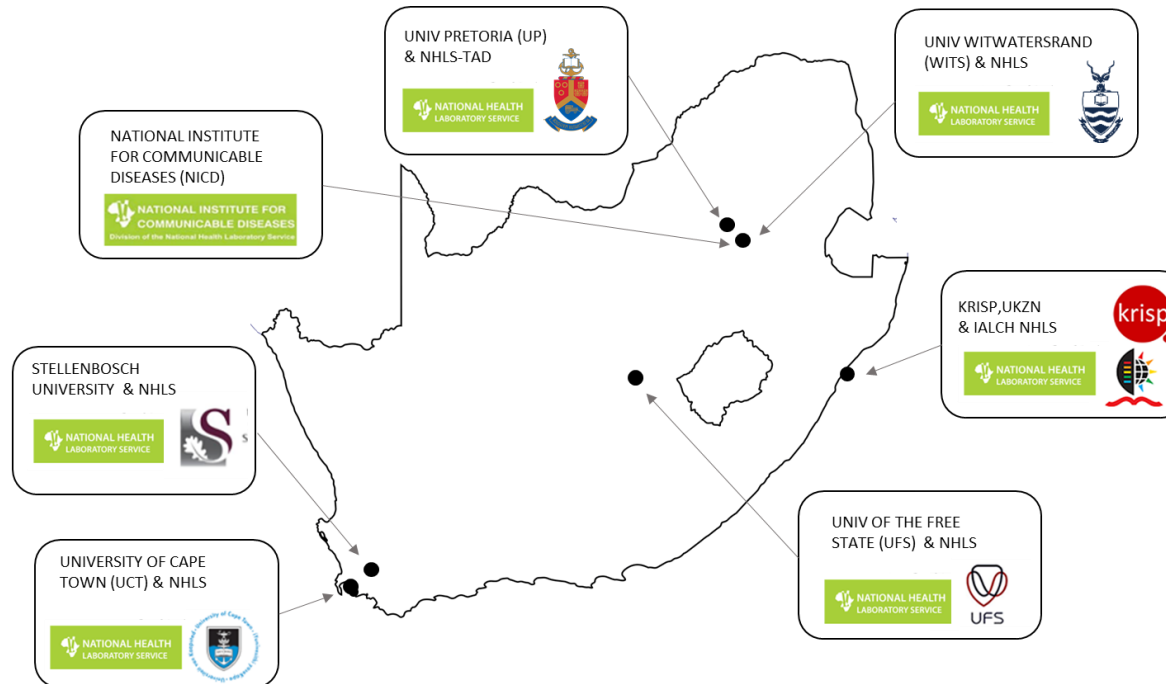


SARS-CoV-2 Sequencing Update 15 October 2021



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) on 15 October at 17h20



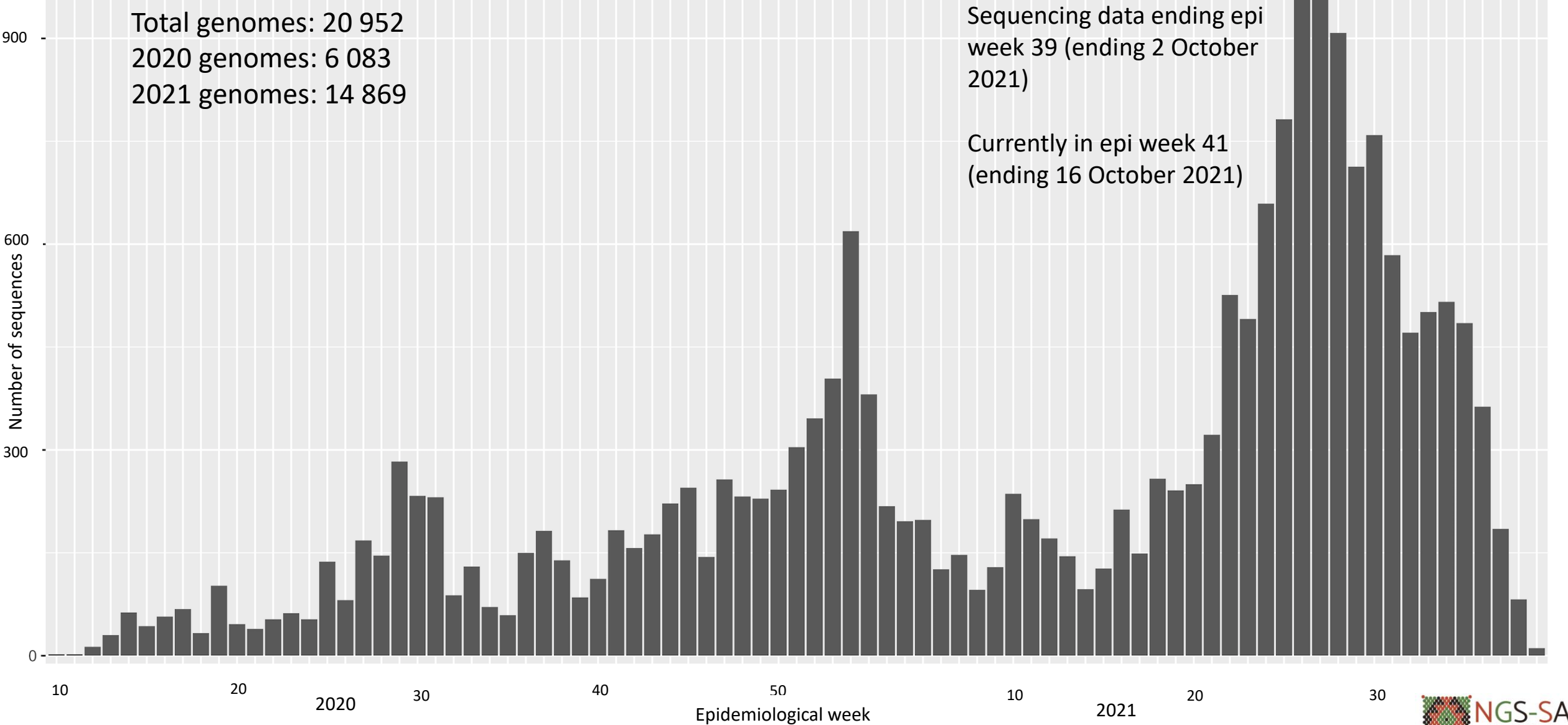
Data license: <https://www.gisaid.org/registration/terms-of-use/>

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

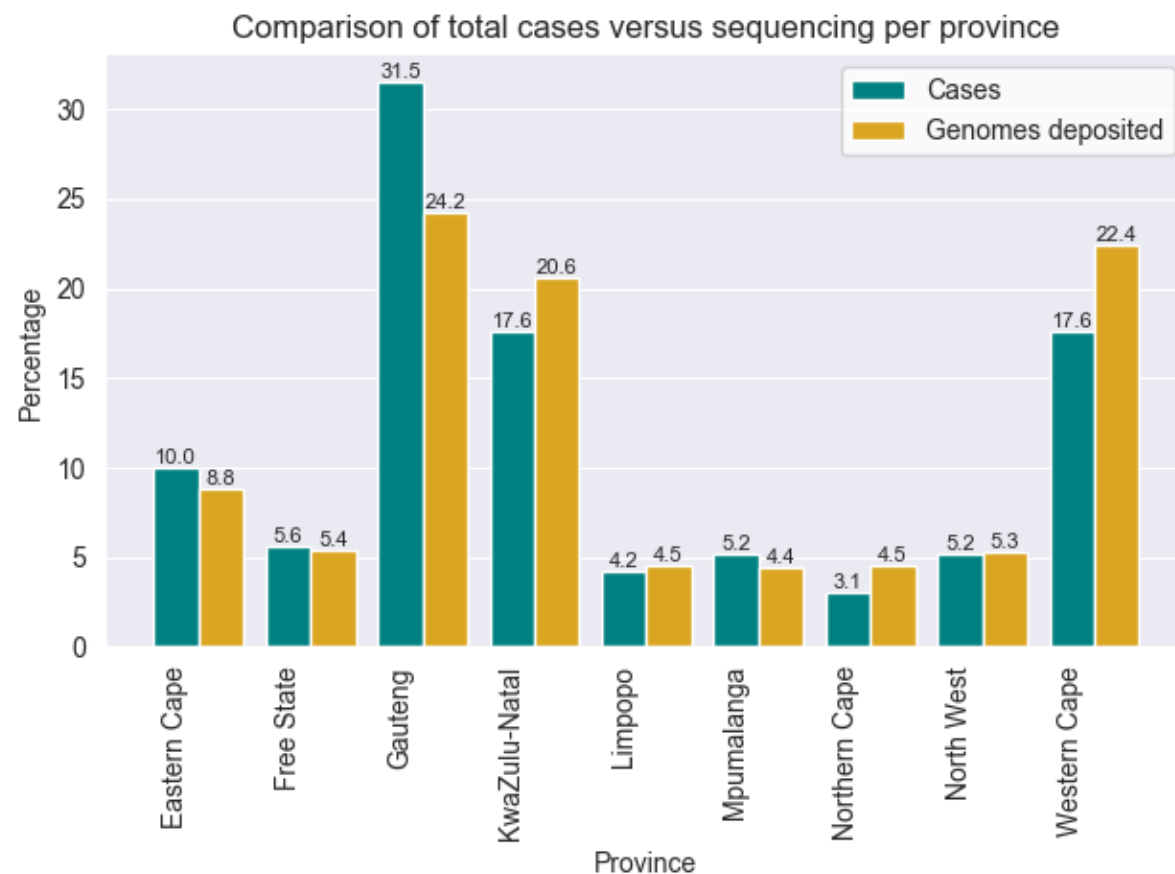
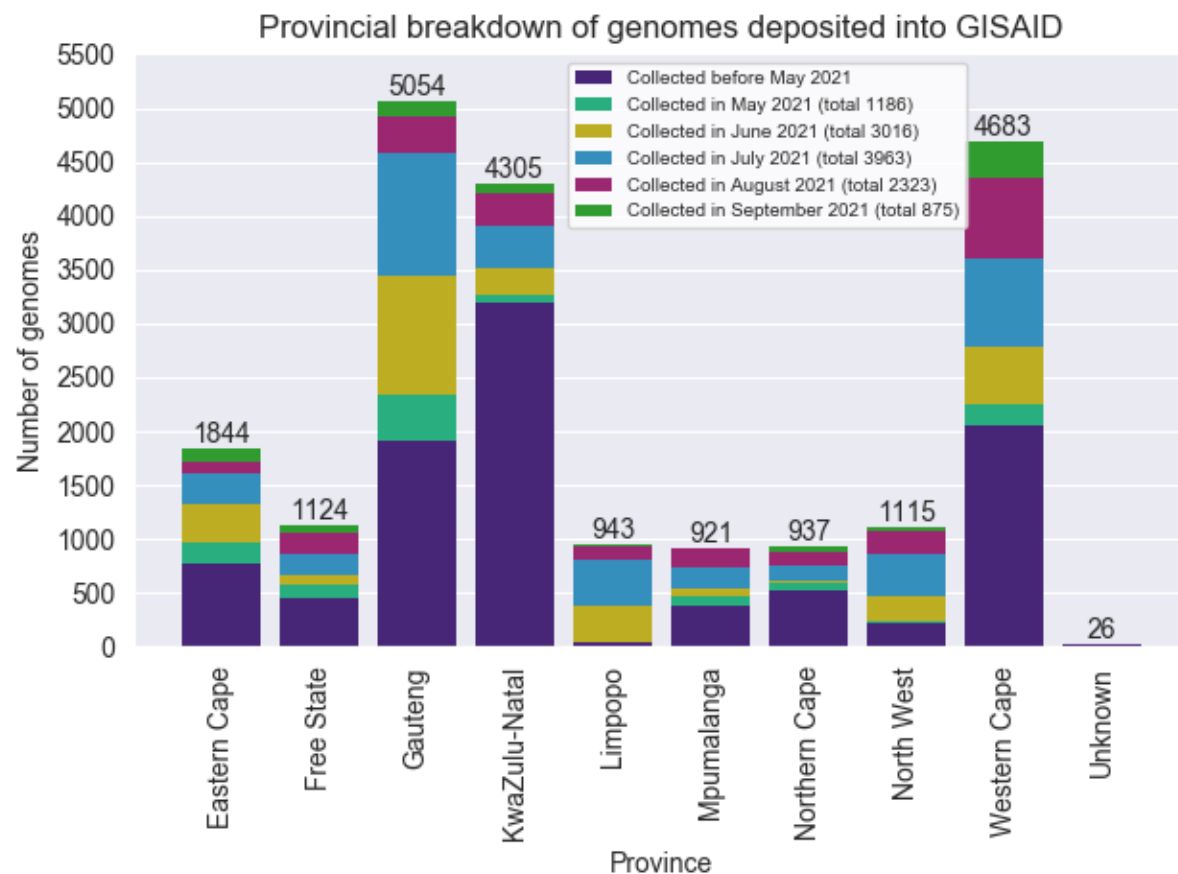
Case data is based on specimen collection date. Cases from <https://www.nicd.ac.za/diseases-a-z-index/disease-index-covid-19/surveillance-reports/weekly-epidemiological-brief/>

Number of South African genomes deposited on GISAID, by specimen collection week, 2020 and 2021 (N=20 952*)



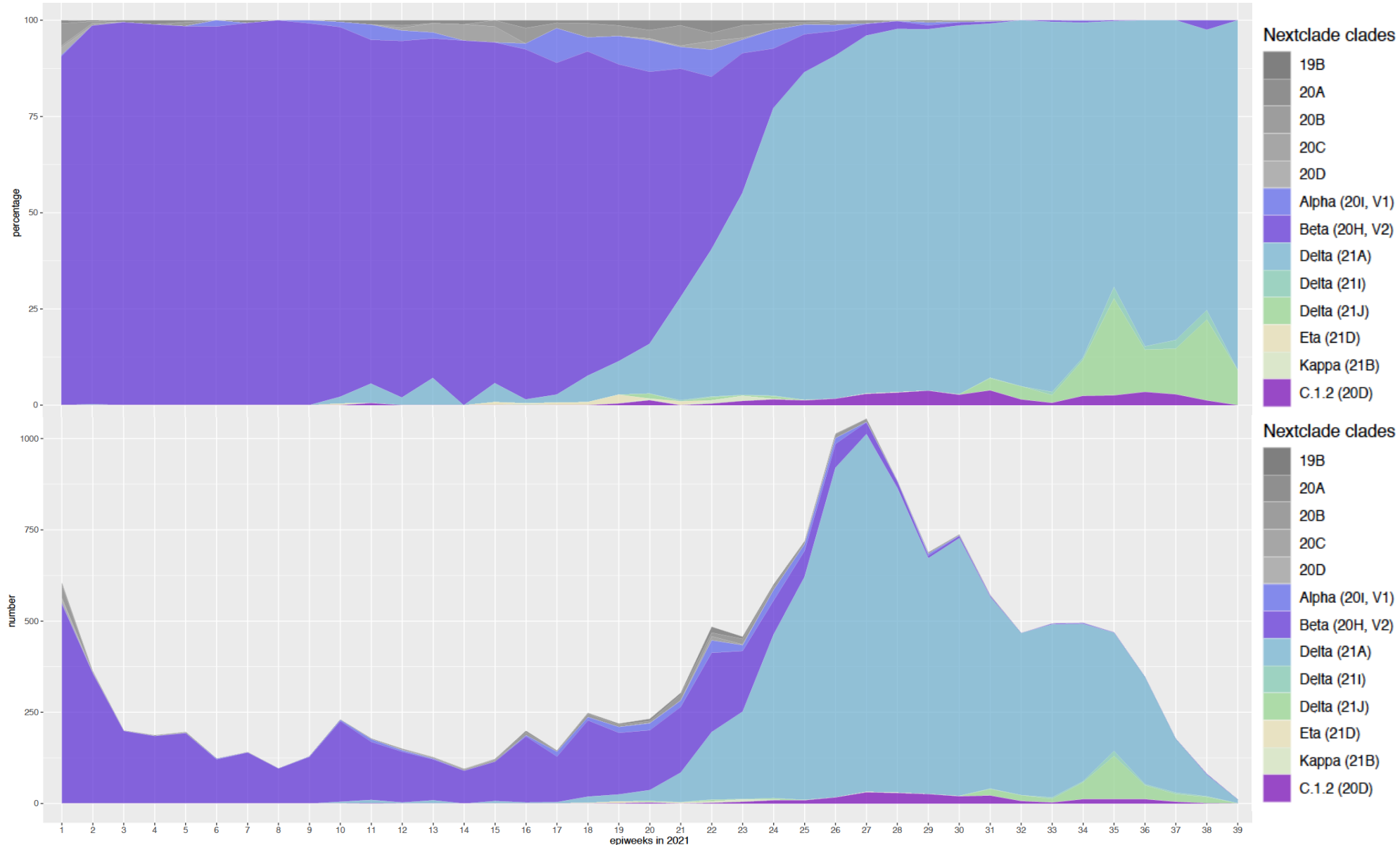
*This represents the cleaned, de-duplicated dataset of unique sequences. This dataset will be used for all further figures.

GISAID genomes vs total cases, 2020 and 2021 (N=20 952)



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= 14 869)



Delta has recently been split into three clades (21A, 21I, 21J). We are in the process of updating the classification of all Delta samples submitted to date.

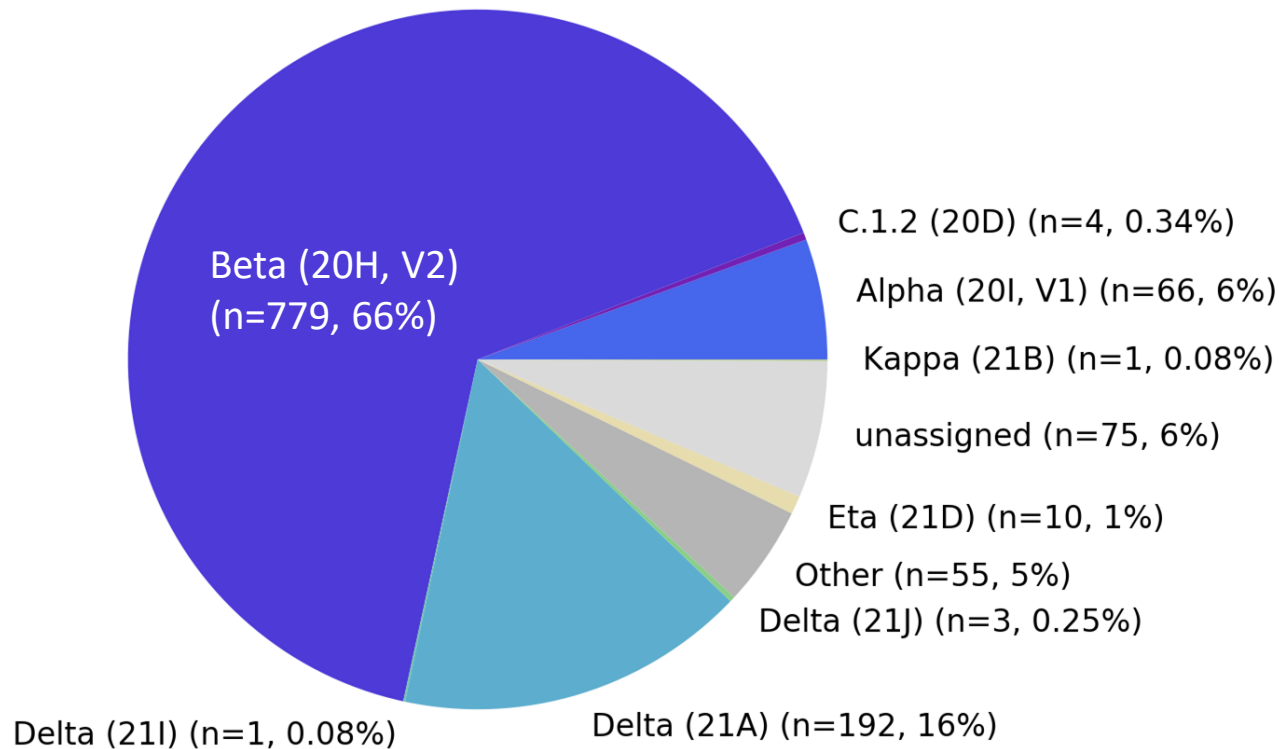
Sequencing data ending epi week 39 (ending 2 October 2021)

Currently in epi week 41 (ending 16 October 2021)

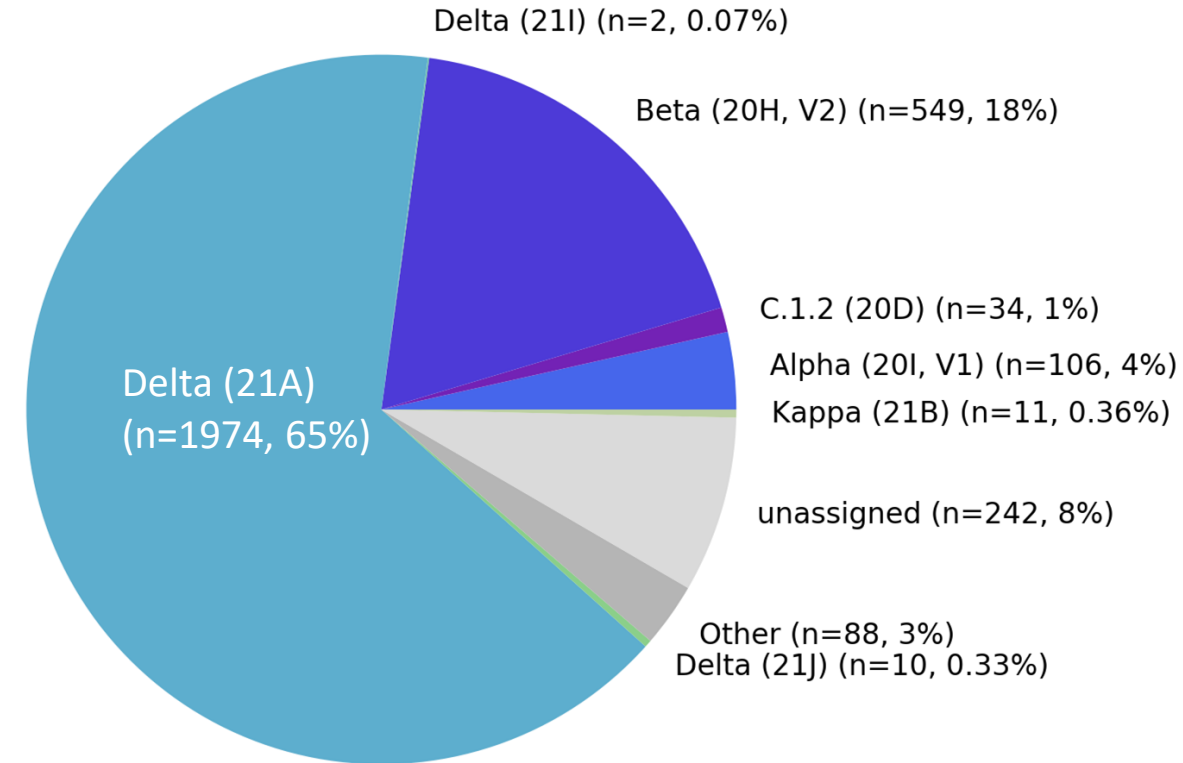
Delta came to dominate by end June at >65% , in July at >85% and in August and September at >90%
C.1.2 present at <4% frequency since March

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

May (N=1186)



June (N=3016)

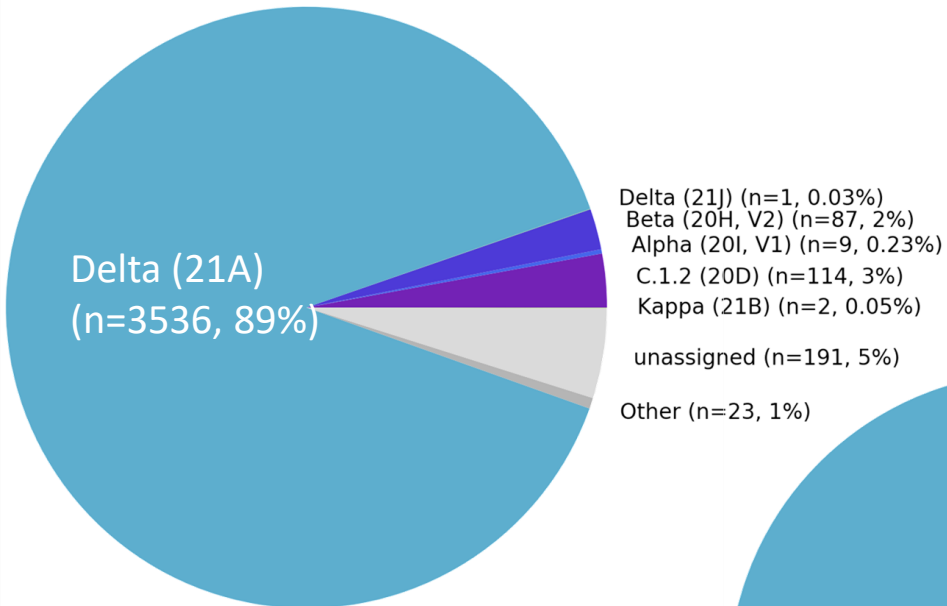


Legend: Beta (20H, V2) Alpha (20I, V1) Delta (21A) Delta (21I) Delta (21J) C.1.2 (20D) Kappa (21B) Eta (21D) Other unassigned

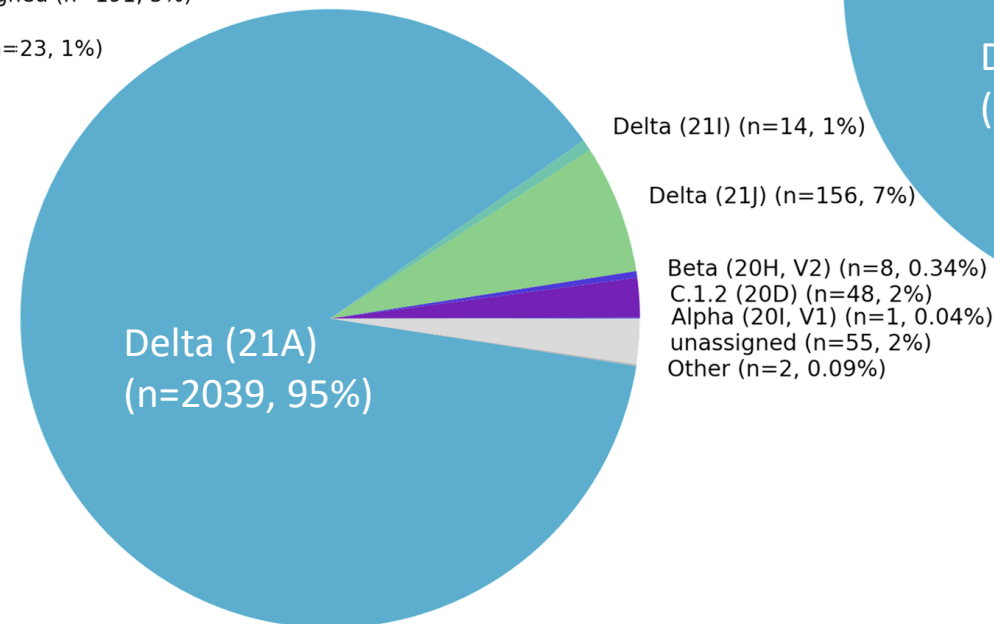
Beta variant dominated in May, but the Delta variant started to dominate in June

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

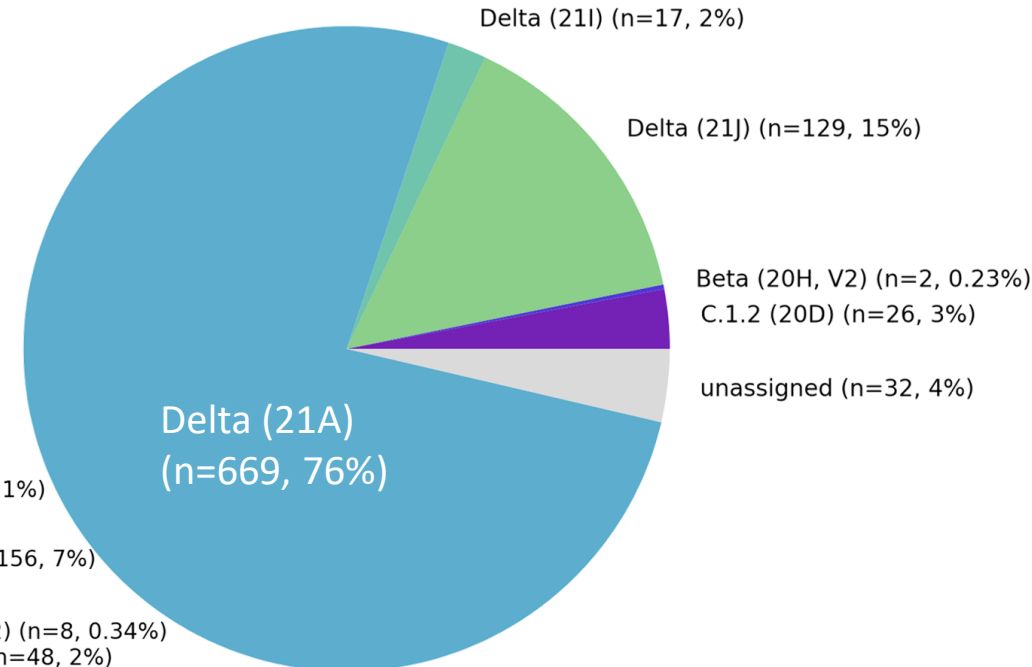
July (N=3963)



August (N=2323)



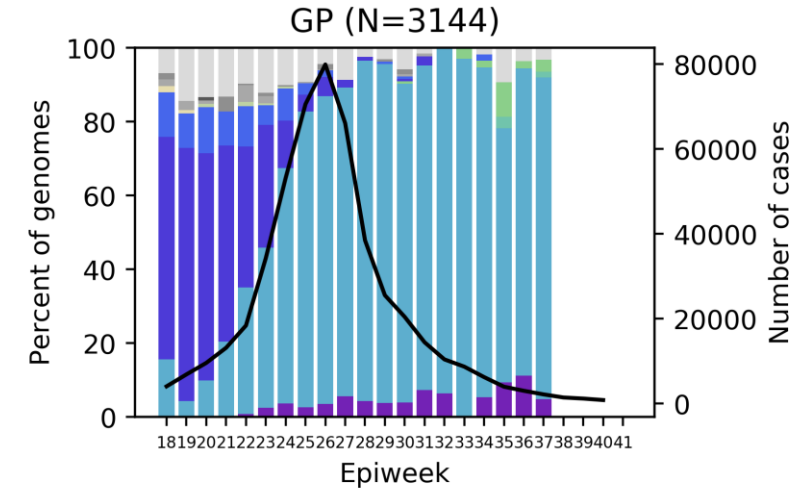
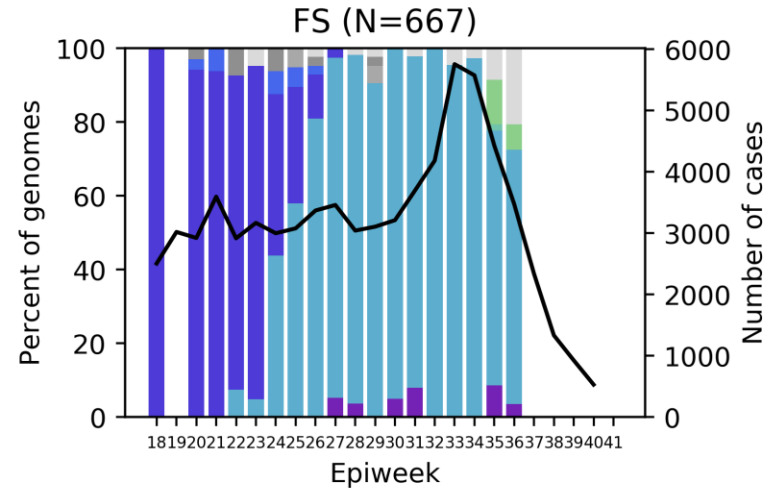
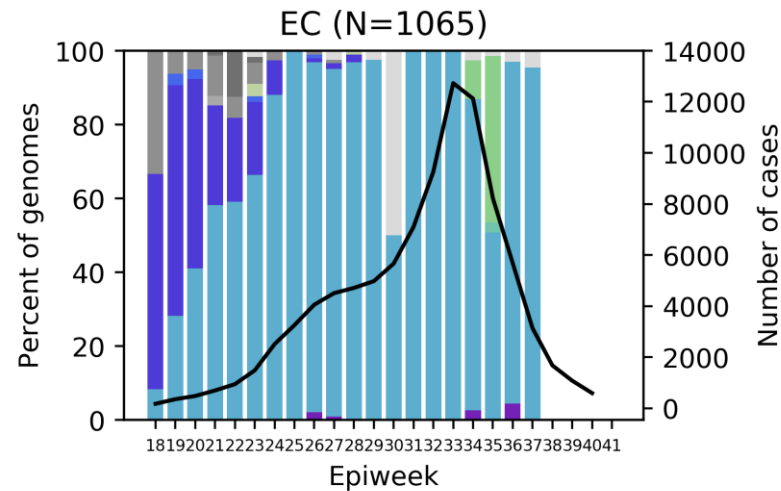
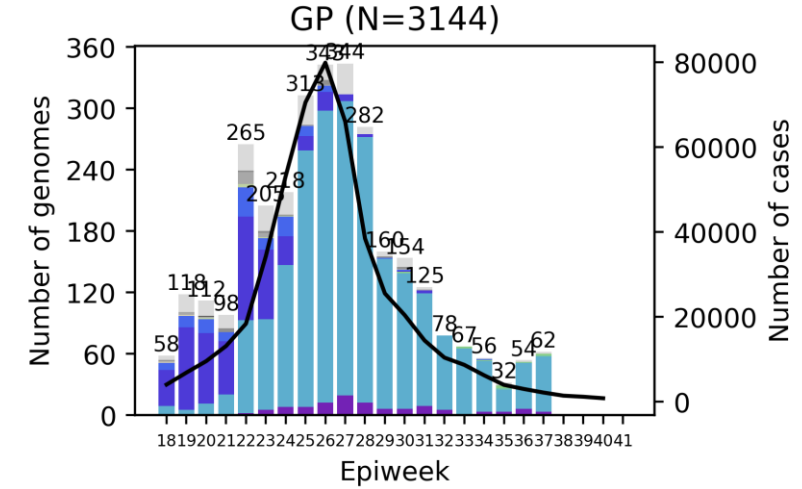
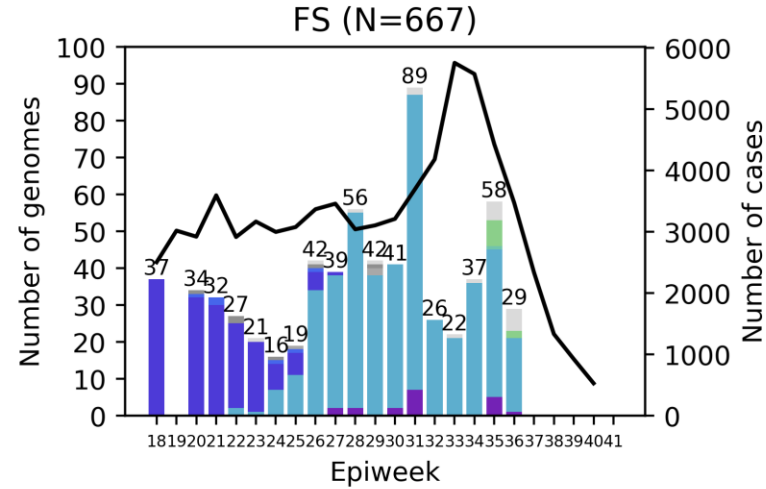
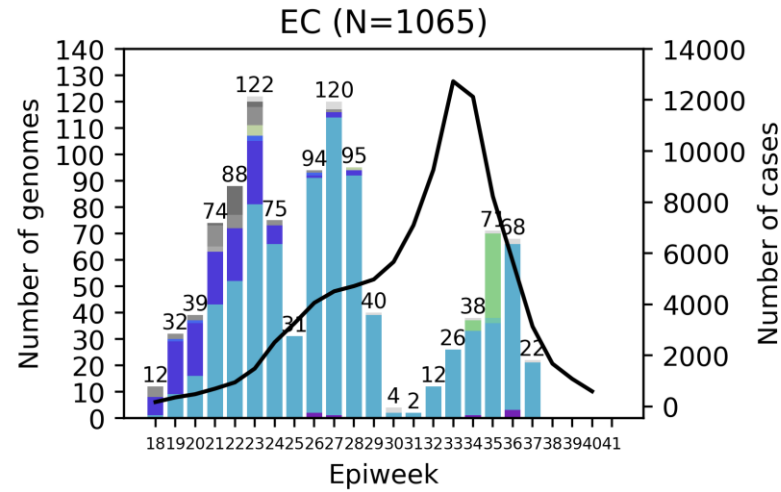
September (N=875)



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

The Delta variant dominated in July and August in South Africa, and appears to still dominate in early September.

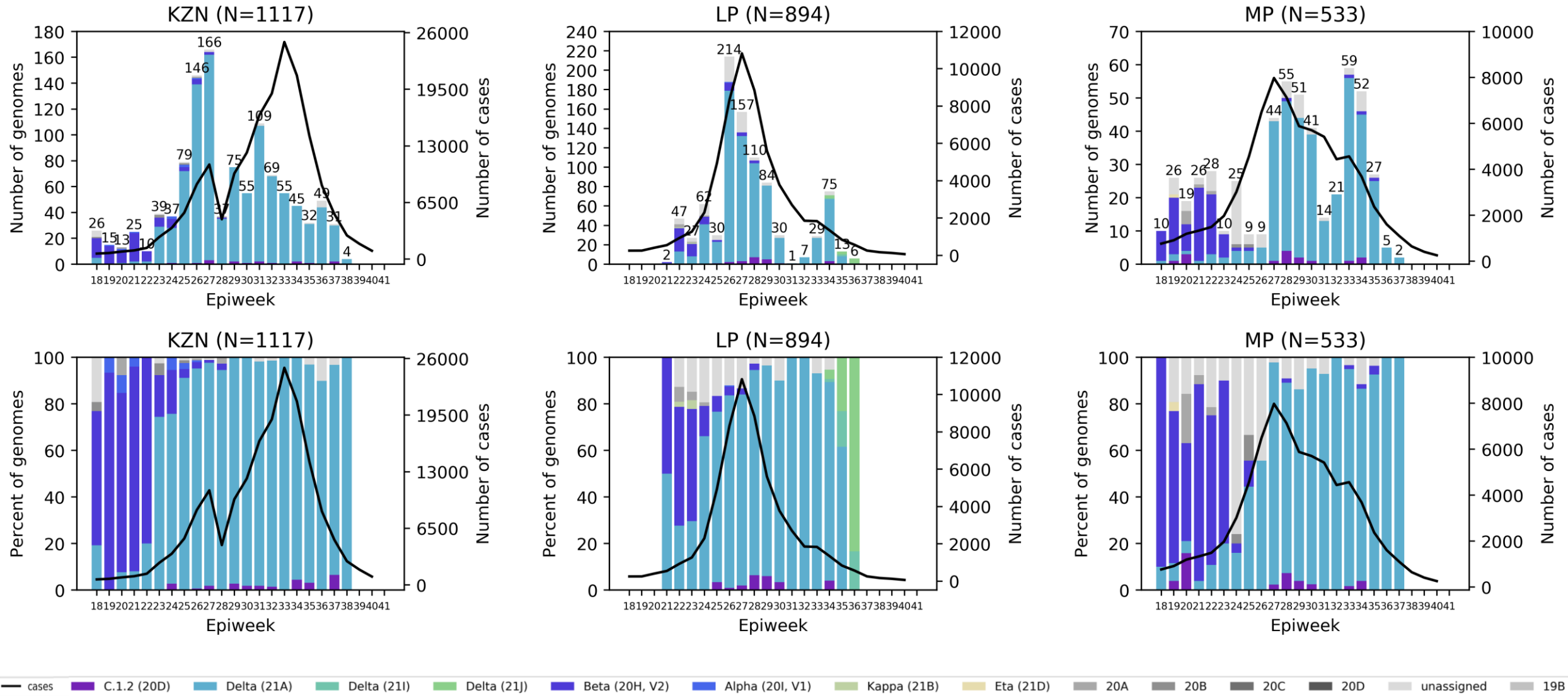
Genomes sequenced from specimens collected in May to mid-September 2021 (epiweeks 18 – 41) from Eastern Cape, Free State and Gauteng Provinces



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

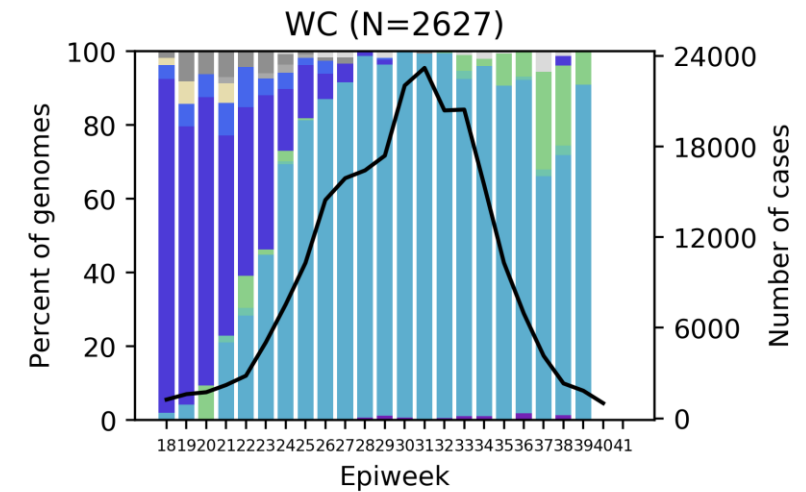
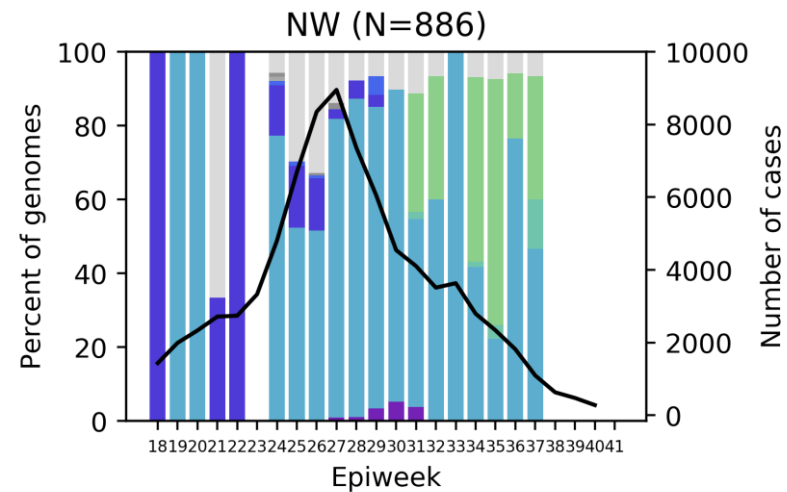
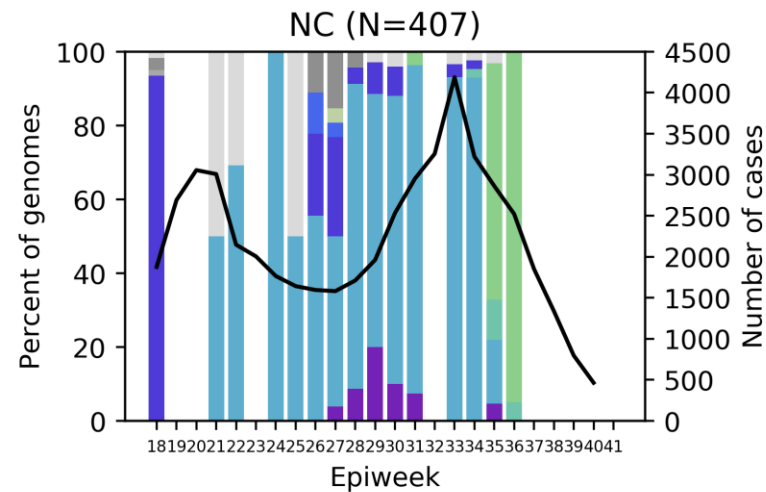
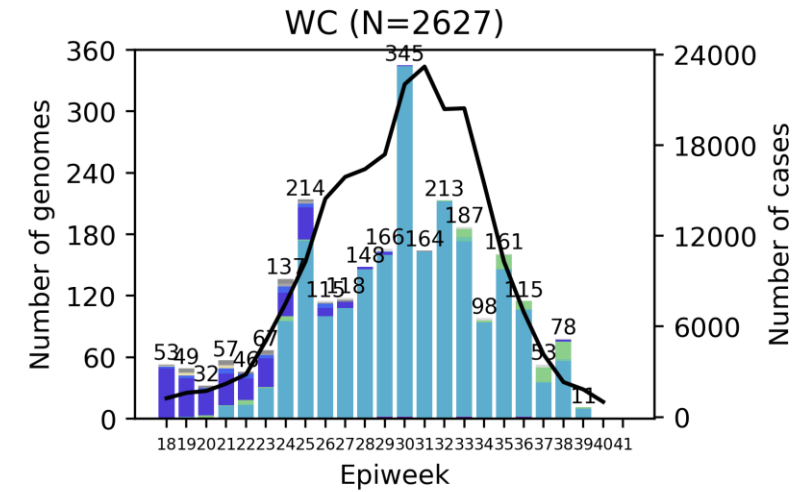
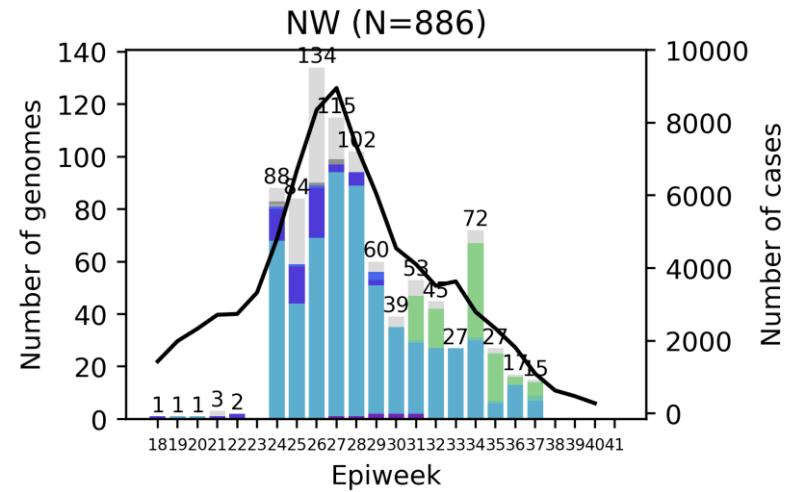
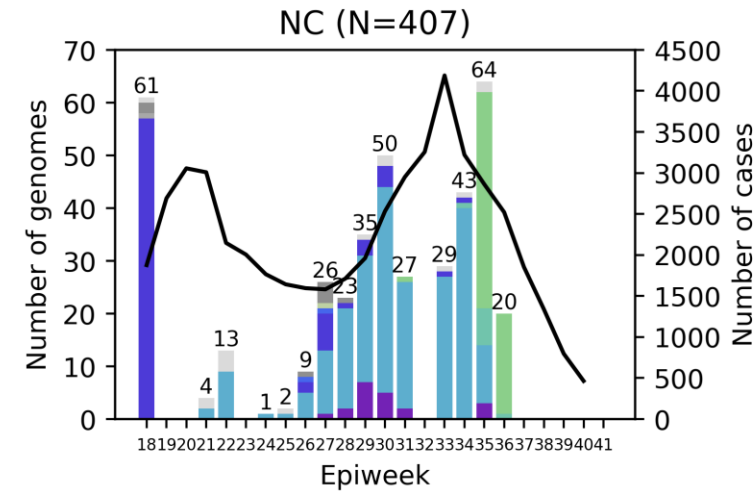
Delta dominates the third wave in Eastern Cape, Free State and Gauteng provinces

Genomes sequenced from specimens collected in May to mid-September 2021 (epiweeks 18 – 41) from KwaZulu-Natal, Limpopo and Mpumalanga Provinces



Delta variant dominates the third wave in KwaZulu-Natal, Limpopo and Mpumalanga Provinces

Genomes sequenced from specimens collected in May to mid-September 2021 (epiweeks 18 – 41) from Northern Cape, North West, and Western Cape Provinces

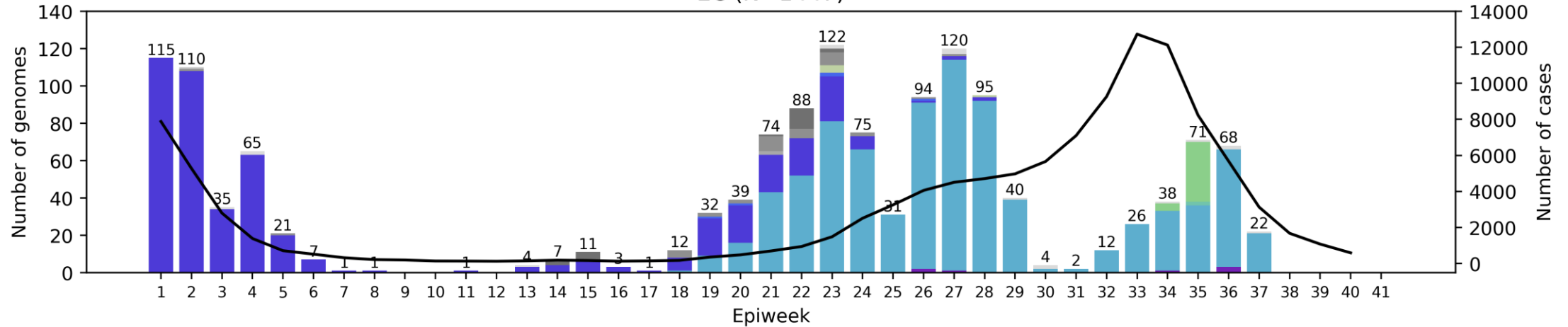


— cases C.1.2 (20D) Delta (21A) Delta (21I) Delta (21J) Beta (20H, V2) Alpha (20I, V1) Kappa (21B) Eta (21D) 20A 20B 20C 20D unassigned 19B

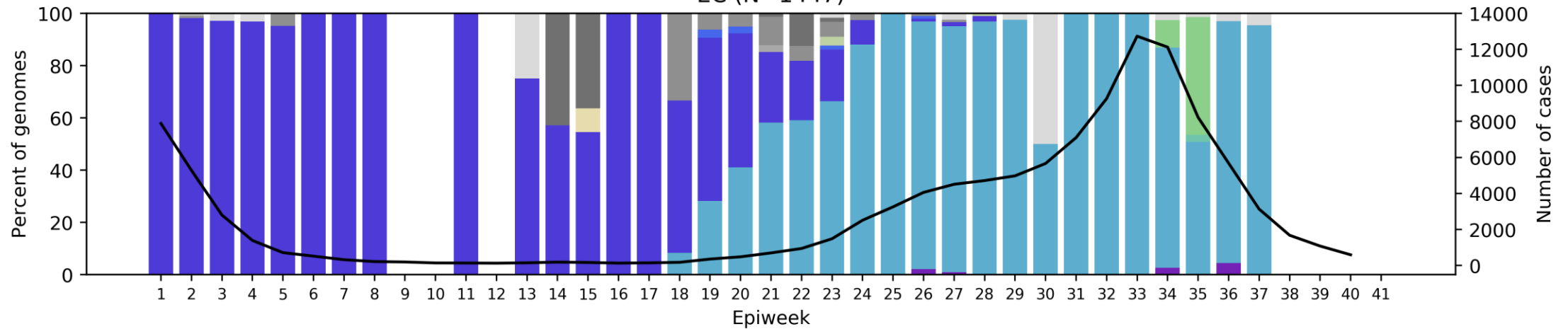
Delta dominates the third wave in Northern Cape, North West, and Western Cape provinces

Eastern Cape Province, 2021, n = 1447

EC (N=1447)

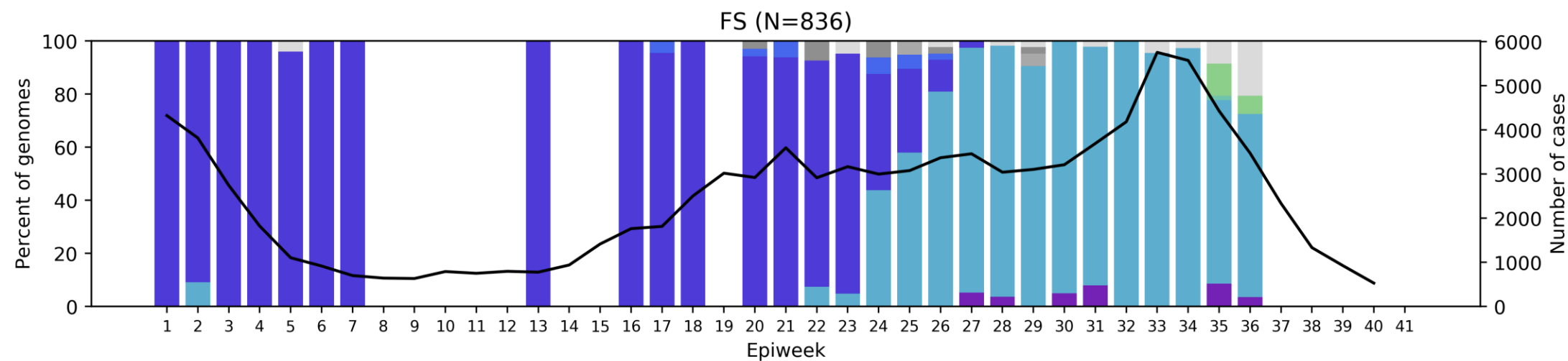
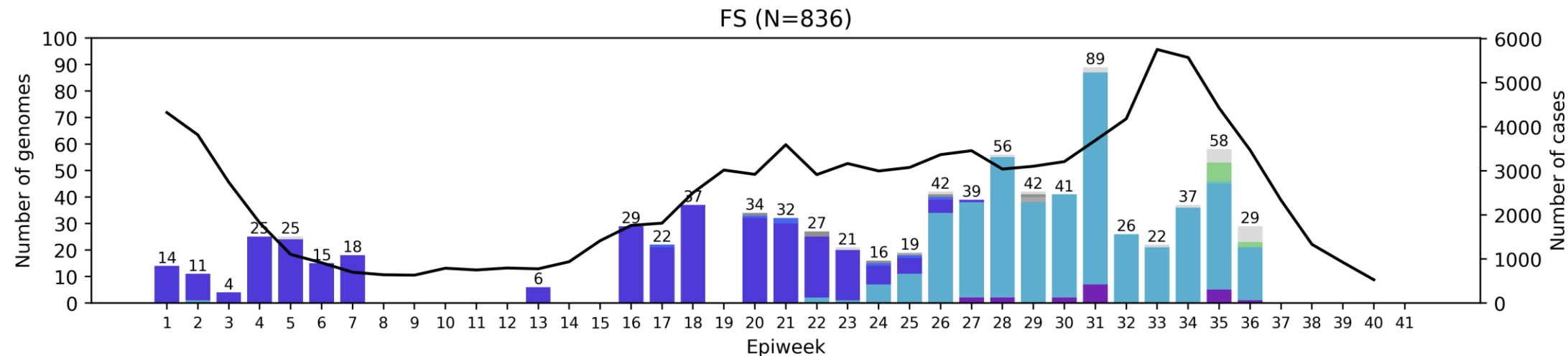


EC (N=1447)



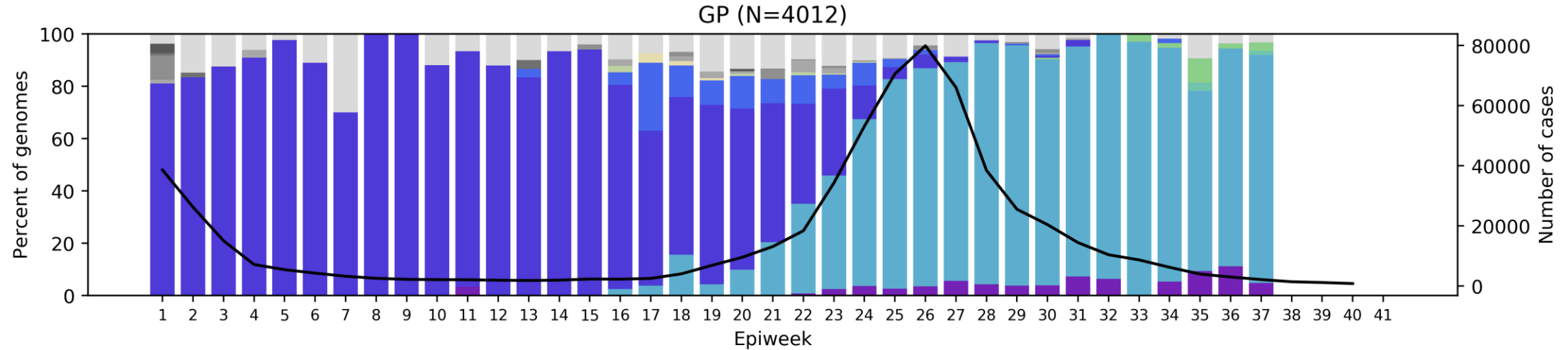
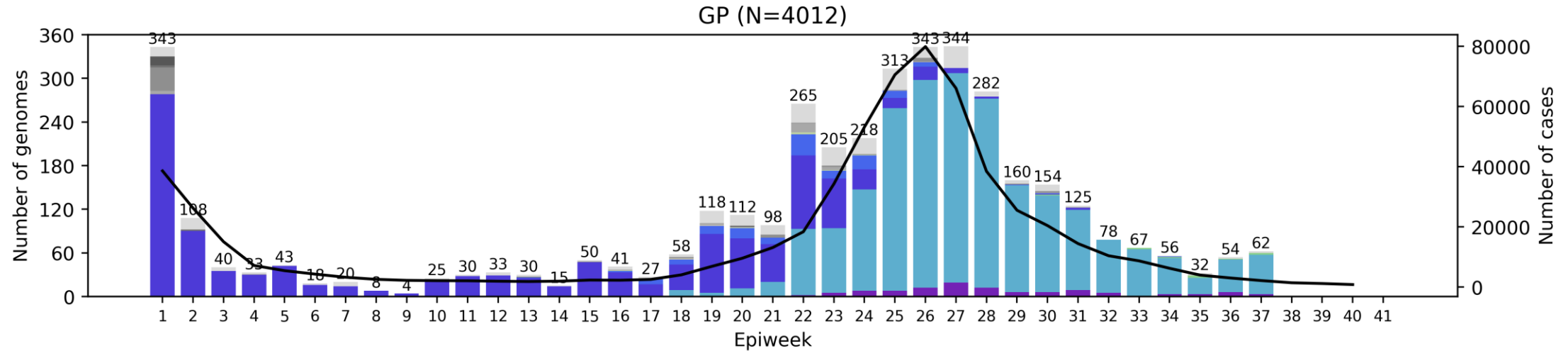
— cases C.1.2 (20D) Delta (21A) Delta (21I) Delta (21J) Beta (20H, V2) Alpha (20I, V1) Kappa (21B) Eta (21D) 20A 20B 20C 20D unassigned 19B

Free State Province, 2021, n = 836



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

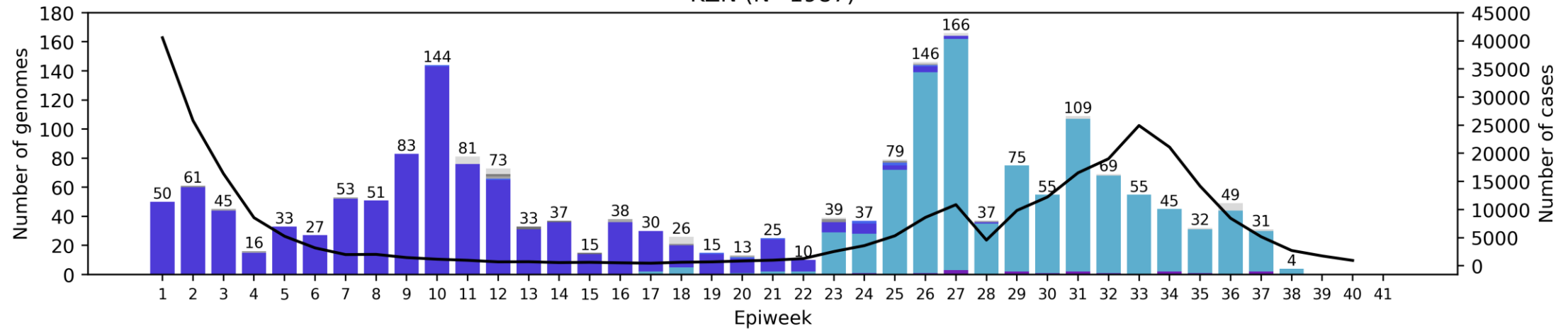
Gauteng Province, 2021, n = 4012



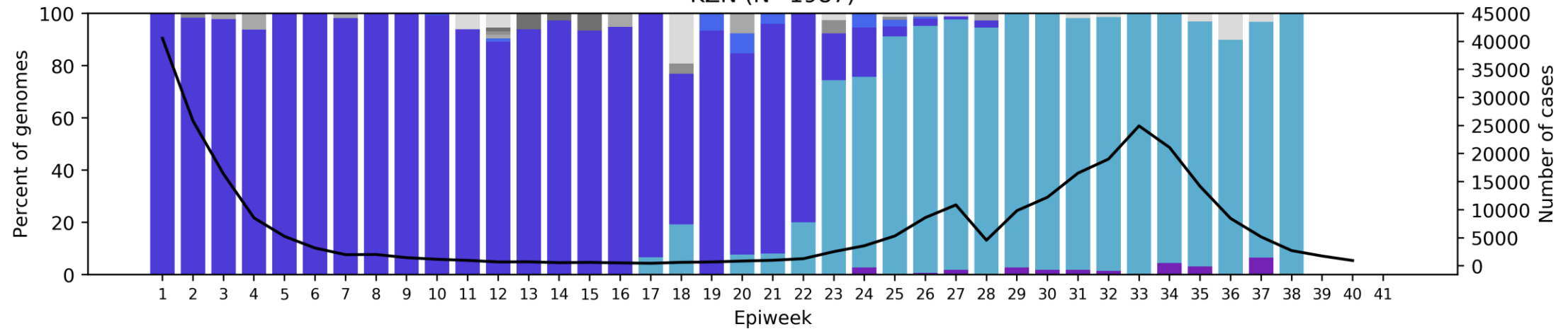
— cases C.1.2 (20D) Delta (21A) Delta (21I) Delta (21J) Beta (20H, V2) Alpha (20I, V1) Kappa (21B) Eta (21D) 20A 20B 20C 20D unassigned 19B

KwaZulu-Natal Province, 2021, n = 1987

KZN (N=1987)



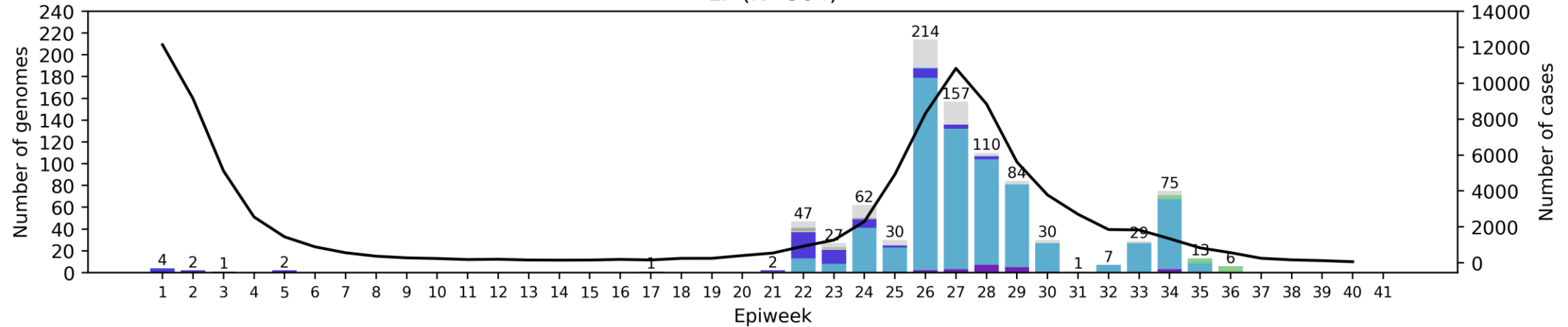
KZN (N=1987)



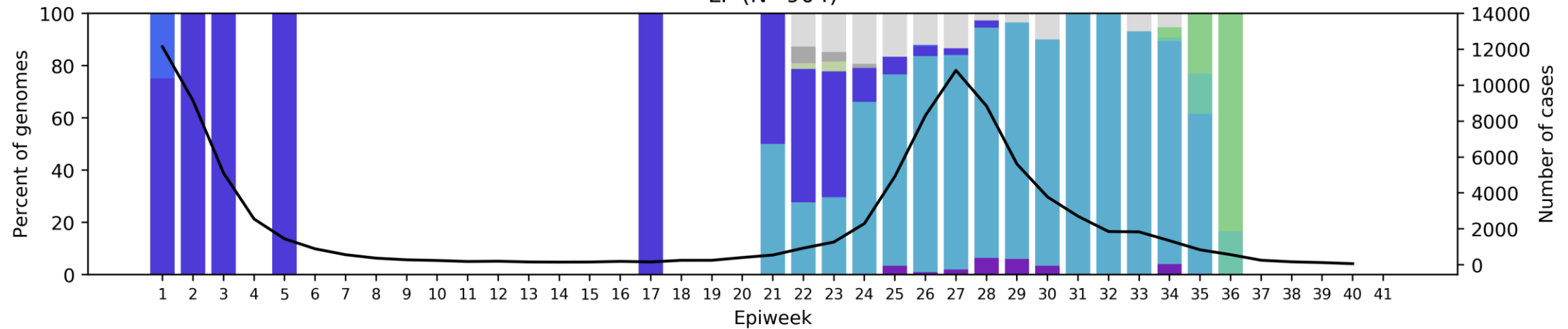
— cases C.1.2 (20D) Delta (21A) Delta (21I) Delta (21J) Beta (20H, V2) Alpha (20I, V1) Kappa (21B) Eta (21D) 20A 20B 20C 20D unassigned 19B

Limpopo Province, 2021, n = 904

LP (N=904)

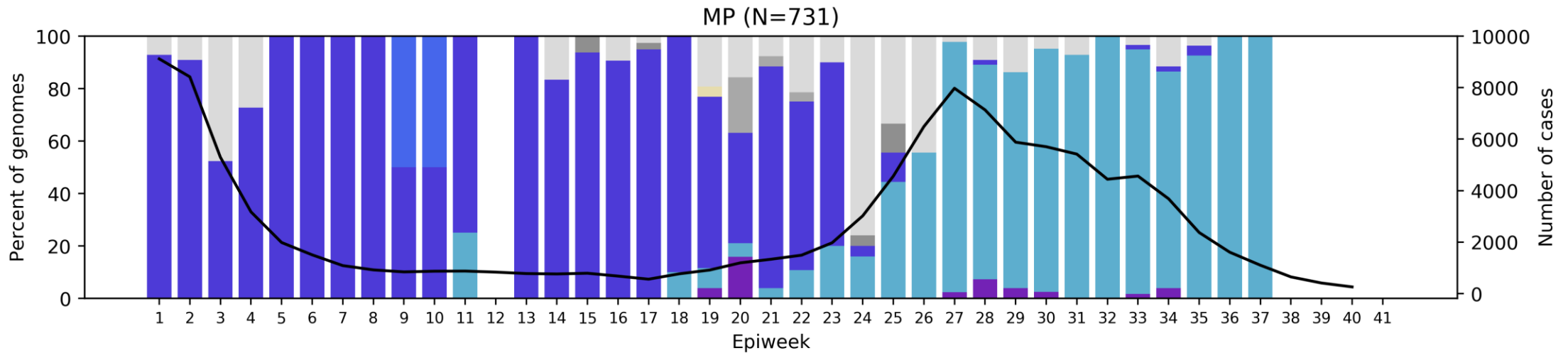
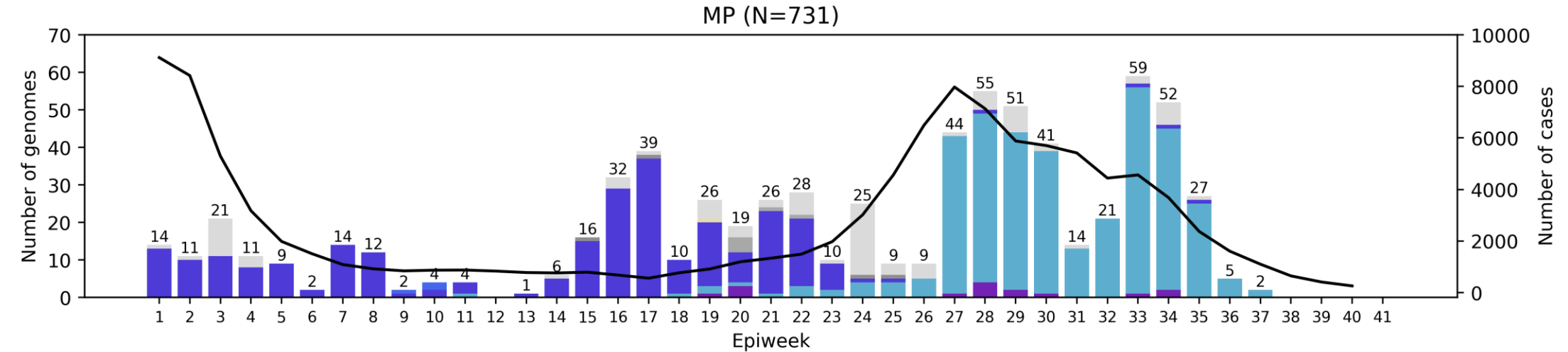


LP (N=904)



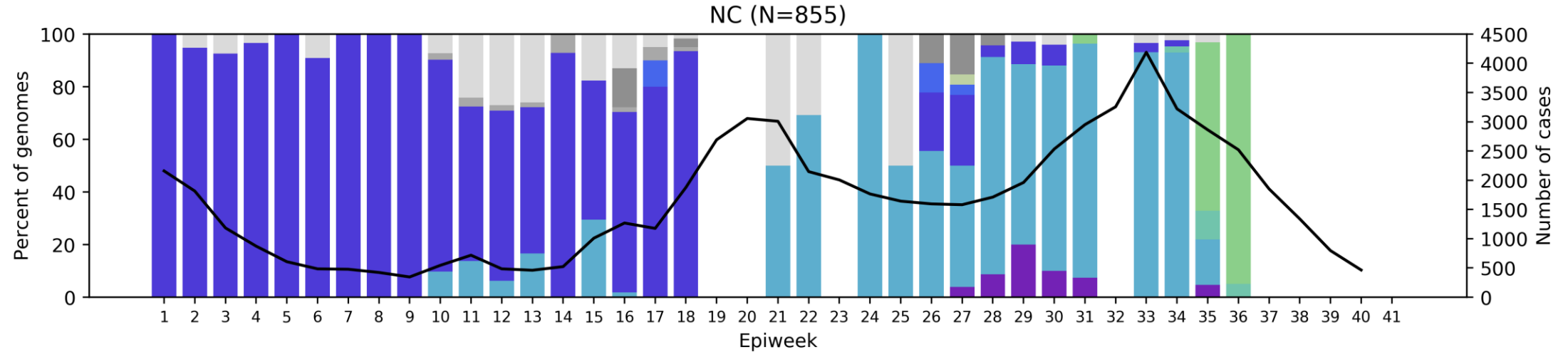
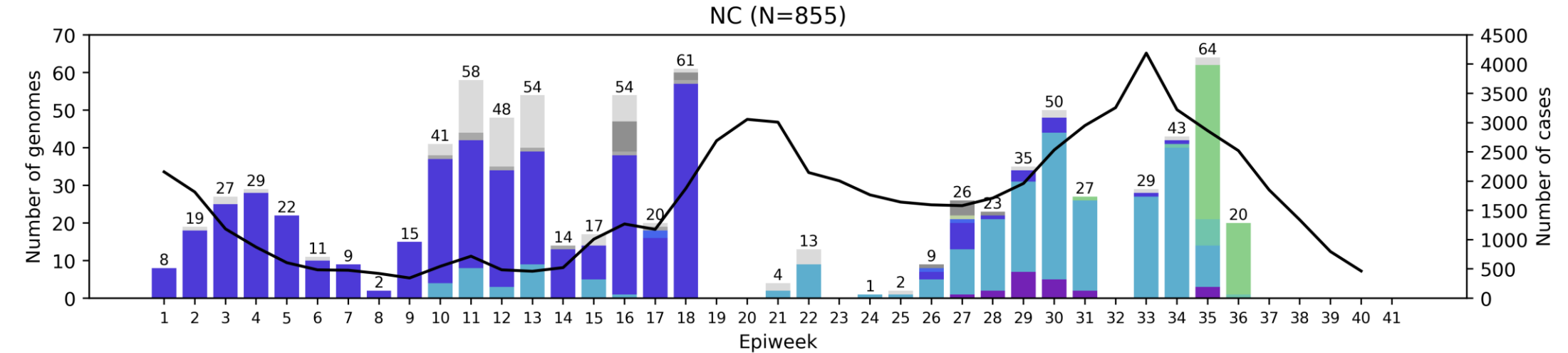
— cases C.1.2 (20D) Delta (21A) Delta (21I) Delta (21J) Beta (20H, V2) Alpha (20I, V1) Kappa (21B) Eta (21D) 20A 20B 20C 20D unassigned 19B

Mpumalanga Province, 2021, n = 731



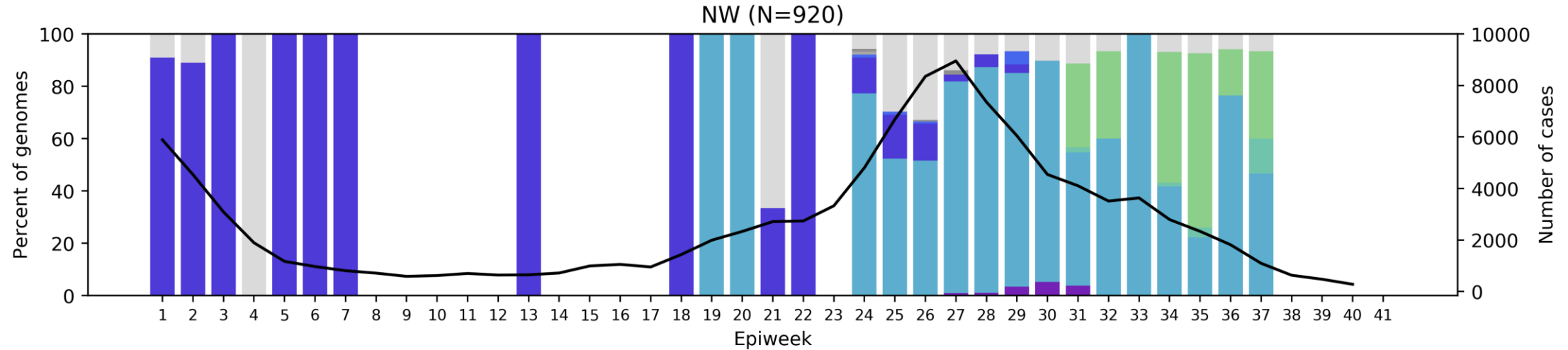
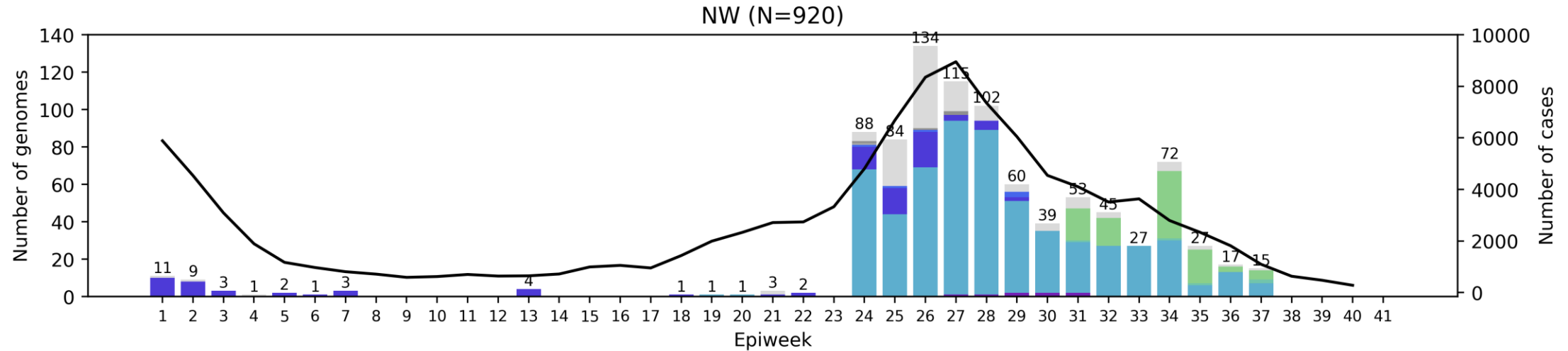
— cases — C.1.2 (20D) — Delta (21A) — Delta (21I) — Delta (21J) — Beta (20H, V2) — Alpha (20I, V1) — Kappa (21B) — Eta (21D) — 20A — 20B — 20C — 20D — unassigned — 19B

Northern Cape Province, 2021, n = 885



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

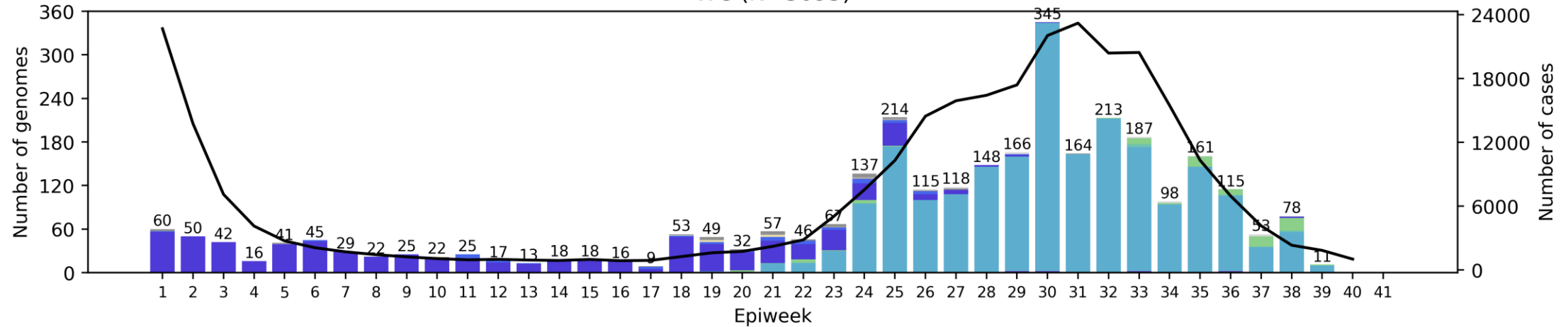
North West Province, 2021, n = 920



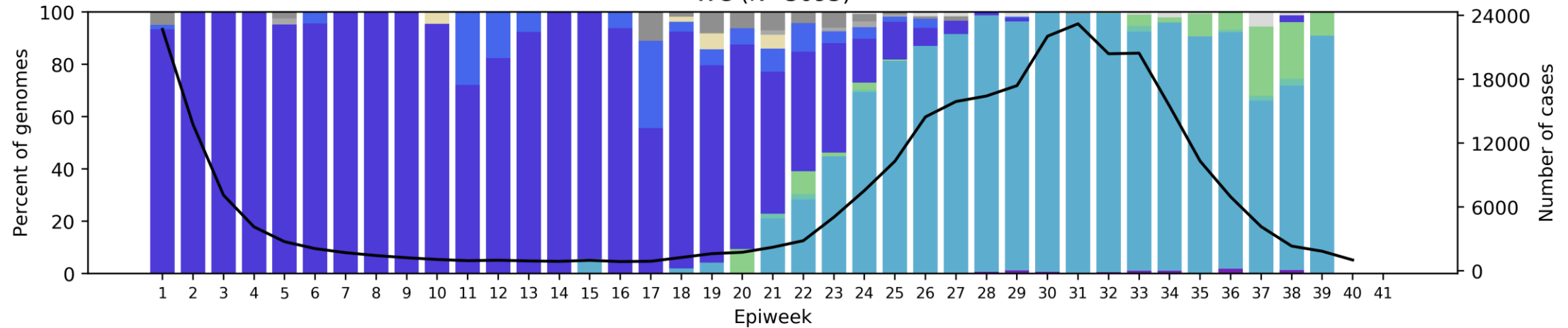
— cases — C.1.2 (20D) — Delta (21A) — Delta (21I) — Delta (21J) — Beta (20H, V2) — Alpha (20I, V1) — Kappa (21B) — Eta (21D) — 20A — 20B — 20C — 20D — unassigned — 19B

Western Cape Province, 2021, n = 3095

WC (N=3095)



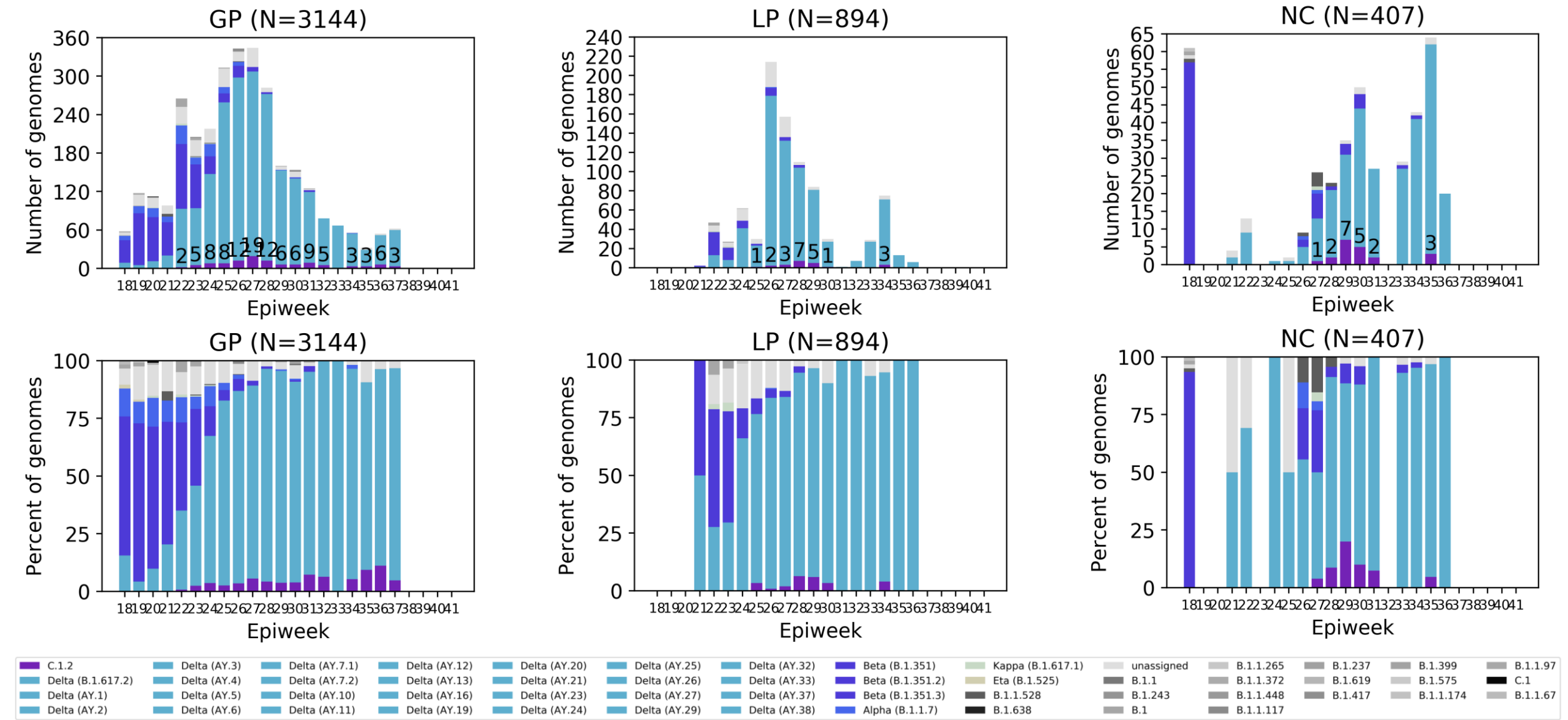
WC (N=3095)



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

C.1.2 (n=226 in SA) in May – August 2021 by epiweek

Number of C.1.2 samples indicated above bar, provinces ordered by number of detections

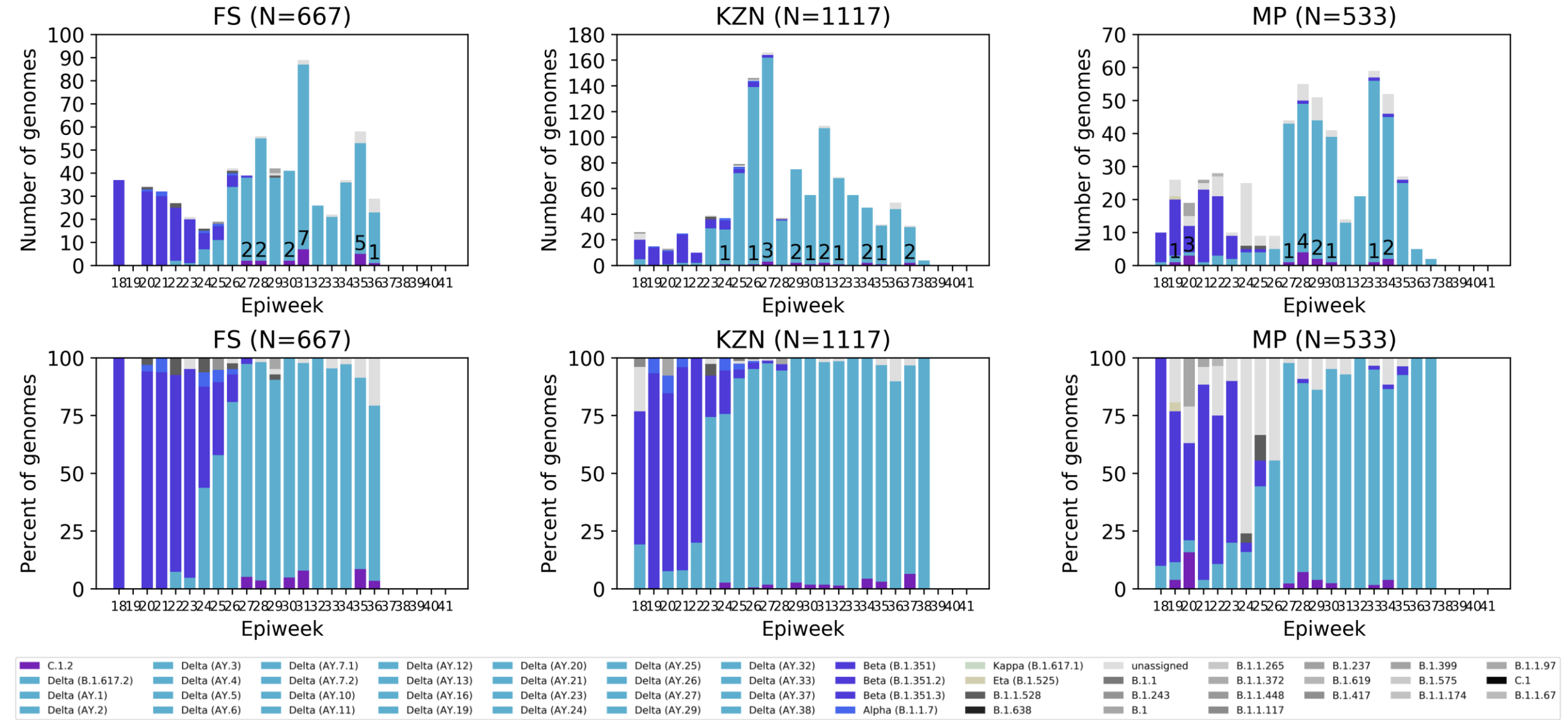


The majority of C.1.2 sequences have been detected in Gauteng (n=107), followed by Limpopo (n=22) and the Northern Cape (n=20).



C.1.2 (n=226 in SA) in May – August 2021 by epiweek

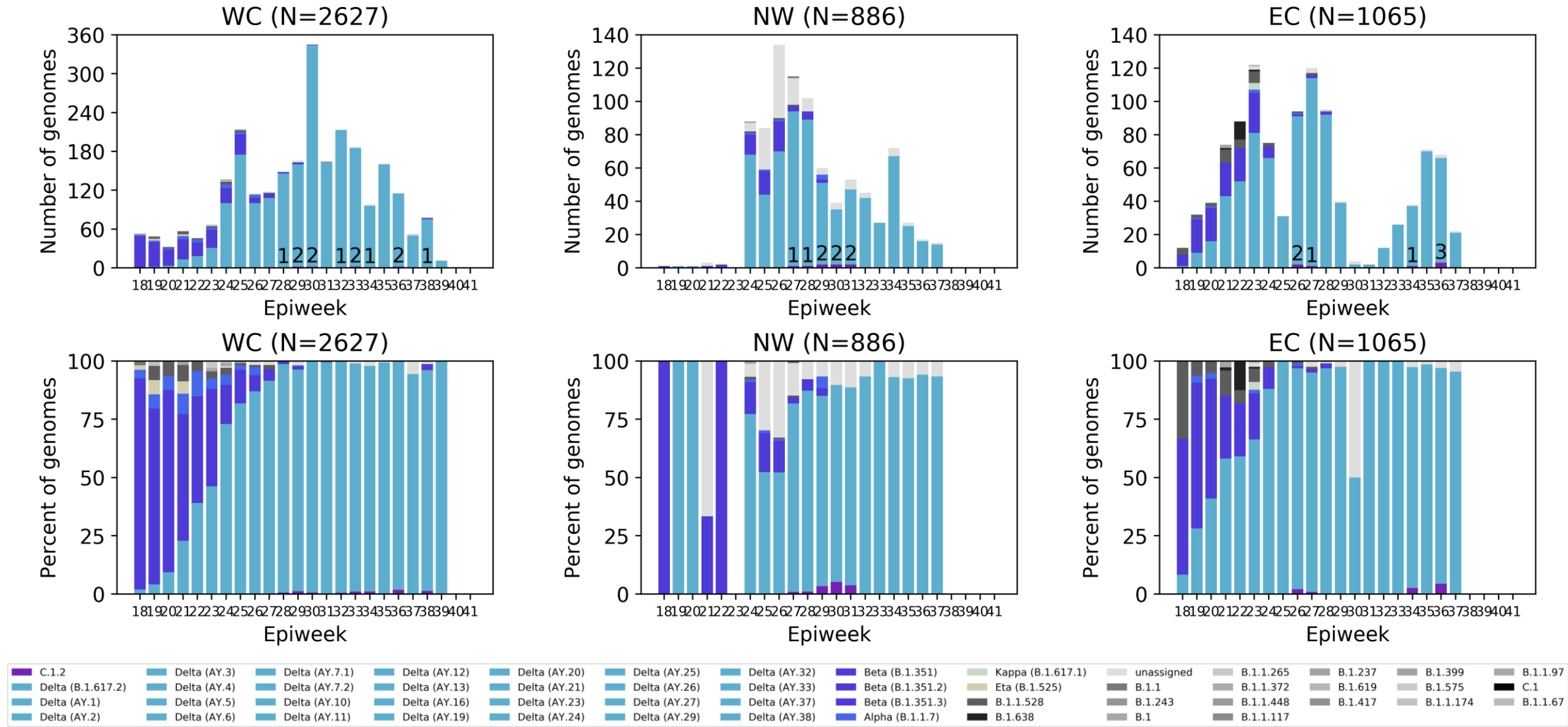
Number of C.1.2 samples indicated above bar, provinces ordered by number of detections



19 C.1.2 sequences have been detected in the Free State, 16 in KwaZulu-Natal, and 15 in Mpumalanga.

C.1.2 (n=226 in SA) in May – August 2021 by epiweek

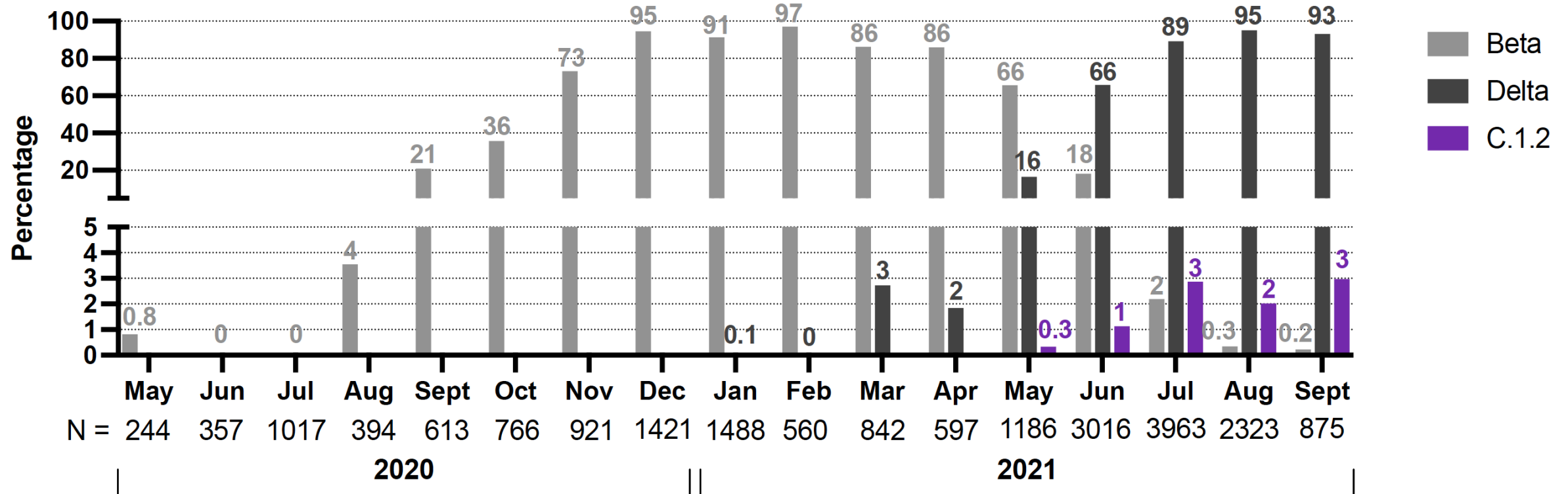
Number of C.1.2 samples indicated above bar, provinces ordered by number of detections



The Western Cape has 12 sequences, the North West has 8, and the Eastern Cape has 7 detections of C.1.2.

C.1.2 growth compared to Beta and Delta

Detection Rates



C.1.2 continues to be detected at low levels (less than 4% of genomes per month)

Summary

- Delta has recently been split into three clades.
 - New clades have been assigned due to >20% global circulation of particular sequences for more than 2 months
 - We are in the process of updating the classification of all Delta samples submitted to date.
- Delta continues to dominate in all provinces from specimens collected in September
- Overall number of lineages detected 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 4% of genomes from May through early September.
- Lambda and Mu variants not detected in South Africa



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NICD SARS-CoV-2 Sequencing Group

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Mushal Allam
Florah Mnyameni
Arshad Ismail



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Amy Strydom (Postdoc)
Michaela Davis (MSc, intern medical scientist)



NHLS Tshwane

Prof Simnikiwe Mayaphi (HOD)

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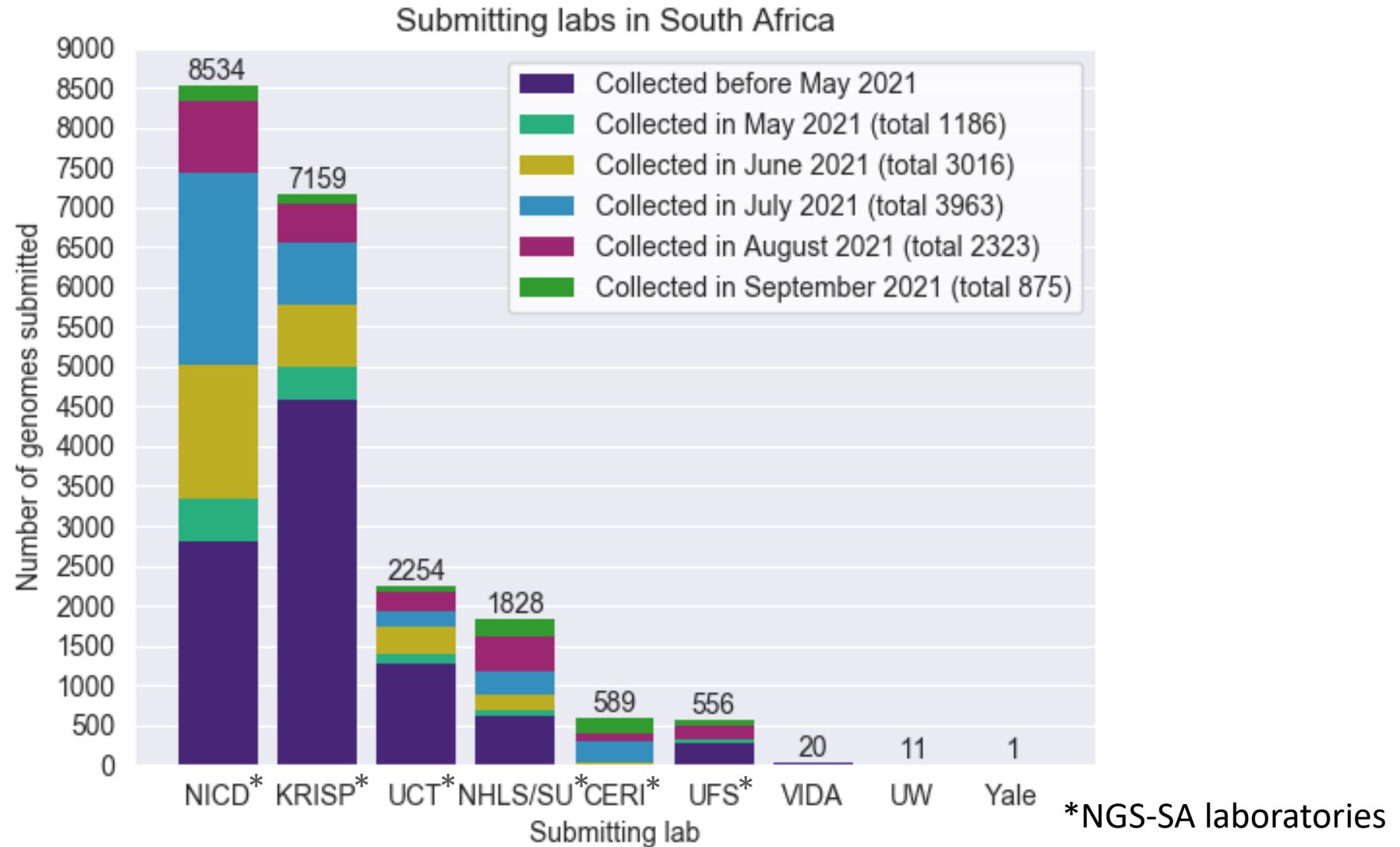
Glaudina Loots

SA MRC

Glenda Gray



South African genomes submitted per sequencing lab, 2020 and 2021 (N=20 952)



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	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 [§]	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

⁺Includes all descendant lineages.

[#]Includes all Q.* lineages in the PANGO nomenclature system.

[§]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 (≥ 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.)