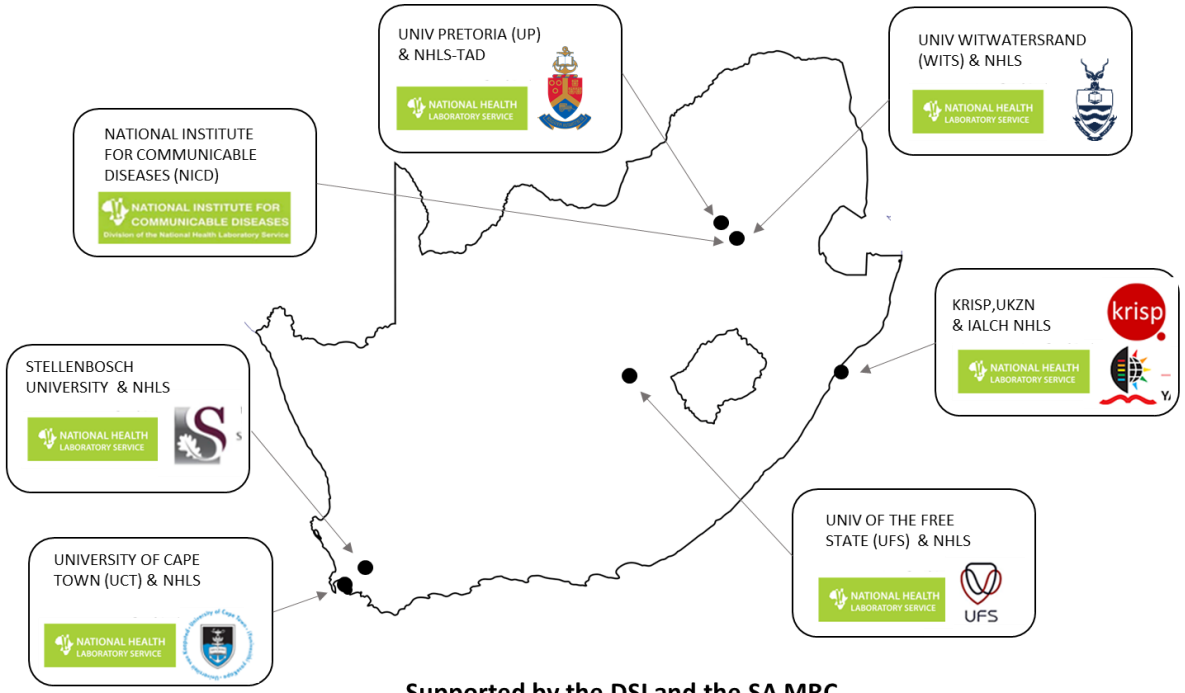
Network for Genomic Surveillance in South Africa (NGS-SA)

SARS-CoV-2 Sequencing Update
8 April 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 8 April 2022 at 10h46*

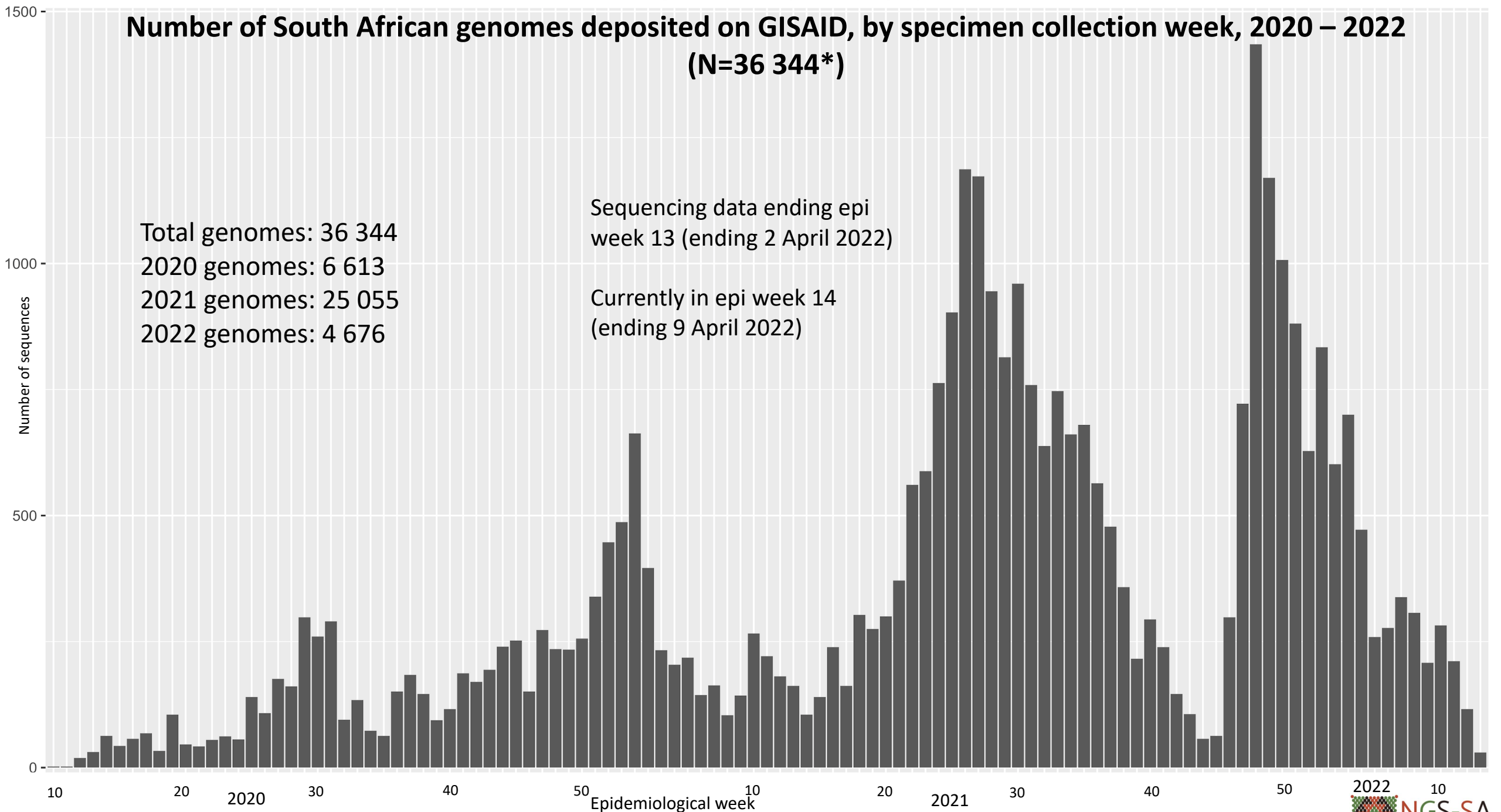
Data license: https://www.gisaid.org/registration/terms-of-use/

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

*Pangolin v4 has recently been released and sequences are in the process of being re-designated. Total numbers and proportions of the various lineages are likely to change over the next few weeks as the data are updated. All sequences deposited since 1 November 2021 have been run through the latest Pangolin update (v4.0.3, pangolin-data v.1.2.133.2, scorpio v0.3.2).
Case data is based on specimen collection date. Cases from https://www.nicd.ac.za/diseases-a-z-index/disease-index-covid-19/surveillance-reports/weekly-epidemiological-brief/
Test data gives weekly percentage testing positive rates, from https://www.nicd.ac.za/diseases-a-z-index/disease-index-covid-19/surveillance-reports/weekly-testing-summary/

Number of South African genomes deposited on GISAID, by specimen collection week, 2020 – 2022 (N=36 344*)



*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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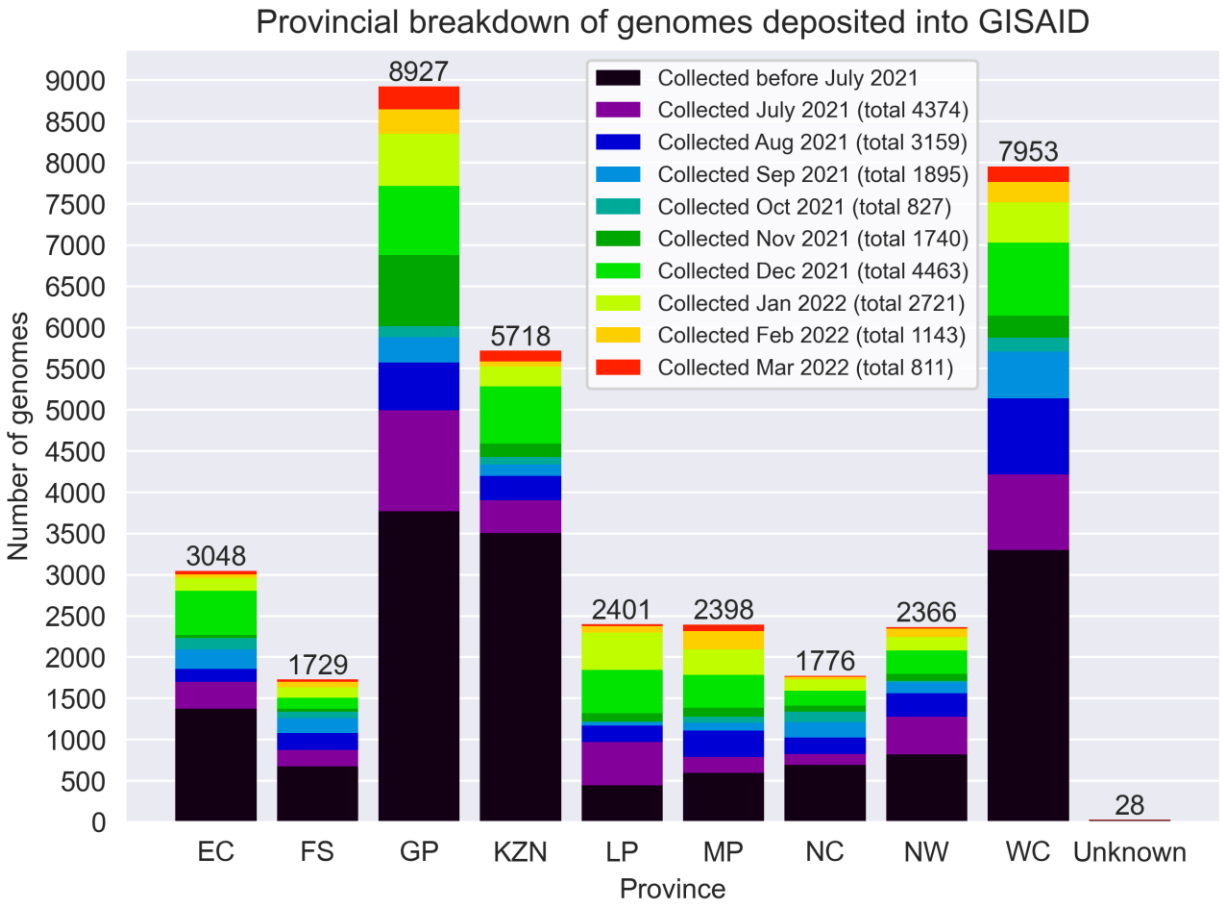
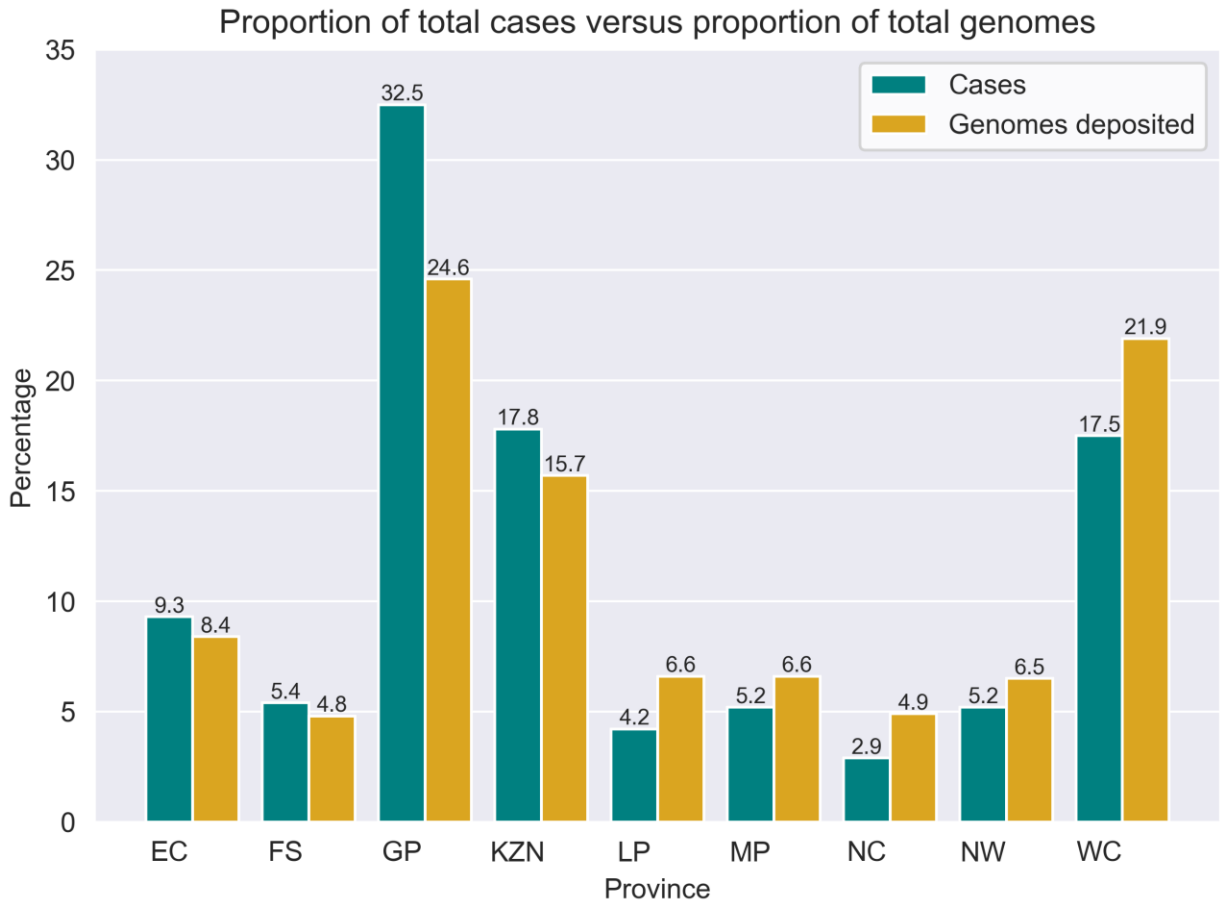
GISAID genomes vs total cases, 2020 – 2022 (N=36 344)





All provinces, apart from GP, KZN, LP, NC and WC, have comparable percentages of overall cases and overall sequenced genomes.

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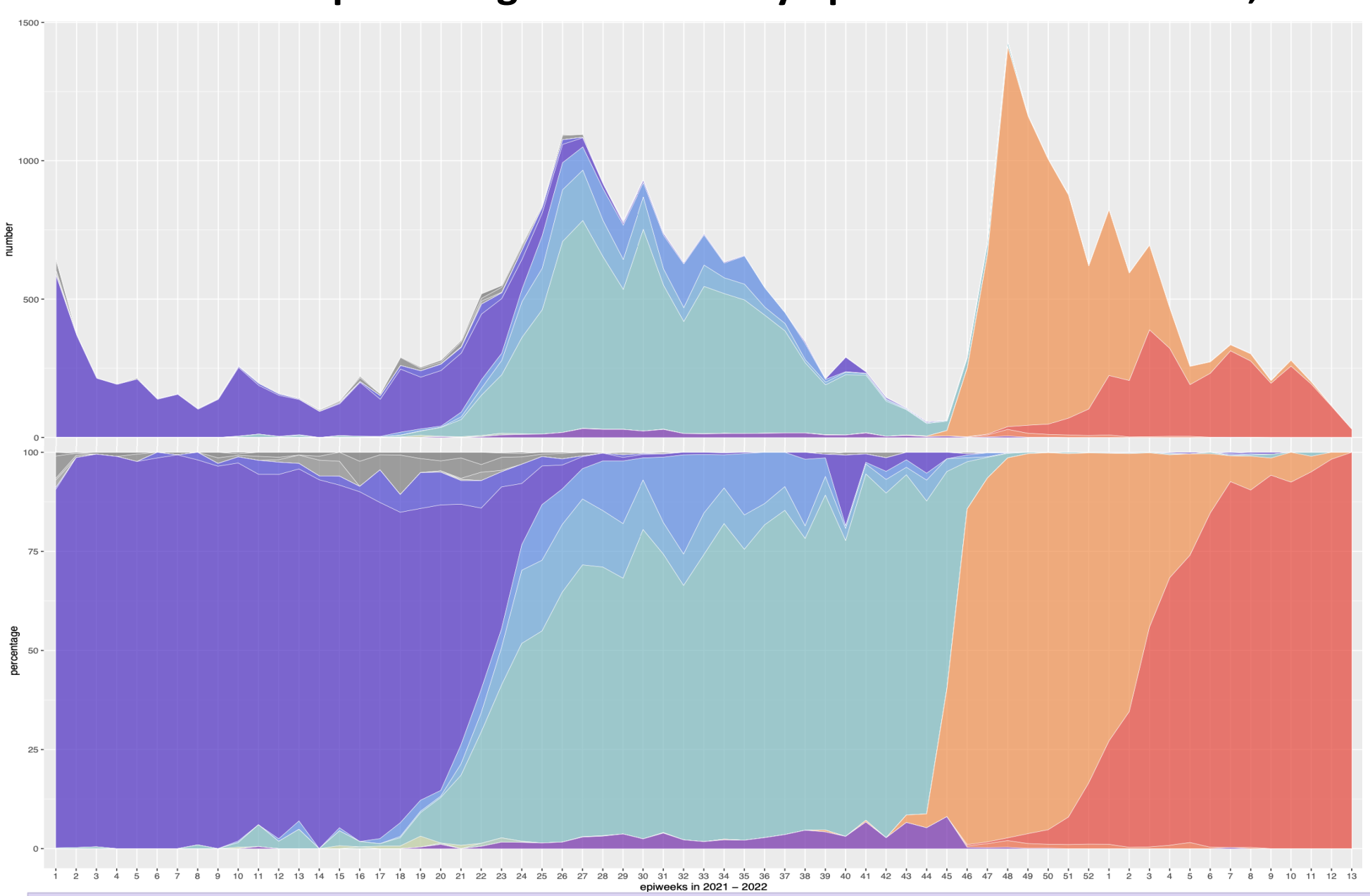
Number and percentage of clades* by epiweek in South Africa, 2021 - 2022 (N=29 731)



Sequencing data ending epi week 13 (ending 2 April 2022)

Currently in epi week 14 (ending 9 April 2022)

*Pangolin v4 has recently been released and sequences are in the process of being re-designated. Total numbers and proportions of the various sub-lineages are likely to change over the next few weeks as the data are updated.

Delta dominated in South Africa until October at >80%. Omicron has dominated from November onwards.

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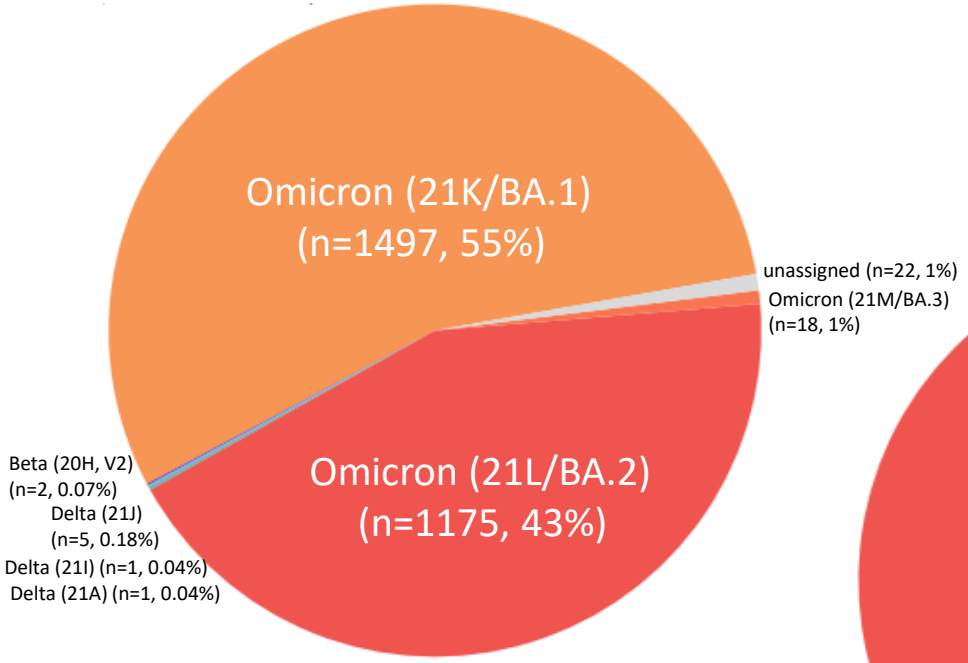
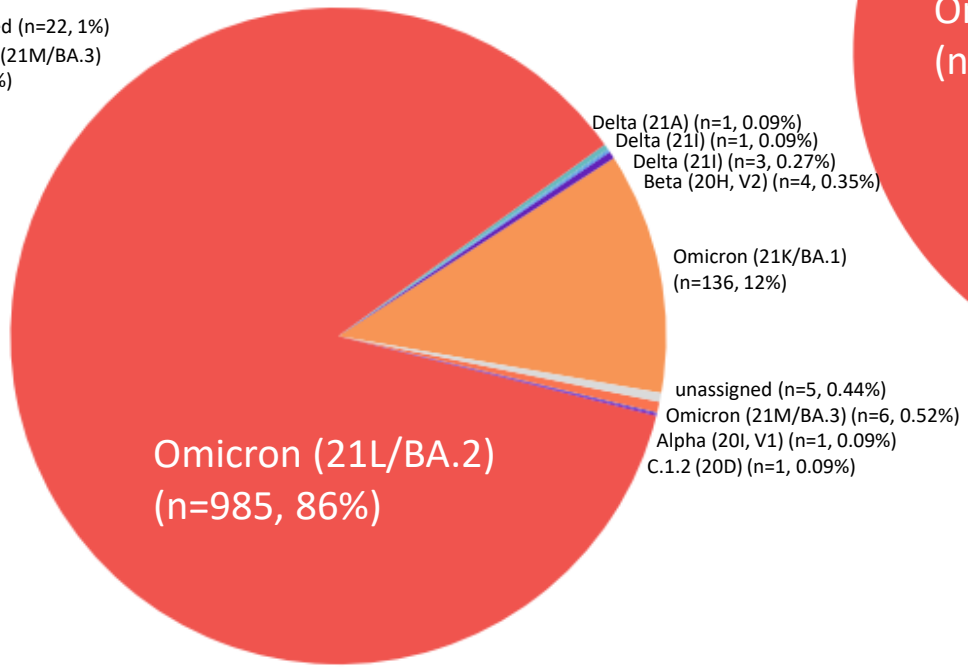
Prevalence of Variants of Concern (VOC) and Variants of Interest (VOI) in Jan – Mar 2022

January (N=2721)



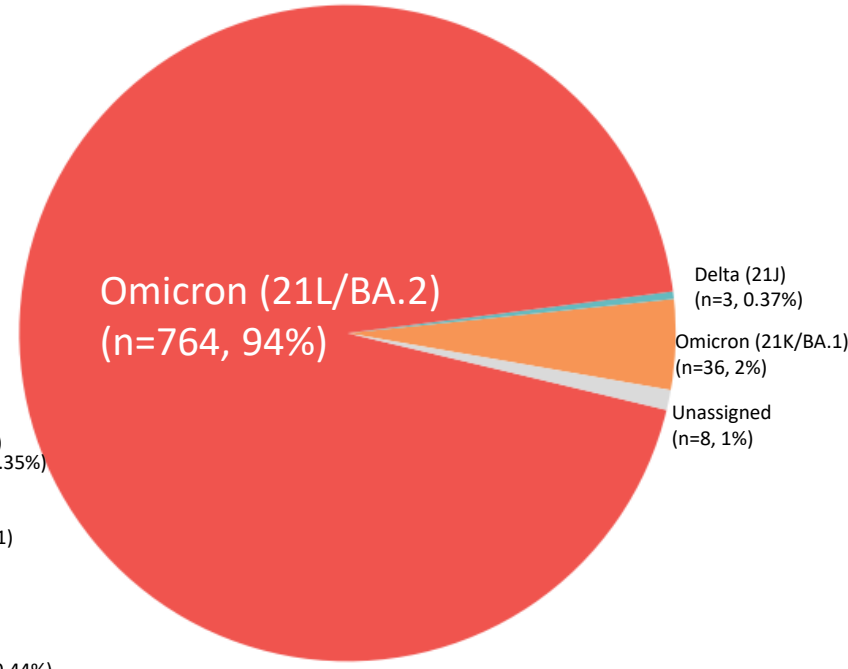
Total Omicron in Jan: 2690 (98.9%)

February (N=1143)



Total Omicron in Feb: 1127 (98.6%)

March (N=811)



Total Omicron in Mar: 800 (98.6%)

***Pangolin v4 has recently been released and sequences are in the process of being re-designated. Total numbers and proportions of the various sub-lineages are likely to change over the next few weeks as the data are updated.**

Omicron (21K) | Omicron (21L) | Omicron (21M) | C.1.2 (20D) | Beta (20H, V2) | Alpha (20I, V1) | Delta (21A) | Delta (21I) | Delta (21J) | Kappa (21B) | Eta (21D) | Other | unassigned

Omicron dominated in January (98.9%, 2690/2721), February (98.6%, 1127/1143) and March (98.6%, 800/811). BA.2 increased in prevalence throughout January and was dominant in February and March.

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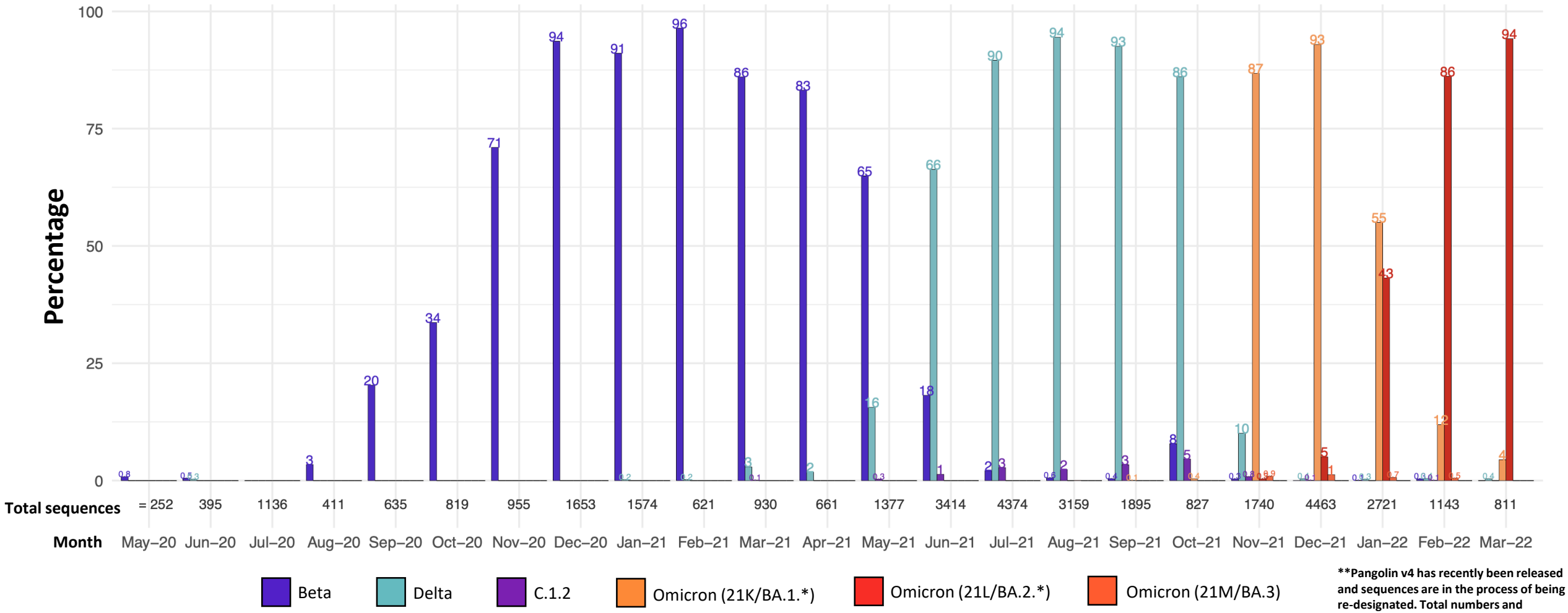
Detection Rates: Beta, Delta, C.1.2 and Omicron

Detection rates of variants** being monitored in South Africa*



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

**Pangolin v4 has recently been released and sequences are in the process of being re-designated. Total numbers and proportions of the various sub-lineages are likely to change over the next few weeks as the data are updated.

**Omicron has been dominant since November (>80% in November, >98% in December, January, February and March).
BA.2 has increased in frequency, making up 43% of genomes in January, 86% in February and 94% in March.
BA.3 and other VOCs continue to be detected at low levels.**

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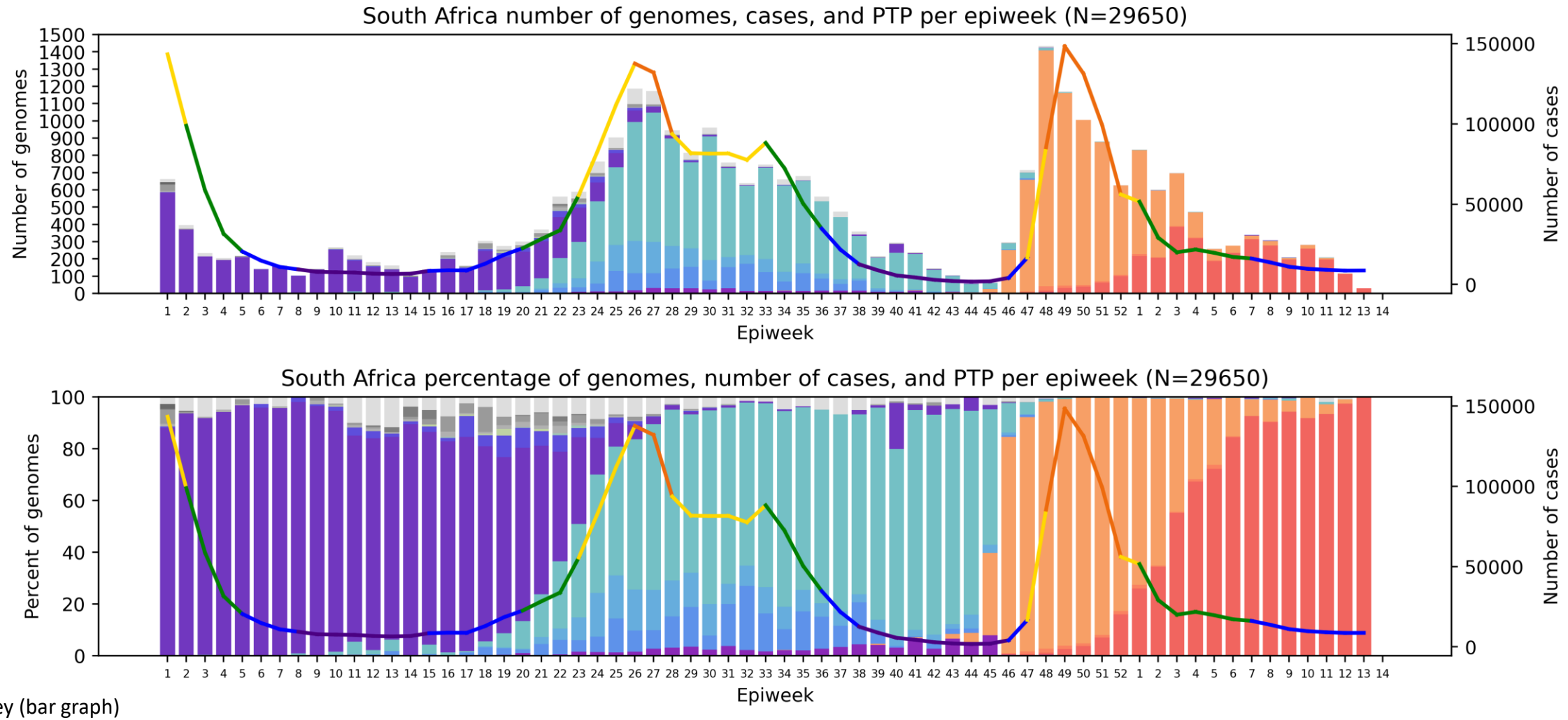
South Africa, 2021-2022, n = 29650*



**Pangolin v4 has recently been released and sequences are in the process of being re-designated. Total numbers and proportions of the various sub-lineages are likely to change over the next few weeks as the data are updated.

*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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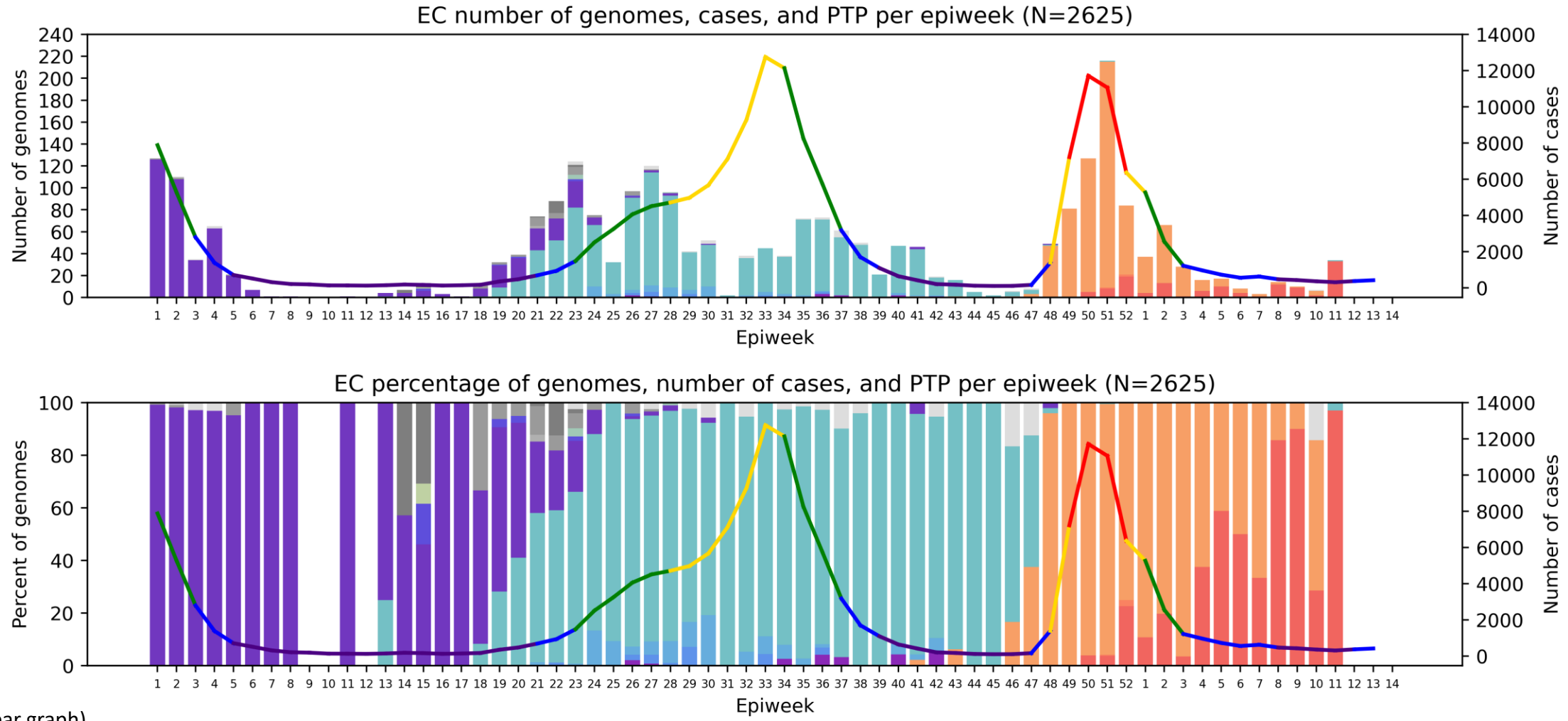
Eastern Cape Province, 2021-2022, n = 2625



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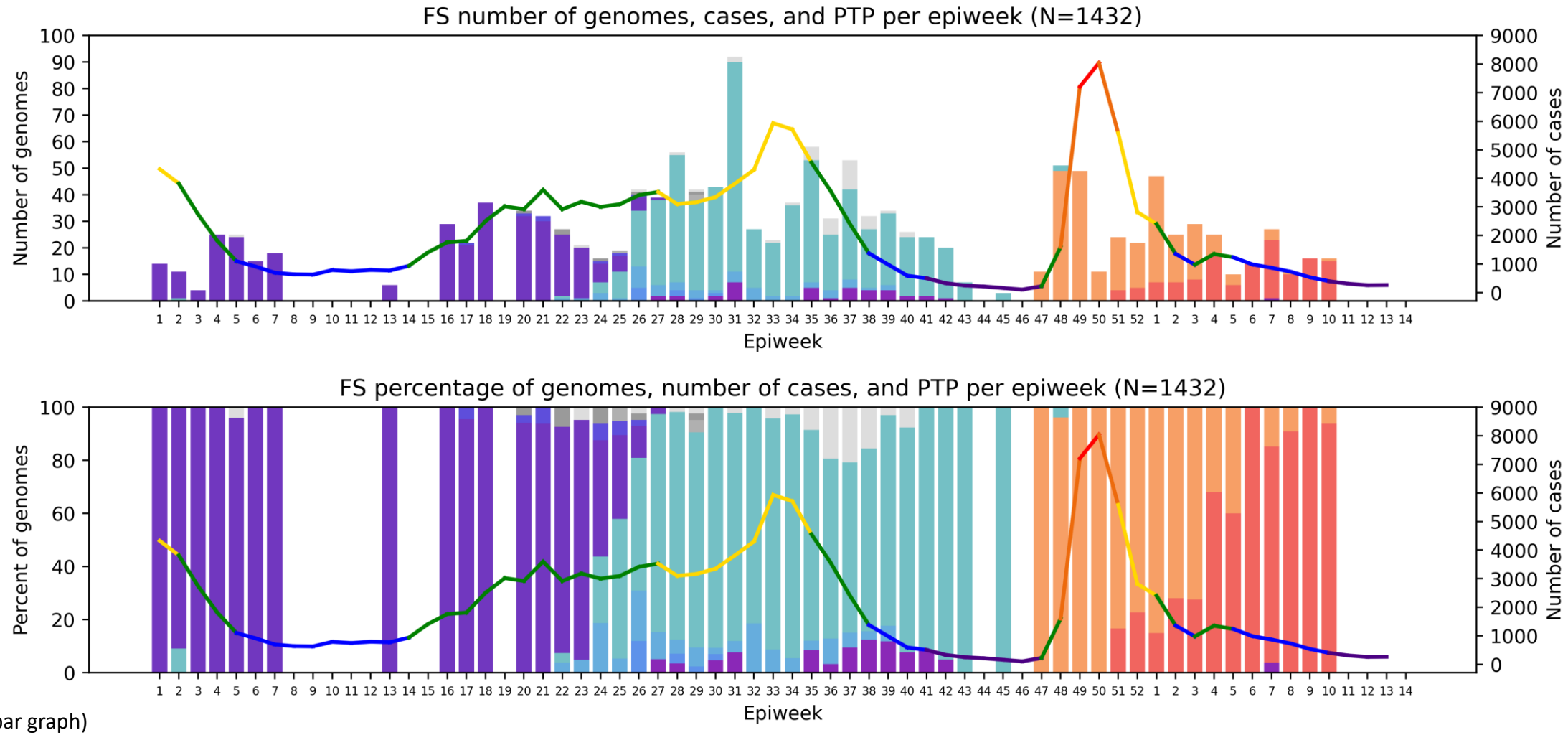
Free State Province, 2021-2022, n = 1432



Clade key (bar graph)

Omicron (21L/BA.2) | Omicron (21M/BA.3) | Omicron (21K/BA.1.1) | Omicron (21K/BA.1) | C.1.2 (20D) | Delta (21A) | Delta (21I) | Delta (21J) | Beta (20H, V2) | Cases | Alpha (20I, V1) | Kappa (21B) | Eta (21D) | 20A | 20B | 20C | 20D | unassigned | 19A | 19B

Weekly percentage testing positive key (line graph)

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

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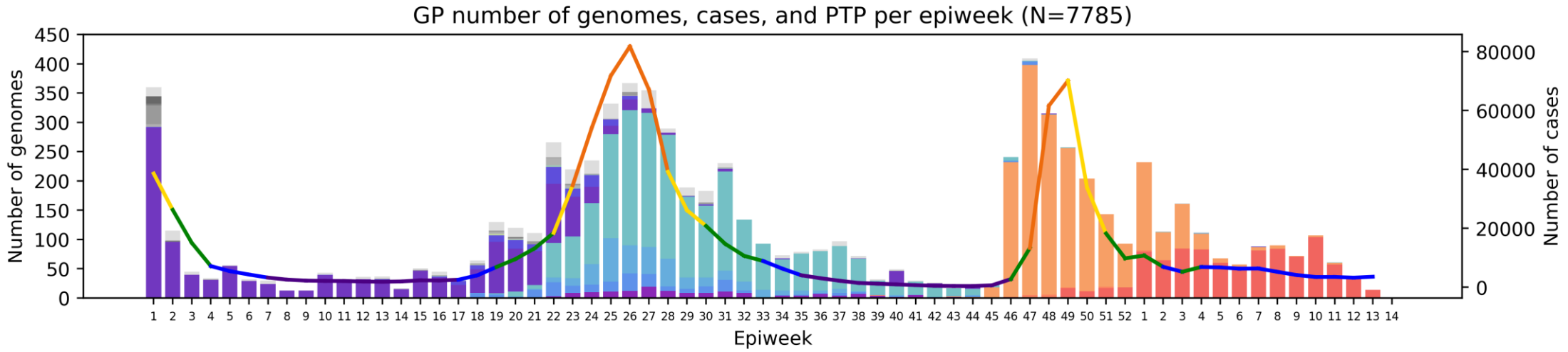
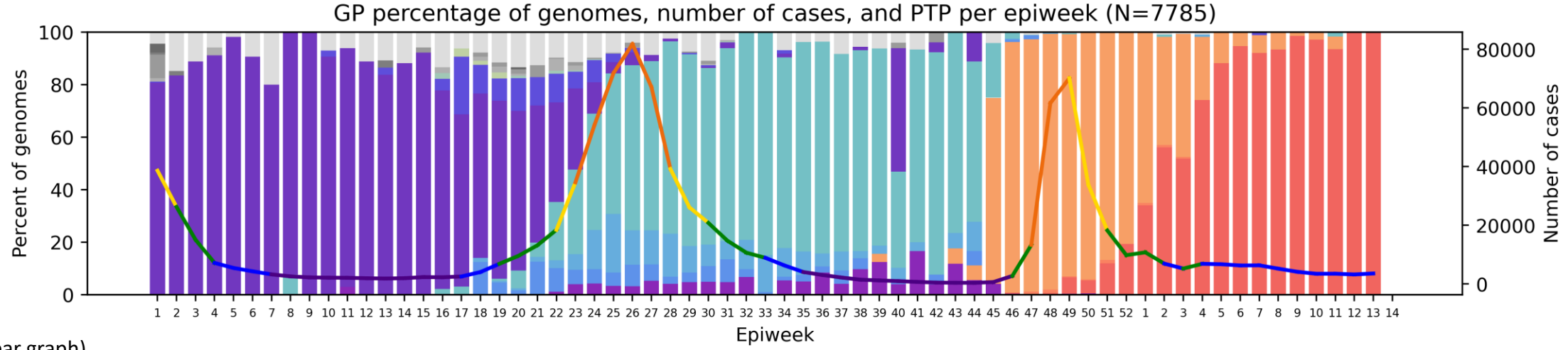
Gauteng Province, 2021-2022, n = 7785





Clade key (bar graph)

Omicron (21L/BA.2) | Omicron (21M/BA.3) | Omicron (21K/BA.1.1) | Omicron (21K/BA.1) | C.1.2 (20D) | Delta (21A) | Delta (21I) | Delta (21J) | Beta (20H, V2) | Cases | Alpha (20I, V1) | Kappa (21B) | Eta (21D) | 20A | 20B | 20C | 20D | unassigned | 19A | 19B

Weekly percentage testing positive key (line graph)

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

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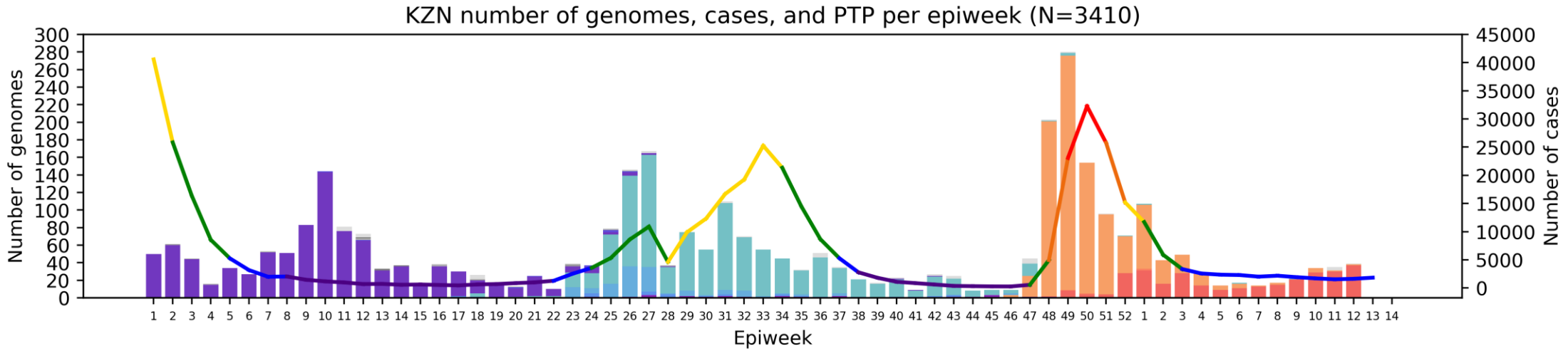
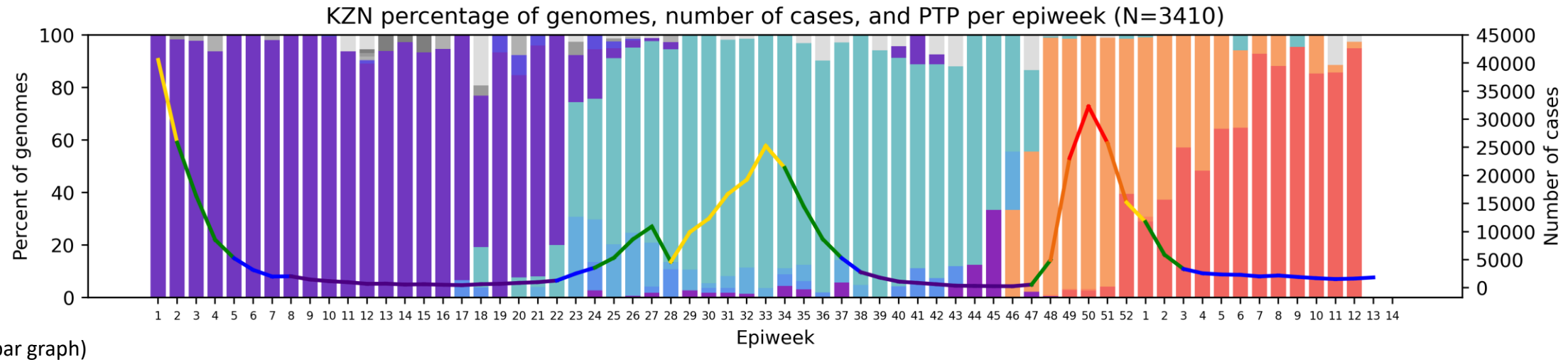
KwaZulu-Natal Province, 2021-2022, n = 3140





Clade key (bar graph)

Omicron (21L/BA.2) | Omicron (21M/BA.3) | Omicron (21K/BA.1.1) | Omicron (21K/BA.1) | C.1.2 (20D) | Delta (21A) | Delta (21I) | Delta (21J) | Beta (20H, V2) | Cases | Alpha (20I, V1) | Kappa (21B) | Eta (21D) | 20A | 20B | 20C | 20D | unassigned | 19A | 19B

Weekly percentage testing positive key (line graph)

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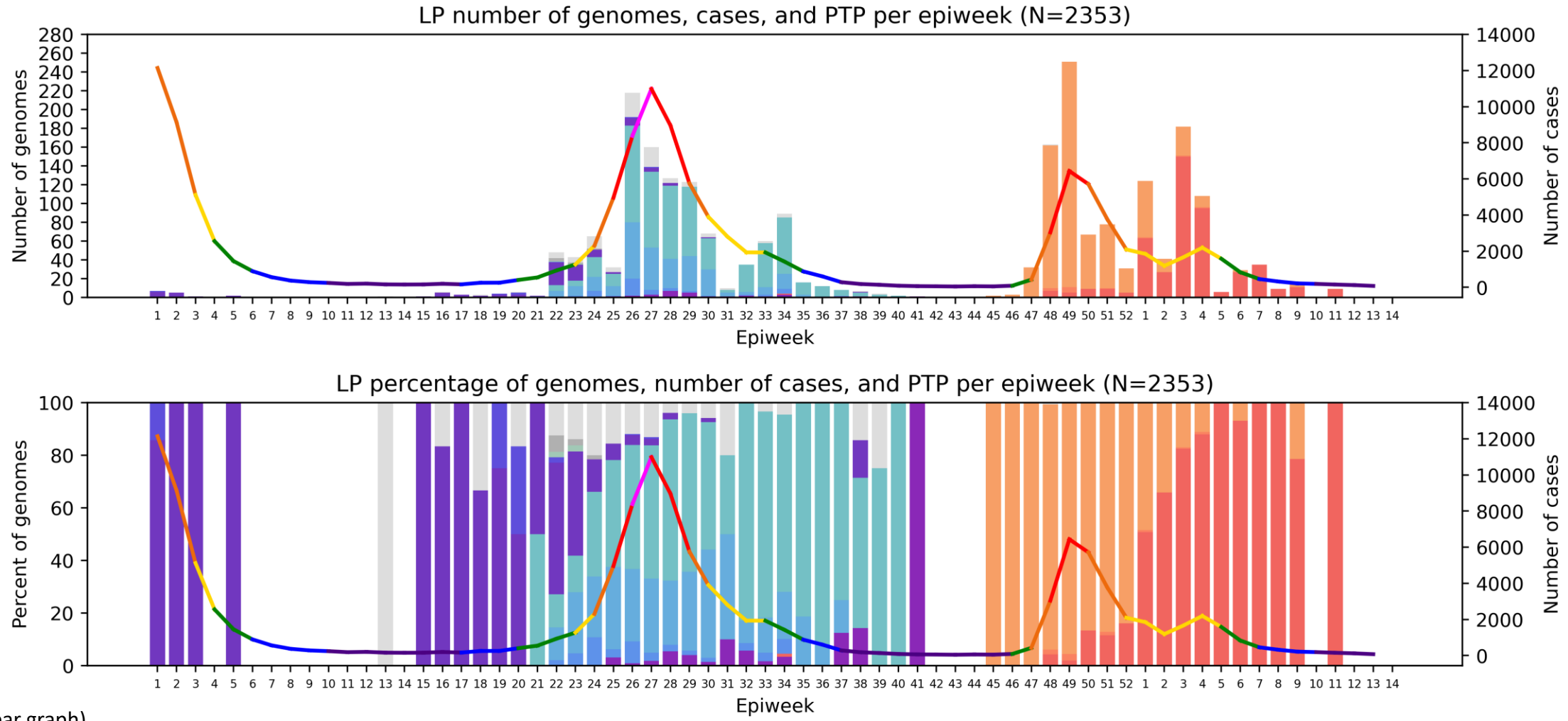
Limpopo Province, 2021-2022, n = 2353



Clade key (bar graph)

Omicron (21L/BA.2) | Omicron (21M/BA.3) | Omicron (21K/BA.1.1) | Omicron (21K/BA.1) | C.1.2 (20D) | Delta (21A) | Delta (21I) | Delta (21J) | Beta (20H, V2) | Cases | Alpha (20I, V1) | Kappa (21B) | Eta (21D) | 20A | 20B | 20C | 20D | unassigned | 19A | 19B

Weekly percentage testing positive key (line graph)

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

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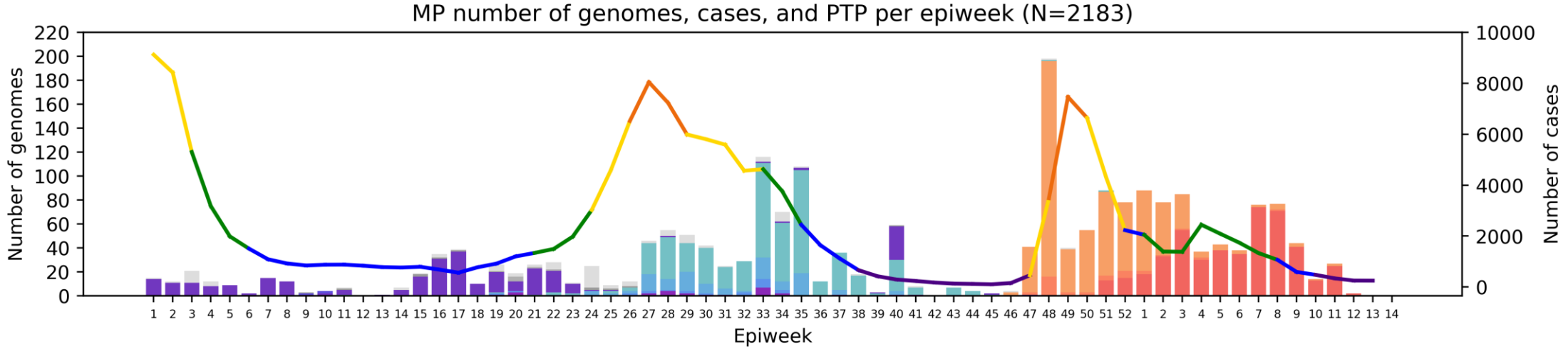
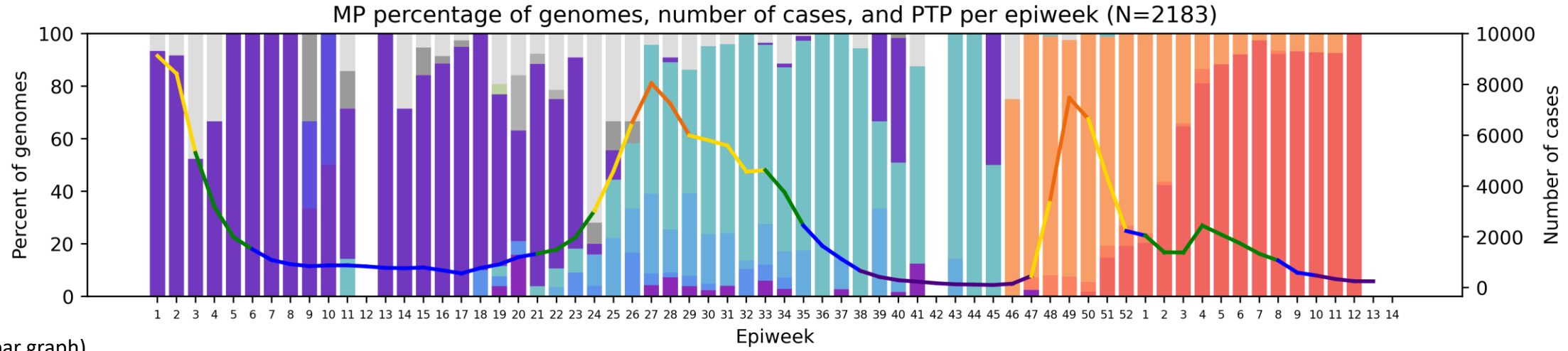
Mpumalanga Province, 2021-2022, n = 2183





Clade key (bar graph)

Omicron (21L/BA.2) | Omicron (21M/BA.3) | Omicron (21K/BA.1.1) | Omicron (21K/BA.1) | C.1.2 (20D) | Delta (21A) | Delta (21I) | Delta (21J) | Beta (20H, V2) | Alpha (20I, V1) | Kappa (21B) | Eta (21D) | 20A | 20B | 20C | 20D | unassigned | 19A | 19B | Cases

Weekly percentage testing positive key (line graph)

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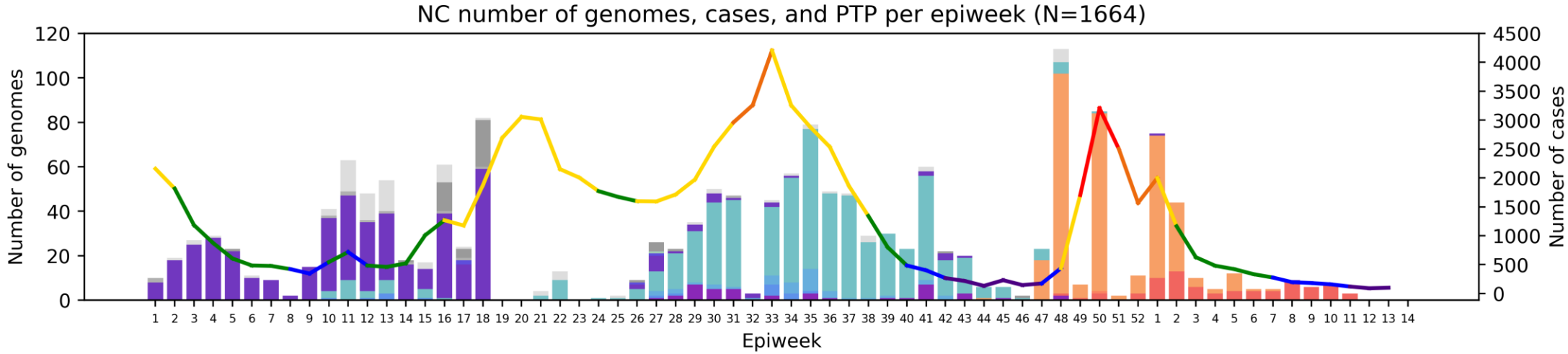
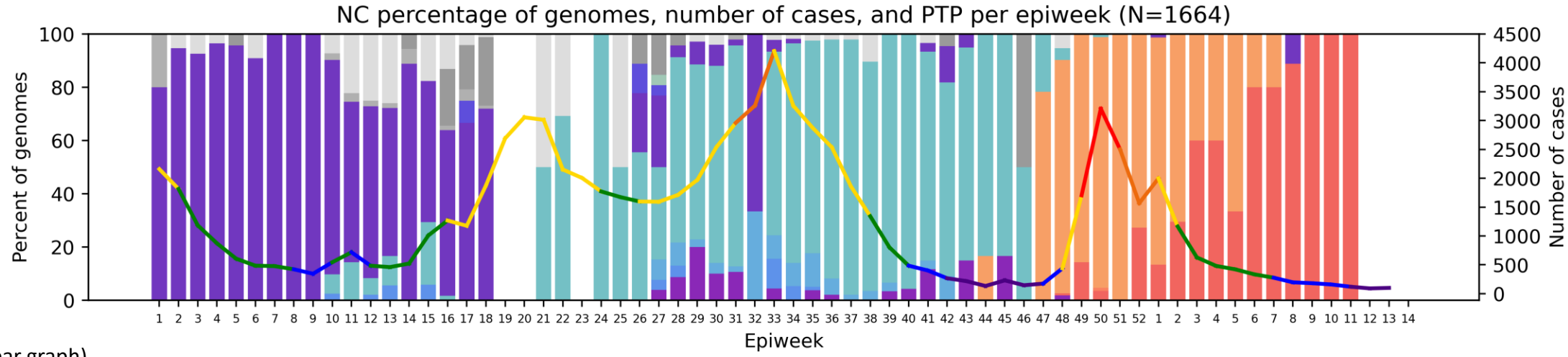
Northern Cape Province, 2021-2022, n = 1664





Clade key (bar graph)

Omicron (21L/BA.2) | Omicron (21M/BA.3) | Omicron (21K/BA.1.1) | Omicron (21K/BA.1) | C.1.2 (20D) | Delta (21A) | Delta (21I) | Delta (21J) | Beta (20H, V2) | Cases | Alpha (20I, V1) | Kappa (21B) | Eta (21D) | 20A | 20B | 20C | 20D | unassigned | 19A | 19B

Weekly percentage testing positive key (line graph)

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

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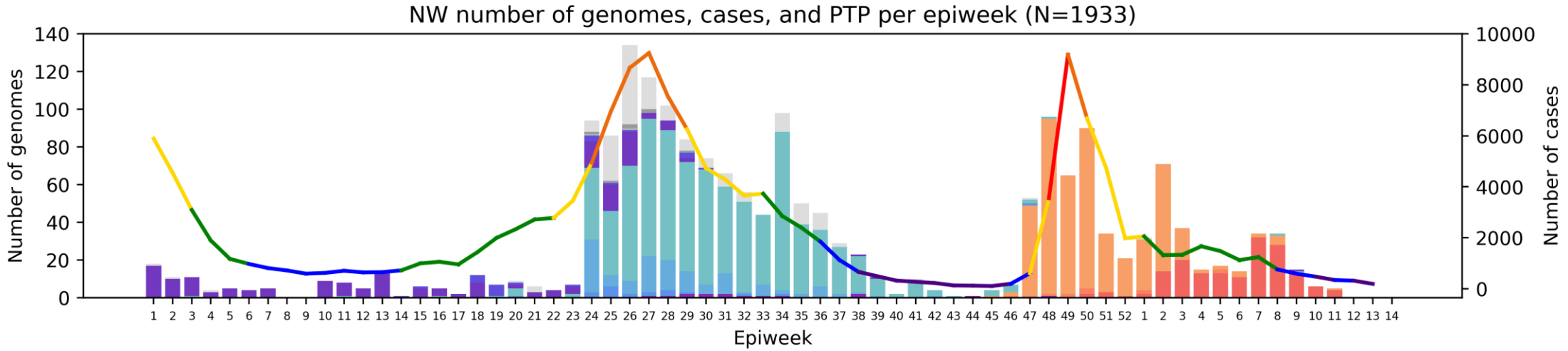
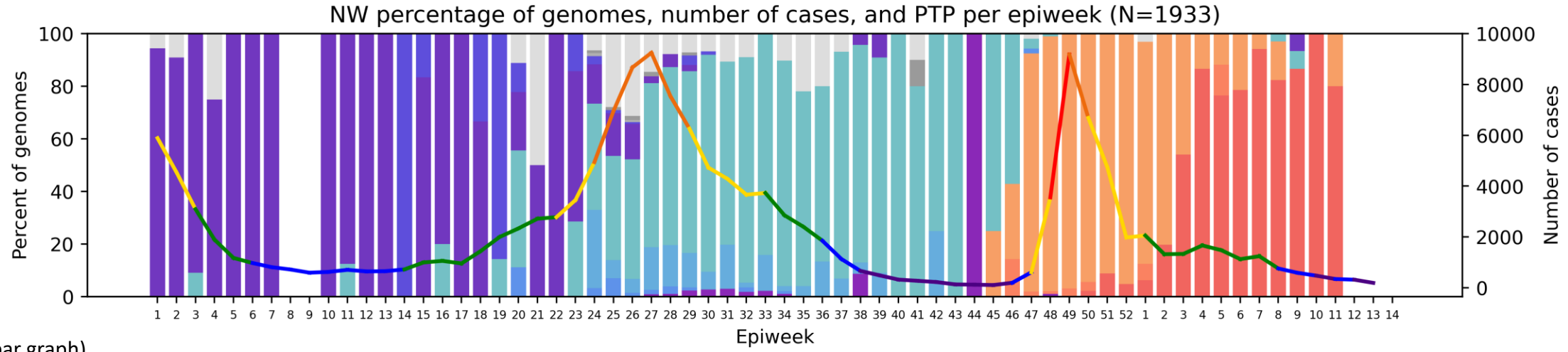
North West Province, 2021, n = 1993





Clade key (bar graph)

Omicron (21L/BA.2) | Omicron (21M/BA.3) | Omicron (21K/BA.1.1) | Omicron (21K/BA.1) | C.1.2 (20D) | Delta (21A) | Delta (21I) | Delta (21J) | Beta (20H, V2) | Cases | Alpha (20I, V1) | Kappa (21B) | Eta (21D) | 20A | 20B | 20C | 20D | unassigned | 19A | 19B

Weekly percentage testing positive key (line graph)

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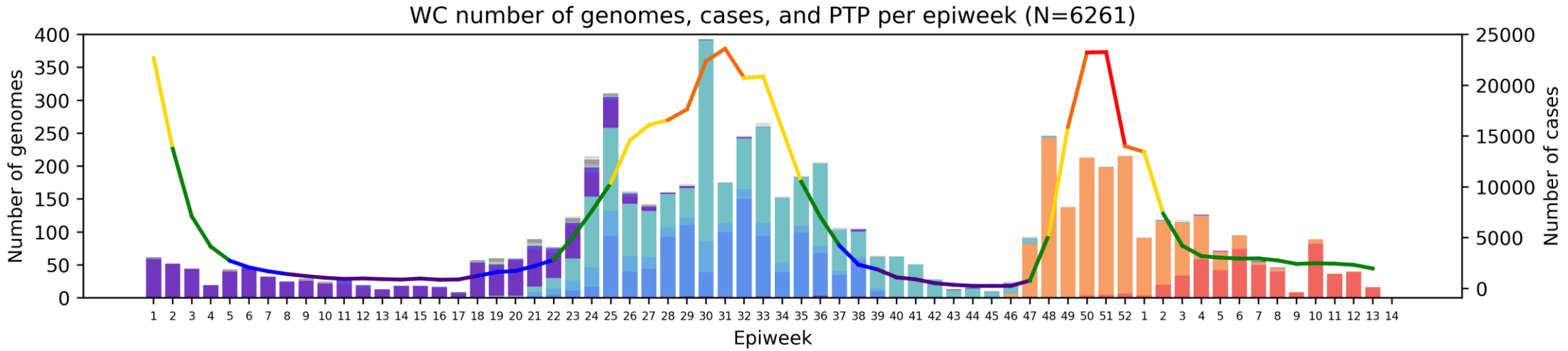
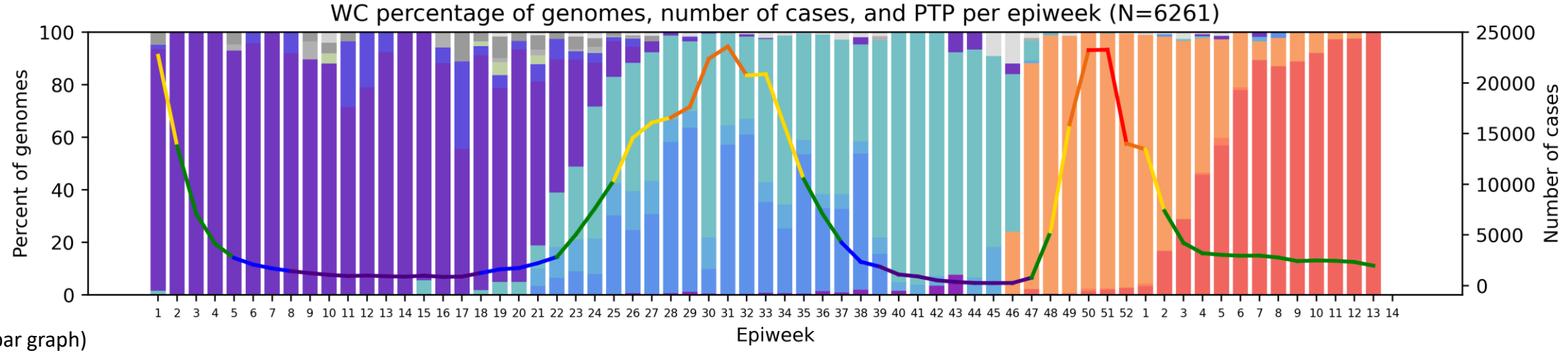
Western Cape Province, 2021-2022, n = 6261





Clade key (bar graph)

Omicron (21L/BA.2) | Omicron (21M/BA.3) | Omicron (21K/BA.1.1) | Omicron (21K/BA.1) | C.1.2 (20D) | Delta (21A) | Delta (21I) | Delta (21J) | Beta (20H, V2) | Cases | Alpha (20I, V1) | Kappa (21B) | Eta (21D) | 20A | 20B | 20C | 20D | unassigned | 19A | 19B

Weekly percentage testing positive key (line graph)

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Summary

- **Variant of Concern Omicron in South Africa**
  - Dominates 2022 sequencing data at >99% of genomes
  - While BA.1 (and sub-lineages) was the predominant sub-lineage in January (55%), the proportion of BA.2 increased from 43% in January to 86% in February and 94% in March
  - BA.3 continues to be detected at low levels
  - NGS-SA teams are monitoring sequencing data for recombinants
  - Two additional Omicron sub-lineages (BA.4 and BA.5) have recently been designated by Pangolin[1] but do not yet reflect on GISAID. Once available, data will be updated accordingly.

- Low frequency of previously circulating variants such as Delta and Beta still detected in recent data

[1] https://github.com/cov-lineages/pango-designation/releases/tag/v1.3

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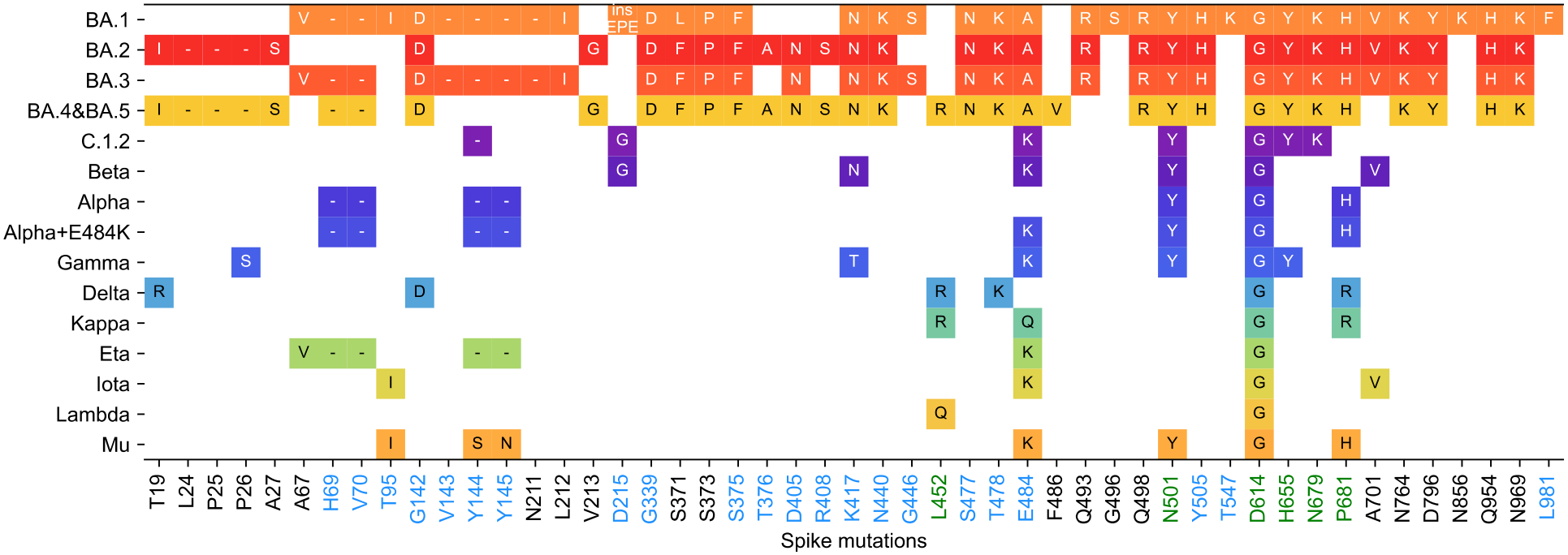
Omicron spike mutations compared to other VOC/VOIs



Only lineage-defining mutations are pictured here. Low prevalence mutations can be seen on the following slide.

Mutation impact key

- Unknown or unconfirmed impact
- Known/predicted immune escape
- Enhanced infectivity

- 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

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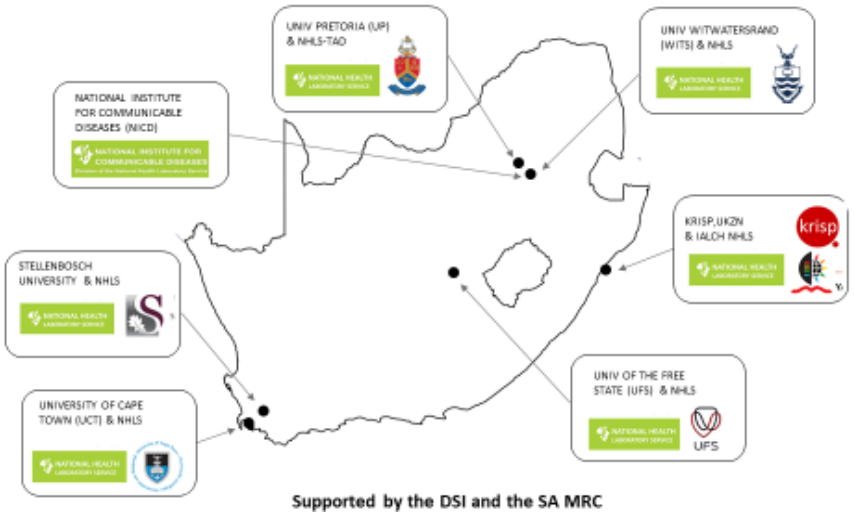

Supported by the DSI and the SA MRC

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Division of the National Health Laboratory Service

EDCTP

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Thabang Serakge
Bruna Galvão
Arghavan Alisoltani (U. California)
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Darren Martin
Nicola Mulder
Wendy Burgers
Ntobeko Ntusi
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Amy Strydom (Postdoc)
Michaela Davis (MSc, intern medical scientist)
Carien van Niekerk

NHLS Tshwane
Prof Simnikiwe Mayaphi (HOD)

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GIZ/BMBF: African Network for Improved diagnostics and epidemiology of common and emerging infectious agents (ANDEMIA)
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National Institute for Communicable Diseases

Centre for Respiratory Diseases & Meningitis
Anne von Gottberg
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NGS-SA
Network for Genomic Surveillance in South Africa

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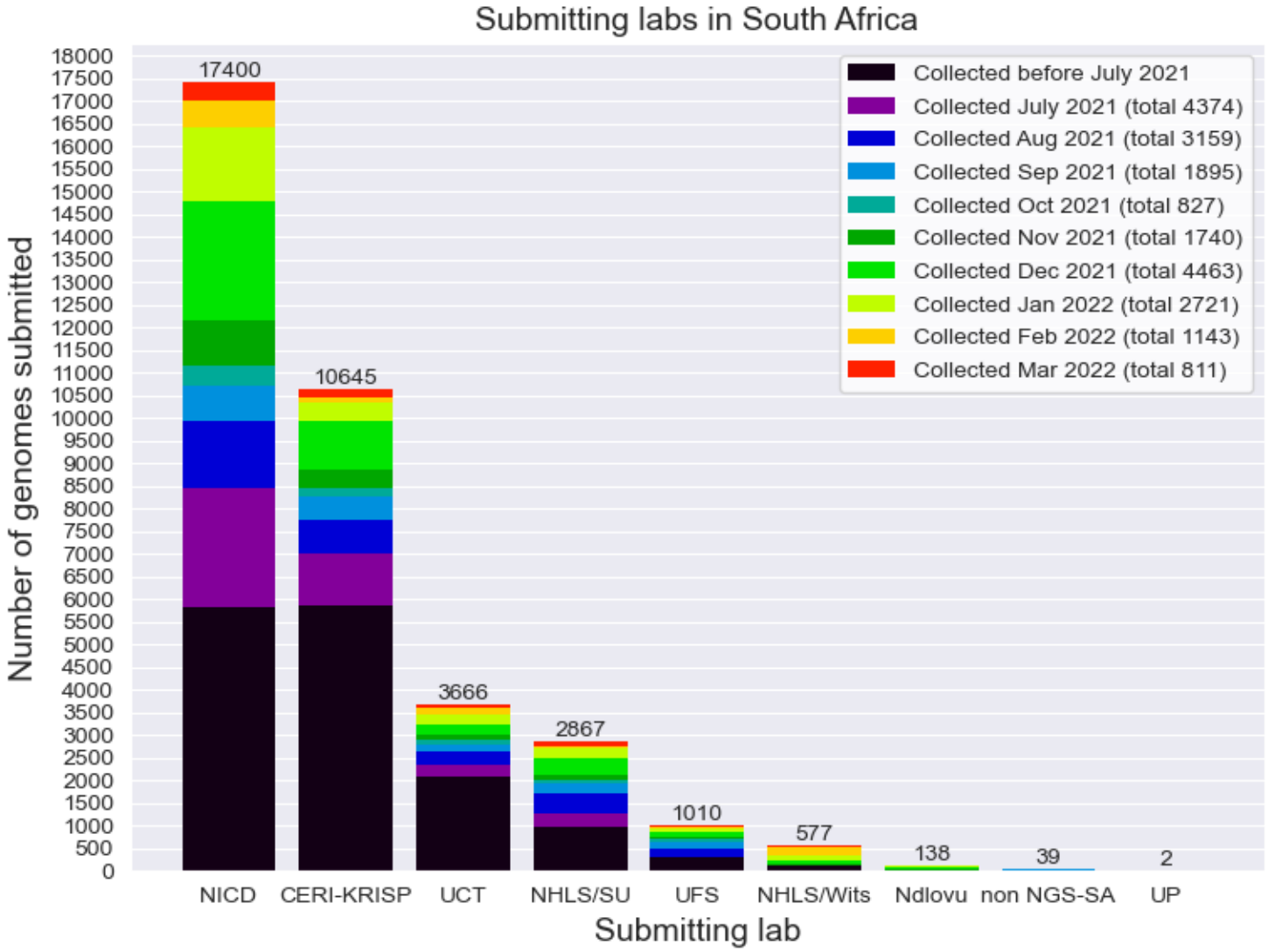
South African genomes submitted per submitting lab, 2020 - 2022 (N=36 344)



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
Delta	B.1.617.2	G/478K.V1	21A, 21I, 21J	+S:K417N +S:K484K	India, Oct-2020	VOI: 4-Apr-2021 VOC: 11-May-2021
Omicron*	B.1.1.529	GR/484A	21K	+S:R346K	Multiple countries, Nov-2021	VUM: 24-Nov-2021 VOC: 26-Nov-2021

https://www.who.int/en/activities/tracking-SARS-CoV-2-variants/ accessed 18 March 2022

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

° Only found in a subset of sequences

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

https://www.who.int/en/activities/tracking-SARS-CoV-2-variants/ accessed 18 March 2022

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

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.)