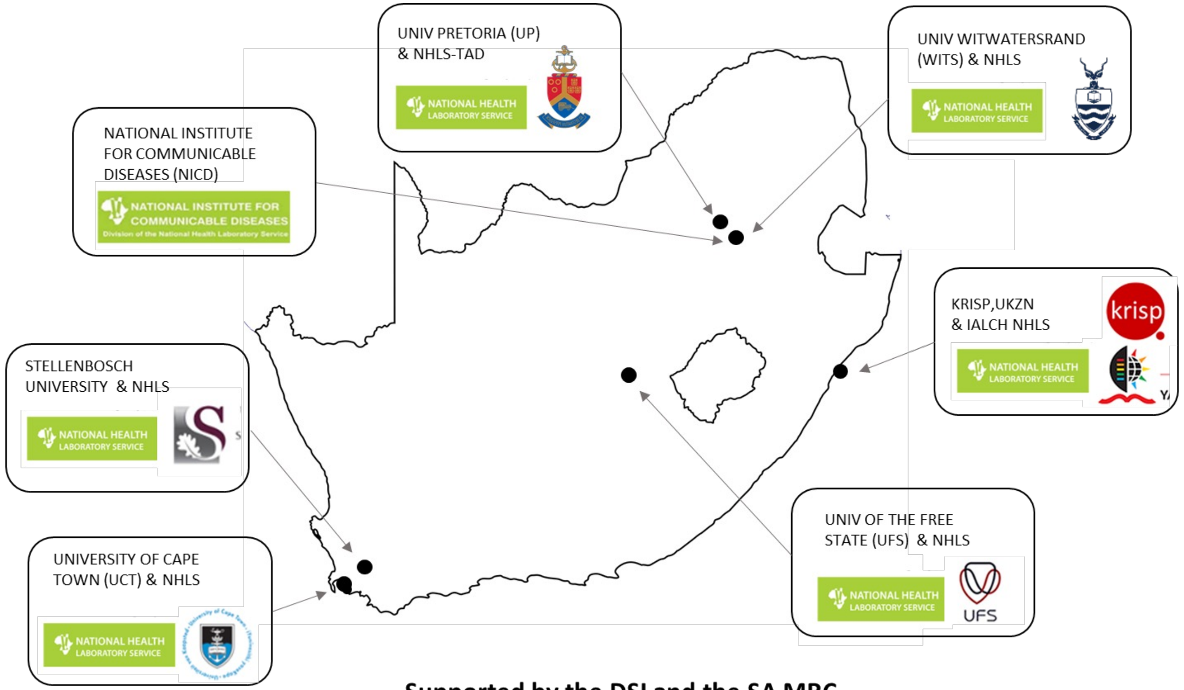
Network for Genomic Surveillance in South Africa (NGS-SA)

SARS-CoV-2 Sequencing Update
14 December 2023



Supported by the DSI and the SA MRC

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

Prepared by the National Institute for Communicable Diseases (NICD) of the National Health Laboratory (NHLS) on behalf of the Network for Genomics Surveillance in South Africa (NGS-SA)

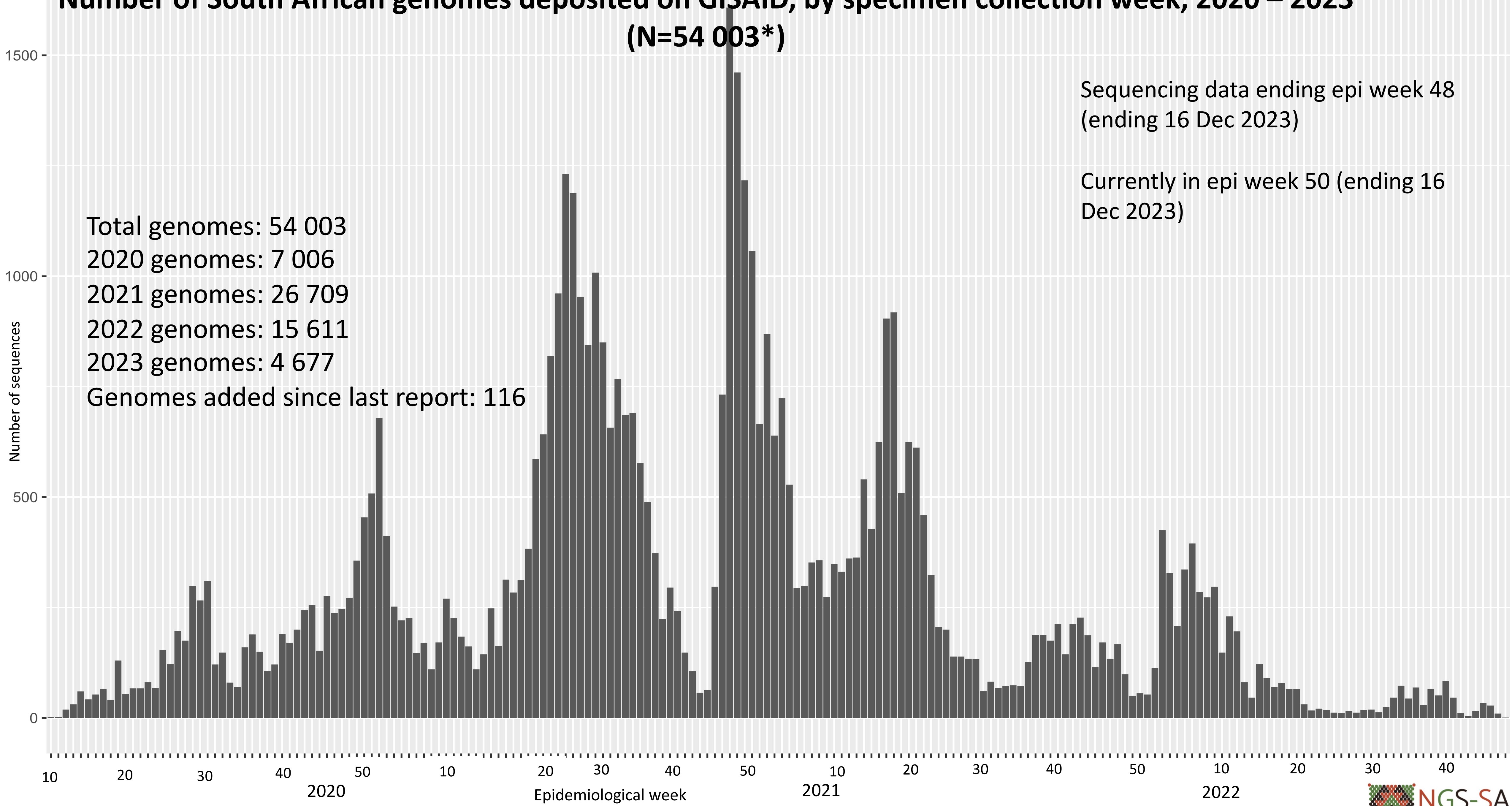
The genomic data presented here are based on South African SARS-CoV-2 sequence data downloaded from GISAID (www.gisaid.org) on 14 December 2023 at 08h30

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=54 003*)



Total genomes: 54 003
2020 genomes: 7 006
2021 genomes: 26 709
2022 genomes: 15 611
2023 genomes: 4 677
Genomes added since last report: 116

Sequencing data ending epi week 48 (ending 16 Dec 2023)

Currently in epi week 50 (ending 16 Dec 2023)

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

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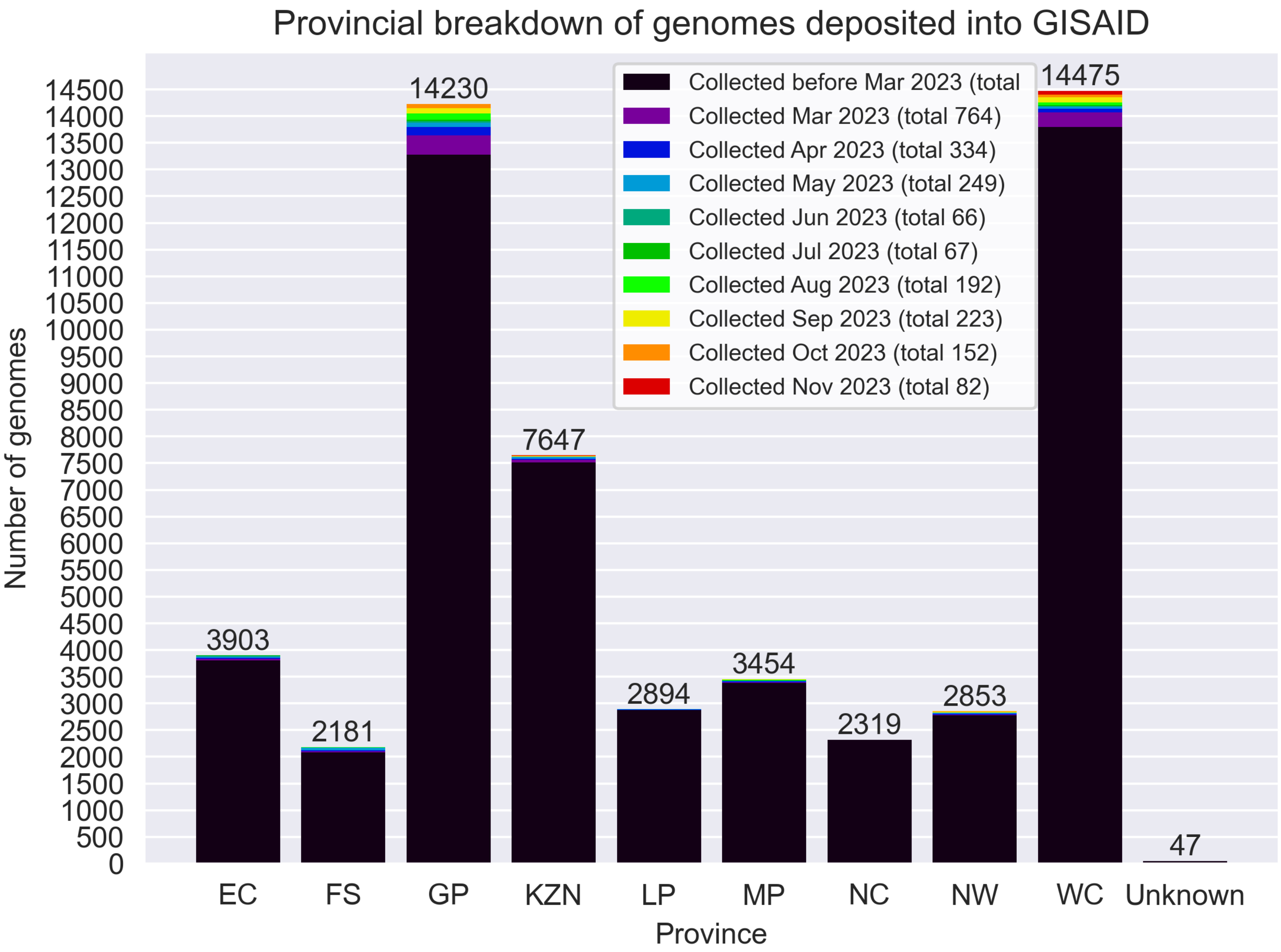
GISAID genomes vs total cases, 2020 – 2023 (N= 54 003)



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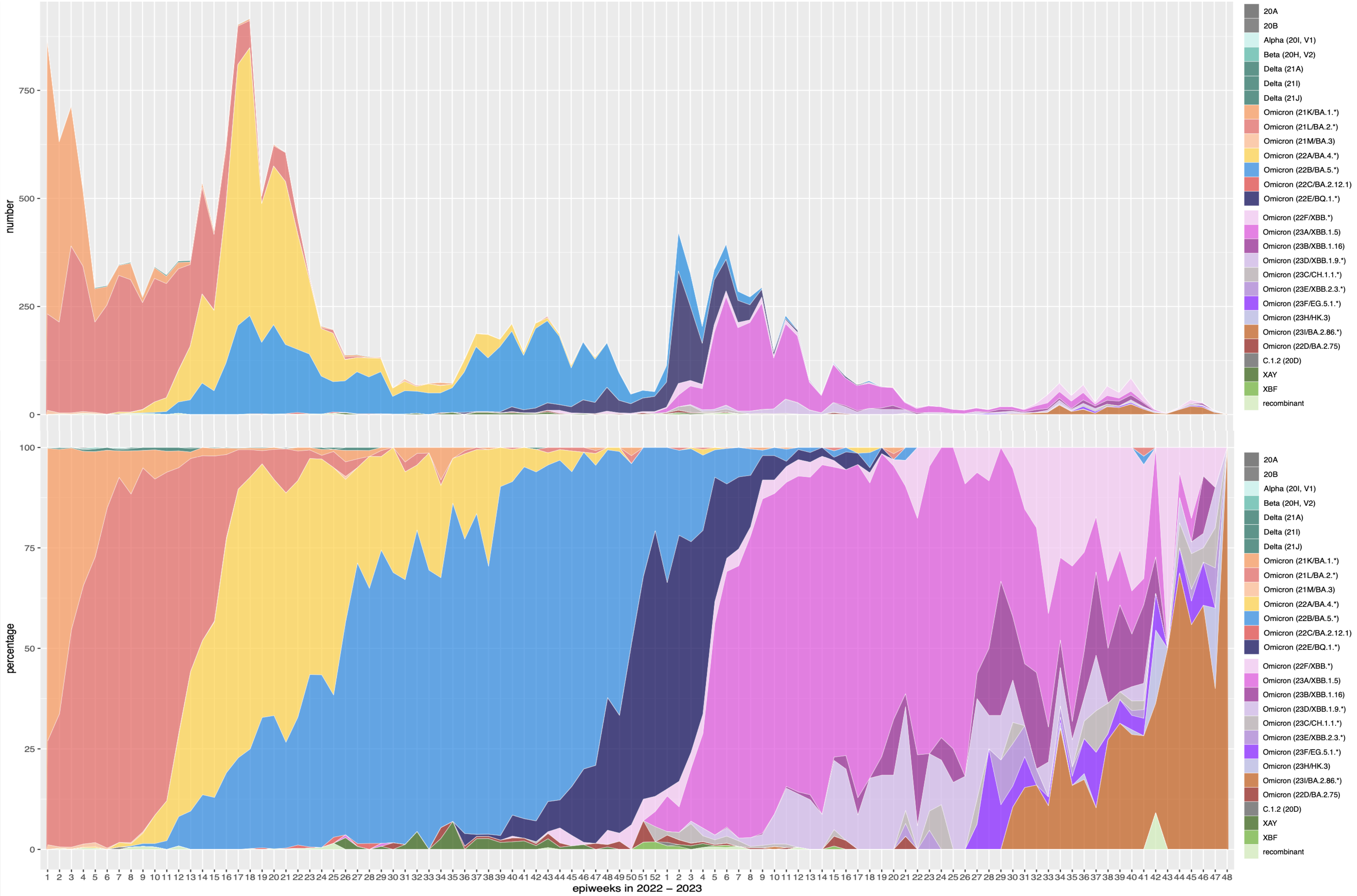
Number and percentage of clades by epiweek in South Africa, 2022-2023 (20 245*)



Sequencing data ending epi week 48 (ending 2 Dec 2023)

Currently in epi week 50 (ending 16 Dec 2023)

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

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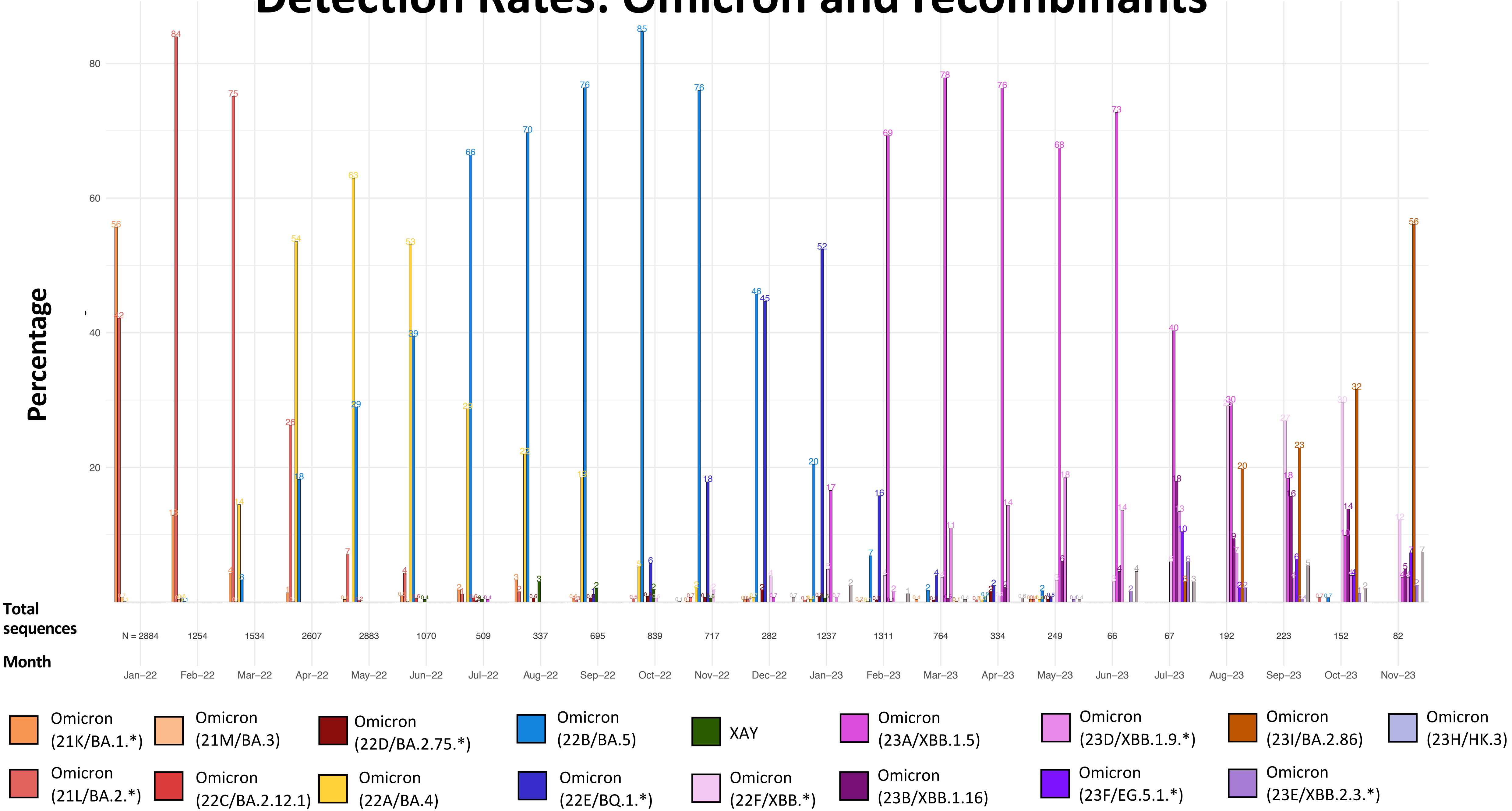
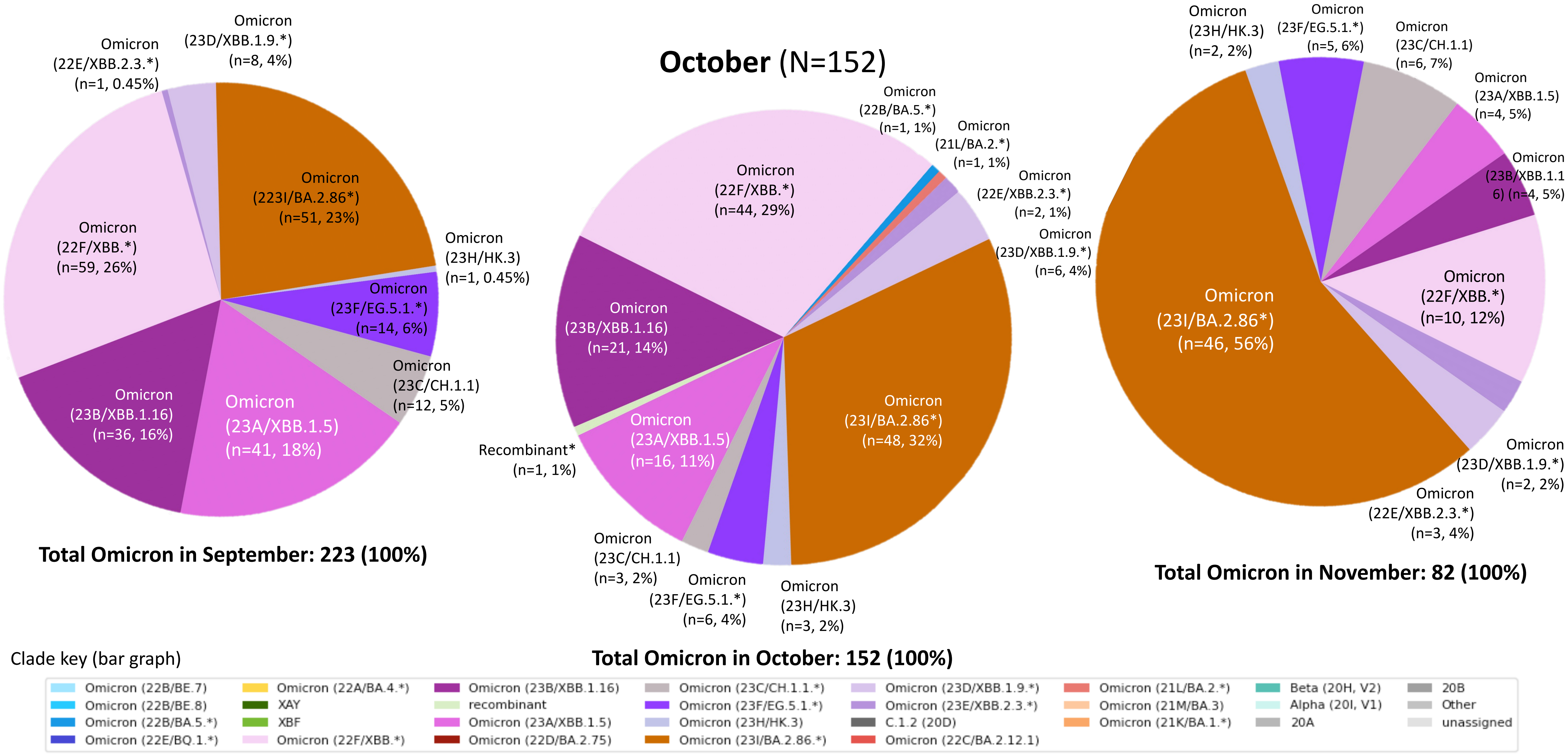
Detection Rates: Omicron and recombinants



*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 September – November 2023



September (N=223)

October (N=152)

November (N=82)

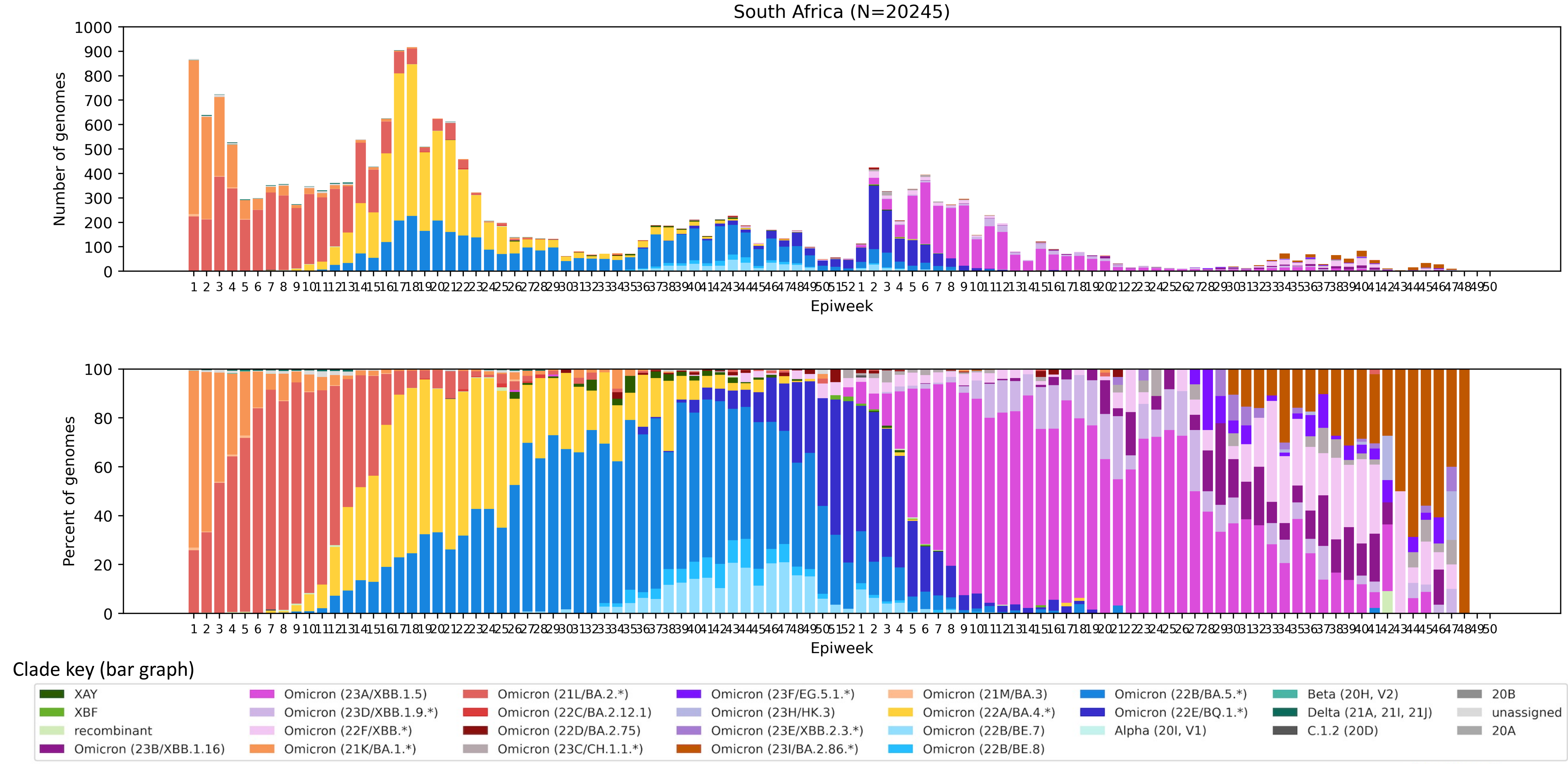
Total Omicron in September: 223 (100%)

Total Omicron in October: 152 (100%)

Total Omicron in November: 82 (100%)

* XCH.1: Recombinant lineage of GK.1.3 (XBB.1.5.*) and XBB.1.9 (or XBB.1.16)

South Africa, 2022-2023, n = 20 245*



*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.

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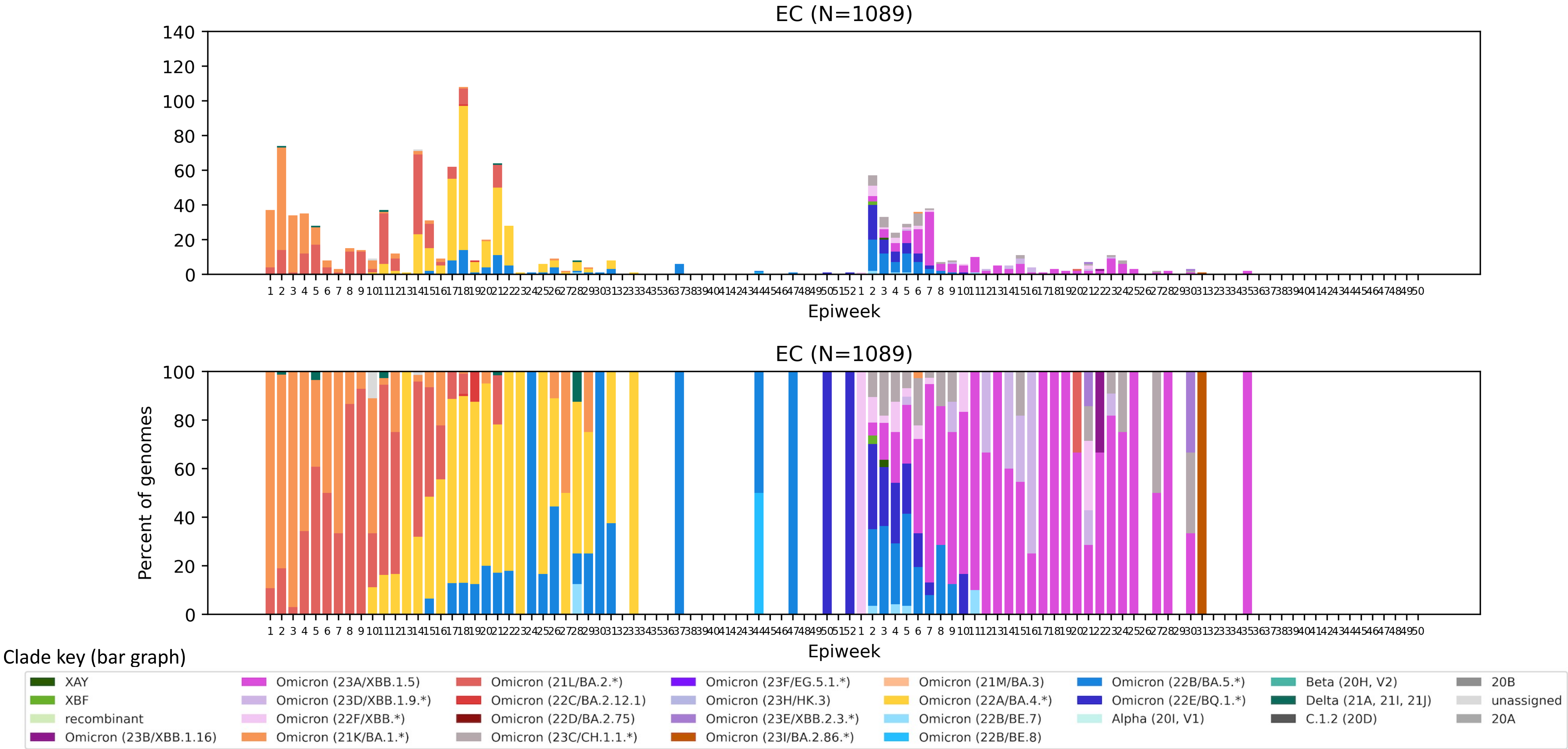
Eastern Cape Province, 2022-2023, n = 1089

Genomes added since last report: 0*



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

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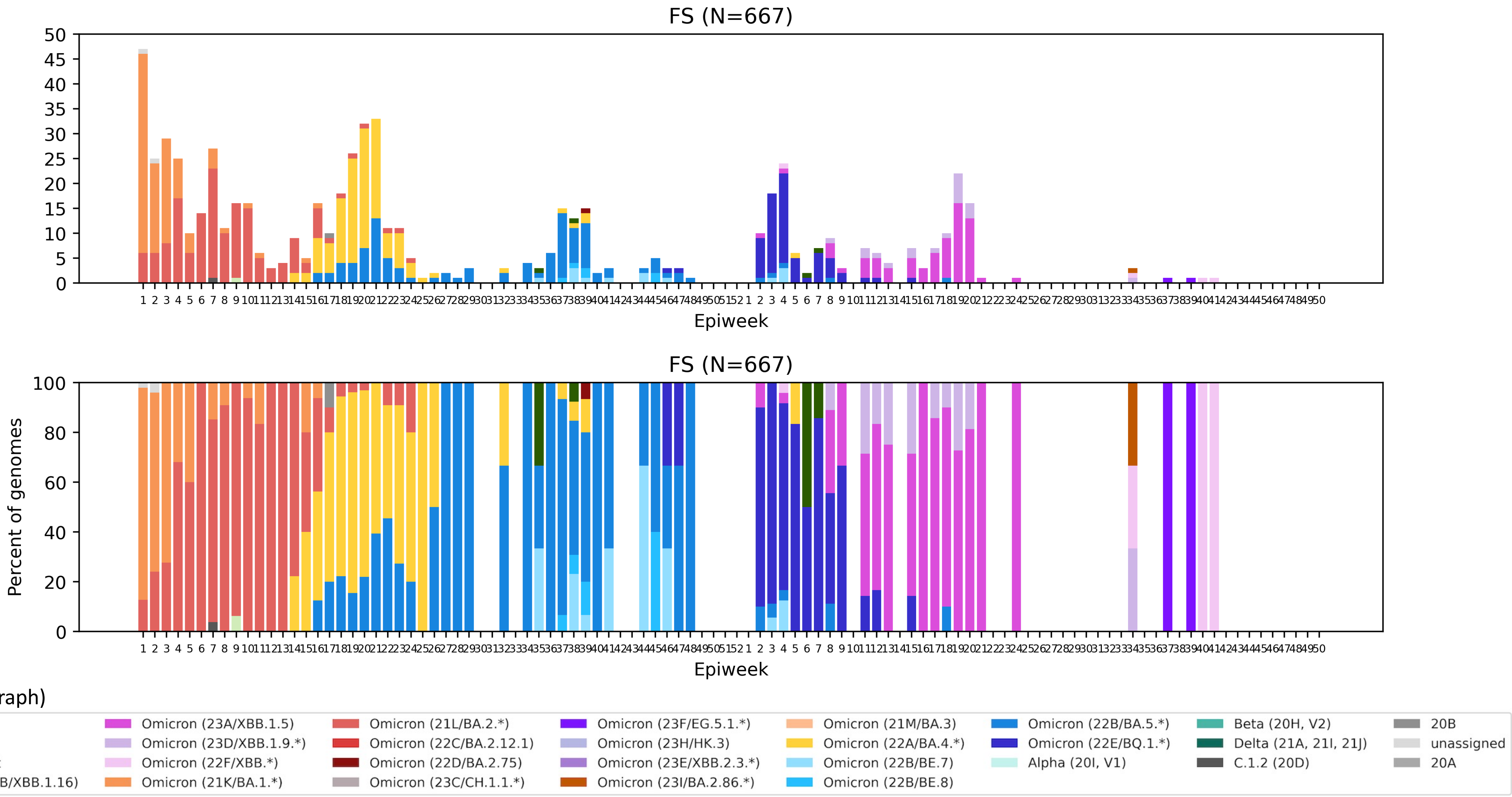
Free State Province, 2022-2023, n = 667

Genomes added since last report: 0*



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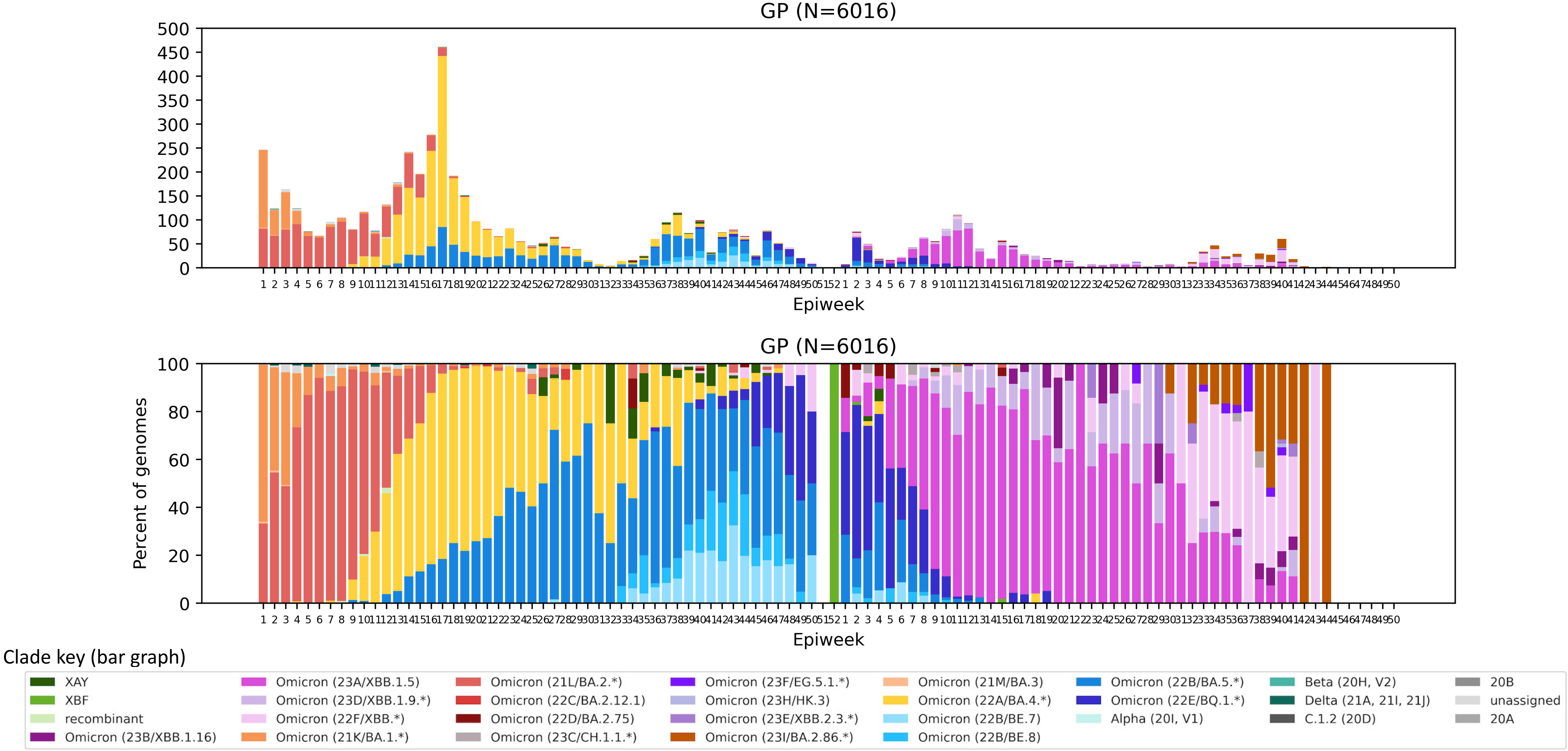
Gauteng Province, 2022-2023, n = 6016

Genomes added since last report: 32*



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

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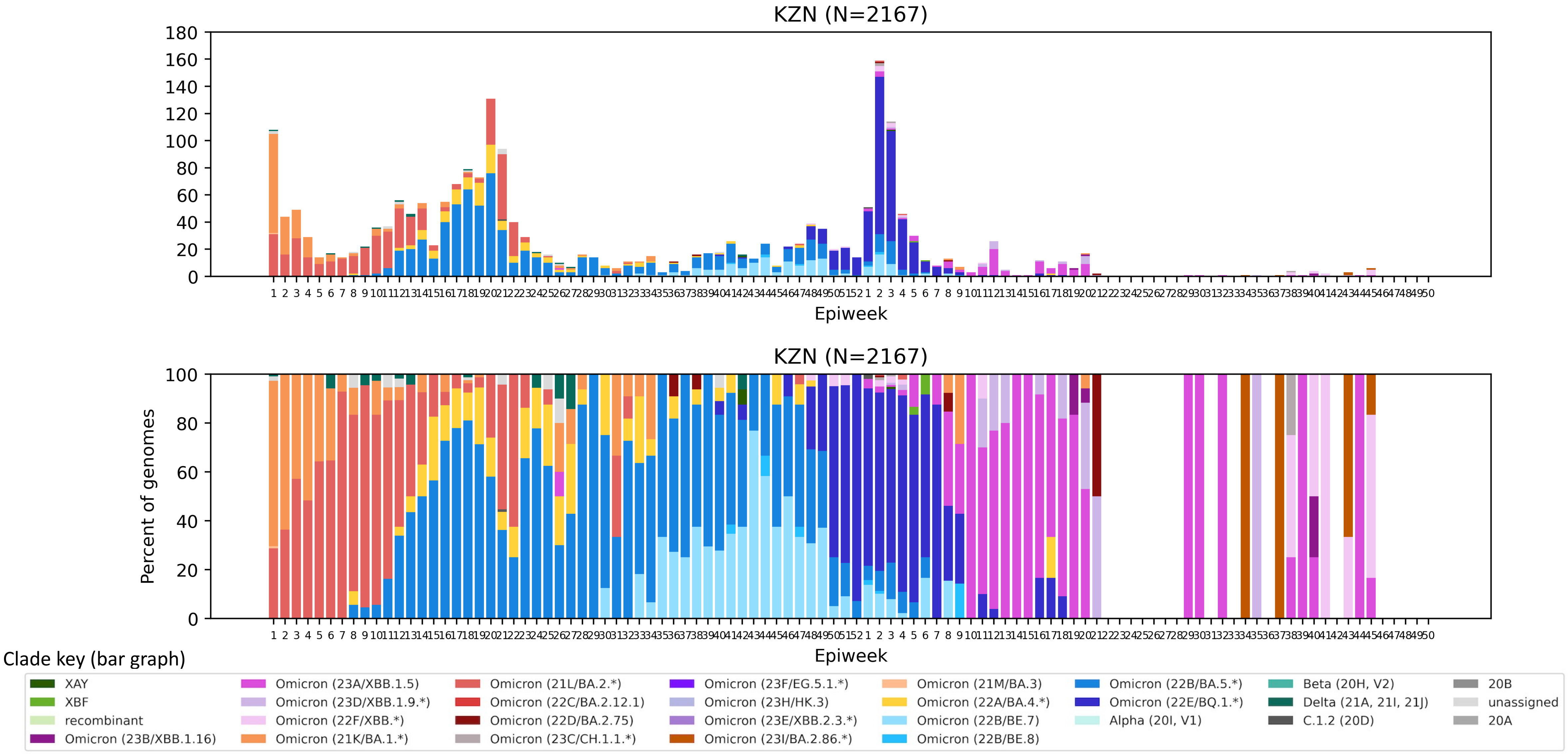
KwaZulu-Natal Province, 2022-2023, n = 2167

Genomes added since last report: 6*



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

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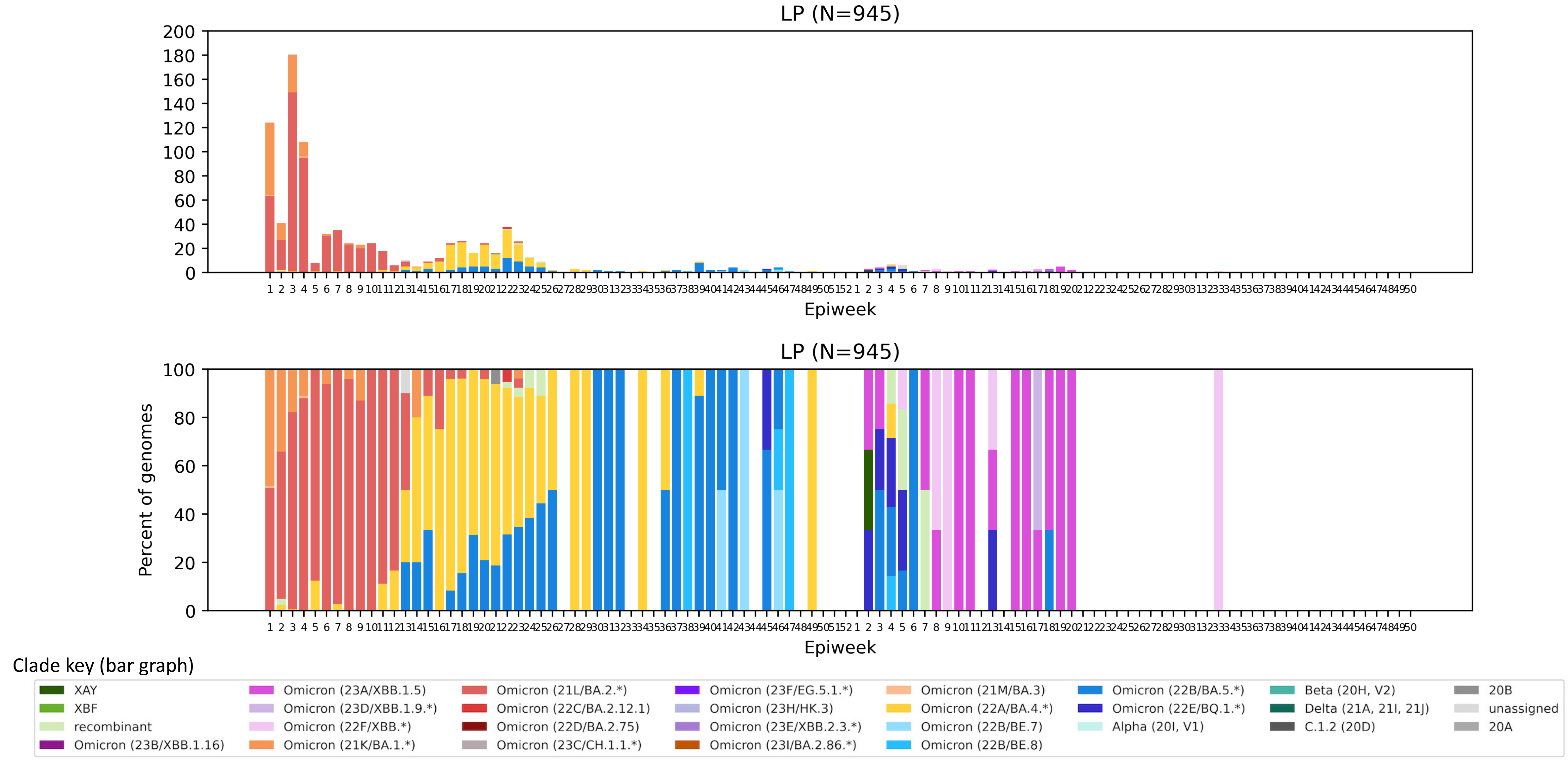
Limpopo Province, 2022-2023, n = 945

Genomes added since last report: 0*



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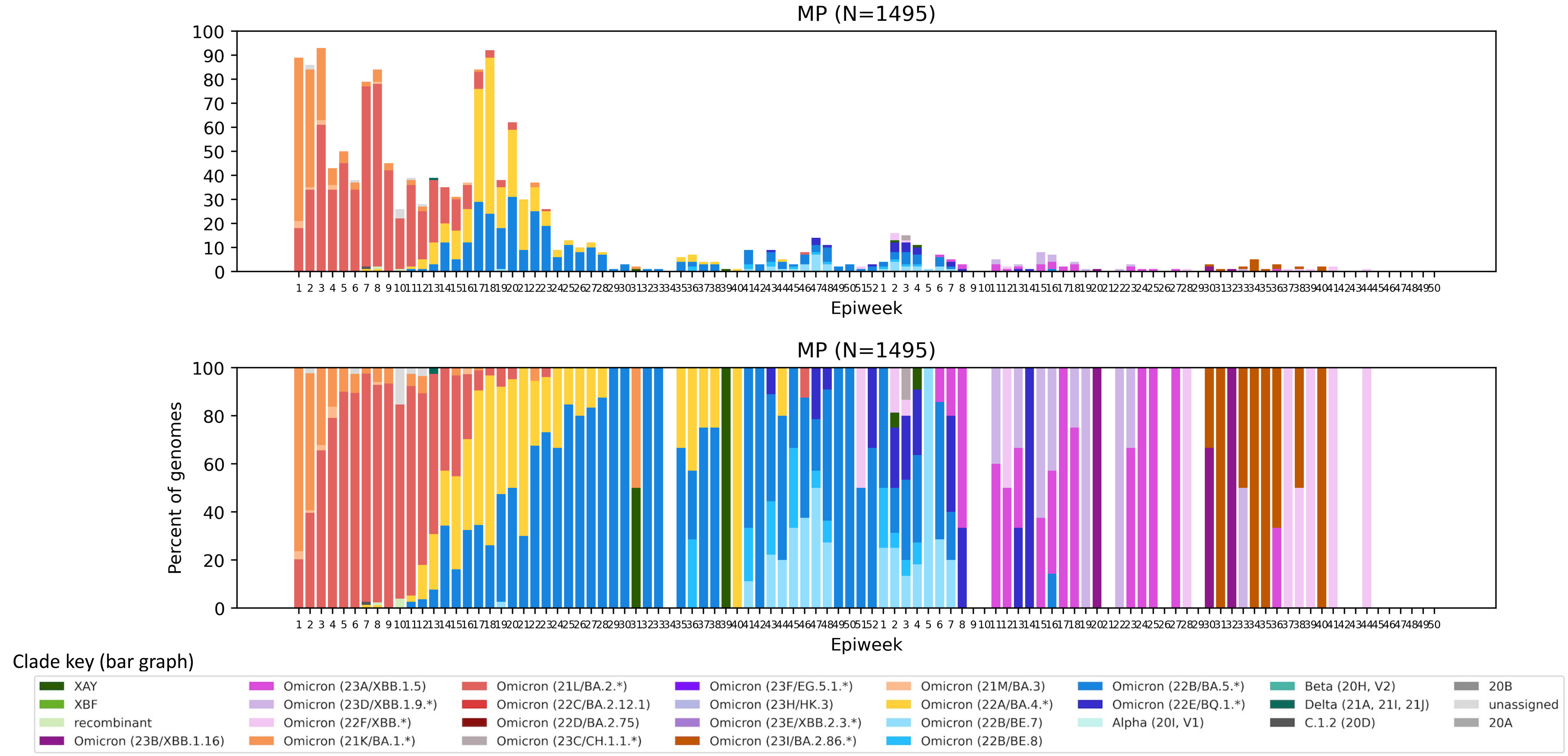
*May include genomes from 2020 and 2021 which are not pictured here and are not included in the slide total.

Mpumalanga Province, 2022-2023, n = 1495

Genomes added since last report: 0*



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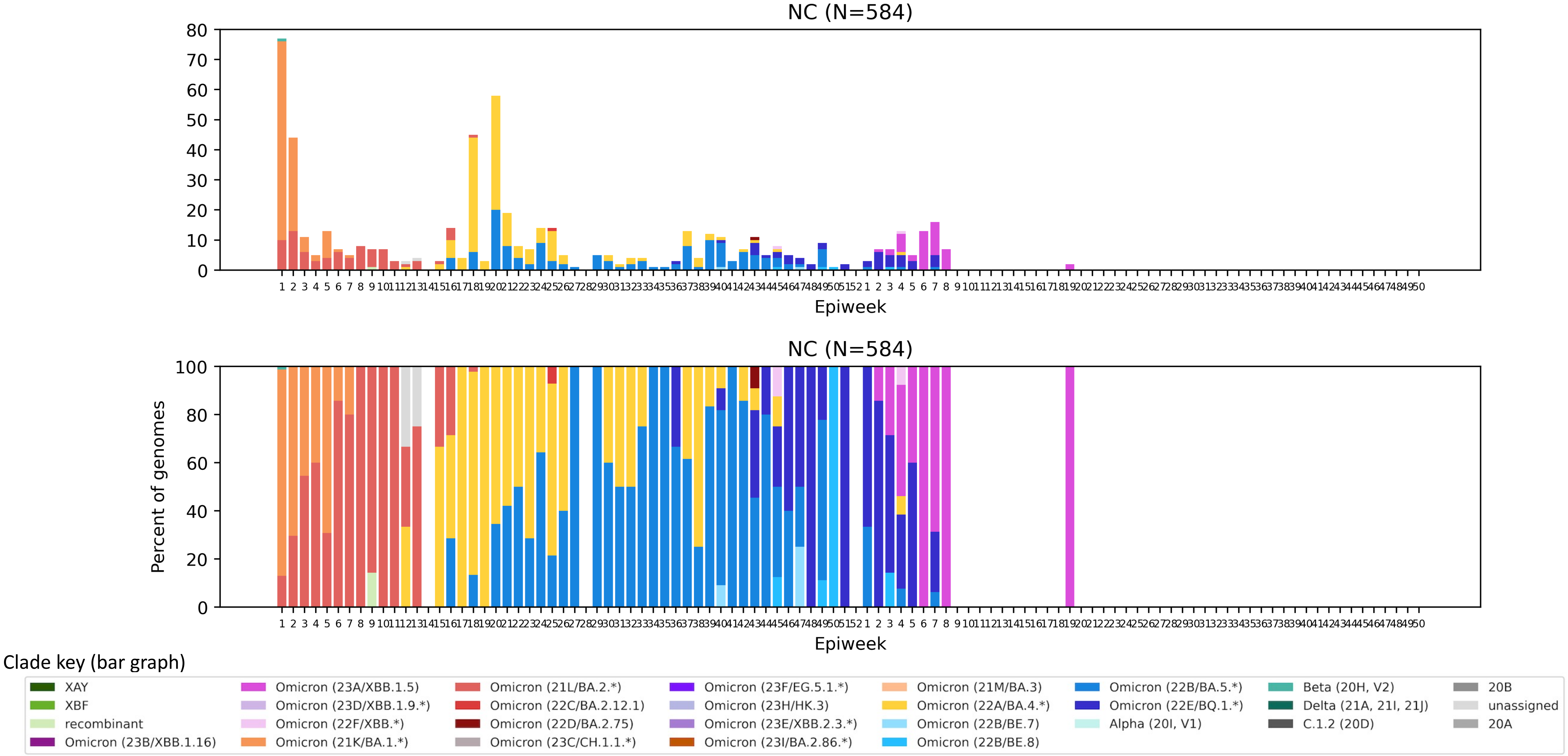
*May include genomes from 2020 and 2021 which are not pictured here and are not included in the slide total.

Northern Cape Province, 2022-2023, n = 584

Genomes added since last report: 0*



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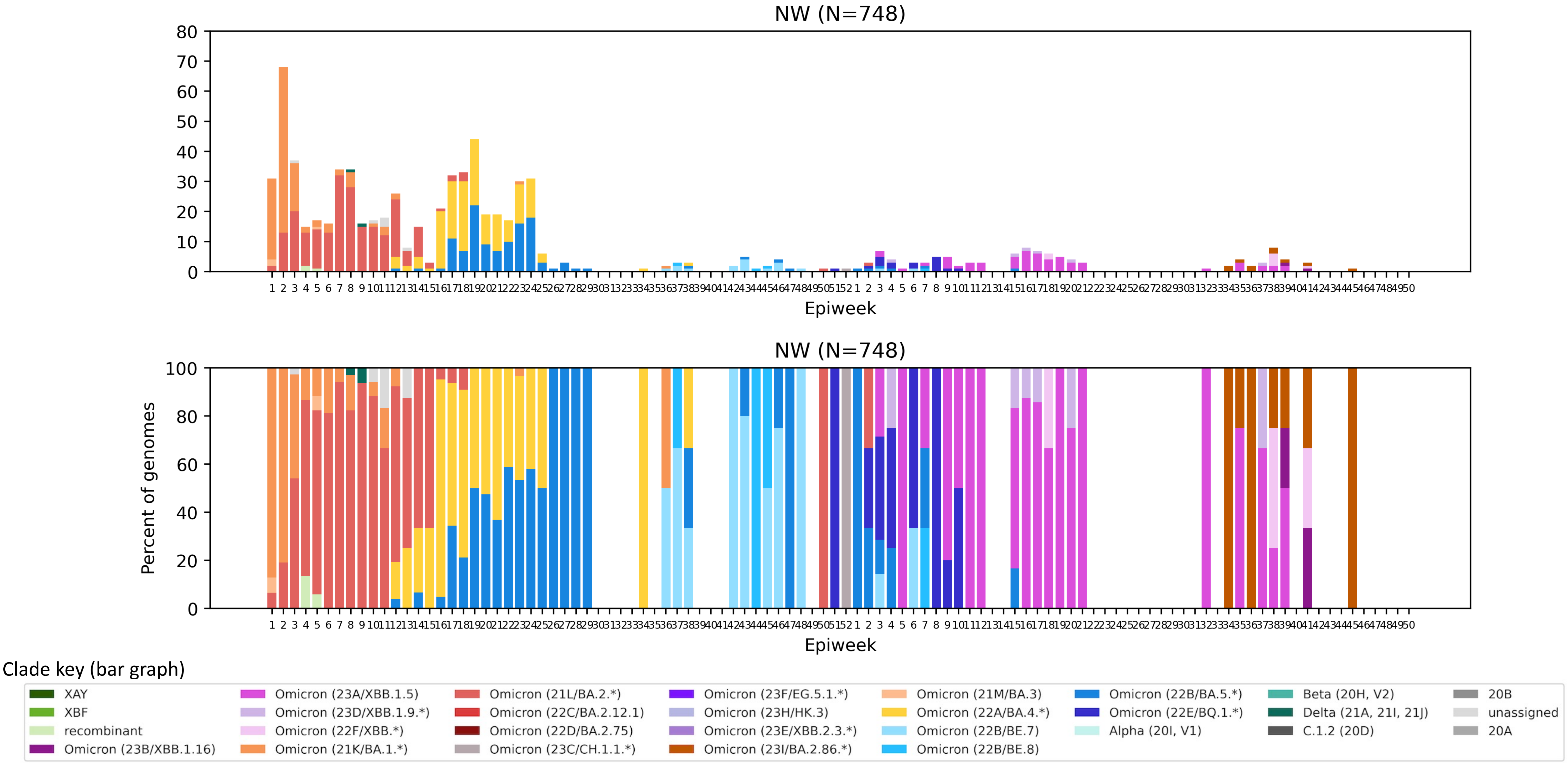
*May include genomes from 2020 and 2021 which are not pictured here and are not included in the slide total.

North West Province, 2022-2023, n = 748

Genomes added since last report: 0*



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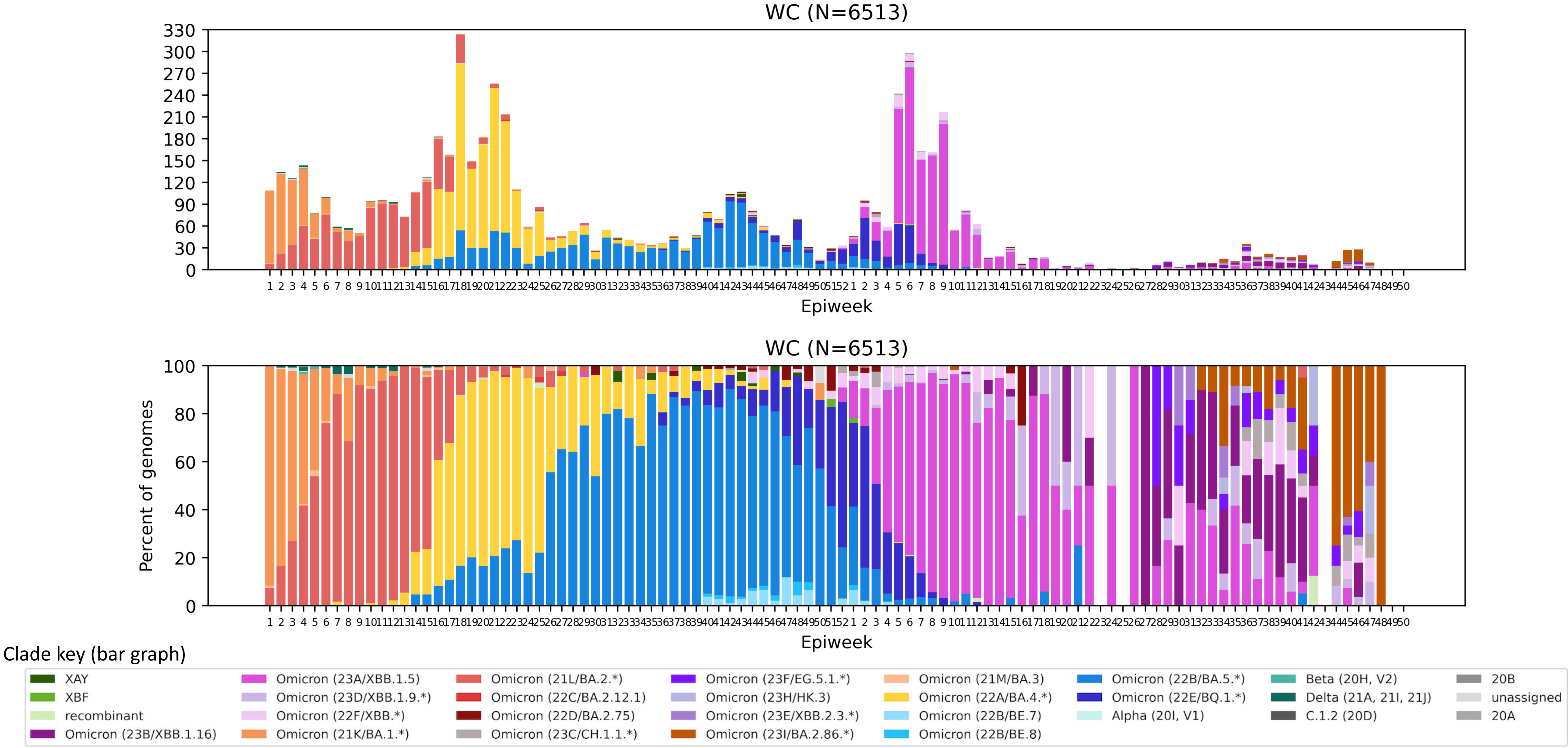
*May include genomes from 2020 and 2021 which are not pictured here and are not included in the slide total.

Western Cape Province, 2022-2023, n = 6513

Genomes added since last report: 78*



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

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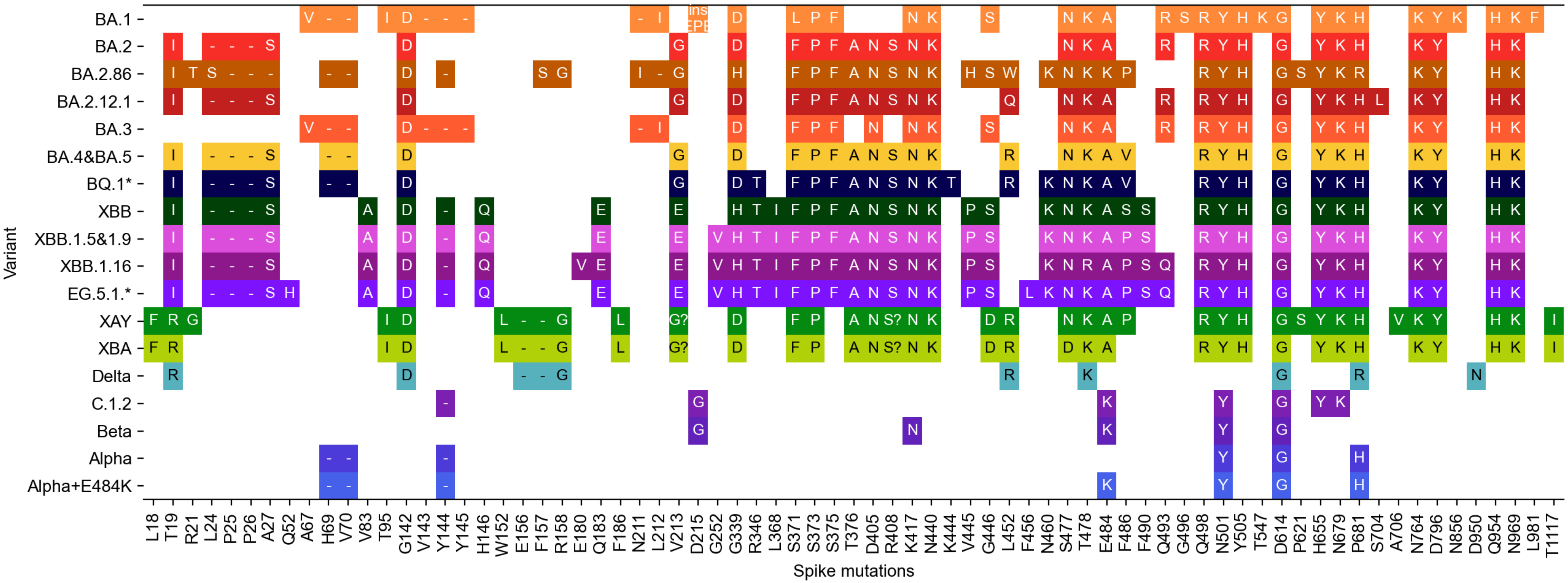
Summary

- **Sequencing update**
  - September sequences (n=223) are from all provinces except Northern Cape and Limpopo. October sequences (n=152) are from all provinces except Northern Cape, Eastern Cape and Limpopo. November sequences (n=82) are from the Western Cape, Gauteng, Mpumalanga, North West and KwaZulu-Natal.

- **Variant of Concern Omicron in South Africa**
  - Omicron dominated in September (100%), October (100%), and November (100%)
  - XBB.1.5 constituted 18% of September, 11% of October and 5% of November sequences
  - XBB.1.16 has been detected in September (16%), October (14%), and November (5%)
  - XBB.1.9.* (clade 23D) was detected in sequences from September(4%), October (4%) and November (2%)
  - 36 sequences of the EG.5.1.* lineage (clade 23F) have been detected in July (n=7), August (n=4), September (n=14), October (n=6) and November (n=5)
  - BA.2.86 has been detected at a prevalence of 23% in September, 32% in October and 56% in November.
  - 5 JN.1 sequences have been detected in the Western Cape in November

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

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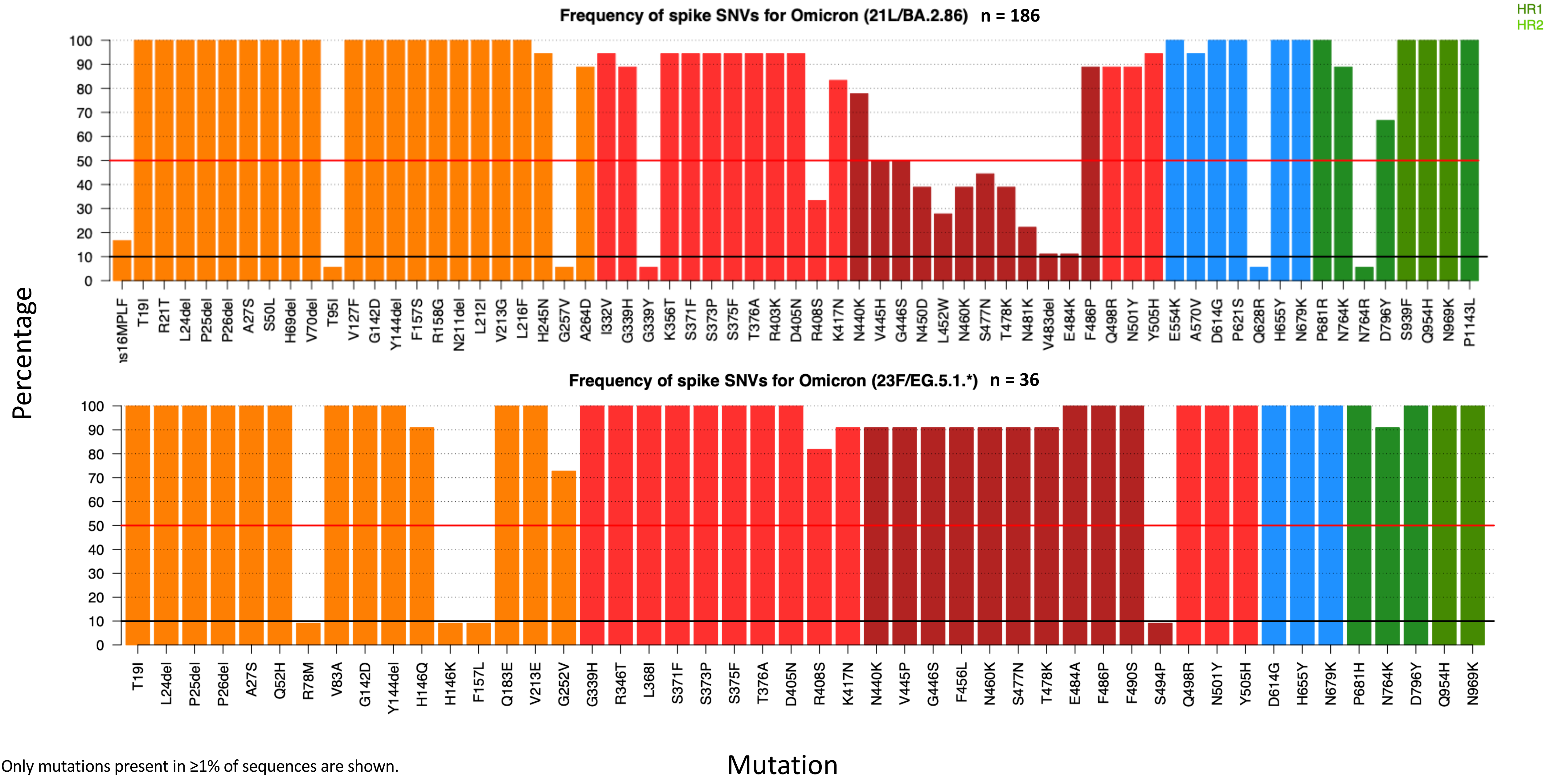
BA.2.86 and EG.5.1 spike mutations*



Frequency of spike SNVs for Omicron (21L/BA.2.86) n = 186

Frequency of spike SNVs for Omicron (23F/EG.5.1.*) n = 36

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

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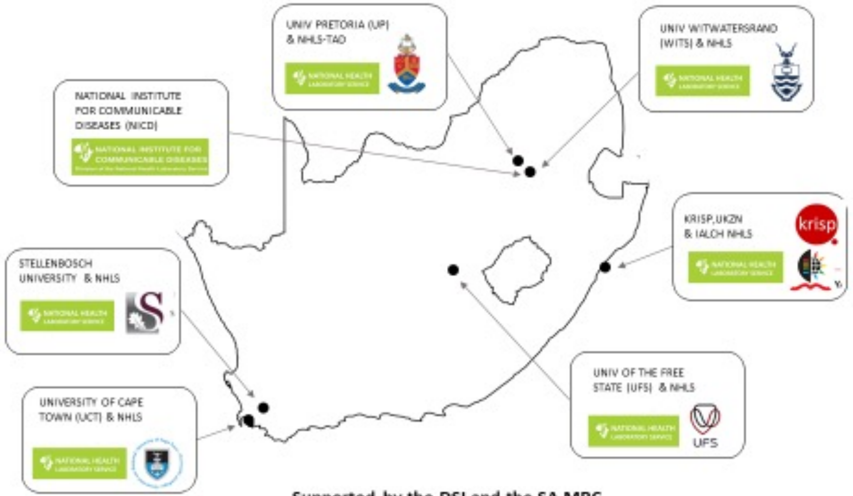

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Division of the National Health Laboratory Service

EDCTP

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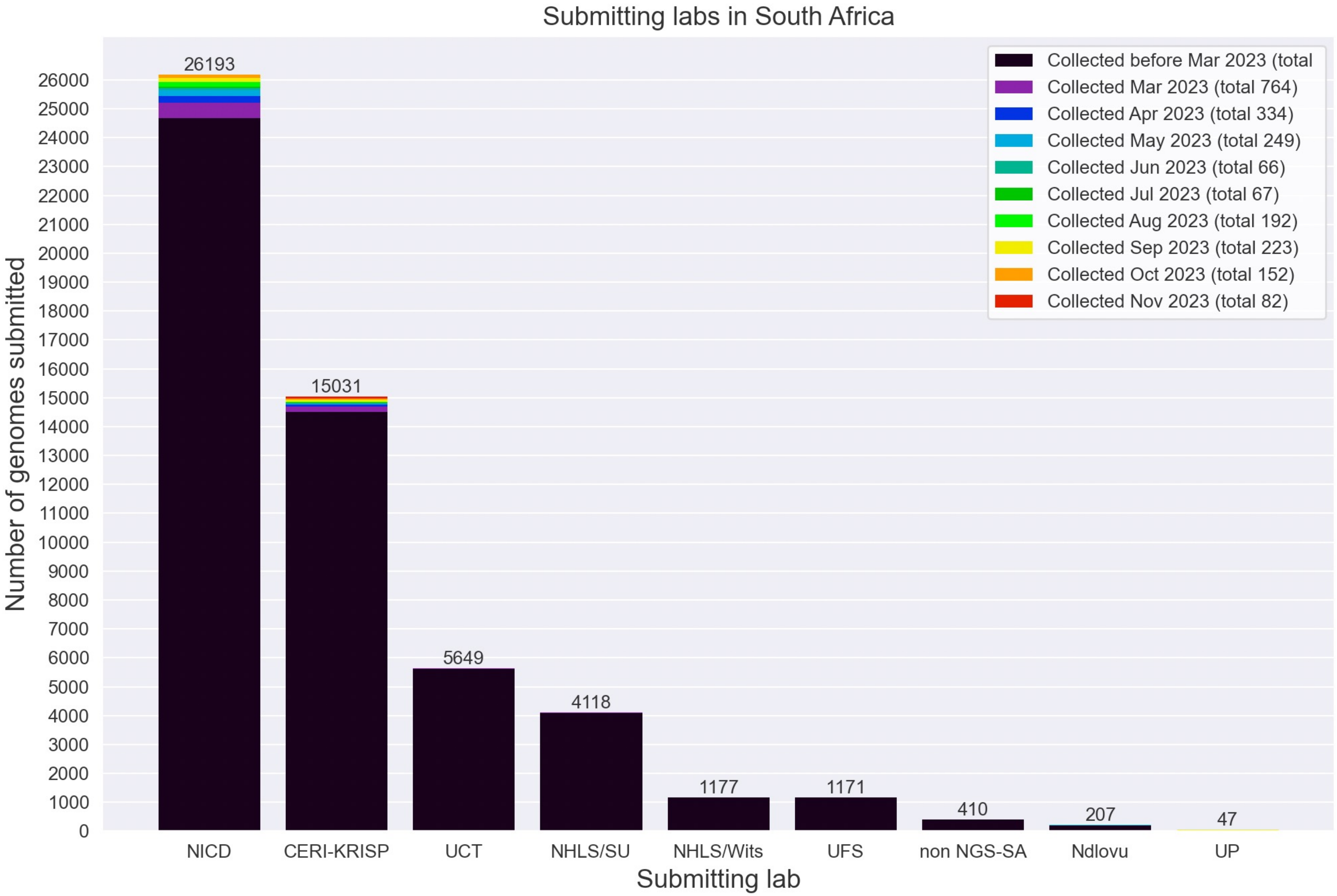
NATIONAL HEALTH LABORATORY SERVICE

South African genomes submitted per submitting lab, 2020 - 2023 (N= 54 003)



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.

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Currently circulating Variants of Interest (VOI) as of 09 Aug 2023

Pango lineage	Nextstrain clade	Genetic features	Earliest documented samples	Date of designation and risk assessments
XBB.1.5	23A	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. XBB.1 + S:F486P (similar Spike genetic profile as XBB.1.9.1)	21-10-2022	11-01-2023 XBB.1.5 Rapid Risk Assessment, 11 January 2023 XBB.1.5 Updated Rapid Risk Assessment, 25 January 2023 XBB.1.5 Updated Risk Assessment, 24 February 2023 XBB.1.5 Updated Risk Assessment, 20 June 2023
XBB.1.16	23B	Recombinant of BA.2.10.1 and BA.2.75 sublineages, i.e. BJ.1 and BM.1.1.1 XBB.1 + S:E180V, S:K478R and S:F486P	09-01-2023	17-04-2023 XBB.1.16 Initial Risk Assessment, 17 April 2023 XBB.1.16 Updated Risk Assessment, 05 June 2023
EG.5	Not assigned	XBB.1.9.2 + S:F456L Includes EG.5.1: EG.5 + S:Q52H	17-02-2023	09-08-2023 EG.5 Initial Risk Evaluation, 09 August 2023

https://www.who.int/en/activities/tracking-SARS-CoV-2-variants/ accessed 11 Aug 2023

Currently circulating variants under monitoring (VUMs)

Pango lineage[#] (+ 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	06-07-2022
CH.1.1	22D	BA.2.75 + S:L452R, S:F486S	27-07-2022	08-02-2023
BQ.1	22E	BA.5 + S:R346T, S:K444T, S:N460K	07-02-2022	21-09-2022
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	12-10-2022
XBB.1.9.1	23D	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
XBB.1.9.2	23D	Recombinant of BA.2.10.1 and BA.2.75 sublineages, i.e. BJ1 and BM.1.1.1 XBB.1 + S:F486P, S:Q613H	05-12-2022	26-04-2023
XBB.2.3	22E	Recombinant of BA.2.10.1 and BA.2.75 sublineages, i.e. BJ1 and BM.1.1.1 XBB + S:D253G, S:F486P, S:P521S	09-12-2022	17-05-2023
BA.2.86	Not assigned	Mutations relative to putative ancestor BA.2	24-07-2023	17-08-2023

[*] Excludes XBB sublineages listed here as VOIs and VUMs

https://www.who.int/en/activities/tracking-SARS-CoV-2-variants/ accessed 24 Aug 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 (≥14 days after vaccine), especially if hospitalised and clinically severe
- Suspected re-infection (≥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.)