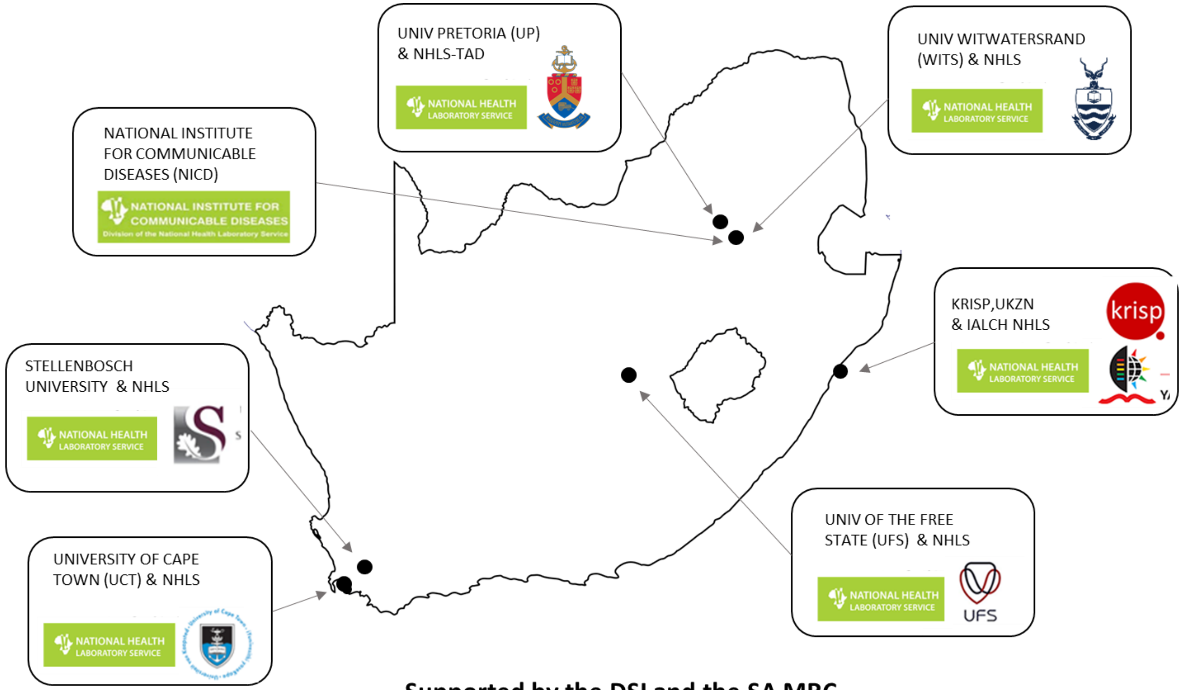
NGS-SA
Network for Genomic
Surveillance in South Africa

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

SARS-CoV-2 Sequencing Update
02 February 2024



Supported by the DSI and the SA MRC

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

science & innovation
Department:
Science and Innovation
REPUBLIC OF SOUTH AFRICA

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)

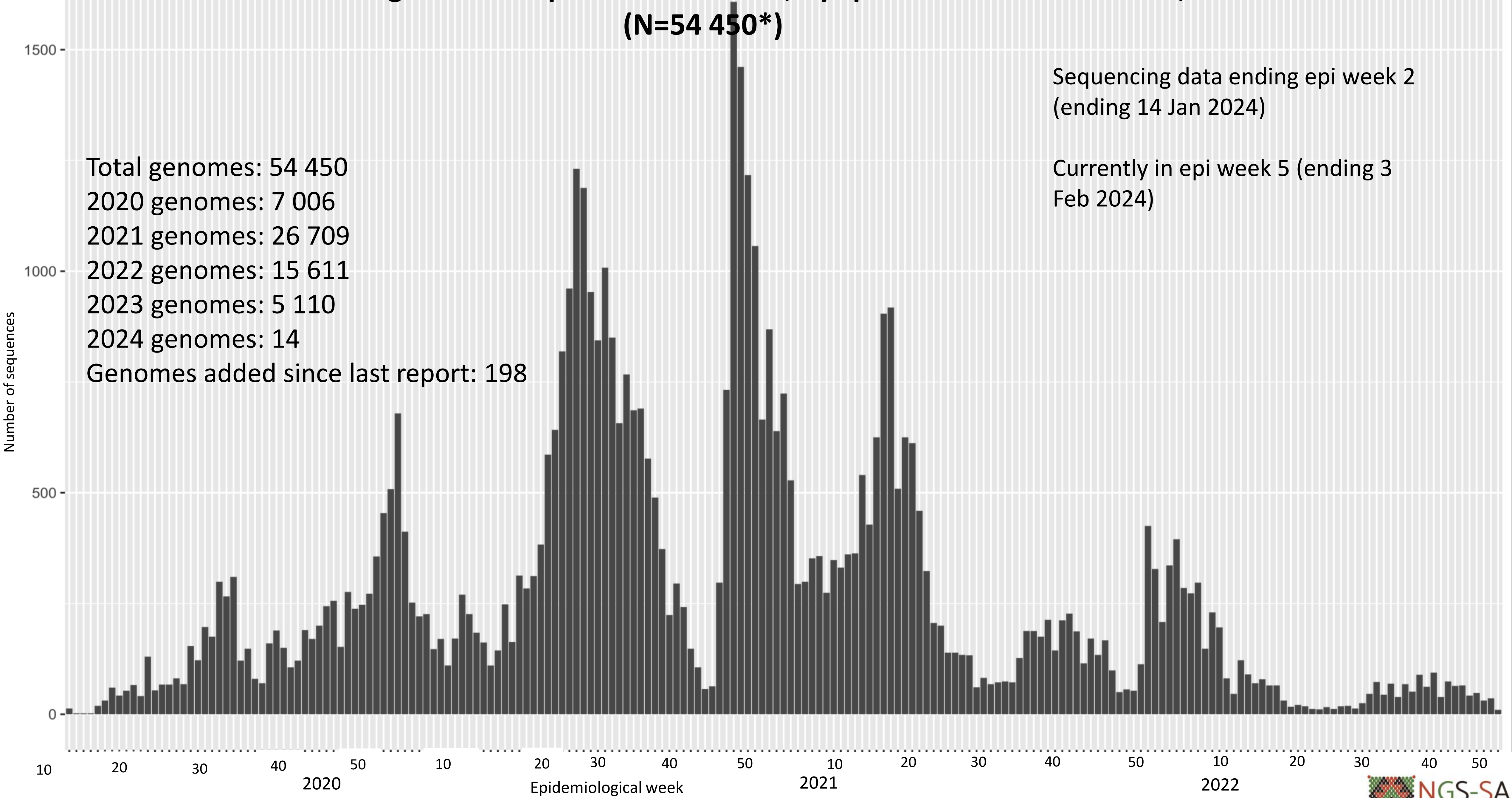
The genomic data presented here are based on South African SARS-CoV-2 sequence data downloaded from GISAID (www.gisaid.org) on 02 February 2024 at 09h30

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=54 450*)



Total genomes: 54 450
2020 genomes: 7 006
2021 genomes: 26 709
2022 genomes: 15 611
2023 genomes: 5 110
2024 genomes: 14
Genomes added since last report: 198

Sequencing data ending epi week 2 (ending 14 Jan 2024)

Currently in epi week 5 (ending 3 Feb 2024)

*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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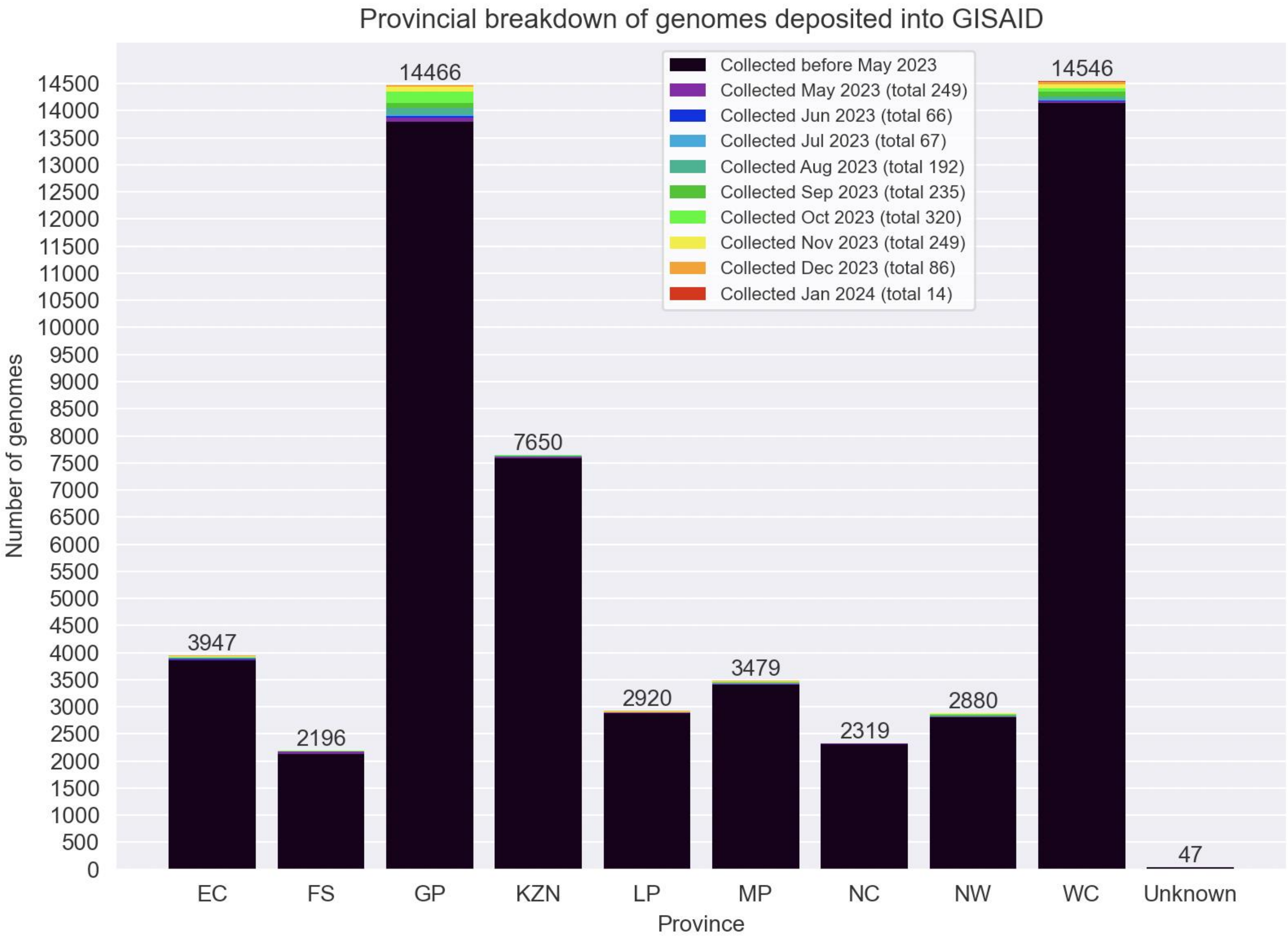
GISAID genomes vs total cases, 2020 – 2024 (N= 54 450)



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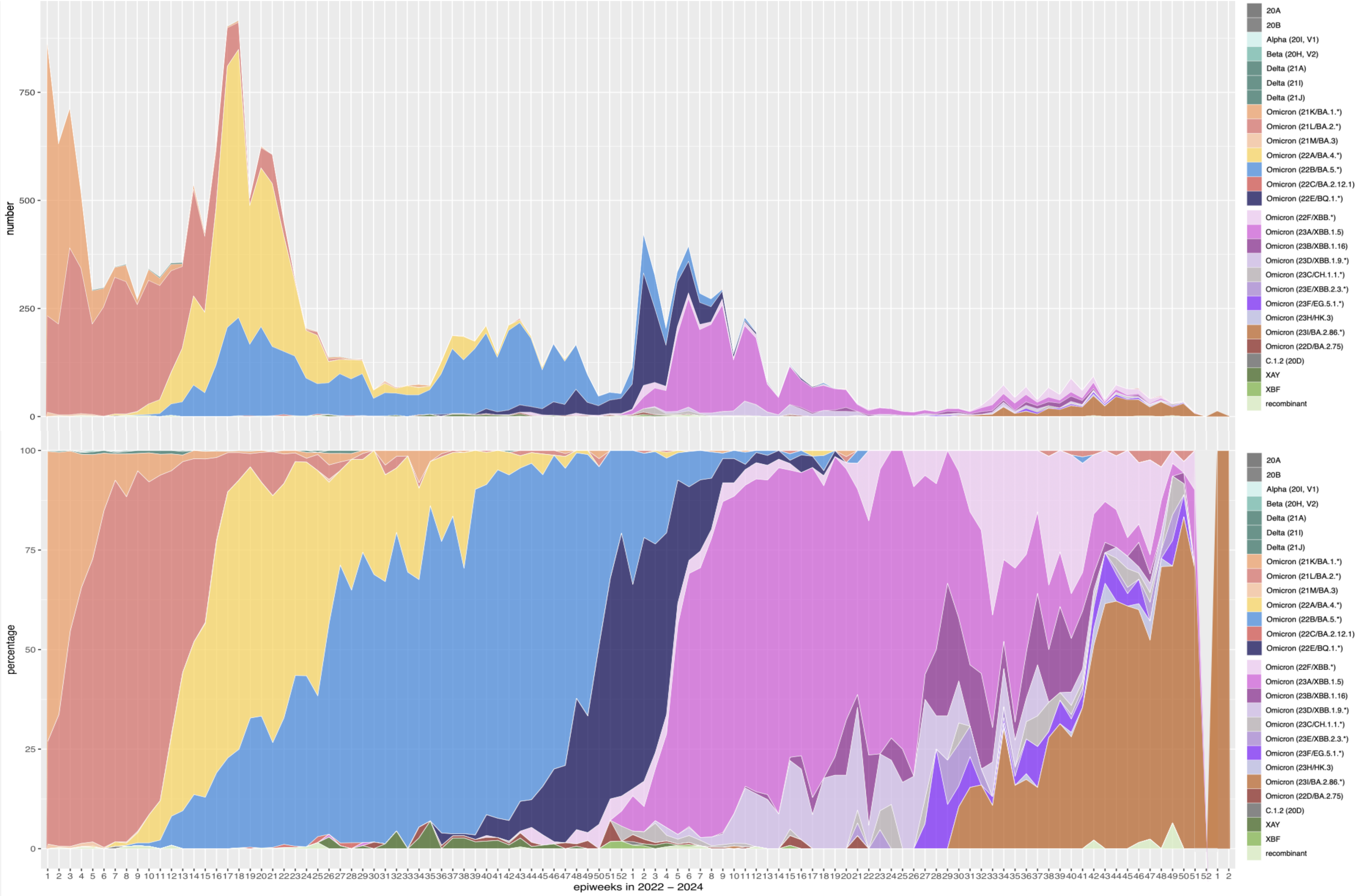
Number and percentage of clades by epiweek in South Africa, 2022-2024 (20 692*)



Sequencing data ending epi week 2 (ending 14 Jan 2024)

Currently in epi week 5 (ending 3 Feb 2024)

*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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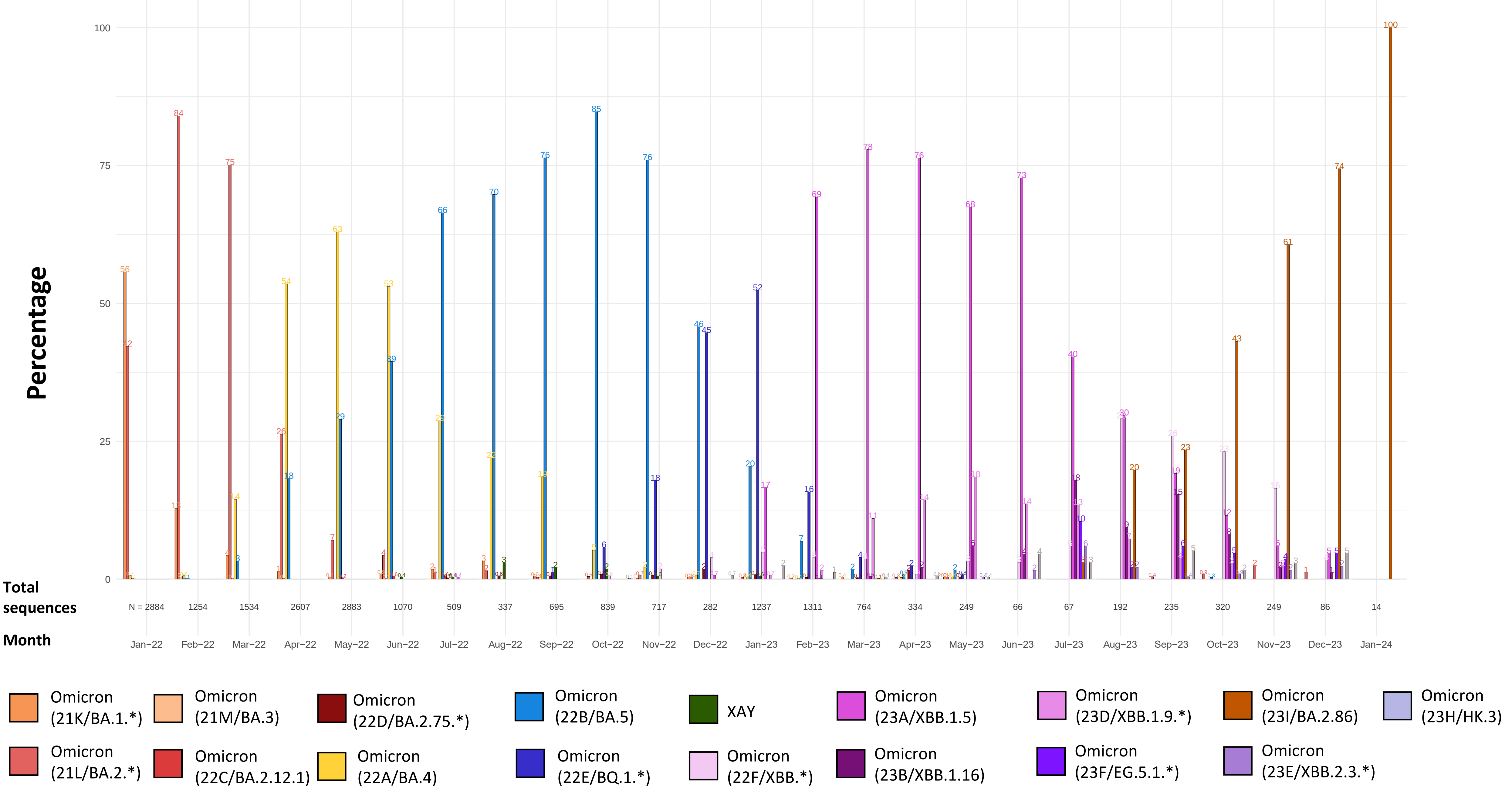
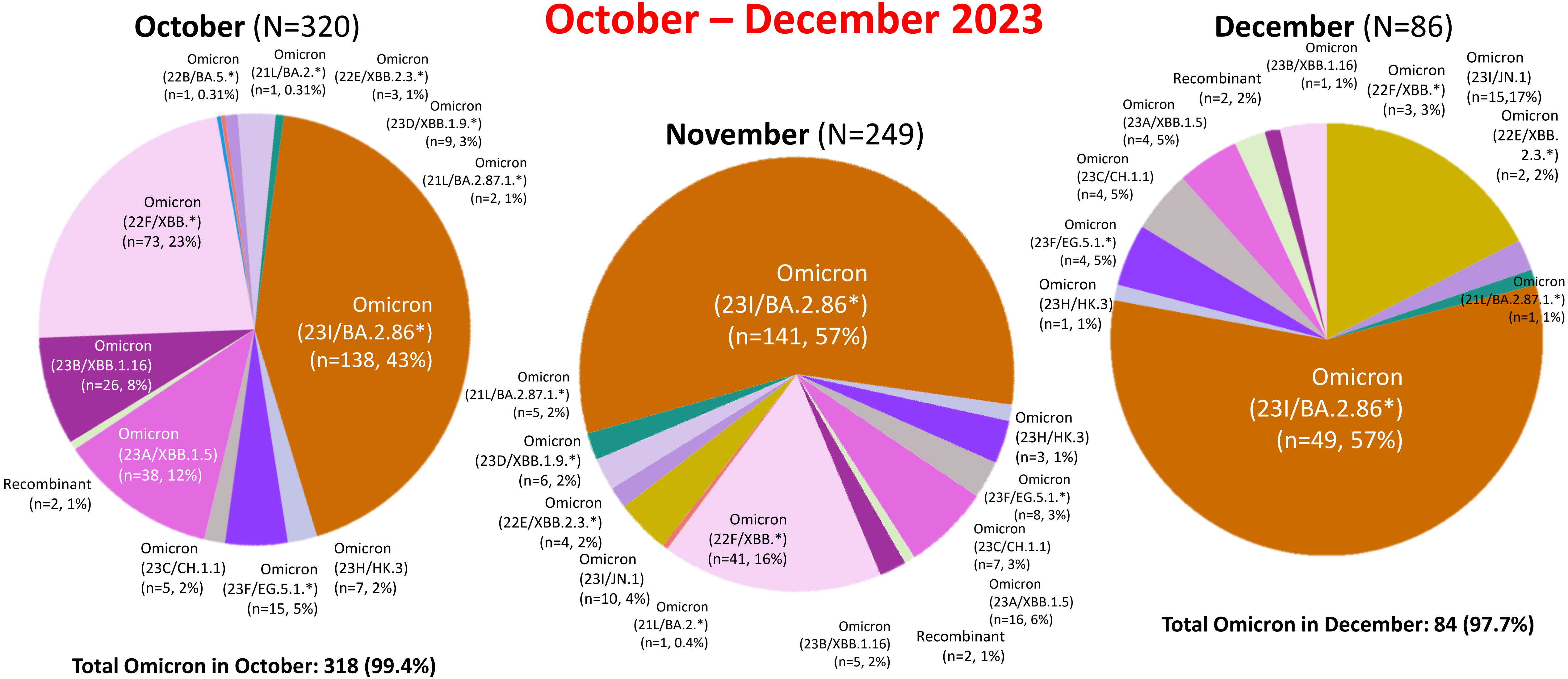
Detection Rates: Omicron and recombinants



*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 **October – December 2023**



October (N=320)

Total Omicron in October: 318 (99.4%)

November (N=249)

Total Omicron in November: 247 (99.2%)

December (N=86)

Total Omicron in December: 84 (97.7%)

Clade key (bar graph)

- ■ XAY
- ■ XBF
- ■ recombinant
- ■ Omicron (23B/XBB.1.16)
- ■ Omicron (23A/XBB.1.5)
- ■ Omicron (23D/XBB.1.9.*)
- ■ Omicron (22F/XBB.*)
- ■ Omicron (21K/BA.1.*)
- ■ Omicron (21L/BA.2.*)
- ■ Omicron (22C/BA.2.12.1)
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- ■ Omicron (23E/XBB.2.3.*)
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- ■ Alpha (20I, V1)
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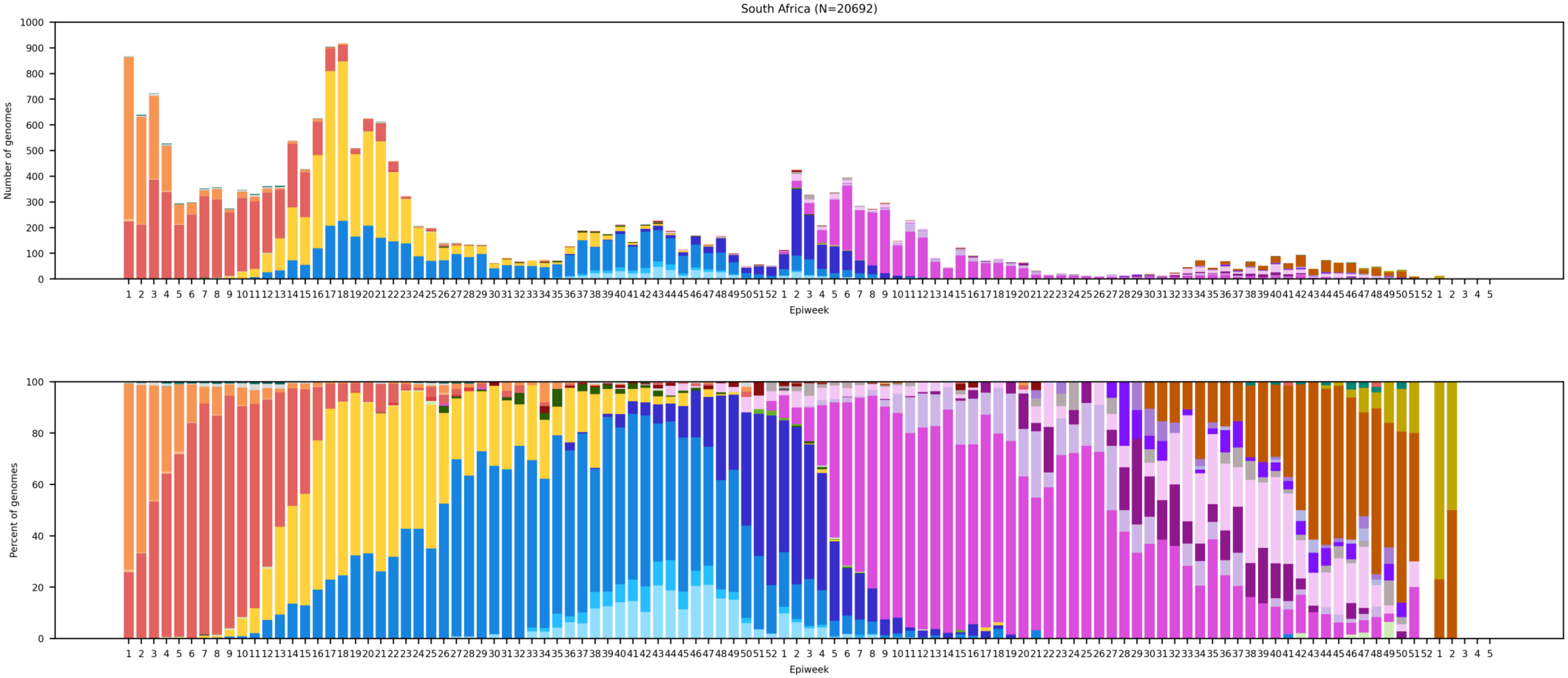
- ■ Delta (21A, 21I, 21J)
- ■ C.1.2 (20D)
- ■ 20B
- ■ unassigned
- ■ 20A

South Africa, 2022-2024, n = 20 692*



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*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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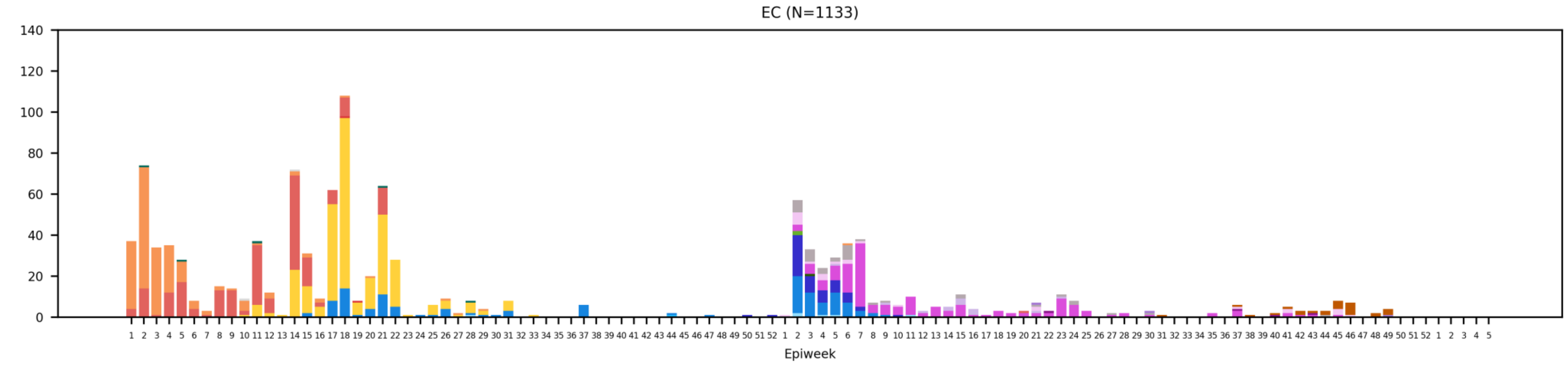
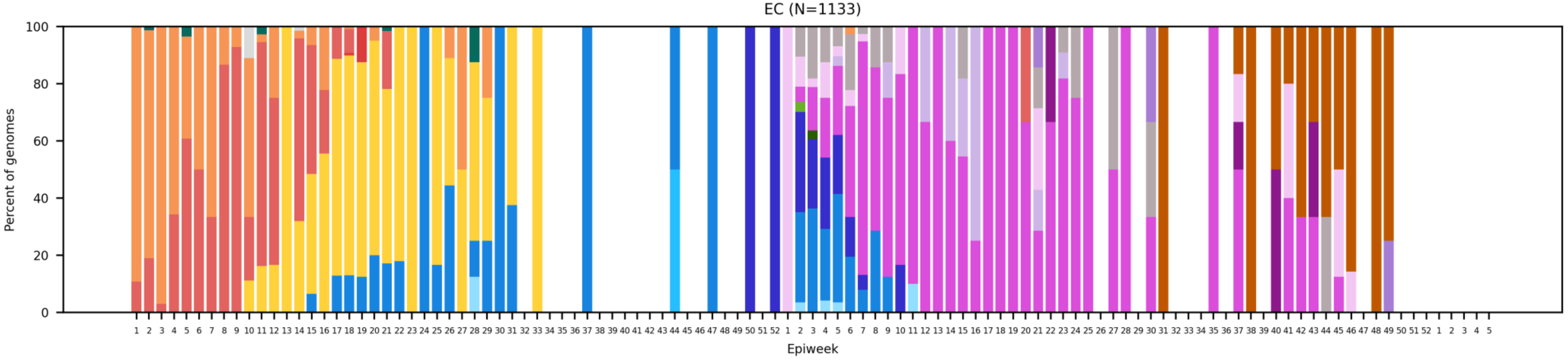
Eastern Cape Province, 2022-2024, n = 1133

Genomes added since last report: 7*





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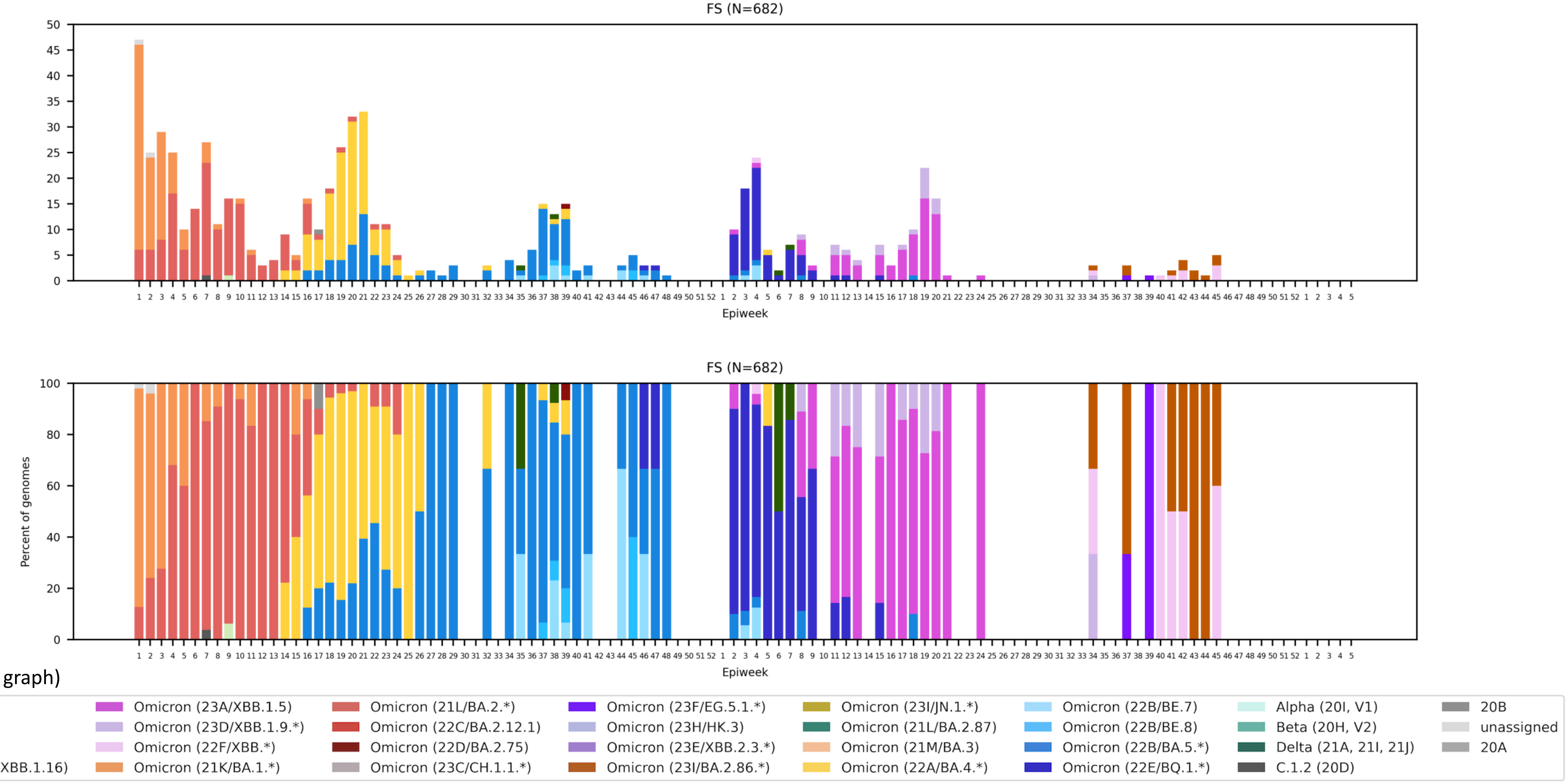
*May include genomes from 2020 and 2021 which are not pictured here and are not included in the slide total.

Free State Province, 2022-2024, n = 682

Genomes added since last report: 7*



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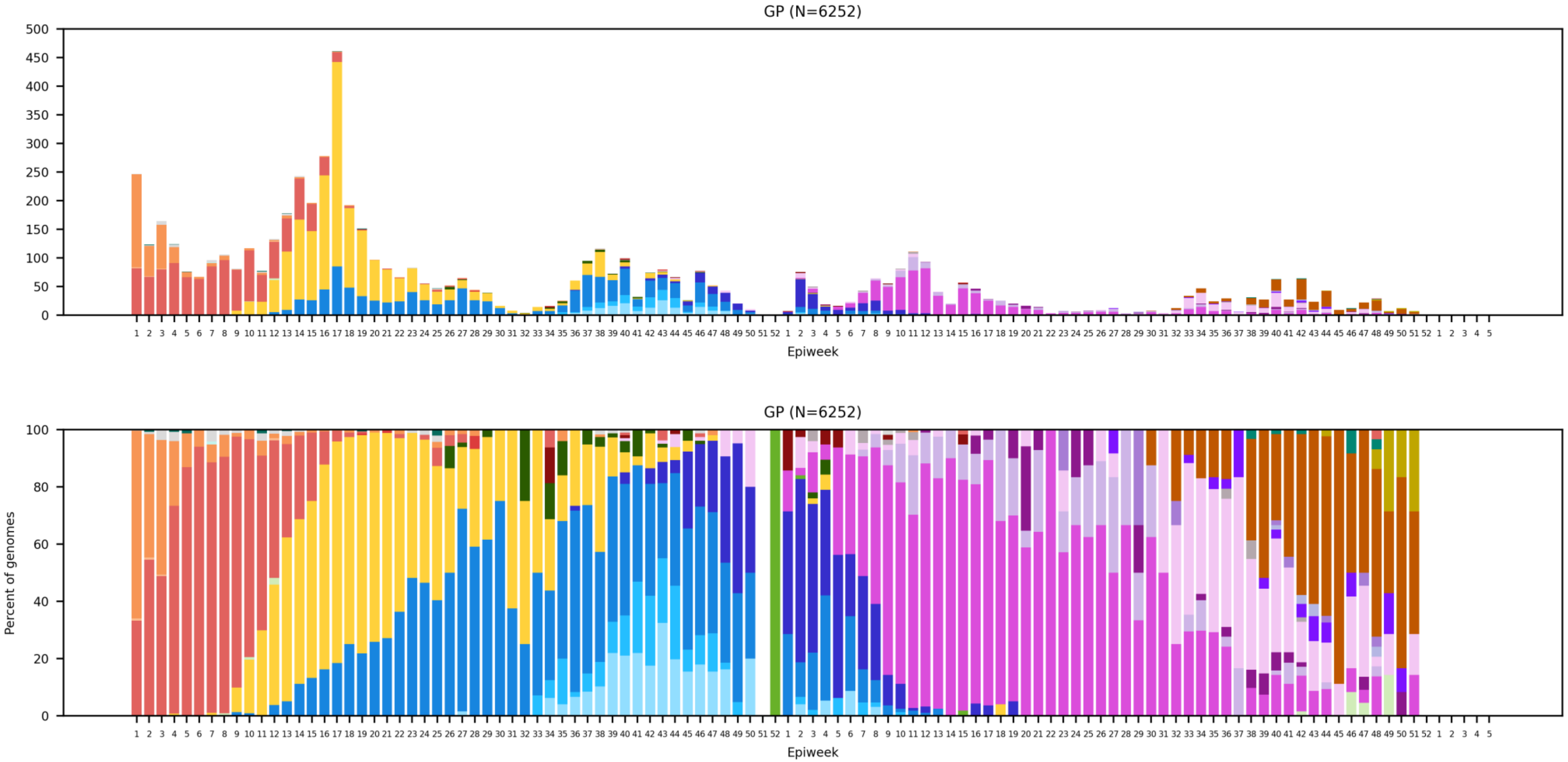
Gauteng Province, 2022-2024, n = 6252

Genomes added since last report: 127*



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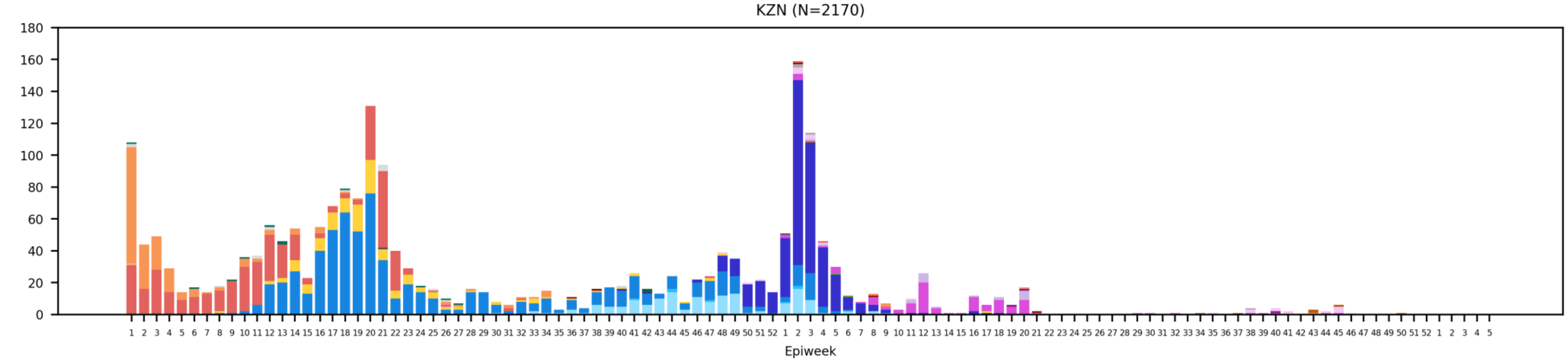
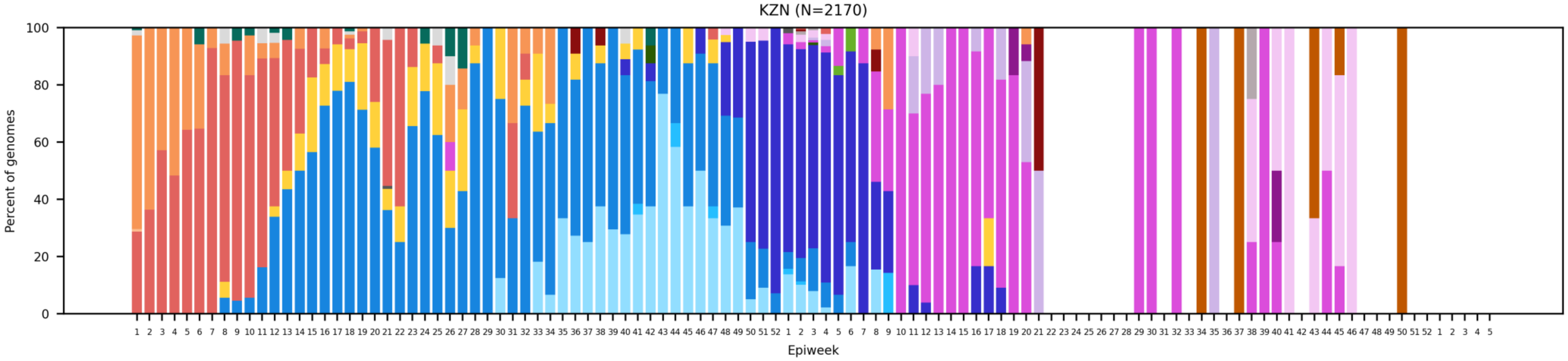
KwaZulu-Natal Province, 2022-2024, n = 2170

Genomes added since last report: 2*





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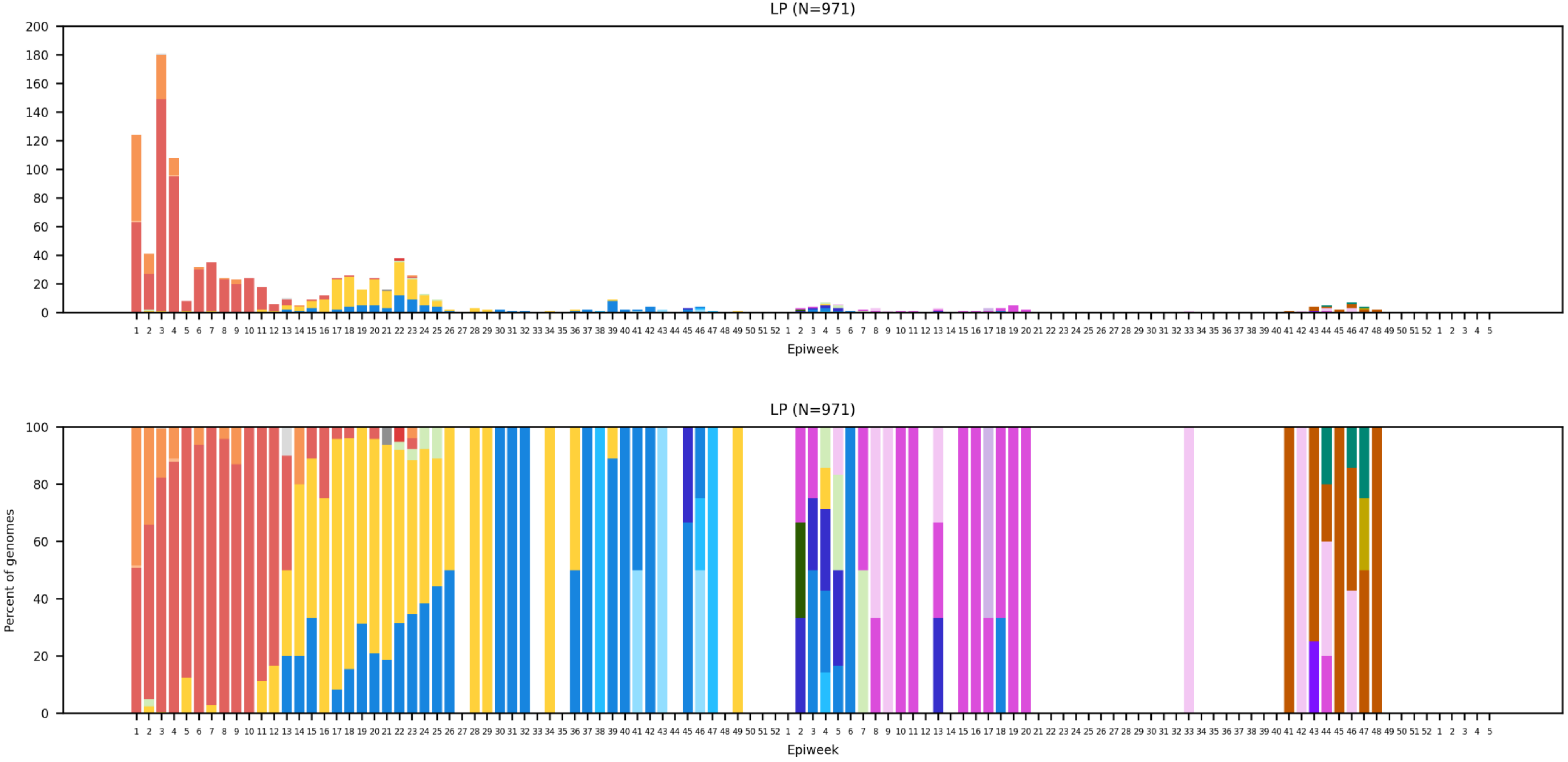
Limpopo Province, 2022-2024, n = 971

Genomes added since last report: 8*



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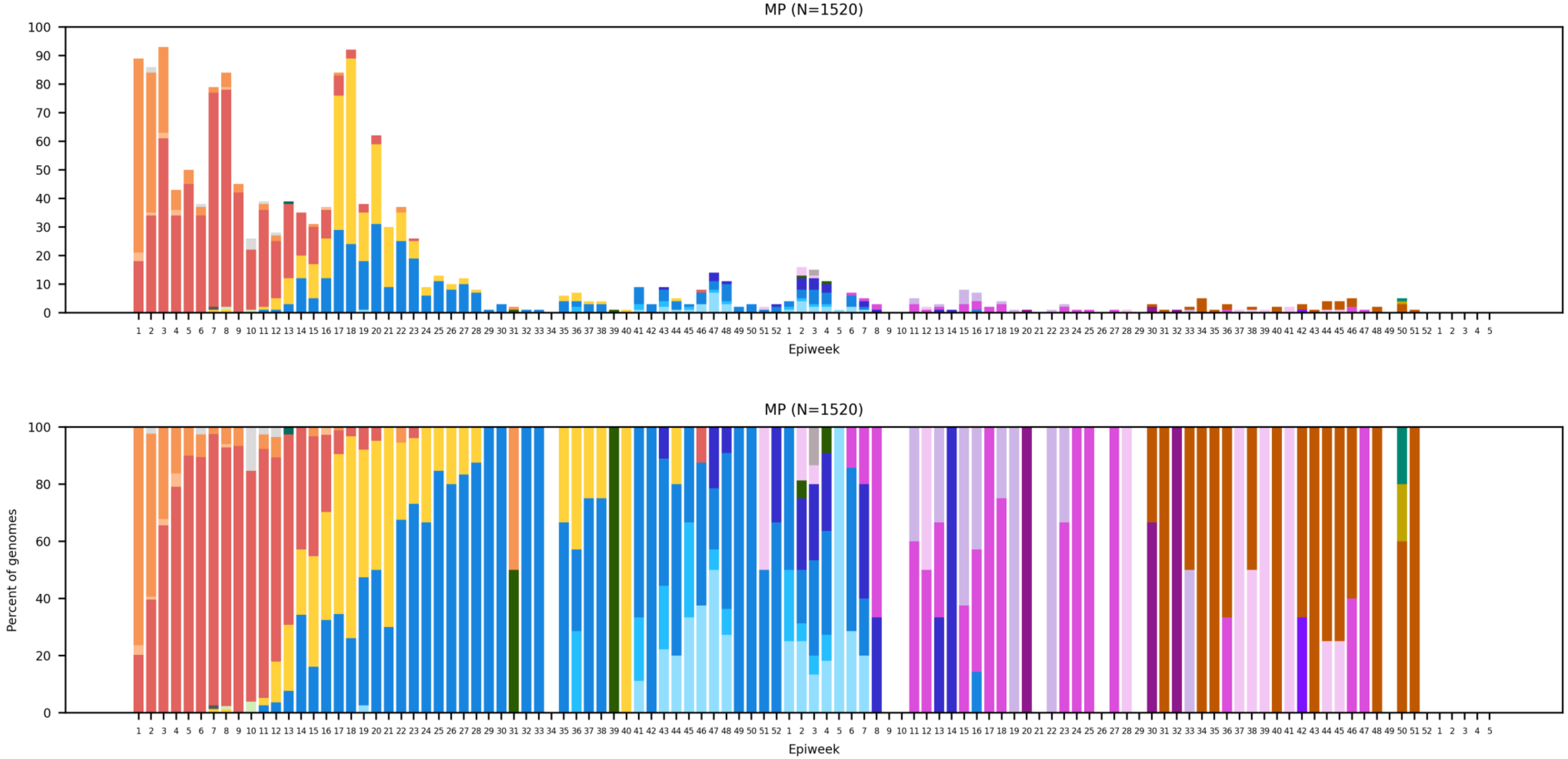
Mpumalanga Province, 2022-2024, n = 1520

Genomes added since last report: 13*



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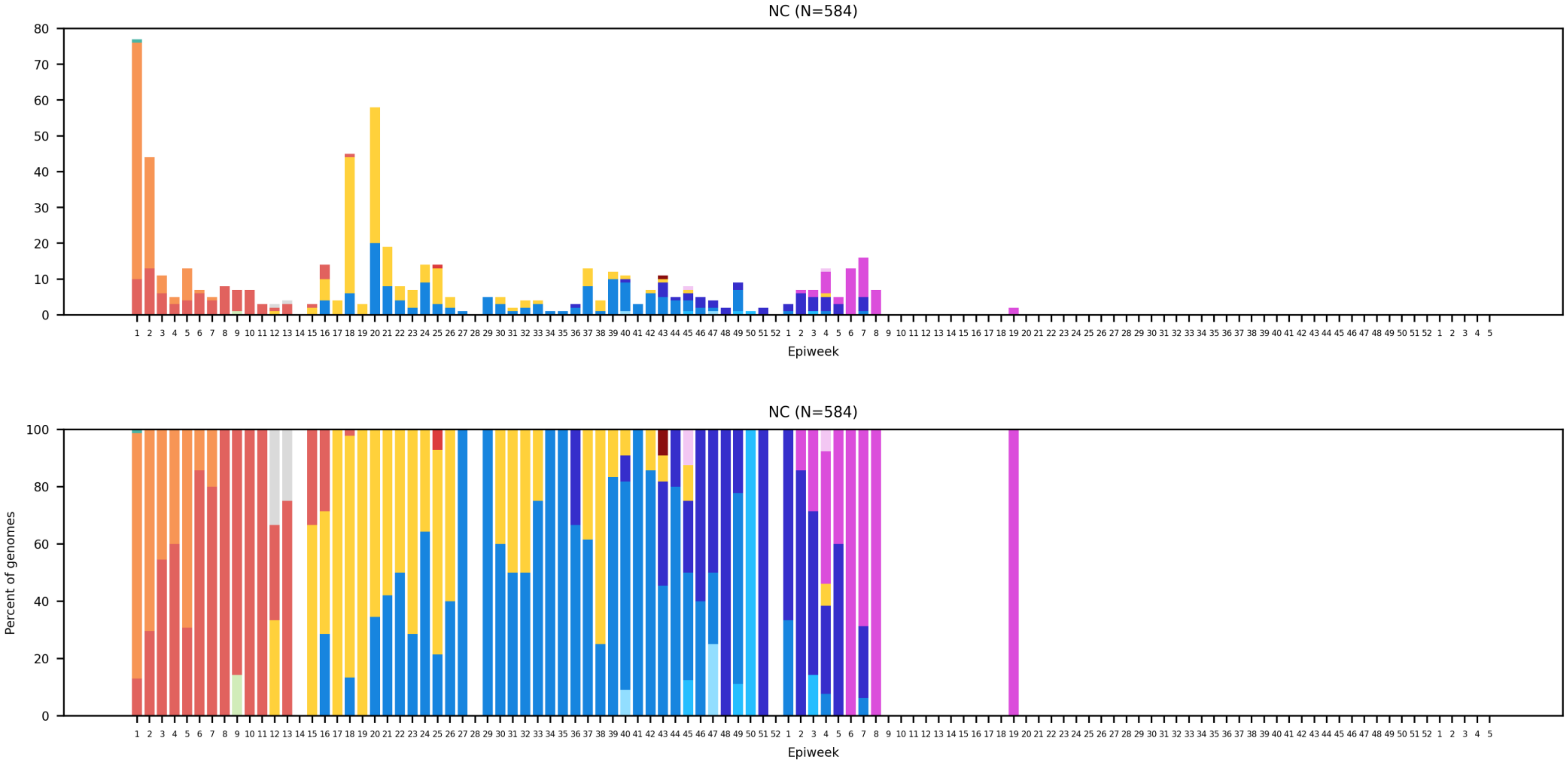
Northern Cape Province, 2022-2025, n = 584

Genomes added since last report: 0*



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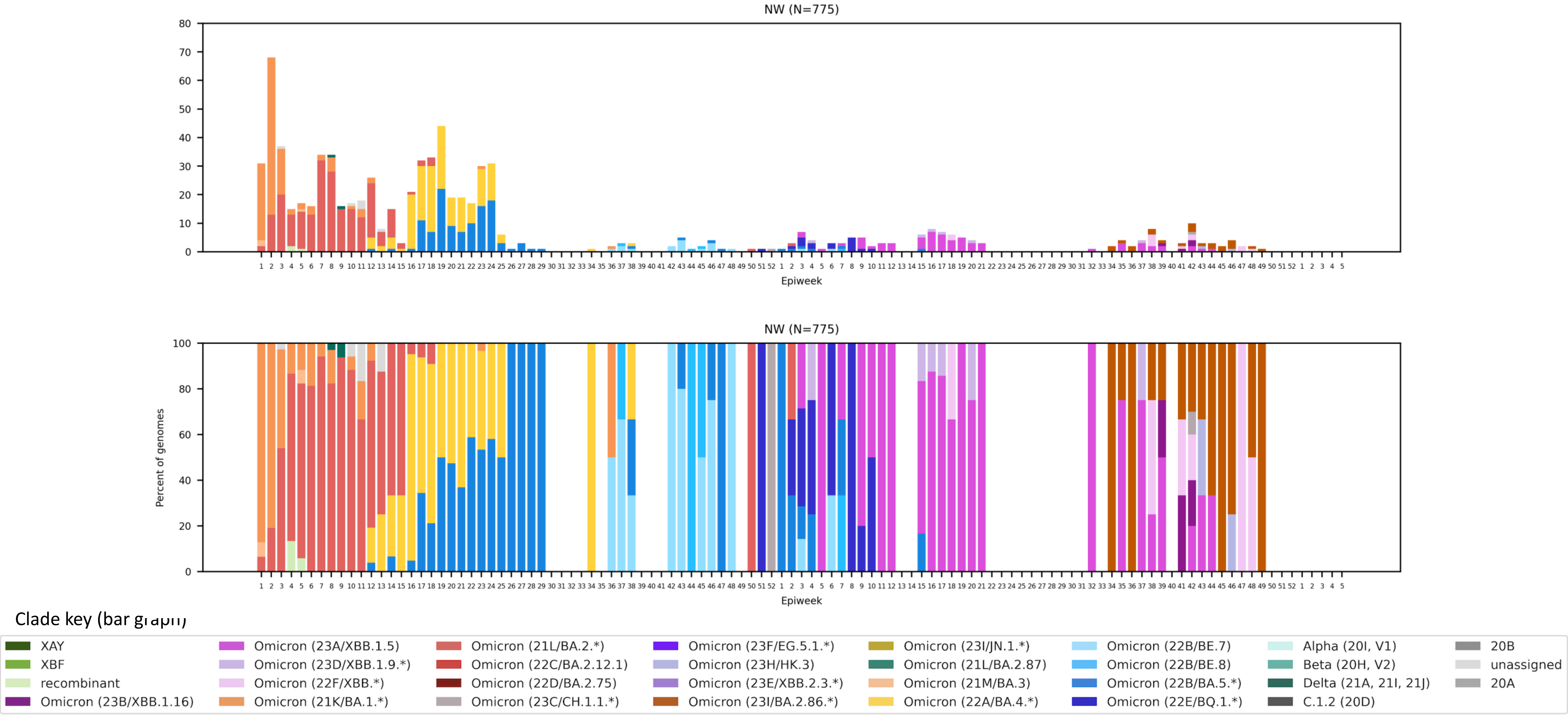
North West Province, 2022-2024, n = 775

Genomes added since last report: 9*



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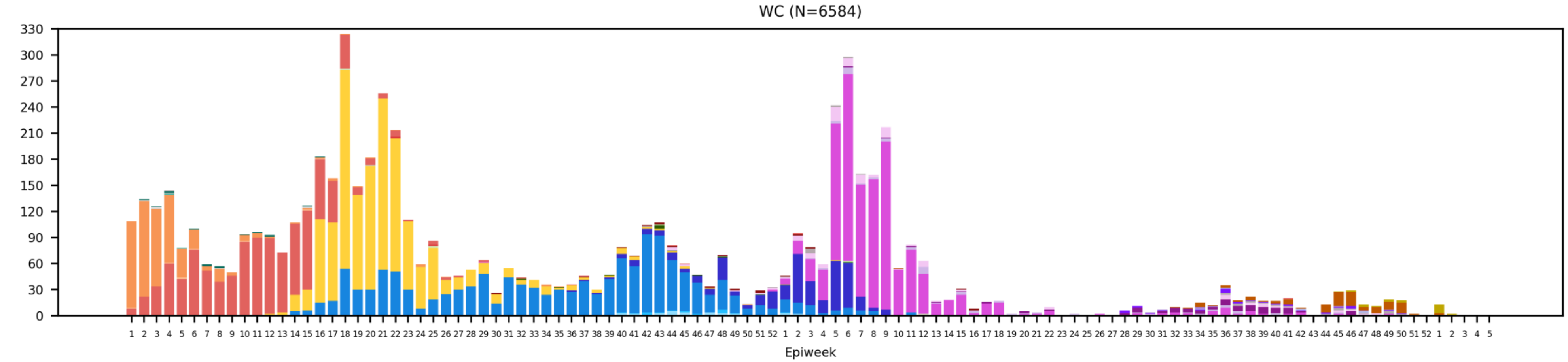
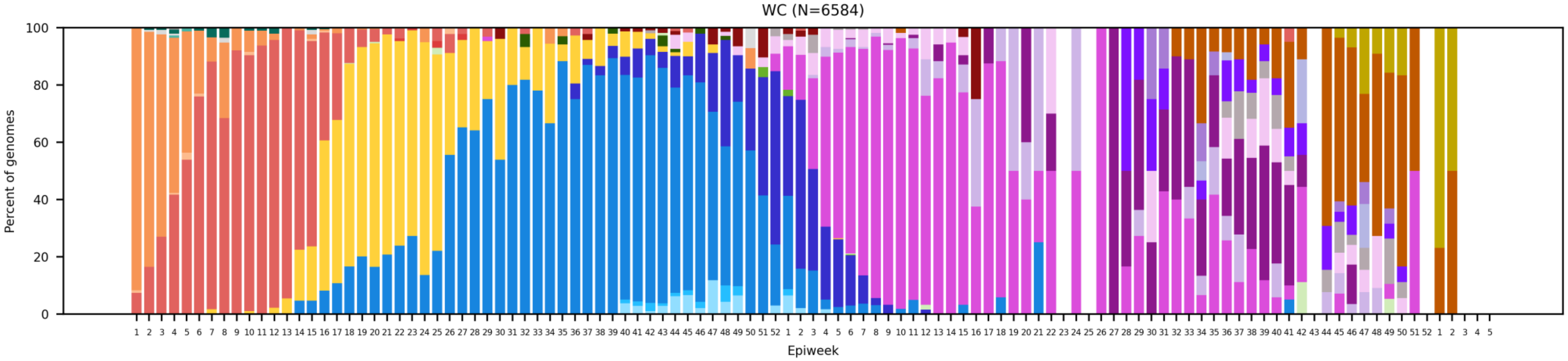
Western Cape Province, 2022-2024, n = 6584

Genomes added since last report: 25*





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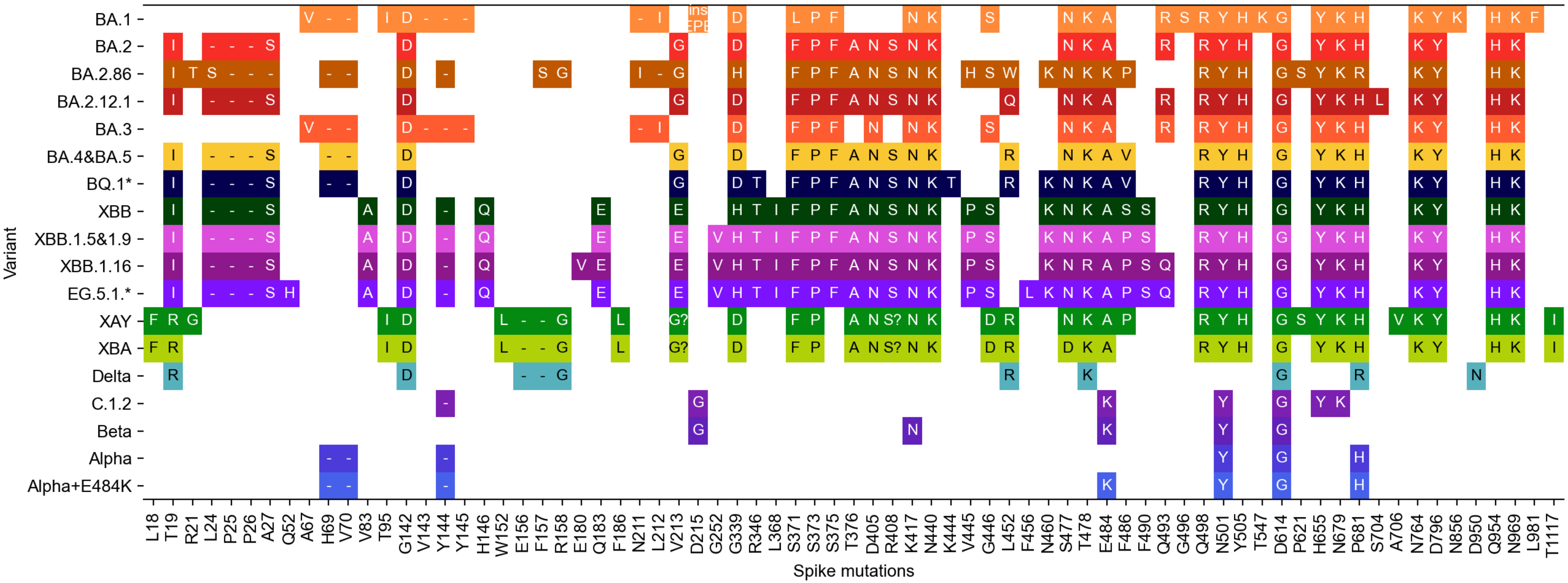
Summary

- **Sequencing update**
  - October sequences (n=320) and November sequences (n=249) are from all provinces except the Northern Cape. December sequences (n=86) are from all provinces except the Northern Cape and Free State

- **Variant of Concern Omicron in South Africa**
  - Omicron dominated in October (99.4%), November (99.2%) and December (99.7%)
  - BA.2.86 was detected at a prevalence of 43% in October, and dominated at 57% in November and 57% in December
  - 35 JN.1 sequences have been detected in the Western Cape (n=24), Gauteng (n=9), Limpopo (n=1), and Mpumalanga (n=1) in November (4%) and December (17%), and January (71%)
  - XBB.1.5 constituted 12% of October, 6% of November and 5% of December sequences
  - XBB.1.16 was detected in October (8%) and November (2%), and December (1%)
  - EG.5.1.* lineage (clade 23F) was detected at a prevalence of 5% in October, 3% in November and 5% in December
  - Nine sequences of newly designated BA.2.87.1 lineage have been detected in SA in Sep-Dec 2023 (details in slides 21-24)

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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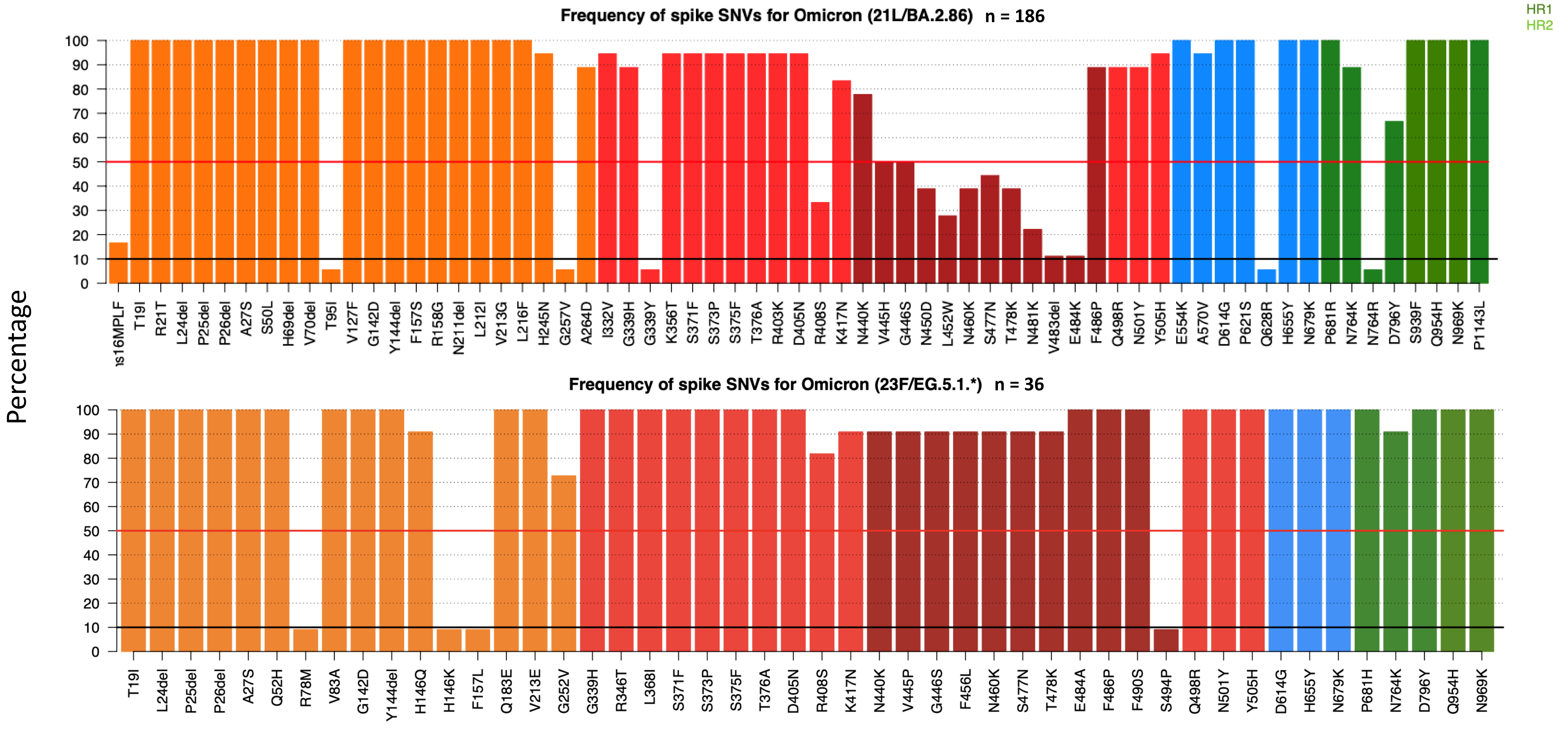
Network for Genomic Surveillance in South Africa

BA.2.86 and EG.5.1 spike mutations*

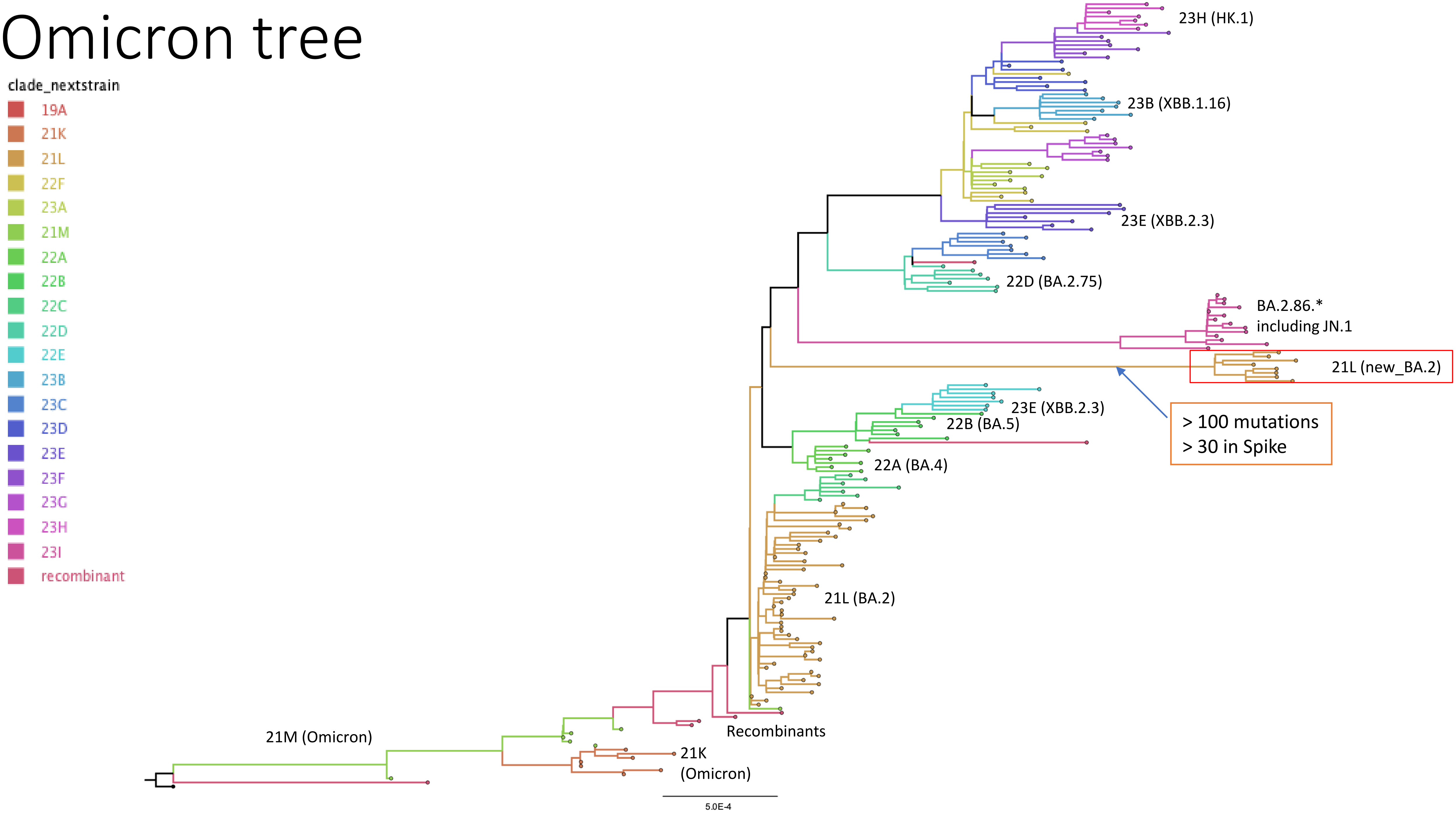


*Only mutations present in ≥1% of sequences are shown.

BA.2.87.1 summary

- NGS-SA has detected a **new lineage** in South Africa **assigned Omicron BA.2.87.1**
- This lineage has been detected in **nine samples** from **three provinces** (Mpumalanga, Limpopo and Gauteng) between **20 September and 12 December 2023**
- All nine genomes were from **SARS-CoV-2 genomic surveillance** (routine diagnostic samples) or **syndromic influenza-like illness surveillance** (Viral Watch)
- Initial analysis suggests no similar sequences have been identified outside South Africa at this stage
- The lineage is **genetically distinct from currently circulating Omicron lineages** (particularly BA.2.86 and JN.1), and initial analysis suggests it has likely emerged from BA.2 or from the basal node of Omicron

Omicron tree

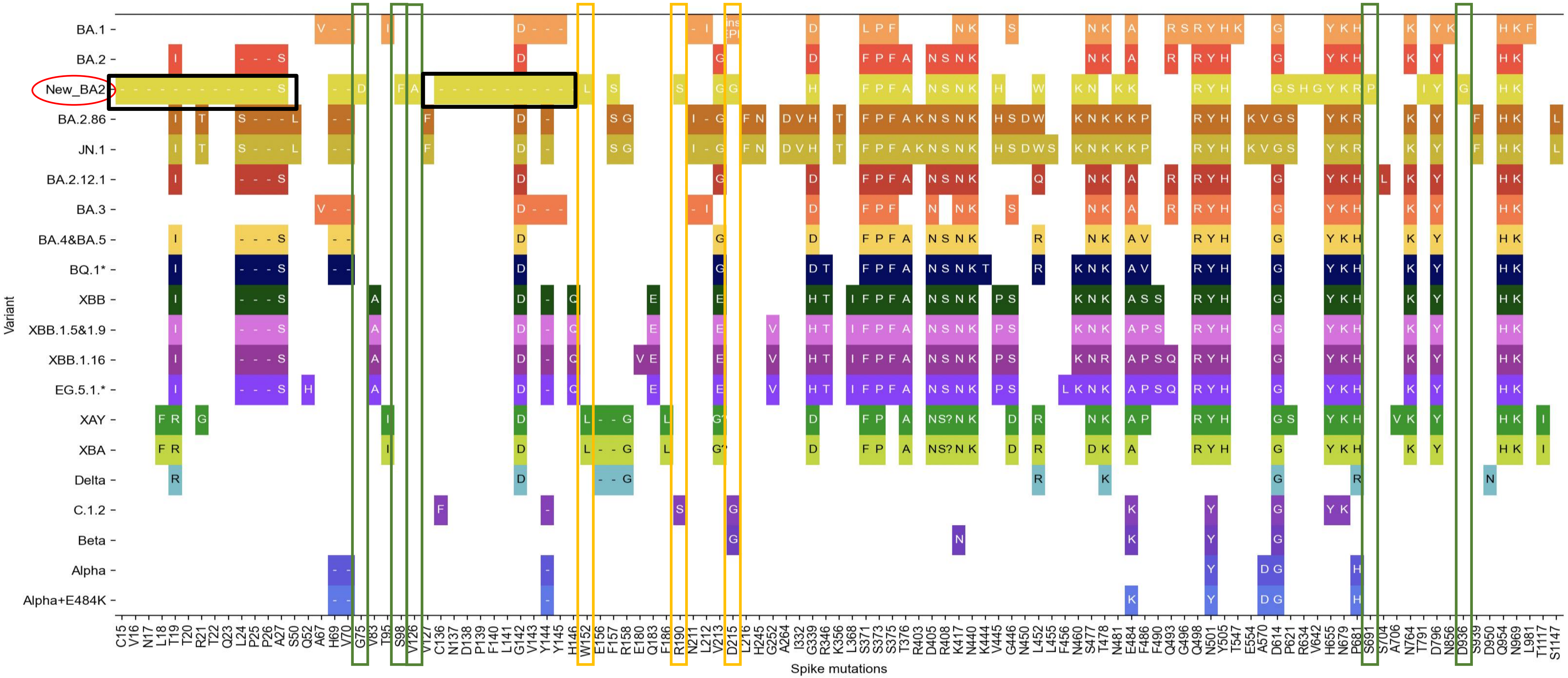


> 100 mutations
> 30 in Spike

Genomic profile

- Relative to BA.2, this lineage has >30 non-synonymous substitutions (concentrated in spike) and 7 deletions (3 in spike)
- Mutations are concentrated in important regions of the spike protein:
    - Two large deletions in the antigenic supersite of the N-terminal domain (15-26del and 136-146del)
    - Multiple mutations at important antigenic sites in receptor-binding domain (e.g. K417T, K444N, V445G, L452M, N460K, N481K)
    - Mutations close to the furin cleavage site (N679R, S691P)

Spike protein mutation profile



Deletions

Private mutations

Mutations shared with one or two lineages

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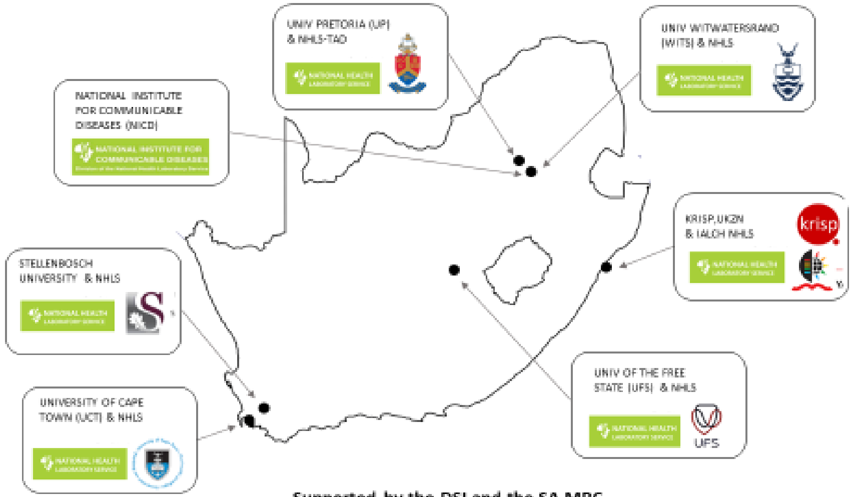

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EDCTP

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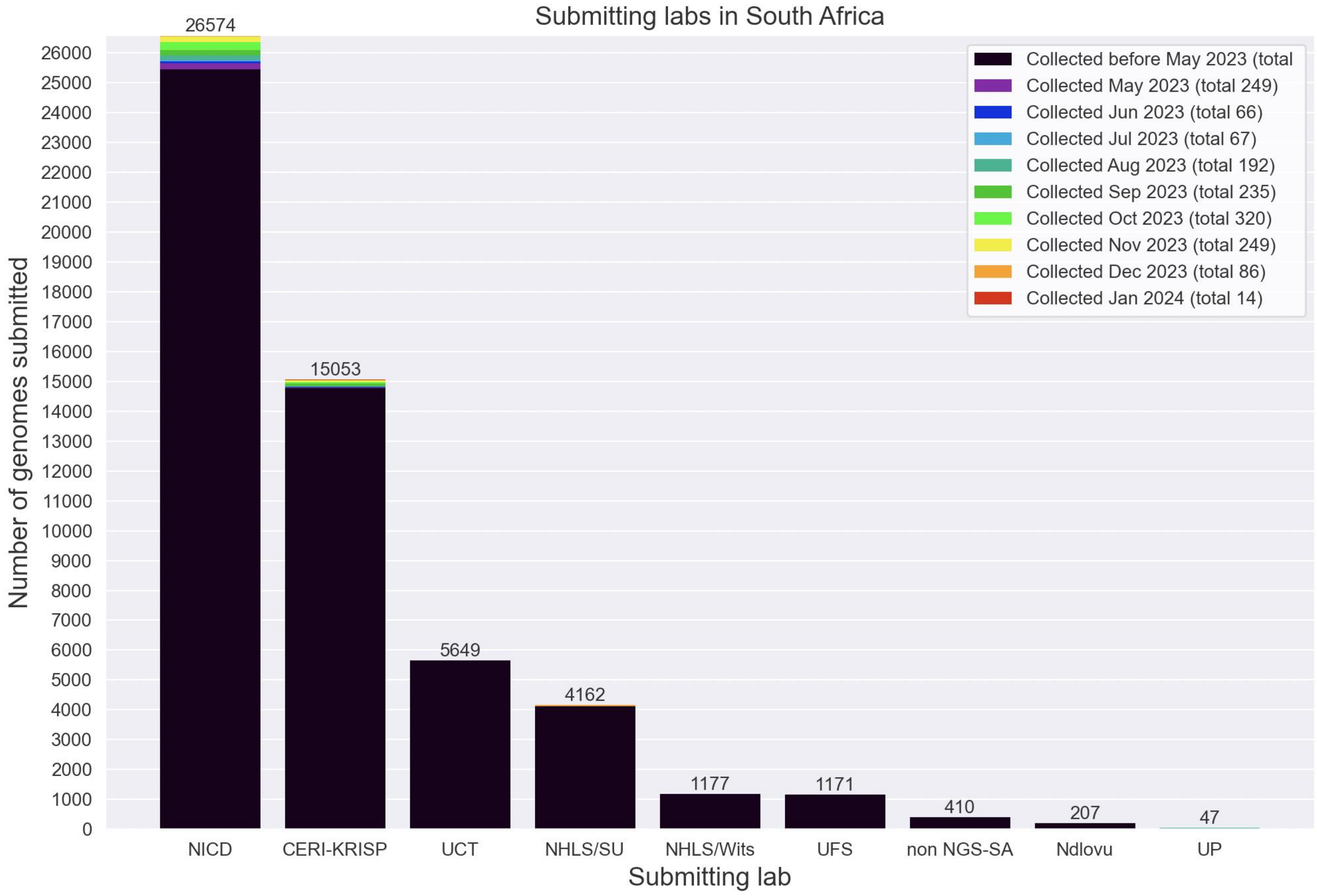
South African genomes submitted per submitting lab, 2020 - 2024 (N= 54 450)



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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Network for Genomic Surveillance in South Africa

Currently circulating Variants of Interest (VOI) as of 18 December 2023

ango 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) Includes XBB.1.5.70 (23G): XBB.1.5 + S:L455F and S:F456L	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 (23F): EG.5 + S:Q52H HK.3 (23H): EG.5 + S:Q52H, S:L455F HV.1: EG.5 + S:Q52H, S:F157L, S:L452R	17-02-2023	09-08-2023 EG.5 Initial Risk Evaluation, 09 August 2023 EG.5 Updated Risk Evaluation, 21 September 2023 EG.5 Updated Risk Evaluation, 21 November 2023
BA.2.86[$]	23I	Mutations relative to BA.2	24-07-2023	21-11-2023 BA.2.86 Initial Risk Evaluation, 21 November 2023
JN.1	Not assigned	BA.2.86 + S:L455S	25-08-2023	18-12-2023 JN.1 Initial Risk Evaluation 18 December 2023

https://www.who.int/en/activities/tracking-SARS-CoV-2-variants/ accessed 5 Jan 2024

Currently circulating variants under monitoring (VUMs) as of 21 November 2023

Pango lineage	Nextstrain clade	Genetic features	Earliest documented samples	Date of designation and risk assessments
DV.7	23C	CH.1.1 + S:N185D, S:L858I	19-01-2023	23-10-2023
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.1.9.2[#]	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, S:Q613H	05-12-2022	26-04-2023
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

https://www.who.int/en/activities/tracking-SARS-CoV-2-variants/ accessed 5 Jan 2024

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.)