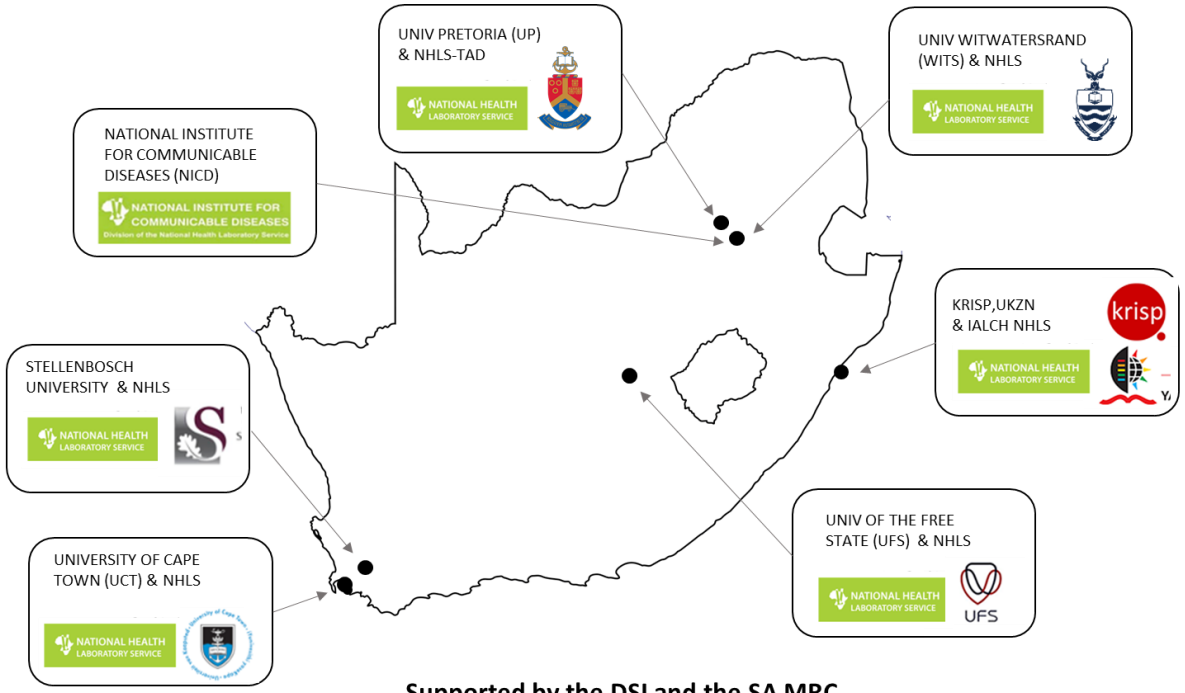
Network for Genomic Surveillance in South Africa (NGS-SA)

SARS-CoV-2 Sequencing Update
20 October 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)

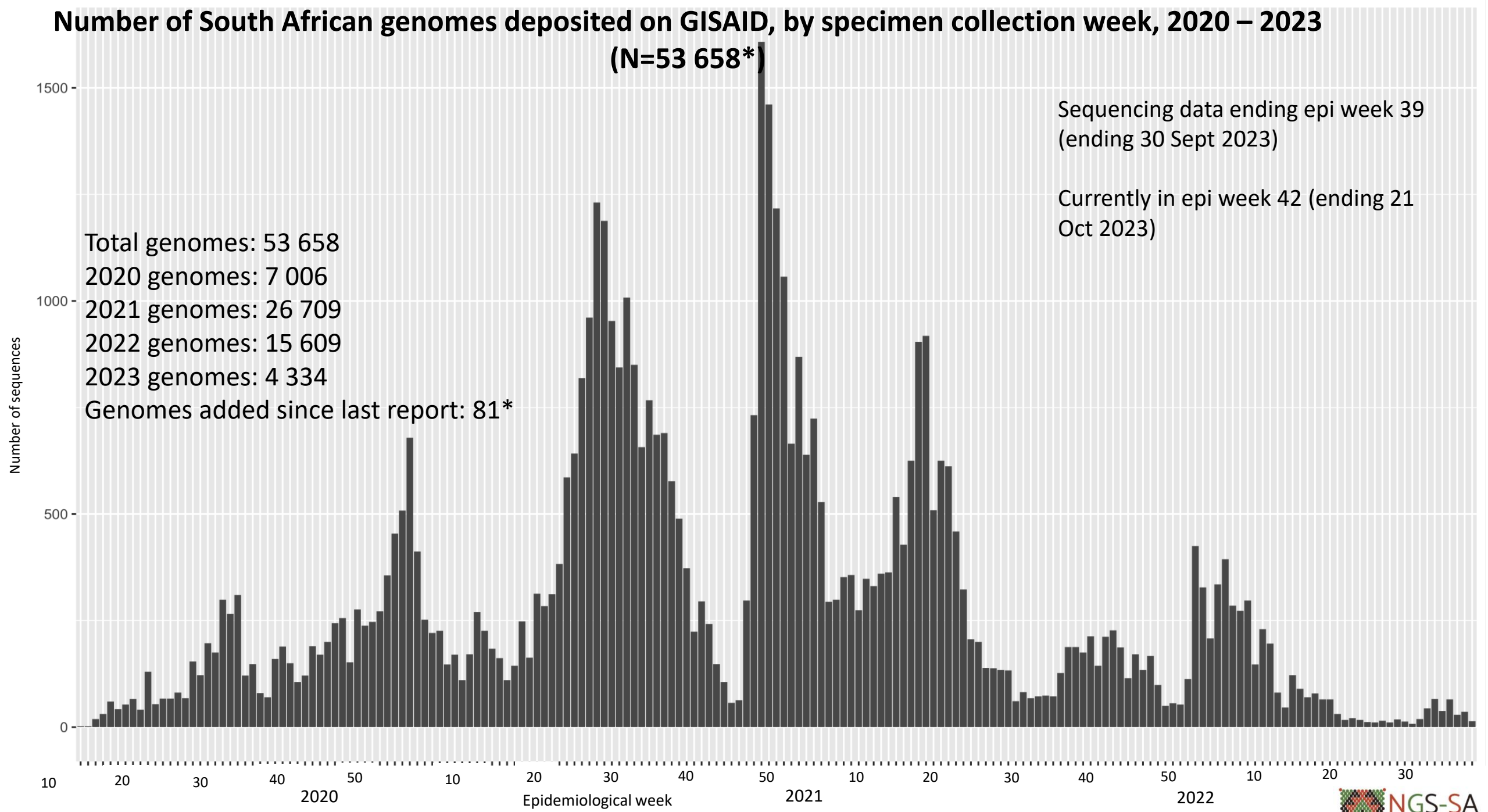
The genomic data presented here are based on South African SARS-CoV-2 sequence data downloaded from GISAID (www.gisaid.org) on 20 October 2023 at 13h00

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=53 658*)



*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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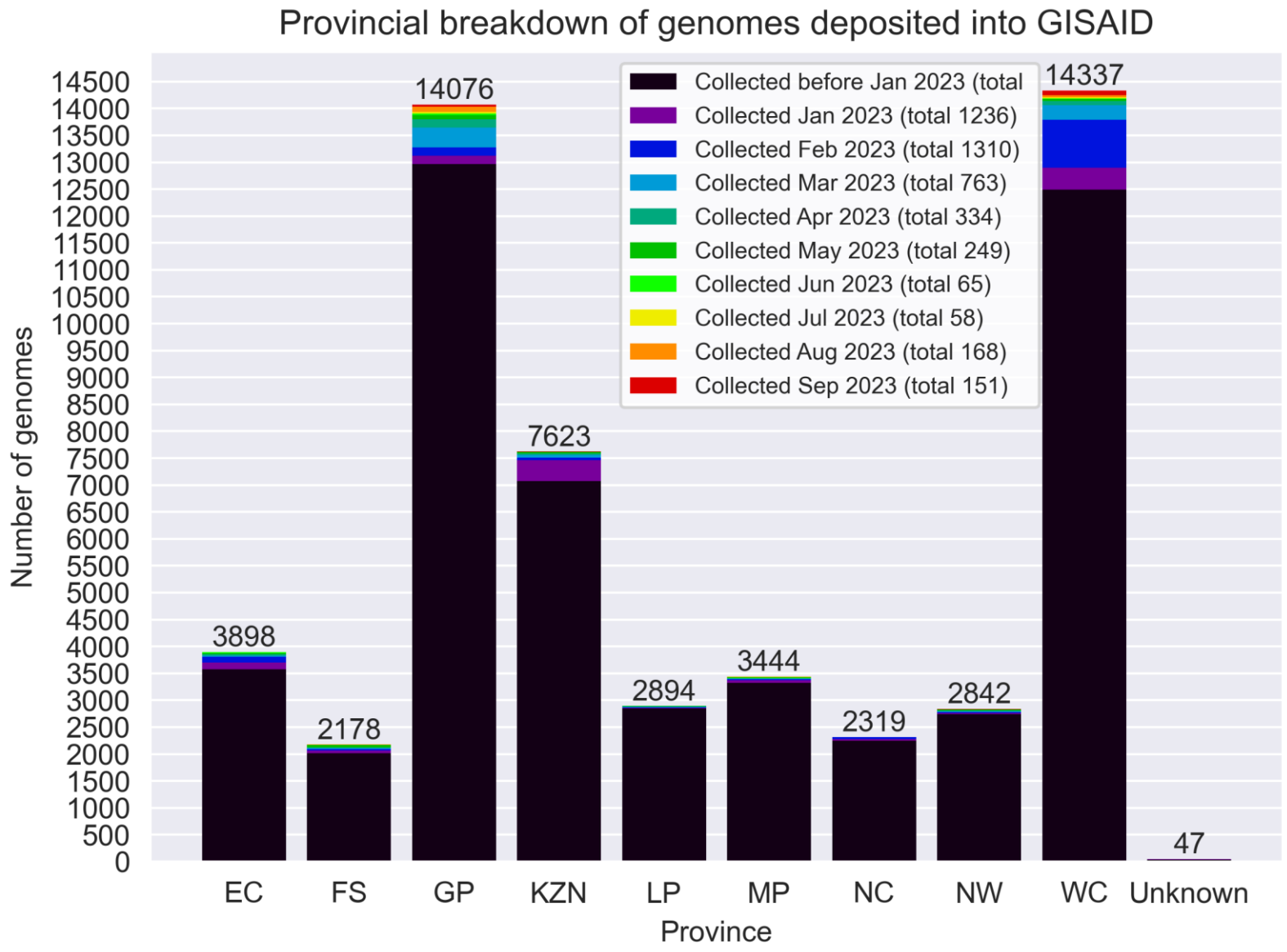
GISAID genomes vs total cases, 2020 – 2023 (N= 53 658)



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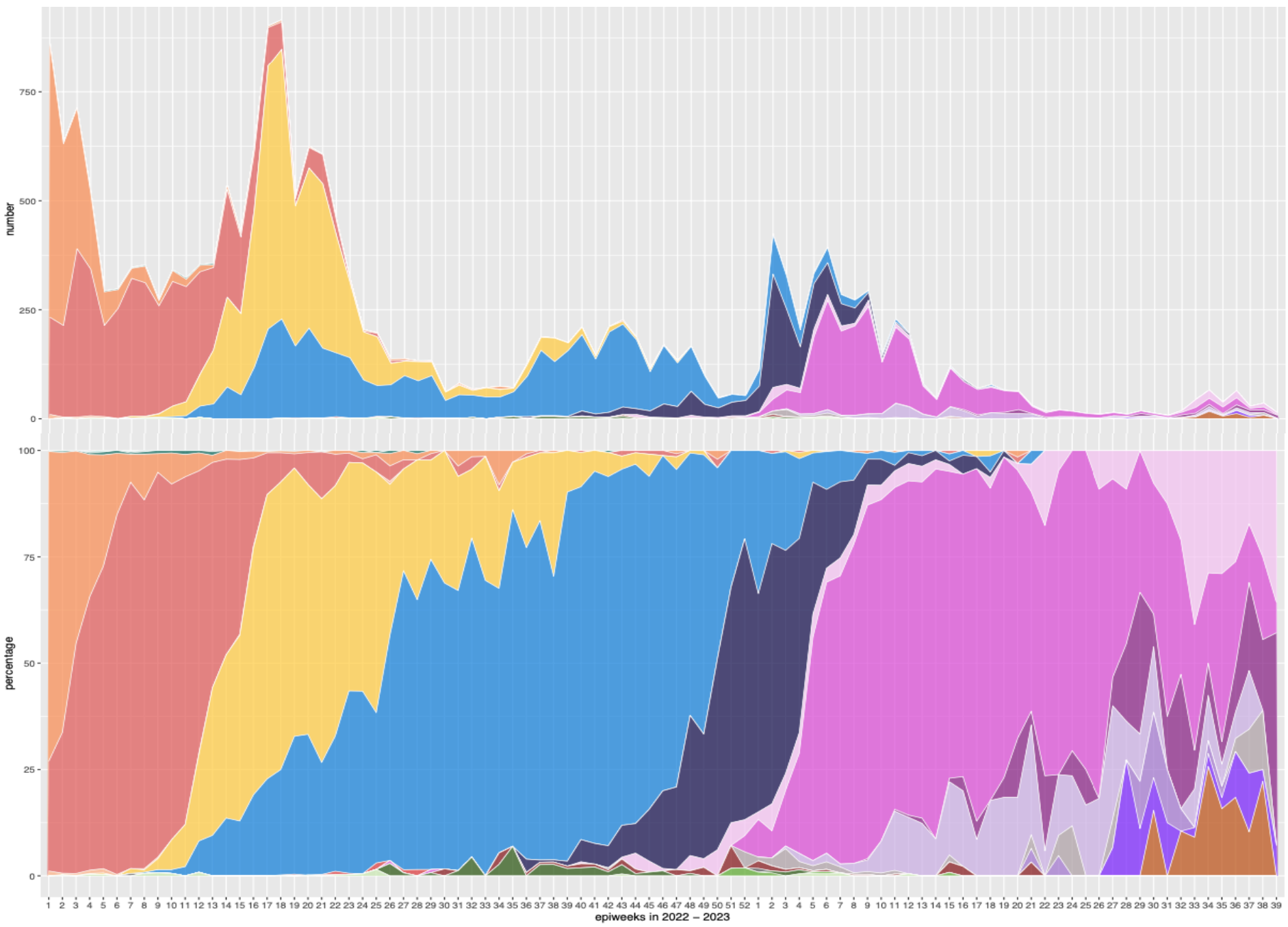
Number and percentage of clades by epiweek in South Africa, 2022-2023 (19 900*)



Sequencing data ending epi week 39 (ending 30 Sep 2023

Currently in epi week 42 (ending 21 Oct 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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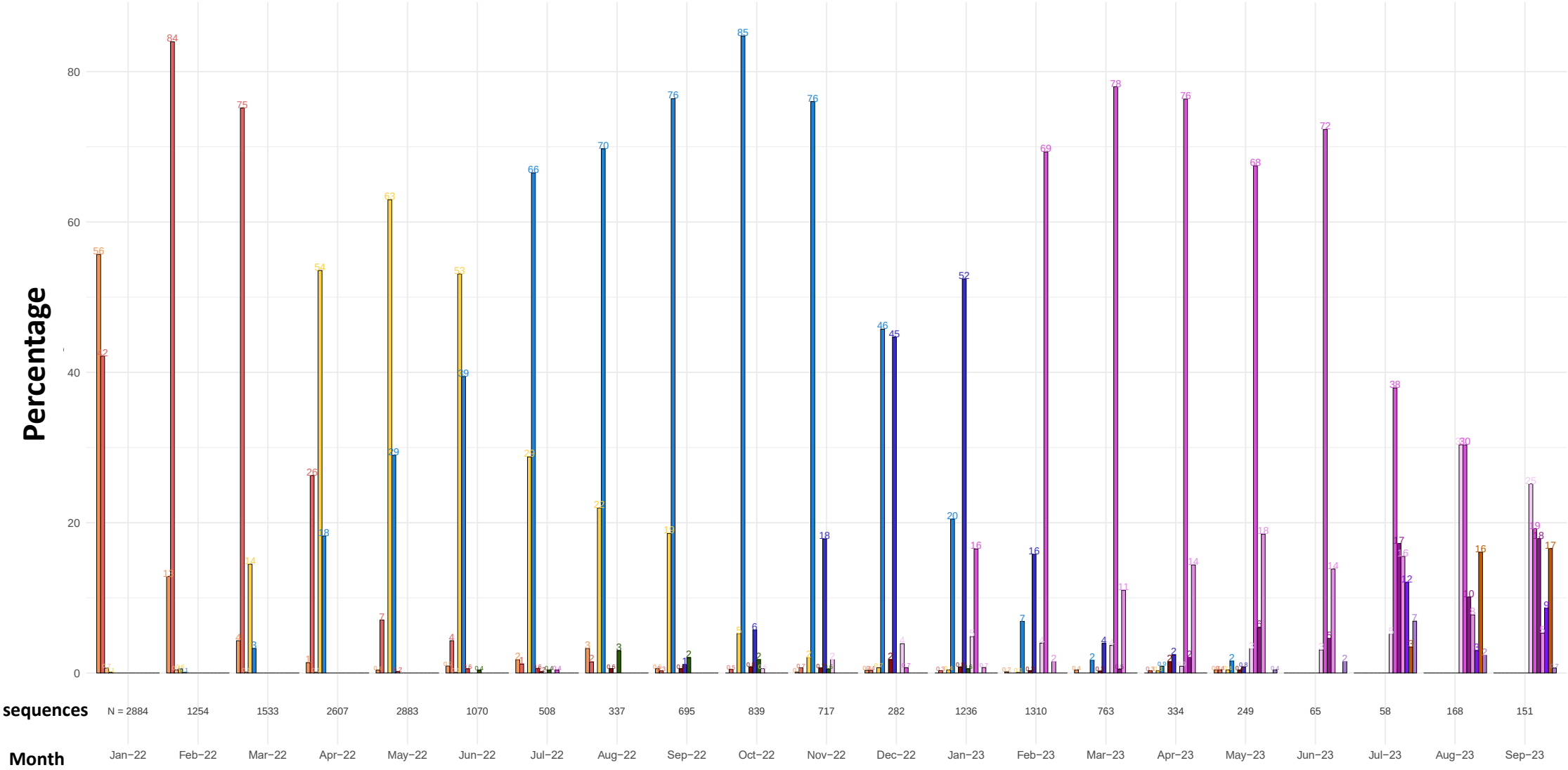
Detection Rates: Omicron and recombinants



Omicron (21K/BA.1.*)

Omicron (21M/BA.3)

Omicron (22D/BA.2.75.*)

Omicron (22B/BA.5)

XAY

Omicron (23A/XBB.1.5)

Omicron (23D/XBB.1.9.*)

Omicron (23D/BA.2.86)

Omicron (21L/BA.2.*)

Omicron (22C/BA.2.12.1)

Omicron (22A/BA.4)

Omicron (22E/BQ.1.*)

Omicron (22F/XBB.*)

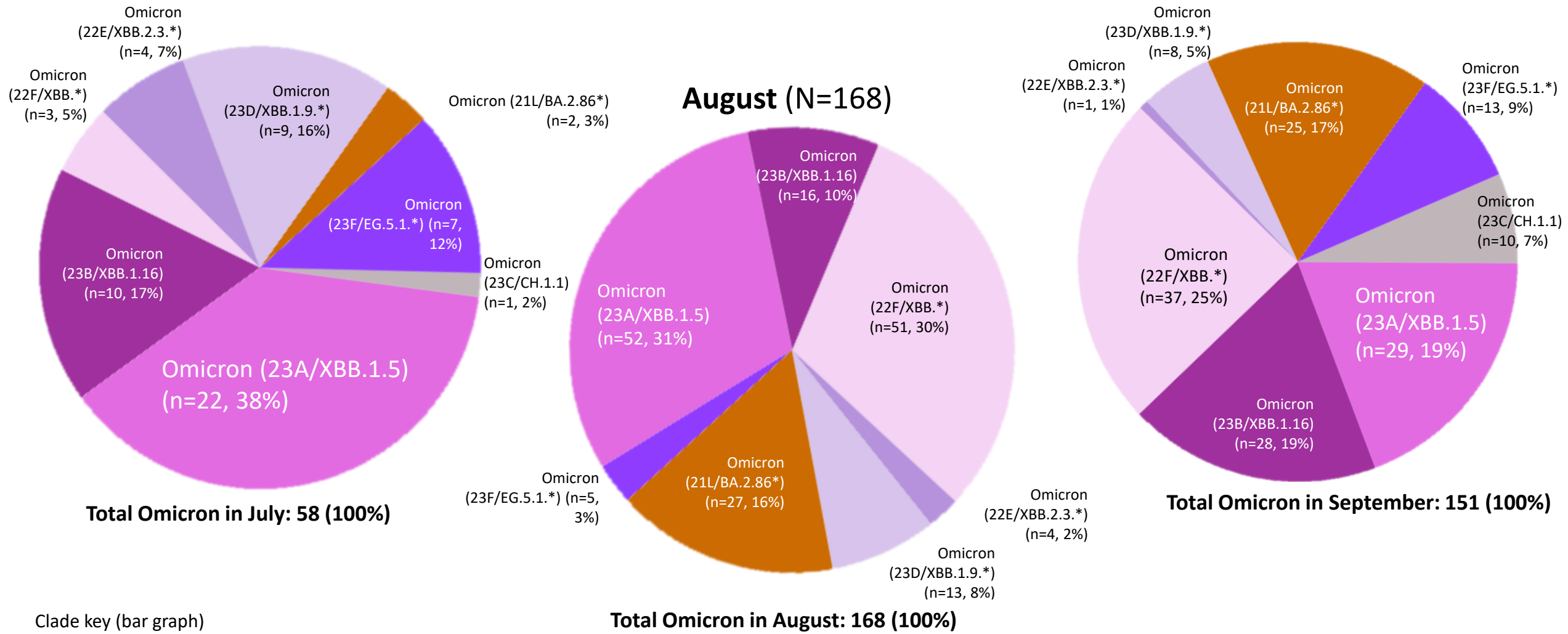
Omicron (23B/XBB.1.16)

Omicron (23F/EG.5.1.*)

Omicron (23E/XBB.2.3.*)

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

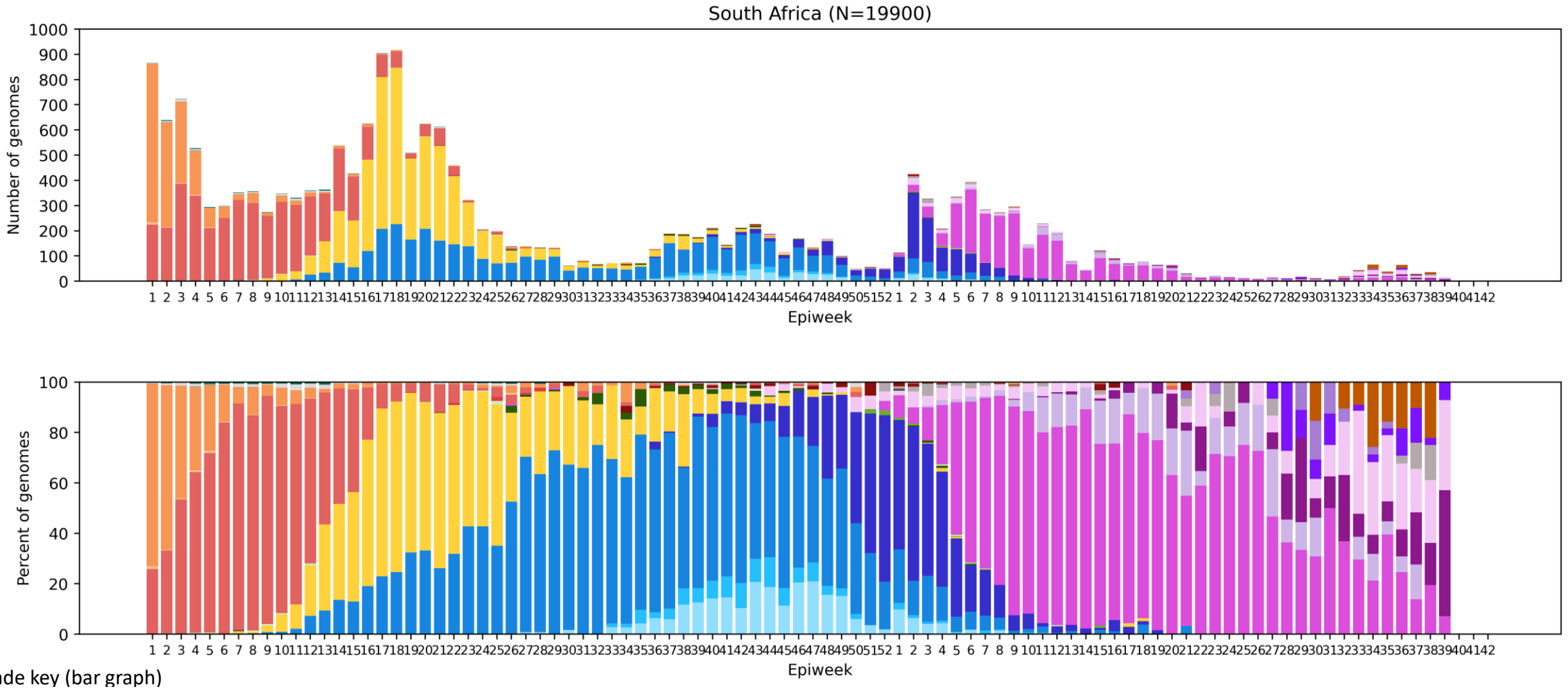
Prevalence of Variants of Concern (VOC) and Variants of Interest (VOI) in July – September 2023



Clade key (bar graph)

XAY	Omicron (23A/XBB.1.5)	Omicron (21L/BA.2.*)	Omicron (23F/EG.5.1.*)	Omicron (21M/BA.3)	Omicron (22B/BE.8)	Alpha (20I, V1)	C.1.2 (20D)
XBF	Omicron (23D/XBB.1.9.*)	Omicron (22C/BA.2.12.1)	Omicron (23E/XBB.2.3.*)	Omicron (22A/BA.4.*)	Omicron (22B/BA.5.*)	Beta (20H, V2)	20B
recombinant	Omicron (22F/XBB.*)	Omicron (22D/BA.2.75)	Omicron (21L/BA.2.86)	Omicron (22B/BE.7)	Omicron (22E/BQ.1.*)	Delta (21A, 21I, 21J)	unassigned
Omicron (23B/XBB.1.16)	Omicron (21K/BA.1.*)	Omicron (23C/CH.1.1.*)					

South Africa, 2022-2023, n = 19 900*



*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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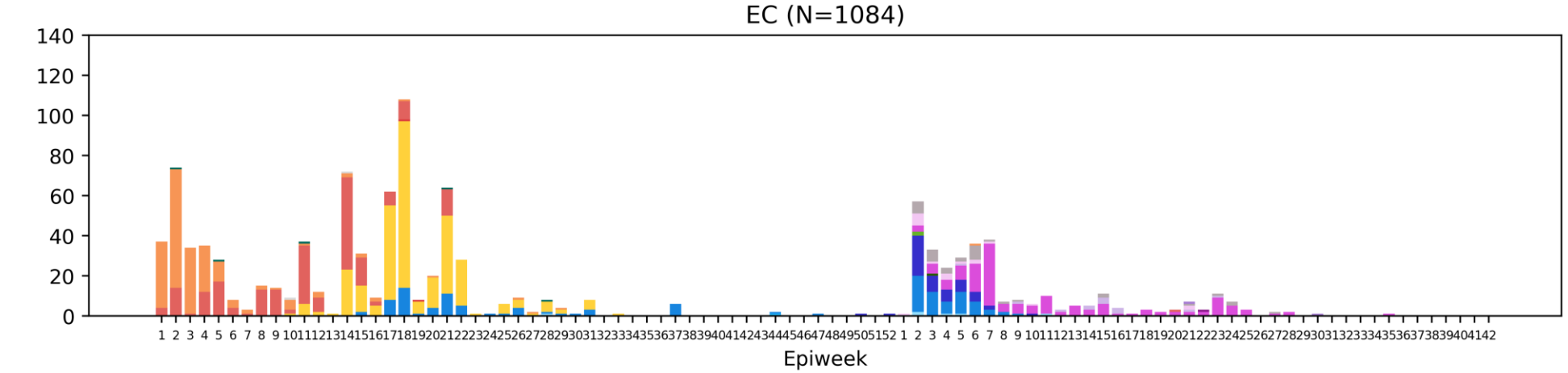
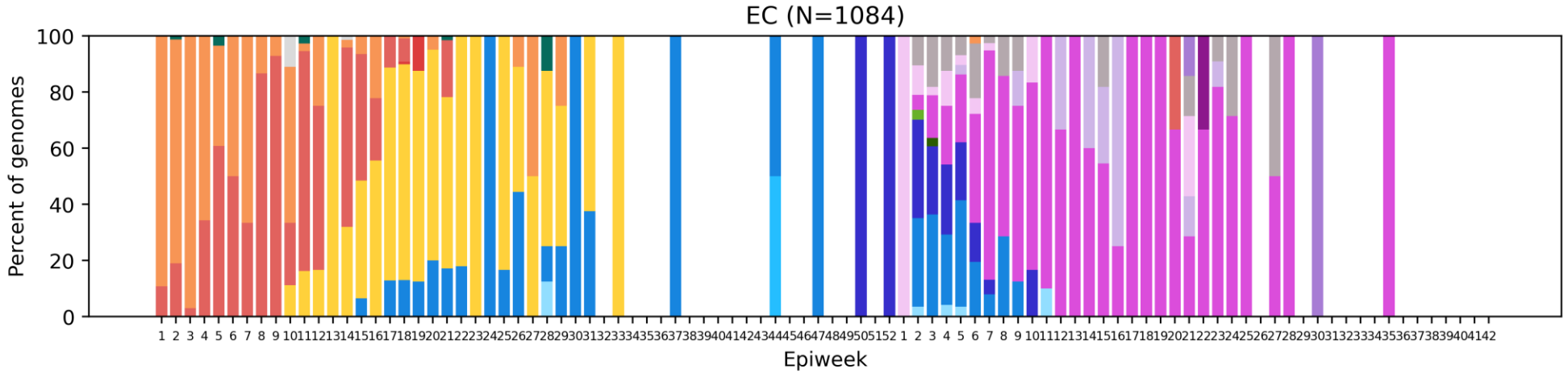
Eastern Cape Province, 2022-2023, n = 1084

Genomes added since last report: 0*





Clade key (bar graph)

XAY	Omicron (23A/XBB.1.5)	Omicron (21L/BA.2.*)	Omicron (23F/EG.5.1.*)	Omicron (21M/BA.3)	Omicron (22B/BE.8)	Alpha (20I, V1)	C.1.2 (20D)
XBF	Omicron (23D/XBB.1.9.*)	Omicron (22C/BA.2.12.1)	Omicron (23E/XBB.2.3.*)	Omicron (22A/BA.4.*)	Omicron (22B/BA.5.*)	Beta (20H, V2)	20B
recombinant	Omicron (22F/XBB.*)	Omicron (22D/BA.2.75)	Omicron (21L/BA.2.86)	Omicron (22B/BE.7)	Omicron (22E/BQ.1.*)	Delta (21A, 21I, 21J)	unassigned
Omicron (23B/XBB.1.16)	Omicron (21K/BA.1.*)	Omicron (23C/CH.1.1.*)					

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

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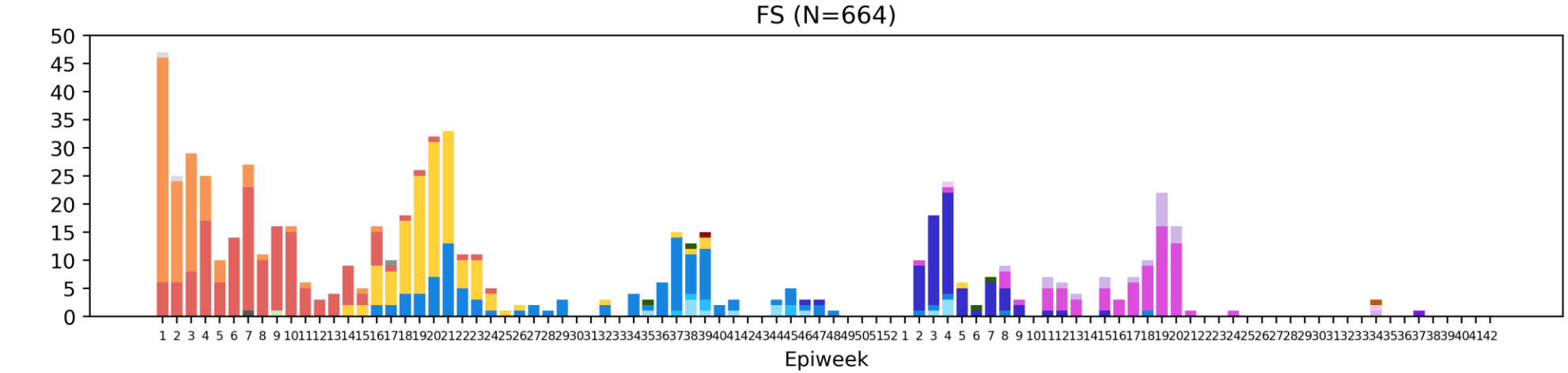
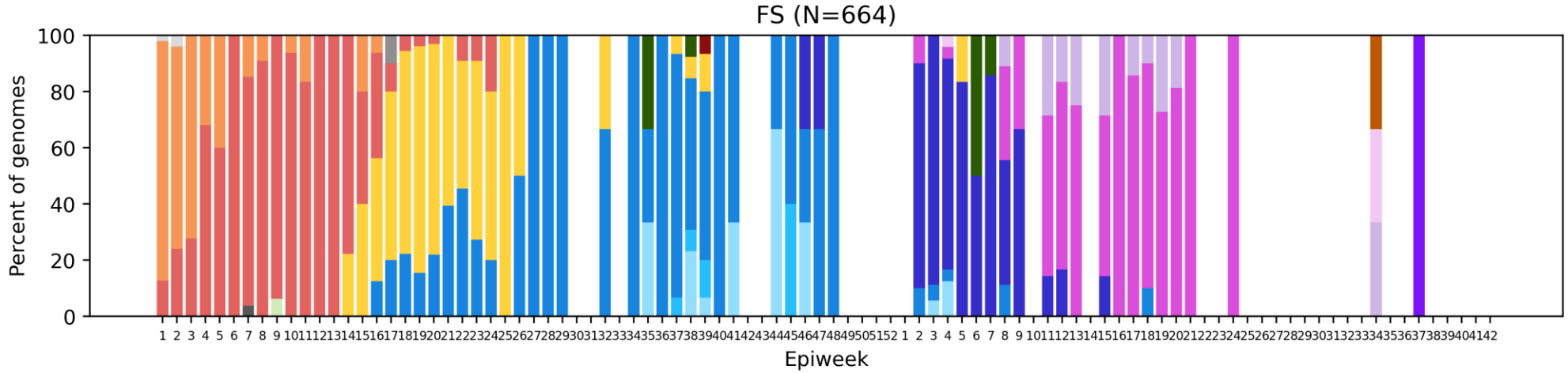
Free State Province, 2022-2023, n = 664

Genomes added since last report: 1*





Clade key (bar graph)

XAY	Omicron (23A/XBB.1.5)	Omicron (21L/BA.2.*)	Omicron (23F/EG.5.1.*)	Omicron (21M/BA.3)	Omicron (22B/BE.8)	Alpha (20I, V1)	C.1.2 (20D)
XBF	Omicron (23D/XBB.1.9.*)	Omicron (22C/BA.2.12.1)	Omicron (23E/XBB.2.3.*)	Omicron (22A/BA.4.*)	Omicron (22B/BA.5.*)	Beta (20H, V2)	20B
recombinant	Omicron (22F/XBB.*)	Omicron (22D/BA.2.75)	Omicron (21L/BA.2.86)	Omicron (22B/BE.7)	Omicron (22E/BQ.1.*)	Delta (21A, 21I, 21J)	unassigned
Omicron (23B/XBB.1.16)	Omicron (21K/BA.1.*)	Omicron (23C/CH.1.1.*)					

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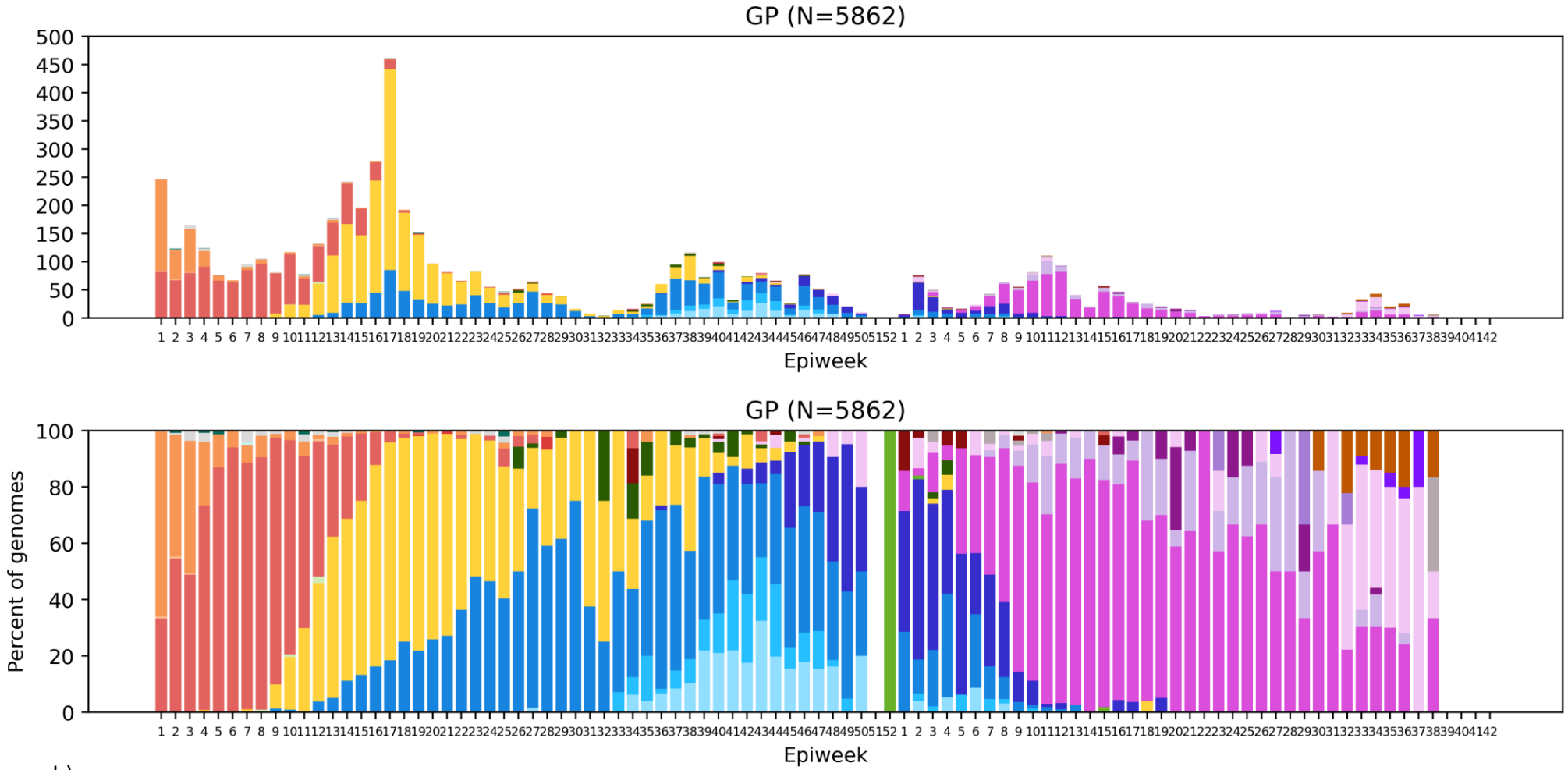
Gauteng Province, 2022-2023, n = 5862

Genomes added since last report: 7*



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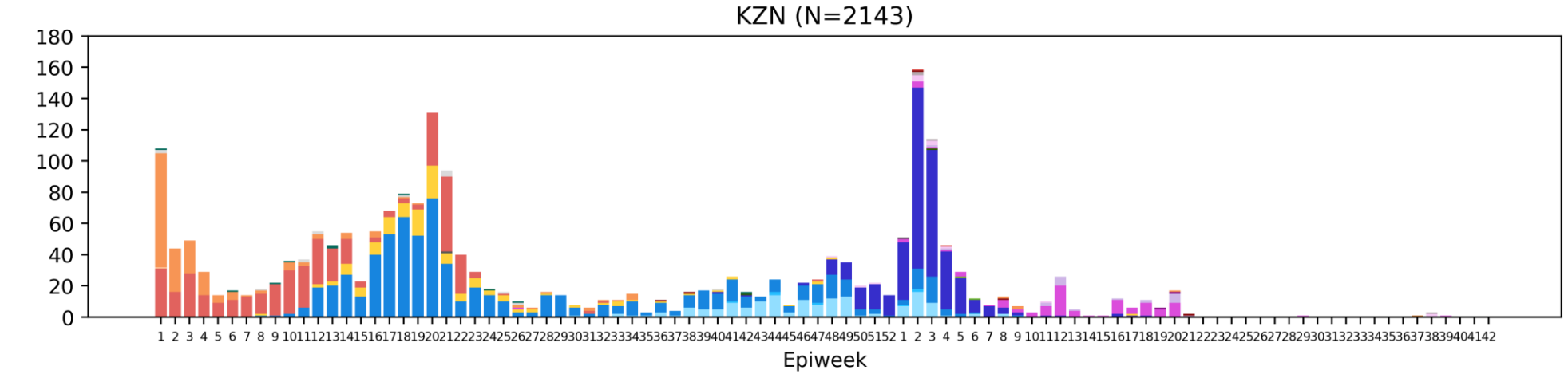
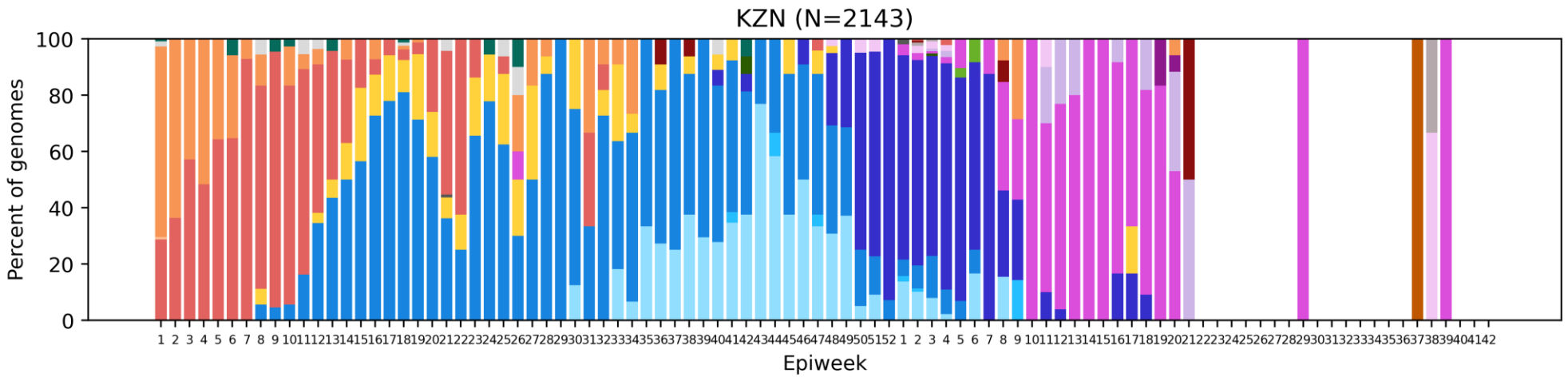
KwaZulu-Natal Province, 2022-2023, n = 2143

Genomes added since last report: 5*





Clade key (bar graph)

XAY	Omicron (23A/XBB.1.5)	Omicron (21L/BA.2.*)	Omicron (23F/EG.5.1.*)	Omicron (21M/BA.3)	Omicron (22B/BE.8)	Alpha (20I, V1)	C.1.2 (20D)
XBF	Omicron (23D/XBB.1.9.*)	Omicron (22C/BA.2.12.1)	Omicron (23E/XBB.2.3.*)	Omicron (22A/BA.4.*)	Omicron (22B/BA.5.*)	Beta (20H, V2)	20B
recombinant	Omicron (22F/XBB.*)	Omicron (22D/BA.2.75)	Omicron (21L/BA.2.86)	Omicron (22B/BE.7)	Omicron (22E/BQ.1.*)	Delta (21A, 21I, 21J)	unassigned
Omicron (23B/XBB.1.16)	Omicron (21K/BA.1.*)	Omicron (23C/CH.1.1.*)					

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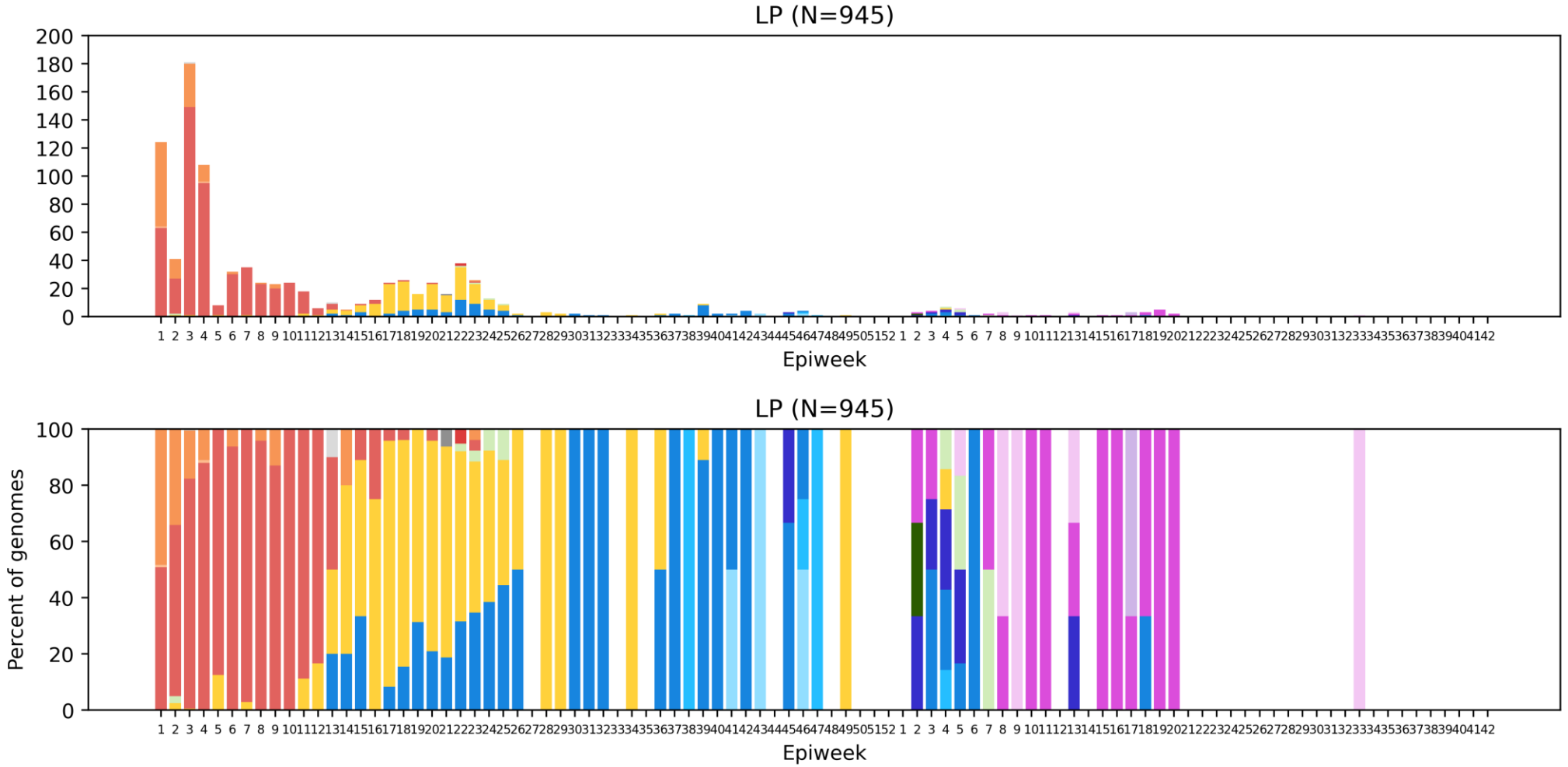
Limpopo Province, 2022-2023, n = 945

Genomes added since last report: 0*



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)
- Omicron (22D/BA.2.75)
- Omicron (23C/CH.1.1.*)
- Omicron (23F/EG.5.1.*)
- Omicron (23E/XBB.2.3.*)
- Omicron (21L/BA.2.86)
- Omicron (21M/BA.3)
- Omicron (22A/BA.4.*)
- Omicron (22B/BE.7)
- Omicron (22B/BE.8)
- Omicron (22B/BA.5.*)
- Omicron (22E/BQ.1.*)
- Alpha (20I, V1)
- Beta (20H, V2)
- Delta (21A, 21I, 21J)
- C.1.2 (20D)
- 20B
- unassigned

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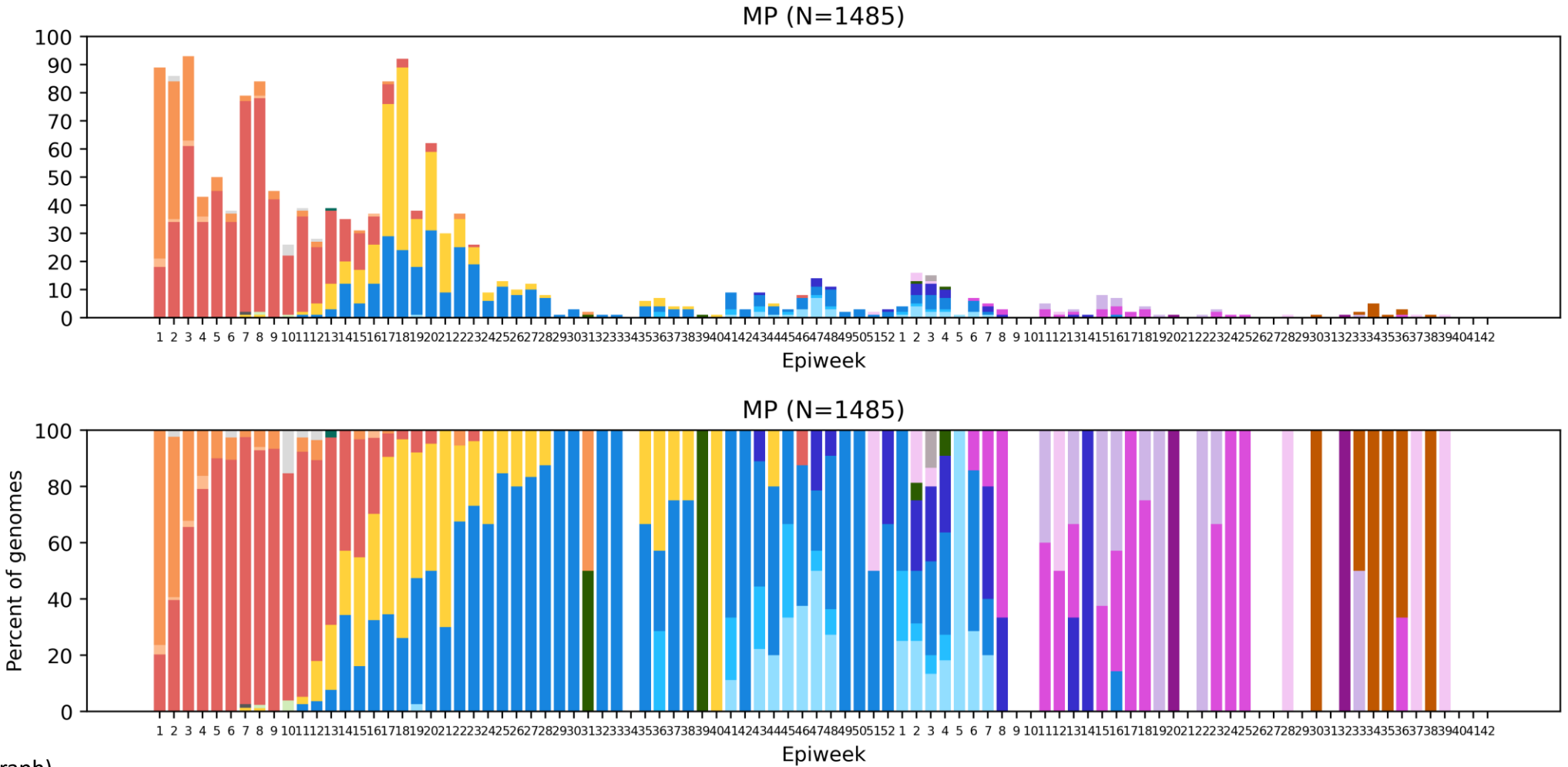
Mpumalanga Province, 2022-2023, n = 1485

Genomes added since last report: 5*



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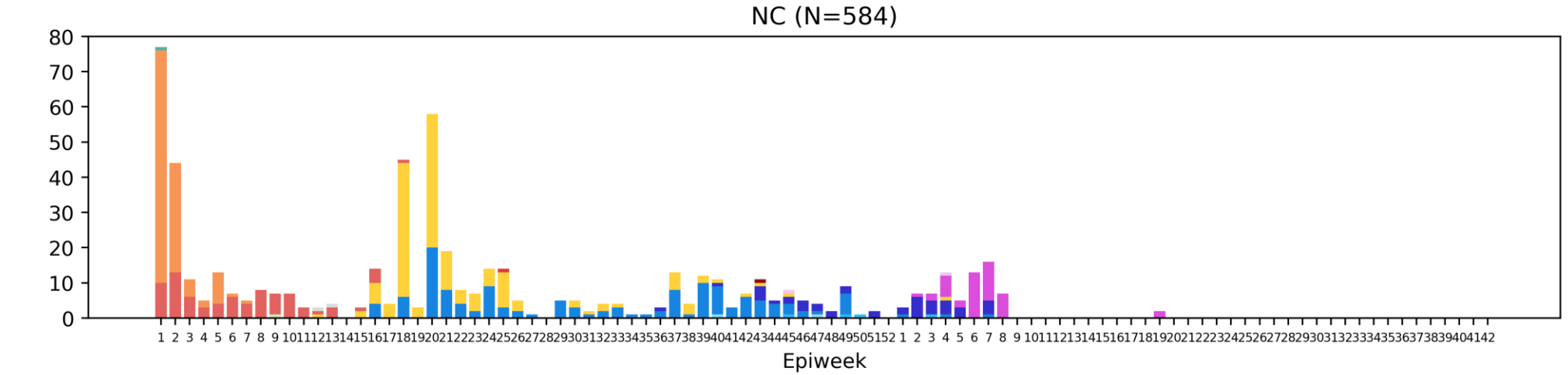
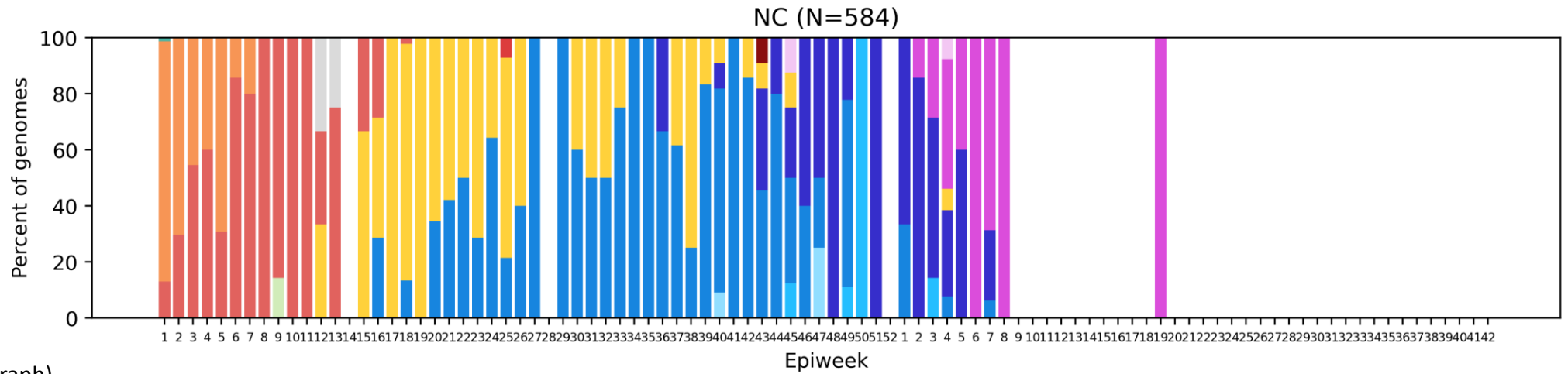
Northern Cape Province, 2022-2023, n = 584

Genomes added since last report: 0*





Clade key (bar graph)

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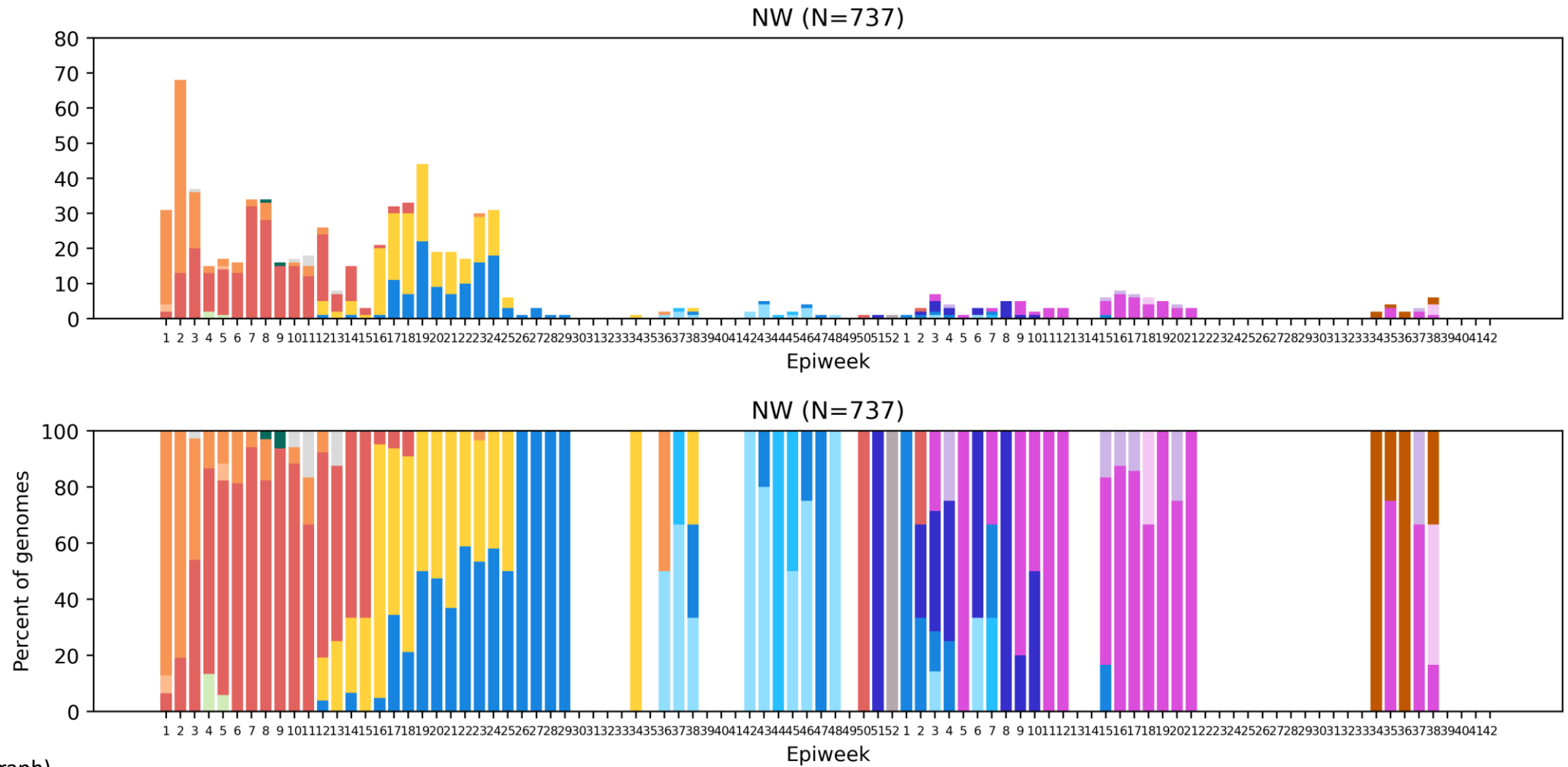
North West Province, 2022-2023, n = 737

Genomes added since last report: 10*



Clade key (bar graph)

XAY	Omicron (23A/XBB.1.5)	Omicron (21L/BA.2.*)	Omicron (23F/EG.5.1.*)	Omicron (21M/BA.3)	Omicron (22B/BE.8)	Alpha (20I, V1)	C.1.2 (20D)
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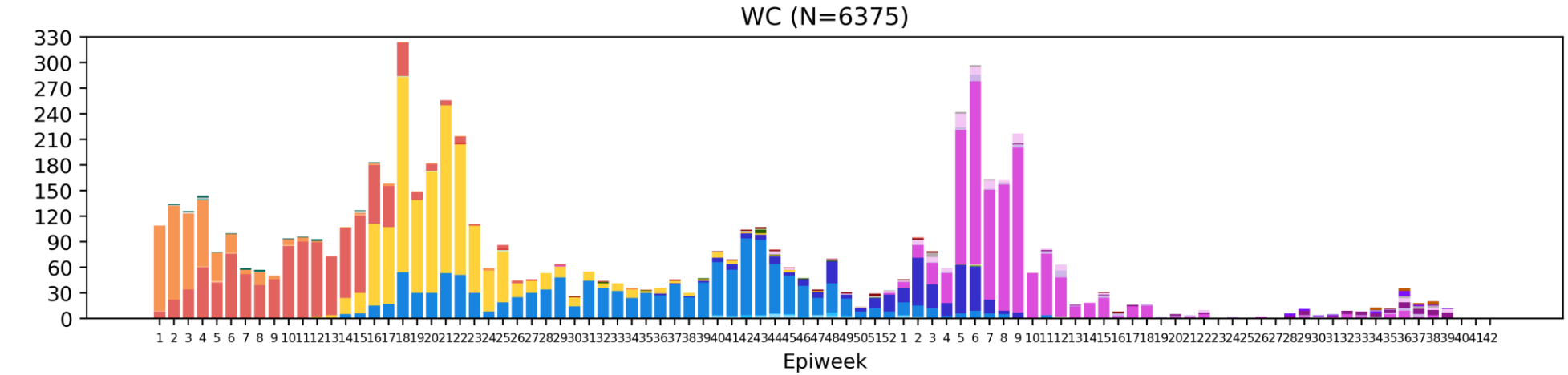
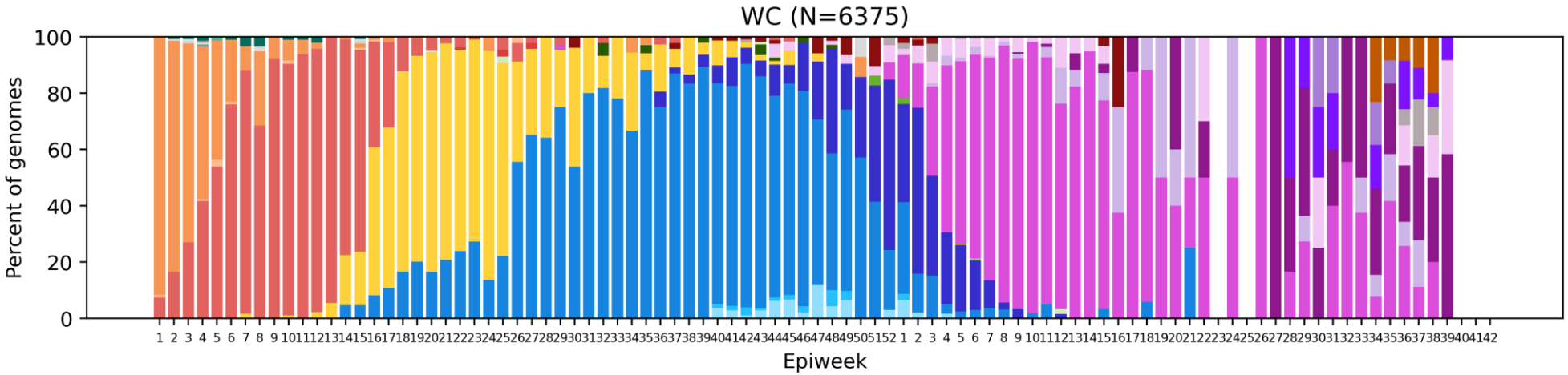
Western Cape Province, 2022-2023, n = 6375

Genomes added since last report: 53*





Clade key (bar graph)

XAY	Omicron (23A/XBB.1.5)	Omicron (21L/BA.2.*)	Omicron (23F/EG.5.1.*)	Omicron (21M/BA.3)	Omicron (22B/BE.8)	Alpha (20I, V1)	C.1.2 (20D)
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recombinant	Omicron (22F/XBB.*)	Omicron (22D/BA.2.75)	Omicron (21L/BA.2.86)	Omicron (22B/BE.7)	Omicron (22E/BQ.1.*)	Delta (21A, 21I, 21J)	unassigned
Omicron (23B/XBB.1.16)	Omicron (21K/BA.1.*)	Omicron (23C/CH.1.1.*)					

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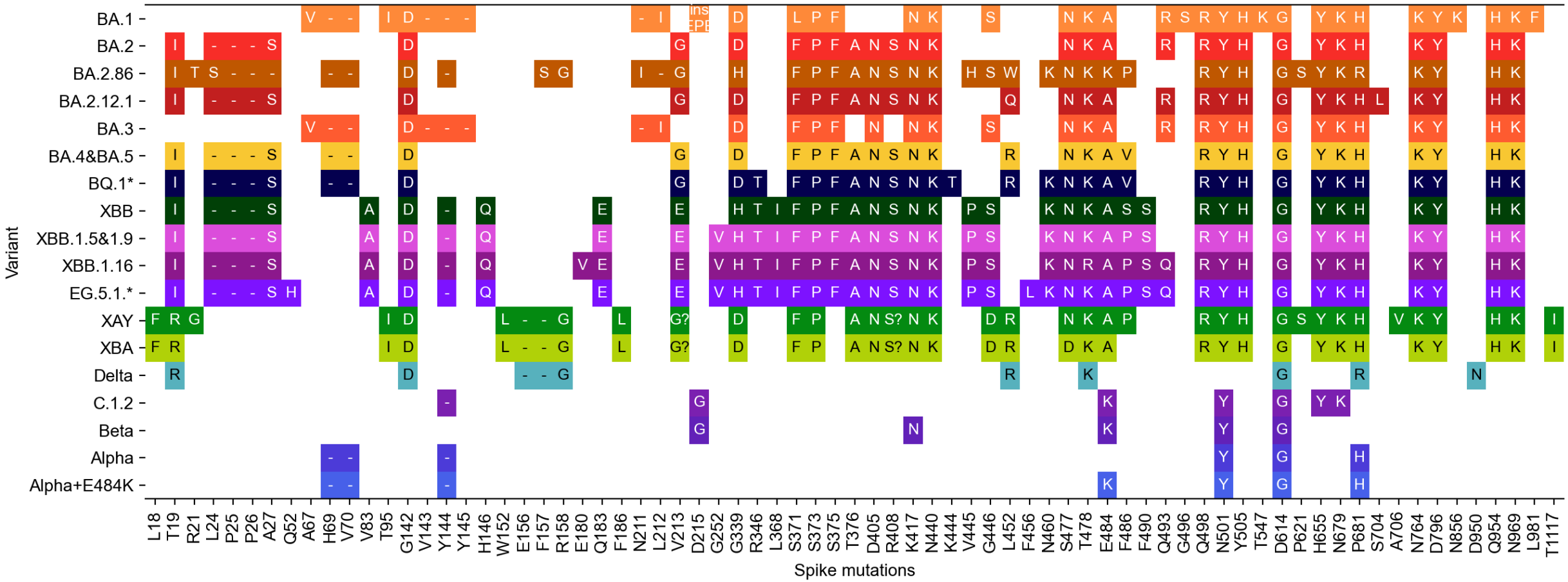
Summary

- **Sequencing update**
  - July sequences (n=58) are from the Eastern Cape, KwaZulu-Natal, Gauteng, Mpumalanga, and the Western Cape. August sequences (n=168) are from all provinces except Northern Cape and KwaZulu-Natal. September sequences (n=151) are from the Western Cape, Gauteng, Mpumalanga, Free State, KwaZulu-Natal, and North West.

- **Variant of Concern Omicron in South Africa**
  - Omicron dominated in July (100%), August (100%), and September (100%)
  - XBB.1.5 constituted 38% of July, 31% of August and 19% of September sequences
  - XBB.1.16 has been detected in July (17%), August (16%), and September (19%)
  - XBB.1.9.* (clade 23D) was detected in sequences from July (16%), August (8%) and September (5%)
  - Twenty-five sequences of the EG.5.1.* lineage (clade 23F) have been detected in Gauteng (n=5), Western Cape (n=19), and Free State (n=1) in July (n=7), August (n=5), and September (n=13)
  - Fifty-four sequences of the BA.2.86 lineage have been detected in Gauteng (n=21), Mpumalanga (n=11), Western Cape (n=13), North West (n=7), KwaZulu-Natal (n=1) and Free State (n=1), and the lineage constituted 3% of sequences in July, 16% in August and 17% in September

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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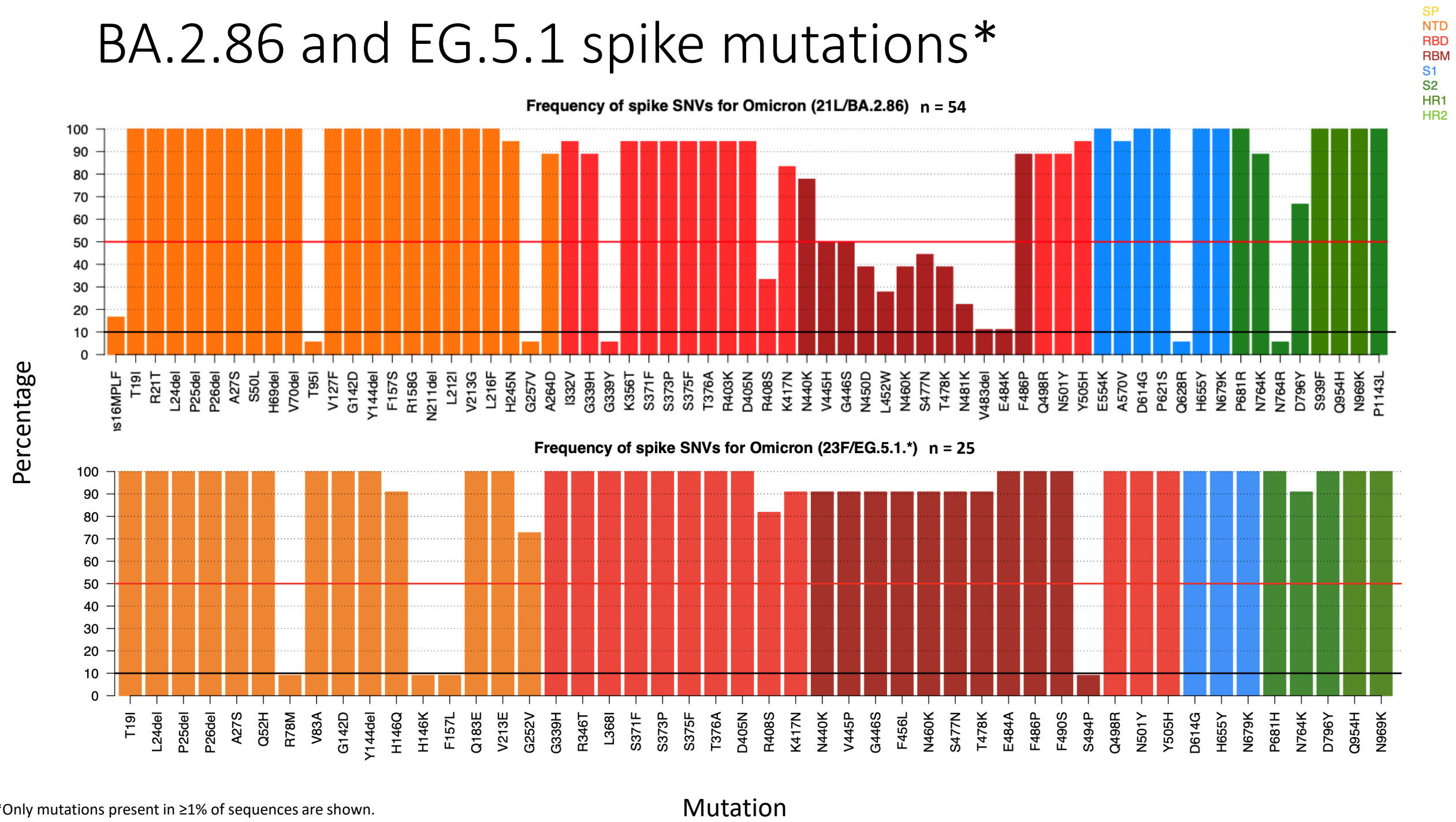
BA.2.86 and EG.5.1 spike mutations*



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

University of Stellenbosch & NHLS Tygerberg Virology

Susan Engelbrecht
Wolfgang Preiser
Gert van Zyl
Tongai Maponga
Bronwyn Kleinhans
Shannon Wilson
Karabo Phadu
Tania Stander
Kamela Mahlakwane
Mathilda Claassen
Diagnostic laboratory staff

UKZN-Inkosi Albert Luthuli Central Hospital

Dr Khanyi Msomi
Dr Kerusha Govender
Dr Pravi Moodley
Dr Aabida Khan
Dr Lili Gounder
Dr Kerri Francois
Dr Cherise Naicker
Dr Joedene Chetty
Dr Neli Ngcaba
Dr Tshepiso Mosito
Mr Malcolm Ellapen
Mr Kubendran Reddy
The COVID-19 Bench team

University of KwaZulu-Natal & Africa Health Research Institute

KRISP at UKZN:
Tulio de Oliveira
Richard Lessels
Houriiyah Tegally
Eduan Wilkinson
Jennifer Giandhari
Sureshnee Pillay
Emmanuel James San

AHRI
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University of Cape Town, NHLS & Western Cape Government

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Theuns Jacobs
Erna Morden

NHLS Greenpoint
Annabel Enoch

This project has received funding from the European Union's Horizon Europe Research and Innovation Actions under grant No. 101046041

UCT, IDM and CIDRI-Africa
Deelan Doolabh
Arash Iranzadeh
Lynn Tyers
Innocent Mudau
Nokuzola Mbhele
Fezokuhle Khumalo
Thabang Serakge
Bruna Galvão
Arghavan Alisoltani
(U. California)
Robert Wilkinson
Darren Martin
Nicola Mulder
Wendy Burgers
Ntobeko Ntusi
Rageema Joseph
Sean Wasserman
Linda Boloko

Zoonotic arbo and respiratory virus program
Centre for Viral Zoonoses
Department Medical Virology/ NHLS Tshwane Academic division
University of Pretoria

ZARV research program/UP
Marietjie Venter (Head: ZARV)
Adriano Mendes (Postdoc)
Amy Strydom (Postdoc)
Michaela Davis (MSc, intern medical scientist)
Carien van Niekerk

NHLS Tshwane
Prof Simnikiwe Mayaphi (HOD)

Funders:
GIZ/BMBF: African Network for Improved diagnostics and epidemiology of common and emerging infectious agents (ANDEMIA)
G7 Global Health fund, Robert Koch Institute, Dr Fabian Leendertz

National Institute for Communicable Diseases

Centre for Respiratory Diseases & Meningitis
Anne von Gottberg
Thabo Mohale
Daniel Amoako
Josie Everatt
Boitshoko Mahlangu
Noxolo Ntuli
Anele Mnguni
Amelia Buys
Cardia Fourie
Noluthando Duma
Linda de Gouveia
Jackie Kleynhans
Nicole Wolter
Sibongile Walaza
Mignon du Plessis
Stefano Tempia
Mvuyo Makhasi
Cheryl Cohen

Centre for HIV and STIs
Jinal Bhiman
Cathrine Scheepers
Constantinos Kurt Wibmer
Thandeka Moyo
Tandile Hermanus
Frances Ayres
Zanele Molaudzi
Bronwen Lambson
Tandile Hermanus
Mashudu Madzivhandila
Prudence Kgagudi
Brent Oosthuysen
Penny Moore
Lynn Morris

Sequencing Core Facility
Zamantungwa Khumalo
Annie Chan
Morne du Plessis
Stanford Kwenda
Phillip Senzo Mtshali
Mushal Allam
Florah Mnyameni
Arshad Ismail

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

University of the Free State

UFS
Dominique Goedhals
Armand Bester
Martin Myaga
Peter Mwangi
Emmanuel Ogunbayo
Milton Mogotsi
Makgotso Maotoana
Lutfiyya Mohamed

NHLS Division of Virology
Sabeehah Vawda
Felicity Burt
Thokozani Mkhize
Diagnostic laboratory staff

NGS-SA
Network for Genomic Surveillance in South Africa

Additional support and collaborators

NHLS
Koleka Mlisana
Zinhle Makatini
Eugene Elliot
Florette K. Treurnicht
Kathleen Subramoney
Oluwakemi Laguda-Akingba
Shareef Abrahams
Greta Hoyland
Gloria Selabe
Elias Bereda
Jeannette Wadula

Hyrax Biosciences
Simon Travers

Cape Town HVTN Laboratory
Erica Anderson-Nissen
Anneta Naidoo

Ndlovu Research
Hugo Tempelman
CJ Umunnakwe

Lancet
Allison J. Glass
Raquel Viana

Ampath
Terry Marshall
Cindy van Deventer
Eddie Silberbauer

Pathcare Vermaak
Andries Dreyer
Howard Newman
Riaan Writes
Marianne Wolfaardt
Warren Lowman

Bridge-the-Gap
Raymond Rott

Cytespace Africa Laboratories
Christa Viljoen

ARC-OVI
Lia Rotherham

CAPRISA
Salim Abdool Karim
Nigel Garret

UKZN - Big Data
Francesco Pettruccione
Ilya Sinayskiy

University of Oxford
José Lourenço

FioCruz, Brazil
Vagner Fonseca
Marta Giovanetti
Luiz Carlos Junior Alcantara

Africa CDC and Africa PGI
John Nkengasong
Sofonias Tessema

Netcare
Richard Friedland
Craig Murphy
Caroline Maslo
Liza Sitharam

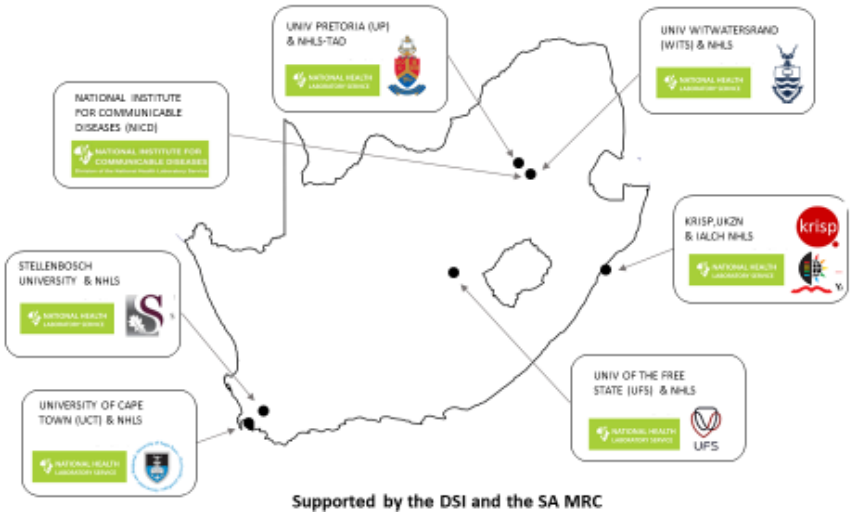
DSI
Glaudina Loots

SA MRC
Glenda Gray

Pathcare N1 City
Jean Maritz
Nadine Cronje
Petra Raimond
Kim Hoek

NGS-SA

Network for Genomic Surveillance in South Africa



Supported by the DSI and the SA MRC

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UNIVERSITY OF PRETORIA
YUNIBESITHI YA PRETORIA

UNIVERSITEIT iYUNIVESITHI STELLENBOSCH UNIVERSITY

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

UFS

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Division of the National Health Laboratory Service

EDCTP

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

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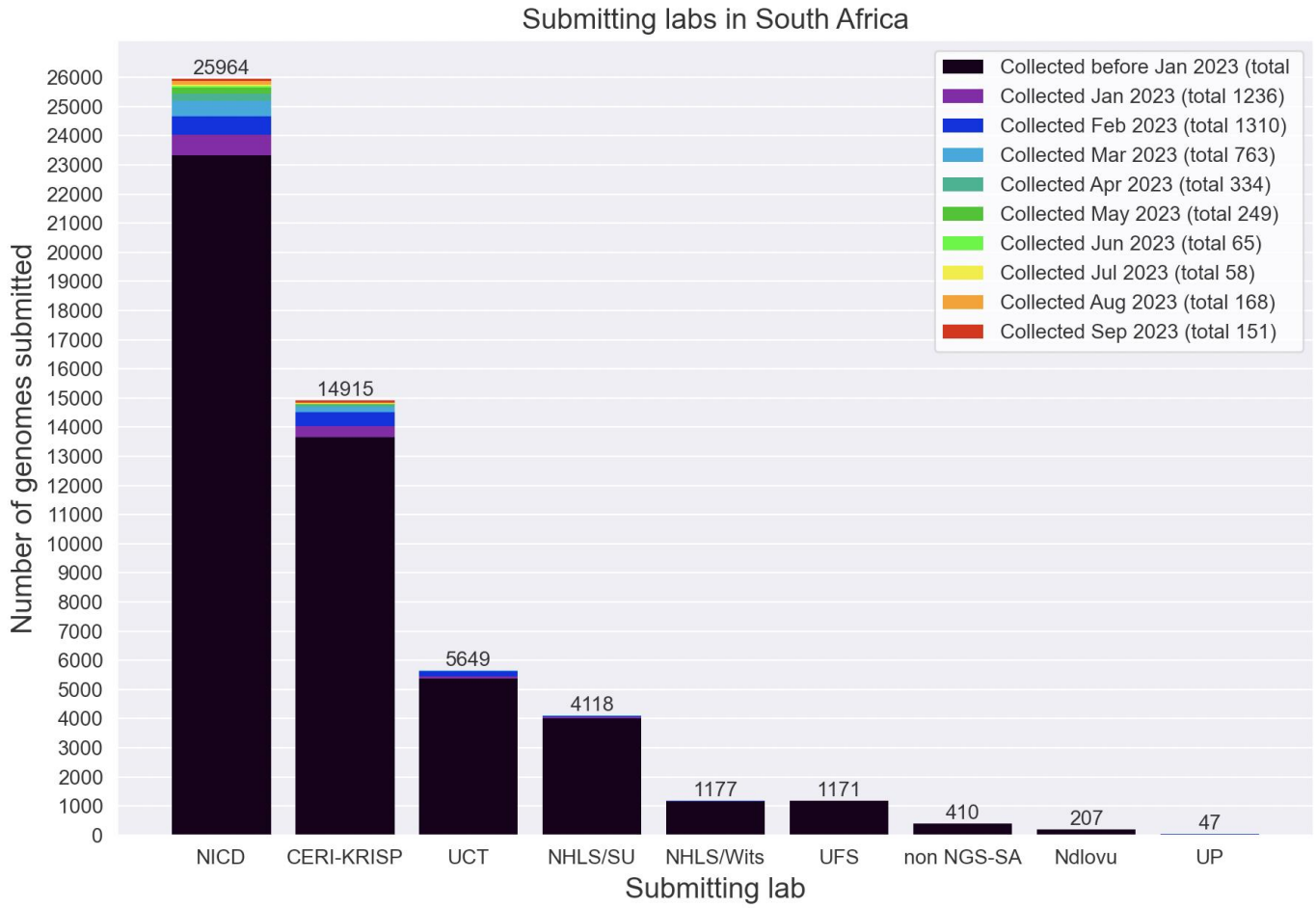
INYUVESI YAKWAZULU-NATALI

NATIONAL HEALTH LABORATORY SERVICE

South African genomes submitted per submitting lab, 2020 - 2023 (N= 53 658)



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.

NGS-SA
Network for Genomic Surveillance in South Africa

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.)