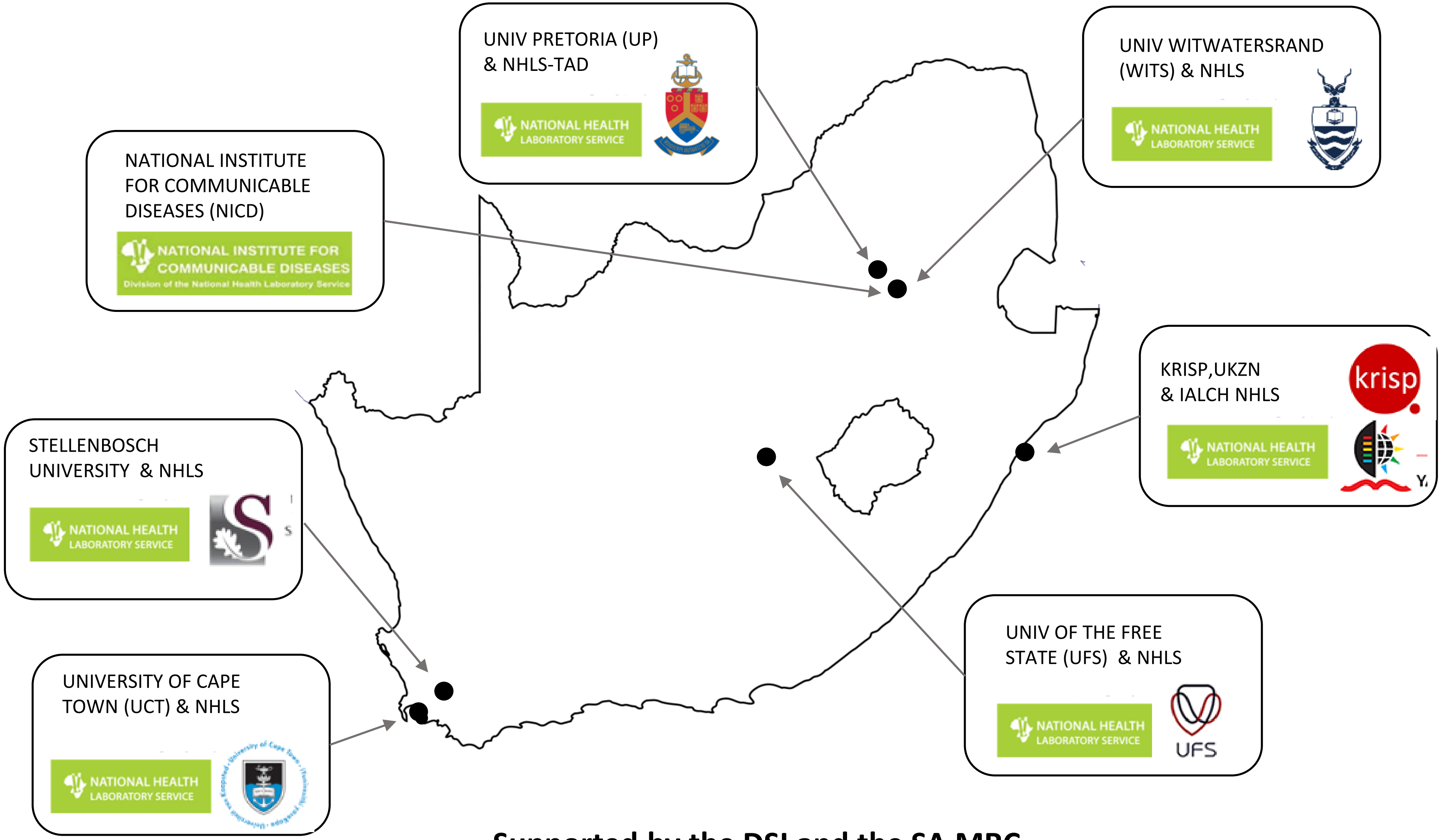
# NGS-SA SARS-CoV-2 Sequencing Update

## 12 July 2021

## Network for Genomic Surveillance South Africa (NGS-SA)

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)

# Network for Genomic Surveillance in South Africa (NGS-SA)



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**Supported by the DSI and the SA MRC**

Msomi N, Mlisana K, et al. Lancet Microbe 2020

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The genomic data presented here are based on South African SARS-CoV-2 sequence data downloaded from GISAID (www.gisaid.org) on 12 July at 12h30

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

# 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<br>+S:452R | United Kingdom, Sep-2020 | 18-Dec-2020 |
| **Beta** | B.1.351<br>B.1.351.2<br>B.1.351.3 | GH/501Y.V2 | 20H (V2) | +S:L18F | South Africa, May-2020 | 18-Dec-2020 |
| **Gamma** | P.1<br>P.1.1<br>P.1.2 | GR/501Y.V3 | 20J (V3) | +S:681H | Brazil, Nov-2020 | 11-Jan-2021 |
| **Delta** | B.1.617.2<br>AY.1<br>AY.2 | G/478K.V1 | 21A | +S:417N | India, Oct-2020 | VOI: 4-Apr-2021<br>VOC: 11-May-2021 |

https://www.who.int/en/activities/tracking-SARS-CoV-2-variants/

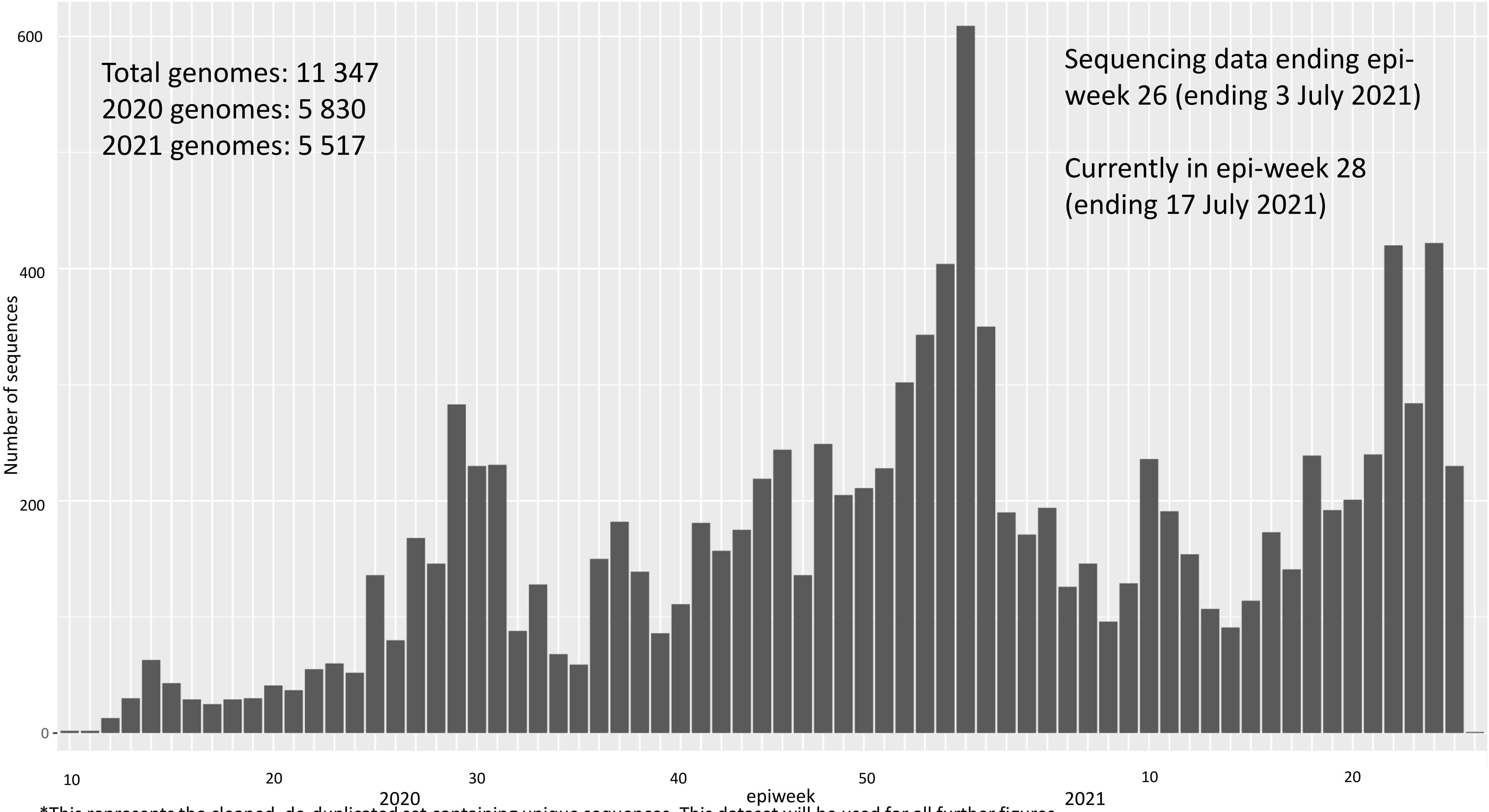
*Notable spike (S) amino acid changes under monitoring, which are currently reported in a minority of sequenced samples

# 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 |

https://www.who.int/en/activities/tracking-SARS-CoV-2-variants/

# Number of South African genomes deposited on GISAID, by specimen collection week, 2020 and 2021 (N=11 347*, downloaded 12 July)



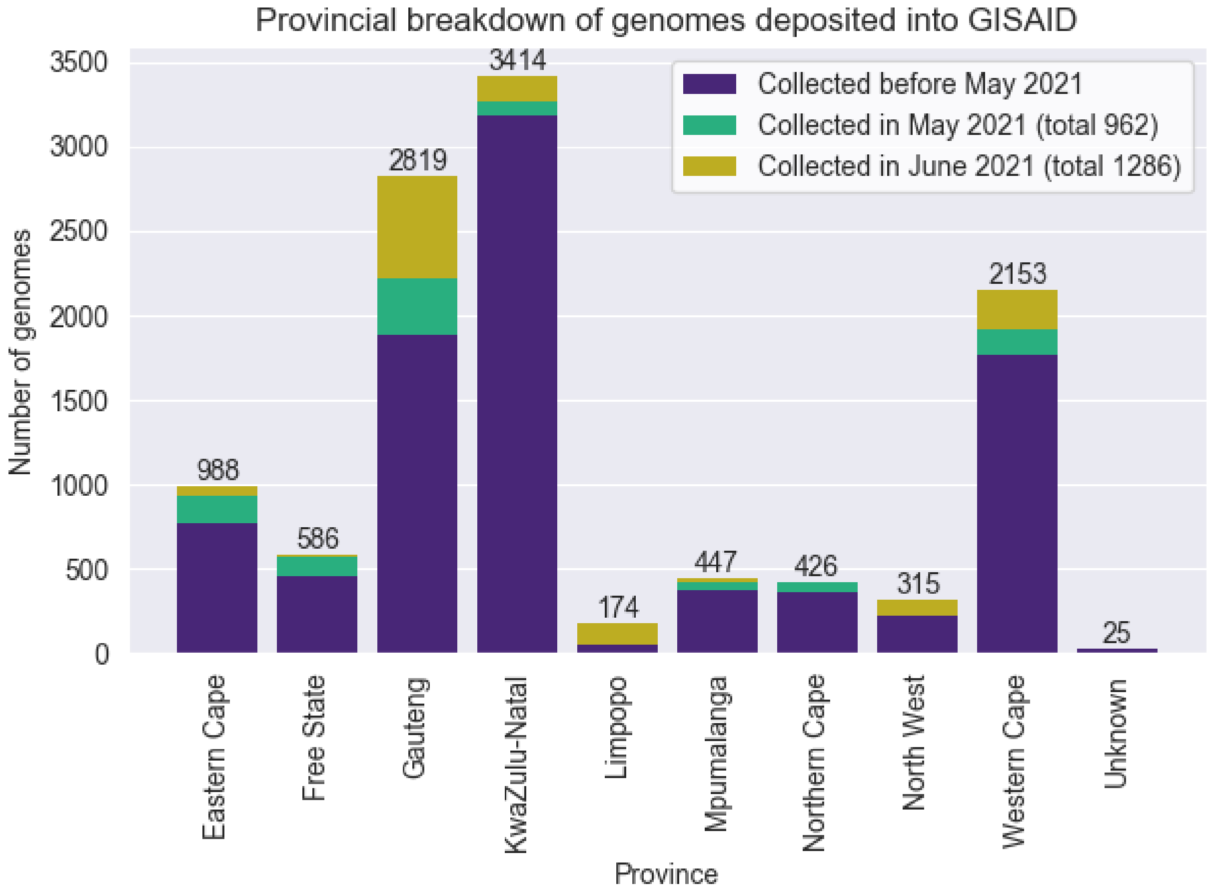
Total genomes: 11 347
2020 genomes: 5 830
2021 genomes: 5 517

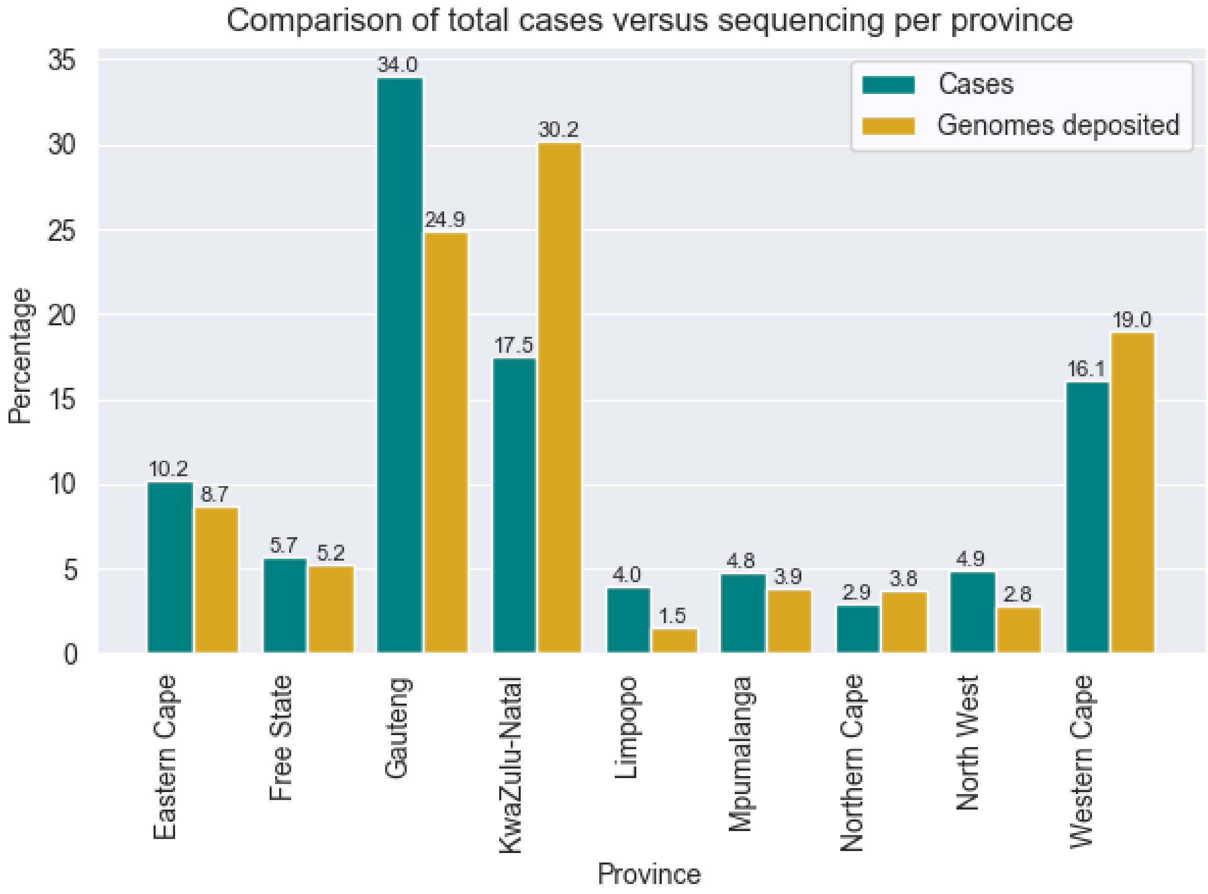
Sequencing data ending epi-week 26 (ending 3 July 2021)

Currently in epi-week 28 (ending 17 July 2021)

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

# GISAID genomes vs total cases, 2020 and 2021 (N=11 347)

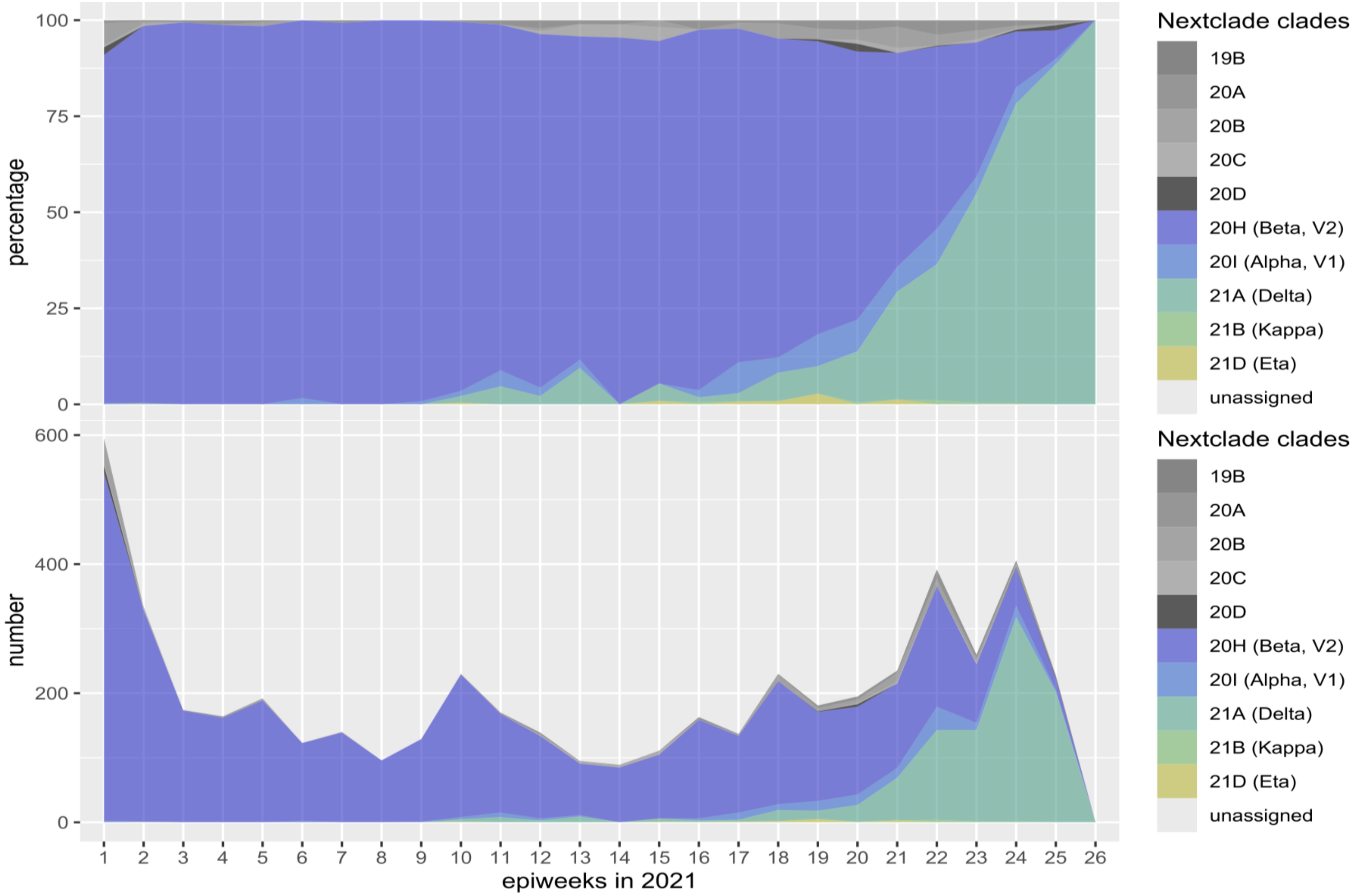




**All provinces, apart from Limpopo (less), Gauteng (less) and KZN (more), have a similar percentage of cases as sequenced genomes.**

Case data from https://www.nicd.ac.za/wp-content/uploads/2021/07/COVID-19-Weekly-Epidemiology-Brief-week-26-2021.pdf

# Distribution and number of clades in South Africa, 2021 (N=5 517)



Sequencing data ending epi-week 26 (ending 3 July 2021)
Currently in epi-week 28 (ending 17 July 2021)

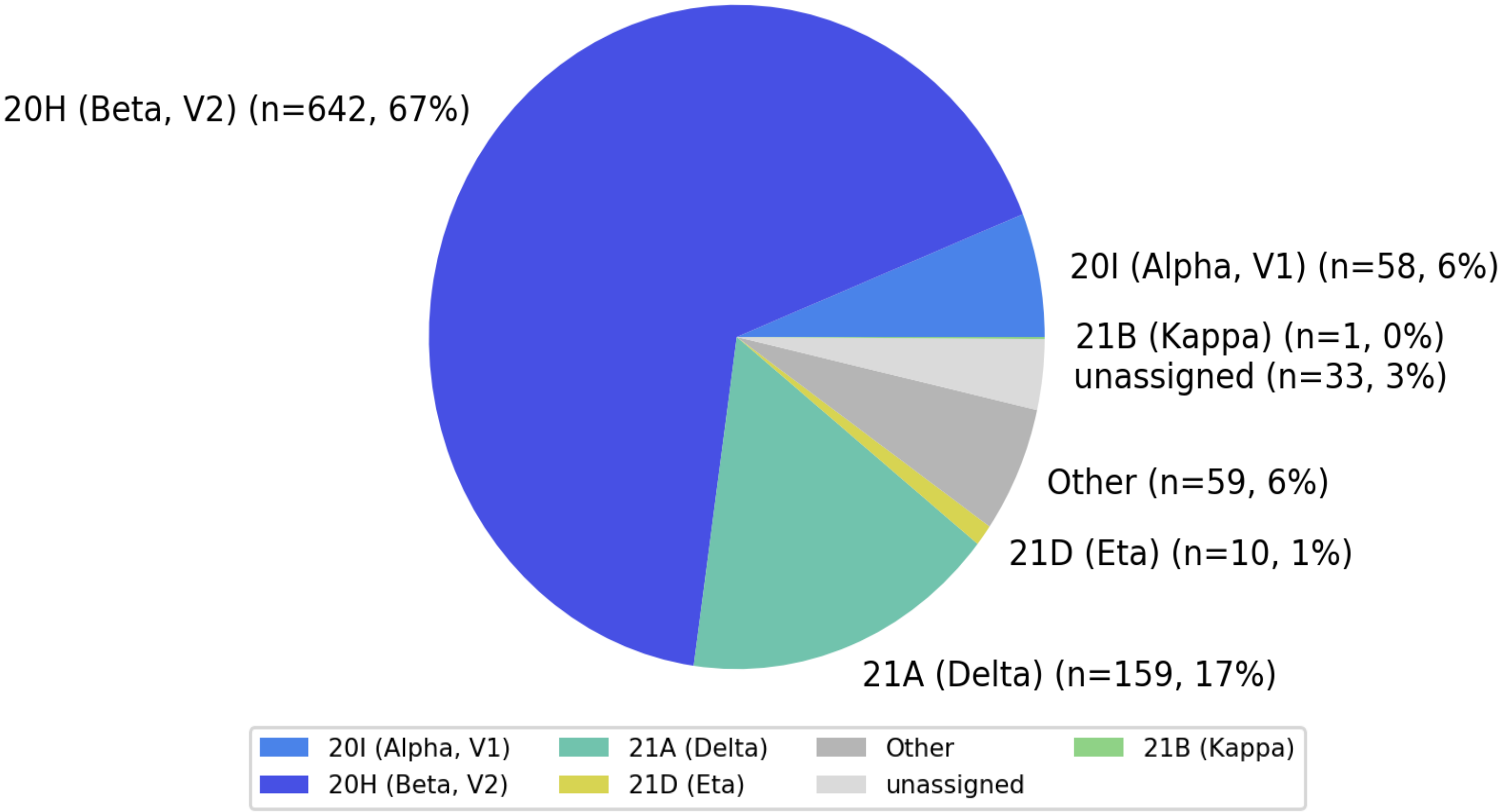
**Alpha, Delta and Eta variant frequency increasing as of the beginning of May (epi-week 18, 2 May). Delta becoming dominant by end of June (317/422, 75% in week 24; 203/230, 88% in week 25)**

# Prevalence of Variants of Concern (VOC) and Variants of Interest (VOI) in May 2021 sequences, South Africa (N=962)

- 91% of sequences are from a VOC (Alpha, Beta, Delta) or VOI (Eta).

- Greater than 10%
  - Beta variant (67%) dominated
  - Delta (17%)

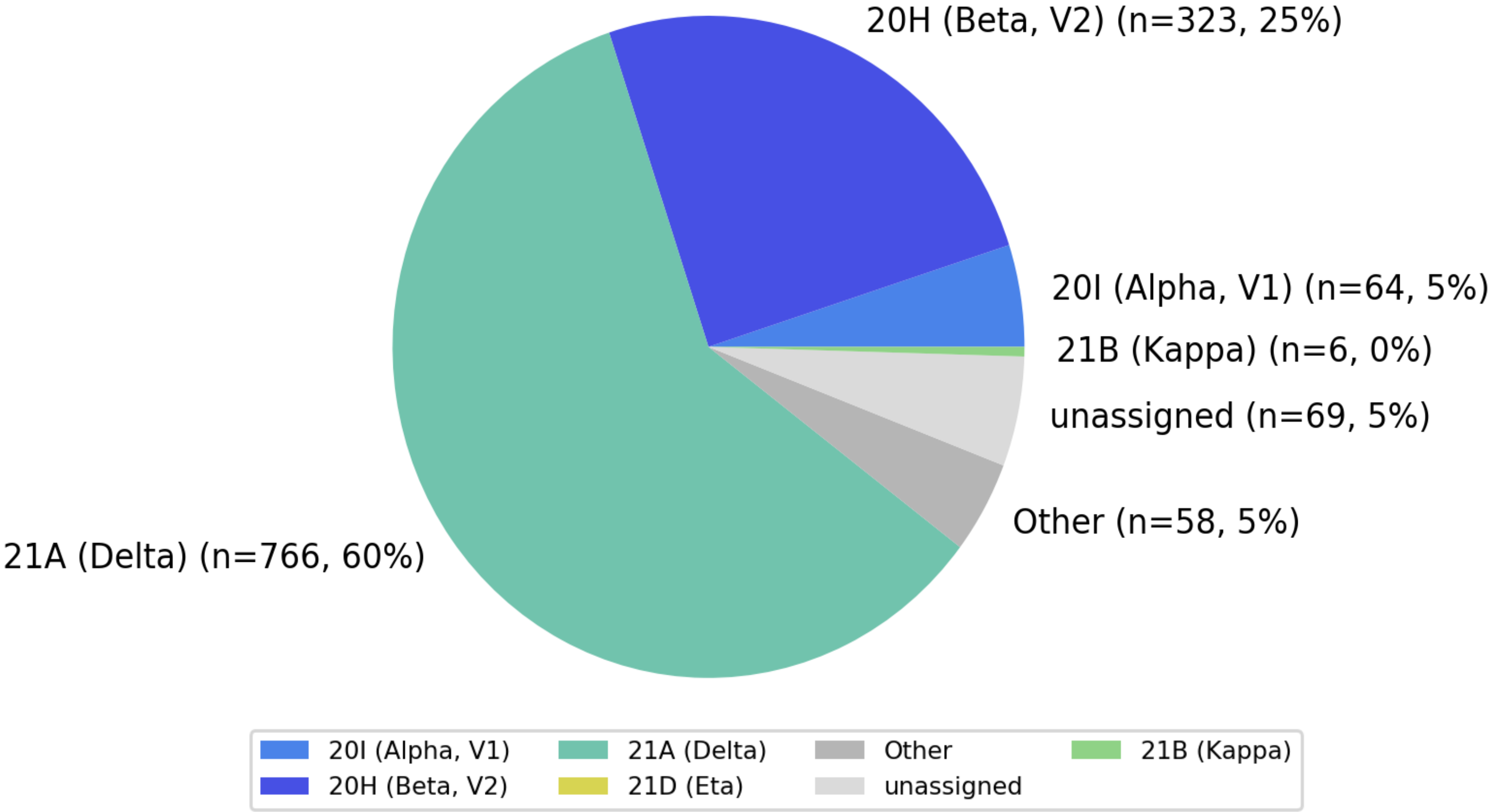
- Less than 10%
  - Alpha (6%).
  - Eta (VOI, 1%)
  - Kappa is present in only one sample (0.001%).



**Overall, the Beta variant dominated in May in South Africa**

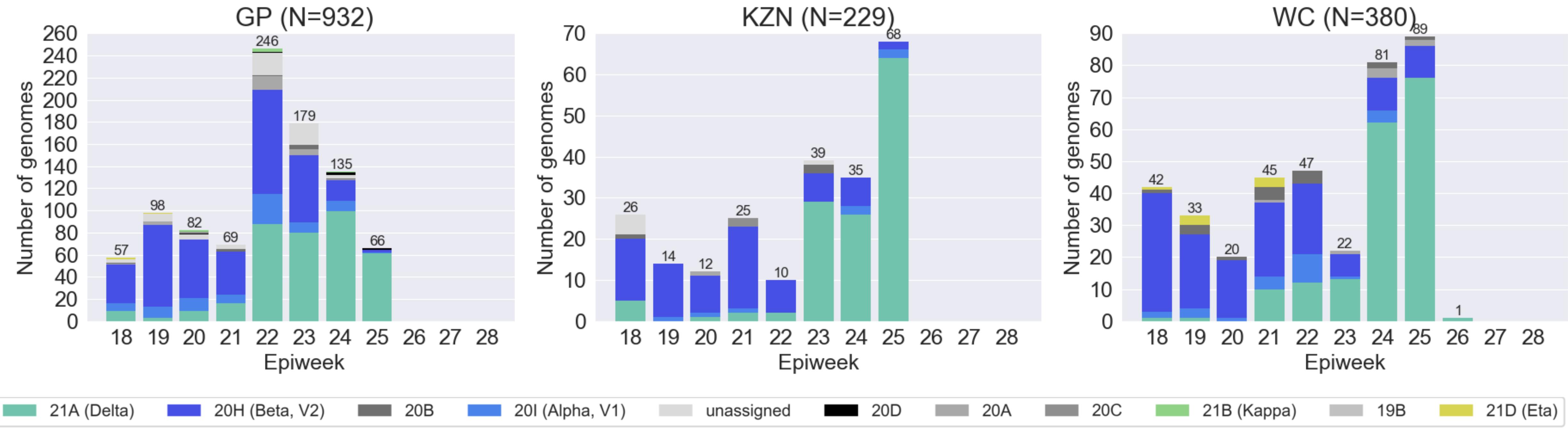
# Prevalence of Variants of Concern (VOC) and Variants of Interest (VOI) in June 2021 sequences, South Africa (N=1 286)

- 90% of sequences are from a VOC (Alpha, Beta, Delta) or VOI (Eta).
- Greater than 10%
  - Delta variant now dominates (60%)
  - Beta variant (25%)
- Less than 10%
  - Alpha (5%).
  - Kappa is present in five sample (0.004%).
  - Eta not yet detected in June



**Overall the Delta variant dominated in June in South Africa**

# Genomes sequenced from specimens collected in May and June 2021 from KwaZulu-Natal, Gauteng, Western Cape Provinces



**Gauteng**

- Delta is present in early weeks (May) but increases in later weeks (June)
- Eta detected in May but is not present in June. Kappa detected in May and June

**KwaZulu-Natal**

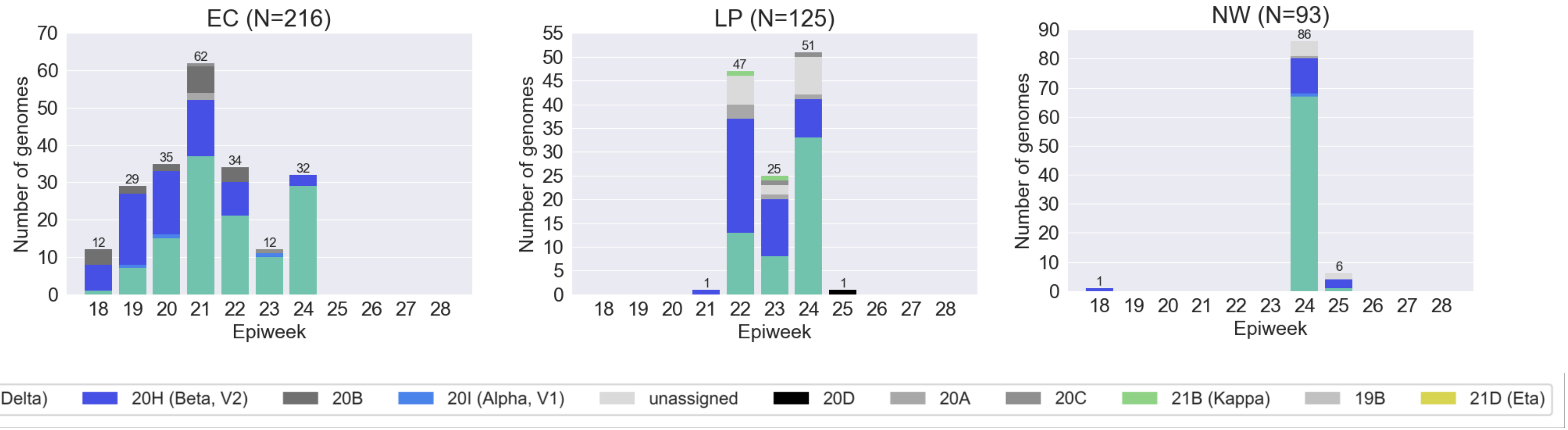
- Delta is proportionately higher compared to GP and WC until epiweek 25
- Eta was not detected

**Western Cape**

- Beta dominates until week 23, when Delta increases
- Eta is detected in higher numbers than in GP and KZN, but not detected in most recent weeks

**Beta dominates in all provinces in May, however following its first detection in week 18, Delta rapidly begins to dominate in all three provinces by mid-June**

# Genomes sequenced from specimens collected in May and June 2021 from Eastern Cape, Limpopo, Mpumalanga and North-West Provinces



**Eastern Cape**

- Delta detected in early May and rapidly increases to predominate by end of May
- Alpha detected at low frequency in May and only once in June

**Limpopo**

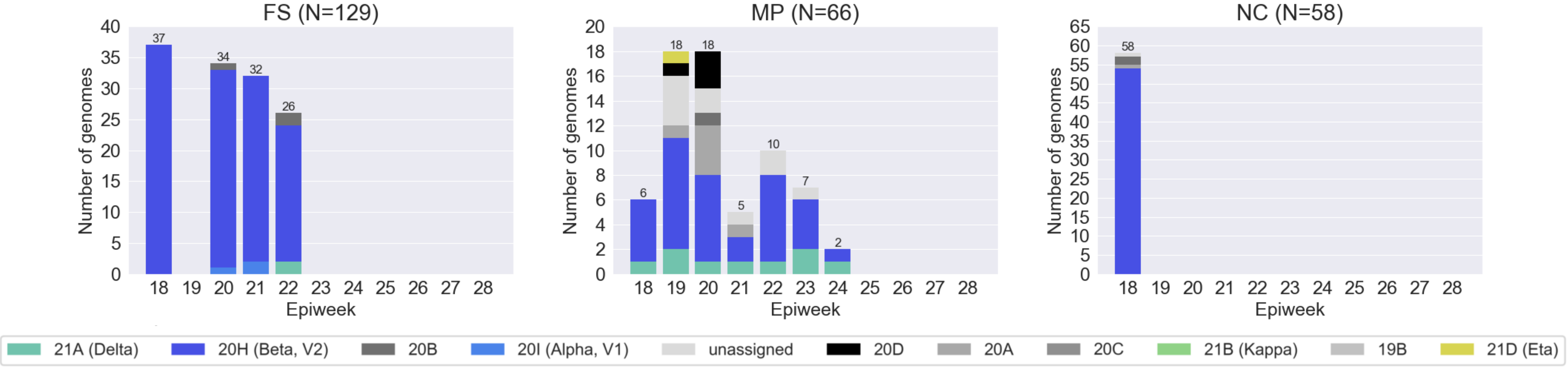
- Delta detected at the end of May and predominates by early June
- Kappa detected at low frequency in May and early June

**North-West**

- Delta detected at high proportion in June, but additional time points required for sequencing

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

# Genomes sequenced from specimens collected in May and June 2021 from Free State and Northern Cape Provinces



**Free State**

- Delta has been detected at low frequency in June
- Recent sequences are required to determine whether Delta has begun to dominate

**Mpumalanga**

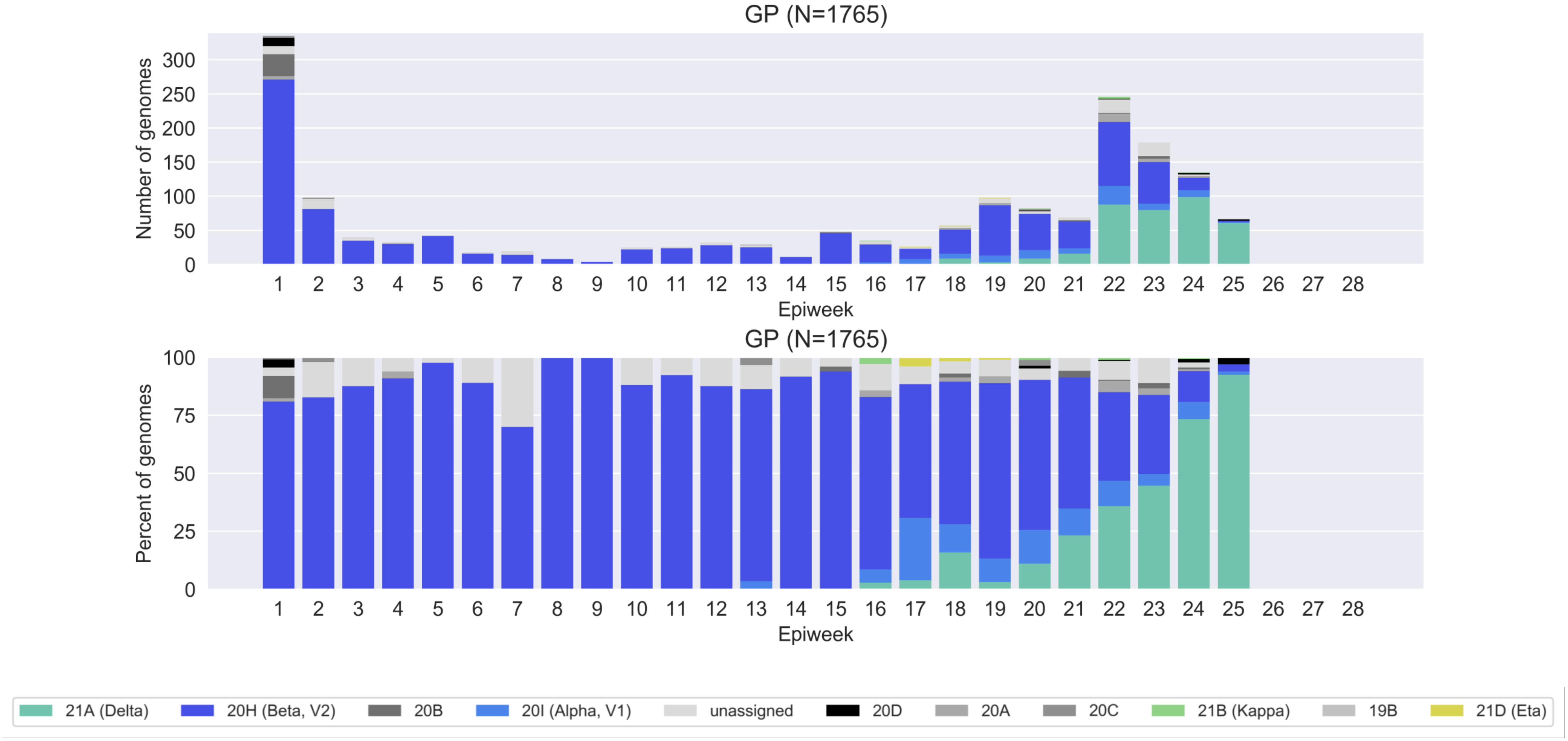
- Delta detected in early May, however increased specimen numbers required to estimate predominance of a particular variant

**Northern Cape**

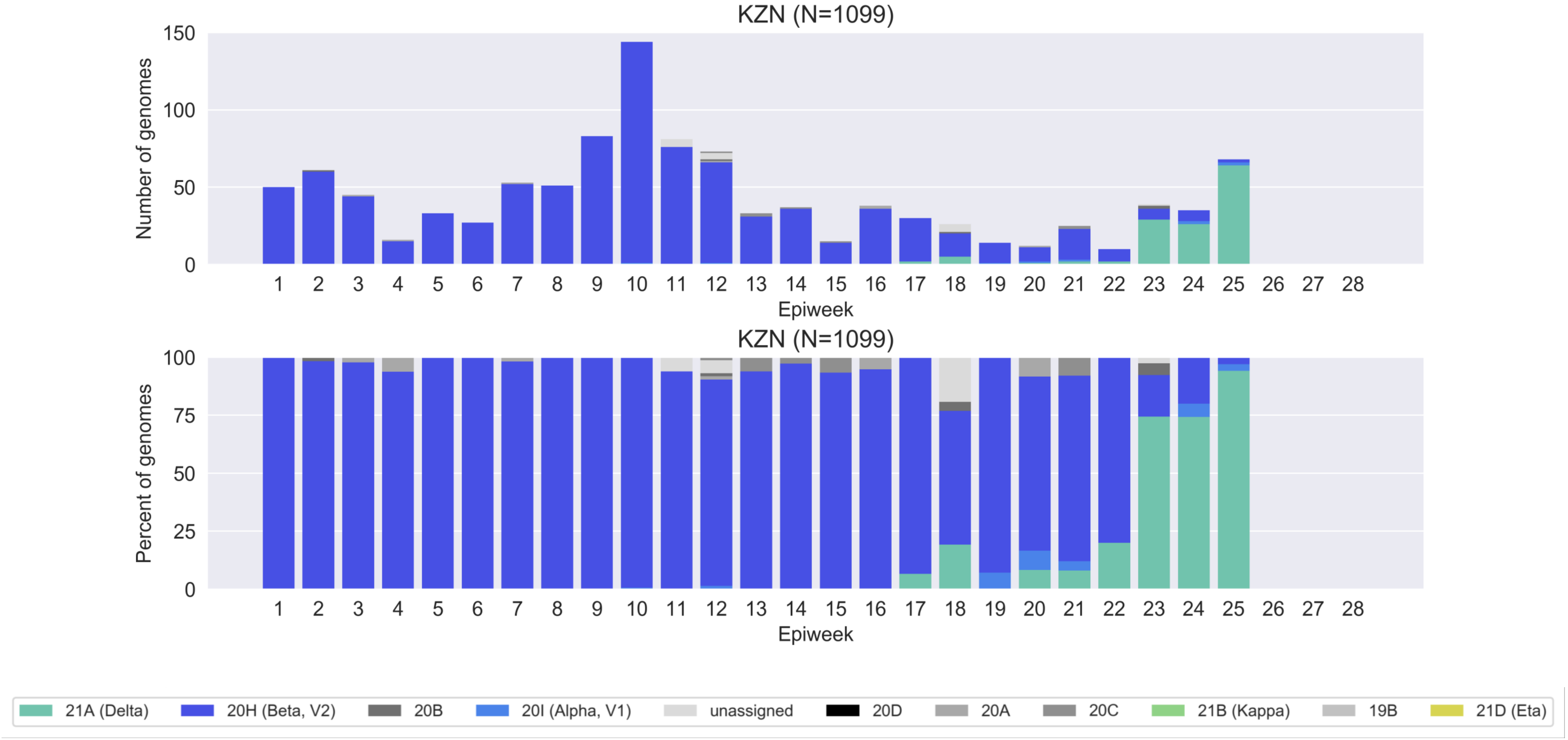
- Delta has been detected in March (not shown, see later slides) in Northern Cape, but the Beta variant continued to cause a significant number of infections
- Recent sequences are required to determine whether Delta has begun to dominate

**Recent data is required from these provinces to estimate the frequency of the Delta variant**

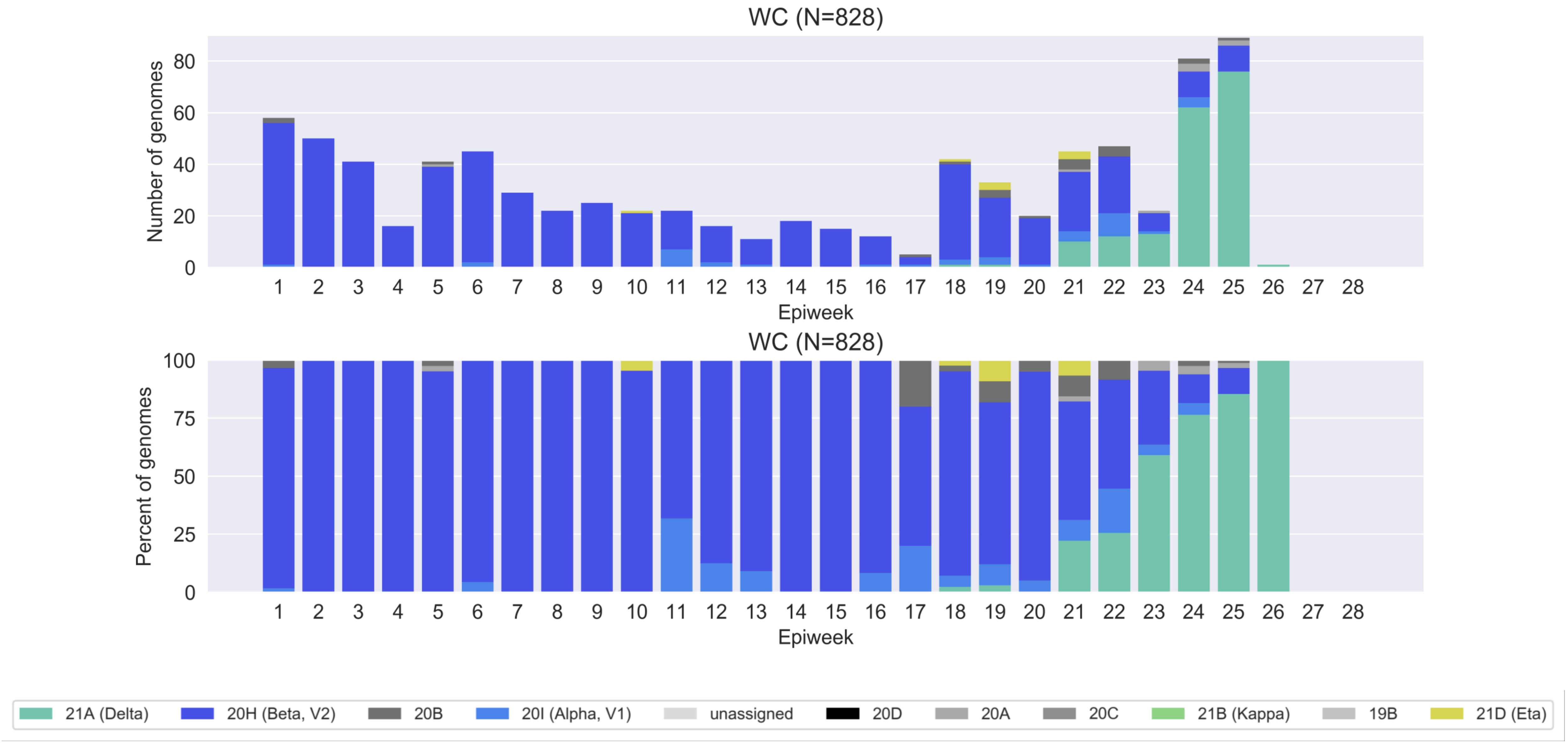
# Gauteng Province, 2021, n = 1,765



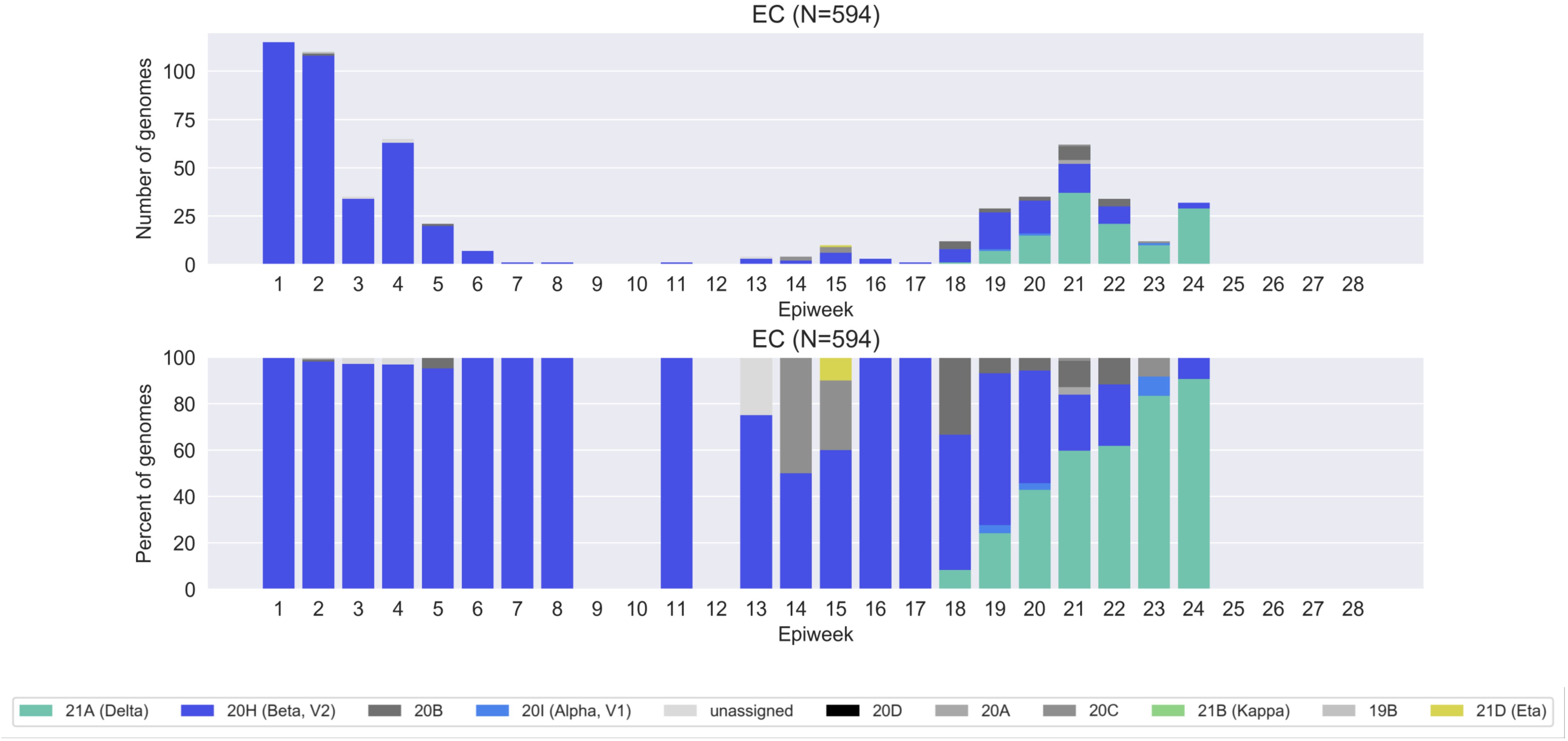
# KwaZulu-Natal Province, 2021, n = 1,099



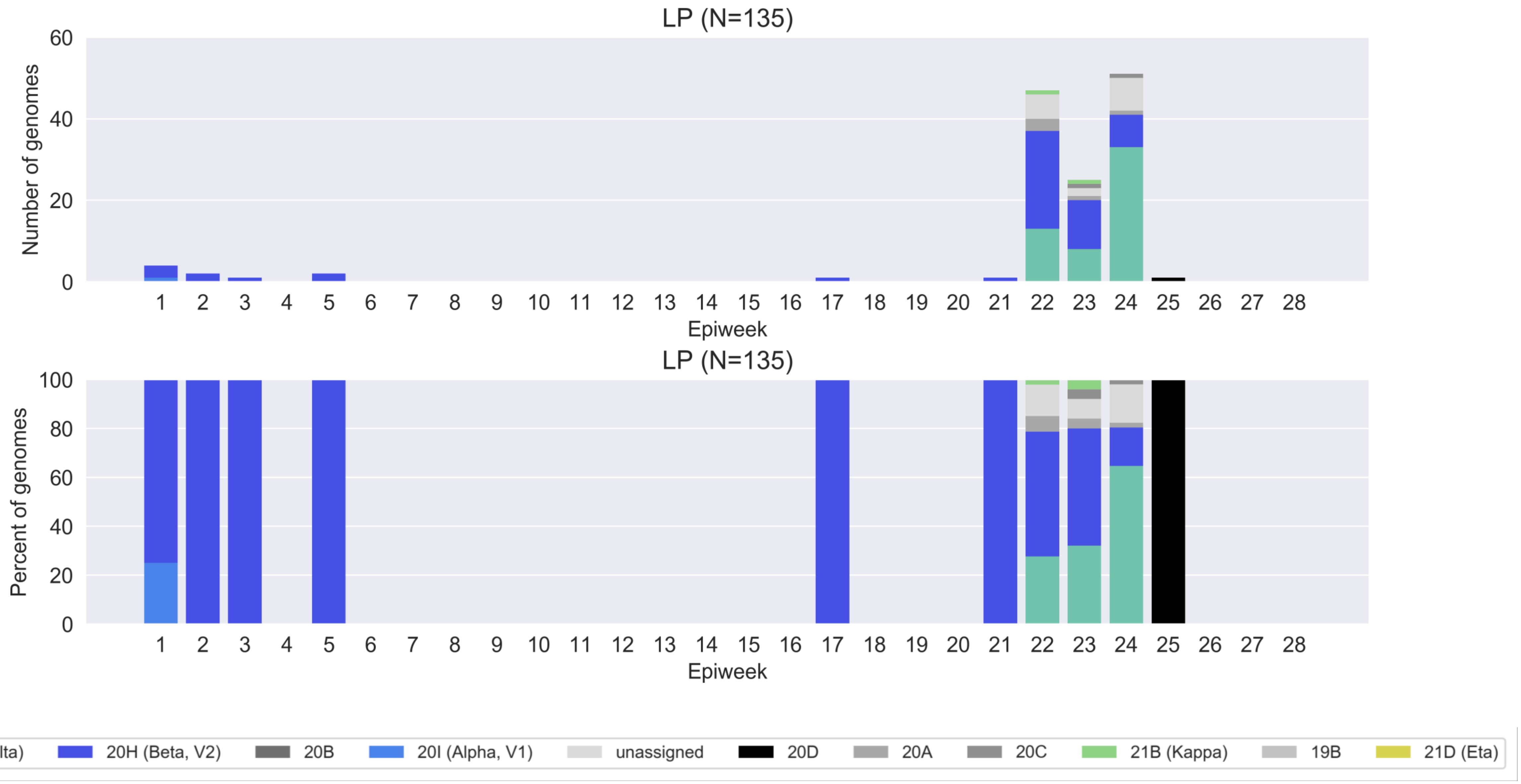
# Western Cape Province, 2021, n =828



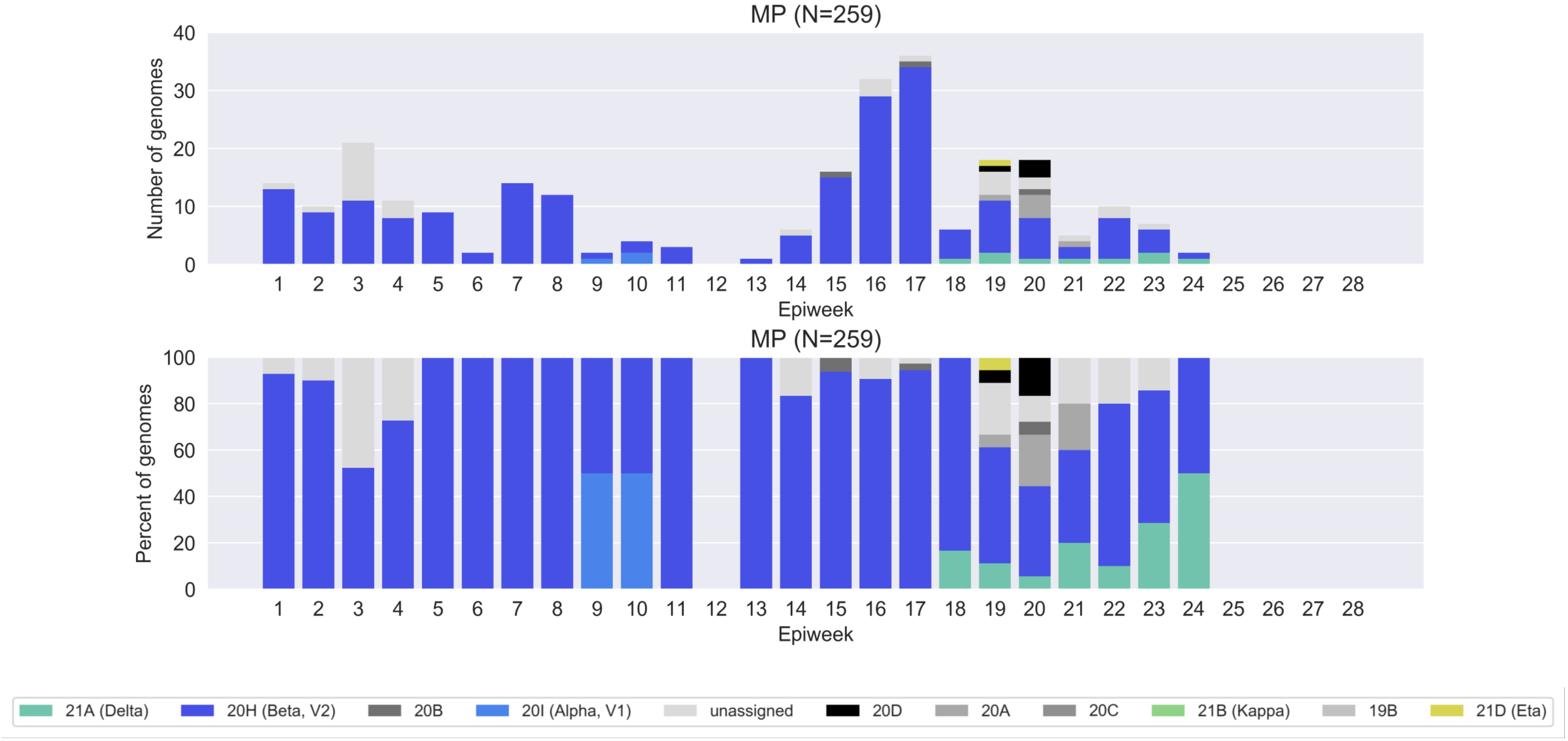
# Eastern Cape Province, 2021, n =594



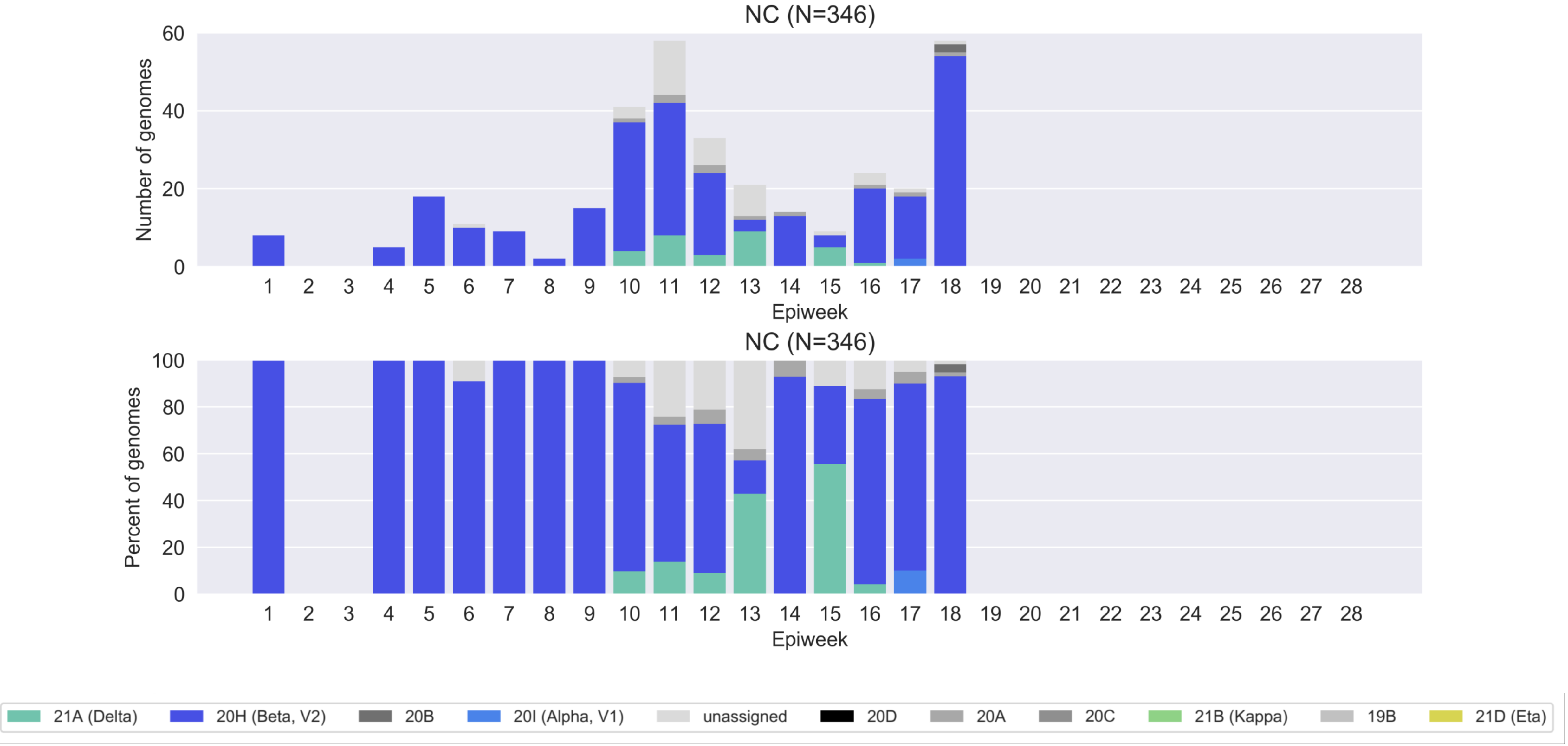
# Limpopo Province, 2021, n = 135



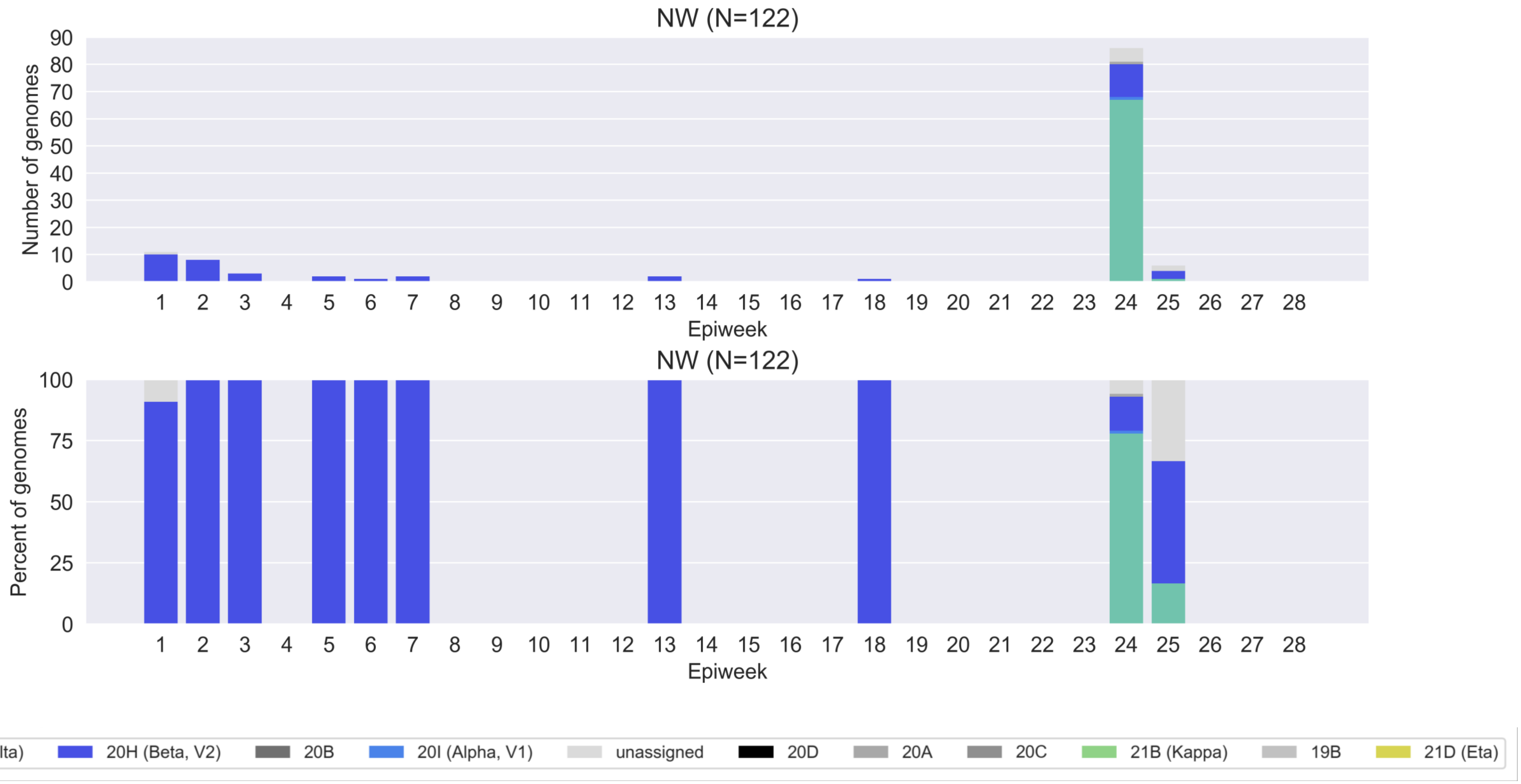
# Mpumalanga Province, 2021, n=259



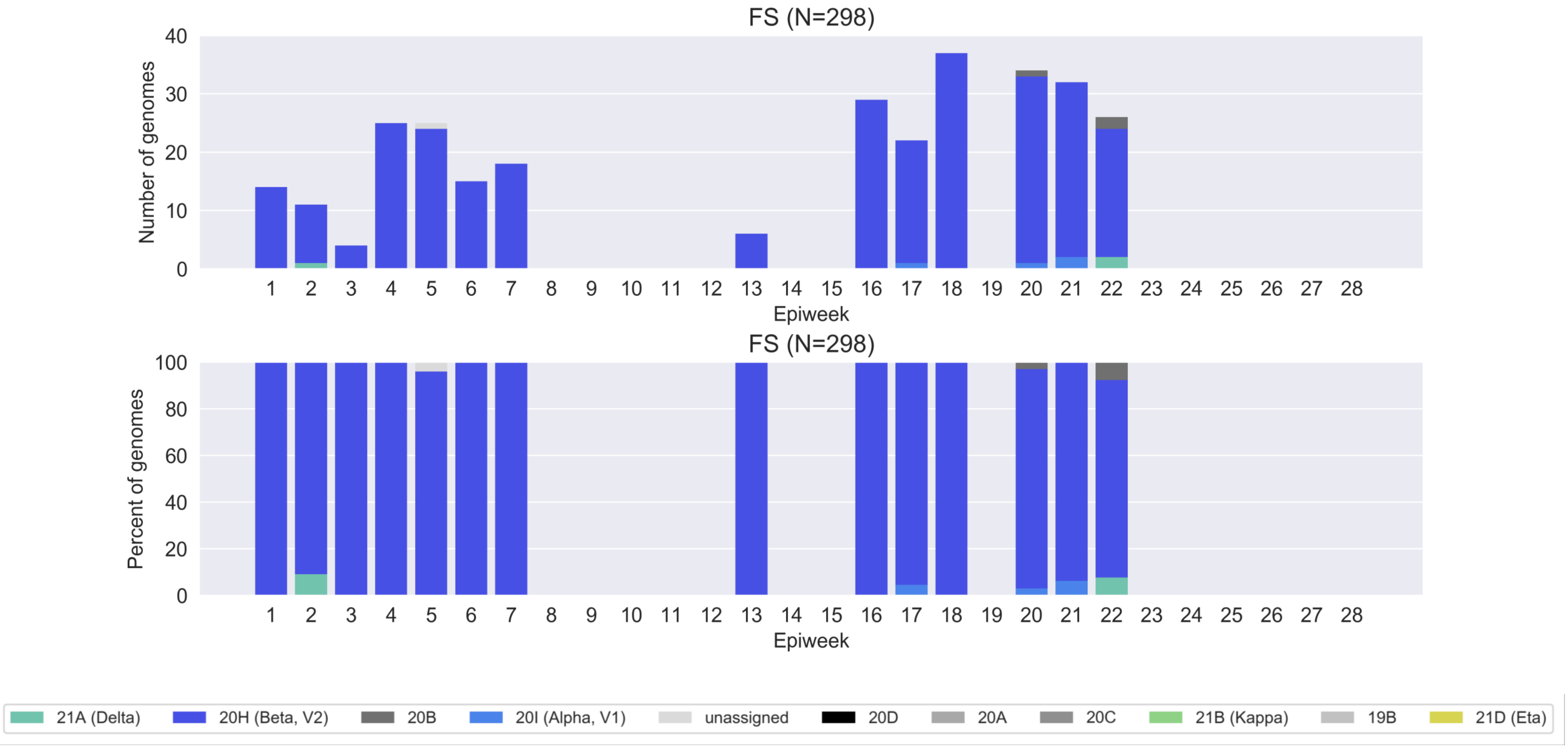
# Northern Cape Province, 2021, n = 346



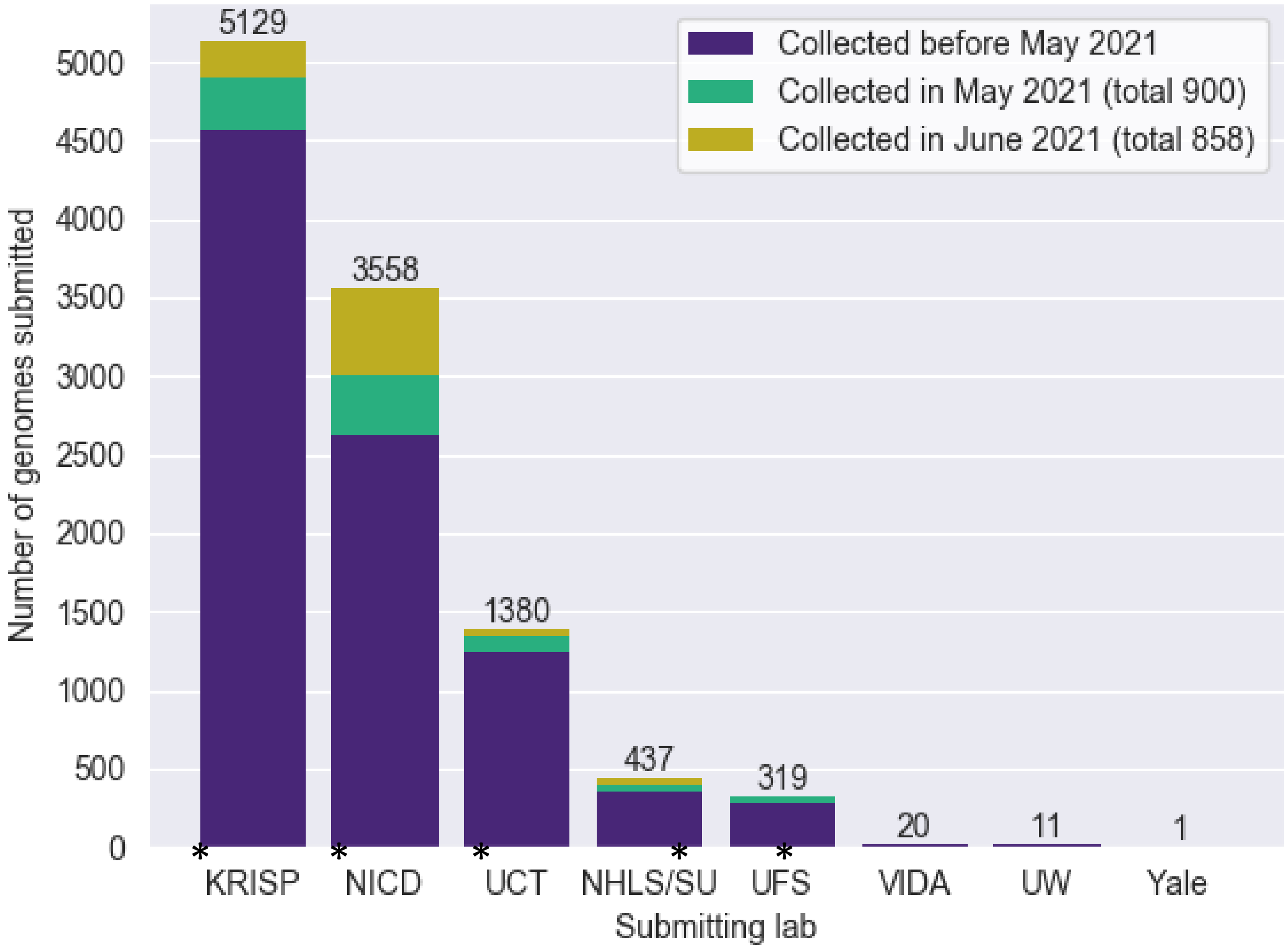
# North West Province, 2021, n = 122



# Free State Province, 2021, n = 298



# South African genomes submitted per sequencing lab, 2020 and 2021 (N=11 347)

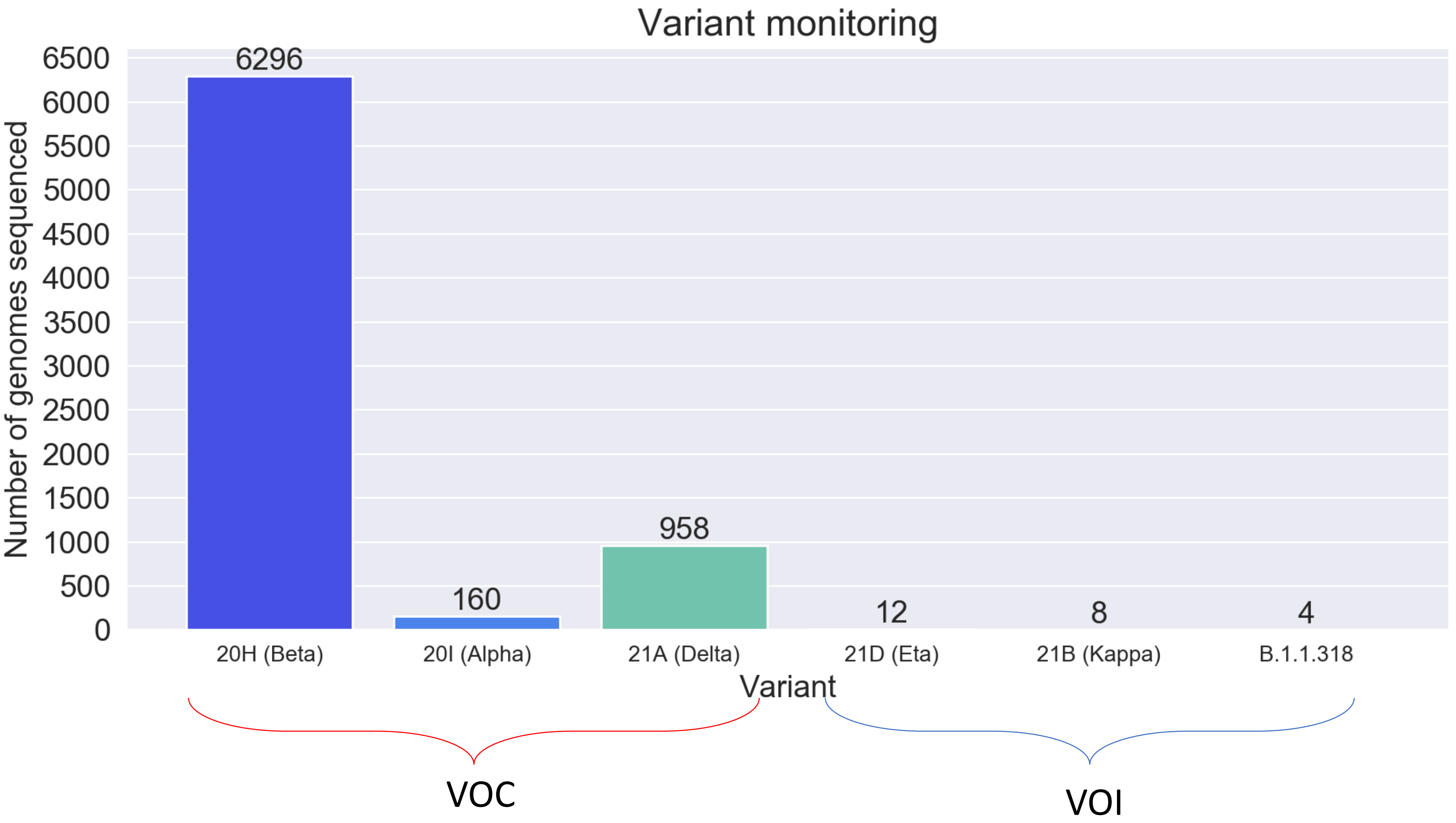


*NGS-SA laboratories

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

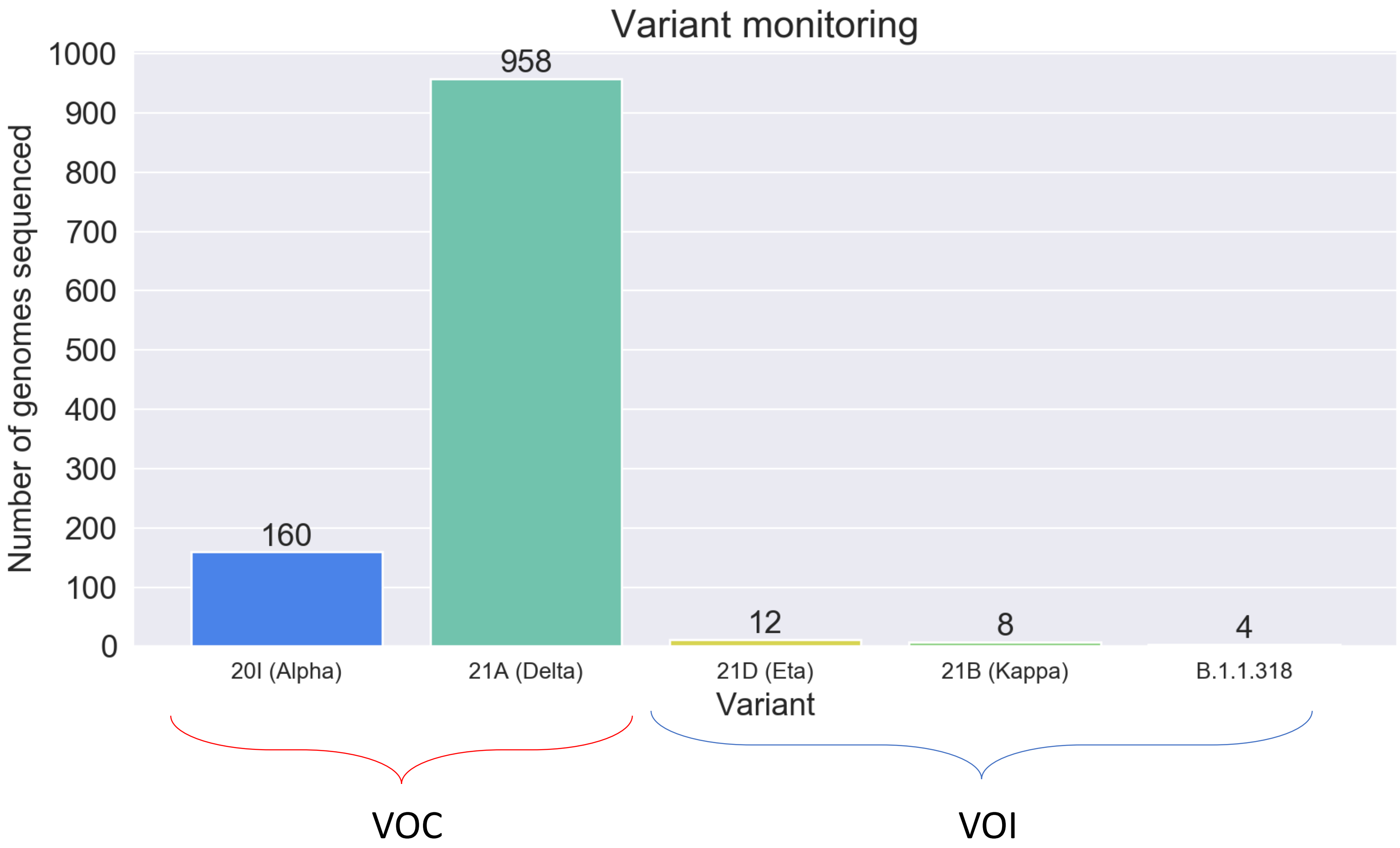
# Monitoring VOCs and VOIs in South Africa (N=7 438, 66% of all sequences)

## (2020 – 2021)



**Variant monitoring has detected a number of VOCs and VOIs. Within these, no unusual mutations have yet been detected.**

# Monitoring VOCs and VOIs in South Africa (excluding 20H, Beta; 2020 – 2021)



**Variant monitoring has detected a number of VOCs and VOIs. Within these, no unusual mutations have yet been detected. Lambda variant not yet detected**

# Summary

- In June, Delta increases significantly and dominates in most provinces with recent data available
- Variant diversity appears to have decreased with the dominance of Delta
- Lambda has not been detected in South Africa

# NICD Acknowledgements

- **Thabo Mohale**
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- **Lynn Morris**
- **Jinal Bhiman**

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- Anneta Naidoo
- Raymond Rott
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**NICD COVID-19 response team**
**COVID Incident Management Team**

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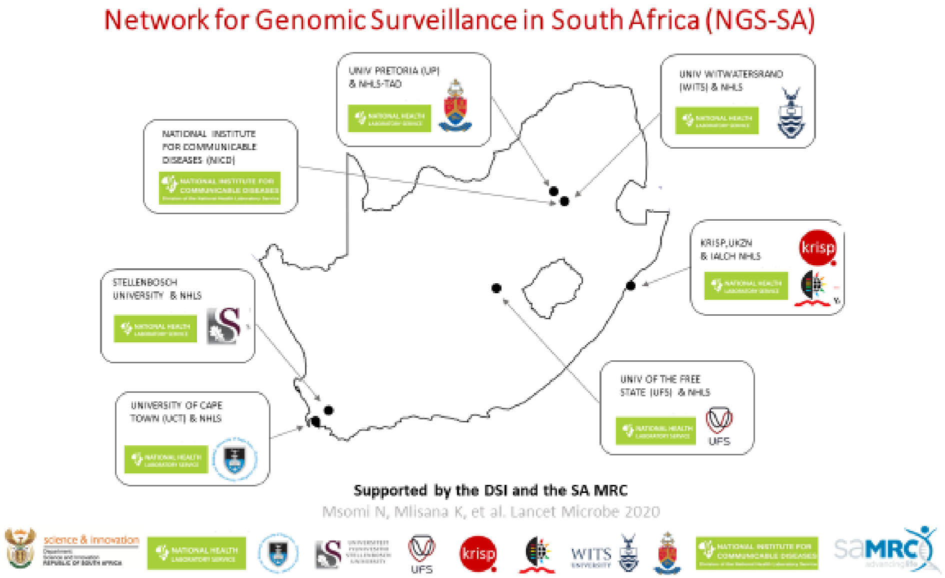
# Multi-institute, multi-disciplinary NGS team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Supported by the DSI and the SA MRC

Msomi N, Mlisana K, et al. Lancet Microbe 2020

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UFS

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INYUVESI YAKWAZULU-NATALI

NATIONAL HEALTH LABORATORY SERVICE

# 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 the NICD (or 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 (NICD 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.)