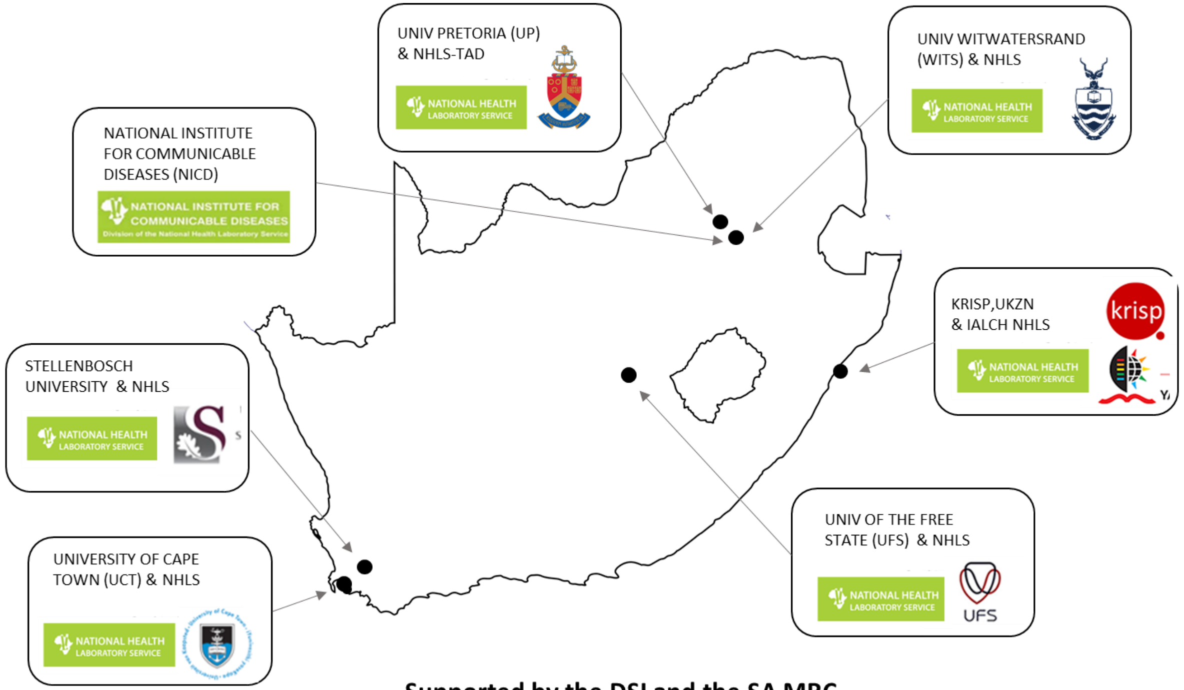
Network for Genomic Surveillance South Africa (NGS-SA)

SARS-CoV-2 Sequencing Update
22 October 2021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NATIONAL INSTITUTE FOR COMMUNICABLE DISEASES (NICD)

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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 22 October at 08h16

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

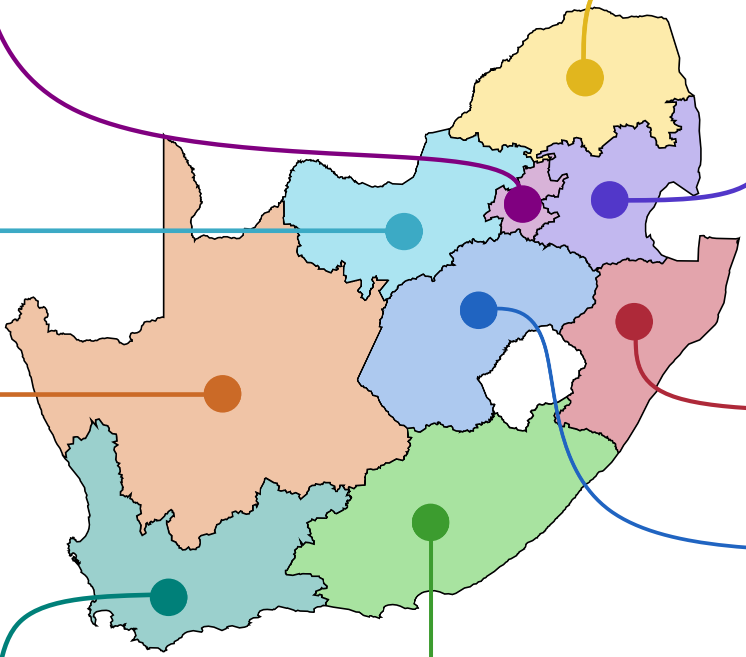
Elbe, S., and Buckland-Merrett, G. (2017) Data, disease and diplomacy: GISAID's innovative contribution to global health. Global Challenges, 1:33-46. DOI: 10.1002/gch2.1018 PMCID: 31565258

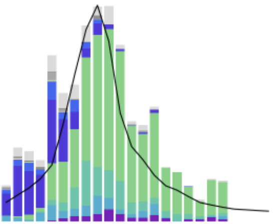
Shu, Y., McCauley, J. (2017) GISAID: Global initiative on sharing all influenza data – from vision to reality. EuroSurveillance, 22(13) DOI: 10.2807/1560-7917.ES.2017.22.13.30494 PMCID: PMC5388101

Case data is based on specimen collection date. Cases 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 - 41





Gauteng

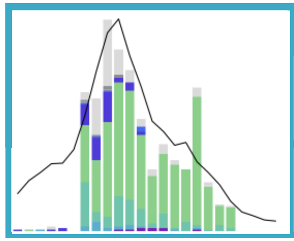
PTP: 1.3%

Genomes 3 243 (27.6%)

Cases 493 668 (37.1%)

Genomes deposited in the last week

🟦 9 🟩 4 🟩 81 🟦 2 🟪 2 ⬜ 2



North West

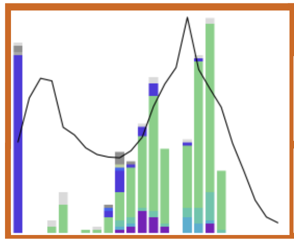
PTP: 3.1%

Genomes 935 (0.8%)

Cases 82 244 (6.2%)

Genomes deposited in the last week

🟦 2 🟩 9 🟩 35 🟪 1 ⬜ 3



Northern Cape

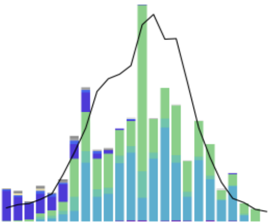
PTP: 8.8%

Genomes 427 (3.6%)

Cases 51 413 (3.9%)

Genomes deposited in the last week

🟦 2 🟩 18



Western Cape

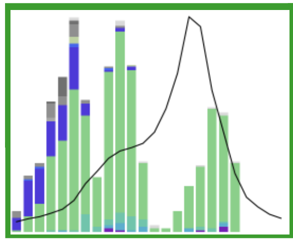
PTP: 3.4%

Genomes 2 674 (22.7%)

Cases 225 641 (17.0%)

Genomes deposited in the last week

🟦 1 🟩 4 🟩 42



Eastern Cape

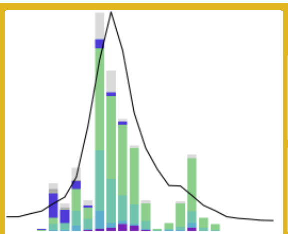
PTP: 3.1%

Genomes 1 083 (9.2%)

Cases 95 804 (7.2%)

Genomes deposited in the last week

🟩 18



Limpopo

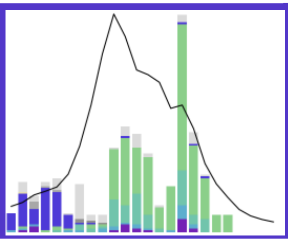
PTP: 1.6%

Genomes 897 (7.6%)

Cases 58 096 (4.4%)

Genomes deposited in the last week

🟩 3



Mpumalanga

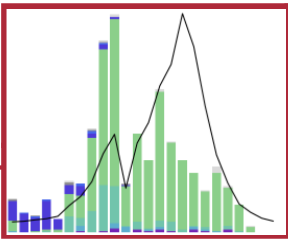
PTP: 2.5%

Genomes 604 (5.1%)

Cases 73 149 (5.5%)

Genomes deposited in the last week

🟦 7 🟩 7 🟩 49 🟪 6 ⬜ 2



KwaZulu-Natal

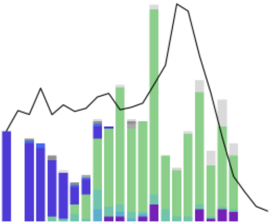
PTP: 2.4%

Genomes 1 144 (9.7%)

Cases 177 708 (13.4%)

Genomes deposited in the last week

🟩 1 🟩 25 ⬜ 1



Free State

PTP: 5.4%

Genomes 750 (6.4%)

Cases 73 074 (5.5%)

Genomes deposited in the last week

🟩 2 🟩 56 🟪 9 ⬜ 16

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

Bar graphs represent genomes sequenced per epiweek, with lines representing cases by collection date (weeks 18 – 41)
Genomes and cases presented as provincial total (percentage of national total) for epiweeks 18 – 41
PTP: percentage testing positive

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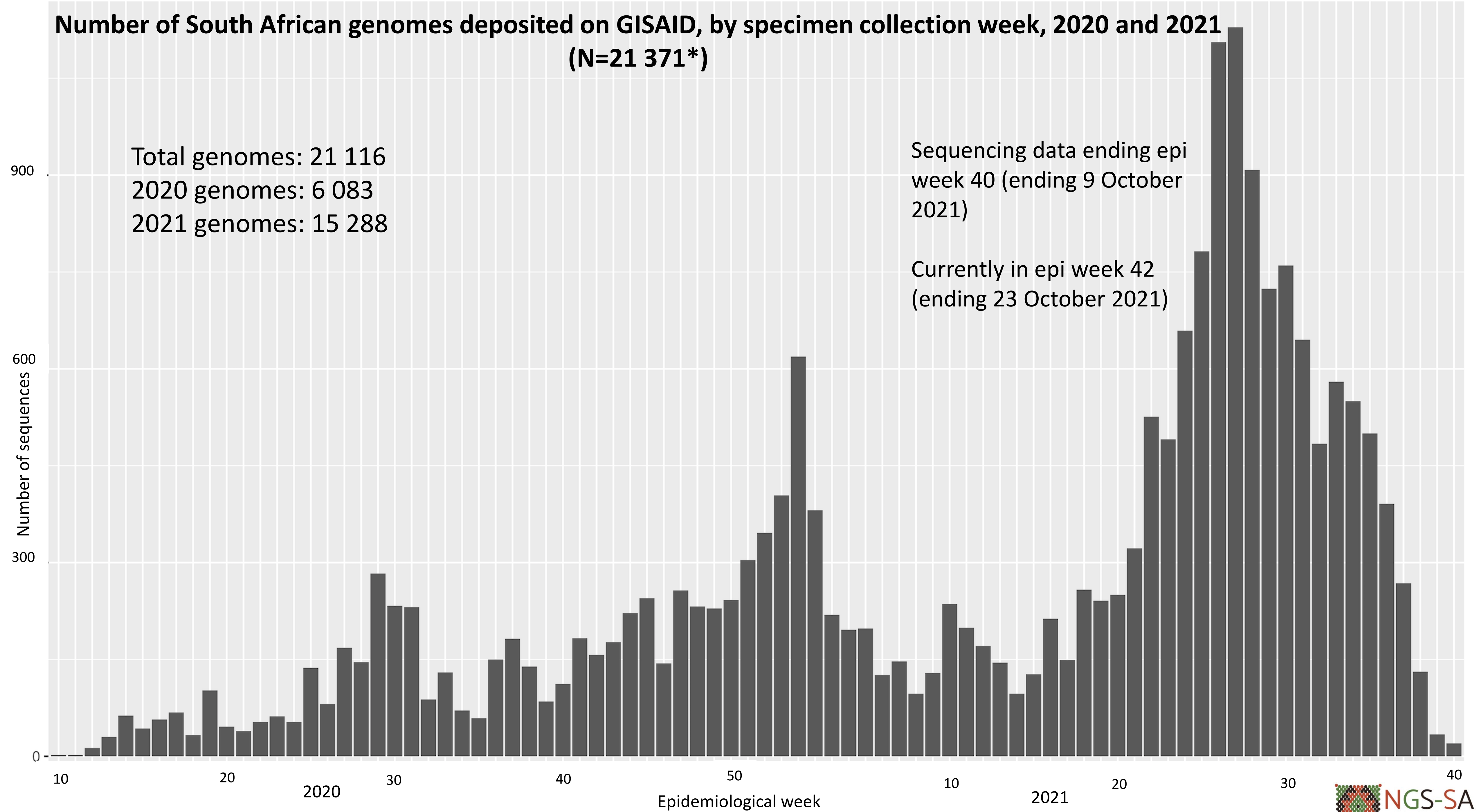
Number of South African genomes deposited on GISAID, by specimen collection week, 2020 and 2021
(N=21 371*)



Total genomes: 21 116
2020 genomes: 6 083
2021 genomes: 15 288

Sequencing data ending epi week 40 (ending 9 October 2021)

Currently in epi week 42 (ending 23 October 2021)

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

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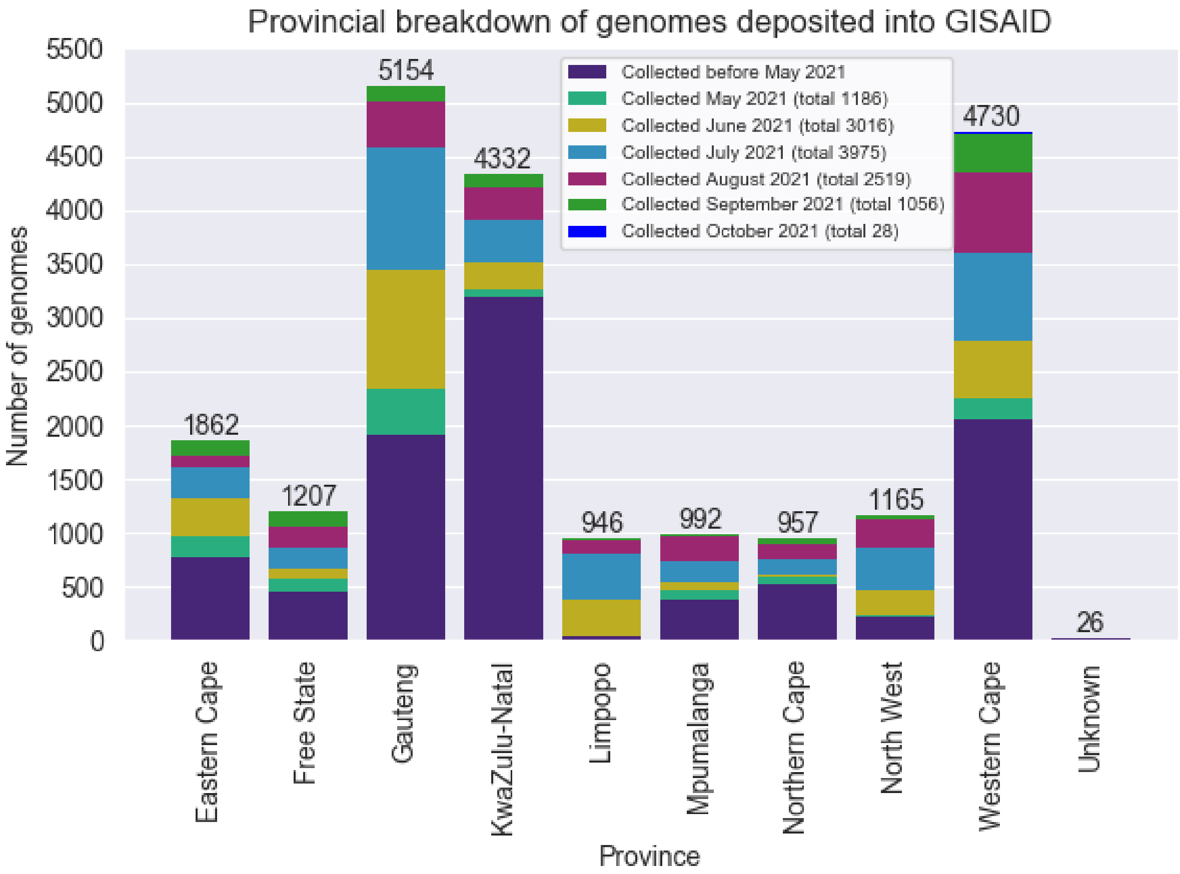
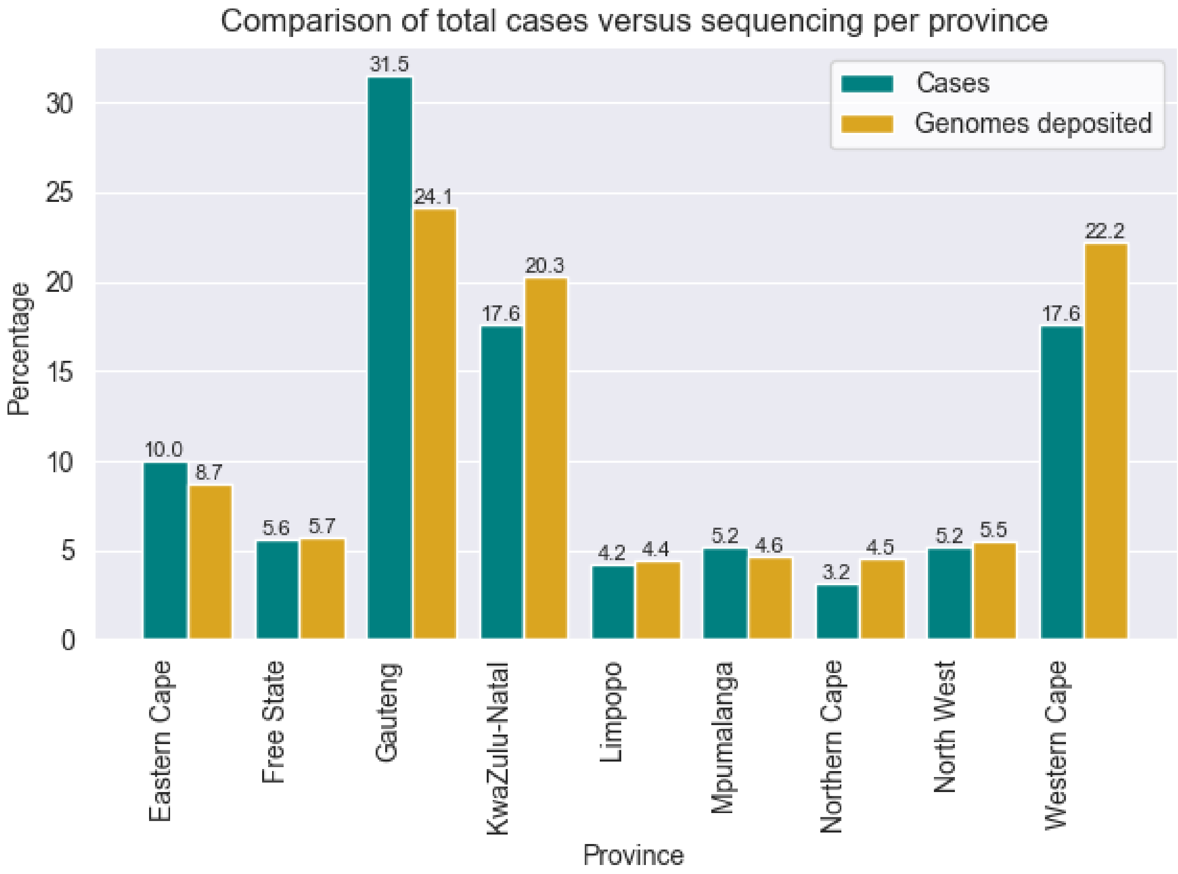
GISAID genomes vs total cases, 2020 and 2021 (N=21 371)





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

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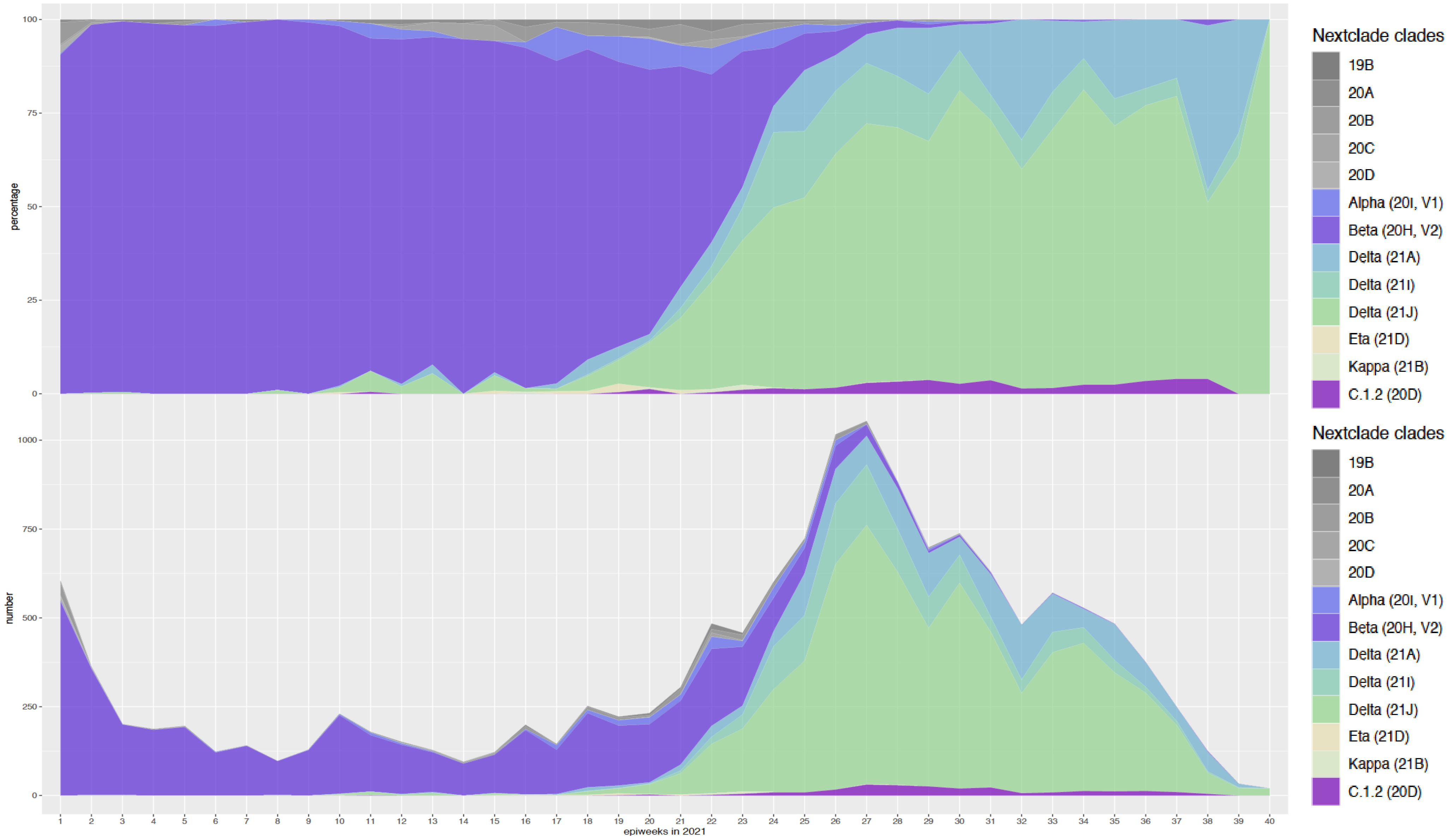
Surveillance in South Africa

Distribution and number of clades in South Africa, 2021 (N= 15 288)



Delta has recently been split into three clades (21A, 21I, 21J).

Sequencing data ending epi week 40 (ending 9 October 2021)

Currently in epi week 42 (ending 23 October 2021)

Delta came to dominate by end June at >65% , in July at >85% and in August and September at >90%
C.1.2 present at <4% frequency since March

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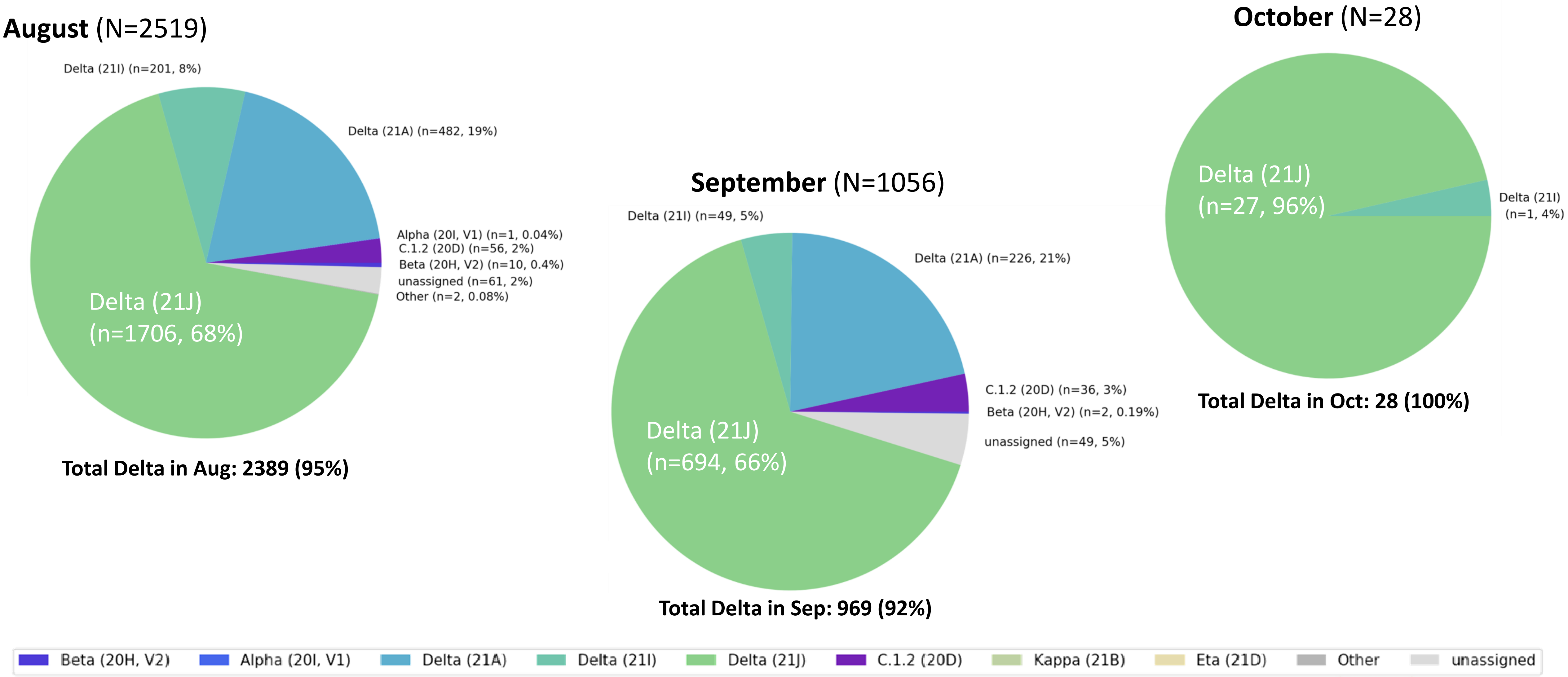
Prevalence of Variants of Concern (VOC) and Variants of Interest (VOI) in August – October 2021 sequences, South Africa



Total Delta in Aug: 2389 (95%)

Total Delta in Sep: 969 (92%)

Total Delta in Oct: 28 (100%)

The Delta variant dominated in July and August in South Africa, and appears to still dominate in early September.

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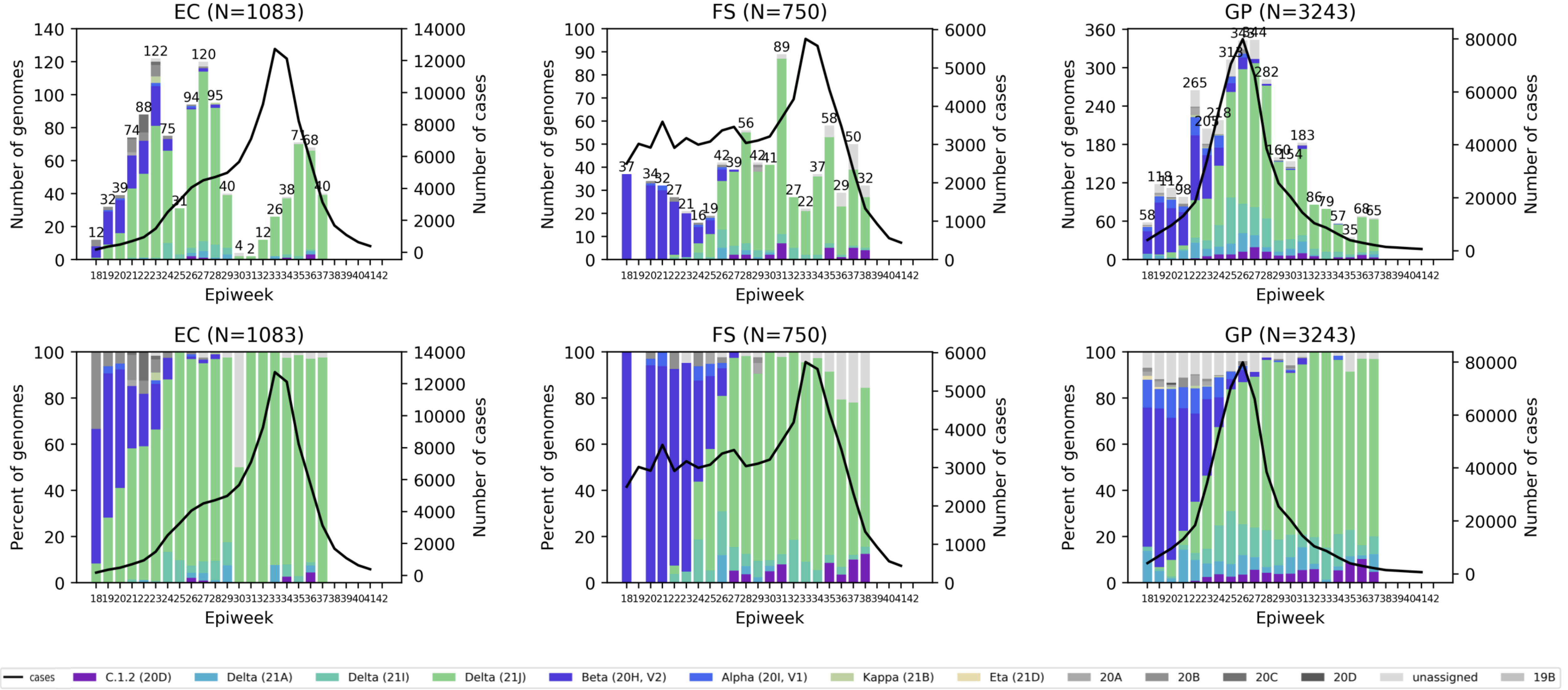
Genomes sequenced from specimens collected in May to mid-September 2021 (epiweeks 18 – 42) from Eastern Cape, Free State and Gauteng Provinces



Delta dominates the third wave in Eastern Cape, Free State and Gauteng provinces

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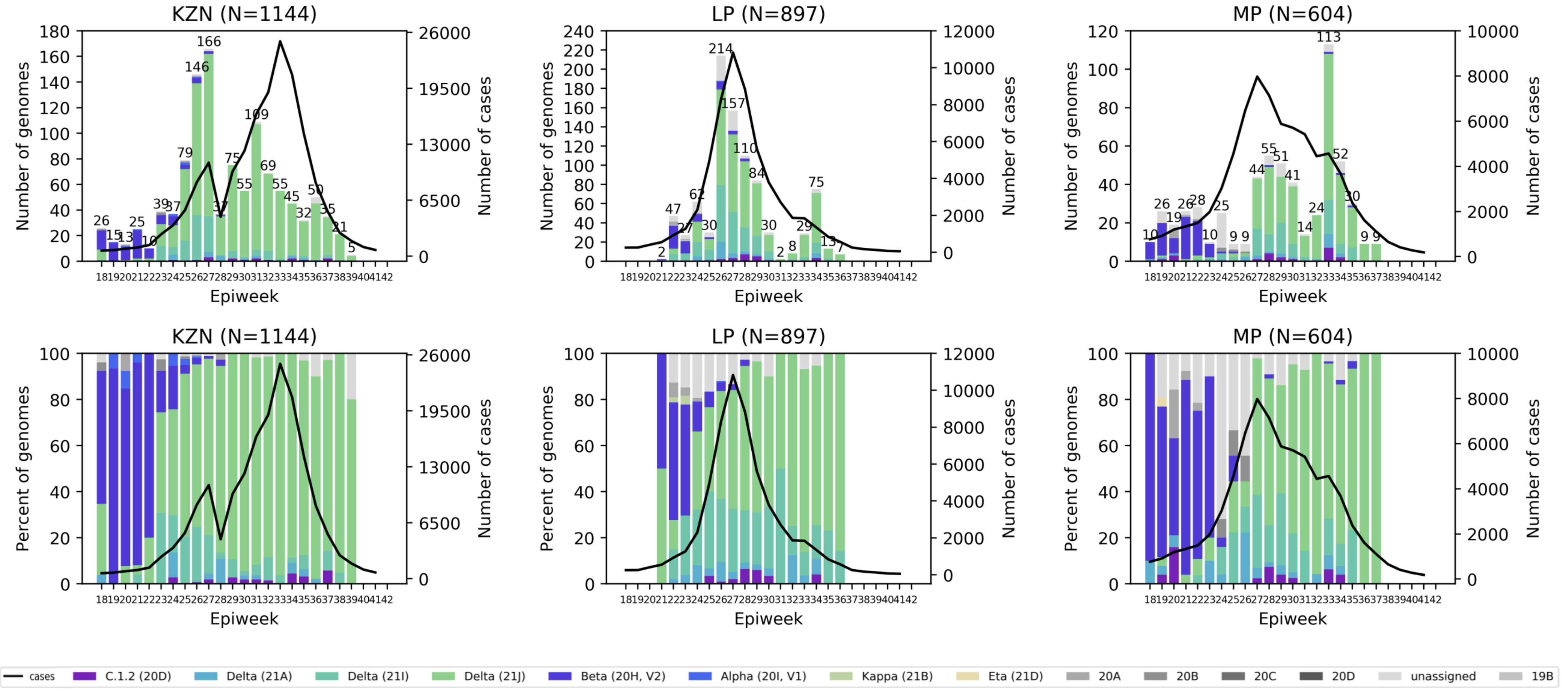
Genomes sequenced from specimens collected in May to mid-September 2021 (epiweeks 18 – 42) from KwaZulu-Natal, Limpopo and Mpumalanga Provinces



Delta variant dominates the third wave in KwaZulu-Natal, Limpopo and Mpumalanga Provinces

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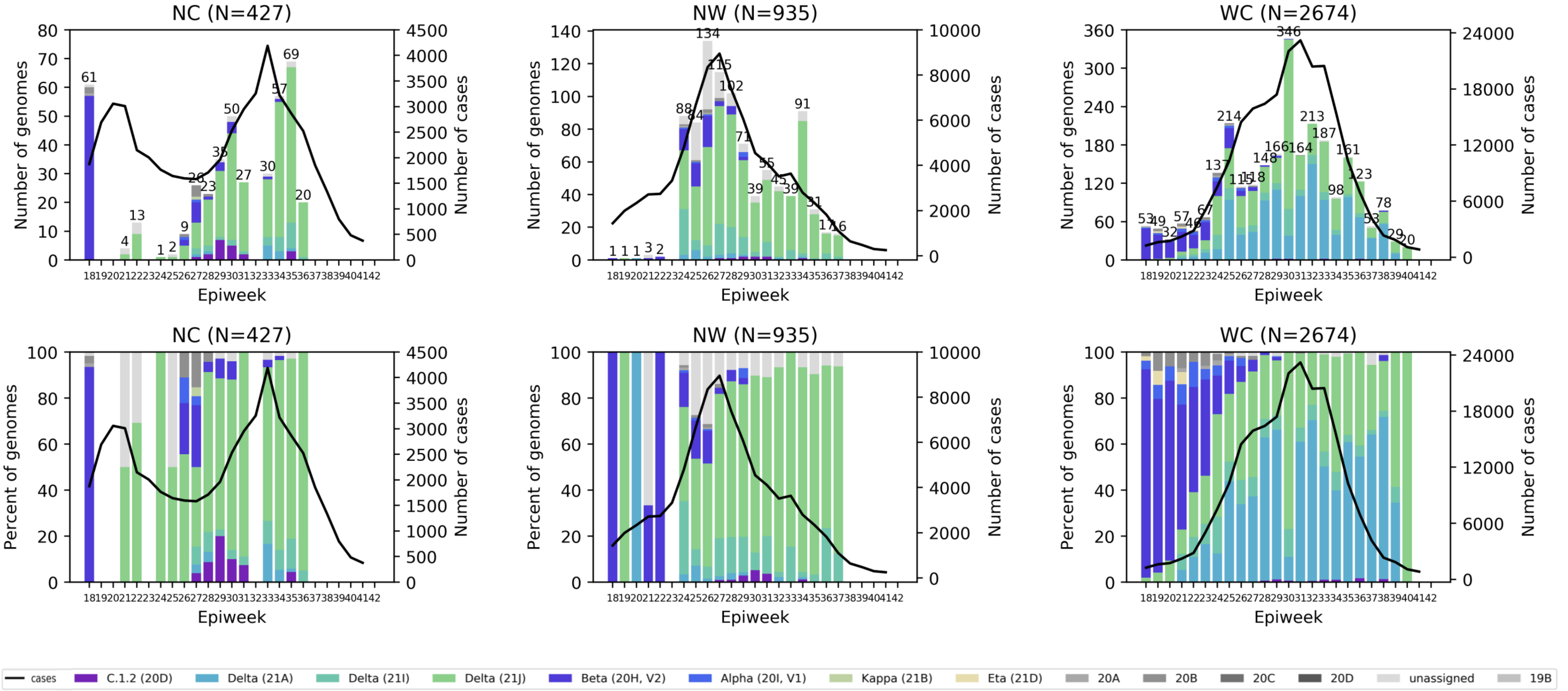
Genomes sequenced from specimens collected in May to mid-September 2021 (epiweeks 18 – 42) from Northern Cape, North West, and Western Cape Provinces



Delta dominates the third wave in Northern Cape, North West, and Western Cape provinces

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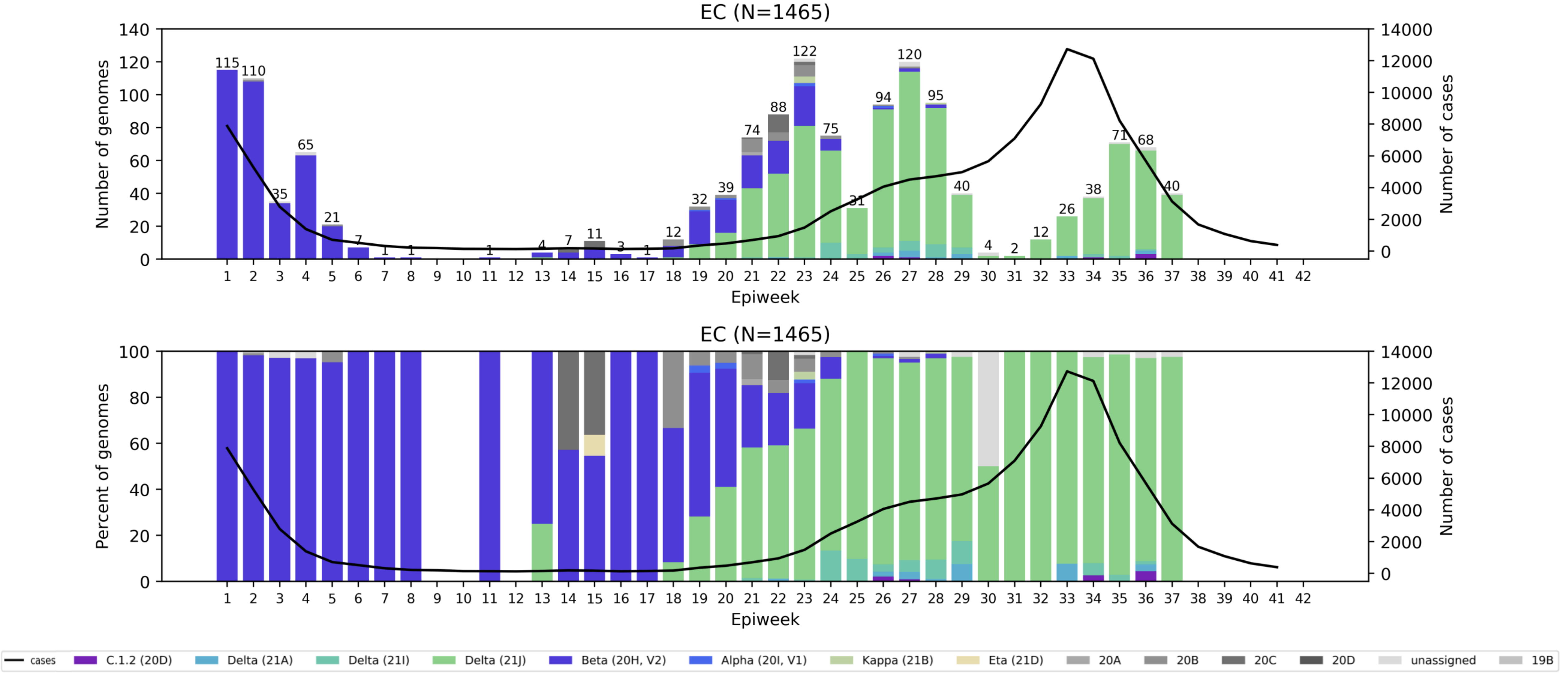
Eastern Cape Province, 2021, n = 1465



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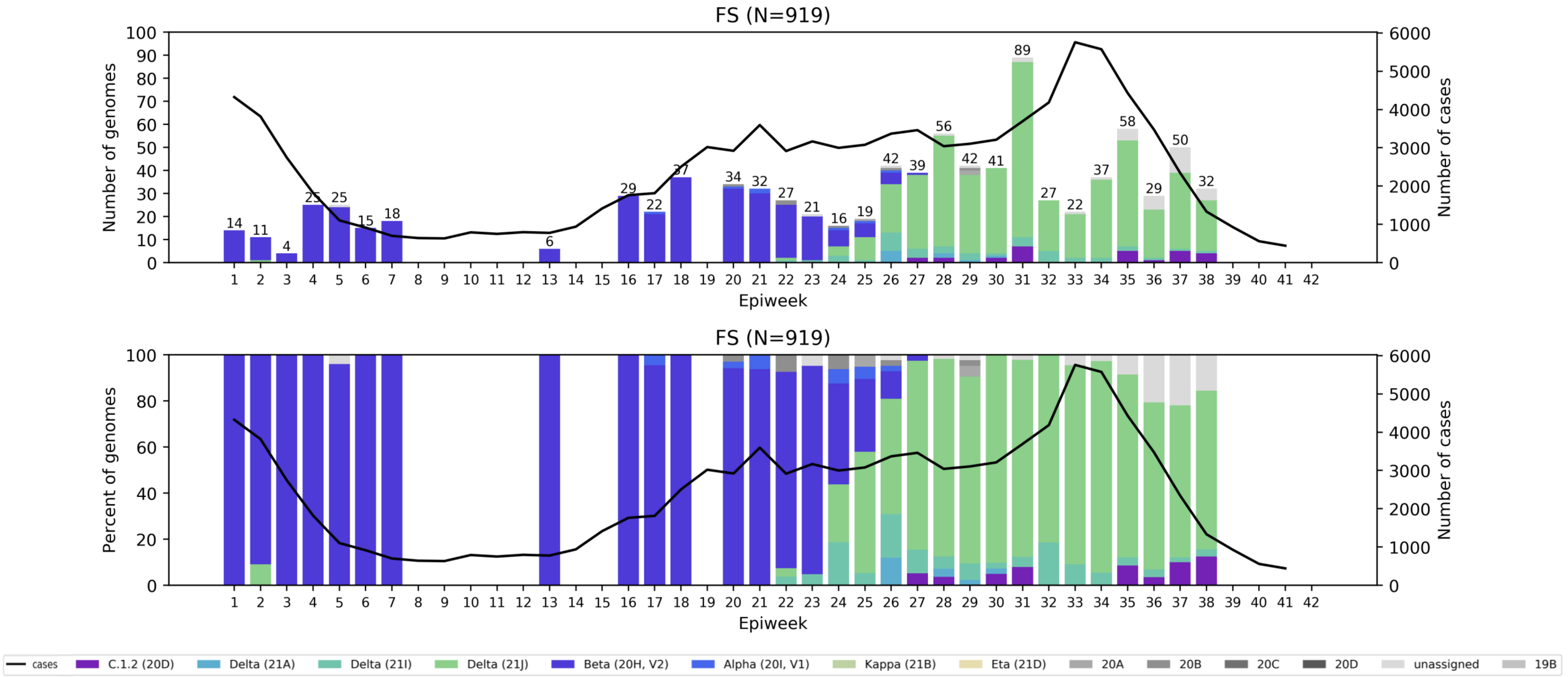
Free State Province, 2021, n = 919



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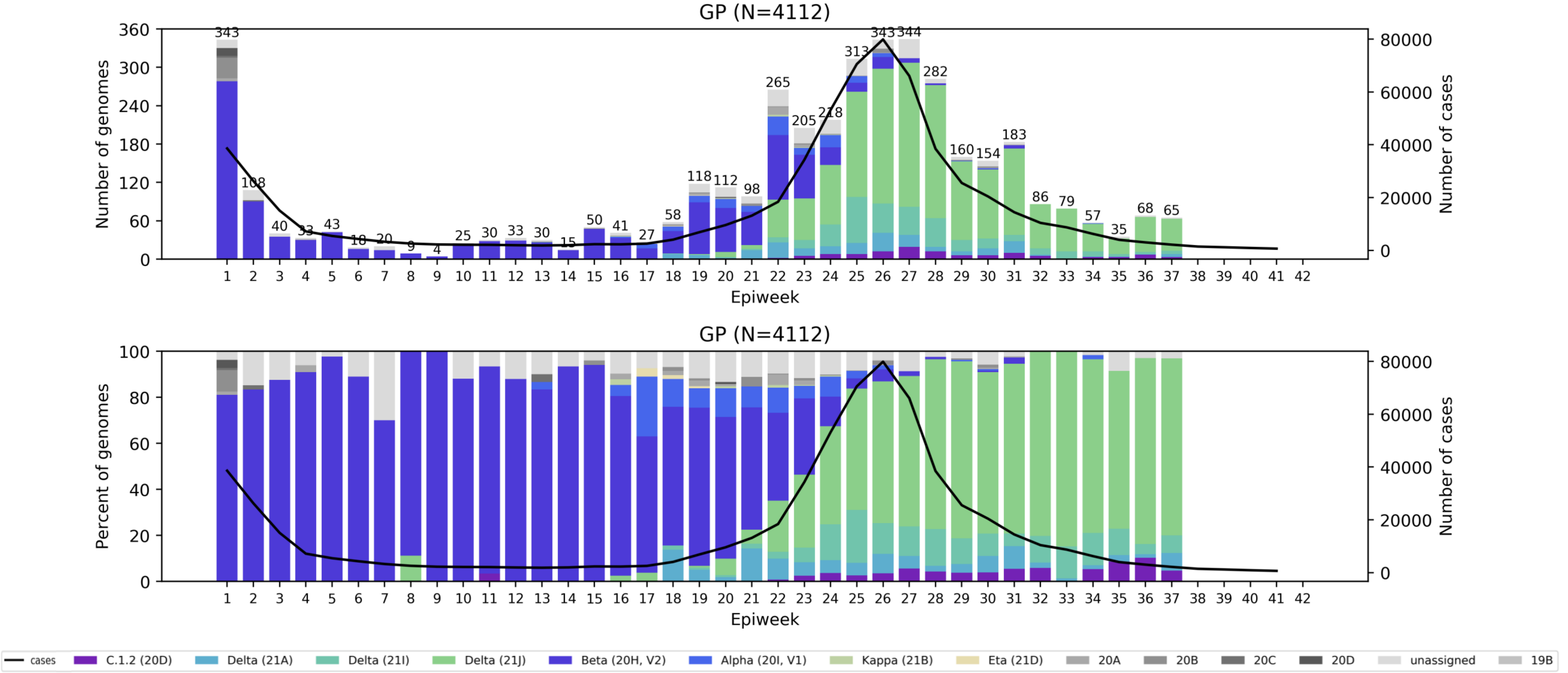
Gauteng Province, 2021, n = 4112



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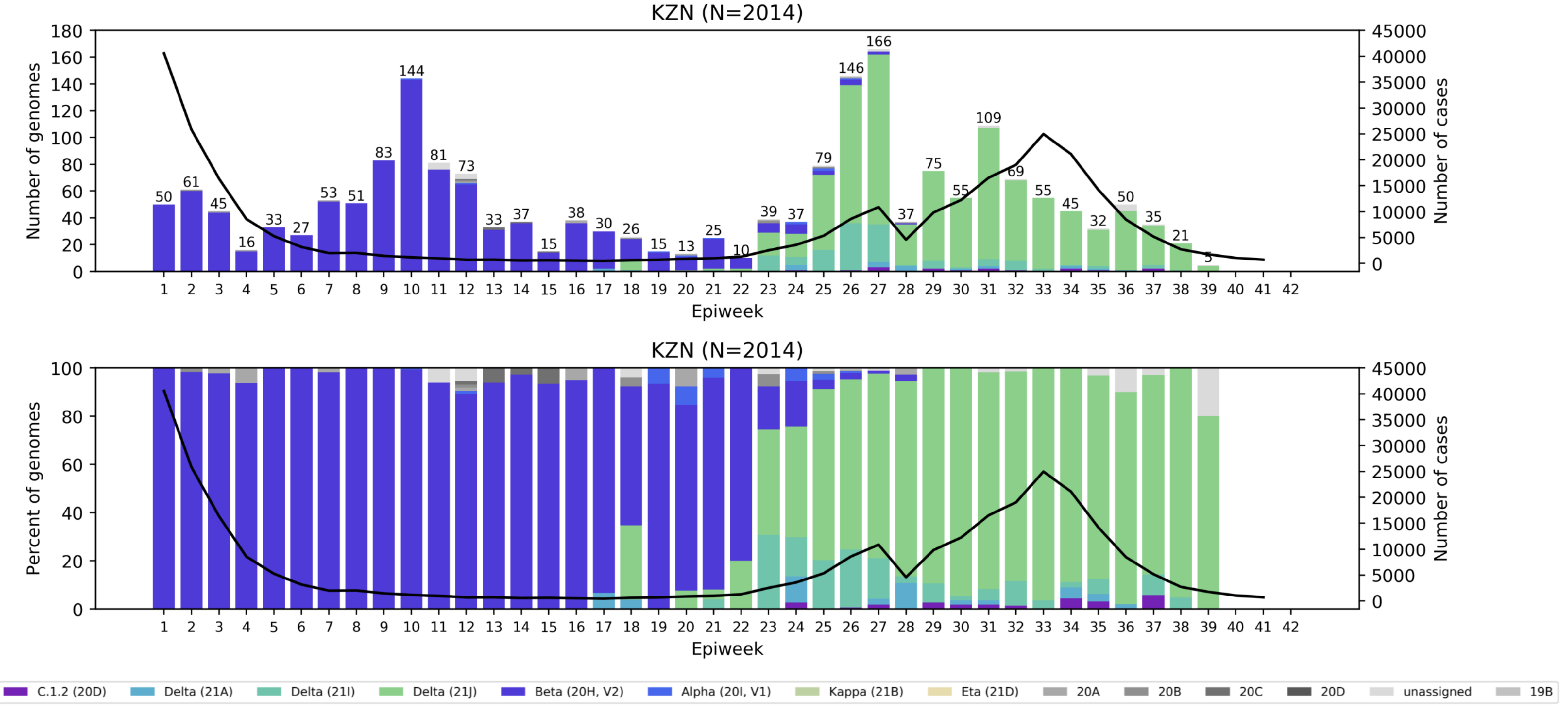
KwaZulu-Natal Province, 2021, n = 2014



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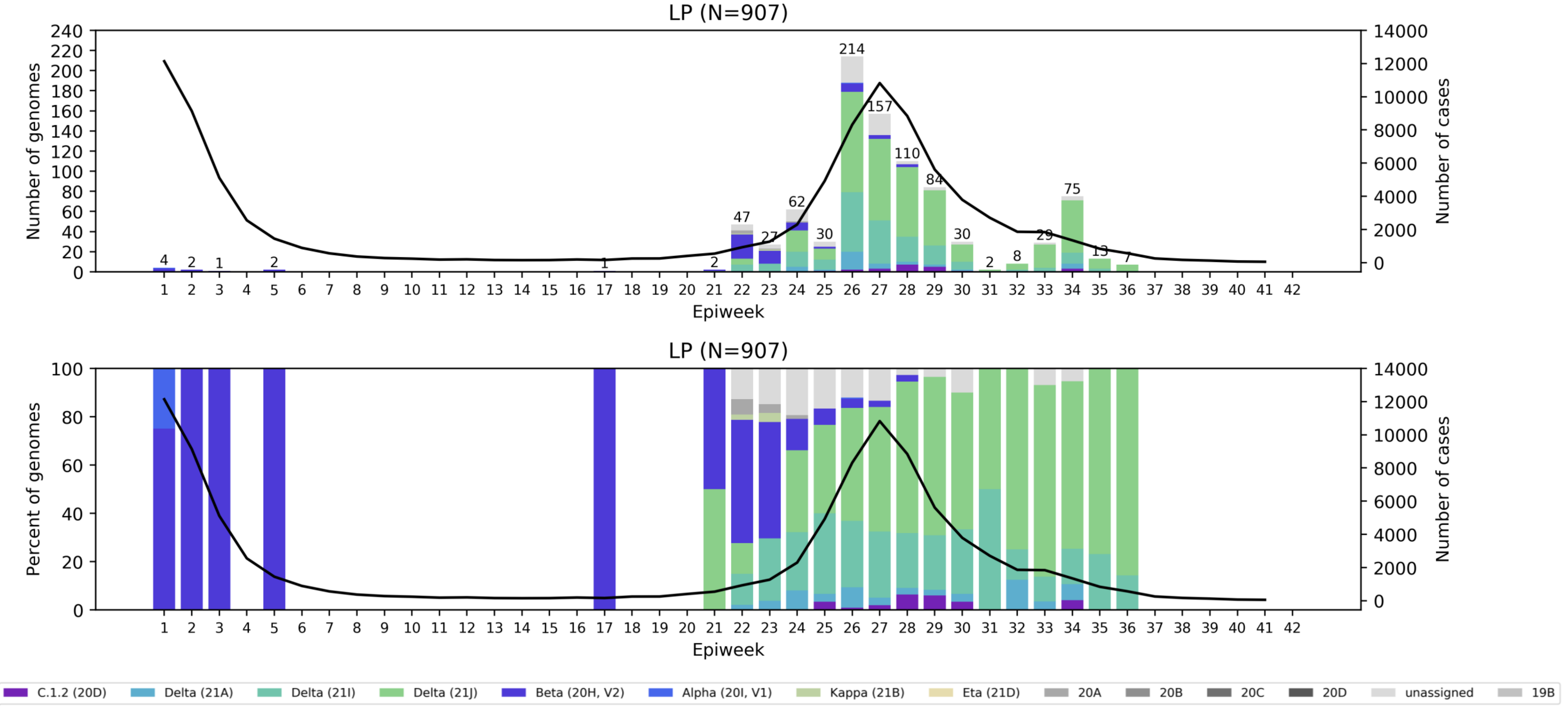
Limpopo Province, 2021, n = 907



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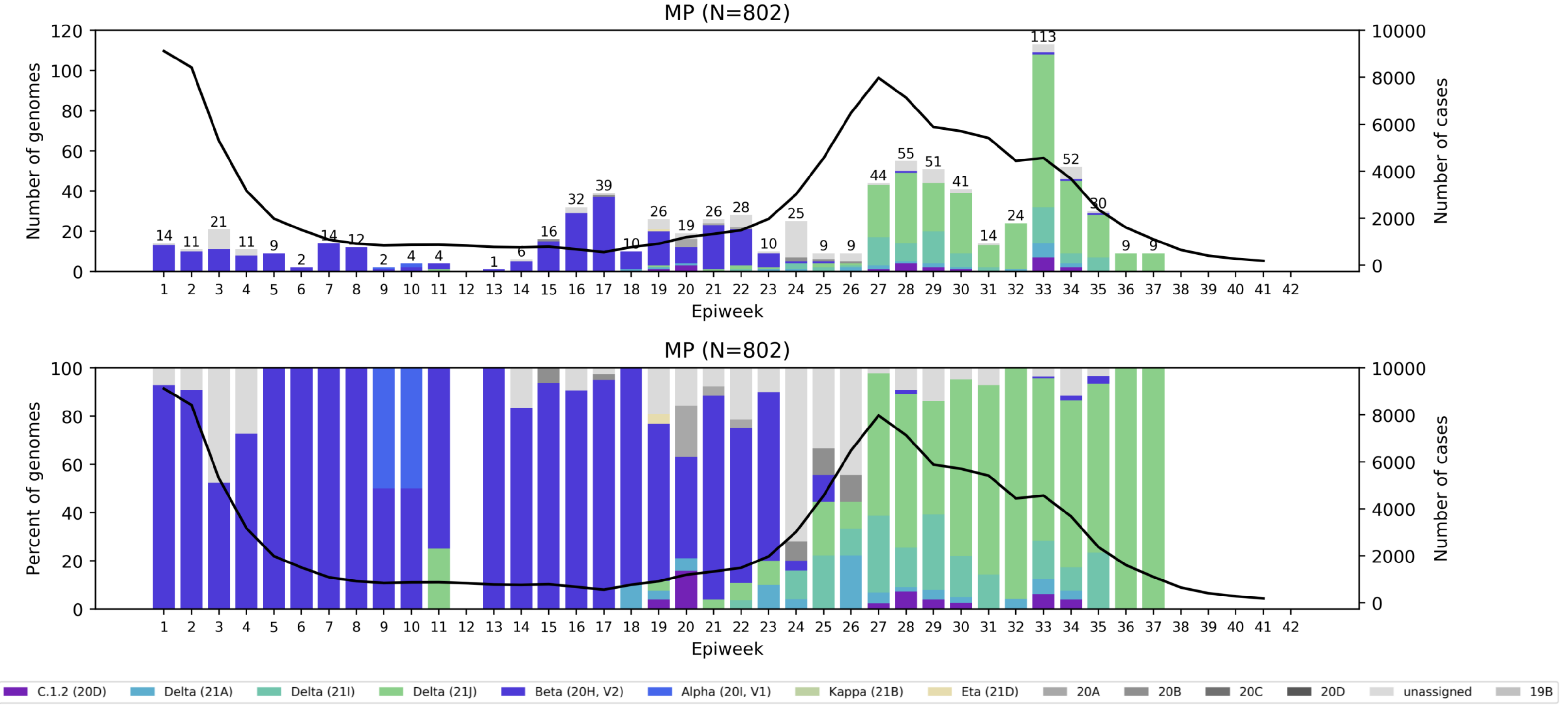
Mpumalanga Province, 2021, n = 802



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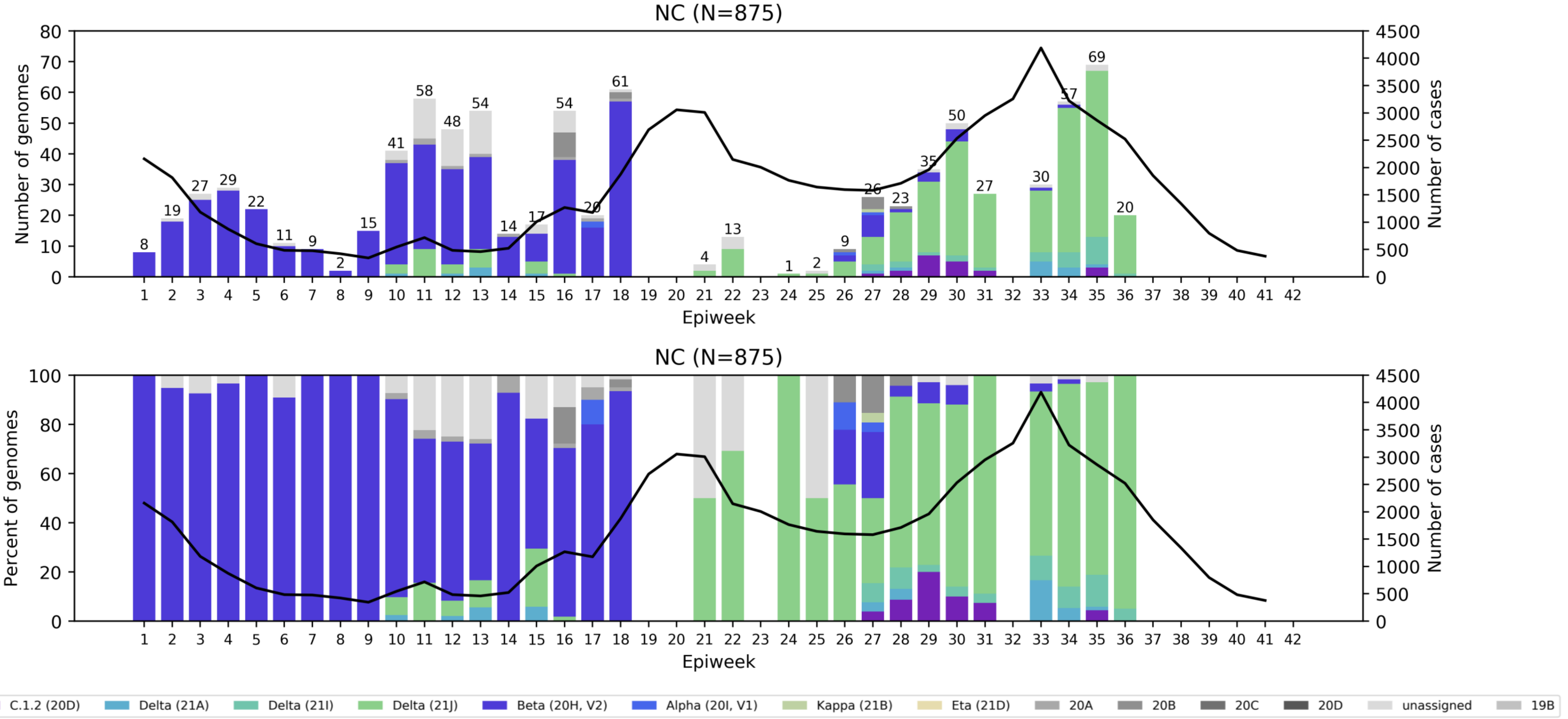
Northern Cape Province, 2021, n = 875



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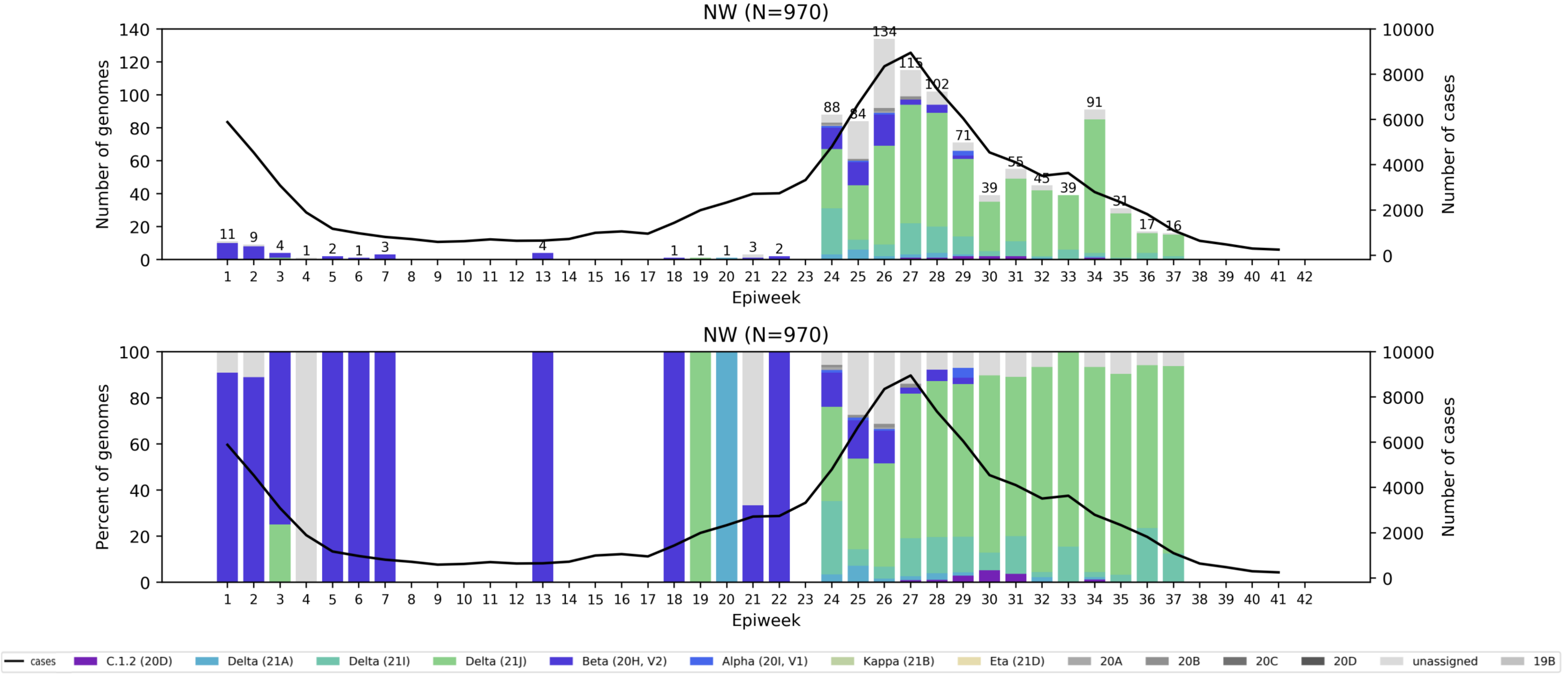
North West Province, 2021, n = 970



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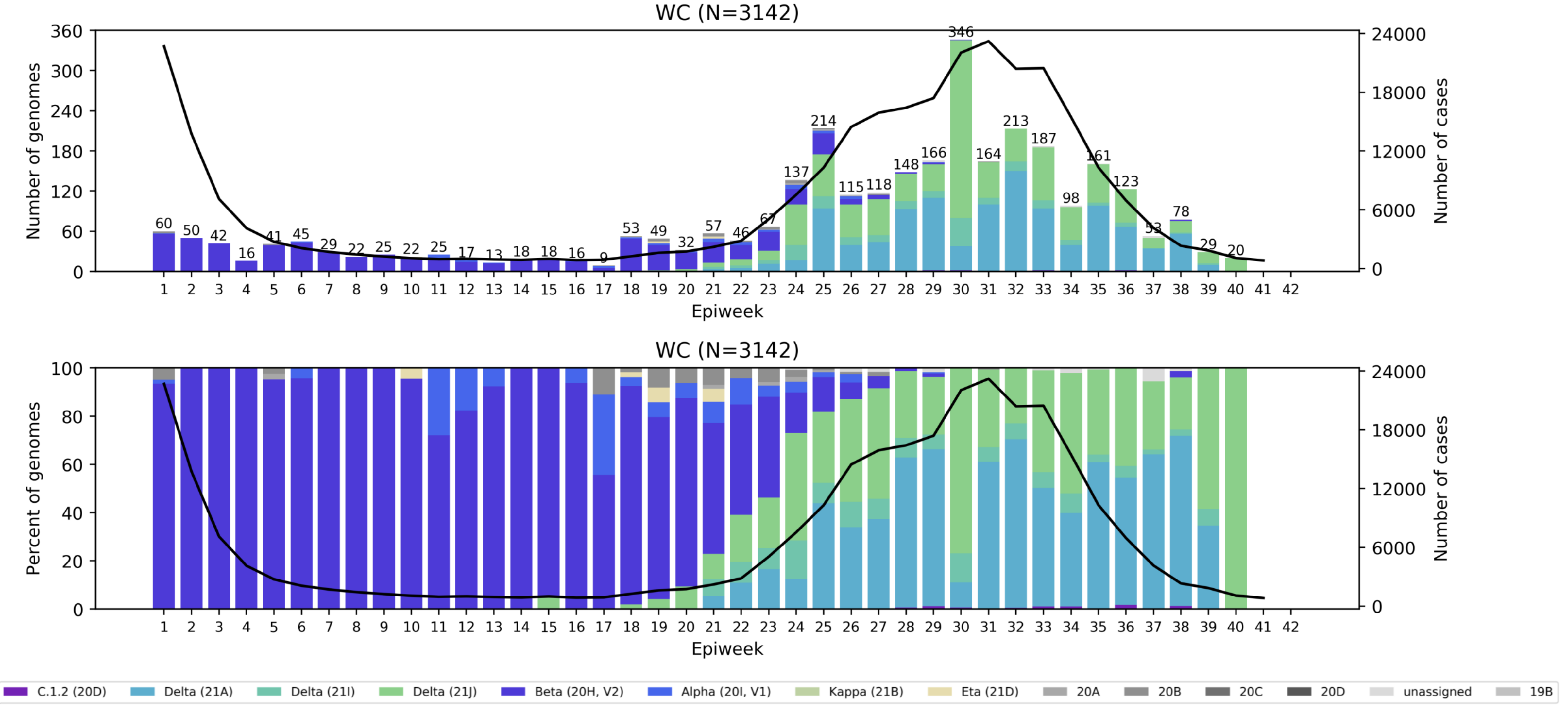
Western Cape Province, 2021, n = 3142



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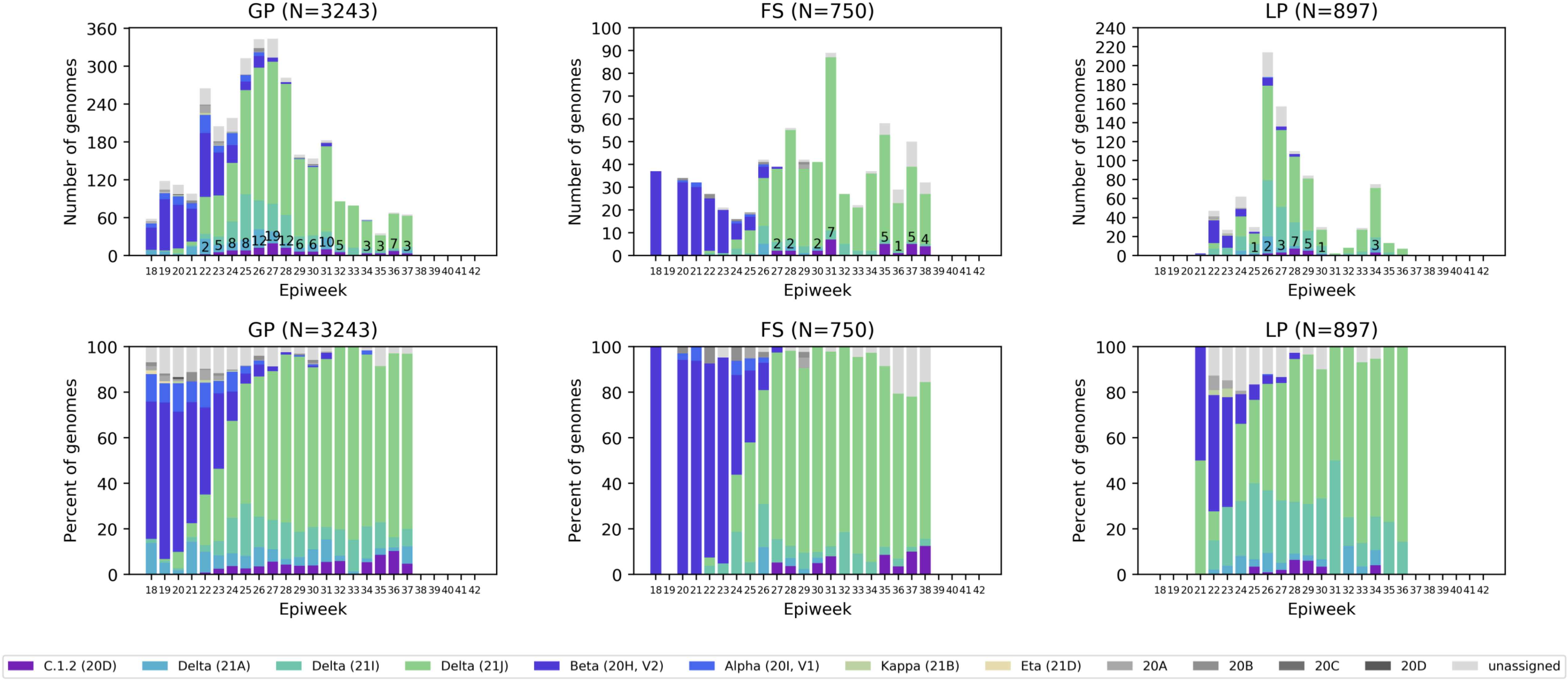
C.1.2 (n=244 in SA) in May – August 2021 by epiweek

Number of C.1.2 samples indicated above bar, provinces ordered by number of detections



The majority of C.1.2 sequences have been detected in Gauteng (n=109), followed by the Free State (n=28) and then Limpopo (n=22).

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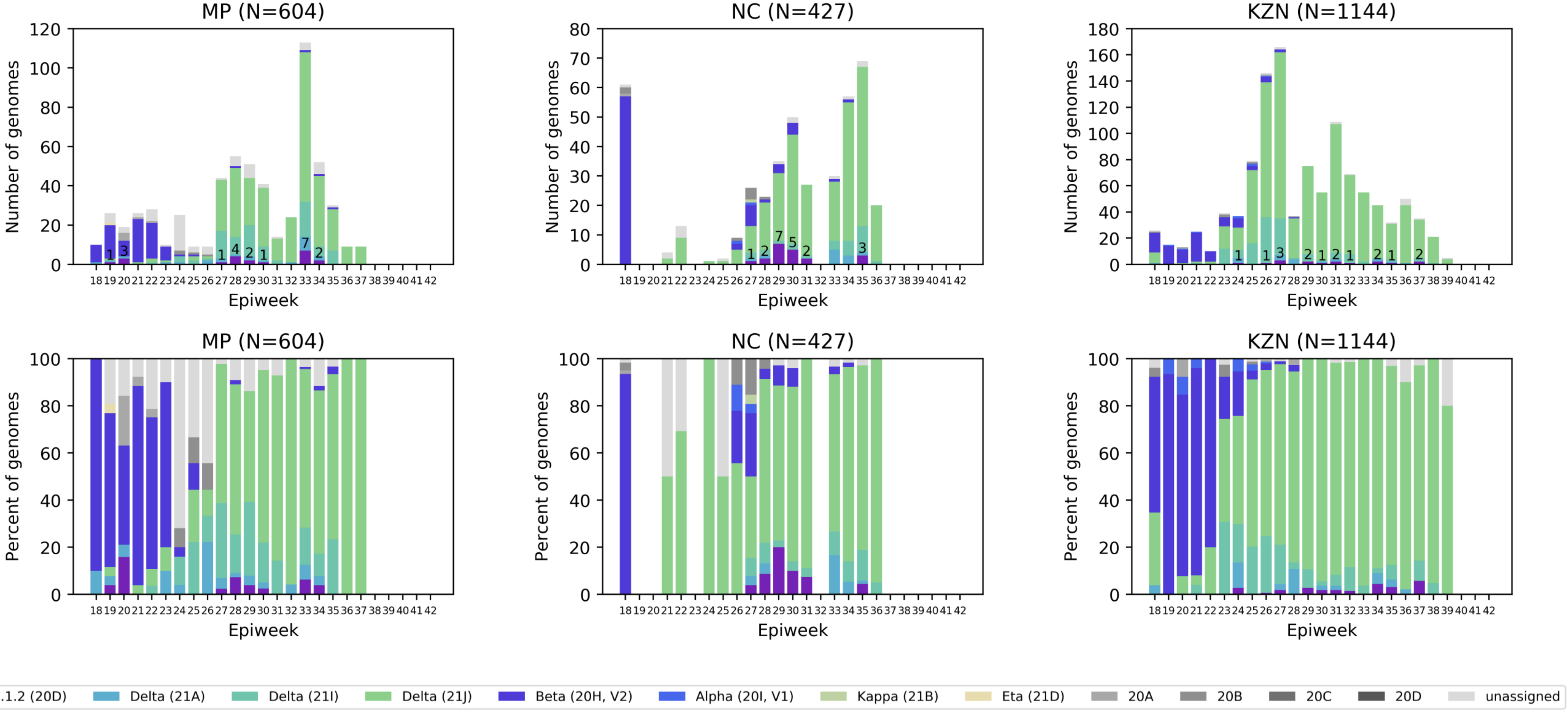
C.1.2 (n=244 in SA) in May – August 2021 by epiweek

Number of C.1.2 samples indicated above bar, provinces ordered by number of detections



21 C.1.2 sequences have been detected in Mpumalanga, 20 in the Northern Cape, and 16 in KwaZulu-Natal.

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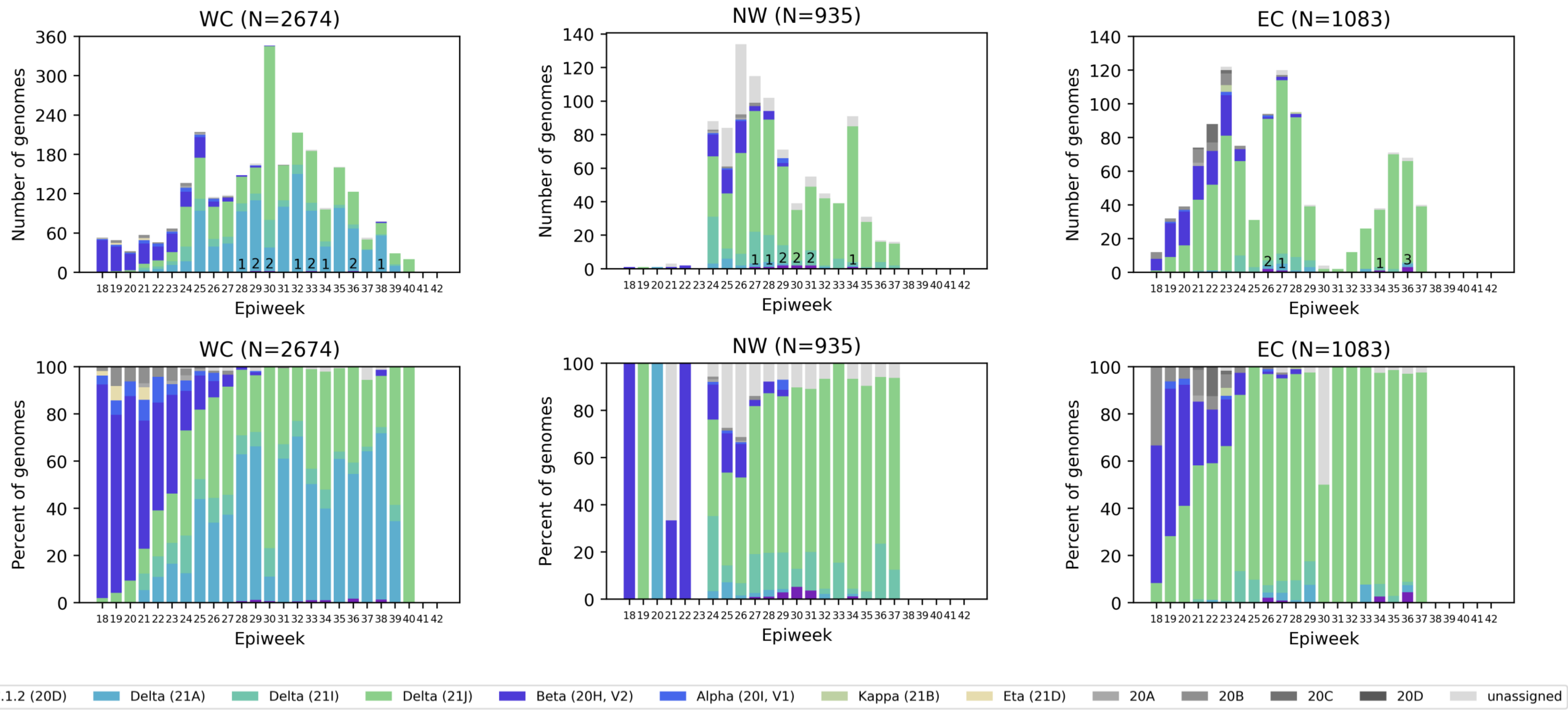
C.1.2 (n=244 in SA) in May – August 2021 by epiweek

Number of C.1.2 samples indicated above bar, provinces ordered by number of detections



The Western Cape has 12 sequences, the North West has 9, and the Eastern Cape has 7 detections of C.1.2.

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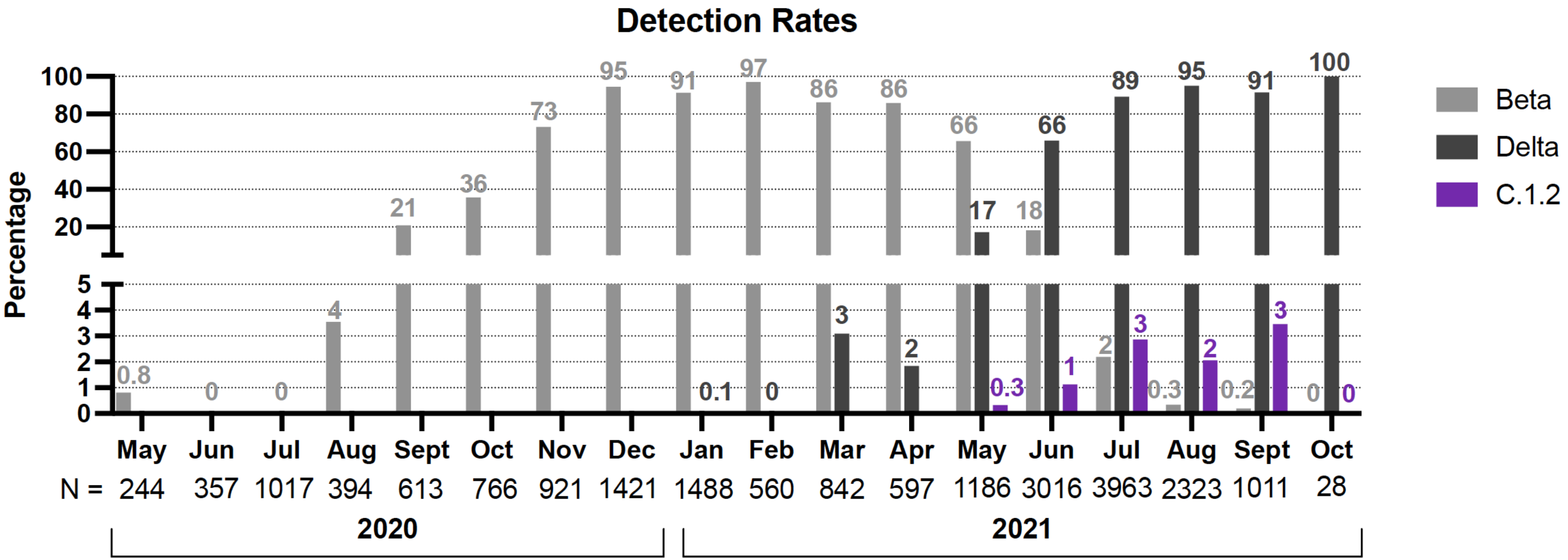
C.1.2 growth compared to Beta and Delta



C.1.2 continues to be detected at low levels (less than 4% of genomes per month)

Summary

- Delta continues to dominate in all provinces from specimens collected in September and October
  - Delta has recently been split into three clades.
    - New clades have been assigned due to >20% global circulation of particular sequences for more than 2 months
    - All SA Delta samples have been updated
    - Delta 21J is the dominant clade globally and in SA
- The new Delta sub-lineage AY.4.2 has not been identified in South Africa
  - At least 2 of 4 lineage-defining mutations must be present for an accurate assignment to the AY.4.2 lineage[1, 2]
- Mutated C.1.2 lineage detected in all provinces of South Africa at less than 4% of genomes
- Lambda and Mu variants not detected in South Africa

1. https://github.com/cov-lineages/constellations/blob/main/constellations/definitions/cAY.4.2.json
2. https://assets.publishing.service.gov.uk/government/uploads/system/uploads/attachment_data/file/1028113/Technical_Briefing_26.pdf

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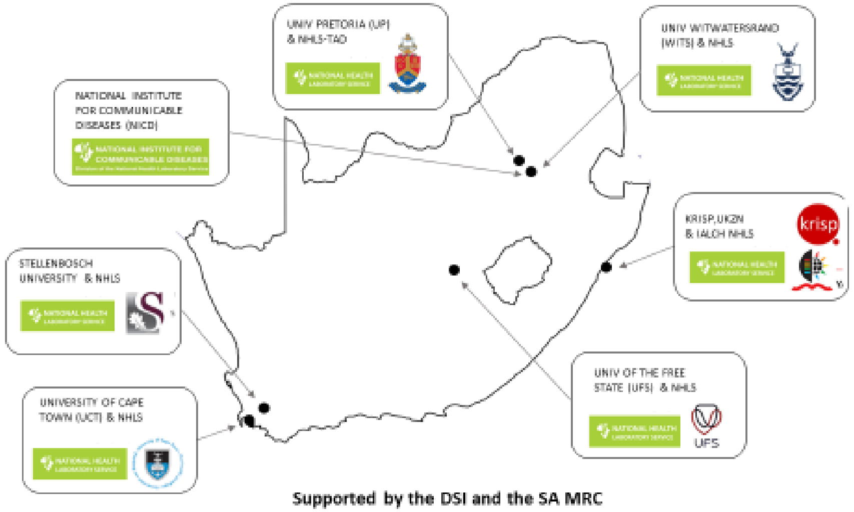

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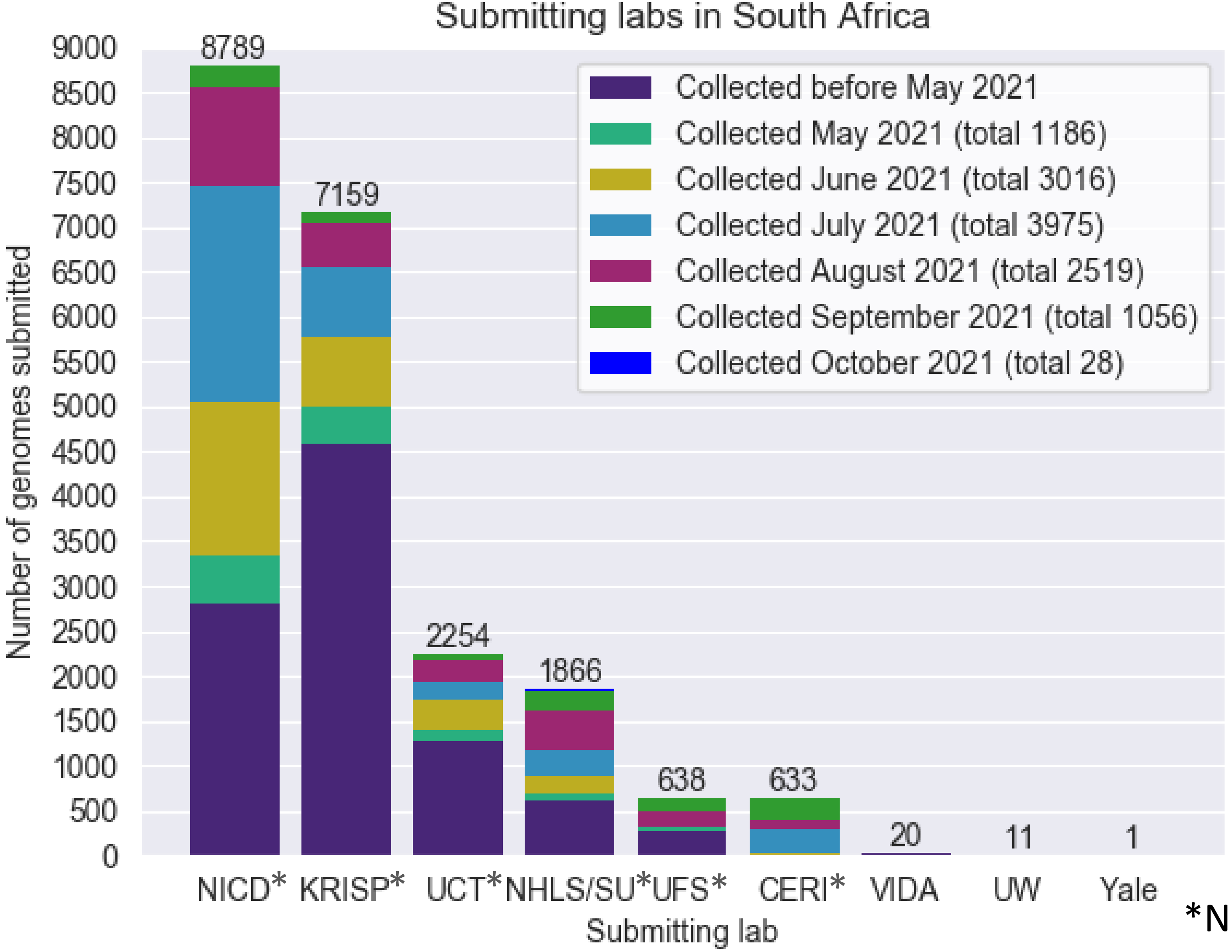
South African genomes submitted per sequencing lab, 2020 and 2021 (N=21 371)



*NGS-SA laboratories

Multiple labs from NGS-SA are contributing to the sequencing effort. Sequencing efforts 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	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 22 October 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 22 October 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.)