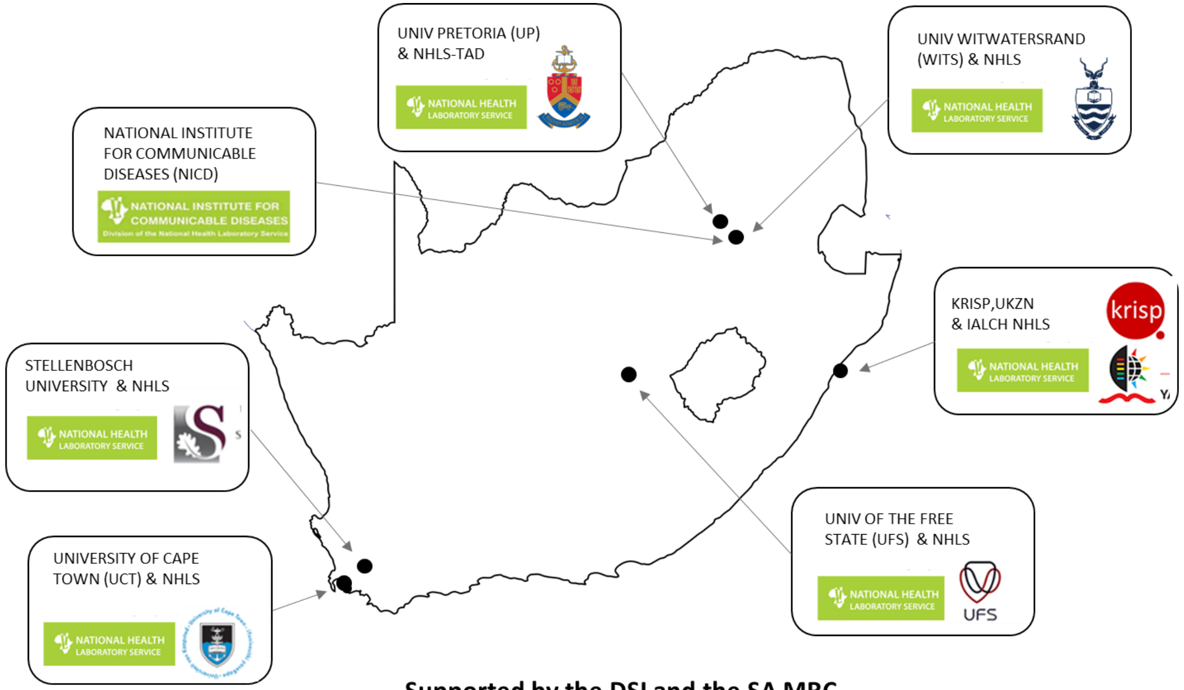
Network for Genomic Surveillance in South Africa (NGS-SA)

SARS-CoV-2 Sequencing Update
14 October 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)

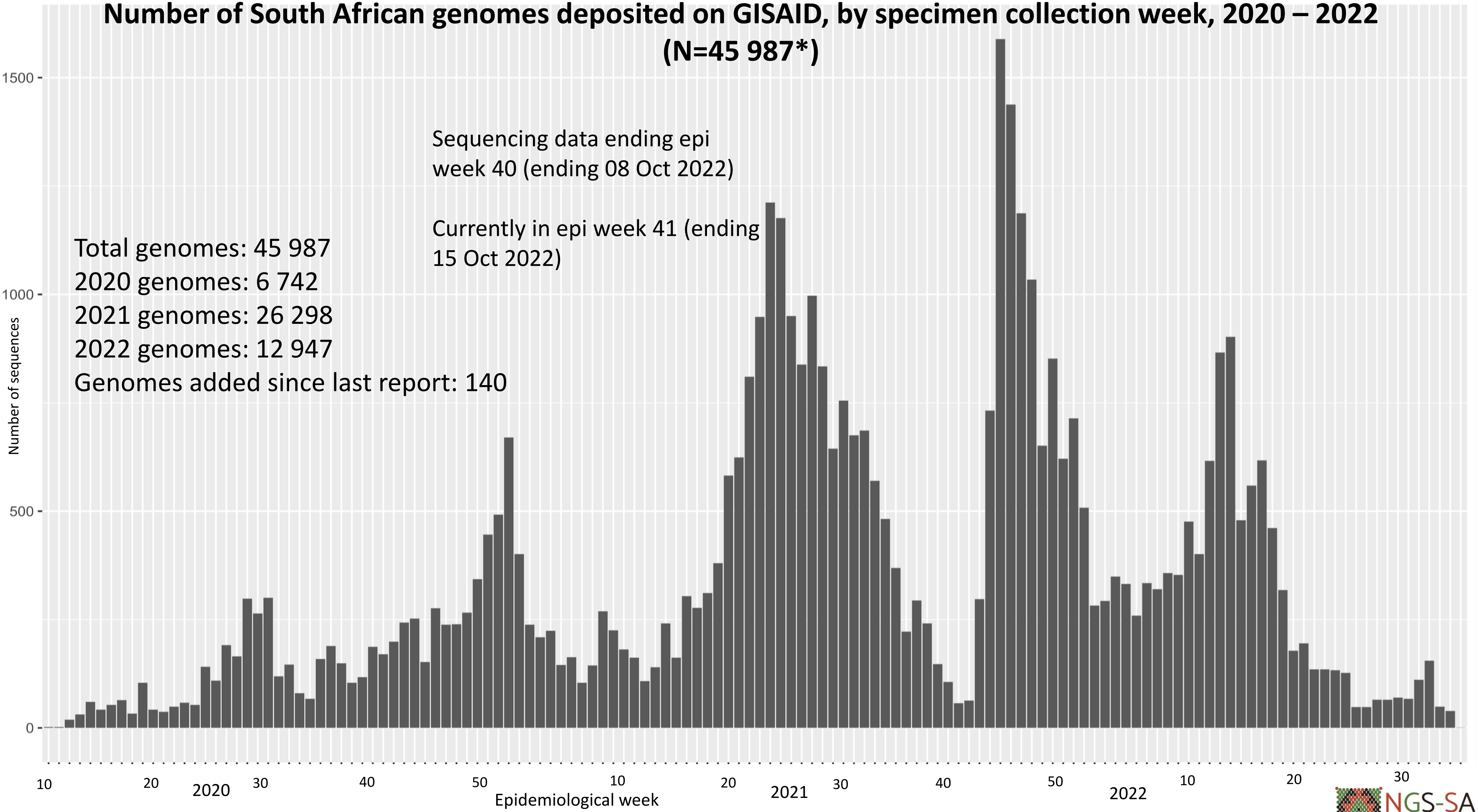
The genomic data presented here are based on South African SARS-CoV-2 sequence data downloaded from GISAID (www.gisaid.org) on 14 October 2022 at 09h30

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=45 987*)



Sequencing data ending epi week 40 (ending 08 Oct 2022)

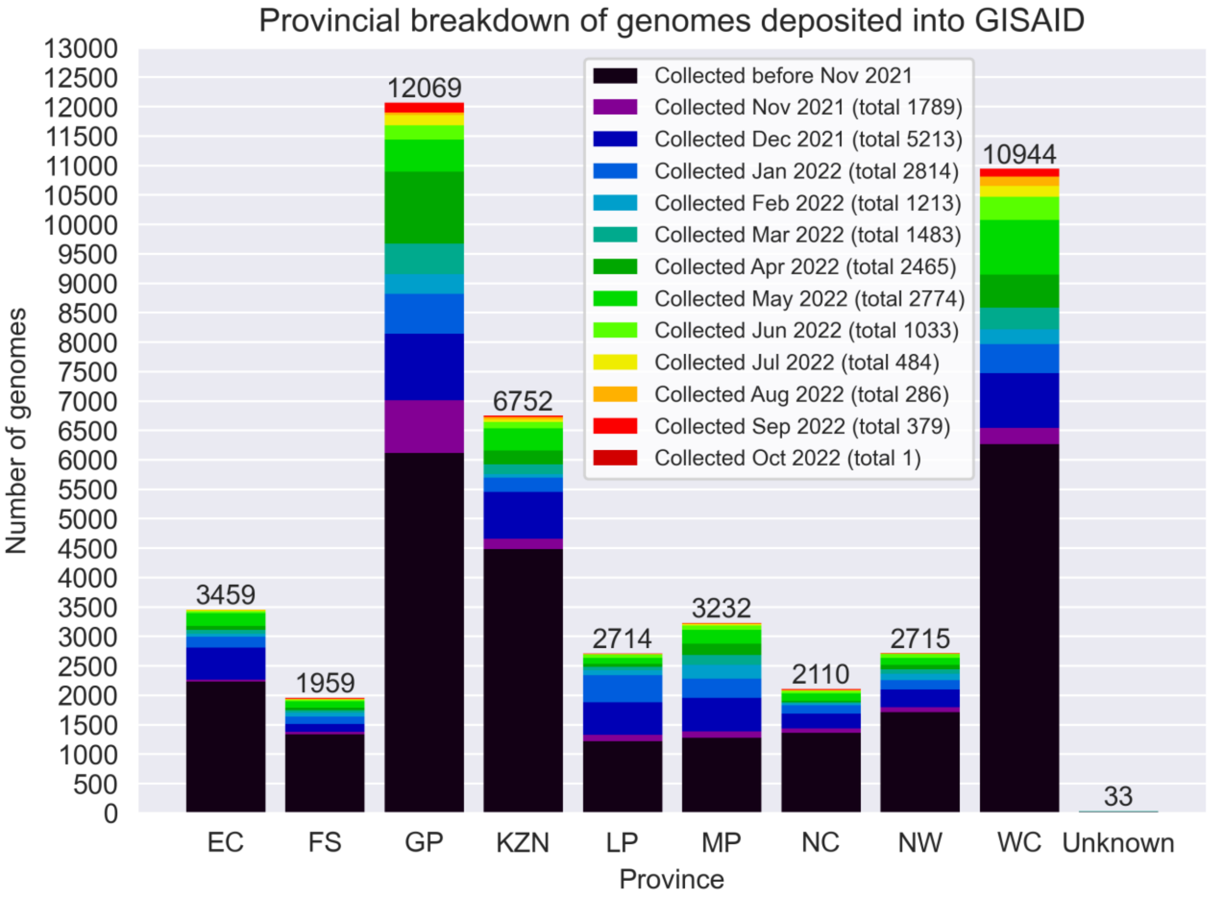
Currently in epi week 41 (ending 15 Oct 2022)

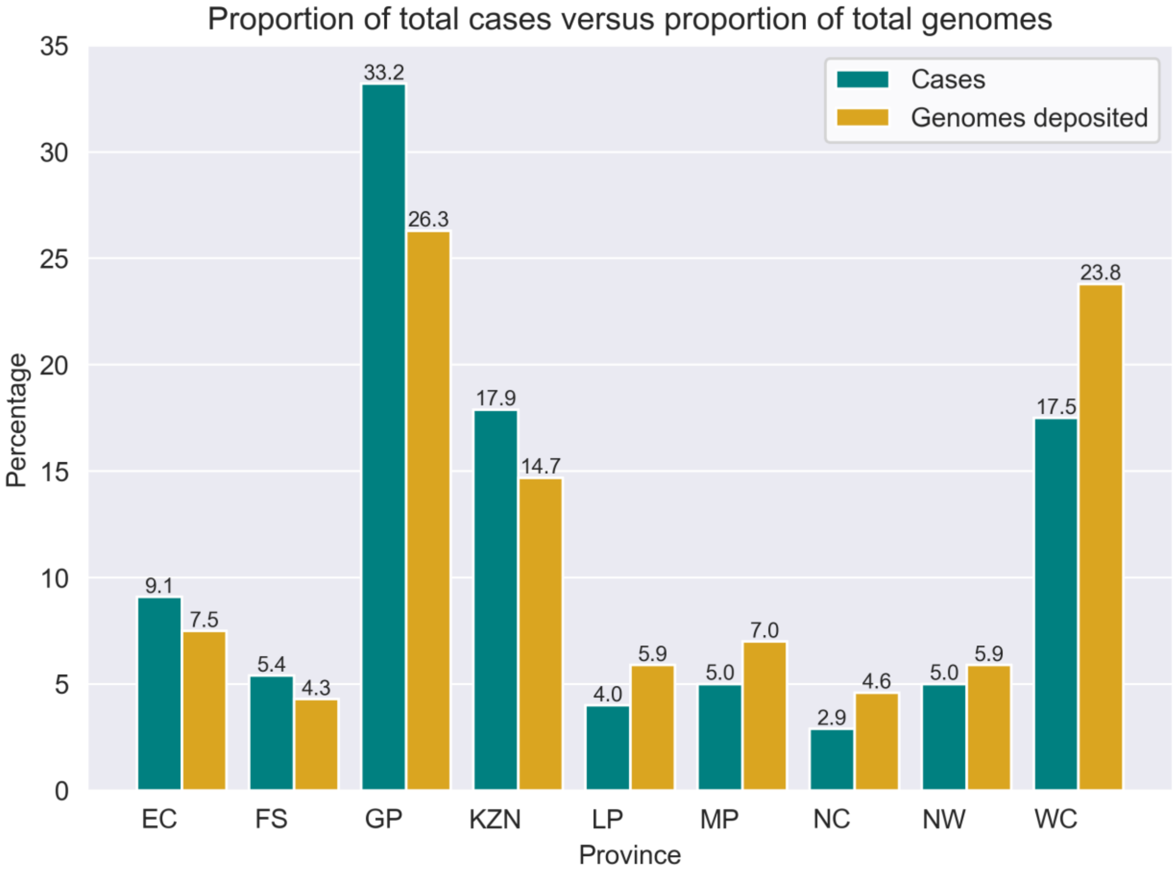
Total genomes: 45 987
2020 genomes: 6 742
2021 genomes: 26 298
2022 genomes: 12 947
Genomes added since last report: 140

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

NGS-SA
Network for Genomic Surveillance in South Africa

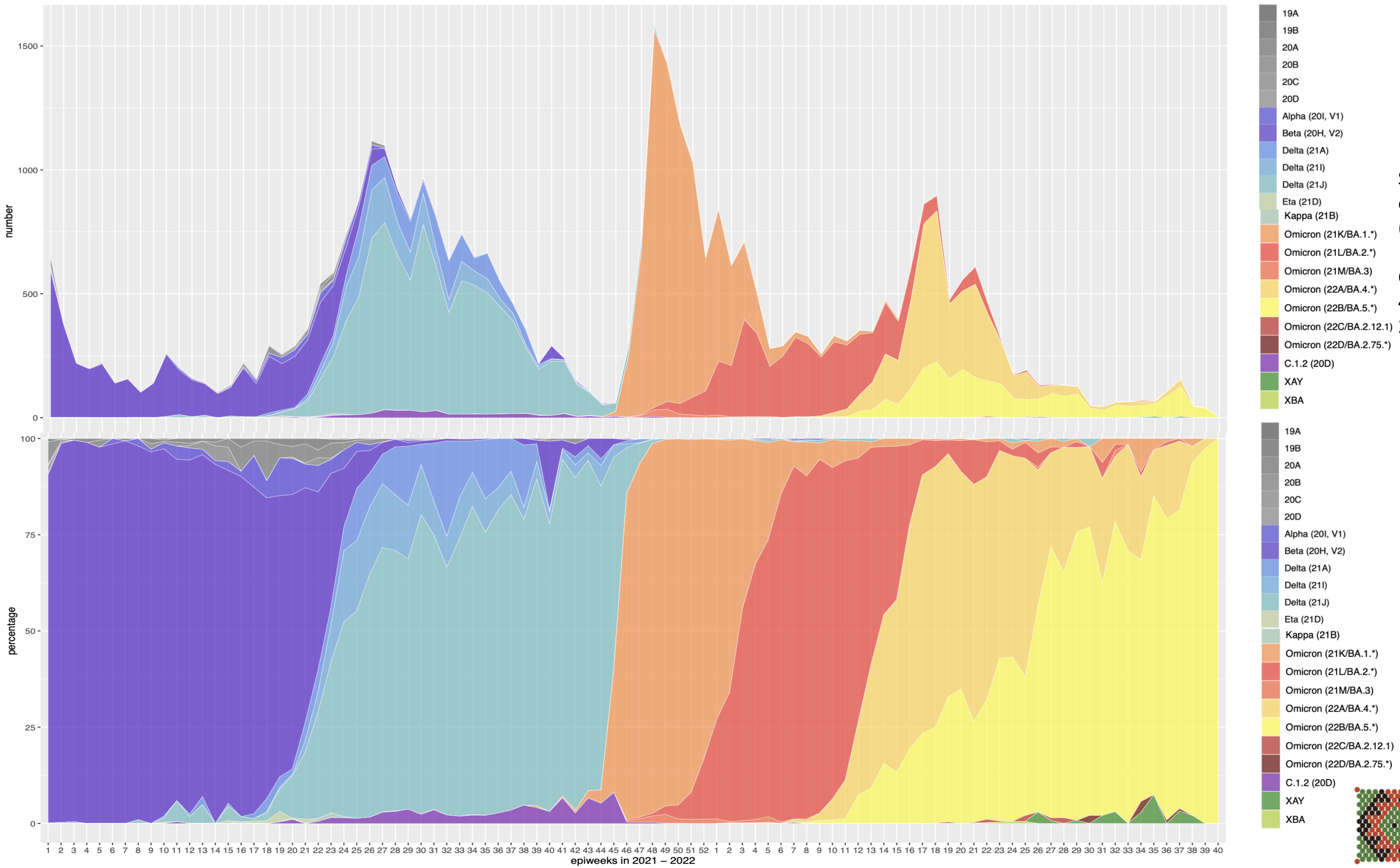
GISAID genomes vs total cases, 2020 – 2022 (N=45 987)





NGS-SA
Network for Genomic Surveillance in South Africa

Number and percentage of clades by epiweek in South Africa, 2021 – 2022 (39 158*)



Sequencing data ending epi week 40 (ending 08 Oct 2022)

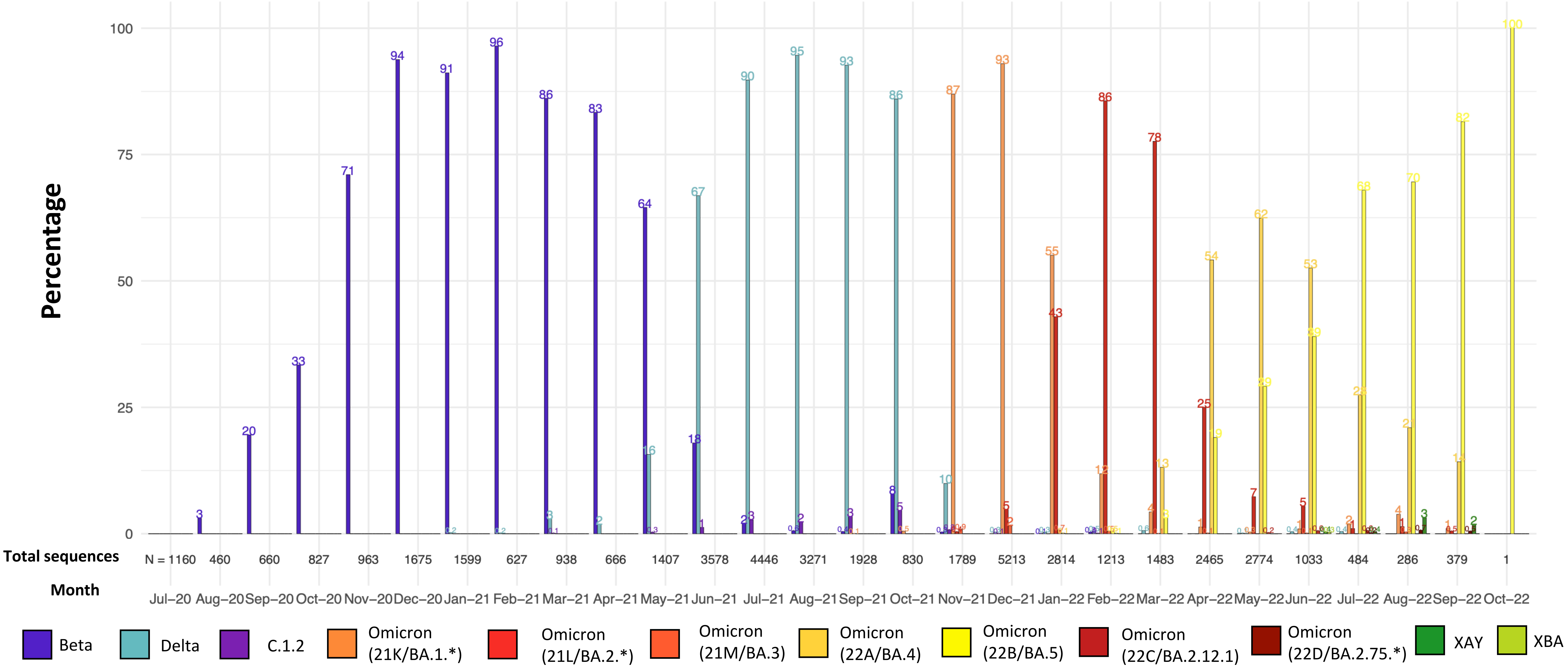
Currently in epi week 41 (ending 15 Oct 2022)

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

NGS-SA
Network for Genomic Surveillance in South Africa

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

Detection rates of variants being monitored in South Africa

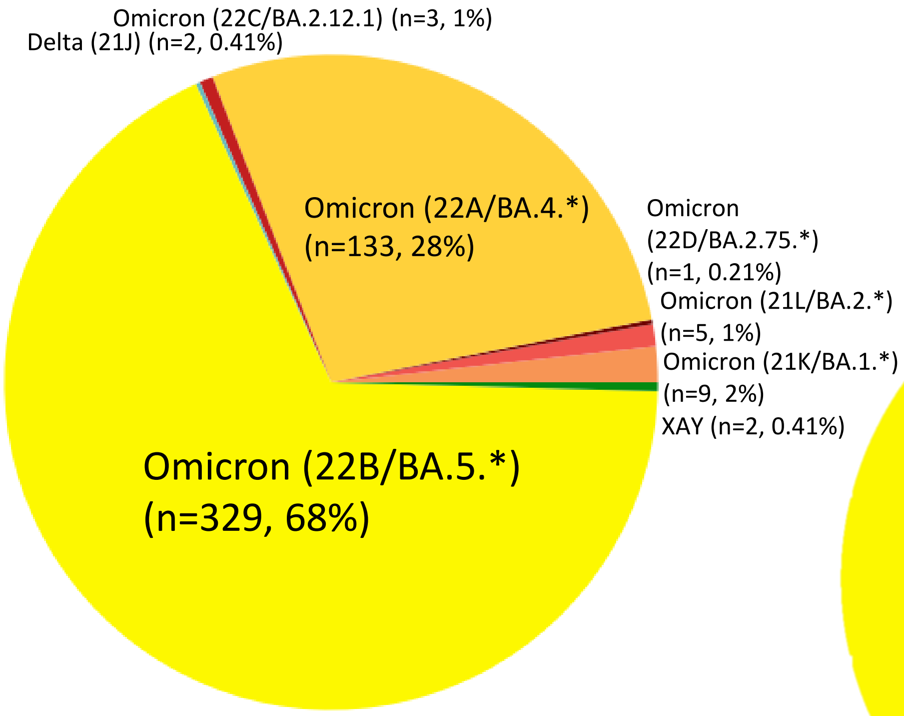


*Bars represent percentage prevalence of variant for the month; total number sequences collected for the month are given below the bar

NGS-SA
Network for Genomic Surveillance in South Africa

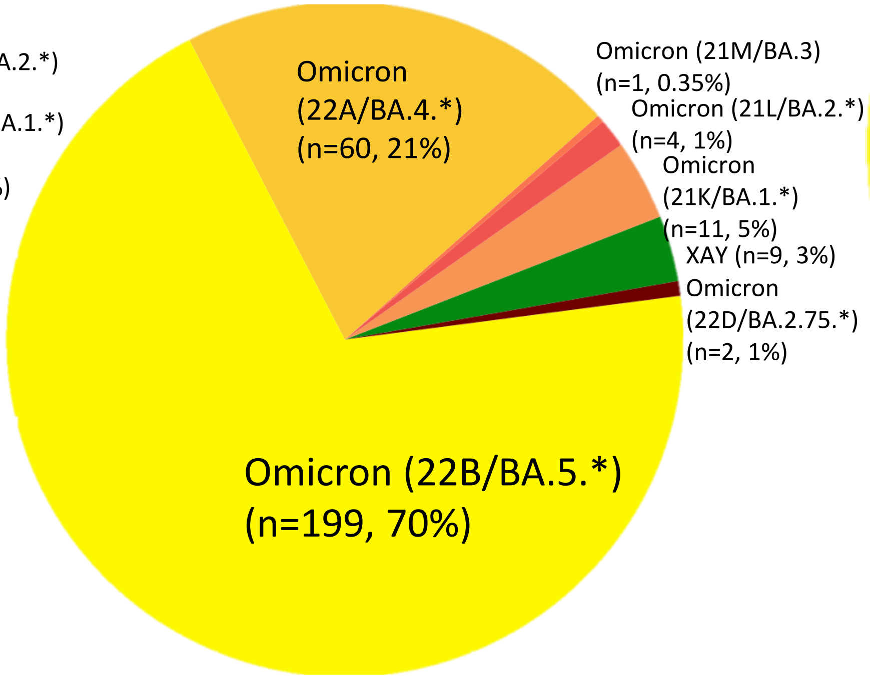
Prevalence of Variants of Concern (VOC) and Variants of Interest (VOI) in July – September 2022

July (N=484)



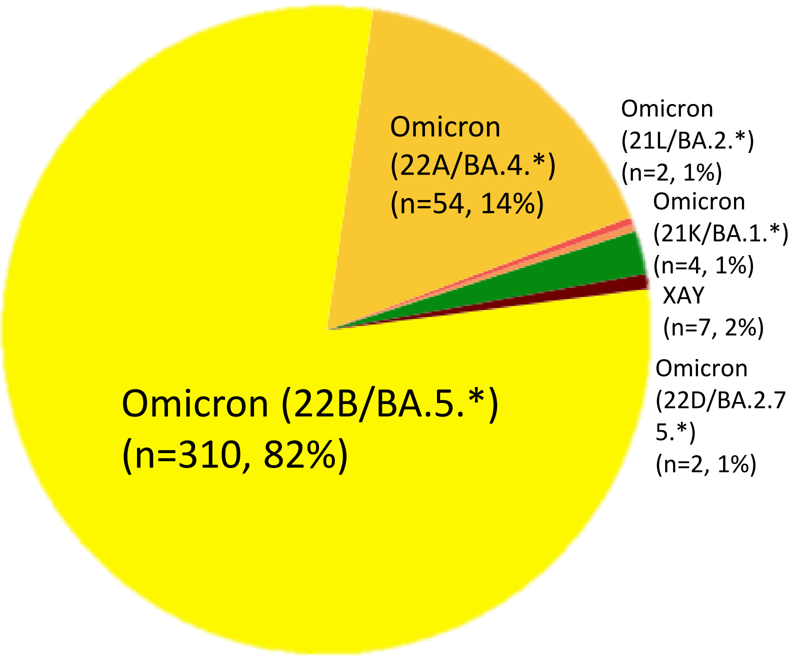
Total Omicron in July: 480 (99.2%)

August (N=286)



Total Omicron in August: 277 (96.9%)

September (N=379)

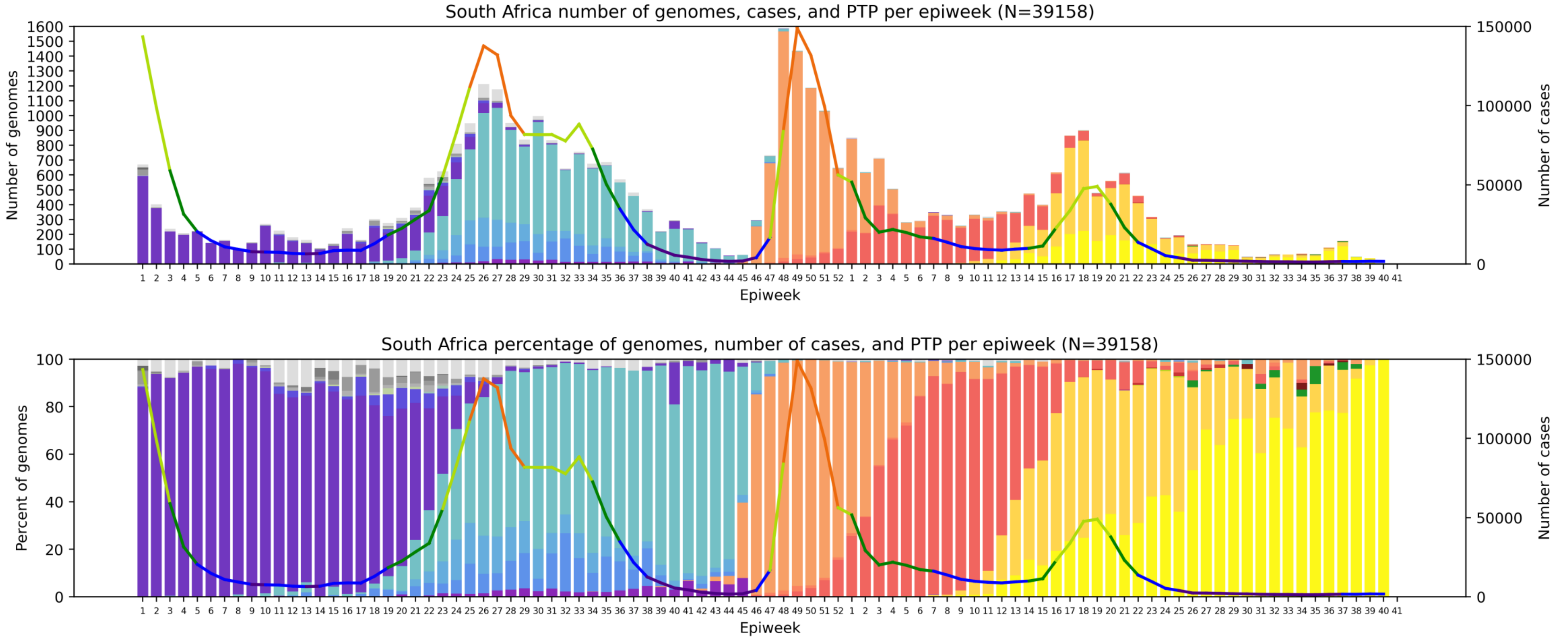


Total Omicron in September: 372 (98.2%)

XAY
XBA
Omicron (21K/BA.1.*)
Omicron (21L/BA.2.*)
Omicron (22C/BA.2.12.1)
Omicron (22D/BA.2.75)
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)
Other
unassigned

NGS-SA
Network for Genomic Surveillance in South Africa

South Africa, 2021-2022, n = 39 158*


South Africa number of genomes, cases, and PTP per epiweek (N=39158)

South Africa percentage of genomes, number of cases, and PTP per epiweek (N=39158)

Clade key (bar graph)

- 🟩 XAY
- 🟩 XBA
- 🟧 Omicron (21K/BA.1.*)
- 🟥 Omicron (21L/BA.2.*)
- 🟥 Omicron (22C/BA.2.12.1)
- 🟫 Omicron (22D/BA.2.75.*)
- 🟧 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
- ⬛ 20C
- — Cases
- ⬛ 20B
- ⬛ 20A
- ⬜ 19B
- ⬜ 19A
- ⬜ unassigned

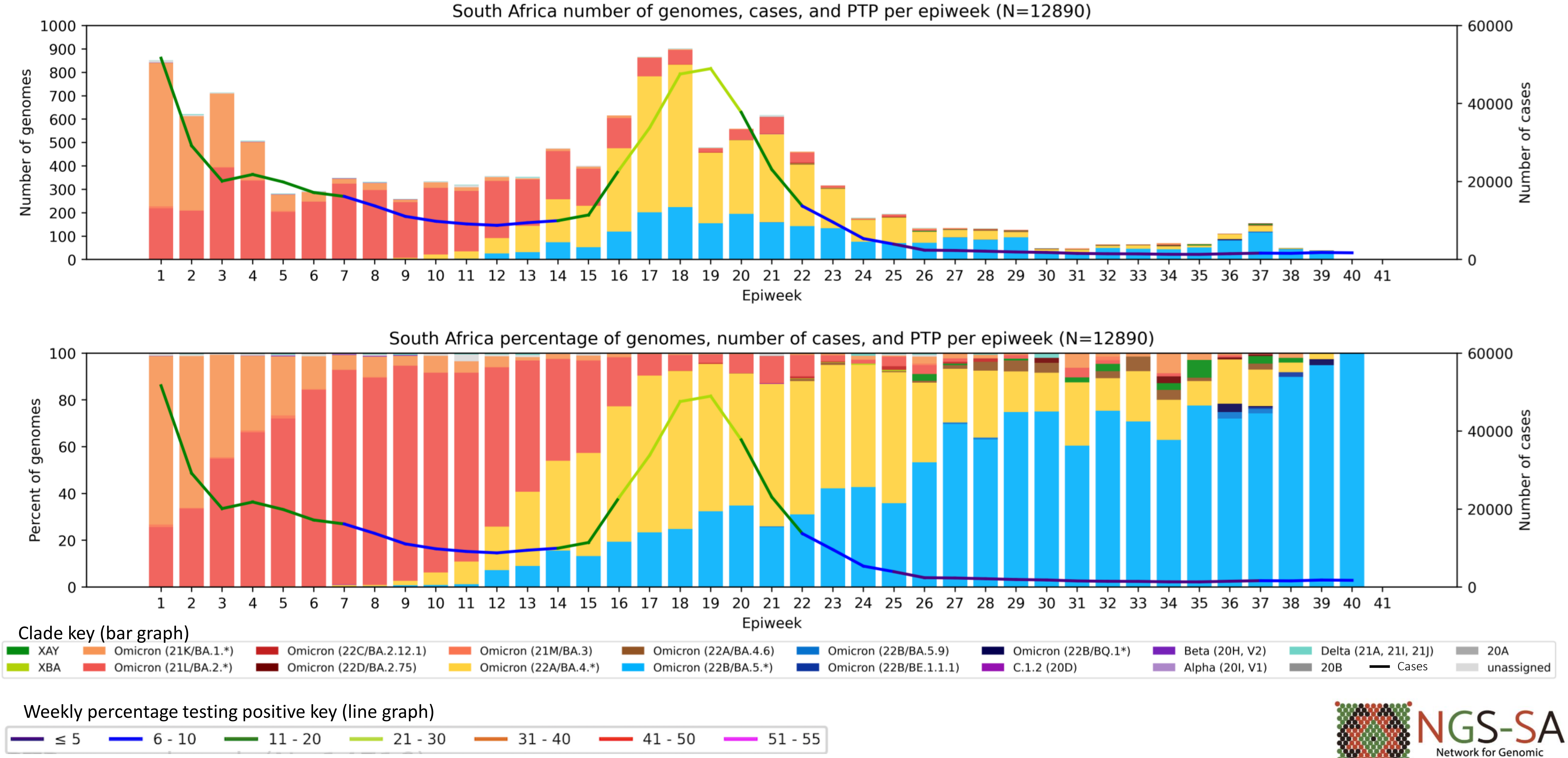
Weekly percentage testing positive key (line graph)

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

NGS-SA
Network for Genomic
Surveillance in South Africa

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

South Africa, 2022, n = 12 890*

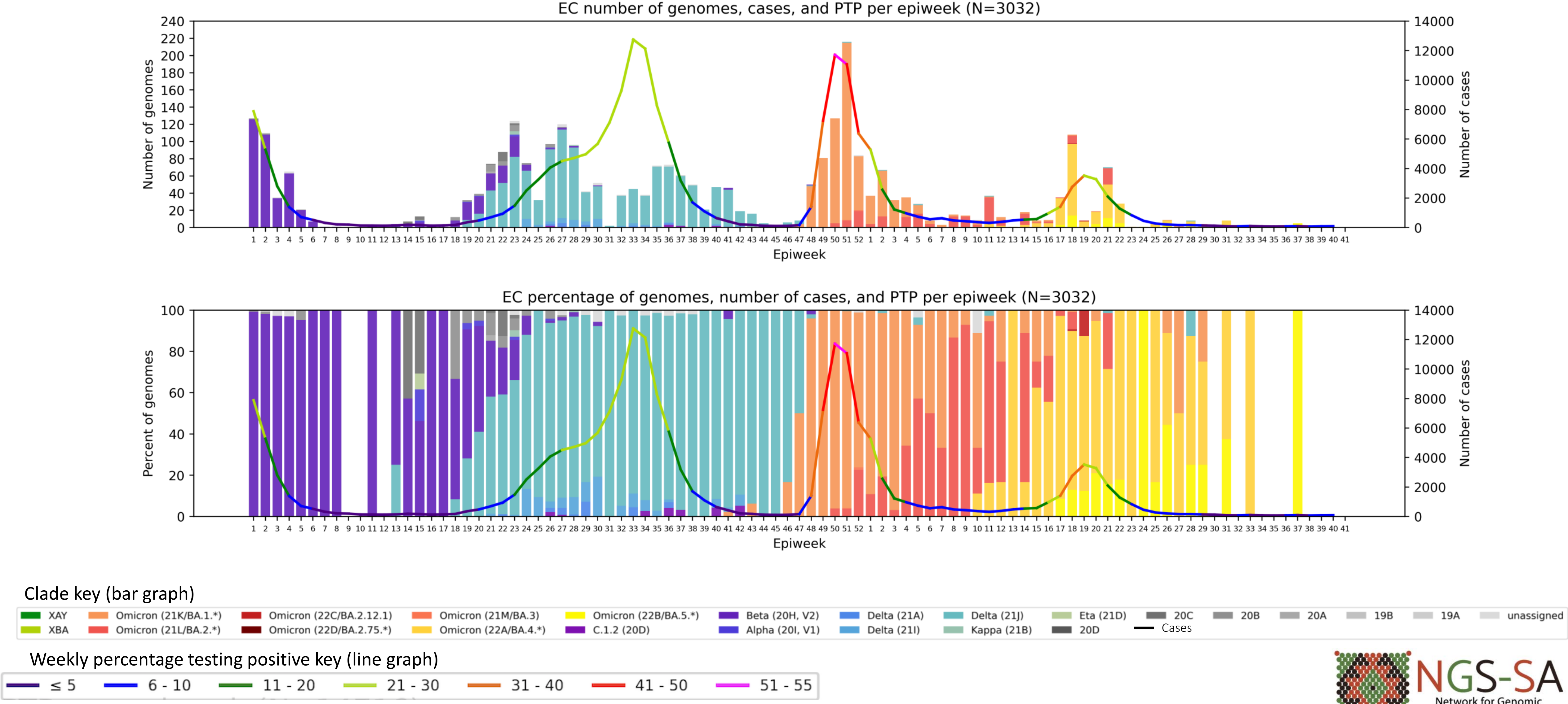


*Excludes sequences missing collection dates. Lineages of particular interest (currently WHO Omicron subvariants under monitoring) are separate from the main clade groupings.

NGS-SA
Network for Genomic Surveillance in South Africa

Eastern Cape Province, 2021-2022, n = 3032

Genomes added since last report: 3*



EC number of genomes, cases, and PTP per epiweek (N=3032)

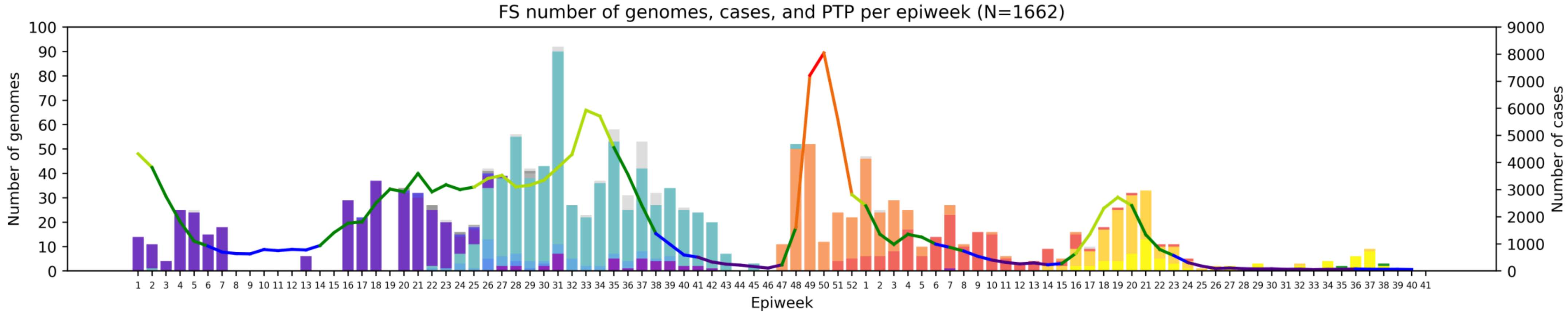
EC percentage of genomes, number of cases, and PTP per epiweek (N=3032)

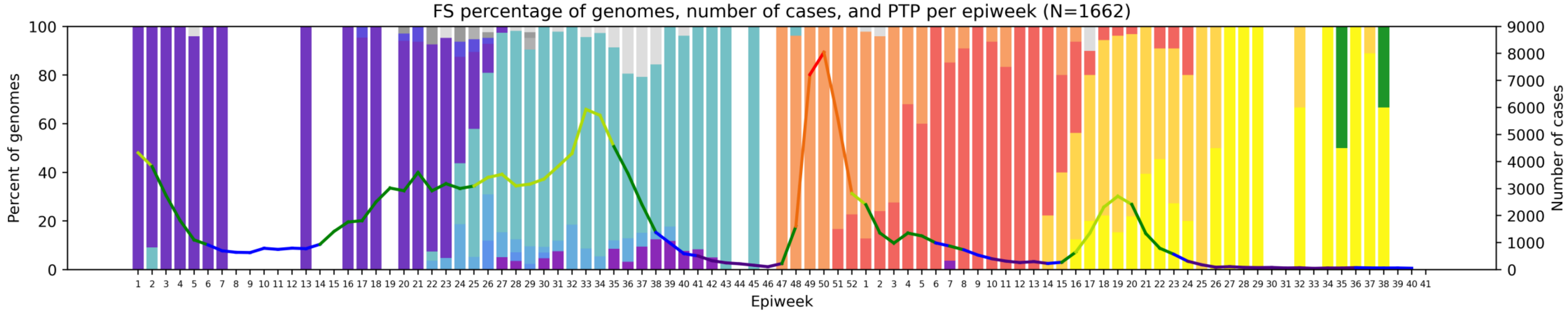
NGS-SA
Network for Genomic Surveillance in South Africa

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

Free State Province, 2021-2022, n = 1662

Genomes added since last report: 1*


FS number of genomes, cases, and PTP per epiweek (N=1662)


FS percentage of genomes, number of cases, and PTP per epiweek (N=1662)

Clade key (bar graph)

- 🟩 XAY
- 🟩 XBA
- 🟧 Omicron (21K/BA.1.*)
- 🟥 Omicron (21L/BA.2.*)
- 🟥 Omicron (22C/BA.2.12.1)
- 🟫 Omicron (22D/BA.2.75.*)
- 🟧 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
- ⬛ 20C
- ⬜ 20B
- ⬜ 20A
- ⬜ 19B
- ⬜ 19A
- ⬜ unassigned
- — Cases

Weekly percentage testing positive key (line graph)

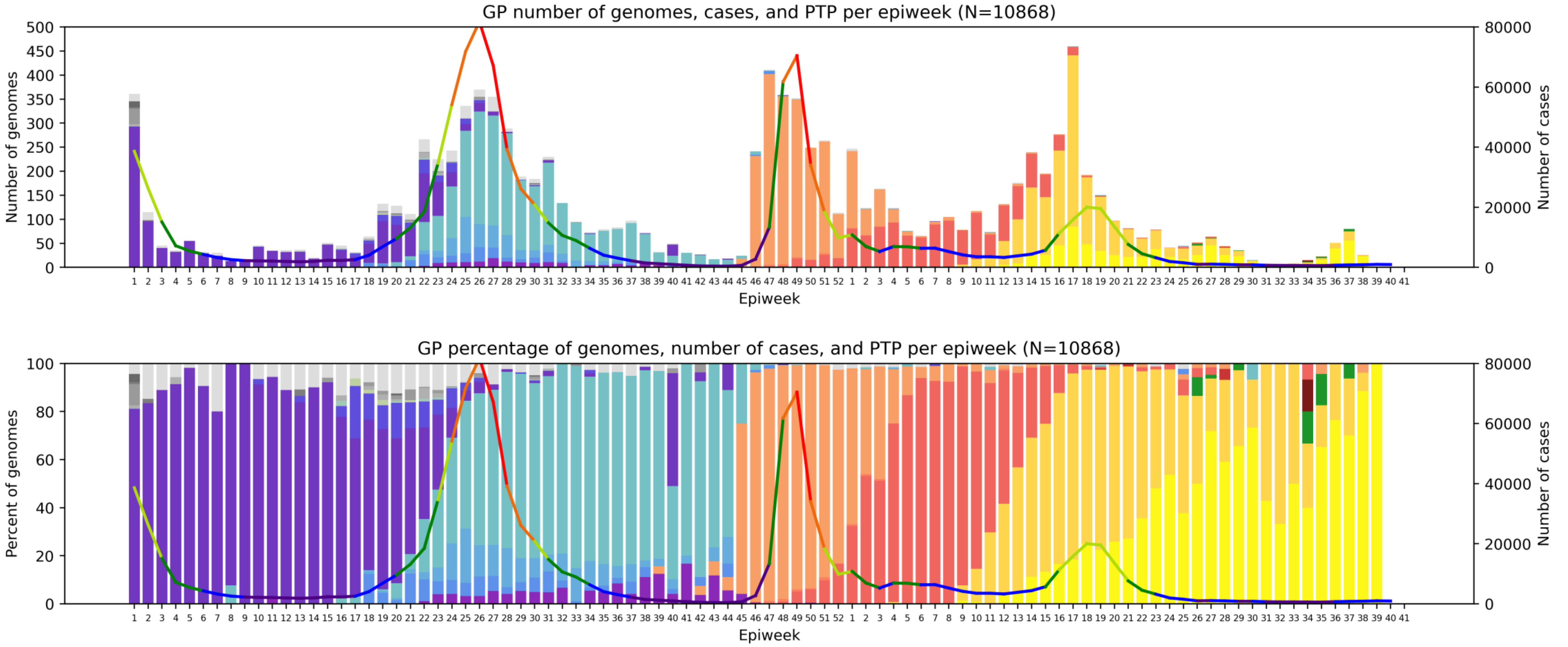
- — ≤ 5
- — 6 - 10
- — 11 - 20
- — 21 - 30
- — 31 - 40
- — 41 - 50
- — 51 - 55

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

NGS-SA
Network for Genomic Surveillance in South Africa

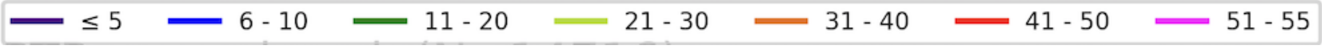
Gauteng Province, 2021-2022, n = 10 868

Genomes added since last report: 39*



Clade key (bar graph)

Weekly percentage testing positive key (line graph)

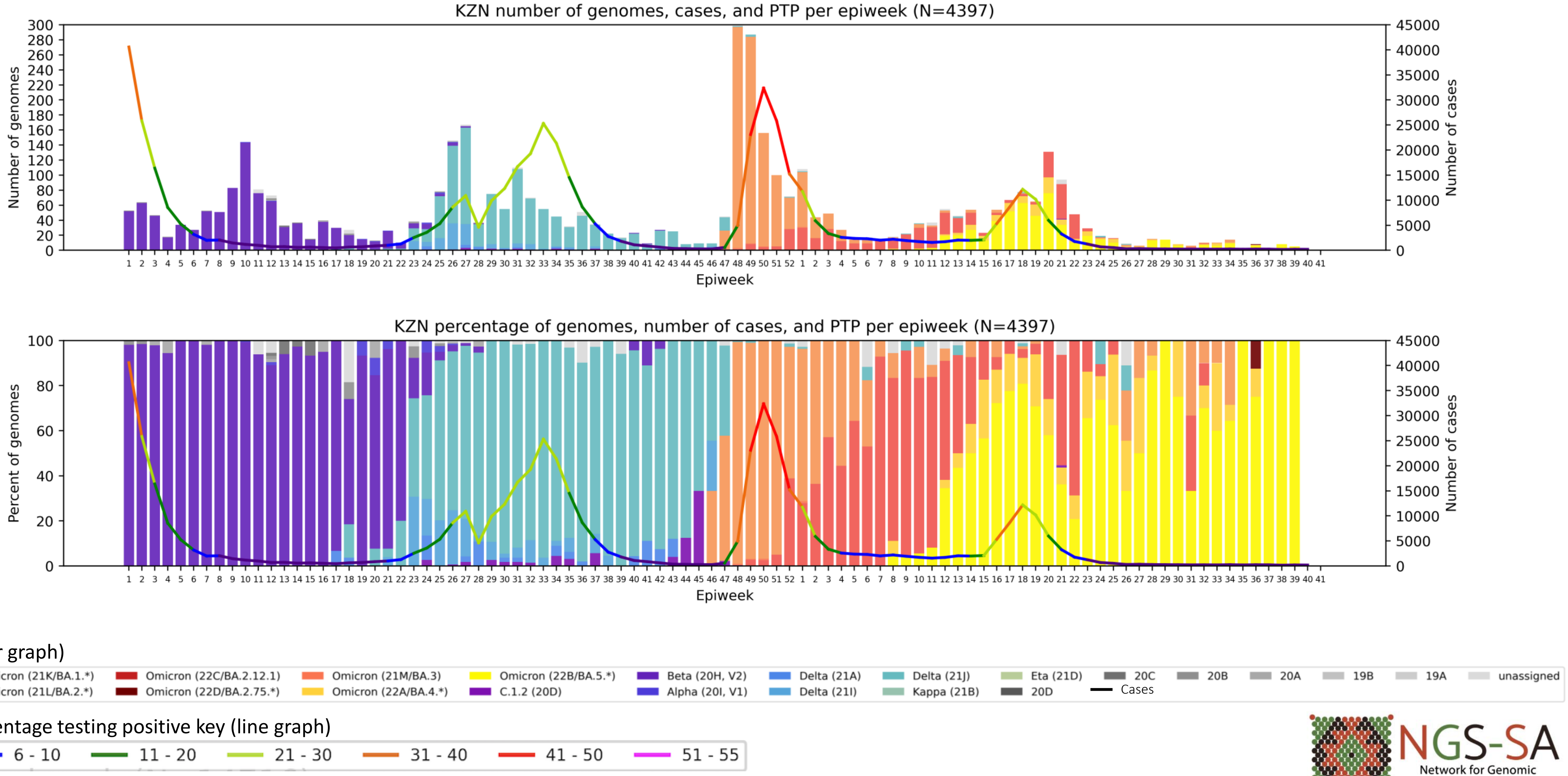


*May include genomes from 2020 which are not pictured here and are not included in the slide total.

NGS-SA
Network for Genomic
Surveillance in South Africa

KwaZulu-Natal Province, 2021-2022, n = 4397

Genomes added since last report: 20*

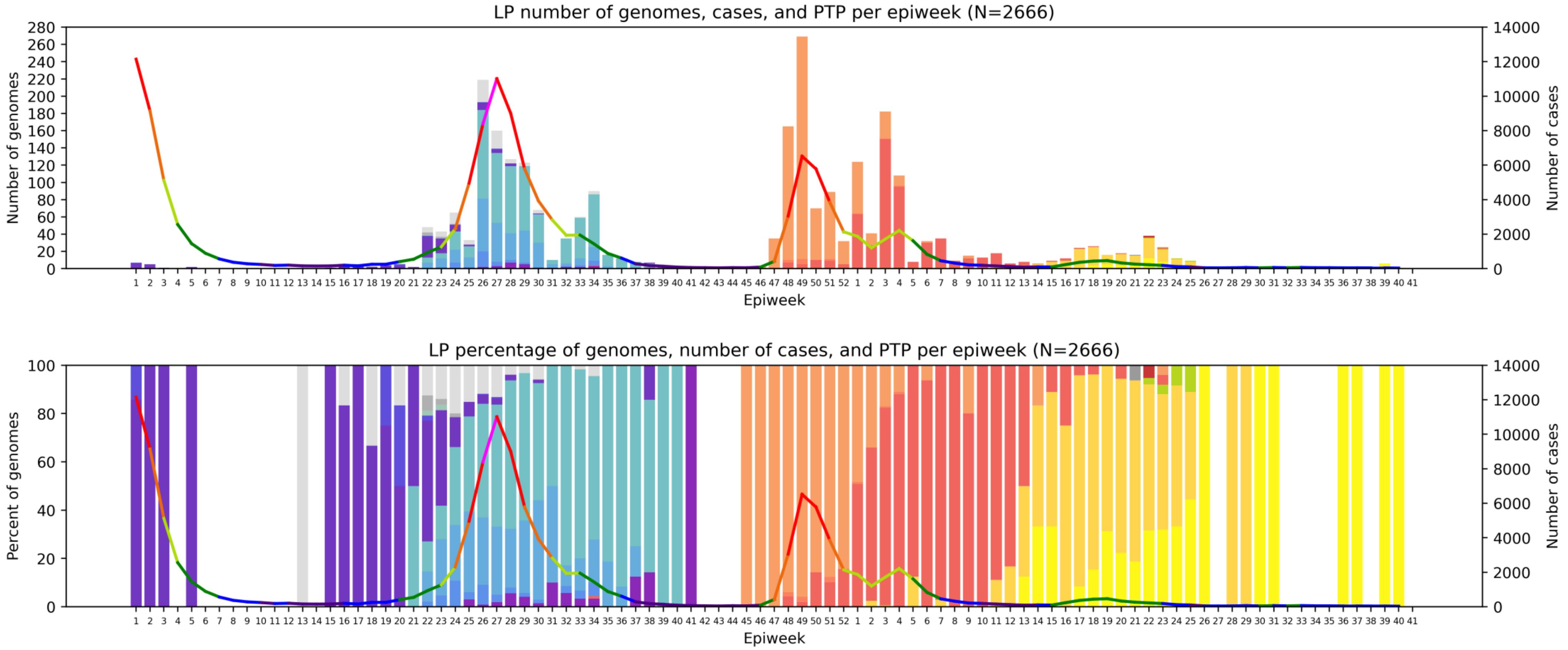


NGS-SA
Network for Genomic Surveillance in South Africa

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

Limpopo Province, 2021-2022, n = 2666

Genomes added since last report: 11*



LP number of genomes, cases, and PTP per epiweek (N=2666)

LP percentage of genomes, number of cases, and PTP per epiweek (N=2666)

Clade key (bar graph)

- 🟩 XAY
- 🟩 XBA
- 🟧 Omicron (21K/BA.1.*)
- 🟥 Omicron (21L/BA.2.*)
- 🟥 Omicron (22C/BA.2.12.1)
- 🟥 Omicron (22D/BA.2.75.*)
- 🟧 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
- ⬛ 20C
- ⬛ 20B
- ⬛ 20A
- ⬜ 19B
- ⬜ 19A
- ⬜ unassigned
- — Cases

Weekly percentage testing positive key (line graph)

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

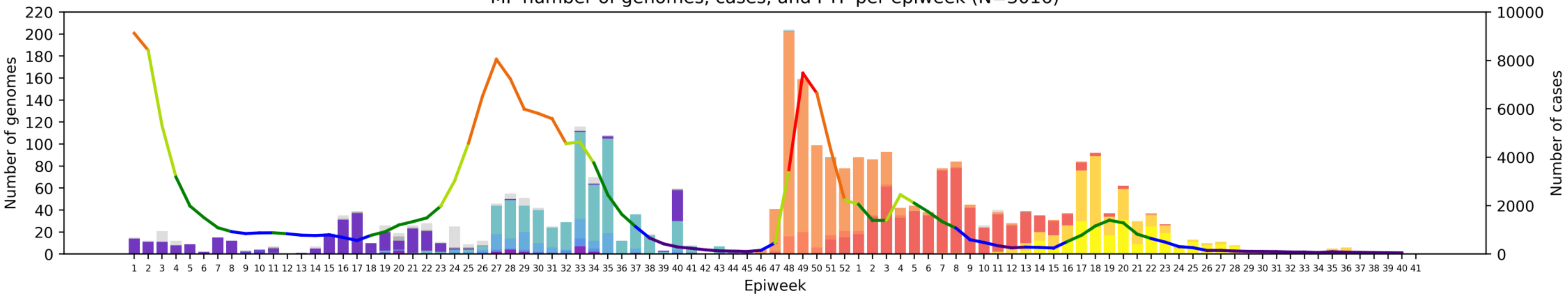
NGS-SA
Network for Genomic
Surveillance in South Africa

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

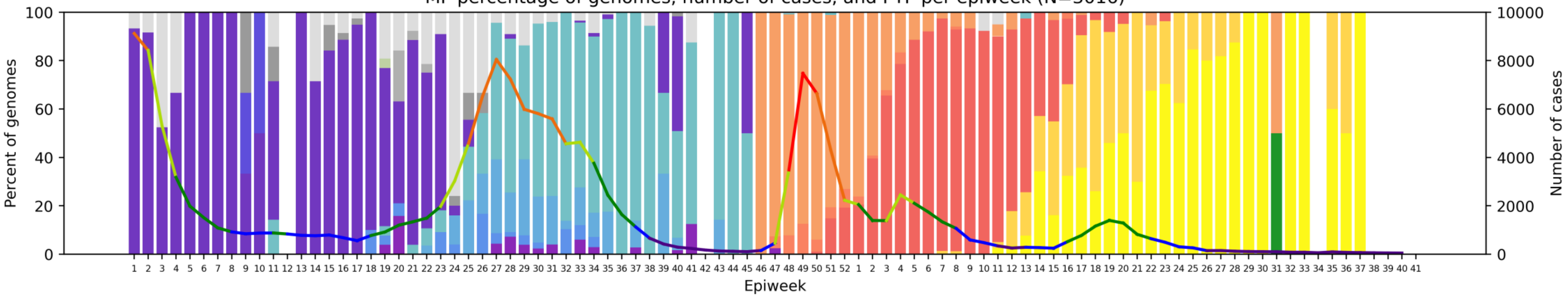
Mpumalanga Province, 2021-2022, n = 3016

Genomes added since last report: 1*

MP number of genomes, cases, and PTP per epiweek (N=3016)



MP percentage of genomes, number of cases, and PTP per epiweek (N=3016)



Clade key (bar graph)

- 🟩 XAY
- 🟩 XBA
- 🟧 Omicron (21K/BA.1.*)
- 🟥 Omicron (21L/BA.2.*)
- 🟥 Omicron (22C/BA.2.12.1)
- 🟥 Omicron (22D/BA.2.75.*)
- 🟧 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
- ⬛ 20C
- ⬛ 20B
- ⬛ 20A
- ⬜ 19B
- ⬜ 19A
- ⬜ unassigned
- — Cases

Weekly percentage testing positive key (line graph)

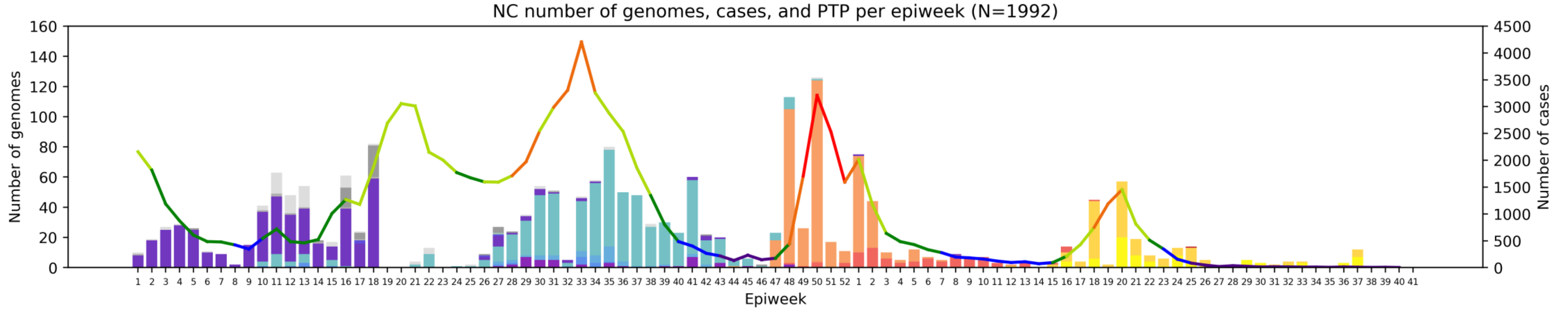
- — ≤ 5
- — 6 - 10
- — 11 - 20
- — 21 - 30
- — 31 - 40
- — 41 - 50
- — 51 - 55

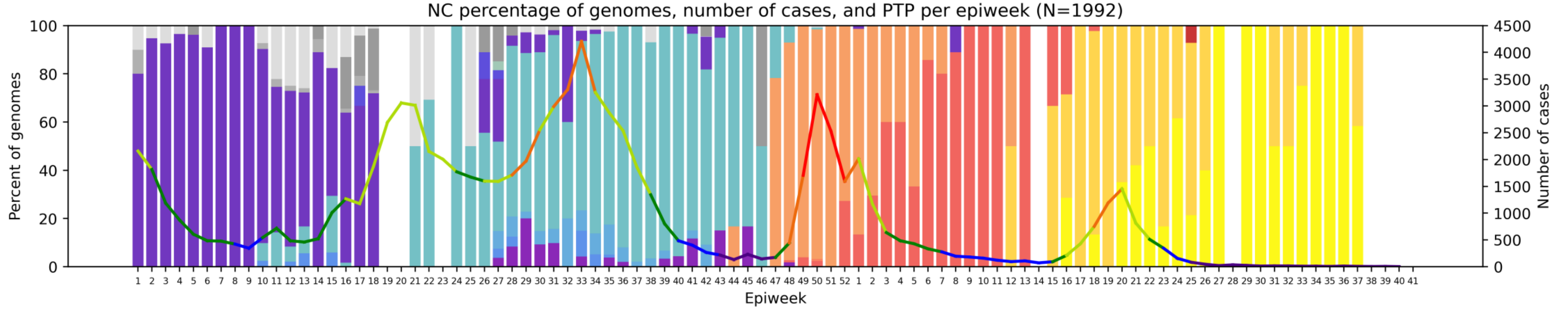
NGS-SA
Network for Genomic Surveillance in South Africa

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

Northern Cape Province, 2021-2022, n = 1992

Genomes added since last report: 0*





Clade key (bar graph)

- 🟩 XAY
- 🟩 XBA
- 🟧 Omicron (21K/BA.1.*)
- 🟥 Omicron (21L/BA.2.*)
- 🟥 Omicron (22C/BA.2.12.1)
- 🟫 Omicron (22D/BA.2.75.*)
- 🟧 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
- ⬛ 20C
- ⬛ 20B
- ⬜ 20A
- ⬜ 19B
- ⬜ 19A
- ⬜ unassigned
- — Cases

Weekly percentage testing positive key (line graph)

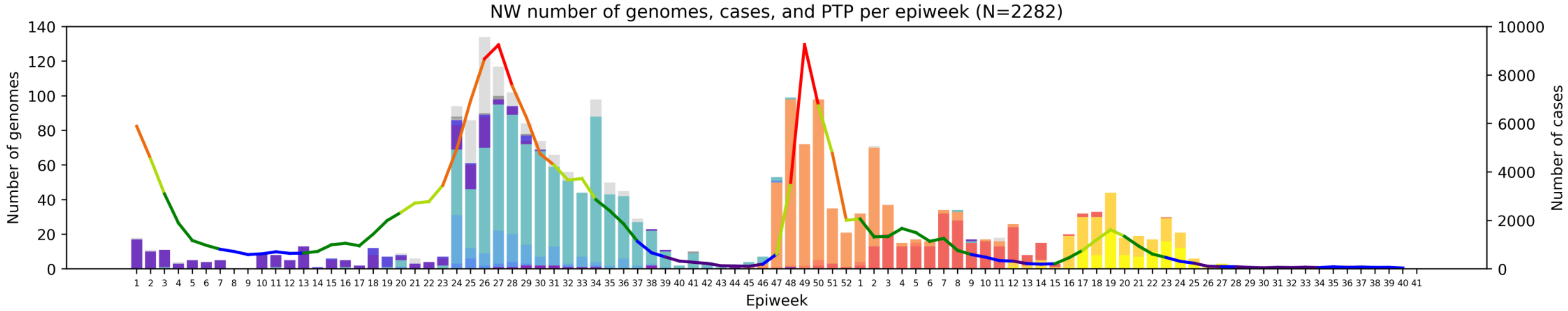
- — ≤ 5
- — 6 - 10
- — 11 - 20
- — 21 - 30
- — 31 - 40
- — 41 - 50
- — 51 - 55

NGS-SA
Network for Genomic
Surveillance in South Africa

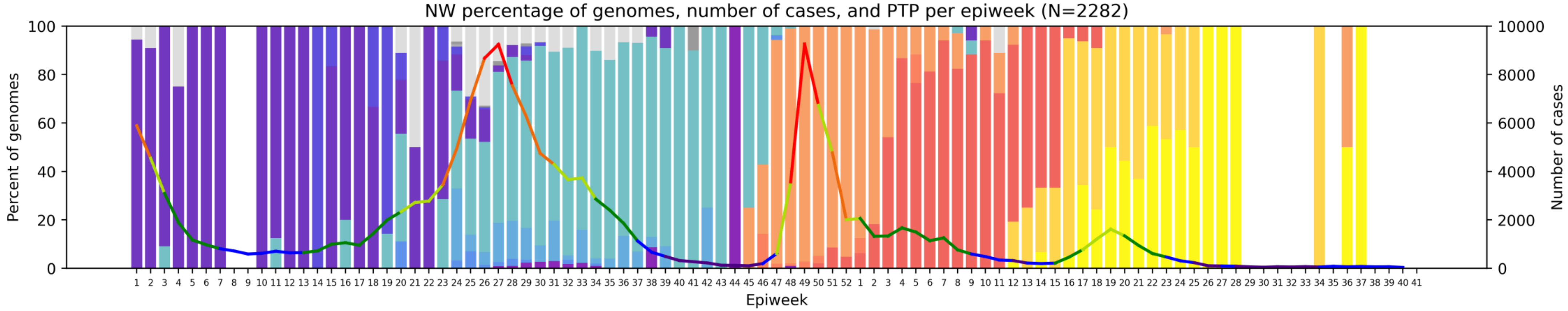
*May include genomes from 2020 which are not pictured here and are not included in the slide total.

North West Province, 2021-2022, n = 2282

Genomes added since last report: 10*



NW number of genomes, cases, and PTP per epiweek (N=2282)



NW percentage of genomes, number of cases, and PTP per epiweek (N=2282)

Clade key (bar graph)

■ XAY
■ XBA
■ Omicron (21K/BA.1.*)
■ Omicron (21L/BA.2.*)
■ Omicron (22C/BA.2.12.1)
■ Omicron (22D/BA.2.75.*)
■ 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
■ 20C
— Cases
■ 20B
■ 20A
■ 19B
■ 19A
■ unassigned

Weekly percentage testing positive key (line graph)

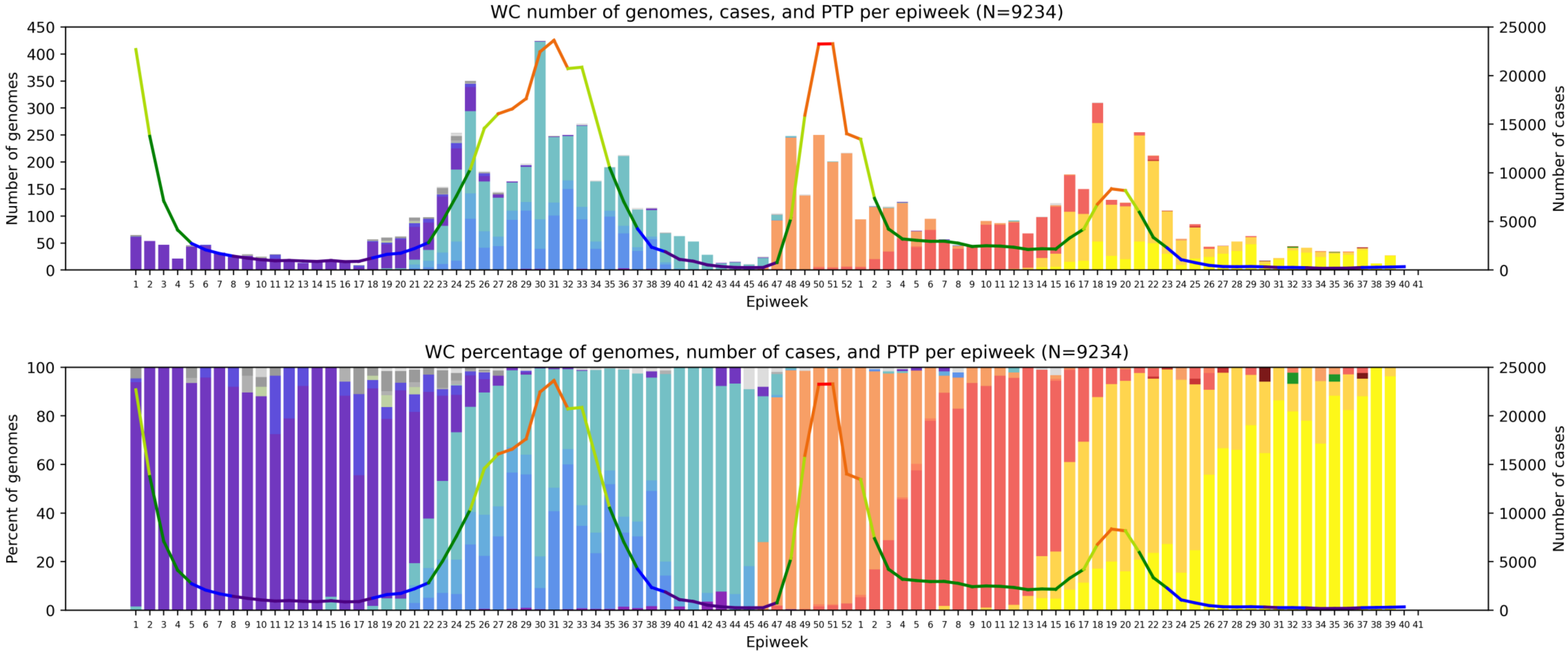
— ≤ 5
— 6 - 10
— 11 - 20
— 21 - 30
— 31 - 40
— 41 - 50
— 51 - 55

NGS-SA
Network for Genomic Surveillance in South Africa

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

Western Cape Province, 2021-2022, n = 9234

Genomes added since last report: 55*



Clade key (bar graph)

- XAY
- XBA
- Omicron (21K/BA.1.*)
- Omicron (21L/BA.2.*)
- Omicron (22C/BA.2.12.1)
- Omicron (22D/BA.2.75.*)
- 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
- 20C
- Cases
- 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

NGS-SA
Network for Genomic
Surveillance in South Africa

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

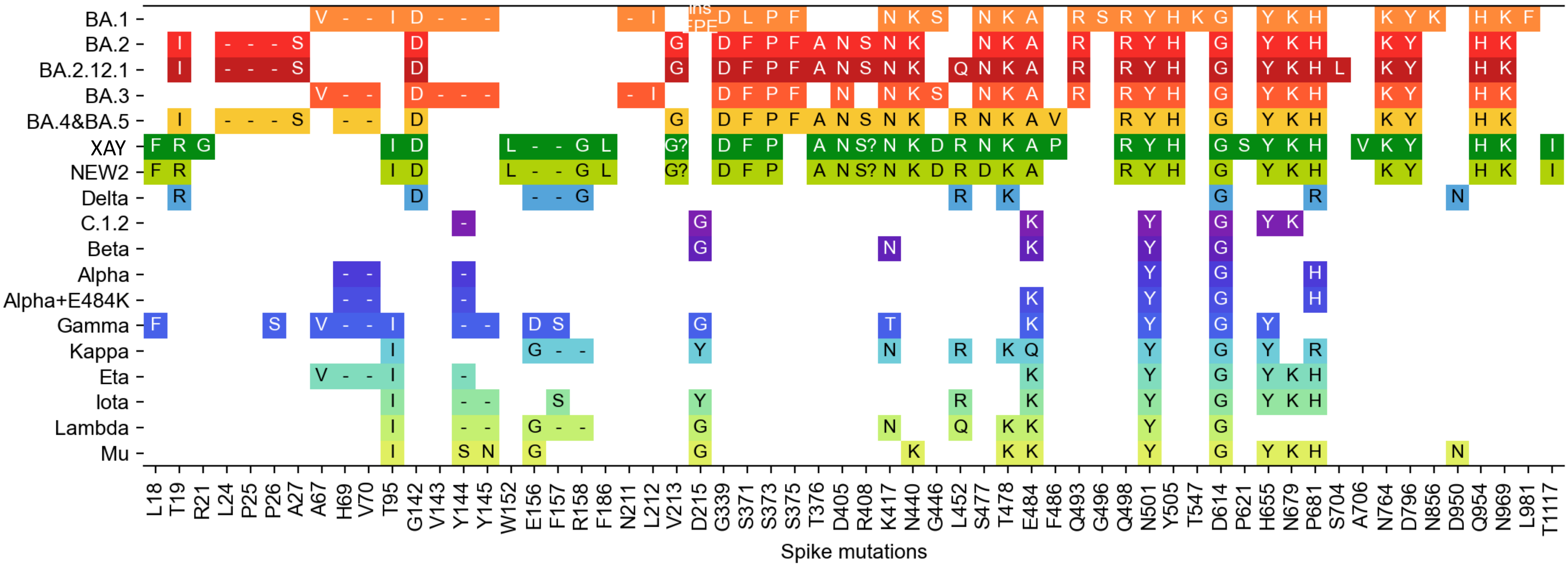
Summary

- **Sequencing update**
  - All provinces have sequences for August and September.
- **Variant of Concern Omicron in South Africa**
  - Omicron continued to dominate in June (99%), July (99%), August (97%), and currently makes up 98% of September sequences.
  - Omicron BA.5 was dominant in July (68%) and August (70%), and makes up 82% of September data.
  - BA.2.12.1 was detected in South Africa at low prevalence in May, June and July (<1%).
  - BA.2.75.* has been detected in July, August and September at a low prevalence (≤1%).
  - XAY (New1) continues to be detected at a low prevalence (n = 22, predominantly from Gauteng)
    - XAY has also been detected in Denmark (n=3) and the USA (n=2)
  - BQ.1 and BQ.1.1 have been detected in South Africa at low prevalence in September (<1%; BQ.1: n=1 in the Northern Cape, n=2 in the Western Cape; BQ.1.1: n=1 in Gauteng, n=2 in the Western Cape)
- Low frequency of previously circulating variants such as Delta not detected since July.

---

[1] https://github.com/cov-lineages/pango-designation/issues/844

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
XAY	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		
XAY	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				

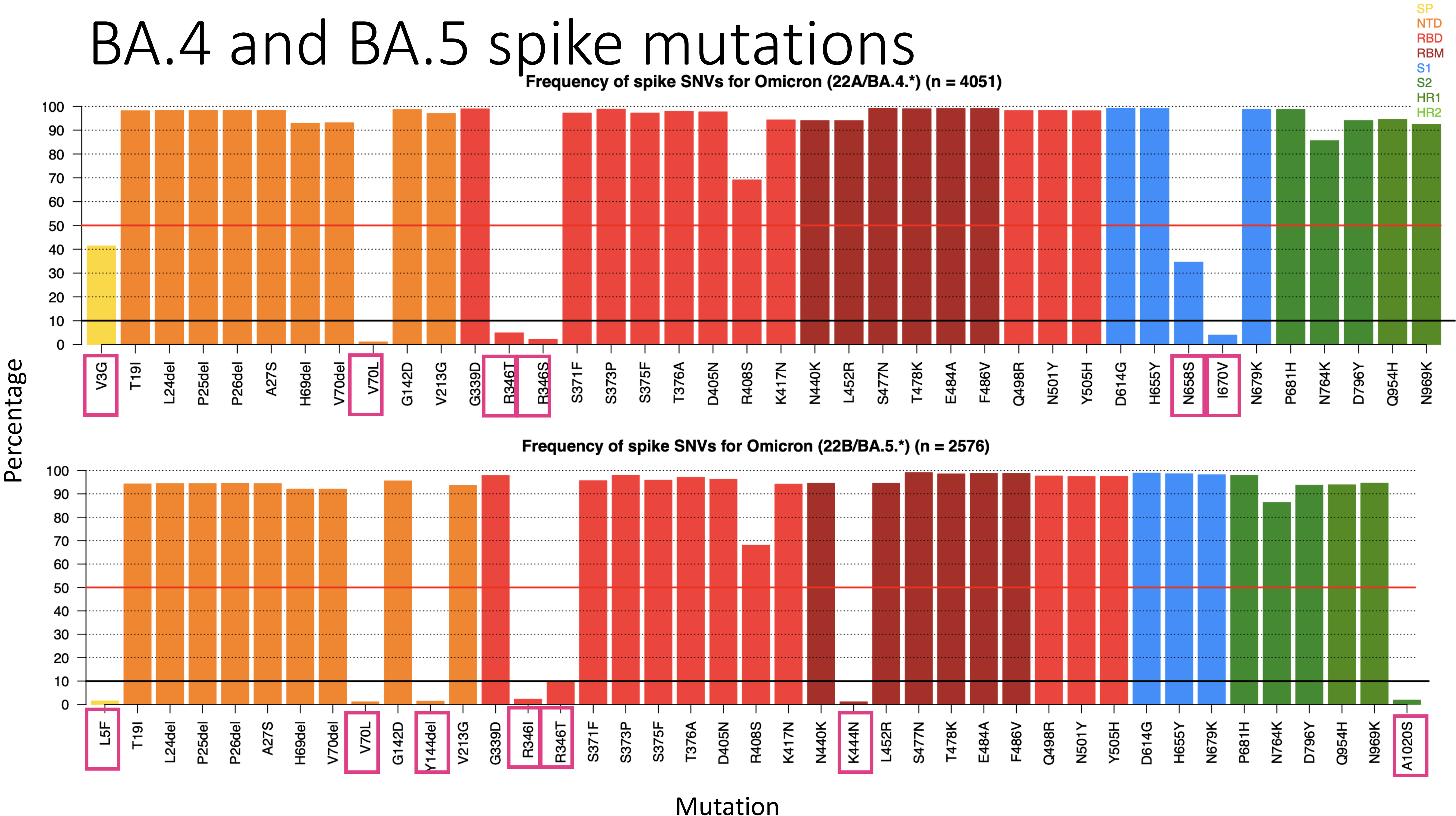
Spike mutations

- 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

NGS-SA
Network for Genomic
Surveillance in South Africa

BA.4 and BA.5 spike mutations

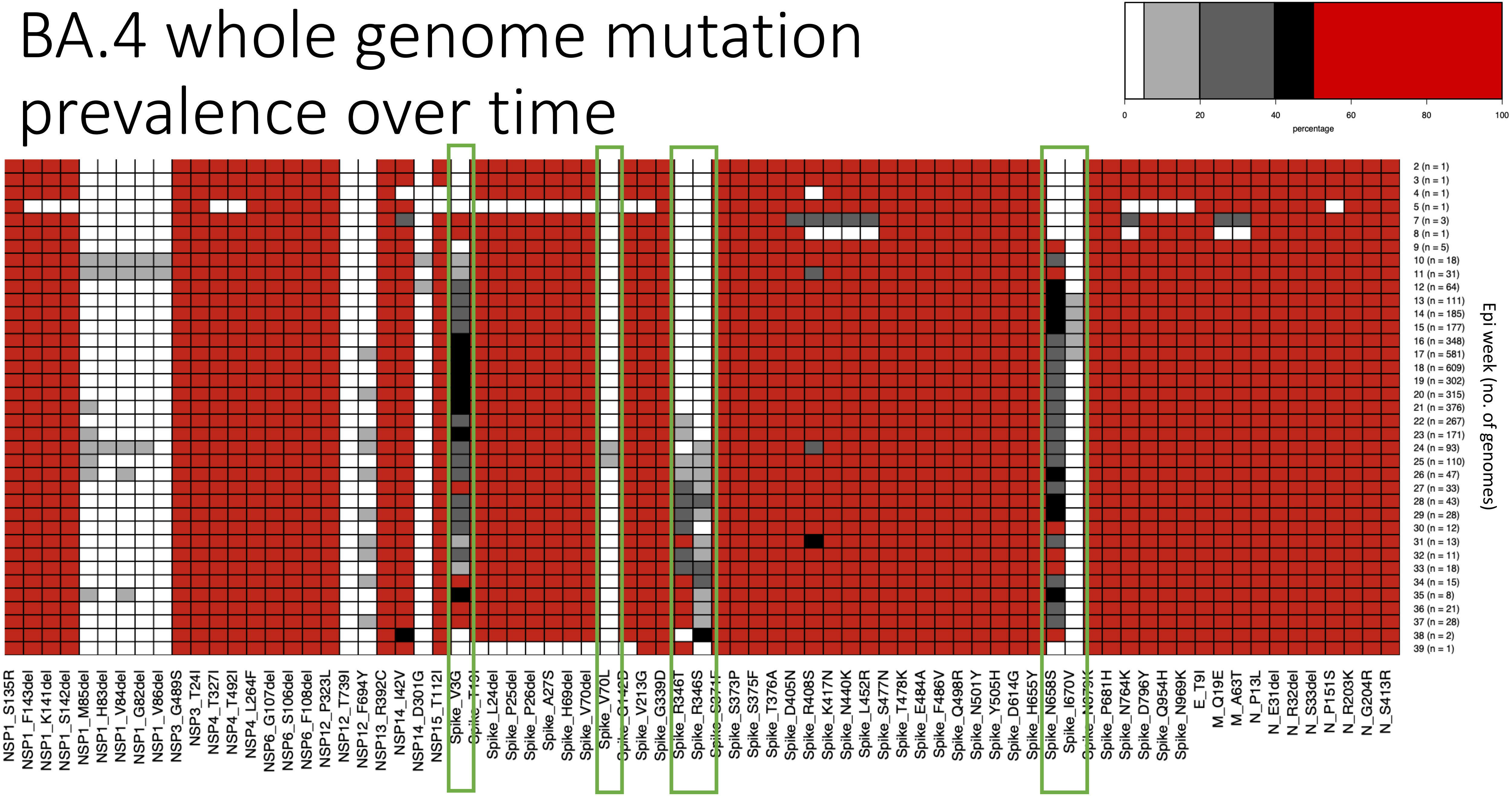


Frequency of spike SNVs for Omicron (22A/BA.4.*) (n = 4051)

Frequency of spike SNVs for Omicron (22B/BA.5.*) (n = 2576)

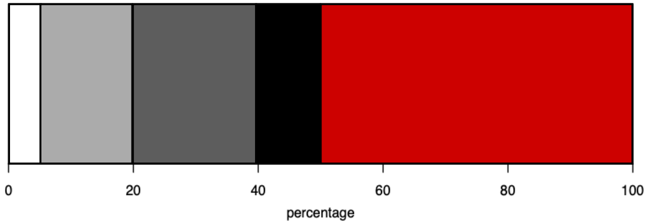
*as of 23 September 2022

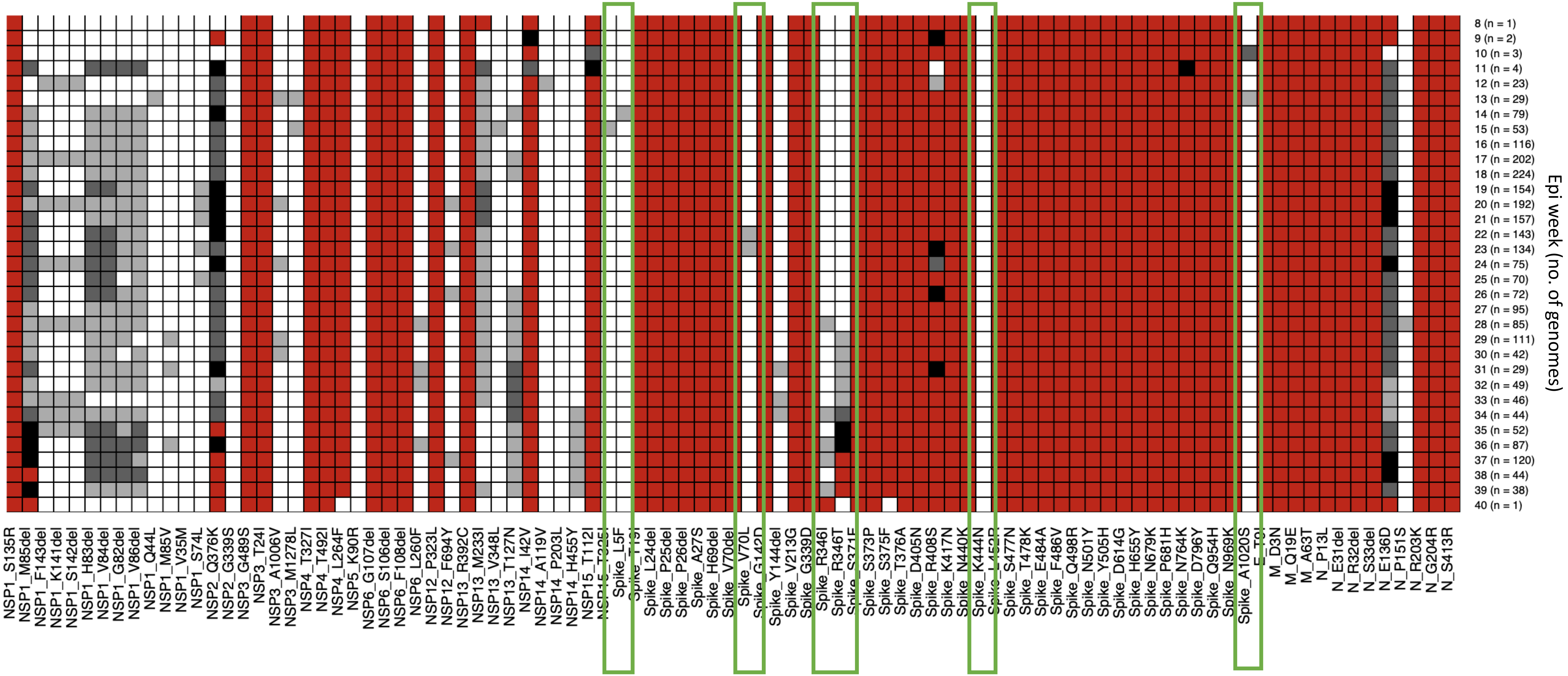
BA.4 whole genome mutation prevalence over time



*as of 23 September 2022

BA.5 whole genome mutation prevalence over time

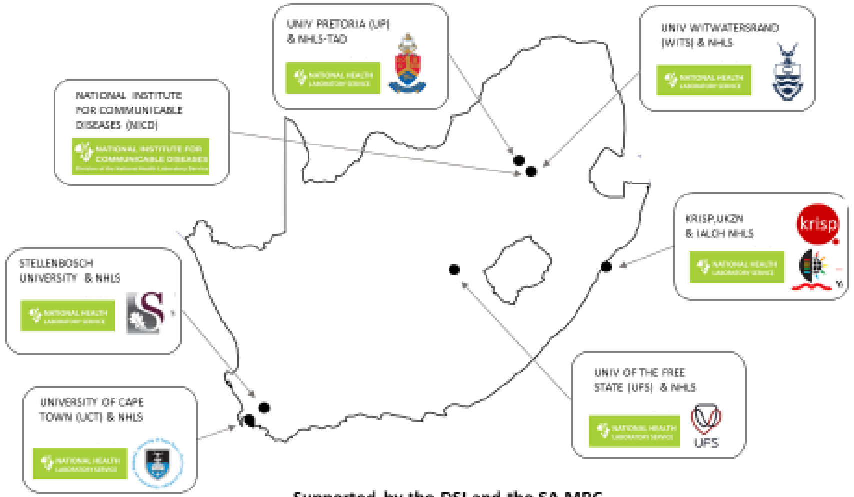




*as of 23 September 2022

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

EDCTP

This project (RIA2020EF-3030) is part of the EDCTP2 programme supported by the European Union”

UNIVERSITY OF CAPE TOWN
IYUNIVESITHI YASEKAPA • UNIVERSITEIT VAN KAAPSTAD

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

This project has received funding from the European Union's Horizon Europe Research and Innovation Actions under grant No. 101046041

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)

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

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

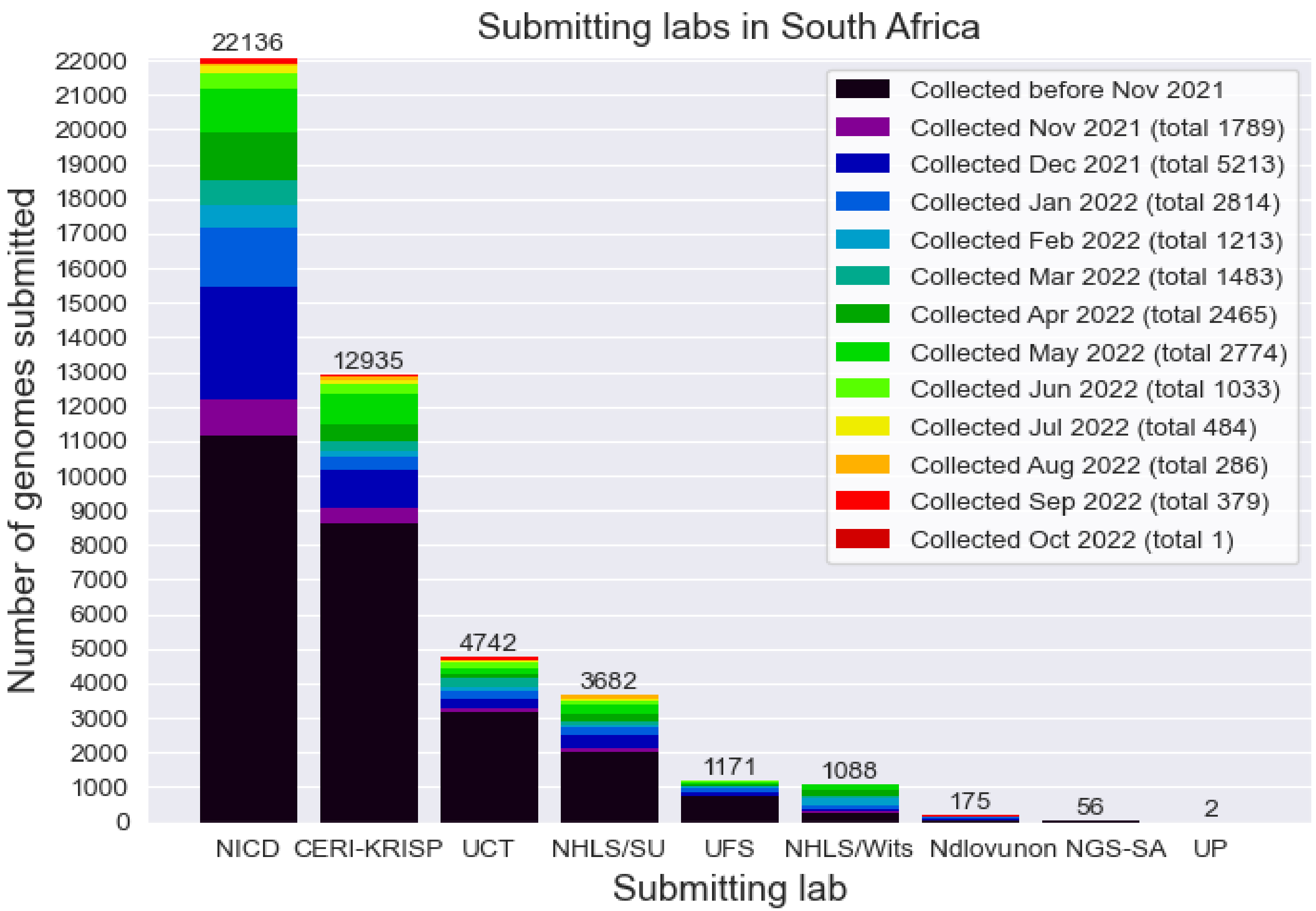
Africa CDC
John Nkengasong
Sofonias Tessema

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=45 987)



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.

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
Omicron*	B.1.1.529	GR/484A	21K, 21L, 21M, 22A, 22B, 22C, 22D	+S:R346K +S:L452X +S:F486V	Multiple countries, Nov-2021	VUM: 24-Nov-2021 VOC: 26-Nov-2021

* Includes BA.1, BA.2, BA.3, BA.4, BA.5 and descendent lineages. It also includes BA.1/BA.2 circulating recombinant forms such as XE. WHO emphasizes that these descendant lineages should be monitored as distinct lineages by public health authorities and comparative assessments of their virus characteristics should be undertaken.

° Only found in a subset of sequences

https://www.who.int/en/activities/tracking-SARS-CoV-2-variants/ accessed 12 August 2022

Omicron subvariants under monitoring

Pango lineage[#] (+ mutation)	GISAID clade	Nextstrain **clade**	**Relationship to circulating VOC lineages**	Spike genetic features	Earliest documented **samples**
BA.5** (+R346X or +K444X or +V445X or +N450D or +N460X)	GRA	22B	BA.5 sublineages (e.g. BF.7, BF.14, BQ.1)	BA.5 + one or more of these mutations: S:R346X, S:K444X, S:V445X , S:N450D or S:N460X	07-02-2022
BA.2.75***	GRA	22D	BA.2 sublineage	BA.2.75: BA.2 + S:K147E, S:W152R, S:F157L, S:I210V, S:G257S, S:D339H, S:G446S, S:N460K, S:Q493R reversion BA.2.75.2: BA.2.75 + S:R346T, S:F486S, S:D1199N	31-12-2021
BJ.1****	GRA	21L	BA.2 sublineage (B.1.1.529.2.10.1.1)	BA.2+S:V83A, S:Y144-, S:H146Q, S:Q183E, S:V213E, S:G339H, S:R346T, S:L368I, S:V445P, S:G446S, S:V483A, S:F490V, S:G798D, S:S1003I	06-09-2021
BA.4.6	GRA	22A	BA.4 sublineage	BA.4+S:R346T, S:N658S	20-07-2020
XBB[$]		recombinant	Recombinant of BA.2.10.1 and BA.2.75 sublineages, i.e. BJ1 and BM.1.1.1, with a breakpoint in S1	BA.2+ S:V83A, S:Y144-, S:H146Q, S:Q183E, S:V213E, S:G252V, S:G339H, S:R346T, S:L368I, S:V445P, S:G446S, S:N460K, S:F486S, S:F490S	13-08-2022
BA.2.3.20[§]	GRA	21L	BA.2 sublineage	BA.2+ S:M153T, S:N164K, S:H245N, S:G257D, S:K444R, S:N450D, S:L452M, S:N460K, S:E484R	15-08-2022

* these subvariants are tracked under Omicron unless/until sufficient evidence arises that the virus characteristics are substantially different from what is known about the VOC they belong to. If this evidence arises, WHO will decide, in consultation with the TAG-VE, if designation of the emerging variant warrants a separate WHO label.

[#] includes descendent lineages

** additional mutations outside of the spike protein: N:G30-, N:S33F, N:E136D, ORF1a:Q556K, ORF1a:L3829F, ORF1b:Y264H, ORF1b:M1156I, ORF9b:P10F, ORF9b:D16G, ORF9b:M26-, ORF9b:A29I, ORF9b:V30L.

*** additional mutation outside the spike protein: ORF1a:S1221L, ORF1a:P1640S, ORF1a:N4060S; ORF1b:G662S; E:T11A

**** additional mutations outside of the spike protein: Mutations: M:D3Y, N:T282I, ORF1a:K47R, ORF1b:G662S, ORF1b:S959P, ORF7a:I110T

[$] additional mutations outside of the spike protein: E:T11A, ORF1a:K47R, ORF1b:G662S, ORF1b:S959P, ORF8:G8*

[§] additional mutations outside of the spike protein: ORF1a:T727I, ORF1a:I1714T, ORF1a:M2169V, ORF1a:T2174I, ORF1a:T2648I, ORF1a:A2909V, ORF1a:Q3922R, ORF1b:T1404M, ORF3a:L140F, ORF9b:D89E

https://www.who.int/en/activities/tracking-SARS-CoV-2-variants/ accessed 14 October 2022

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
Delta	B.1.617.2	G/478K.V1	21A, 21I, 21J	India, Oct-2020	VOI: 4-Apr-2021 VOC: 11-May-2021 Previous VOC: 7-Jun-2022

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

https://www.who.int/en/activities/tracking-SARS-CoV-2-variants/ accessed 12 August 2022

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.)