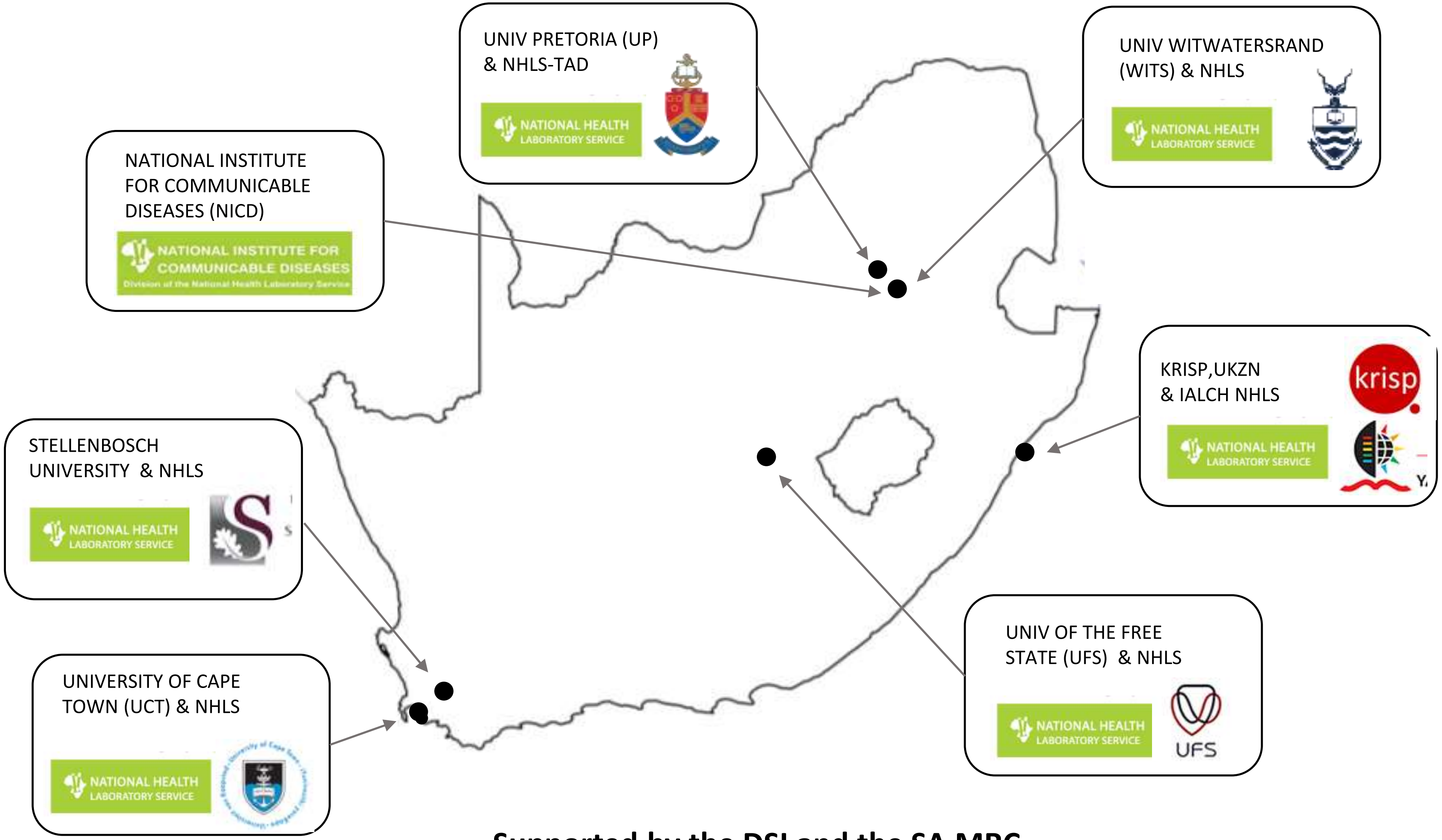
NGS-SA SARS-CoV-2 Sequencing Update

7 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)



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

The genomic data presented here are based on South African SARS-CoV-2 sequence data downloaded from GISAID (www.gisaid.org) on 06 July at 12h00

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 +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/

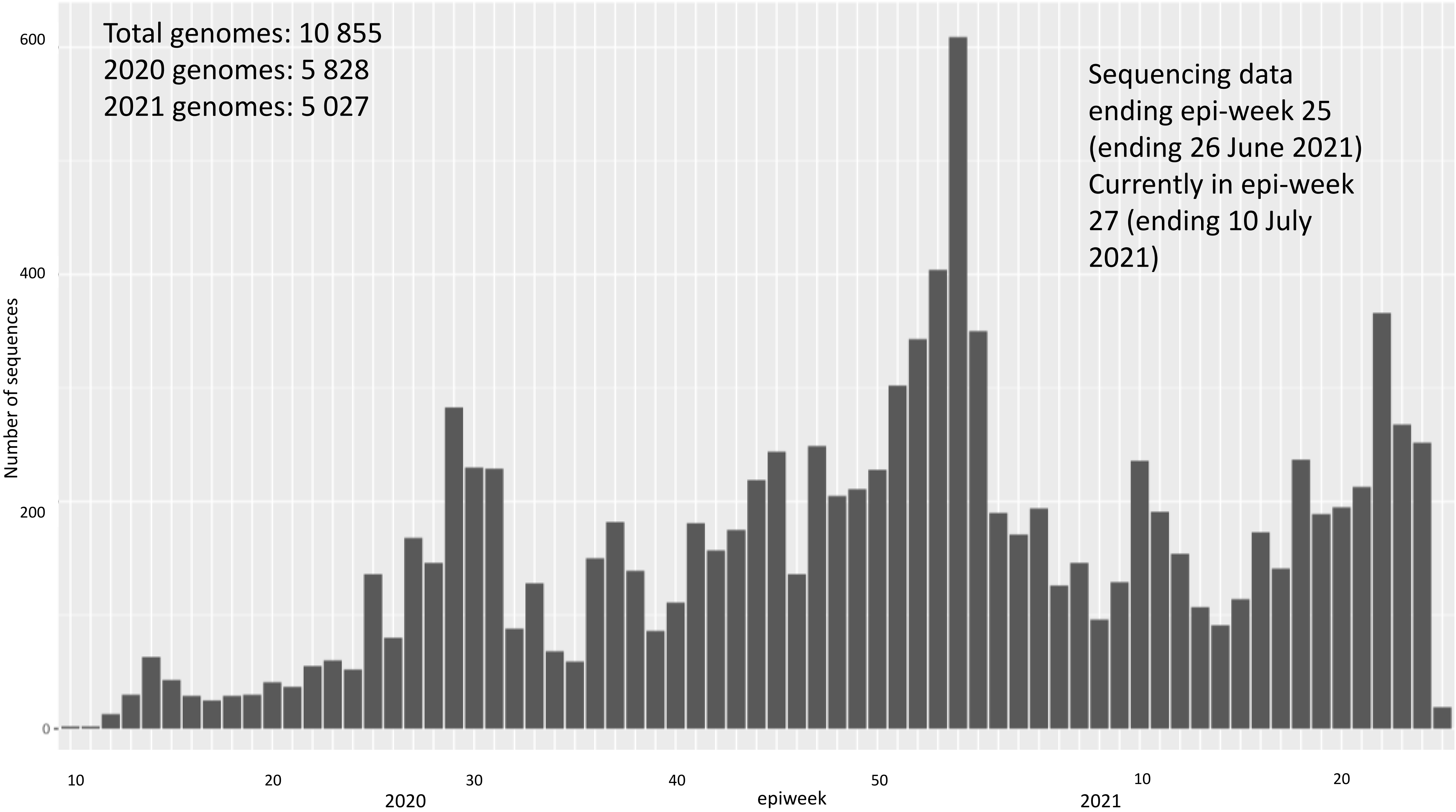
*Notable spike (S) amino acid changes under monitoring, which are currently reported in a minority of sequenced samples

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=10 855*, downloaded 6 July)

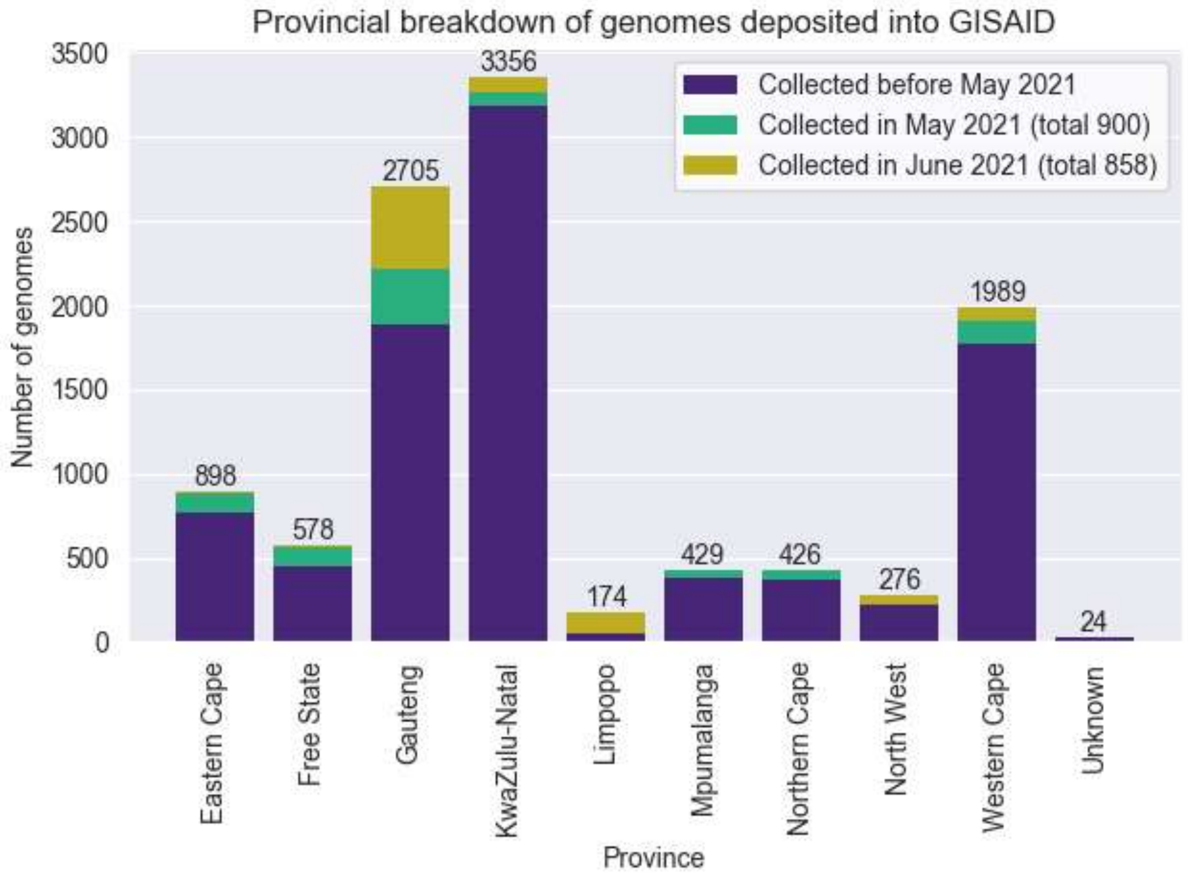


Total genomes: 10 855
2020 genomes: 5 828
2021 genomes: 5 027

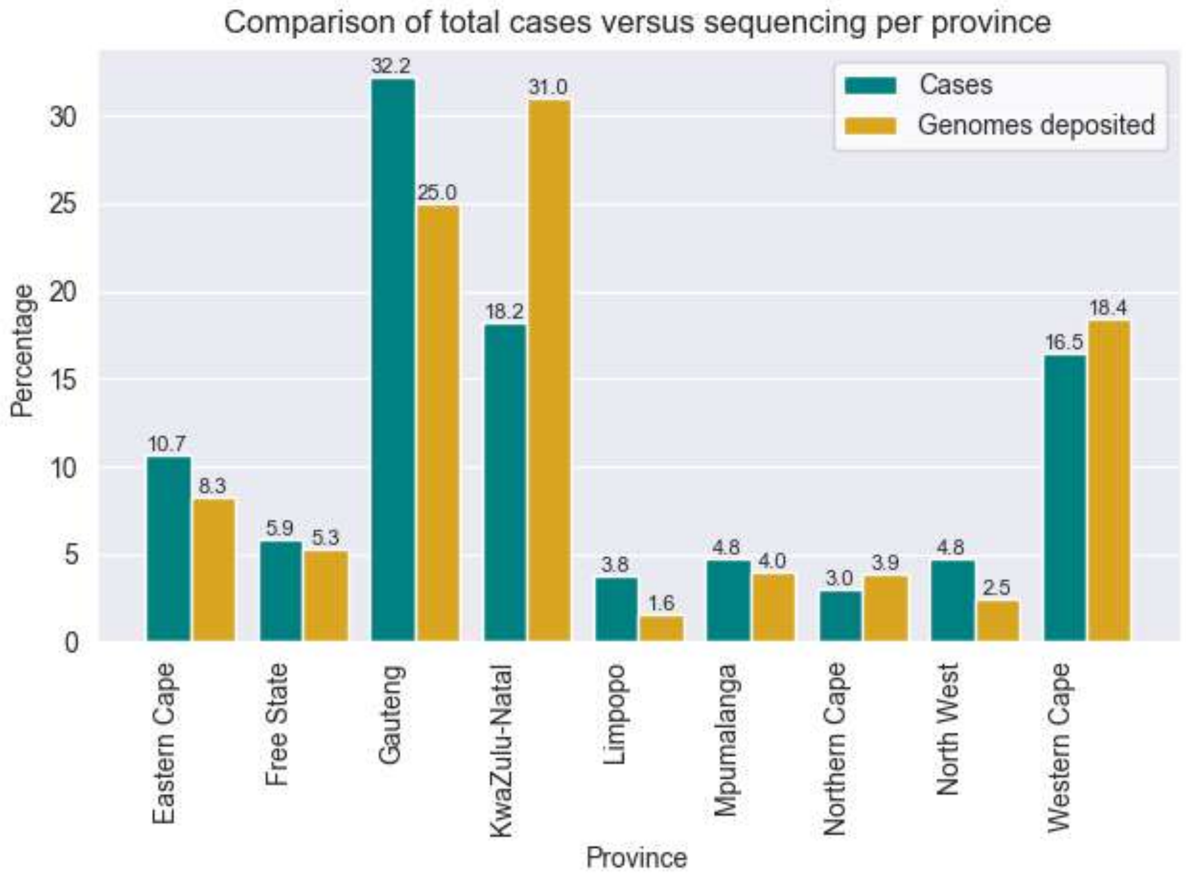
Sequencing data ending epi-week 25 (ending 26 June 2021) Currently in epi-week 27 (ending 10 July 2021)

*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=10 855)



Provincial breakdown of genomes deposited into GISAID

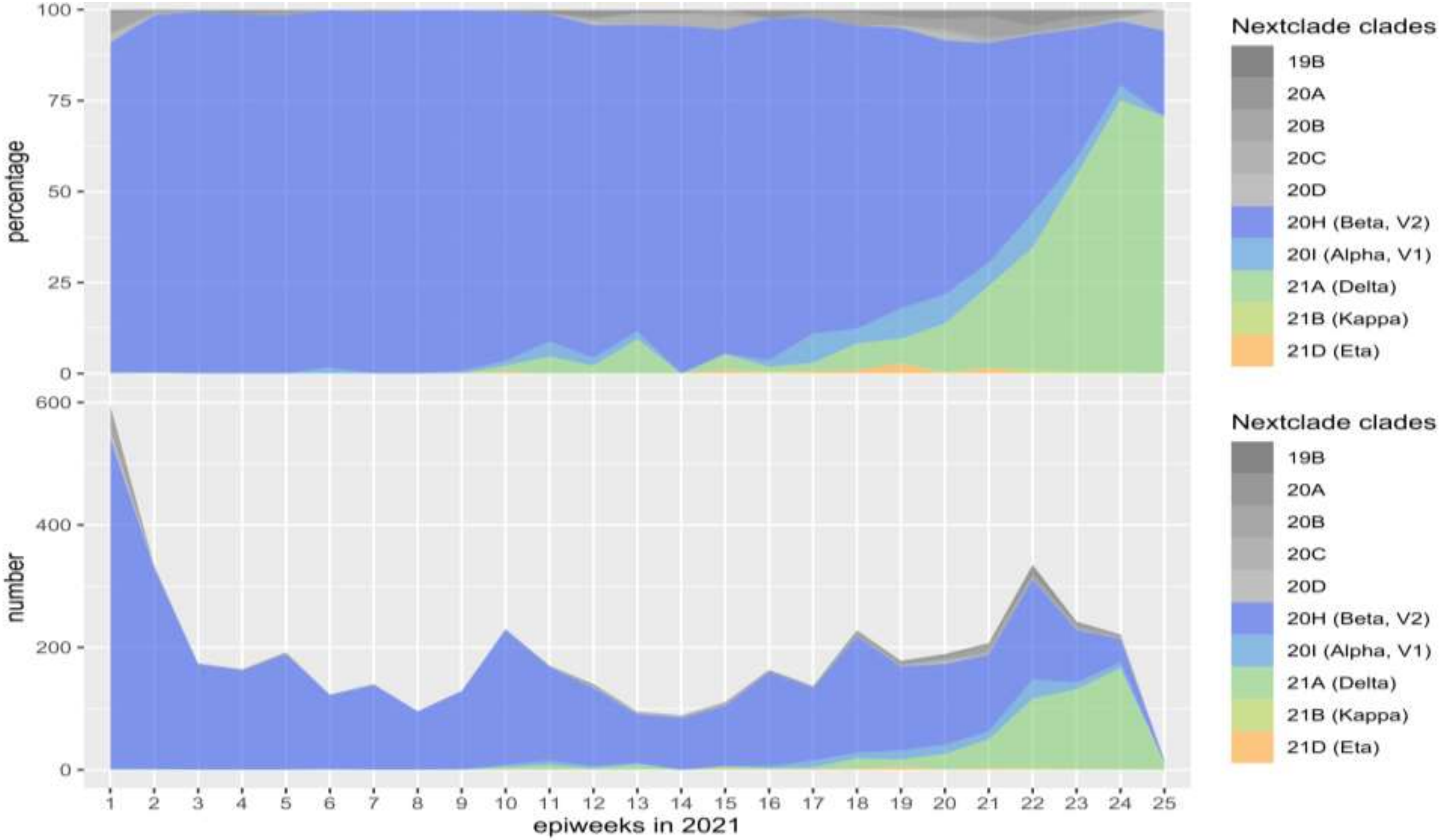


Comparison of total cases versus sequencing per province

All provinces, apart from Limpopo (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-25-2021.pdf

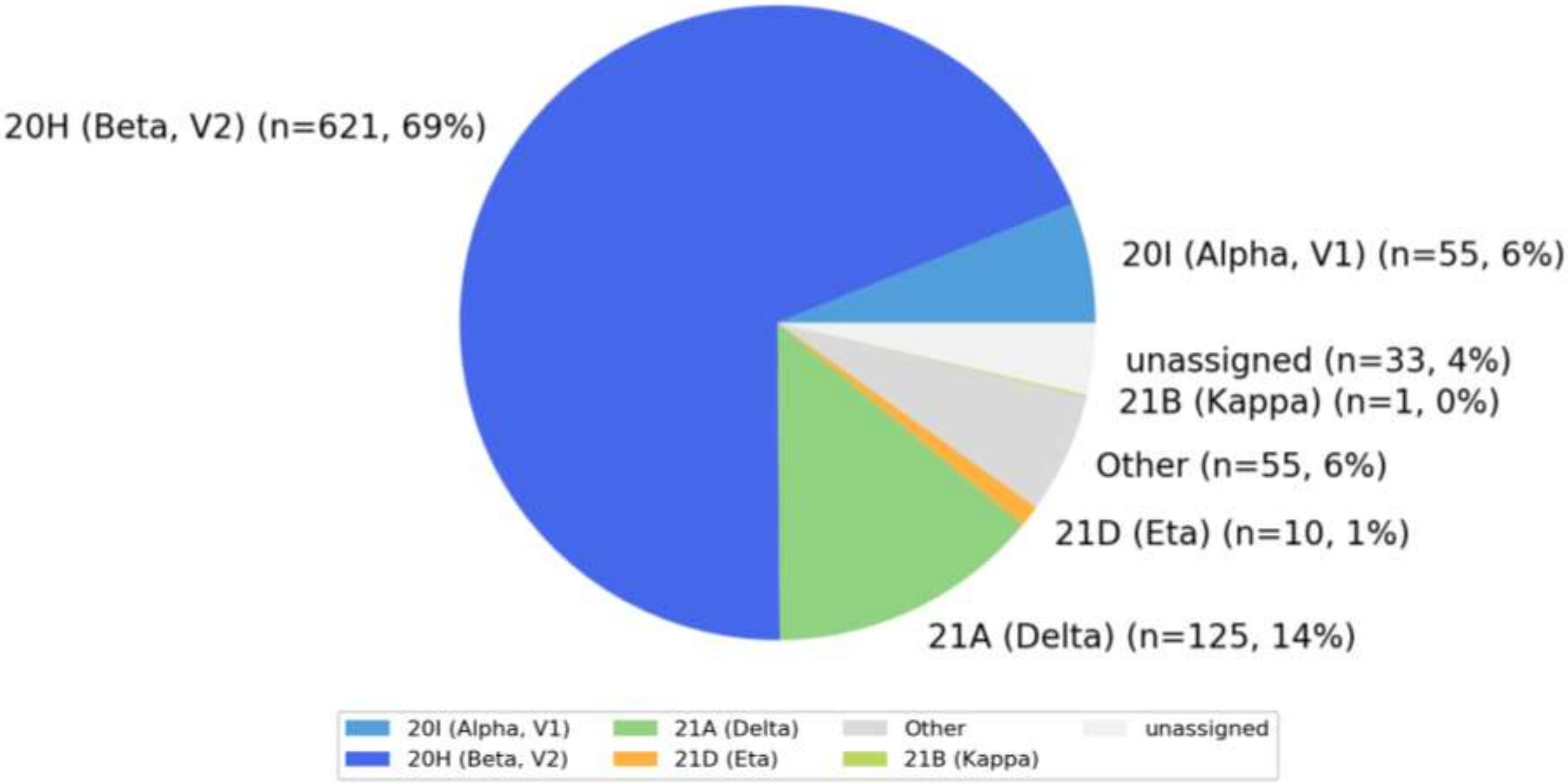
Distribution and number of clades in South Africa, 2021 (N=5 027)



Sequencing data ending epi-week 25 (ending 26 June 2021)
Currently in epi-week 27 (ending 10 July 2021)

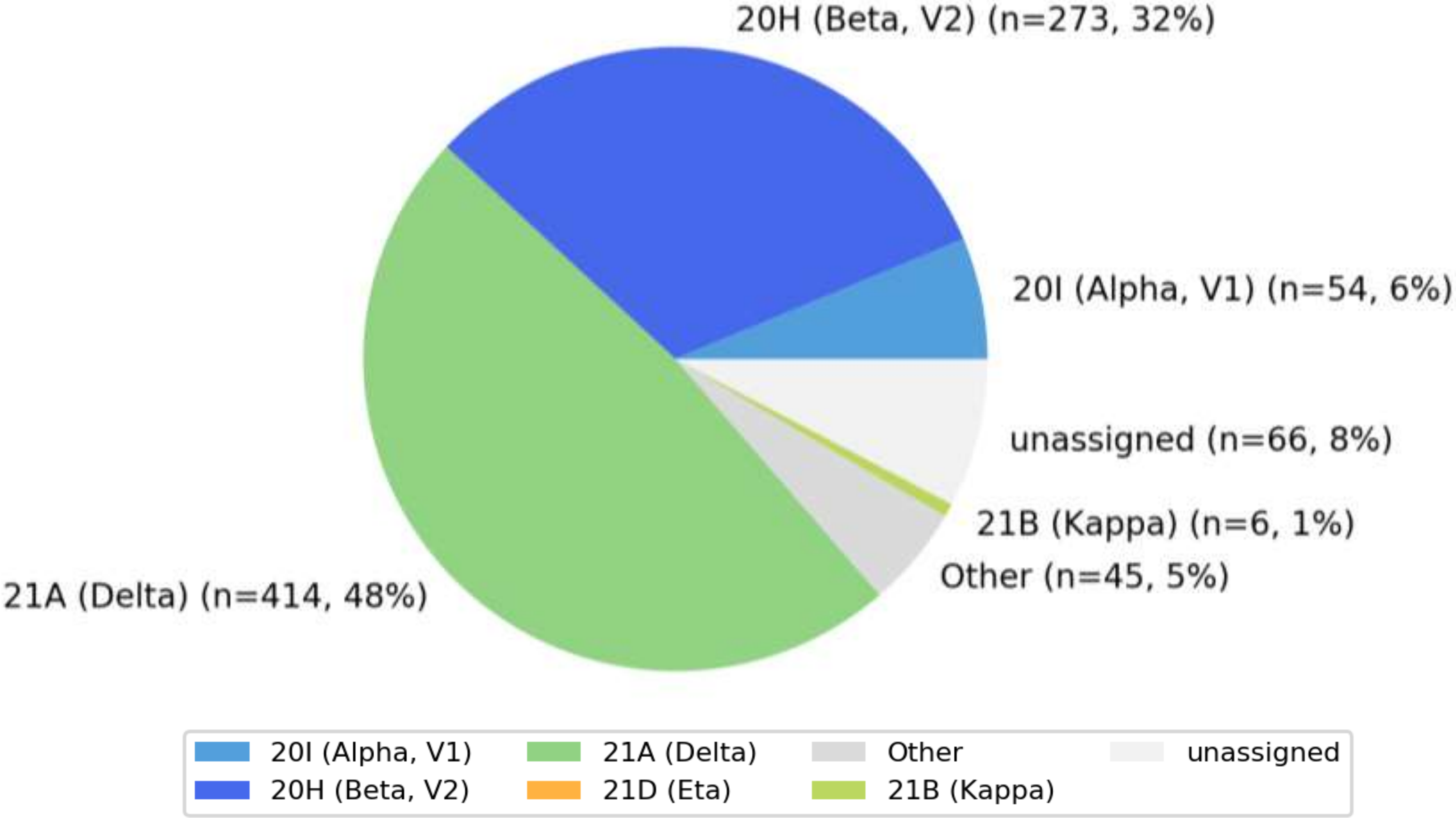
Alpha, Delta and Eta variant frequency increasing as of the beginning of May (epi-week 18, 2 May). Delta becoming dominant by end of June (175/237, 74% in week 24; 12/18, 67% in week 25; calculated using sequences with a clade assignment)

Prevalence of Variants of Concern (VOC) and Variants of Interest (VOI) in May 2021 sequences, South Africa (N=900)



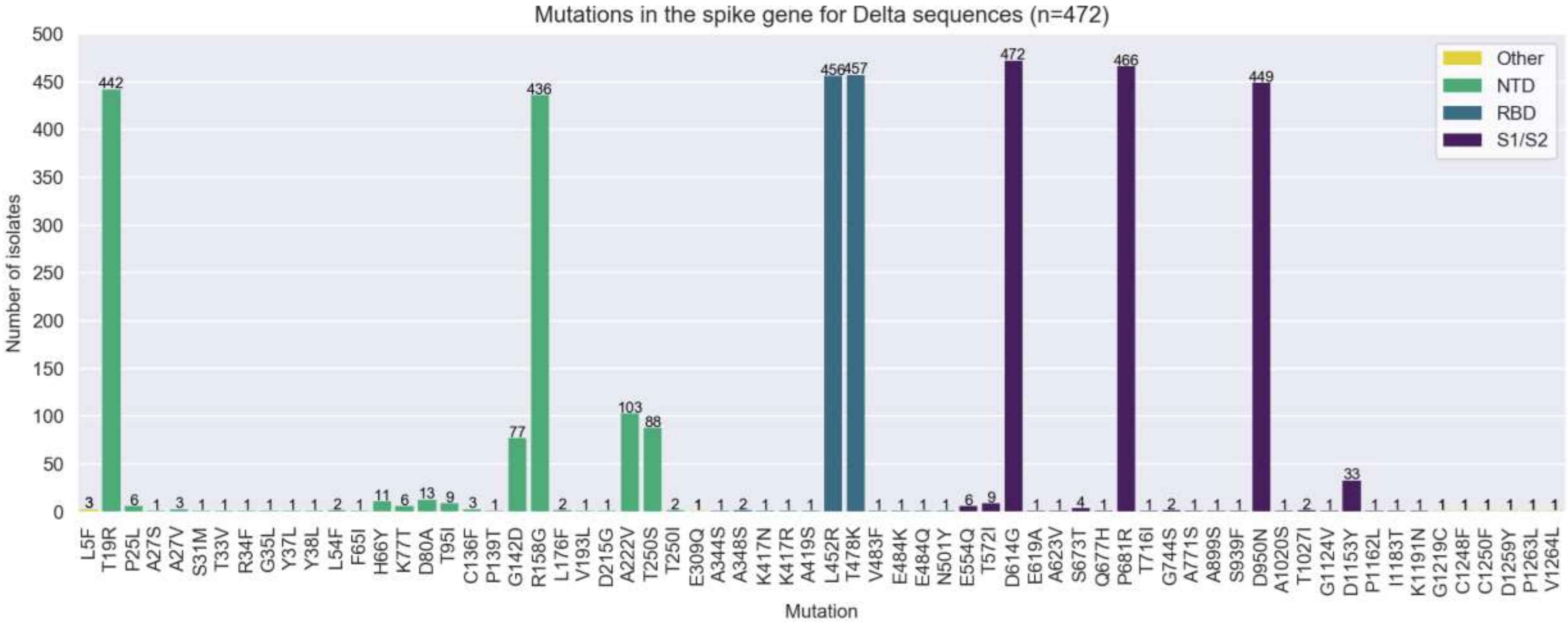
90% of sequences are from a VOC (Alpha, Beta, Delta) or VOI (Eta). Sequences were still dominated by the Beta variant (69%), followed by Delta (14%) and then Alpha (6%). Eta (VOI, 1%) was present in a small percentage of samples. Kappa is present in only one sample (0%).

Prevalence of Variants of Concern (VOC) and Variants of Interest (VOI) in June 2021 sequences, South Africa (N=858)

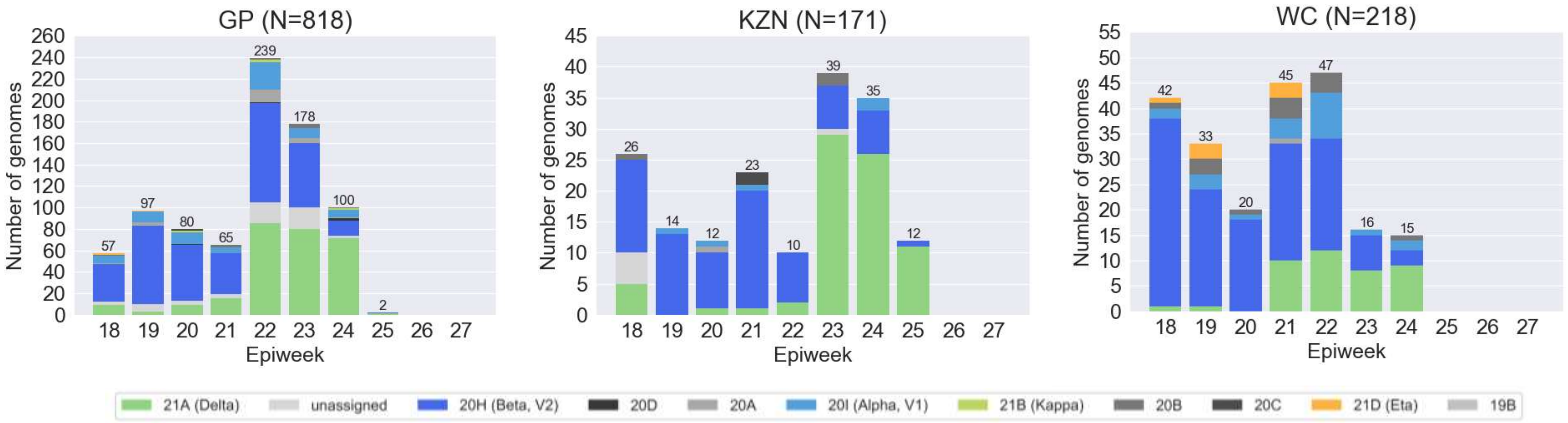


87% of sequences are from a VOC (Alpha, Beta, Delta) or VOI (Eta). The Delta variant now dominates (48%), followed by the Beta variant (32%). Alpha has remained at 6%, and Kappa has increased to (1%). Eta (VOI) has not yet been identified in June.

Delta spike mutations



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



Beta dominates in all provinces in earlier epiweeks; Delta detected from week 18, dominating in all three provinces by weeks 24 and 25

Gauteng

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

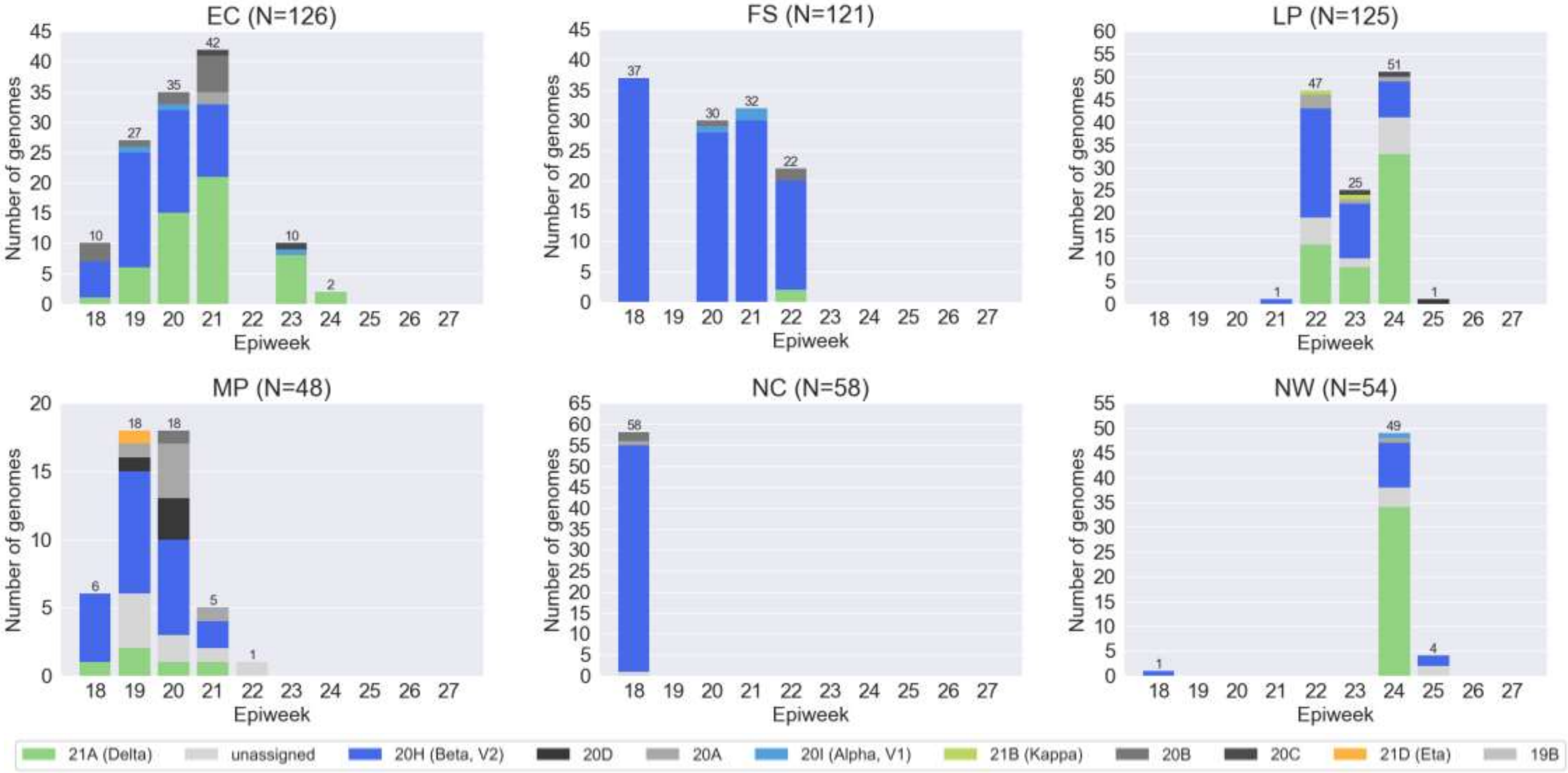
KwaZulu Natal

- **Delta is proportionately higher compared to GP and WC.**
- **Eta** was not detected.

Western Cape

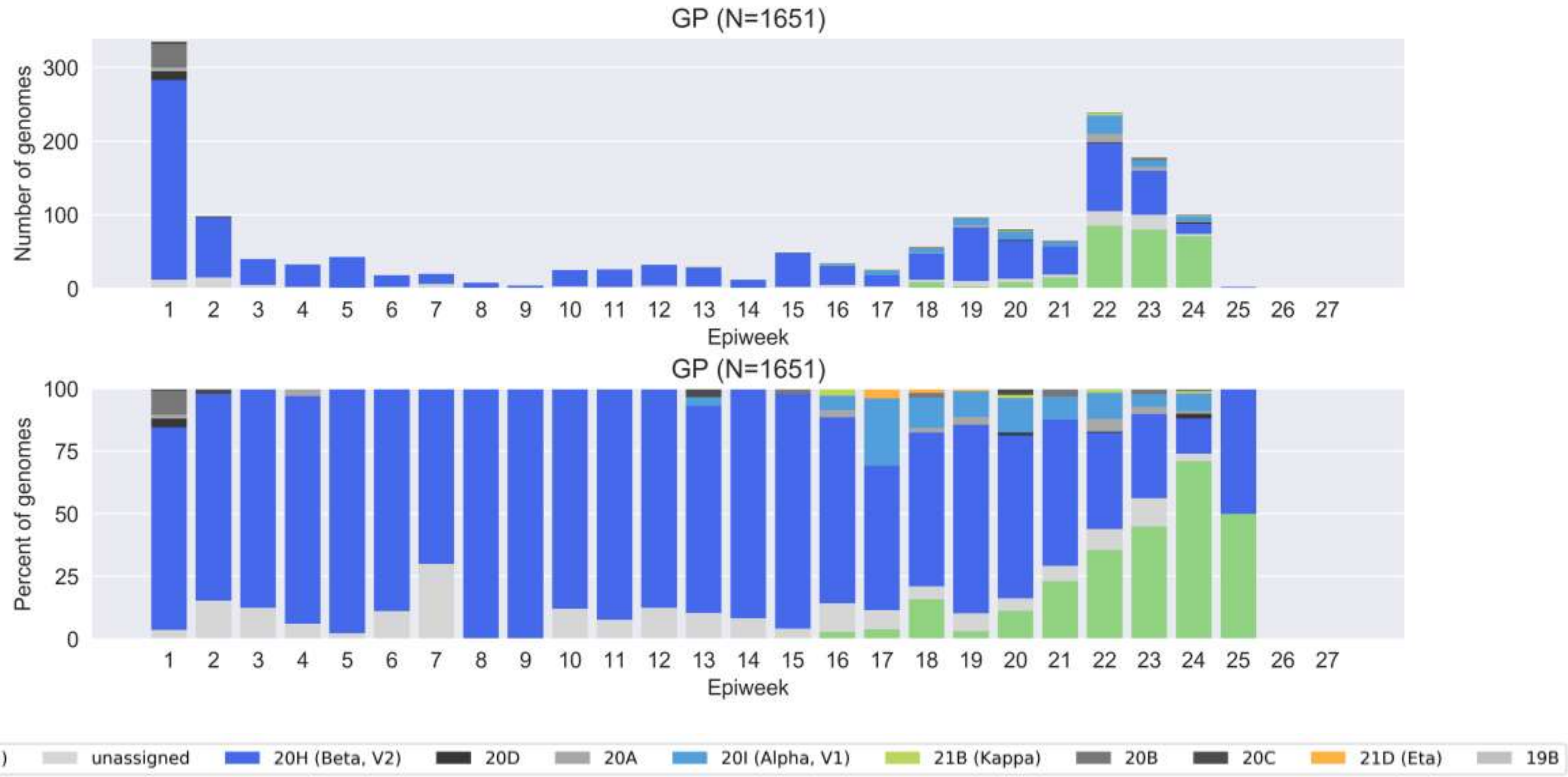
- **Beta dominates until week 23, when Delta increases.**
- **Eta** is detected in higher numbers than in GP and KZN, but not detected in most recent weeks.

Genomes sequenced from specimens collected in May and June 2021 in other South African provinces

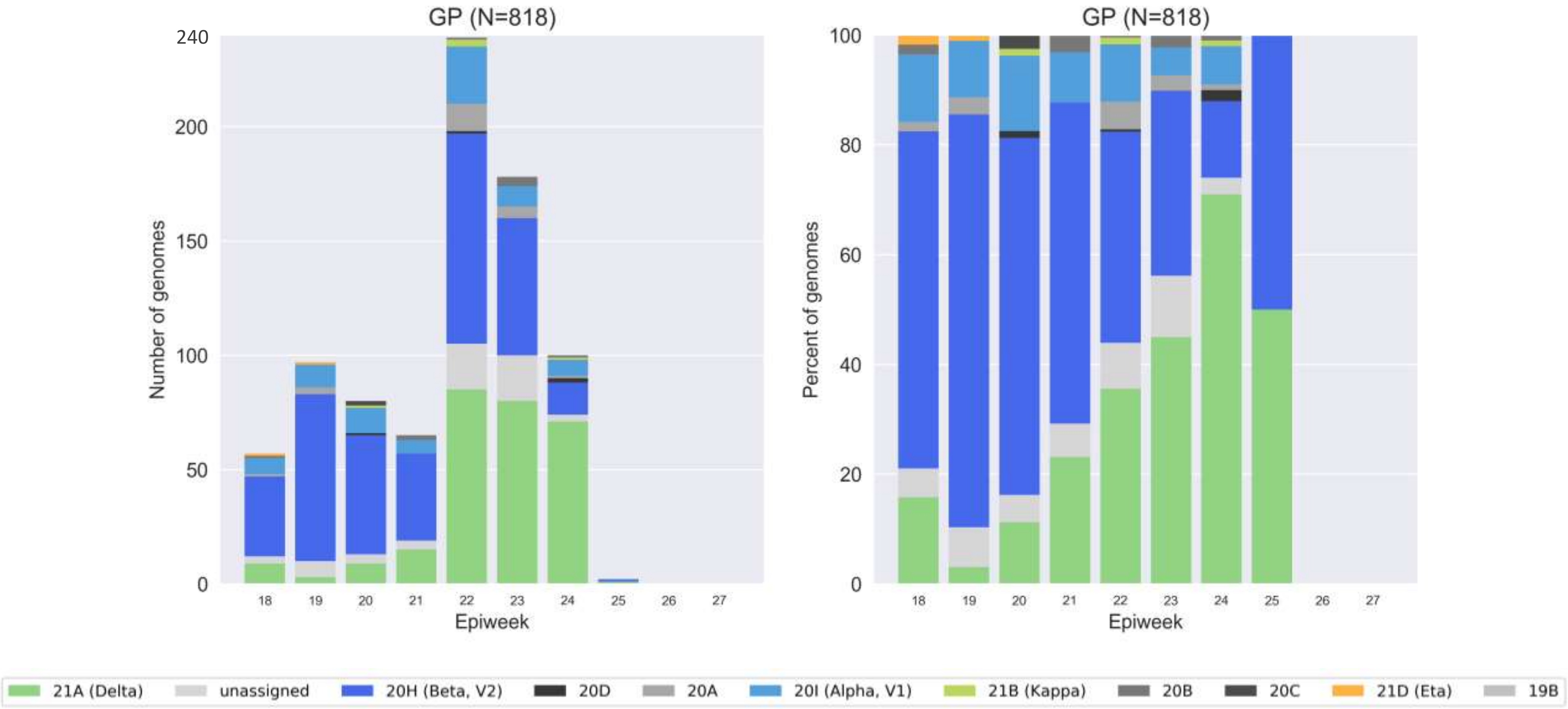


Variant dominance changes by province. Delta now detected in all provinces. Delta was detected in the Northern Cape in March and April (see later).

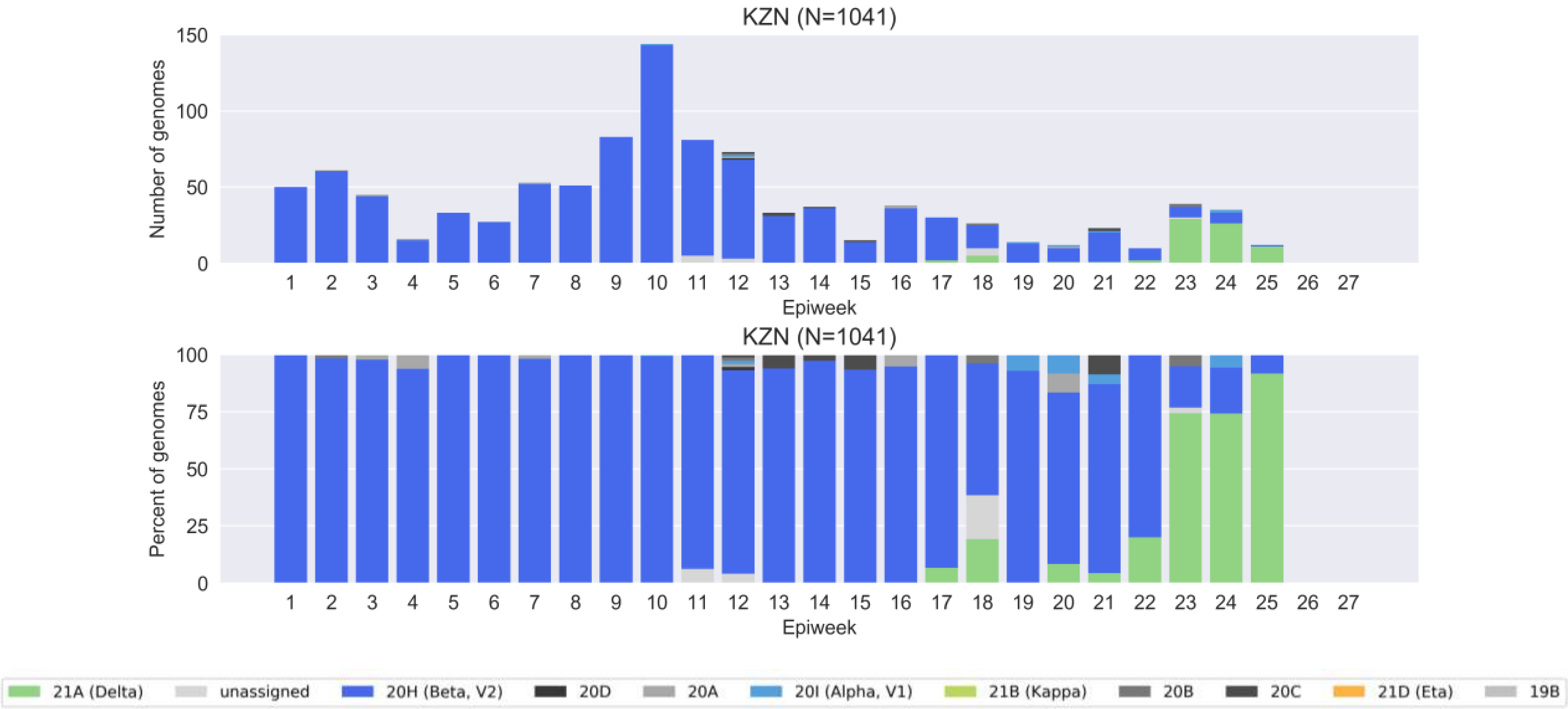
Gauteng (2021)



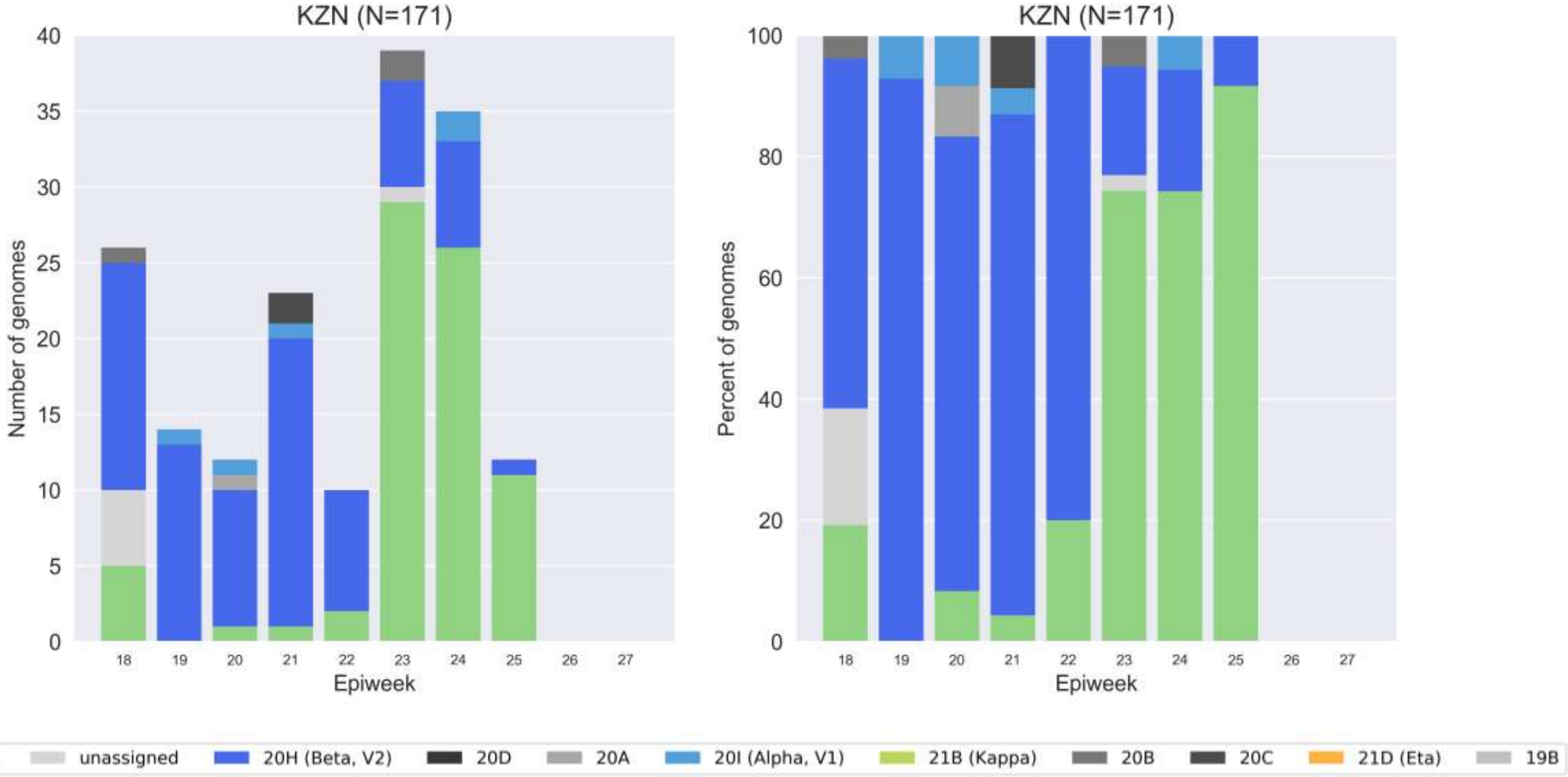
Gauteng (May and June 2021)



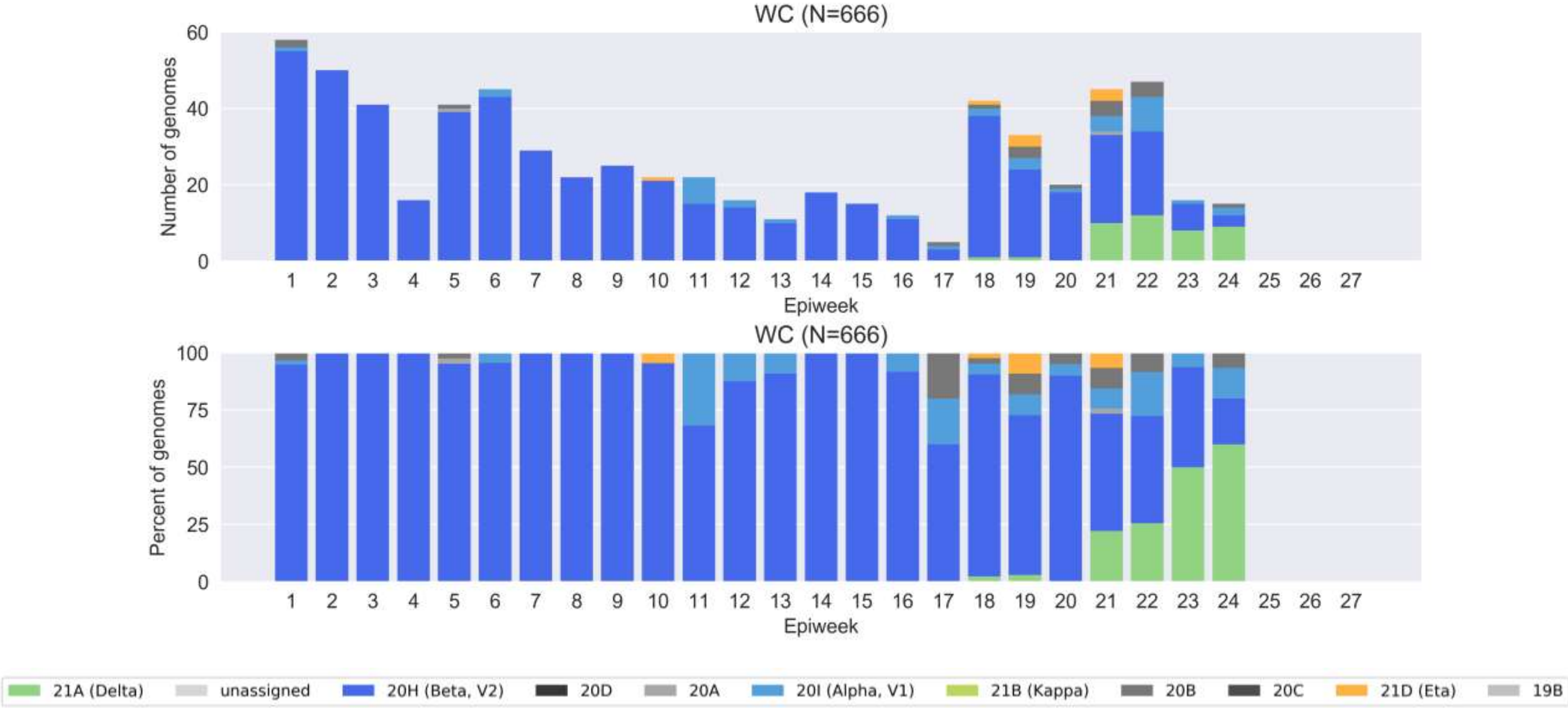
KwaZulu-Natal (2021)



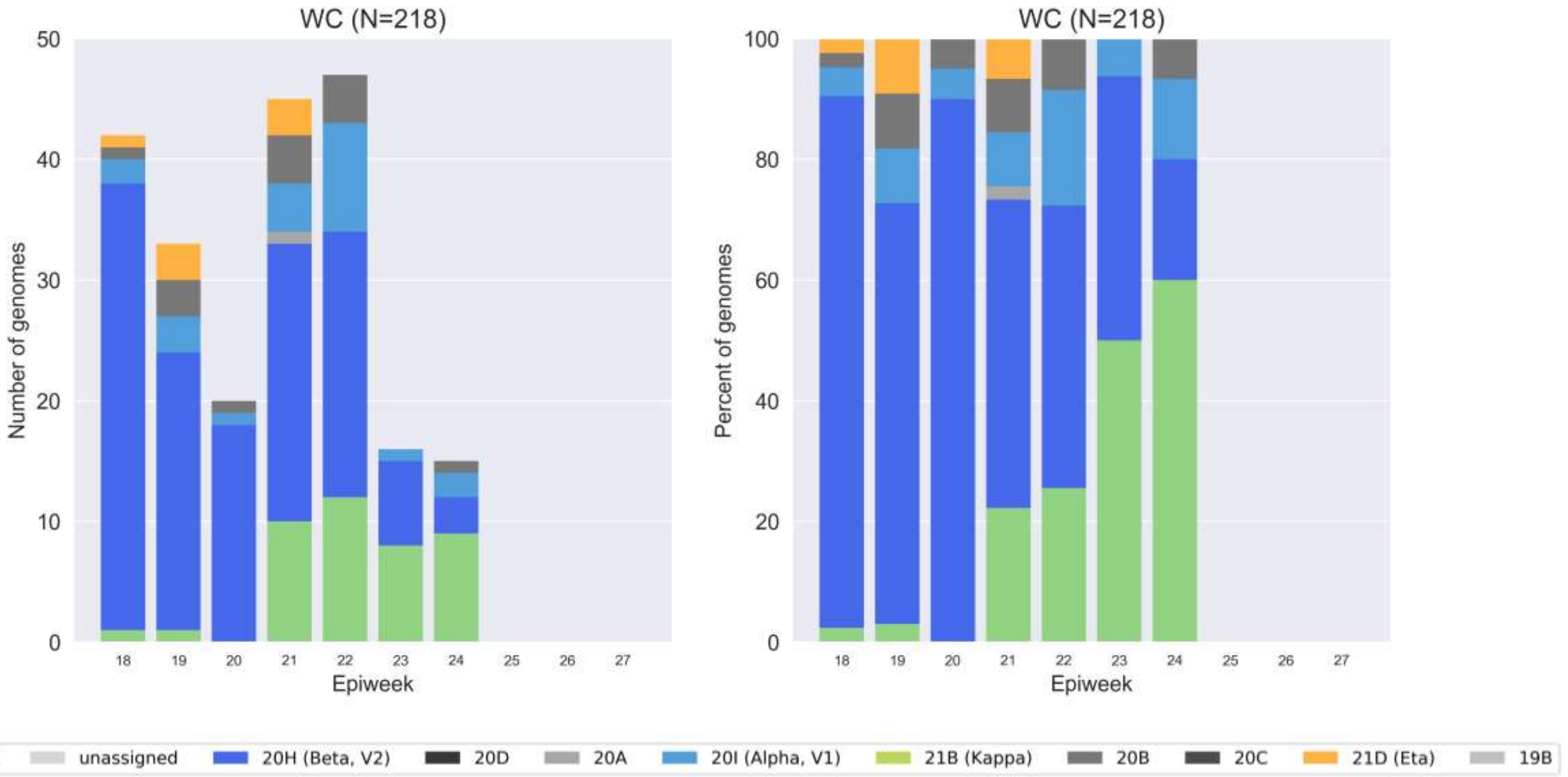
KwaZulu-Natal (May and June 2021)



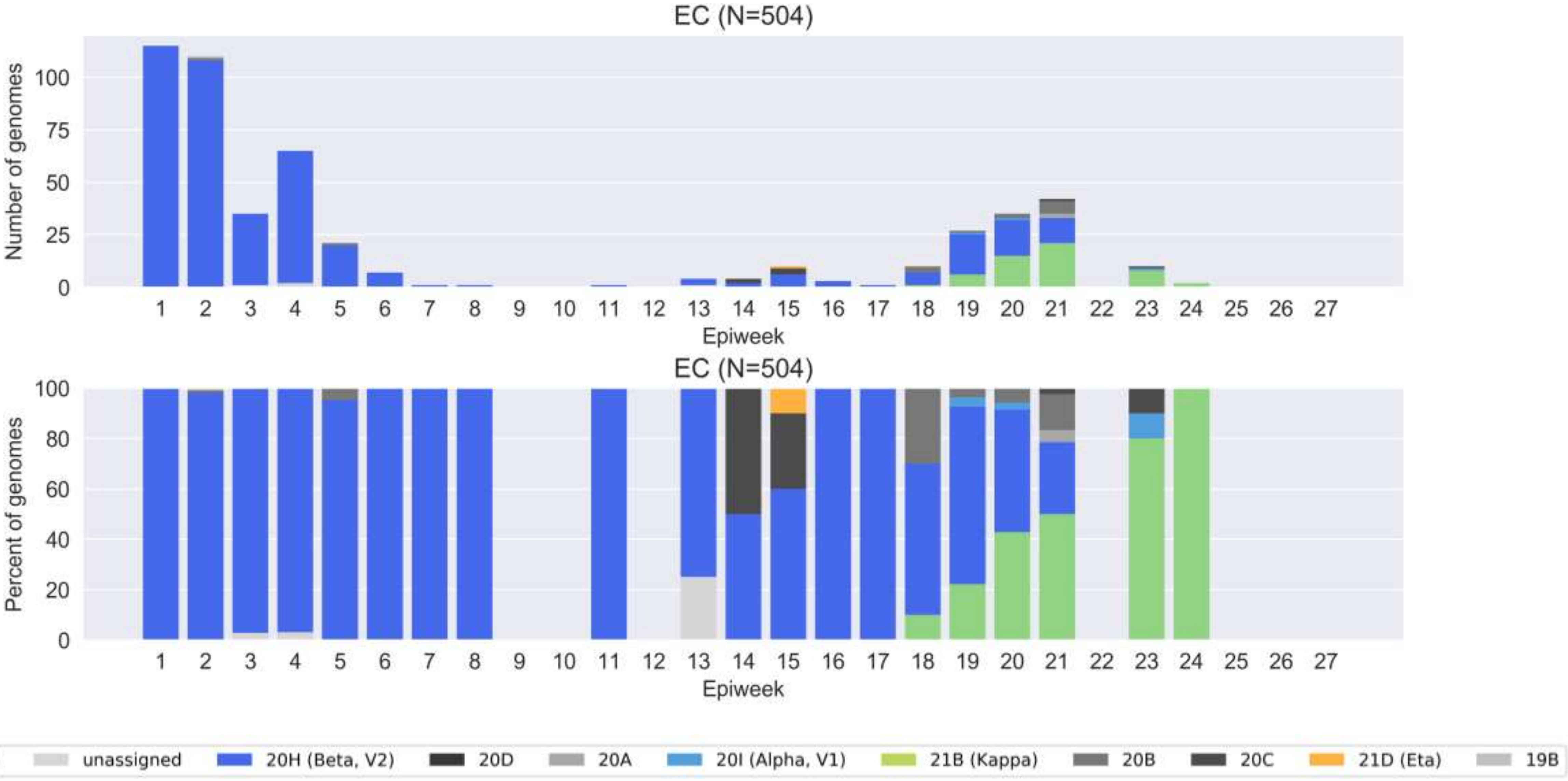
Western Cape (2021)



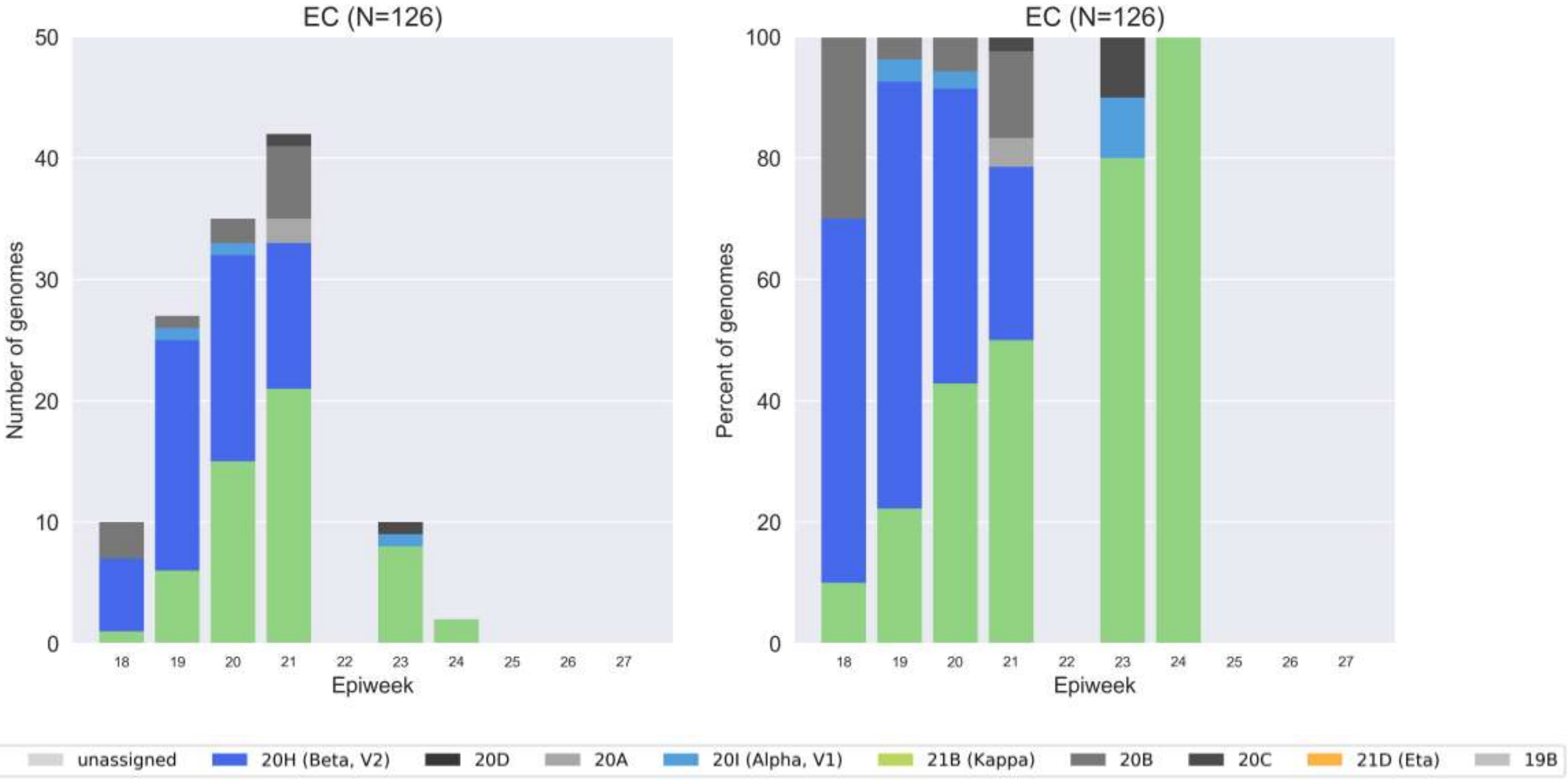
Western Cape (May and June 2021)



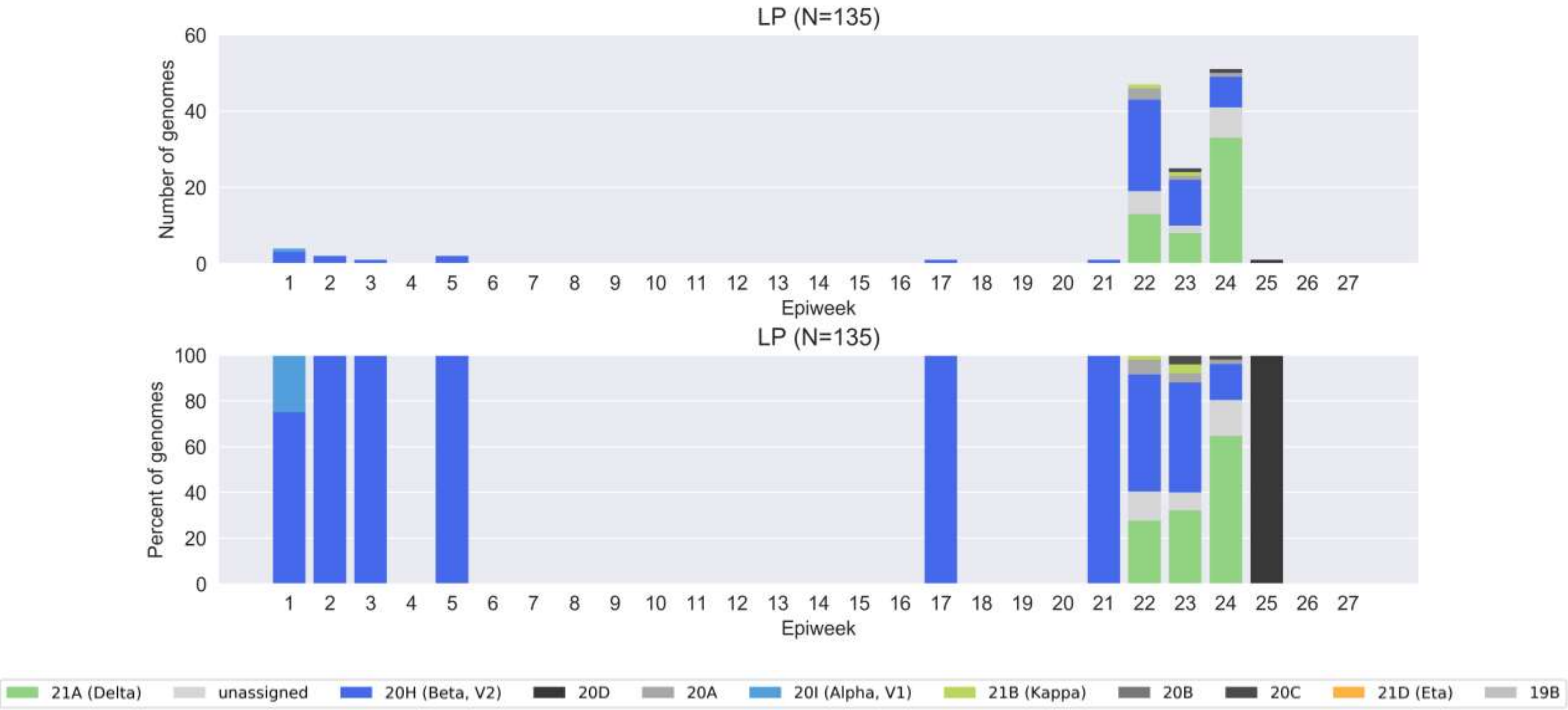
Eastern Cape (2021)



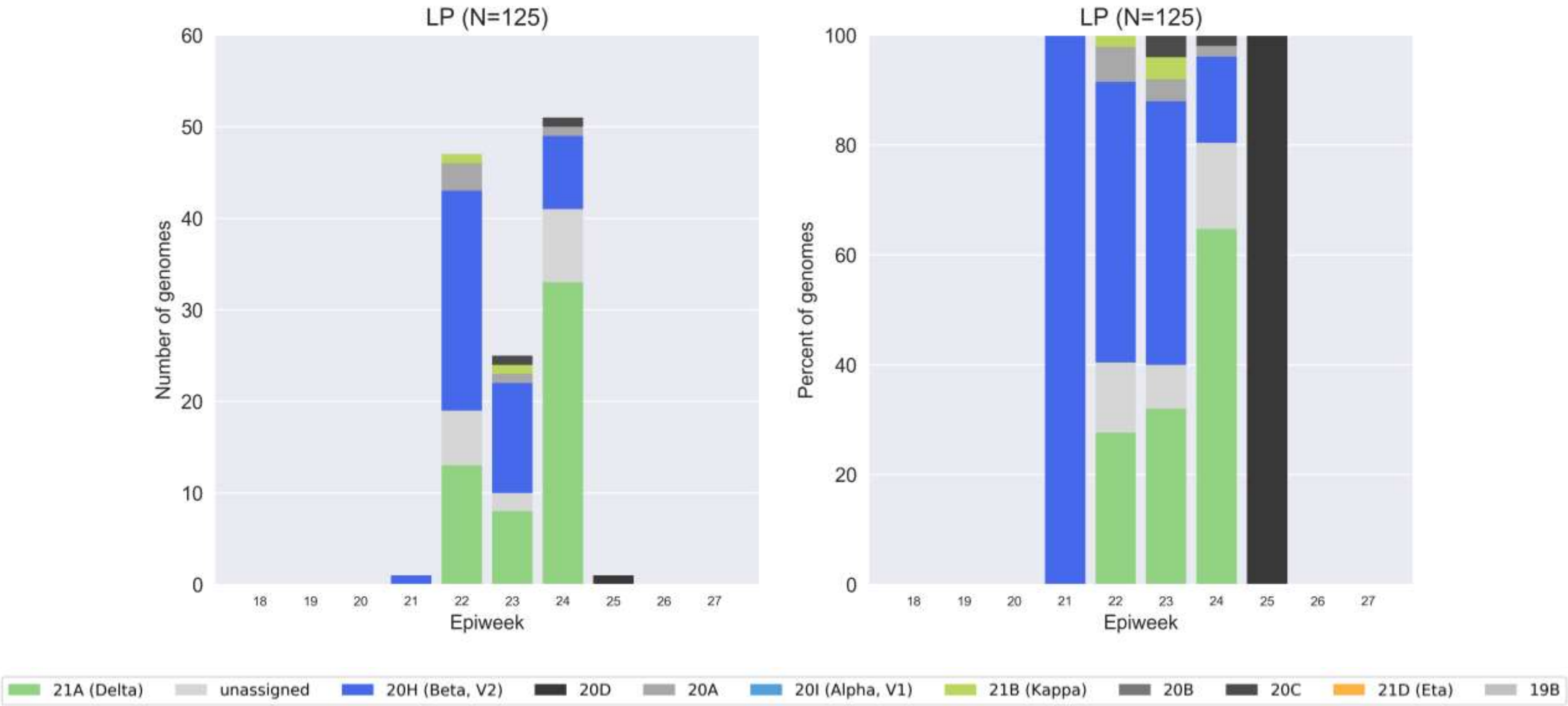
Eastern Cape (May and June 2021)



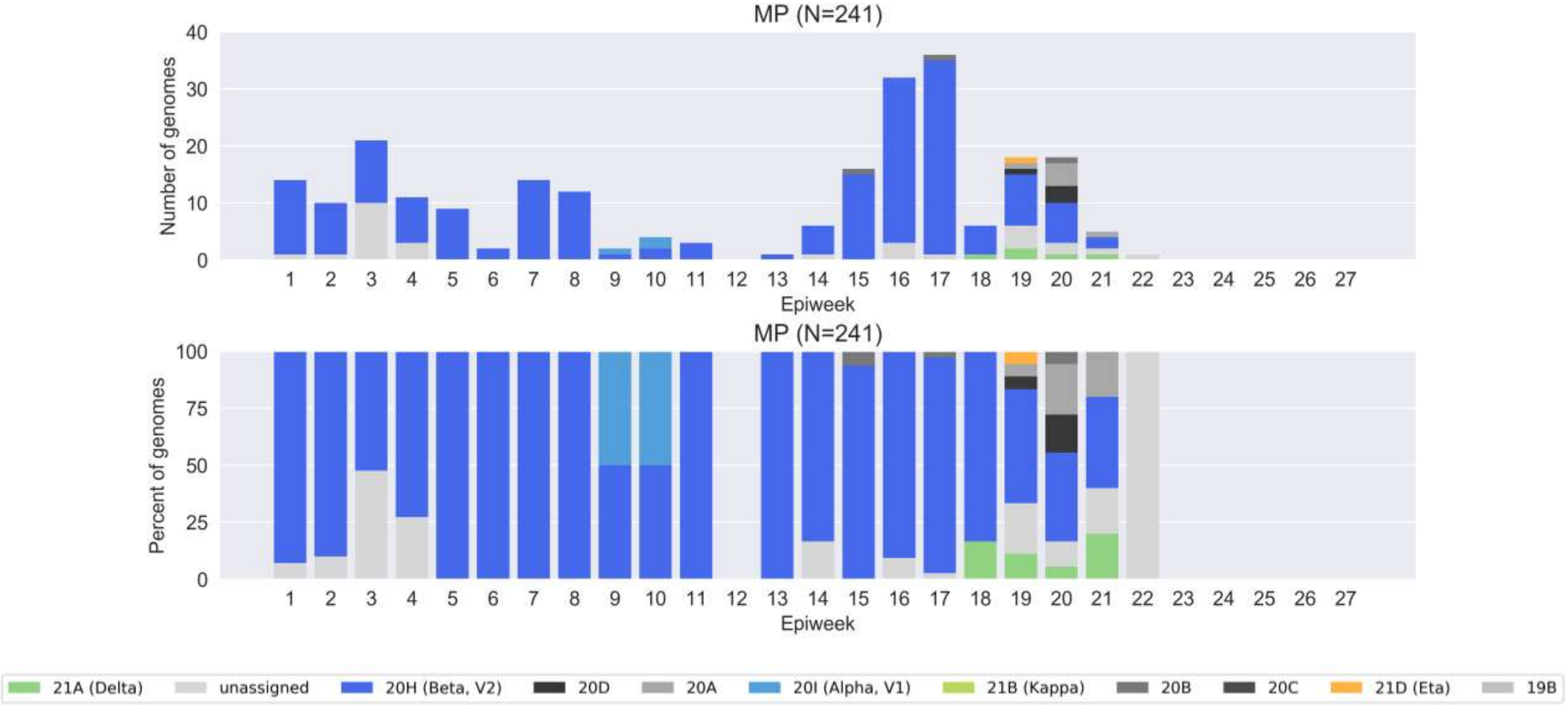
Limpopo (2021)



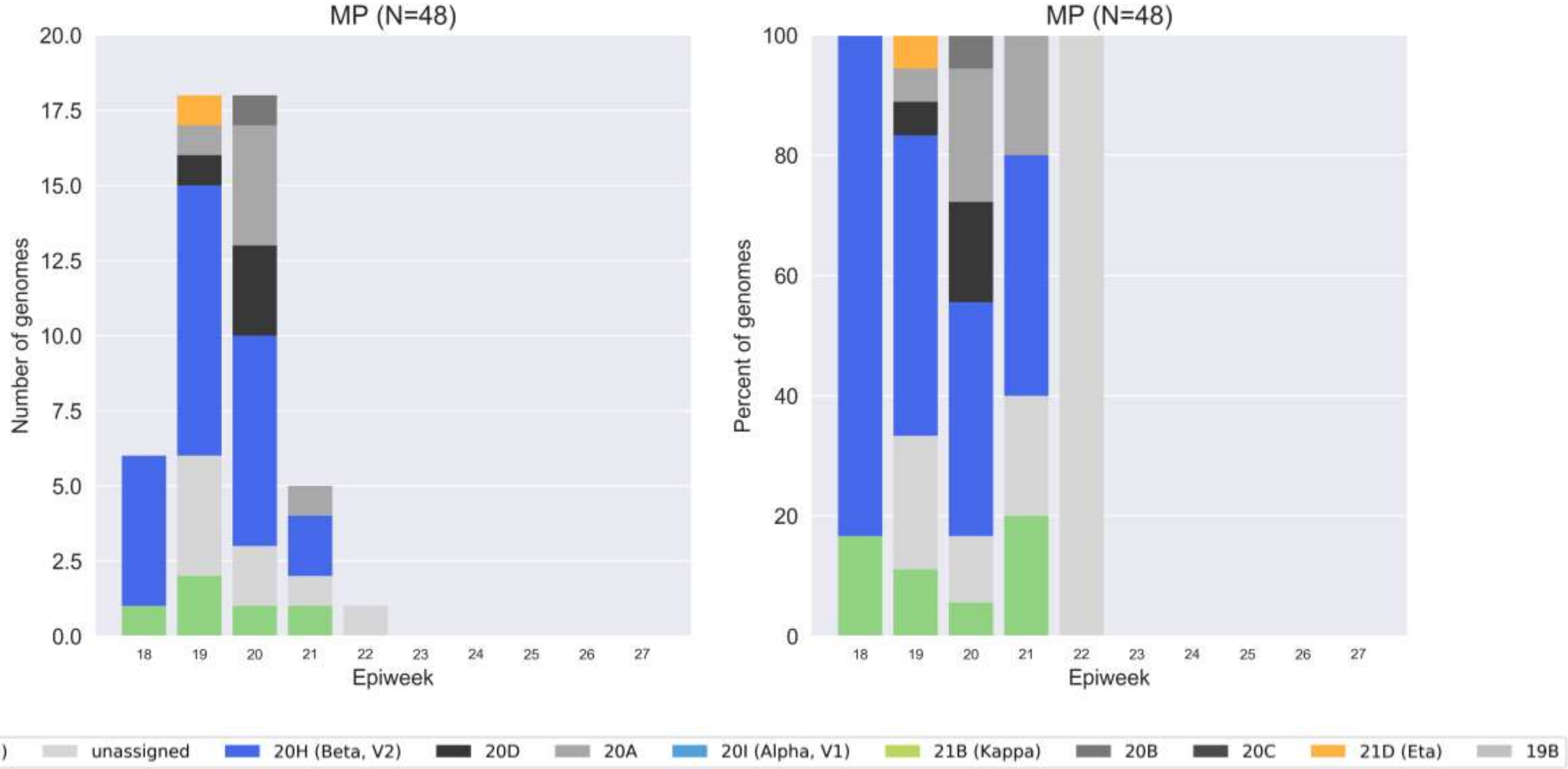
Limpopo (May and June 2021)



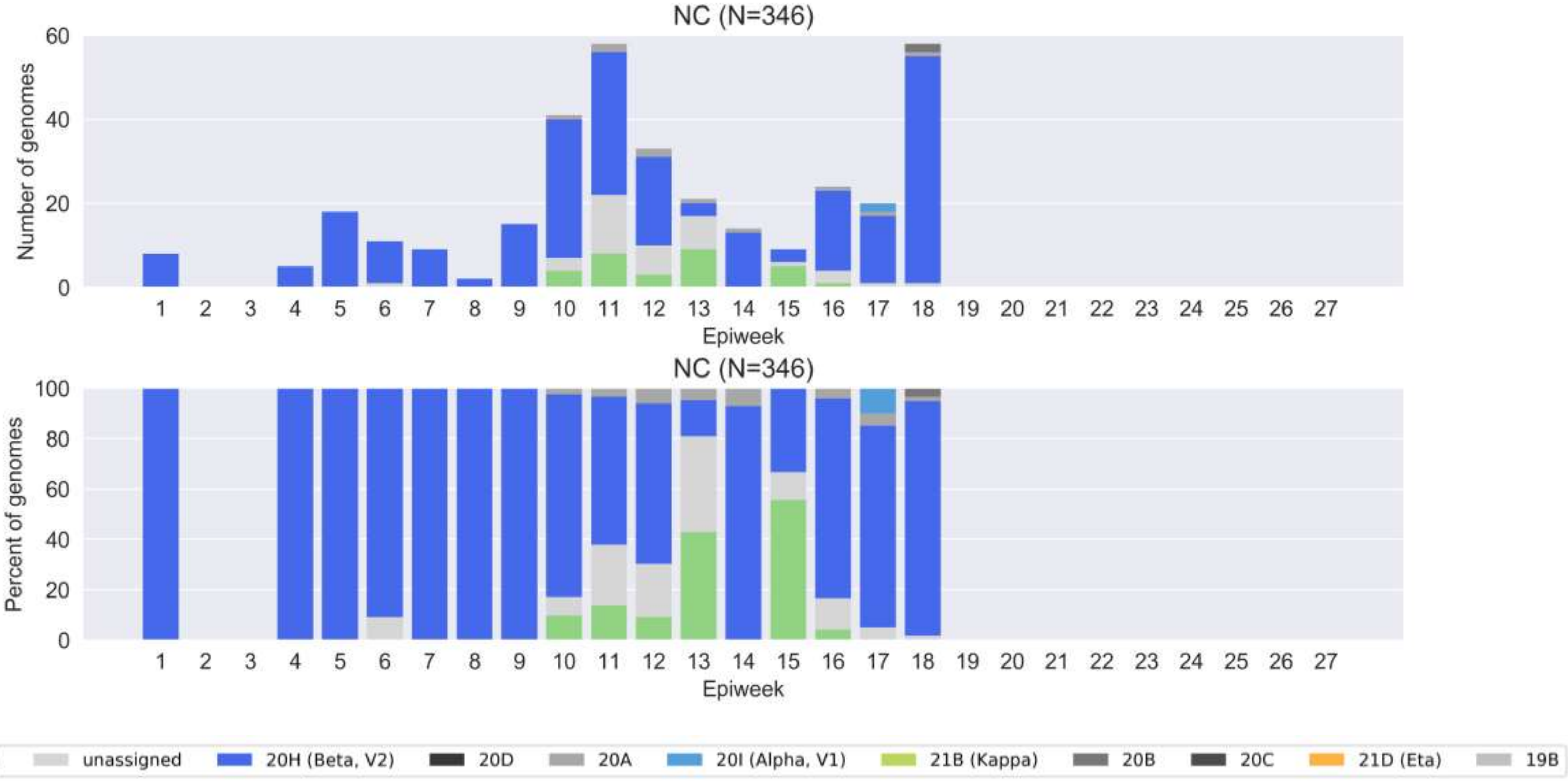
Mpumalanga (2021)



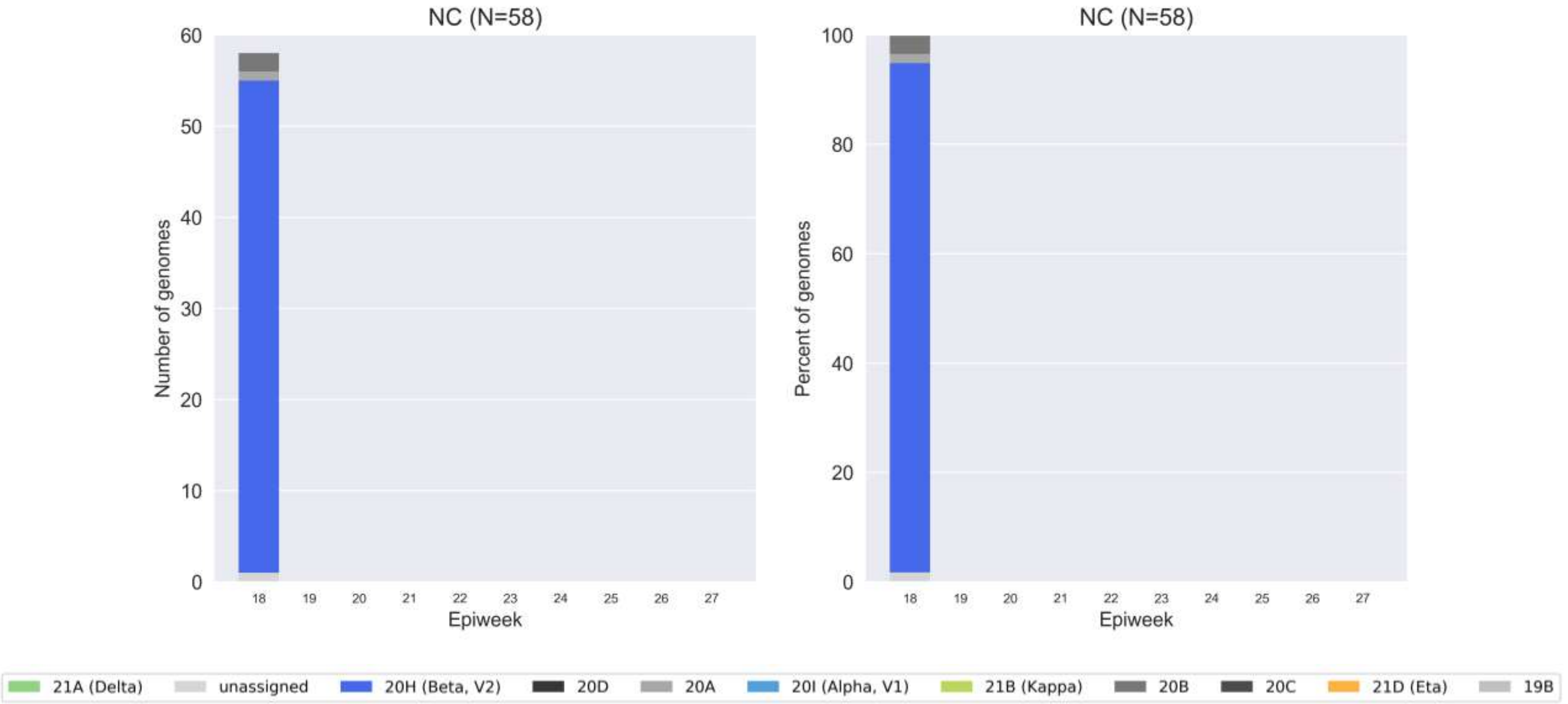
Mpumalanga (May and June 2021)



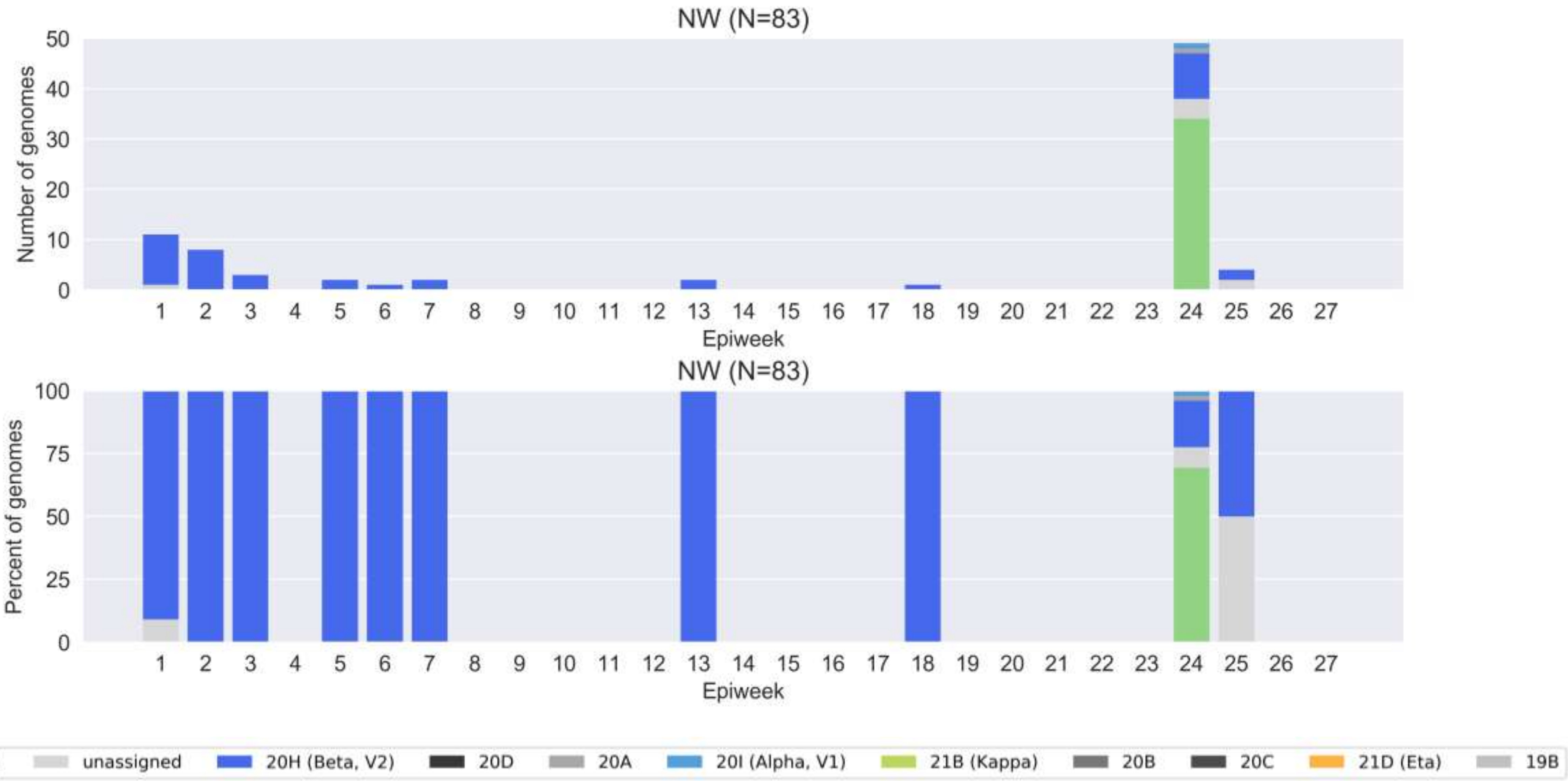
Northern Cape (2021)



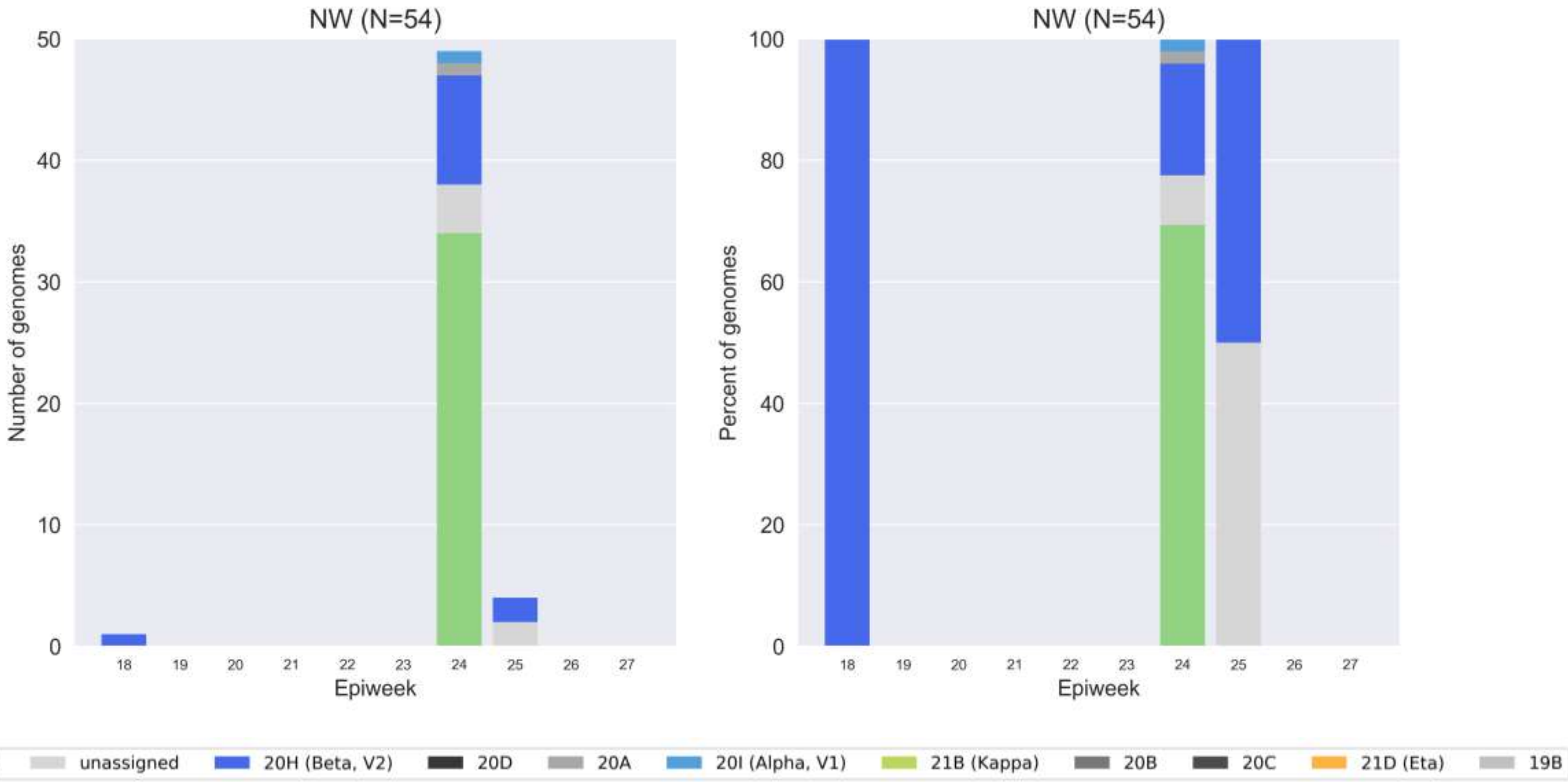
Northern Cape (May and June 2021)



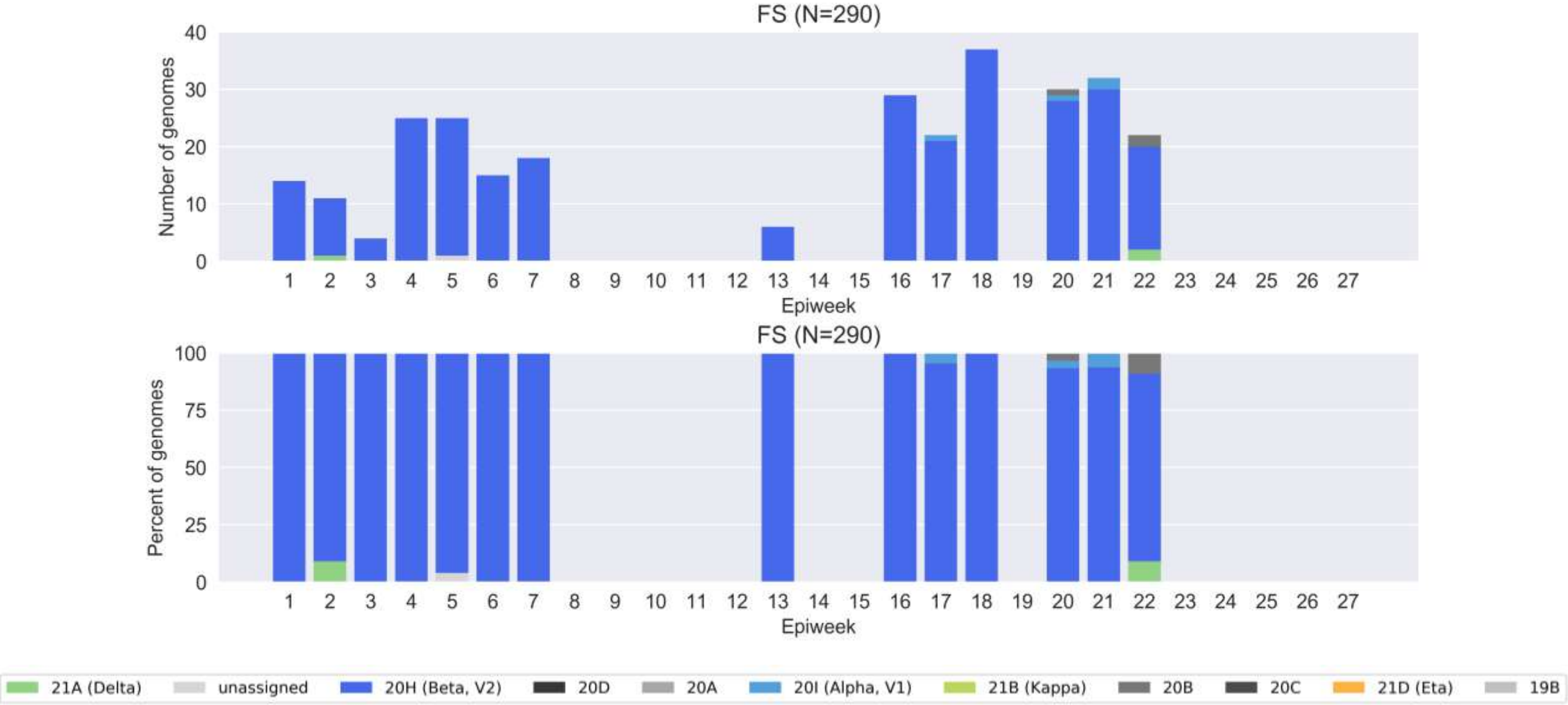
North West (2021)



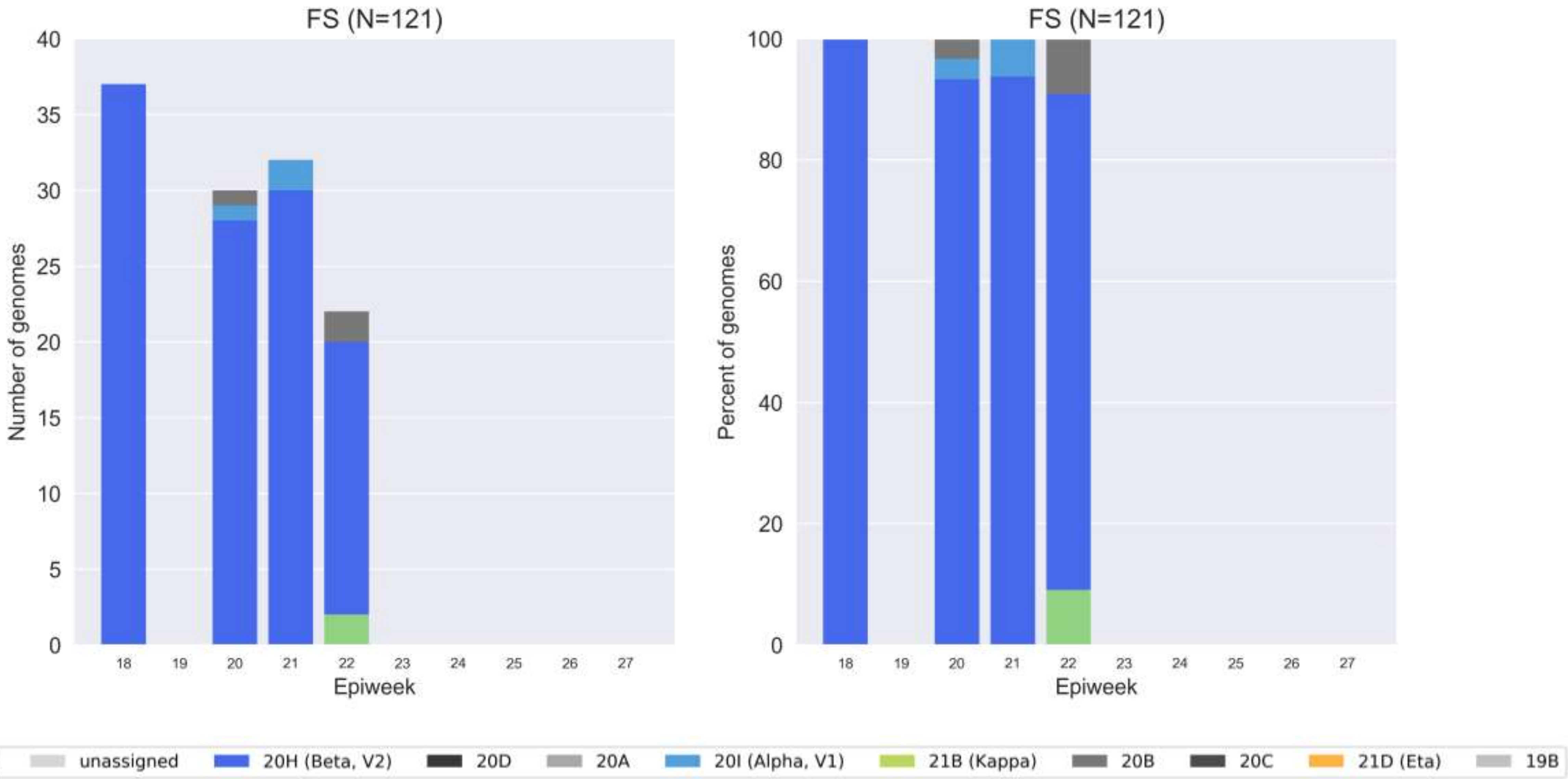
North West (May and June 2021)



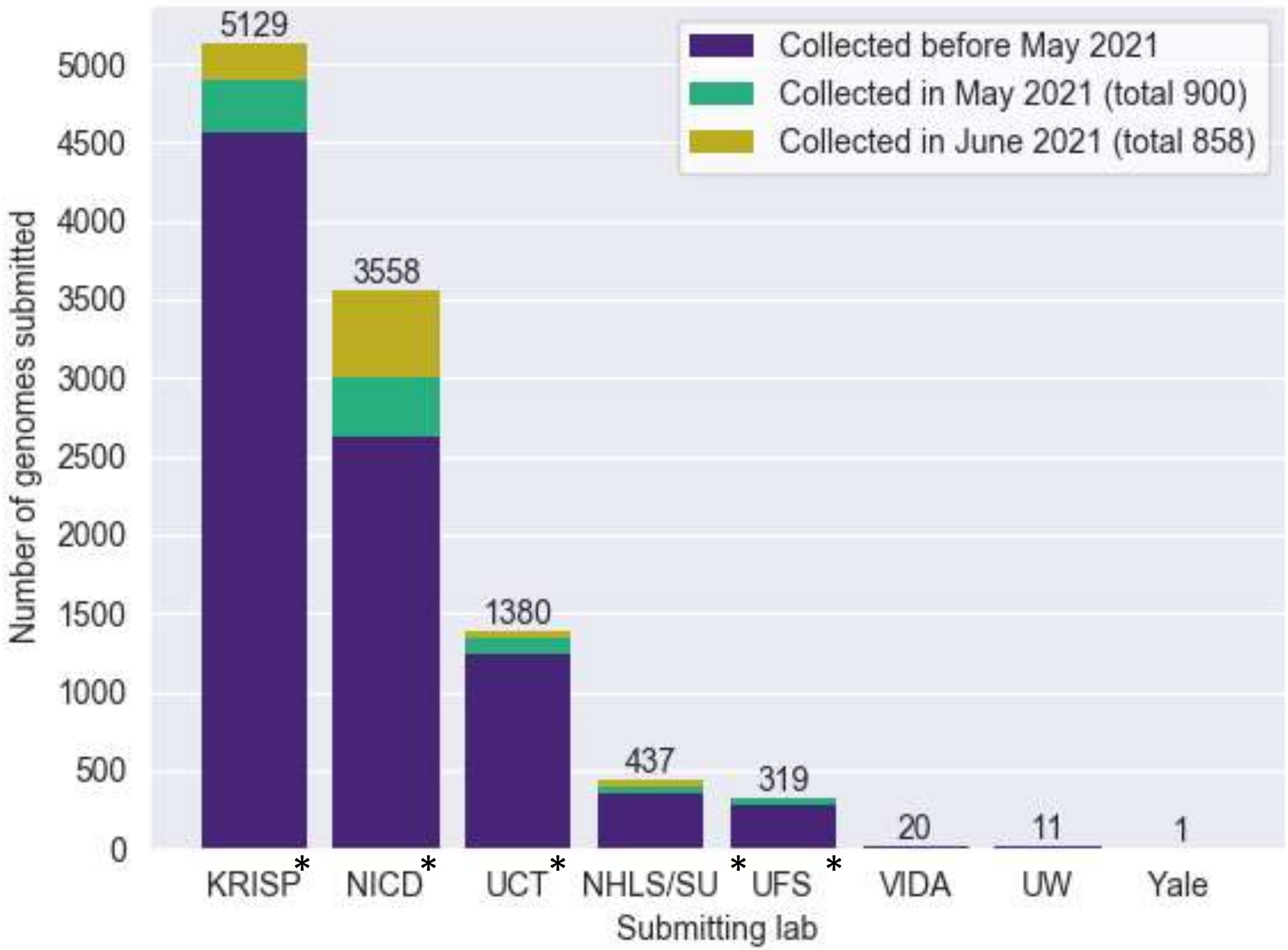
Free State (2021)



Free State (May and June 2021)



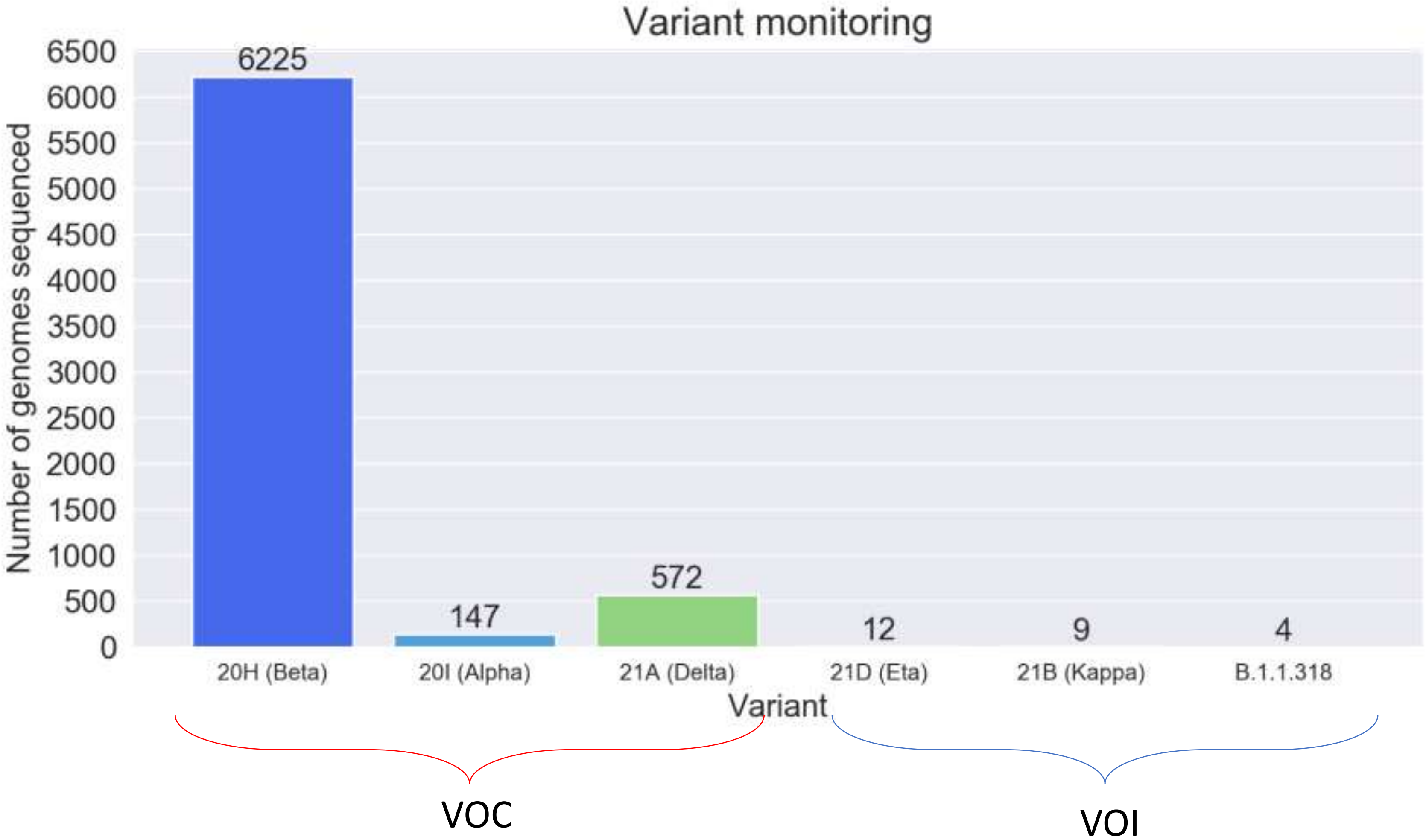
South African genomes submitted per sequencing lab, 2020 and 2021 (N=10 855)



*NGS-SA laboratories

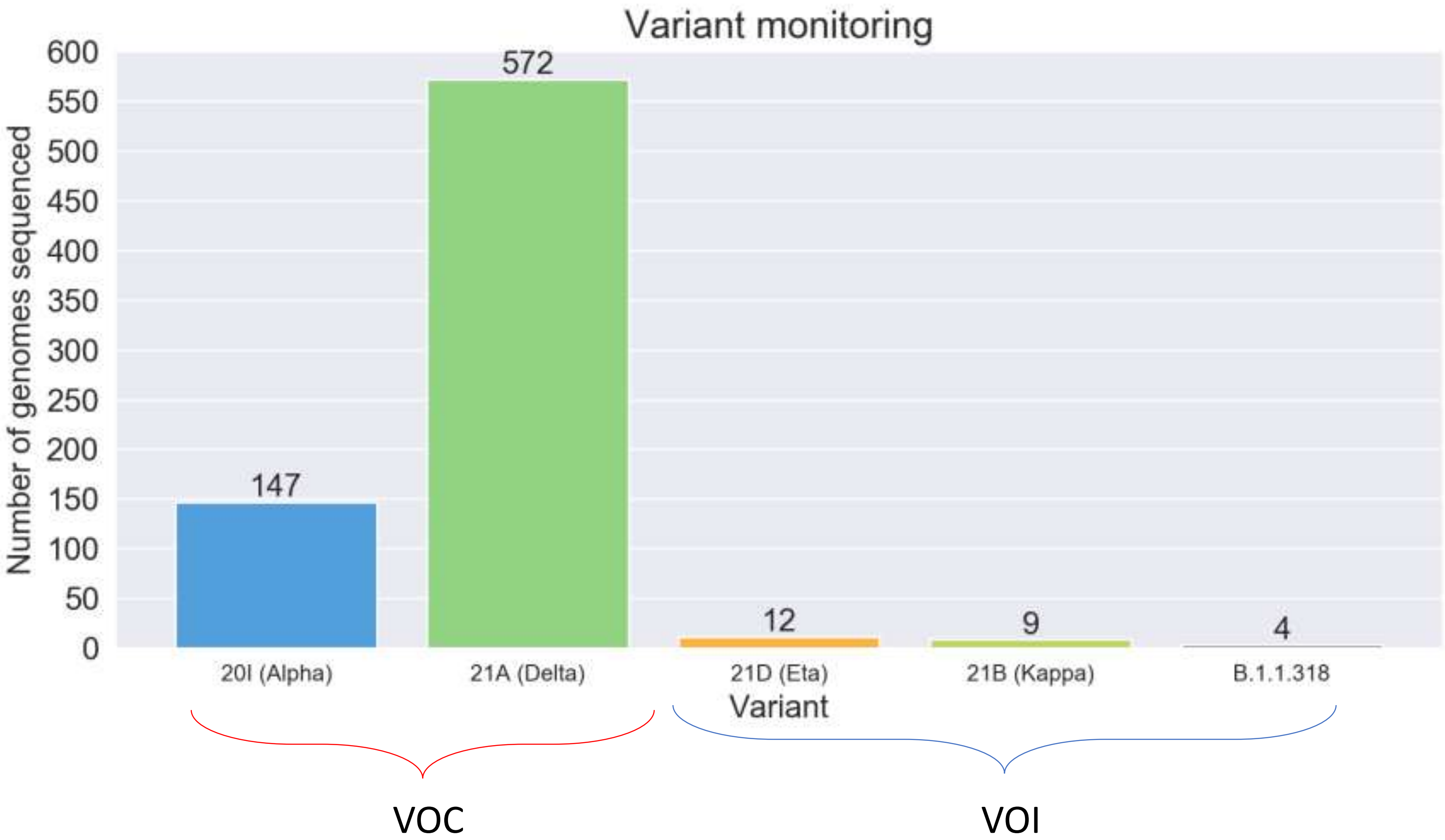
Multiple labs from NGS-SA are contributing to the sequencing effort. Sequencing is increasing with the third wave.

Monitoring VOCs and VOIs in South Africa (N=6 969, 64% of all sequences) (2020 – 2021)



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

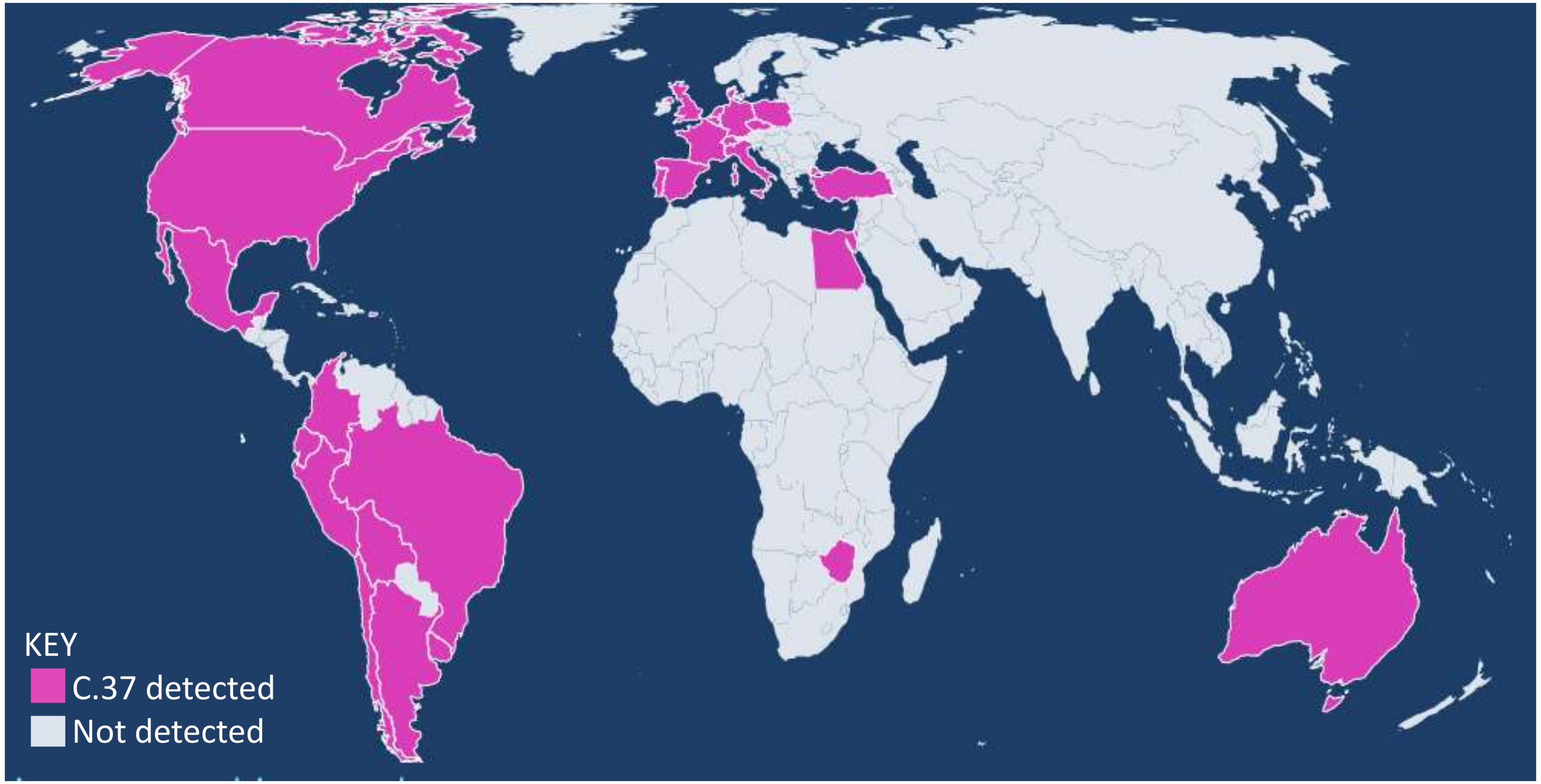
Monitoring VOCs and VOIs in South Africa (excluding 20H, Beta; 2020 - 2021)



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

Lambda Variant (C.37) – what we know so far

Geographic distribution

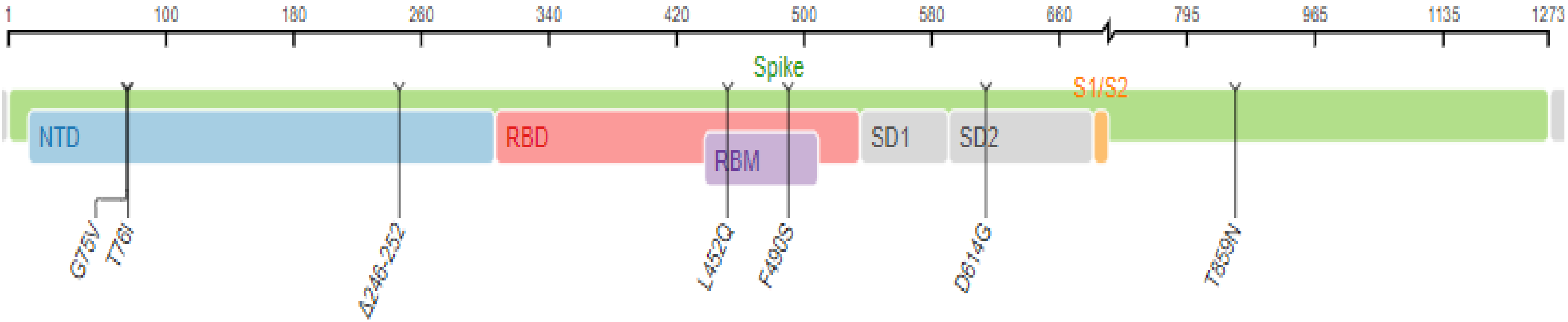


https://outbreak.info/situation-reports?pango=C.37 accessed 12pm on 7 July 2021

- The Lambda variant detected first in South America
  - now detected in 37 countries
- In Africa
  - reported in only Egypt (n=8)
  - and Zimbabwe (n=1)
  - but not in South Africa (as on 7th July 2021)

WHO listed “variant of interest” (VOI) on the on 14 June 2021

Lambda Variant-Spike Mutations



- Two Substitutions (**G75V, T76I**) and a deletion (**246-252del**) in N-terminal domain (NTD)
- Two mutations (**L452Q** & **F490S**) in receptor-binding domain (RBD)

Summary

- In June, Delta increases significantly and dominates in most provinces with recent data available
- Variant diversity and dominance changes with province
- Lambda variant has not been detected in South Africa

NICD Acknowledgements

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- **Simon Travers (Hyrax Biosciences)**

NICD COVID-19 response team
COVID Incident Management Team

health
Department:
Health
REPUBLIC OF SOUTH AFRICA

science & technology
Department:
Science and Technology
REPUBLIC OF SOUTH AFRICA

AFRICA CDC
Centres for Disease Control and Prevention
Safeguarding Africa's Health

NRF National Research Foundation

saMRC advancinglife

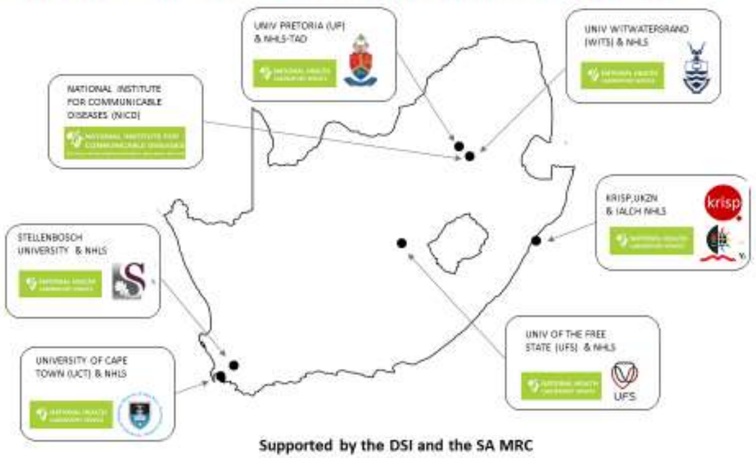
wellcome

CDC
CENTERS FOR DISEASE CONTROL AND PREVENTION

The Fleming Fund

Multi-institute, multi-disciplinary NGS team

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



Supported by the DSI and the SA MRC

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Contributors of samples to NICD:

Adriano Mendes
Allison J. Glass
Amy Strydom
Andries Dreyer
Christa Viljoen
Eddie Silberbauer
Elias Bereda
Eugene Elliot
Florah Mnyameni
Florette K. Treurnicht
Gloria Selabe
Greta Hoyland
Howard Newman
Jeannette Wadula
Kathleen Subramoney
Lia Rotherham
Marianne Wolfaardt
Marietjie Venter
Michaela Davis
Oluwakemi Laguda-Akingba
Riaan Writes
Shareef Abrahams
Simnikiwe Mayaphi
Terry Marshall
Warren Lowman
Zinhle Makatini

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.)