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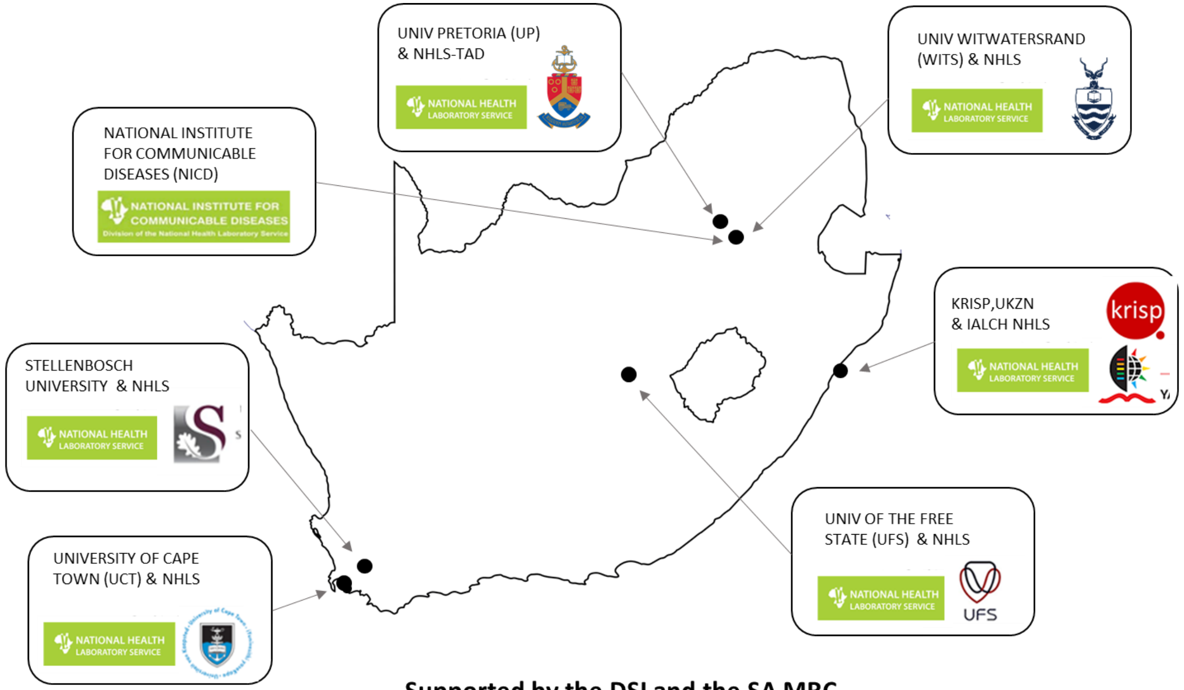
Network for Genomic
Surveillance in South Africa

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

SARS-CoV-2 Sequencing Update
15 July 2022



UNIV PRETORIA (UP)
& NHLS-TAD

UNIV WITWATERSRAND
(WITS) & NHLS

NATIONAL INSTITUTE
FOR COMMUNICABLE
DISEASES (NICD)

KRISP,UKZN
& IALCH NHLS

STELLENBOSCH
UNIVERSITY & NHLS

UNIVERSITY OF CAPE
TOWN (UCT) & NHLS

UNIV OF THE FREE
STATE (UFS) & NHLS

Supported by the DSI and the SA MRC

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

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

Prepared by the National Institute for Communicable Diseases (NICD) of the National Health Laboratory (NHLS) on behalf of the Network for Genomics Surveillance in South Africa (NGS-SA)

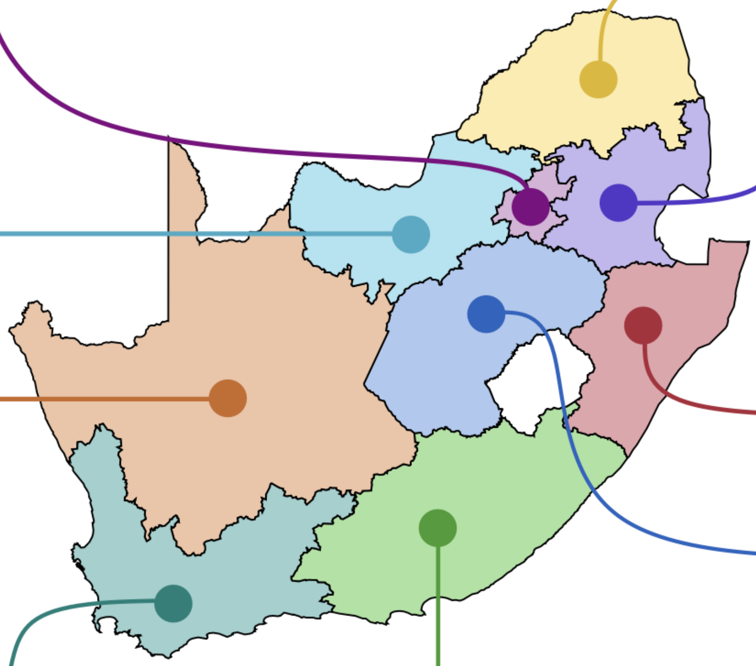
The genomic data presented here are based on South African SARS-CoV-2 sequence data downloaded from GISAID (www.gisaid.org) on 15 July 2022 at 15h28

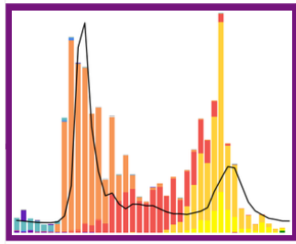
Data license: https://www.gisaid.org/registration/terms-of-use/

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) - 27 (2022)



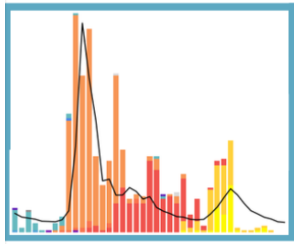


Gauteng ↑ PTP: 5.0%

Genomes	Cases
5 443 (29.5%)	398 744 (37.0%)

Genomes deposited in the last week

🟧1 🟥2 🟨44 🟨29 🟩4

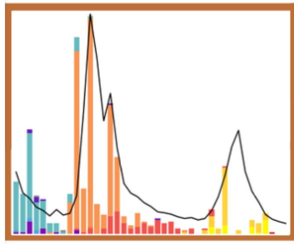


North West - PTP: 3.5%

Genomes	Cases
903 (4.9%)	50 130 (4.6%)

Genomes deposited in the last week

🟨3 🟨3

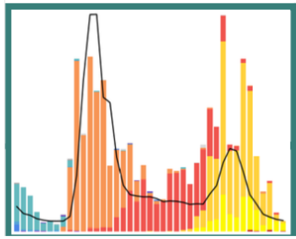


Northern Cape ↓PTP: 1.9%

Genomes	Cases
761 (4.1%)	24 632 (2.3%)

Genomes deposited in the last week

🟥1 🟨7 🟨8

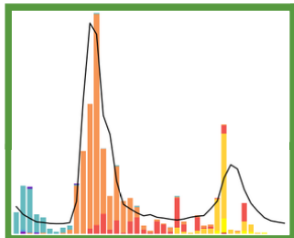


Western Cape - PTP: 6.4%

Genomes	Cases
4 390 (23.8%)	188 561 (17.5%)

Genomes deposited in the last week

🟧3 🟥6 🟥1 🟨132 🟨42

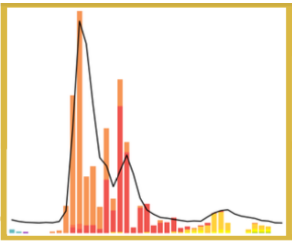


Eastern Cape - PTP: 3.6%

Genomes	Cases
1 243 (6.7%)	73 569 (6.8%)

Genomes deposited in the last week

🟥18 🟨21 🟨3

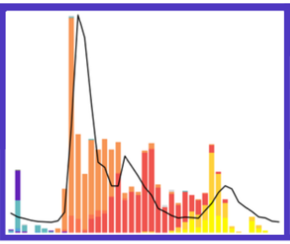


Limpopo - PTP: 4.8%

Genomes	Cases
1 367 (7.4%)	36 317 (3.4%)

Genomes deposited in the last week

🟧1 🟨14 🟨29 🟩3

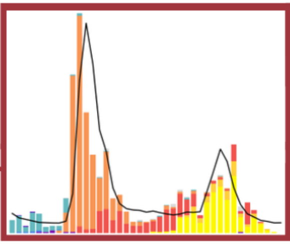


Mpumalanga - PTP: 5.6%

Genomes	Cases
1 658 (9.0%)	50 102 (4.6%)

Genomes deposited in the last week

🟧1 🟥10 🟨14 🟨29

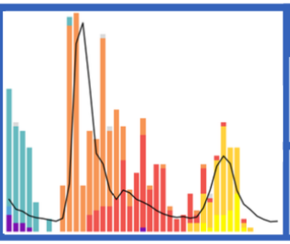


KwaZulu-Natal - PTP: 2.5%

Genomes	Cases
2 032 (11.0%)	203 255 (18.8%)

Genomes deposited in the last week

🟥54 🟨24 🟨84 🟪1



Free State - PTP: 4.6%

Genomes	Cases
645 (3.5%)	53 689 (5.0%)

Genomes deposited in the last week

🟨1

🟩 New1
🟩 New2
🟧 Omicron (BA.1.*)
🟥 Omicron (BA.2.*)
🟨 Omicron (BA.4)
🟨 Omicron (BA.5)
🟥 Omicron (BA.2.12.1)
🟧 Omicron (BA.3)
🟪 Beta
🟦 Delta (21A)
🟦 Delta (21I)
🟦 Alpha
🟪 C.1.2
🟦 Delta (21J)
⬜ 20A
⬜ 20B
⬜ 20C
⬜ 20D
⬜ Unassigned
— Cases

578 genomes added since the previous report

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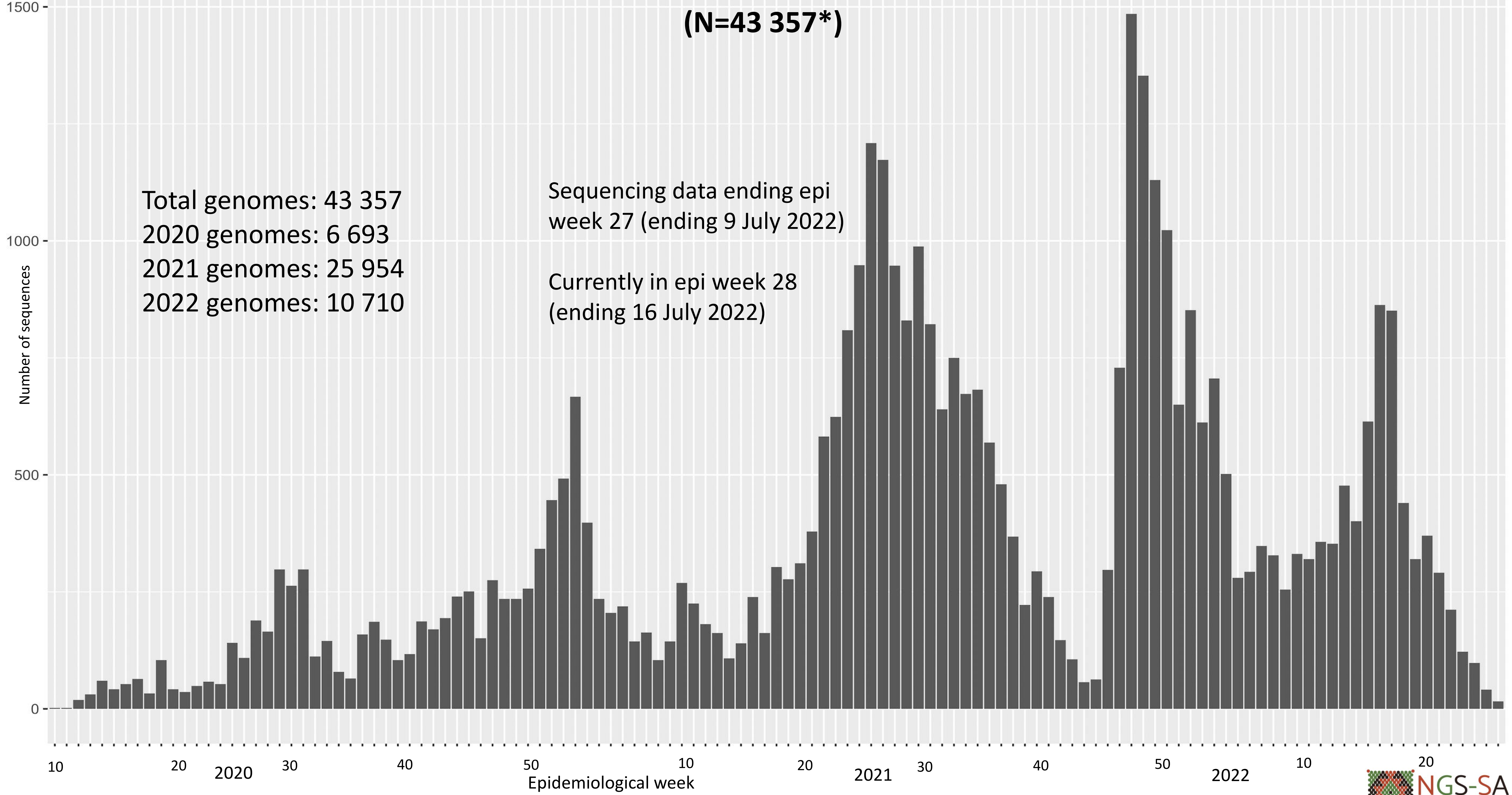
Bar graphs represent genomes sequenced per epiweek, with lines representing cases by collection date (weeks 39 [2021] – 27 [2022])
Genomes and cases presented as provincial total (percentage of national total) for epiweeks 39 (2021) – 27 (2022)
PTP: percentage testing positive in week 27 (03 July 2022 – 09 July 2022); arrow indicates direction of change since previous week (26 June 2022 – 02 July 2022) if change was significant (P<0.05)

Number of South African genomes deposited on GISAID, by specimen collection week, 2020 – 2022 (N=43 357*)



Total genomes: 43 357
2020 genomes: 6 693
2021 genomes: 25 954
2022 genomes: 10 710

Sequencing data ending epi week 27 (ending 9 July 2022)

Currently in epi week 28 (ending 16 July 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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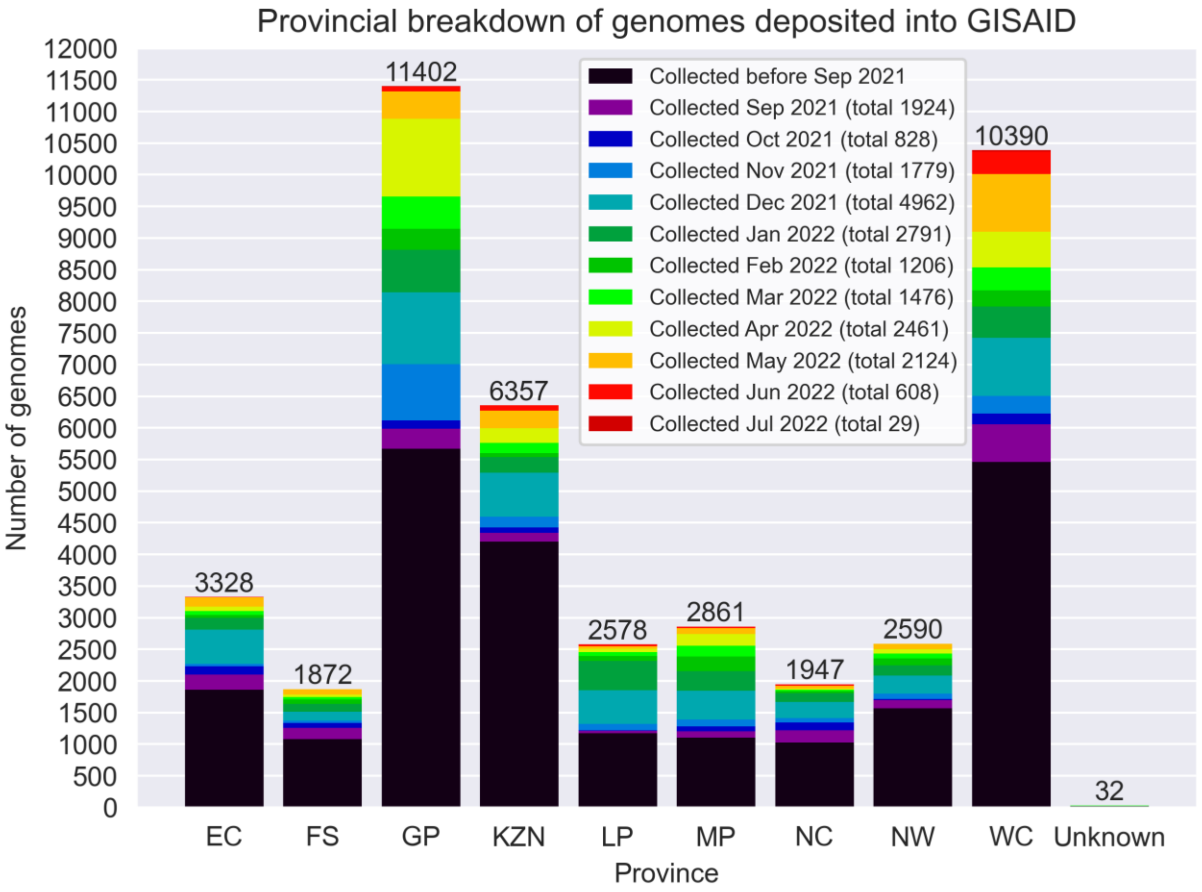
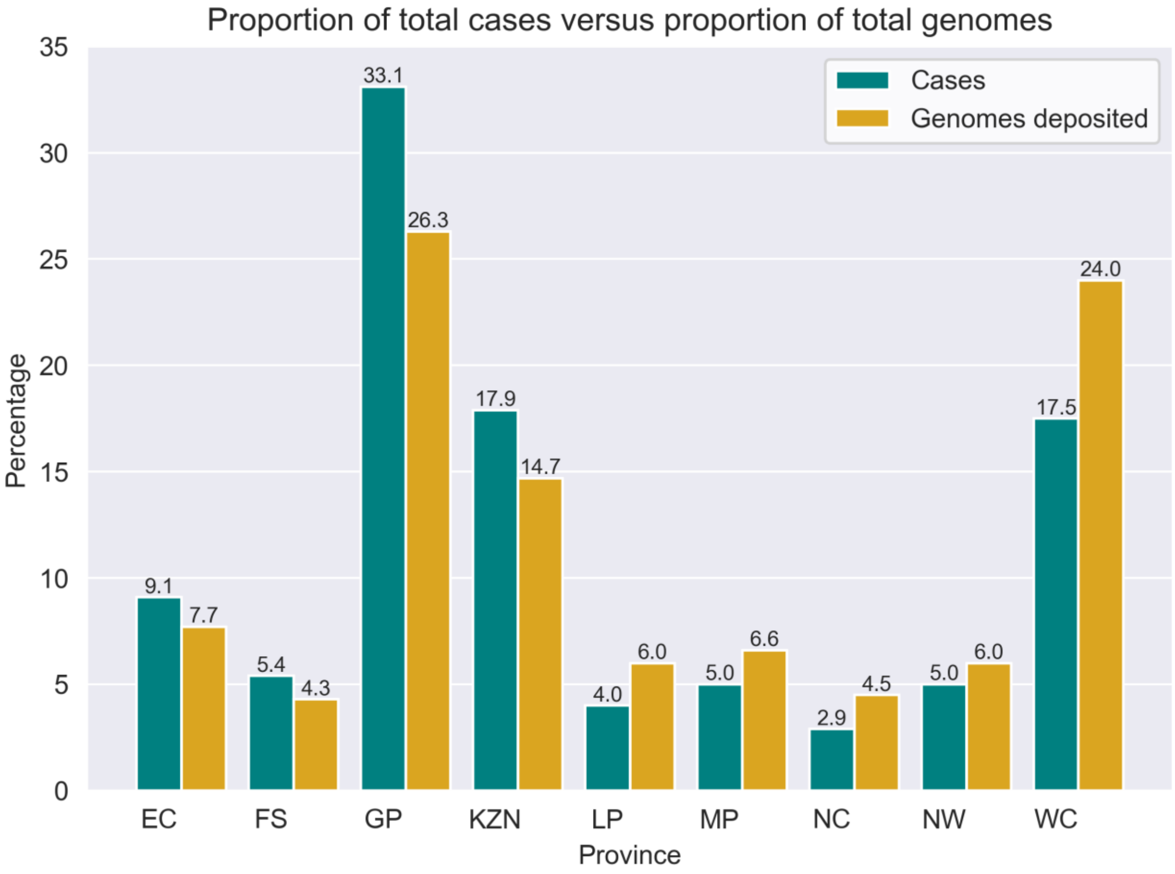
GISAID genomes vs total cases, 2020 – 2022 (N=43 357)





All provinces, apart from GP, KZN and WC, have comparable percentages of overall cases and sequenced genomes. All provinces have contributed sequences for April, May, and June.
July sequences are from WC and GP.

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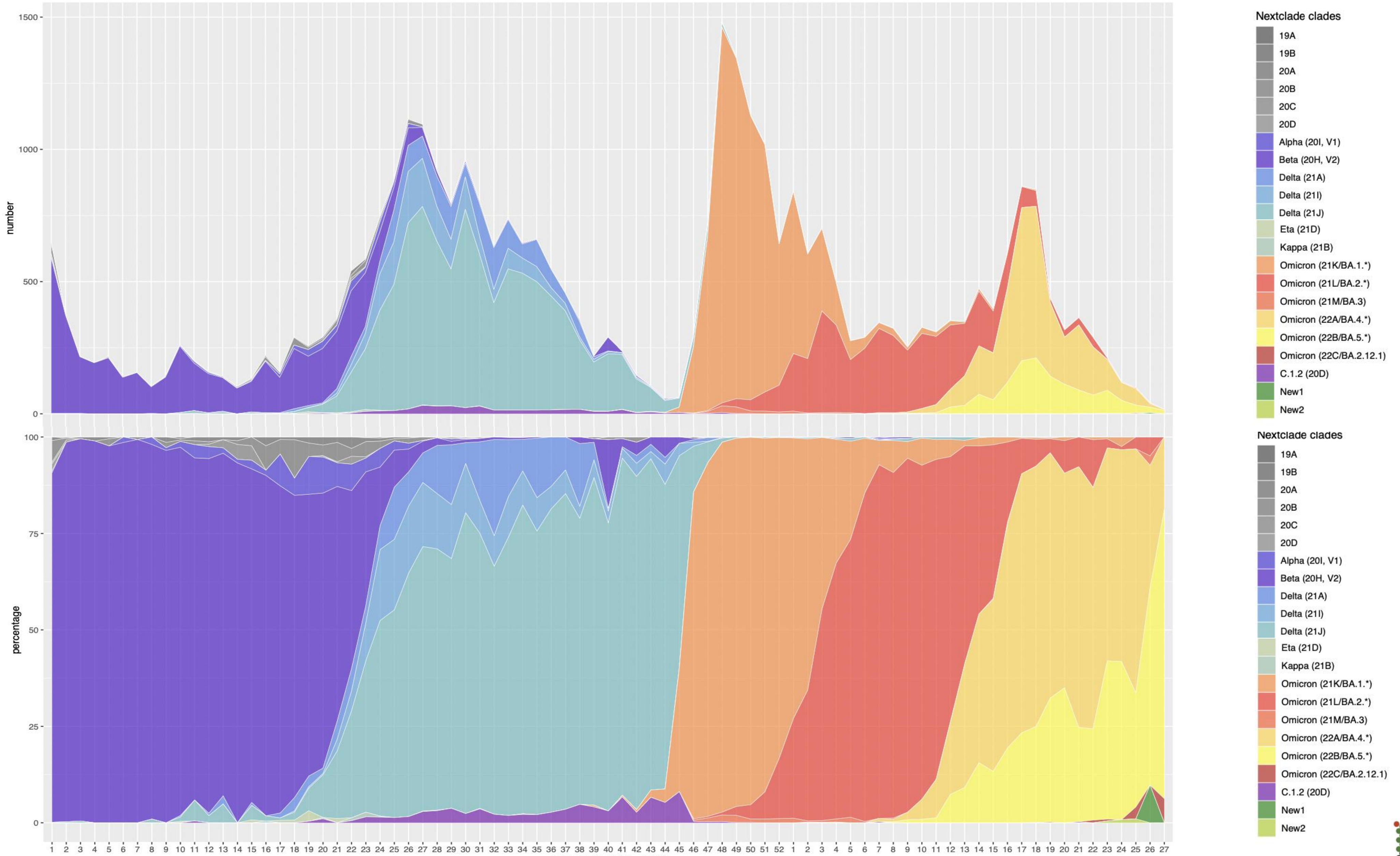
Number and percentage of clades by epiweek in South Africa, 2021 – 2022 (36 577*)



Sequencing data ending epi week 27 (ending 9 July 2022)

Currently in epi week 28 (ending 16 July 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.

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

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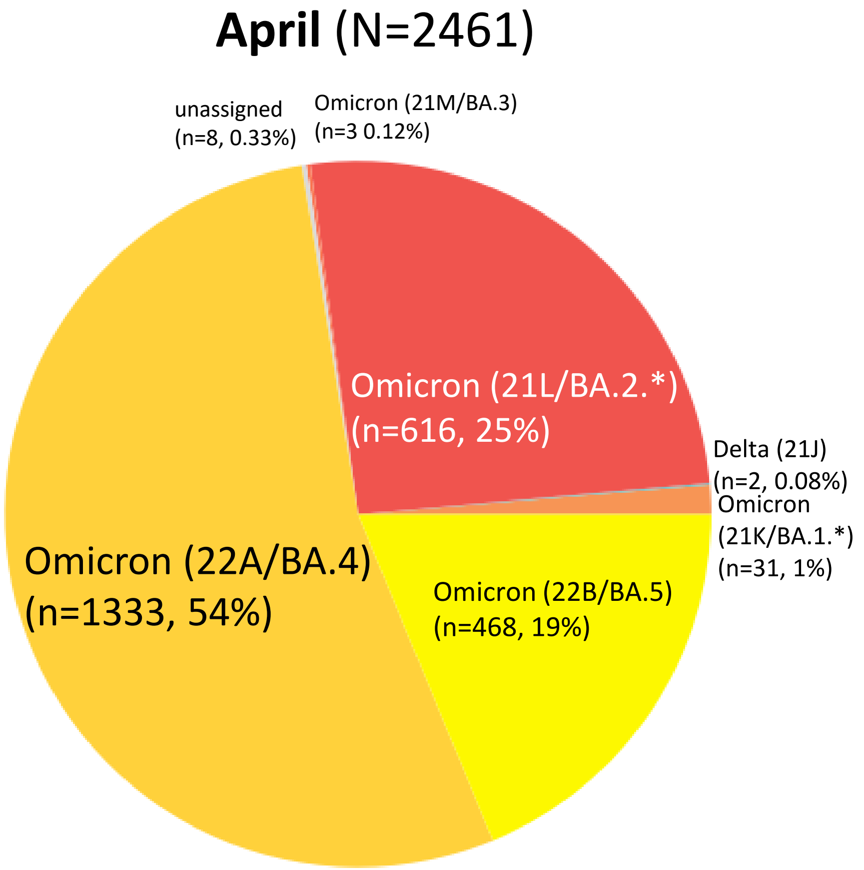
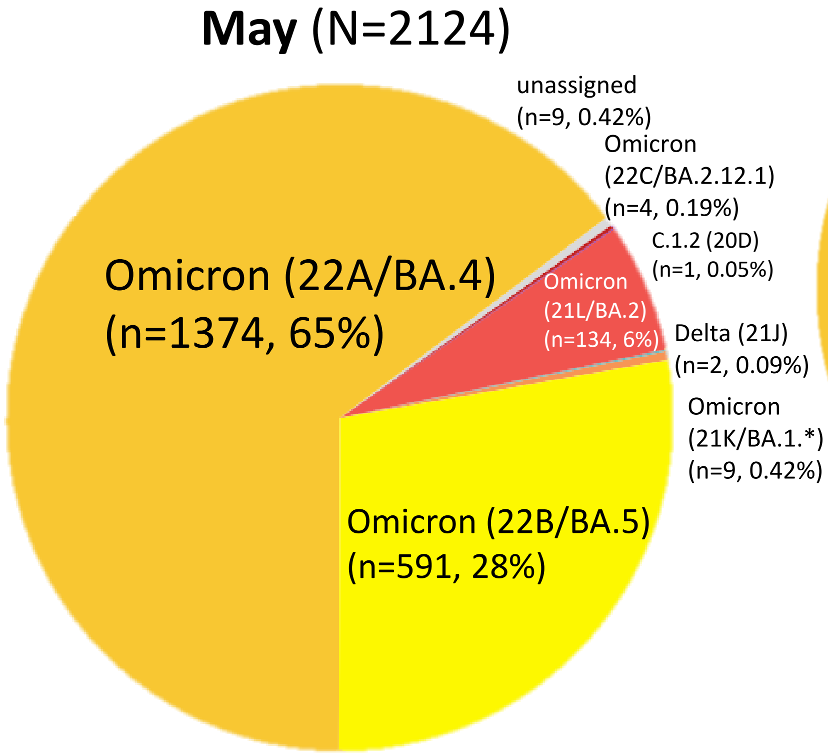
Prevalence of Variants of Concern (VOC) and Variants of Interest (VOI) in April – June 2022



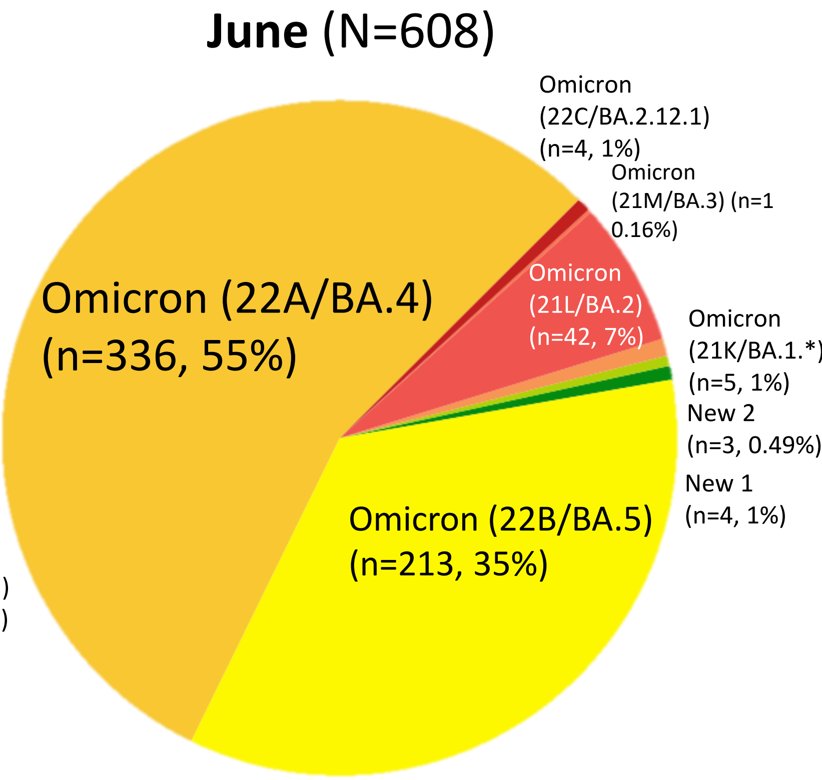
April (N=2461)

Total Omicron in Apr: 2451 (99.6%)



May (N=2124)

Total Omicron in May: 2112 (99.4%)



June (N=608)

Total Omicron in June: 601 (98.8%)

Clade key (bar graph)

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

Omicron dominated in April (99.6%, 2451/2461), May (99.4%, 2112/2124) and June (98.8%, 601/608). BA.4 and BA.5 together were dominant in April, May and June. BA.2.12.1 was detected at low levels in May and June.

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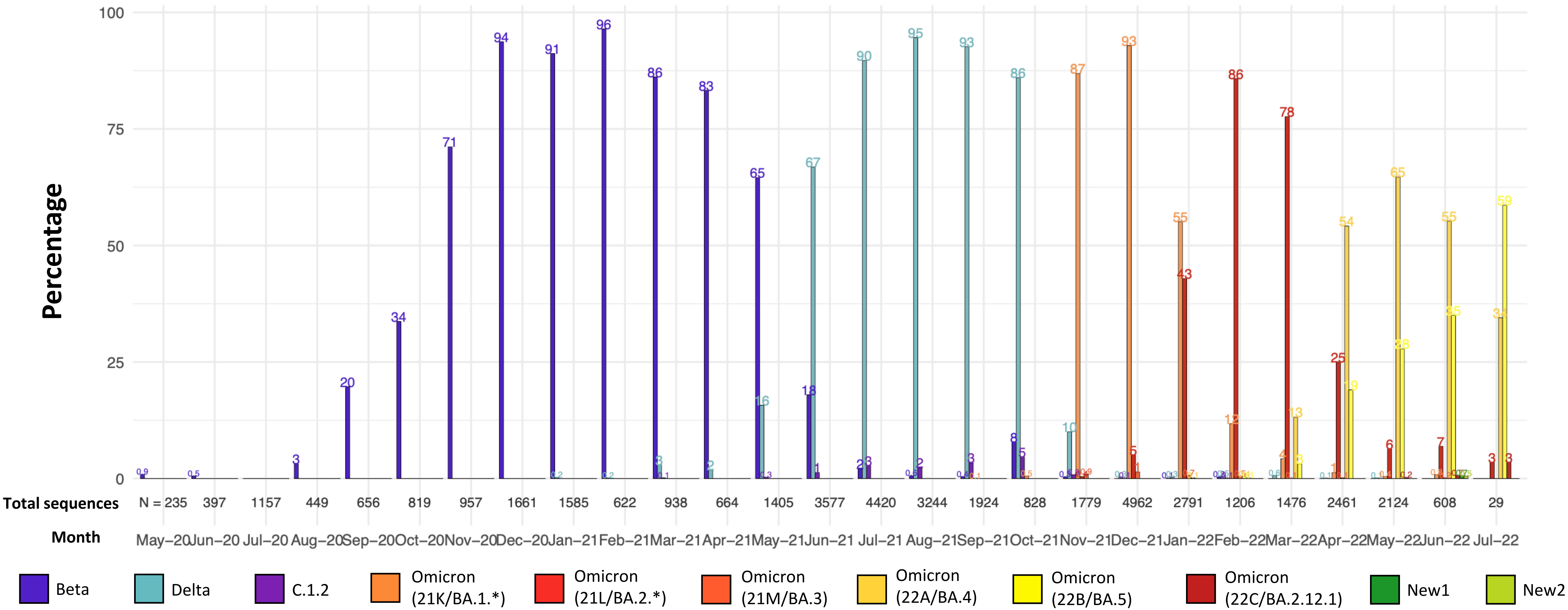
Detection Rates: Beta, Delta, C.1.2 and Omicron

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 – July).
BA.4 and BA.5 together dominated in April at 73%, May at 93%, June at 90% and currently make up 93% of July sequences, although with a small number of genomes.

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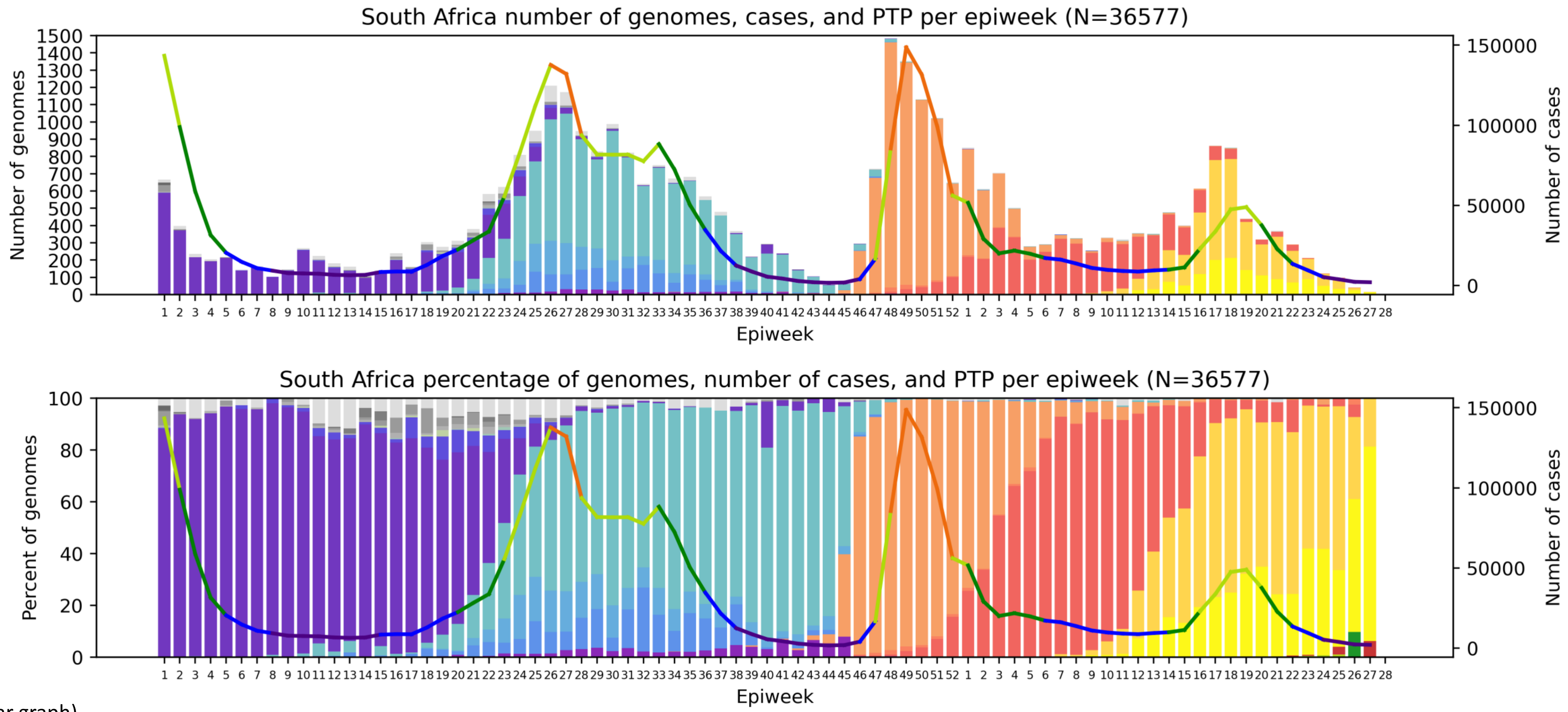
South Africa, 2021-2022, n = 36 577*


South Africa number of genomes, cases, and PTP per epiweek (N=36577)

South Africa percentage of genomes, number of cases, and PTP per epiweek (N=36577)

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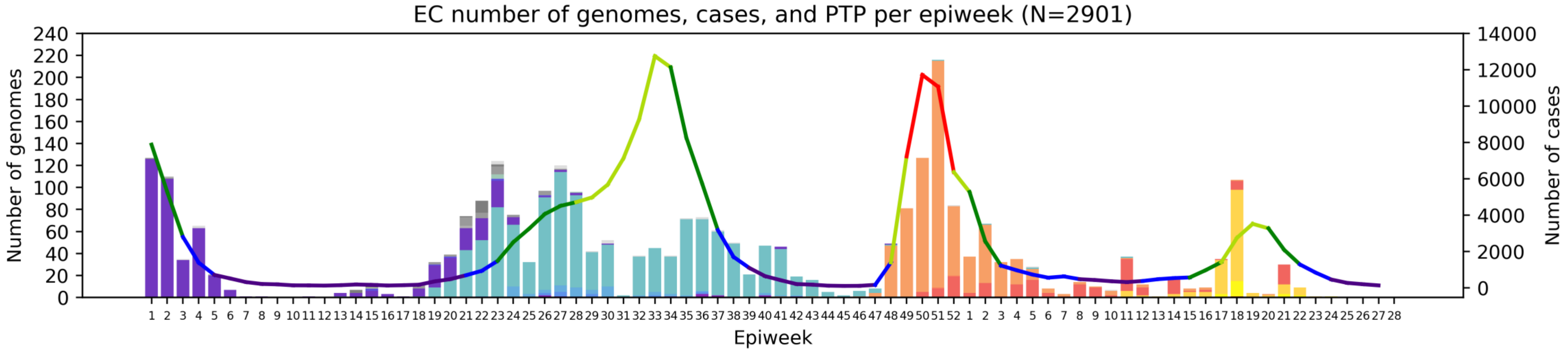
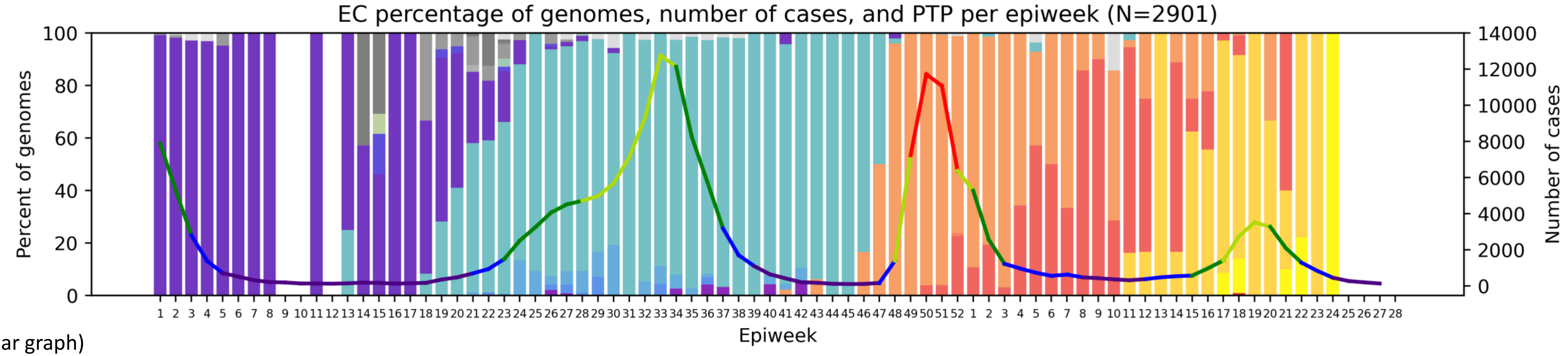
*Excludes sequences missing collection dates, as well as those collected January 1st and 2nd 2021 as they are part of epiweek 53 of 2020.

Eastern Cape Province, 2021-2022, n = 2901





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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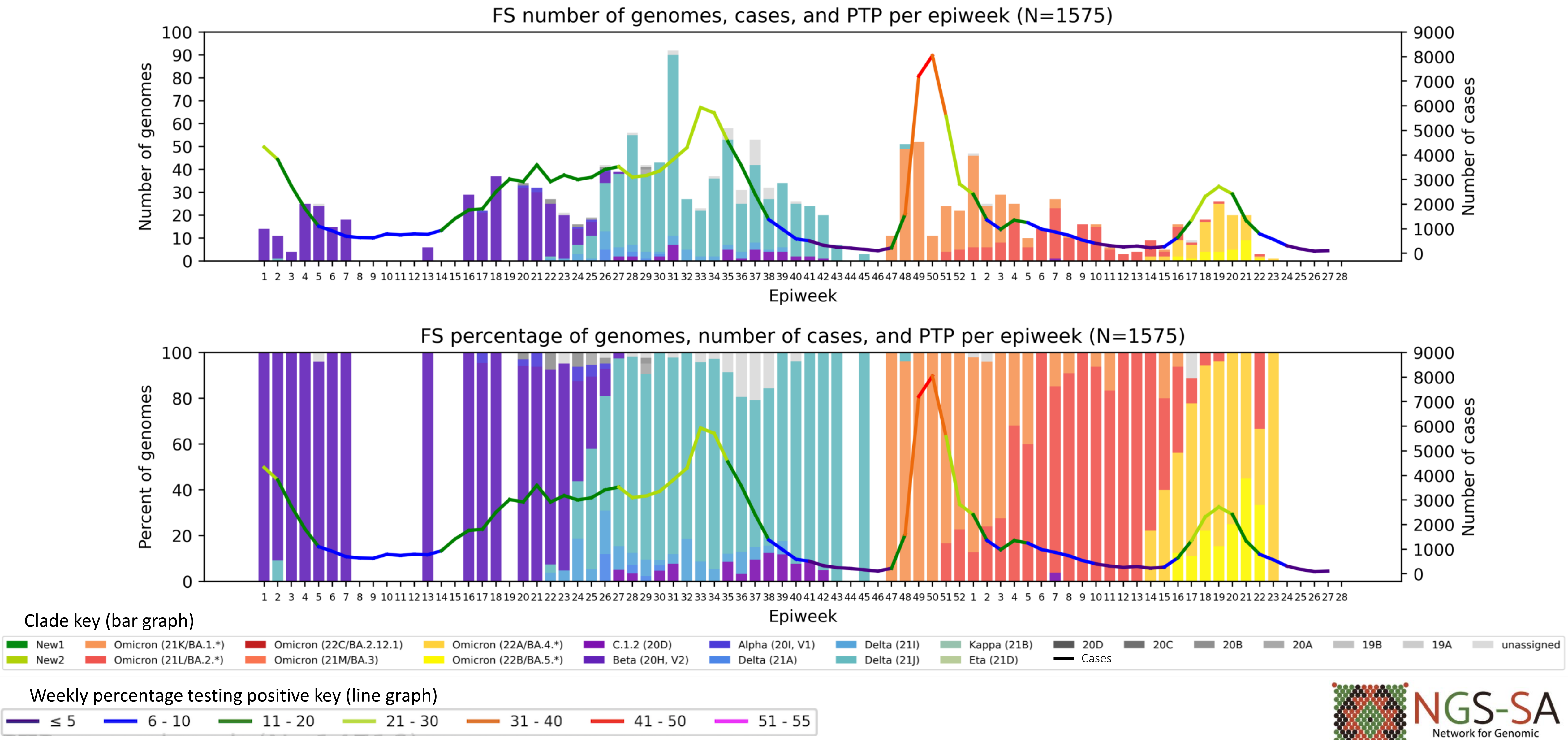
Free State Province, 2021-2022, n = 1575



FS number of genomes, cases, and PTP per epiweek (N=1575)

FS percentage of genomes, number of cases, and PTP per epiweek (N=1575)

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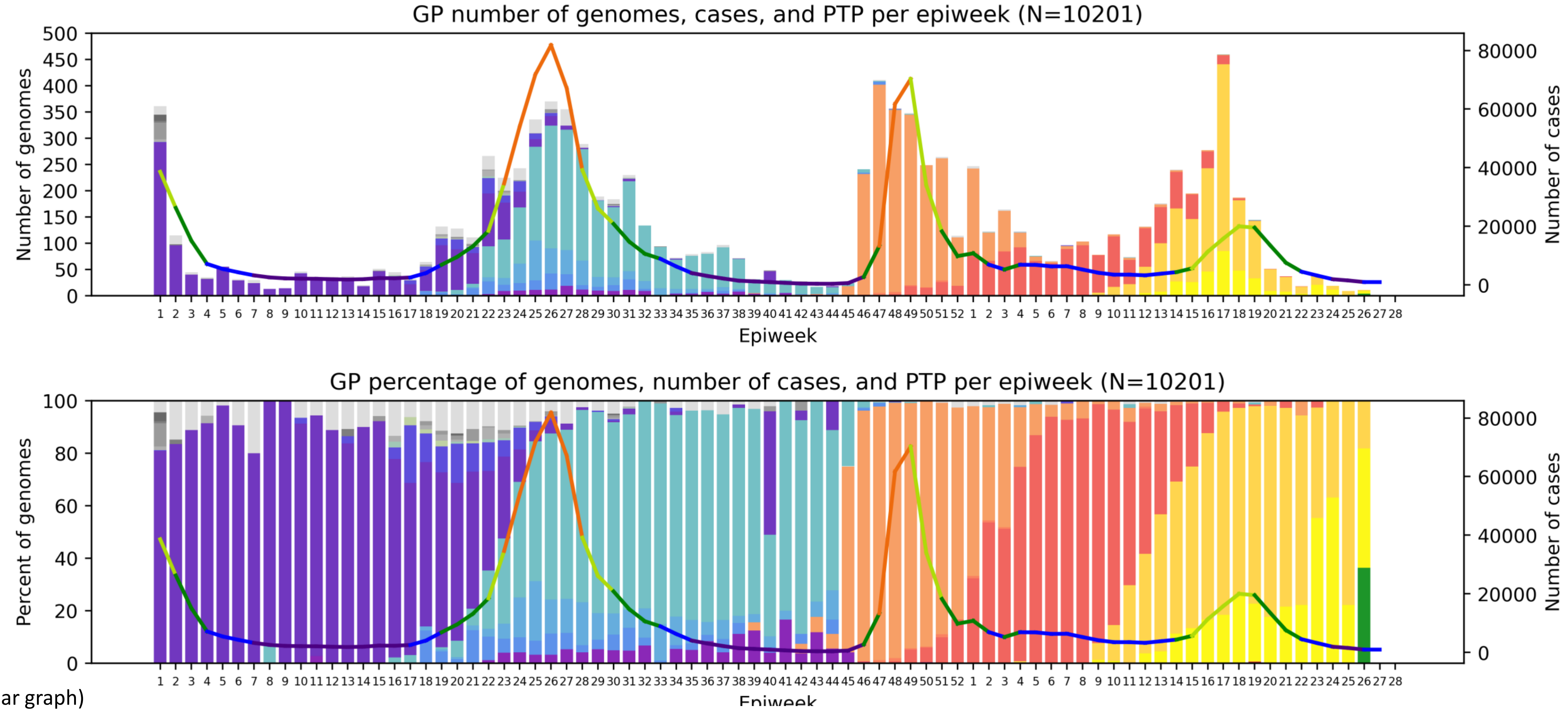
Gauteng Province, 2021-2022, n = 10 201



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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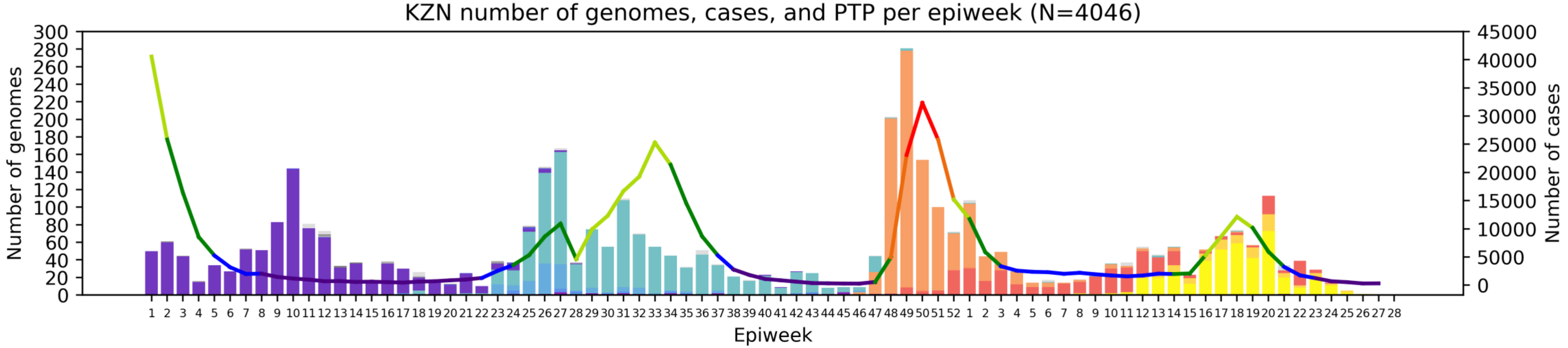
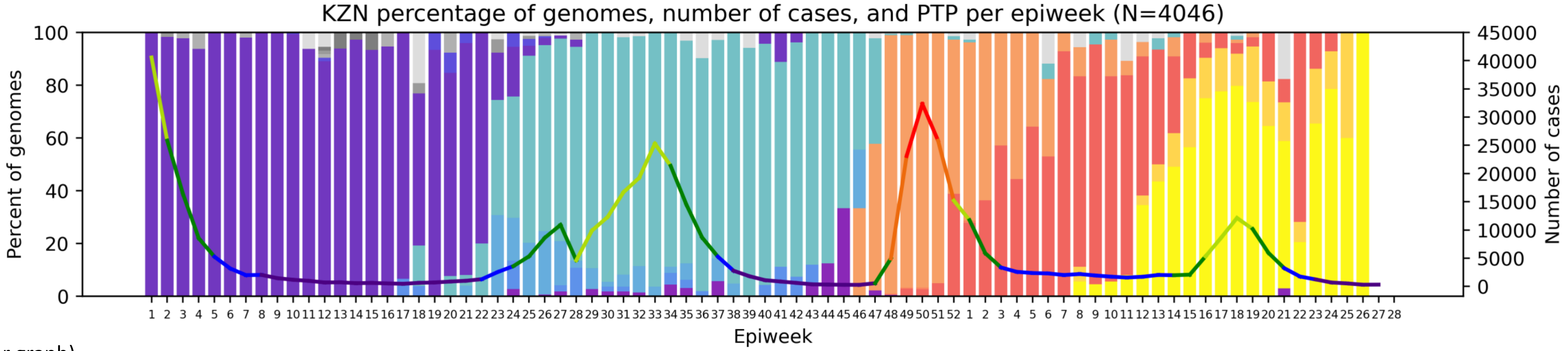
KwaZulu-Natal Province, 2021-2022, n = 4046





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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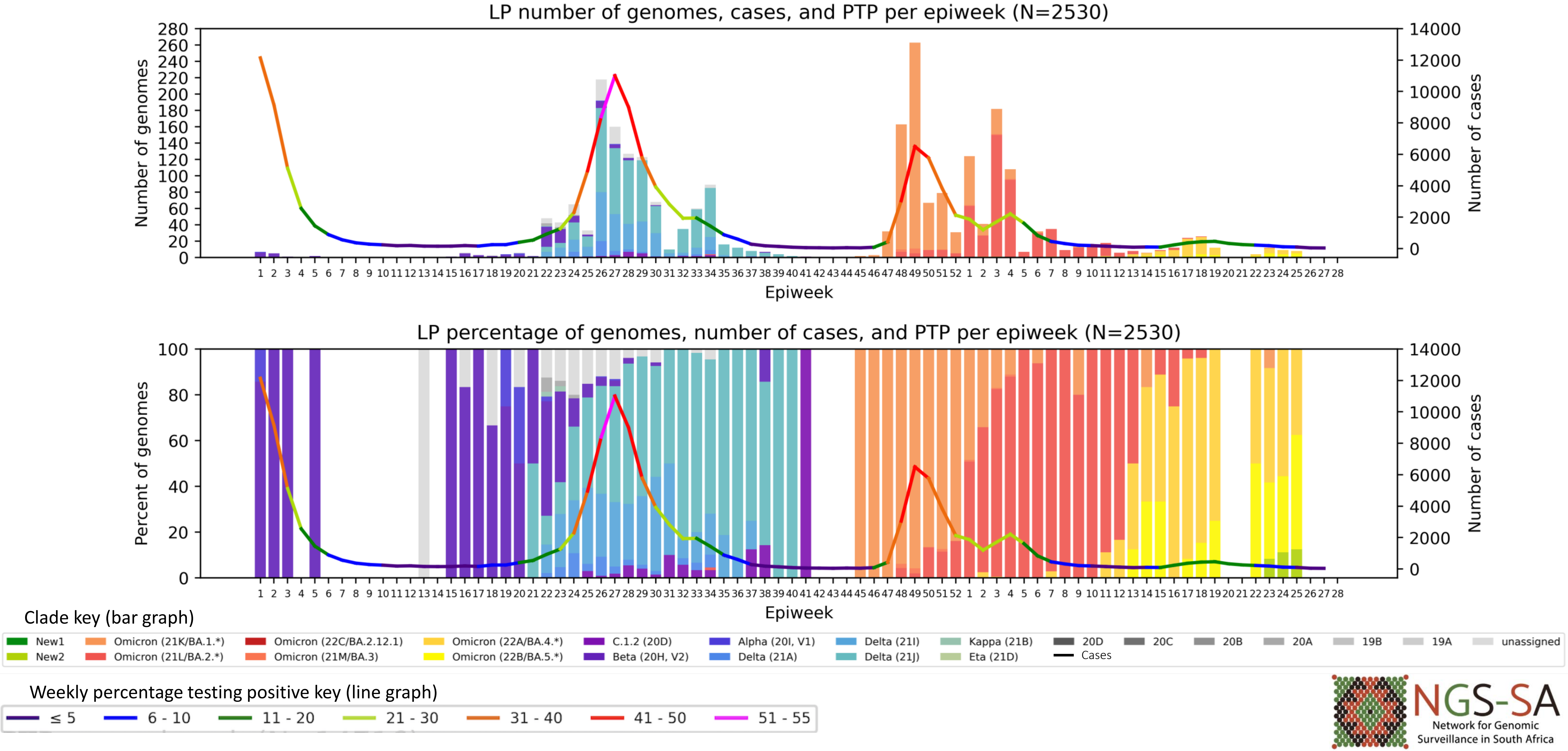
Limpopo Province, 2021-2022, n = 2530



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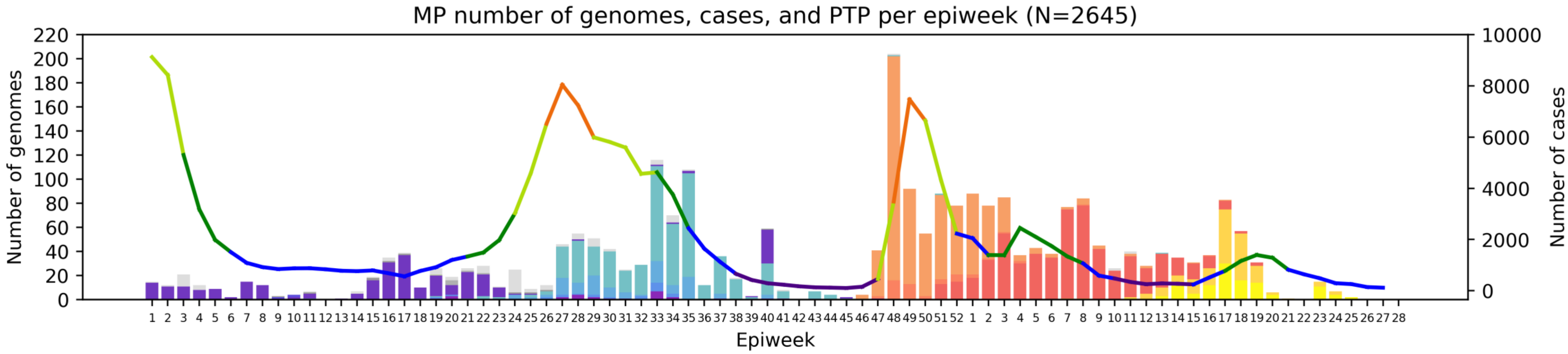
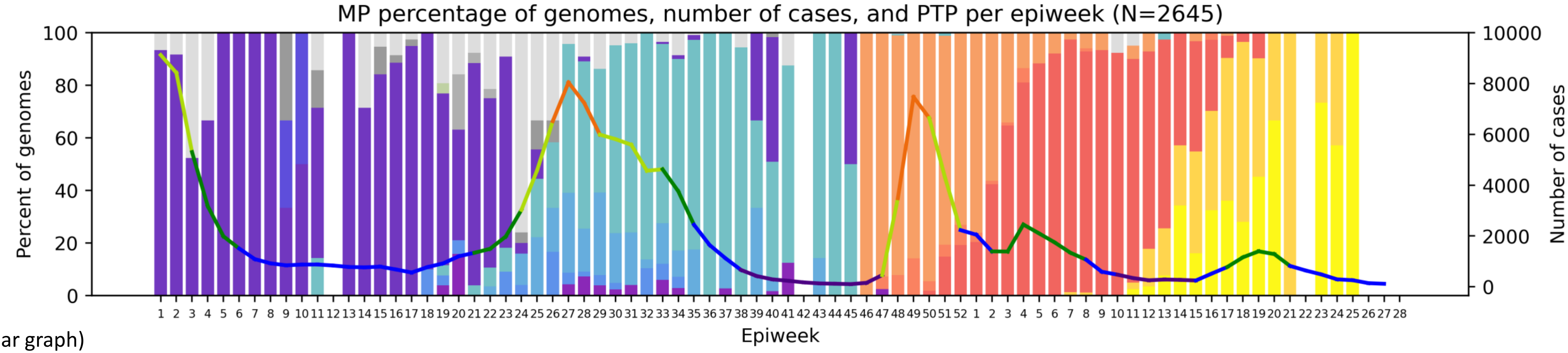
Mpumalanga Province, 2021-2022, n = 2645





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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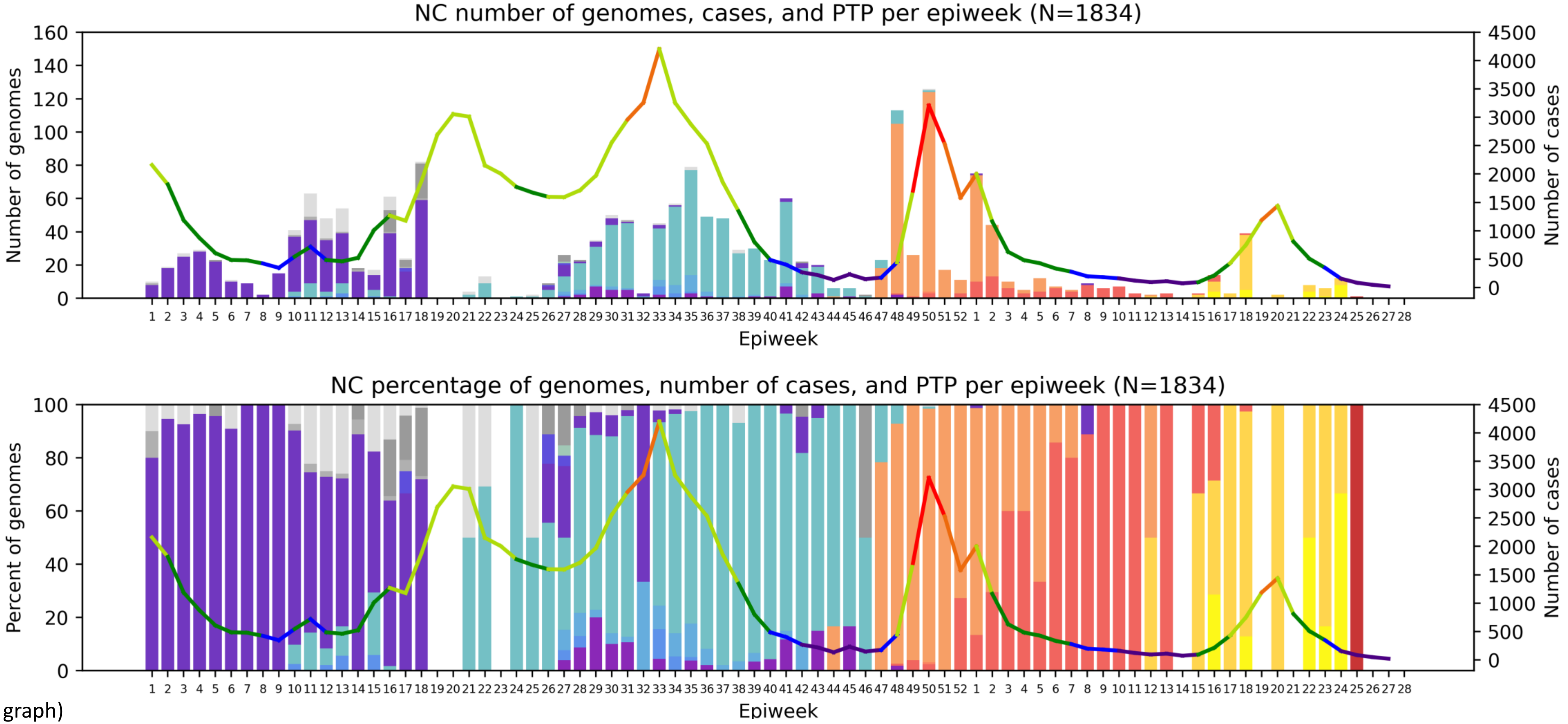
Northern Cape Province, 2021-2022, n = 1834



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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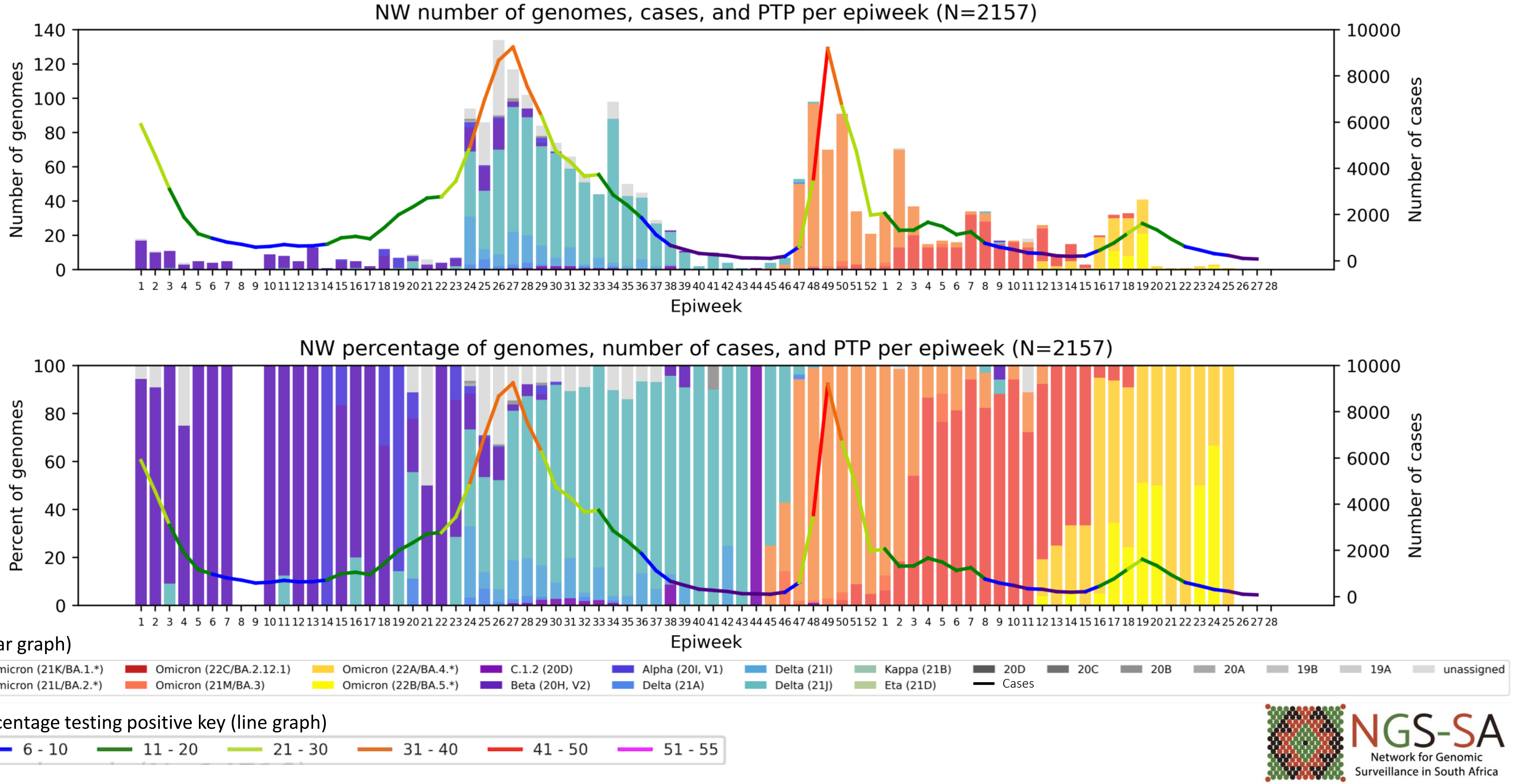
North West Province, 2021-2022, n = 2157



NW number of genomes, cases, and PTP per epiweek (N=2157)

NW percentage of genomes, number of cases, and PTP per epiweek (N=2157)

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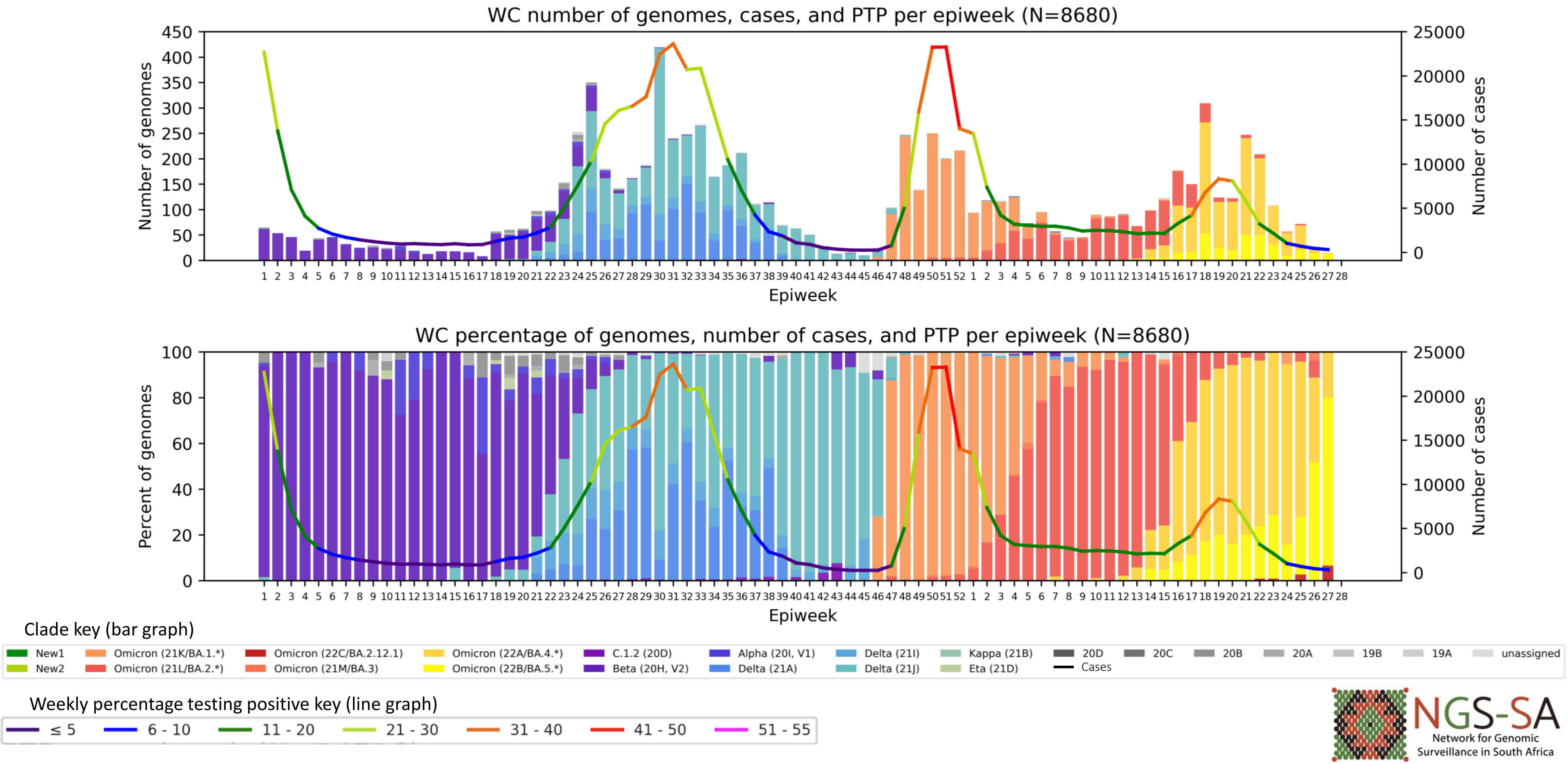
Western Cape Province, 2021-2022, n = 8680



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7 SARS-CoV-2 SGTP (S-gene target positive) sequences with novel mutations

Whole genome profiles

Both batches are flagged for private mutations in NextClade:

- New1 sequences (21M) are flagged for containing many 21J mutations
- New2 samples (21J) are flagged for containing many 21K and 21L mutations
- Sequences contain a mixture of mutations from Omicron and Delta

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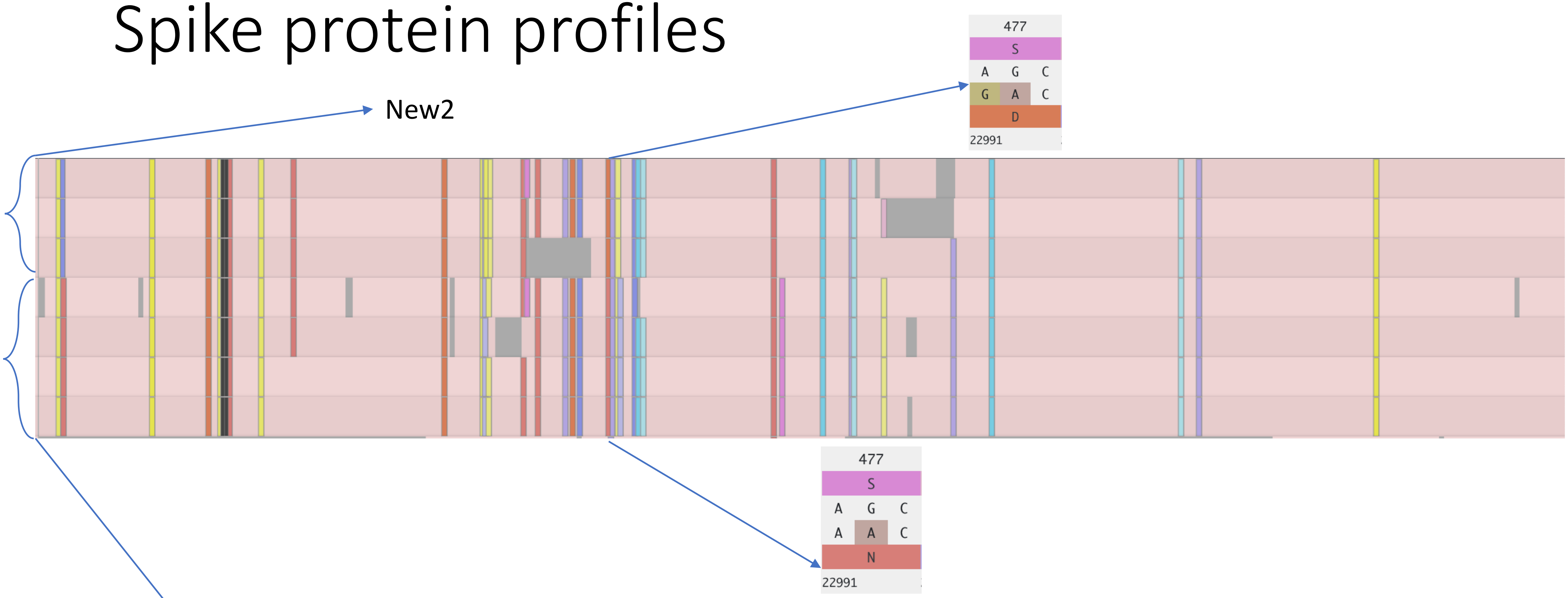
Spike protein profiles



- Shared additional mutations: L18F, T19R, T95I, W152L, 156-157del, R158G, F186L, G446D, wildtype Q493, T1117I, additional synonymous nucleotide change in L452R compared to BA.4/5
- Unique to New1 batch: R21G, F486P, A706V (A706T present in 1 surveillance sample but different nucleotide change in different position)
- Unique to New2 batch: S477D instead of S477N

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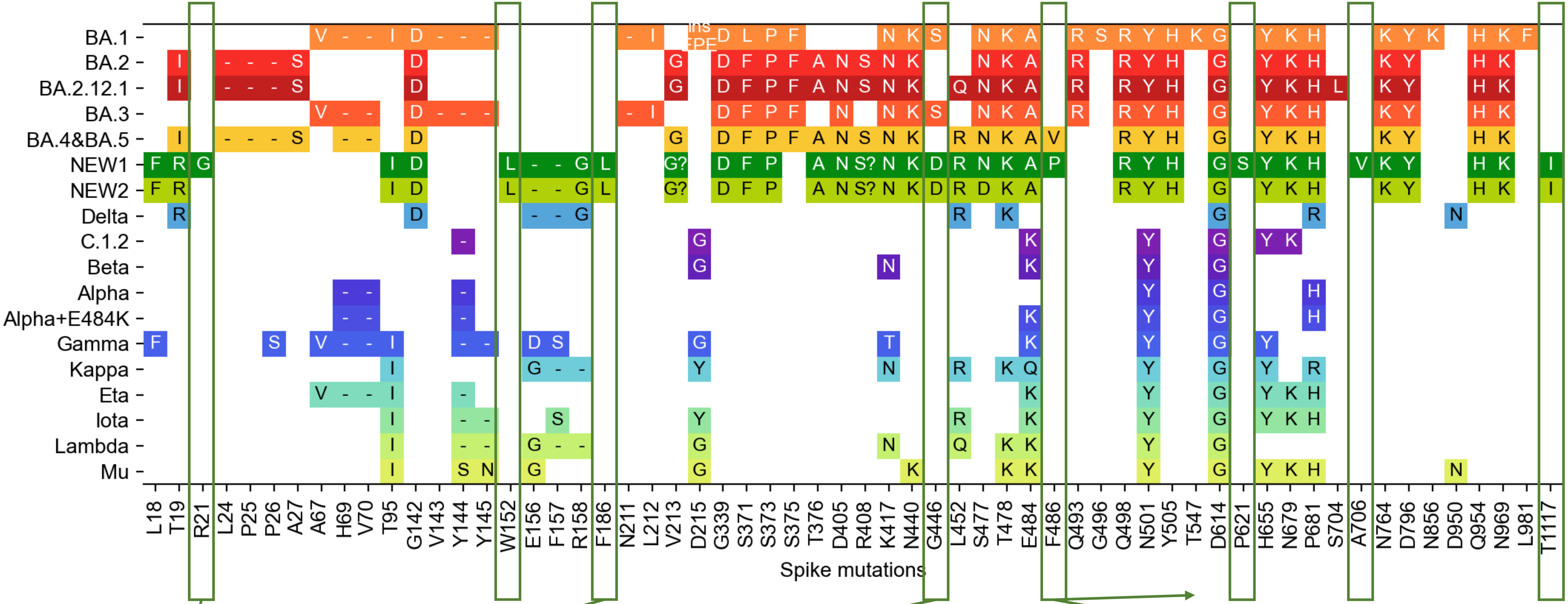
Spike protein mutation profile (1)*



	L18	T19	R21	L24	P25	P26	A27	A67	H69	V70	T95	G142	V143	Y144	Y145	W152	E156	F157	R158	F186
BA.1								V	-	-	I	D	-	-	-					
BA.2		I		-	-	-	S					D								
BA.2.12.1		I		-	-	-	S					D								
BA.3								V	-	-		D	-	-	-					
BA.4&BA.5		I		-	-	-	S		-	-		D								
NEW1	F	R	G								I	D				L	-	-	G	L
NEW2	F	R									I	D				L	-	-	G	L
Delta		R										D					-	-	G	
C.1.2														-						
Beta																				
Alpha									-	-				-						
Alpha+E484K									-	-				-						
Gamma	F					S		V	-	-	I			-	-		D	S		
Kappa											I						G	-	-	
Eta								V	-	-	I			-						
Iota											I			-	-			S		
Lambda											I			-	-		G	-	-	
Mu											I			S	N		G			

	N211	L212	V213	D215	G339	S371	S373	S375	T376	D405	R408	K417	N440	G446	L452	S477	T478	E484	F486	Q493
BA.1	-	I		ins EPE	D	L	P	F				N	K	S		N	K	A		R
BA.2			G		D	F	P	F	A	N	S	N	K			N	K	A		R
BA.2.12.1			G		D	F	P	F	A	N	S	N	K		Q	N	K	A		R
BA.3	-	I			D	F	P	F		N		N	K	S		N	K	A		R
BA.4&BA.5			G		D	F	P	F	A	N	S	N	K		R	N	K	A	V	
NEW1			G?		D	F	P		A	N	S?	N	K	D	R	N	K	A	P	
NEW2			G?		D	F	P		A	N	S?	N	K	D	R	D	K	A		
Delta															R		K			
C.1.2				G														K		
Beta				G								N						K		
Alpha																				
Alpha+E484K																		K		
Gamma				G								T						K		
Kappa				Y								N			R		K	Q		
Eta																		K		
Iota				Y											R			K		
Lambda				G								N			Q		K	K		
Mu				G									K				K	K		

	G496	Q498	N501	Y505	T547	D614	P621	H655	N679	P681	S704	A706	N764	D796	N856	D950	Q954	N969	L981	T1117
BA.1	S	R	Y	H	K	G		Y	K	H			K	Y	K		H	K	F	
BA.2		R	Y	H		G		Y	K	H			K	Y			H	K		
BA.2.12.1		R	Y	H		G		Y	K	H	L		K	Y			H	K		
BA.3		R	Y	H		G		Y	K	H			K	Y			H	K		
BA.4&BA.5		R	Y	H		G		Y	K	H			K	Y			H	K		
NEW1		R	Y	H		G	S	Y	K	H		V	K	Y			H	K		I
NEW2		R	Y	H		G		Y	K	H			K	Y			H	K		I
Delta						G				R						N				
C.1.2			Y			G		Y	K											
Beta			Y			G														
Alpha			Y			G				H										
Alpha+E484K			Y			G				H										
Gamma			Y			G		Y												
Kappa			Y			G		Y		R										
Eta			Y			G		Y	K	H										
Iota			Y			G		Y	K	H										
Lambda			Y			G														
Mu			Y			G		Y	K	H						N				

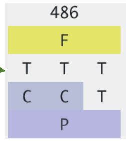
Seen in 578 seqs on GISAID

Seen in 1,424 seqs on GISAID

Seen in 485 seqs on GISAID
Different aa to BA.1
High predicted Ab escape (Bloom lab)

Seen in 9 seqs on GISAID
- 7 human, 2 bat

Different aa to BA.4/5
High predicted Ab escape (Bloom lab)
– know immune escape in BA.4/5 when F→V



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

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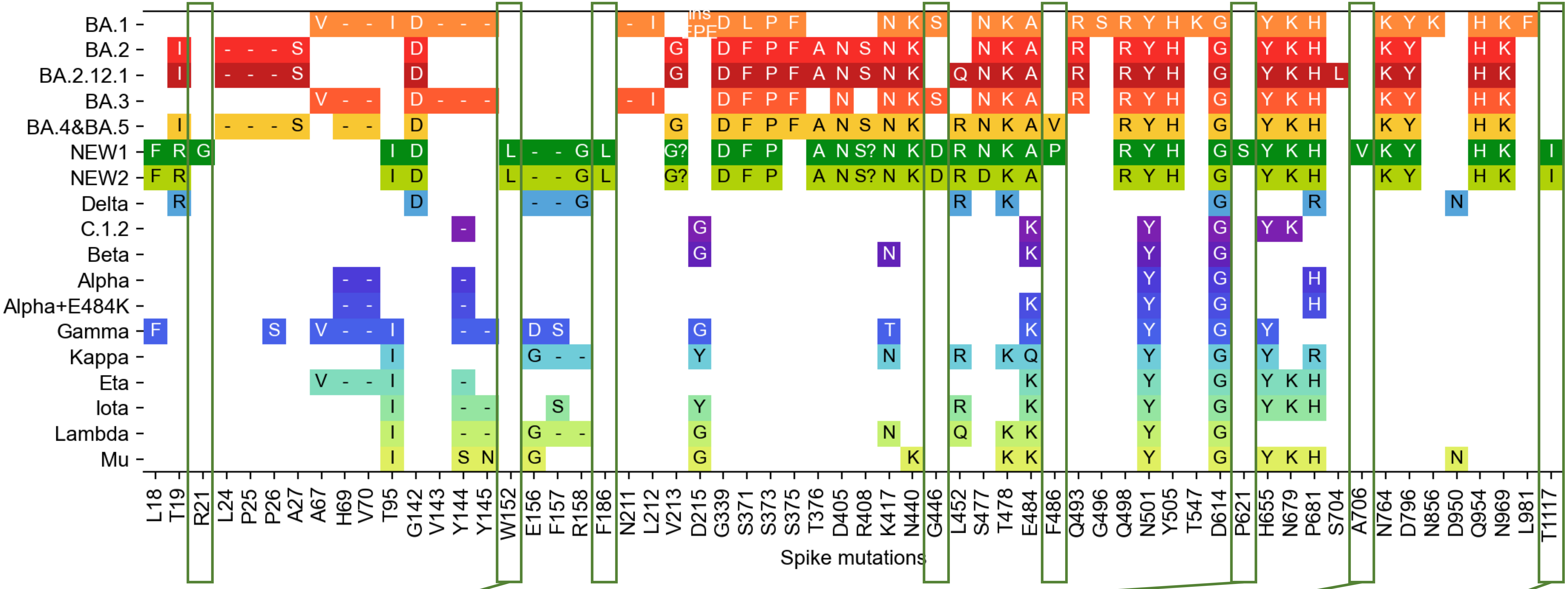
Spike protein mutation profile (2)*



Seen in 18,434 seqs on GISAID

Seen in 1,765 seqs on GISAID ~near FCS

Seen in 4,639 seqs on GISAID

Seen in 13,470 seqs on GISAID

Note V213, S375, D405 and R408 sometimes drop out on Ion Torrent – need confirmation on different platform

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

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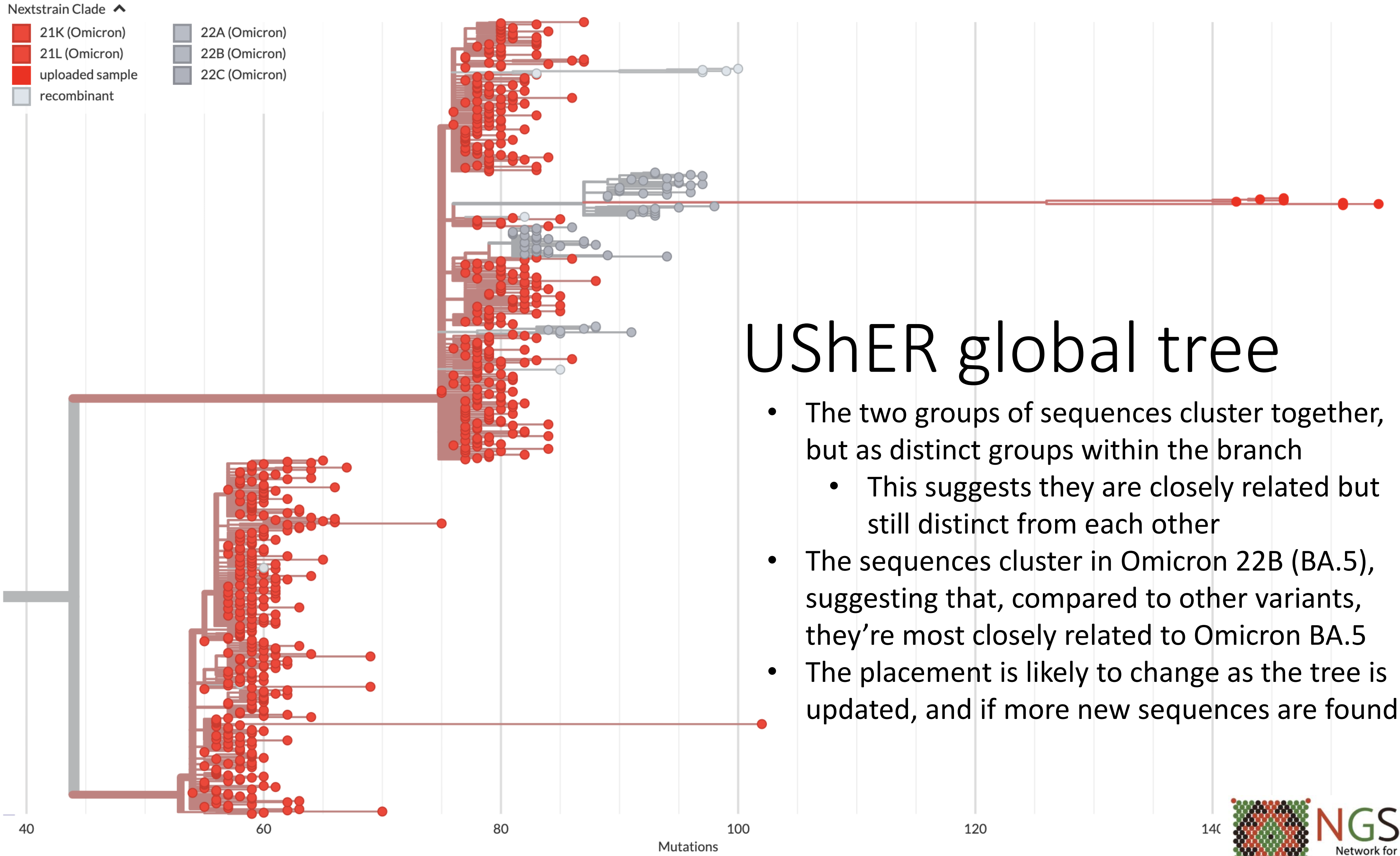

UShER global tree

- The two groups of sequences cluster together, but as distinct groups within the branch
  - This suggests they are closely related but still distinct from each other
- The sequences cluster in Omicron 22B (BA.5), suggesting that, compared to other variants, they're most closely related to Omicron BA.5
- The placement is likely to change as the tree is updated, and if more new sequences are found

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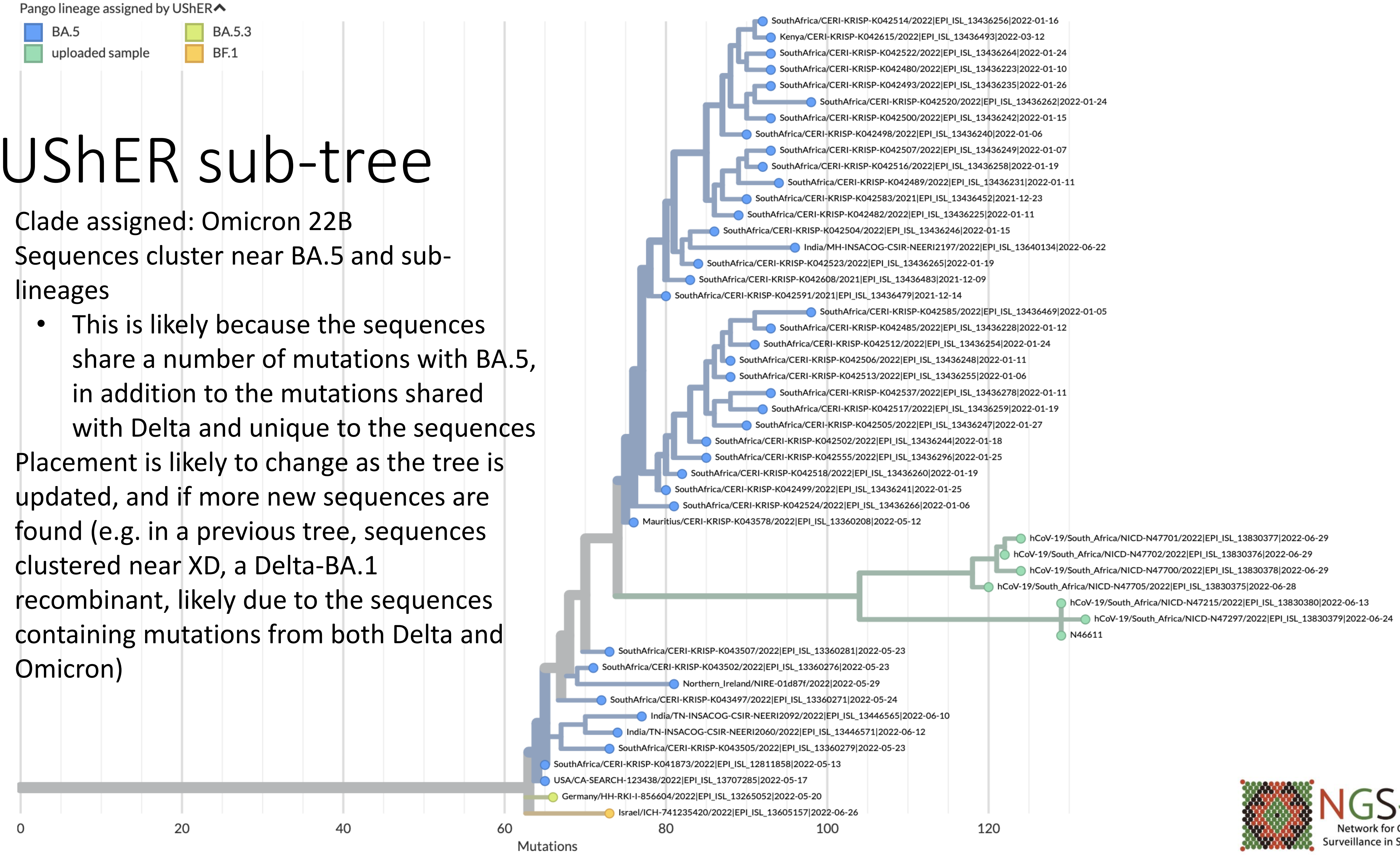
UShER sub-tree

- Clade assigned: Omicron 22B
- Sequences cluster near BA.5 and sub-lineages
  - This is likely because the sequences share a number of mutations with BA.5, in addition to the mutations shared with Delta and unique to the sequences
- Placement is likely to change as the tree is updated, and if more new sequences are found (e.g. in a previous tree, sequences clustered near XD, a Delta-BA.1 recombinant, likely due to the sequences containing mutations from both Delta and Omicron)



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Summary

- **N=7 sequences with novel mutational profile**
  - NGS-SA teams are currently analysing the data to confirm the mutational profile

- **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%) and June (90%).
  - BA.2.12.1 was detected in South Africa at low prevalence in May and June (<1%)

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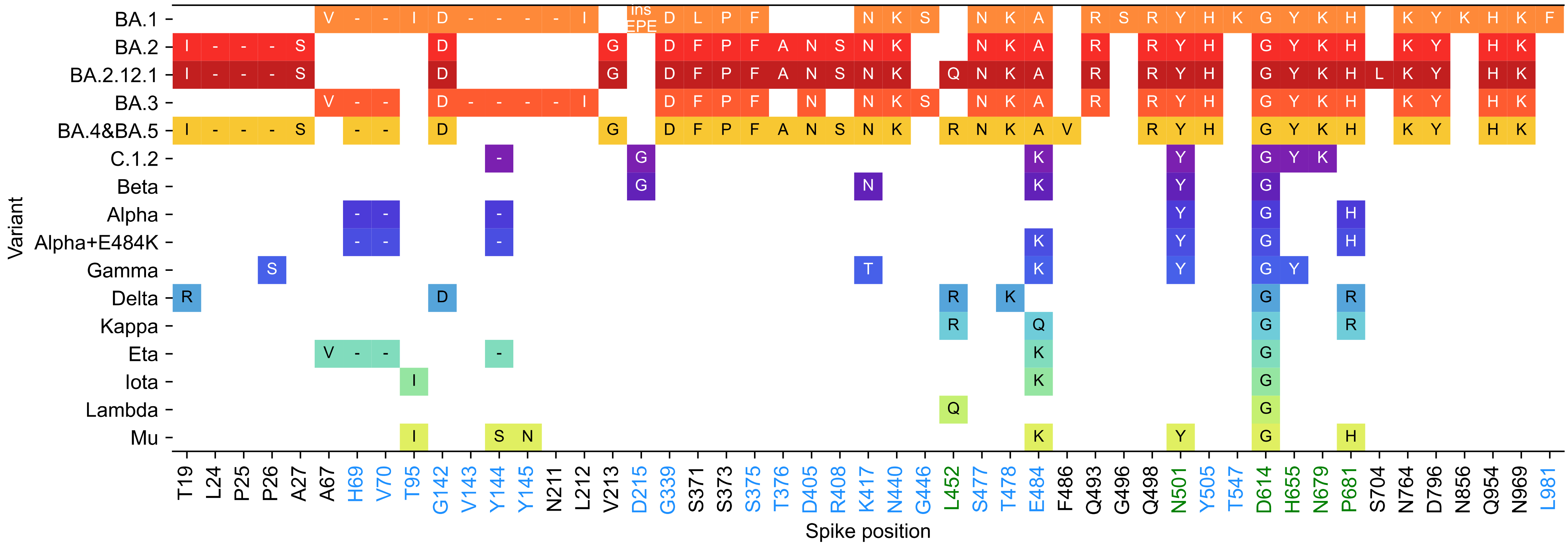
[1] https://github.com/cov-lineages/pango-designation/releases/tag/v1.3

Omicron spike mutations compared to other VOC/VOIs



Variant	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	S704	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		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		K	Y		H	K	
BA.2.12.1	I	-	-	-	S					D						G		D	F	P	F	A	N	S	N	K		Q	N	K	A		R		R	Y	H		G	Y	K	H	L	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		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										
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										
Lambda																												Q											G										
Mu									I			S	N																		K					Y			G			H							

Mutation impact key ⬛ Unknown/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

Only lineage-defining mutations are pictured.

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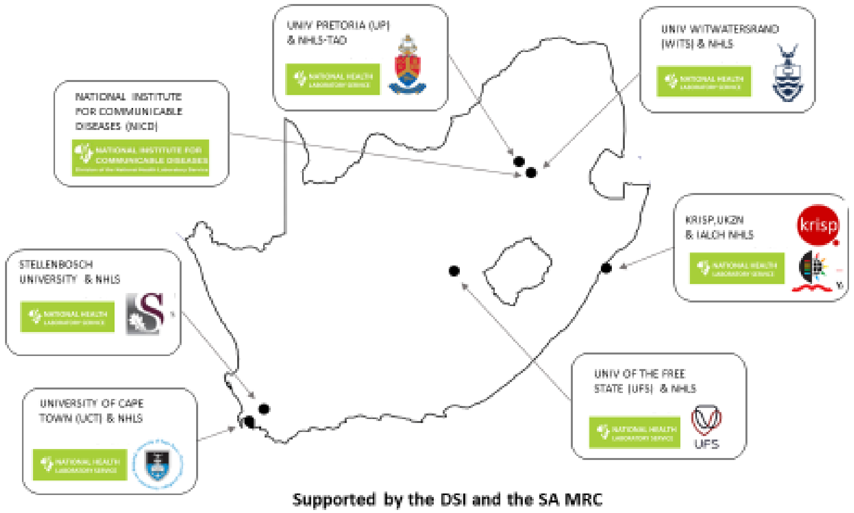

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EDCTP

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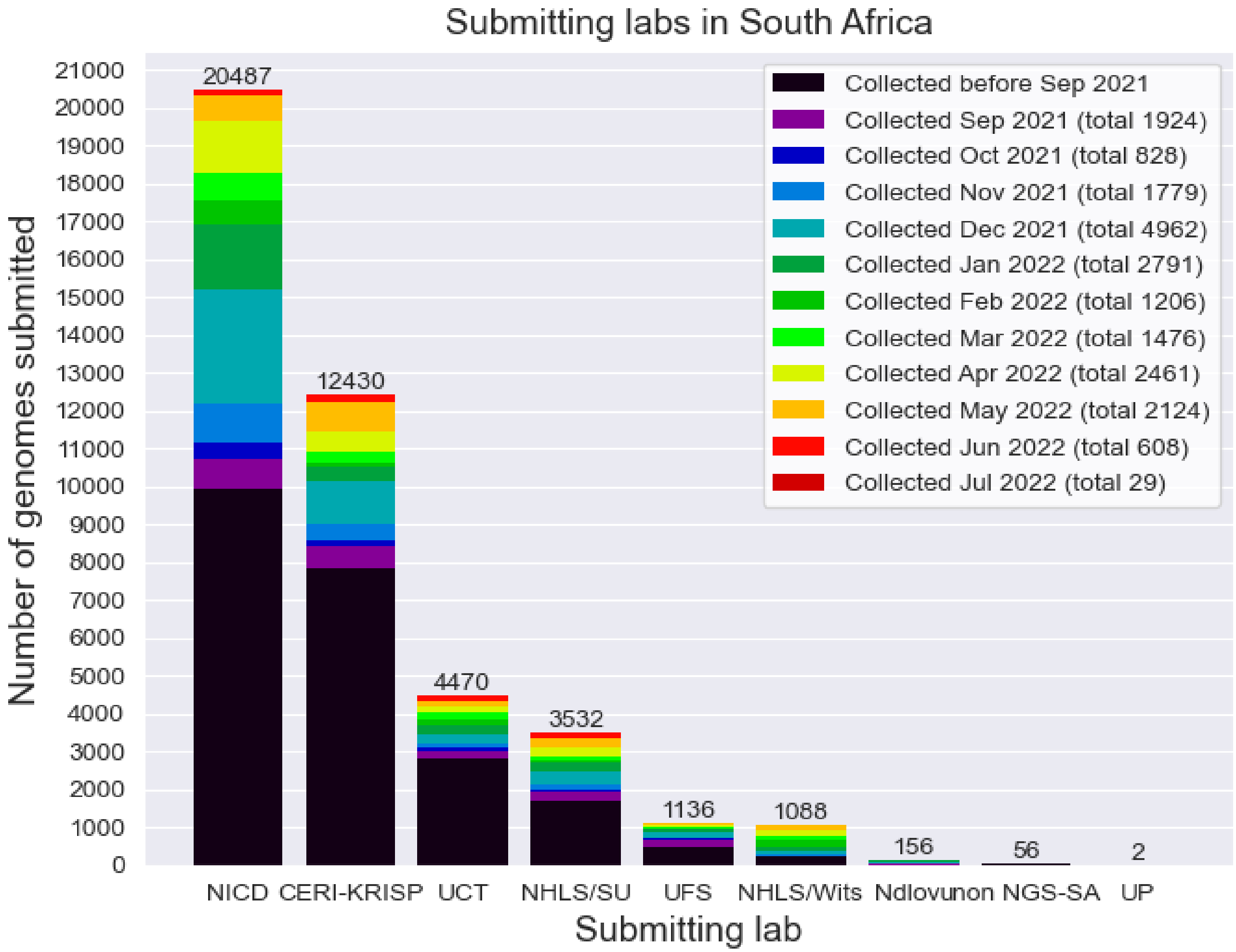
South African genomes submitted per submitting lab, 2020 - 2022 (N=43 357)



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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.)