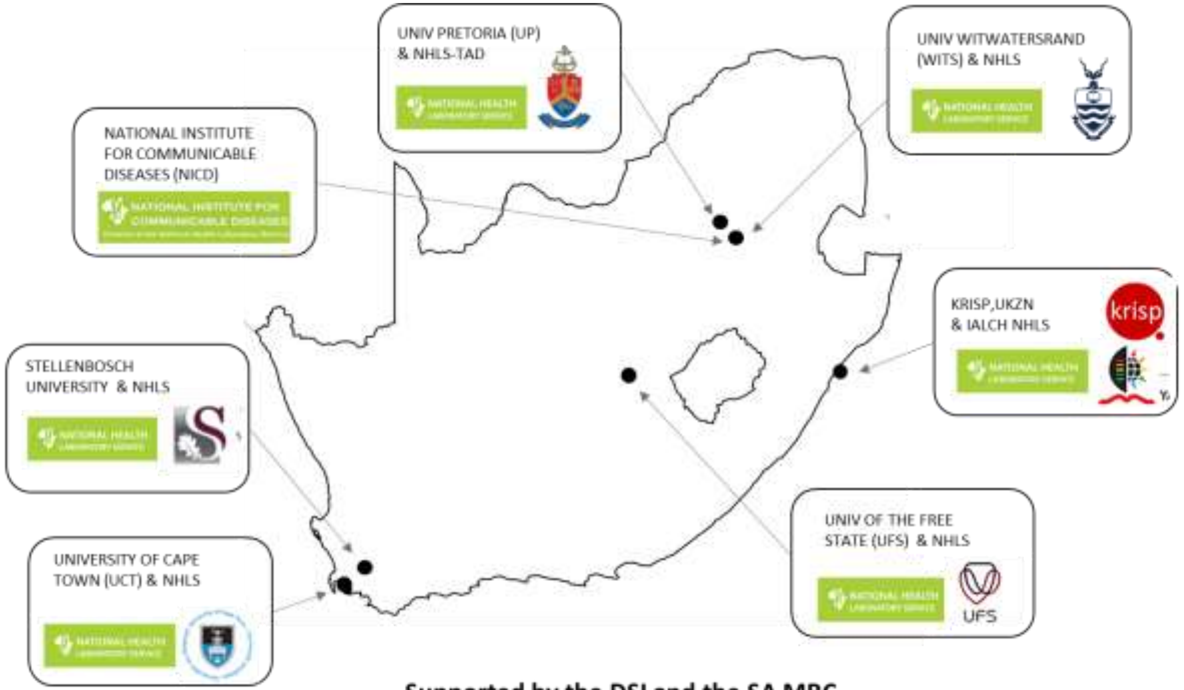
Network for Genomic Surveillance in South Africa (NGS-SA)

SARS-CoV-2 Sequencing Update
30 September 2022



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)

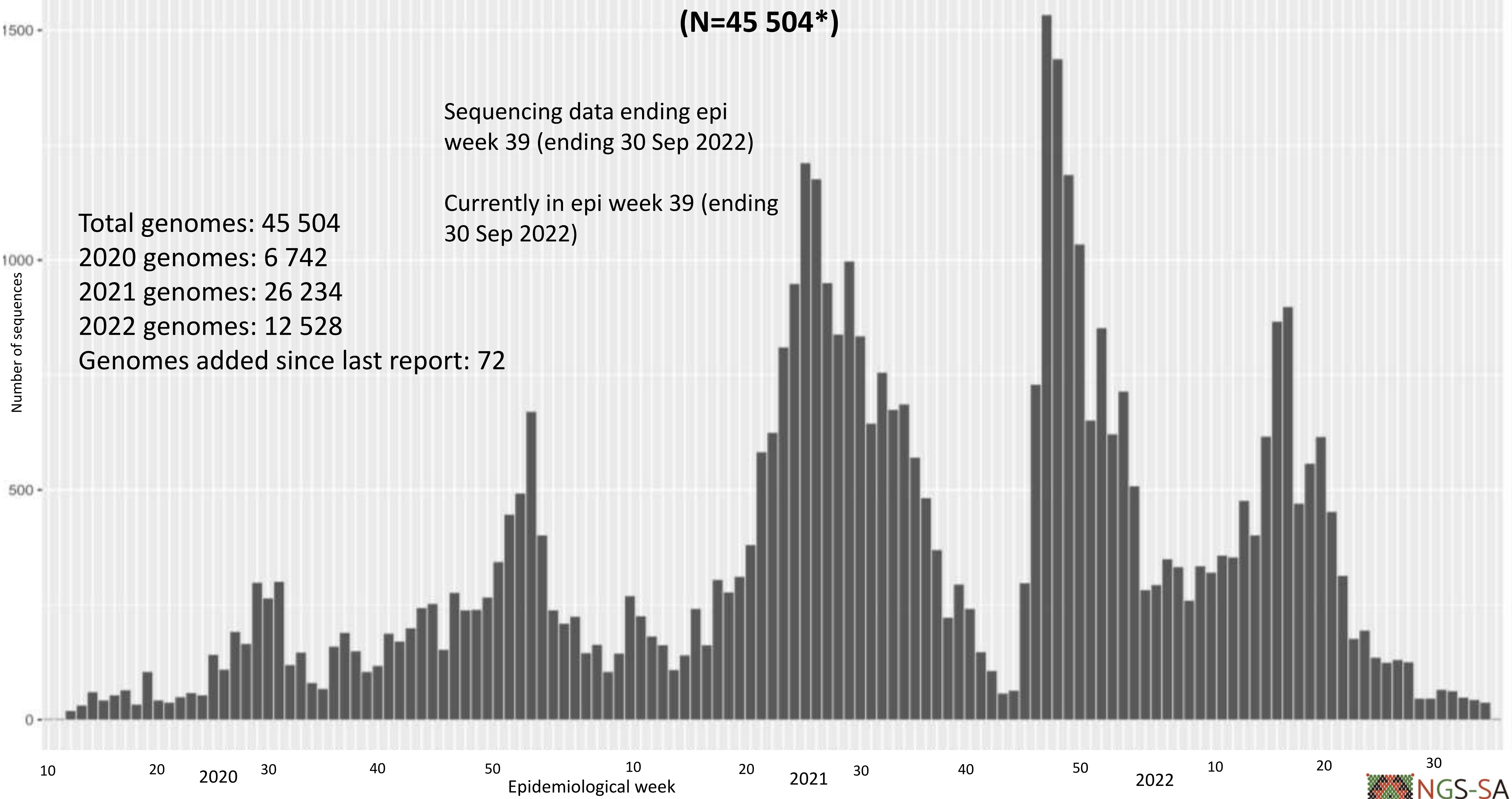
The genomic data presented here are based on South African SARS-CoV-2 sequence data downloaded from GISAID (www.gisaid.org) on 30 September 2022 at 08h08

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 – 2022 (N=45 504*)



Sequencing data ending epi week 39 (ending 30 Sep 2022)

Currently in epi week 39 (ending 30 Sep 2022)

Total genomes: 45 504
2020 genomes: 6 742
2021 genomes: 26 234
2022 genomes: 12 528
Genomes added since last report: 72

*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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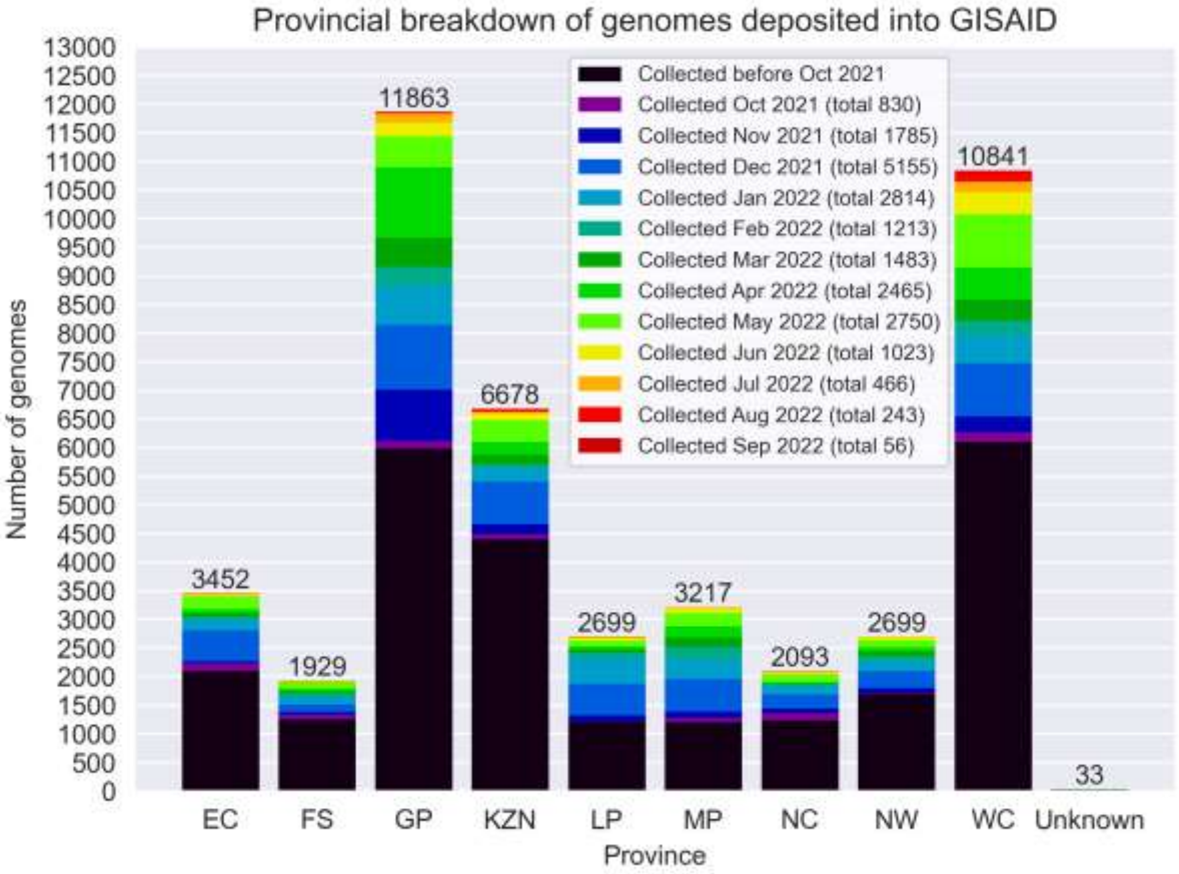
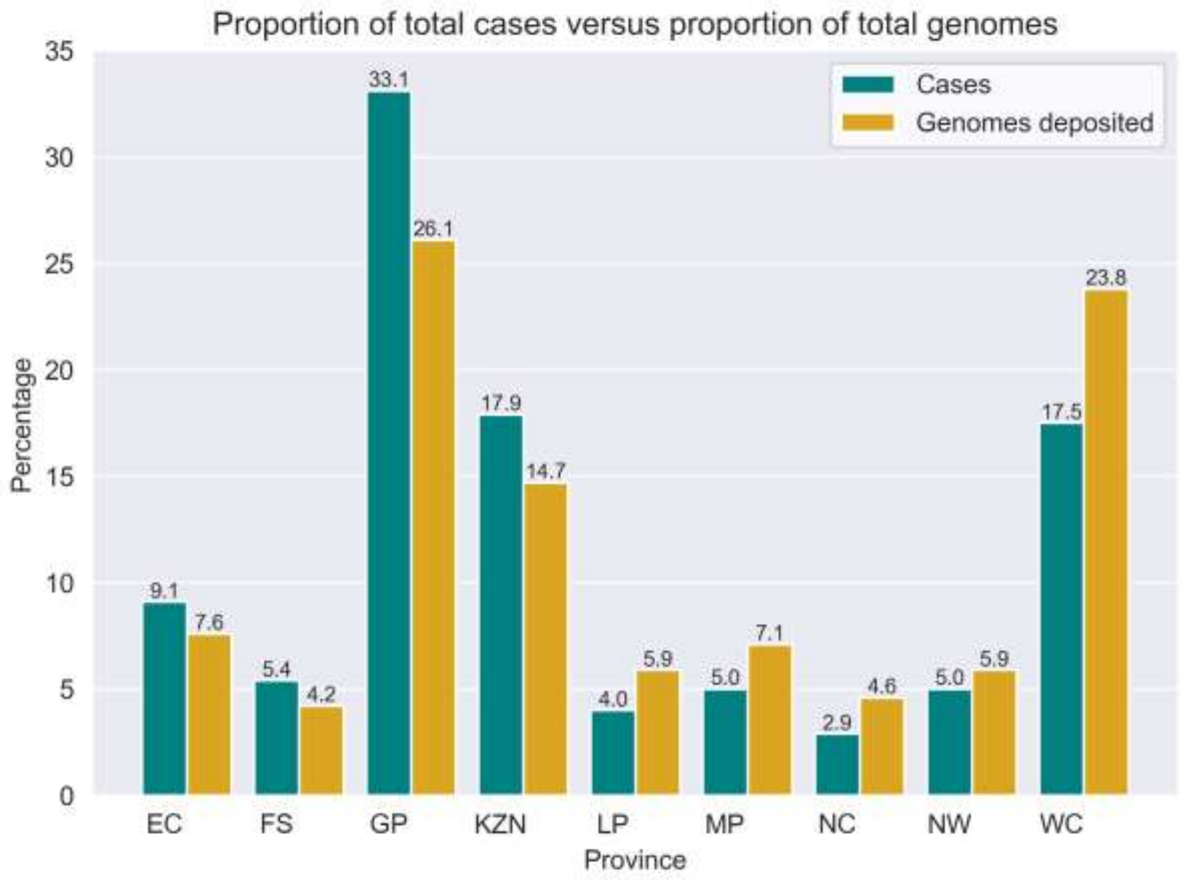
GISAID genomes vs total cases, 2020 – 2022 (N=45 504)





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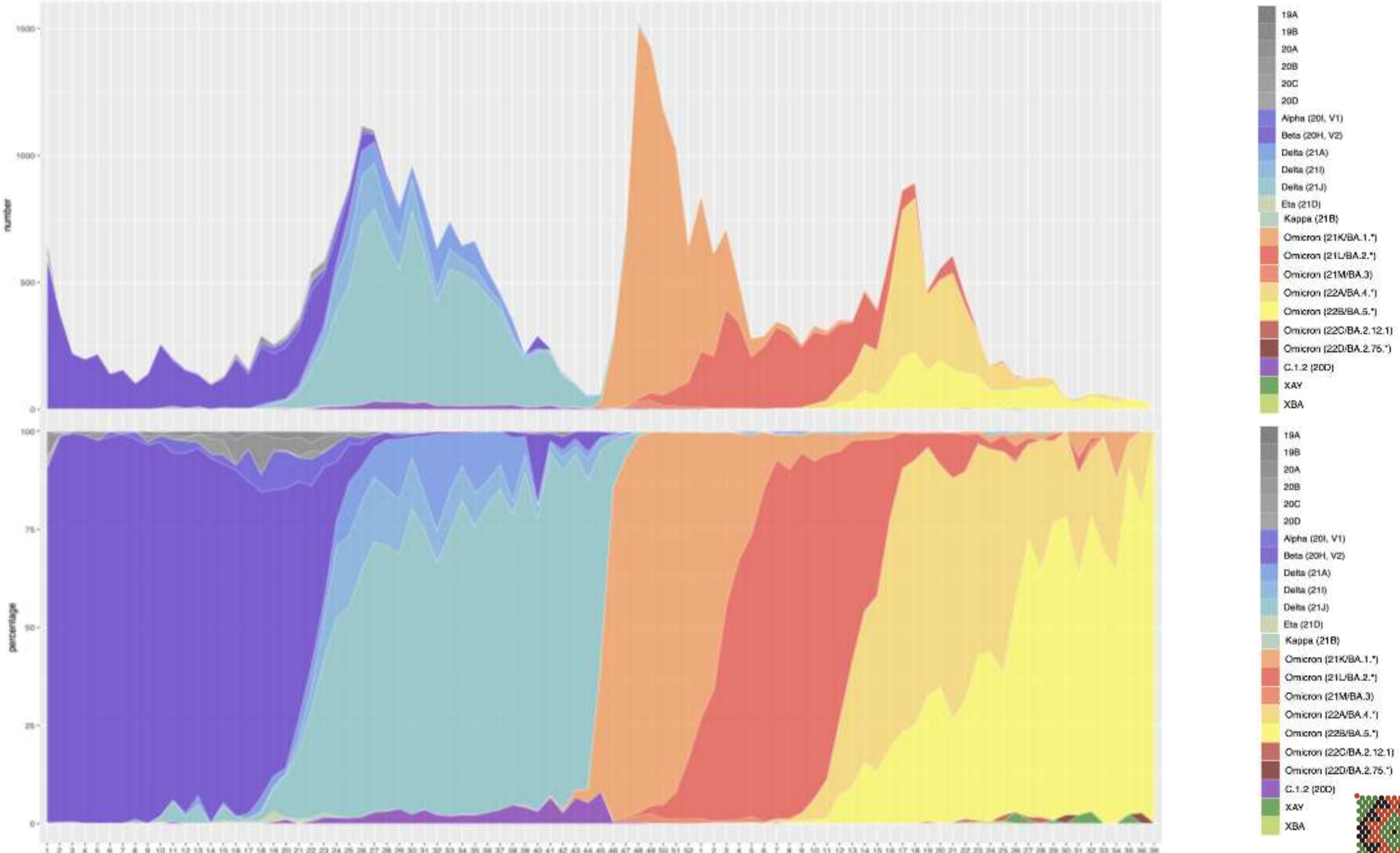
Number and percentage of clades by epiweek in South Africa, 2021 – 2022 (38 675*)



Sequencing data ending epi week 39 (ending 30 Sep 2022)

Currently in epi week 39 (ending 30 Sep 2022)

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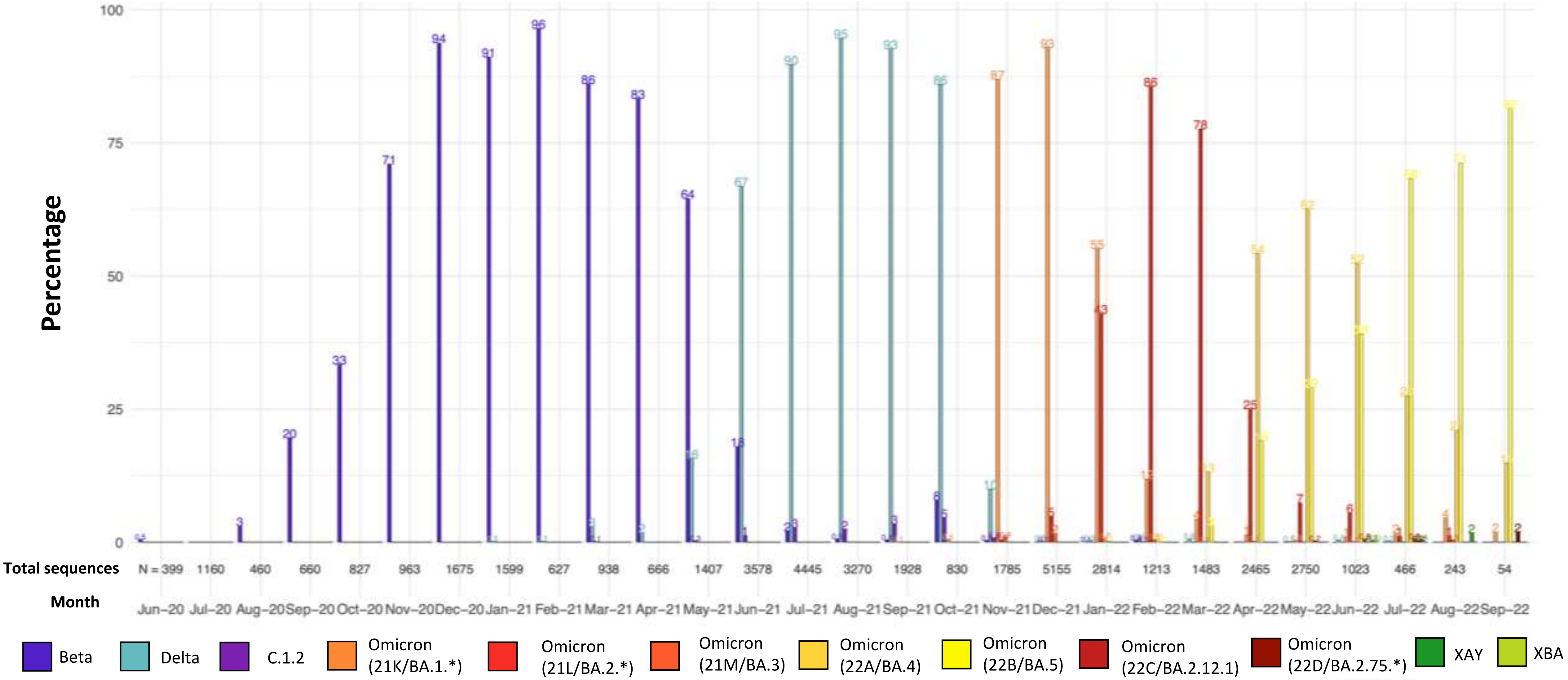
Detection Rates: Beta, Delta, C.1.2 and Omicron

Detection rates of variants being monitored in South Africa



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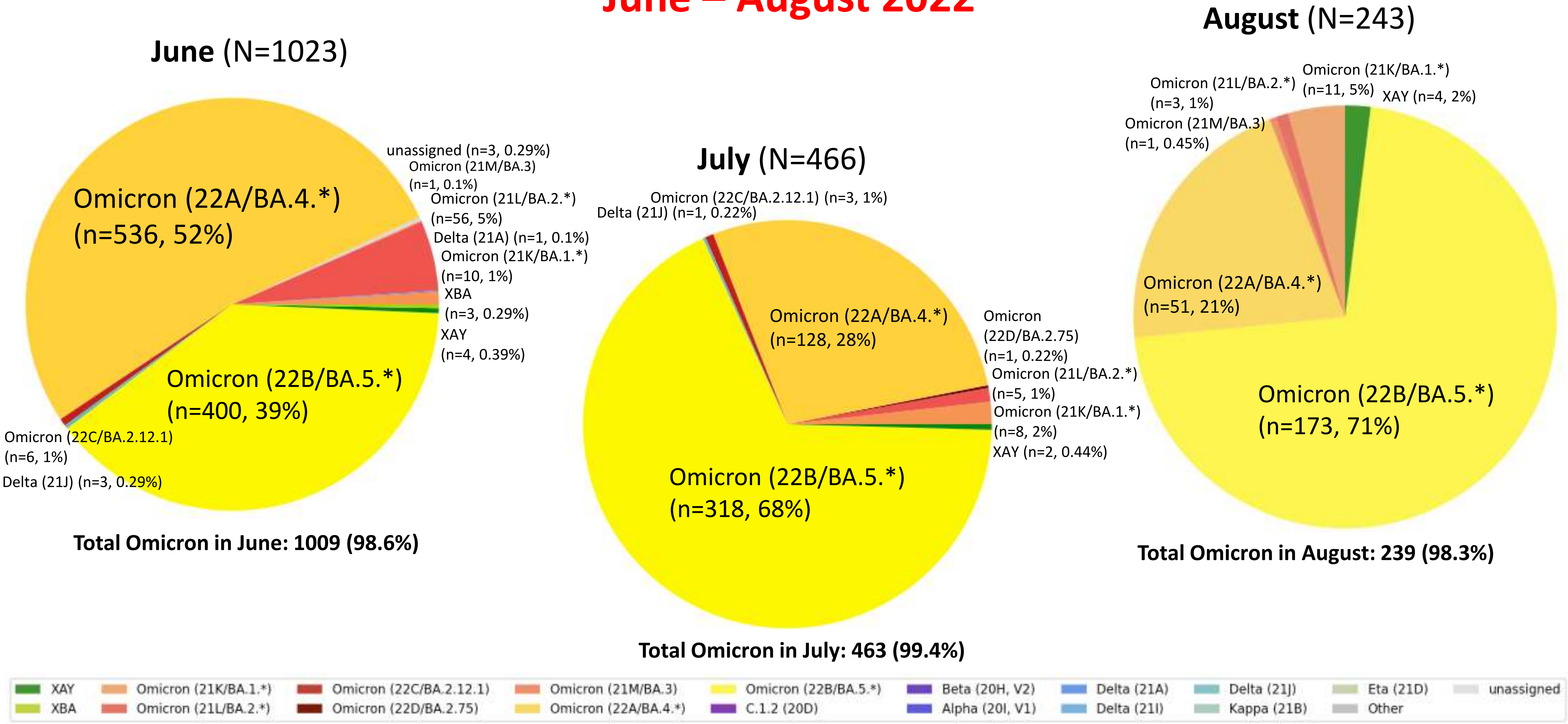
*Bars represent percentage prevalence of variant for the month; total number sequences collected for the month are given below the bar

Prevalence of Variants of Concern (VOC) and Variants of Interest (VOI) in June – August 2022



June (N=1023)

Total Omicron in June: 1009 (98.6%)

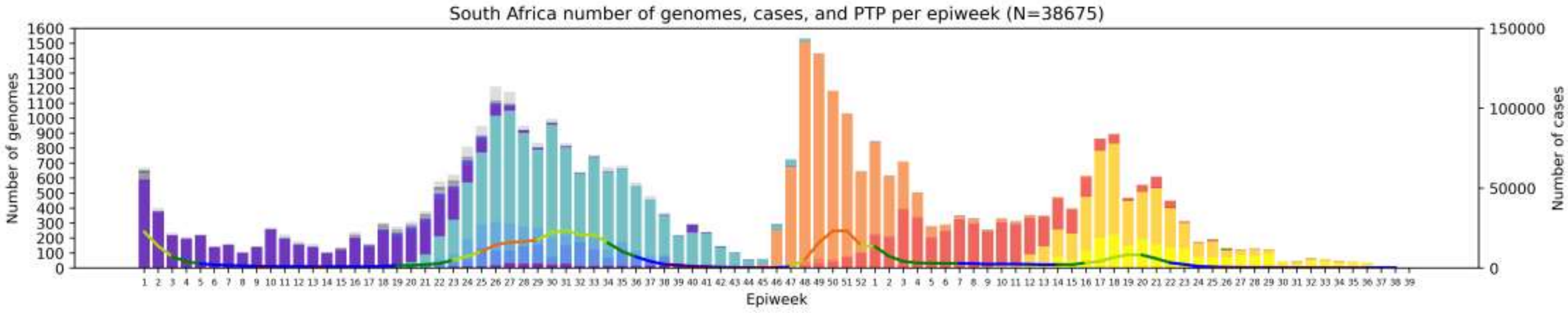
July (N=466)

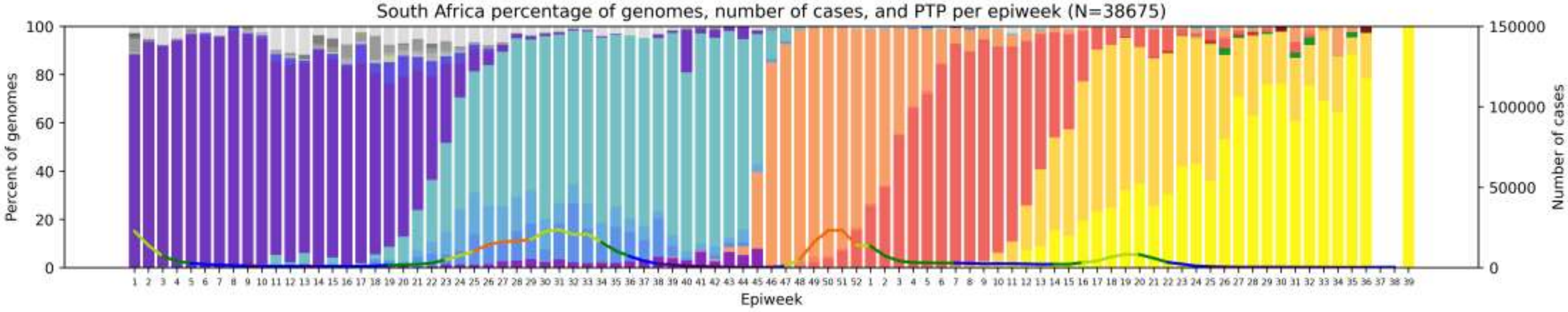
Total Omicron in July: 463 (99.4%)

August (N=243)

Total Omicron in August: 239 (98.3%)

South Africa, 2021-2022, n = 38 675*





Clade key (bar graph)

- XAY
- XBA
- Omicron (21K/BA.1.*)
- Omicron (21L/BA.2.*)
- Omicron (22C/BA.2.12.1)
- Omicron (22D/BA.2.75.*)
- Omicron (21M/BA.3)
- Omicron (22A/BA.4.*)
- Omicron (22B/BA.5.*)
- C.1.2 (20D)
- Beta (20H, V2)
- Alpha (20I, V1)
- Delta (21A)
- Delta (21I)
- Delta (21J)
- Kappa (21B)
- Eta (21D)
- 20D
- 20C
- Cases
- 20B
- 20A
- 19B
- 19A
- unassigned

Weekly percentage testing positive key (line graph)

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

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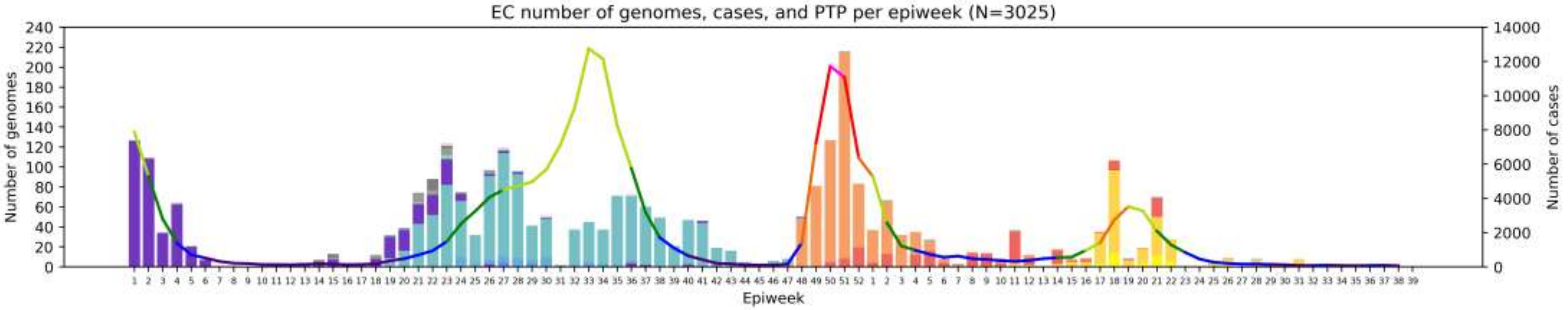
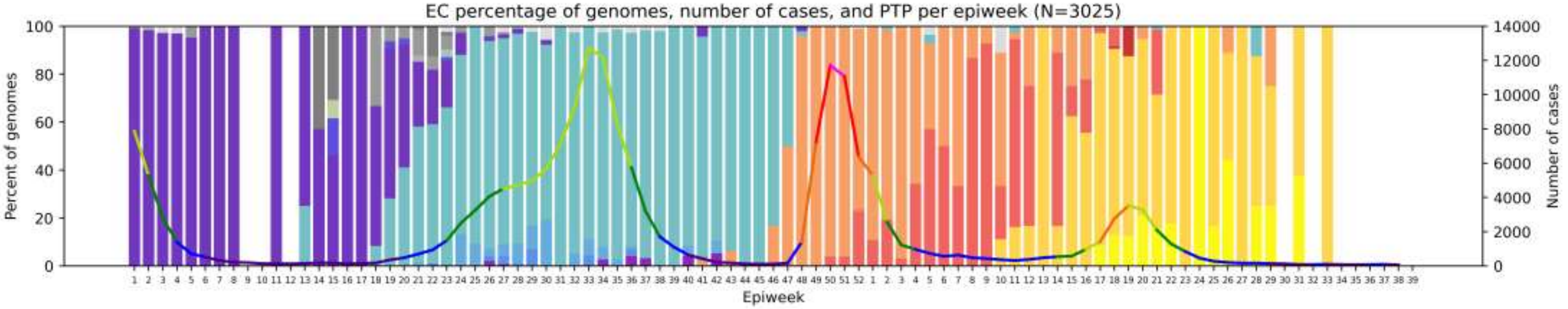
*Excludes sequences missing collection dates, as well as those collected January 1st and 2nd 2021 as they are part of epiweek 53 of 2020.

Eastern Cape Province, 2021-2022, n = 3025

Genomes added since last report: 0*





Clade key (bar graph)

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- Omicron (21M/BA.3)
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- Omicron (22B/BA.5.*)
- C.1.2 (20D)
- Beta (20H, V2)
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Weekly percentage testing positive key (line graph)

- ≤ 5
- 6 - 10
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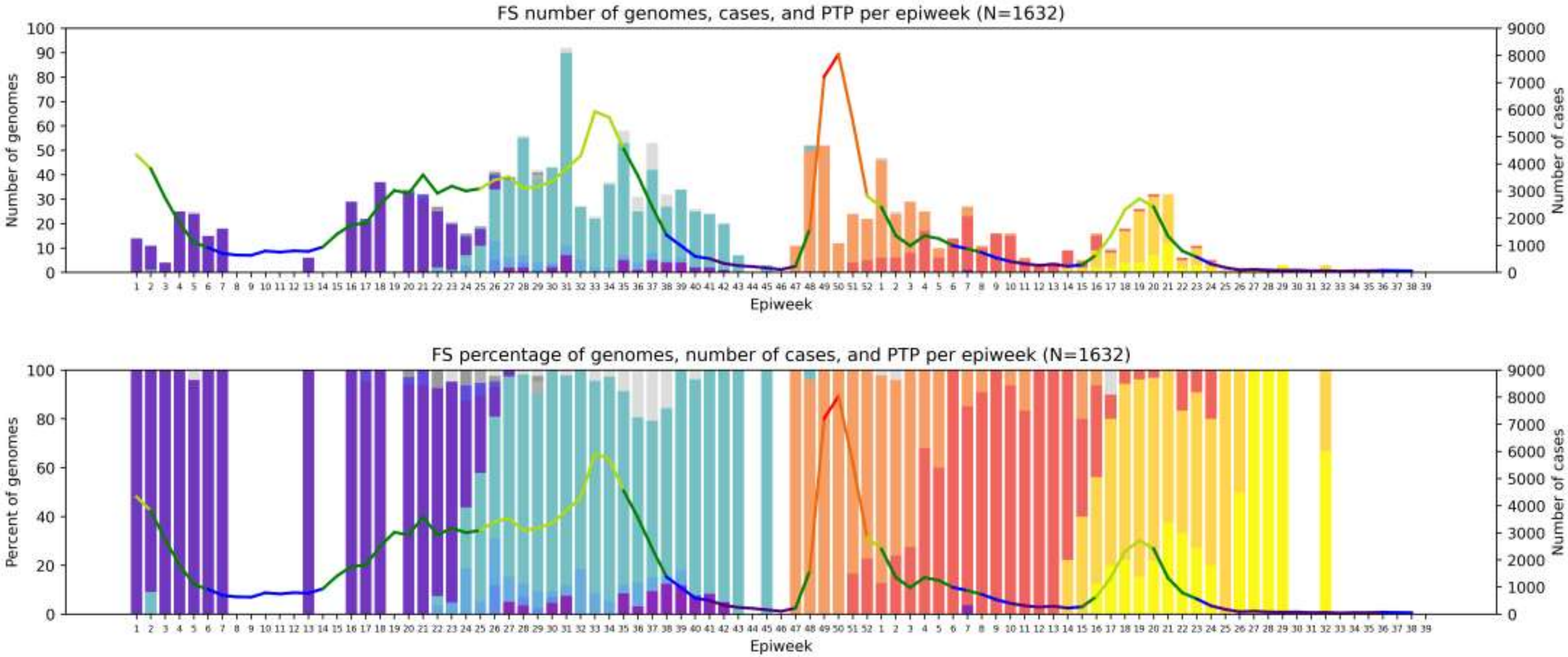
*May include genomes from 2020 which are not pictured here and are not included in the slide total.

Free State Province, 2021-2022, n = 1632

Genomes added since last report: 0*



Clade key (bar graph)

- 🟩 XAY
- 🟩 XBA
- 🟧 Omicron (21K/BA.1.*)
- 🟥 Omicron (21L/BA.2.*)
- 🟥 Omicron (22C/BA.2.12.1)
- 🟫 Omicron (22D/BA.2.75.*)
- 🟧 Omicron (21M/BA.3)
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- 🟪 Beta (20H, V2)
- 🟦 Alpha (20I, V1)
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- 🟦 Delta (21I)
- 🟦 Delta (21J)
- 🟩 Kappa (21B)
- 🟩 Eta (21D)
- ⬛ 20D
- ⬛ 20C
- ⬛ 20B
- ⬜ 20A
- ⬜ 19B
- ⬜ 19A
- ⬜ unassigned
- — Cases

Weekly percentage testing positive key (line graph)

- — ≤ 5
- — 6 - 10
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- — 51 - 55

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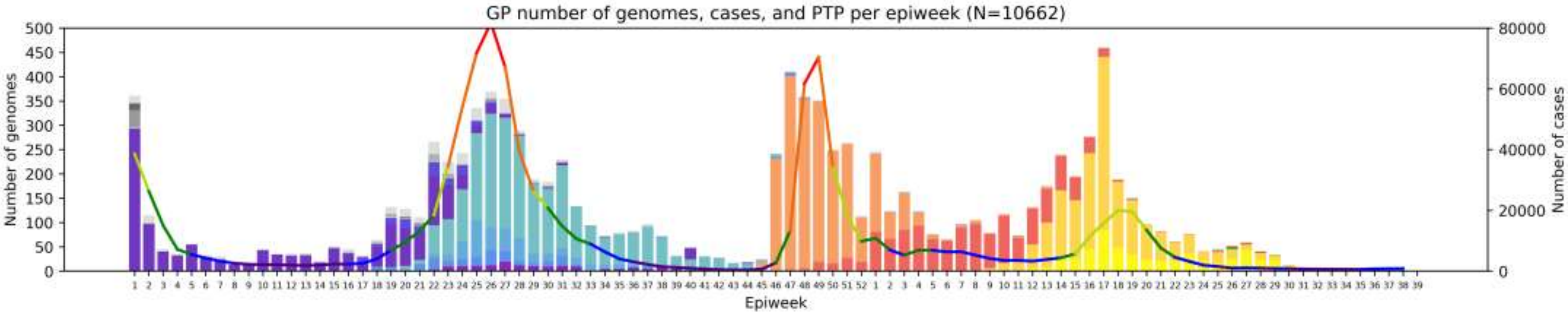
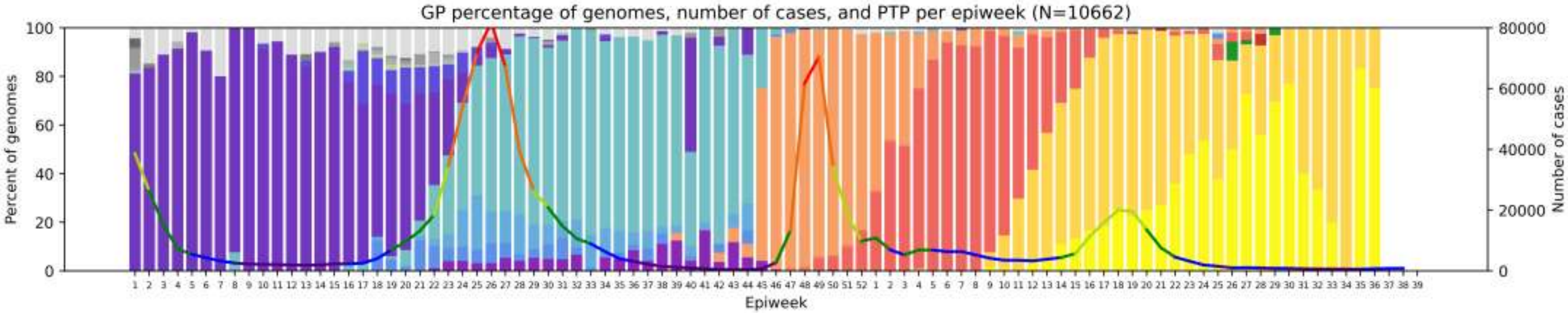
Gauteng Province, 2021-2022, n = 10 662

Genomes added since last report: 0*





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Weekly percentage testing positive key (line graph)

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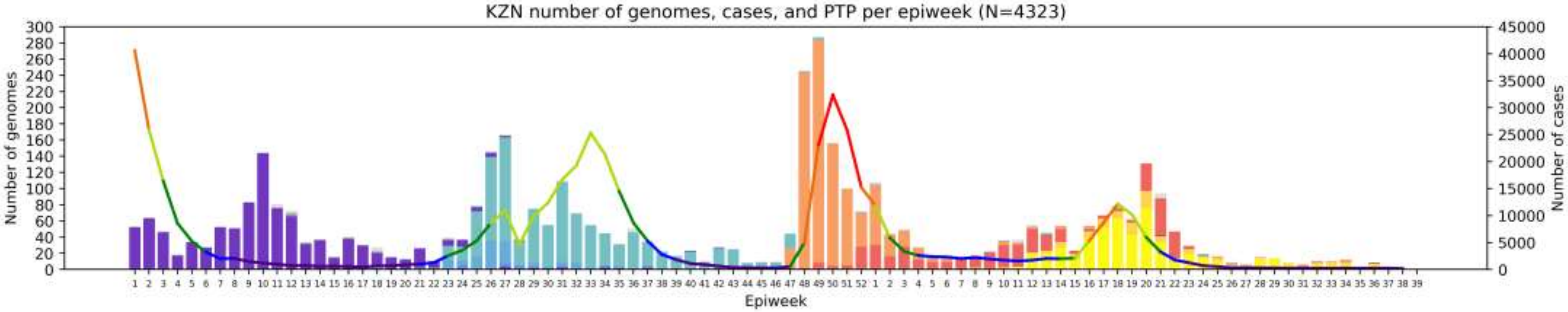
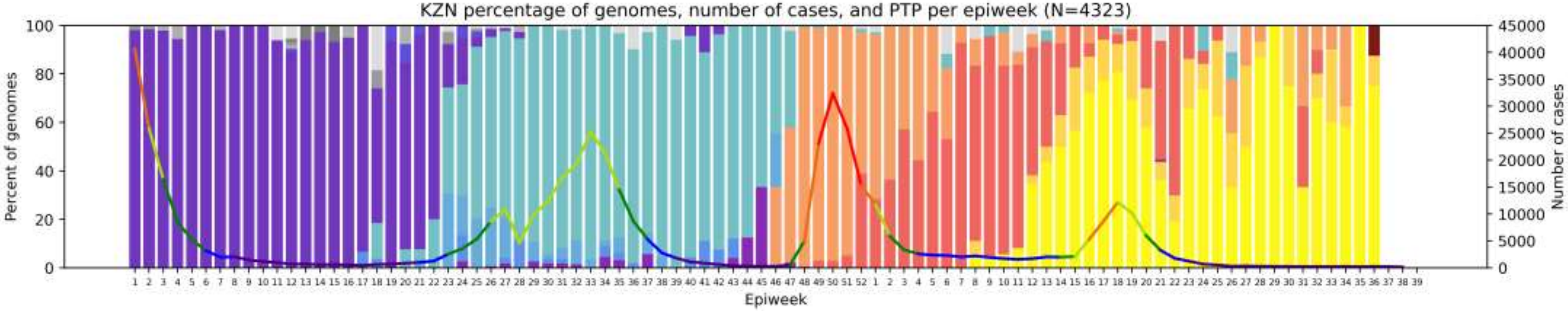
KwaZulu-Natal Province, 2021-2022, n = 4323

Genomes added since last report: 17*





Clade key (bar graph)

XAY
XBA
Omicron (21K/BA.1.*)
Omicron (21L/BA.2.*)
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Eta (21D)
20D
20C
20B
20A
19B
19A
unassigned
Cases

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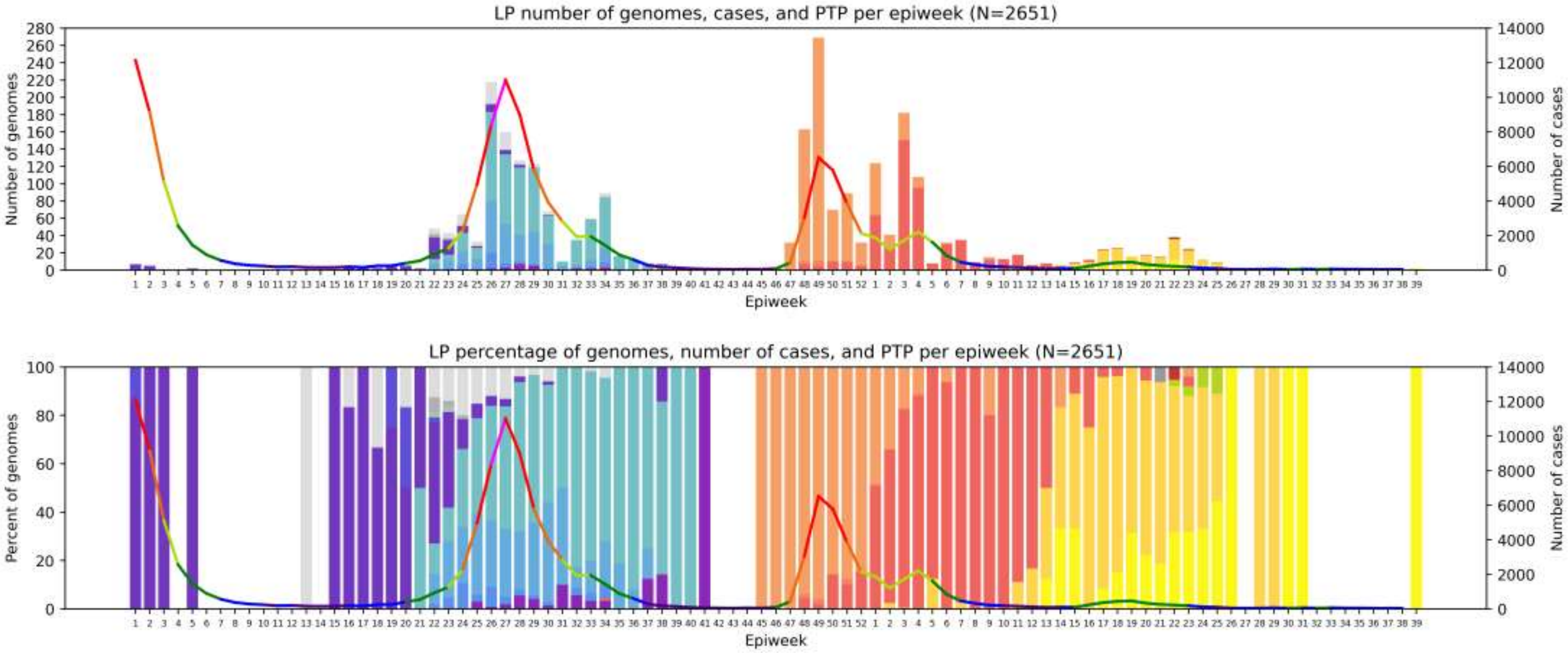
*May include genomes from 2020 which are not pictured here and are not included in the slide total.

Limpopo Province, 2021-2022, n = 2651

Genomes added since last report: 2*


LP number of genomes, cases, and PTP per epiweek (N=2651)

LP percentage of genomes, number of cases, and PTP per epiweek (N=2651)

Clade key (bar graph)

- XAY
- XBA
- Omicron (21K/BA.1.*)
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- 19A
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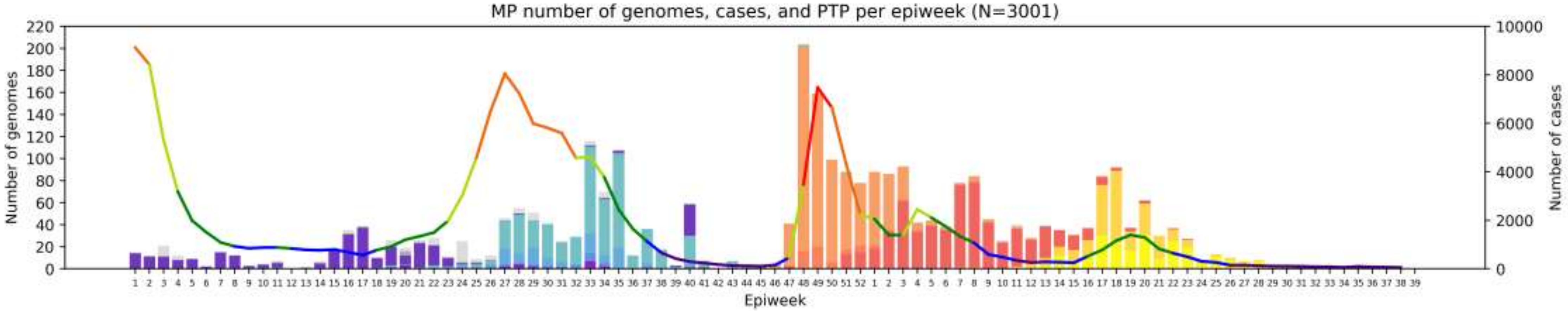
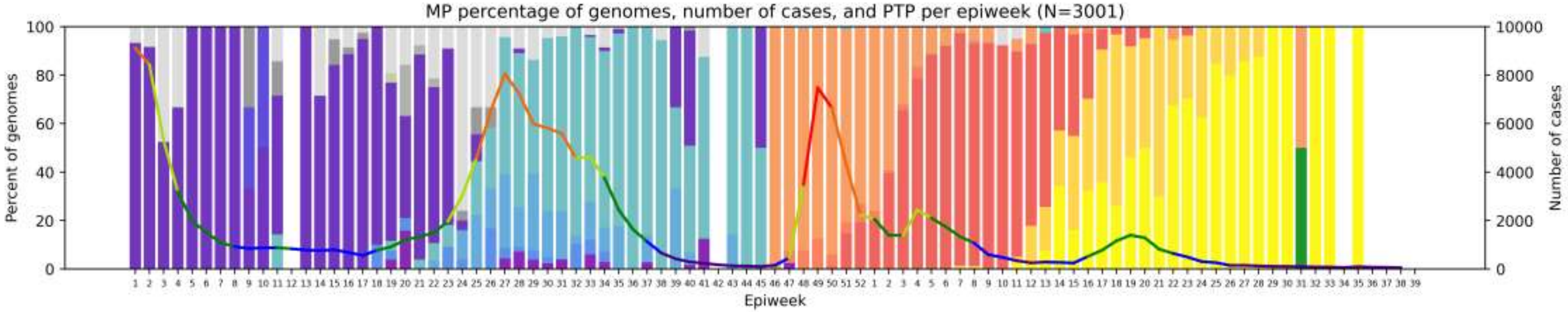
*May include genomes from 2020 which are not pictured here and are not included in the slide total.

Mpumalanga Province, 2021-2022, n = 3001

Genomes added since last report: 0*





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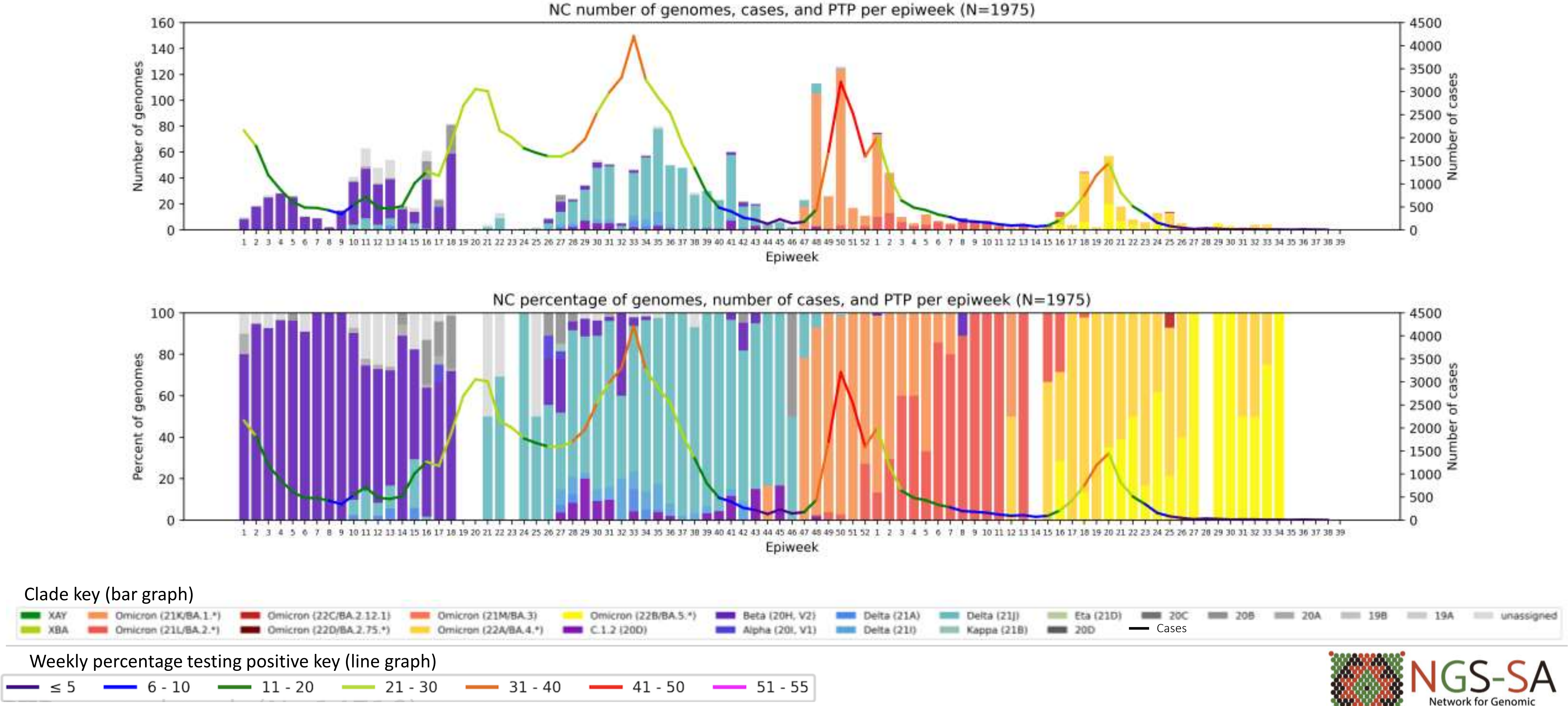
Northern Cape Province, 2021-2022, n = 1975

Genomes added since last report: 0*



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

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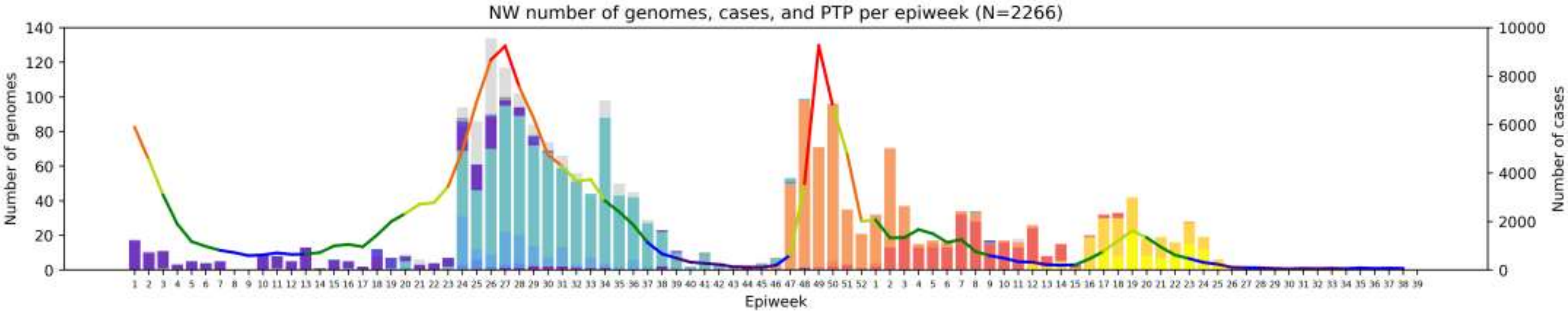
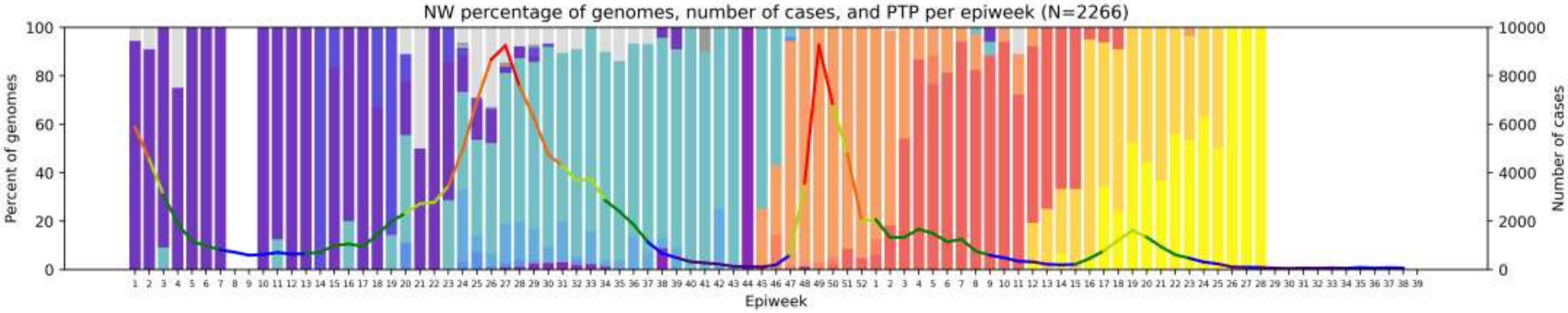
North West Province, 2021-2022, n = 2266

Genomes added since last report: 0*



NW number of genomes, cases, and PTP per epiweek (N=2266)



NW percentage of genomes, number of cases, and PTP per epiweek (N=2266)

Clade key (bar graph)

XAY
XBA
Omicron (21K/BA.1.*)
Omicron (21L/BA.2.*)
Omicron (22C/BA.2.12.1)
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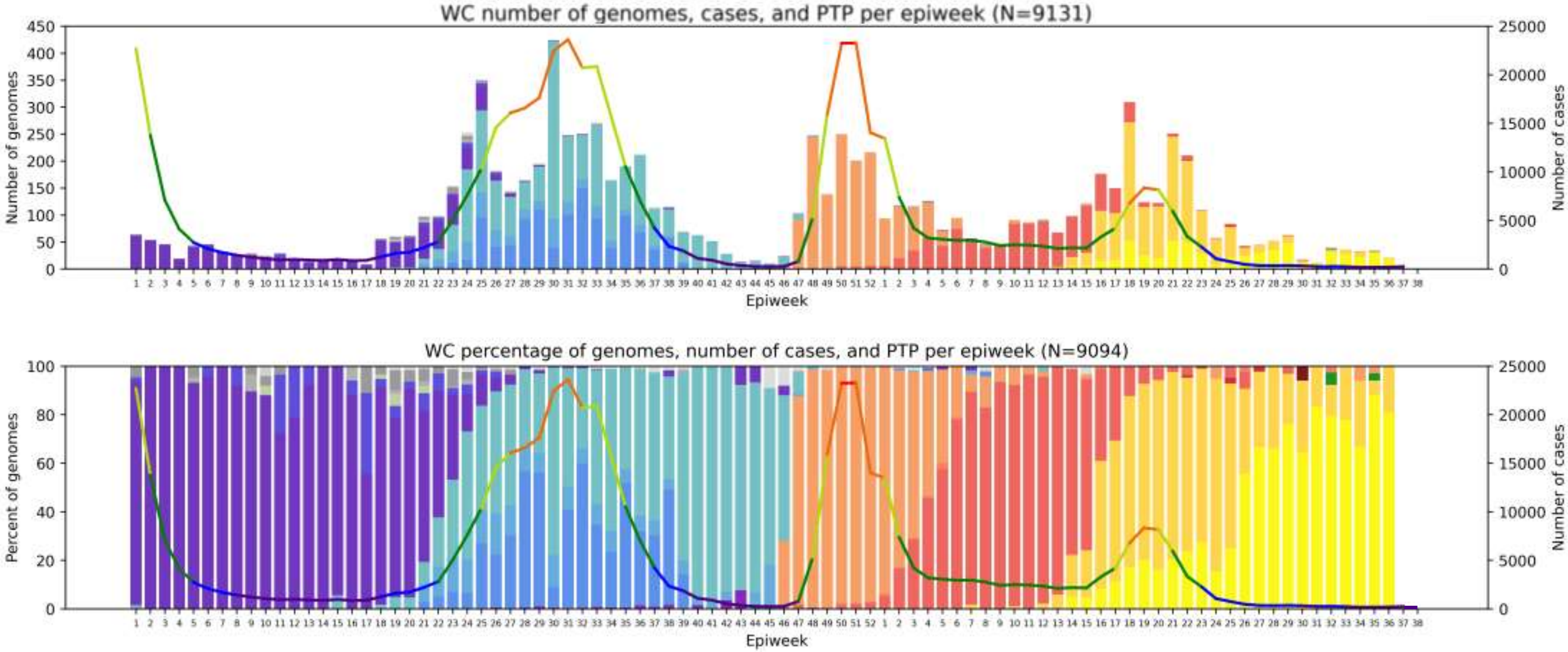
Western Cape Province, 2021-2022, n = 9131



Clade key (bar graph)

- ▬ XAY
- ▬ XBA
- ▬ Omicron (21K/BA.1.*)
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- ▬ Omicron (22C/BA.2.12.1)
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Summary

- **Sequencing update**
  - All provinces have sequences for June and July. Only the North West does not have August data. Gauteng, Kwa-Zulu Natal, Limpopo and the Western Cape have September data.
- **Variant of Concern Omicron in South Africa**
  - Omicron continued to dominate in June (99%), July (99%), August (98%), and currently makes up 100% of September sequences although numbers are small.
  - Omicron BA.5 was dominant in July (68%) and August (71%), and makes up 82% of September data.
  - BA.2.12.1 was detected in South Africa at low prevalence in May, June and July (<1%)
  - BA.2.75.* has been detected twice in Western Cape and Kwa-Zulu Natal (n=2).
- **N=14 sequences with novel mutational profile**
  - The New1 cluster (n = 10, predominantly from Gauteng) has been designated “XAY”, and the New2 cluster (n = 4, Limpopo) has been designated “XBA”[1]..
- Low frequency of previously circulating variants such as Delta not detected since July.

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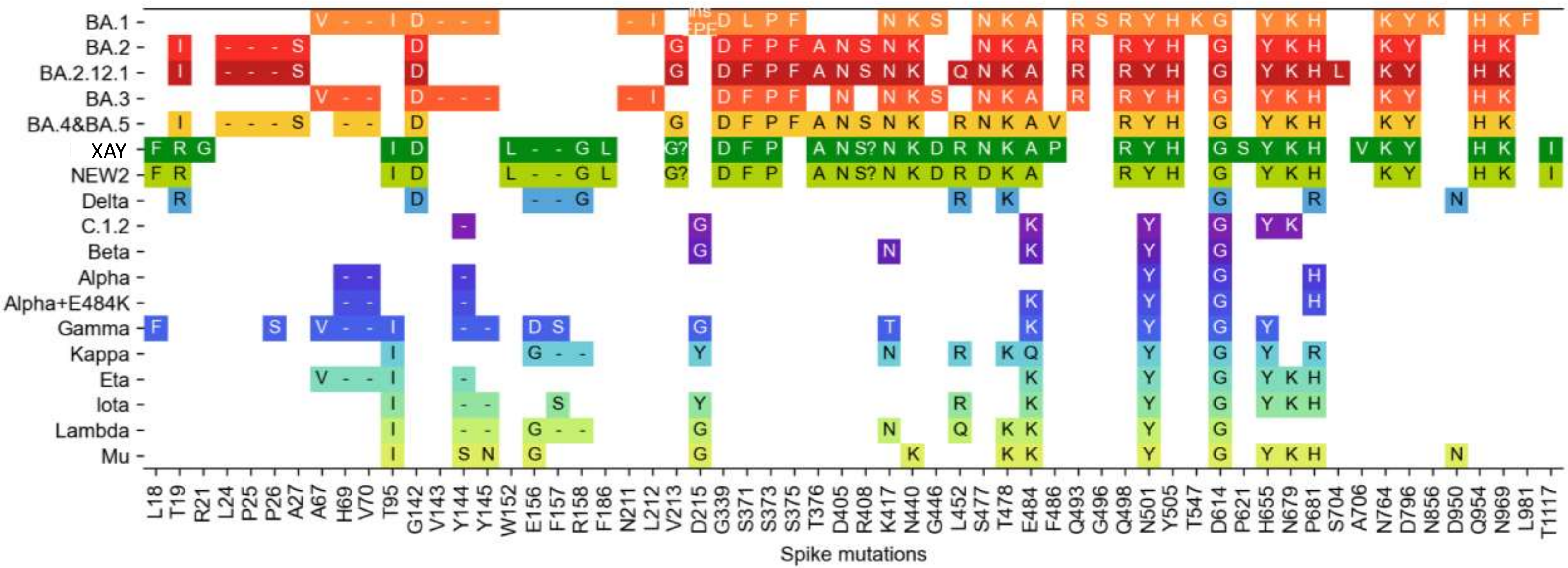
[1] https://github.com/cov-lineages/pango-designation/issues/844

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 the new SGTP sequences are pictured

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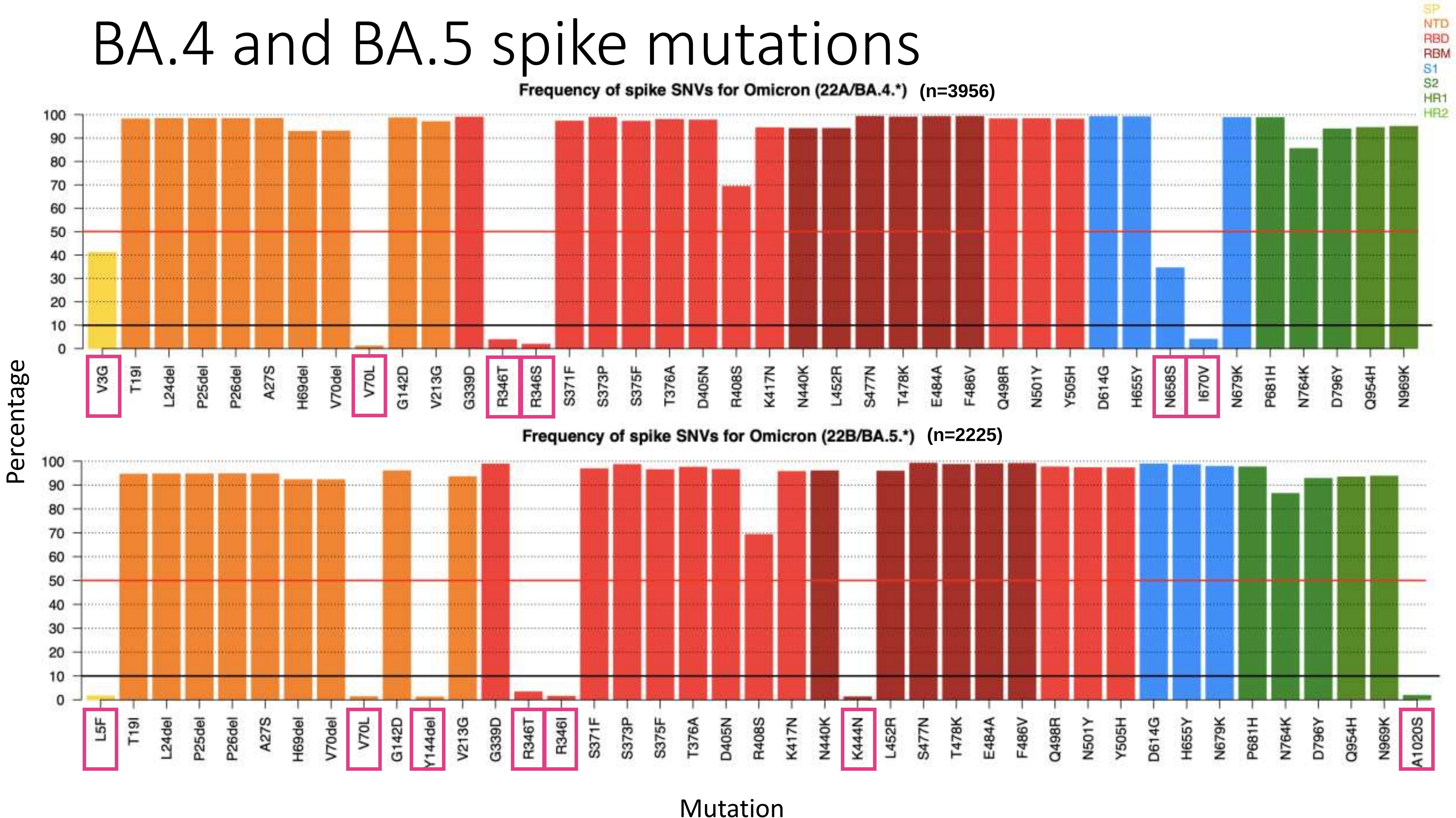
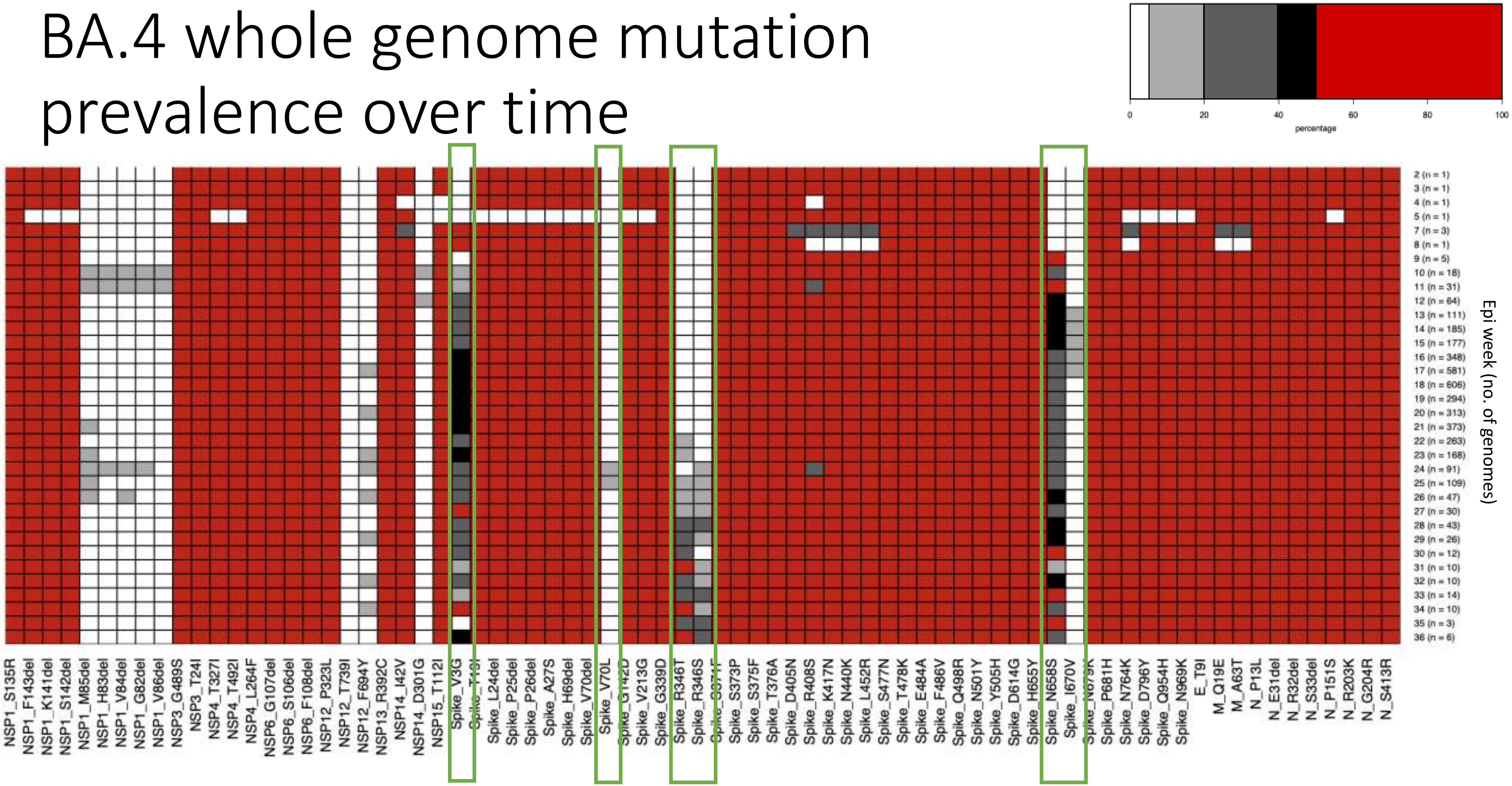
BA.4 and BA.5 spike mutations



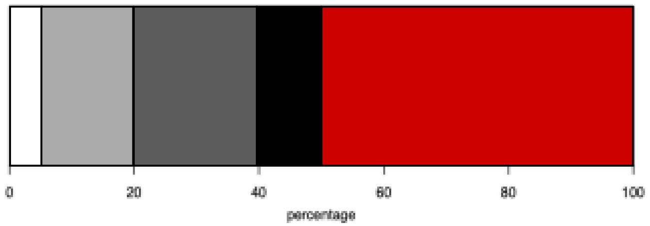
*as of 23 September 2022

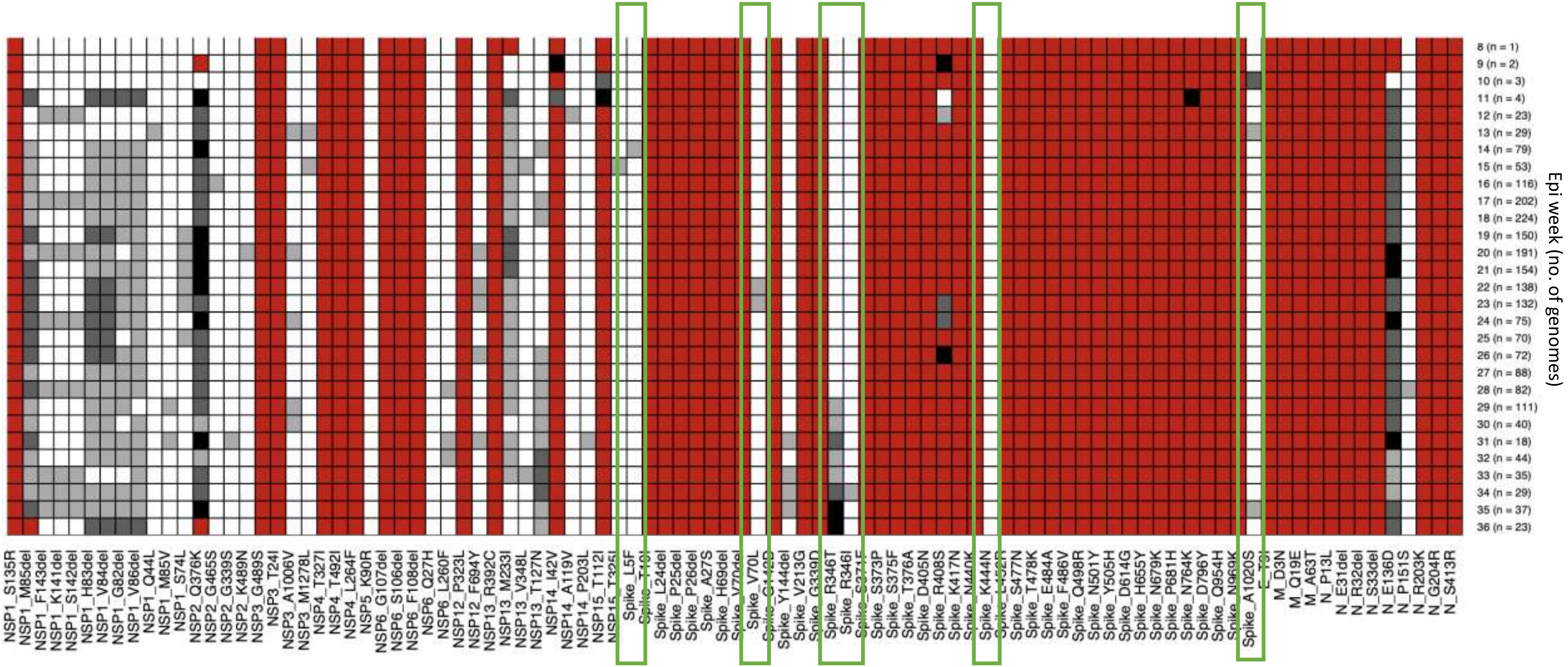
BA.4 whole genome mutation prevalence over time



*as of 23 September 2022

BA.5 whole genome mutation prevalence over time





*as of 23 September 2022

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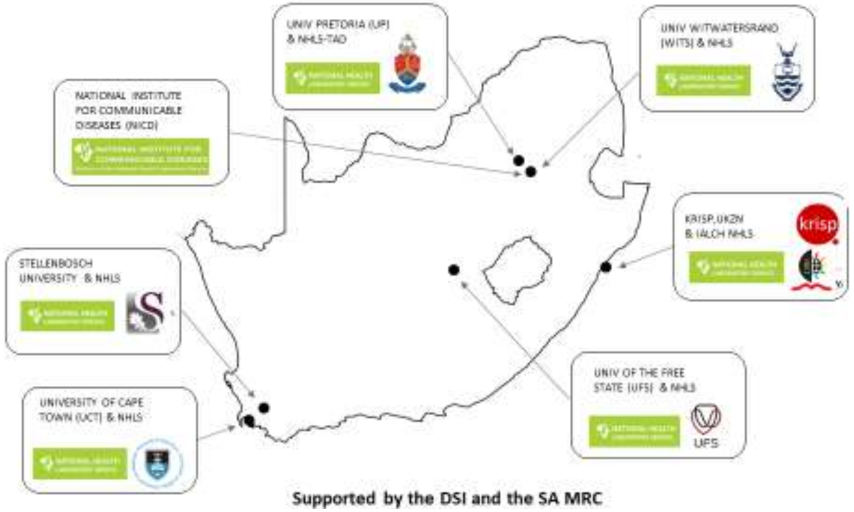

Supported by the DSI and the SA MRC

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

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
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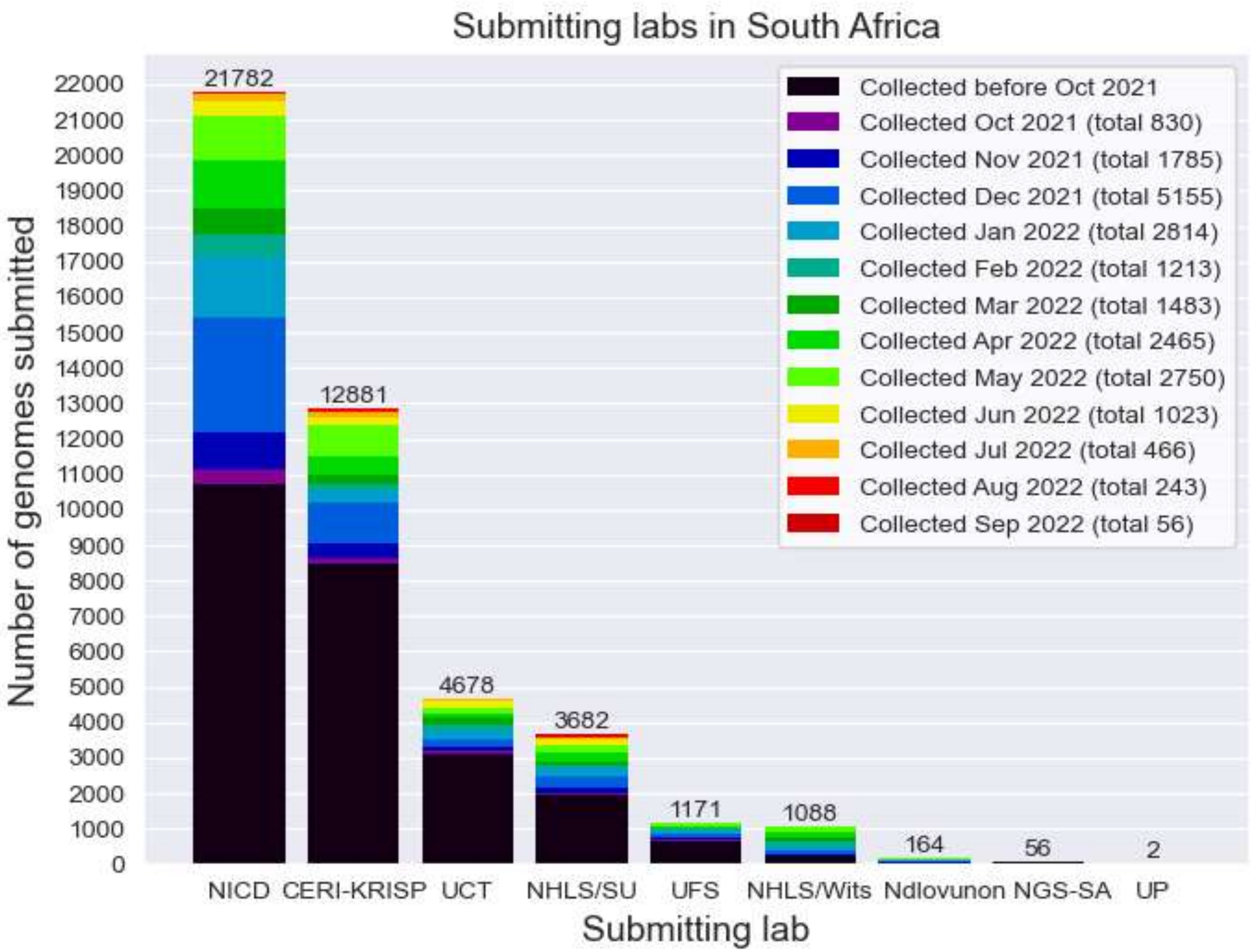
South African genomes submitted per submitting lab, 2020 - 2022 (N=45 504)



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 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 12 August 2022

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 12 August 2022

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.)