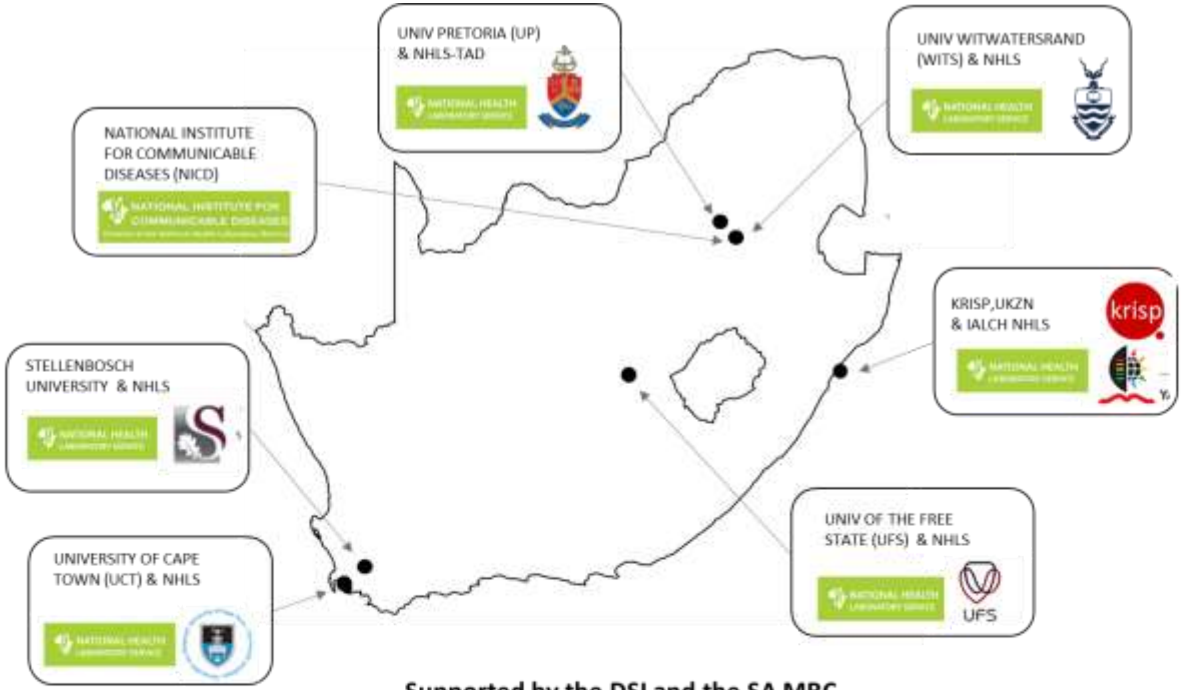
NGS-SA
Network for Genomic
Surveillance in South Africa

Network for Genomic Surveillance South Africa (NGS-SA)

SARS-CoV-2 Sequencing Update
19 November 2021



NATIONAL INSTITUTE FOR COMMUNICABLE DISEASES (NICD)

UNIV PRETORIA (UP) & NHLS-TAD

UNIV WITWATERSRAND (WITS) & NHLS

KRISP,UKZN & IALCH NHLS

STELLENBOSCH UNIVERSITY & NHLS

UNIVERSITY OF CAPE TOWN (UCT) & NHLS

UNIV OF THE FREE STATE (UFS) & NHLS

Supported by the DSI and the SA MRC

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

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

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 19 November at 10h45

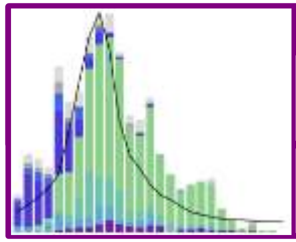
Data license: https://www.gisaid.org/registration/terms-of-use/

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

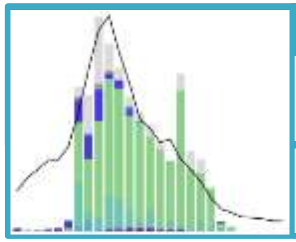
Case data is based on specimen collection date. Cases from https://www.nicd.ac.za/diseases-a-z-index/disease-index-covid-19/surveillance-reports/weekly-epidemiological-brief/ Test data from https://www.nicd.ac.za/diseases-a-z-index/disease-index-covid-19/surveillance-reports/weekly-testing-summary/

SARS-CoV-2
GENOMIC SURVEILLANCE
epiweeks 18 - 45



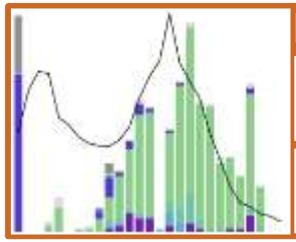
Gauteng ↑ PTP: 1.0%
Genomes 3 619 (26.8%)
Cases 495 992 (37.0%)

Genomes deposited in the last week
🟦3 🟩10 🟩54 🟪6 🟩1 ⬜3



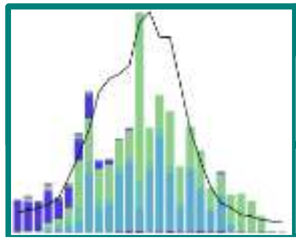
North West - PTP: 1.3%
Genomes 1 098 (8.1%)
Cases 82 822 (6.2%)

Genomes deposited in the last week
🟩3 🟩44 🟪1 ⬛1



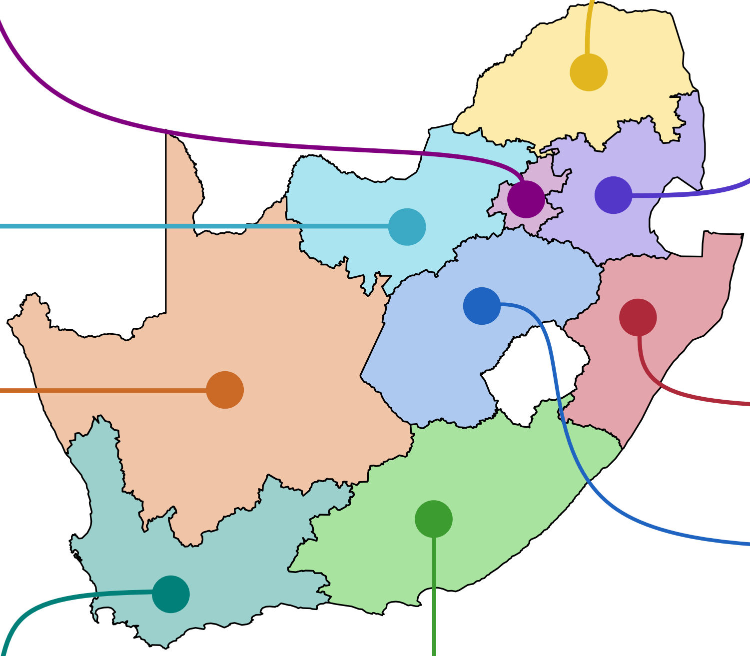
Northern Cape ↑PTP: 3.6%
Genomes 715 (5.3%)
Cases 52 186 (3.9%)

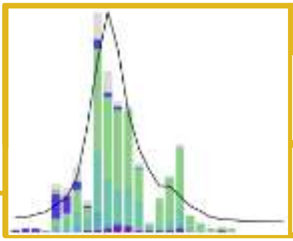
Genomes deposited in the last week
🟩3 🟩35 🟪3 ⬛1



Western Cape ↓PTP: 1.1%
Genomes 3 010 (22.3%)
Cases 227 111 (16.9%)

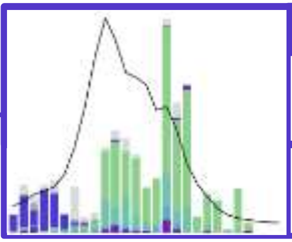
Genomes deposited in the last week
🟦5 🟦1 🟦1 🟩5 🟩73 🟪2 ⬛1 ⬜3





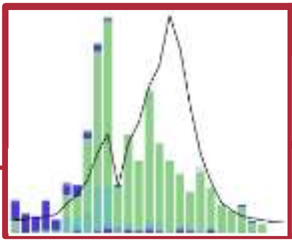
Limpopo ↑ PTP: 1.2%
Genomes 1 106 (8.2%)
Cases 58 319 (4.4%)

Genomes deposited in the last week
🟦1 🟩14 🟩38 🟪3



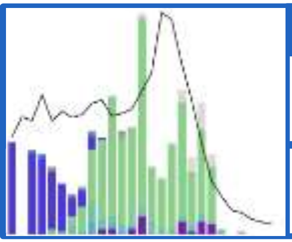
Mpumalanga ↓PTP: 1.1%
Genomes 758 (5.6%)
Cases 73 781 (5.5%)

Genomes deposited in the last week
🟦2 🟩5 🟩32 🟪1



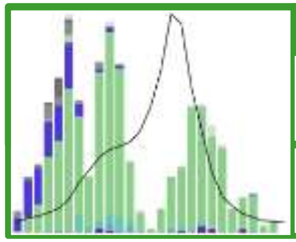
KwaZulu-Natal ↓PTP: 0.8%
Genomes 1 196 (8.9%)
Cases 179 341 (13.4%)

Genomes deposited in the last week
🟦1 🟩15



Free State ↓PTP: 1.6%
Genomes 761 (5.6%)
Cases 74 134 (5.5%)

Genomes deposited in the last week
🟩1



Eastern Cape ↓PTP: 0.7%
Genomes 1 251 (9.3%)
Cases 96 427 (7.2%)

Genomes deposited in the last week
🟦1 🟩2 🟩97 🟪2 ⬜2

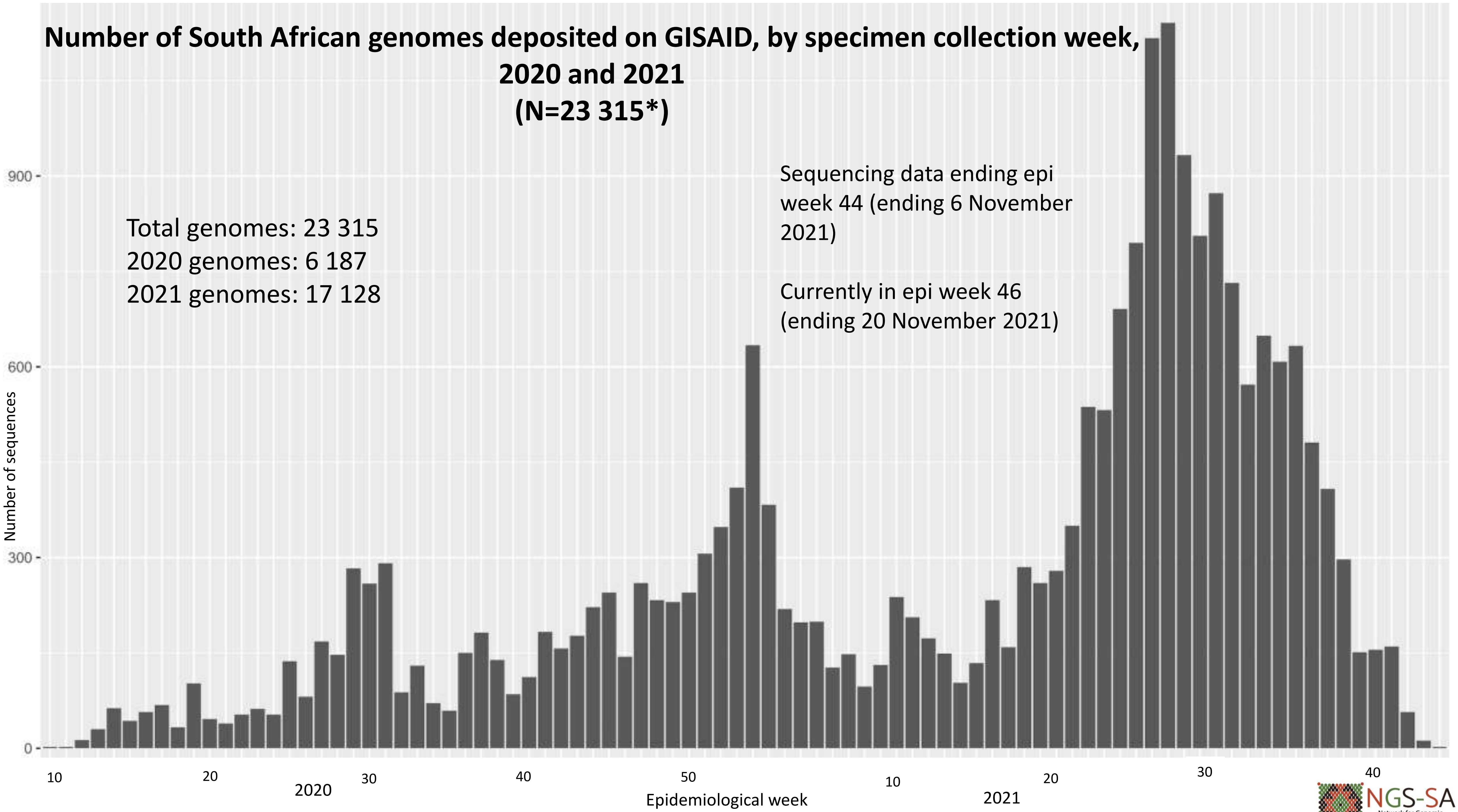
🟪 C.1.2 (20D)
🟦 Beta (20H, V2)
🟦 Alpha (20I, V1)
🟦 Delta (21A)
🟩 Delta (21I)
🟩 Delta (21J)
🟩 Kappa (21B)
🟨 Eta (21D)
⬜ 20A
⬛ 20B
⬛ 20C
⬛ 20D
⬜ Unassigned
— Cases

476 genomes deposited in the past week

Bar graphs represent genomes sequenced per epiweek, with lines representing cases by collection date (weeks 18 – 45)
Genomes and cases presented as provincial total (percentage of national total) for epiweeks 18 – 45
PTP: percentage testing positive in week 44 (7 Nov – 13 Nov); the arrow indicates direction of change since the previous week (31 Oct – 6 Nov)

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=23 315*)



Total genomes: 23 315
2020 genomes: 6 187
2021 genomes: 17 128

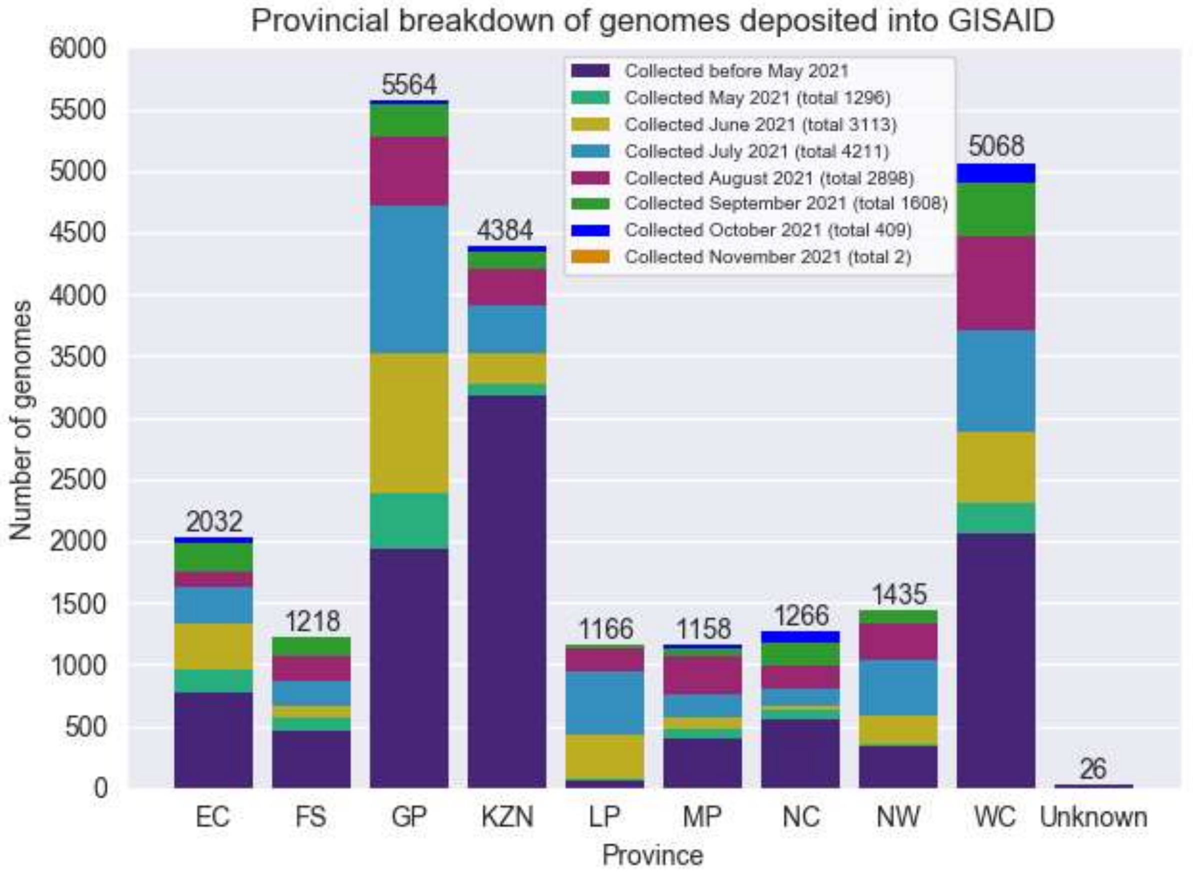
Sequencing data ending epi week 44 (ending 6 November 2021)

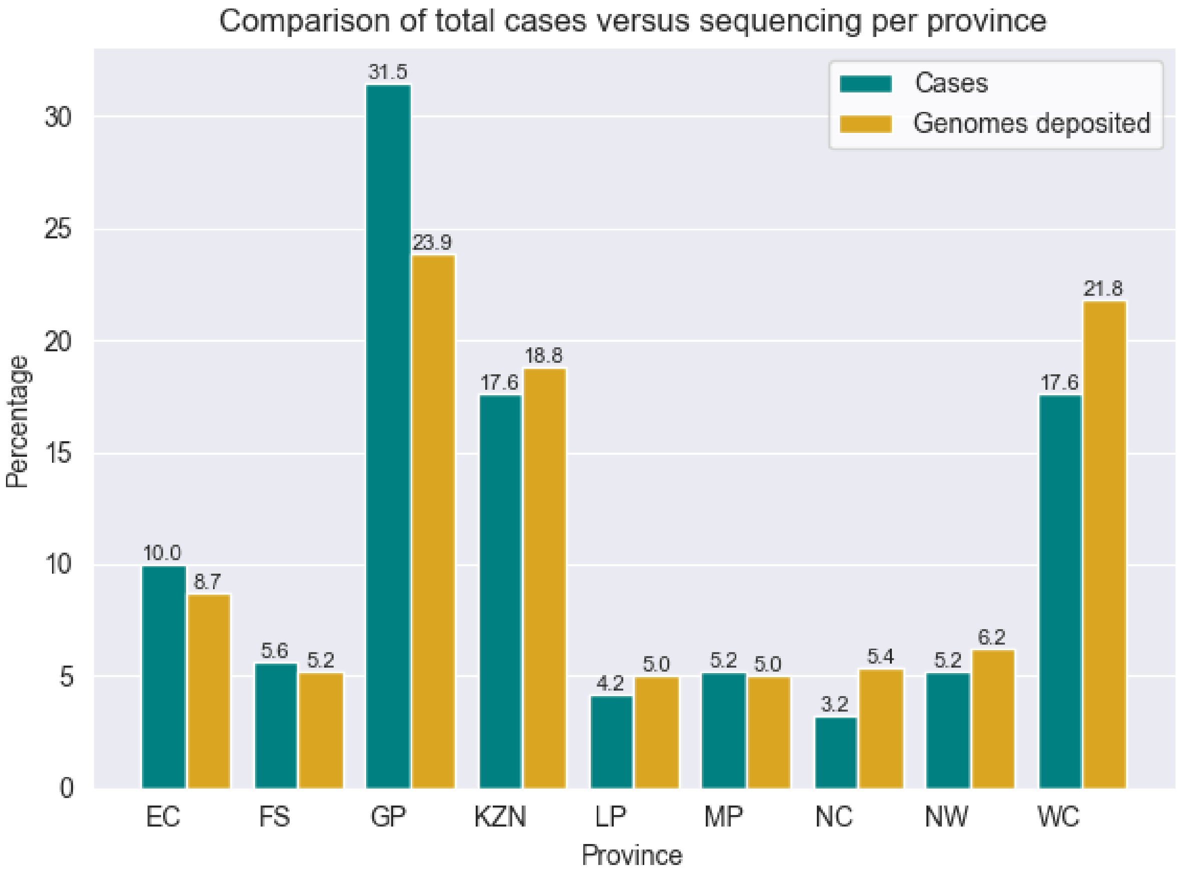
Currently in epi week 46 (ending 20 November 2021)

*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=23 315)

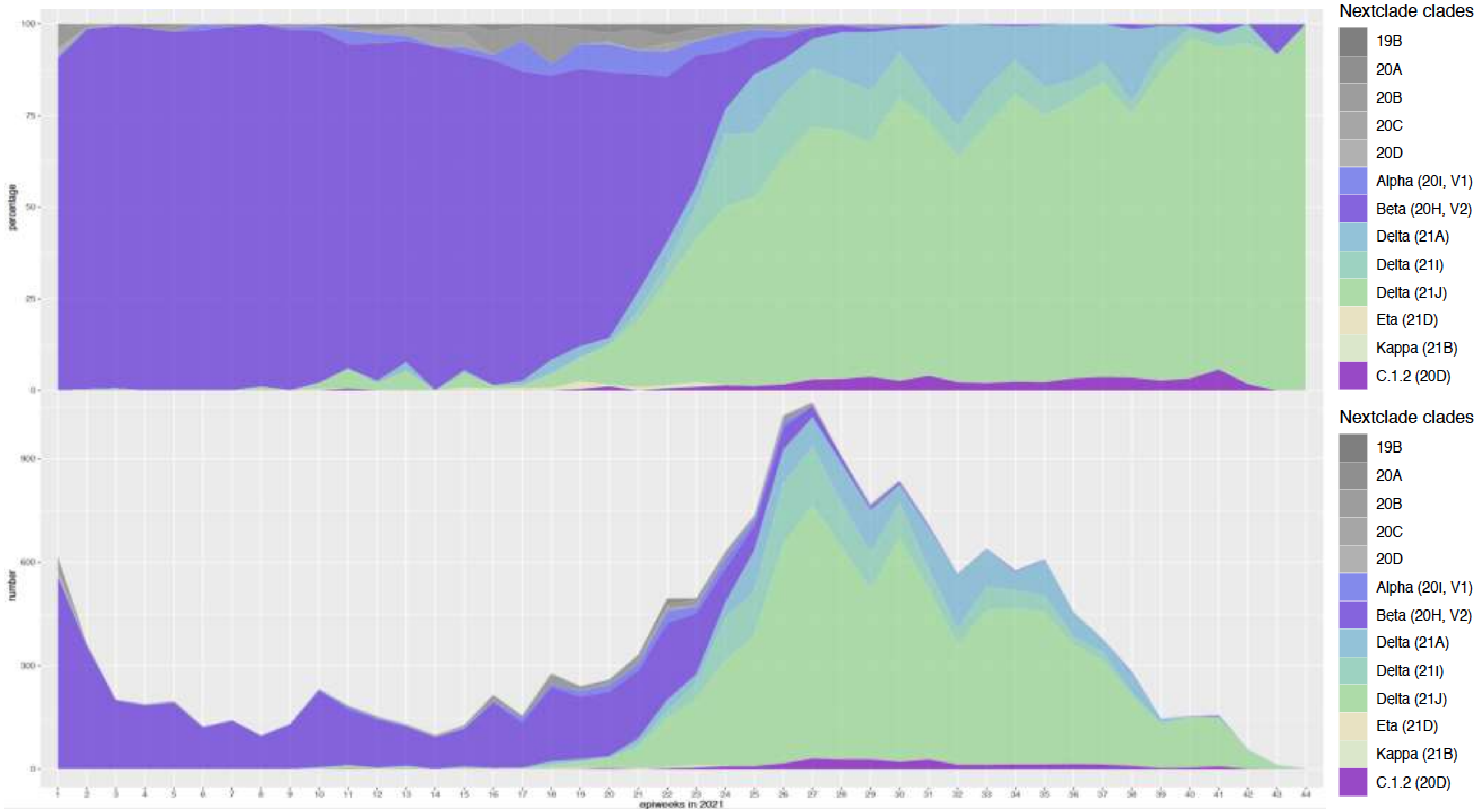




All provinces, apart from GP, KZN, NC and WC, have comparable percentage of overall cases and overall sequenced genomes

NGS-SA
Network for Genomic Surveillance in South Africa

Distribution and number of clades in South Africa, 2021 (N= 17 128)



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

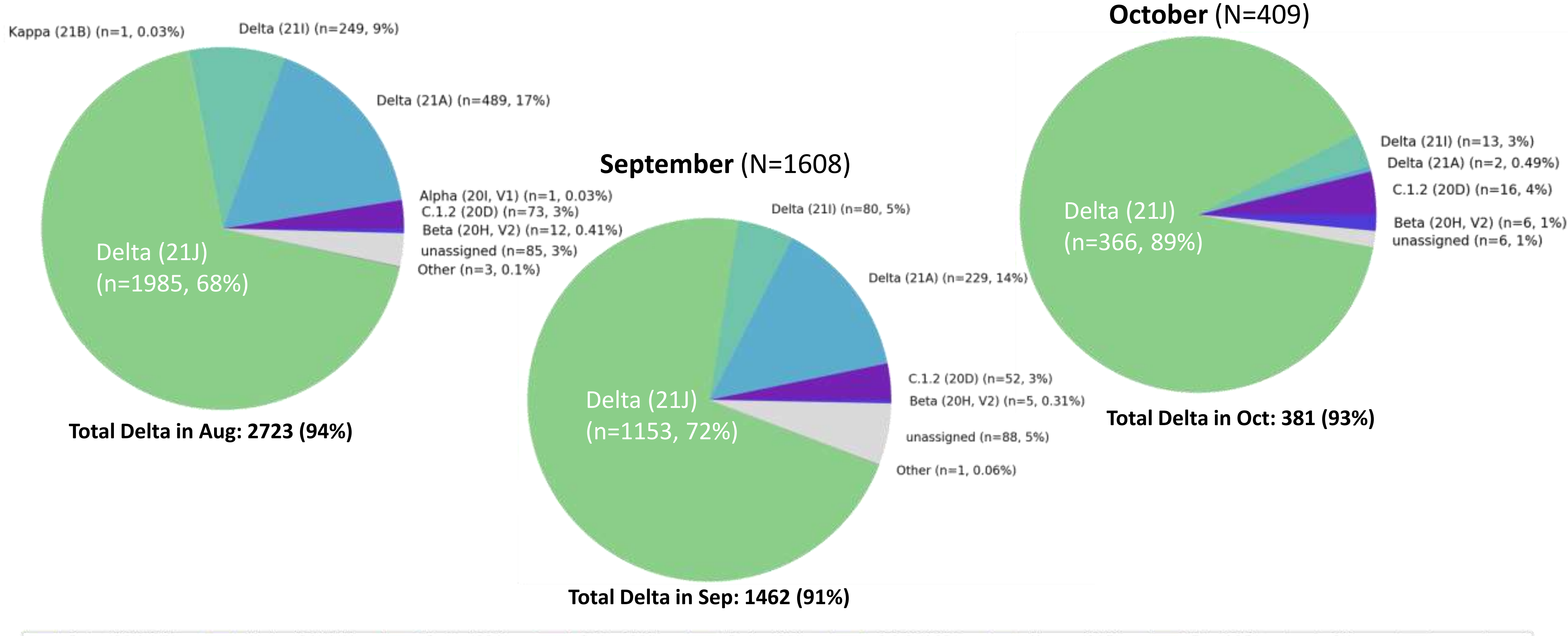
Sequencing data ending epi week 44 (ending 6 November 2021)

Currently in epi week 46 (ending 20 November 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


August (N=2898)

September (N=1608)

October (N=409)

Total Delta in Aug: 2723 (94%)

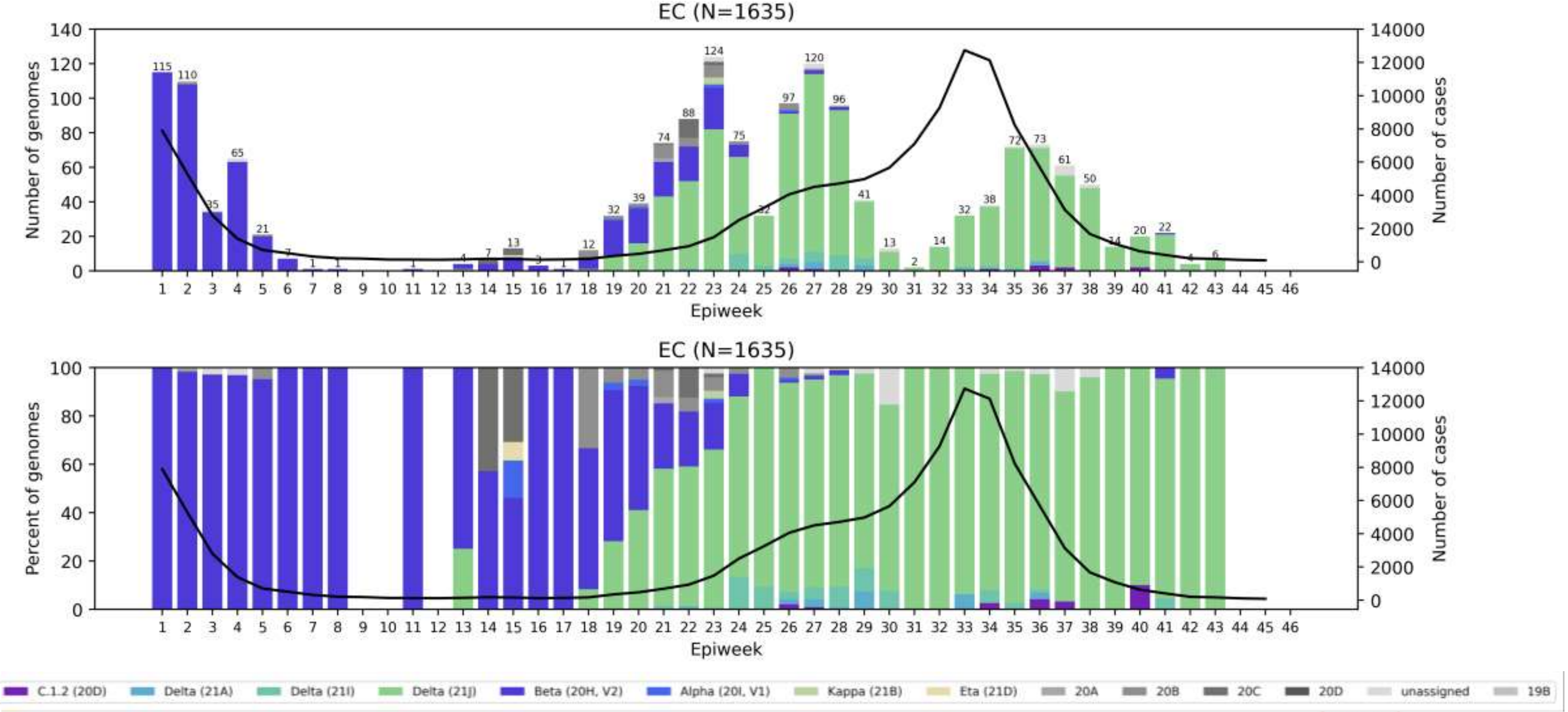
Total Delta in Sep: 1462 (91%)

Total Delta in Oct: 381 (93%)

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

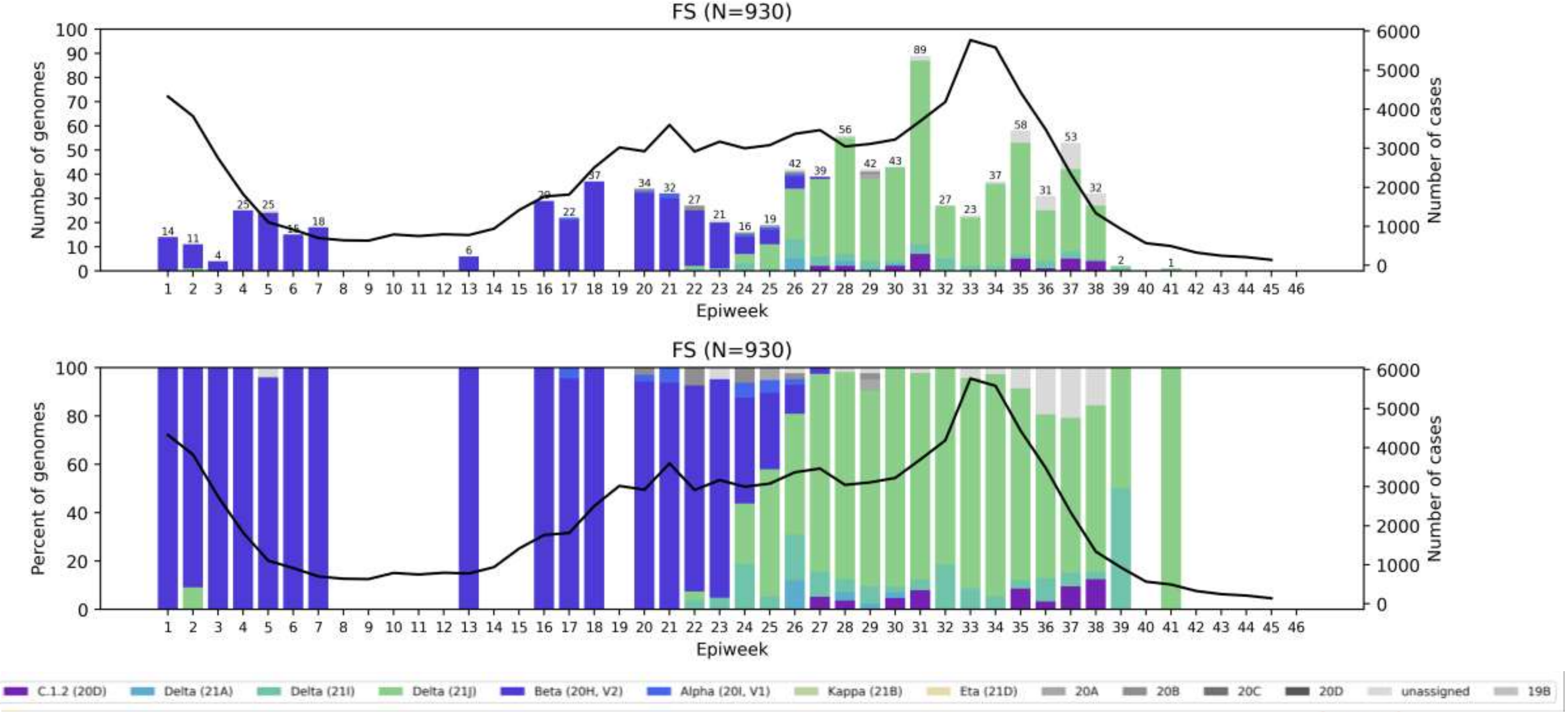
NGS-SA
Network for Genomic Surveillance in South Africa

Eastern Cape Province, 2021, n = 1635



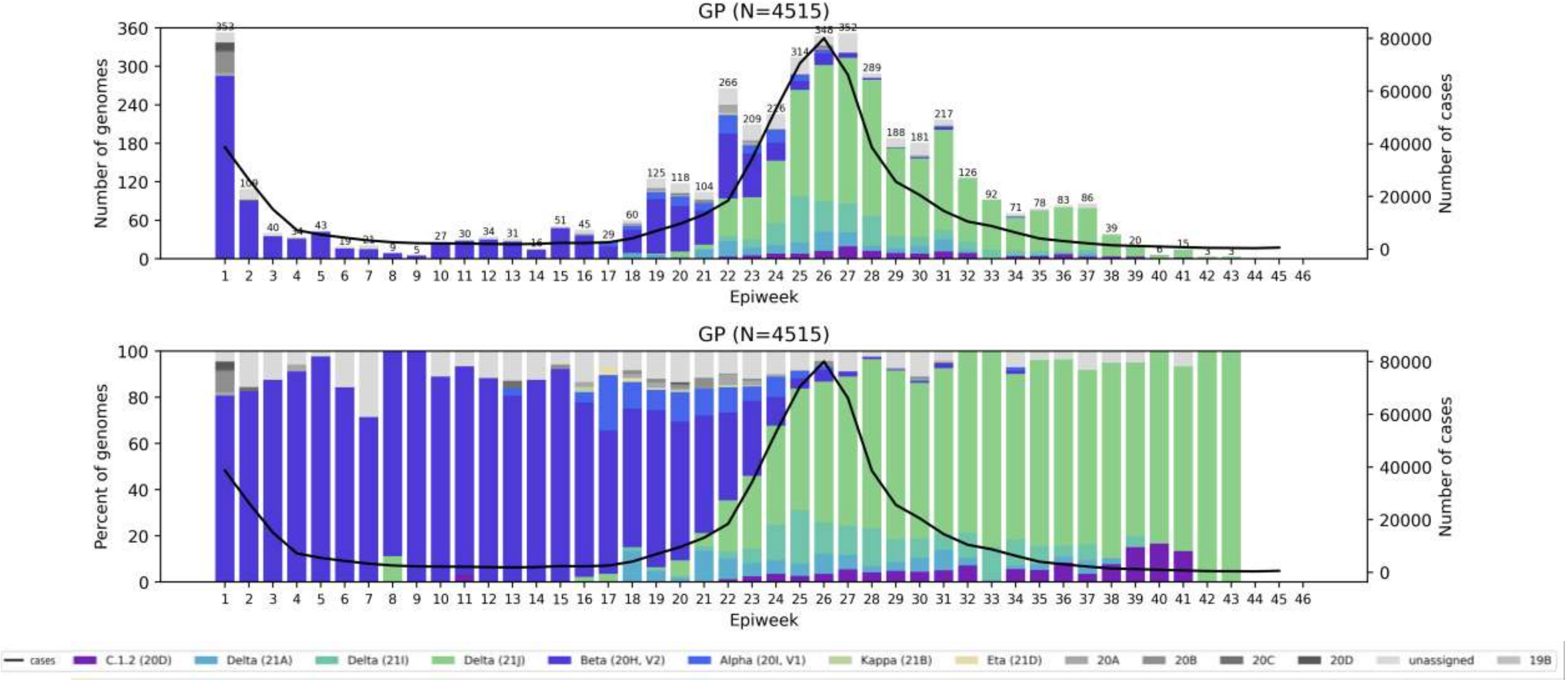
NGS-SA
Network for Genomic
Surveillance in South Africa

Free State Province, 2021, n = 930



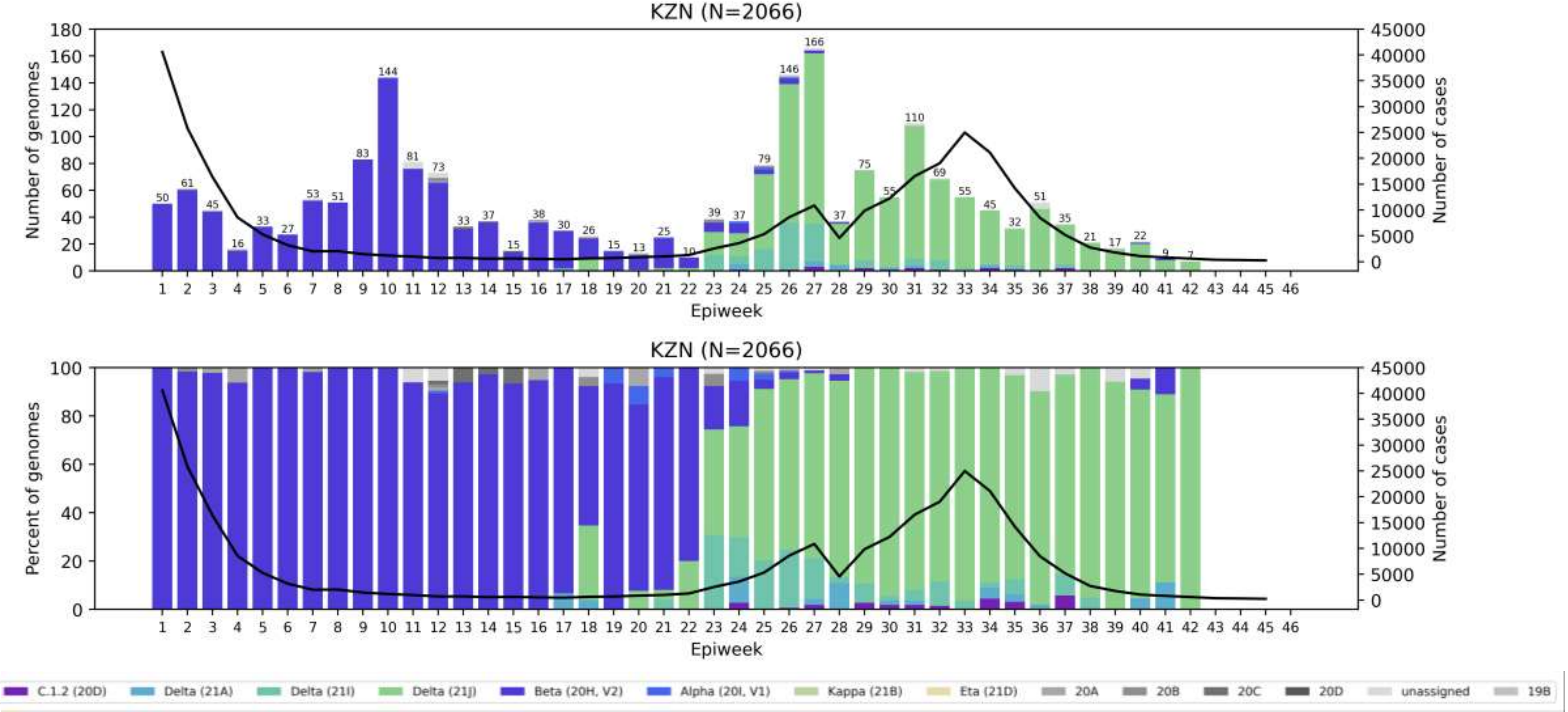
NGS-SA
Network for Genomic
Surveillance in South Africa

Gauteng Province, 2021, n =4515



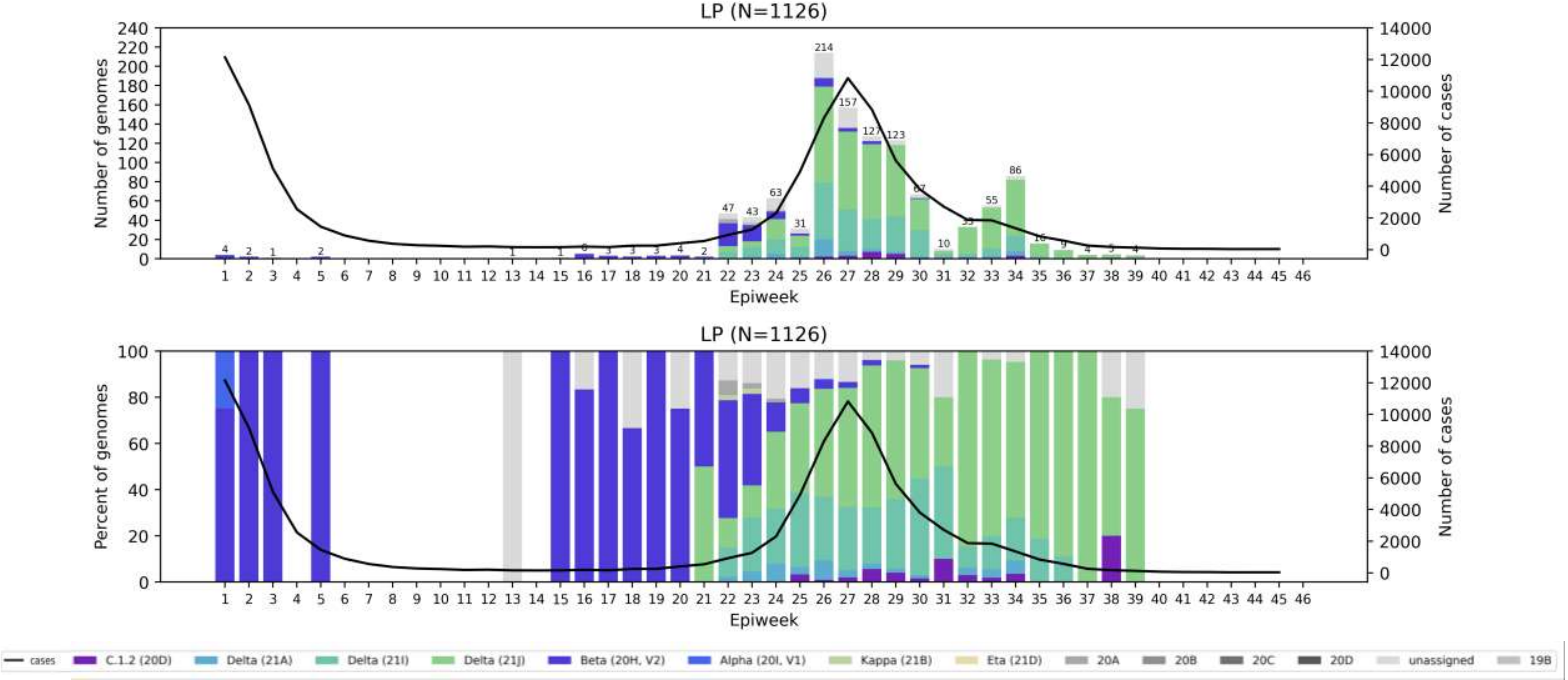
NGS-SA
Network for Genomic
Surveillance in South Africa

KwaZulu-Natal Province, 2021, n = 2066



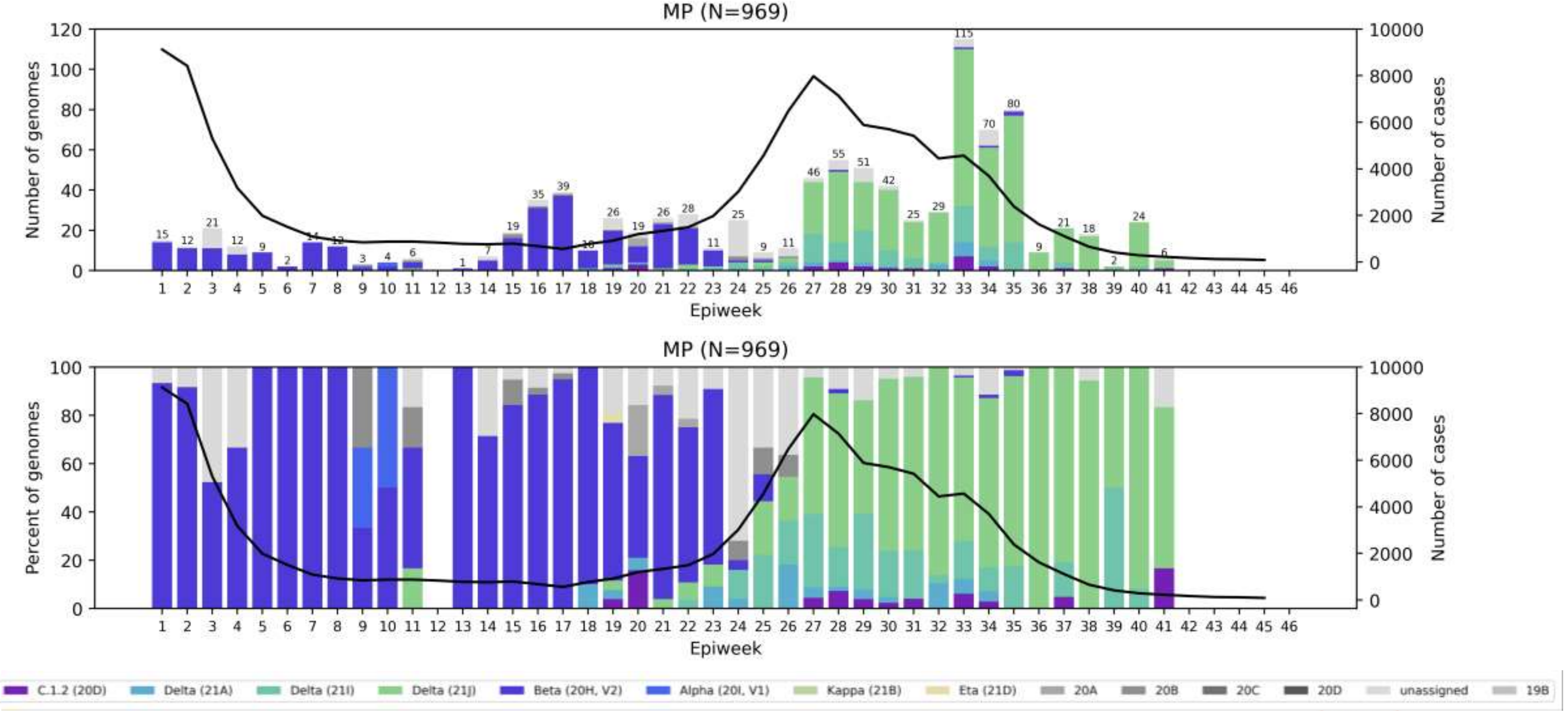
NGS-SA
Network for Genomic
Surveillance in South Africa

Limpopo Province, 2021, n = 1126



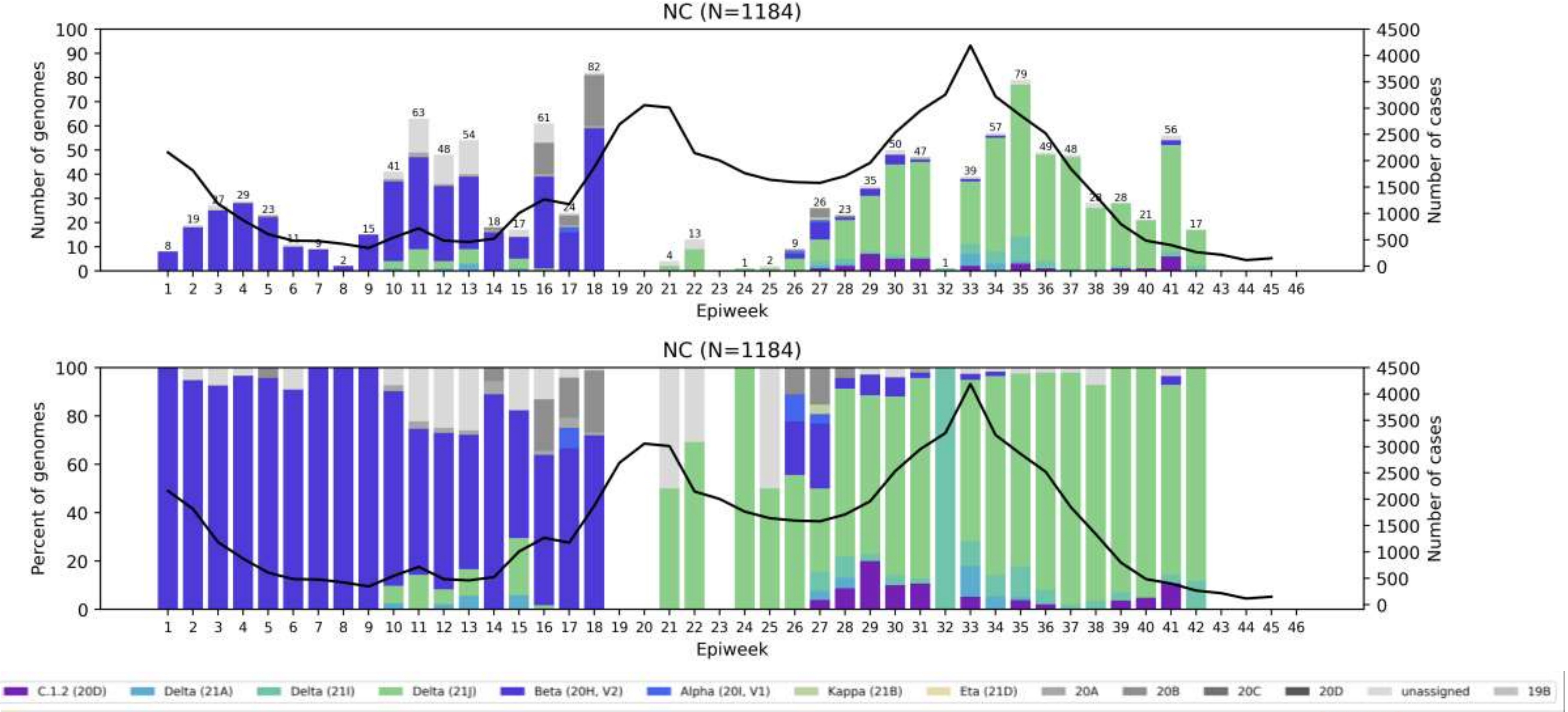
NGS-SA
Network for Genomic
Surveillance in South Africa

Mpumalanga Province, 2021, n = 969



NGS-SA
Network for Genomic
Surveillance in South Africa

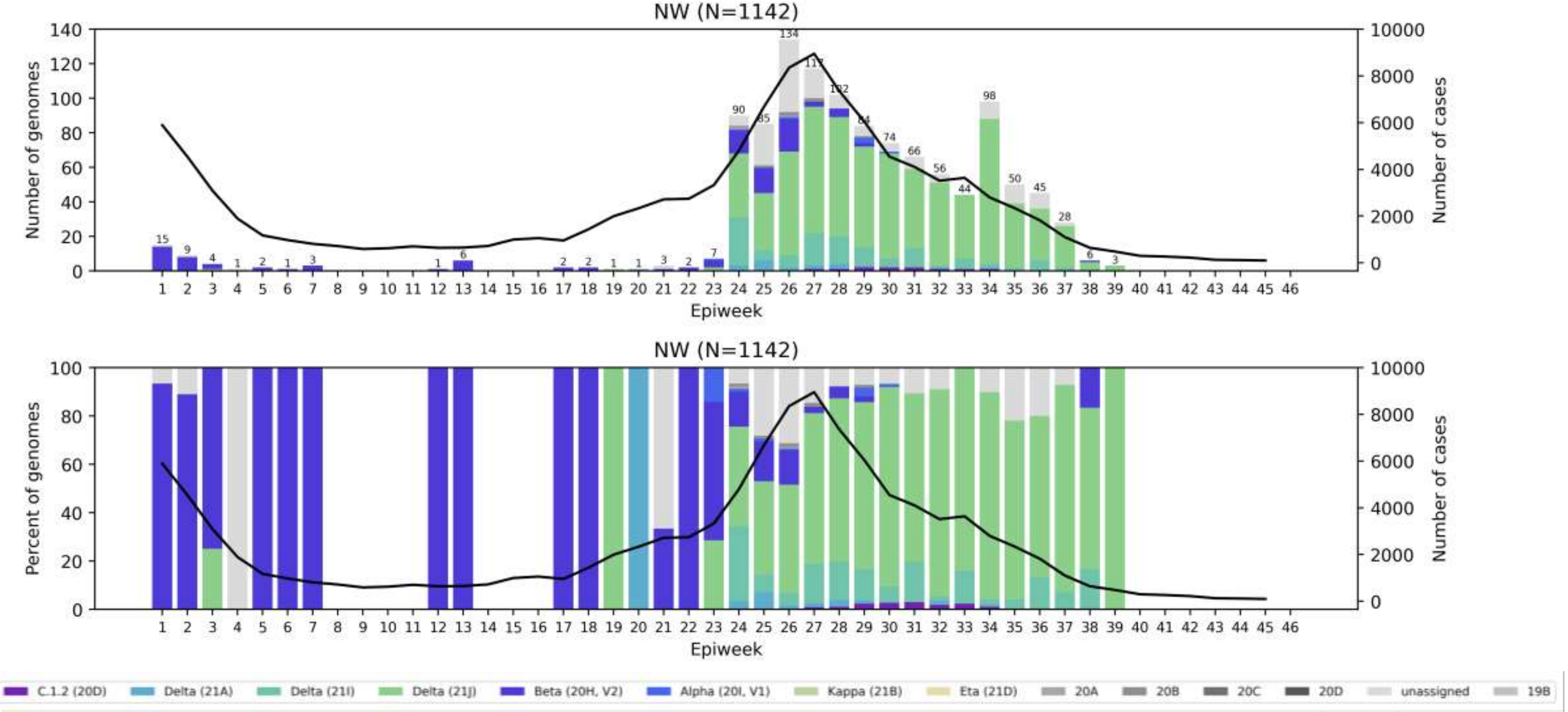
Northern Cape Province, 2021, n = 1184



NGS-SA

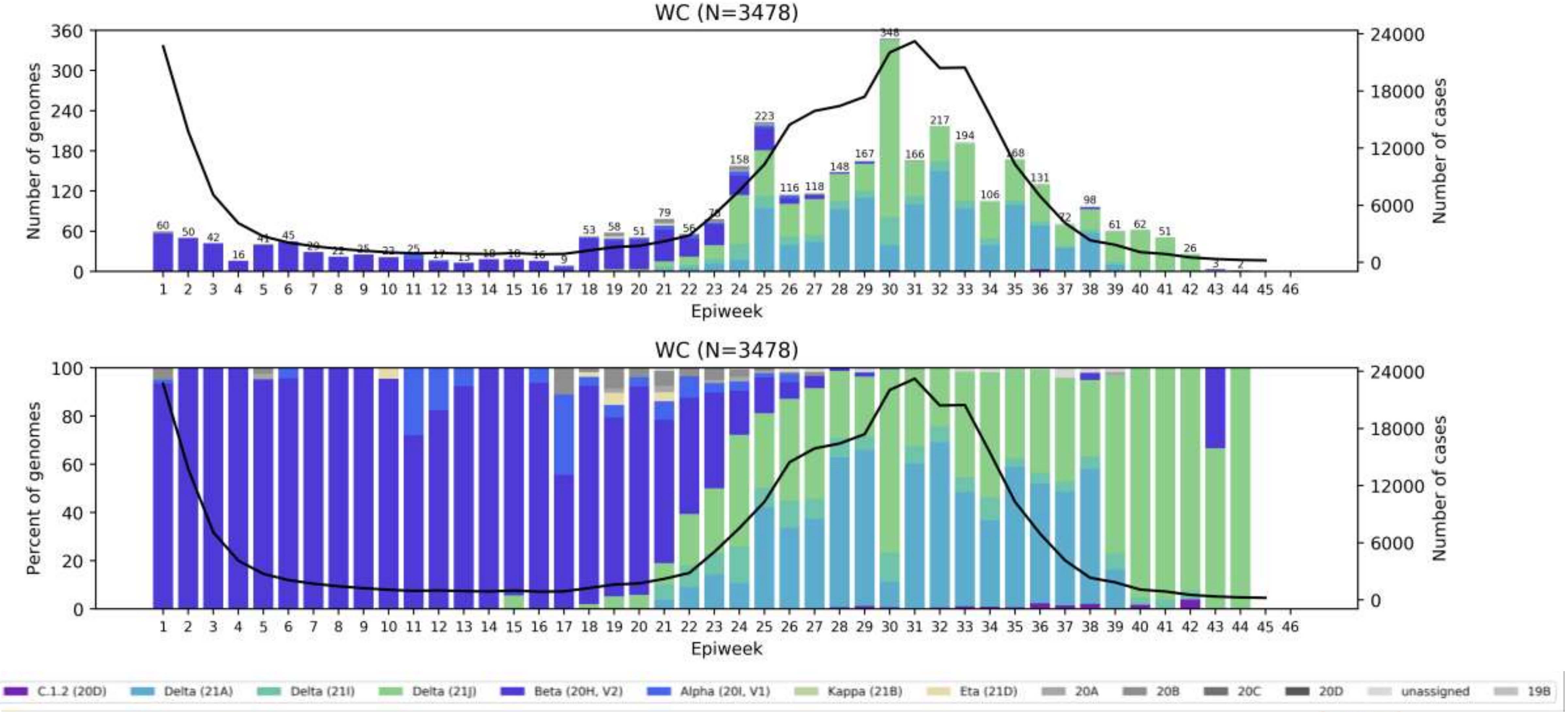
Network for Genomic Surveillance in South Africa

North West Province, 2021, n = 1142



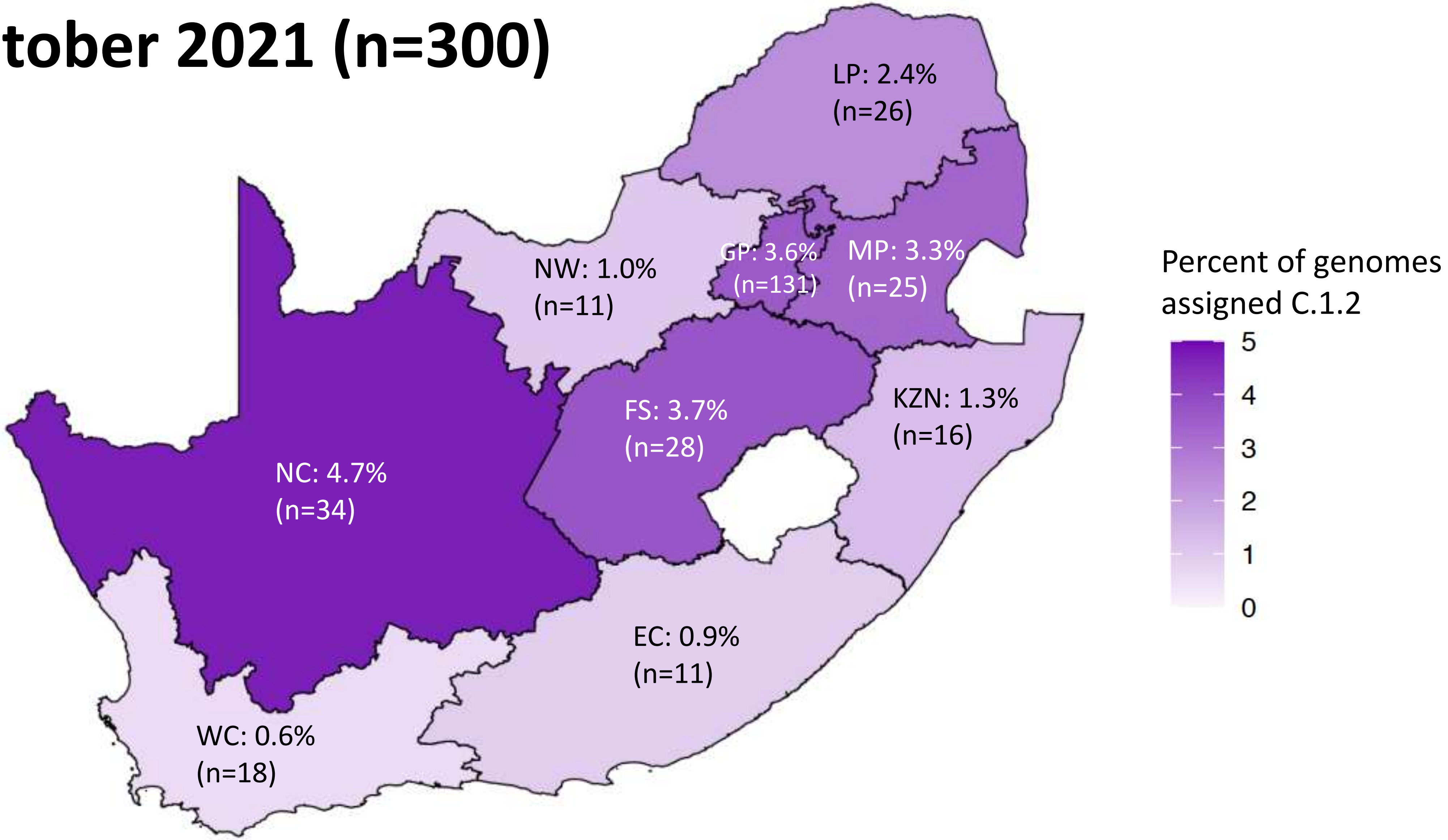
NGS-SA
Network for Genomic
Surveillance in South Africa

Western Cape Province, 2021, n = 3478



NGS-SA
Network for Genomic
Surveillance in South Africa

Percentage of sequences assigned C.1.2 in South Africa, May – October 2021 (n=300)

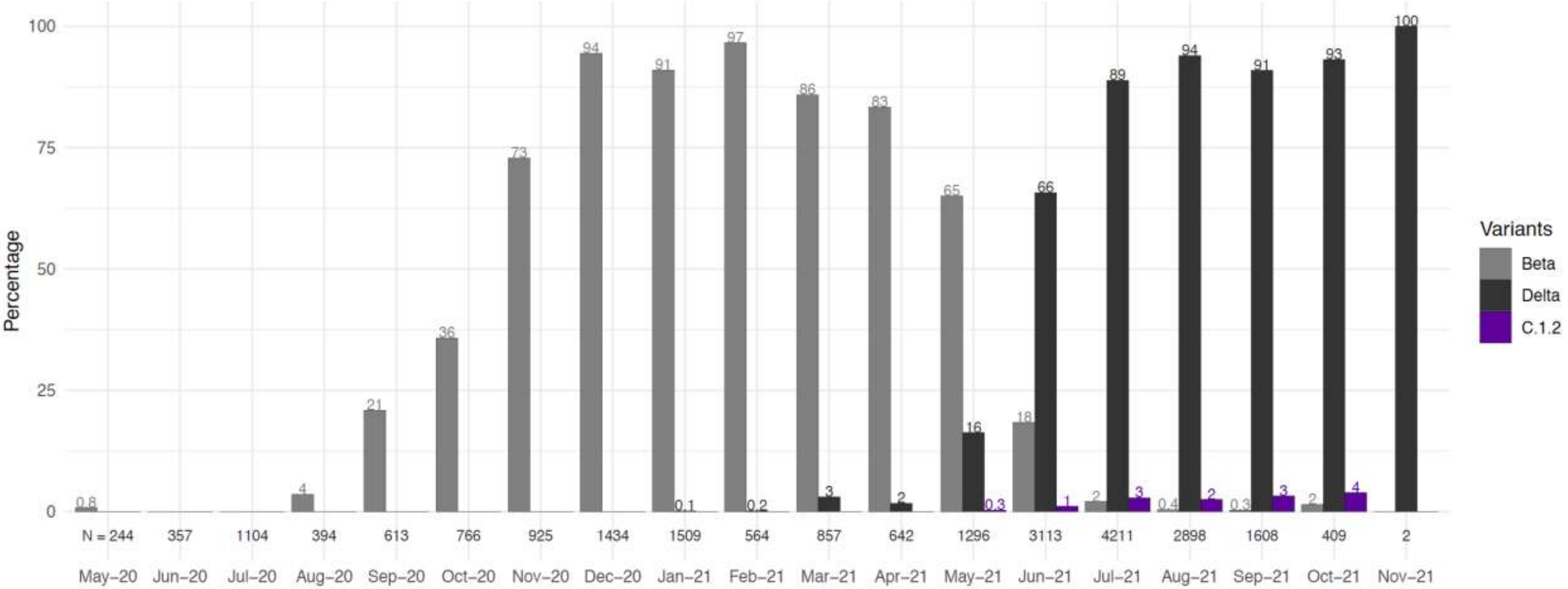


The majority of C.1.2 sequences have been detected in Gauteng, followed by the Northern Cape, the Free State, Mpumalanga, and Limpopo.

NGS-SA
Network for Genomic Surveillance in South Africa

C.1.2 growth compared to Beta and Delta

Detection of variants of concern (VOCs) in South Africa

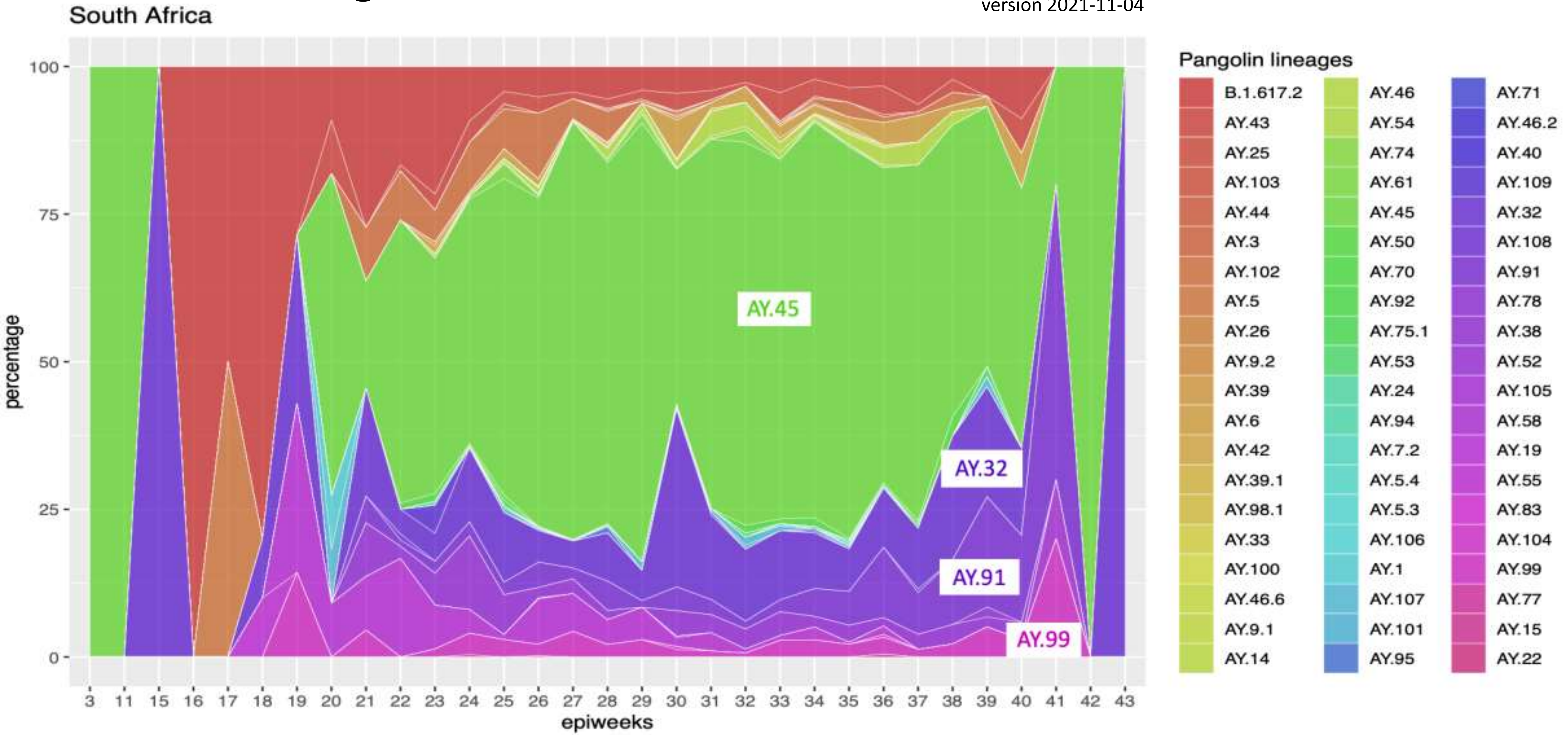


C.1.2 continues to be detected at low levels (≤ 4% of genomes per month)

NGS-SA
Network for Genomic Surveillance in South Africa

Delta sub-lineages* in South Africa

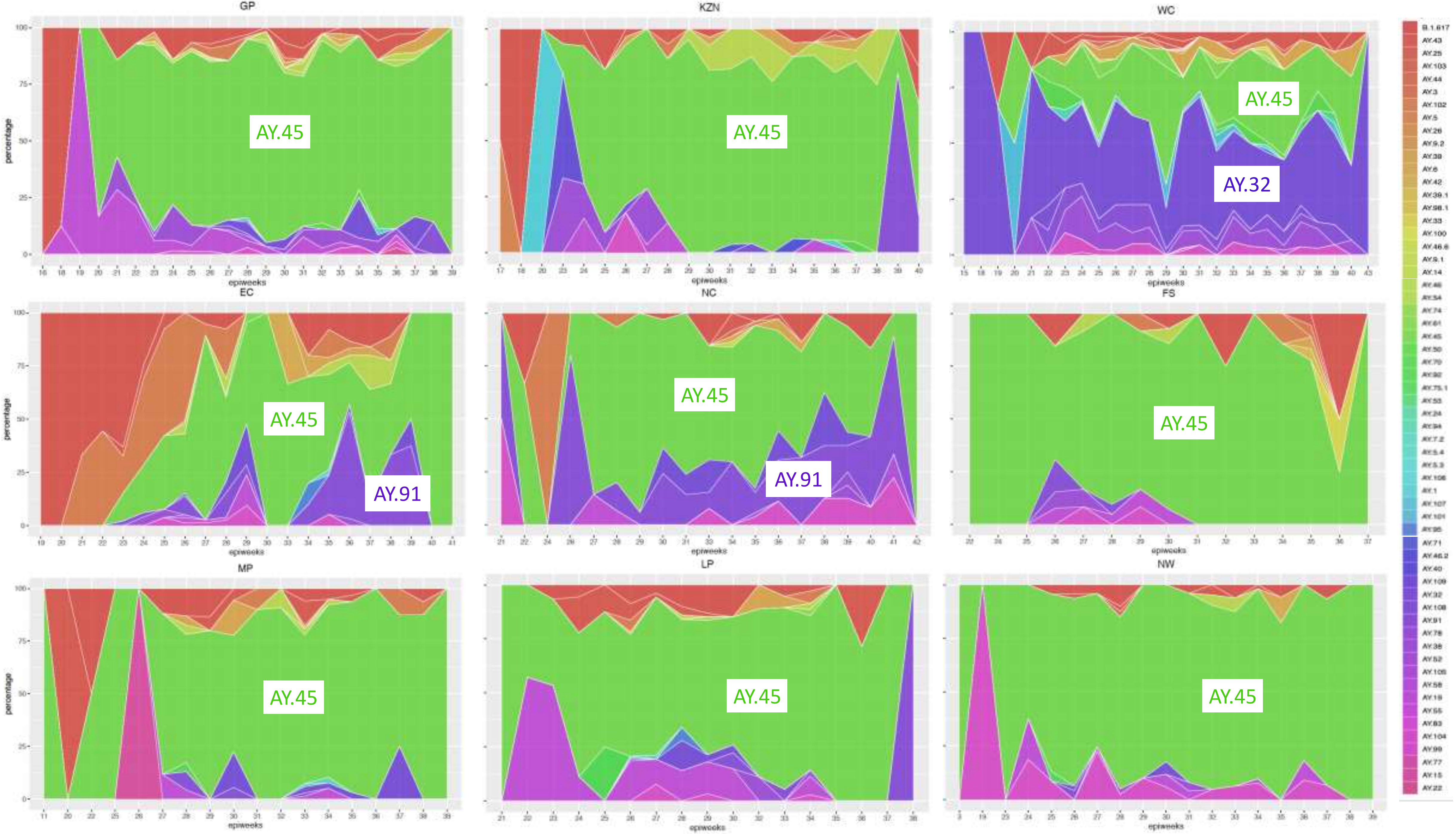
*Data sourced from the GISAID variant surveillance file, downloaded 17 Nov 2021, high coverage sequences only, lineages assigned using lineages version 2021-11-04



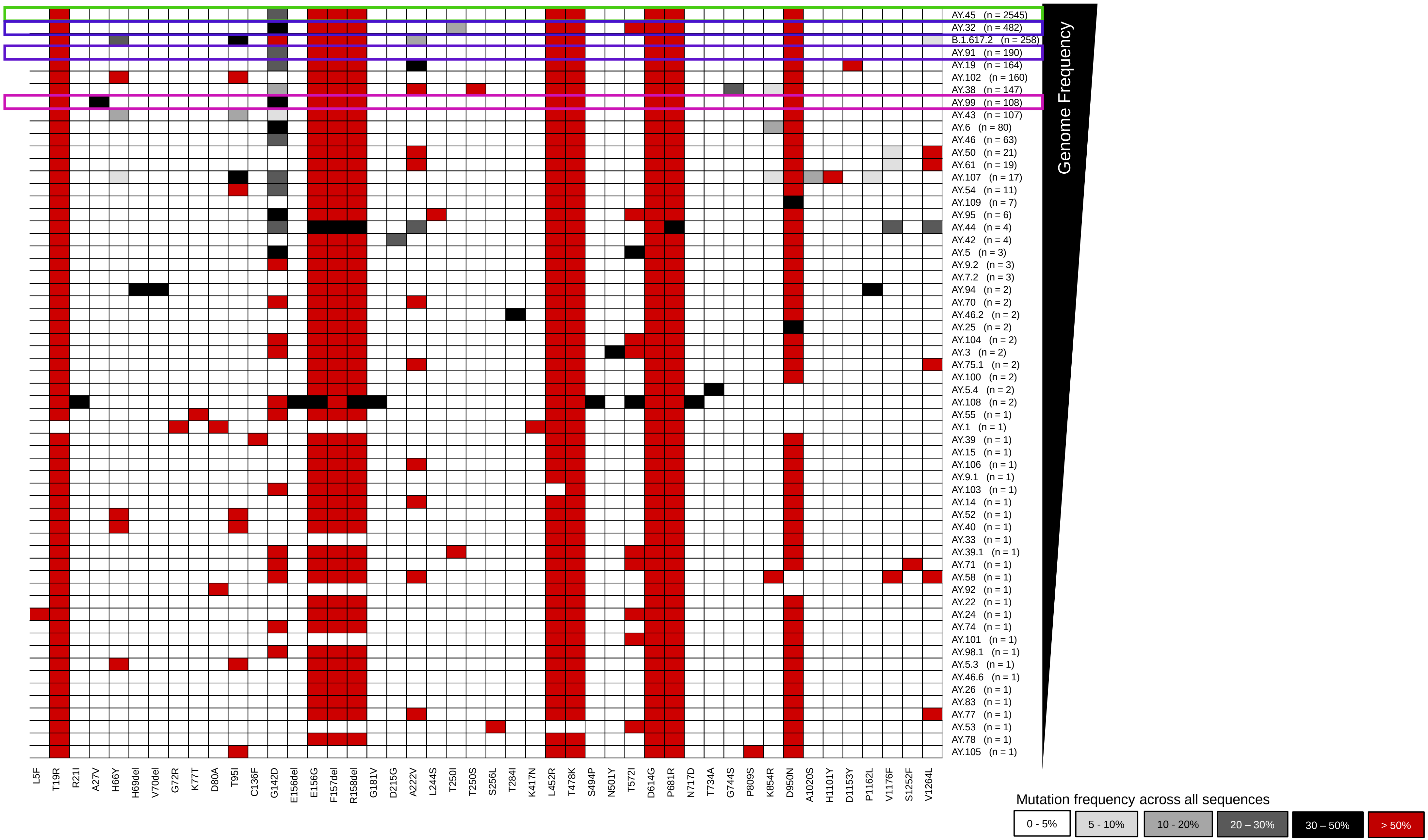
Delta in South Africa is dominated by the AY.45, B.1.617.2, AY.32, AY.91 and AY.99 sub-lineages, although the dominance of sub-lineages varies with province. None of these are known to have a fitness advantage.

NGS-SA
Network for Genomic Surveillance in South Africa

Delta by province (epiweeks 15 – 42, depending on data available per province)



Spike Mutation Frequency for AY.x in South Africa



Summary as on 19 November 2021

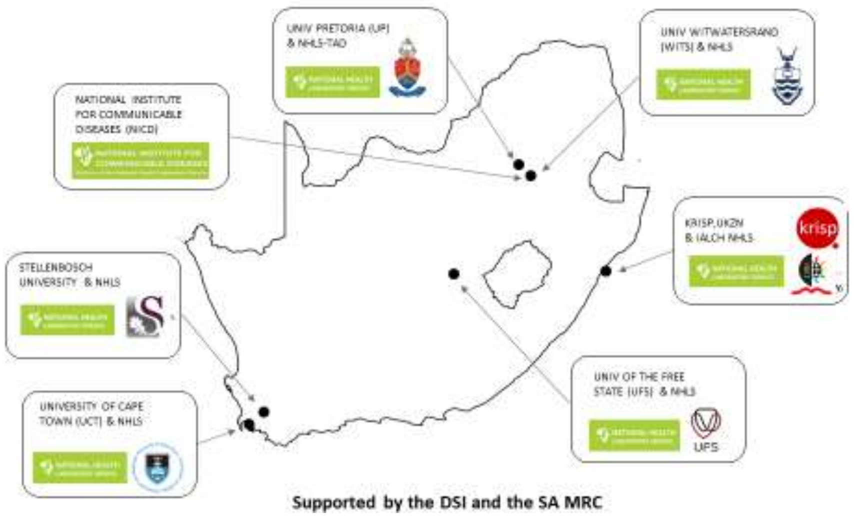
- Delta continues to dominate in all provinces from specimens collected in September and October
  - Delta has recently been split into three clades.
    - New clades have been assigned due to >20% global circulation of particular sequences for more than 2 months
    - All South African Delta samples have been updated
    - Delta 21J is the dominant clade globally and in South Africa
    - The Delta sub-lineages vary by province

- Mutated C.1.2 lineage detected in all provinces of South Africa at less than 5% of genomes

- Lambda, Mu and the Delta AY.4.2 variants not yet detected in South Africa

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

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

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 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

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

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

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

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

National Institute for Communicable Diseases

Centre for Respiratory Diseases & Meningitis
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
Jinal Bhiman
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

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

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

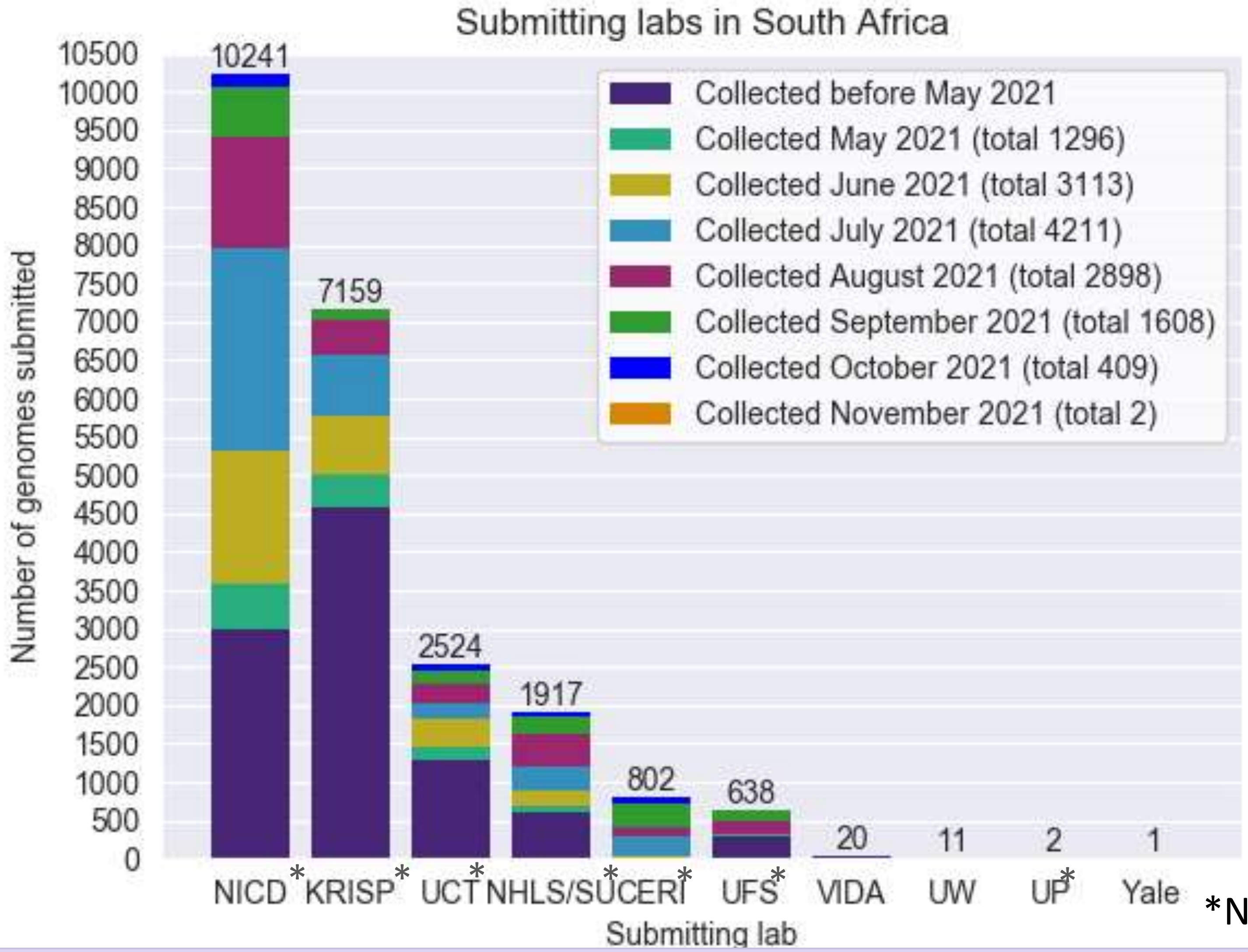
Africa CDC
John Nkengasong
Sofonias Tessema

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=23 315)



*NGS-SA laboratories

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

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 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.)