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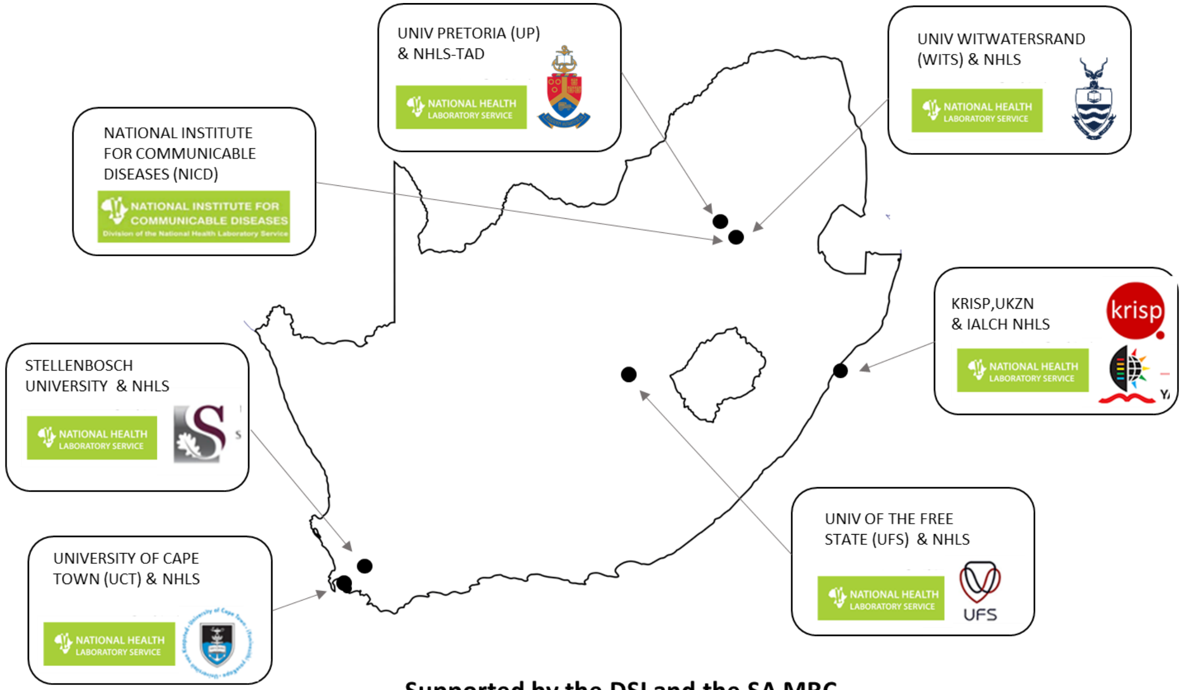
Network for Genomic
Surveillance in South Africa

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

SARS-CoV-2 Sequencing Update

14 April 2022



Supported by the DSI and the SA MRC

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

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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)

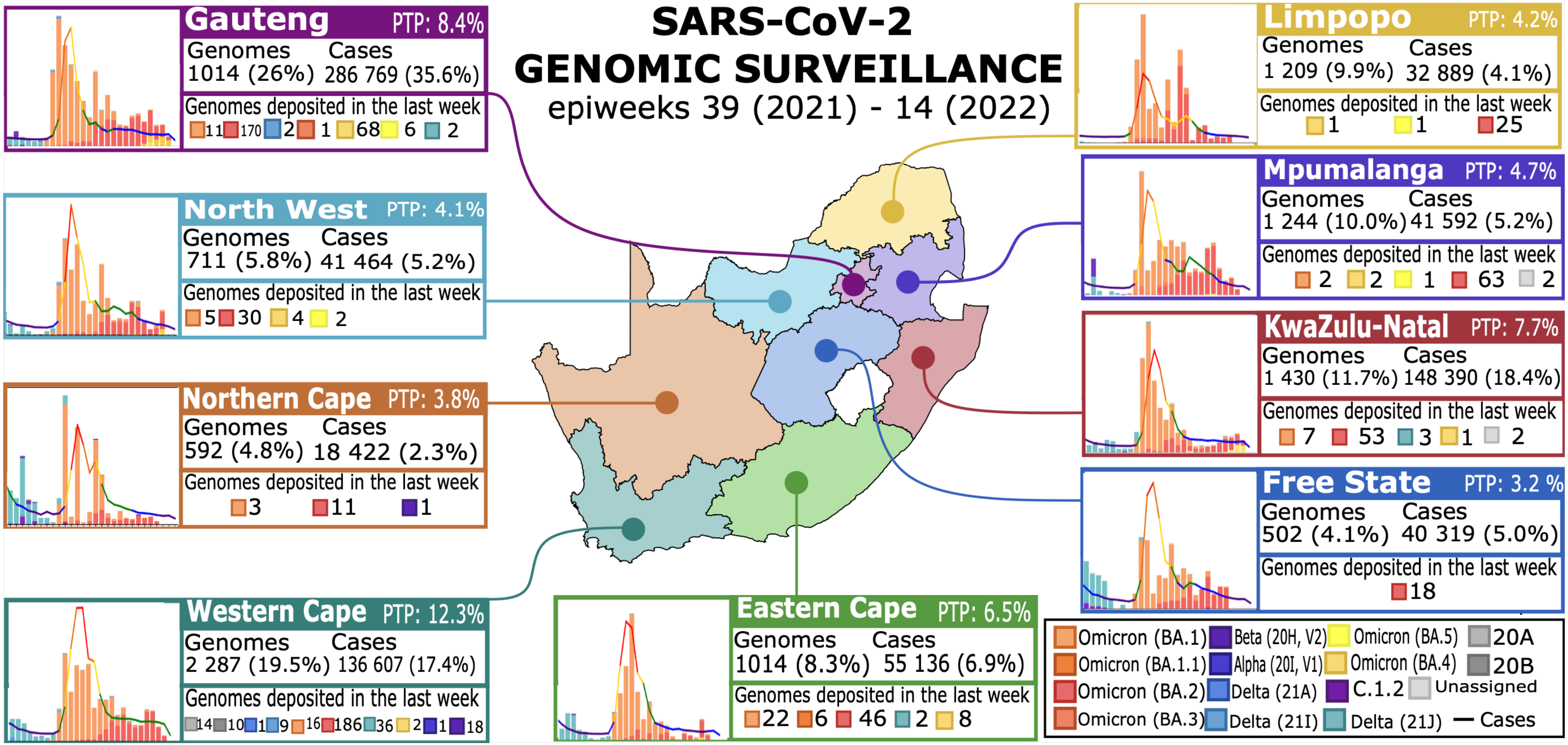
The genomic data presented here are based on South African SARS-CoV-2 sequence data downloaded from GISAID (www.gisaid.org) on 13 April 2022 at 15h00

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

SARS-CoV-2
GENOMIC SURVEILLANCE
epiweeks 39 (2021) - 14 (2022)



Gauteng PTP: 8.4%
Genomes Cases
1014 (26%) 286 769 (35.6%)
Genomes deposited in the last week
🟧11 🟥170 🟦2 🟧1 🟨68 🟨6 🟩2

North West PTP: 4.1%
Genomes Cases
711 (5.8%) 41 464 (5.2%)
Genomes deposited in the last week
🟧5 🟥30 🟨4 🟨2

Northern Cape PTP: 3.8%
Genomes Cases
592 (4.8%) 18 422 (2.3%)
Genomes deposited in the last week
🟧3 🟥11 🟪1

Western Cape PTP: 12.3%
Genomes Cases
2 287 (19.5%) 136 607 (17.4%)
Genomes deposited in the last week
⬜14 ⬛10 🟦1 🟦9 🟧16 🟥186 🟩36 🟨2 🟦1 🟪18

Eastern Cape PTP: 6.5%
Genomes Cases
1014 (8.3%) 55 136 (6.9%)
Genomes deposited in the last week
🟧22 🟧6 🟥46 🟩2 🟨8

Limpopo PTP: 4.2%
Genomes Cases
1 209 (9.9%) 32 889 (4.1%)
Genomes deposited in the last week
🟨1 🟨1 🟥25

Mpumalanga PTP: 4.7%
Genomes Cases
1 244 (10.0%) 41 592 (5.2%)
Genomes deposited in the last week
🟧2 🟨2 🟨1 🟥63 ⬜2

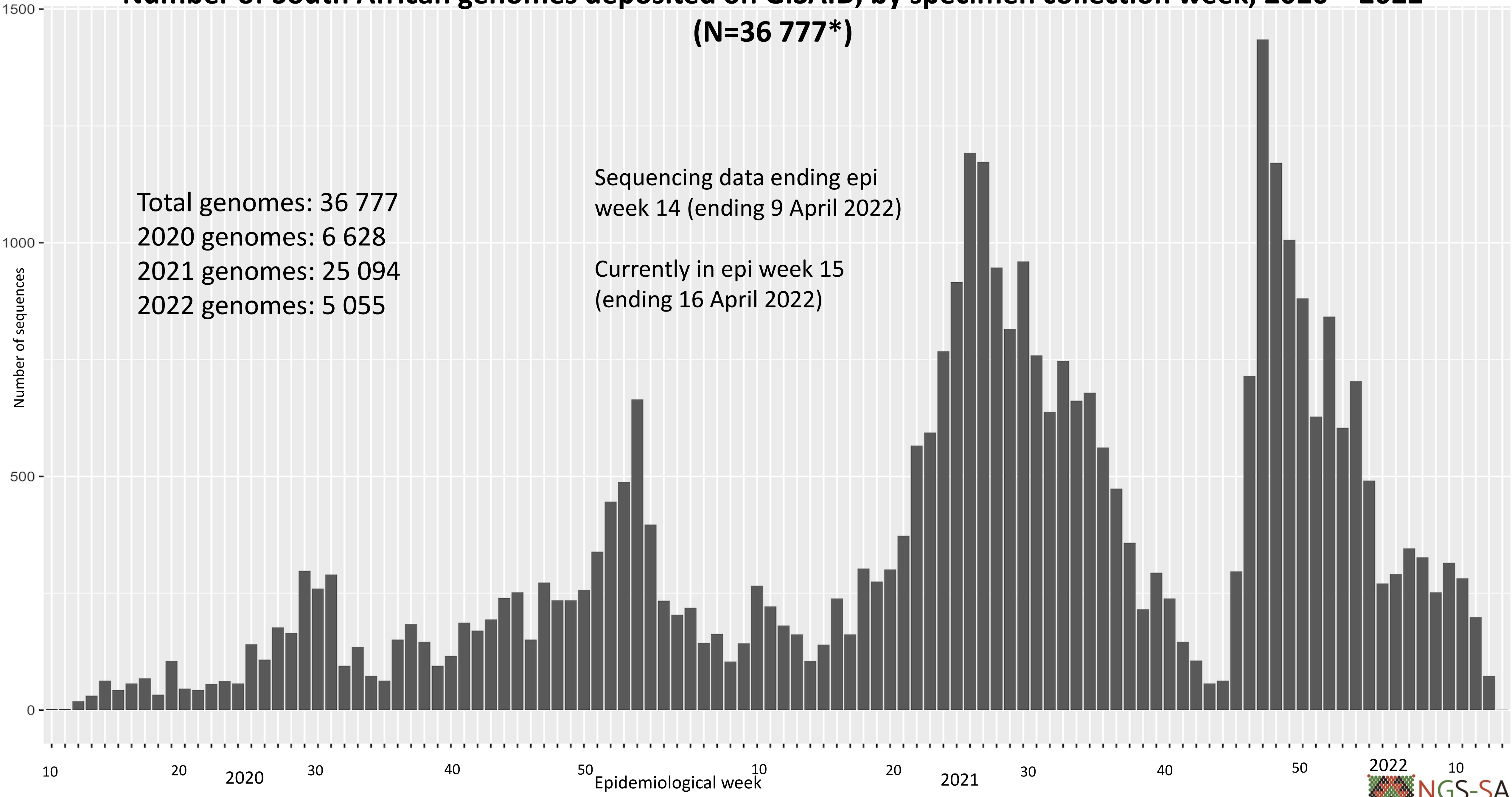
KwaZulu-Natal PTP: 7.7%
Genomes Cases
1 430 (11.7%) 148 390 (18.4%)
Genomes deposited in the last week
🟧7 🟥53 🟩3 🟨1 ⬜2

Free State PTP: 3.2 %
Genomes Cases
502 (4.1%) 40 319 (5.0%)
Genomes deposited in the last week
🟥18

🟧 Omicron (BA.1)
🟧 Omicron (BA.1.1)
🟥 Omicron (BA.2)
🟥 Omicron (BA.3)
🟪 Beta (20H, V2)
🟦 Alpha (20I, V1)
🟦 Delta (21A)
🟦 Delta (21I)
🟨 Omicron (BA.5)
🟨 Omicron (BA.4)
🟪 C.1.2
🟩 Delta (21J)
⬜ 20A
⬛ 20B
⬜ Unassigned
— Cases

Bar graphs represent genomes sequenced per epiweek, with lines representing cases by collection date (weeks 39 [2021] – 14 [2022])
Genomes and cases presented as provincial total (percentage of national total) for epiweeks 39 (2021) – 14 (2022)
PTP: percentage testing positive in week 14 (3 Apr – 9 Apr); the arrow indicates direction of change since the previous week (27 Mar 2022 – 2 Apr 2022)

Number of South African genomes deposited on GISAID, by specimen collection week, 2020 – 2022 (N=36 777*)



Total genomes: 36 777
2020 genomes: 6 628
2021 genomes: 25 094
2022 genomes: 5 055

Sequencing data ending epi week 14 (ending 9 April 2022)

Currently in epi week 15 (ending 16 April 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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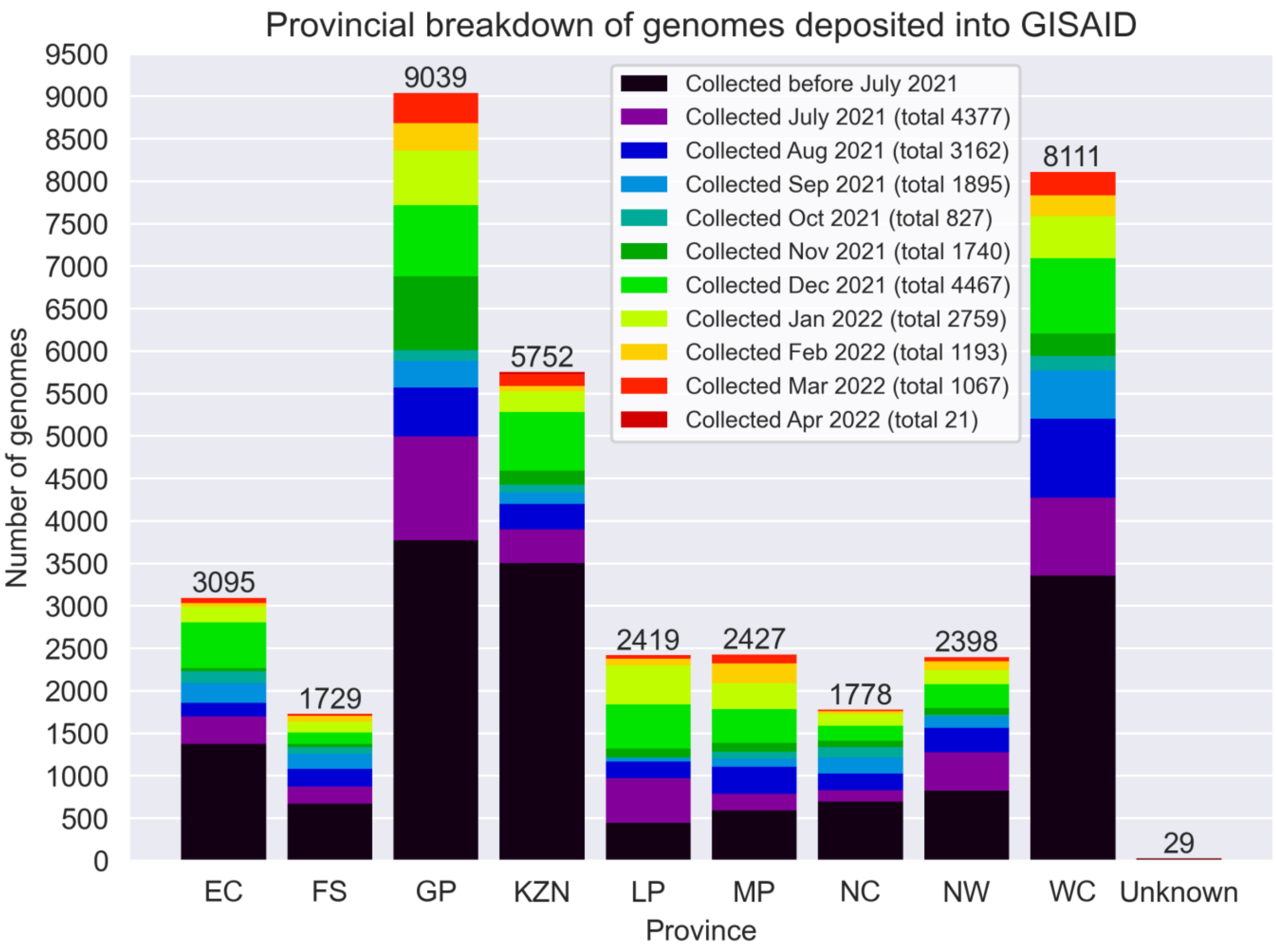
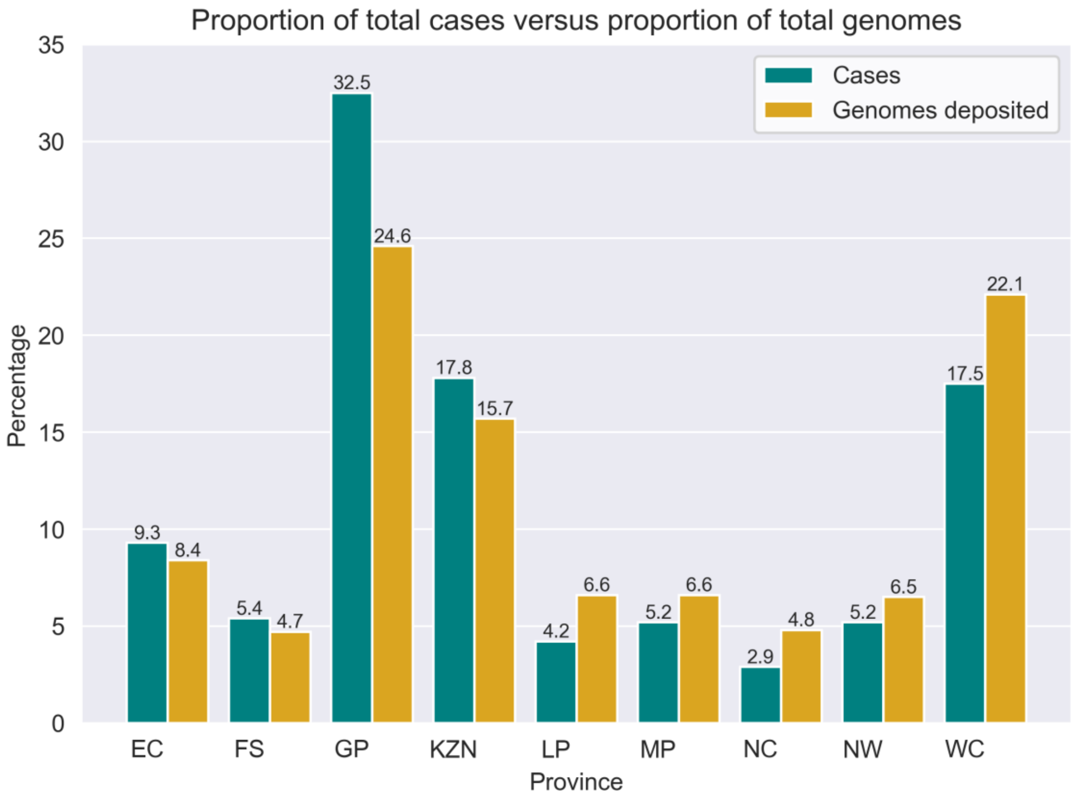
GISAID genomes vs total cases, 2020 – 2022 (N=36 777)





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

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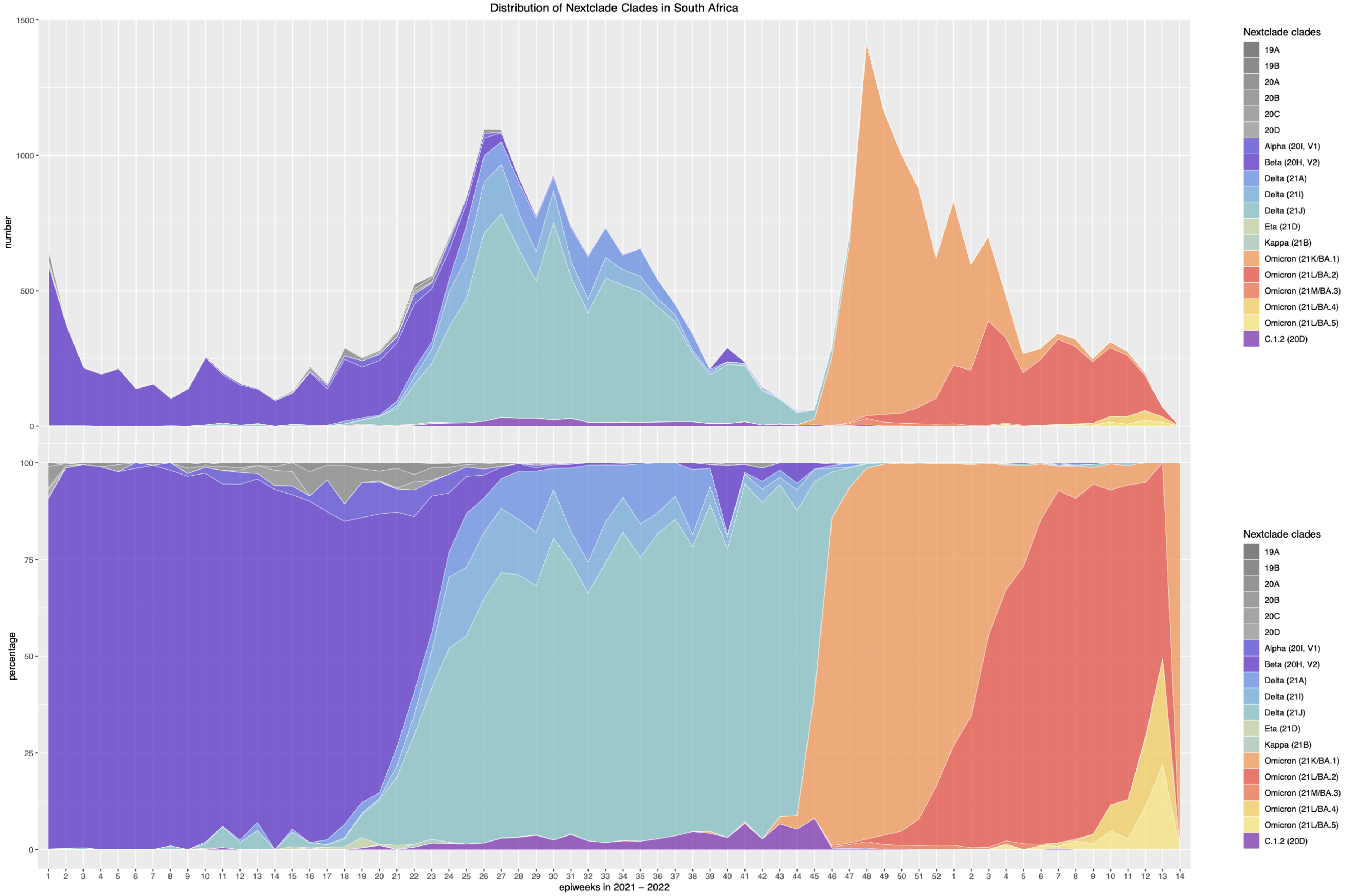
Number and percentage of clades by epiweek in South Africa, 2021 – 2022 (30 149)



Sequencing data ending epi week 14 (ending 9 April 2022)

Currently in epi week 15 (ending 16 April 2022)

Delta dominated in South Africa until October at >80%. Omicron has dominated from November onwards.

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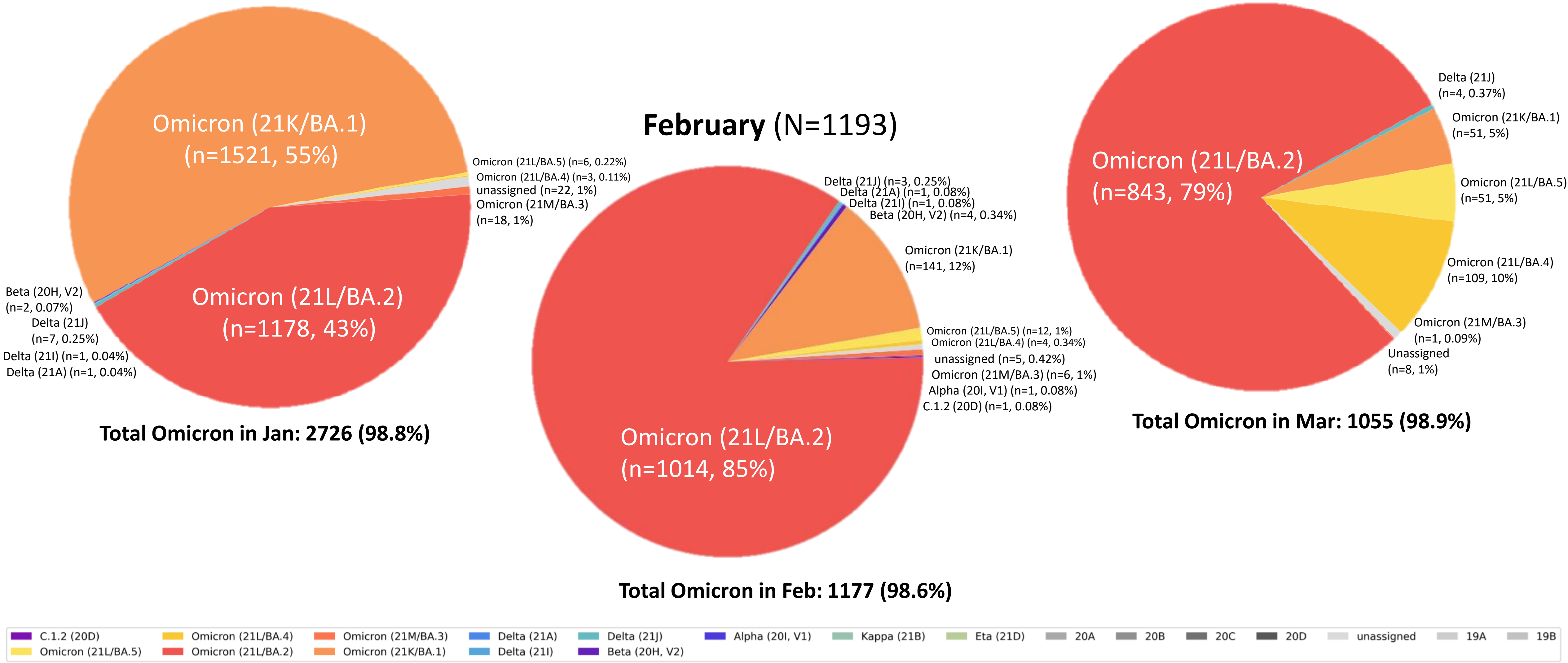
Prevalence of Variants of Concern (VOC) and Variants of Interest (VOI) in

Jan – Mar 2022



January (N=2759)

Total Omicron in Jan: 2726 (98.8%)

February (N=1193)

Total Omicron in Feb: 1177 (98.6%)

March (N=1067)

Total Omicron in Mar: 1055 (98.9%)

Omicron dominated in January (98.8%), February (98.6%) and March (98.6%). Sub-lineage BA.2 was dominant in February and March, while the prevalence of the newly assigned BA.4 and BA.5 sub-lineages increased in March.

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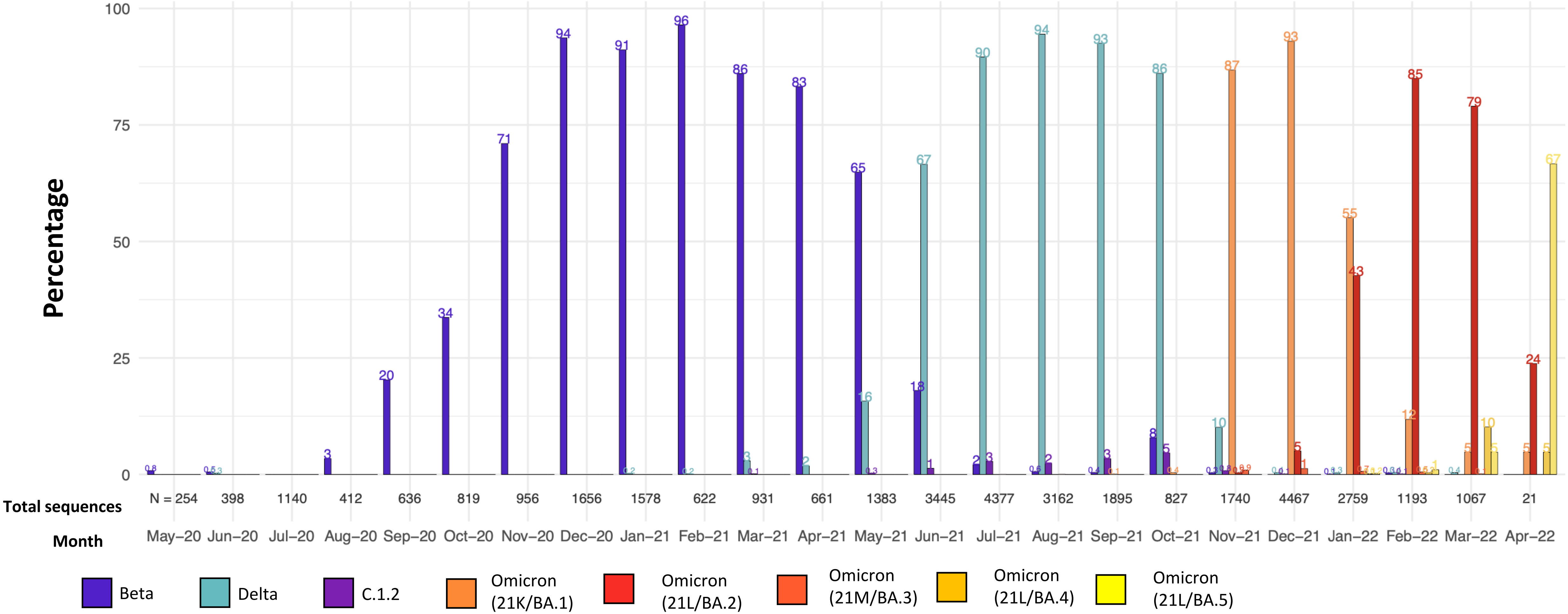
Detection Rates: Beta, Delta, C.1.2 and Omicron

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

Omicron has been dominant since November (>85% in November, >98% in December, January, February and March). BA.2 made up 43% of genomes in January, 85% in February and 79% in March. Newly designated sub-lineages BA.4 and BA.5 appear to be dominant in April, however additional sequence data is needed for recent weeks.

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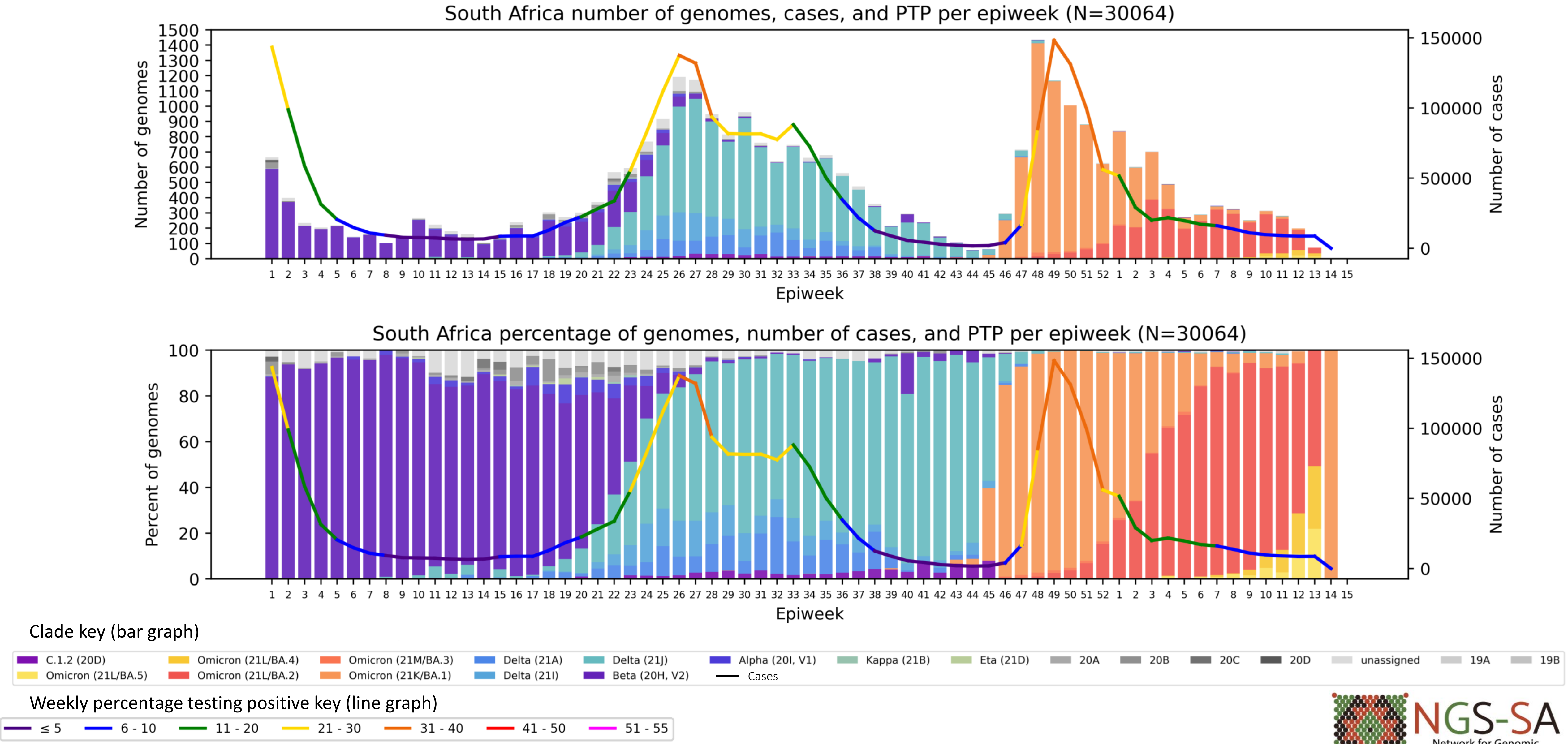
South Africa, 2021-2022, n = 30064*



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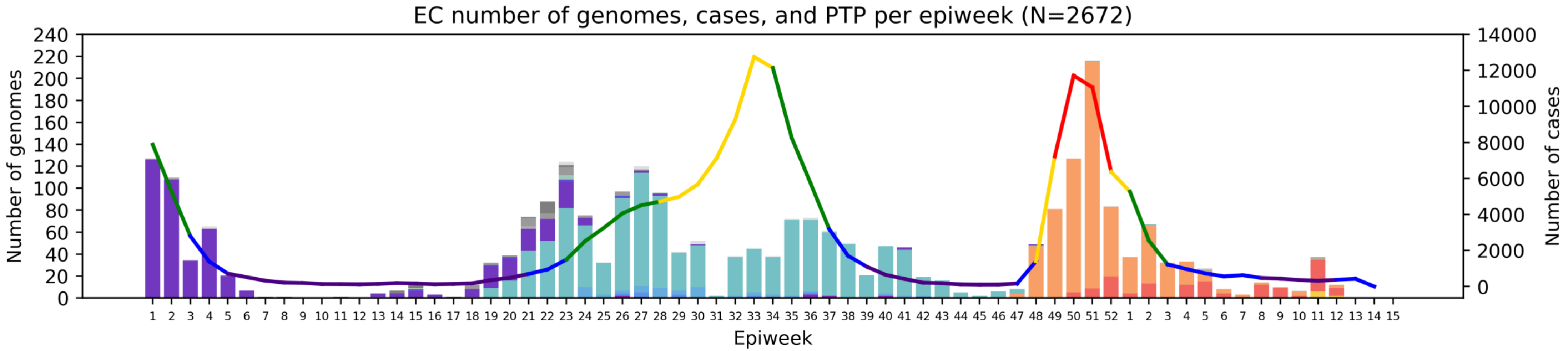
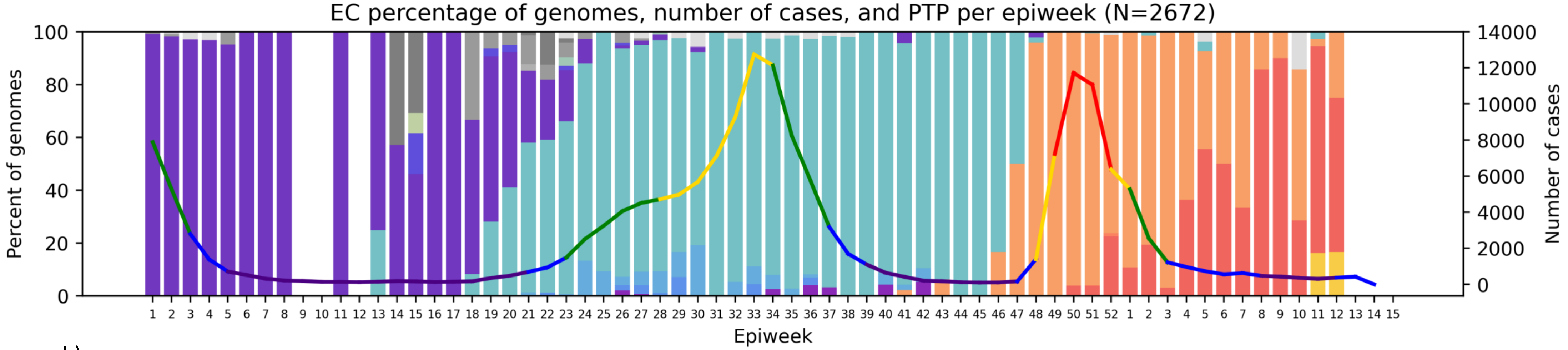
*Excludes sequences missing collection dates, as well as those collected January 1st and 2nd 2021 as they are part of epiweek 53 of 2020.

Eastern Cape Province, 2021-2022, n = 2672





Clade key (bar graph)

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

Weekly percentage testing positive key (line graph)

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

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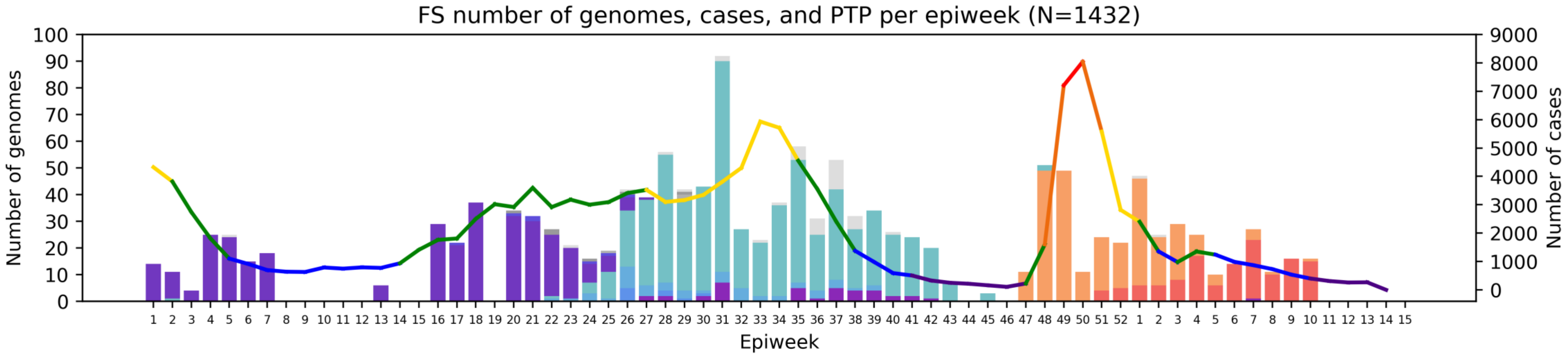
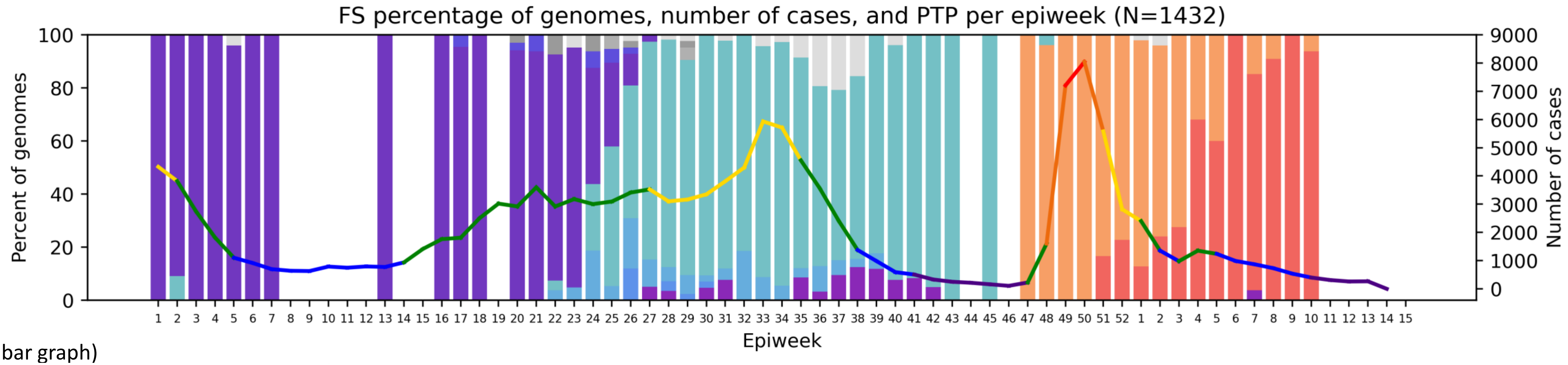
Free State Province, 2021-2022, n = 1432





Clade key (bar graph)

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

Weekly percentage testing positive key (line graph)

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

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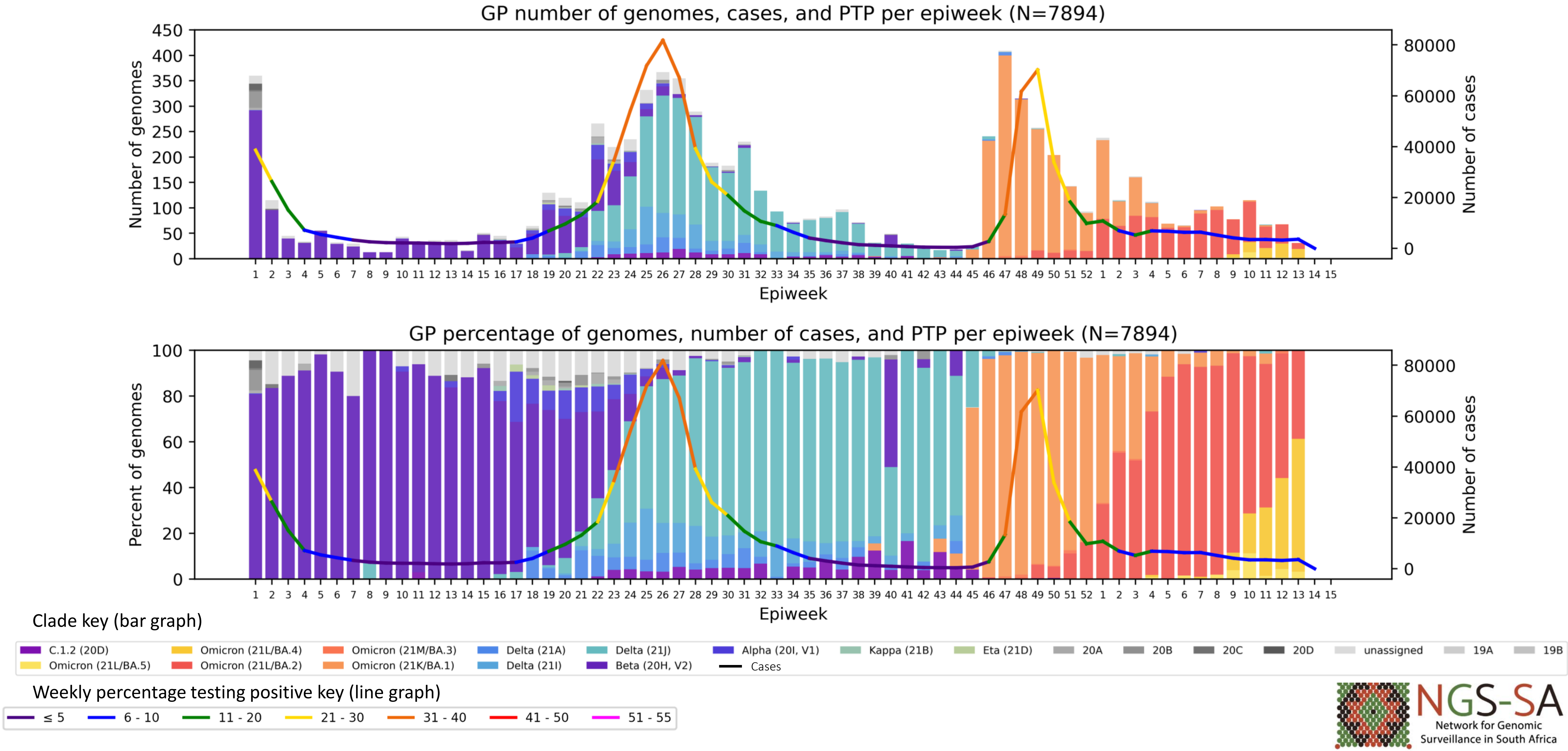
Gauteng Province, 2021-2022, n = 7894



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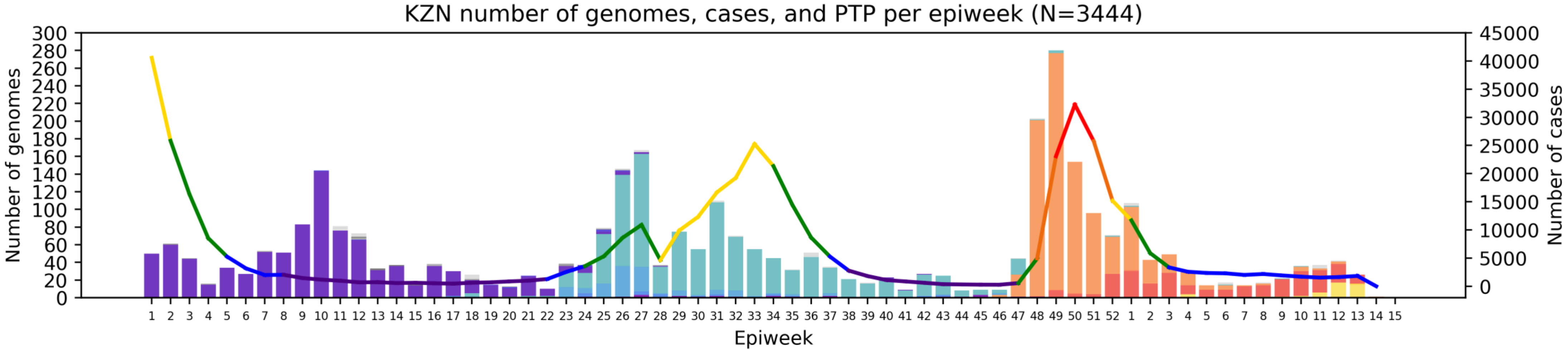
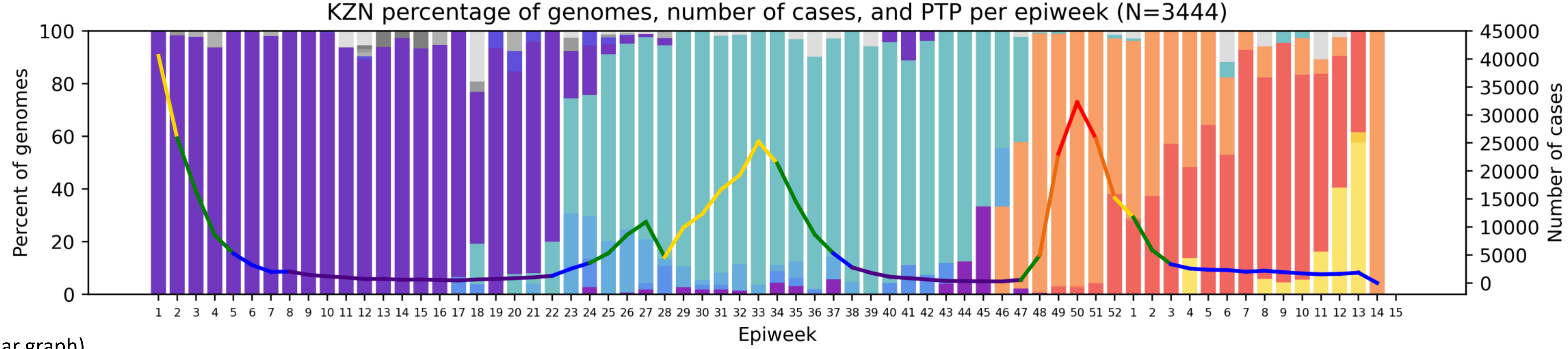
KwaZulu-Natal Province, 2021-2022, n = 3444


KZN number of genomes, cases, and PTP per epiweek (N=3444)


KZN percentage of genomes, number of cases, and PTP per epiweek (N=3444)

Clade key (bar graph)

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

Weekly percentage testing positive key (line graph)

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

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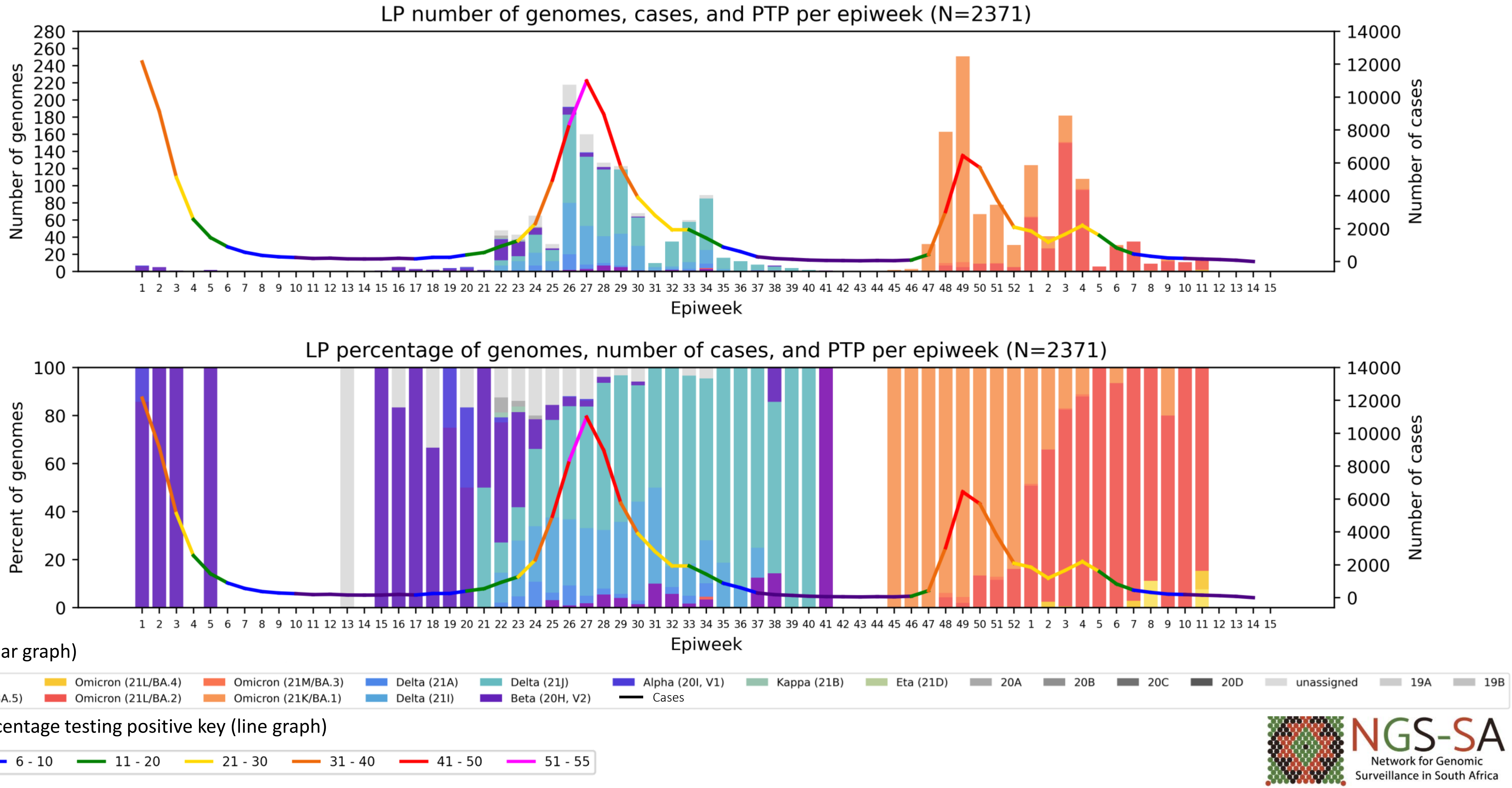
Limpopo Province, 2021-2022, n = 2371



LP number of genomes, cases, and PTP per epiweek (N=2371)

LP percentage of genomes, number of cases, and PTP per epiweek (N=2371)

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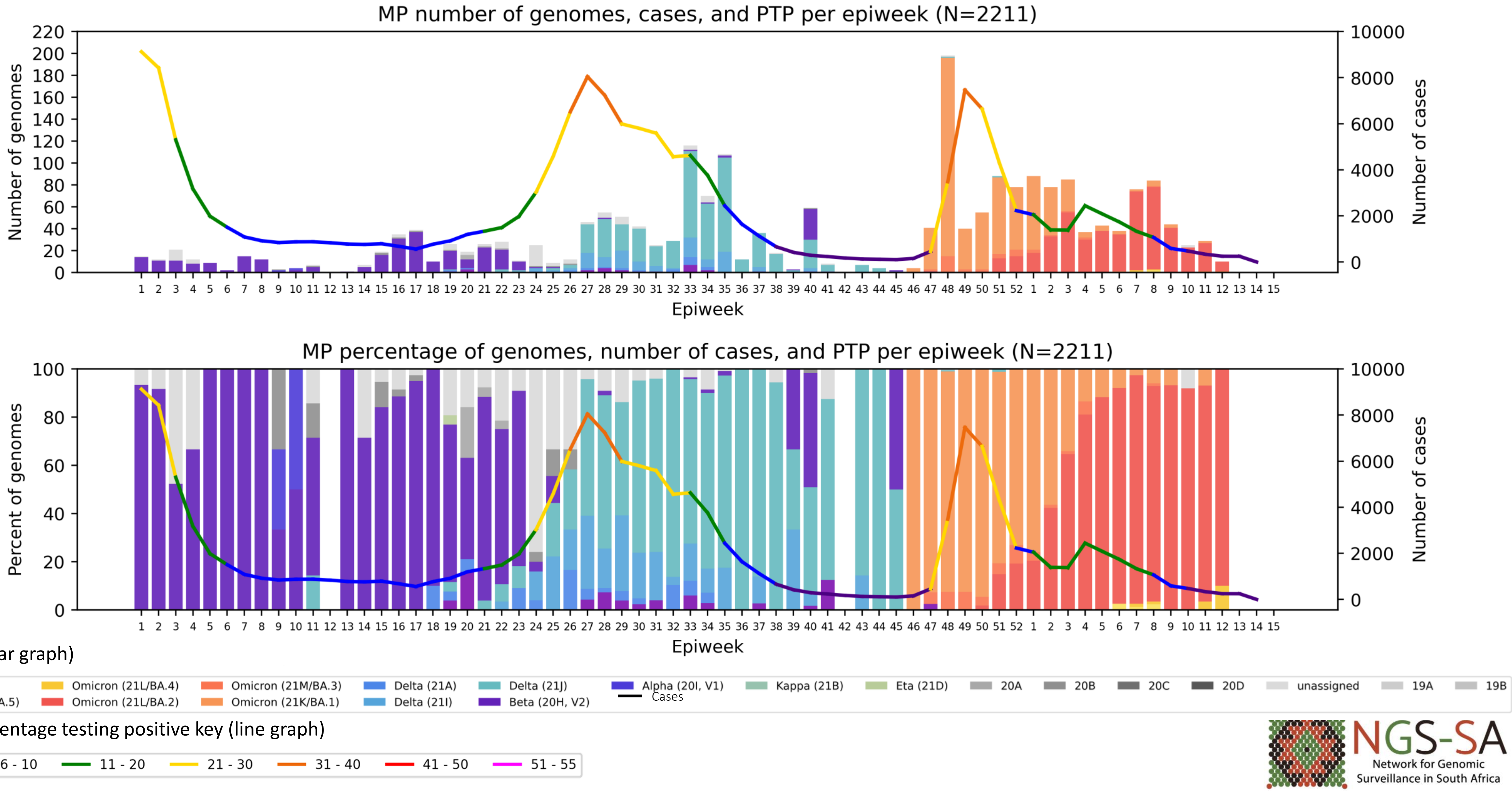
Mpumalanga Province, 2021-2022, n = 2211



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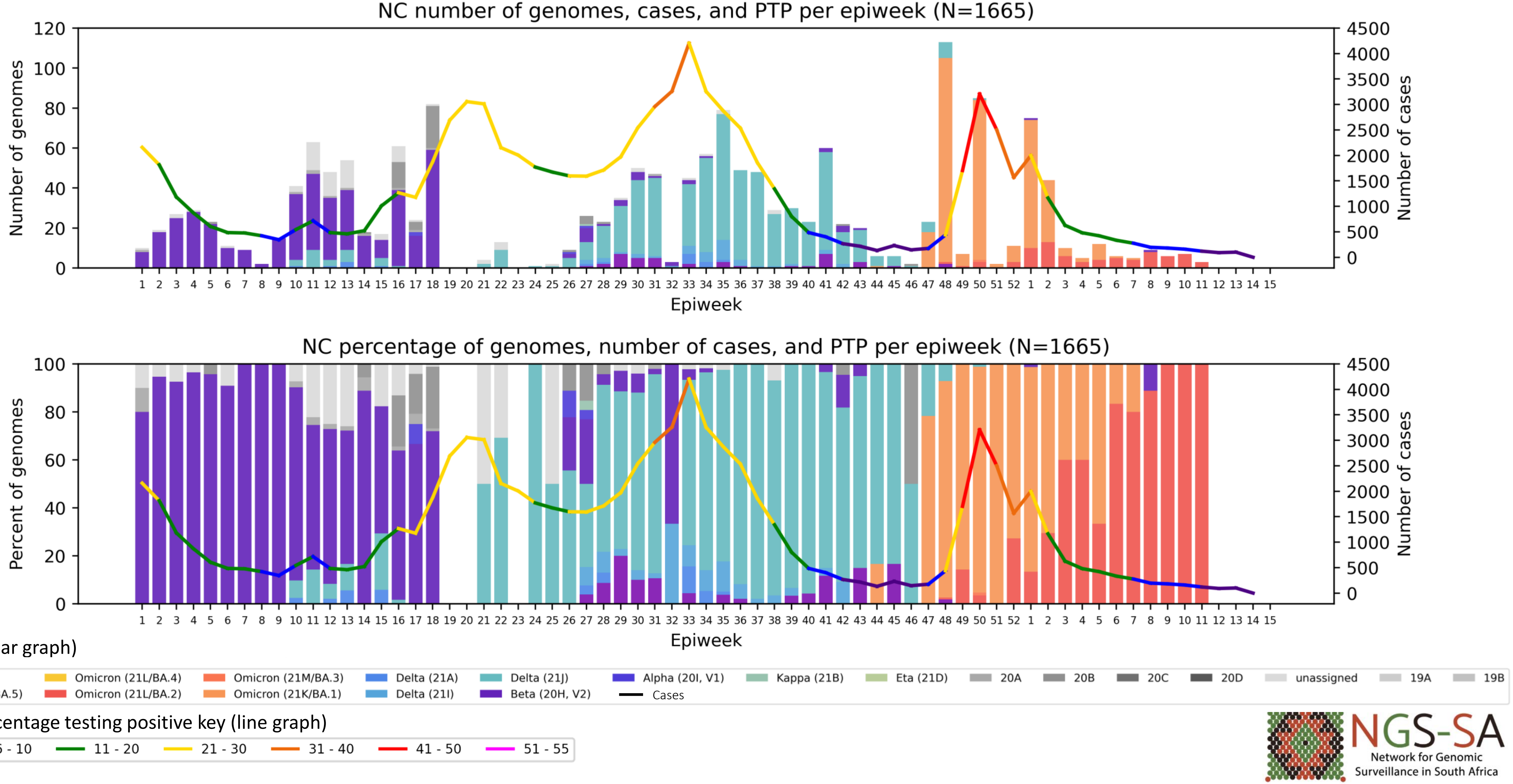
Northern Cape Province, 2021-2022, n = 1665



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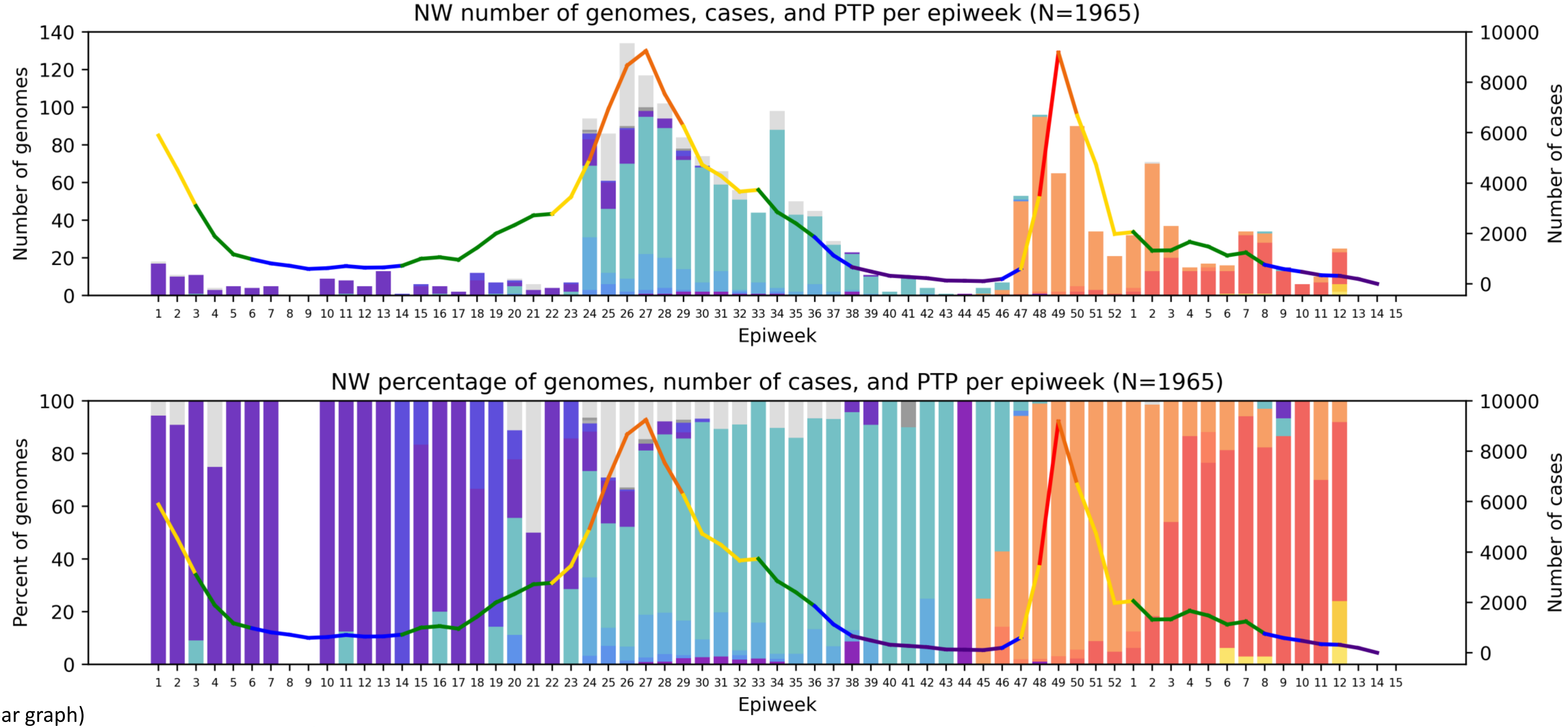
North West Province, 2021, n = 1965



Clade key (bar graph)

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

▨ 20D ▨ unassigned ▨ 19A ▨ 19B

Weekly percentage testing positive key (line graph)

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

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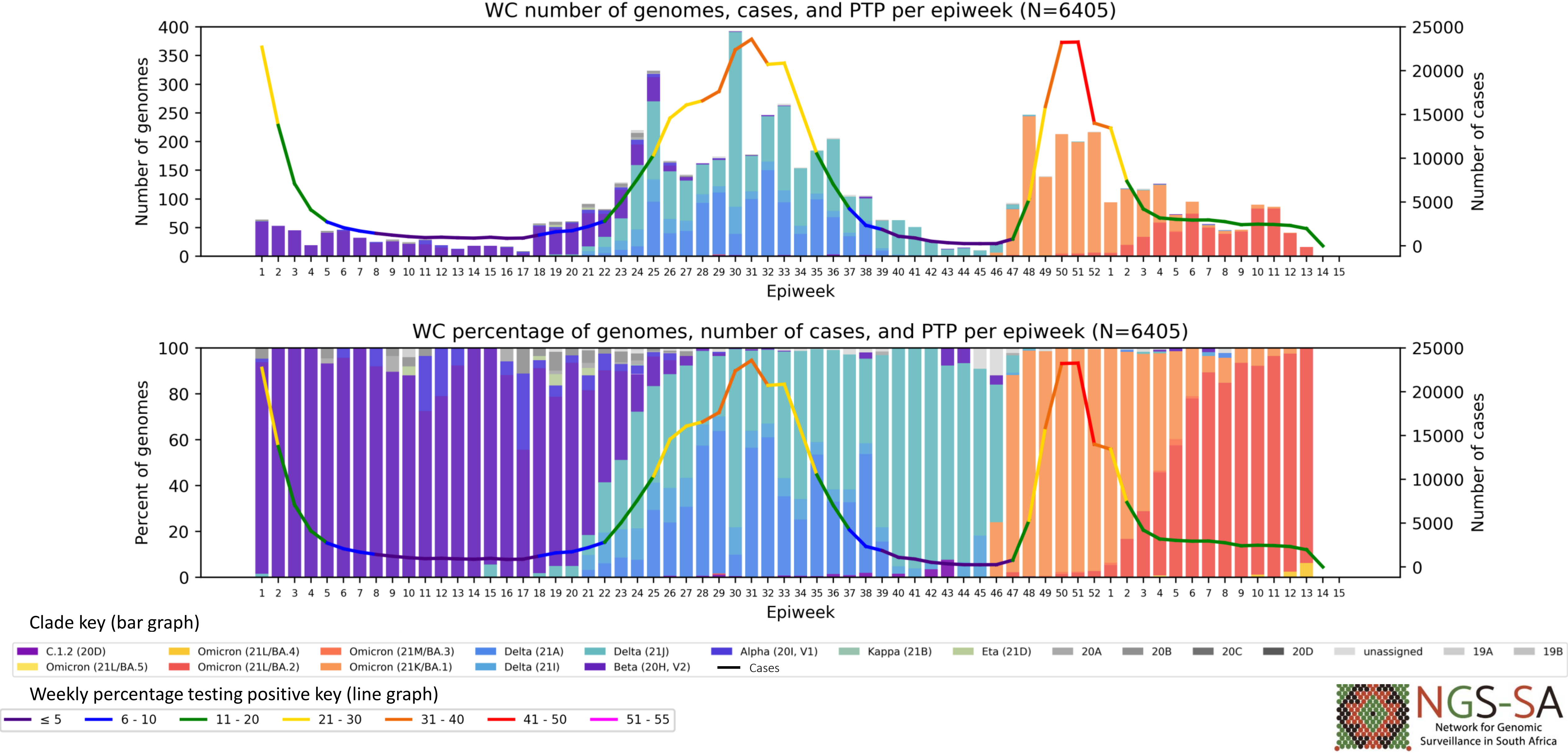
Western Cape Province, 2021-2022, n = 6405



WC number of genomes, cases, and PTP per epiweek (N=6405)

WC percentage of genomes, number of cases, and PTP per epiweek (N=6405)

Clade key (bar graph)

Weekly percentage testing positive key (line graph)

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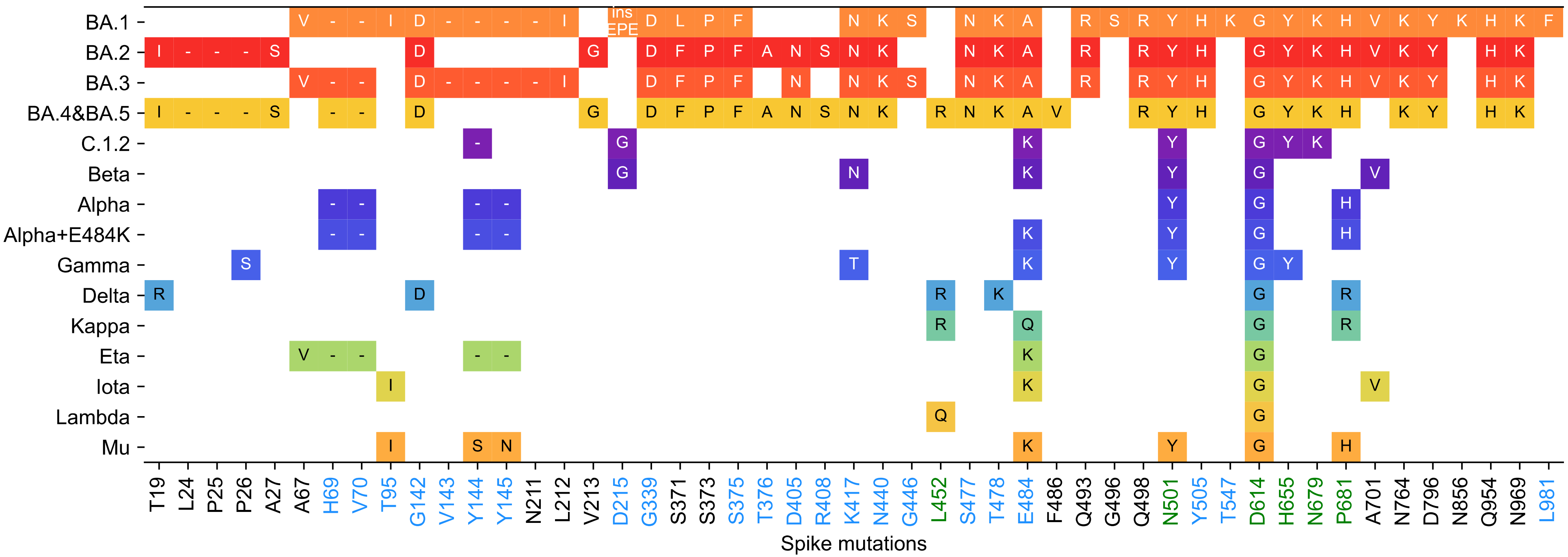
Summary

- **Variant of Concern Omicron in South Africa**
  - Dominates 2022 sequencing data at >98% of genomes
  - While BA.1 (and sub-lineages) was the predominant sub-lineage in January (55%), BA.2 dominated in February (85%) and March (79%).
  - Two additional Omicron sub-lineages (BA.4 and BA.5) have recently been designated by Pangolin. BA.4 and BA.5 increased in prevalence in March (15%), and appear to be dominant in April although additional sequencing data is needed for this period.
  - BA.3 continues to be detected at low levels.
  - NGS-SA teams are monitoring sequencing data for recombinants.
- Low frequency of previously circulating variants such as Delta still detected in recent data

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

Omicron spike mutations compared to other VOC/VOIs



	T19	L24	P25	P26	A27	A67	H69	V70	T95	G142	V143	Y144	Y145	N211	L212	V213	D215	G339	S371	S373	S375	T376	D405	R408	K417	N440	G446	L452	S477	T478	E484	F486	Q493	G496	Q498	N501	Y505	T547	D614	H655	N679	P681	A701	N764	D796	N856	Q954	N969	L981
BA.1						V	-	-	I	D	-	-	-	-	I		ins EPE	D	L	P	F				N	K	S		N	K	A		R	S	R	Y	H	K	G	Y	K	H	V	K	Y	K	H	K	F
BA.2	I	-	-	-	S					D						G		D	F	P	F	A	N	S	N	K			N	K	A		R		R	Y	H		G	Y	K	H	V	K	Y		H	K	
BA.3						V	-	-		D	-	-	-	-	I			D	F	P	F		N		N	K	S		N	K	A		R		R	Y	H		G	Y	K	H	V	K	Y		H	K	
BA.4&BA.5	I	-	-	-	S		-	-		D						G		D	F	P	F	A	N	S	N	K		R	N	K	A	V			R	Y	H		G	Y	K	H		K	Y		H	K	
C.1.2												-					G														K					Y			G	Y	K								
Beta																	G								N						K					Y			G				V						
Alpha							-	-				-	-																							Y			G			H							
Alpha+E484K							-	-				-	-																		K					Y			G			H							
Gamma				S																					T						K					Y			G	Y									
Delta	R									D																		R		K									G			R							
Kappa																												R			Q								G			R							
Eta						V	-	-				-	-																		K								G										
Iota									I																						K								G				V						
Lambda																												Q											G										
Mu									I			S	N																		K					Y			G			H							

Spike mutations

Only lineage-defining mutations are pictured here. Low prevalence mutations can be seen on the following slide.

Mutation impact key

⬛ Unknown or unconfirmed impact

🟦 Known/predicted immune escape

🟩 Enhanced infectivity

- 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

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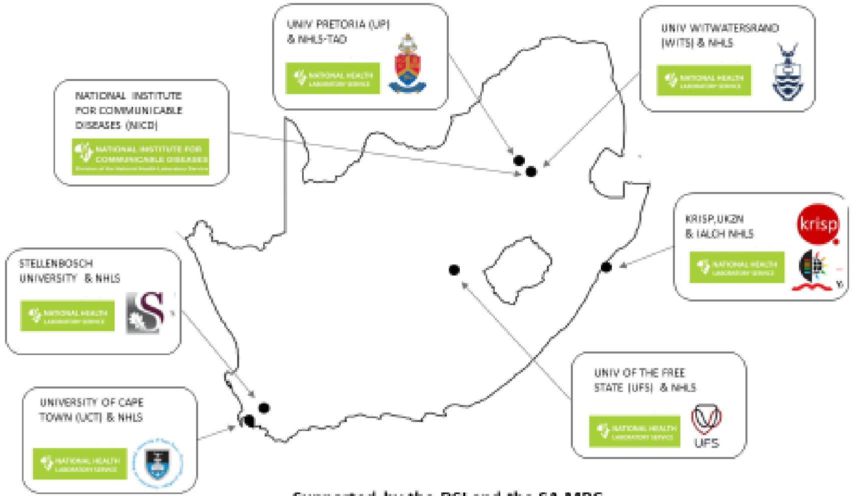

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Division of the National Health Laboratory Service

EDCTP

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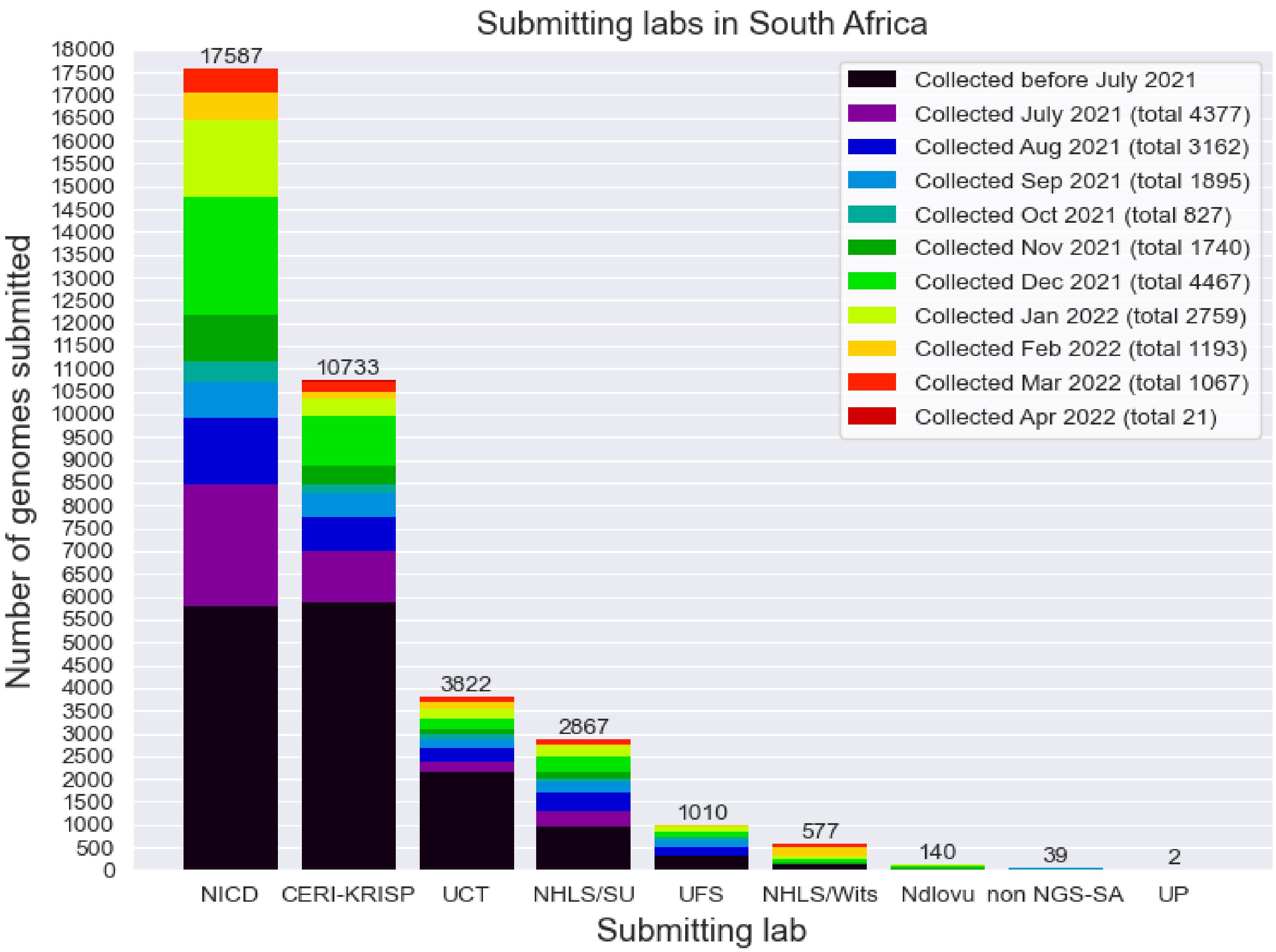
South African genomes submitted per submitting lab, 2020 - 2022 (N=36 777)



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.

NGS-SA
Network for Genomic Surveillance in South Africa

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.)