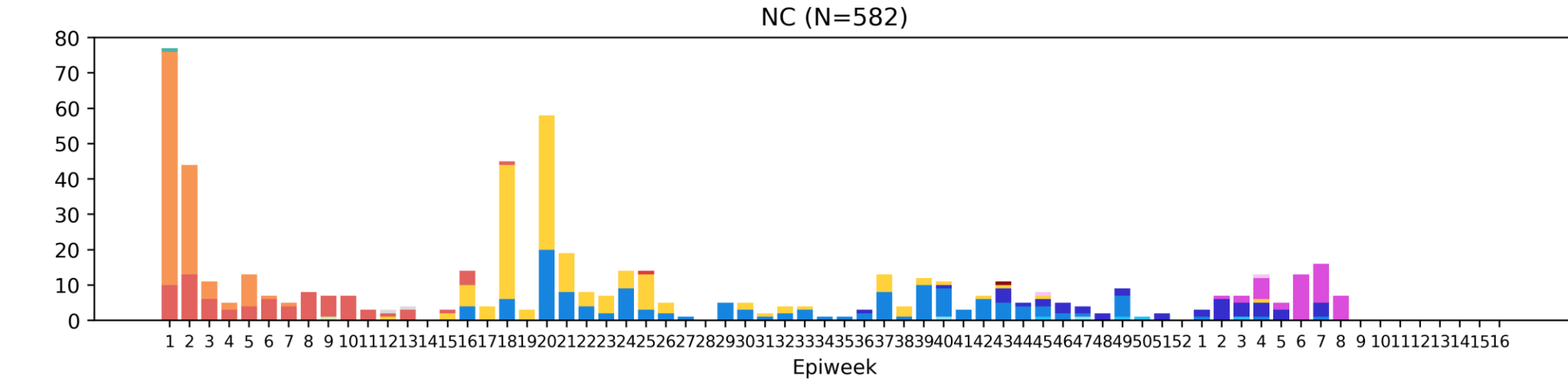
Clade key (bar graph)



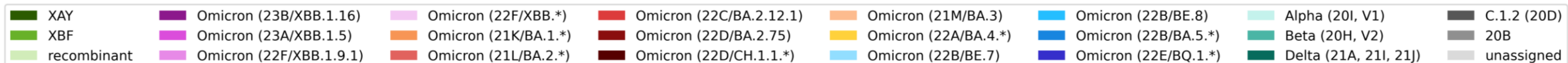
\*May include genomes from 2020 and 2021 which are not pictured here and are not included in the slide total.

# Northern Cape Province, 2022-2023, n = 582

Genomes added since last report: 0\*



Clade key (bar graph)

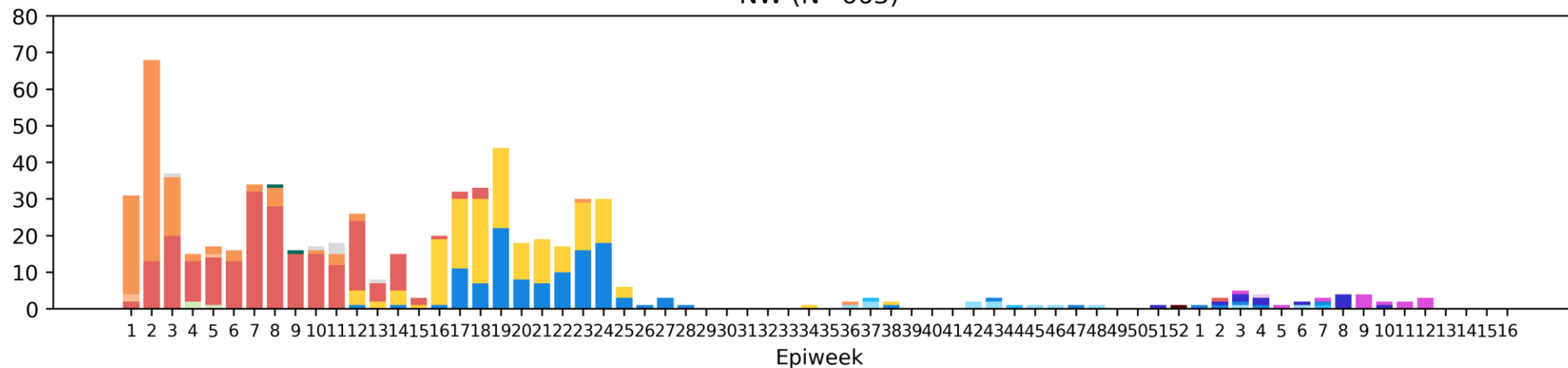


\*May include genomes from 2020 and 2021 which are not pictured here and are not included in the slide total.

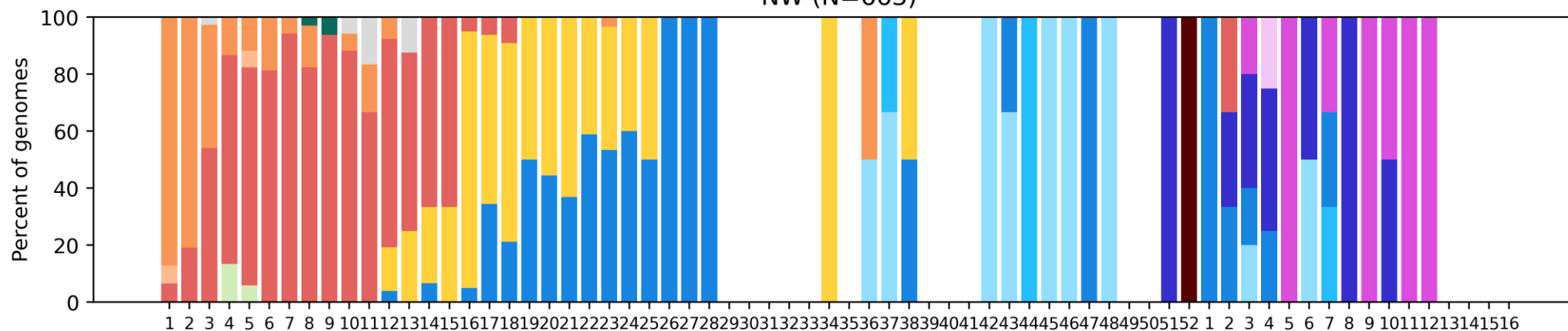
# North West Province, 2022-2023, n = 663

Genomes added since last report: 3\*

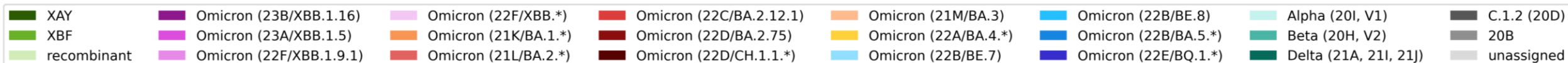
NW (N=663)



NW (N=663)



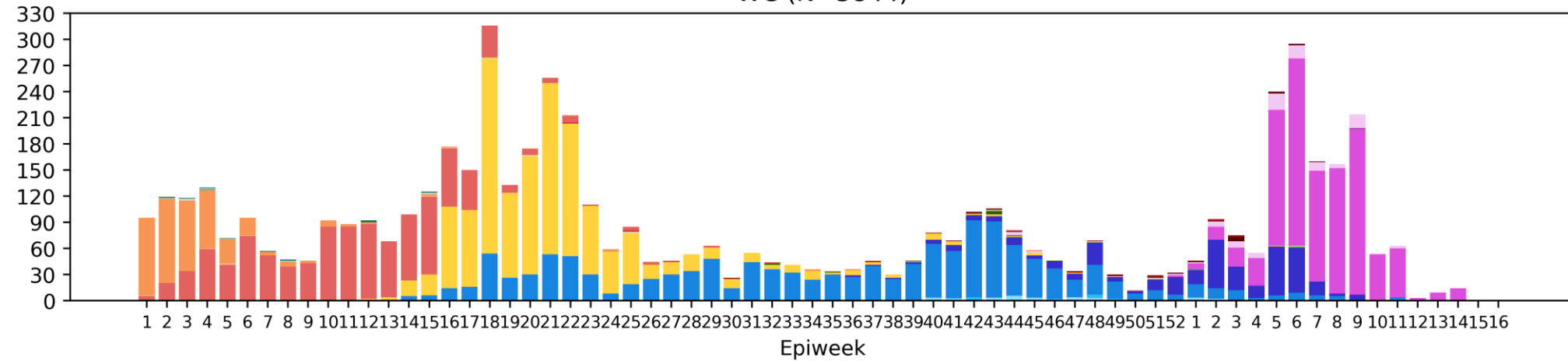
Clade key (bar graph)



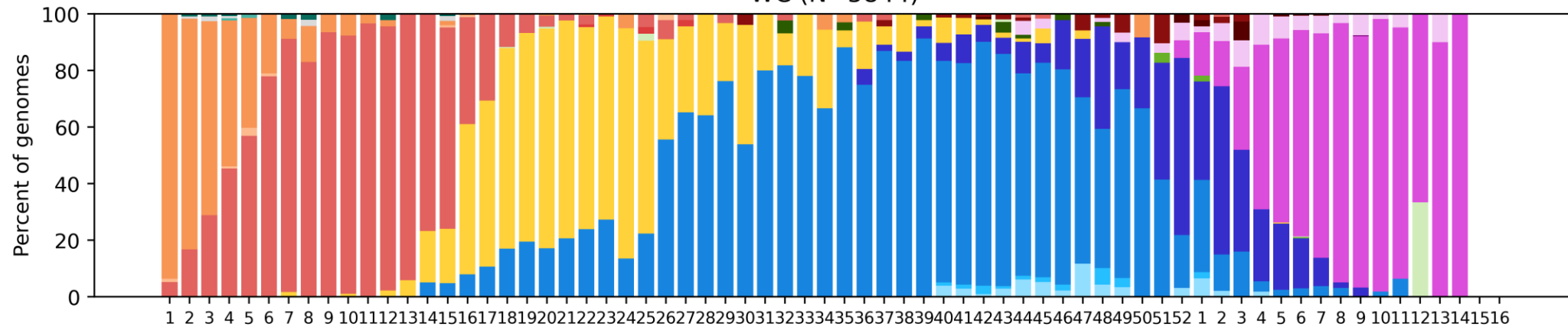
# Western Cape Province, 2022-2023, n = 5844

Genomes added since last report: 58\*

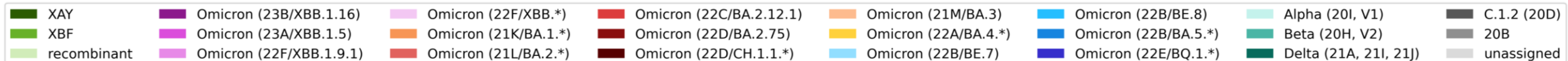
WC (N=5844)



WC (N=5844)



Clade key (bar graph)



# Summary

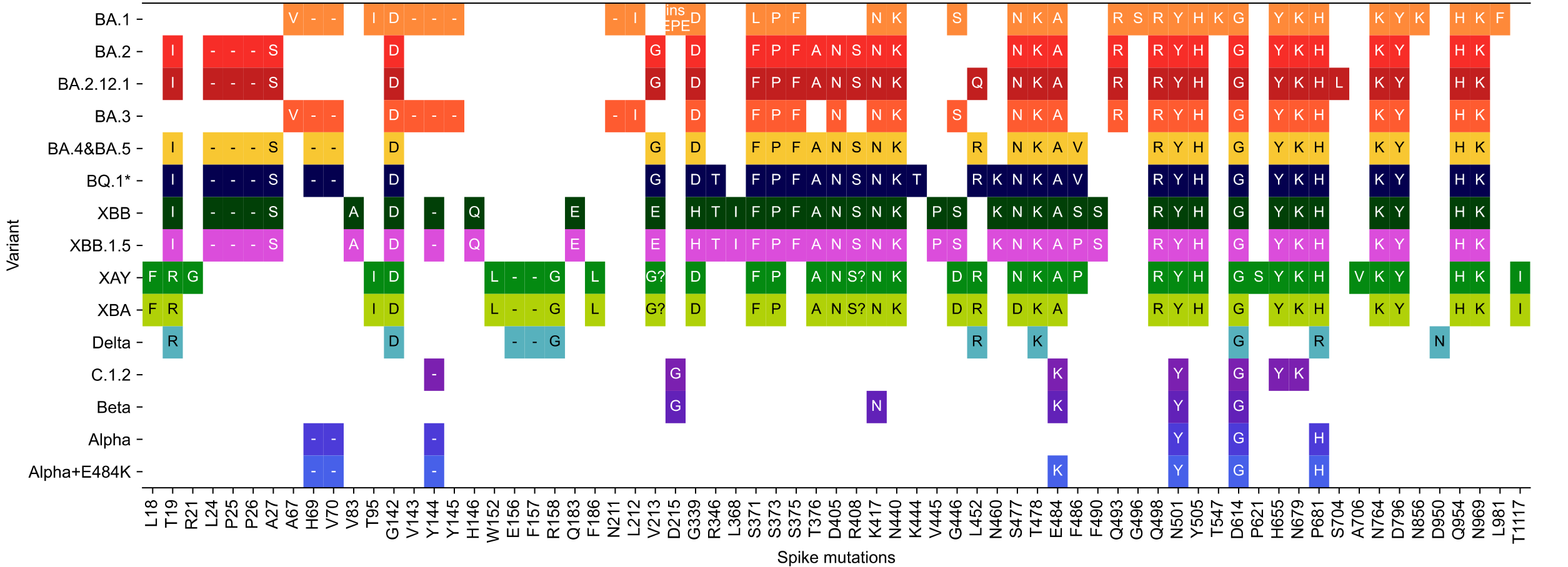
- **Sequencing update**

- All provinces have sequences for January and February 2023. March sequences are from all provinces, except the Northern Cape. April sequence data is from the Western Cape

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

- Omicron continued to dominate in January (99%), February (100%) and March (100%)
- BQ.1 and sub-lineages were the dominant Omicron lineage in December (46%) and January (53%)
- XBB.1.5 was detected in December 2022 (0.8%) and January 2023 (16%), and was the dominant lineage in February (70%) and March (80%). It is currently dominant in April (100%), although this is based on low numbers (n=15)
- XBB.1.16 has been detected at a low prevalence in March (<1%) in Gauteng (n=1) and the Western Cape (n=1)
- BA.2.75.\* continued to be detected at a low prevalence in January through March ( $\leq 1\%$ )

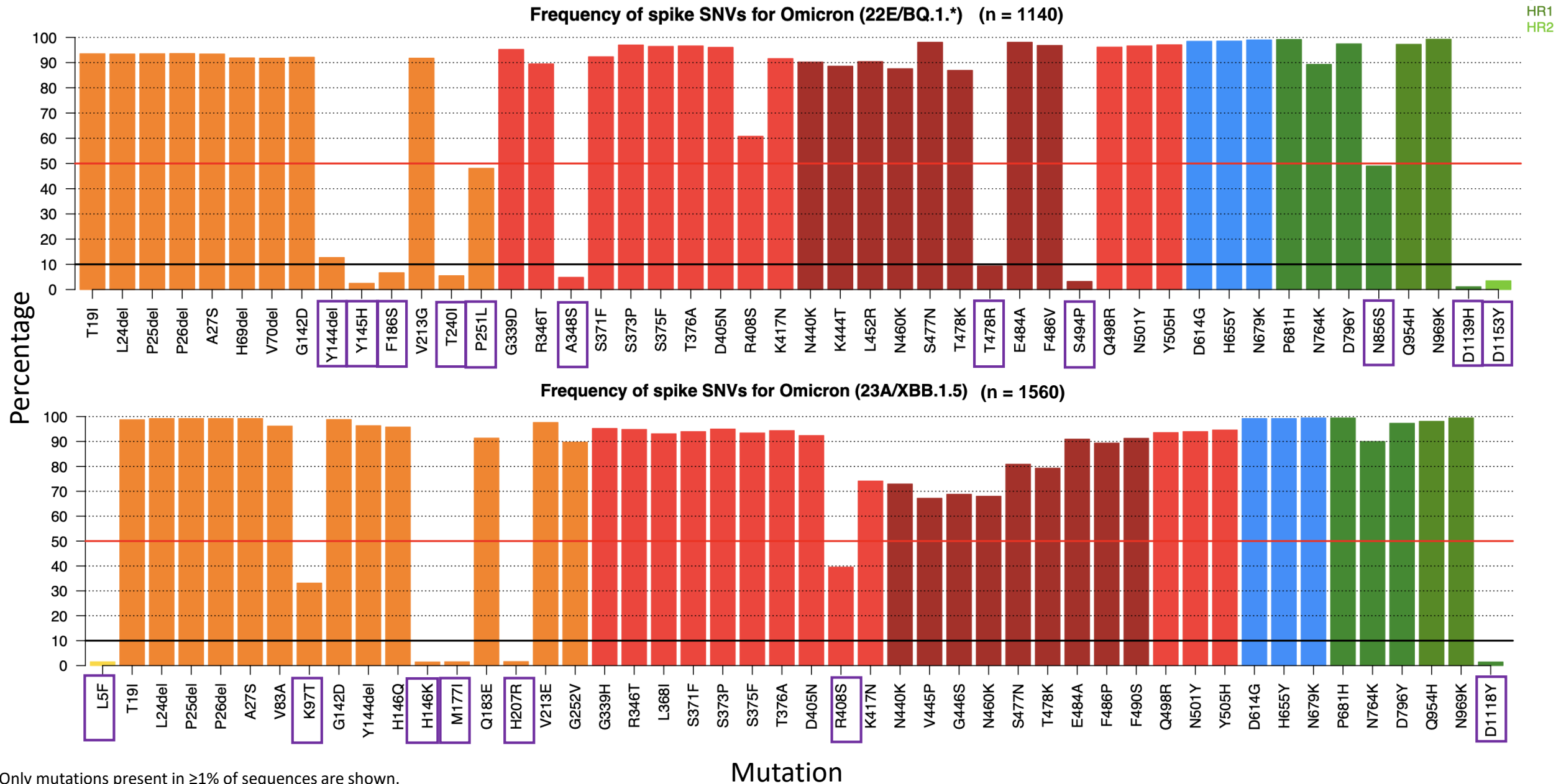
# Spike protein mutation\* profile of Variants of Interest and Concern



- 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

# BQ.1\* and XBB.1.5\* spike mutations\*



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KWAZULU-NATAL  
INYUVESI  
YAKWAZULU-NATALI



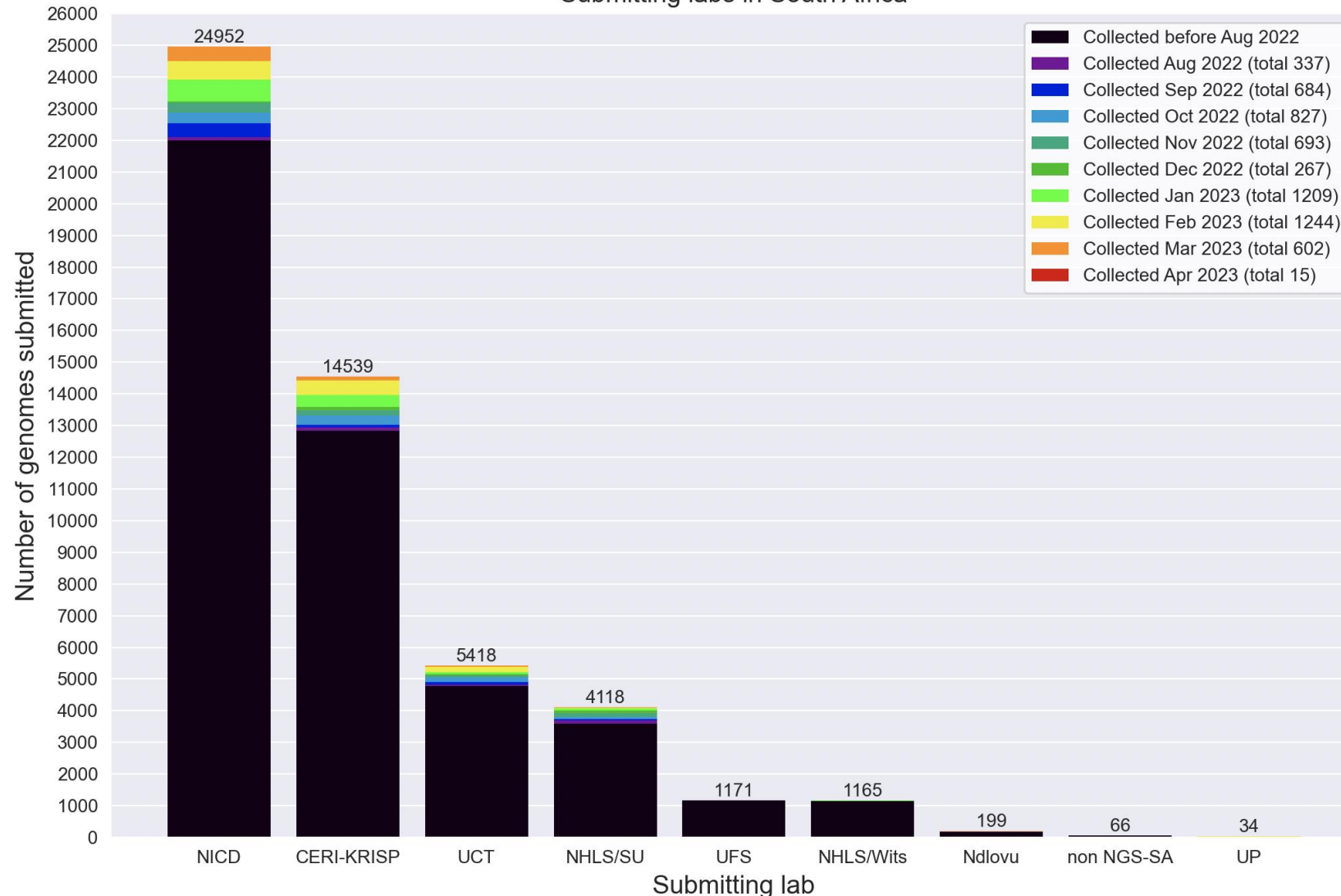
EDCTP

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



# South African genomes submitted per submitting lab, 2020 - 2023 (N=51 662)

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 Interest (VOI) as of 15 March 2023

Pango lineage	Nextstrain clade	Genetic features	Earliest documented samples	Date of designation
XBB.1.5	23A	<p>Recombinant of BA.2.10.1 and BA.2.75 sublineages, i.e. BJ1 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>	05-01-2022	<p>11-Jan-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>

# Currently circulating variants under monitoring (VUMs)

Pango lineage <sup>#</sup> (+ mutation)	Nextstrain clade	Spike genetic features	Earliest documented samples	Date of designation and risk assessments
BA.2.75	22D	BA.2 + S:K147E, S:W152R, S:F157L, S:I210V, S:G257S, S:D339H, S:G446S, S:N460K, S:Q493R reversion	31-12-2021	06-Jul-2022
CH.1.1	22D	BA.2.75 + S:L452R, S:F486S	27-07-2022	08-Feb-2023
BQ.1	22E	BA.5 + S:R346T, S:K444T, S:N460K	07-02-2022	21-Sep-2022
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	13-08-2022	12-Oct-2022
XBB.1.16	23B	Recombinant of BA.2.10.1 and BA.2.75 sublineages, i.e. BJ1 and BM.1.1.1 XBB.1 + S:E180V, S:K478R and S:F486P	23-01-2023	22-03-2023
XBB.1.9.1	Not assigned	Recombinant of BA.2.10.1 and BA.2.75 sublineages, i.e. BJ1 and BM.1.1.1 XBB.1 + S:F486P (similar Spike genetic profile as XBB.1.5)	05-12-2022	30-03-2022
XBF	Not assigned	Recombinant of BA.5.2.3 and CJ.1 (BA.2.75.3 sublineage) BA.5 + S:K147E, S:W152R, S:F157L, S:I210V, S:G257S, S:G339H, S:R346T, S:G446S, S:N460K, S:F486P, S:F490S	27-07-2022	08-Feb-2023

# 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.)