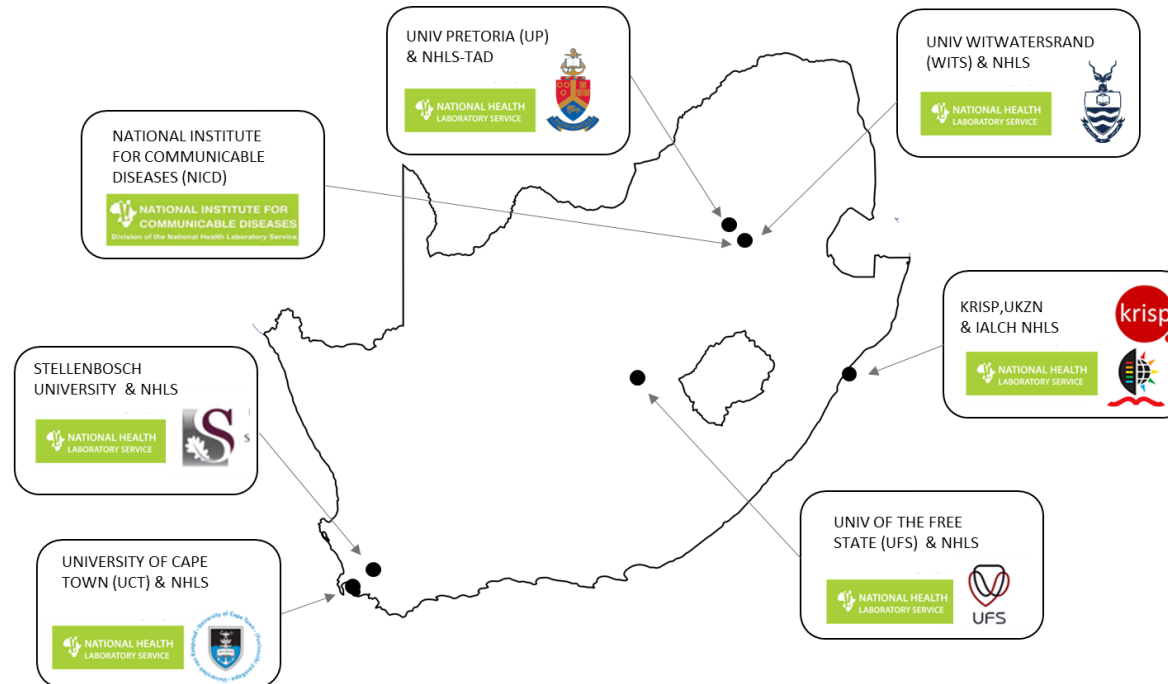


## SARS-CoV-2 Sequencing Update 30 September 2021



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 30 September at 09h00



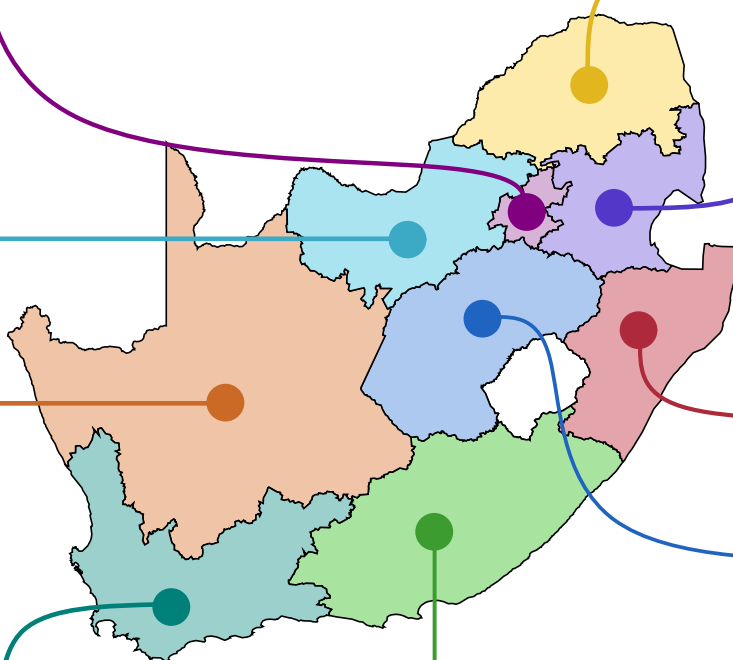
Data license: <https://www.gisaid.org/registration/terms-of-use/>

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 - 39



## Gauteng

Genomes Cases  
2 898 (30.6%) 490 783 (37.4%)

Genomes deposited in the last week

■ 1 ■ 30 ■ 3 ■ 1

## North West

Genomes Cases  
667 (7.0%) 81 143 (6.2%)

Genomes deposited in the last week

## Northern Cape

Genomes Cases  
227 (2.4%) 49 685 (3.8%)

Genomes deposited in the last week

## Western Cape

Genomes Cases  
2 086 (22.0%) 221 630 (16.9%)

Genomes deposited in the last week

■ 4 ■ 73 ■ 1

## Eastern Cape

Genomes Cases  
934 (9.9%) 93 589 (7.1%)

Genomes deposited in the last week

■ 103 ■ 2

## Limpopo

Genomes Cases  
754 (8.0%) 57 724 (4.4%)

Genomes deposited in the last week

## Mpumalanga

Genomes Cases  
286 (3.0%) 72 202 (5.5%)

Genomes deposited in the last week

## KwaZulu-Natal

Genomes Cases  
1 043 (11.0%) 173 466 (13.2%)

Genomes deposited in the last week

■ 53 ■ 5

## Free State

Genomes Cases  
568 (5.4%) 70 937 (5.4%)

Genomes deposited in the last week

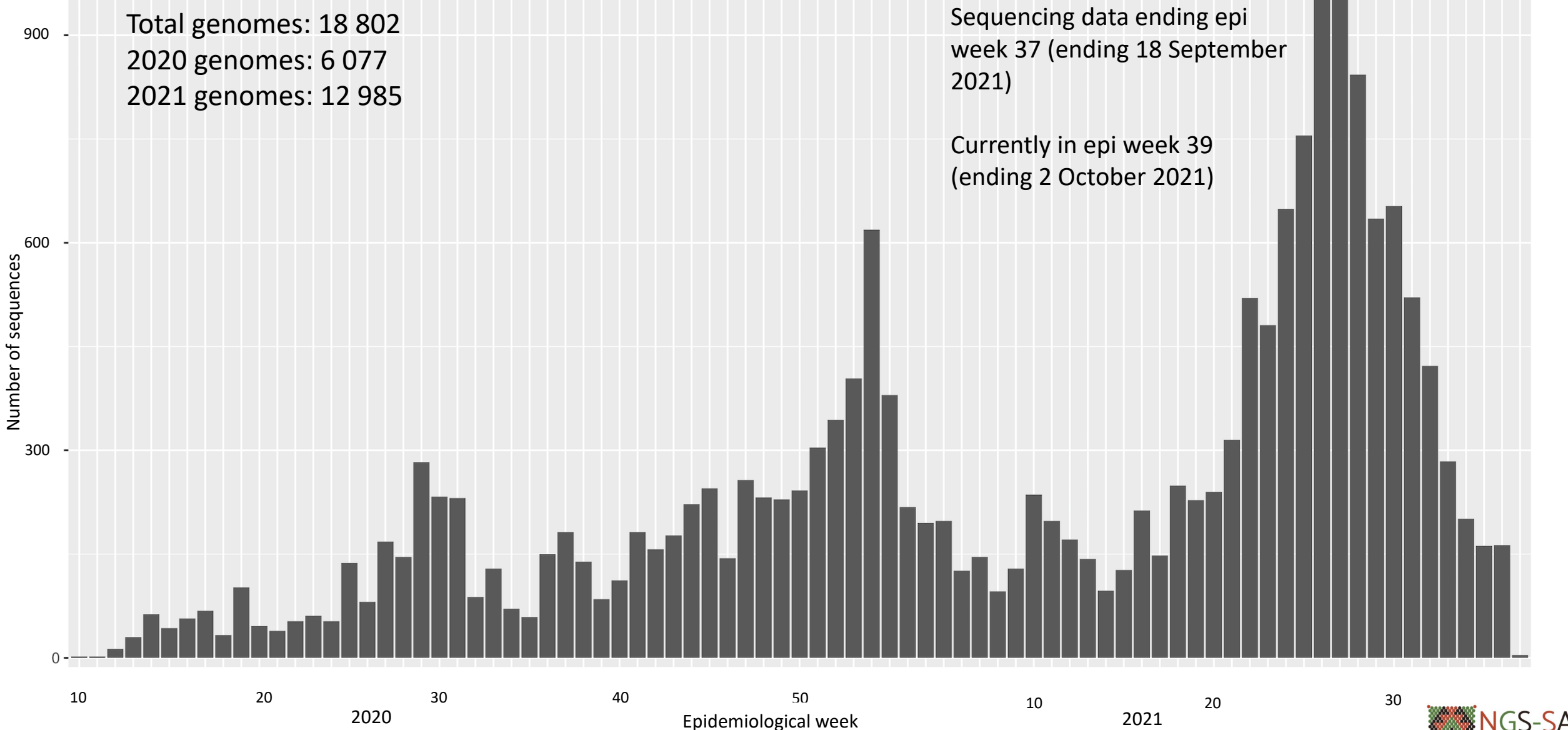
■ 19 ■ 2

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

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

Number of South African genomes deposited on GISAID, by specimen collection week, 2020 and 2021  
(N=19 063\*)

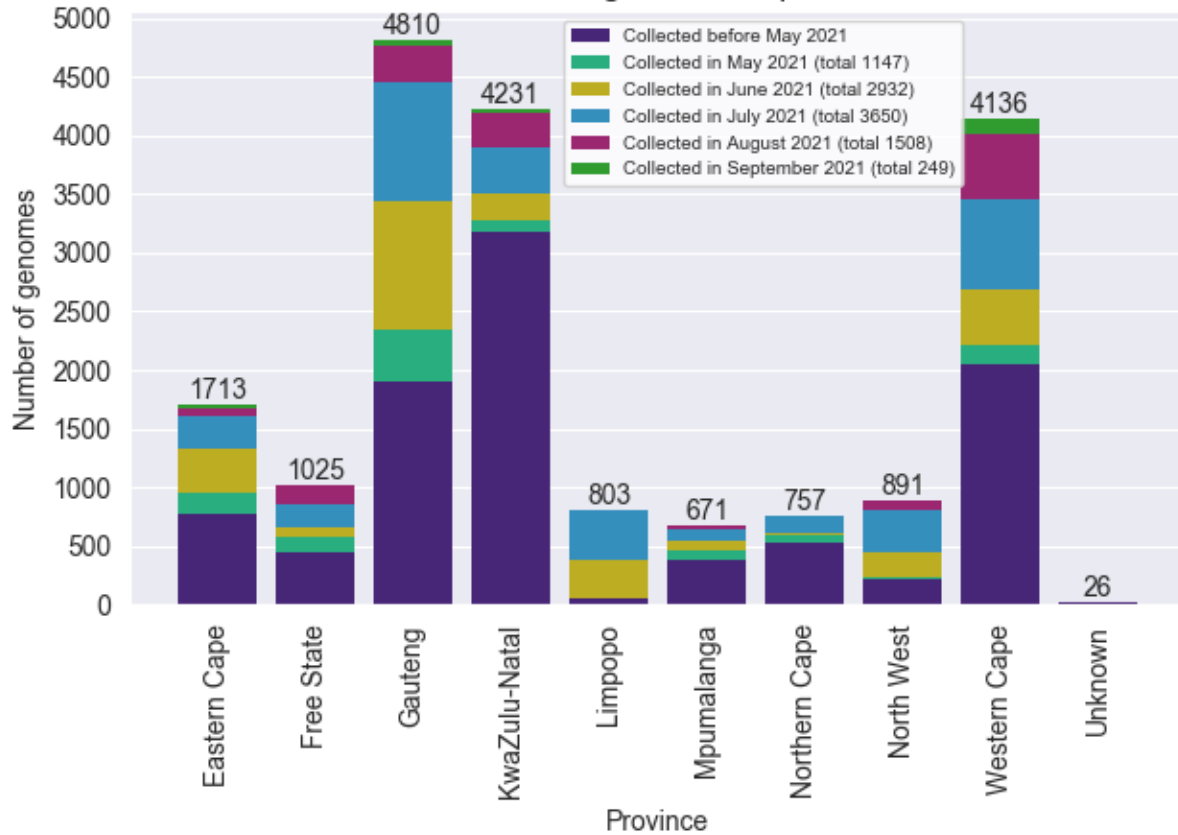


\*This represents the cleaned, de-duplicated dataset of unique sequences. This dataset will be used for all further figures.

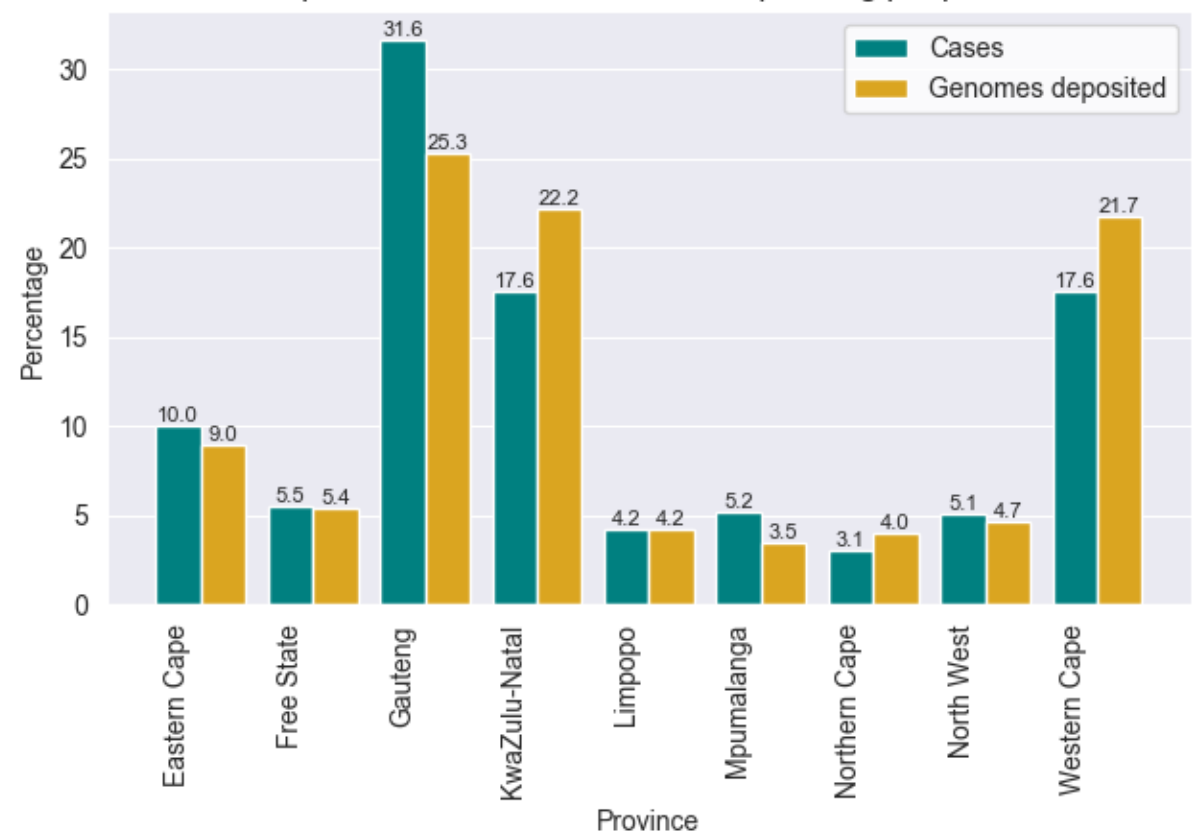


# GISAID genomes vs total cases, 2020 and 2021 (N=19 063)

Provincial breakdown of genomes deposited into GISAID

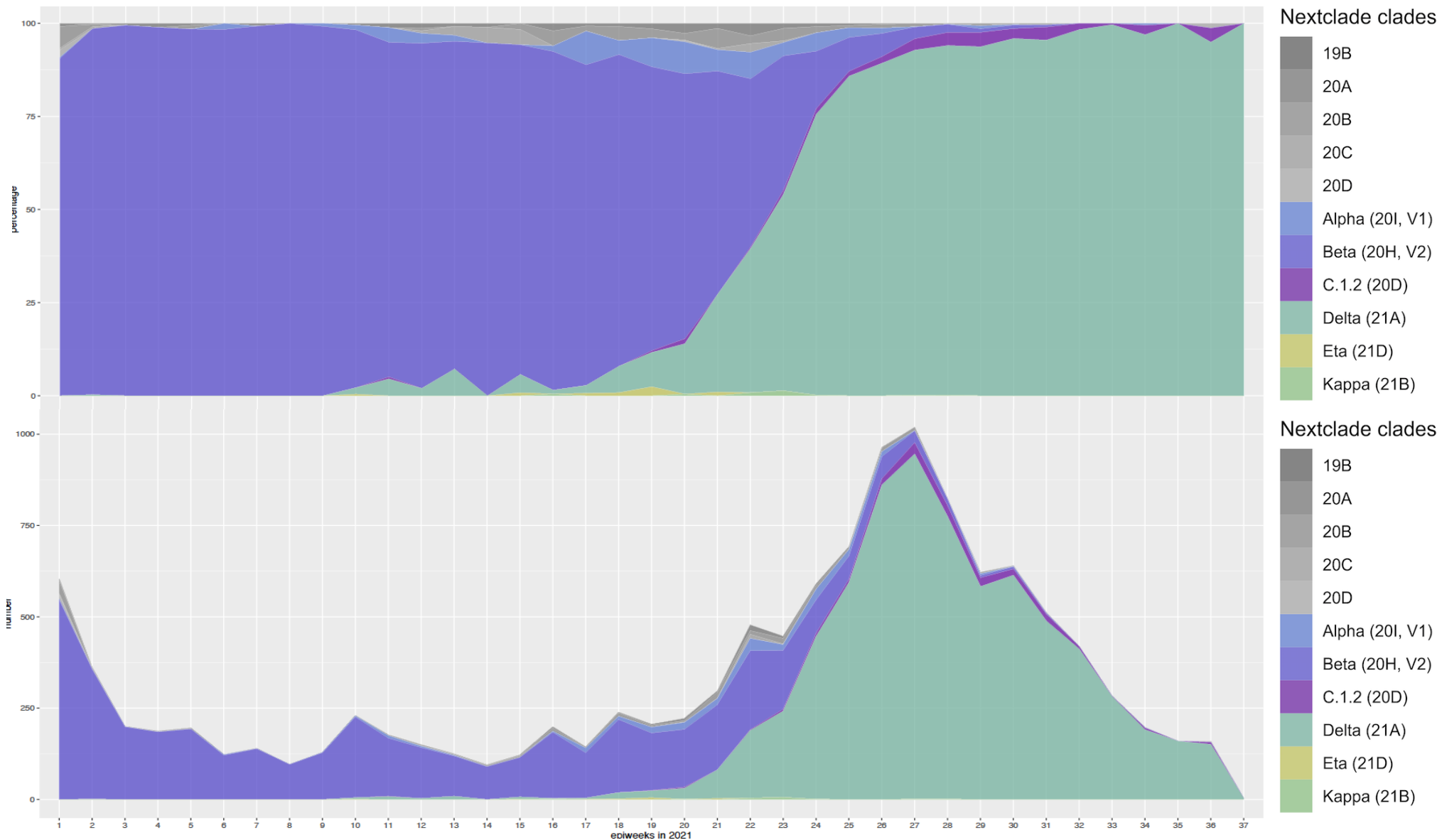


Comparison of total cases versus sequencing per province



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

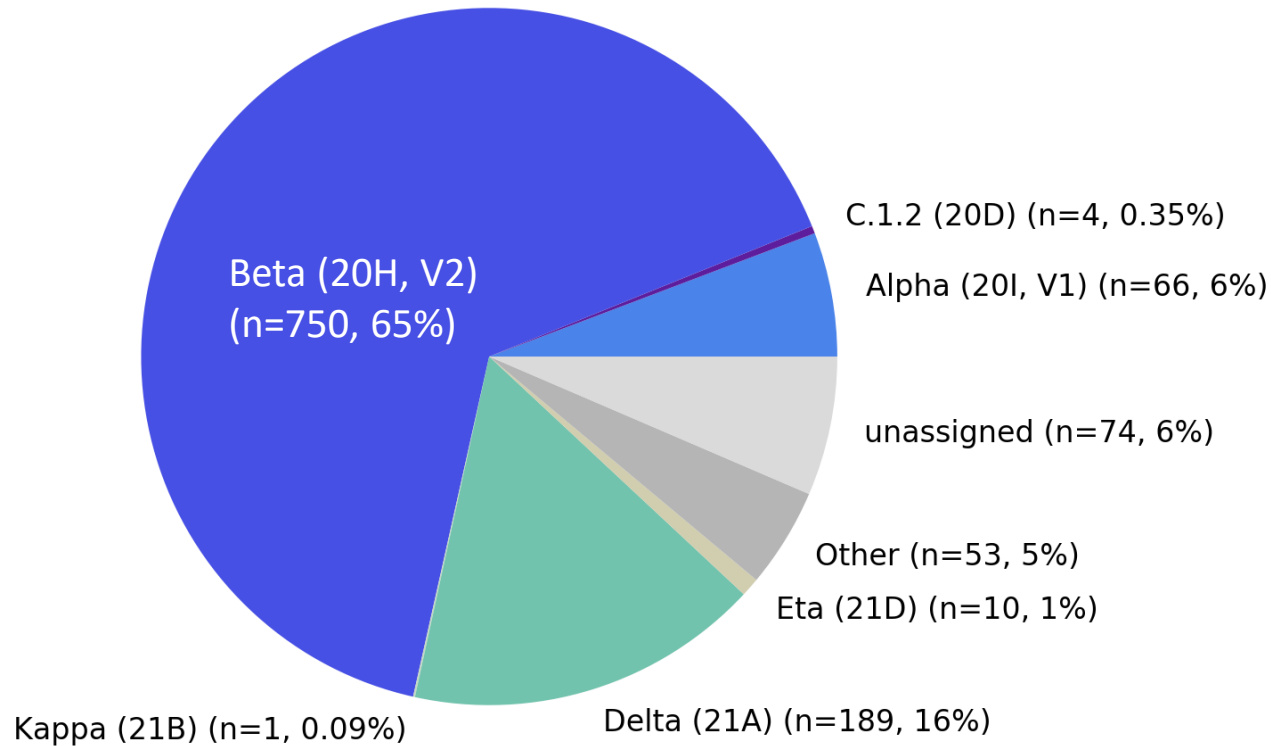
# Distribution and number of clades in South Africa, 2021 (N= 12 985)



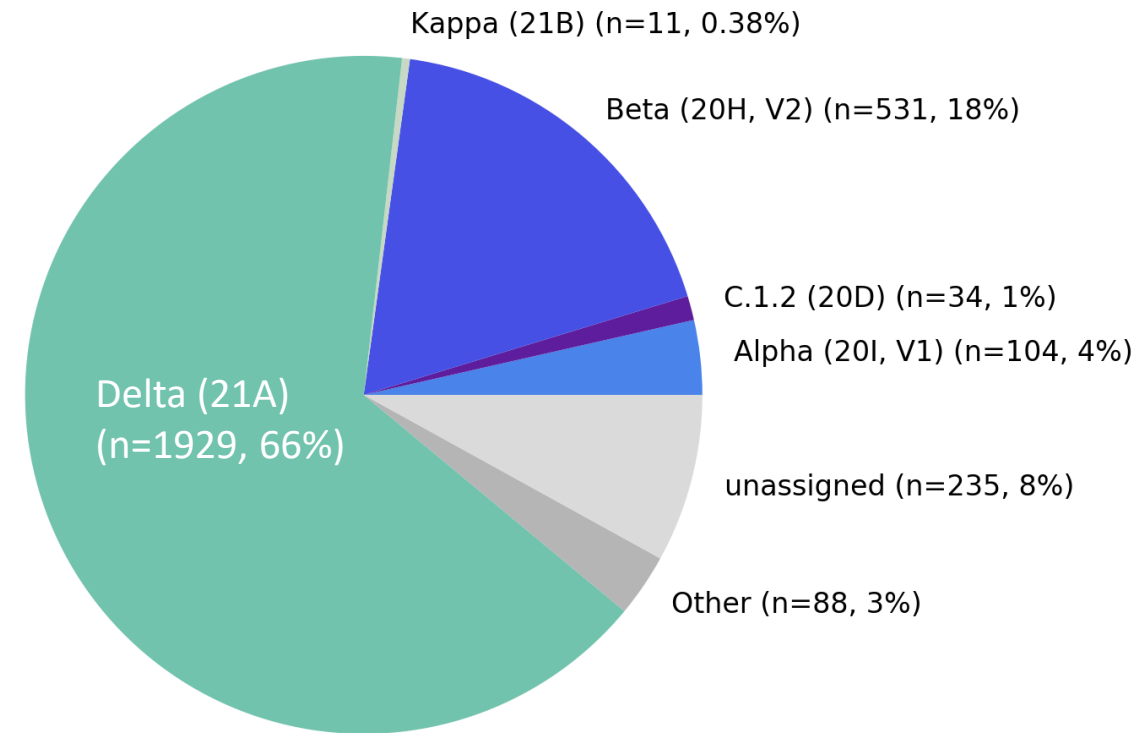
**Delta came to dominate by end June at >65% , in July at >85% and in August and September at >90%**  
**C.1.2 present at <4% frequency since March**

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

**May (N=1147)**



**June (N=2932)**

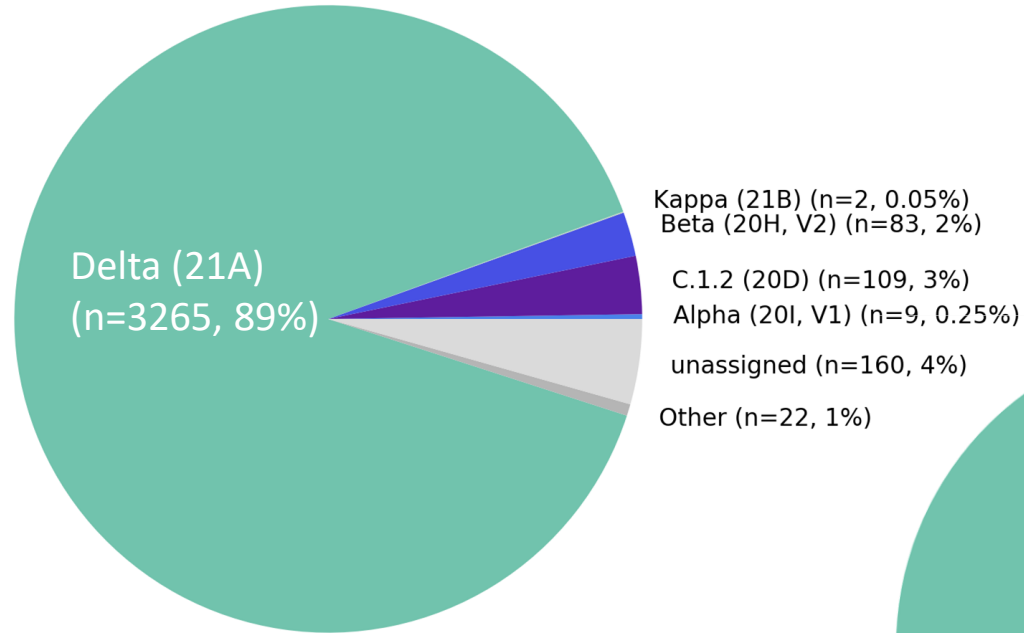


Delta (21A) C.1.2 (20D) Beta (20H, V2) Alpha (20I, V1) Kappa (21B) Eta (21D) Other unassigned

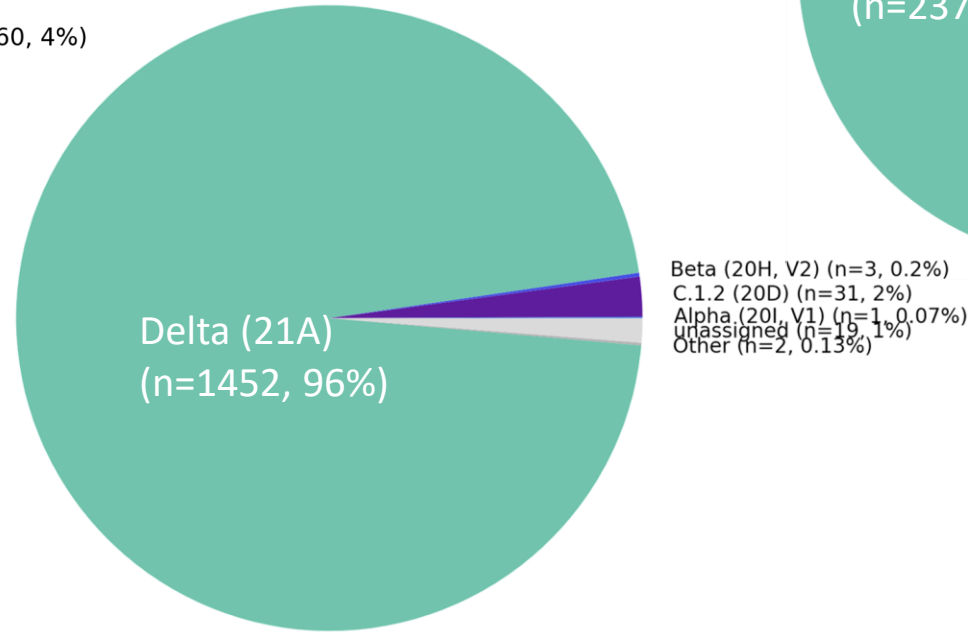
**Beta variant dominated in May, but the Delta variant started to dominate in June**

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

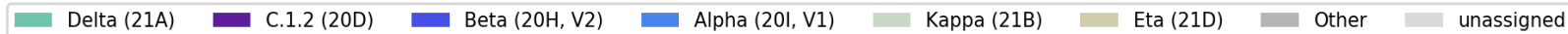
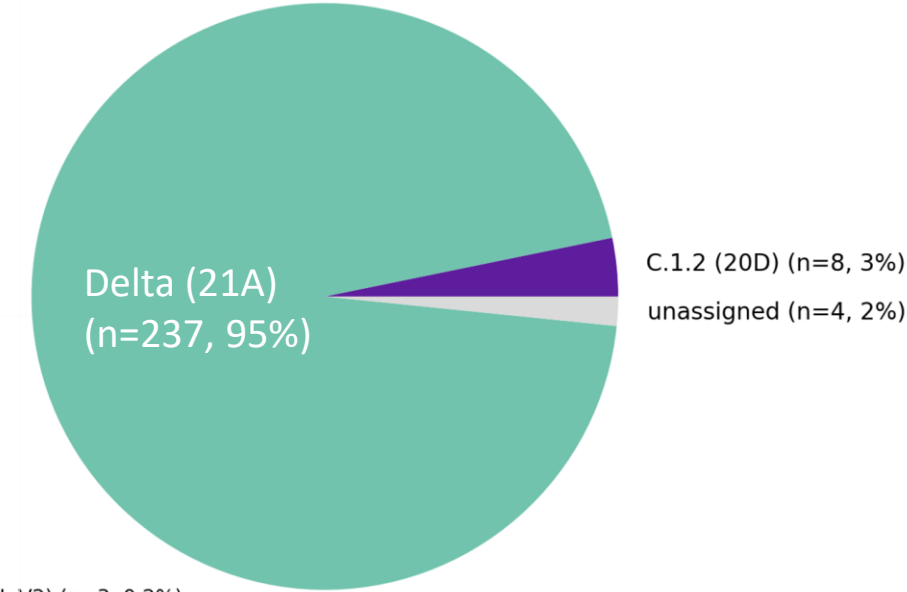
**July (N=3626)**



**August (N=1508)**

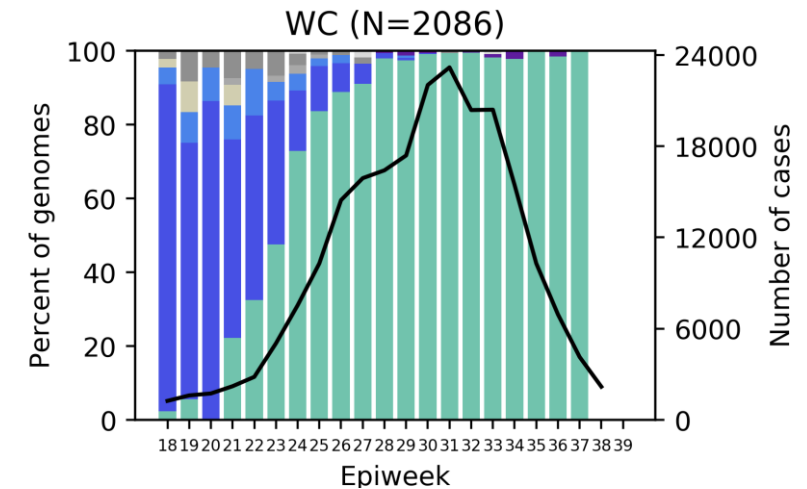
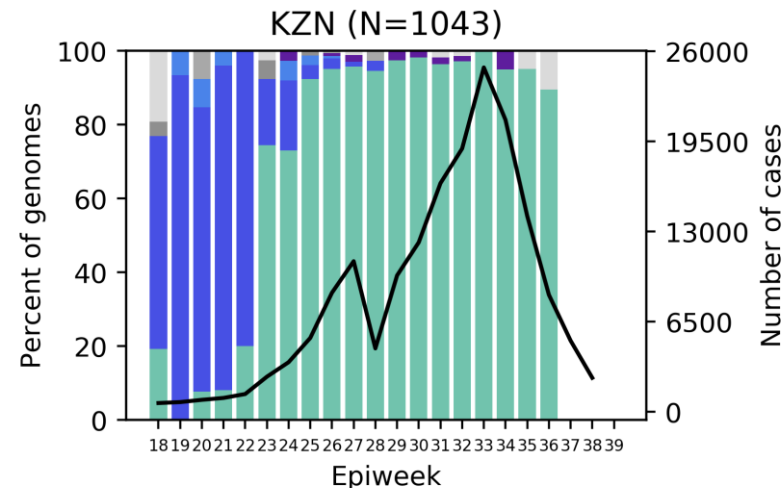
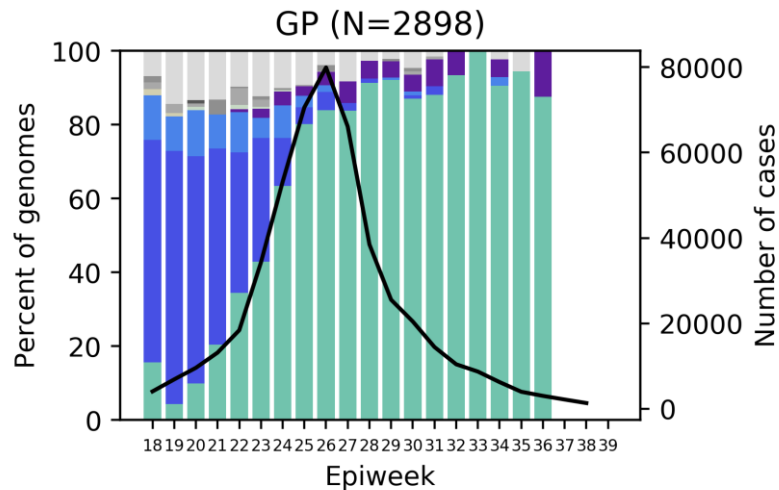
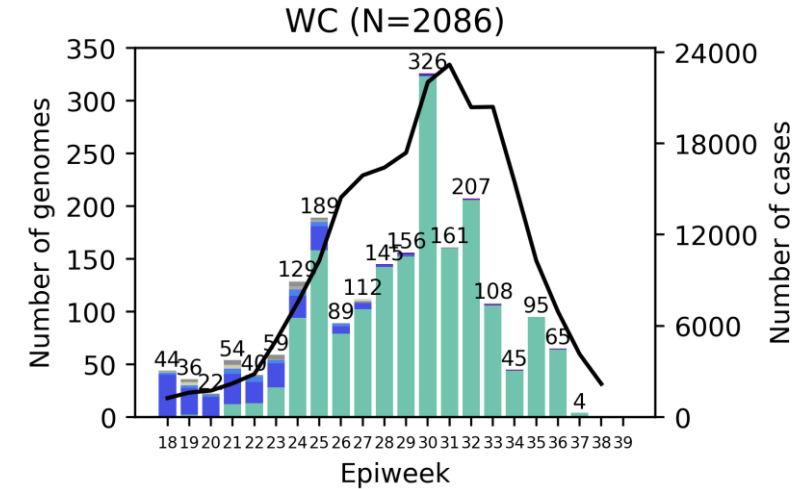
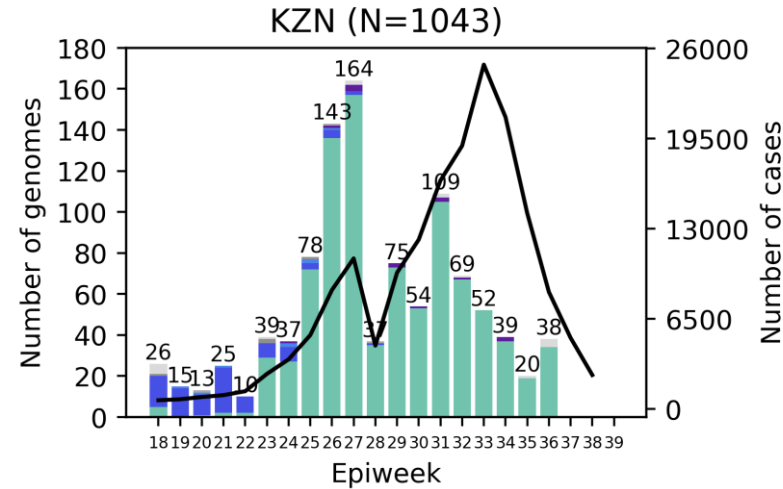
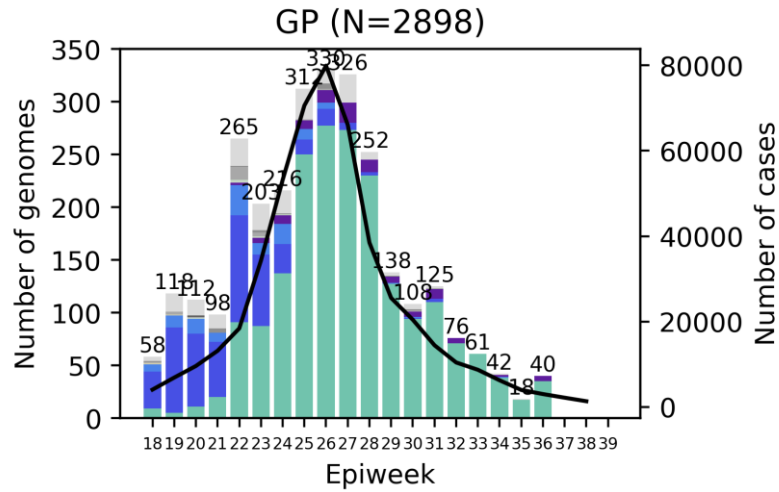


**September (N=249)**



**The Delta variant dominated in July and August in South Africa.**

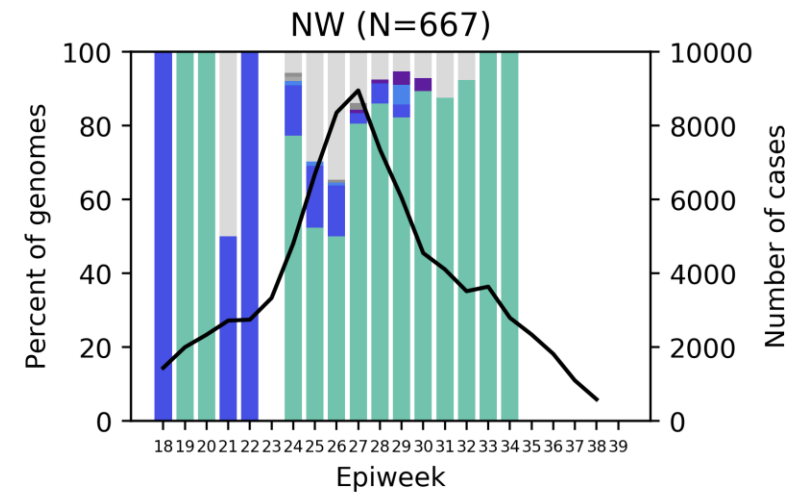
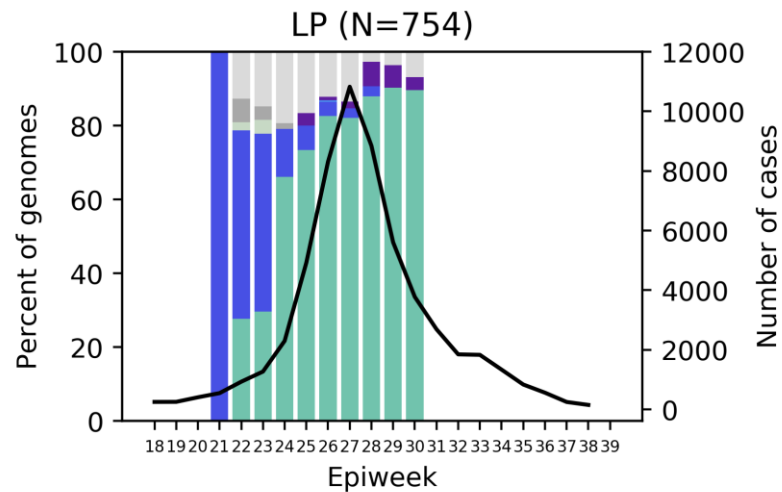
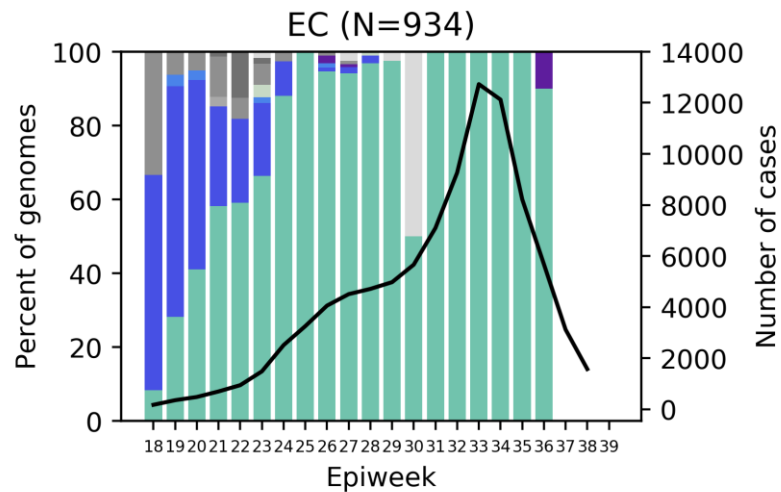
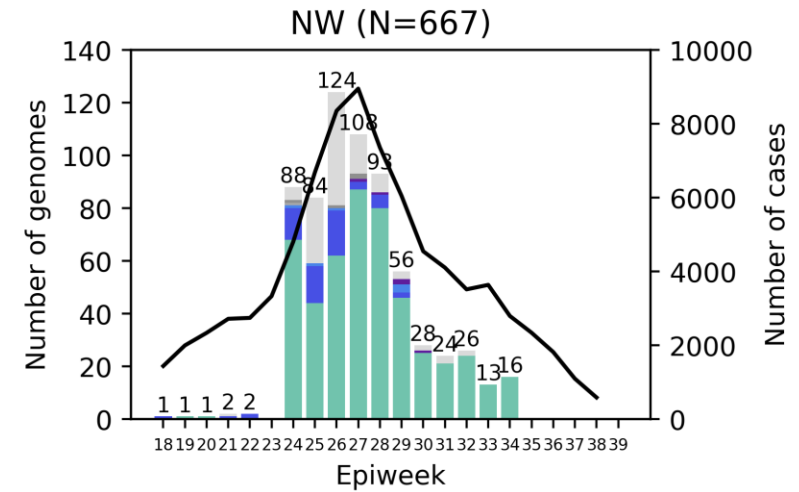
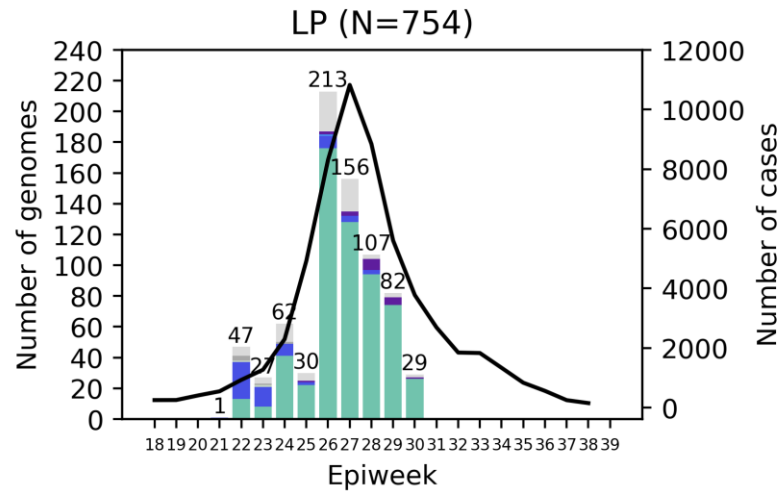
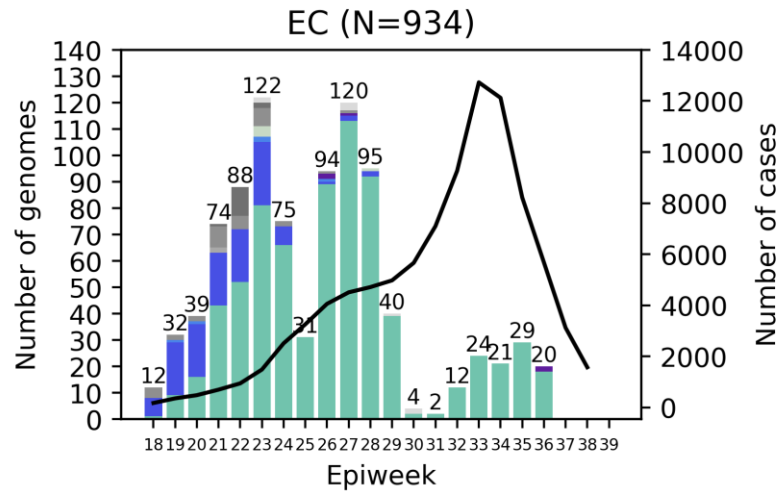
# Genomes sequenced from specimens collected in May to mid-August 2021 (epiweeks 18 – 39) from KwaZulu-Natal, Gauteng, Western Cape Provinces



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

**Delta dominates the third wave in Gauteng, KwaZulu-Natal and Western Cape provinces**

# Genomes sequenced from specimens collected in May to mid-August 2021 (epiweeks 18 – 39) from Eastern Cape, Limpopo and North-West Provinces

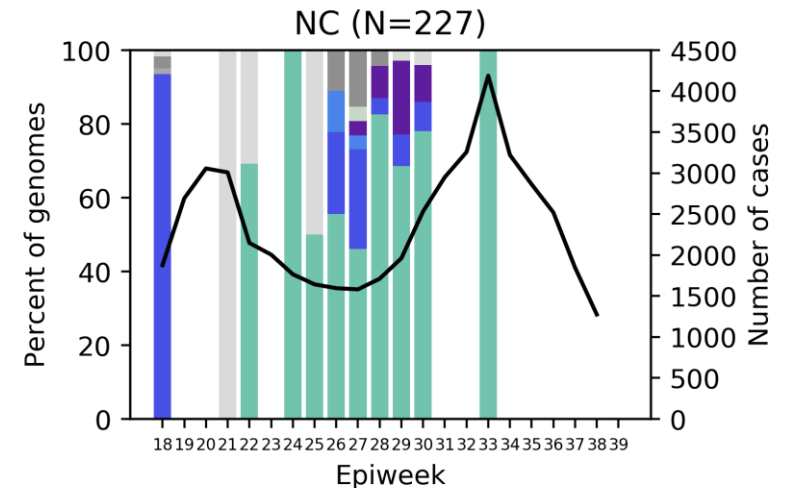
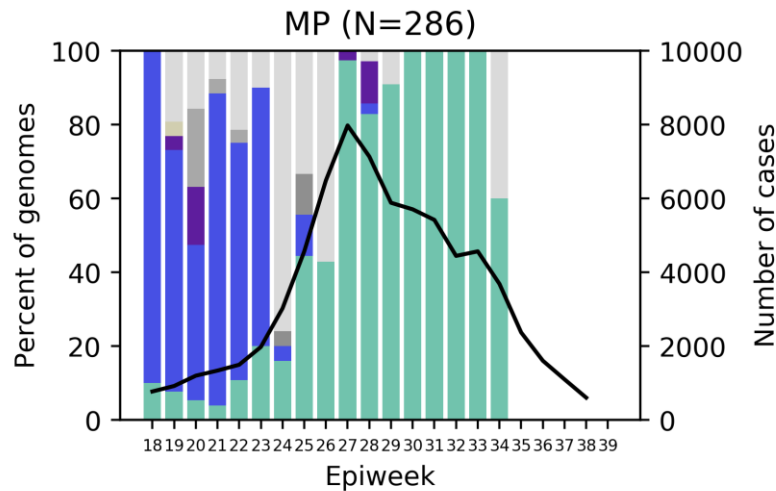
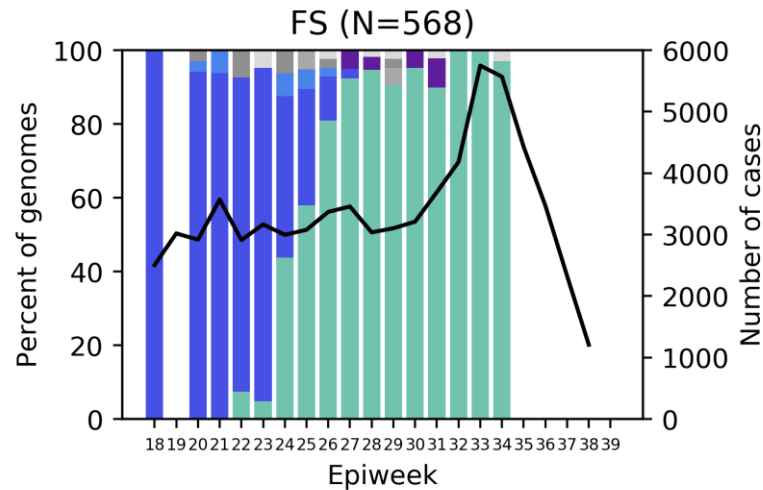
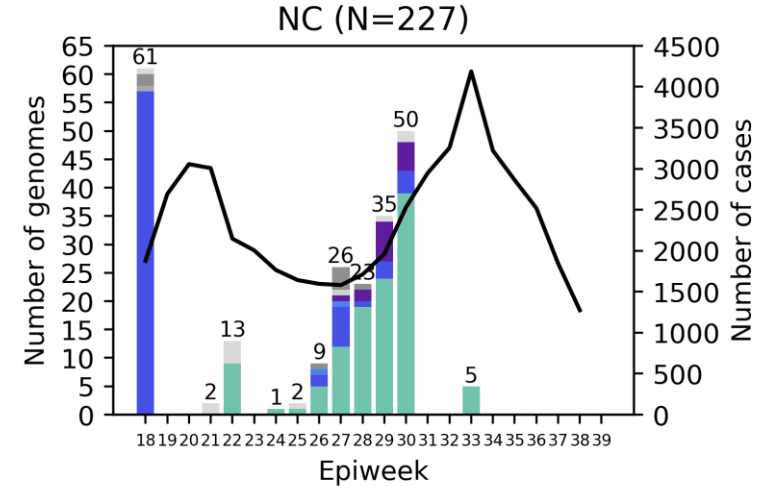
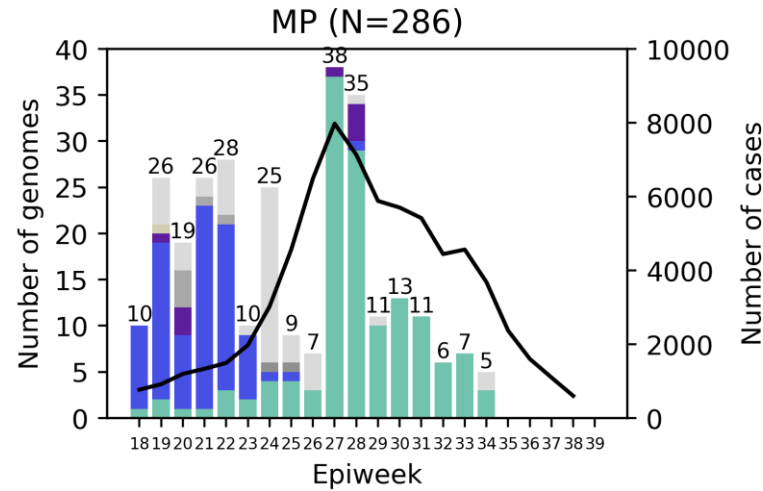
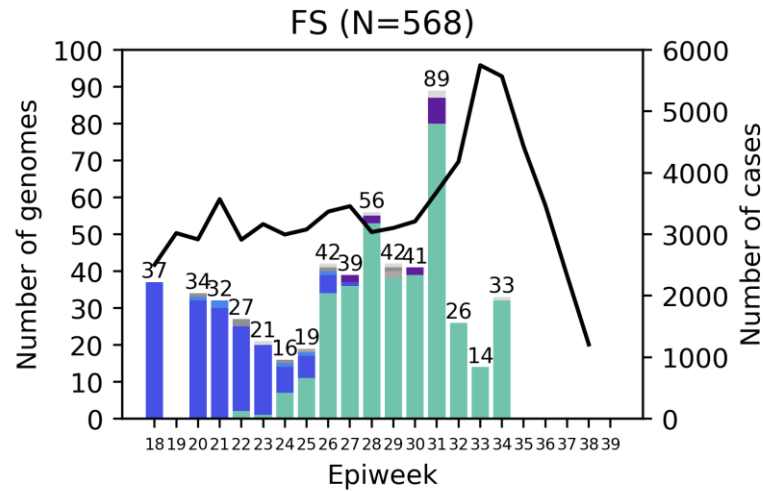


— cases Delta (21A) Beta (20H, V2) Alpha (20I, V1) C.1.2 (20D) Kappa (21B) Eta (21D) 20A 20B 20C 20D unassigned 19B

Delta variant dominates the third wave in Eastern Cape, Limpopo and North-West Provinces



# Genomes sequenced from specimens collected in May to mid-August 2021 (epiweeks 18 – 38) from Free State, Mpumalanga and Northern Cape Provinces

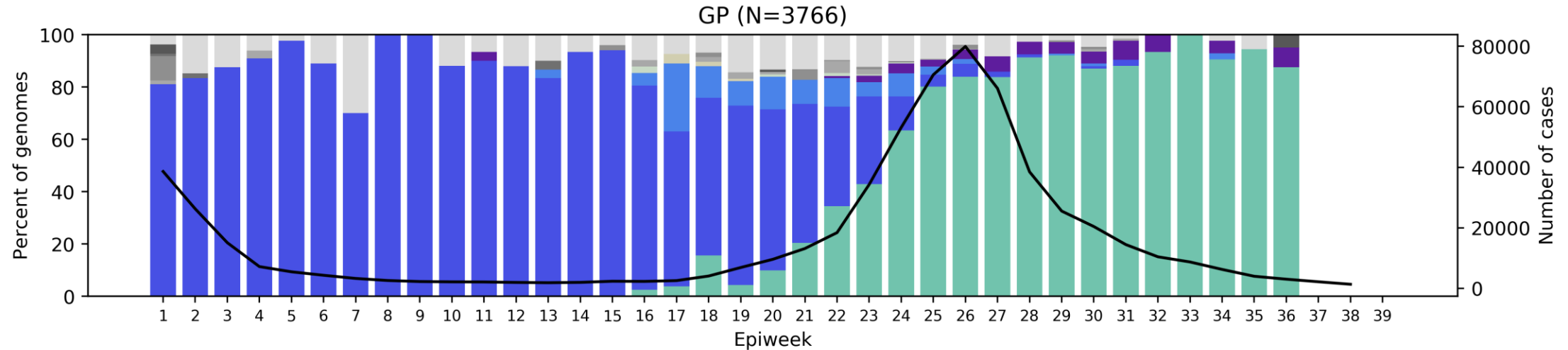
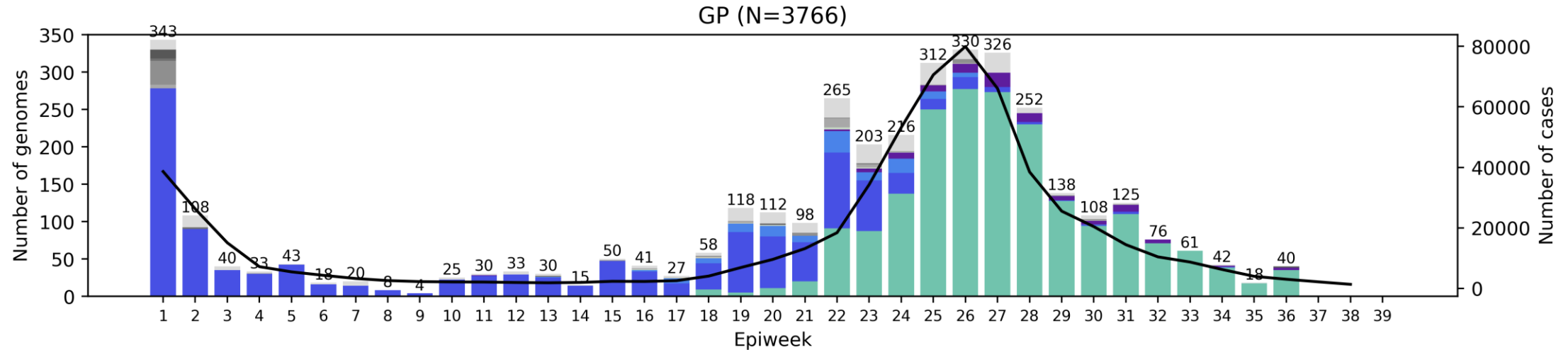


— cases   Delta (21A)   Beta (20H, V2)   Alpha (20I, V1)   C.1.2 (20D)   Kappa (21B)   Eta (21D)   20A   20B   20C   20D   unassigned   19B

**Delta dominates the third wave in Free State, Mpumalanga and Northern Cape provinces**



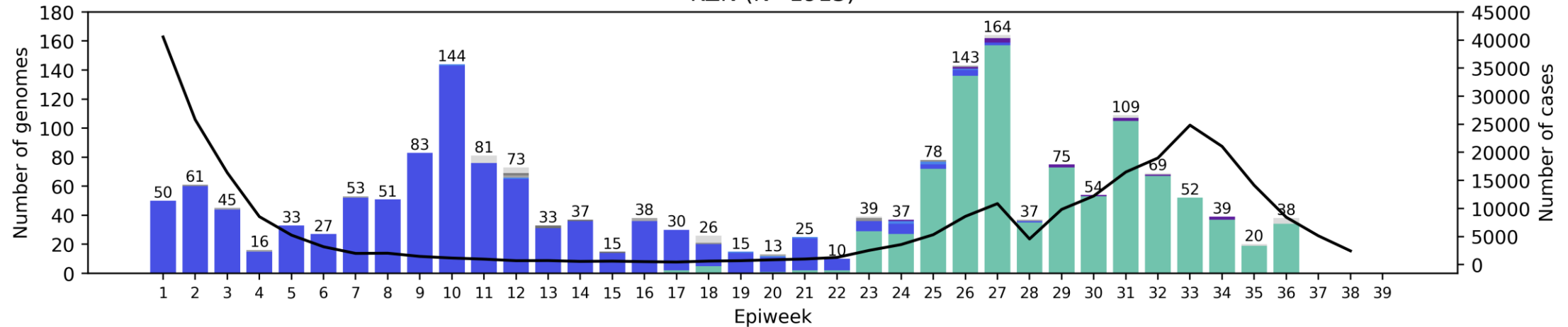
# Gauteng Province, 2021, n = 3562



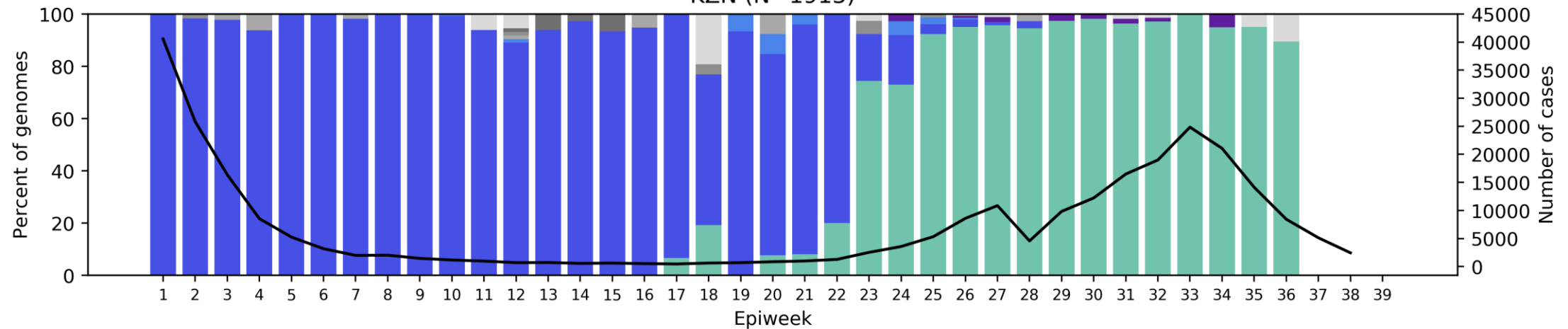
— cases Delta (21A) Beta (20H, V2) Alpha (20I, V1) C.1.2 (20D) Kappa (21B) Eta (21D) 20A 20B 20C 20D unassigned 19B

# KwaZulu-Natal Province, 2021, n = 1913

KZN (N=1913)



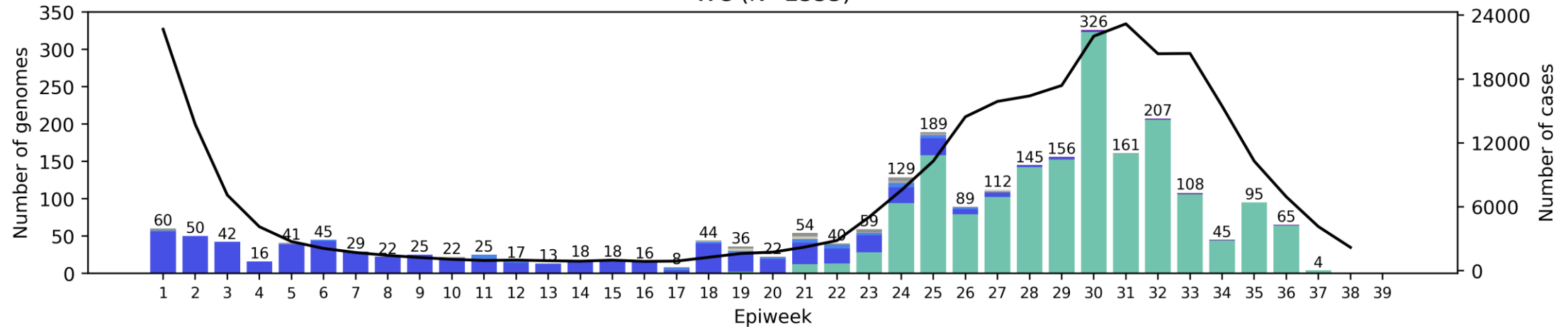
KZN (N=1913)



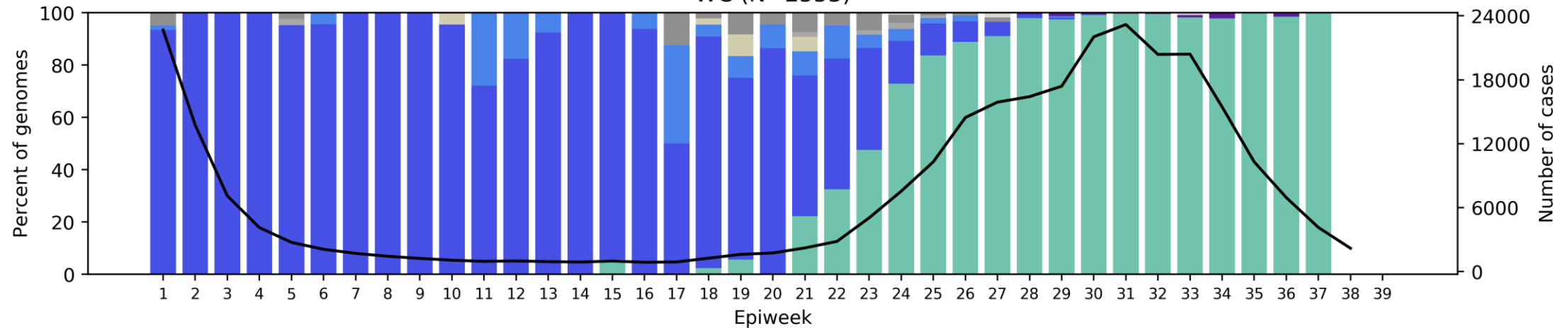
— cases Delta (21A) Beta (20H, V2) Alpha (20I, V1) C.1.2 (20D) Kappa (21B) Eta (21D) 20A 20B 20C 20D unassigned 19B

# Western Cape Province, 2021, n = 2553

WC (N=2553)



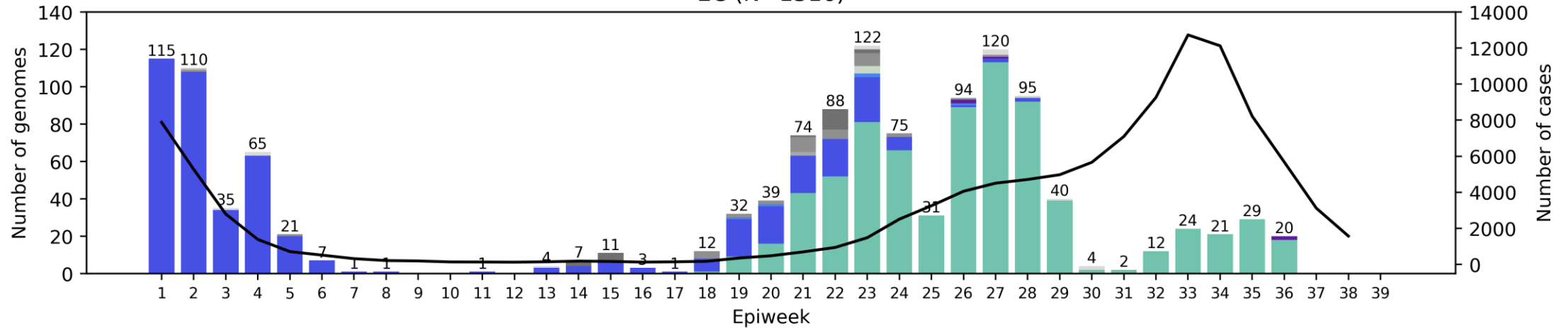
WC (N=2553)



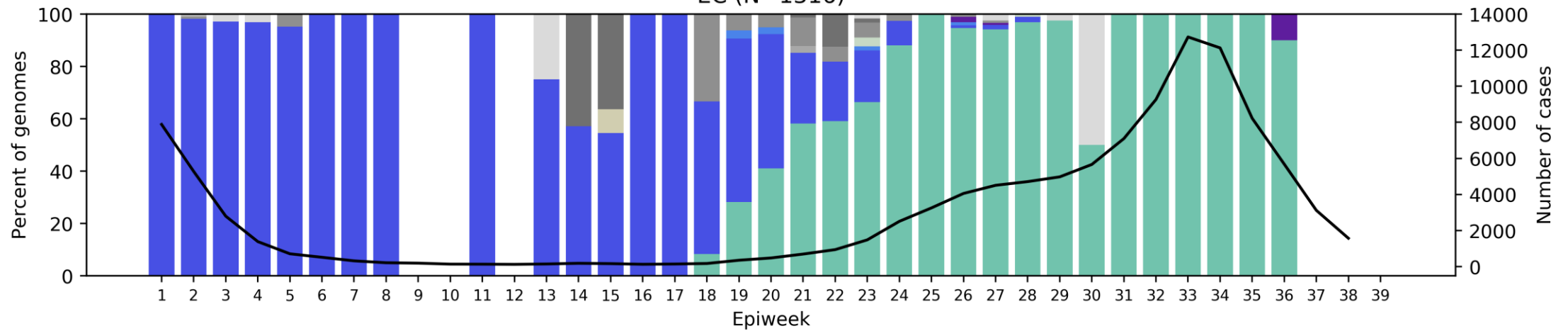
— cases Delta (21A) Beta (20H, V2) Alpha (20I, V1) C.1.2 (20D) Kappa (21B) Eta (21D) 20A 20B 20C 20D unassigned 19B

# Eastern Cape Province, 2021, n = 1316

EC (N=1316)



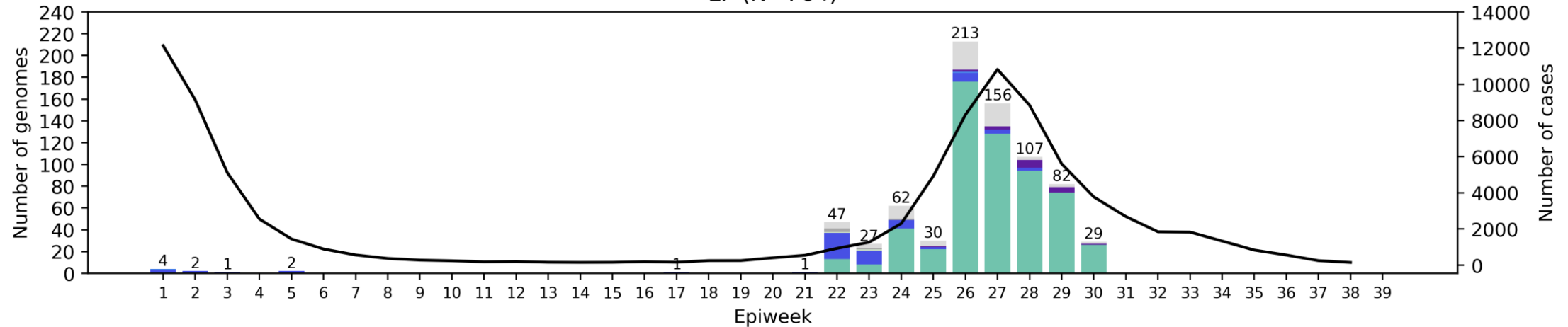
EC (N=1316)



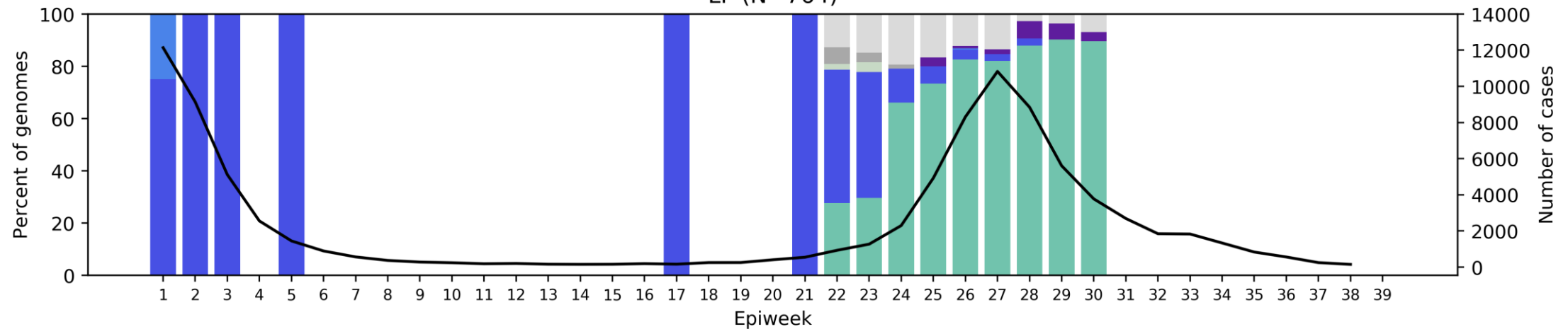
— cases Delta (21A) Beta (20H, V2) Alpha (20I, V1) C.1.2 (20D) Kappa (21B) Eta (21D) 20A 20B 20C 20D unassigned 19B

# Limpopo Province, 2021, n = 764

LP (N=764)

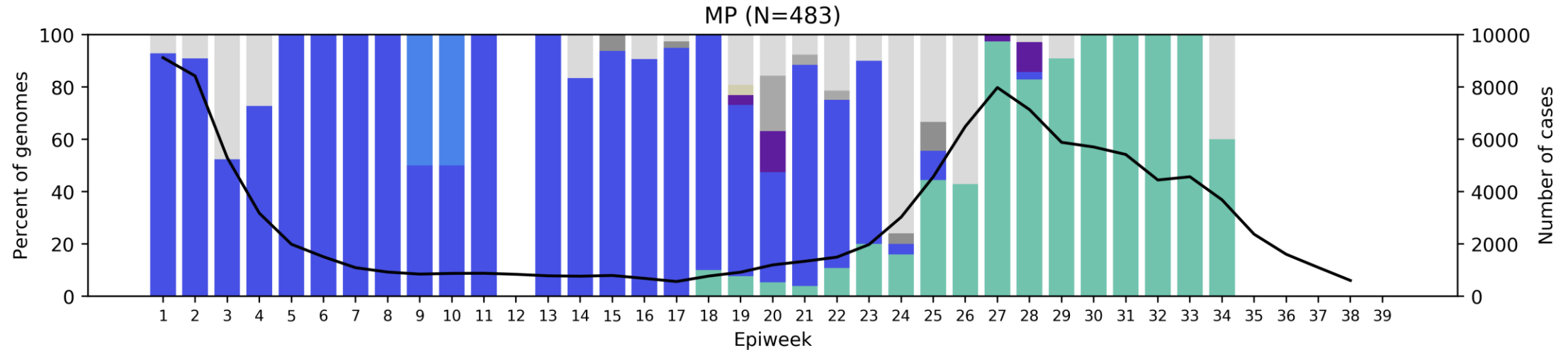
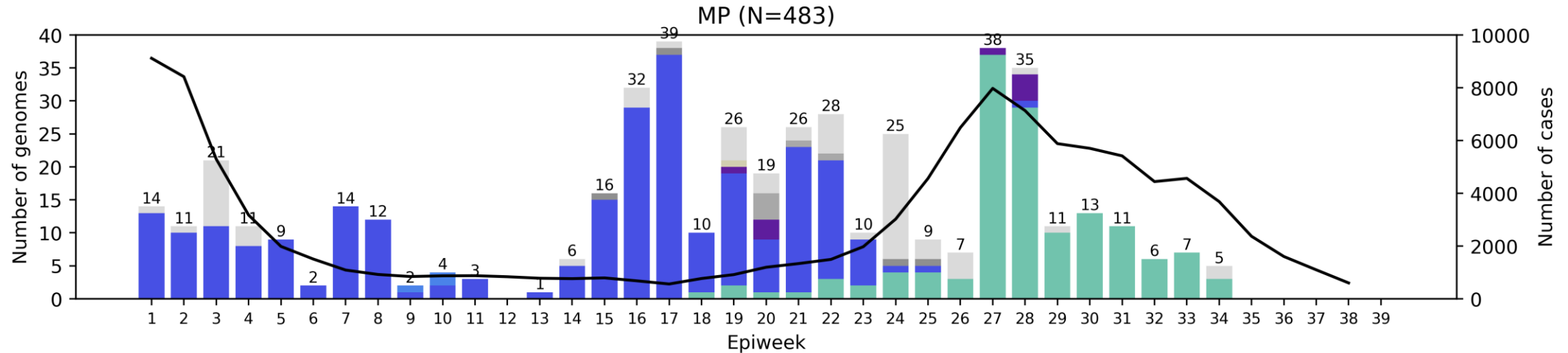


LP (N=764)

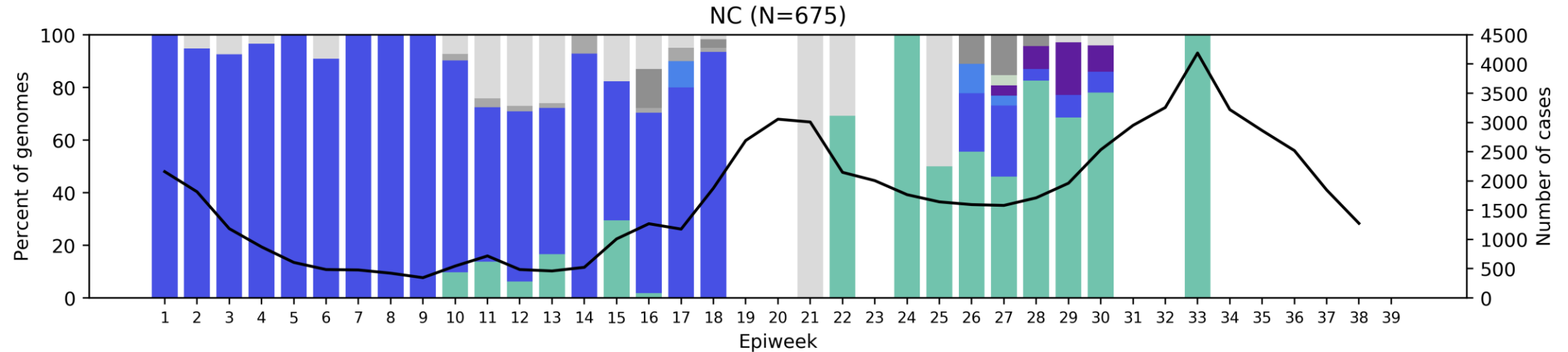
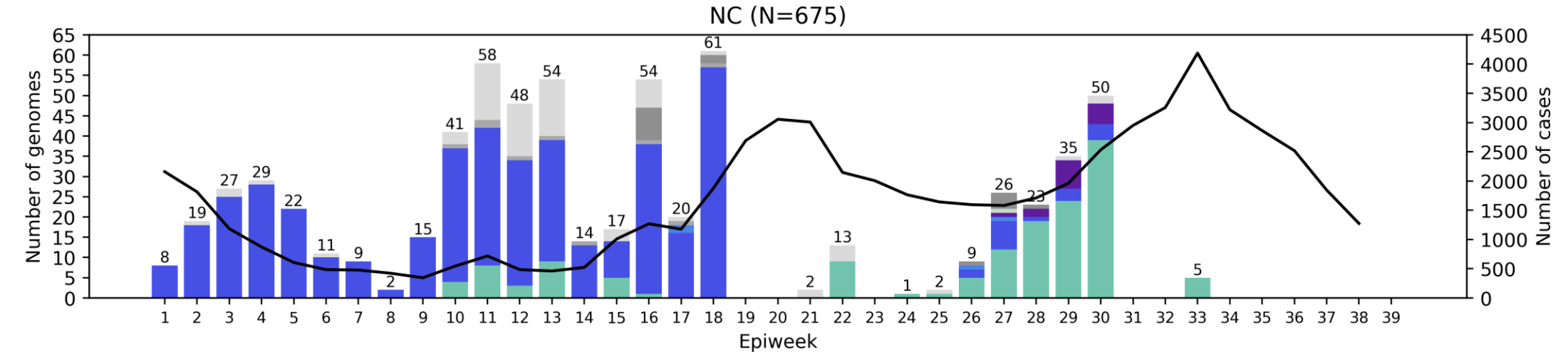


— cases   Delta (21A)   Beta (20H, V2)   Alpha (20I, V1)   C.1.2 (20D)   Kappa (21B)   Eta (21D)   20A   20B   20C   20D   unassigned   19B

# Mpumalanga Province, 2021, n = 483



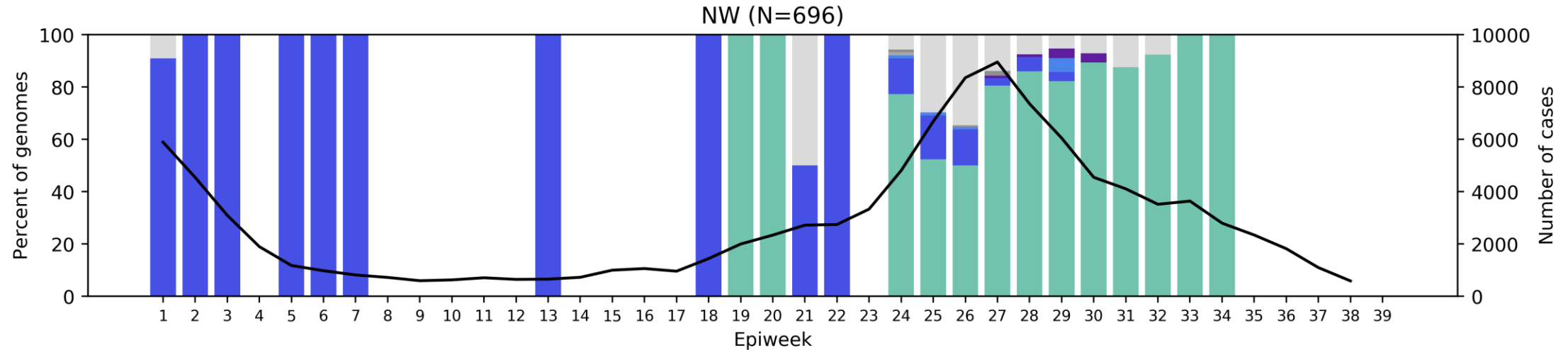
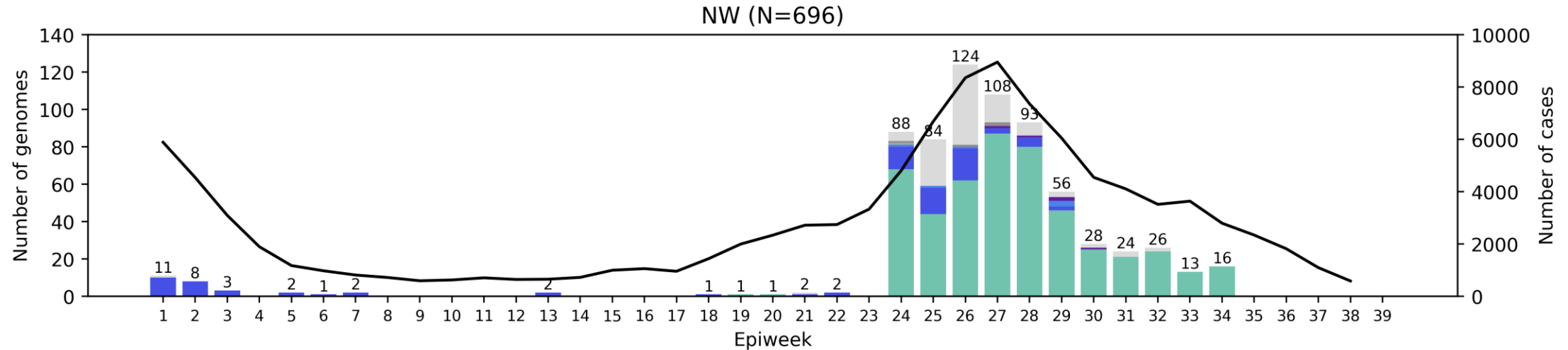
# Northern Cape Province, 2021, n = 675



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

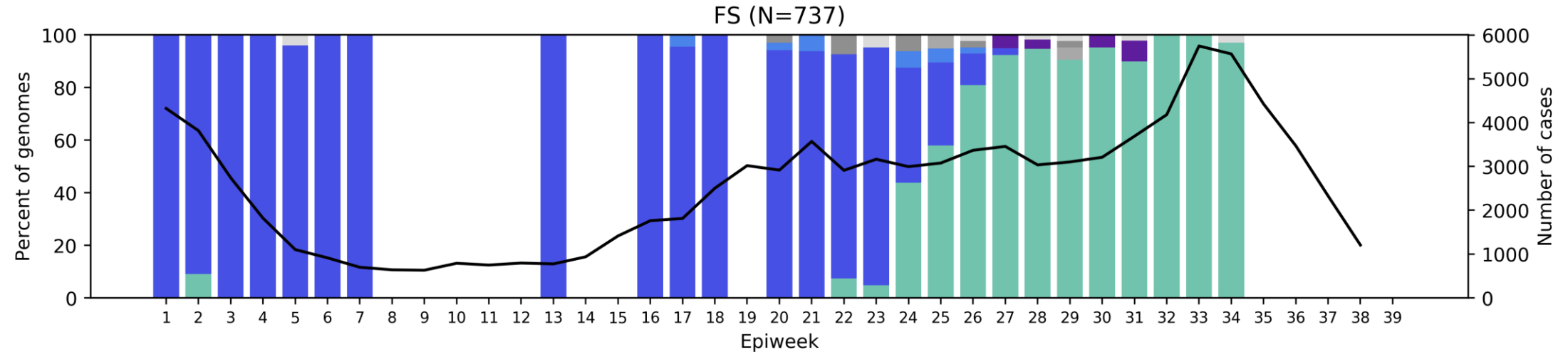
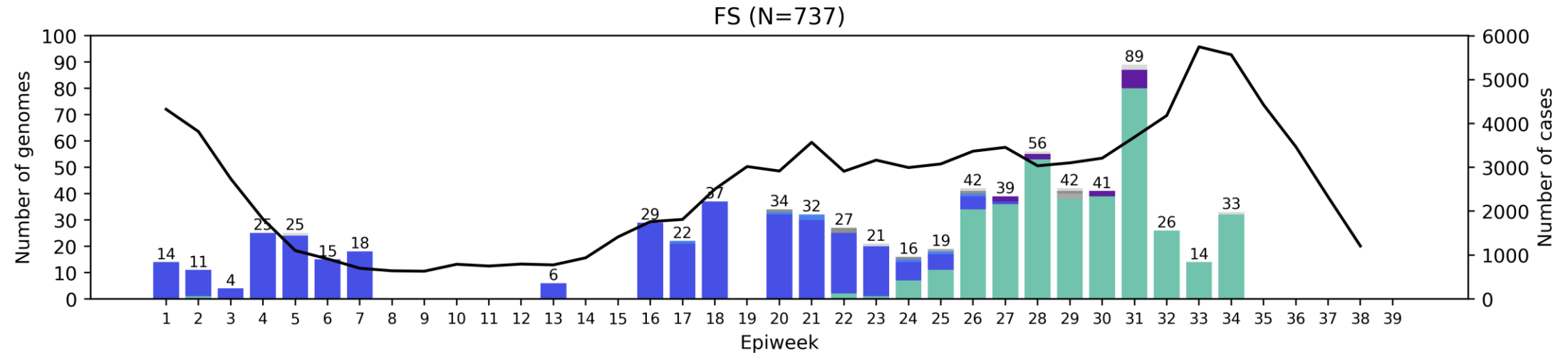


# North West Province, 2021, n = 696



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

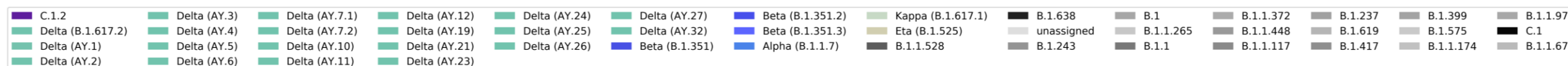
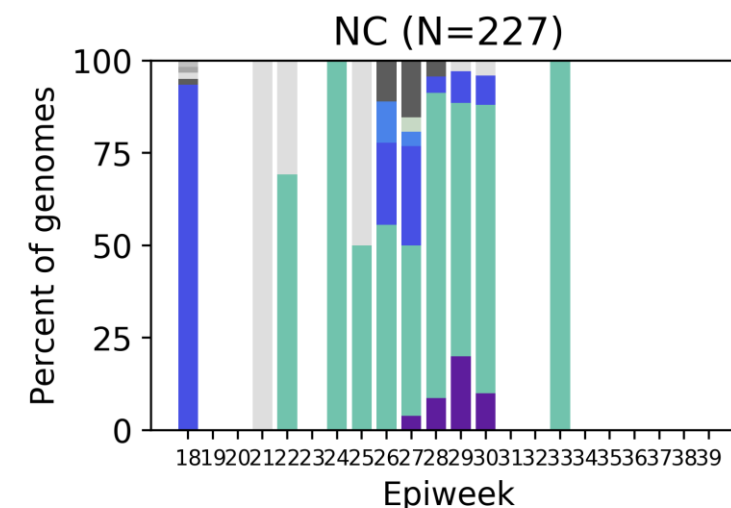
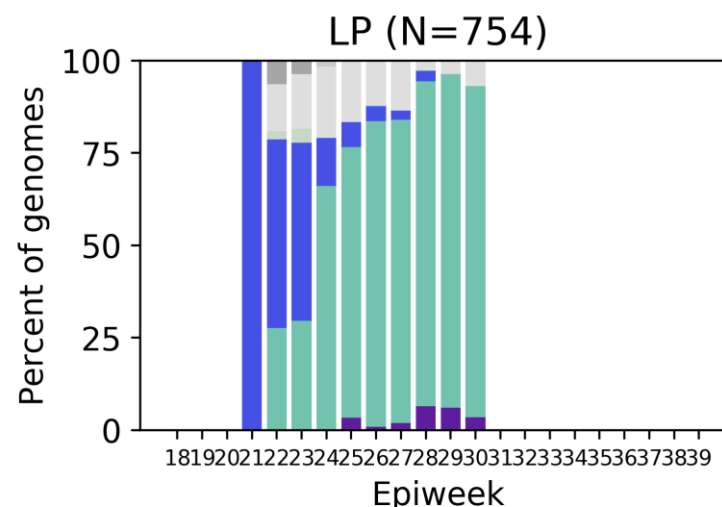
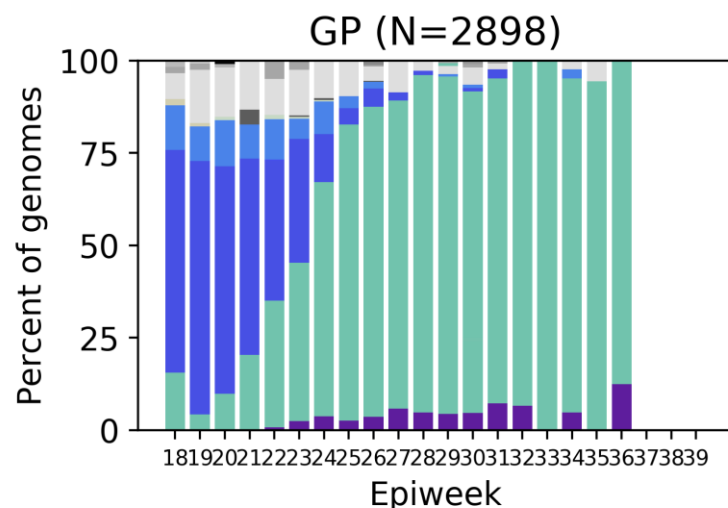
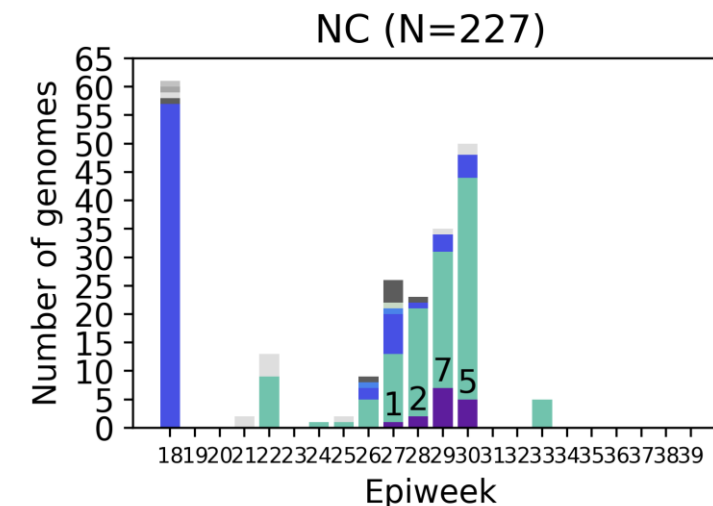
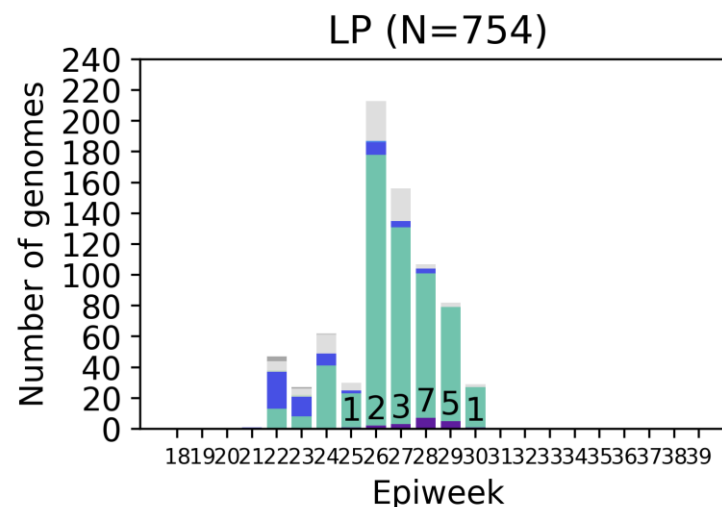
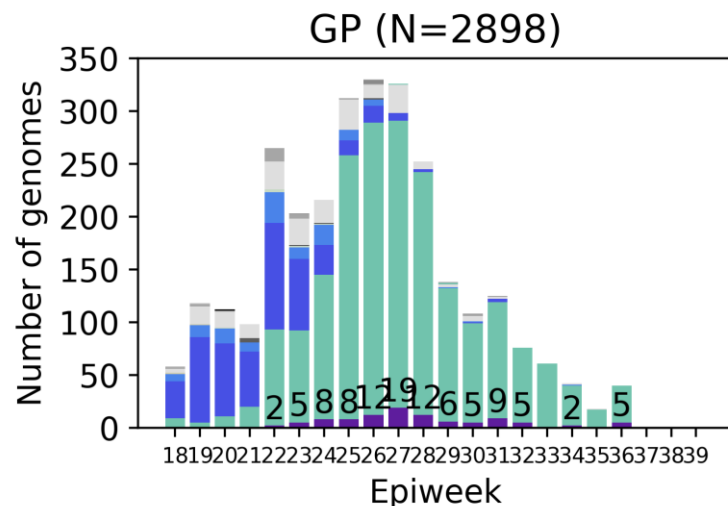
# Free State Province, 2021, n = 737



— 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=186 in SA) in May – August 2021 by epiweek

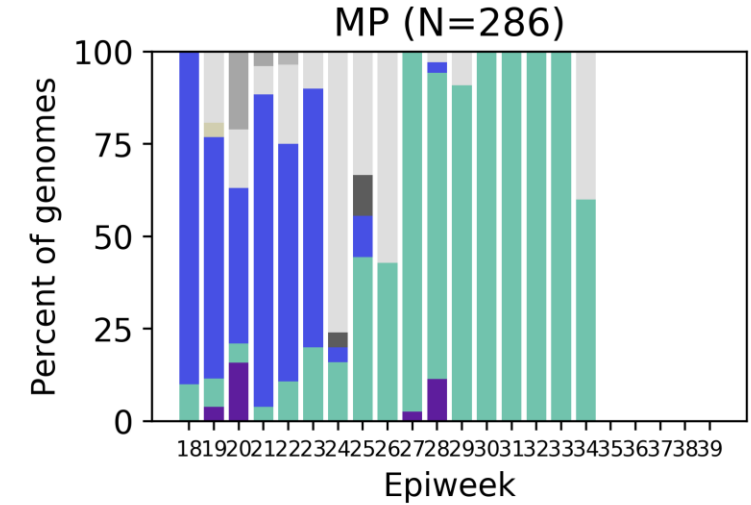
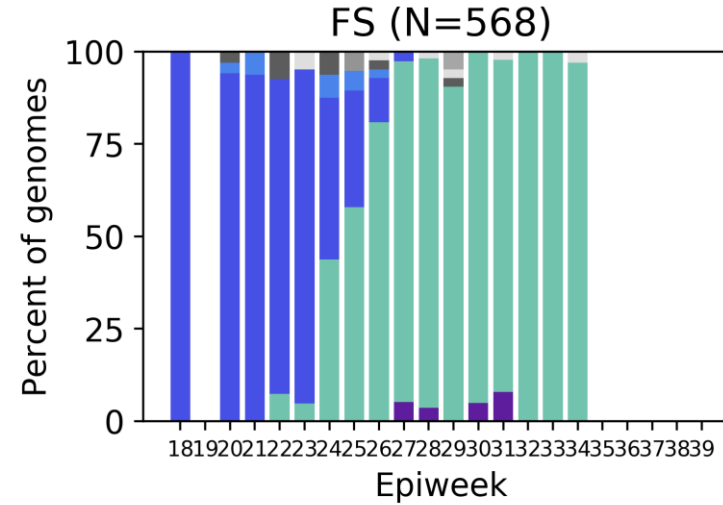
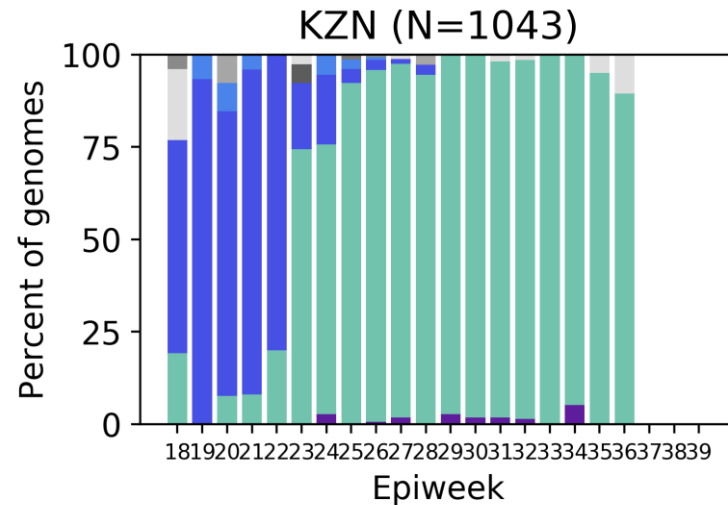
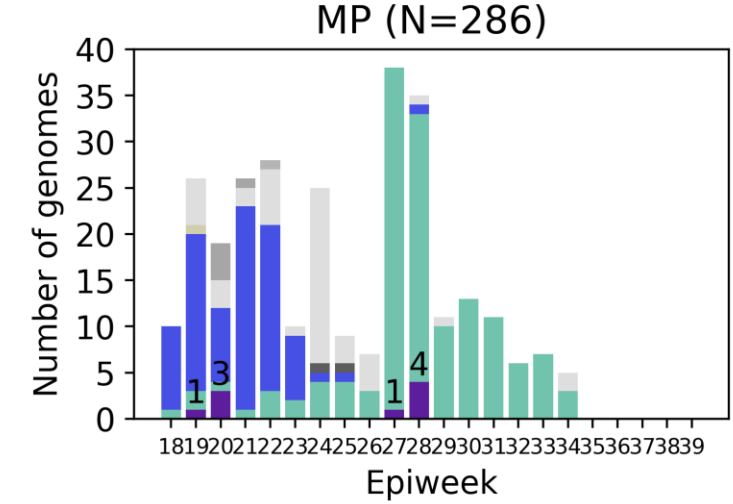
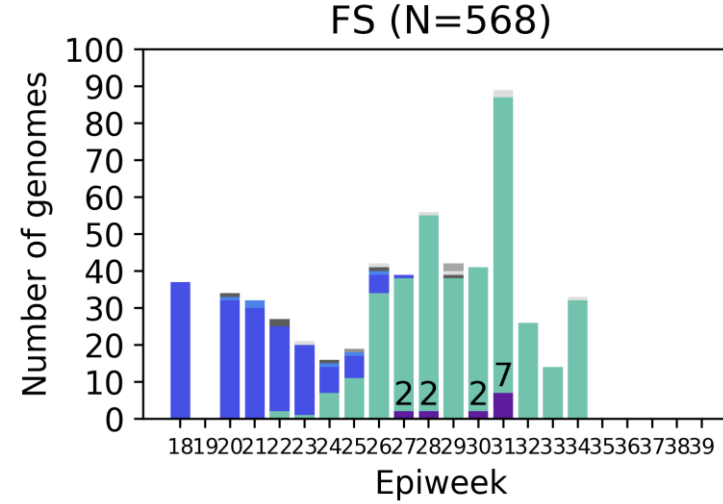
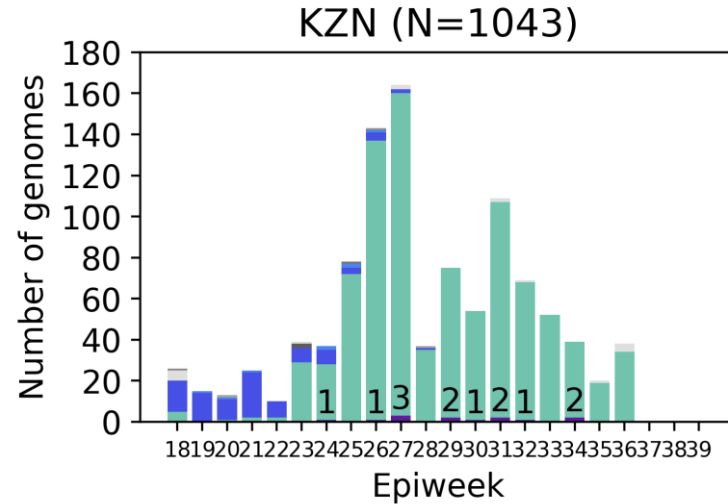
Number of C.1.2 samples indicated above bar



The majority of C.1.2 sequences have been detected in Gauteng (n=98), followed by Limpopo (n=19) and the Northern Cape (n=15).

# C.1.2 (n=186 in SA) in May – August 2021 by epiweek

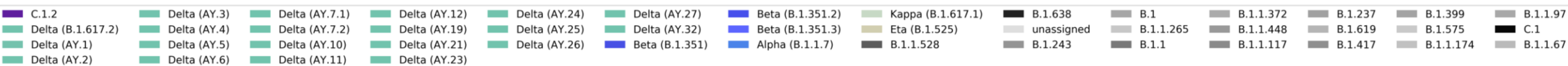
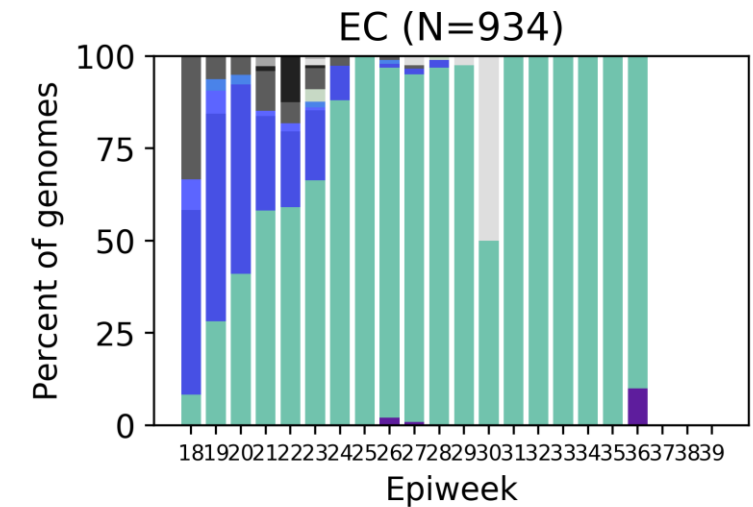
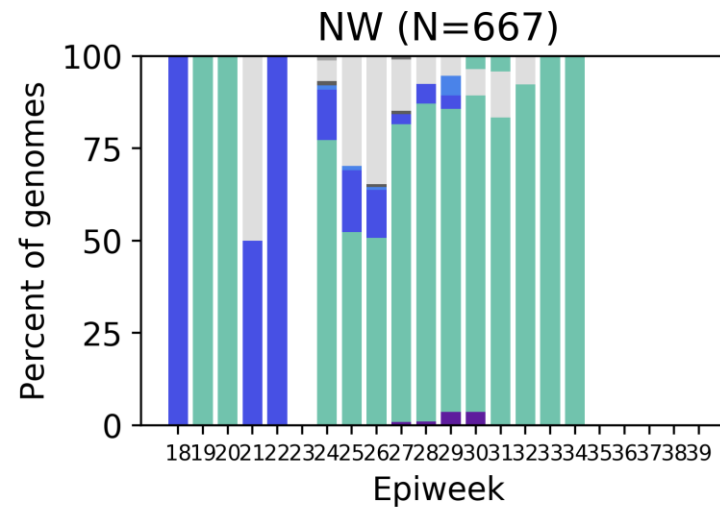
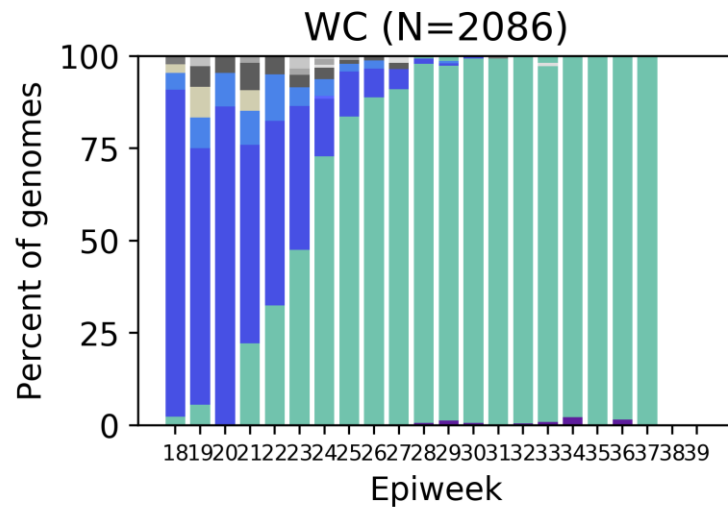
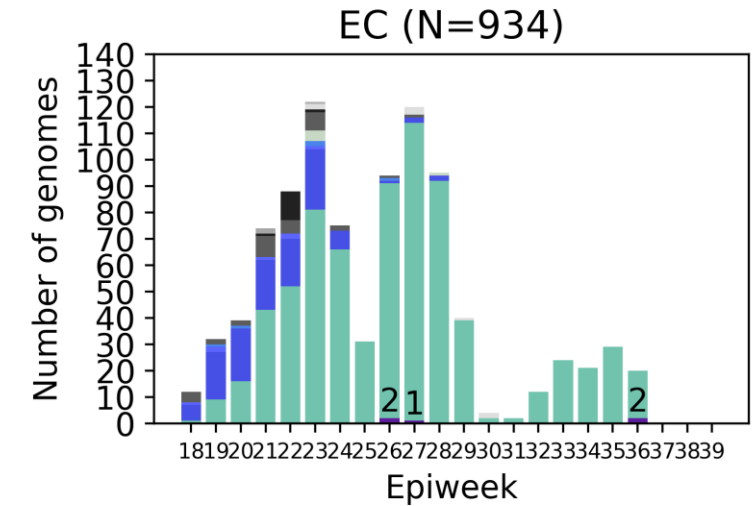
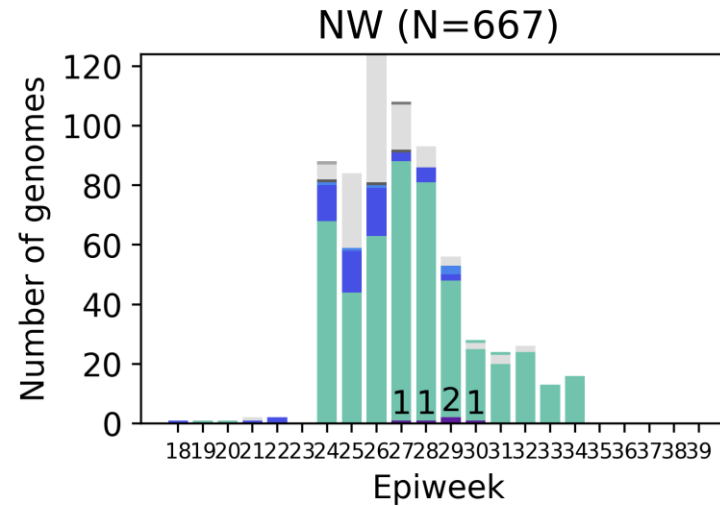
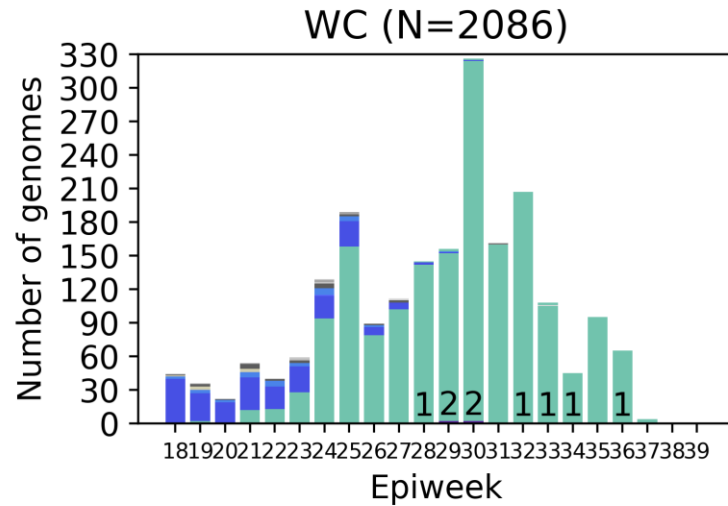
Number of C.1.2 samples indicated above bar



13 C.1.2 sequences have been detected in KwaZulu-Natal and the Free State, and 9 in Mpumalanga.

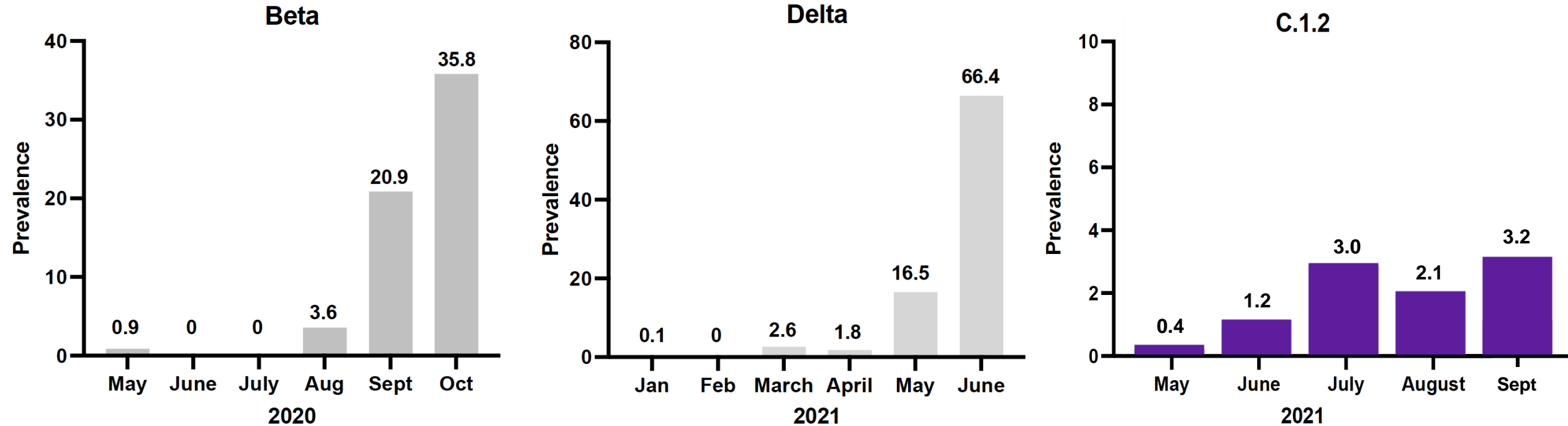
# C.1.2 (n=186 in SA) in May – August 2021 by epiweek

Number of C.1.2 samples indicated above bar



The Western Cape has 9 sequences, the North West Eastern Cape each have 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

# Summary

- Delta continues to dominate in all provinces from specimens collected in September
- Overall diversity of lineages decreased as Delta became dominant
- 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 from May through August. C.1.2 has been detected at 3.2% frequency in September.
- Lambda and Mu variants not detected in South Africa





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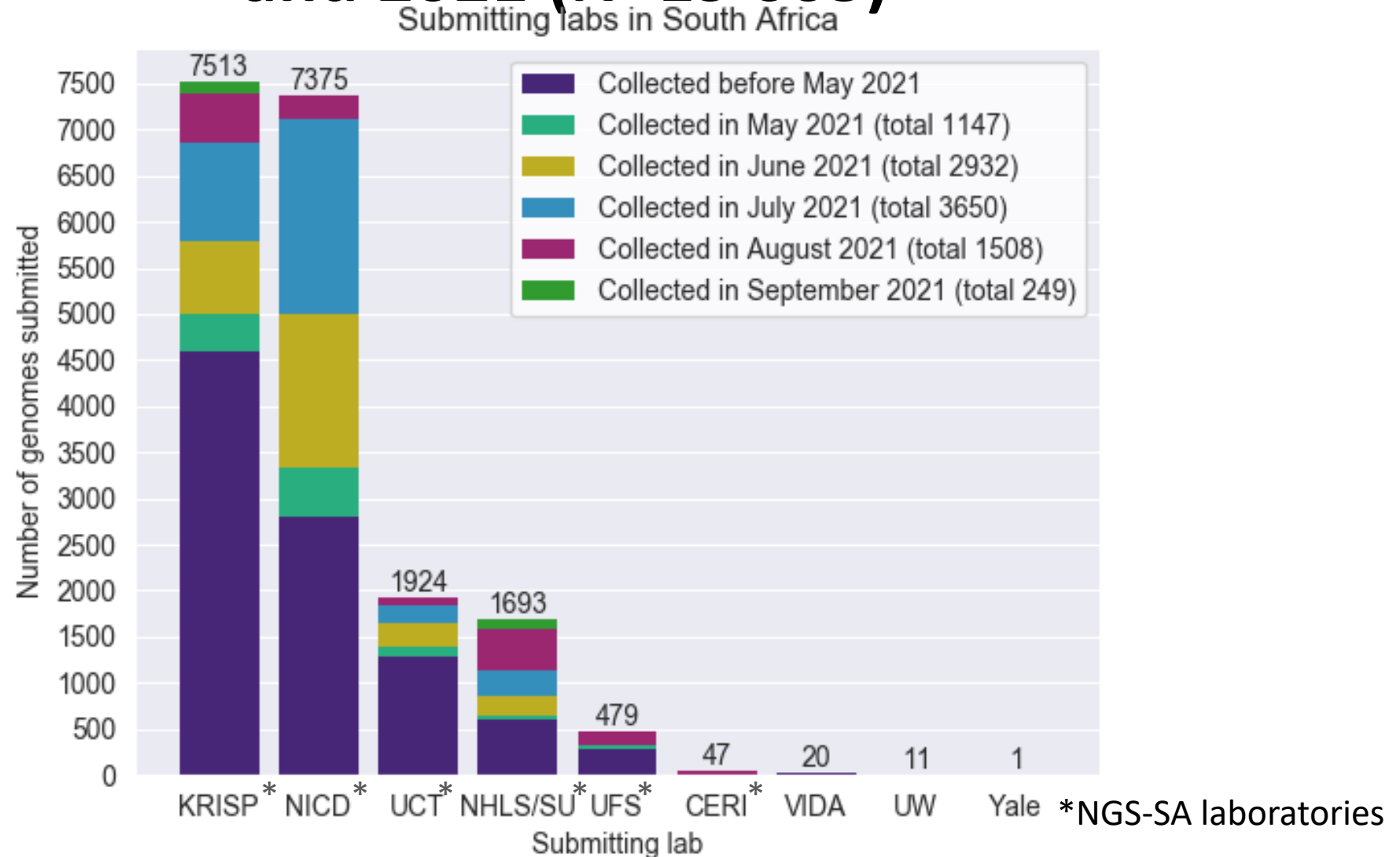
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# South African genomes submitted per sequencing lab, 2020 and 2021 (N=19 063)



**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 <sup>+</sup>	GISAID clade	Nextstrain clade	Additional amino acid changes monitored*	Earliest documented samples	Date of designation
Alpha	B.1.1.7 <sup>#</sup>	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 <sup>§</sup>	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

<sup>+</sup>Includes all descendant lineages.

<sup>#</sup>Includes all Q.\* lineages in the PANGO nomenclature system.

<sup>§</sup>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 ( $\geq 14$  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.)