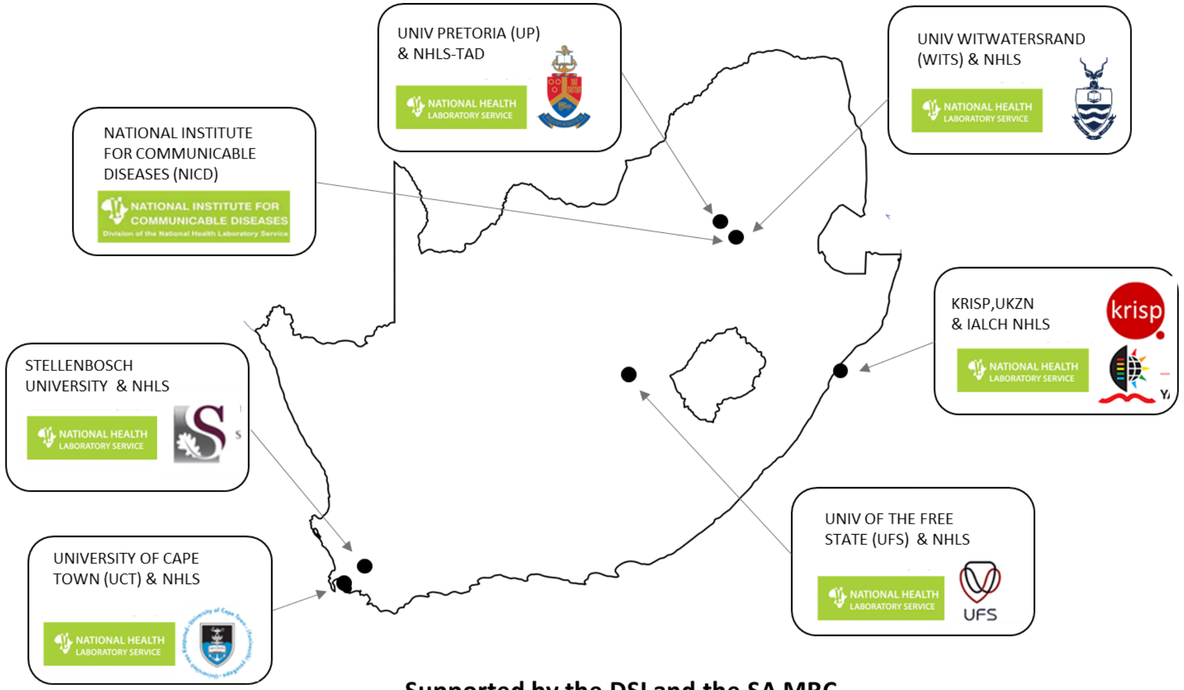
Network for Genomic Surveillance in South Africa (NGS-SA)

SARS-CoV-2 Sequencing Update
05 August 2022



UNIV PRETORIA (UP) & NHLS-TAD

UNIV WITWATERSRAND (WITS) & NHLS

NATIONAL INSTITUTE FOR COMMUNICABLE DISEASES (NICD)

KRISP,UKZN & IALCH NHLS

STELLENBOSCH UNIVERSITY & NHLS

UNIV OF THE FREE STATE (UFS) & NHLS

UNIVERSITY OF CAPE TOWN (UCT) & NHLS

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)

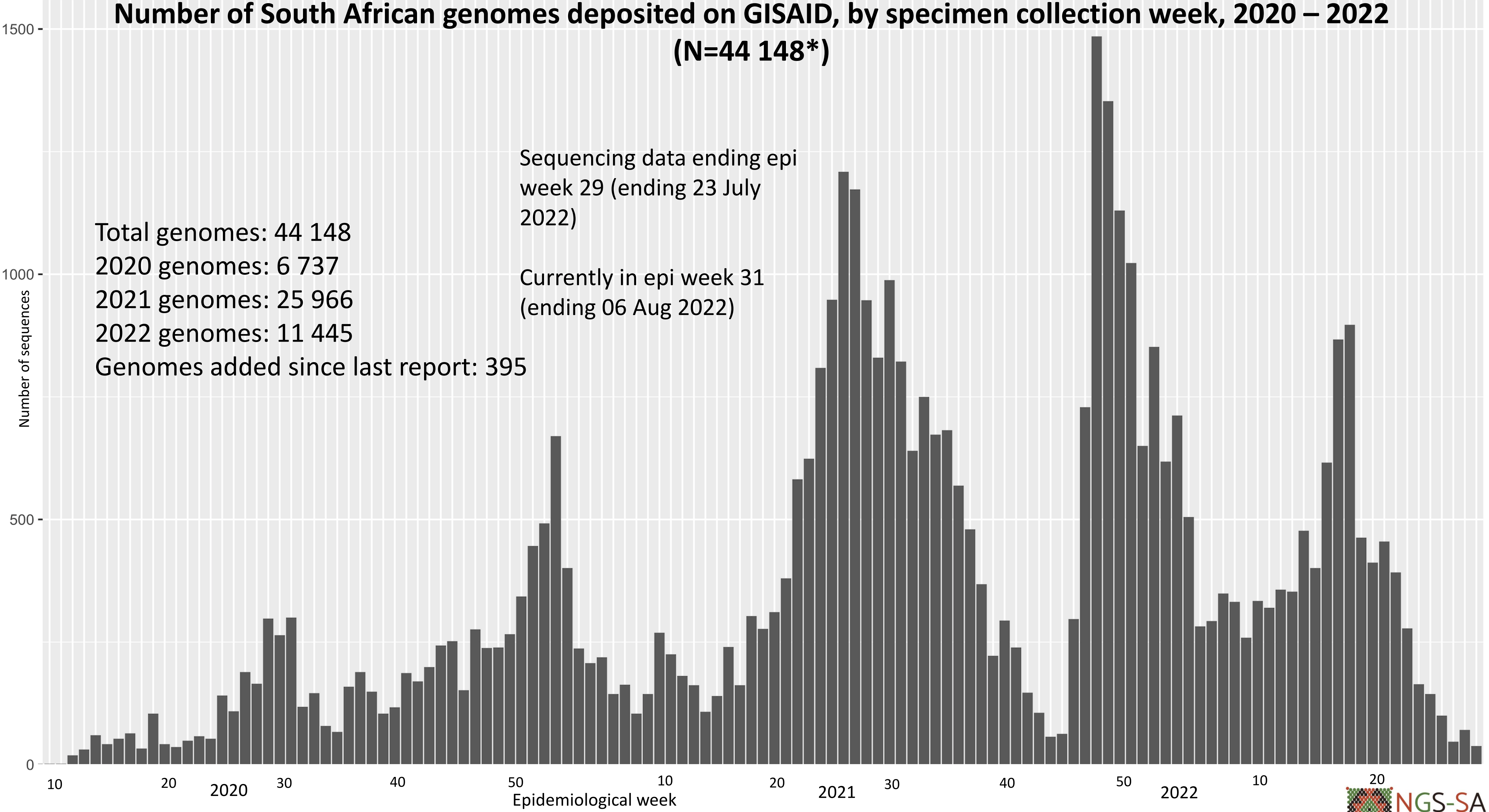
The genomic data presented here are based on South African SARS-CoV-2 sequence data downloaded from GISAID (www.gisaid.org) on 04 August 2022 at 09h11

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

Number of South African genomes deposited on GISAID, by specimen collection week, 2020 – 2022 (N=44 148*)



Total genomes: 44 148
2020 genomes: 6 737
2021 genomes: 25 966
2022 genomes: 11 445
Genomes added since last report: 395

Sequencing data ending epi week 29 (ending 23 July 2022)

Currently in epi week 31 (ending 06 Aug 2022)

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

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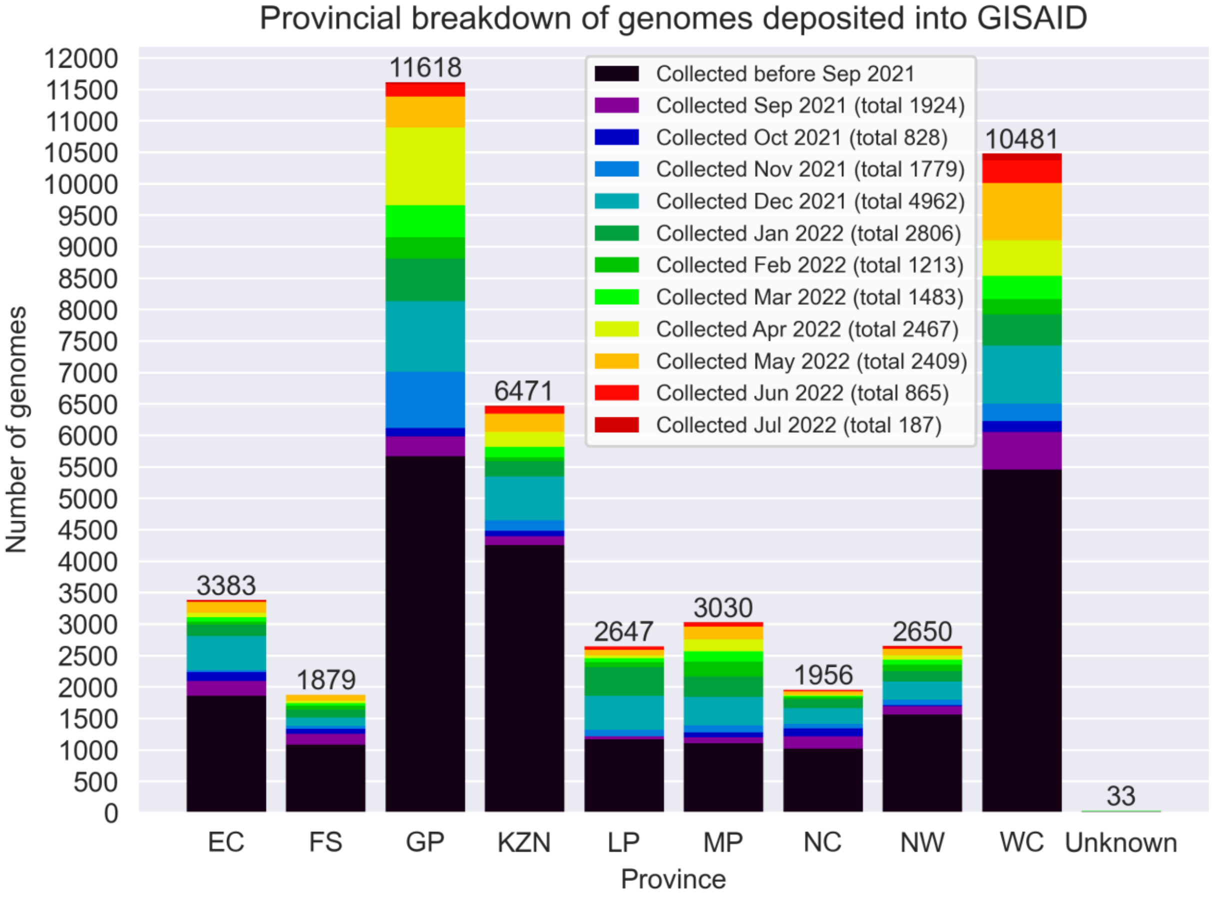
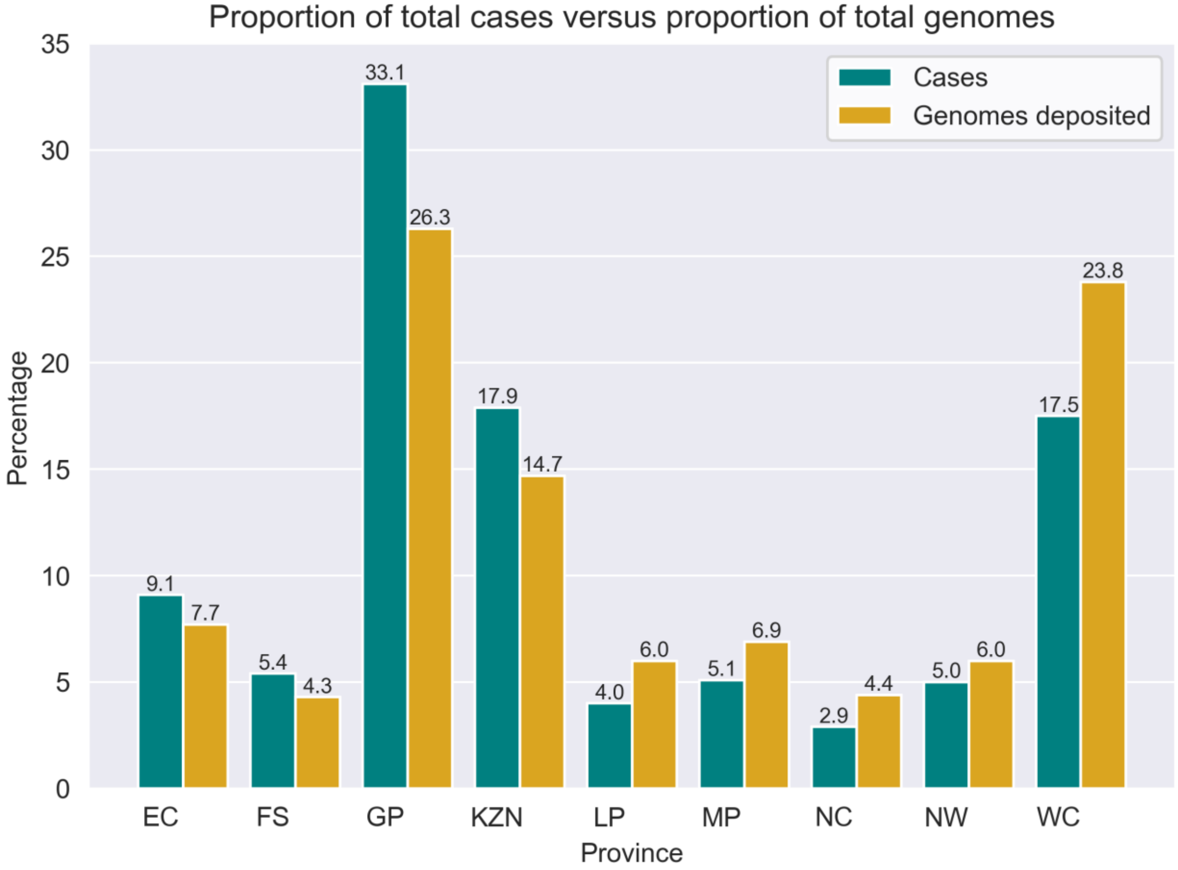
GISAID genomes vs total cases, 2020 – 2022 (N=44 148)


Provincial breakdown of genomes deposited into GISAID


Proportion of total cases versus proportion of total genomes

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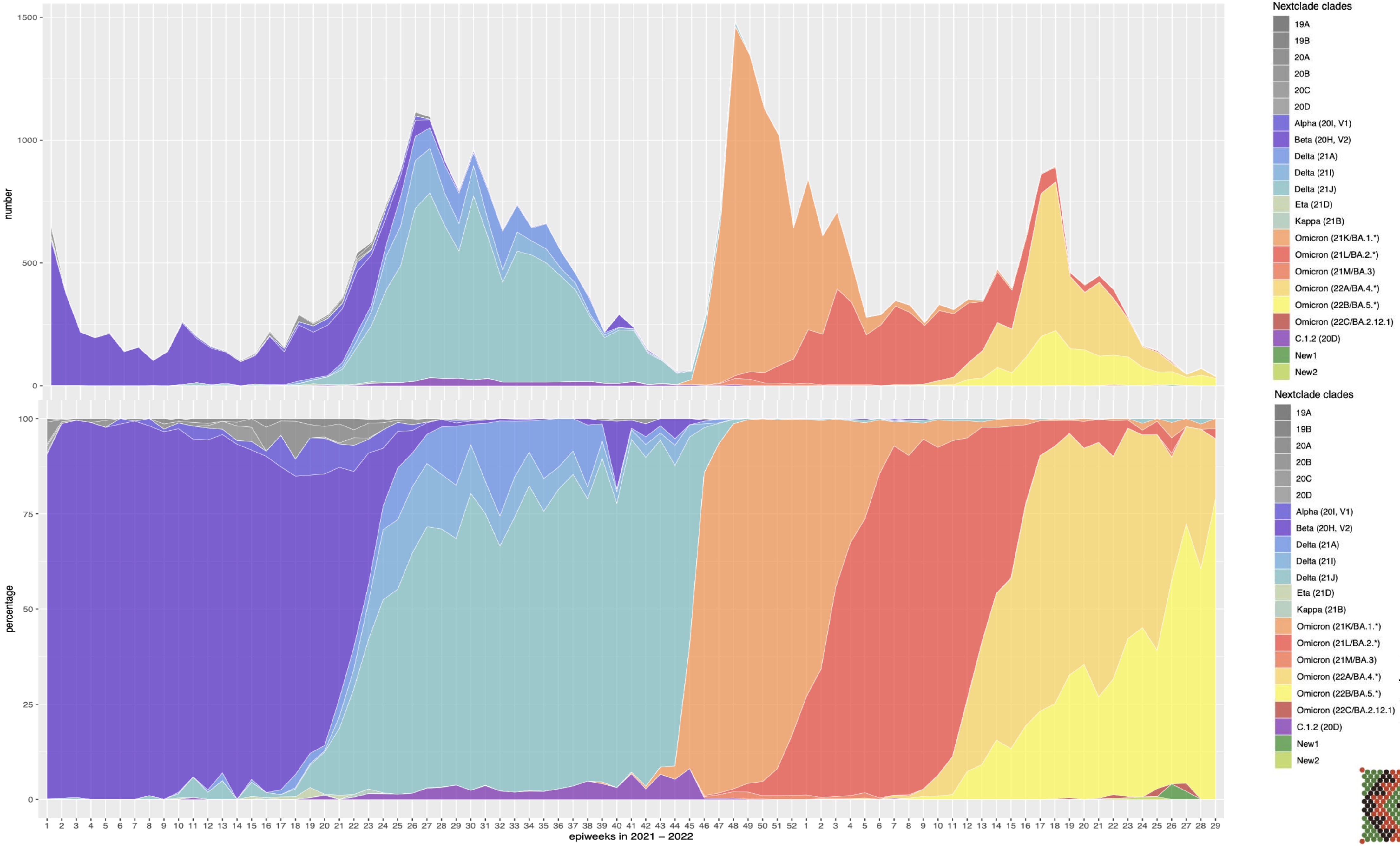
Number and percentage of clades by epiweek in South Africa, 2021 – 2022 (37 324*)



Sequencing data ending epi week 29 (ending 23 July 2022)

Currently in epi week 31 (ending 06 Aug 2022)

*Excludes sequences missing collection dates, as well as those collected January 1st and 2nd 2021 as they are part of epiweek 53 of 2020.

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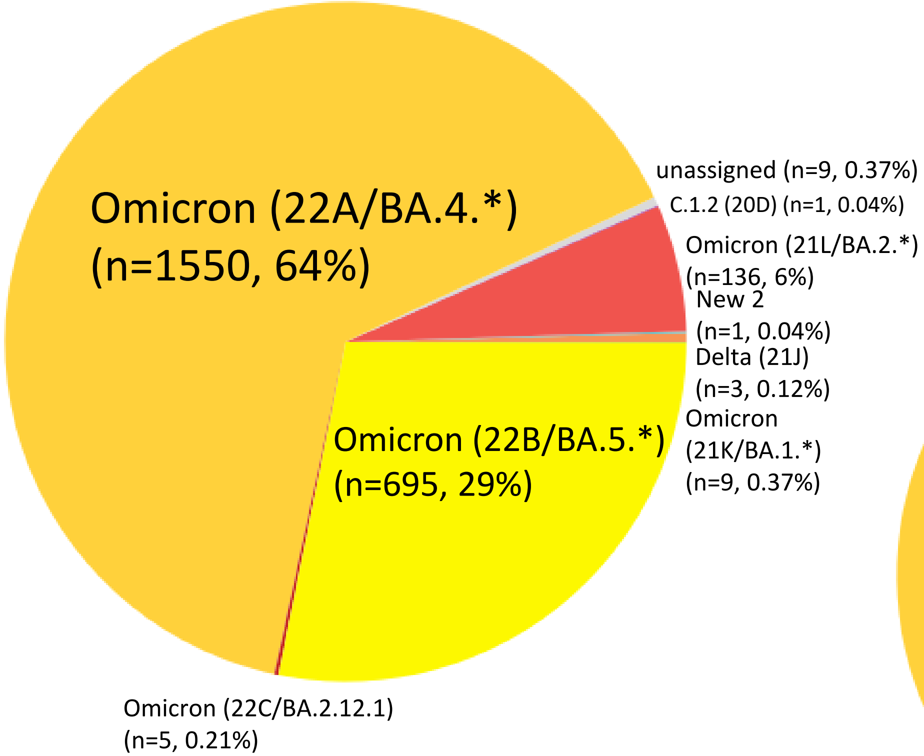
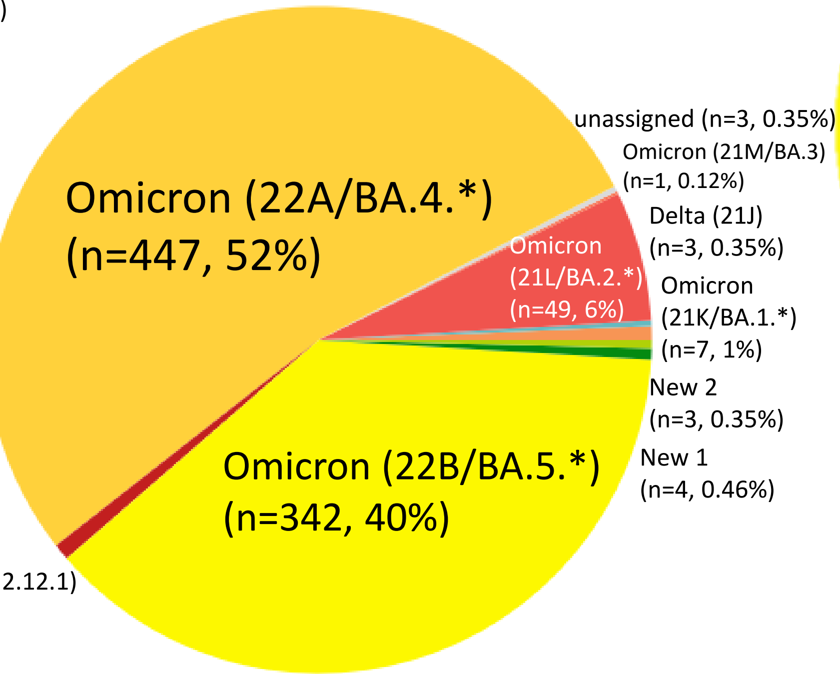
Prevalence of Variants of Concern (VOC) and Variants of Interest (VOI) in May – July 2022

May (N=2409)



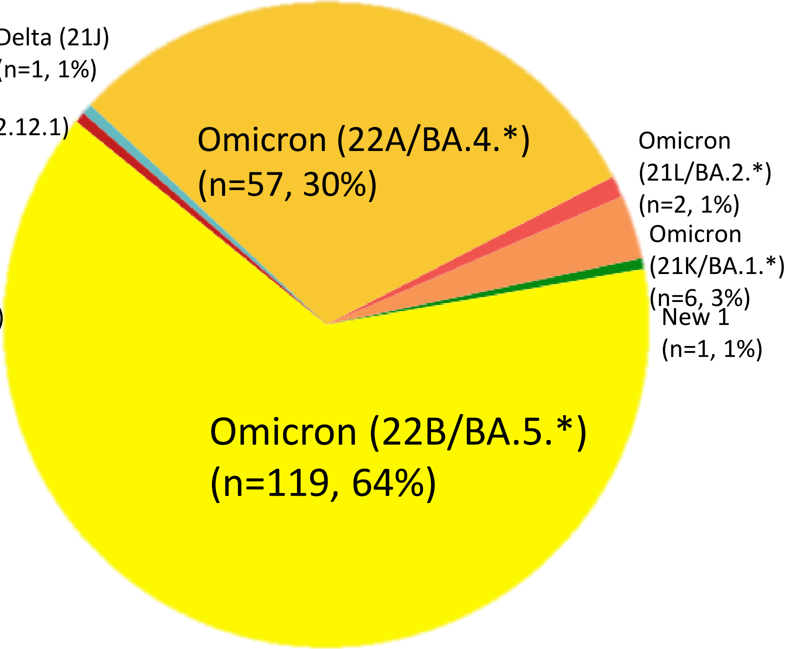
Total Omicron in May: 2398 (99.5%)

June (N=865)



Total Omicron in June: 852 (98.5%)

July (N=187)



Total Omicron in July: 185 (98.9%)

Clade key (bar graph)

🟩 New1
🟩 New2
🟧 Omicron (21K/BA.1.*)
🟥 Omicron (21L/BA.2.*)
🟥 Omicron (22C/BA.2.12.1)
🟧 Omicron (21M/BA.3)
🟨 Omicron (22A/BA.4.*)
🟨 Omicron (22B/BA.5.*)
🟪 C.1.2 (20D)
🟪 Beta (20H, V2)
🟦 Alpha (20I, V1)
🟦 Delta (21A)
🟦 Delta (21I)
🟦 Delta (21J)
🟩 Kappa (21B)
🟩 Eta (21D)
⬛ 20D
— Cases
⬛ 20C
⬛ 20B
⬛ 20A
⬜ 19B
⬜ 19A
⬜ unassigned

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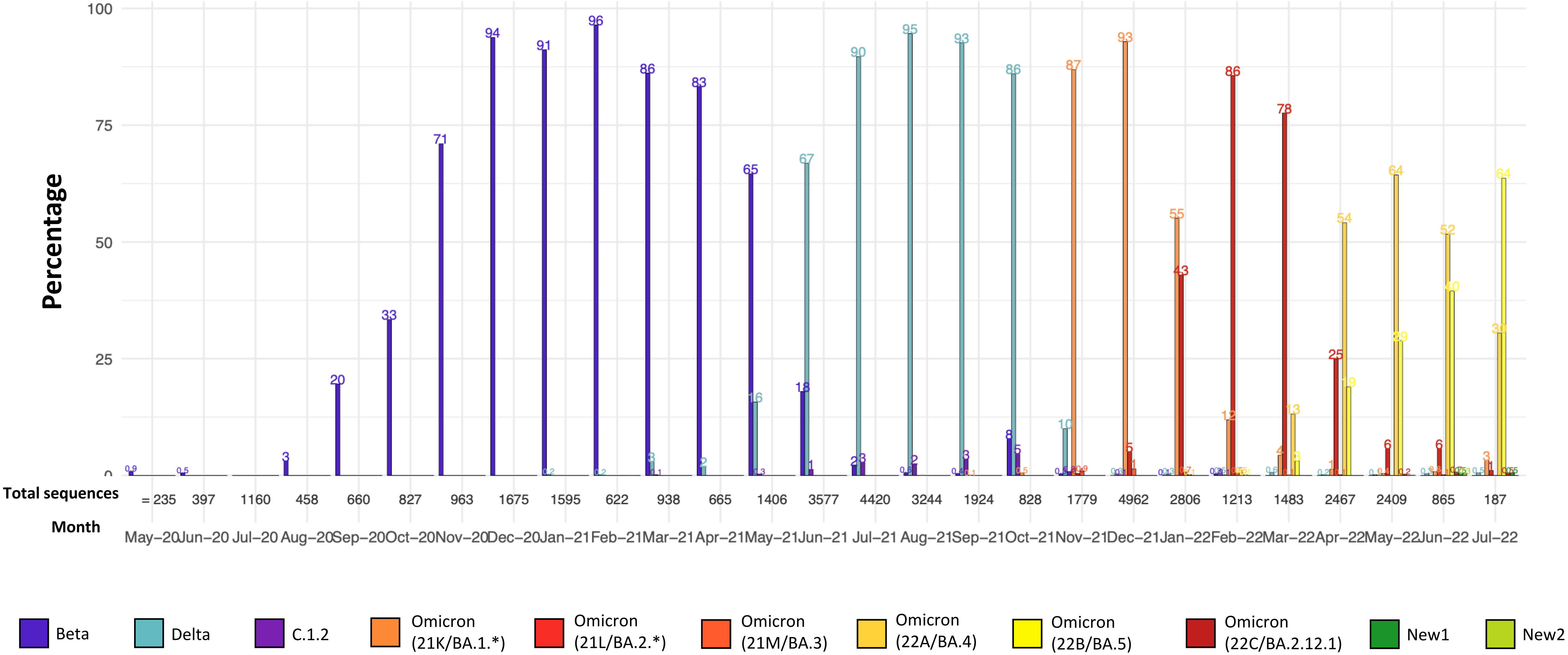
Detection Rates: Beta, Delta, C.1.2 and Omicron

Detection rates of variants being monitored in South Africa



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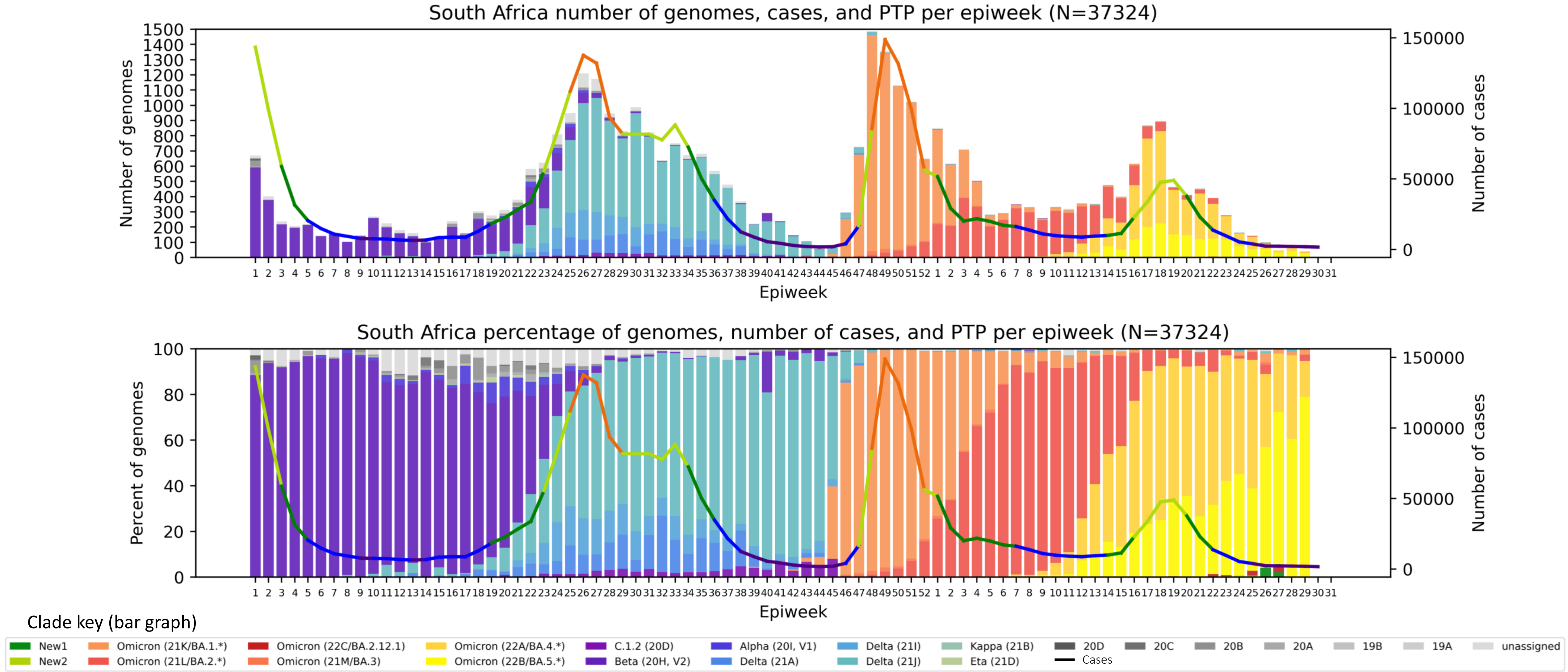
*Bars represent percentage prevalence of variant for the month; total number sequences collected for the month are given below the bar

South Africa, 2021-2022, n = 37 324*


South Africa number of genomes, cases, and PTP per epiweek (N=37324)

South Africa percentage of genomes, number of cases, and PTP per epiweek (N=37324)

Weekly percentage testing positive key (line graph)

- ≤ 5
- 6 - 10
- 11 - 20
- 21 - 30
- 31 - 40
- 41 - 50
- 51 - 55

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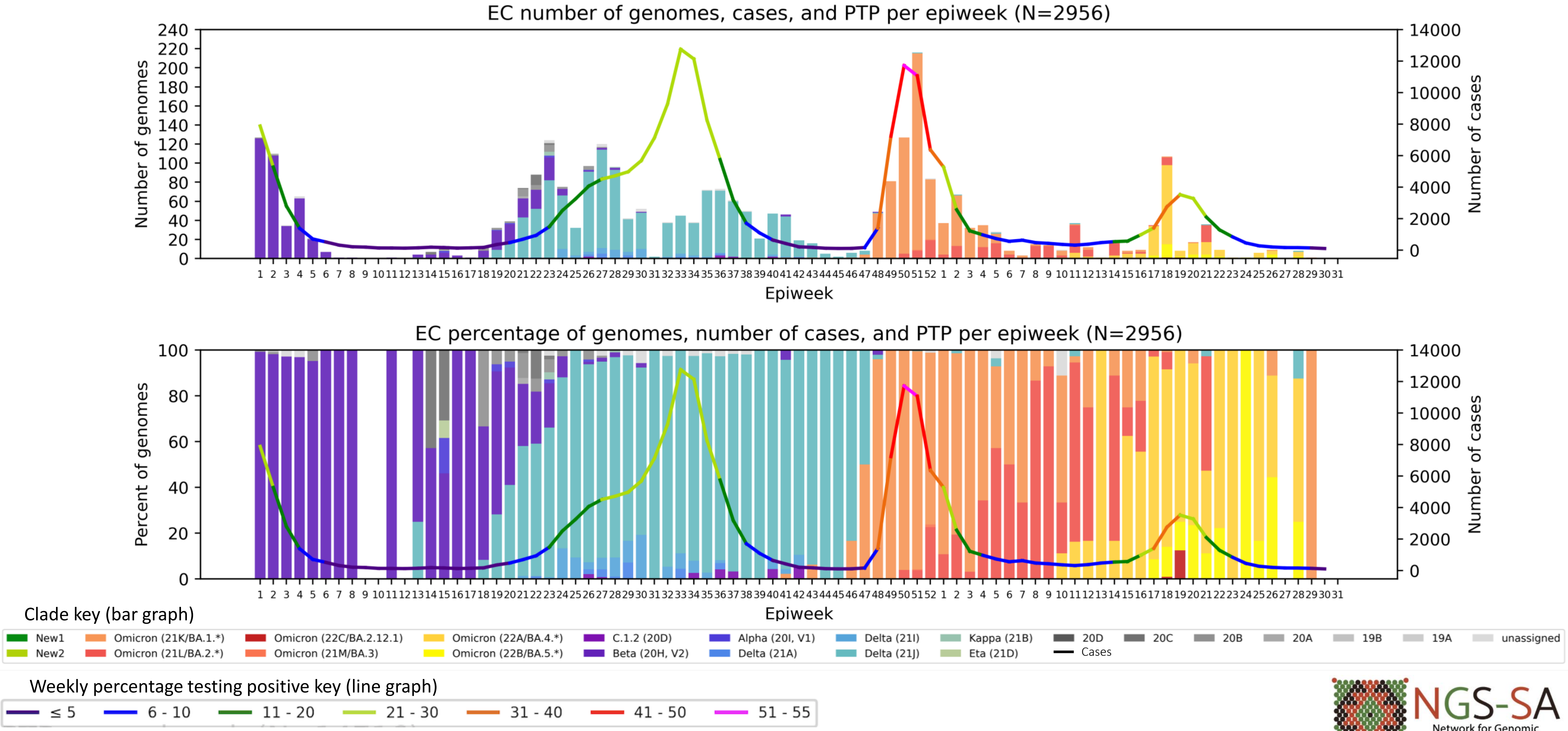
*Excludes sequences missing collection dates, as well as those collected January 1st and 2nd 2021 as they are part of epiweek 53 of 2020.

Eastern Cape Province, 2021-2022, n = 2956

Genomes added since last report: 54*



EC number of genomes, cases, and PTP per epiweek (N=2956)

EC percentage of genomes, number of cases, and PTP per epiweek (N=2956)

*May include genomes from 2020 which are not pictured here and are not included in the slide total.

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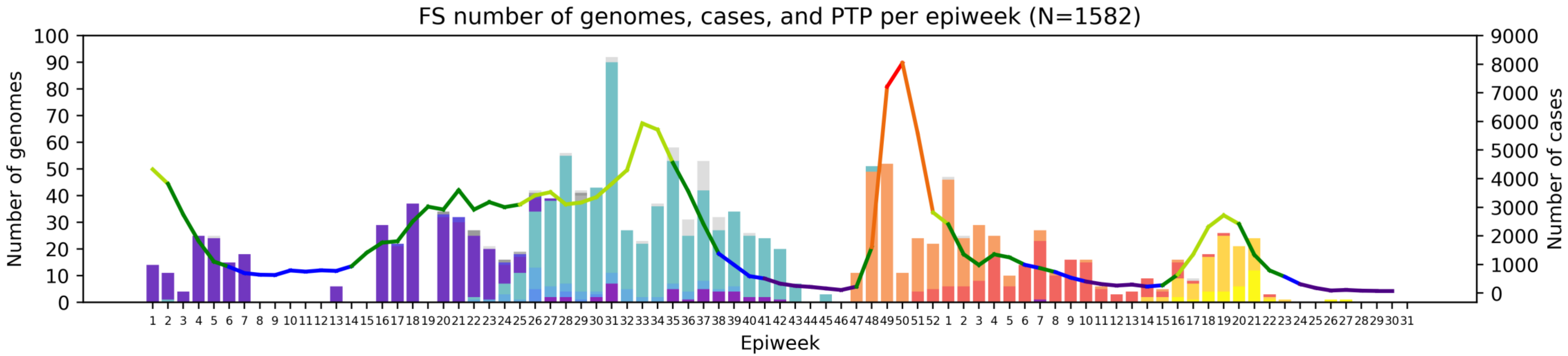
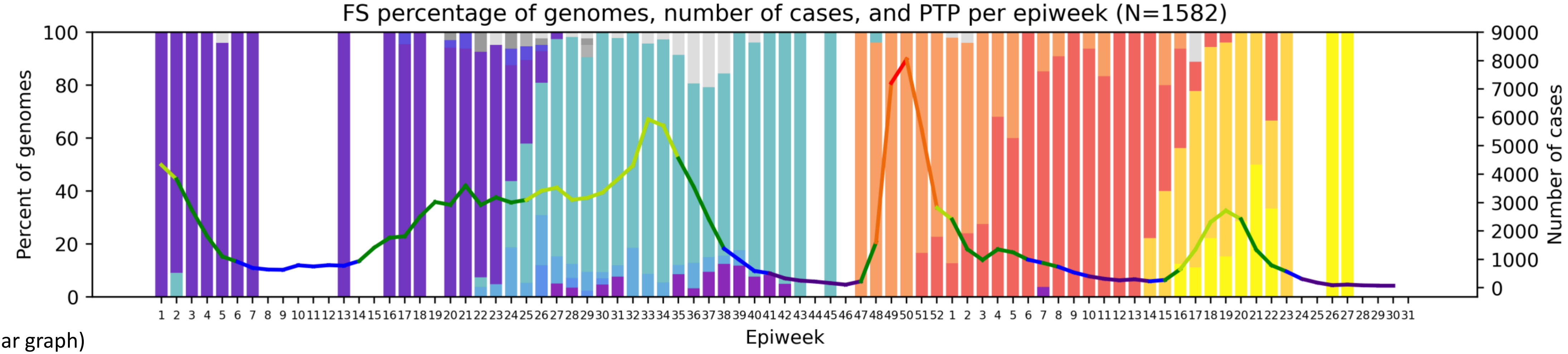
Free State Province, 2021-2022, n = 1582

Genomes added since last report: 7*





Clade key (bar graph)

- ■ New1
- ■ New2
- ■ Omicron (21K/BA.1.*)
- ■ Omicron (21L/BA.2.*)
- ■ Omicron (22C/BA.2.12.1)
- ■ Omicron (21M/BA.3)
- ■ Omicron (22A/BA.4.*)
- ■ Omicron (22B/BA.5.*)
- ■ C.1.2 (20D)
- ■ Beta (20H, V2)
- ■ Alpha (20I, V1)
- ■ Delta (21A)
- ■ Delta (21I)
- ■ Delta (21J)
- ■ Kappa (21B)
- ■ Eta (21D)
- ■ 20D
- — Cases
- ■ 20C
- ■ 20B
- ■ 20A
- ■ 19B
- ■ 19A
- ■ unassigned

Weekly percentage testing positive key (line graph)

- — ≤ 5
- — 6 - 10
- — 11 - 20
- — 21 - 30
- — 31 - 40
- — 41 - 50
- — 51 - 55

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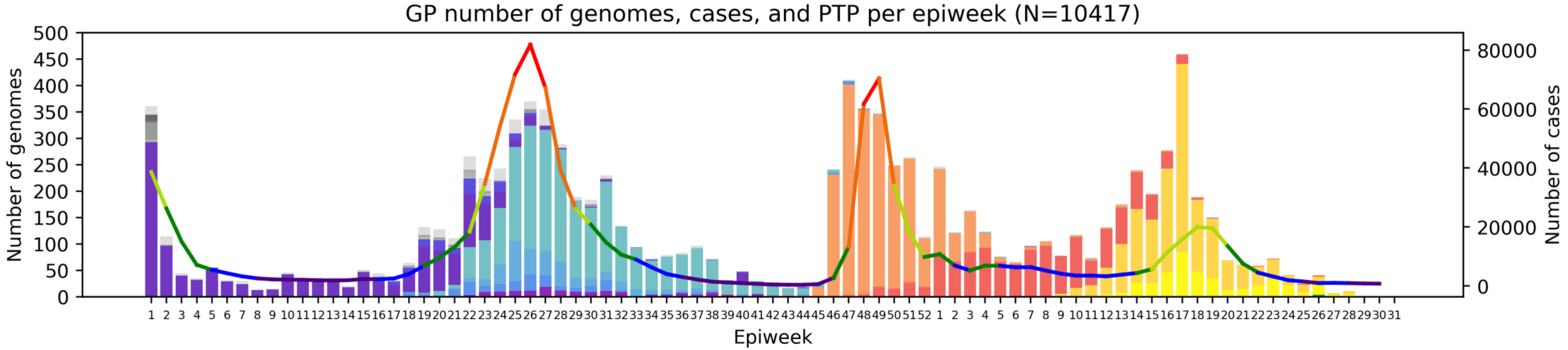
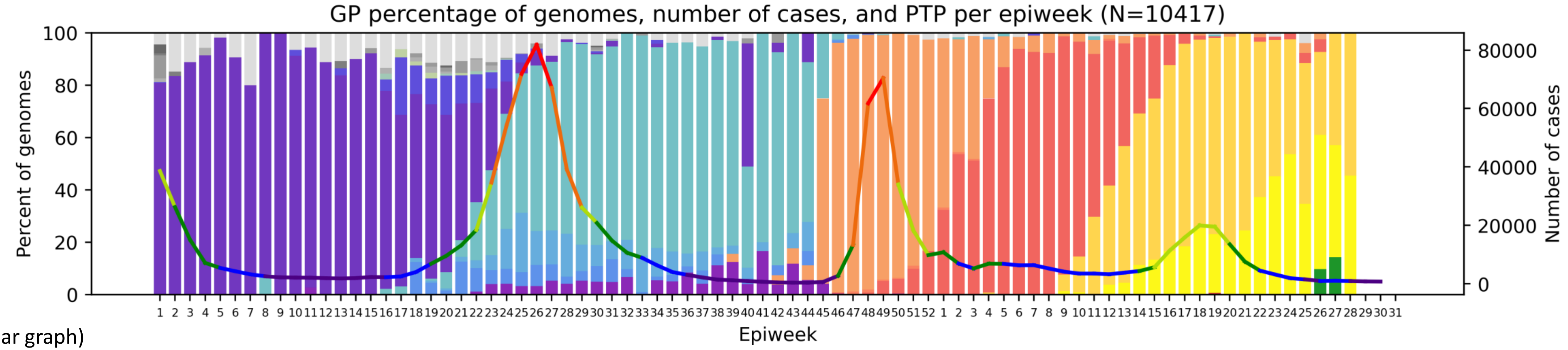
*May include genomes from 2020 which are not pictured here and are not included in the slide total.

Gauteng Province, 2021-2022, n = 10 417

Genomes added since last report: 125*





Clade key (bar graph)

- New1
- New2
- Omicron (21K/BA.1.*)
- Omicron (21L/BA.2.*)
- Omicron (22C/BA.2.12.1)
- Omicron (21M/BA.3)
- Omicron (22A/BA.4.*)
- Omicron (22B/BA.5.*)
- C.1.2 (20D)
- Beta (20H, V2)
- Alpha (20I, V1)
- Delta (21A)
- Delta (21I)
- Delta (21J)
- Kappa (21B)
- Eta (21D)
- 20D
- Cases
- 20C
- 20B
- 20A
- 19B
- 19A
- unassigned

Weekly percentage testing positive key (line graph)

- ≤ 5
- 6 - 10
- 11 - 20
- 21 - 30
- 31 - 40
- 41 - 50
- 51 - 55

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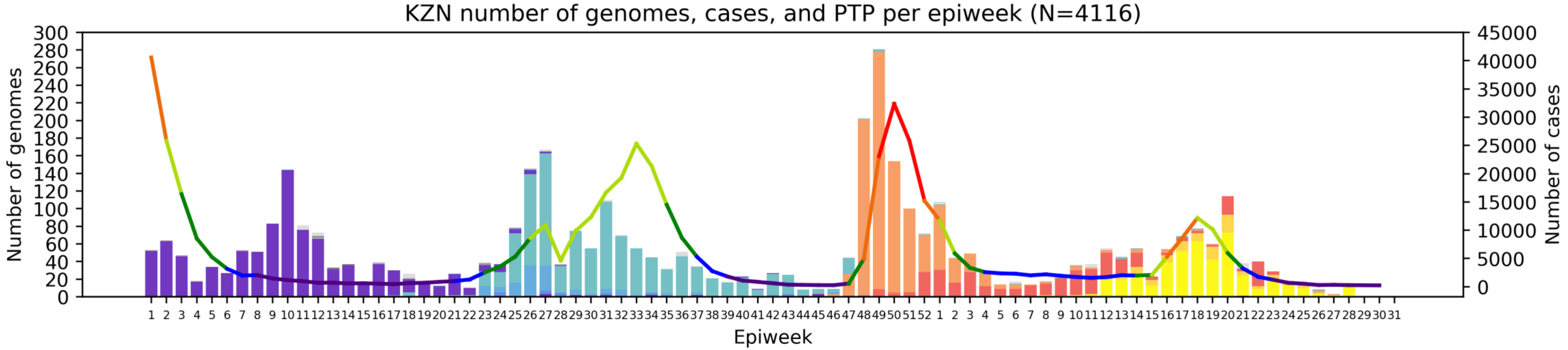
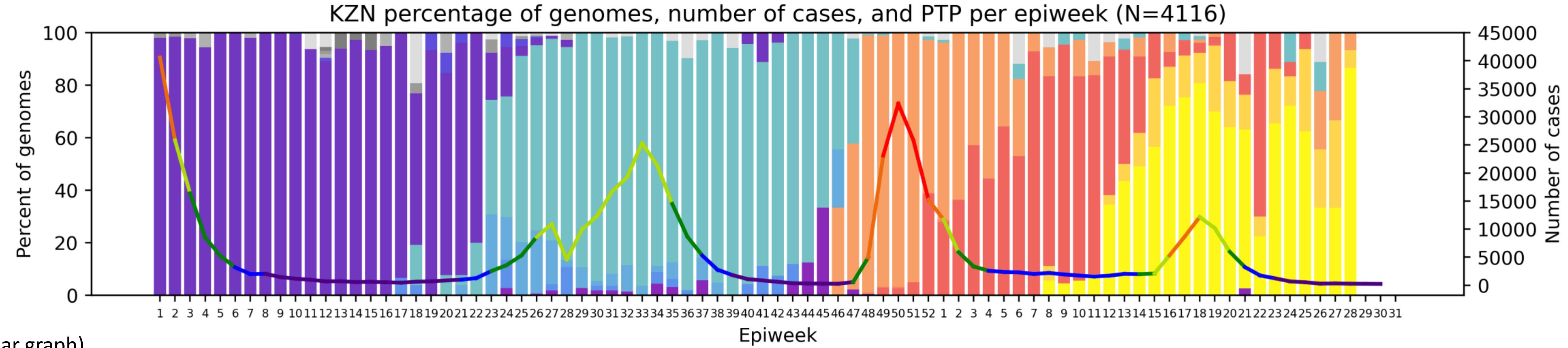
*May include genomes from 2020 which are not pictured here and are not included in the slide total.

KwaZulu-Natal Province, 2021-2022, n = 4116

Genomes added since last report: 36*


KZN number of genomes, cases, and PTP per epiweek (N=4116)


KZN percentage of genomes, number of cases, and PTP per epiweek (N=4116)

Clade key (bar graph)

- New1
- New2
- Omicron (21K/BA.1.*)
- Omicron (21L/BA.2.*)
- Omicron (22C/BA.2.12.1)
- Omicron (21M/BA.3)
- Omicron (22A/BA.4.*)
- Omicron (22B/BA.5.*)
- C.1.2 (20D)
- Beta (20H, V2)
- Alpha (20I, V1)
- Delta (21A)
- Delta (21I)
- Delta (21J)
- Kappa (21B)
- Eta (21D)
- 20D
- Cases
- 20C
- 20B
- 20A
- 19B
- 19A
- unassigned

Weekly percentage testing positive key (line graph)

- ≤ 5
- 6 - 10
- 11 - 20
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- 41 - 50
- 51 - 55

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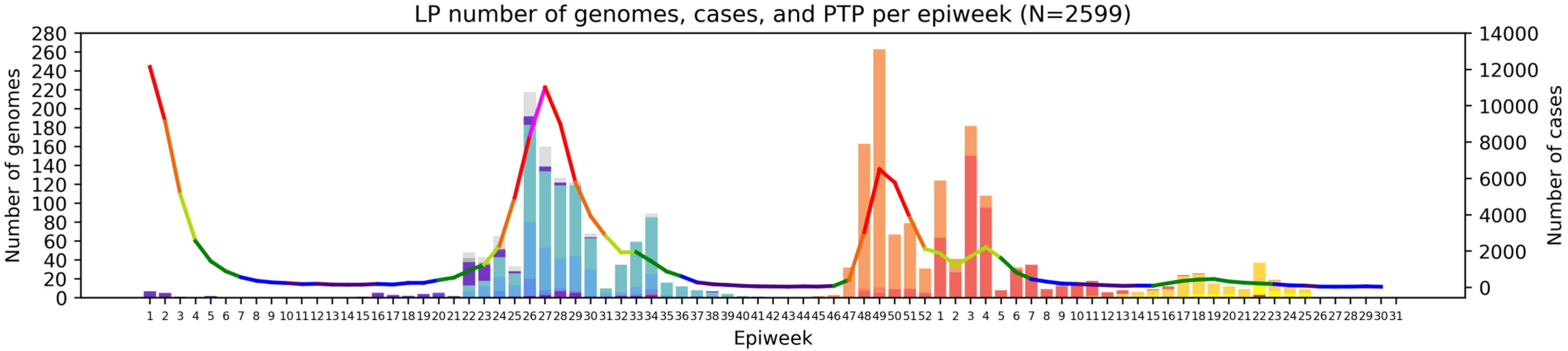
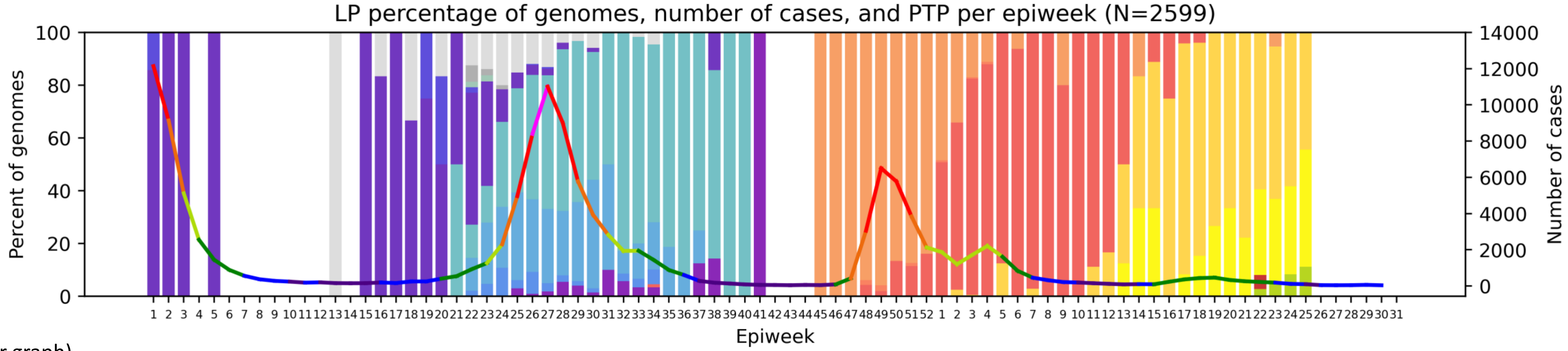
Limpopo Province, 2021-2022, n = 2599

Genomes added since last report: 25*





Clade key (bar graph)

- 🟩 New1
- 🟩 New2
- 🟧 Omicron (21K/BA.1.*)
- 🟥 Omicron (21L/BA.2.*)
- 🟥 Omicron (22C/BA.2.12.1)
- 🟧 Omicron (21M/BA.3)
- 🟨 Omicron (22A/BA.4.*)
- 🟨 Omicron (22B/BA.5.*)
- 🟪 C.1.2 (20D)
- 🟪 Beta (20H, V2)
- 🟦 Alpha (20I, V1)
- 🟦 Delta (21A)
- 🟦 Delta (21I)
- 🟦 Delta (21J)
- 🟩 Kappa (21B)
- 🟩 Eta (21D)
- ⬛ 20D
- — Cases
- ⬛ 20C
- ⬛ 20B
- ⬛ 20A
- ⬜ 19B
- ⬜ 19A
- ⬜ unassigned

Weekly percentage testing positive key (line graph)

- — ≤ 5
- — 6 - 10
- — 11 - 20
- — 21 - 30
- — 31 - 40
- — 41 - 50
- — 51 - 55

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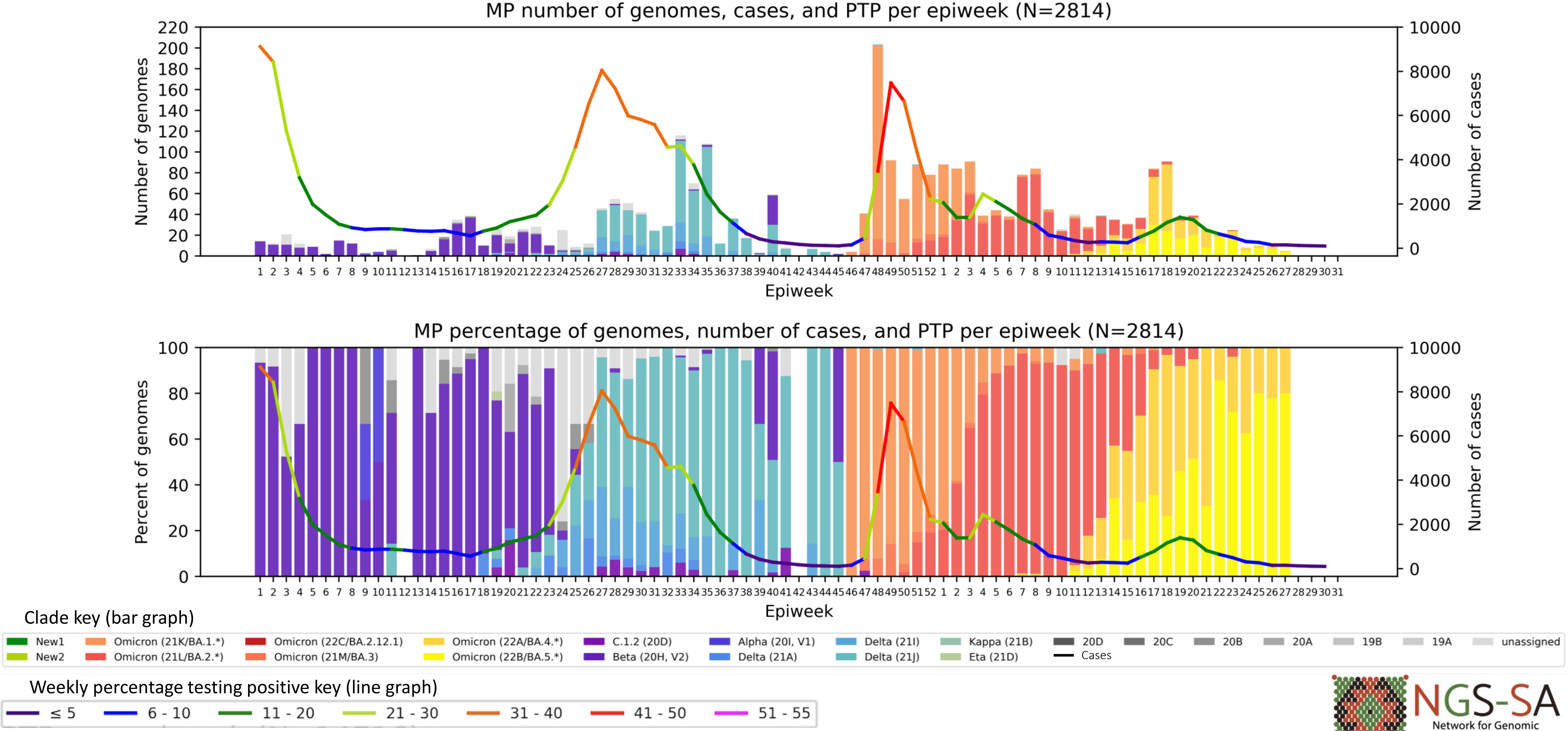
*May include genomes from 2020 which are not pictured here and are not included in the slide total.

Mpumalanga Province, 2021-2022, n = 2814

Genomes added since last report: 110*



*May include genomes from 2020 which are not pictured here and are not included in the slide total.

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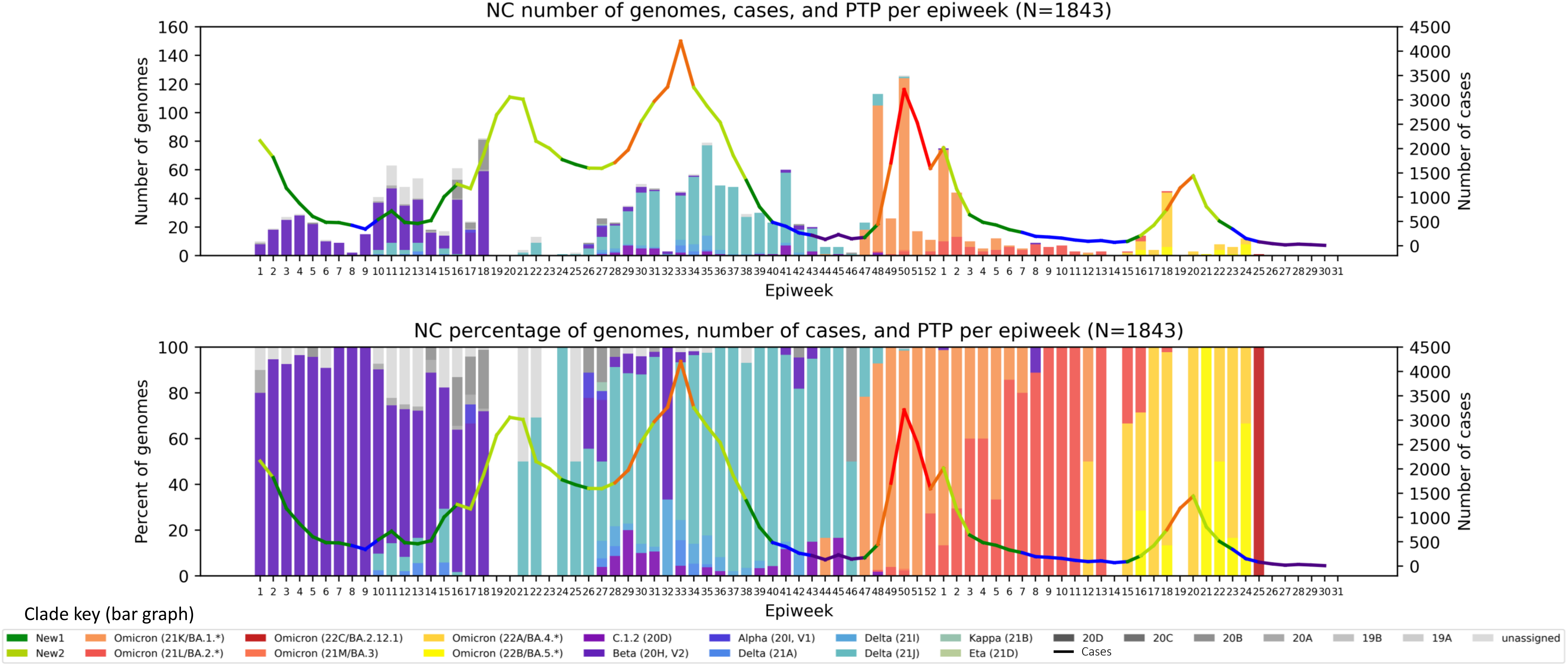
Northern Cape Province, 2021-2022, n = 1843

Genomes added since last report: 2*


NC number of genomes, cases, and PTP per epiweek (N=1843)

NC percentage of genomes, number of cases, and PTP per epiweek (N=1843)

Weekly percentage testing positive key (line graph)

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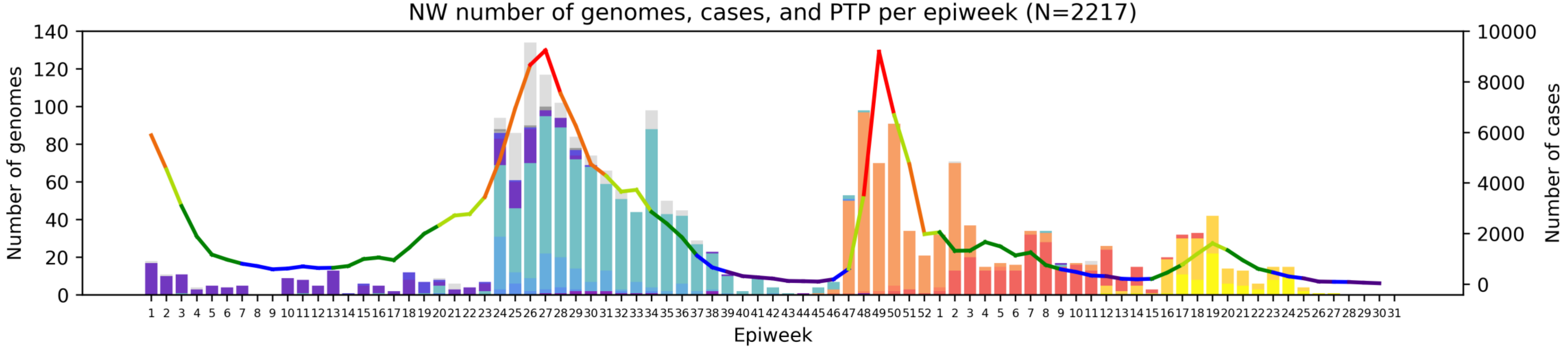
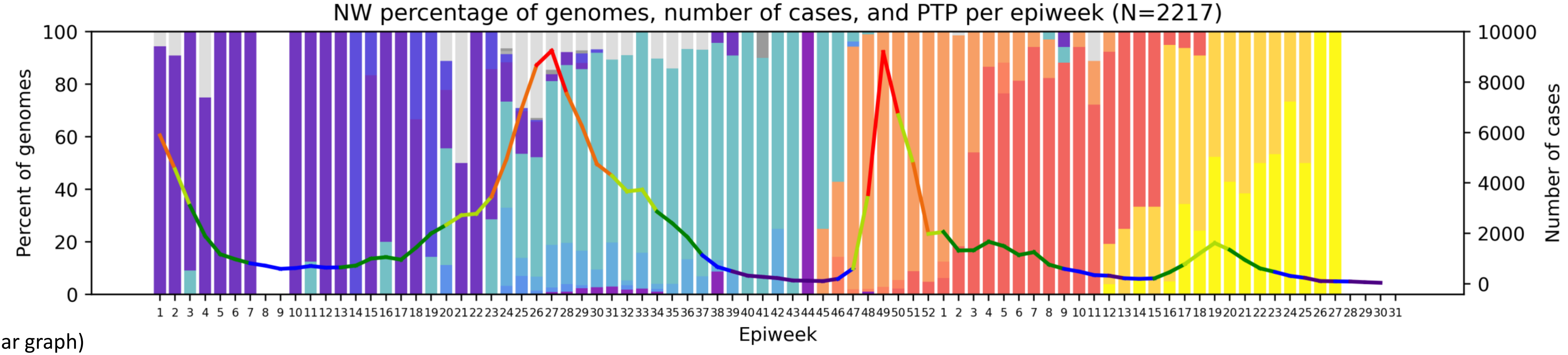
*May include genomes from 2020 which are not pictured here and are not included in the slide total.

North West Province, 2021-2022, n = 2217

Genomes added since last report: 36*


NW number of genomes, cases, and PTP per epiweek (N=2217)


NW percentage of genomes, number of cases, and PTP per epiweek (N=2217)

Clade key (bar graph)

- New1
- New2
- Omicron (21K/BA.1.*)
- Omicron (21L/BA.2.*)
- Omicron (22C/BA.2.12.1)
- Omicron (21M/BA.3)
- Omicron (22A/BA.4.*)
- Omicron (22B/BA.5.*)
- C.1.2 (20D)
- Beta (20H, V2)
- Alpha (20I, V1)
- Delta (21A)
- Delta (21I)
- Delta (21J)
- Kappa (21B)
- Eta (21D)
- 20D
- Cases
- 20C
- 20B
- 20A
- 19B
- 19A
- unassigned

Weekly percentage testing positive key (line graph)

- ≤ 5
- 6 - 10
- 11 - 20
- 21 - 30
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- 41 - 50
- 51 - 55

*May include genomes from 2020 which are not pictured here and are not included in the slide total.

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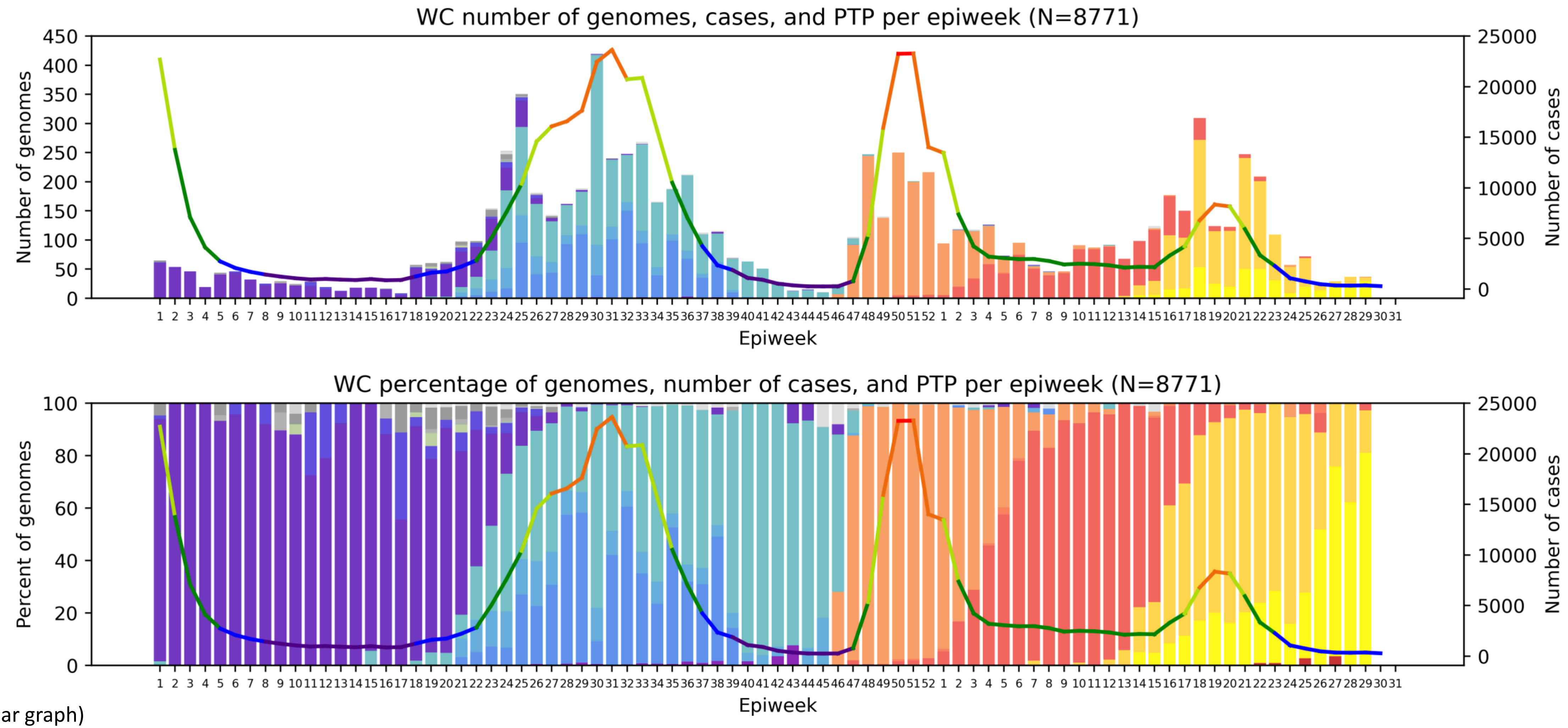
Western Cape Province, 2021-2022, n = 8771

Genomes added since last report: 0*



WC number of genomes, cases, and PTP per epiweek (N=8771)

WC percentage of genomes, number of cases, and PTP per epiweek (N=8771)

Clade key (bar graph)

- 🟩 New1
- 🟩 New2
- 🟧 Omicron (21K/BA.1.*)
- 🟥 Omicron (21L/BA.2.*)
- 🟥 Omicron (22C/BA.2.12.1)
- 🟧 Omicron (21M/BA.3)
- 🟨 Omicron (22A/BA.4.*)
- 🟨 Omicron (22B/BA.5.*)
- 🟪 C.1.2 (20D)
- 🟪 Beta (20H, V2)
- 🟦 Alpha (20I, V1)
- 🟦 Delta (21A)
- 🟦 Delta (21I)
- 🟦 Delta (21J)
- 🟩 Kappa (21B)
- 🟩 Eta (21D)
- ⬛ 20D
- — Cases
- ⬛ 20C
- ⬛ 20B
- ⬜ 20A
- ⬜ 19B
- ⬜ 19A
- ⬜ unassigned

Weekly percentage testing positive key (line graph)

- — ≤ 5
- — 6 - 10
- — 11 - 20
- — 21 - 30
- — 31 - 40
- — 41 - 50
- — 51 - 55

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Summary

- **Sequencing update**
  - All provinces have contributed sequences for April, May, and June. July sequences are from all provinces except LP and NC.
  - Omicron dominated in May (99.5%), June (98.5%) and July (98.9%). BA.4 and BA.5 together were dominant in May, June and July.
- **N=9 sequences with novel mutational profile**
  - One additional sequence has been detected (collection date 18th July 2022)
  - No recent sequences have been detected but NGS-SA teams are closely monitoring the data
- **Variant of Concern Omicron in South Africa**
  - Dominates 2022 sequencing data at >98% of genomes.
  - While BA.1 was the predominant lineage in January (55%), BA.2 dominated in February (86%) and March (78%).
  - Omicron lineages BA.4 and BA.5 increased in prevalence in March (16%), and together are dominant in April (73%), May (93%), June (92%) and July (94%).
  - BA.2.12.1 was detected in South Africa at low prevalence in May, June and July (<1%)
- Low frequency of previously circulating variants such as Delta still detected in recent data.

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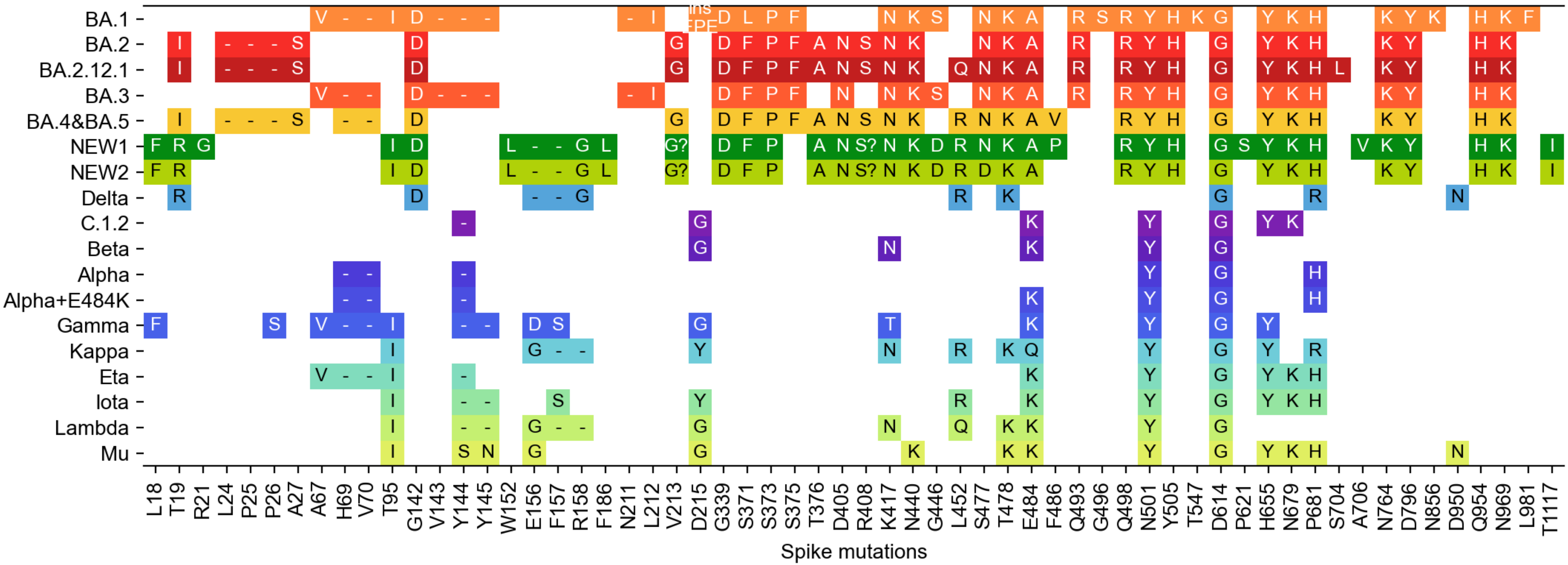
[1] https://github.com/cov-lineages/pango-designation/releases/tag/v1.3

Spike protein mutation* profile of Variants of Interest and Concern



	L18	T19	R21	L24	P25	P26	A27	A67	H69	V70	T95	G142	V143	Y144	Y145	W152	E156	F157	R158	F186	N211	L212	V213	D215	G339	S371	S373	S375	T376	D405
BA.1								V	-	-	I	D	-	-	-						-	I		ins EPE	D	L	P	F		
BA.2		I		-	-	-	S					D											G		D	F	P	F	A	N
BA.2.12.1		I		-	-	-	S					D											G		D	F	P	F	A	N
BA.3								V	-	-		D	-	-	-						-	I			D	F	P	F		N
BA.4&BA.5		I		-	-	-	S		-	-		D											G		D	F	P	F	A	N
NEW1	F	R	G								I	D				L	-	-	G	L			G?		D	F	P		A	N
NEW2	F	R									I	D				L	-	-	G	L			G?		D	F	P		A	N
Delta		R										D					-	-	G											
C.1.2														-										G						
Beta																								G						
Alpha									-	-				-																
Alpha+E484K									-	-				-																
Gamma	F					S		V	-	-	I			-	-		D	S						G						
Kappa											I						G	-	-					Y						
Eta								V	-	-	I			-																
Iota											I			-	-			S						Y						
Lambda											I			-	-		G	-	-					G						
Mu											I			S	N		G							G						

	R408	K417	N440	G446	L452	S477	T478	E484	F486	Q493	G496	Q498	N501	Y505	T547	D614	P621	H655	N679	P681	S704	A706	N764	D796	N856	D950	Q954	N969	L981	T1117
BA.1		N	K	S		N	K	A		R	S	R	Y	H	K	G		Y	K	H			K	Y	K		H	K	F	
BA.2	S	N	K			N	K	A		R		R	Y	H		G		Y	K	H			K	Y			H	K		
BA.2.12.1	S	N	K		Q	N	K	A		R		R	Y	H		G		Y	K	H	L		K	Y			H	K		
BA.3		N	K	S		N	K	A		R		R	Y	H		G		Y	K	H			K	Y			H	K		
BA.4&BA.5	S	N	K		R	N	K	A	V			R	Y	H		G		Y	K	H			K	Y			H	K		
NEW1	S?	N	K	D	R	N	K	A	P			R	Y	H		G	S	Y	K	H		V	K	Y			H	K		I
NEW2	S?	N	K	D	R	D	K	A				R	Y	H		G		Y	K	H			K	Y			H	K		I
Delta					R		K									G				R						N				
C.1.2								K					Y			G		Y	K											
Beta		N						K					Y			G														
Alpha													Y			G				H										
Alpha+E484K								K					Y			G				H										
Gamma		T						K					Y			G		Y												
Kappa		N			R		K	Q					Y			G		Y		R										
Eta								K					Y			G		Y	K	H										
Iota					R			K					Y			G		Y	K	H										
Lambda		N			Q		K	K					Y			G														
Mu			K				K	K					Y			G		Y	K	H						N				

Spike mutations

- 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, but may be linked to immune escape

*Only mutations present in Omicron, Delta, or the new SGTP sequences are pictured

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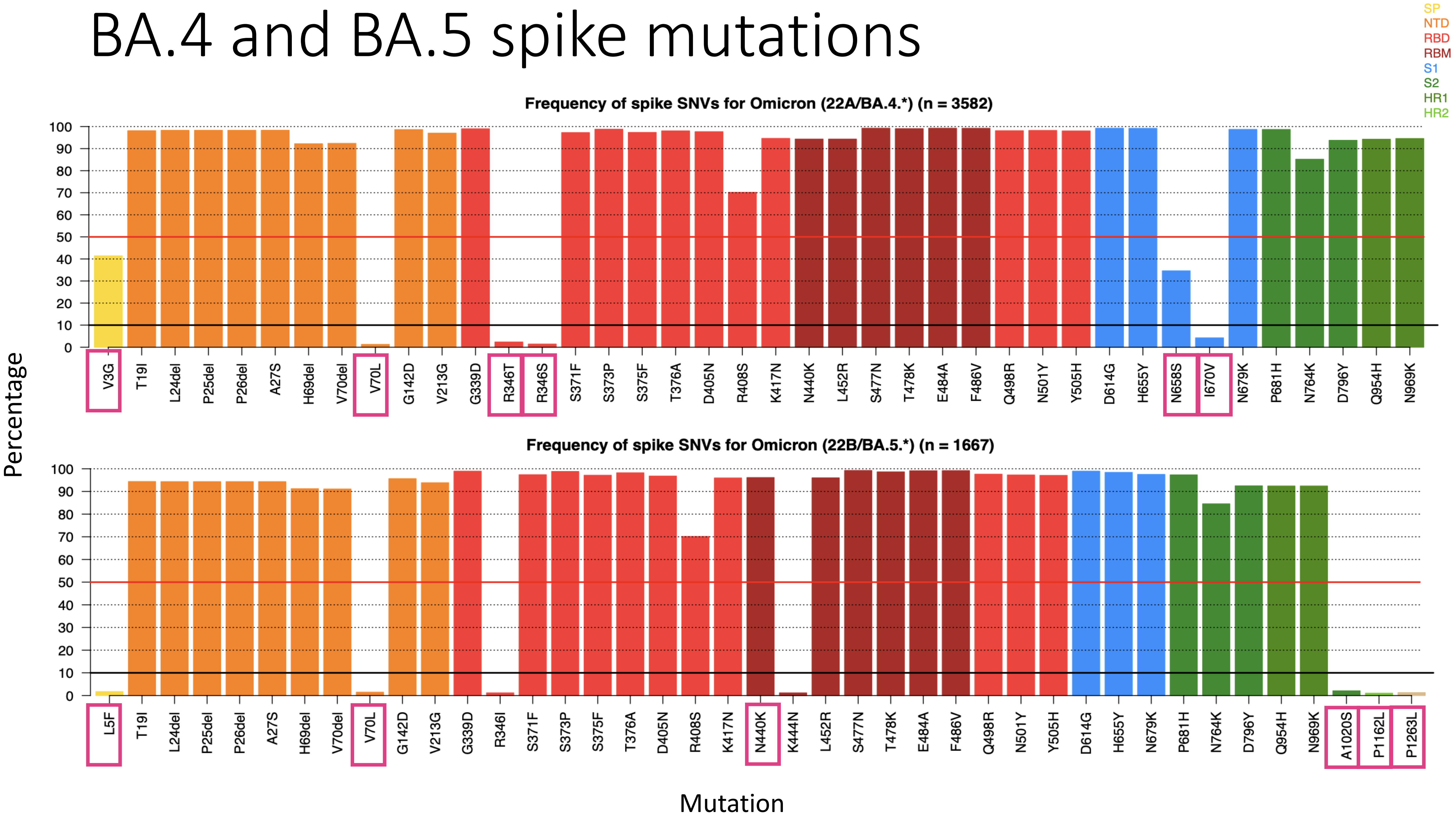
BA.4 and BA.5 spike mutations



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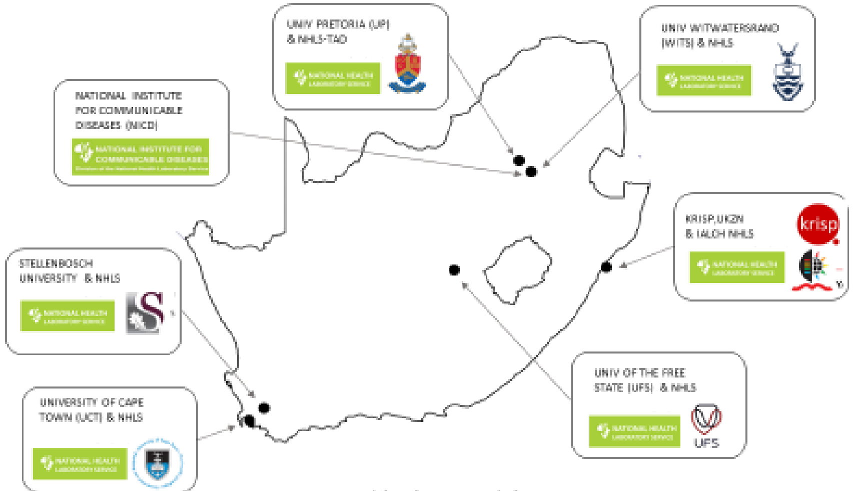

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EDCTP

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WITS
UNIVERSITY

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 & Western Cape Government

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

NHLS Greenpoint
Annabel Enoch

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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

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)
Carien van Niekerk

NHLS Tshwane
Prof Simnikiwe Mayaphi (HOD)

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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

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
Raquel Viana

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

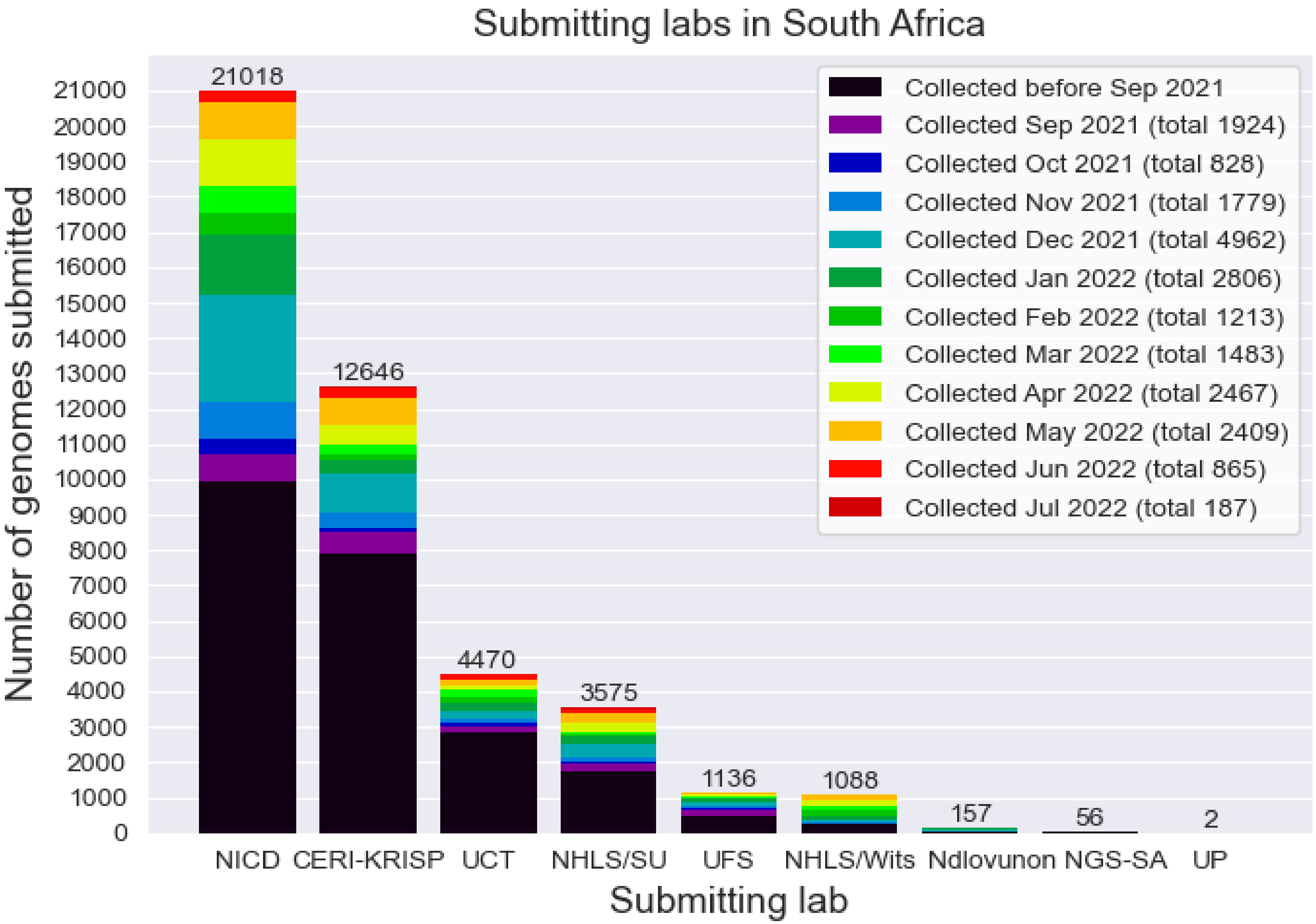
Africa CDC
John Nkengasong
Sofonias Tessema

Netcare:
Richard Friedland
Craig Murphy
Caroline Maslo
Liza Sitharam

DSI
Glaudina Loots

SA MRC
Glenda Gray

South African genomes submitted per submitting lab, 2020 - 2022 (N=44 148)



NGS-SA Labs

CERI: Centre for Epidemic Response and Innovation
KRISP: KZN Research Innovation and Sequencing Platform
NDLOVU: Ndlovu Research Laboratories
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 and collaborating public and private laboratories are contributing to sequencing, both as originating and as submitting (pictured here) laboratories.

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Currently circulating Variants of Concern (VOC)

WHO label	Pango lineage•	GISAID clade	Nextstrain clade	Additional amino acid changes monitored°	Earliest documented samples	Date of designation
Delta	B.1.617.2	G/478K.V1	21A, 21I, 21J	+S:K417N +S:K484K	India, Oct-2020	VOI: 4-Apr-2021 VOC: 11-May-2021
Omicron*	B.1.1.529	GR/484A	21K	+S:R346K	Multiple countries, Nov-2021	VUM: 24-Nov-2021 VOC: 26-Nov-2021

https://www.who.int/en/activities/tracking-SARS-CoV-2-variants/ accessed 18 March 2022

•Includes all descendant lineages. See the cov-lineages.org and the Pango network websites for further details.

° Only found in a subset of sequences

Previously circulating Variants of Concern

WHO label	**Pango lineage•**	**GISAID clade**	**Nextstrain clade**	**Earliest documented samples**	**Date of designation**
Alpha	B.1.1.7	GRY	20I (V1)	United Kingdom, Sep-2020	VOC: 18-Dec-2020 Previous VOC: 09-Mar-2022
Beta	B.1.351	GH/501Y.V2	20H (V2)	South Africa, May-2020	VOC: 18-Dec-2020 Previous VOC: 09-Mar-2022
Gamma	P.1	GR/501Y.V3	20J (V3)	Brazil, Nov-2020	VOC: 11-Jan-2021 Previous VOC: 09-Mar-2022

https://www.who.int/en/activities/tracking-SARS-CoV-2-variants/ accessed 18 March 2022

- Includes all descendant lineages. See the cov-lineages.org and the Pango network websites for further details.

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.)