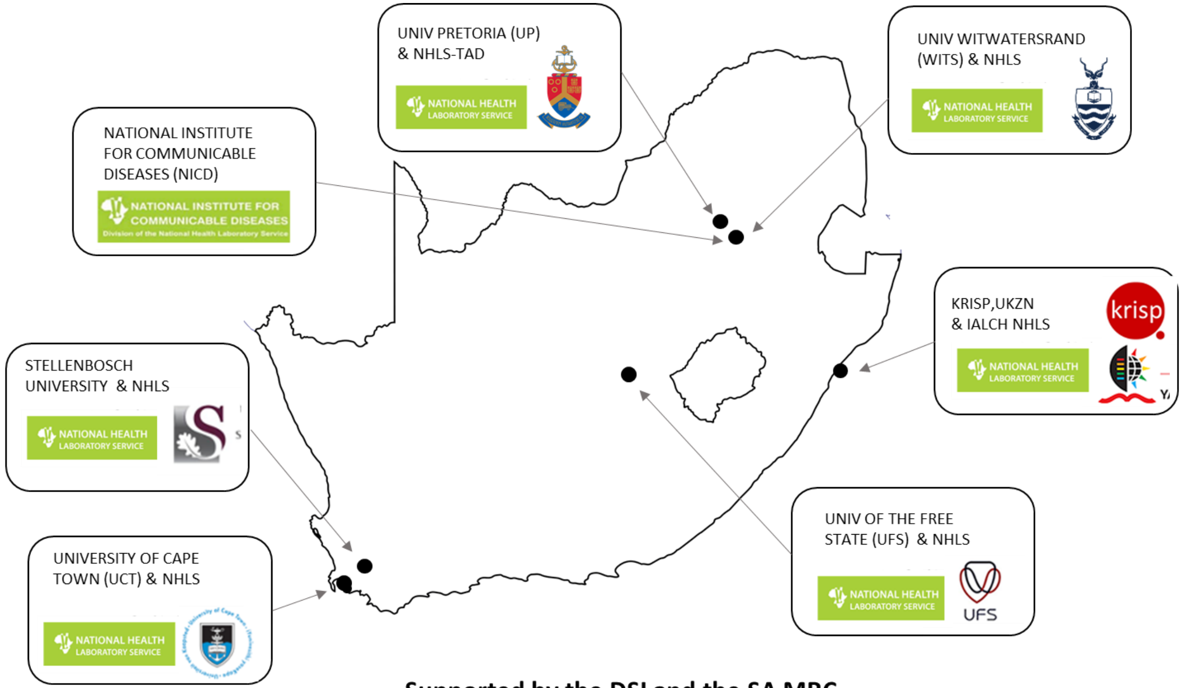
Network for Genomic Surveillance in South Africa (NGS-SA)

SARS-CoV-2 Sequencing Update

25 August 2023



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& NHLS-TAD

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(WITS) & NHLS

NATIONAL INSTITUTE
FOR COMMUNICABLE
DISEASES (NICD)

KRISP,UKZN
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TOWN (UCT) & NHLS

Supported by the DSI and the SA MRC

Msomi N, Mlisana K, et al. Lancet Microbe 2020

Prepared by the National Institute for Communicable Diseases (NICD) of the National Health Laboratory (NHLS) on behalf of the Network for Genomics Surveillance in South Africa (NGS-SA)

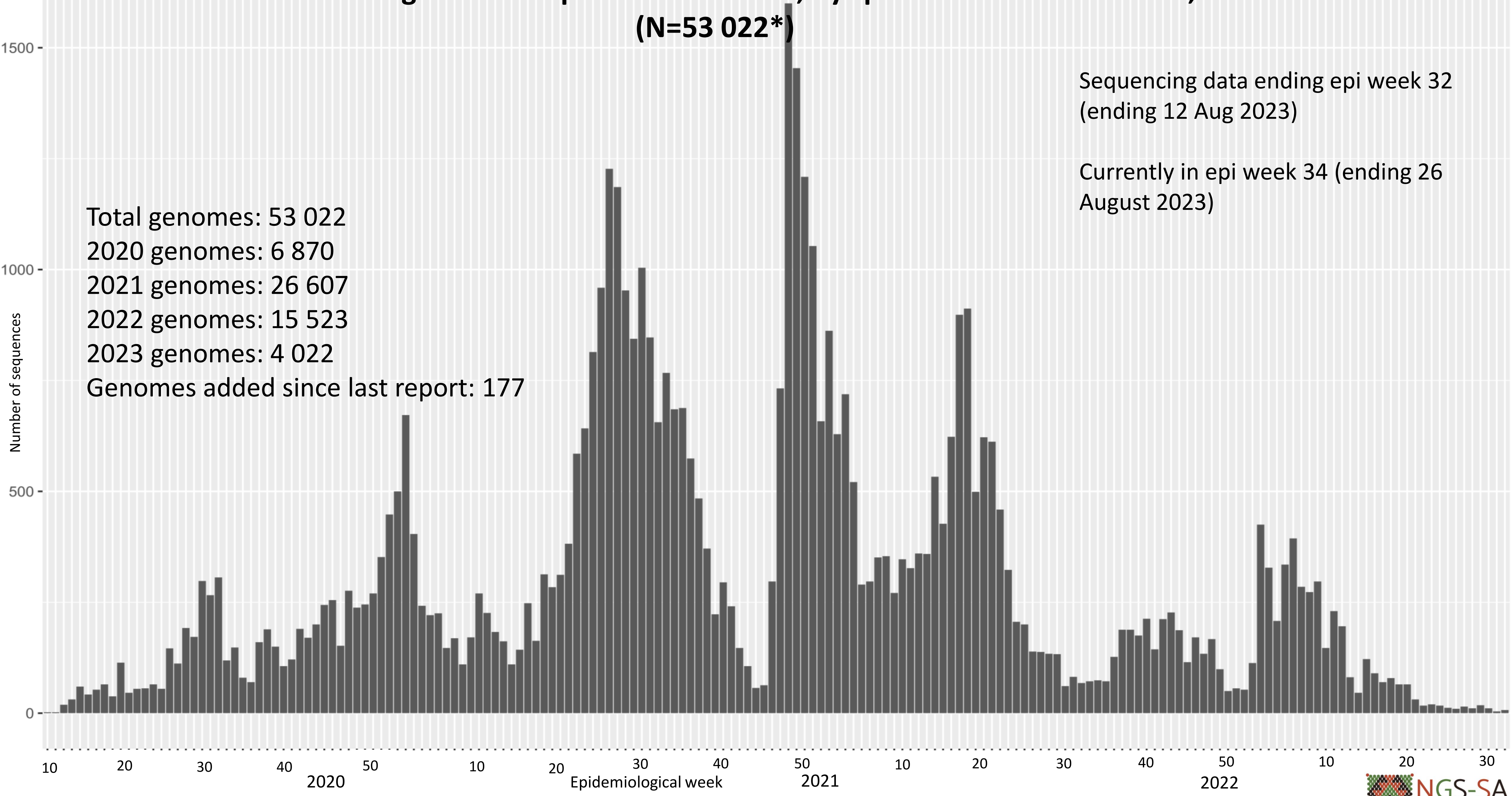
The genomic data presented here are based on South African SARS-CoV-2 sequence data downloaded from GISAID (www.gisaid.org) on 25 August 2023 at 08h45

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 – 2023 (N=53 022*)



Total genomes: 53 022
2020 genomes: 6 870
2021 genomes: 26 607
2022 genomes: 15 523
2023 genomes: 4 022
Genomes added since last report: 177

Sequencing data ending epi week 32 (ending 12 Aug 2023)

Currently in epi week 34 (ending 26 August 2023)

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

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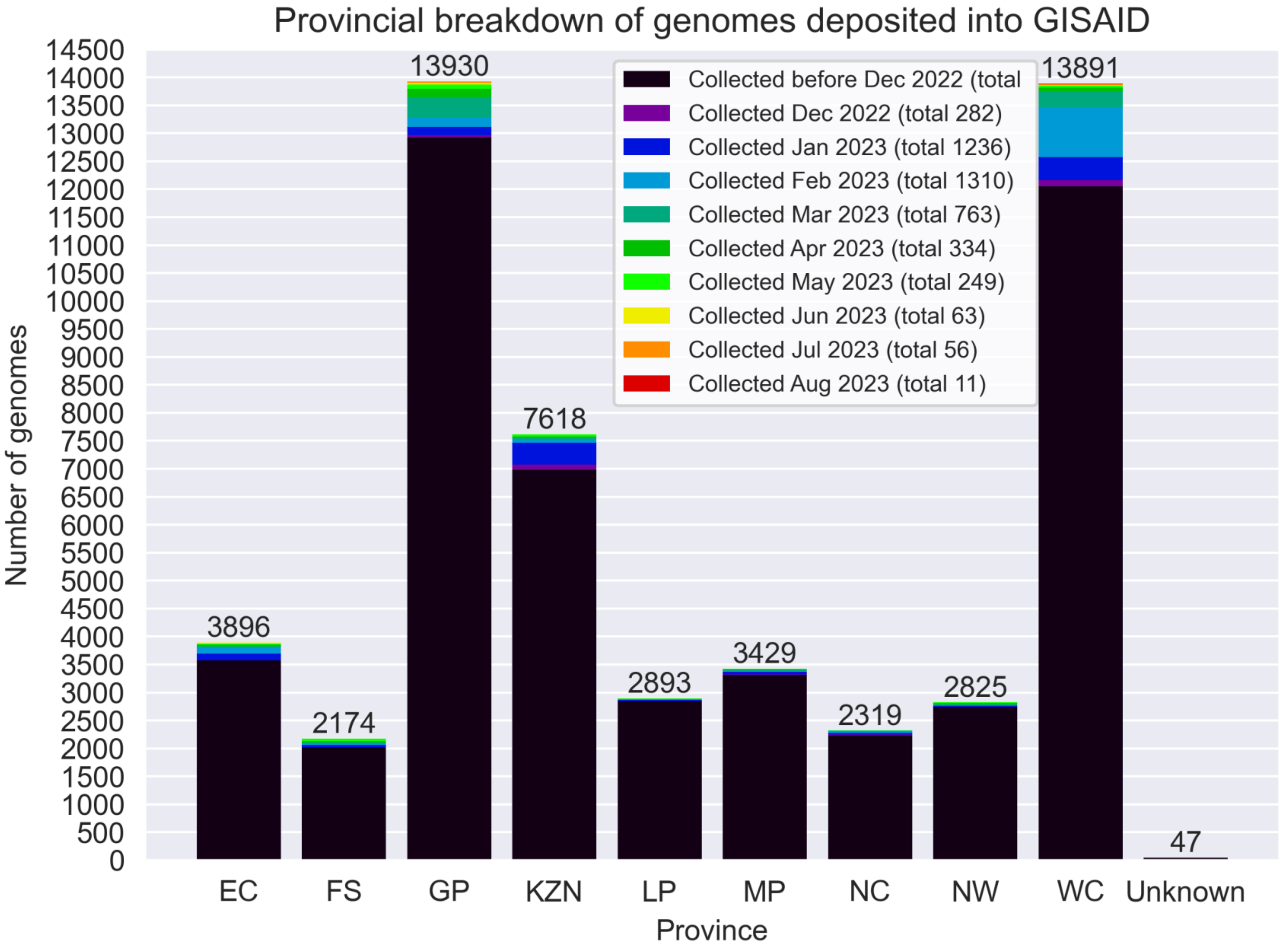
GISAID genomes vs total cases, 2020 – 2023 (N= 53 022)



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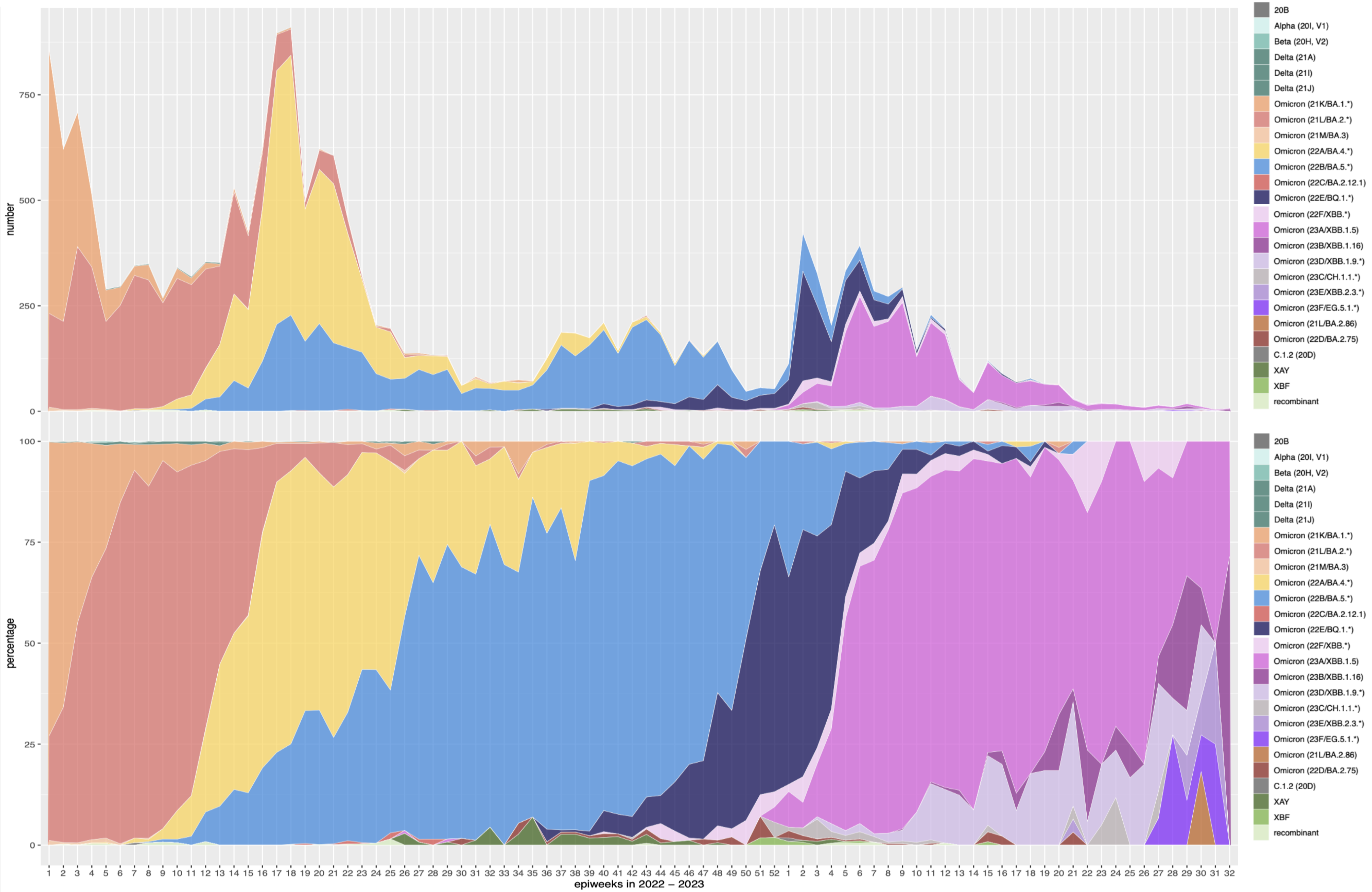
Number and percentage of clades by epiweek in South Africa, 2022-2023 (19 502*)



Sequencing data ending epi week 32 (ending 12 Aug 2023)

Currently in epi week 34 (ending 26 August 2023)

*Excludes sequences missing collection dates, as well as those collected January 1st 2022 as they are part of epiweek 52 of 2021.

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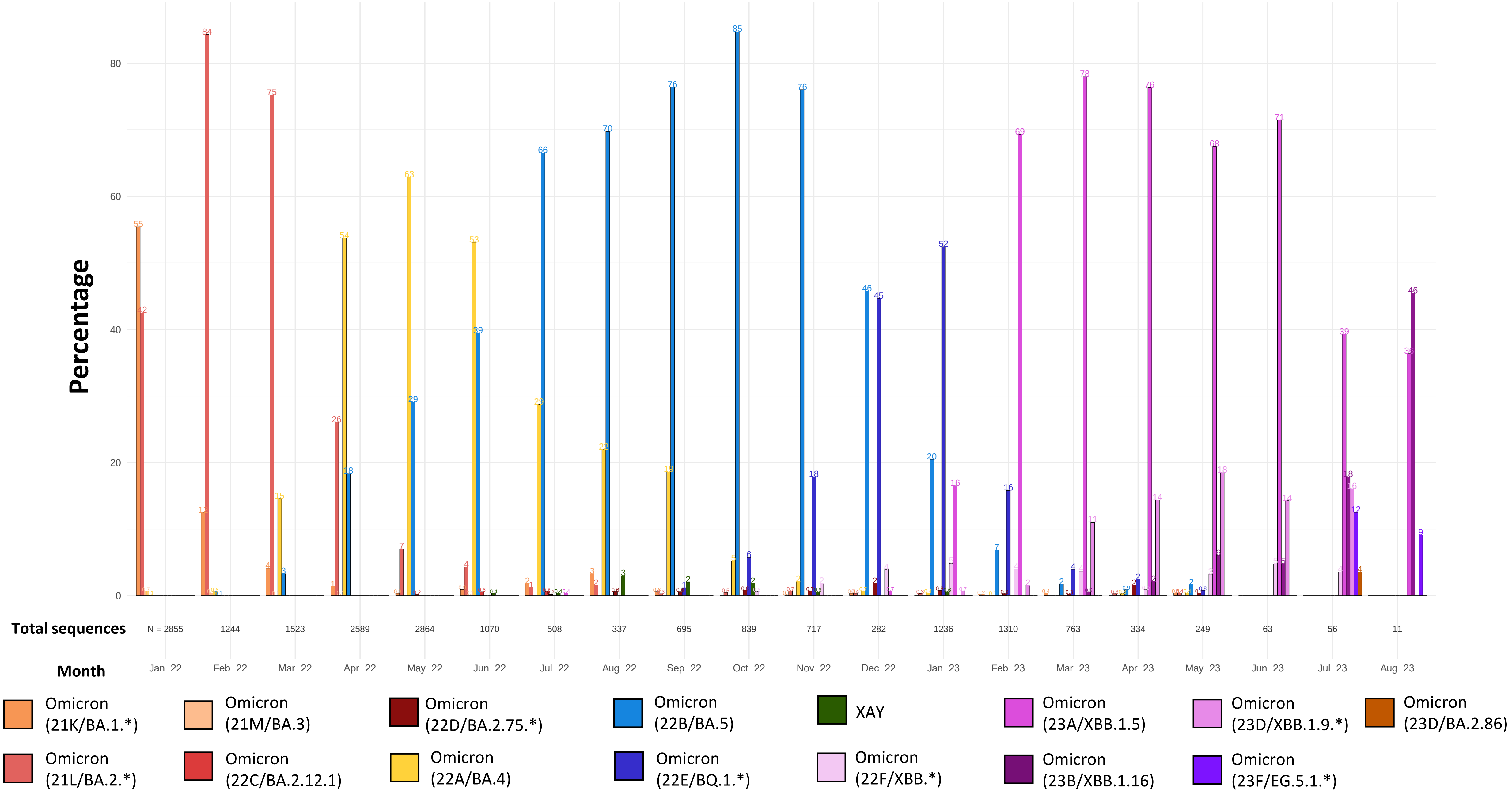
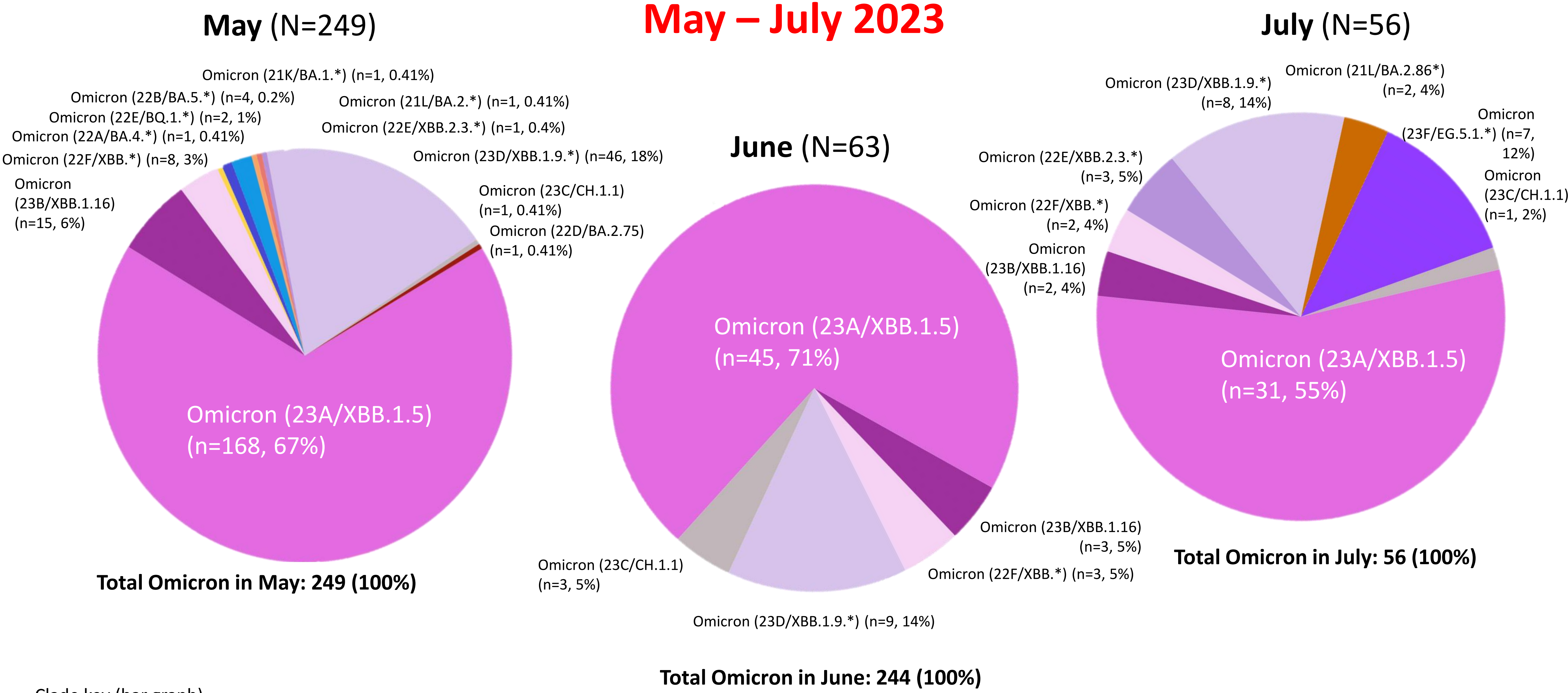
Detection Rates: Omicron and recombinants



*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 May – July 2023

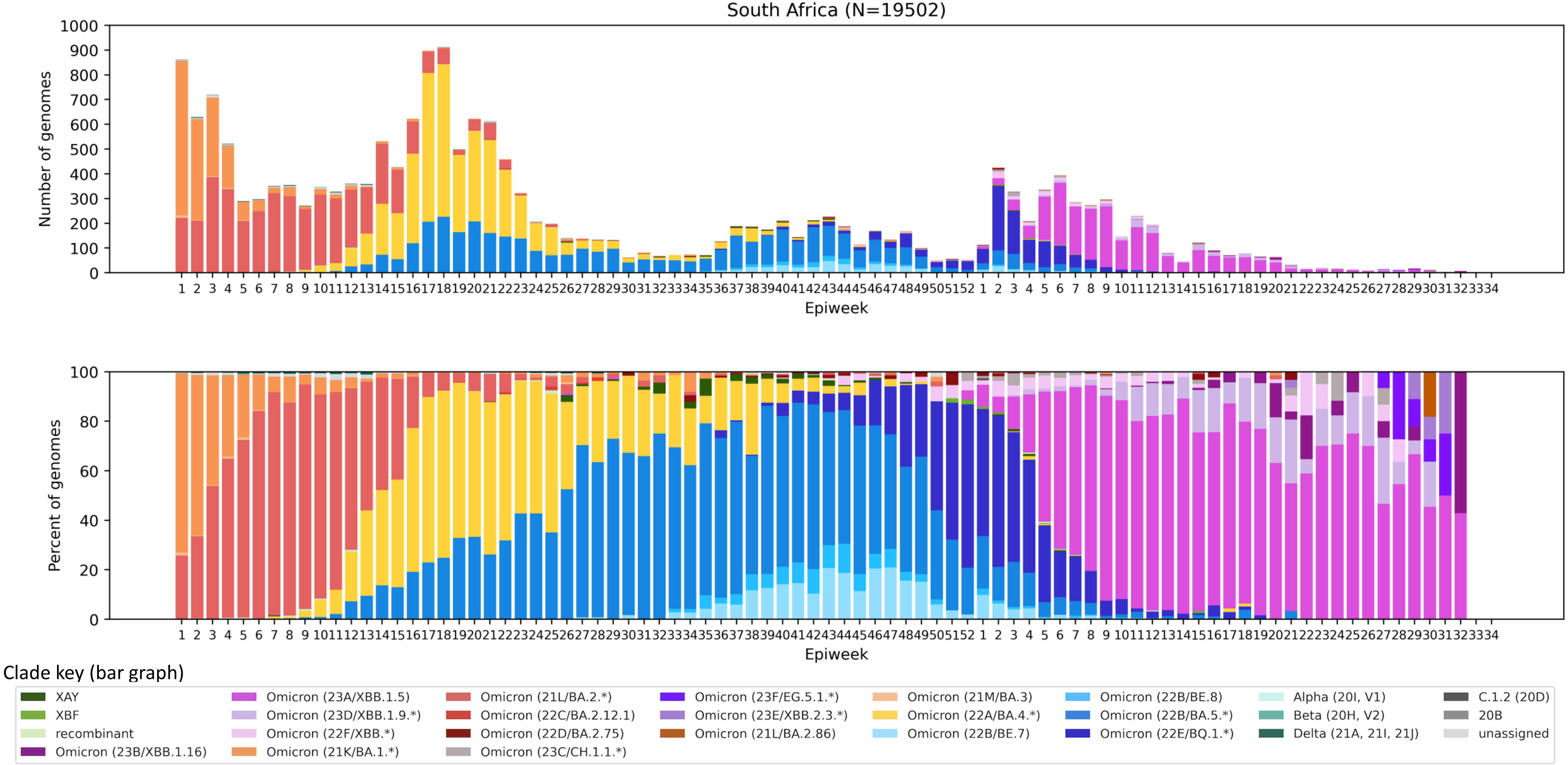


Clade key (bar graph)

■ XAY	■ Omicron (23B/XBB.1.16)	■ Omicron (22F/XBB.*)	■ Omicron (22C/BA.2.12.1)	■ Omicron (21M/BA.3)	■ Omicron (22B/BE.8)	■ Alpha (20I, V1)	■ C.1.2 (20D)
■ XBF	■ Omicron (23A/XBB.1.5)	■ Omicron (21K/BA.1.*)	■ Omicron (22D/BA.2.75)	■ Omicron (22A/BA.4.*)	■ Omicron (22B/BA.5.*)	■ Beta (20H, V2)	■ 20B
■ recombinant	■ Omicron (23D/XBB.1.9.*)	■ Omicron (21L/BA.2.*)	■ Omicron (22D/CH.1.1.*)	■ Omicron (22B/BE.7)	■ Omicron (22E/BQ.1.*)	■ Delta (21A, 21I, 21J)	■ unassigned

Note: XBF is an Omicron-Omicron recombinant and so is counted in the total number of Omicrons.

South Africa, 2022-2023, n = 19 502*



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

[#] Recombinants include all recombinant lineages (viruses consisting of segments of two different lineages) detected in South Africa at low levels. Currently it consists of XT, XAS, XAZ, XBA, XBF.

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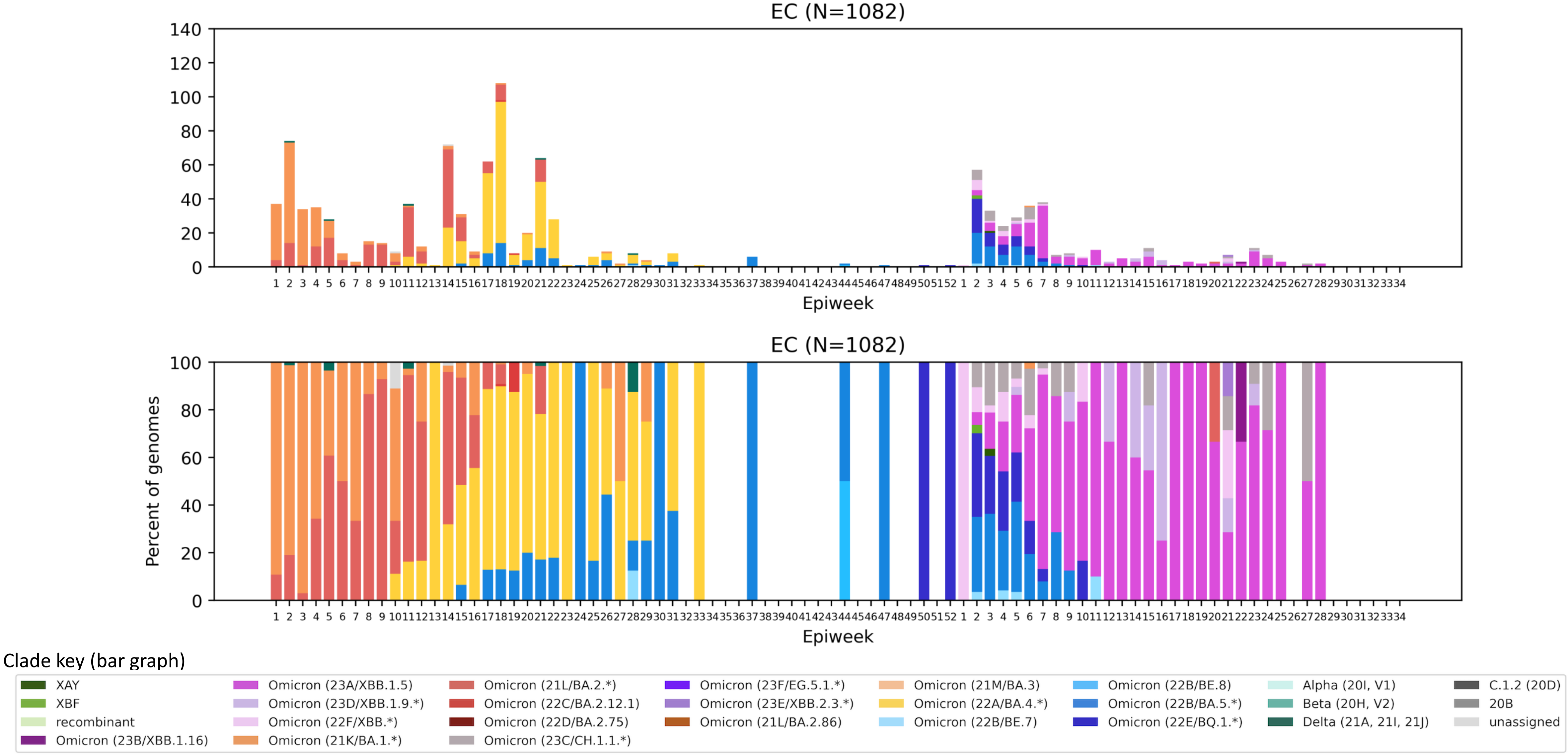
Eastern Cape Province, 2022-2023, n = 1082

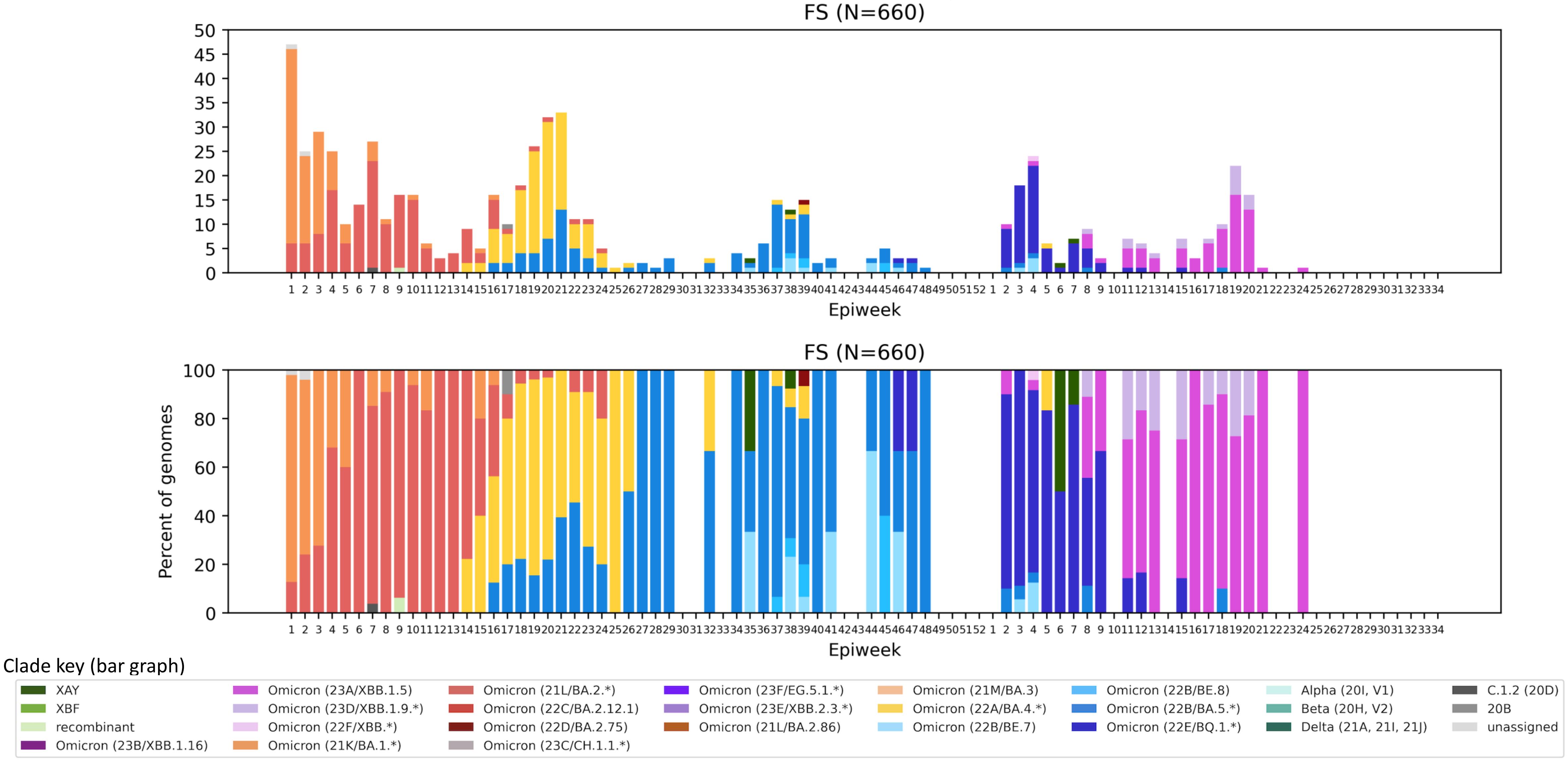
Genomes added since last report: 28*



*May include genomes from 2020 and 2021 which are not pictured here and are not included in the slide total.

Free State Province, 2022-2023, n = 660

Genomes added since last report: 0*



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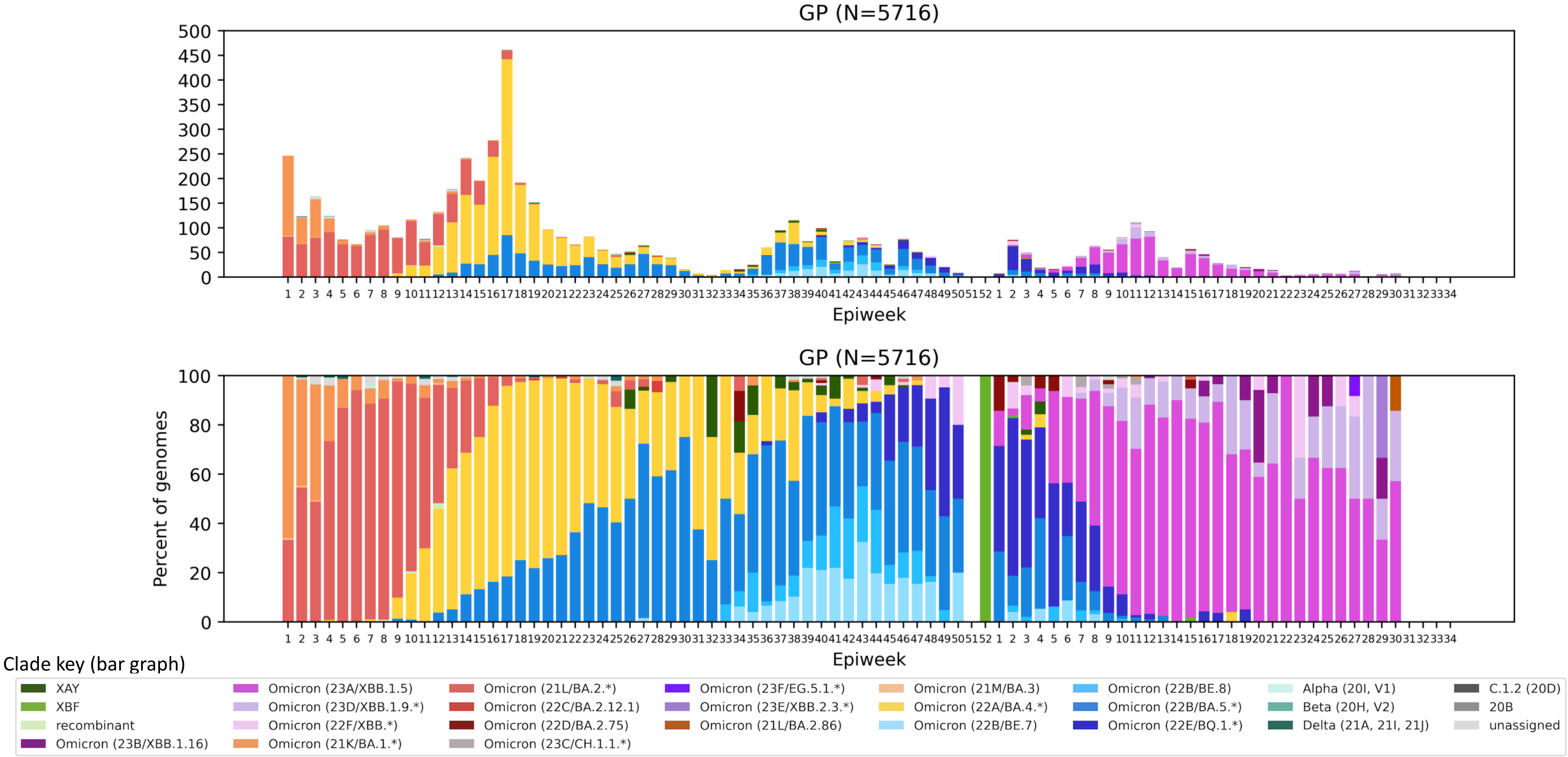
*May include genomes from 2020 and 2021 which are not pictured here and are not included in the slide total.

Gauteng Province, 2022-2023, n = 5716

Genomes added since last report: 35*



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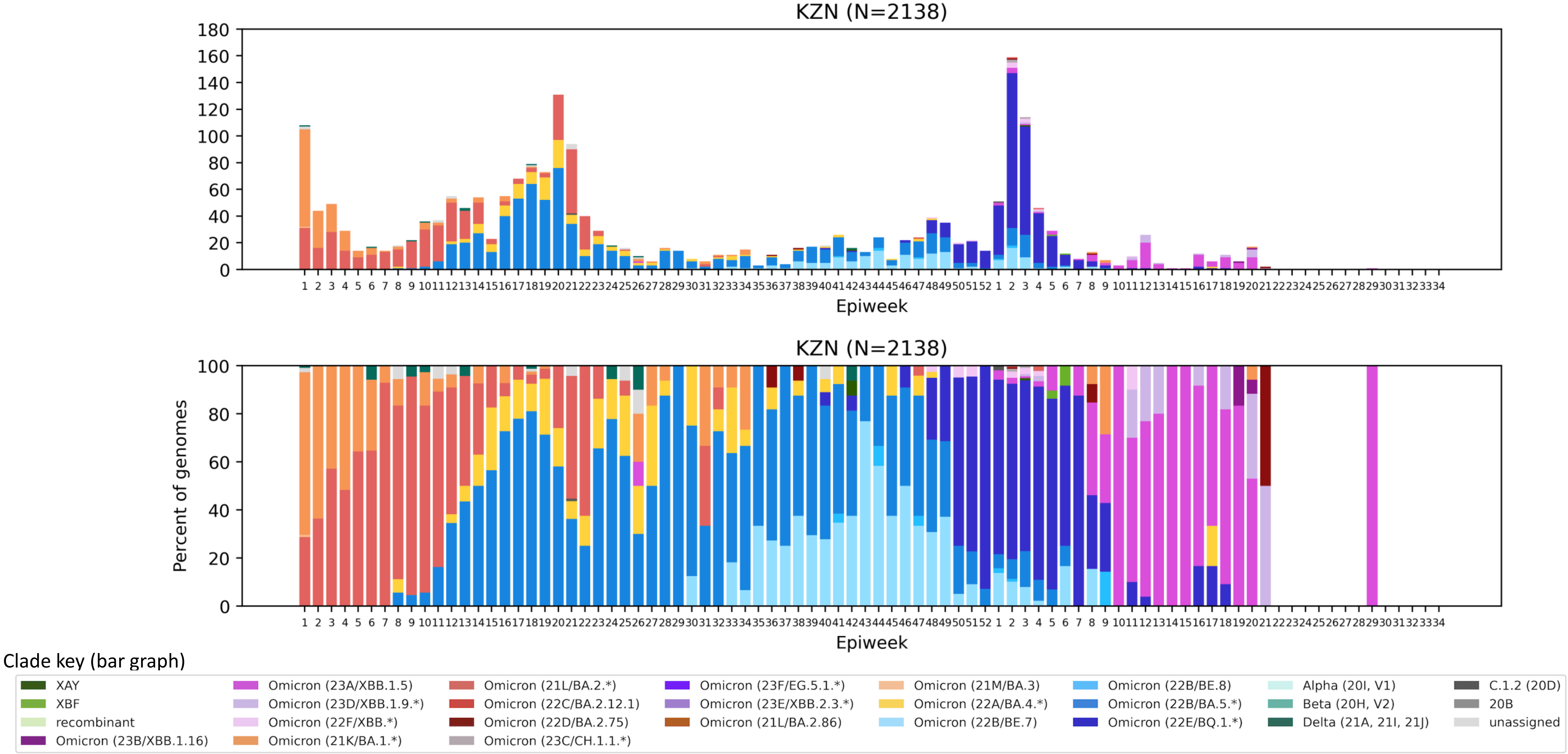
*May include genomes from 2020 and 2021 which are not pictured here and are not included in the slide total.

KwaZulu-Natal Province, 2022-2023, n = 2138

Genomes added since last report: 2*



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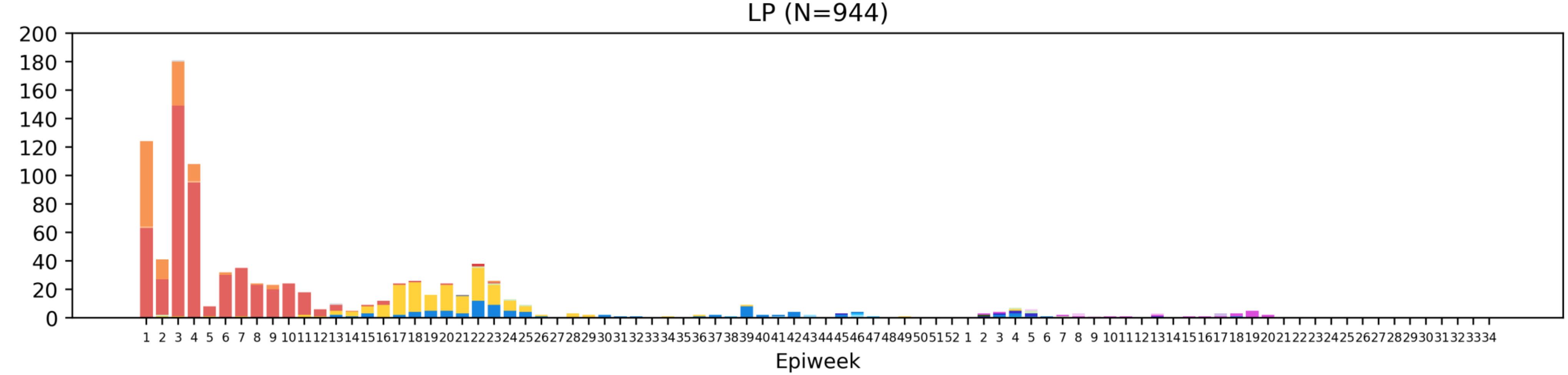
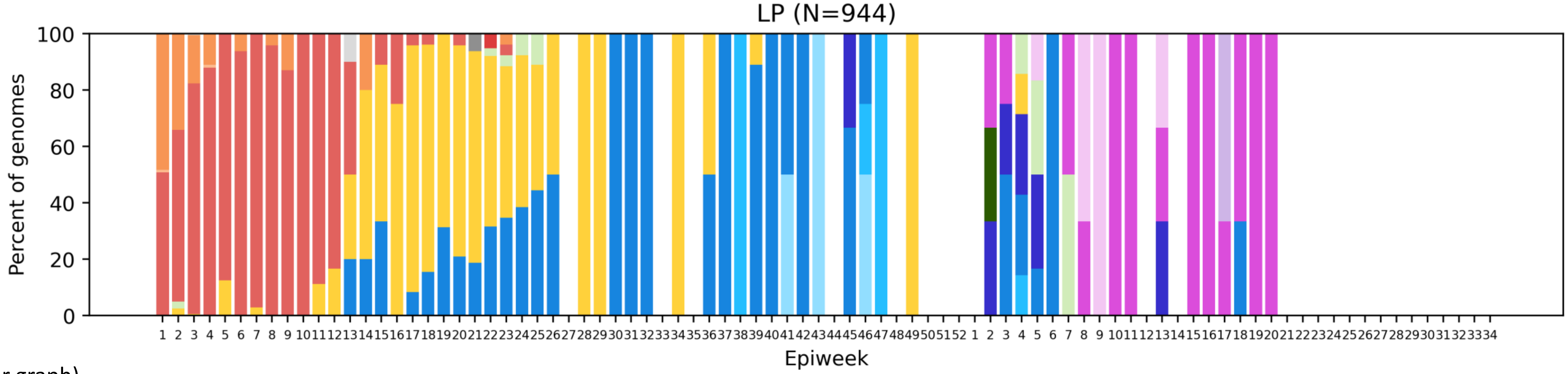
*May include genomes from 2020 and 2021 which are not pictured here and are not included in the slide total.

Limpopo Province, 2022-2023, n = 944

Genomes added since last report: 0*


LP (N=944)


LP (N=944)

Clade key (bar graph)

■ XAY
■ XBF
■ recombinant
■ Omicron (23B/XBB.1.16)
■ Omicron (23A/XBB.1.5)
■ Omicron (23D/XBB.1.9.*)
■ Omicron (22F/XBB.*)
■ Omicron (21K/BA.1.*)
■ Omicron (21L/BA.2.*)
■ Omicron (22C/BA.2.12.1)
■ Omicron (22D/BA.2.75)
■ Omicron (23C/CH.1.1.*)
■ Omicron (23F/EG.5.1.*)
■ Omicron (23E/XBB.2.3.*)
■ Omicron (21L/BA.2.86)
■ Omicron (21M/BA.3)
■ Omicron (22A/BA.4.*)
■ Omicron (22B/BE.7)
■ Omicron (22B/BE.8)
■ Omicron (22B/BA.5.*)
■ Omicron (22E/BQ.1.*)
■ Alpha (20I, V1)
■ Beta (20H, V2)
■ Delta (21A, 21I, 21J)
■ C.1.2 (20D)
■ 20B
■ unassigned

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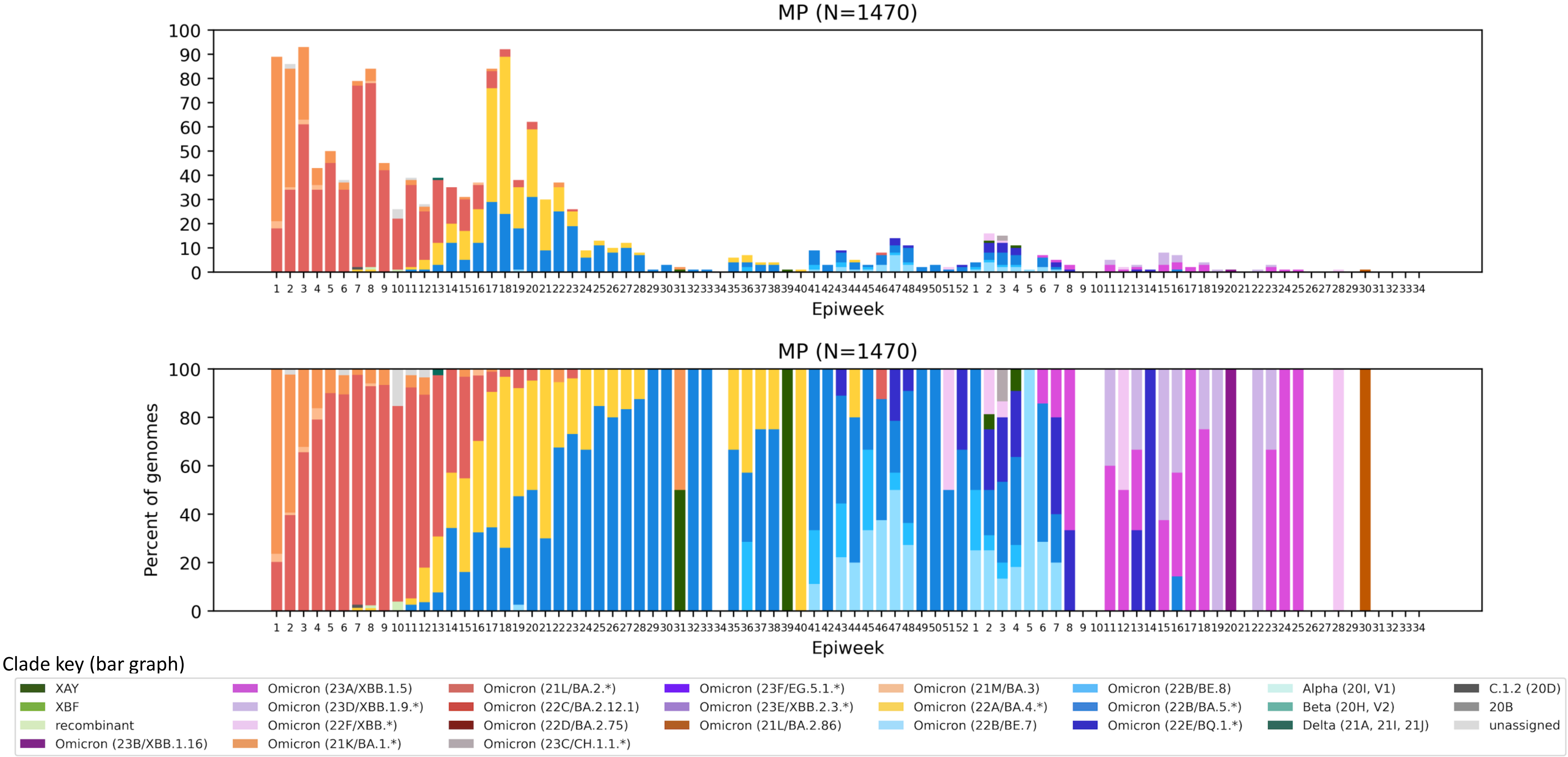
*May include genomes from 2020 and 2021 which are not pictured here and are not included in the slide total.

Mpumalanga Province, 2022-2023, n = 1470

Genomes added since last report: 2*



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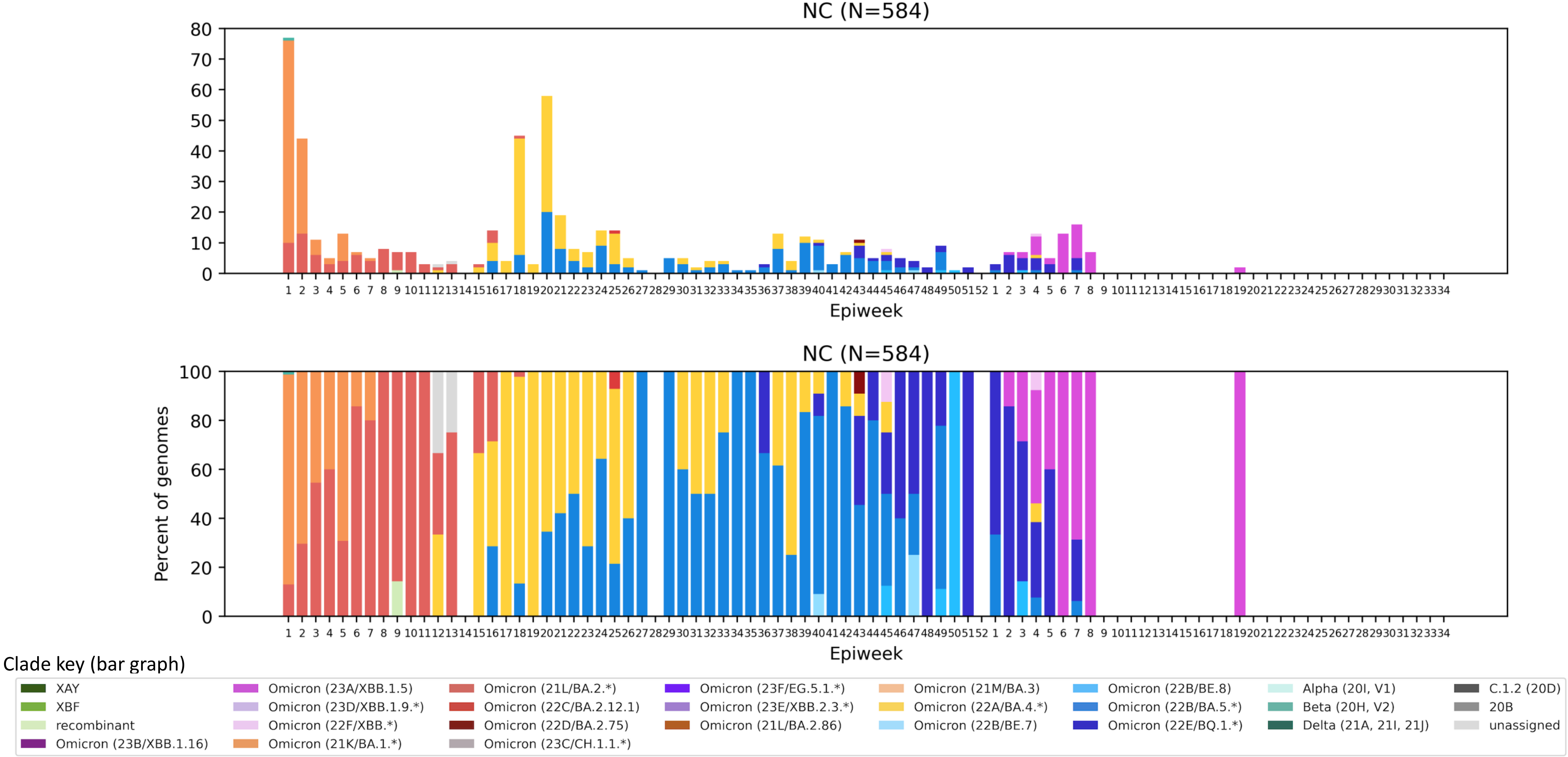
*May include genomes from 2020 and 2021 which are not pictured here and are not included in the slide total.

Northern Cape Province, 2022-2023, n = 584

Genomes added since last report: 0*



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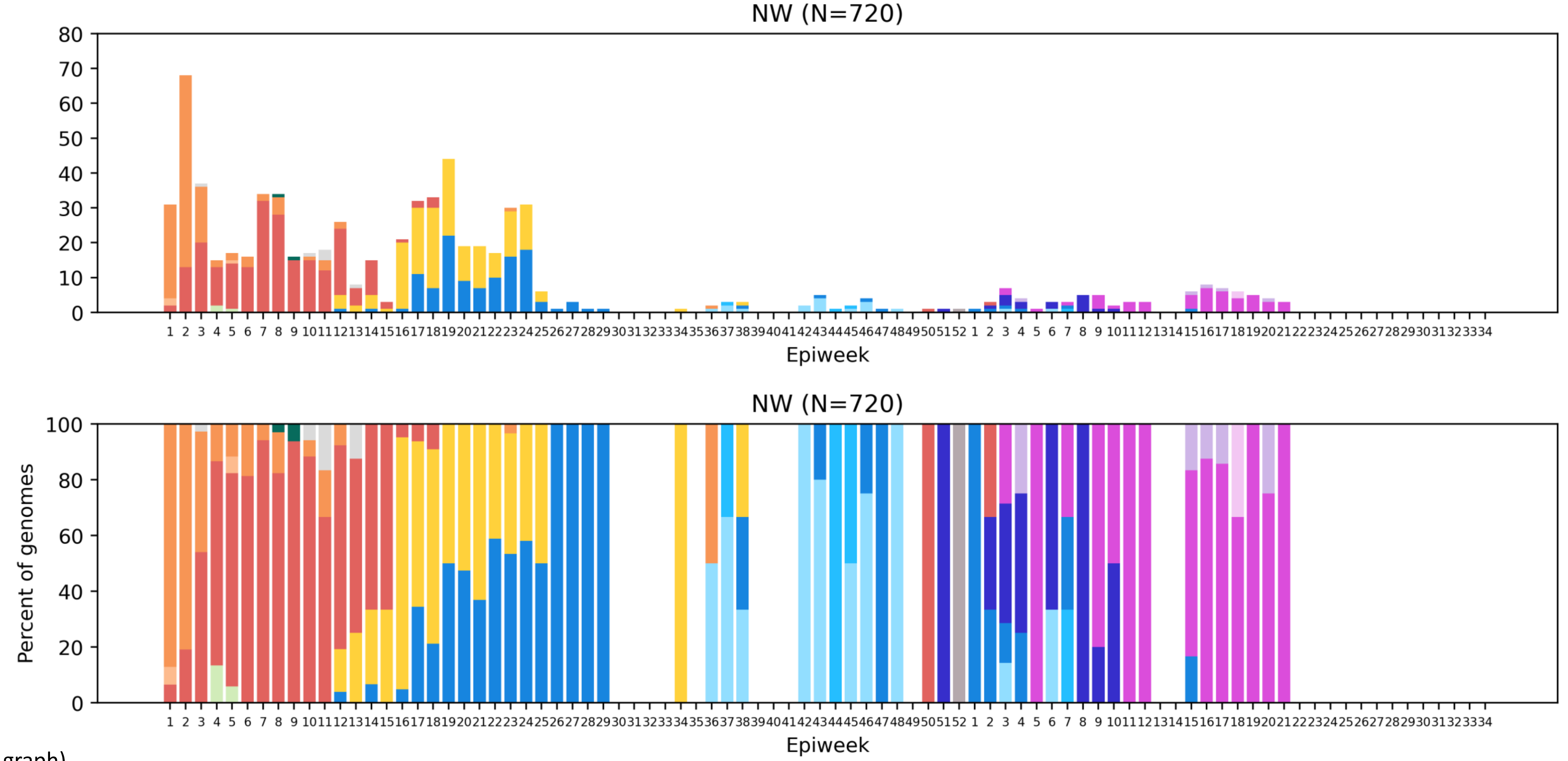
*May include genomes from 2020 and 2021 which are not pictured here and are not included in the slide total.

North West Province, 2022-2023, n = 720

Genomes added since last report: 0*



Clade key (bar graph)

- 🟩 XAY
- 🟩 XBF
- 🟩 recombinant
- 🟪 Omicron (23B/XBB.1.16)
- 🟪 Omicron (23A/XBB.1.5)
- 🟪 Omicron (23D/XBB.1.9.*)
- 🟪 Omicron (22F/XBB.*)
- 🟧 Omicron (21K/BA.1.*)
- 🟥 Omicron (21L/BA.2.*)
- 🟥 Omicron (22C/BA.2.12.1)
- 🟥 Omicron (22D/BA.2.75)
- ⬜ Omicron (23C/CH.1.1.*)
- 🟪 Omicron (23F/EG.5.1.*)
- 🟪 Omicron (23E/XBB.2.3.*)
- 🟫 Omicron (21L/BA.2.86)
- 🟧 Omicron (21M/BA.3)
- 🟨 Omicron (22A/BA.4.*)
- 🟦 Omicron (22B/BE.7)
- 🟦 Omicron (22B/BE.8)
- 🟦 Omicron (22B/BA.5.*)
- 🟦 Omicron (22E/BQ.1.*)
- 🟩 Alpha (20I, V1)
- 🟩 Beta (20H, V2)
- 🟩 Delta (21A, 21I, 21J)
- ⬛ C.1.2 (20D)
- ⬛ 20B
- ⬜ unassigned

*May include genomes from 2020 and 2021 which are not pictured here and are not included in the slide total.

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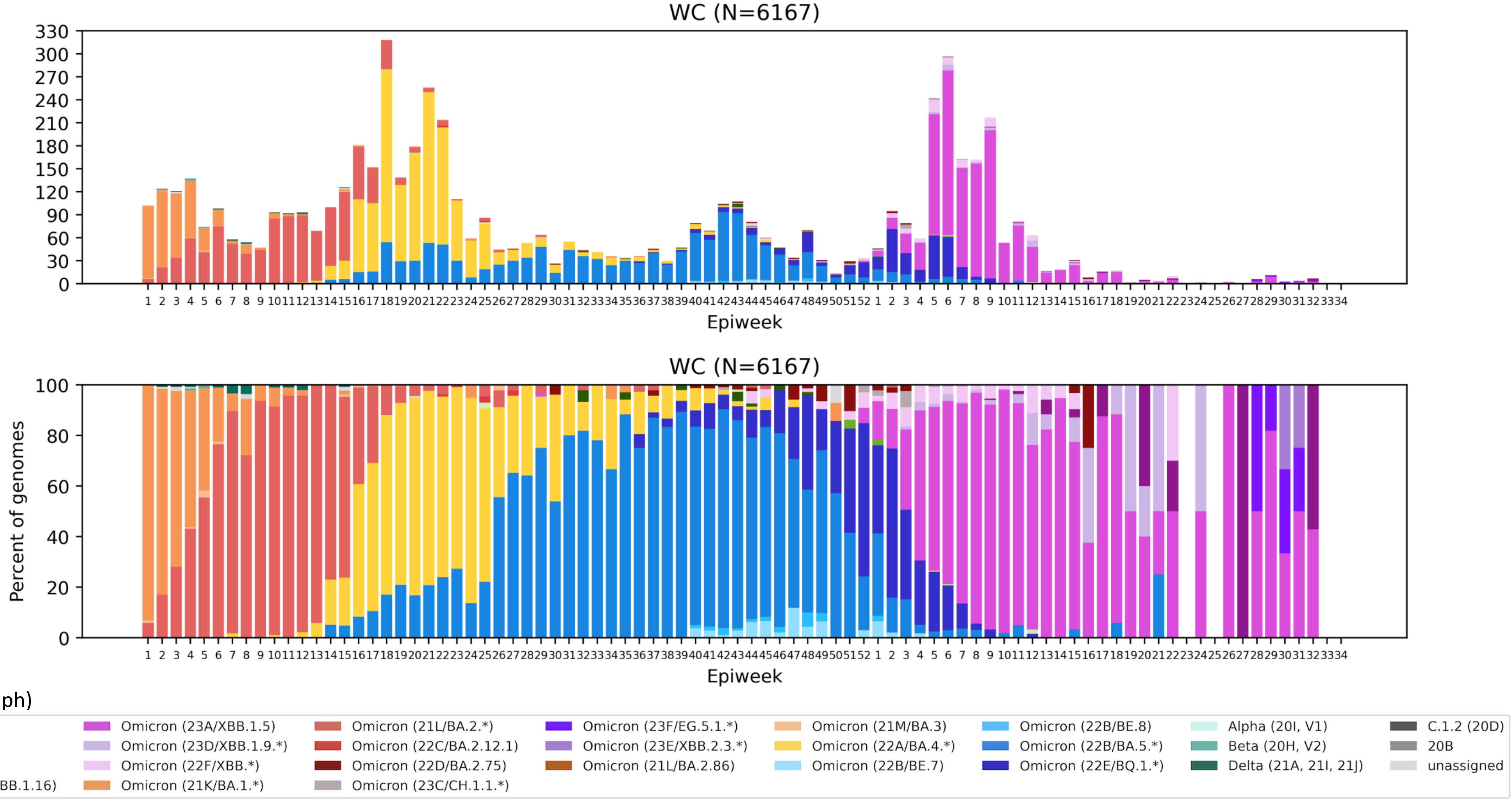
Western Cape Province, 2022-2023, n = 6167

Genomes added since last report: 110*



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*May include genomes from 2020 and 2021 which are not pictured here and are not included in the slide total.

Summary

- **Sequencing update**
  - All provinces have data for May 2023. June sequences (n=63) are from the Eastern Cape, Free State, Gauteng, Mpumalanga, and the Western Cape. July sequences (n=56) are from the Eastern Cape, KwaZulu-Natal, Gauteng, Mpumalanga, and the Western Cape. All (n=11) August sequences are from the Eastern Cape

- **Variant of Concern Omicron in South Africa**
  - Omicron dominated in May (100%), and appears to dominate in June (100%) and July (100%), although this is based on low numbers (n=63 and 56 respectively)
  - XBB.1.5 was the dominant lineage in May (68%) and June (71%), and constitutes 39% of July sequences
  - XBB.1.16 has been detected at a low prevalence in May (6%), June (5%), and July (4%)
  - XBB.1.9.* (newly designated clade 23D) was detected in sequences from May (18%), June (14%), and July (14%)
  - One sequence of the EG.5.2.3 (23D) lineage has been detected in Gauteng in June
  - Eight sequences of the EG.5.1.* lineage (newly designated clade 23F) have been detected in Gauteng (n = 1) and Western Cape (n = 7) in July (n=7) and August (n=1)
  - BA.2.86 has been added to the variants under monitoring (VUMs) list. Two sequences have been detected in Gauteng (n=1) and Mpumalanga (n=1) in July

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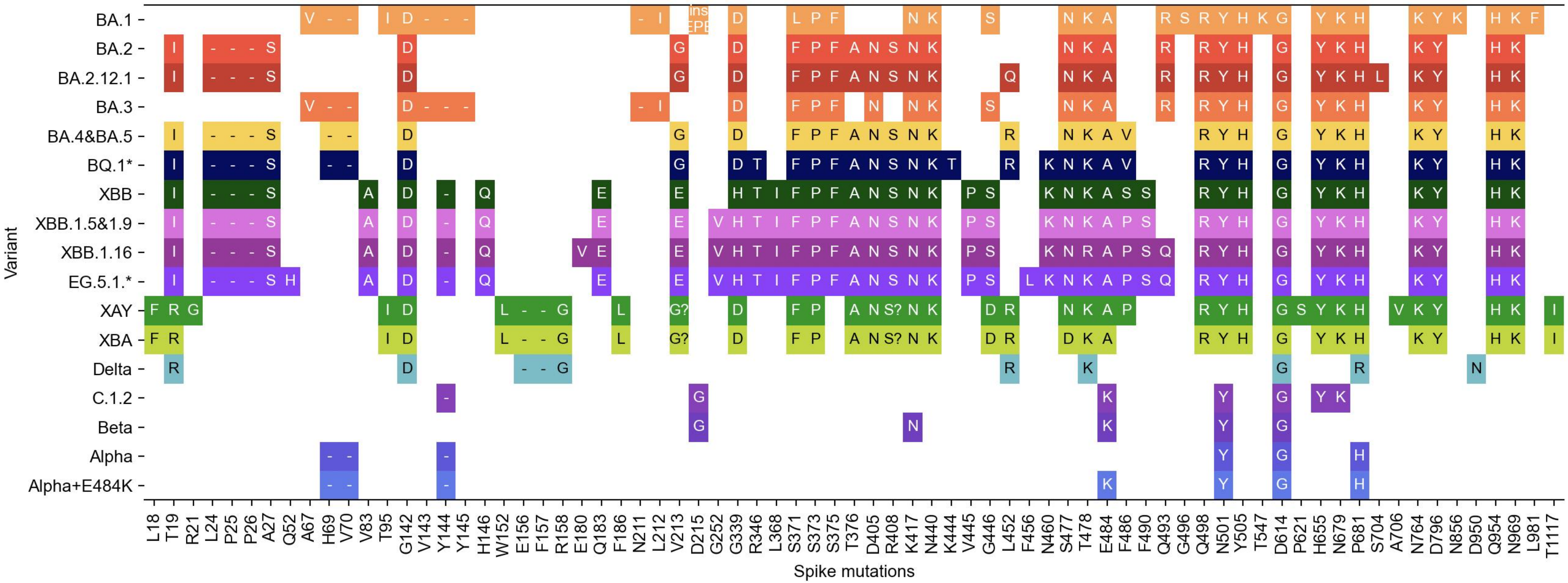
Spike protein mutation* profile of Variants of Interest and Concern



Variant	L18	T19	R21	L24	P25	P26	A27	Q52	A67	H69	V70	V83	T95	G142	V143	Y144	Y145	H146	W152	E156	F157	R158	E180	Q183	F186	N211	L212	V213	D215	G252	G339	R346	L368	S371	S373	S375	T376	D405	R408	K417	N440	K444	V445	G446	L452	F456	N460	S477	T478	E484	F486	F490	Q493	G496	Q498	N501	Y505	T547	D614	P621	H655	N679	P681	S704	A706	N764	D796	N856	D950	Q954	N969	L981	T1117
BA.1									V	-	-		I	D	-	-	-									-	I		ins EPE		D			L	P	F				N	K			S				N	K	A			R	S	R	Y	H	K	G		Y	K	H			K	Y	K		H	K	F	
BA.2		I		-	-	-	S							D														G			D			F	P	F	A	N	S	N	K							N	K	A			R		R	Y	H		G		Y	K	H			K	Y			H	K		
BA.2.12.1		I		-	-	-	S							D														G			D			F	P	F	A	N	S	N	K				Q			N	K	A			R		R	Y	H		G		Y	K	H	L		K	Y			H	K		
BA.3									V	-	-			D	-	-	-									-	I				D			F	P	F		N		N	K			S				N	K	A			R		R	Y	H		G		Y	K	H			K	Y			H	K		
BA.4&BA.5		I		-	-	-	S			-	-			D														G			D			F	P	F	A	N	S	N	K				R			N	K	A	V				R	Y	H		G		Y	K	H			K	Y			H	K		
BQ.1*		I		-	-	-	S			-	-			D														G			D	T		F	P	F	A	N	S	N	K	T			R		K	N	K	A	V				R	Y	H		G		Y	K	H			K	Y			H	K		
XBB		I		-	-	-	S					A		D		-		Q						E				E			H	T	I	F	P	F	A	N	S	N	K		P	S			K	N	K	A	S	S			R	Y	H		G		Y	K	H			K	Y			H	K		
XBB.1.5&1.9		I		-	-	-	S					A		D		-		Q						E				E		V	H	T	I	F	P	F	A	N	S	N	K		P	S			K	N	K	A	P	S			R	Y	H		G		Y	K	H			K	Y			H	K		
XBB.1.16		I		-	-	-	S					A		D		-		Q					V	E				E		V	H	T	I	F	P	F	A	N	S	N	K		P	S			K	N	R	A	P	S	Q		R	Y	H		G		Y	K	H			K	Y			H	K		
EG.5.1.*		I		-	-	-	S	H				A		D		-		Q						E				E		V	H	T	I	F	P	F	A	N	S	N	K		P	S		L	K	N	K	A	P	S	Q		R	Y	H		G		Y	K	H			K	Y			H	K		
XAY	F	R	G										I	D					L	-	-	G			L			G?			D			F	P		A	N	S?	N	K			D	R			N	K	A	P				R	Y	H		G	S	Y	K	H		V	K	Y			H	K		I
XBA	F	R											I	D					L	-	-	G			L			G?			D			F	P		A	N	S?	N	K			D	R			D	K	A					R	Y	H		G		Y	K	H			K	Y			H	K		I
Delta		R												D						-	-	G																							R				K										G				R						N				
C.1.2																-													G																					K						Y			G		Y	K											
Beta																													G											N										K						Y			G														
Alpha										-	-					-																																								Y			G				H										
Alpha+E484K										-	-					-																																		K						Y			G				H										

- 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

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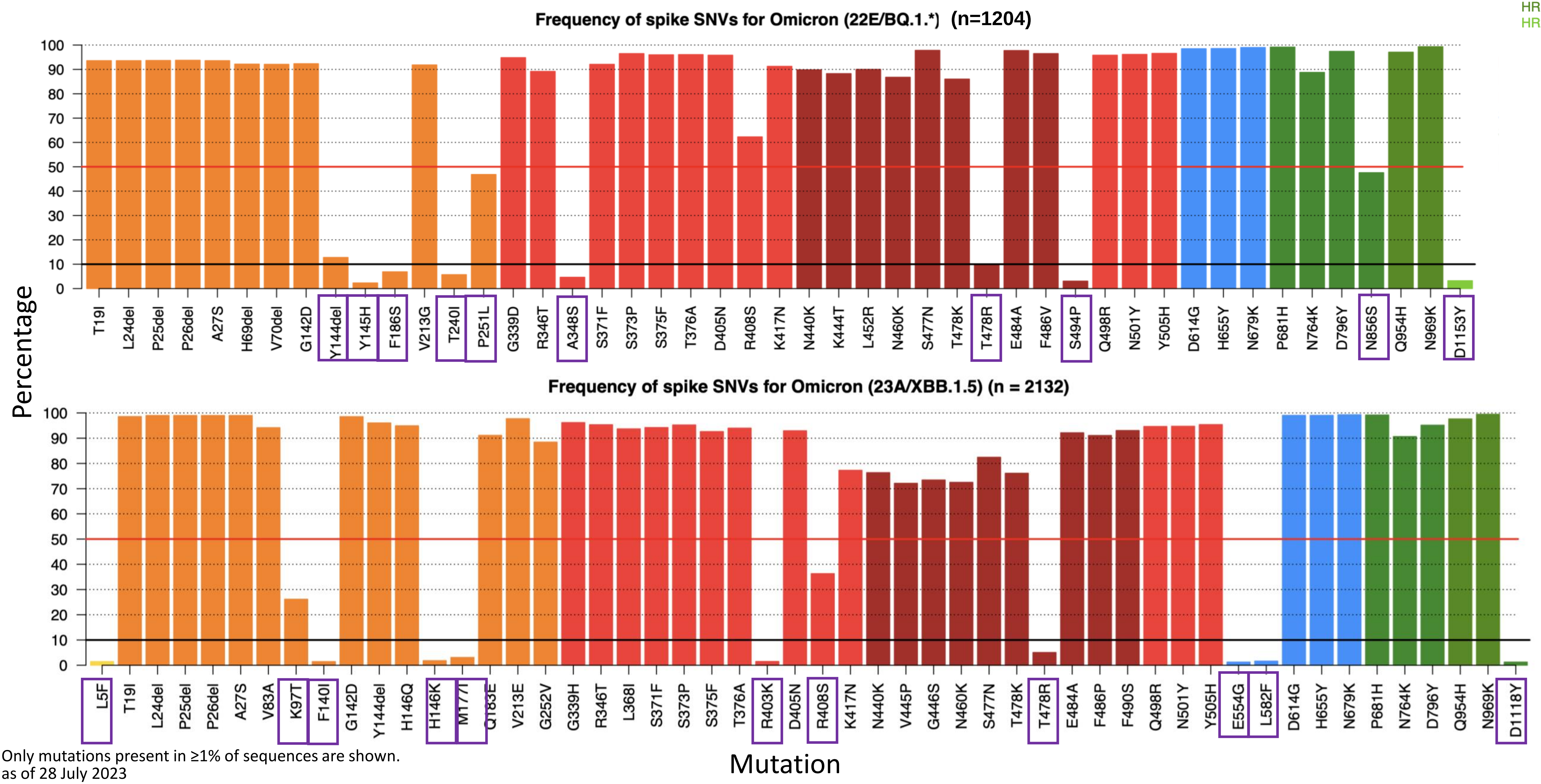
BQ.1* and XBB.1.5* spike mutations*



*Only mutations present in ≥1% of sequences are shown.
*as of 28 July 2023

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NHLS Tshwane
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NICD SARS-CoV-2 Sequencing Group

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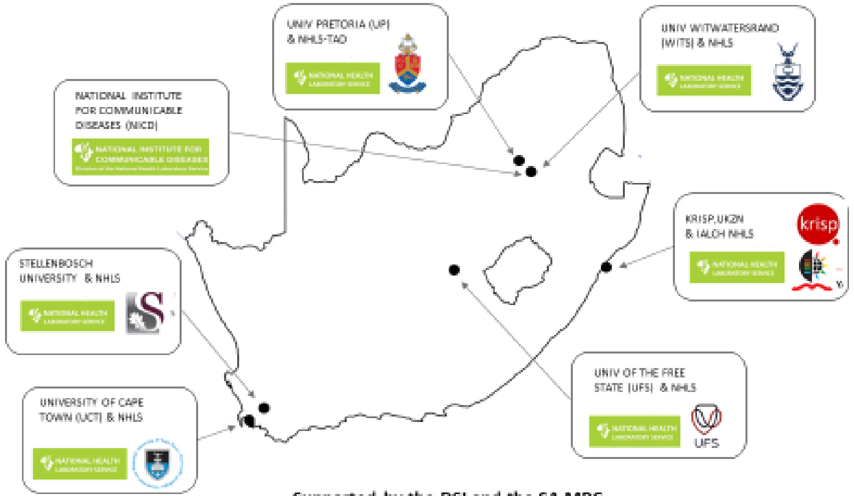
NGS-SA
Network for Genomic
Surveillance in South Africa



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EDCTP

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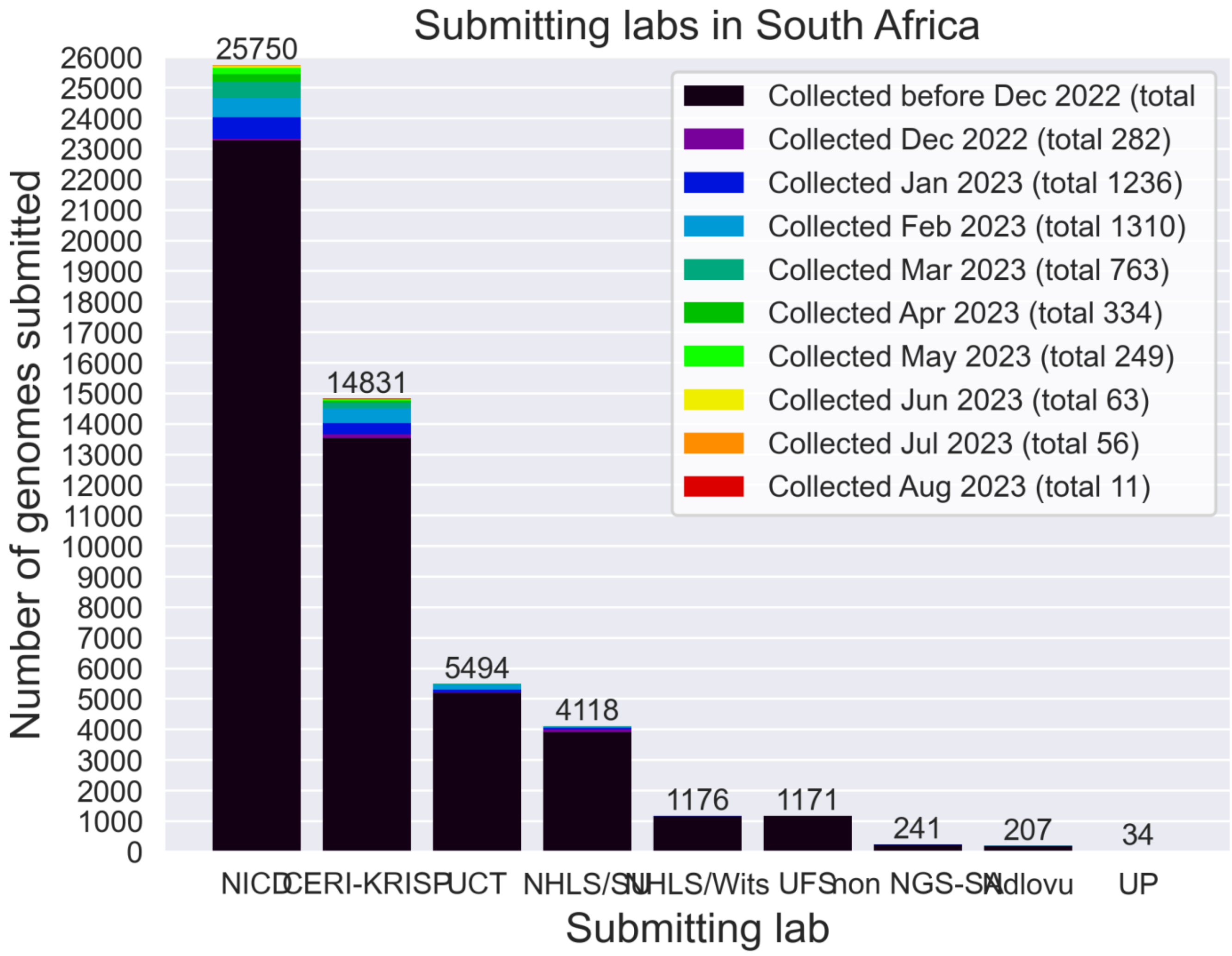
South African genomes submitted per submitting lab, 2020 - 2023 (N= 53 022)



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.

NGS-SA
Network for Genomic Surveillance in South Africa

Currently circulating Variants of Interest (VOI) as of 09 Aug 2023

Pango lineage	Nextstrain clade	Genetic features	Earliest documented samples	Date of designation and risk assessments
XBB.1.5	23A	Recombinant of BA.2.10.1 and BA.2.75 sublineages, i.e. BJ.1 and BM.1.1.1, with a breakpoint in S1. XBB.1 + S:F486P (similar Spike genetic profile as XBB.1.9.1)	21-10-2022	11-01-2023 XBB.1.5 Rapid Risk Assessment, 11 January 2023 XBB.1.5 Updated Rapid Risk Assessment, 25 January 2023 XBB.1.5 Updated Risk Assessment, 24 February 2023 XBB.1.5 Updated Risk Assessment, 20 June 2023
XBB.1.16	23B	Recombinant of BA.2.10.1 and BA.2.75 sublineages, i.e. BJ.1 and BM.1.1.1 XBB.1 + S:E180V, S:K478R and S:F486P	09-01-2023	17-04-2023 XBB.1.16 Initial Risk Assessment, 17 April 2023 XBB.1.16 Updated Risk Assessment, 05 June 2023
EG.5	Not assigned	XBB.1.9.2 + S:F456L Includes EG.5.1: EG.5 + S:Q52H	17-02-2023	09-08-2023 EG.5 Initial Risk Evaluation, 09 August 2023

https://www.who.int/en/activities/tracking-SARS-CoV-2-variants/ accessed 11 Aug 2023

Currently circulating variants under monitoring (VUMs)

Pango lineage[#] (+ mutation)	Nextstrain clade	Spike genetic features	Earliest documented samples	Date of designation and risk assessments
BA.2.75	22D	BA.2 + S:K147E, S:W152R, S:F157L, S:I210V, S:G257S, S:D339H, S:G446S, S:N460K, S:Q493R reversion	31-12-2021	06-07-2022
CH.1.1	22D	BA.2.75 + S:L452R, S:F486S	27-07-2022	08-02-2023
BQ.1	22E	BA.5 + S:R346T, S:K444T, S:N460K	07-02-2022	21-09-2022
XBB*	22F	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	12-10-2022
XBB.1.9.1	23D	Recombinant of BA.2.10.1 and BA.2.75 sublineages, i.e. BJ1 and BM.1.1.1 XBB.1 + S:F486P (similar Spike genetic profile as XBB.1.5)	05-12-2022	30-03-2022
XBB.1.9.2	23D	Recombinant of BA.2.10.1 and BA.2.75 sublineages, i.e. BJ1 and BM.1.1.1 XBB.1 + S:F486P, S:Q613H	05-12-2022	26-04-2023
XBB.2.3	22E	Recombinant of BA.2.10.1 and BA.2.75 sublineages, i.e. BJ1 and BM.1.1.1 XBB + S:D253G, S:F486P, S:P521S	09-12-2022	17-05-2023
BA.2.86	Not assigned	Mutations relative to putative ancestor BA.2	24-07-2023	17-08-2023

[*] Excludes XBB sublineages listed here as VOIs and VUMs

https://www.who.int/en/activities/tracking-SARS-CoV-2-variants/ accessed 24 Aug 2023

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.)