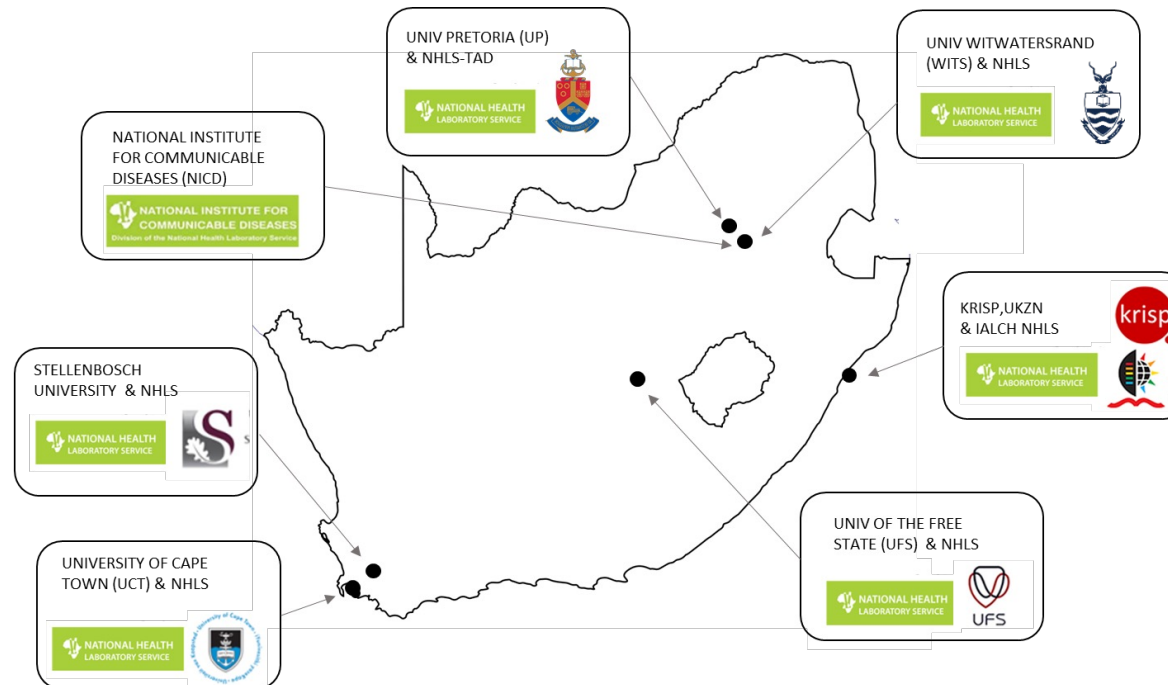


SARS-CoV-2 Sequencing Update 14 July 2023



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) on 14 July 2023 at 10h20



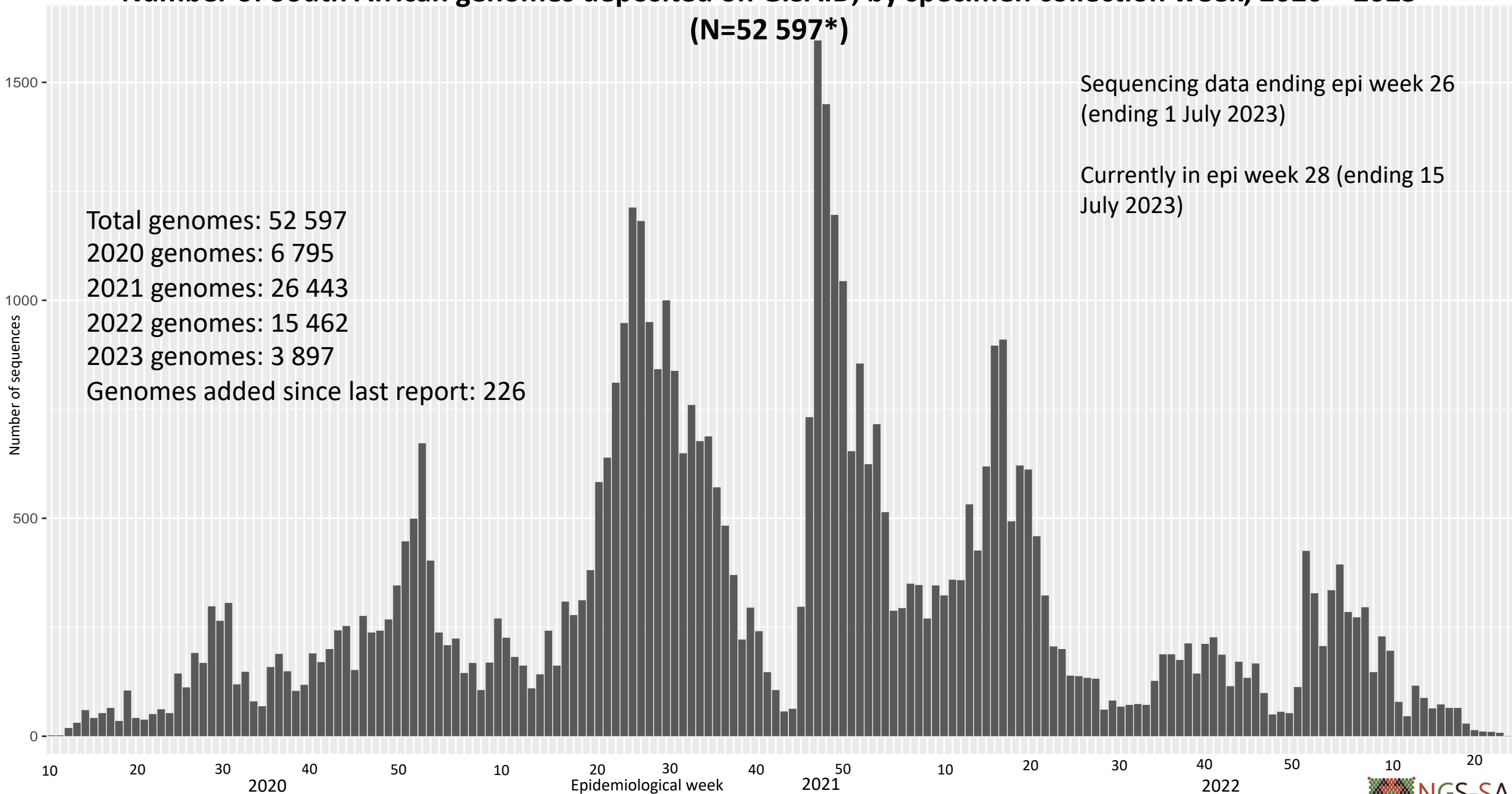
Data license: <https://www.gisaid.org/registration/terms-of-use/>

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

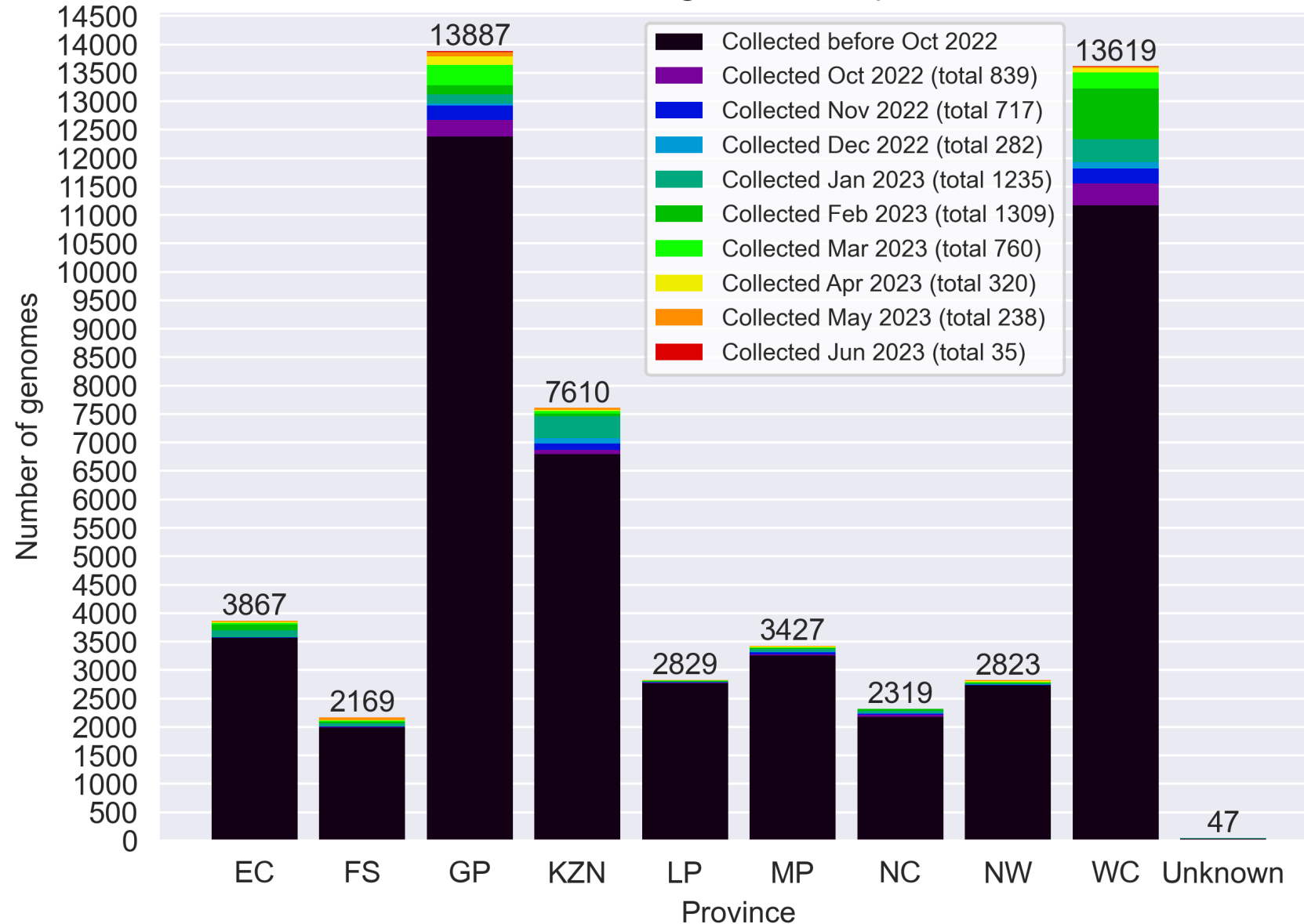
(N=52 597*)



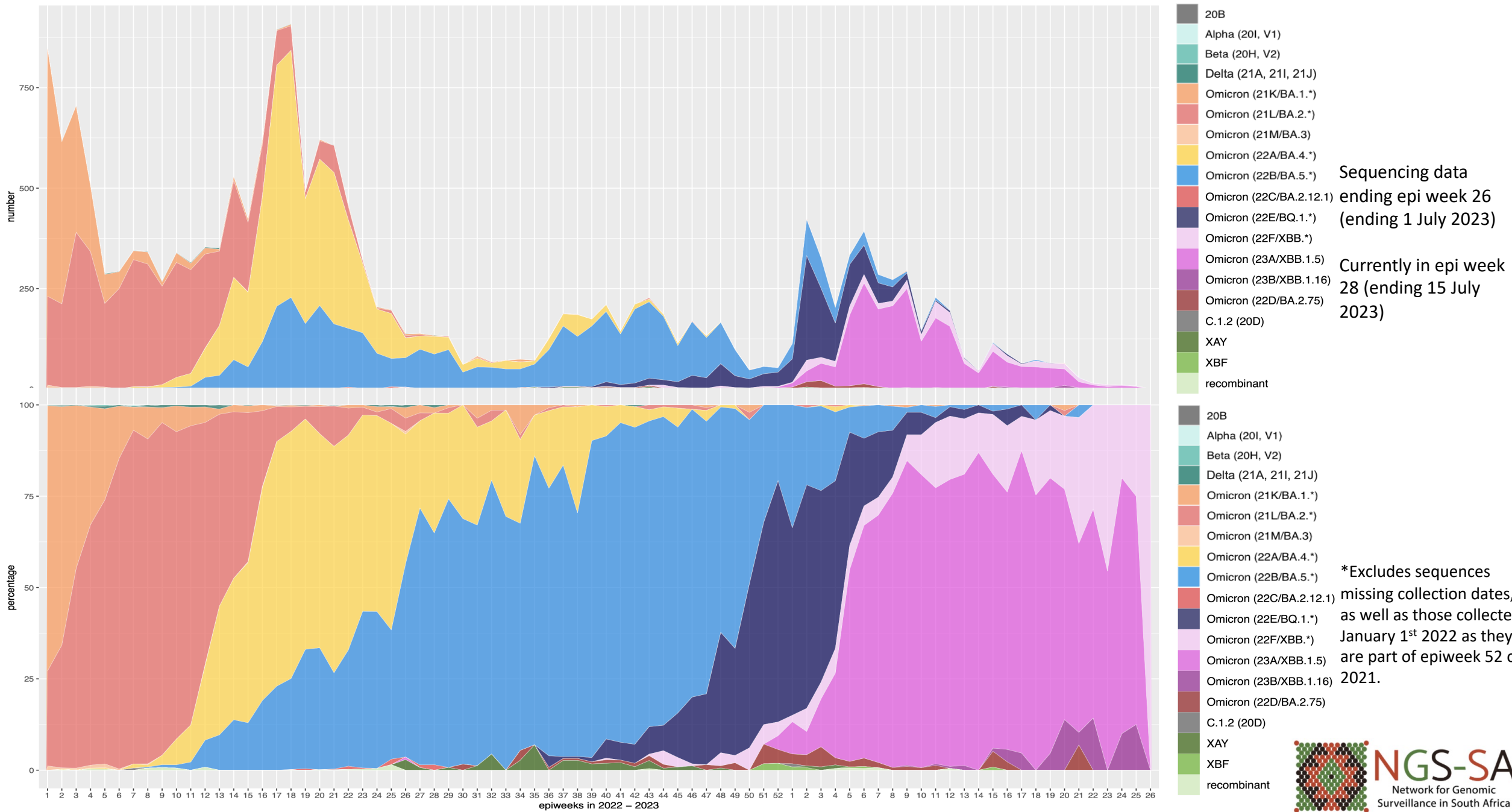
*This represents the cleaned, de-duplicated dataset of unique **National and Pneumonia Surveillance** sequences. This dataset will be used for all further figures

GISAID genomes vs total cases, 2020 – 2023 (N= 52 597)

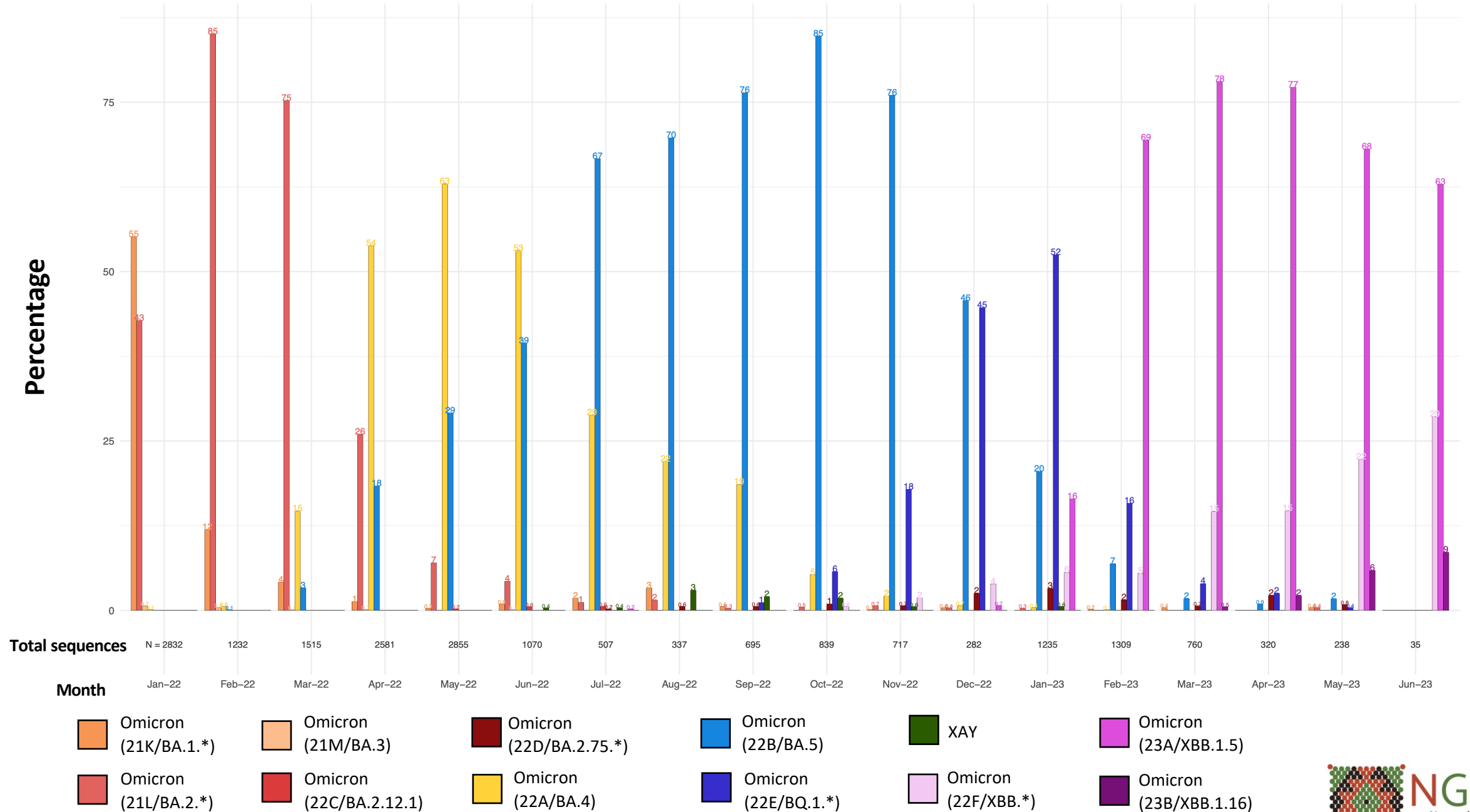
Provincial breakdown of genomes deposited into GISAID



Number and percentage of clades by epiweek in South Africa, 2022-2023 (19 316*)



Detection Rates: Omicron and recombinants

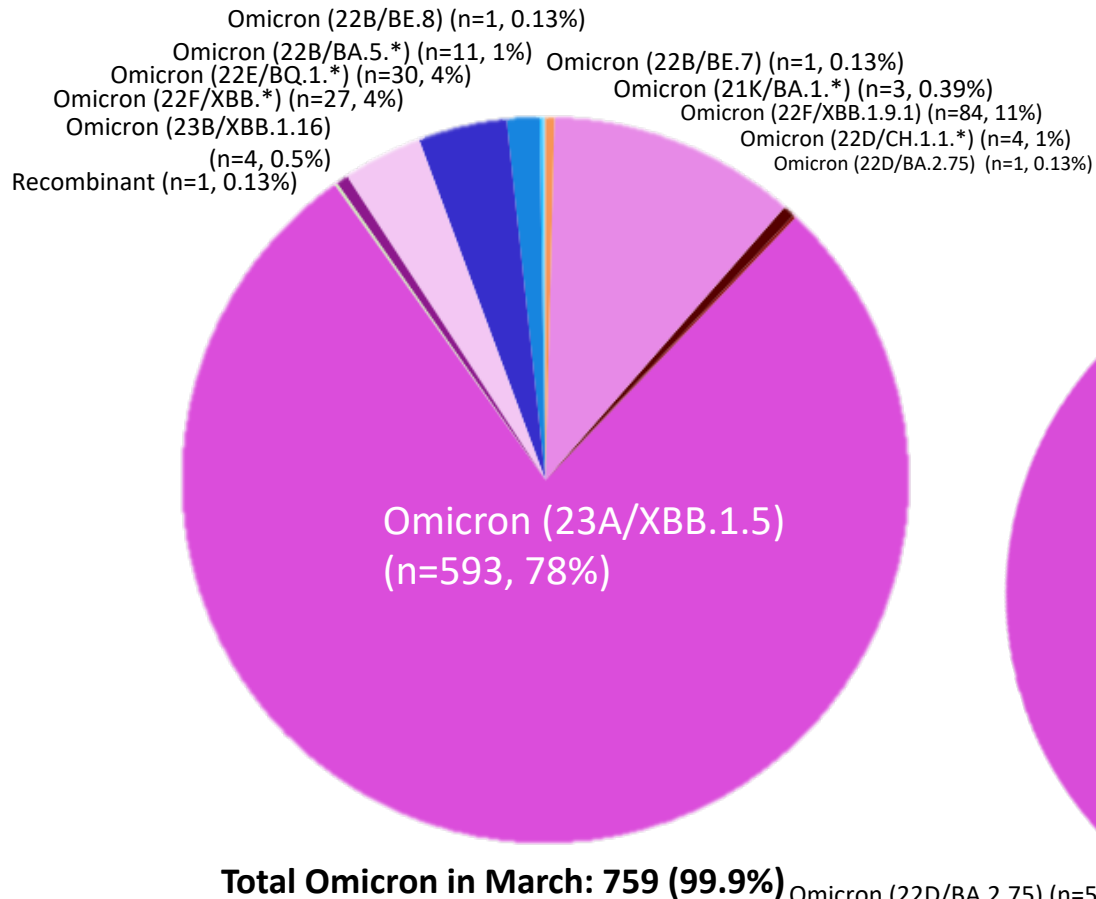


Prevalence of Variants of Concern (VOC) and Variants of Interest (VOI) in

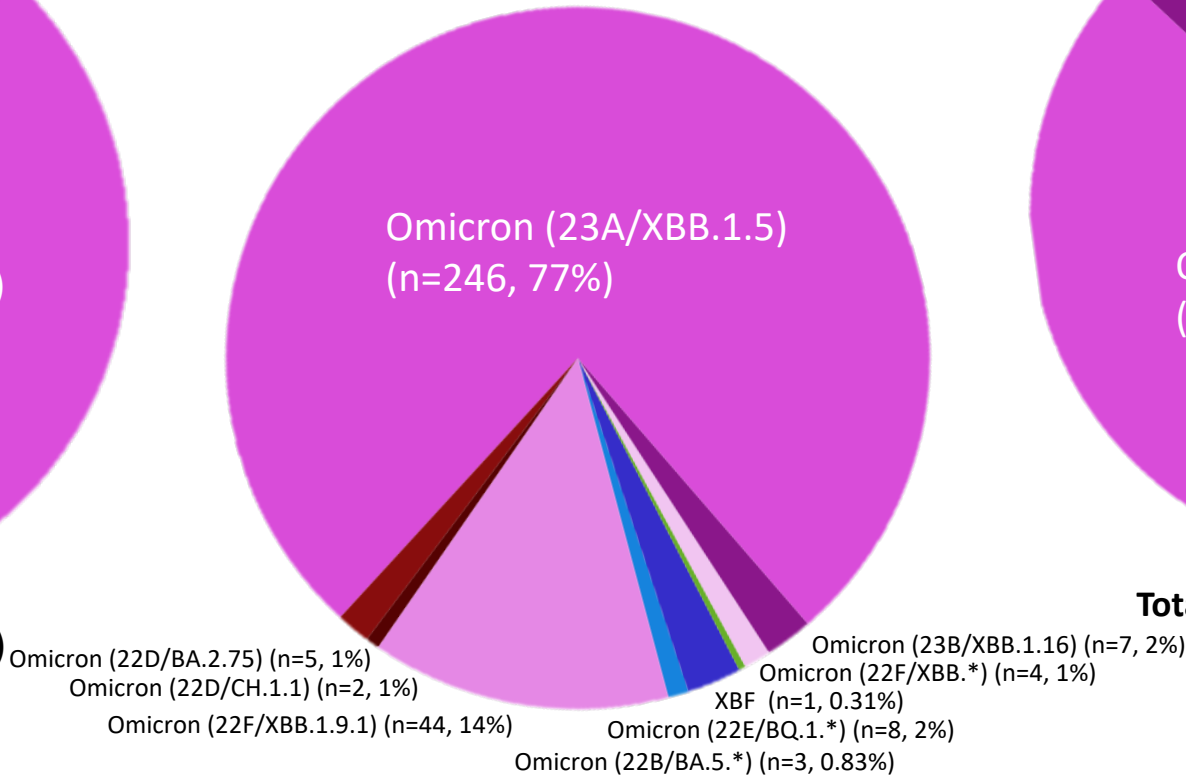
Mar (N=760)

Mar – May 2023

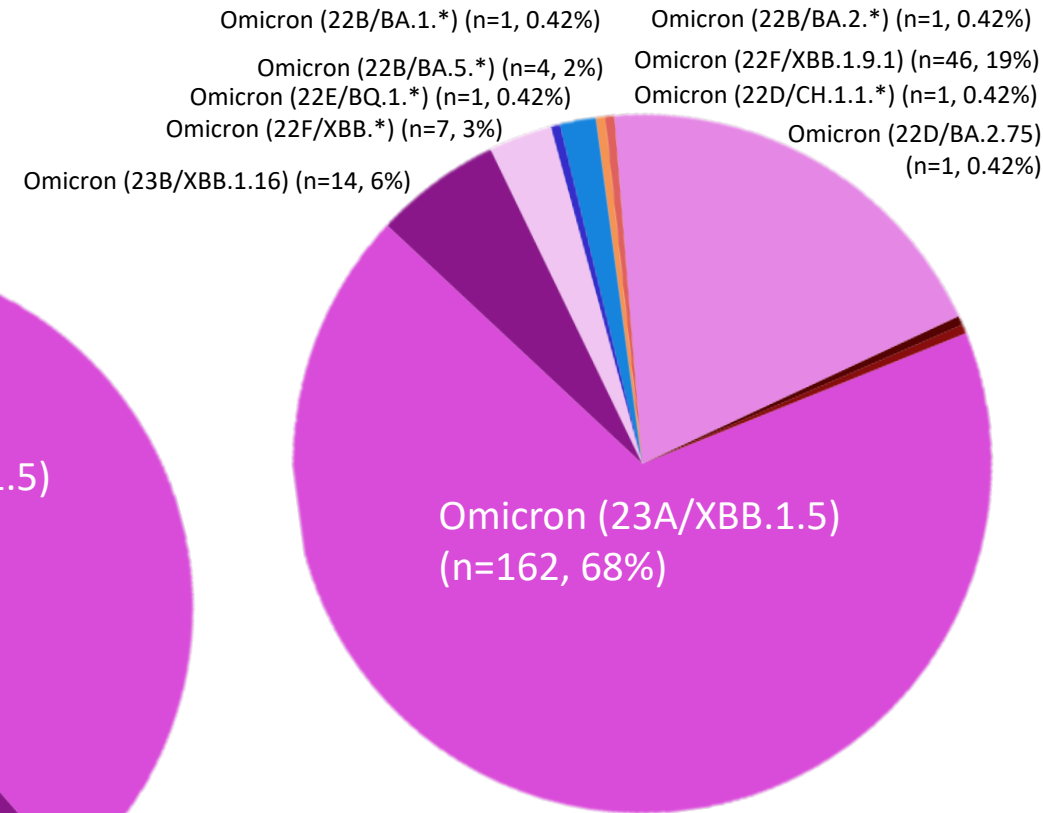
May (N=238)



Apr (N=320)



Total Omicron in May: 238 (100%)

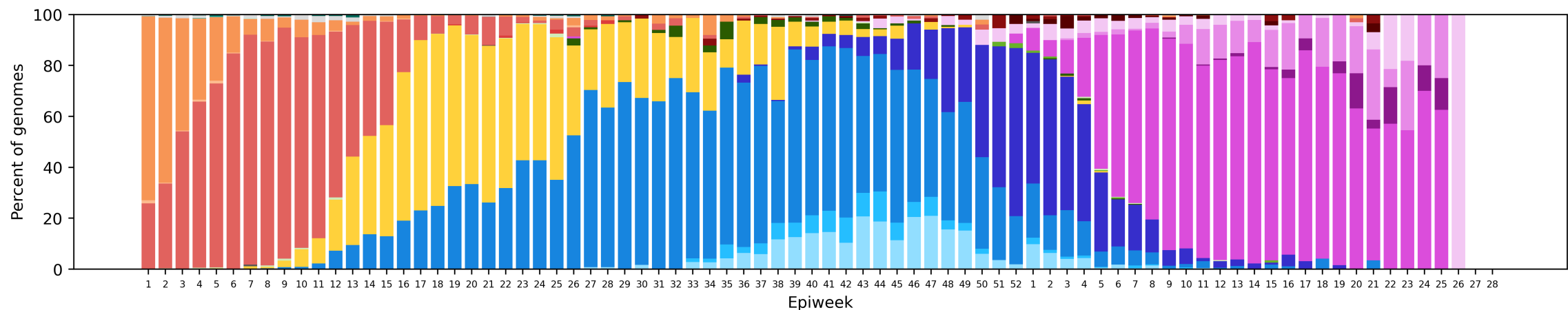
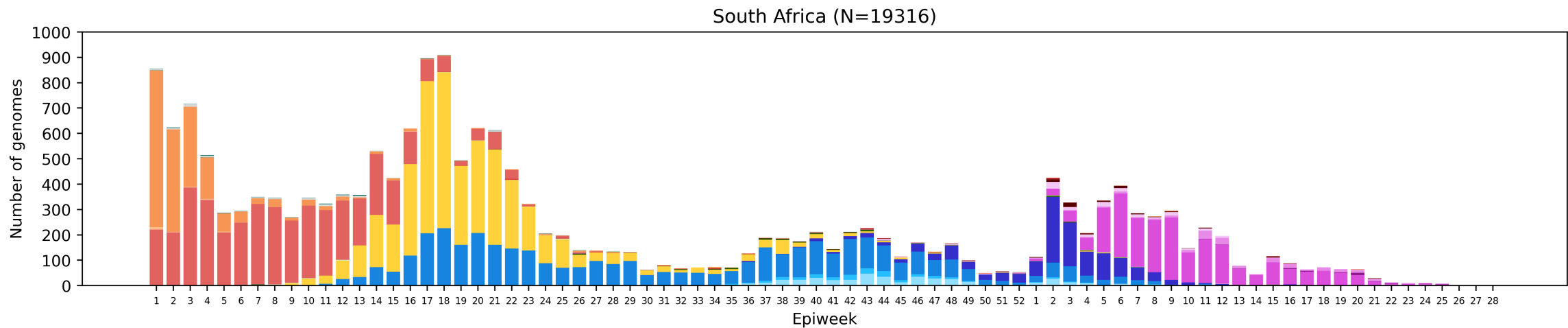


Clade key (bar graph)

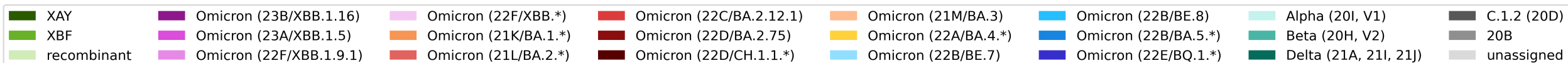
| | | | | | | | |
|-------------|-------------------------|----------------------|-------------------------|----------------------|----------------------|-----------------------|-------------|
| XAY | Omicron (23B/XBB.1.16) | Omicron (22F/XBB.*) | Omicron (22C/BA.2.12.1) | Omicron (21M/BA.3) | Omicron (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 = 19 316*



Clade key (bar graph)



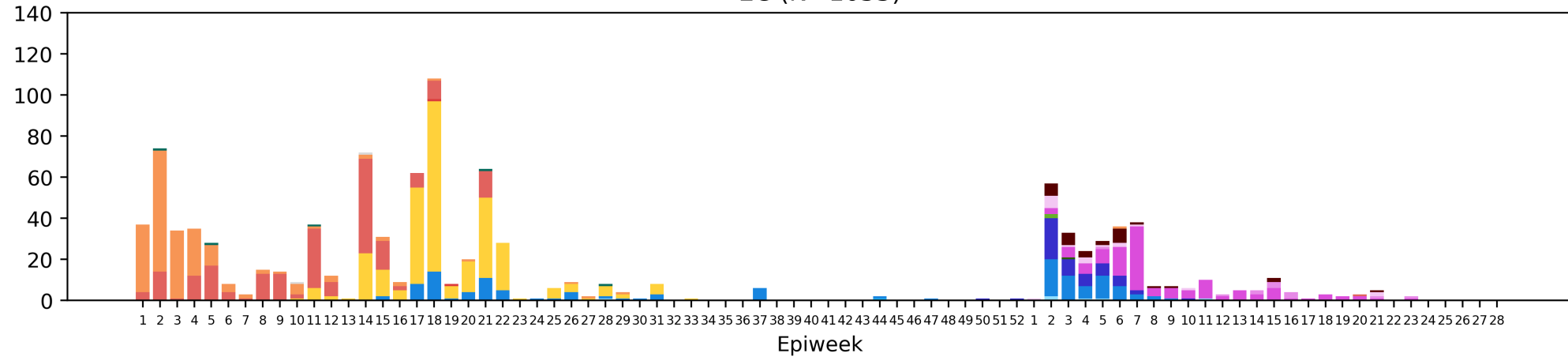
*Excludes sequences missing collection dates. Lineages of particular interest (mainly WHO Omicron subvariants under monitoring) are separate from the main clade groupings.

#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.

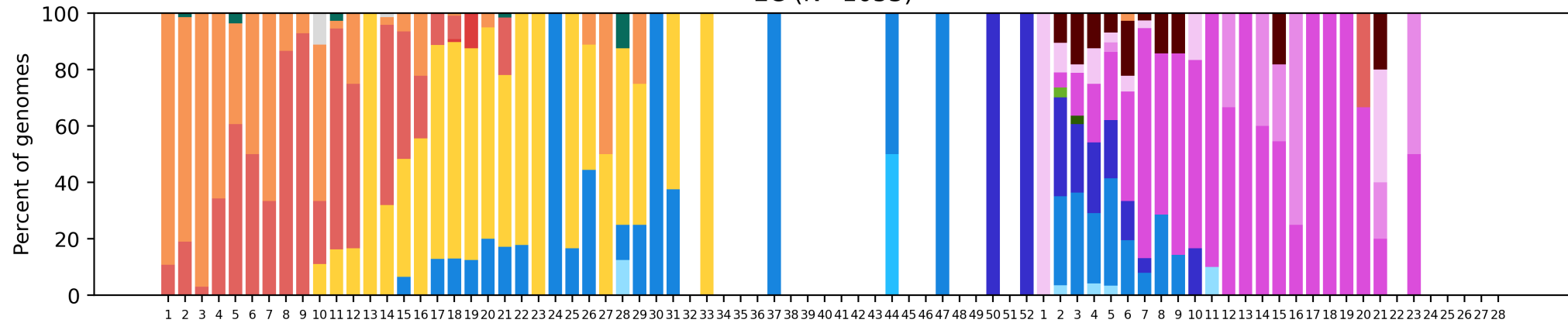
Eastern Cape Province, 2022-2023, n = 1053

Genomes added since last report: 82*

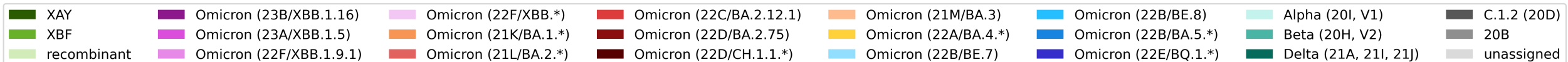
EC (N=1053)



EC (N=1053)



Clade key (bar graph)

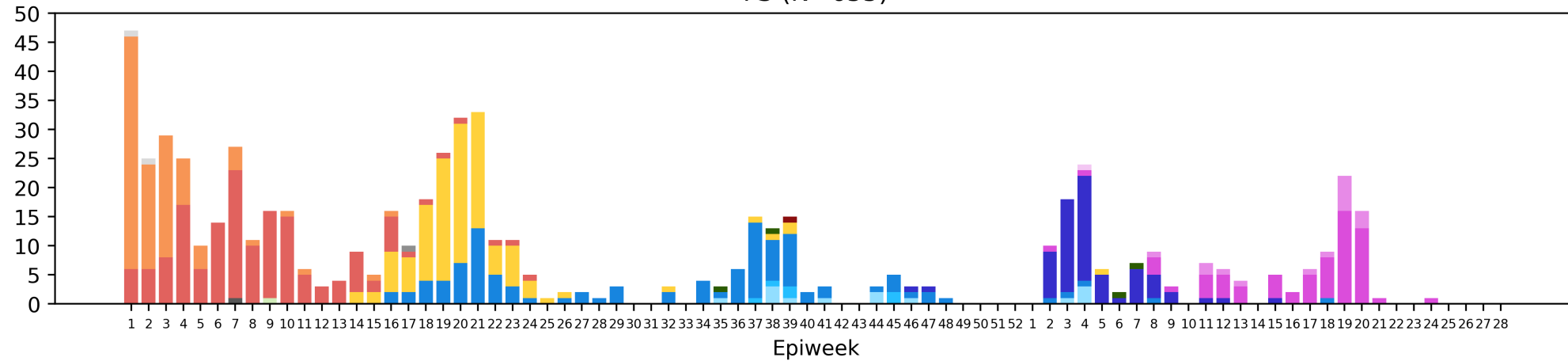


*May include genomes from 2020 and 2021 which are not pictured here and are not included in the slide total.

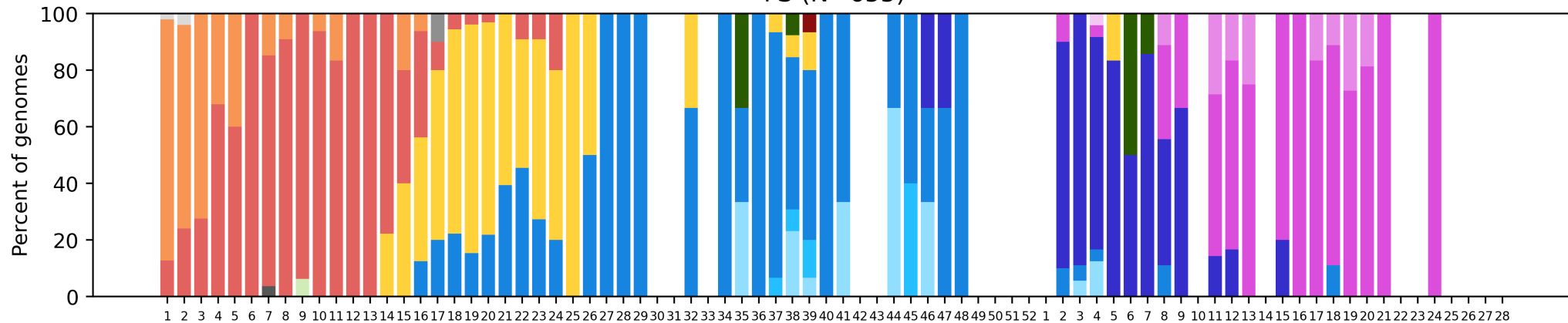
Free State Province, 2022-2023, n = 655

Genomes added since last report: 7*

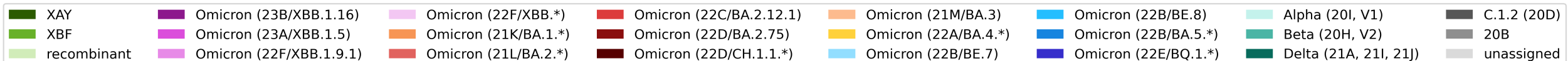
FS (N=655)



FS (N=655)



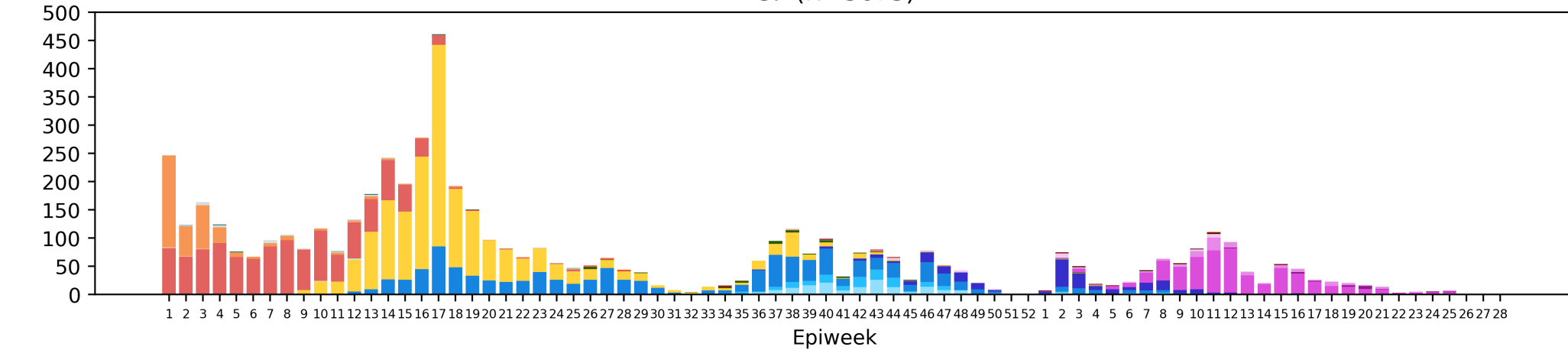
Clade key (bar graph)



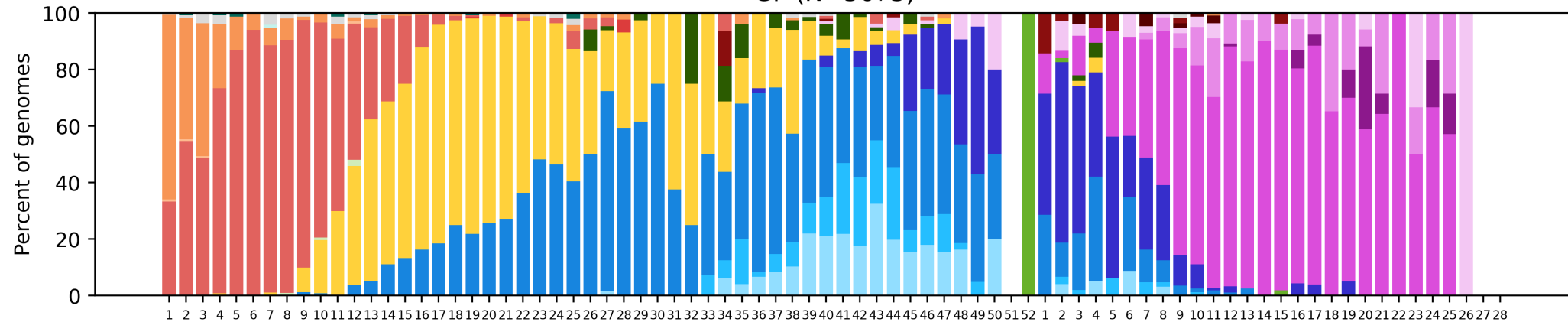
Gauteng Province, 2022-2023, n = 5673

Genomes added since last report: 85*

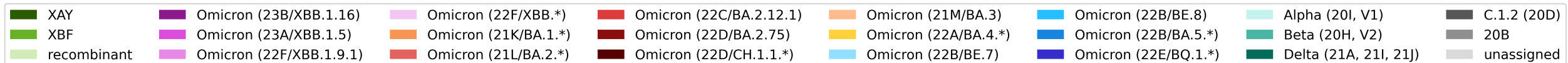
GP (N=5673)



GP (N=5673)



Clade key (bar graph)

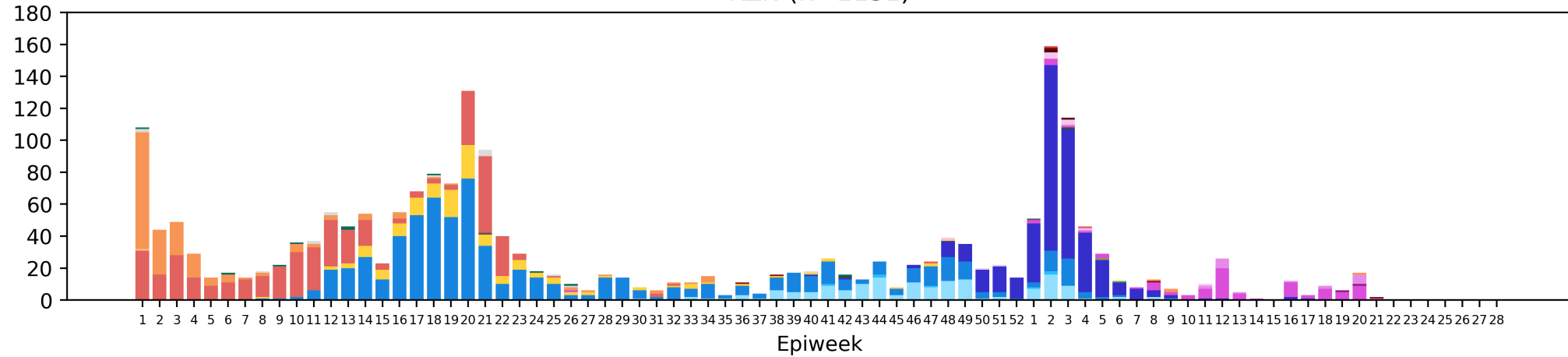


*May include genomes from 2020 and 2021 which are not pictured here and are not included in the slide total.

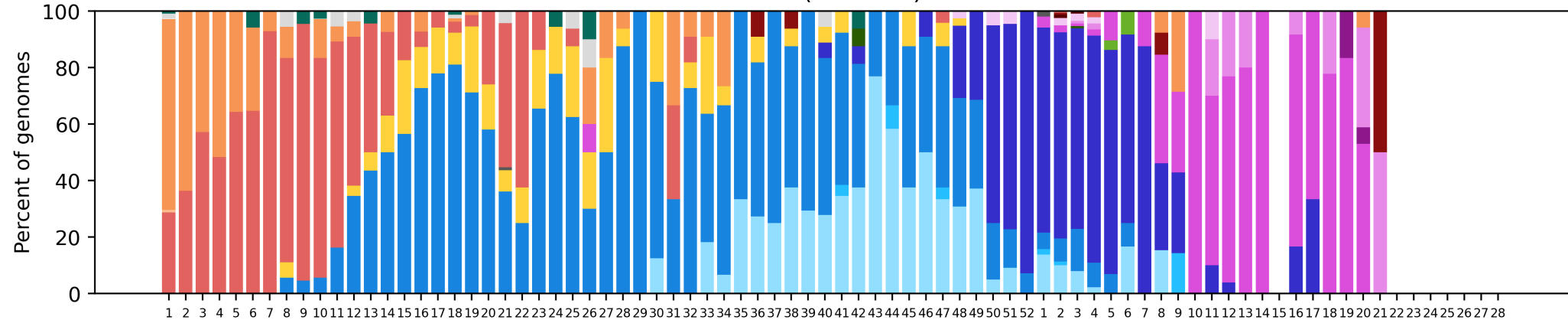
KwaZulu-Natal Province, 2022-2023, n = 2131

Genomes added since last report: 2*

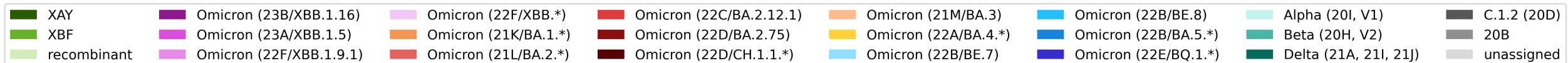
KZN (N=2131)



KZN (N=2131)



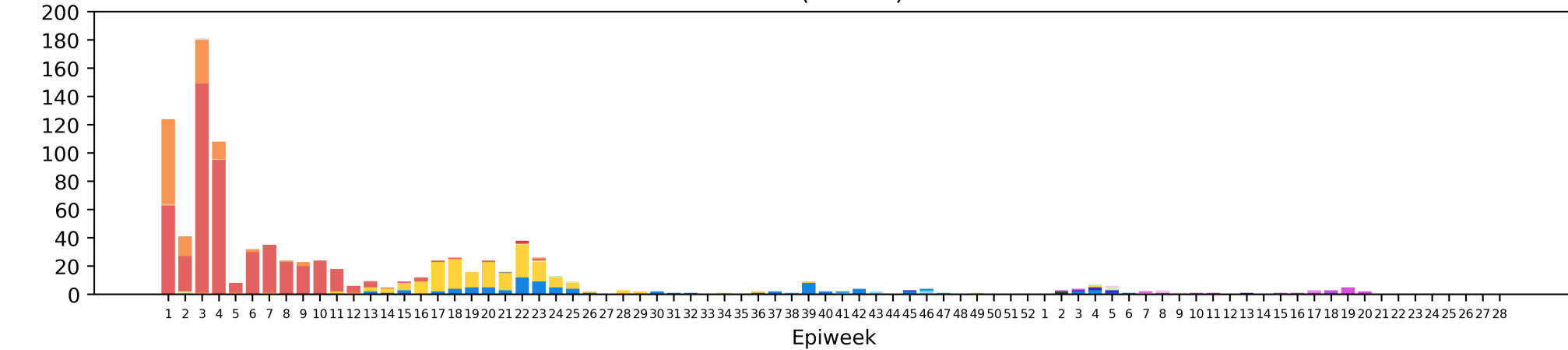
Clade key (bar graph)



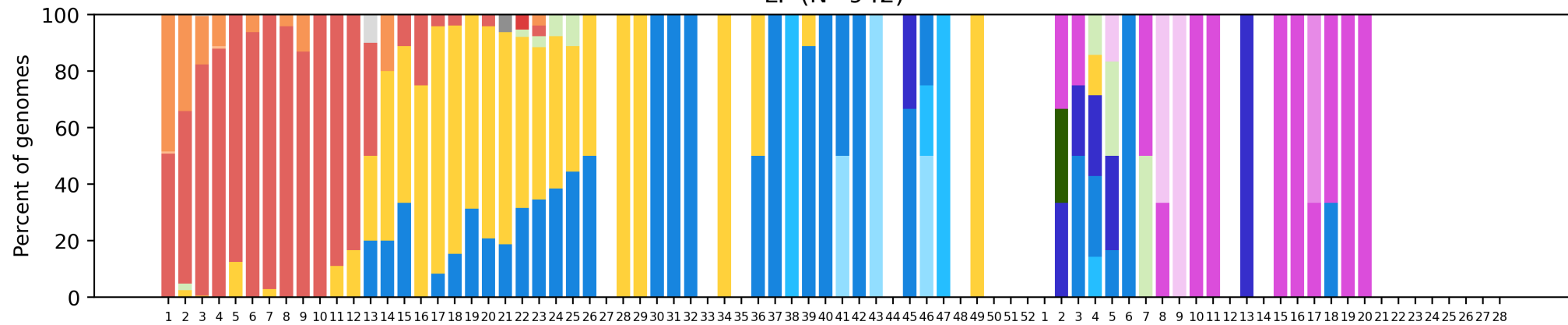
Limpopo Province, 2022-2023, n = 942

Genomes added since last report: 8*

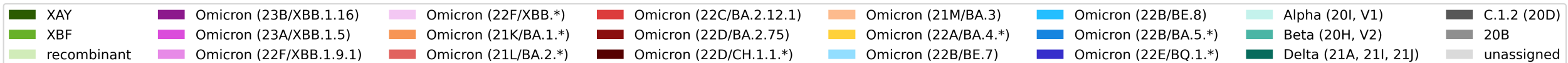
LP (N=942)



LP (N=942)



Clade key (bar graph)

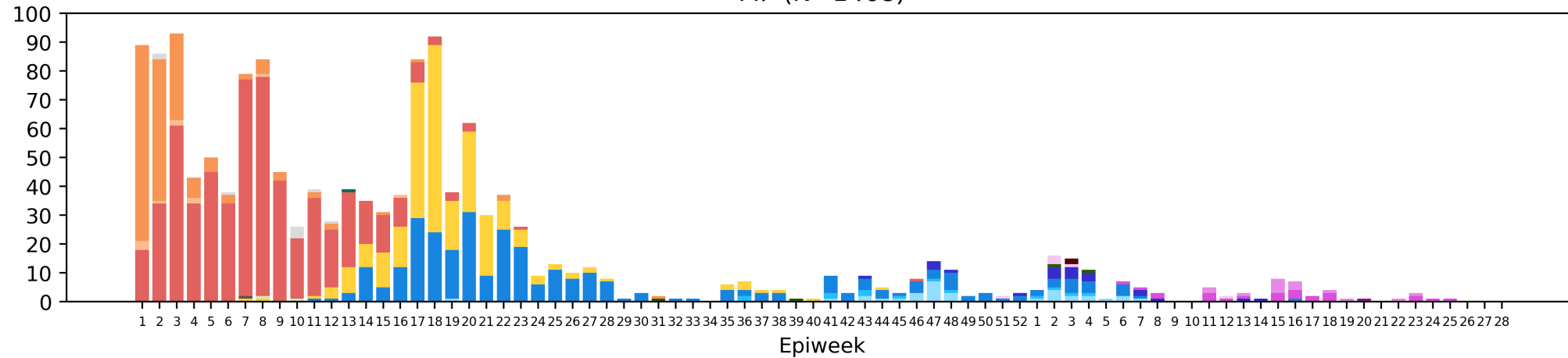


*May include genomes from 2020 and 2021 which are not pictured here and are not included in the slide total.

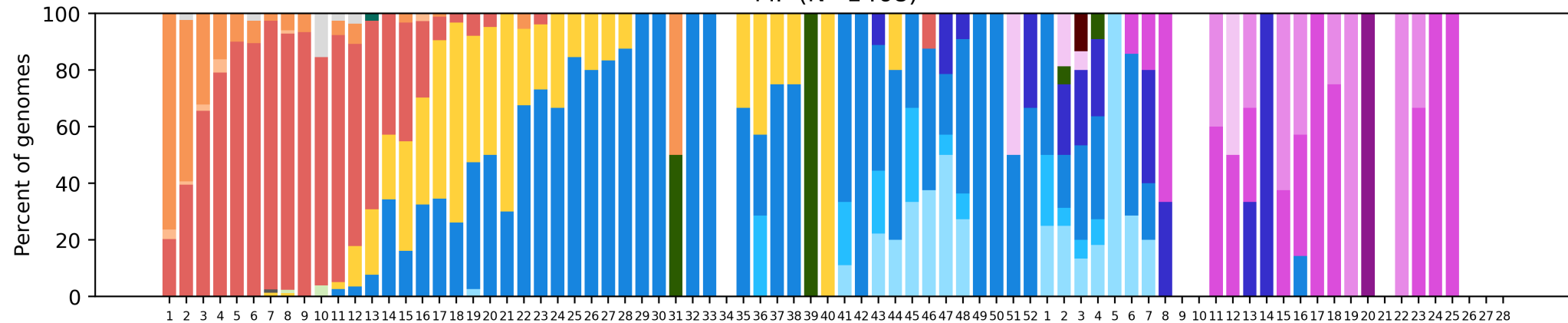
Mpumalanga Province, 2022-2023, n = 1468

Genomes added since last report: 14*

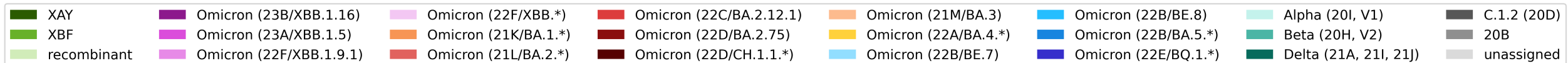
MP (N=1468)



MP (N=1468)



Clade key (bar graph)

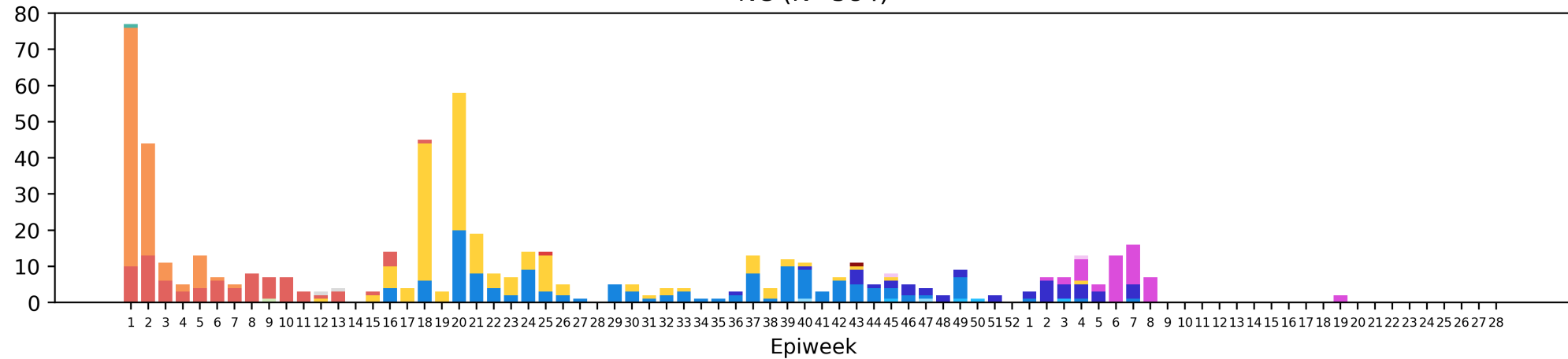


*May include genomes from 2020 and 2021 which are not pictured here and are not included in the slide total.

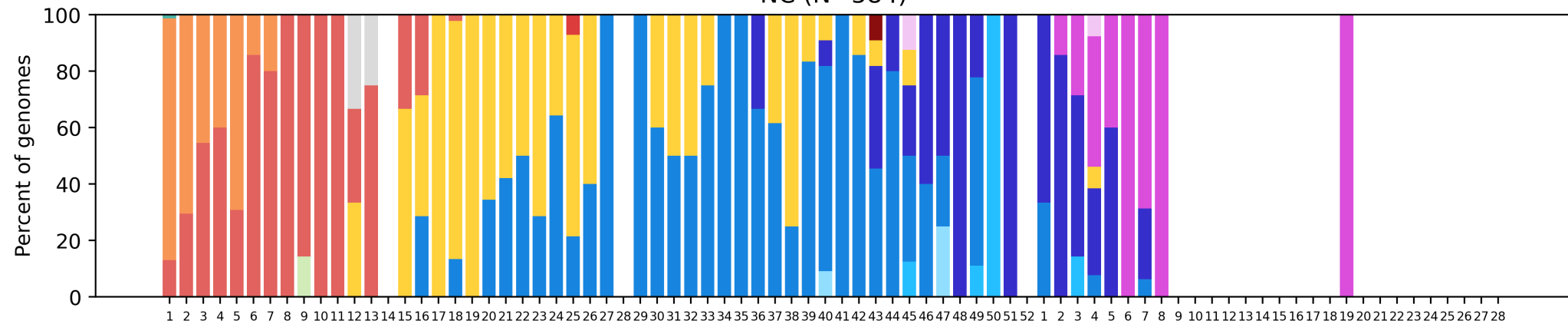
Northern Cape Province, 2022-2023, n = 584

Genomes added since last report: 0*

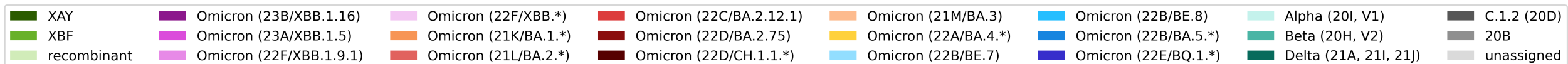
NC (N=584)



NC (N=584)



Clade key (bar graph)

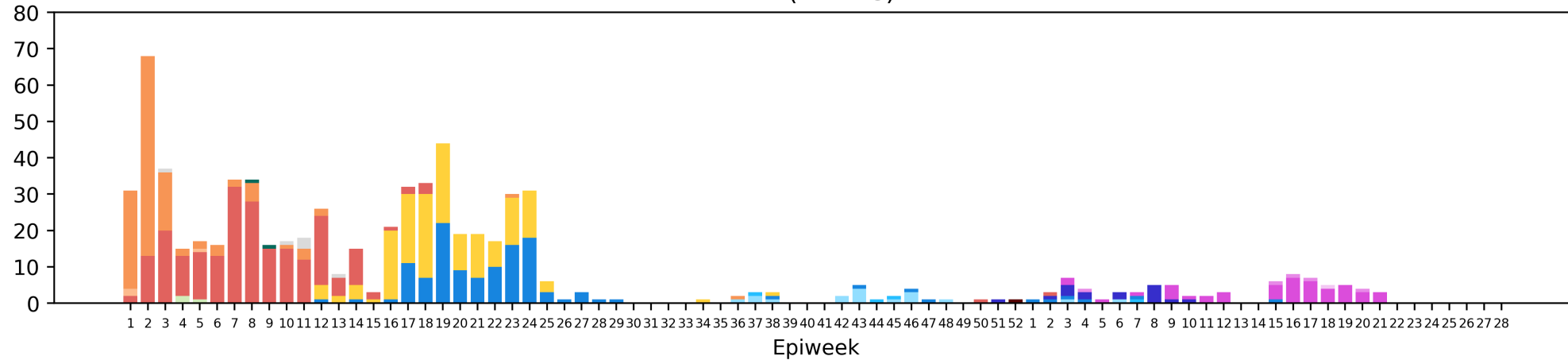


*May include genomes from 2020 and 2021 which are not pictured here and are not included in the slide total.

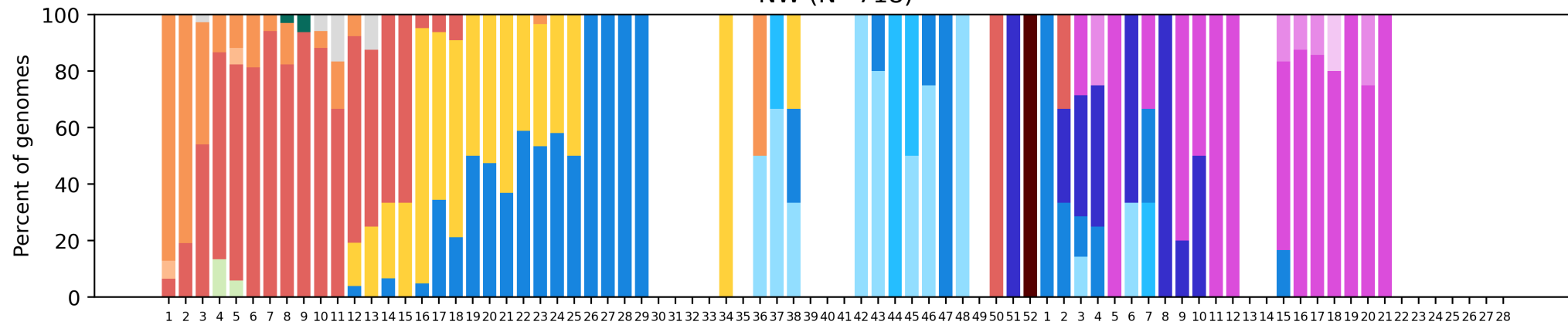
North West Province, 2022-2023, n = 718

Genomes added since last report: 3*

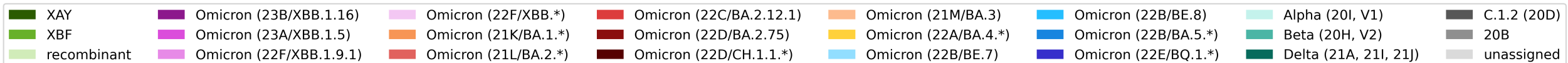
NW (N=718)



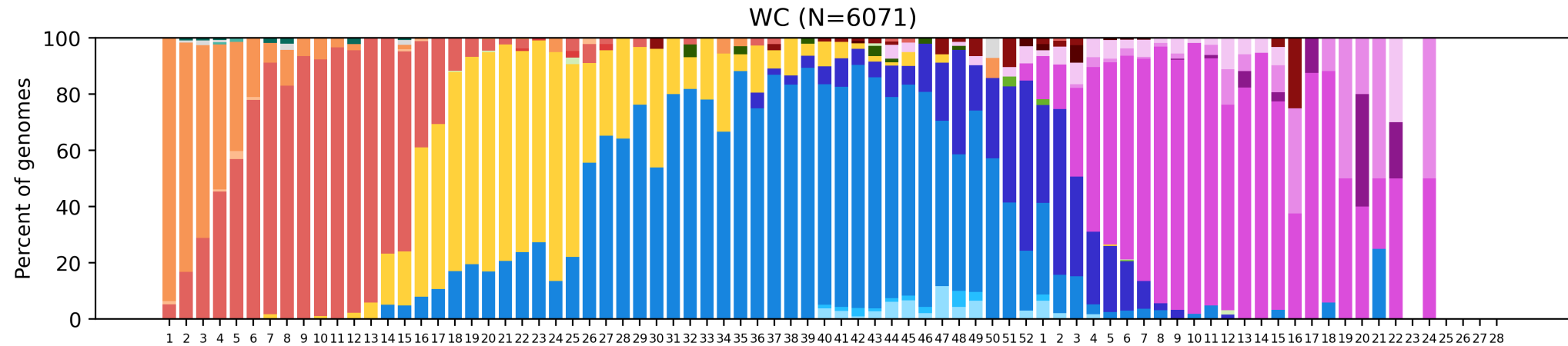
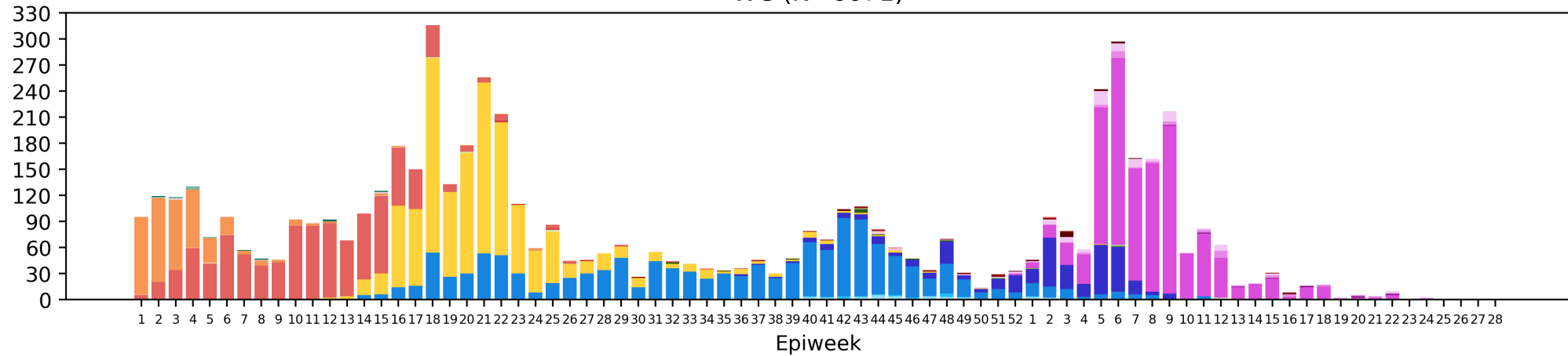
NW (N=718)



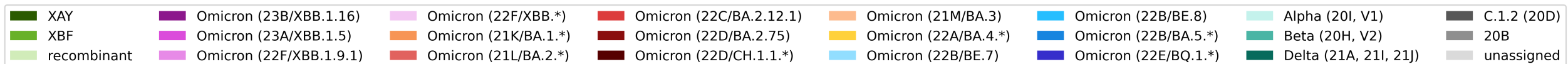
Clade key (bar graph)



Genomes added since last report: 25*
WC (N=6071)



Clade key (bar graph)



Summary

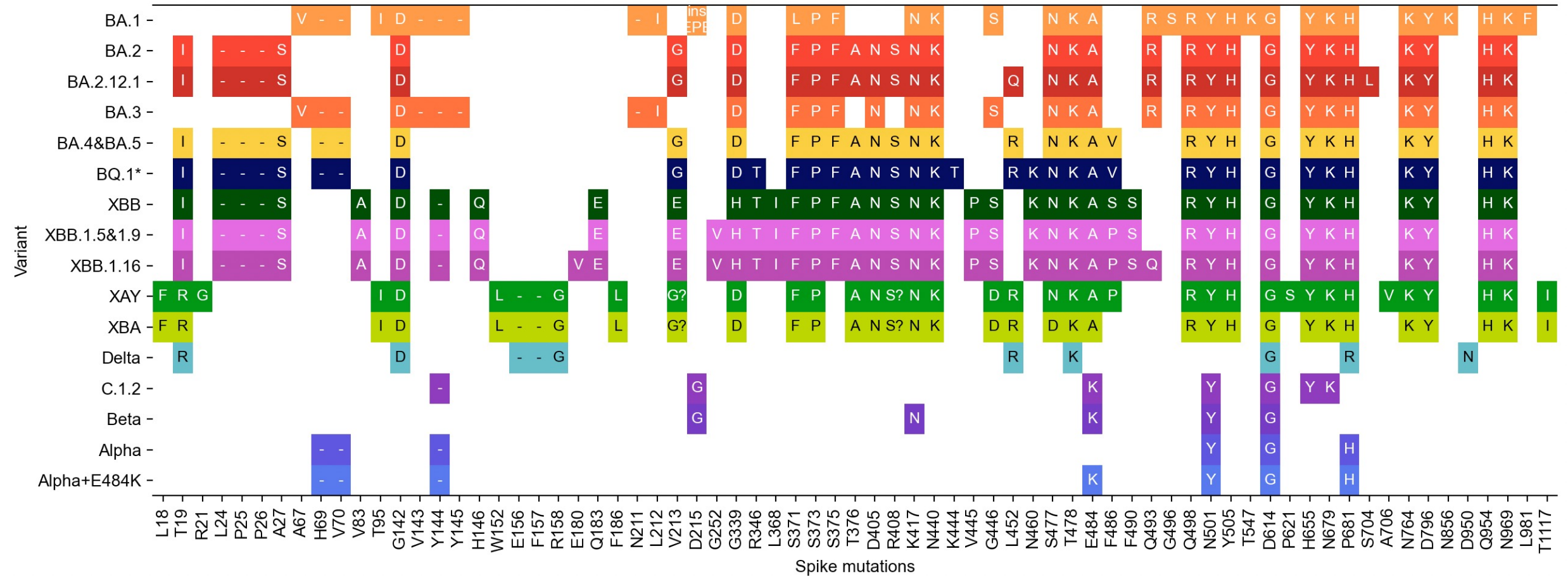
- **Sequencing update**

- All provinces except the Northern Cape have sequences for March and April. All provinces have data for May 2023. June sequences (n=35) are from the Eastern Cape, Free State, Gauteng, Mpumalanga, and the Western Cape.

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

- Omicron continued to dominate in March (99.9%), April (99.7%) and May (100%), and appears to dominate in June (100%), although this is based on low numbers (n=35)
- XBB.1.5 was the dominant lineage in March (78%) and April (77%), and continued to be dominant in May (68%)
- XBB.1.16 has been detected at a low prevalence in March (<1%), April (2%) and May (6%)
- XBB.1.9.1 was detected in sequences from March (11%), April (14%) and May (19%)

Spike protein mutation* profile of Variants of Interest and Concern

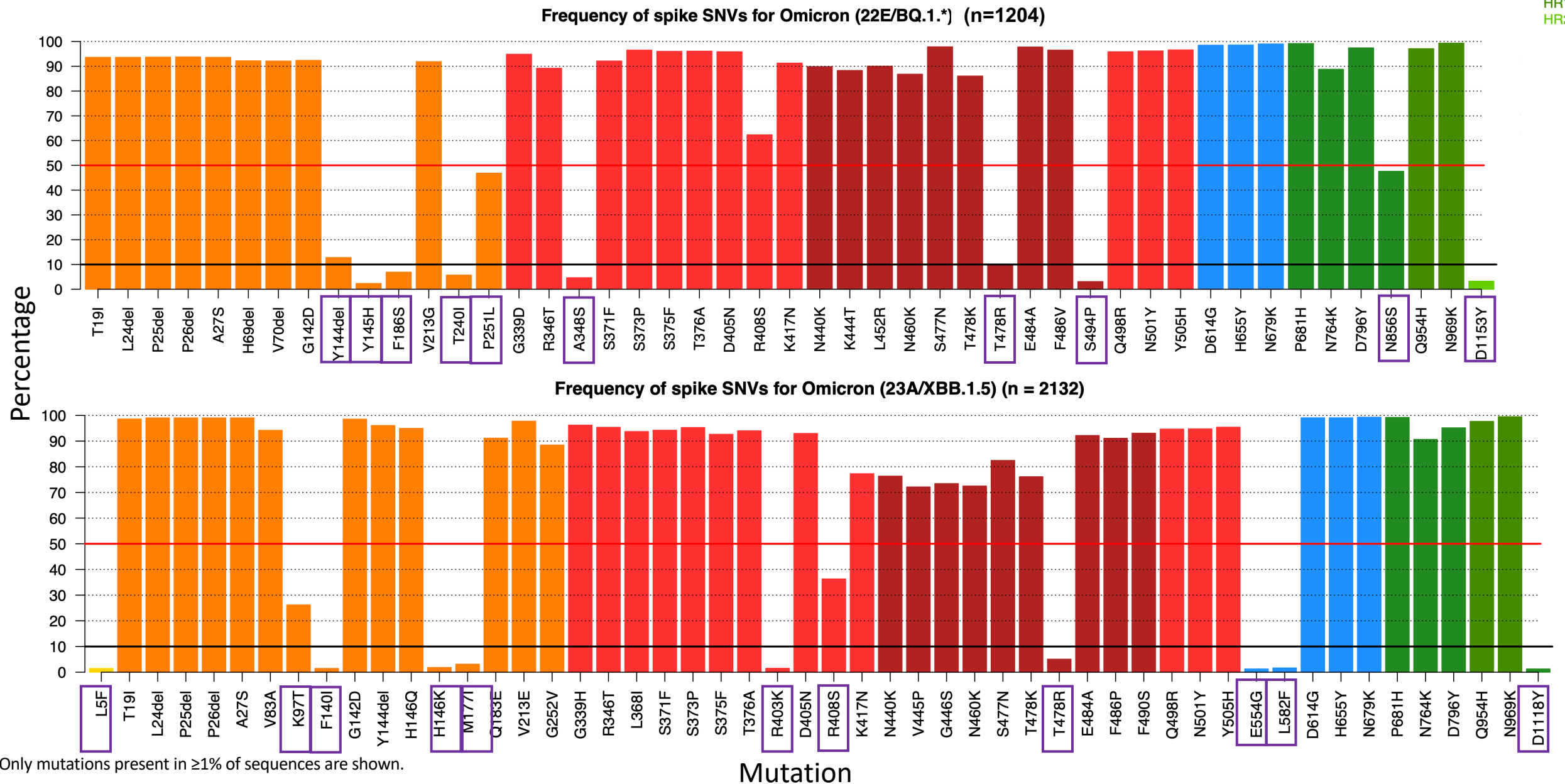


- Multiple changes within the two immunogenic regions in S1 (NTD and RBD)
 - Including a three amino acid insertion
- Accumulation of mutations surrounding the furin cleavage site
 - Including combination of N679K and P681H
- Effect of most spike S2 subunit changes have not been defined, but may be linked to immune escape

*Only mutations present in Omicron, Delta, or recombinant sequences are pictured

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

SP
NTD
RBD
RBM
S1
S2
HR1
HR2



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
Alex Sigal
Sandile Cele
Willem Hanekom

University of Cape Town, NHLS & Western Cape Government



NHLS-UCT
Carolyn Williamson
Nei-yuan Hsiao
Diana Hardie
Kruger Marais
Stephen Korsman
Ziyaad Valley-Omar

WCG-UCT
Mary-Anne Davies
Hannah Hussey
Andrew Boule
Masudah Paleker
Theuns Jacobs
Erna Morden

NHLS Greenpoint
Annabel Enoch



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UCT, IDM and CIDRI-Africa

Deelan Doolabh
Arash Iranzadeh
Lynn Tyers
Innocent Mudau
Nokuzola Mbhele
Fezokuhle Khumalo
Thabang Serake
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)

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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

NICD Groups

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

Sequencing Core Facility

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



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



Additional support and collaborators



NHLS

Koeleka 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

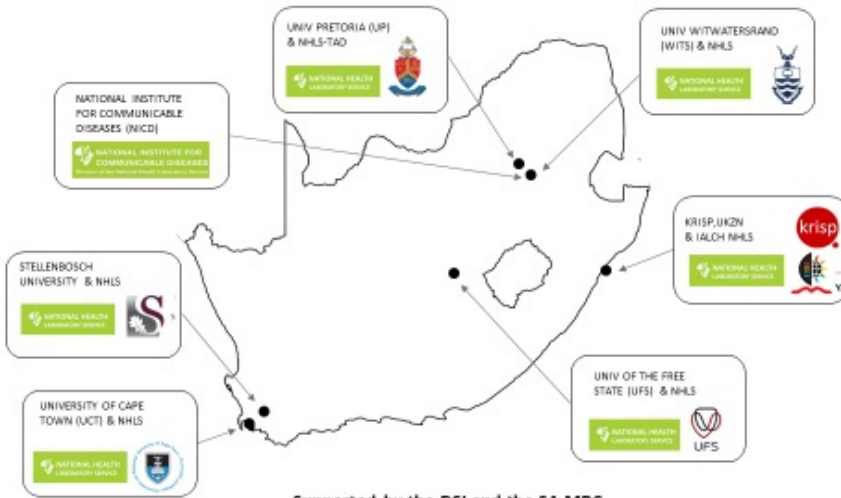
SA MRC

Glenda Gray

Pathcare N1 City

Jean Maritz
Nadine Cronje
Petra Raimond
Kim Hoek





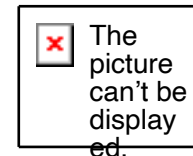
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UNIVERSITY OF PRETORIA
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UNIVERSITY OF CAPE TOWN
IYUNIBESITHI YASEKAPA • UNIVERSITEIT VAN KAAPSTAD



WITS
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UNIVERSITY OF
KWAZULU-NATAL
INYUVESI
YAKWAZULU-NATALI

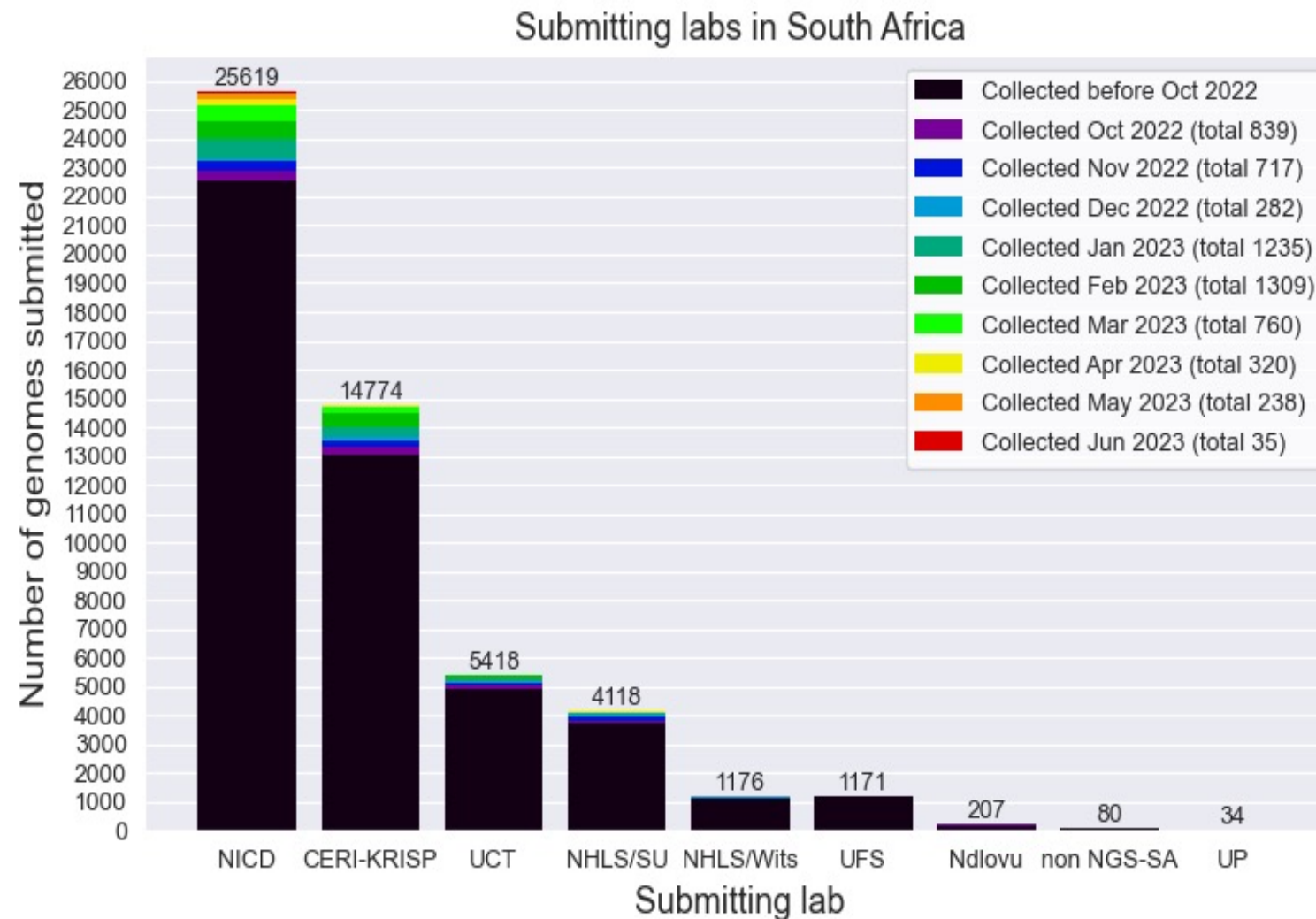


EDCTP

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=52 597)



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 5 June 2023

| Pango lineage | Nextstrain clade | Genetic features | Earliest documented samples | Date of designation |
|---------------|------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| XBB.1.5 | 23A | Recombinant of BA.2.10.1 and BA.2.75 sublineages, i.e. BJ1 and BM.1.1.1, with a breakpoint in S1. XBB.1 + S:F486P (similar Spike genetic profile as XBB.1.9.1) | 05-01-2022 | 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.1.16 | 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 | 09-01-2023 | 17-04-2023 XBB.1.16 Initial Risk Assessment 17 April 2023 XBB.1.16 Updated Risk Assessment, 05 June 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 | 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 |
| XBB.1.9.2 | 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, S:Q613H | 05-12-2022 | 26-04-2023 |
| XBB.2.3 | Not assigned | 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 |

* Excludes XBB sublineages listed here as VOIs and VUMs

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.)