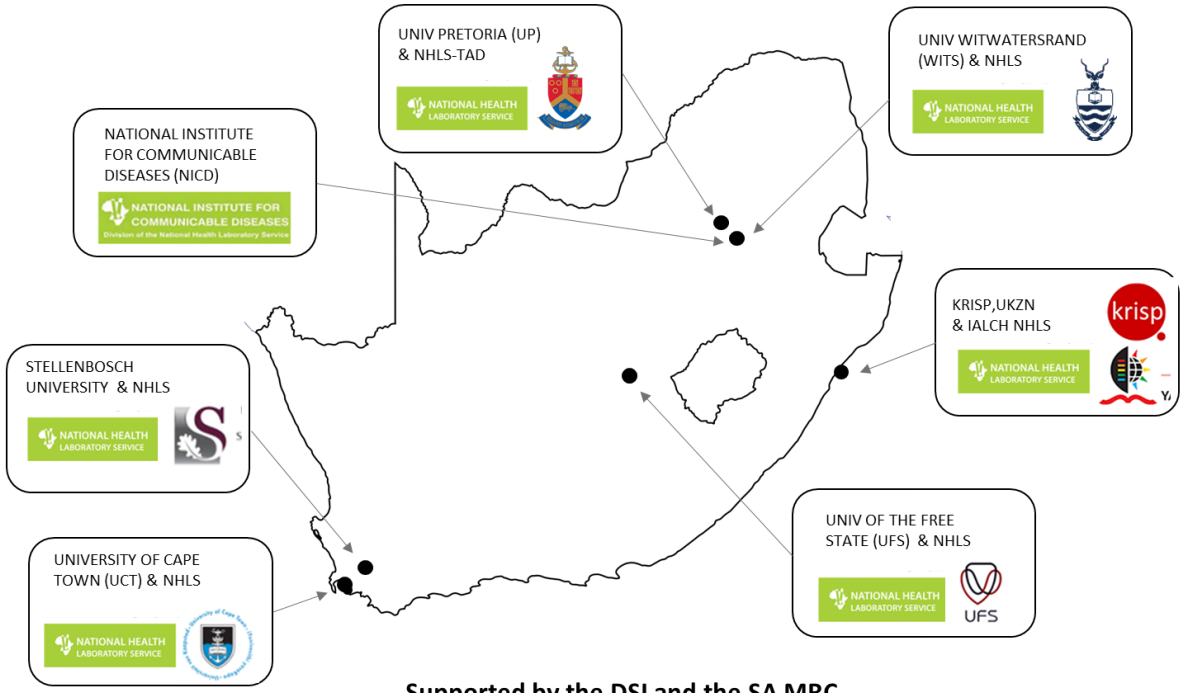
Network for Genomic Surveillance in South Africa (NGS-SA)

SARS-CoV-2 Sequencing Update
17 June 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)

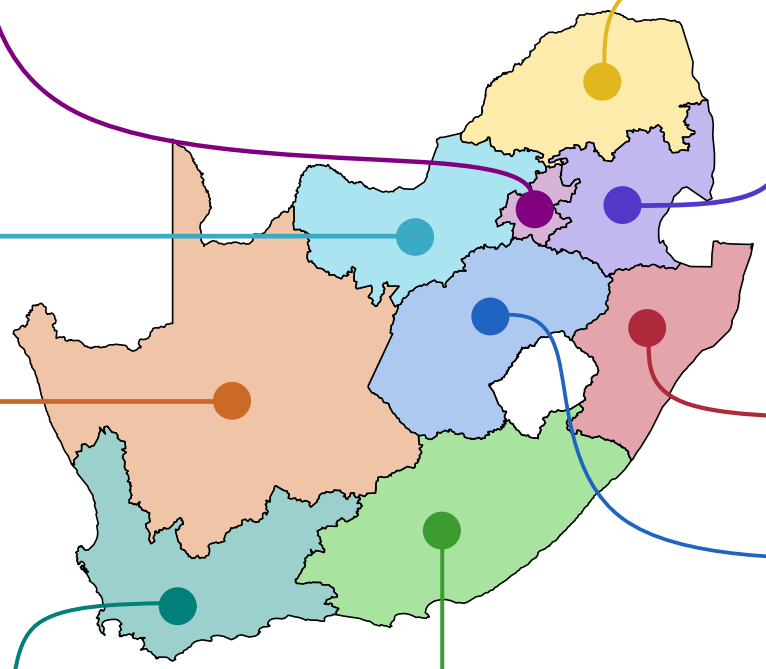
The genomic data presented here are based on South African SARS-CoV-2 sequence data downloaded from GISAID (www.gisaid.org) on 17 June 2022 at 14h05

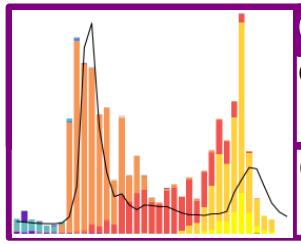
Data license: https://www.gisaid.org/registration/terms-of-use/

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

SARS-CoV-2
GENOMIC SURVEILLANCE
epiweeks 39 (2021) - 23 (2022)

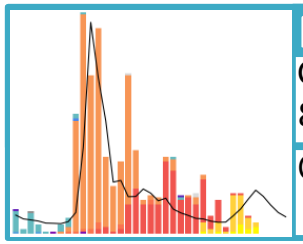




Gauteng ↓ PTP: 7.9%

Genomes	Cases
5 242 (30.3%)	390 970 (36.9%)

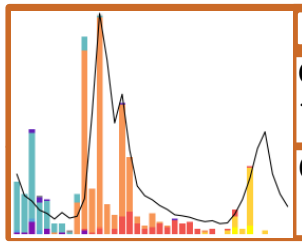
Genomes deposited in the last week



North West ↓ PTP: 9.1%

Genomes	Cases
816 (4.7%)	49 230 (4.6%)

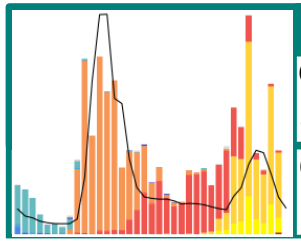
Genomes deposited in the last week



Northern Cape ↓ PTP: 12.2%

Genomes	Cases
734 (4.2%)	24 225 (2.3%)

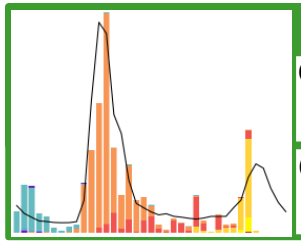
Genomes deposited in the last week



Western Cape ↓ PTP: 14.5%

Genomes	Cases
3 949 (22.9%)	185 117 (17.5%)

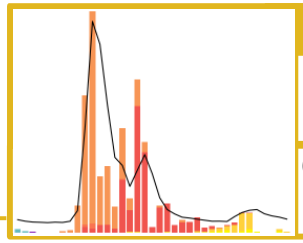
Genomes deposited in the last week
2 2 68 16 1 3



Eastern Cape ↓ PTP: 9.9%

Genomes	Cases
1 191 (6.9%)	72 202 (6.8%)

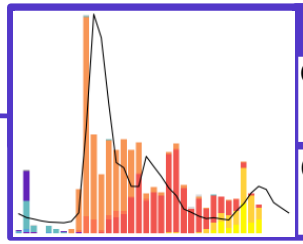
Genomes deposited in the last week



Limpopo - PTP: 8.9%

Genomes	Cases
1 326 (7.7%)	35 763 (3.4%)

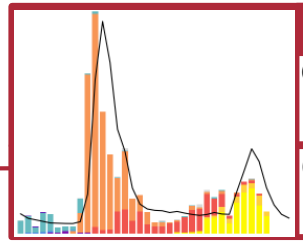
Genomes deposited in the last week
3 2



Mpumalanga - PTP: 9.8%

Genomes	Cases
1 568 (9.1%)	49 152 (4.6%)

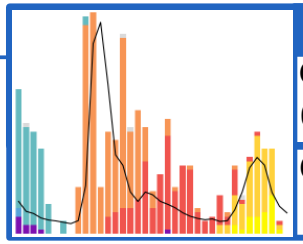
Genomes deposited in the last week



KwaZulu-Natal ↓ PTP: 5.9%

Genomes	Cases
1 814 (10.5%)	200 547 (18.9%)

Genomes deposited in the last week



Free State ↓ PTP: 10.2%

Genomes	Cases
642 (3.7%)	52 864 (5.0%)

Genomes deposited in the last week
3 57 23 1

Omicron (BA.1.*)
Omicron (BA.2.*)
Omicron (BA.3)
Omicron (BA.4)
Omicron (BA.5)
Omicron (BA.2.12.1)
Beta (20H, V2)
Alpha (20I, V1)
Delta (21A)
Delta (21I)
C.1.2
Delta (21J)
20A
20B
20C
20D
Unassigned
Cases

181 genomes added since the previous report

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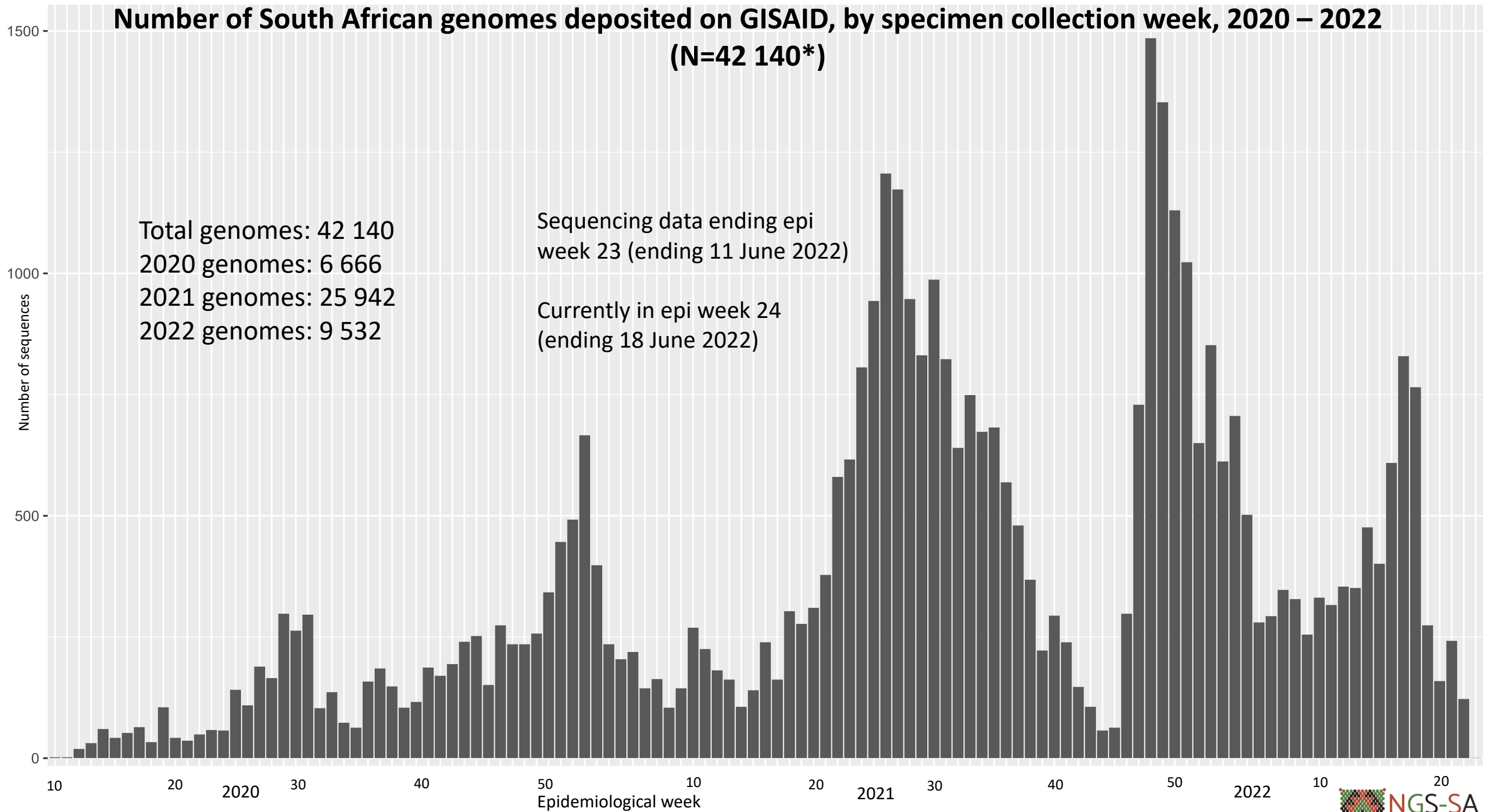
Bar graphs represent genomes sequenced per epiweek, with lines representing cases by collection date (weeks 39 [2021] – 23 [2022])
Genomes and cases presented as provincial total (percentage of national total) for epiweeks 39 (2021) – 23 (2022)
PTP: percentage testing positive in week 23 (5 June 2022 – 11 June 2022); arrow indicates direction of change since previous week (29 May 2022 – 4 June 2022) if change was significant (P<0.05)

Number of South African genomes deposited on GISAID, by specimen collection week, 2020 – 2022 (N=42 140*)



*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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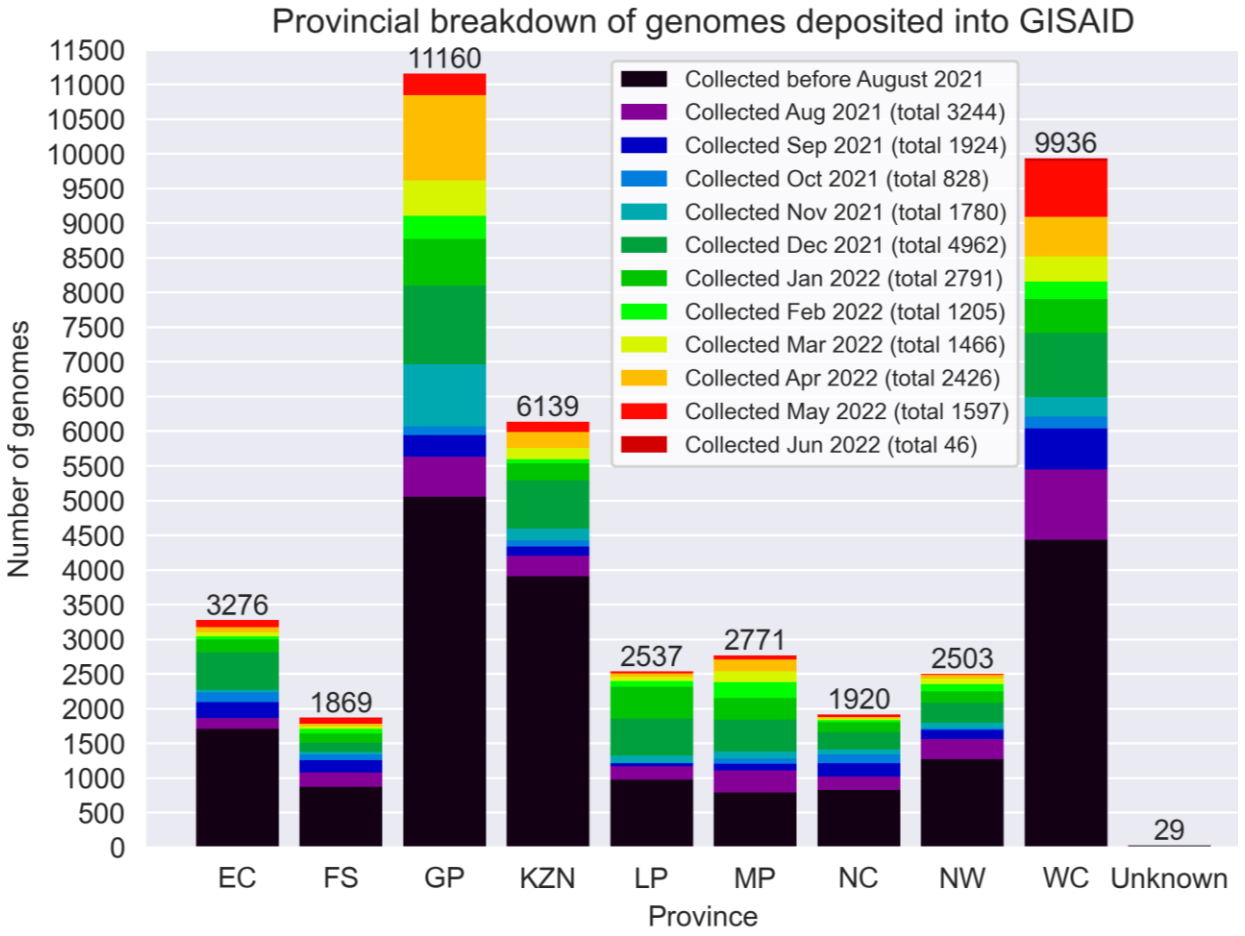
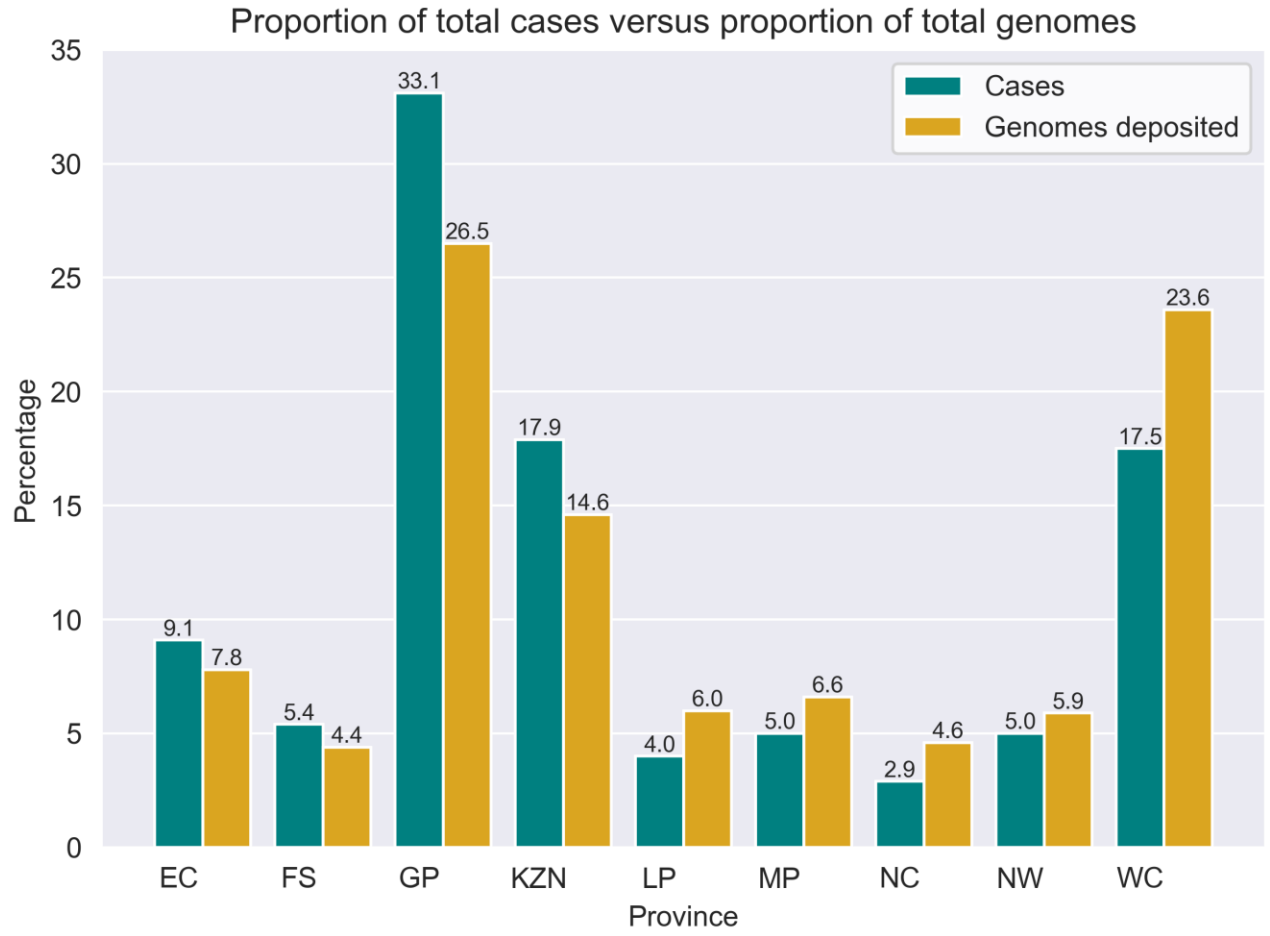
GISAID genomes vs total cases, 2020 – 2022 (N=42 140)





All provinces, apart from GP, KZN and WC, have comparable percentages of overall cases and sequenced genomes. All provinces have contributed sequences for April and May. June sequences are from WC.

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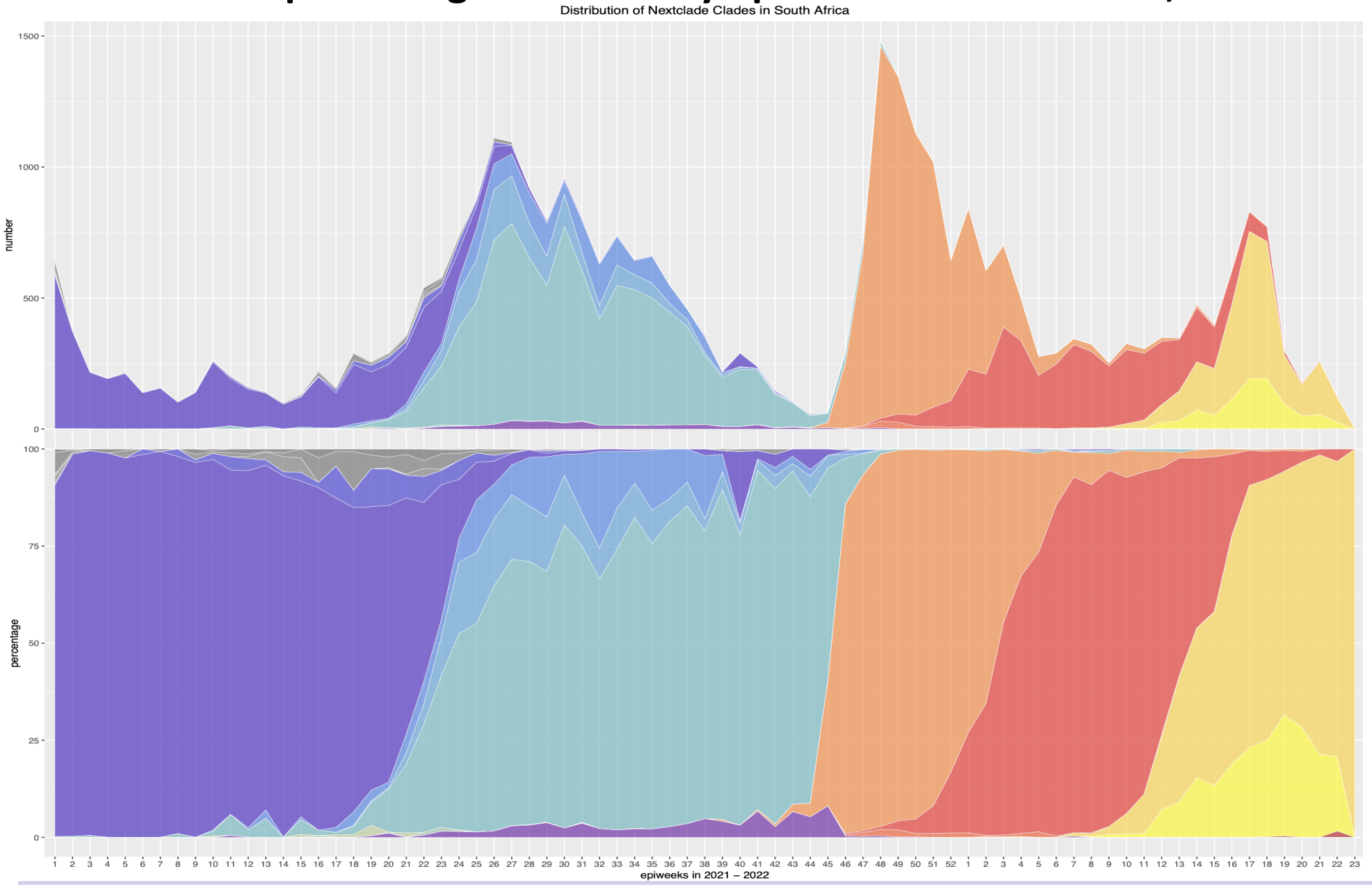
Number and percentage of clades by epiweek in South Africa, 2021 – 2022 (35 387*)



Sequencing data ending epi week 23 (ending 11 June 2022)

Currently in epi week 24 (ending 18 June 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.

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

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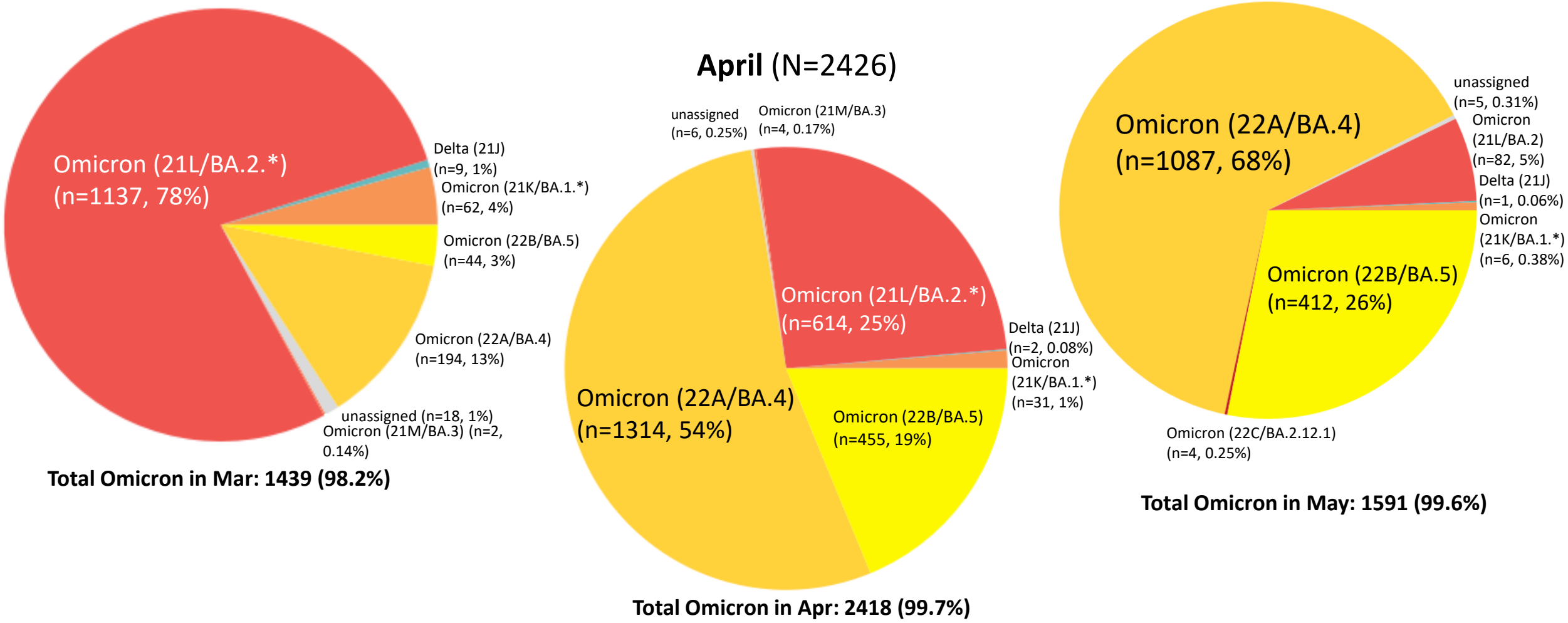
Prevalence of Variants of Concern (VOC) and Variants of Interest (VOI) in March – May 2022



Omicron dominated in March (98.2%, 1439/1466), April (99.7%, 2418/2426) and May (99.6%, 1591/1597). BA.2 was dominant in March. BA.4 and BA.5 together were dominant in April and May. BA.2.12.1 was detected at low levels in May (0.25%).

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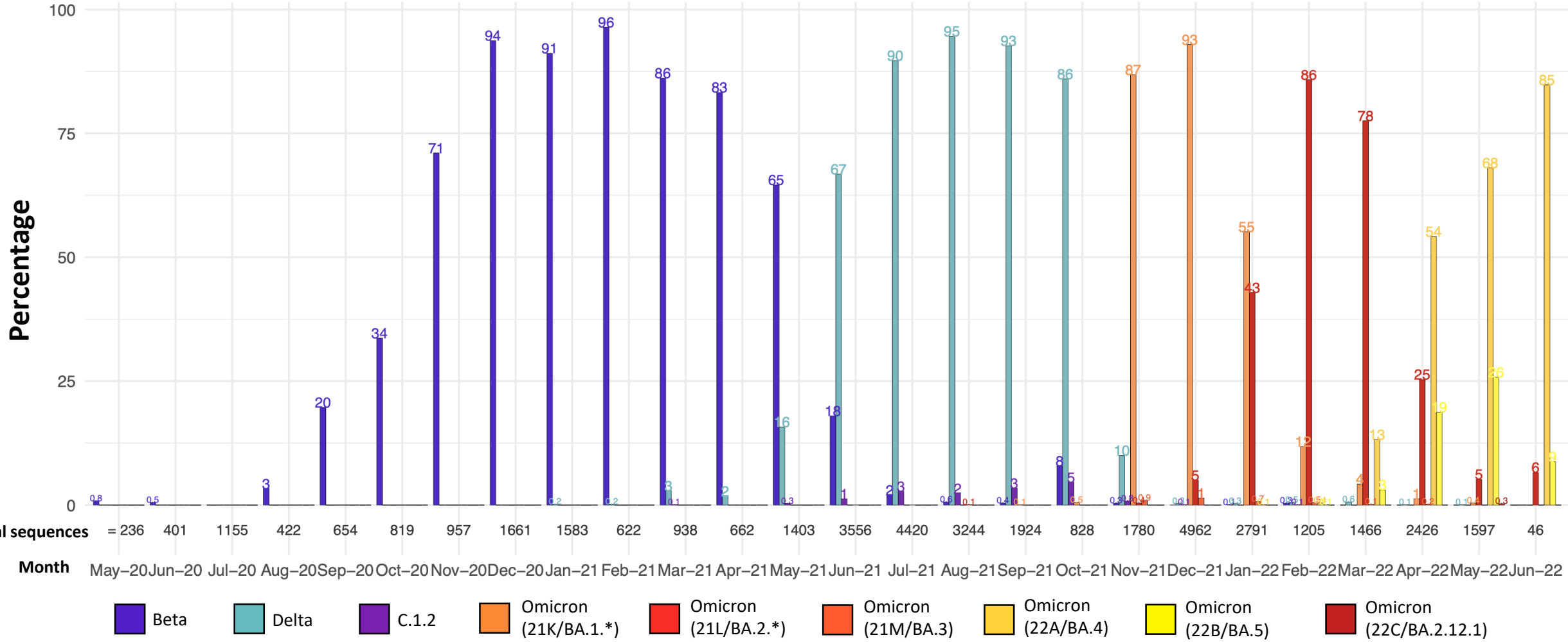
Detection Rates: Beta, Delta, C.1.2 and Omicron

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

Omicron has been dominant since November (>85% in November, >98% in December – June).
BA.2 was dominant in February and March. BA.4 and BA.5 together dominated in April at 73%, and in May at 94%, and currently make up 94% of June sequences, although with a small number of genomes.

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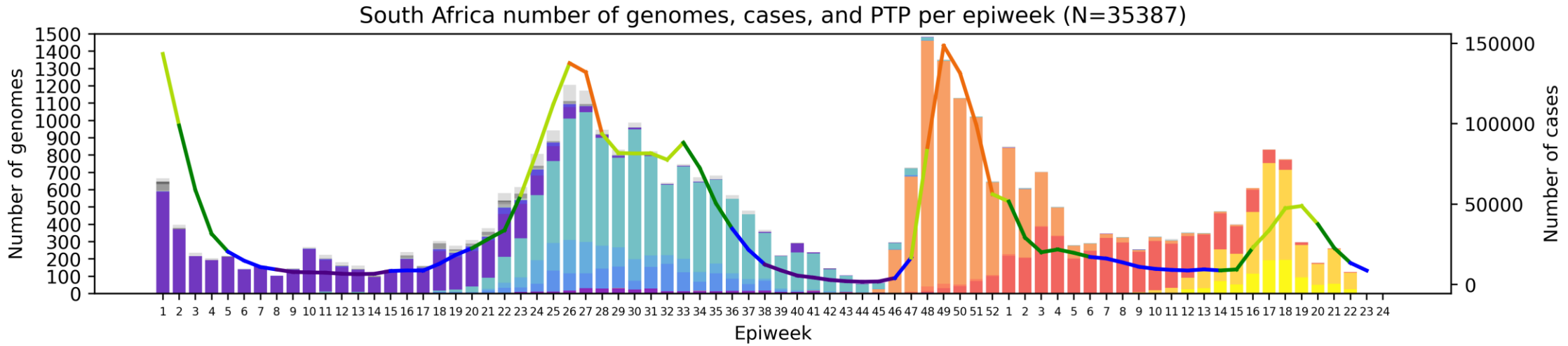
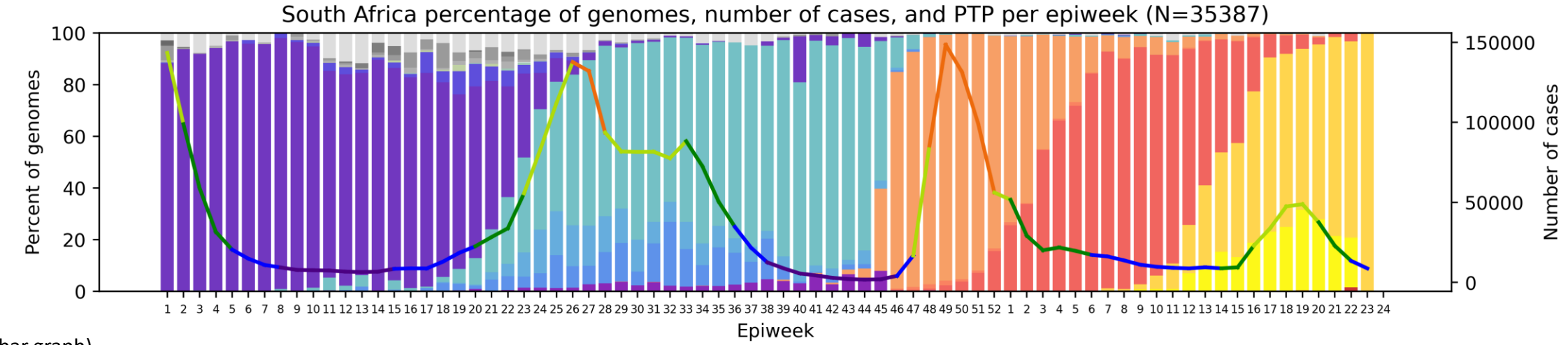
South Africa, 2021-2022, n = 35 387*





Clade key (bar graph)

Omicron (21K/BA.1.*) | Omicron (21L/BA.2.*) | Omicron (22C/BA.2.12.1) | 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) | Cases | Eta (21D) | 20D | 20C | 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

*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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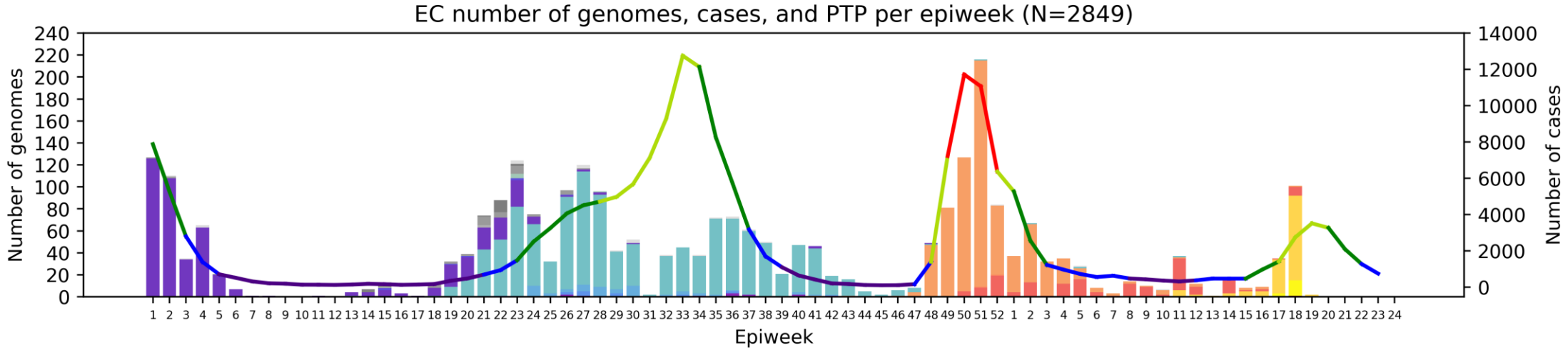
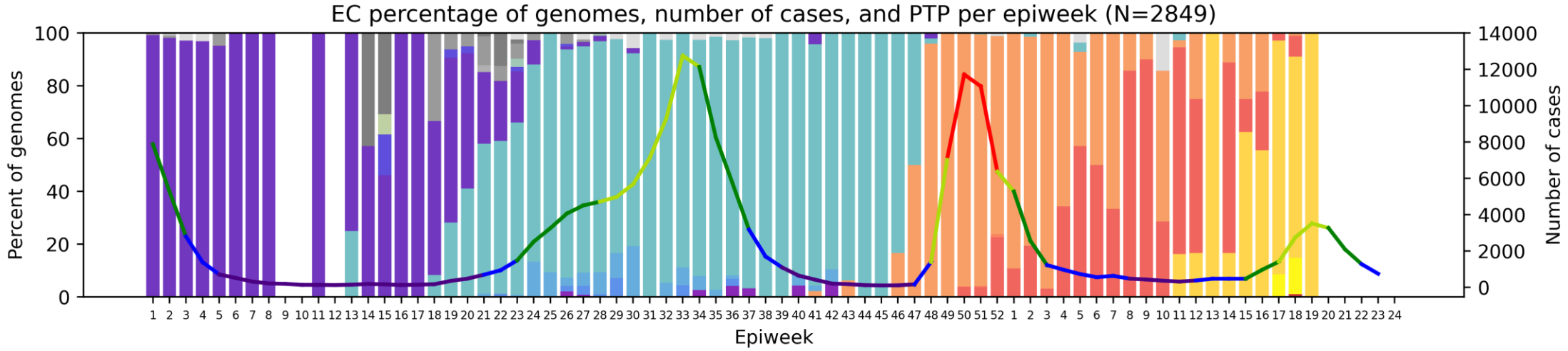
Eastern Cape Province, 2021-2022, n = 2849





Clade key (bar graph)

Omicron (21K/BA.1.*) | Omicron (21L/BA.2.*) | Omicron (22C/BA.2.12.1) | 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) | Cases | Eta (21D) | 20D | 20C | 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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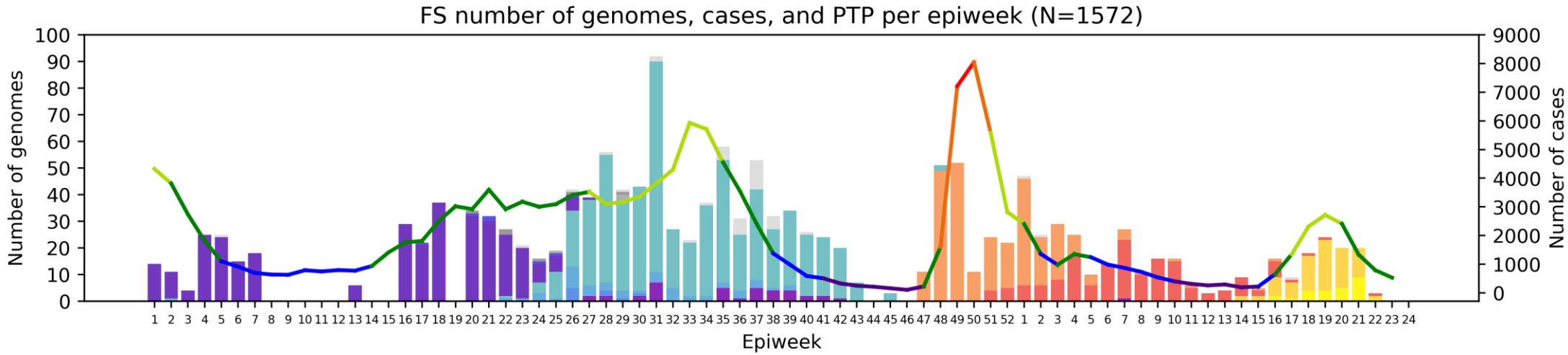
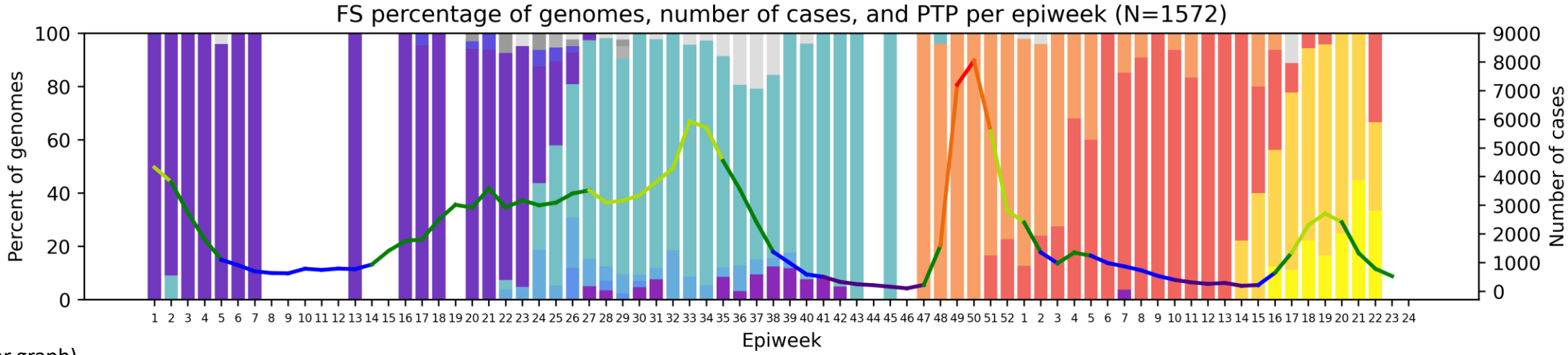
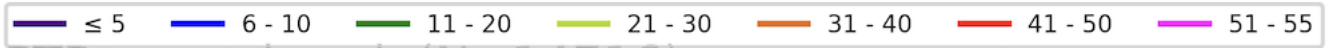
Free State Province, 2021-2022, n = 1572





Clade key (bar graph)

Weekly percentage testing positive key (line graph)



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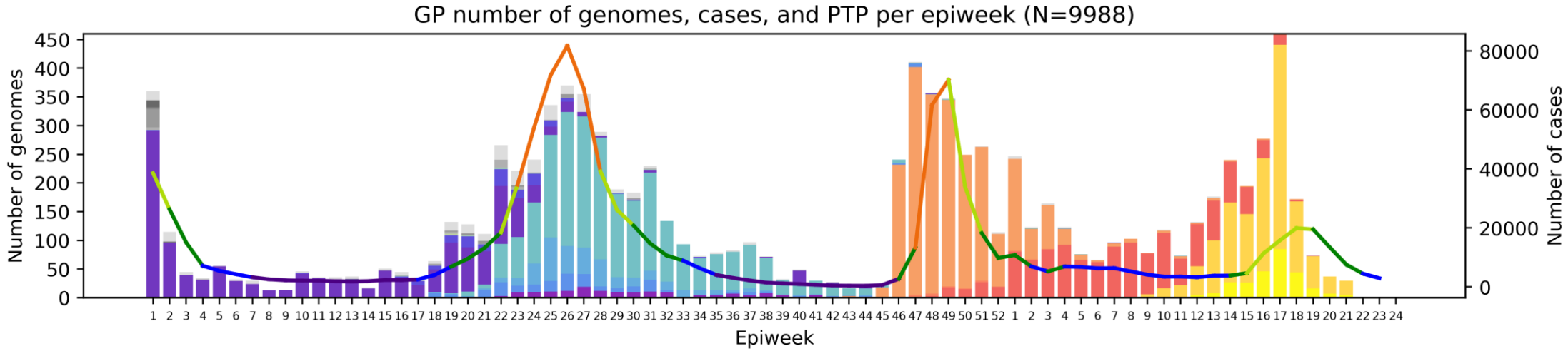
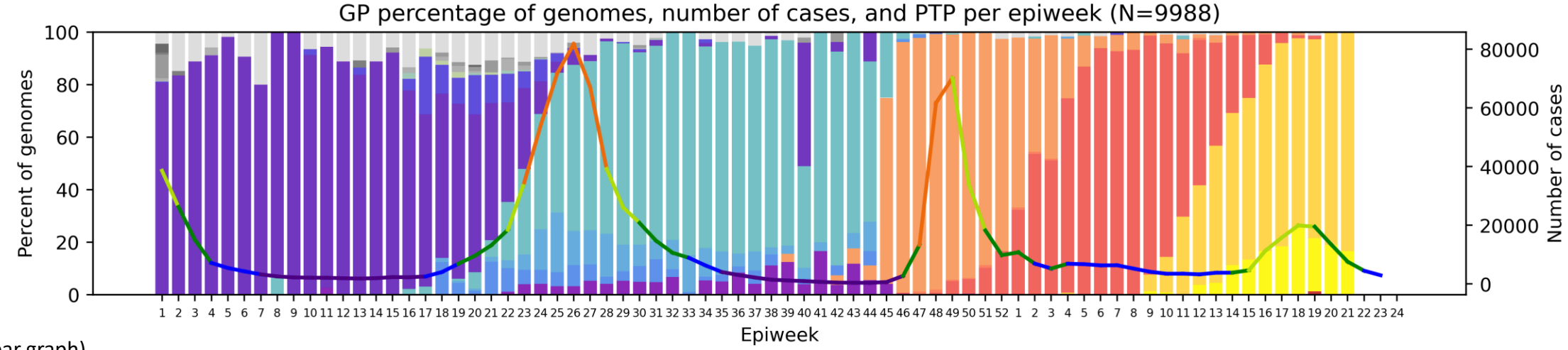
Gauteng Province, 2021-2022, n = 9988





Clade key (bar graph)

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Weekly percentage testing positive key (line graph)

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

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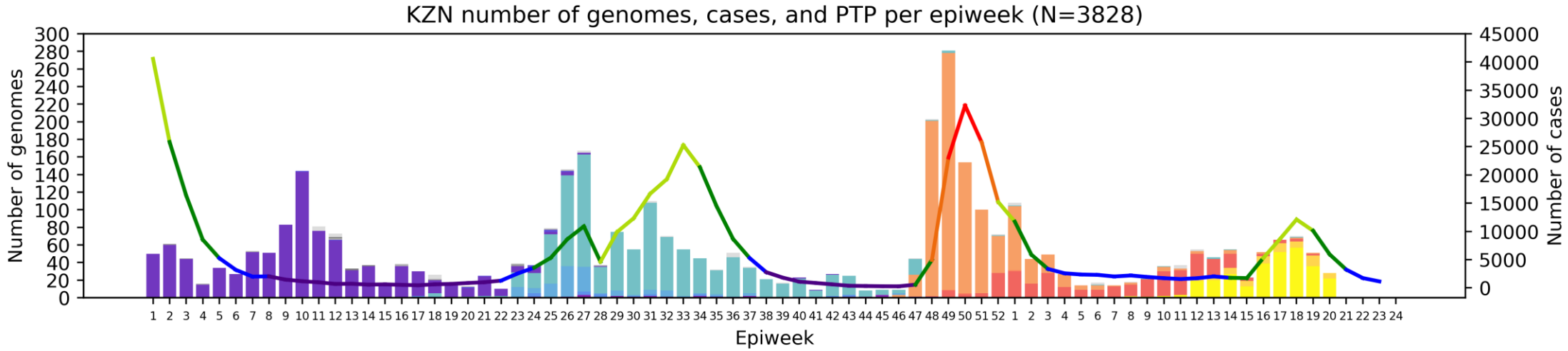
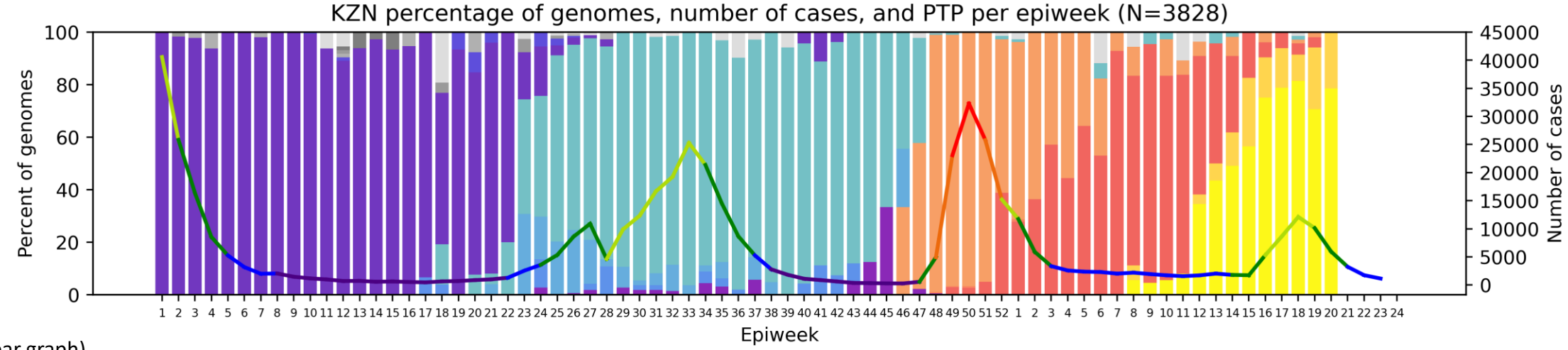
KwaZulu-Natal Province, 2021-2022, n = 3828





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Weekly percentage testing positive key (line graph)

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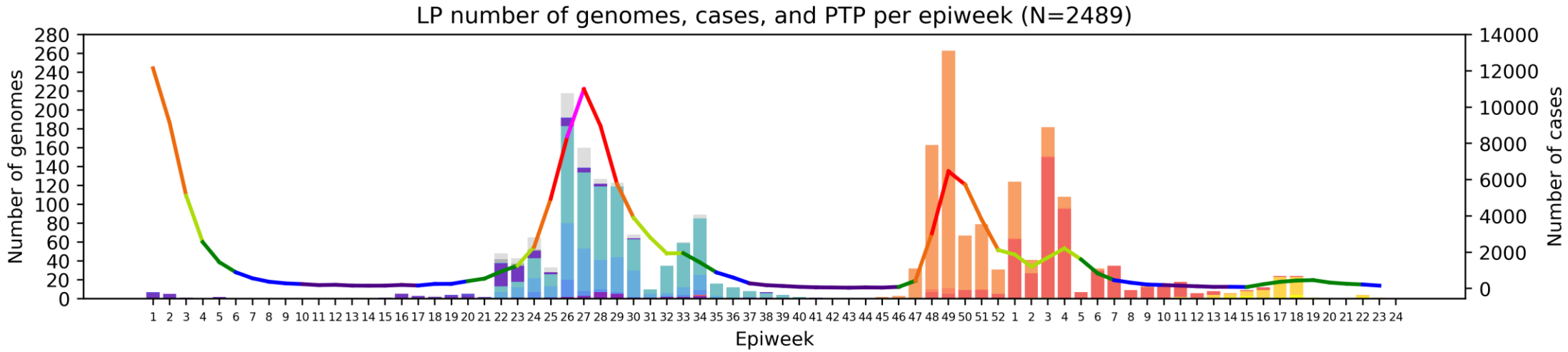
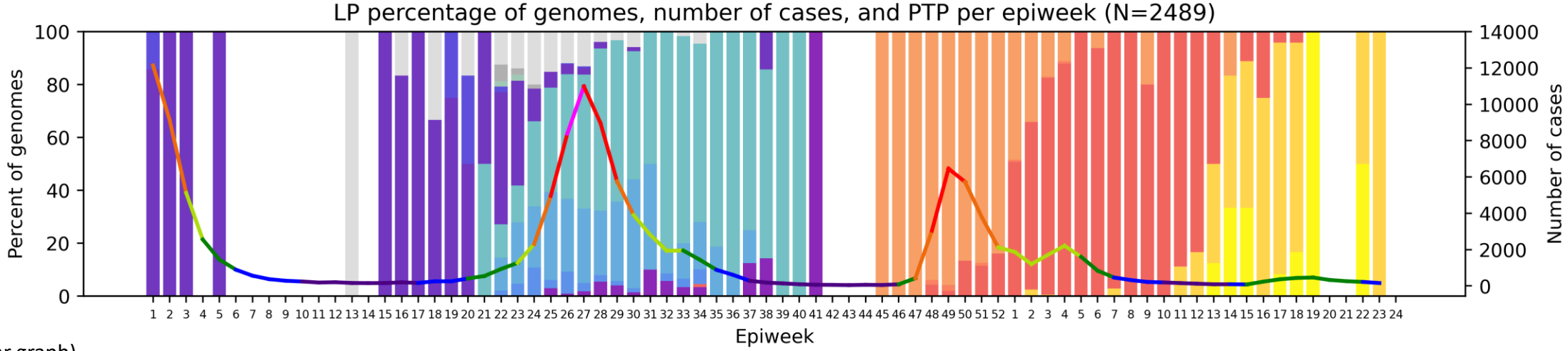
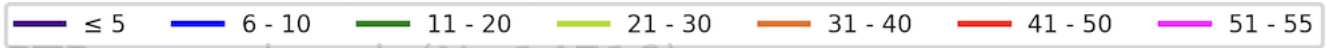
Limpopo Province, 2021-2022, n = 2489





Clade key (bar graph)

Weekly percentage testing positive key (line graph)



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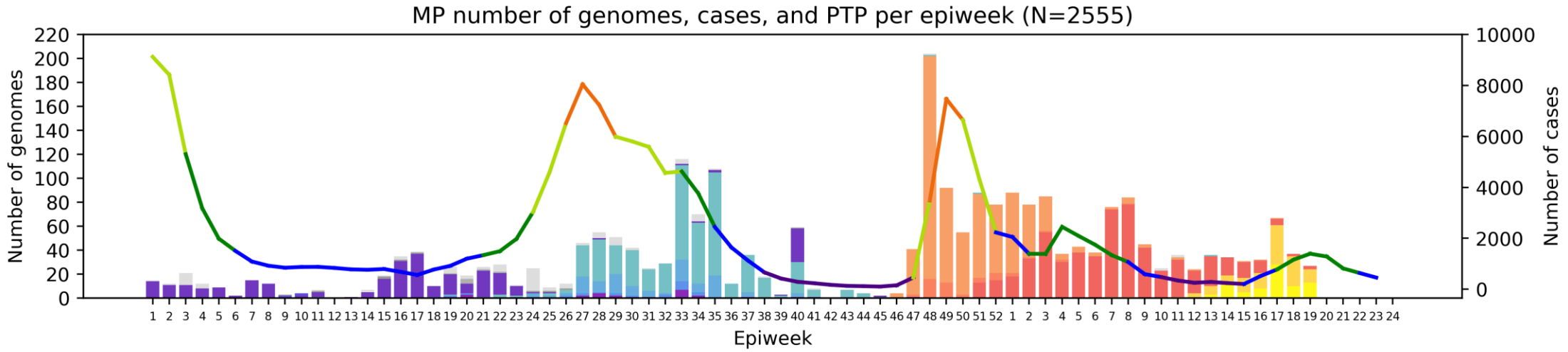
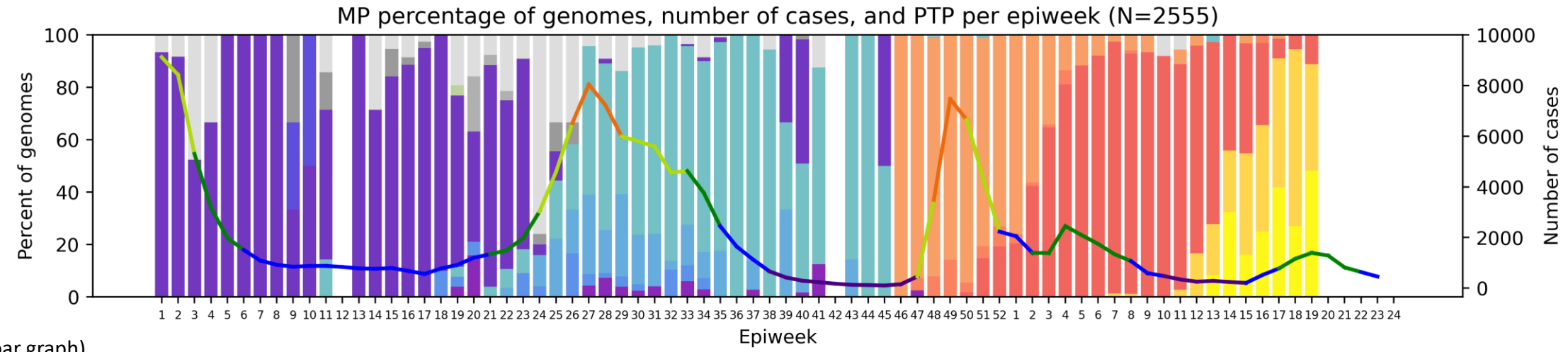
Mpumalanga Province, 2021-2022, n = 2555





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Weekly percentage testing positive key (line graph)

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

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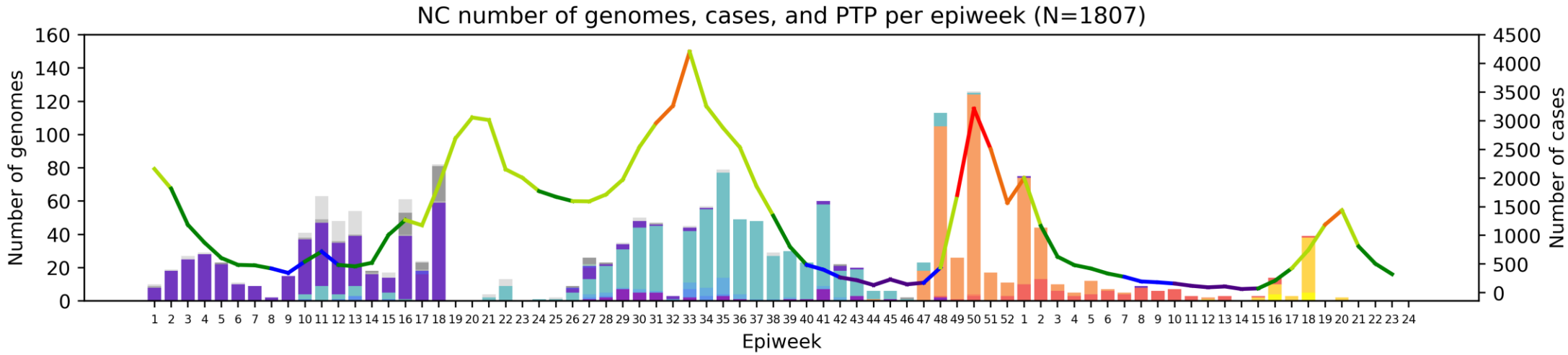
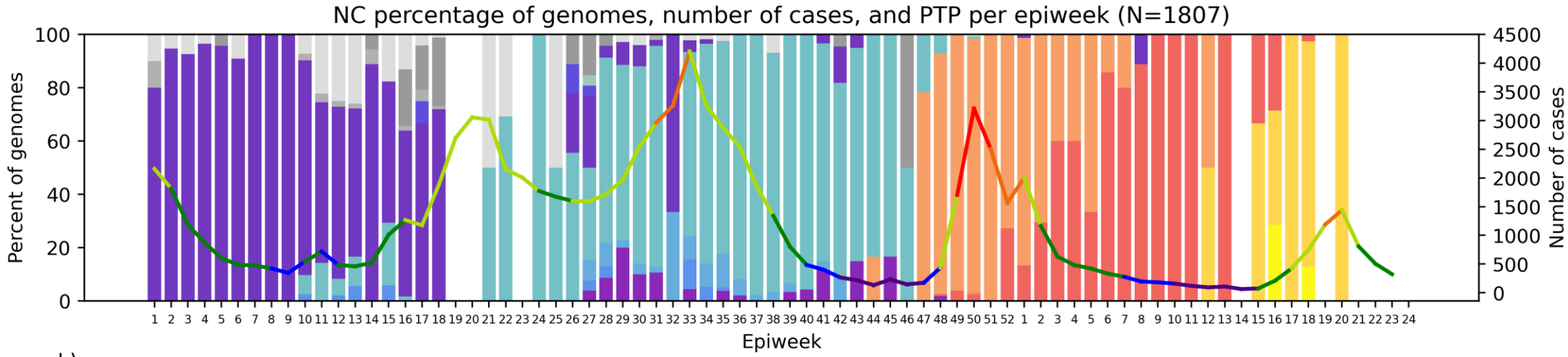
Northern Cape Province, 2021-2022, n = 1807





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Weekly percentage testing positive key (line graph)

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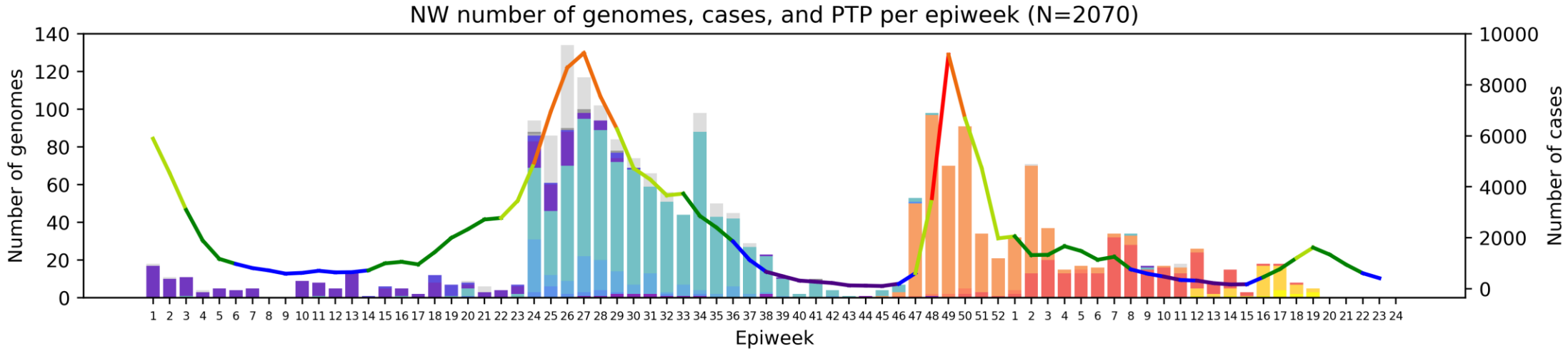
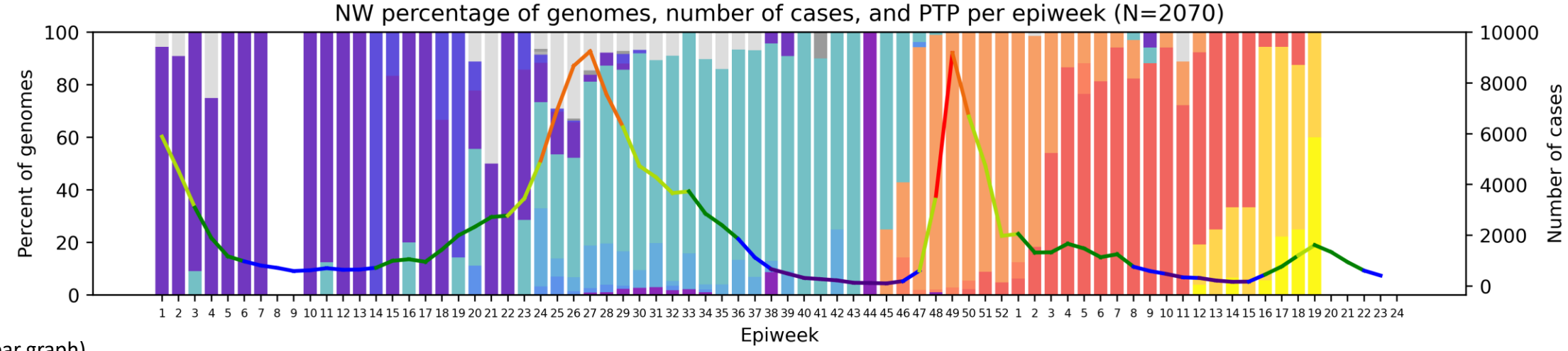
North West Province, 2021-2022, n = 2070





Clade key (bar graph)

Omicron (21K/BA.1.*) | Omicron (21L/BA.2.*) | Omicron (22C/BA.2.12.1) | 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 | 20B | 20A | 19B | 19A | unassigned | Cases

Weekly percentage testing positive key (line graph)

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

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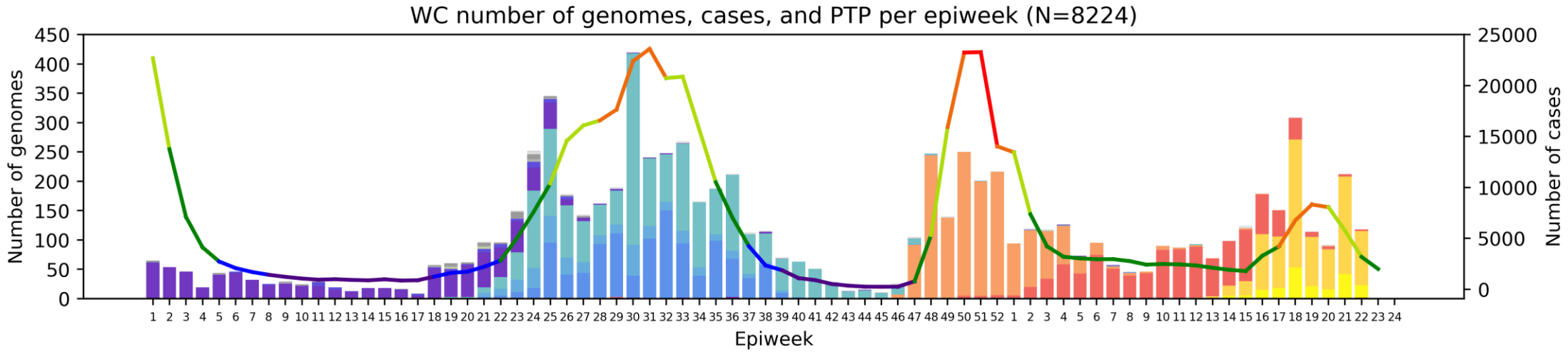
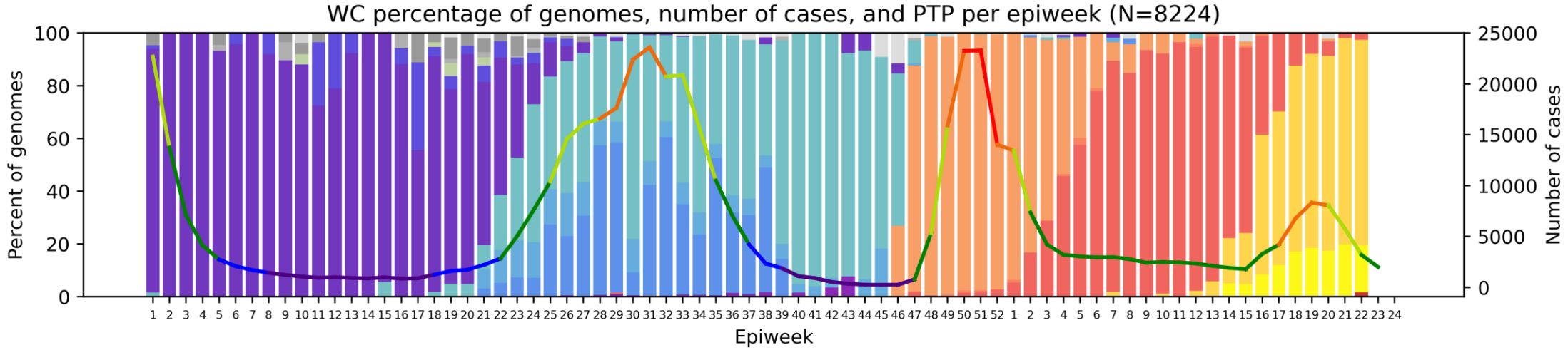
Western Cape Province, 2021-2022, n = 8224





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Weekly percentage testing positive key (line graph)

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Summary

- **Variant of Concern Omicron in South Africa**
  - Dominates 2022 sequencing data at >98% of genomes.
  - While BA.1 (and sub-lineages) was the predominant lineage in January (55%), BA.2 dominated in February (86%) and March (78%).
  - Omicron lineages BA.4 and BA.5 increased in prevalence in March (16%), and together are dominant in April (73%), May (94%) and June (94%).
  - BA.2.12.1 was detected in South Africa at low prevalence in May (0.25%)
- Low frequency of previously circulating variants such as Delta still detected in recent data.

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

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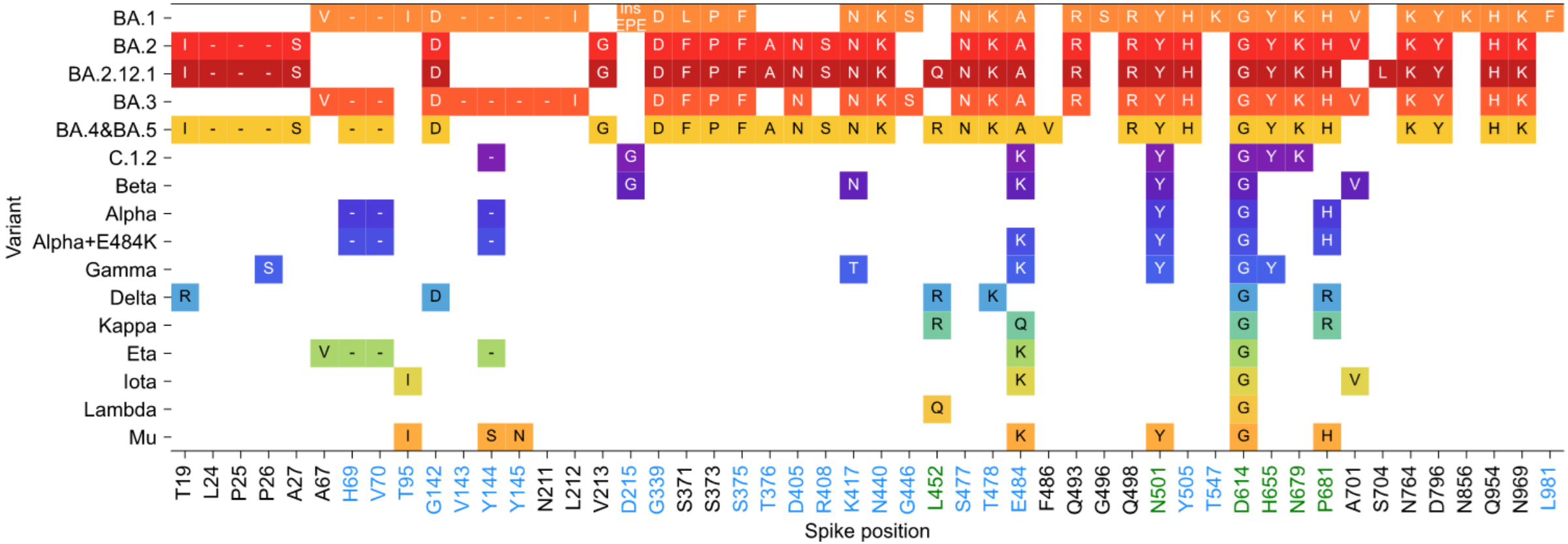
Omicron spike mutations compared to other VOC/VOIs



Mutation impact key

- Unknown/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

Only lineage-defining mutations are pictured.

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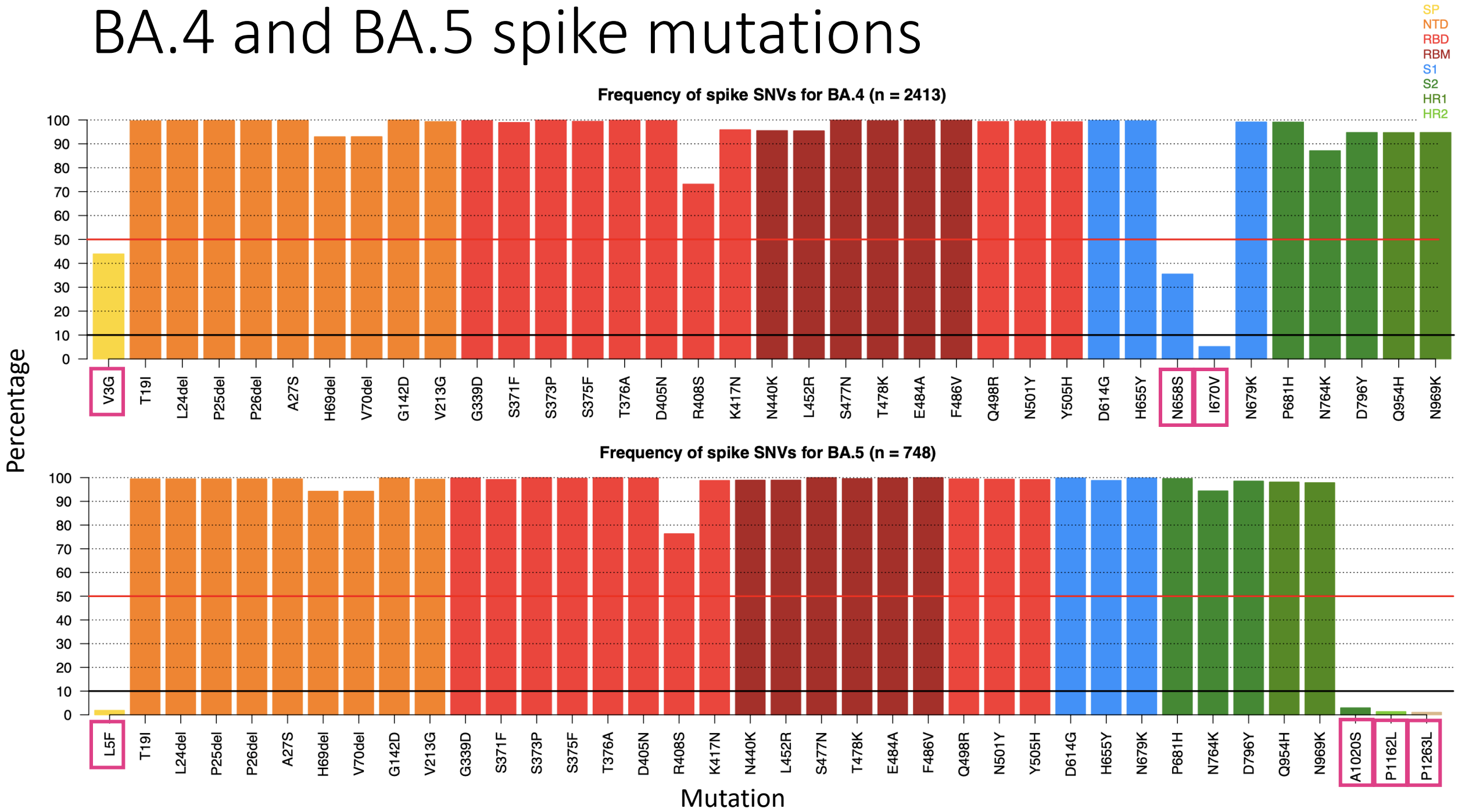
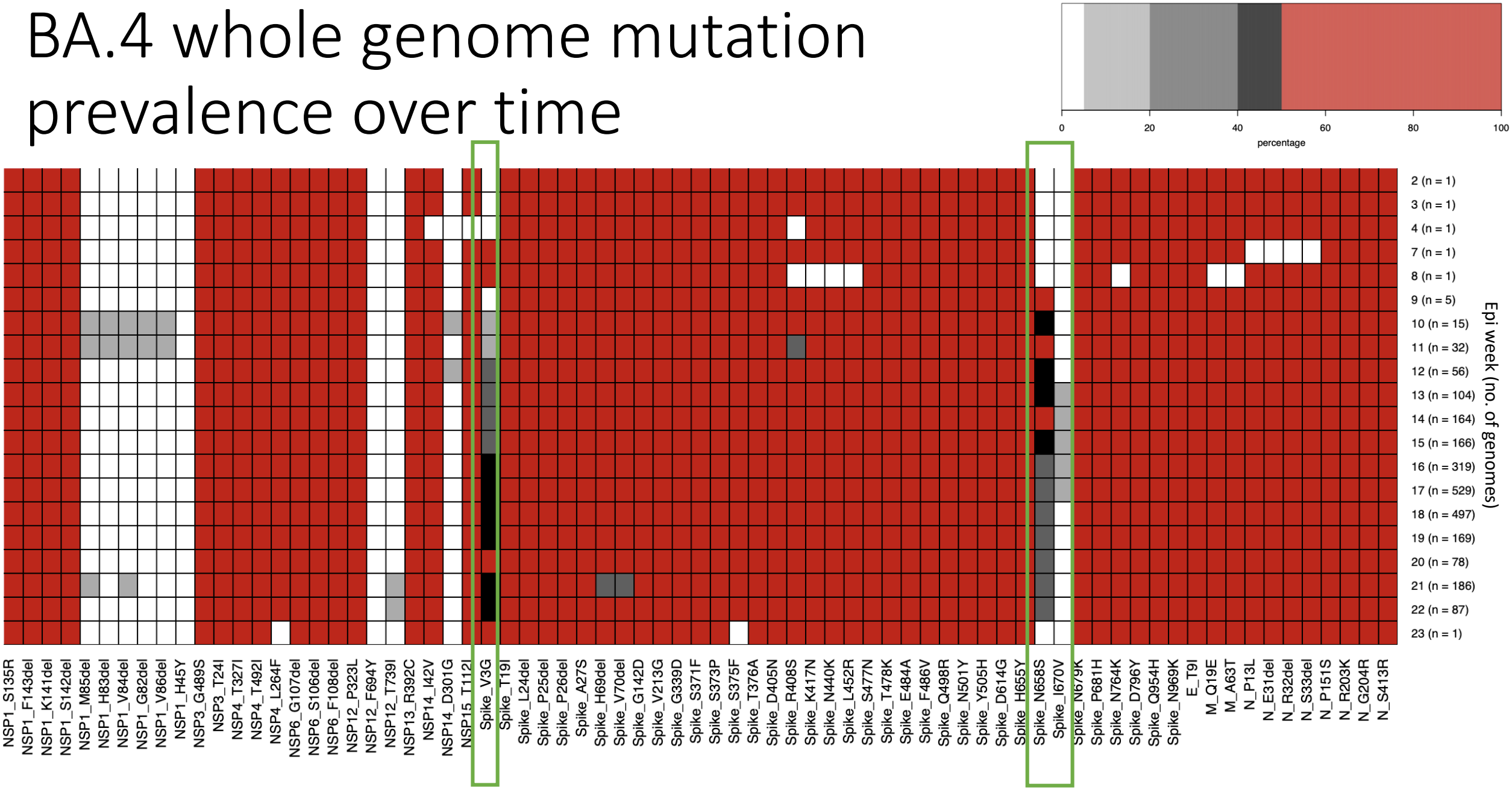
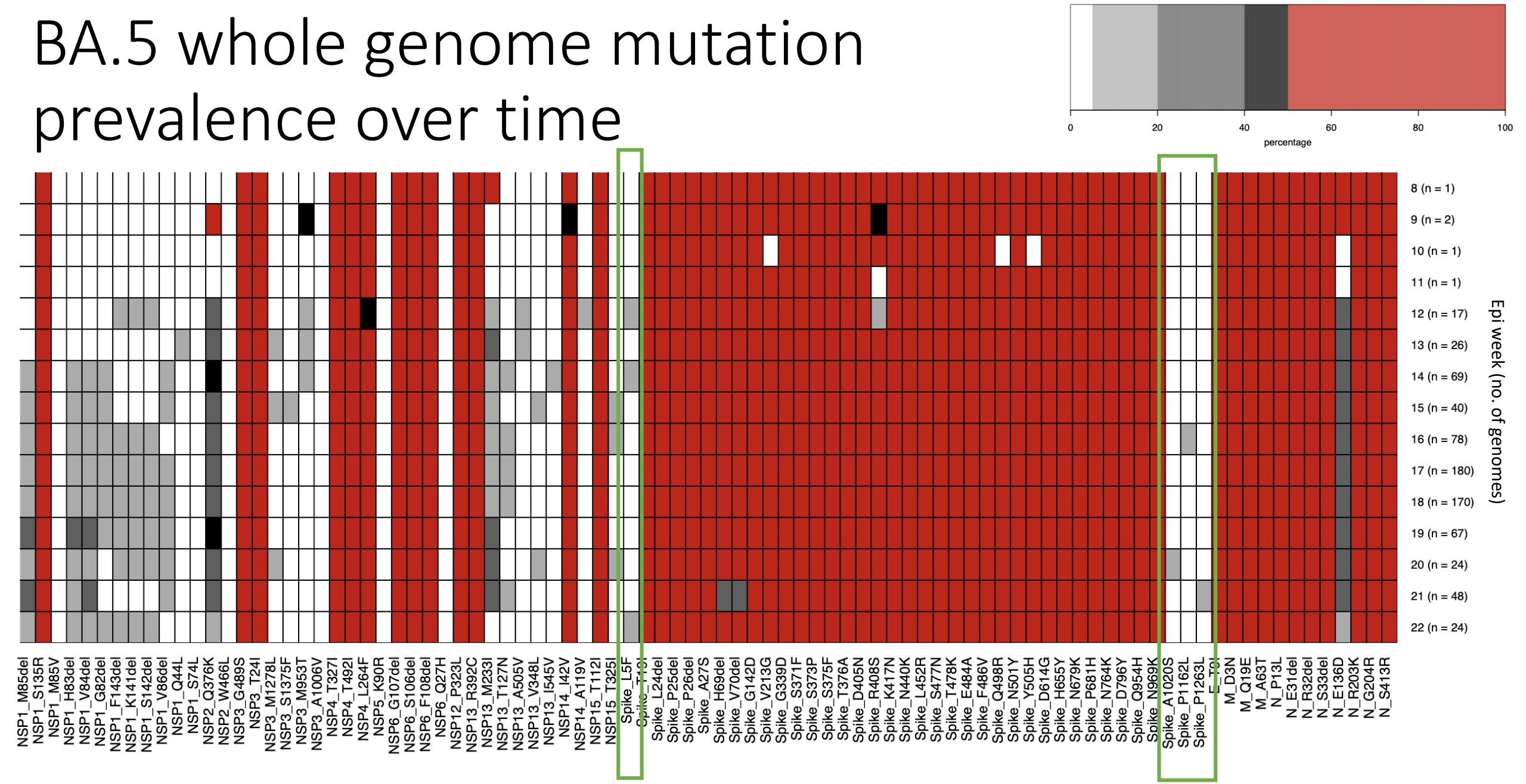
BA.4 and BA.5 spike mutations



BA.4 whole genome mutation prevalence over time



BA.5 whole genome mutation prevalence over time



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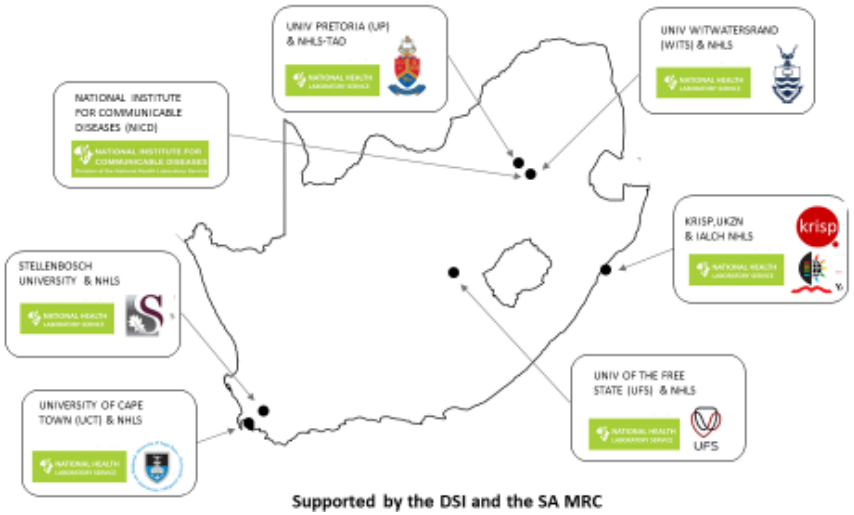

Supported by the DSI and the SA MRC

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Division of the National Health Laboratory Service

EDCTP

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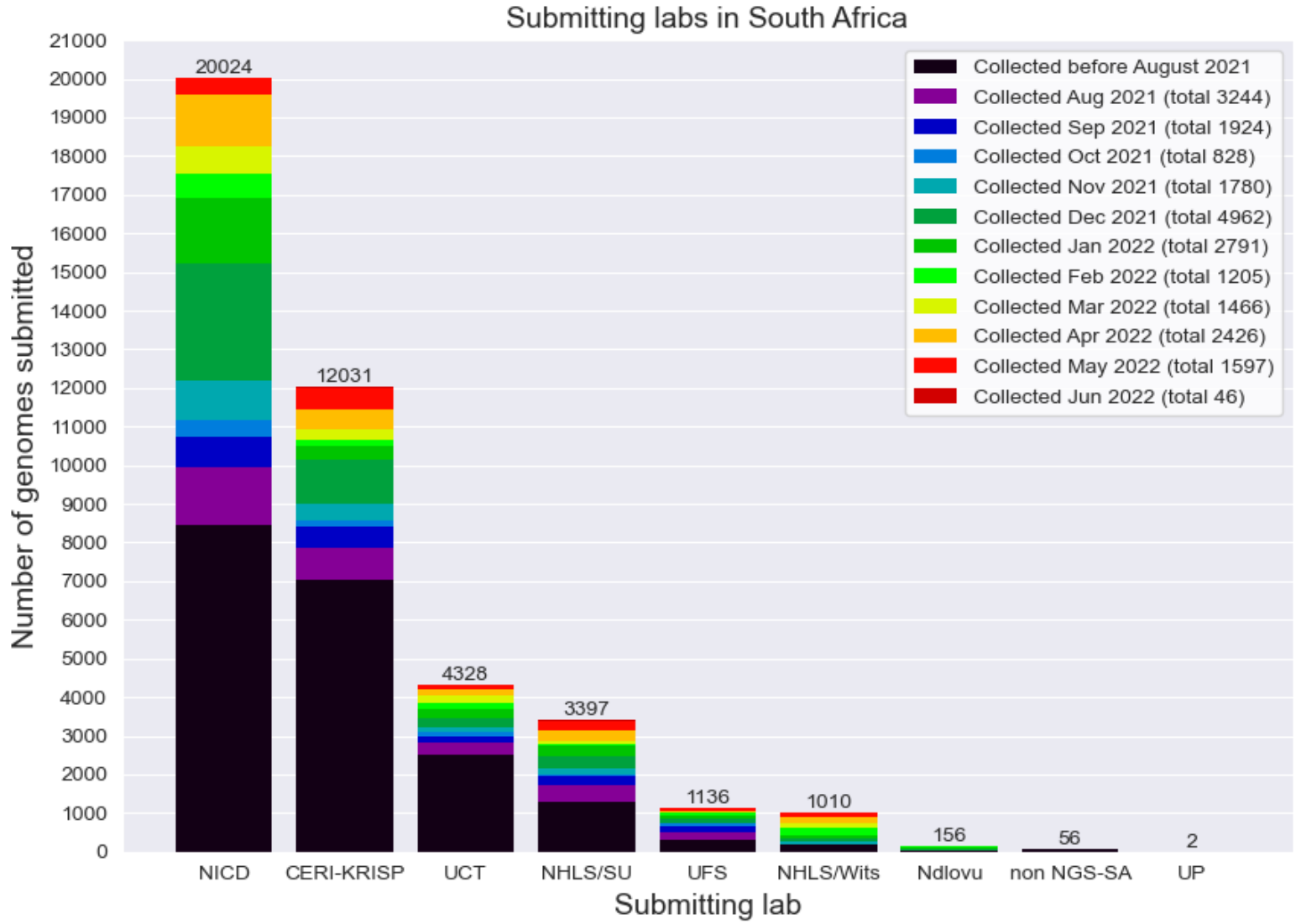
South African genomes submitted per submitting lab, 2020 - 2022 (N=42 140)



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
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.)