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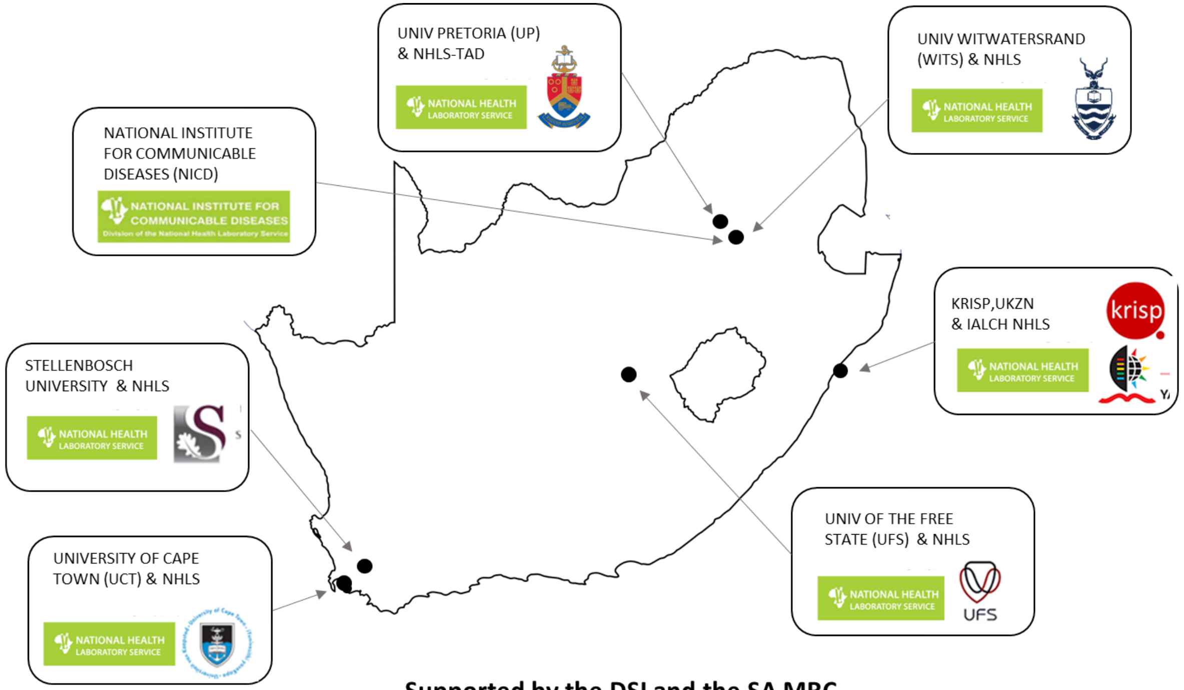
Network for Genomic Surveillance in South Africa

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

SARS-CoV-2 Sequencing Update
11 February 2022


UNIV PRETORIA (UP) & NHLS-TAD

UNIV WITWATERSRAND (WITS) & NHLS

NATIONAL INSTITUTE FOR COMMUNICABLE DISEASES (NICD)

KRISP,UKZN & IALCH NHLS

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Supported by the DSI and the SA MRC

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

science & innovation
Department:
Science and Innovation
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NATIONAL HEALTH LABORATORY SERVICE

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

saMRC advancinglife

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 10 February 2022 at 08h56

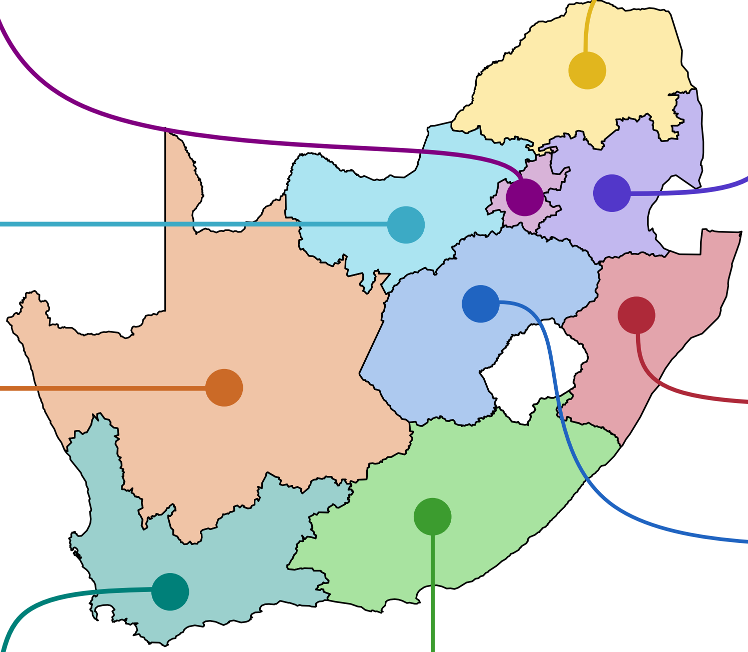
Data license: https://www.gisaid.org/registration/terms-of-use/

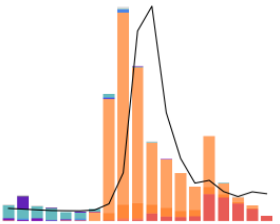
Elbe, S., and Buckland-Merrett, G. (2017) Data, disease and diplomacy: GISAID's innovative contribution to global health. Global Challenges, 1:33-46. DOI: 10.1002/gch2.1018 PMCID: 31565258

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 gives weekly percentage testing positive rates, 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 39 (2021) - 5 (2022)



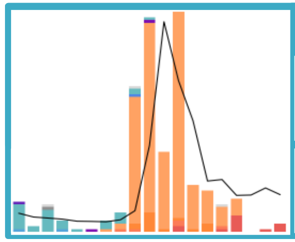


Gauteng ↓ PTP: 10.0%

Genomes	Cases
1 883 (27.7%)	250 208 (35.5%)

Genomes deposited in the last week

🟧44 🟧6 🟥63 🟧1 🟦1

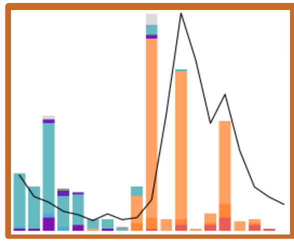


North West ↓ PTP: 14.8%

Genomes	Cases
338 (5.0%)	35 796 (5.1%)

Genomes deposited in the last week

🟧8 🟧1 🟥5

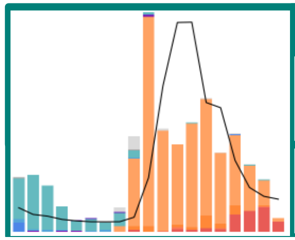


Northern Cape ↑ PTP: 14.9%

Genomes	Cases
474 (7.0%)	16 881 (2.4%)

Genomes deposited in the last week

🟧2 🟥4

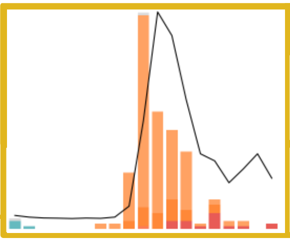


Western Cape ↓ PTP: 12.0%

Genomes	Cases
1 443 (21.2%)	118 967 (16.9%)

Genomes deposited in the last week

🟧81 🟧12 🟥42 🟪1 🟦1 🟦2 🟦7 ⬜1

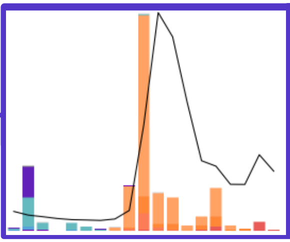


Limpopo ↓ PTP: 22.8%

Genomes	Cases
242 (3.6%)	29 396 (4.2%)

Genomes deposited in the last week

🟧86 🟧18 🟥7

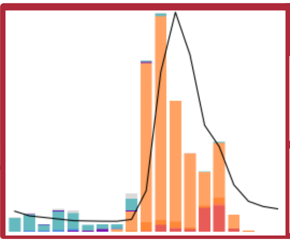


Mpumalanga ↓ PTP: 21.1%

Genomes	Cases
463 (6.8%)	35 140 (5.0%)

Genomes deposited in the last week

🟧19 🟧7 🟥5 🟪2 🟦1

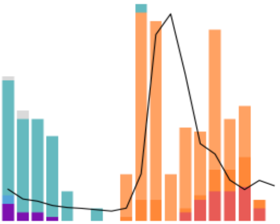


KwaZulu-Natal ↓ PTP: 8.4%

Genomes	Cases
1 076 (15.8%)	132 197 (18.7%)

Genomes deposited in the last week

🟧49 🟧10 🟥2 🟦1

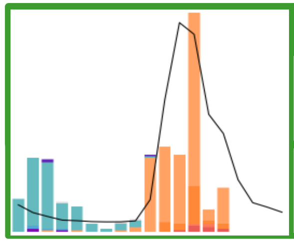


Free State ↓ PTP: 10.7%

Genomes	Cases
378 (5.6%)	35 771 (5.1%)

Genomes deposited in the last week

🟧55 🟧15 🟥21



Eastern Cape ↓ PTP: 7.0%

Genomes	Cases
503 (7.4%)	50 667 (7.4%)

Genomes deposited in the last week

🟧81 🟧12 🟥48 🟦2

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

792 genomes deposited in the past week

Bar graphs represent genomes sequenced per epiweek, with lines representing cases by collection date (weeks 39 [2021] – 5 [2022])
Genomes and cases presented as provincial total (percentage of national total) for epiweeks 39 (2021) – 5 (2022)
PTP: percentage testing positive in week 5 (30 Jan 2022 – 5 Feb 2022); the arrow indicates direction of change since the previous week (23 Jan 2022 – 29 Jan 2022)

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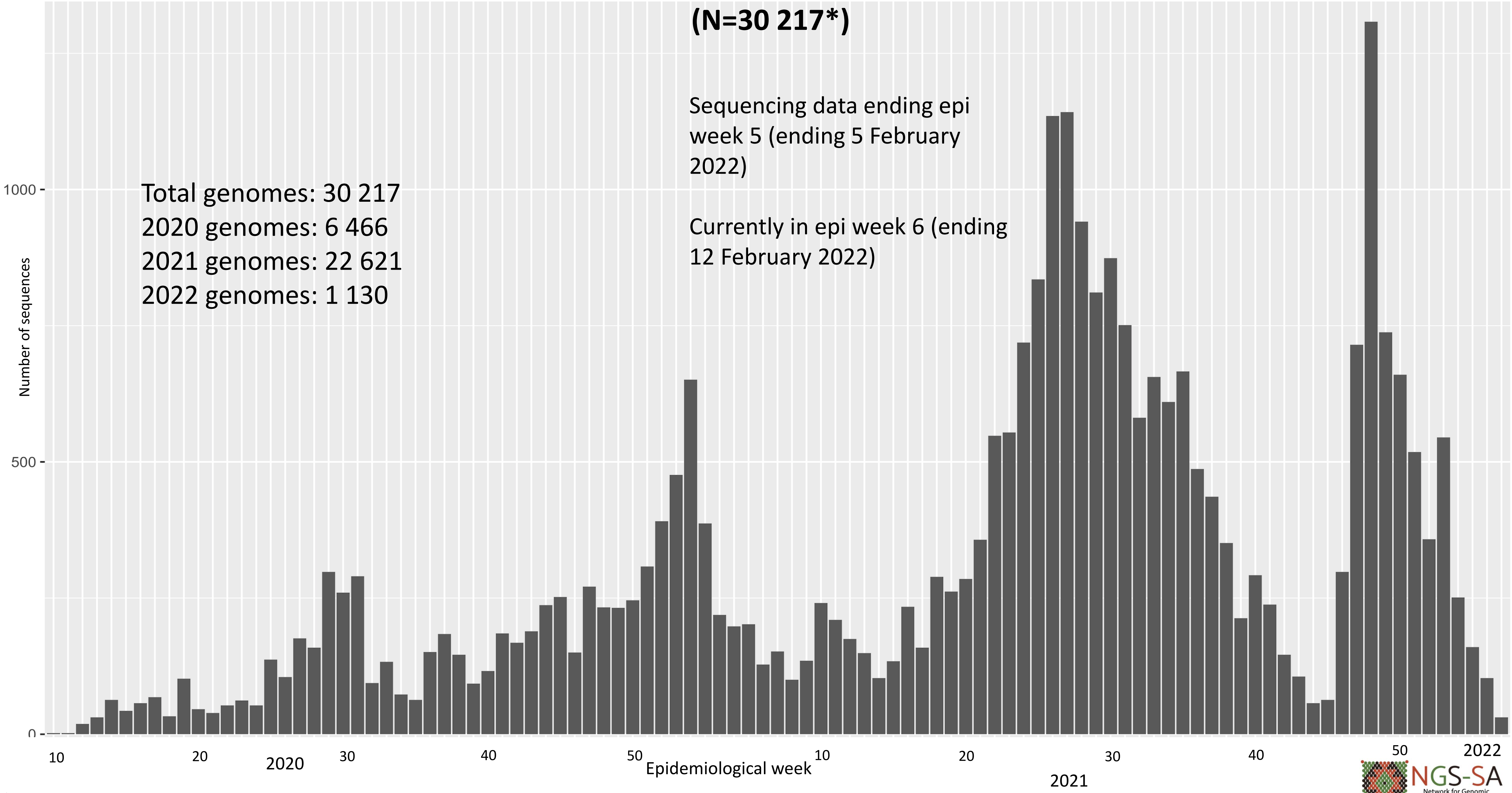
Number of South African genomes deposited on GISAID, by specimen collection week, 2020 – 2022 (N=30 217*)



Total genomes: 30 217
2020 genomes: 6 466
2021 genomes: 22 621
2022 genomes: 1 130

Sequencing data ending epi week 5 (ending 5 February 2022)

Currently in epi week 6 (ending 12 February 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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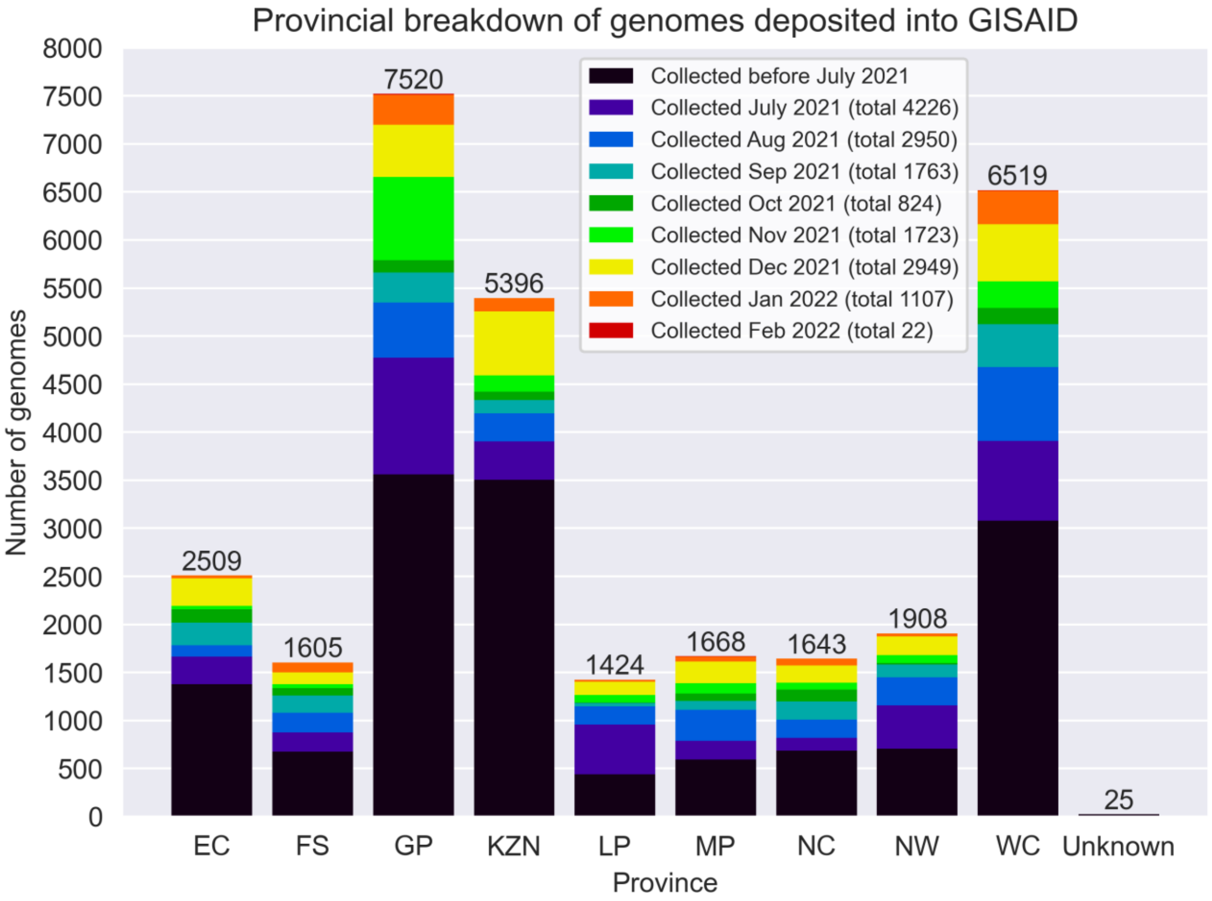
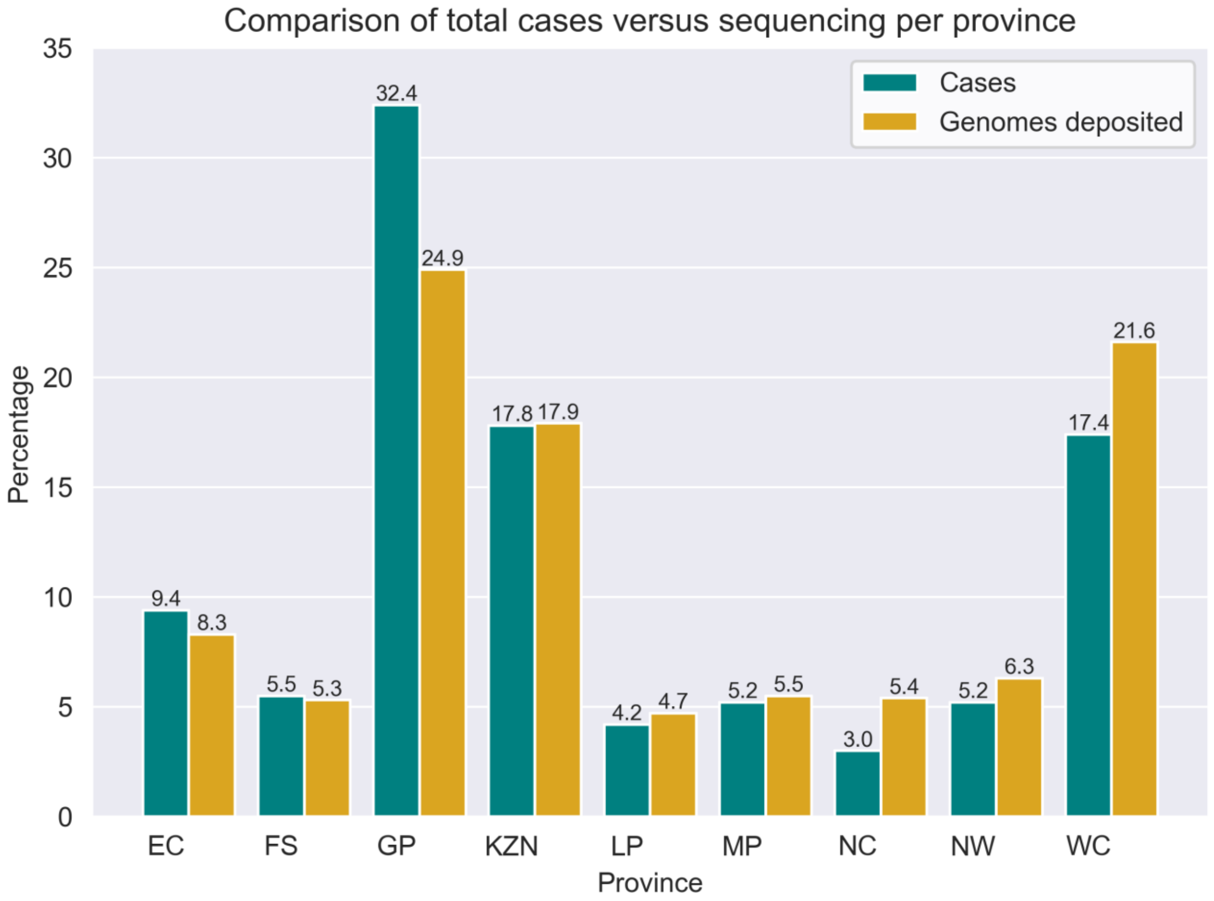
GISAID genomes vs total cases, 2020 – 2022 (N=30 217)



Provincial breakdown of genomes deposited into GISAID



Comparison of total cases versus sequencing per province

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

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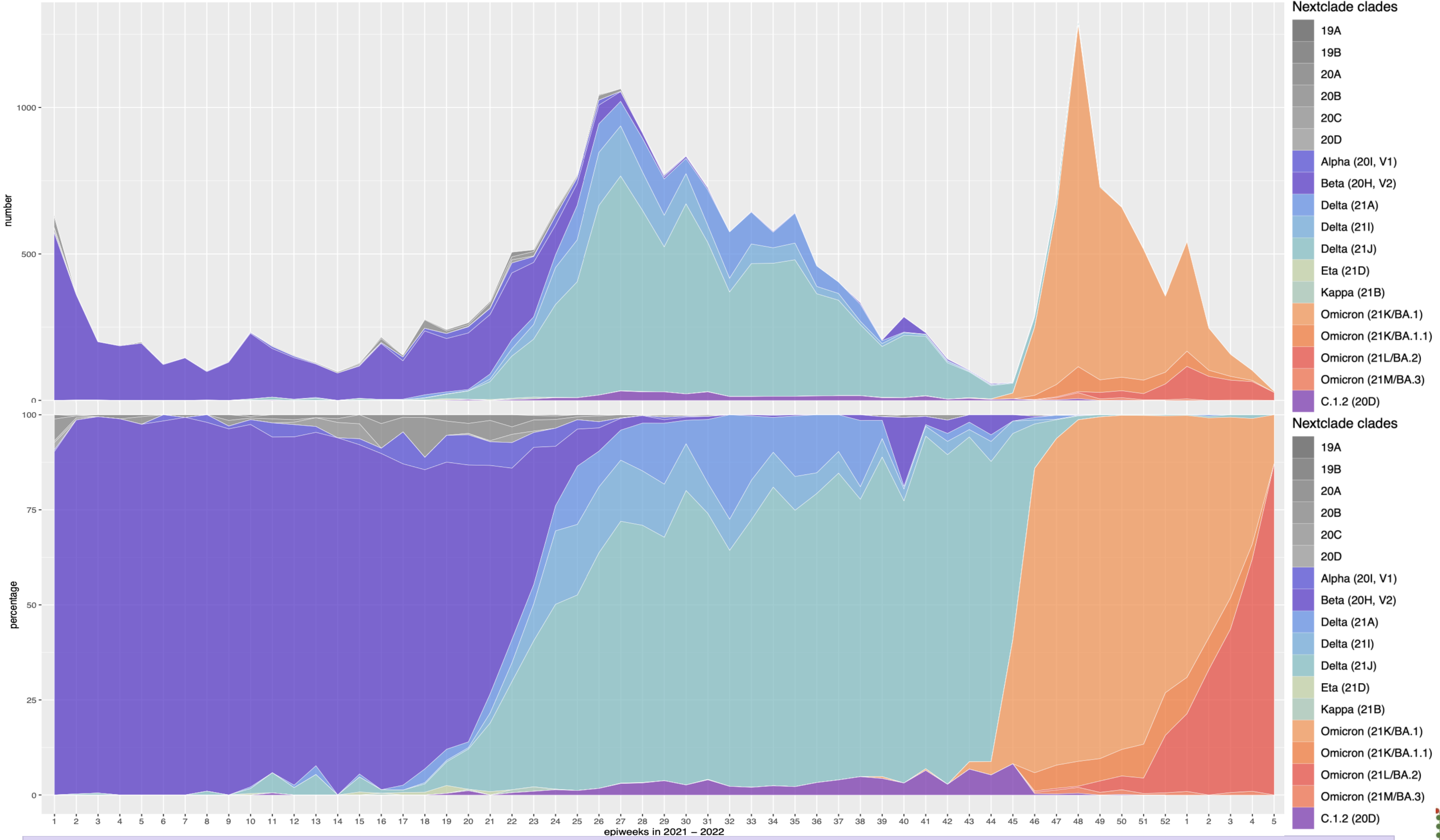
Percentage and number of clades by epiweek in South Africa, 2021 - 2022 (N=23 751)



Sequencing data ending epi week 5 (ending 5 February 2022)

Currently in epi week 6 (ending 12 February 2022)

Delta dominated in South Africa until October at >80%. Omicron dominated November and December at >95%.

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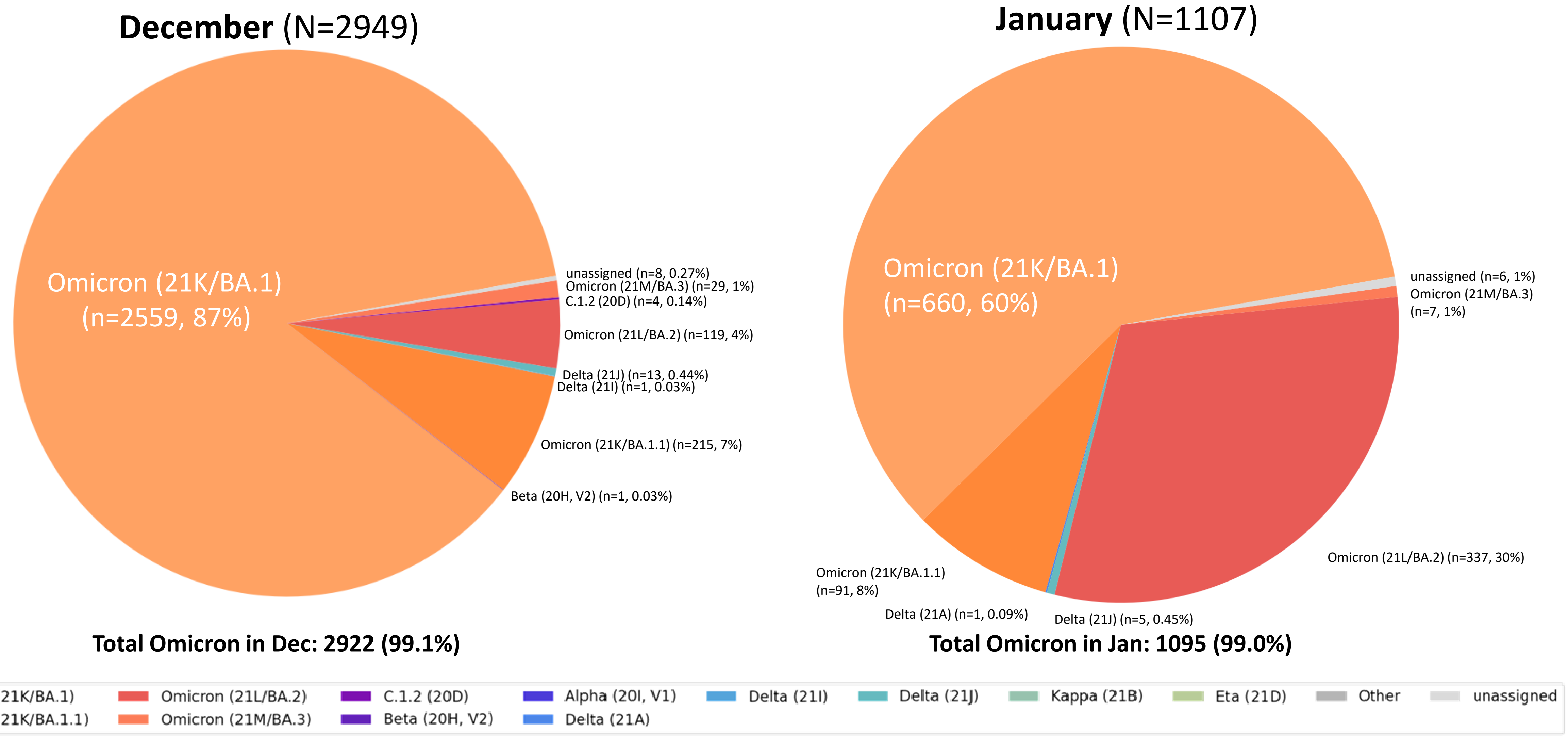
Prevalence of Variants of Concern (VOC) and Variants of Interest (VOI) in Dec 2021 – Jan 2022



Total Omicron in Dec: 2922 (99.1%)

Total Omicron in Jan: 1095 (99.0%)

Omicron dominated in December (99%, 2922/2949). Omicron continues to dominate in January (99%, 1095/1107), with BA.2 increasing in prevalence.

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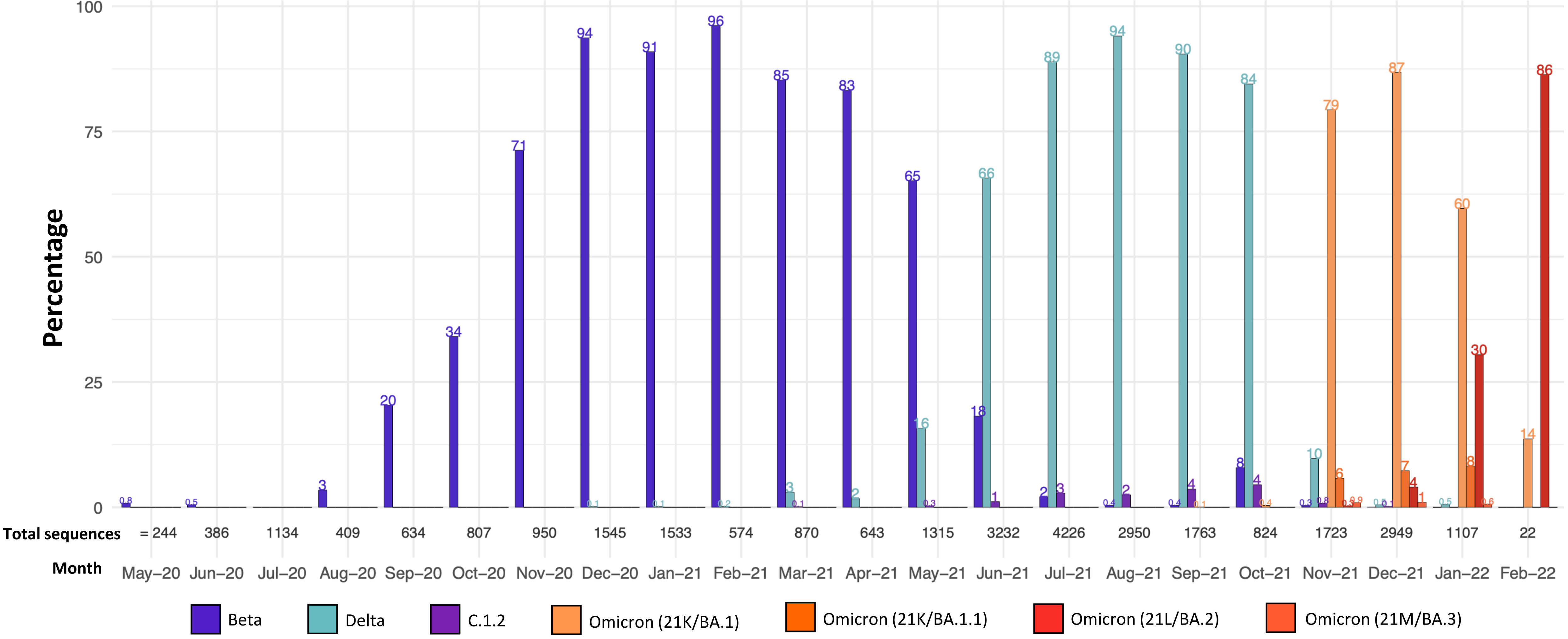
Detection Rates: Beta, Delta, C.1.2 and Omicron


Detection rates of variants being monitored in South Africa*

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

Omicron has been dominant since November (>80% in November, >98% in December and January). BA.2 has significantly increased in frequency in January, now making up 29% of genomes. BA.2 dominates February but more sequencing data is required to confirm its prevalence.

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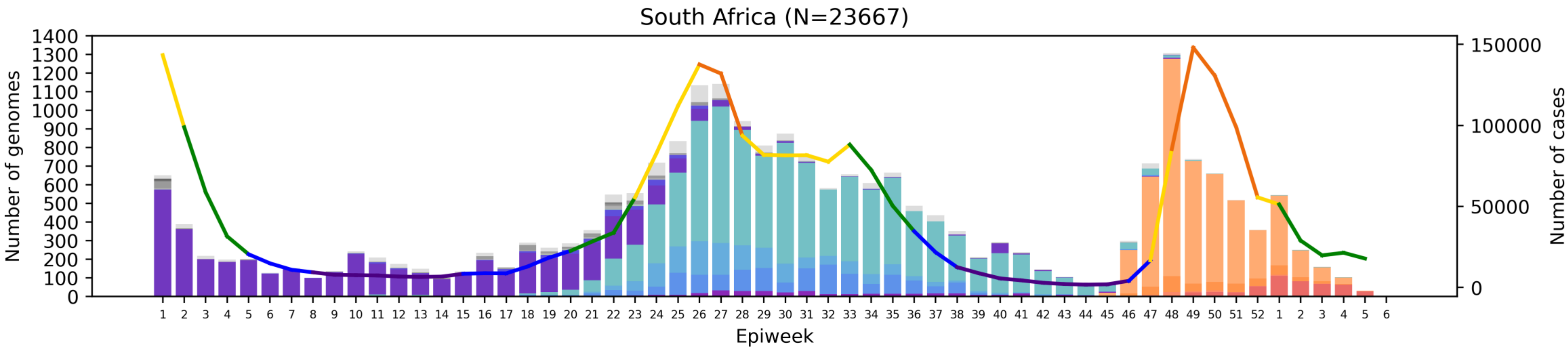
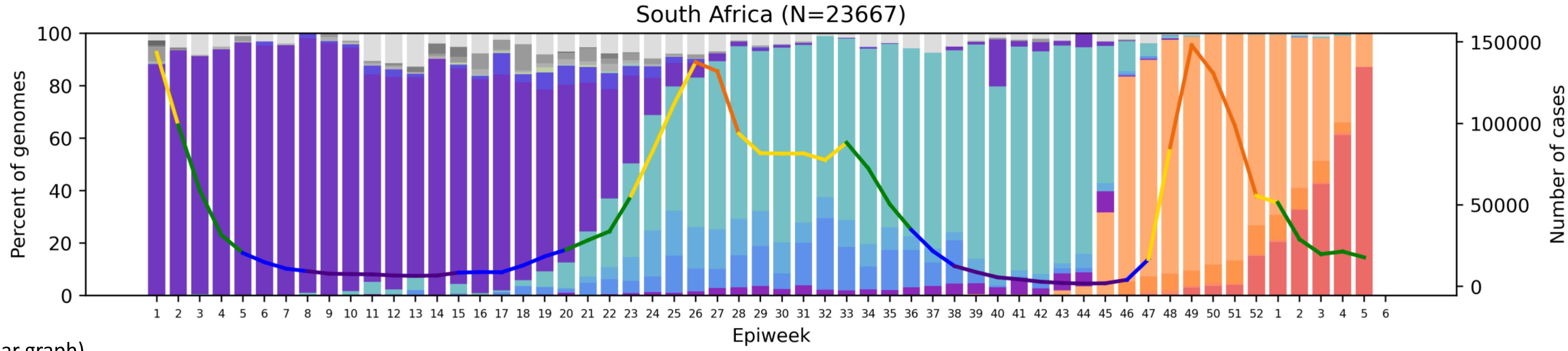
South Africa, 2021-2022, n = 23667*





Clade key (bar graph)

🟥 Omicron (21L/BA.2) 🟧 Omicron (21K/BA.1.1) 🟪 C.1.2 (20D) 🟦 Delta (21I) 🟪 Beta (20H, V2) 🟦 Alpha (20I, V1) 🟩 Kappa (21B) 🟩 Eta (21D) ■ 20A ■ 20B ■ 20C ■ 20D ■ unassigned ■ 19A ■ 19B
🟧 Omicron (21M/BA.3) 🟧 Omicron (21K/BA.1) 🟦 Delta (21A) 🟦 Delta (21J) — Cases

Weekly percentage testing positive key (line graph)

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

*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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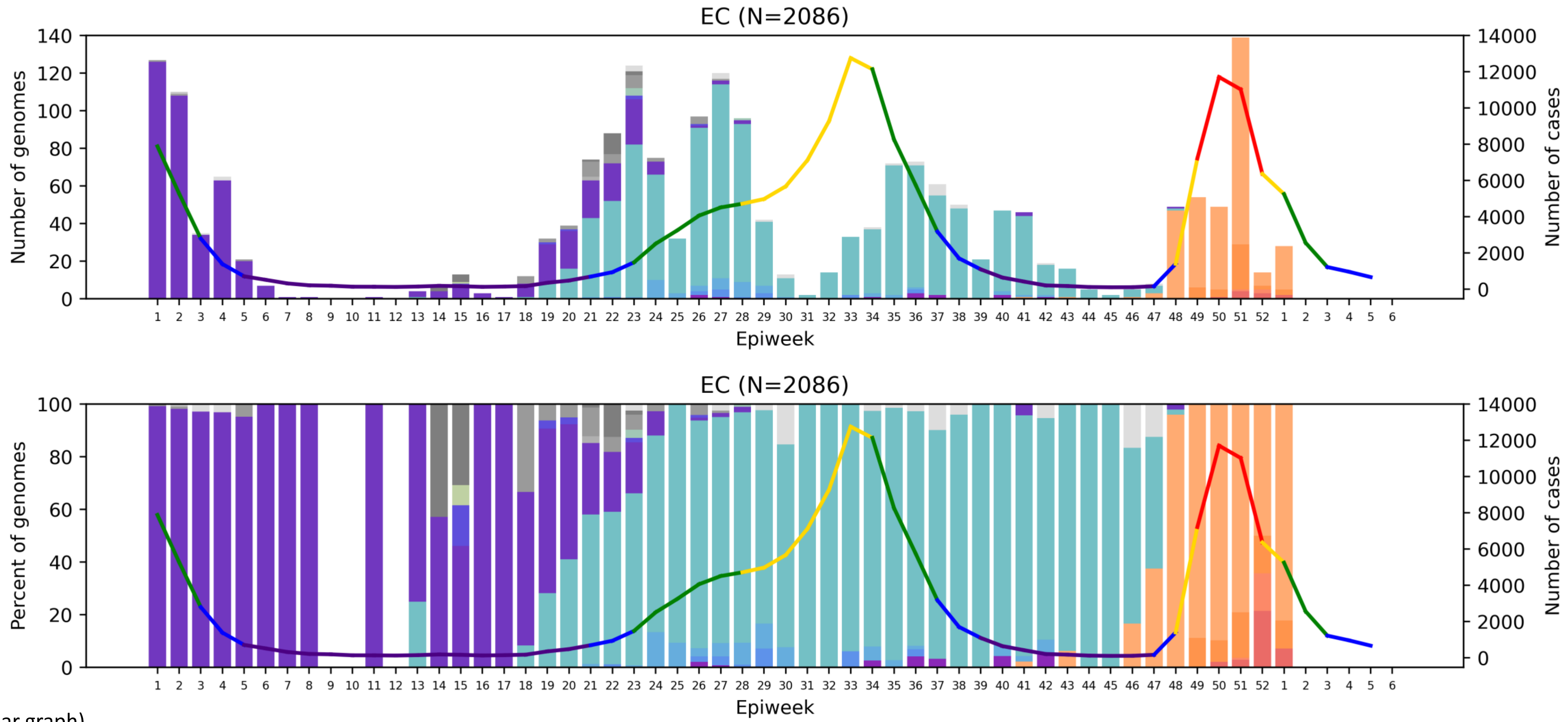
Eastern Cape Province, 2021-2022, n = 2086



Clade key (bar graph)

- 🟥 Omicron (21L/BA.2)
- 🟧 Omicron (21M/BA.3)
- 🟧 Omicron (21K/BA.1.1)
- 🟧 Omicron (21K/BA.1)
- 🟪 C.1.2 (20D)
- 🟦 Delta (21A)
- 🟦 Delta (21I)
- 🟩 Delta (21J)
- 🟪 Beta (20H, V2)
- — Cases
- 🟦 Alpha (20I, V1)
- 🟩 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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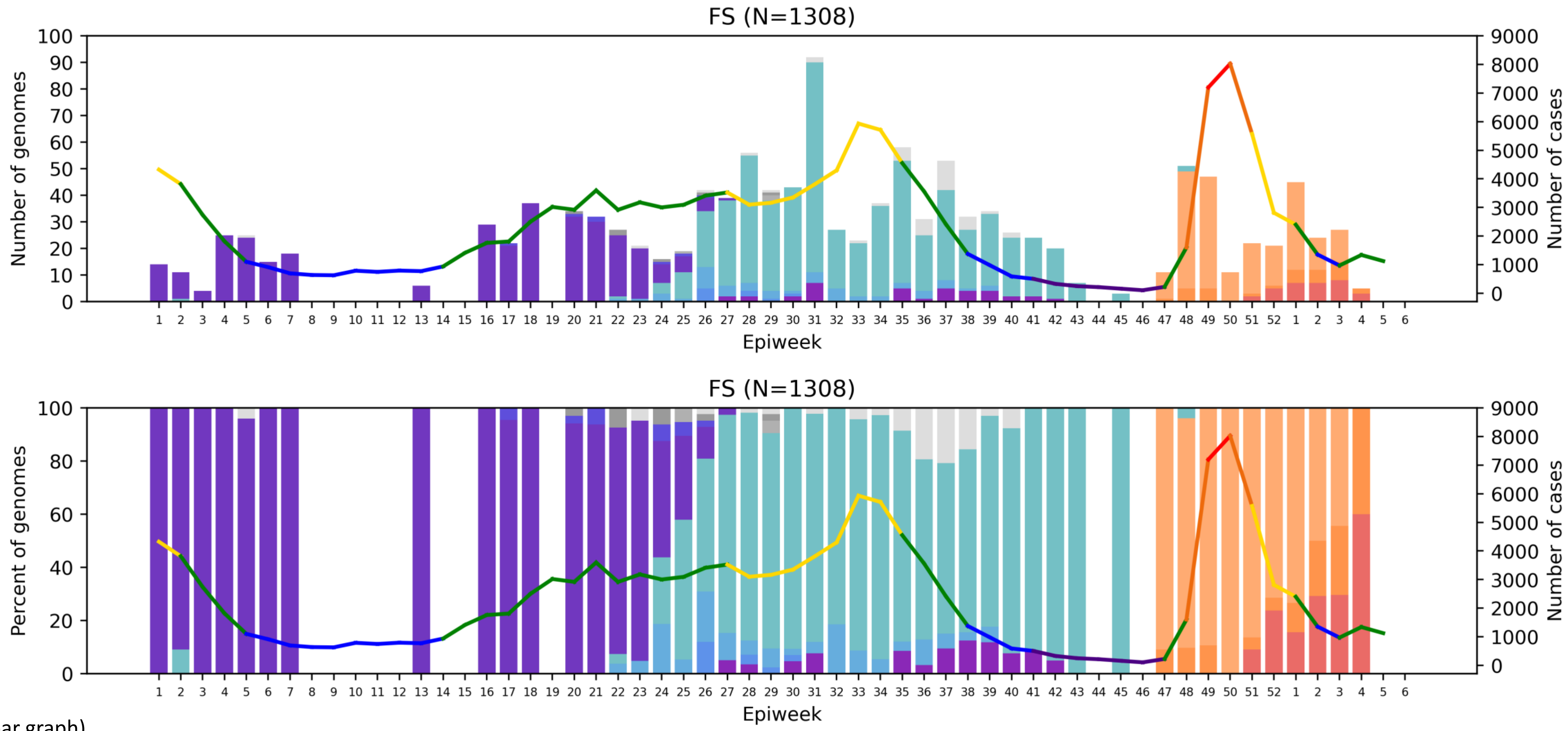
Free State Province, 2021-2022, n = 1308



Clade key (bar graph)

Omicron (21L/BA.2)	Omicron (21K/BA.1.1)	C.1.2 (20D)	Delta (21I)	Beta (20H, V2)	Alpha (20I, V1)	Kappa (21B)	Eta (21D)	20A	20B	20C	20D
Omicron (21M/BA.3)	Omicron (21K/BA.1)	Delta (21A)	Delta (21J)	Cases							

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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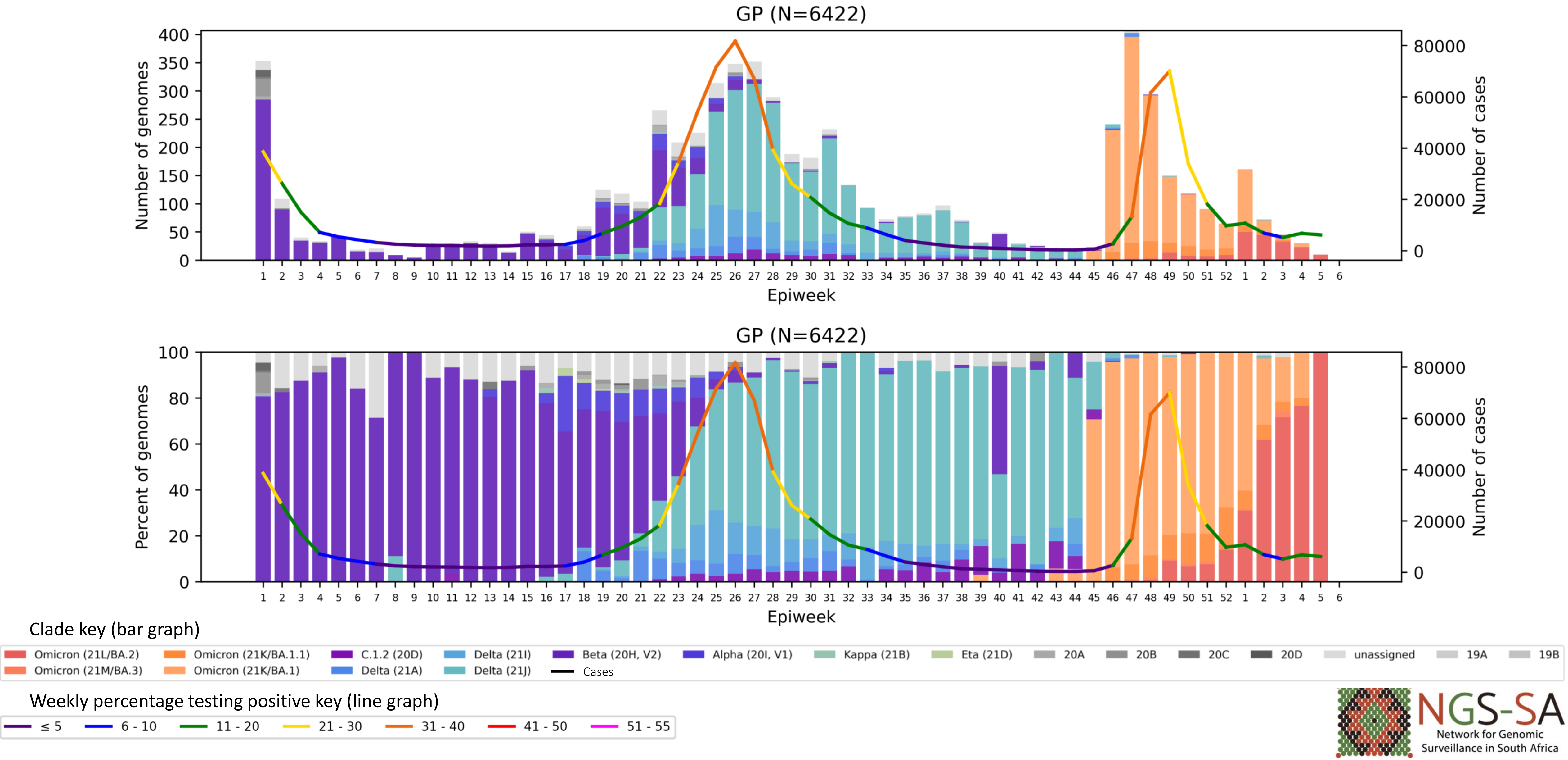
Gauteng Province, 2021-2022, n = 6422



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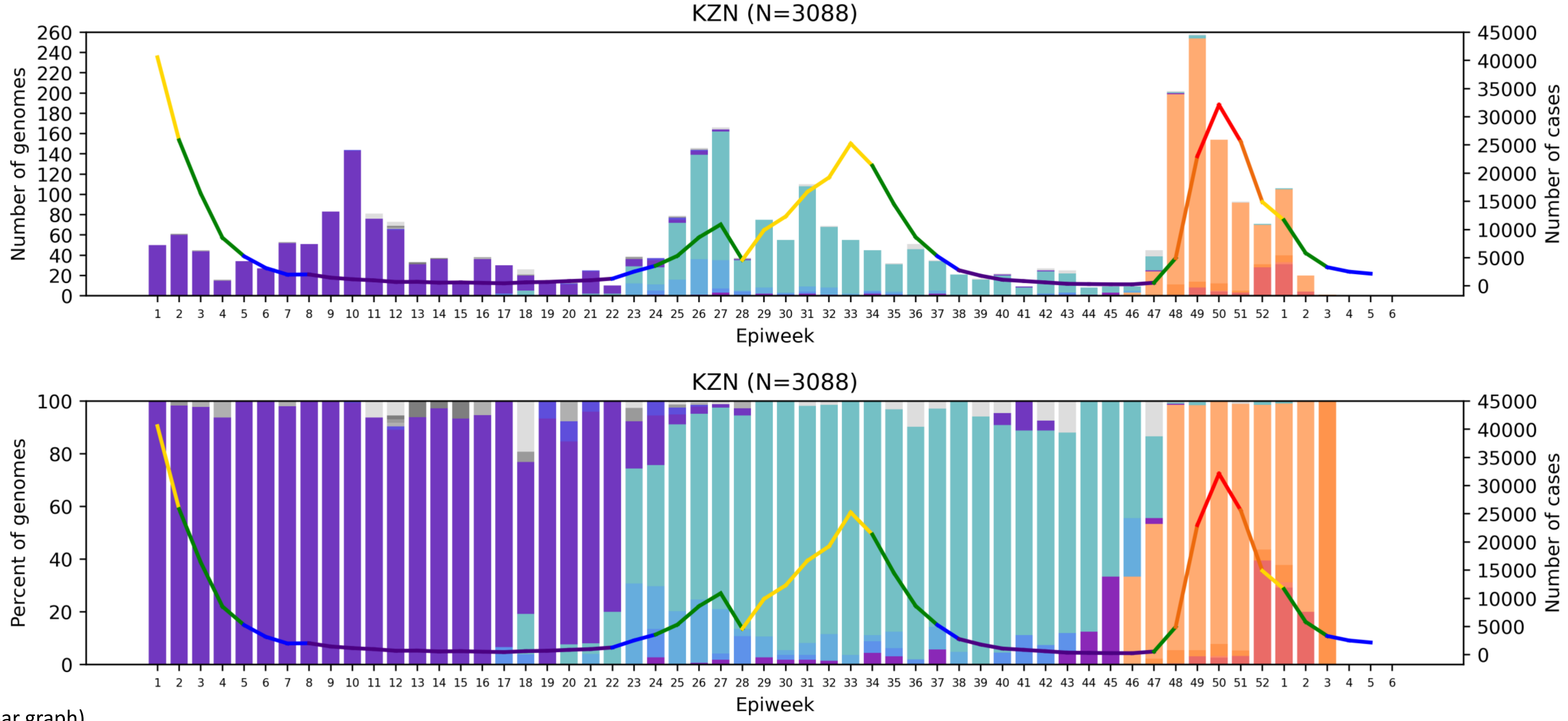
KwaZulu-Natal Province, 2021-2022, n = 3088



Clade key (bar graph)

- Omicron (21L/BA.2)
- Omicron (21M/BA.3)
- Omicron (21K/BA.1.1)
- Omicron (21K/BA.1)
- C.1.2 (20D)
- Delta (21A)
- Delta (21I)
- Delta (21J)
- Beta (20H, V2)
- Cases
- Alpha (20I, V1)
- 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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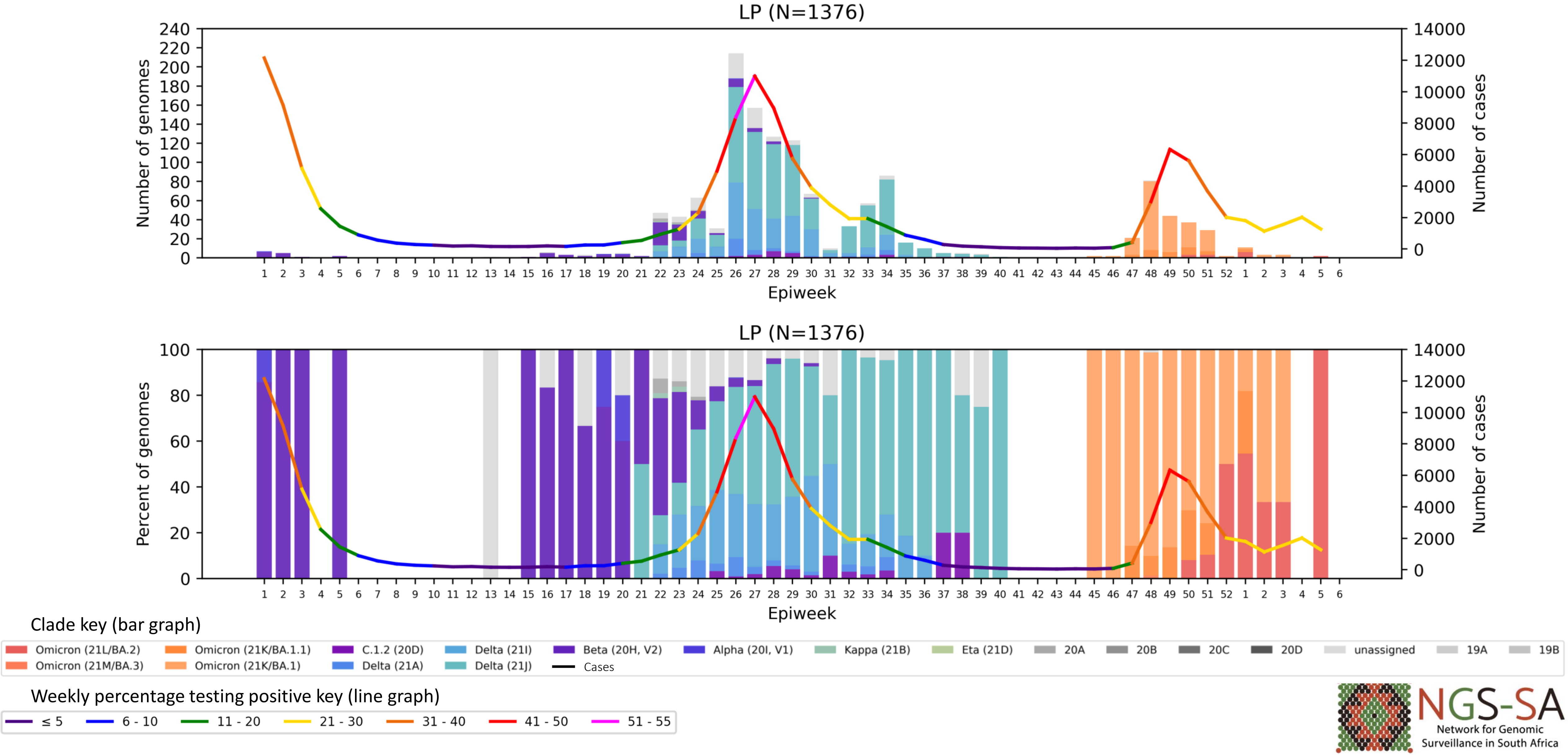
Limpopo Province, 2021-2022, n = 1376



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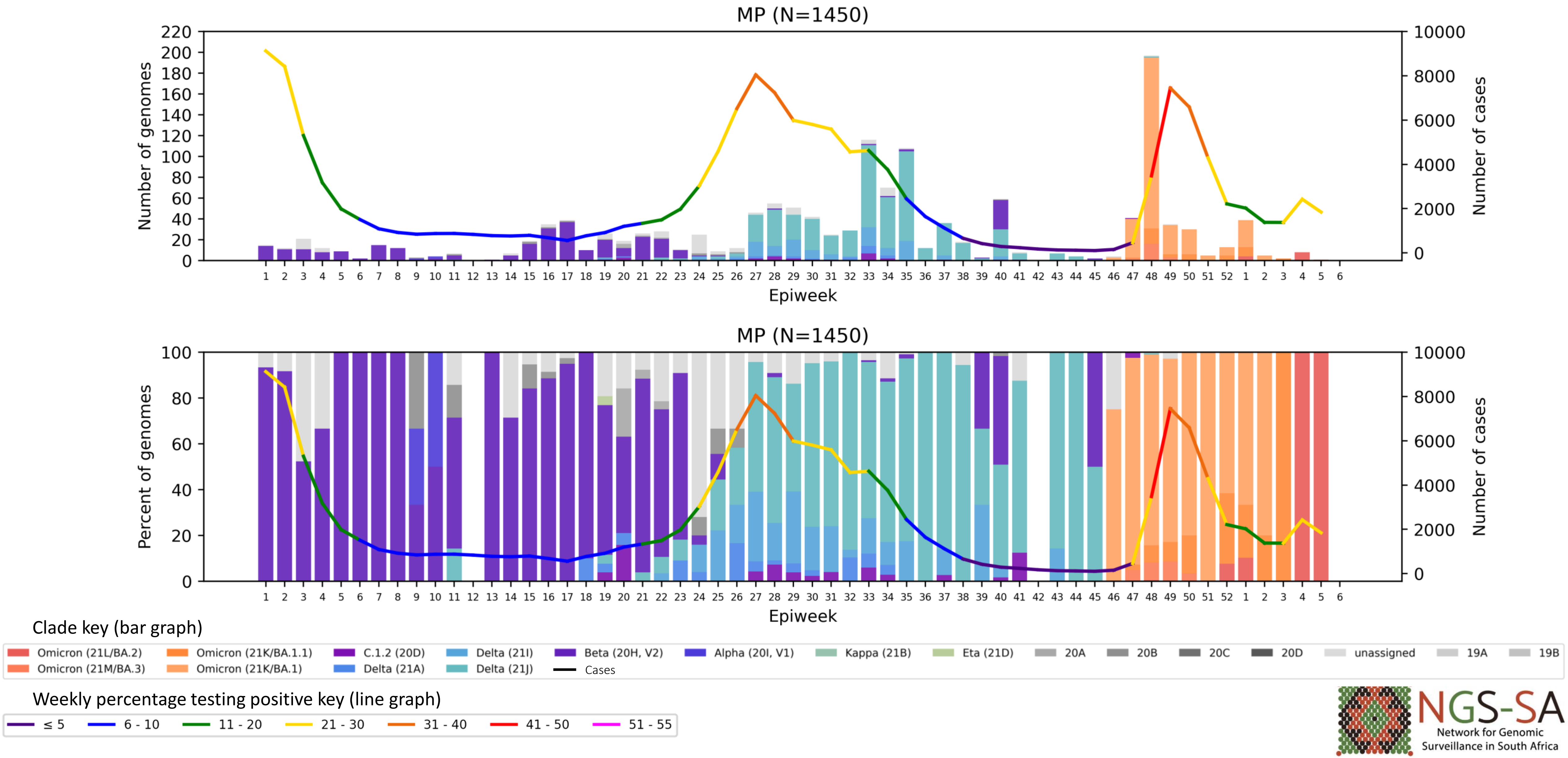
Mpumalanga Province, 2021-2022, n = 1450



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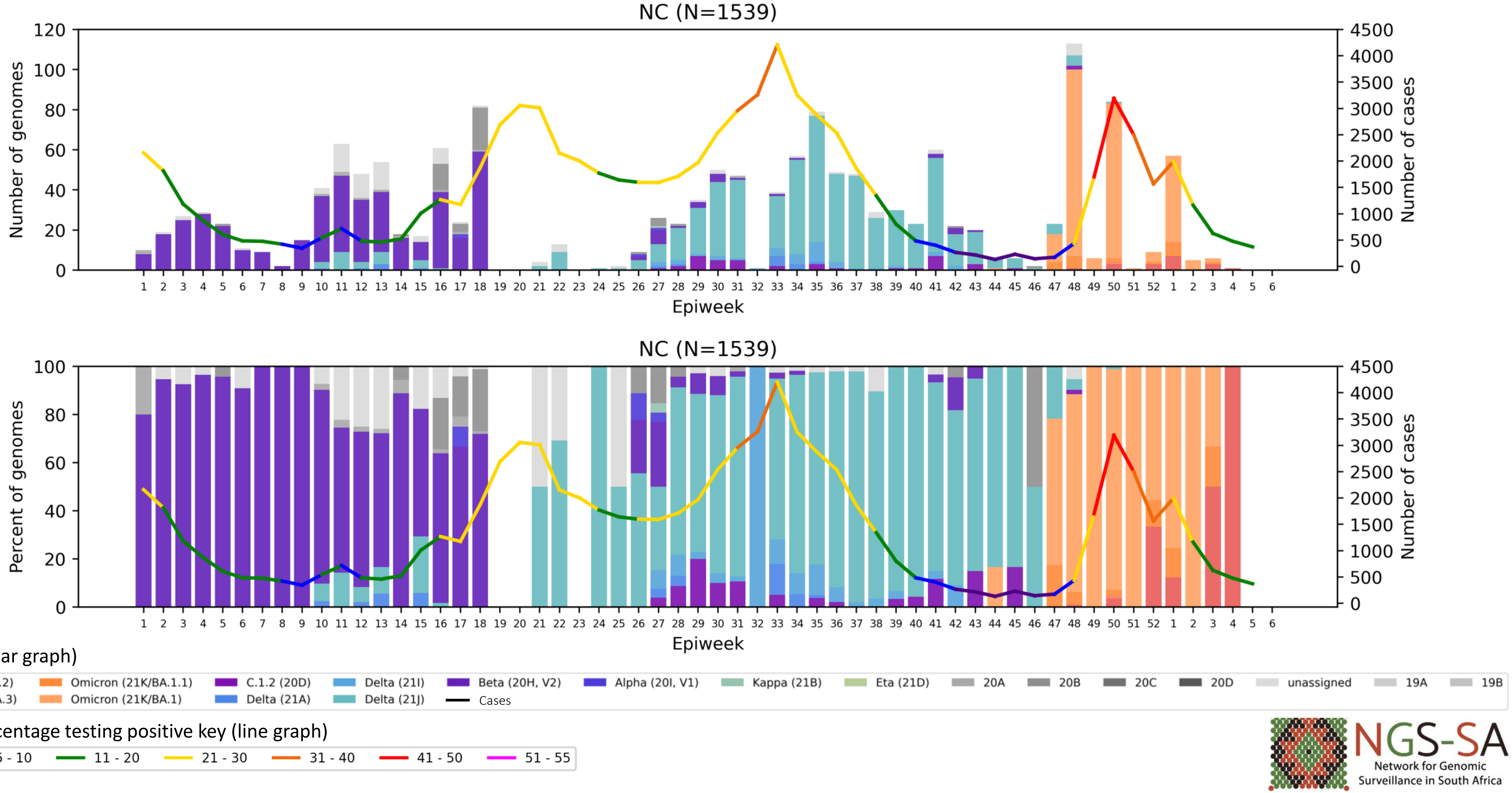
Northern Cape Province, 2021-2022, n = 1539



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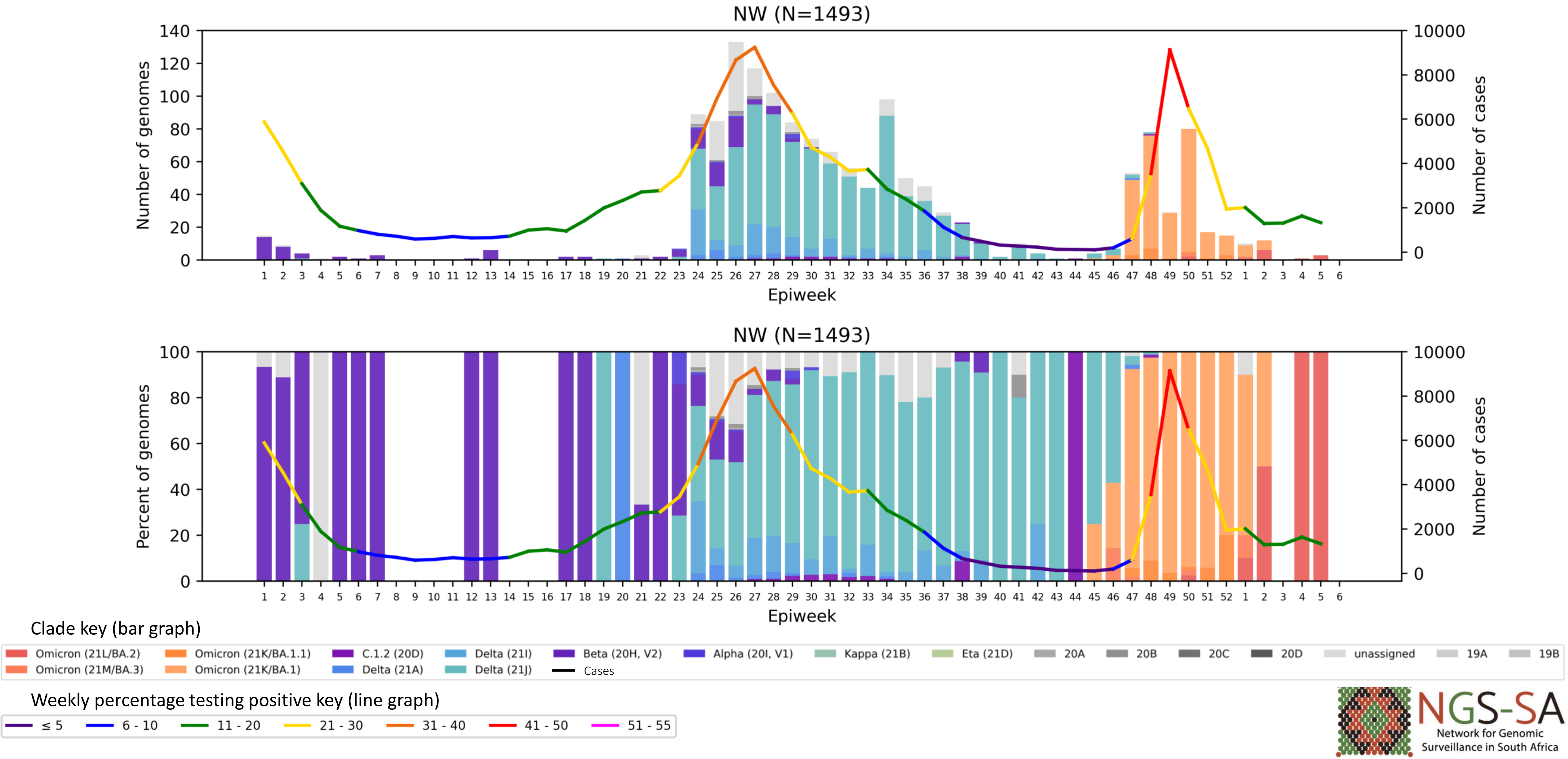
North West Province, 2021, n = 1493



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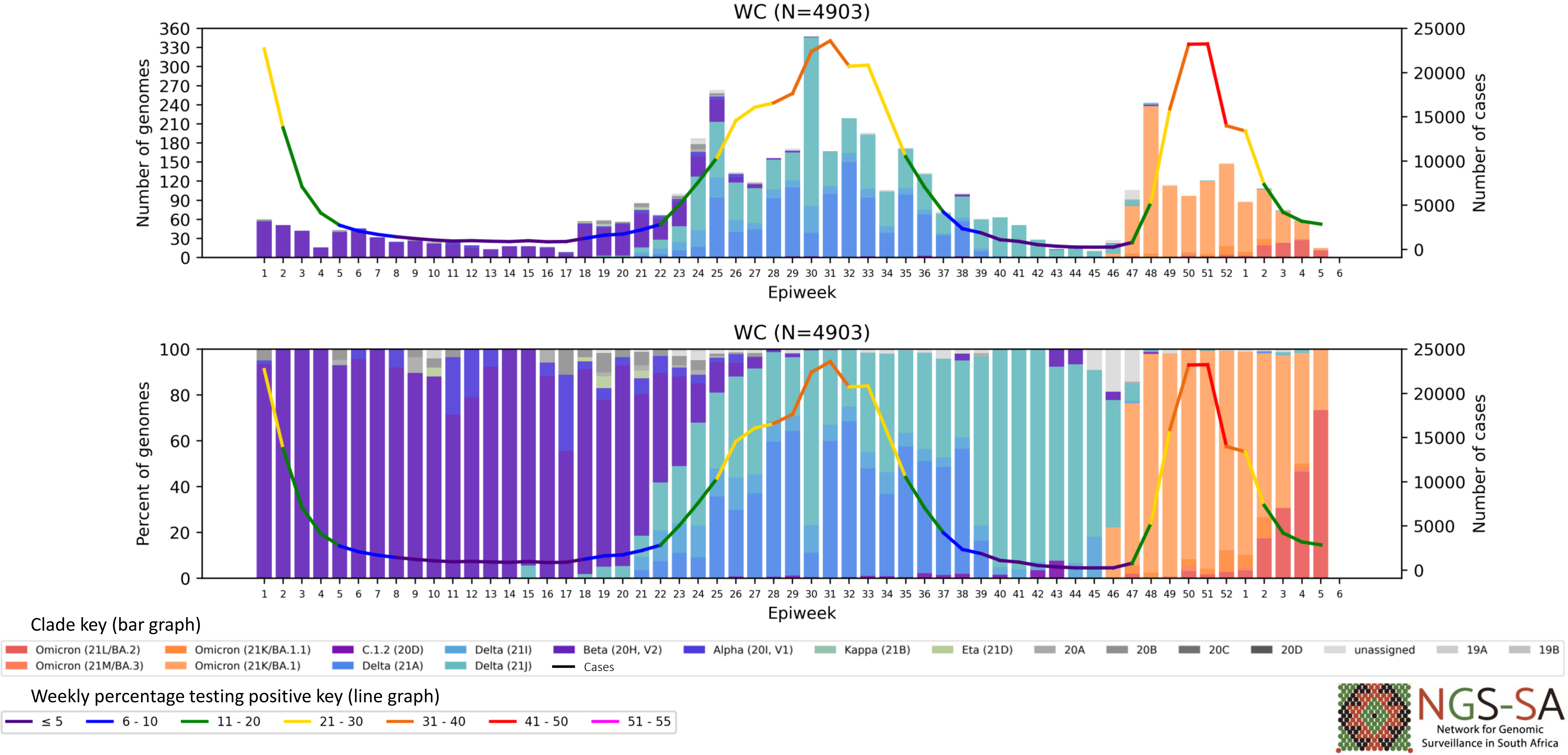
Western Cape Province, 2021-2022, n = 4903



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Summary

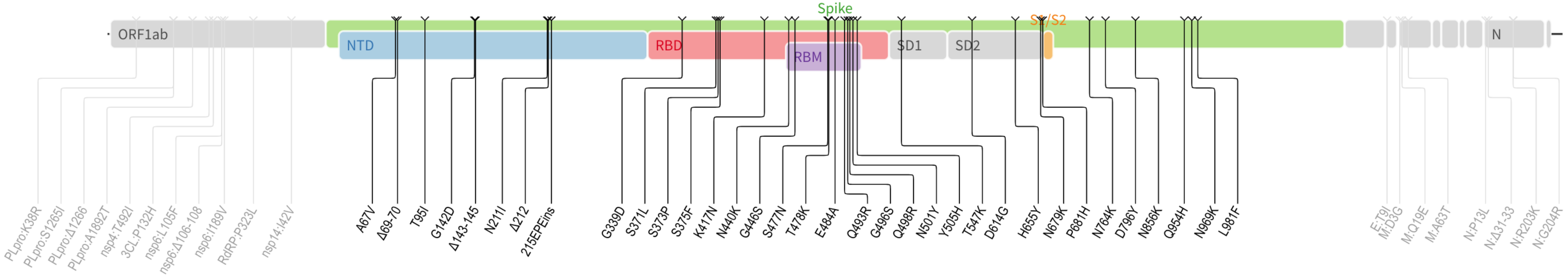
- **Variant of Concern Omicron**
  - Detected in at least 145 countries and dominating globally
  - Split into different lineages based on different mutational profiles: BA.1 (21K), BA.1.1 (21K, BA.1+spike R346K), BA.2 (21L), BA.3 (remains in 21M as does not meet requirements for new clade), B.1.1.529 (parent lineage, 21M)

  - South Africa (detected in all provinces):
    - Dominated December sequencing data at 99% of genomes
    - Sequence data for January shows continued dominance of Omicron, with increase of BA.2 to 30% of sequences
      - BA.2 has increased in recent epiweeks in the Free State, Gauteng, Limpopo, Mpumalanga, the North West and the Western Cape.
    - Limited data for February shows BA.2 at 86% prevalence

- Low frequency of previously circulating variants such as Delta still detected in recent data

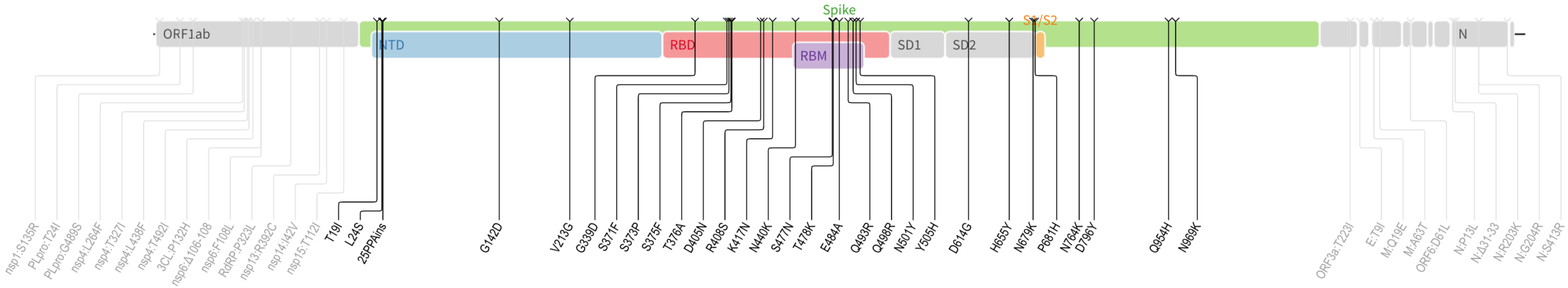
Omicron sub-lineage spike mutation profiles

BA.1
21K

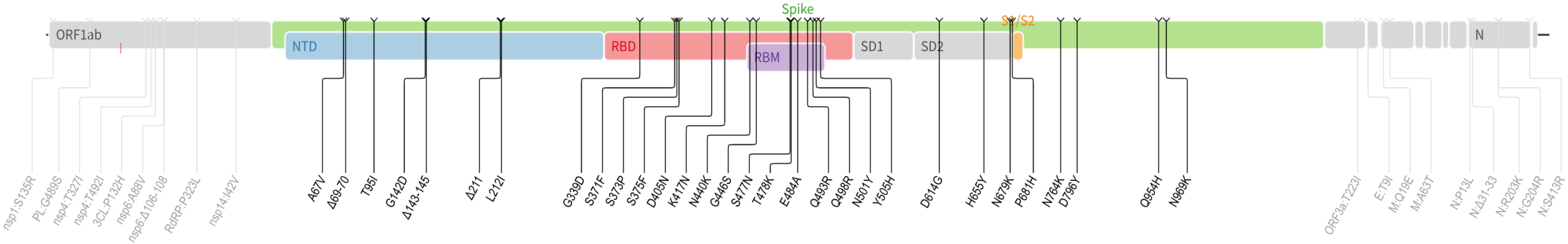


BA.2
21L

Lacks 69-70del
Not detectable by
S-Gene Target
Failure



BA.3
21M



Lineage definitions based on https://github.com/cov-lineages/pango-designation/issues/367
Images from https://covdb.stanford.edu/page/mutation-viewer/

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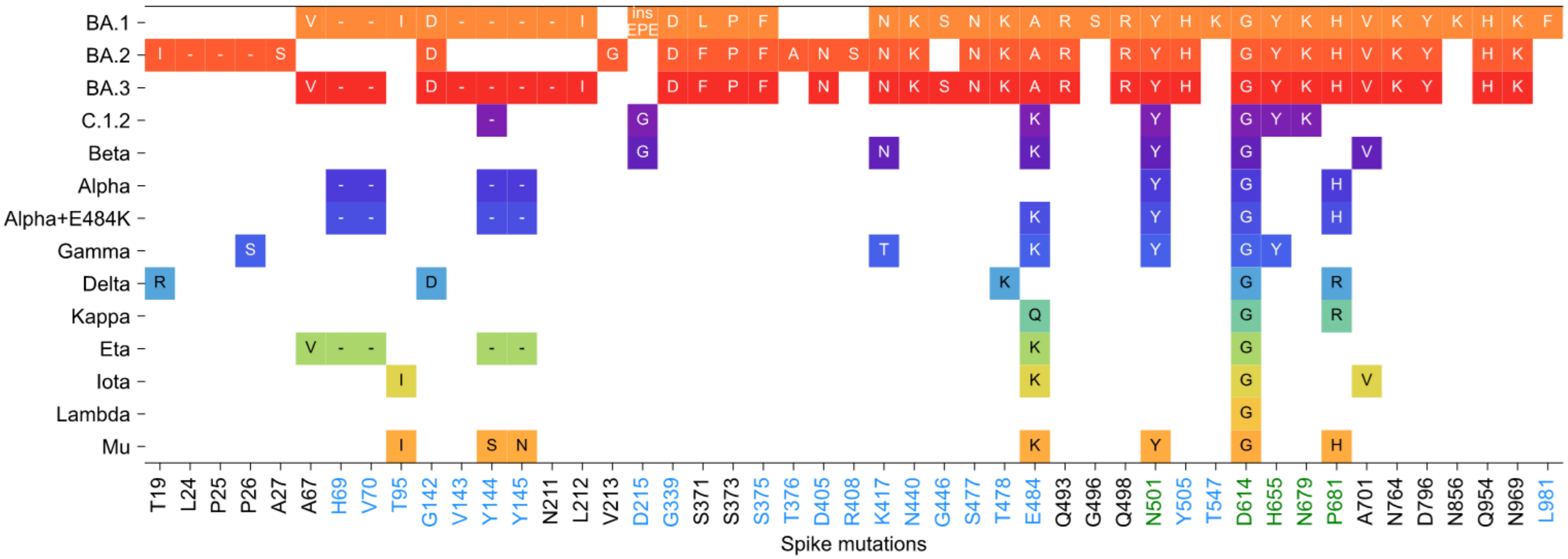
Omicron spike mutations compared to other VOC/VOIs



	T19	L24	P25	P26	A27	A67	H69	V70	T95	G142	V143	Y144	Y145	N211	L212	V213
BA.1						V	-	-	I	D	-	-	-	-	I	
BA.2	I	-	-	-	S					D						G
BA.3						V	-	-		D	-	-	-	-	I	
C.1.2												-				
Beta																
Alpha							-	-				-	-			
Alpha+E484K							-	-				-	-			
Gamma				S												
Delta	R									D						
Kappa																
Eta						V	-	-				-	-			
Iota									I							
Lambda																
Mu									I			S	N			

	D215	G339	S371	S373	S375	T376	D405	R408	K417	N440	G446	S477	T478	E484	Q493	G496
BA.1	ins EPE	D	L	P	F				N	K	S	N	K	A	R	S
BA.2		D	F	P	F	A	N	S	N	K		N	K	A	R	
BA.3		D	F	P	F		N		N	K	S	N	K	A	R	
C.1.2	G													K		
Beta	G								N					K		
Alpha																
Alpha+E484K														K		
Gamma									T					K		
Delta													K			
Kappa														Q		
Eta														K		
Iota														K		
Lambda																
Mu														K		

	Q498	N501	Y505	T547	D614	H655	N679	P681	A701	N764	D796	N856	Q954	N969	L981
BA.1	R	Y	H	K	G	Y	K	H	V	K	Y	K	H	K	F
BA.2	R	Y	H		G	Y	K	H	V	K	Y		H	K	
BA.3	R	Y	H		G	Y	K	H	V	K	Y		H	K	
C.1.2		Y			G	Y	K								
Beta		Y			G				V						
Alpha		Y			G			H							
Alpha+E484K		Y			G			H							
Gamma		Y			G	Y									
Delta					G			R							
Kappa					G			R							
Eta					G										
Iota					G				V						
Lambda					G										
Mu		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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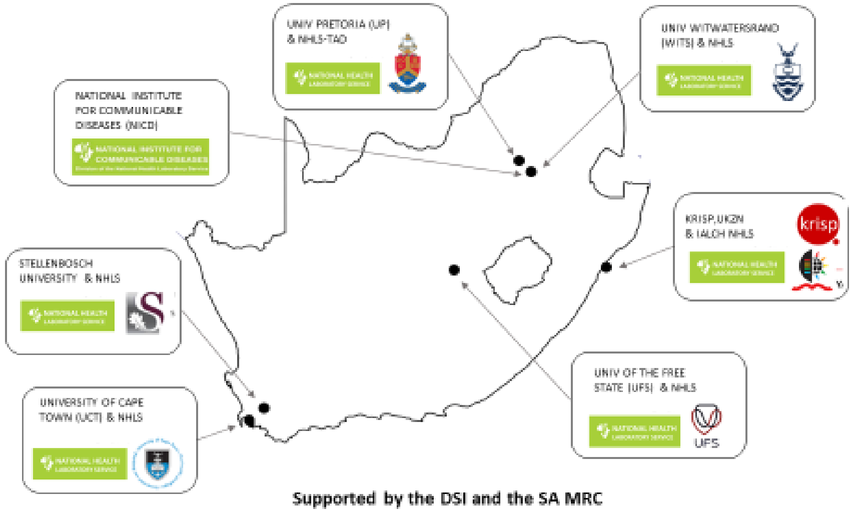

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NATIONAL INSTITUTE FOR COMMUNICABLE DISEASES
Division of the National Health Laboratory Service

EDCTP

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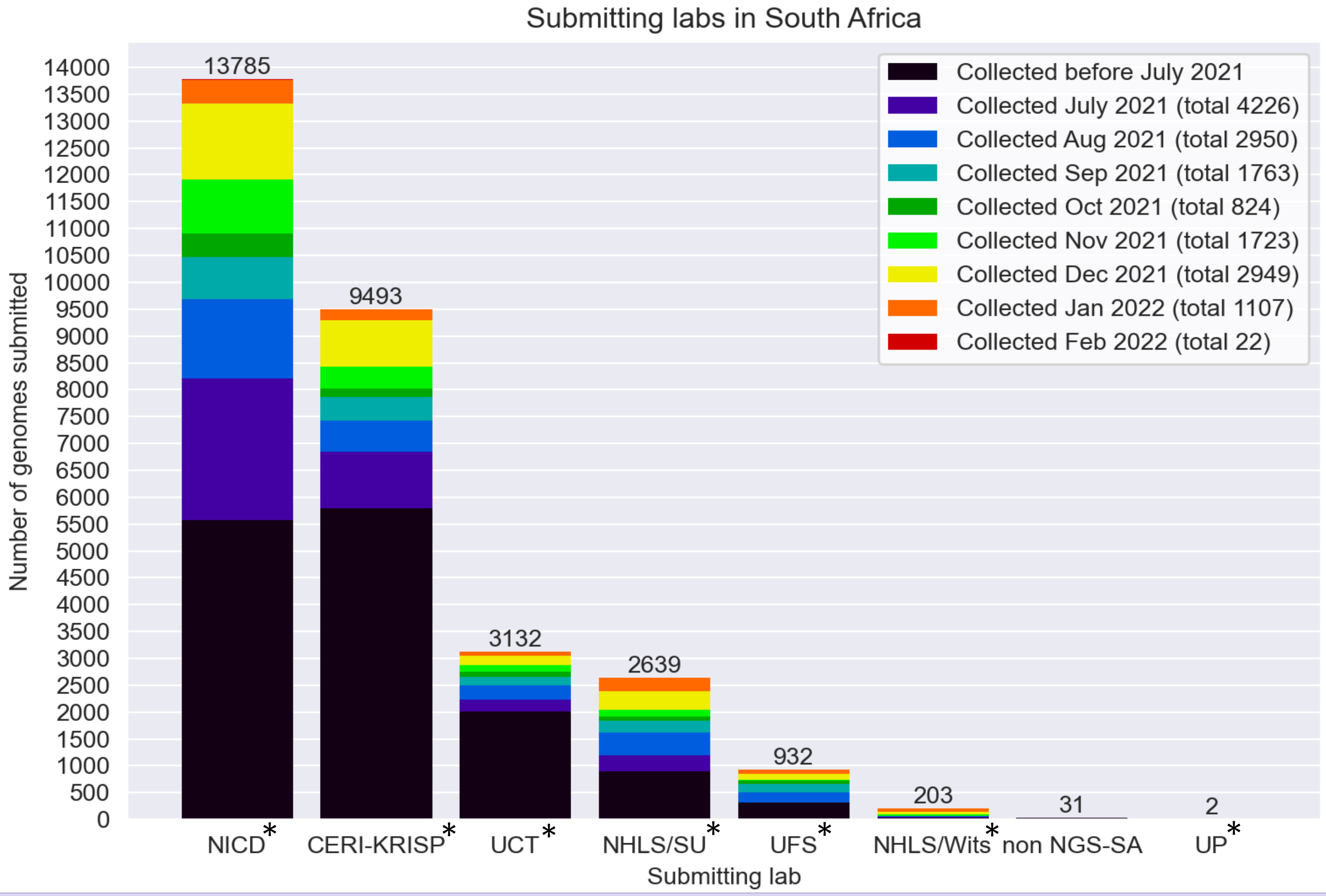
South African genomes submitted per submitting lab, 2020 - 2022 (N=30 217)



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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 and collaborating public and private laboratories are contributing to sequencing, both as originating and as submitting (pictured here) laboratories.

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Network for Genomic Surveillance in South Africa

Variants of Concern (VOC)

WHO label	Pango lineage•	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 +S:E484K	India, Oct-2020	VOI: 4-Apr-2021 VOC: 11-May-2021
Omicron*	B.1.1.529	GRA	21K, 21L, 21M	+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 14 January 2022

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

* See TAG-VE statement issued on 26 November 2021

° Only found in a subset of sequences

Currently designated Variants of Interest (VOI)

WHO label	Pango lineage*	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 17 December 2021

*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.)