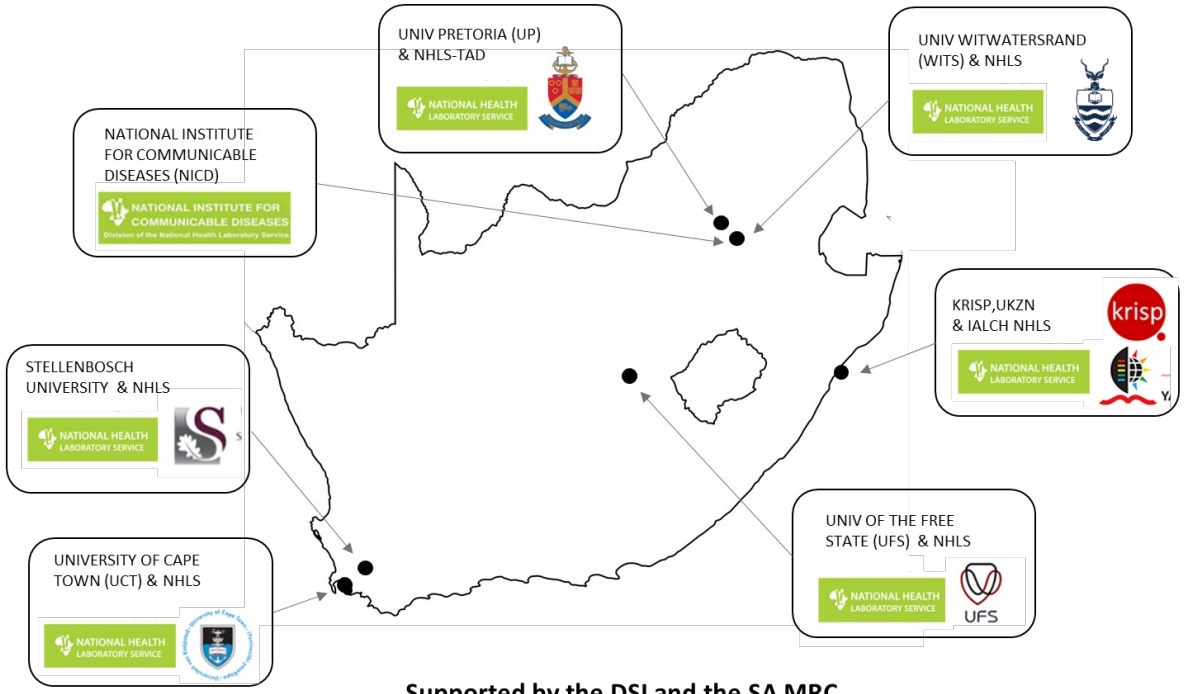
Network for Genomic Surveillance in South Africa (NGS-SA)

SARS-CoV-2 Sequencing Update
1 July 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)

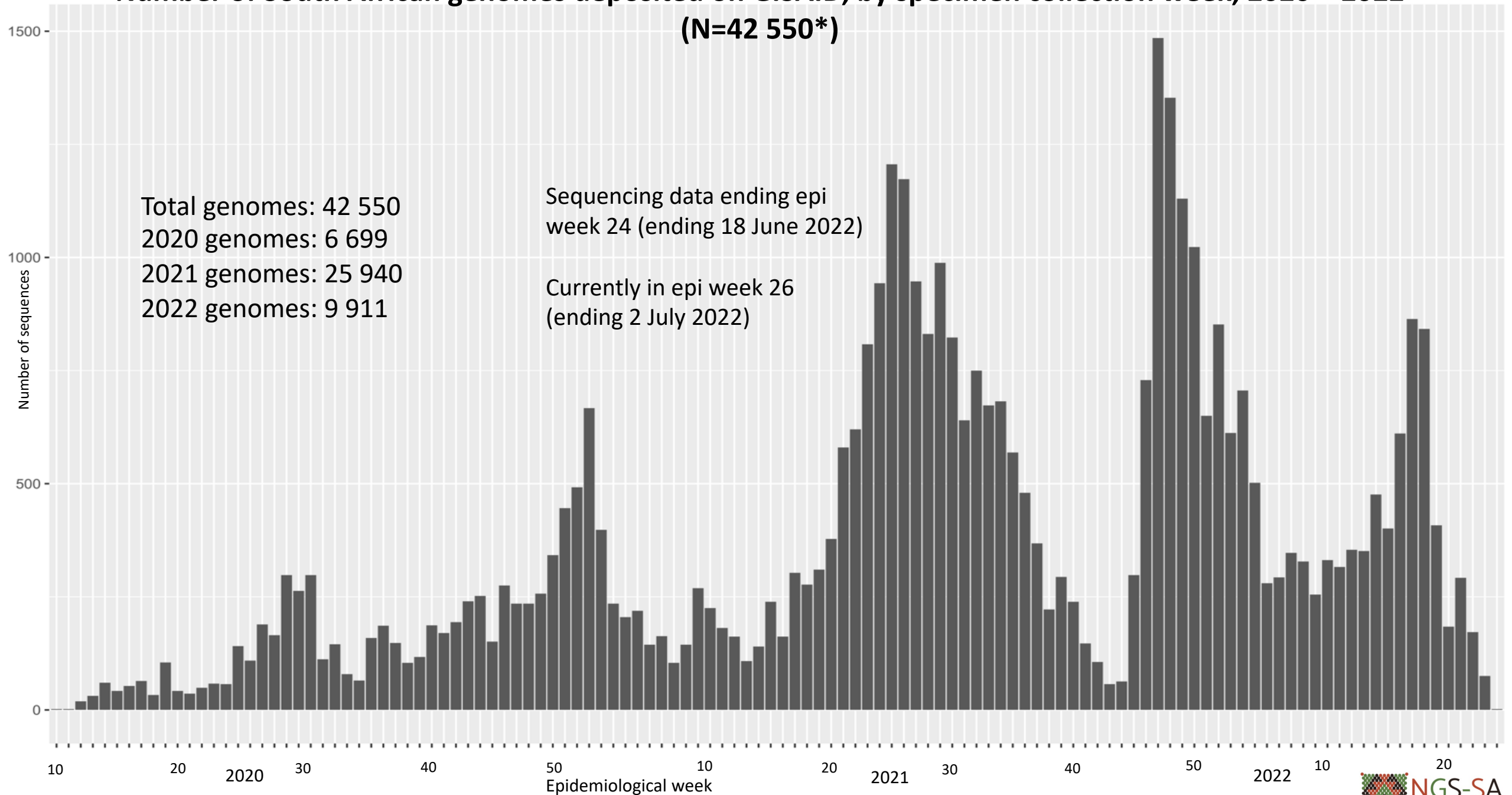
The genomic data presented here are based on South African SARS-CoV-2 sequence data downloaded from GISAID (www.gisaid.org) on 1st July 2022 at 12h50

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=42 550*)



*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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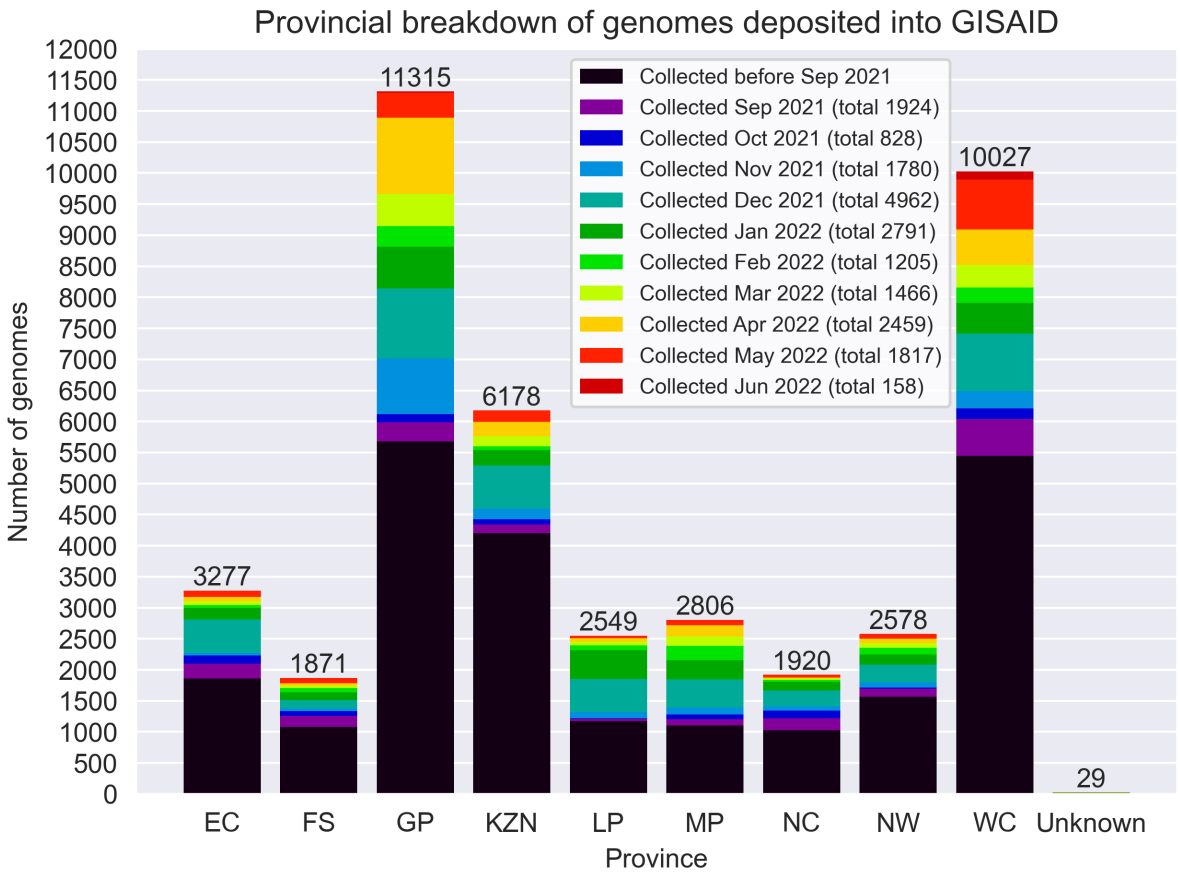
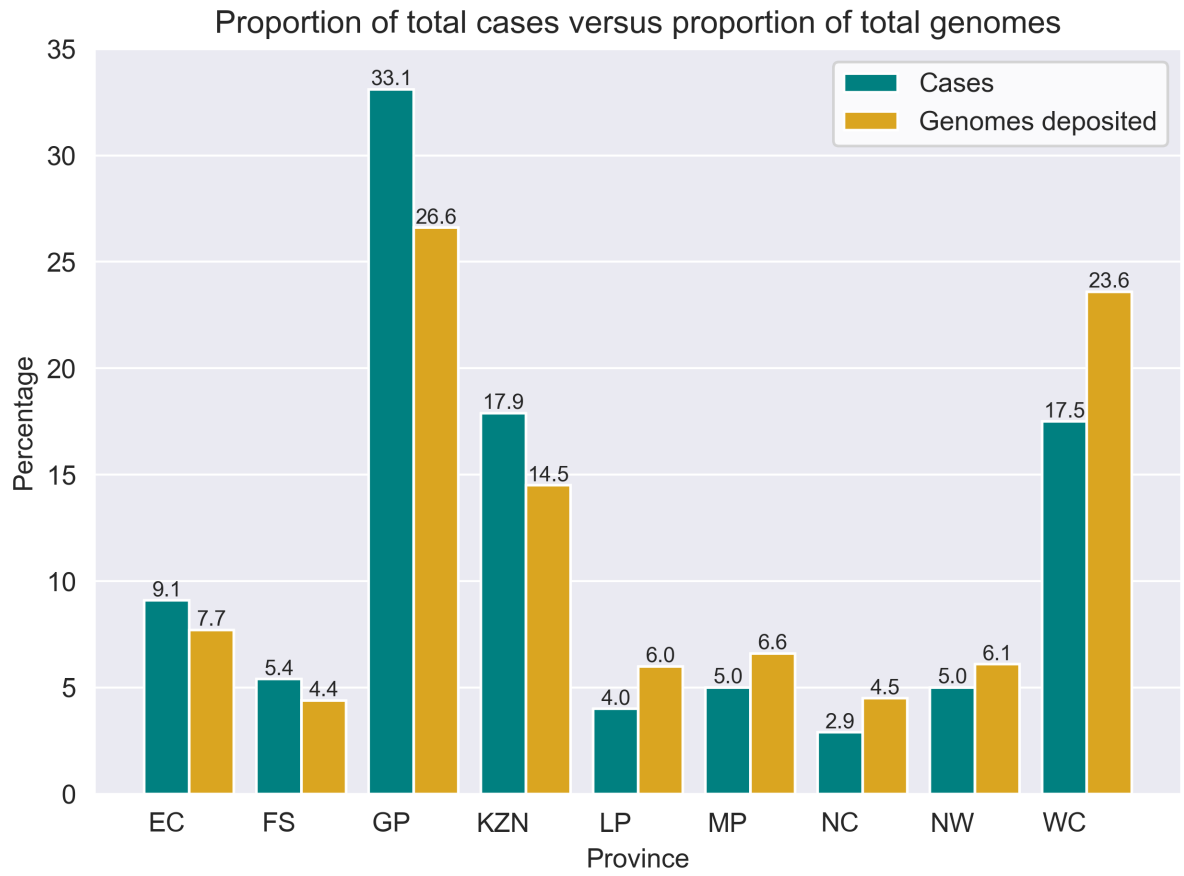
GISAID genomes vs total cases, 2020 – 2022 (N=42 550)





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, GP, FS and LP.

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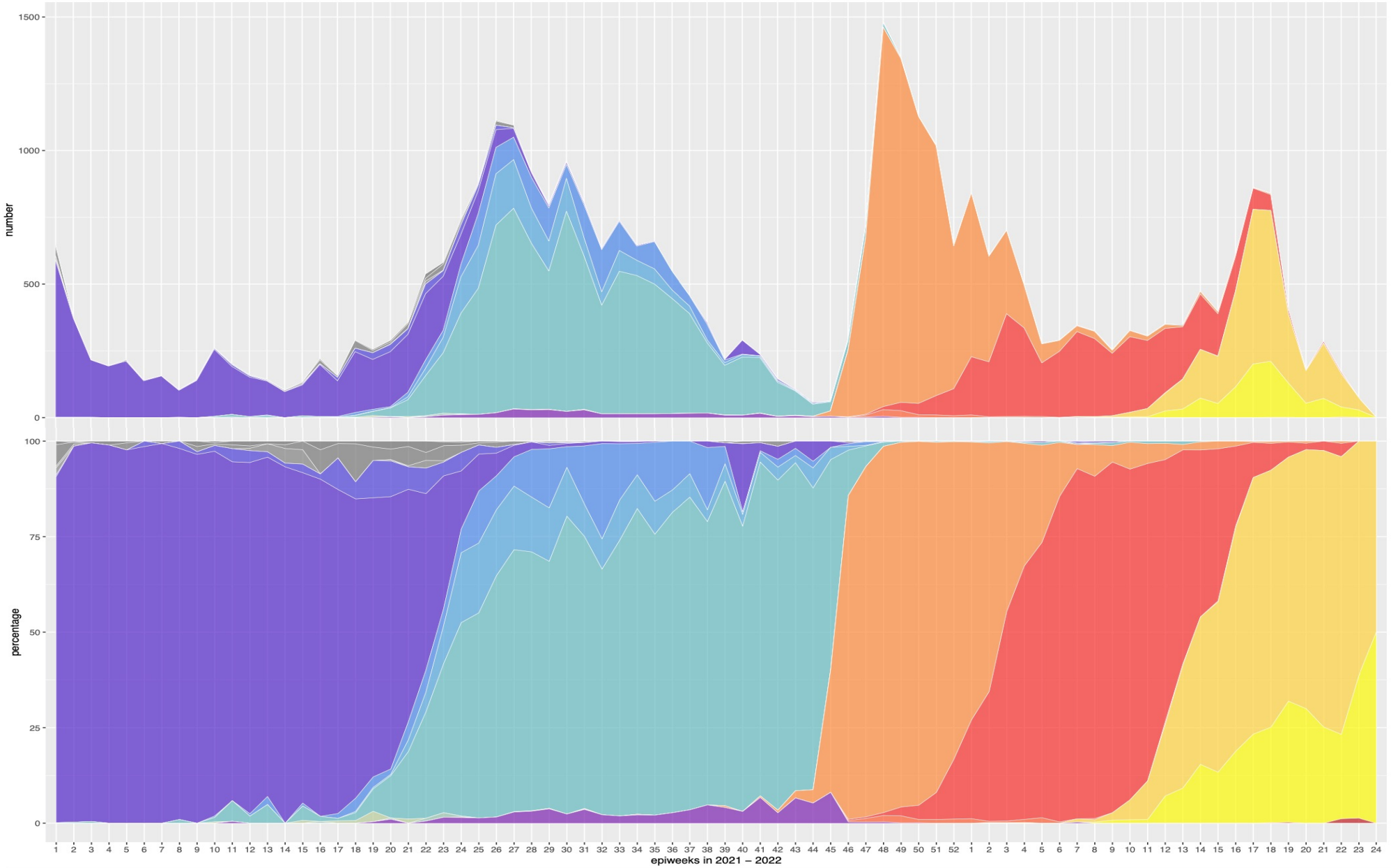
Number and percentage of clades by epiweek in South Africa, 2021 – 2022 (35 764*)



Sequencing data ending epi week 24 (ending 18 June 2022)

Currently in epi week 26 (ending 2 July 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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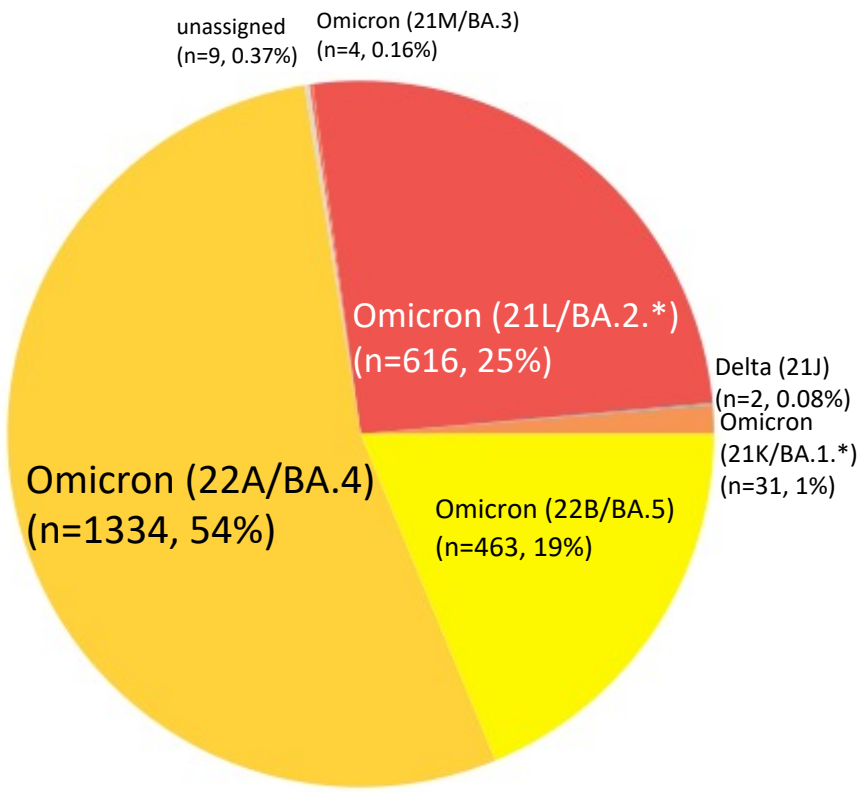
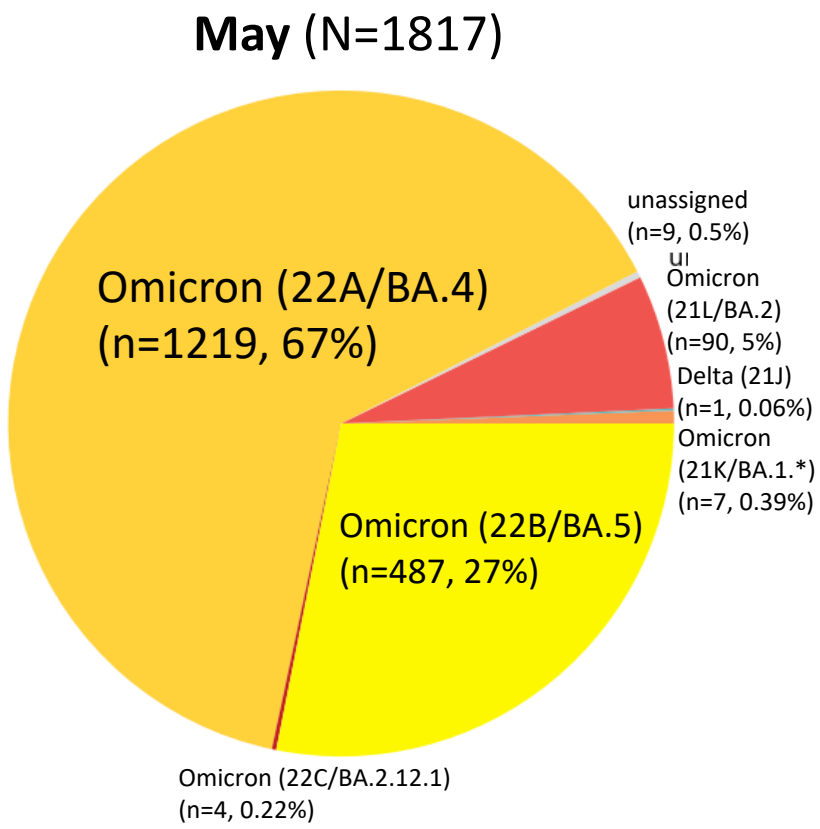
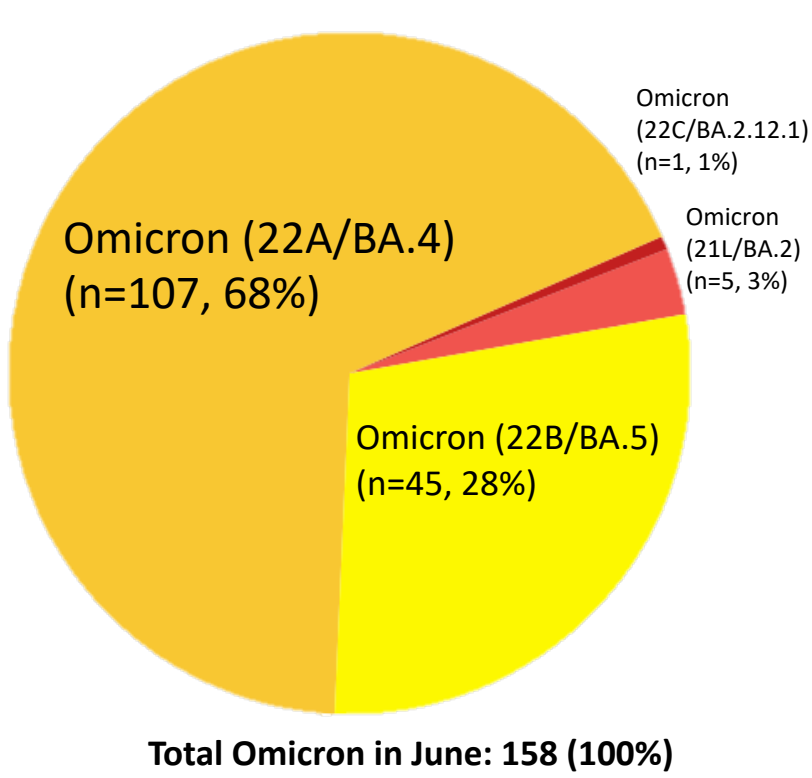
Prevalence of Variants of Concern (VOC) and Variants of Interest (VOI) in April – June 2022



Total Omicron in Apr: 2448 (99.6%)



Total Omicron in May: 1806 (99.4%)



Total Omicron in June: 158 (100%)

Omicron dominated in April (99.6%, 2448/2459), May (99.4%, 1806/1817) and June (100%, 158/158). BA.4 and BA.5 together were dominant in April, May and June. BA.2.12.1 was detected at low levels in May and June.

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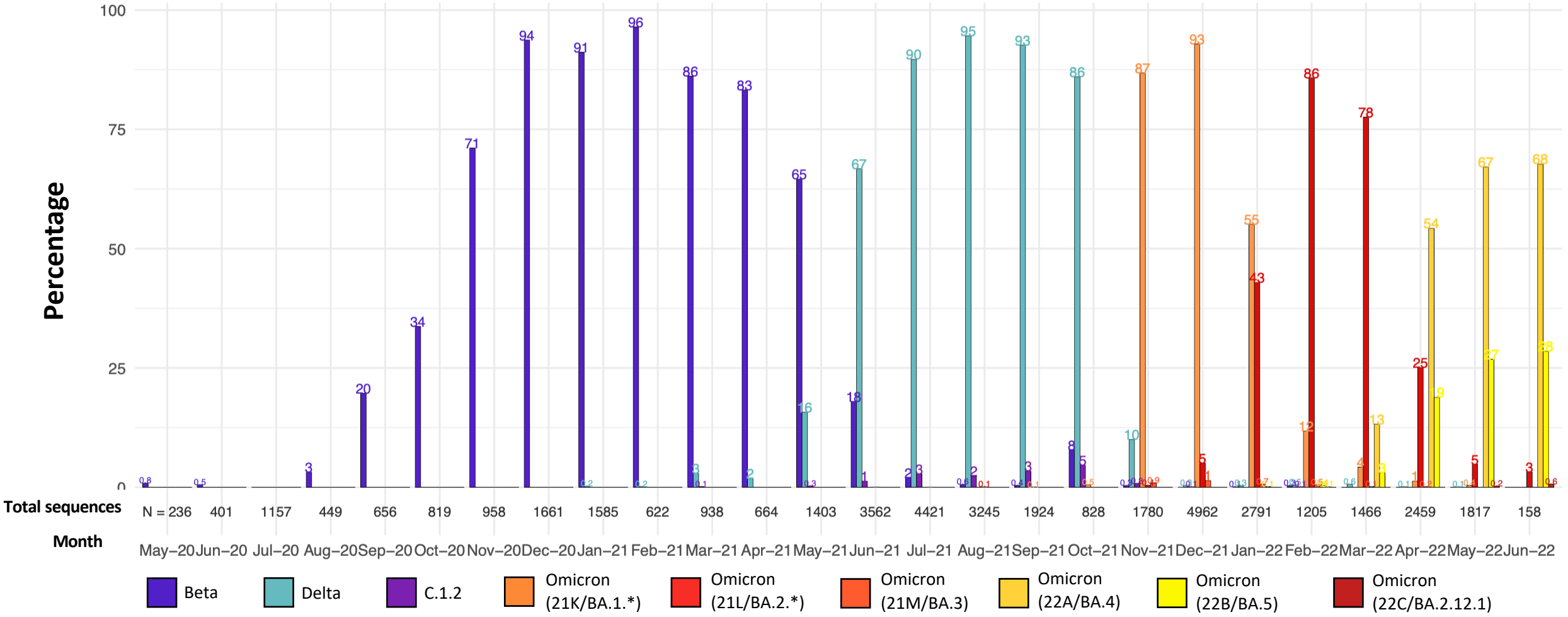
Detection Rates: Beta, Delta, C.1.2 and Omicron

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.4 and BA.5 together dominated in April at 73%, in May at 94%, and currently make up 96% of June sequences, although with a small number of genomes.

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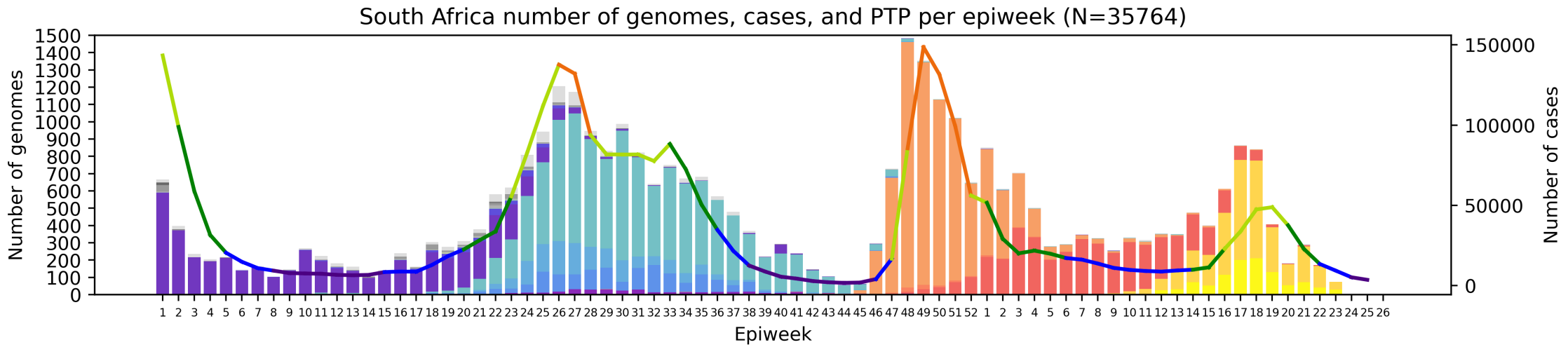
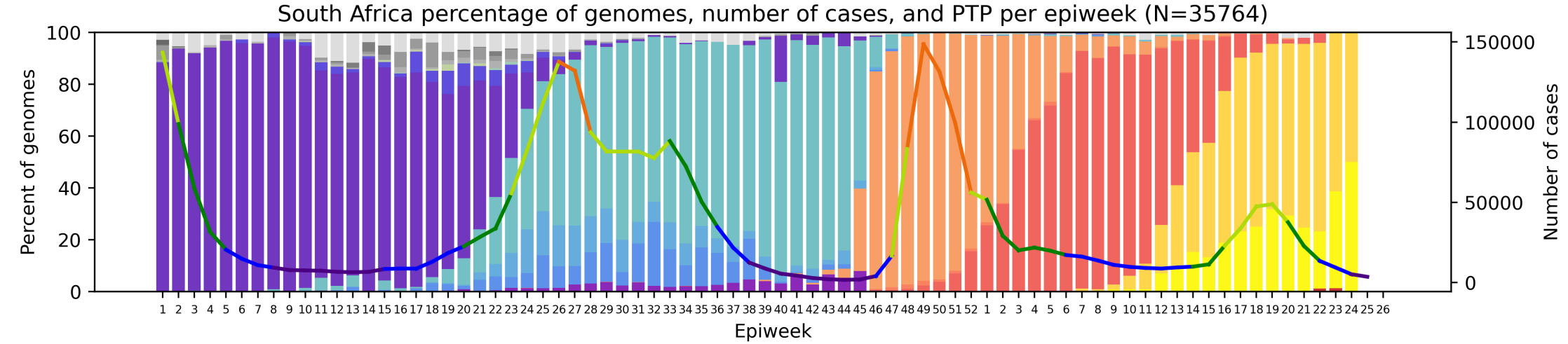
South Africa, 2021-2022, n = 35 764*





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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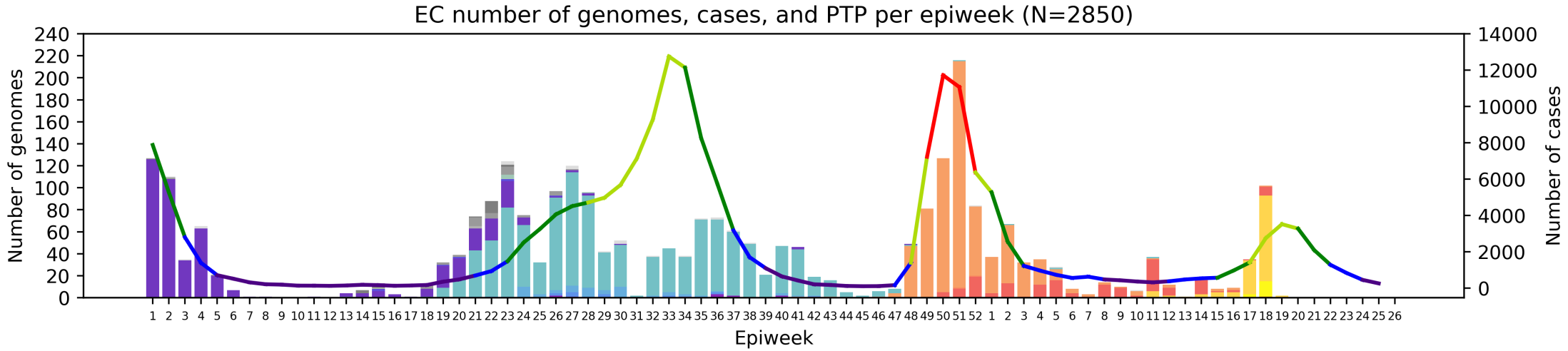
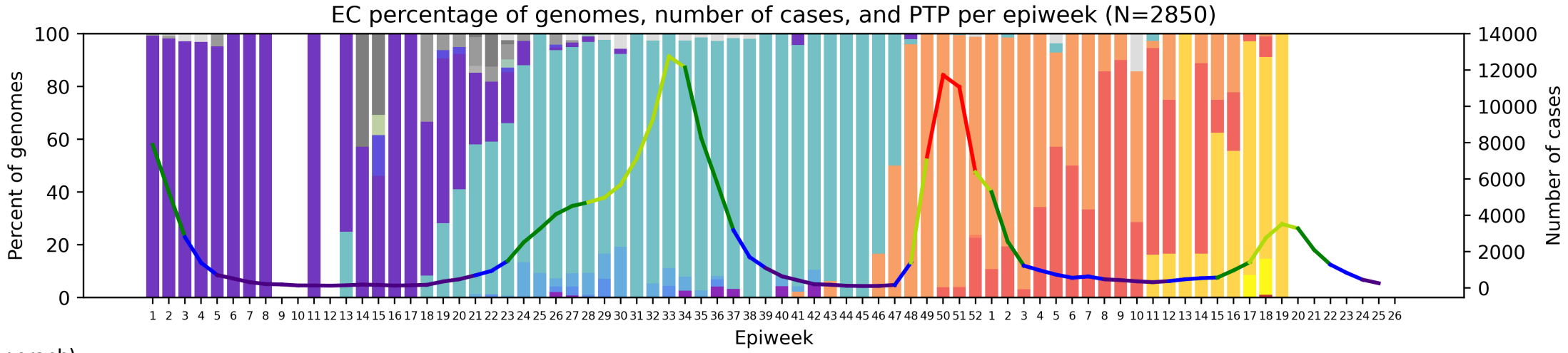
Eastern Cape Province, 2021-2022, n = 2850





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)

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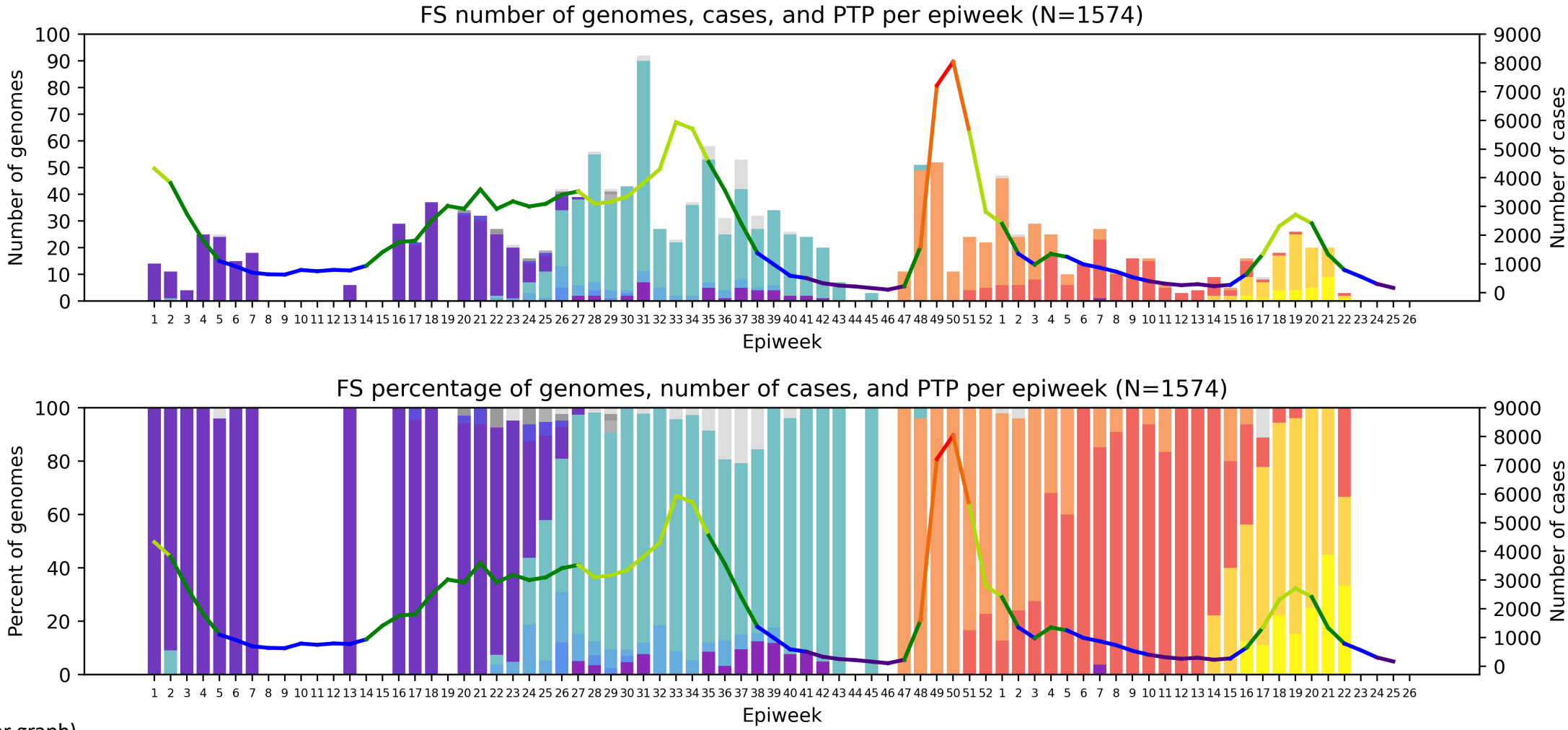
Free State Province, 2021-2022, n = 1574



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)

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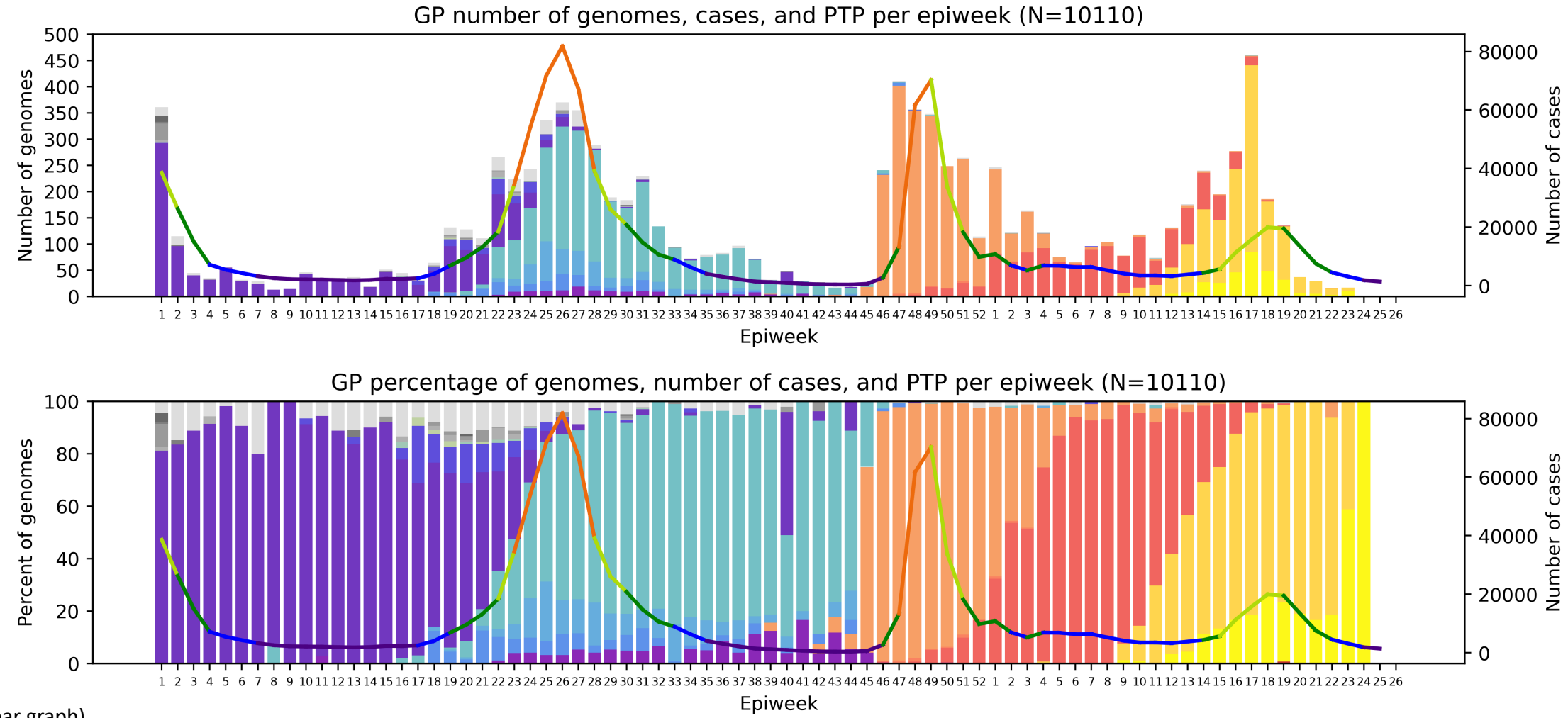
Gauteng Province, 2021-2022, n = 10 110



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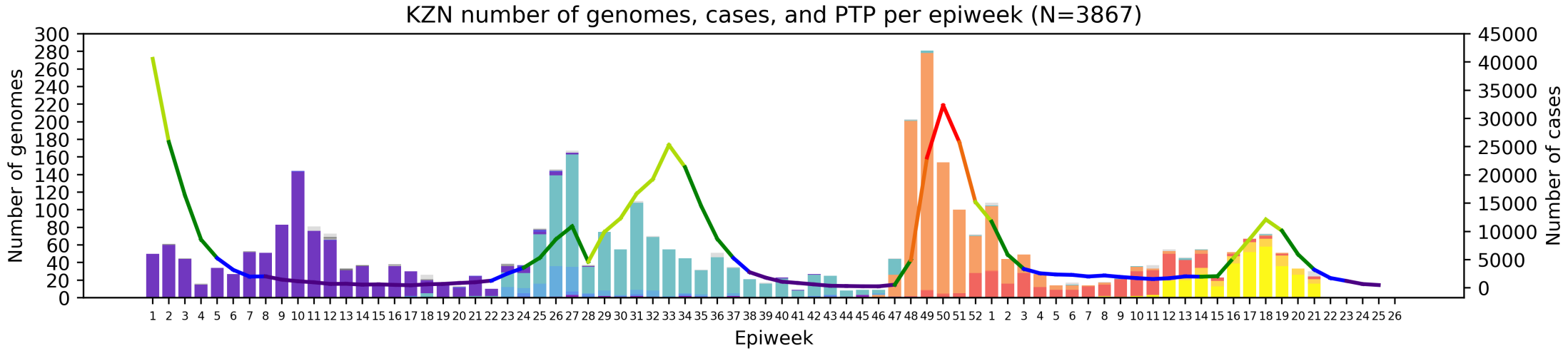
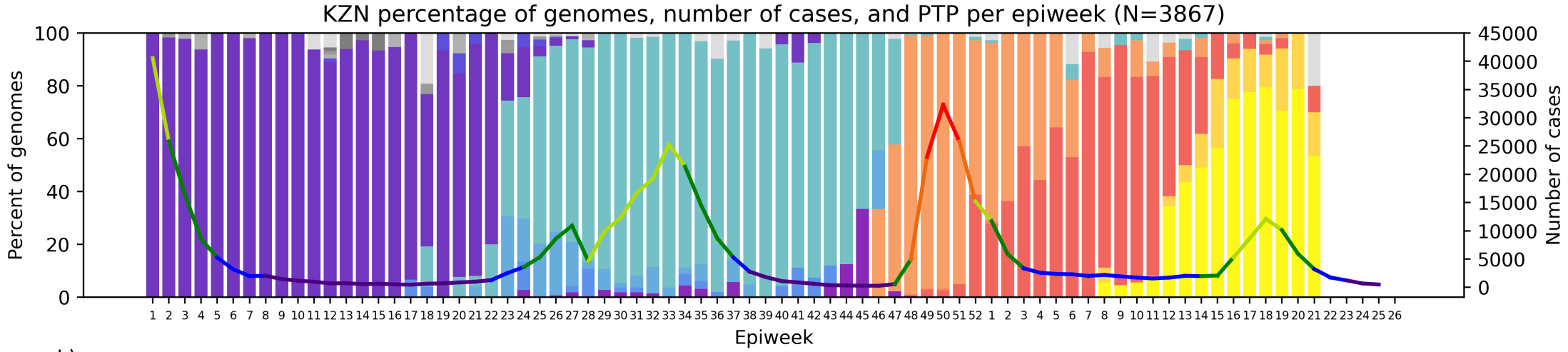
KwaZulu-Natal Province, 2021-2022, n = 3867





Clade key (bar graph)

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Weekly percentage testing positive key (line graph)

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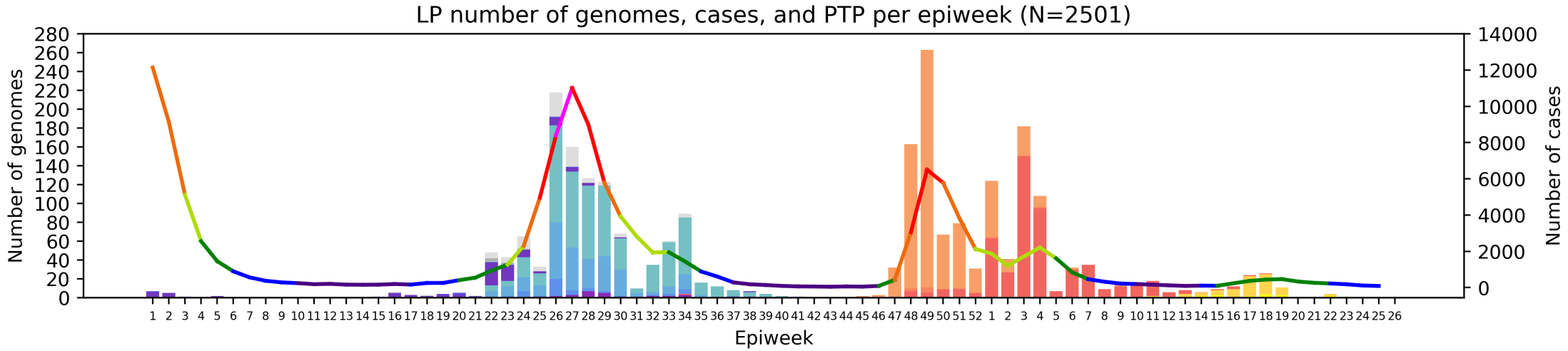
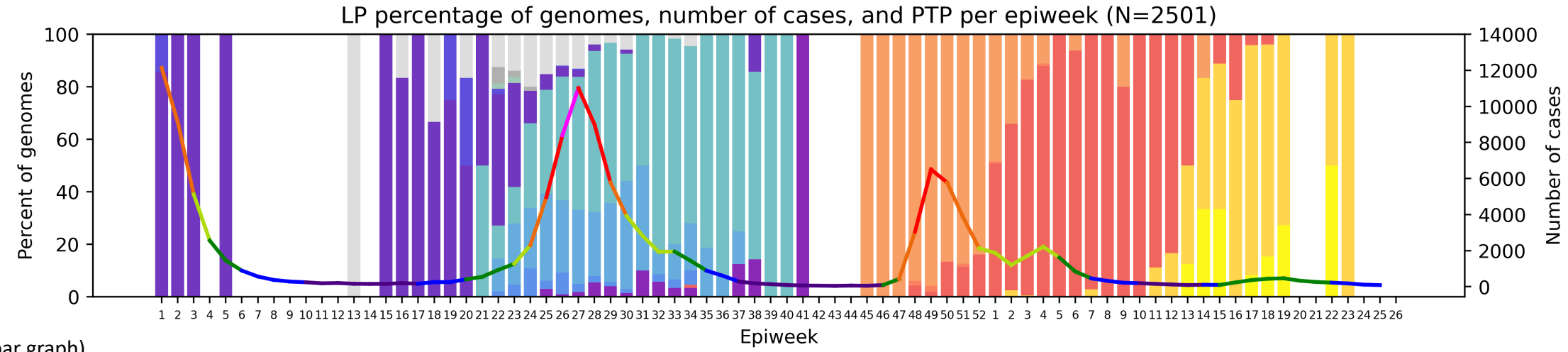
Limpopo Province, 2021-2022, n = 2501





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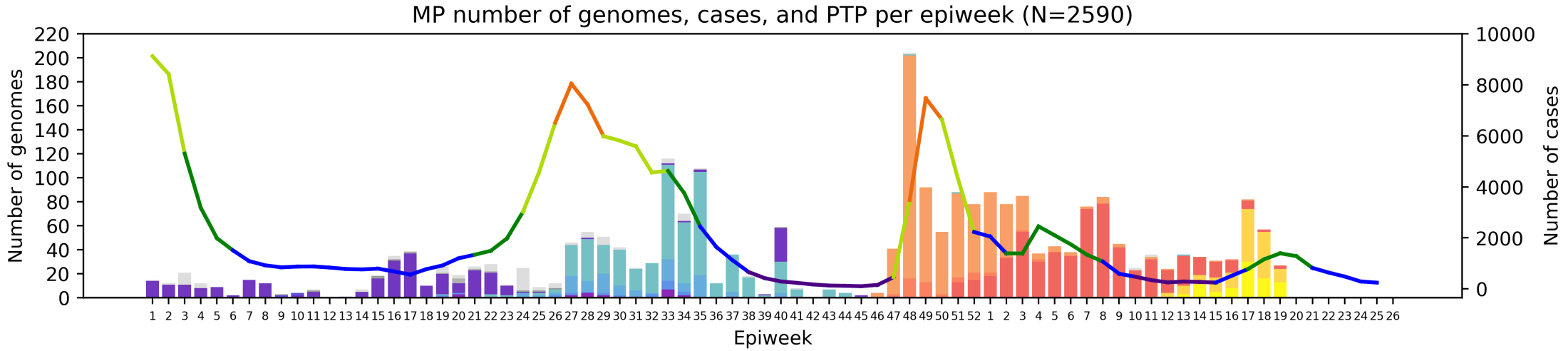
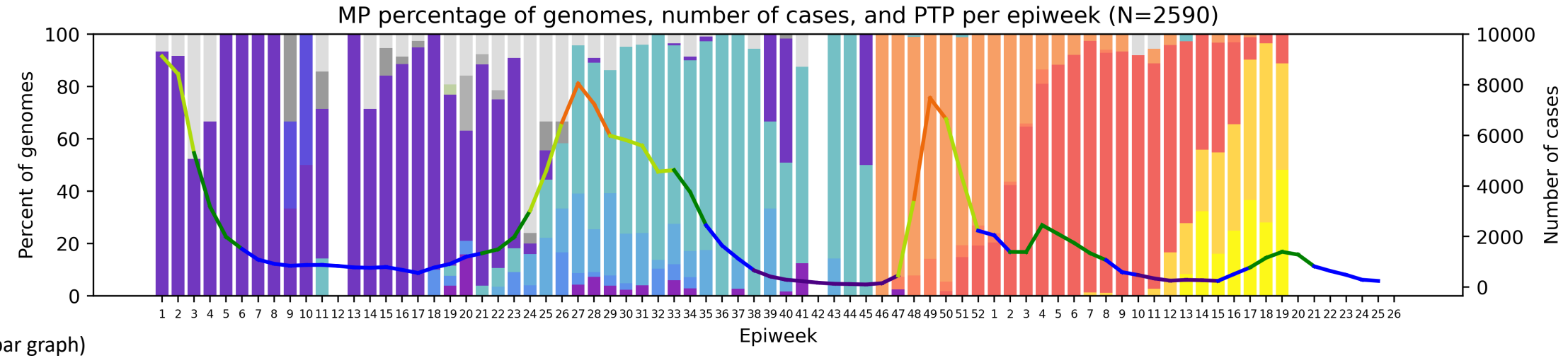
Mpumalanga Province, 2021-2022, n = 2590





Clade key (bar graph)

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Weekly percentage testing positive key (line graph)

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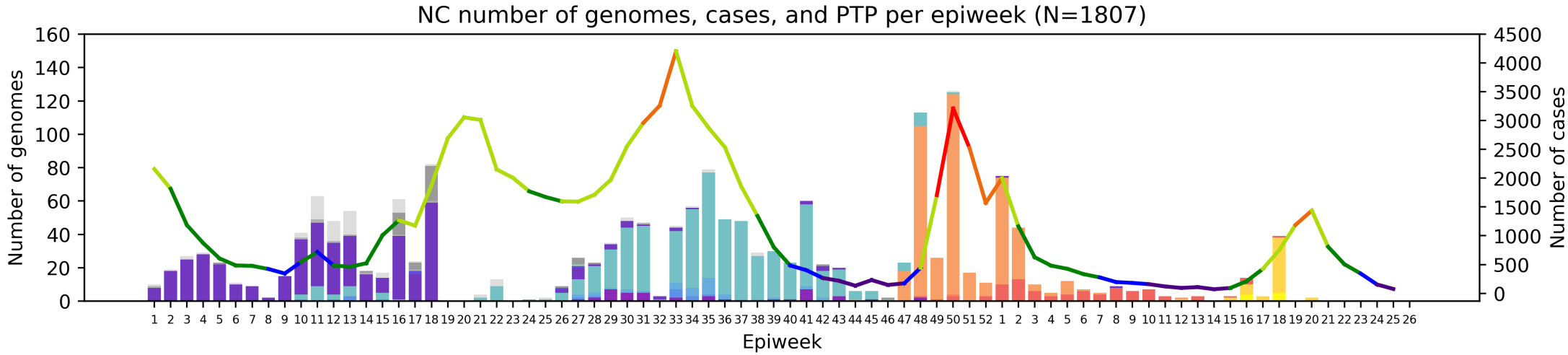
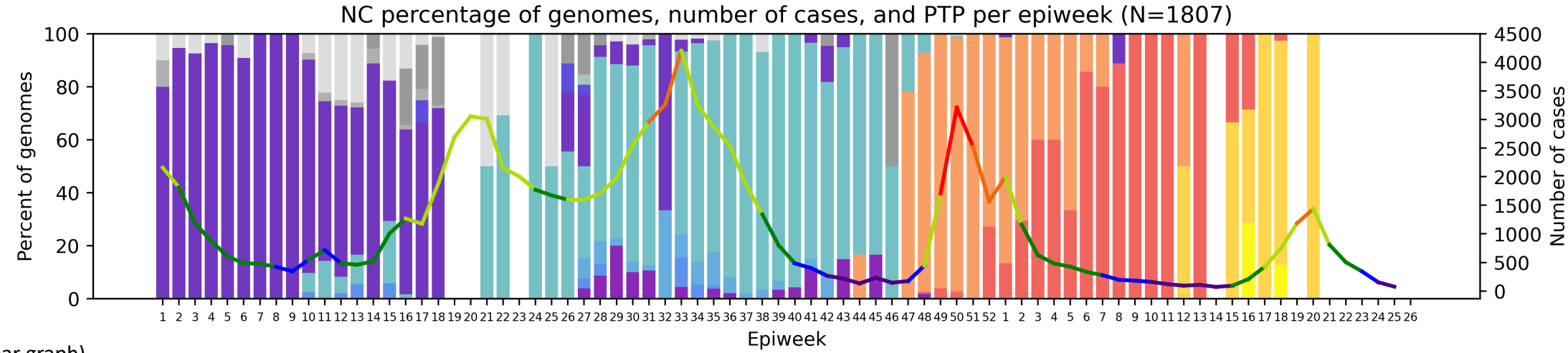
Northern Cape Province, 2021-2022, n = 1807





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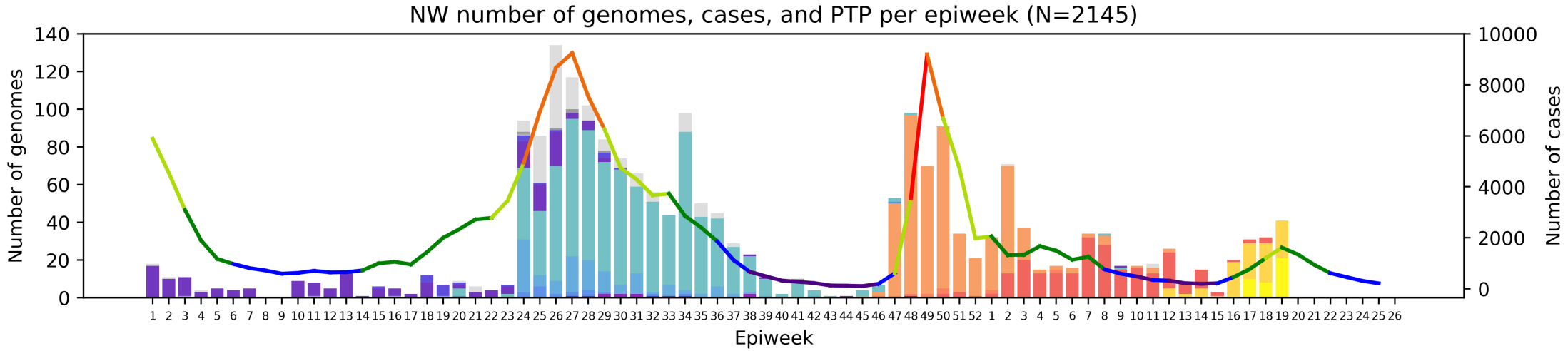
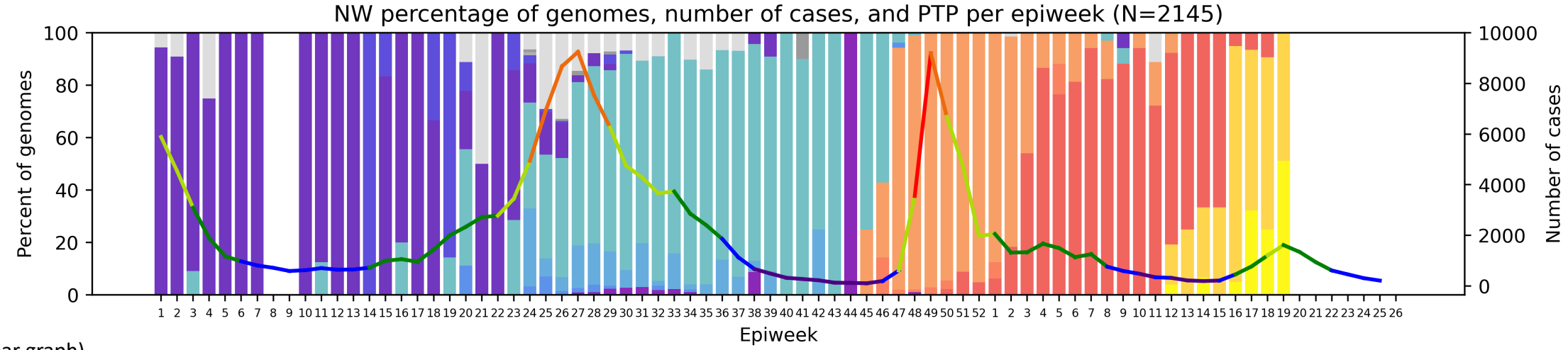
North West Province, 2021-2022, n = 2145





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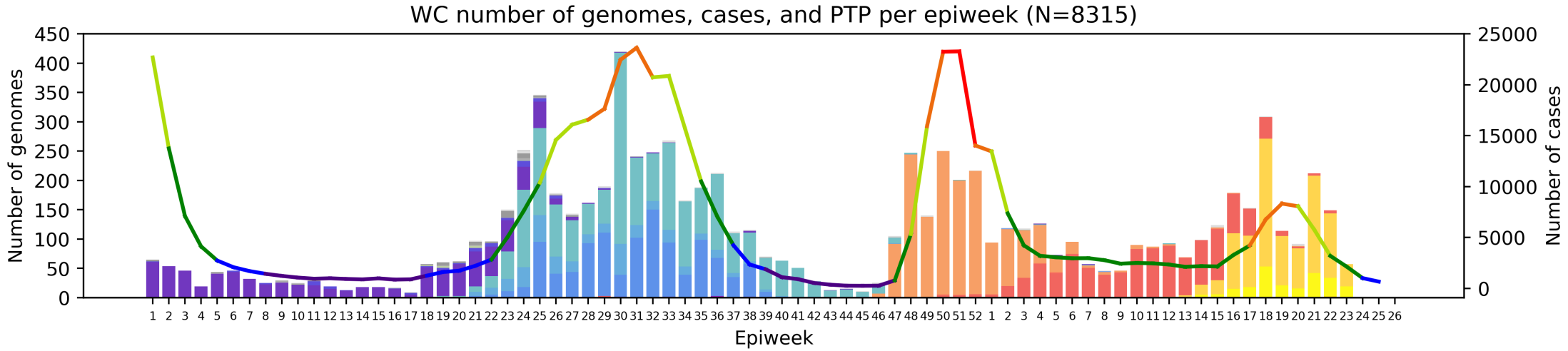
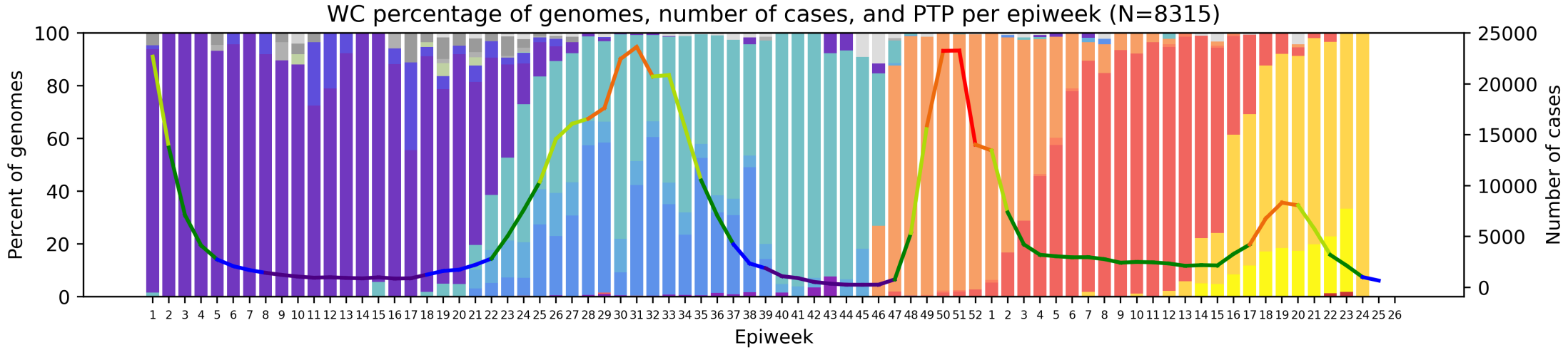
Western Cape Province, 2021-2022, n = 8315





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Summary

- **Variant of Concern Omicron in South Africa**
  - Dominates 2022 sequencing data at >98% of genomes.
  - While BA.1 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 (96%).
  - BA.2.12.1 was detected in South Africa at low prevalence in May and June (<1%)
- 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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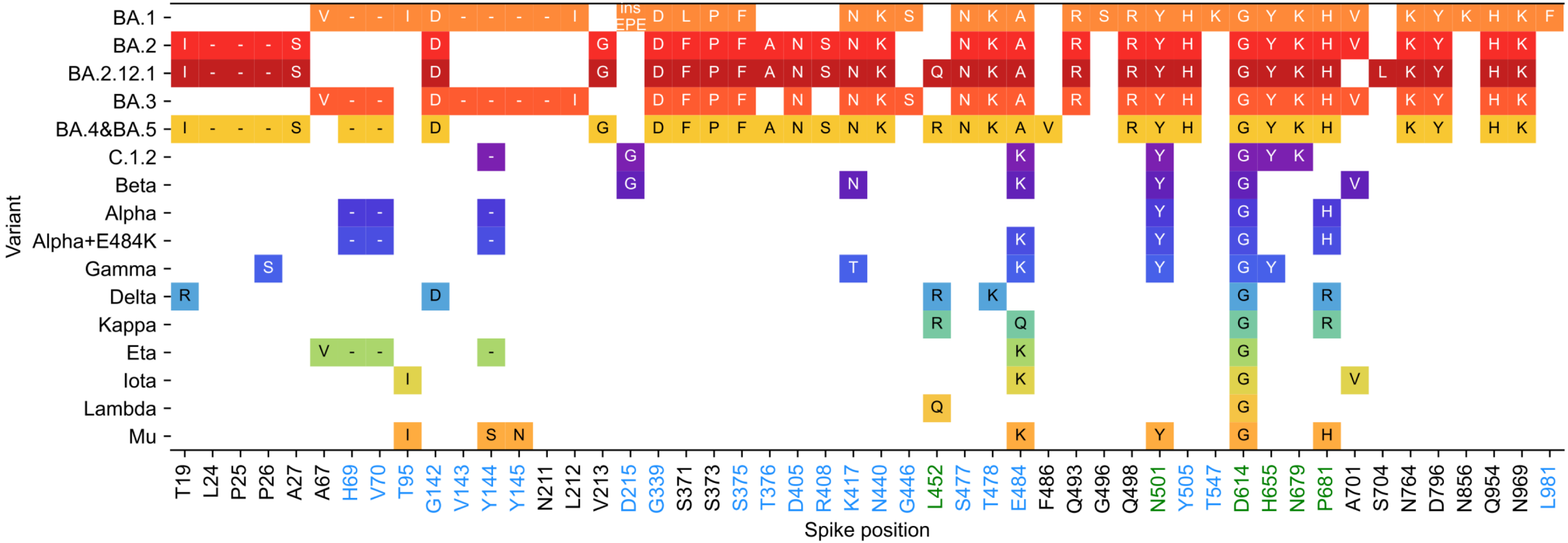
Omicron spike mutations compared to other VOC/VOIs



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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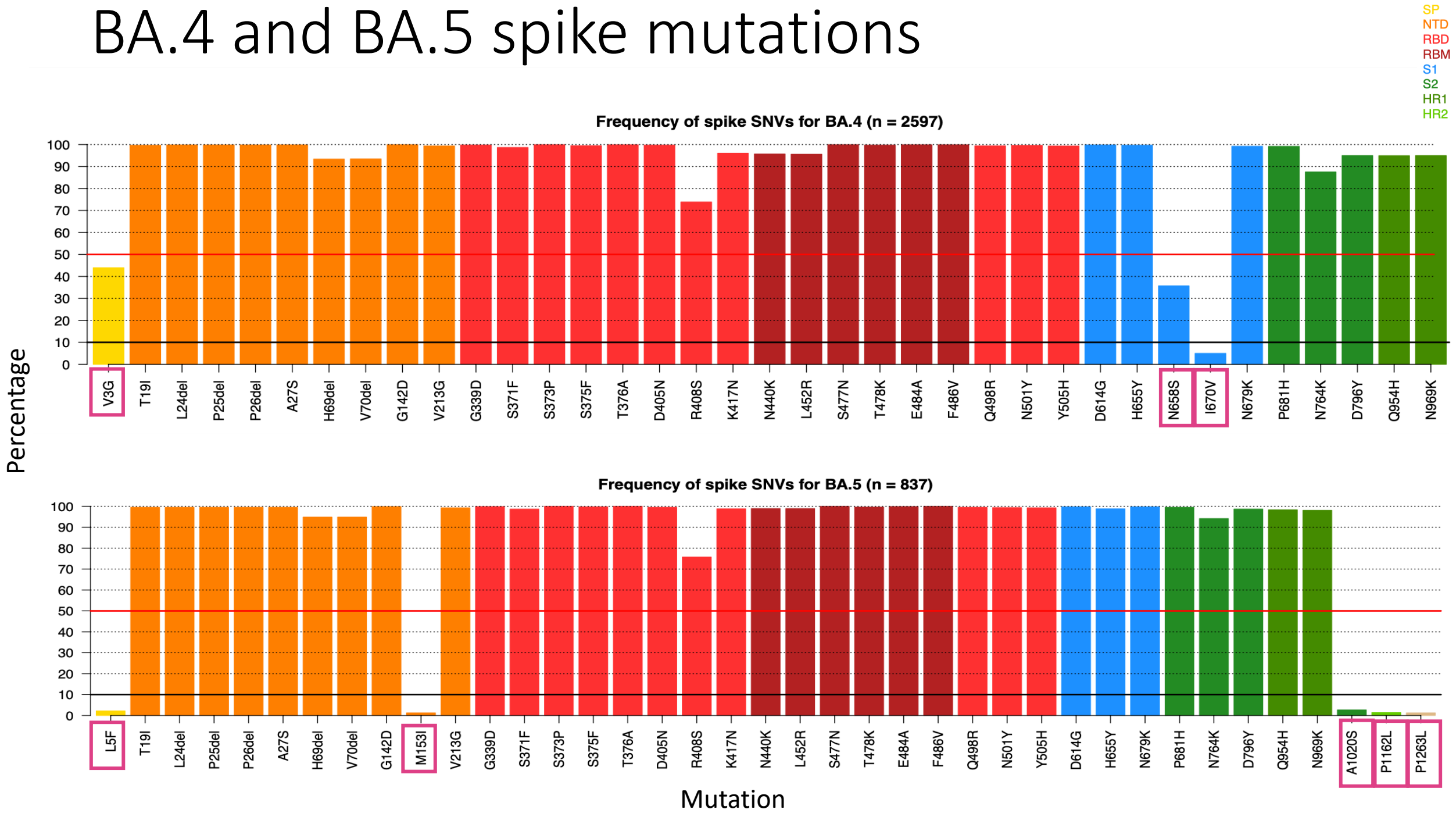
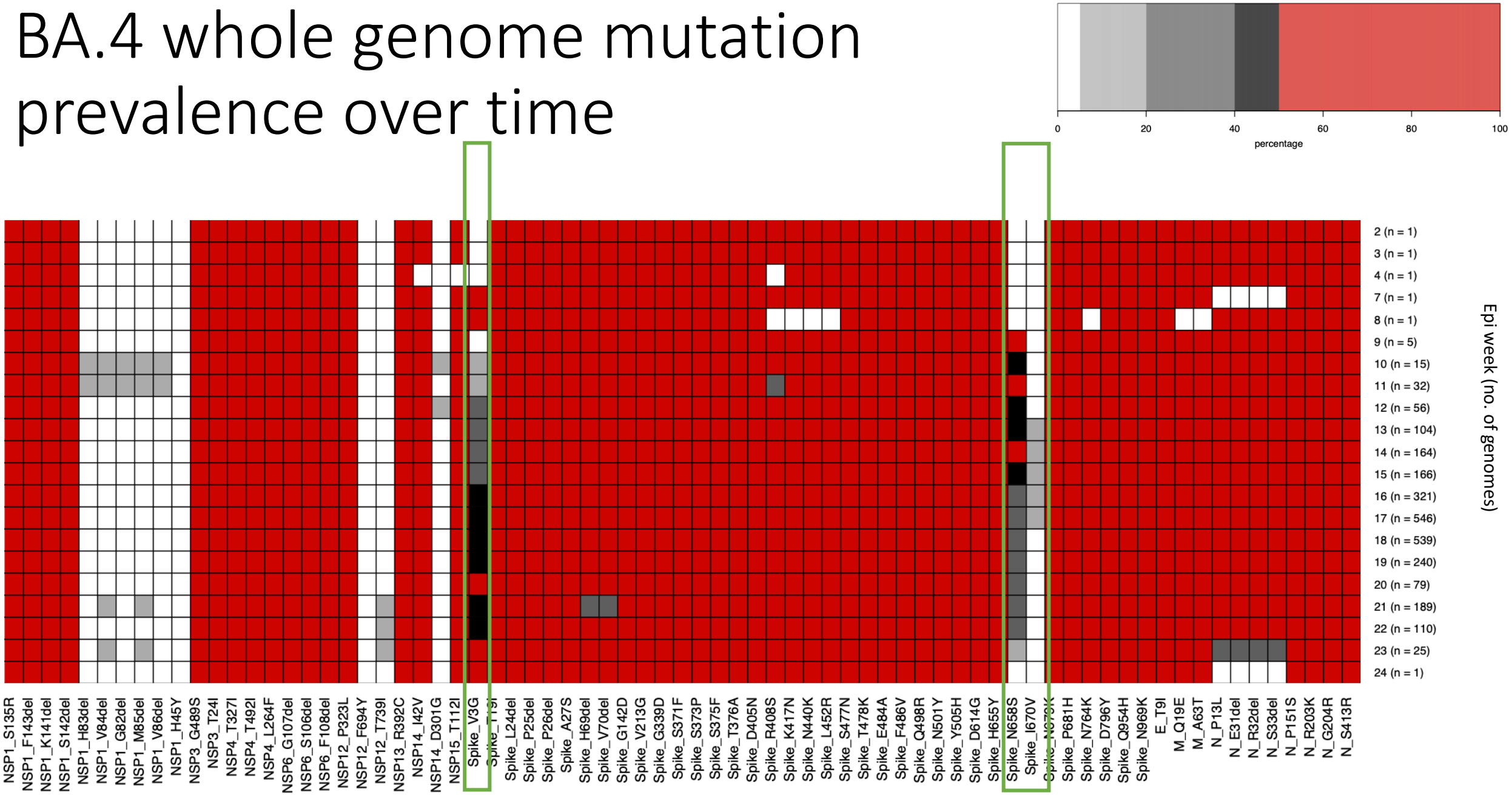
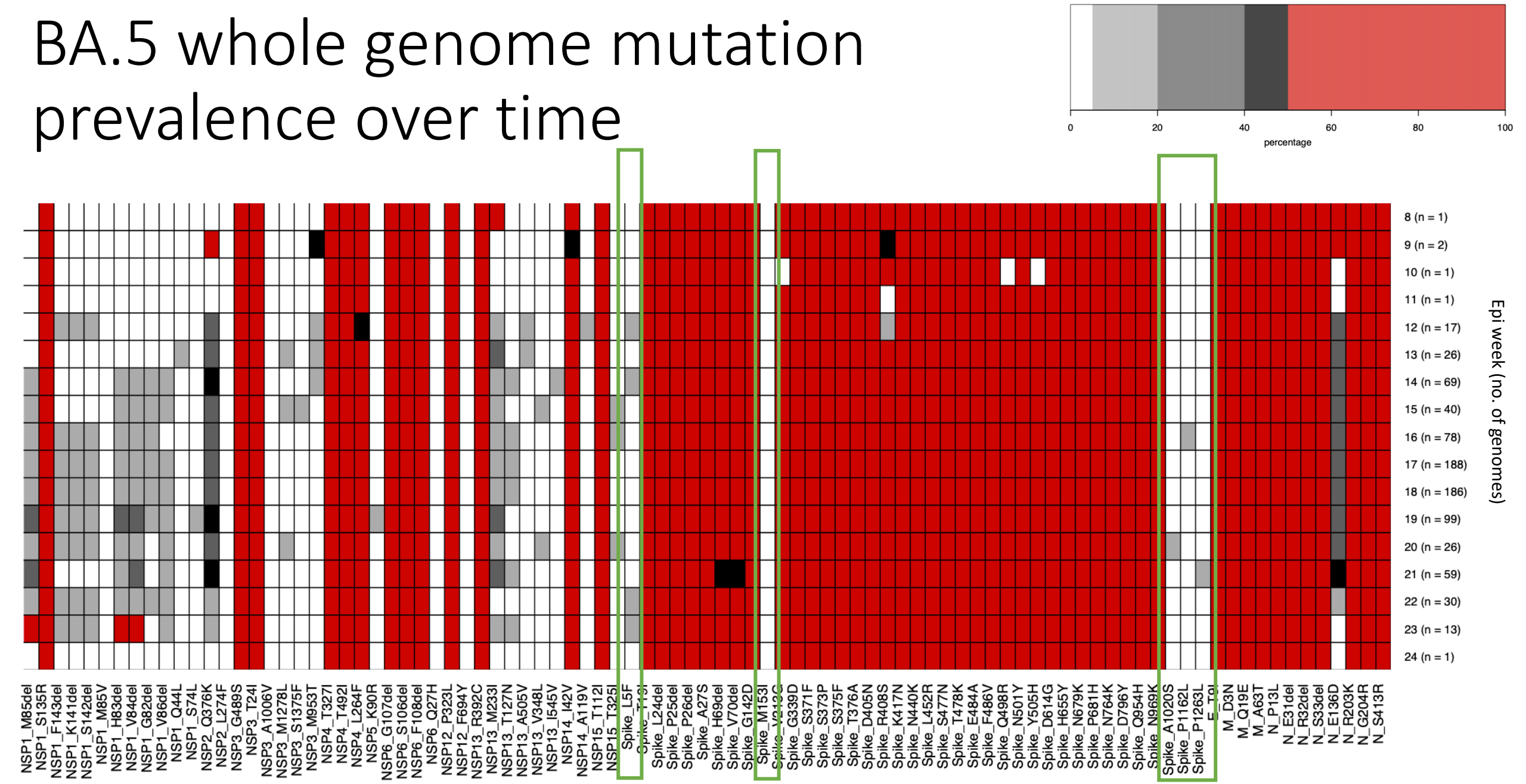
BA.4 and BA.5 spike mutations



BA.4 whole genome mutation prevalence over time



BA.5 whole genome mutation prevalence over time



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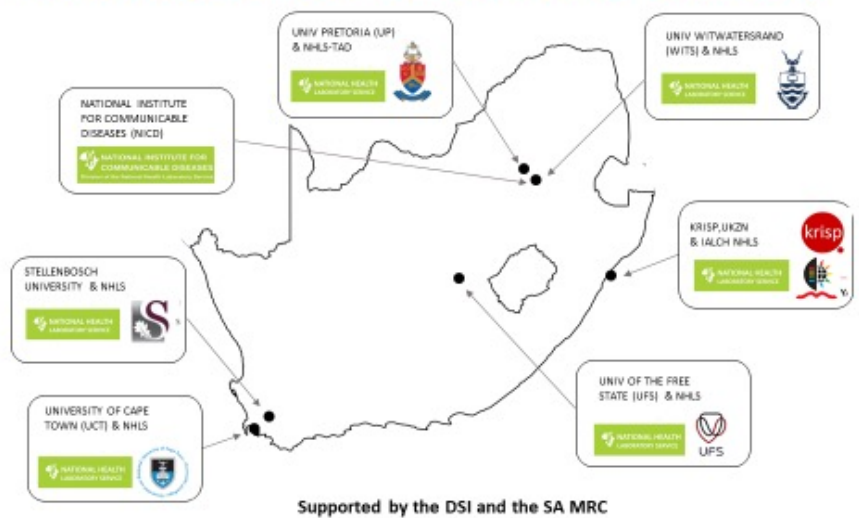

Supported by the DSI and the SA MRC

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saMRC advancinglife

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

EDCTP

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

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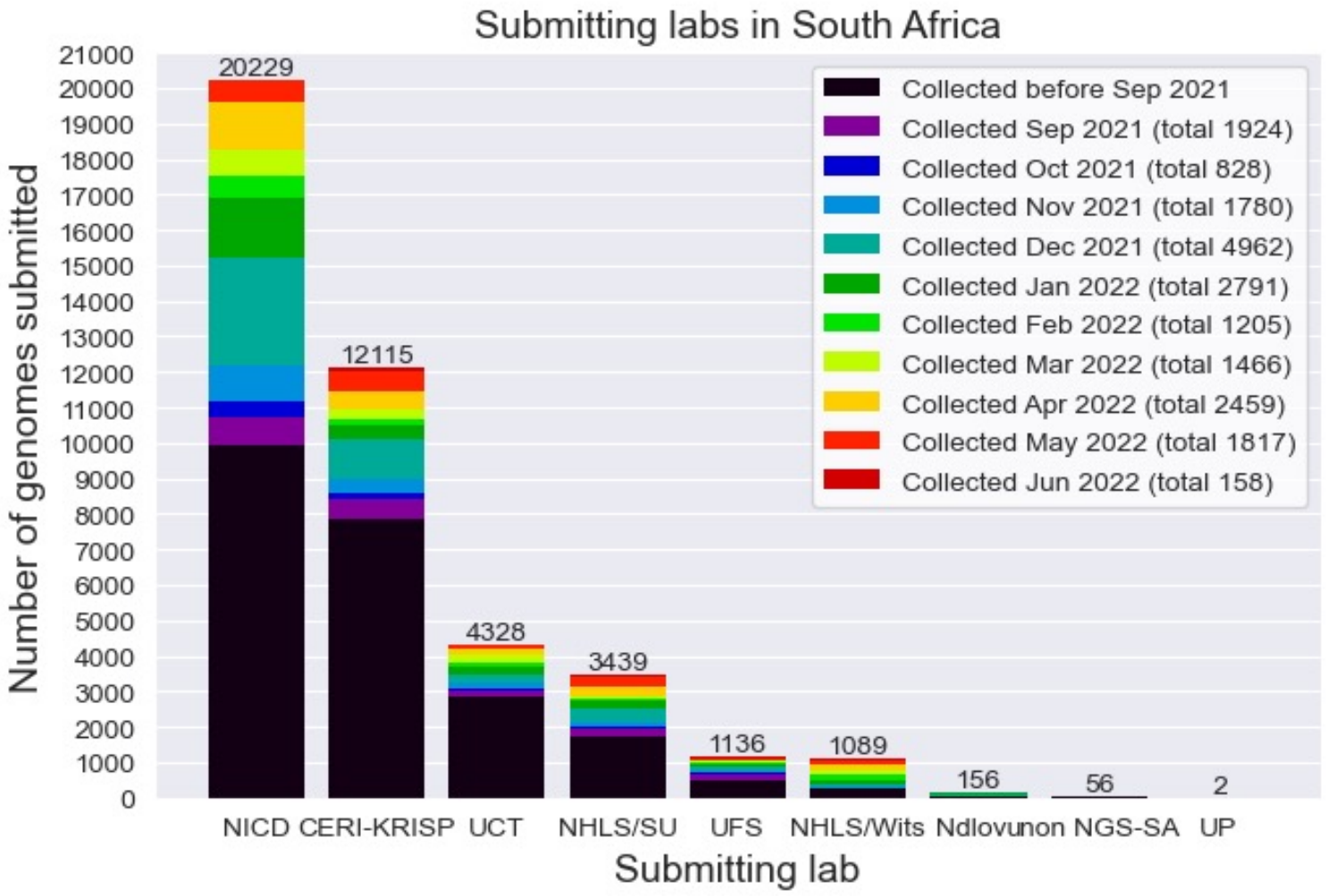
South African genomes submitted per submitting lab, 2020 - 2022 (N=42 550)



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.)