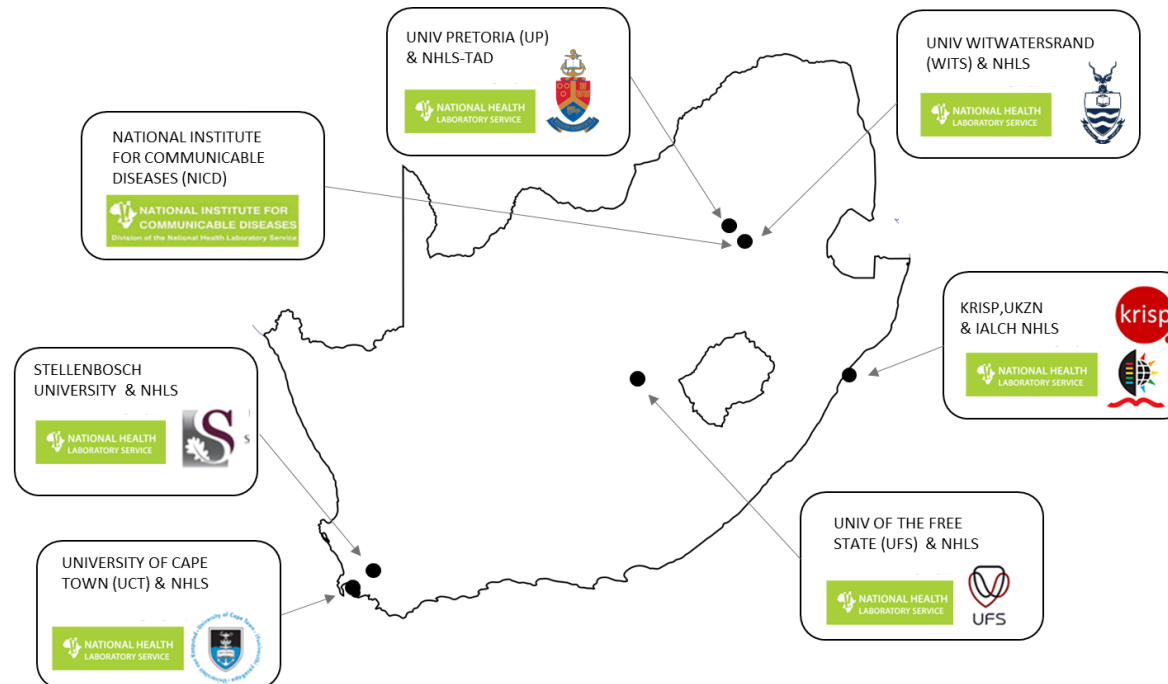


SARS-CoV-2 Sequencing Update 25 February 2022



Supported by the DSI and the SA MRC

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

The genomic data presented here are based on South African SARS-CoV-2 sequence data downloaded from GISAID (www.gisaid.org) on 25 February 2022 at 11h11



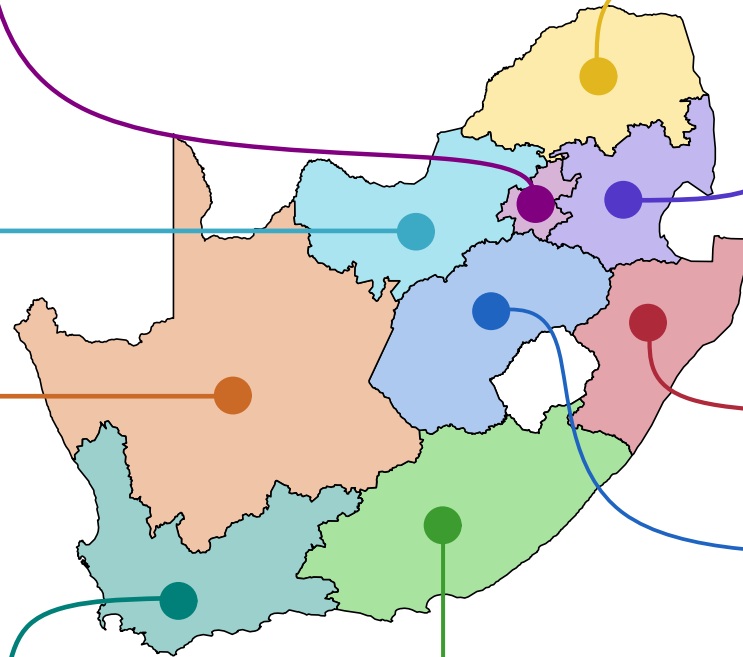
Data license: <https://www.gisaid.org/registration/terms-of-use/>

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 PMID: 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 PMID: PMC5388101

SARS-CoV-2

GENOMIC SURVEILLANCE epiweeks 39 (2021) - 7 (2022)



Gauteng ↑ PTP: 9.8%

Genomes Cases
2 194 (26.4%) 262 979 (35.5%)

Genomes deposited in the last week

49 12 47 1 1

North West ↑ PTP: 14.5%

Genomes Cases
415 (5.0%) 38 198 (5.2%)

Genomes deposited in the last week

29 5 11 2

Northern Cape ↓ PTP: 11.5%

Genomes Cases
493 (5.9%) 17 549 (2.4%)

Genomes deposited in the last week

8 3 3 1

Western Cape ↑ PTP: 12.8%

Genomes Cases
1 586 (19.1%) 124 893 (16.9%)

Genomes deposited in the last week

45 3 30 10 14 2 2

Eastern Cape ↑ PTP: 6.5%

Genomes Cases
780 (9.4%) 52 674 (7.1%)

Genomes deposited in the last week

142 10 8

Limpopo ↓ PTP: 10.6%

Genomes Cases
541 (6.5%) 31 180 (4.2%)

Genomes deposited in the last week

78 10 50 1

Mpumalanga ↓ PTP: 16.2%

Genomes Cases
704 (7.5%) 38 353 (5.2%)

Genomes deposited in the last week

65 22 55 3 1

KwaZulu-Natal ↓ PTP: 7.4%

Genomes Cases
1 208 (14.5%) 136 789 (18.5%)

Genomes deposited in the last week

10 3 3 1

Free State ↓ PTP: 8.9%

Genomes Cases
384 (4.6%) 37 693 (5.1%)

Genomes deposited in the last week

2 1 1

Omicron (BA.1) Beta (20H, V2) 20A 20C
 Omicron (BA.1.1) Alpha (20I, V1) 20B 20D
 Omicron (BA.2) Delta (21A) C.1.2 Unassigned
 Omicron (BA.3) Delta (21I) Delta (21J) Cases

743 genomes deposited in the past week

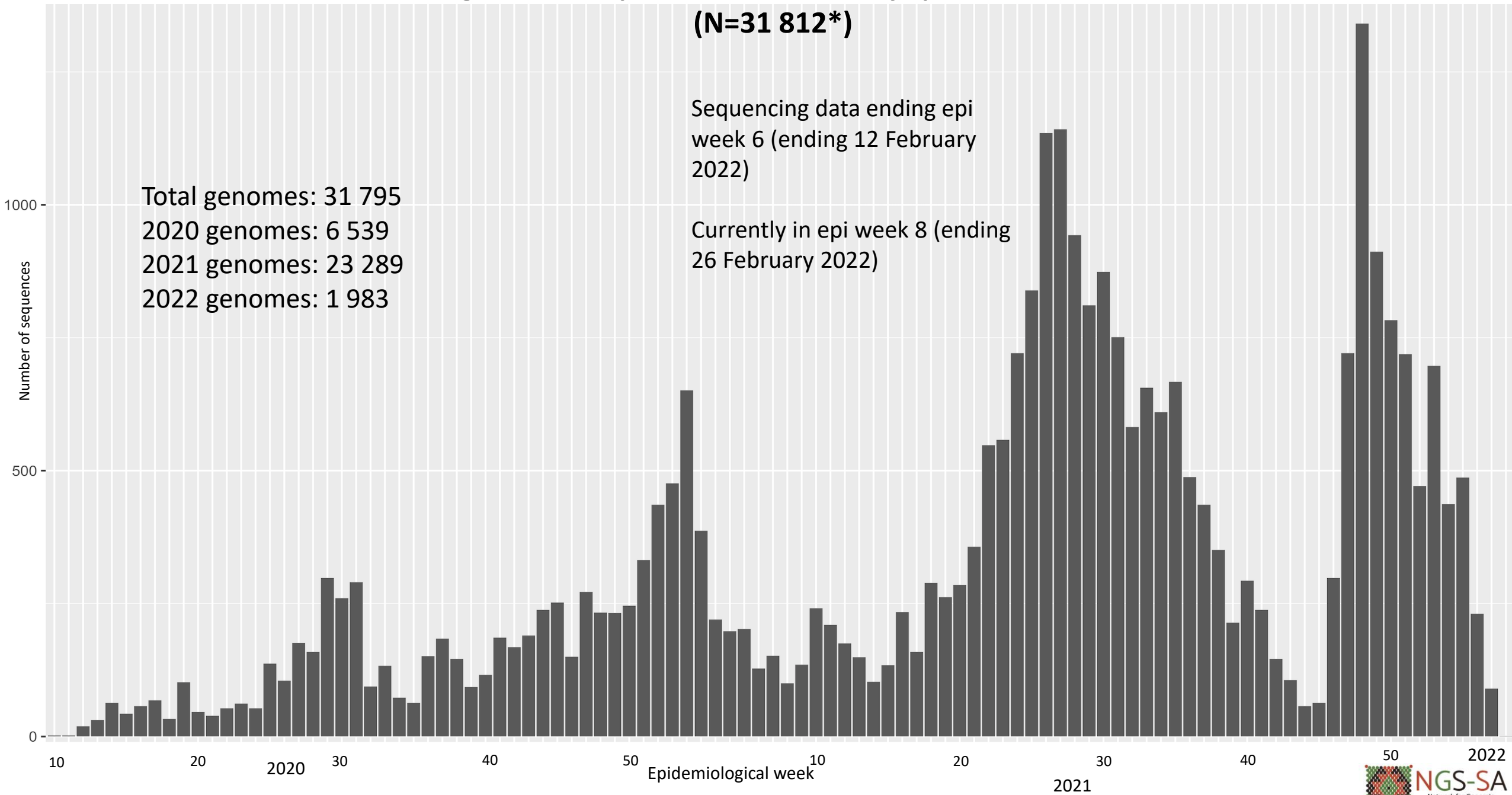
Bar graphs represent genomes sequenced per epiweek, with lines representing cases by collection date (weeks 39 [2021] – 7 [2022])

Genomes and cases presented as provincial total (percentage of national total) for epiweeks 39 (2021) – 7 (2022)

PTP: percentage testing positive in week 7 (13 Feb 2022 – 19 Feb 2022); the arrow indicates direction of change since the previous week (6 Feb 2022 – 12 Feb 2022)

Number of South African genomes deposited on GISAID, by specimen collection week, 2020 – 2022

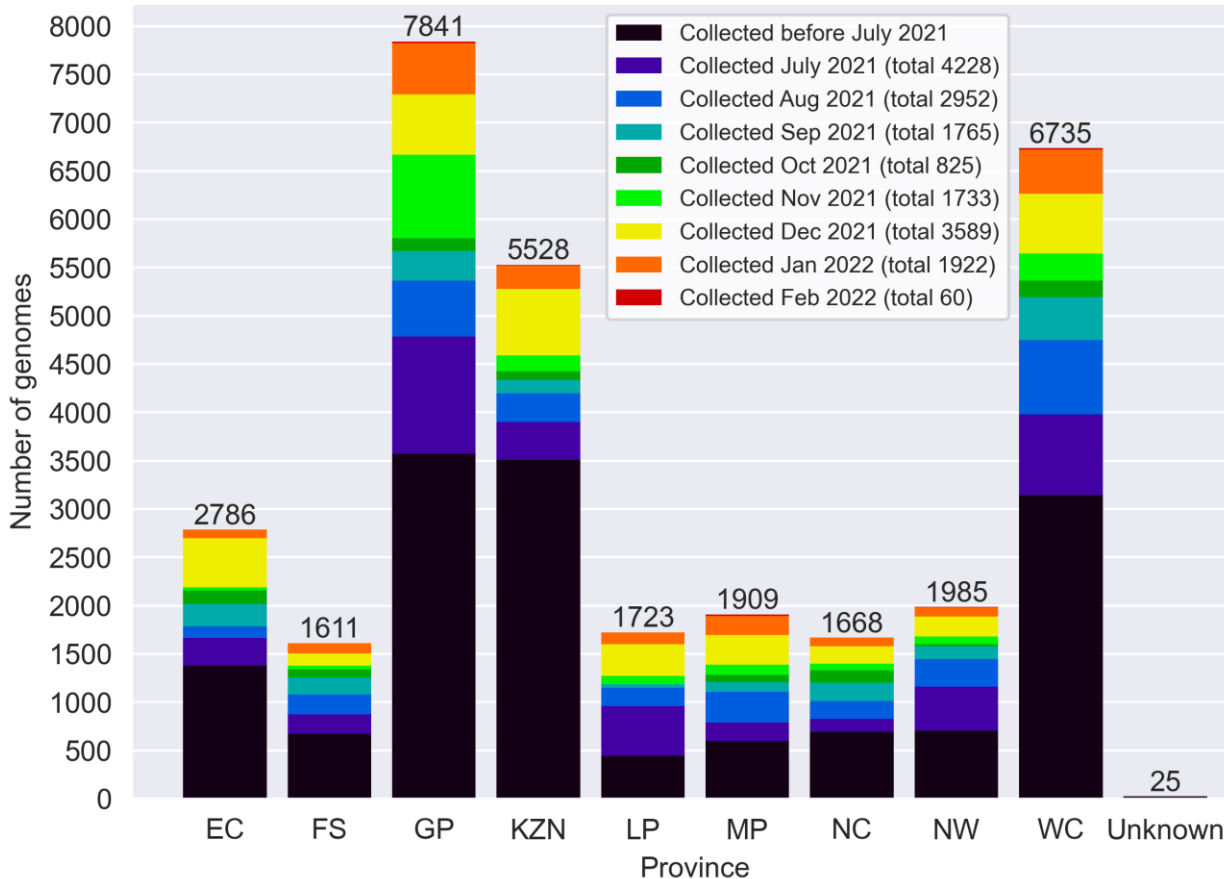
(N=31 812*)



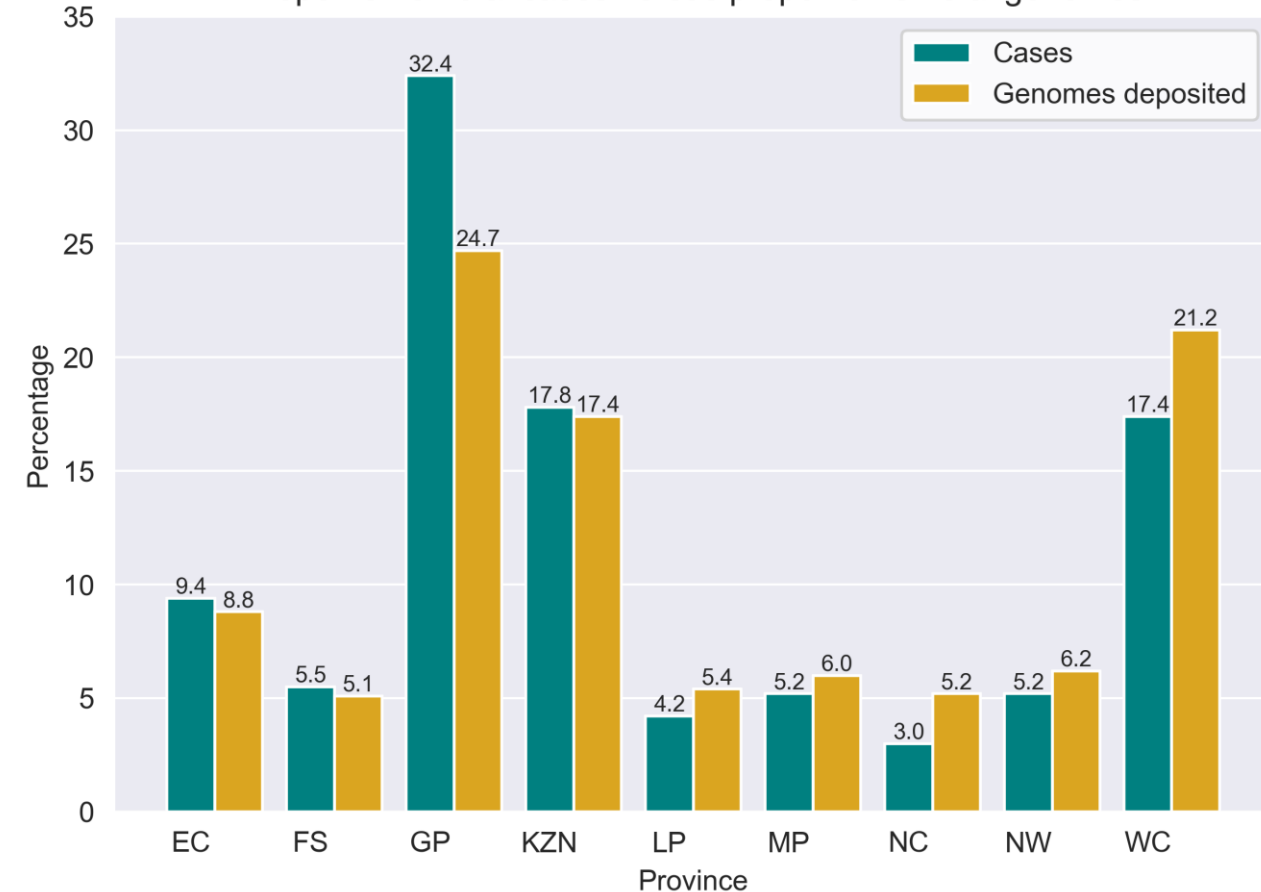
*This represents the cleaned, de-duplicated dataset of unique **National and Pneumonia Surveillance** sequences. This dataset will be used for all further figures.

GISAID genomes vs total cases, 2020 – 2022 (N=31 812)

Provincial breakdown of genomes deposited into GISAID

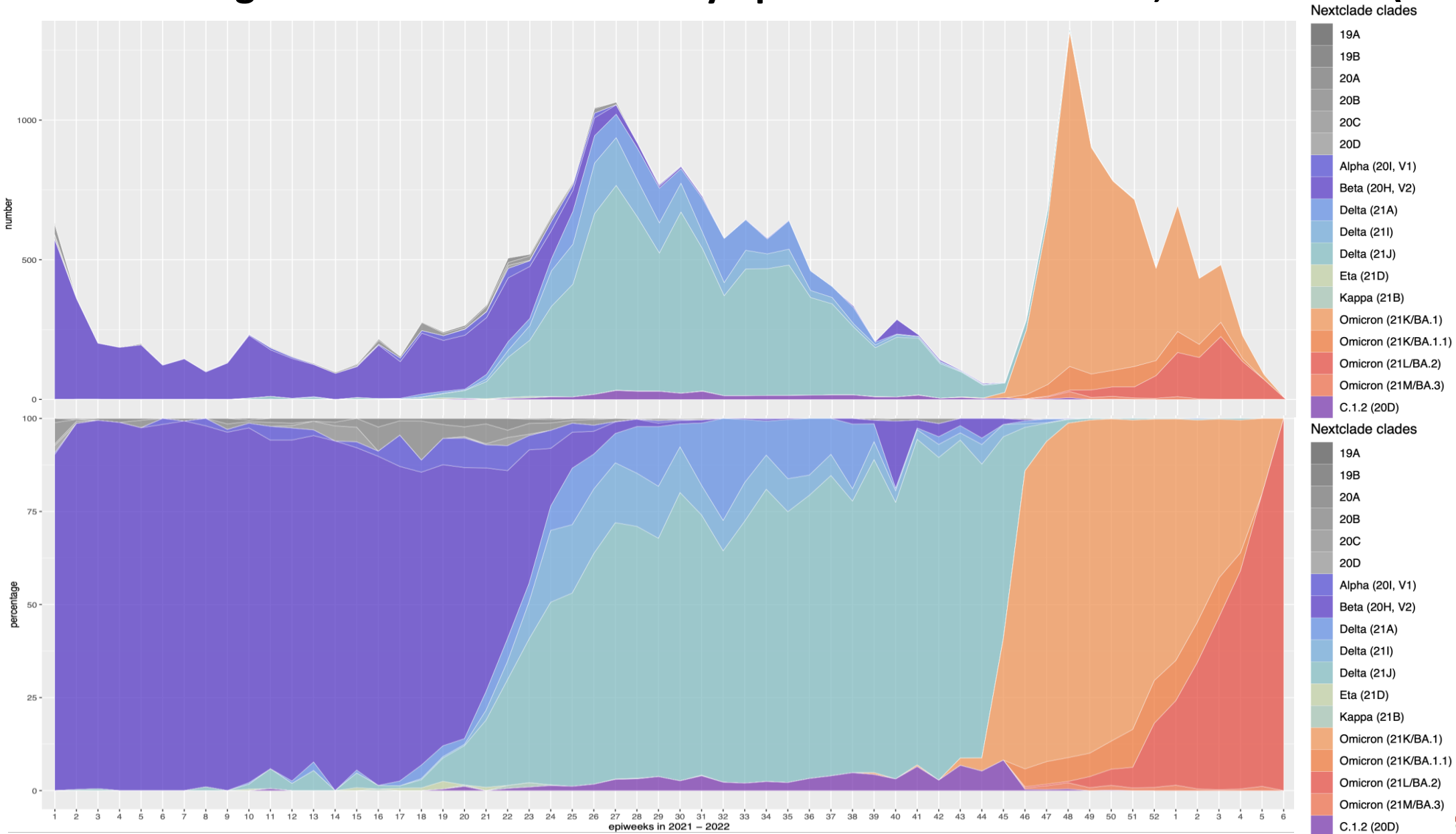


Proportion of total cases versus proportion of total genomes



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

Percentage and number of clades by epiweek in South Africa, 2021 - 2022 (N=25 272)



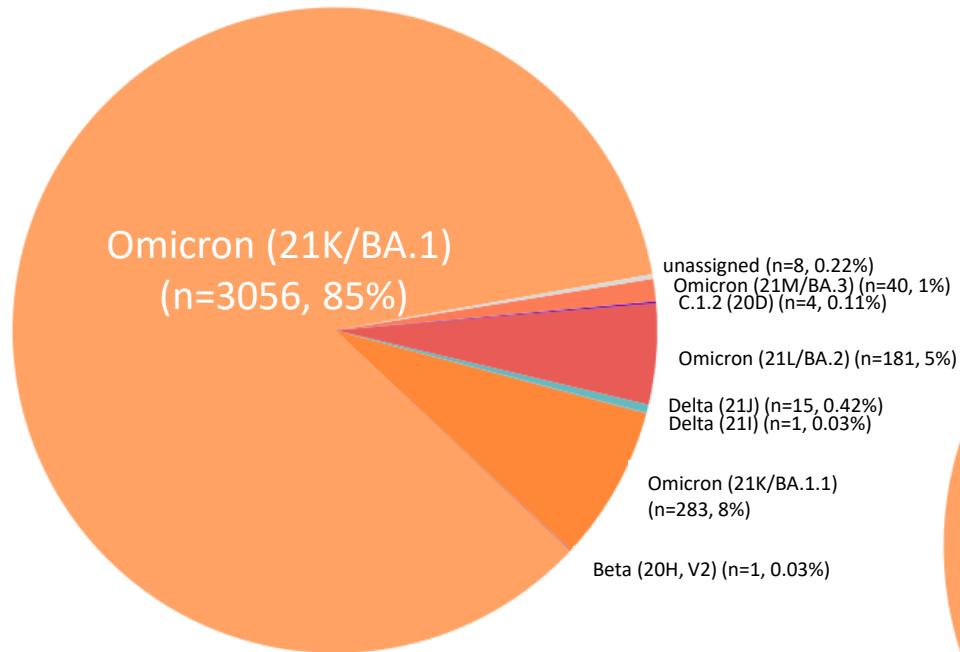
Sequencing data
ending epi week 6
(ending 12
February 2022)

Currently in epi
week 8 (ending 26
February 2022)

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

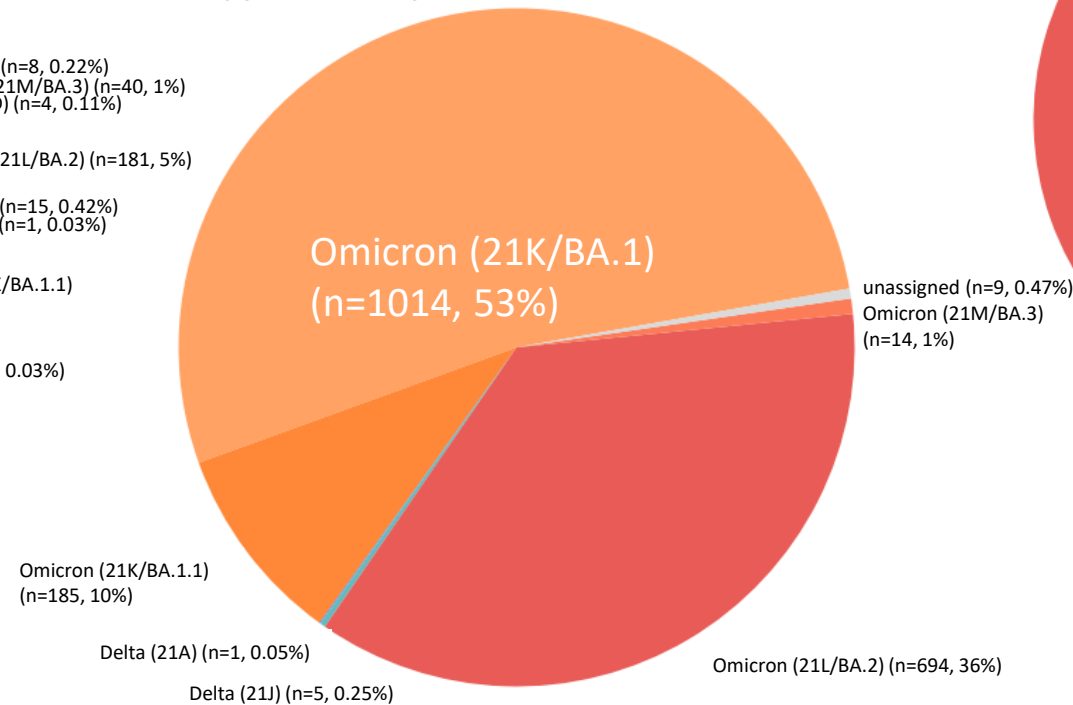
Prevalence of Variants of Concern (VOC) and Variants of Interest (VOI) in Dec 2021 – Feb 2022

December (N=3589)



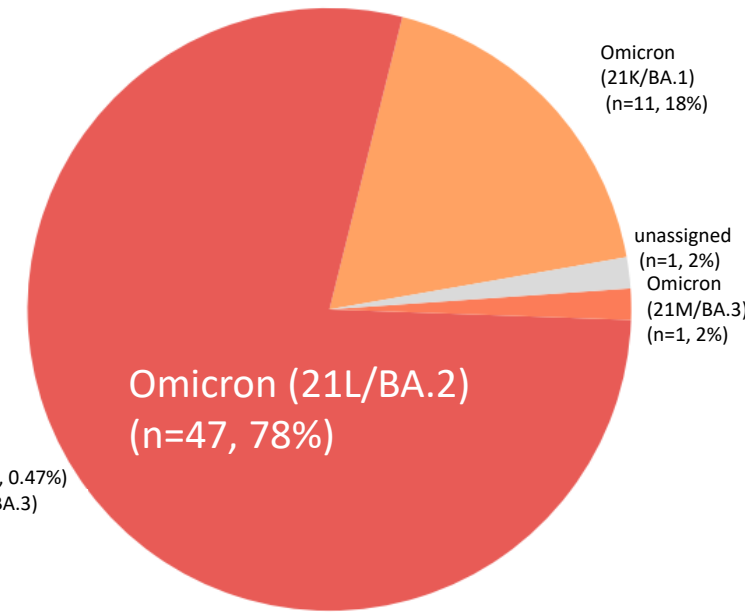
Total Omicron in Dec: 3560 (99.2%)

January (N=1922)



Total Omicron in Jan: 1907 (99.2%)

February (N=60)



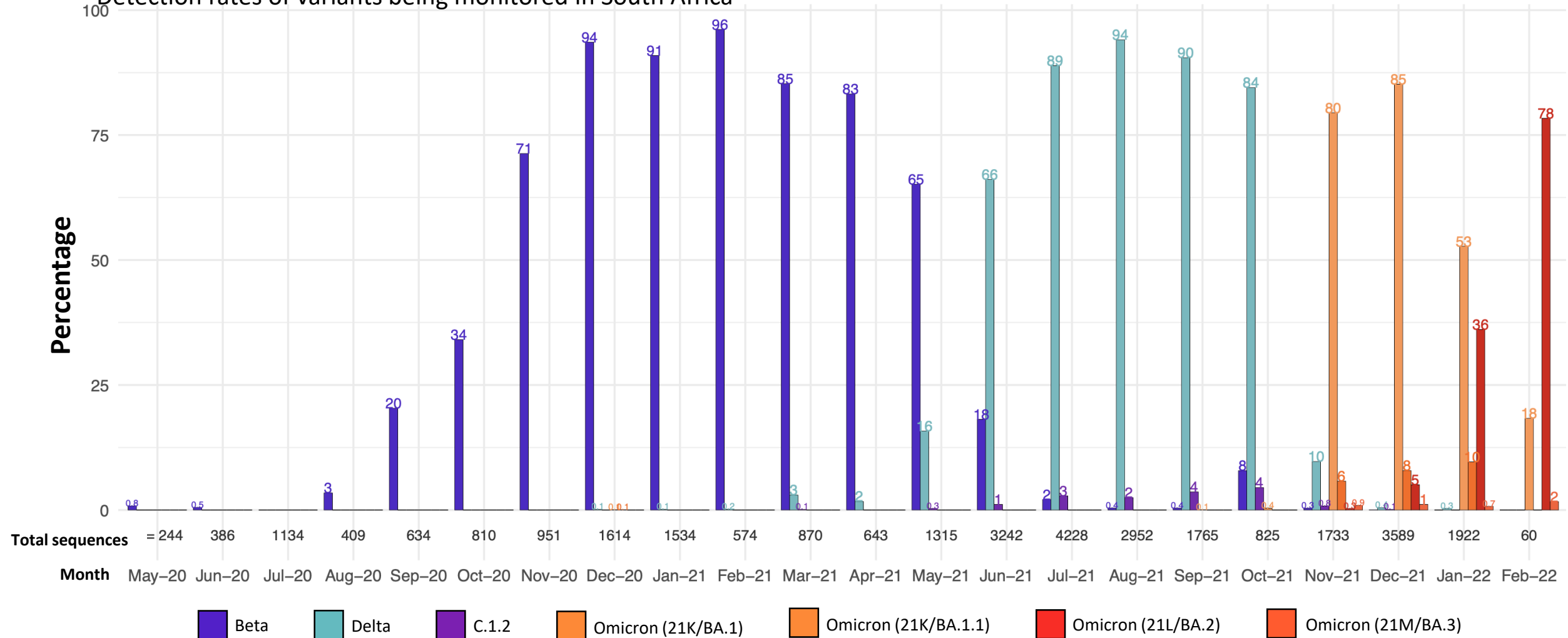
Total Omicron in Feb: 59 (98.3%)



Omicron dominated in December (99%, 3560/3589) and January (99%, 1907/1922), and continues to dominate in February (98%, 59/60) with sub-lineage BA.2 increasing in prevalence.

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

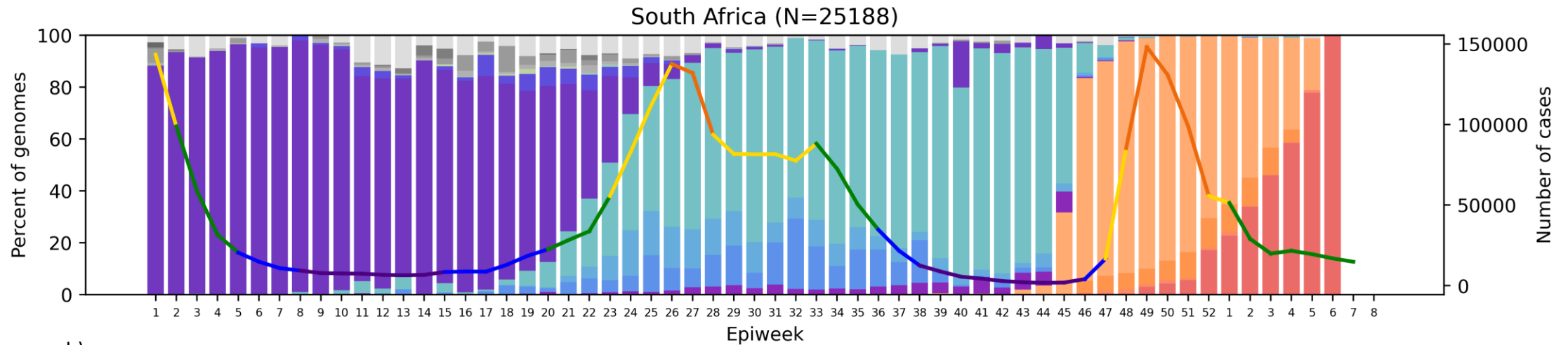
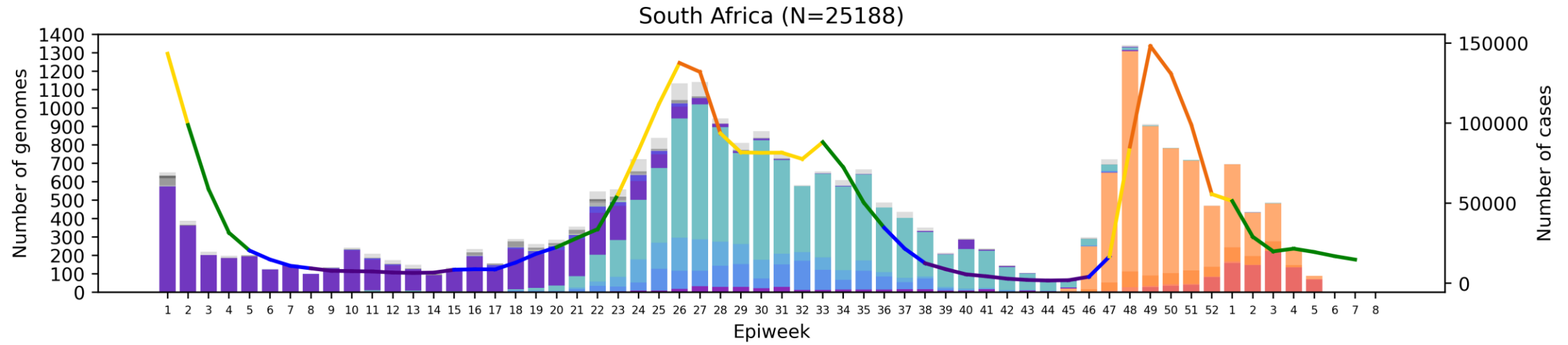
Detection rates of variants being monitored in South Africa*



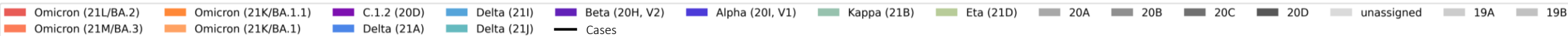
*Bars represent percentage prevalence of variant for the month; total sequences collected for the month are given below

Omicron has been dominant since November (>80% in November, >99% in December and January). BA.2 increased in frequency in January, making up 36% of genomes. BA.2 dominates in February (78%) but more sequencing data is required to confirm its prevalence.

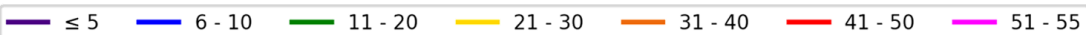
South Africa, 2021-2022, n = 25188*



Clade key (bar graph)

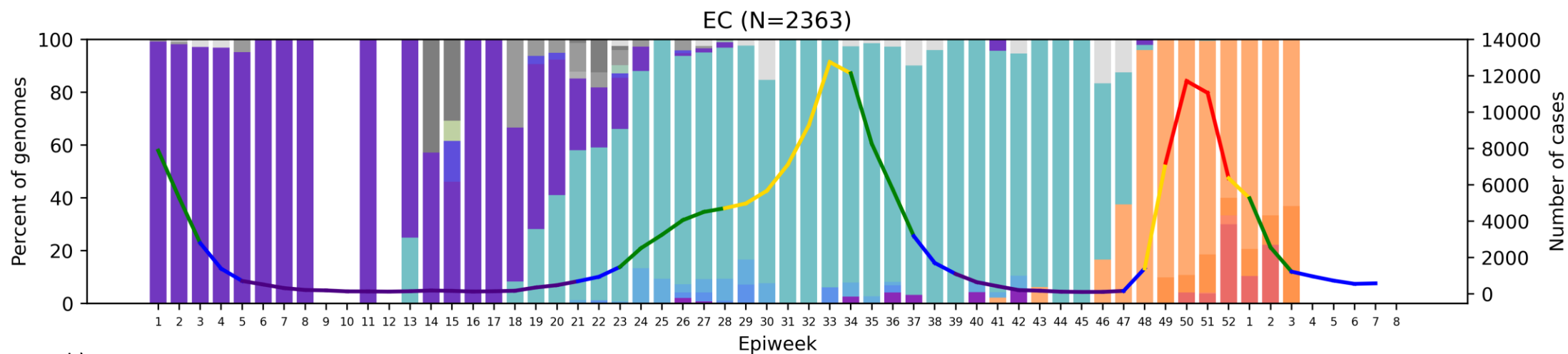
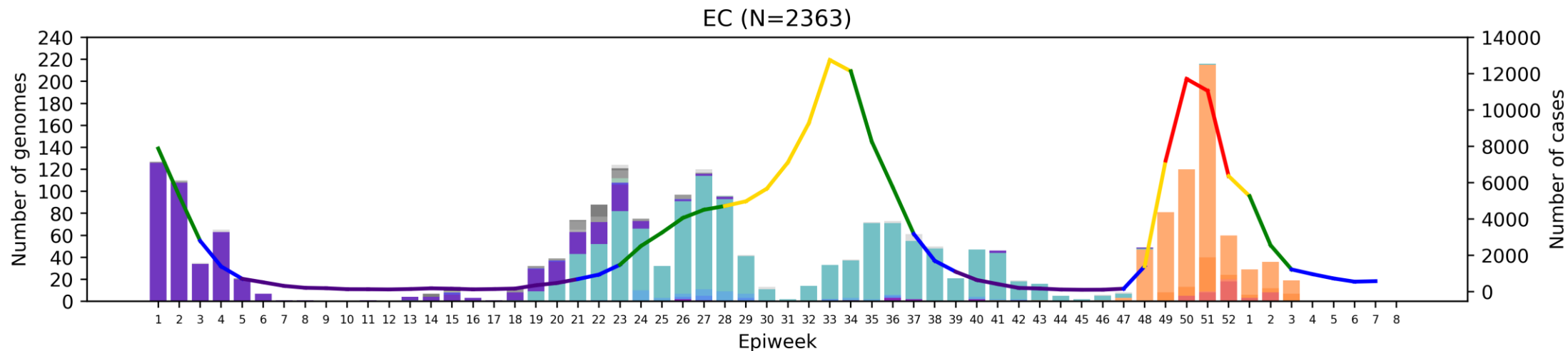


Weekly percentage testing positive key (line graph)

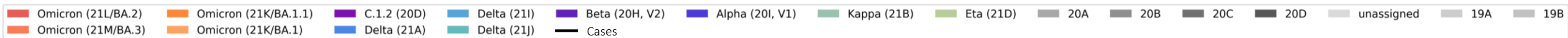


*Excludes sequences missing collection dates, as well as those collected January 1st and 2nd 2021 as they are part of epiweek 53 of 2020.

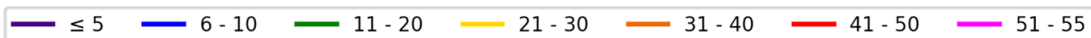
Eastern Cape Province, 2021-2022, n = 2363



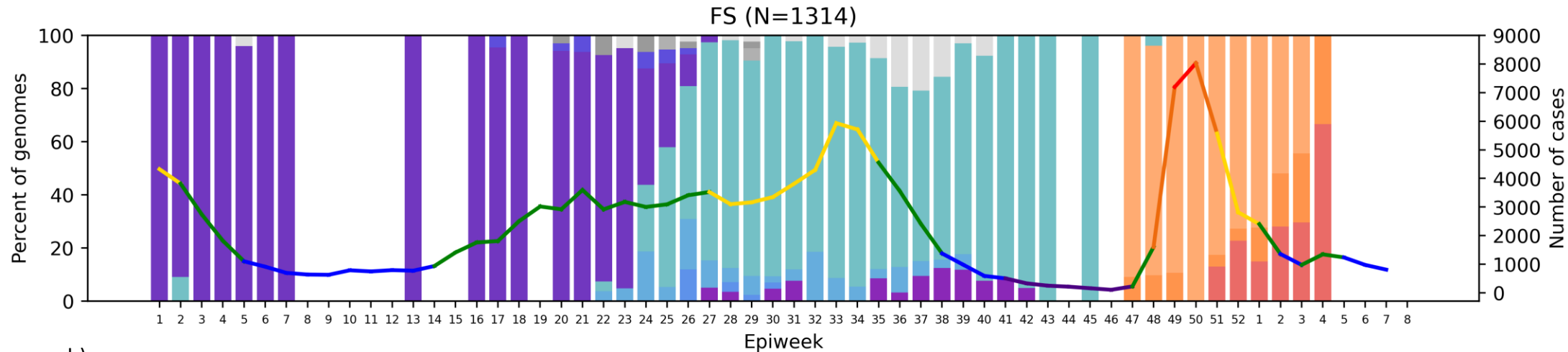
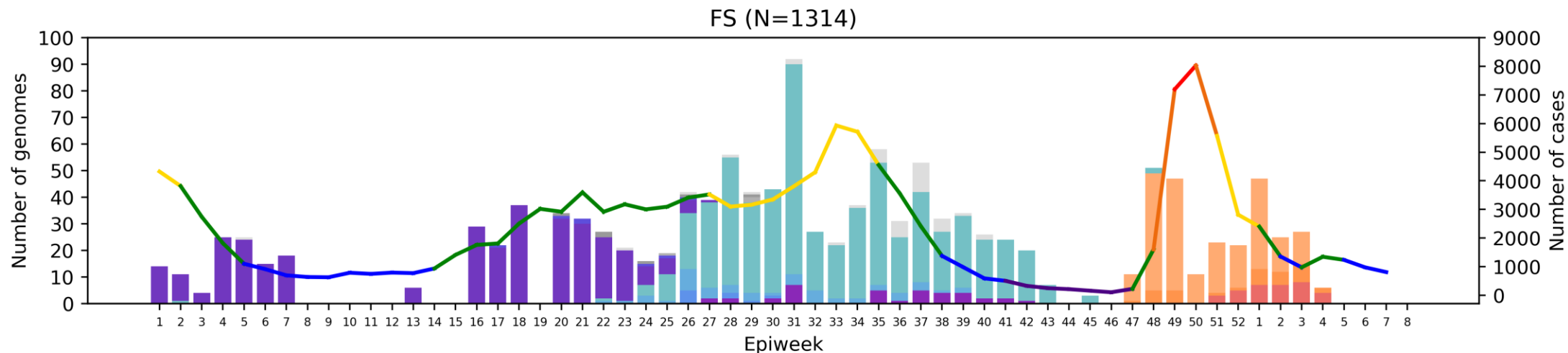
Clade key (bar graph)



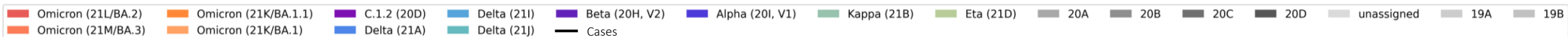
Weekly percentage testing positive key (line graph)



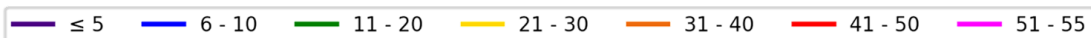
Free State Province, 2021-2022, n = 1314



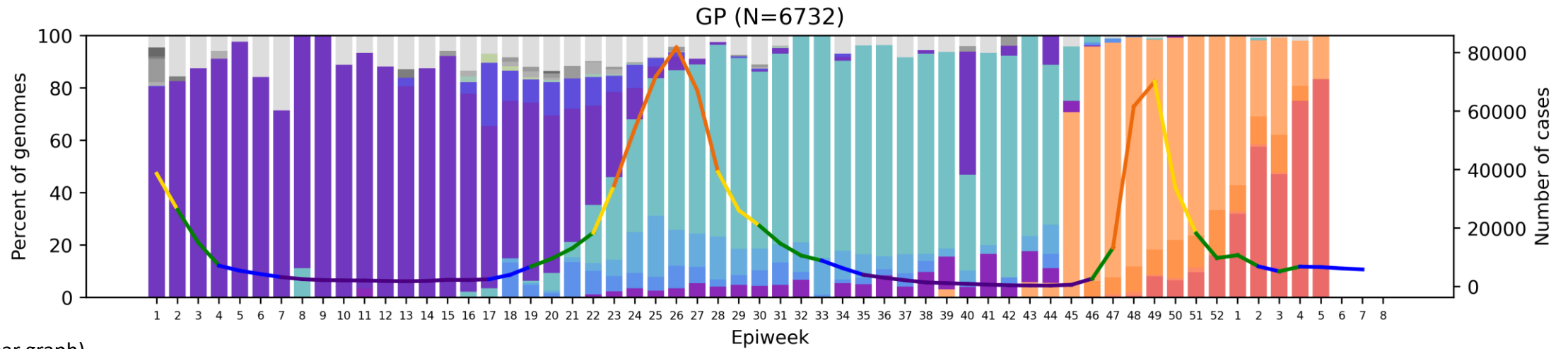
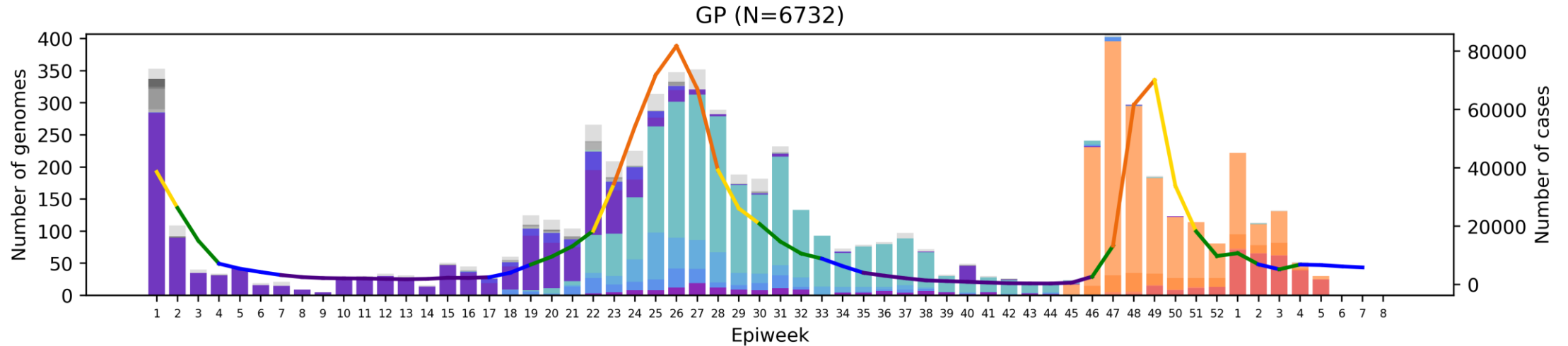
Clade key (bar graph)



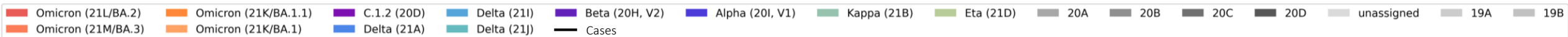
Weekly percentage testing positive key (line graph)



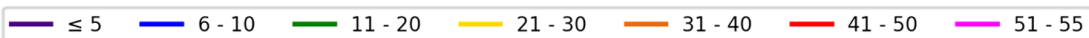
Gauteng Province, 2021-2022, n = 6732



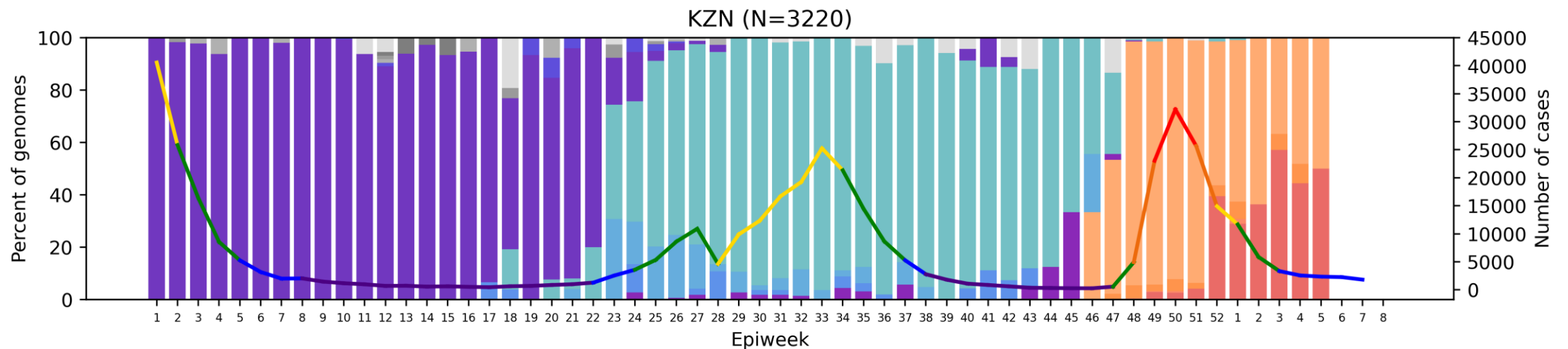
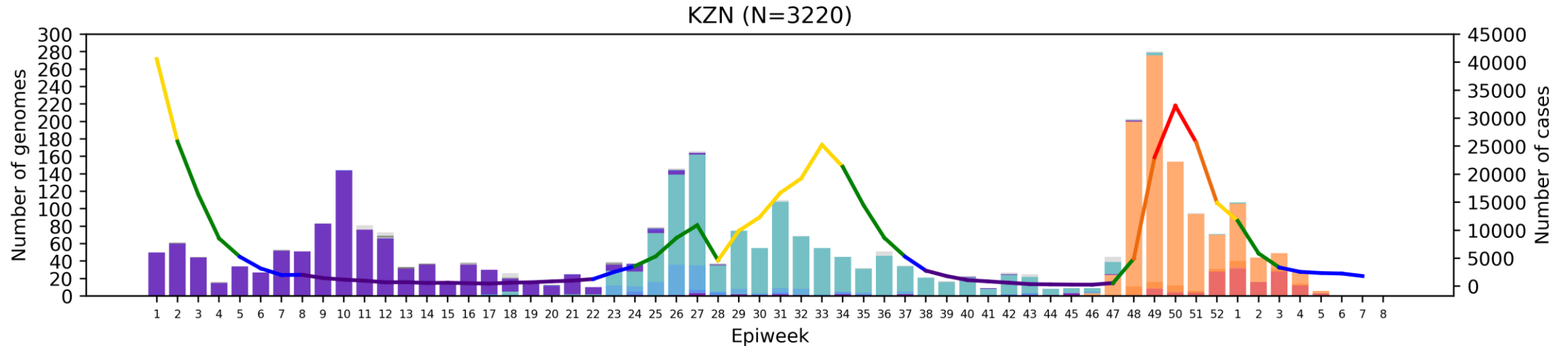
Clade key (bar graph)



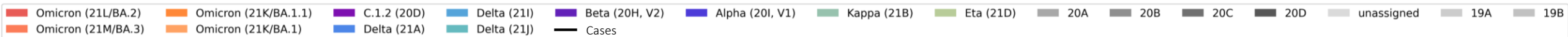
Weekly percentage testing positive key (line graph)



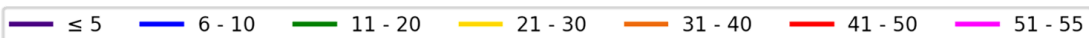
KwaZulu-Natal Province, 2021-2022, n = 3220



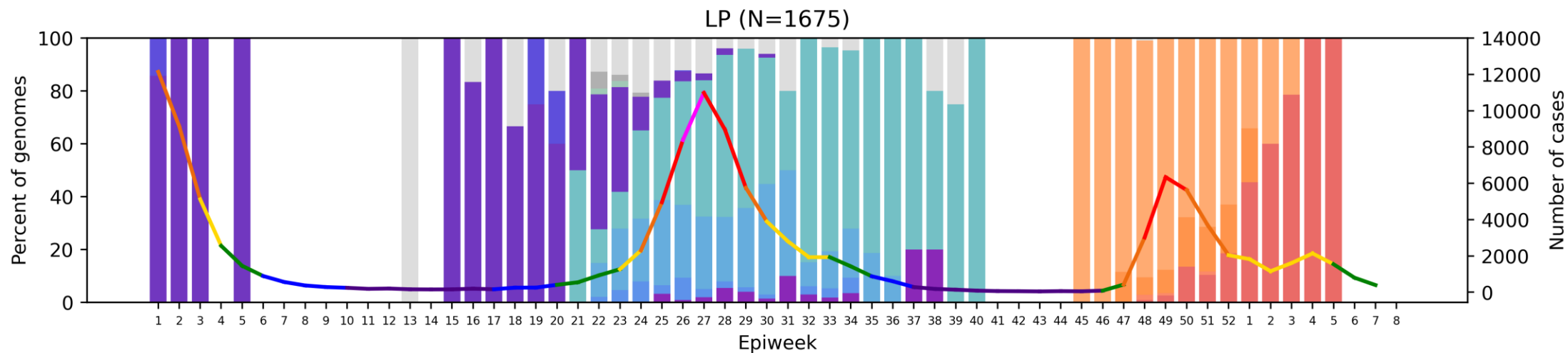
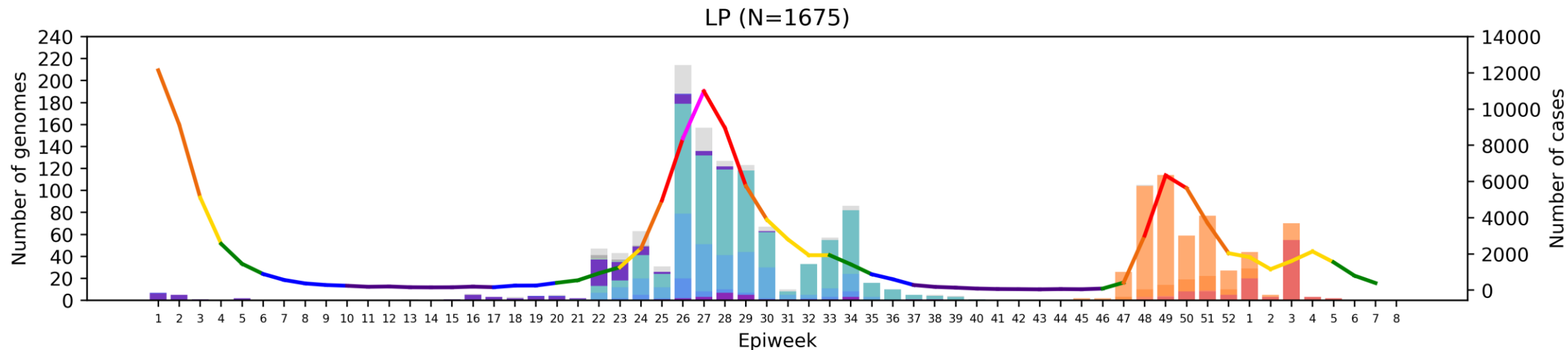
Clade key (bar graph)



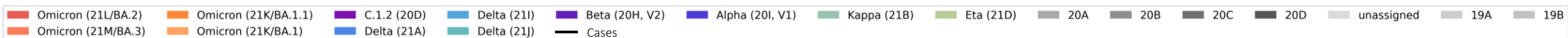
Weekly percentage testing positive key (line graph)



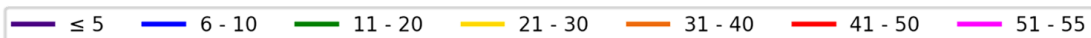
Limpopo Province, 2021-2022, n = 1675



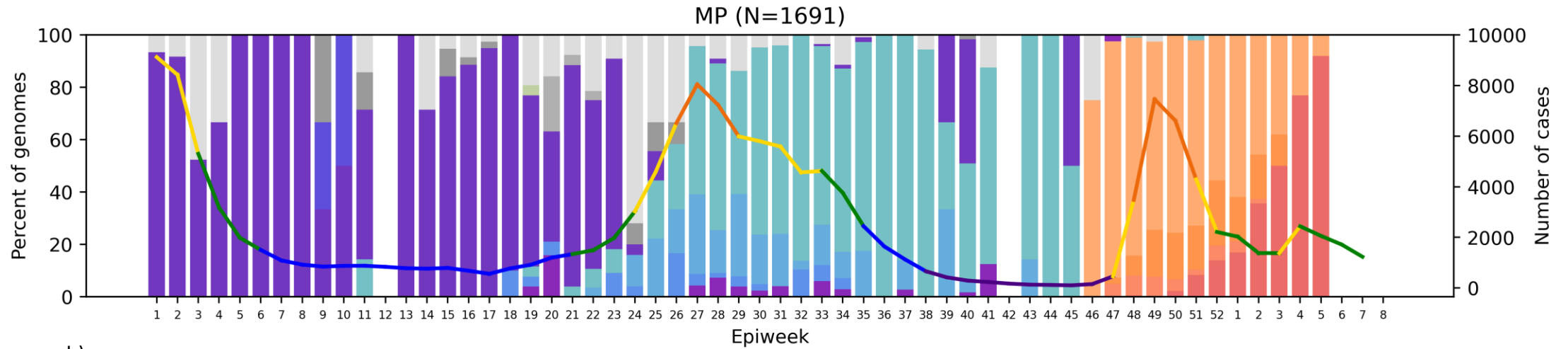
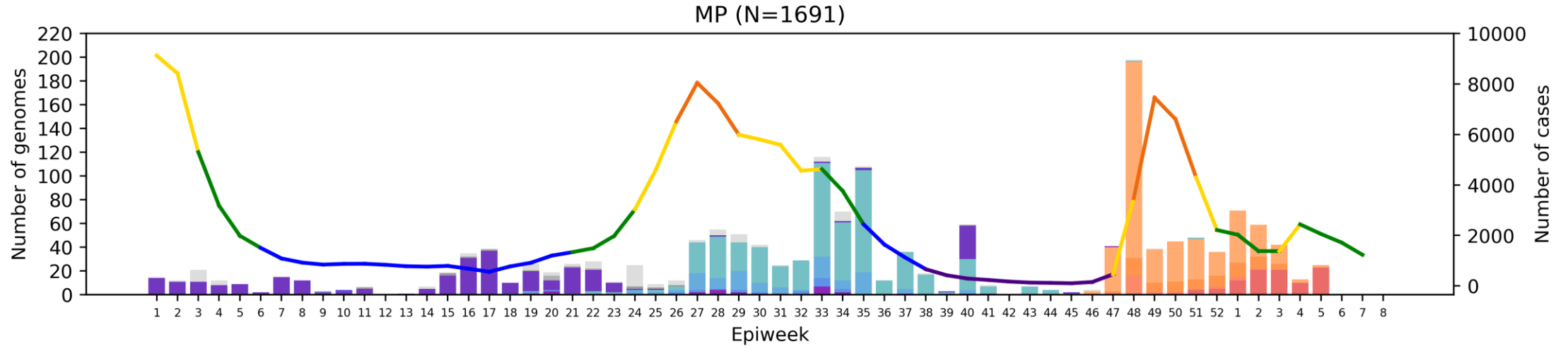
Clade key (bar graph)



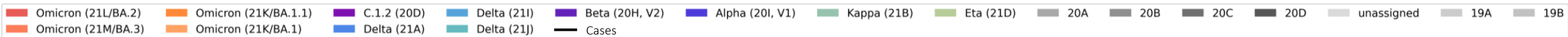
Weekly percentage testing positive key (line graph)



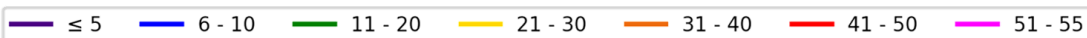
Mpumalanga Province, 2021-2022, n = 1691



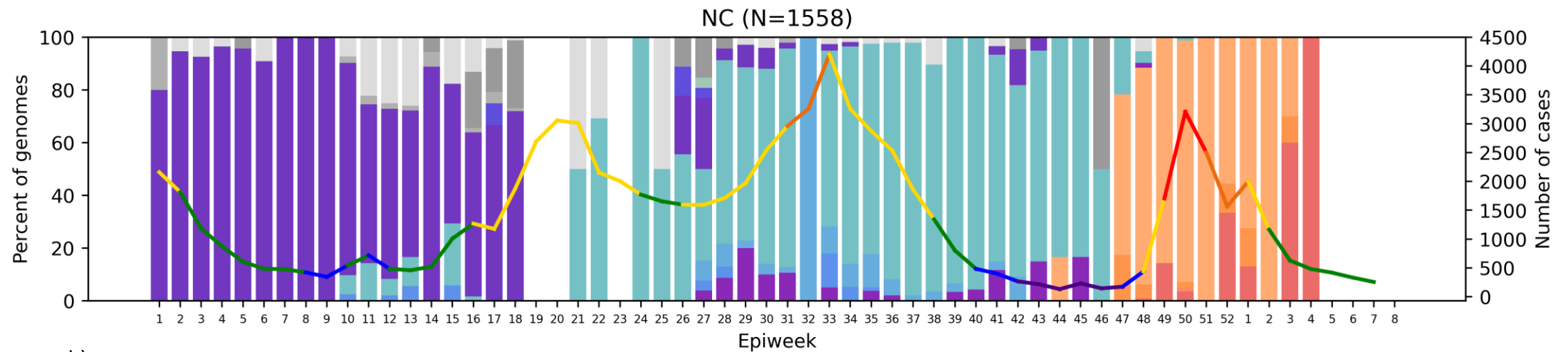
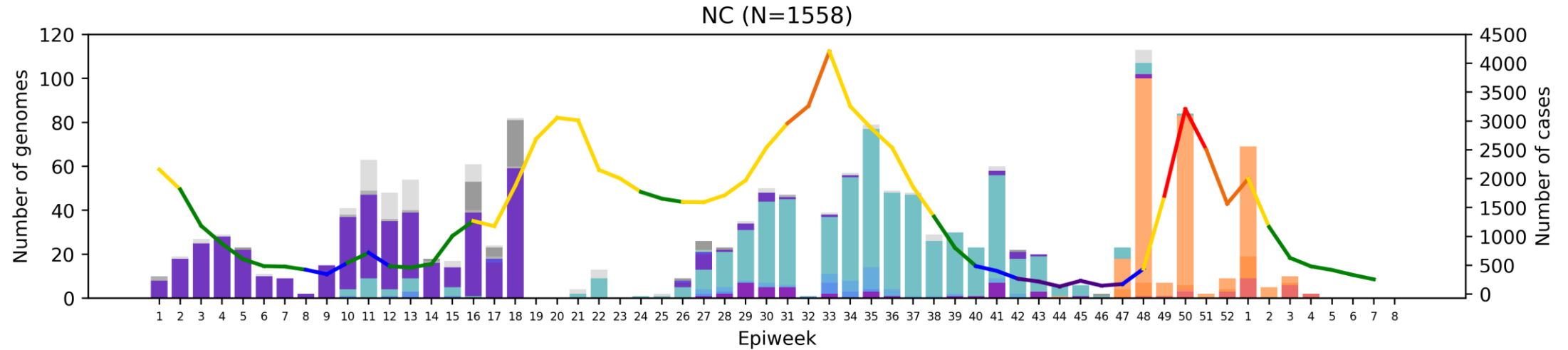
Clade key (bar graph)



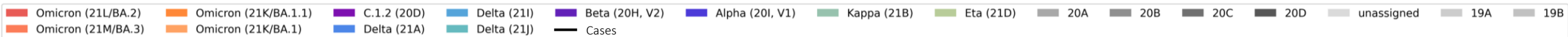
Weekly percentage testing positive key (line graph)



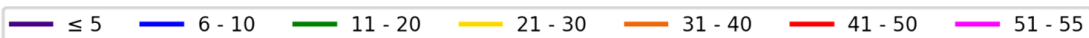
Northern Cape Province, 2021-2022, n = 1558



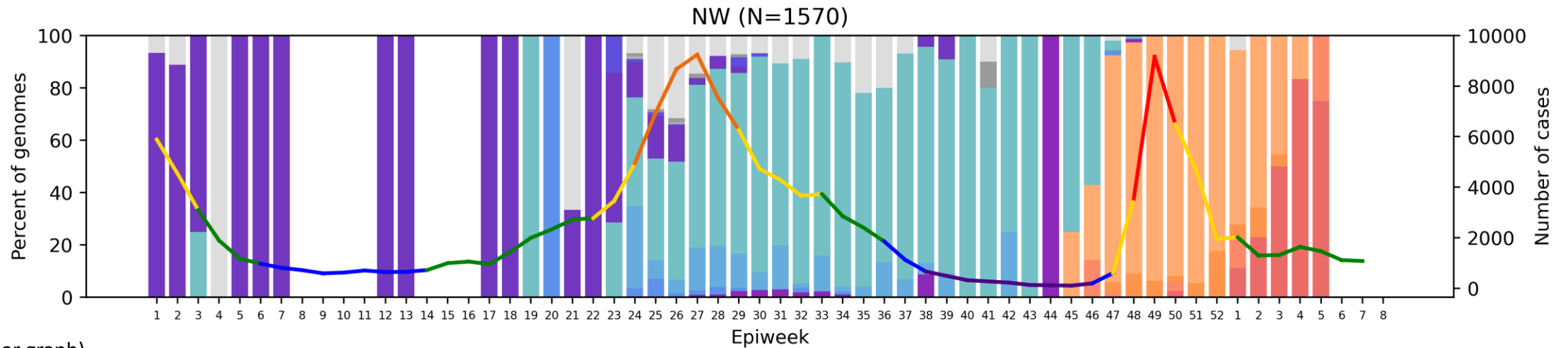
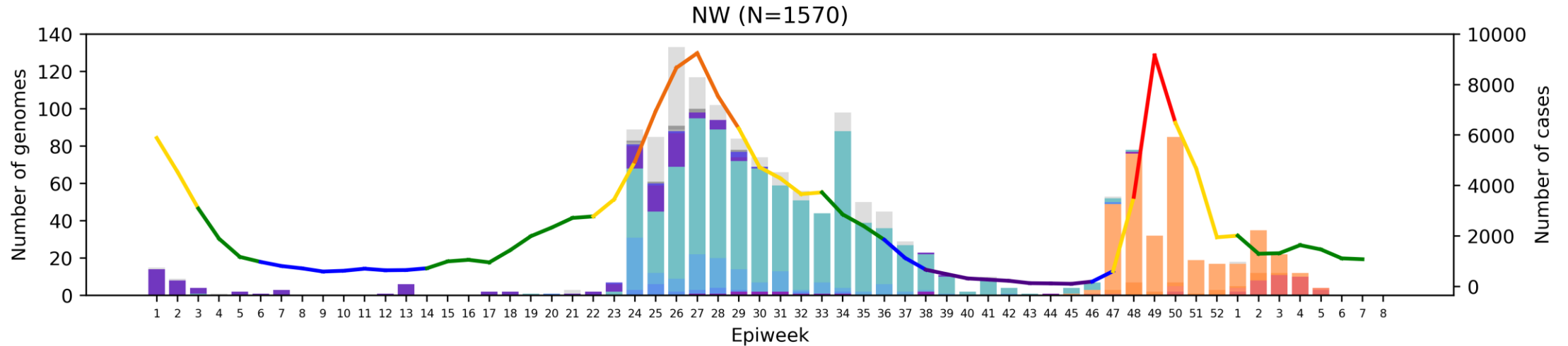
Clade key (bar graph)



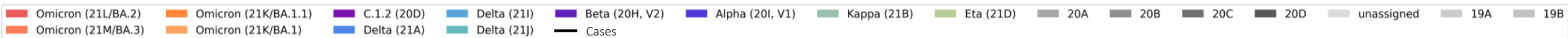
Weekly percentage testing positive key (line graph)



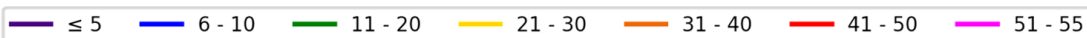
North West Province, 2021, n = 1570



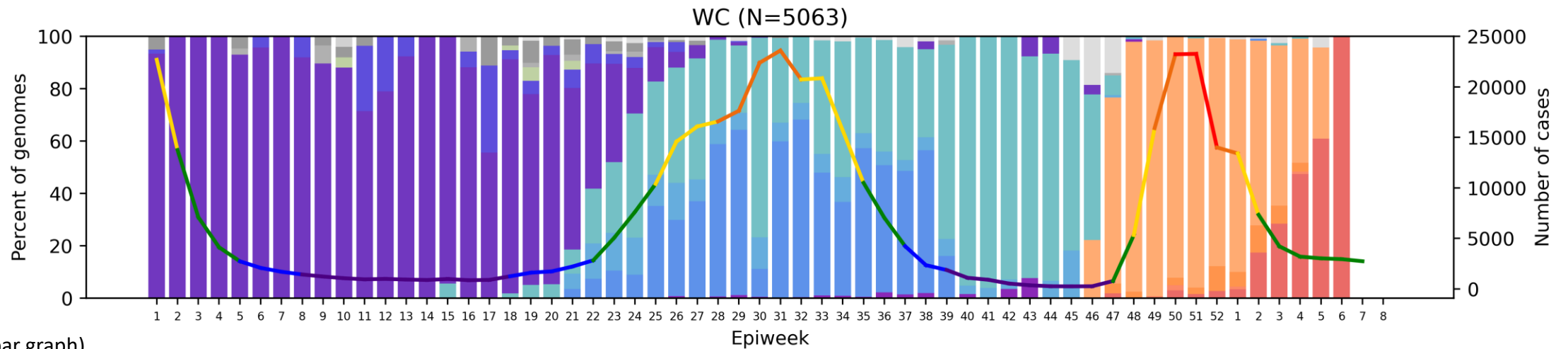
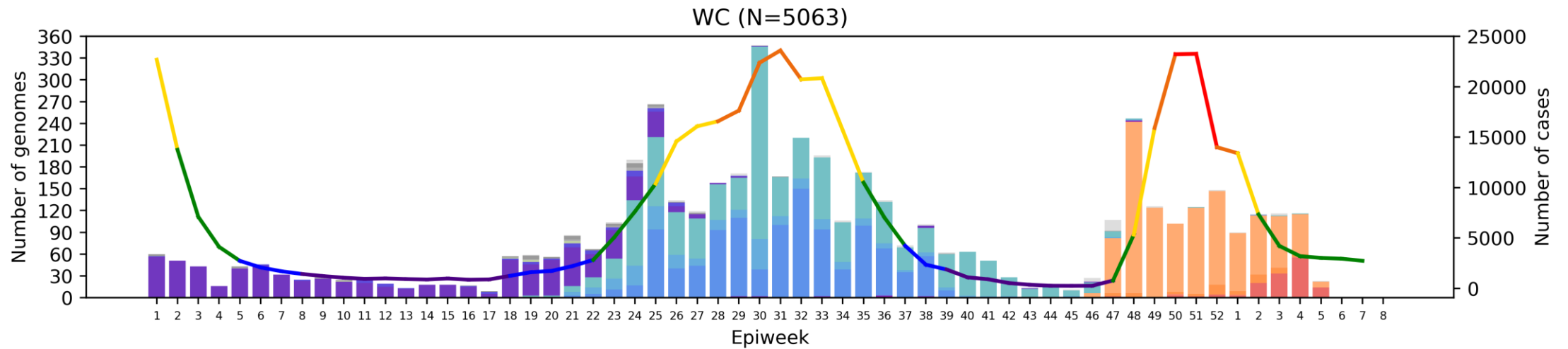
Clade key (bar graph)



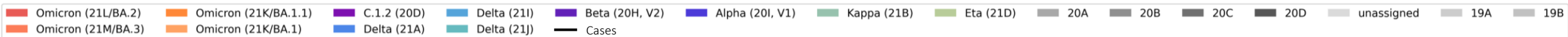
Weekly percentage testing positive key (line graph)



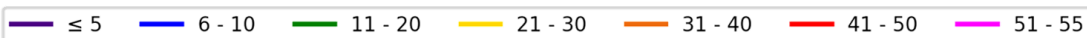
Western Cape Province, 2021-2022, n = 5063



Clade key (bar graph)



Weekly percentage testing positive key (line graph)

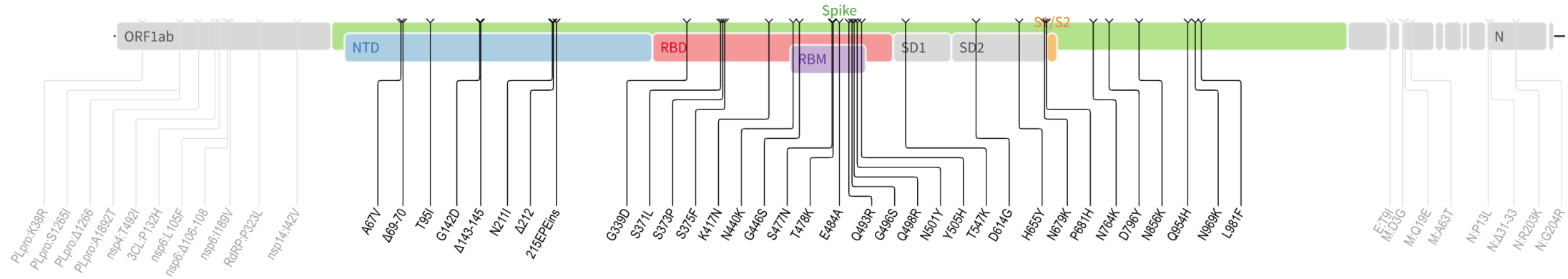


Summary

- **Variant of Concern Omicron**
 - Detected in at least 153 countries and dominating globally
 - Split into different lineages based on different mutational profiles. Predominant lineages currently BA.1 (21K), BA.1.1 (21K, BA.1+spike R346K), BA.2 (21L), BA.3 (21M). More lineages are being assigned but defining mutations are not yet available.
 - South Africa (detected in all provinces):
 - Dominated December, January and February sequencing data at >99% of genomes
 - While BA.1 was the predominant sub-lineage in December (85%) and January (53%), the proportion of BA.2 increased from 5% in December and 36% in January to 78% in February
- Low frequency of previously circulating variants such as Delta still detected in recent data

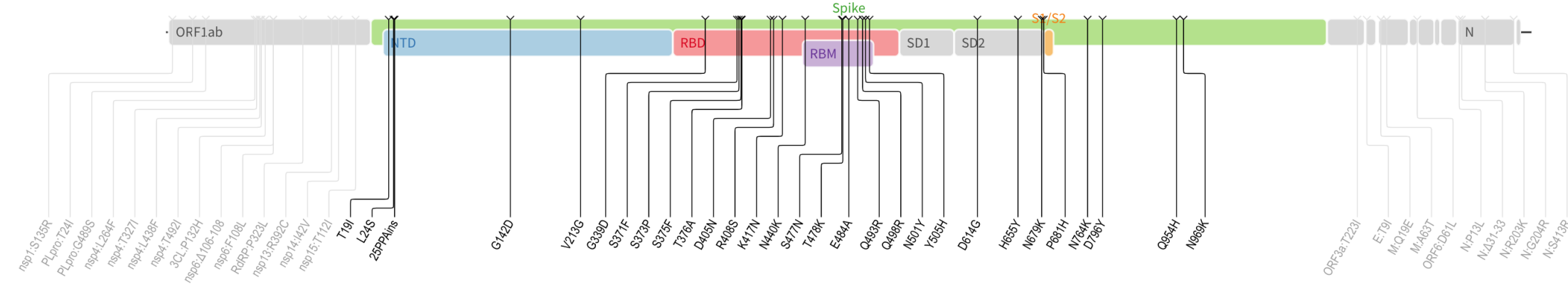
Omicron sub-lineage spike mutation profiles

**BA.1
21K**

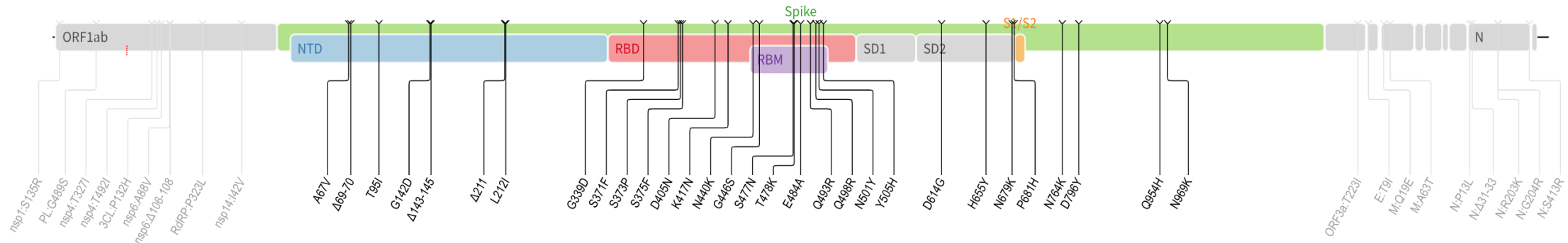


**BA.2
21L**

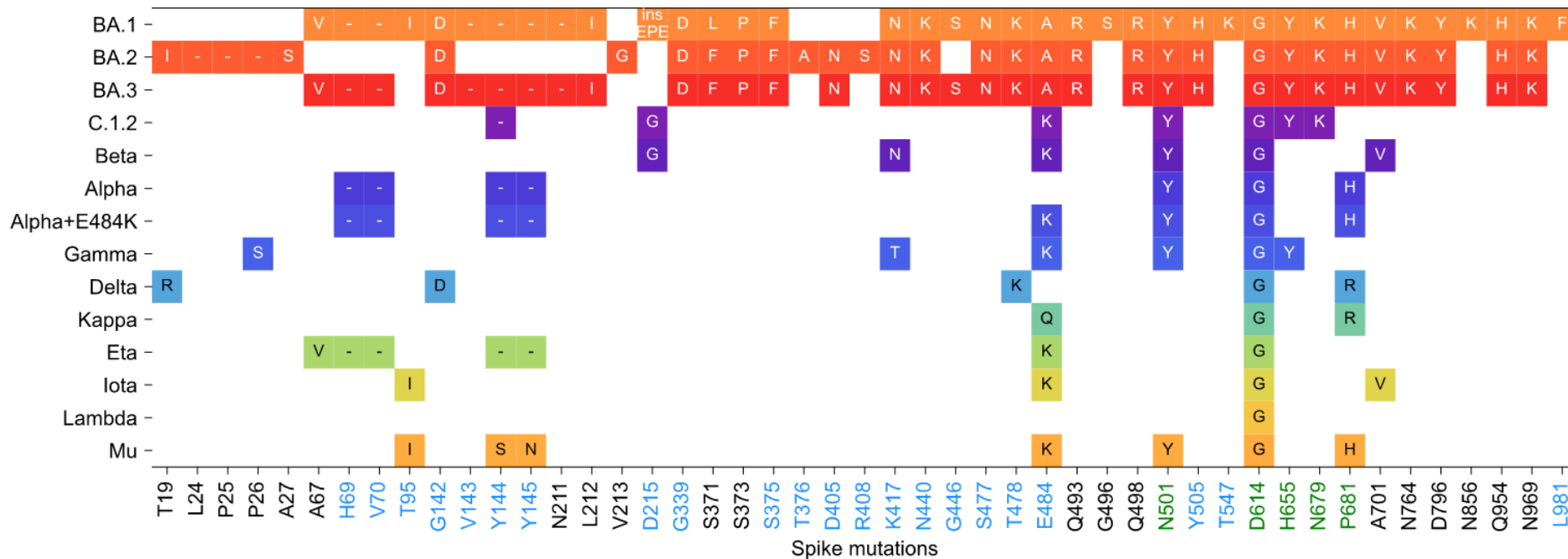
Lacks 69-70del
Not detectable by
S-Gene Target
Failure



**BA.3
21M**



Omicron spike mutations compared to other VOC/VOIs



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

- 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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EDCTP

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National Institute for Communicable Diseases



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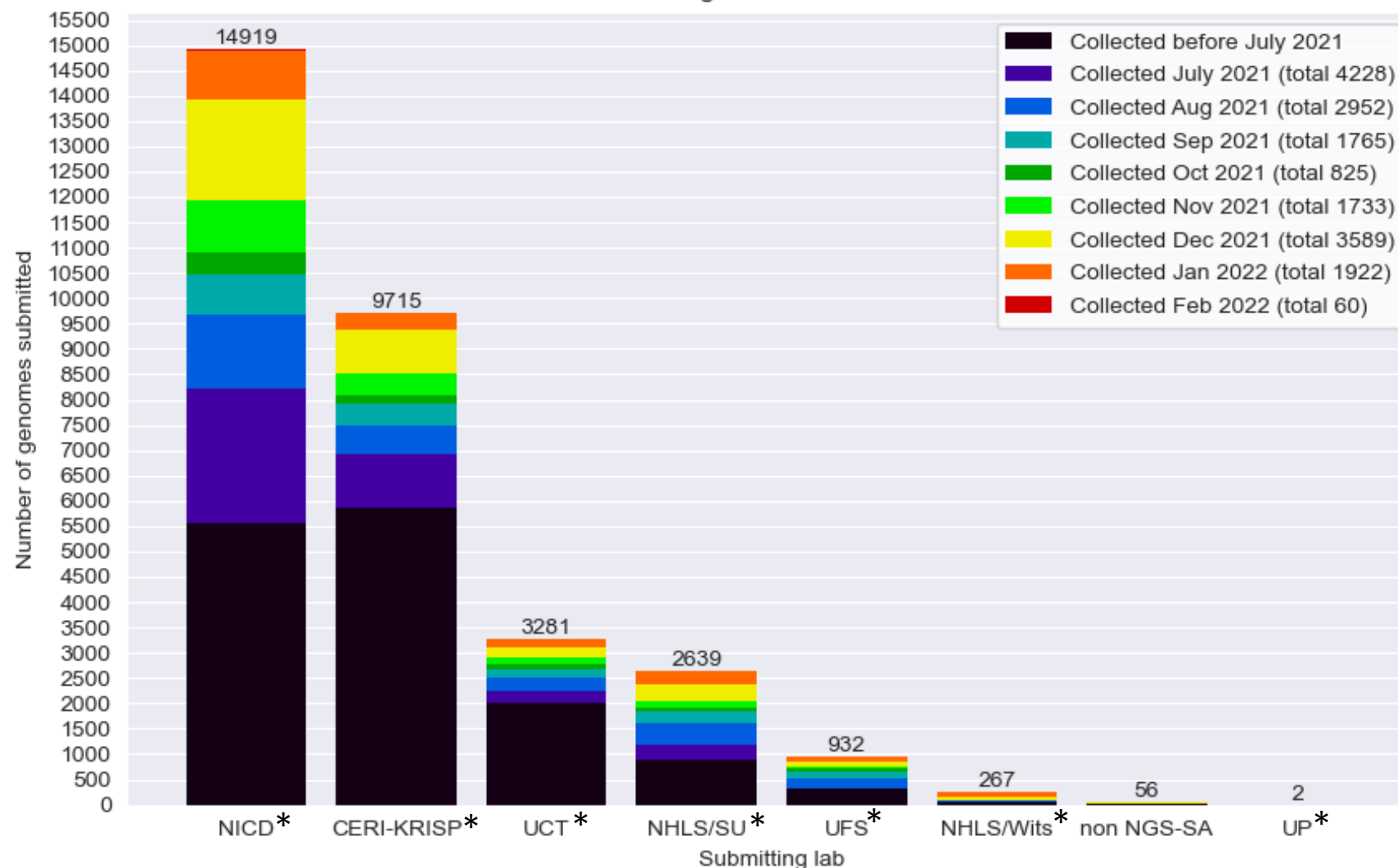
SA MRC

Glenda Gray



South African genomes submitted per submitting lab, 2020 - 2022 (N=31 812)

Submitting labs in South Africa



*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, 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.)