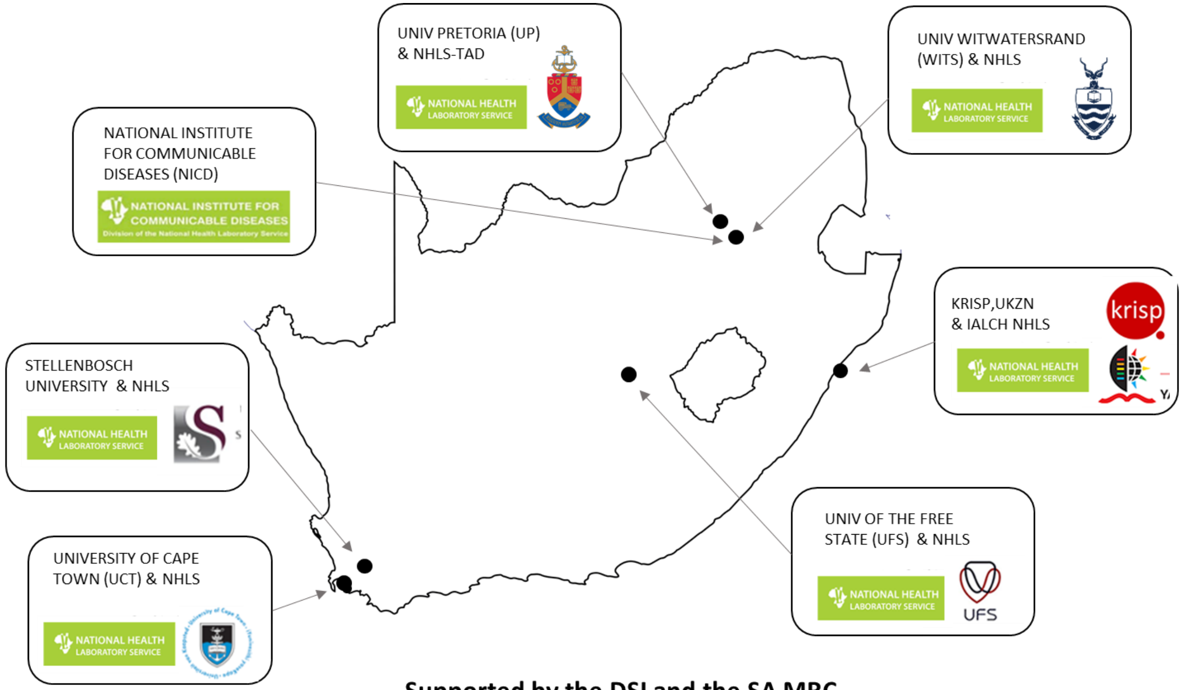
Network for Genomic Surveillance South Africa (NGS-SA)

SARS-CoV-2 Sequencing Update
17 September 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 17 September at 08h58

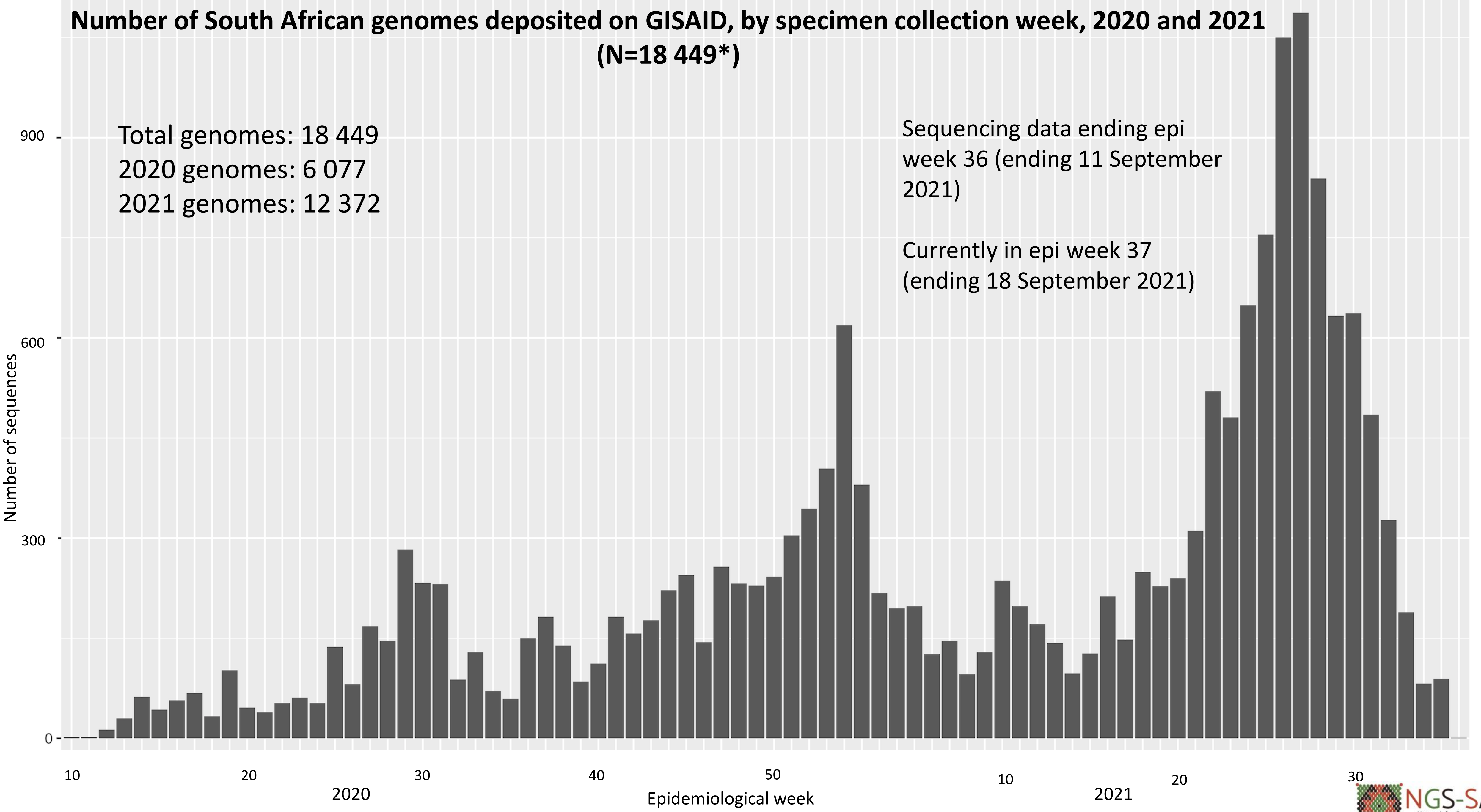
Data license: https://www.gisaid.org/registration/terms-of-use/

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/

Number of South African genomes deposited on GISAID, by specimen collection week, 2020 and 2021 (N=18 449*)



Total genomes: 18 449
2020 genomes: 6 077
2021 genomes: 12 372

Sequencing data ending epi week 36 (ending 11 September 2021)

Currently in epi week 37 (ending 18 September 2021)

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

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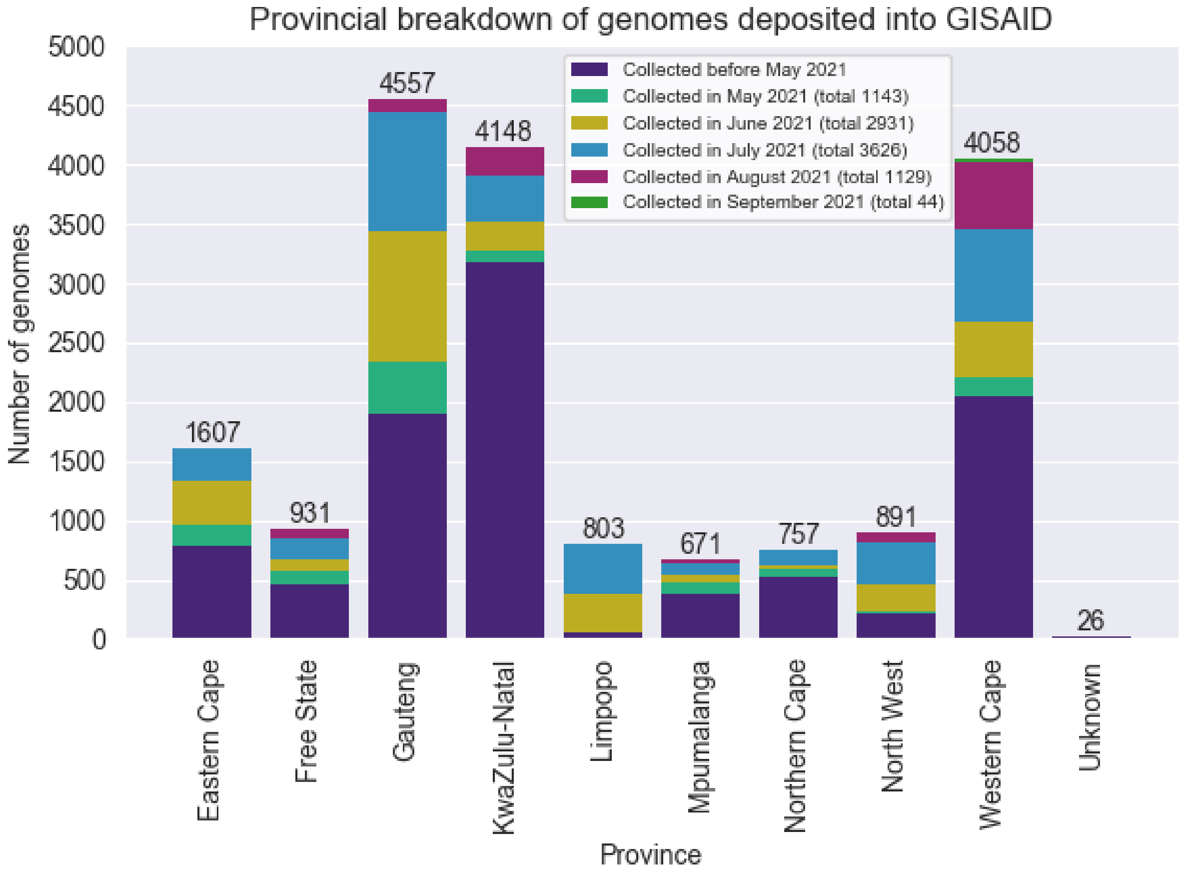
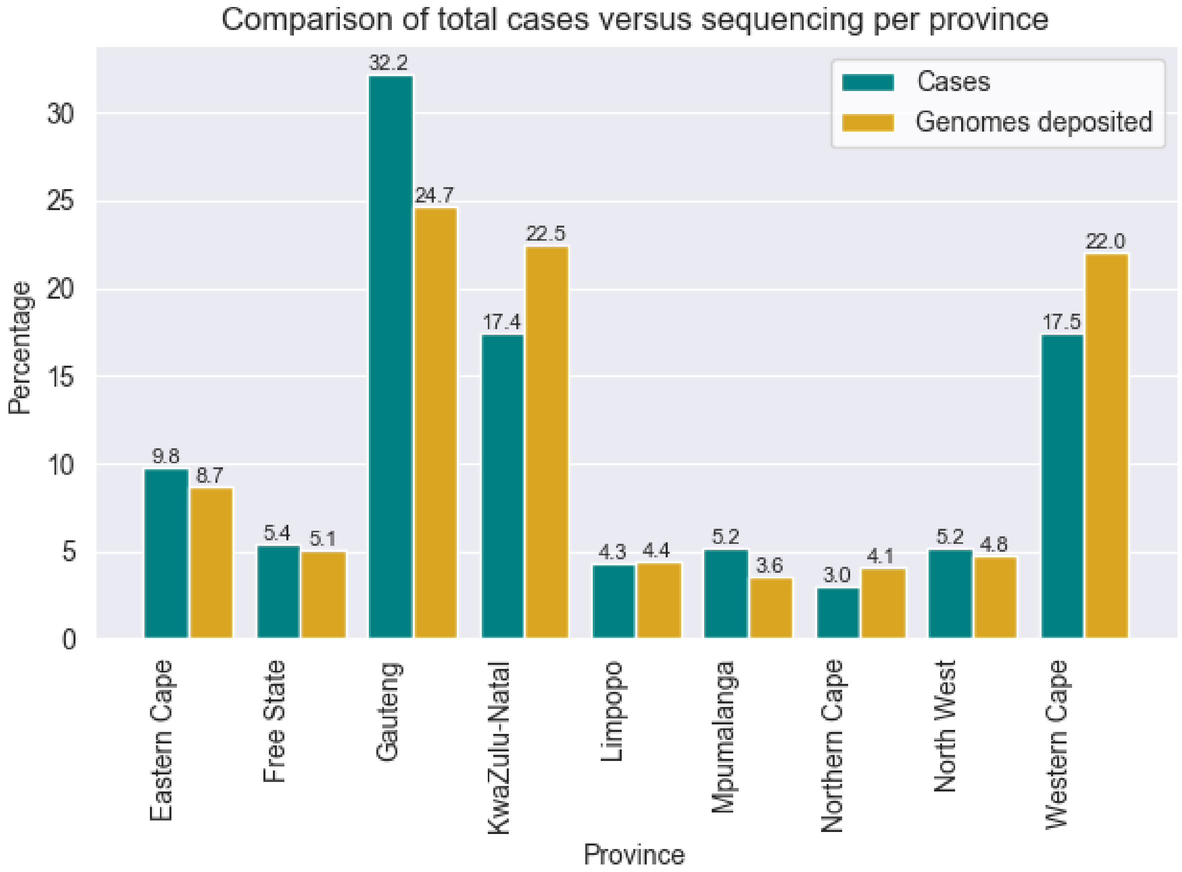
GISAID genomes vs total cases, 2020 and 2021 (N=18 449)

Provincial breakdown of genomes deposited into GISAID



Comparison of total cases versus sequencing per province



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

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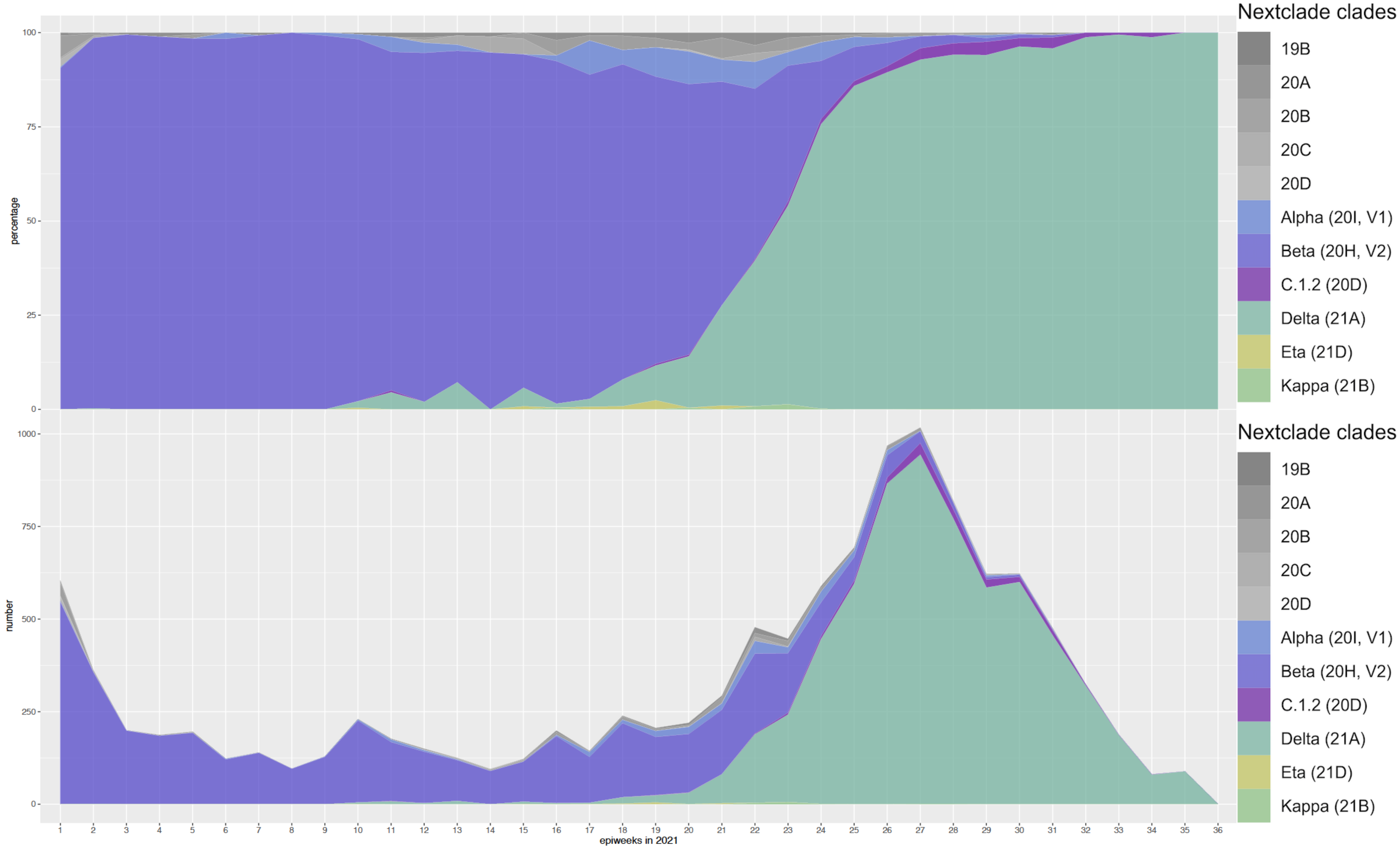
Distribution and number of clades in South Africa, 2021 (N= 12 140)



Sequencing data ending epi week 36 (ending 11 September 2021)

Currently in epi week 37 (ending 18 September 2021)

Delta came to dominate by end June at >65% , in July at >85% and in August at >90%
C.1.2 present at <3% frequency since March

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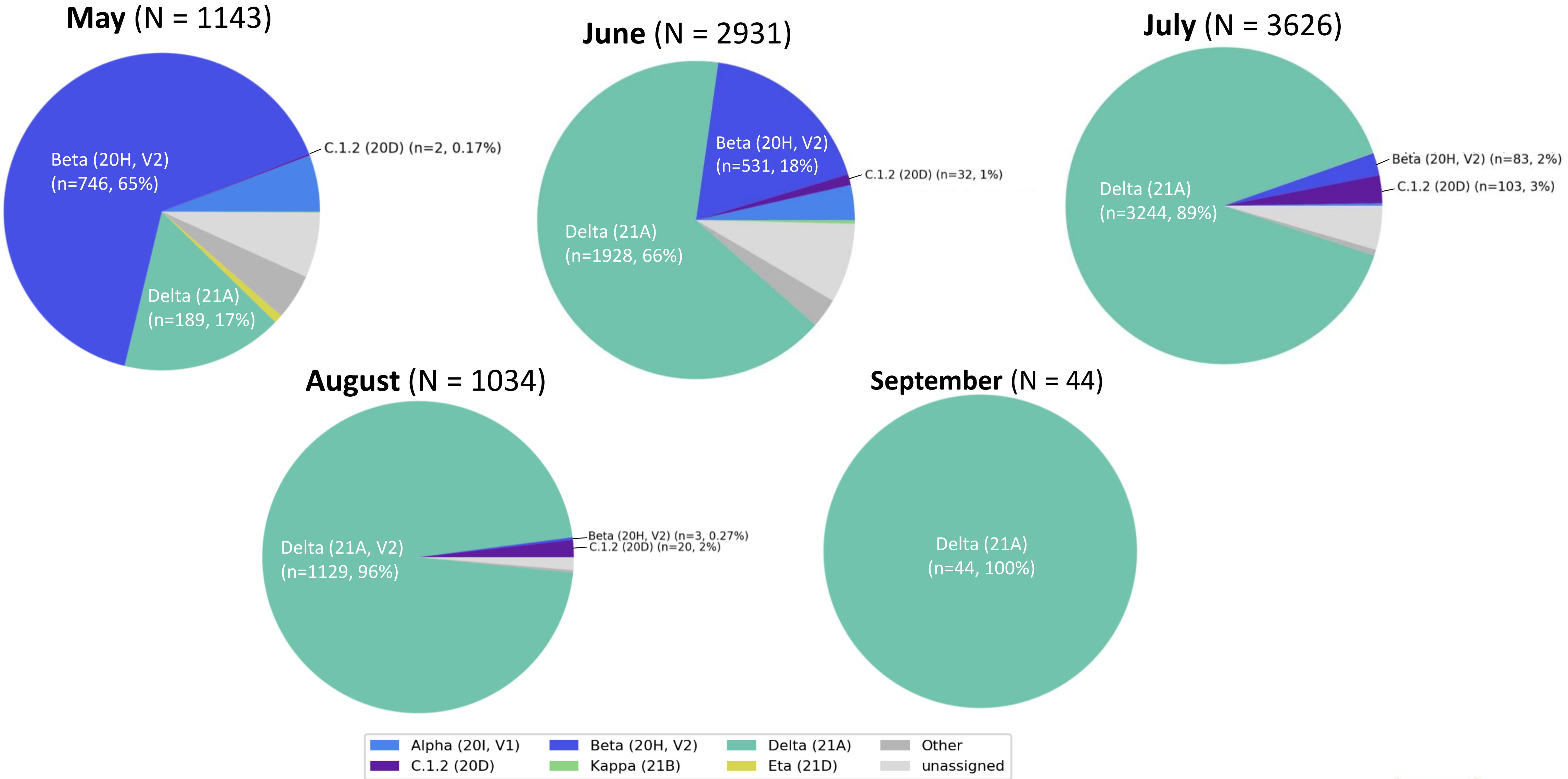
Prevalence of Variants of Concern (VOC) and Variants of Interest (VOI) in May – early September 2021 sequences, South Africa



Beta variant dominated in May, while the Delta variant dominated in June-August in South Africa

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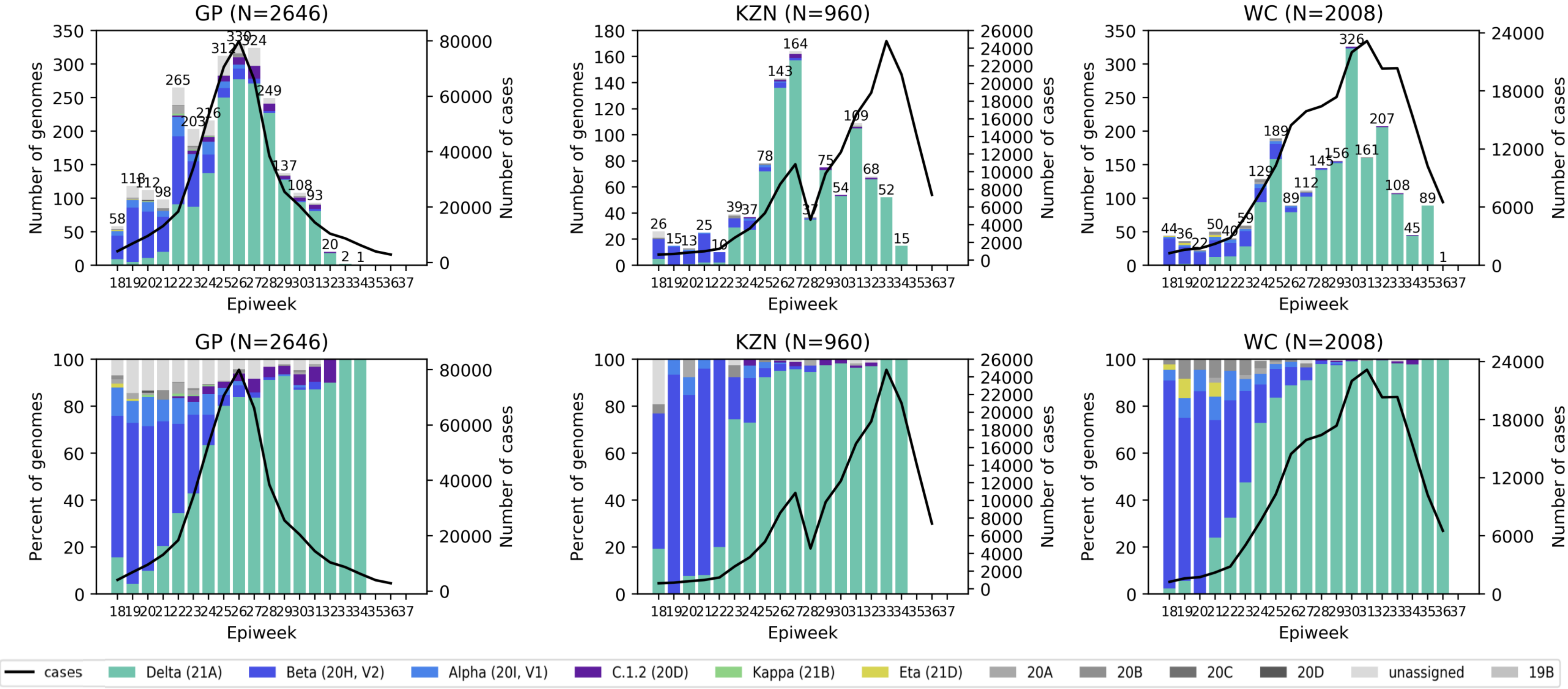
Genomes sequenced from specimens collected in May to mid-August 2021 (epiweeks 18 – 37) from KwaZulu-Natal, Gauteng, Western Cape Provinces



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 and continues to dominate in July and August

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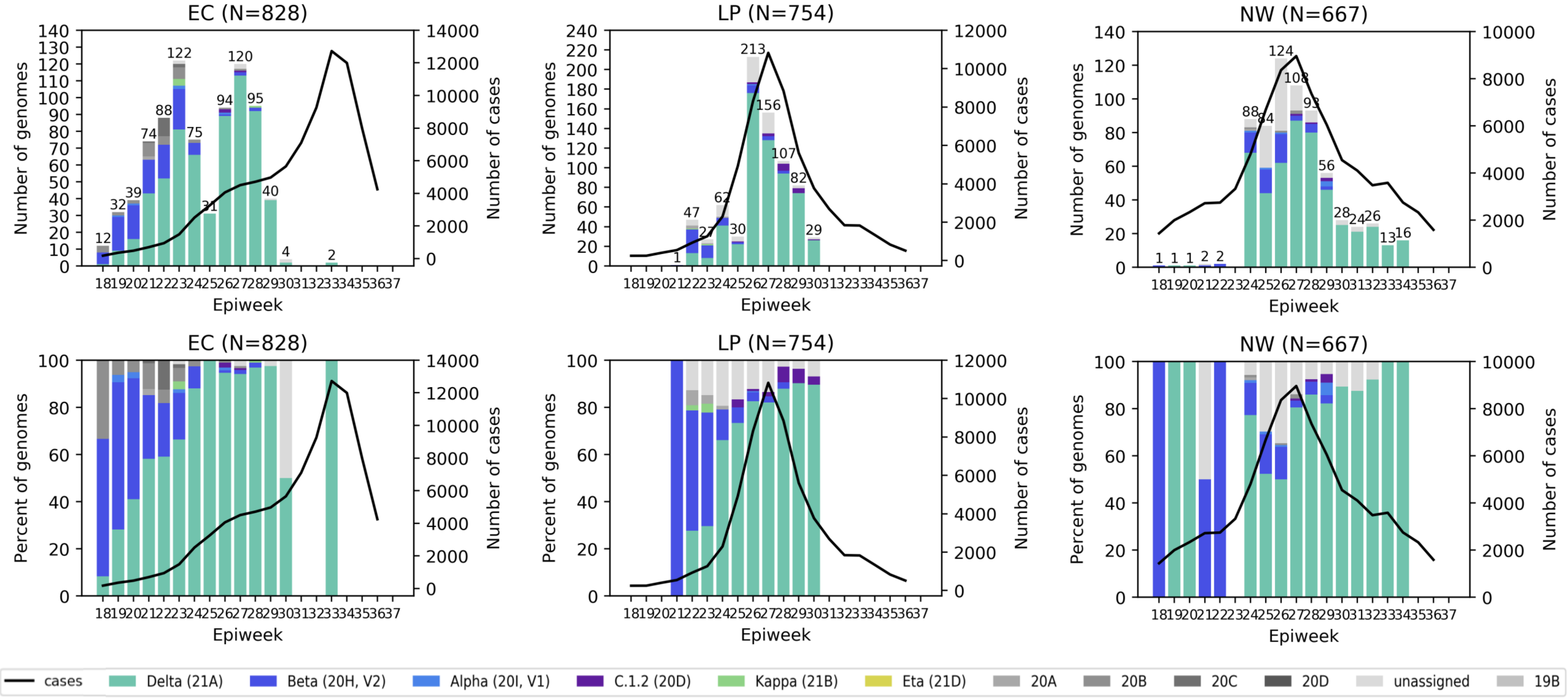
Genomes sequenced from specimens collected in May to mid-August 2021 (epiweeks 18 – 37) from Eastern Cape, Limpopo and North-West Provinces



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

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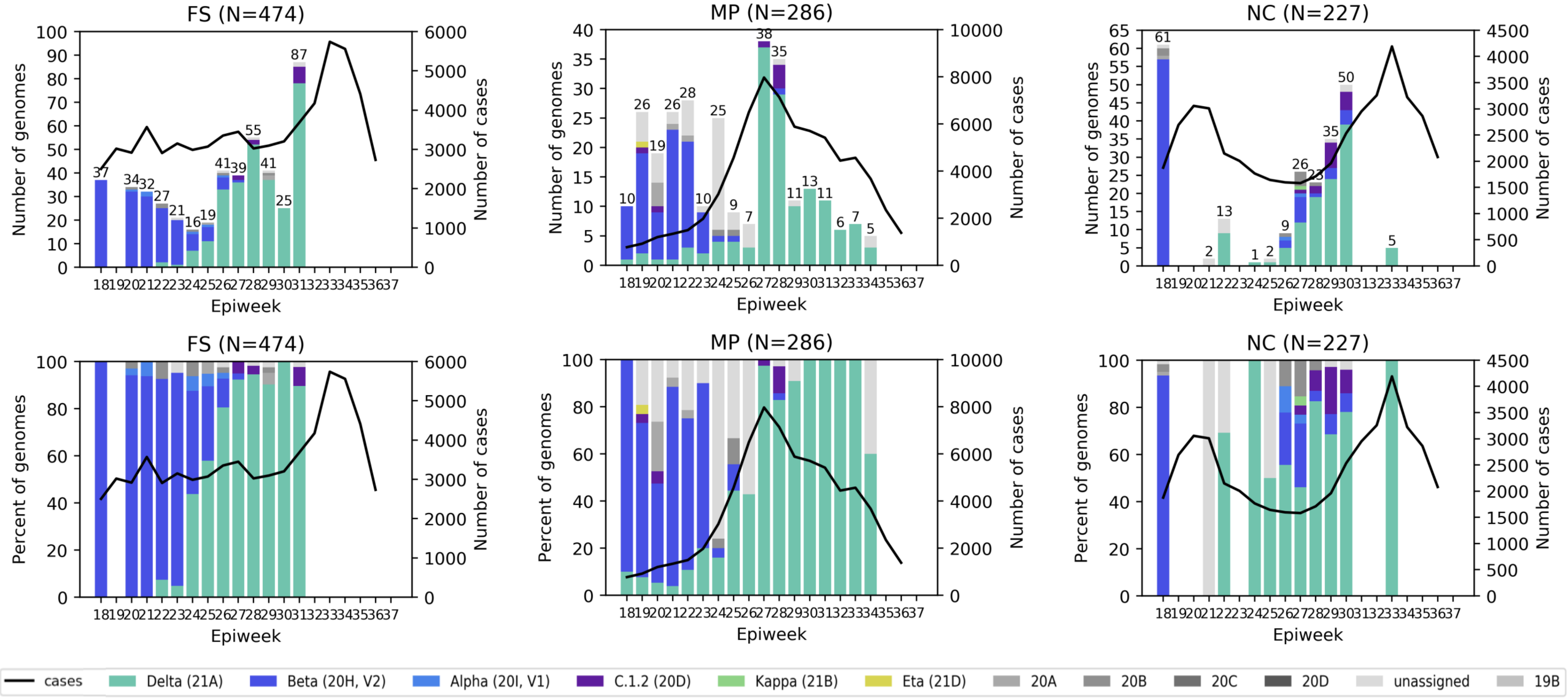
Genomes sequenced from specimens collected in May to mid-August 2021 (epiweeks 18 – 37) from Free State, Mpumalanga and Northern Cape Provinces



Despite small number of genomes, Delta dominating in FS, MP and NC provinces

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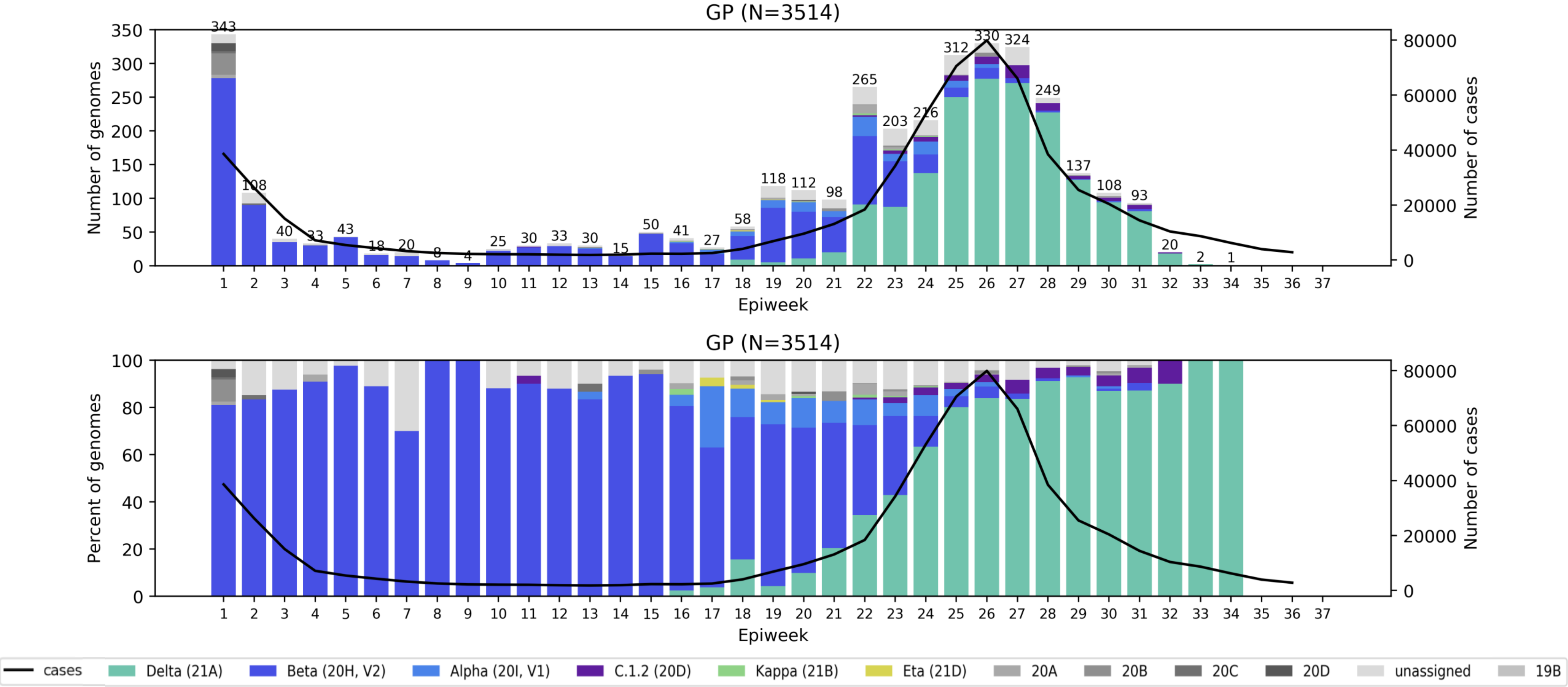
Gauteng Province, 2021, n = 3514



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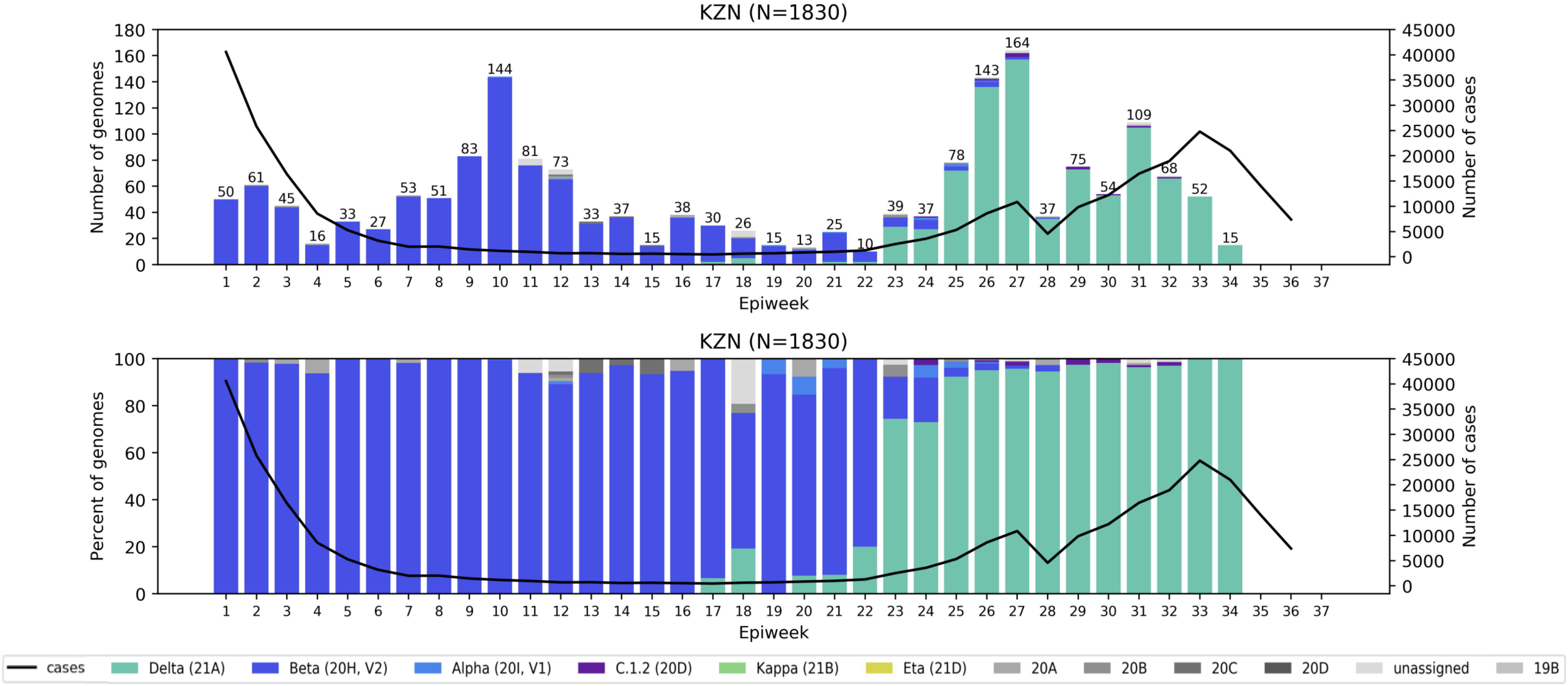
KwaZulu-Natal Province, 2021, n = 1830



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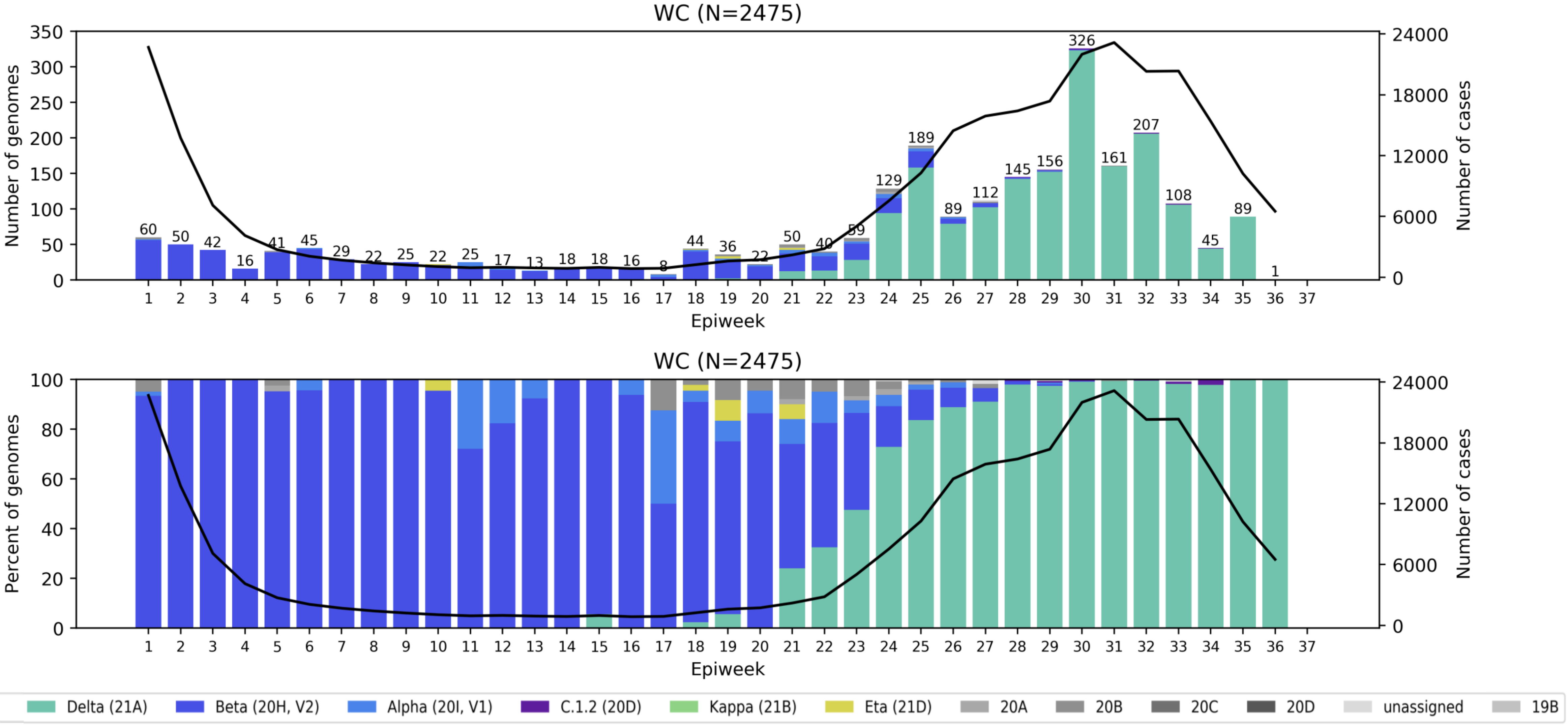
Western Cape Province, 2021, n = 2475



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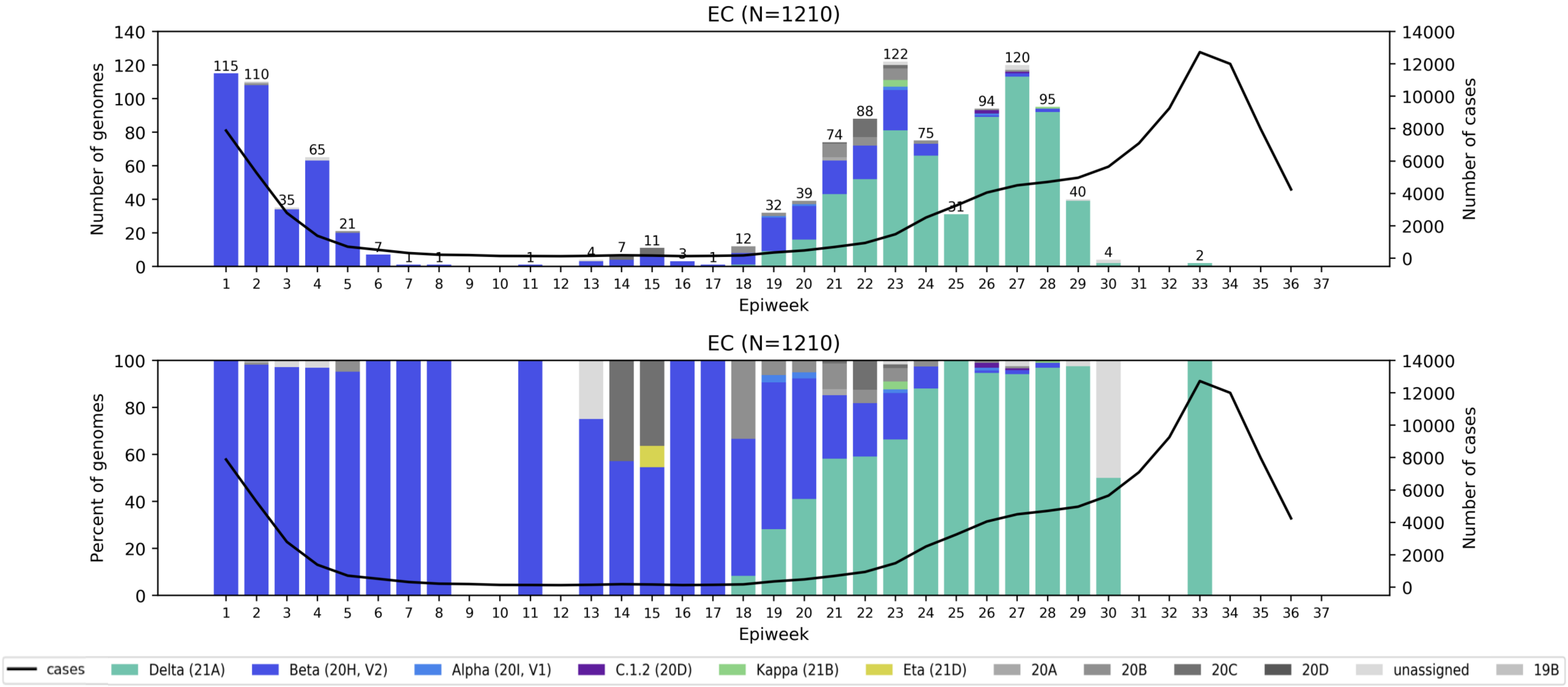
Eastern Cape Province, 2021, n = 1210



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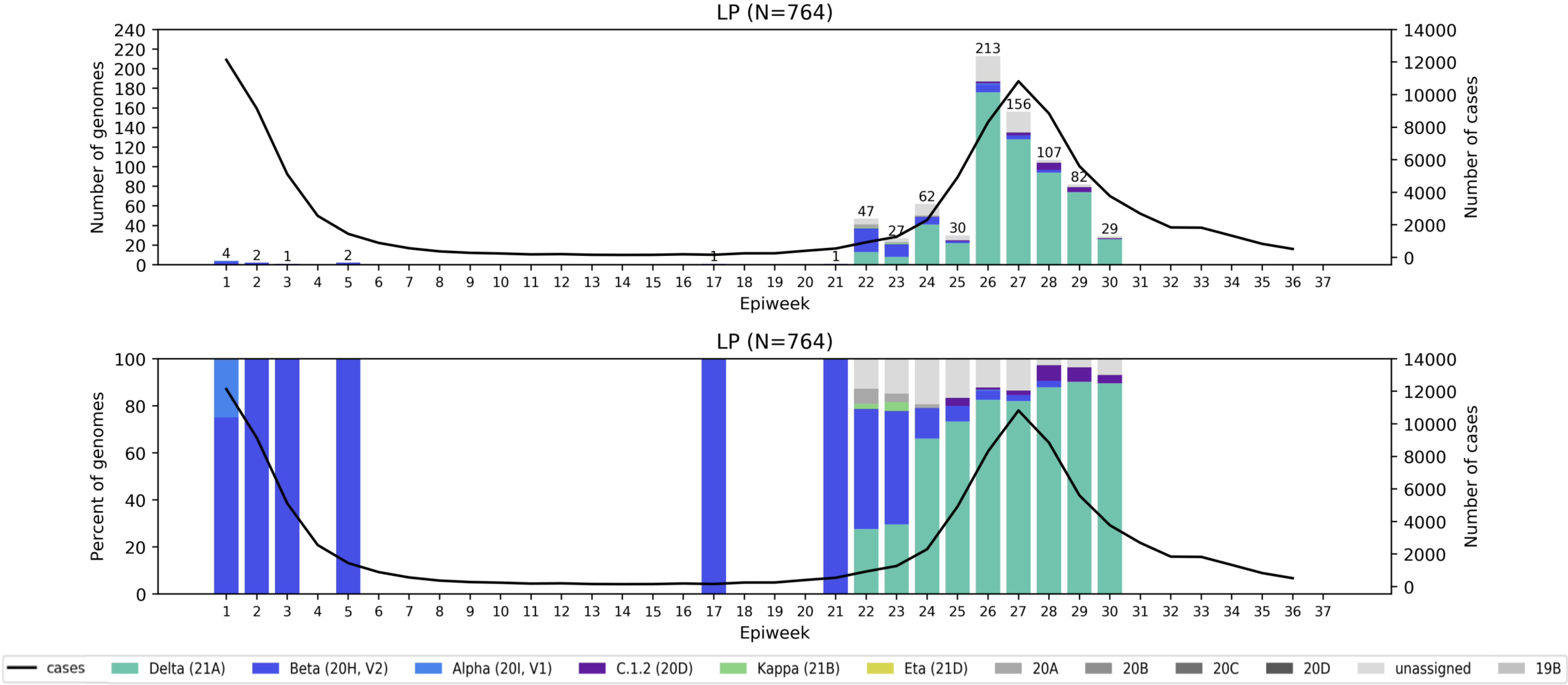
Limpopo Province, 2021, n = 764



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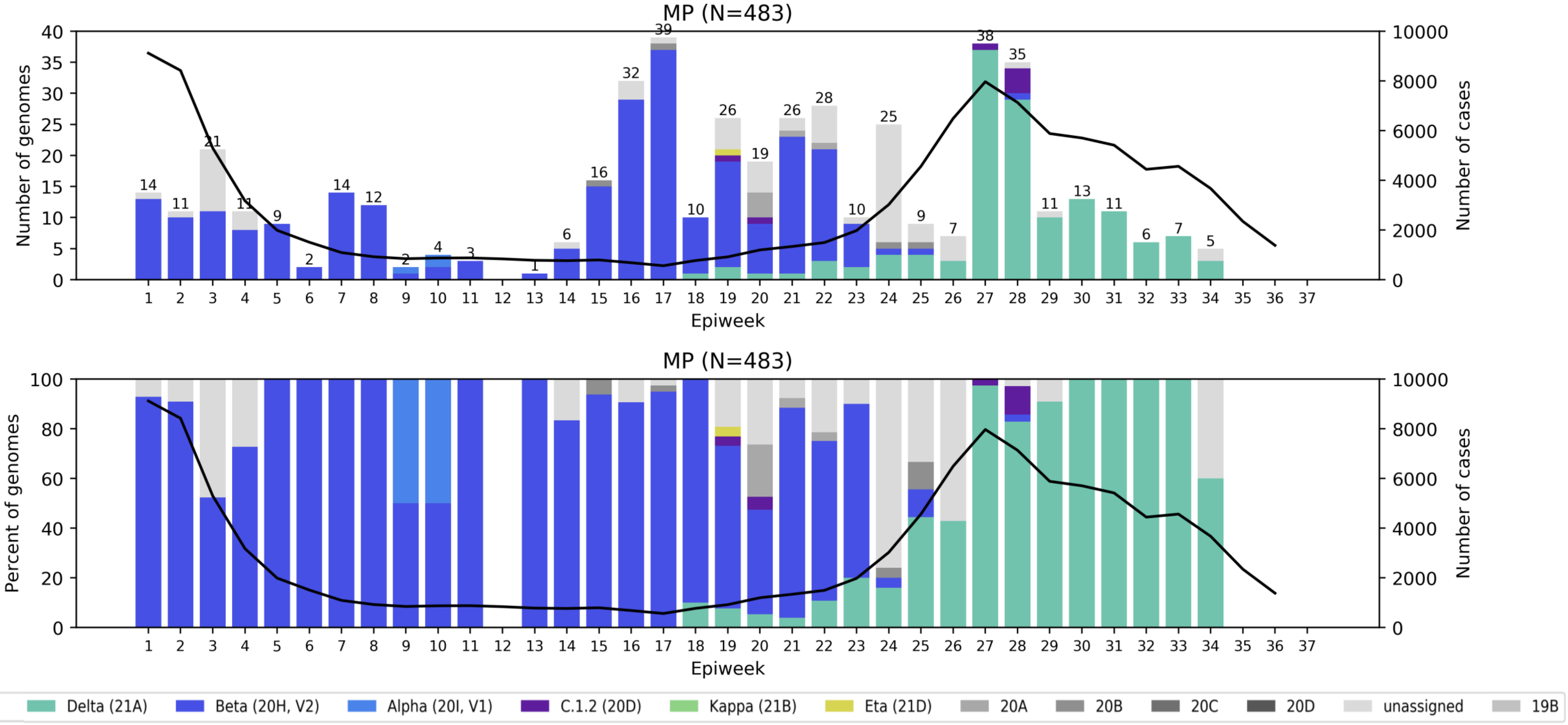
Mpumalanga Province, 2021, n = 483



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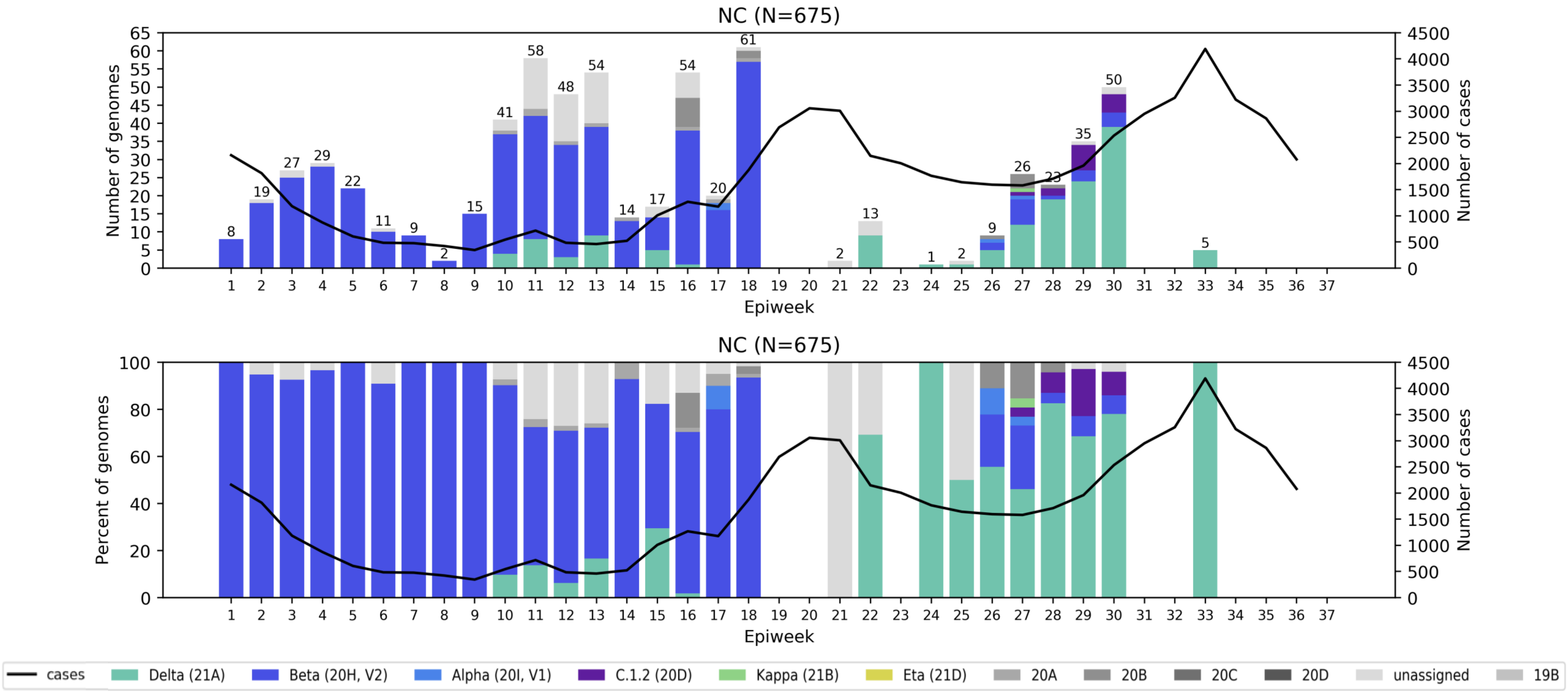
Northern Cape Province, 2021, n = 675



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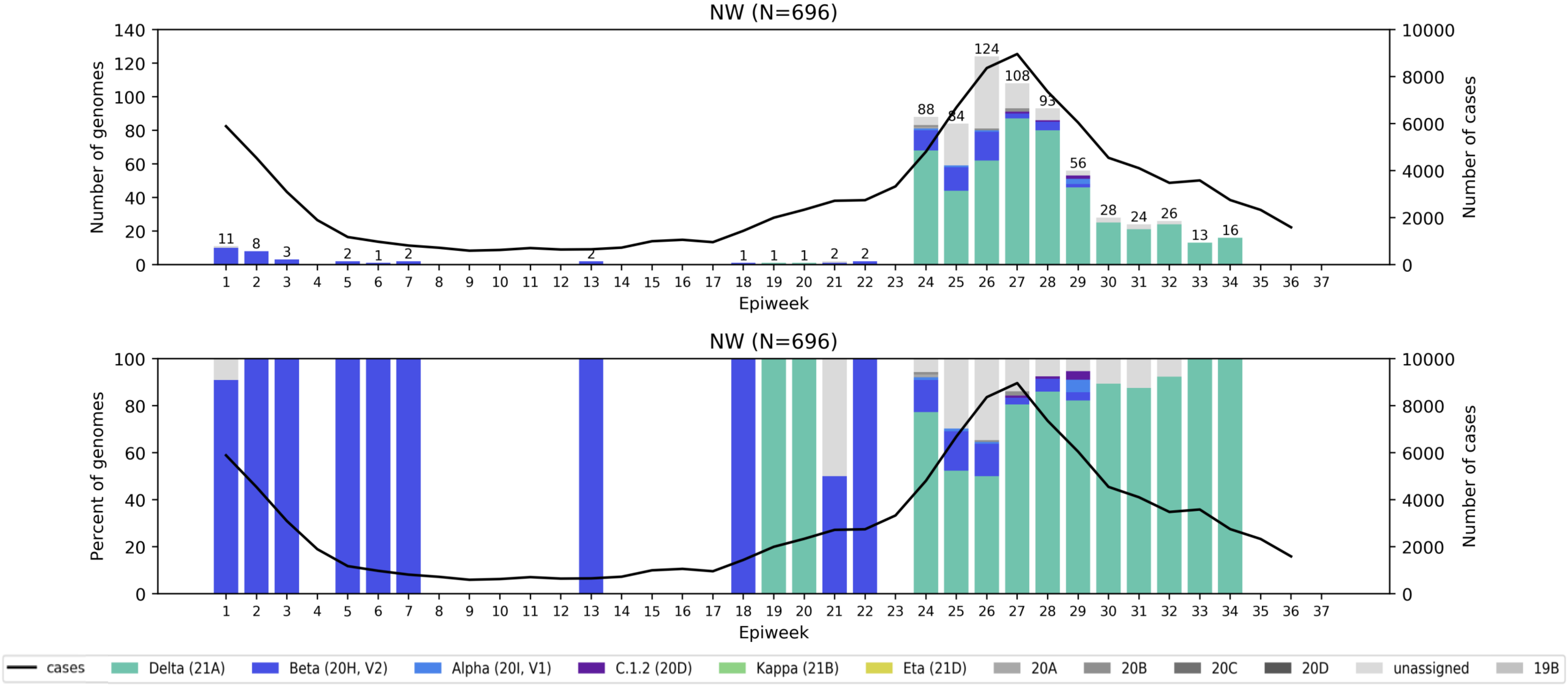
North West Province, 2021, n = 696



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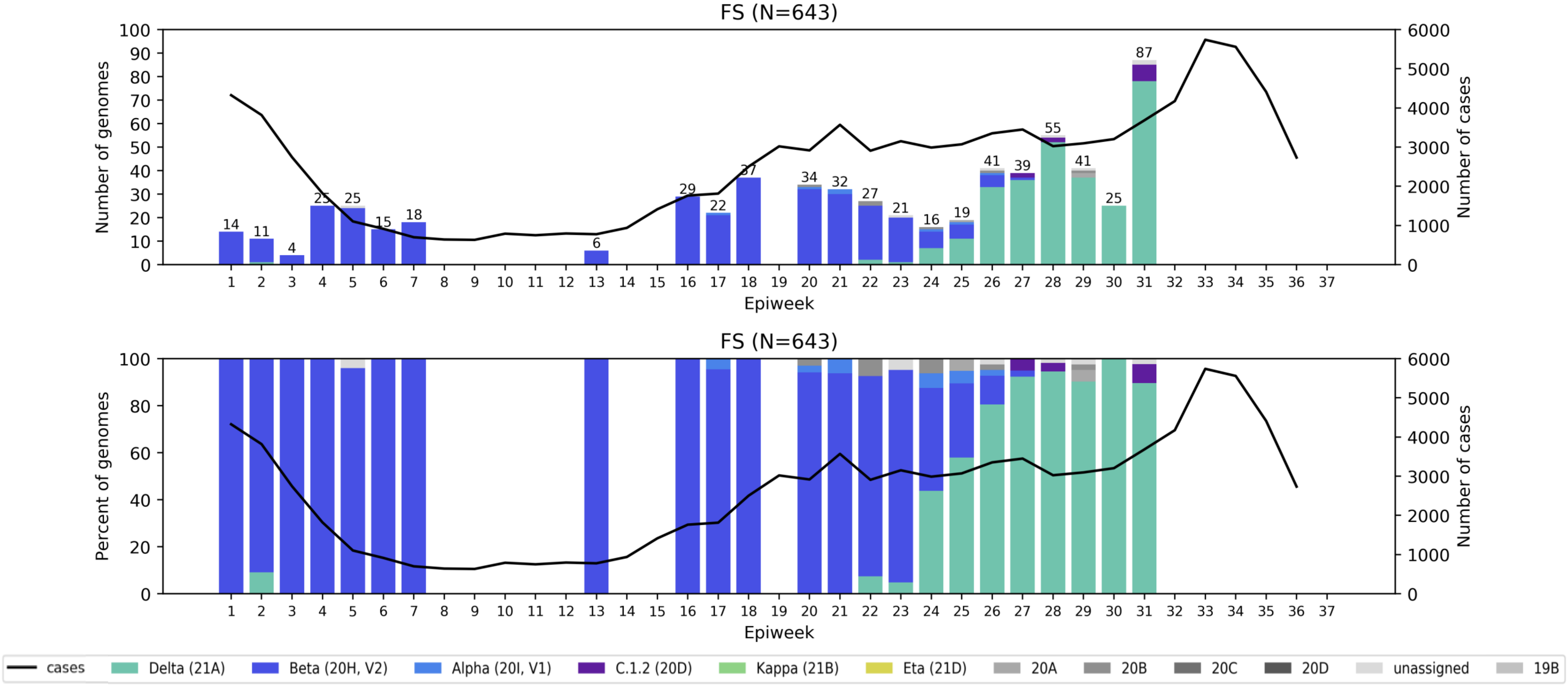
Free State Province, 2021, n = 643



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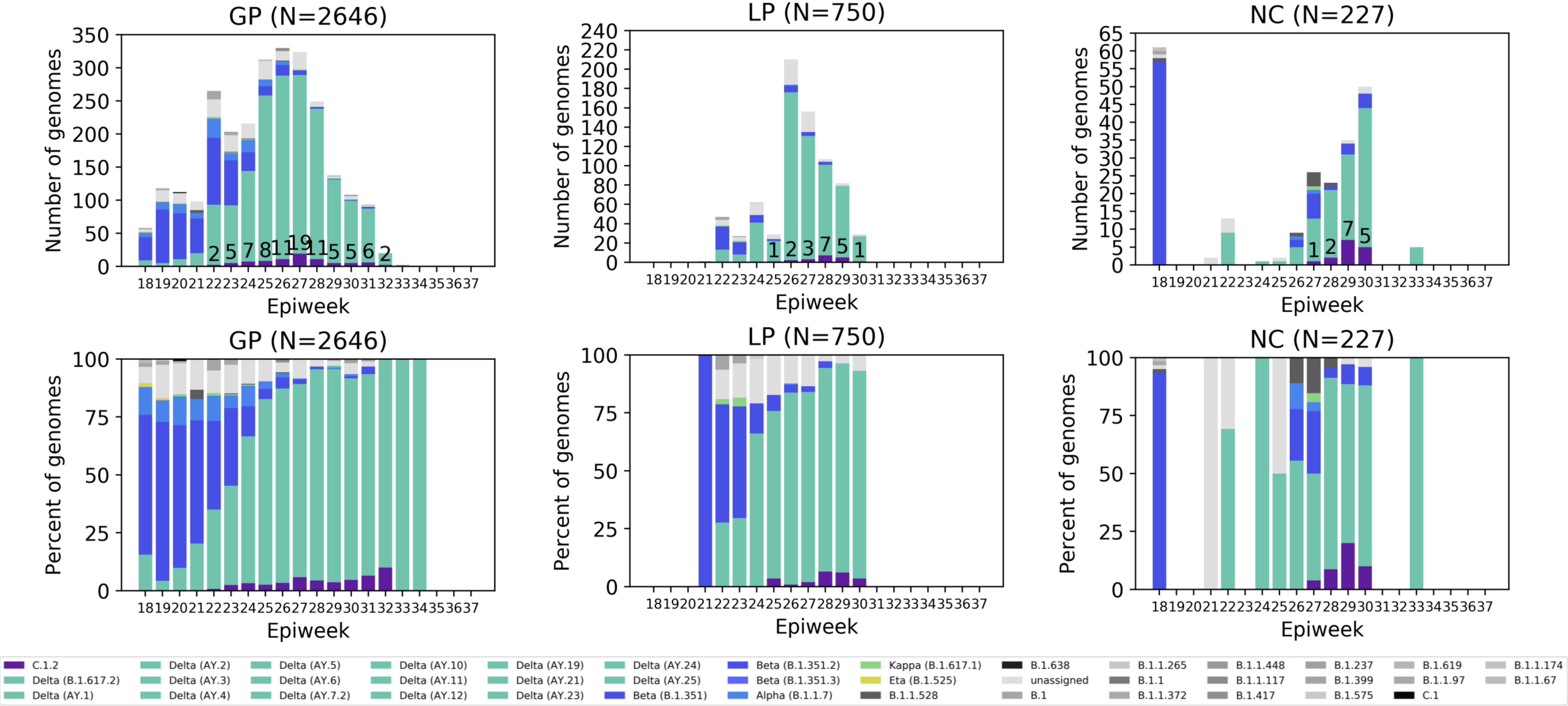
C.1.2 (n=150 in SA) in May – August 2021 by epiweek

Number of C.1.2 samples indicated above bar



C.1.2 has now been detected in all provinces. The majority of samples have been detected in Gauteng (n=81), followed by Limpopo (n=19) and the Northern Cape (n=15).

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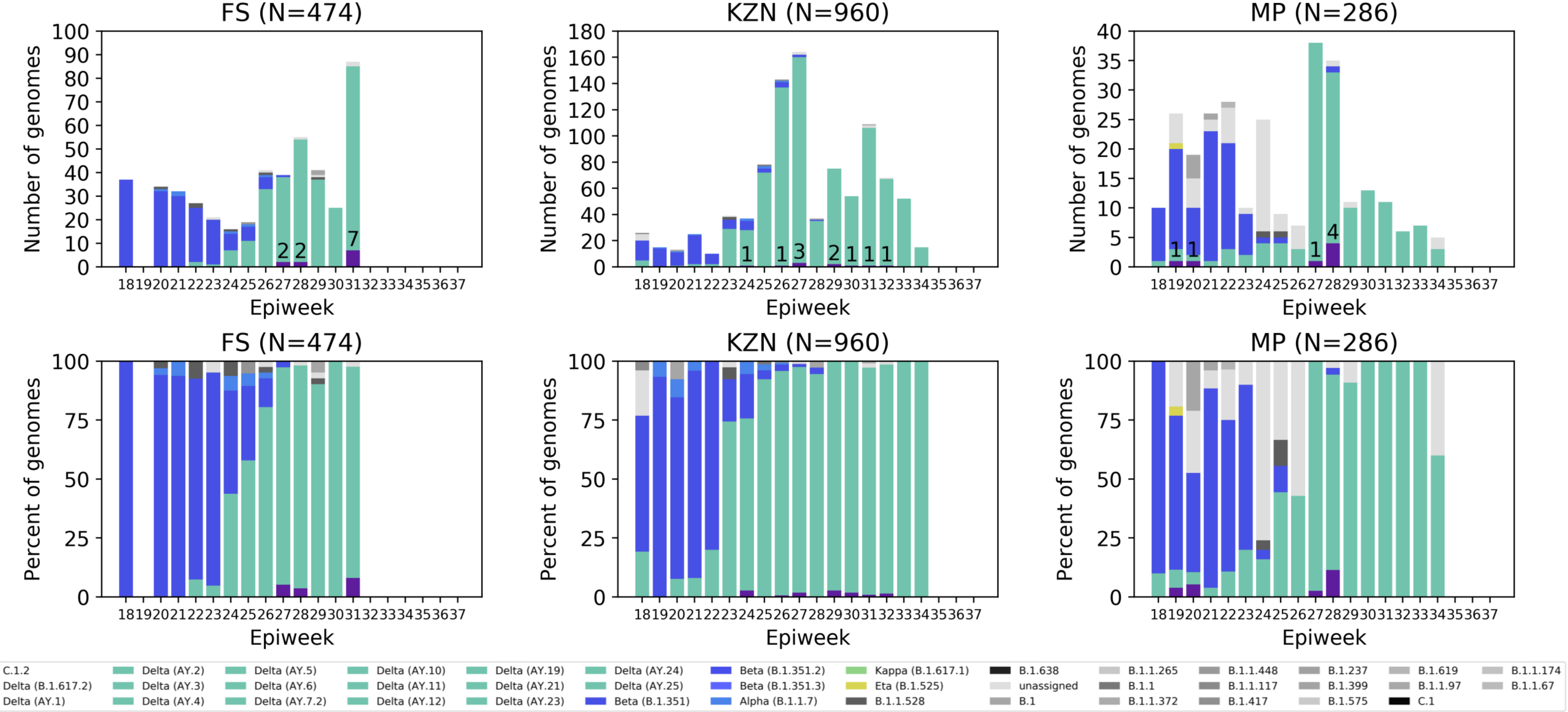
C.1.2 (n=150 in SA) in May – August 2021 by epiweek

Number of C.1.2 samples indicated above bar



C.1.2 has now been detected in all provinces. 11 sequences have been detected in the Free State, 10 in KwaZulu-Natal, and 7 in Mpumalanga.

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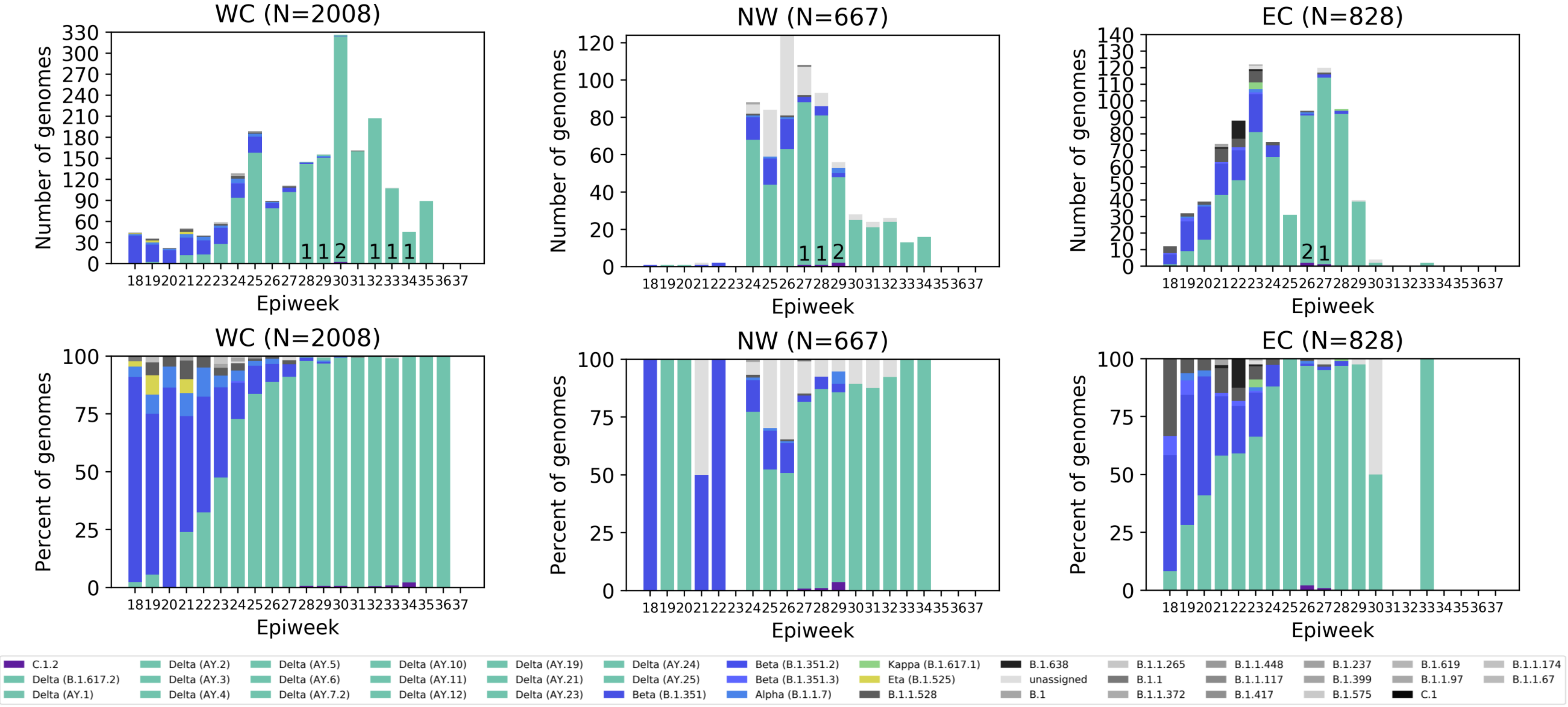
C.1.2 (n=150 in SA) in May – August 2021 by epiweek

Number of C.1.2 samples indicated above bar



The Western Cape has 7 sequences, the North West has 4, and the Eastern Cape has 3 detections of C.1.2.

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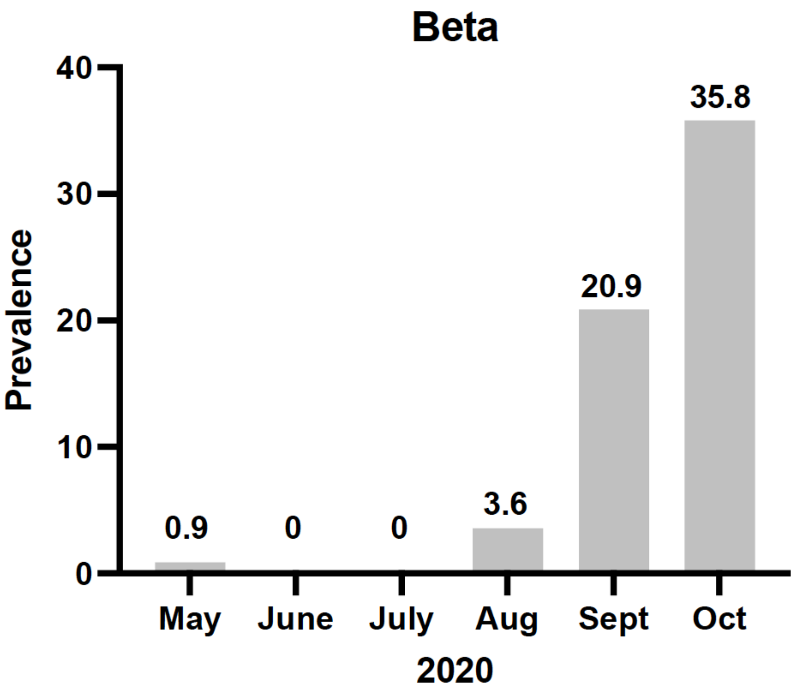
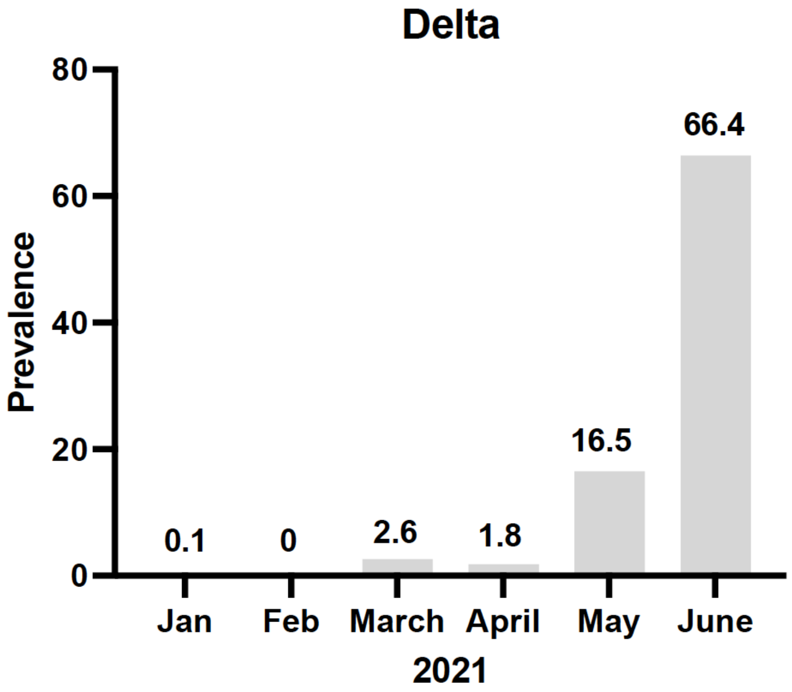
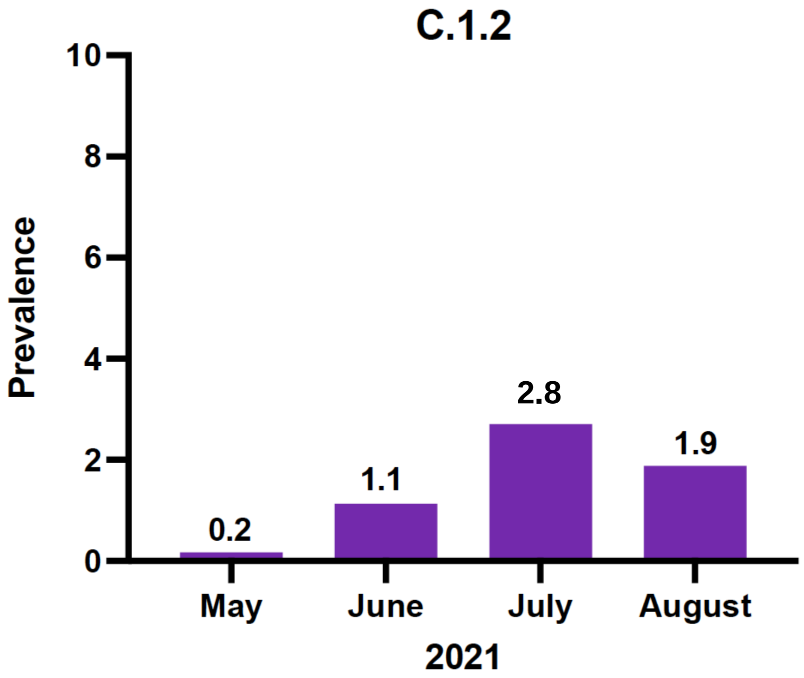
C.1.2 growth compared to Beta and Delta







C.1.2 is being continually monitored and is currently only detected at low levels

Summary

- Delta continues to dominate in all provinces from specimens collected in August

- Overall diversity of lineages decreased as Delta became dominant

- Lambda and Mu variants not detected in South Africa

- Mutated C.1.2 lineage has now been detected in all provinces of South Africa
  - The frequency of C.1.2 at less than 3% of genomes

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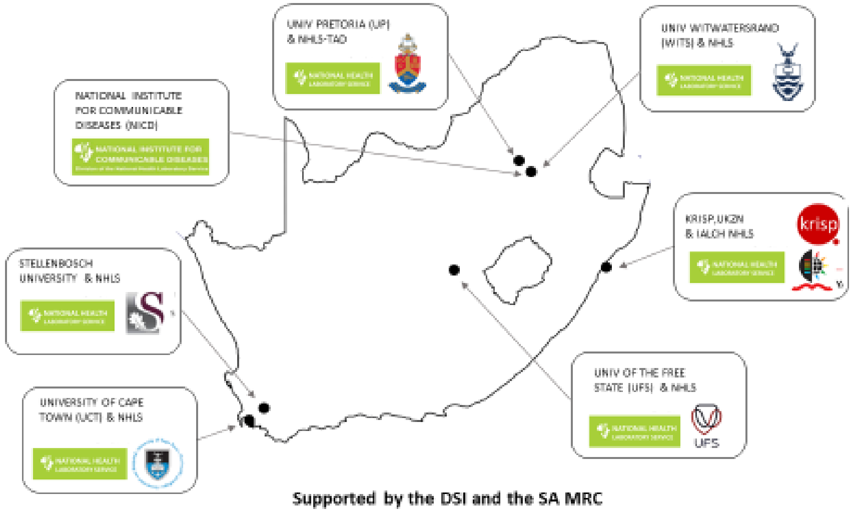

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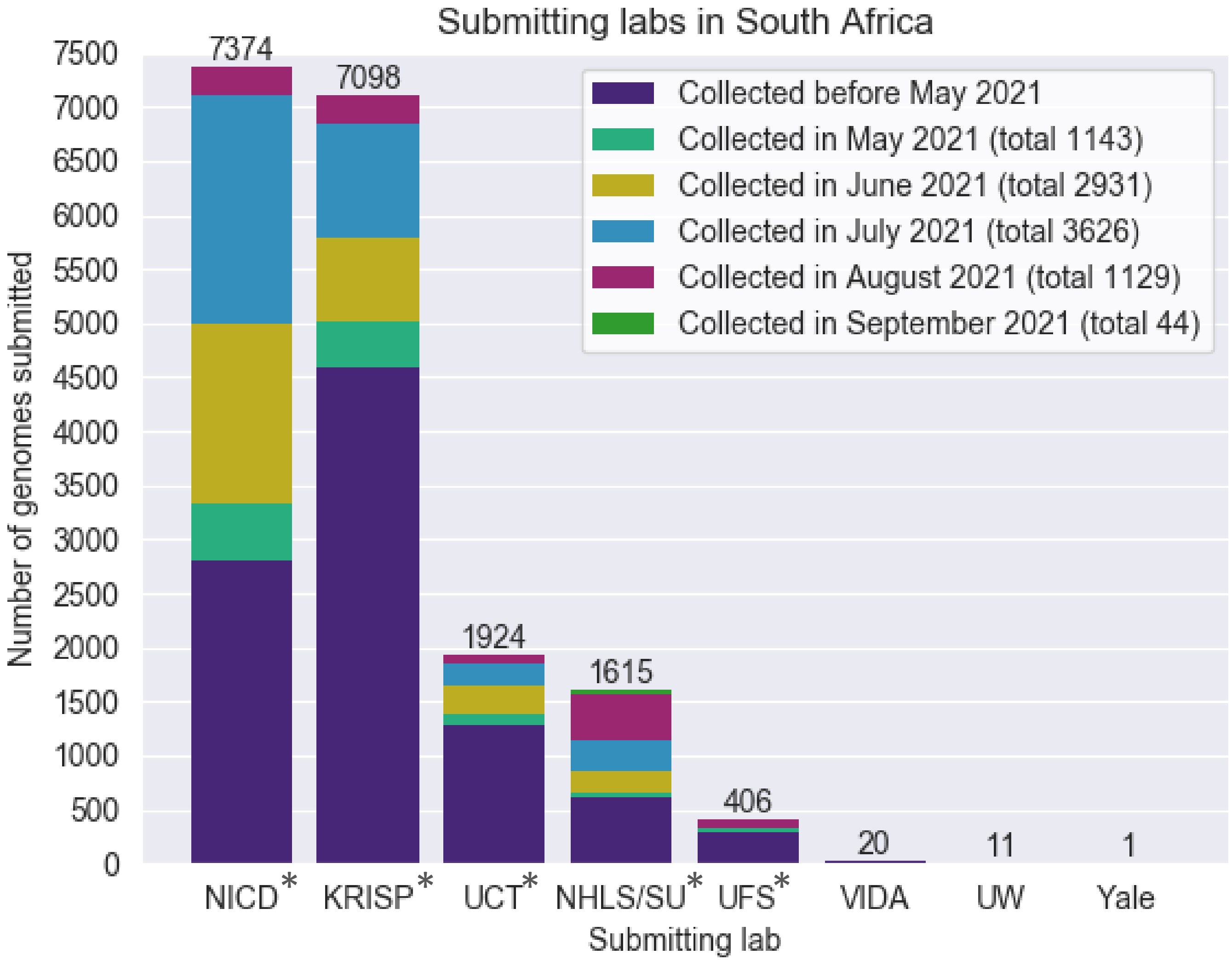
South African genomes submitted per sequencing lab, 2020 and 2021 (N=18 449)



*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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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	GH/501Y.V2	20H (V2)	+S:L18F	South Africa, May-2020	18-Dec-2020
Gamma	P.1	GR/501Y.V3	20J (V3)	+S:681H	Brazil, Nov-2020	11-Jan-2021
Delta	B.1.617.2[§]	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 17 September 2021

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

[+] Includes all descendant lineages.

[#] Includes all Q.* lineages in the PANGO nomenclature system.

[§] Includes all AY.* lineages in the PANGO nomenclature system.

Currently designated Variants of Interest (VOI)

WHO label	Pango* lineages	GISAID clade	Nextstrain clade	Earliest documented samples	Date of designation
Lambda	C.37	GR/452Q.V1	21G	Peru, Dec-2020	14-Jun-2021
Mu	B.1.631	GH	21H	Colombia, Jan-2021	30-Aug-2021

https://www.who.int/en/activities/tracking-SARS-CoV-2-variants/ accessed 17 September 2021

*Includes all descendant lineages.

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.)