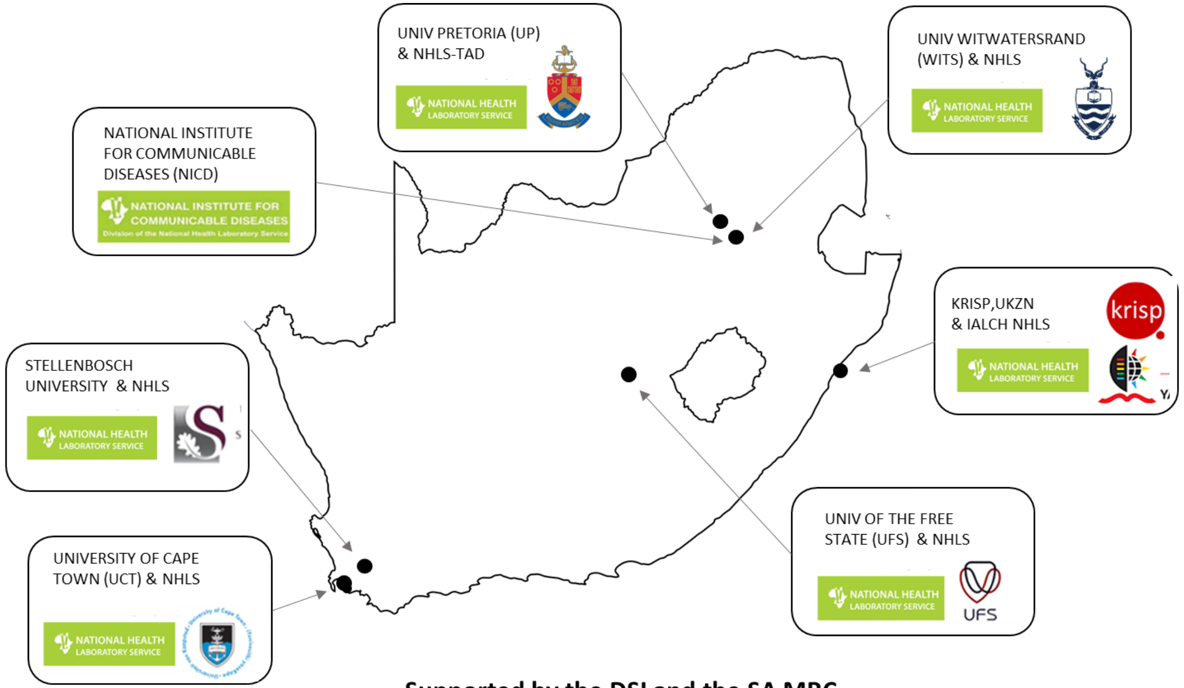
NGS-SA
Network for Genomic
Surveillance in South Africa

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

SARS-CoV-2 Sequencing Update

07 June 2024


UNIV PRETORIA (UP) & NHLS-TAD

UNIV WITWATERSRAND (WITS) & NHLS

NATIONAL INSTITUTE FOR COMMUNICABLE DISEASES (NICD)

KRISP,UKZN & IALCH NHLS

STELLENBOSCH UNIVERSITY & NHLS

UNIV OF THE FREE STATE (UFS) & NHLS

UNIVERSITY OF CAPE TOWN (UCT) & NHLS

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)

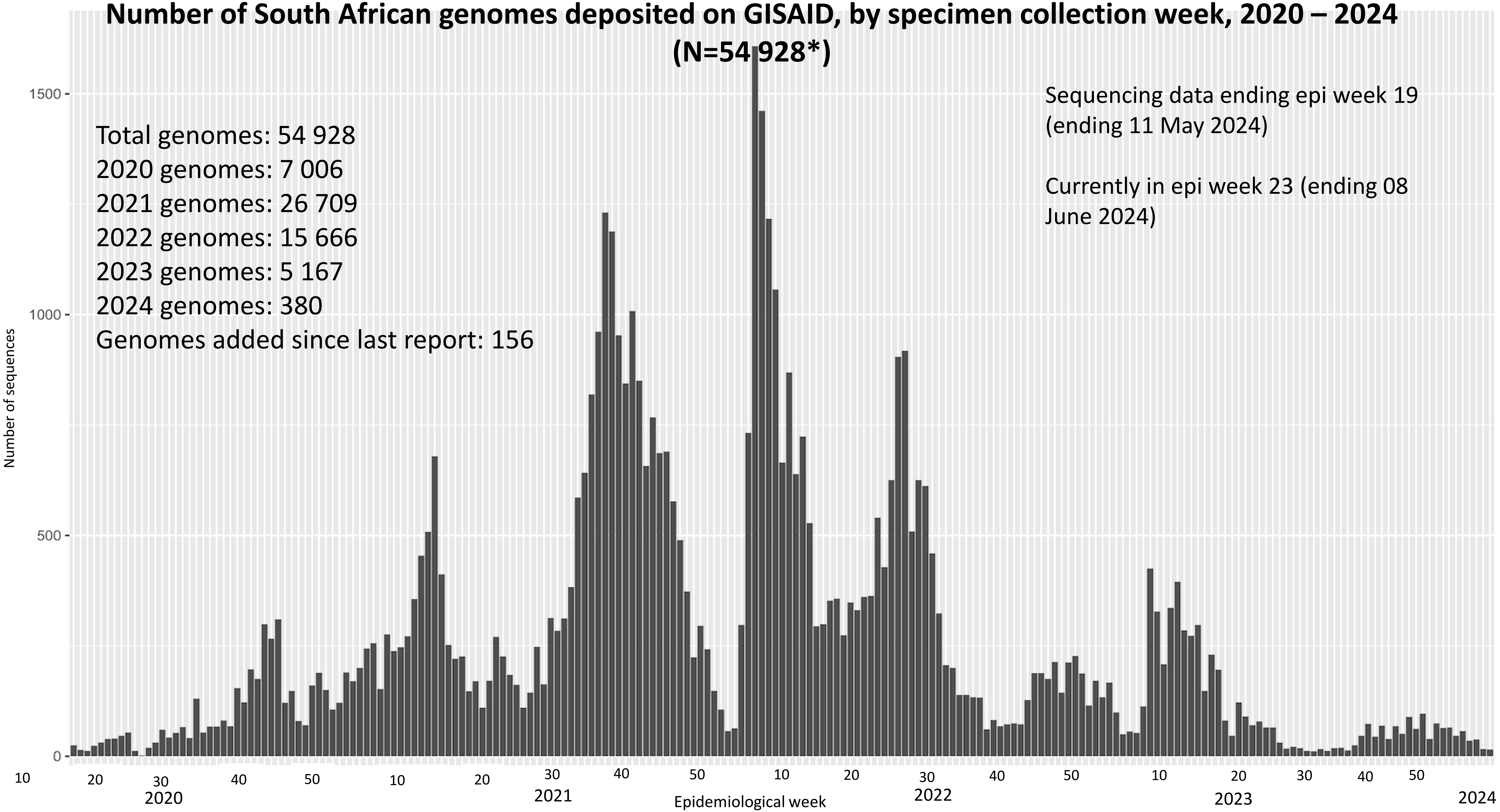
The genomic data presented here are based on South African SARS-CoV-2 sequence data downloaded from GISAID (www.gisaid.org) on 07 June 2024 at 08h30

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 – 2024 (N=54 928*)



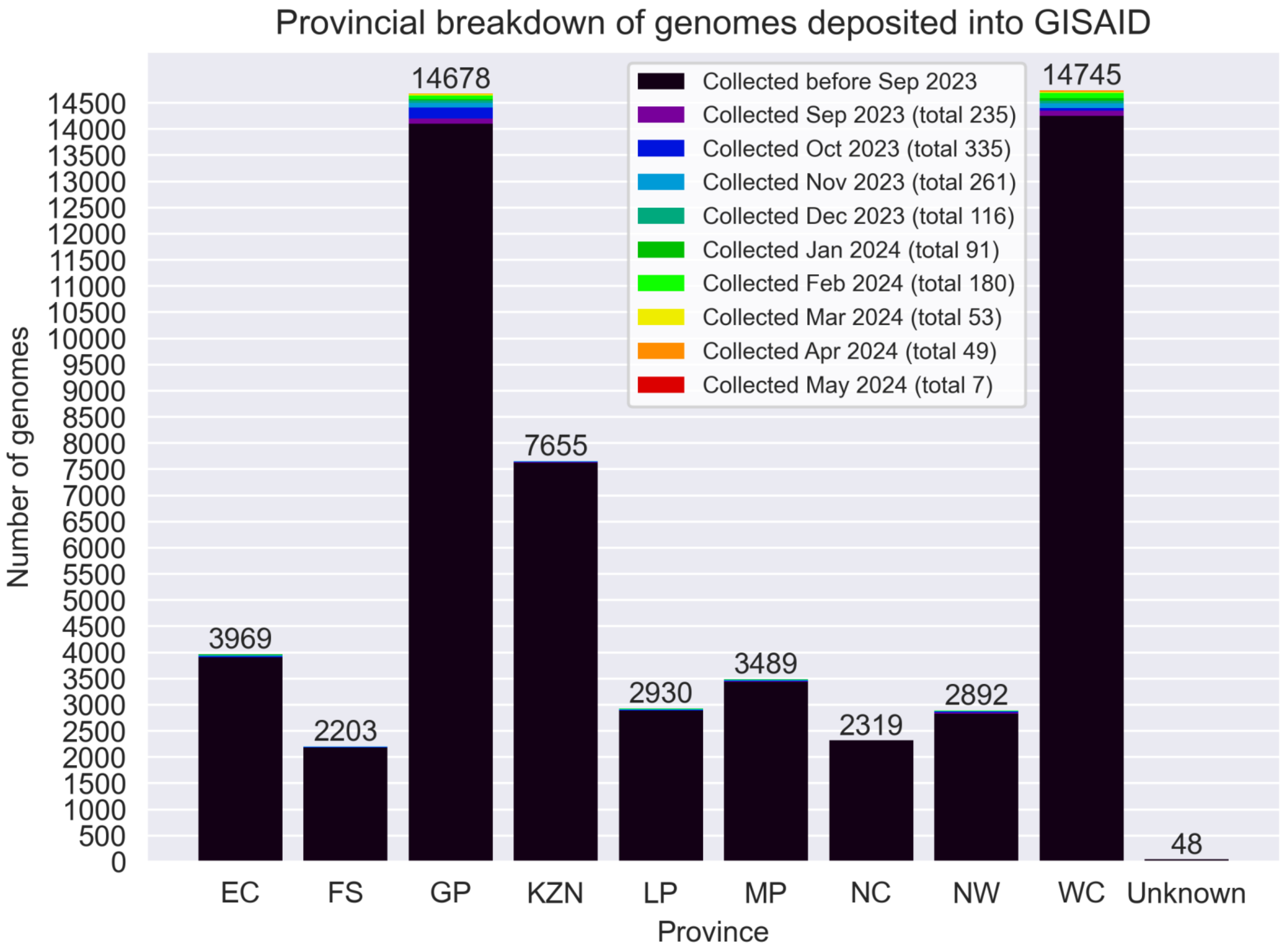
Total genomes: 54 928
2020 genomes: 7 006
2021 genomes: 26 709
2022 genomes: 15 666
2023 genomes: 5 167
2024 genomes: 380
Genomes added since last report: 156

Sequencing data ending epi week 19 (ending 11 May 2024)

Currently in epi week 23 (ending 08 June 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= 54 928)



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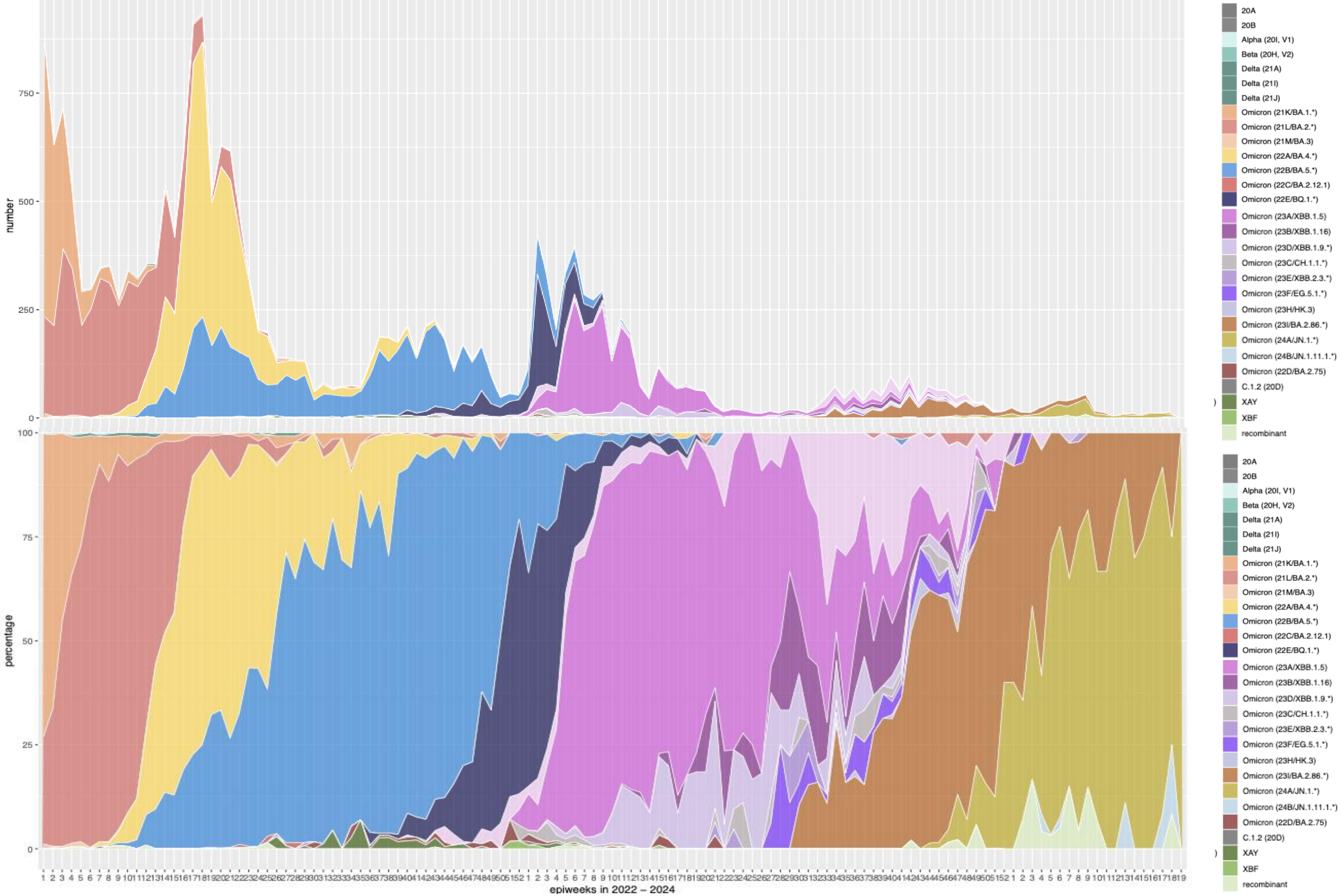
Number and percentage of clades by epiweek in South Africa, 2022-2024 (21 710*)



Sequencing data ending epi week 19 (ending 11 May 2024)

Currently in epi week 23 (ending 08 June 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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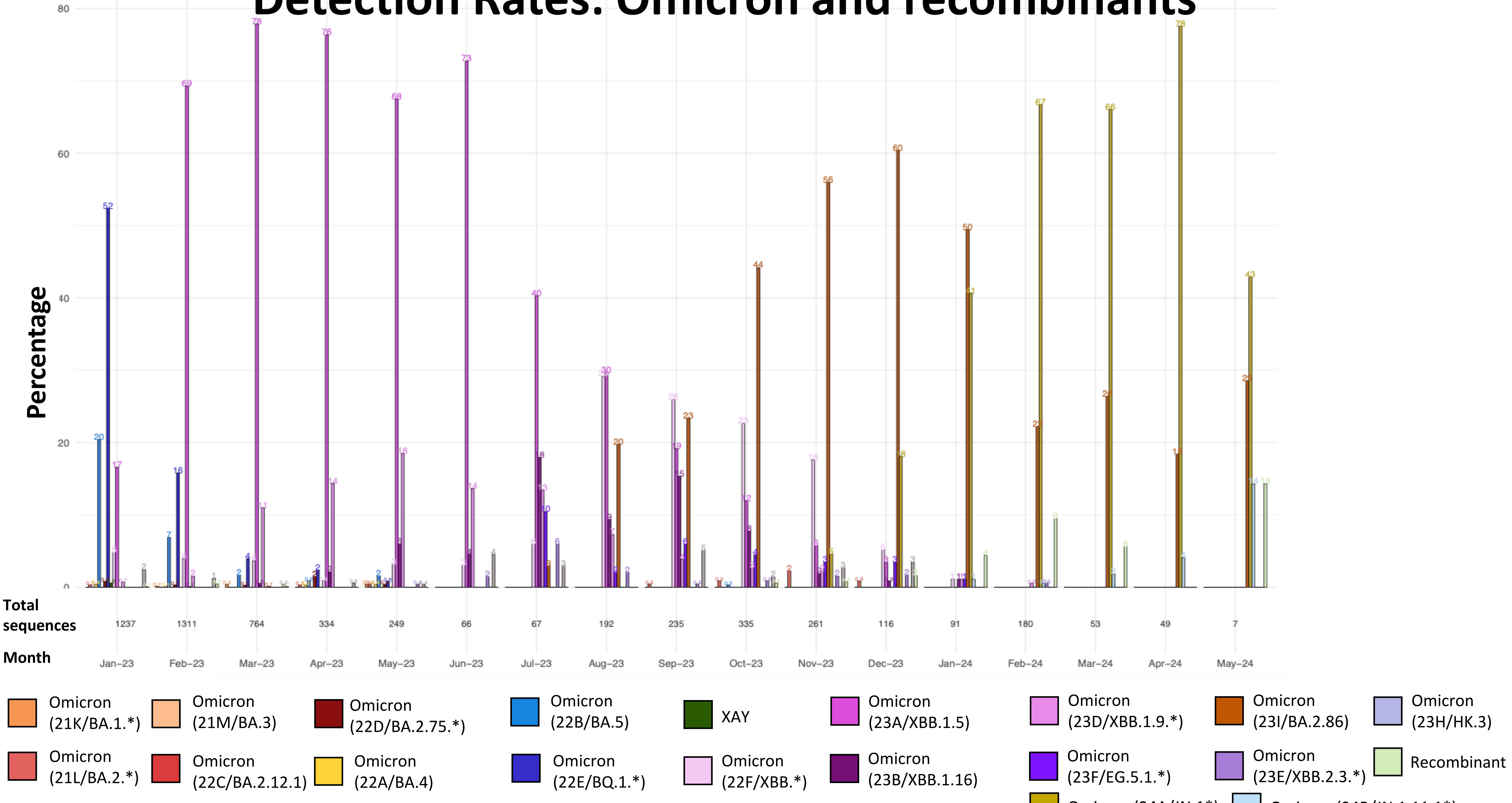
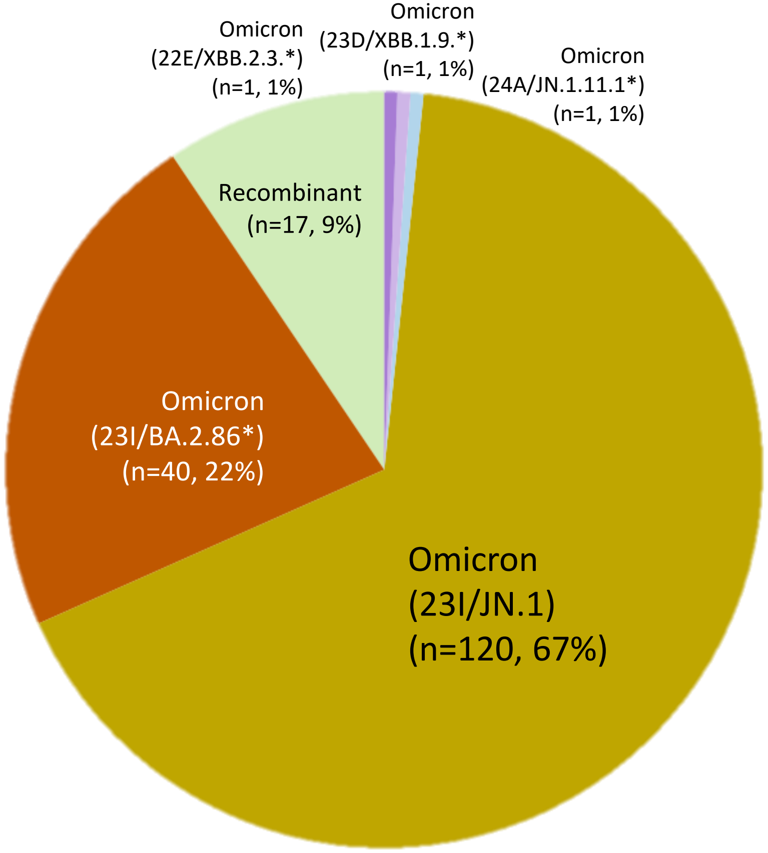
Detection Rates: Omicron and recombinants



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

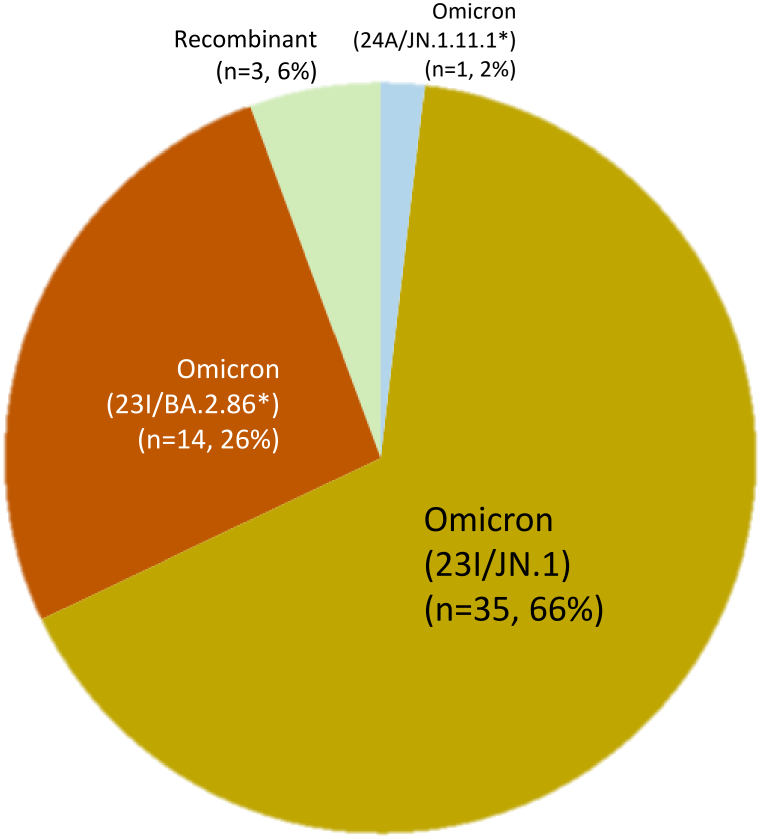
Prevalence of Variants of Concern (VOC) and Variants of Interest (VOI) in February – April 2024

February (N=180)



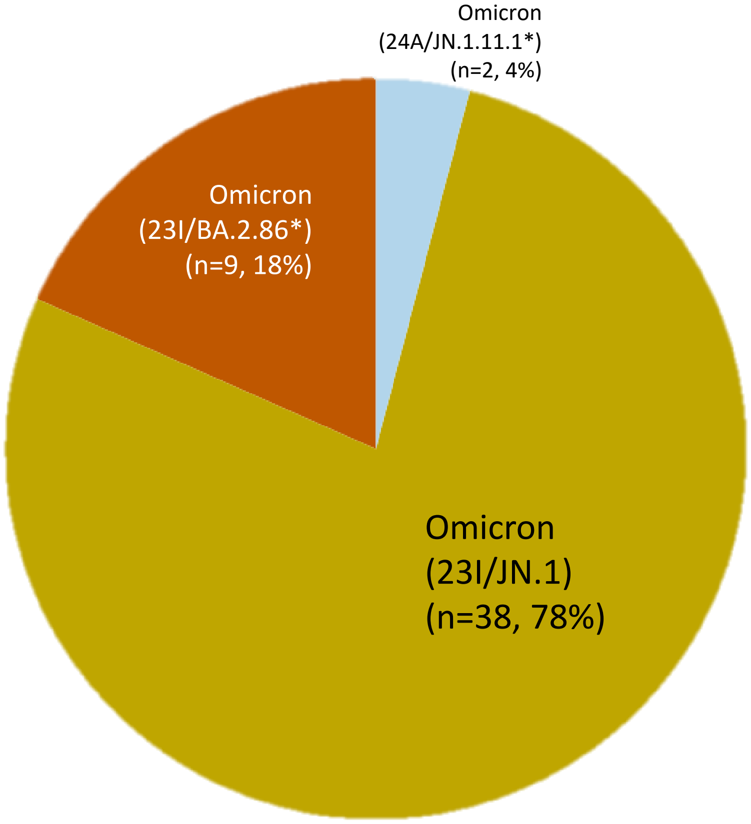
Total Omicron in February: 180 (100%)

March (N=53)



Total Omicron in March: 53 (100%)

April (N=49)



Total Omicron in April: 49 (100%)

Clade key

- ■ 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)
- ■ Omicron (22D/BA.2.75)
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- ■ Omicron (23H/HK.3)
- ■ Omicron (23E/XBB.2.3.*)
- ■ Omicron (23I/BA.2.86.*)
- ■ Omicron (24A/JN.1.*)
- ■ Omicron (24B/JN.1.11.1.*)
- ■ Omicron (21L/BA.2.87.1)
- ■ Omicron (21M/BA.3)
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- ■ Omicron (22B/BE.7)
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- ■ Omicron (22B/BA.5.*)
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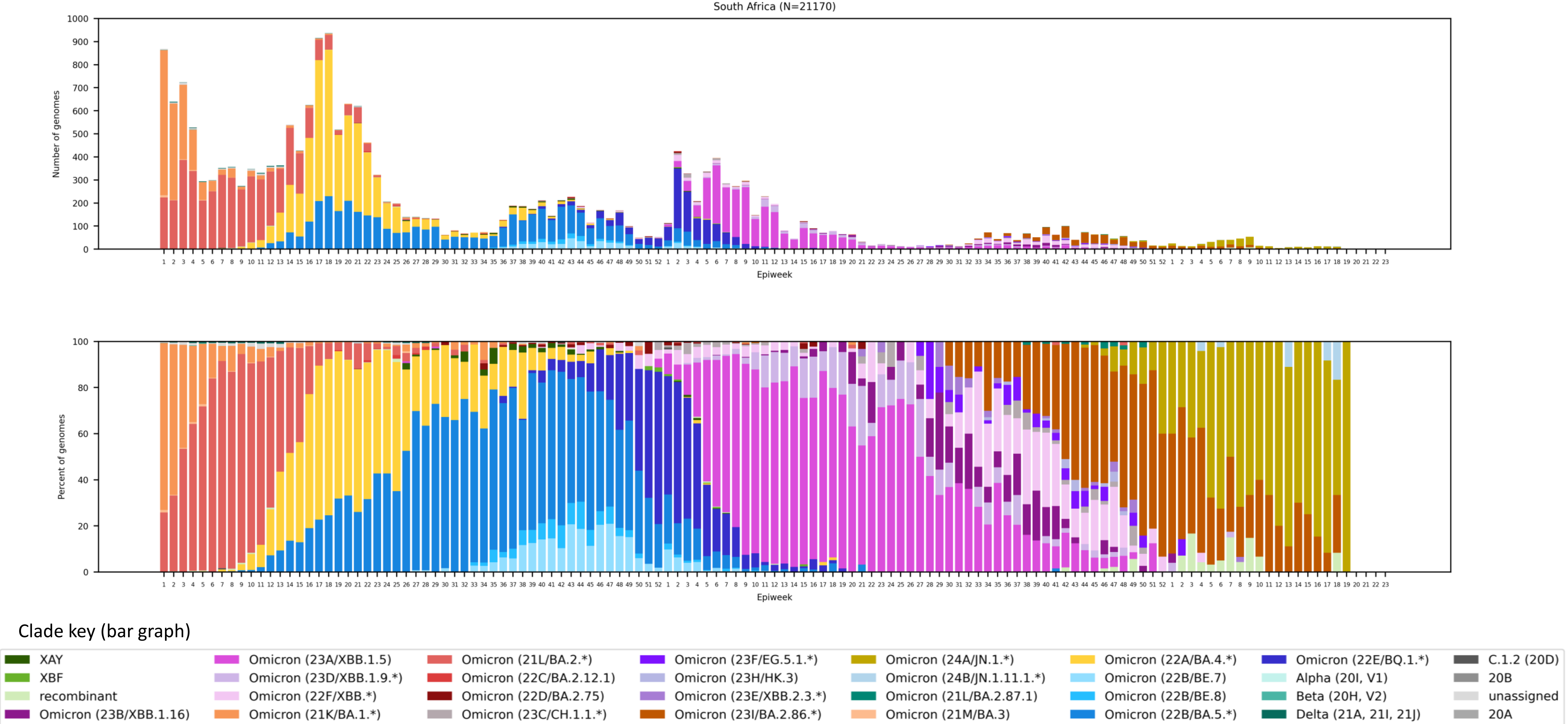
- ■ Beta (20H, V2)
- ■ Delta (21A, 21I, 21J)
- ■ C.1.2 (20D)
- ■ 20B
- ■ unassigned
- ■ 20A

South Africa, 2022-2024, n = 21 170*



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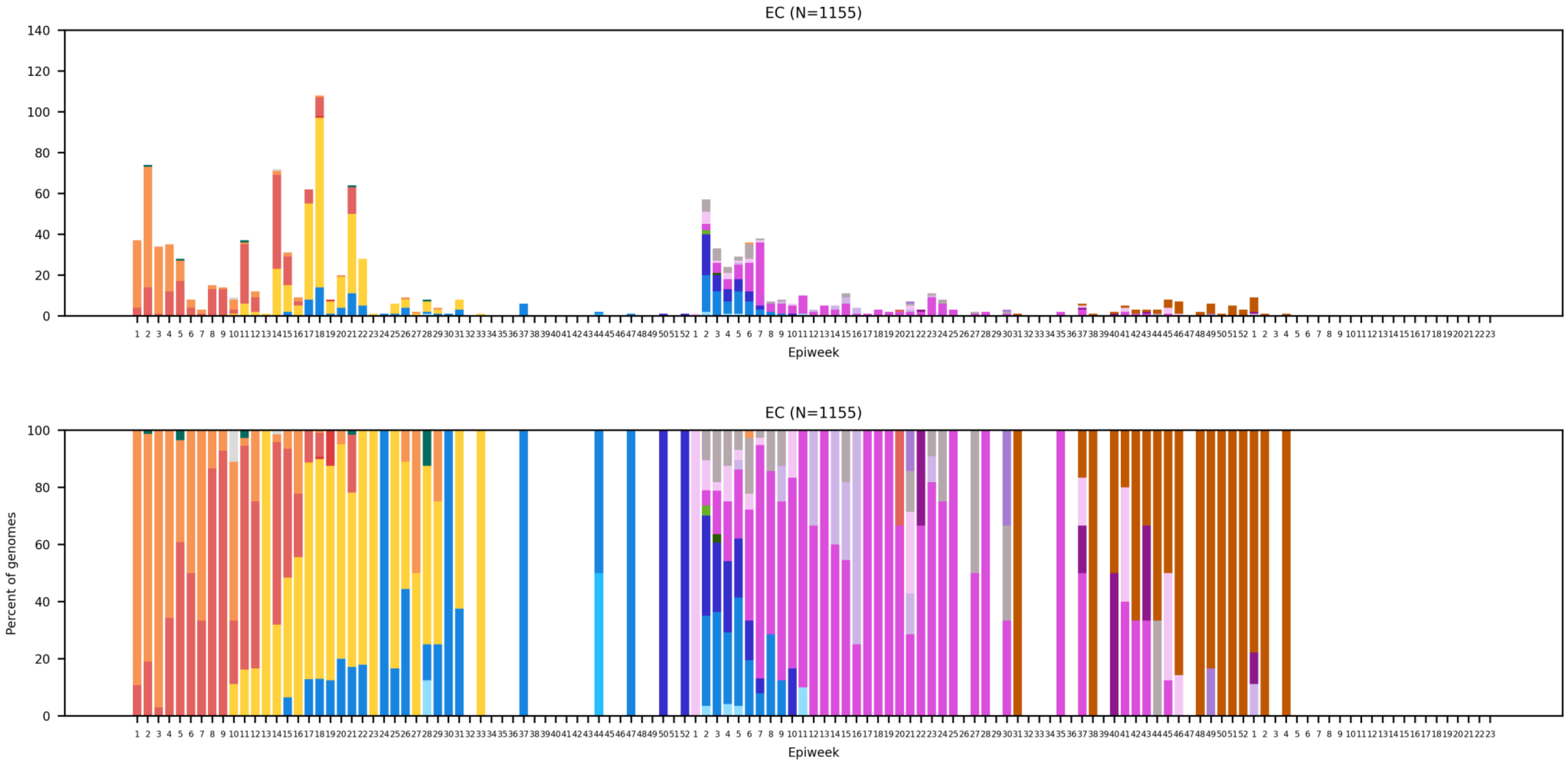
Eastern Cape Province, 2022-2024, n = 1155

Genomes added since last report: 0*



Clade key (bar graph)

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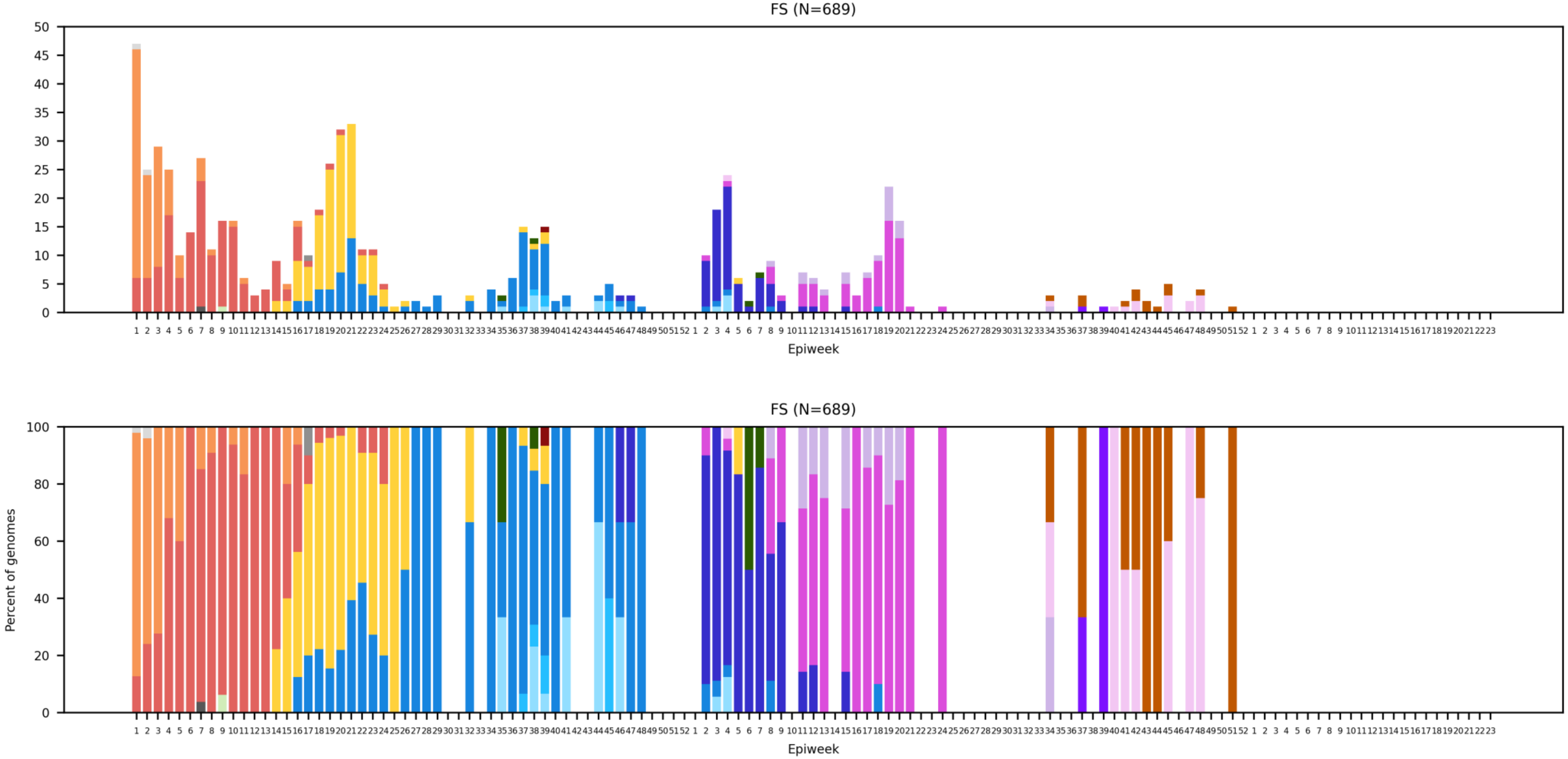
Free State Province, 2022-2024, n = 689

Genomes added since last report: 0*



Clade key (bar graph)

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- ⬛ 20B
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- ⬜ 20A

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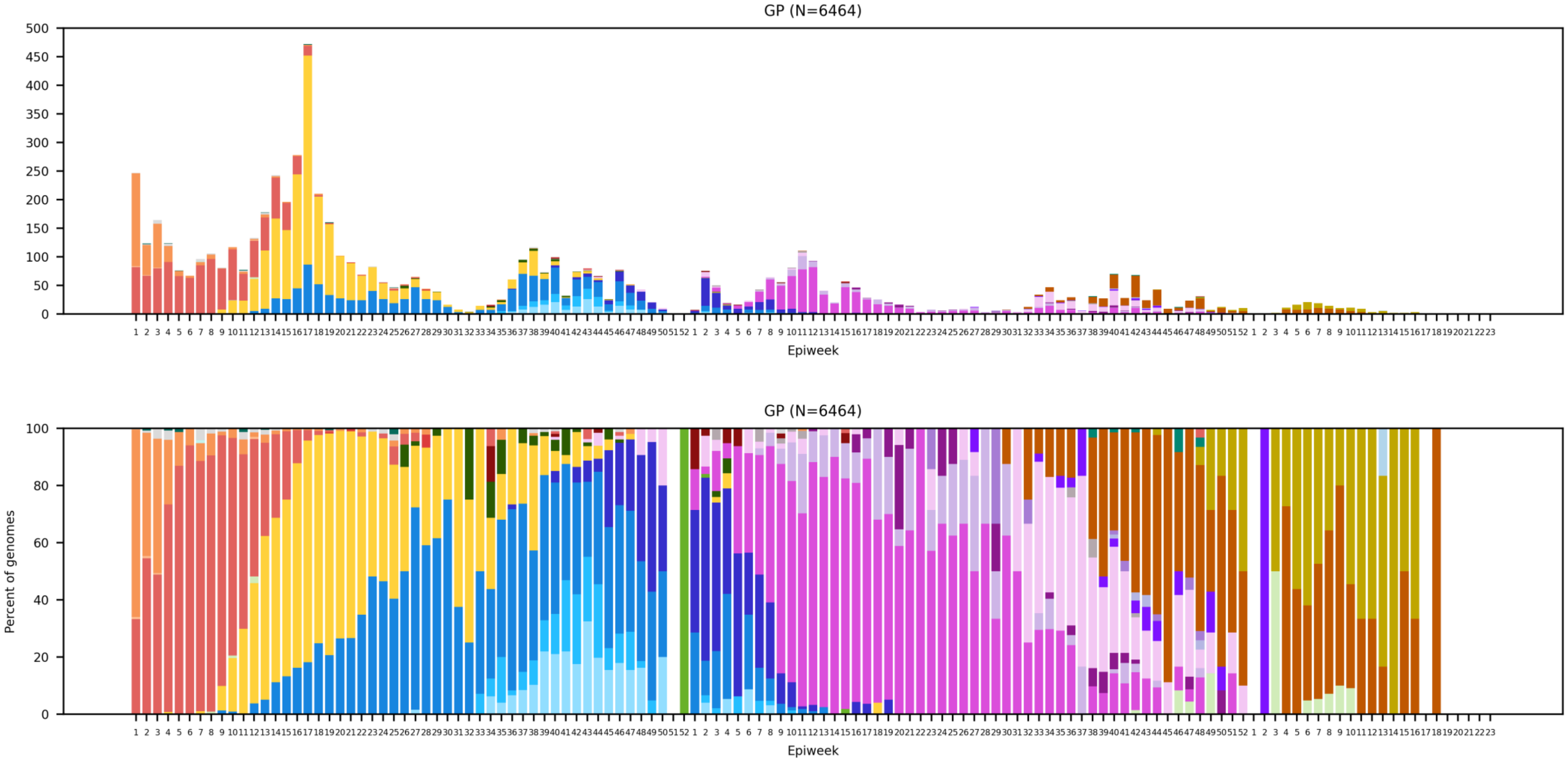
Gauteng Province, 2022-2024, n = 6464

Genomes added since last report: 96*



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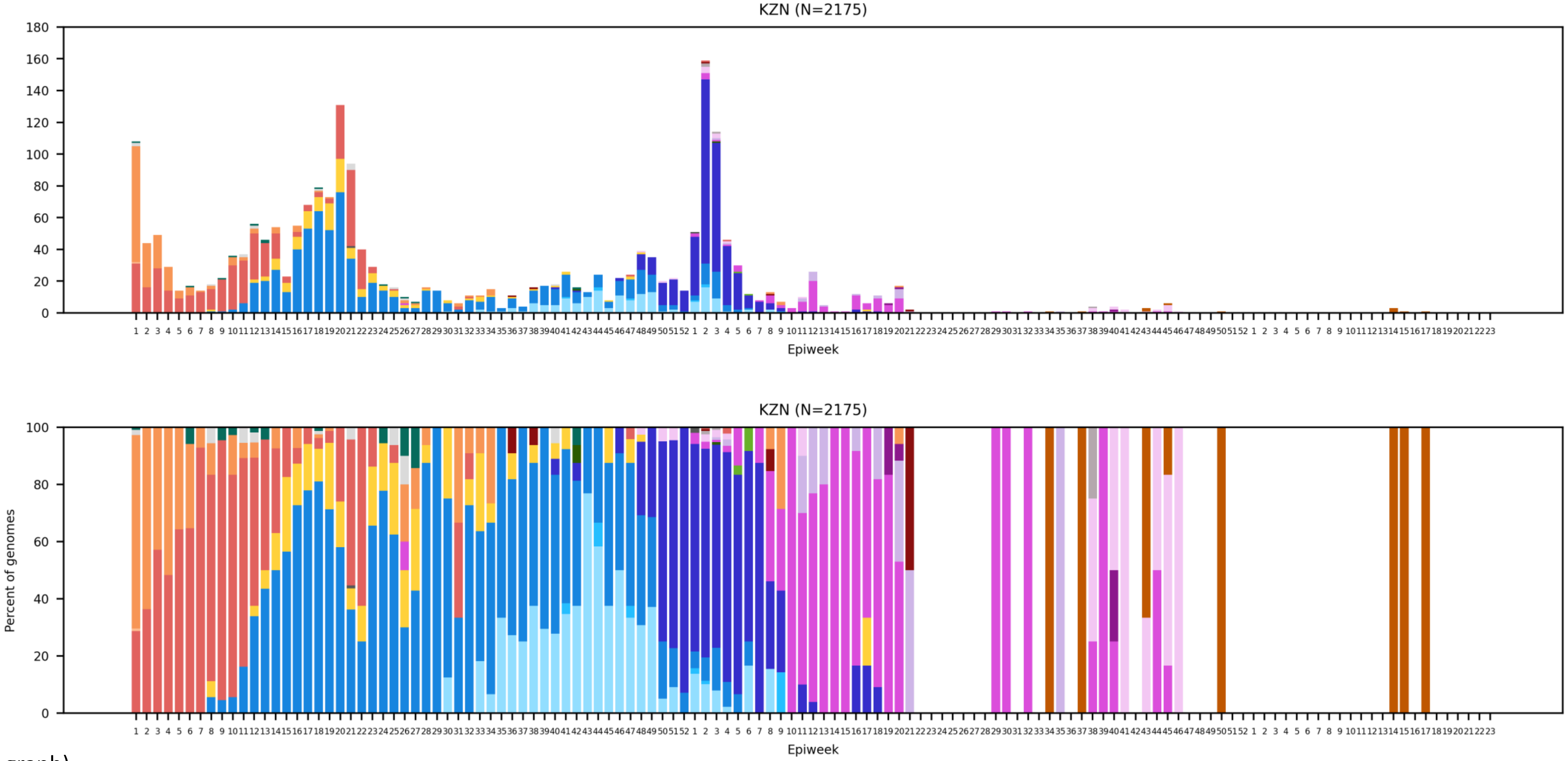
KwaZulu-Natal Province, 2022-2024, n = 2175

Genomes added since last report: 5*



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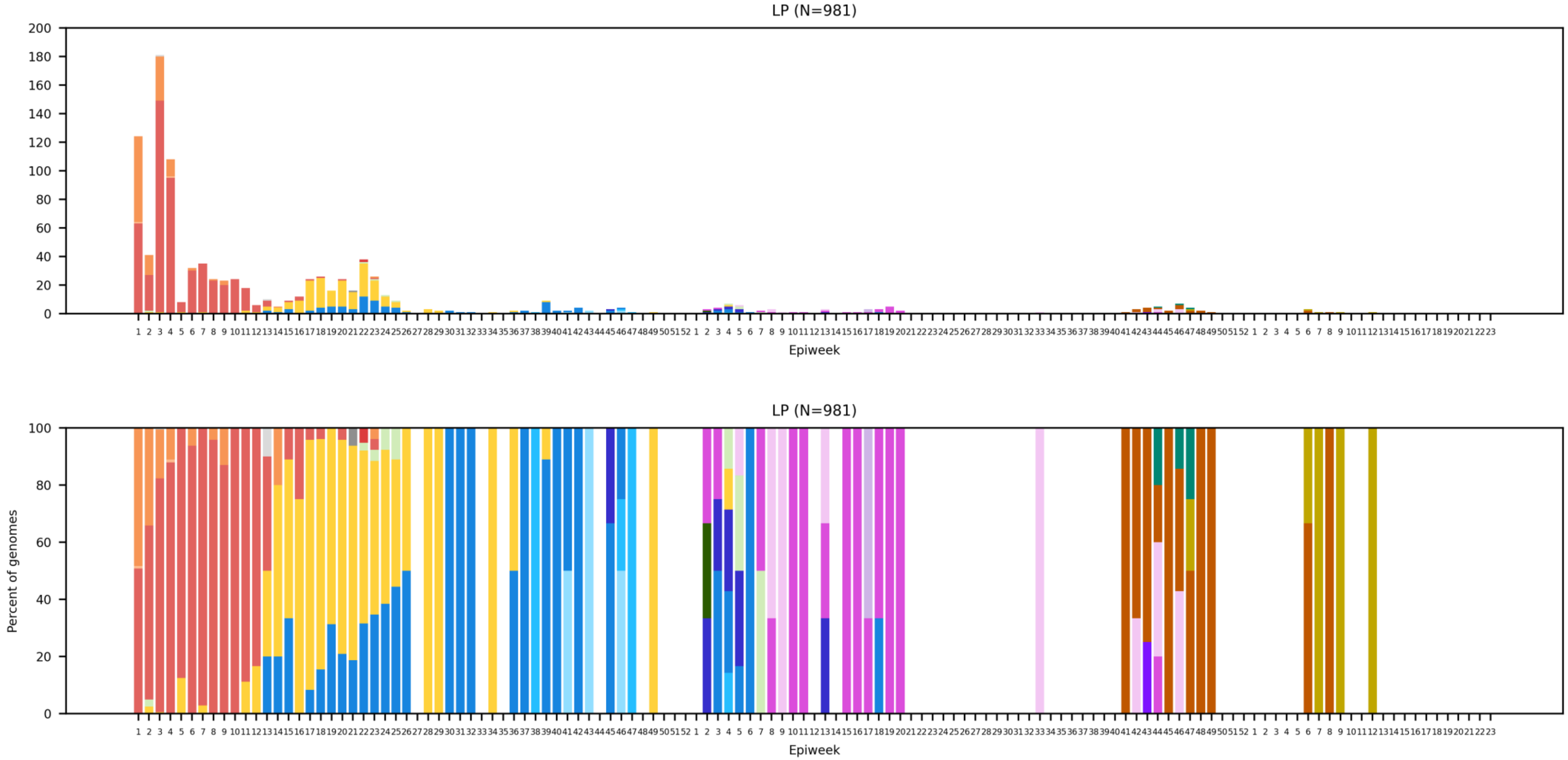
Limpopo Province, 2022-2024, n = 981

Genomes added since last report: 1*



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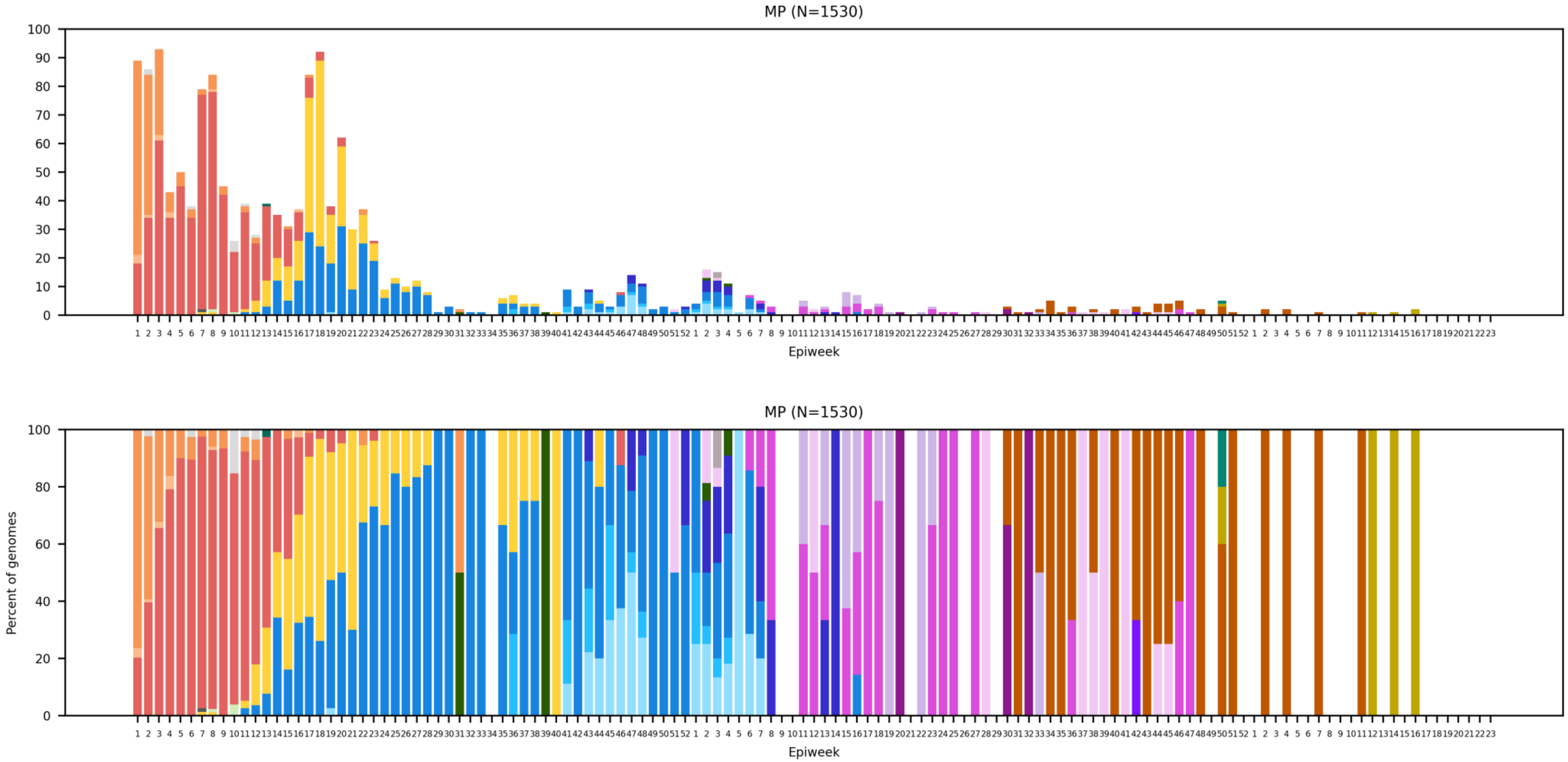
Mpumalanga Province, 2022-2024, n = 1530

Genomes added since last report: 5*



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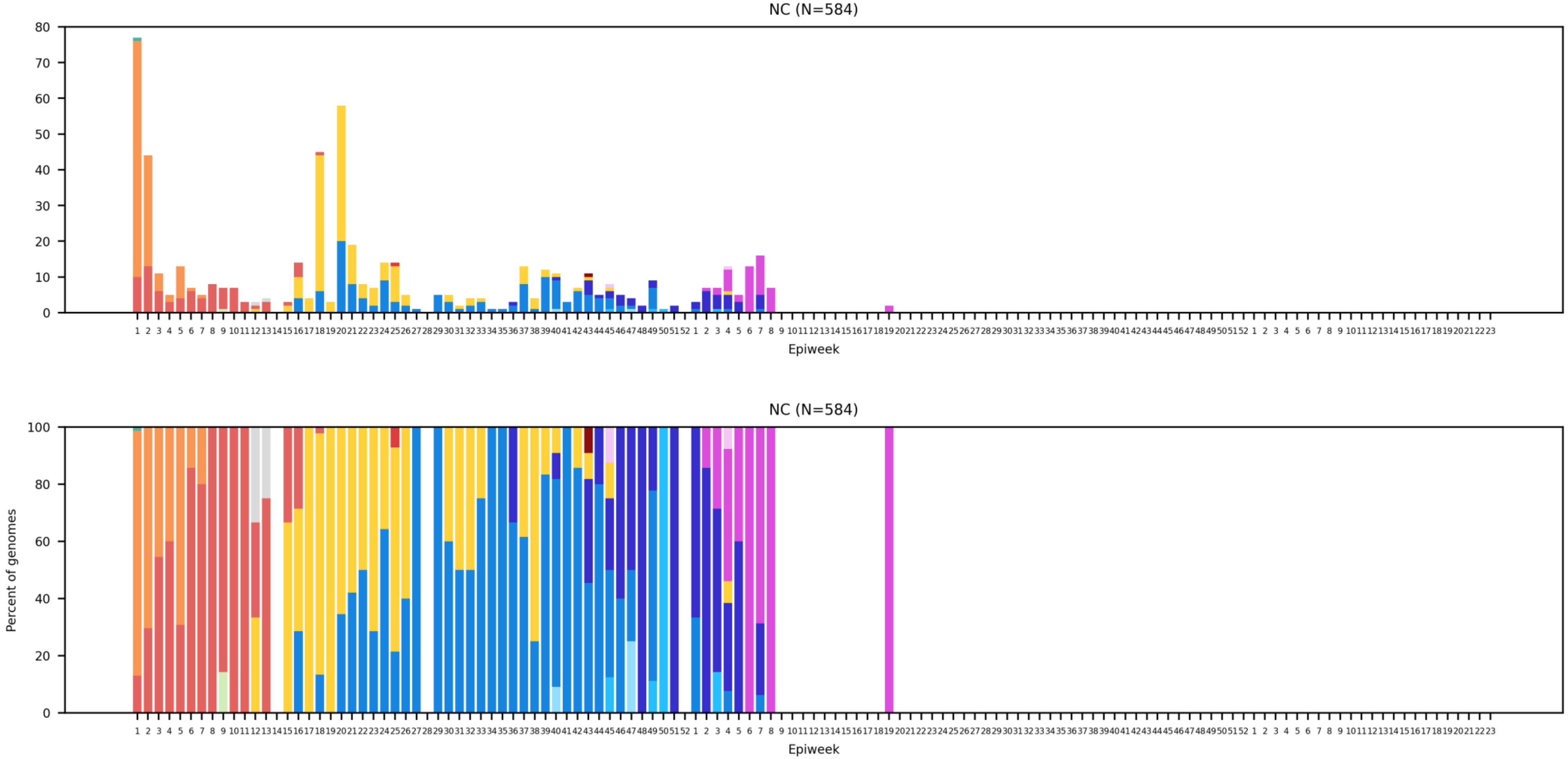
Northern Cape Province, 2022-2025, n = 584

Genomes added since last report: 0*



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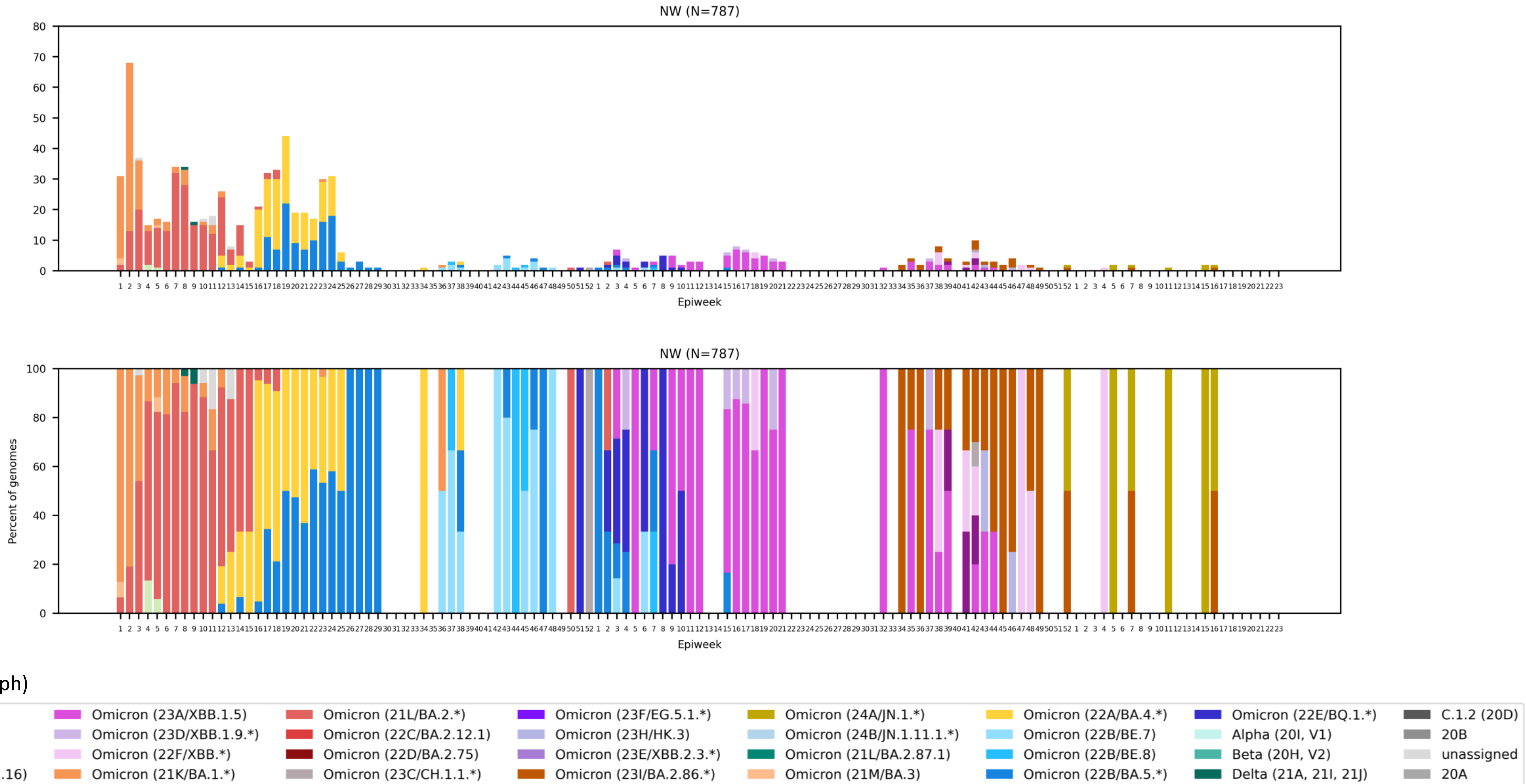
North West Province, 2022-2024, n = 787

Genomes added since last report: 5*



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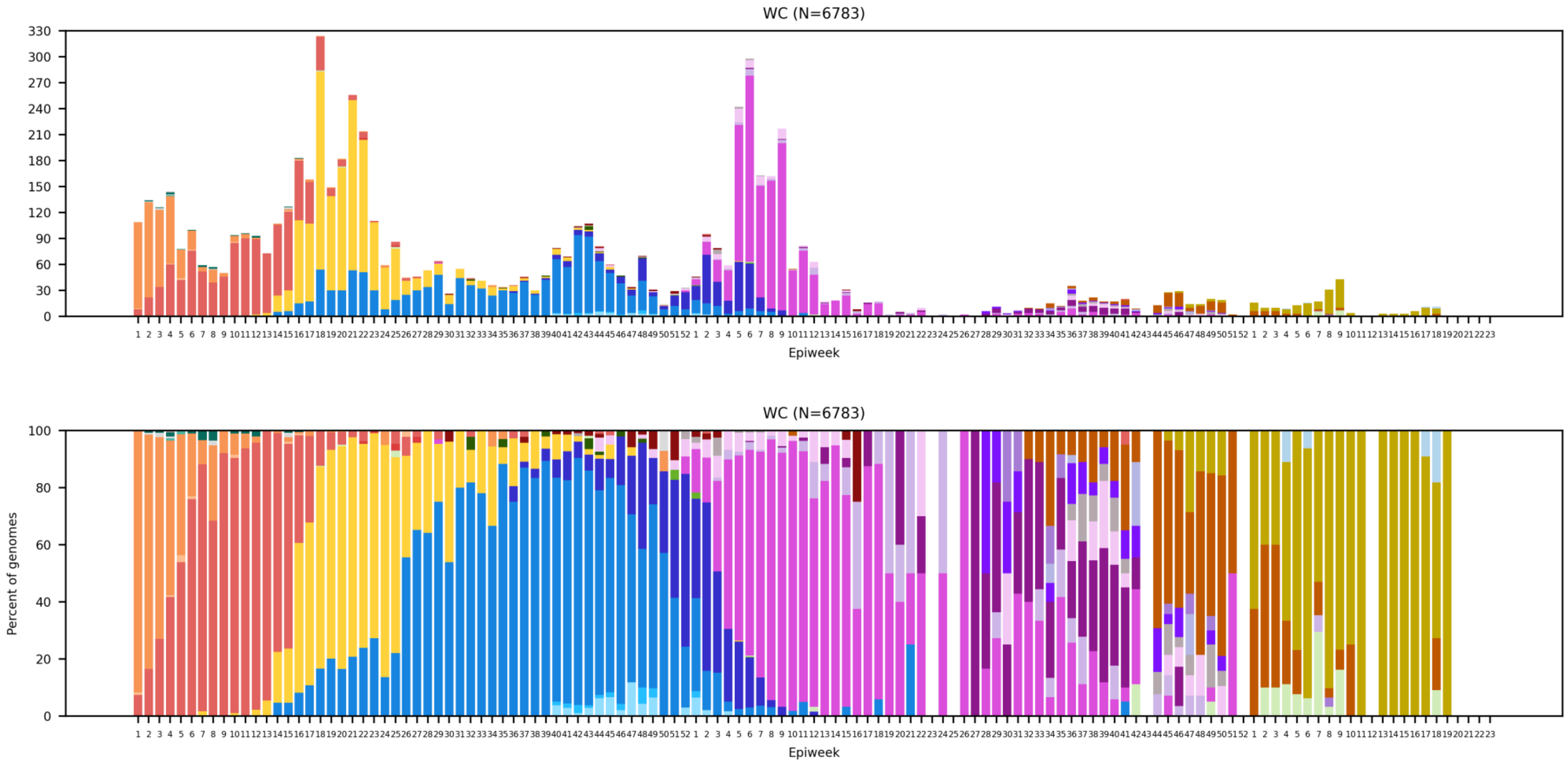
Western Cape Province, 2022-2024, n = 6783

Genomes added since last report: 43*



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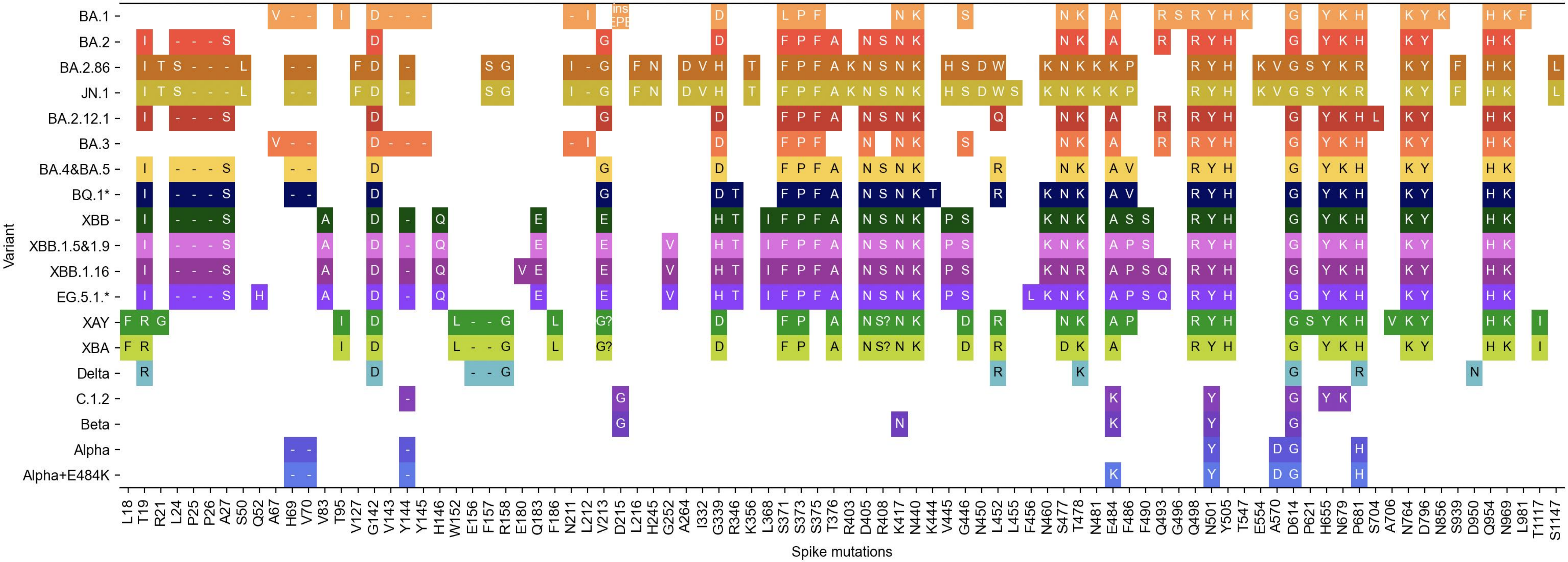
Summary

- **Sequencing update**
  - Testing for SARS-CoV-2 throughout the country is very low, and as a result few specimens are being submitted for sequencing
    - NGS-SA partners are working towards closing the delay to sequencing results during the coming months
  - Systematic testing from sentinel syndromic surveillance has however not indicated an increase in SARS-CoV-2 detections (WEEKLY RESPIRATORY PATHOGENS SURVEILLANCE REPORT WEEK - NICD)

- **Variant of Concern Omicron in South Africa**
  - The JN.1 lineage is currently the dominant lineage, accounting for 68% of all sequences in South Africa in February through May. BA.2.86 lineages (parent lineage of JN.1) are also being detected but declining in dominance due to JN.1
  - Recombinant XDD.1.1 (EG.5.1.1 and JN.1.1) has been detected in Gauteng (n=4) and the Western Cape (n=19) in January through May. It has a cumulative prevalence of <0.5% worldwide
  - JN.1.11.1.* lineages (specifically KP.1.1 and KP.2) have been detected in Gauteng (KP.2, n=1) and the Western Cape (KP.2, n=2 and KP.1.1, n=2)
    - The KP.2 lineage is currently increasing in prevalence in the USA

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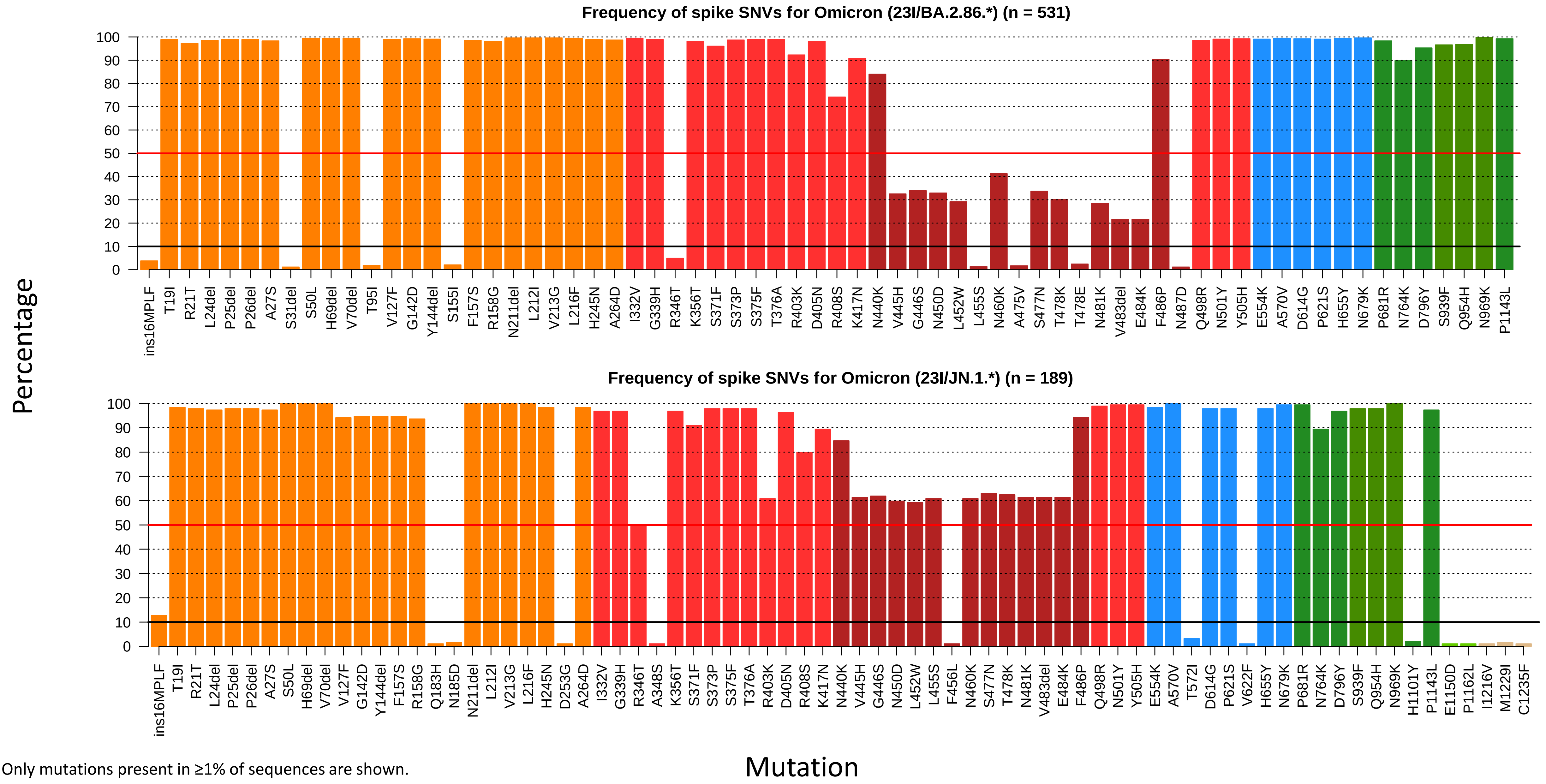
BA.2.86.* and JN.1.* spike mutations*



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

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

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

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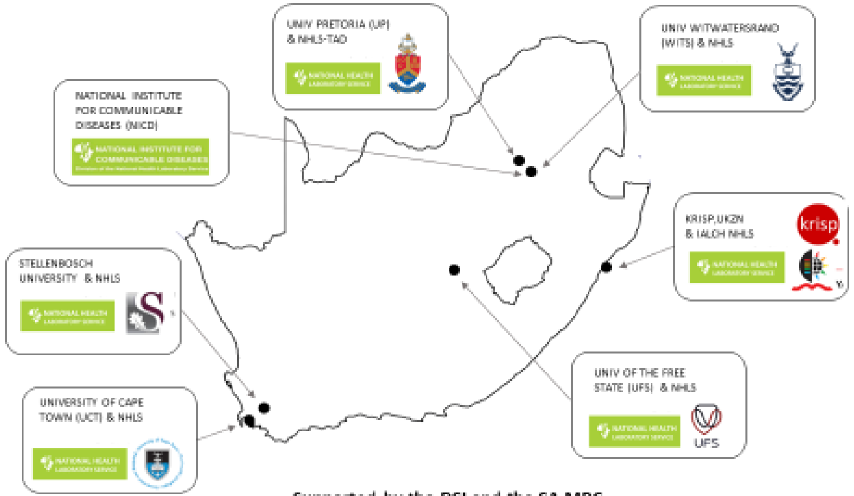

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EDCTP

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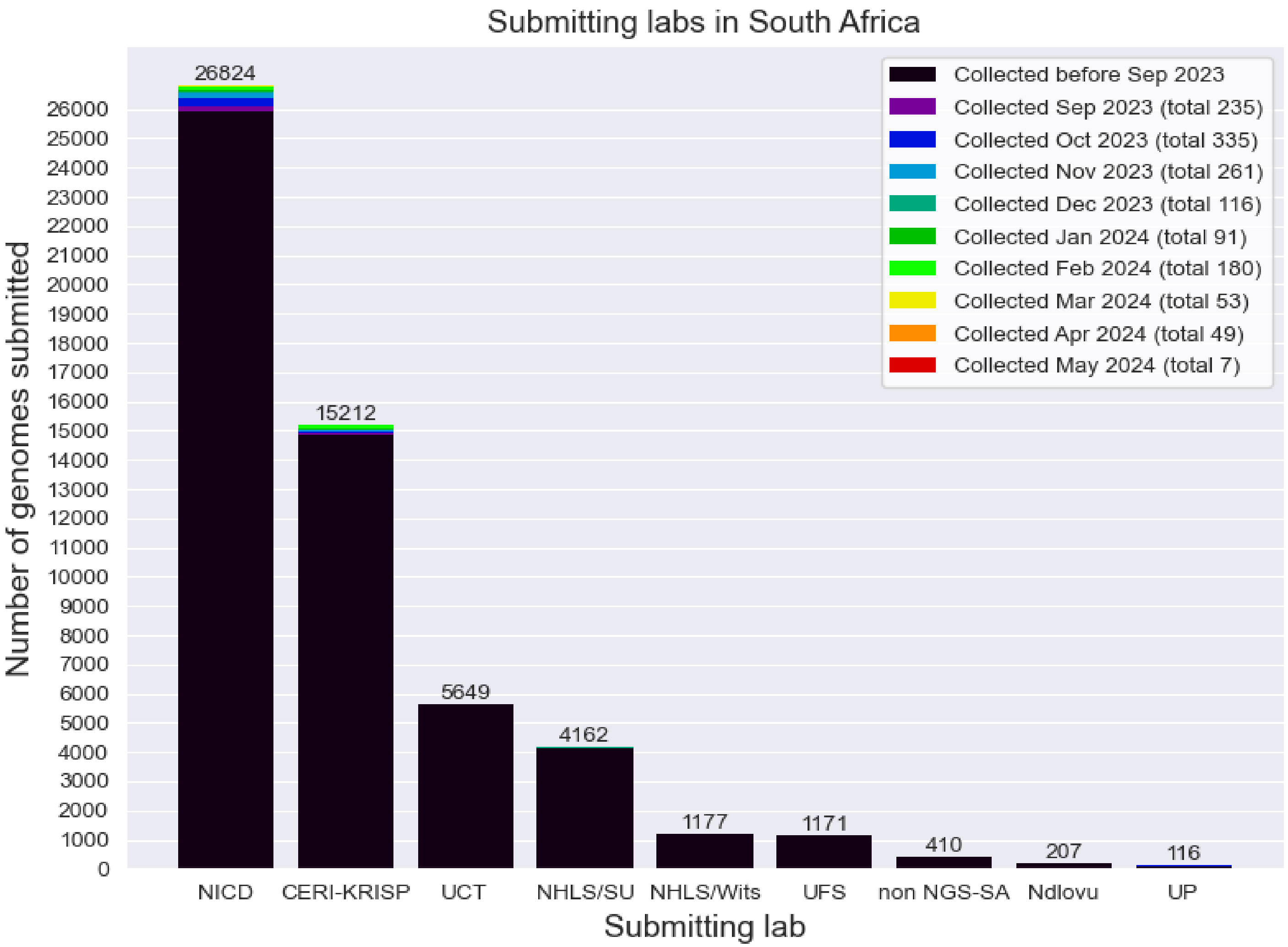
South African genomes submitted per submitting lab, 2020 - 2024 (N= 54 928)



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 (VOIs) (as of 3 May 2024)

Pango lineage	**Next strain clade**	**Genetic features**	**Earliest documented samples**	**Date of designation and risk assessments**
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[#]	24A	BA.2.86 + S:L455S	25-08-2023	18-12-2023 JN.1 Initial Risk Evaluation 18 December 2023 JN.1 Updated Risk Evaluation 9 February 2024 JN.1 Updated Risk Evaluation 15 April 2024

https://www.who.int/en/activities/tracking-SARS-CoV-2-variants/ accessed 07 June 2024

Currently circulating variants under monitoring (VUMs) (as of 3 May 2024)

Pango lineage	Next strain clade	Genetic features	Earliest documented samples	Date of designation
JN.1.7	Not assigned	JN.1 + S:T572I, S:E1150D	25-09-2023	03-05-2024
KP.2	Not assigned	JN.1 + S:R346T, S:F456L, S:V1104L	02-01-2024	03-05-2024
KP.3	Not assigned	JN.1 + S:F456L, S:Q493E, S:V1104L	11-02-2024	03-05-2024
JN.1.18	Not assigned	JN.1 + S:R346T	02-11-2023	03-05-2024

https://www.who.int/en/activities/tracking-SARS-CoV-2-variants/ accessed 07 June 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.)