

SARS-CoV-2 Sequencing Update 07 October 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 07 October 2022 at 08h08

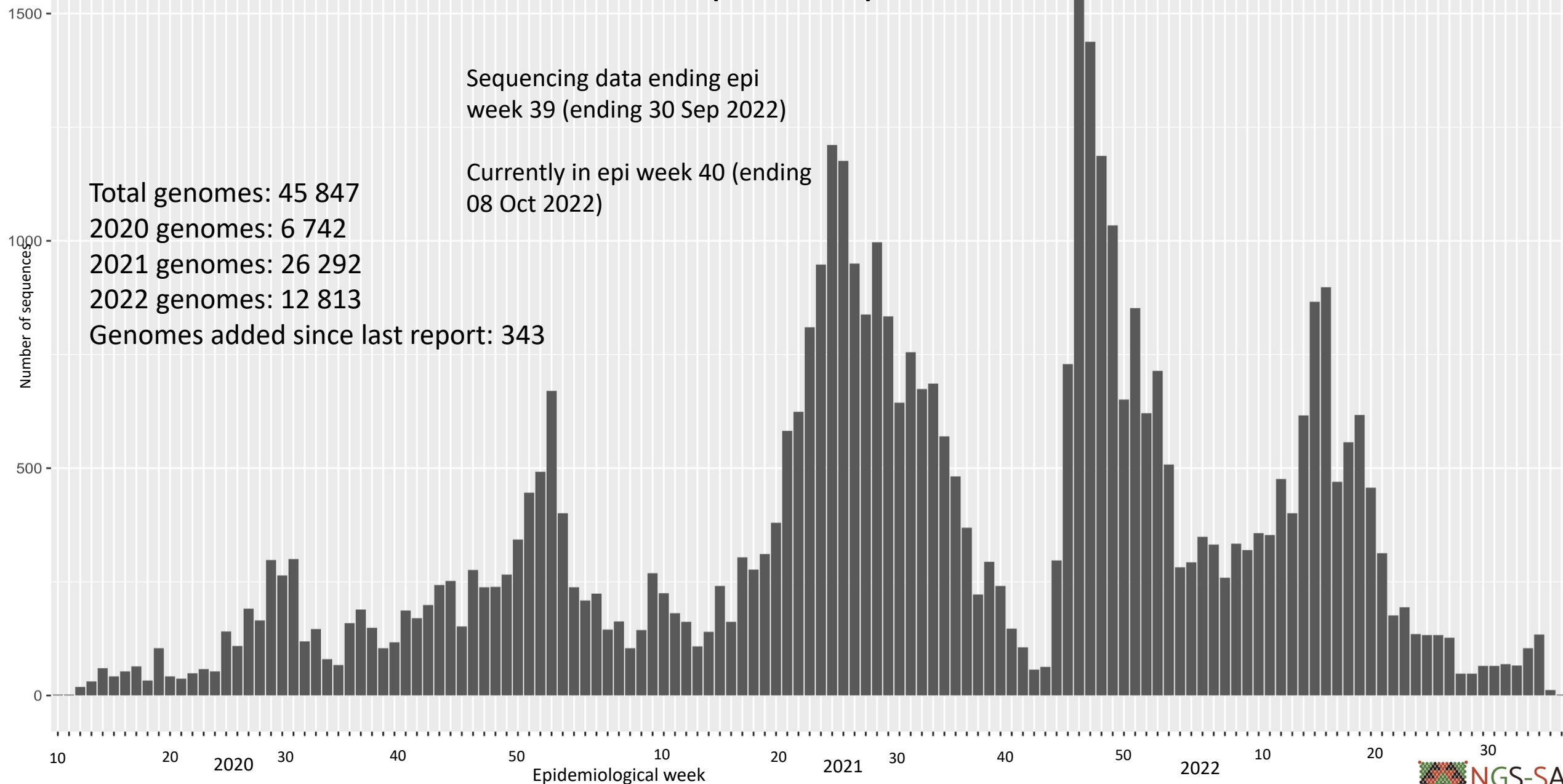


Data license: <https://www.gisaid.org/registration/terms-of-use/>

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

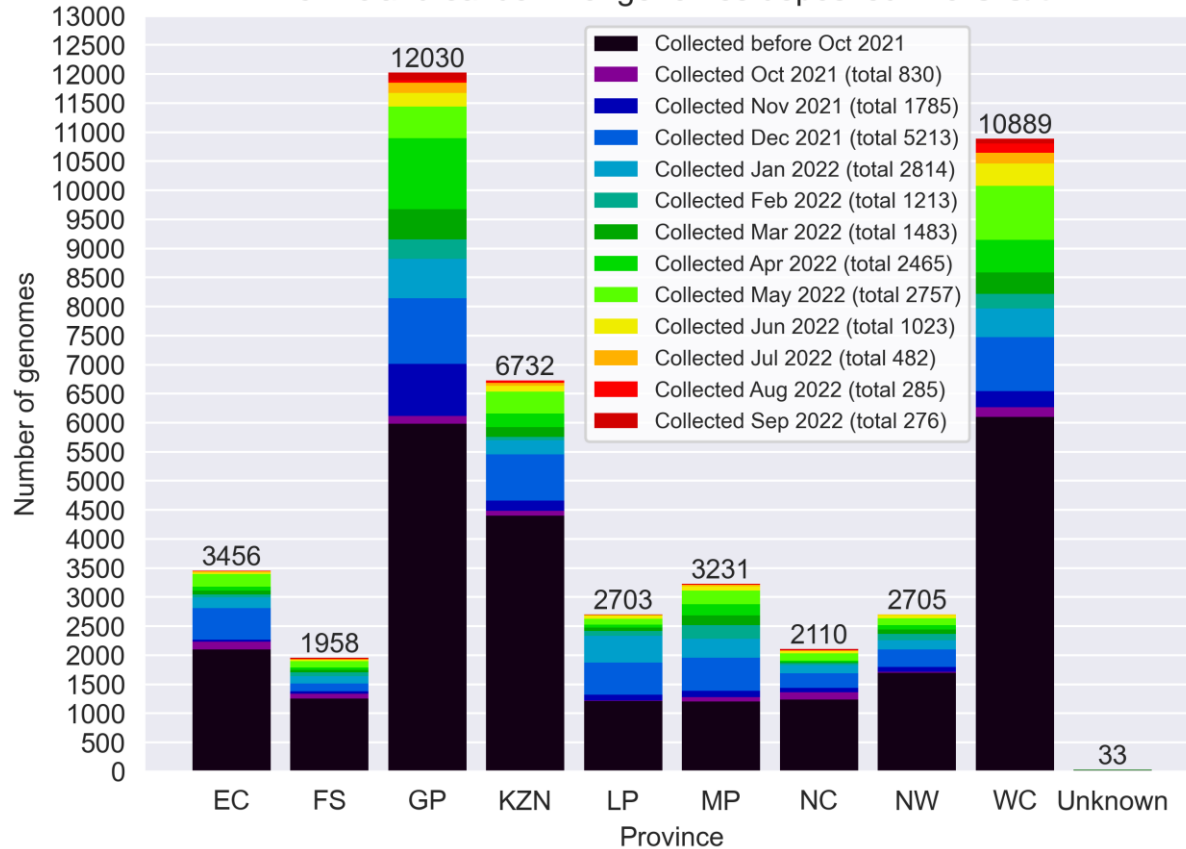
Number of South African genomes deposited on GISAID, by specimen collection week, 2020 – 2022 (N=45 847*)



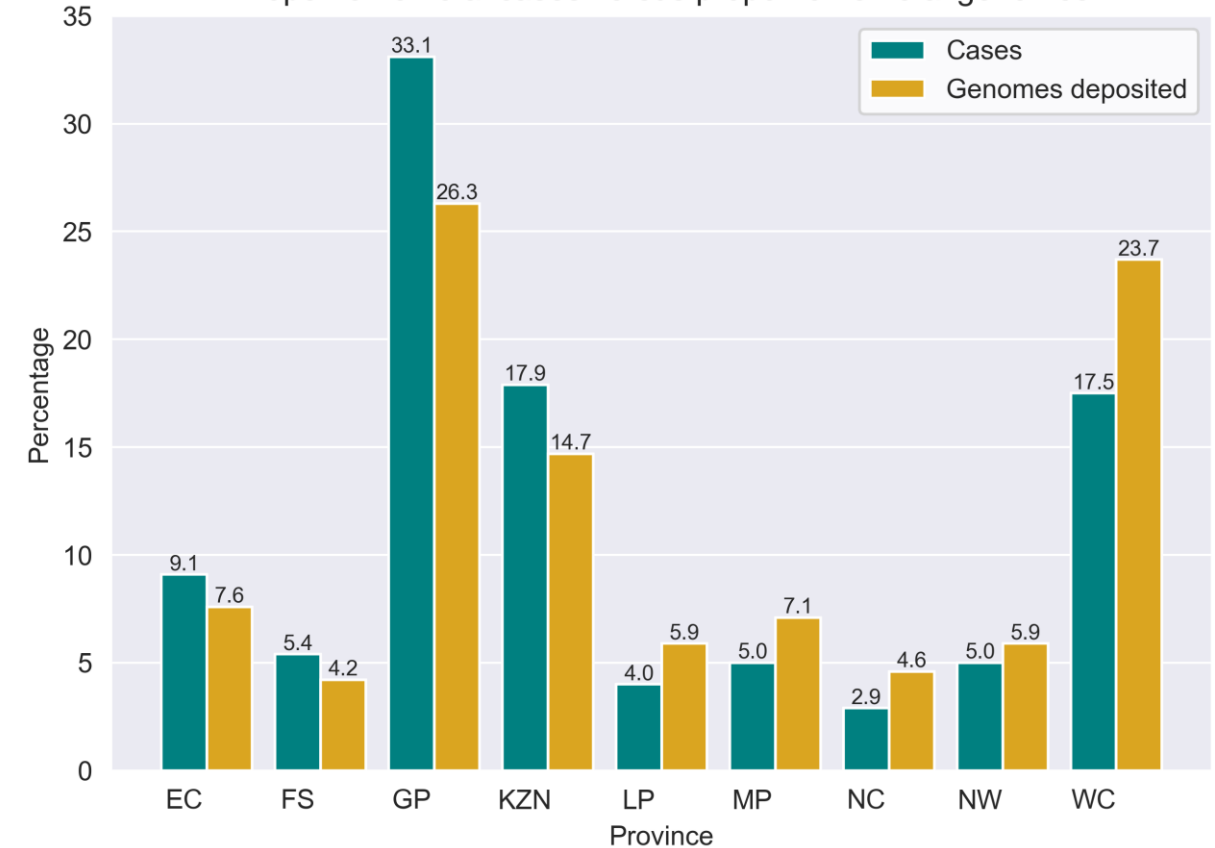
*This represents the cleaned, de-duplicated dataset of unique **National and Pneumonia Surveillance** sequences. This dataset will be used for all further figures.

GISAID genomes vs total cases, 2020 – 2022 (N=45 847)

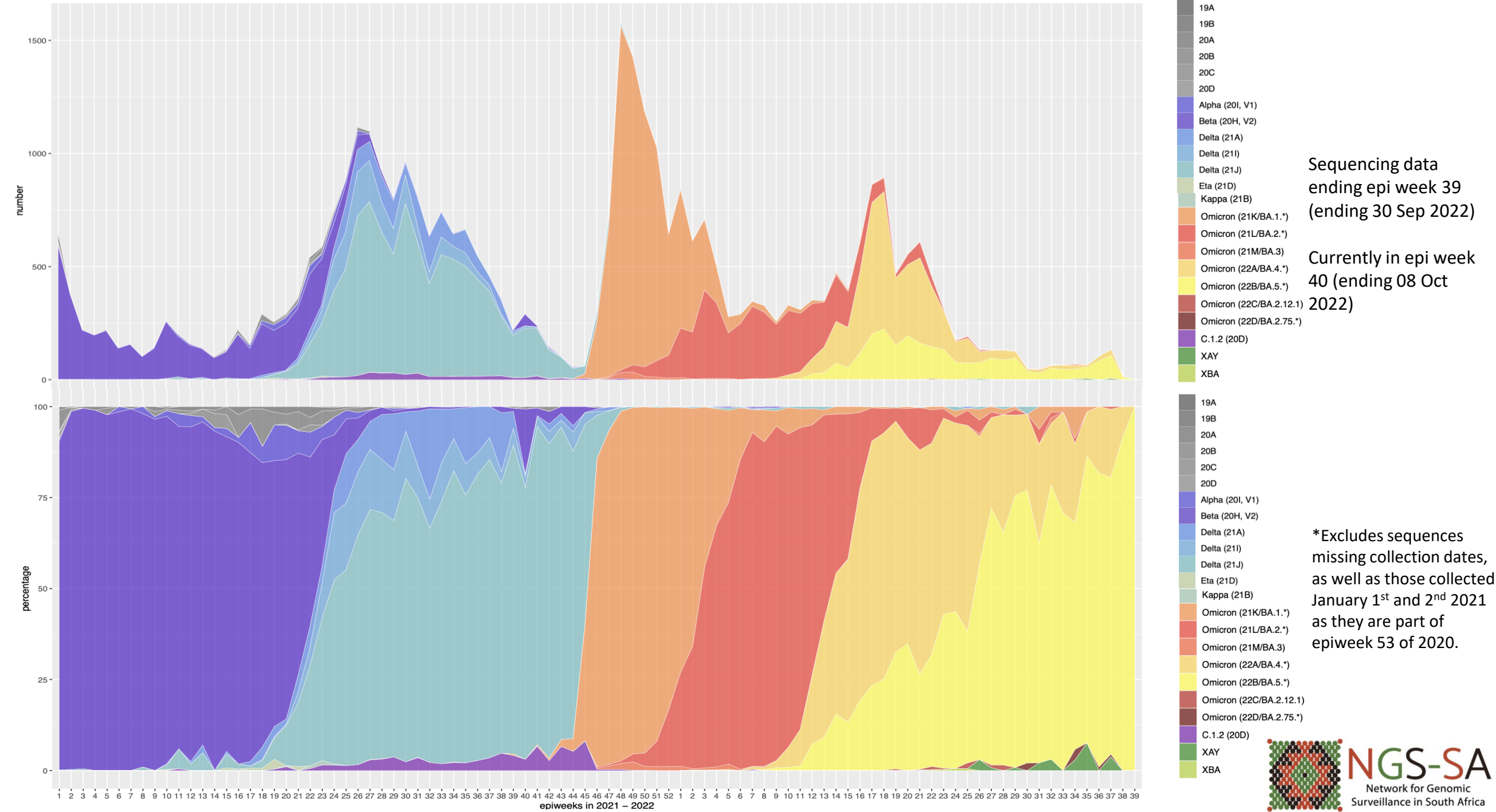
Provincial breakdown of genomes deposited into GISAID



Proportion of total cases versus proportion of total genomes

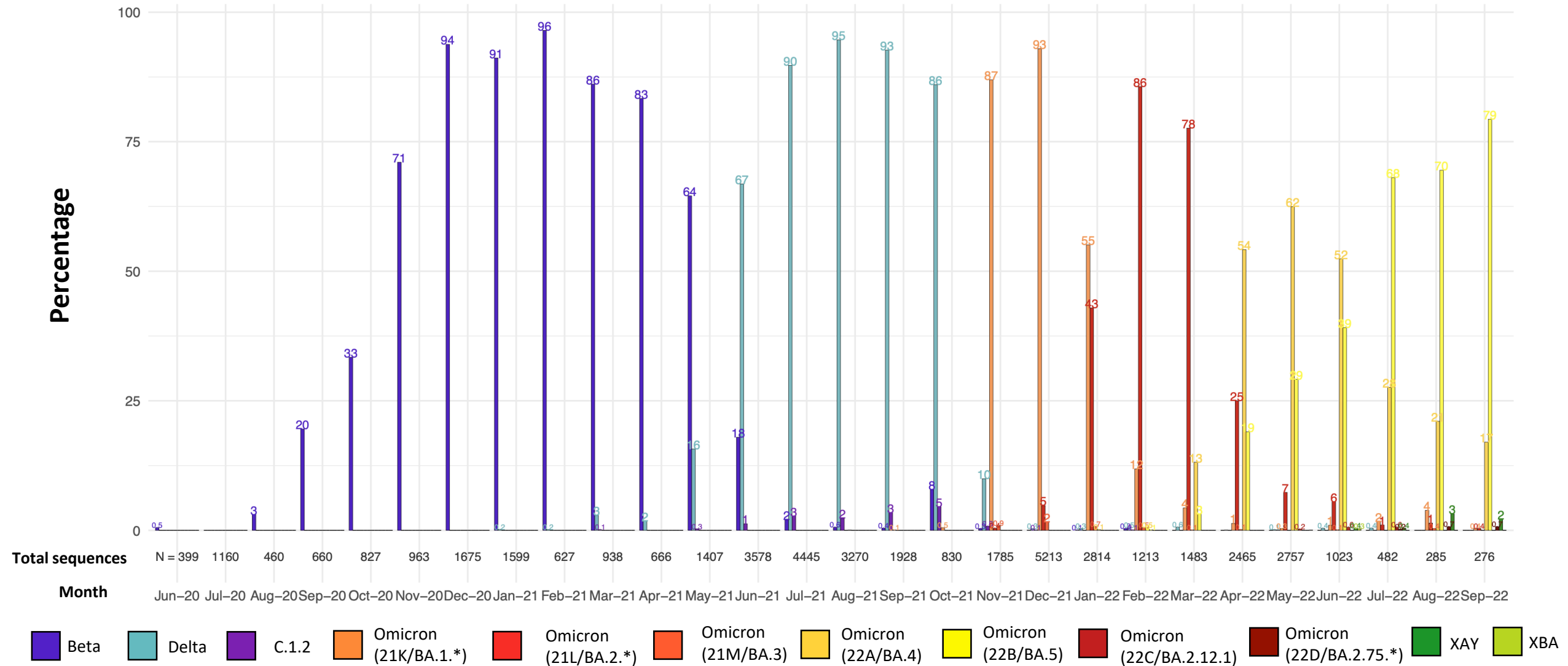


Number and percentage of clades by epiweek in South Africa, 2021 – 2022 (39 018*)



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

Detection rates of variants being monitored in South Africa

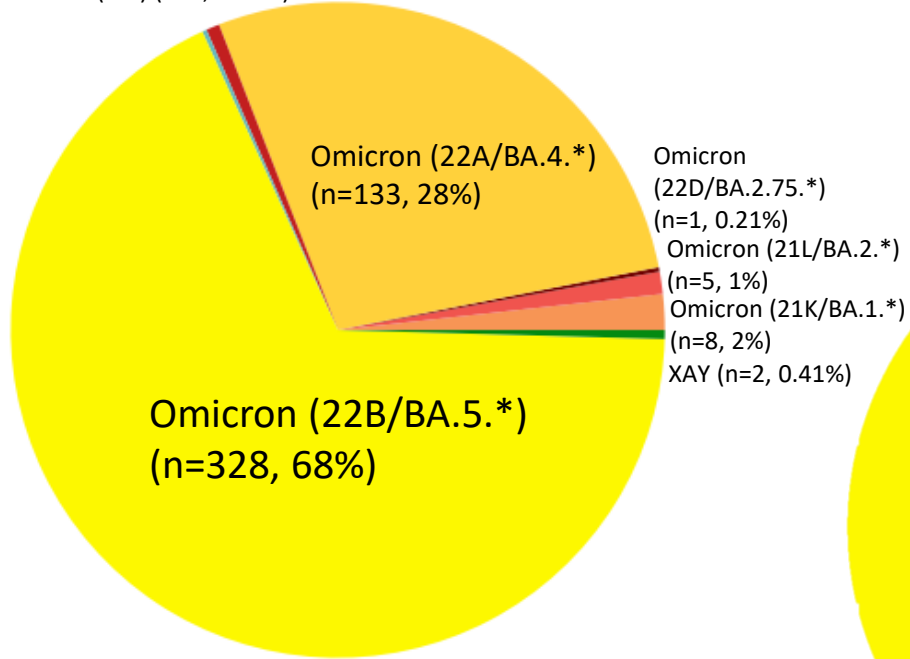


*Bars represent percentage prevalence of variant for the month; total number sequences collected for the month are given below the bar

Prevalence of Variants of Concern (VOC) and Variants of Interest (VOI) in July – September 2022

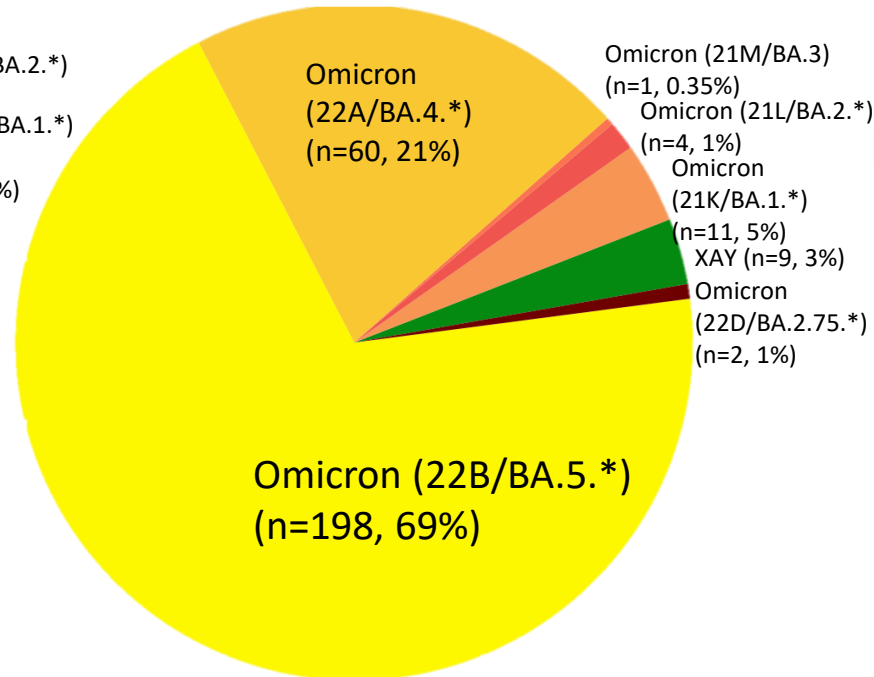
July (N=482)

Omicron (22C/BA.2.12.1) (n=3, 1%)
Delta (21J) (n=2, 0.41%)



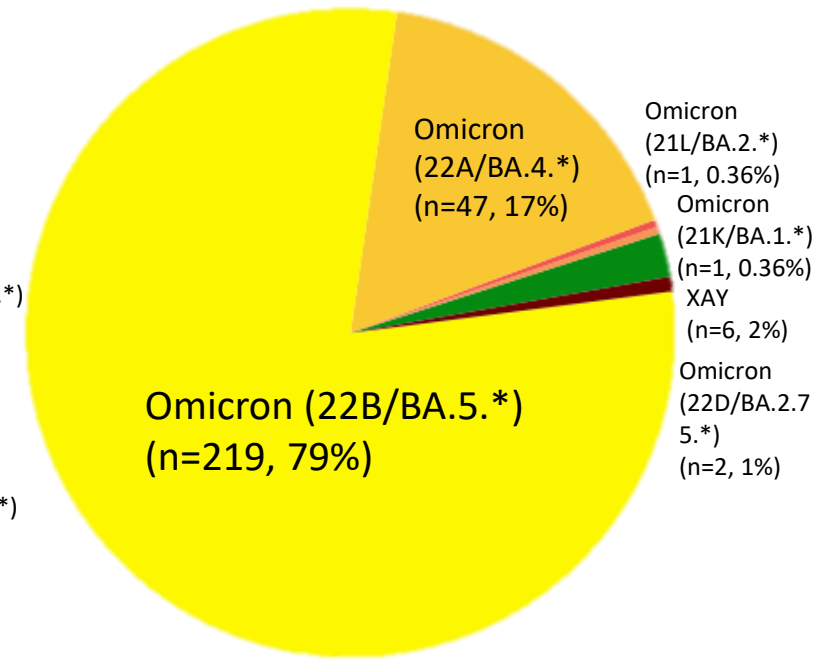
Total Omicron in July: 478 (99.2%)

August (N=285)

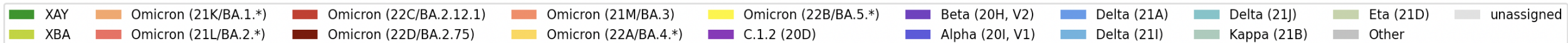


Total Omicron in August: 276 (96.8%)

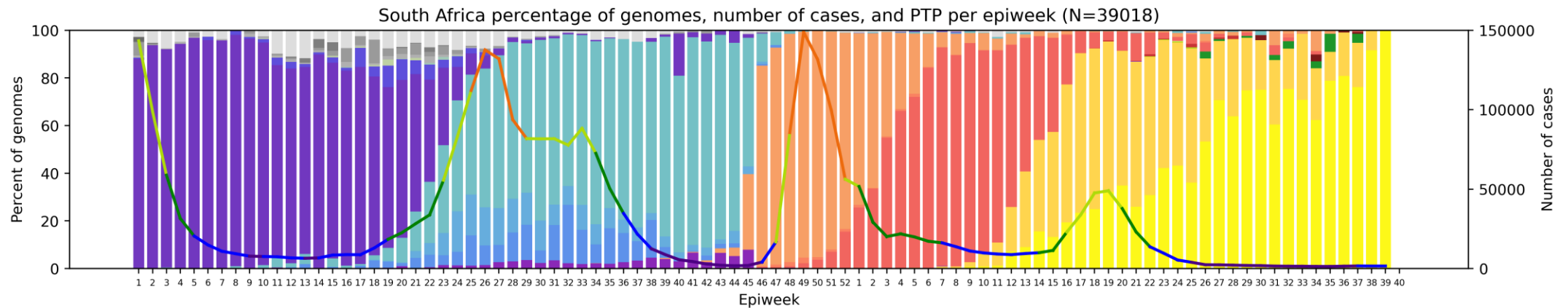
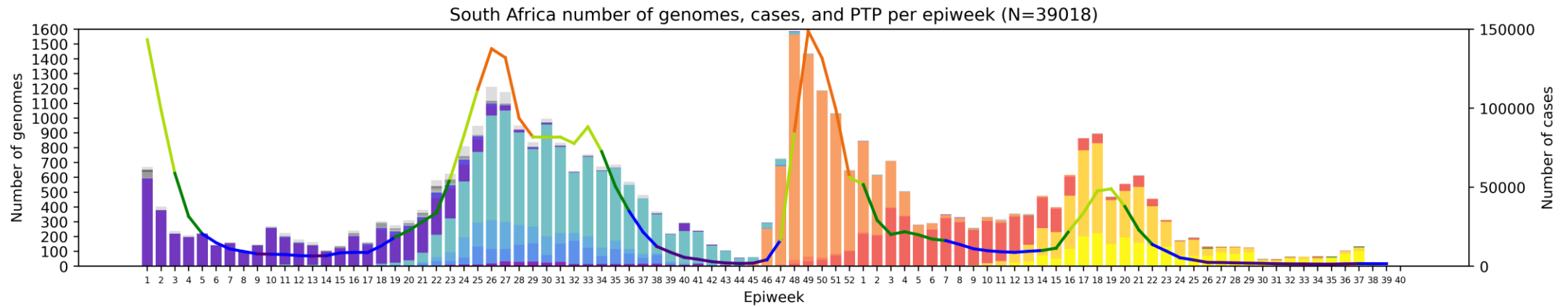
September (N=276)



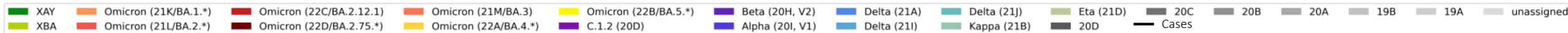
Total Omicron in September: 270 (97.8%)



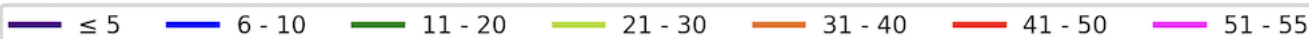
South Africa, 2021-2022, n = 39 018*



Clade key (bar graph)



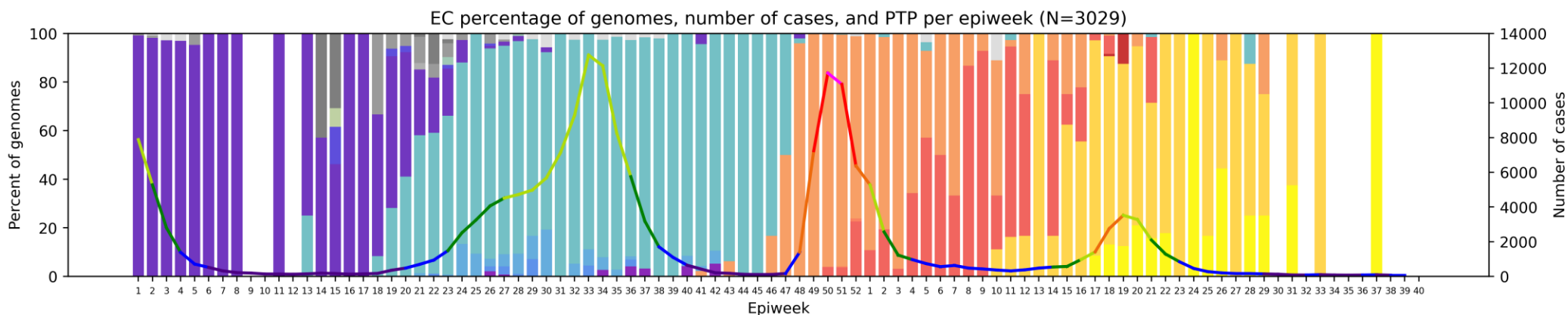
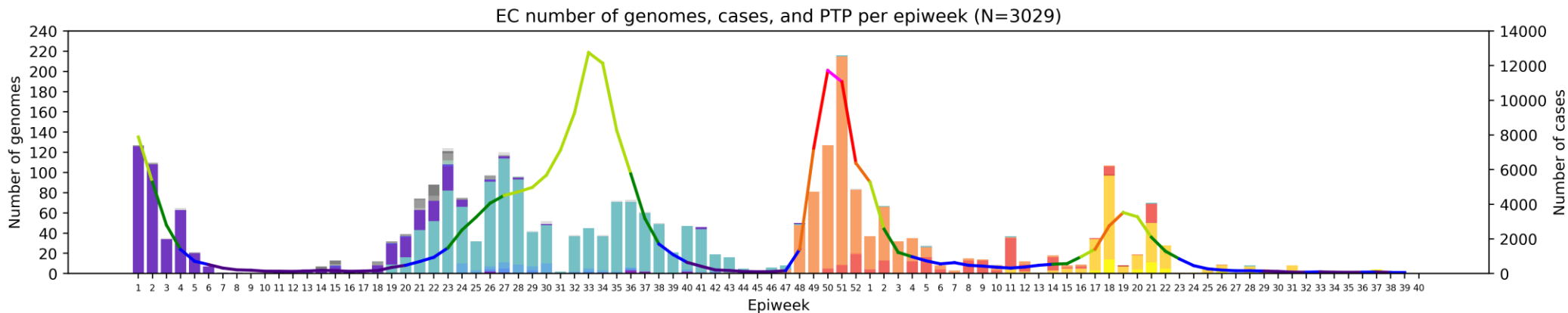
Weekly percentage testing positive key (line graph)



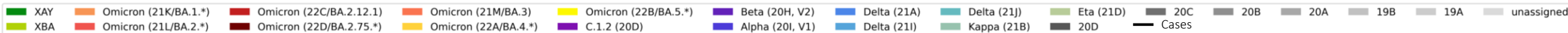
*Excludes sequences missing collection dates, as well as those collected January 1st and 2nd 2021 as they are part of epiweek 53 of 2020.

Eastern Cape Province, 2021-2022, n = 3029

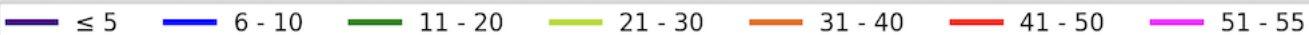
Genomes added since last report: 4*



Clade key (bar graph)



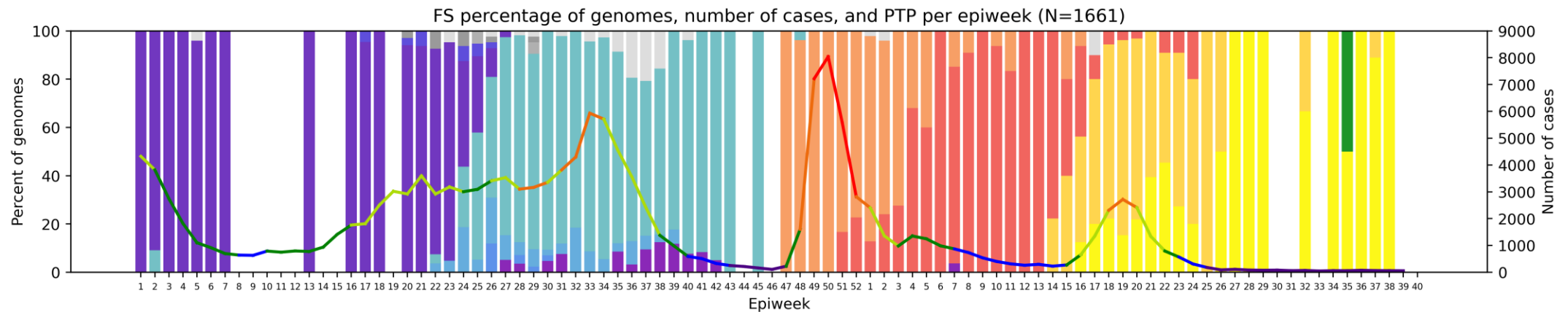
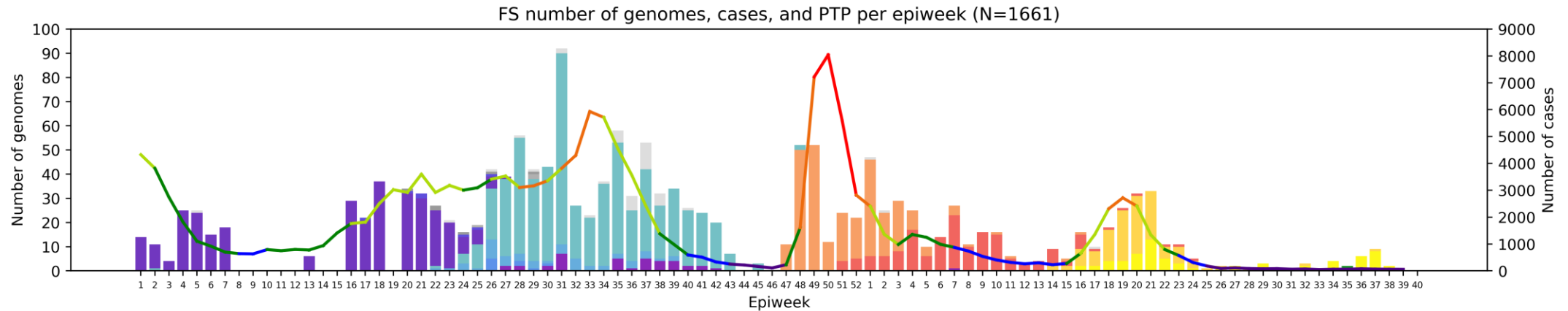
Weekly percentage testing positive key (line graph)



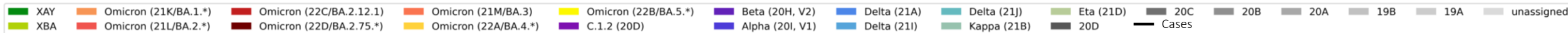
*May include genomes from 2020 which are not pictured here and are not included in the slide total.

Free State Province, 2021-2022, n = 1661

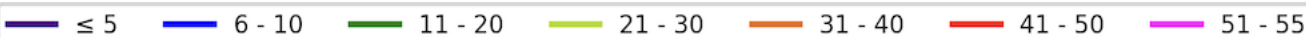
Genomes added since last report: 29*



Clade key (bar graph)



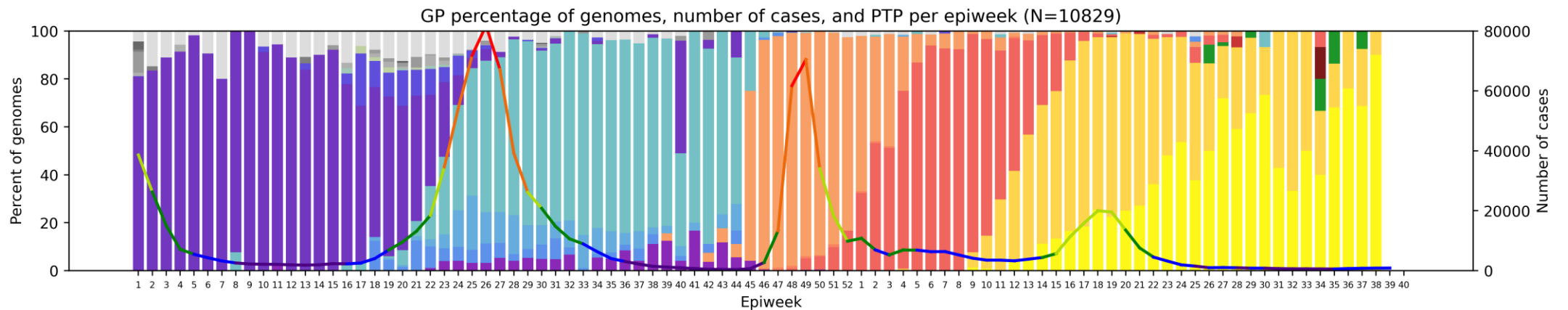
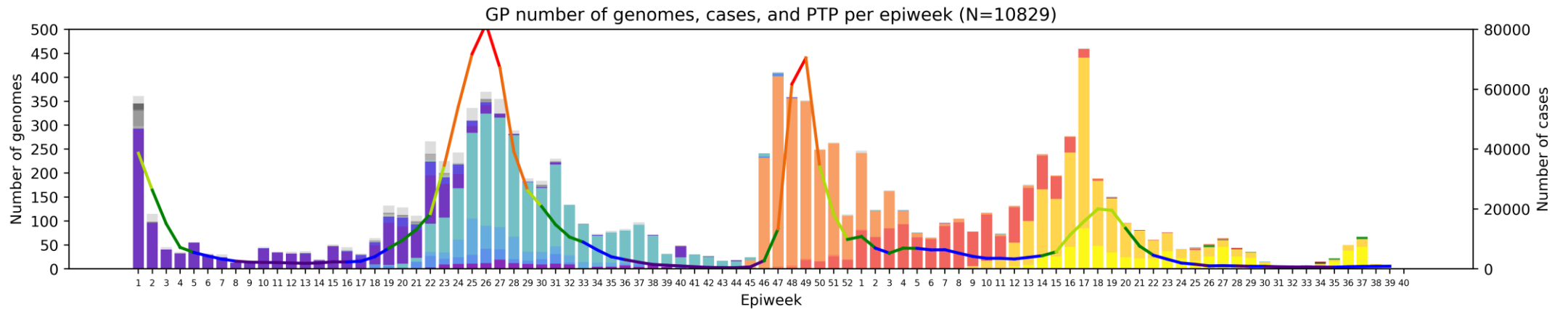
Weekly percentage testing positive key (line graph)



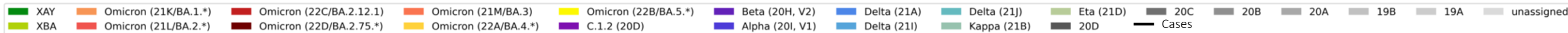
*May include genomes from 2020 which are not pictured here and are not included in the slide total.

Gauteng Province, 2021-2022, n = 10 829

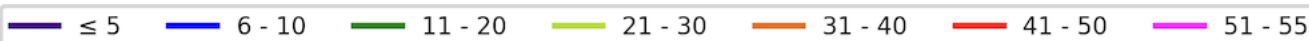
Genomes added since last report: 167*



Clade key (bar graph)



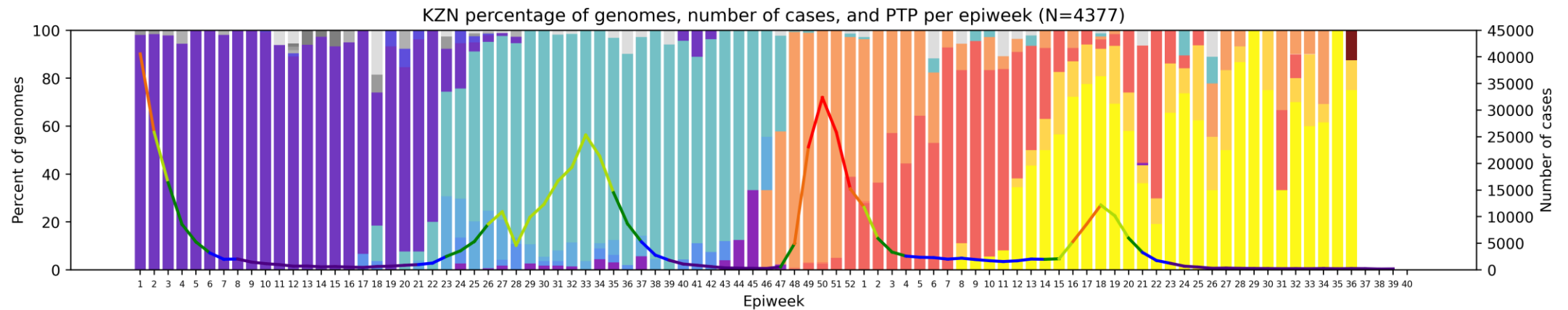
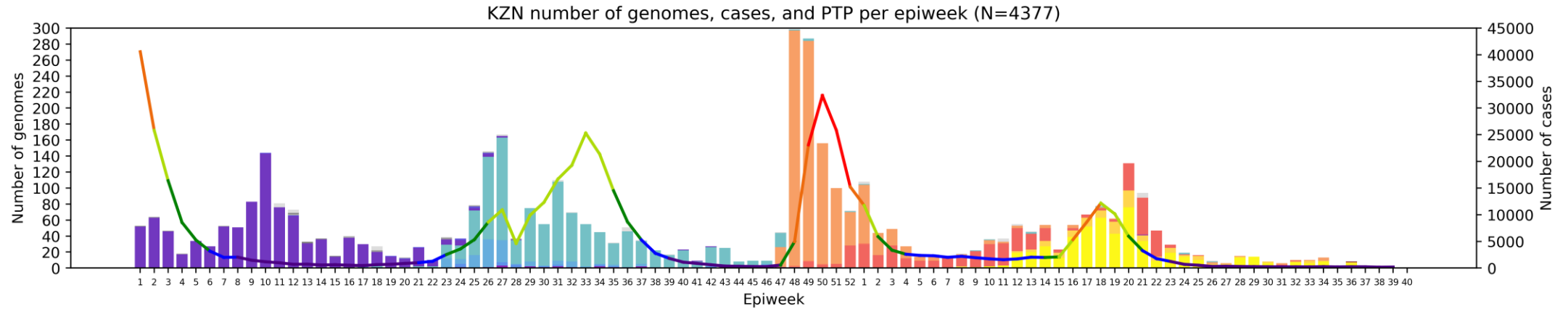
Weekly percentage testing positive key (line graph)



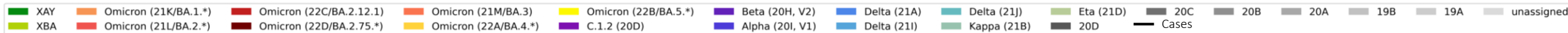
*May include genomes from 2020 which are not pictured here and are not included in the slide total.

KwaZulu-Natal Province, 2021-2022, n = 4377

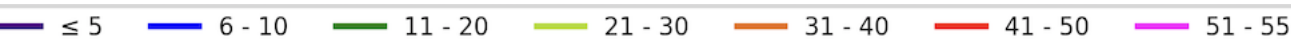
Genomes added since last report: 54*



Clade key (bar graph)



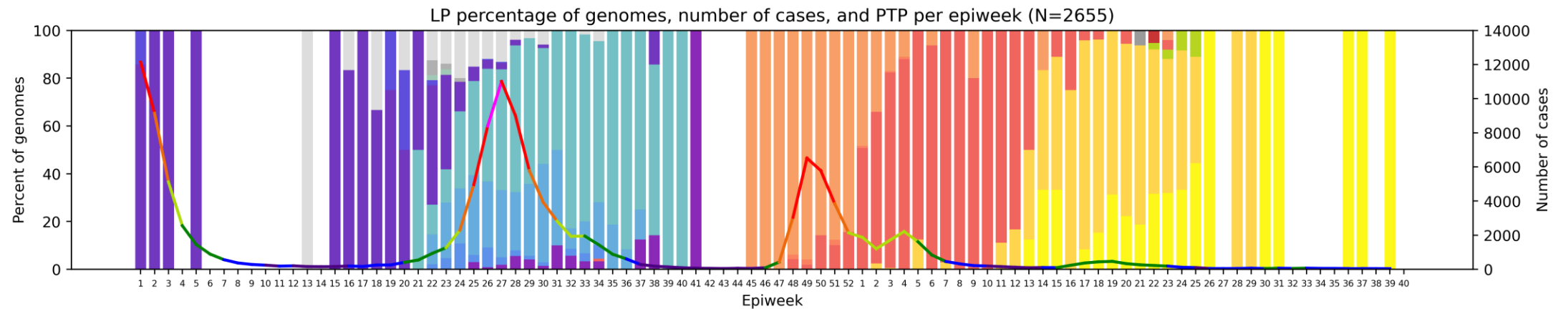
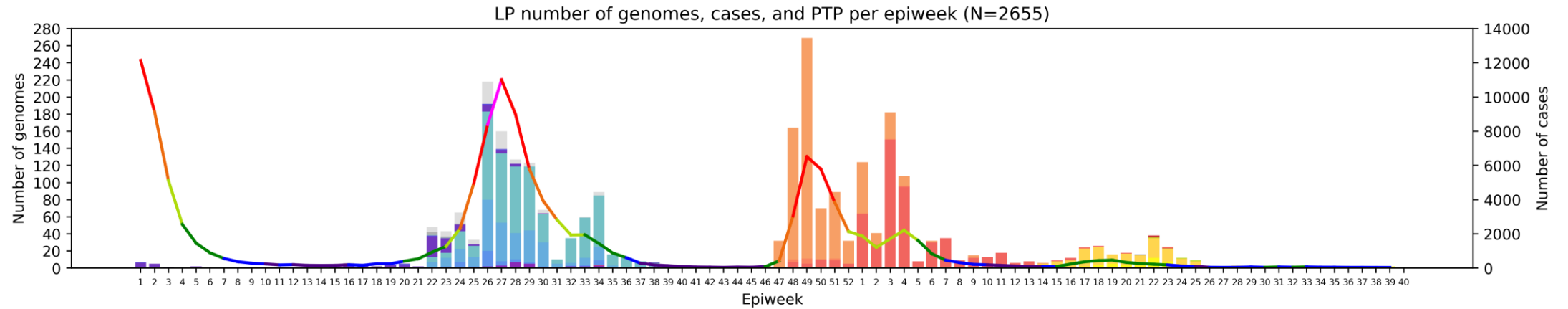
Weekly percentage testing positive key (line graph)



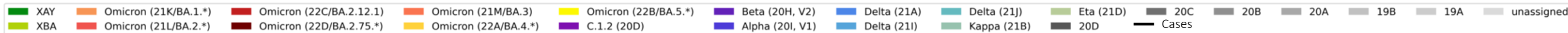
*May include genomes from 2020 which are not pictured here and are not included in the slide total.

Limpopo Province, 2021-2022, n = 2655

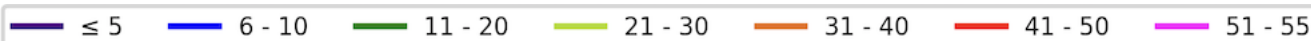
Genomes added since last report: 4*



Clade key (bar graph)



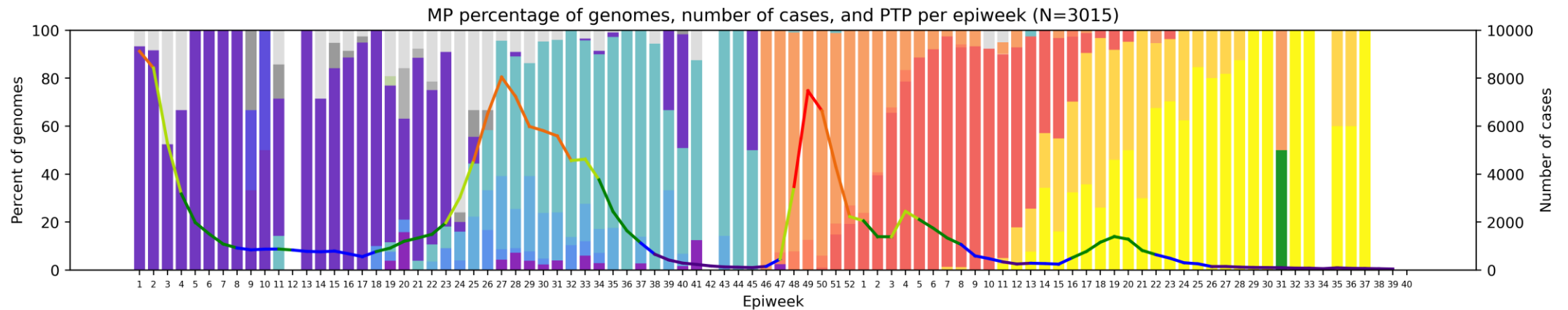
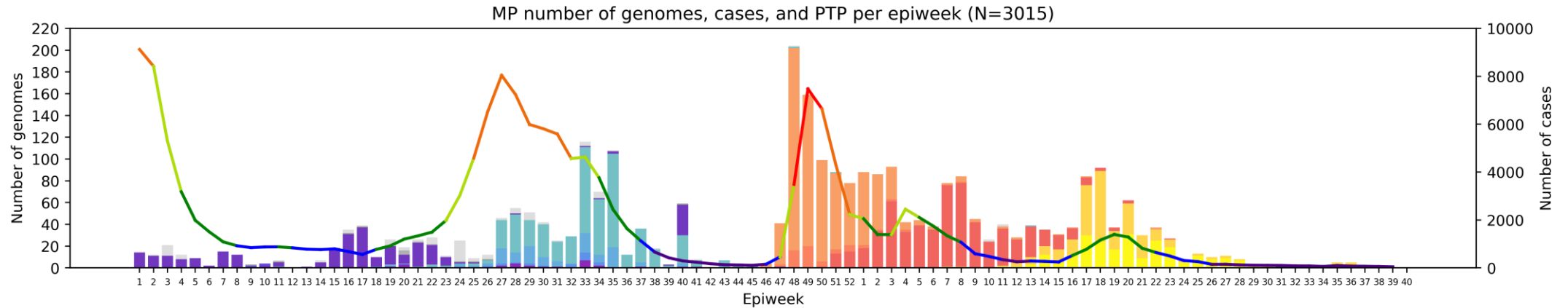
Weekly percentage testing positive key (line graph)



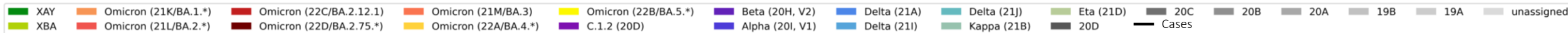
*May include genomes from 2020 which are not pictured here and are not included in the slide total.

Mpumalanga Province, 2021-2022, n = 3015

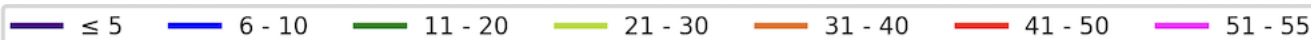
Genomes added since last report: 14*



Clade key (bar graph)



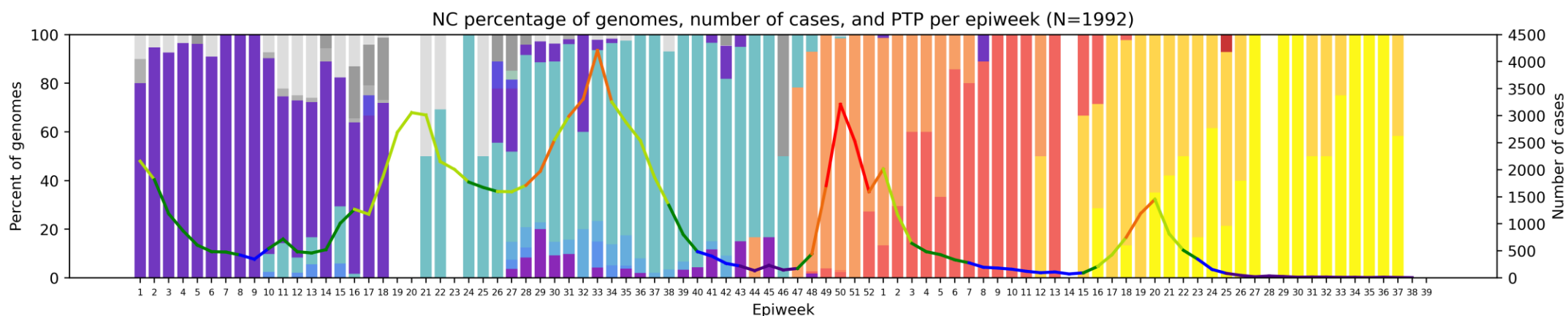
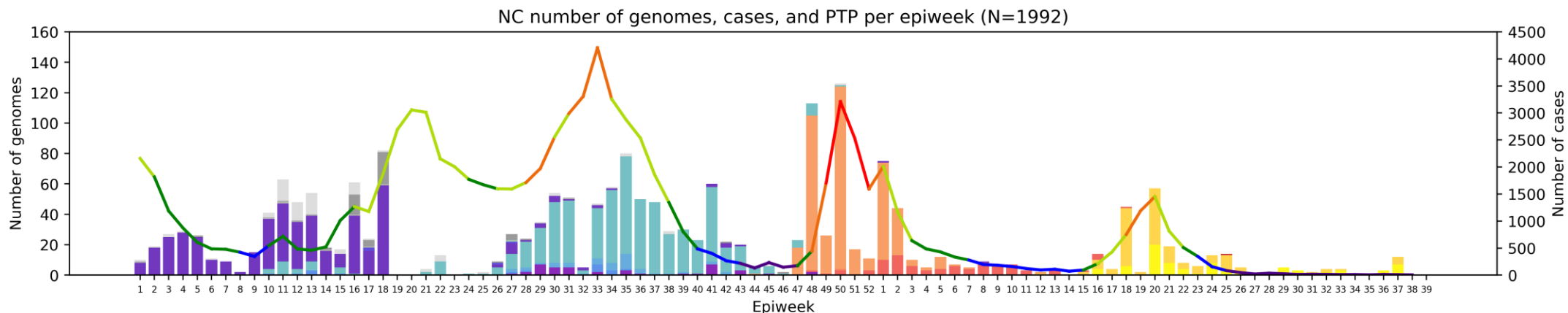
Weekly percentage testing positive key (line graph)



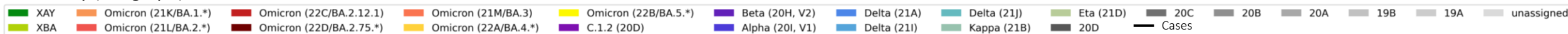
*May include genomes from 2020 which are not pictured here and are not included in the slide total.

Northern Cape Province, 2021-2022, n = 1992

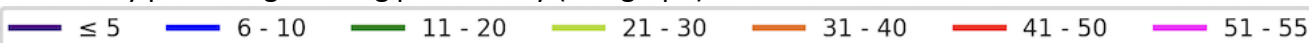
Genomes added since last report: 17*



Clade key (bar graph)



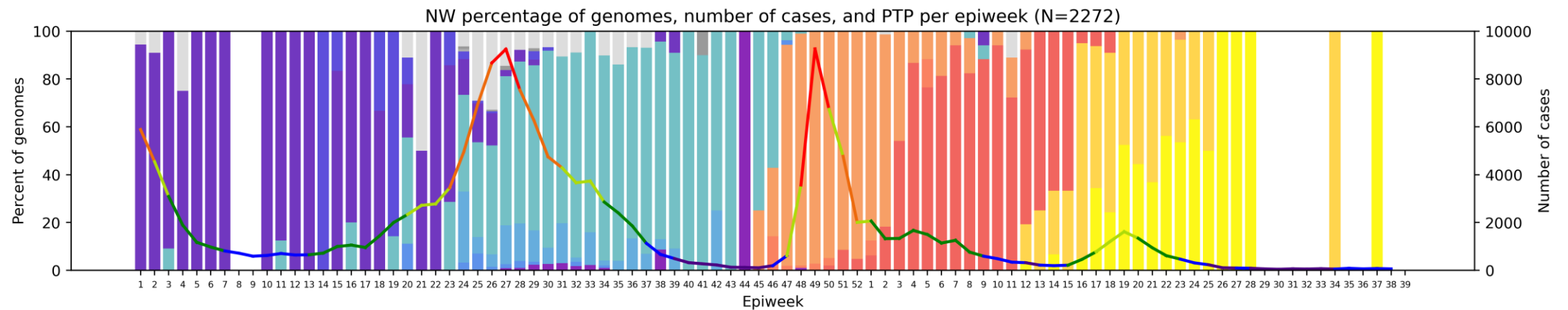
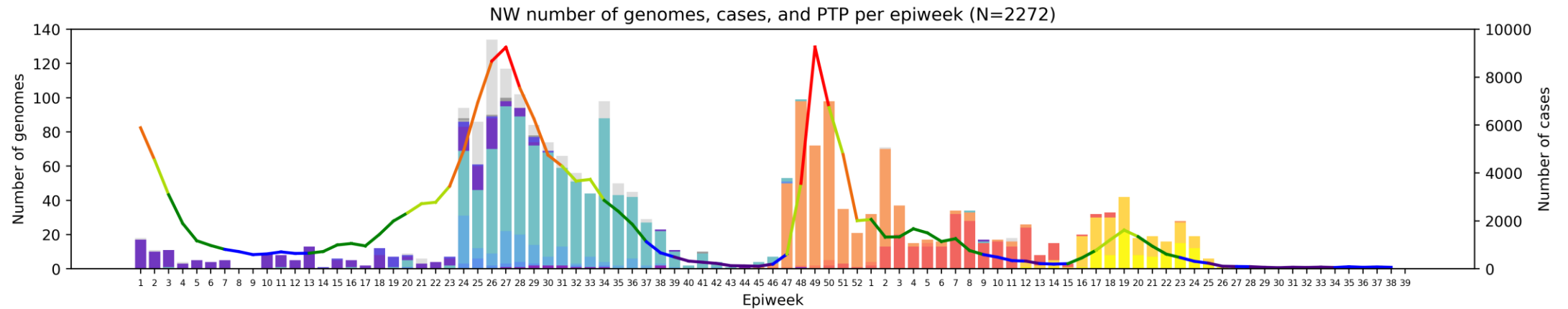
Weekly percentage testing positive key (line graph)



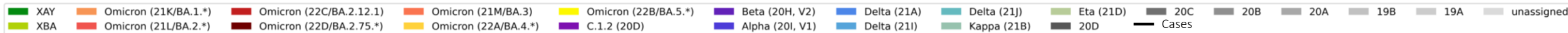
*May include genomes from 2020 which are not pictured here and are not included in the slide total.

North West Province, 2021-2022, n = 2272

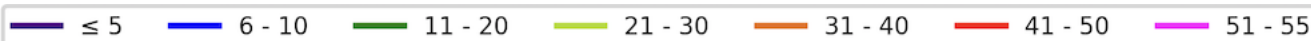
Genomes added since last report: 6*



Clade key (bar graph)



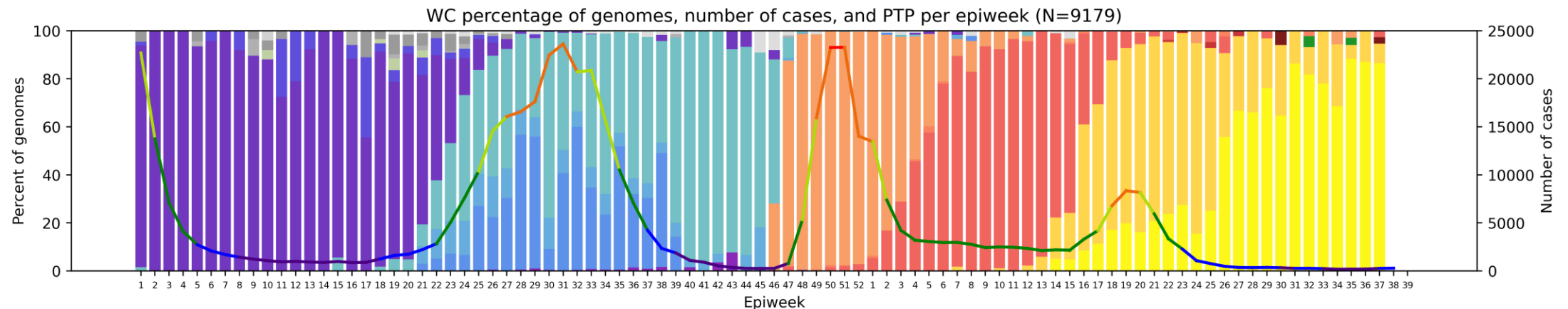
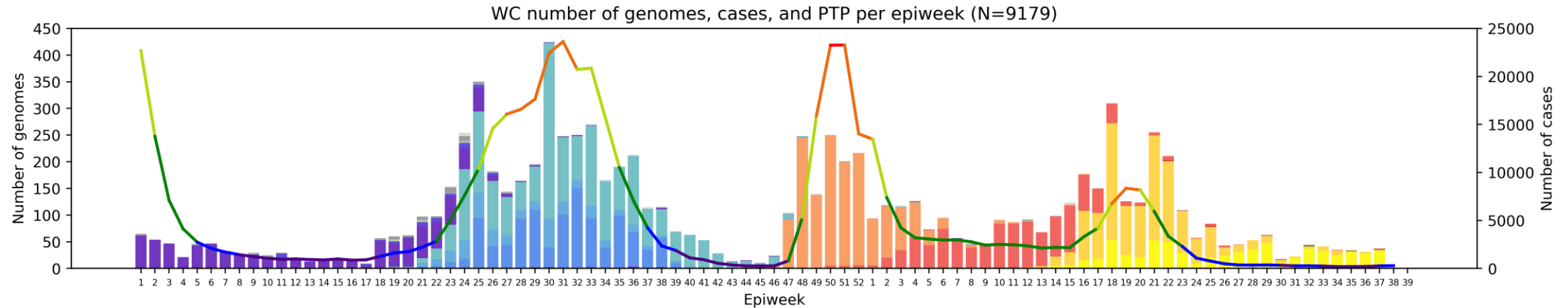
Weekly percentage testing positive key (line graph)



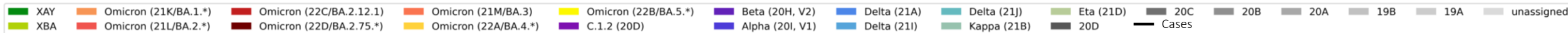
*May include genomes from 2020 which are not pictured here and are not included in the slide total.

Western Cape Province, 2021-2022, n = 9179

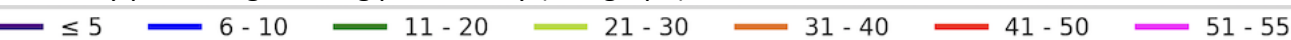
Genomes added since last report: 48*



Clade key (bar graph)



Weekly percentage testing positive key (line graph)



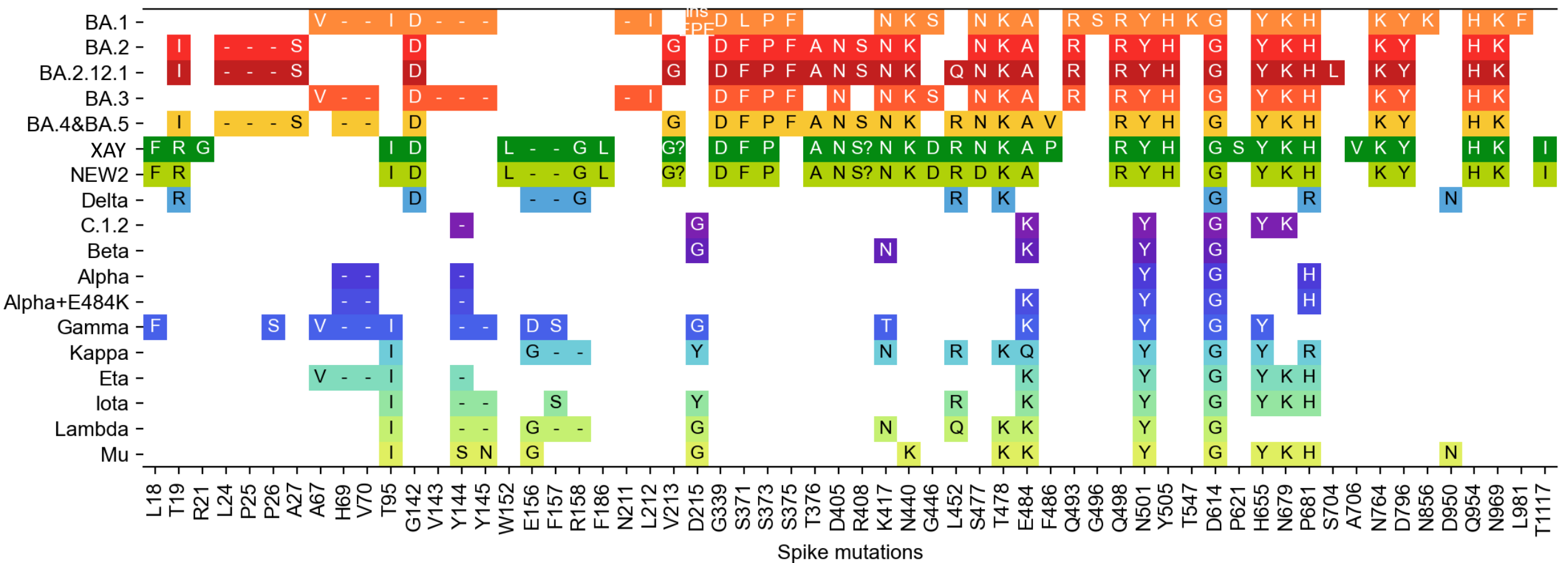
*May include genomes from 2020 which are not pictured here and are not included in the slide total.

Summary

- **Sequencing update**
 - All provinces have sequences for August and September.
- **Variant of Concern Omicron in South Africa**
 - Omicron continued to dominate in June (99%), July (99%), August (97%), and currently makes up 98% of September sequences.
 - Omicron BA.5 was dominant in July (68%) and August (69%), and makes up 79% of September data.
 - BA.2.12.1 was detected in South Africa at low prevalence in May, June and July (<1%)
 - BA.2.75.* has been detected in Western Cape, Gauteng and Kwa-Zulu Natal (n=5).
- **N=14 sequences with novel mutational profile**
 - The New1 cluster (n = 21, predominantly from Gauteng) has been designated “XAY”, and the New2 cluster (n = 4, Limpopo) has been designated “XBA”¹.
- Low frequency of previously circulating variants such as Delta not detected since July.

¹ <https://github.com/cov-lineages/pango-designation/issues/844>

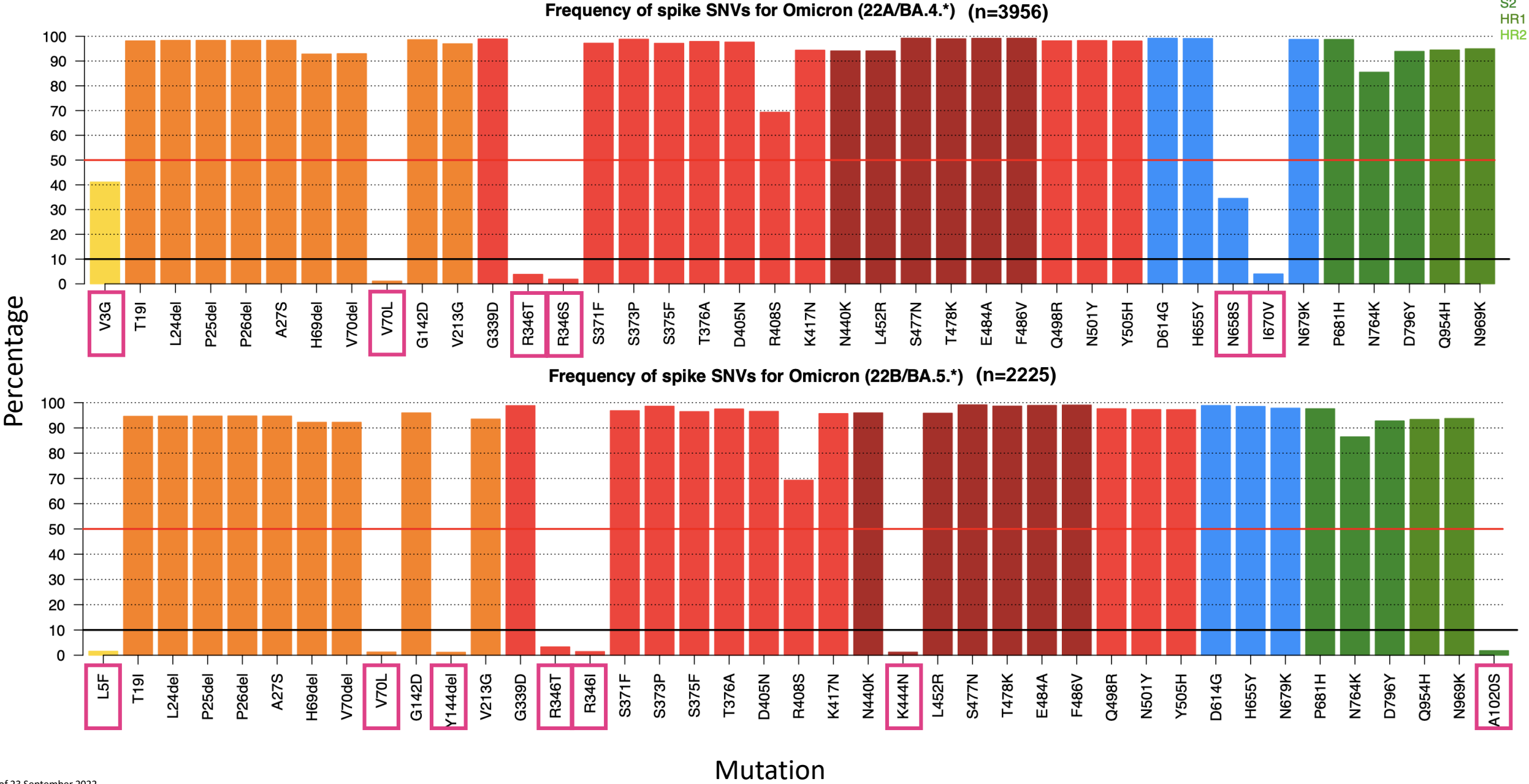
Spike protein mutation* profile of Variants of Interest and Concern



- 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

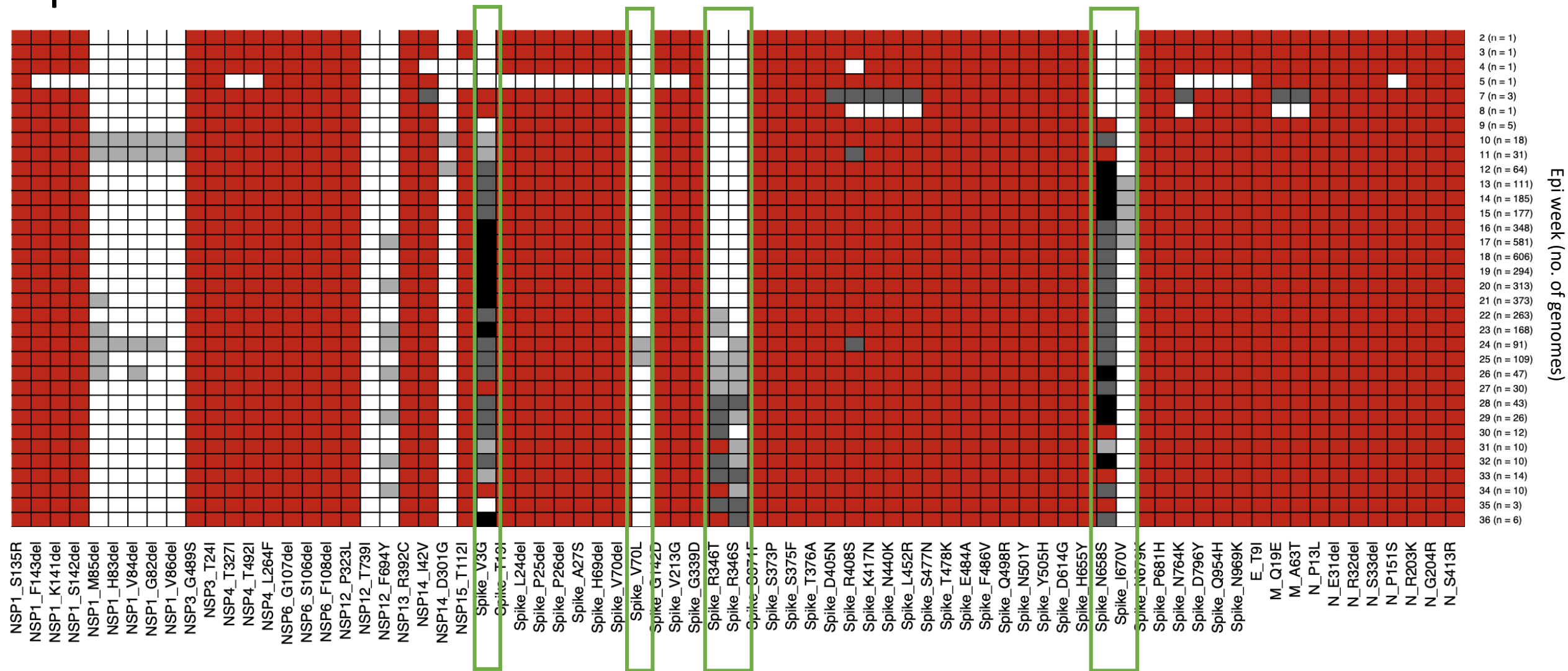
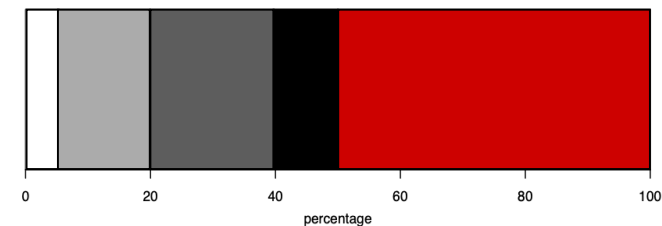
*Only mutations present in Omicron, Delta, or the new SGTP sequences are pictured

BA.4 and BA.5 spike mutations

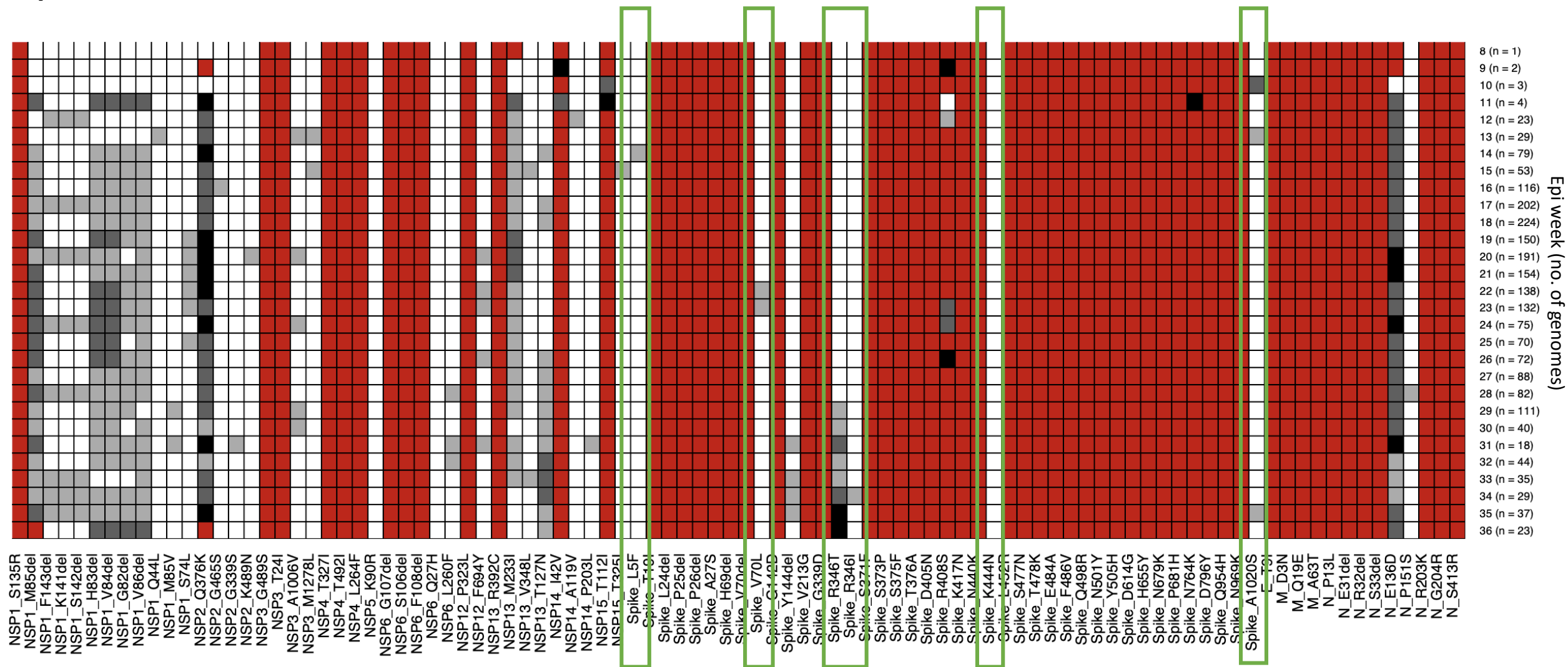
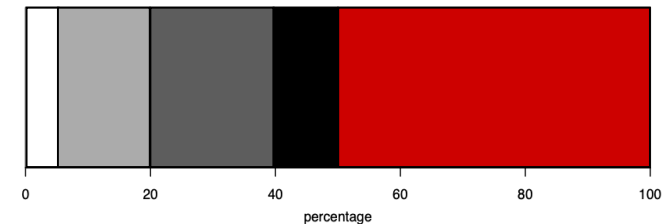


*as of 23 September 2022

BA.4 whole genome mutation prevalence over time



BA.5 whole genome mutation prevalence over time





Supported by the DSI and the SA MRC



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EDCTP

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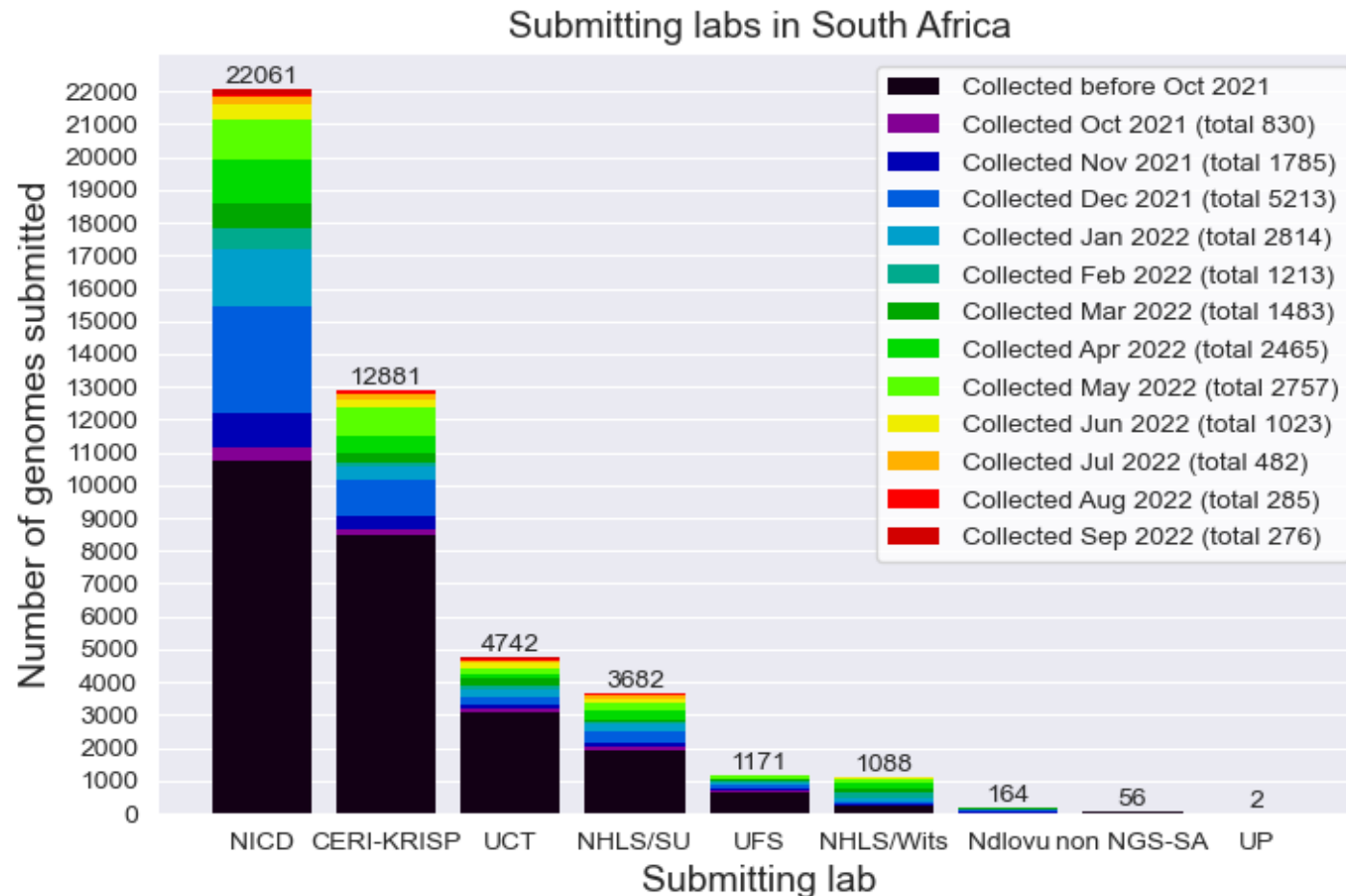
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SA MRC

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South African genomes submitted per submitting lab, 2020 - 2022 (N=45 847)



NGS-SA Labs

CERi: Centre for Epidemic Response and Innovation

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.

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
Omicron*	B.1.1.529	GR/484A	21K, 21L, 21M, 22A, 22B, 22C, 22D	+S:R346K +S:L452X +S:F486V	Multiple countries, Nov-2021	VUM: 24-Nov-2021 VOC: 26-Nov-2021

* Includes BA.1, BA.2, BA.3, BA.4, BA.5 and descendent lineages. It also includes BA.1/BA.2 circulating recombinant forms such as XE. WHO emphasizes that these descendant lineages should be monitored as distinct lineages by public health authorities and comparative assessments of their virus characteristics should be undertaken.

• 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
Delta	B.1.617.2	G/478K.V1	21A, 21I, 21J	India, Oct-2020	VOI: 4-Apr-2021 VOC: 11-May-2021 Previous VOC: 7-Jun-2022

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

<https://www.who.int/en/activities/tracking-SARS-CoV-2-variants/> accessed 12 August 2022

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.)