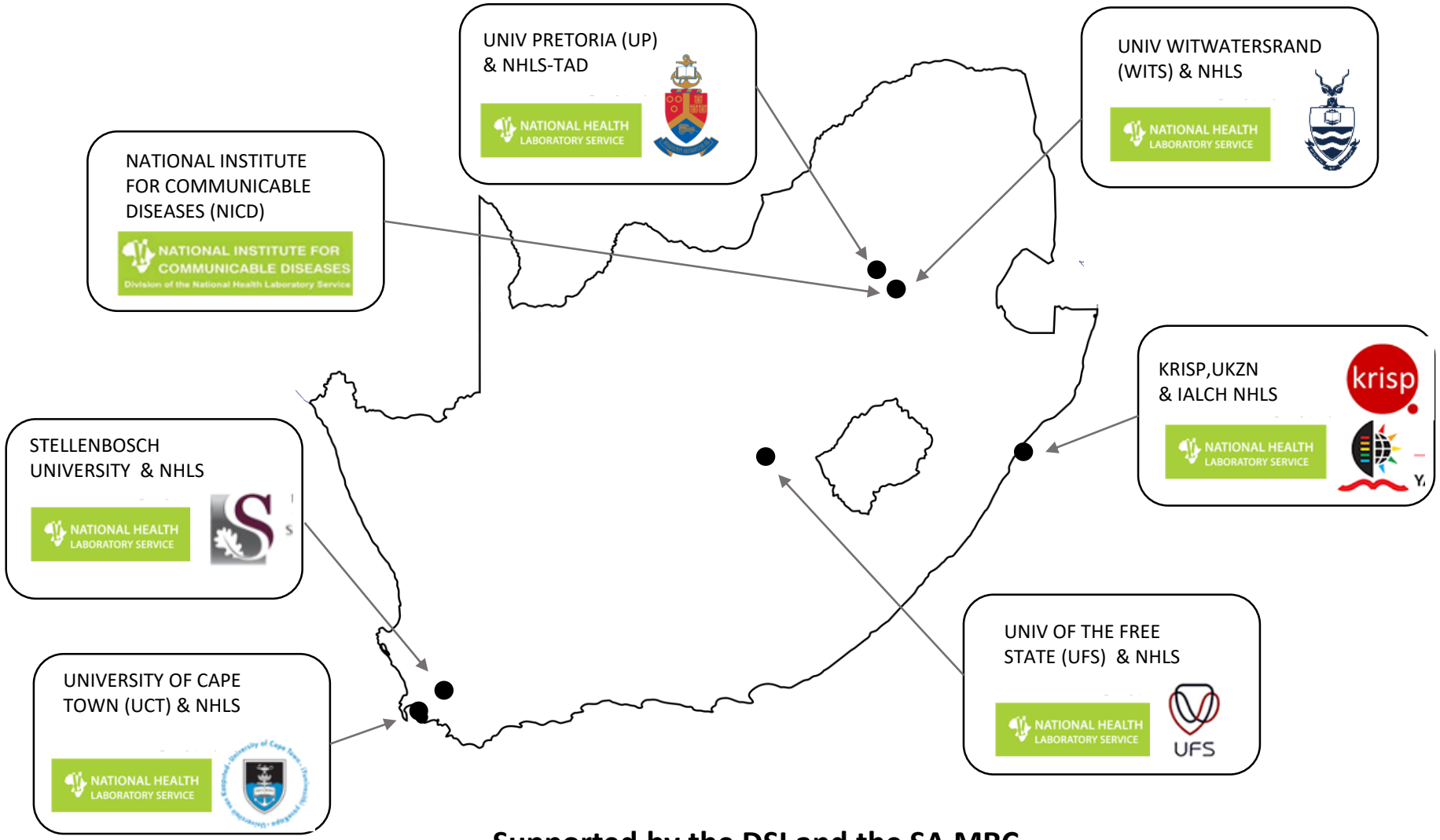
NGS-SA SARS-CoV-2 Sequencing Update

29 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)



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 29 July at 08h15

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/

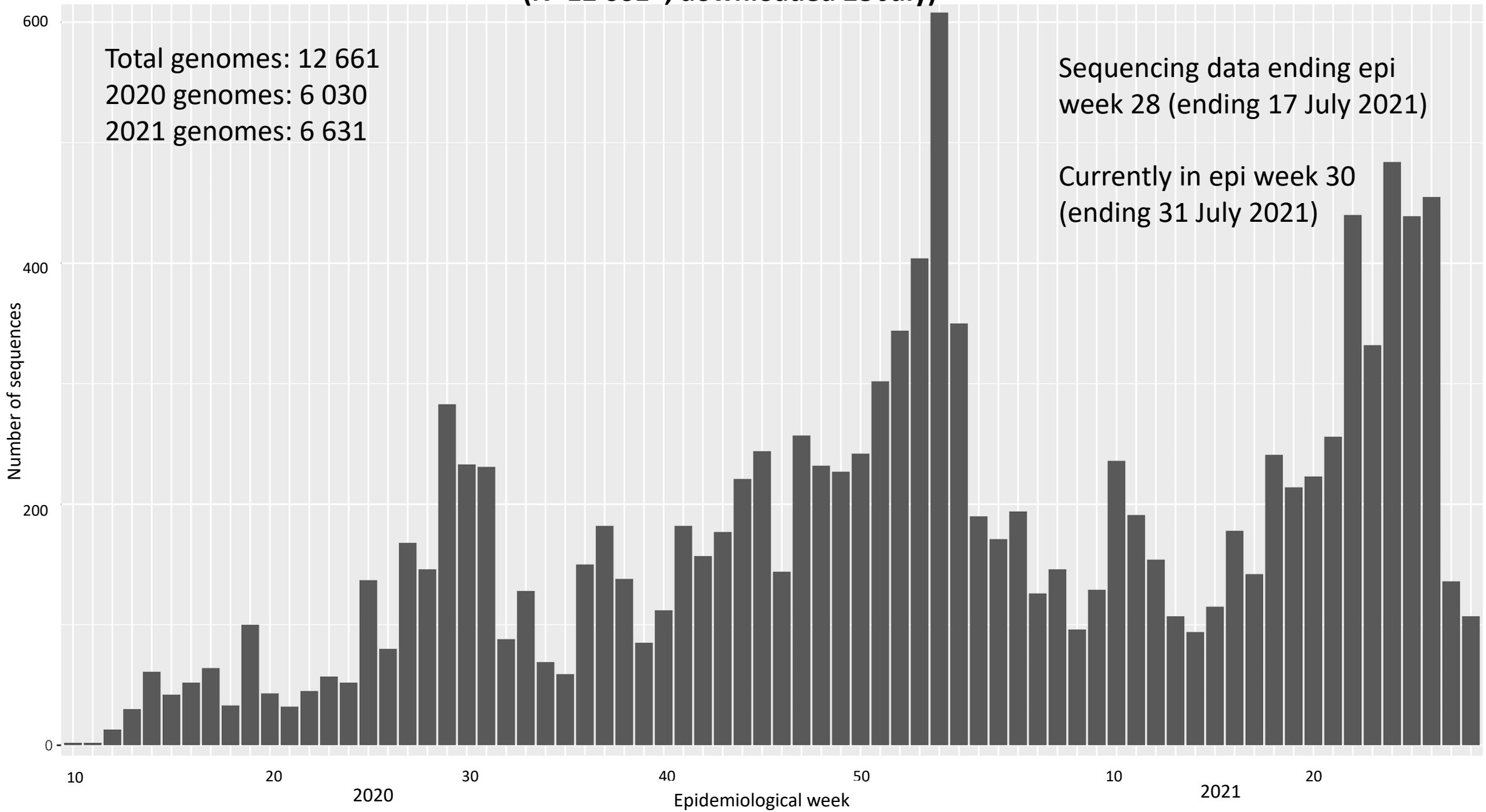
*Notable spike (S) amino acid changes under monitoring, which are currently reported in a minority of sequenced samples

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

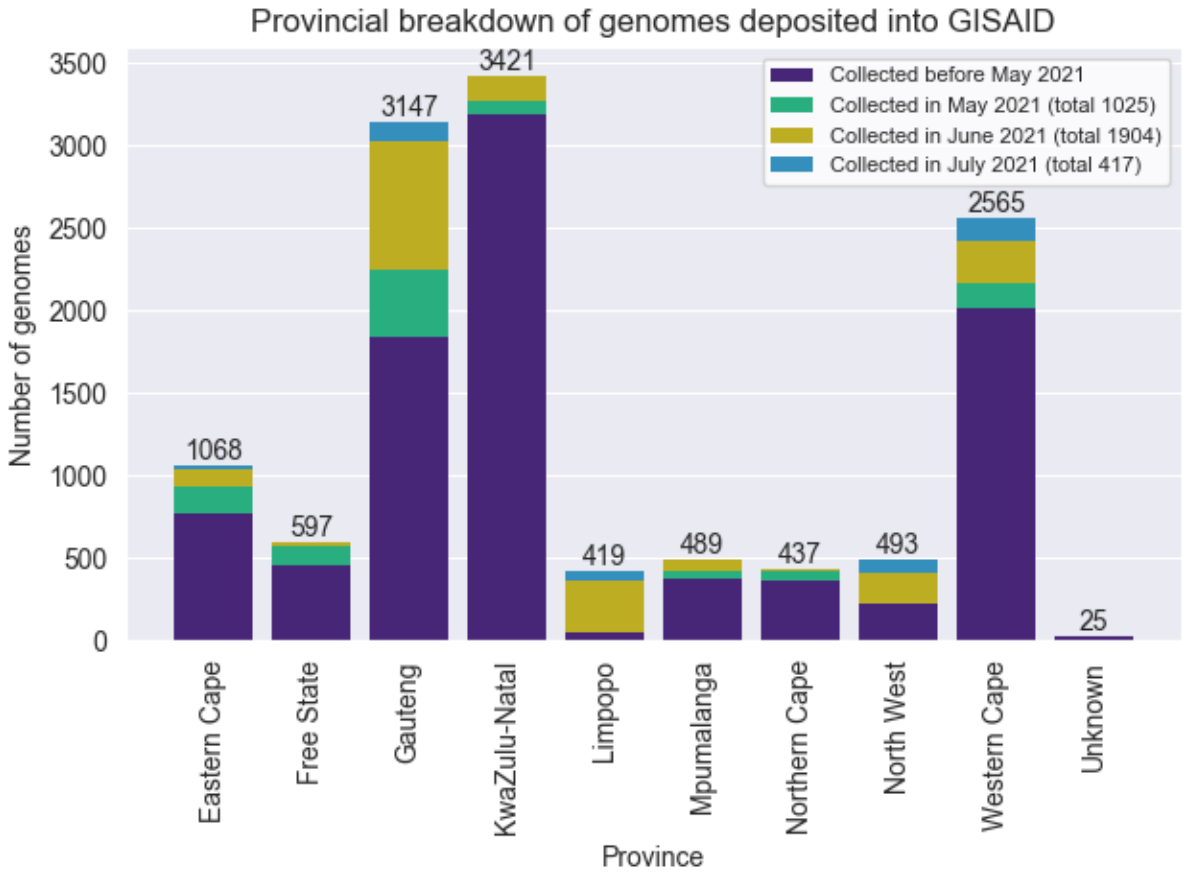
https://www.who.int/en/activities/tracking-SARS-CoV-2-variants/

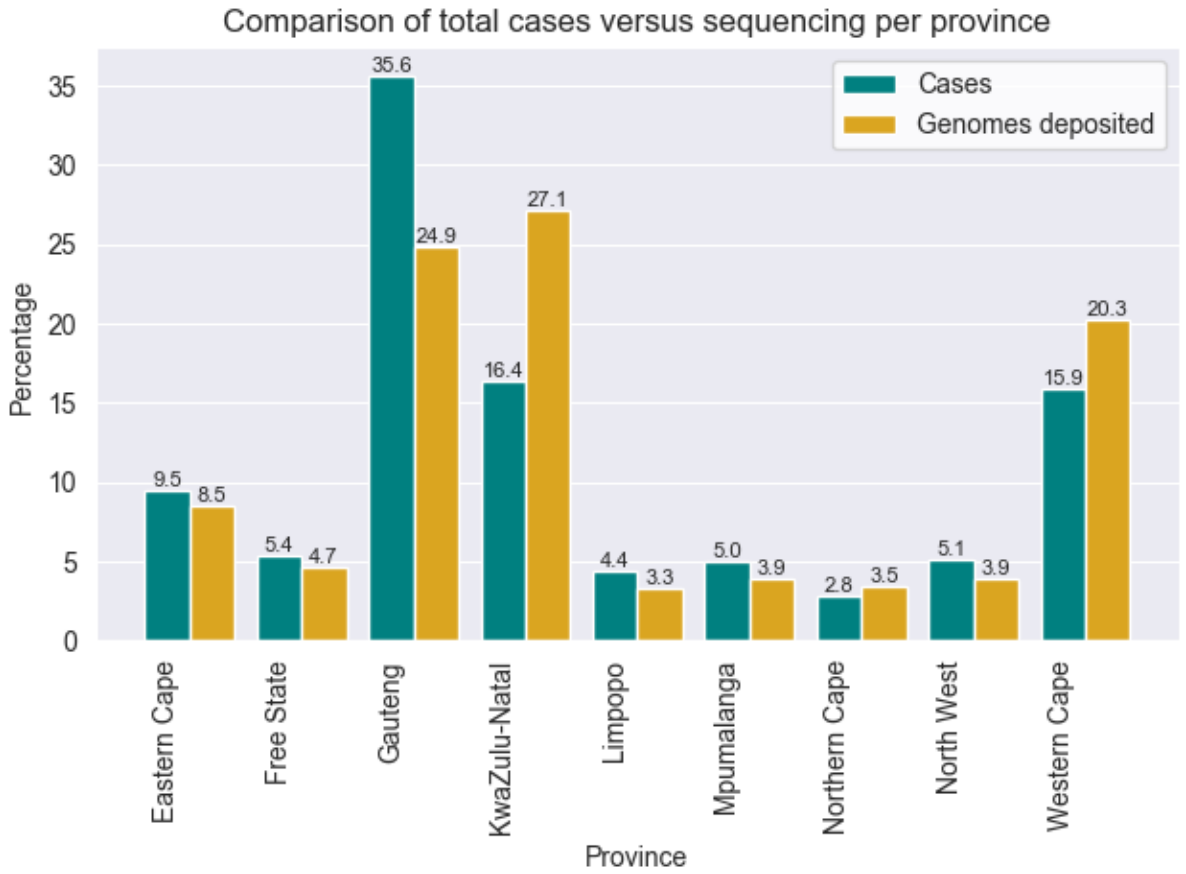
Number of South African genomes deposited on GISAID, by specimen collection week, 2020 and 2021 (N=12 661*, downloaded 28 July)



*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=12 661)

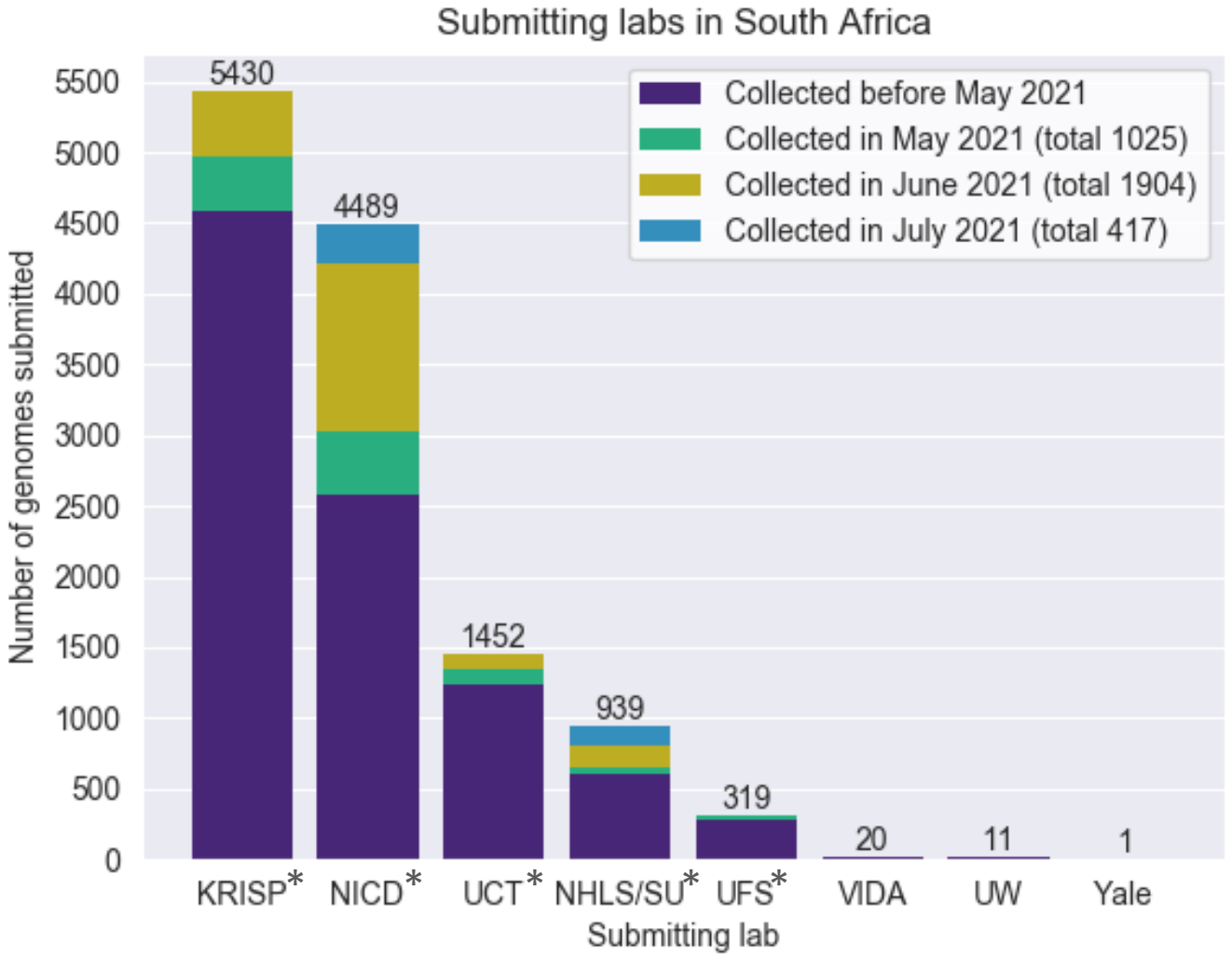




All provinces, apart from Gauteng (less) and KZN (more), have a similar percentage of overall cases as overall sequenced genomes.

Case data from https://www.nicd.ac.za/wp-content/uploads/2021/07/COVID-19-Weekly-Epidemiology-Brief-week-28-2021.pdf

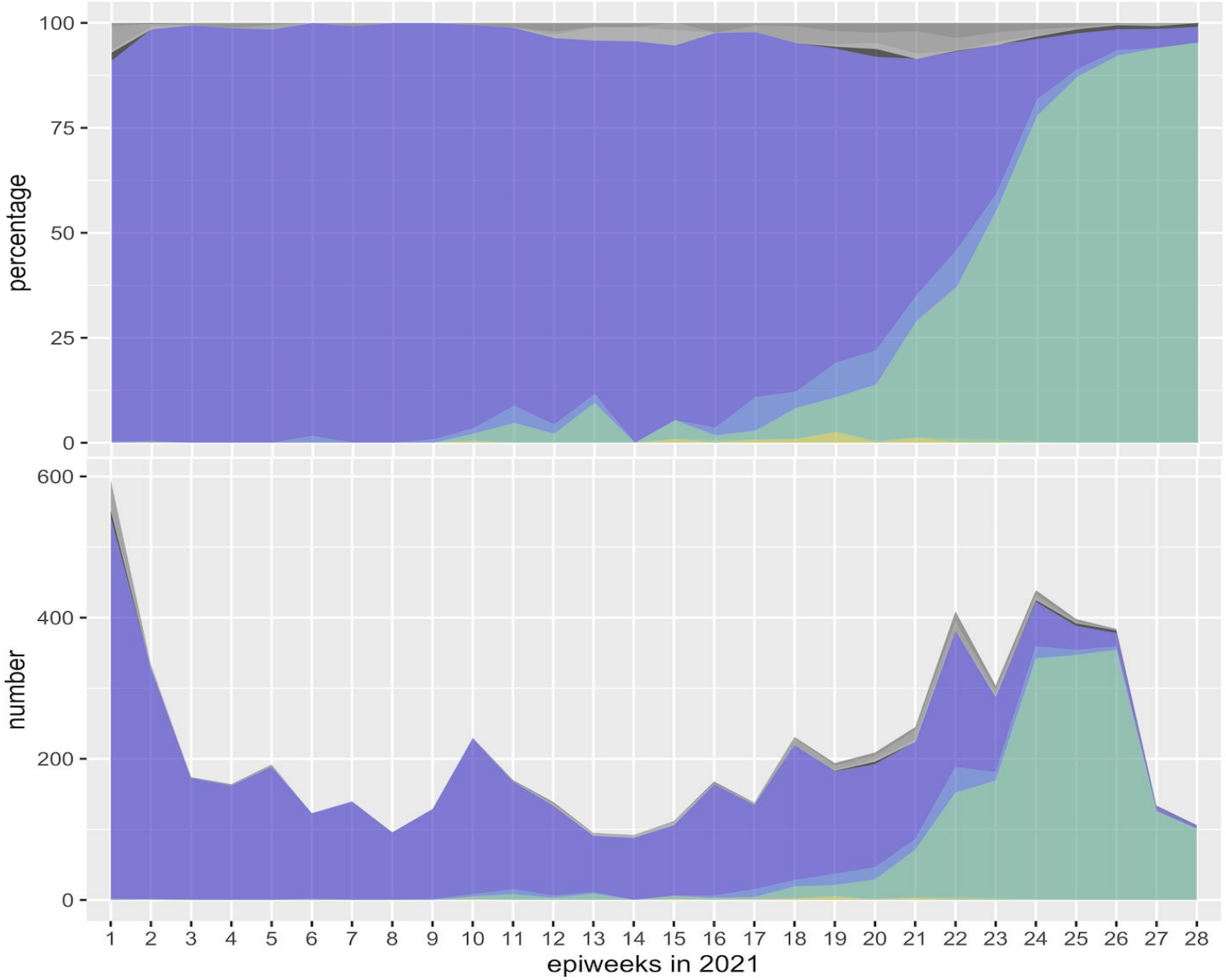
South African genomes submitted per sequencing lab, 2020 and 2021 (N=12 661)



*NGS-SA laboratories

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

Distribution and number of clades in South Africa, 2021 (N=6 631)



Nextclade clades
- 19B
- 20A
- 20B
- 20C
- 20D
- 20H (Beta, V2)
- 20I (Alpha, V1)
- 21A (Delta)
- 21B (Kappa)
- 21D (Eta)

Nextclade clades
- 19B
- 20A
- 20B
- 20C
- 20D
- 20H (Beta, V2)
- 20I (Alpha, V1)
- 21A (Delta)
- 21B (Kappa)
- 21D (Eta)

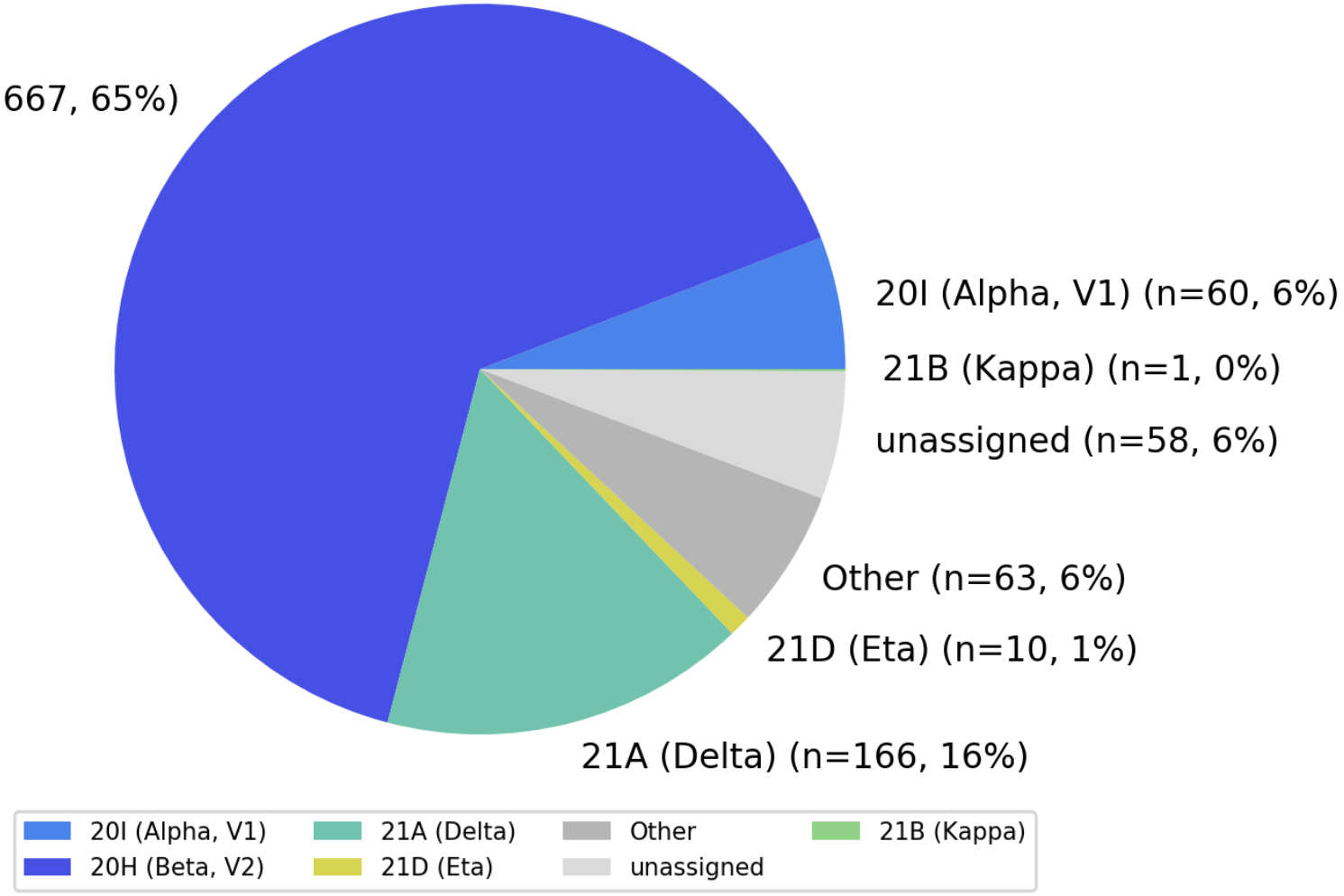
Sequencing data ending epi week 28 (ending 17 July 2021)

Currently in epi week 30 (ending 31 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 (340/439, 77% in week 24; 347/398, 87% in week 25; 354/384, 92% in week 26; 126/134, 94% in week 27 – excluding unassigned sequences)

Prevalence of Variants of Concern (VOC) and Variants of Interest (VOI) in May 2021 sequences, South Africa (N=1 025)

- 88% of sequences are from a VOC (Alpha, Beta, Delta) or VOI (Eta).
- Greater than 10%
  - Beta variant (65%) dominated
  - Delta (16%)
- Less than 10%
  - Alpha (6%).
  - Eta (VOI, 1%)
  - Kappa is present in only one sample (0.1%).



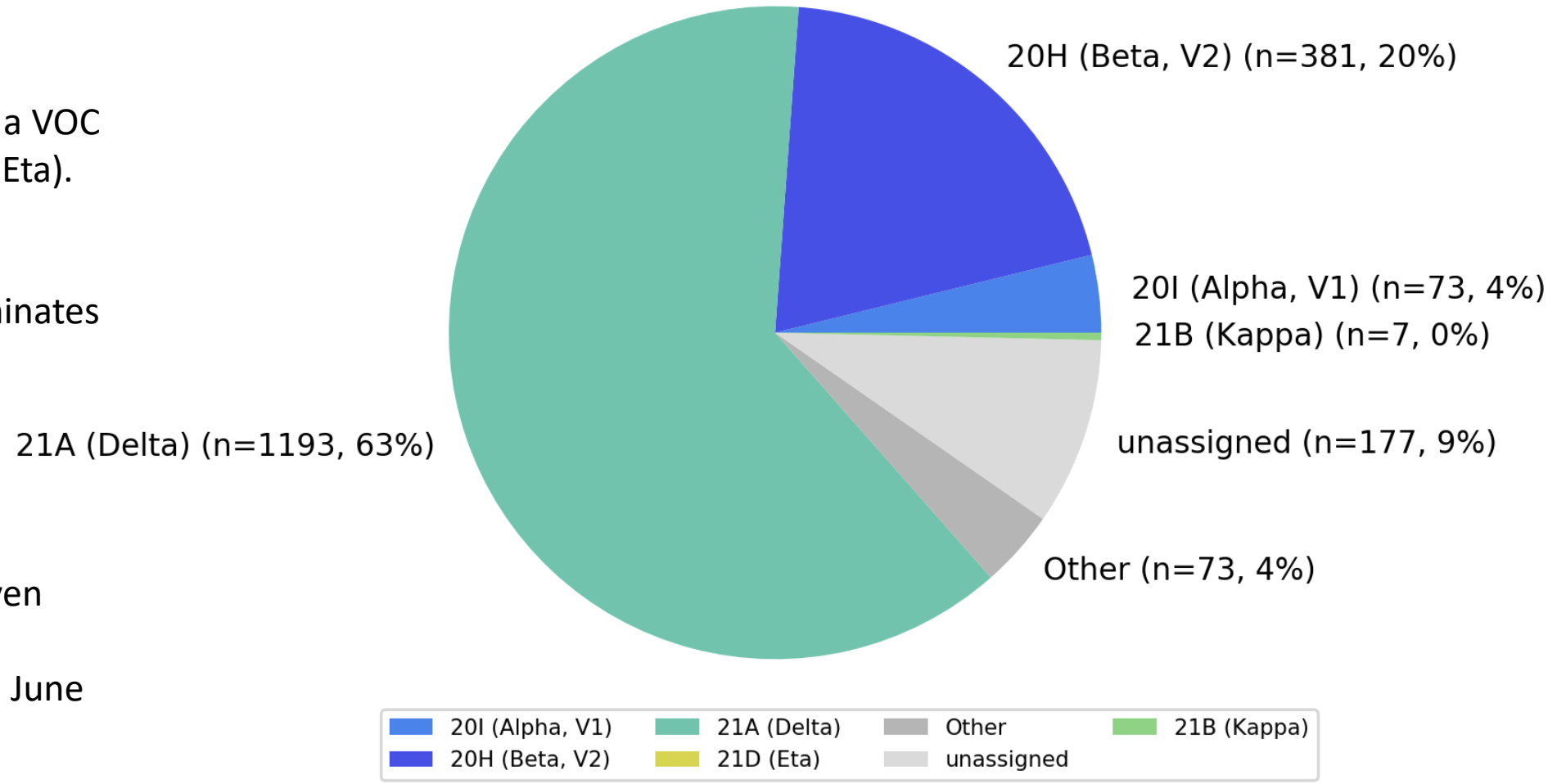
Beta variant dominated in May in South Africa

Prevalence of Variants of Concern (VOC) and Variants of Interest (VOI) in June 2021 sequences, South Africa (N=1 904)

- 87% of sequences are from a VOC (Alpha, Beta, Delta) or VOI (Eta).

- Greater than 10%
  - Delta variant now dominates (63%)
  - Beta variant (20%)

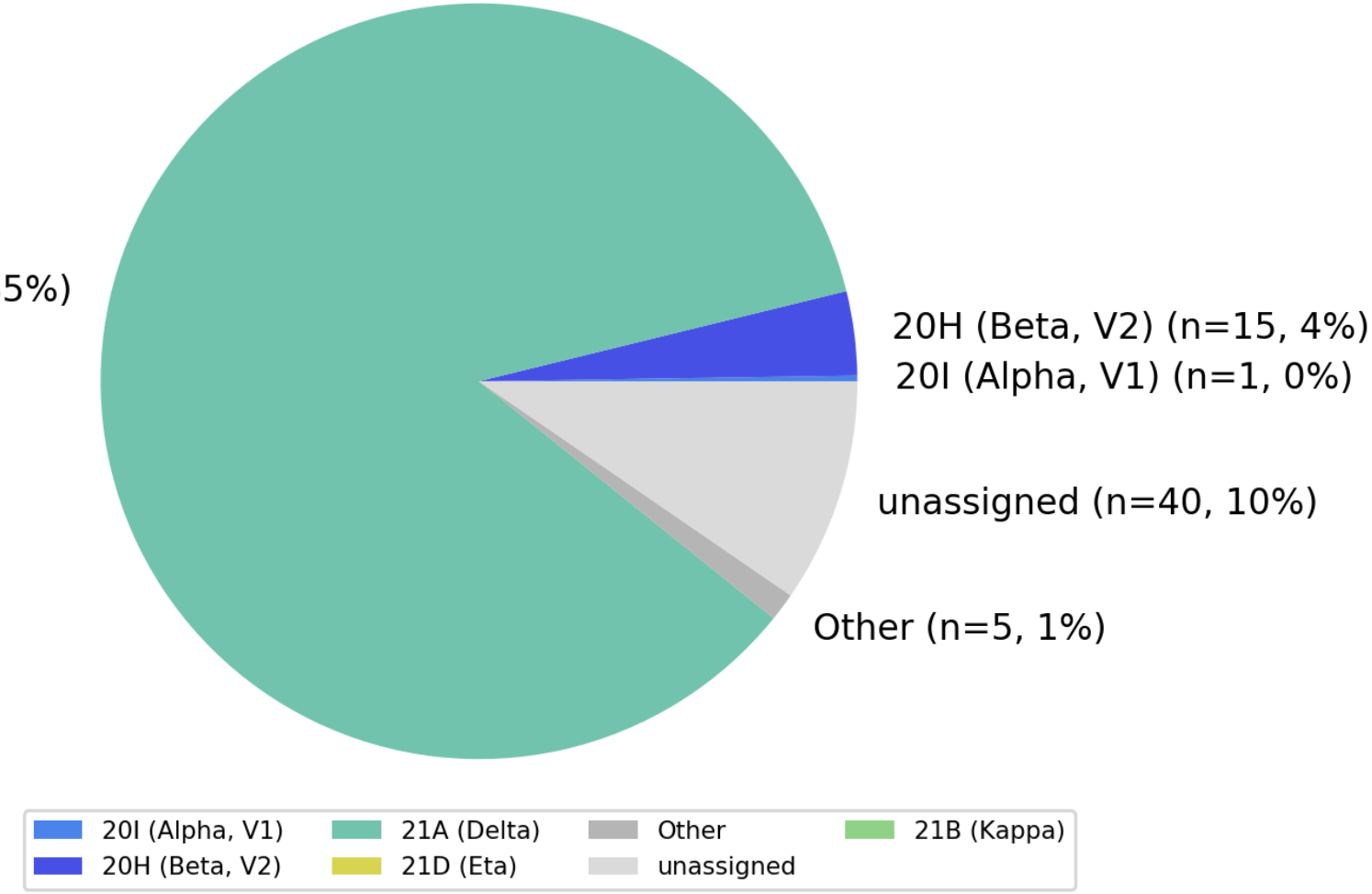
- Less than 10%
  - Alpha (4%).
  - Kappa is present in seven samples (0.4%).
  - Eta not yet detected in June



Delta variant dominated in June in South Africa

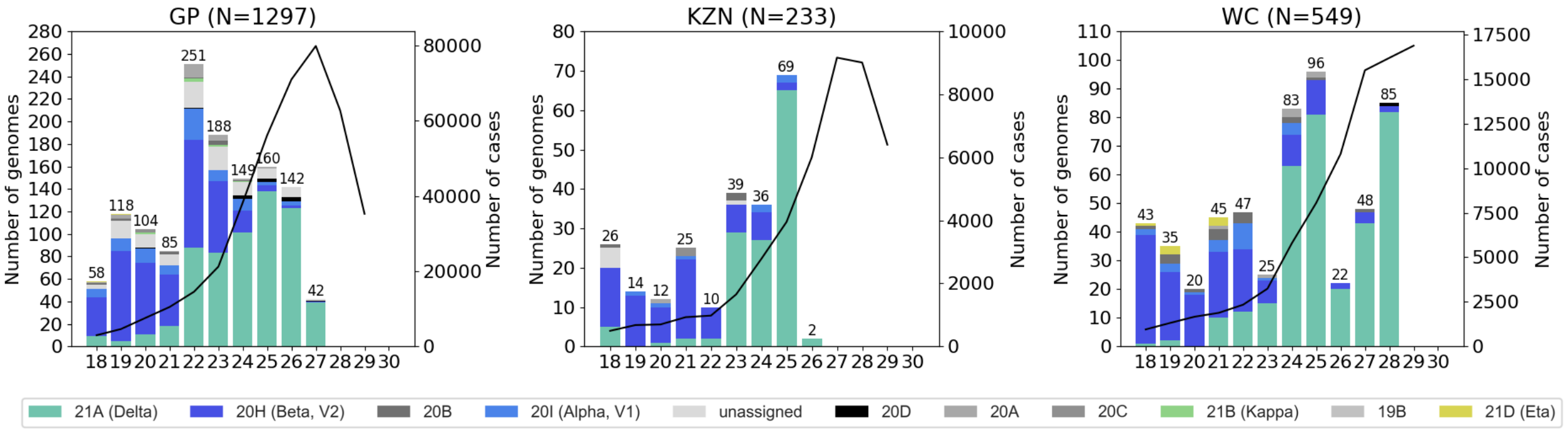
Prevalence of Variants of Concern (VOC) and Variants of Interest (VOI) in July 2021 sequences, South Africa (N=417)

- 89% of sequences are from a VOC (Beta, Delta)
- Greater than 10%
  - Delta variant now dominates (85%)
- Less than 10%
  - Beta (4%)
  - Alpha (0.2%)
- No other VOCs or VOIs detected yet.
- More high quality data is required to establish variant dominance and diversity



Delta variant appears to dominate in July in South Africa so far, but more high quality sequence data is required to confirm this

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) and increases in proportion in later weeks (June and July)
- Eta detected in May but is not present in June and July. Kappa detected in both May and June, but not in July.

KwaZulu-Natal

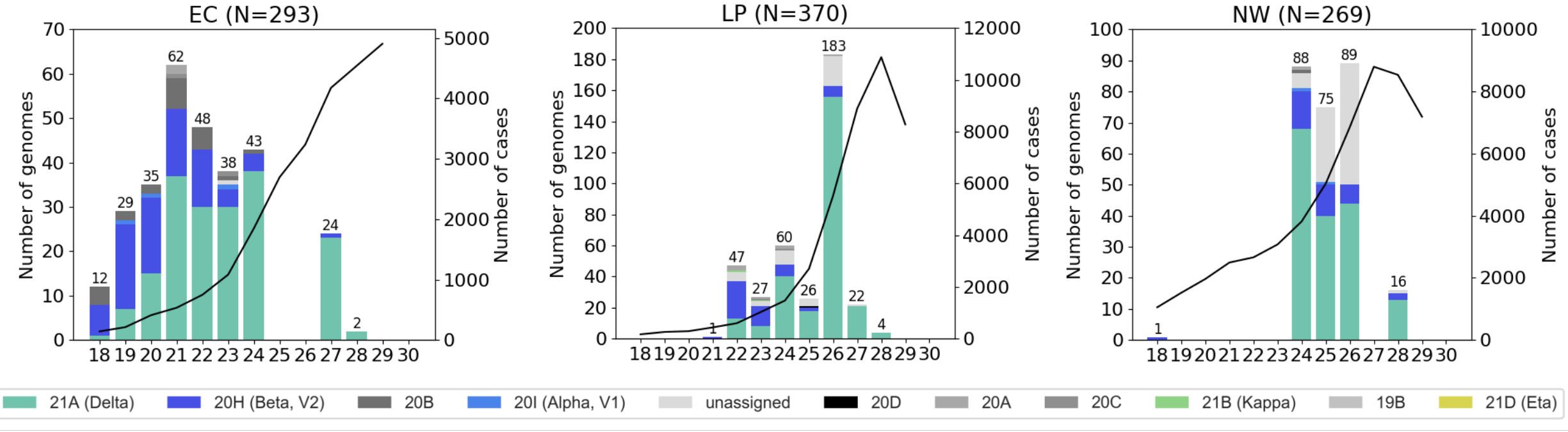
- Delta is present in early weeks (May) and increases in proportion later weeks (June and July)
- Eta and Kappa were not detected.

Western Cape

- Beta dominates until week 22, when Delta increases and rapidly dominates (June). Delta continues to dominate in July.
- Eta is detected in relatively higher numbers than in GP and KZN, but not detected in most recent weeks.

Beta dominates in all provinces in May, however by mid-June Delta dominates in GP, KZN and WC. Delta continues to dominate in July

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



Eastern Cape

- Delta detected in early May, rapidly increases to predominate by end of May, and remains dominant in most recent time points (July)
- Alpha detected at low frequency in May and only once in June.

Limpopo

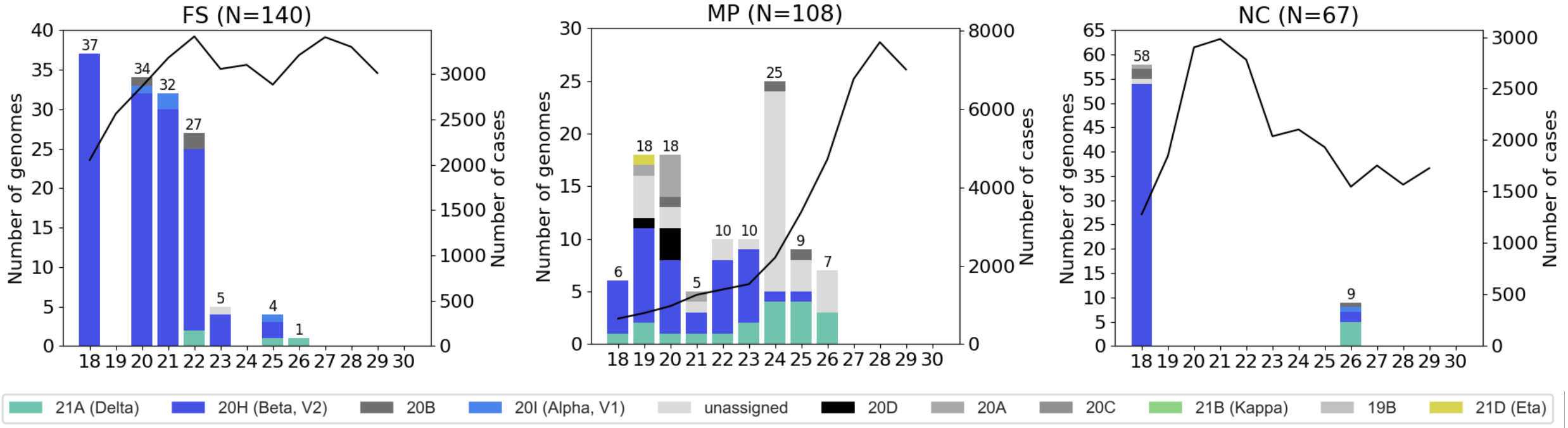
- Delta detected at the end of May and predominates by early June.
- Kappa detected at low frequency in May and early June, but not in July.

North-West

- Delta detected at high proportion in June and July, but additional earlier 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, Mpumalanga 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

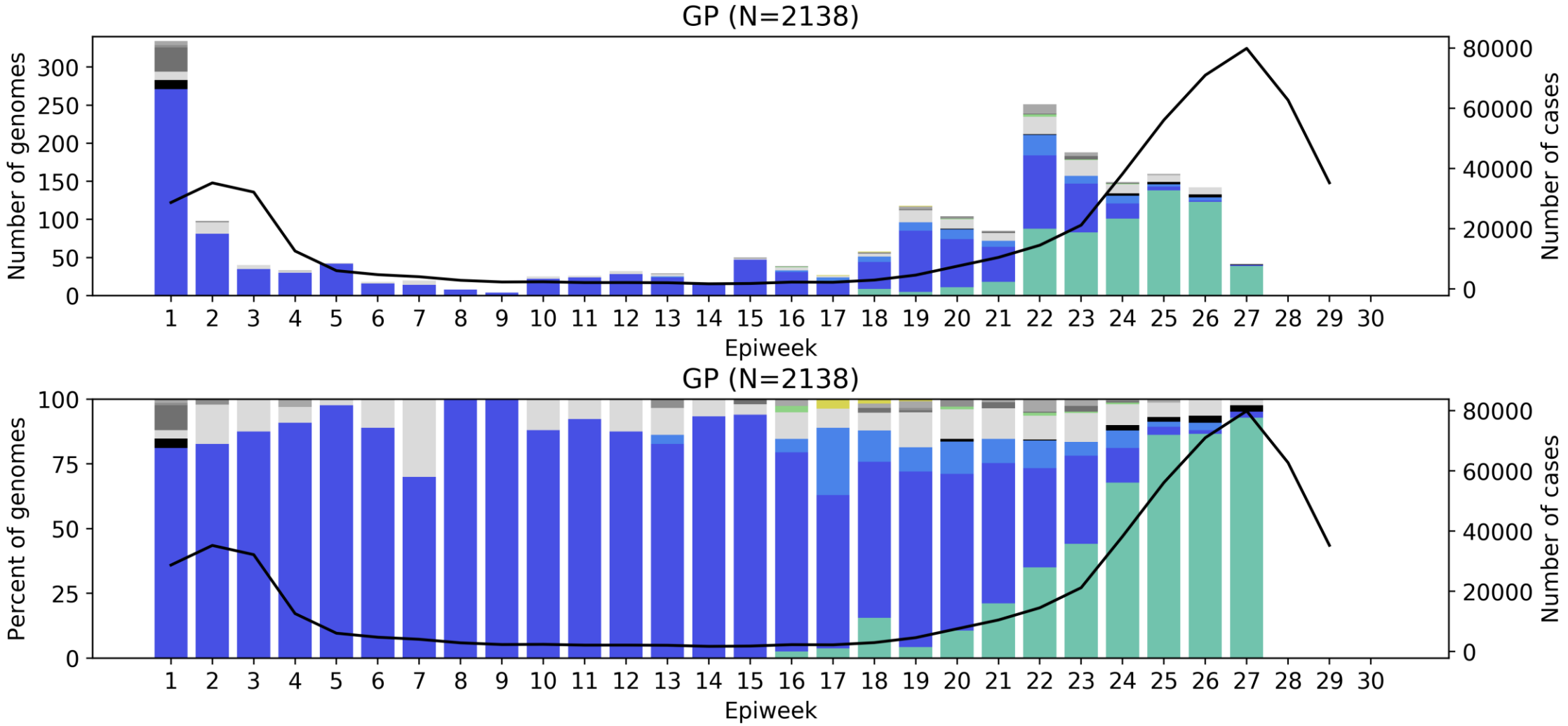
- Delta detected throughout May and June, however increased specimen numbers required to estimate predominance of a particular variant

Northern Cape

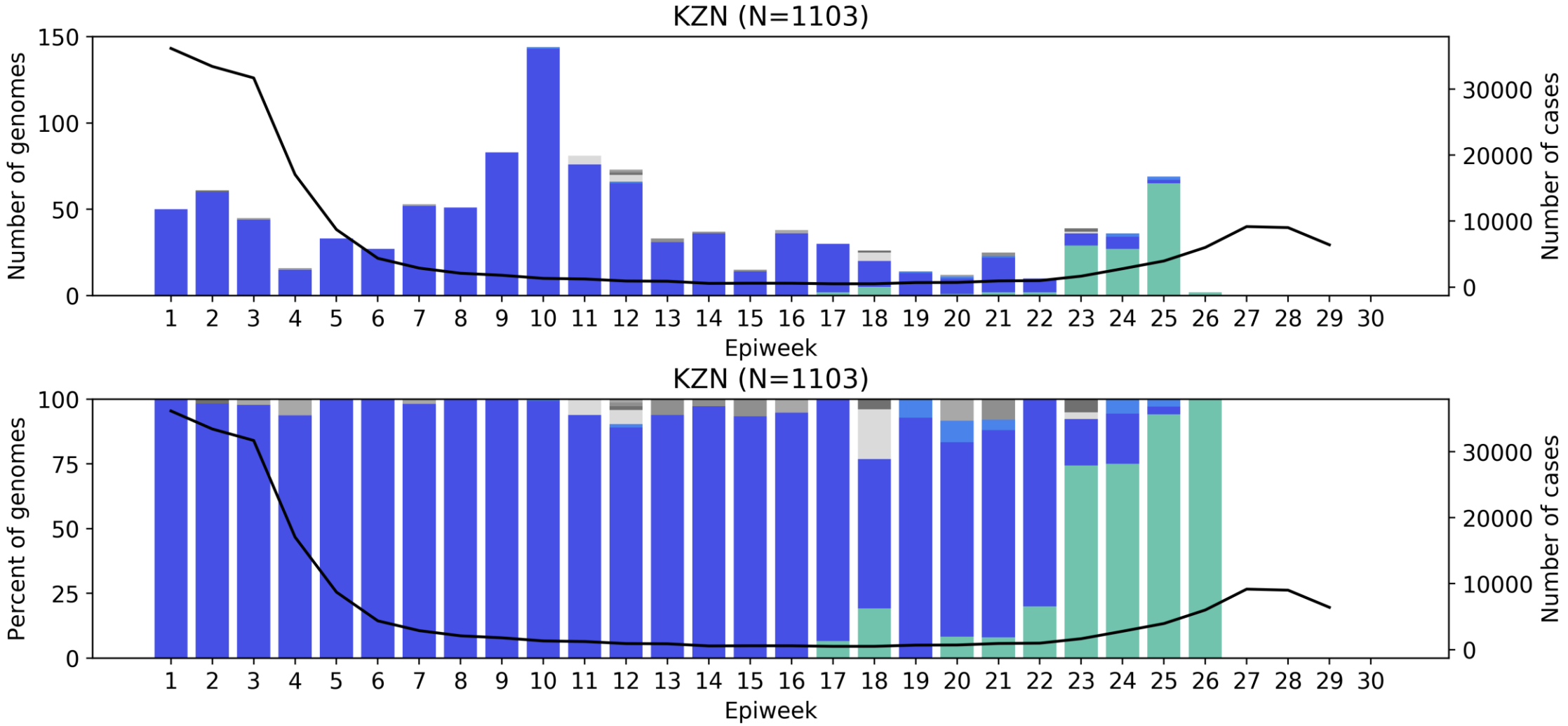
- Delta was detected in March (not shown, see later slides) in Northern Cape, but the Beta variant continued to cause a significant number of infections
- Delta again detected at most recent time point, but more sequences are required to establish prevalence levels

Recent data is required from these provinces to estimate the dominance of Delta

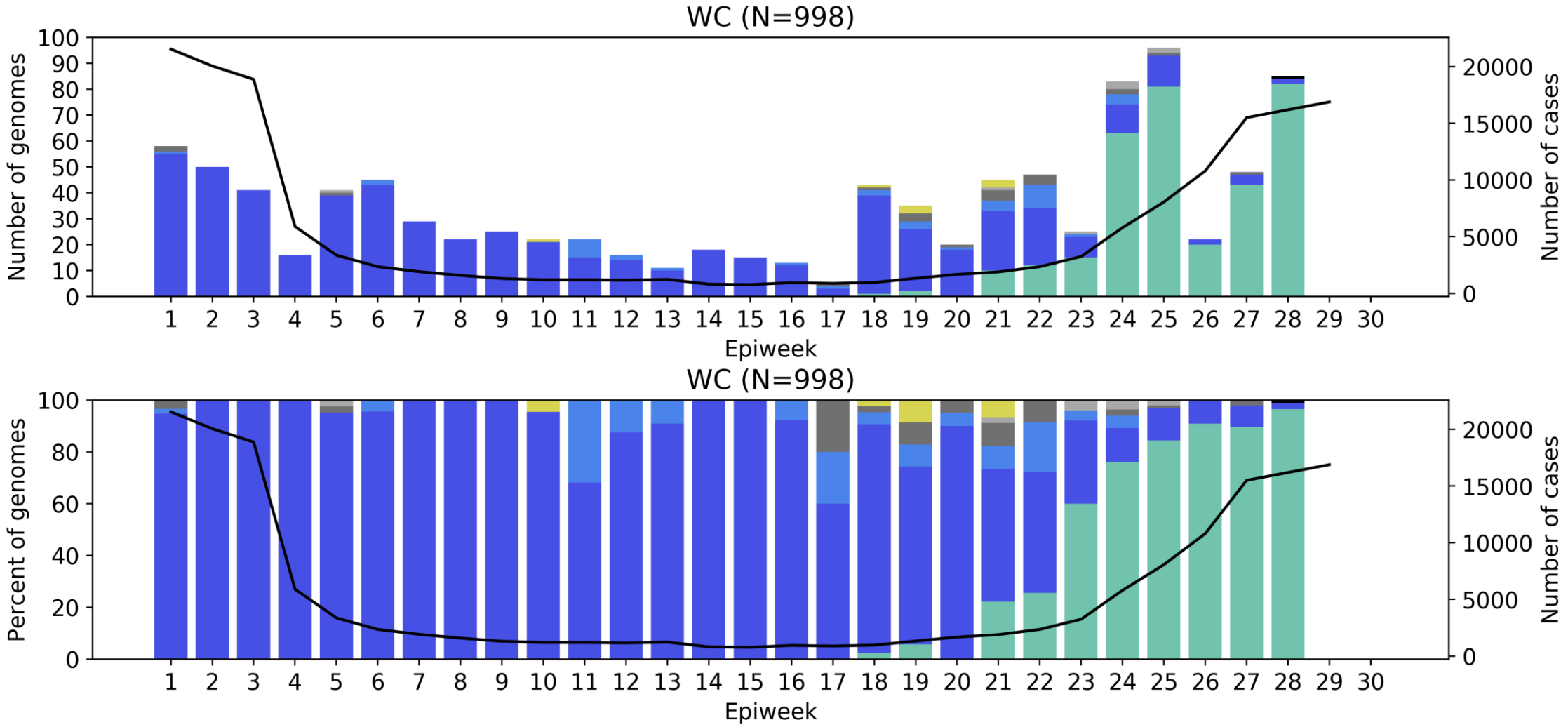
Gauteng Province, 2021, n = 2 138



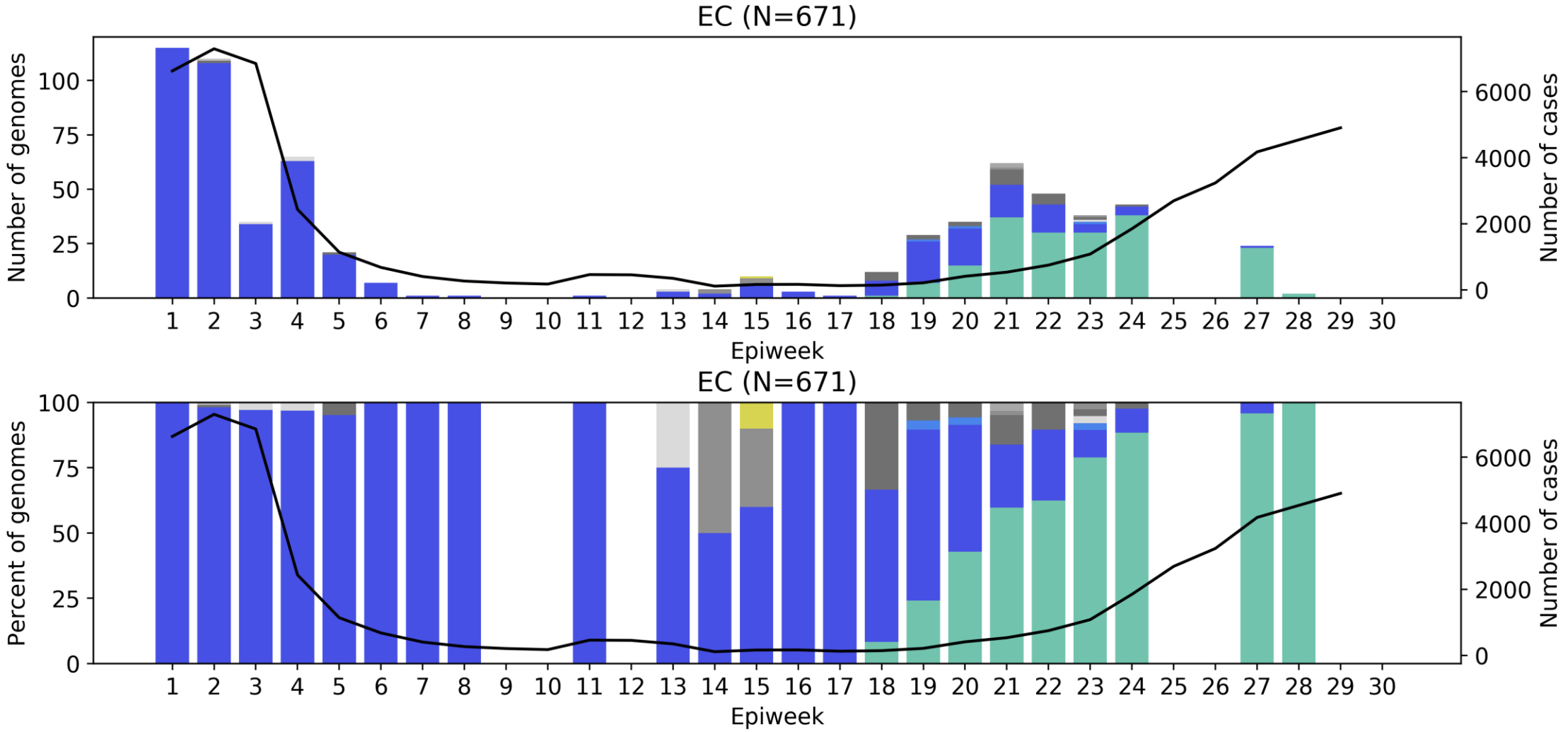
KwaZulu-Natal Province, 2021, n = 1 103



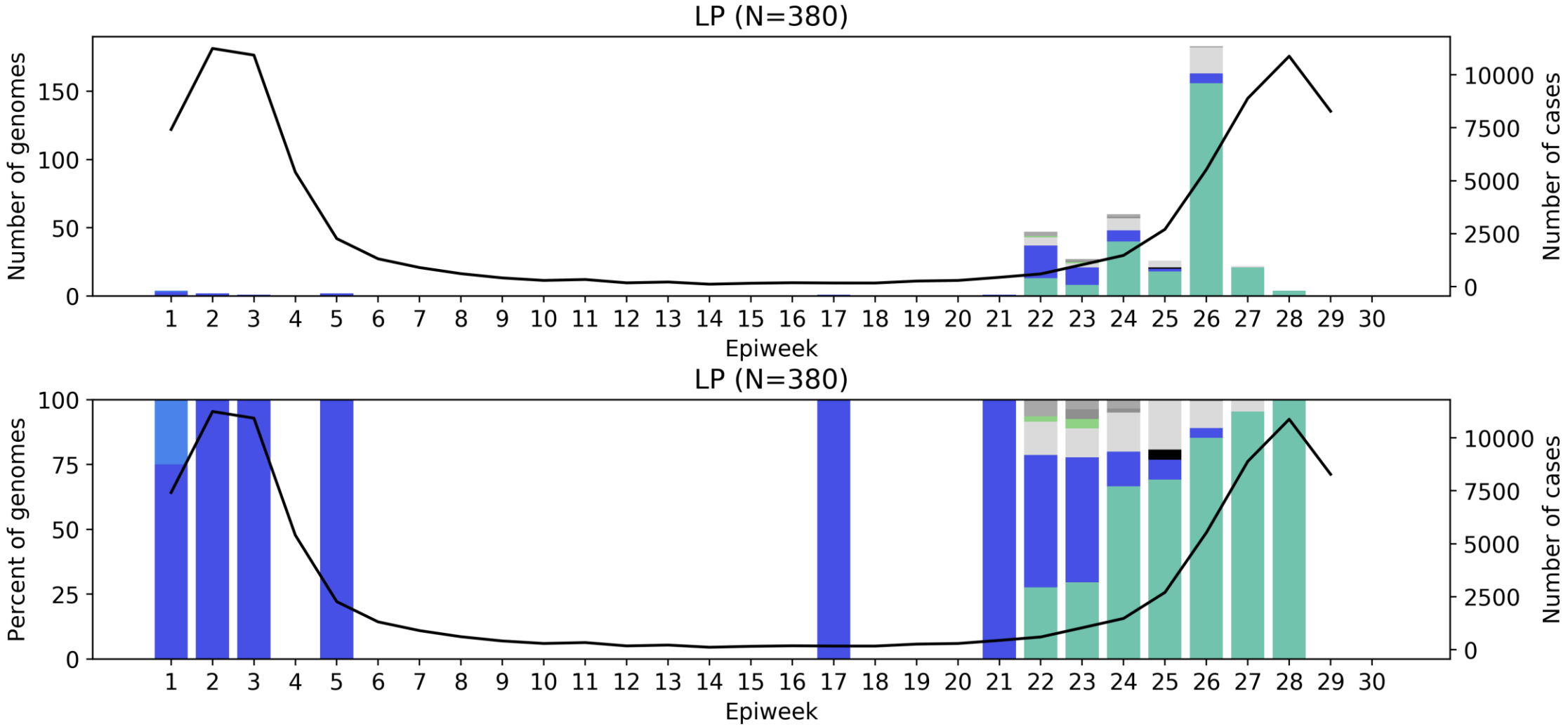
Western Cape Province, 2021, n = 998



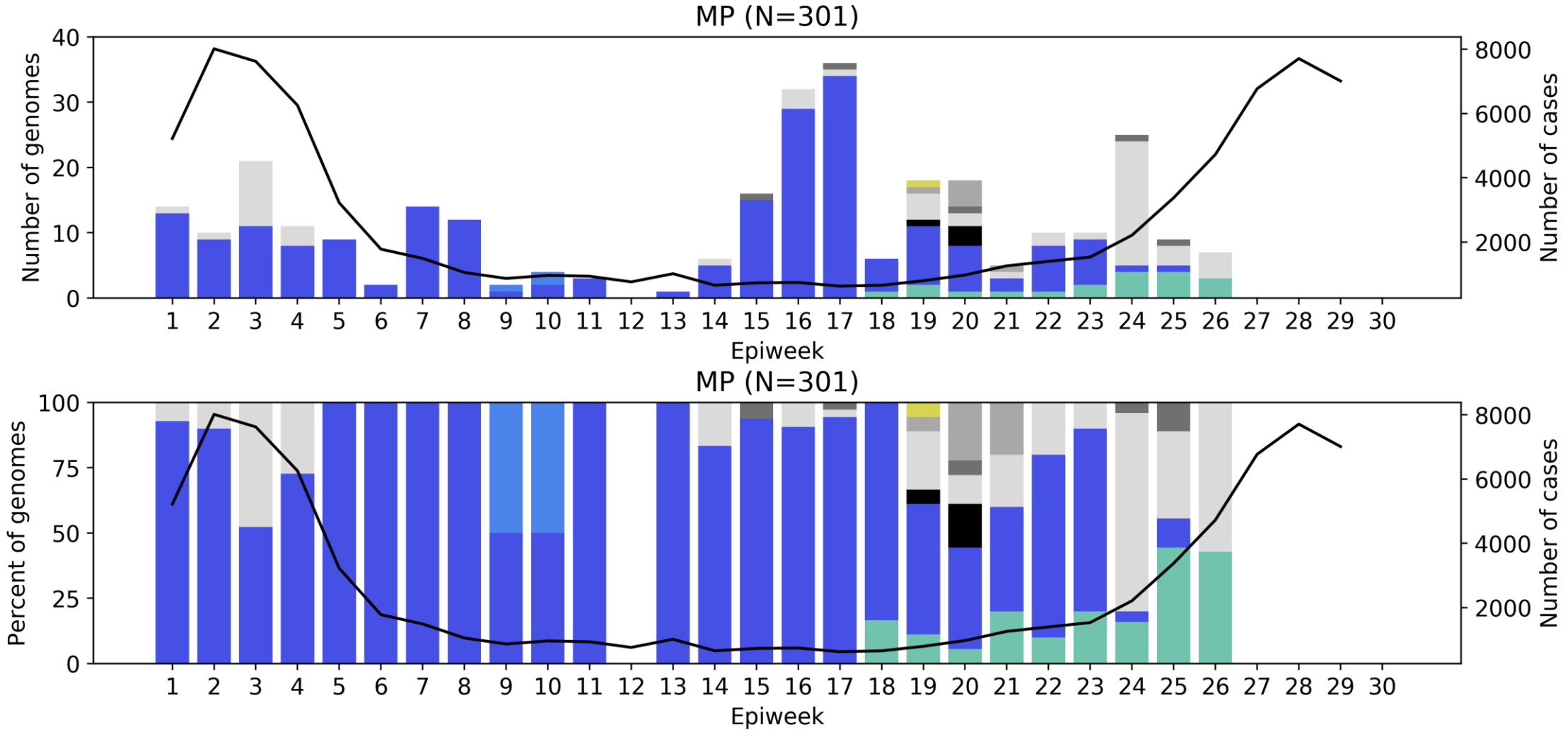
Eastern Cape Province, 2021, n = 671



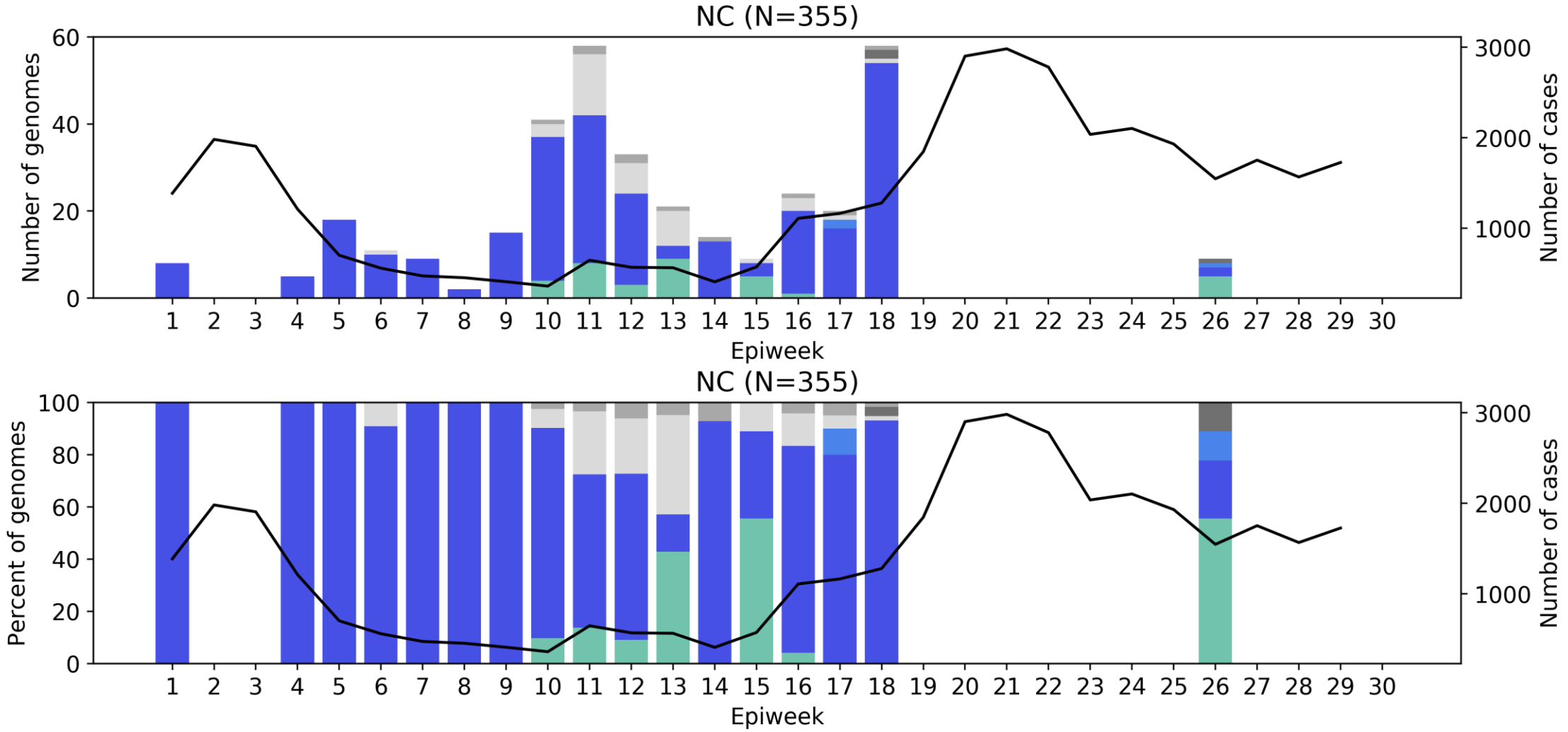
Limpopo Province, 2021, n = 380



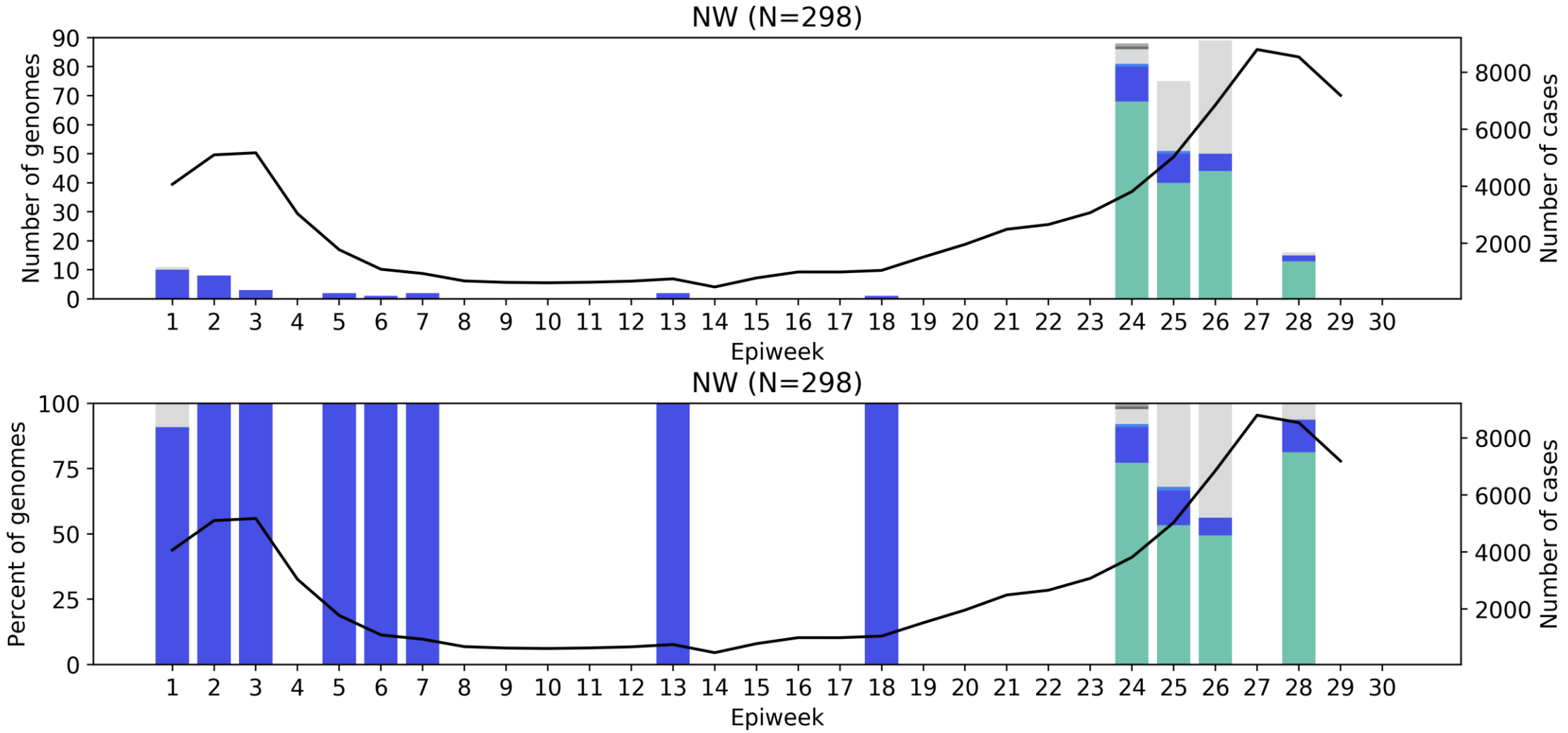
Mpumalanga Province, 2021, n = 301



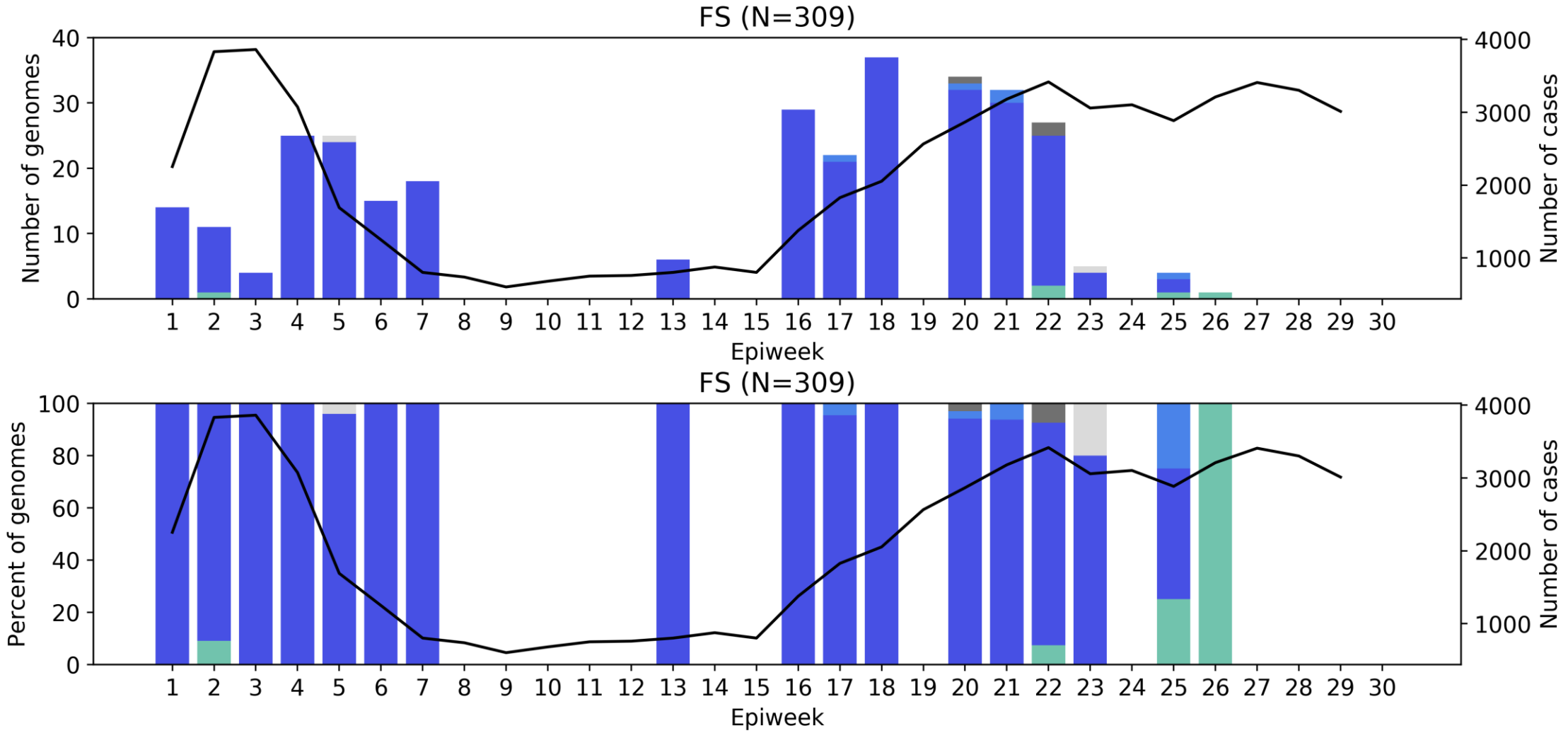
Northern Cape Province, 2021, n = 355



North West Province, 2021, n = 298

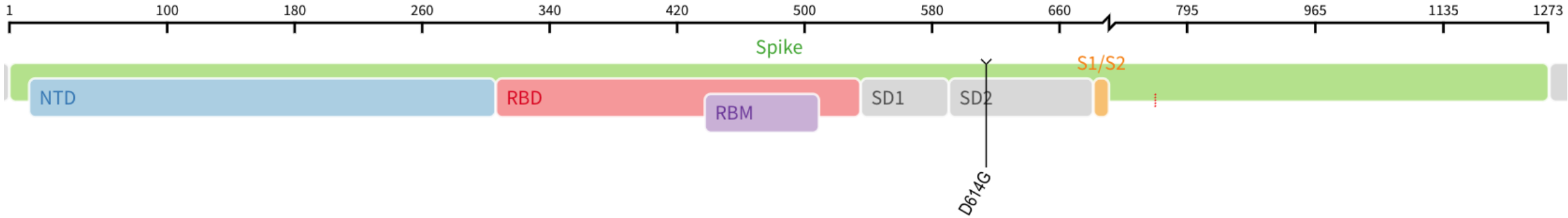


Free State Province, 2021, n = 309

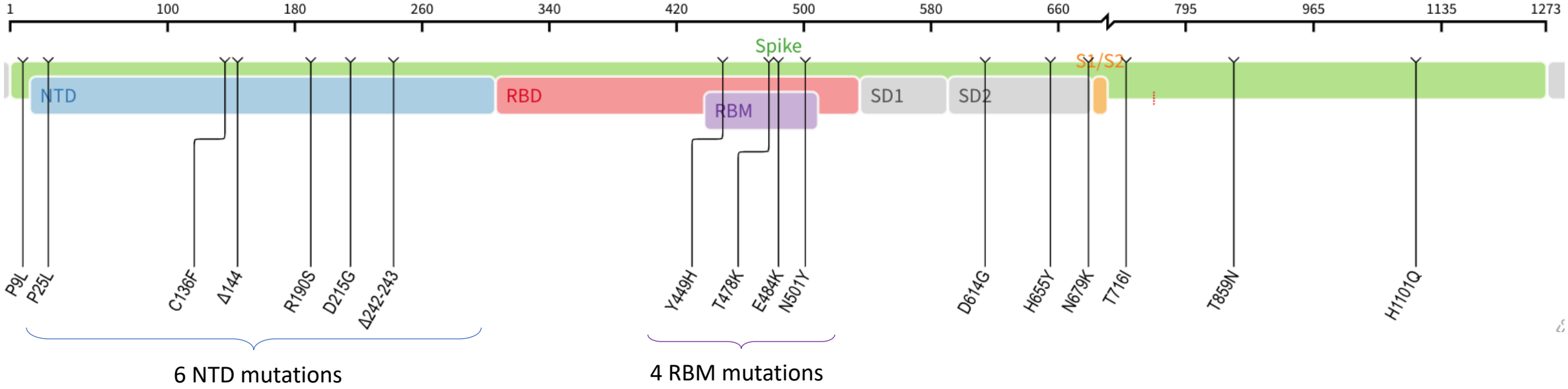


Mutated C.1 spike mutations: January vs June (2021)

Spike mutation profile from N3342 (January 2021).



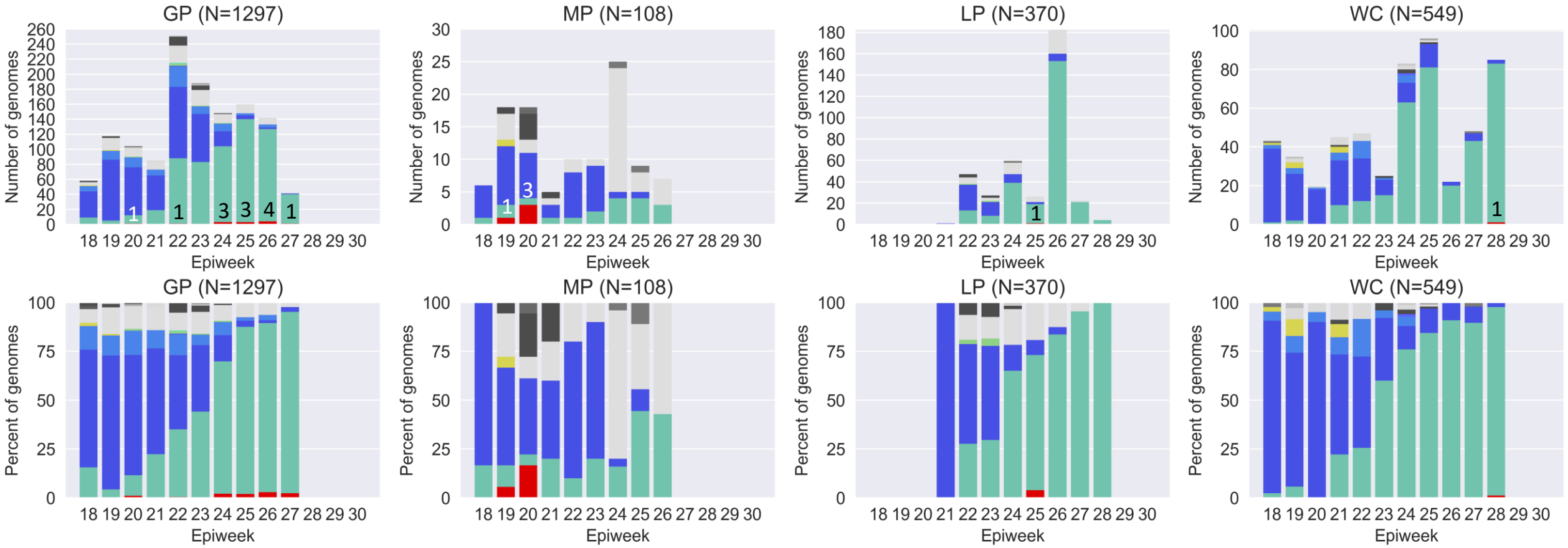
Spike mutation profile from N9382 (June 2021).



C.1 has evolved to include multiple spike mutations, many of which are shared with other VOCs.

C.1 (n=19) in May, June and July 2021 by epi week

Total number of C.1 for each epi week indicated above bar



C.1 continues to be detected in GP and has now been detected in WC at the most recent timepoint (epi week 28, July 14th)

Summary

- In June, Delta increases significantly and dominates in 8/9 provinces with available data.
- For July new data since last week's update from GP, WC, EC and LP shows continued Delta dominance
- Variant diversity appears to have decreased with the dominance of Delta.
- C.1 lineage continues to be detected in Gauteng and has now also been detected in WC.

NICD Acknowledgements

- **Thabo Mohale**
- **Daniel Amoako**
- **Cathrine Scheepers**
- **Josie Everatt**
- **Boitshoko Mahlangu**
- **Noxolo Ntuli**
- **Anele Mnguni**
- **Amelia Buys**
- **Cardia Fourie**
- **Noluthando Duma**
- **Linda de Gouveia**
- **Jackie Kleynhans**
- **Nicole Wolter**
- **Zamantungwa Khumalo**
- **Annie Chan**
- **Morne du Plessis**
- **Constantinos Kurt Wibmer**
- Thandeka Moyo
- Tandile Hermanus
- Frances Ayres
- Zanele Molaudzi
- Bronwen Lambson
- Tandile Hermanus
- Sibongile Walaza
- Mignon du Plessis
- Stefano Tempia
- CRDM lab and epi staff
- Mvuyo Makhasi
- Brent Oosthuysen
- Susan Meiring
- Mashudu Madzivhandila
- Prudence Kgagudi
- Mushal Allam
- NICD SARS-CoV-2 Sequencing Group
- Stanford Kwenda
- Phillip Senzo Mtshali
- Ranmini Kularatne
- **Arshad Ismail**
- **Penny Moore**
- **Anne von Gottberg**
- **Cheryl Cohen**
- **Lynn Morris**
- **Jinal Bhiman**
- Erica Anderson-Nissen
- Anneta Naidoo
- Raymond Rott
- **Simon Travers (Hyrax Biosciences)**

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COVID Incident Management Team

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science & technology
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Science and Technology
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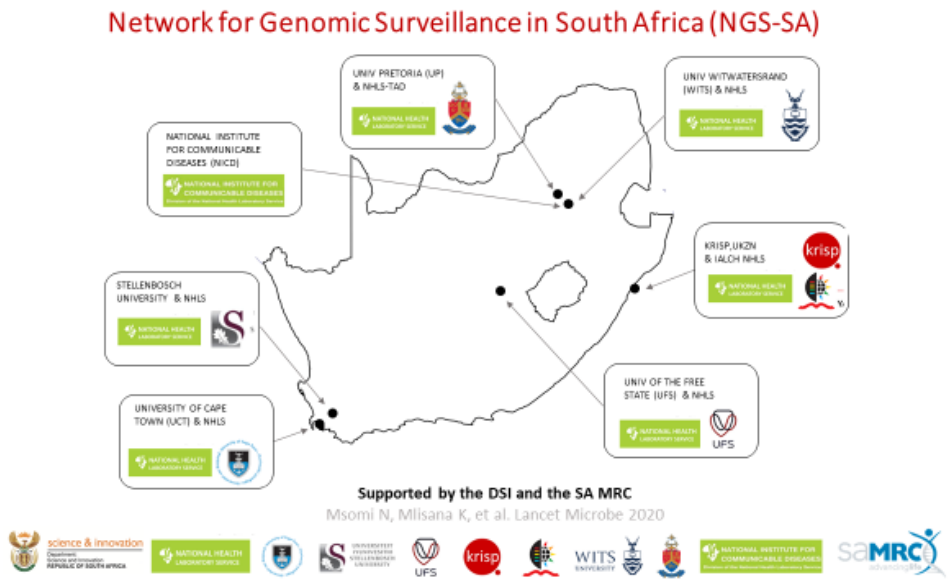
The Fleming Fund

Multi-institute, multi-disciplinary NGS team



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NATIONAL HEALTH LABORATORY SERVICE

UFS Acknowledgements

- Dominique Goedhals
- Armand Bester
- Martin Nyaga
- Peter Mwangi
- Emmanuel Ogunbayo
- Milton Mogotsi
- Makgotso Maotoana
- Lutfiyya Mahomed

NHLS Division of Virology:

- Sabeehah Vawda
- Felicity Burt
- Thokozani Mkhize
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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.)