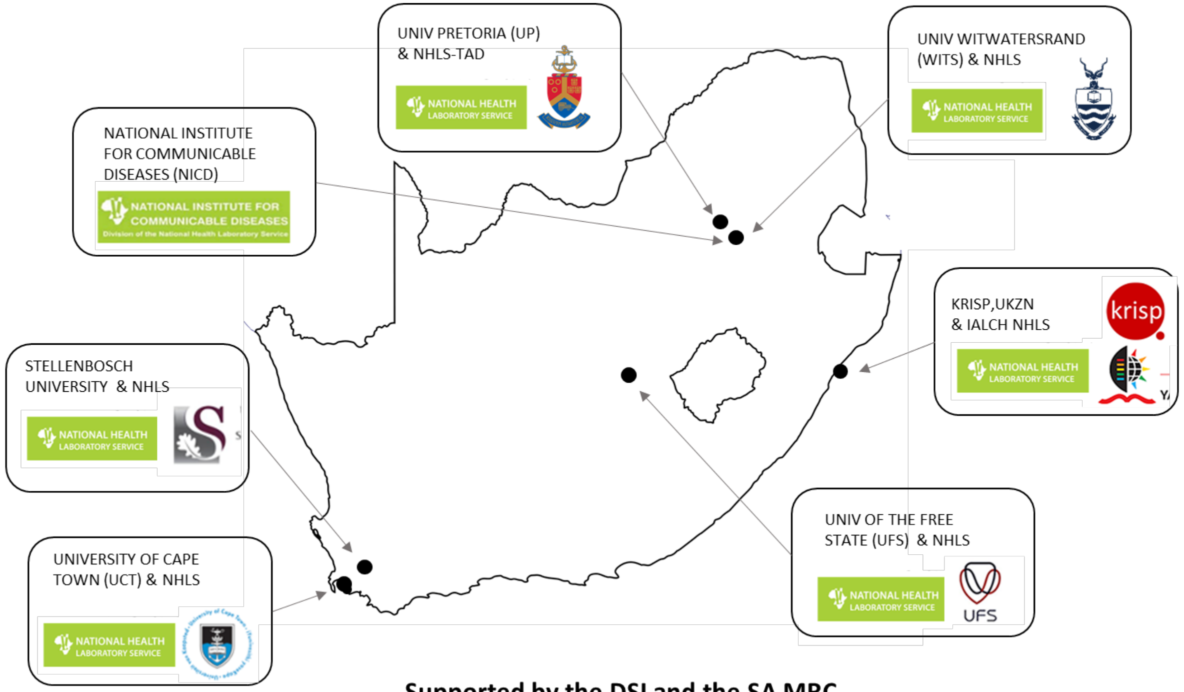
Network for Genomic Surveillance in South Africa (NGS-SA)

SARS-CoV-2 Sequencing Update
31 December 2021



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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 30 December at 08h36

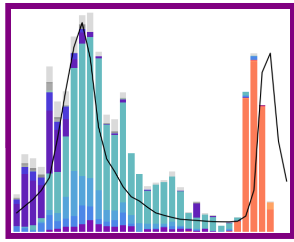
Data license: https://www.gisaid.org/registration/terms-of-use/

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 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 18 - 51

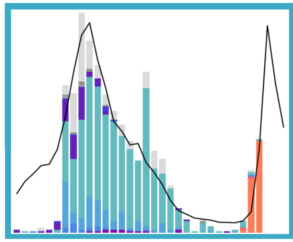


Gauteng ↓PTP: 22.7%

Genomes	Cases
4 578 (28.1%)	700 929 (38.4%)

Genomes deposited in the last week

🟧92 🟧2 🟪6 ⬜1

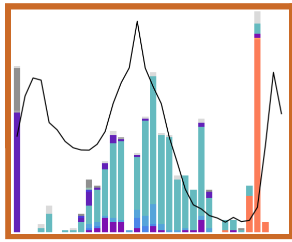


North West ↓PTP: 25.7%

Genomes	Cases
1 232 (7.6%)	109 618 (6.0%)

Genomes deposited in the last week

🟧15 🟩14 🟪2 ⬜1 ⬛17 ⬛3

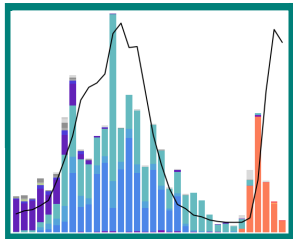


Northern Cape ↑PTP: 43.2%

Genomes	Cases
870 (5.3%)	60 383 (3.3%)

Genomes deposited in the last week

🟧44 🟩4

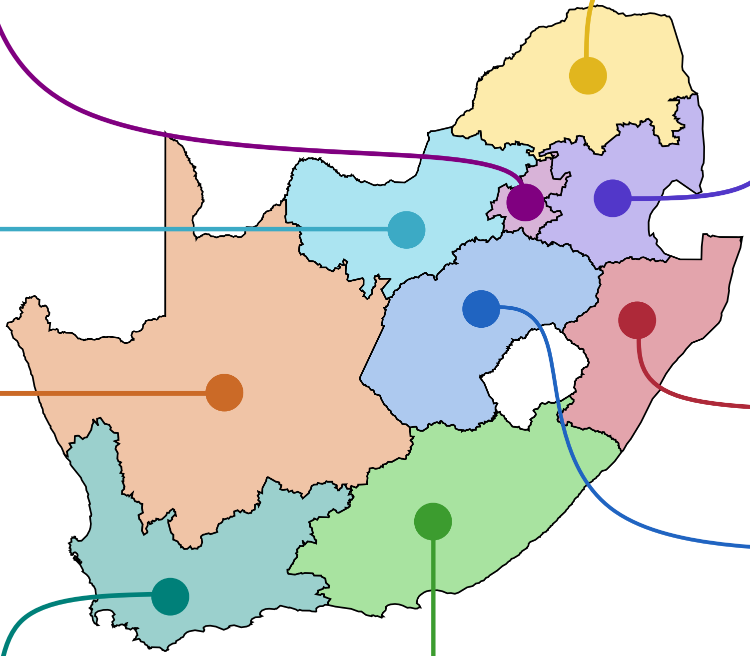


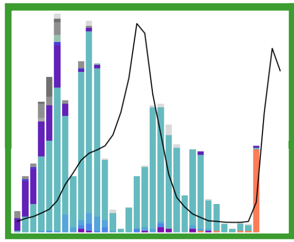
Western Cape ↑PTP: 45.4%

Genomes	Cases
3 642 (22.4%)	296 211 (16.2%)

Genomes deposited in the last week

🟧66 🟧2 🟥3



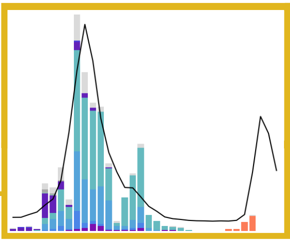


Eastern Cape ↑PTP: 46.6%

Genomes	Cases
1 402 (8.6%)	126 447 (6.9%)

Genomes deposited in the last week

🟧3

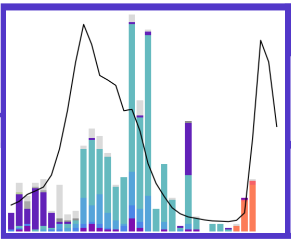


Limpopo ↓PTP: 37.5%

Genomes	Cases
1 142 (7.0%)	76 056 (4.2%)

Genomes deposited in the last week

🟧19

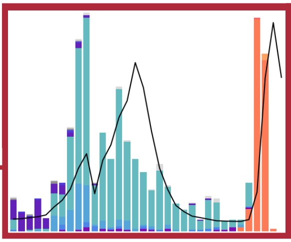


Mpumalanga ↓PTP: 37.0%

Genomes	Cases
903 (5.6%)	96 673 (5.3%)

Genomes deposited in the last week

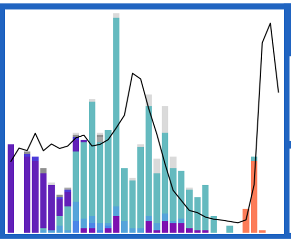
🟧5



KwaZulu-Natal ↑PTP: 43.0%

Genomes	Cases
1 603 (9.9%)	263 558 (14.4%)

Genomes deposited in the last week



Free State ↓PTP: 34.4%

Genomes	Cases
894 (5.5%)	97 617 (5.3%)

Genomes deposited in the last week

- 🟧 Omicron (21K)
- 🟧 Omicron (21L)
- 🟥 Omicron (21M)
- 🟪 C.1.2 (20D)
- 🟪 Beta (20H, V2)
- 🟦 Alpha (20I, V1)
- 🟦 Delta (21A)
- 🟦 Delta (21I)
- 🟩 Delta (21J)
- ⬜ 20A
- ⬛ 20B
- ⬛ 20C
- ⬛ 20D
- ⬜ Unassigned
- — Cases

209 genomes deposited in the past week

Bar graphs represent genomes sequenced per epiweek, with lines representing cases by collection date (weeks 18 – 51)

Genomes and cases presented as provincial total (percentage of national total) for epiweeks 18 – 51

PTP: percentage testing positive in week 50 (19 Dec – 25 Dec); the arrow indicates direction of change since the previous week (12 Dec – 18 Dec)

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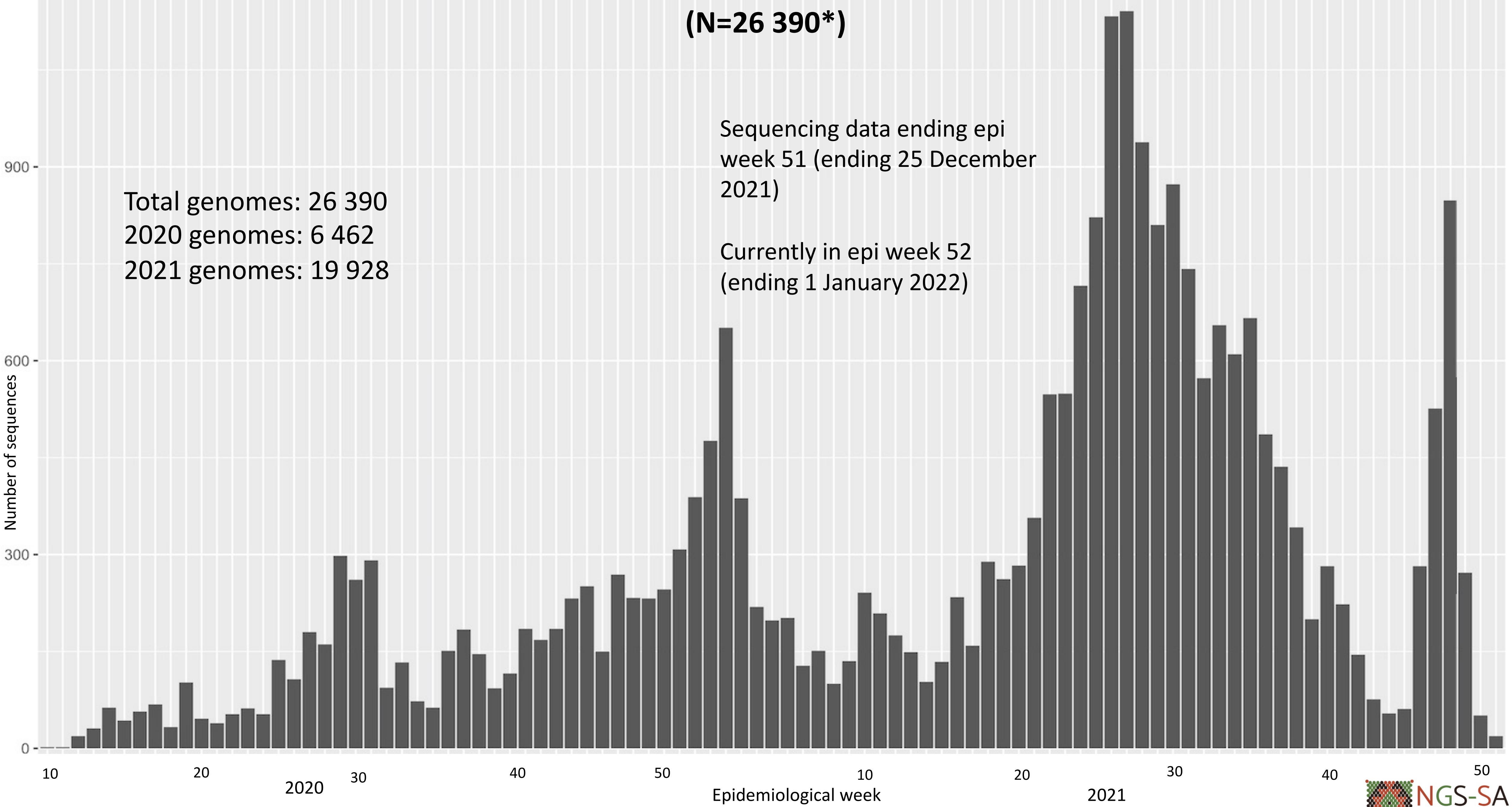
Number of South African genomes deposited on GISAID, by specimen collection week, 2020 and 2021 (N=26 390*)



Total genomes: 26 390
2020 genomes: 6 462
2021 genomes: 19 928

Sequencing data ending epi week 51 (ending 25 December 2021)

Currently in epi week 52 (ending 1 January 2022)

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

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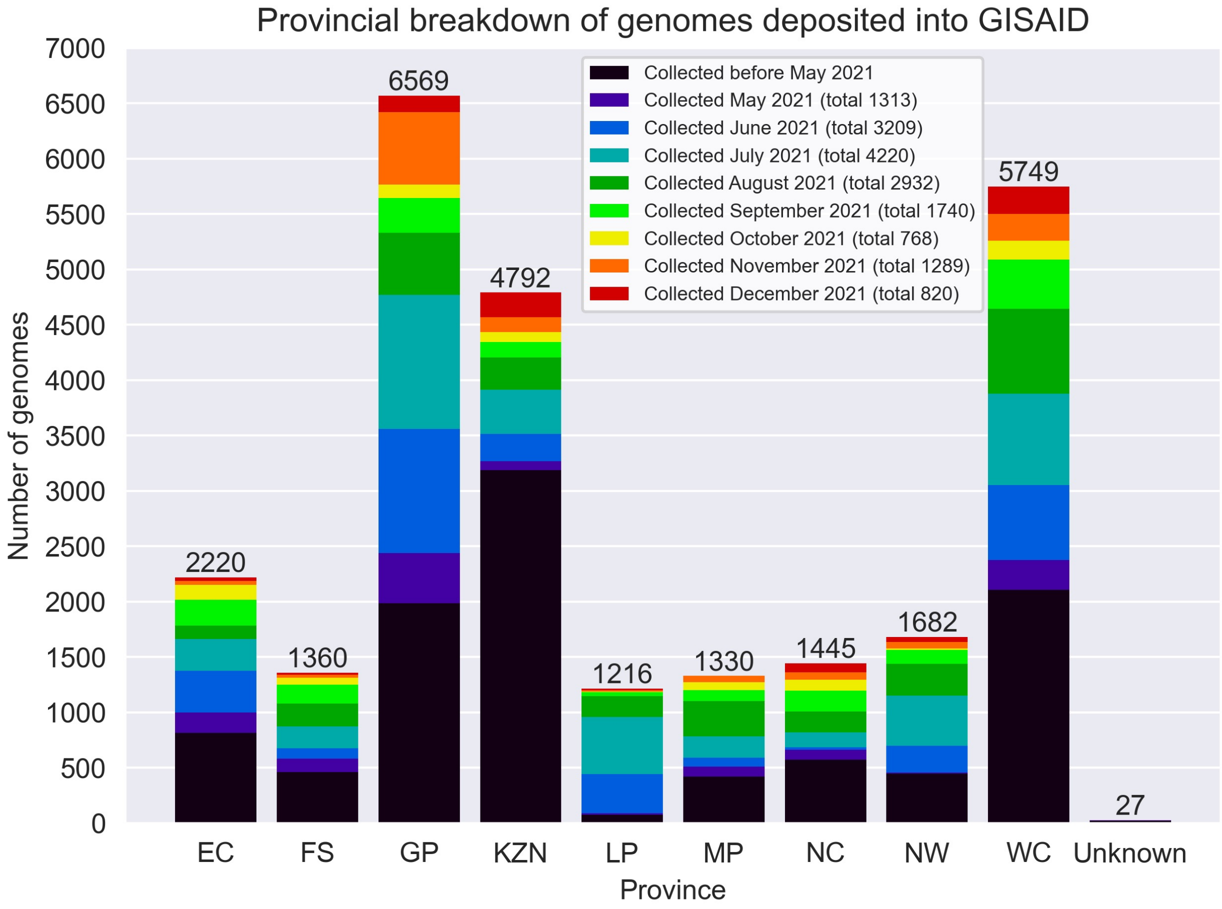
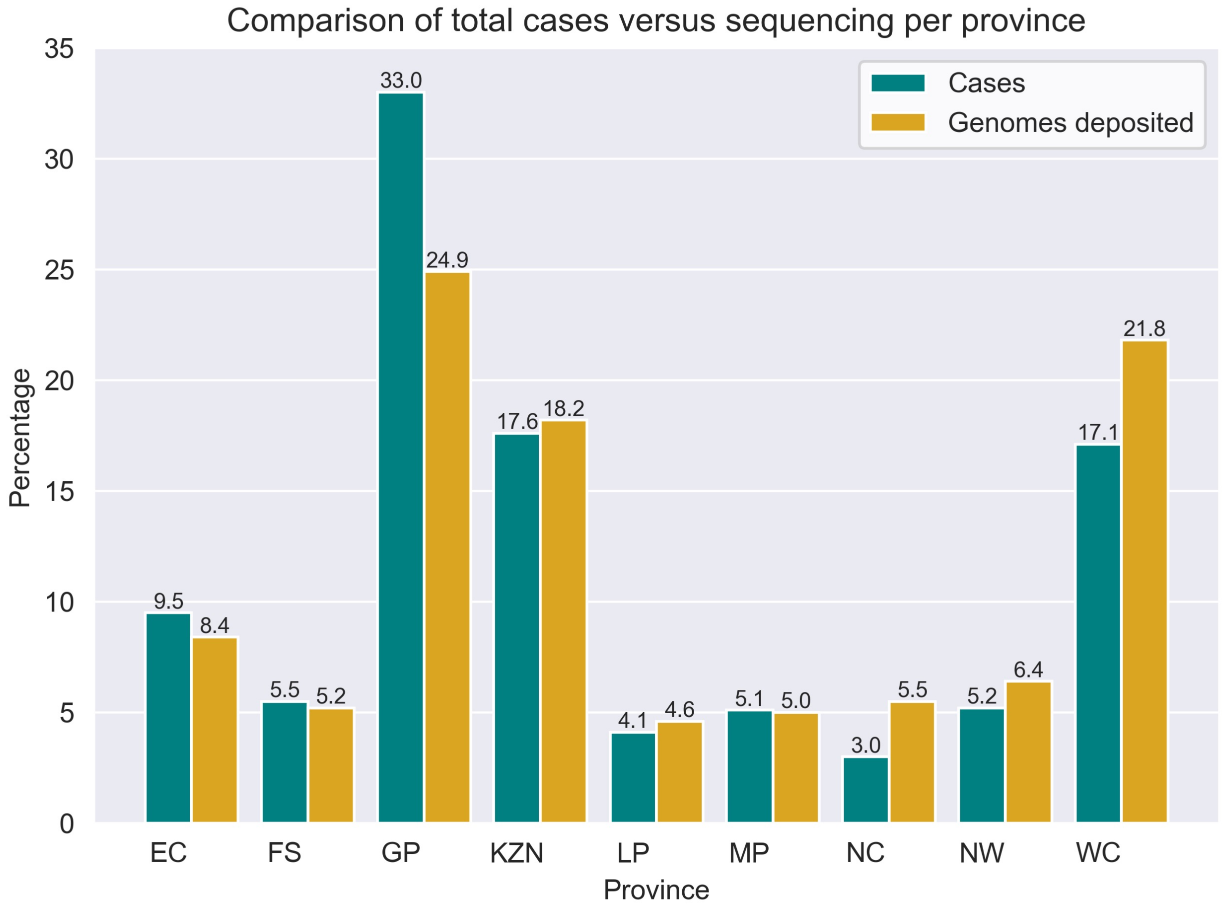
GISAID genomes vs total cases, 2020 and 2021 (N=26 390)


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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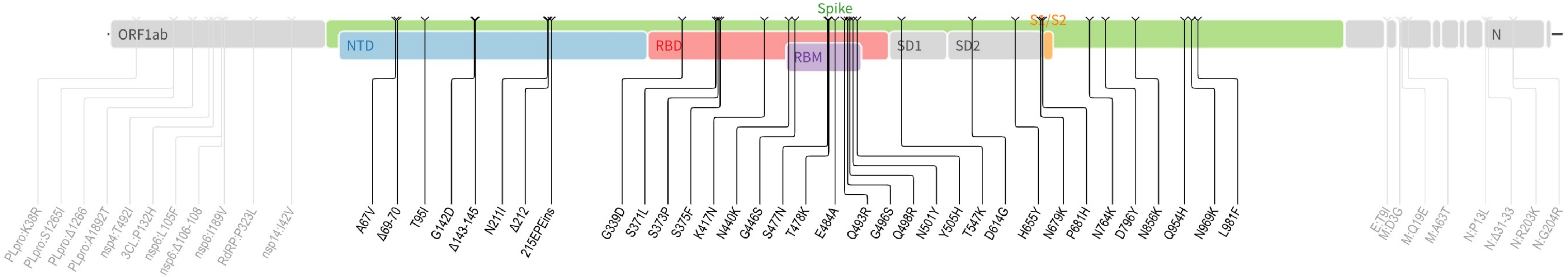
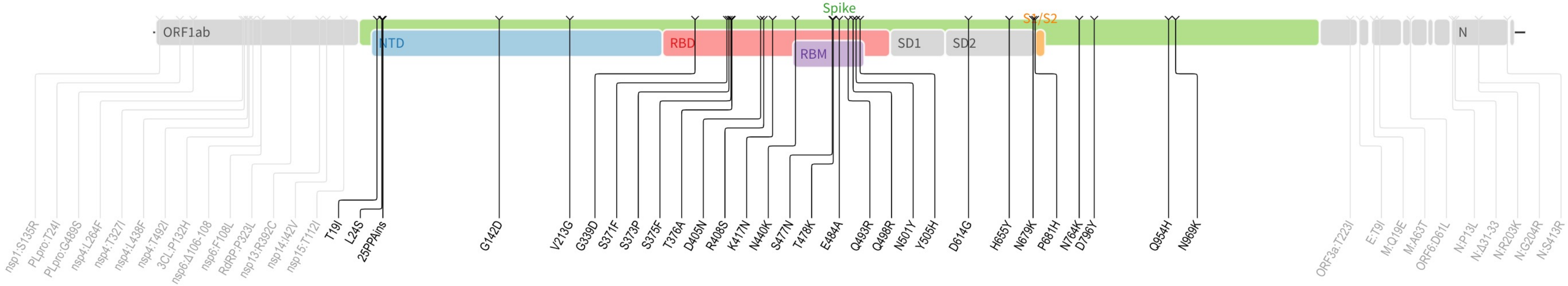
Omicron sub-lineage spike mutation profiles

BA.1
21K

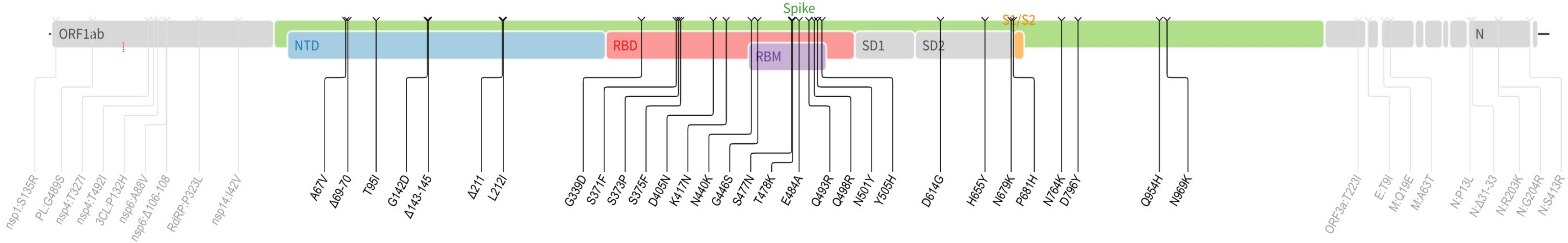


BA.2
21L

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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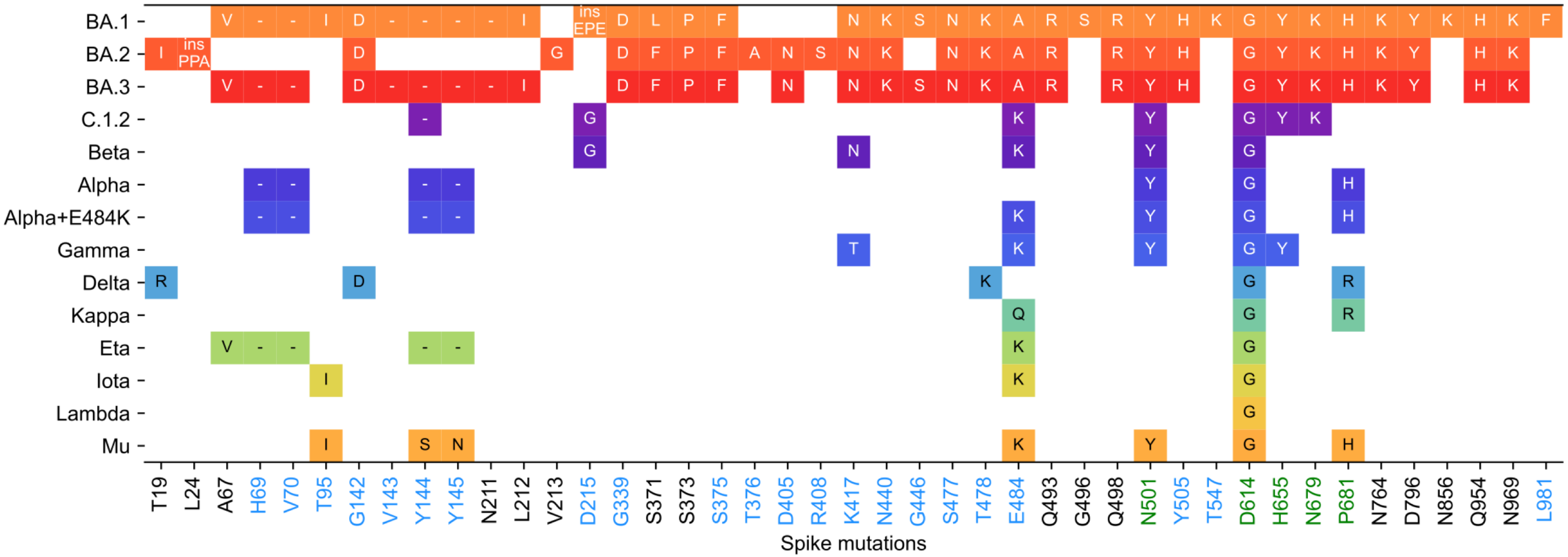
Omicron spike mutations compared to other VOC/VOIs



	T19	L24	A67	H69	V70	T95	G142	V143	Y144	Y145	N211	L212	V213	D215	G339	S371	S373	S375	T376	D405	R408
BA.1			V	-	-	I	D	-	-	-	-	I		ins EPE	D	L	P	F			
BA.2	I	ins PPA					D						G		D	F	P	F	A	N	S
BA.3			V	-	-		D	-	-	-	-	I			D	F	P	F		N	
C.1.2									-					G							
Beta														G							
Alpha				-	-				-	-											
Alpha+E484K				-	-				-	-											
Gamma																					
Delta	R						D														
Kappa																					
Eta			V	-	-				-	-											
Iota						I															
Lambda																					
Mu						I			S	N											

	K417	N440	G446	S477	T478	E484	Q493	G496	Q498	N501	Y505	T547	D614	H655	N679	P681	N764	D796	N856	Q954	N969	L981
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	N	K		N	K	A	R		R	Y	H		G	Y	K	H	K	Y		H	K	
BA.3	N	K	S	N	K	A	R		R	Y	H		G	Y	K	H	K	Y		H	K	
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								
Delta					K								G			R						
Kappa						Q							G			R						
Eta						K							G									
Iota						K							G									
Lambda													G									
Mu						K				Y			G			H						

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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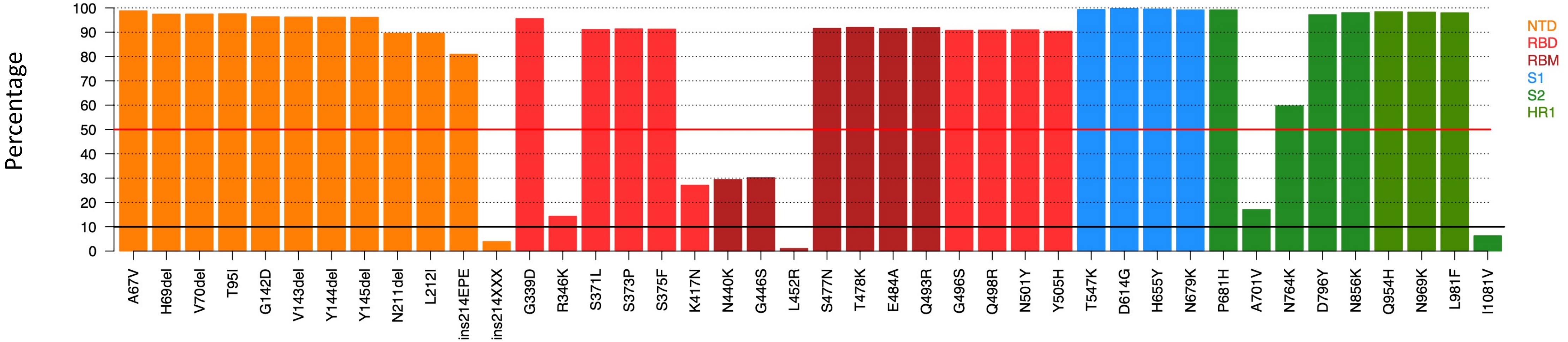
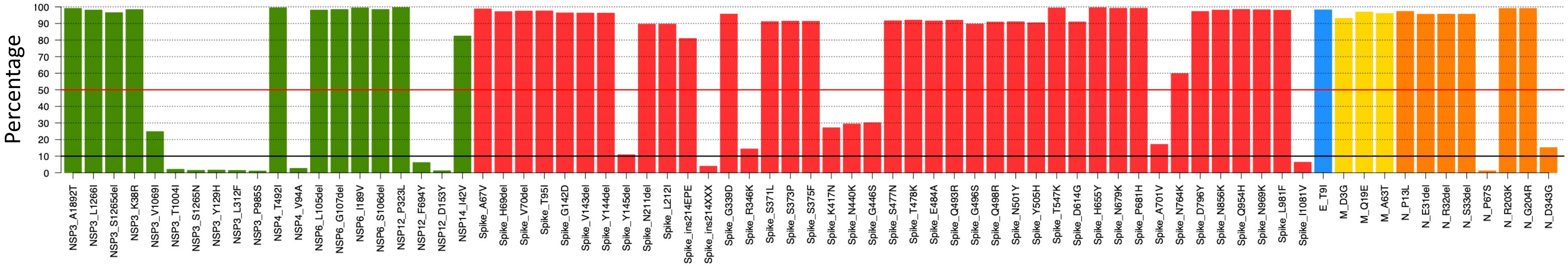
Mutational profile of Omicron sequences

Frequency of Spike SNVs for Omicron (n = 74 613)



Frequency of whole genome SNVs for Omicron (n = 74 613)



Mutational profile of Omicron is largely shared amongst all sequences.
Low mutation frequencies for N417N, N440K, G446S and N764K are most likely a result of poor coverage due to primer drop off.

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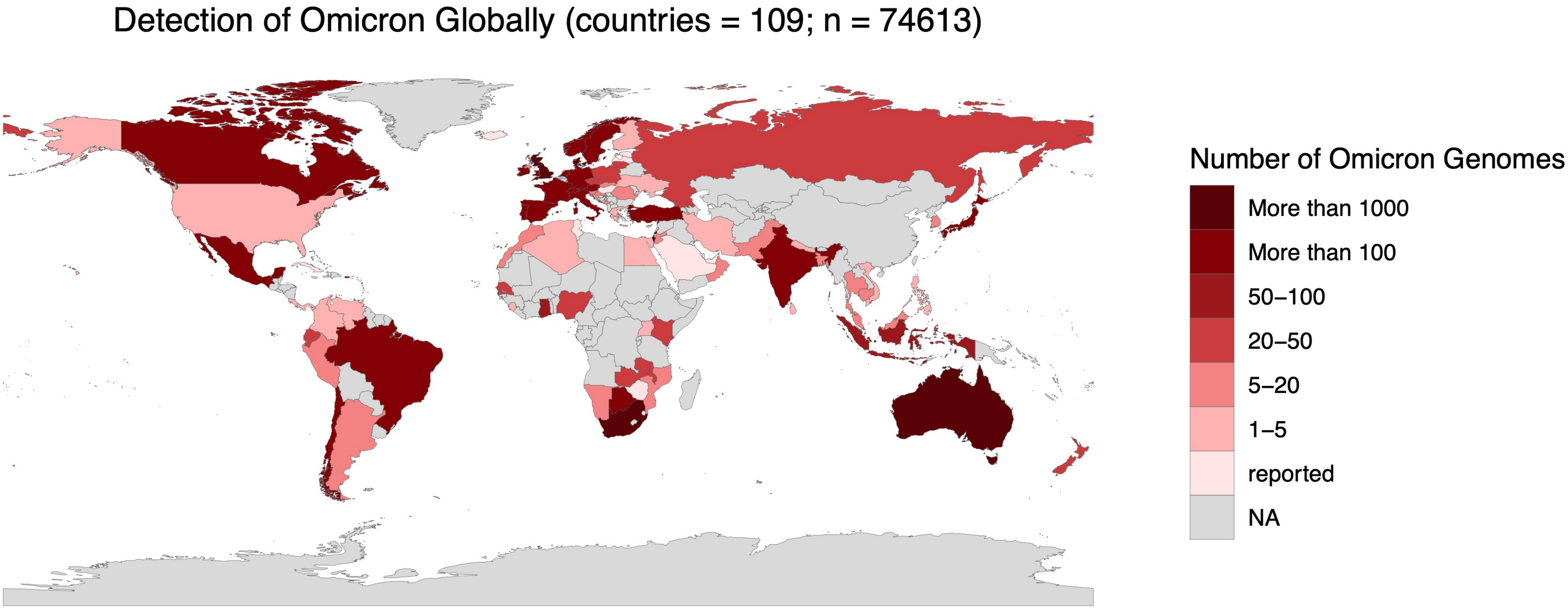
Omicron global prevalence



Omicron has been detected in 109 countries across the globe (detections based on GISAID).

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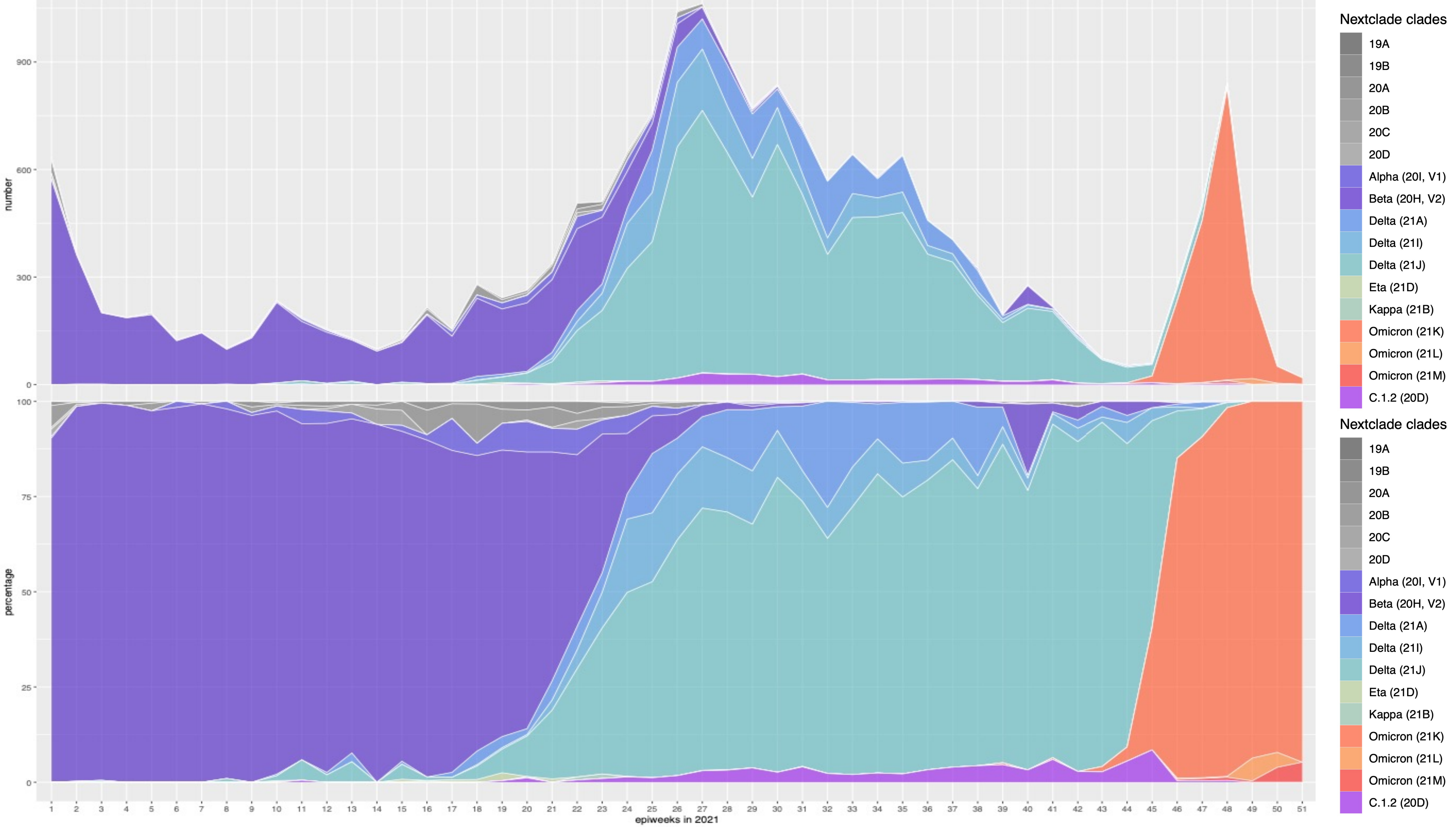
Proportion and number of clades by epiweek in South Africa, 2021 (N= 19 928)



Sequencing data ending epi week 51 (ending 25 December 2021)

Currently in epi week 52 (ending 1 January 2022)

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

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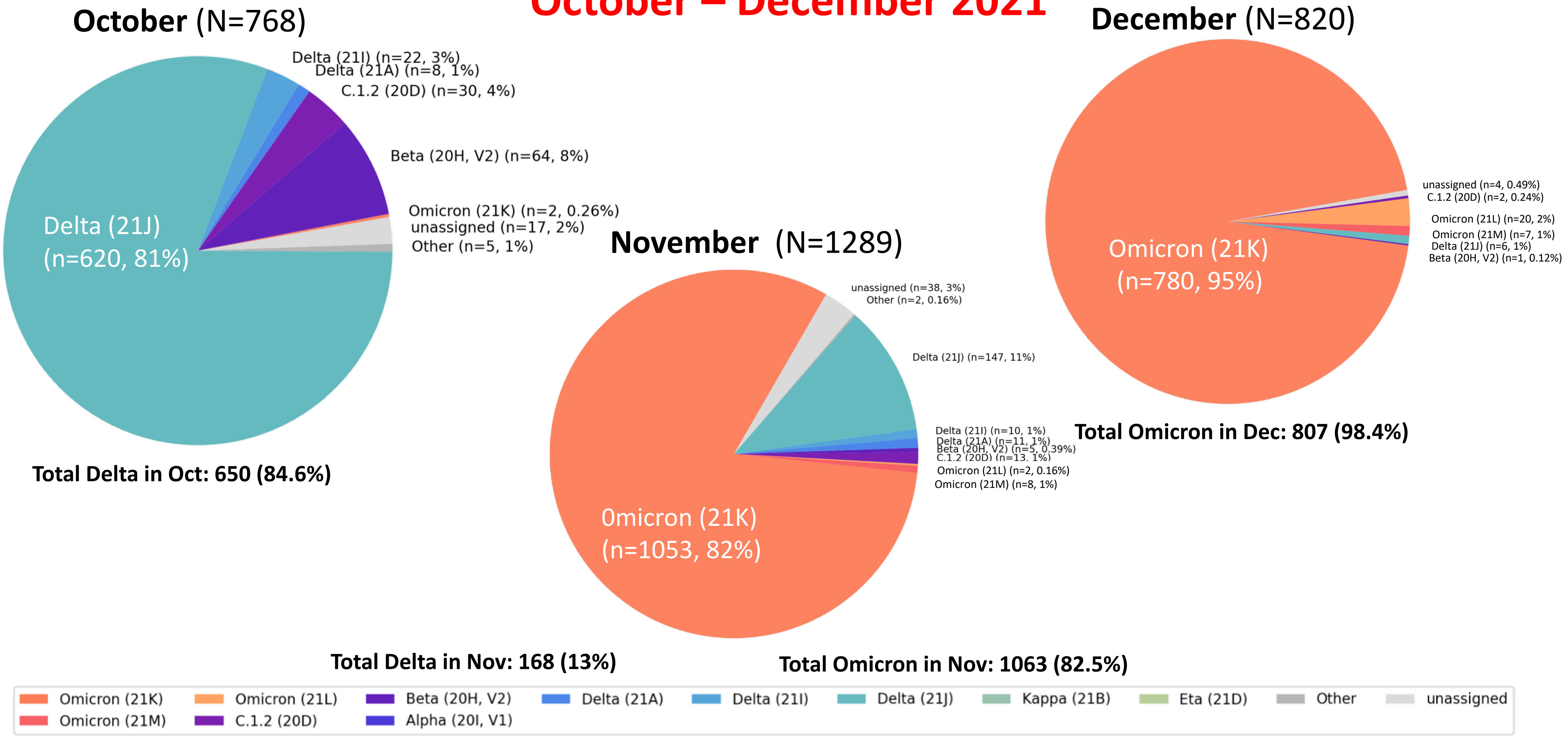
Prevalence of Variants of Concern (VOC) and Variants of Interest (VOI) in October – December 2021



Total Delta in Oct: 650 (84.6%)

Total Delta in Nov: 168 (13%)

Total Omicron in Nov: 1063 (82.5%)

Total Omicron in Dec: 807 (98.4%)

■ Omicron (21K) ■ Omicron (21L) ■ Beta (20H, V2) ■ Delta (21A) ■ Delta (21I) ■ Delta (21J) ■ Kappa (21B) ■ Eta (21D) ■ Other ■ unassigned
■ Omicron (21M) ■ C.1.2 (20D) ■ Alpha (20I, V1)

The Delta variant dominated at >80% in October in South Africa, while Omicron was detected at 0.3% (2/768)
Omicron dominated in November, at 83% (1063/1289) and continues to dominate in December (98%, 807/820)

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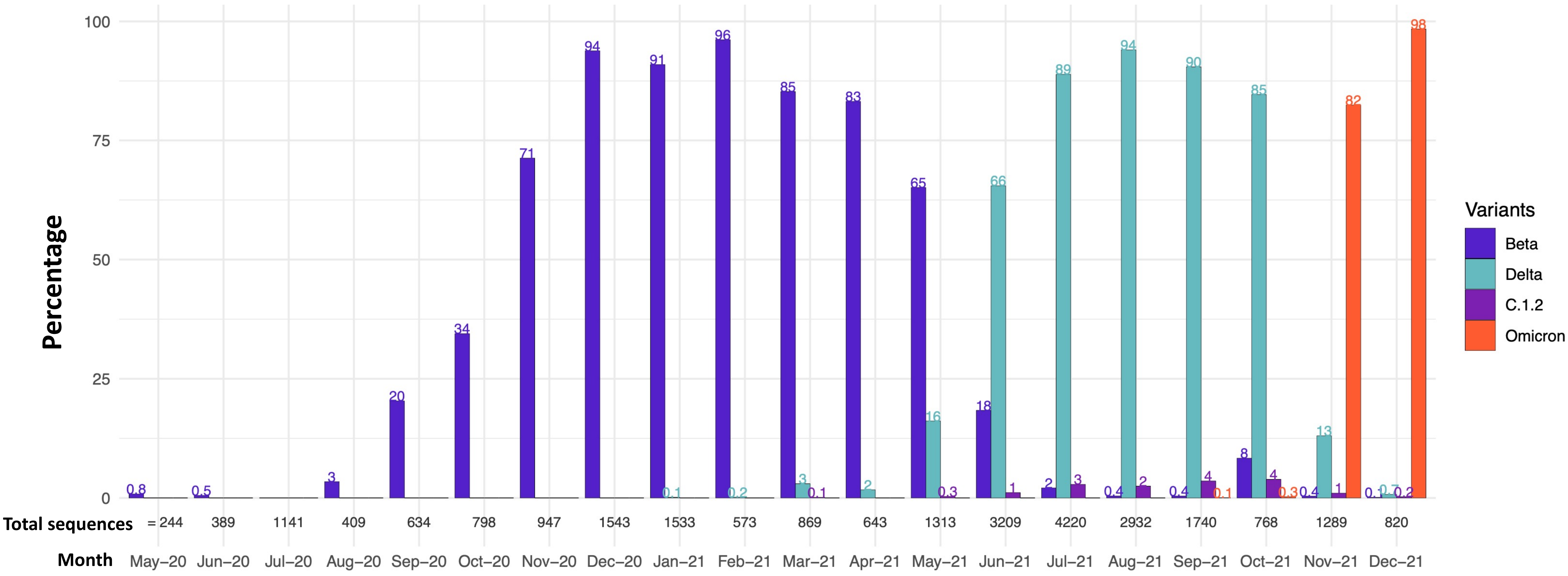
Detection Rates: Beta, Delta, C.1.2 and Omicron

Detection rates of variants being monitored in South Africa



C.1.2 has been detected at ≤ 4% of sequences monthly.
Beta prevalence increased slightly in October but has since remained at low levels in November and December.
Omicron has been dominant since November (>80% in November, >98% in December).

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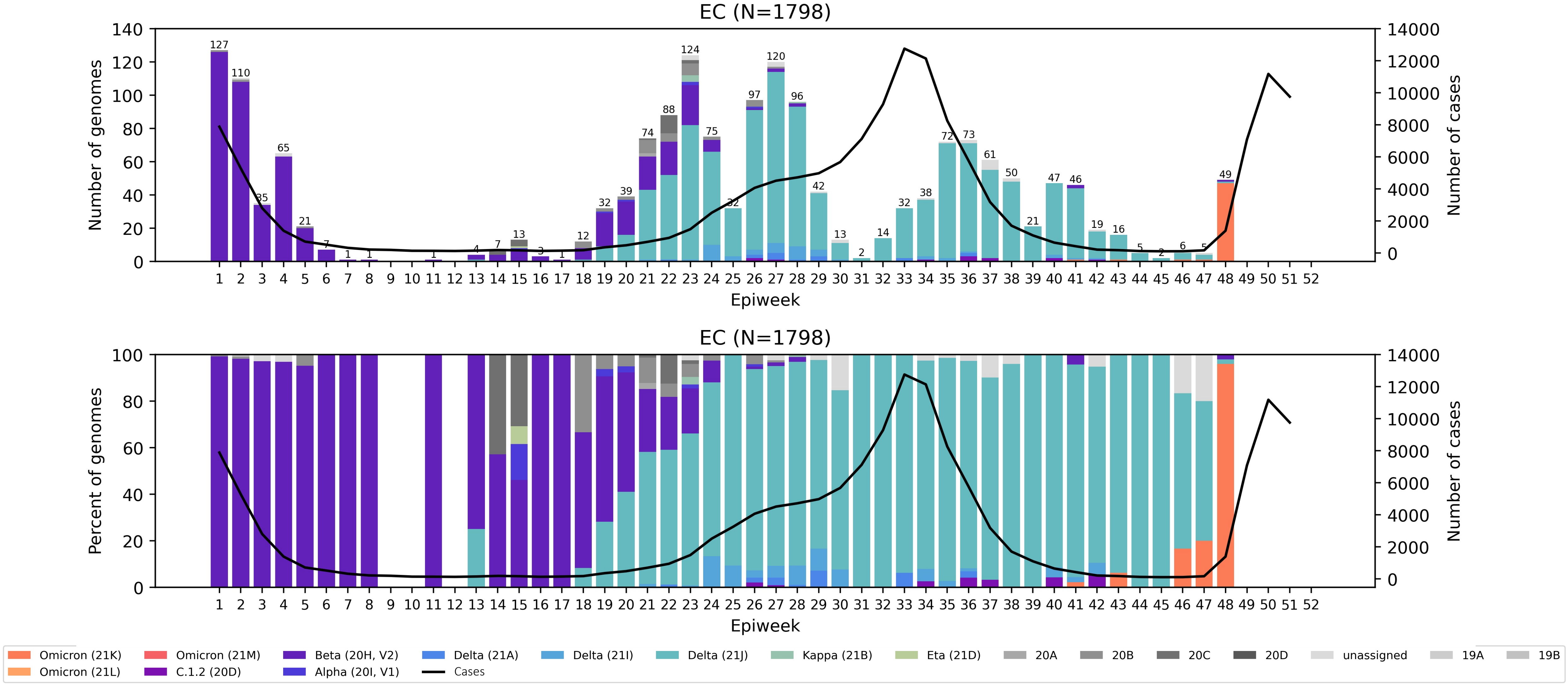
Eastern Cape Province, 2021, n =1798



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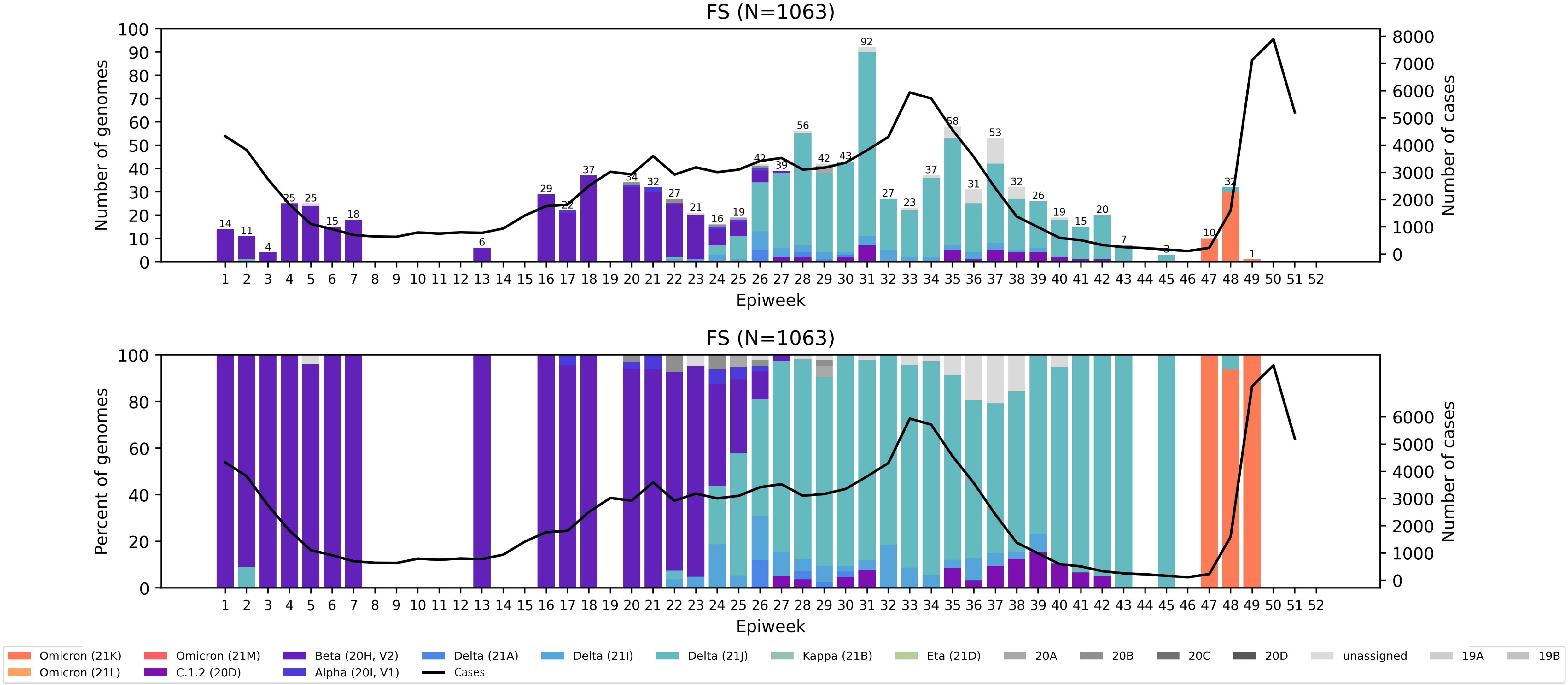
Free State Province, 2021, n = 1063



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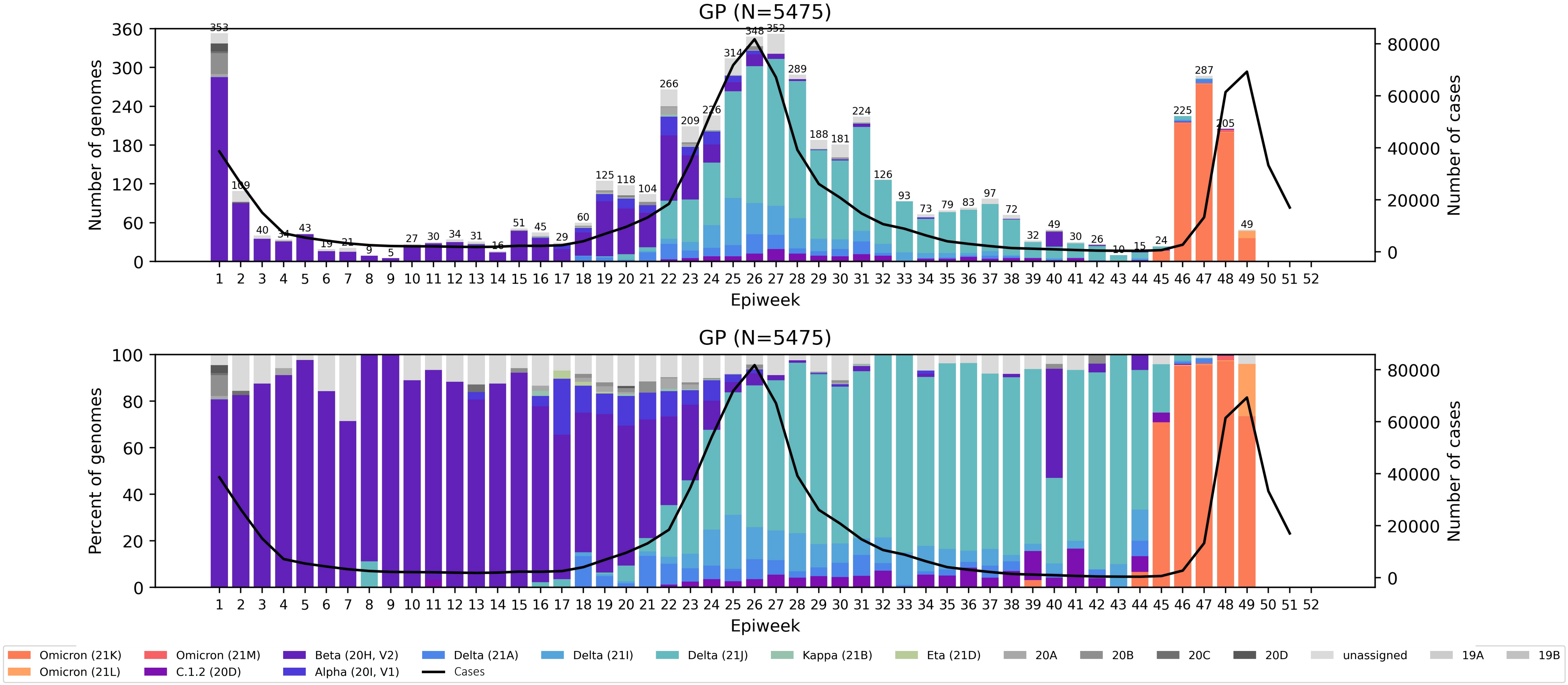
Gauteng Province, 2021, n = 5475



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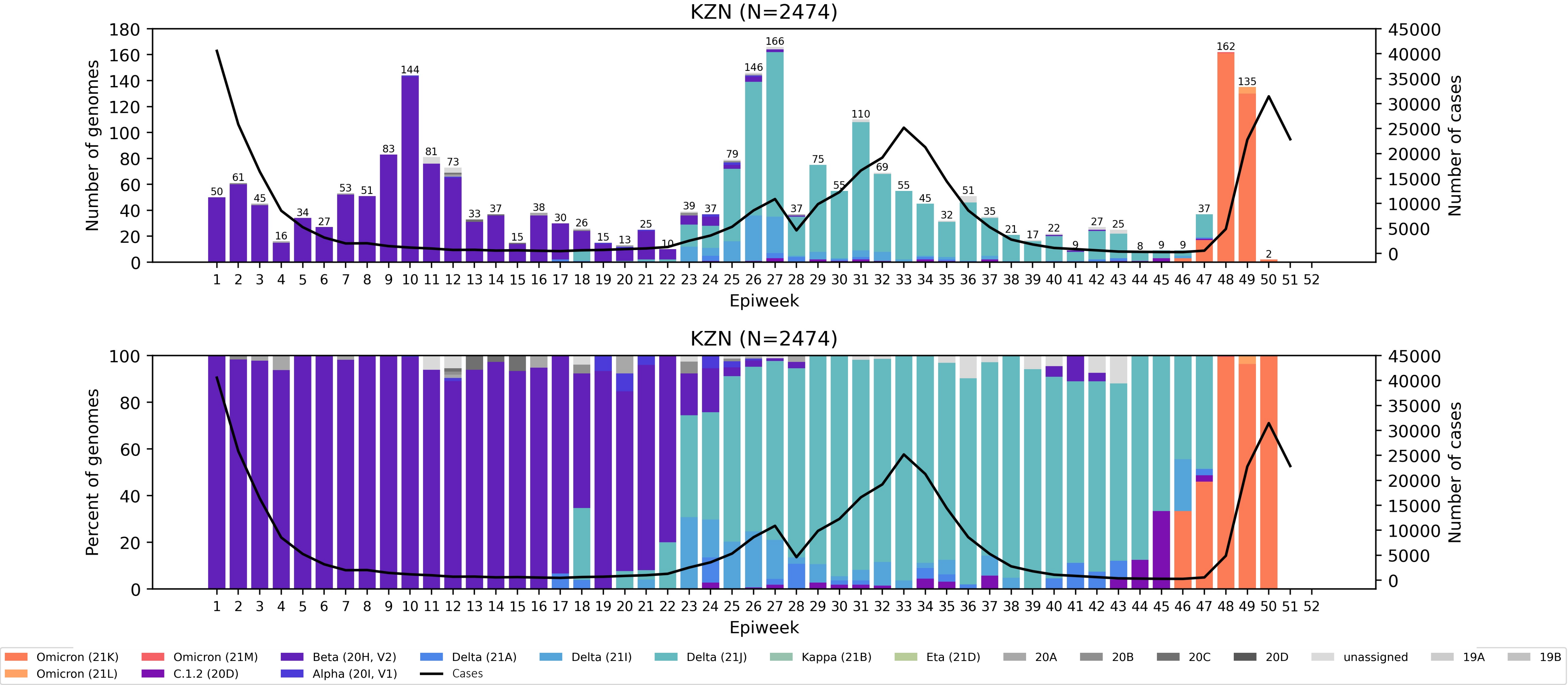
KwaZulu-Natal Province, 2021, n = 2474



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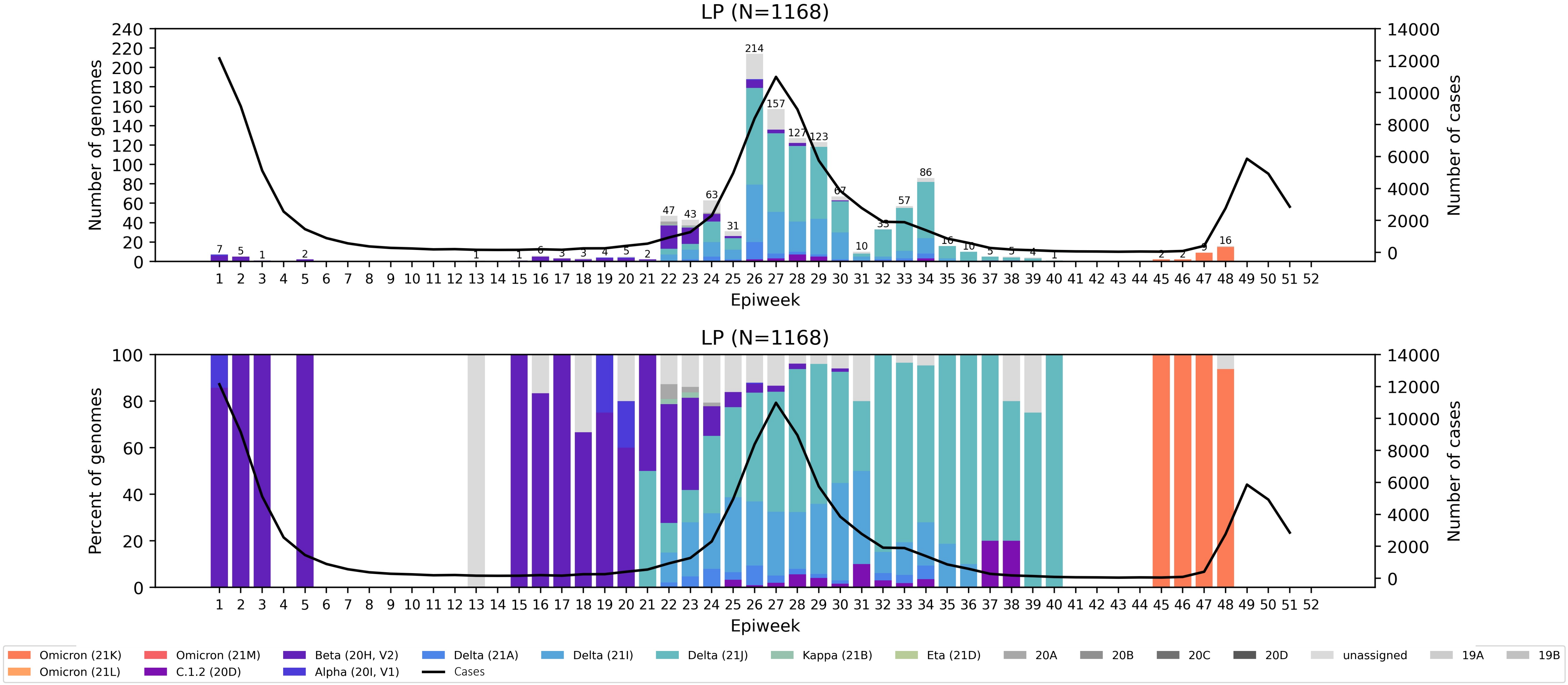
Limpopo Province, 2021, n = 1168



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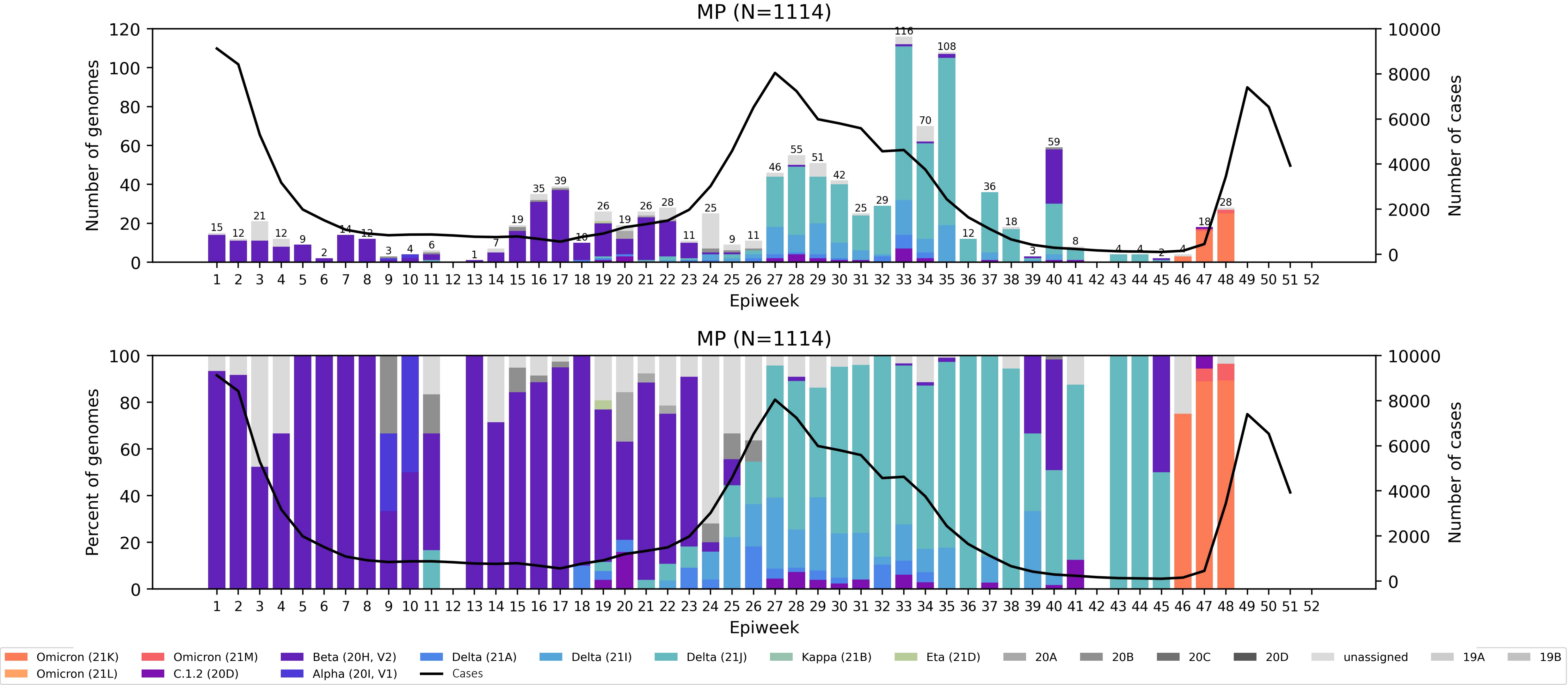
Mpumalanga Province, 2021, n = 1114



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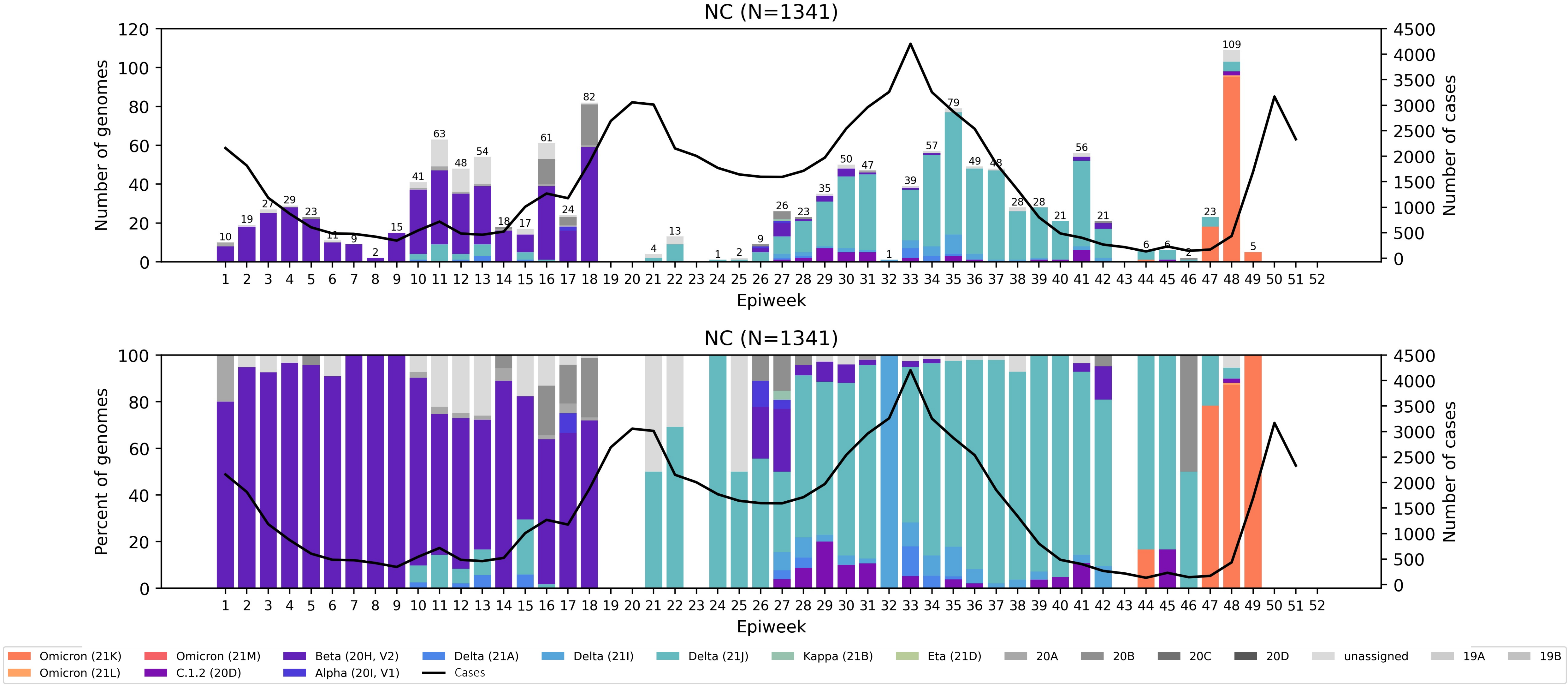
Northern Cape Province, 2021, n = 1341



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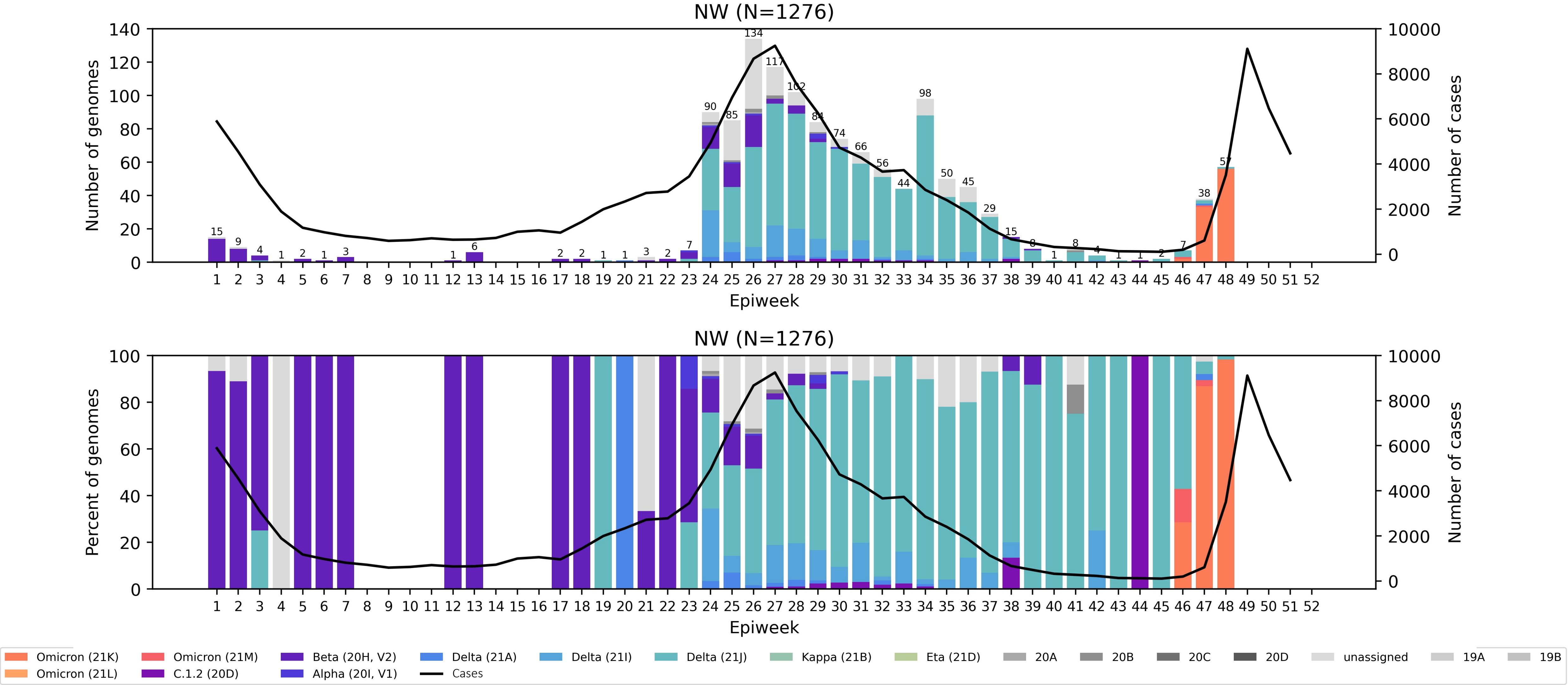
North West Province, 2021, n = 1276



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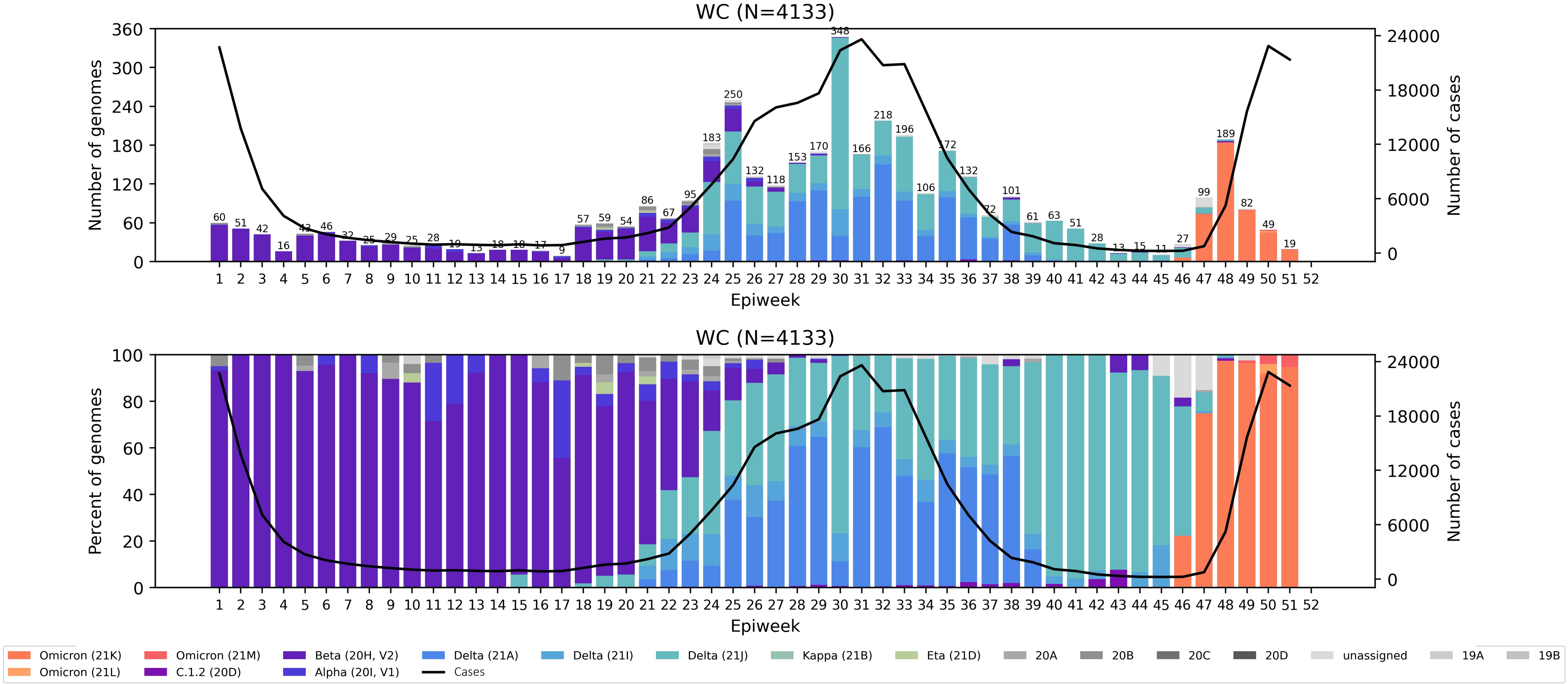
Western Cape Province, 2021, n = 4133



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Summary

- **Variant of Concern Omicron**
  - South Africa:
    - Dominated November sequencing data at 82.5% of genomes (n=1063/1289) and December sequencing data at 98% of genomes (n=807/830)
    - Detected in all provinces
  - Global:
    - Detected in 109 countries worldwide
    - Split into three lineages based on different mutational profiles: BA.1 (21K), BA.2 (21L), BA.3 (remains in 21M with parent lineage B.1.1.529 as does not meet requirements for new clade)
- Delta variant dominated in all provinces until end October
  - Delta sub-lineages varied by province
- C.1.2 lineage detected in all provinces of South Africa with prevalence of <4% of genomes per month and continues to be detected at low frequency

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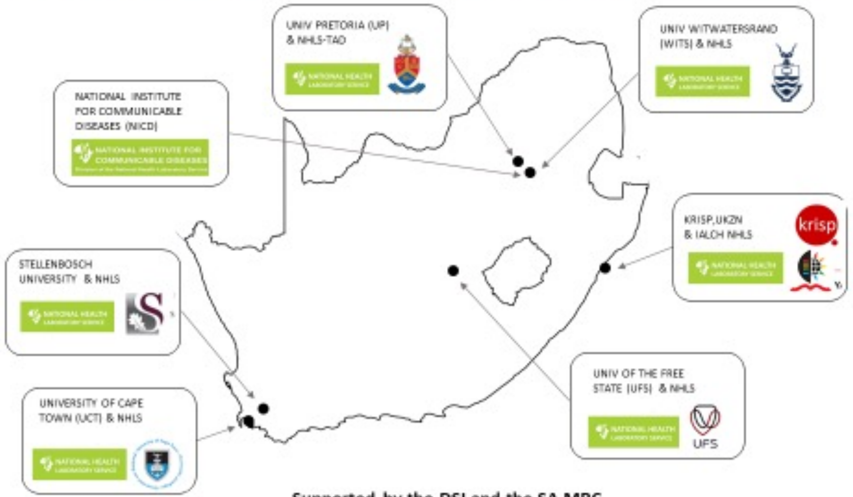

Supported by the DSI and the SA MRC

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Division of the National Health Laboratory Service

EDCTP

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

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GIZ/BMBF: African Network for Improved diagnostics and epidemiology of common and emerging infectious agents (ANDEMIA)
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National Institute for Communicable Diseases

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Division of the National Health Laboratory Service

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saMRC advancinglife

The Fleming Fund

science & technology
Department: Science and Technology
REPUBLIC OF SOUTH AFRICA

health
Department: Health
REPUBLIC OF SOUTH AFRICA

AFRICA CDC
Centres for Disease Control and Prevention
Safeguarding Africa's Health

wellcome

CDC
CENTERS FOR DISEASE CONTROL AND PREVENTION

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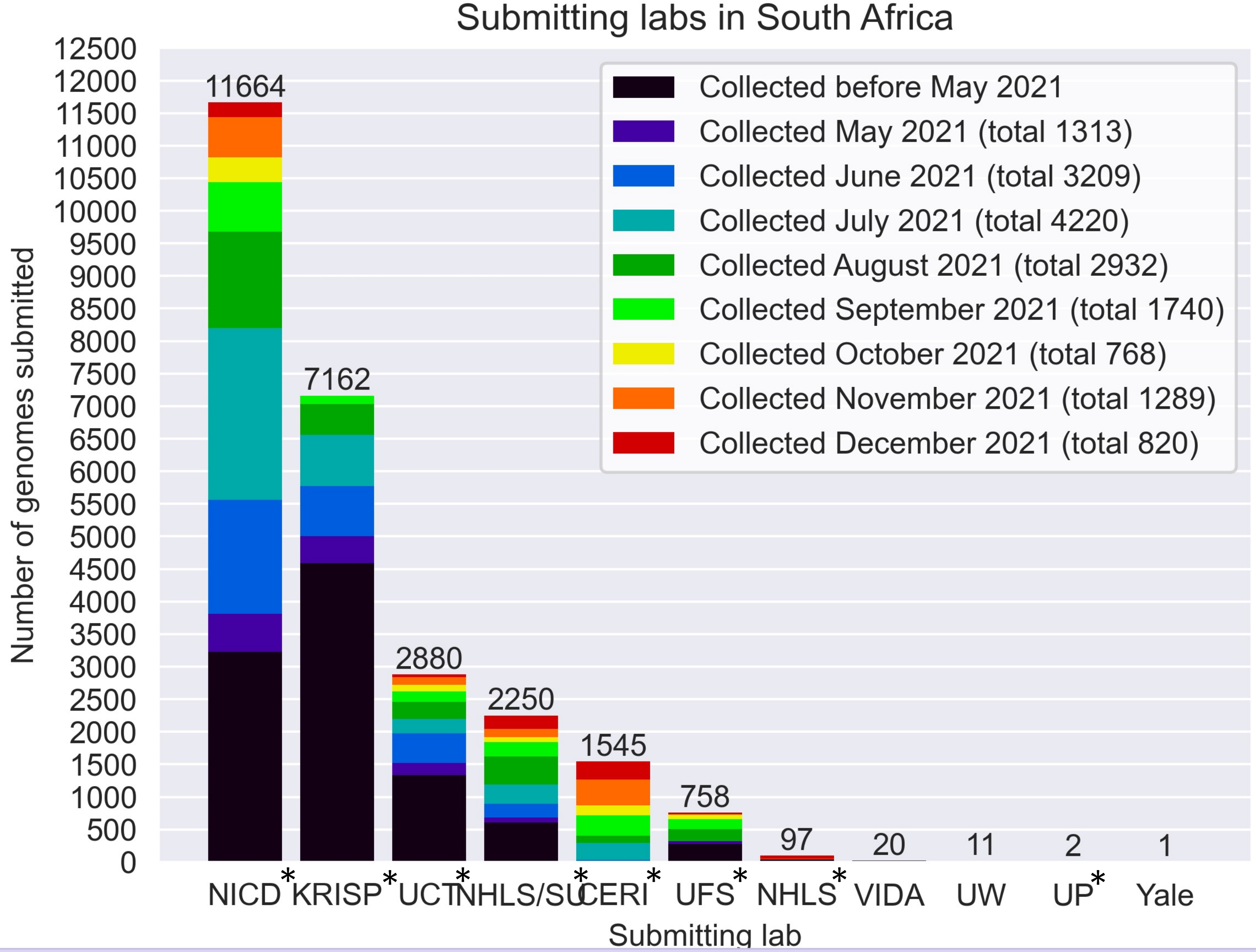
NGS-SA
Network for Genomic Surveillance in South Africa

South African genomes submitted per submitting lab, 2020 and 2021 (N=26 390)



***NGS-SA Labs**

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.

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	+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 17 December 2021

•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.)