

SARS-CoV-2 Sequencing Update 29 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) on 29 April 2022 at 14h25



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

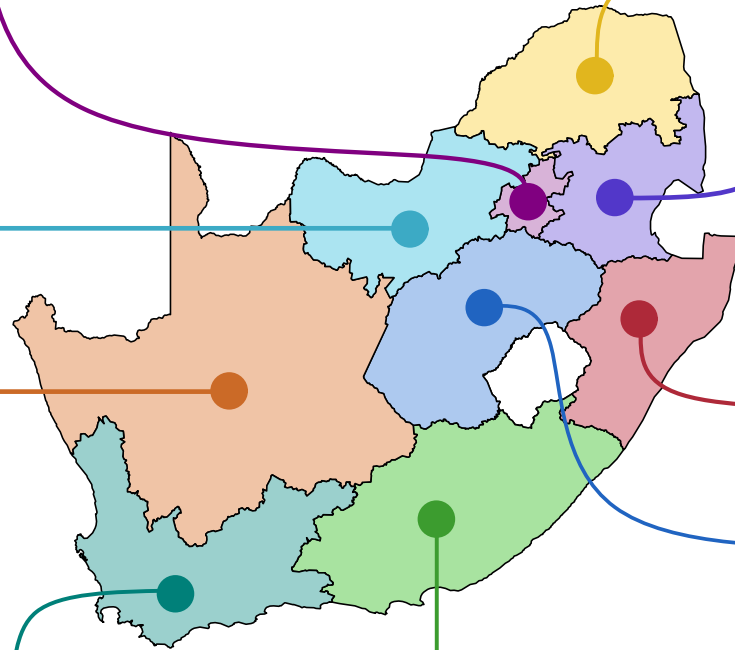
Elbe, S., and Buckland-Merrett, G. (2017) Data, disease and diplomacy: GISAID's innovative contribution to global health. *Global Challenges*, 1:33-46. DOI: 10.1002/gch2.1018 PMCID: 31565258

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

SARS-CoV-2

GENOMIC SURVEILLANCE

epiweeks 39 (2021) - 17 (2022)



Gauteng ↑ PTP: 20.2%

Genomes Cases
3 916 (28.6%) 306 005 (36.2%)

Genomes deposited in the last week

168 118 3 169 46 1

North West ↑ PTP: 9.7%

Genomes Cases
757 (5.5%) 42 251 (5.0%)

Genomes deposited in the last week

7 26 4 1 1

Northern Cape ↑ PTP: 10.9%

Genomes Cases
671 (4.9%) 18 761 (2.2%)

Genomes deposited in the last week

50 2 1

Western Cape ↑ PTP: 17.9%

Genomes Cases
2 629 (19.2%) 146 412 (17.3%)

Genomes deposited in the last week

4 13 4 1

Eastern Cape ↑ PTP: 12.8%

Genomes Cases
1 035 (7.6%) 56 991 (6.7%)

Genomes deposited in the last week

1 6 3

Limpopo ↑ PTP: 10.2%

Genomes Cases
1 248 (9.1%) 33 275 (3.9%)

Genomes deposited in the last week

13 7 6 3 1

Mpumalanga ↑ PTP: 9.7%

Genomes Cases
1 372 (10.0%) 42 564 (5.0%)

Genomes deposited in the last week

44 53 11 23 16 1

KwaZulu-Natal ↑ PTP: 19.9%

Genomes Cases
1 550 (11.3%) 156 943 (18.6%)

Genomes deposited in the last week

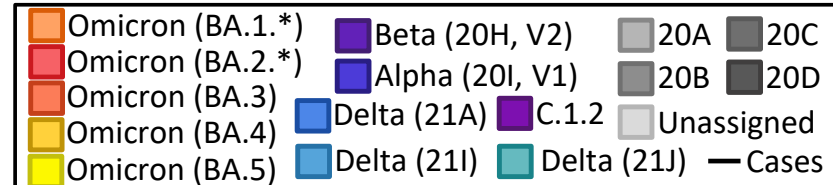
6 10 12 35 1 1

Free State ↑ PTP: 9.4%

Genomes Cases
507 (3.7%) 41 329 (4.9%)

Genomes deposited in the last week

1 1 1



1 288 genomes deposited since the previous report

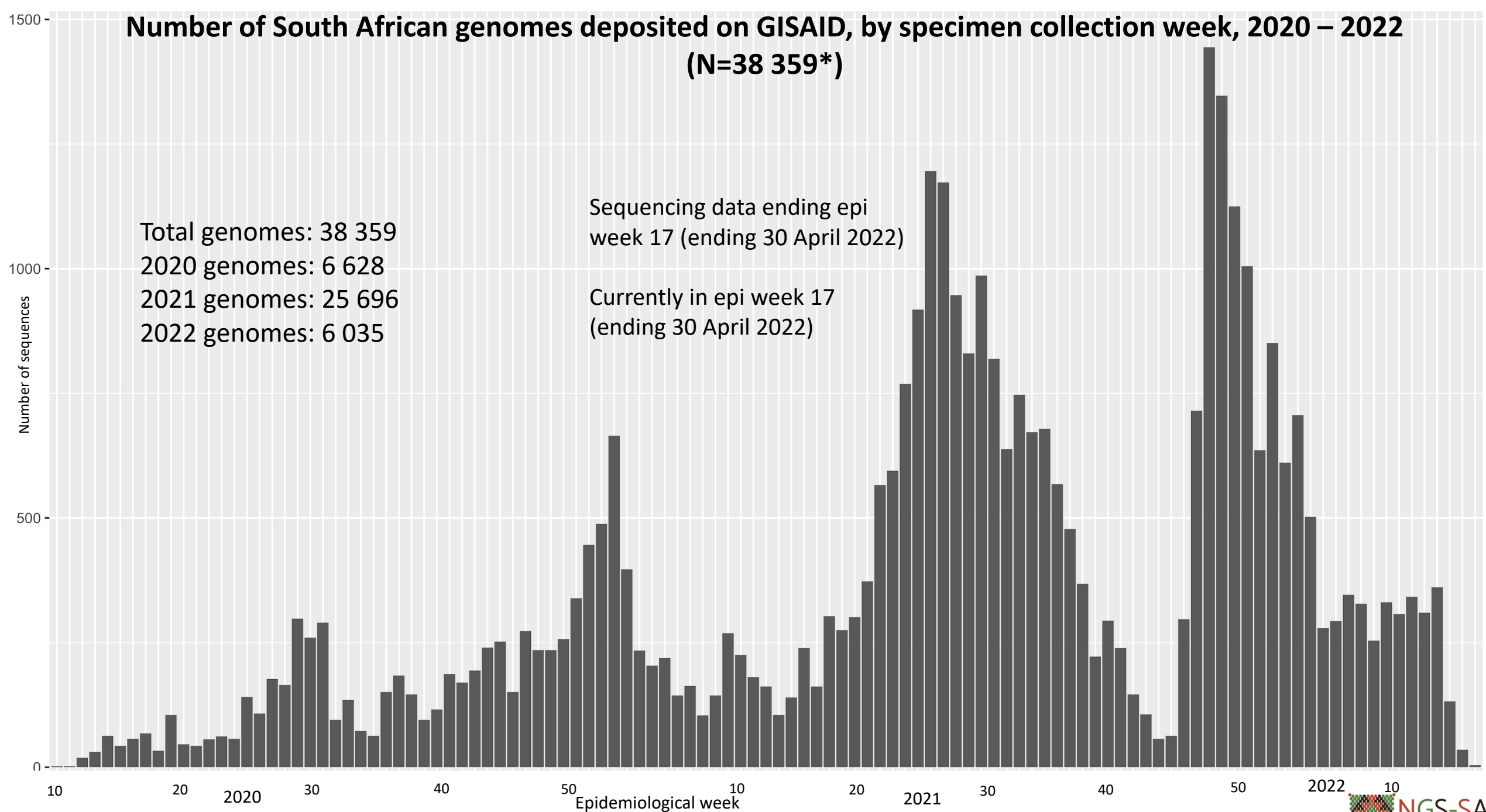


Bar graphs represent genomes sequenced per epiweek, with lines representing cases by collection date (weeks 39 [2021] – 17 [2022])

Genomes and cases presented as provincial total (percentage of national total) for epiweeks 39 (2021) – 17 (2022)

PTP: percentage testing positive in week 16 (17 Apr 2022 – 23 Apr 2022); arrow indicates direction of change since previous week (10 Apr 2022 – 16 Apr 2022) if change was significant ($P < 0.05$)

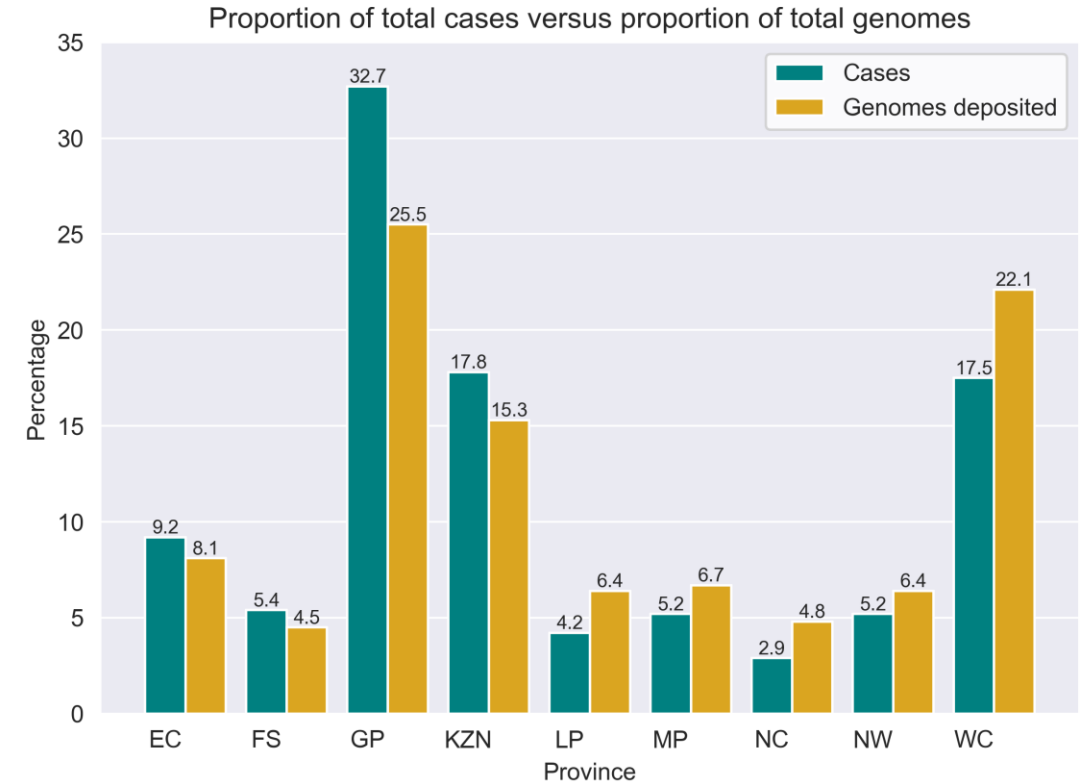
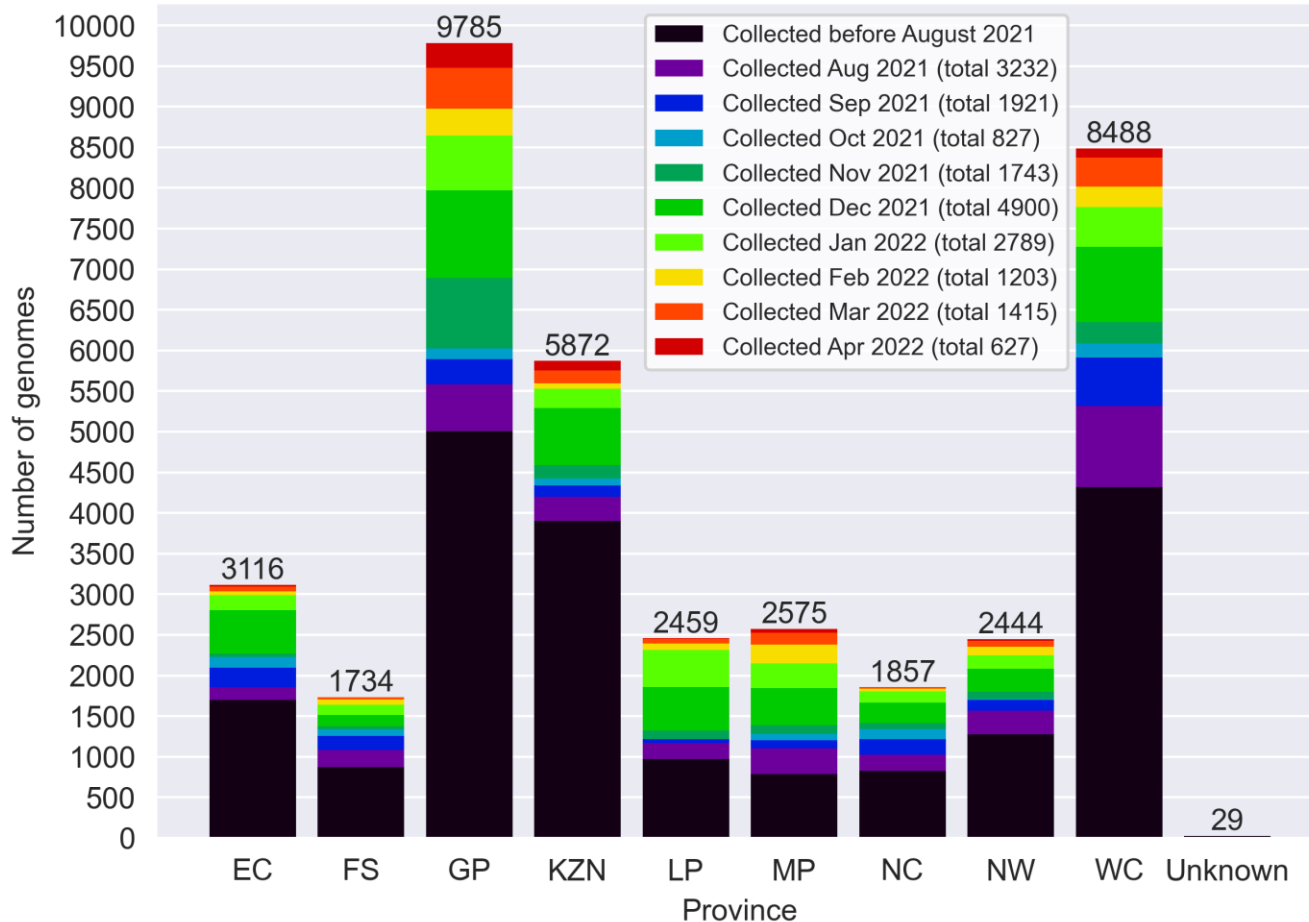
Number of South African genomes deposited on GISAID, by specimen collection week, 2020 – 2022 (N=38 359*)



*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=38 359)

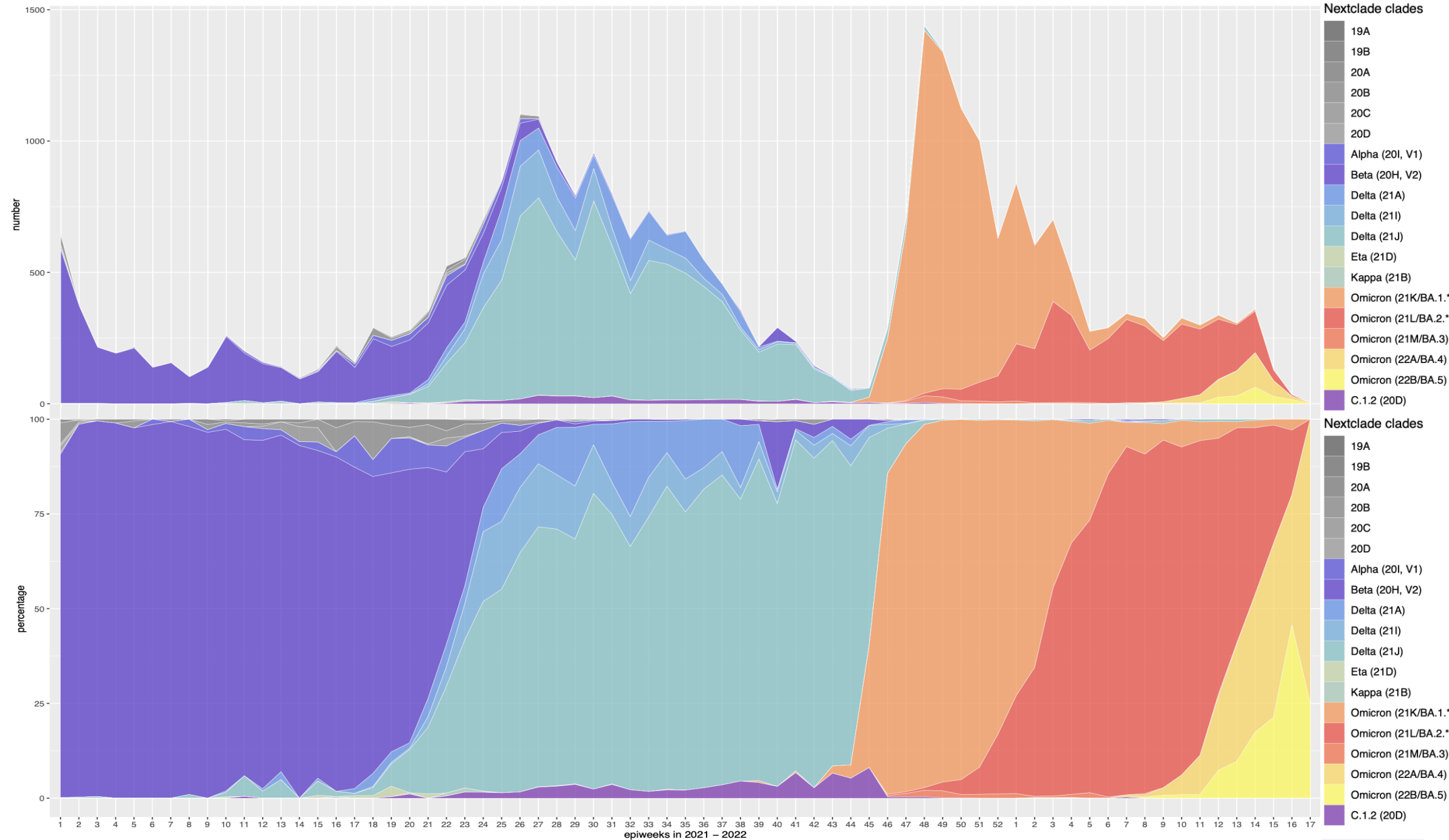
Provincial breakdown of genomes deposited into GISAID



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 (31 646*)

Distribution of Nextclade Clades in South Africa

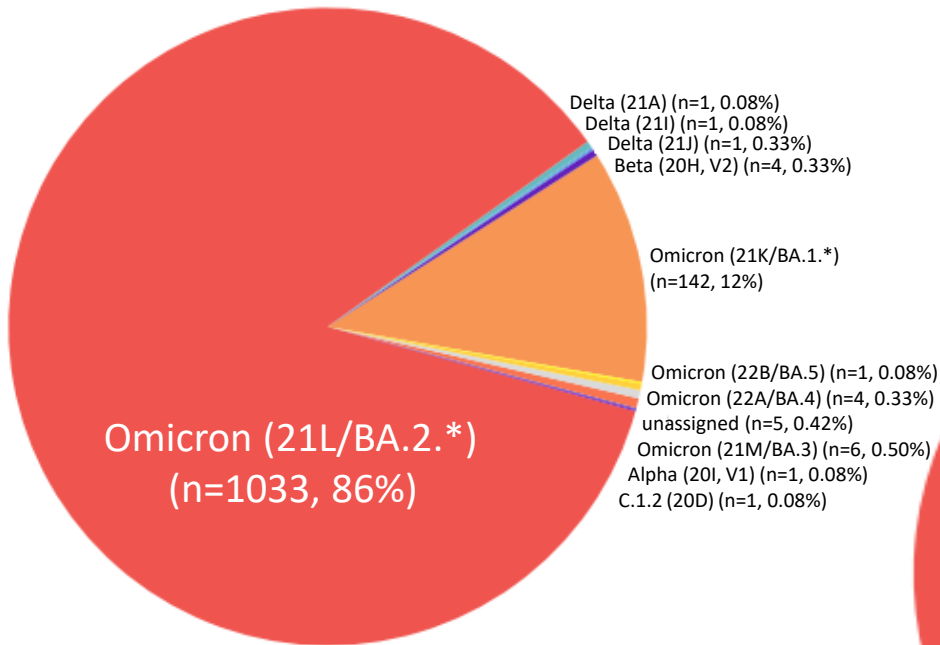


Delta dominated in South Africa until October at >80%. Omicron has dominated from November onwards.

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

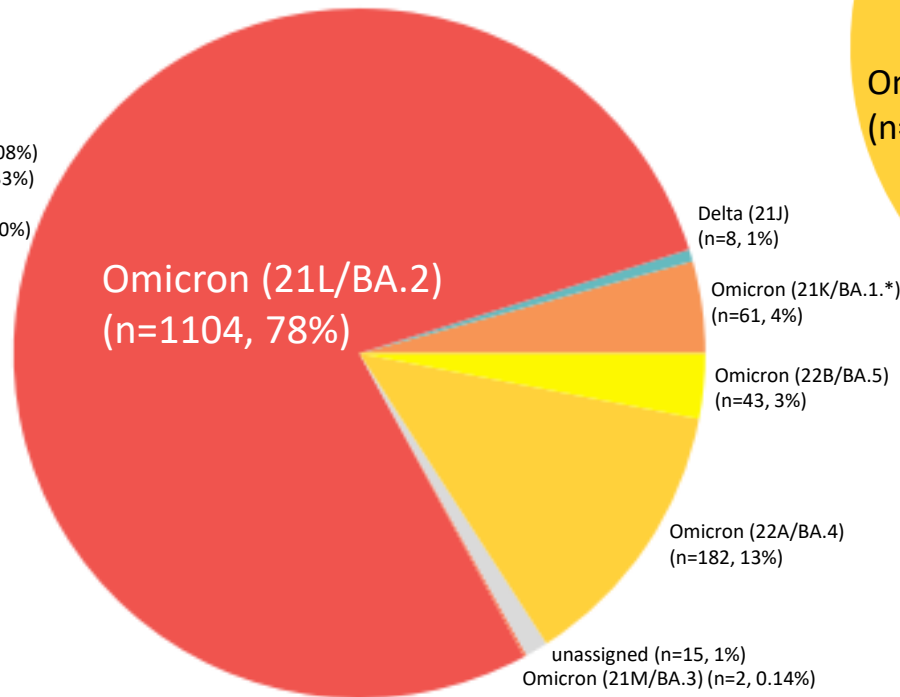
Feb – Apr 2022

February (N=1203)



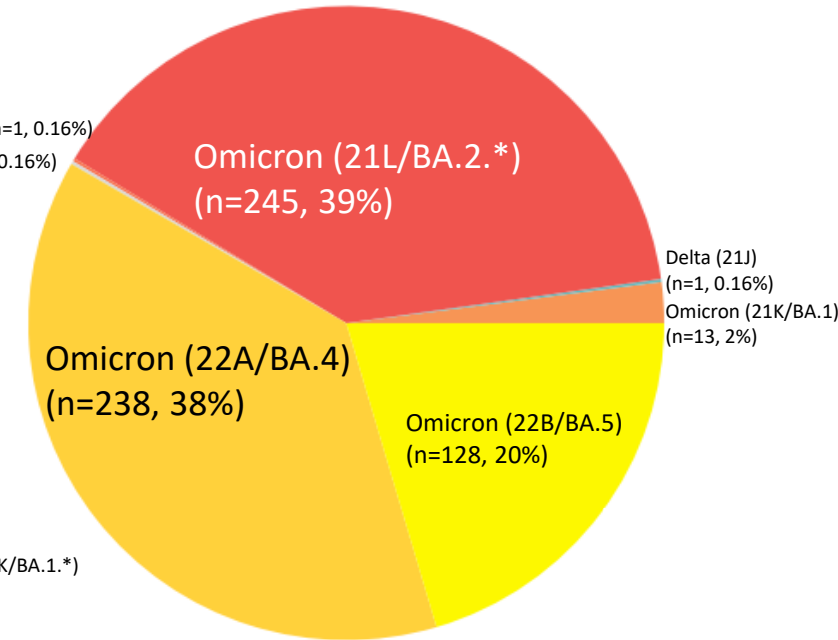
Total Omicron in Feb: 1186 (98.6%)

March (N=1415)



Total Omicron in Mar: 1392 (98.4%)

April (N=627)



Total Omicron in Apr: 625 (99.7%)

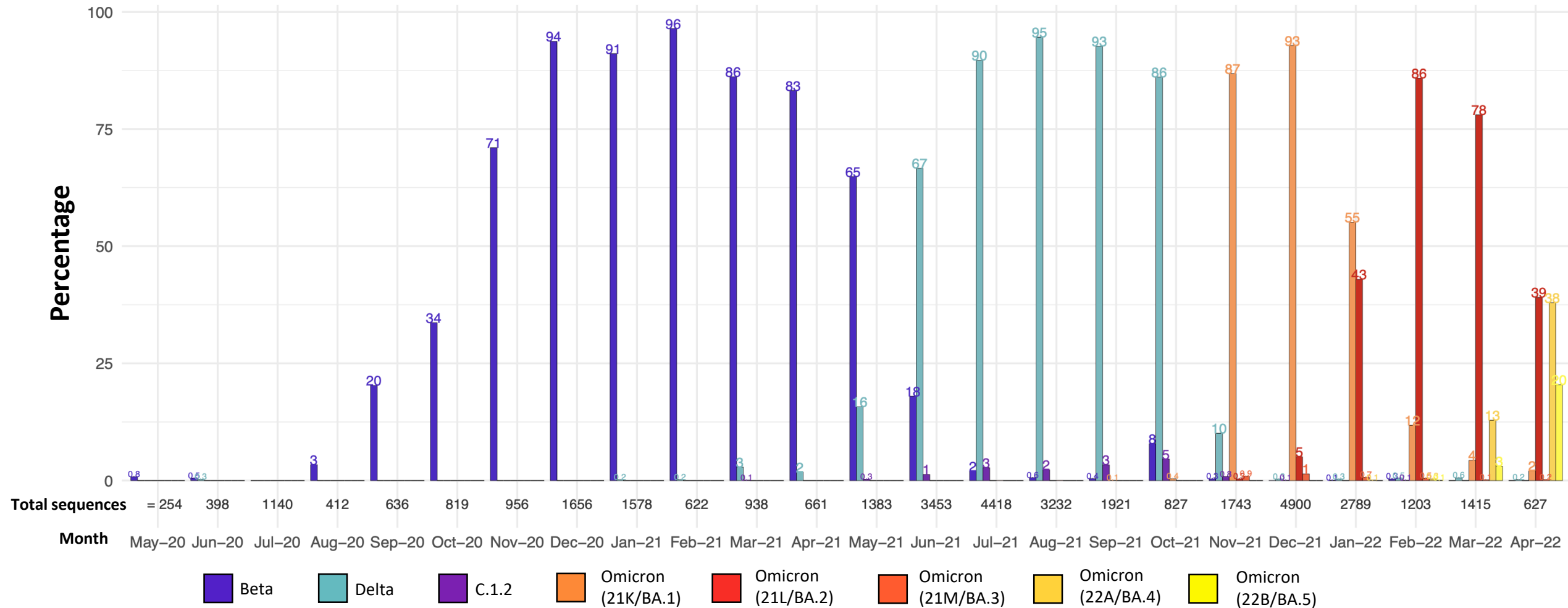
***Pangolin v4 has recently been released and sequences are in the process of being re-designated. Total numbers and proportions of the various sub-lineages are likely to change over the next few weeks as the data are updated.**



Omicron dominated in February (98.6%, 1186/1203), March (98.4%, 1392/1415) and April (99.7%, 625/627). BA.2 was dominant in February and March. BA.4 and BA.5 together are dominant in April (58.4%, 366/627).

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

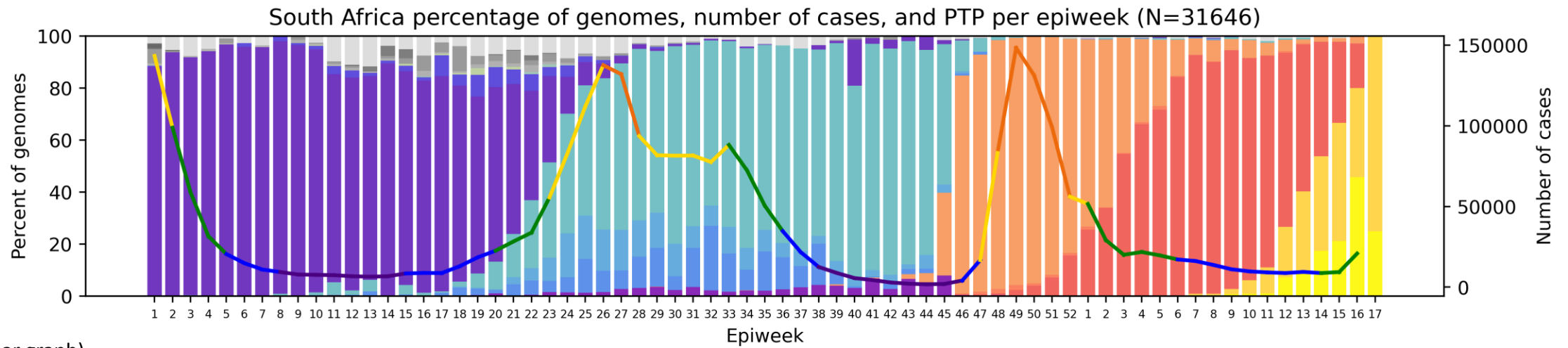
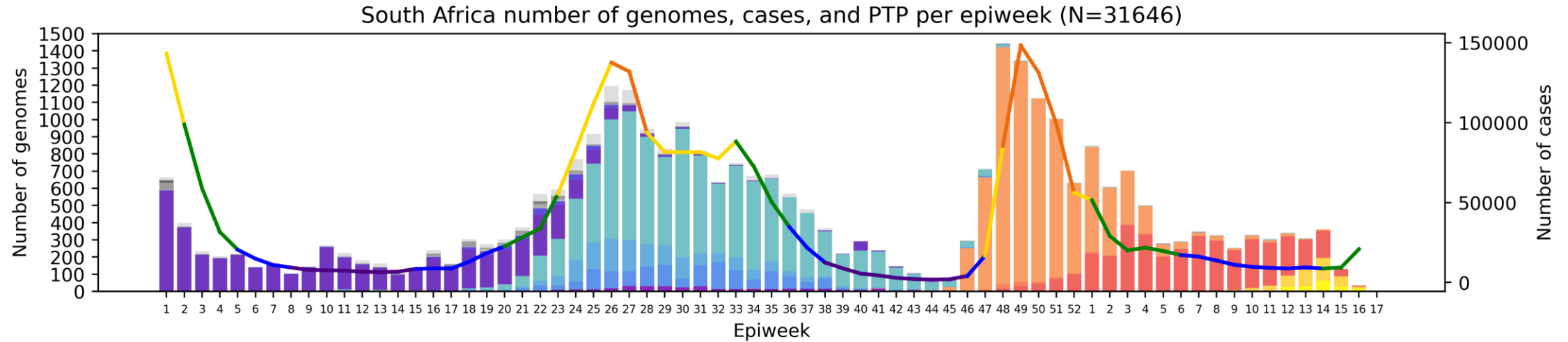
Detection rates of variants being monitored in South Africa



*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 – April). BA.2 made up 43% of genomes in January, 86% in February, 78% in March and 39% in April. Newly designated sub-lineages BA.4 and BA.5 together are dominant in April, at 38% and 20% respectively.

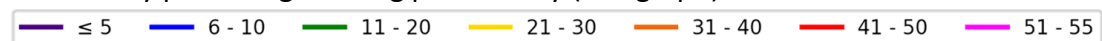
South Africa, 2021-2022, n = 31646*



Clade key (bar graph)

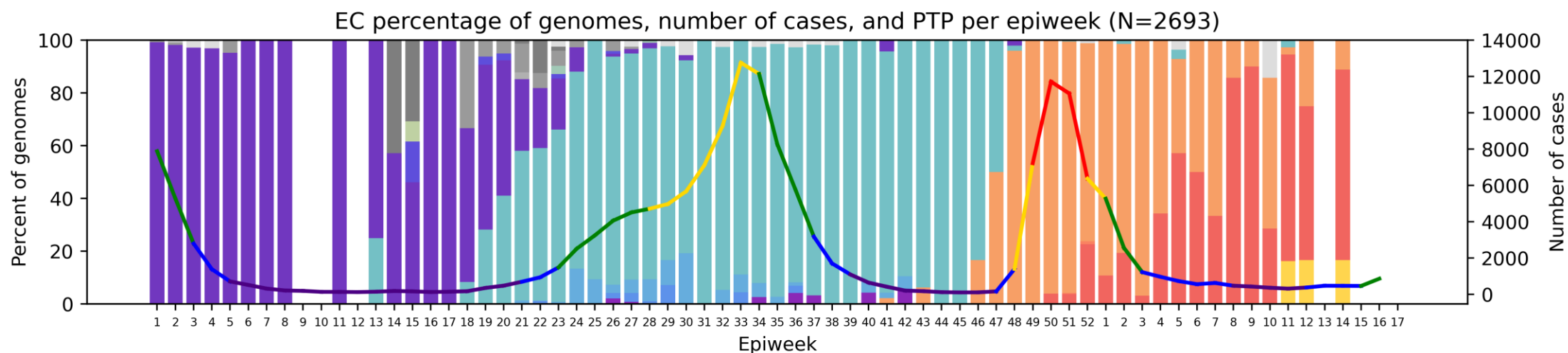
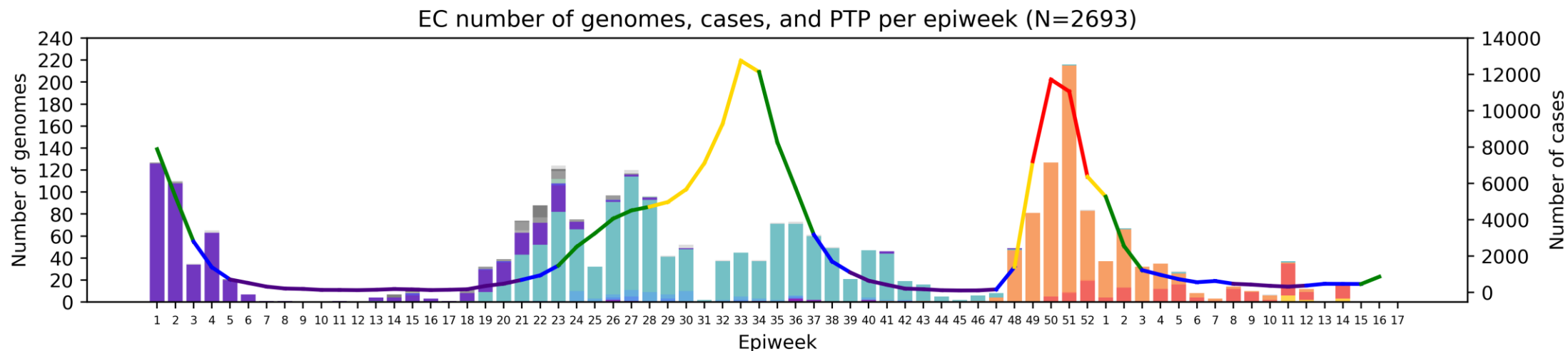


Weekly percentage testing positive key (line graph)



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

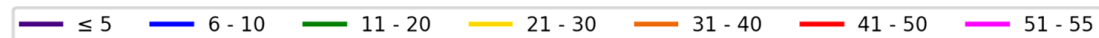
Eastern Cape Province, 2021-2022, n = 2693



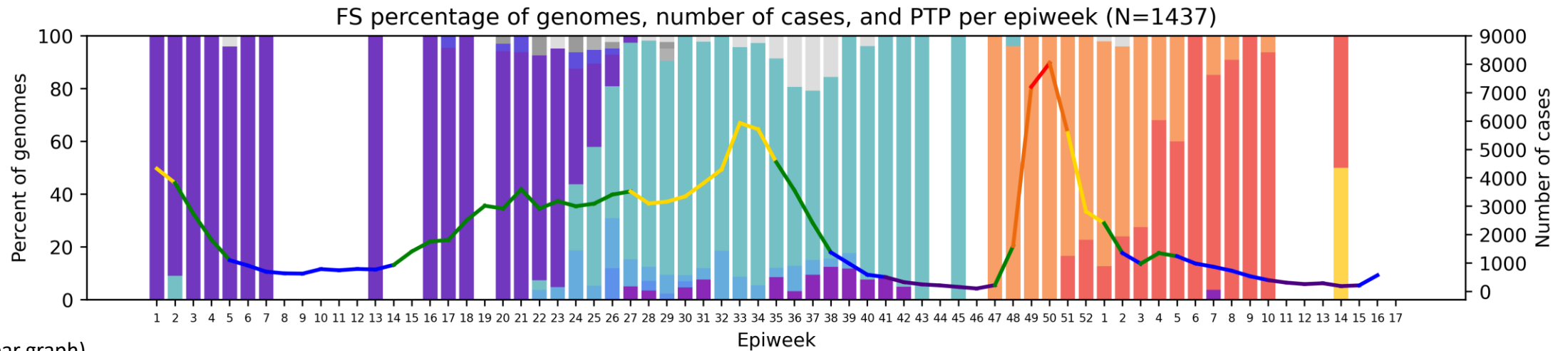
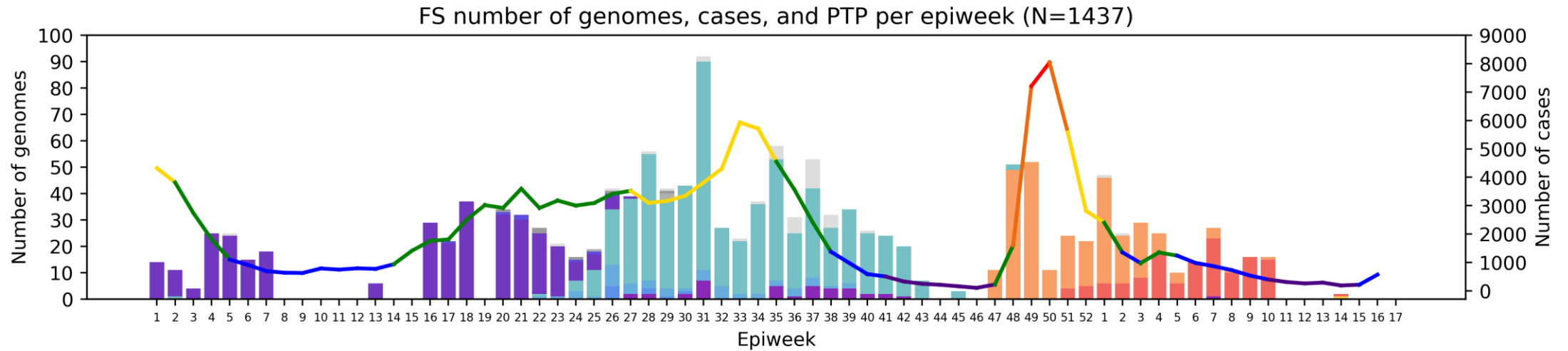
Clade key (bar graph)



Weekly percentage testing positive key (line graph)



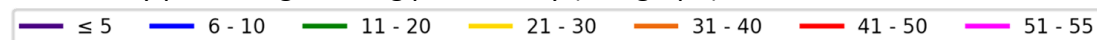
Free State Province, 2021-2022, n = 1437



Clade key (bar graph)

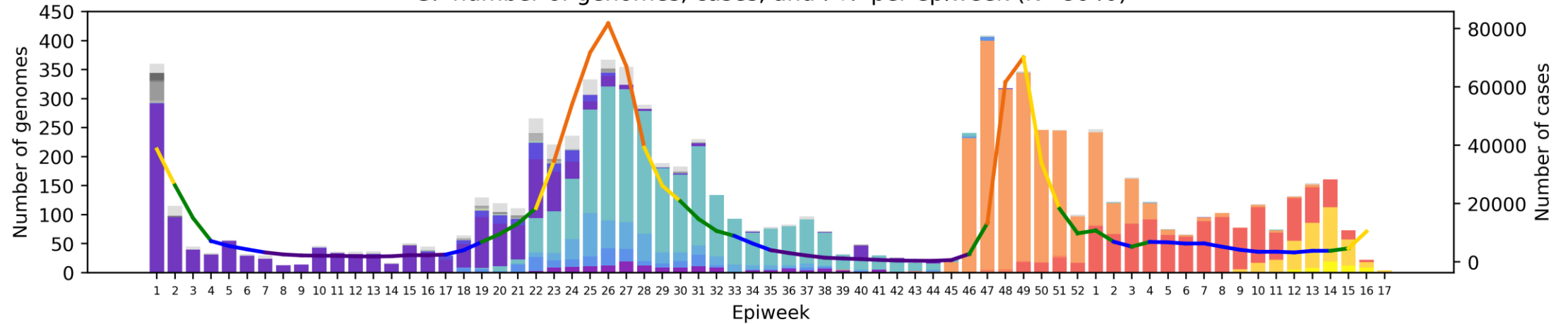


Weekly percentage testing positive key (line graph)

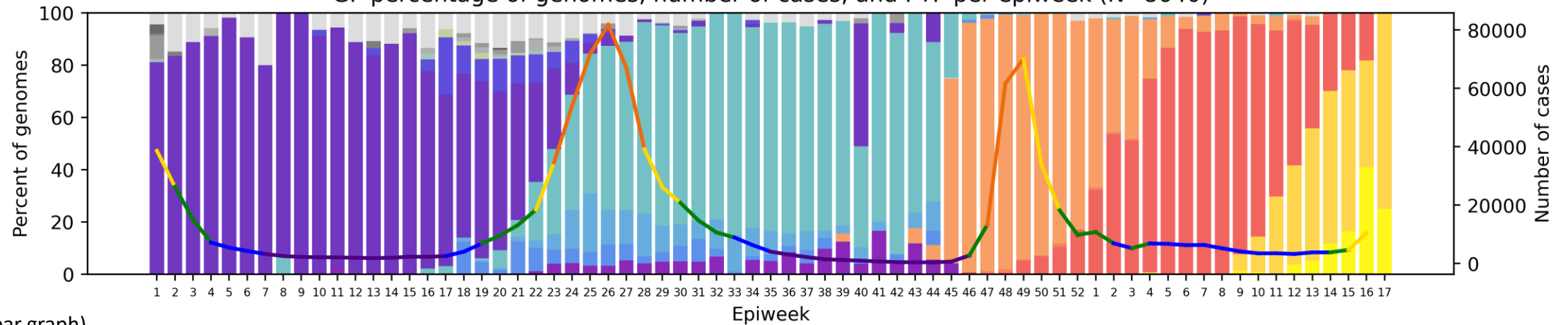


Gauteng Province, 2021-2022, n = 8640

GP number of genomes, cases, and PTP per epiweek (N=8640)



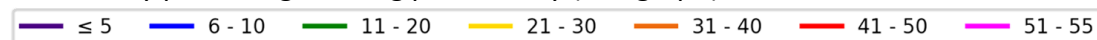
GP percentage of genomes, number of cases, and PTP per epiweek (N=8640)



Clade key (bar graph)

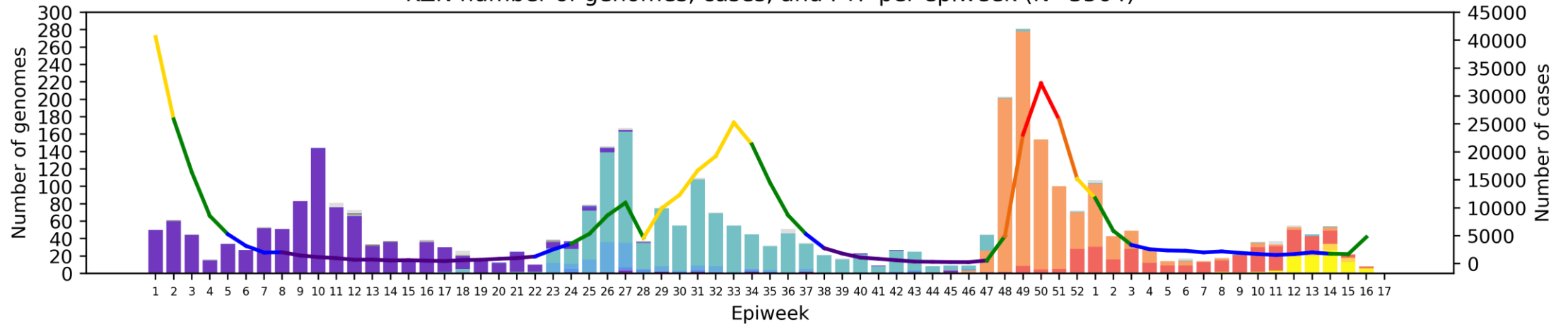


Weekly percentage testing positive key (line graph)

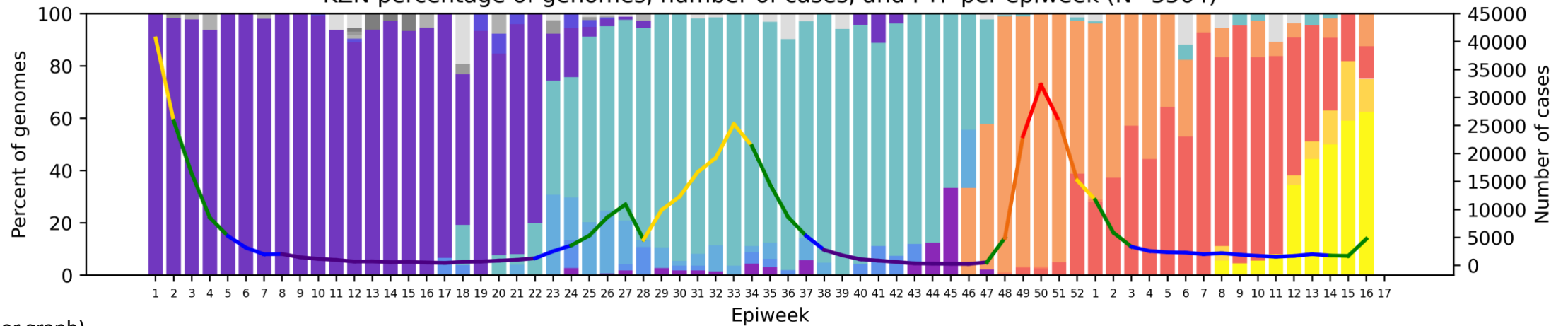


KwaZulu-Natal Province, 2021-2022, n = 3564

KZN number of genomes, cases, and PTP per epiweek (N=3564)



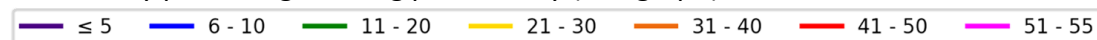
KZN percentage of genomes, number of cases, and PTP per epiweek (N=3564)



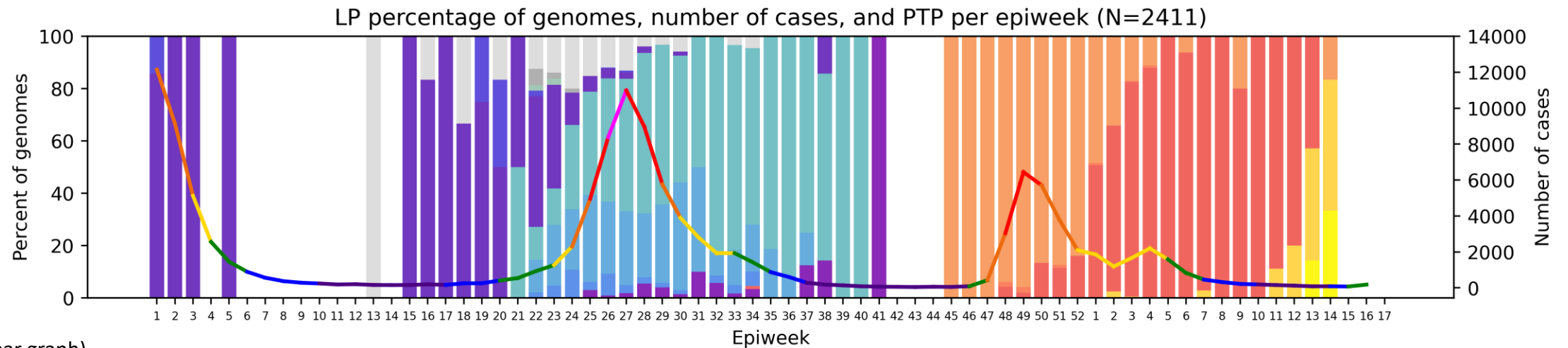
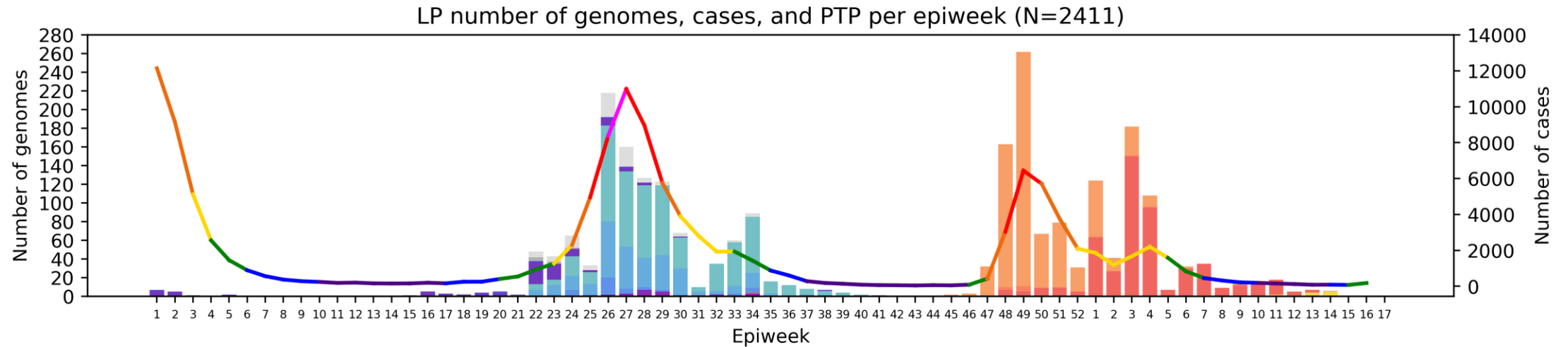
Clade key (bar graph)



Weekly percentage testing positive key (line graph)



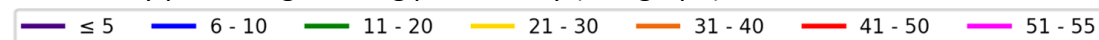
Limpopo Province, 2021-2022, n = 2411



Clade key (bar graph)

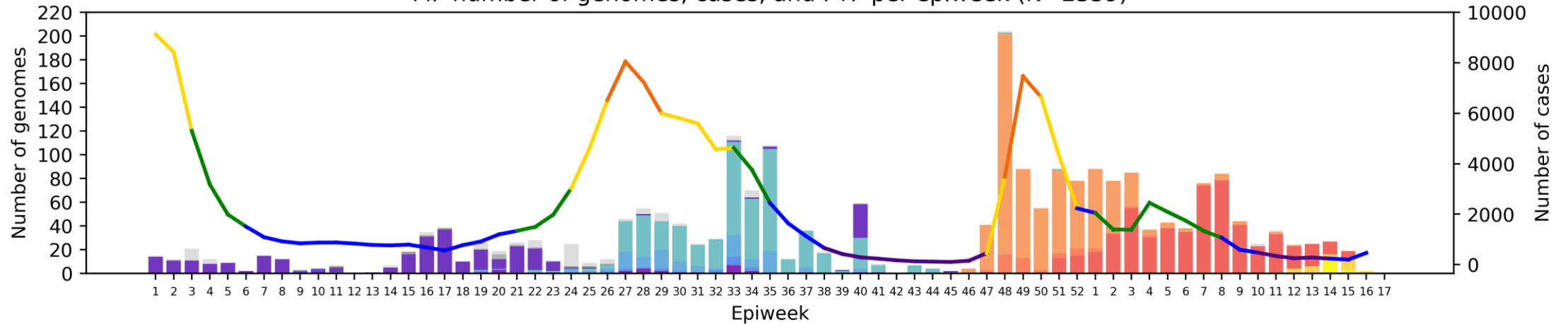


Weekly percentage testing positive key (line graph)

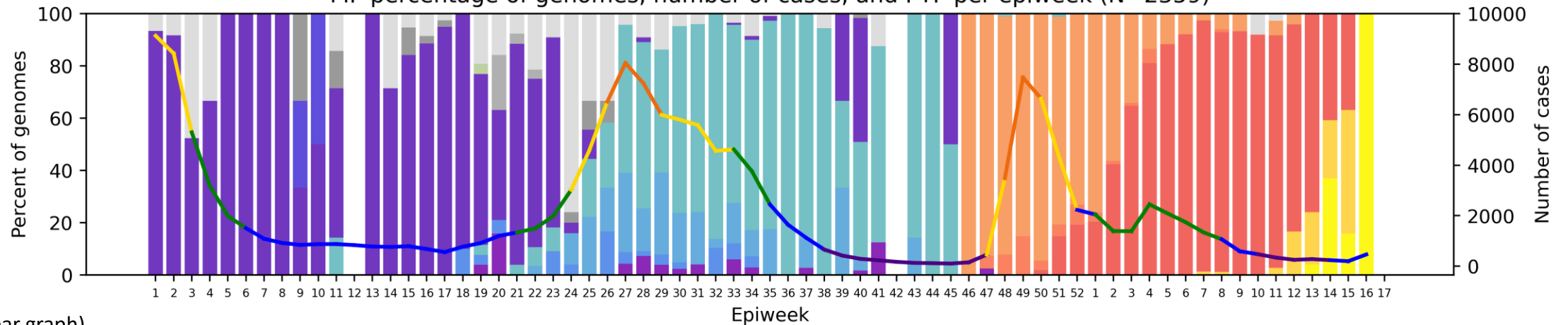


Mpumalanga Province, 2021-2022, n = 2359

MP number of genomes, cases, and PTP per epiweek (N=2359)



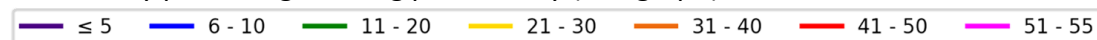
MP percentage of genomes, number of cases, and PTP per epiweek (N=2359)



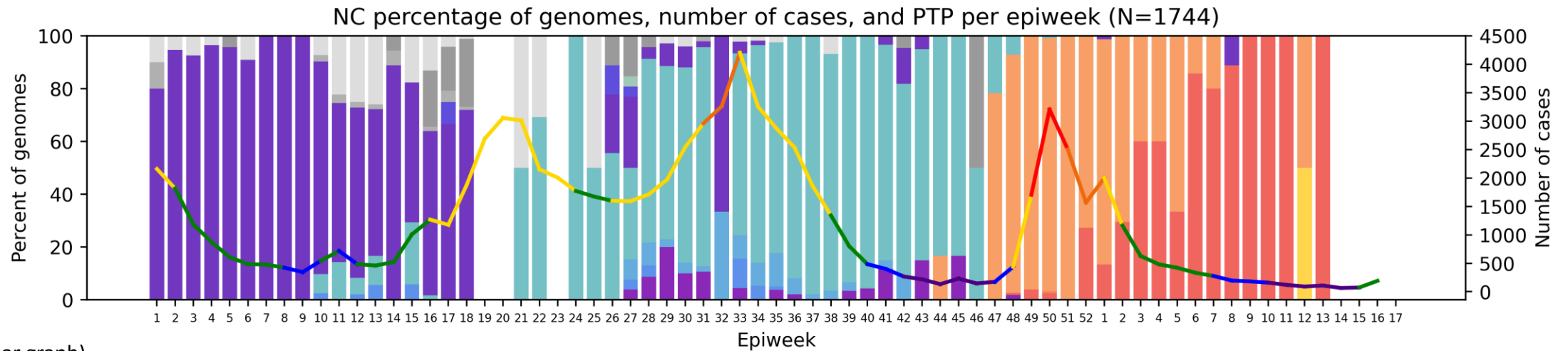
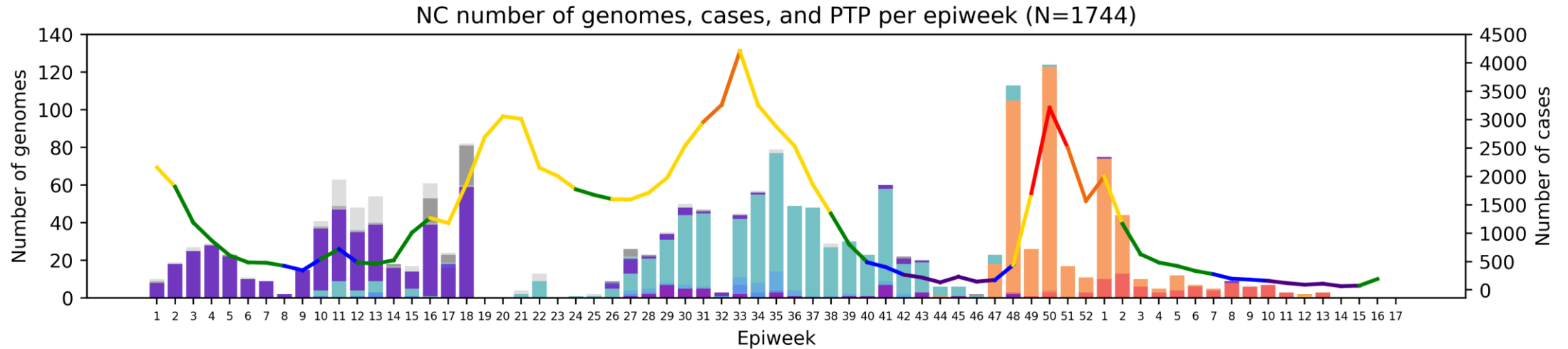
Clade key (bar graph)



Weekly percentage testing positive key (line graph)



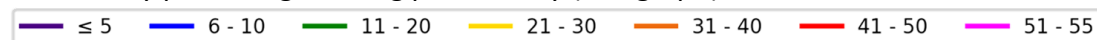
Northern Cape Province, 2021-2022, n = 1744



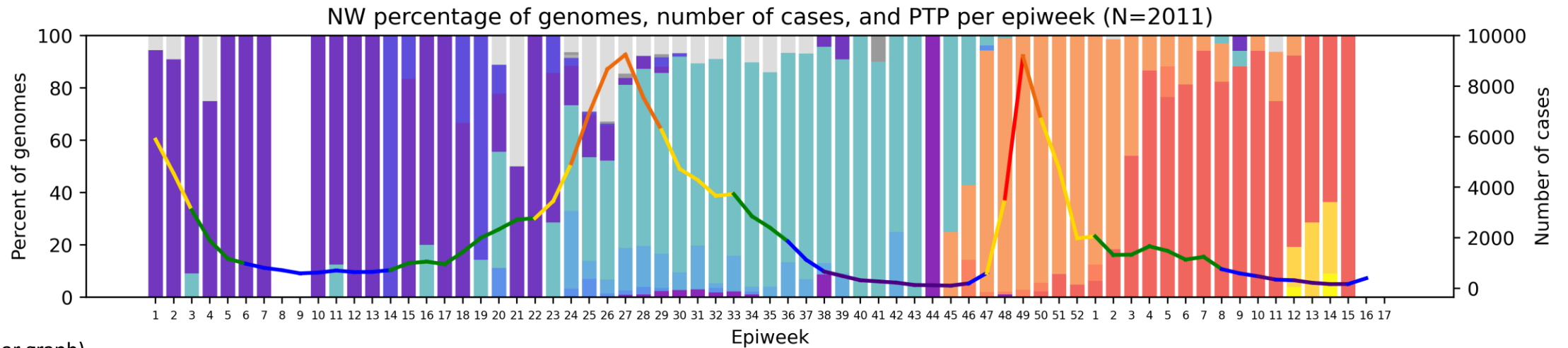
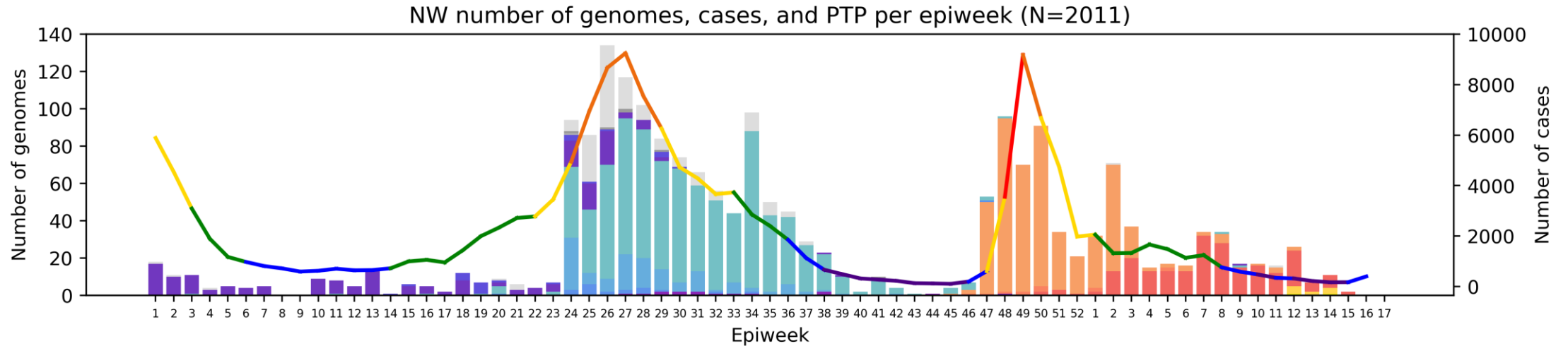
Clade key (bar graph)



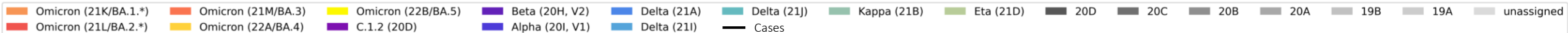
Weekly percentage testing positive key (line graph)



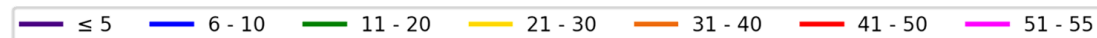
North West Province, 2021, n = 2011



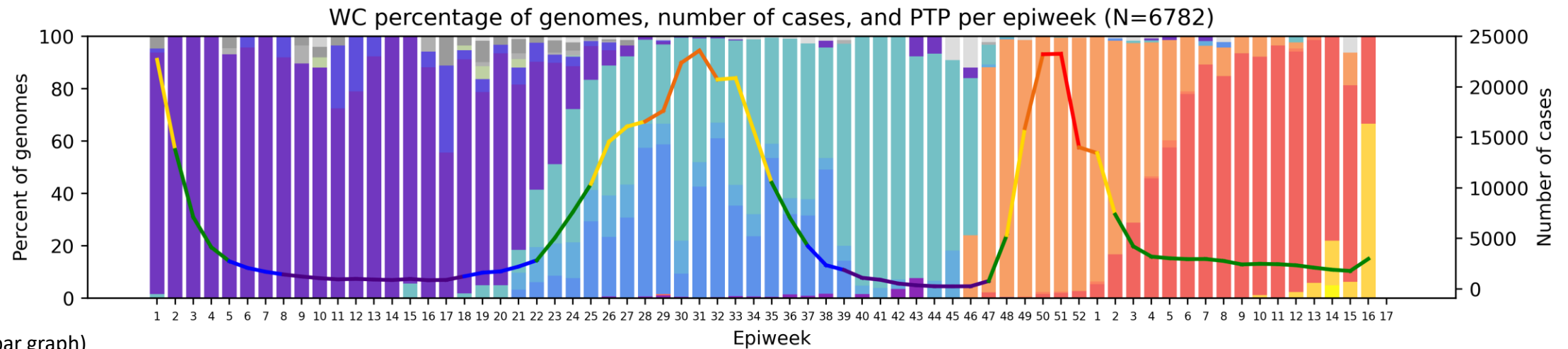
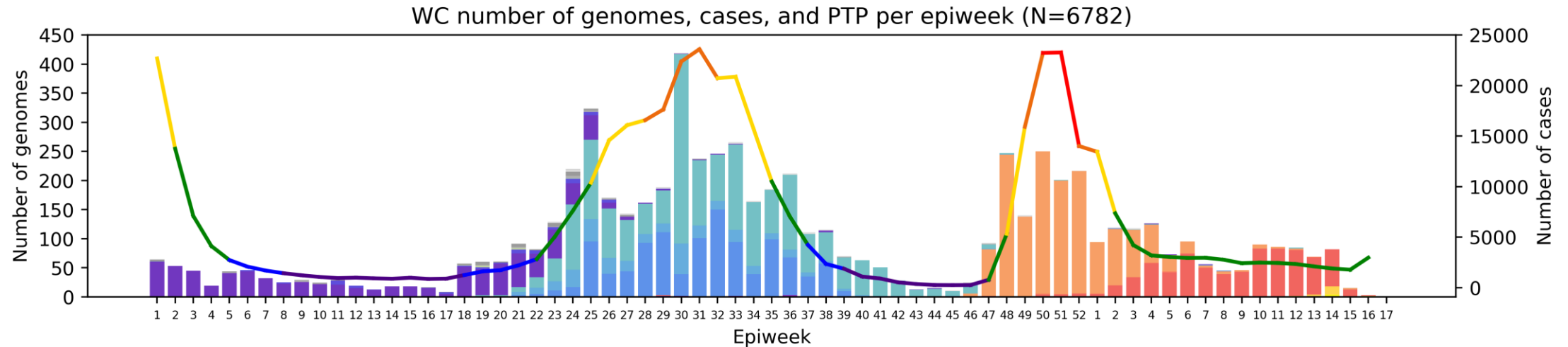
Clade key (bar graph)



Weekly percentage testing positive key (line graph)



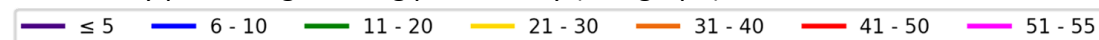
Western Cape Province, 2021-2022, n = 6782



Clade key (bar graph)



Weekly percentage testing positive key (line graph)

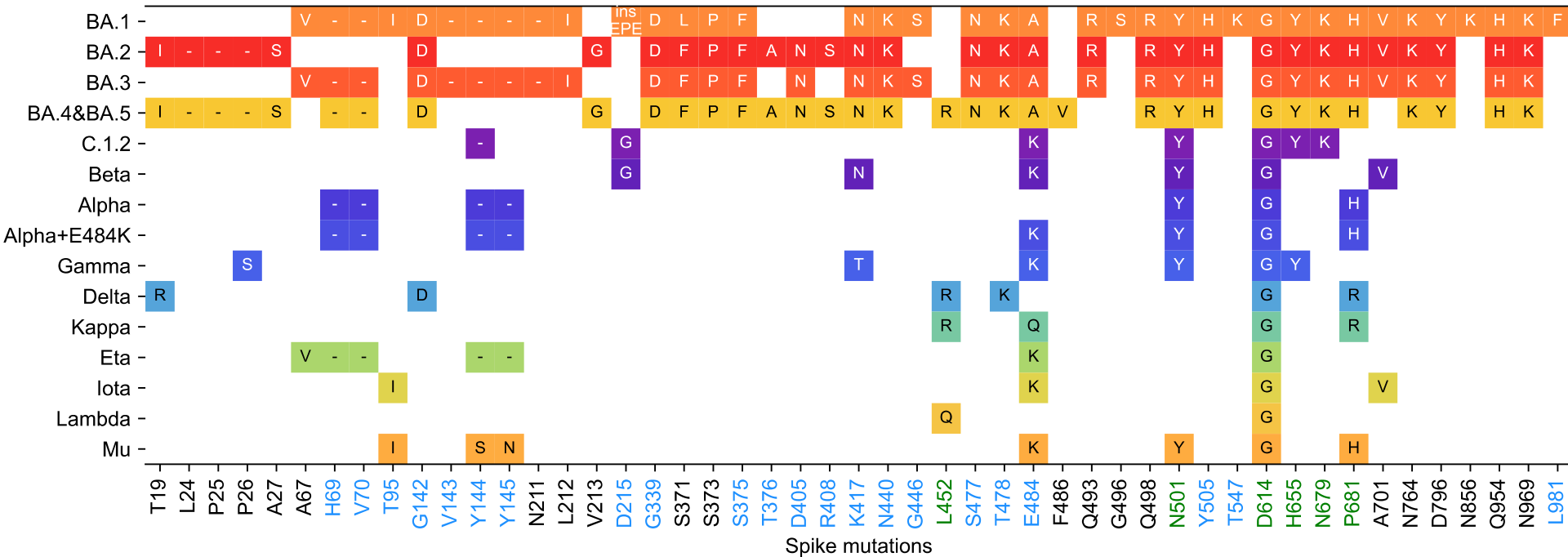


Summary

- **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%) and March (78%).
 - Two additional Omicron sub-lineages (BA.4 and BA.5) have recently been designated. BA.4 and BA.5 increased in prevalence in March (16%), and together are dominant in April (58%).
 - 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

¹ <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



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KWAZULU-NATAL
INYUVESI
YAKWAZULU-NATALI



EDCTP

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University of Stellenbosch & NHLS Tygerberg Virology



Susan Engelbrecht
Wolfgang Preiser
Gert van Zyl
Tongai Maponga
Bronwyn Kleinhans
Shannon Wilson
Karabo Phadu
Tania Stander
Kamela Mahlakwane
Mathilda Claassen
Diagnostic laboratory staff

UKZN-Inkosi Albert Luthuli Central Hospital



Dr Khanyi Msomi
Dr Kerusha Govender
Dr Pravi Moodley
Dr Aabida Khan
Dr Lili Gounder
Dr Kerri Francois
Dr Cherise Naicker
Dr Joedene Chetty

Dr Neli Ngcaba
Dr Tshepiso Mosito
Mr Malcolm Ellapen
Mr Kubendran Reddy
The COVID-19 Bench team

University of KwaZulu-Natal & Africa Health Research Institute



KRISP at UKZN:
Tulio de Oliveira
Richard Lessels
Houriiyah Tegally
Eduan Wilkinson
Jennifer Giandhari
Sureshnee Pillay
Emmanuel James San



AHRI
Alex Sigal
Sandile Cele
Willem Hanekom

University of Cape Town, NHLS & Western Cape Government



NHLS-UCT
Carolyn Williamson
Nei-yuan Hsiao
Diana Hardie
Kruger Marais
Stephen Korsman
Ziyaad Valley-Omar

WCG-UCT
Mary-Anne Davies
Hannah Hussey
Andrew Boule
Masudah Paleker
Theuns Jacobs
Erna Morden

NHLS Greenpoint
Annabel Enoch

Zoonotic arbo and respiratory virus program Centre for Viral Zoonoses Department Medical Virology/ NHLS Tshwane Academic division University of Pretoria



ZARV research program/UP
Marietjie Venter (Head: ZARV)
Adriano Mendes (Postdoc)
Amy Strydom (Postdoc)
Michaela Davis (MSc, intern medical scientist)
Carien van Niekerk



NHLS Tshwane
Prof Simnikiwe Mayaphi (HOD)

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National Institute for Communicable Diseases



Centre for Respiratory Diseases & Meningitis

Anne von Gottberg
Thabo Mohale
Daniel Amoako
Josie Everatt
Boitshoko Mahlangu
Noxolo Ntuli
Anele Mnguni
Amelia Buys
Cardia Fourie
Noluthando Duma
Linda de Gouveia
Jackie Kleynhans
Nicole Wolter
Sibongile Walaza
Mignon du Plessis
Stefano Tempia
Mvuyo Makhasi
Cheryl Cohen

Centre for HIV and STIs

Jinal Bhiman
Cathrine Scheepers
Constantinos Kurt Wibmer
Thandeka Moyo
Tandile Hermanus
Frances Ayres
Zanele Molaudzi
Bronwen Lambson
Tandile Hermanus
Mashudu Madzivhandila
Prudence Kgagudi
Brent Oosthuysen
Penny Moore
Lynn Morris

NICD Groups

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

Sequencing Core Facility

Zamantungwa Khumalo
Annie Chan
Morne du Plessis
Stanford Kwenda
Phillip Senzo Mtshali
Mushal Allam
Florah Mnyameni
Arshad Ismail



University of the Free State



UFS
Dominique Goedhals
Armand Bester
Martin Myaga
Peter Mwangi
Emmanuel Ogunbayo
Milton Mogotsi
Makgotso Maotoana
Lutfiyya Mohamed



NHLS Division of Virology
Sabeehah Vawda
Felicity Burt
Thokozani Mkhize
Diagnostic laboratory staff



Additional support and collaborators



NHLS

Koeleka Mlisana
Zinhle Makatini
Eugene Elliot
Florette K. Treurnicht
Kathleen Subramoney
Oluwakemi Laguda-Akingba
Shareef Abrahams
Greta Hoyland
Gloria Selabe
Elias Bereda
Jeannette Wadula

Hyrax Biosciences

Simon Travers

Cape Town HVTN Laboratory

Erica Anderson-Nissen
Anneta Naidoo

Ndlovu Research

Hugo Tempelman
CJ Umunnakwe

Lancet

Allison J. Glass
Raquel Viana

Ampath

Terry Marshall
Cindy van Deventer
Eddie Silberbauer

Pathcare Vermaak

Andries Dreyer
Howard Newman
Riaan Writes
Marianne Wolfaardt
Warren Lowman

Bridge-the-Gap

Raymond Rott

Cytespace Africa Laboratories

Christa Viljoen

ARC-OVI

Lia Rotherham

CAPRISA

Salim Abdool Karim
Nigel Garret

UKZN - Big Data

Francesco Pettruccione
Ilya Sinayskiy

University of Oxford

José Lourenço

FioCruz, Brazil

Vagner Fonseca
Marta Giovanetti
Luiz Carlos Junior Alcantara

Africa CDC

John Nkengasong
Sofonias Tessema

Netcare:

Richard Friedland
Craig Murphy
Caroline Maslo
Liza Sitharam

DSI

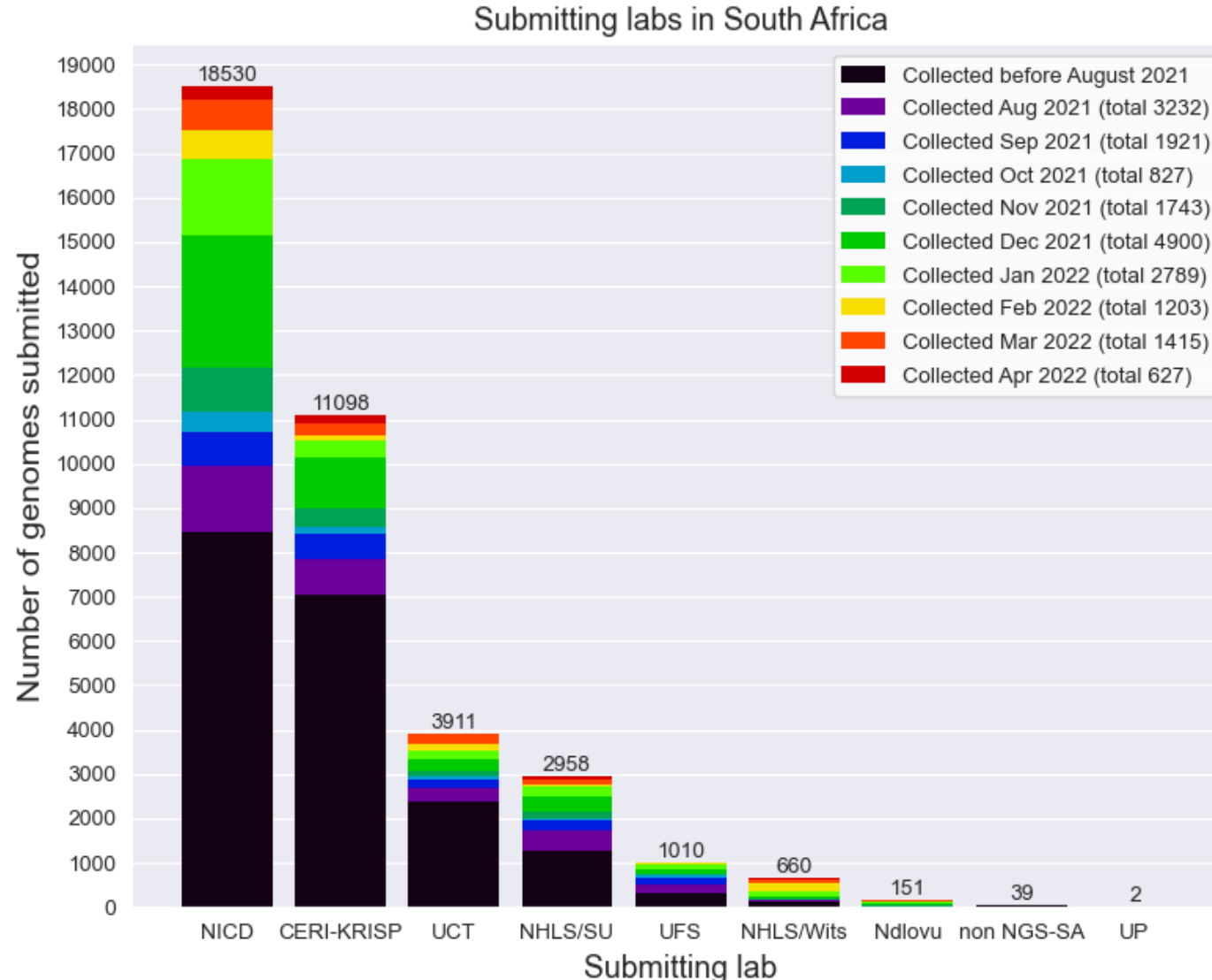
Glaudina Loots

SA MRC

Glenda Gray



South African genomes submitted per submitting lab, 2020 - 2022 (N=38 359)



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 (≥ 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.)