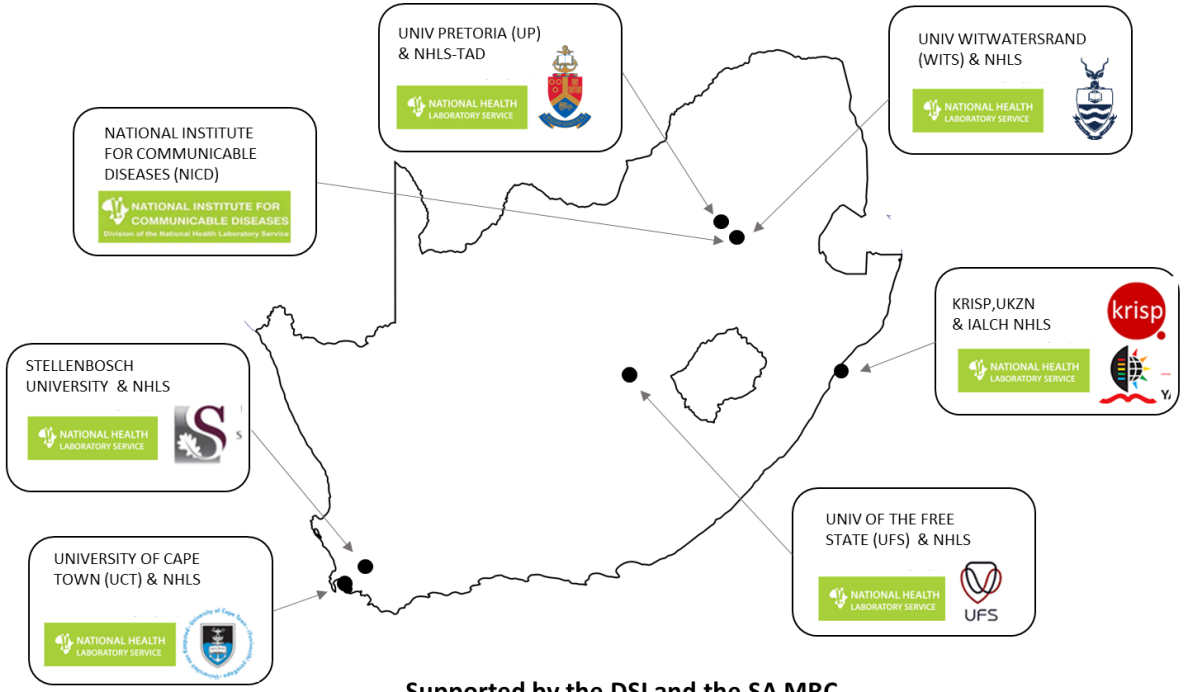
Network for Genomic Surveillance in South Africa (NGS-SA)

SARS-CoV-2 Sequencing Update
1 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 1 April 2022 at 16h05

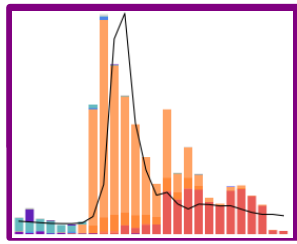
Data license: https://www.gisaid.org/registration/terms-of-use/

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

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/

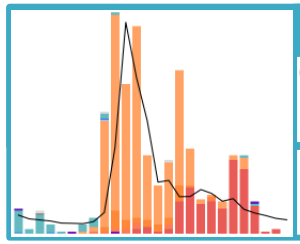
SARS-CoV-2
GENOMIC SURVEILLANCE
epiweeks 39 (2021) - 12 (2022)



Gauteng ↑ PTP: 6.1%

Genomes	Cases
2 923 (25.5%)	282 852 (35.6%)

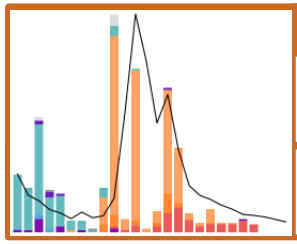
Genomes deposited in the last week: 3, 81, 2, 83, 6, 34, 5, 3



North West ↑ PTP: 5.6%

Genomes	Cases
670 (5.8%)	41 181 (5.2%)

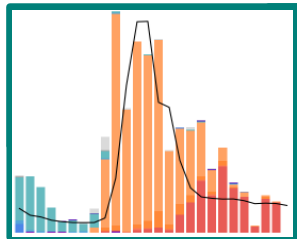
Genomes deposited in the last week: 2, 25, 14, 76, 8, 6, 5, 1



Northern Cape ↓ PTP: 5.3%

Genomes	Cases
577 (5.0%)	18 314 (2.3%)

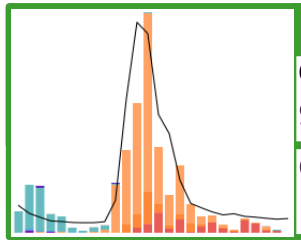
Genomes deposited in the last week: 3, 11, 1



Western Cape ↑ PTP: 12.6%

Genomes	Cases
2 201 (19.2%)	137 518 (17.3%)

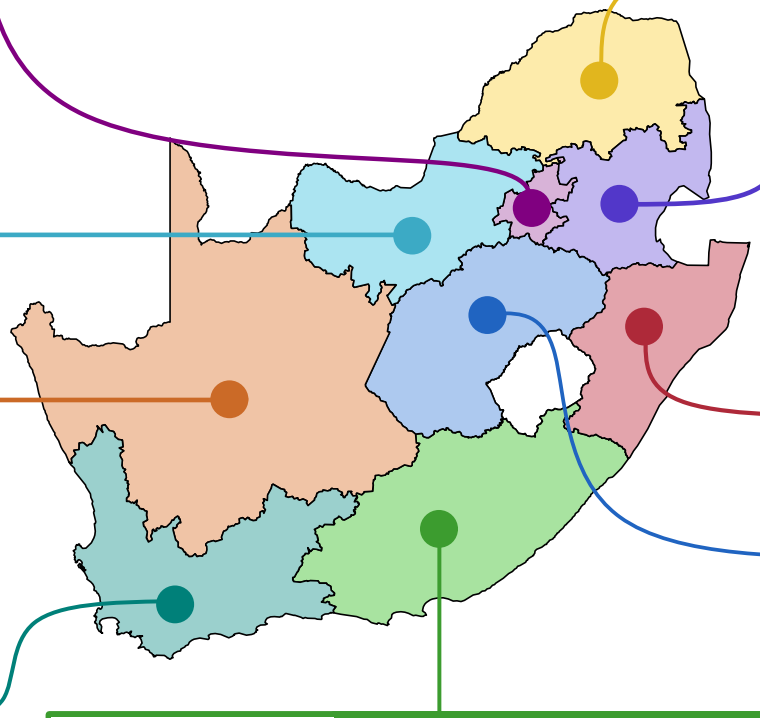
Genomes deposited in the last week: 7, 36, 10, 174

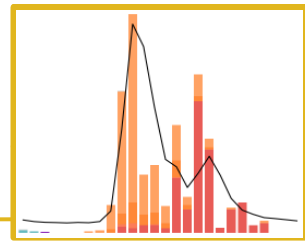


Eastern Cape ↑ PTP: 5.1%

Genomes	Cases
936 (8.2%)	54 680 (6.9%)

Genomes deposited in the last week: 26, 6, 40, 1, 1

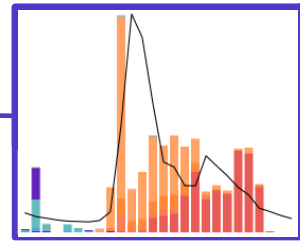




Limpopo ↓ PTP: 4.0%

Genomes	Cases
1 182 (10.3%)	32 706 (4.1%)

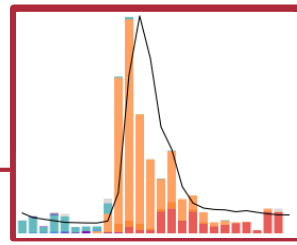
Genomes deposited in the last week: 17, 8, 84



Mpumalanga ↓ PTP: 4.0%

Genomes	Cases
1 155 (10.1%)	41 301 (5.2%)

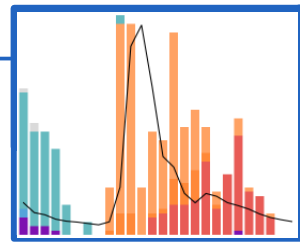
Genomes deposited in the last week: 8, 2, 70



KwaZulu-Natal ↑ PTP: 5.8%

Genomes	Cases
1 331 (11.6%)	146 315 (18.4%)

Genomes deposited in the last week: 1, 33, 4



Free State ↑ PTP: 4.0%

Genomes	Cases
484 (4.2%)	40 020 (5.0%)

Genomes deposited in the last week: 6, 35, 1

Omicron (BA.1) | Beta (20H, V2) | 20A | 20C
Omicron (BA.1.1) | Alpha (20I, V1) | 20B | 20D
Omicron (BA.2) | Delta (21A) | C.1.2 | Unassigned
Omicron (BA.3) | Delta (21I) | Delta (21J) | Cases

941 genomes deposited in the past week

Bar graphs represent genomes sequenced per epiweek, with lines representing cases by collection date (weeks 39 [2021] – 12 [2022])
Genomes and cases presented as provincial total (percentage of national total) for epiweeks 39 (2021) – 12 (2022)
PTP: percentage testing positive in week 12 (20 Mar – 26 Mar); the arrow indicates direction of change since the previous week (13 Mar 2022 – 19 Mar 2022)

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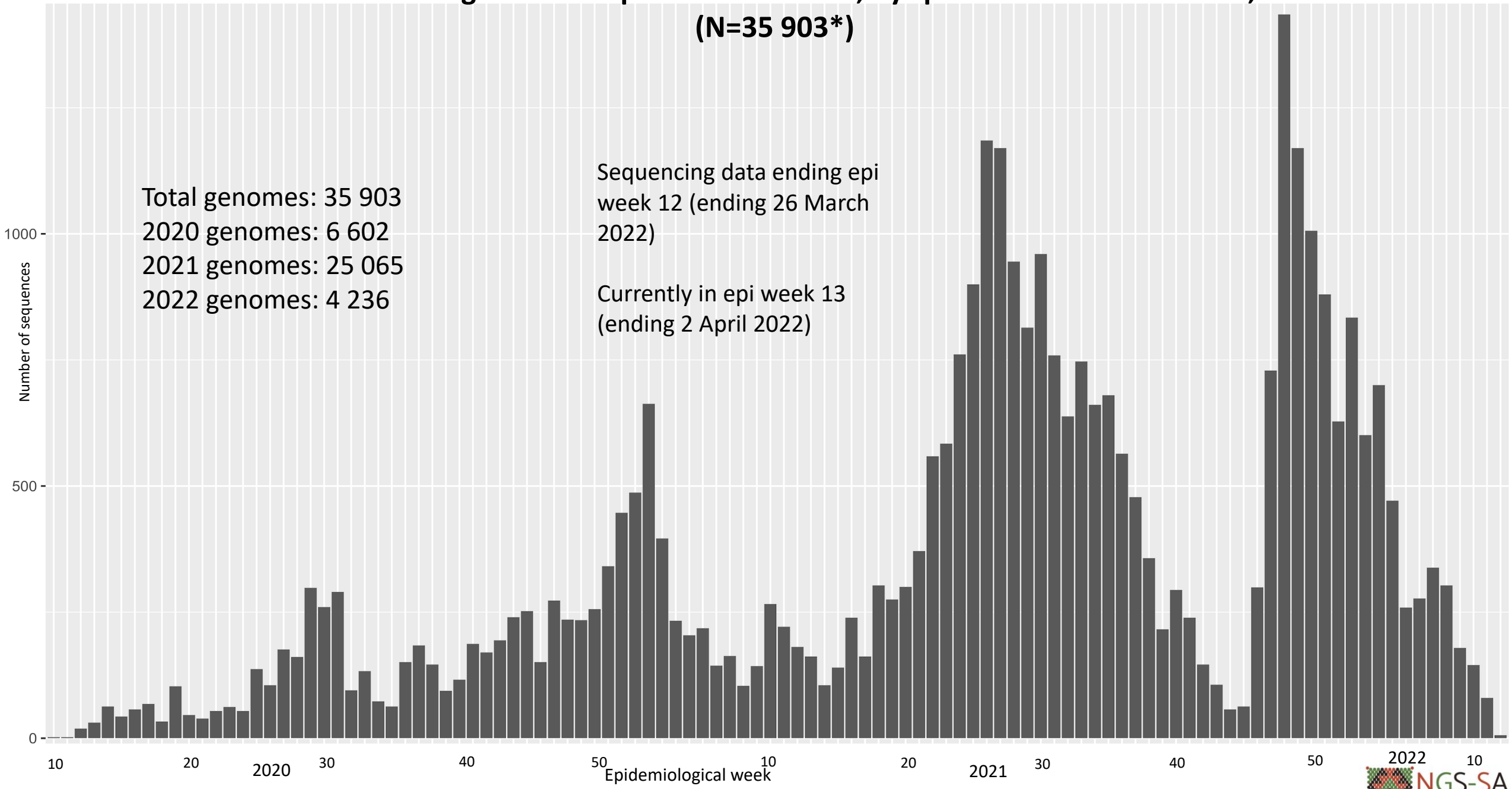
Number of South African genomes deposited on GISAID, by specimen collection week, 2020 – 2022 (N=35 903*)



*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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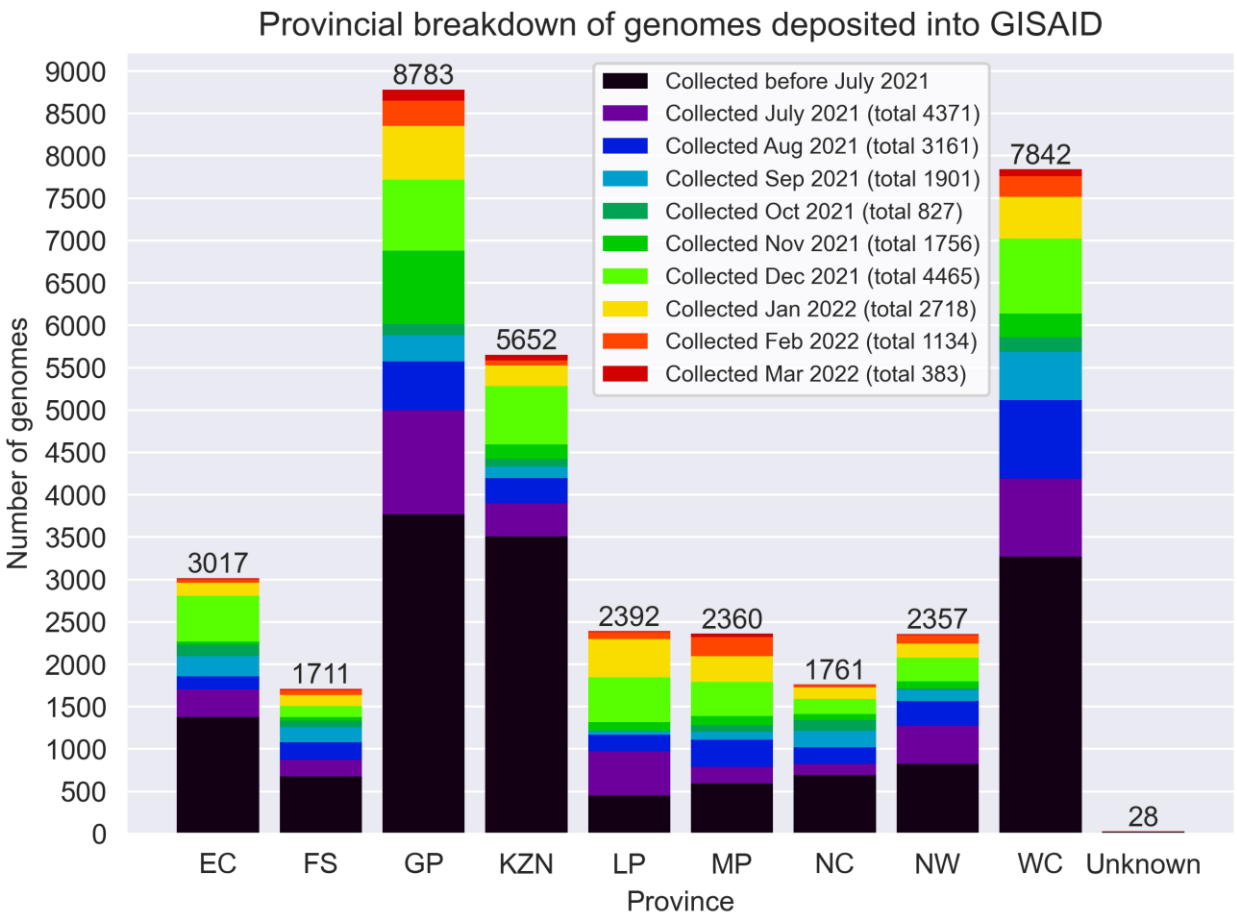
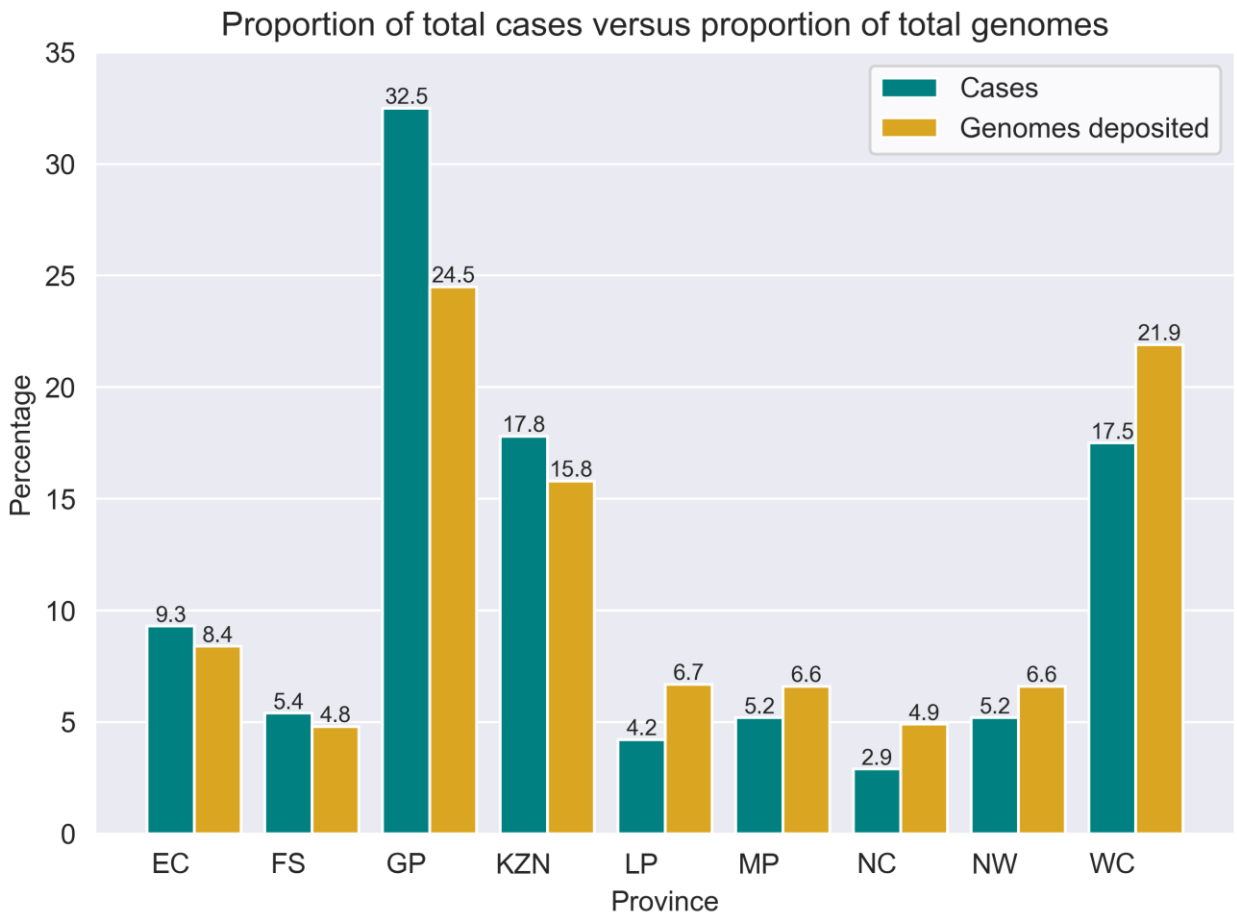
GISAID genomes vs total cases, 2020 – 2022 (N=35 903)





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

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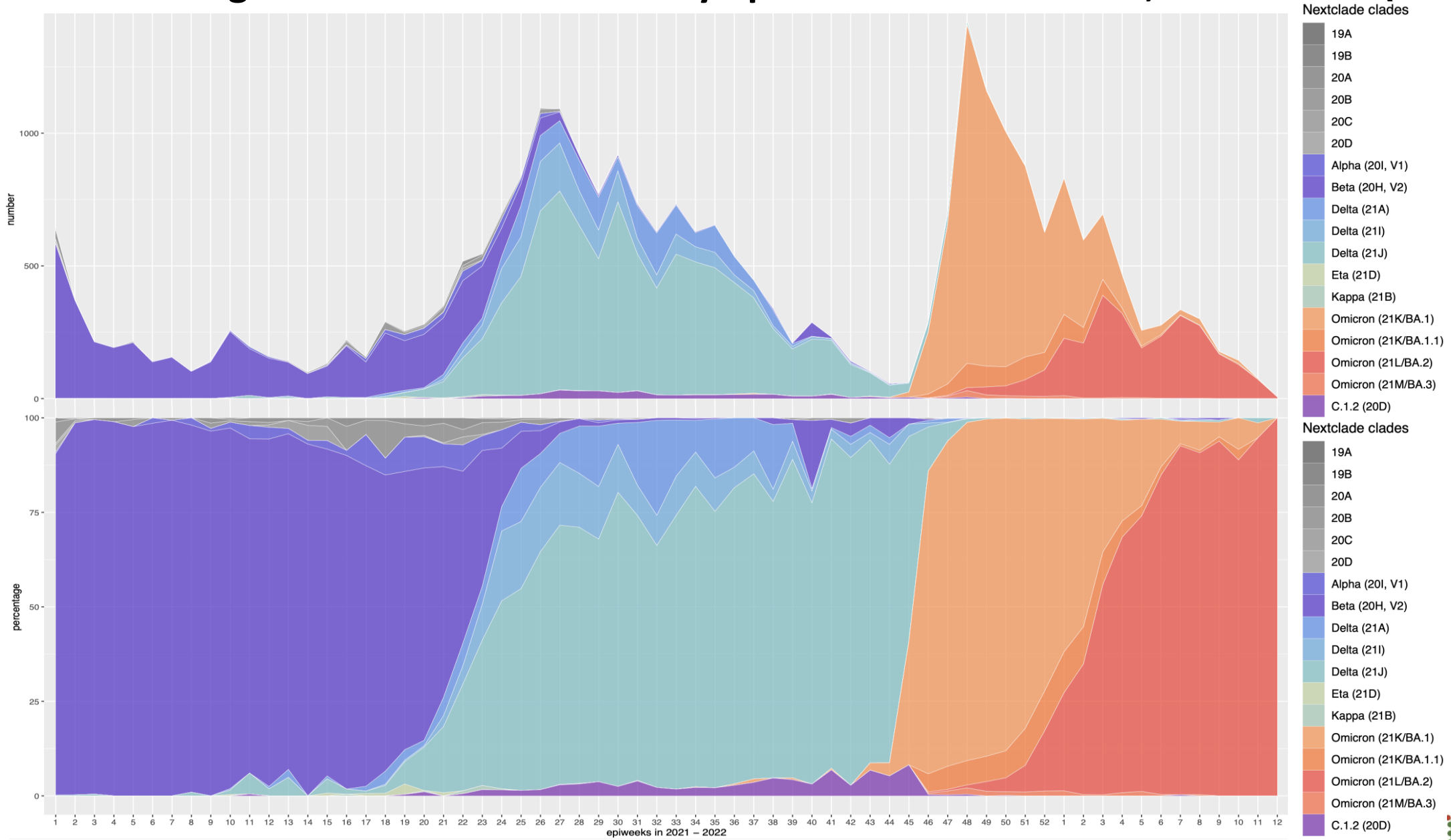
Percentage and number of clades by epiweek in South Africa, 2021 - 2022 (N=29 301)



Sequencing data ending epi week 11 (ending 19 March 2022)

Currently in epi week 13 (ending 2 April 2022)

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

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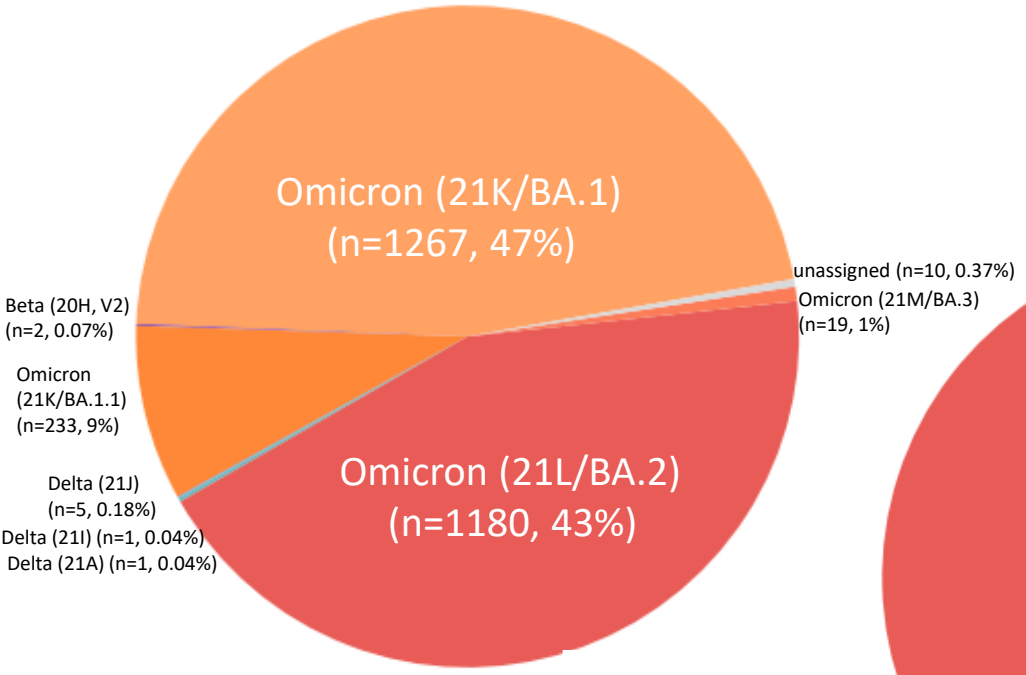
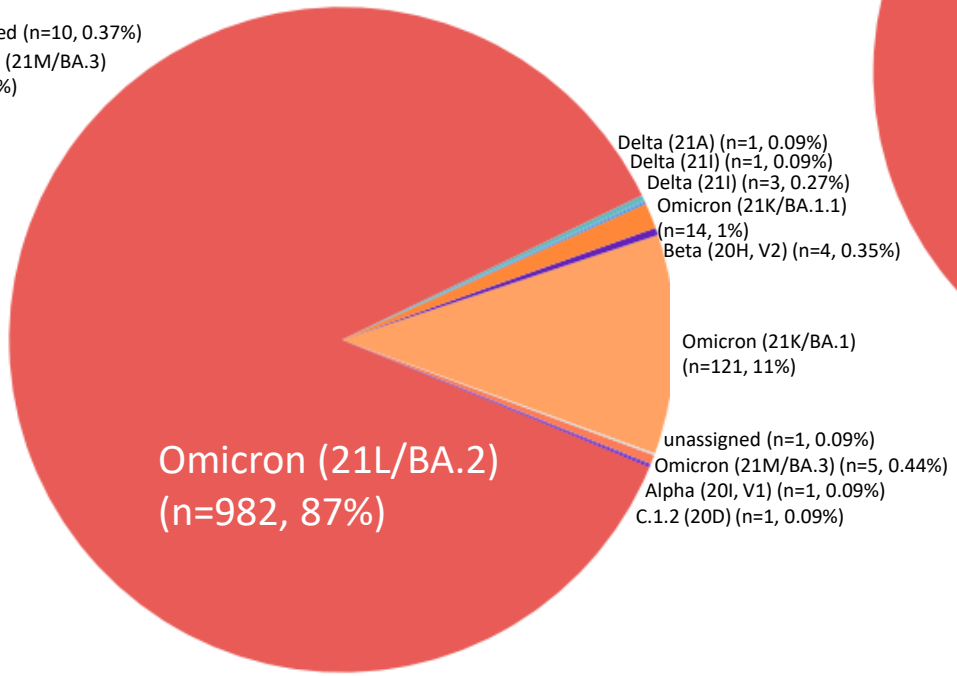
Prevalence of Variants of Concern (VOC) and Variants of Interest (VOI) in Jan – Mar 2022

January (N=2718)



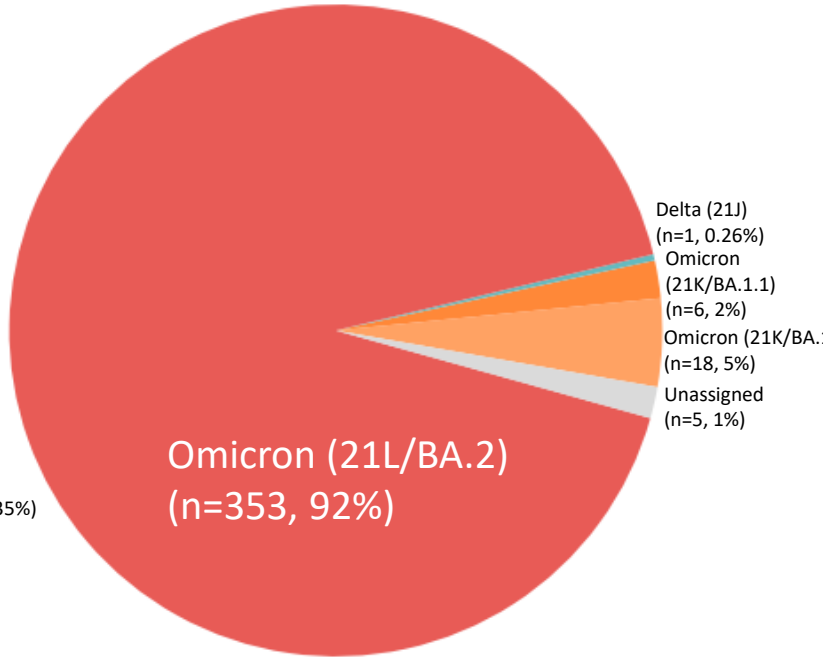
Total Omicron in Jan: 2699 (99.3%)

February (N=1134)



Total Omicron in Feb: 1122 (98.9%)

March (N=383)



Total Omicron in Mar: 377 (98.4%)

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 (99.3%, 2699/2718), February (98.9%, 1122/1134) and March (98.4%, 377/383). BA.2 increased in prevalence throughout January and was dominant in February. It appears to still be dominant in March.

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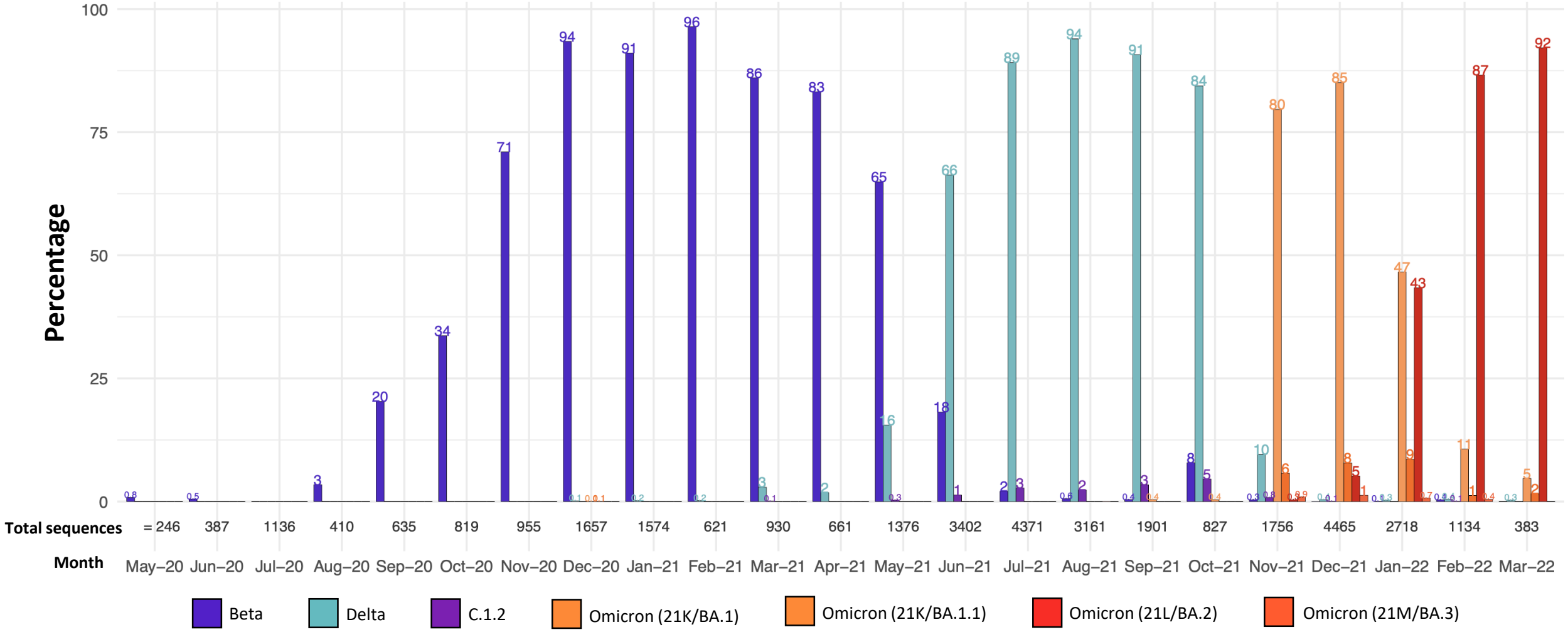
Detection Rates: Beta, Delta, C.1.2 and Omicron

Detection rates of variants being monitored in South Africa*



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

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, 87% in February and 92% in March. BA.3 and other VOCs continue to be detected at low levels.

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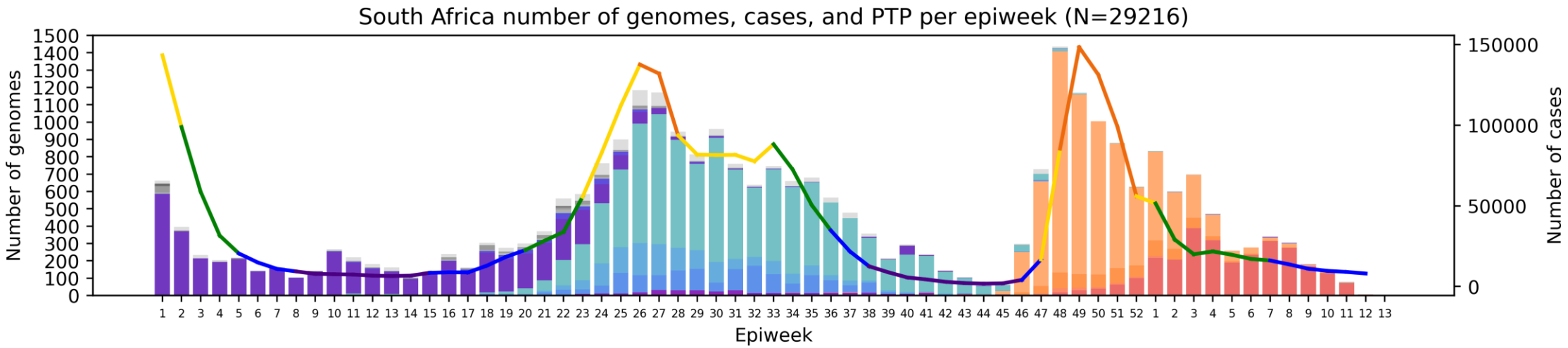
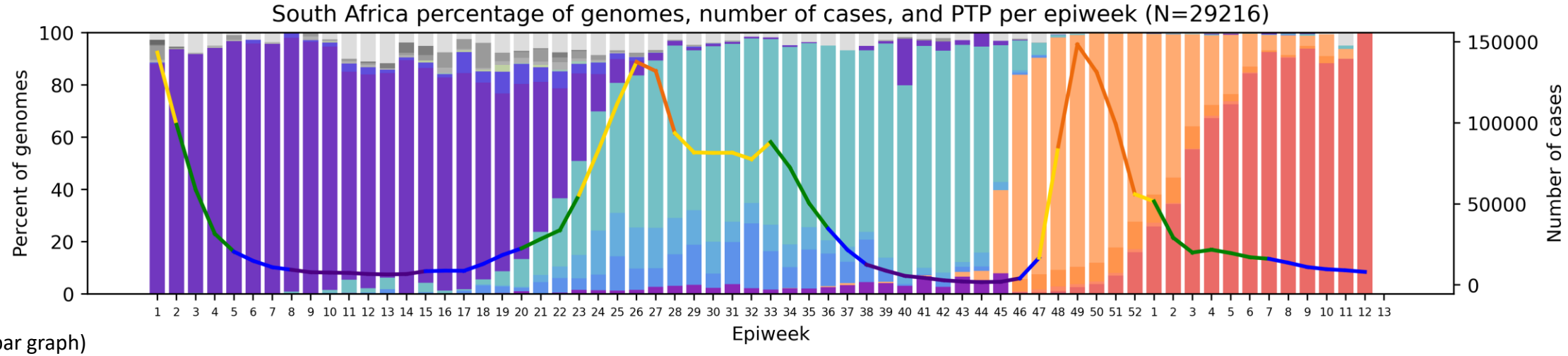
South Africa, 2021-2022, n = 29216*





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

*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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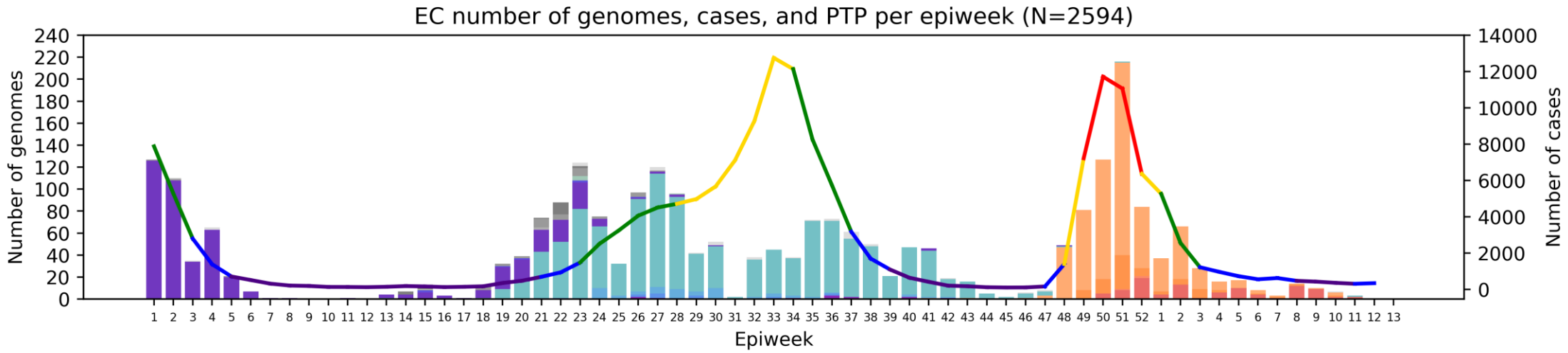
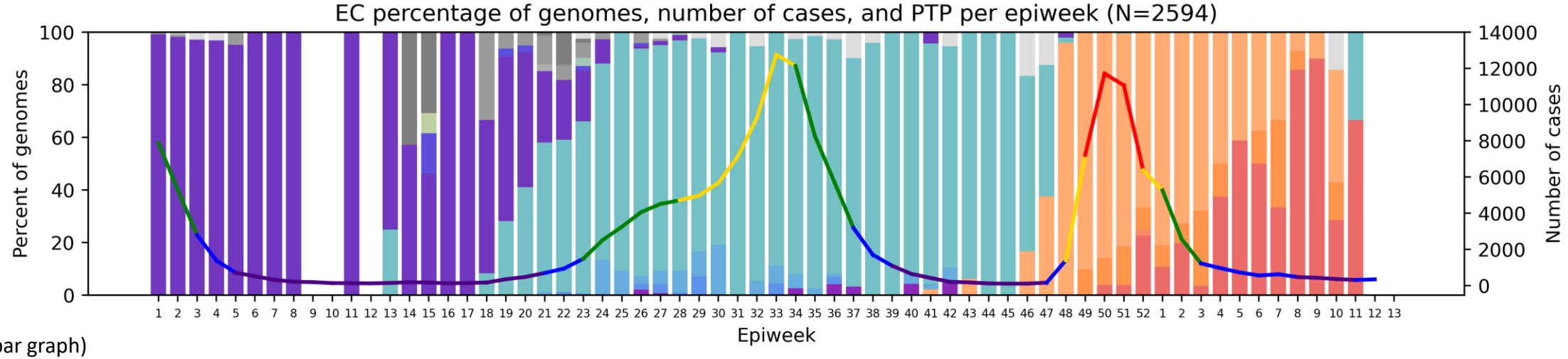
Eastern Cape Province, 2021-2022, n = 2594





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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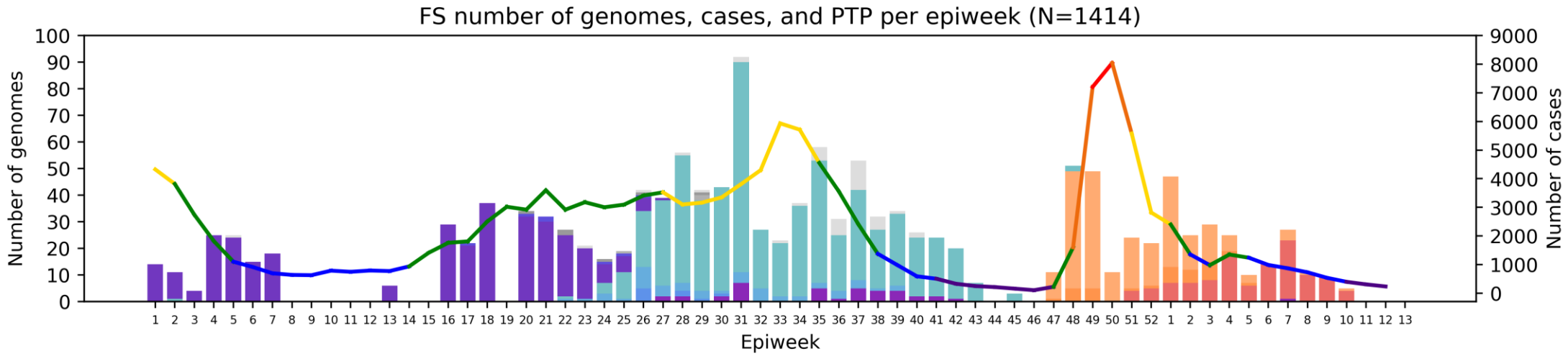
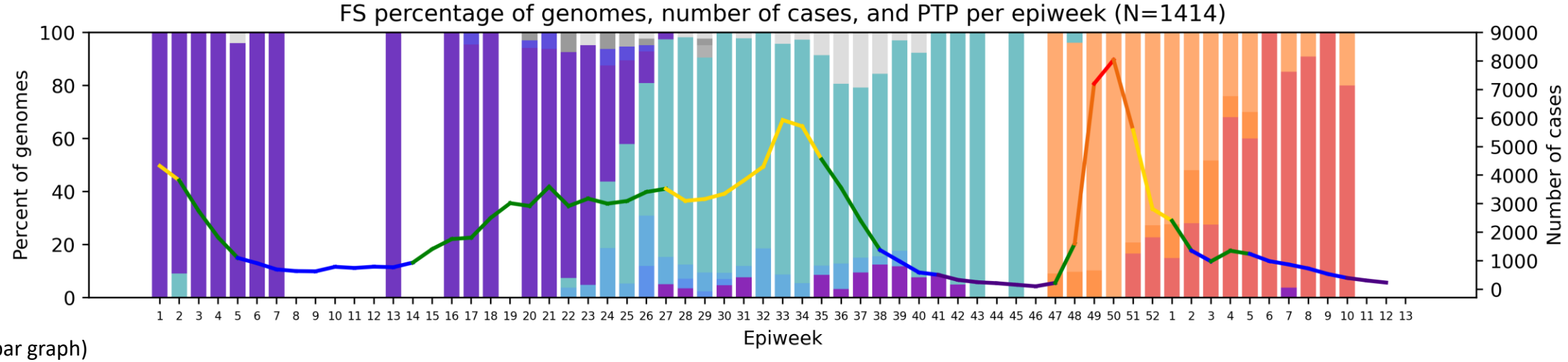
Free State Province, 2021-2022, n = 1414





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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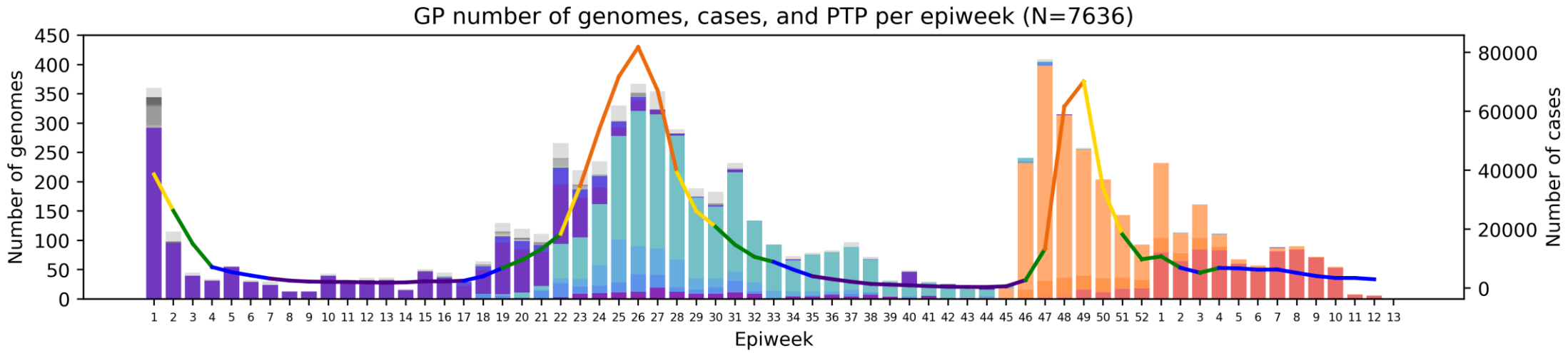
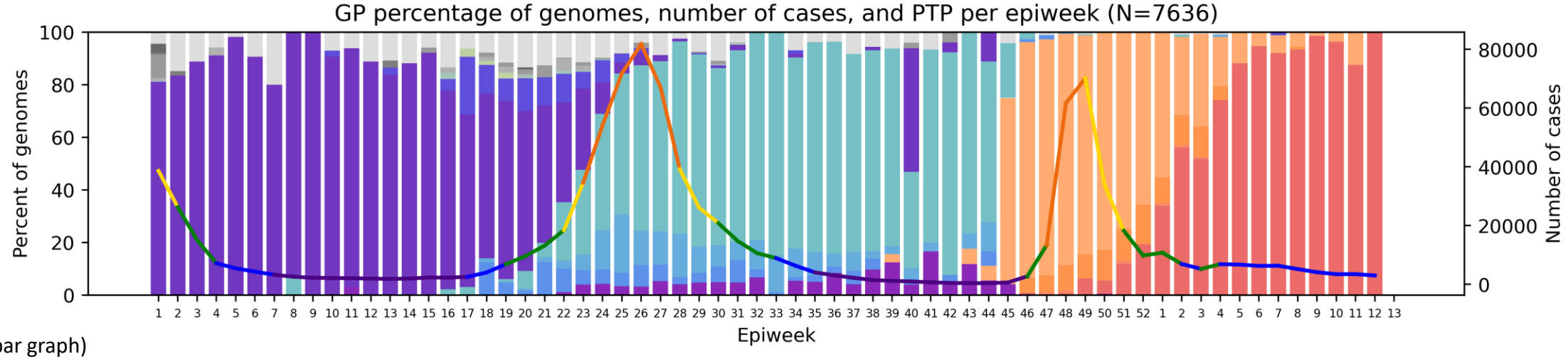
Gauteng Province, 2021-2022, n = 7636





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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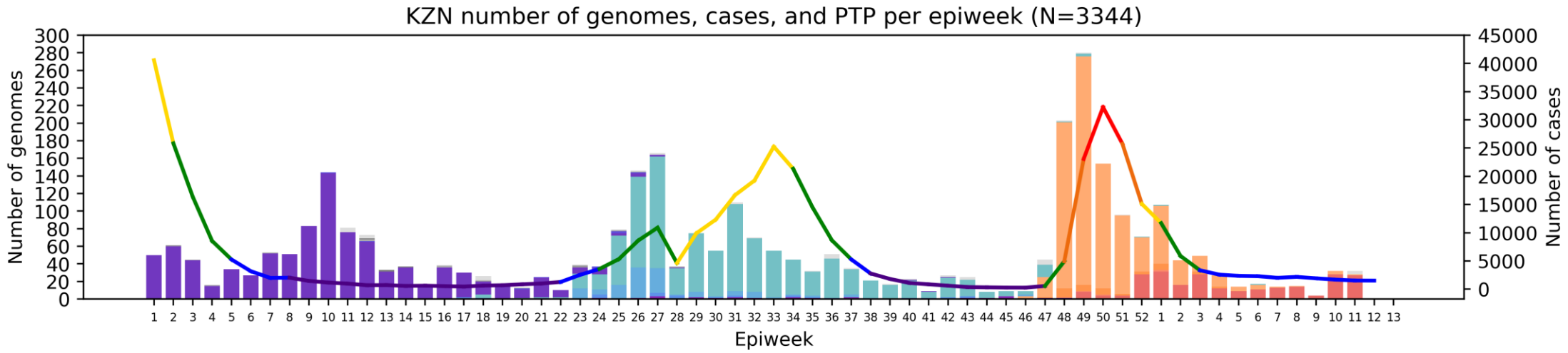
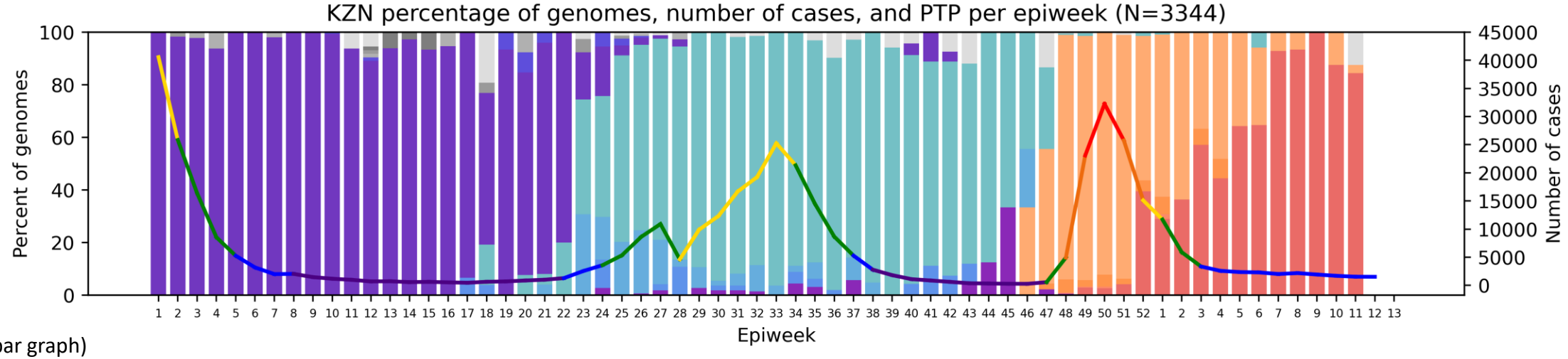
KwaZulu-Natal Province, 2021-2022, n = 3344





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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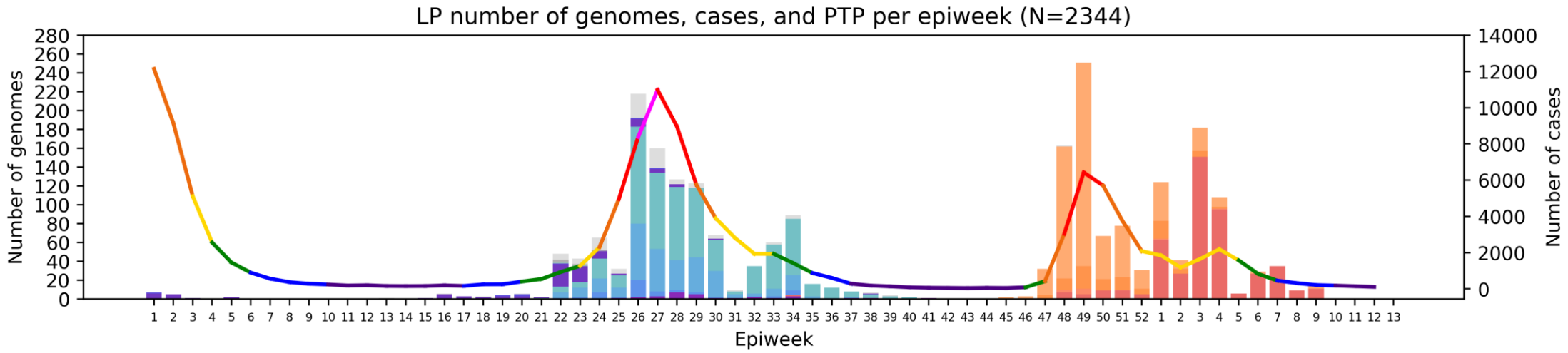
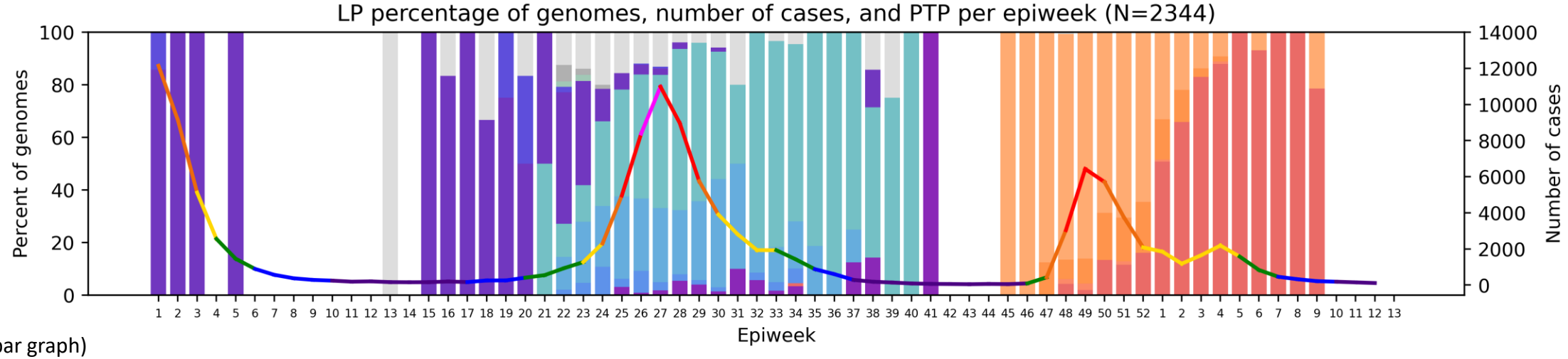
Limpopo Province, 2021-2022, n = 2344





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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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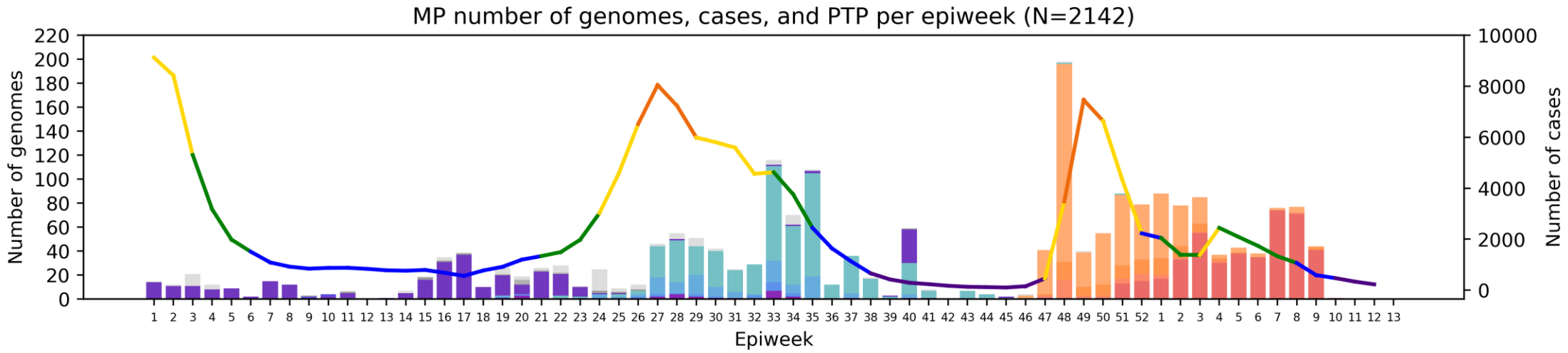
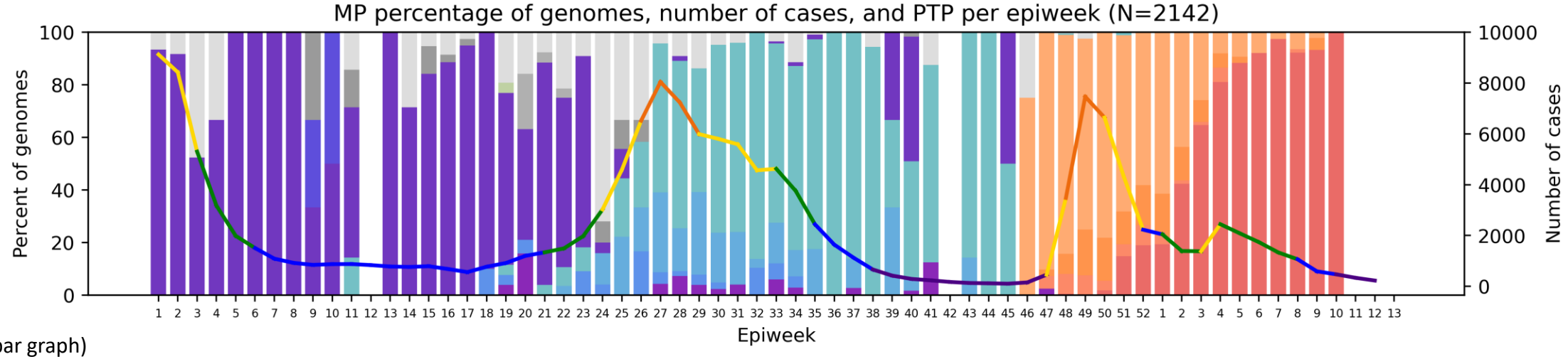
Mpumalanga Province, 2021-2022, n = 2142





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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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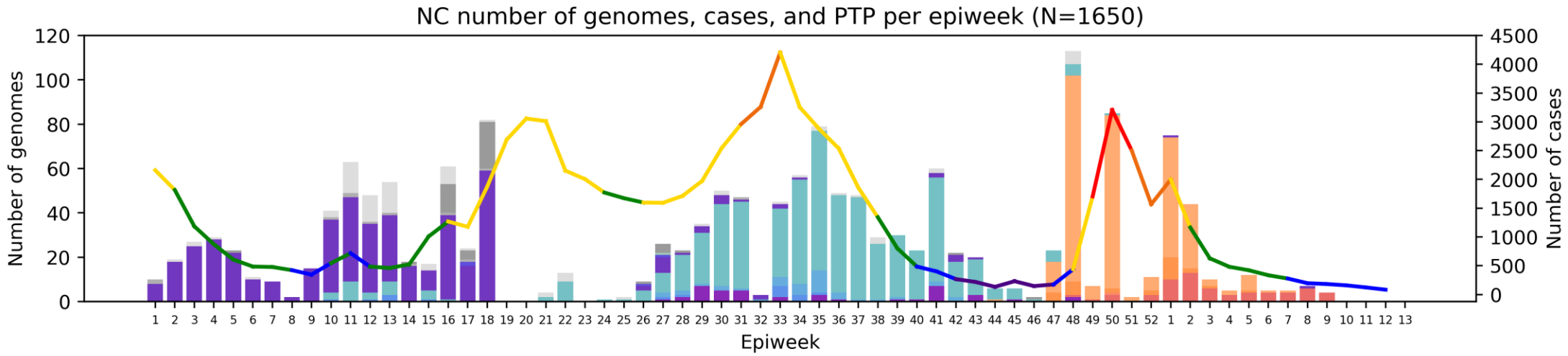
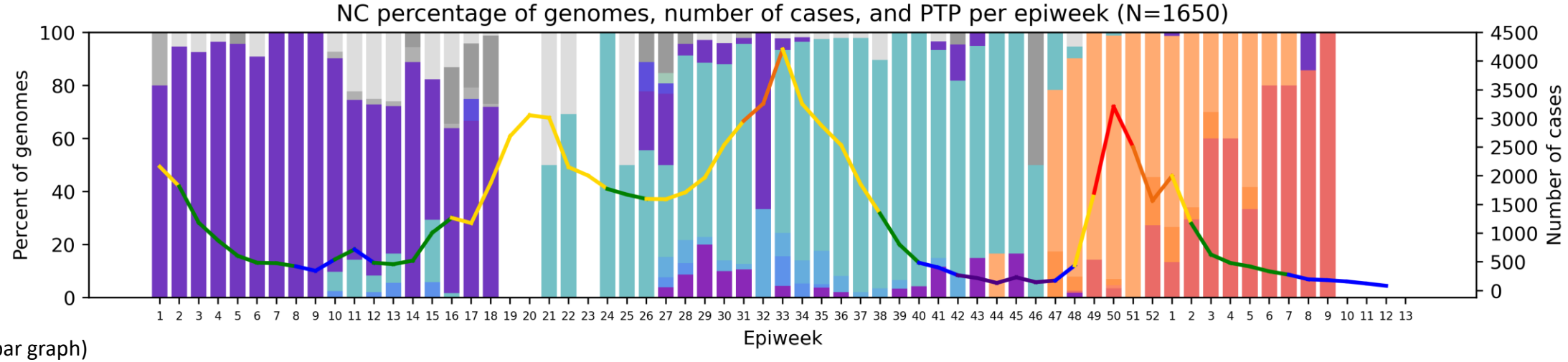
Northern Cape Province, 2021-2022, n = 1650





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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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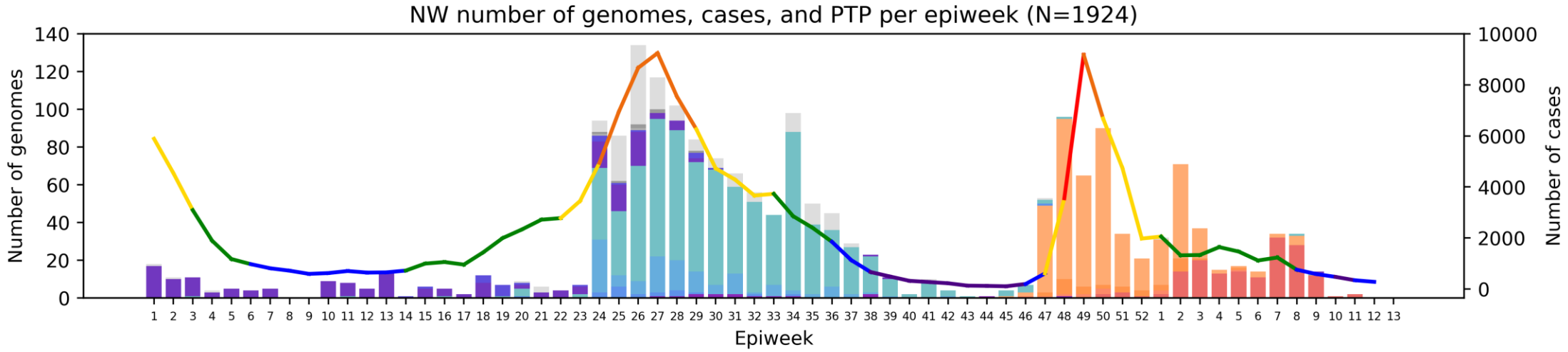
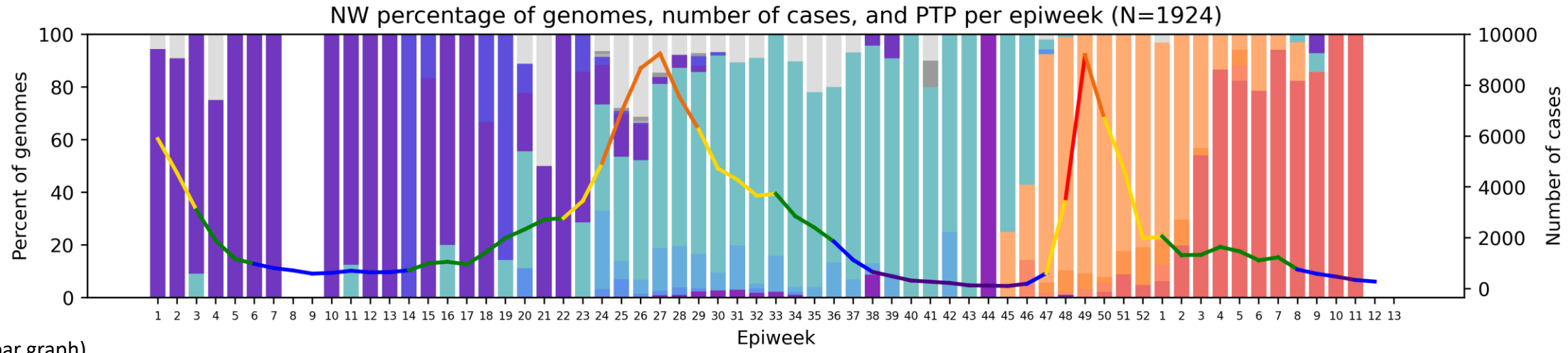
North West Province, 2021, n = 1924





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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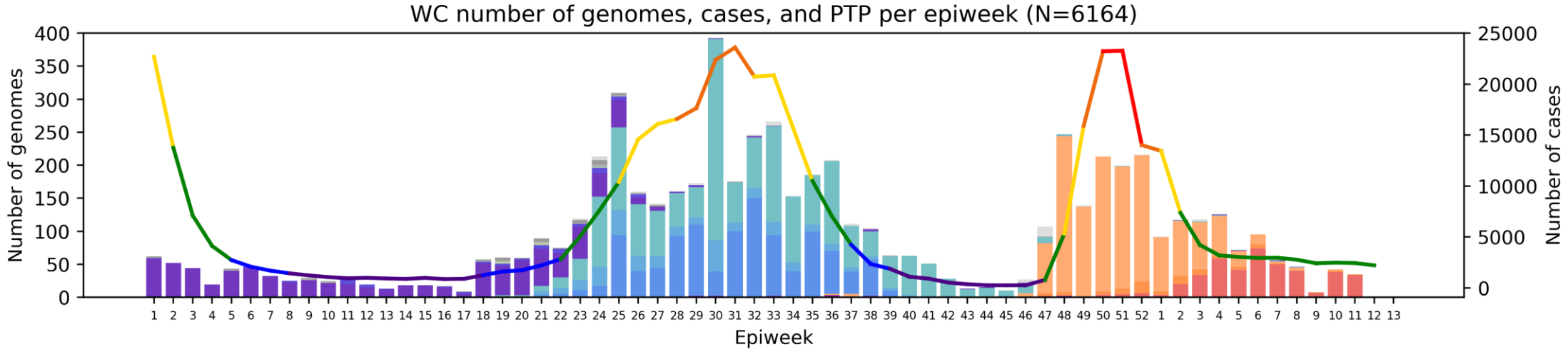
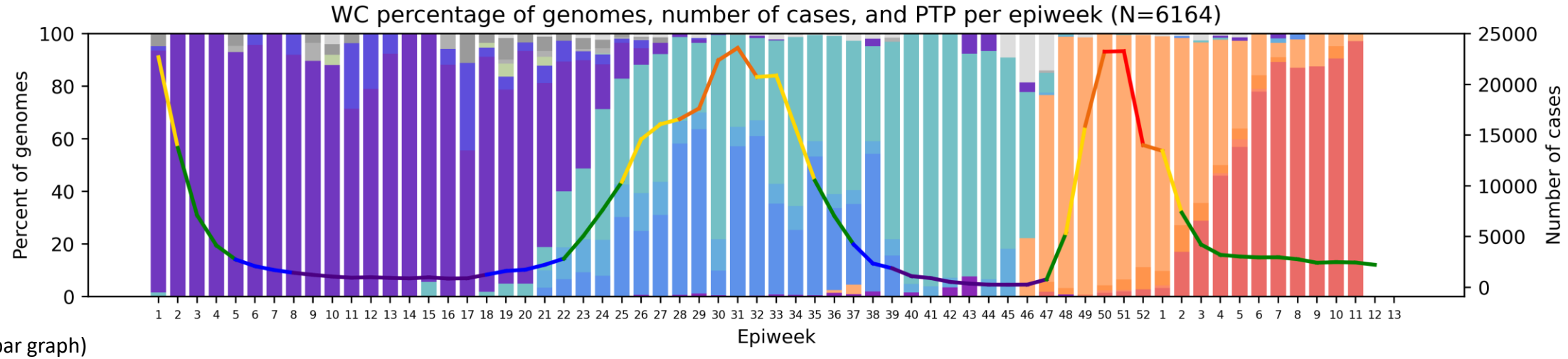
Western Cape Province, 2021-2022, n = 6164





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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Summary

- **Variant of Concern Omicron**
  - Detected in at least 153 countries and dominating globally
  - Split into different lineages based on different mutational profiles. Predominant lineages currently BA.1 (21K), BA.1.1 (21K, BA.1+spike R346K), BA.2 (21L), BA.3 (21M). More lineages are being assigned but defining mutations are not yet available.

  - South Africa (detected in all provinces):
    - Dominated January, February and March sequencing data at >99% of genomes
    - While BA.1 was the predominant sub-lineage in January (47%), the proportion of BA.2 increased from 43% in January to 87% in February and 92% in March
    - BA.3 continues to be detected at low levels

  - NGS-SA teams are monitoring for recombinants
- Low frequency of previously circulating variants such as Delta and Beta still detected in recent data

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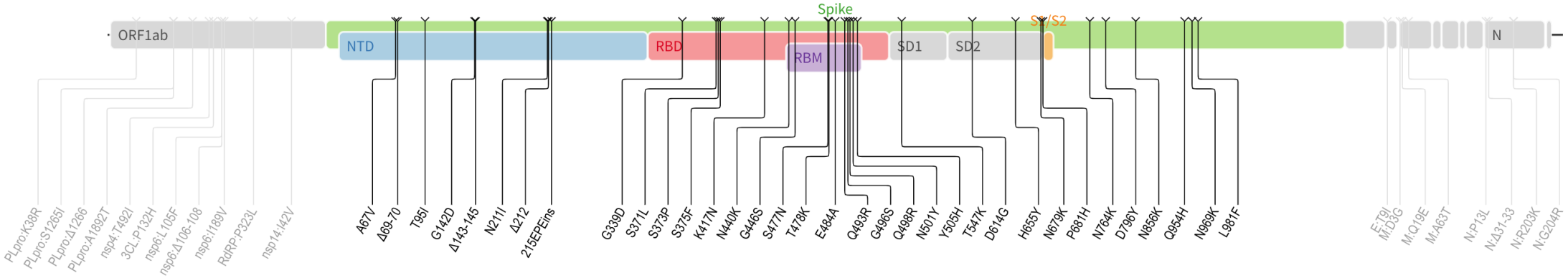
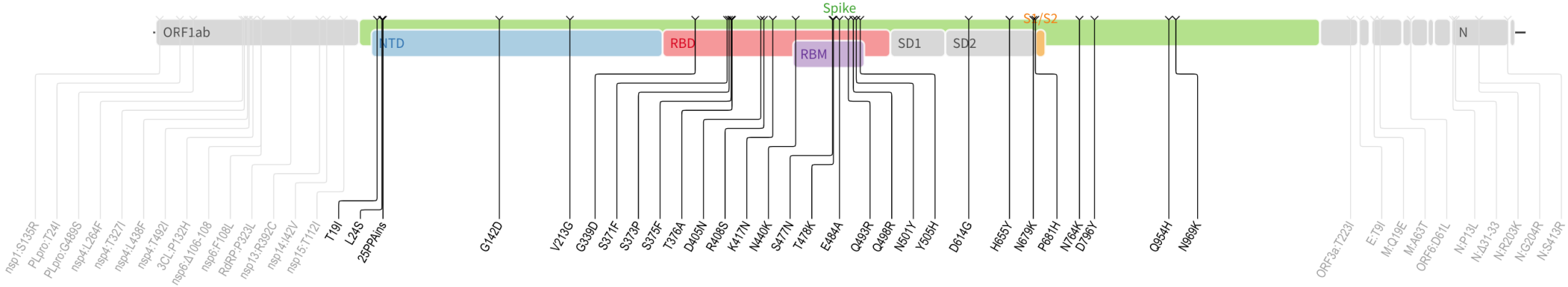
Omicron sub-lineage spike mutation profiles

BA.1
21K

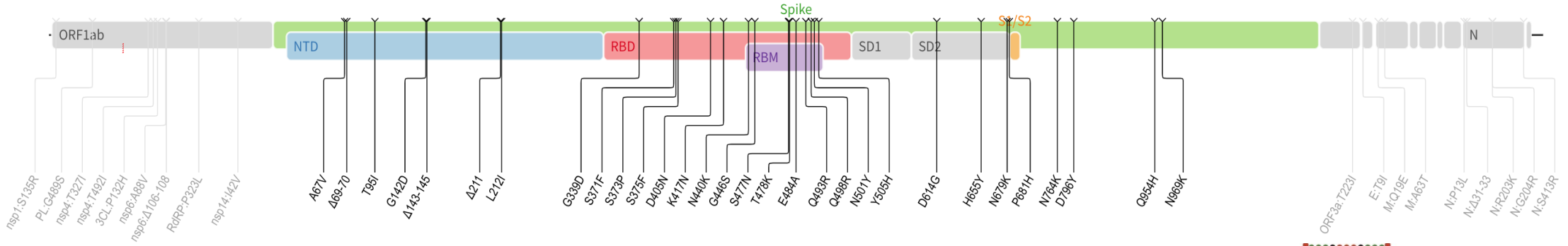


BA.2
21L

Lacks 69-70del
Not detectable by
S-Gene Target
Failure



BA.3
21M



Lineage definitions based on https://github.com/cov-lineages/pango-designation/issues/367
Images from https://covdb.stanford.edu/page/mutation-viewer/

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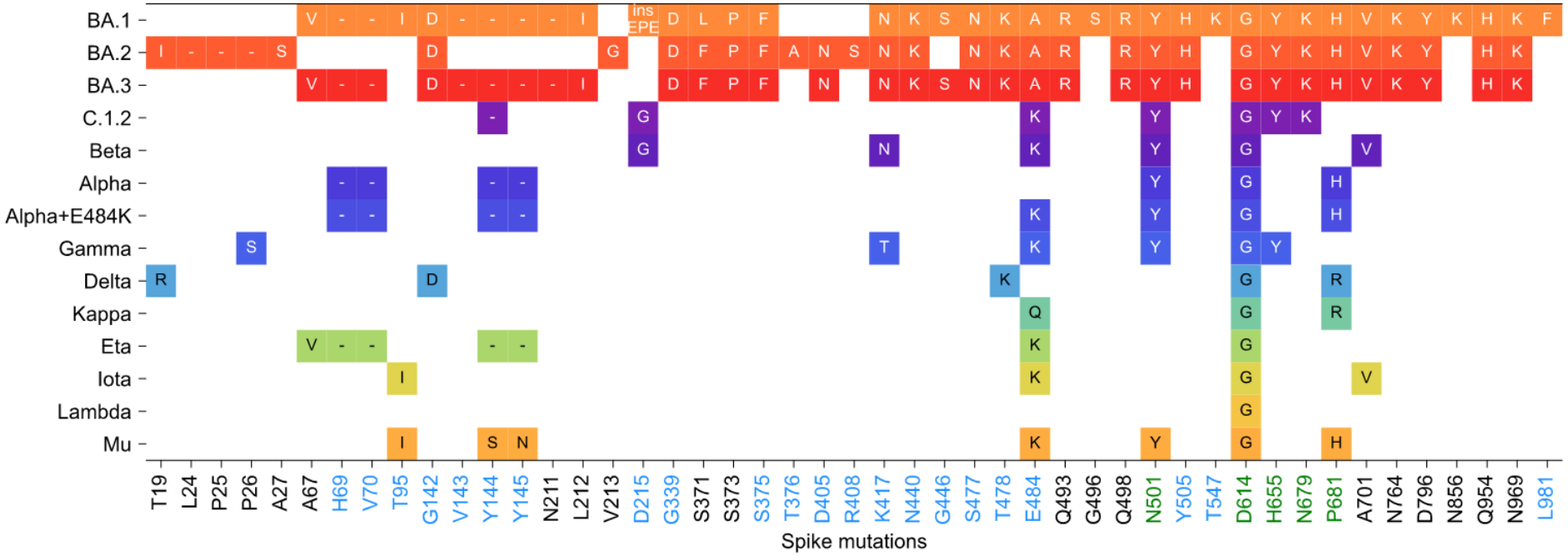
Omicron spike mutations compared to other VOC/VOIs



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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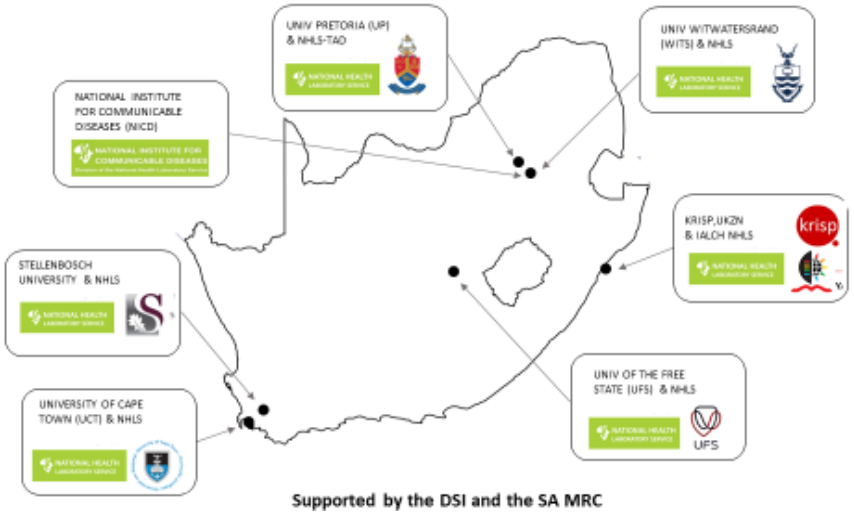

Supported by the DSI and the SA MRC

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Department: Science and Innovation
REPUBLIC OF SOUTH AFRICA

UFS

saMRC advancinglife

NATIONAL INSTITUTE FOR COMMUNICABLE DISEASES
Division of the National Health Laboratory Service

EDCTP

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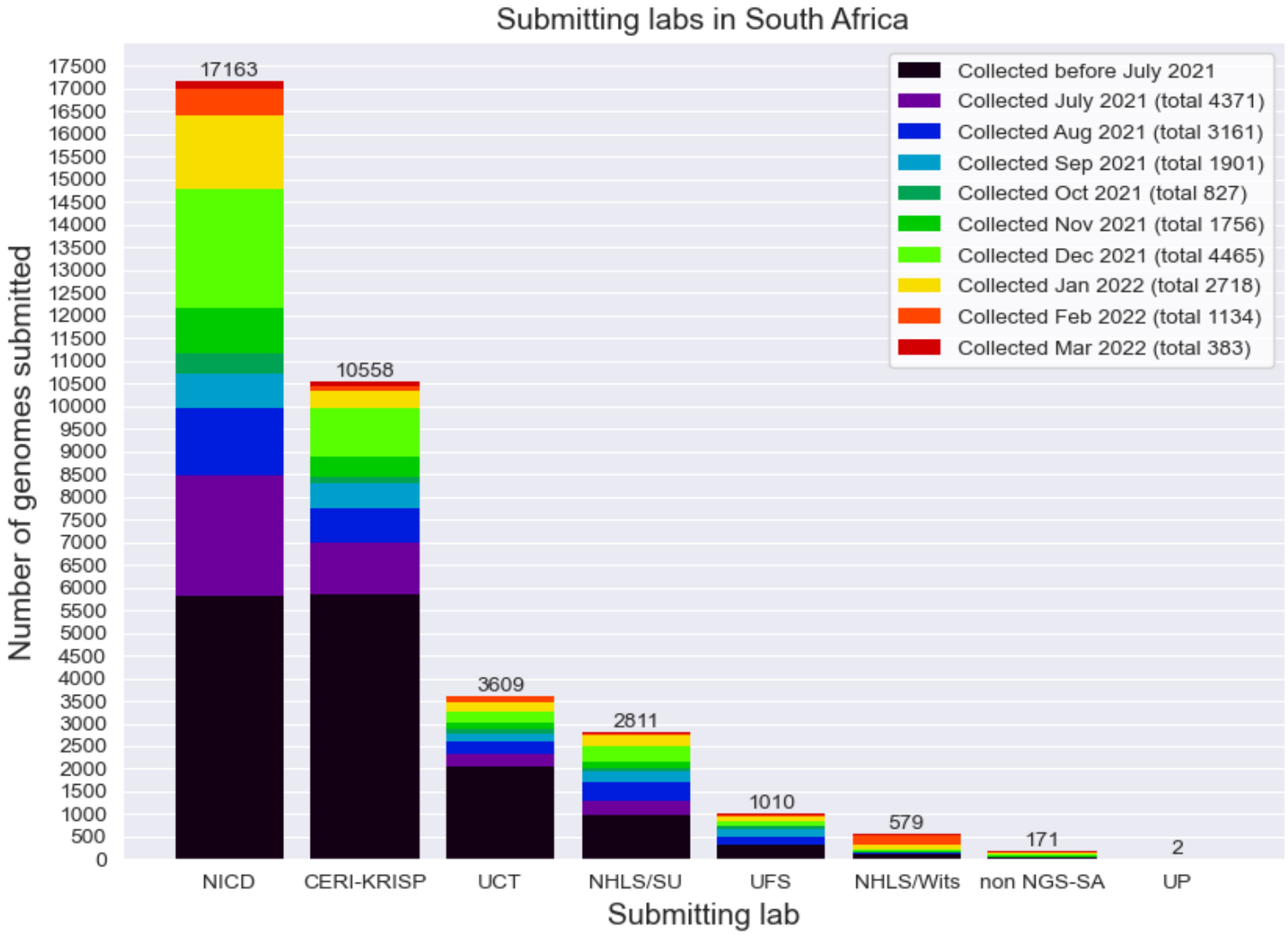
South African genomes submitted per submitting lab, 2020 - 2022 (N=35 903)



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CERI: Centre for Epidemic Response and Innovation
KRISP: KZN Research Innovation and Sequencing Platform
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
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.)