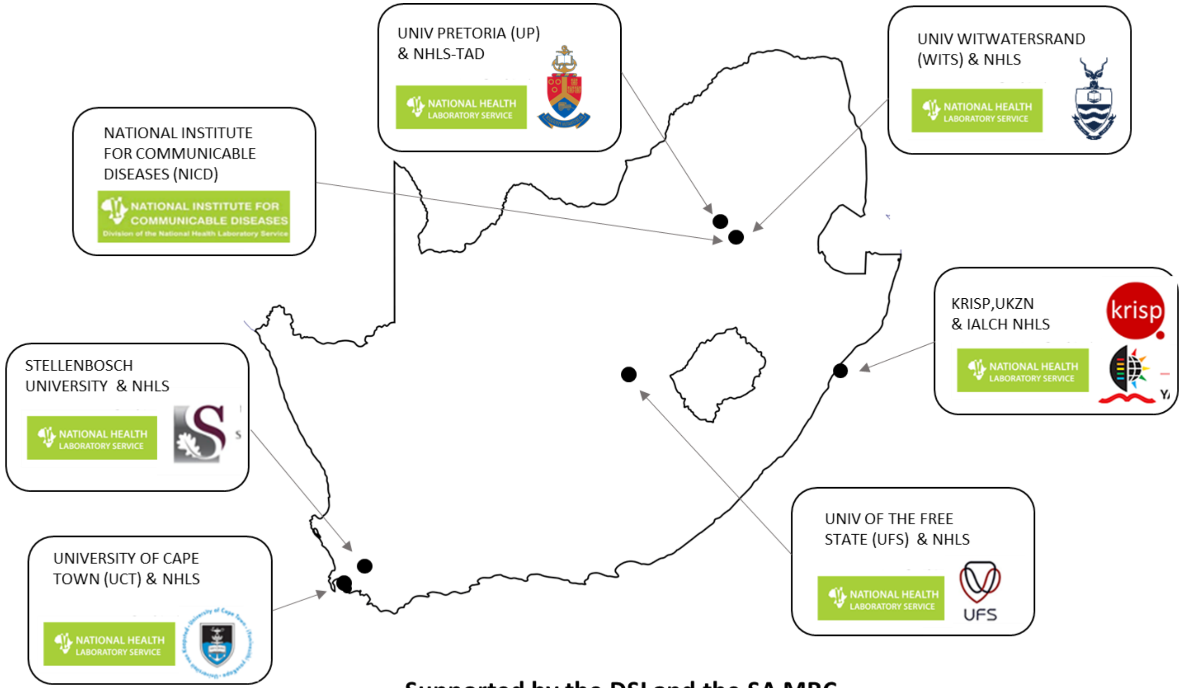
Network for Genomic Surveillance in South Africa (NGS-SA)

SARS-CoV-2 Sequencing Update
26 November 2021



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Supported by the DSI and the SA MRC

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

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)

The genomic data presented here are based on South African SARS-CoV-2 sequence data downloaded from GISAID (www.gisaid.org) on 25 November at 16h01

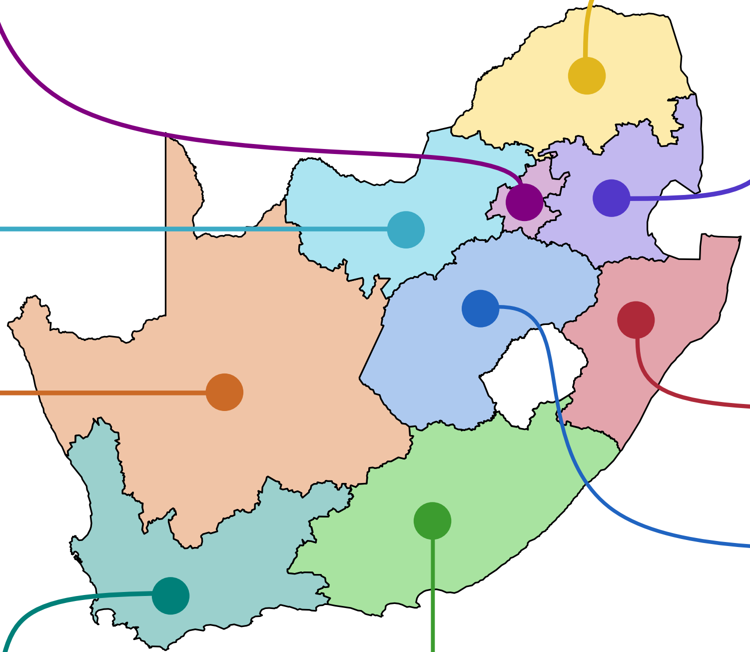
Data license: https://www.gisaid.org/registration/terms-of-use/

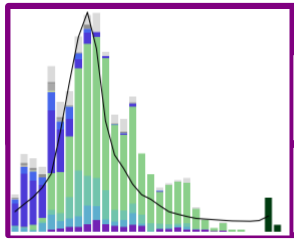
Elbe, S., and Buckland-Merrett, G. (2017) Data, disease and diplomacy: GISAID's innovative contribution to global health. Global Challenges, 1:33-46. DOI: 10.1002/gch2.1018 PMCID: 31565258

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

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/ Test data from https://www.nicd.ac.za/diseases-a-z-index/disease-index-covid-19/surveillance-reports/weekly-testing-summary/

SARS-CoV-2
GENOMIC SURVEILLANCE
epiweeks 18 - 46

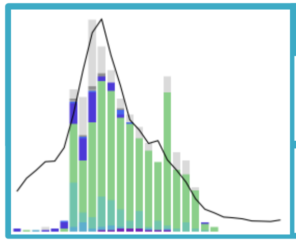




Gauteng ↑ PTP: 4.3%

Genomes	Cases
3 685 (26.9%)	498 540 (37.1%)

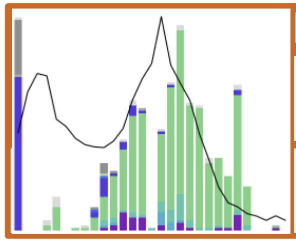
Genomes deposited in the last week
🟩 3 🟦 10 ⬛ 54



North West ↑ PTP: 2.3%

Genomes	Cases
1 098 (8.0%)	83 000 (6.2%)

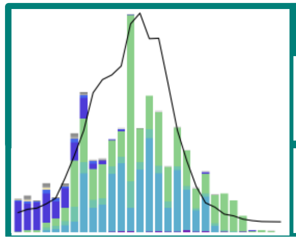
Genomes deposited in the last week
🟦 3 ⬜ 4 ⬛ 27 ⬛ 10 ⬜ 5



Northern Cape ↓ PTP: 3.5%

Genomes	Cases
717 (5.2%)	52 410 (3.9%)

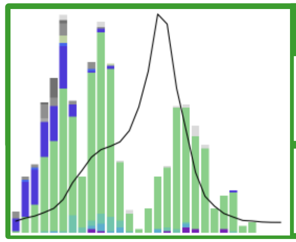
Genomes deposited in the last week
🟦 9 🟩 1 🟪 1 ⬜ 2 ⬛ 2



Western Cape - PTP: 1.1%

Genomes	Cases
3 014 (22.0%)	227 368 (16.9%)

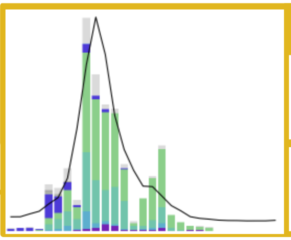
Genomes deposited in the last week
🟩 3 ⬜ 1



Eastern Cape ↑ PTP: 0.8%

Genomes	Cases
1 254 (9.2%)	96 526 (7.2%)

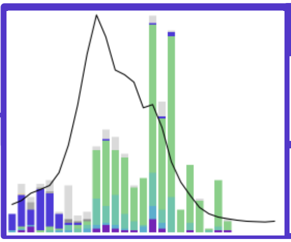
Genomes deposited in the last week
🟩 3



Limpopo ↑ PTP: 2.1%

Genomes	Cases
1 106 (8.1%)	58 425 (4.4%)

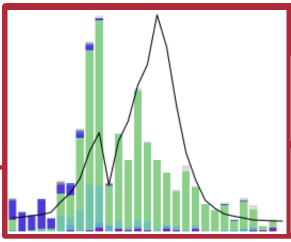
Genomes deposited in the last week
🟦 5 🟪 1



Mpumalanga ↑ PTP: 1.9%

Genomes	Cases
810 (5.9%)	73 926 (5.5%)

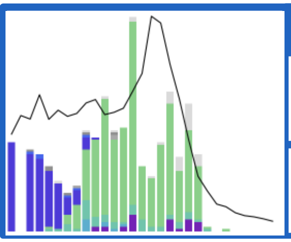
Genomes deposited in the last week
🟦 6 🟩 6 🟩 45 🟪 1 ⬜ 2 ⬛ 14 ⬜ 1



KwaZulu-Natal - PTP: 0.8%

Genomes	Cases
1 248 (9.1%)	179 592 (13.4%)

Genomes deposited in the last week
🟦 2 🟦 4 🟩 37 🟪 5 ⬜ 5



Free State ↓ PTP: 1.1%

Genomes	Cases
761 (5.6%)	74 248 (5.5%)

Genomes deposited in the last week
🟦 1 ⬜ 3 ⬛ 4

🟩 B.1.1.529 (21K)
🟪 C.1.2 (20D)
🟦 Beta (20H, V2)
🟦 Alpha (20I, V1)
🟦 Delta (21A)
🟩 Delta (21I)
🟩 Delta (21J)
⬜ 20A
⬜ 20B
⬜ Unassigned
— Cases
⬛ 20C
⬛ 20D

308 genomes deposited in the past week

Bar graphs represent genomes sequenced per epiweek, with lines representing cases by collection date (weeks 18 – 46)
Genomes and cases presented as provincial total (percentage of national total) for epiweeks 18 – 46
PTP: percentage testing positive in week 46 (14 Nov – 20 Nov); the arrow indicates direction of change since the previous week (7 Nov – 13 Nov)

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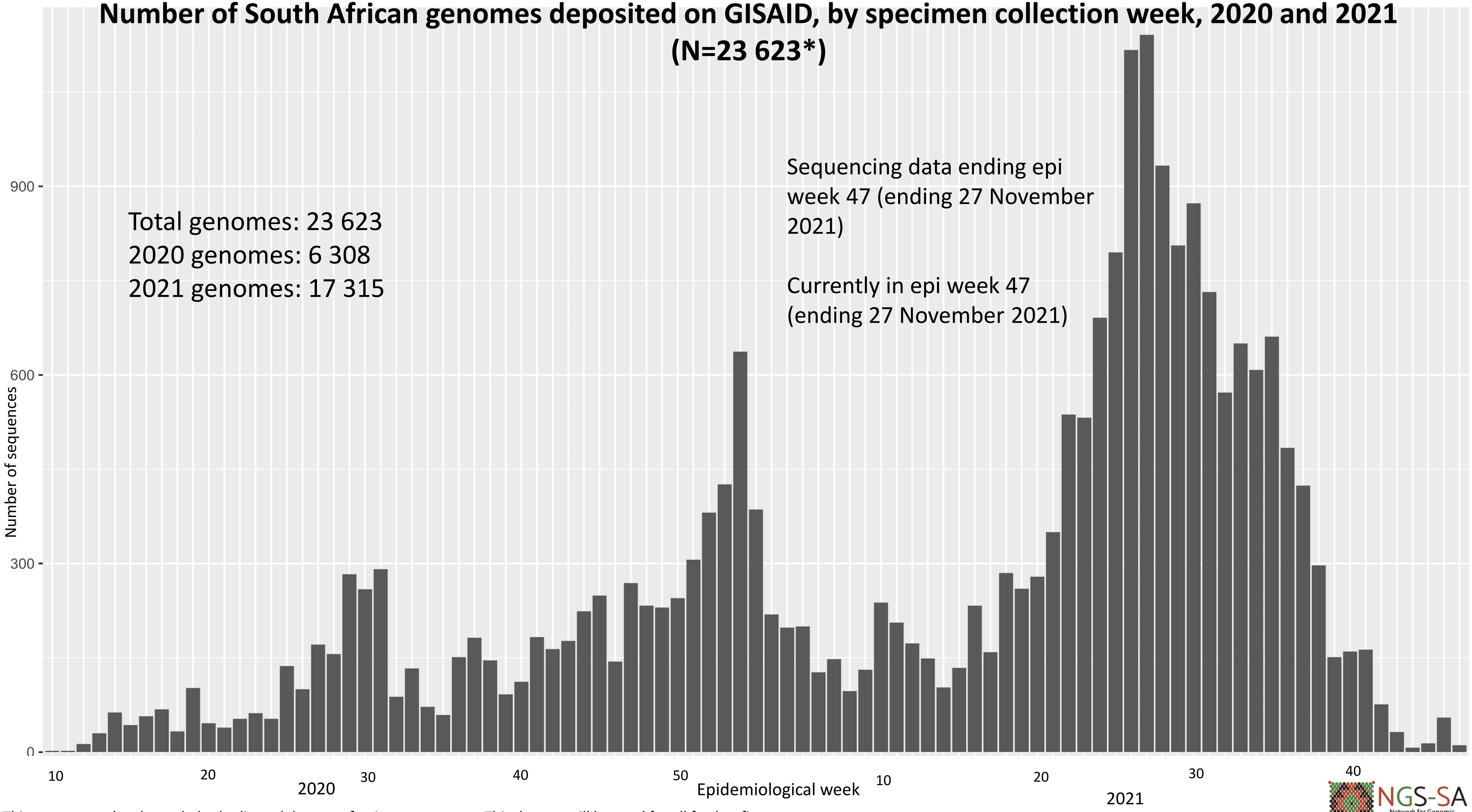
Number of South African genomes deposited on GISAID, by specimen collection week, 2020 and 2021 (N=23 623*)



Total genomes: 23 623
2020 genomes: 6 308
2021 genomes: 17 315

Sequencing data ending epi week 47 (ending 27 November 2021)

Currently in epi week 47 (ending 27 November 2021)

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

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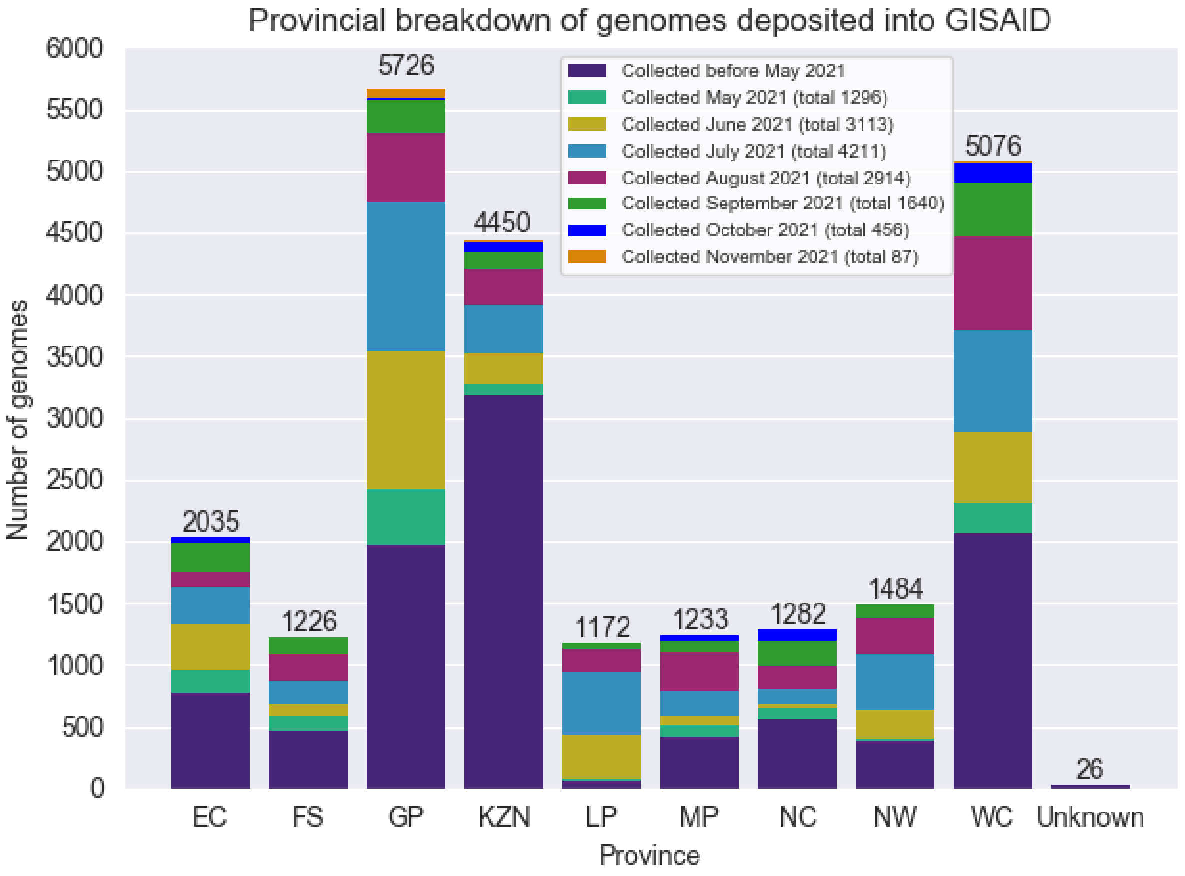
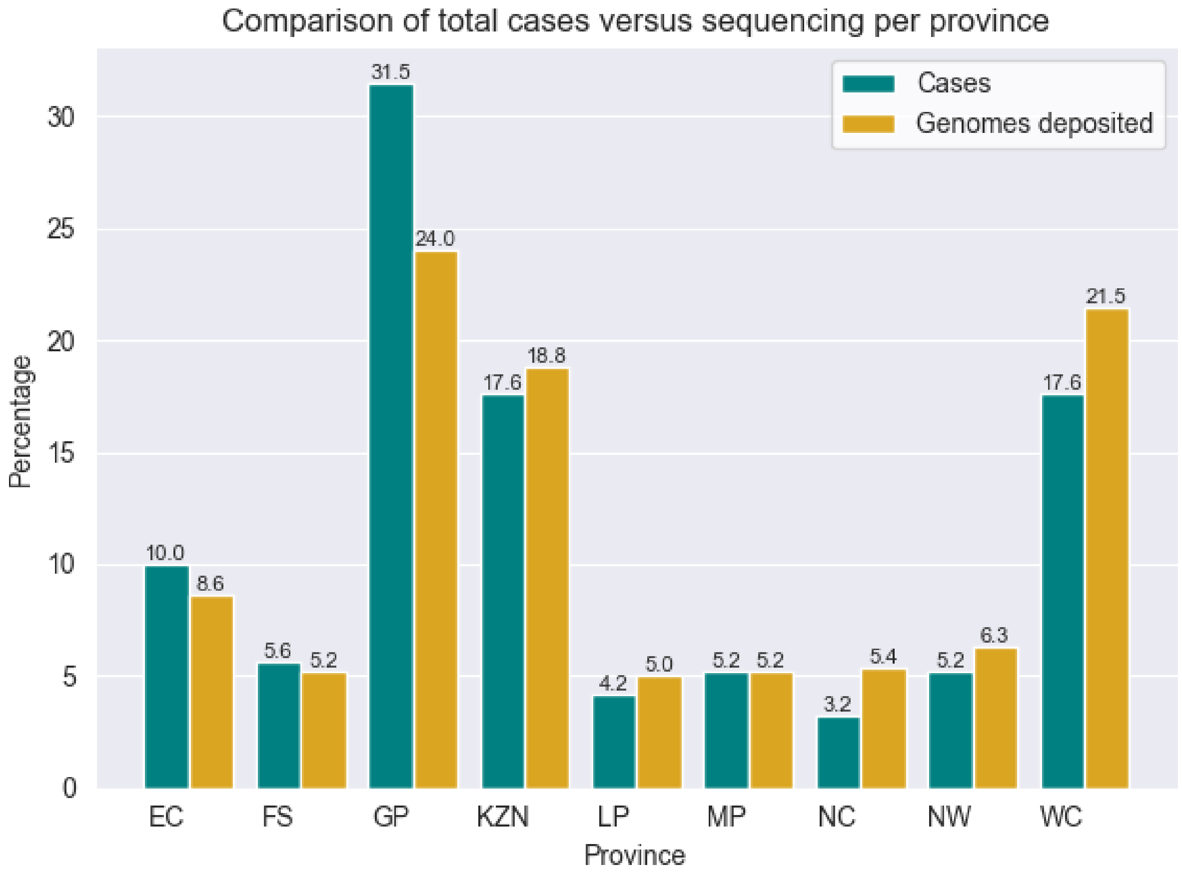
GISAID genomes vs total cases, 2020 and 2021 (N=23 623)


Provincial breakdown of genomes deposited into GISAID


Comparison of total cases versus sequencing per province

All provinces, apart from GP, KZN, NC and WC, have comparable percentage of overall cases and overall sequenced genomes. The majority of November sequencing data is from Gauteng.

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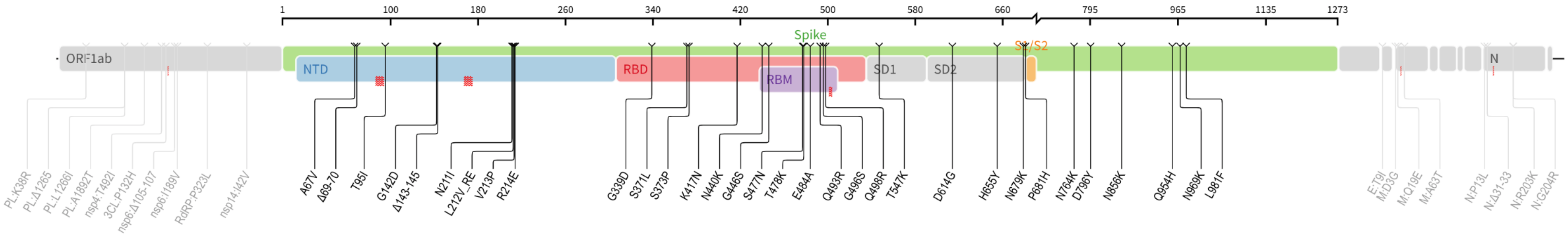
B.1.1.529 lineage mutation profile



- 45-52 amino acid changes (including deletions) across the whole GENOME
  - 26-32 changes in SPIKE

- Does not possess the RdRp G671S change associated with a decrease in Ct value for Delta variants
- Does possess the Δ69-70, which causes the S-Gene Target Failure (SGTF) and was previously seen in the Alpha VOC
- Sequences identified from Botswana, Hong Kong and South Africa

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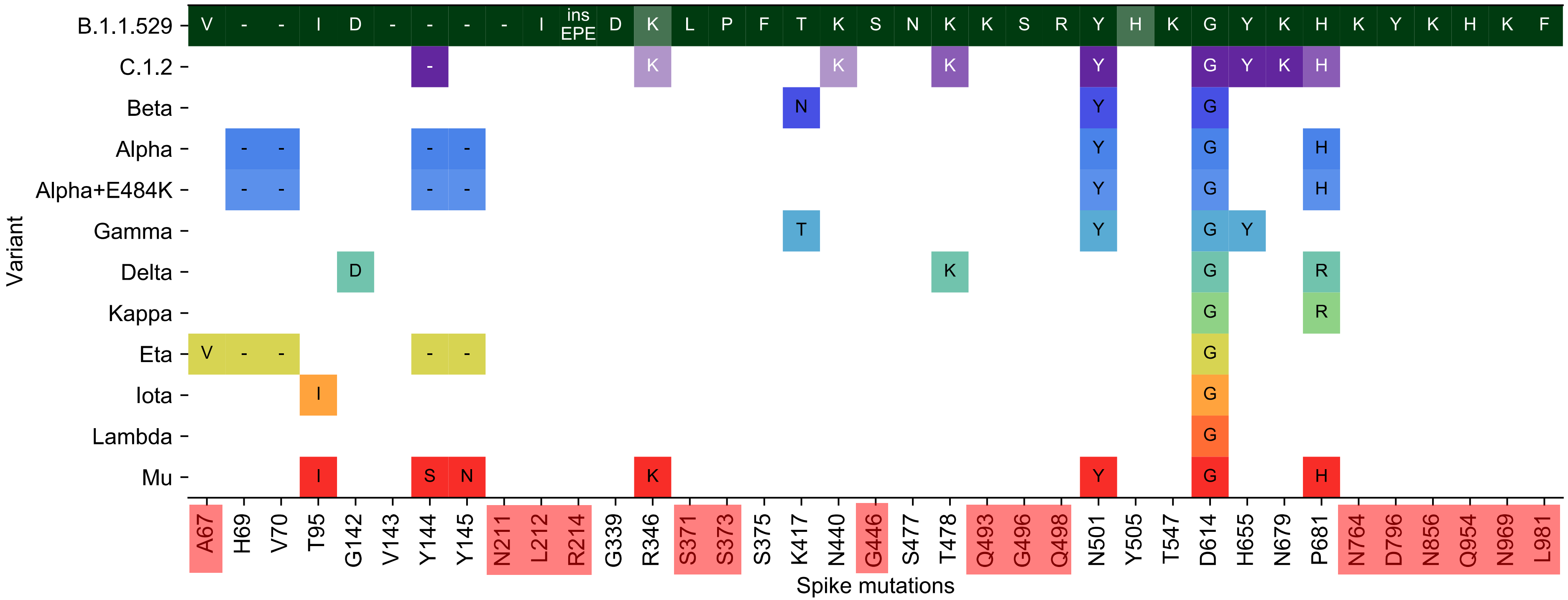
B.1.1.529 spike mutations compared to other VOC/VOIs



Variant	A67	H69	V70	T95	G142	V143	Y144	Y145	N211	L212	R214	G339	R346	S371	S373	S375	K417	N440	G446	S477	T478	Q493	G496	Q498	N501	Y505	T547	D614	H655	N679	P681	N764	D796	N856	Q954	N969	L981
B.1.1.529	V	-	-	I	D	-	-	-	-	I	ins EPE	D	K	L	P	F	T	K	S	N	K	K	S	R	Y	H	K	G	Y	K	H	K	Y	K	H	K	F
C.1.2							-						K					K			K				Y			G	Y	K	H						
Beta																	N								Y			G									
Alpha		-	-				-	-																	Y			G			H						
Alpha+E484K		-	-				-	-																	Y			G			H						
Gamma																	T								Y			G	Y								
Delta					D																K							G			R						
Kappa																												G			R						
Eta	V	-	-				-	-																				G									
Iota				I																								G									
Lambda																												G									
Mu				I			S	N					K												Y			G			H						

🟥 Mutations with unknown or unconfirmed impact

- Multiple changes within the two immunogenic regions in S1 (NTD and RBD)
  - including a three amino acid insertion
- Accumulation of mutations surrounding the furin cleavage site
  - Including combination of N679K and P681H
- Effect of most spike S2 subunit changes have not been defined

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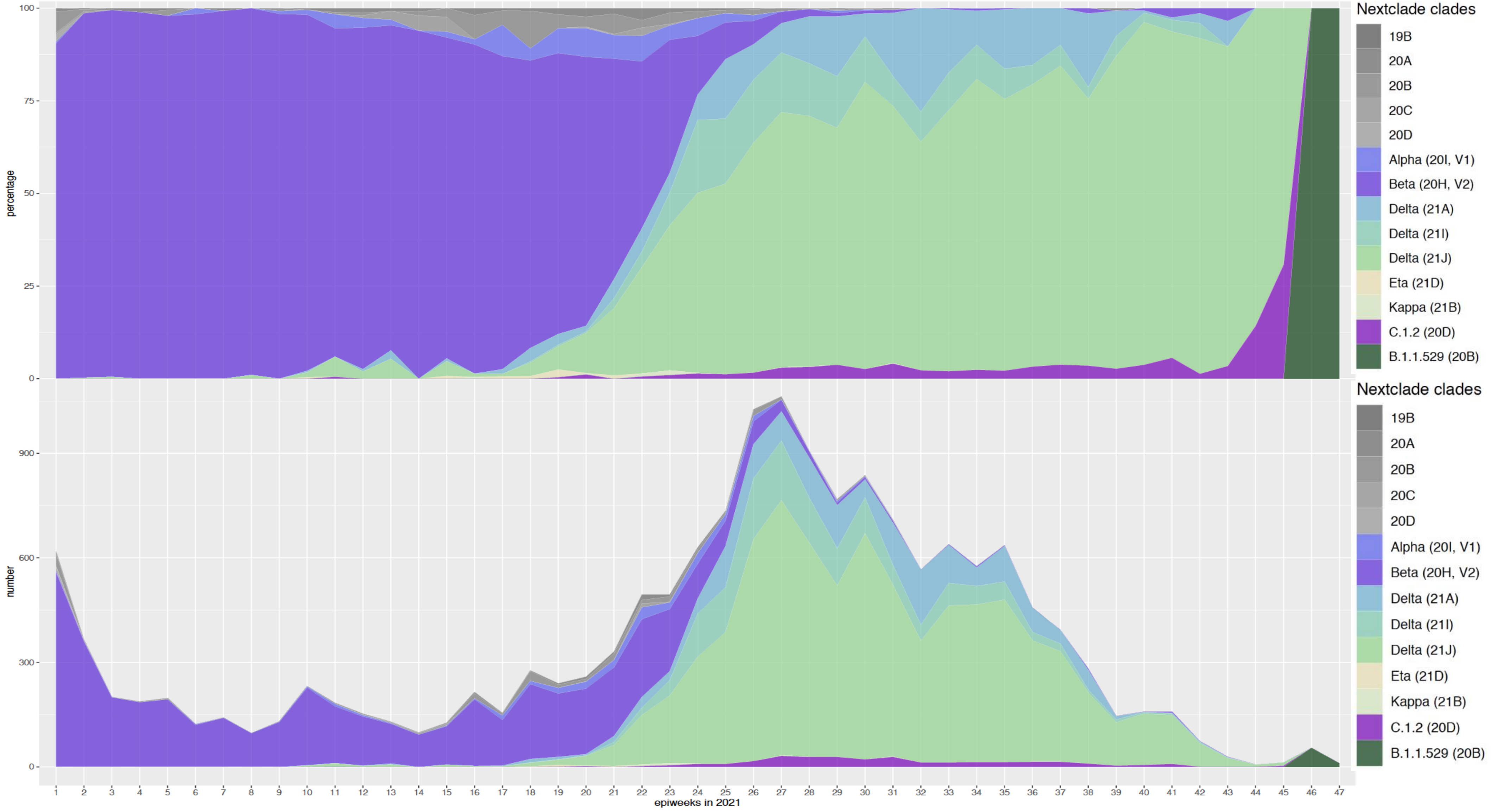
Proportion and number of clades by epiweek in South Africa, 2021 (N= 17 315)



Delta has recently been split into three clades (21A, 21I, 21J).

Sequencing data ending epi week 47 (ending 27 November 2021)

Currently in epi week 47 (ending 27 November 2021)

Delta dominated South Africa’s third wave with >90% frequency in October, with C.1.2 detection remaining <6%. B.1.1.529 dominates November sequencing data but estimates are based on <100 sequences, with the majority of these sequences from Gauteng.

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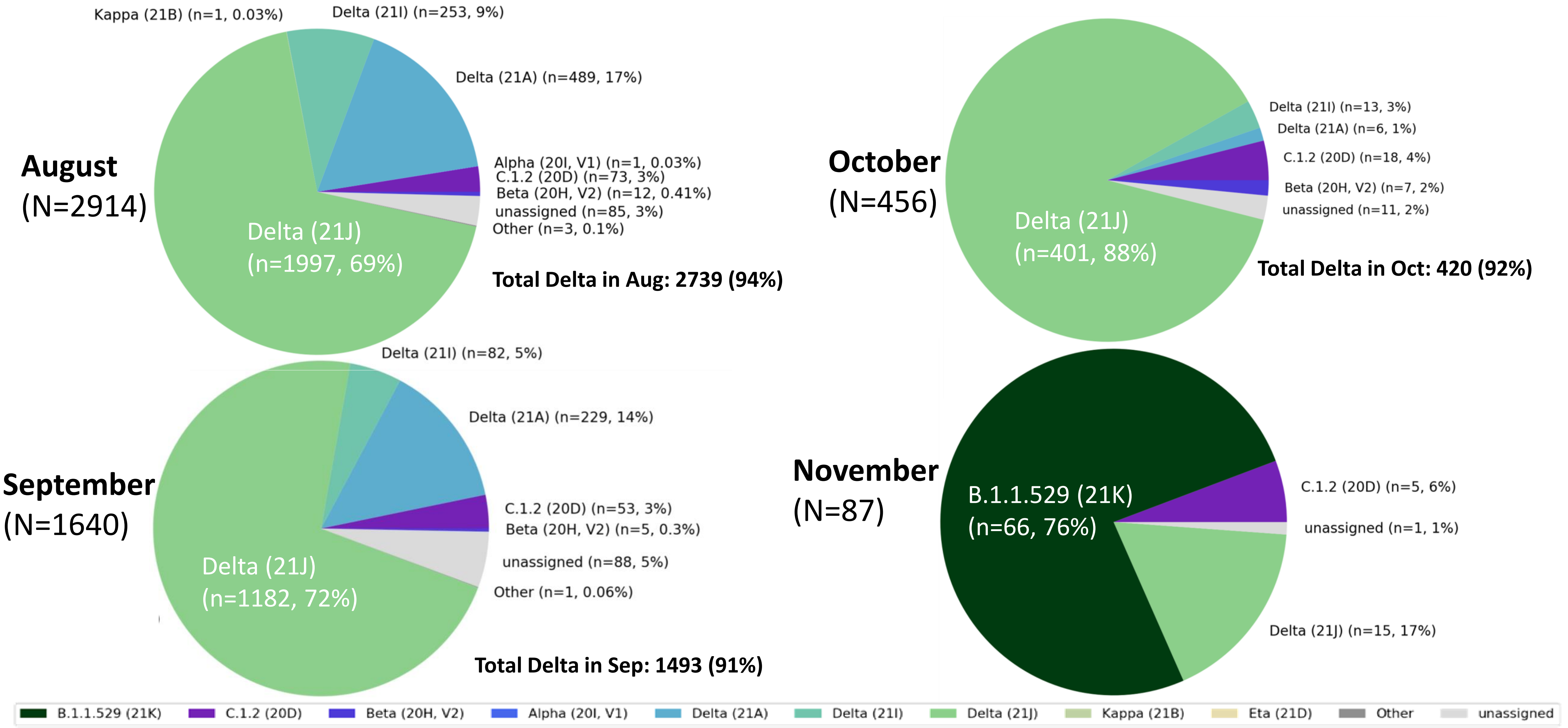
Prevalence of Variants of Concern (VOC) and Variants of Interest (VOI) in August – November 2021



The Delta variant dominated in August, September and October in South Africa.
B.1.1.529 was first detected in South Africa in November, comprising 76% (66/87) of sequences.

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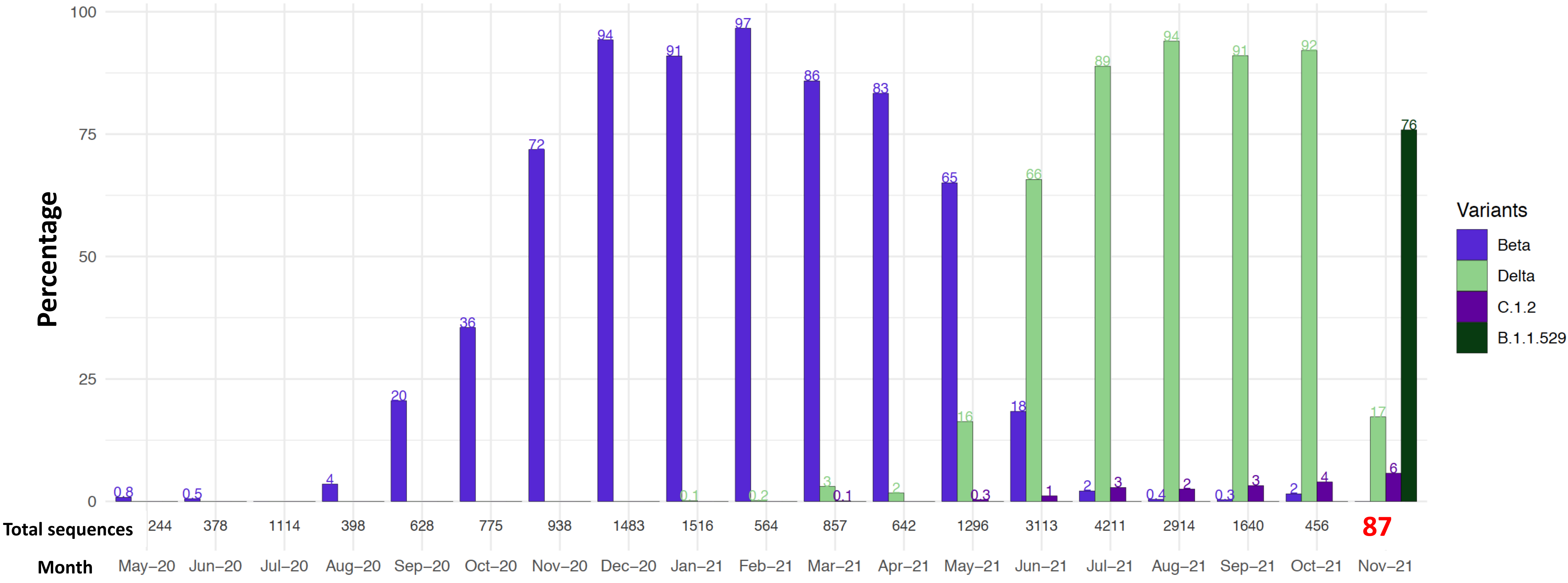
Detection Rates: Beta, Delta, C.1.2 and B.1.1.529

Detection rates of variants being monitored in South Africa



C.1.2 has been detected at ≤ 6% of sequences monthly.
B.1.1.529 was first detected in South Africa on November 14th. It makes up 76% (n=66/87) of November sequences released on GISAID.

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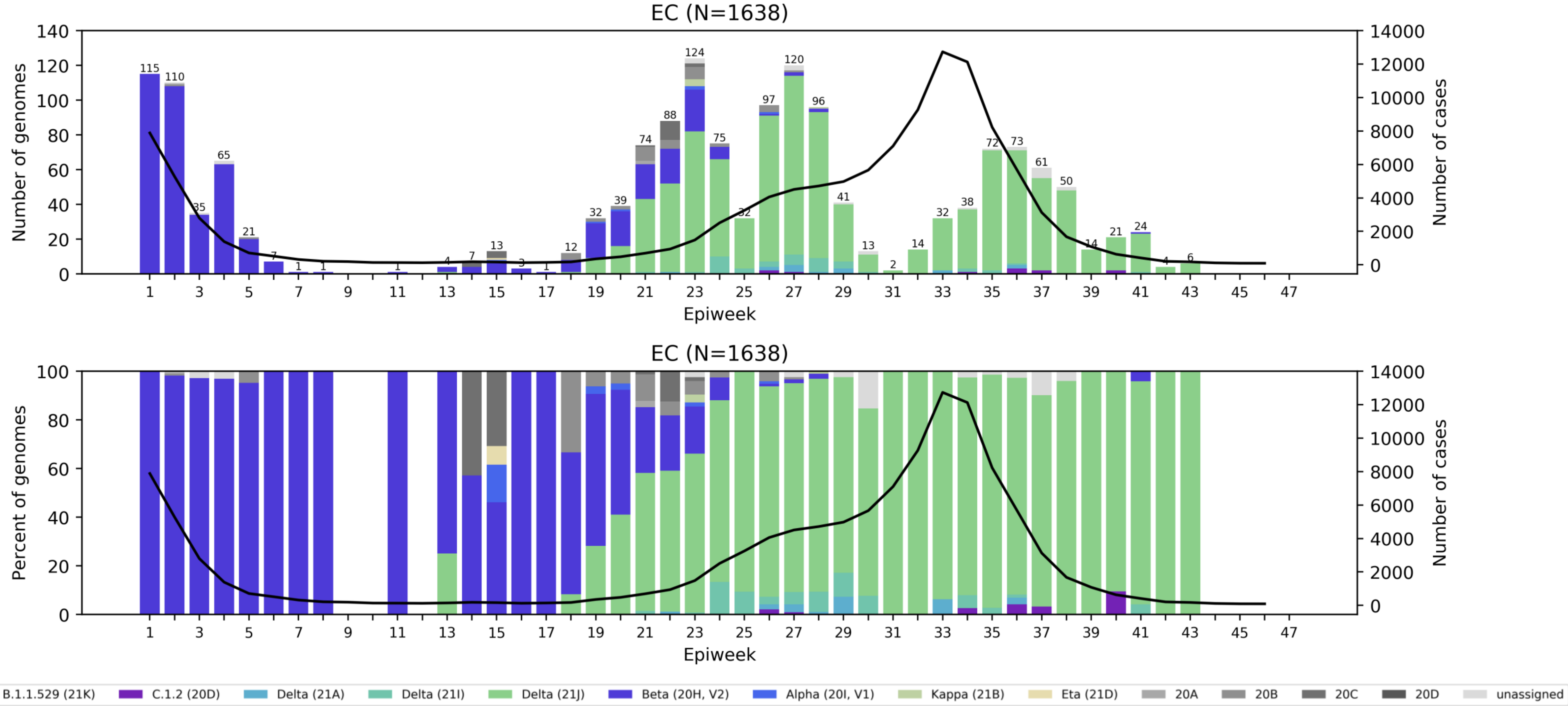
Eastern Cape Province, 2021, n = 1638



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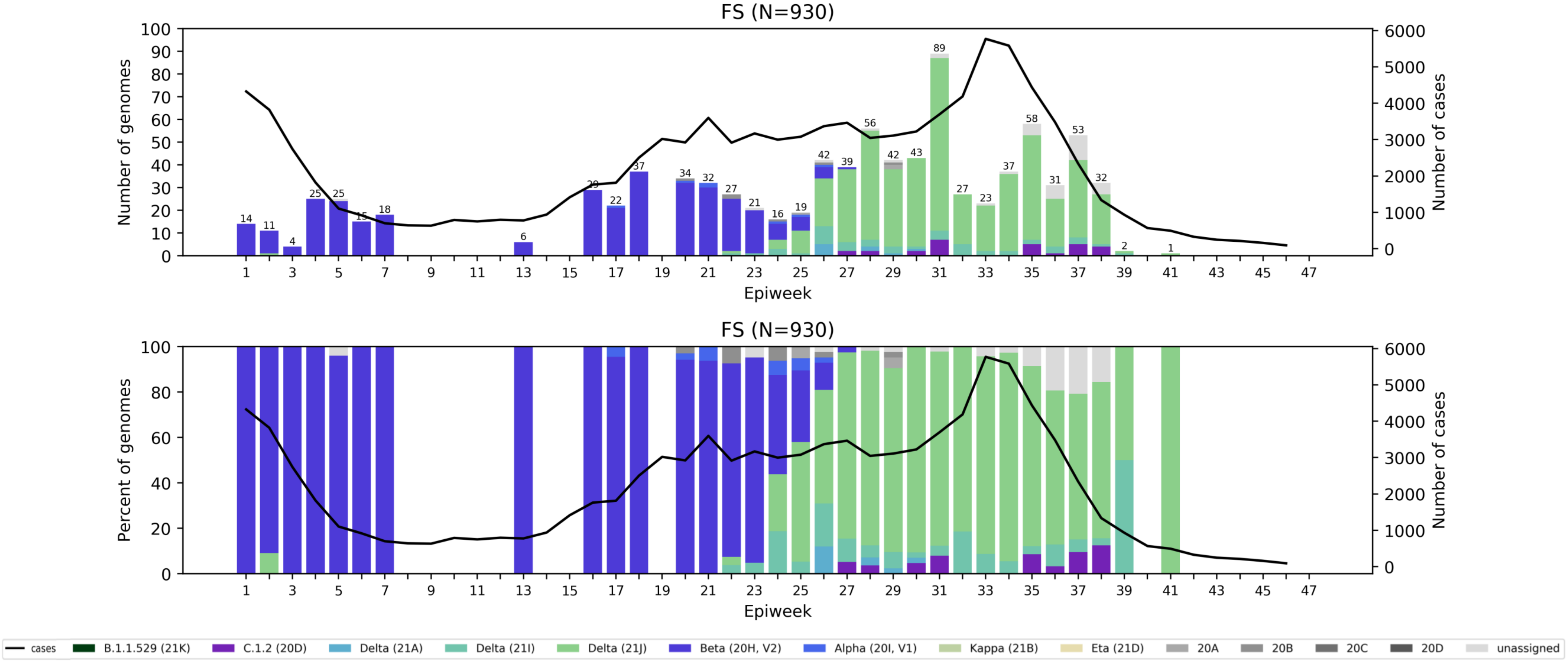
Free State Province, 2021, n = 930



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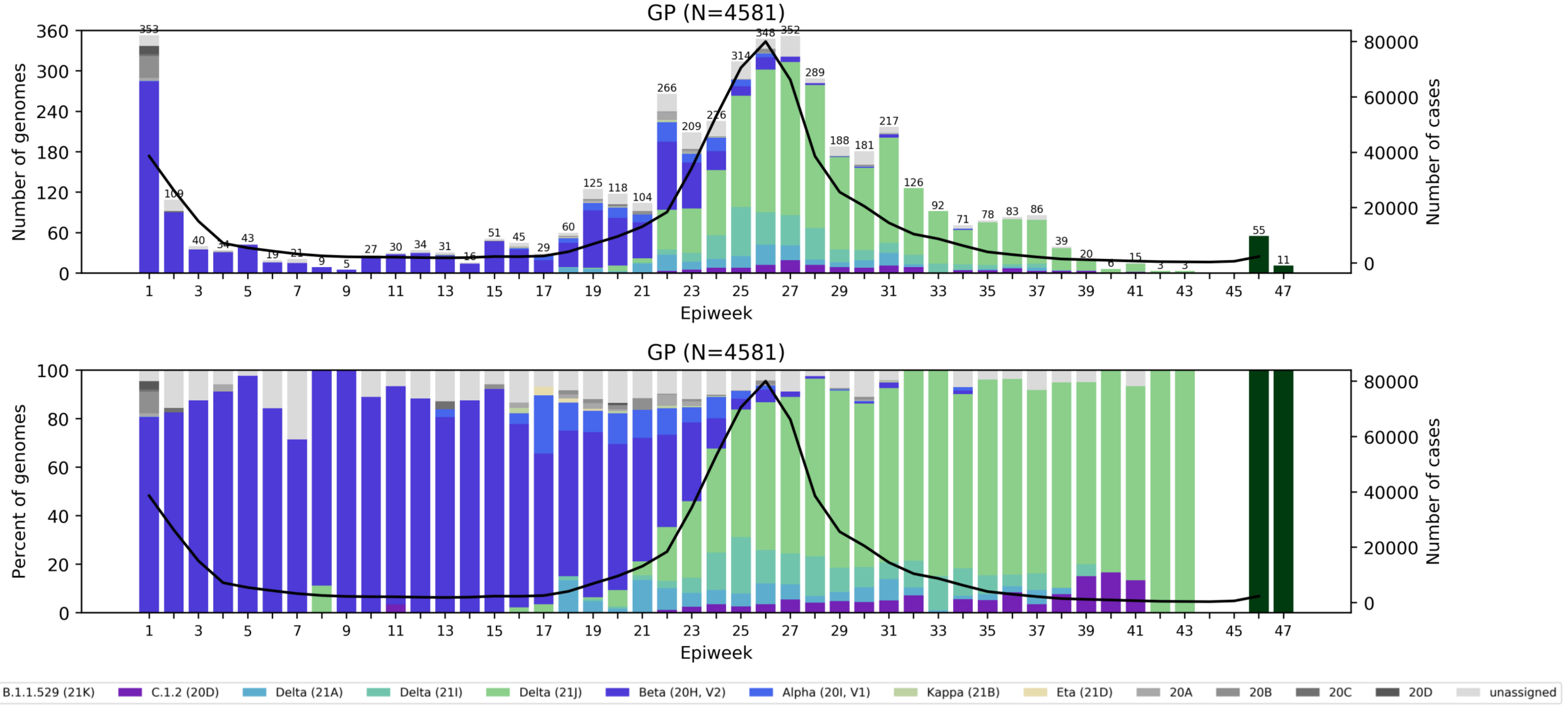
Gauteng Province, 2021, n =4581



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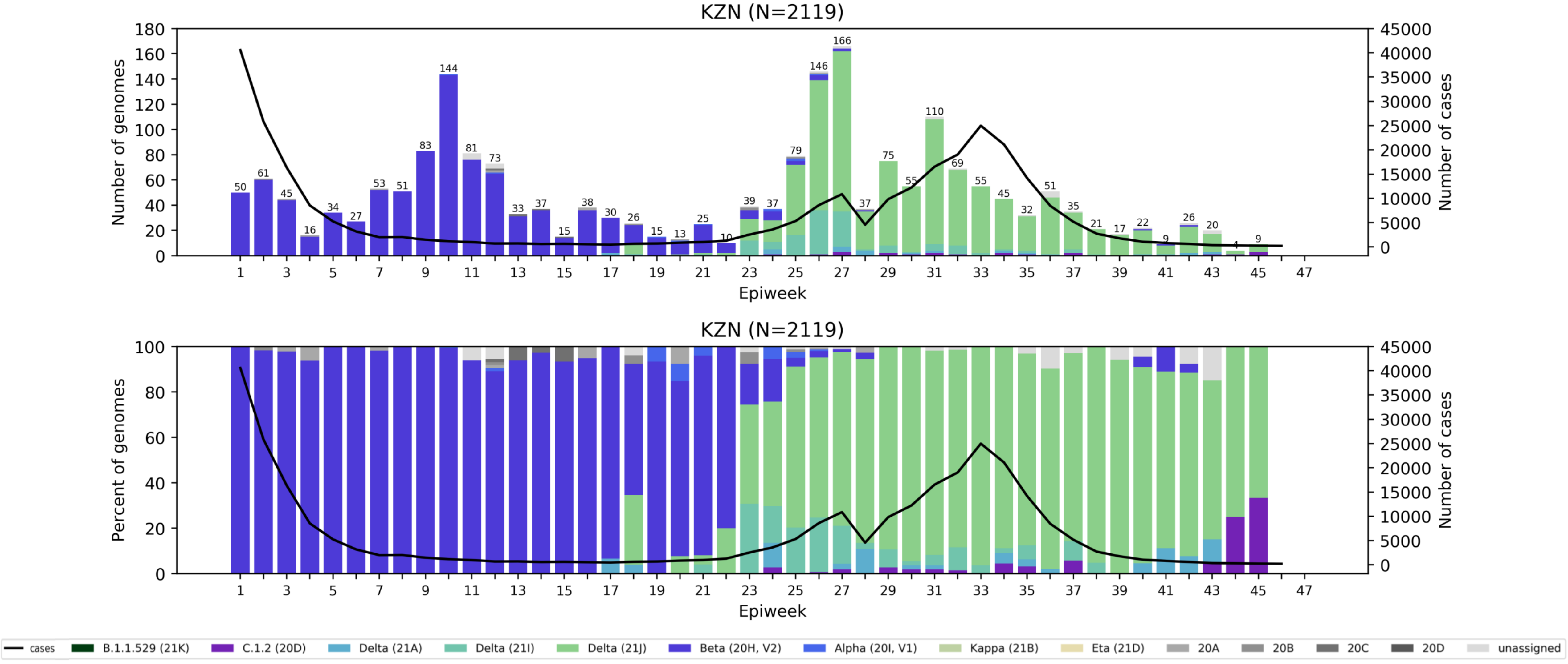
KwaZulu-Natal Province, 2021, n = 2119



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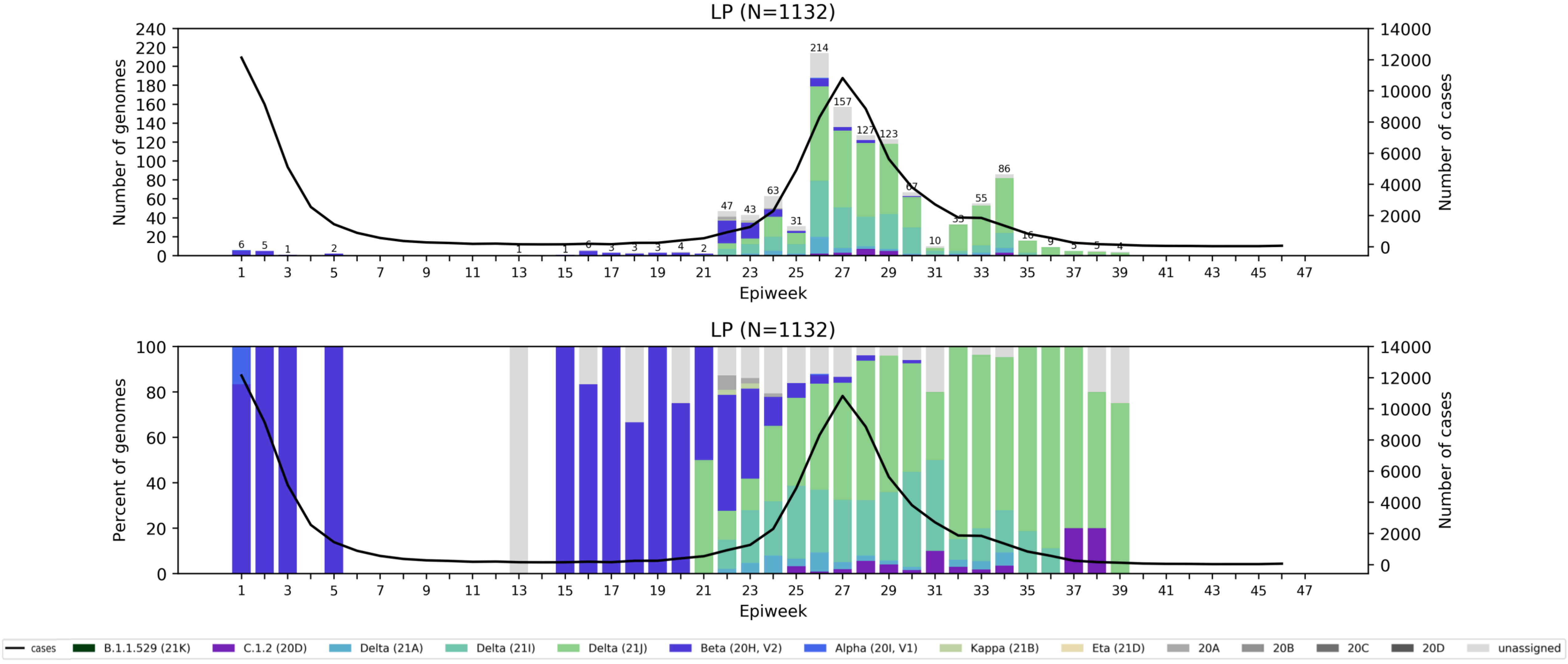
Limpopo Province, 2021, n = 1132



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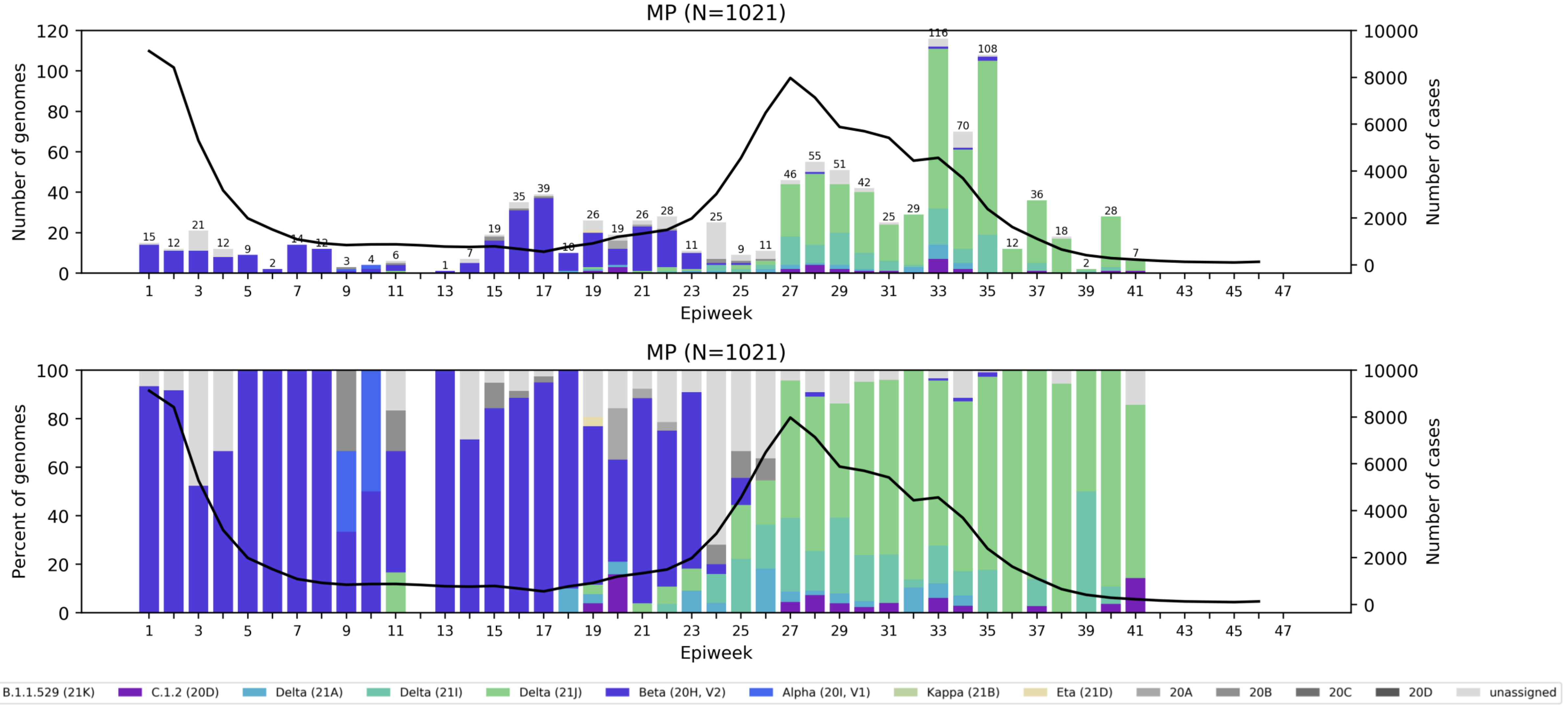
Mpumalanga Province, 2021, n = 1021



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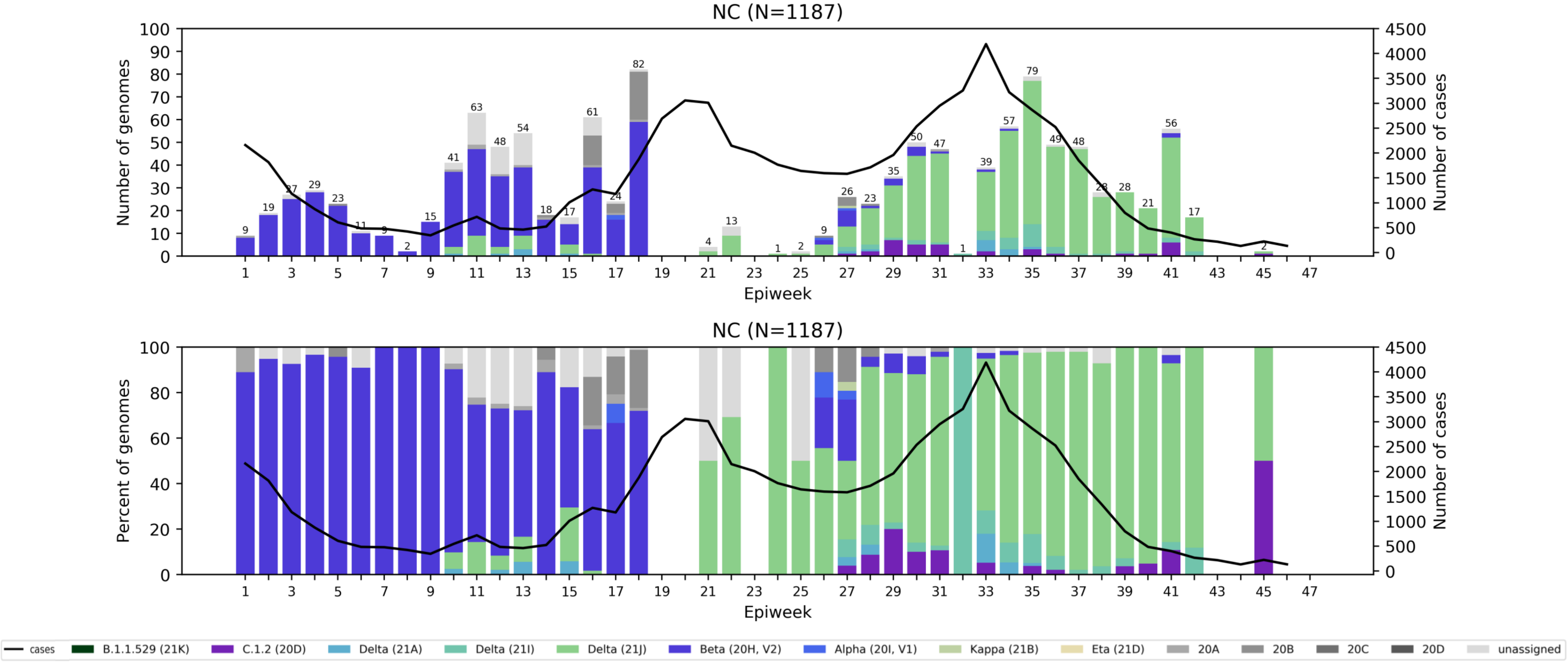
Northern Cape Province, 2021, n = 1187



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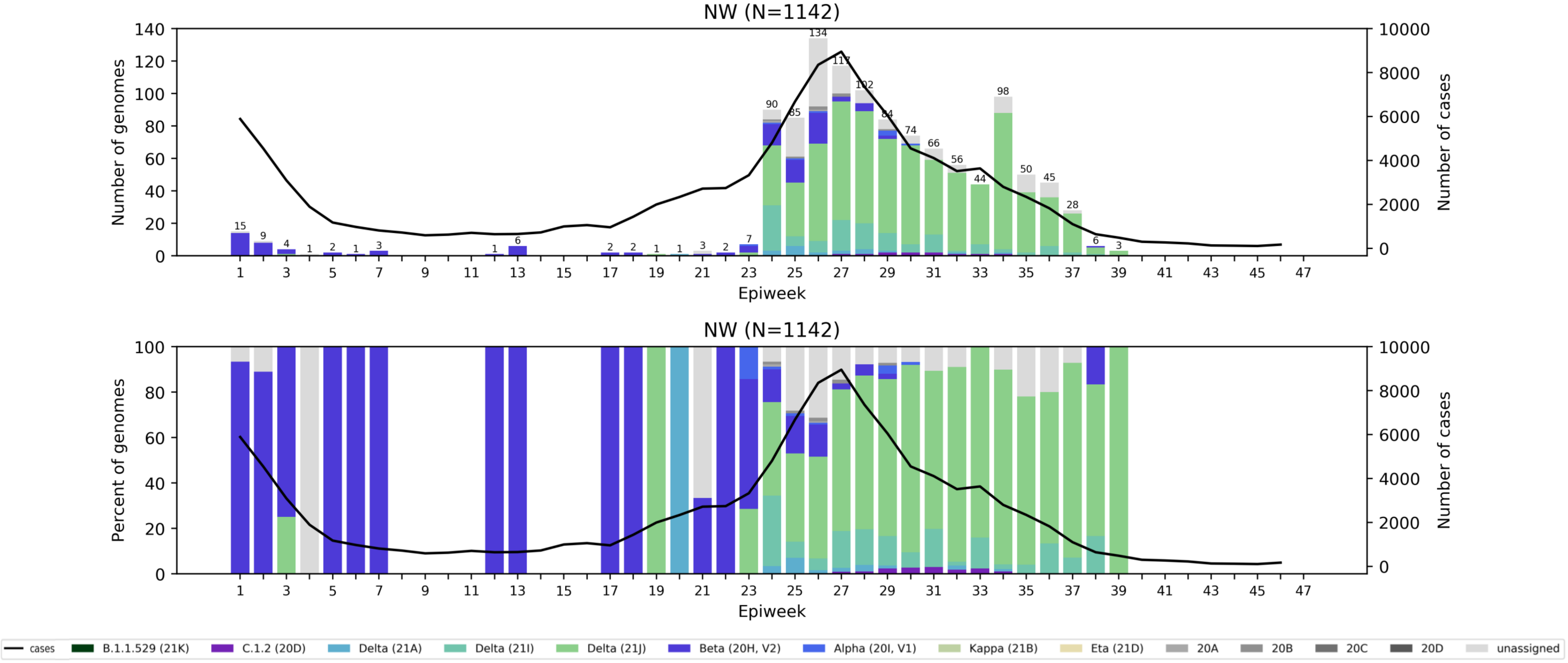
North West Province, 2021, n = 1142



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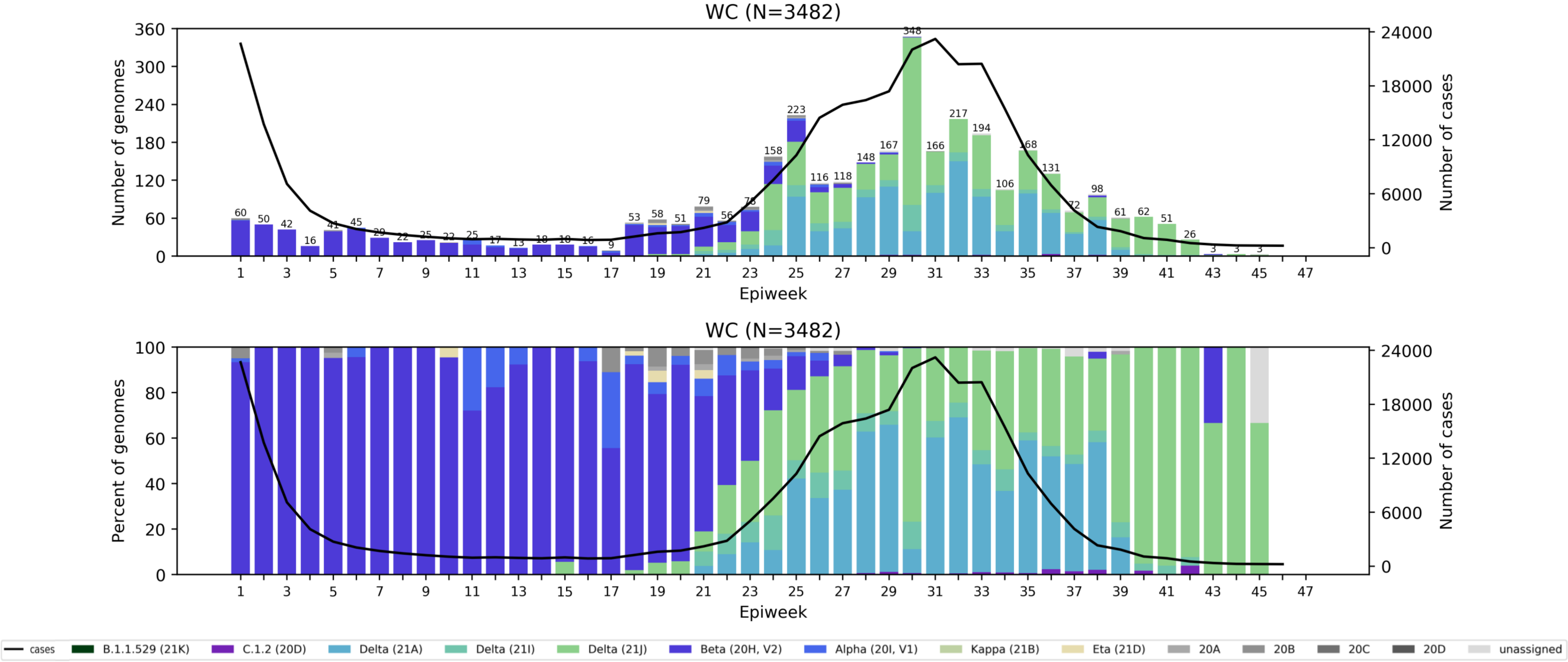
Western Cape Province, 2021, n = 3482



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Summary

- Delta variant dominated in all provinces until end October
  - The Delta sub-lineages vary by province

- C.1.2 lineage detected in all provinces of South Africa with prevalence of <6% of genomes, with increases detected in KZN and NC in November

- New B.1.1.529 lineage first detected from specimens collected in Gauteng on 12 November
  - B.1.1.529 dominates November sequencing data at 76% of genomes (n=66/87). However, total number sequences for November are low.
  - Sequencing is ongoing to determine prevalence of B.1.1.529 in other provinces.
  - Additional detections reported in Botswana and Hong Kong
  - B.1.1.529 has been assigned as NextStrain clade 21K
  - More information can be found at https://www.nicd.ac.za/frequently-asked-questions-for-the-b-1-1-529-mutated-sars-cov-2-lineage-in-south-africa/

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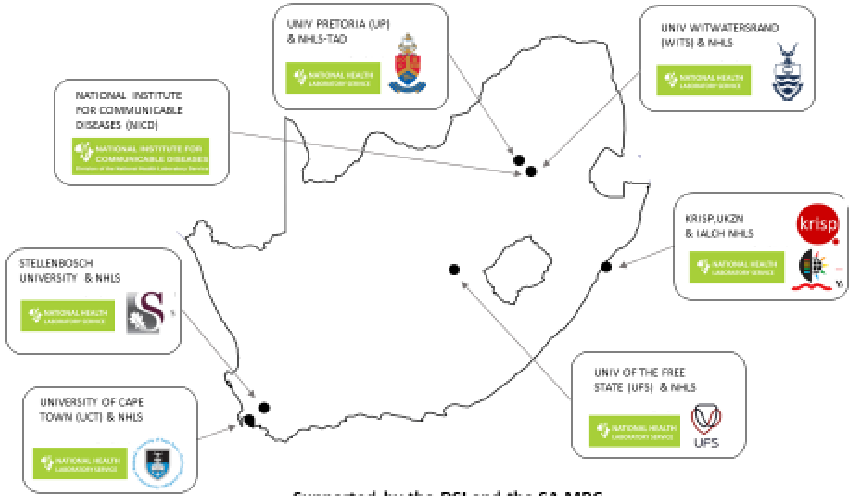

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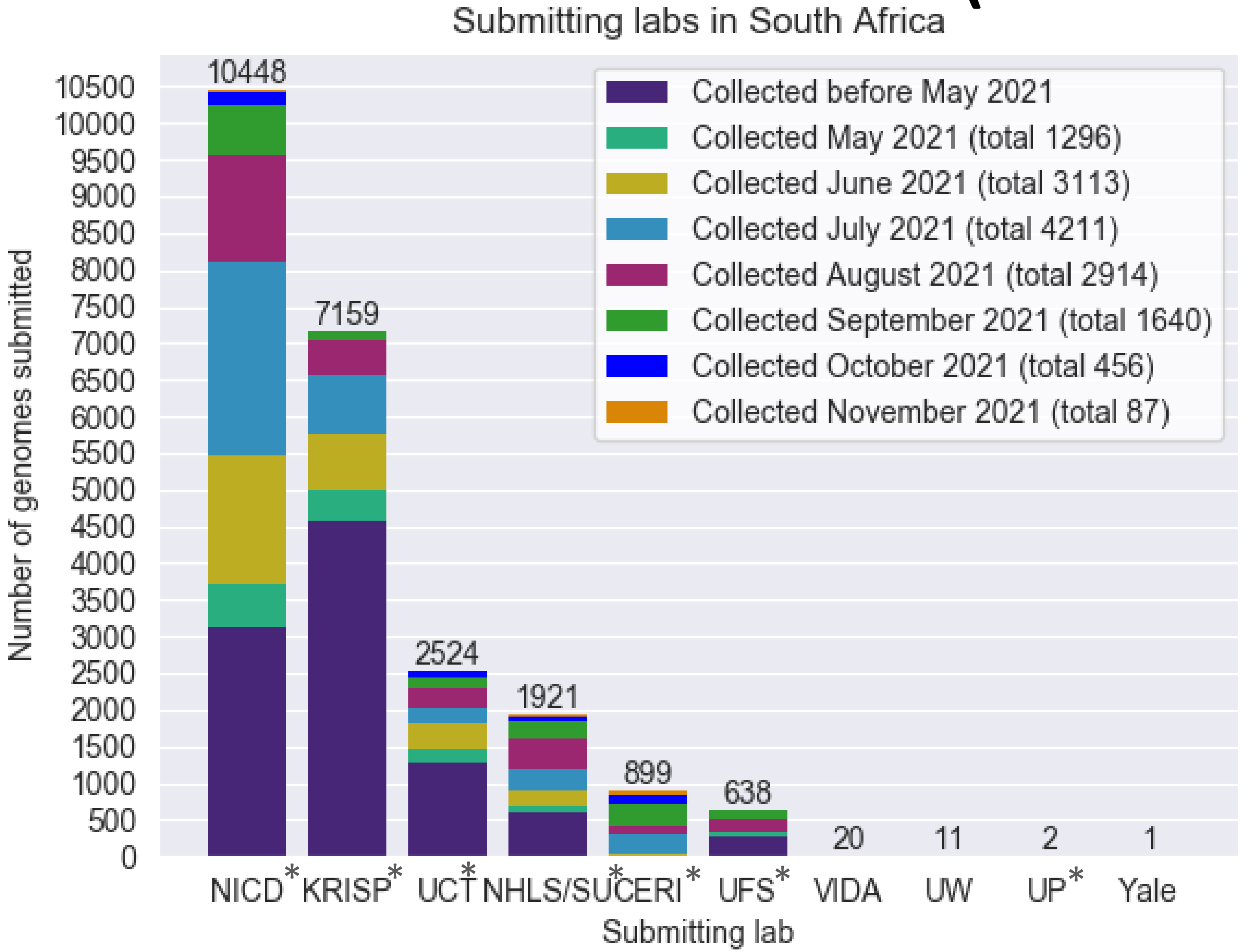
Glenda Gray

South African genomes submitted per submitting lab, 2020 and 2021 (N=23 623)



NGS-SA Labs
CERI: Centre for Epidemic Response and Innovation
KRISP: KZN Research Innovation and Sequencing Platform
NICD: National Institute for Communicable Diseases
NHLS: National Health Laboratory Service
SU: Stellenbosch University
UCT: University of Cape Town
UFS: University of the Free State
UP: University of Pretoria

*NGS-SA laboratories

Multiple labs from NGS-SA and collaborating private laboratories are contributing to the sequencing effort.

NGS-SA
Network for Genomic Surveillance in South Africa

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 11 November 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 11 November 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.)