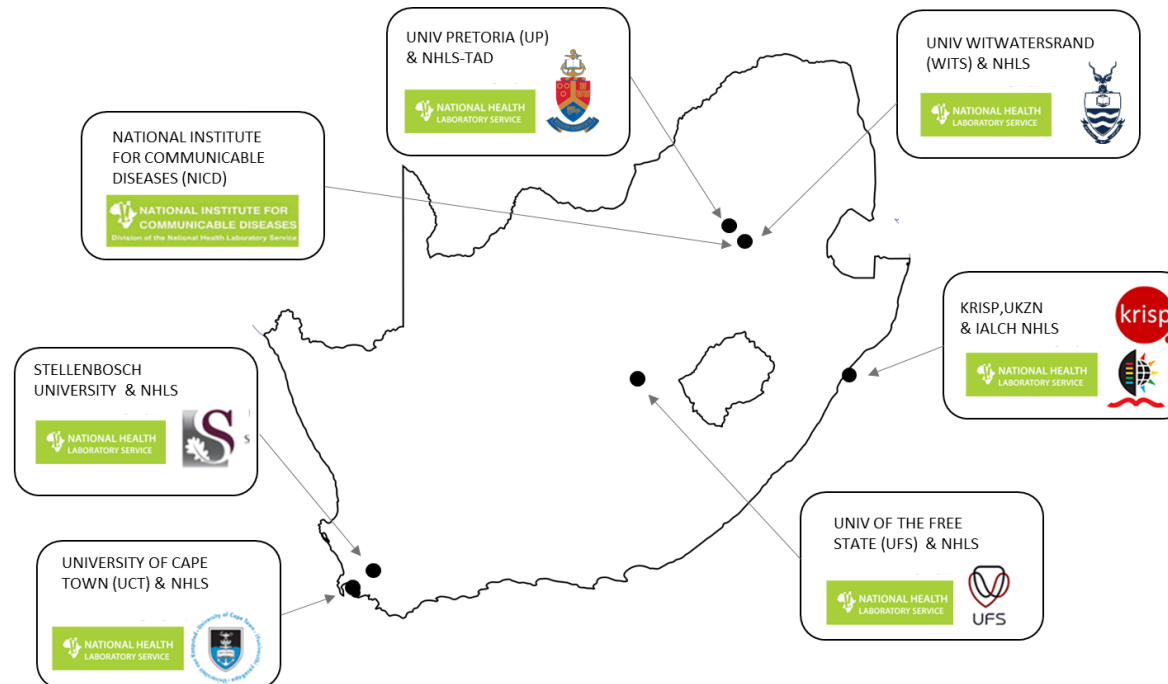


SARS-CoV-2 Sequencing Update 8 October 2021



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 8 October at 09h50



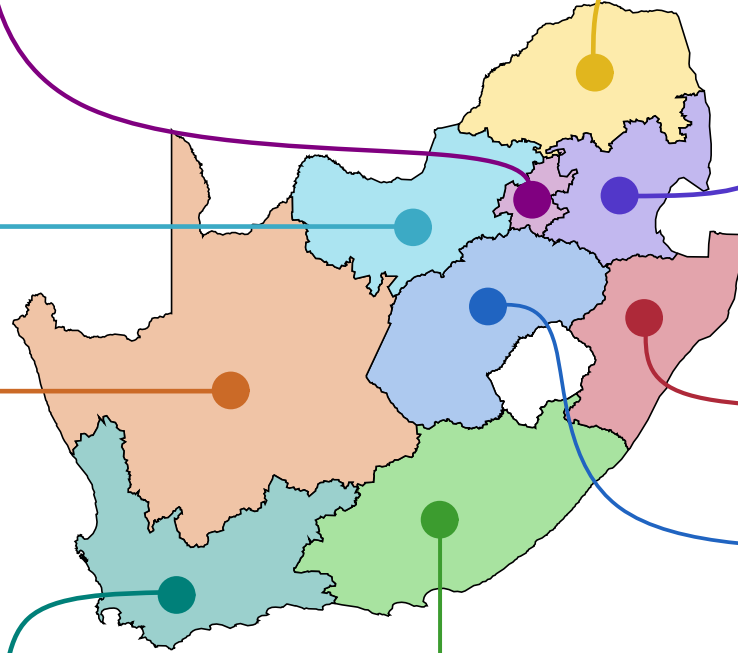
Data license: <https://www.gisaid.org/registration/terms-of-use/>

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 PMID: 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 PMID: PMC5388101

GENOMIC SURVEILLANCE IN THE THIRD WAVE

epiweeks 18 - 39



Gauteng

PTP: 2.0%

Genomes Cases
3 056 (28.4%) 492 021 (37.3%)

Genomes deposited in the last week
■ 2 ■ 142 ■ 1 ■ 1 ■ 12

North West

PTP: 4.9%

Genomes Cases
783 (7.3%) 81 643 (6.2%)

Genomes deposited in the last week
■ 5 ■ 94 ■ 3 ■ 19

Northern Cape

PTP: 13.8%

Genomes Cases
331 (3.1%) 50 507 (3.8%)

Genomes deposited in the last week
■ 2 ■ 98 ■ 2 ■ 2

Western Cape

PTP: 6.2%

Genomes Cases
2 449 (22.7%) 223 569 (16.9%)

Genomes deposited in the last week
■ 1 ■ 39 ■ 312 ■ 2 ■ 1 ■ 4 ■ 9

Eastern Cape

PTP: 6.5%

Genomes Cases
976 (9.1%) 94 736 (7.2%)

Genomes deposited in the last week
■ 40 ■ 2

Limpopo

PTP: 2.7%

Genomes Cases
877 (8.1%) 57 870 (4.4%)

Genomes deposited in the last week
■ 115 ■ 6 ■ 2

Mpumalanga

PTP: 4.0%

Genomes Cases
533 (4.9%) 72 631 (5.5%)

Genomes deposited in the last week
■ 3 ■ 218 ■ 6 ■ 21

KwaZulu-Natal

PTP: 4.7%

Genomes Cases
1 113 (10.3%) 175 677 (13.3%)

Genomes deposited in the last week
■ 63 ■ 3 ■ 4

Free State

PTP: 9.2%

Genomes Cases
657 (6.1%) 71 979 (5.5%)

Genomes deposited in the last week
■ 71 ■ 6 ■ 12



Bar graphs represent genomes sequenced per epiweek, with lines representing cases by collection date (weeks 18 – 39)

Genomes and cases presented as provincial total (percentage of national total) for epiweeks 18 – 39

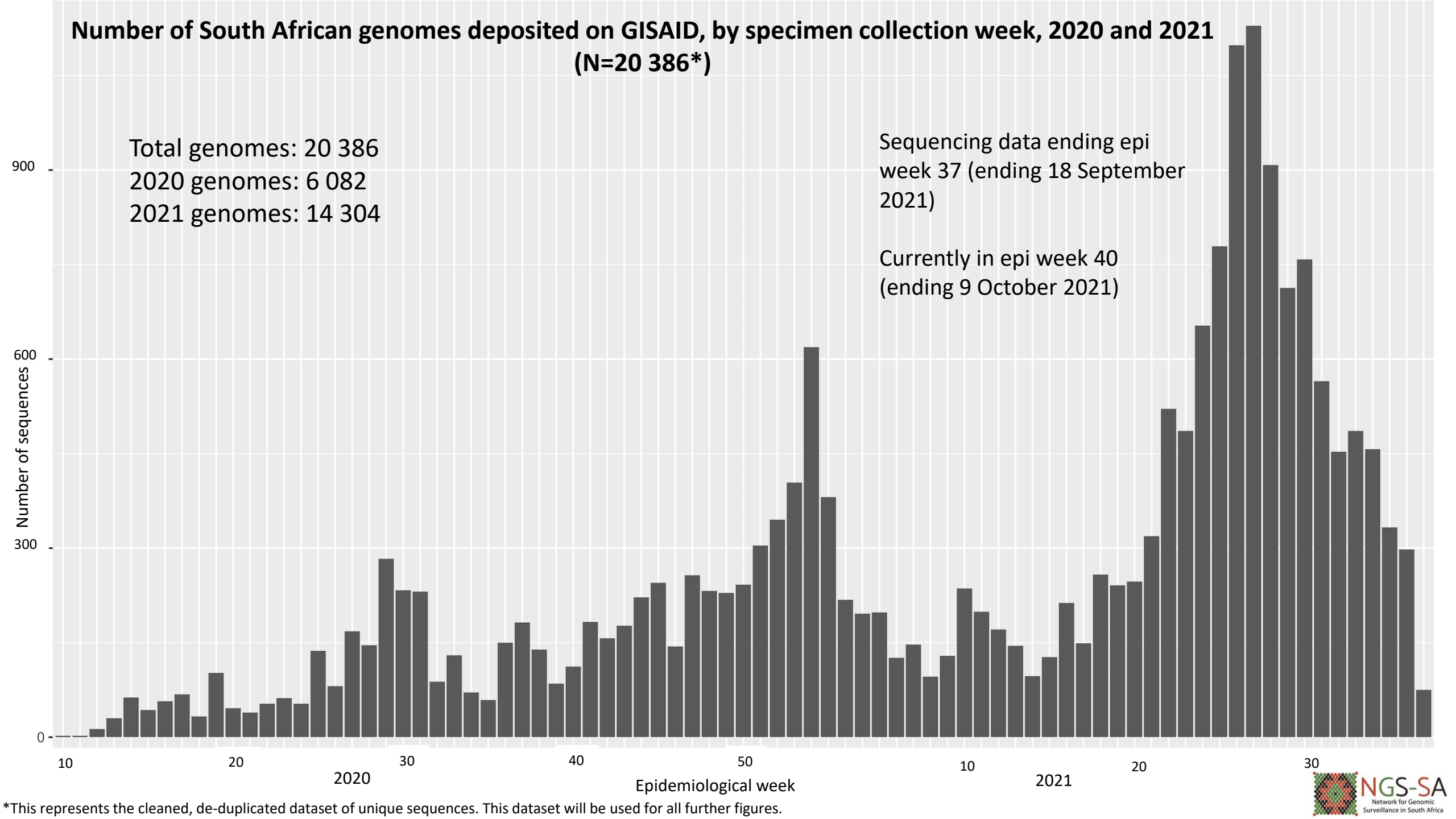
PTP: percentage testing positive

Number of South African genomes deposited on GISAID, by specimen collection week, 2020 and 2021
(N=20 386*)

Total genomes: 20 386
2020 genomes: 6 082
2021 genomes: 14 304

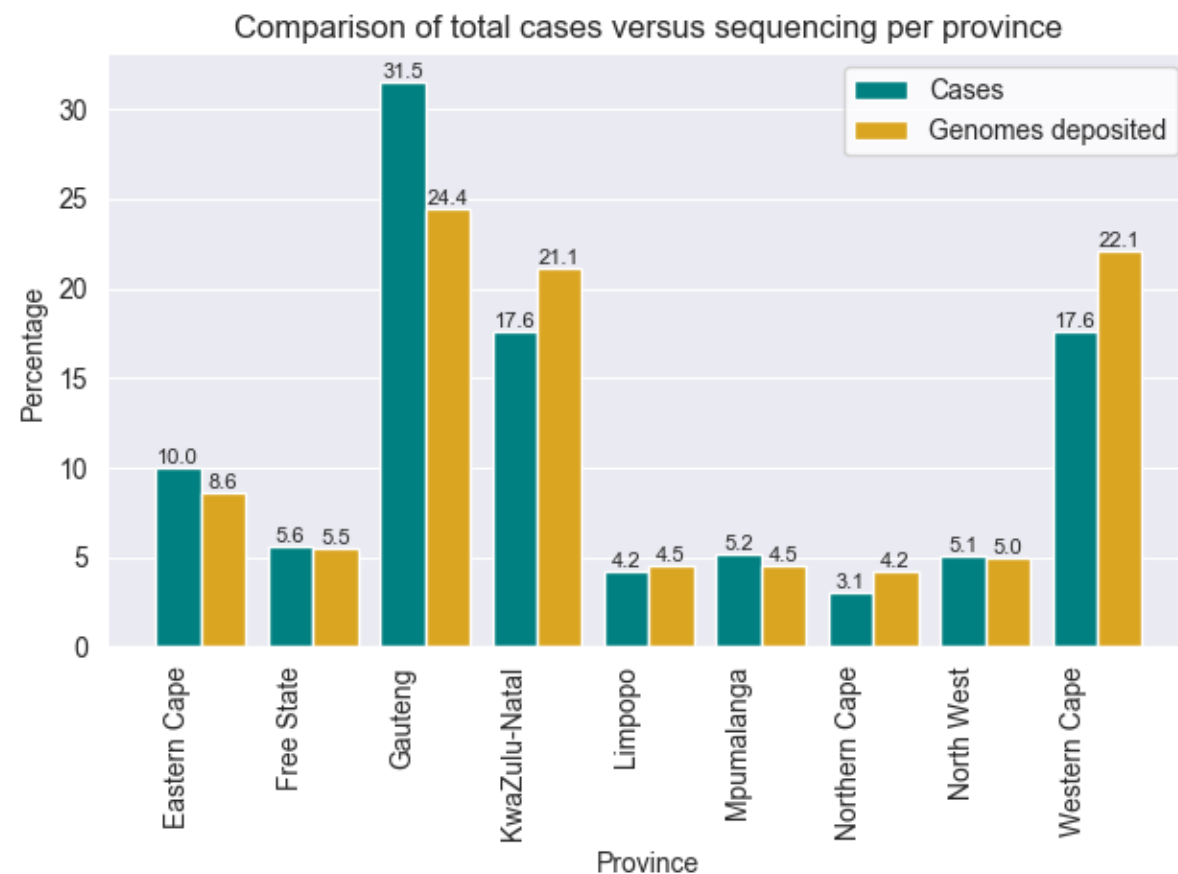
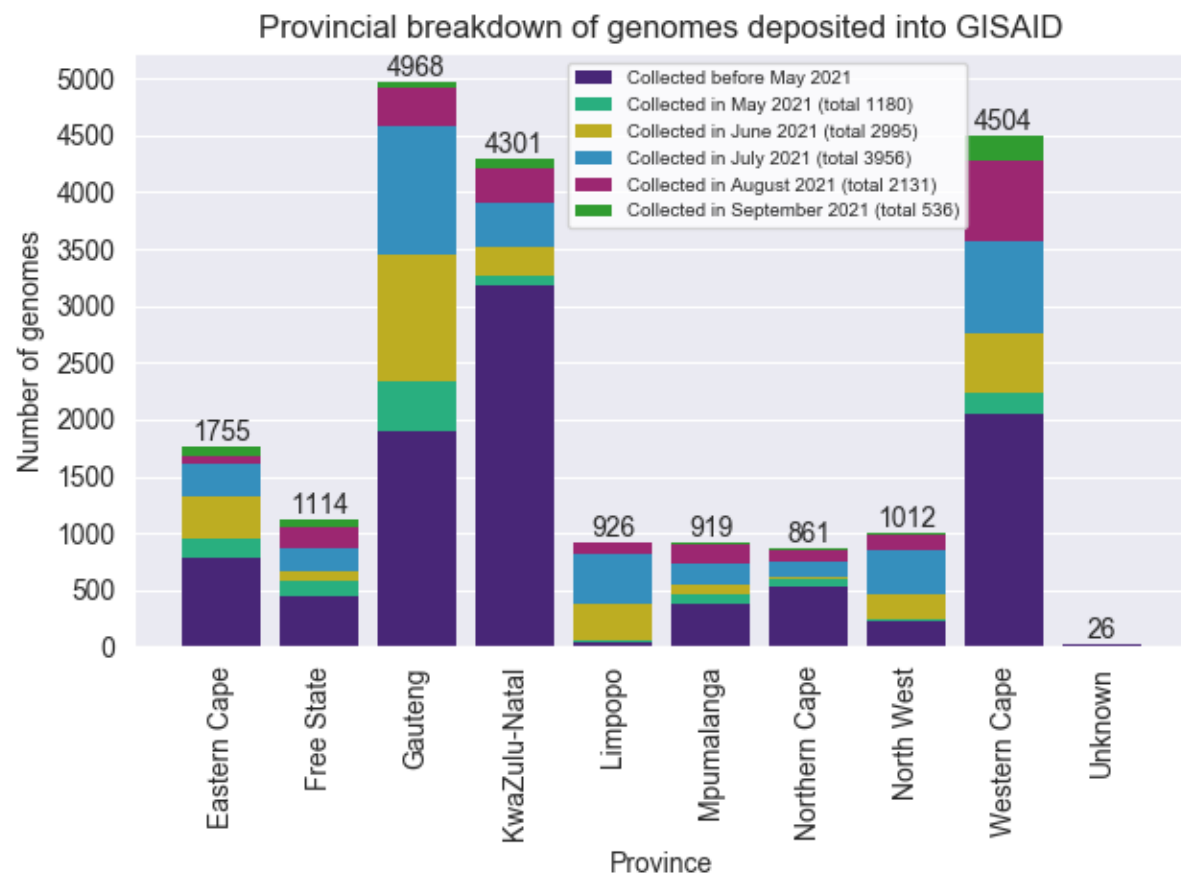
Sequencing data ending epi
week 37 (ending 18 September
2021)

Currently in epi week 40
(ending 9 October 2021)



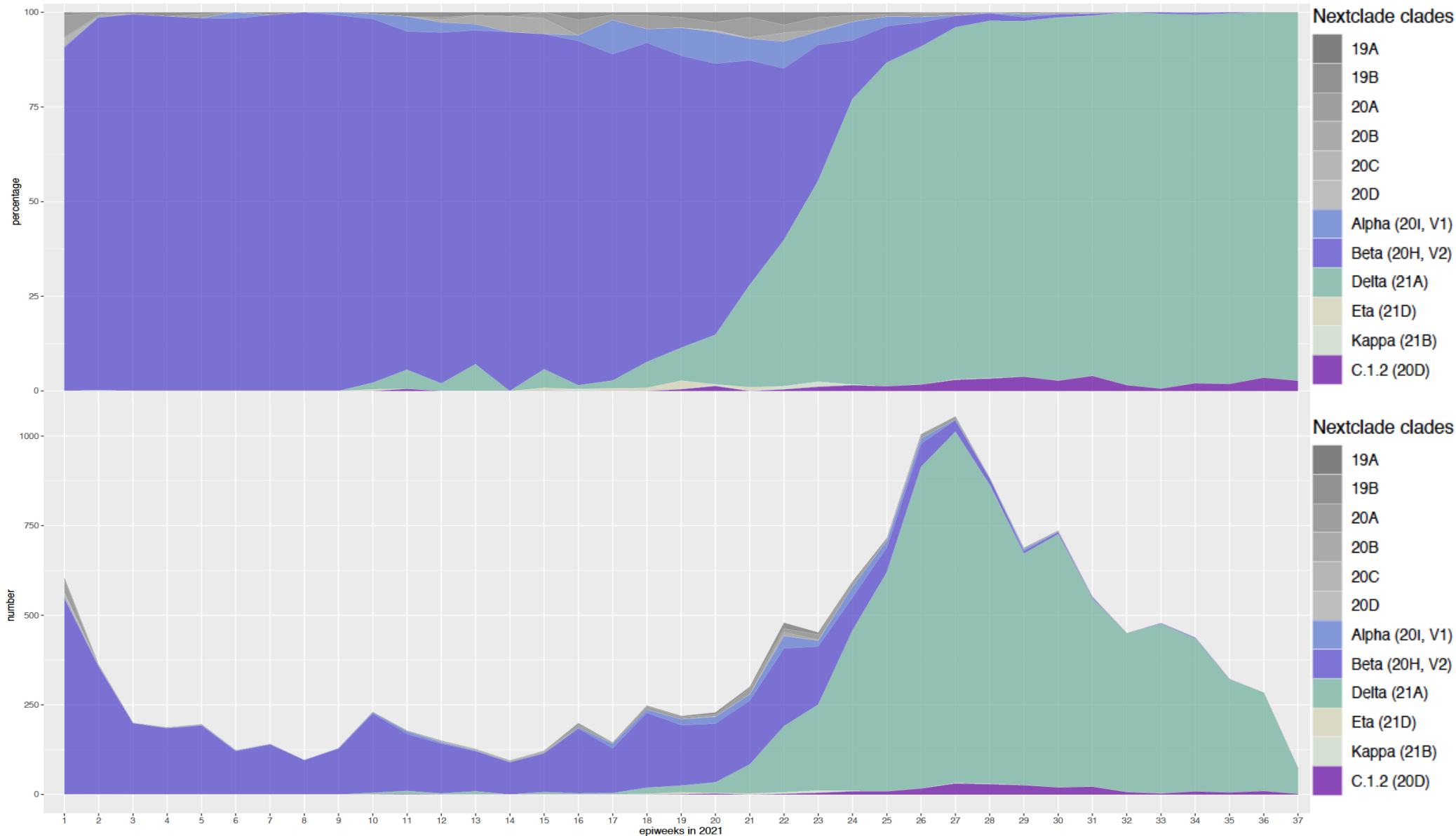
*This represents the cleaned, de-duplicated dataset of unique sequences. This dataset will be used for all further figures.

GISAID genomes vs total cases, 2020 and 2021 (N=20 386)



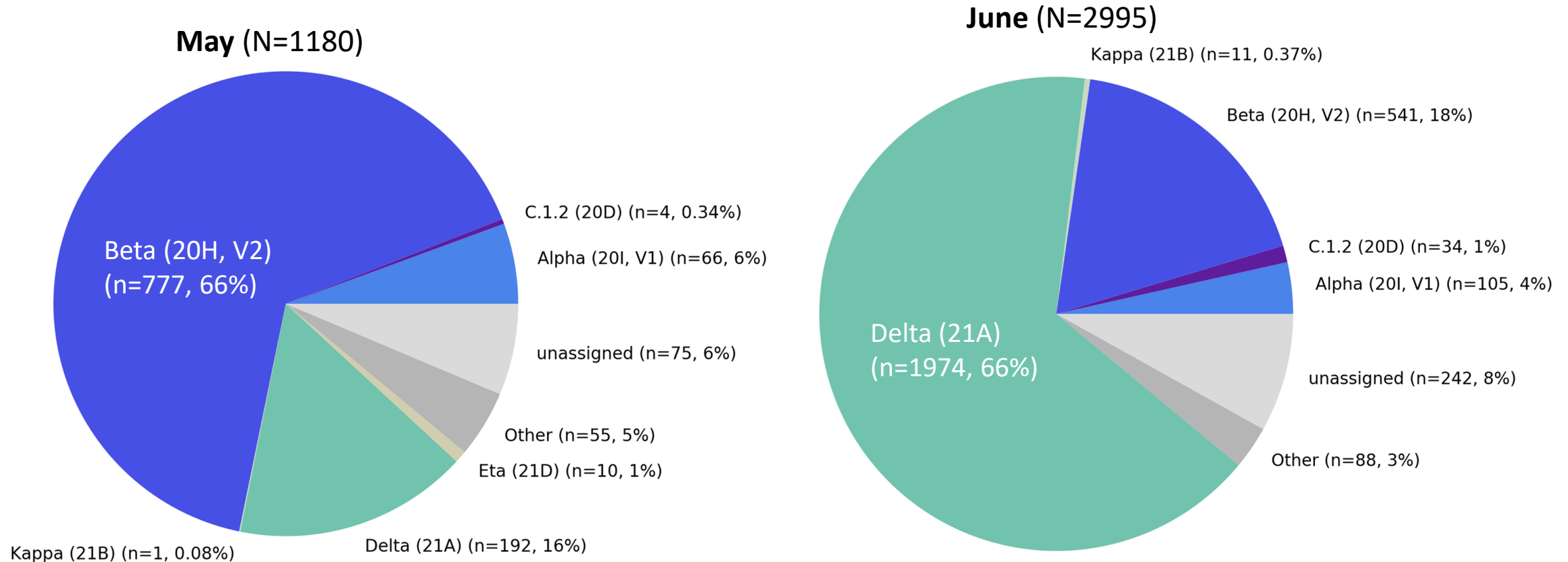
All provinces, apart from GP, KZN, and WC, have comparable percentage of overall cases and overall sequenced genomes

Distribution and number of clades in South Africa, 2021 (N= 14 304)



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. Beta present at <2% frequency since July and not yet detected in September

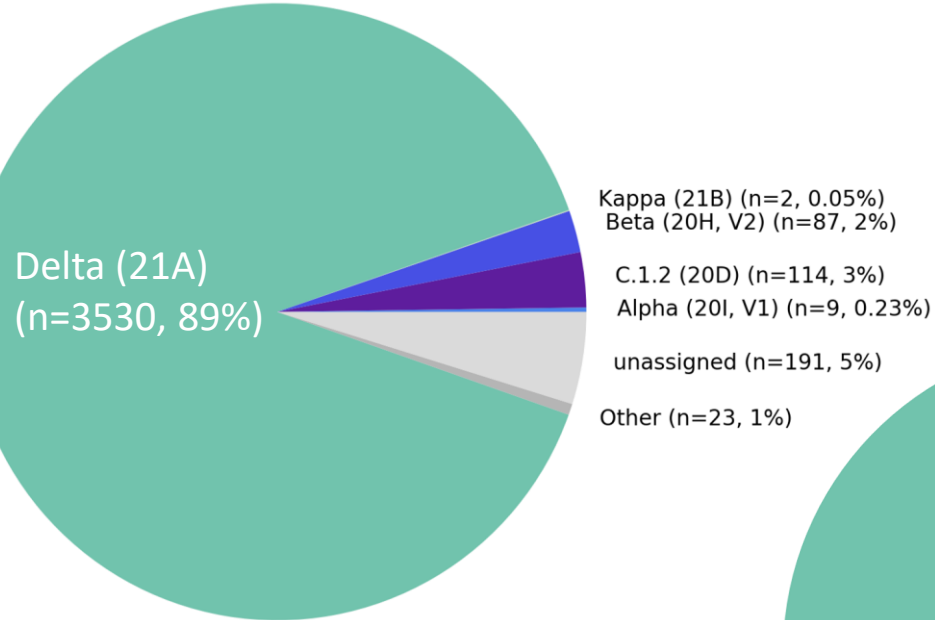
Prevalence of Variants of Concern (VOC) and Variants of Interest (VOI) in **May and June 2021** sequences, South Africa



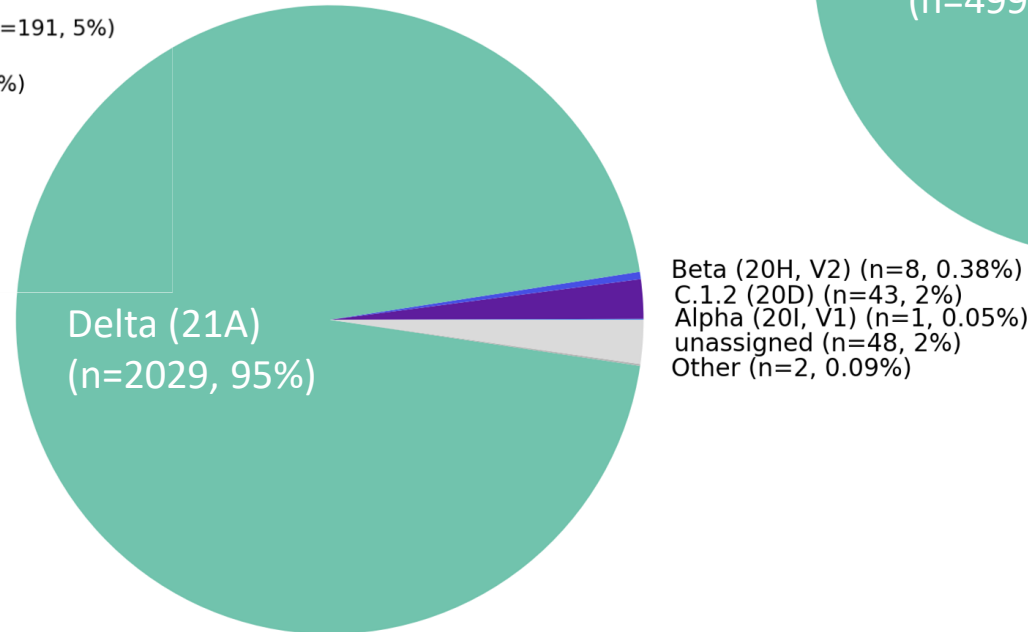
Beta variant dominated in May, but the Delta variant started to dominate in June

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

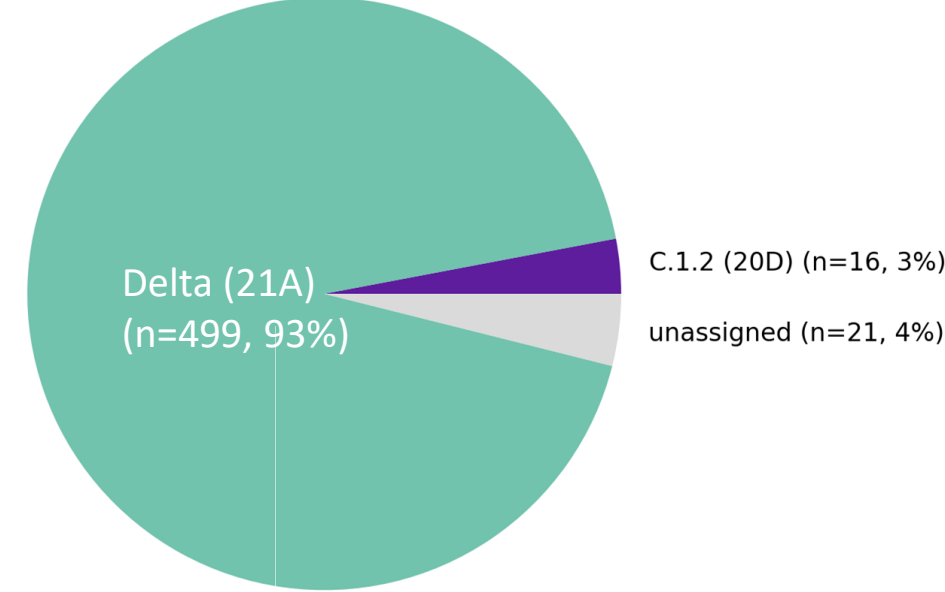
July (N=3956)



August (N=2131)



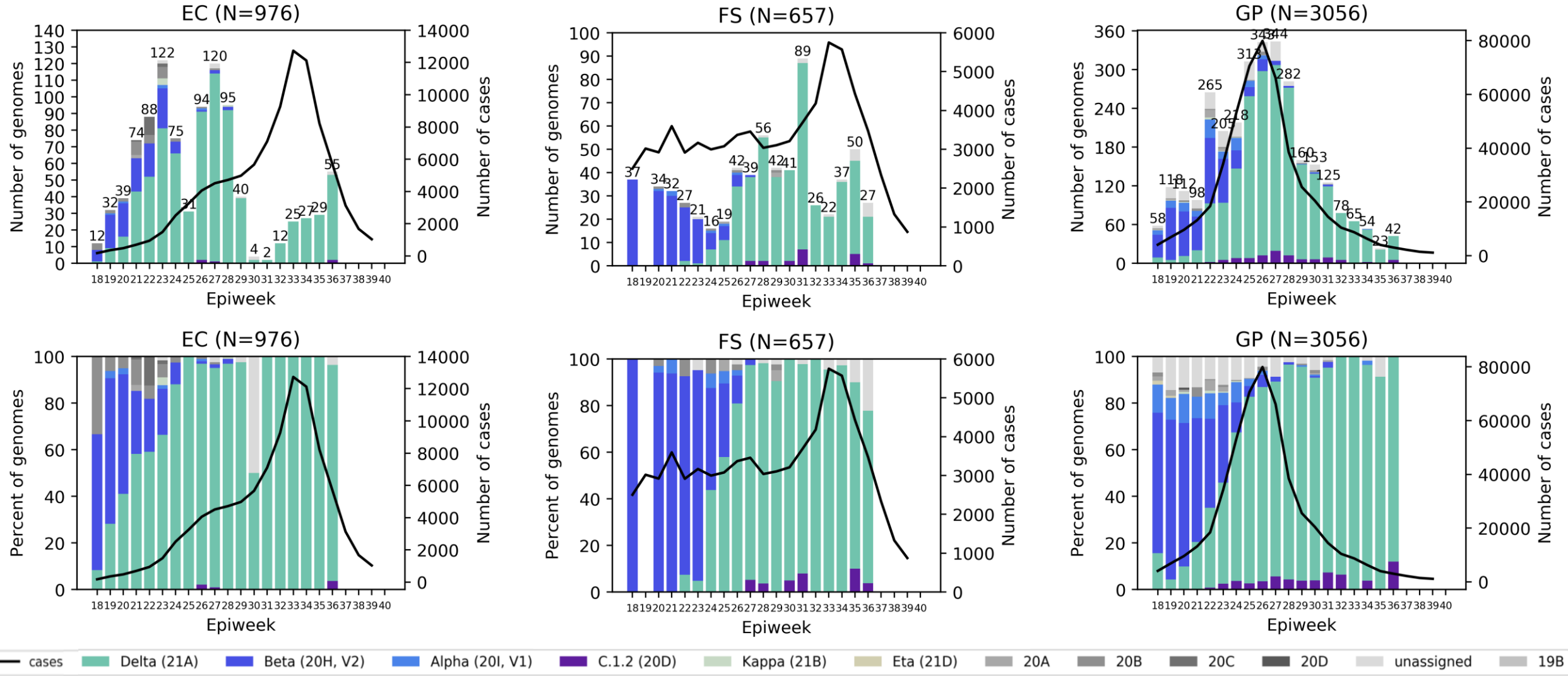
September (N=536)



Delta (21A) C.1.2 (20D) Beta (20H, V2) Alpha (20I, V1) Kappa (21B) Eta (21D) Other unassigned

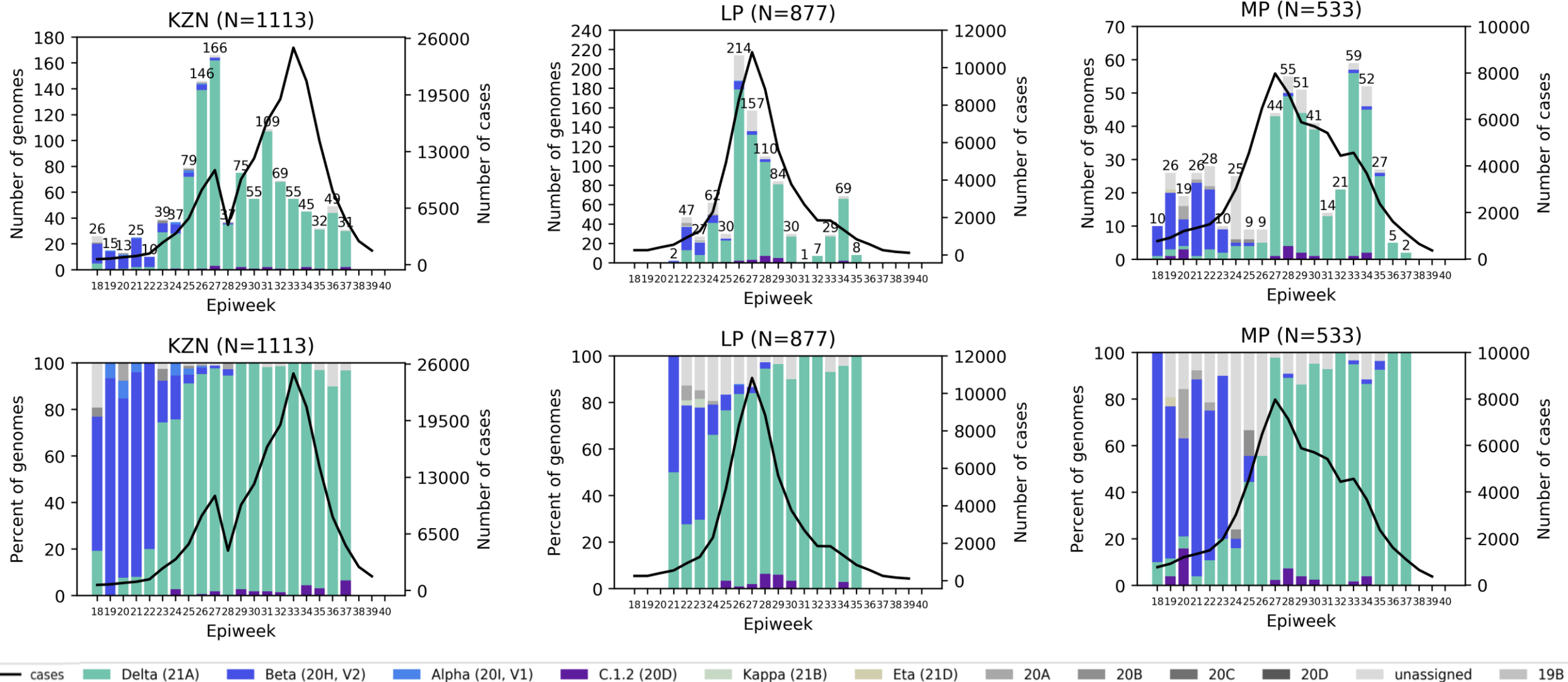
The Delta variant dominated in July and August in South Africa, and continues to dominate in September

Genomes sequenced from specimens collected in May to mid-September 2021 (epiweeks 18 – 40) from Eastern Cape, Free State and Gauteng Provinces



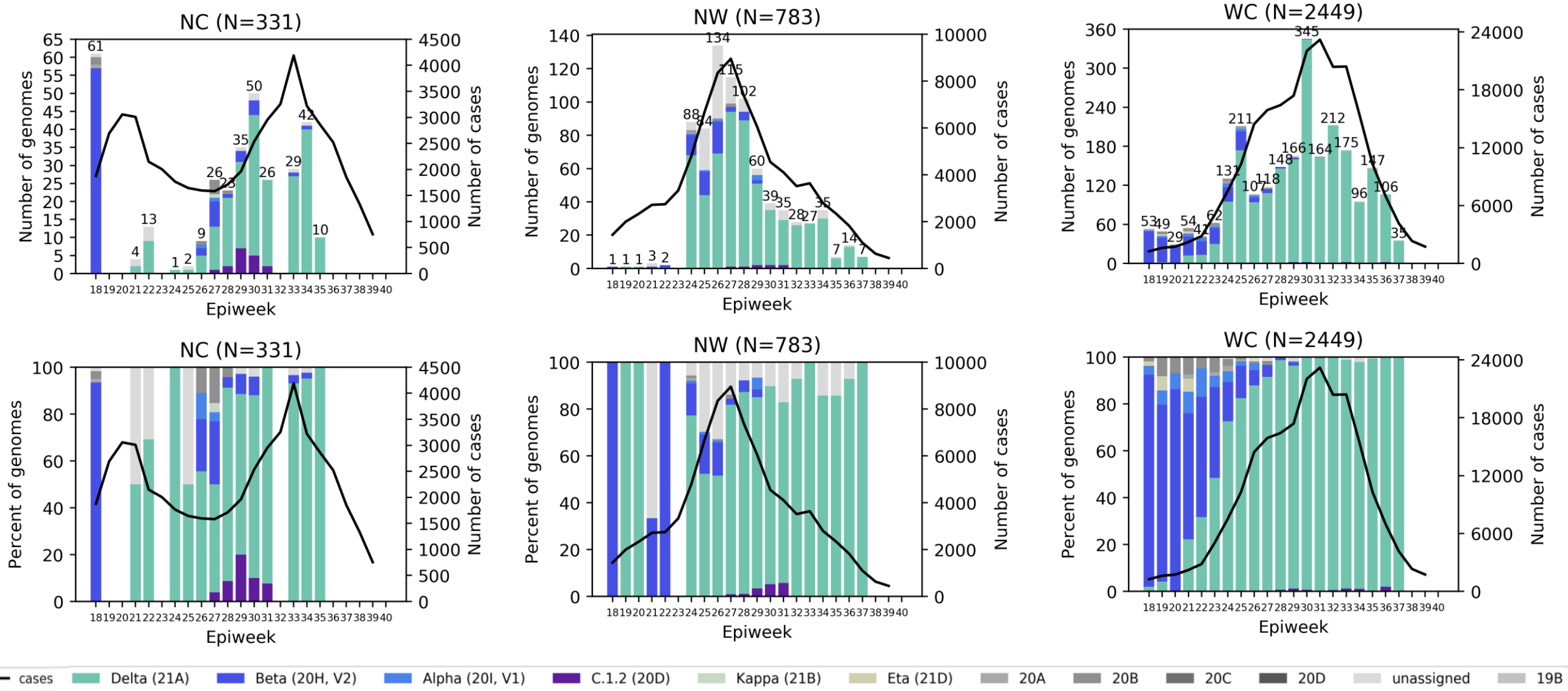
Delta dominates the third wave in Eastern Cape, Free State and Gauteng provinces

Genomes sequenced from specimens collected in May to mid-September 2021 (epiweeks 18 – 40) from KwaZulu-Natal, Limpopo and Mpumalanga Provinces



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

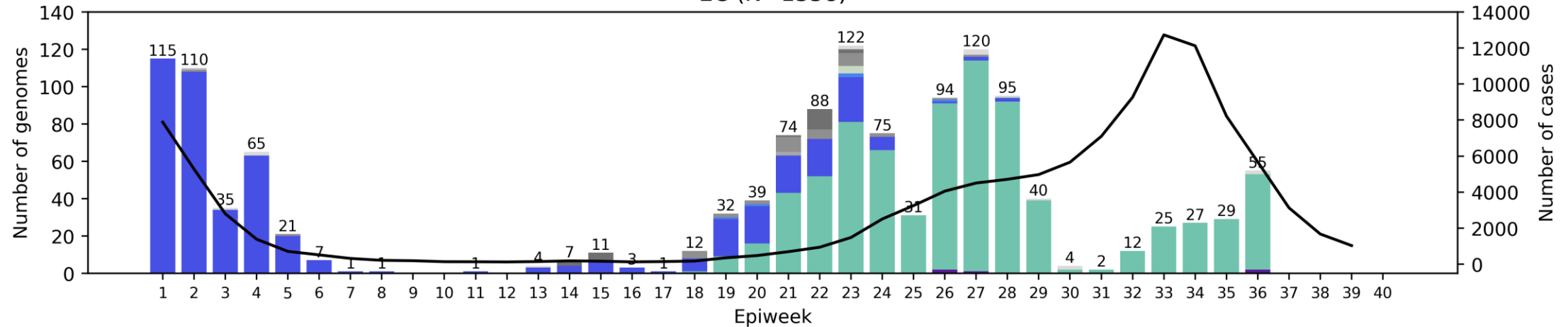
Genomes sequenced from specimens collected in May to mid-September 2021 (epiweeks 18 – 40) from Northern Cape, North West, and Western Cape Provinces



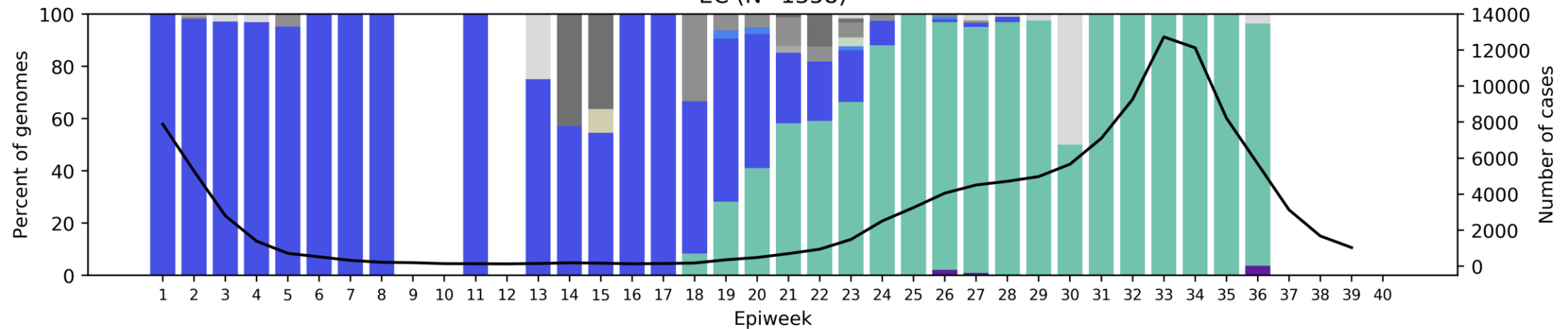
Delta dominates the third wave in Northern Cape, North West, and Western Cape provinces

Eastern Cape Province, 2021, n = 1358

EC (N=1358)

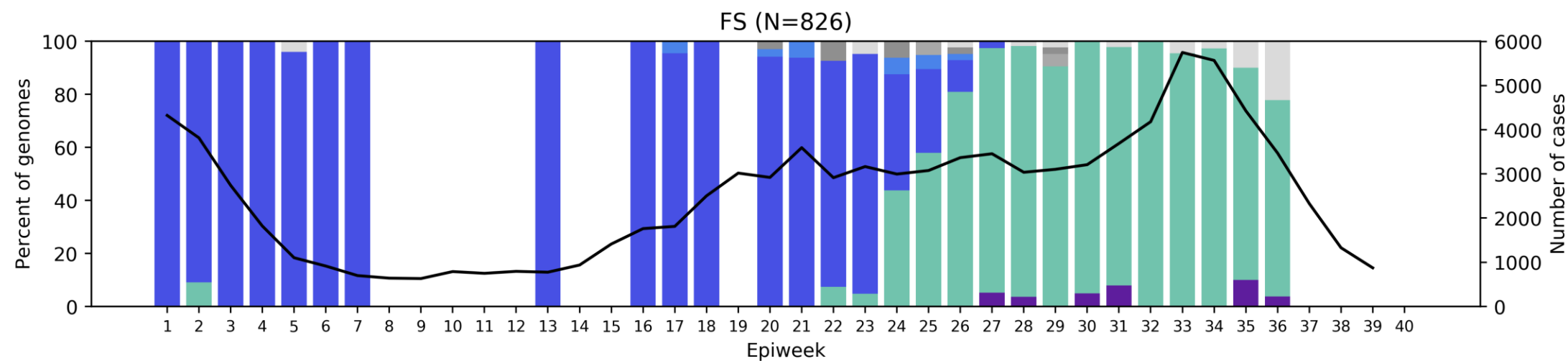
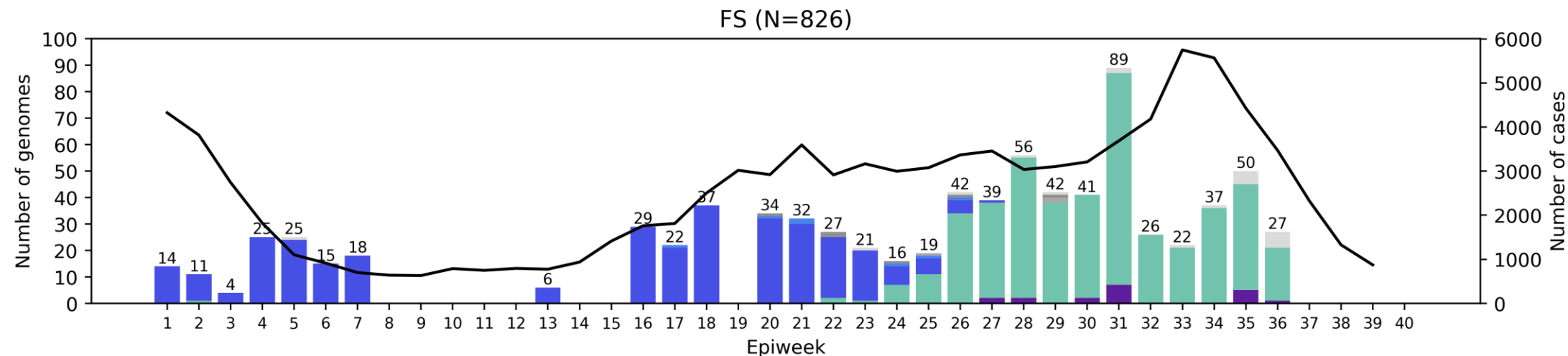


EC (N=1358)

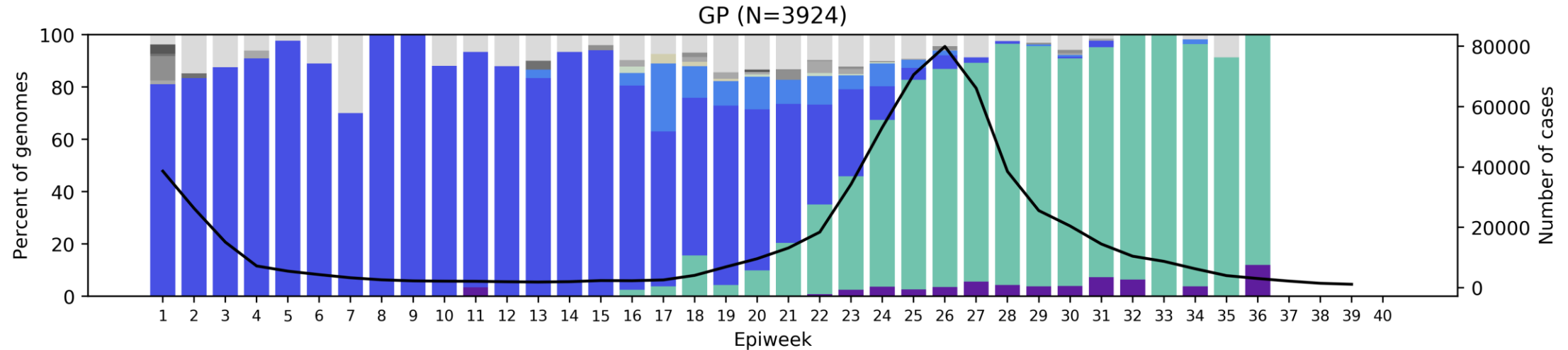
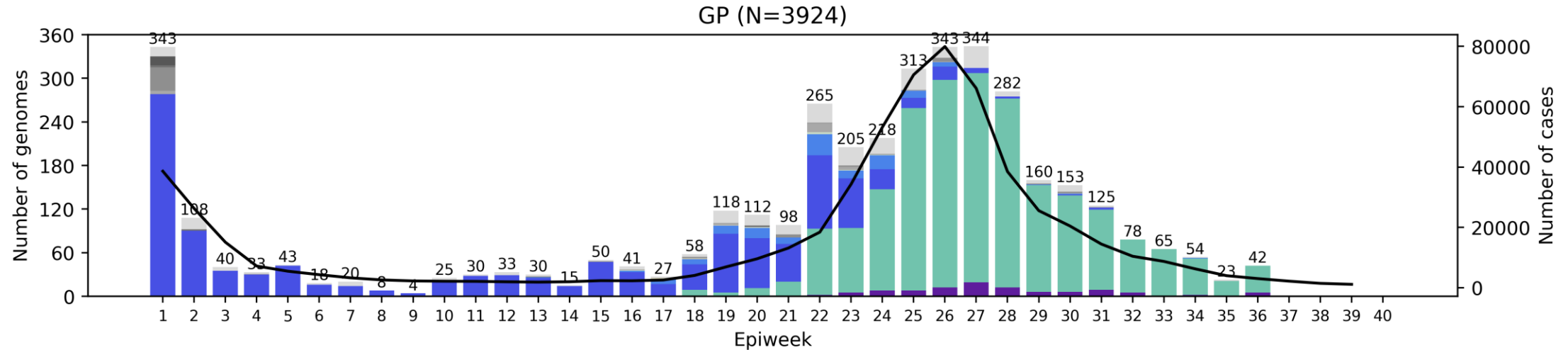


— cases Delta (21A) Beta (20H, V2) Alpha (20I, V1) C.1.2 (20D) Kappa (21B) Eta (21D) 20A 20B 20C 20D unassigned 19B

Free State Province, 2021, n = 826



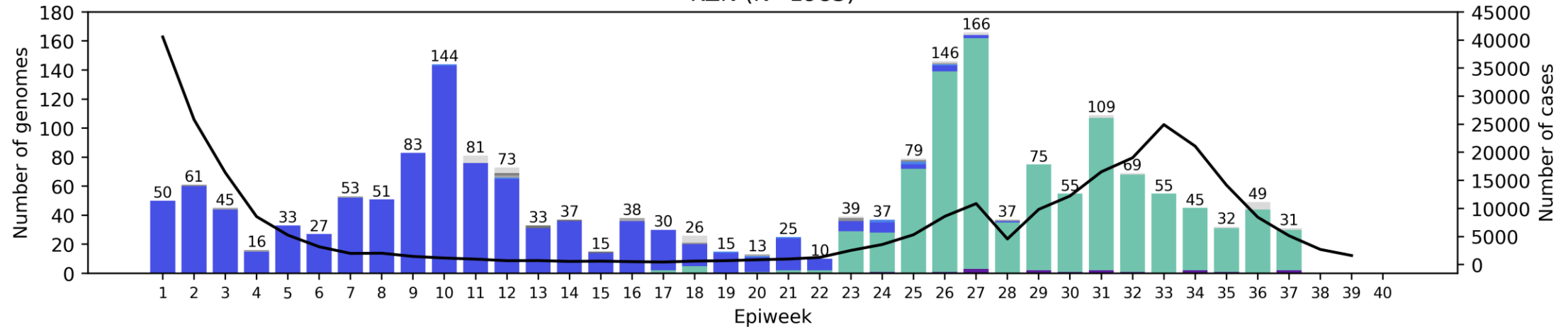
Gauteng Province, 2021, n = 3924



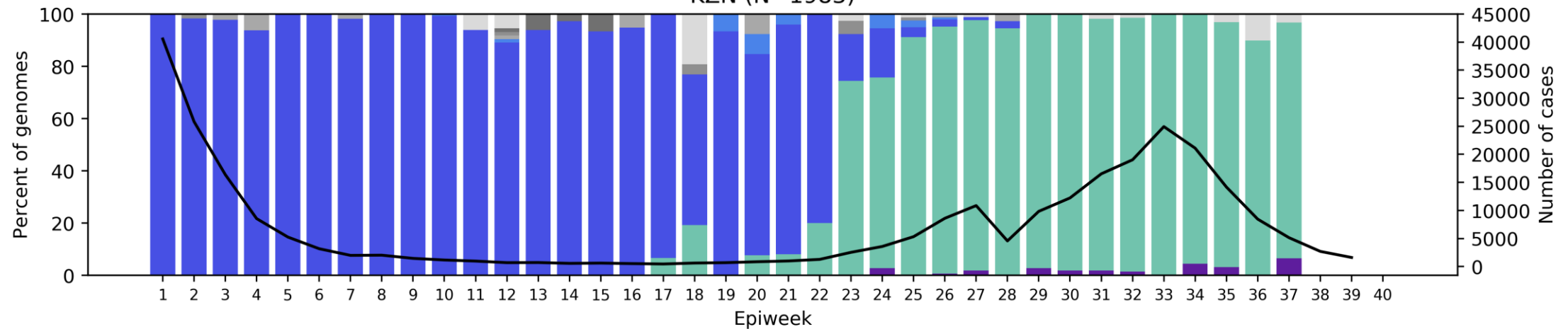
— cases Delta (21A) Beta (20H, V2) Alpha (20I, V1) C.1.2 (20D) Kappa (21B) Eta (21D) 20A 20B 20C 20D unassigned 19B

KwaZulu-Natal Province, 2021, n = 1983

KZN (N=1983)

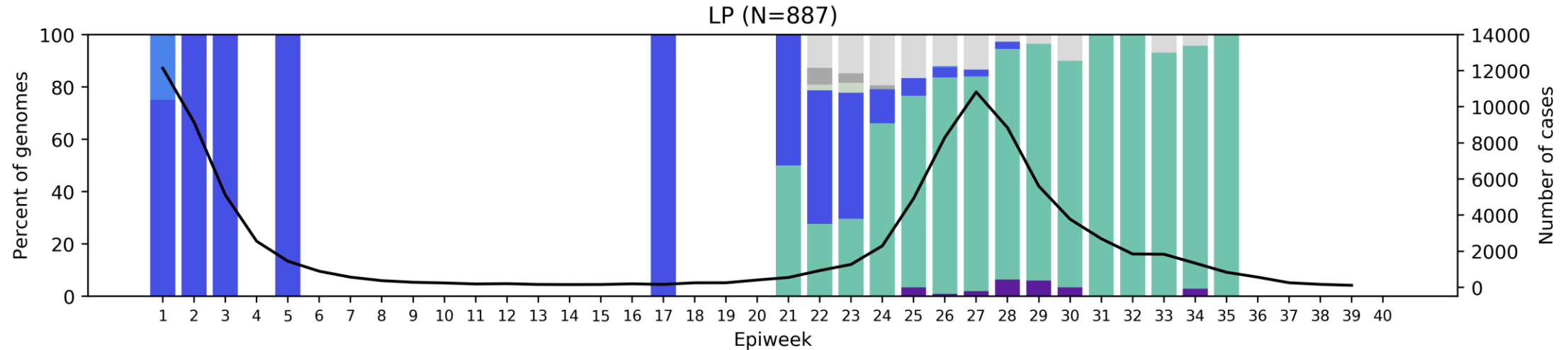
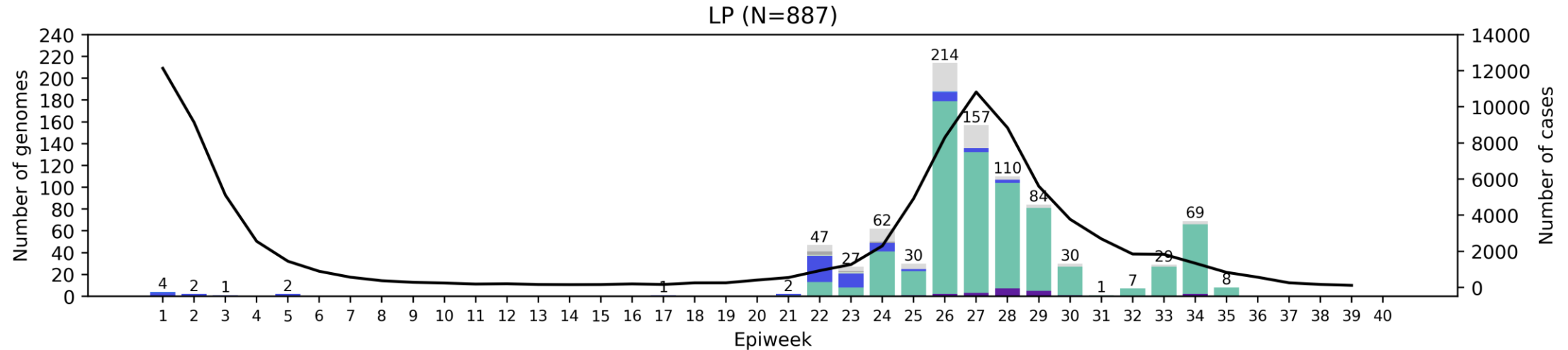


KZN (N=1983)



— cases Delta (21A) Beta (20H, V2) Alpha (20I, V1) C.1.2 (20D) Kappa (21B) Eta (21D) 20A 20B 20C 20D unassigned 19B

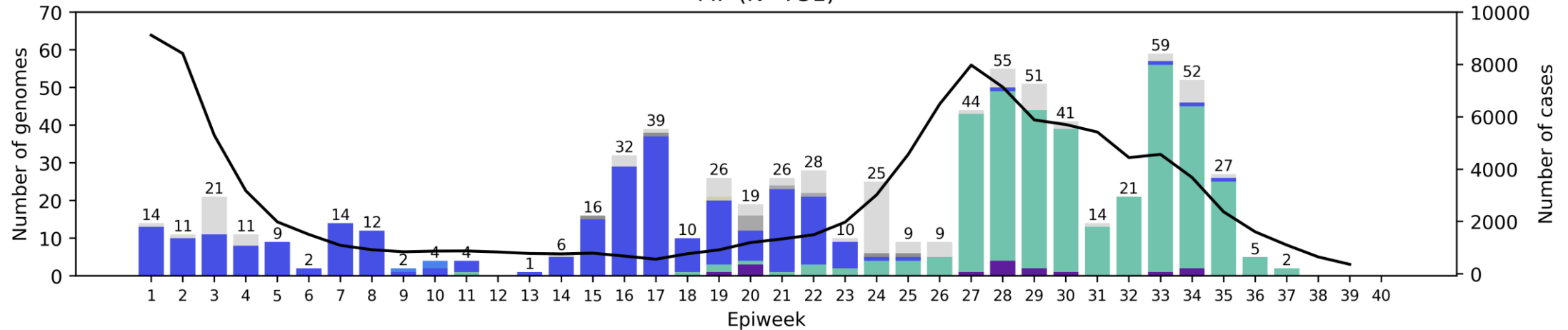
Limpopo Province, 2021, n = 887



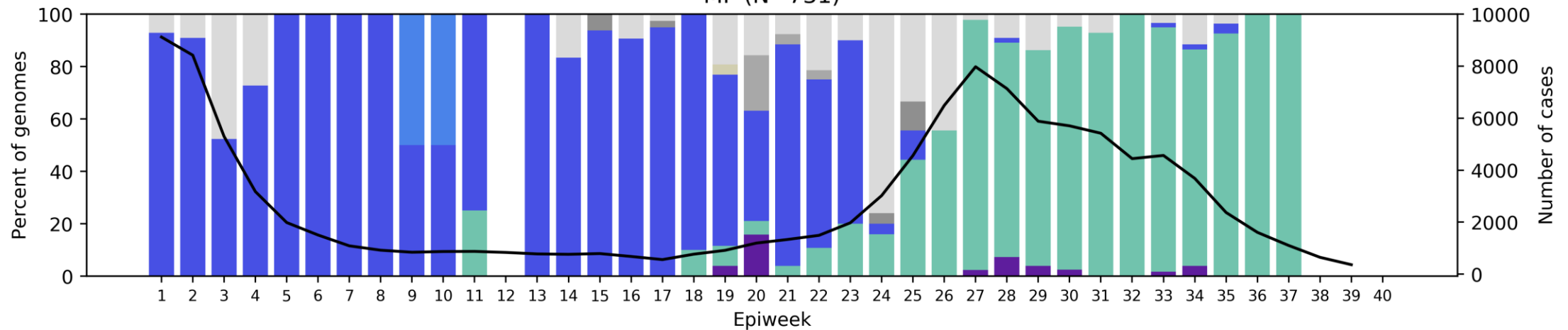
— cases Delta (21A) Beta (20H, V2) Alpha (20I, V1) C.1.2 (20D) Kappa (21B) Eta (21D) 20A 20B 20C 20D unassigned 19B

Mpumalanga Province, 2021, n = 731

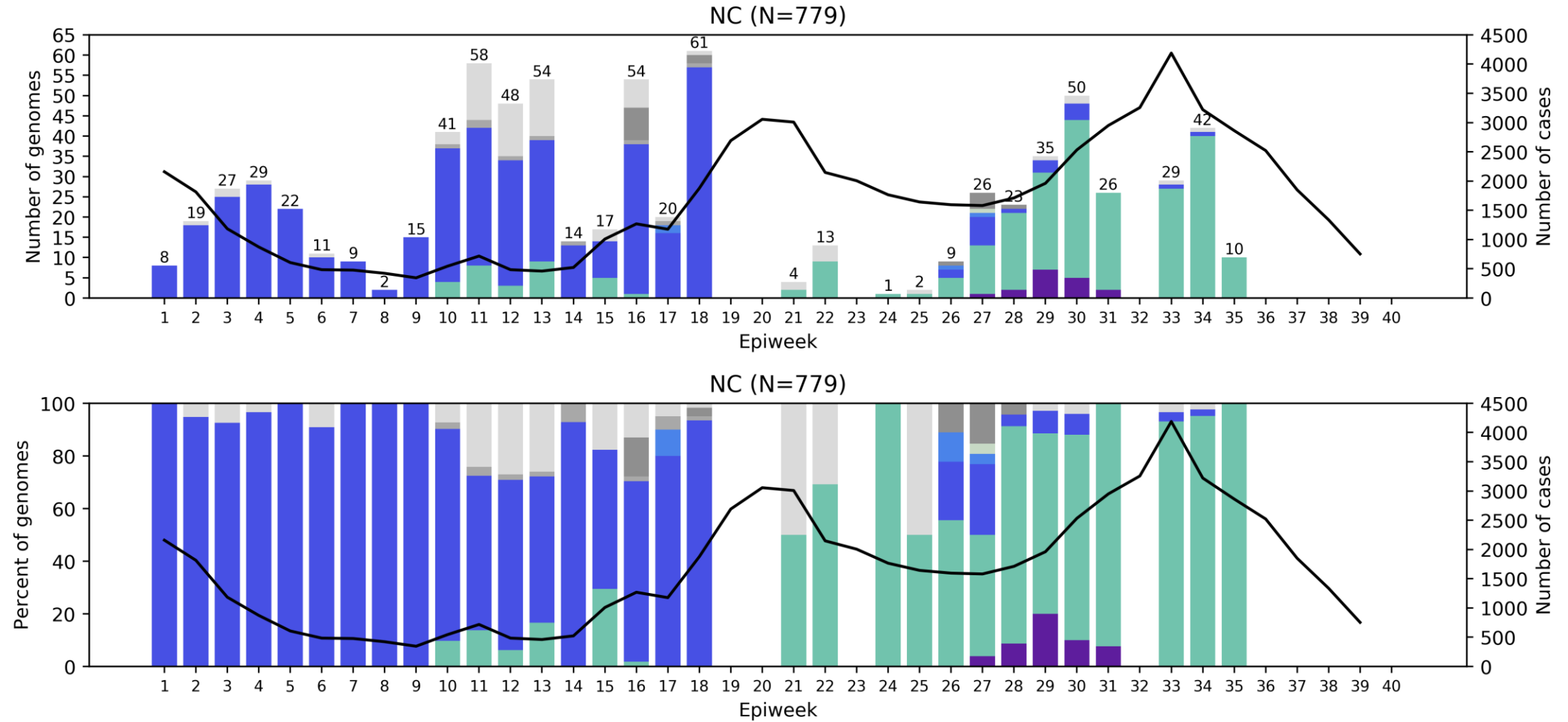
MP (N=731)



MP (N=731)

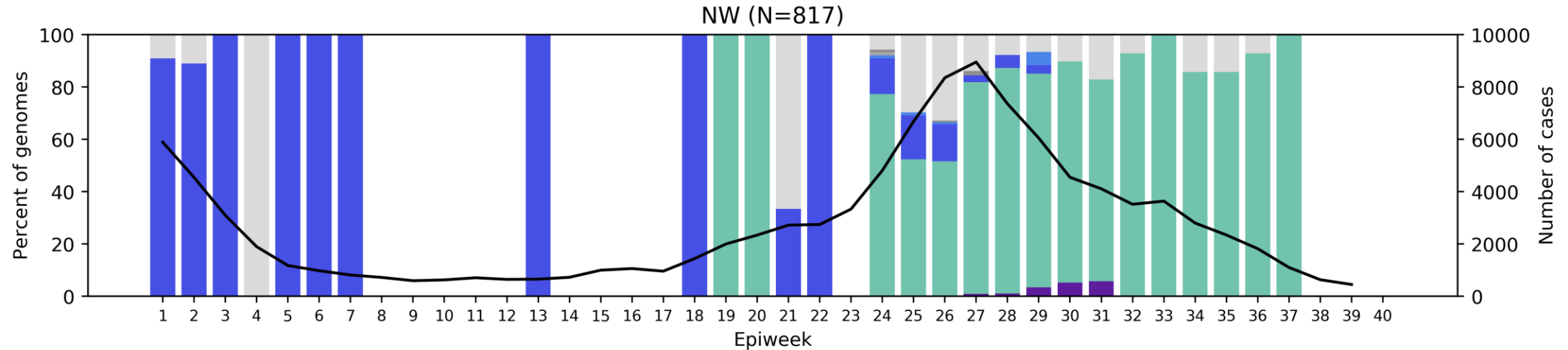
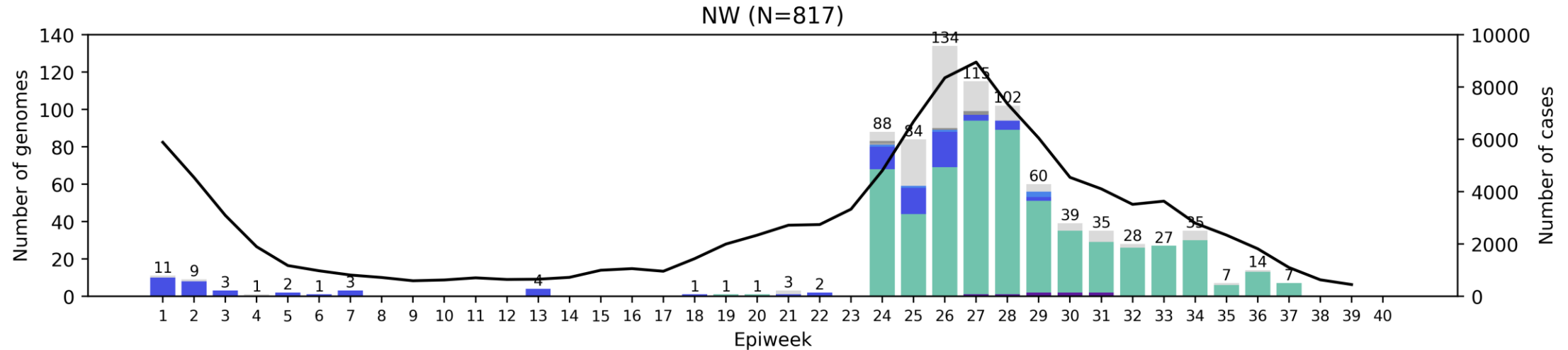


Northern Cape Province, 2021, n = 779



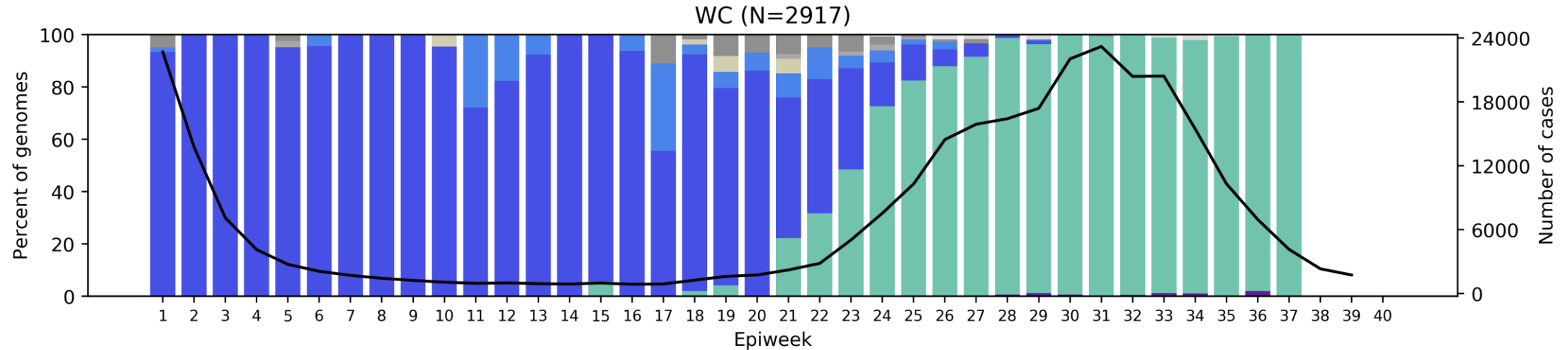
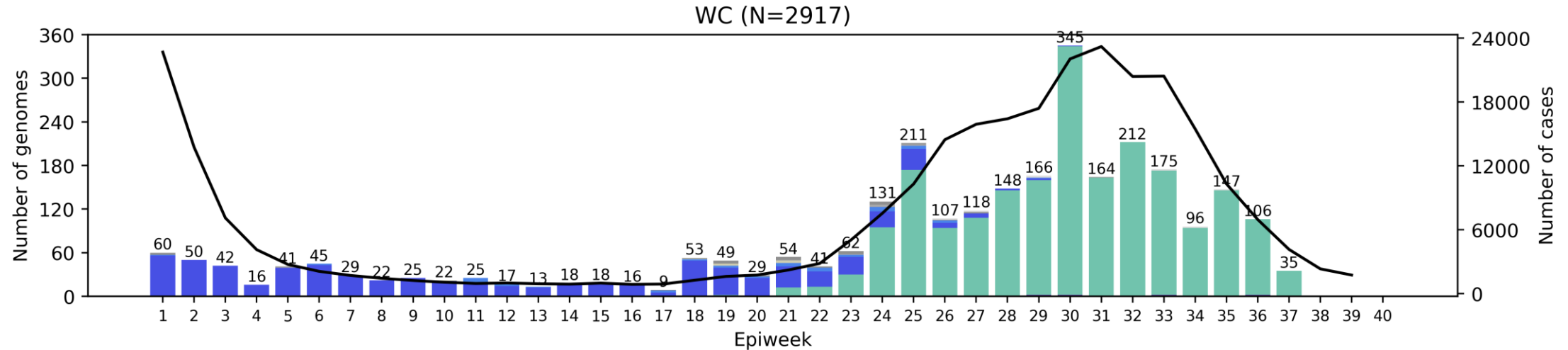
— cases Delta (21A) Beta (20H, V2) Alpha (20I, V1) C.1.2 (20D) Kappa (21B) Eta (21D) 20A 20B 20C 20D unassigned 19B

North West Province, 2021, n = 817



— cases Delta (21A) Beta (20H, V2) Alpha (20I, V1) C.1.2 (20D) Kappa (21B) Eta (21D) 20A 20B 20C 20D unassigned 19B

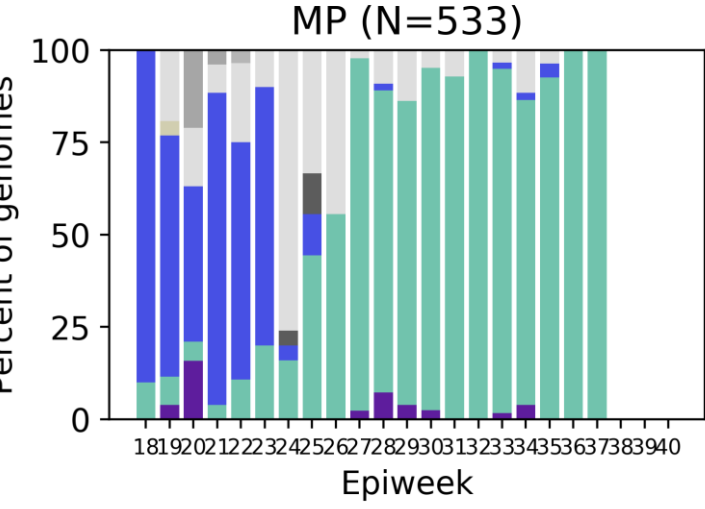
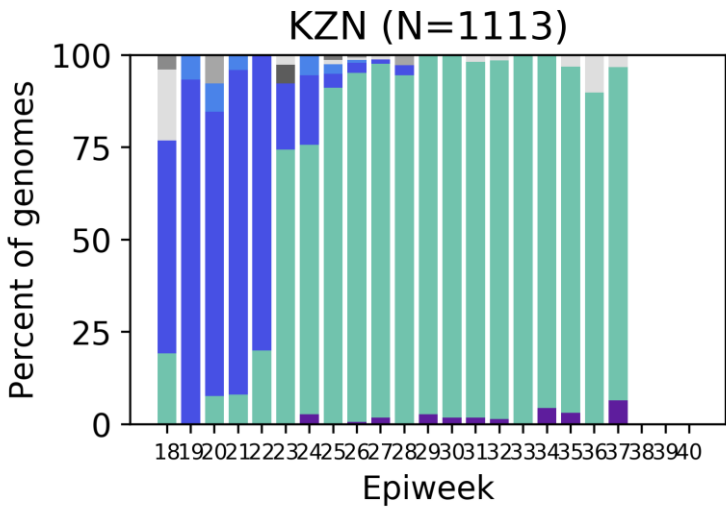
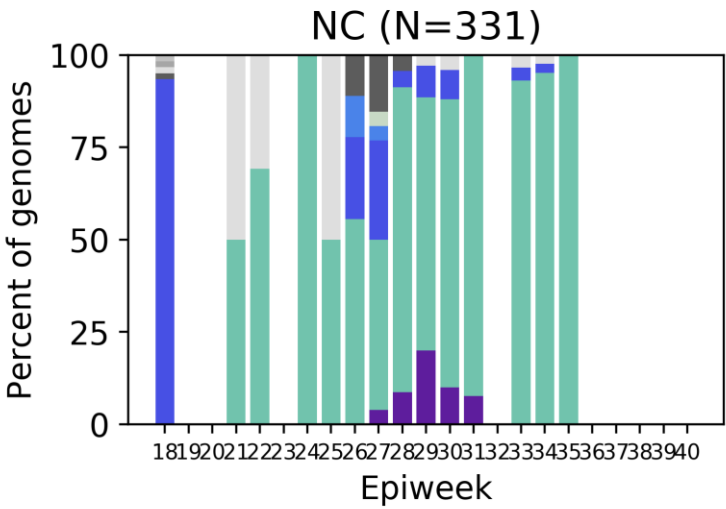
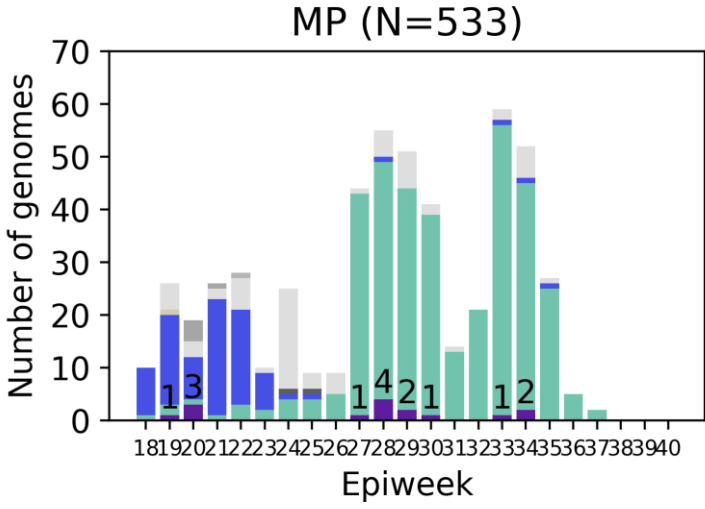
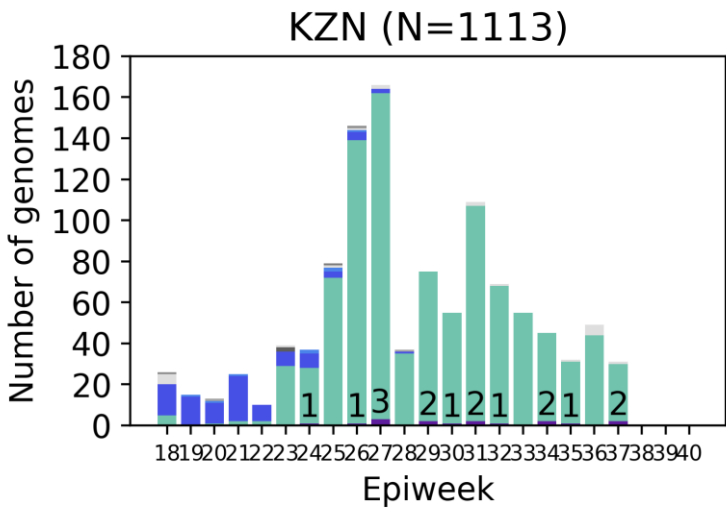
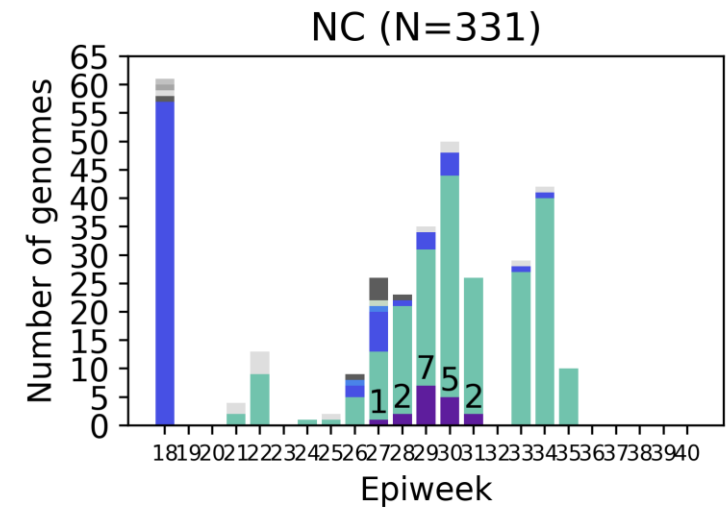
Western Cape Province, 2021, n = 2917



— cases Delta (21A) Beta (20H, V2) Alpha (20I, V1) C.1.2 (20D) Kappa (21B) Eta (21D) 20A 20B 20C 20D unassigned 19B

C.1.2 (n=211 in SA) in May – August 2021 by epiweek

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

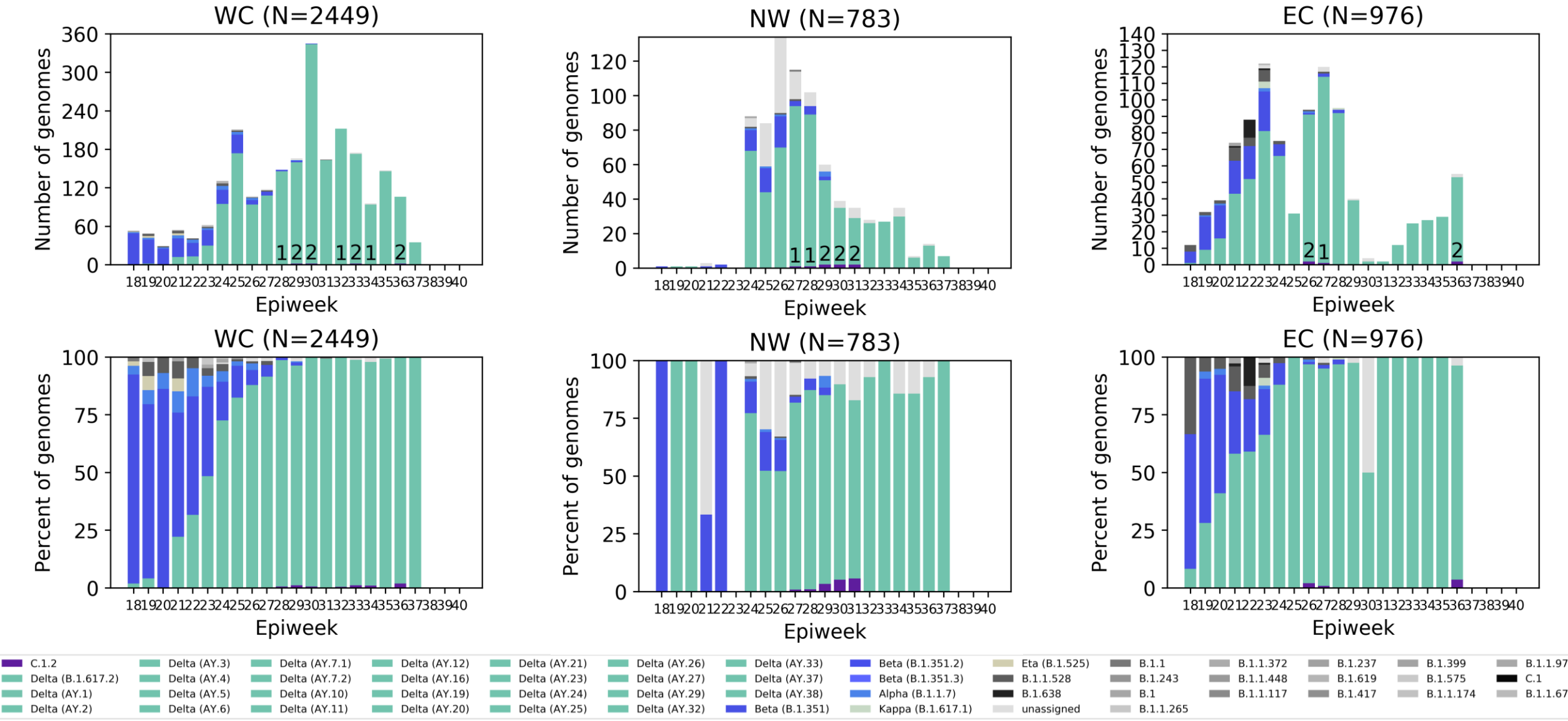


C.1.2 sequences have also been detected in the Northern Cape (n=17), KwaZulu-Natal (n=16), and Mpumalanga (n=15)



C.1.2 (n=211 in SA) in May – August 2021 by epiweek

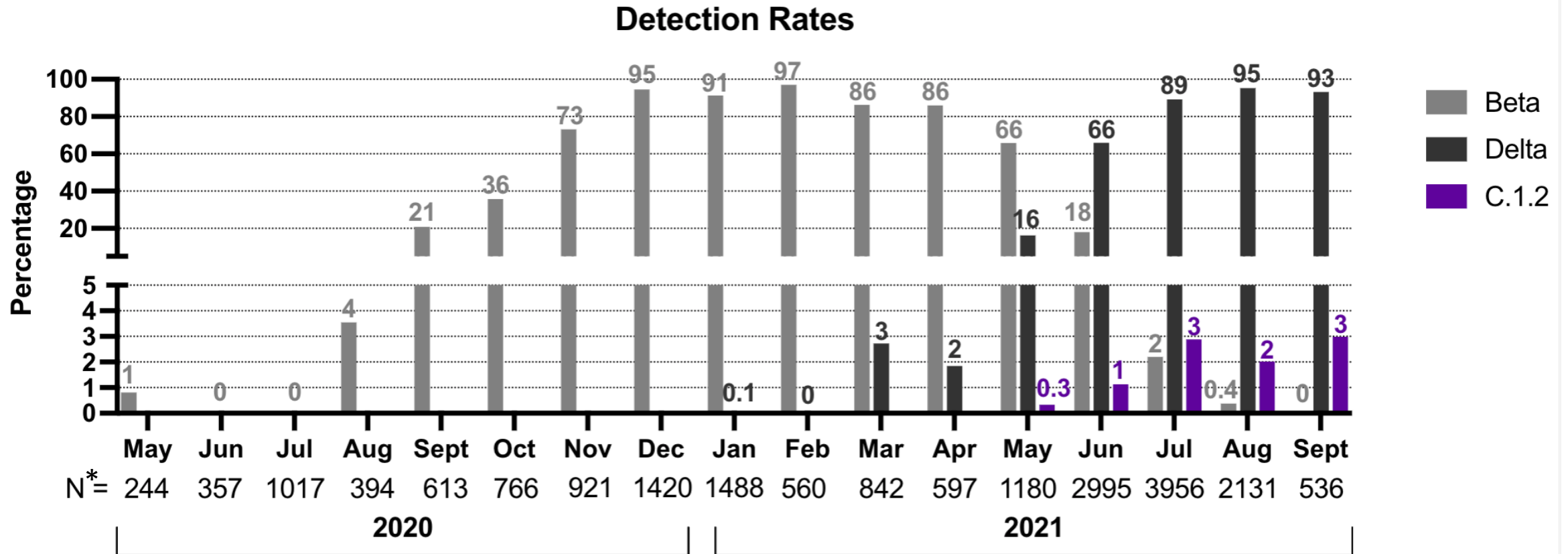
Number of C.1.2 samples indicated above bar, provinces ordered by number of detections



The Western Cape has 11 sequences, the North West has 8, and the Eastern Cape has 5 detections of C.1.2.



C.1.2 growth compared to Beta and Delta



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

N* = total number of sequences collected in each month

Summary

- Delta continues to dominate in all provinces from specimens collected in September
- Overall number of lineages detected has decreased following Delta dominance
- Mutated C.1.2 lineage has now been detected in all provinces of South Africa
 - The frequency of C.1.2 at less than 4% of genomes from May through early September.
- Lambda and Mu variants not detected in South Africa



Supported by the DSI and the SA MRC



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Amy Strydom (Postdoc)
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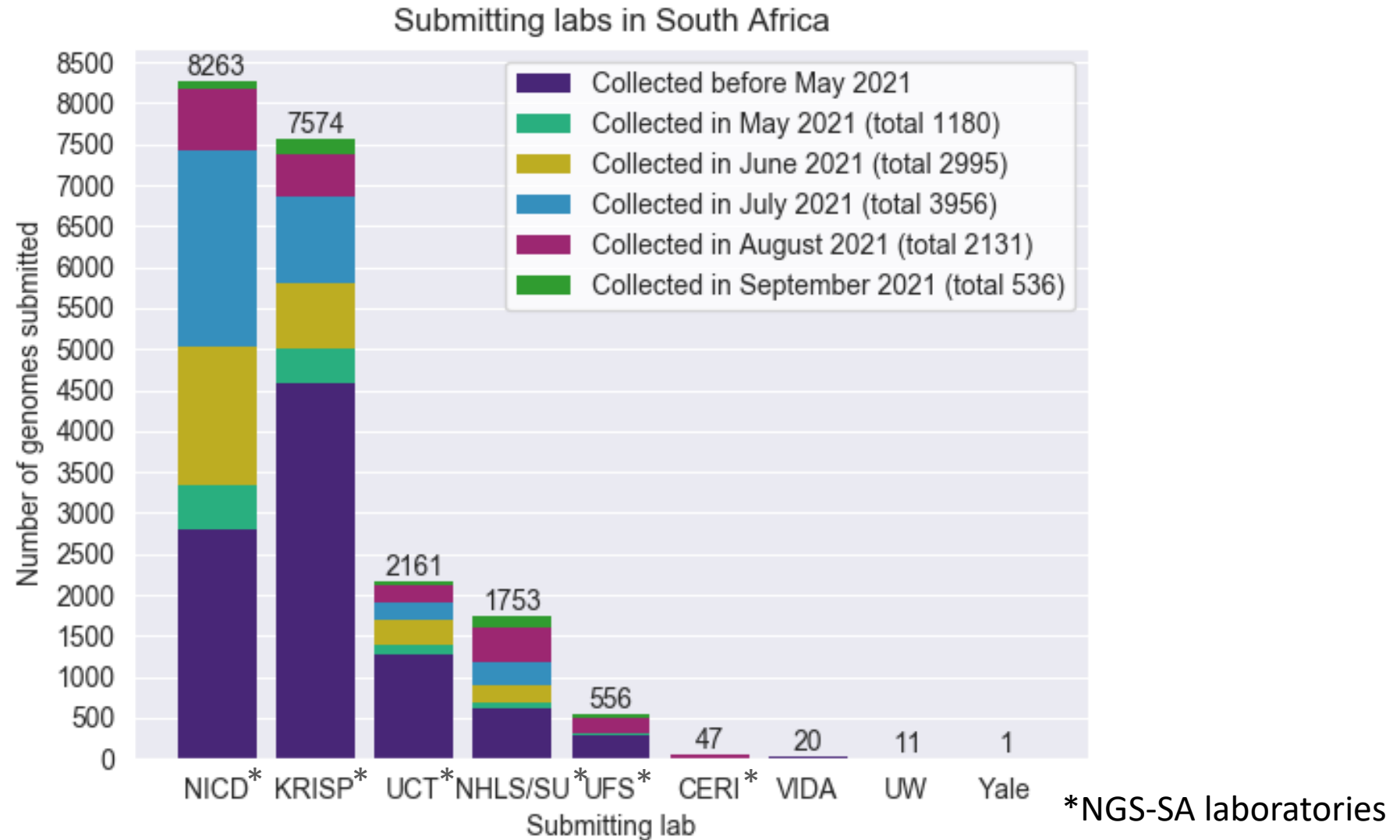
Glaudina Loots

SA MRC

Glenda Gray



South African genomes submitted per sequencing lab, 2020 and 2021 (N=20 386)



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

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 27 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.)