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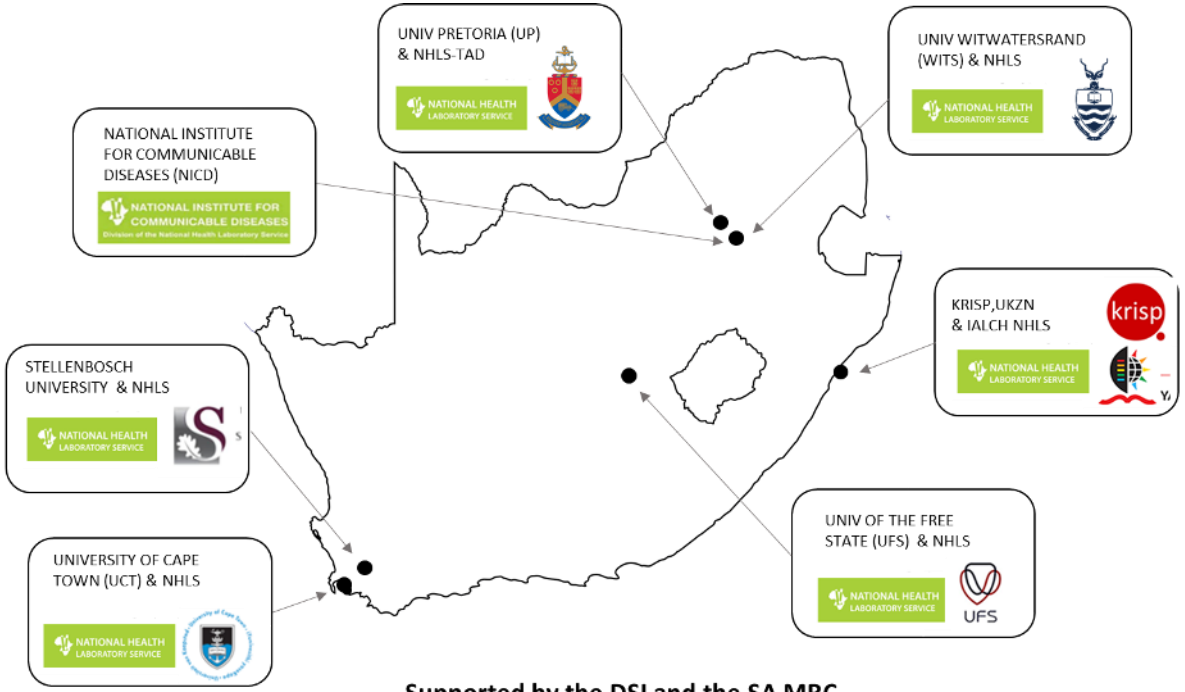
Network for Genomic Surveillance in South Africa

Network for Genomic Surveillance South Africa (NGS-SA)

SARS-CoV-2 Sequencing Update
19 August 2021



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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 19 August at 09h00

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

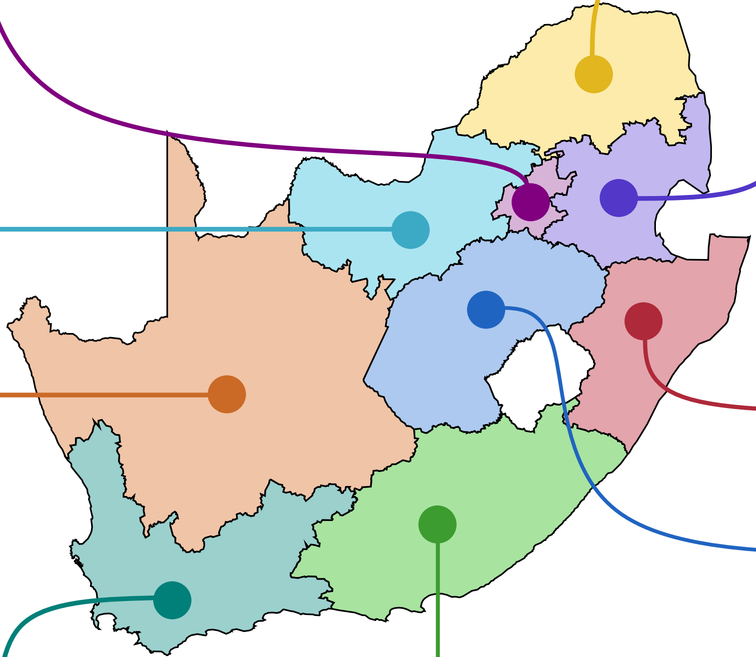
Elbe, S., and Buckland-Merrett, G. (2017) Data, disease and diplomacy: GISAID's innovative contribution to global health. Global Challenges, 1:33-46. DOI: 10.1002/gch2.1018 PMCID: 31565258

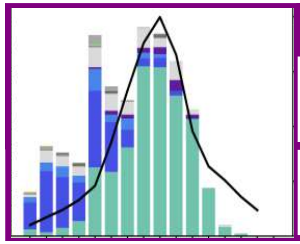
Shu, Y., McCauley, J. (2017) GISAID: Global initiative on sharing all influenza data – from vision to reality. EuroSurveillance, 22(13) DOI: 10.2807/1560-7917.ES.2017.22.13.30494 PMCID: PMC5388101

Case data is based on collection date. Case from https://www.nicd.ac.za/diseases-a-z-index/disease-index-covid-19/surveillance-reports/weekly-epidemiological-brief/

GENOMIC SURVEILLANCE IN THE THIRD WAVE

epiweeks 18 - 33



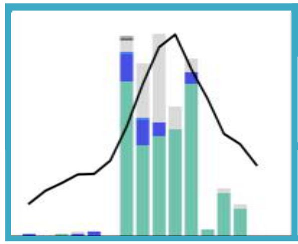


Gauteng

Genomes	Cases
2 033 (36.7%)	464 281 (45.5%)

Genomes deposited in the last week

🟦 11 🟦 26 🟩 195 🟪 9 ⬜ 1 ⬛ 6 ⬜ 15

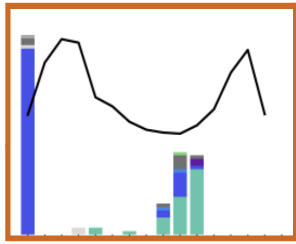


North West

Genomes	Cases
432 (7.8%)	68 246 (6.7%)

Genomes deposited in the last week

🟩 40 ⬜ 4

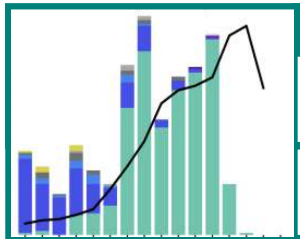


Northern Cape

Genomes	Cases
119 (2.1%)	32 324 (3.2%)

Genomes deposited in the last week

🟦 1 🟦 70 🟩 33 🟪 2 🟩 1 ⬛ 13 ⬜ 20

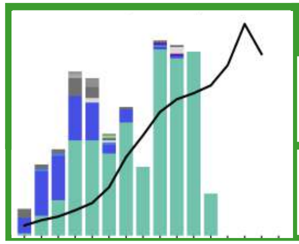


Western Cape

Genomes	Cases
759 (13.7%)	157 541 (15.5%)

Genomes deposited in the last week

🟦 3 🟩 69 🟪 1 ⬜ 1

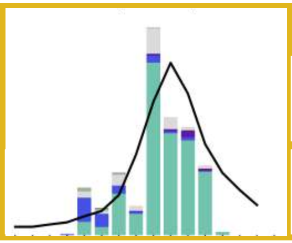


Eastern Cape

Genomes	Cases
639 (11.5%)	46 813 (4.6%)

Genomes deposited in the last week

🟦 1 🟦 5 🟩 219 🟩 1 ⬛ 2 ⬛ 4 ⬜ 2

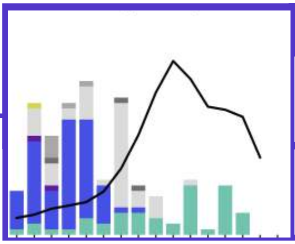


Limpopo

Genomes	Cases
668 (12.1%)	52 419 (5.1%)

Genomes deposited in the last week

🟦 3 🟩 120 🟪 10 ⬜ 6

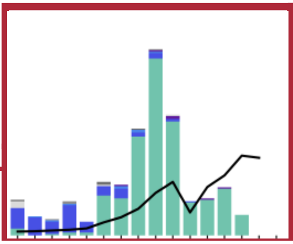


Mpumalanga

Genomes	Cases
179 (3.2%)	57 083 (5.6%)

Genomes deposited in the last week

🟦 40 🟩 14 ⬛ 1 ⬜ 6

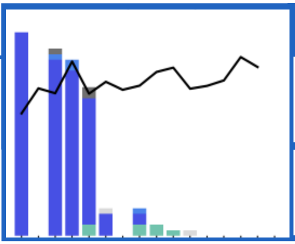


KwaZulu-Natal

Genomes	Cases
567 (10.3%)	93 945 (9.2%)

Genomes deposited in the last week

🟦 1 🟩 127 🟪 3 ⬜ 1



Free State

Genomes	Cases
144 (2.6%)	47 230 (4.6%)

Genomes deposited in the last week

- 🟦 Alpha (20I, V1)
- 🟦 Beta (20H, V2)
- 🟩 Delta (21A)
- 🟩 Kappa (21B)
- 🟨 Eta (21D)
- 🟪 C.1.2 (20D)
- ⬜ 20A
- ⬜ 20B
- ⬛ 20C
- ⬛ 20D
- ⬜ Unassigned
- — Cases

Bar graphs represent genomes sequenced per epiweek, line represents cases by collection date (weeks 18 – 33)
Genomes and cases presented as provincial total (percentage of national total)

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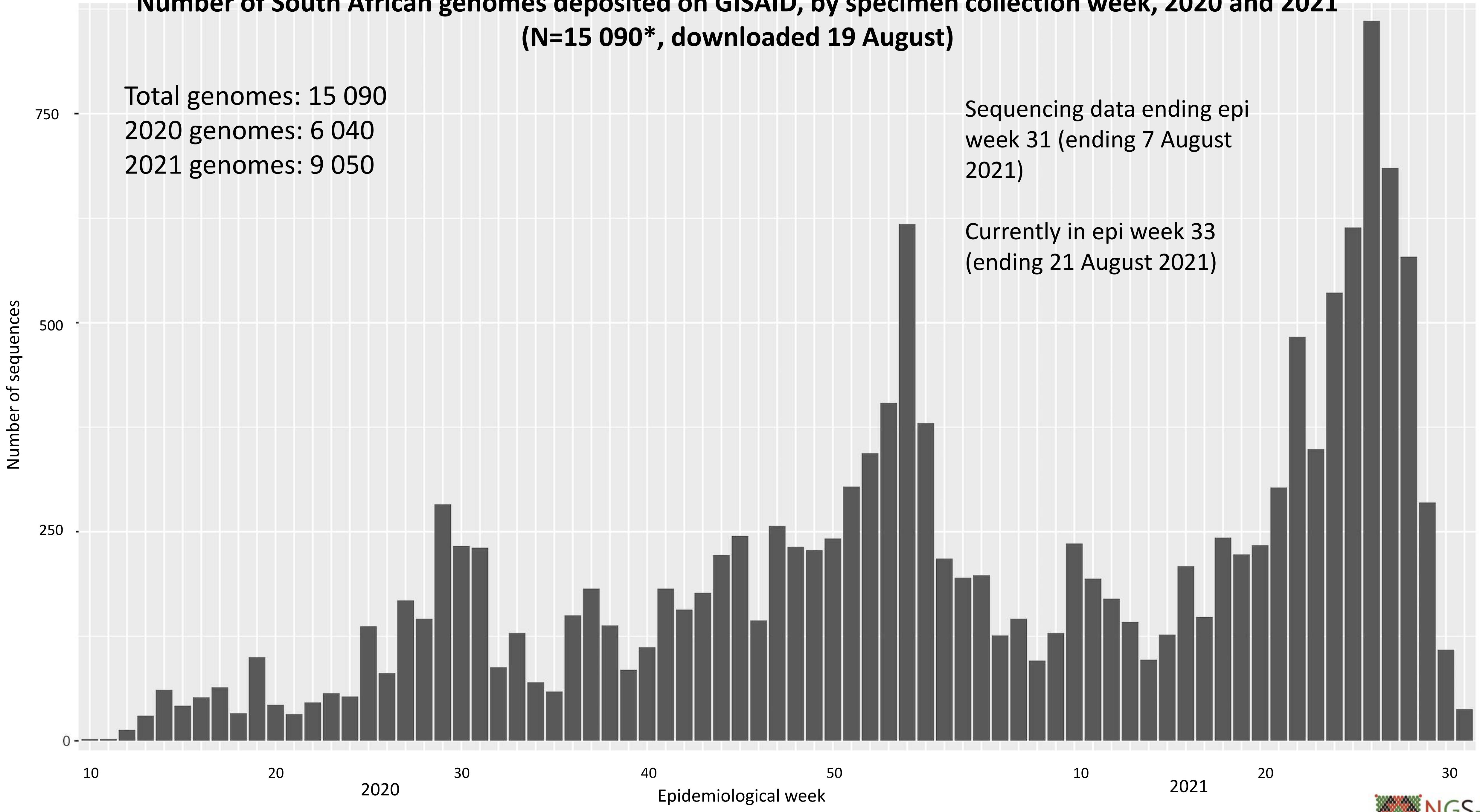
Number of South African genomes deposited on GISAID, by specimen collection week, 2020 and 2021 (N=15 090*, downloaded 19 August)



Total genomes: 15 090
2020 genomes: 6 040
2021 genomes: 9 050

Sequencing data ending epi week 31 (ending 7 August 2021)

Currently in epi week 33 (ending 21 August 2021)

*This represents the cleaned, de-duplicated dataset of unique sequences. This dataset will be used for all further figures.

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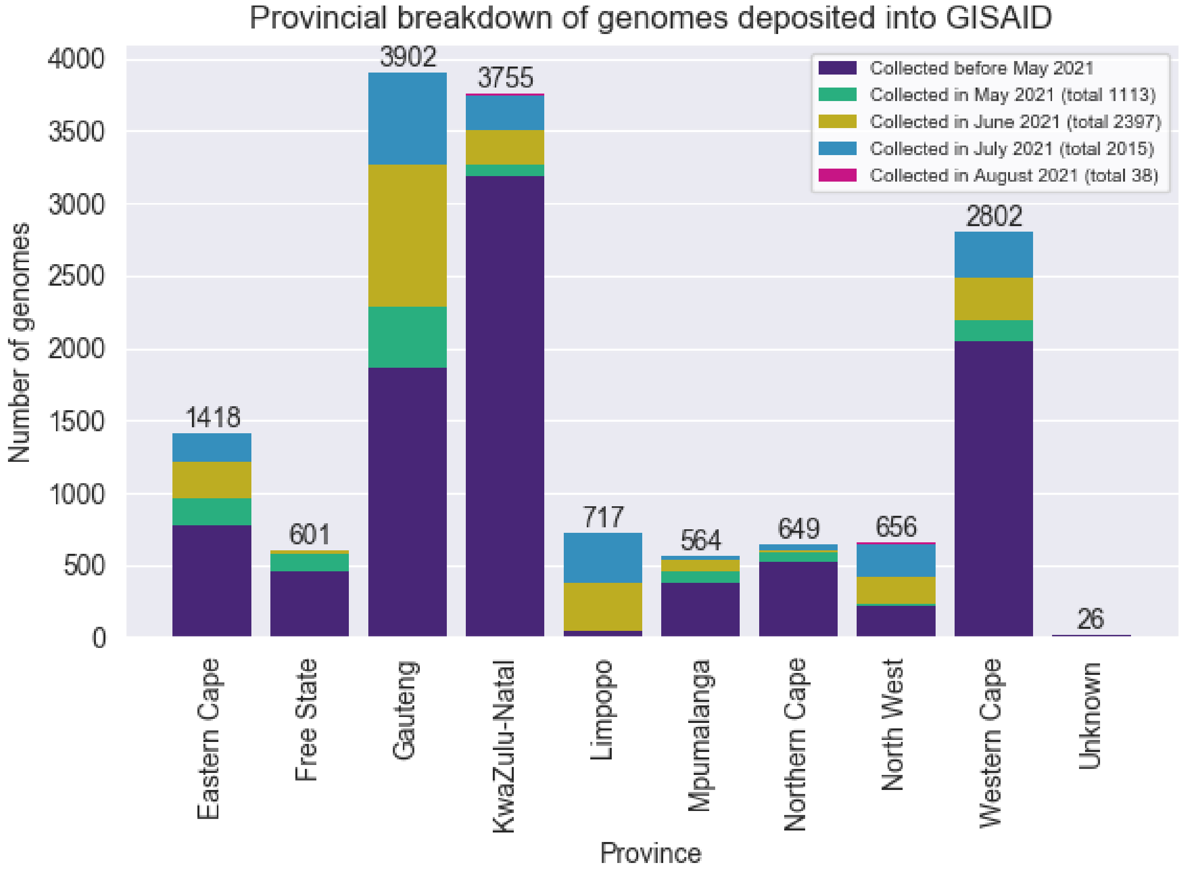
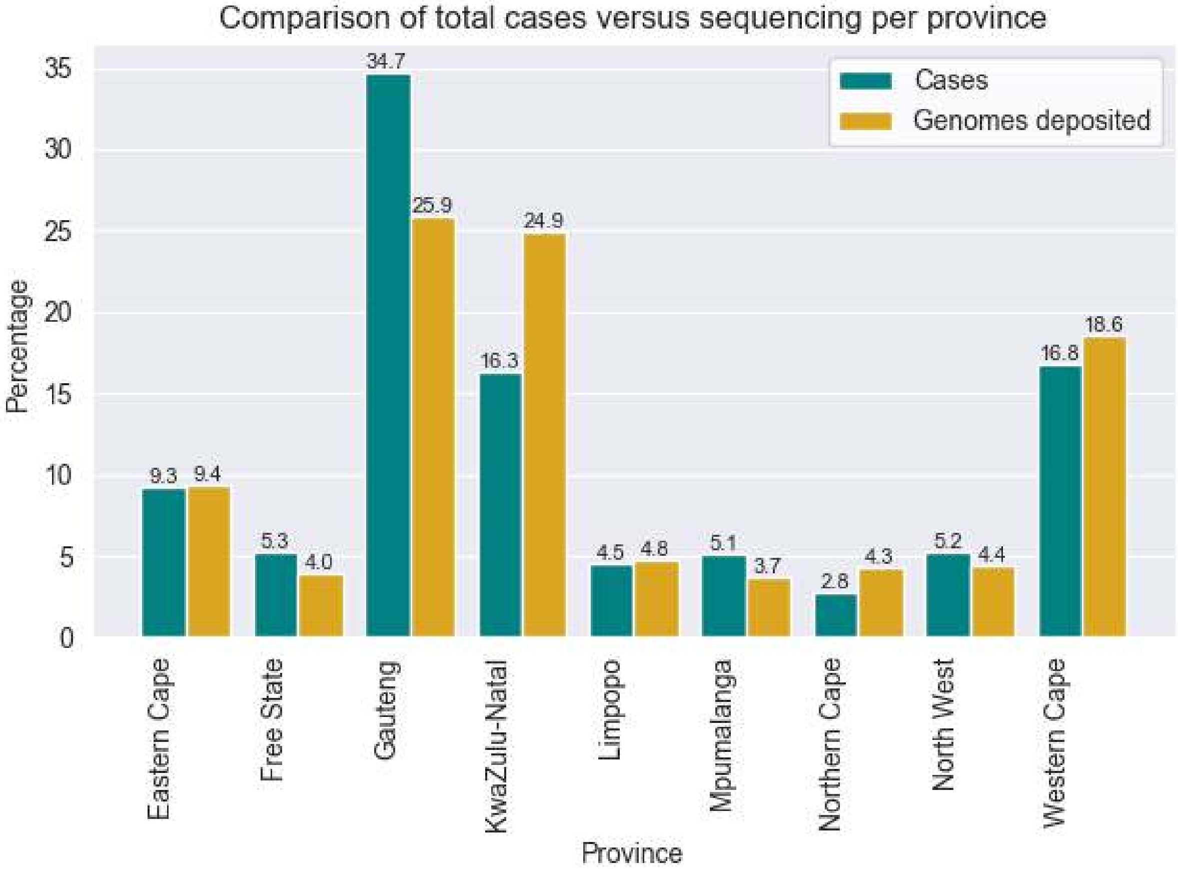
GISAID genomes vs total cases, 2020 and 2021 (N=15 090)





All provinces, apart from GP and KZN, have comparable percentage of overall cases and overall sequenced genomes

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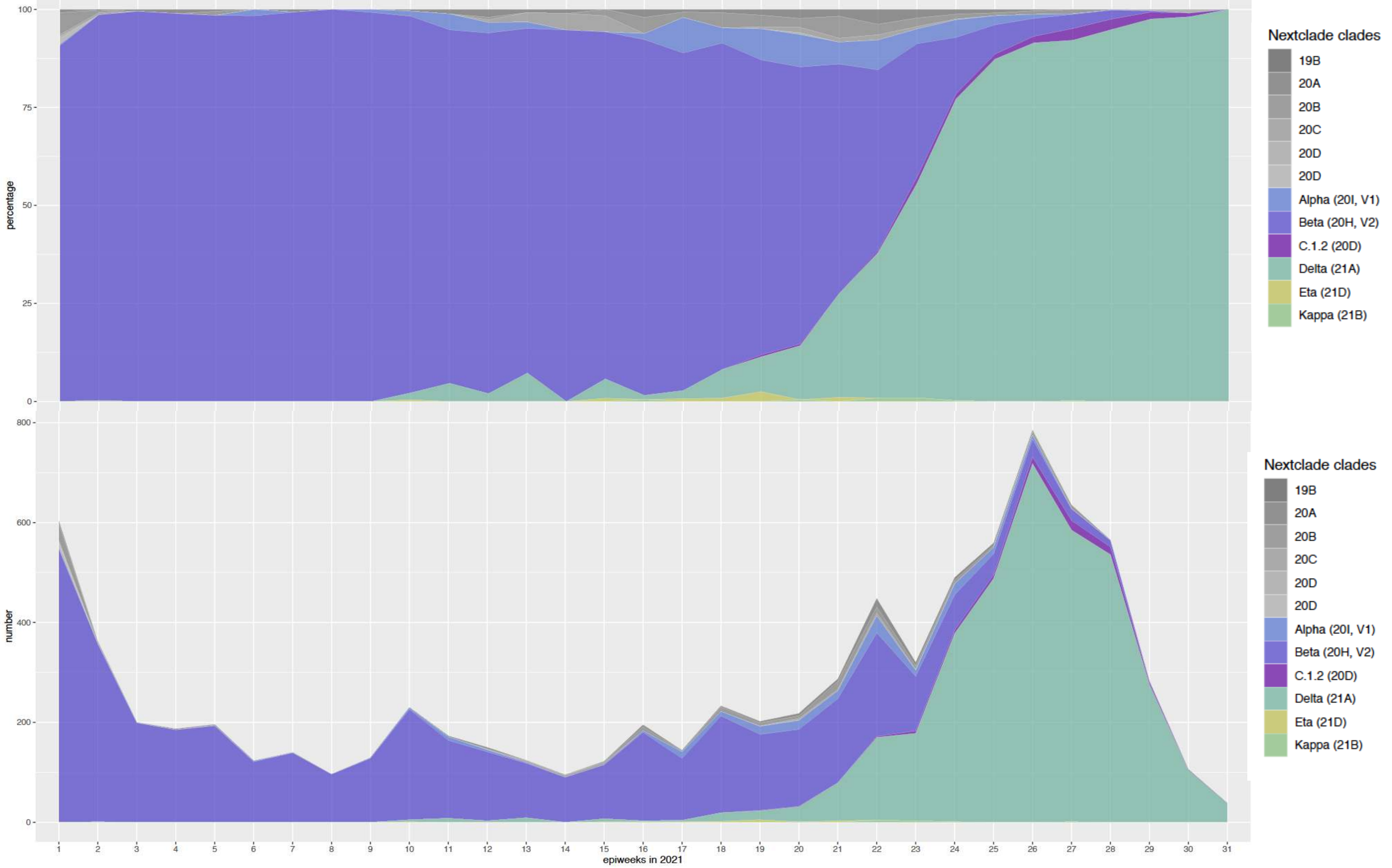
Distribution and number of clades in South Africa, 2021 (N=9050)

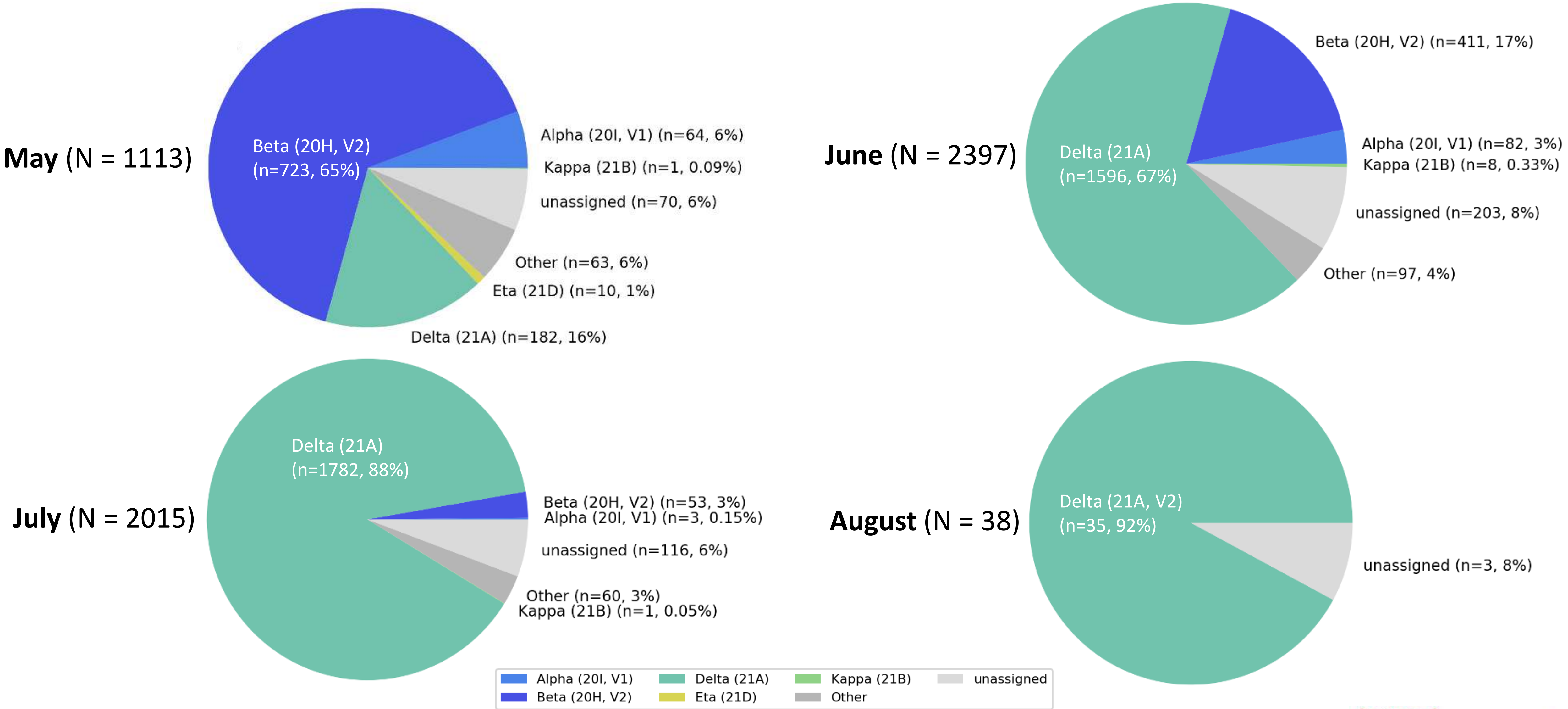


Sequencing data ending epi week 31 (ending 7 August 2021)

Currently in epi week 33 (ending 21 August 2021)

While Alpha, Delta and Eta variant frequency increased from the beginning of May, Delta came to dominate by end June at >75% and in July at >85%

Prevalence of Variants of Concern (VOC) and Variants of Interest (VOI) in May – August 2021 sequences, South Africa



Beta variant dominated in May, while the Delta variant dominated in June and July in South Africa

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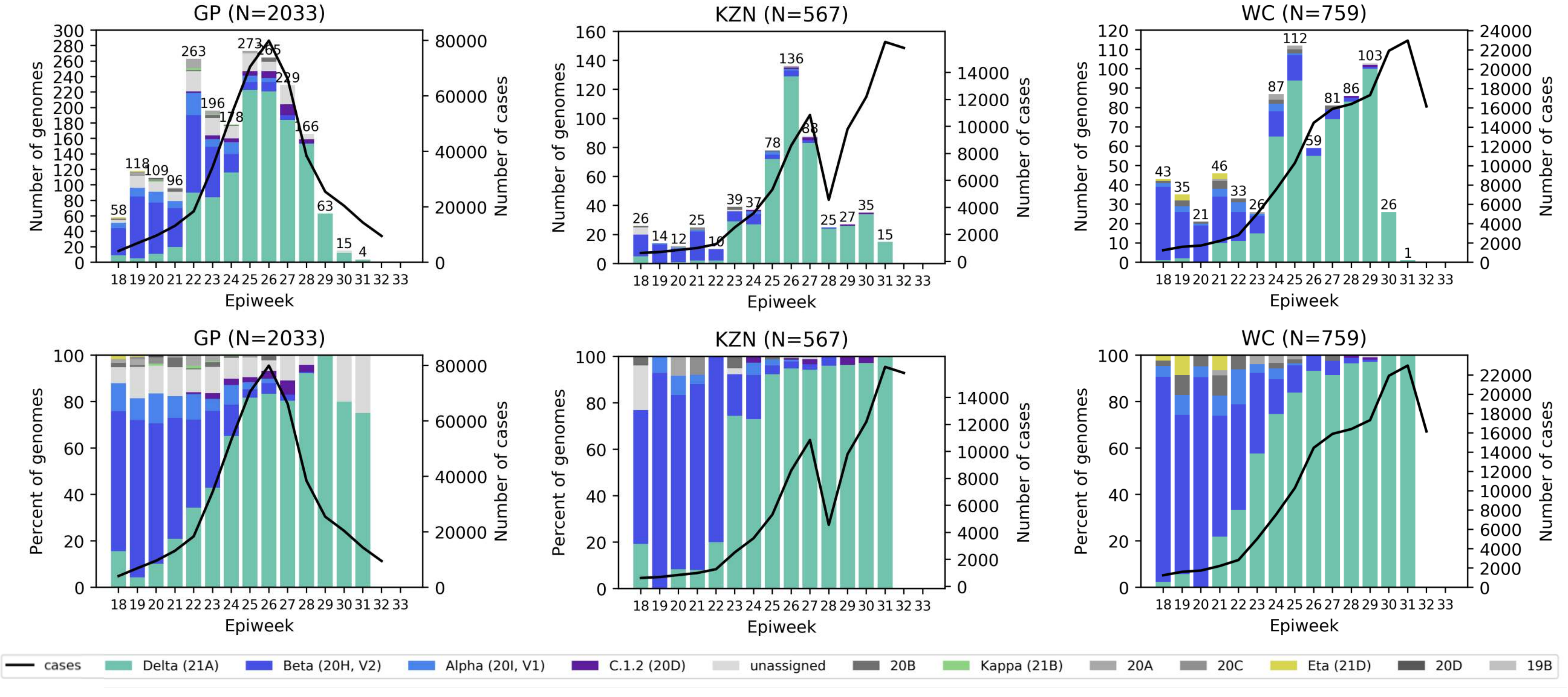
Genomes sequenced from specimens collected in May – mid-August 2021 (epiweeks 18 – 33) from KwaZulu-Natal, Gauteng, Western Cape Provinces



Beta dominates in all provinces in May, however following its detection in week 18, Delta rapidly begins to dominate in all three provinces by mid-June

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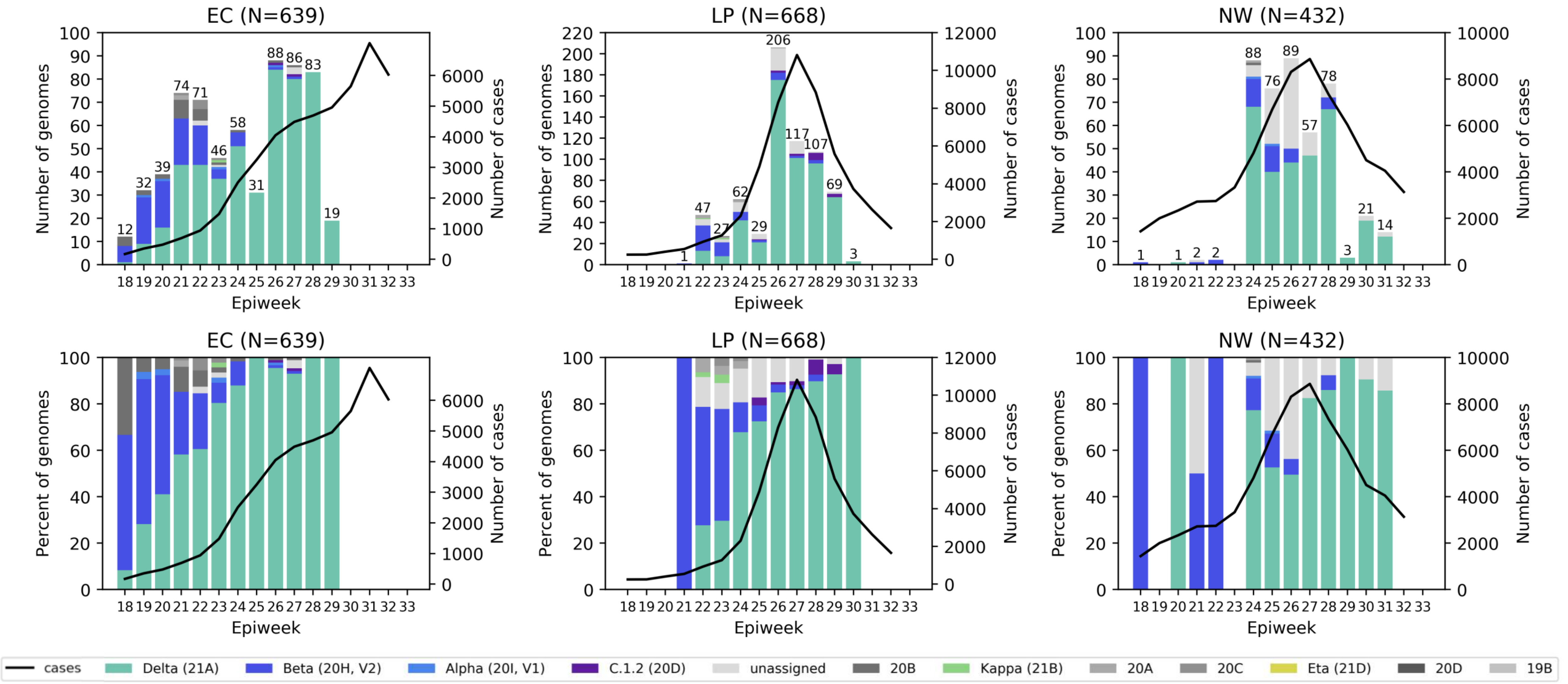
Genomes sequenced from specimens collected in May – mid-August 2021 (epiweeks 18 – 33) from Eastern Cape, Limpopo and North-West Provinces



Delta variant dominating in Eastern Cape, Limpopo and North-West Provinces

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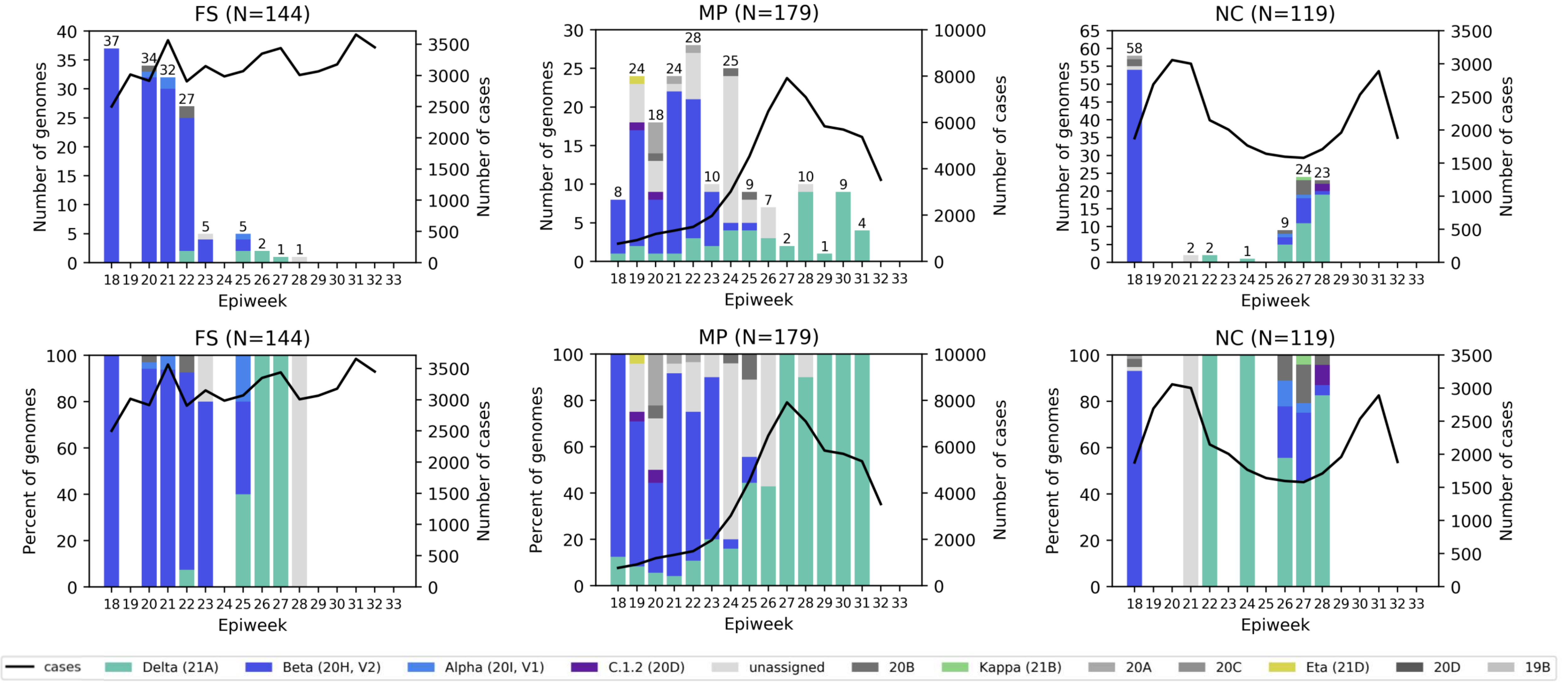
Genomes sequenced from specimens collected in May – mid-August 2021 (epiweeks 18 – 33) from Free State, Mpumalanga and Northern Cape Provinces



Recent data outstanding, specimens currently being sequenced to estimate the dominance of Delta

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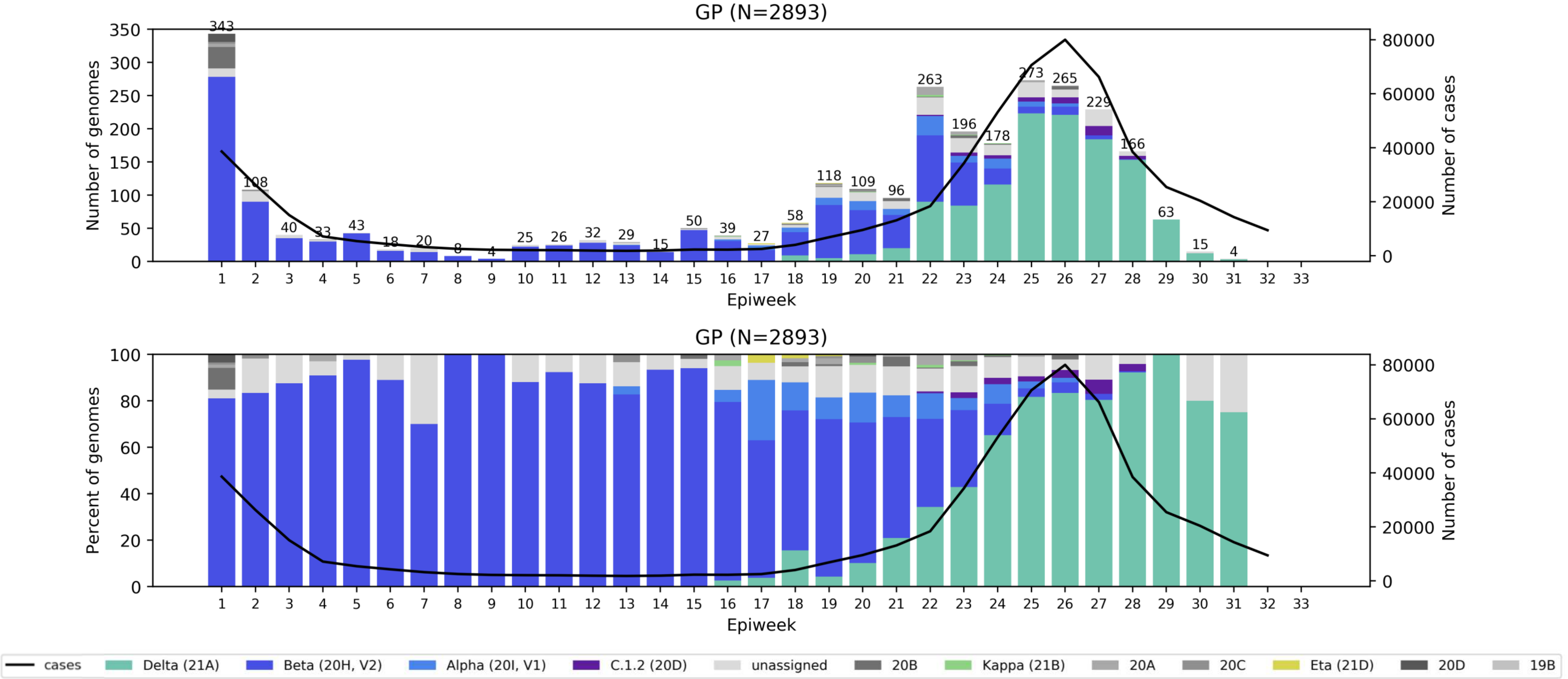
Gauteng Province, 2021, n = 2893



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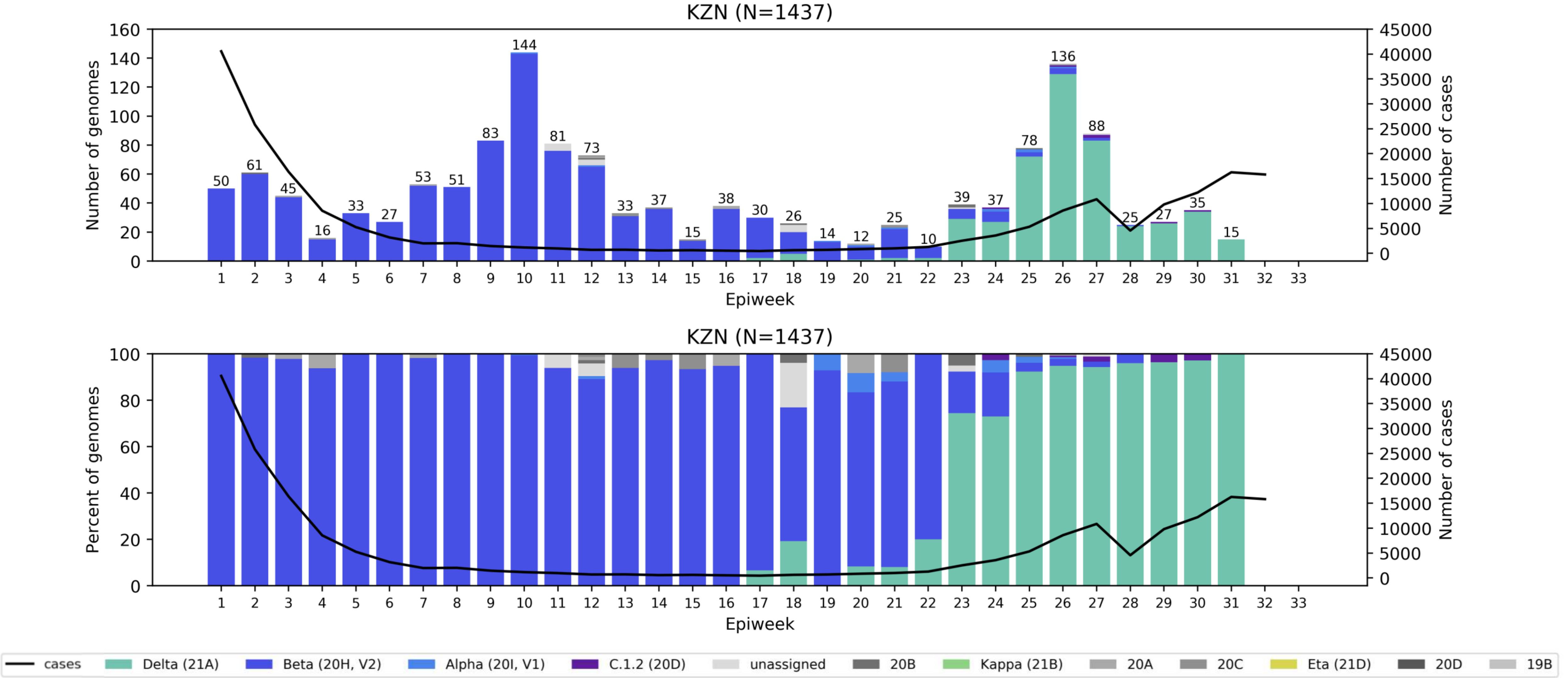
KwaZulu-Natal Province, 2021, n = 1437



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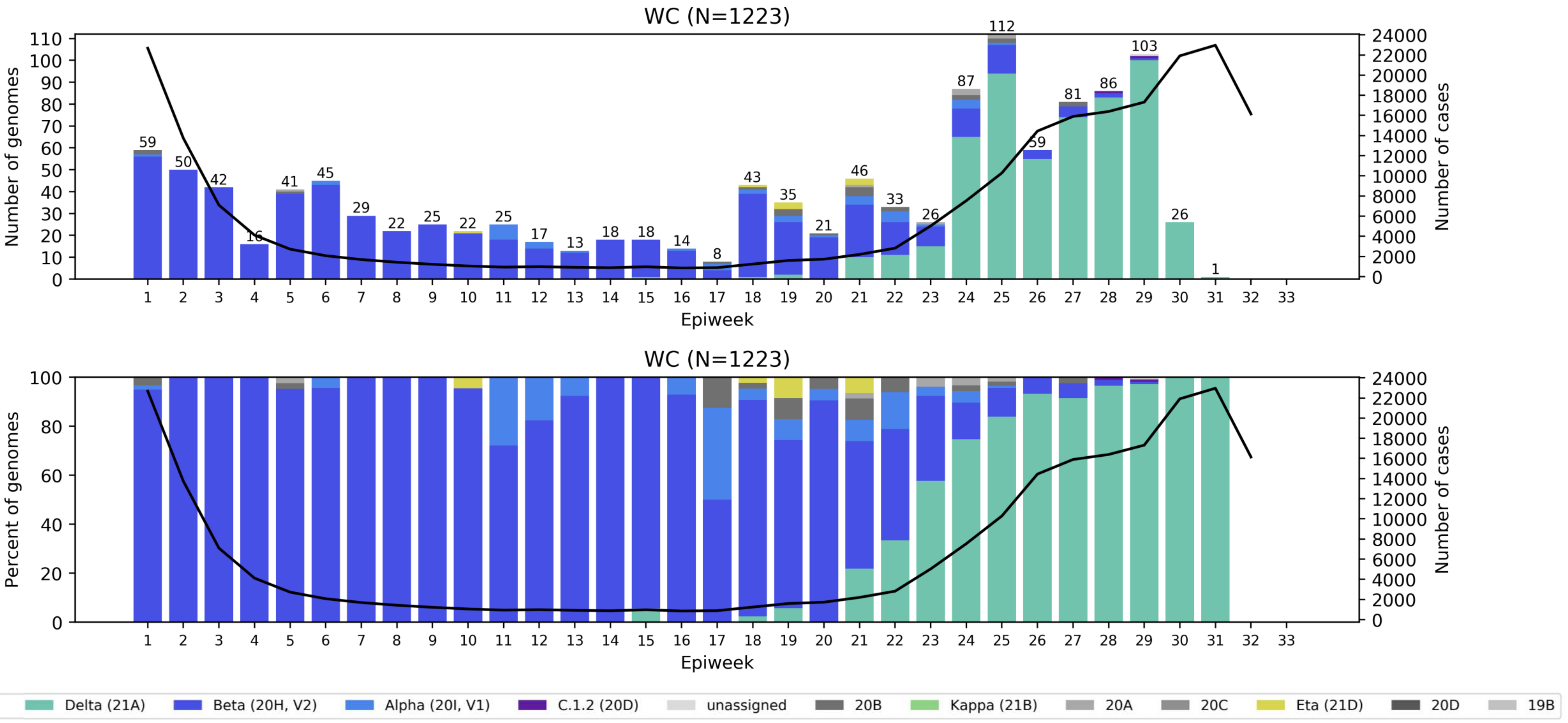
Western Cape Province, 2021, n = 1223



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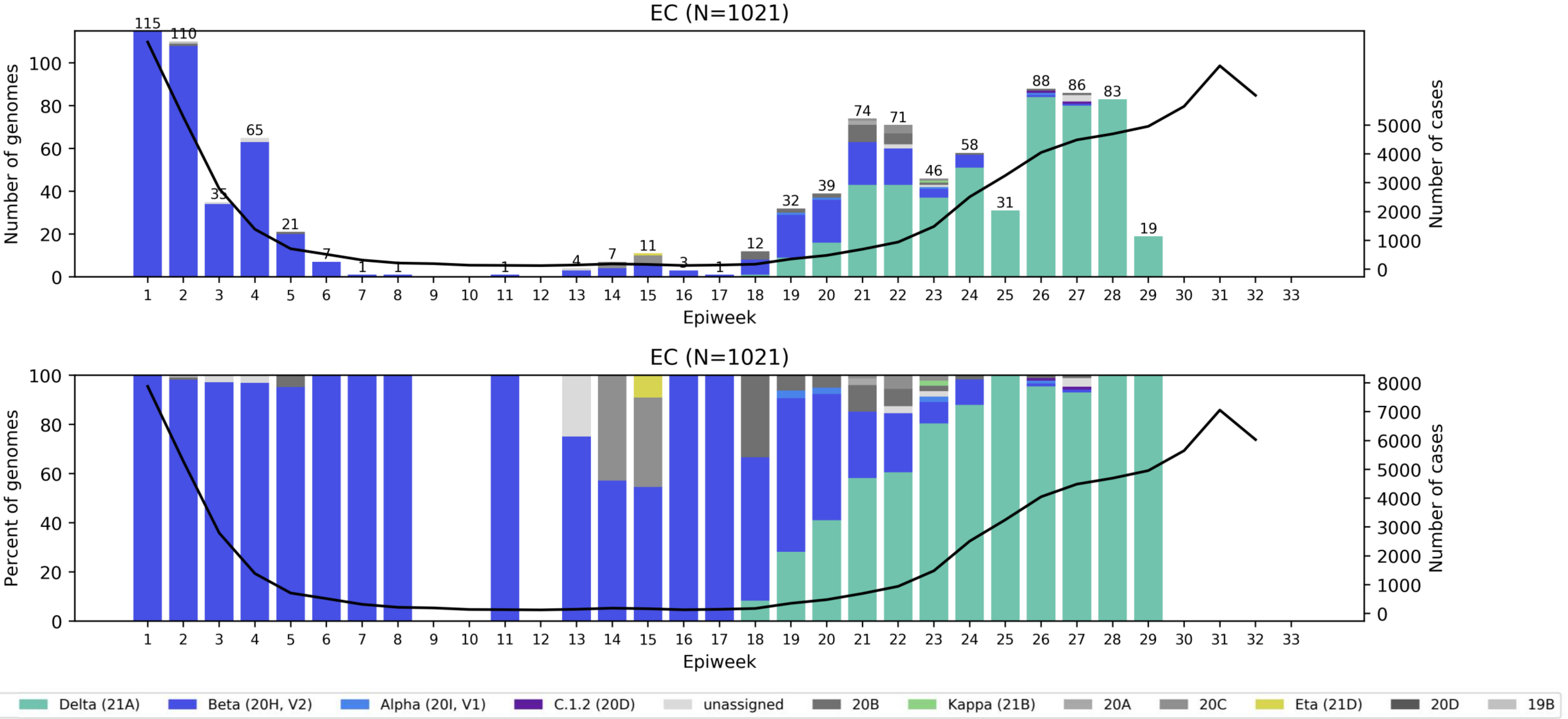
Eastern Cape Province, 2021, n = 1021



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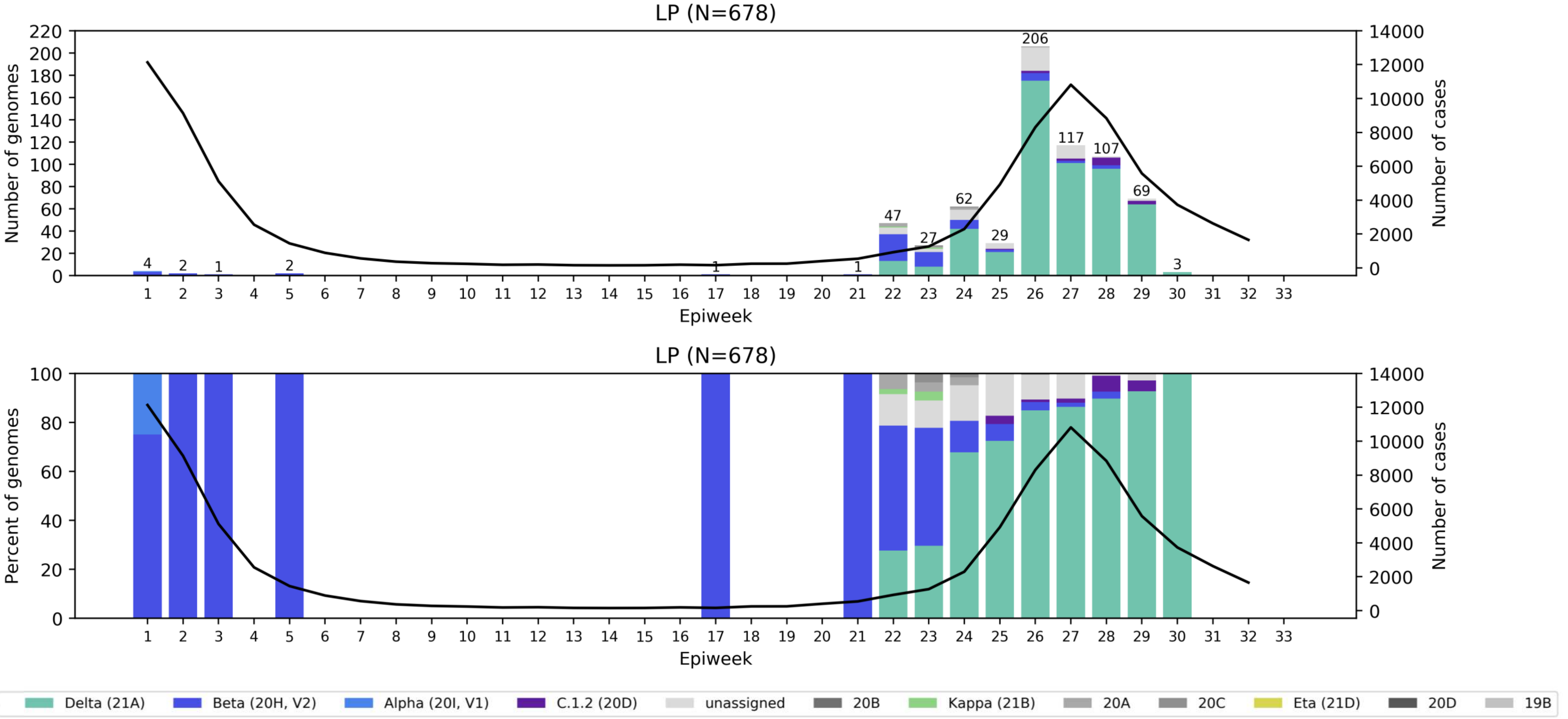
Limpopo Province, 2021, n = 678


LP (N=678)

LP (N=678)

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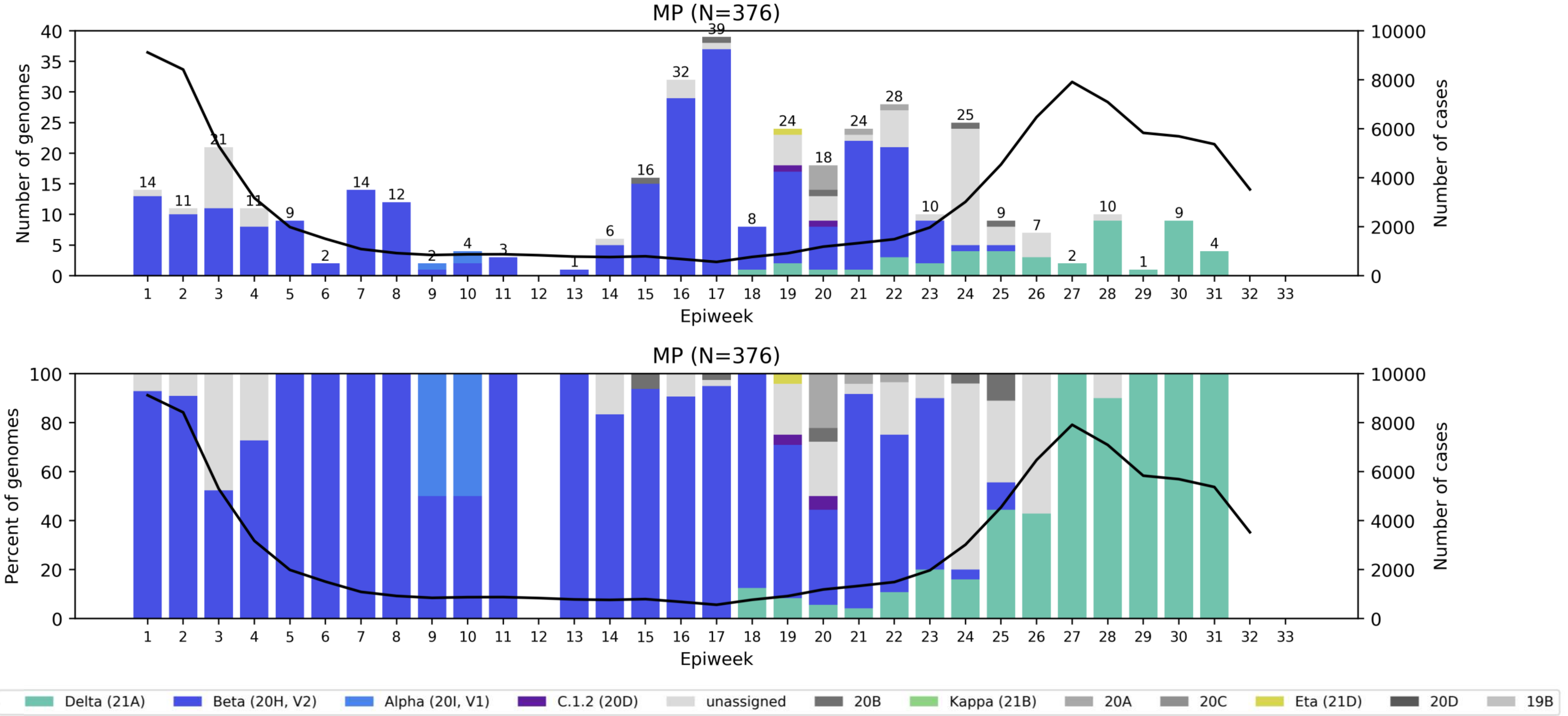
Mpumalanga Province, 2021, n = 376



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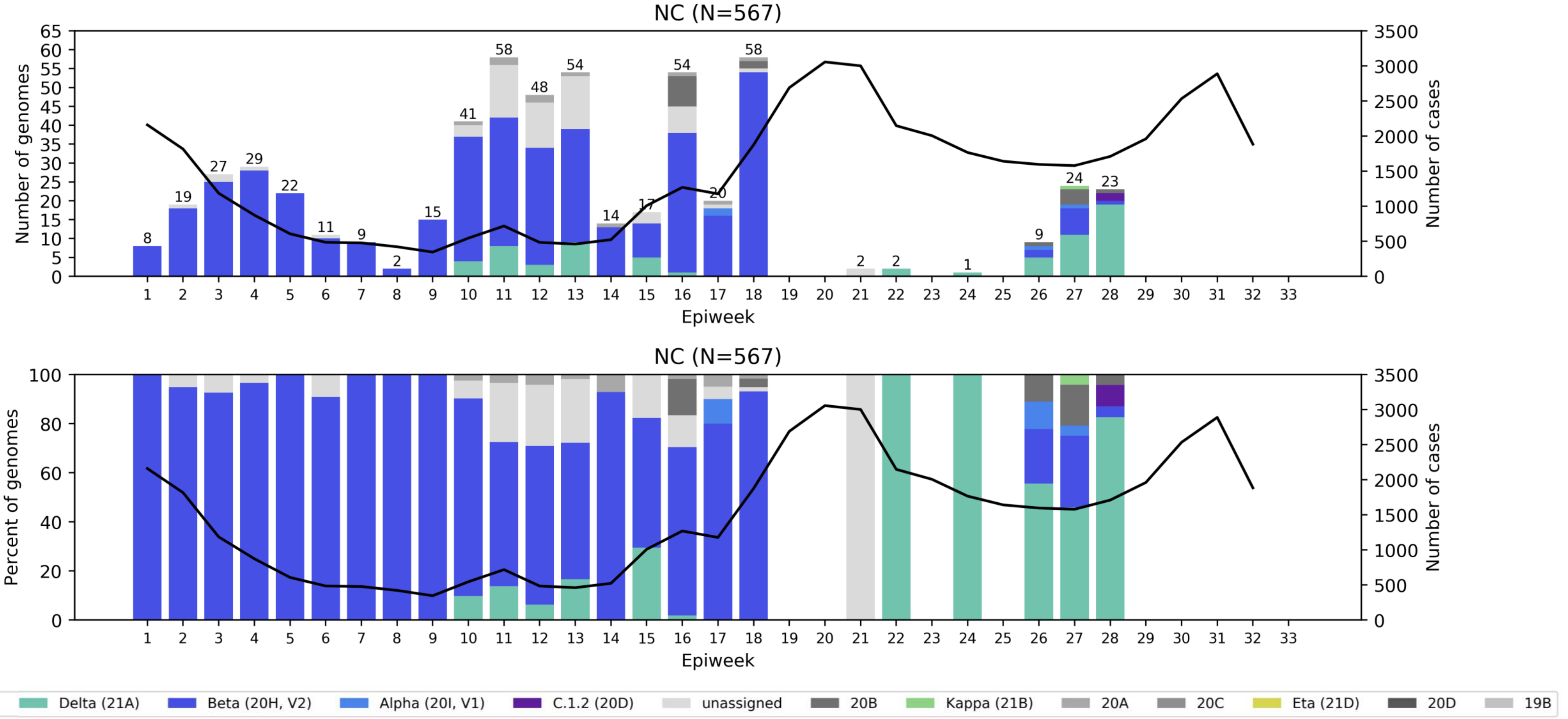
Northern Cape Province, 2021, n = 567



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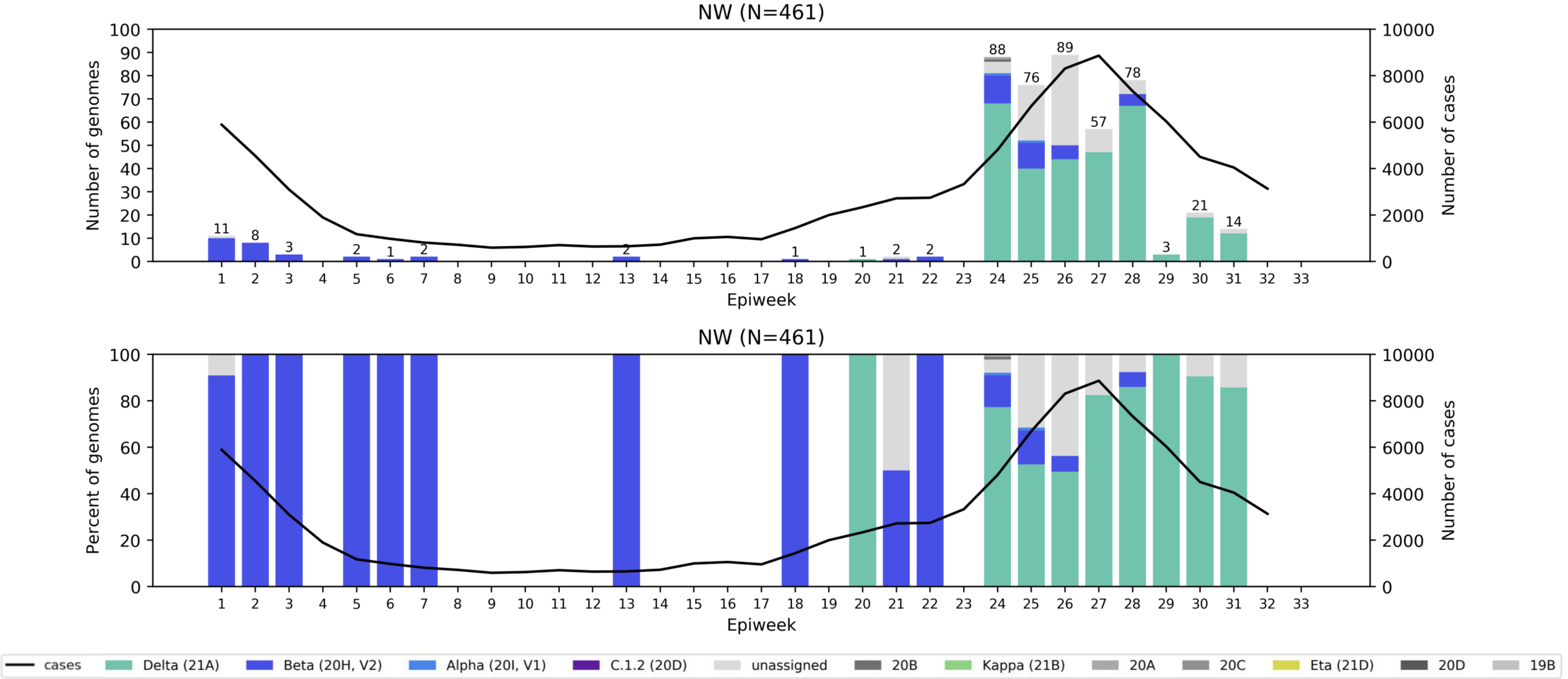
North West Province, 2021, n = 461



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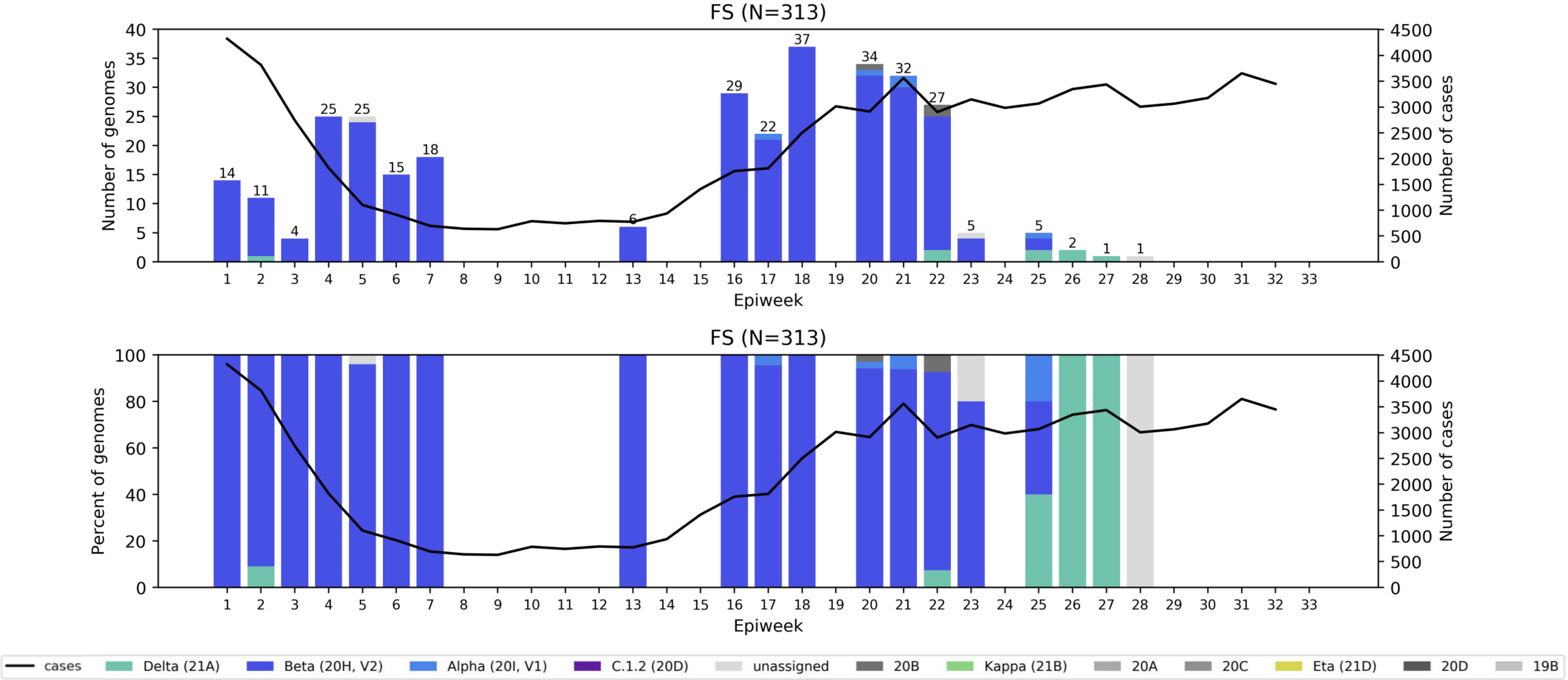
Free State Province, 2021, n = 313



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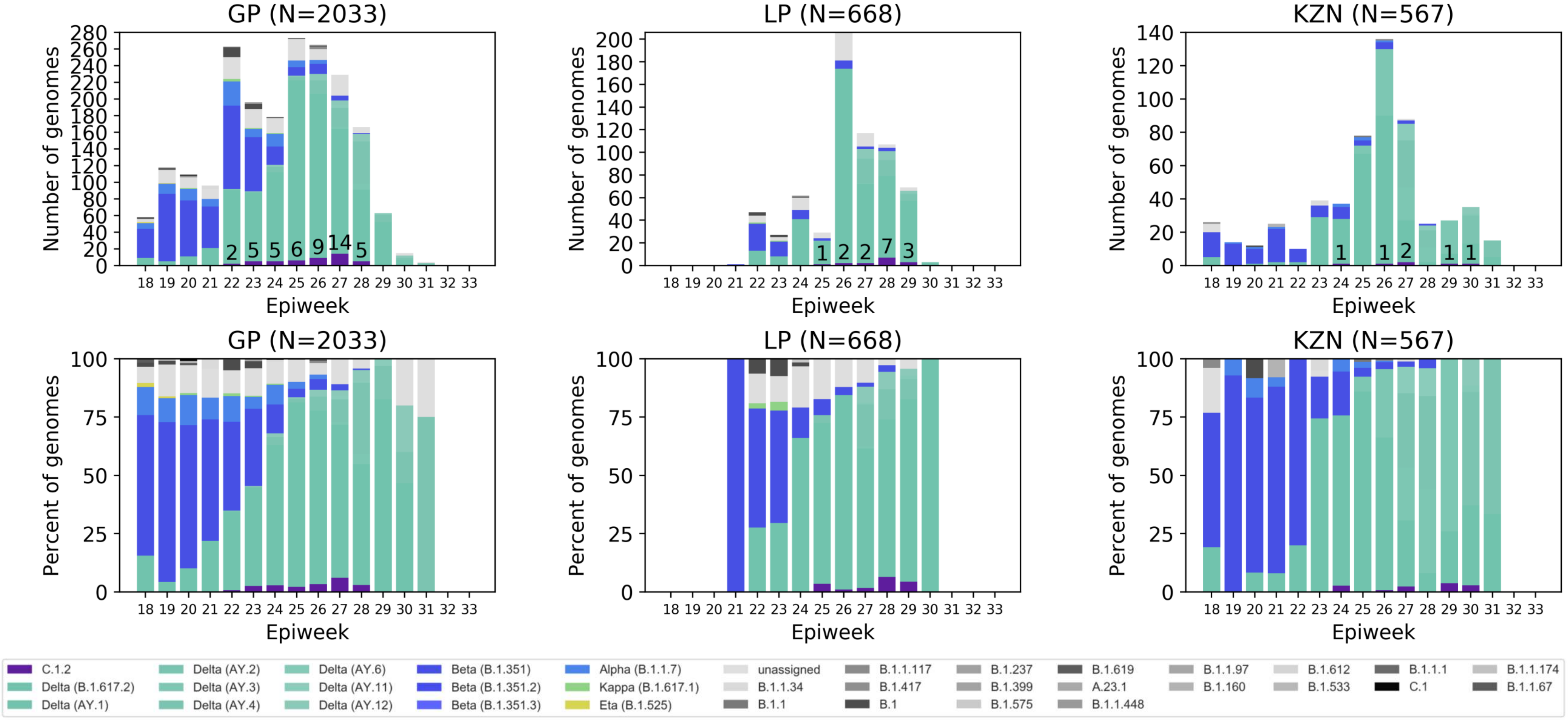
C.1.2 (n=75 in SA) in May – mid-August 2021 by epiweek

Number of C.1.2 samples indicated above bar



C.1.2 has now been detected in seven provinces. The majority of samples have been detected in Gauteng (n=46), followed by Limpopo (n=15) and KwaZulu-Natal (n=6).

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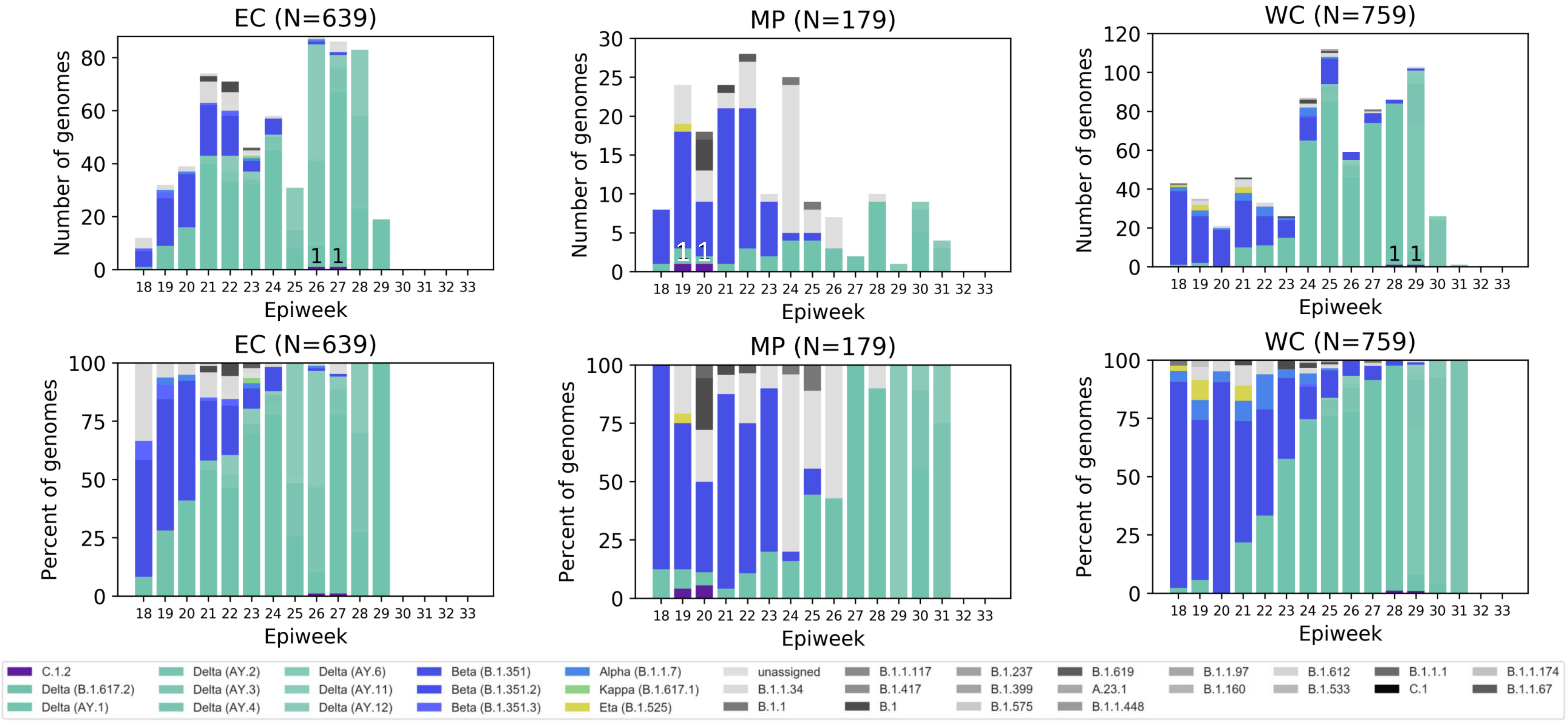
C.1.2 (n=75 in SA) in May – mid-August 2021 by epiweek

Number of C.1.2 samples indicated above bar



C.1.2 has now been detected in seven provinces. Mpumalanga the Eastern Cape and the Western Cape have two C.1.2 detections each.

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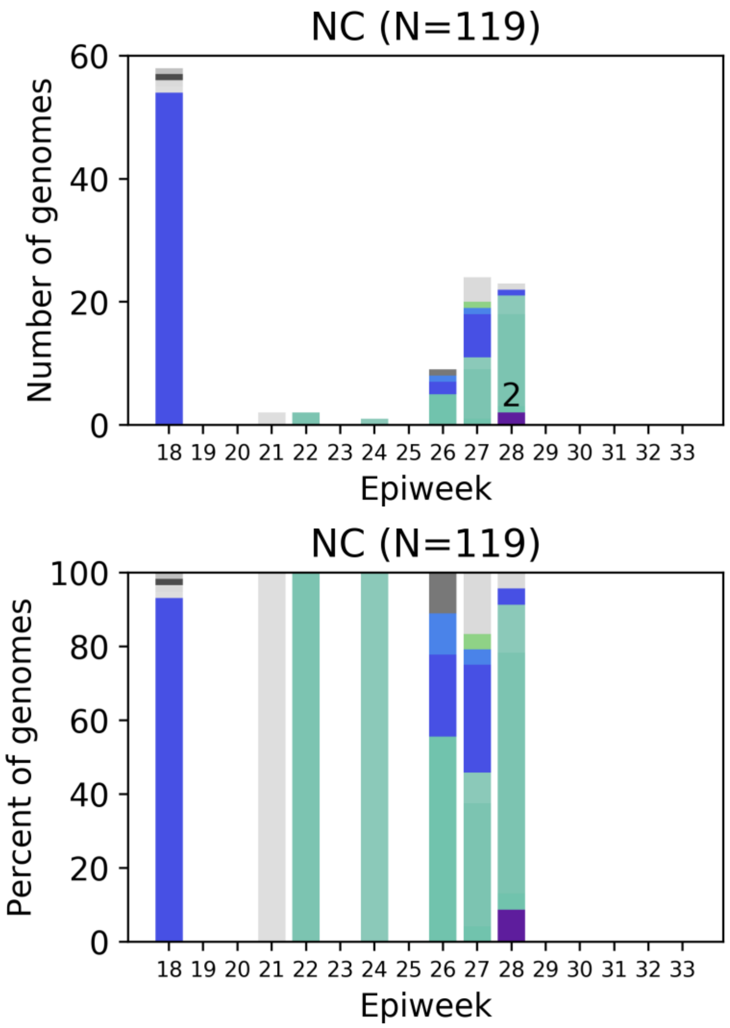
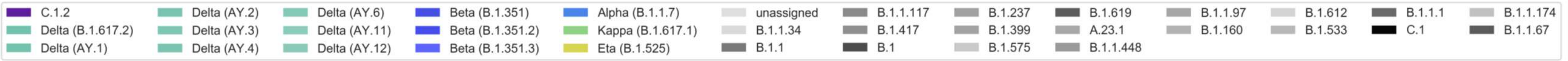
C.1.2 (n=75 in SA) in May – mid-August 2021 by epiweek

Number of C.1.2 samples indicated above bar





- C.1.2 is a newly-identified lineage containing some mutations of interest and concern.
- Work is ongoing to determine the functional impact of these mutations.
- We are continuing to monitor C.1.2 closely through genomic surveillance.

This is the first detection of C.1.2 in the Northern Cape (n=2).

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Summary

- In June, Delta increased to dominated in most provinces with recent data showing this continued Delta dominance.

- Overall diversity of lineages decreased as Delta became dominant.

- Mutated C.1 lineage has been given designation C.1.2 by Pangolin[1] and has now been detected in seven provinces in South Africa: Eastern Cape, Gauteng, Mpumalanga, Limpopo, KwaZulu-Natal, Northern Cape, Western Cape.

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[1] https://github.com/cov-lineages/pango-designation/issues/139

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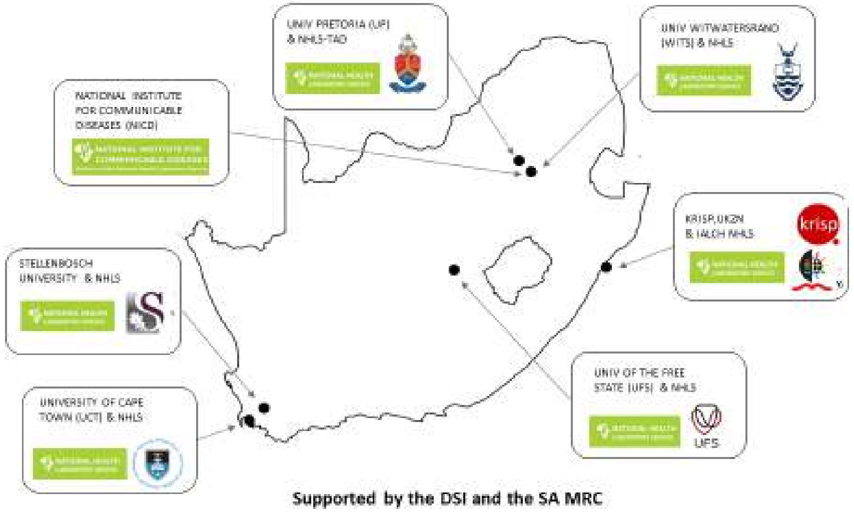

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NICD COVID-19 response team
COVID Incident Management Team

National Research Foundation
NRF

health
Department: Health
REPUBLIC OF SOUTH AFRICA

science & technology
Department: Science and Technology
REPUBLIC OF SOUTH AFRICA

AFRICA CDC
Centres for Disease Control and Prevention
Safeguarding Africa's Health

saMRC advancinglife

wellcome

CDC
CENTERS FOR DISEASE CONTROL AND PREVENTION

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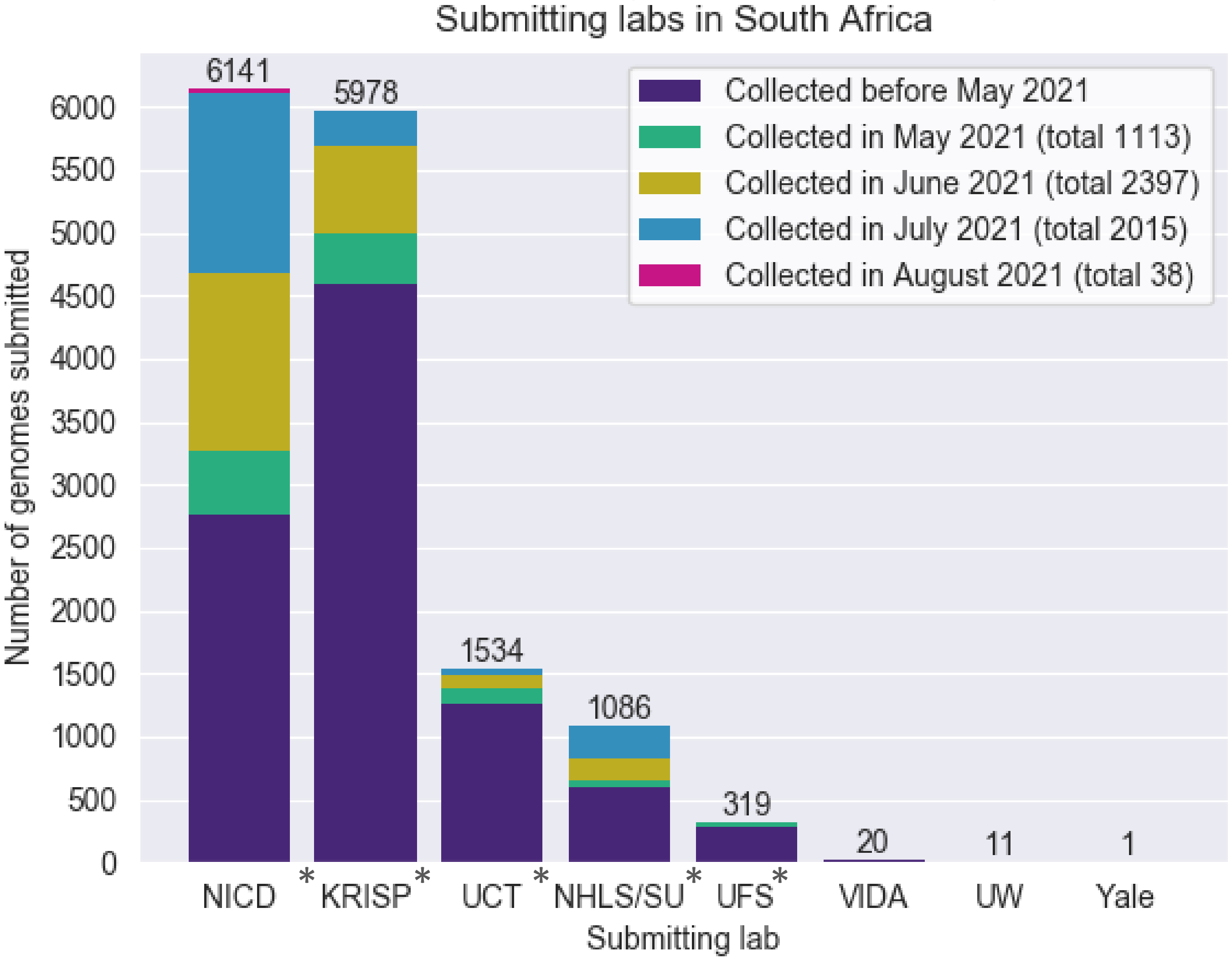
South African genomes submitted per sequencing lab, 2020 and 2021 (N=15 090)



*NGS-SA laboratories

Multiple labs from NGS-SA are contributing to the sequencing effort. Sequencing efforts have increased with the third wave.

NGS-SA
Network for Genomic Surveillance in South Africa

Variants of Concern (VOC)

WHO label	Pango lineages	GISAID clade	Nextstrain clade	Additional amino acid changes monitored*	Earliest documented samples	Date of designation
Alpha	B.1.1.7	GRY	20I (V1)	+S:484K +S:452R	United Kingdom, Sep-2020	18-Dec-2020
Beta	B.1.351 B.1.351.2 B.1.351.3	GH/501Y.V2	20H (V2)	+S:L18F	South Africa, May-2020	18-Dec-2020
Gamma	P.1 P.1.1 P.1.2	GR/501Y.V3	20J (V3)	+S:681H	Brazil, Nov-2020	11-Jan-2021
Delta	B.1.617.2 AY.1 AY.2	G/478K.V1	21A	+S:417N	India, Oct-2020	VOI: 4-Apr-2021 VOC: 11-May-2021

https://www.who.int/en/activities/tracking-SARS-CoV-2-variants/ accessed 12 August 2021

*Notable spike (S) amino acid changes under monitoring, which are currently reported in a minority of sequenced samples

Currently designated Variants of Interest (VOI)

WHO label	Pango lineages	GISAID clade	Nextstrain clade	Earliest documented samples	Date of designation
Eta	B.1.525	G/484K.V3	21D	Multiple countries, Dec-2020	17-Mar-2021
Iota	B.1.526	GH/253G.V1	21F	United States of America, Nov-2020	24-Mar-2021
Kappa	B.1.617.1	G/452R.V3	21B	India, Oct-2020	4-Apr-2021
Lambda	C.37	GR/452Q.V1	21G	Peru, Dec-2020	14-Jun-2021

https://www.who.int/en/activities/tracking-SARS-CoV-2-variants/ accessed 12 August 2021

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.)