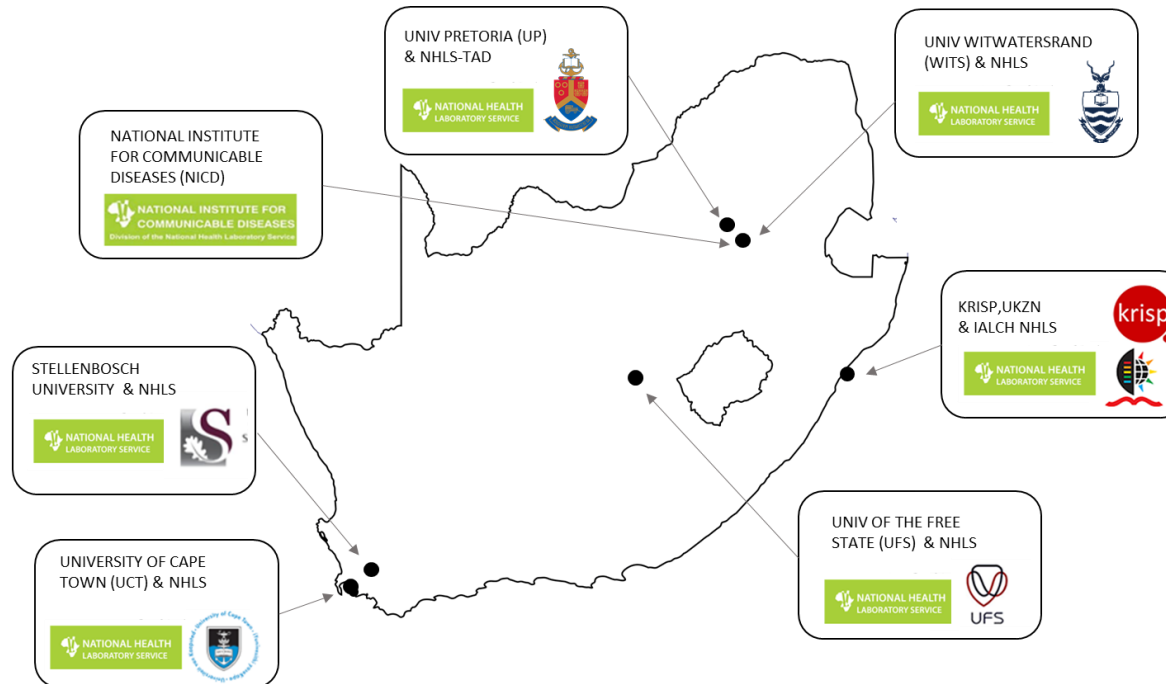


## SARS-CoV-2 Sequencing Update 19 August 2021



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](http://www.gisaid.org)) on 19 August at 09h00



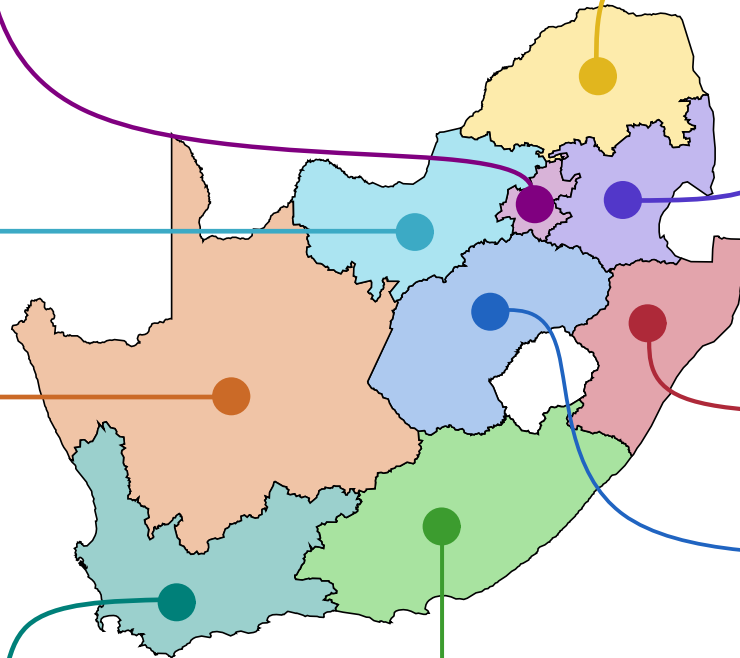
Data license: <https://www.gisaid.org/registration/terms-of-use/>

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 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 - 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

## Limpopo

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

Genomes deposited in the last week  
3 120 10 6

## North West

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

Genomes deposited in the last week  
40 4

## Mpumalanga

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

Genomes deposited in the last week  
40 14 1 6

## Northern Cape

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

Genomes deposited in the last week  
1 70 33 2 1 13 20

## KwaZulu-Natal

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

Genomes deposited in the last week  
1 127 3 1

## 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

## Free State

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

Genomes deposited in the last week



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)

# 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)

Number of sequences

750

500

250

0

10

20

2020

30

40

50

Epidemiological week

10

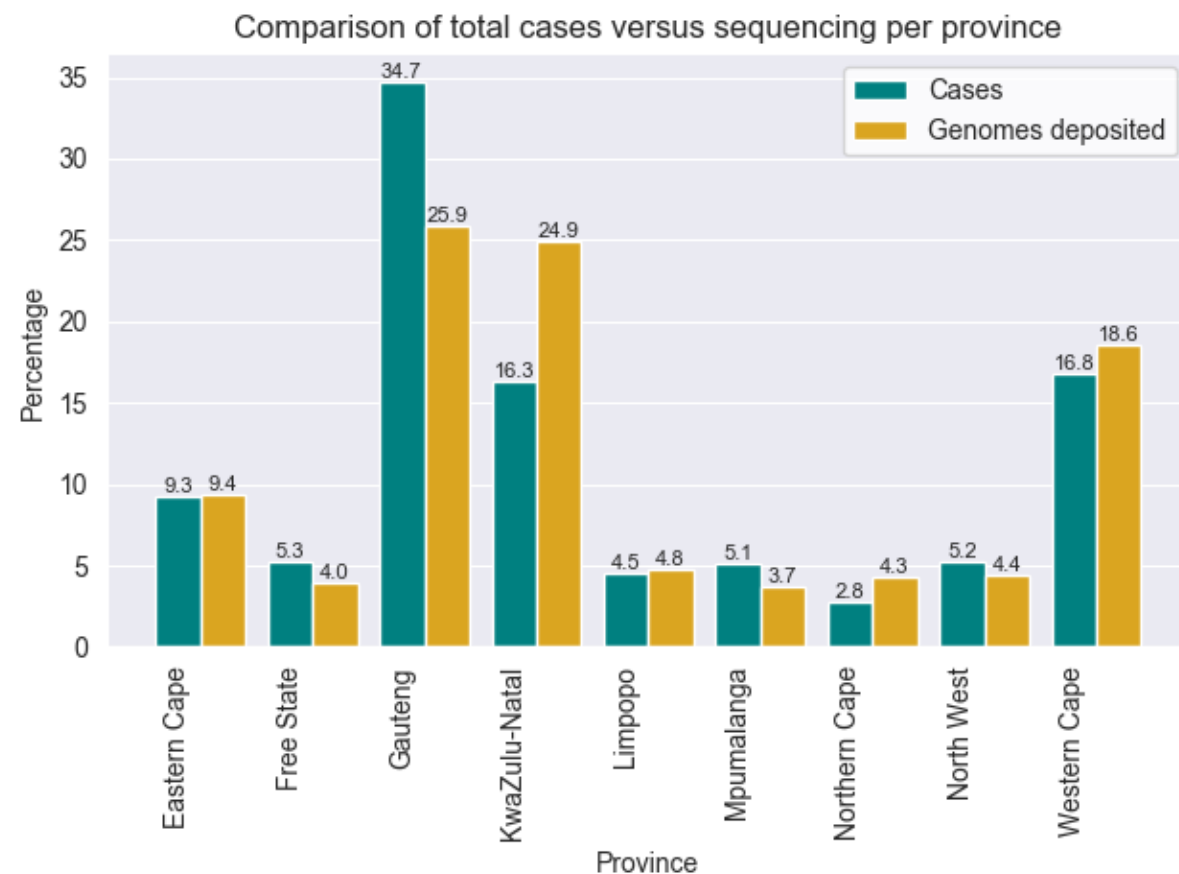
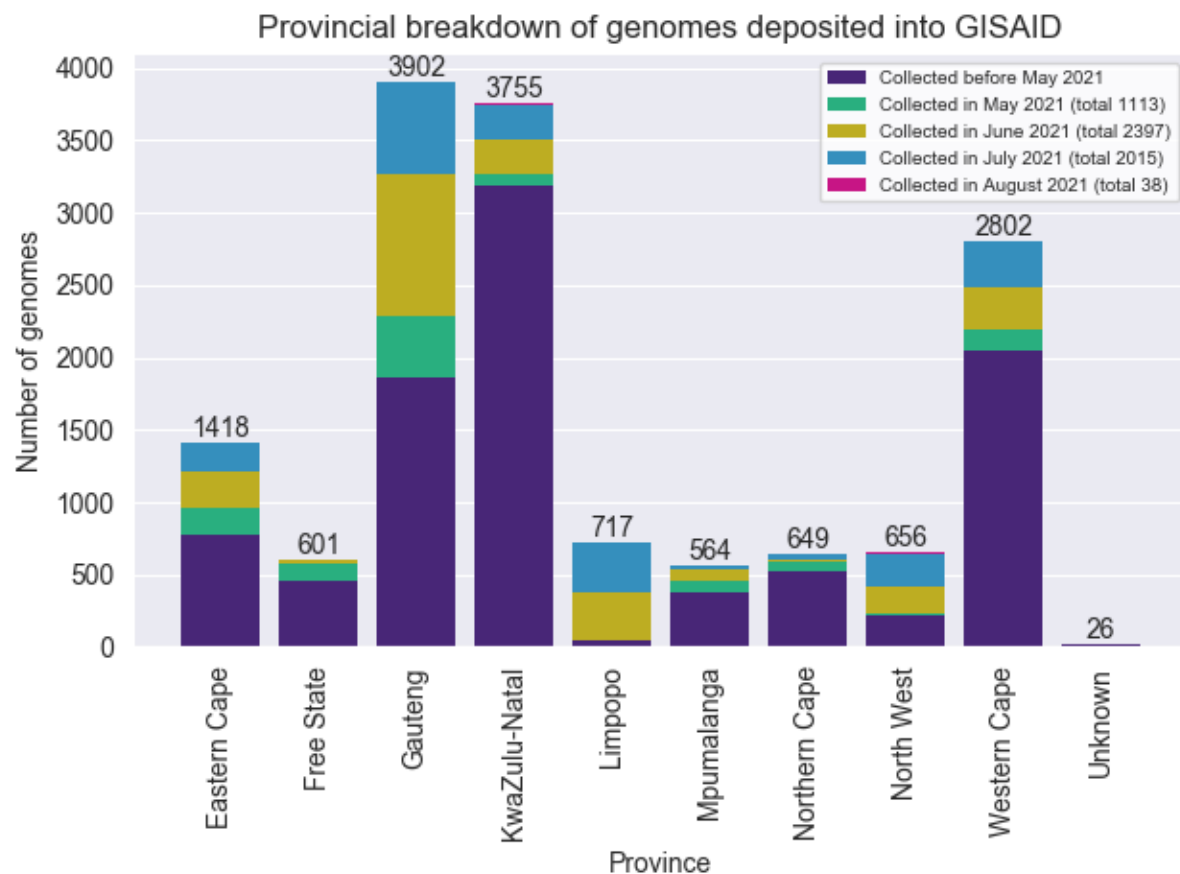
2021

20

30

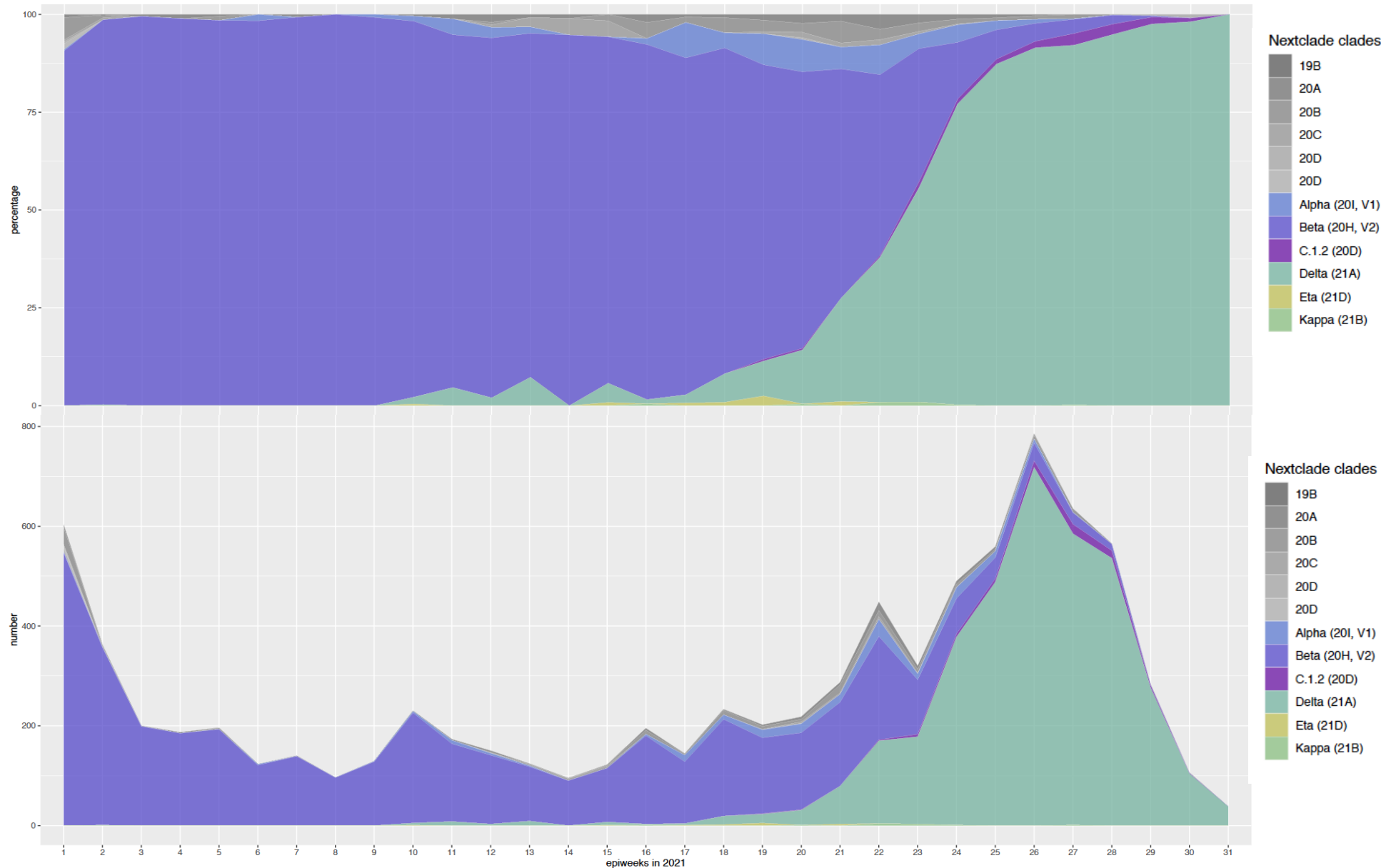
\*This represents the cleaned, de-duplicated dataset of unique sequences. This dataset will be used for all further figures.

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



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

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



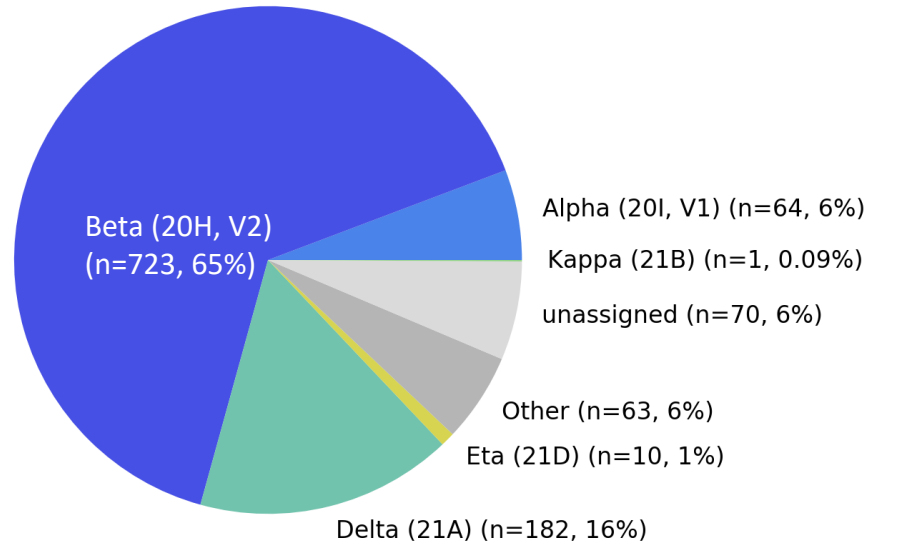
Sequencing data  
ending epi week 31  
(ending 7 August  
2021)

Currently in epi  
week 33 (ending 21  
August 2021)

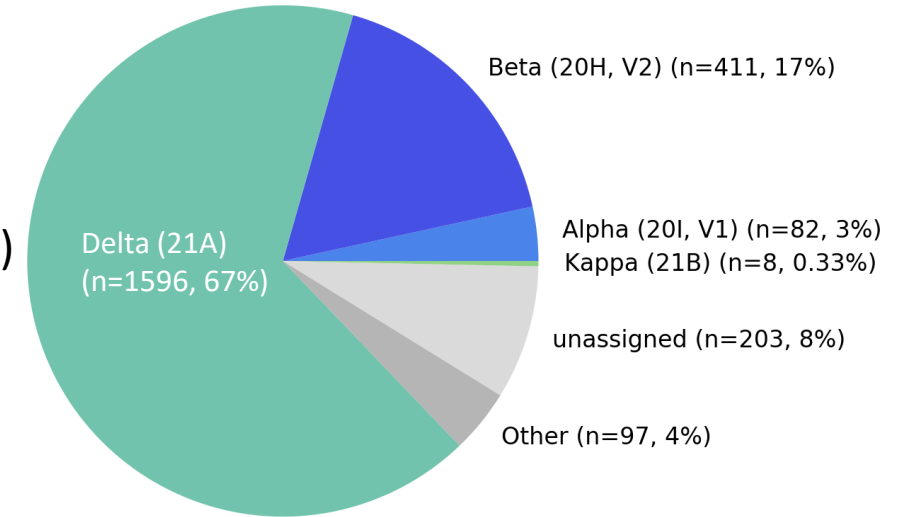
**While Alpha, Delta and Eta variant frequency increased from the beginning of May, Delta came to dominate by end June at >75% and in July at >85%**

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

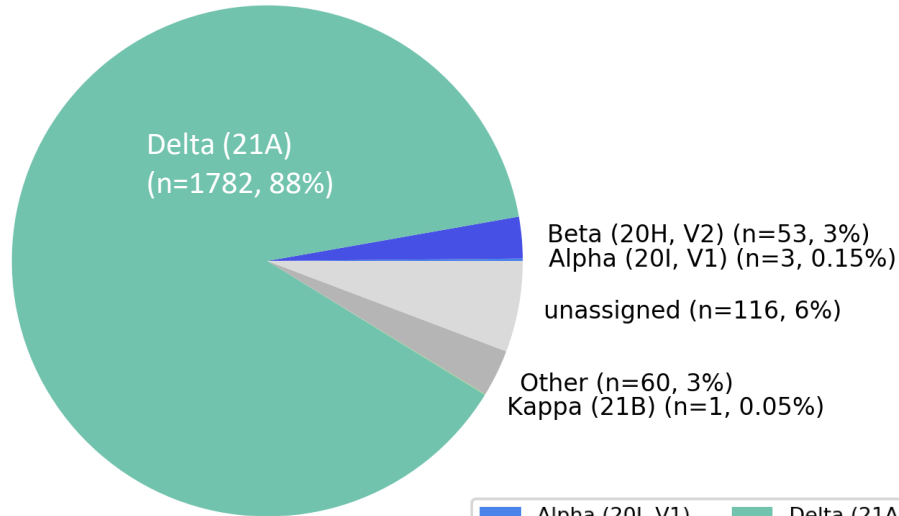
**May (N = 1113)**



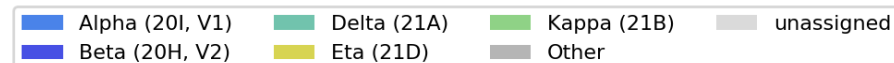
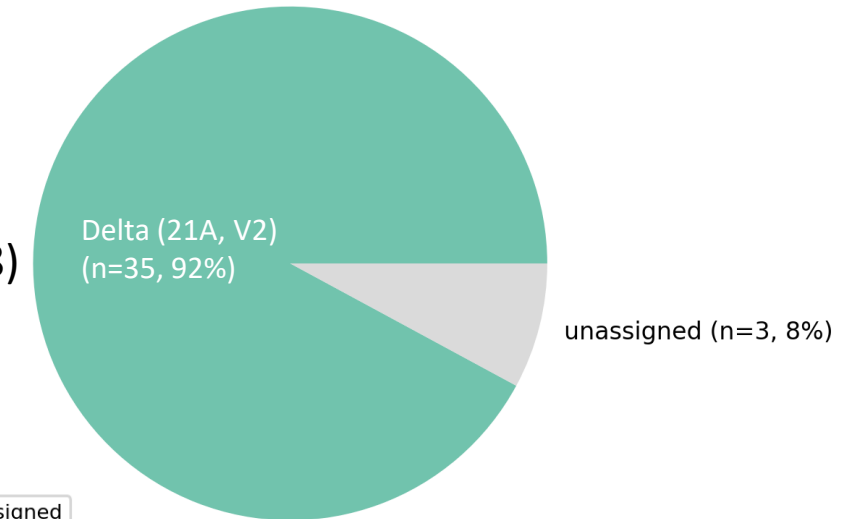
**June (N = 2397)**



**July (N = 2015)**



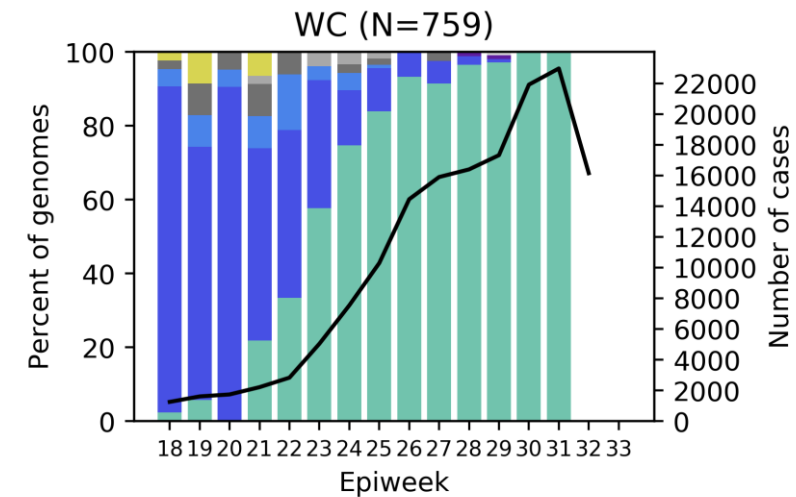
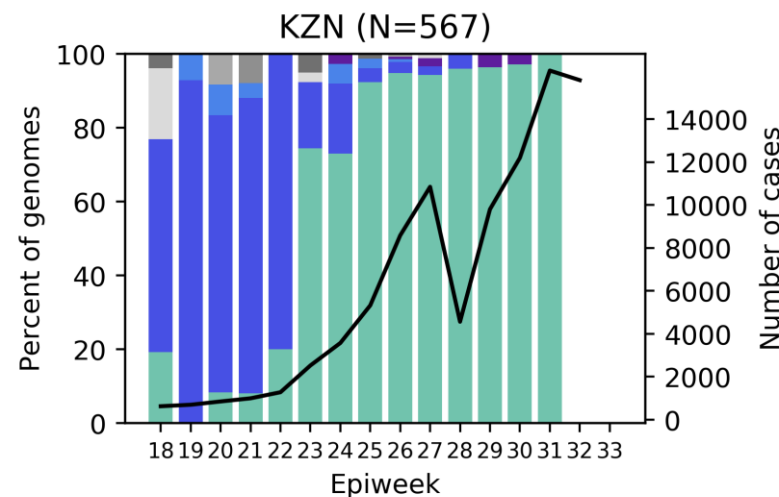
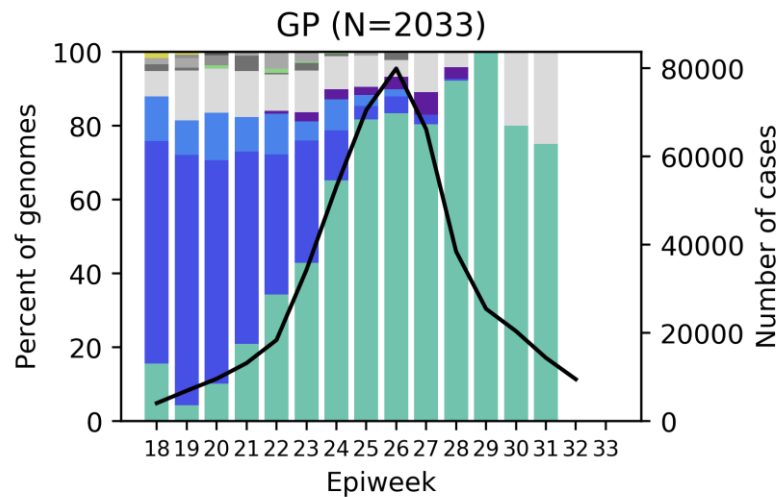
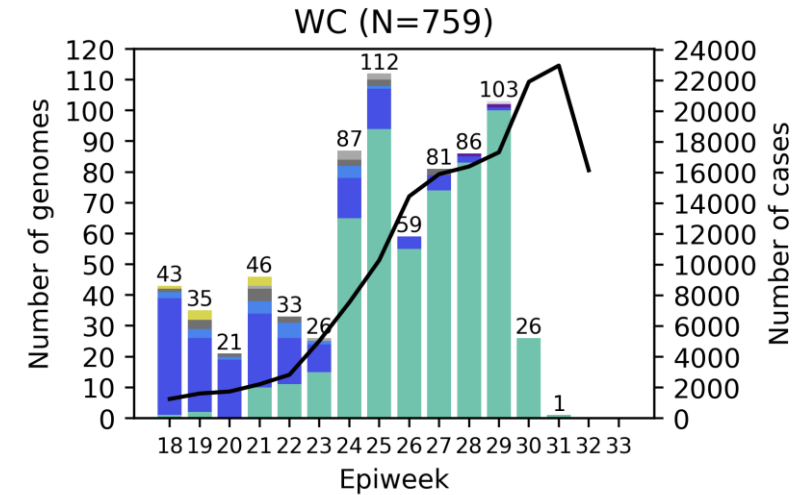
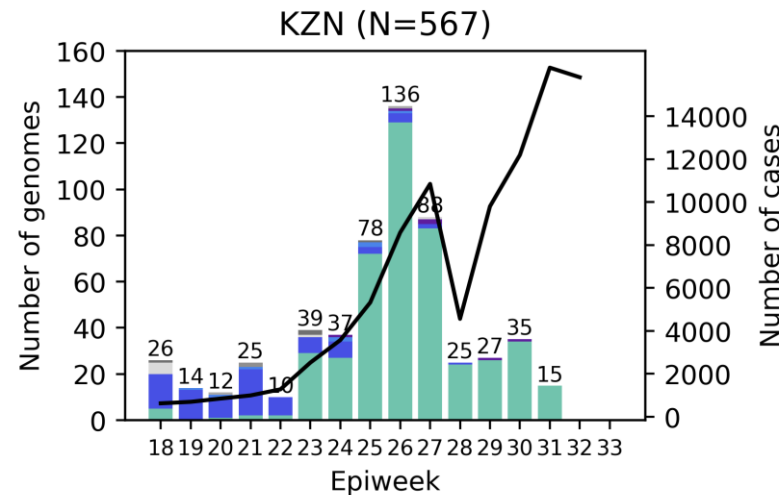
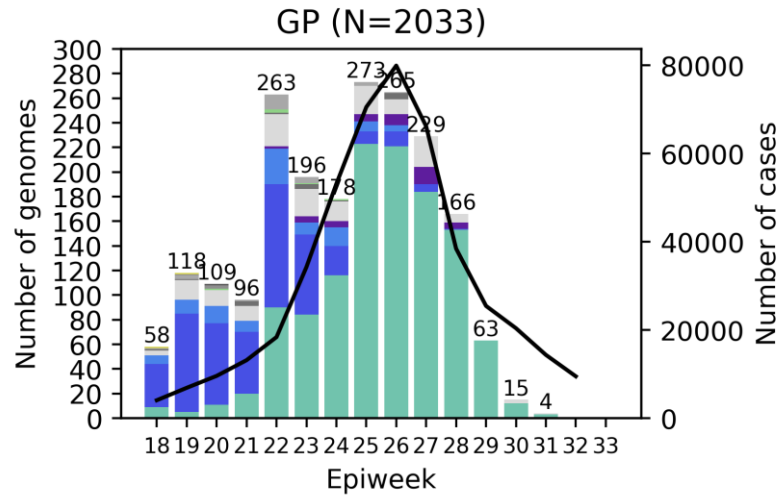
**August (N = 38)**



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



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

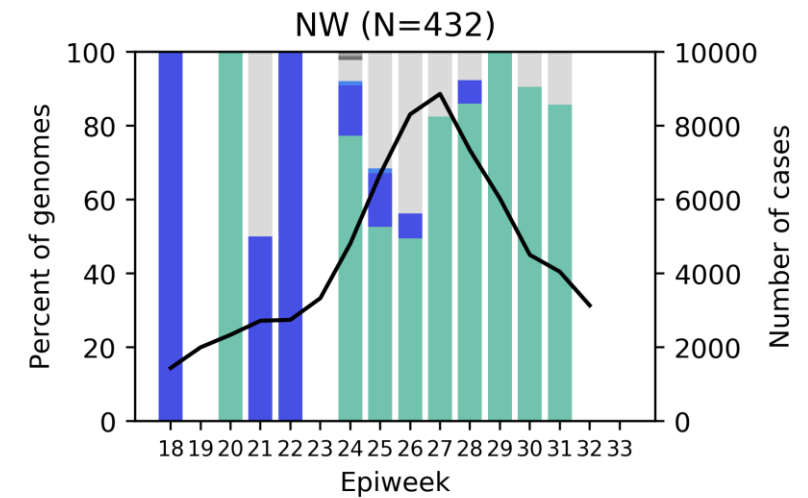
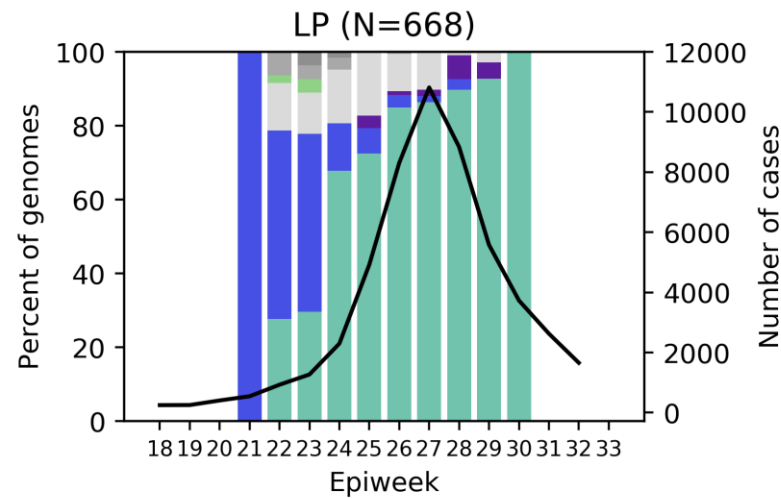
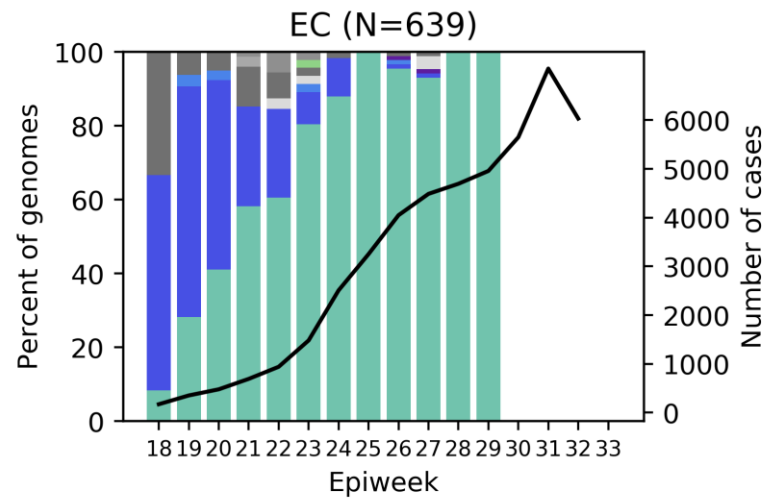
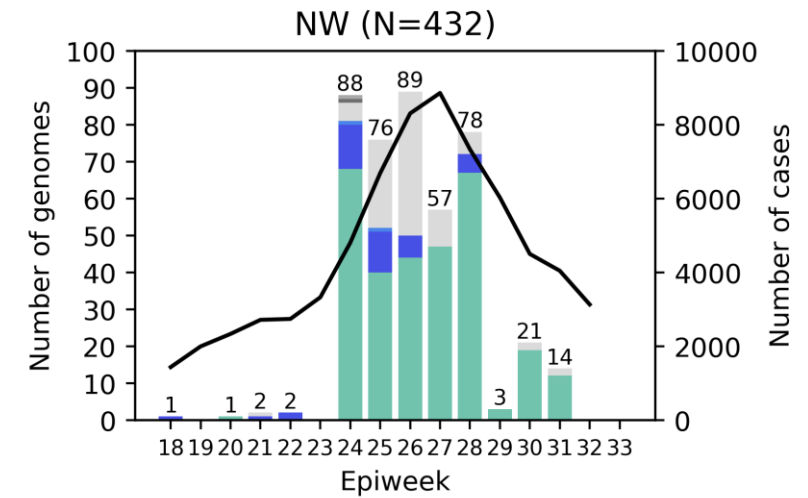
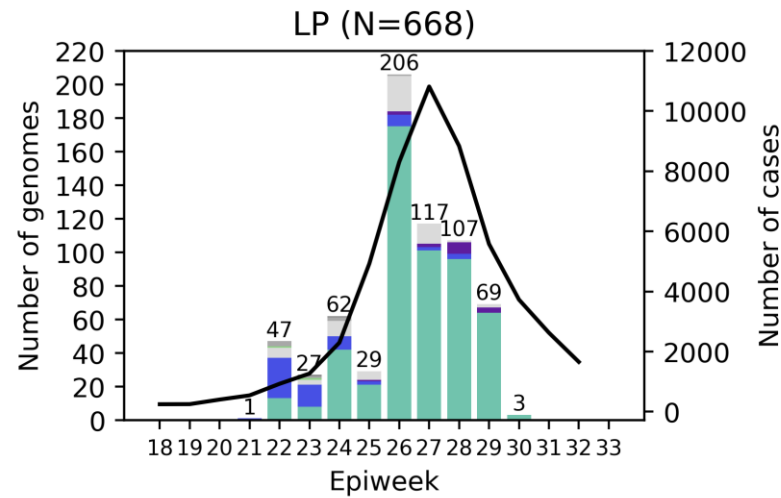
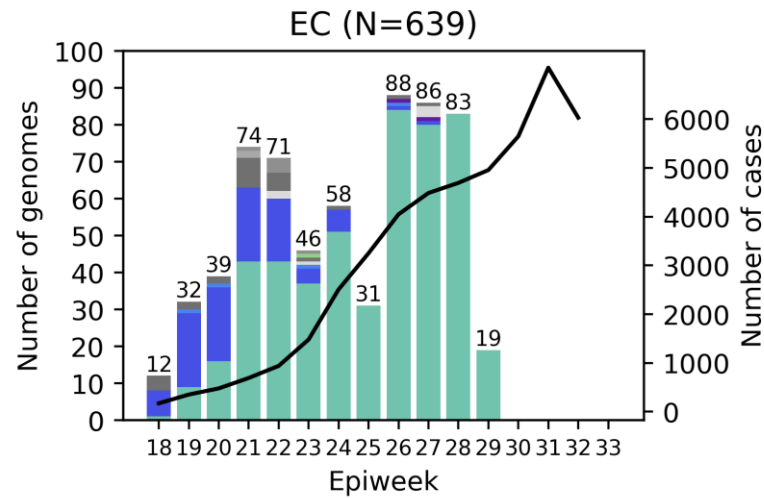


— cases Delta (21A) Beta (20H, V2) Alpha (20I, V1) C.1.2 (20D) unassigned 20B Kappa (21B) 20A 20C Eta (21D) 20D 19B

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



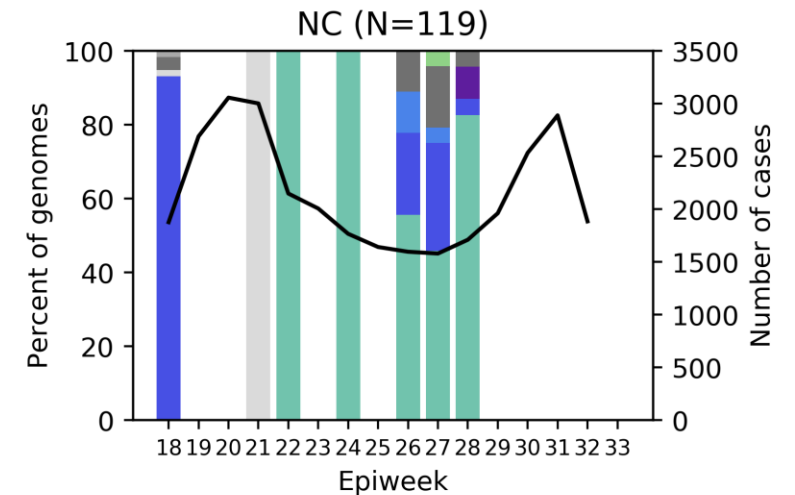
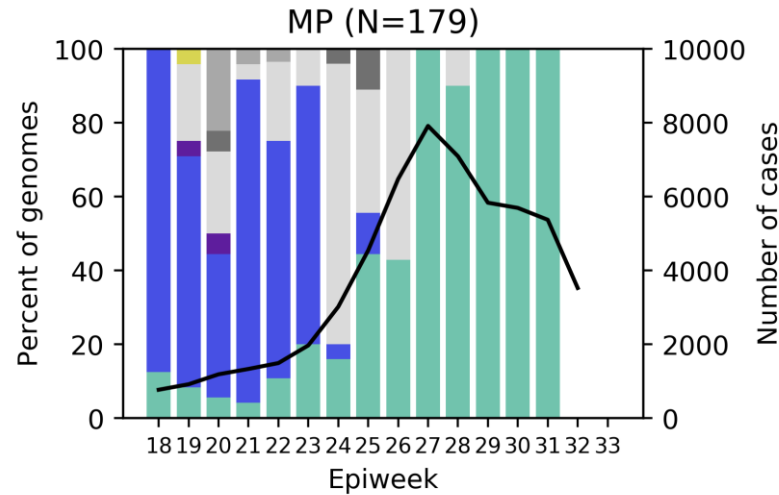
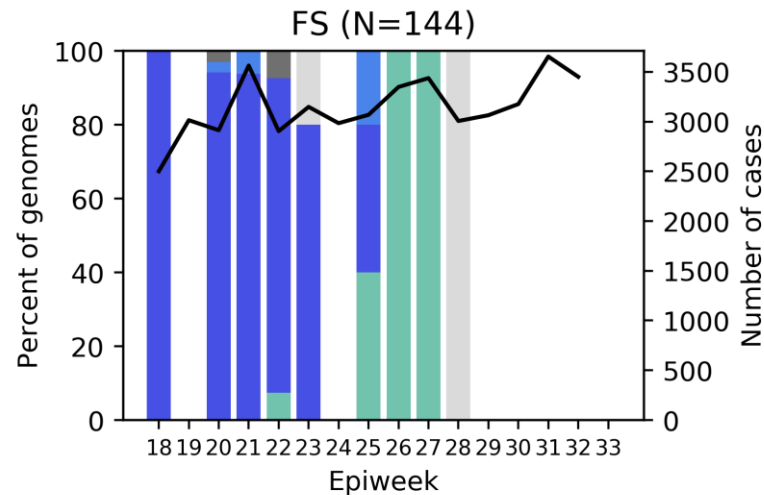
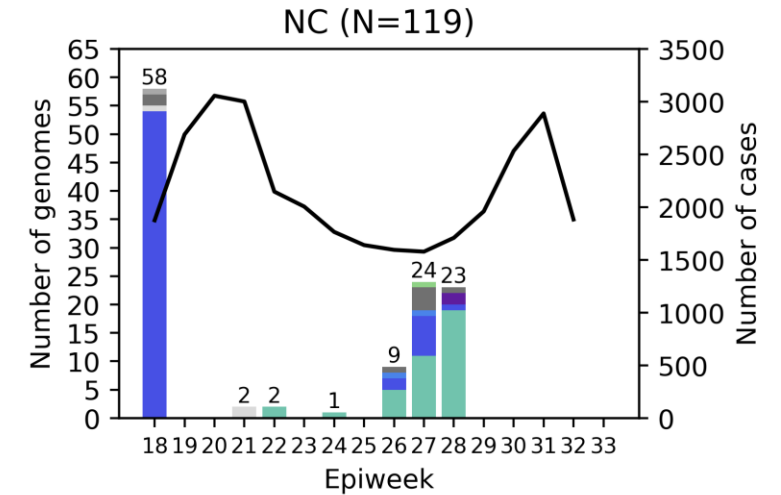
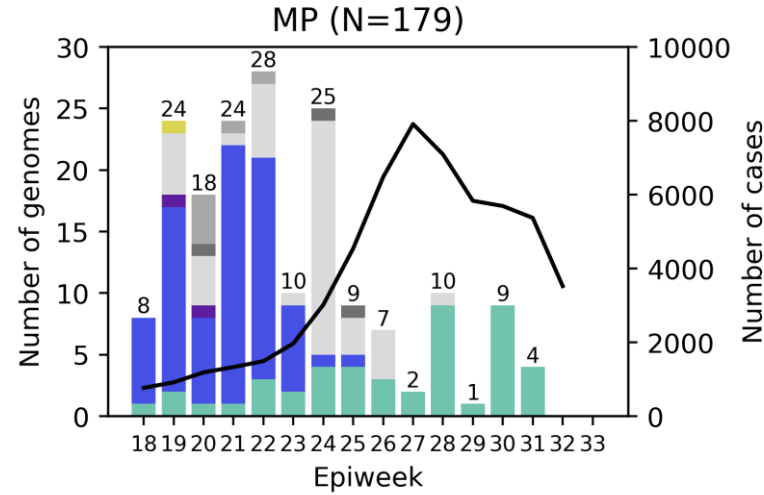
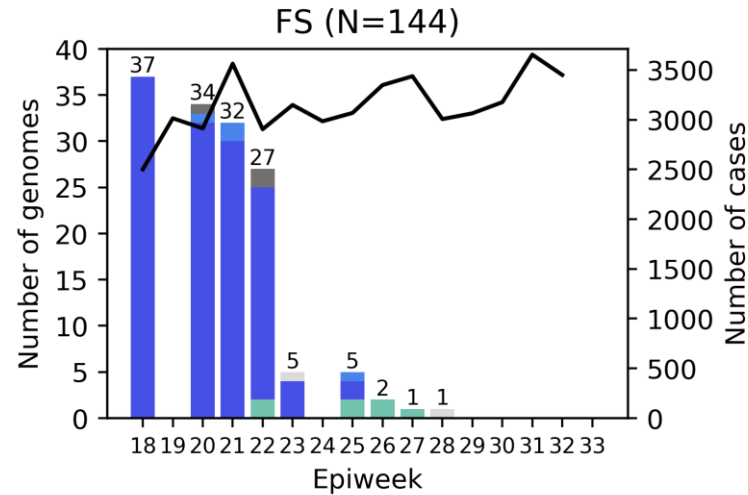
# Genomes sequenced from specimens collected in May – mid-August 2021 (epiweeks 18 – 33) from Eastern Cape, Limpopo and North-West Provinces



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

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

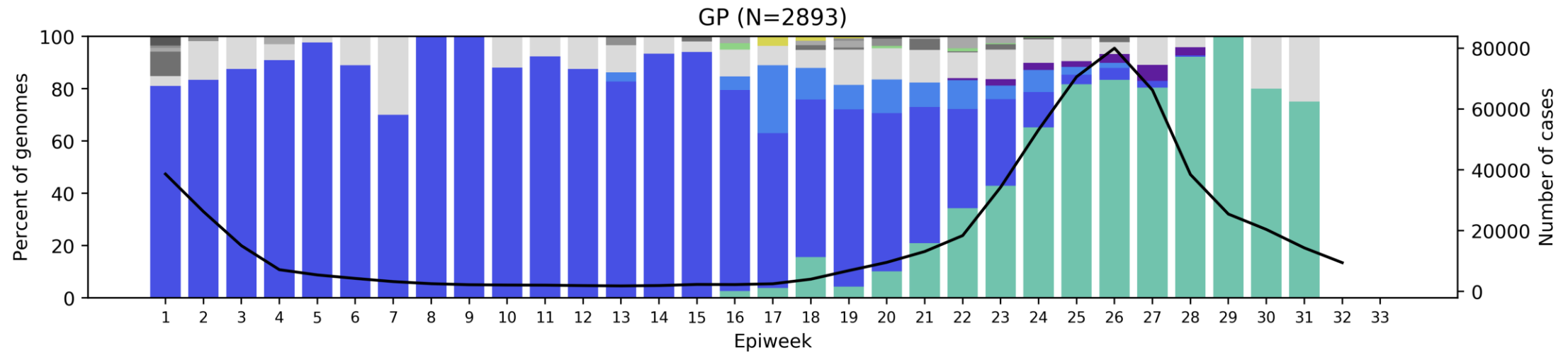
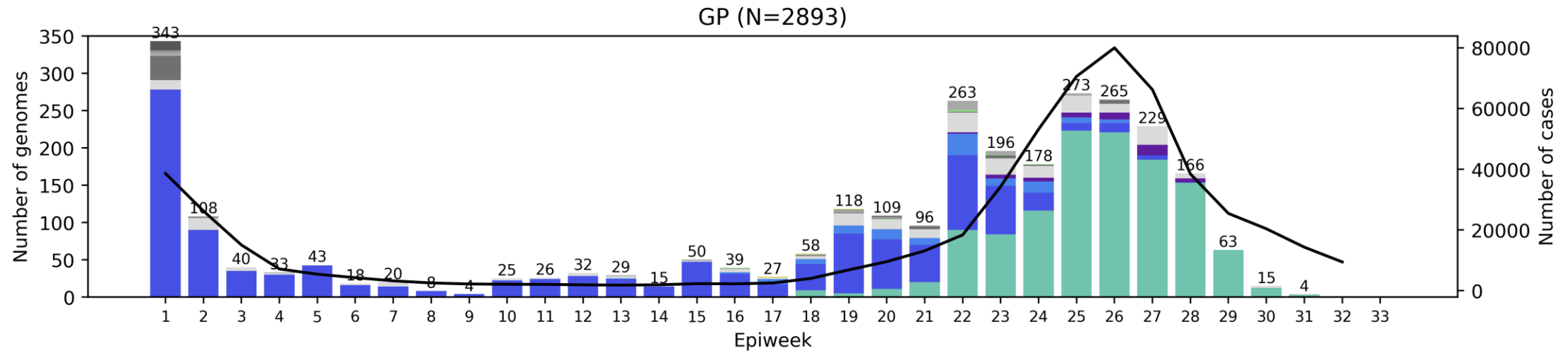
# Genomes sequenced from specimens collected in May – mid-August 2021 (epiweeks 18 – 33) from Free State, Mpumalanga and Northern Cape Provinces



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

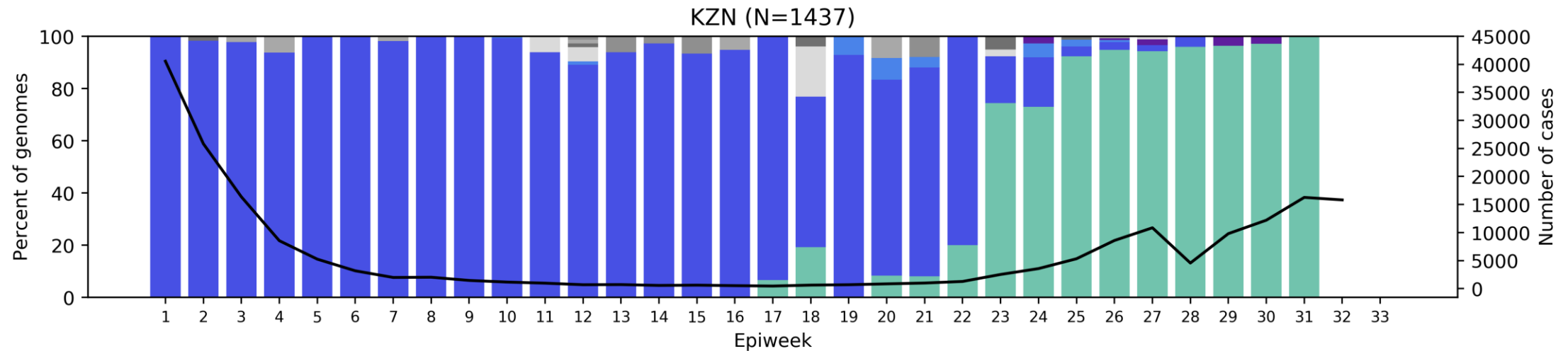
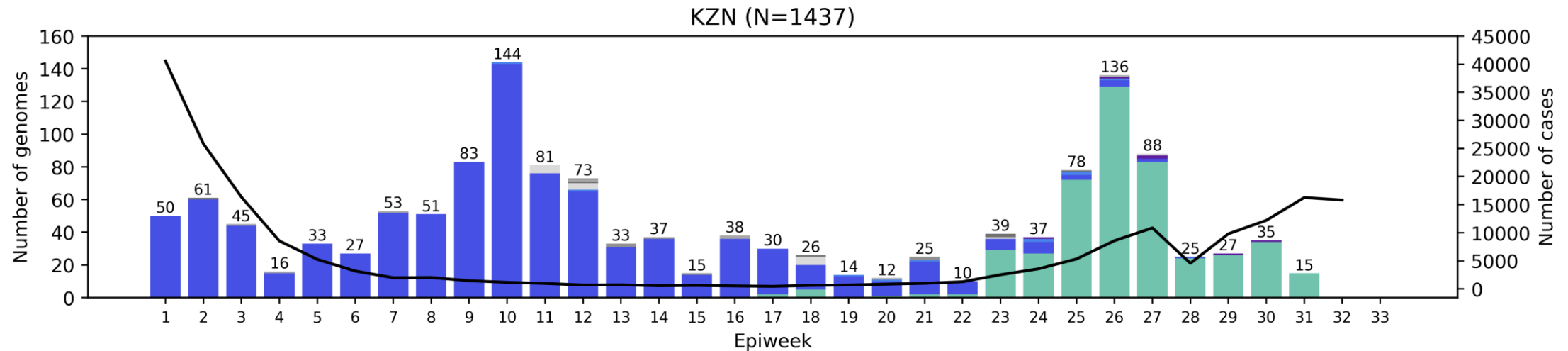
Recent data outstanding, specimens currently being sequenced to estimate the dominance of Delta

# Gauteng Province, 2021, n = 2893



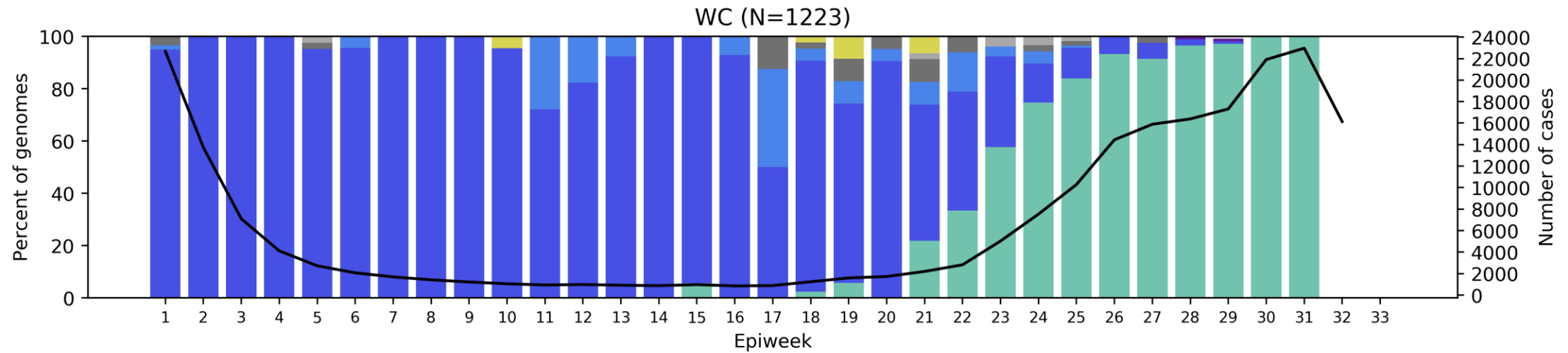
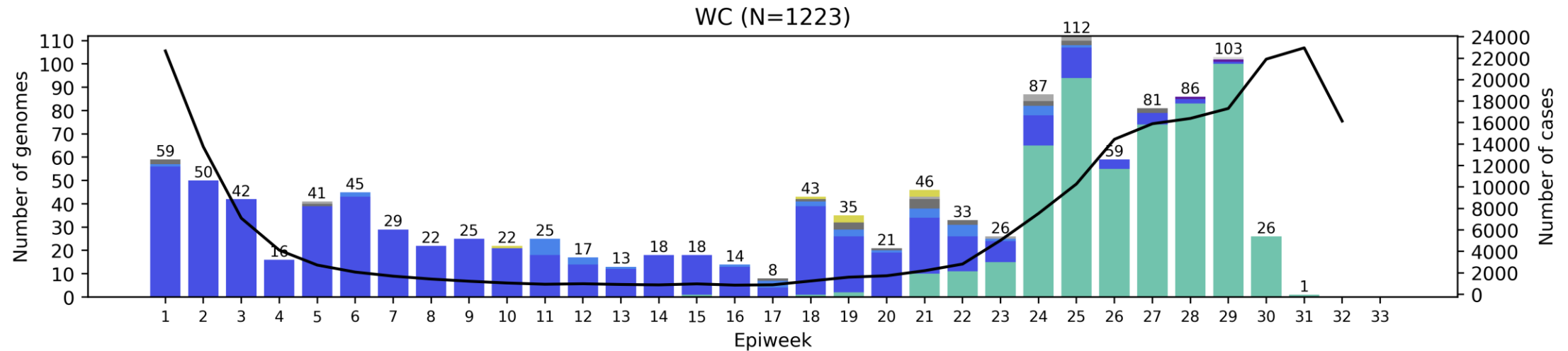
— cases   Delta (21A)   Beta (20H, V2)   Alpha (20I, V1)   C.1.2 (20D)   unassigned   20B   Kappa (21B)   20A   20C   Eta (21D)   20D   19B

# KwaZulu-Natal Province, 2021, n = 1437



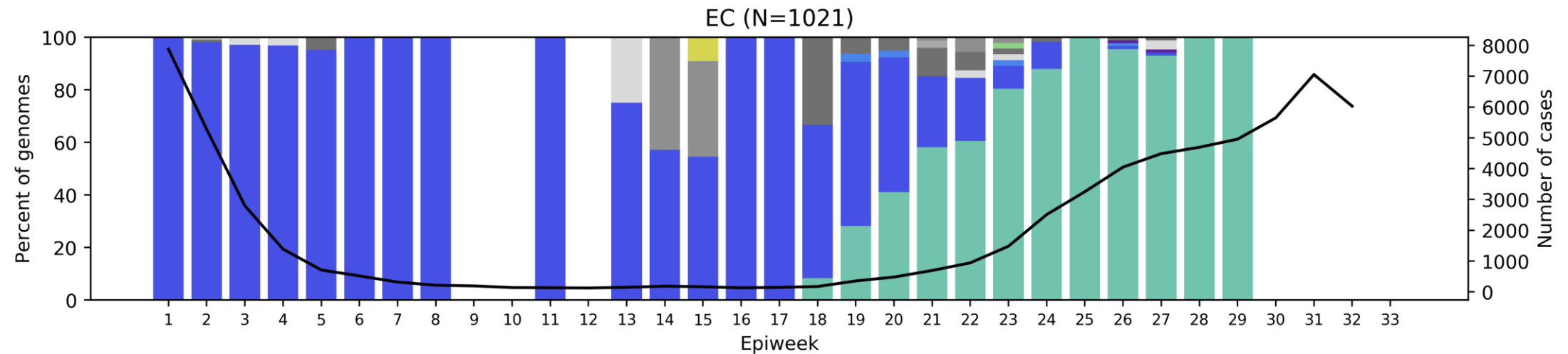
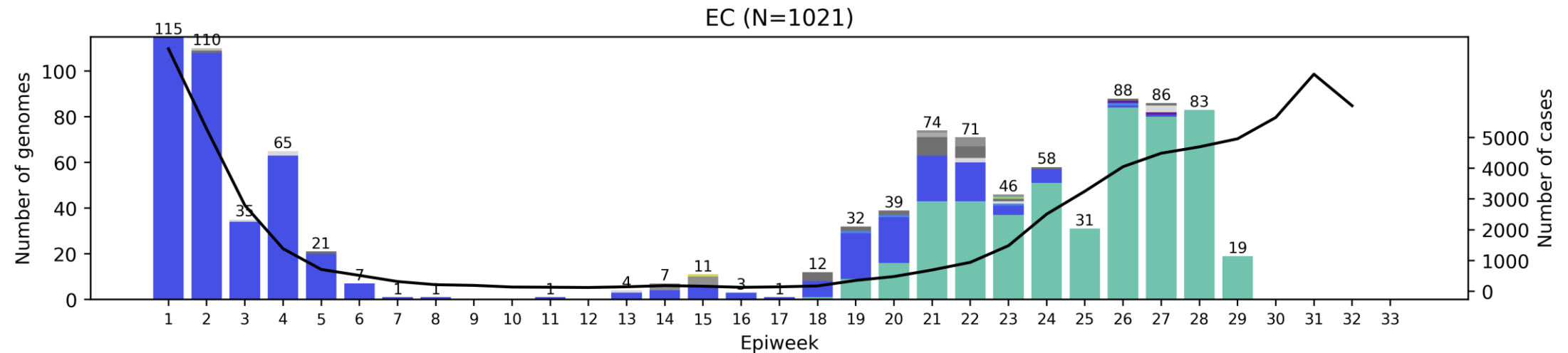
— cases Delta (21A) Beta (20H, V2) Alpha (20I, V1) C.1.2 (20D) unassigned 20B Kappa (21B) 20A 20C Eta (21D) 20D 19B

# Western Cape Province, 2021, n = 1223



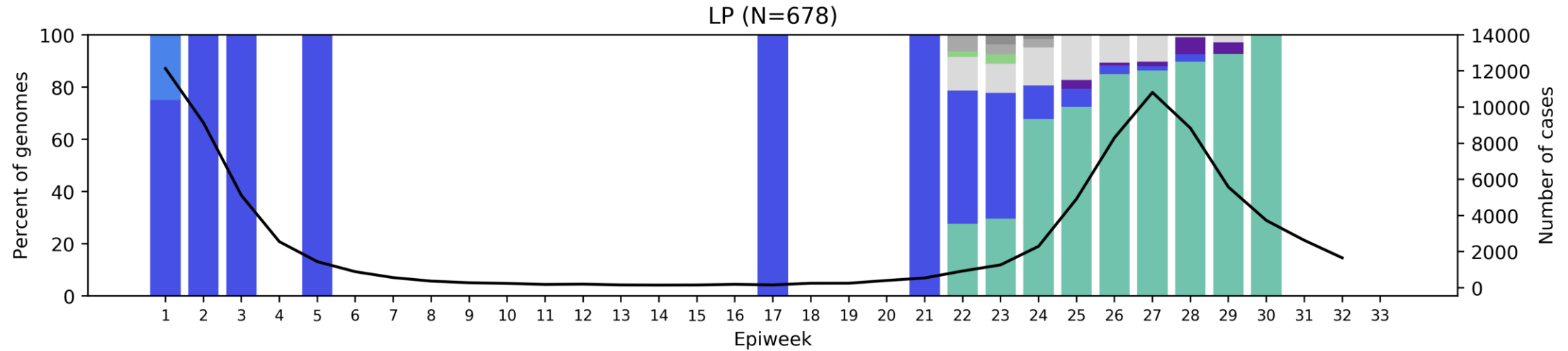
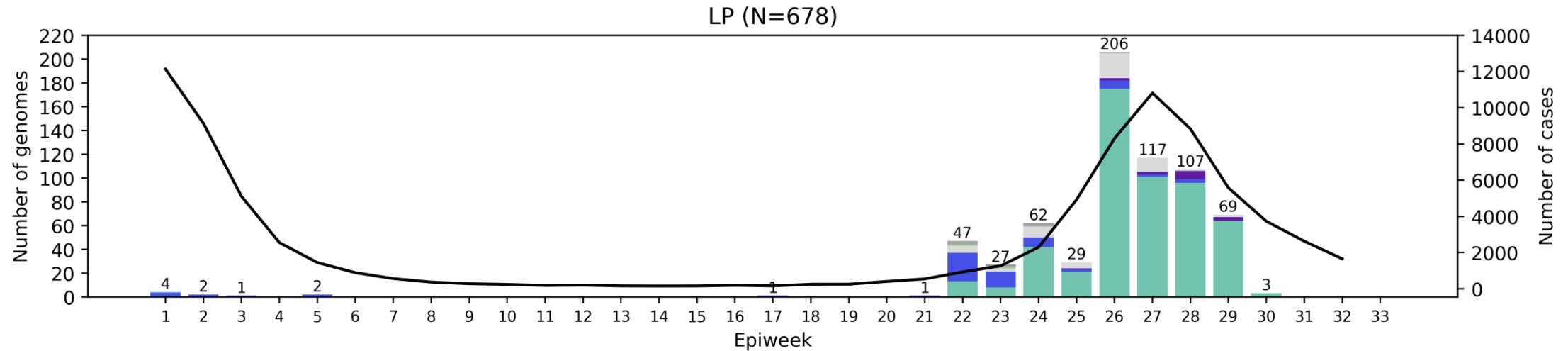
— cases Delta (21A) Beta (20H, V2) Alpha (20I, V1) C.1.2 (20D) unassigned 20B Kappa (21B) 20A 20C Eta (21D) 20D 19B

# Eastern Cape Province, 2021, n = 1021



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

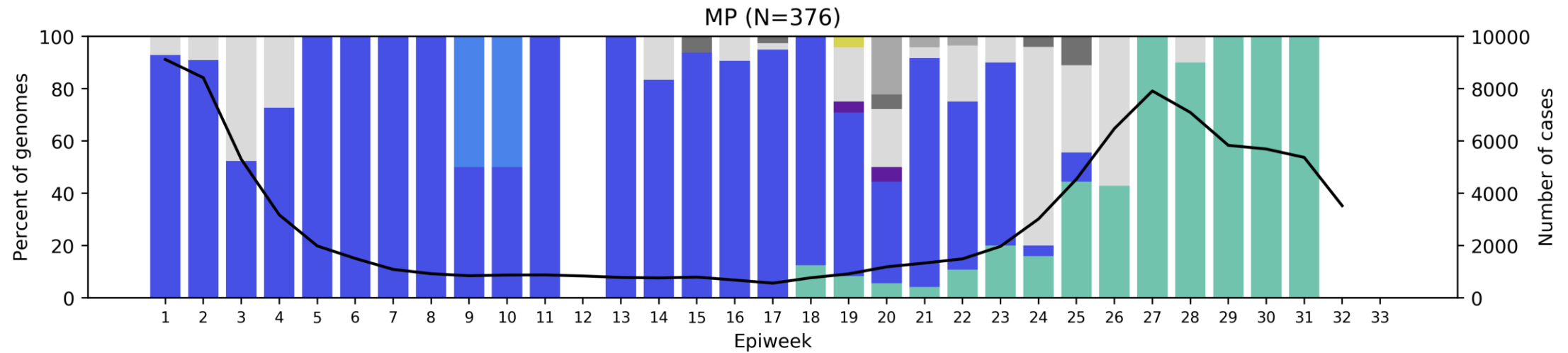
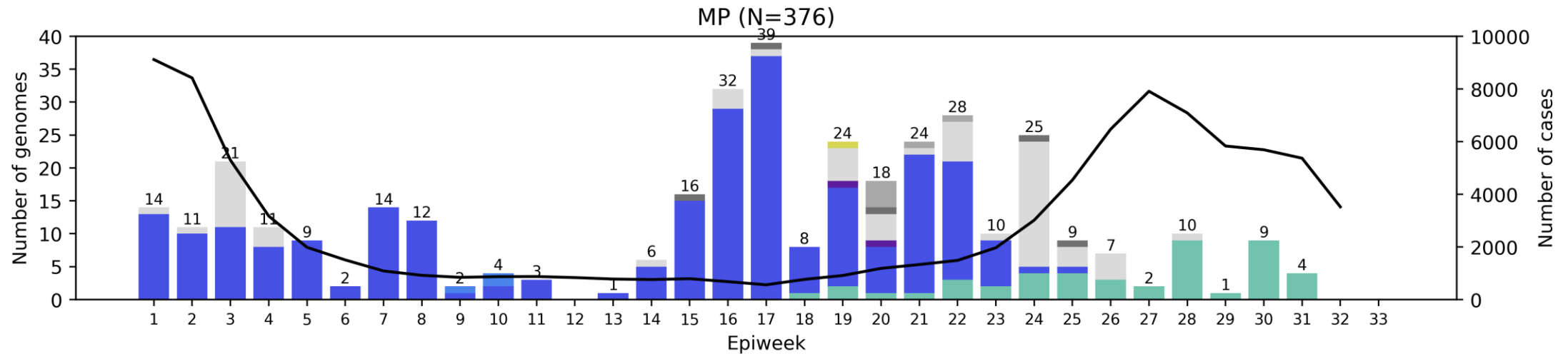
# Limpopo Province, 2021, n = 678



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

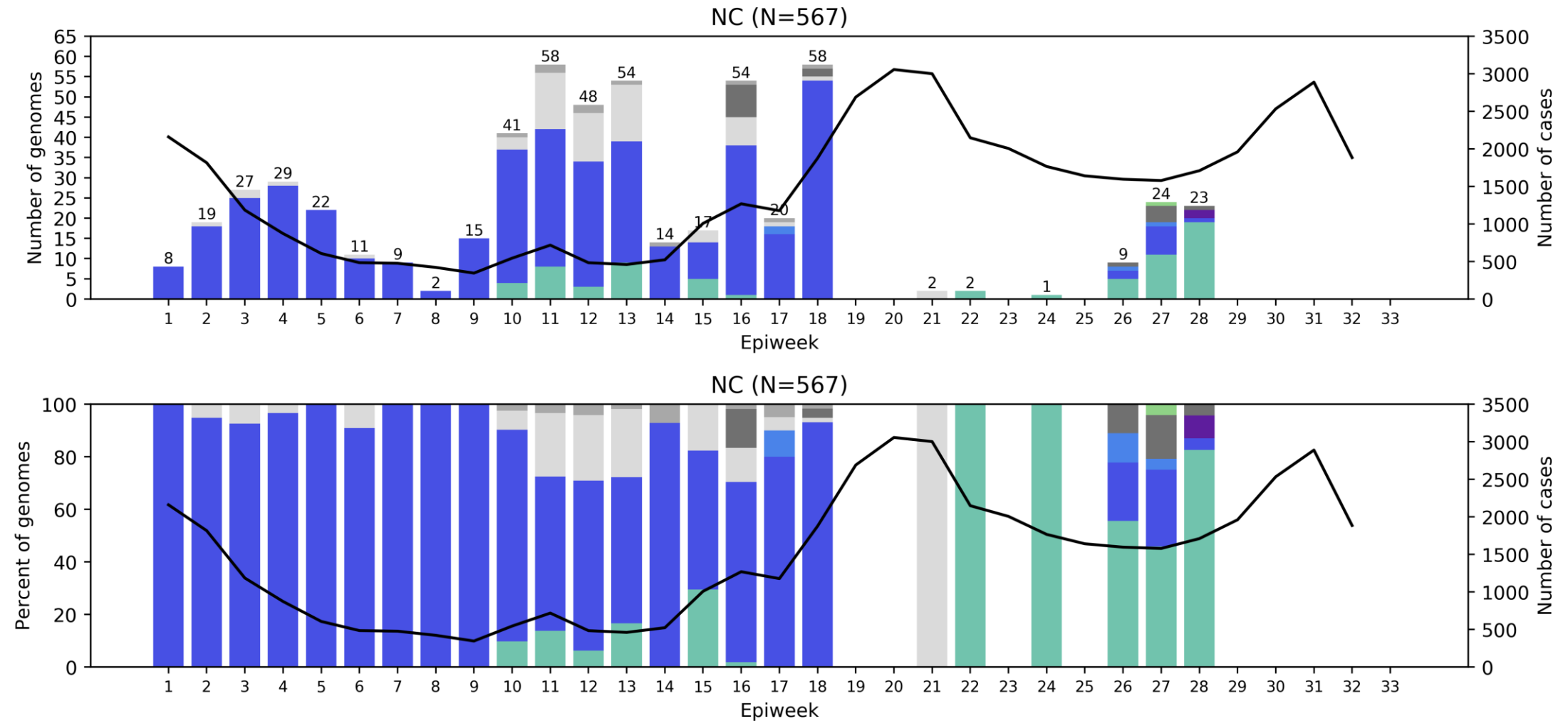


# Mpumalanga Province, 2021, n = 376



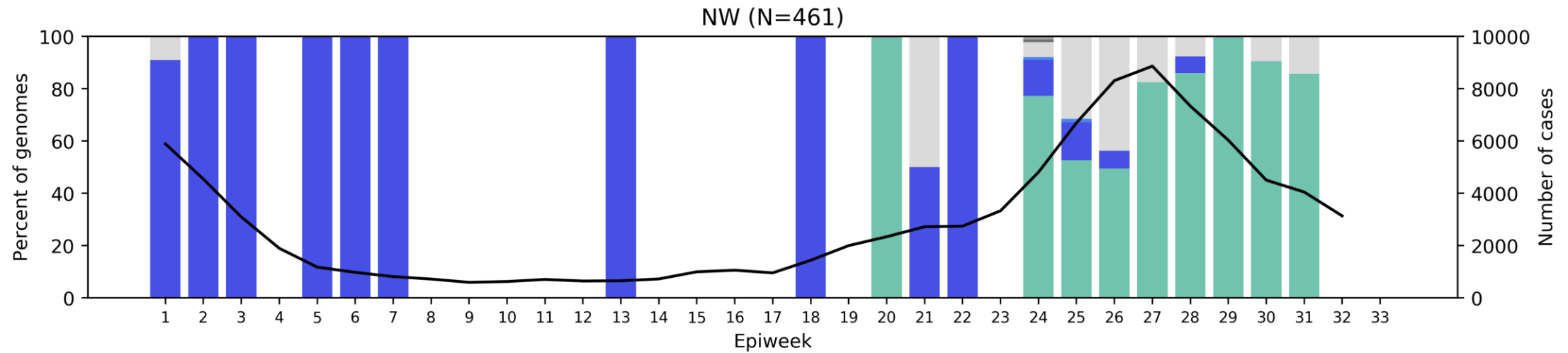
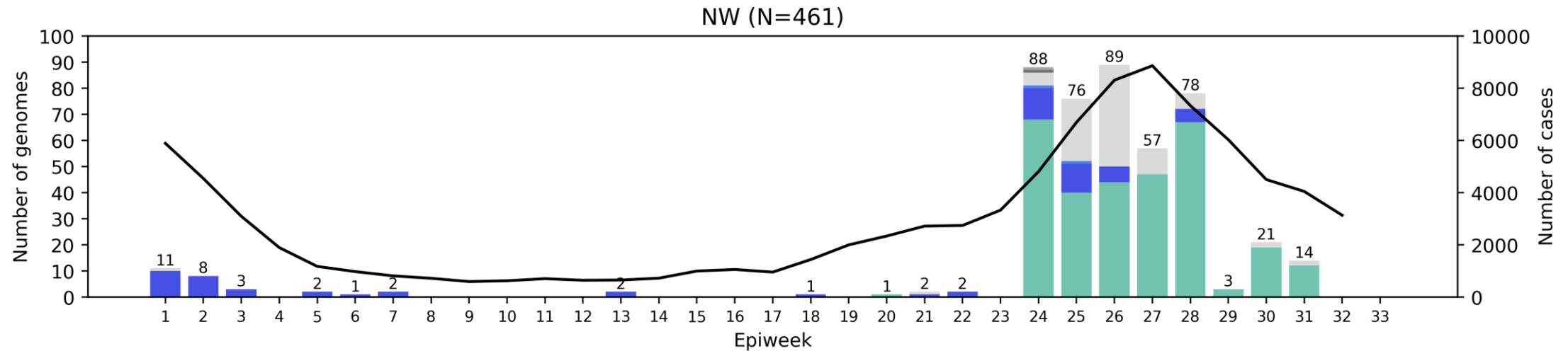
— cases   Delta (21A)   Beta (20H, V2)   Alpha (20I, V1)   C.1.2 (20D)   unassigned   20B   Kappa (21B)   20A   20C   Eta (21D)   20D   19B

# Northern Cape Province, 2021, n = 567



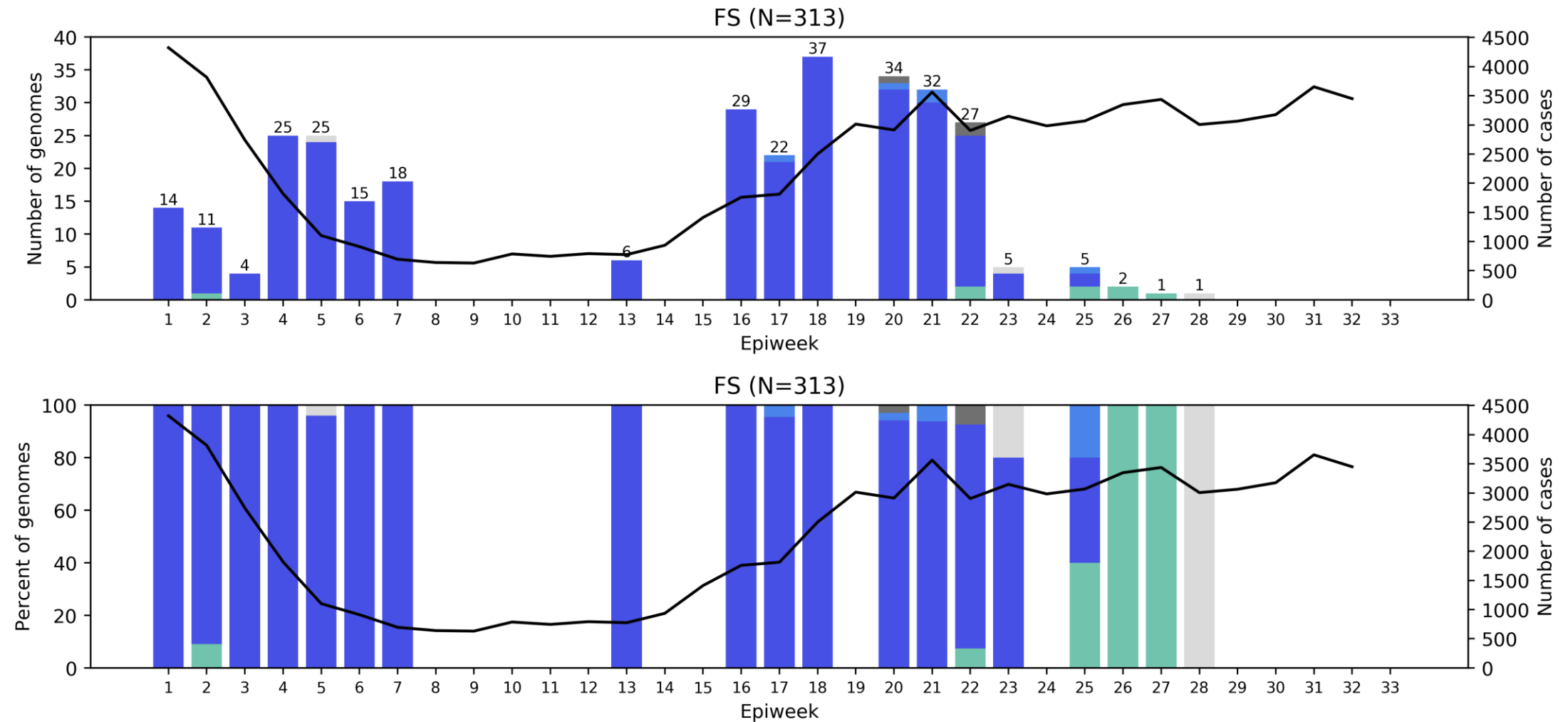
— cases   Delta (21A)   Beta (20H, V2)   Alpha (20I, V1)   C.1.2 (20D)   unassigned   20B   Kappa (21B)   20A   20C   Eta (21D)   20D   19B

# North West Province, 2021, n = 461



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

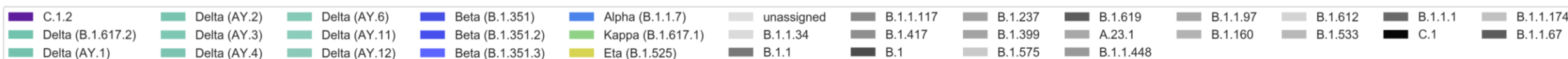
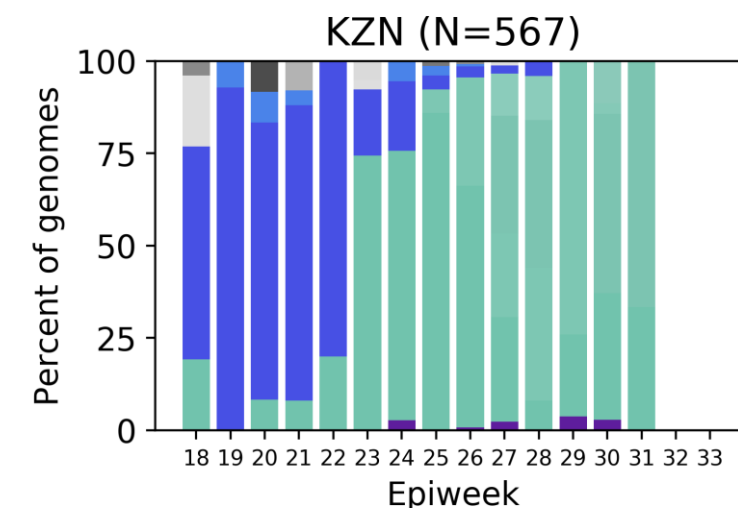
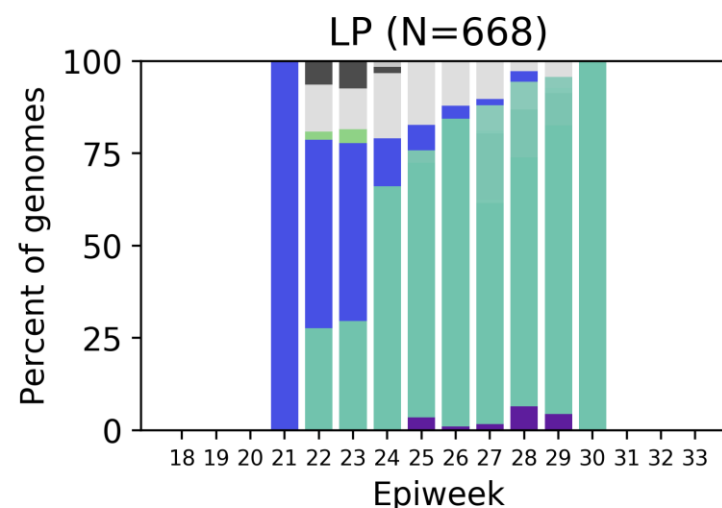
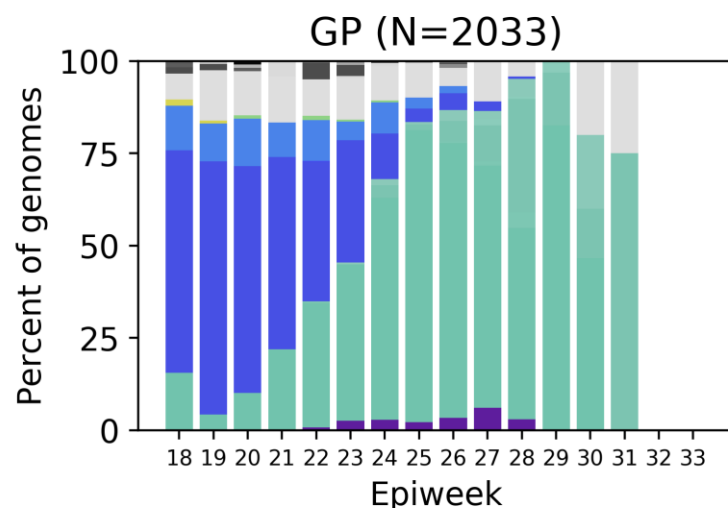
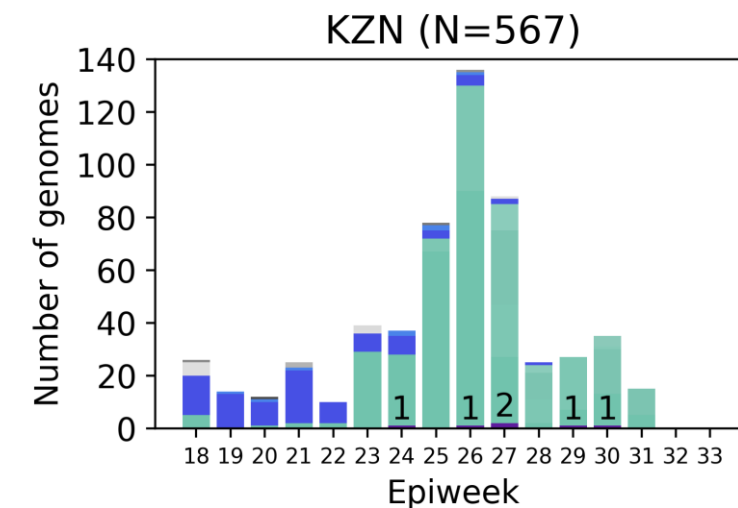
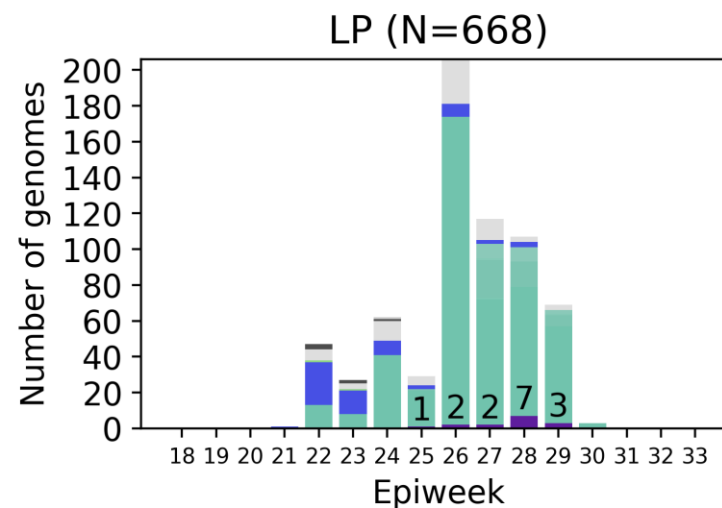
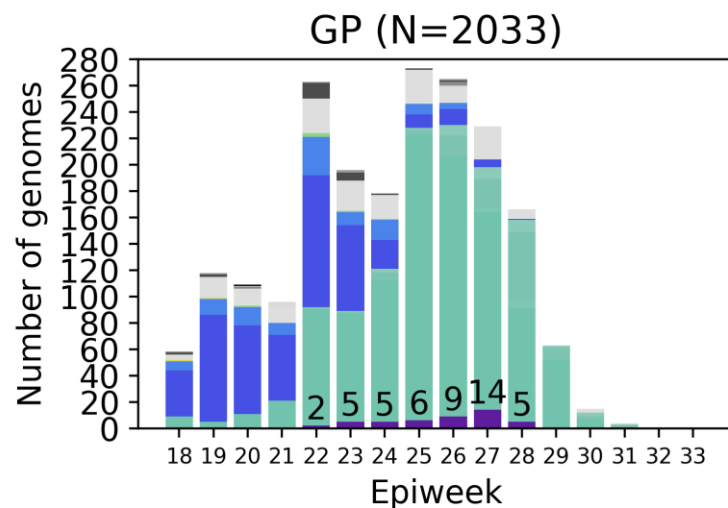
# Free State Province, 2021, n = 313



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

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

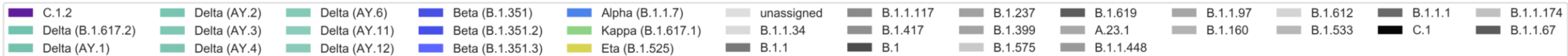
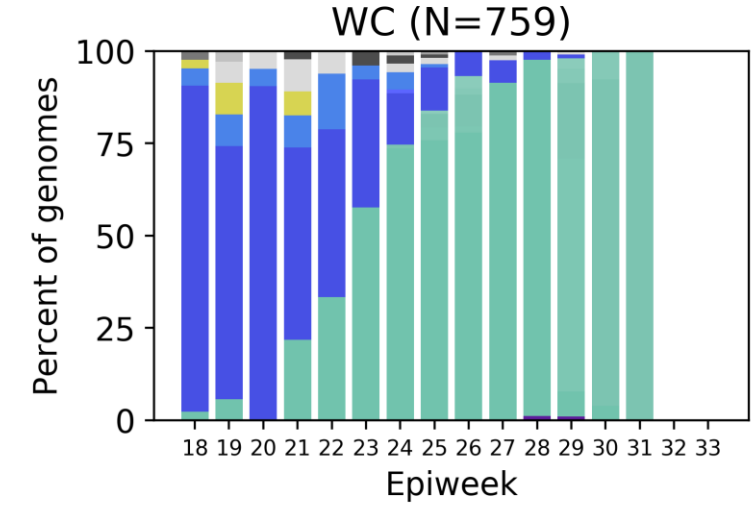
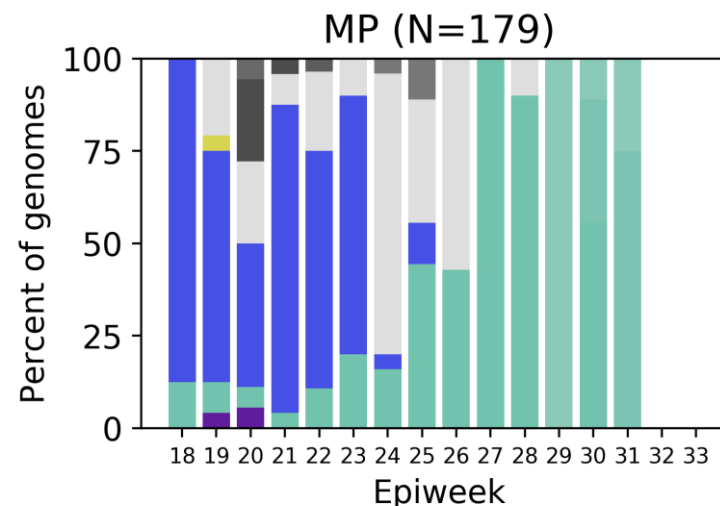
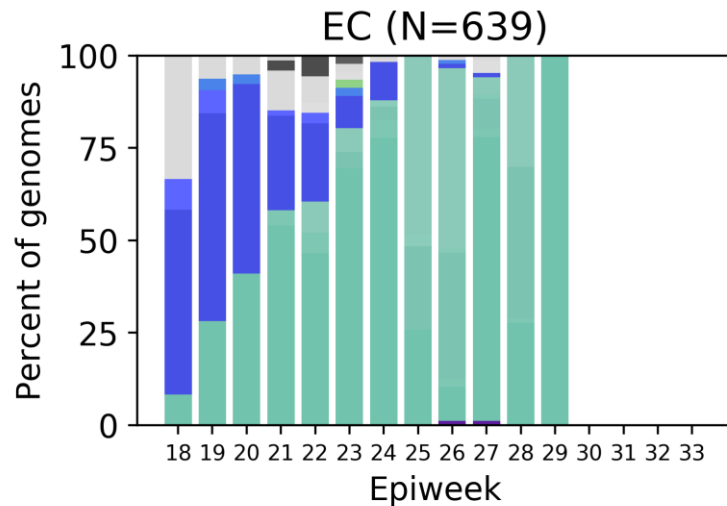
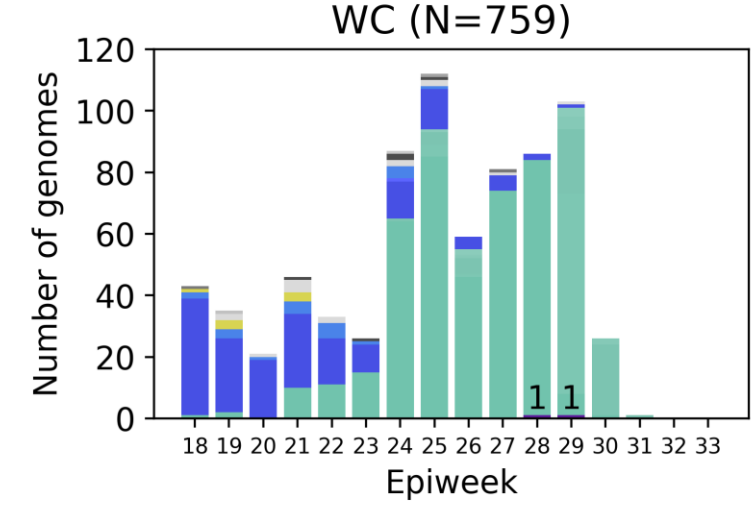
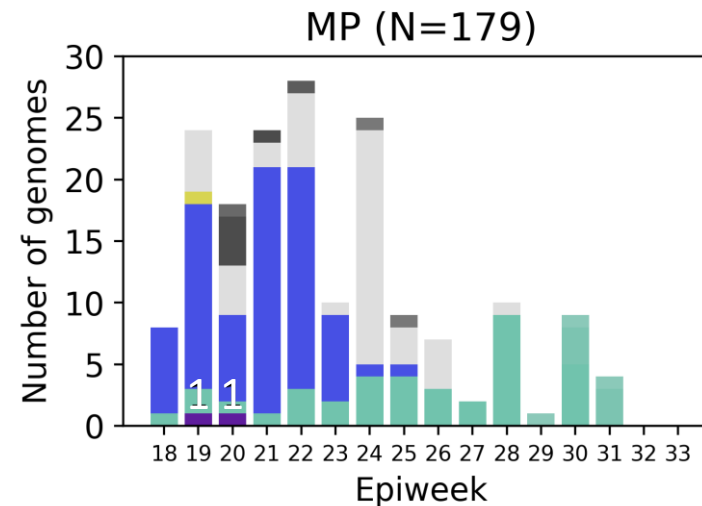
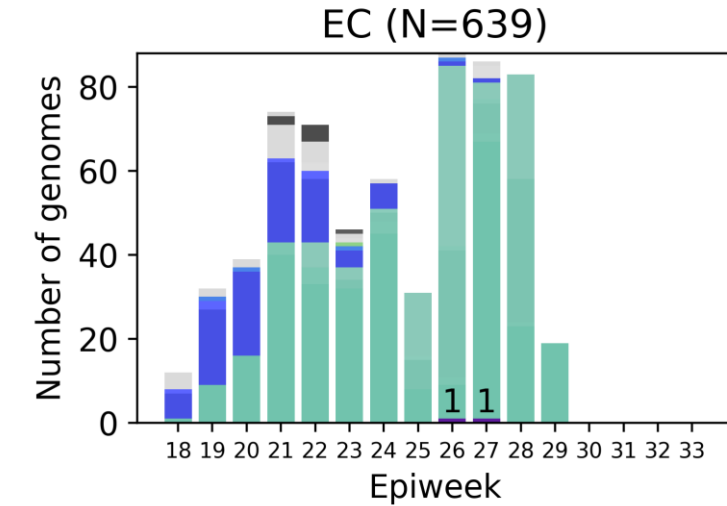
Number of C.1.2 samples indicated above bar



**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).**

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

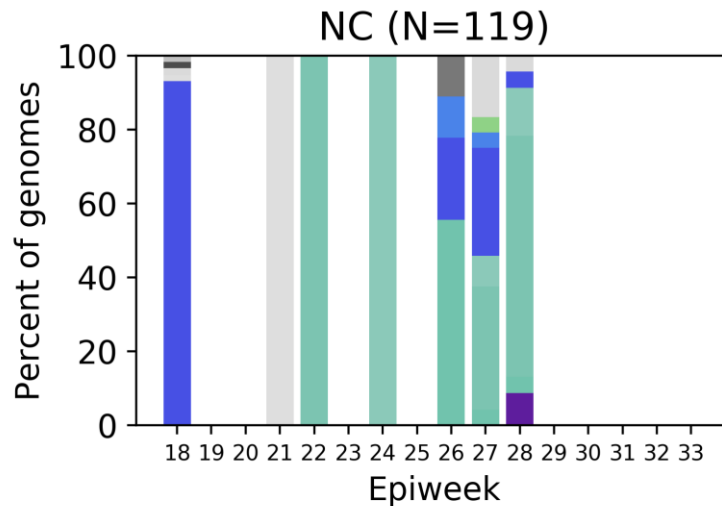
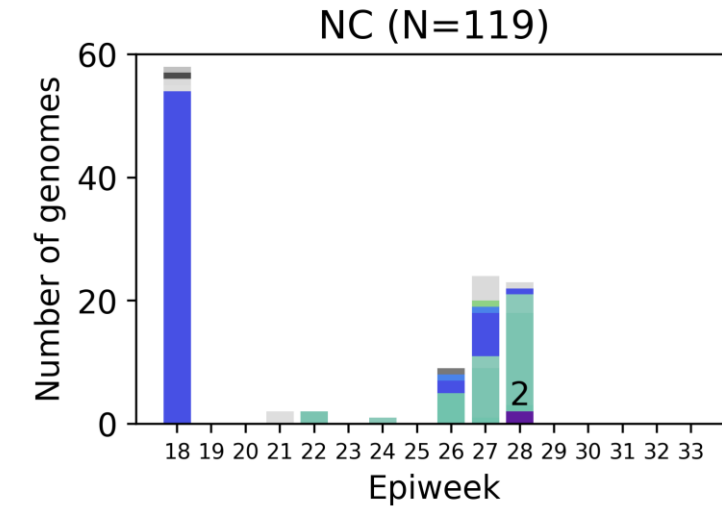
Number of C.1.2 samples indicated above bar



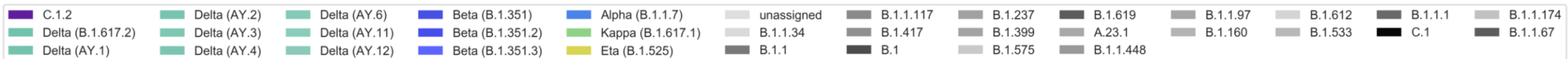
**C.1.2 has now been detected in seven provinces. Mpumalanga the Eastern Cape and the Western Cape have two C.1.2 detections each.**

# 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).



# 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<sup>1</sup> and has now been detected in seven provinces in South Africa: Eastern Cape, Gauteng, Mpumalanga, Limpopo, KwaZulu-Natal, Northern Cape, Western Cape.

<sup>1</sup> <https://github.com/cov-lineages/pango-designation/issues/139>



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INYUVESI  
YAKWAZULU-NATALI



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Nei-yuan Hsiao  
Diana Hardie  
Kruger Marais  
Stephen Korsman  
Ziyaad Valley-Omar



## UCT, IDM and CIDRI-Africa

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Arash Iranzadeh	Darren Martin
Lynn Tyers	Nicola Mulder
Innocent Mudau	Wendy Burgers
Nokuzola Mbhele	Ntobeko Ntusi
Fezokuhle Khumalo	Rageema Joseph
Thabang Serakge	Sean Wasserman
Bruna Galvão	Linda Boloko
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Hannah Hussey  
Andrew Boule  
Masudah Paleker  
Theuns Jacobs  
Erna Morden



## Tulio de Oliveira (PI)

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Wolfgang Prieser  
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Eduan Wilkinson  
Houriiyah Tegally  
San James  
Koleka Mlisana  
Jinal Bhiman  
Penny Moore  
Anne von Gottberg  
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**health**

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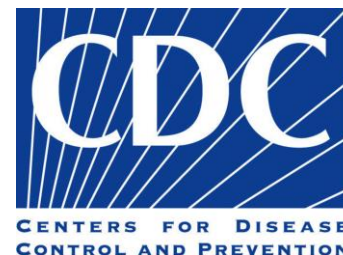


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**NICD COVID-19 response team**  
**COVID Incident Management Team**



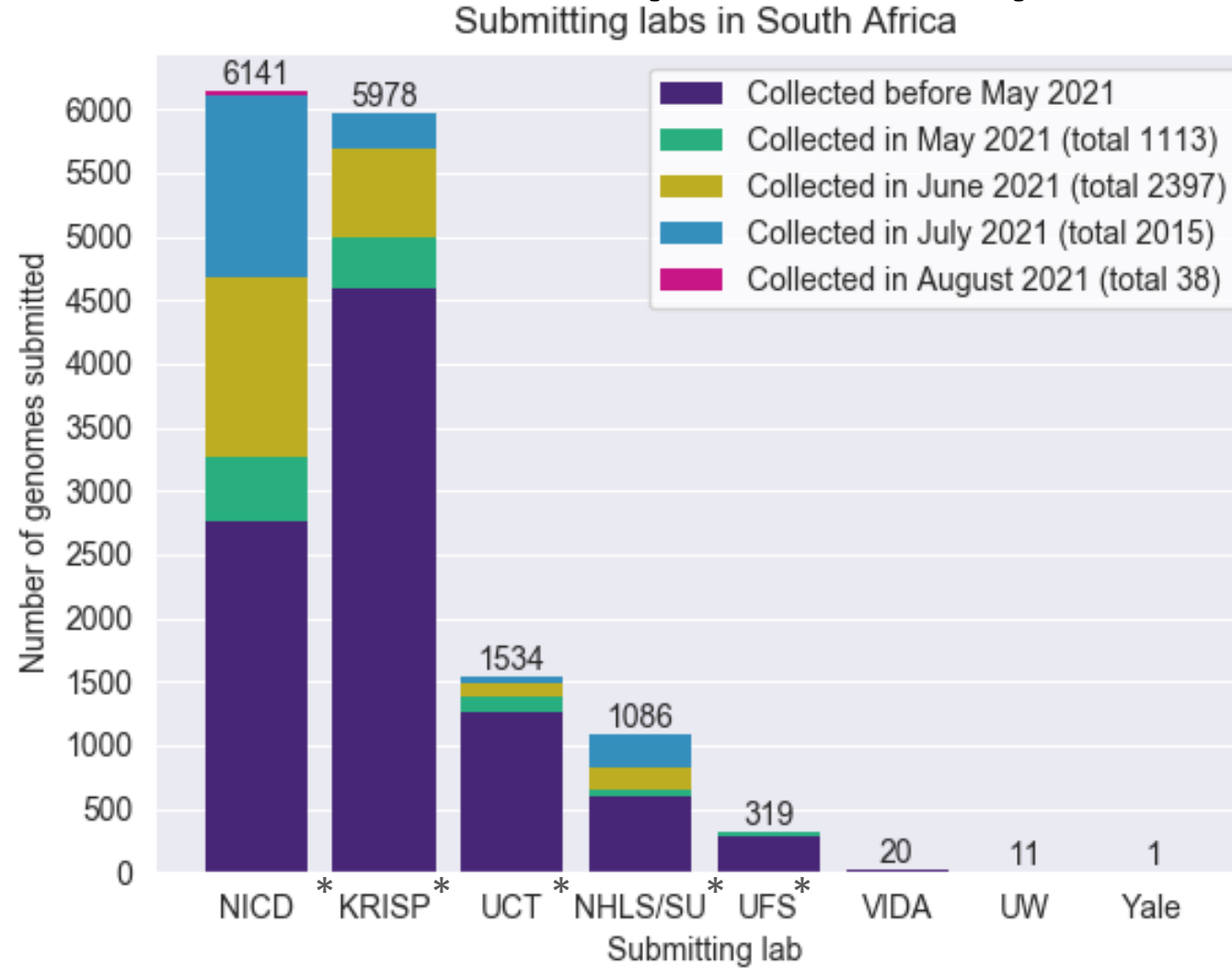
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# South African genomes submitted per sequencing lab, 2020 and 2021 (N=15 090)



\*NGS-SA laboratories

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

# 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

# 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 ( $\geq 14$  days after vaccine), especially if hospitalised and clinically severe
- Suspected re-infection ( $\geq 90$  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.)