

SARS-CoV-2 Sequencing Update 11 November 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 11 November 2022 at 10h48

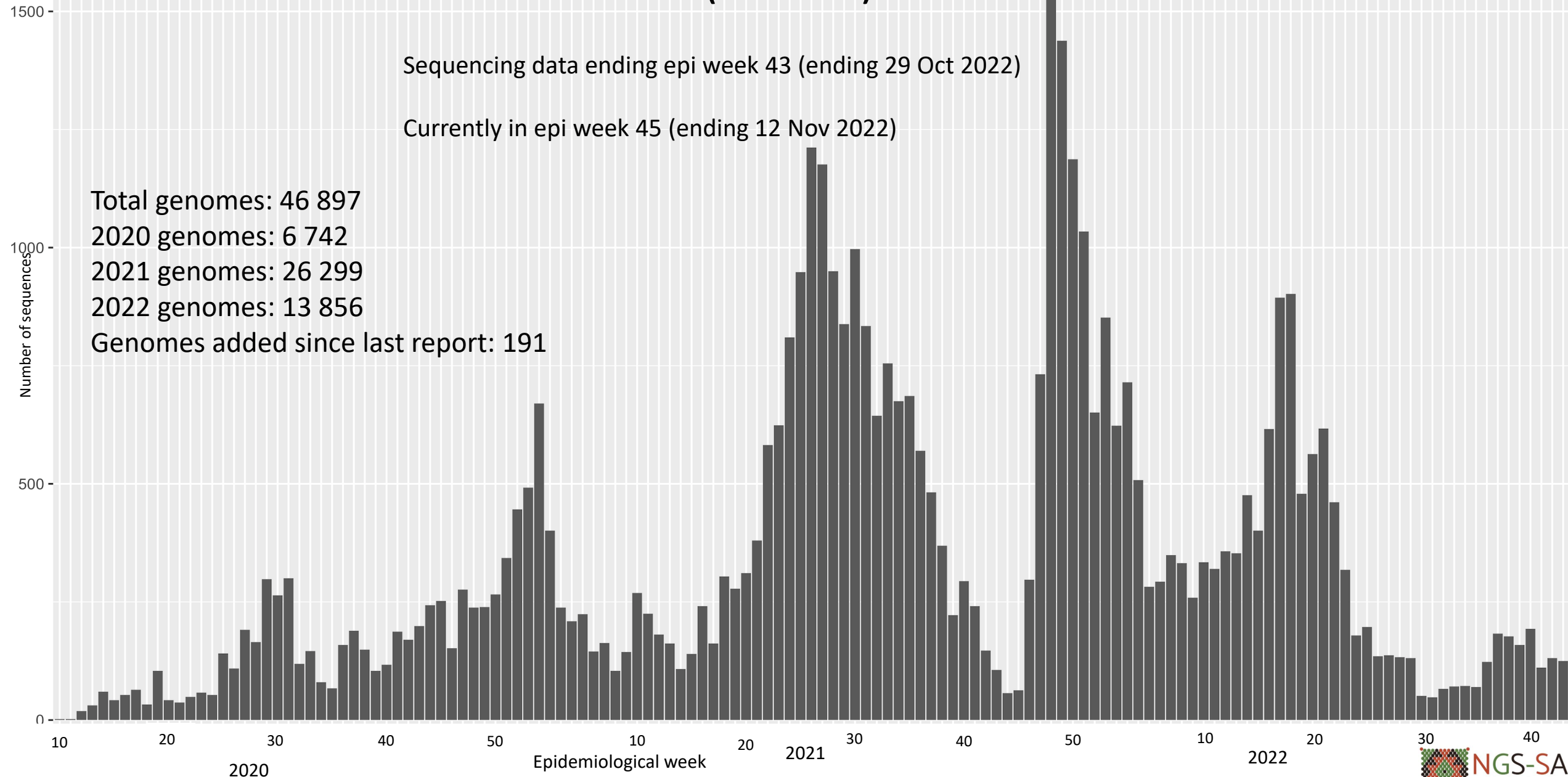


Data license: <https://www.gisaid.org/registration/terms-of-use/>

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

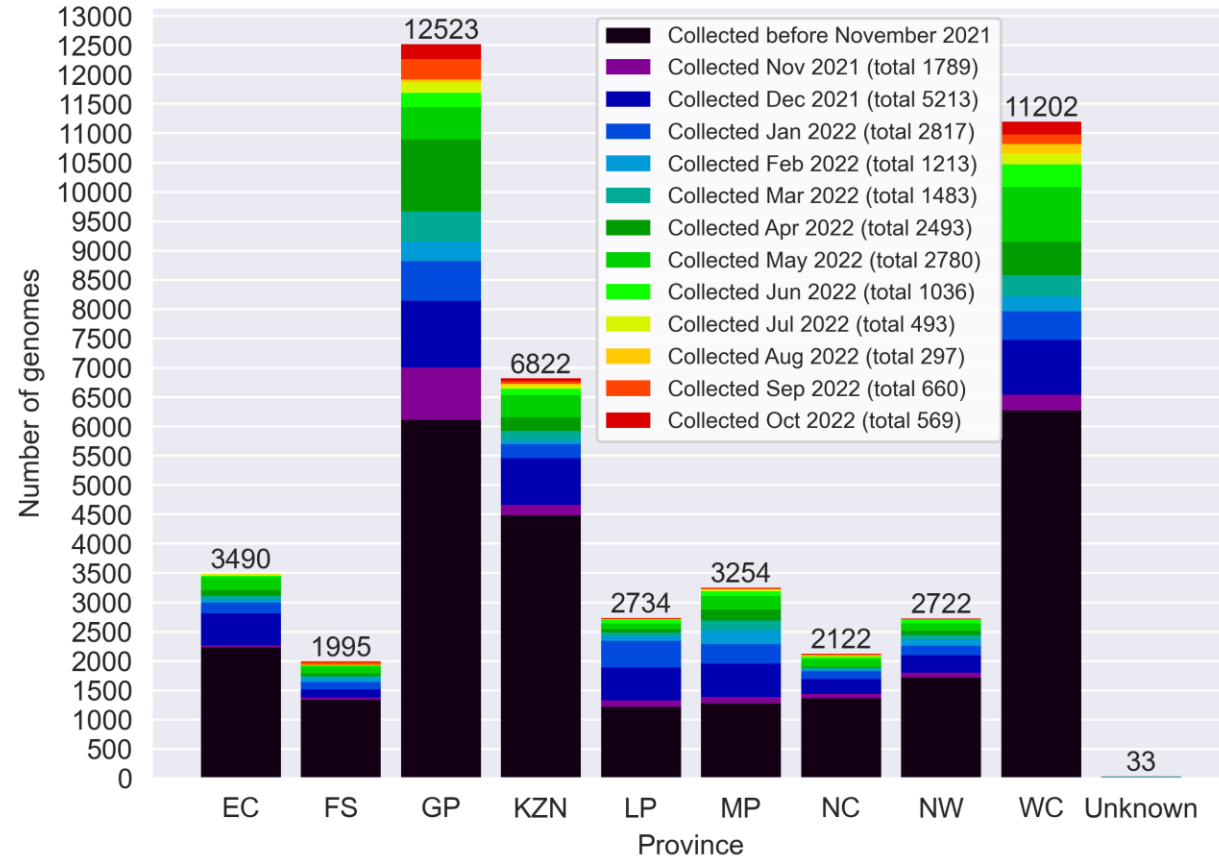
Number of South African genomes deposited on GISAID, by specimen collection week, 2020 – 2022
(N=46 897*)



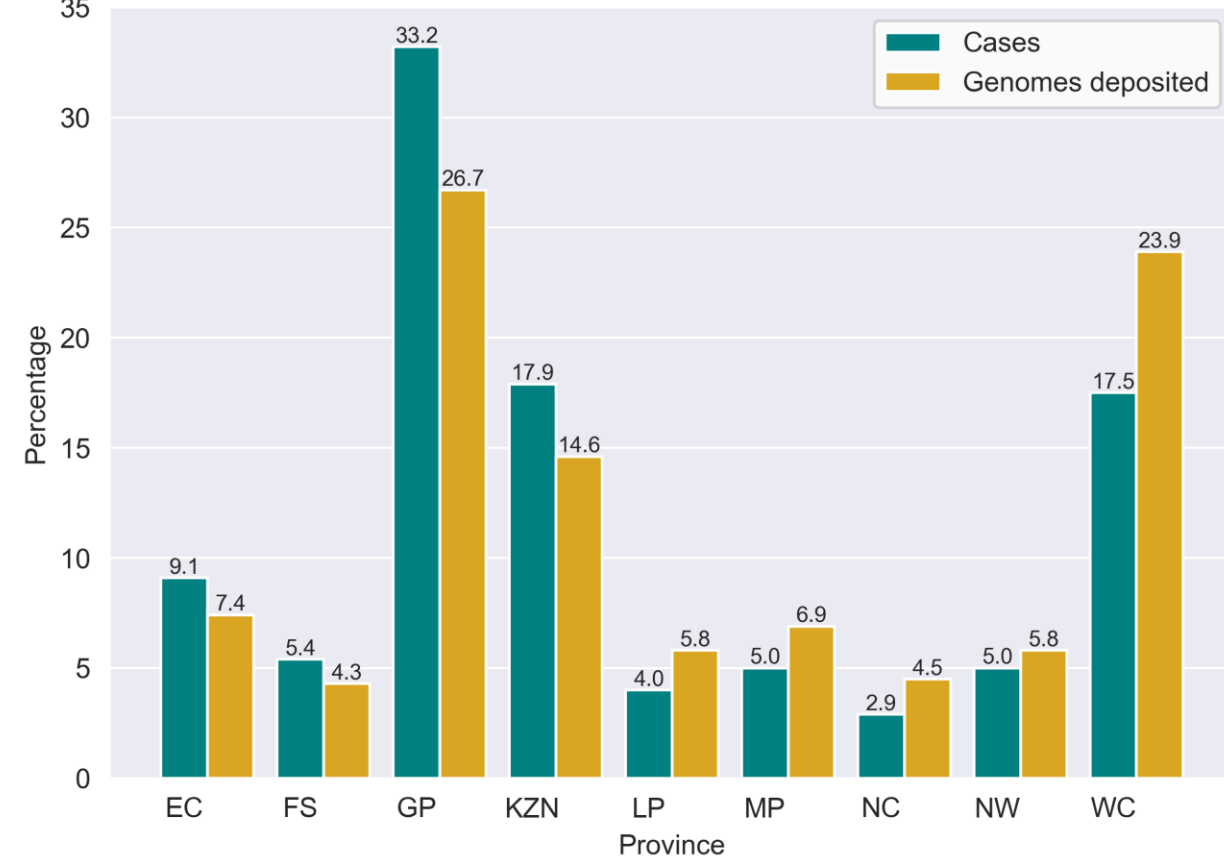
*This represents the cleaned, de-duplicated dataset of unique **National and Pneumonia Surveillance** sequences. This dataset will be used for all further figures.

GISAID genomes vs total cases, 2020 – 2022 (N=46 897)

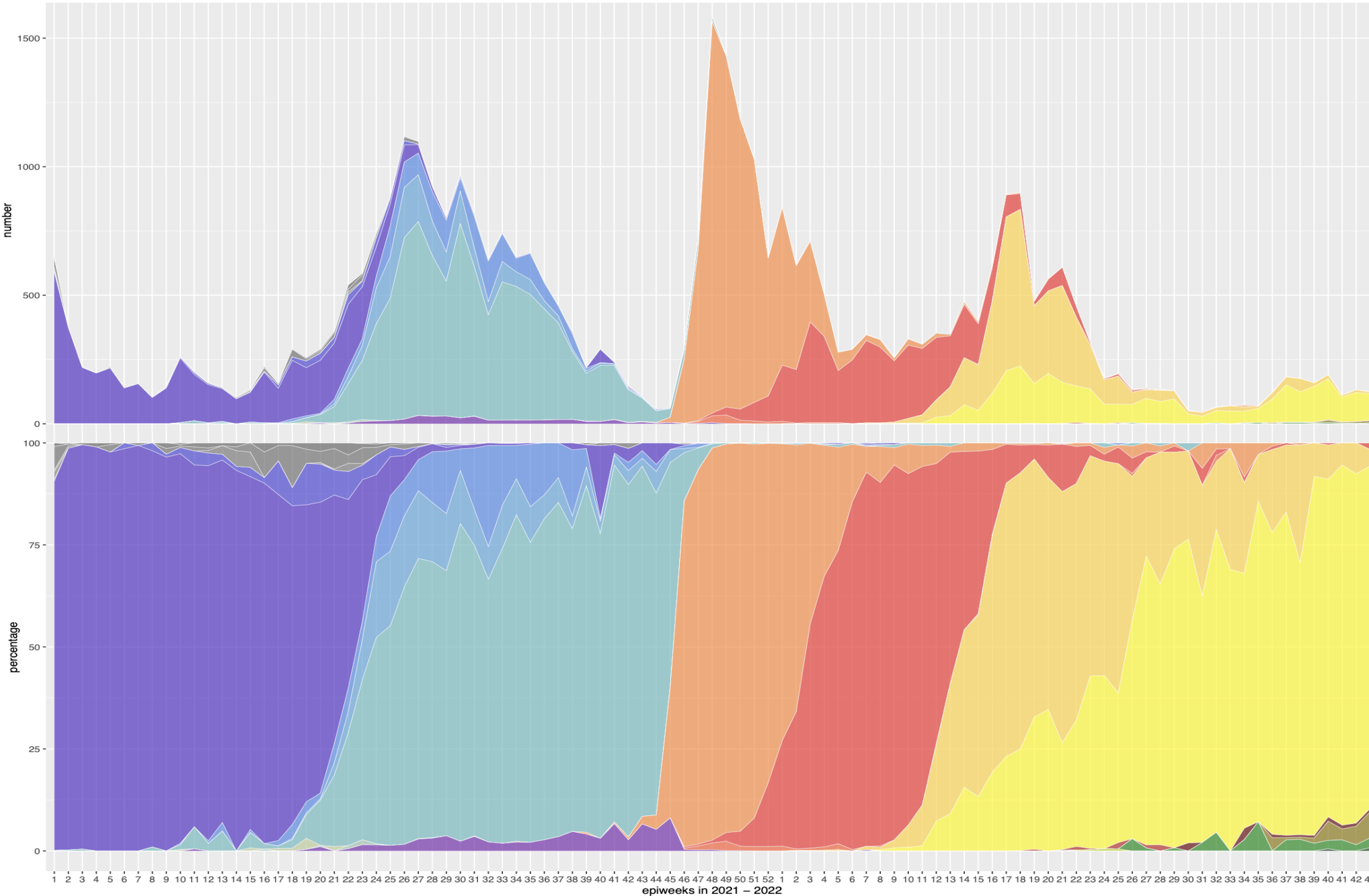
Provincial breakdown of genomes deposited into GISAID



Proportion of total cases versus proportion of total genomes



Number and percentage of clades by epiweek in South Africa, 2021 – 2022 (40 068*)



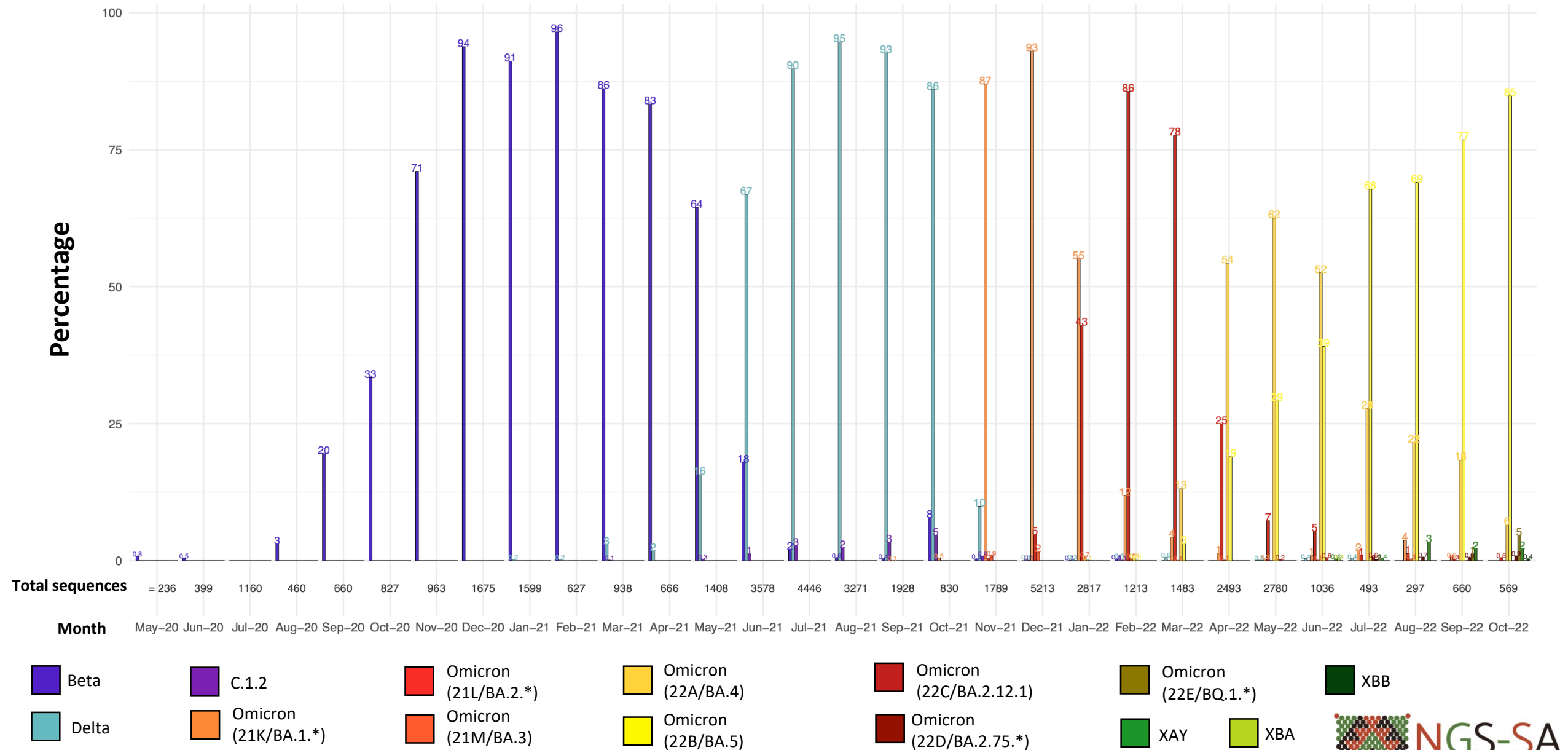
Sequencing data
ending epi week 43
(ending 29 Oct
2022)

Currently in epi
week 45 (ending 12
Nov 2022)

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

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

Detection rates of variants being monitored in South Africa

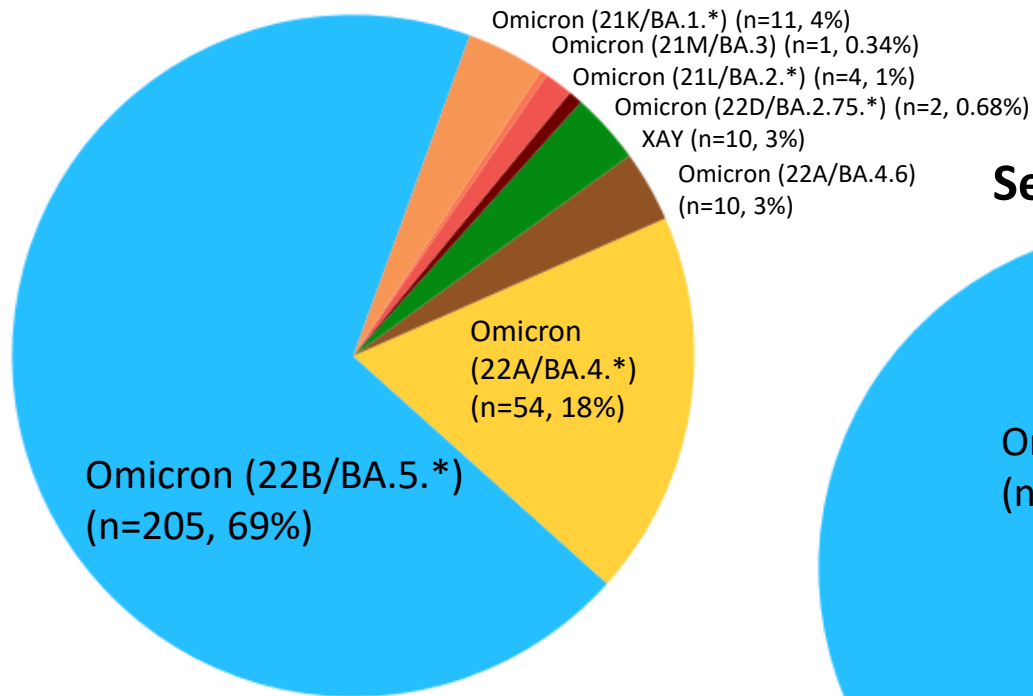


*Bars represent percentage prevalence of variant for the month; total number sequences collected for the month are given below the bar

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

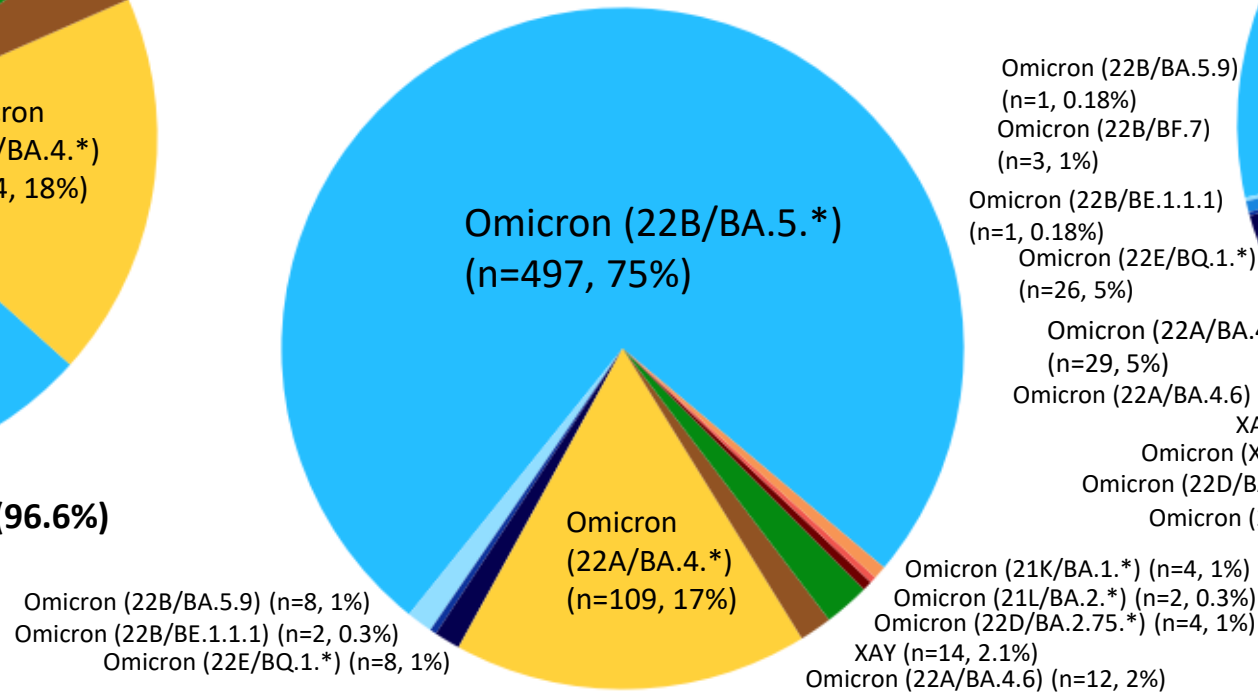
August – October 2022

August (N=297)



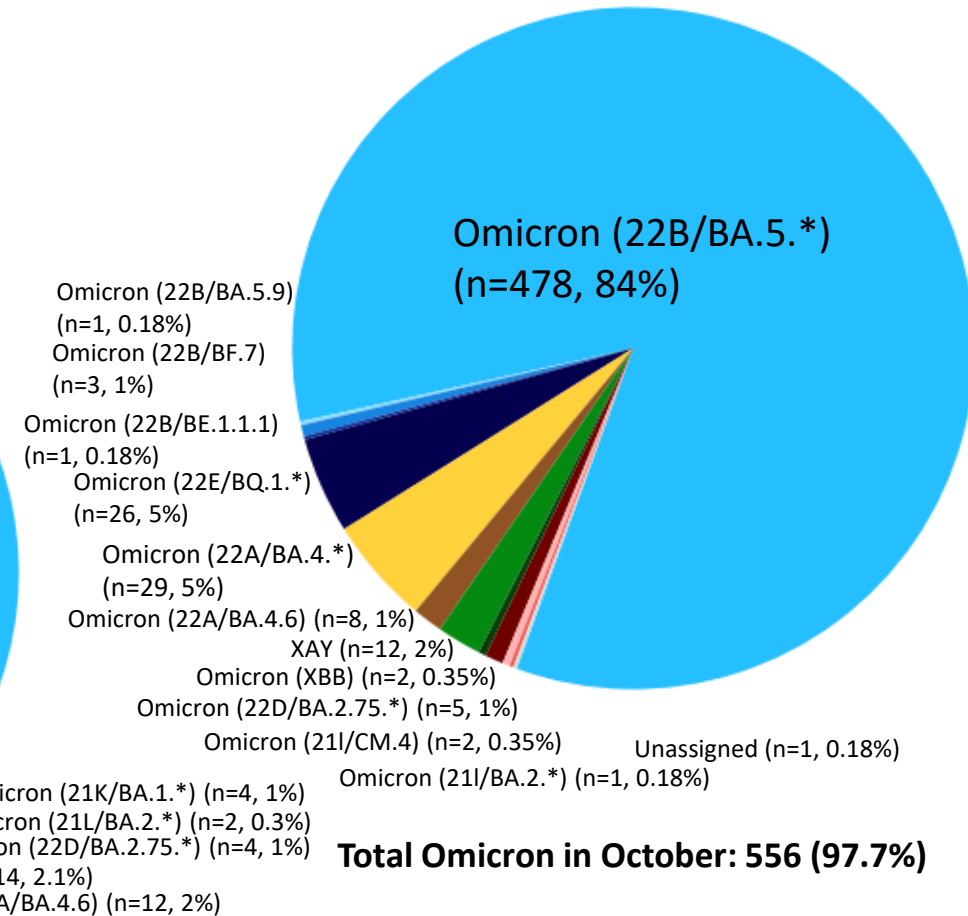
Total Omicron in August: 287 (96.6%)

September (N=660)

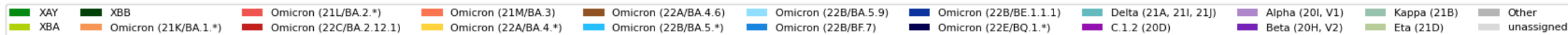


Total Omicron in September: 646 (97.9%)

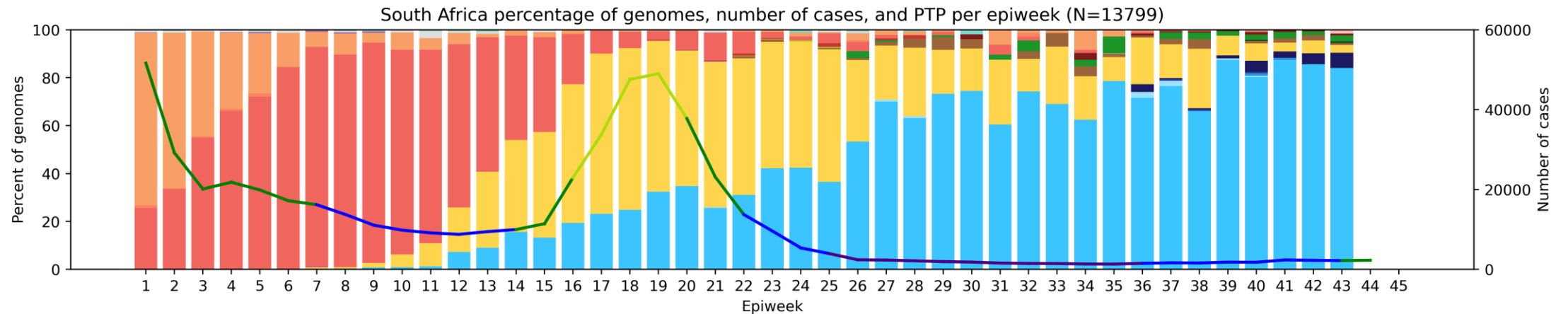
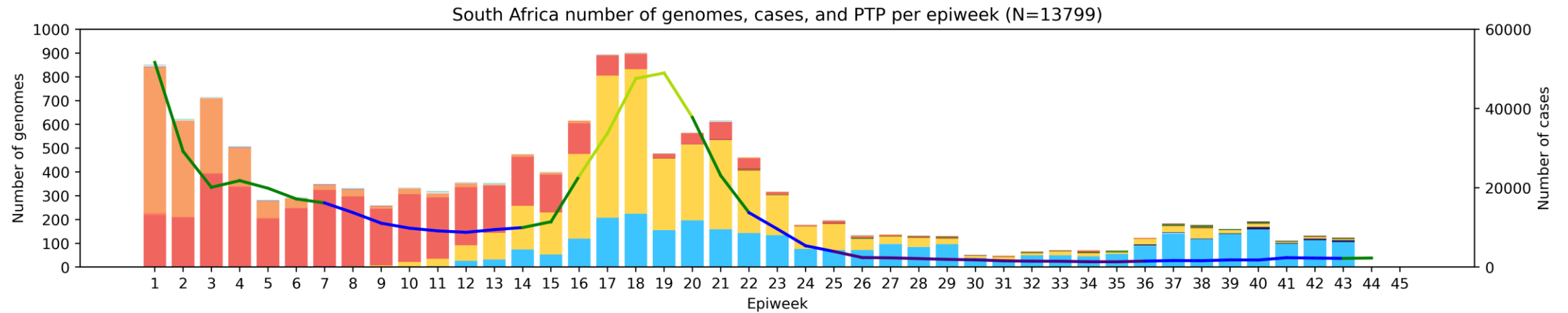
October (N=569)



Total Omicron in October: 556 (97.7%)



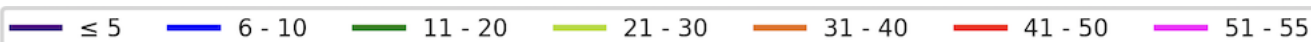
South Africa, 2022, n = 13 799*



Clade key (bar graph)



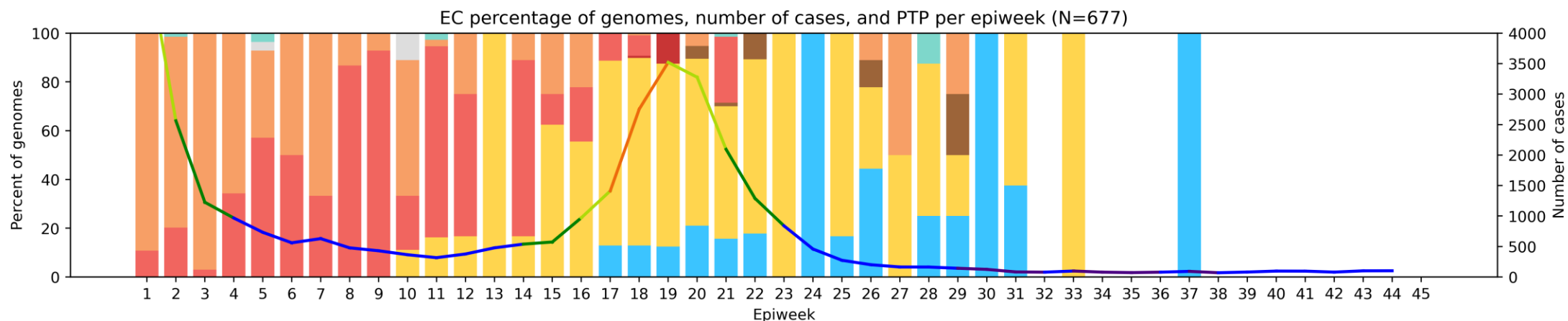
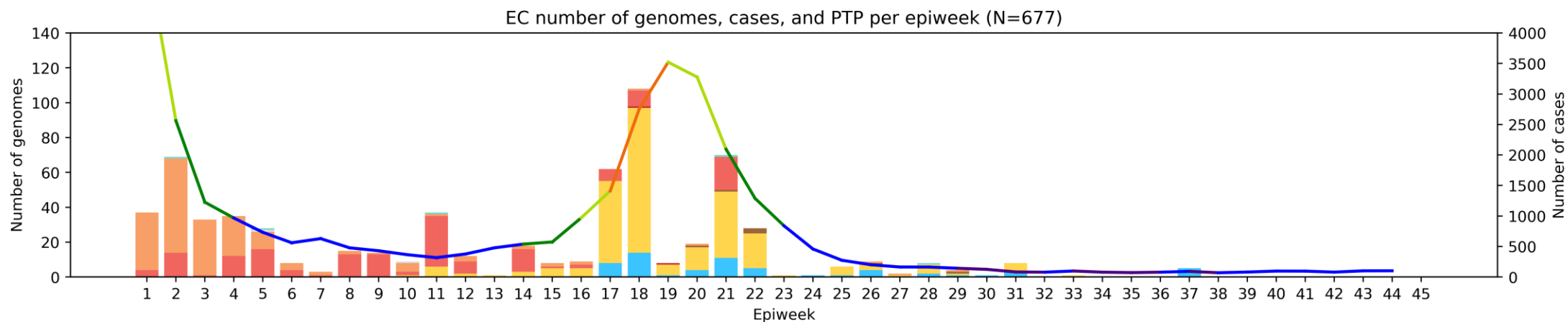
Weekly percentage testing positive key (line graph)



*Excludes sequences missing collection dates. Lineages of particular interest (currently WHO Omicron subvariants under monitoring) are separate from the main clade groupings.

Eastern Cape Province, 2022, n = 677

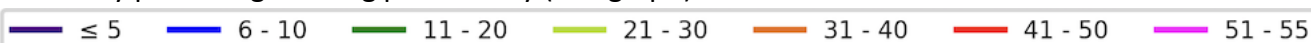
Genomes added since last report: 3*



Clade key (bar graph)



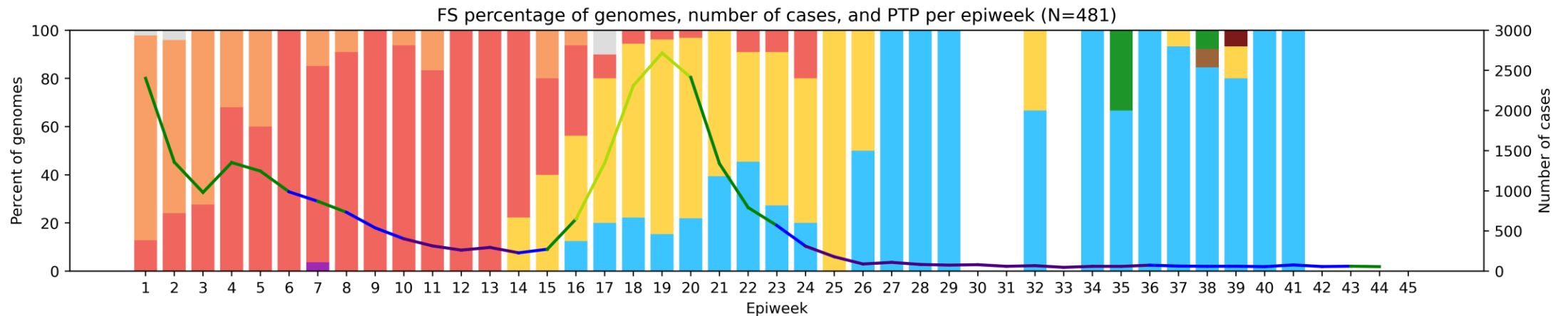
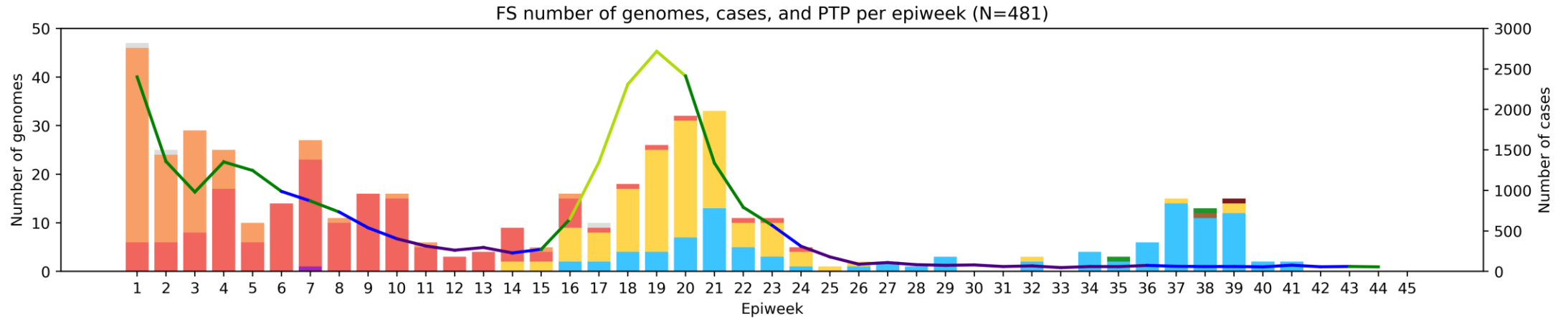
Weekly percentage testing positive key (line graph)



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

Free State Province, 2022, n = 481

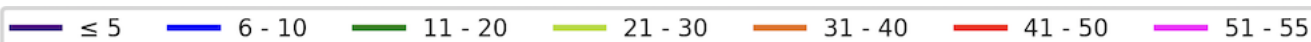
Genomes added since last report: 0*



Clade key (bar graph)



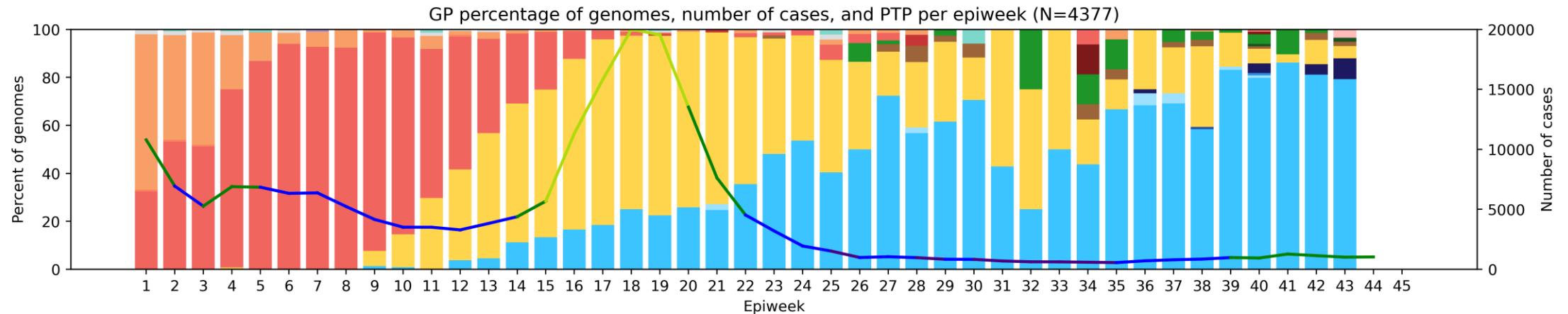
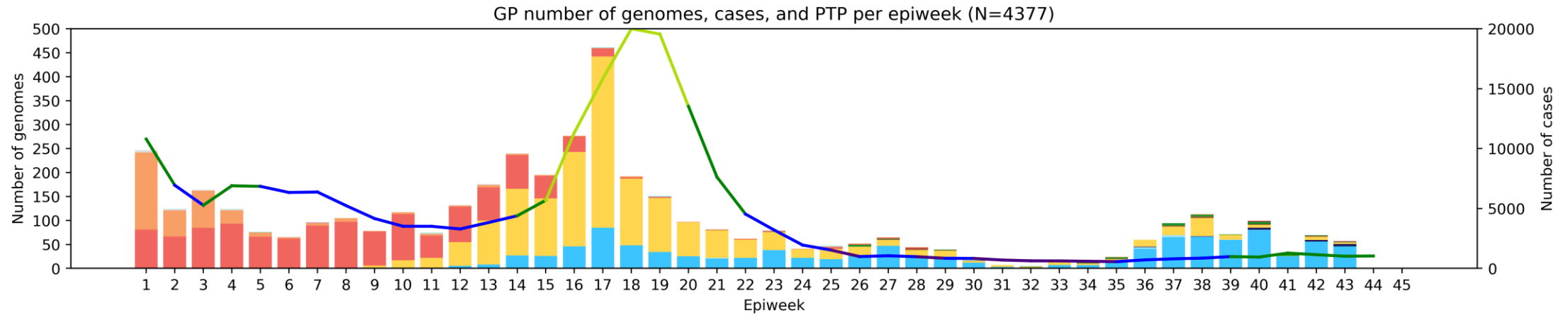
Weekly percentage testing positive key (line graph)



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

Gauteng Province, 2022, n = 4377

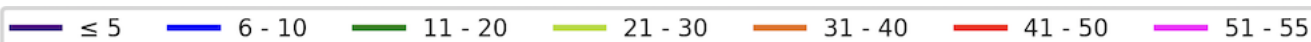
Genomes added since last report: 77*



Clade key (bar graph)



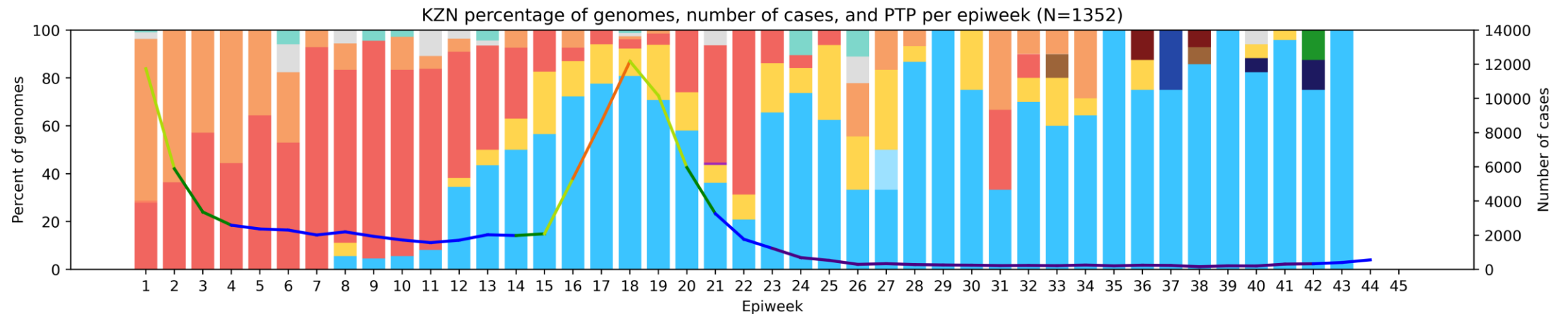
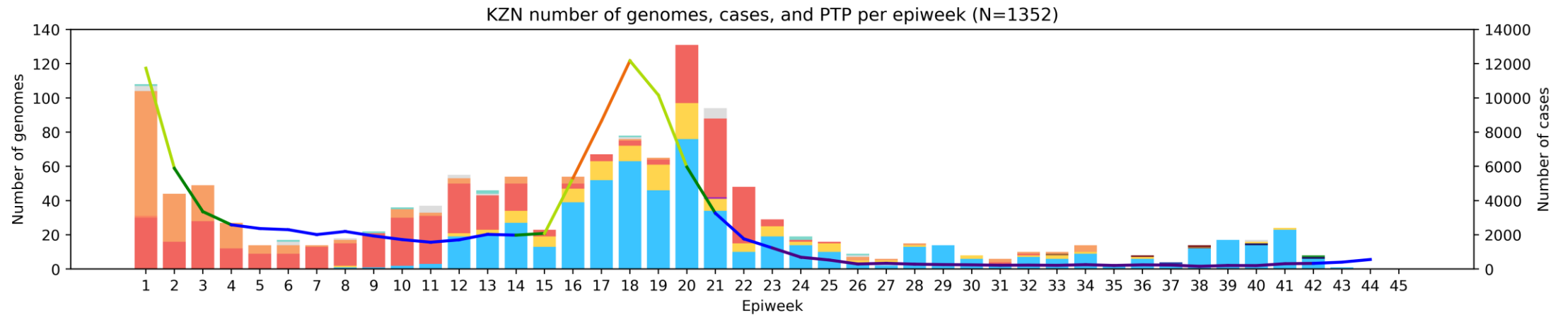
Weekly percentage testing positive key (line graph)



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

KwaZulu-Natal Province, 2022, n = 1352

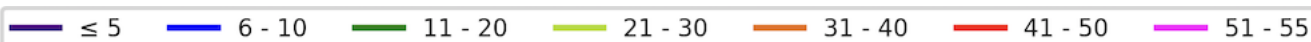
Genomes added since last report: 9*



Clade key (bar graph)



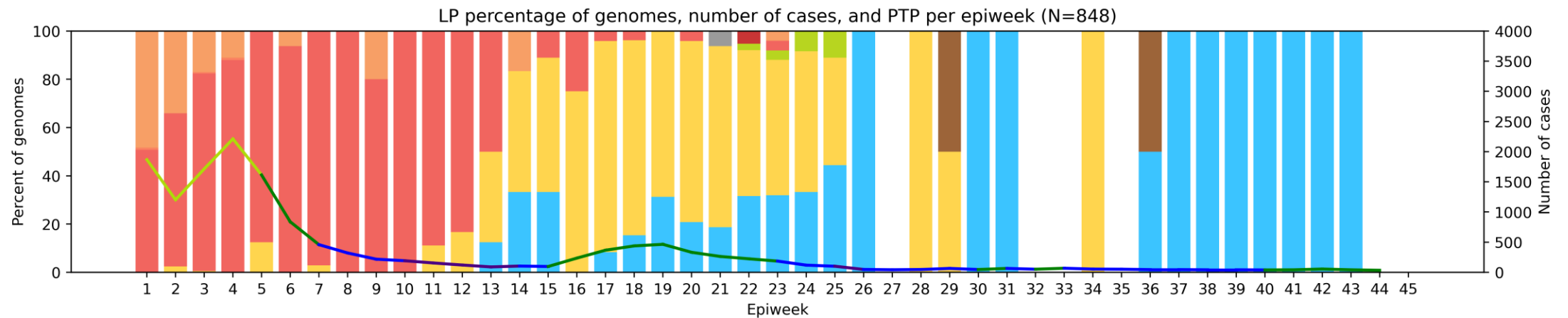
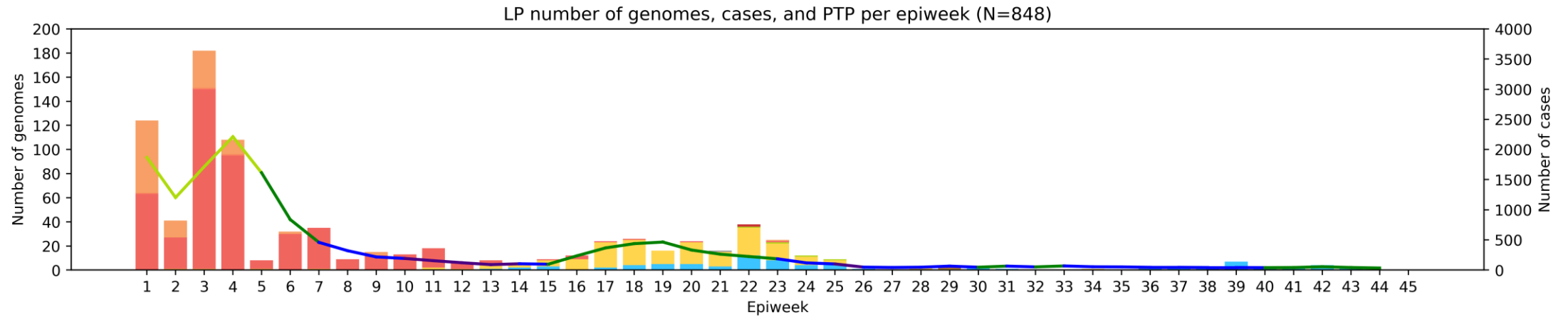
Weekly percentage testing positive key (line graph)



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

Limpopo Province, 2022, n = 848

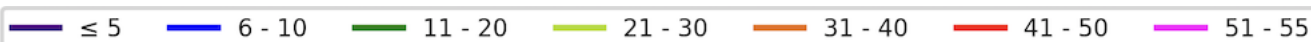
Genomes added since last report: 11*



Clade key (bar graph)



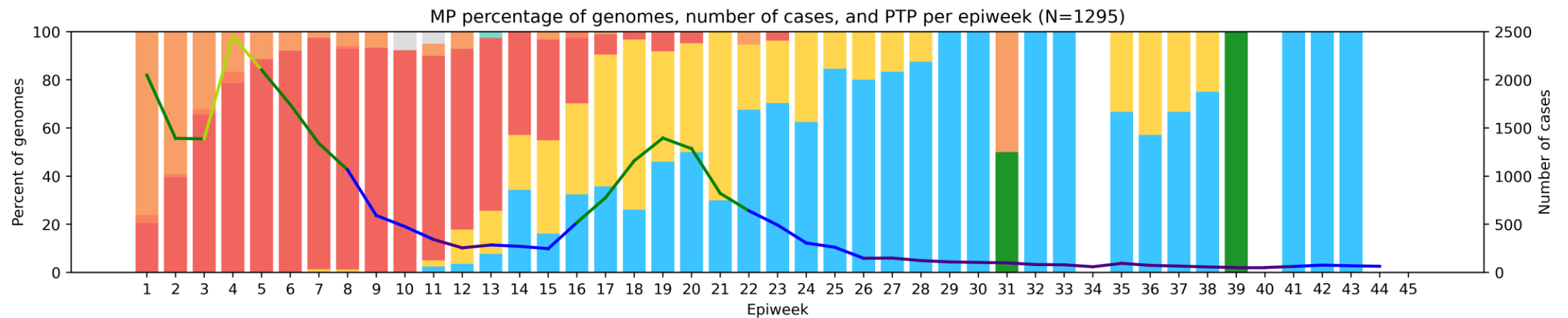
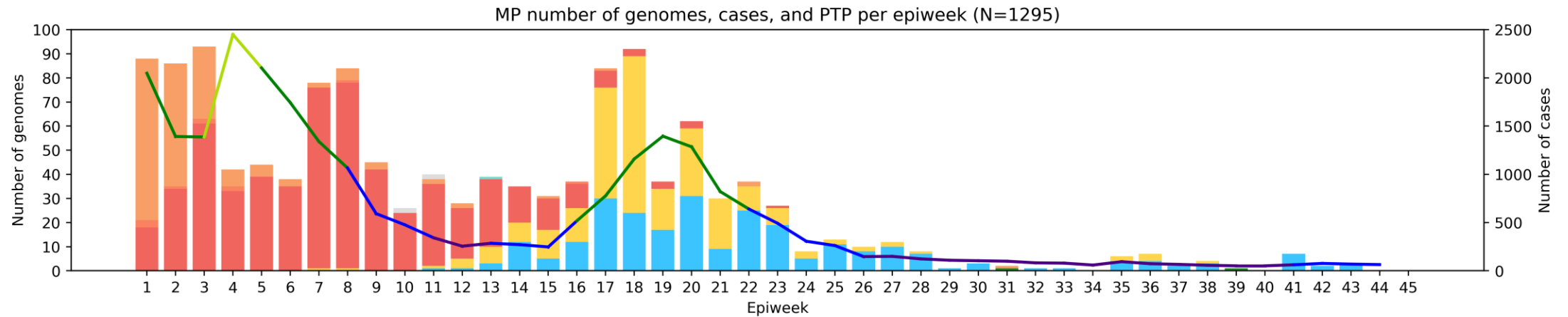
Weekly percentage testing positive key (line graph)



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

Mpumalanga Province, 2022, n = 1295

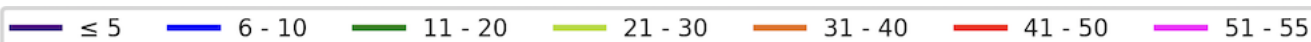
Genomes added since last report: 4*



Clade key (bar graph)



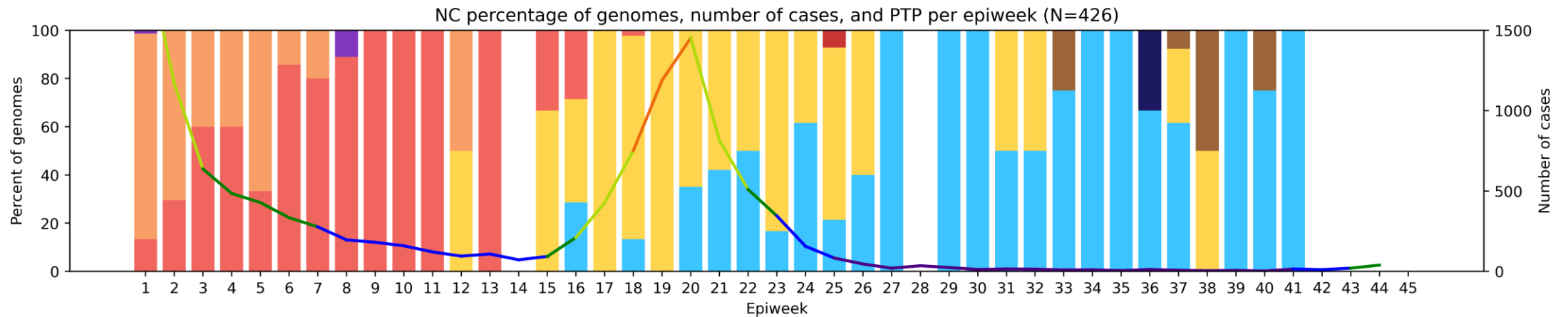
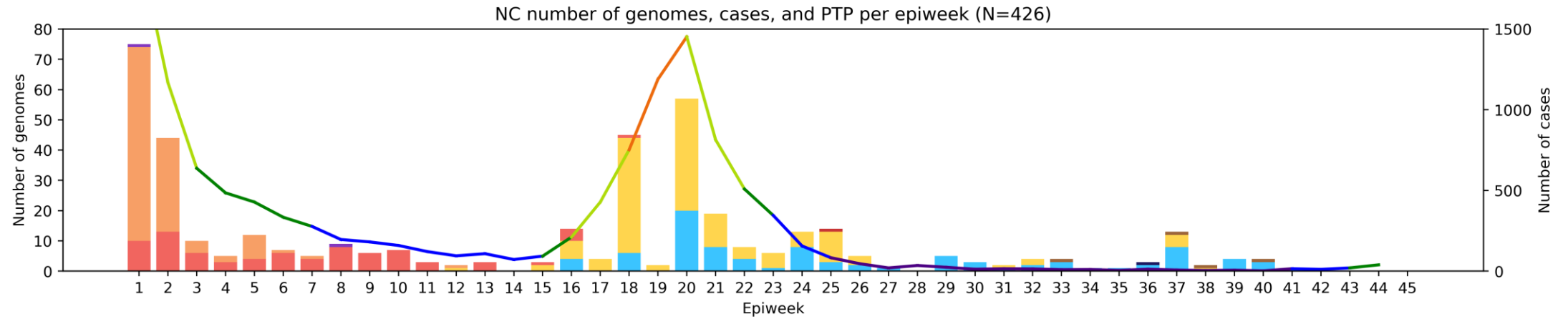
Weekly percentage testing positive key (line graph)



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

Northern Cape Province, 2022, n = 426

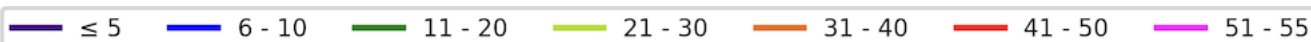
Genomes added since last report: 0*



Clade key (bar graph)



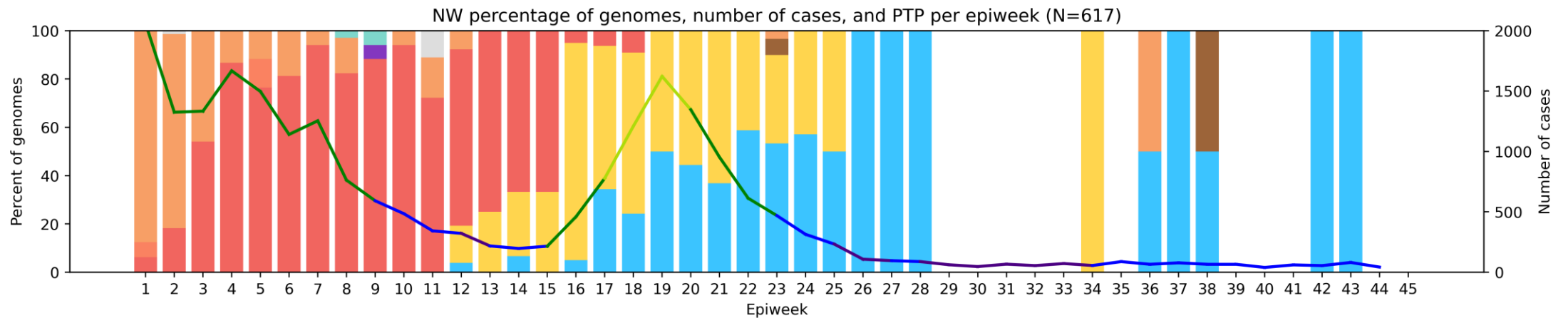
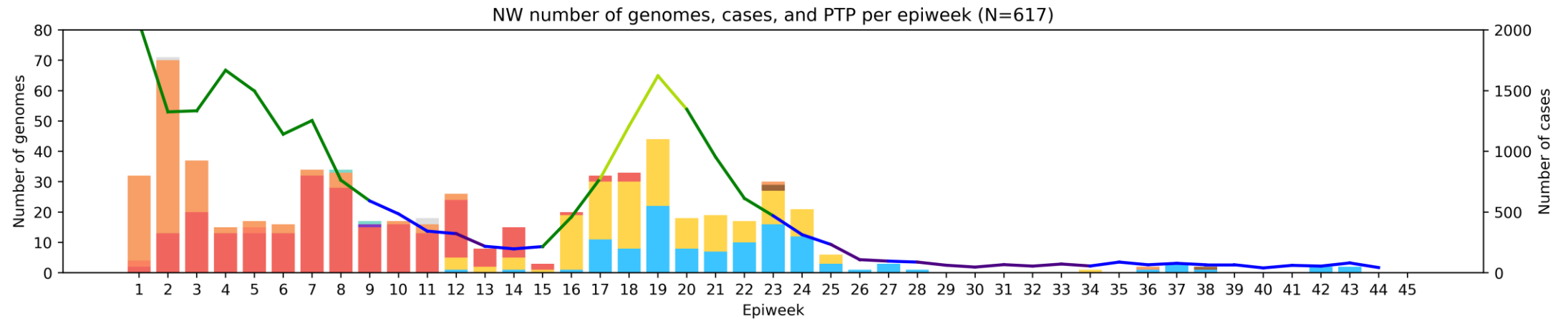
Weekly percentage testing positive key (line graph)



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

North West Province, 2022, n = 617

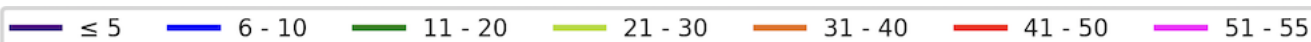
Genomes added since last report: 2*



Clade key (bar graph)



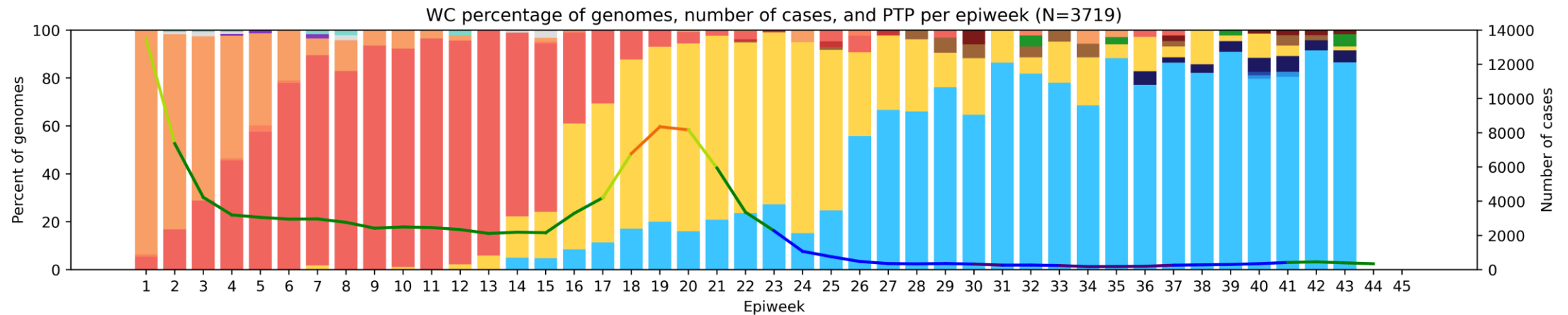
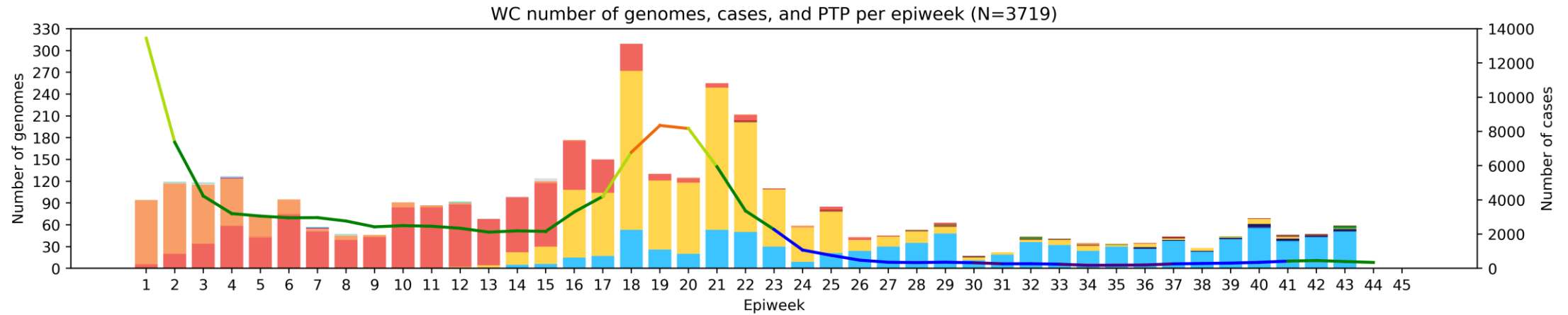
Weekly percentage testing positive key (line graph)



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

Western Cape Province, 2022, n = 3719

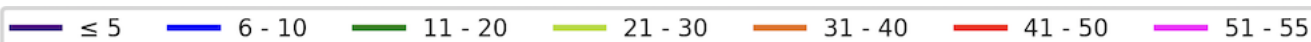
Genomes added since last report: 85*



Clade key (bar graph)



Weekly percentage testing positive key (line graph)

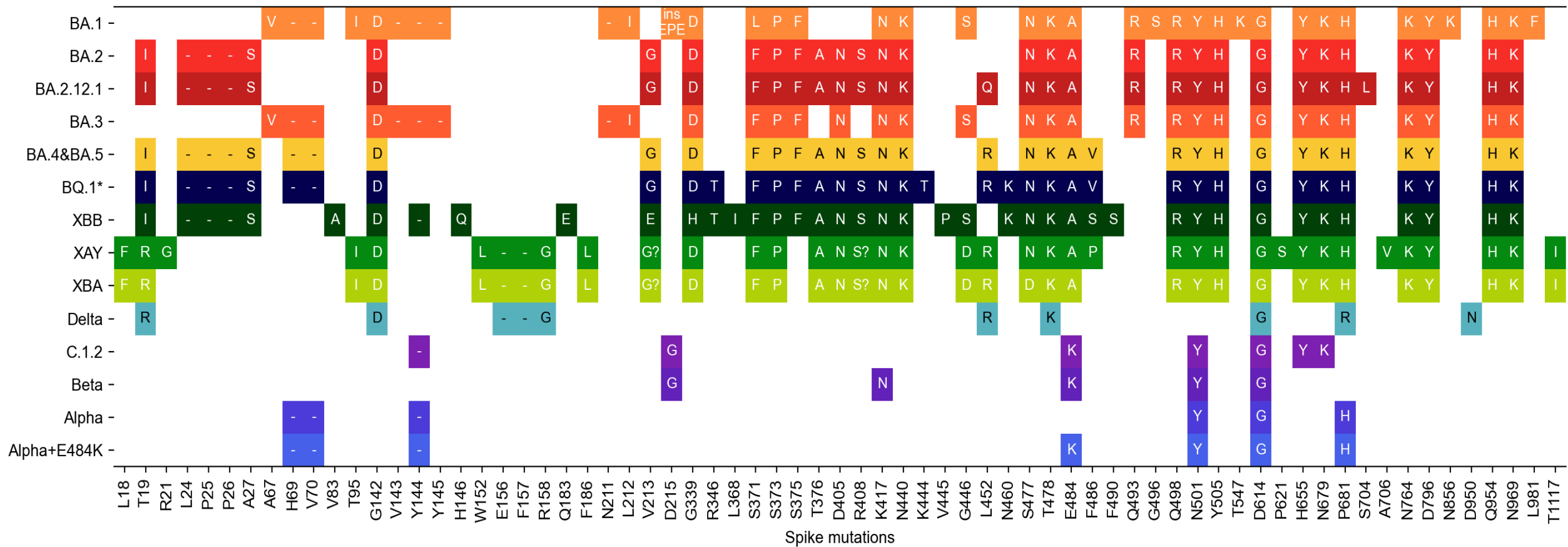


*May include genomes from 2020 which are not pictured here and are not included in the slide total.

Summary

- **Sequencing update**
 - All provinces have sequences for August and September.
 - All provinces, except the Eastern Cape, have sequences for October.
- **Variant of Concern Omicron in South Africa**
 - Omicron continued to dominate in August (97%), September (98%) and currently makes up 98% of October sequences.
 - Omicron BA.5 and sub-lineages were dominant in August (69%), September (78%) and currently make up 90% of October data.
 - BA.2.75.* has been detected in July through October at a low prevalence ($\leq 1\%$).
 - XAY continues to be detected at a low prevalence ($\leq 3\%$)
 - XAY has also been detected in Denmark (n=18), Israel (n=2), the USA (n=2), England (n=1), and Sweden (n=1)
 - BQ.1 and BQ.1.1 have been detected in South Africa in September and October
 - September (1%) - BQ.1: n=1 in the Northern Cape, n=4 in the Western Cape; BQ.1.1: n=1 in Gauteng, n=2 in the Western Cape
 - October (5%) - BQ.1: n=1 in KwaZulu-Natal, n=4 in Gauteng, n=8 in the Western Cape; BQ.1.1: n=8 in Gauteng, n=4 in the Western Cape, n=1 in KwaZulu-Natal
 - XBB has been detected in South Africa in October (n=2, Gauteng)
- Low frequency of previously circulating variants such as Delta not detected since July.

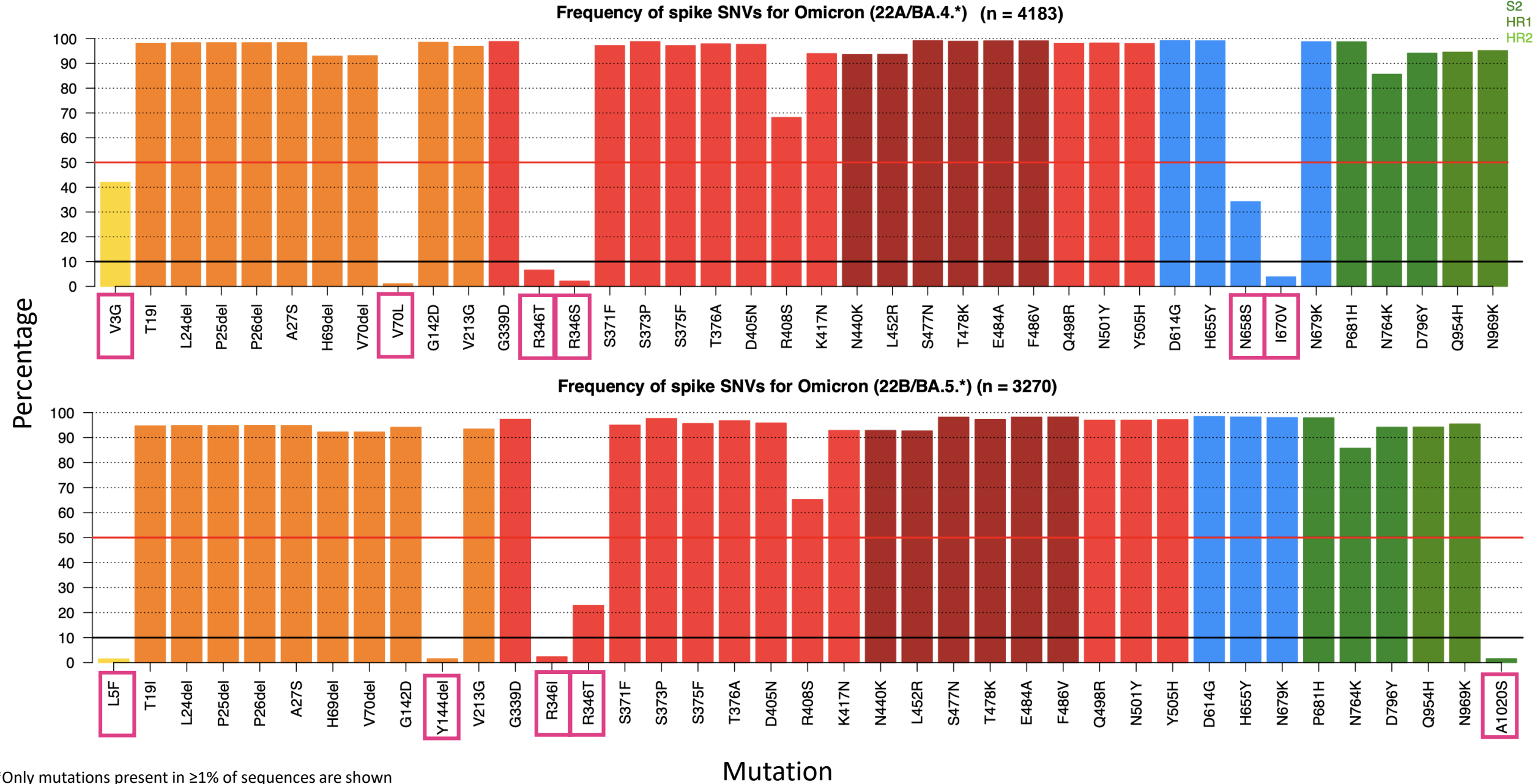
Spike protein mutation* profile of Variants of Interest and Concern



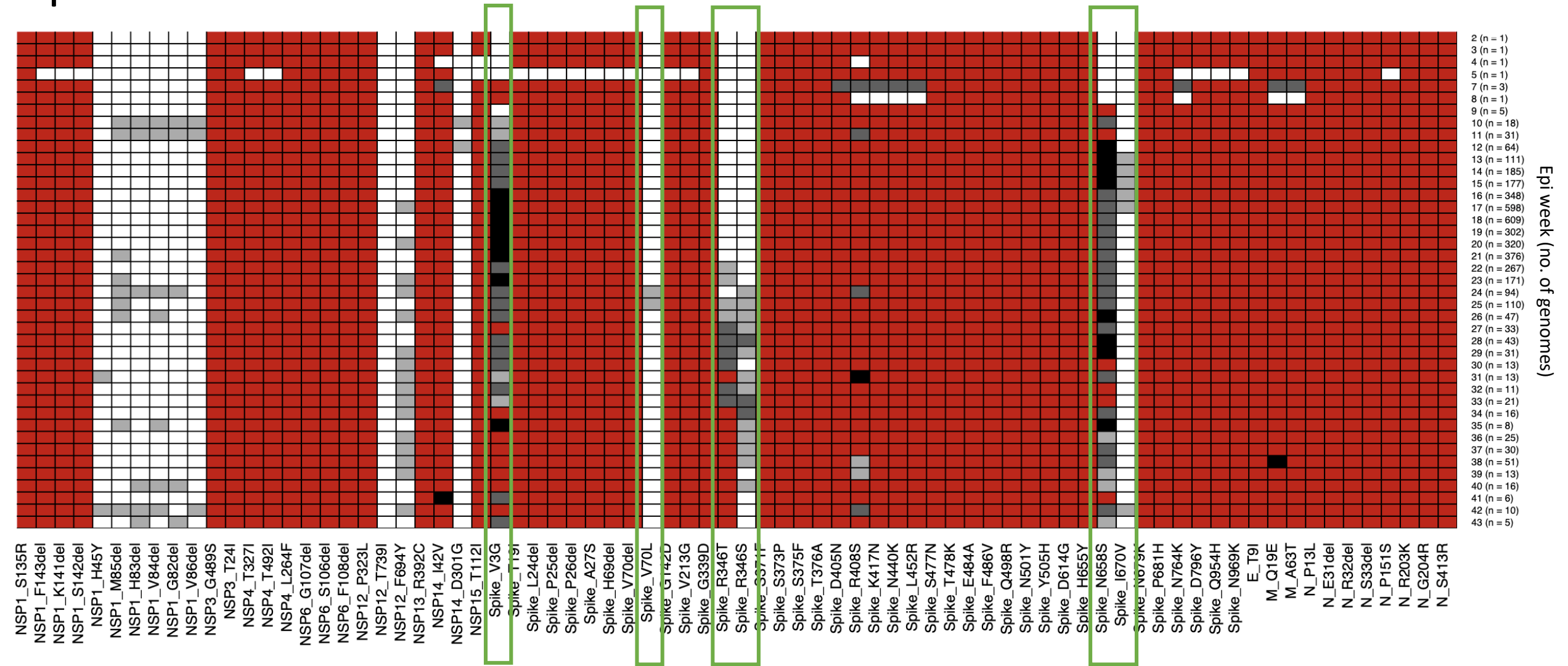
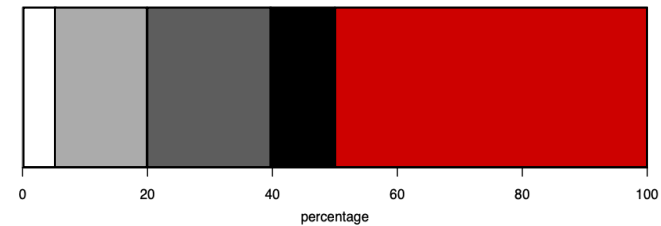
- Multiple changes within the two immunogenic regions in S1 (NTD and RBD)
 - Including a three amino acid insertion
- Accumulation of mutations surrounding the furin cleavage site
 - Including combination of N679K and P681H
- Effect of most spike S2 subunit changes have not been defined, but may be linked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

*Only mutations present in Omicron, Delta, or recombinant sequences are pictured

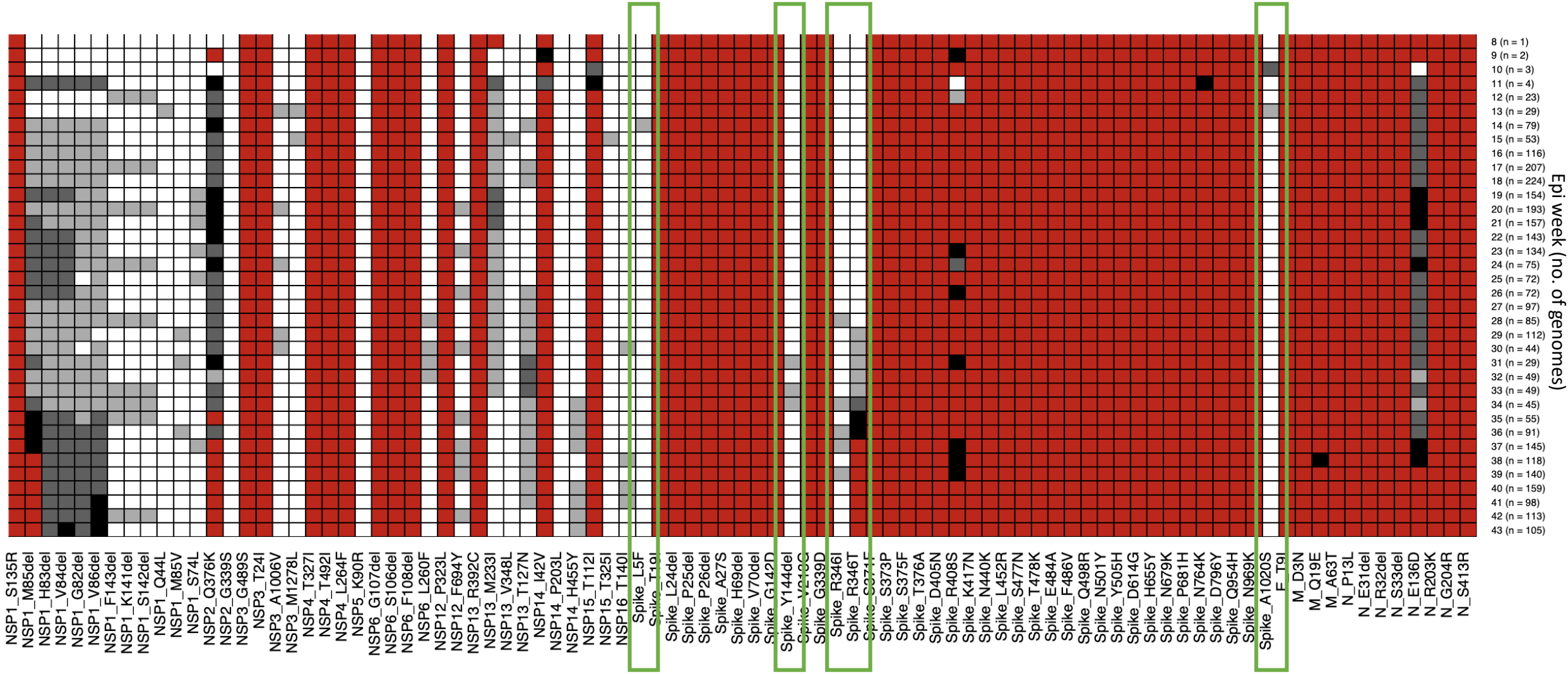
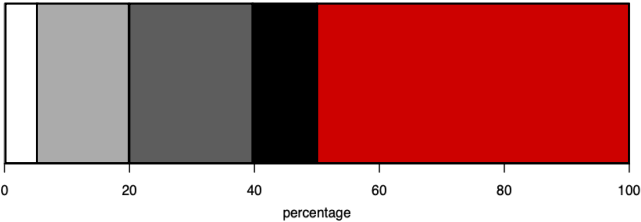
BA.4 and BA.5 spike mutations*



BA.4 whole genome mutation prevalence over time



BA.5 whole genome mutation prevalence over time





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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

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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



UCT, IDM and CIDRI-Africa

Deelan Doolabh
Arash Iranzadeh
Lynn Tyers
Innocent Mudau
Nokuzola Mbhele
Fezokuhle Khumalo
Thabang Serake
Bruna Galvão
Arghavan Alisoltani
(U. California)

Robert Wilkinson
Darren Martin
Nicola Mulder
Wendy Burgers
Ntobeko Ntusi
Rageema Joseph
Sean Wasserman
Linda Boloko



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

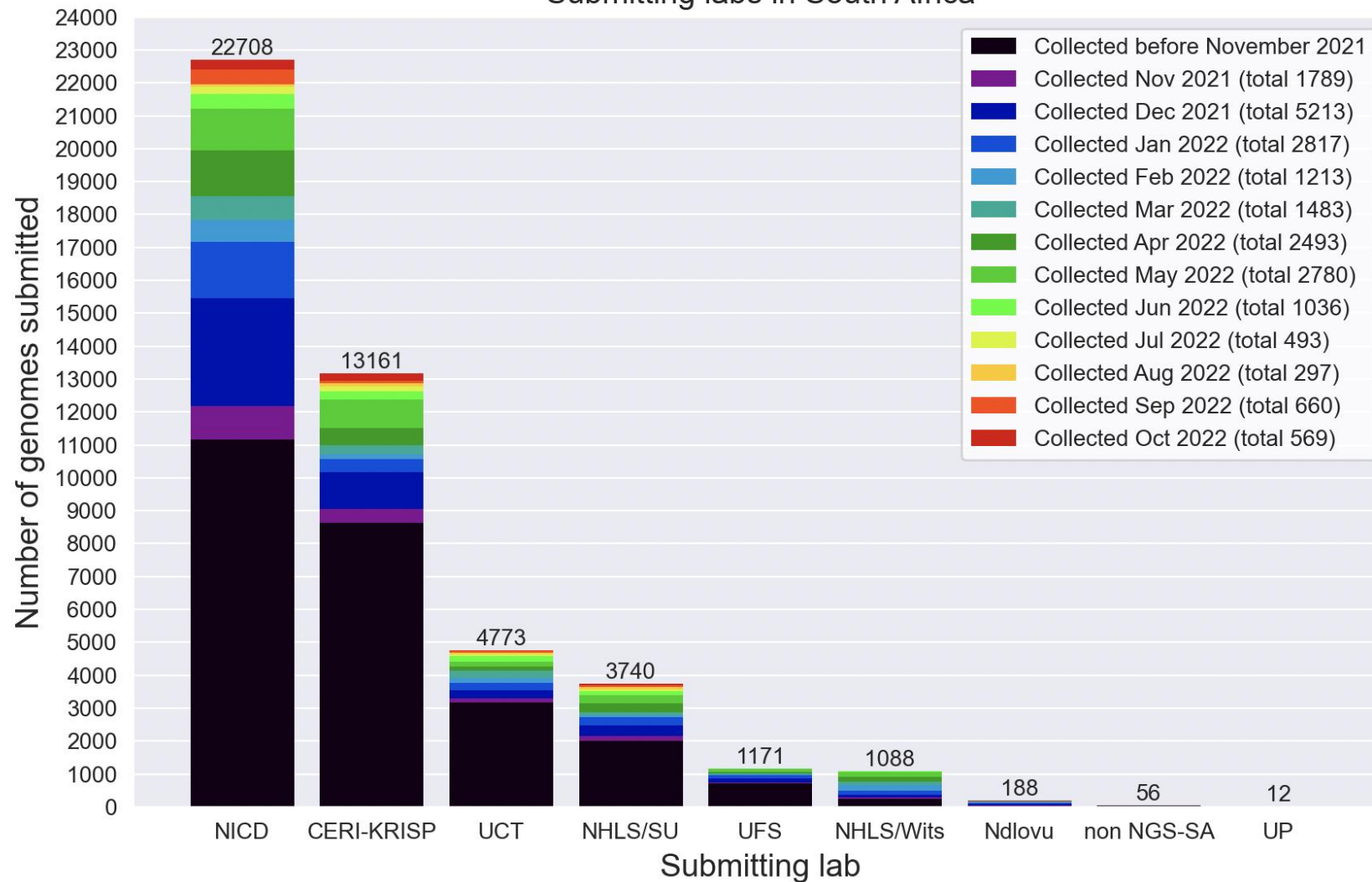
SA MRC

Glenda Gray



South African genomes submitted per submitting lab, 2020 - 2022 (N=46 897)

Submitting labs in South Africa



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

Omicron subvariants under monitoring

Pango lineage [#] (+ mutation)	GISAID clade	Nextstrain clade	Relationship to circulating VOC lineages	Spike genetic features	Earliest documented samples
BA.5** (+R346X or +K444X or +V445X or +N450D or +N460X)	GRA	22B	BA.5 sublineages (e.g. BF.7, BF.14, BQ.1)	BA.5 + one or more of these mutations: S:R346X, S:K444X, S:V445X, S:N450D or S:N460X	07-02-2022
BA.2.75***	GRA	22D	BA.2 sublineage	BA.2.75: BA.2 + S:K147E, S:W152R, S:F157L, S:I210V, S:G257S, S:D339H, S:G446S, S:N460K, S:Q493R reversion BA.2.75.2: BA.2.75 + S:R346T, S:F486S, S:D1199N	31-12-2021
BJ.1****	GRA	21L	BA.2 sublineage (B.1.1.529.2.10.1.1)	BA.2+S:V83A, S:Y144-, S:H146Q, S:Q183E, S:V213E, S:G339H, S:R346T, S:L368I, S:V445P, S:G446S, S:V483A, S:F490V, S:G798D, S:S1003I	06-09-2021
BA.4.6	GRA	22A	BA.4 sublineage	BA.4+S:R346T, S:N658S	20-07-2020
XBB [§]		recombinant	Recombinant of BA.2.10.1 and BA.2.75 sublineages, i.e. BJ1 and BM.1.1.1, with a breakpoint in S1	BA.2+ S:V83A, S:Y144-, S:H146Q, S:Q183E, S:V213E, S:G252V, S:G339H, S:R346T, S:L368I, S:V445P, S:G446S, S:N460K, S:F486S, S:F490S	13-08-2022
BA.2.3.20 [§]	GRA	21L	BA.2 sublineage	BA.2+ S:M153T, S:N164K, S:H245N, S:G257D, S:K444R, S:N450D, S:L452M, S:N460K, S:E484R	15-08-2022

* these subvariants are tracked under Omicron unless/until sufficient evidence arises that the virus characteristics are substantially different from what is known about the VOC they belong to. If this evidence arises, WHO will decide, in consultation with the TAG-VE, if designation of the emerging variant warrants a separate WHO label.

[#] includes descendent lineages

** additional mutations outside of the spike protein: N:G30-, N:S33F, N:E136D, ORF1a:Q556K, ORF1a:L3829F, ORF1b:Y264H, ORF1b:M1156I, ORF9b:P10F, ORF9b:D16G, ORF9b:M26-, ORF9b:A29I, ORF9b:V30L.

*** additional mutation outside the spike protein: ORF1a:S1221L, ORF1a:P1640S, ORF1a:N4060S; ORF1b:G662S; E:T11A

**** additional mutations outside of the spike protein: Mutations: M:D3Y, N:T282I, ORF1a:K47R, ORF1b:G662S, ORF1b:S959P, ORF7a:I110T

[§] additional mutations outside of the spike protein: E:T11A, ORF1a:K47R, ORF1b:G662S, ORF1b:S959P, ORF8:G8*

[§] additional mutations outside of the spike protein: ORF1a:T727I, ORF1a:I1714T, ORF1a:M2169V, ORF1a:T2174I, ORF1a:T2648I, ORF1a:A2909V, ORF1a:Q3922R, ORF1b:T1404M, ORF3a:L140F, ORF9b:D89E

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.)