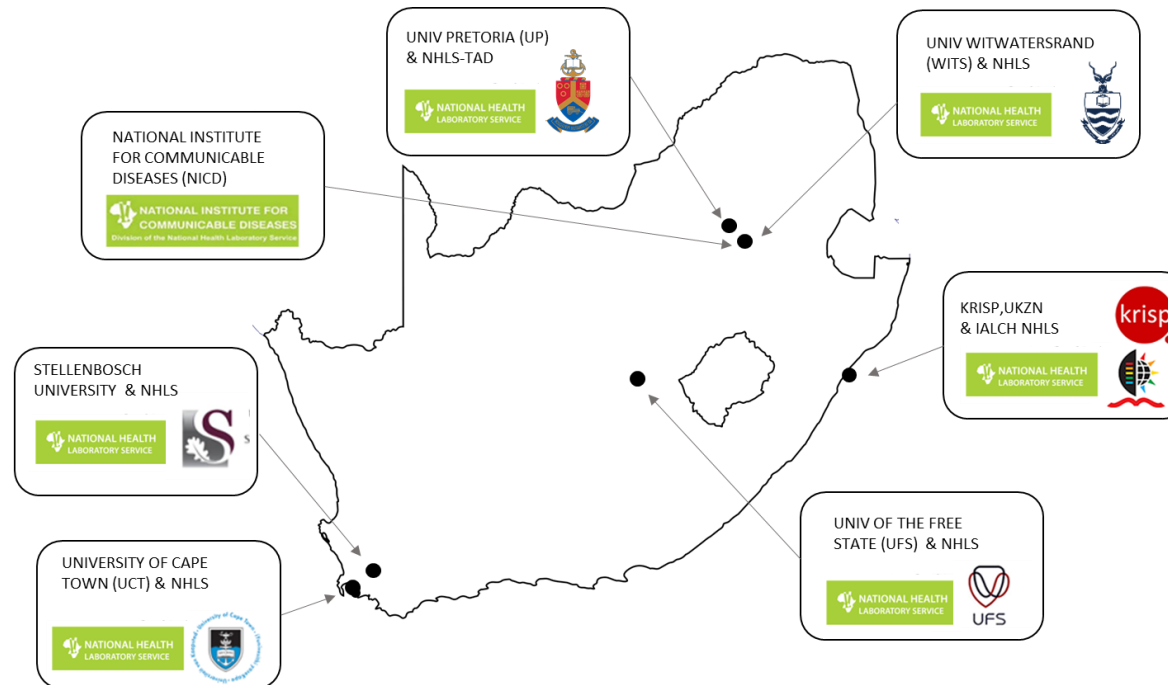


## SARS-CoV-2 Sequencing Update 22 April 2022



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](http://www.gisaid.org)) on 21 April 2022 at 22h10

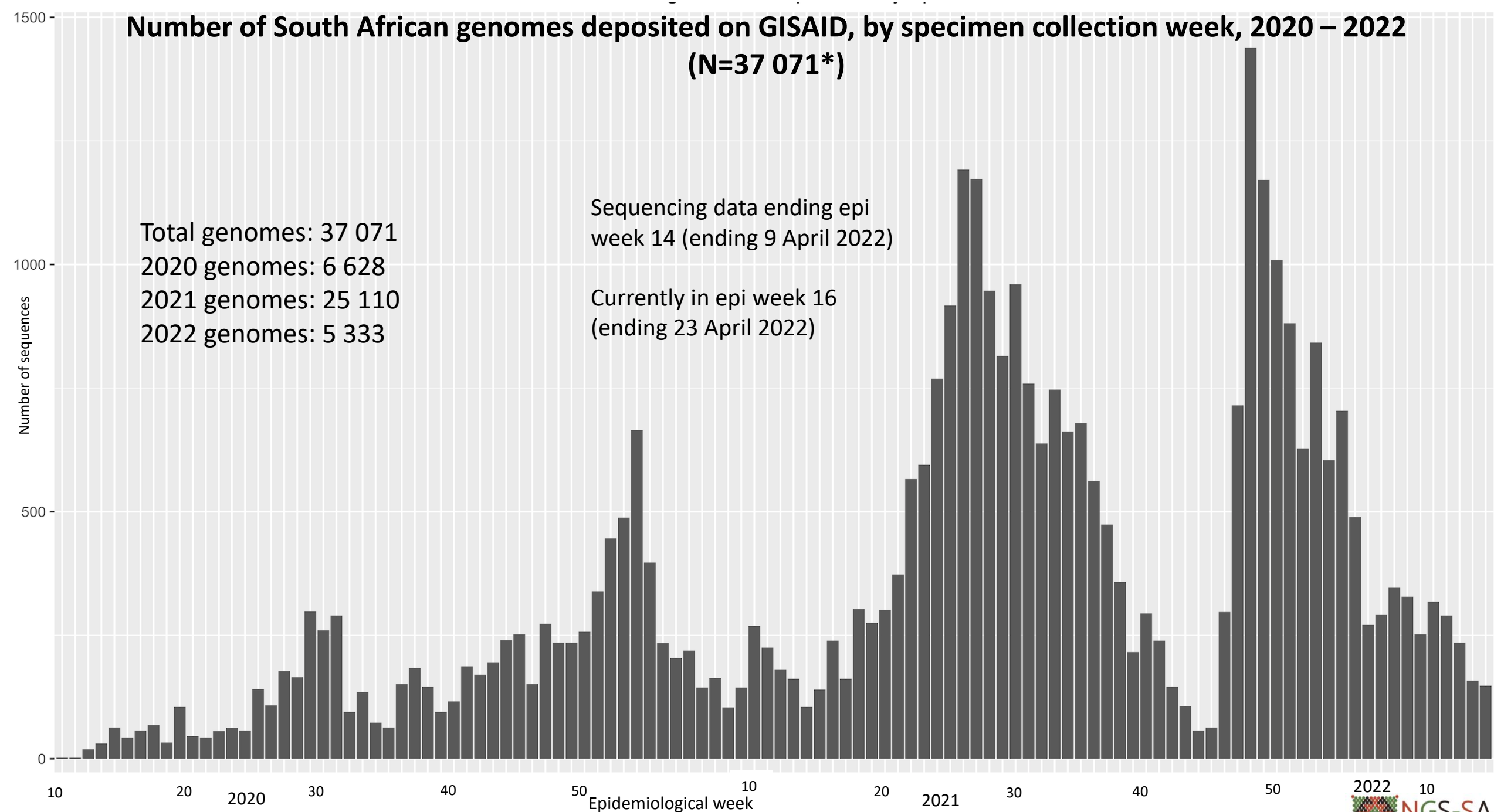


Data license: <https://www.gisaid.org/registration/terms-of-use/>

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

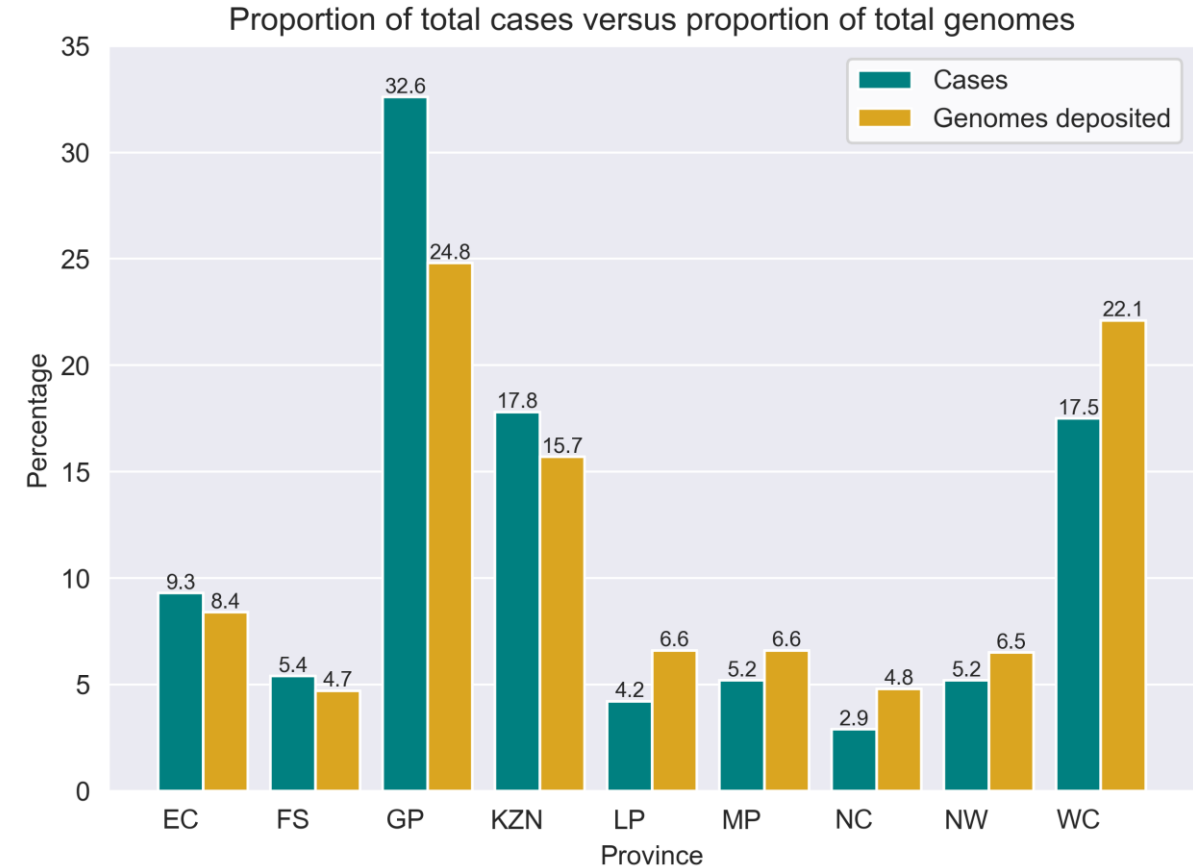
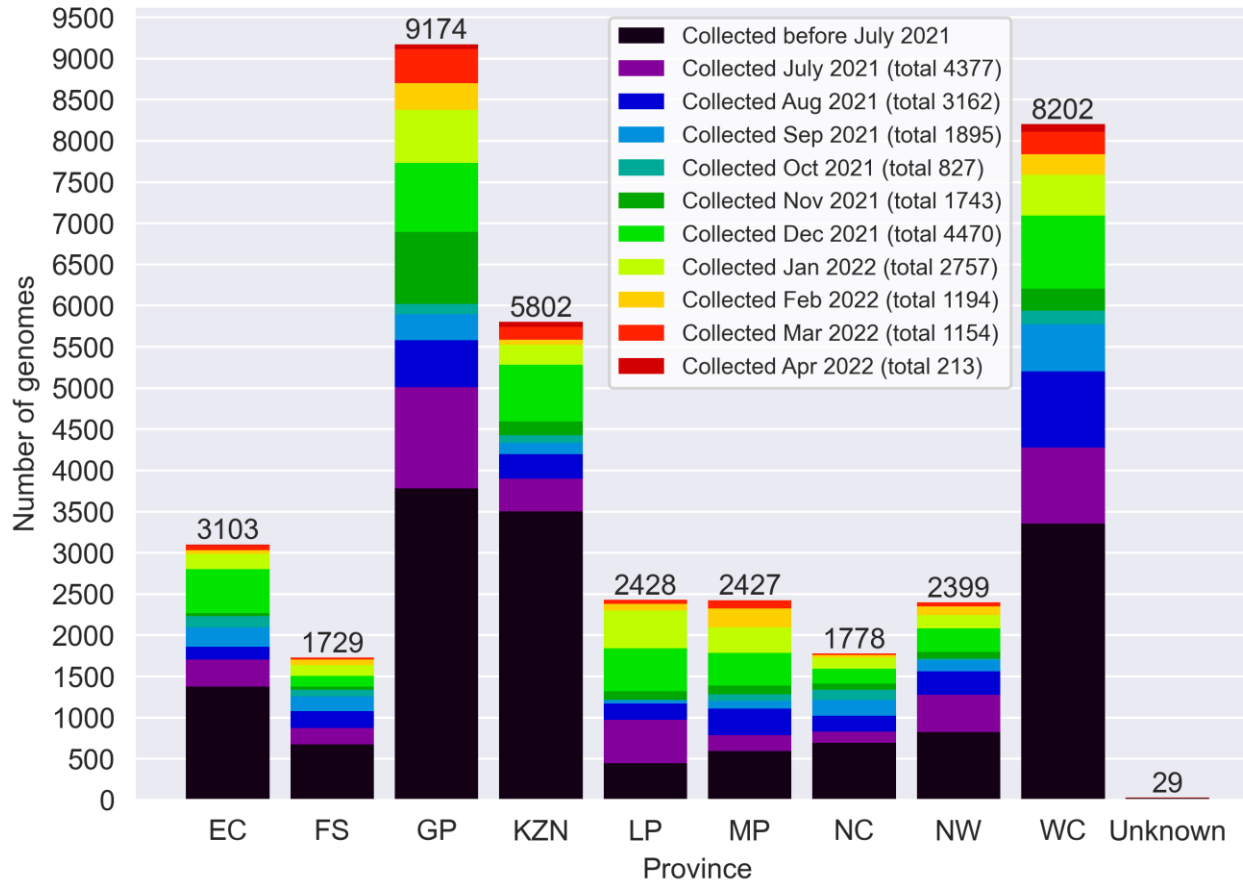
# Number of South African genomes deposited on GISAID, by specimen collection week, 2020 – 2022 (N=37 071\*)



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

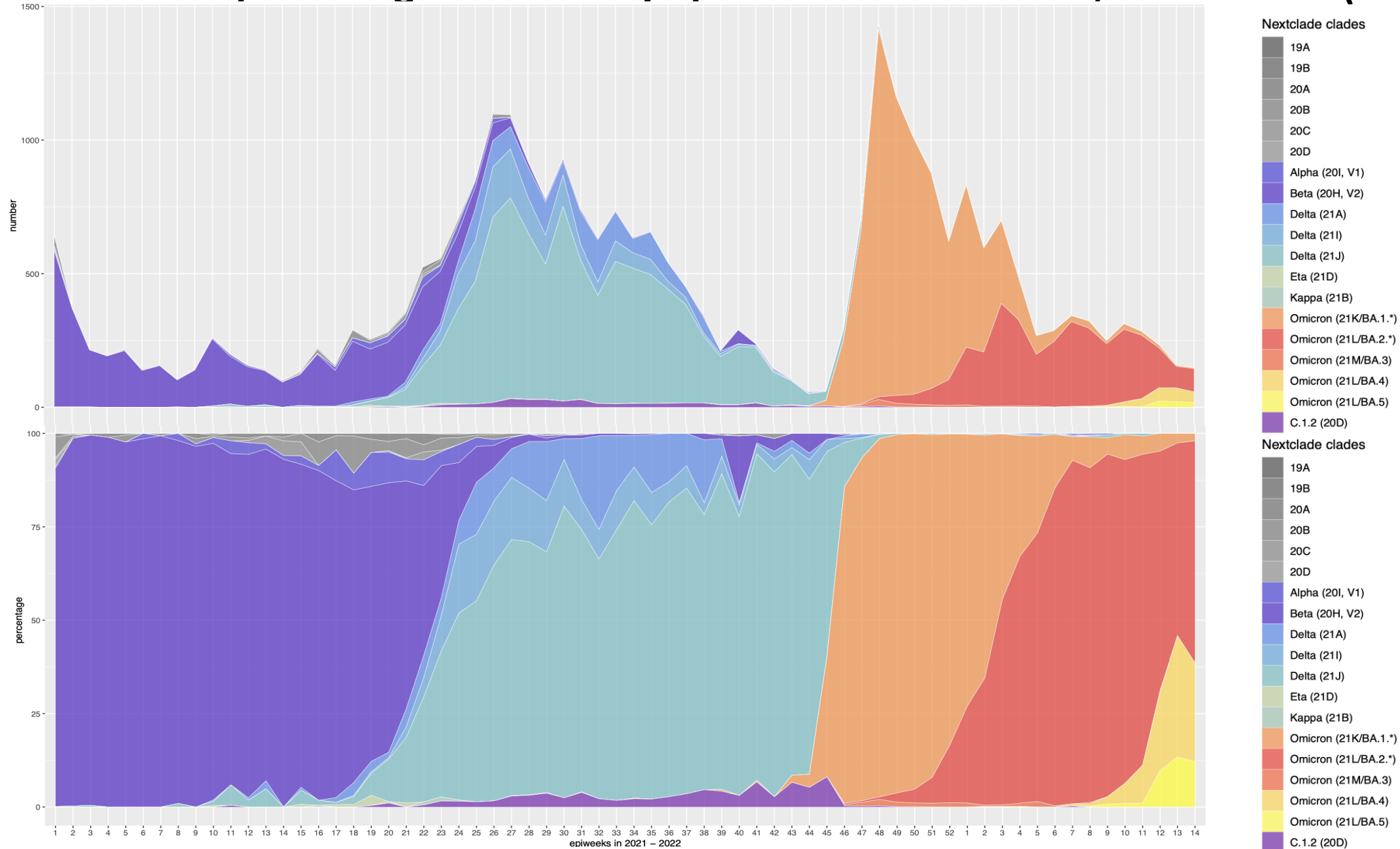
# GISAID genomes vs total cases, 2020 – 2022 (N=37 071)

Provincial breakdown of genomes deposited into GISAID



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

# Number and percentage of clades by epiweek in South Africa, 2021 – 2022 (30 358)



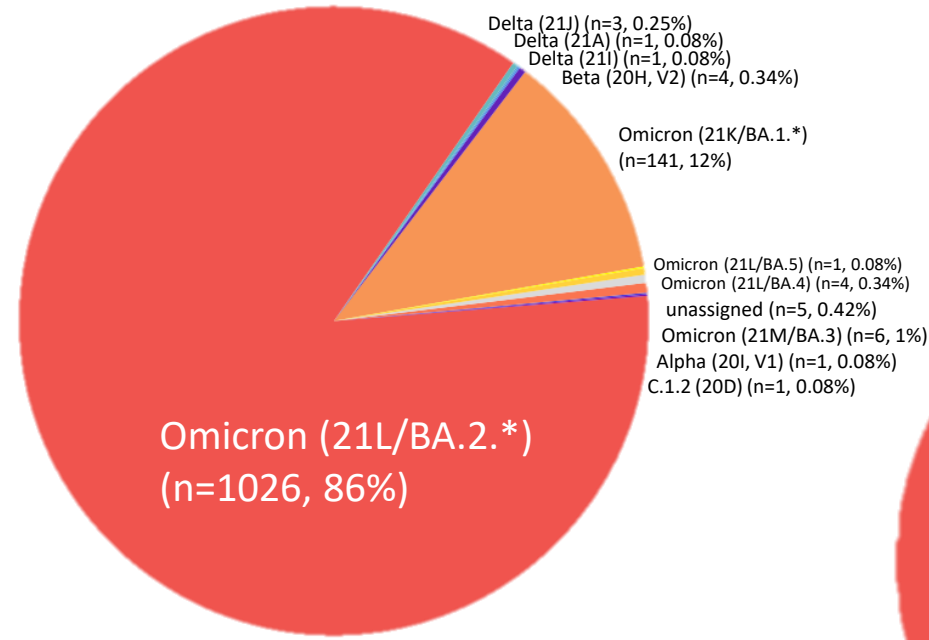
Sequencing data  
ending epi week 14  
(ending 9 April  
2022)

Currently in epi  
week 16 (ending 23  
April 2022)

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

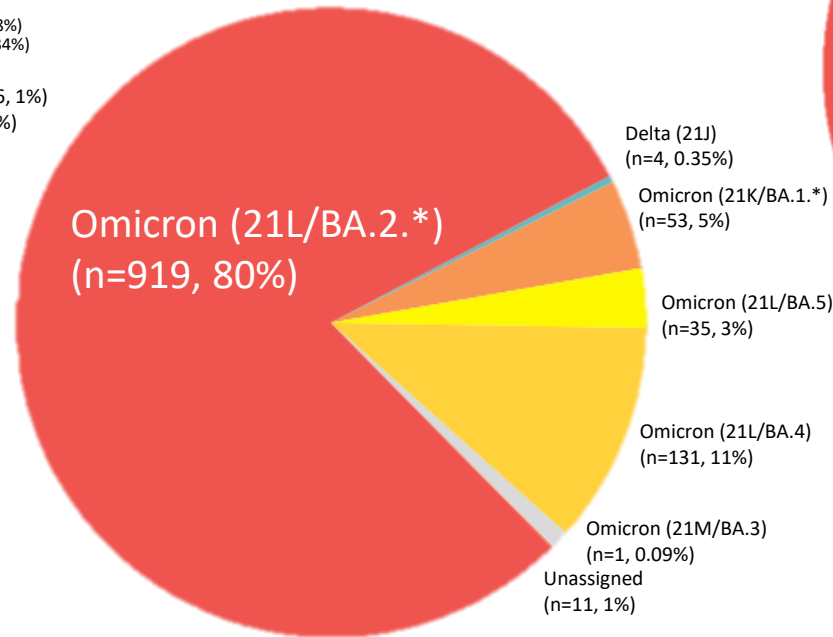
# Prevalence of Variants of Concern (VOC) and Variants of Interest (VOI) in Feb – Apr 2022

February (N=1194)



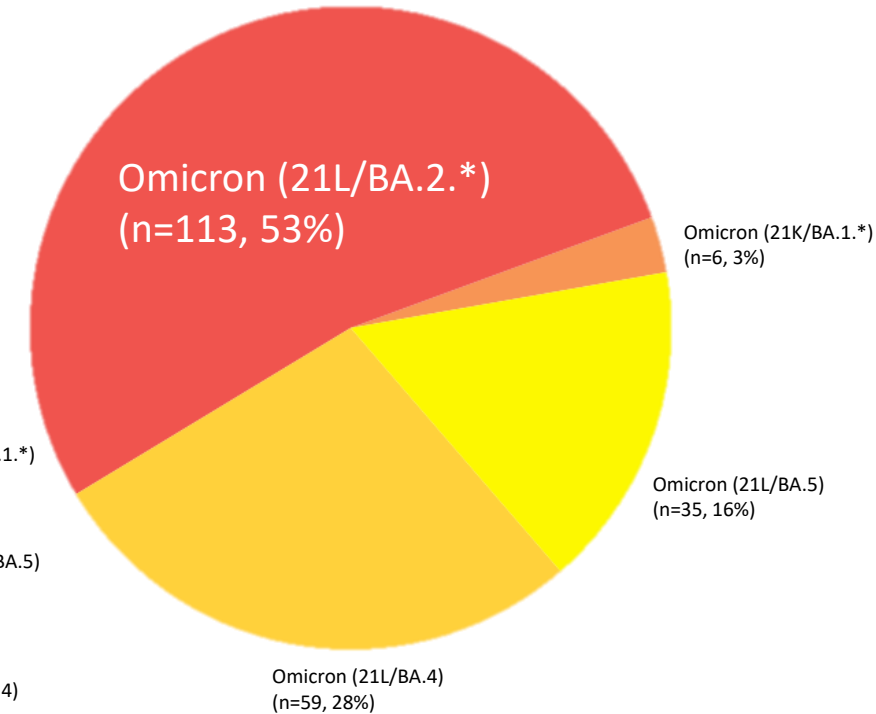
Total Omicron in Feb: 1178 (98.6%)

March (N=1154)



Total Omicron in Mar: 1139 (98.7%)

April (N=213)



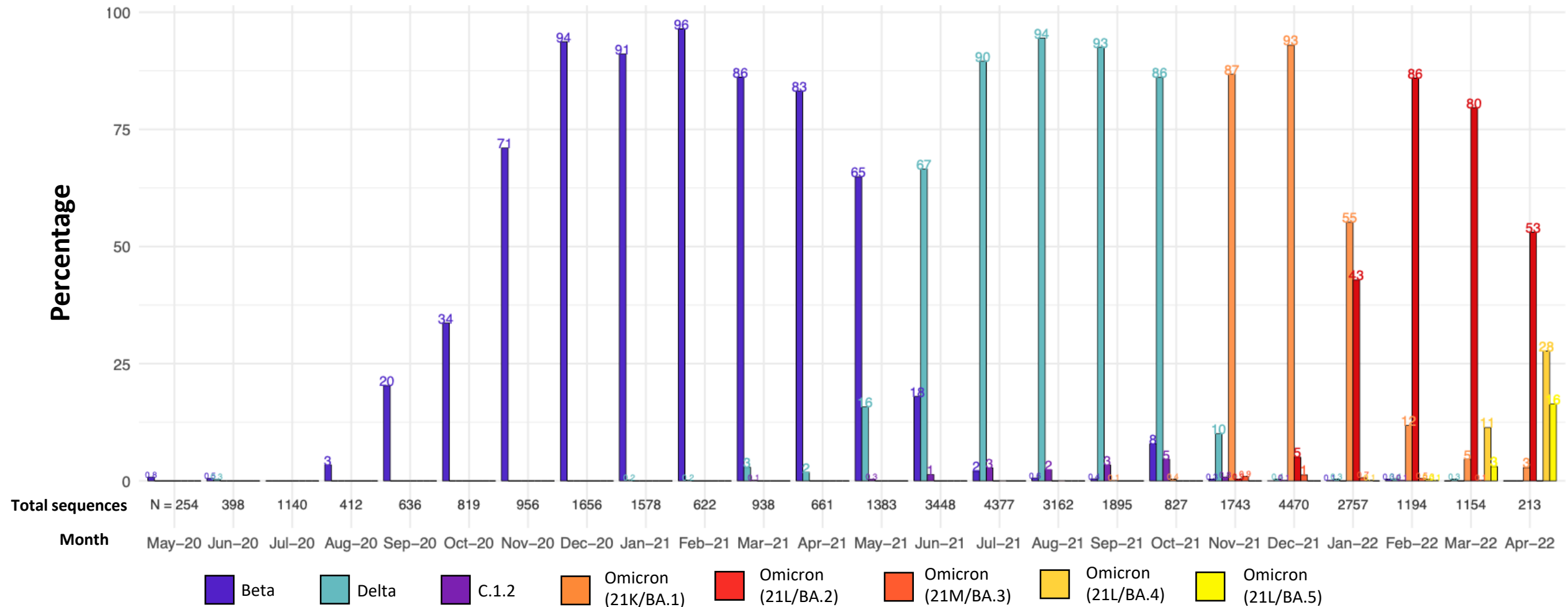
Total Omicron in Apr: 213 (100%)



Omicron dominated in February (98.6%, 1178/1194), March (90%, 1039/1154) and April (100%, 213/213), . BA.2 increased was dominant in February and March while the prevalence of the newly assigned BA.4 and BA5 lineages increasing from February to April.

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

Detection rates of variants being monitored in South Africa



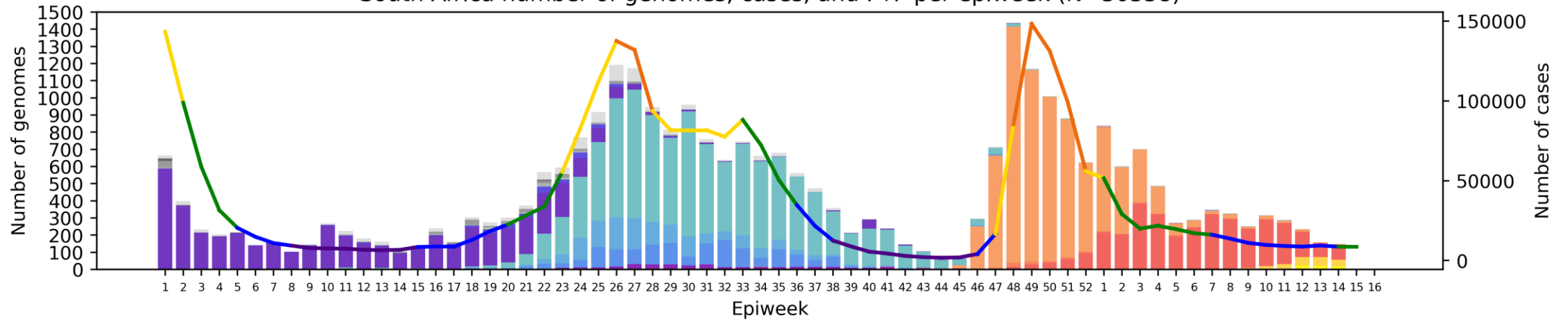
\*Bars represent percentage prevalence of variant for the month; total number sequences collected for the month are given below the bar

**Omicron has been dominant since November (>85% in November, >98% in December, January, February and March). BA.2 made up 43% of genomes in January, 86% in February, 80% in March and 53% in April. Newly designated sub-lineages BA.4 and BA.5 steadily increasing in April.**

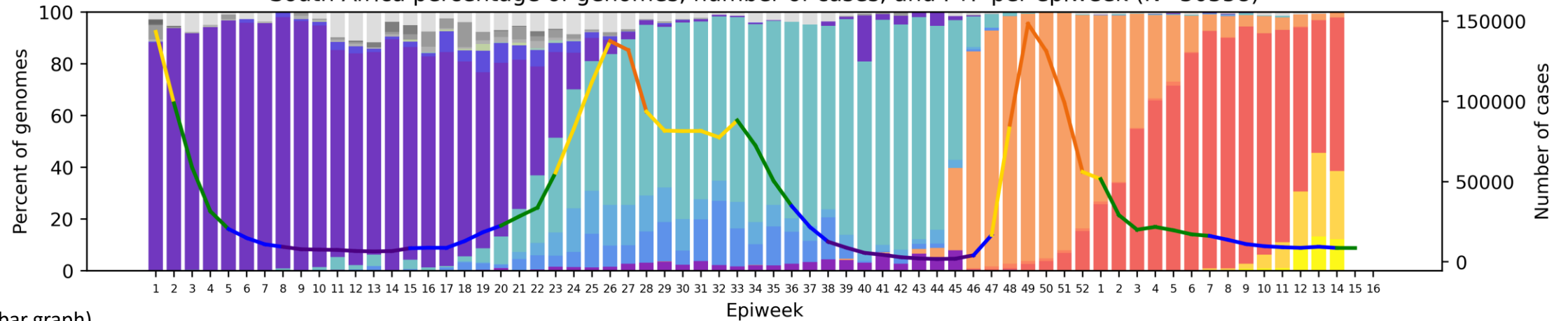


# South Africa, 2021-2022, n = 30358\*

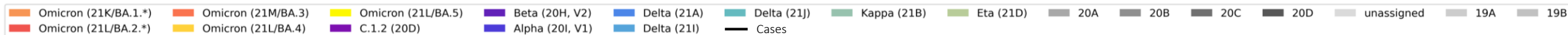
South Africa number of genomes, cases, and PTP per epiweek (N=30358)



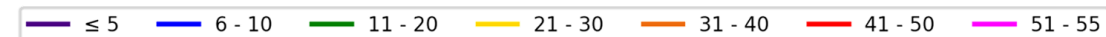
South Africa percentage of genomes, number of cases, and PTP per epiweek (N=30358)



Clade key (bar graph)



Weekly percentage testing positive key (line graph)

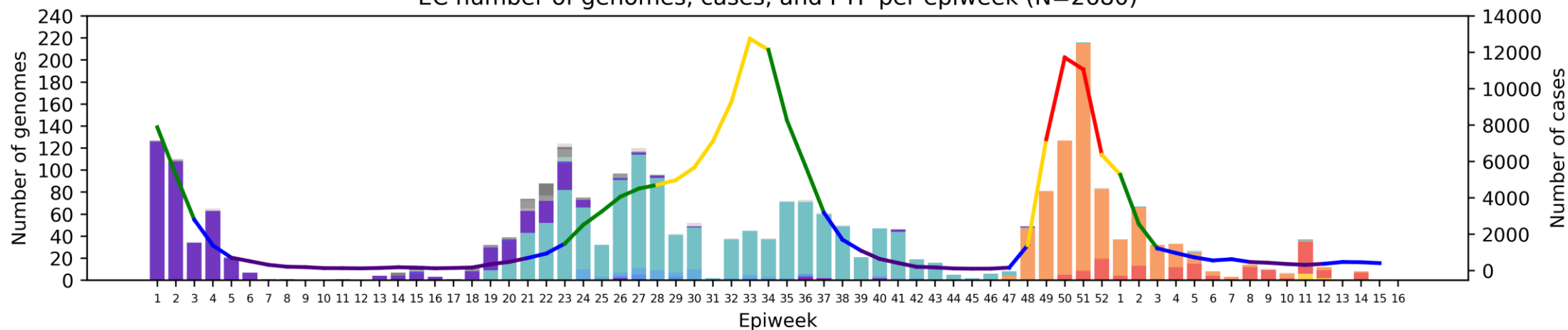


\*Excludes sequences missing collection dates, as well as those collected January 1<sup>st</sup> and 2<sup>nd</sup> 2021 as they are part of epiweek 53 of 2020.

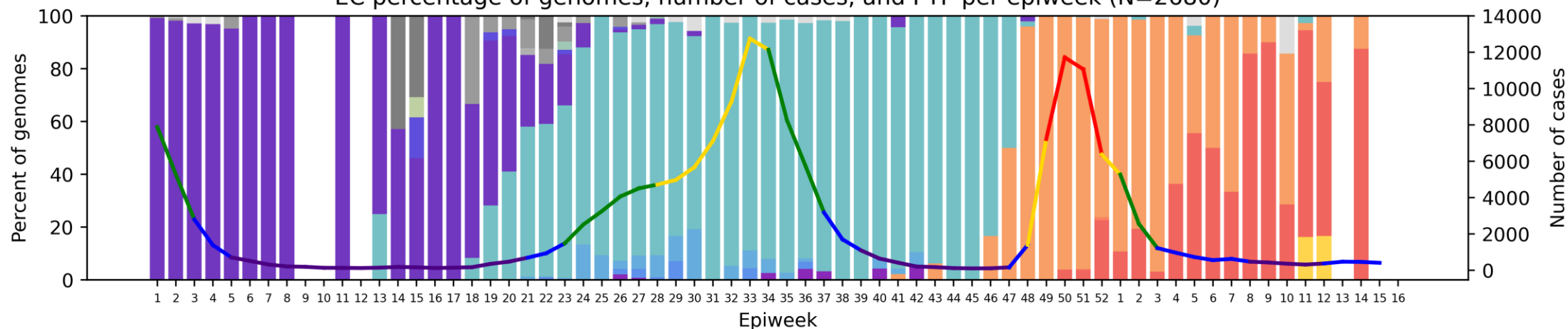


# Eastern Cape Province, 2021-2022, n = 2680

EC number of genomes, cases, and PTP per epiweek (N=2680)



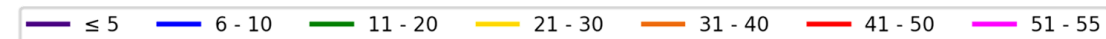
EC percentage of genomes, number of cases, and PTP per epiweek (N=2680)



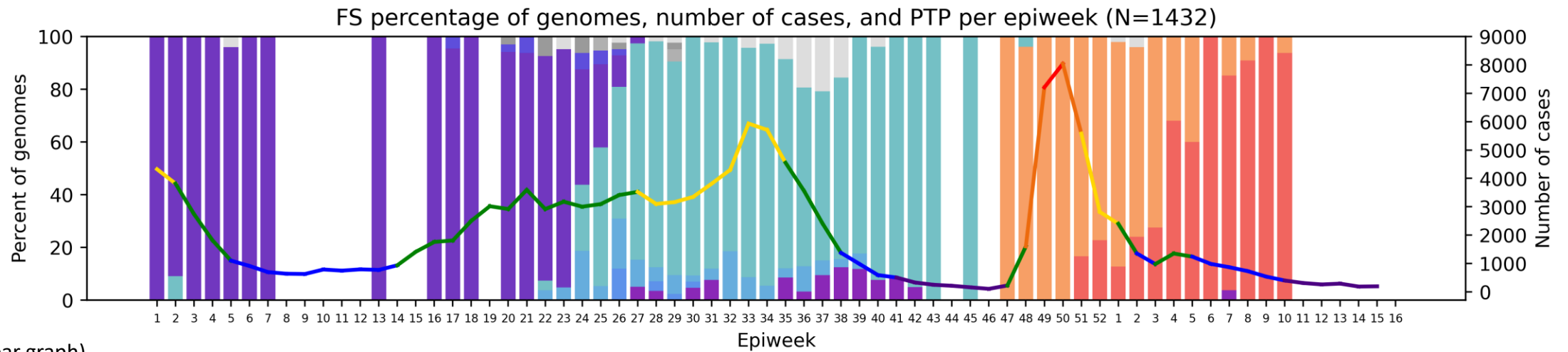
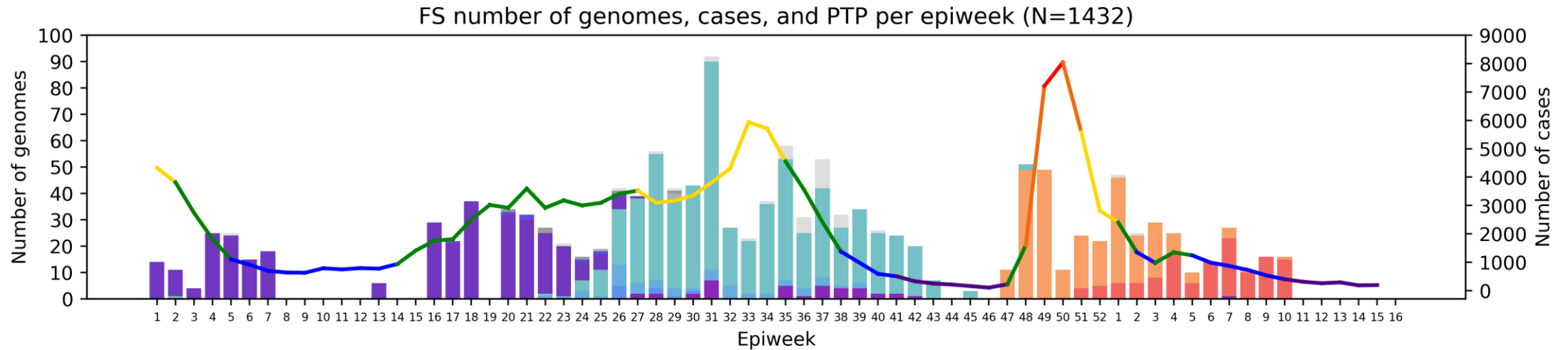
Clade key (bar graph)



Weekly percentage testing positive key (line graph)



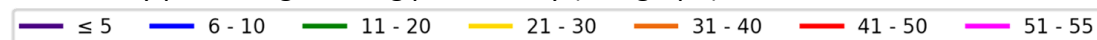
# Free State Province, 2021-2022, n = 1432



Clade key (bar graph)

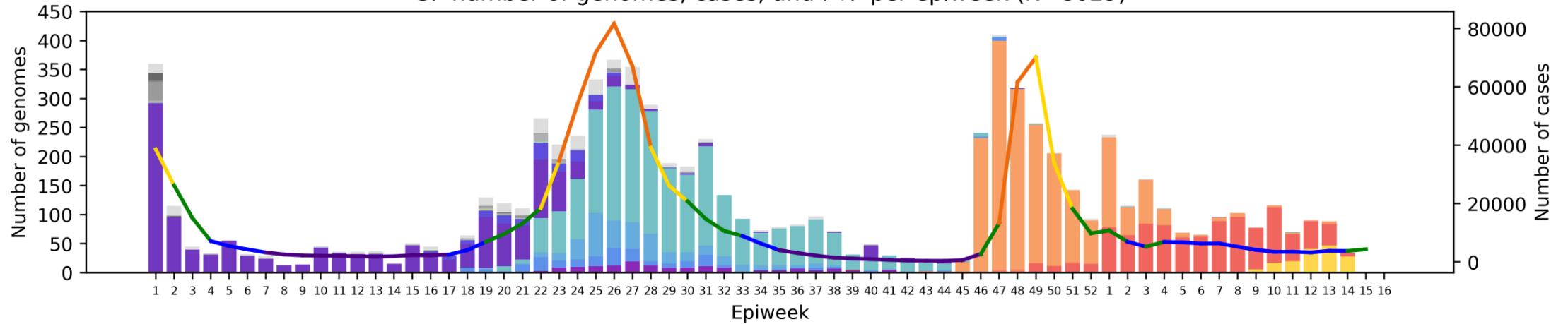


Weekly percentage testing positive key (line graph)

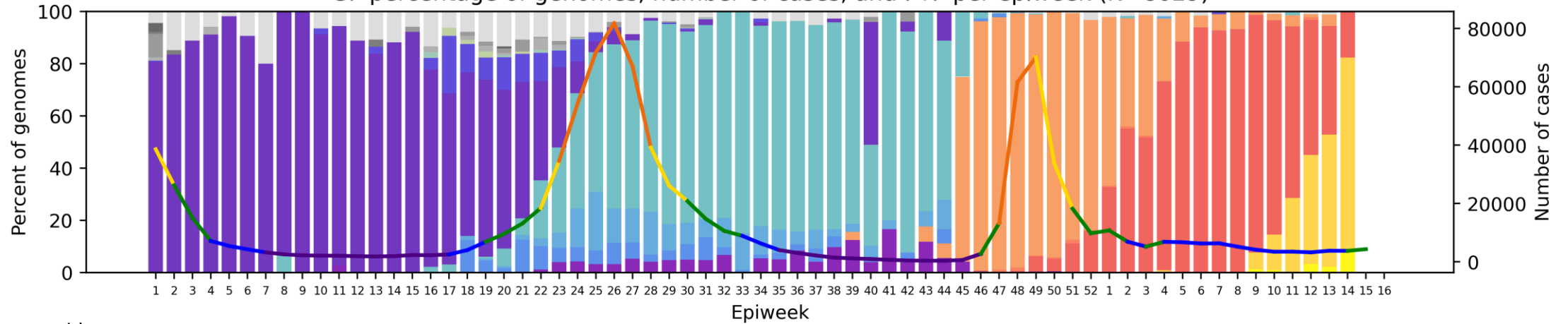


# Gauteng Province, 2021-2022, n = 8029

GP number of genomes, cases, and PTP per epiweek (N=8029)



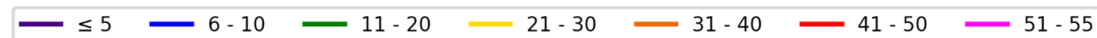
GP percentage of genomes, number of cases, and PTP per epiweek (N=8029)



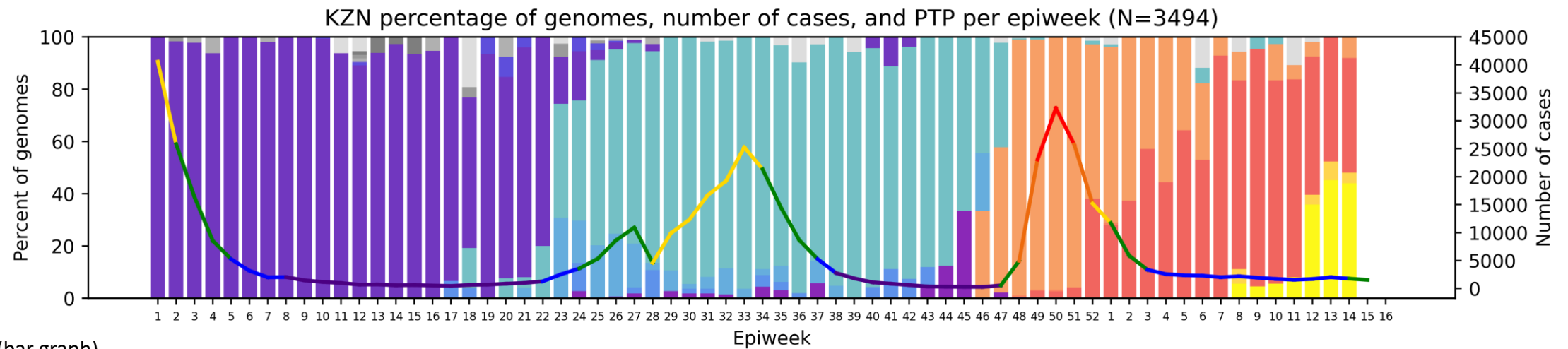
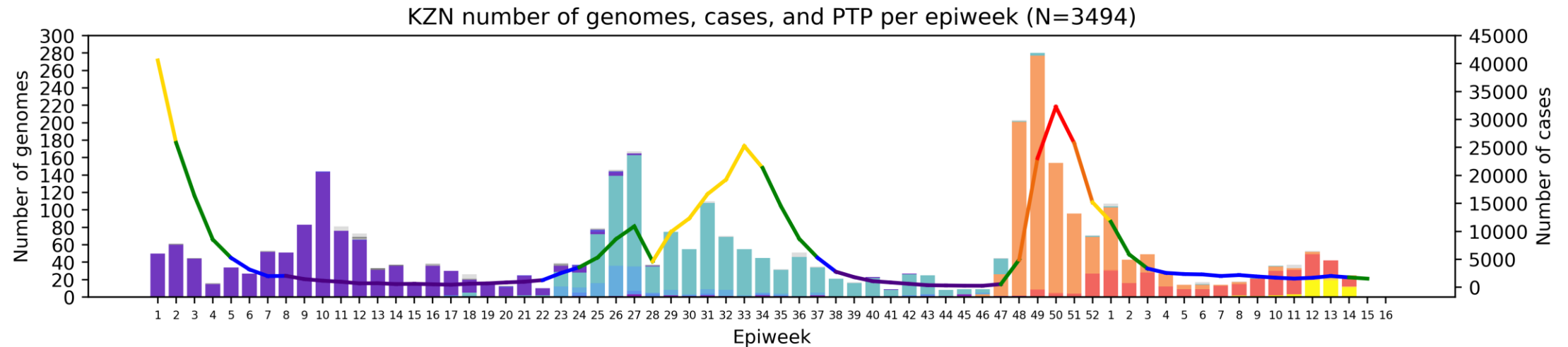
Clade key (bar graph)



Weekly percentage testing positive key (line graph)



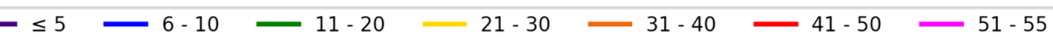
# KwaZulu-Natal Province, 2021-2022, n = 3494



Clade key (bar graph)

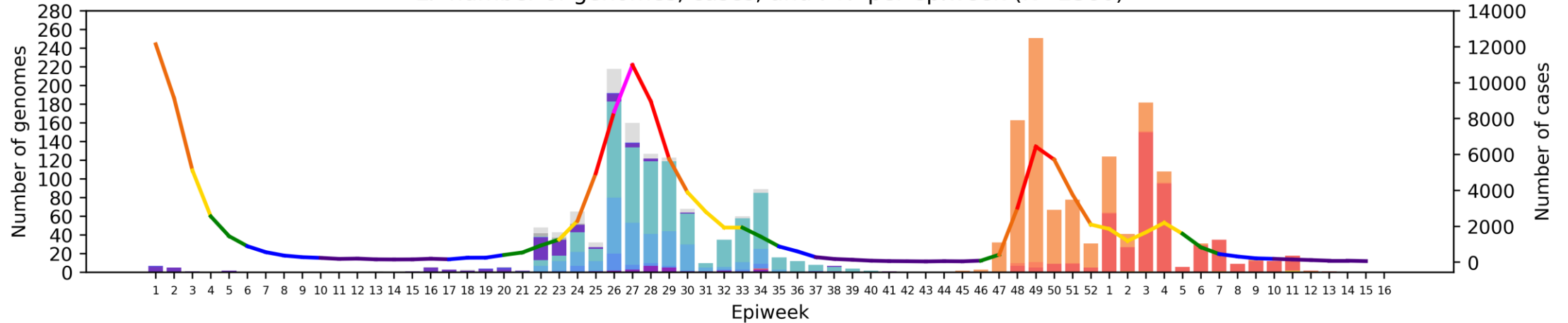


Weekly percentage testing positive key (line graph)

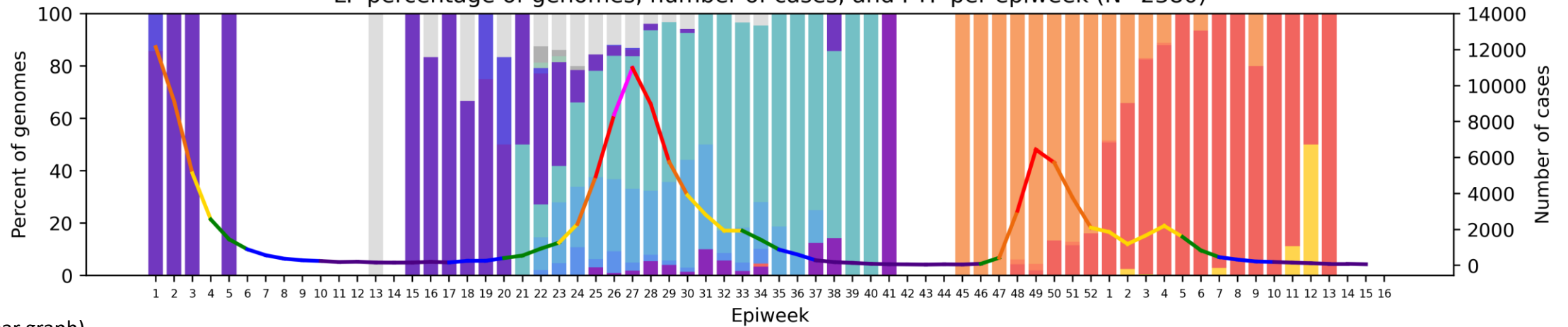


# Limpopo Province, 2021-2022, n = 2380

LP number of genomes, cases, and PTP per epiweek (N=2380)



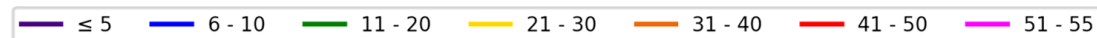
LP percentage of genomes, number of cases, and PTP per epiweek (N=2380)



Clade key (bar graph)

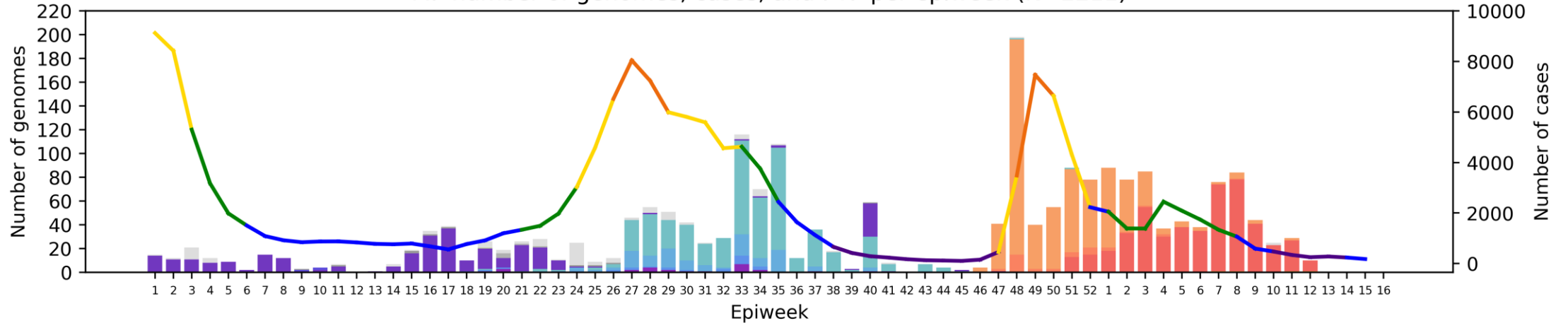


Weekly percentage testing positive key (line graph)

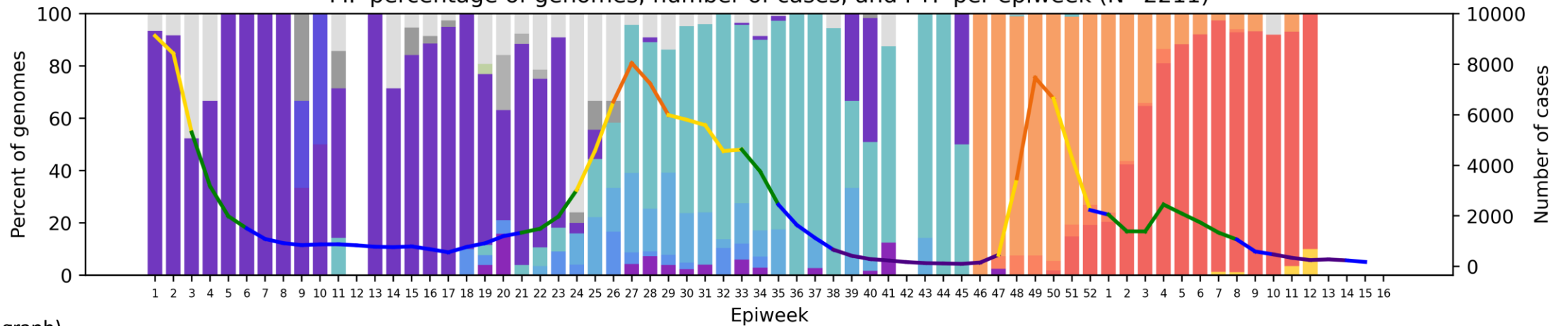


# Mpumalanga Province, 2021-2022, n = 2211

MP number of genomes, cases, and PTP per epiweek (N=2211)



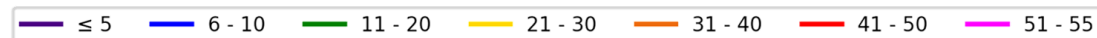
MP percentage of genomes, number of cases, and PTP per epiweek (N=2211)



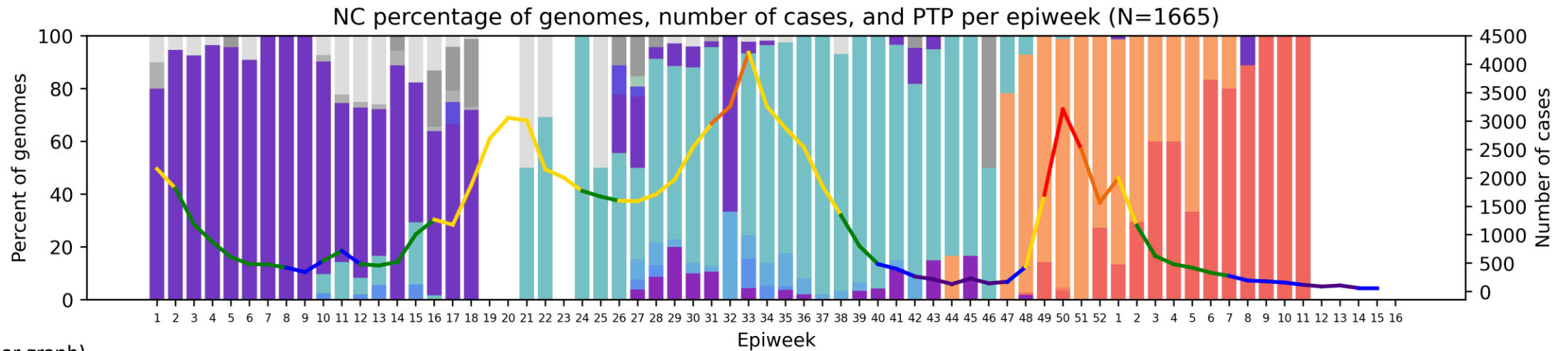
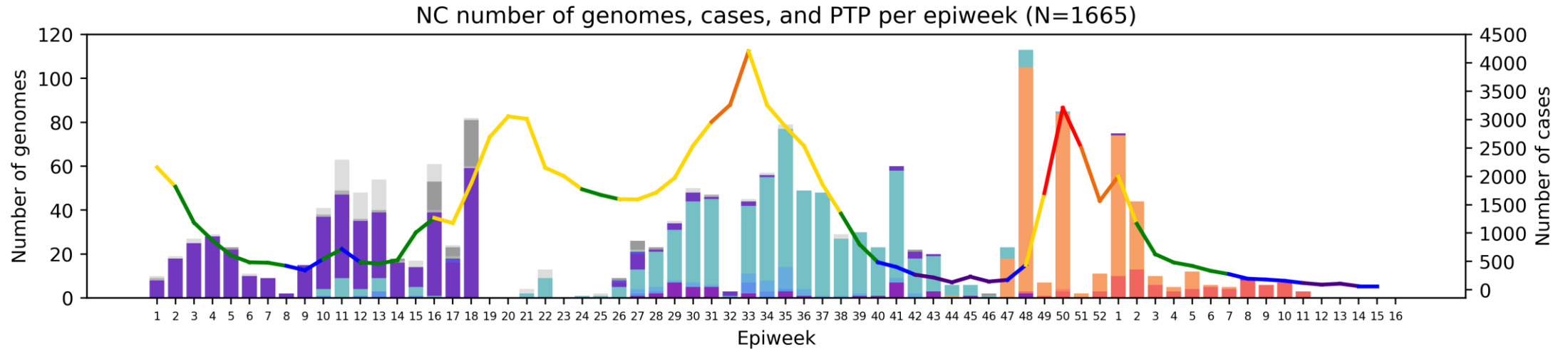
Clade key (bar graph)



Weekly percentage testing positive key (line graph)



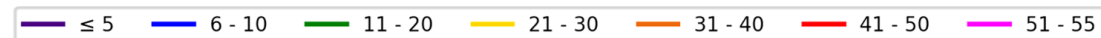
# Northern Cape Province, 2021-2022, n = 1665



Clade key (bar graph)

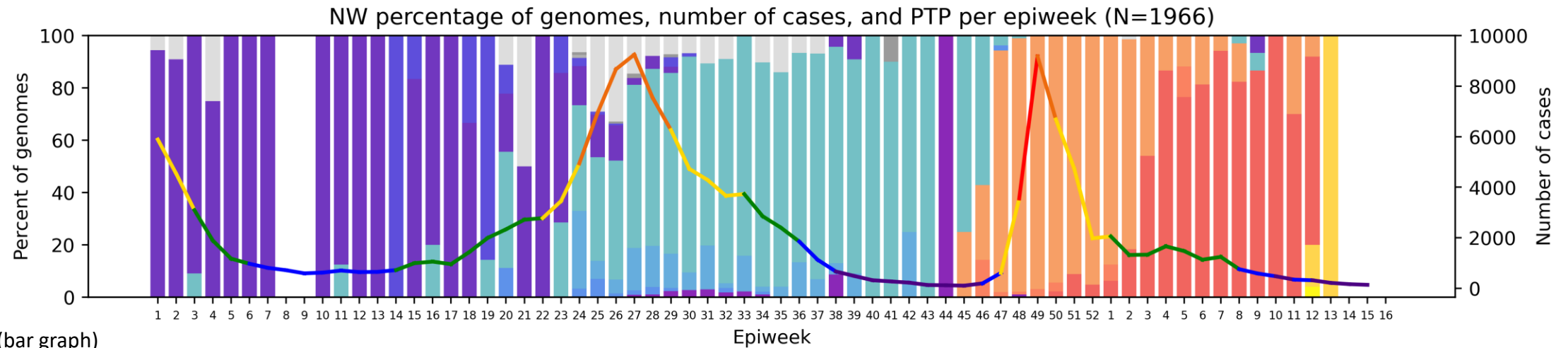
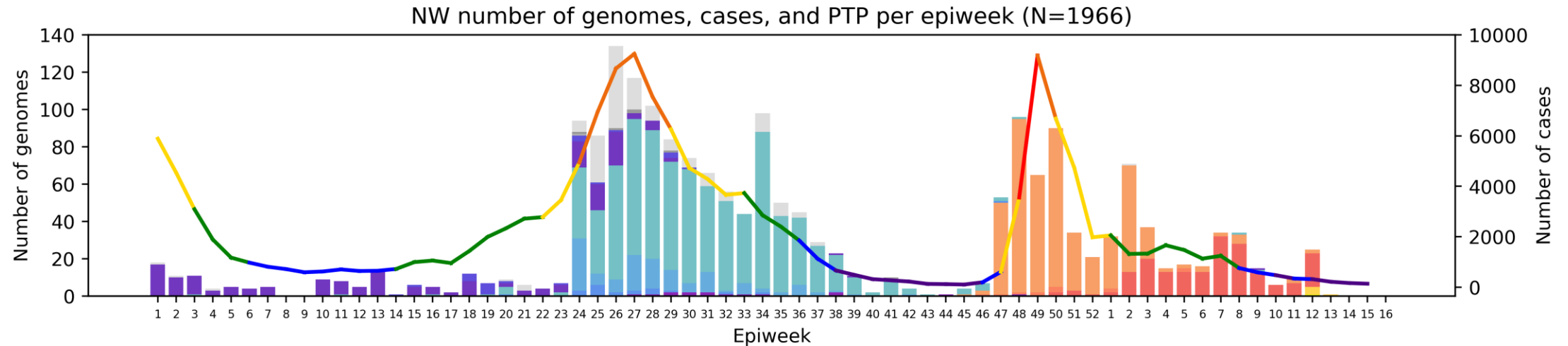


Weekly percentage testing positive key (line graph)





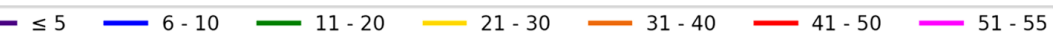
# North West Province, 2021, n = 1966



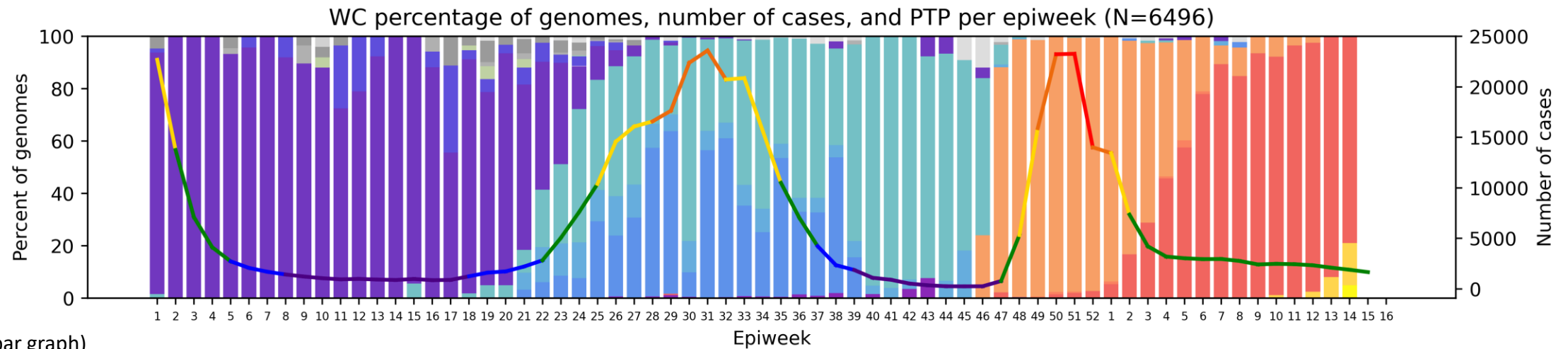
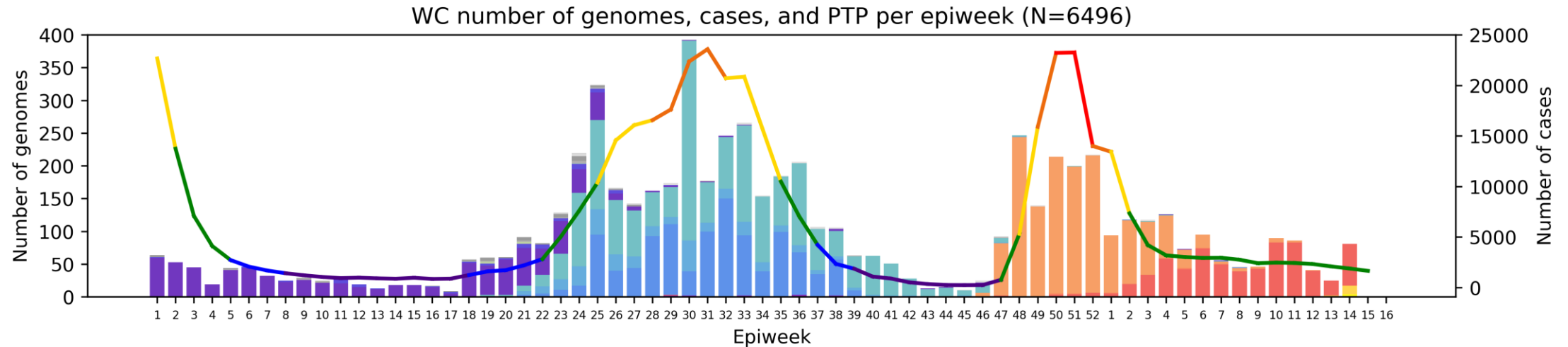
Clade key (bar graph)



Weekly percentage testing positive key (line graph)



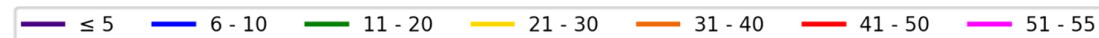
# Western Cape Province, 2021-2022, n = 6496



Clade key (bar graph)



Weekly percentage testing positive key (line graph)

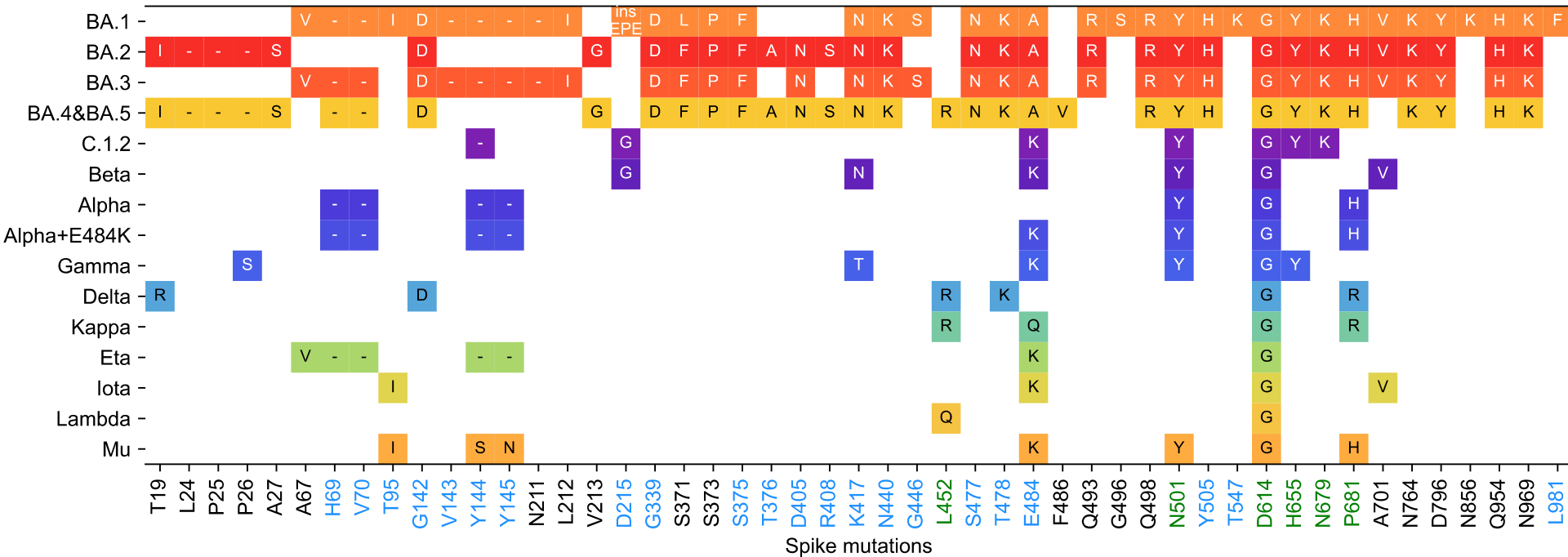


# Summary

- **Variant of Concern Omicron in South Africa**
  - Dominates 2022 sequencing data at >98% of genomes
  - While BA.1 (and sub-lineages) was the predominant sub-lineage in January (55%), BA.2 dominated in February (86%), March (80%) and April (53%).
  - Two additional Omicron sub-lineages (BA.4 and BA.5) have recently been designated by Pangolin. BA.4 and BA.5 increased in prevalence in March (16%), and appear to be increasing in April (44%) although additional sequencing data is needed for this period.
    - These numbers are likely to change as new versions of the assignment tool are released.
  - BA.3 continues to be detected at low levels.
  - NGS-SA teams are monitoring sequencing data for recombinants.
- Low frequency of previously circulating variants such as Delta still detected in recent data

<sup>1</sup> <https://github.com/cov-lineages/pango-designation/releases/tag/v1.3>

# 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



Supported by the DSI and the SA MRC



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EDCTP

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





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**Funders:**  
GIZ/BMBF: African Network for Improved  
diagnostics and epidemiology of common and  
emerging infectious agents (ANDEMIA)  
G7 Global Health fund, Robert Koch Institute, Dr  
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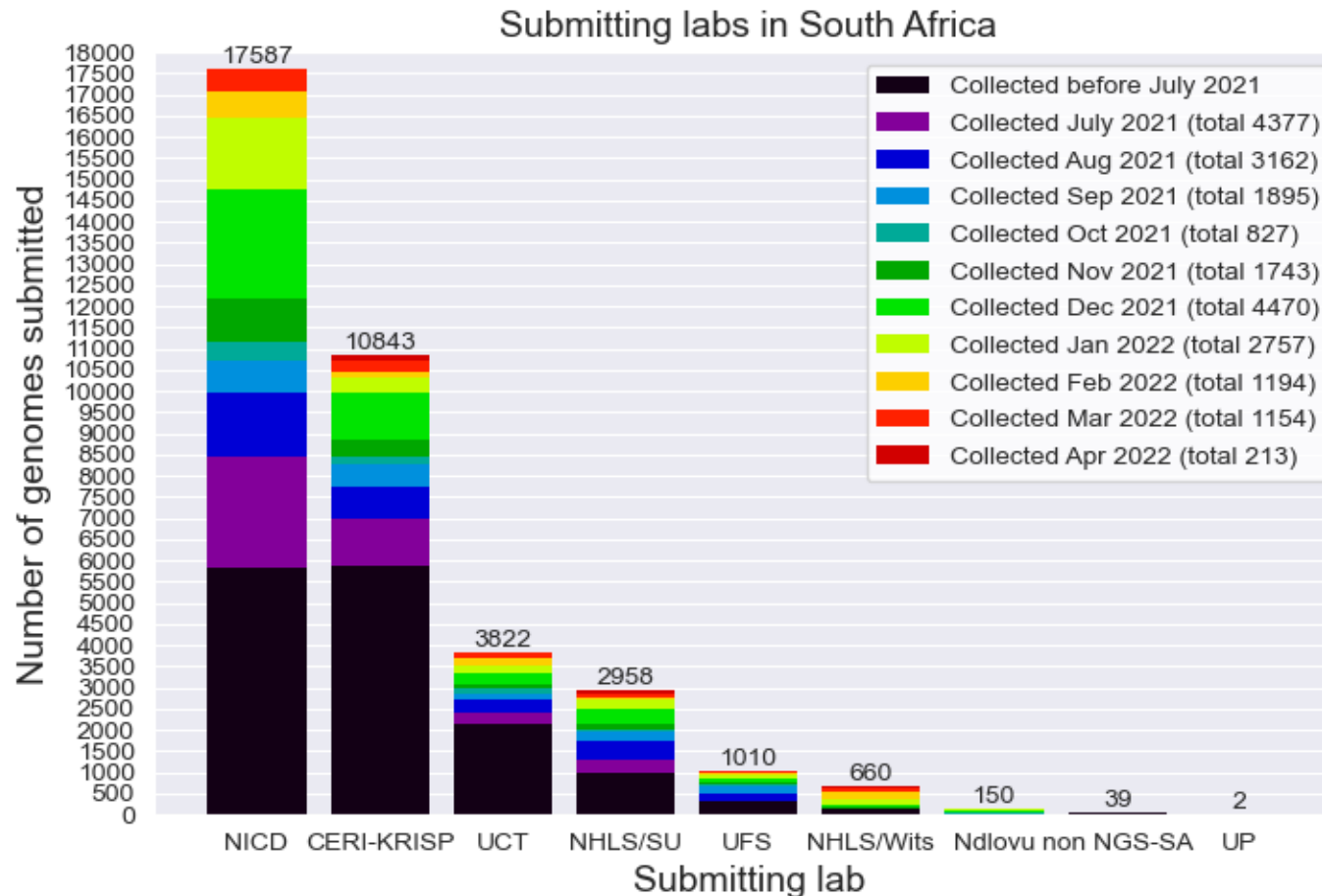
## SA MRC

Glenda Gray





# South African genomes submitted per submitting lab, 2020 - 2022 (N=37 071)



## 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
Delta	B.1.617.2	G/478K.V1	21A, 21I, 21J	+S:K417N +S:K484K	India, Oct-2020	VOI: 4-Apr-2021 VOC: 11-May-2021
Omicron*	B.1.1.529	GR/484A	21K	+S:R346K	Multiple countries, Nov-2021	VUM: 24-Nov-2021 VOC: 26-Nov-2021

<https://www.who.int/en/activities/tracking-SARS-CoV-2-variants/> accessed 18 March 2022

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

° Only found in a subset of sequences

# Previously circulating Variants of Concern

WHO label	Pango lineage•	GISAID clade	Nextstrain clade	Earliest documented samples	Date of designation
Alpha	B.1.1.7	GRY	20I (V1)	United Kingdom, Sep-2020	VOC: 18-Dec-2020 Previous VOC: 09-Mar-2022
Beta	B.1.351	GH/501Y.V2	20H (V2)	South Africa, May-2020	VOC: 18-Dec-2020 Previous VOC: 09-Mar-2022
Gamma	P.1	GR/501Y.V3	20J (V3)	Brazil, Nov-2020	VOC: 11-Jan-2021 Previous VOC: 09-Mar-2022

<https://www.who.int/en/activities/tracking-SARS-CoV-2-variants/> accessed 18 March 2022

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

# Submission of routine specimens for sequencing

- representative of multiple geographic regions (provinces/districts/health facilities) from individuals of
  - all ages
  - over as many time periods during the SARS-CoV-2 epidemic in South Africa
- requested that testing laboratories in both the private and public sectors, submit respiratory samples to their closest NGS-SA sequencing laboratory on a routine basis (ideally every week) as follows, depending on the capacity of the testing laboratory:
  - All positives samples should be sent every week (NGS-SA laboratory will perform random sampling as described below) **OR**
  - A weekly selection of approximately 10%-20% of randomly selected positive samples should be sent every week. Number of selected samples will depend on the size of laboratory and how many other laboratories are drained by the submitting laboratory.

# Submission of special interest specimens for sequencing

In addition to routine samples mentioned above, please send specimens separately to above and clearly marked if:

- Suspected vaccine breakthrough ( $\geq 14$  days after vaccine), especially if hospitalised and clinically severe
- Suspected re-infection ( $\geq 90$  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.)