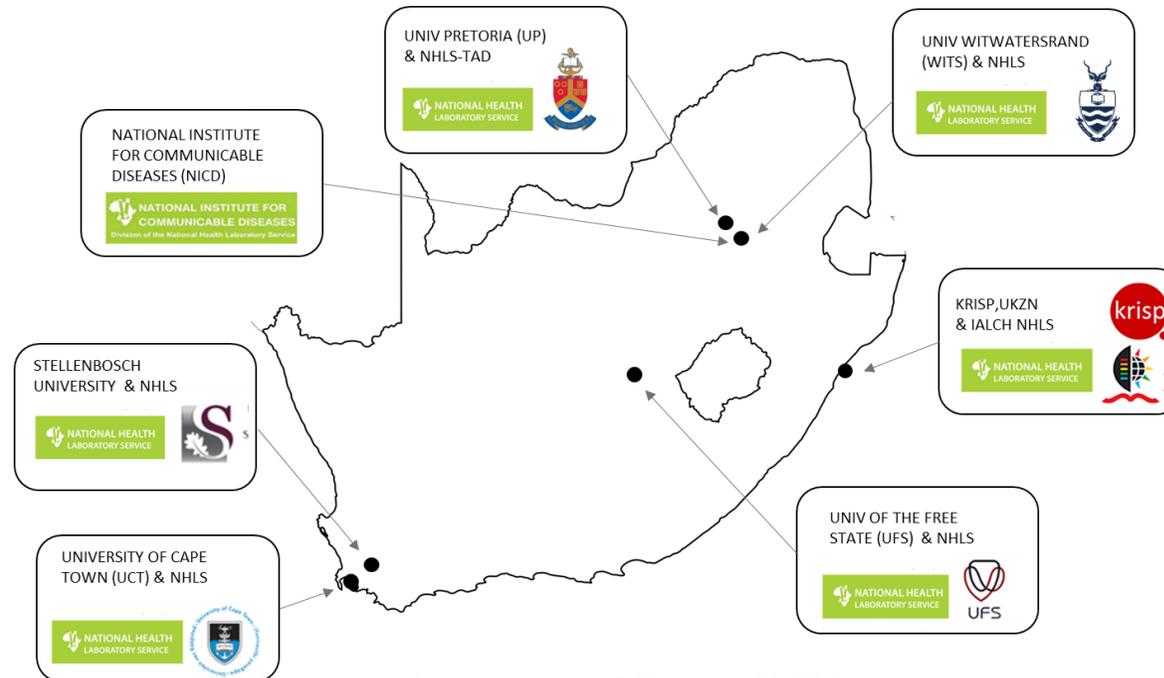


SARS-CoV-2 Sequencing Update 14 January 2022



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 14 January 2022 at 08h20



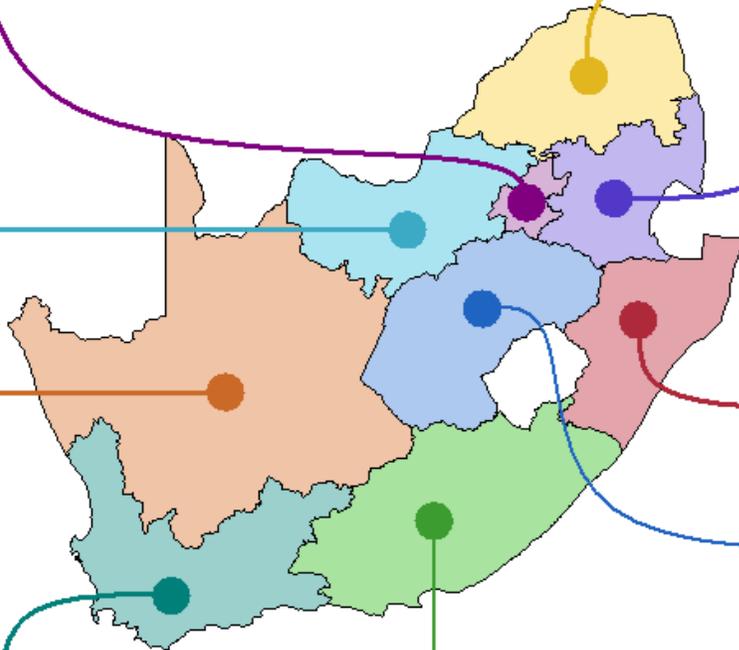
Data license: <https://www.gisaid.org/registration/terms-of-use/>

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) - 2 (2022)



Gauteng ↓PTP: 16.4%

Genomes Cases
1 209 (30.6%) 224 012 (36.8%)

Genomes deposited in the last week

■ 199 ■ 7 ■ 3 ■ 1 ■ 3 ■ 1

Limpopo ↓PTP: 24.6%

Genomes Cases
100 (2.5%) 21 094 (3.5%)

Genomes deposited in the last week

■ 17

North West ↓PTP: 21.4%

Genomes Cases
203 (5.1%) 29 966 (4.9%)

Genomes deposited in the last week

■ 51 ■ 1

Mpumalanga ↓PTP: 21.3%

Genomes Cases
218 (5.5%) 27 728 (4.6%)

Genomes deposited in the last week

■ 42 ■ 1 ■ 2

Northern Cape ↓PTP: 35.5%

Genomes Cases
313 (7.9%) 14 011 (2.3%)

Genomes deposited in the last week

KwaZulu-Natal ↑PTP: 27.8%

Genomes Cases
684 (17.3%) 116 325 (19.1%)

Genomes deposited in the last week

■ 165 ■ 28 ■ 1 ■ 1 ■ 1

Western Cape ↓PTP: 33.9%

Genomes Cases
868 (22.0%) 99 544 (16.4%)

Genomes deposited in the last week

■ 58 ■ 3

Free State ↓PTP: 21.3%

Genomes Cases
141 (3.6%) 30 557 (5.0%)

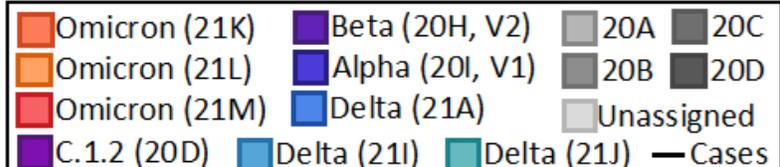
Genomes deposited in the last week

■ 1

Eastern Cape ↓PTP: 29.4%

Genomes Cases
216 (5.5%) 44 996 (7.4%)

Genomes deposited in the last week



583 genomes deposited in the past week

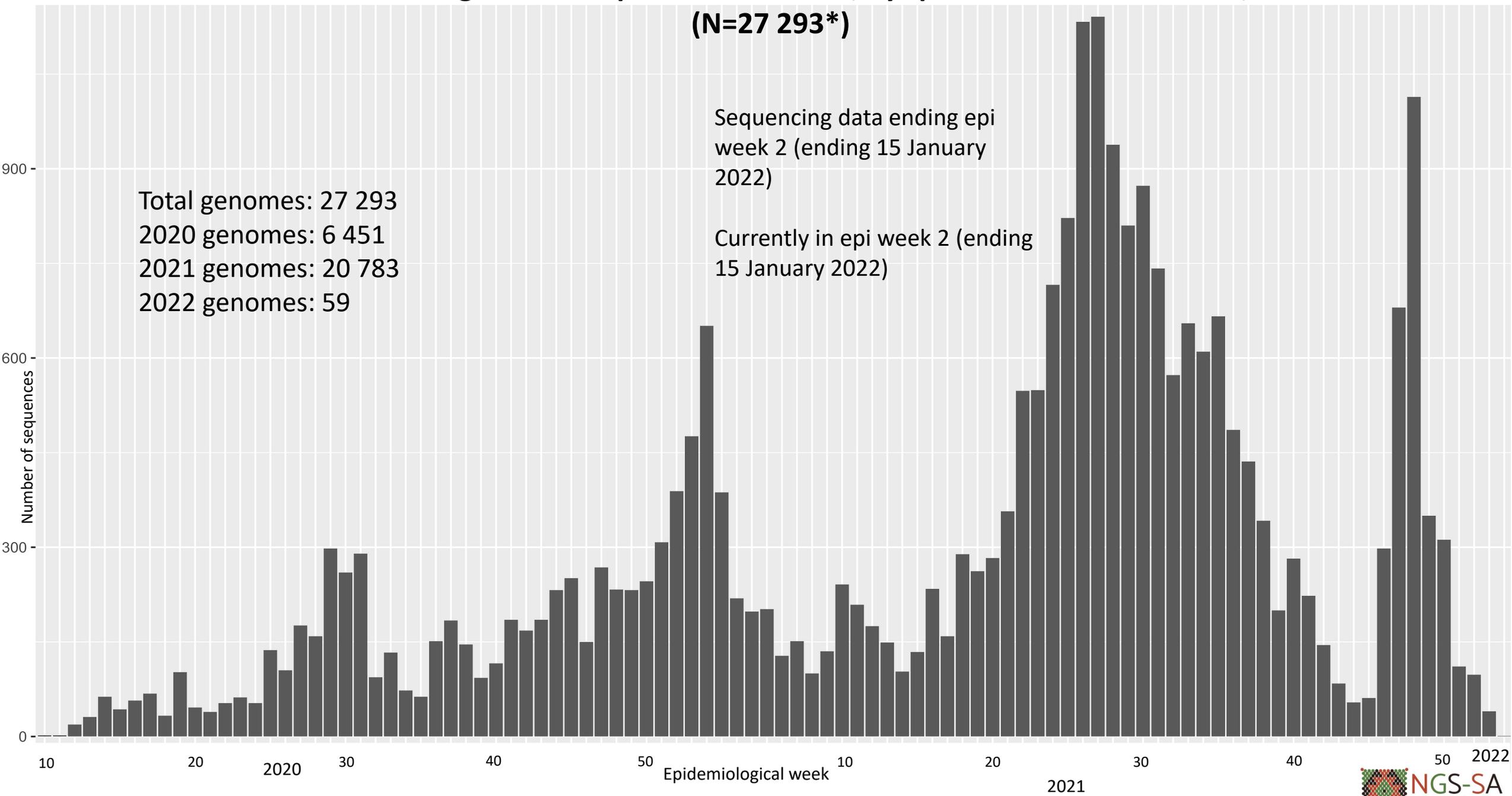
Bar graphs represent genomes sequenced per epiweek, with lines representing cases by collection date (weeks 39 [2021] – 2 [2022])

Genomes and cases presented as provincial total (percentage of national total) for epiweeks 39 (2021) – 2 (2022)

PTP: percentage testing positive in week 1 (2 Jan 2022 – 8 Jan 2022); the arrow indicates direction of change since the previous week (26 Dec 2021 – 1 Jan 2022)

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

(N=27 293*)



Total genomes: 27 293
2020 genomes: 6 451
2021 genomes: 20 783
2022 genomes: 59

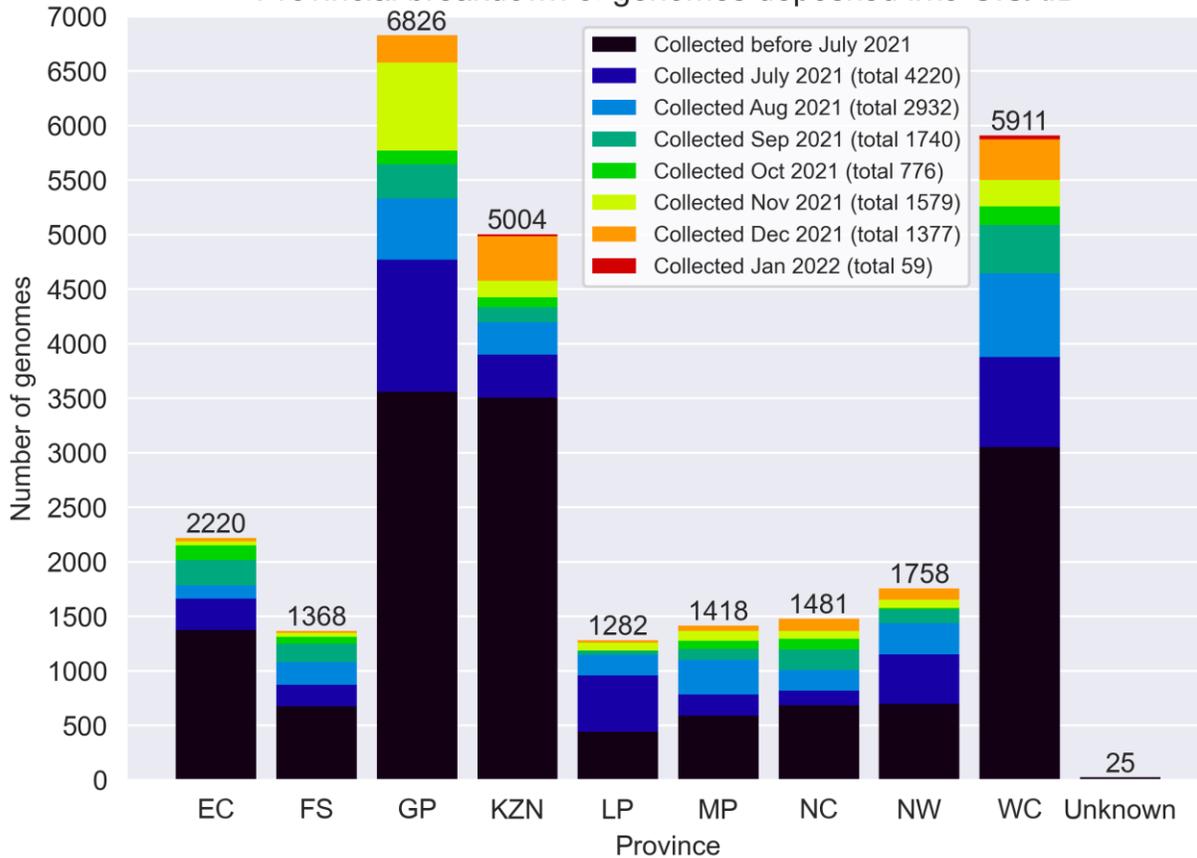
Sequencing data ending epi week 2 (ending 15 January 2022)

Currently in epi week 2 (ending 15 January 2022)

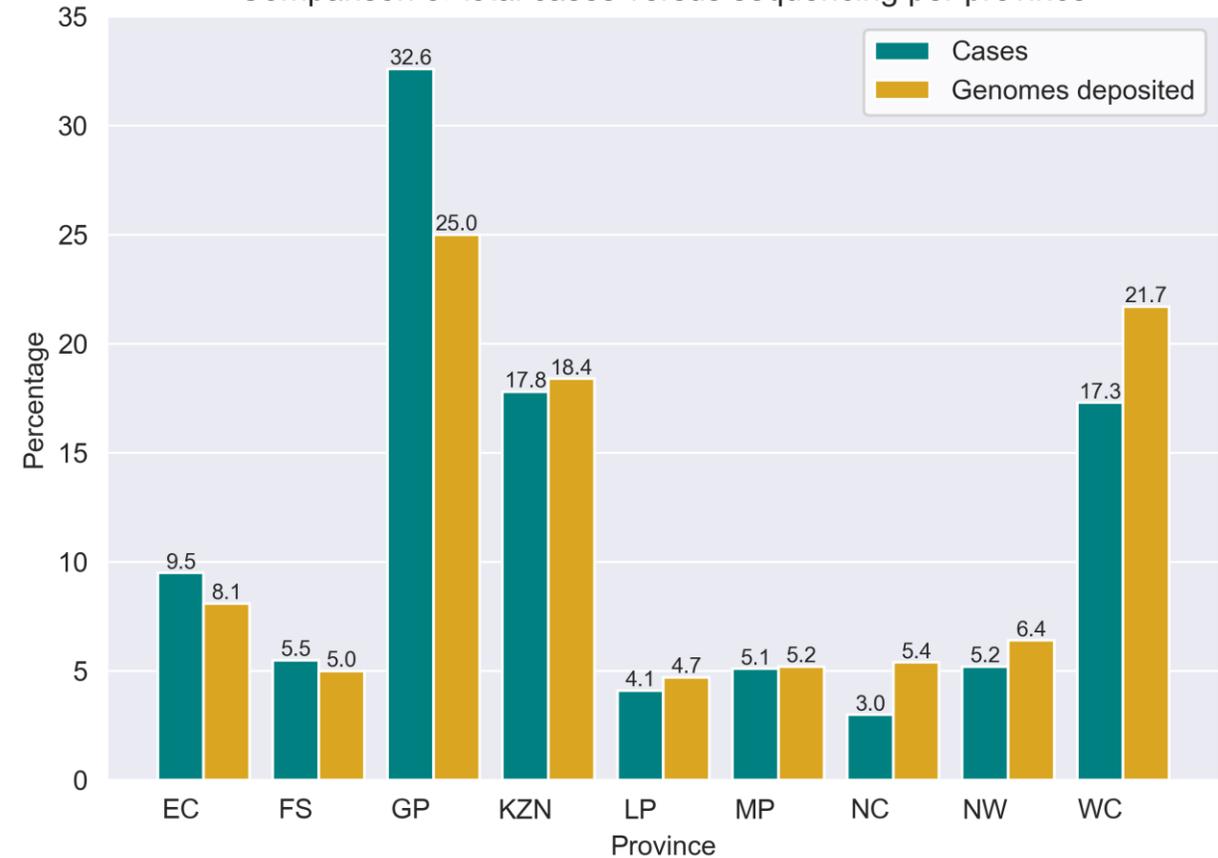
*This represents the cleaned, de-duplicated dataset of unique **National Surveillance** sequences. This dataset will be used for all further figures.

GISAID genomes vs total cases, 2020 – 2022 (N=27 293)

Provincial breakdown of genomes deposited into GISAID



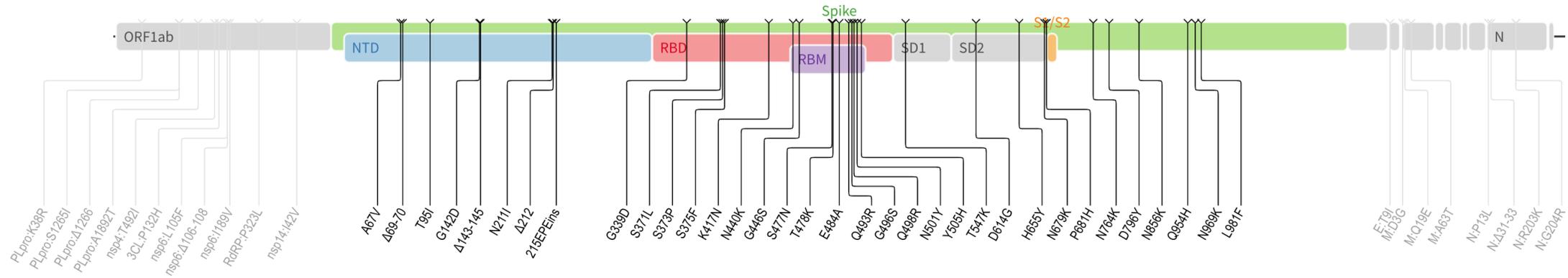
Comparison of total cases versus sequencing per province



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

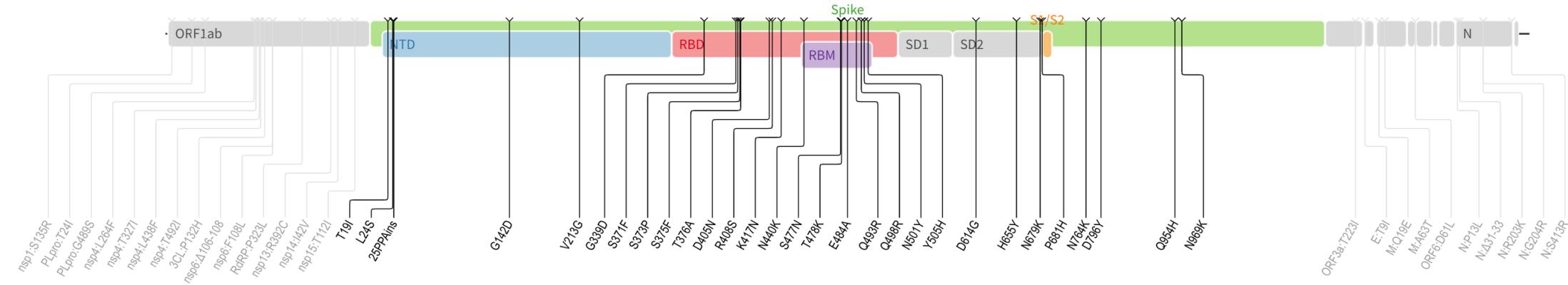
Omicron sub-lineage spike mutation profiles

**BA.1
21K**

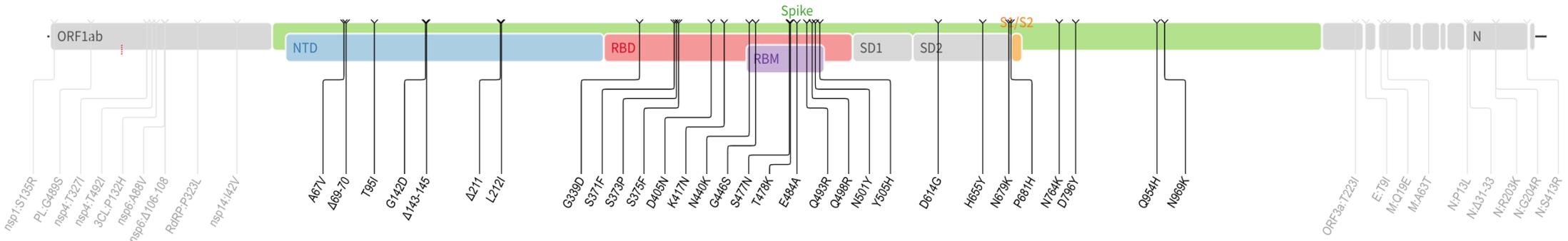


**BA.2
21L**

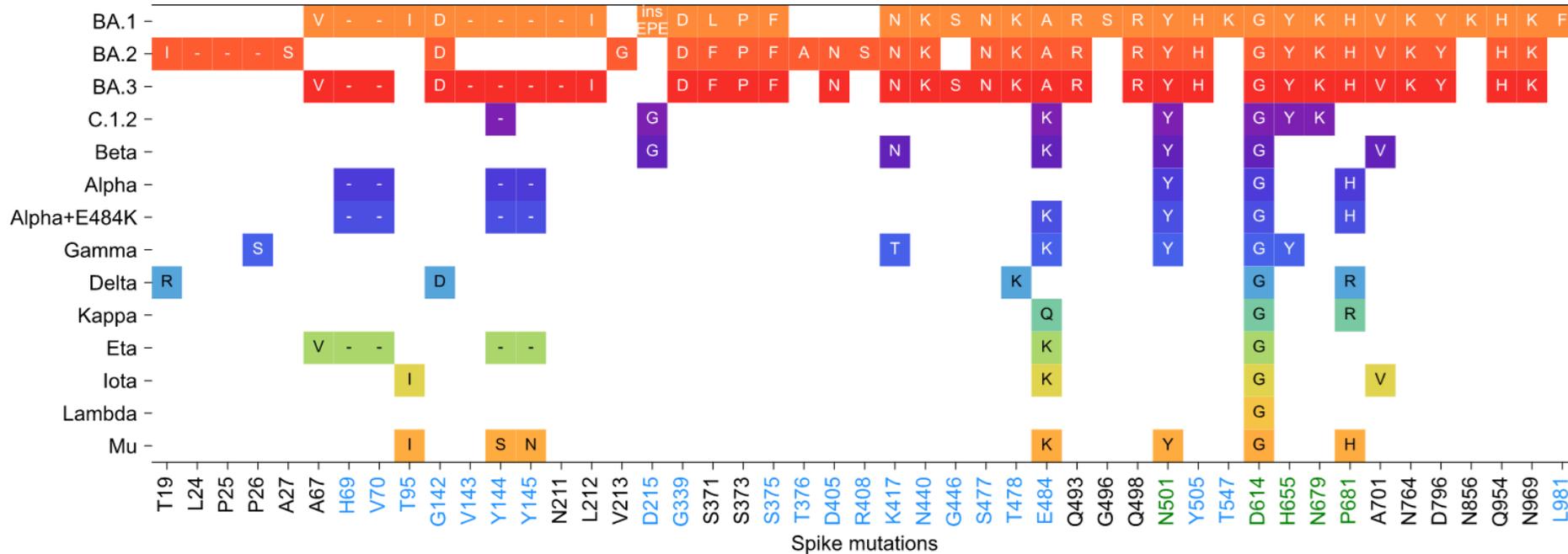
Lacks 69-70del
Not detectable by
S-Gene Target
Failure



**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.

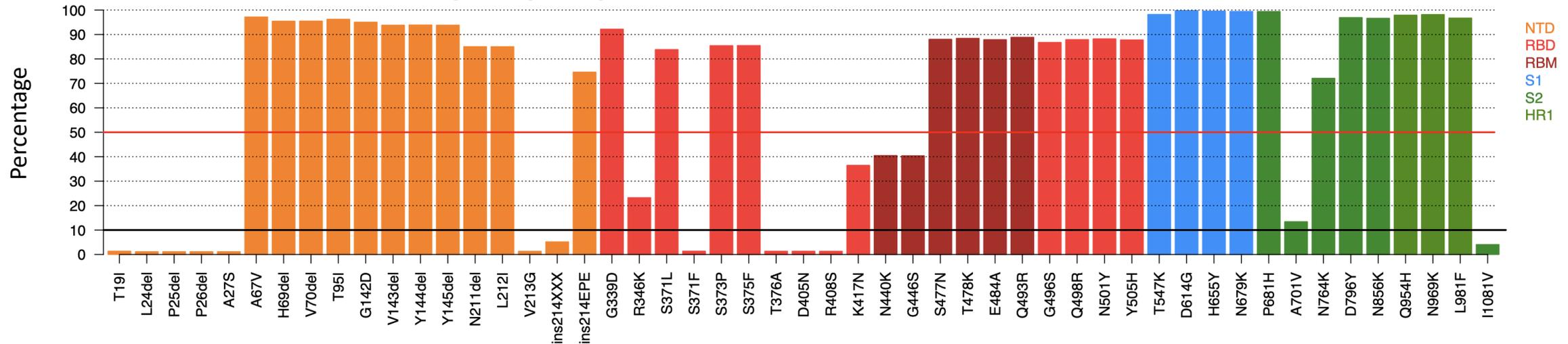
Mutation impact key

- Unknown or unconfirmed impact
- Known/predicted immune escape
- Enhanced infectivity

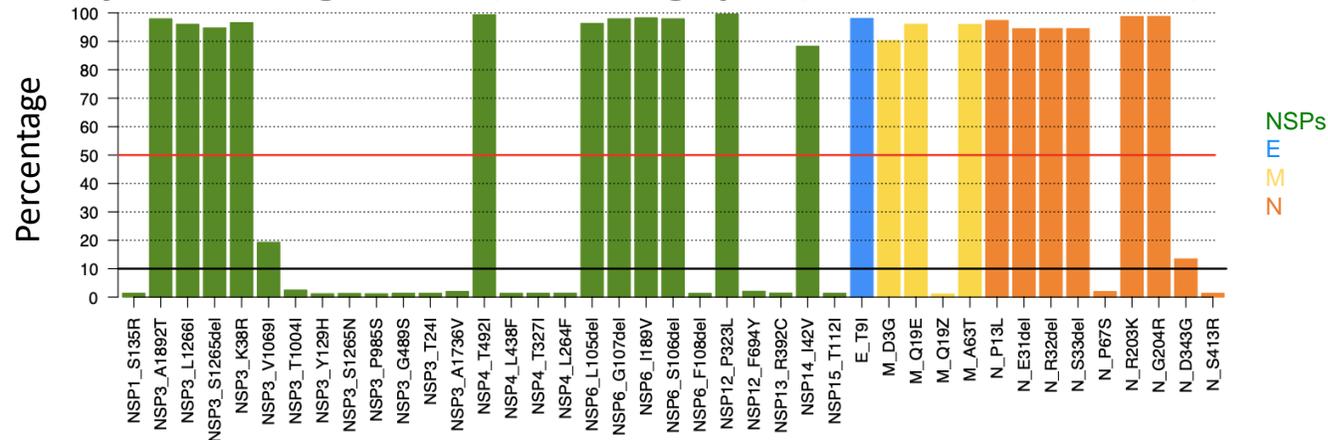
- Multiple changes within the two immunogenic regions in S1 (NTD and RBD)
 - including a three amino acid insertion
- Accumulation of mutations surrounding the furin cleavage site
 - Including combination of N679K and P681H
- Effect of most spike S2 subunit changes have not been defined, but may be linked to immune escape

Mutational profile of Omicron sequences

Frequency of Spike SNVs for Omicron (n = 328 190)



Frequency of whole genome (excluding spike) SNVs for Omicron (n = 328 190)

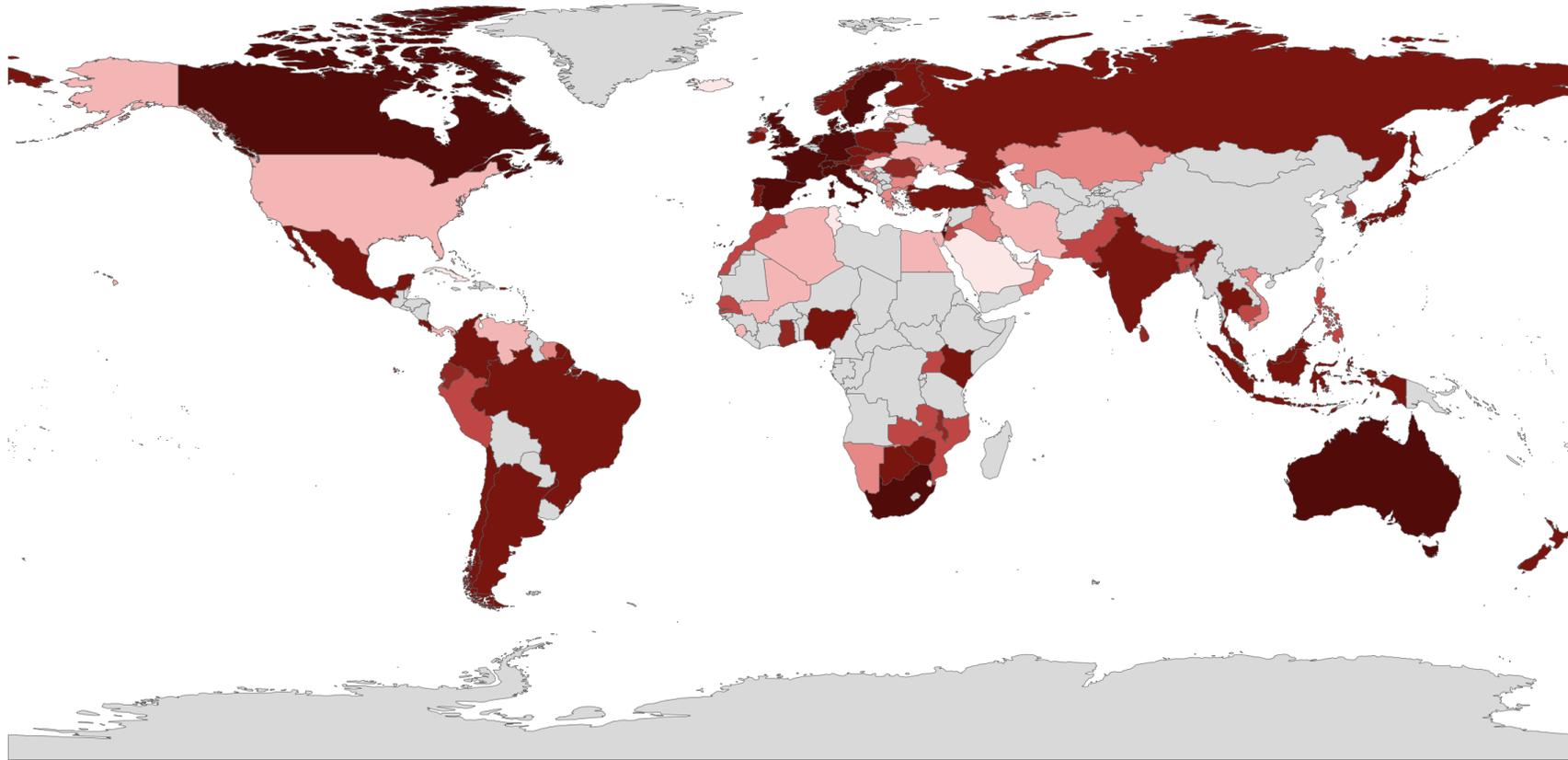


Mutational profile of Omicron is largely shared amongst all sequences.

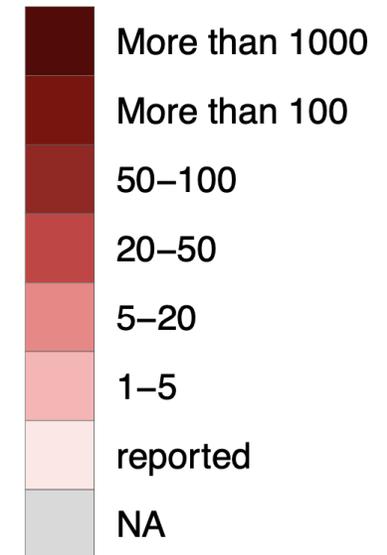
Low mutation frequencies for N417N, N440K, G446S and N764K are most likely a result of poor coverage due to primer drop off.

Omicron global prevalence

Detection of Omicron Globally (countries = 139; n = 328190)

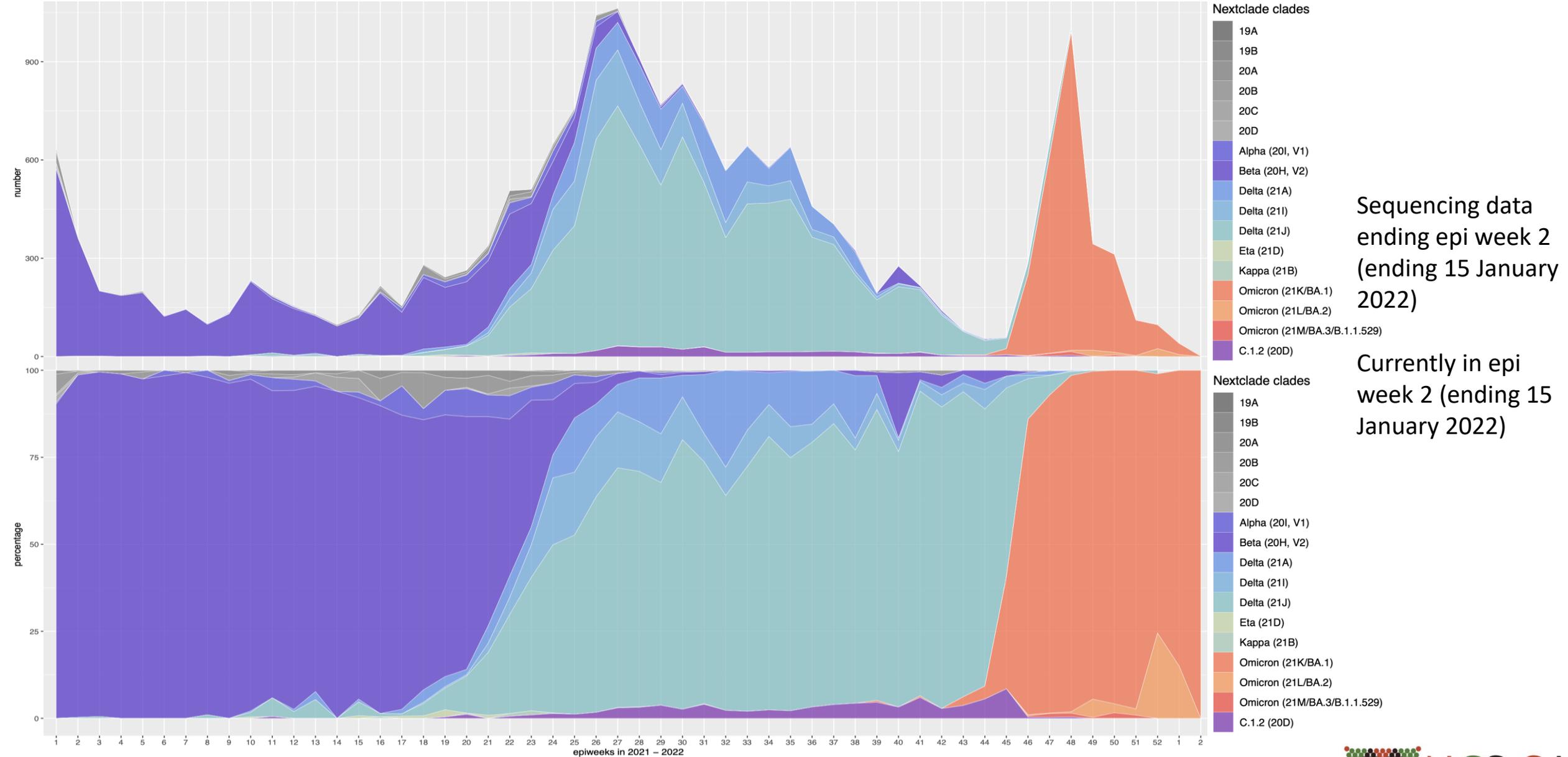


Number of Omicron Genomes



Omicron has been detected in 139 countries across the globe (detections based on GISAID).

Proportion and number of clades by epiweek in South Africa, 2021 - 2022 (N=20 783)



Sequencing data
ending epi week 2
(ending 15 January
2022)

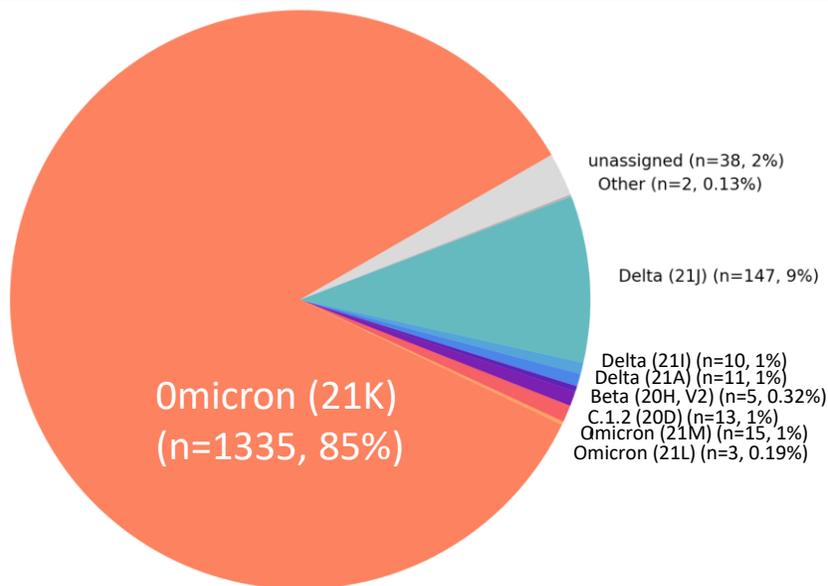
Currently in epi
week 2 (ending 15
January 2022)

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

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

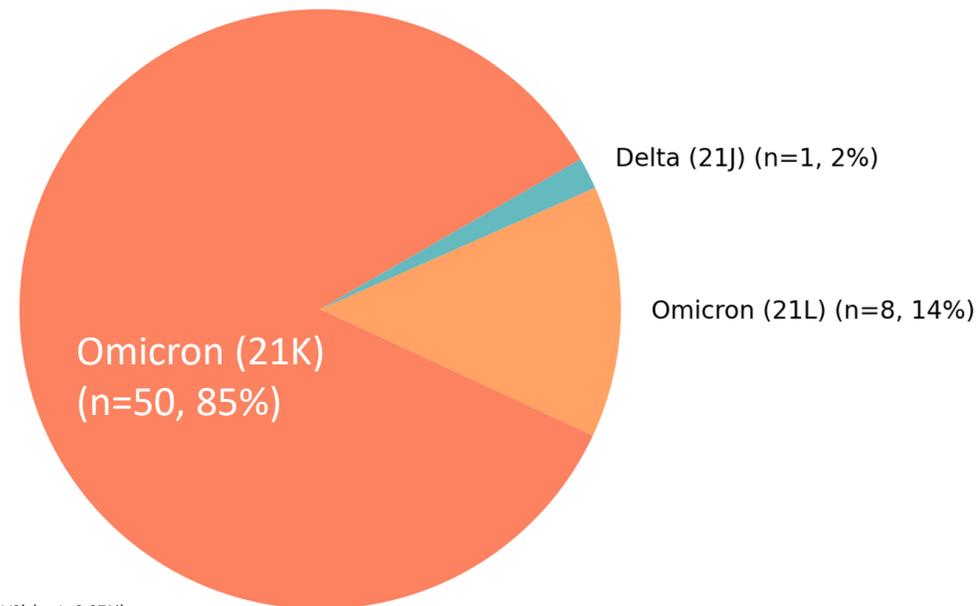
Nov 2021 – Jan 2022

November (N=1579)



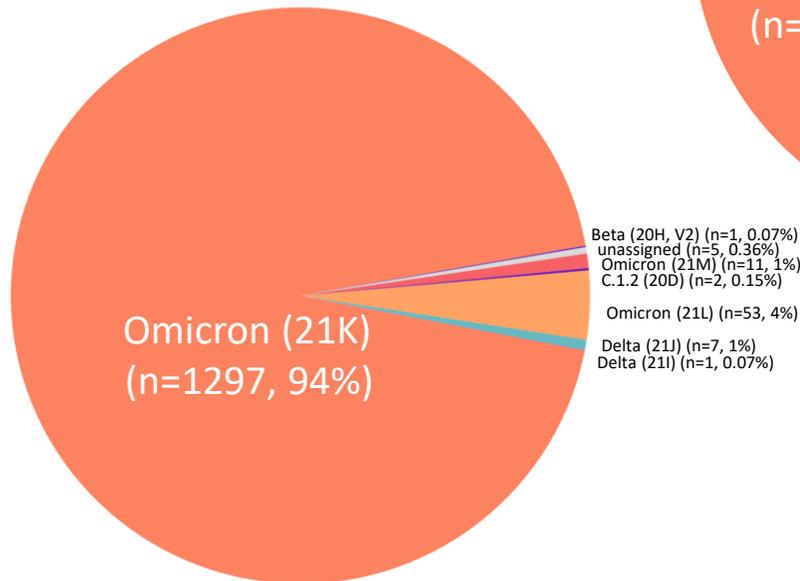
Total Omicron in Nov: 1252 (85.6%)
Total Delta in Nov: 168 (10.6%)

January (N=59)



Total Omicron in Jan: 58 (98.3%)

December (N=1377)



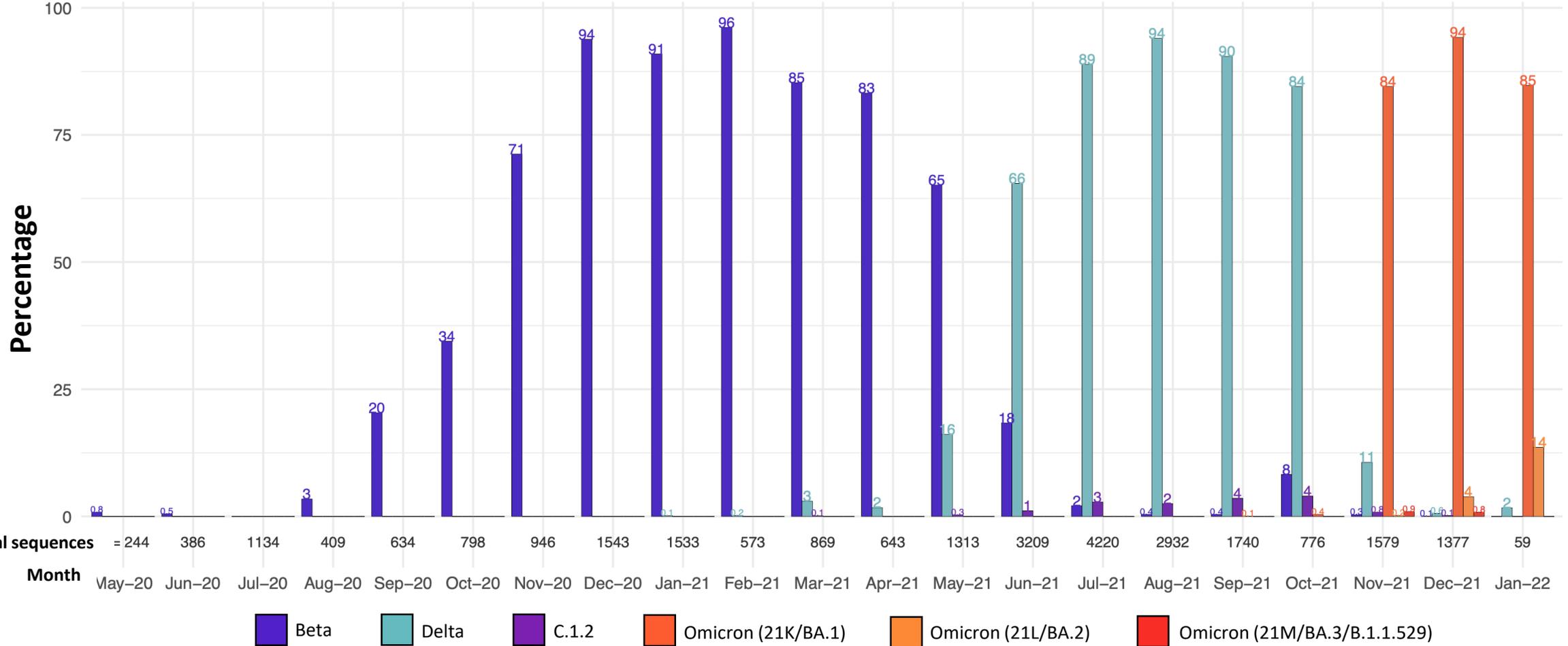
Total Omicron in Dec: 1361 (98.8%)



Omicron dominated in November, at 86% (1252/1579) and continued to dominate in December (99%, 1361/1377). Omicron appears to continue dominating in January (98%, 58/59), although more sequencing data is needed to confirm this trend and the BA.2 increase.

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

Detection rates of variants being monitored in South Africa*

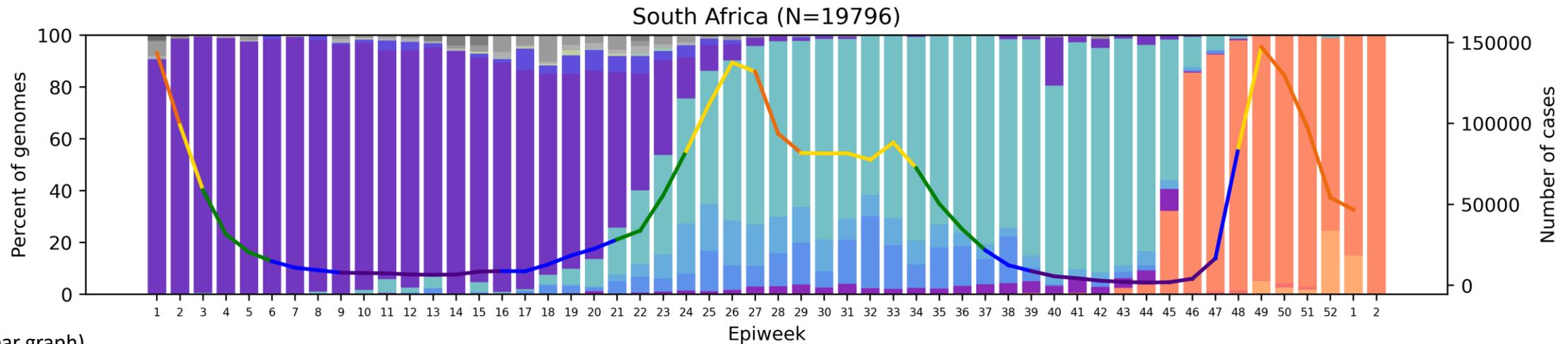
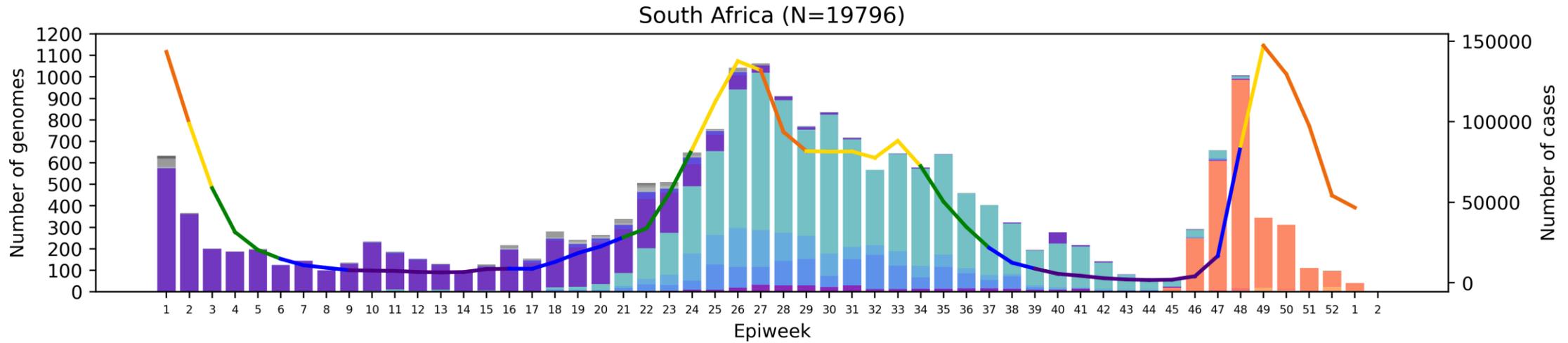


*Bars represent percentage prevalence of variant for the month; total sequences collected for the month are given below

C.1.2 has been detected at $\leq 4\%$ of sequences monthly since May 2021.
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 and January).



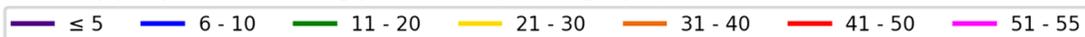
South Africa, 2021-2022, n = 19796



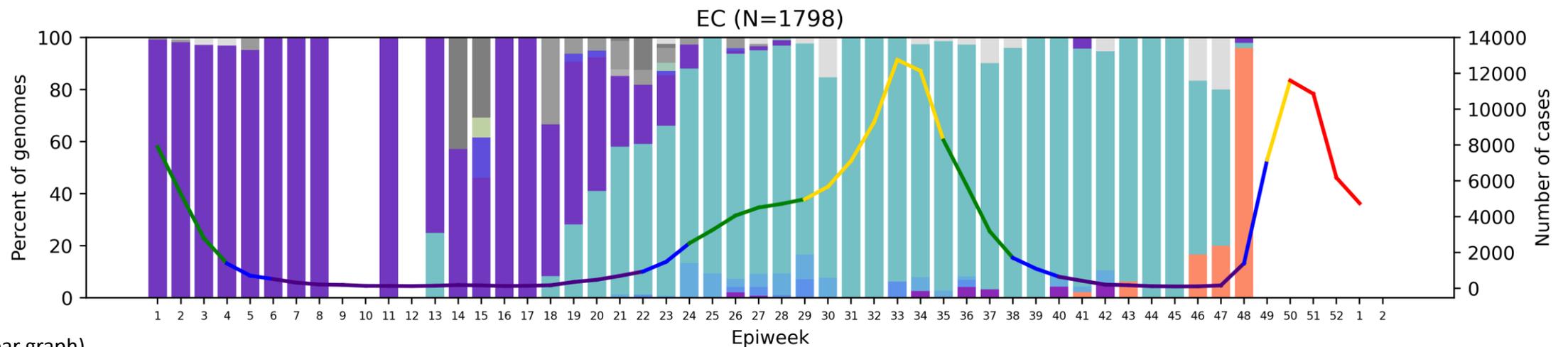
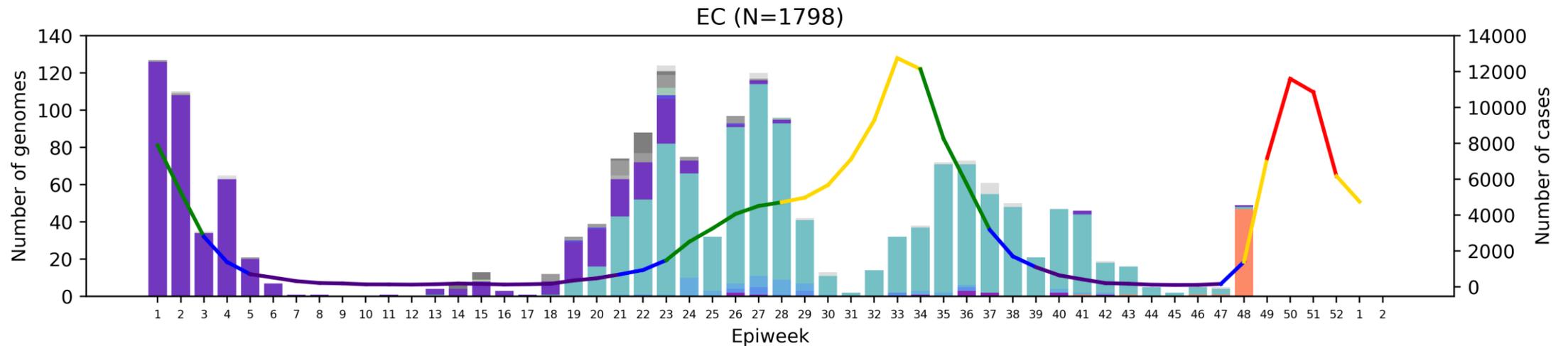
Clade key (bar graph)



Weekly proportion testing positive key (line graph)



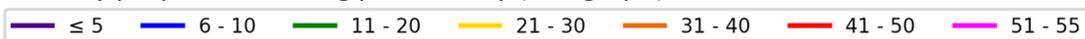
Eastern Cape Province, 2021-2022, n = 1798



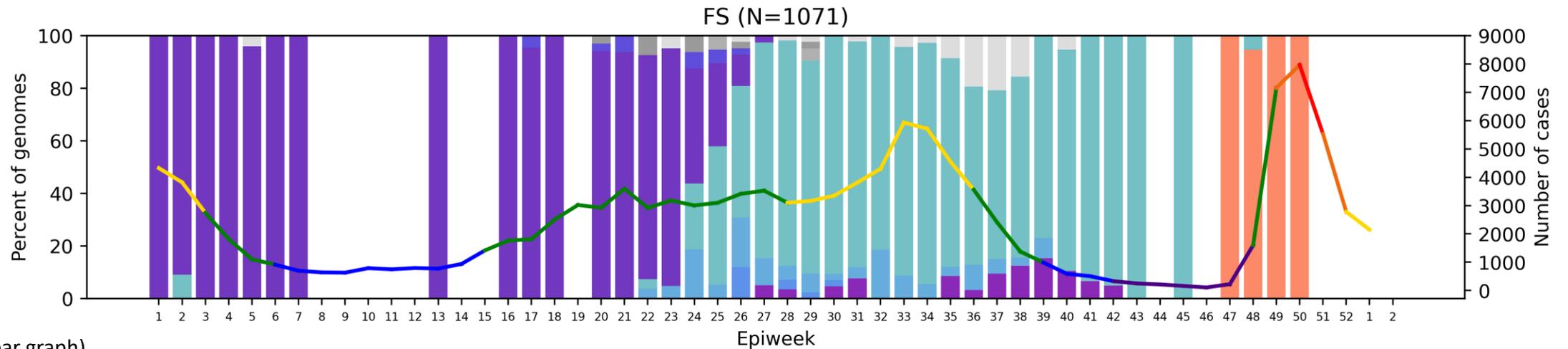
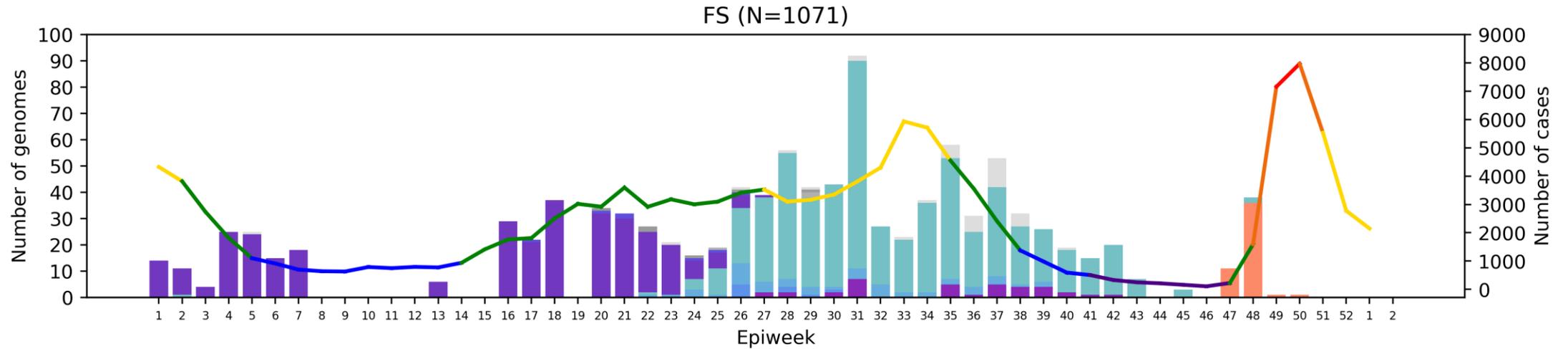
Clade key (bar graph)



Weekly proportion testing positive key (line graph)



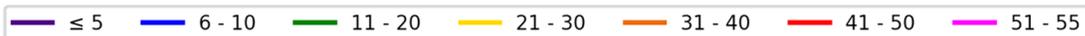
Free State Province, 2021-2022, n = 1071



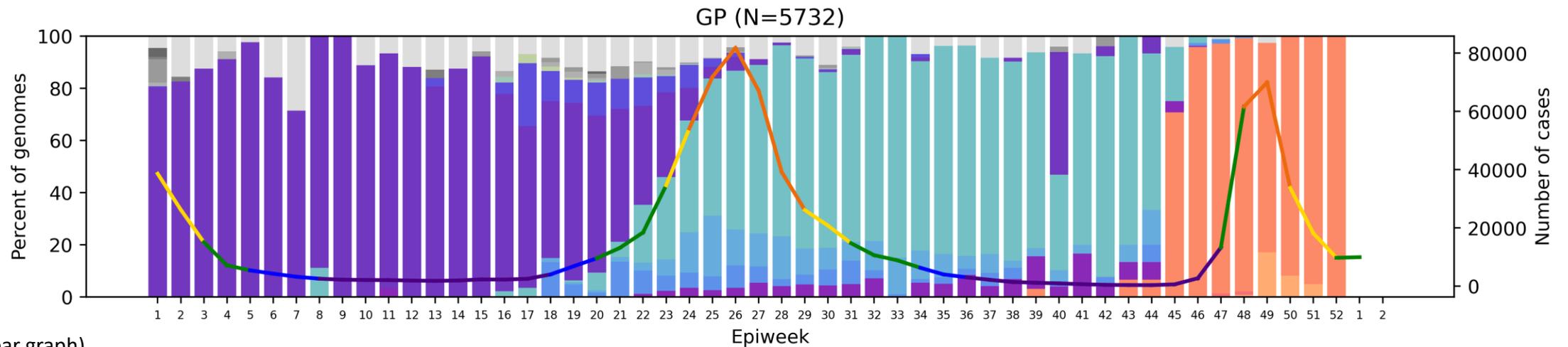
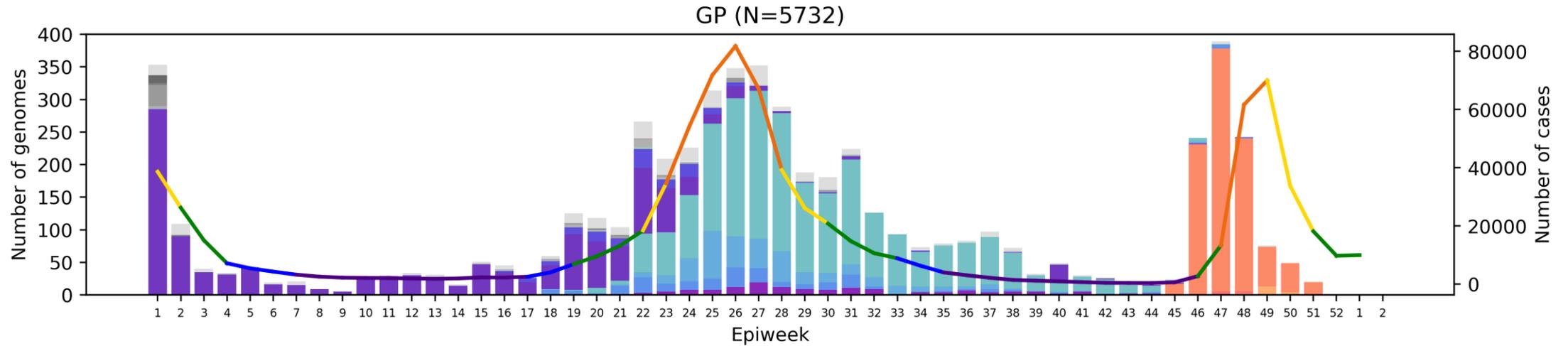
Clade key (bar graph)



Weekly proportion testing positive key (line graph)



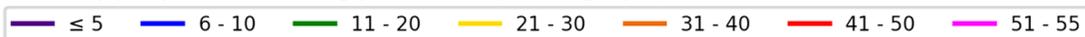
Gauteng Province, 2021-2022, n = 5732



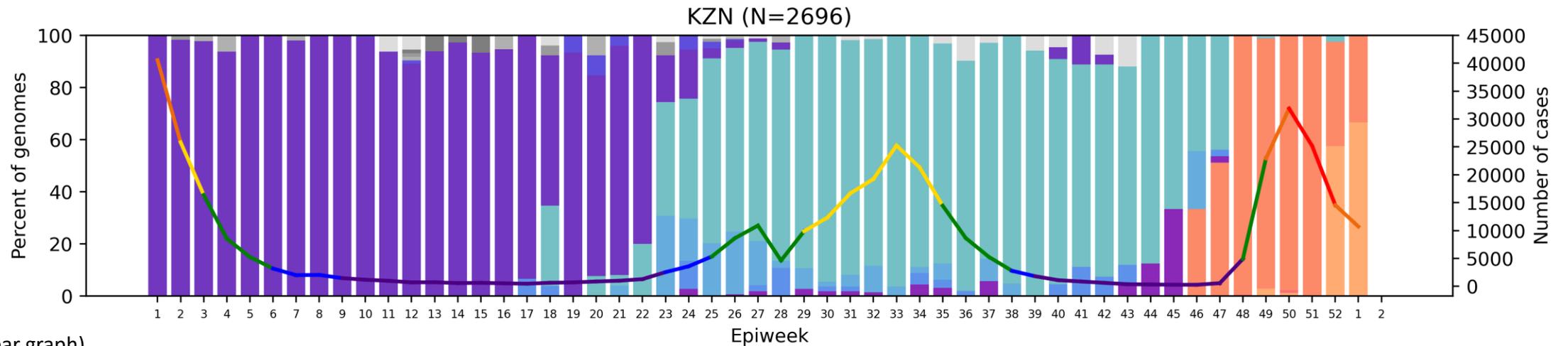
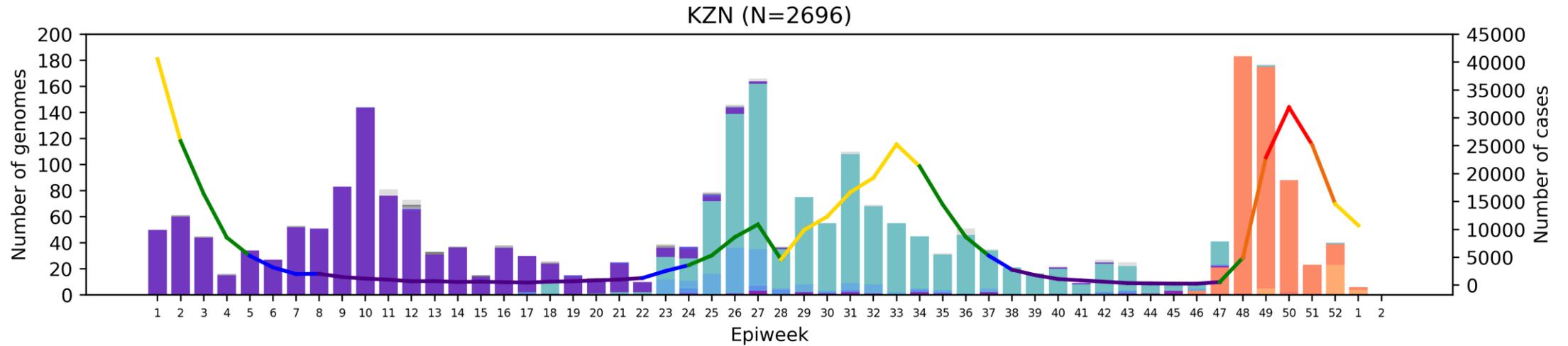
Clade key (bar graph)



Weekly proportion testing positive key (line graph)



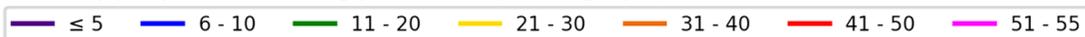
KwaZulu-Natal Province, 2021-2022, n = 2696



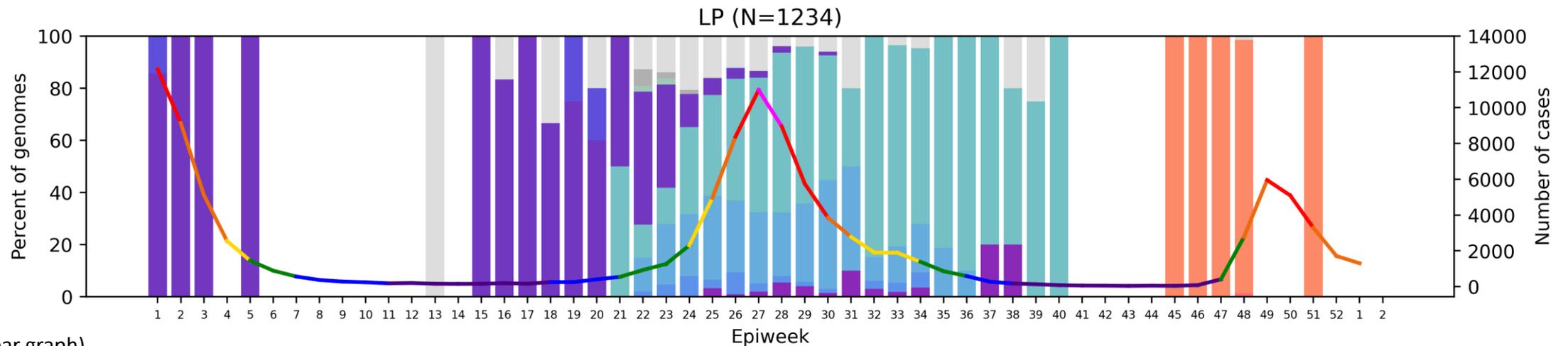
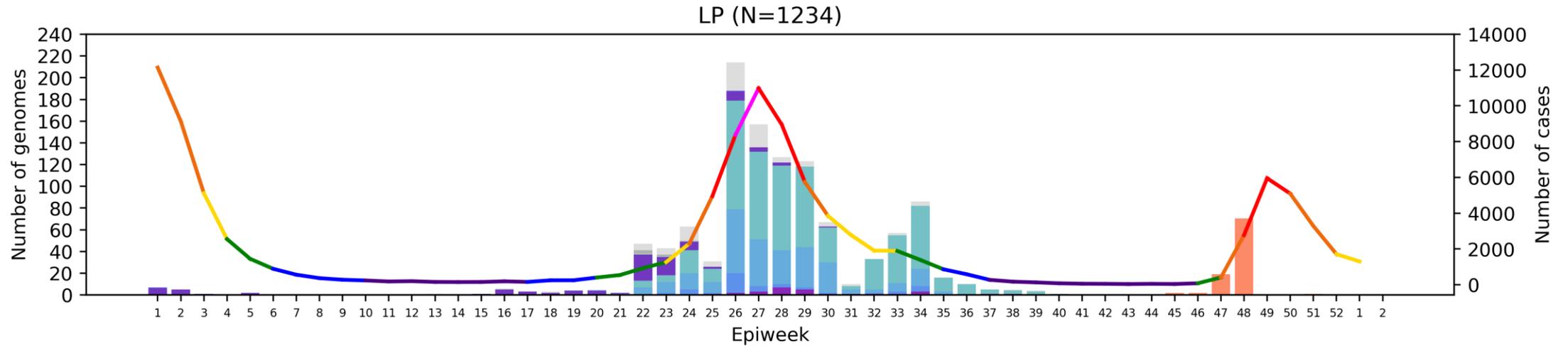
Clade key (bar graph)



Weekly proportion testing positive key (line graph)



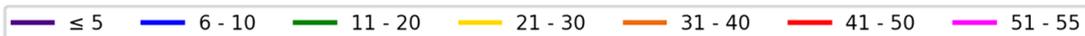
Limpopo Province, 2021-2022, n = 1234



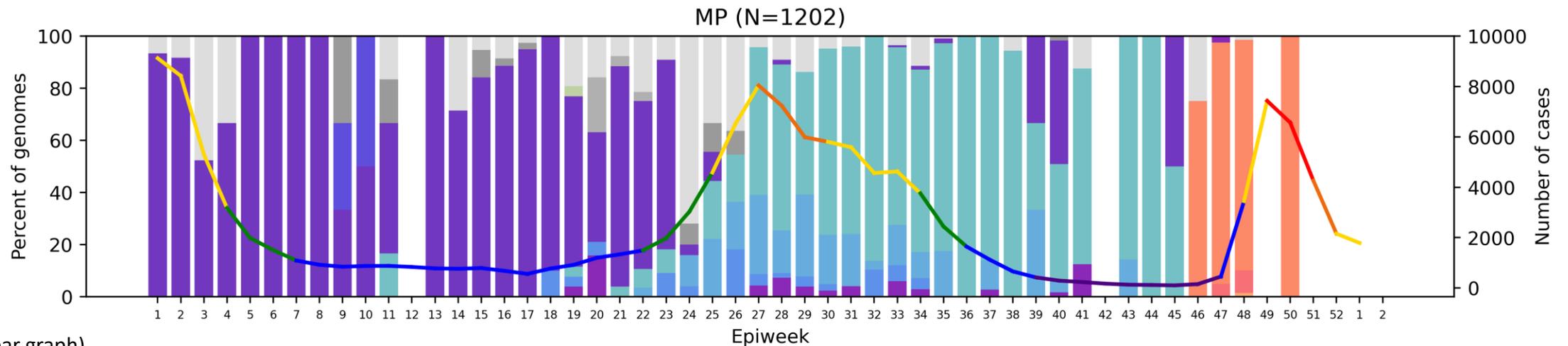
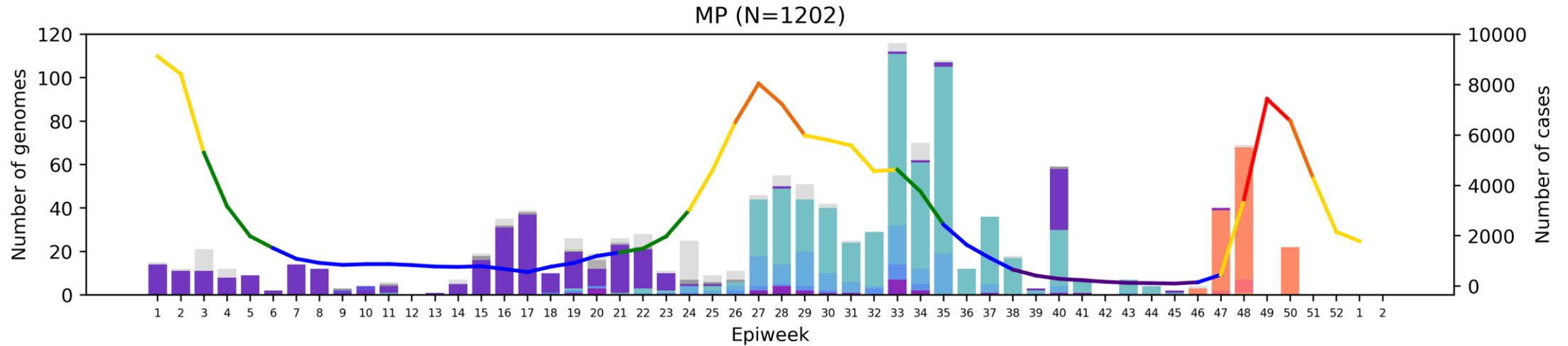
Clade key (bar graph)



Weekly proportion testing positive key (line graph)



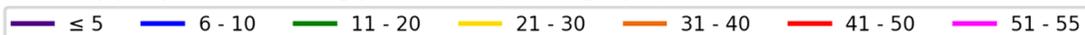
Mpumalanga Province, 2021-2022, n = 1202



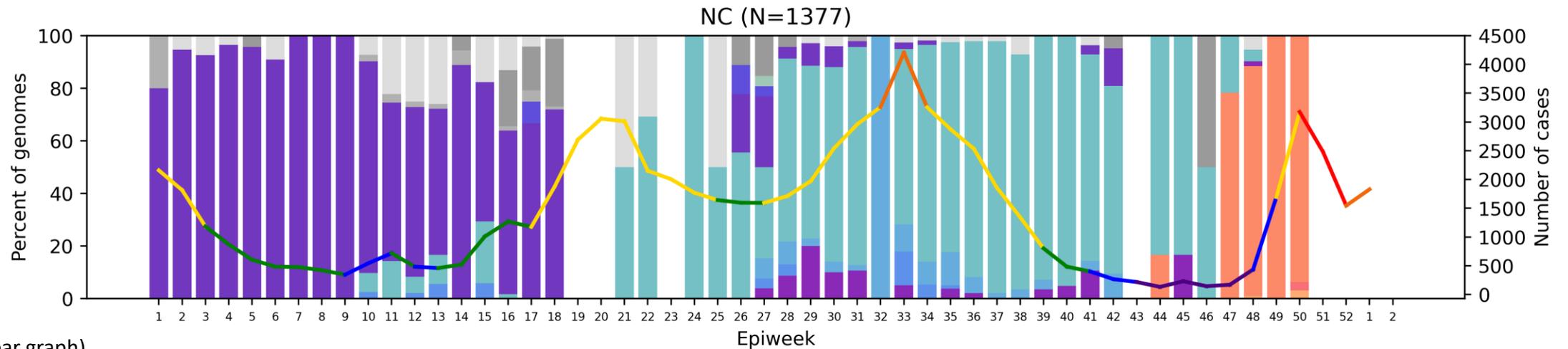
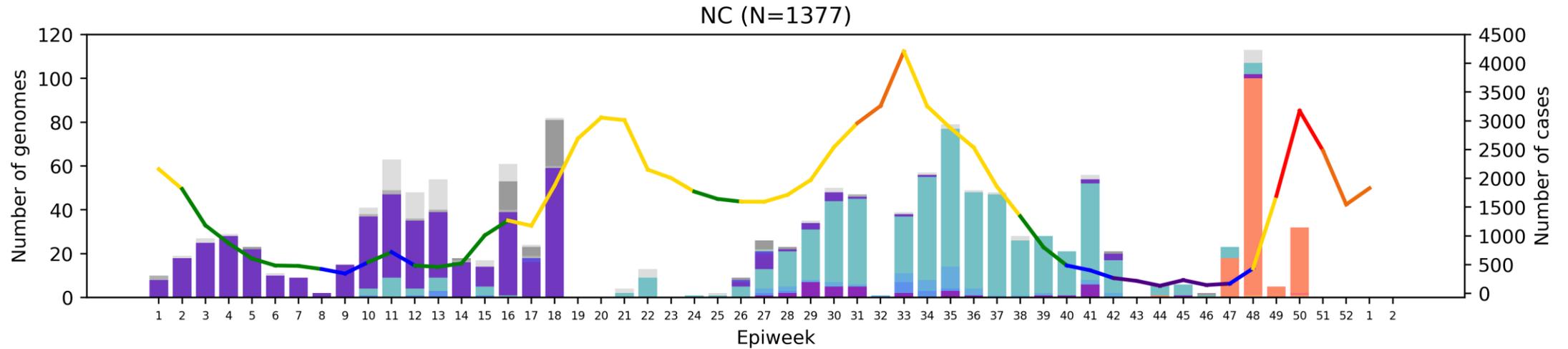
Clade key (bar graph)



Weekly proportion testing positive key (line graph)



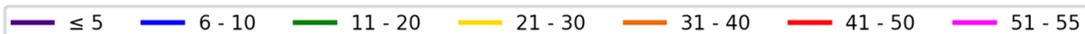
Northern Cape Province, 2021-2022, n = 1377



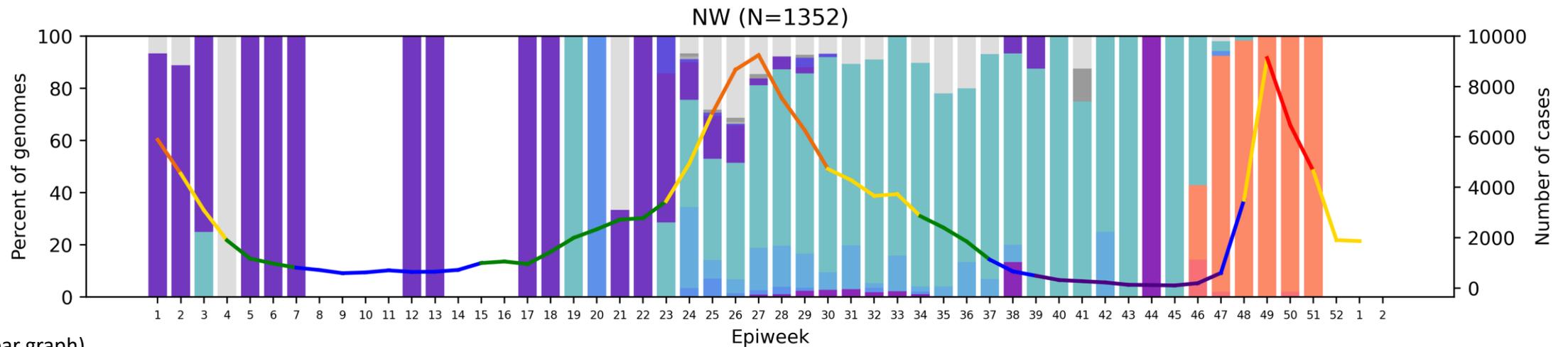
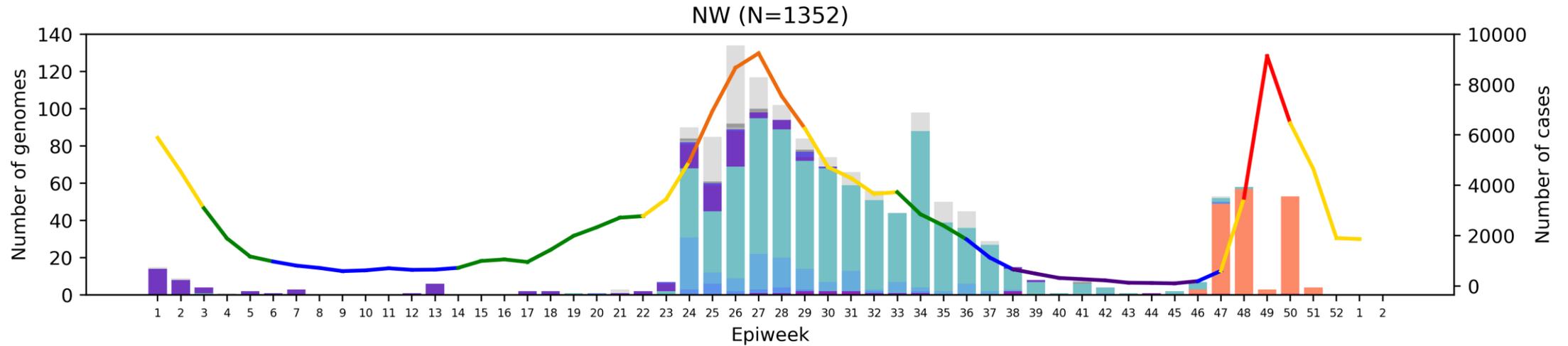
Clade key (bar graph)



Weekly proportion testing positive key (line graph)



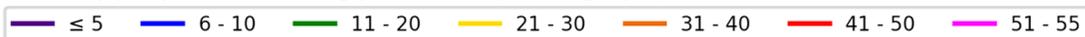
North West Province, 2021, n = 1352



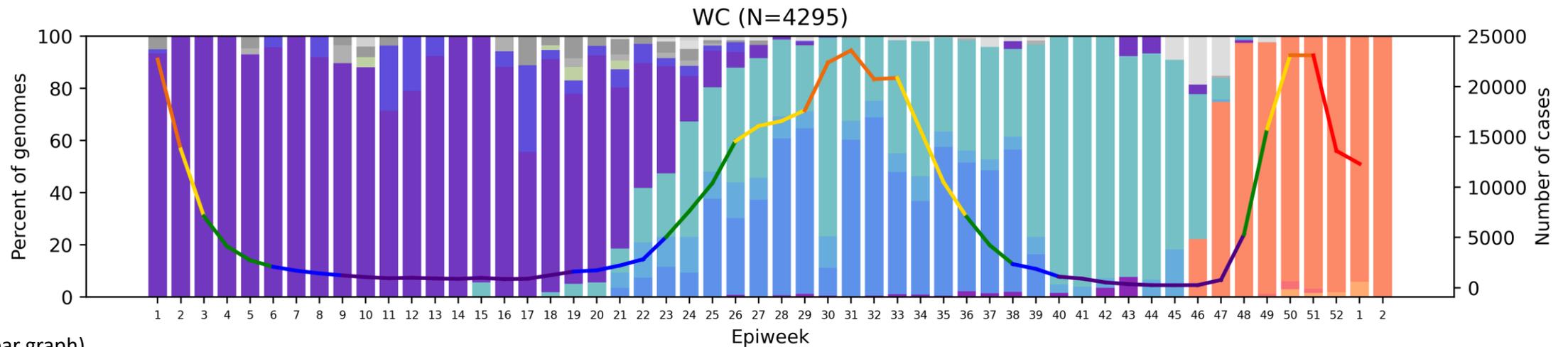
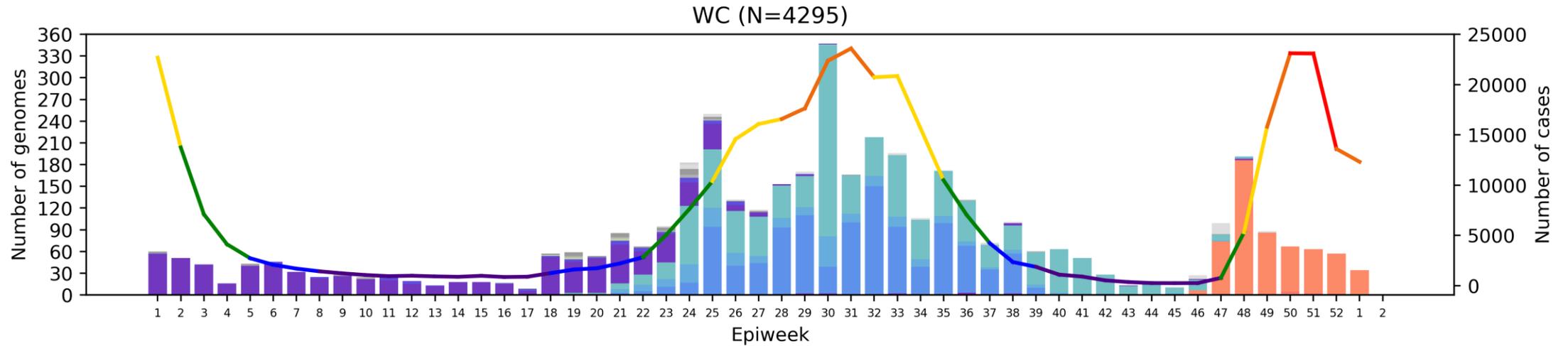
Clade key (bar graph)



Weekly proportion testing positive key (line graph)



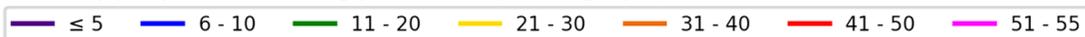
Western Cape Province, 2021-2022, n = 4295



Clade key (bar graph)

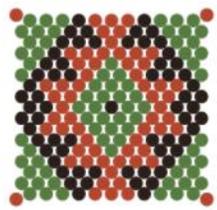


Weekly proportion testing positive key (line graph)



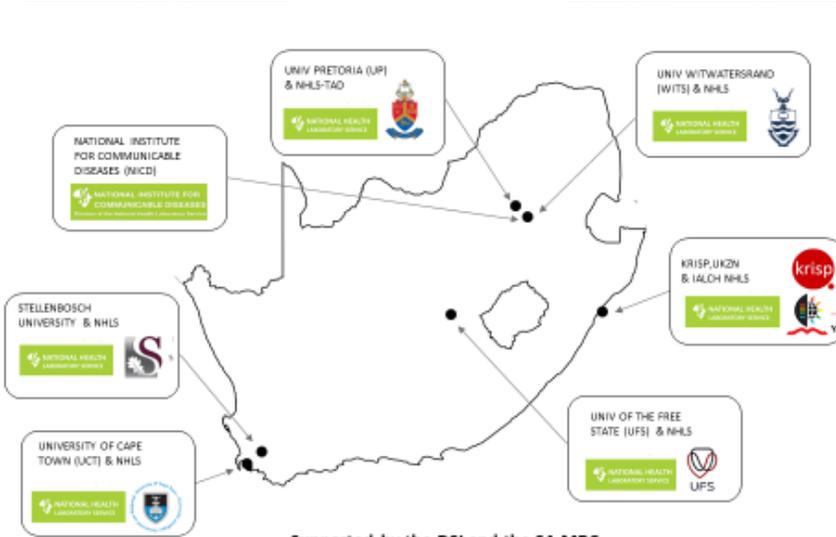
Summary

- **Variant of Concern Omicron**
 - Detected in 139 countries and dominating globally
 - 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)
 - New sub-lineage has been designated: BA.1.1. This contains lineage-defining BA.1.1 + spike:R346K
 - South Africa (detected in all provinces):
 - Dominated November sequencing data at 86% of genomes (n=1252/1579) and December sequencing data at 99% of genomes (n=1361/1377)
 - Limited sequence data for January shows continued dominance of Omicron (n=58/59)
 - BA.1 dominant in SA, with BA.2 increase recently observed and to be confirmed by additional data
- Low frequency of previously circulating variants such as Delta and C.1.2 still detected in recent data



NGS-SA

Network for Genomic Surveillance in South Africa



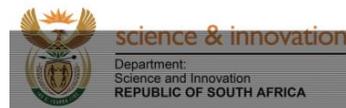
Supported by the DSI and the SA MRC



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WITS
UNIVERSITY



UNIVERSITY OF KWAZULU-NATAL
INYUVESI YAKWAZULU-NATALI



EDCTP

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National Institute for Communicable Diseases



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Mashudu Madzivhandila
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Brent Oosthuysen
Penny Moore
Lynn Morris

NICD Groups
NICD COVID-19 response team
NICD SARS-CoV-2 Sequencing Group

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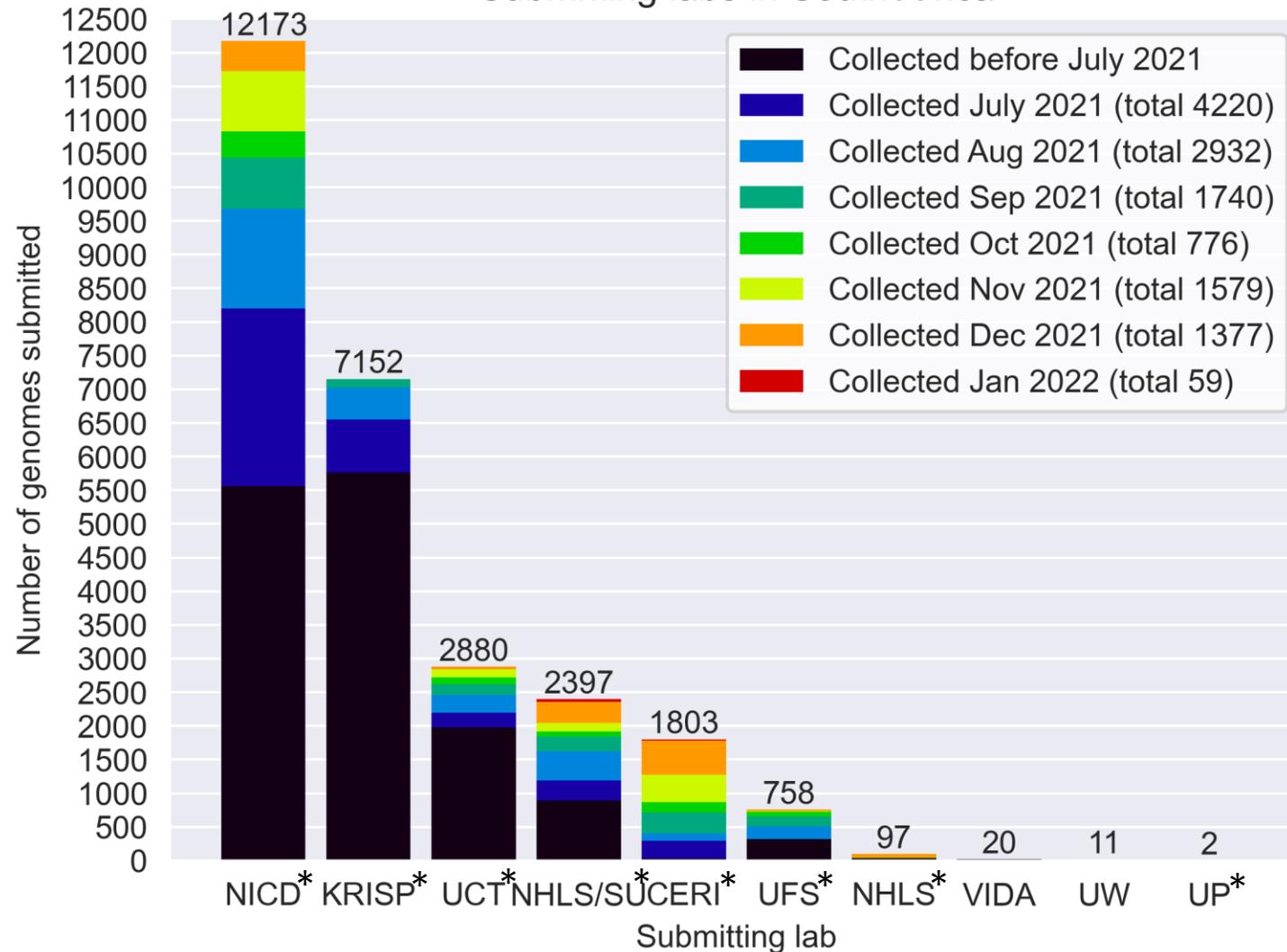
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G7 Global Health fund, Robert Koch Institute, Dr Fabian Leendertz



South African genomes submitted per submitting lab, 2020 and 2021 (N=27 293)

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.)