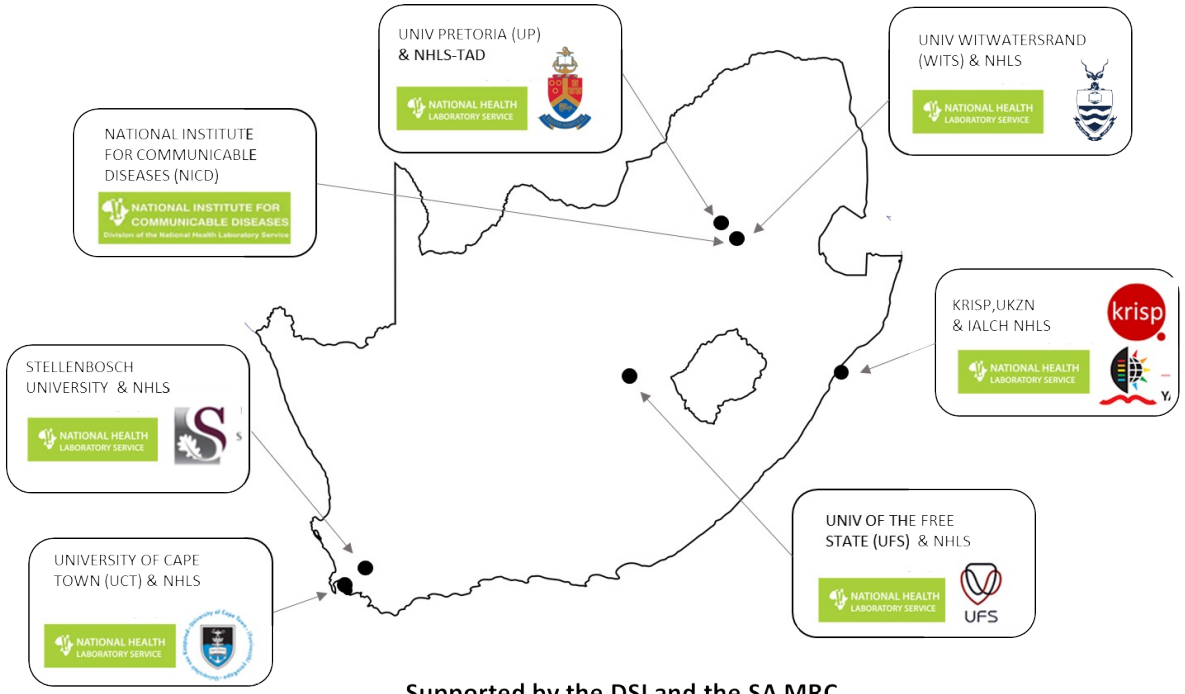
Network for Genomic Surveillance in South Africa (NGS-SA)

SARS-CoV-2 Sequencing Update
10 March 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)

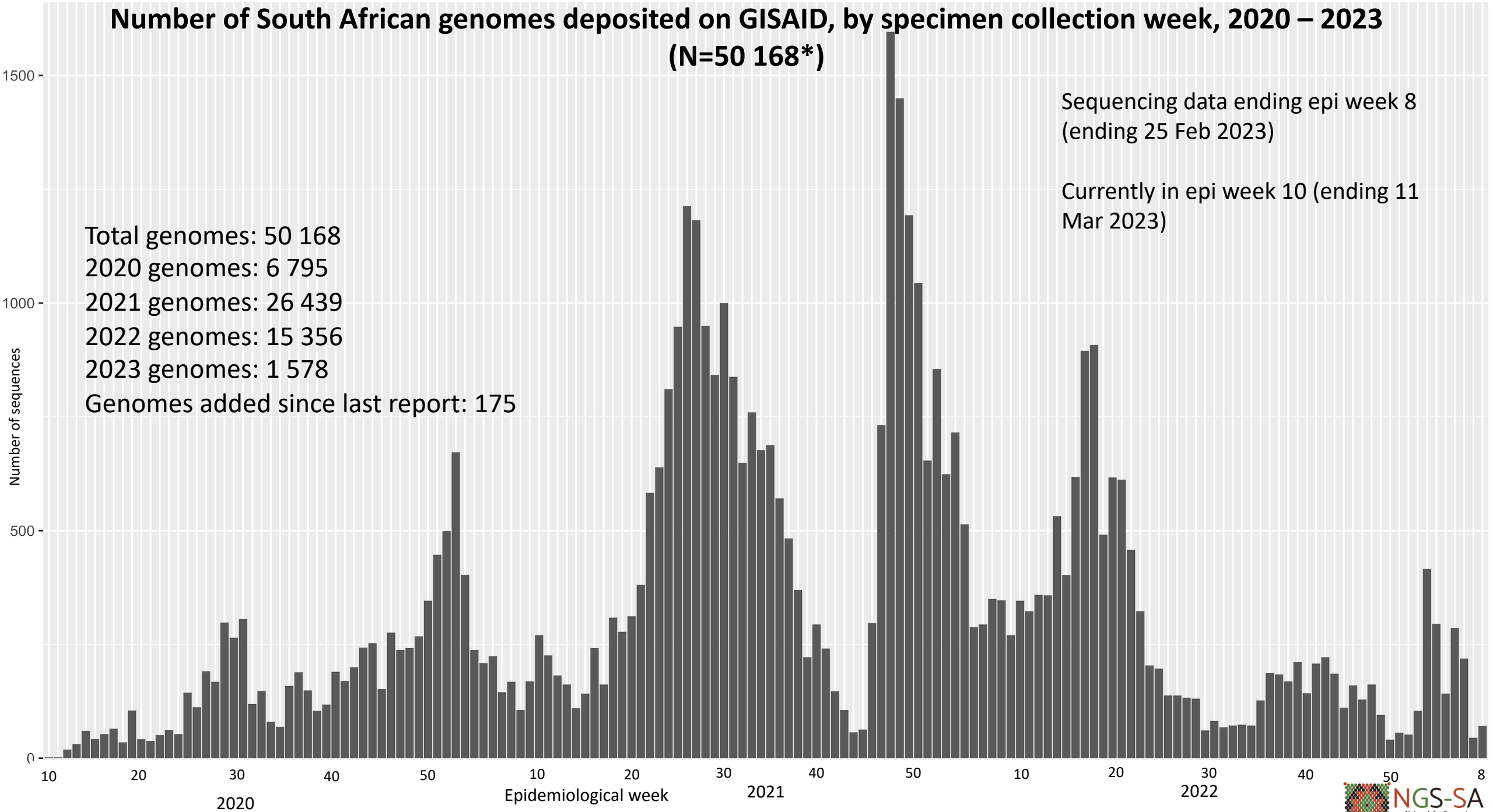
The genomic data presented here are based on South African SARS-CoV-2 sequence data downloaded from GISAID (www.gisaid.org) on 10 March 2023 at 09h00

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=50 168*)



*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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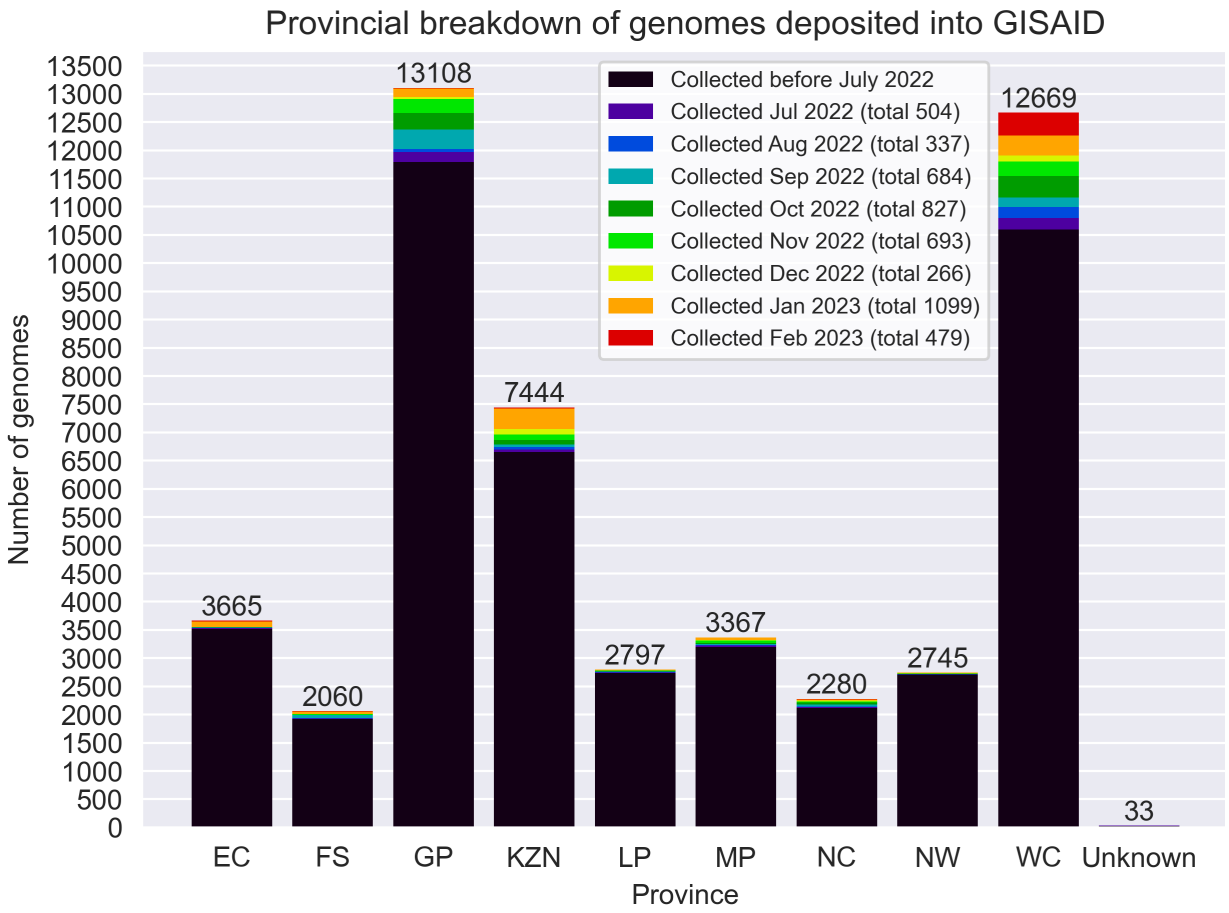
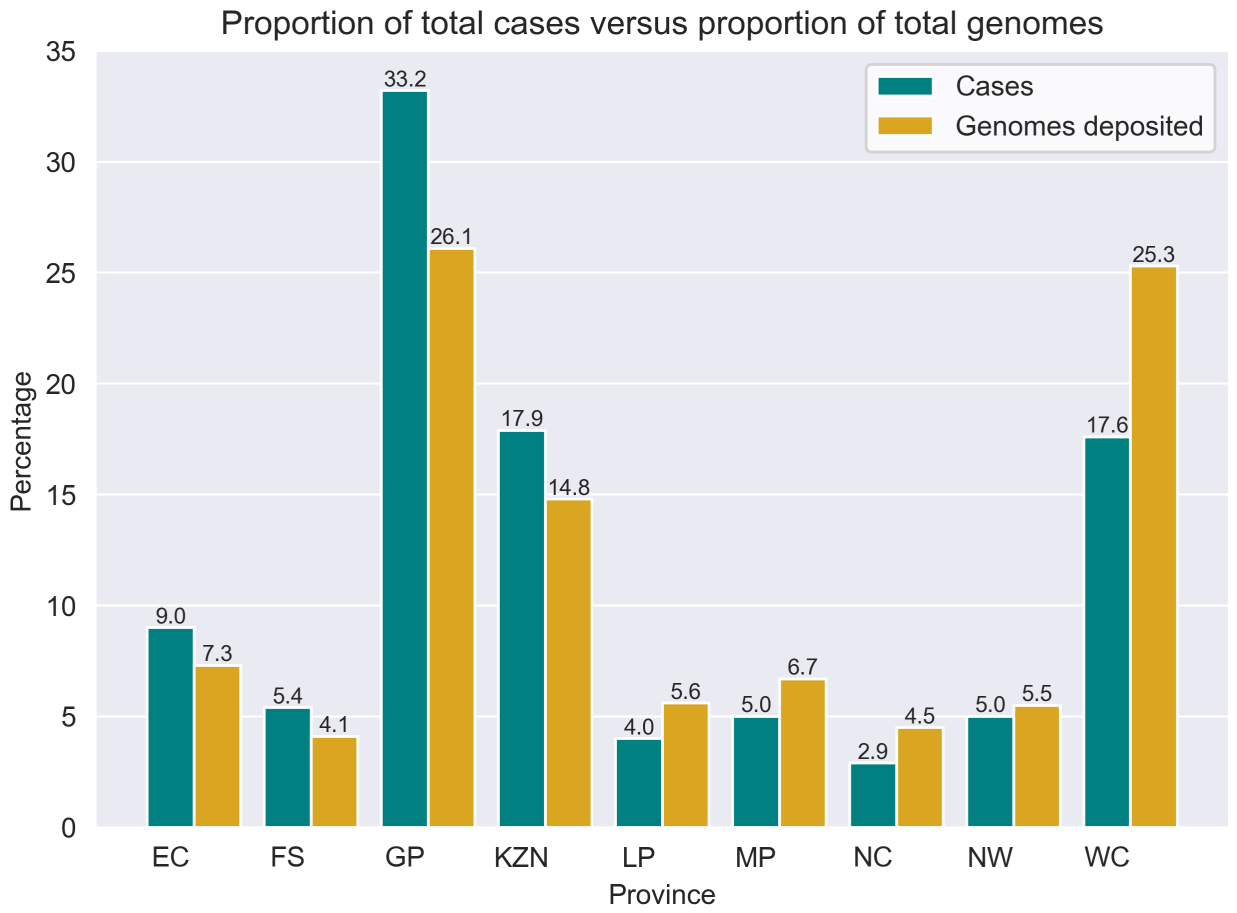
GISAID genomes vs total cases, 2020 – 2023 (N=50 168)





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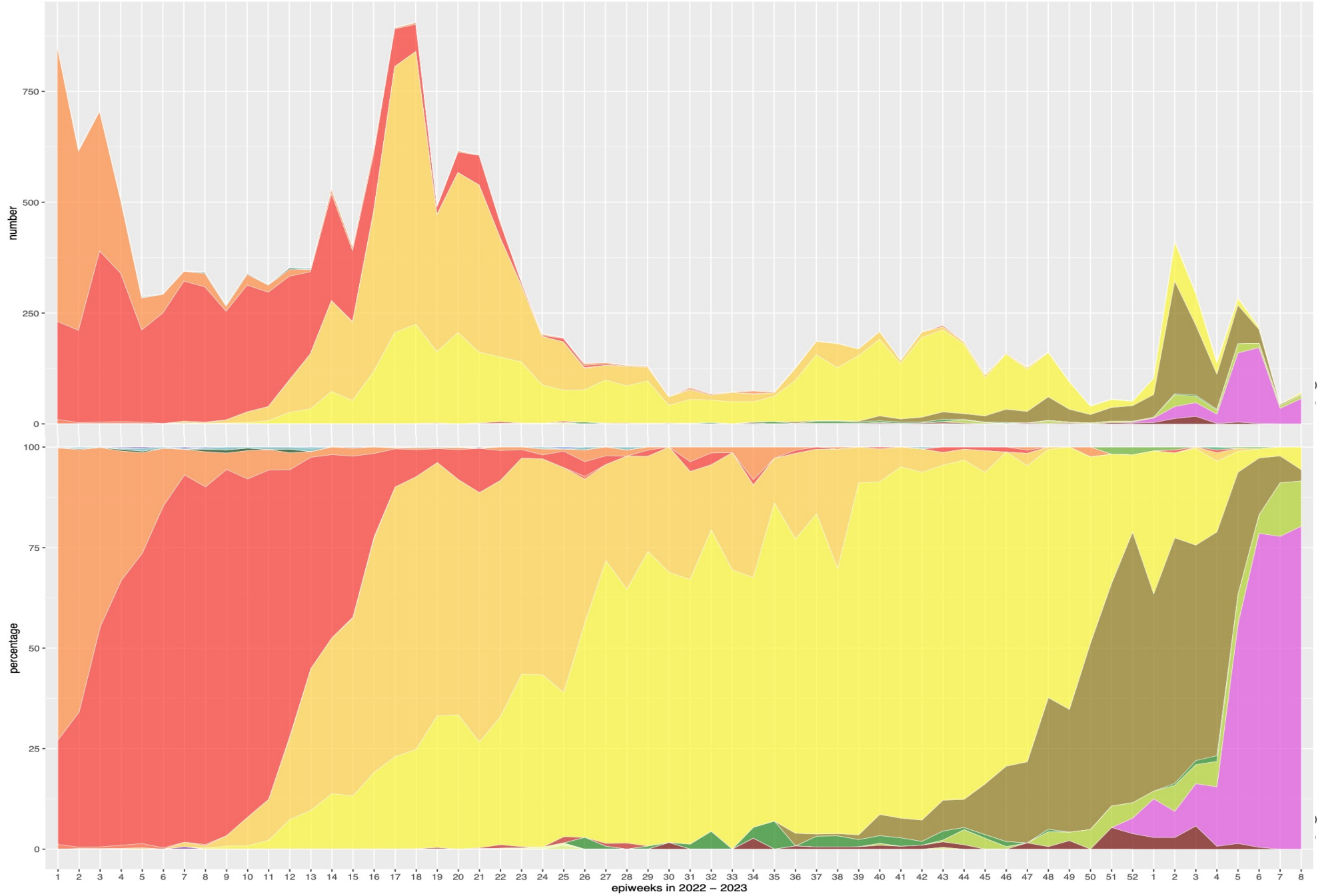
Number and percentage of clades by epiweek in South Africa, 2022-2023 (16 891*)



Sequencing data ending epi week 8 (ending 25 Feb 2023)

Currently in epi week 10 (ending 11 Mar 2023)

*Excludes sequences missing collection dates, as well as those collected January 1st and 2nd 2021 as they are part of epiweek 53 of 2020.

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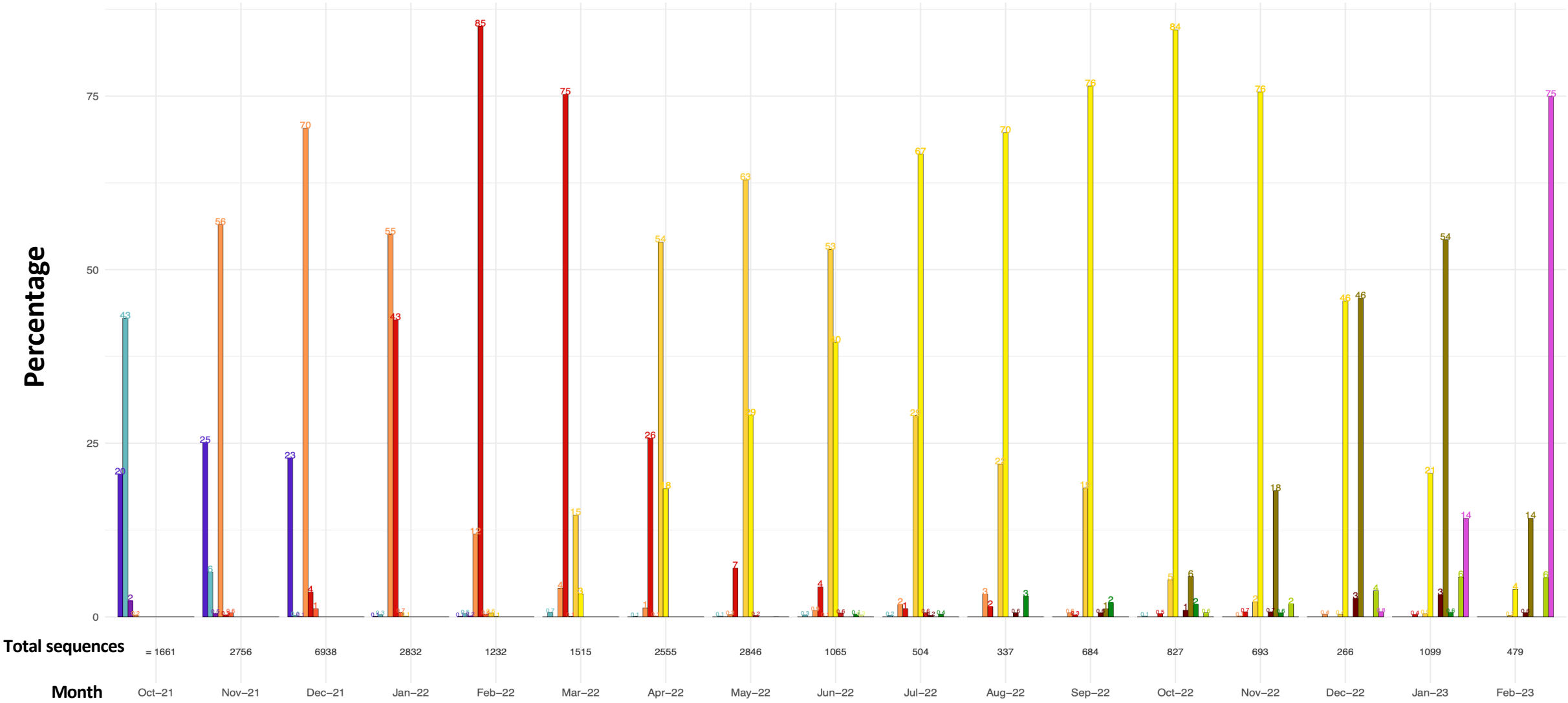
Detection Rates: Beta, Delta, C.1.2, recombinants, and Omicron



Beta

Delta

C.1.2

Omicron (21K/BA.1.*)

Omicron (21L/BA.2.*)

Omicron (21M/BA.3)

Omicron (22A/BA.4)

Omicron (22B/BA.5)

Omicron (22C/BA.2.12.1)

Omicron (22D/BA.2.75.*)

Omicron (22E/BQ.1.*)

XAY

XBA

Omicron (22F/XBB.*)

Omicron (23A/XBB.1.5)

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

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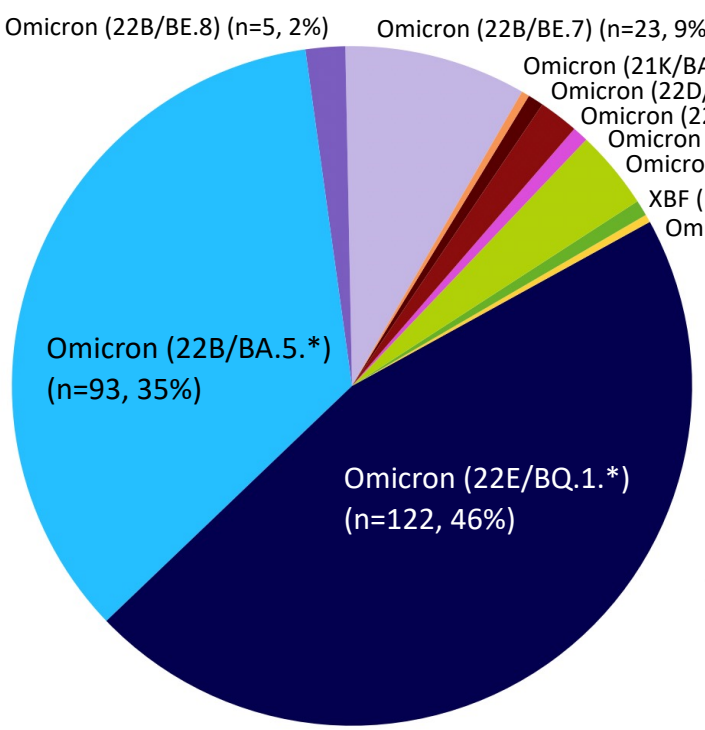
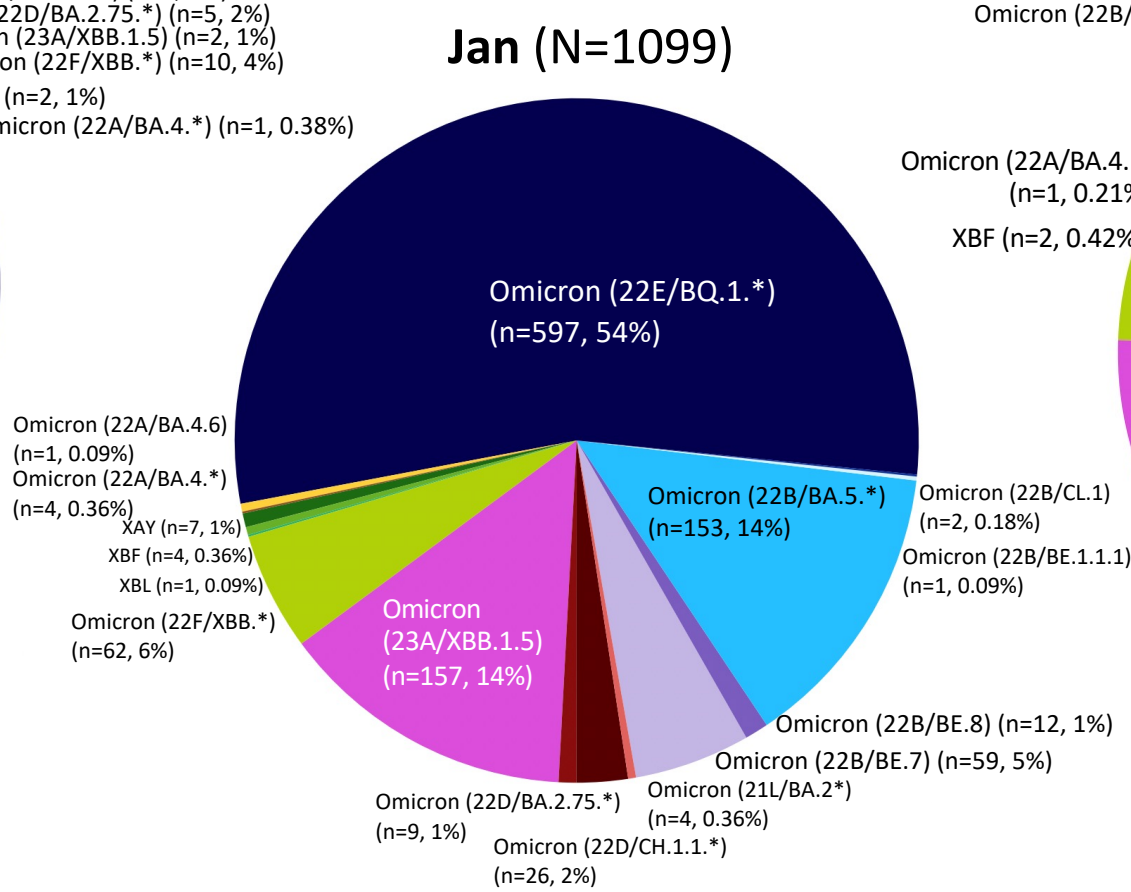
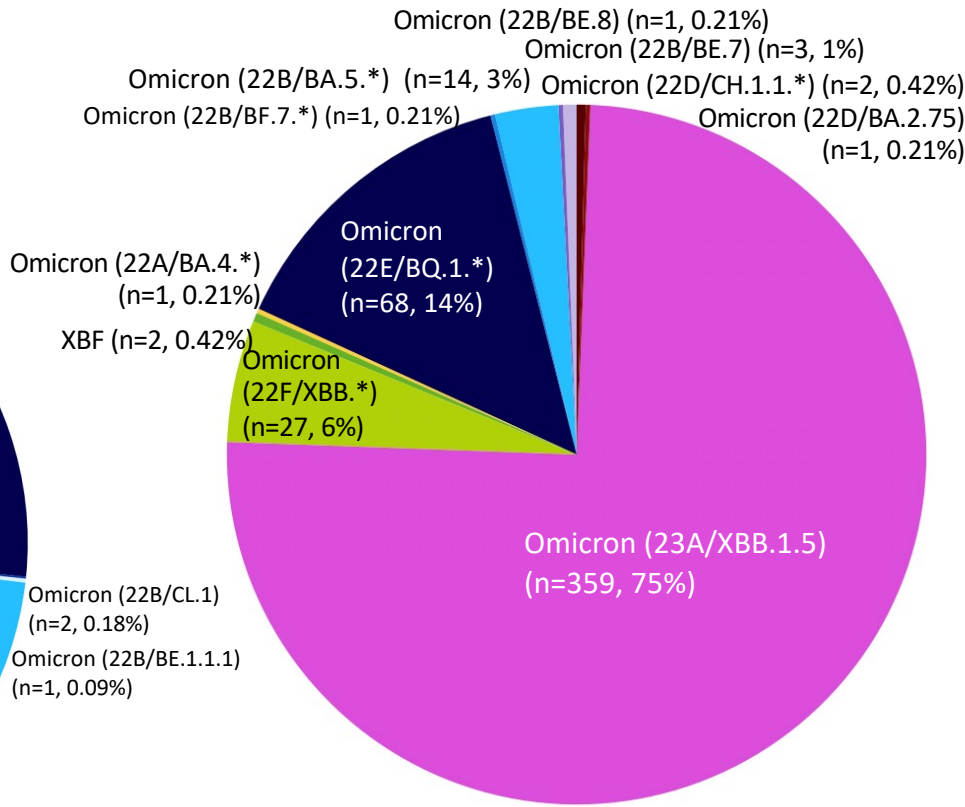
Prevalence of Variants of Concern (VOC) and Variants of Interest (VOI) in Dec 2022– Feb 2023



Total Omicron in December: 266 (100%)



Total Omicron in January: 1092 (99.4%)

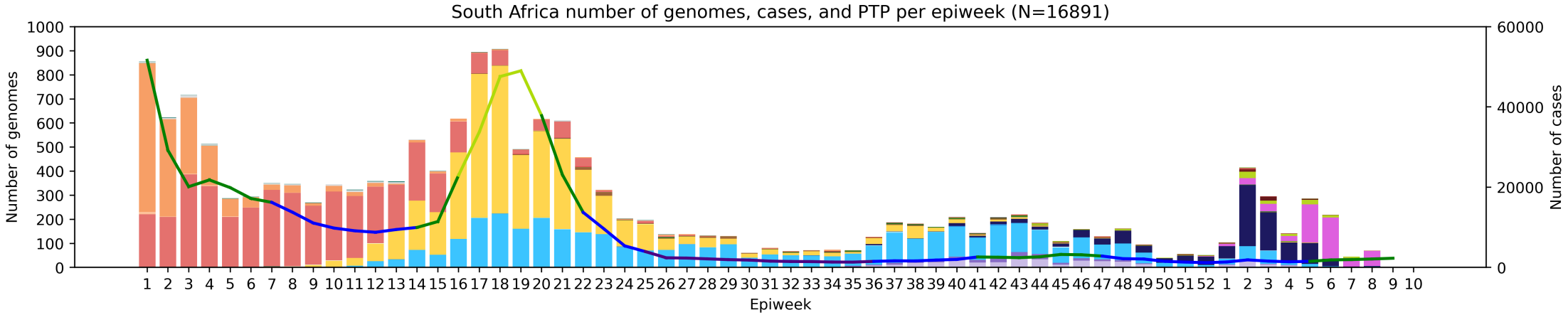


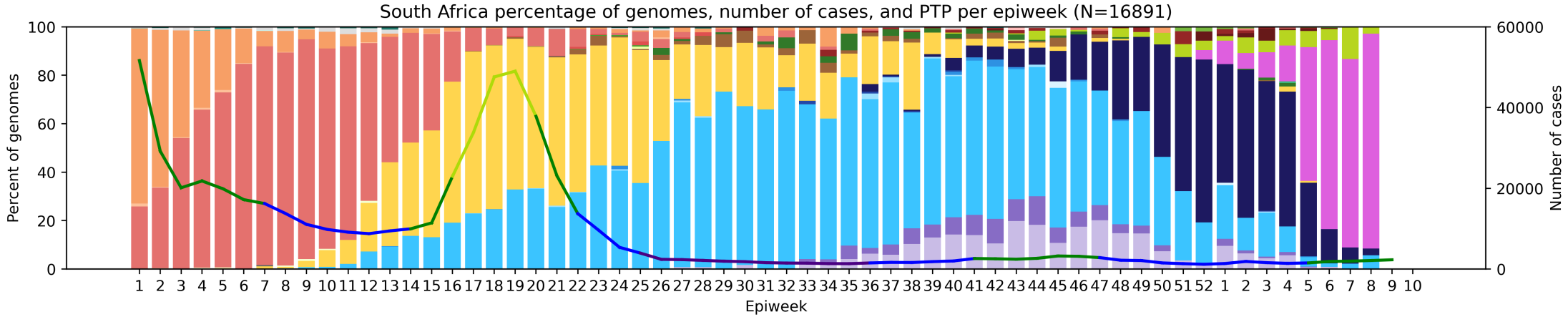
Total Omicron in February: 479 (100%)

Omicron (23A/XBB.1.5) | Omicron (22F/XBB.*) | XAY | XBA | XBF | XAS | XAZ | XT | XBL | Omicron (21K/BA.1.*) | Omicron (21L/BA.2.*) | Omicron (21L/CM.4) | Omicron (21L/BA.2.3.20) | Omicron (22C/BA.2.12.1) | Omicron (22D/BA.2.75) | Omicron (22D/CH.1.1.*) | Omicron (21M/BA.3) | Omicron (22A/BA.4.*) | Omicron (22A/BA.4.6.*) | Omicron (22B/BA.5.*) | Omicron (22B/BF.7.*) | Omicron (22B/BA.5.9) | Omicron (22B/CL.1) | Omicron (22B/BE.1.1.1) | Omicron (22E/BQ.1.*) | Omicron (22B/BE.7) | Omicron (22B/BE.8) | Alpha (20I, V1) | Beta (20H, V2) | Delta (21A, 21I, 21J) | C.1.2 (20D) | 20B | unassigned

Note: XBF and XBL are Omicron-Omicron recombinants and so are counted in the total number of Omicrons.

South Africa, 2022-2023, n = 16 891*





Clade key (bar graph)

Omicron (23A/XBB.1.5)
Omicron (22F/XBB.*)
XAY
XBA
XBF
XAS
XAZ
XT
XBL
Omicron (21K/BA.1.*)
Omicron (21L/BA.2.*)
Omicron (21L/CM.4)
Omicron (21L/BA.2.3.20)
Omicron (22C/BA.2.12.1)
Omicron (22D/BA.2.75)
Omicron (22D/CH.1.1.*)
Omicron (21M/BA.3)
Omicron (22A/BA.4.*)
Omicron (22A/BA.4.6.*)
Omicron (22B/BA.5.*)
Omicron (22B/BF.7.*)
Omicron (22B/BA.5.9)
Omicron (22B/CL.1)
Omicron (22B/BE.1.1.1)
Omicron (22E/BQ.1.*)
Omicron (22B/BE.7)
Omicron (22B/BE.8)
Alpha (20I, V1)
Beta (20H, V2)
Delta (21A, 21I, 21J)
C.1.2 (20D)
20B
unassigned
Cases

Weekly percentage testing positive key (line graph)

≤ 5
6 - 10
11 - 20
21 - 30
31 - 40
41 - 50
51 - 55

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

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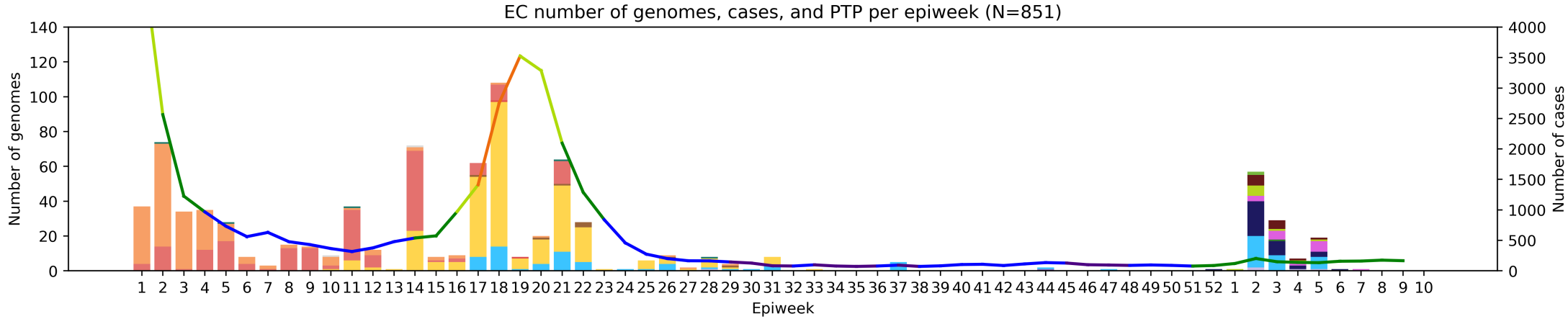
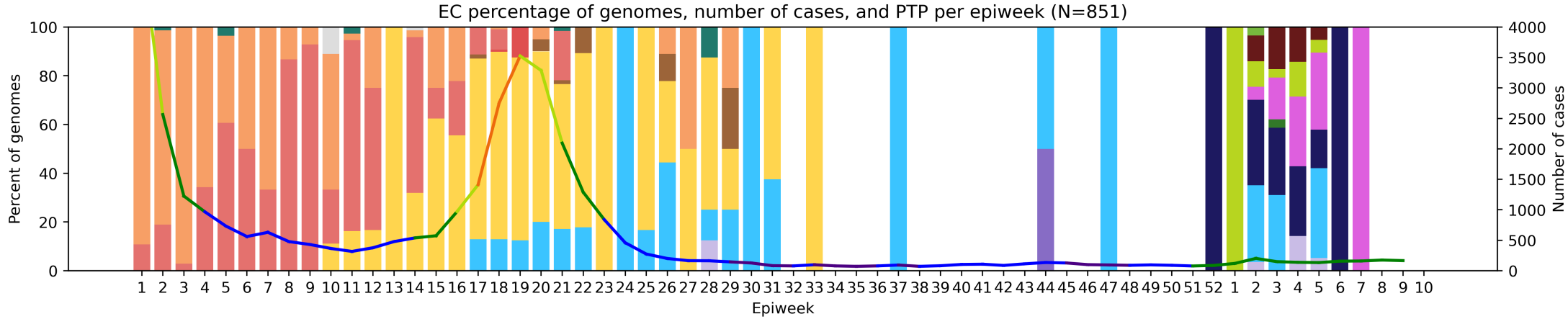
Eastern Cape Province, 2022-2023, n = 851

Genomes added since last report: 0*





Clade key (bar graph)

Omicron (23A/XBB.1.5)
Omicron (22F/XBB.*)
XAY
XBA
XBF
XAS
XAZ
XT
XBL
Omicron (21K/BA.1.*)
Omicron (21L/BA.2.*)
Omicron (21L/CM.4)
Omicron (21L/BA.2.3.20)
Omicron (22C/BA.2.12.1)
Omicron (22D/BA.2.75)
Omicron (22D/CH.1.1.*)
Omicron (21M/BA.3)
Omicron (22A/BA.4.*)
Omicron (22A/BA.4.6.*)
Omicron (22B/BA.5.*)
Omicron (22B/BF.7.*)
Omicron (22B/BA.5.9)
Omicron (22B/CL.1)
Omicron (22B/BE.1.1.1)
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Omicron (22B/BE.7)
Omicron (22B/BE.8)
Alpha (20I, V1)
Beta (20H, V2)
Delta (21A, 21I, 21J)
C.1.2 (20D)
20B
unassigned
Cases

Weekly percentage testing positive key (line graph)

≤ 5
6 - 10
11 - 20
21 - 30
31 - 40
41 - 50
51 - 55

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

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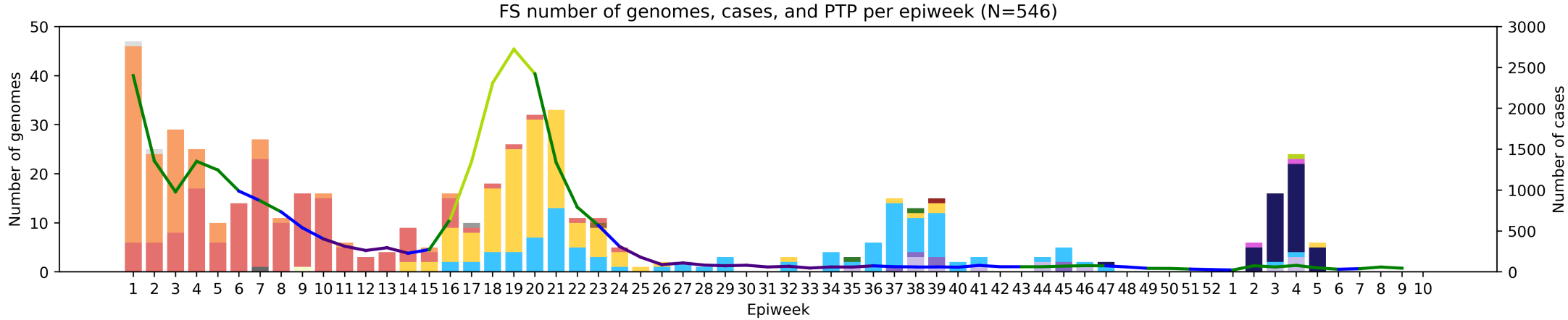
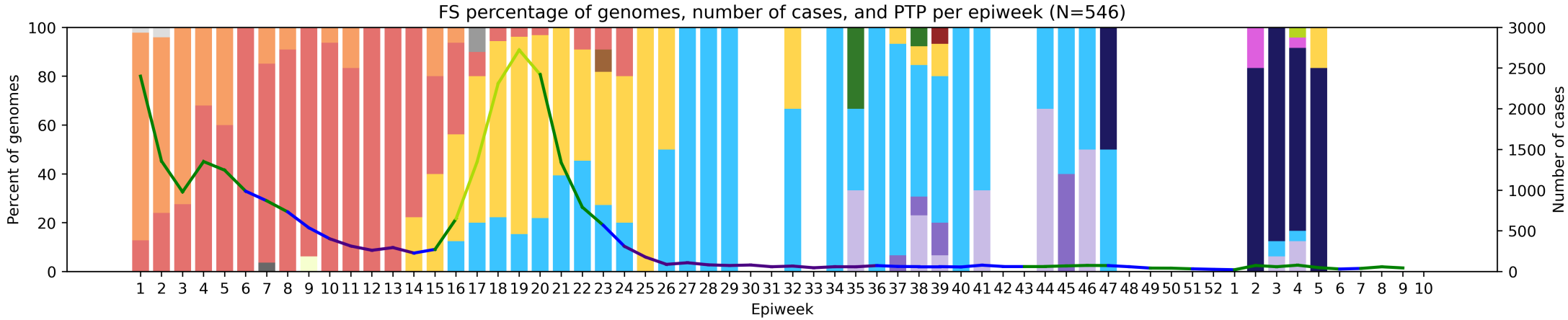
Free State Province, 2022-2023, n = 546

Genomes added since last report: 0*





Clade key (bar graph)

Omicron (23A/XBB.1.5)
Omicron (22F/XBB.*)
XAY
XBA
XBF
XAS
XAZ
XT
XBL
Omicron (21K/BA.1.*)
Omicron (21L/BA.2.*)
Omicron (21L/CM.4)
Omicron (21L/BA.2.3.20)
Omicron (22C/BA.2.12.1)
Omicron (22D/BA.2.75)
Omicron (22D/CH.1.1.*)
Omicron (21M/BA.3)
Omicron (22A/BA.4.*)
Omicron (22A/BA.4.6.*)
Omicron (22B/BA.5.*)
Omicron (22B/BF.7.*)
Omicron (22B/BA.5.9)
Omicron (22B/CL.1)
Omicron (22B/BE.1.1.1)
Omicron (22E/BQ.1.*)
Omicron (22B/BE.7)
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Alpha (20I, V1)
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Delta (21A, 21I, 21J)
C.1.2 (20D)
20B
unassigned
Cases

Weekly percentage testing positive key (line graph)

≤ 5
6 - 10
11 - 20
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31 - 40
41 - 50
51 - 55

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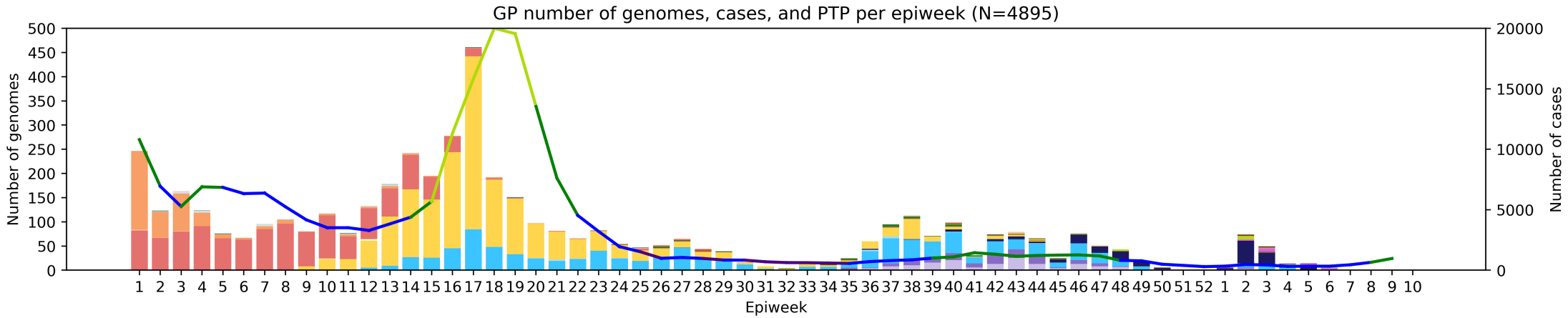
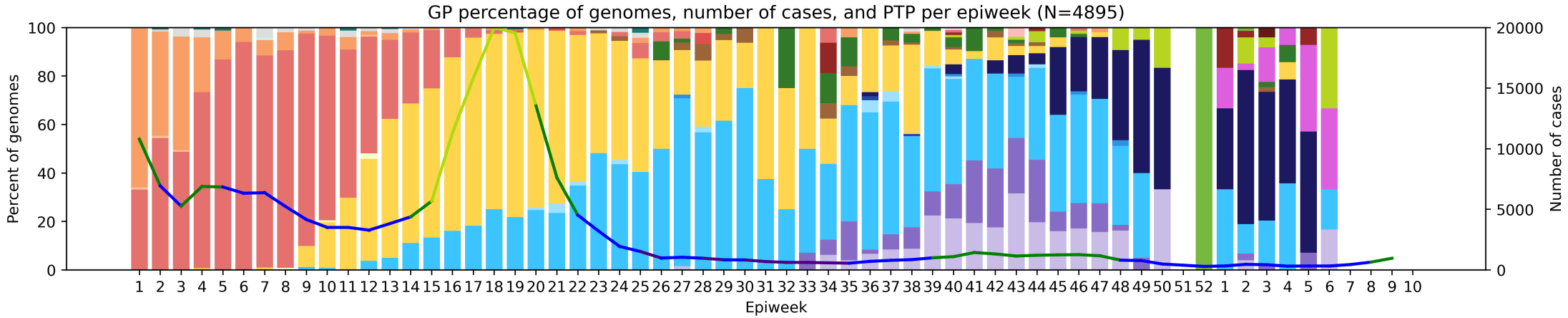
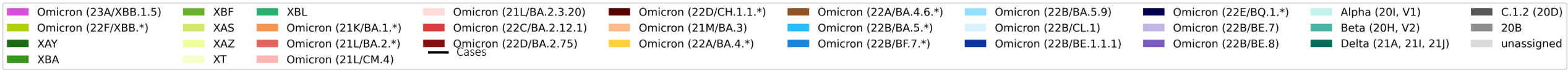
Gauteng Province, 2022-2023, n = 4895

Genomes added since last report: 0*

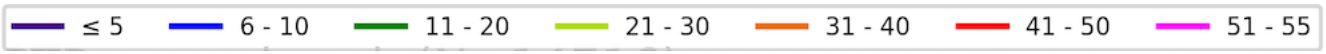




Clade key (bar graph)



Weekly percentage testing positive key (line graph)



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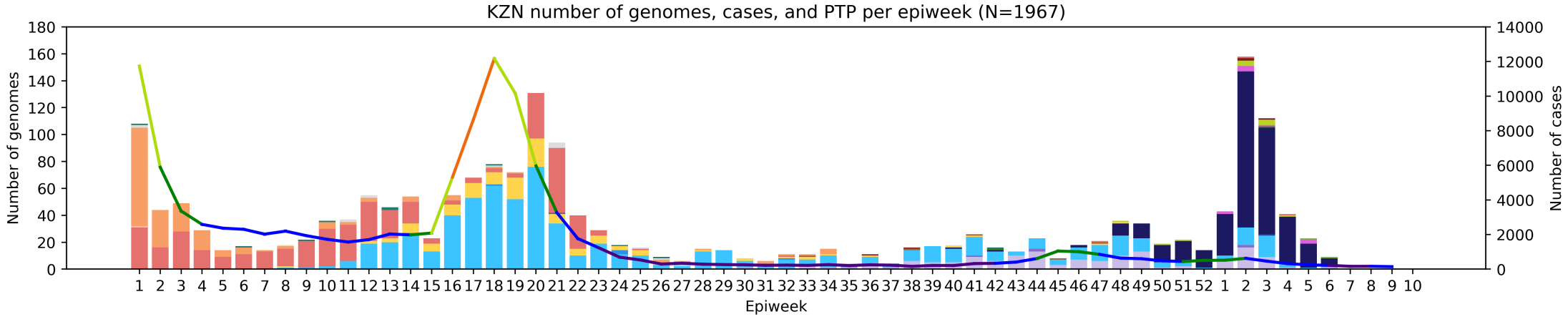
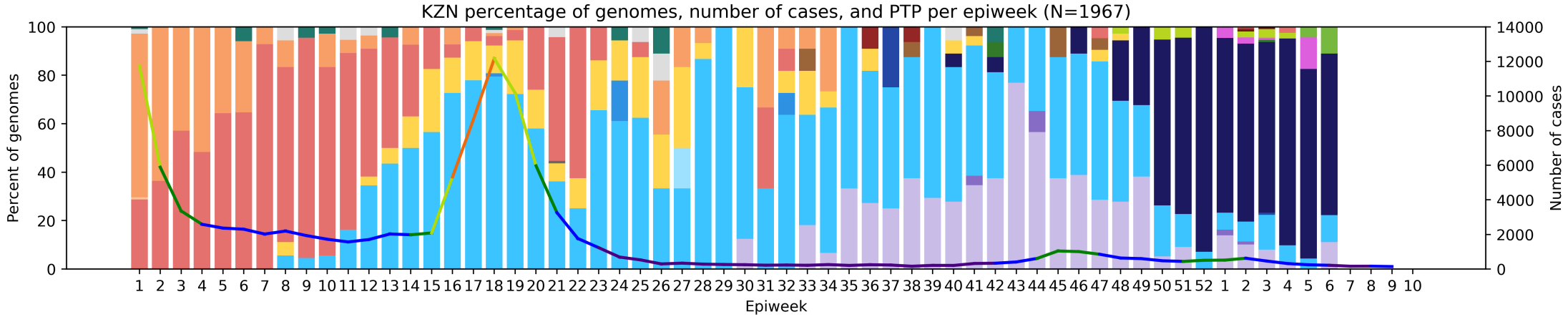
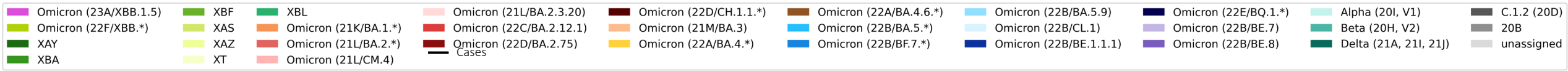
KwaZulu-Natal Province, 2022-2023, n = 1967

Genomes added since last report: 0*

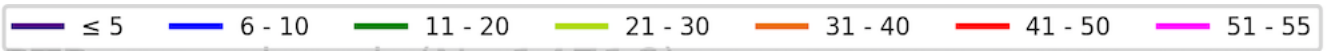




Clade key (bar graph)



Weekly percentage testing positive key (line graph)



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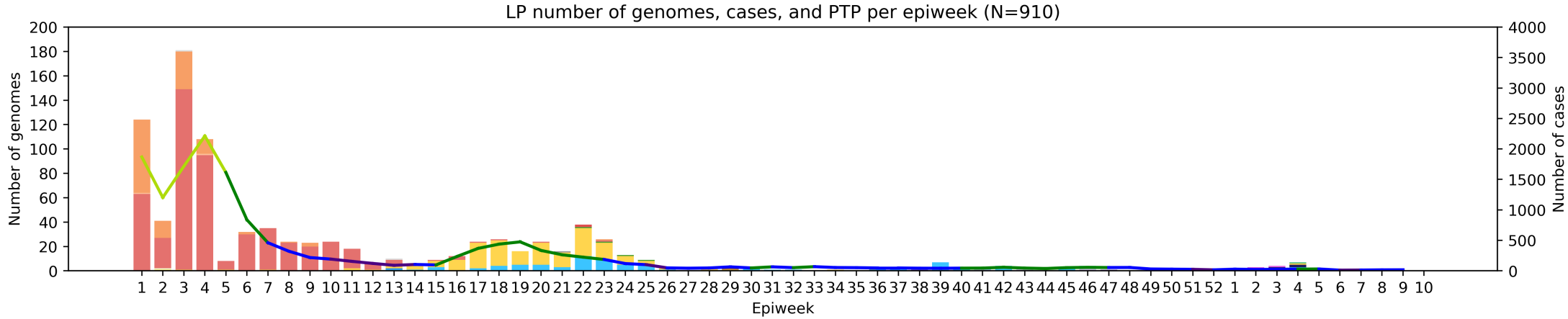
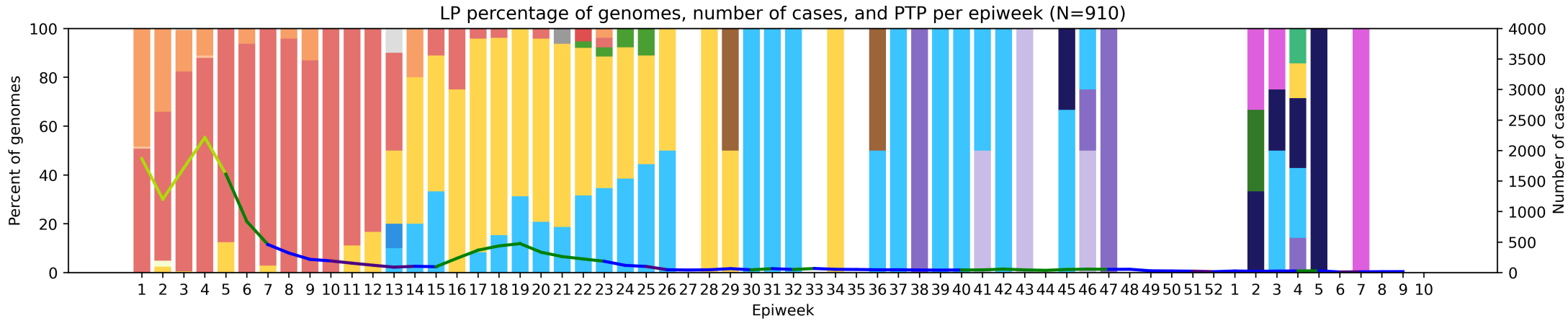
Limpopo Province, 2022-2023, n = 910

Genomes added since last report: 0*





Clade key (bar graph)

Omicron (23A/XBB.1.5)
Omicron (22F/XBB.*)
XAY
XBA
XBF
XAS
XAZ
XT
XBL
Omicron (21K/BA.1.*)
Omicron (21L/BA.2.*)
Omicron (21L/CM.4)
Omicron (21L/BA.2.3.20)
Omicron (22C/BA.2.12.1)
Omicron (22D/BA.2.75)
Omicron (22D/CH.1.1.*)
Omicron (21M/BA.3)
Omicron (22A/BA.4.*)
Omicron (22A/BA.4.6.*)
Omicron (22B/BA.5.*)
Omicron (22B/BF.7.*)
Omicron (22B/BA.5.9)
Omicron (22B/CL.1)
Omicron (22B/BE.1.1.1)
Omicron (22E/BQ.1.*)
Omicron (22B/BE.7)
Omicron (22B/BE.8)
Alpha (20I, V1)
Beta (20H, V2)
Delta (21A, 21I, 21J)
C.1.2 (20D)
20B
unassigned
Cases

Weekly percentage testing positive key (line graph)

≤ 5
6 - 10
11 - 20
21 - 30
31 - 40
41 - 50
51 - 55

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

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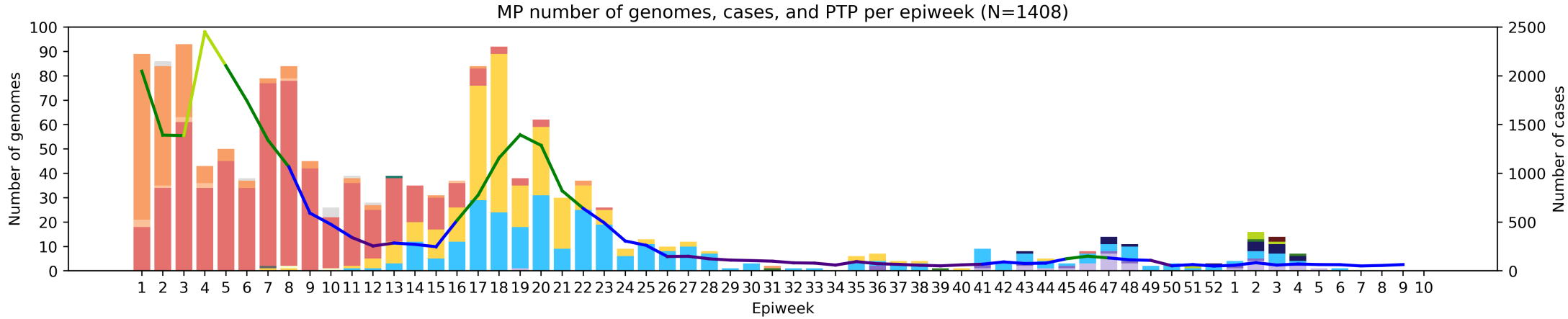
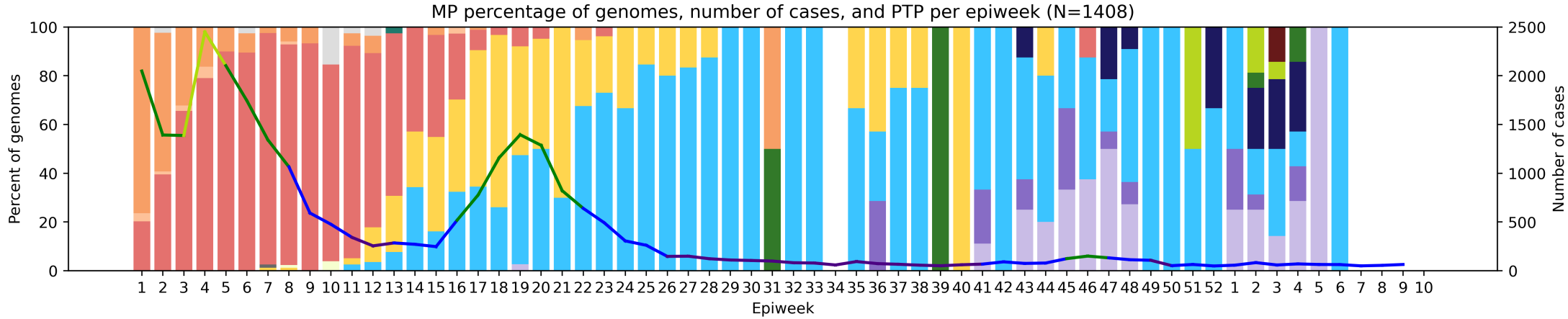
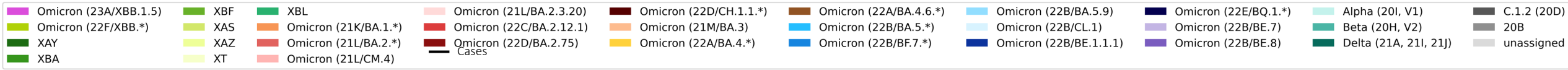
Mpumalanga Province, 2022-2023, n = 1408

Genomes added since last report: 0*

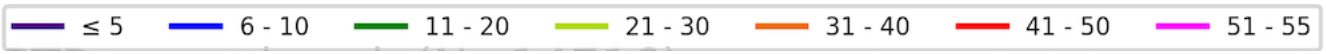




Clade key (bar graph)



Weekly percentage testing positive key (line graph)



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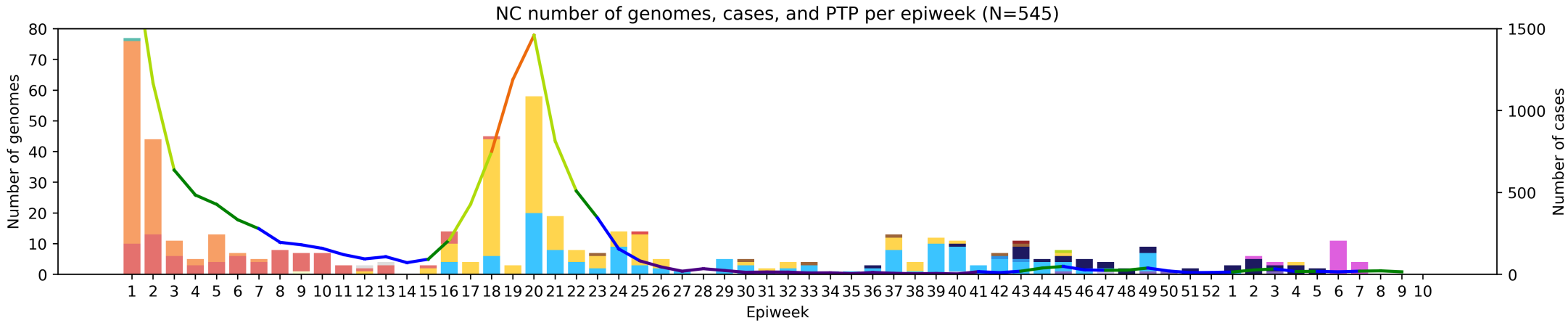
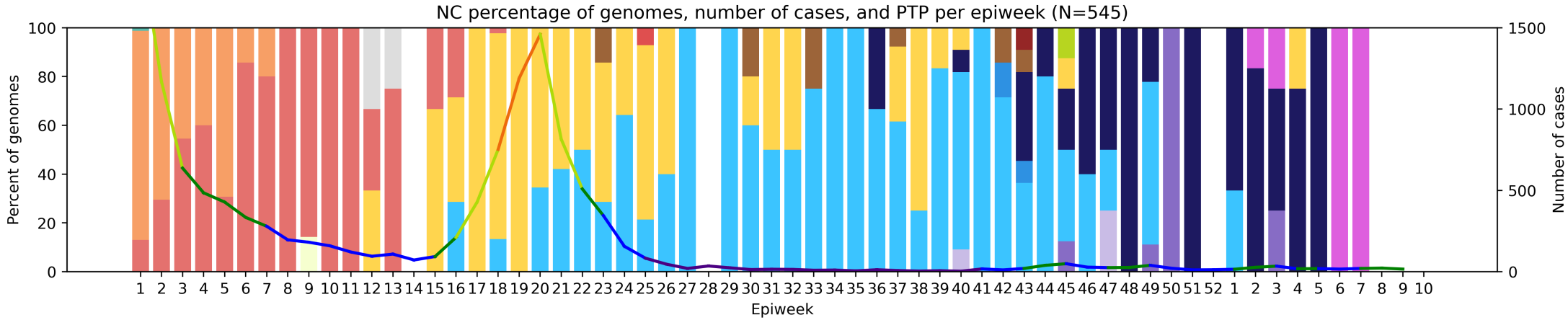
Northern Cape Province, 2022-2023, n = 545

Genomes added since last report: 17*





Clade key (bar graph)

Omicron (23A/XBB.1.5)
Omicron (22F/XBB.*)
XAY
XBA
XBF
XAS
XAZ
XT
XBL
Omicron (21K/BA.1.*)
Omicron (21L/BA.2.*)
Omicron (21L/CM.4)
Omicron (21L/BA.2.3.20)
Omicron (22C/BA.2.12.1)
Omicron (22D/BA.2.75)
Cases
Omicron (22D/CH.1.1.*)
Omicron (21M/BA.3)
Omicron (22A/BA.4.*)
Omicron (22A/BA.4.6.*)
Omicron (22B/BA.5.*)
Omicron (22B/BF.7.*)
Omicron (22B/BA.5.9)
Omicron (22B/CL.1)
Omicron (22B/BE.1.1.1)
Omicron (22E/BQ.1.*)
Omicron (22B/BE.7)
Omicron (22B/BE.8)
Alpha (20I, V1)
Beta (20H, V2)
Delta (21A, 21I, 21J)
C.1.2 (20D)
20B
unassigned

Weekly percentage testing positive key (line graph)

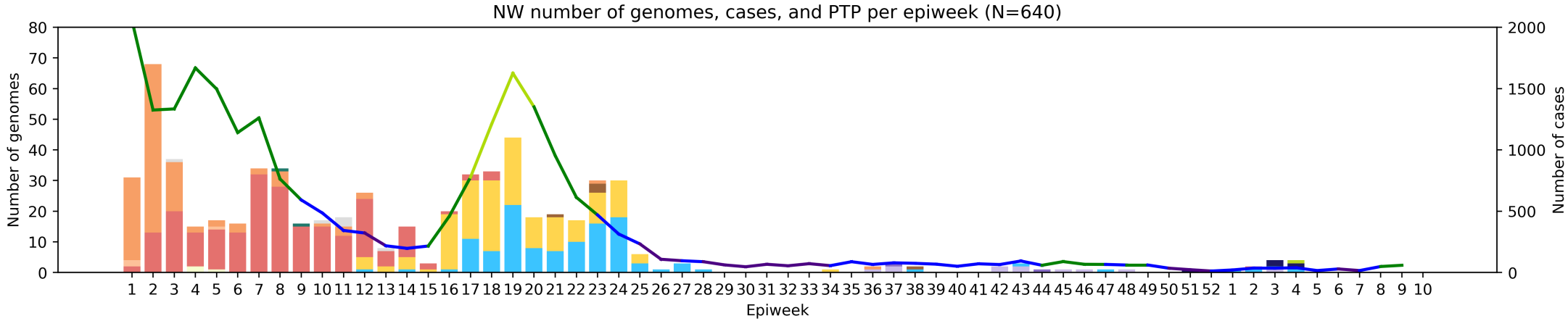
≤ 5
6 - 10
11 - 20
21 - 30
31 - 40
41 - 50
51 - 55

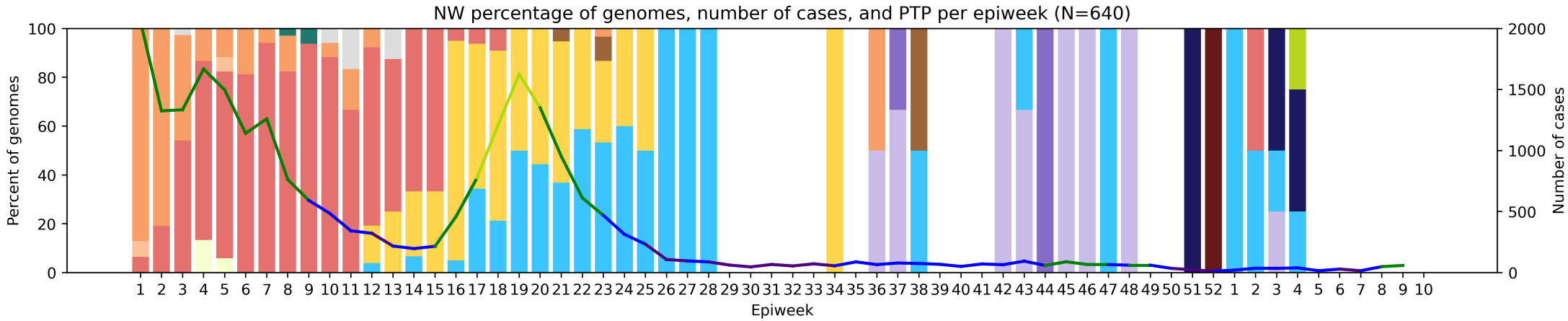
*May include genomes from 2020 and 2021 which are not pictured here and are not included in the slide total.

NGS-SA
Network for Genomic Surveillance in South Africa

North West Province, 2022-2023, n = 640

Genomes added since last report: 0*





Clade key (bar graph)

Omicron (23A/XBB.1.5)
Omicron (22F/XBB.*)
XAY
XBA
XBF
XAS
XAZ
XT
XBL
Omicron (21K/BA.1.*)
Omicron (21L/BA.2.*)
Omicron (21L/CM.4)
Omicron (21L/BA.2.3.20)
Omicron (22C/BA.2.12.1)
Omicron (22D/BA.2.75)
Cases
Omicron (22D/CH.1.1.*)
Omicron (21M/BA.3)
Omicron (22A/BA.4.*)
Omicron (22A/BA.4.6.*)
Omicron (22B/BA.5.*)
Omicron (22B/BF.7.*)
Omicron (22B/BA.5.9)
Omicron (22B/CL.1)
Omicron (22B/BE.1.1.1)
Omicron (22E/BQ.1.*)
Omicron (22B/BE.7)
Omicron (22B/BE.8)
Alpha (20I, V1)
Beta (20H, V2)
Delta (21A, 21I, 21J)
C.1.2 (20D)
20B
unassigned

Weekly percentage testing positive key (line graph)

≤ 5
6 - 10
11 - 20
21 - 30
31 - 40
41 - 50
51 - 55

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

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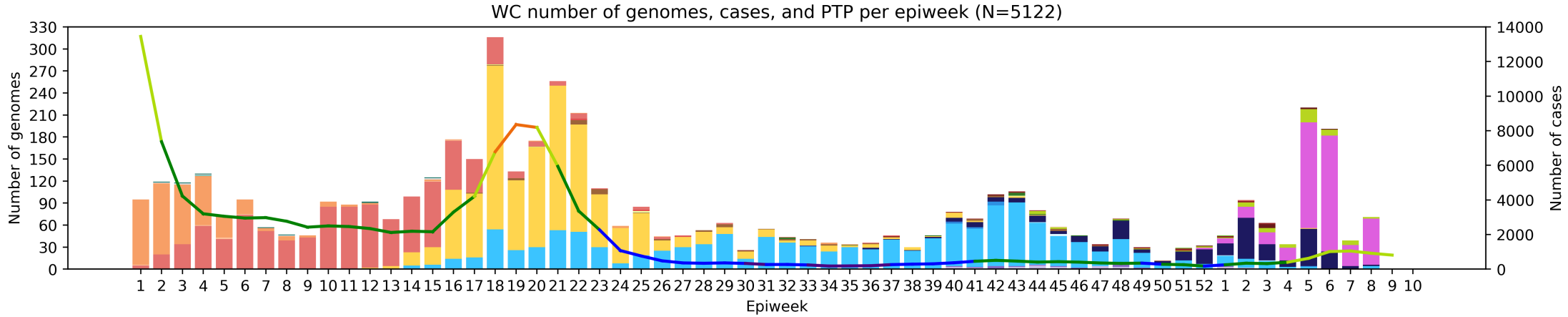
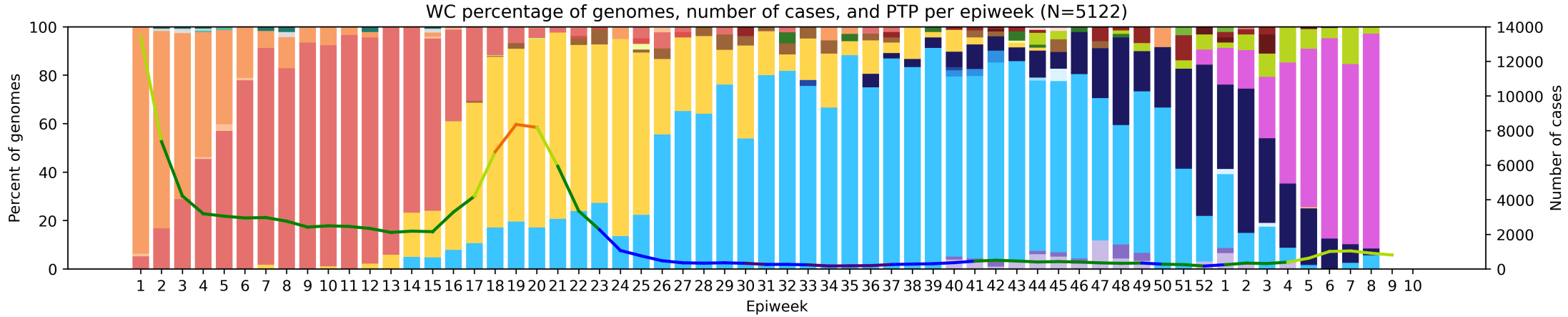
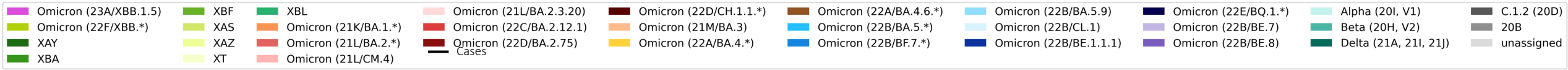
Western Cape Province, 2022-2023, n = 5122

Genomes added since last report: 158*

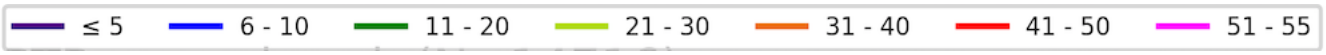




Clade key (bar graph)



Weekly percentage testing positive key (line graph)



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

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Summary

- **Sequencing update**
  - Eastern Cape, Gauteng, KwaZulu-Natal, Mpumalanga, the Northern Cape, the North West and the Western Cape have sequences for December 2022. All provinces have sequences for January 2023. All provinces, except the North West, have sequences for February 2023

- **Variant of Concern Omicron in South Africa**
  - Omicron continued to dominate in December (100%), January (99%) and makes up 100% of February sequences
  - BQ.1 and sub-lineages were the dominant Omicron lineage in December (46%) and January (54%).
  - XBB.1.5 was detected in December 2022 (n=2, 1%) and January 2023 (n=157, 14%), and is the dominant lineage in February 2023 (n=359, 75%)
  - BA.2.75.* continued to be detected at a low prevalence in December, January and February (≤3%)

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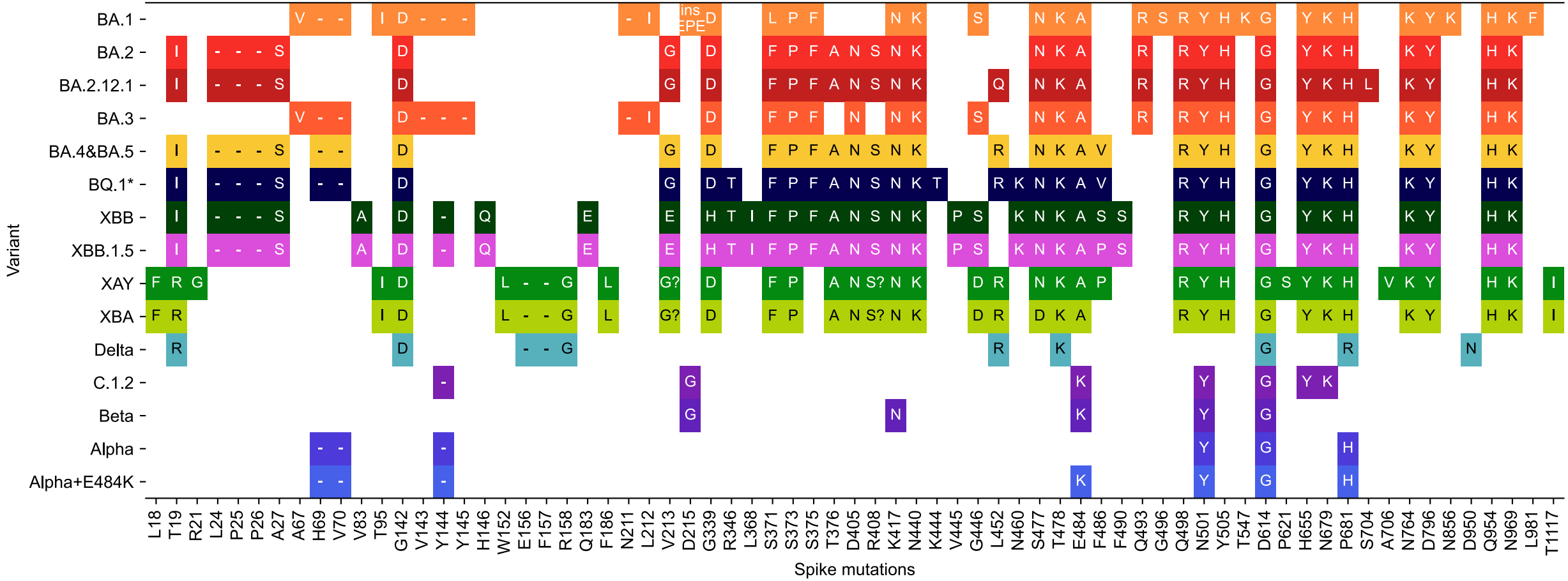
Spike protein mutation* profile of Variants of Interest and Concern



- 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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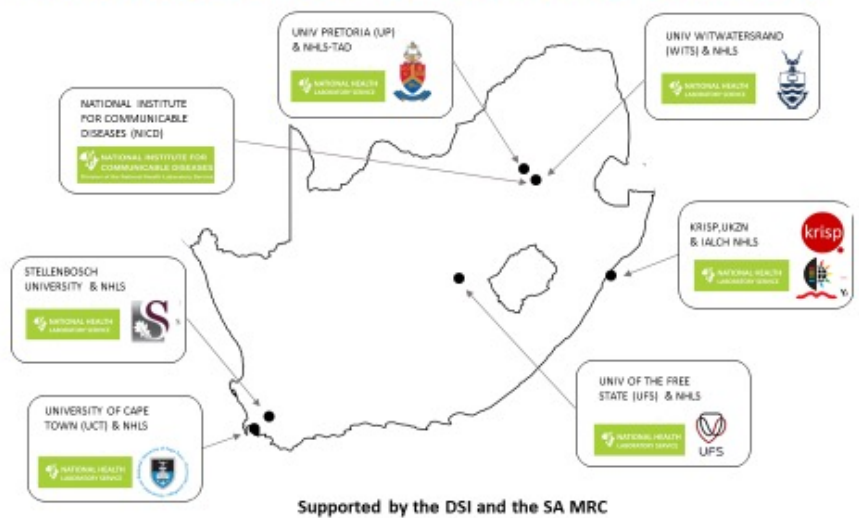

Supported by the DSI and the SA MRC

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REPUBLIC OF SOUTH AFRICA

UFS

saMRC advancinglife

NATIONAL INSTITUTE FOR COMMUNICABLE DISEASES
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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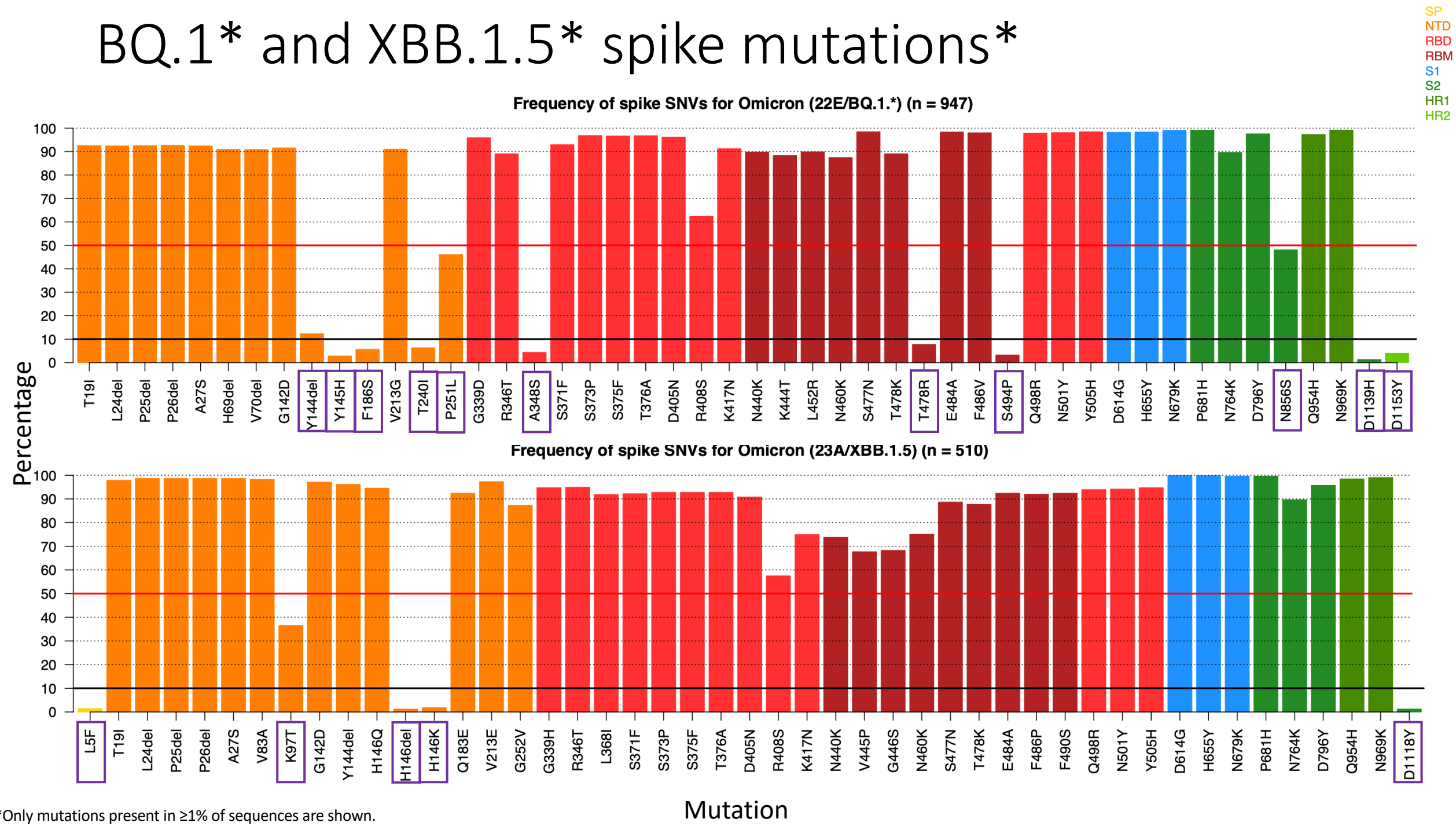
The picture can't be displayed.

UNIVERSITY OF KWAZULU-NATAL
INYUVESI YAKWAZULU-NATALI

NATIONAL HEALTH LABORATORY SERVICE

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



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

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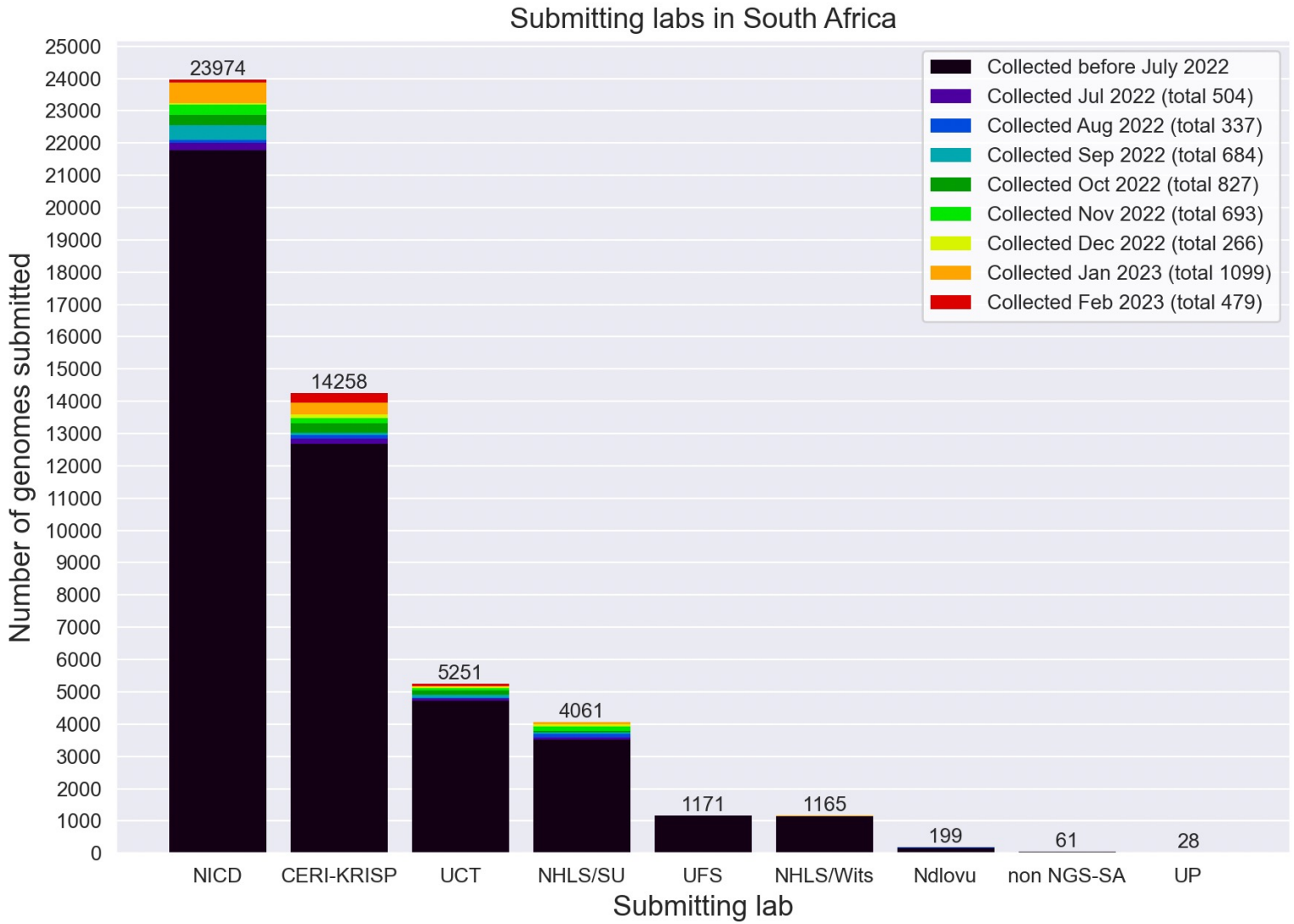
South African genomes submitted per submitting lab, 2020 - 2023 (N=50 168)



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 Concern (VOC)

WHO label	Pango lineage•	GISAID clade	Nextstrain clade	Additional amino acid changes monitored°	Earliest documented samples	Date of designation
Omicron*	B.1.1.529	GR/484A	21K, 21L, 21M, 22A, 22B, 22C, 22D	+S:R346K +S:L452X +S:F486V	Multiple countries, Nov-2021	VUM: 24-Nov-2021 VOC: 26-Nov-2021

* Includes BA.1, BA.2, BA.3, BA.4, BA.5 and descendent lineages. It also includes BA.1/BA.2 circulating recombinant forms such as XE. WHO emphasizes that these descendant lineages should be monitored as distinct lineages by public health authorities and comparative assessments of their virus characteristics should be undertaken.

° Only found in a subset of sequences

https://www.who.int/en/activities/tracking-SARS-CoV-2-variants/ accessed 24 February 2023

Omicron subvariants under monitoring

Pango lineage[#] (+ mutation)	GISAID clade	Nextstrain clade	Relationship to circulating VOC lineages	Spike genetic features	Earliest documented samples
BF.7*	GRA	22B	BA.5 sublineage	BA.5 + S:R346T	24-01-2022
BQ.1[$]	GRA	22E	BA.5 sublineage	BQ.1 and BQ.1.1: BA.5 + S:R346T, S:K444T, S:N460K	07-02-2022
BA.2.75[§]	GRA	22D	BA.2 sublineage	BA.2.75: BA.2 + S:K147E, S:W152R, S:F157L, S:I210V, S:G257S, S:D339H, S:G446S, S:N460K, S:Q493R reversion	31-12-2021
CH.1.1[§]	GRA	22D	BA.2 sublineage	BA.2.75 + S:L452R, S:F486S	27-07-2022
XBB[µ]	GRA	22F	Recombinant of BA.2.10.1 and BA.2.75 sublineages, i.e. BJ1 and BM.1.1.1, with a breakpoint in S1	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
XBB.1.5	GRA	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 + S:F486P (see rapid risk assessment)	05-01-2022
XBF	GRA		Recombinant of BA.5.2.3 and CJ.1 (BA.2.75.3 sublineage)	BA.5 + S:K147E, S:W152R, S:F157L, S:I210V, S:G257S, S:G339H, S:R346T, S:G446S, S:N460K, S:F486P, S:F490S	27-07-2022

includes descendent lineages
* additional mutations outside of the spike protein: N: G30-, S33F, ORF9b: M26-, A29I, V30L
$ additional mutation outside the spike protein: ORF1a: Q556K, L3829F, ORF1b: Y264H, M1156I, N1191S, N: E136D, ORF9b: P10F
§ additional mutations outside of the spike protein: ORF1a: S1221L, P1640S, N4060S, ORF1b: G662S, E: T11A
µ additional mutations outside of the spike protein: ORF1a: K47R, ORF1b: G662S, S959P, E: T11A, ORF8: G8*

https://www.who.int/en/activities/tracking-SARS-CoV-2-variants/ accessed 24 February 2023

Previously circulating Variants of Concern

WHO label	Pango lineage•	GISAID clade	Nextstrain clade	Earliest documented samples	Date of designation
Alpha	B.1.1.7	GRY	20I (V1)	United Kingdom, Sep-2020	VOC: 18-Dec-2020 Previous VOC: 09-Mar-2022
Beta	B.1.351	GH/501Y.V2	20H (V2)	South Africa, May-2020	VOC: 18-Dec-2020 Previous VOC: 09-Mar-2022
Gamma	P.1	GR/501Y.V3	20J (V3)	Brazil, Nov-2020	VOC: 11-Jan-2021 Previous VOC: 09-Mar-2022
Delta	B.1.617.2	G/478K.V1	21A, 21I, 21J	India, Oct-2020	VOI: 4-Apr-2021 VOC: 11-May-2021 Previous VOC: 7-Jun-2022

• Includes all descendant lineages. See the cov-lineages.org and the Pango network websites for further details.

https://www.who.int/en/activities/tracking-SARS-CoV-2-variants/ accessed 24 February 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.)