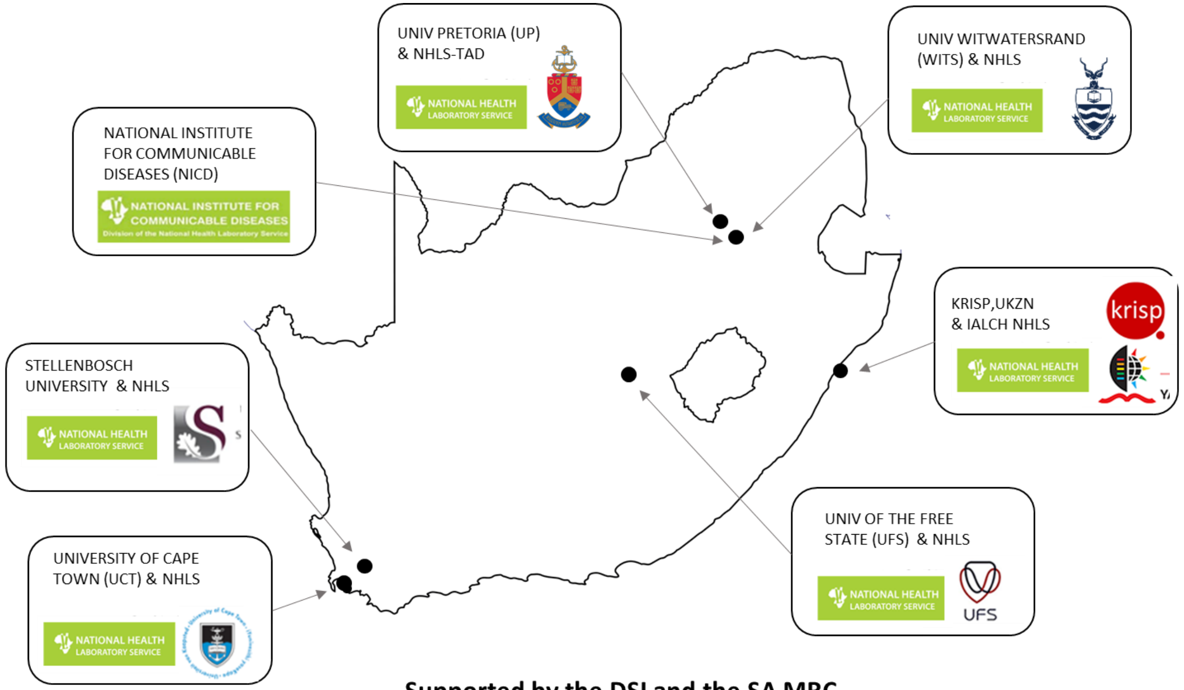
NGS-SA
Network for Genomic Surveillance in South Africa

Network for Genomic Surveillance South Africa (NGS-SA)

SARS-CoV-2 Sequencing Update
29 October 2021



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 29 October at 09h16

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

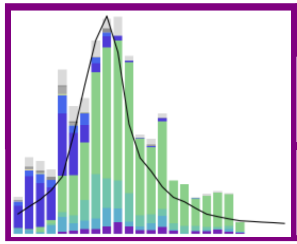
Elbe, S., and Buckland-Merrett, G. (2017) Data, disease and diplomacy: GISAID’s innovative contribution to global health. Global Challenges, 1:33-46. DOI: 10.1002/gch2.1018 PMCID: 31565258

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/

GENOMIC SURVEILLANCE IN THE THIRD WAVE

epiweeks 18 - 42



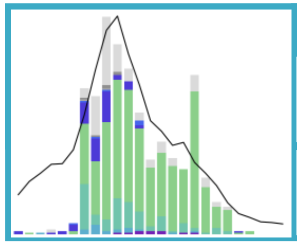
Gauteng

PTP: 0.9%

Genomes	Cases
3 355 (27.3%)	494 121 (37.0%)

Genomes deposited in the last week

🟦 28 🟦 6 🟦 7 🟩 7 🟩 47 🟪 5 ⬛ 5 ⬜ 6



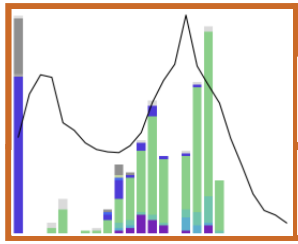
North West

PTP: 2.5%

Genomes	Cases
983 (8.0%)	82 466 (6.2%)

Genomes deposited in the last week

🟦 15 🟦 1 🟩 23 🟪 1 ⬜ 17



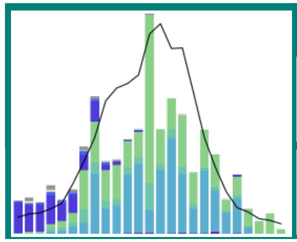
Northern Cape

PTP: 5.7%

Genomes	Cases
460 (3.6%)	51 685 (3.9%)

Genomes deposited in the last week

🟦 11 🟩 1 🟩 8 🟪 2 ⬛ 30 ⬜ 2



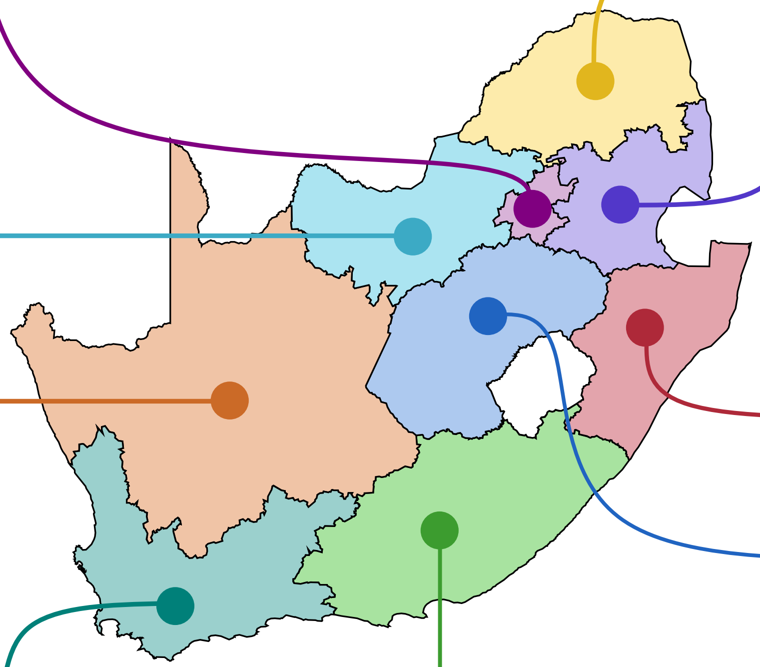
Western Cape

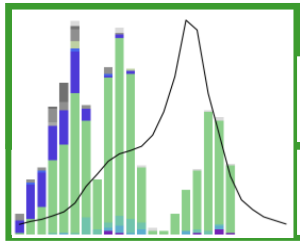
PTP: 2.2%

Genomes	Cases
2 808 (22.9%)	226 208 (17.0%)

Genomes deposited in the last week

🟦 48 🟩 6 🟩 73 🟪 2 ⬜ 3 ⬛ 2





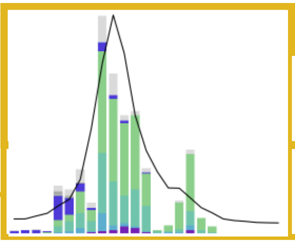
Eastern Cape

PTP: 1.7%

Genomes	Cases
1 092 (8.9%)	96 028 (7.2%)

Genomes deposited in the last week

🟦 2 🟩 4 ⬛ 3 ⬜ 1



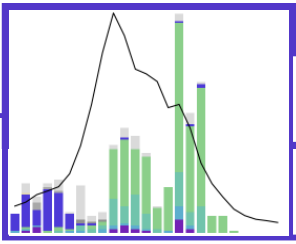
Limpopo

PTP: 1.4%

Genomes	Cases
1013 (7.6%)	58 158 (4.4%)

Genomes deposited in the last week

🟦 21 🟦 1 🟩 43 🟩 50 ⬜ 12



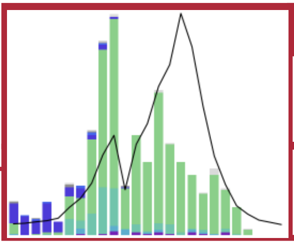
Mpumalanga

PTP: 2.3%

Genomes	Cases
673 (5.5%)	73 355 (5.5%)

Genomes deposited in the last week

🟦 7 🟩 11 🟩 54 🟪 1 ⬛ 4 ⬜ 4

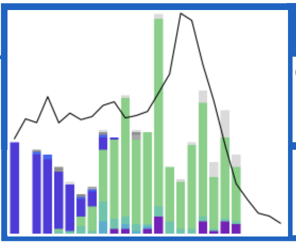


KwaZulu-Natal

PTP: 1.8%

Genomes	Cases
1 144 (93%)	178 359 (13.4%)

Genomes deposited in the last week



Free State

PTP: 3.8%

Genomes	Cases
750 (6.1%)	73 452 (5.5%)

Genomes deposited in the last week

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

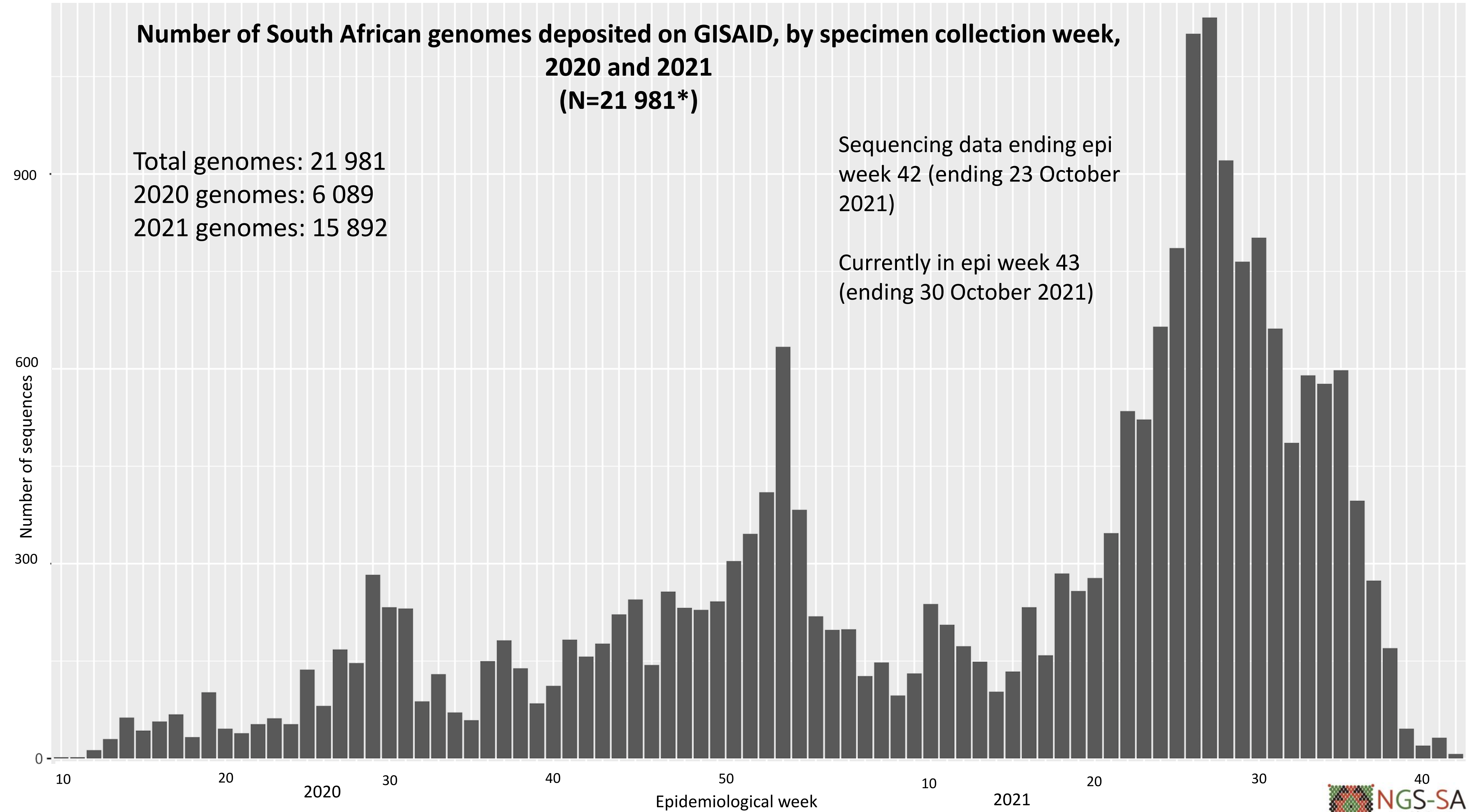
Bar graphs represent genomes sequenced per epiweek, with lines representing cases by collection date (weeks 18 – 42)

Genomes and cases presented as provincial total (percentage of national total) for epiweeks 18 – 42

PTP: percentage testing positive

NGS-SA
Network for Genomic Surveillance in South Africa

Number of South African genomes deposited on GISAID, by specimen collection week, 2020 and 2021
(N=21 981*)



Total genomes: 21 981
2020 genomes: 6 089
2021 genomes: 15 892

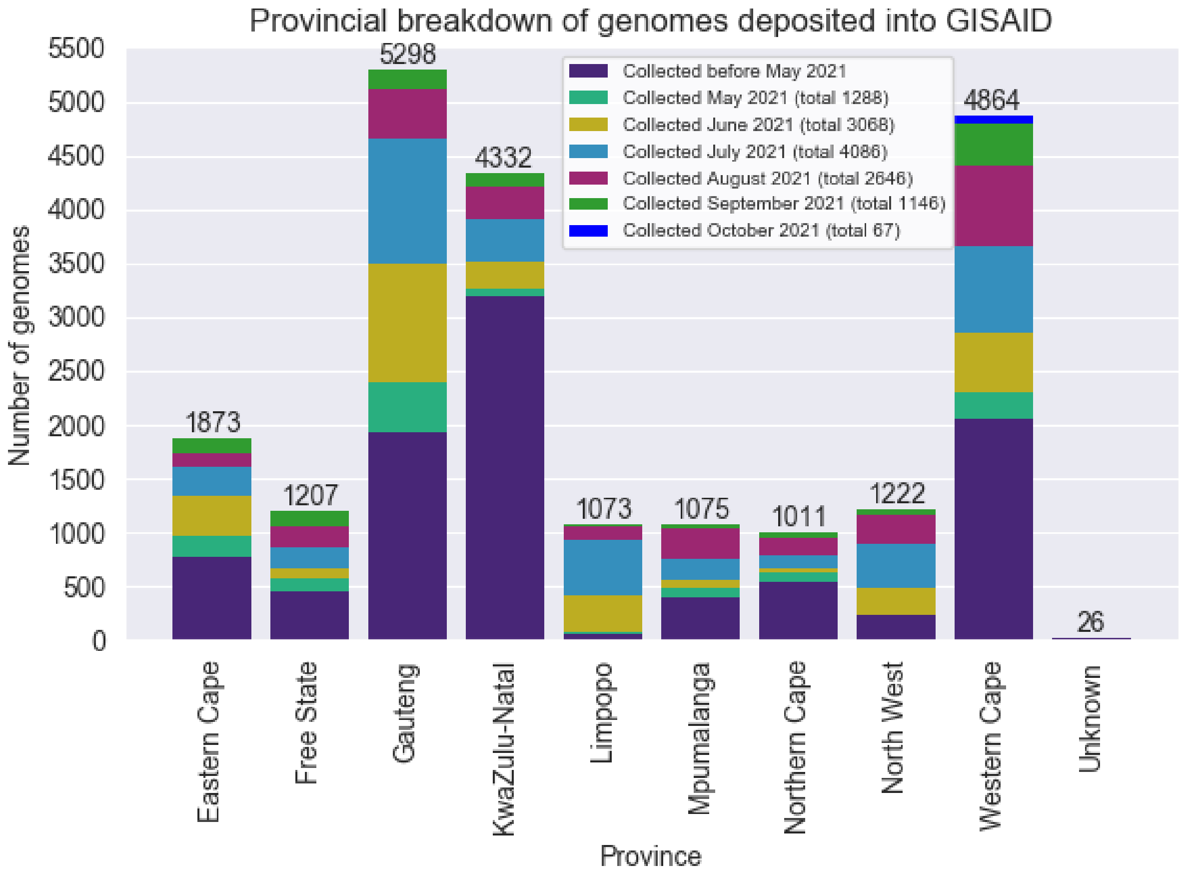
Sequencing data ending epi week 42 (ending 23 October 2021)

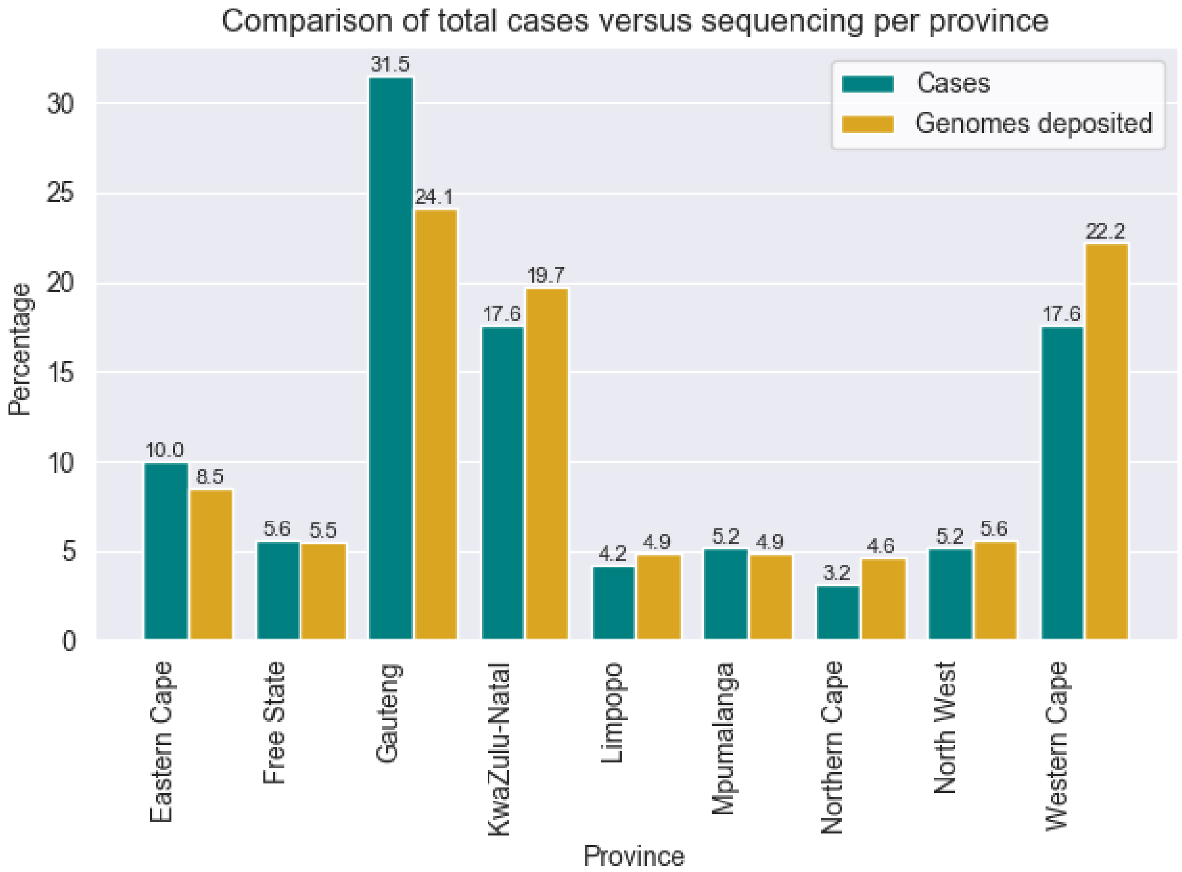
Currently in epi week 43 (ending 30 October 2021)

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

NGS-SA
Network for Genomic Surveillance in South Africa

GISAID genomes vs total cases, 2020 and 2021 (N=21 981)

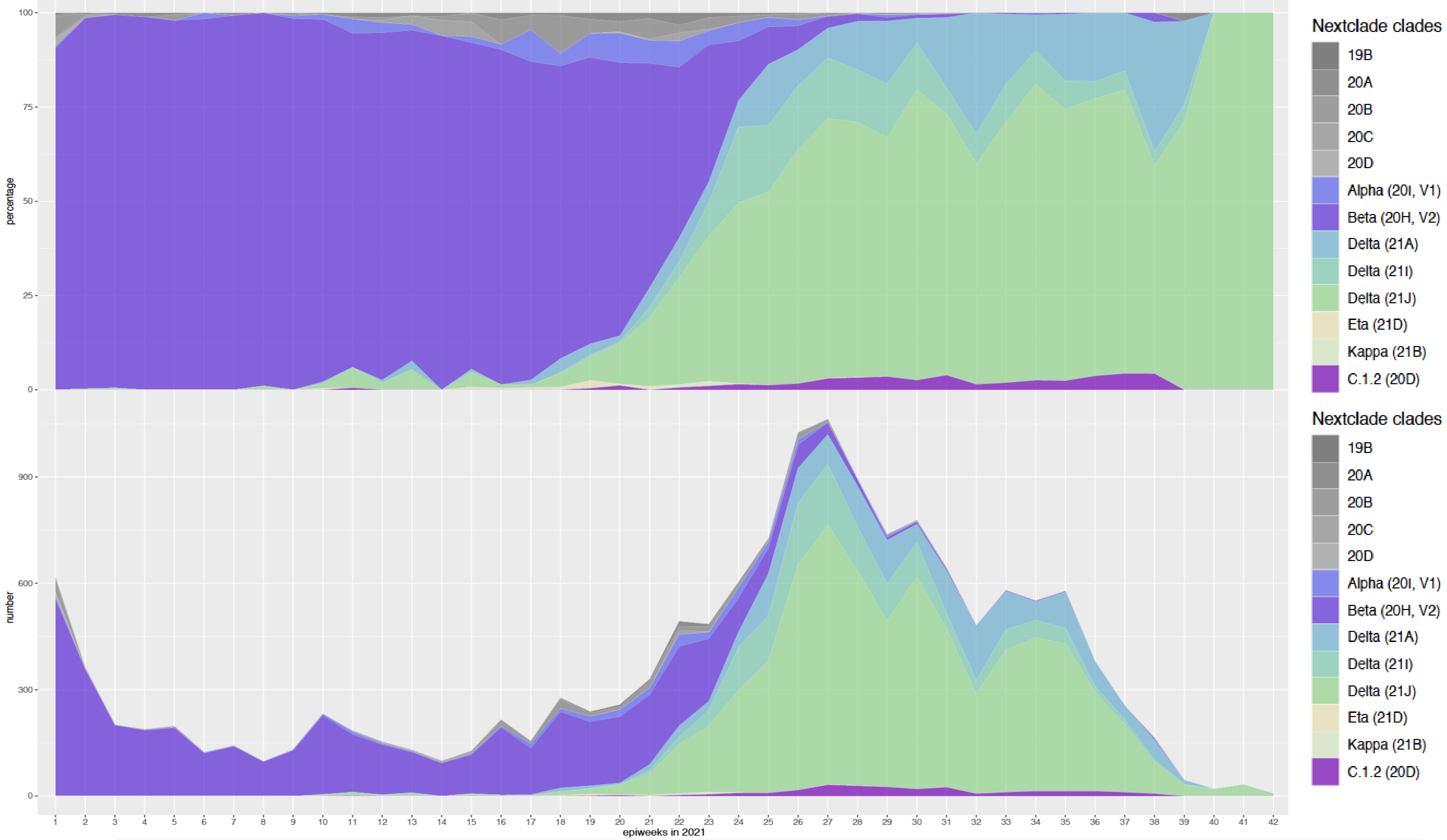




All provinces, apart from GP, KZN, and WC, have comparable percentage of overall cases and overall sequenced genomes

NGS-SA
Network for Genomic Surveillance in South Africa

Distribution and number of clades in South Africa, 2021 (N= 15 892)



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

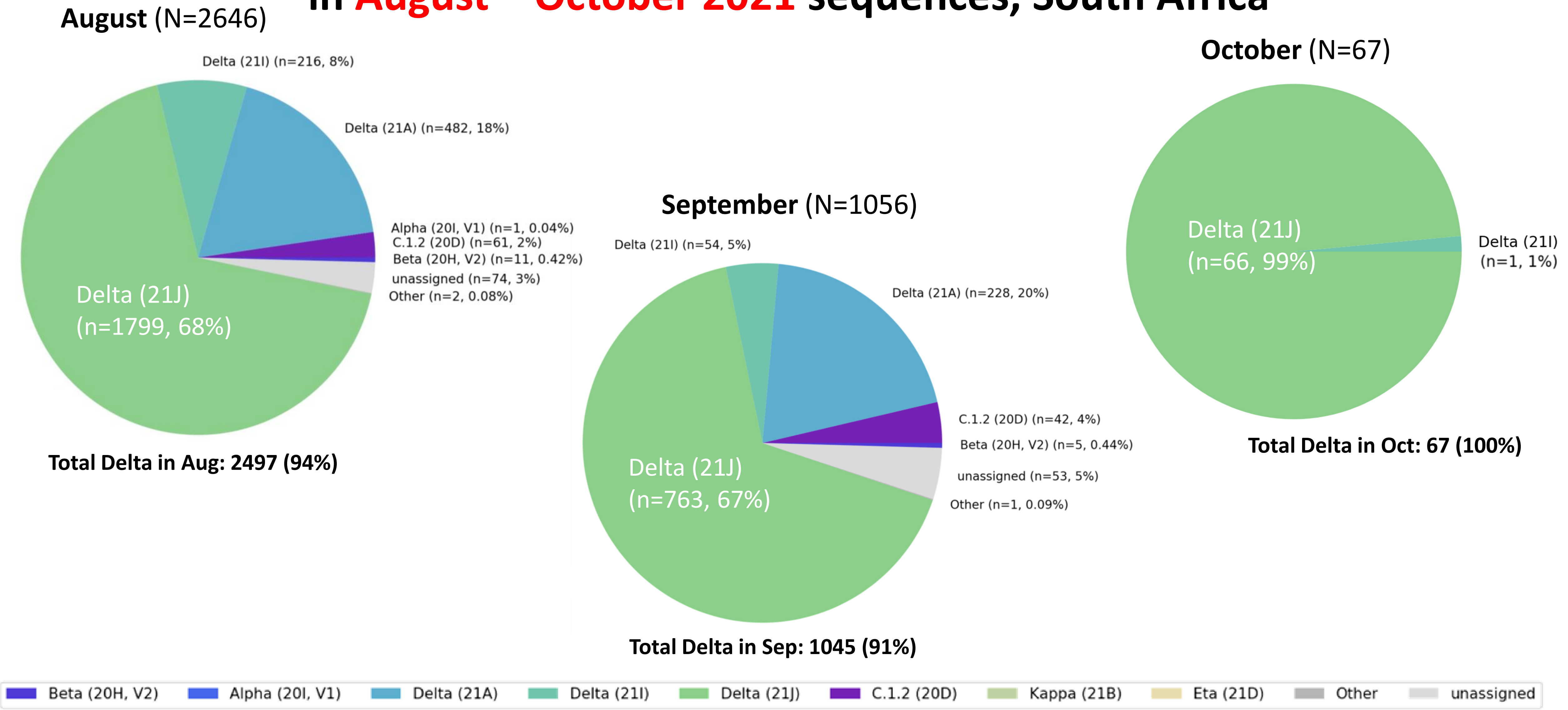
Sequencing data ending epi week 42 (ending 23 October 2021)

Currently in epi week 43 (ending 30 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

NGS-SA
Network for Genomic Surveillance in South Africa

Prevalence of Variants of Concern (VOC) and Variants of Interest (VOI) in August – October 2021 sequences, South Africa



Total Delta in Aug: 2497 (94%)

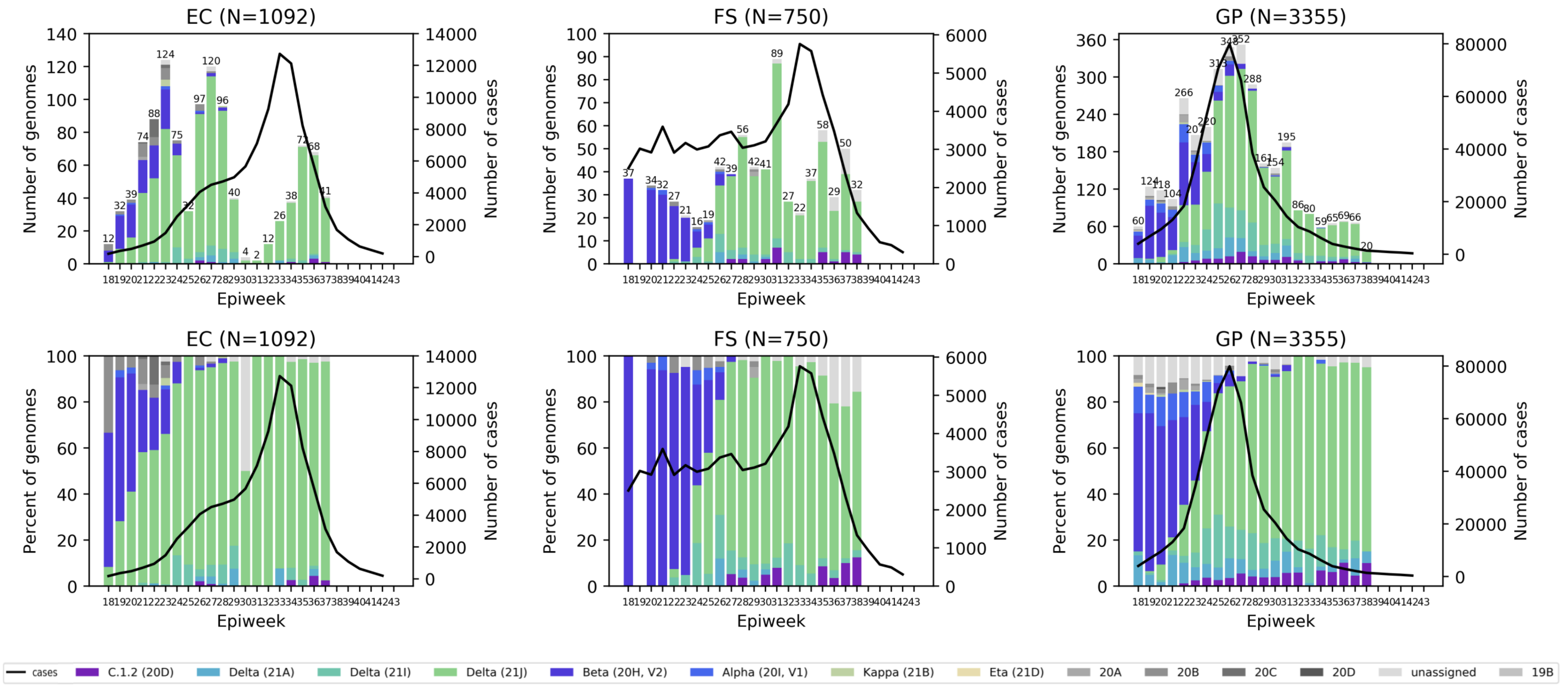
Total Delta in Sep: 1045 (91%)

Total Delta in Oct: 67 (100%)

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

NGS-SA
Network for Genomic
Surveillance in South Africa

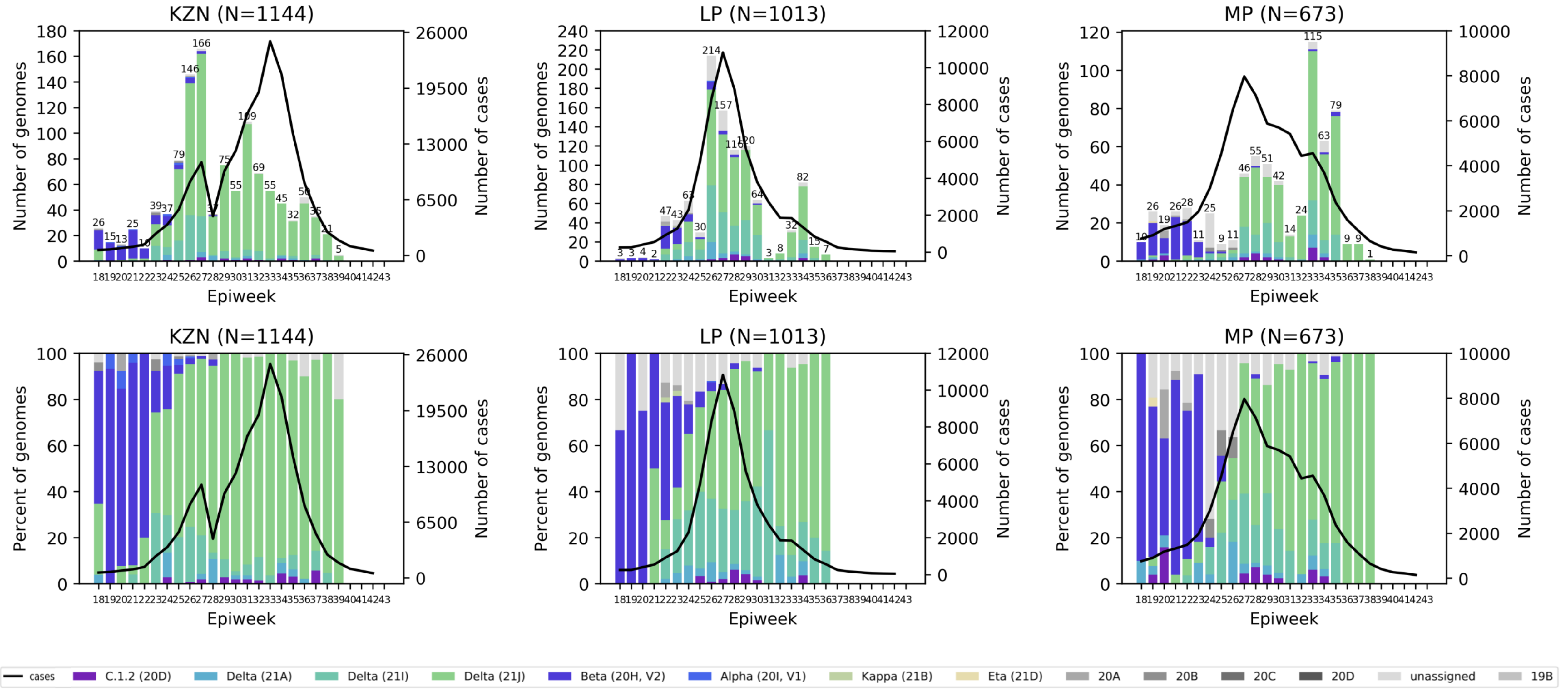
Genomes sequenced from specimens collected in May to mid-September 2021 (epiweeks 18 – 43) from Eastern Cape, Free State and Gauteng Provinces



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

NGS-SA
Network for Genomic
Surveillance in South Africa

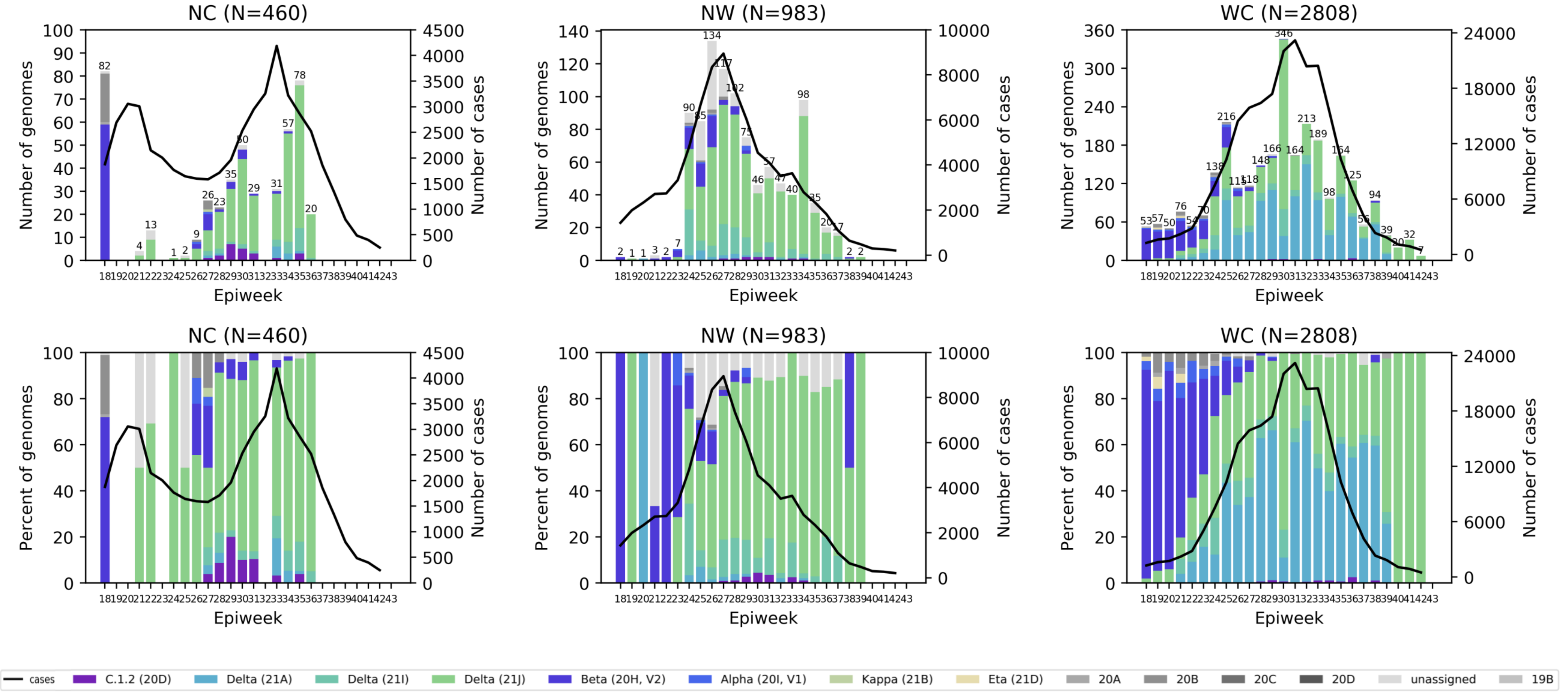
Genomes sequenced from specimens collected in May to mid-September 2021 (epiweeks 18 – 43) from KwaZulu-Natal, Limpopo and Mpumalanga Provinces



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

NGS-SA
Network for Genomic Surveillance in South Africa

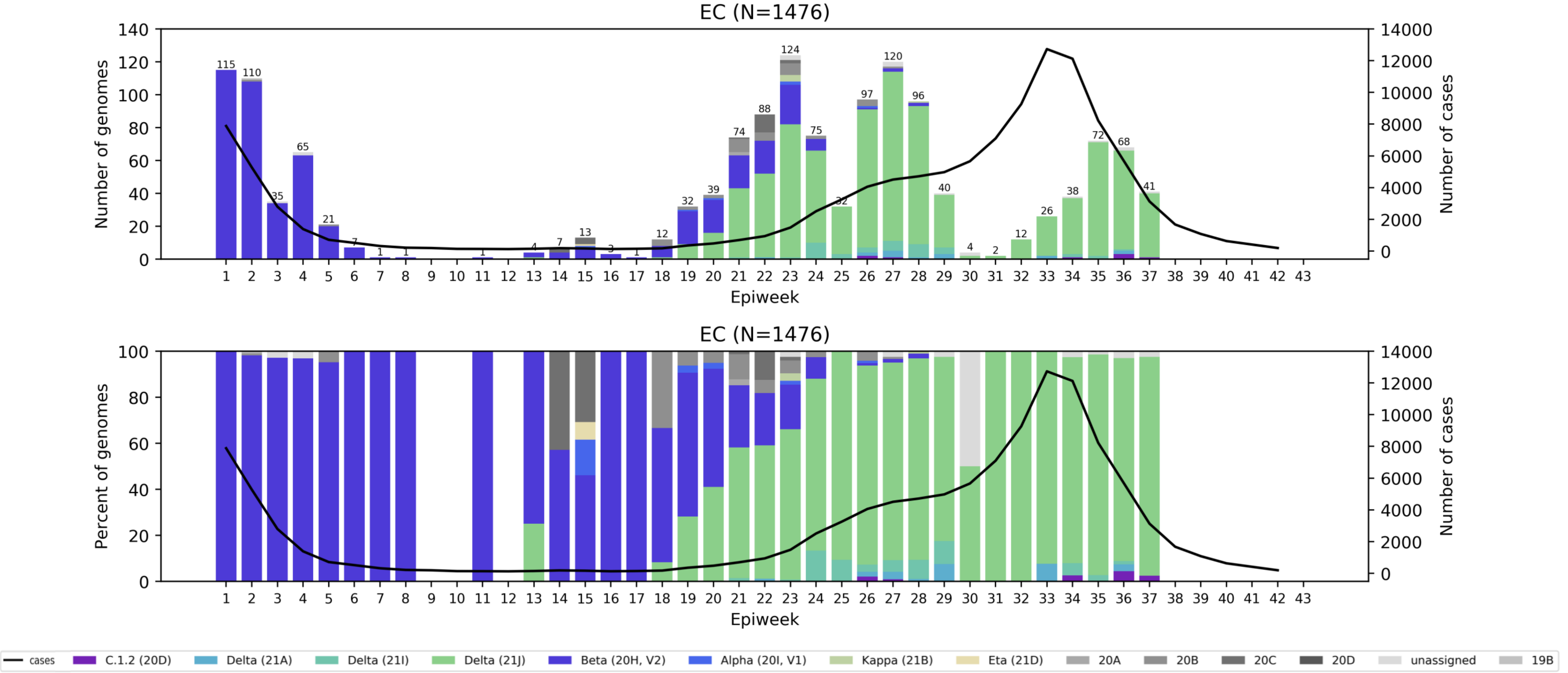
Genomes sequenced from specimens collected in May to mid-September 2021 (epiweeks 18 – 43) from Northern Cape, North West, and Western Cape Provinces



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

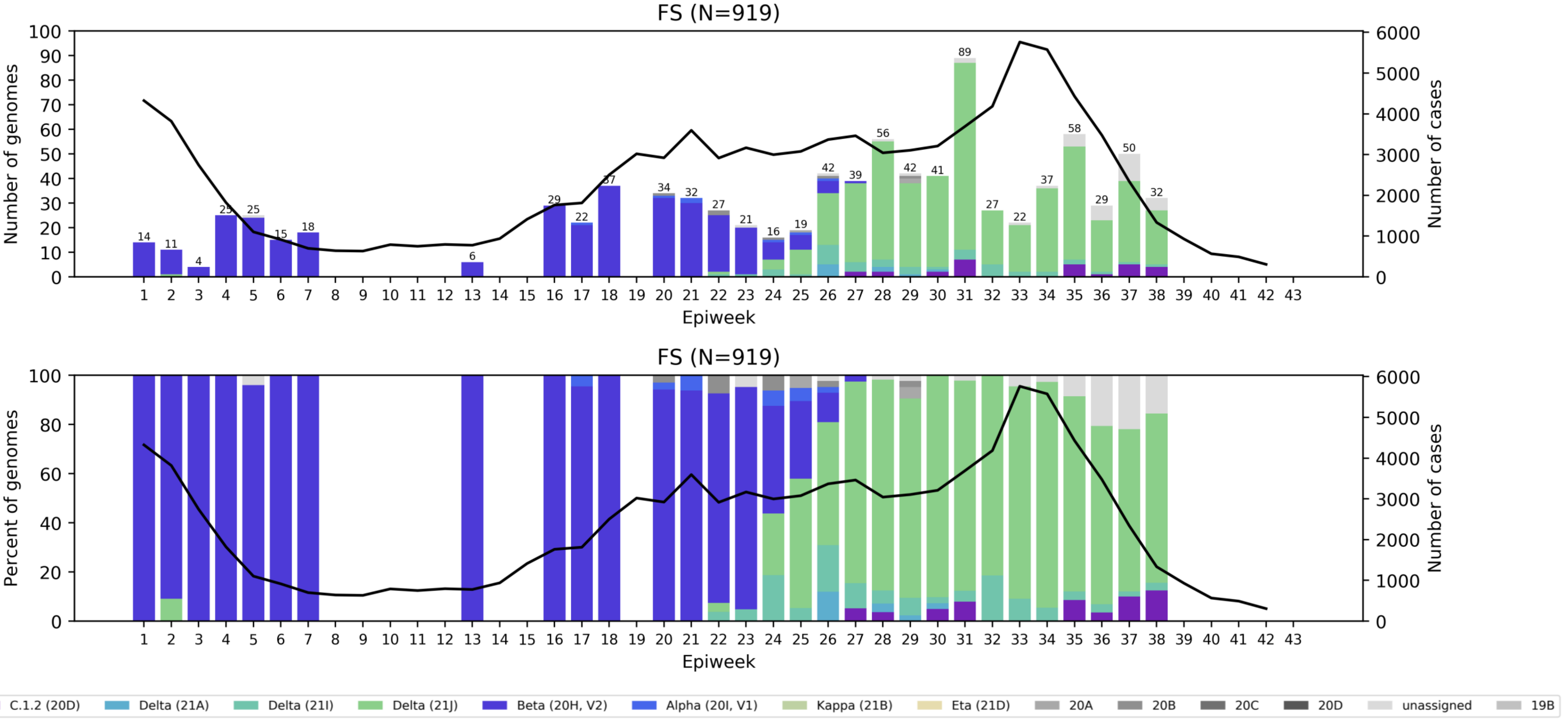
NGS-SA
Network for Genomic Surveillance in South Africa

Eastern Cape Province, 2021, n = 1476



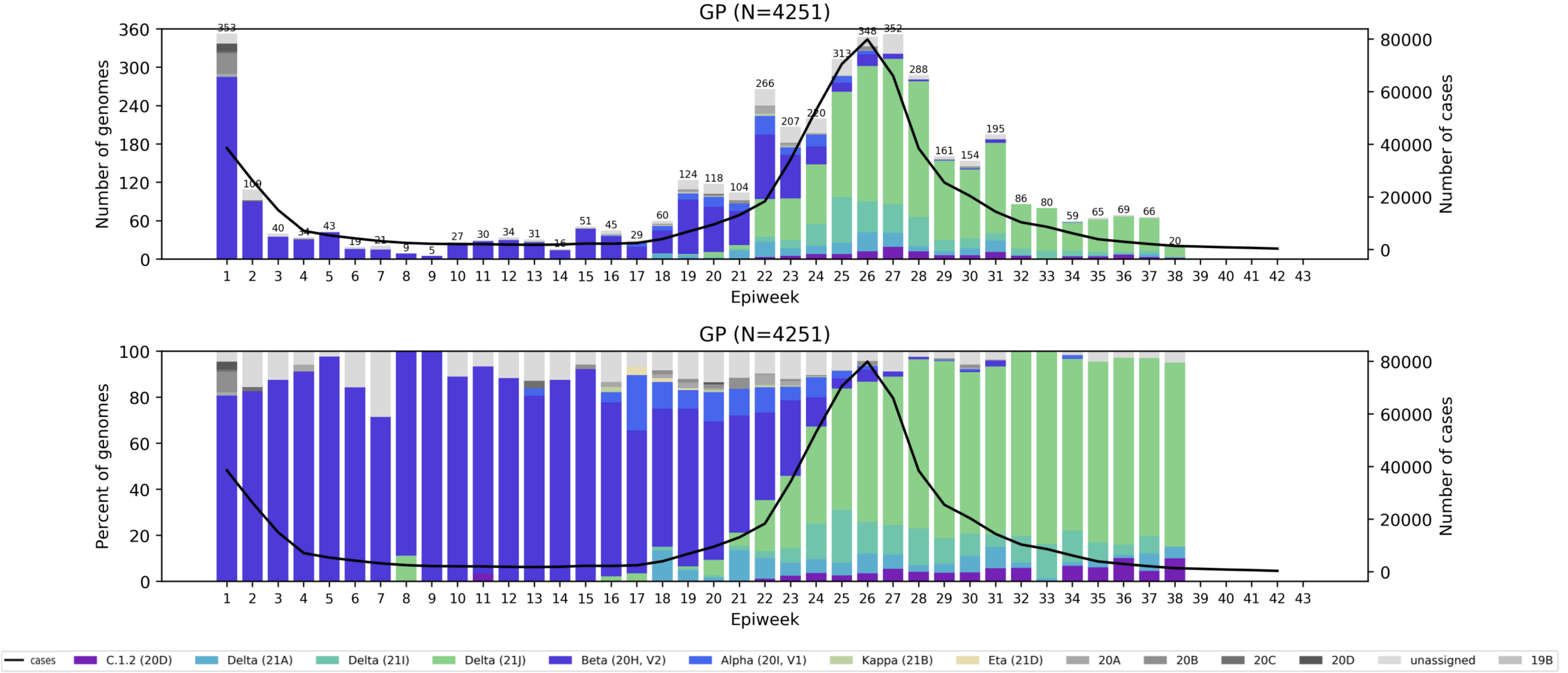
NGS-SA
Network for Genomic
Surveillance in South Africa

Free State Province, 2021, n = 919



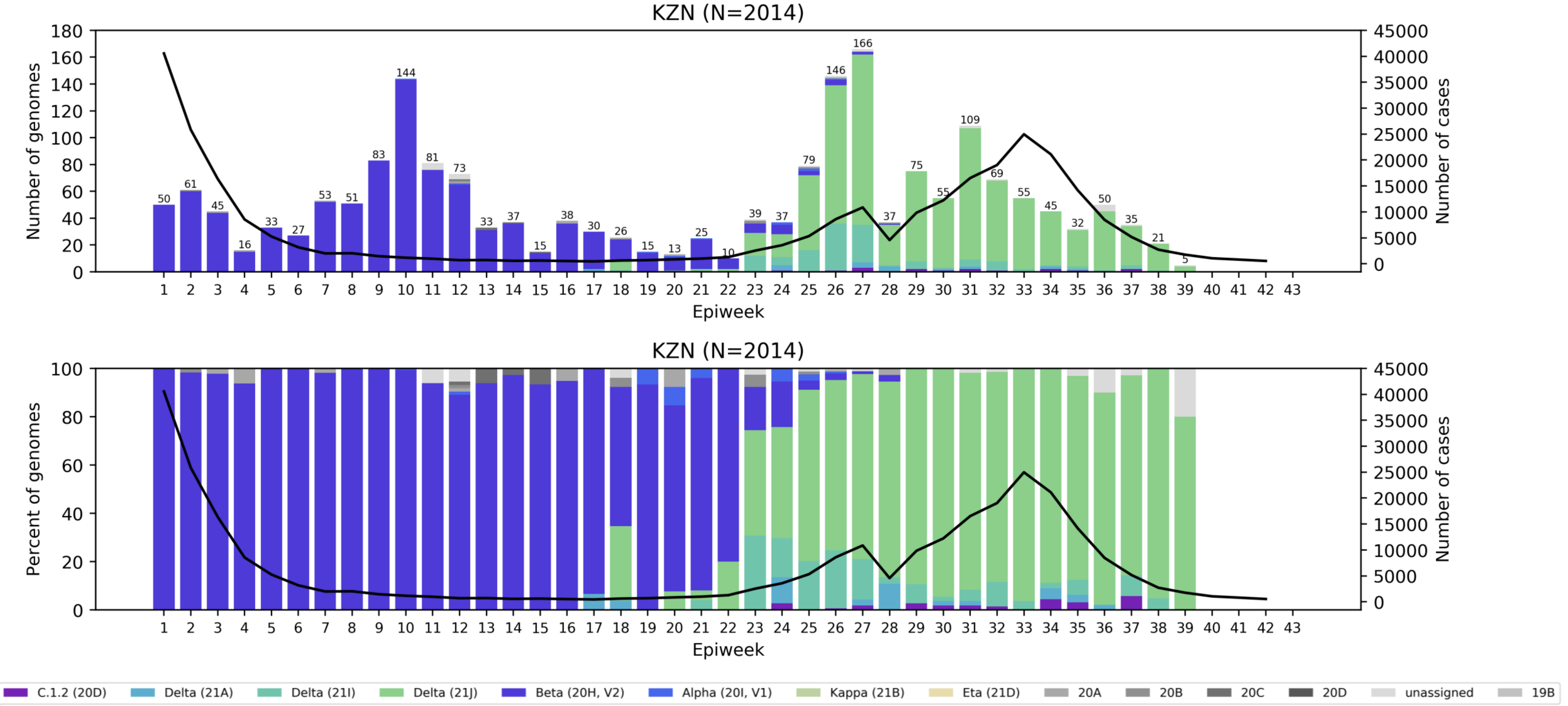
NGS-SA
Network for Genomic
Surveillance in South Africa

Gauteng Province, 2021, n = 4251



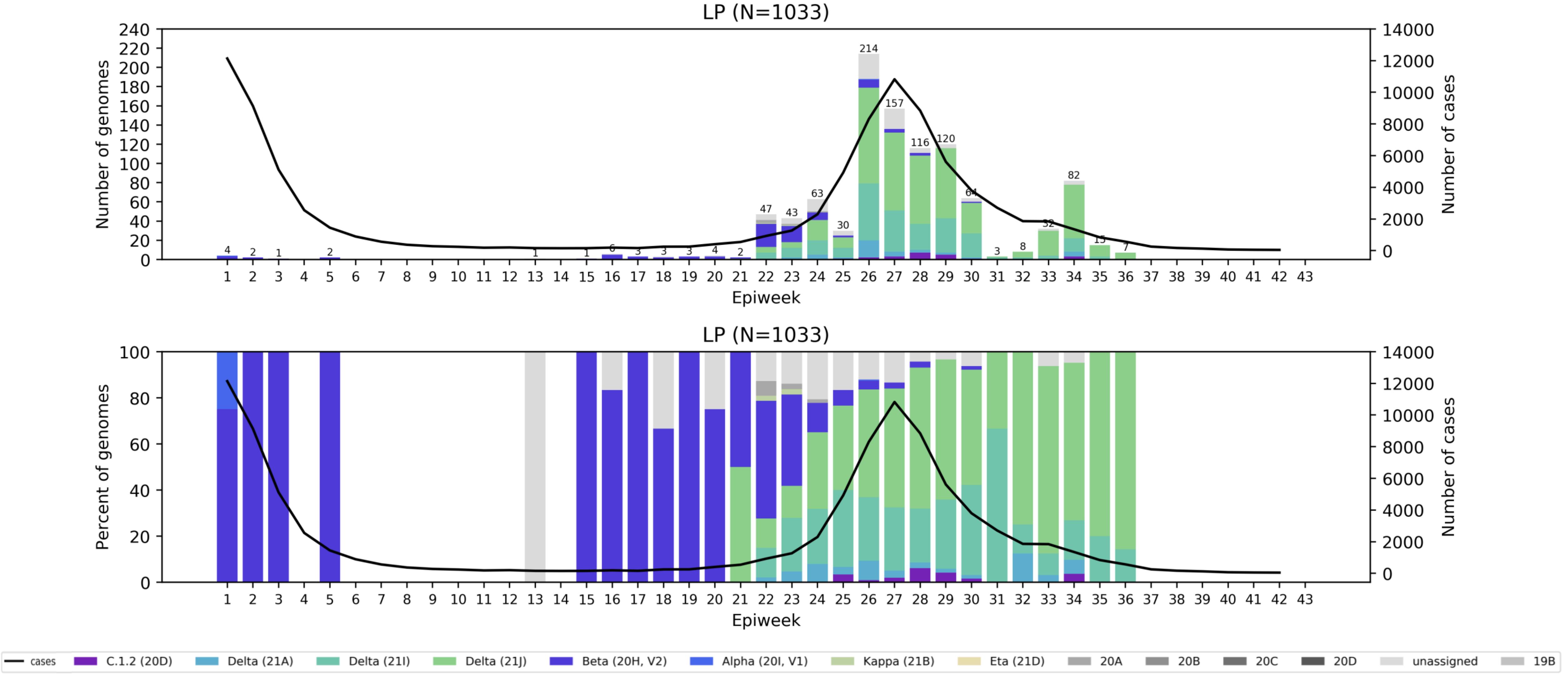
NGS-SA
Network for Genomic
Surveillance in South Africa

KwaZulu-Natal Province, 2021, n = 2014



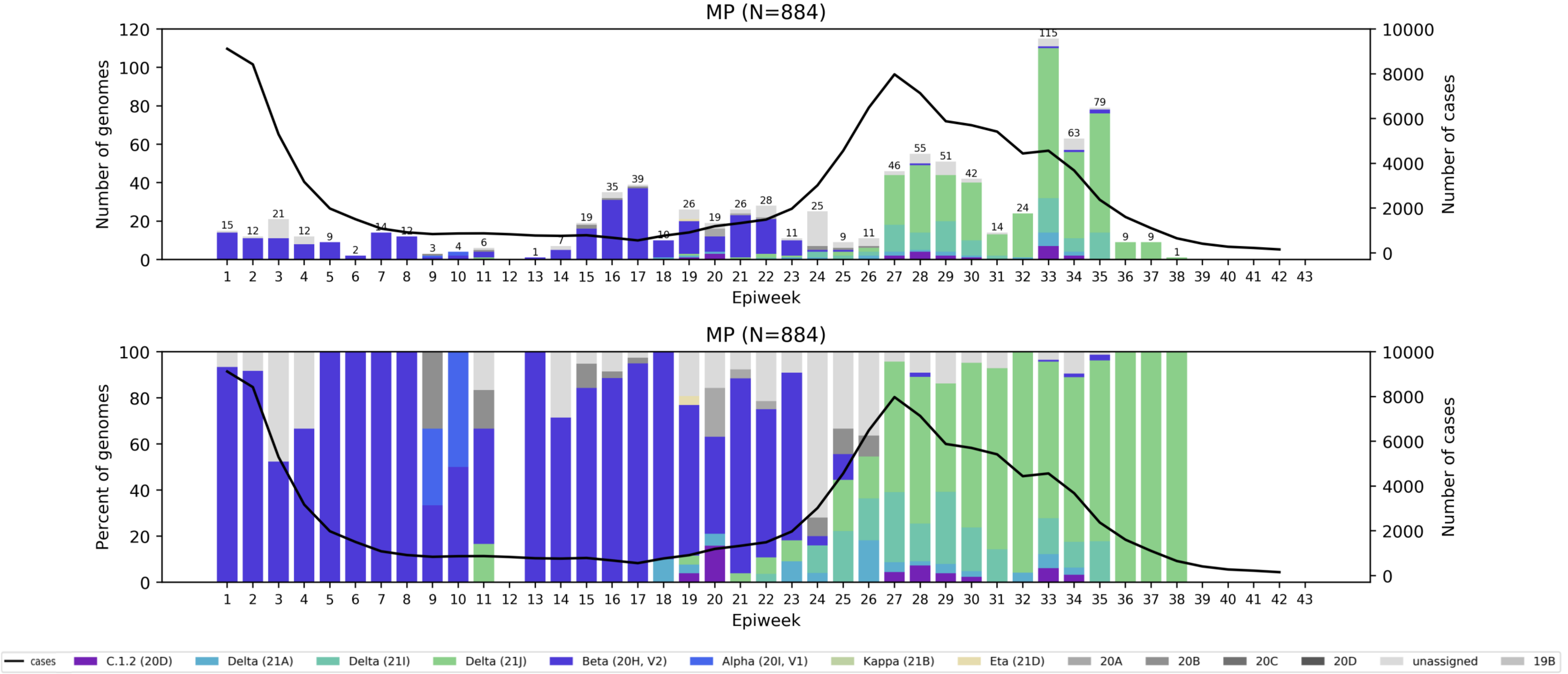
NGS-SA
Network for Genomic
Surveillance in South Africa

Limpopo Province, 2021, n = 1033



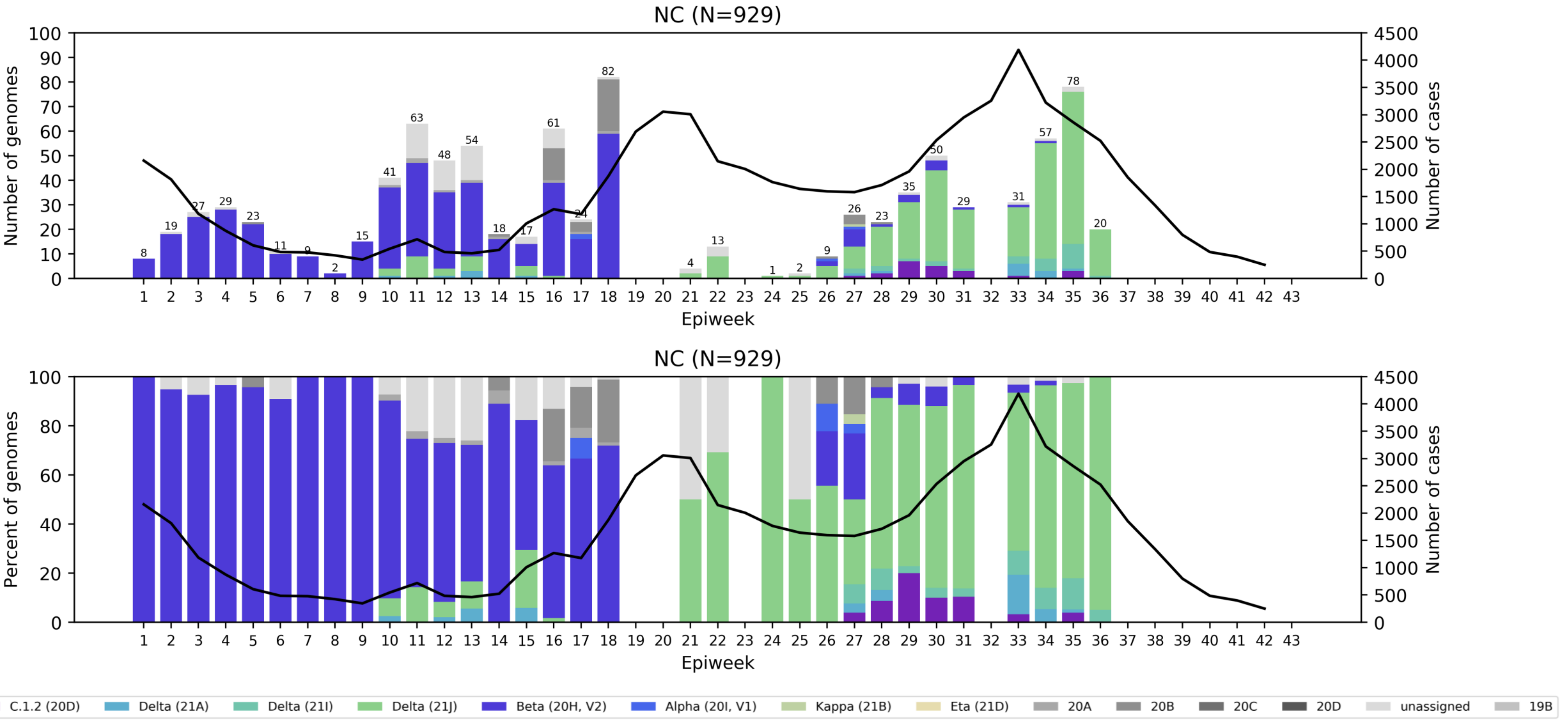
NGS-SA
Network for Genomic
Surveillance in South Africa

Mpumalanga Province, 2021, n = 884



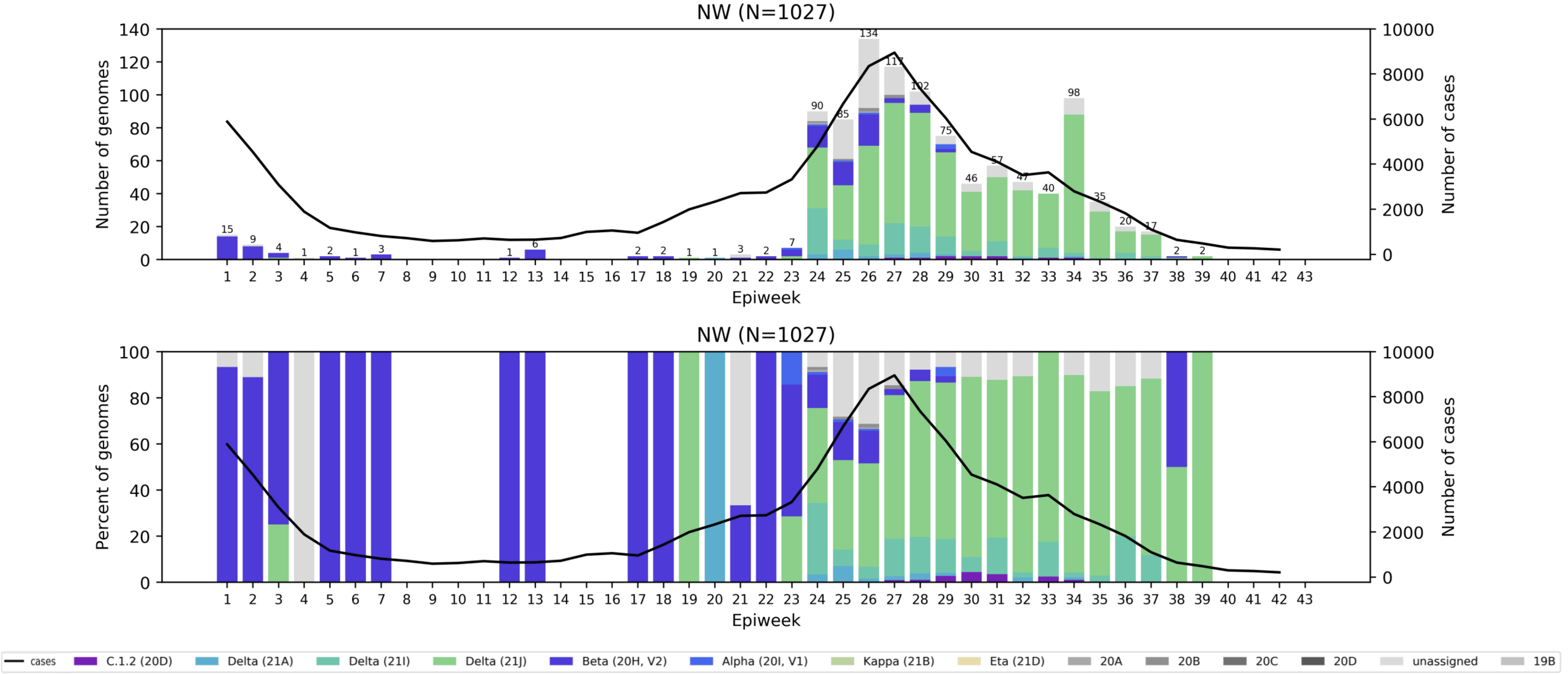
NGS-SA
Network for Genomic
Surveillance in South Africa

Northern Cape Province, 2021, n = 929



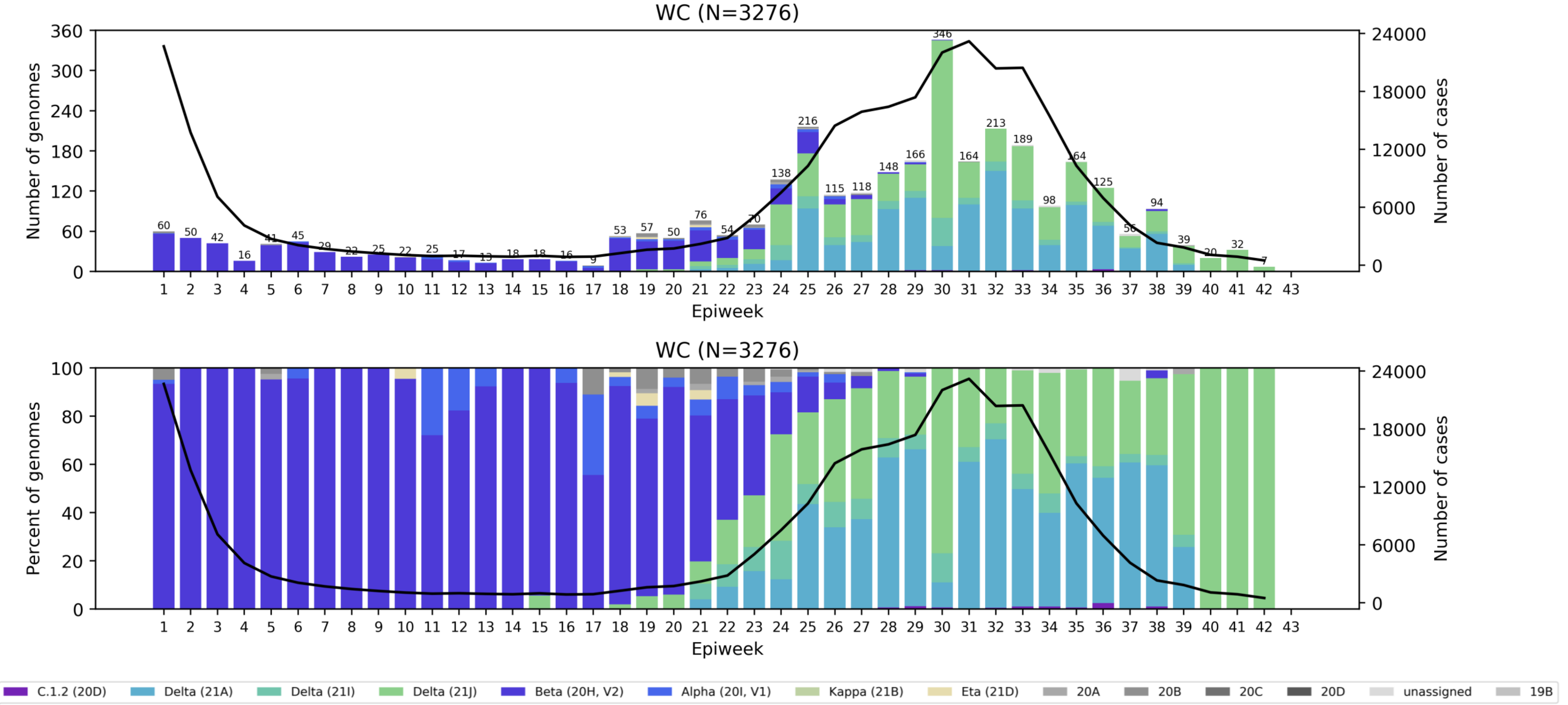
NGS-SA
Network for Genomic
Surveillance in South Africa

North West Province, 2021, n = 970



NGS-SA
Network for Genomic
Surveillance in South Africa

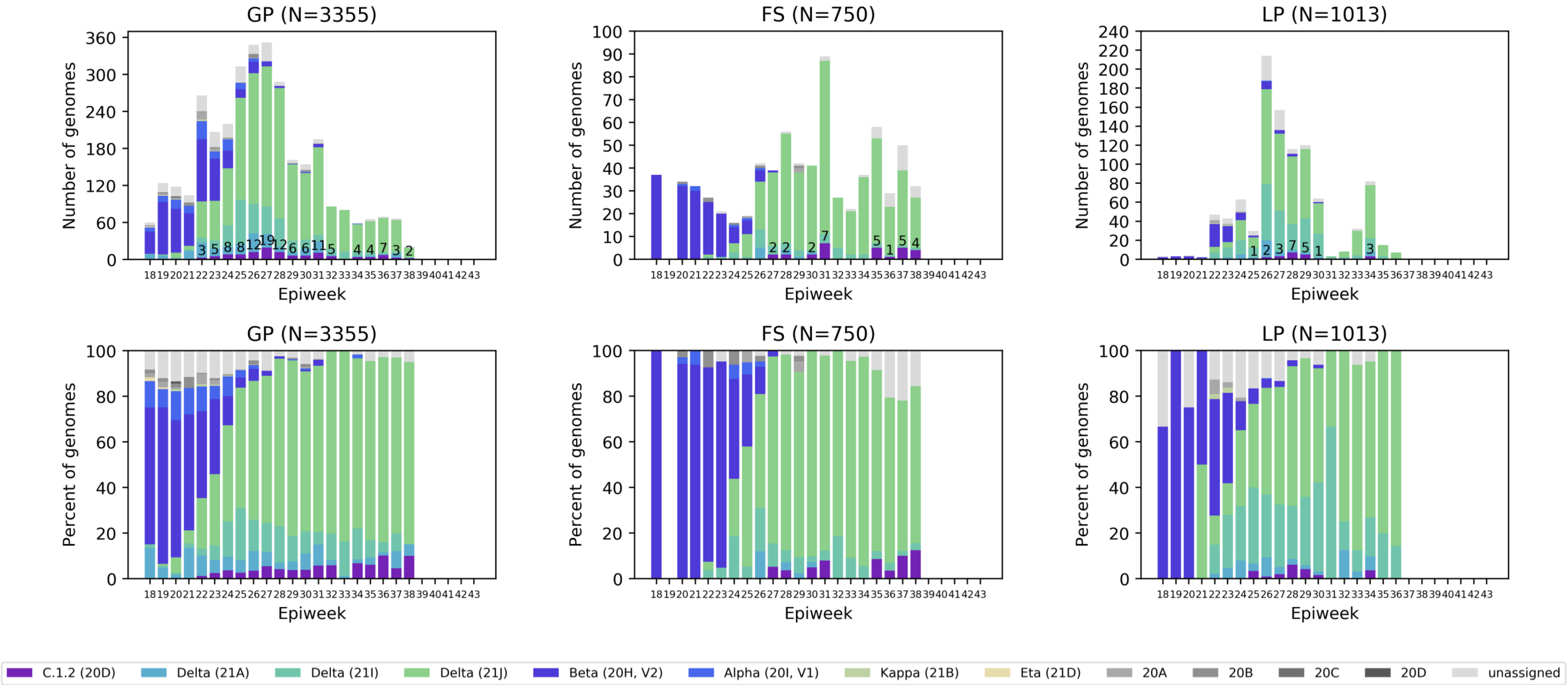
Western Cape Province, 2021, n = 3276



NGS-SA
Network for Genomic
Surveillance in South Africa

C.1.2 (n=257 in SA) in May – August 2021 by epiweek

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

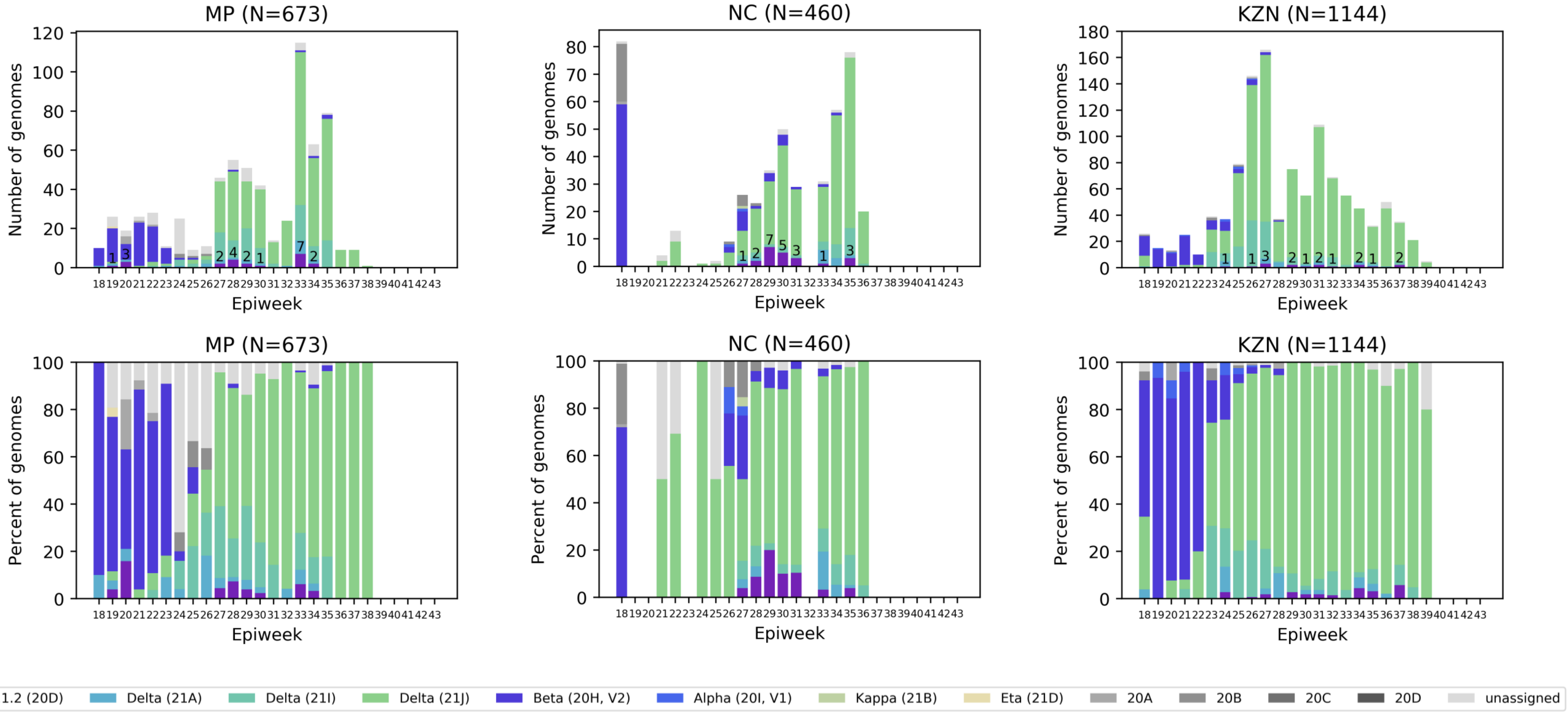


The majority of C.1.2 sequences have been detected in Gauteng (n=115), followed by the Free State (n=28) and then Limpopo (n=22).

NGS-SA
Network for Genomic Surveillance in South Africa

C.1.2 (n=257 in SA) in May – August 2021 by epiweek

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

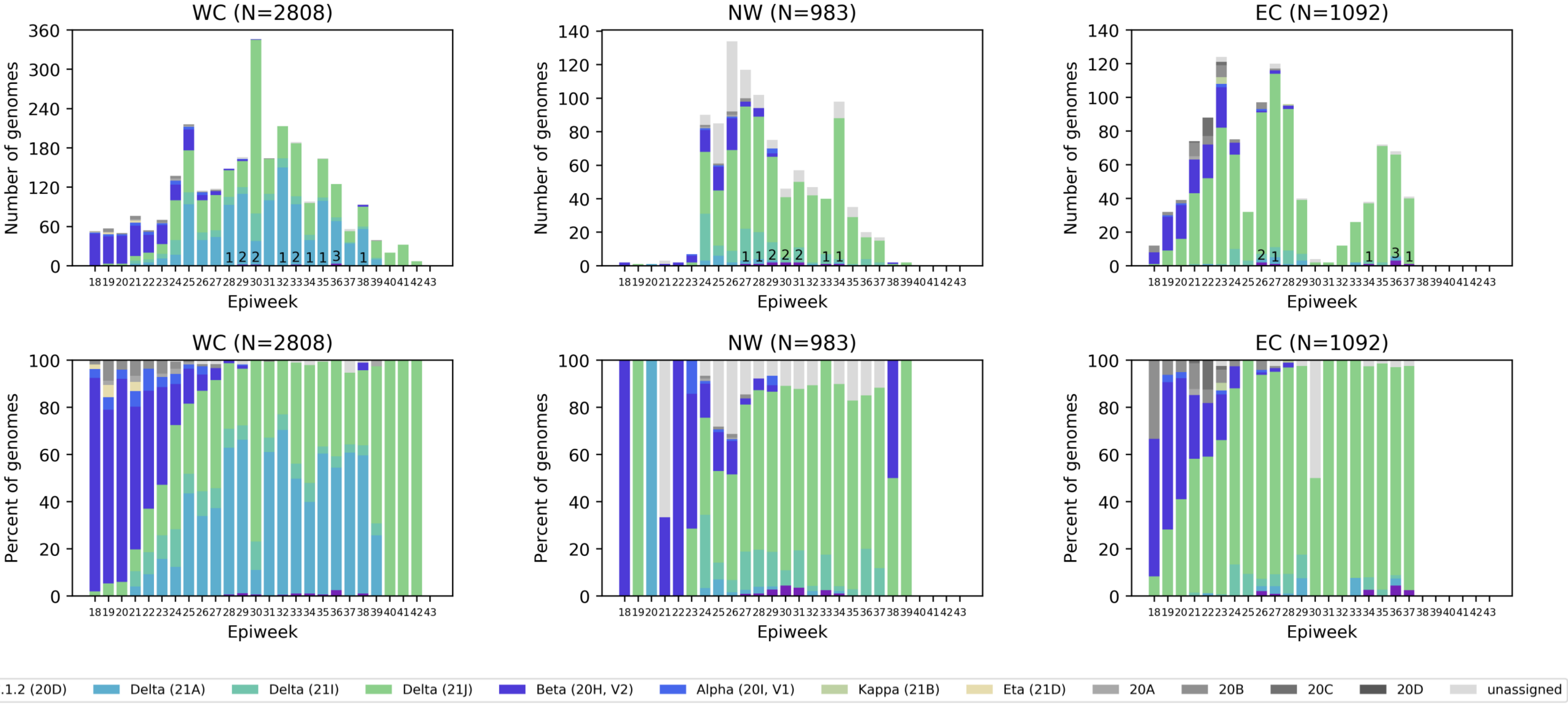


22 C.1.2 sequences have been detected in Mpumalanga, 22 in the Northern Cape, and 16 in KwaZulu-Natal.

NGS-SA
Network for Genomic Surveillance in South Africa

C.1.2 (n=257 in SA) in May – August 2021 by epiweek

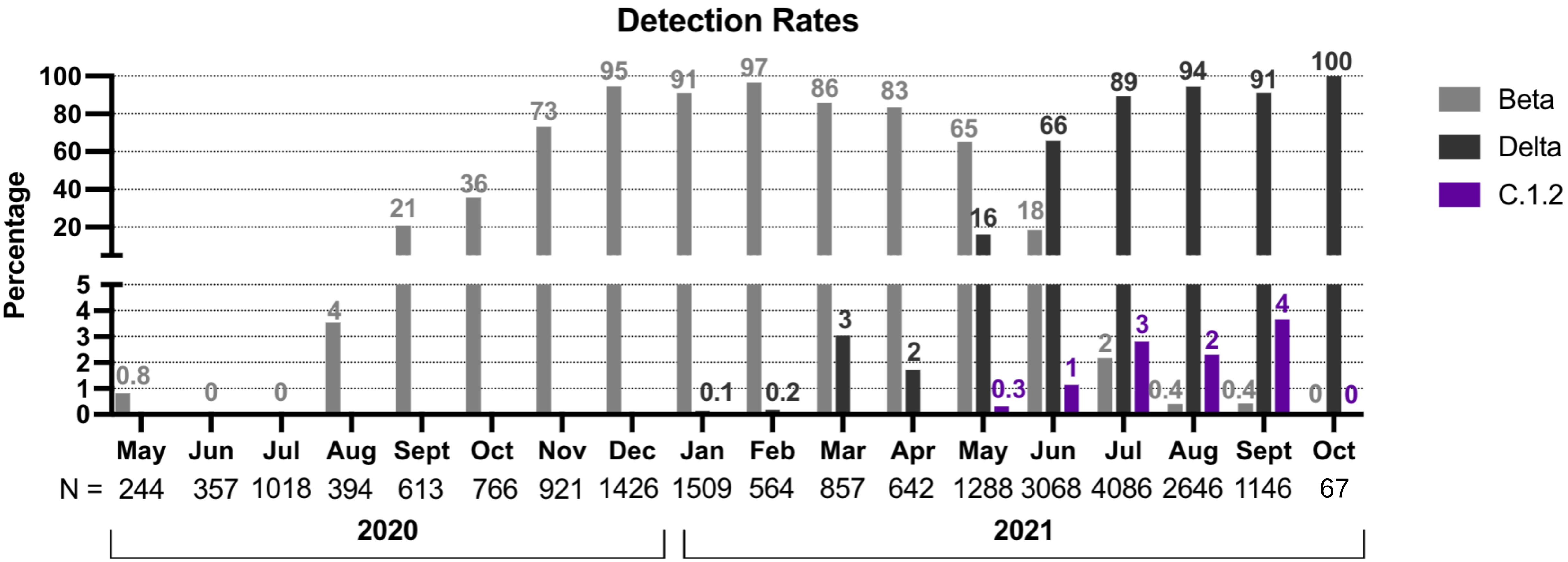
Number of C.1.2 samples indicated above bar, provinces ordered by number of detections



The Western Cape has 14 sequences, the North West has 10, and the Eastern Cape has 8 detections of C.1.2.

NGS-SA
Network for Genomic Surveillance in South Africa

C.1.2 growth compared to Beta and Delta



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

NGS-SA
Network for Genomic Surveillance in South Africa

Summary

- Delta continues to dominate in all provinces from specimens collected in September and October
  - 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
    - All SA Delta samples have been updated
    - Delta 21J is the dominant clade globally and in SA
    - Based on updated definitions of AY.4.2[1,2], this sub-lineage has not been detected in the country

- Mutated C.1.2 lineage detected in all provinces of South Africa at less than 4% of genomes

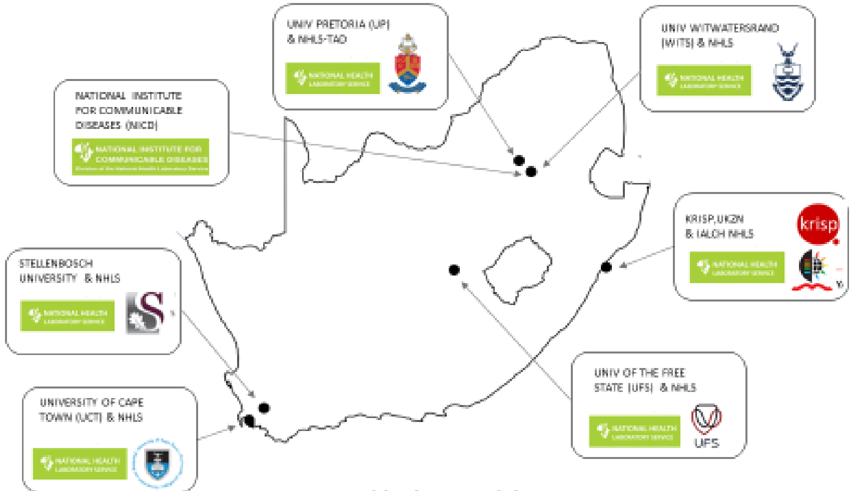
- Lambda and Mu variants not detected in South Africa

---

1. https://github.com/cov-lineages/constellations/blob/main/constellations/definitions/cAY.4.2.json
2. https://assets.publishing.service.gov.uk/government/uploads/system/uploads/attachment_data/file/1028113/Technical_Briefing_26.pdf

NGS-SA

Network for Genomic
Surveillance in South Africa



Supported by the DSI and the SA MRC

UNIVERSITEIT VAN PRETORIA
UNIVERSITY OF PRETORIA
YUNIBESITHI YA PRETORIA

UNIVERSITEIT
iYUNIVESITHI
STELLENBOSCH
UNIVERSITY

science & innovation
Department:
Science and Innovation
REPUBLIC OF SOUTH AFRICA

UFS

saMRC
advancinglife

NATIONAL INSTITUTE FOR COMMUNICABLE DISEASES
Division of the National Health Laboratory Service

UNIVERSITY OF CAPE TOWN
IYUNIVESITHI YASEKAPA • UNIVERSITEIT VAN KAAPSTAD

WITS
UNIVERSITY

krisp

UNIVERSITY OF KWAZULU-NATAL
INYUVESI YAKWAZULU-NATALI

NATIONAL HEALTH LABORATORY SERVICE

UKZN-Inkosi Albert Luthuli Central Hospital

Dr Khanyi Msomi
Dr Kerusha Govender
Dr Pravi Moodley
Dr Aabida Khan
Dr Lili Gounder
Dr Kerri Francois
Dr Cherise Naicker
Dr Joedene Chetty
Dr Neli Ngcaba
Dr Tshepiso Mosito
Mr Malcolm Ellapen
Mr Kubendran Reddy
The COVID-19 Bench team

University of KwaZulu-Natal & Africa Health Research Institute

KRISP at UKZN:
Tulio de Oliveira
Richard Lessels
Houriiyah Tegally
Eduan Wilkinson
Jennifer Giandhari
Sureshnee Pillay
Emmanuel James San

AHRI
Alex Sigal
Sandile Cele
Willem Hanekom

University of Stellenbosch & NHLS Tygerberg Virology

Susan Engelbrecht
Wolfgang Preiser
Gert van Zyl
Tongai Maponga
Bronwyn Kleinhans
Shannon Wilson
Karabo Phadu
Tania Stander
Kamela Mahlakwane
Mathilda Claassen
Diagnostic laboratory staff

NGS-SA
Network for Genomic Surveillance in South Africa

University of Cape Town, NHLS & WCG

NHLS-UCT

Carolyn Williamson
Nei-yuan Hsiao
Diana Hardie
Kruger Marais
Stephen Korsman
Ziyaad Valley-Omar

WCG-UCT

Mary-Anne Davies
Hannah Hussey
Andrew Boulle
Masudah Paleker
Theuns Jacobs
Erna Morden

UCT, IDM and CIDRI-Africa

Deelan Doolabh
Arash Iranzadeh
Lynn Tyers
Innocent Mudau
Nokuzola Mbhele
Fezokuhle Khumalo
Thabang Serakge
Bruna Galvão
Arghavan Alisoltani
(U. California)

Robert Wilkinson
Darren Martin
Nicola Mulder
Wendy Burgers
Ntobeko Ntusi
Rageema Joseph
Sean Wasserman
Linda Boloko

University of the Free State

UFS

Dominique Goedhals
Armand Bester
Martin Myaga
Peter Mwangi
Emmanuel Ogunbayo
Milton Mogotsi
Makgotso Maotoana
Lutfiyya Mohamed

NHLS Division of Virology

Sabeehah Vawda
Felicity Burt
Thokozani Mkhize
Diagnostic laboratory staff

National Institute for Communicable Diseases

NATIONAL INSTITUTE FOR COMMUNICABLE DISEASES
Division of the National Health Laboratory Service

Centre for Respiratory Diseases & Meningitis
Jinal Bhiman
Anne von Gottberg
Thabo Mohale
Daniel Amoako
Josie Everatt
Boitshoko Mahlangu
Noxolo Ntuli
Anele Mnguni
Amelia Buys
Cardia Fourie
Noluthando Duma
Linda de Gouveia
Jackie Kleynhans
Nicole Wolter
Sibongile Walaza
Mignon du Plessis
Stefano Tempia
Mvuyo Makhasi
Cheryl Cohen

Centre for HIV and STIs
Cathrine Scheepers
Constantinos Kurt Wibmer
Thandeka Moyo
Tandile Hermanus
Frances Ayres
Zanele Molaudzi
Bronwen Lambson
Tandile Hermanus
Mashudu Madzivhandila
Prudence Kgagudi
Brent Oosthuysen
Penny Moore
Lynn Morris

NICD Groups
NICD COVID-19 response team
NICD SARS-CoV-2 Sequencing Group

Sequencing Core Facility
Zamantungwa Khumalo
Annie Chan
Morne du Plessis
Stanford Kwenda
Phillip Senzo Mtshali
Mushal Allam
Florah Mnyameni
Arshad Ismail

saMRC advancinglife

The Fleming Fund

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

health
Department: Health
REPUBLIC OF SOUTH AFRICA

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

wellcome

CDC
CENTERS FOR DISEASE CONTROL AND PREVENTION

Zoonotic arbo and respiratory virus program
Centre for Viral Zoonoses
Department Medical Virology/ NHLS Tshwane Academic division
University of Pretoria

UNIVERSITEIT VAN PRETORIA
UNIVERSITY OF PRETORIA
YUNIBESITHI YA PRETORIA

ZARV research program/UP
Marietjie Venter (Head: ZARV)
Adriano Mendes (Postdoc)
Amy Strydom (Postdoc)
Michaela Davis (MSc, intern medical scientist)

NATIONAL HEALTH LABORATORY SERVICE

NHLS Tshwane
Prof Simnikiwe Mayaphi (HOD)

Funders:
GIZ/BMBF: African Network for Improved diagnostics and epidemiology of common and emerging infectious agents (ANDEMIA)
G7 Global Health fund, Robert Koch Institute, Dr Fabian Leendertz

NGS-SA
Network for Genomic Surveillance in South Africa

Additional support and collaborators

NHLS
Koeleka Mlisana
Zinhle Makatini
Eugene Elliot
Florette K. Treurnicht
Kathleen Subramoney
Oluwakemi Laguda-Akingba
Shareef Abrahams
Greta Hoyland
Gloria Selabe
Elias Bereda
Jeannette Wadula

Hyrax Biosciences
Simon Travers

Cape Town HVTN Laboratory
Erica Anderson-Nissen
Anneta Naidoo

Ndlovu Research
Hugo Tempelman
CJ Umunnakwe

Lancet
Allison J. Glass

Ampath
Terry Marshall
Cindy van Deventer
Eddie Silberbauer

Pathcare Vermaak
Andries Dreyer
Howard Newman
Riaan Writes
Marianne Wolfaardt
Warren Lowman

Bridge-the-Gap
Raymond Rott

Cytespace Africa Laboratories
Christa Viljoen

ARC-OVI
Lia Rotherham

CAPRISA
Salim Abdool Karim
Nigel Garret

UKZN - Big Data
Francesco Pettruccione
Ilya Sinayskiy

University of Oxford
José Lourenço

FioCruz, Brazil
Vagner Fonseca
Marta Giovanetti
Luiz Carlos Junior Alcantara

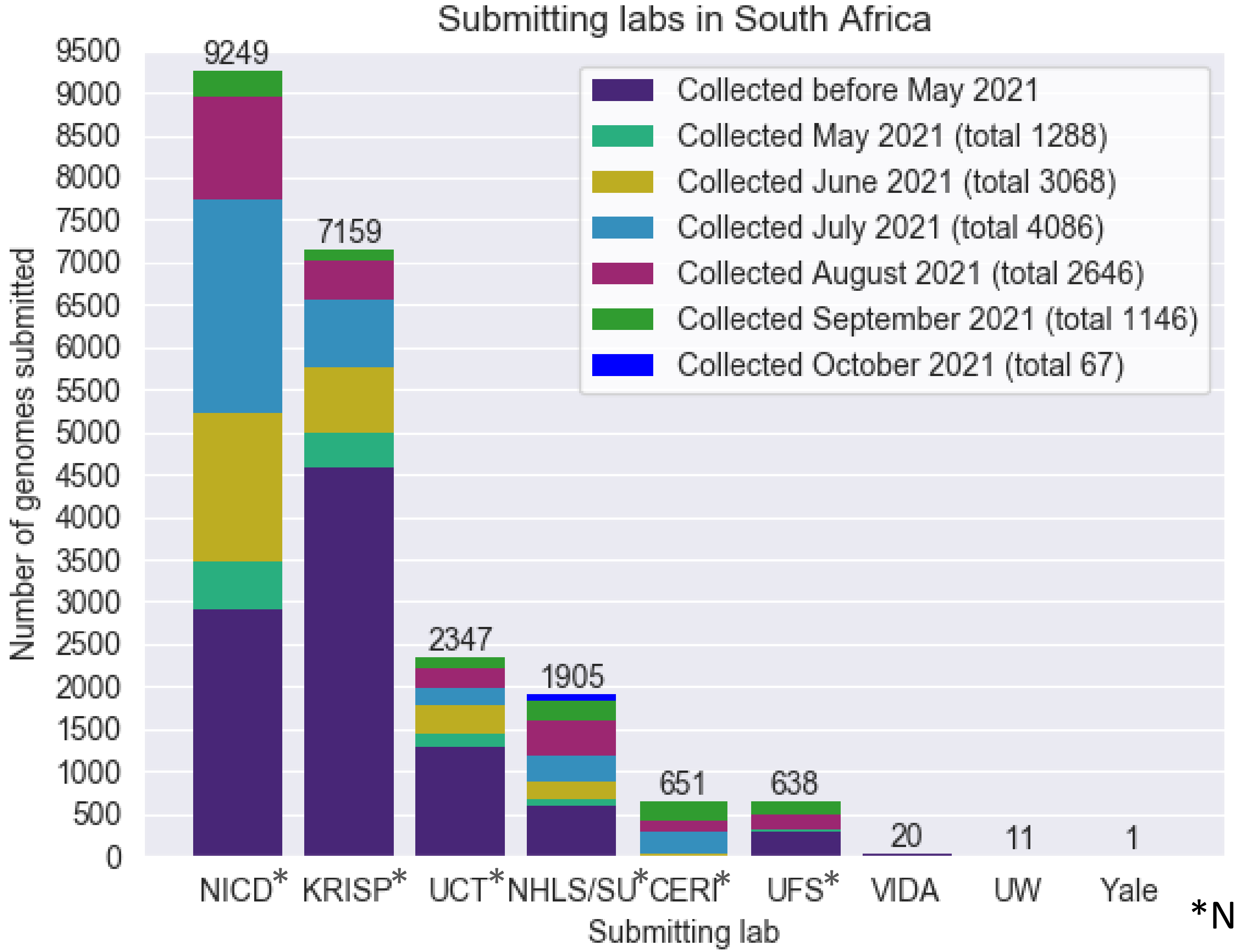
Africa CDC
John Nkengasong
Sofonias Tessema

Netcare:
Richard Friedland
Craig Murphy
Caroline Maslo
Liza Sitharam

DSI
Glaudina Loots

SA MRC
Glenda Gray

South African genomes submitted per sequencing lab, 2020 and 2021 (N=21 981)



*NGS-SA laboratories

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

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 22 October 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 22 October 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.)