NGS-SA SARS-CoV-2 Sequencing Update

12 August 2021

Network for Genomic Surveillance South Africa (NGS-SA)

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Surveillance in South Africa

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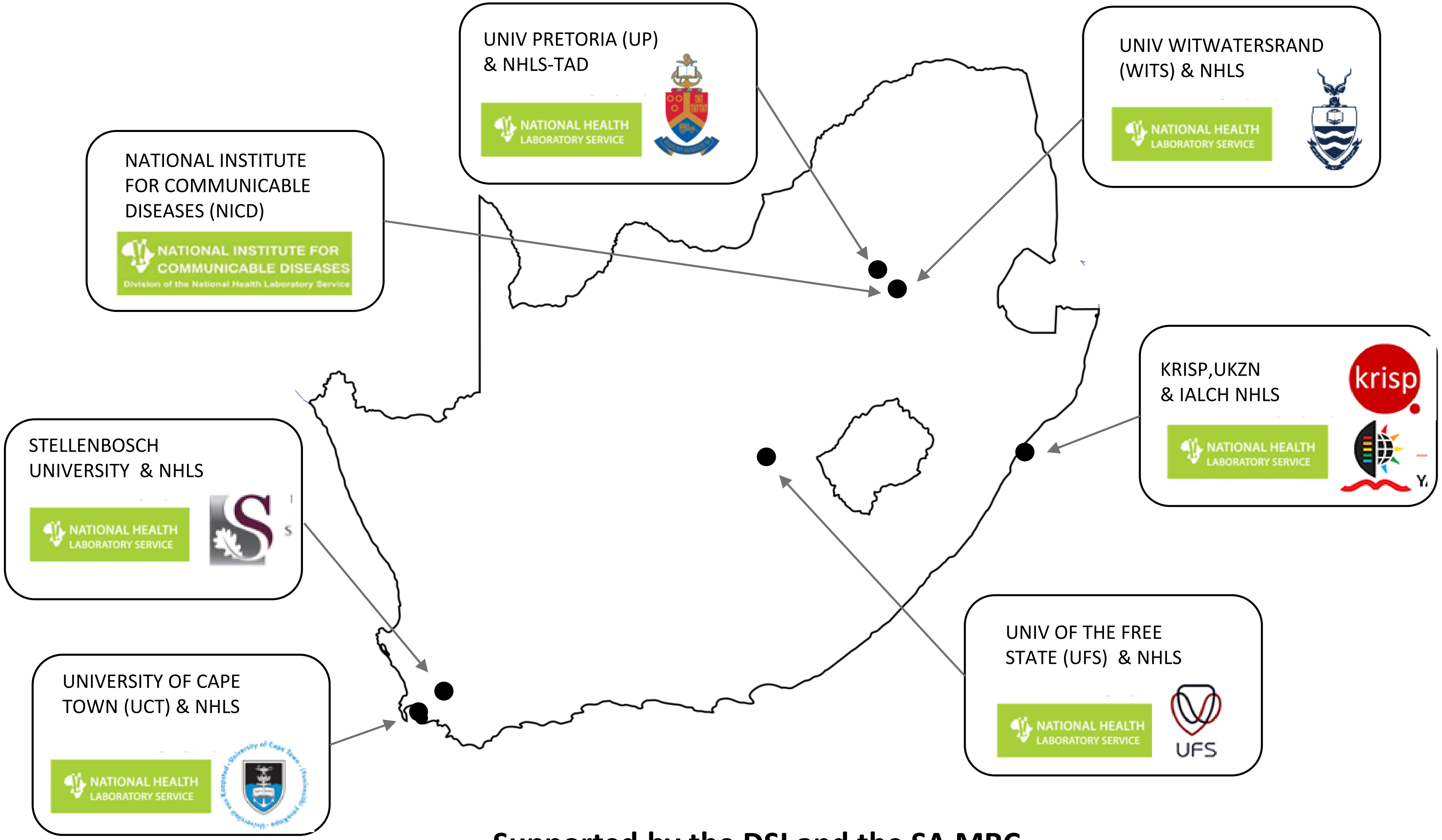
Division of the National Health Laboratory Service

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)

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



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Supported by the DSI and the SA MRC

Msomi N, Mlisana K, et al. Lancet Microbe 2020

The genomic data presented here are based on South African SARS-CoV-2 sequence data downloaded from GISAID (www.gisaid.org) on 11 August at 18h00

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/

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

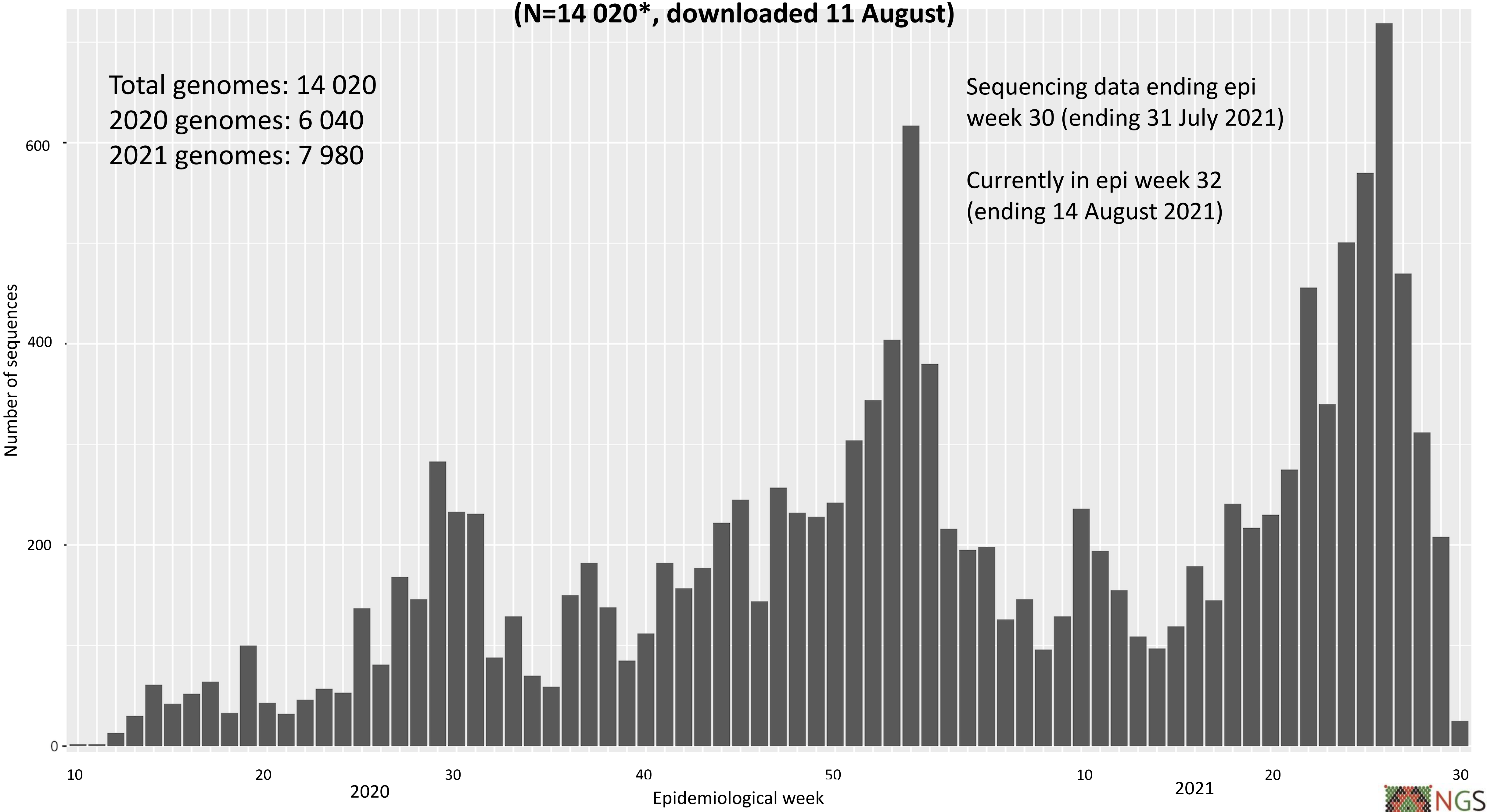
*Notable spike (S) amino acid changes under monitoring, which are currently reported in a minority of sequenced samples

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

Number of South African genomes deposited on GISAID, by specimen collection week, 2020 and 2021 (N=14 020*, downloaded 11 August)



Total genomes: 14 020
2020 genomes: 6 040
2021 genomes: 7 980

Sequencing data ending epi week 30 (ending 31 July 2021)

Currently in epi week 32 (ending 14 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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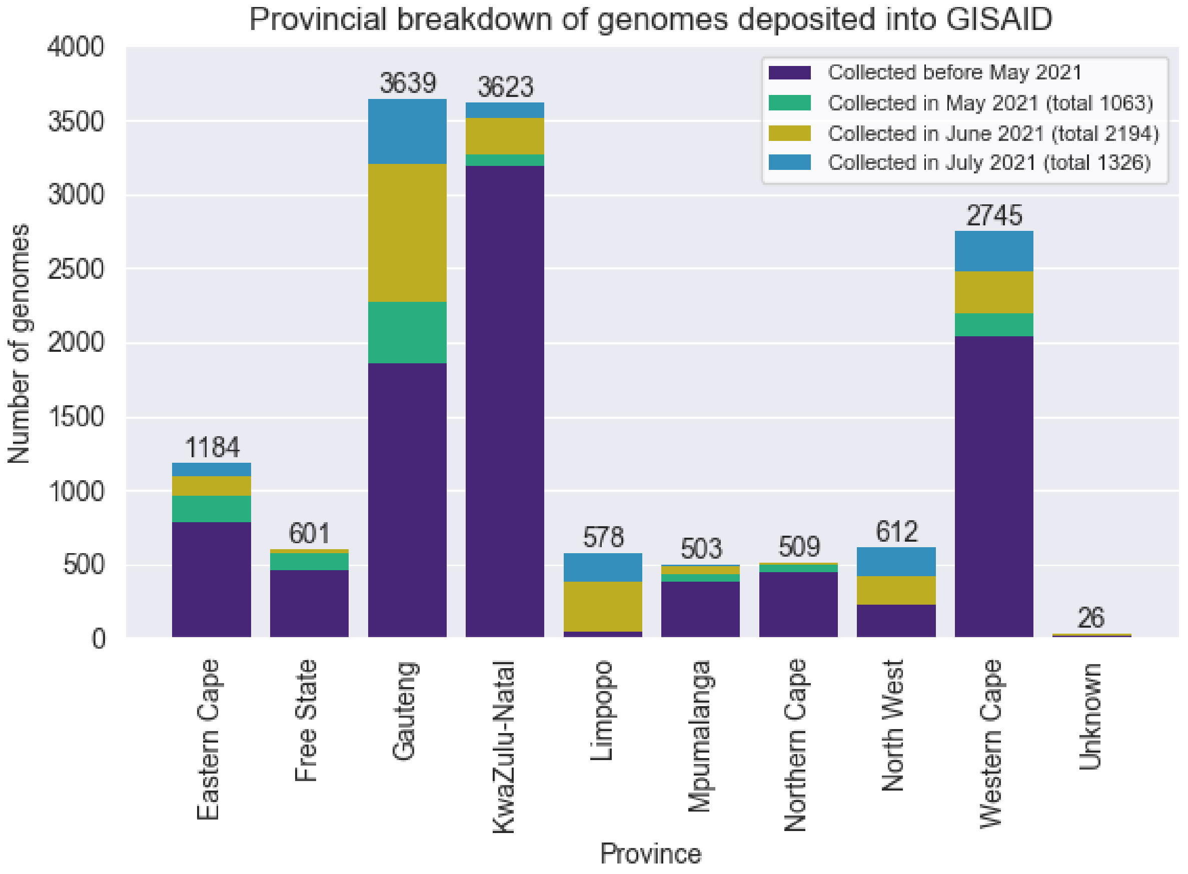
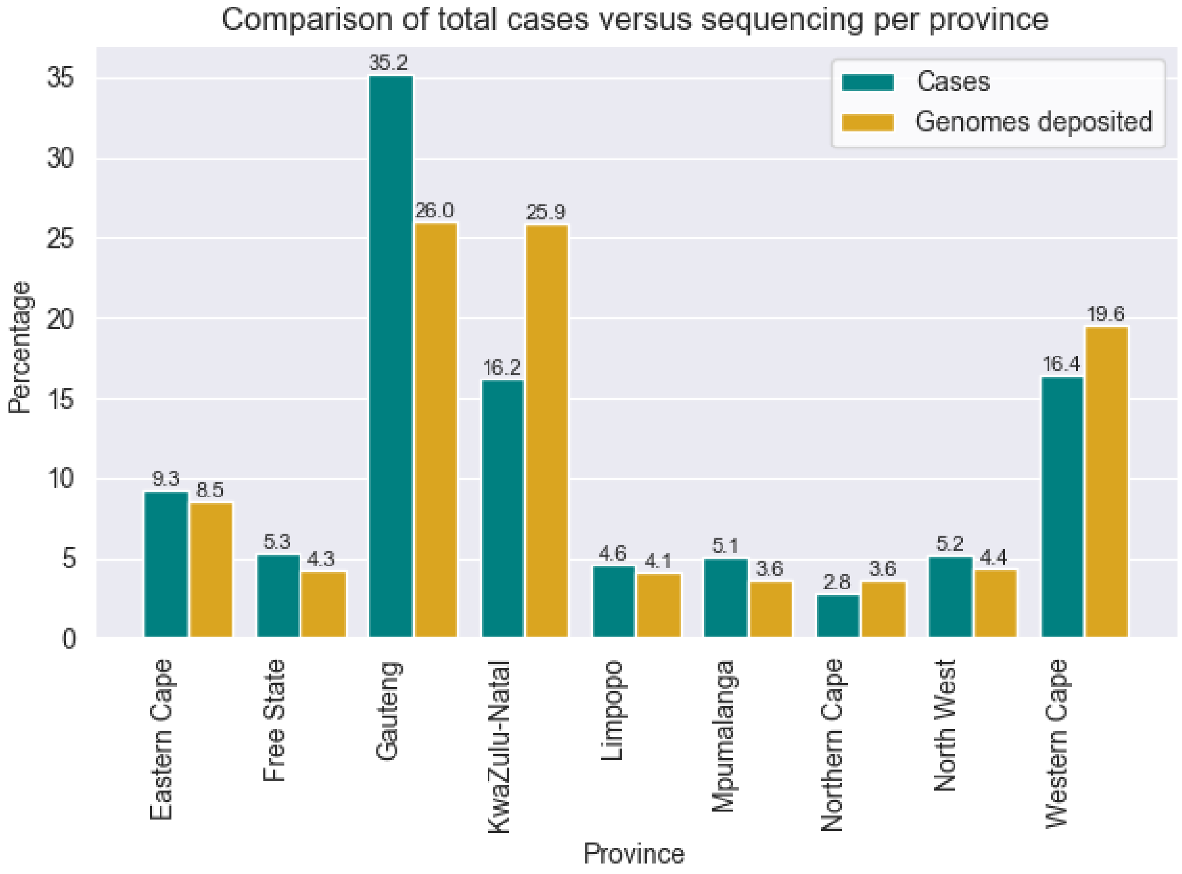
GISAID genomes vs total cases, 2020 and 2021 (N=14 020)





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

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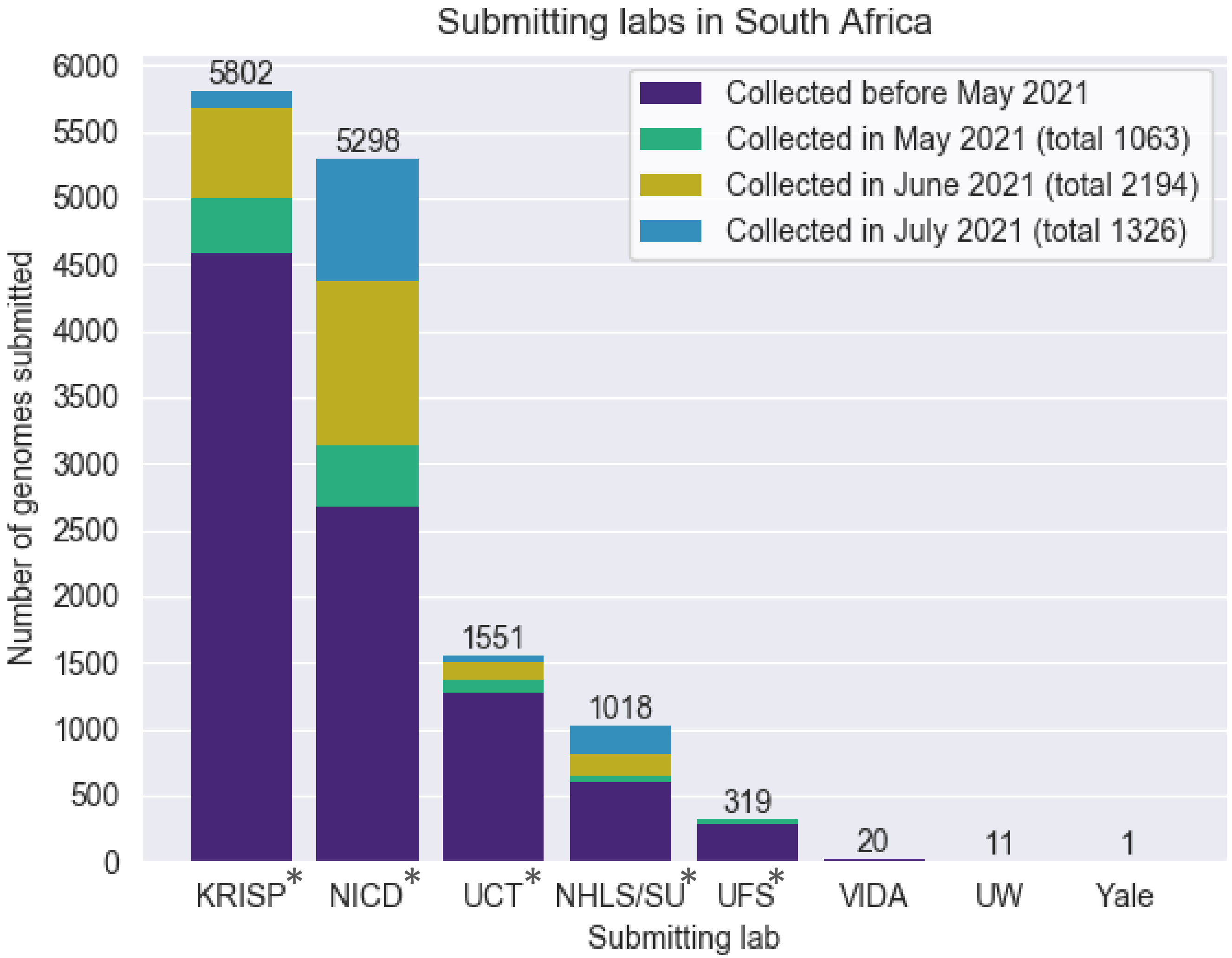
South African genomes submitted per sequencing lab, 2020 and 2021 (N=14 020)



*NGS-SA laboratories

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

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Distribution and number of clades in South Africa, 2021 (N=7 980)

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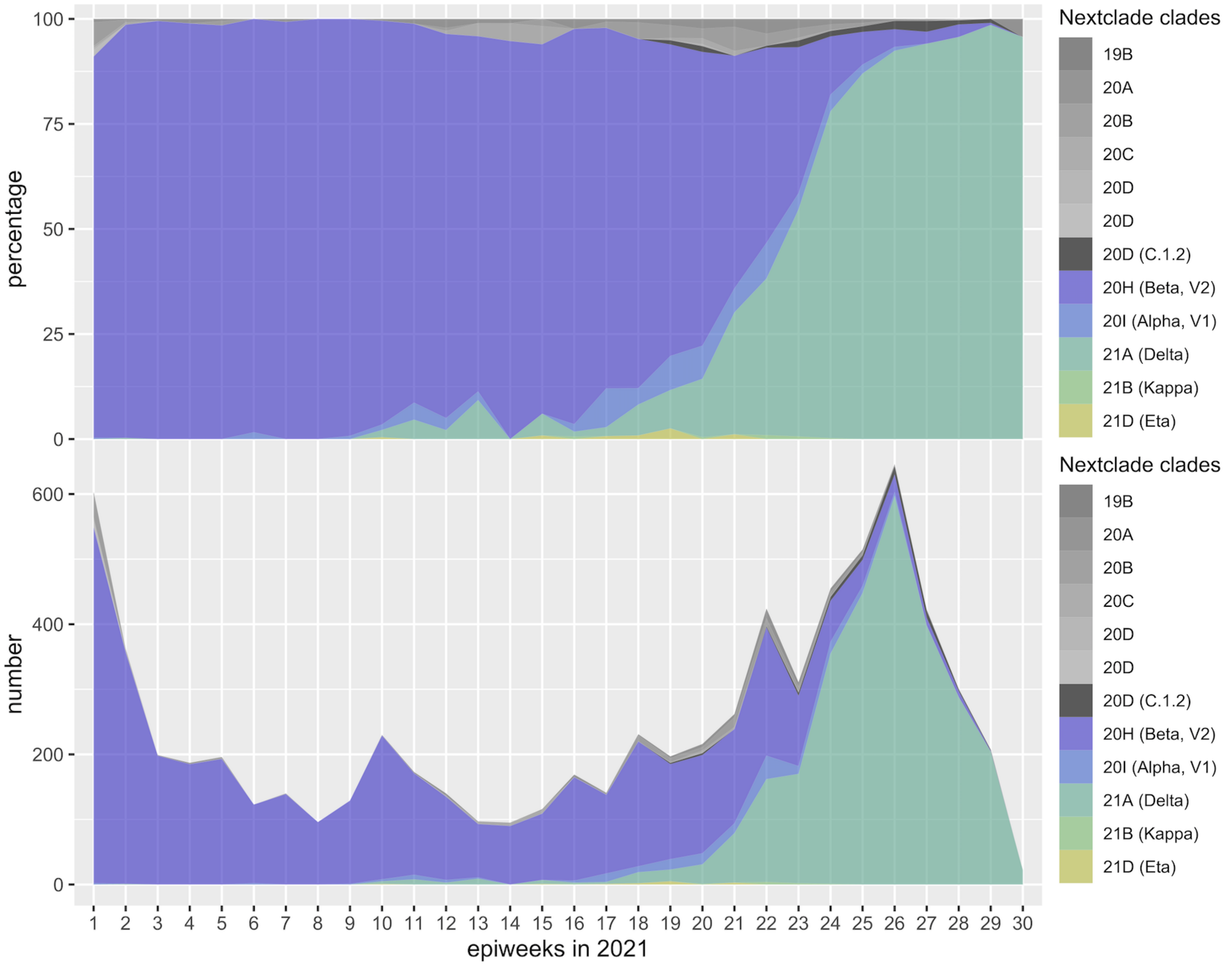
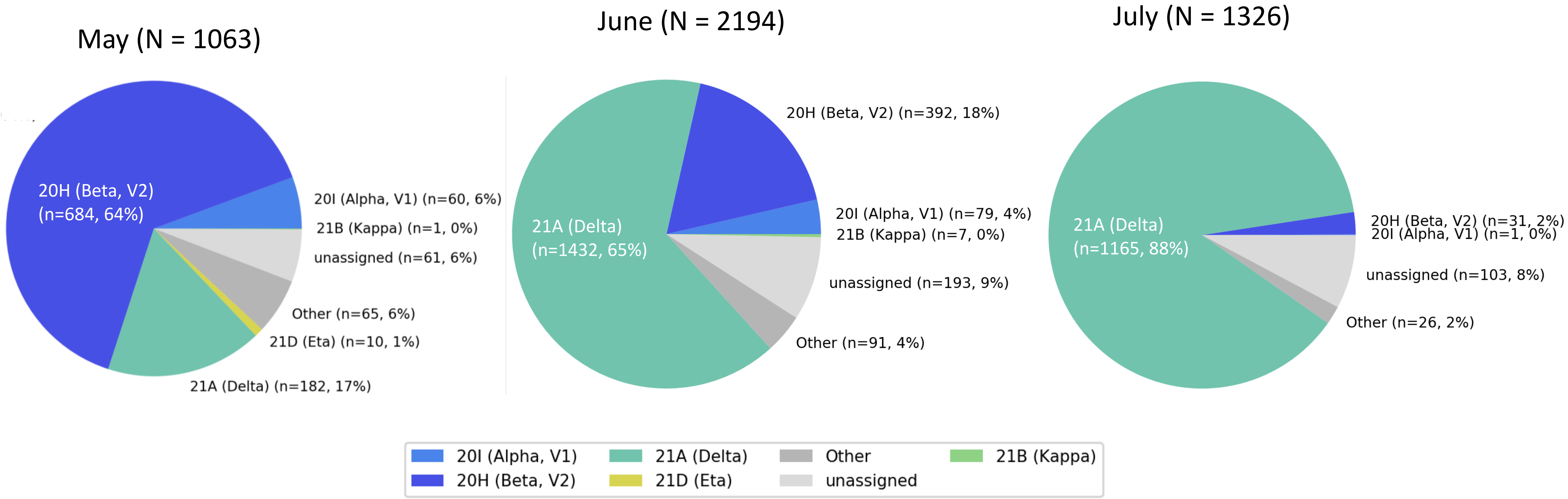


Sequencing data ending epi week 30 (ending 31 July 2021)

Currently in epi week 32 (ending 14 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, June and July 2021 sequences, South Africa


May (N = 1063)

June (N = 2194)

July (N = 1326)

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

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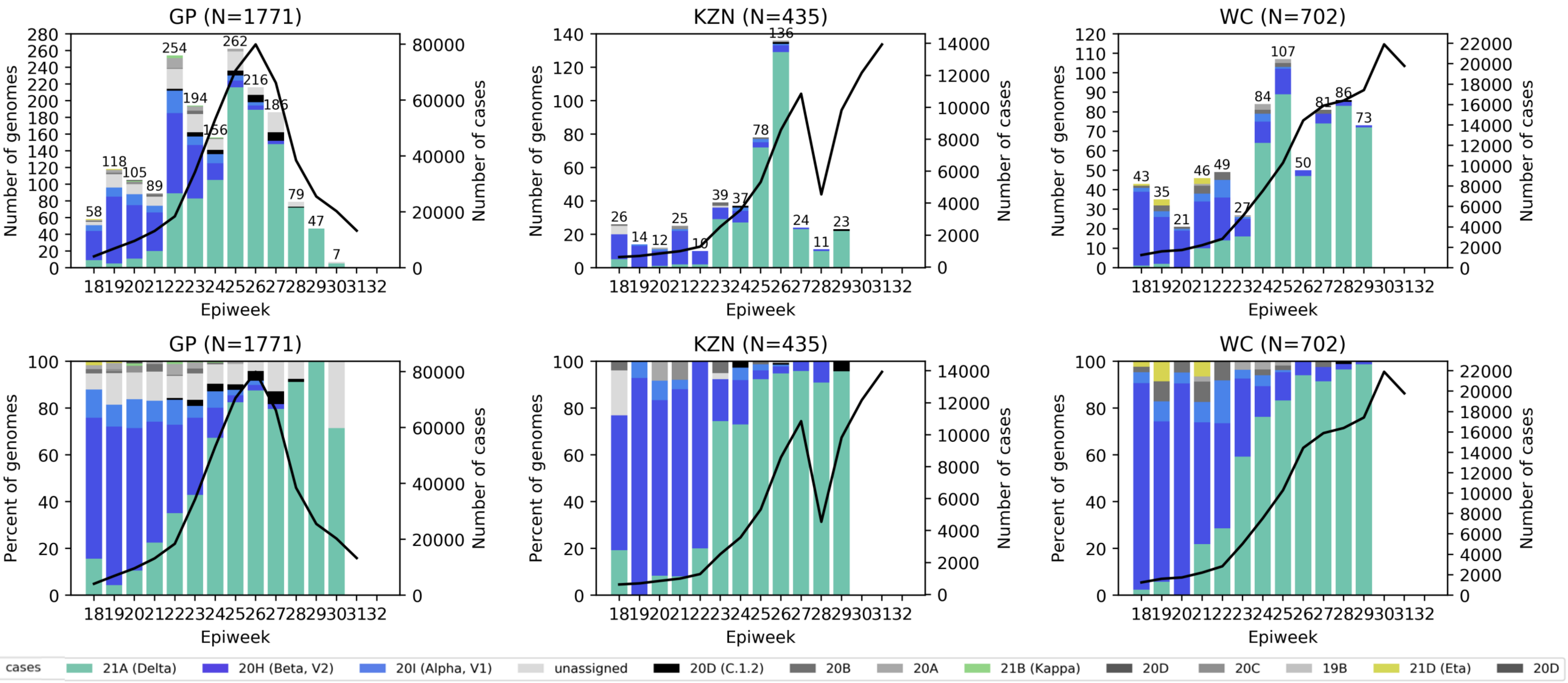
Genomes sequenced from specimens collected in May – mid-August 2021 (epiweeks 18 – 32) from KwaZulu-Natal, Gauteng, Western Cape Provinces



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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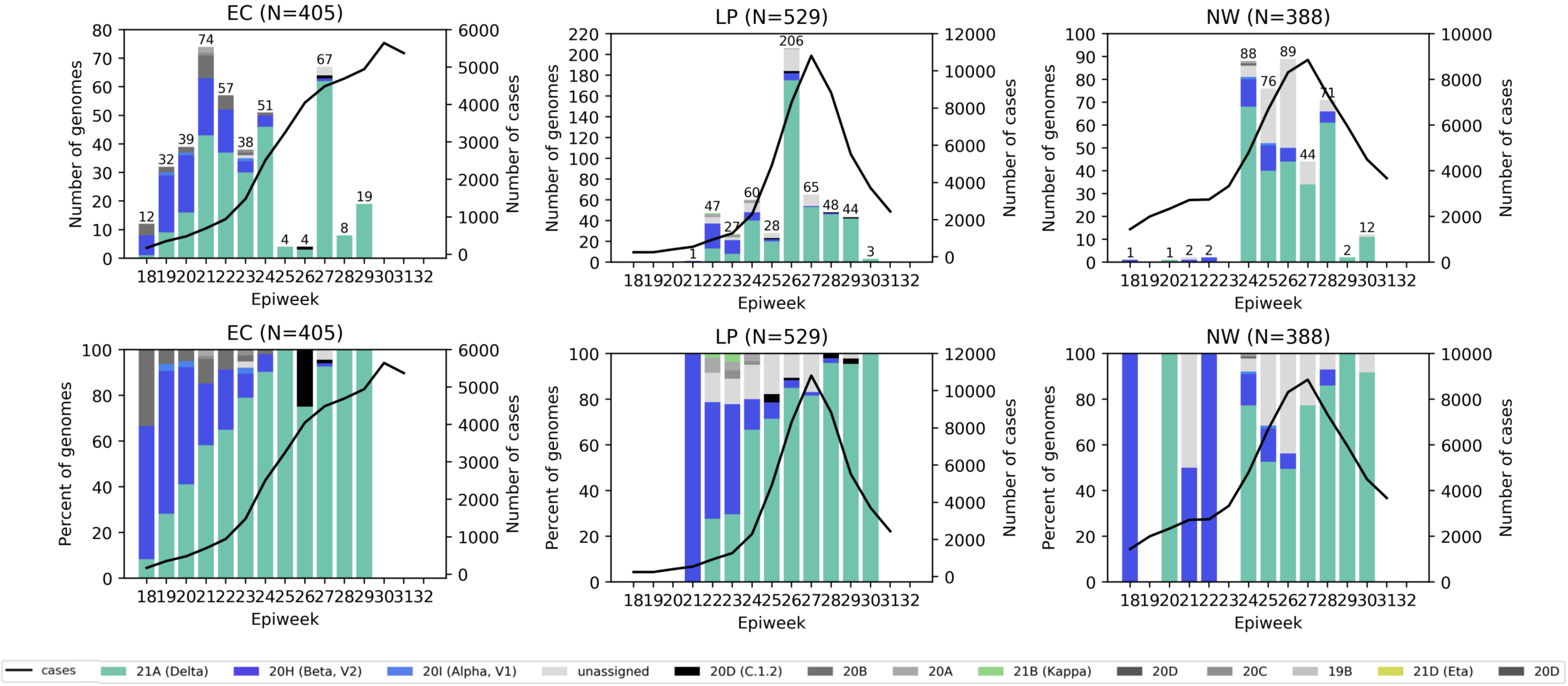
Genomes sequenced from specimens collected in May – mid-August 2021 (epiweeks 18 – 31) from Eastern Cape, Limpopo and North-West Provinces



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

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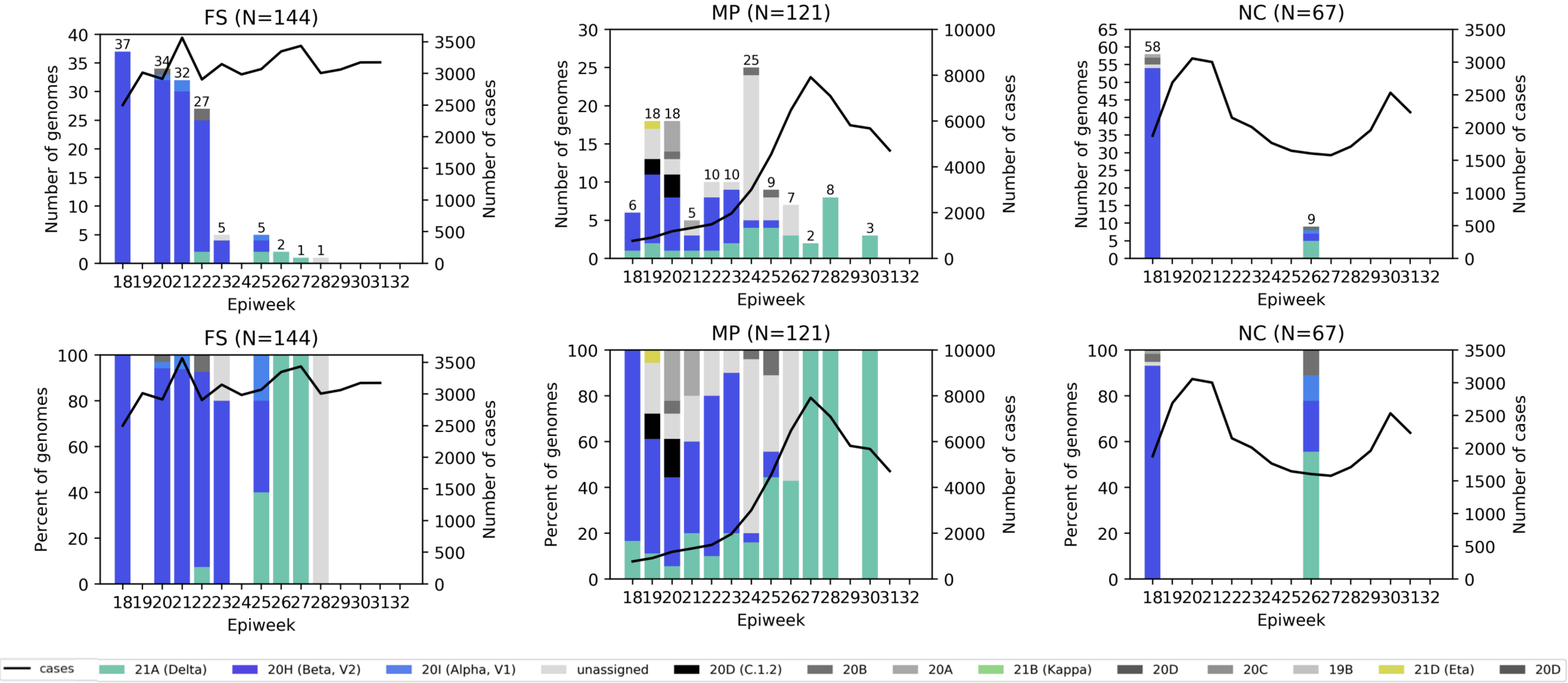
Genomes sequenced from specimens collected in May – mid-August 2021 (epiweeks 18 – 31) from Free State, Mpumalanga and Northern Cape Provinces



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

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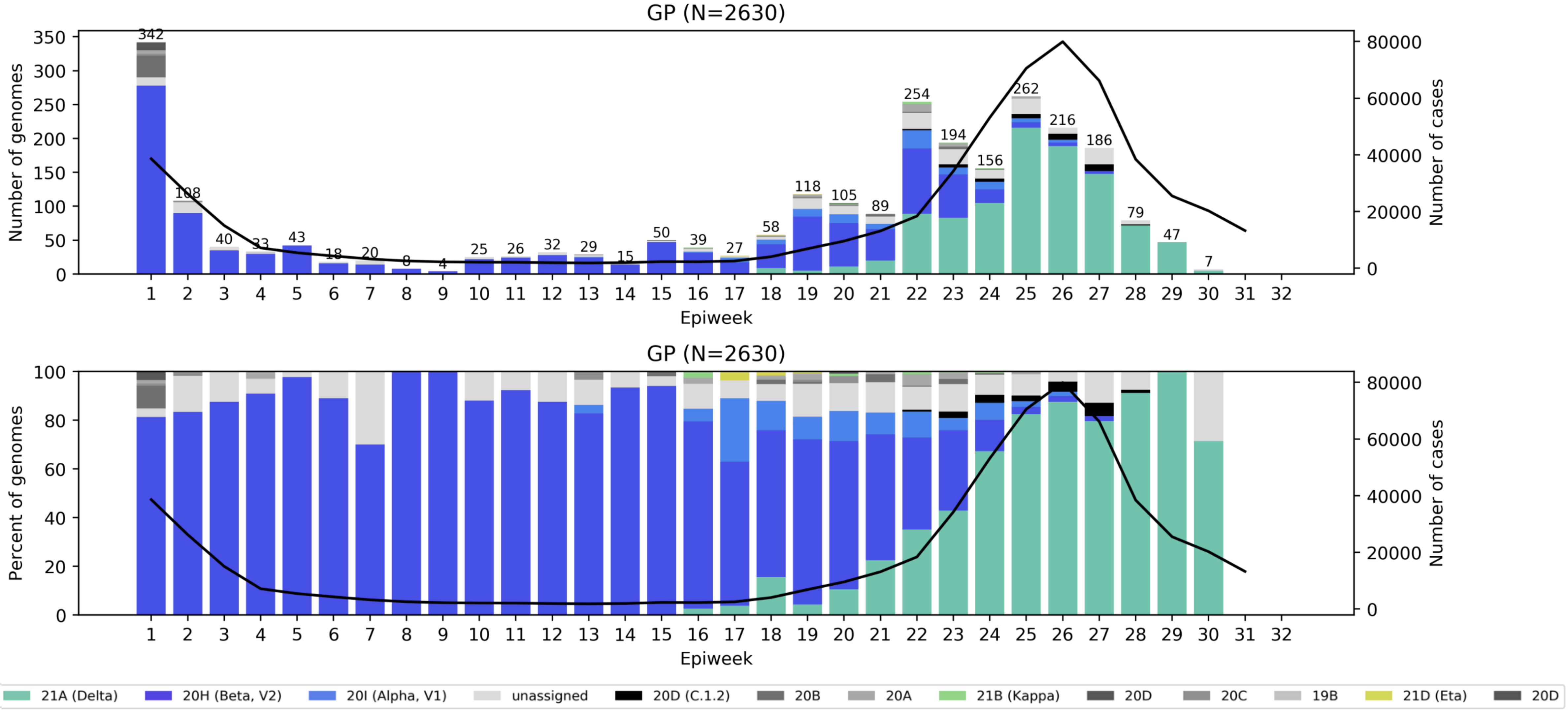
Gauteng Province, 2021, n = 2630



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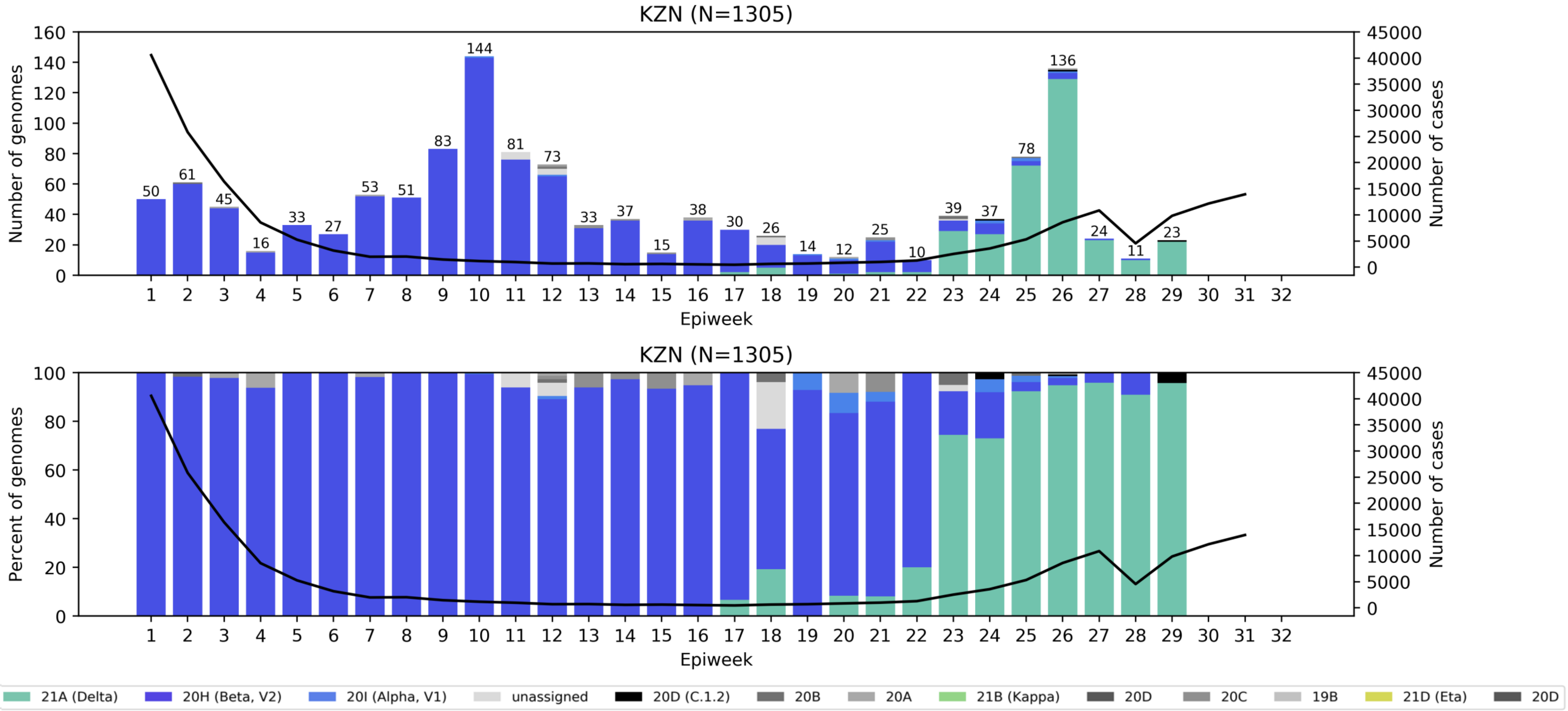
KwaZulu-Natal Province, 2021, n = 1305



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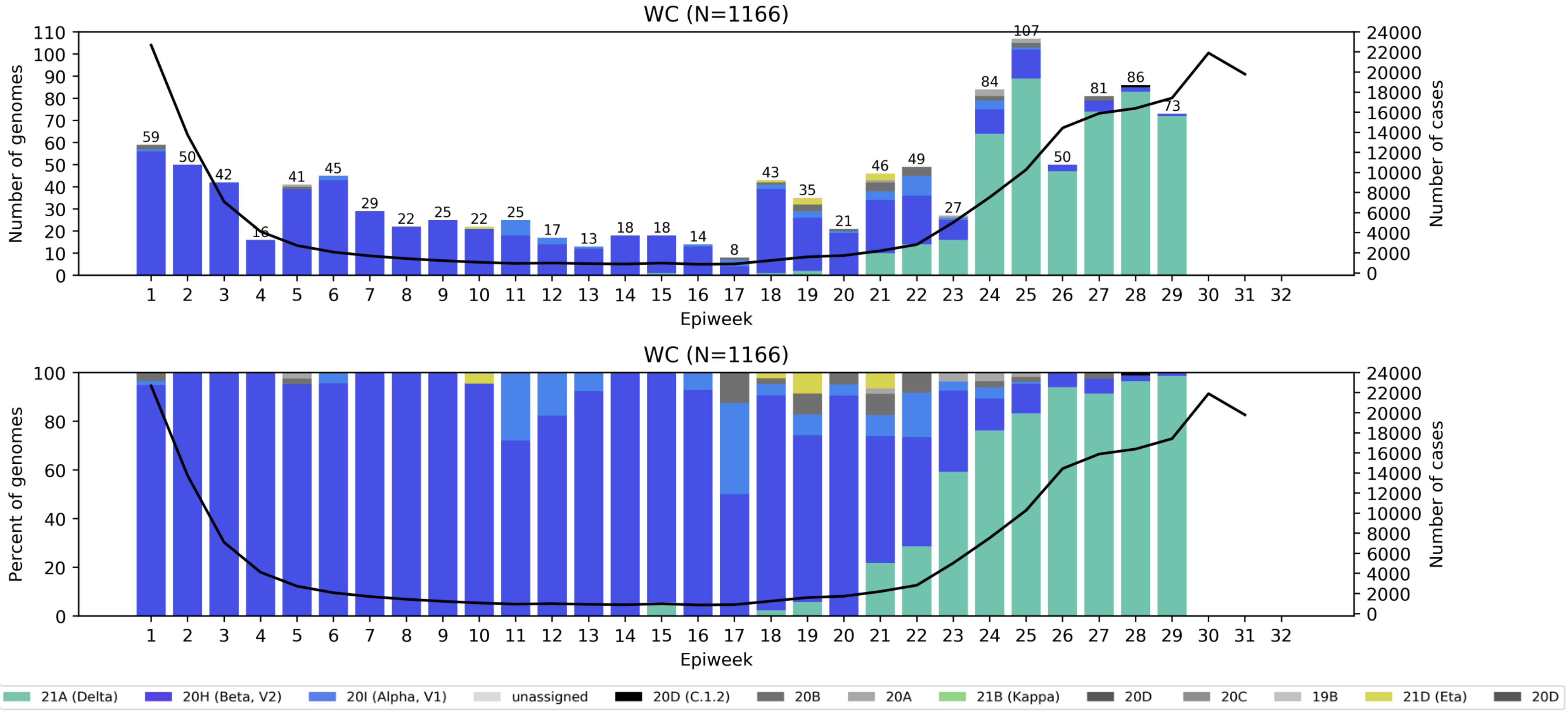
Western Cape Province, 2021, n = 1166



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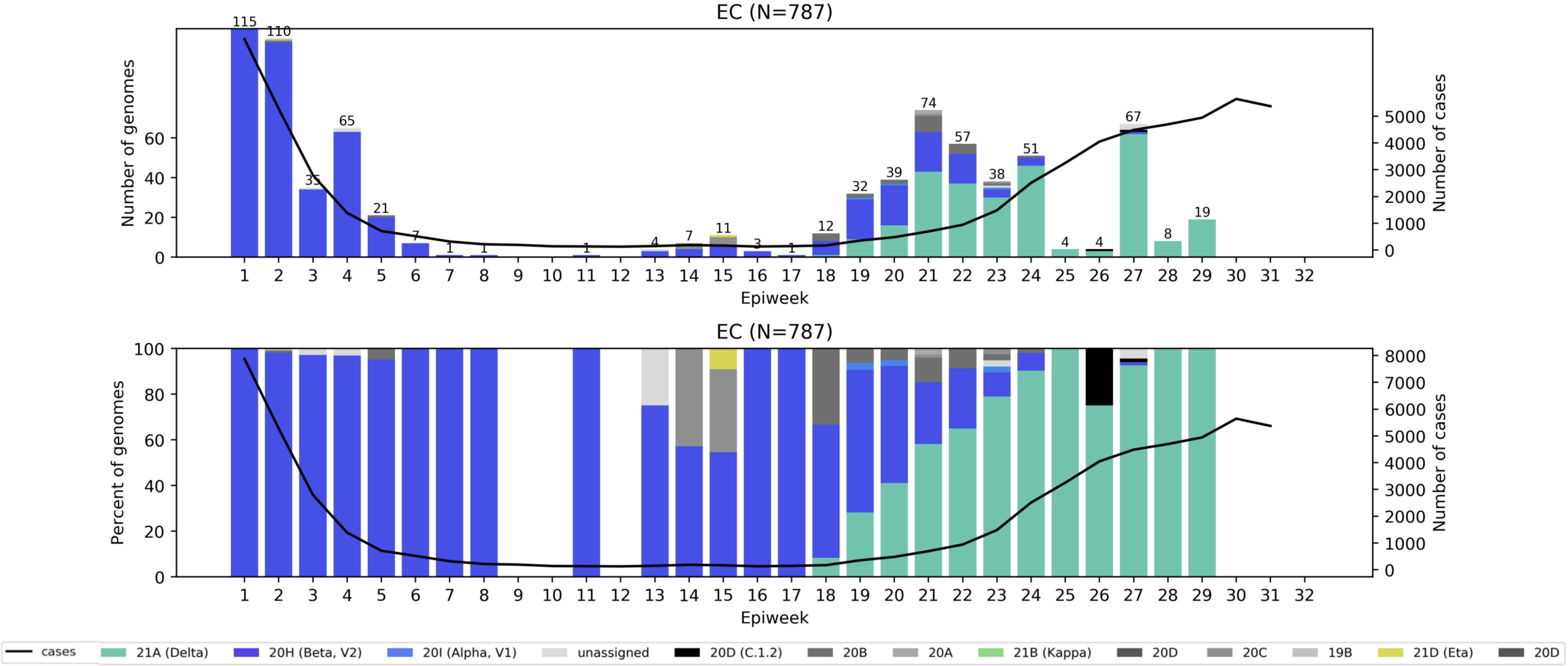
Eastern Cape Province, 2021, n = 787



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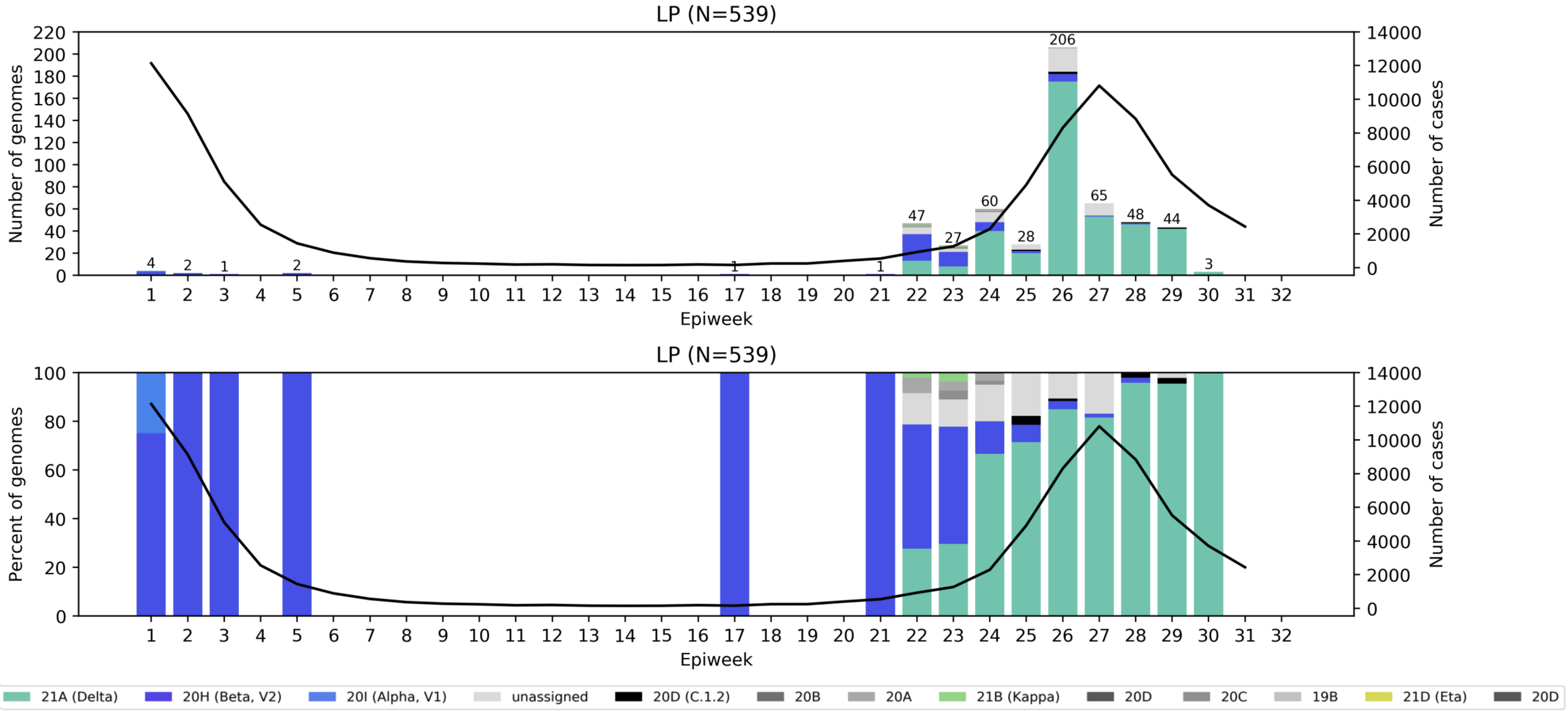
Limpopo Province, 2021, n = 539



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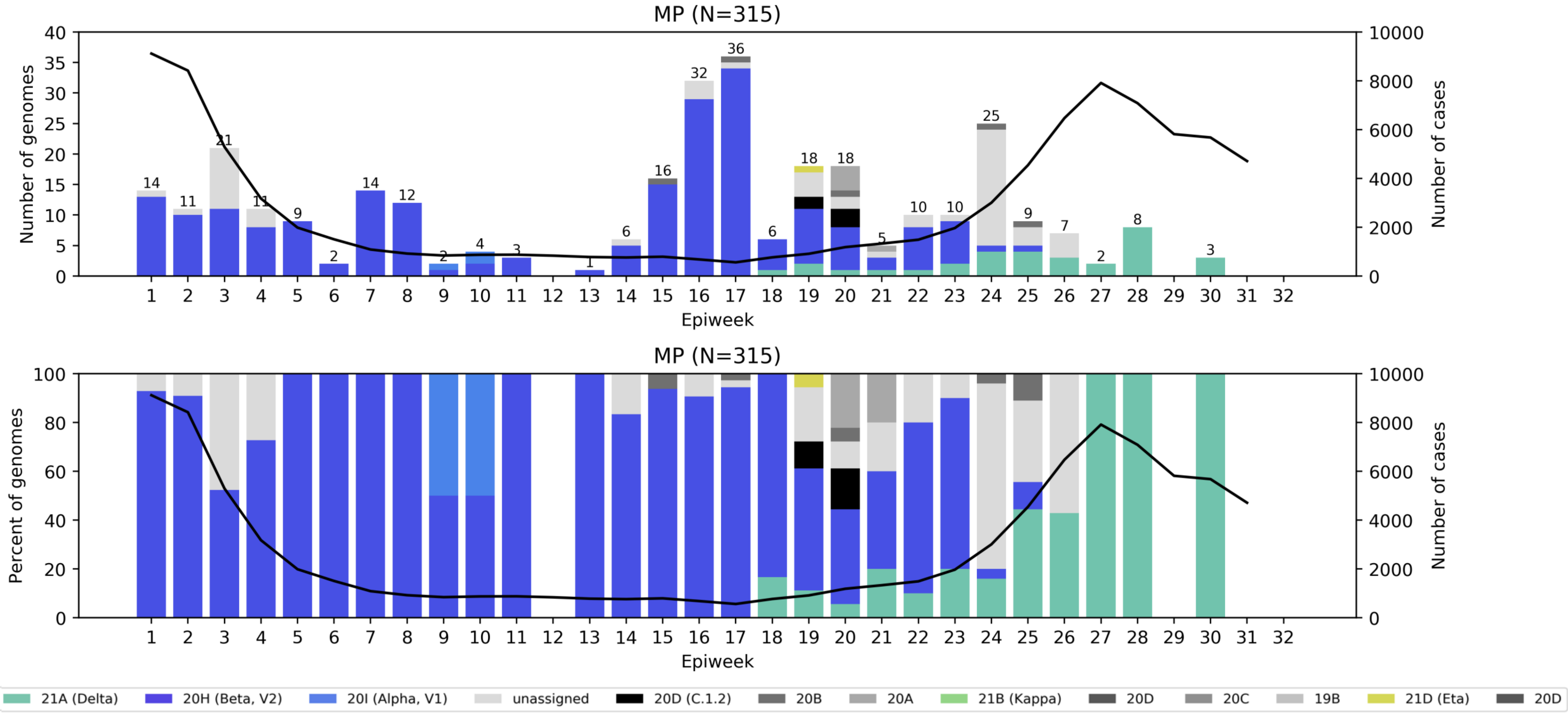
Mpumalanga Province, 2021, n = 315



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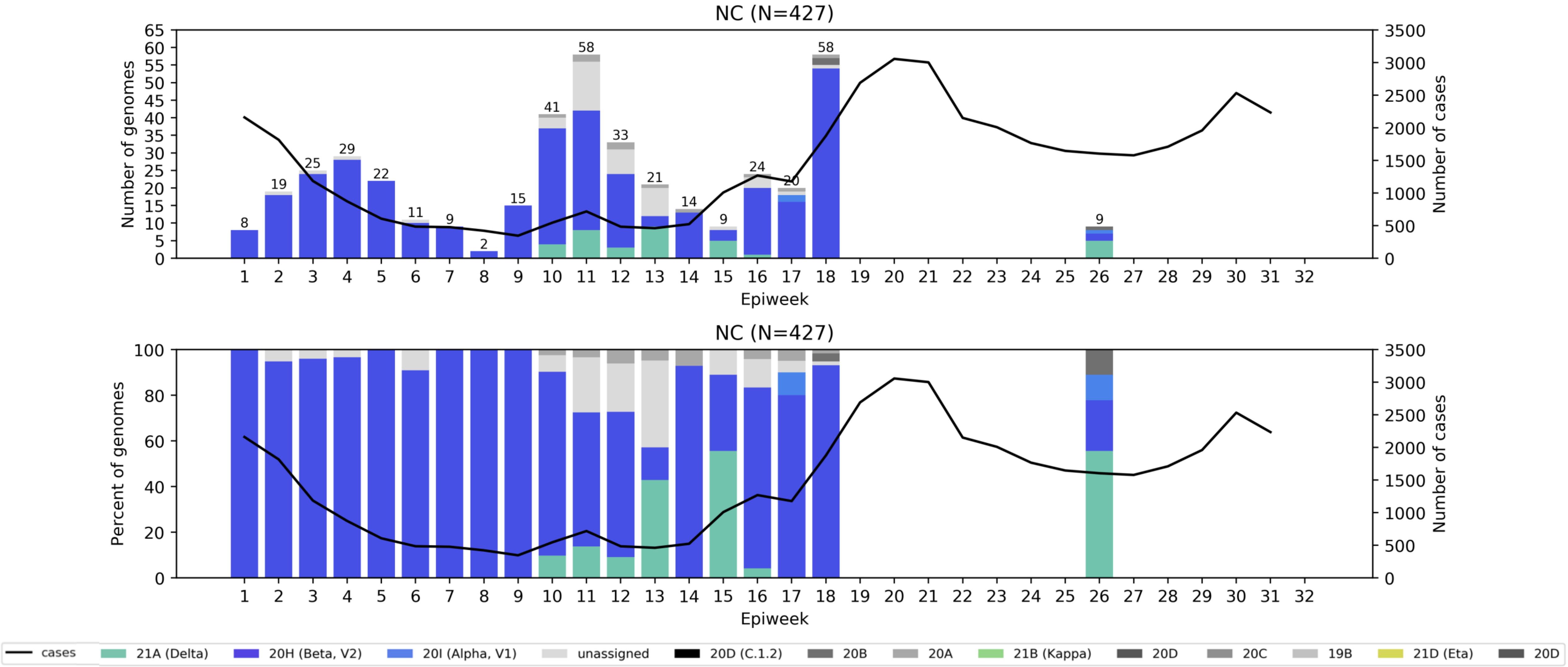
Northern Cape Province, 2021, n = 427



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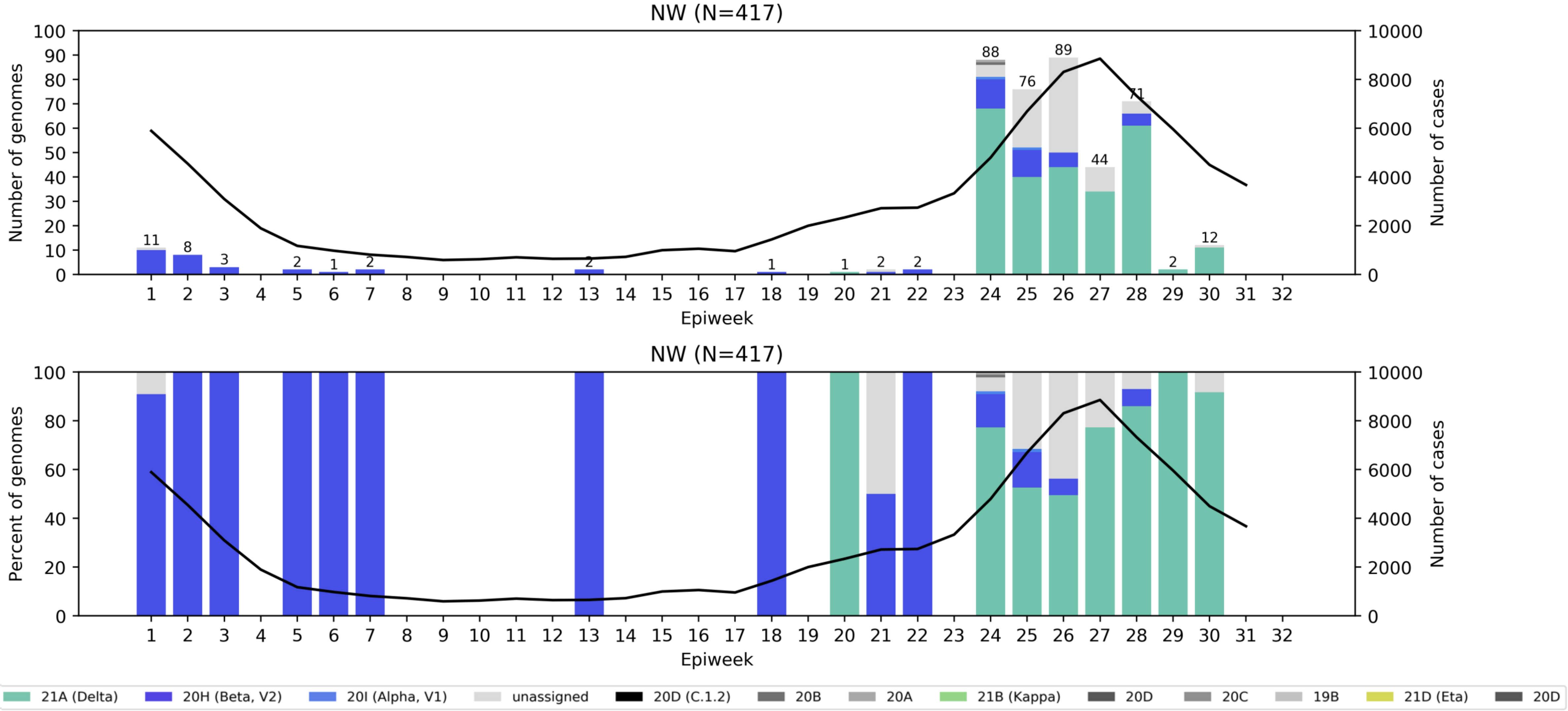
North West Province, 2021, n = 417



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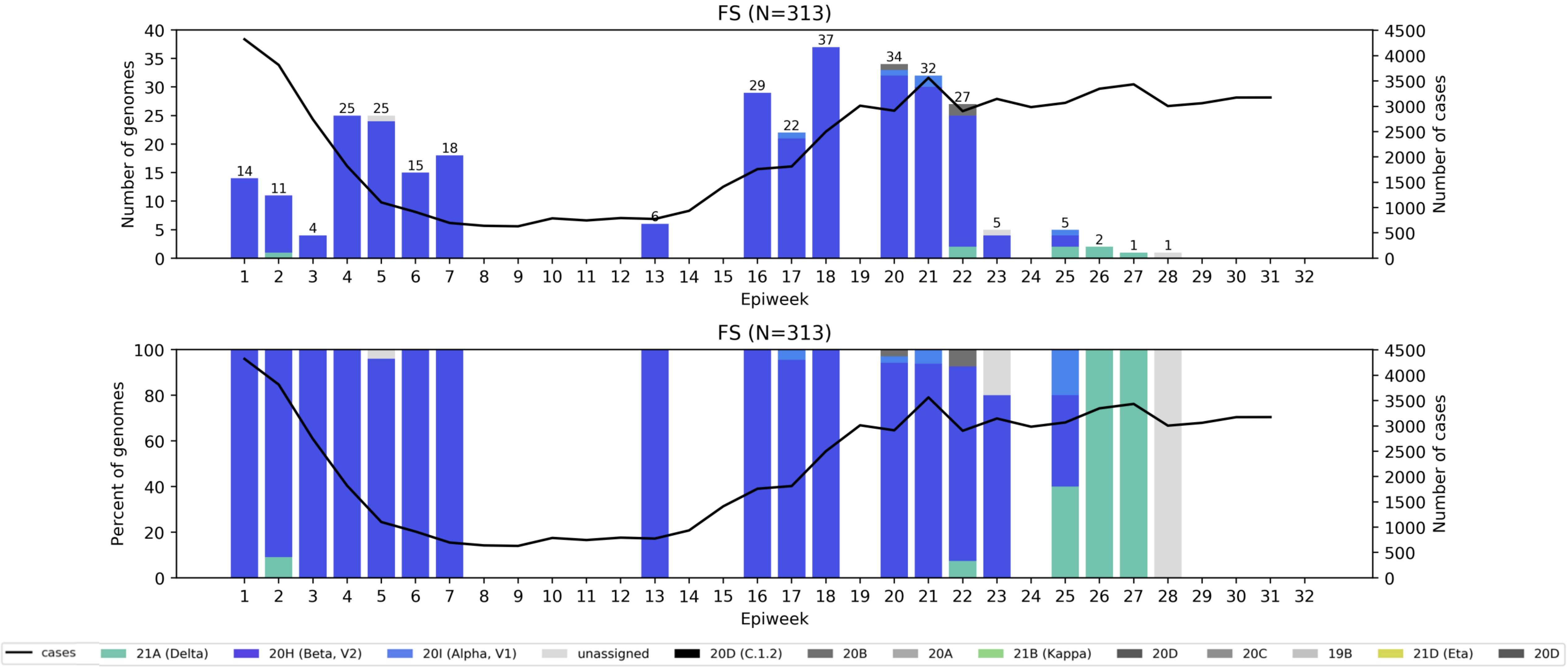
Free State Province, 2021, n = 313



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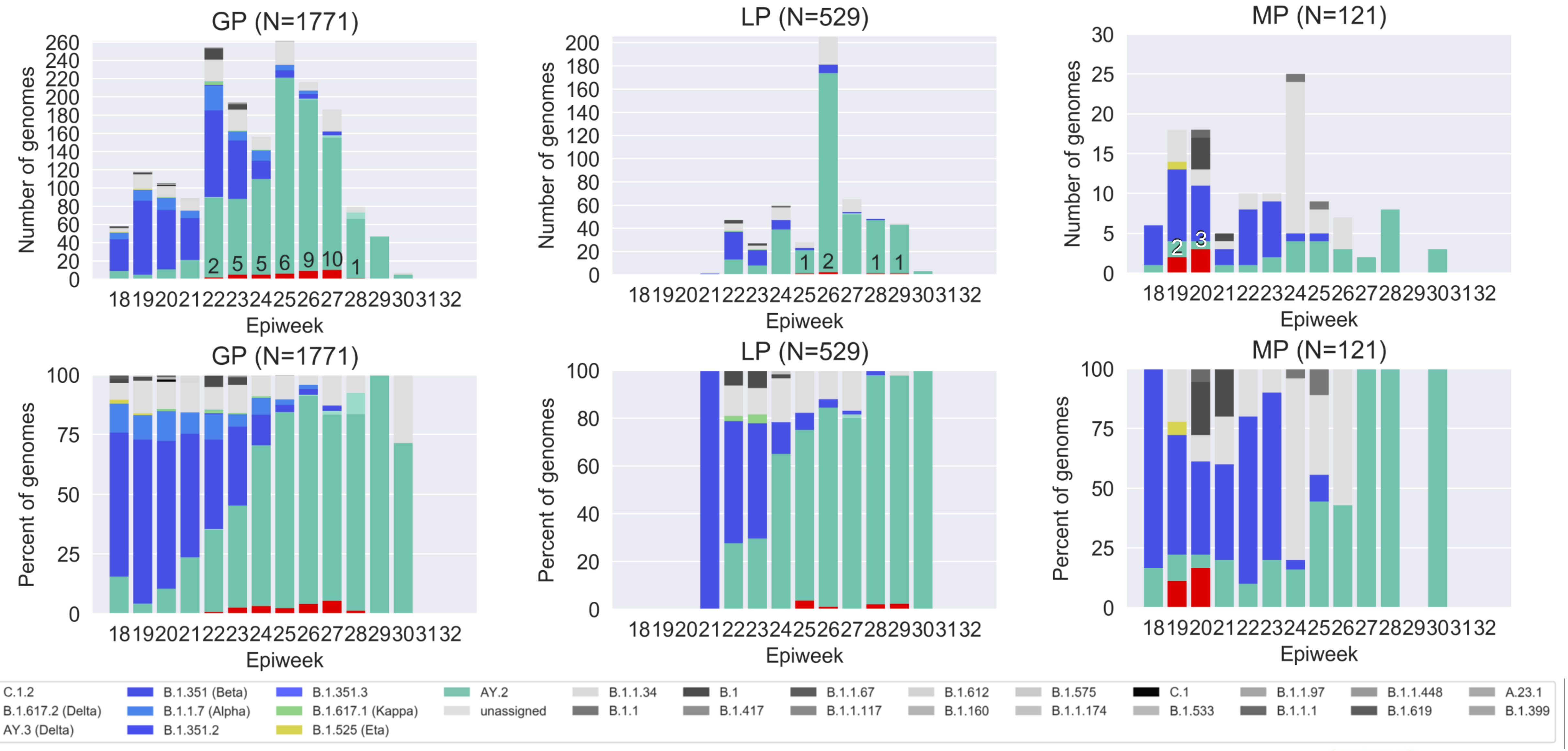
C.1.2 (n=54 in SA) in May – mid-August 2021 by epiweek

Number of C.1.2 samples indicated above bar



C.1.2 has now been detected in six provinces. The majority of samples have been detected in Gauteng (n=37), followed by Limpopo (n=5) and Mpumalanga (n=5).

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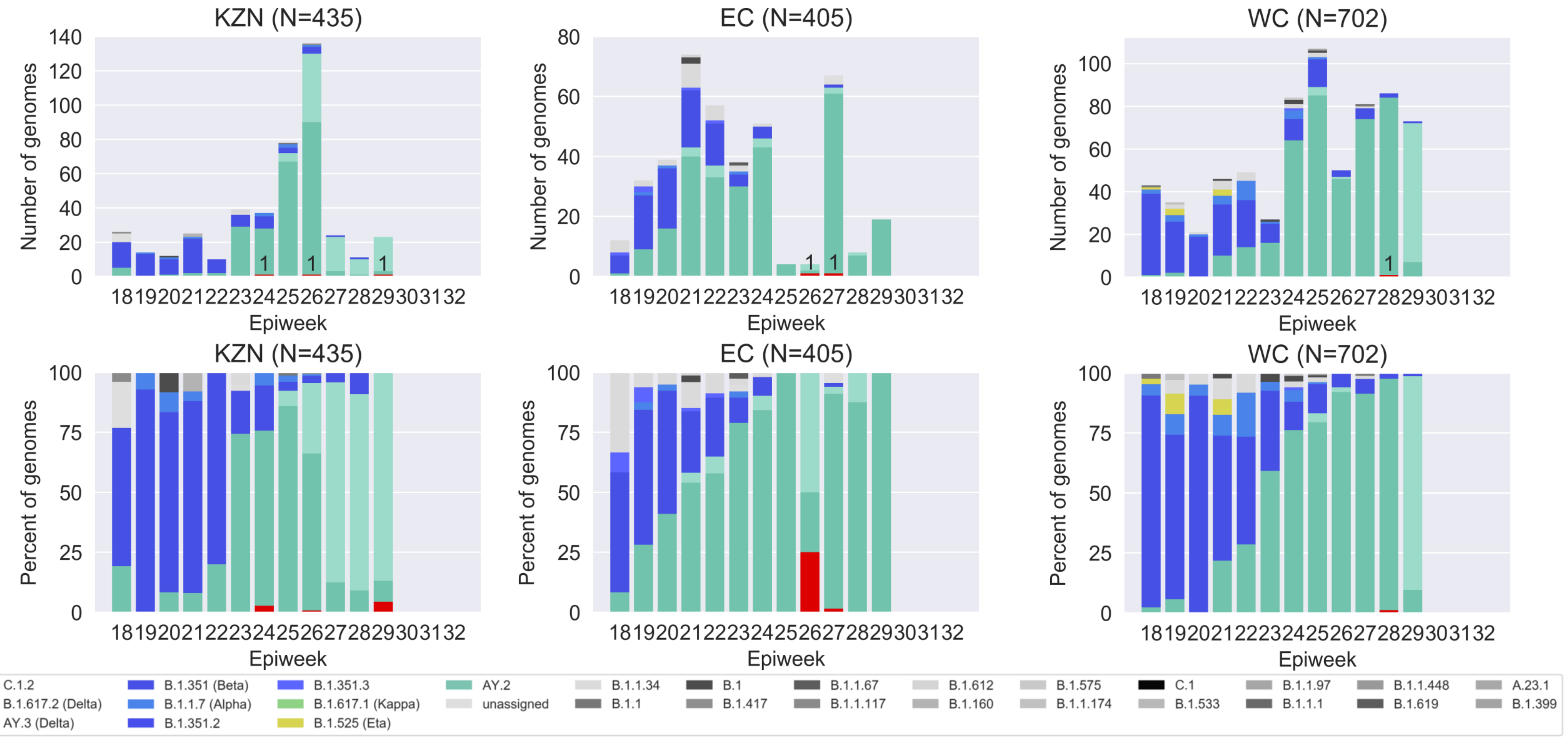
C.1.2 (n=54 in SA) in May – mid-August 2021 by epiweek

Number of C.1.2 samples indicated above bar



C.1.2 has now been detected in six provinces. KwaZulu-Natal now has 3 C.1.2 detections, followed by the Eastern Cape with 2 and the Western Cape with 1.

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Summary

- In June, Delta increased significantly and dominated in most provinces with recent data available.

- Delta remained dominant in July, but additional sequencing data required to confirm these estimates in all provinces.

- 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 six provinces in South Africa: Eastern Cape, Gauteng, Mpumalanga, Limpopo, KwaZulu-Natal, Western Cape.

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

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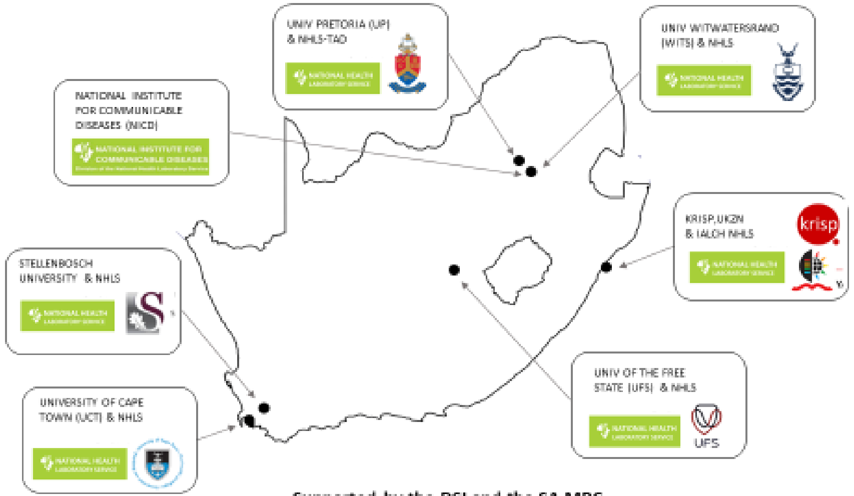

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Zinhle Makatini

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 the NICD (or 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 (NICD 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.)