

SARS-CoV-2 Sequencing Update 06 October 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 06 October 2023 at 09h45



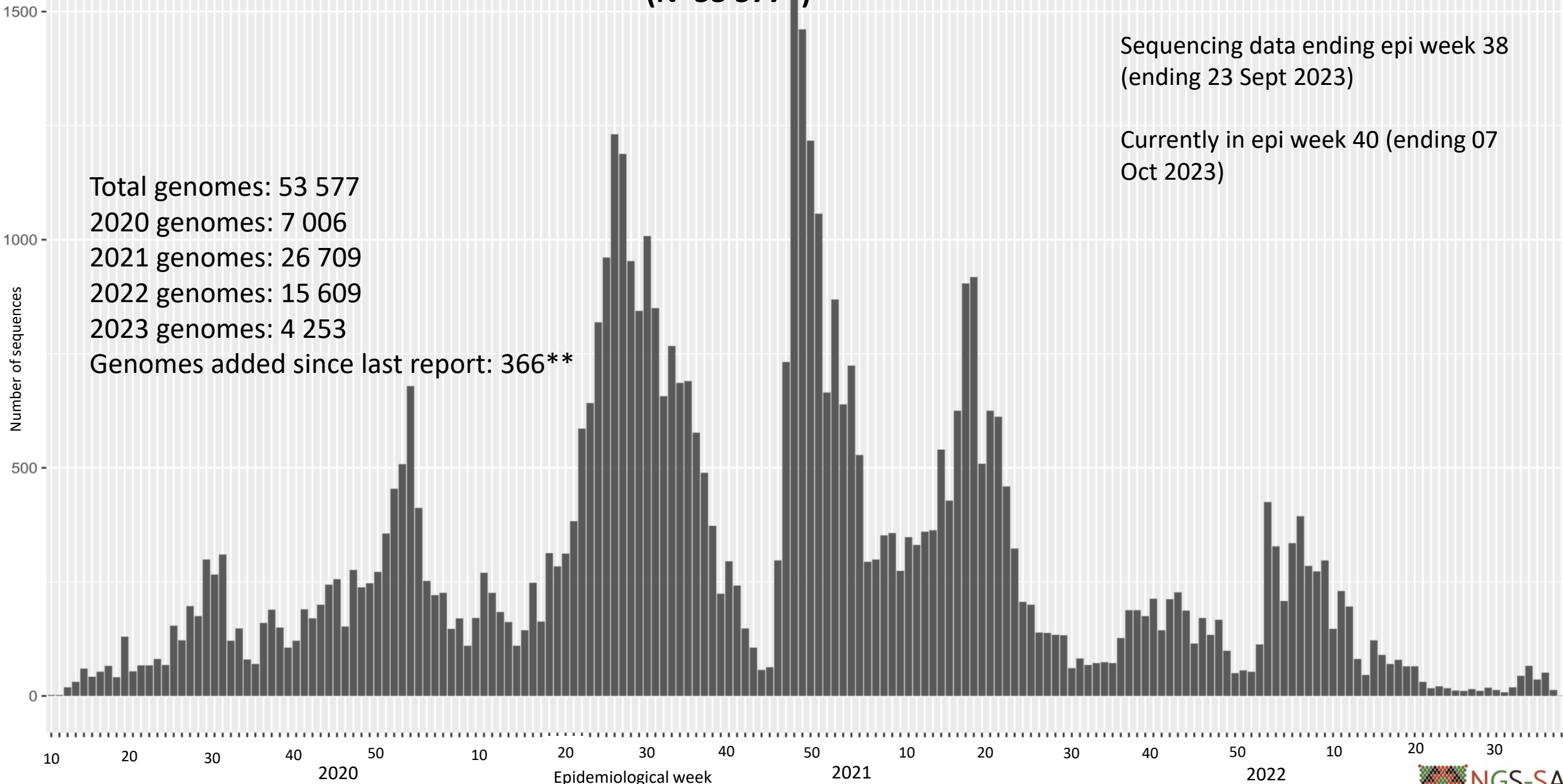
Data license: <https://www.gisaid.org/registration/terms-of-use/>

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

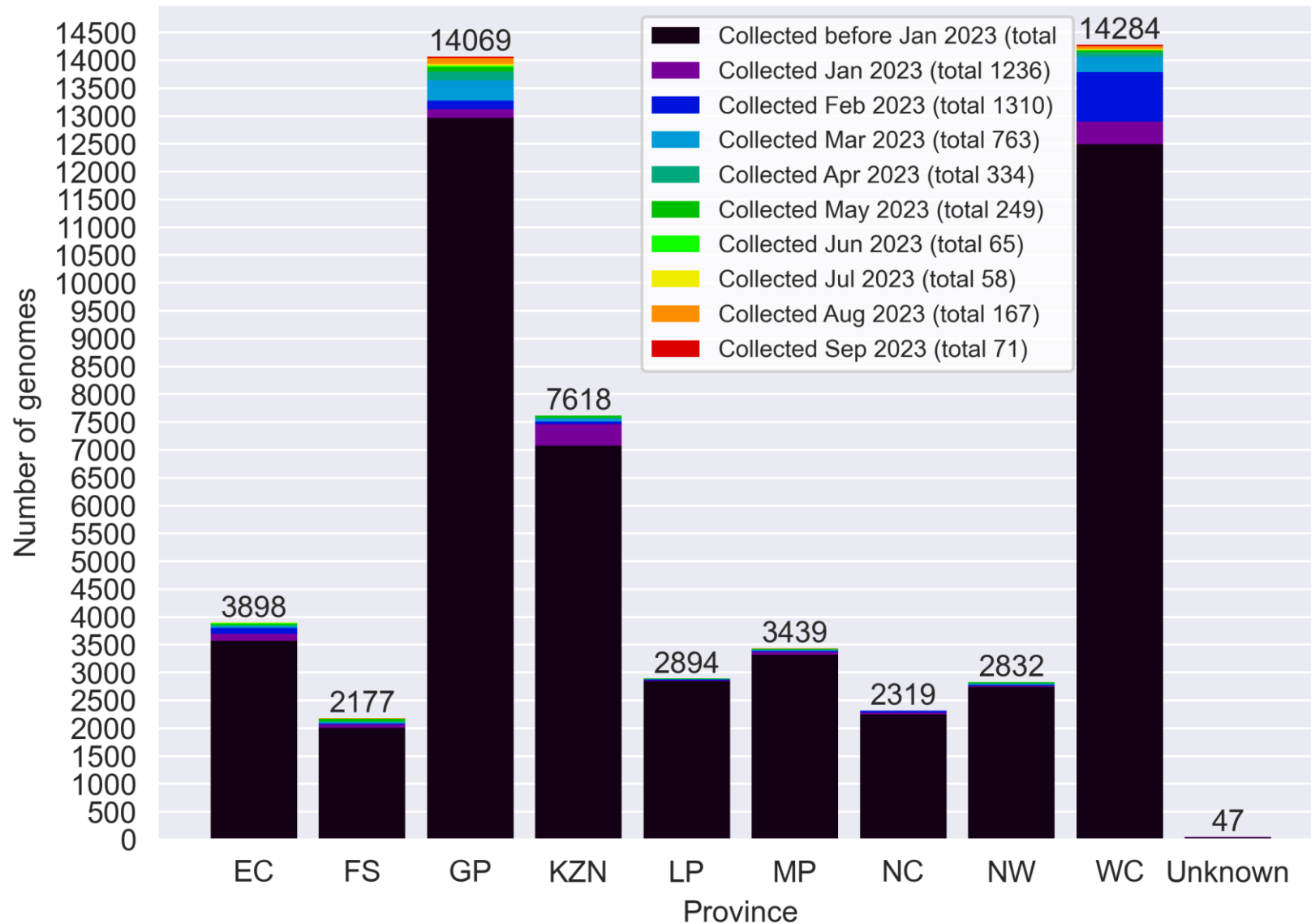
(N=53 577*)



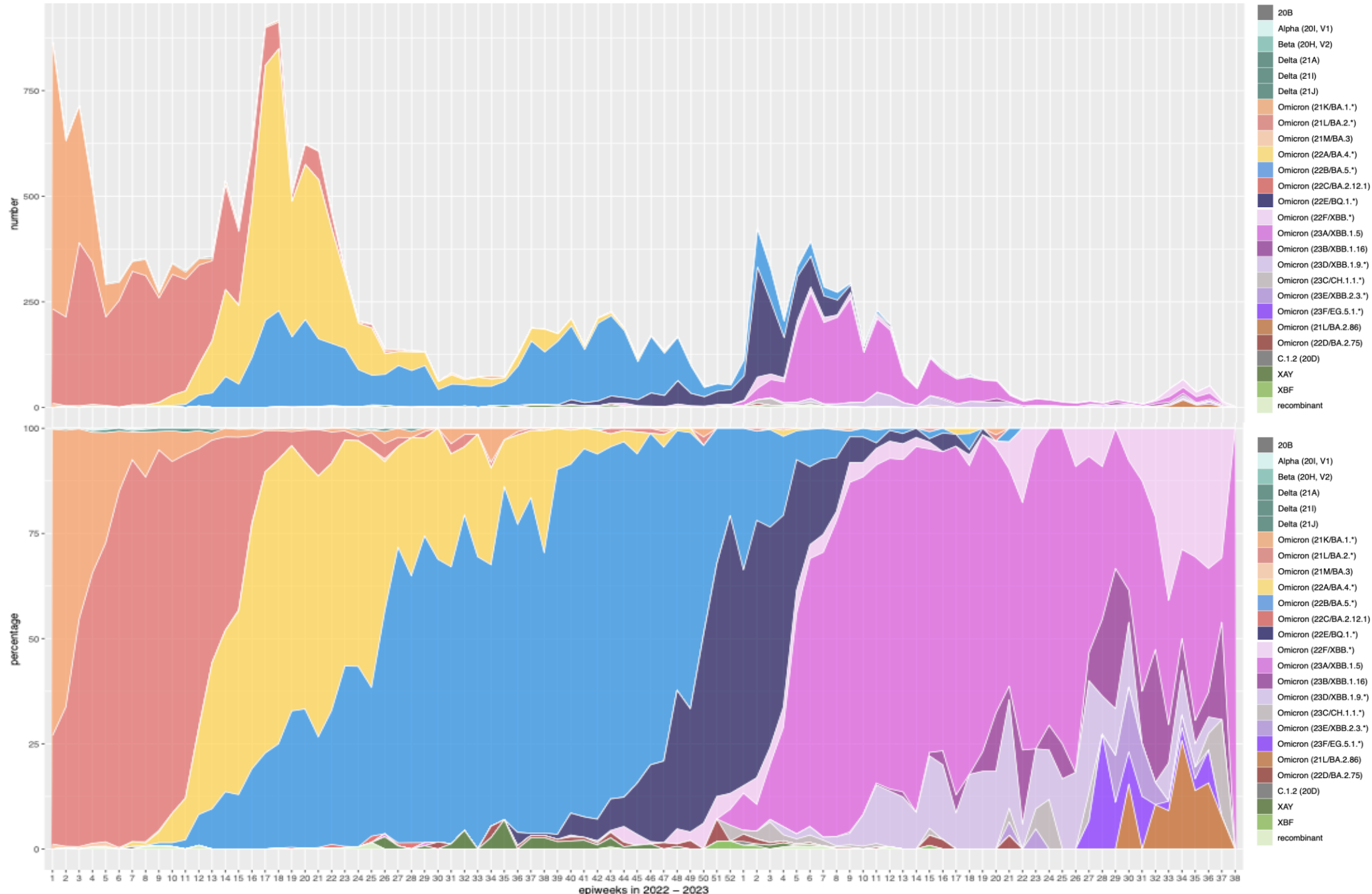
*This represents the cleaned, de-duplicated dataset of unique **National and Pneumonia Surveillance** sequences. This dataset will be used for all further figures. ** Also includes retrospective sequences from 2020-2022

GISAID genomes vs total cases, 2020 – 2023 (N= 53 577)

Provincial breakdown of genomes deposited into GISAID



Number and percentage of clades by epiweek in South Africa, 2022-2023 (19 819*)

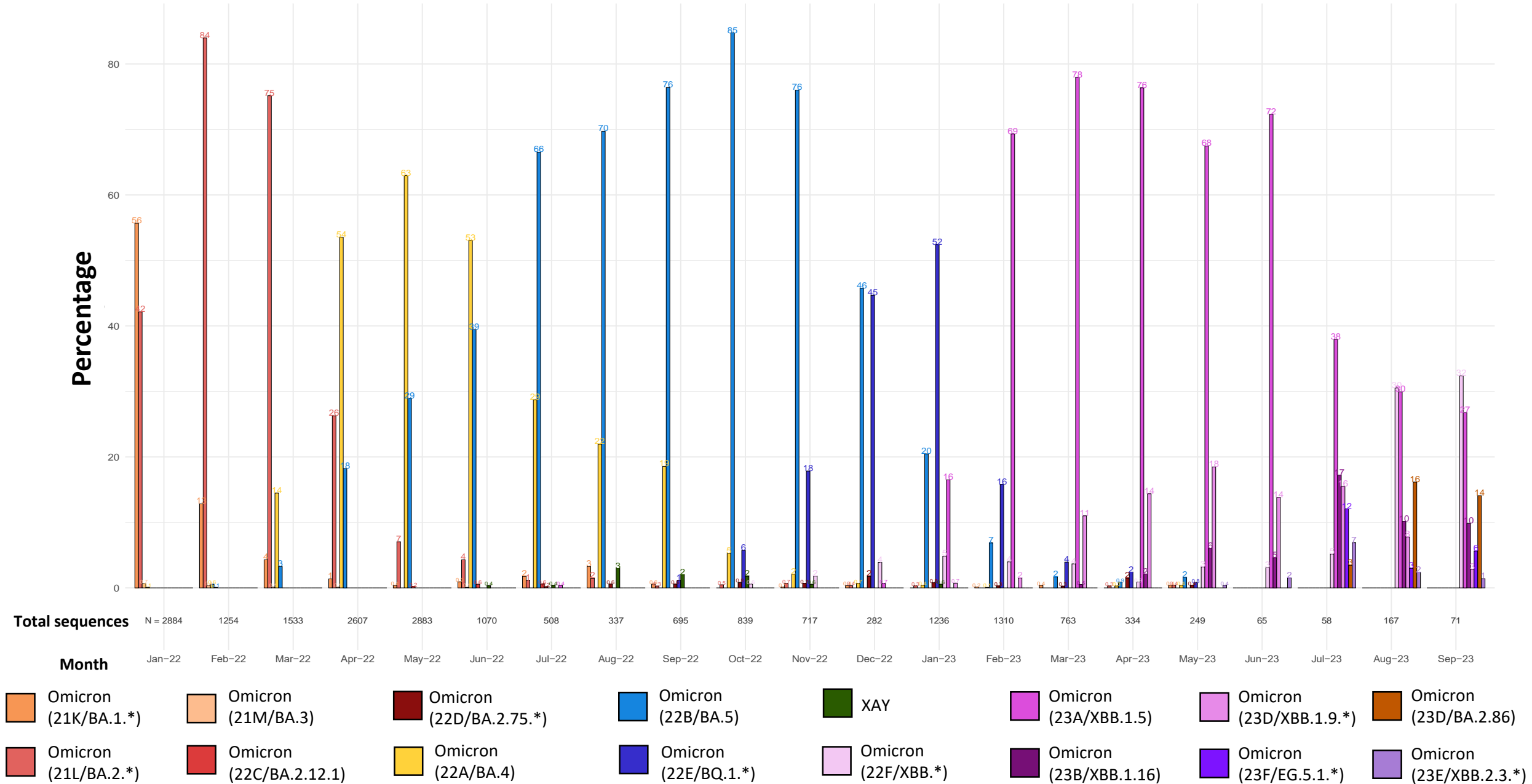


Sequencing data
ending epi week 38
(ending 23 Sep 2023)

Currently in epi week
40 (ending 07 Oct
2023)

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

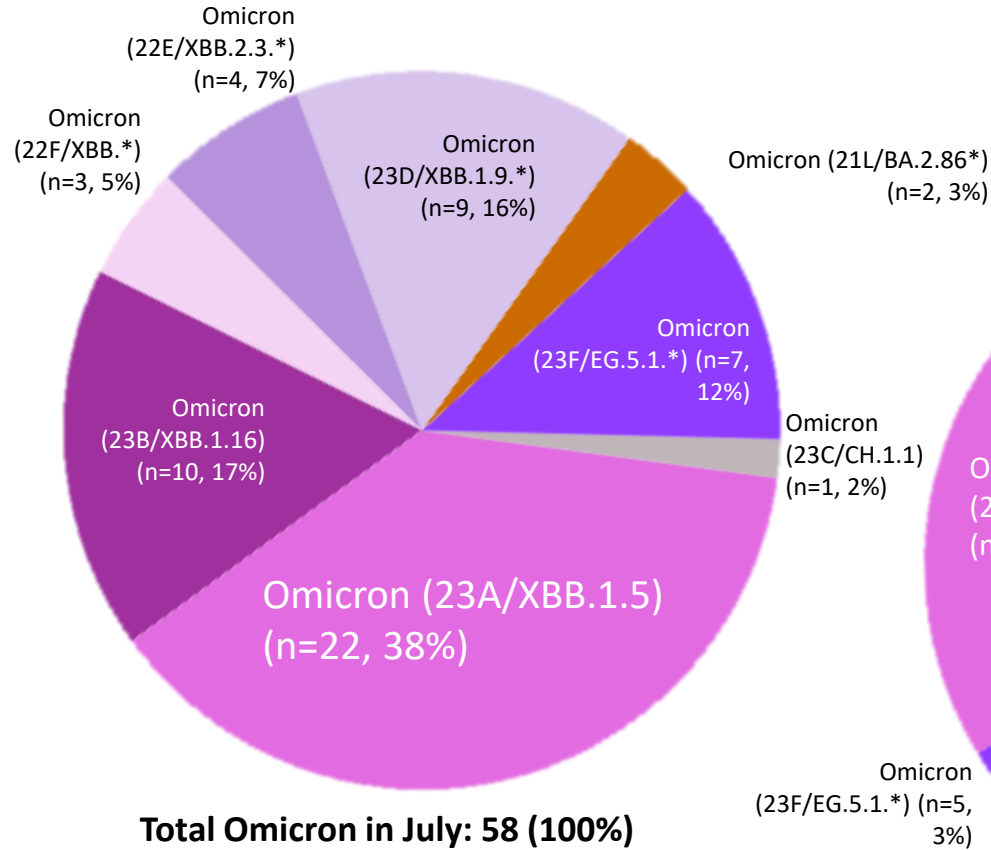
Detection Rates: Omicron and recombinants



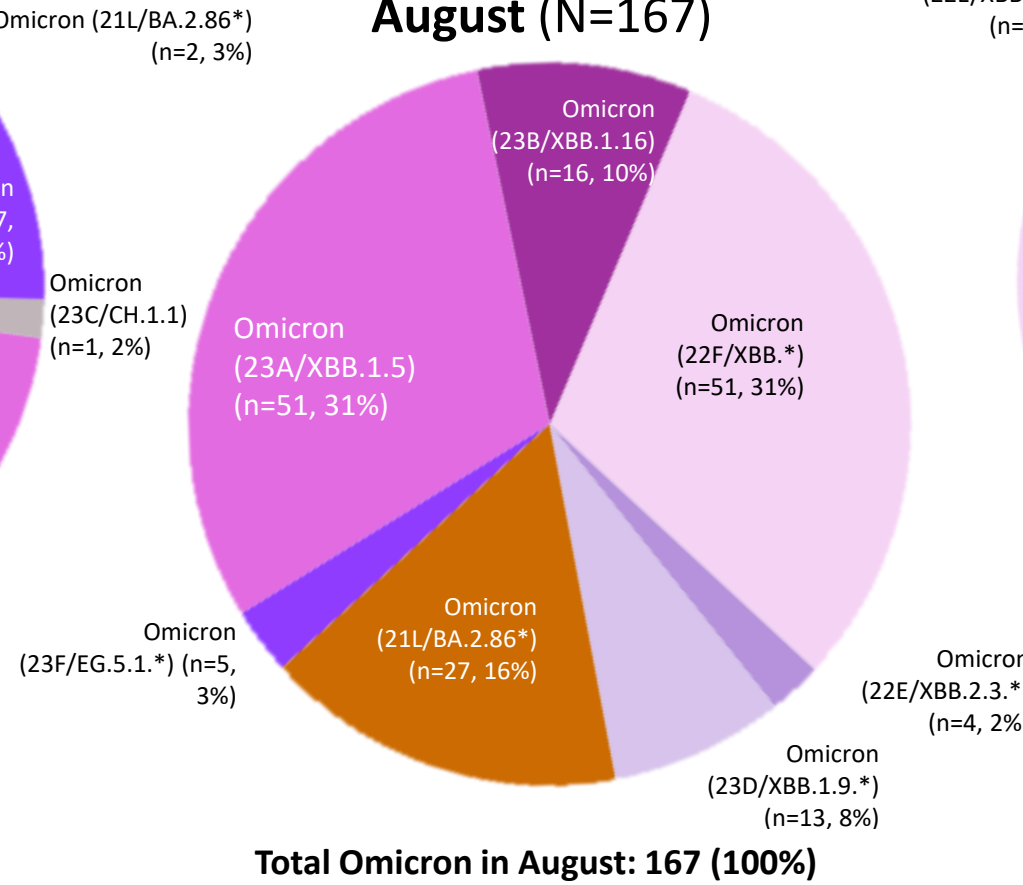
*Bars represent percentage prevalence of variant for the month; total number sequences collected for the month are given below the bar

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

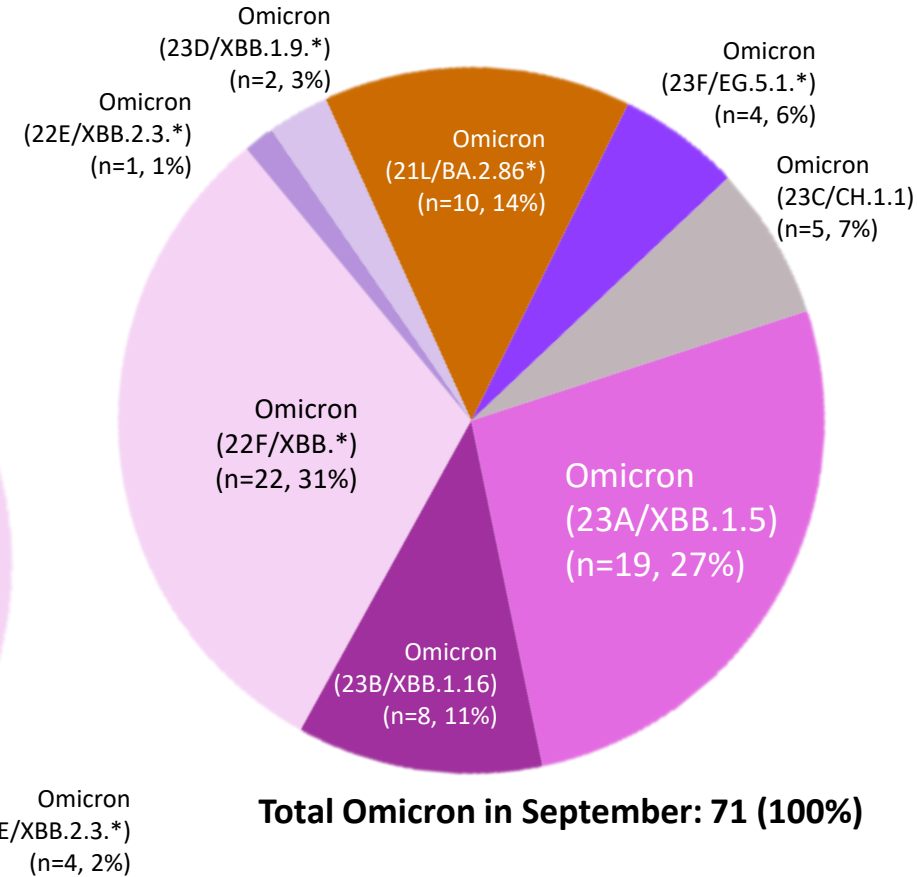
July (N=58)



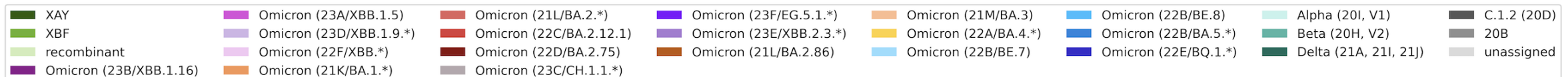
August (N=167)



September (N=71)

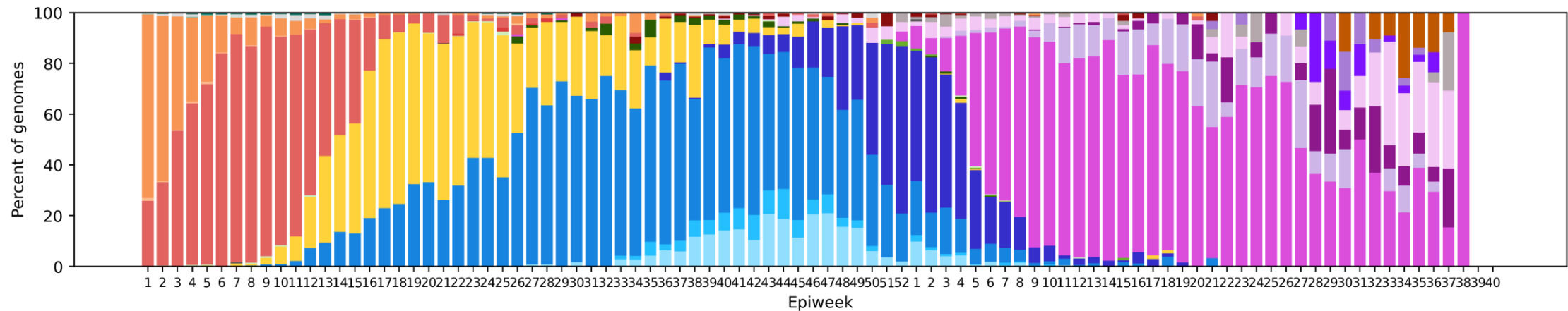
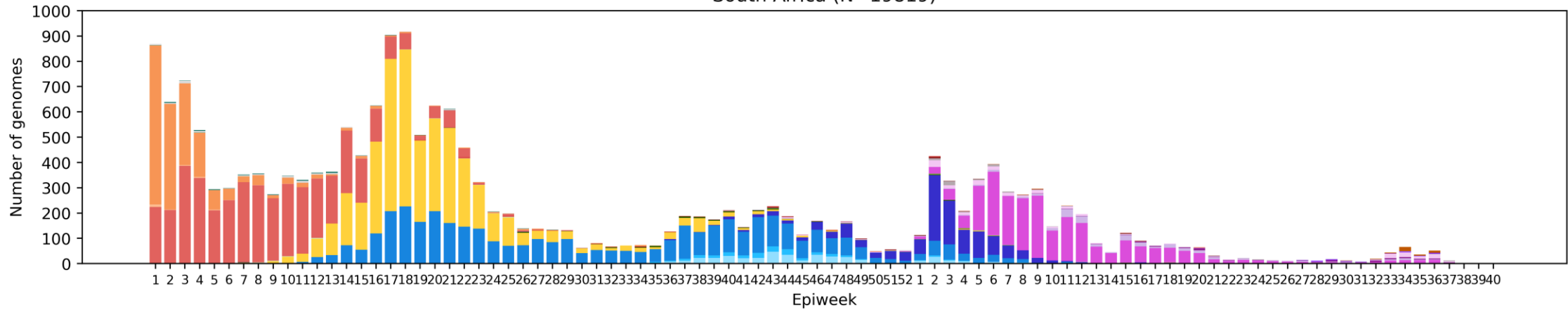


Clade key (bar graph)

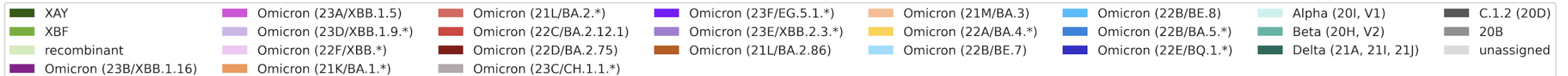


South Africa, 2022-2023, n = 19 819*

South Africa (N=19819)



Clade key (bar graph)



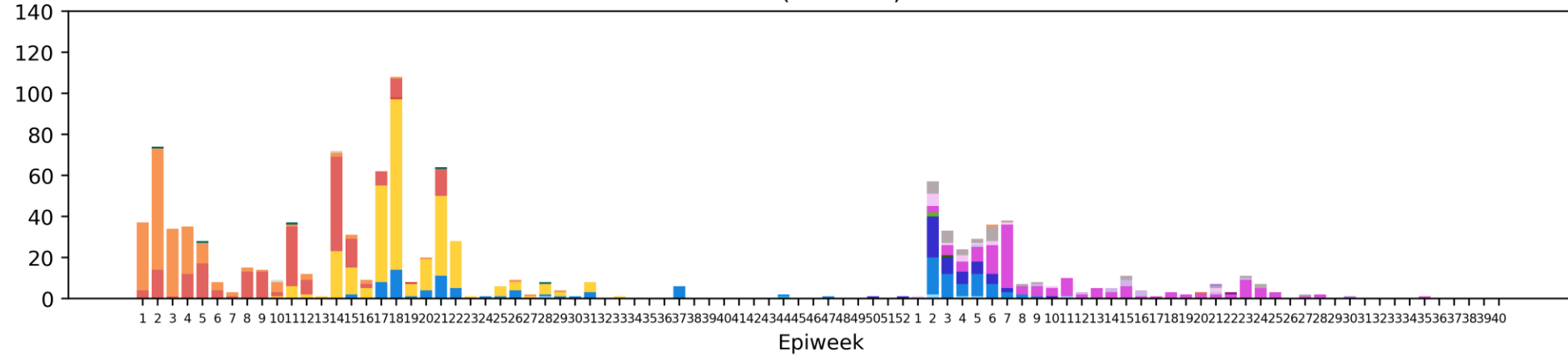
*Excludes sequences missing collection dates. Lineages of particular interest (mainly WHO Omicron subvariants under monitoring) are separate from the main clade groupings.

#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.

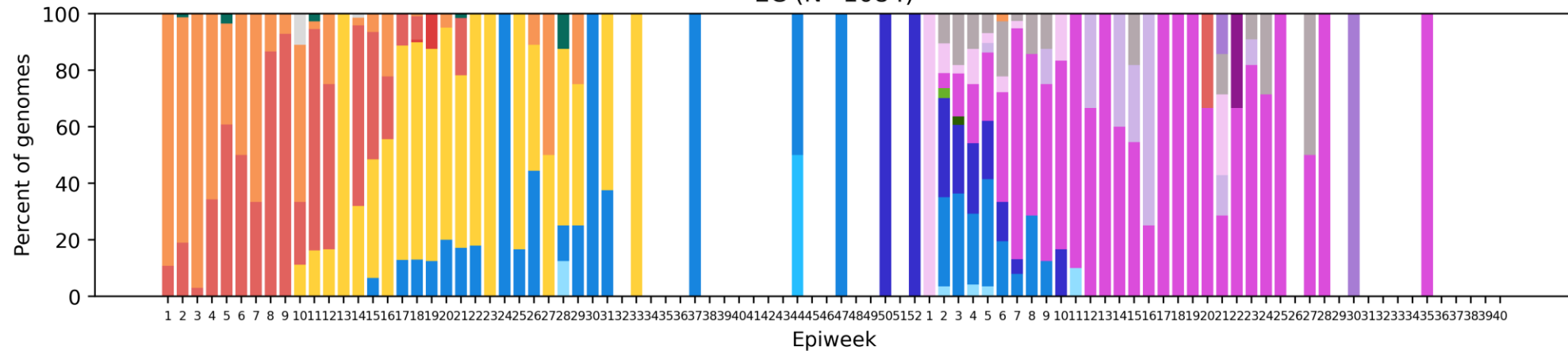
Eastern Cape Province, 2022-2023, n = 1084

Genomes added since last report: 1*

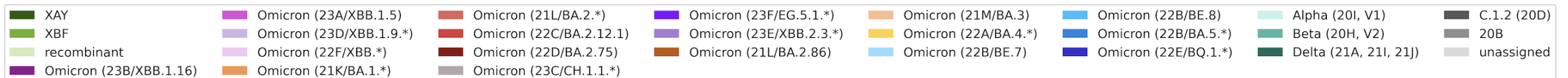
EC (N=1084)



EC (N=1084)



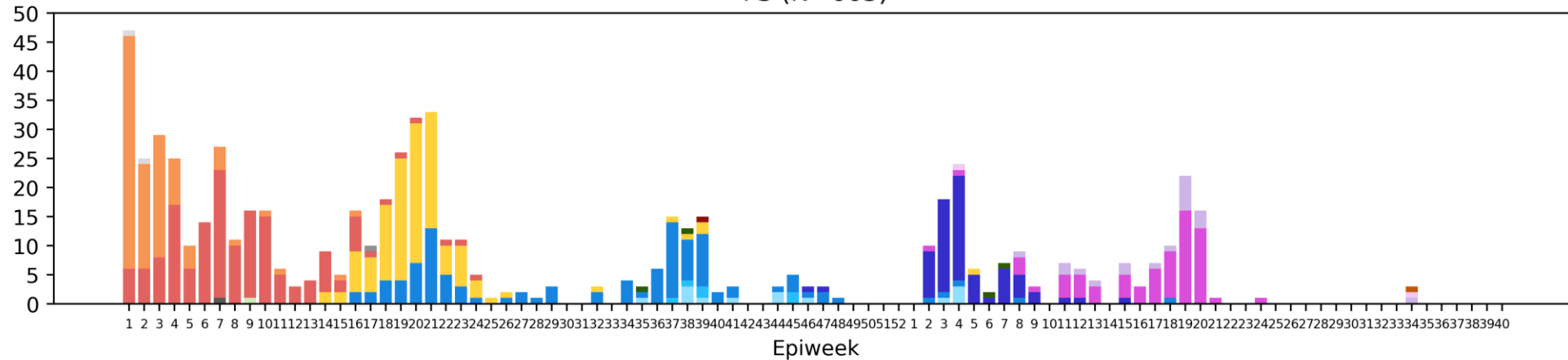
Clade key (bar graph)



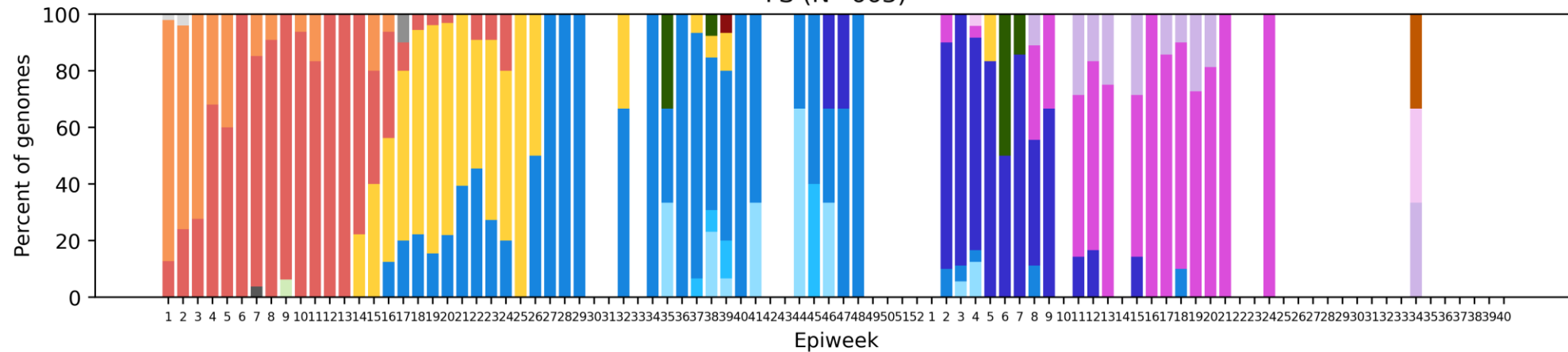
Free State Province, 2022-2023, n = 663

Genomes added since last report: 3*

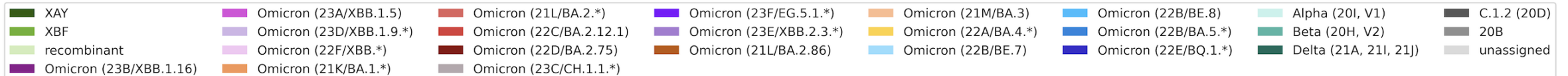
FS (N=663)



FS (N=663)



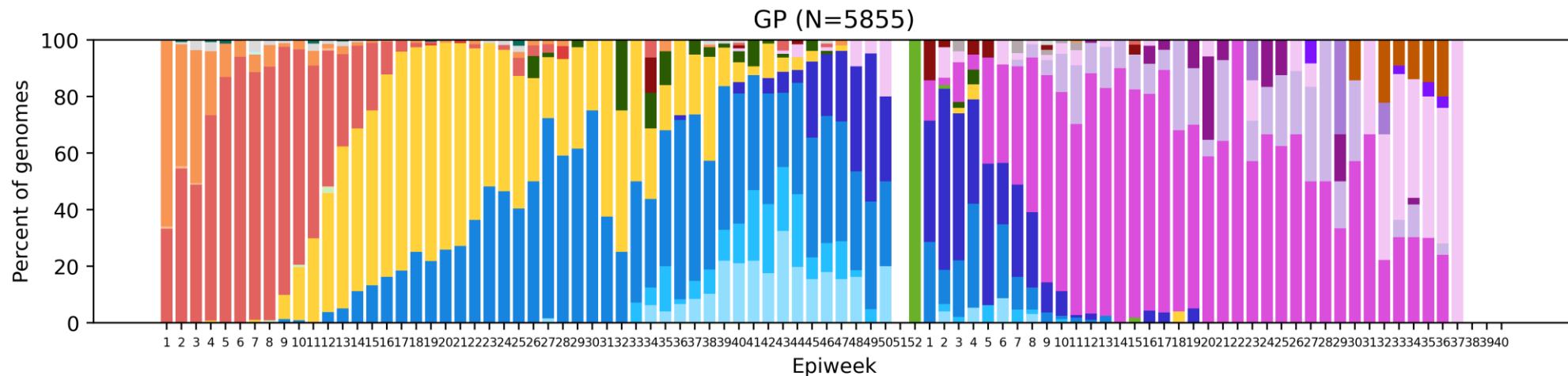
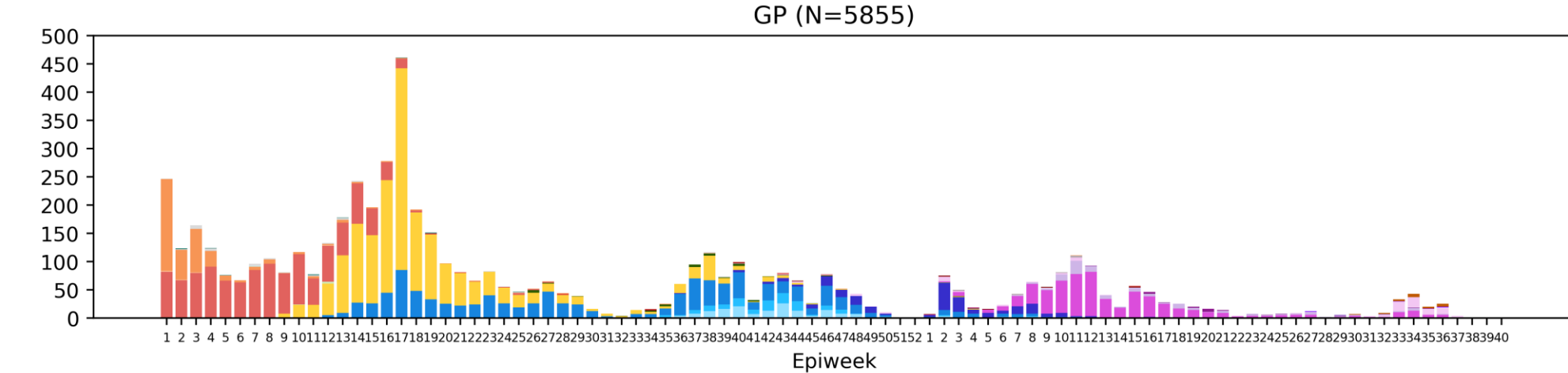
Clade key (bar graph)



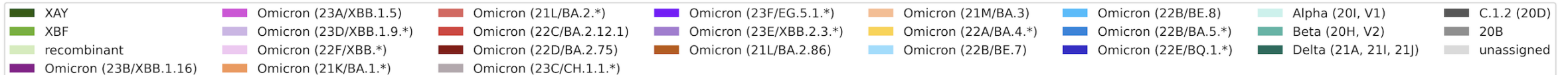
*May include genomes from 2020 and 2021 which are not pictured here and are not included in the slide total.

Gauteng Province, 2022-2023, n = 5855

Genomes added since last report: 87*



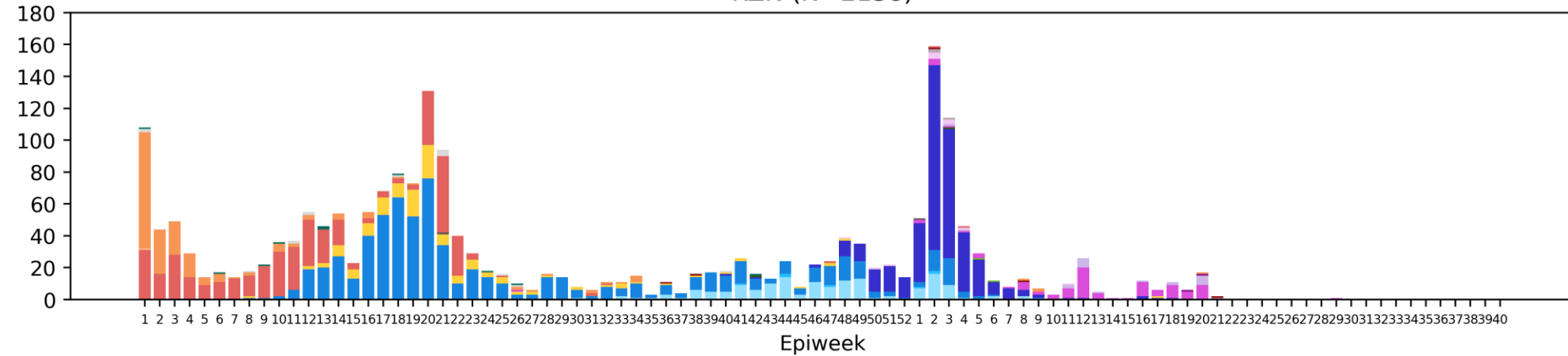
Clade key (bar graph)



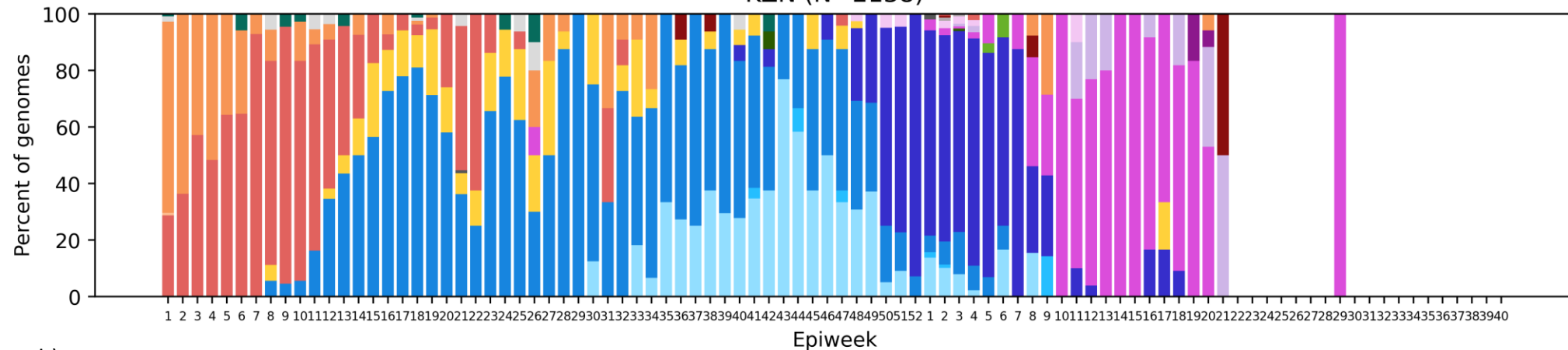
KwaZulu-Natal Province, 2022-2023, n = 2138

Genomes added since last report: 0*

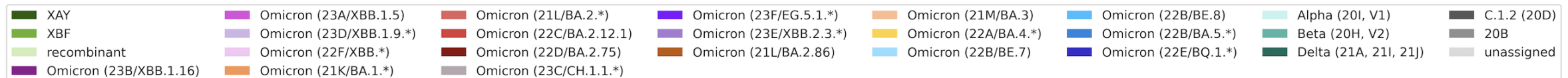
KZN (N=2138)



KZN (N=2138)



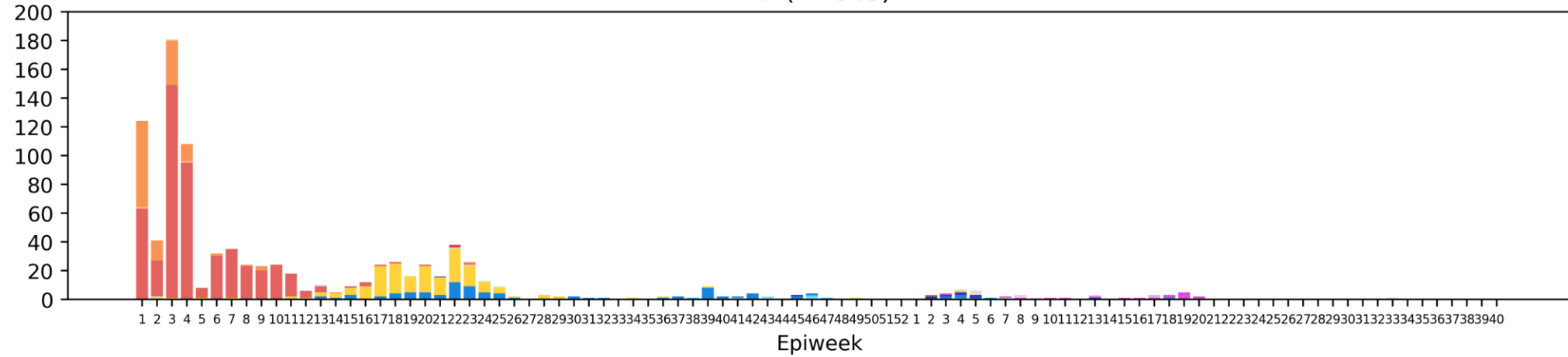
Clade key (bar graph)



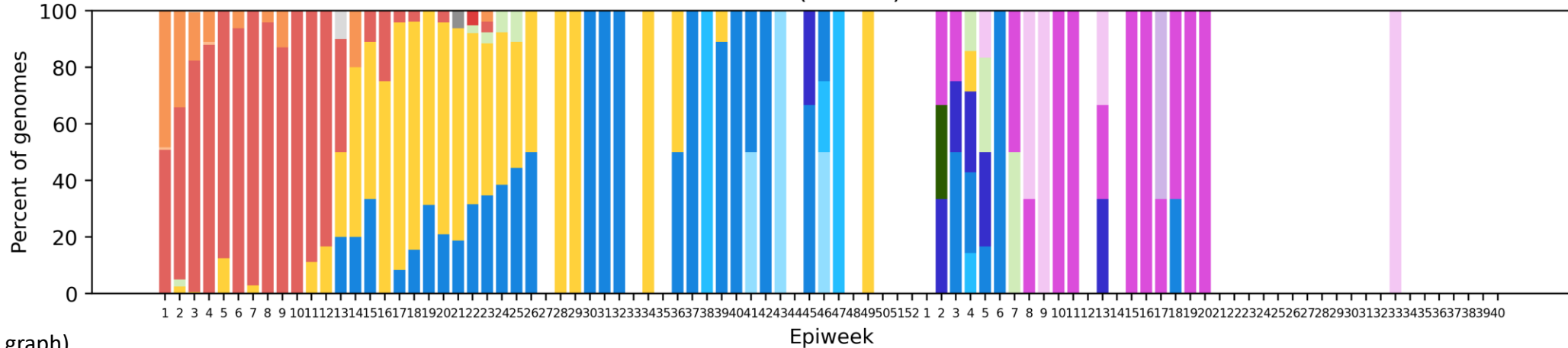
Limpopo Province, 2022-2023, n = 945

Genomes added since last report: 0*

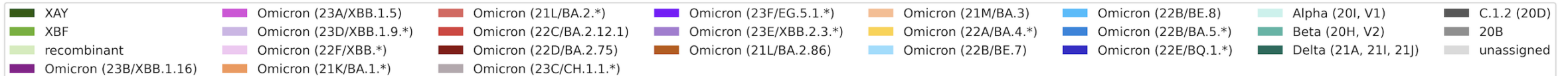
LP (N=945)



LP (N=945)



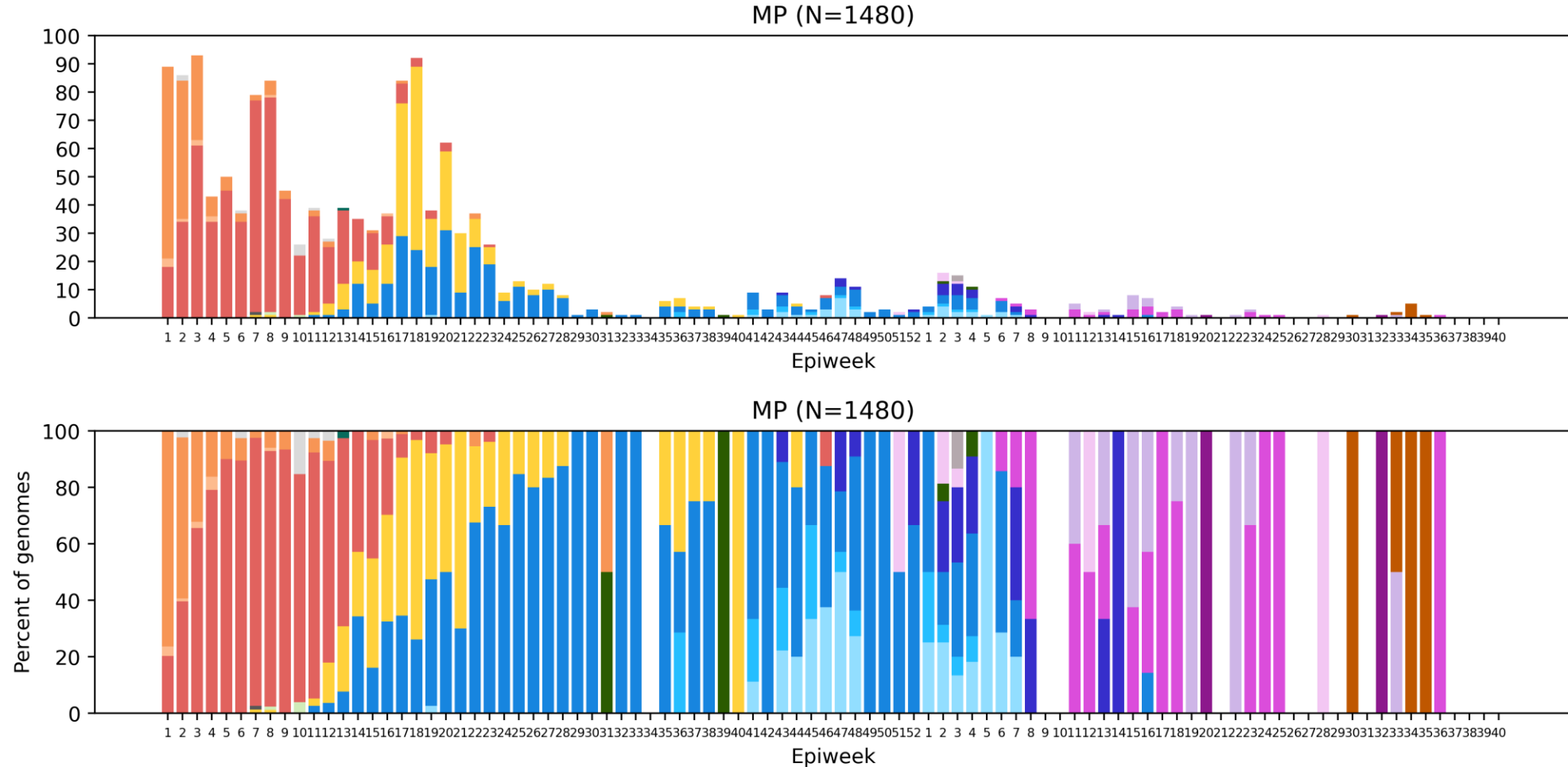
Clade key (bar graph)



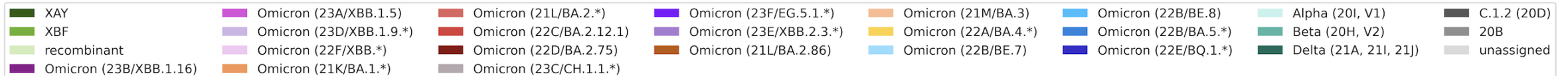
*May include genomes from 2020 and 2021 which are not pictured here and are not included in the slide total.

Mpumalanga Province, 2022-2023, n = 1480

Genomes added since last report: 5*



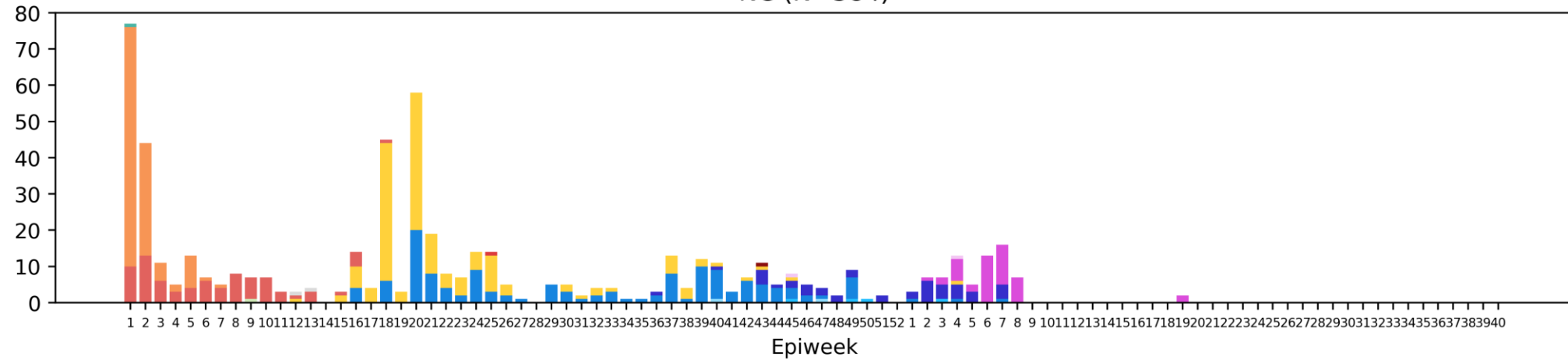
Clade key (bar graph)



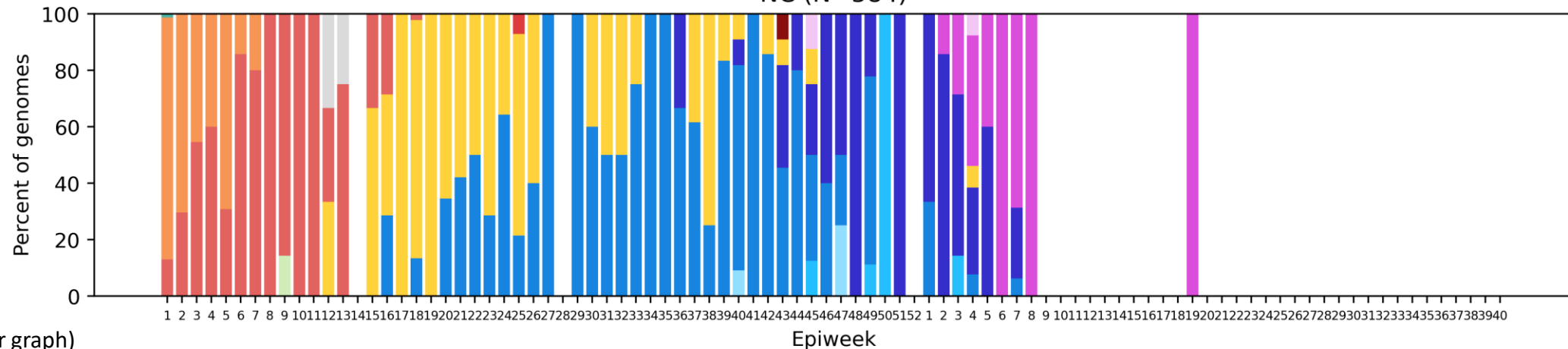
Northern Cape Province, 2022-2023, n = 584

Genomes added since last report: 0*

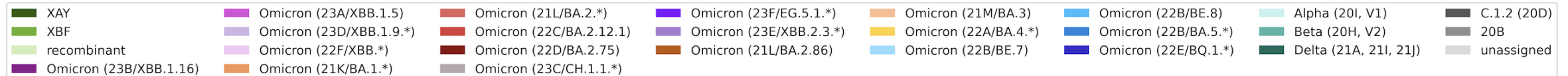
NC (N=584)



NC (N=584)



Clade key (bar graph)

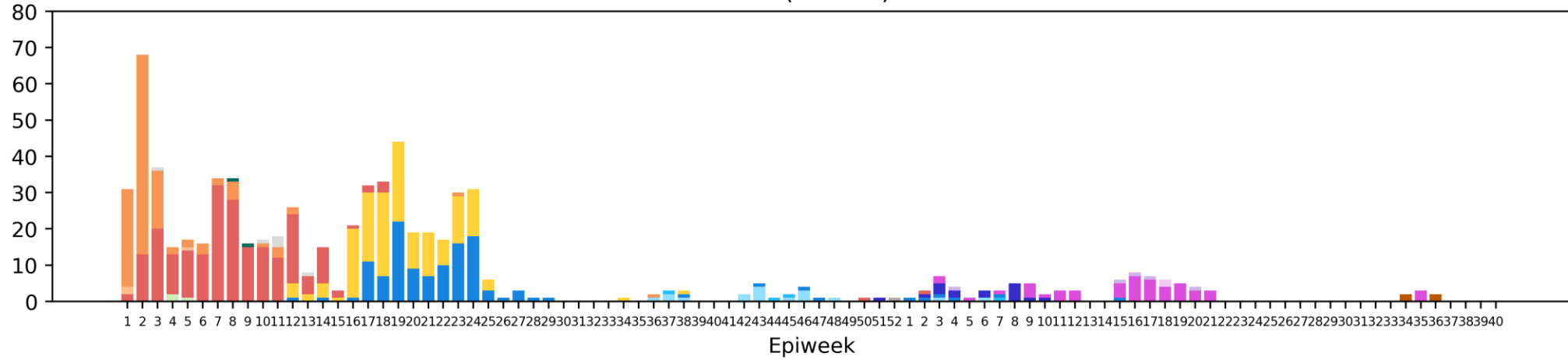


*May include genomes from 2020 and 2021 which are not pictured here and are not included in the slide total.

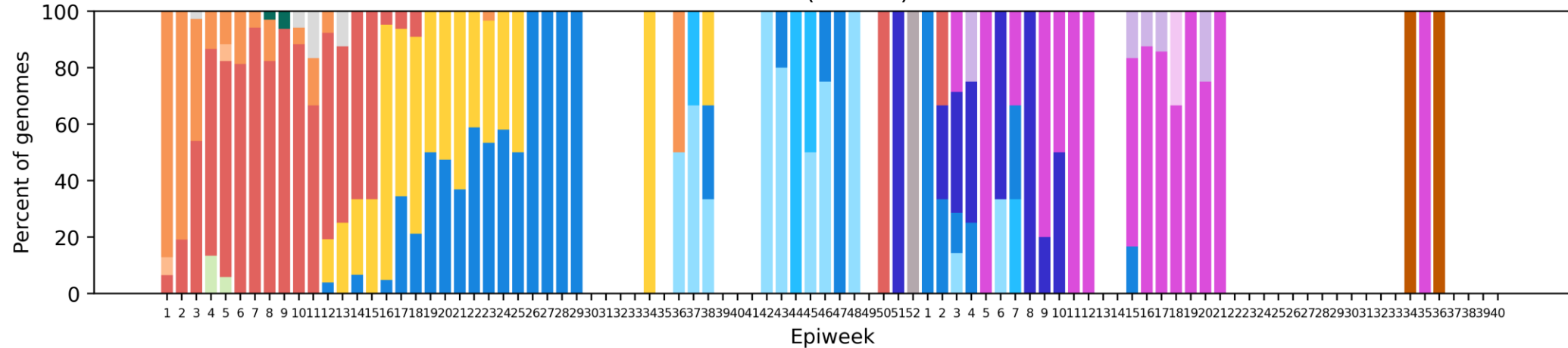
North West Province, 2022-2023, n = 727

Genomes added since last report: 5*

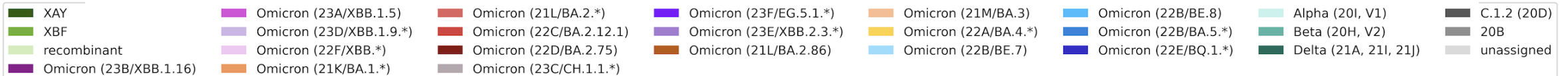
NW (N=727)



NW (N=727)



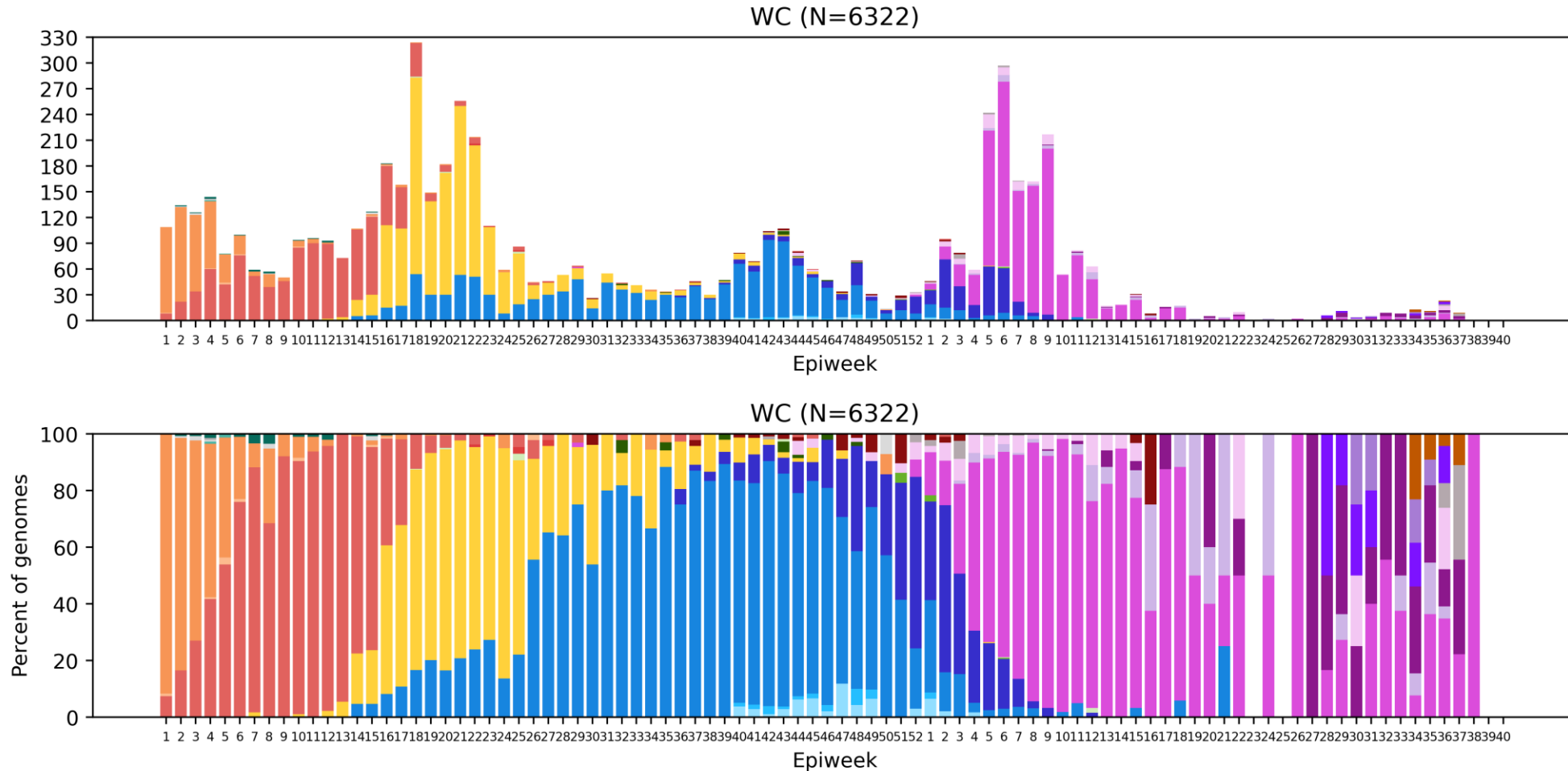
Clade key (



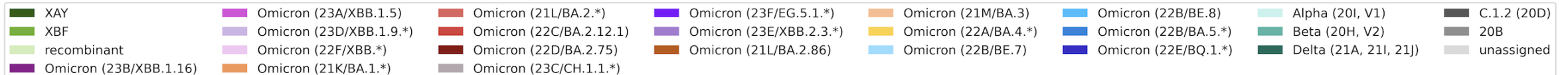
*May include genomes from 2020 and 2021 which are not pictured here and are not included in the slide total.

Western Cape Province, 2022-2023, n = 6322

Genomes added since last report: 265*



Clade key (bar graph)



Summary

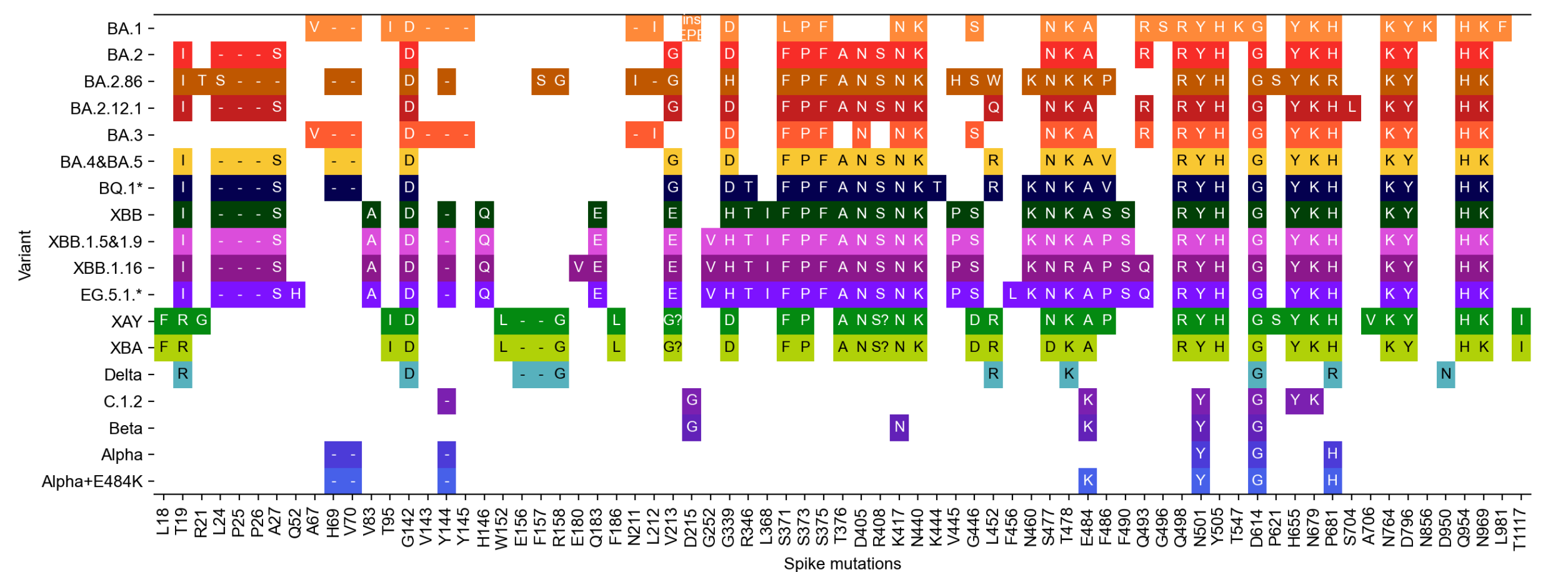
- **Sequencing update**

- July sequences (n=58) are from the Eastern Cape, KwaZulu-Natal, Gauteng, Mpumalanga, and the Western Cape. August sequences (n=167) are from all provinces except the Northern Cape and KwaZulu-Natal. September sequences (n=71) are from the Western Cape, Gauteng, Mpumalanga, 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 27% of September sequences
- XBB.1.16 has been detected in July (17%), August (10%), and September (11%)
- XBB.1.9.* (clade 23D) was detected in sequences from July (16%), August (8%) and September (3%)
- Sixteen sequences of the EG.5.1.* lineage (clade 23F) have been detected in Gauteng (n=3) and the Western Cape (n=13) in July (n=7, 12%), August (n=5, 3%), and September (n=4, 6%)
- Thirty-nine sequences of the BA.2.86 lineage have been detected in Gauteng (n=20), Mpumalanga (n=8), Western Cape (n=6), North West (n=4), and Free State (n=1), in July (n=2, 3%), August (n=27, 16%), and September (n=10, 14%)

Spike protein mutation* profile of Variants of Interest and Concern

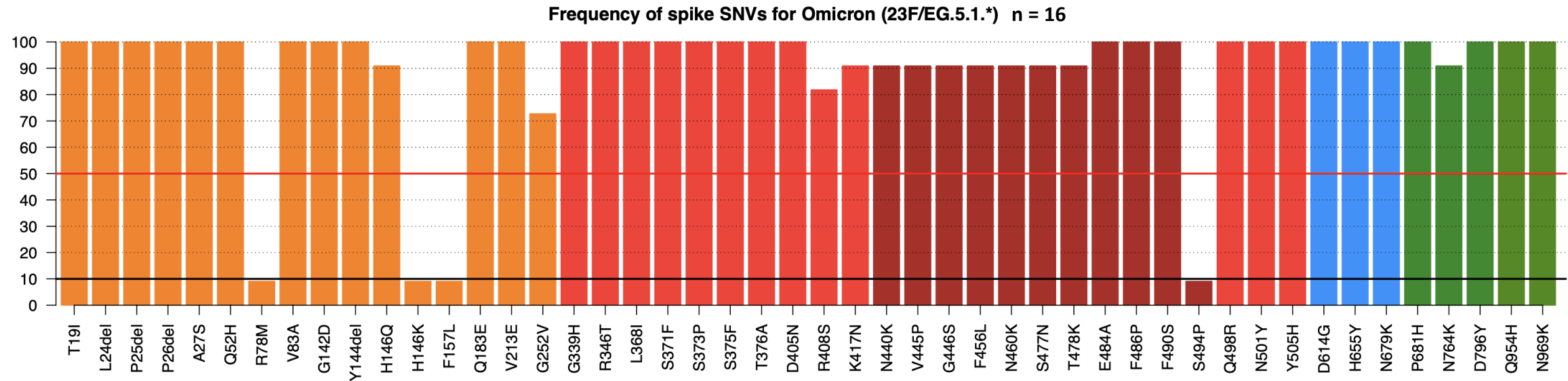
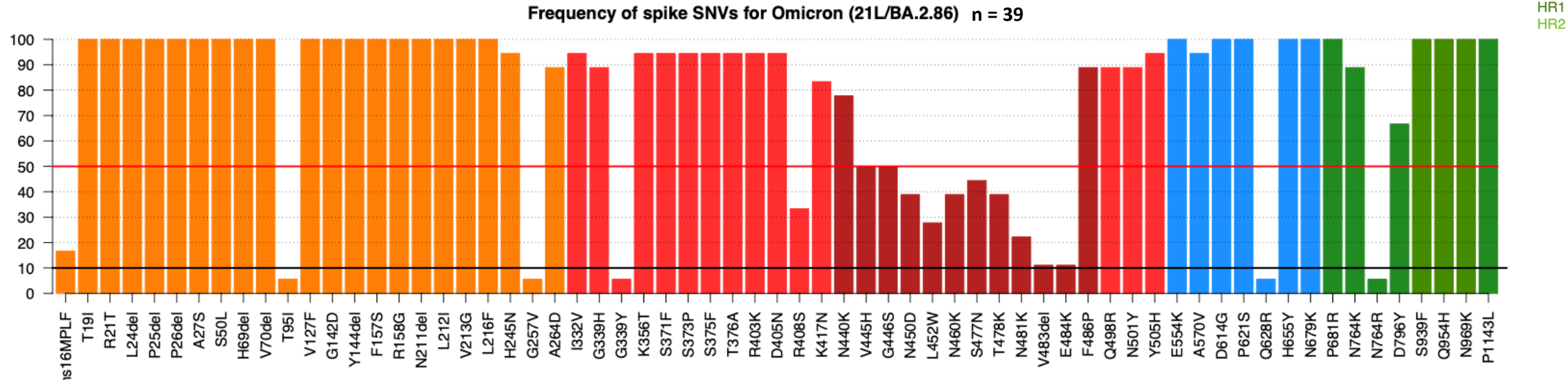


- Multiple changes within the two immunogenic regions in S1 (NTD and RBD)
 - Including a three amino acid insertion
- Accumulation of mutations surrounding the furin cleavage site
 - Including combination of N679K and P681H
- Effect of most spike S2 subunit changes have not been defined, but may be linked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

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

BA.2.86 and EG.5.1 spike mutations*

Percentage



SP
NTD
RBD
RBM
S1
S2
HR1
HR2

Mutation

*Only mutations present in $\geq 1\%$ of sequences are shown.

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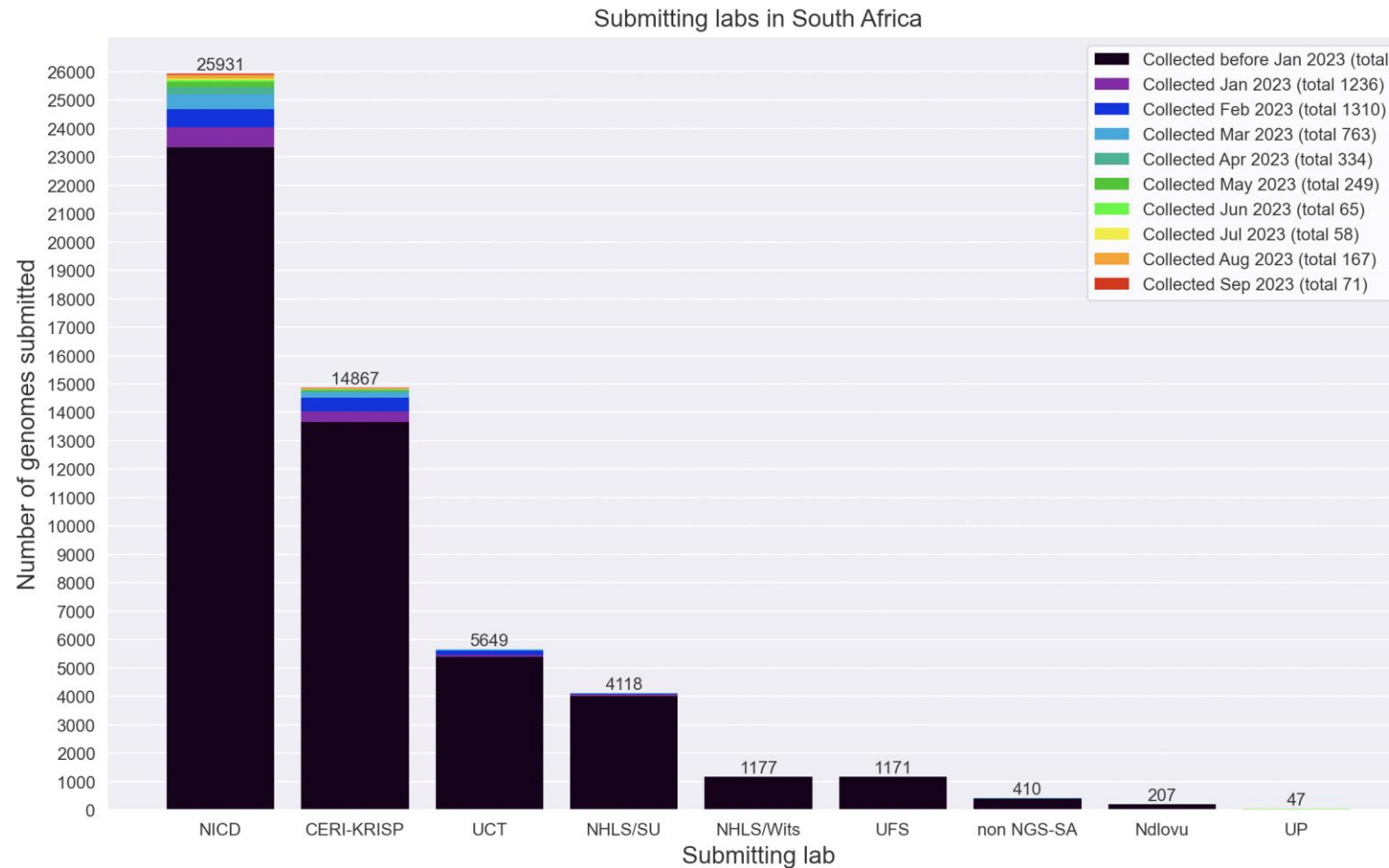


EDCTP

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= 53 577)



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 09 Aug 2023

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

<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

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.)