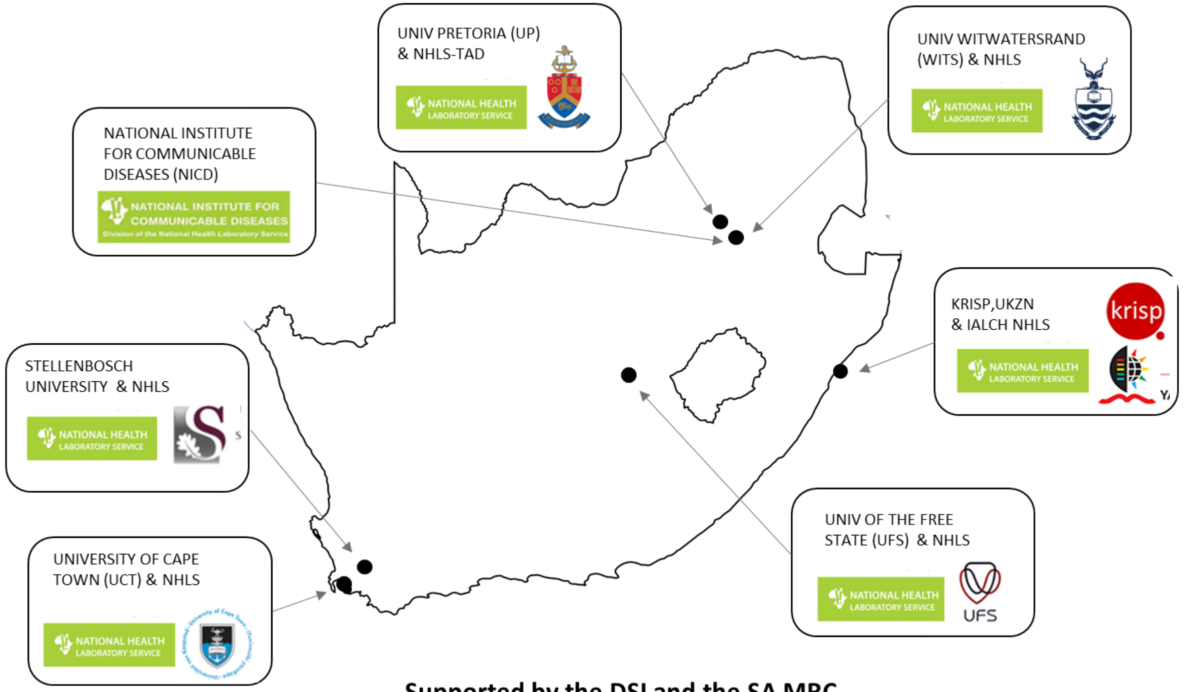
Network for Genomic Surveillance in South Africa (NGS-SA)

SARS-CoV-2 Sequencing Update
22 September 2023


UNIV PRETORIA (UP) & NHLS-TAD

UNIV WITWATERSRAND (WITS) & NHLS

NATIONAL INSTITUTE FOR COMMUNICABLE DISEASES (NICD)

KRISP,UKZN & IALCH NHLS

STELLENBOSCH UNIVERSITY & NHLS

UNIV OF THE FREE STATE (UFS) & NHLS

UNIVERSITY OF CAPE 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)

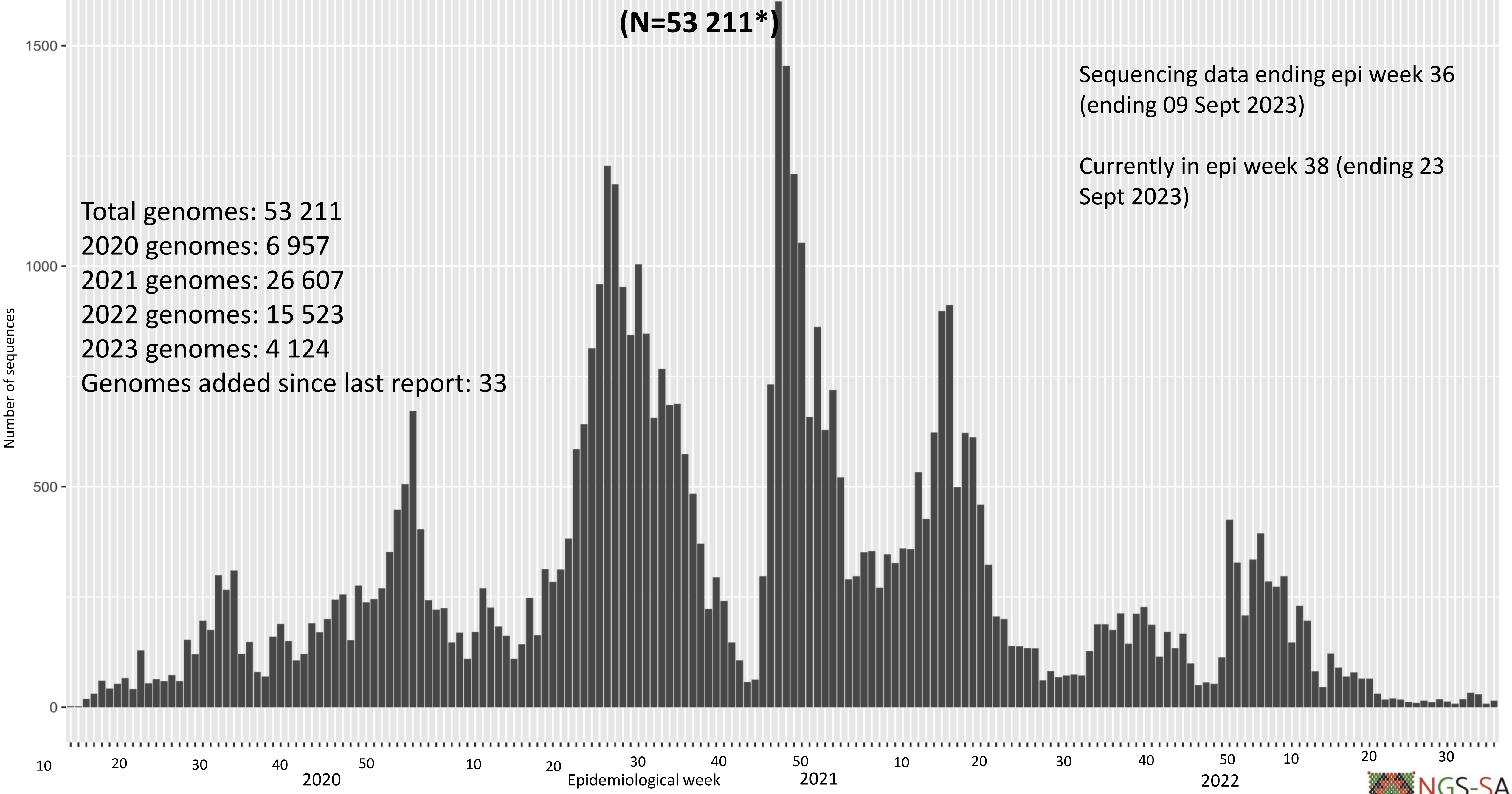
The genomic data presented here are based on South African SARS-CoV-2 sequence data downloaded from GISAID (www.gisaid.org) on 21 September 2023 at 07h45

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=53 211*)



Total genomes: 53 211
2020 genomes: 6 957
2021 genomes: 26 607
2022 genomes: 15 523
2023 genomes: 4 124
Genomes added since last report: 33

Sequencing data ending epi week 36 (ending 09 Sept 2023)

Currently in epi week 38 (ending 23 Sept 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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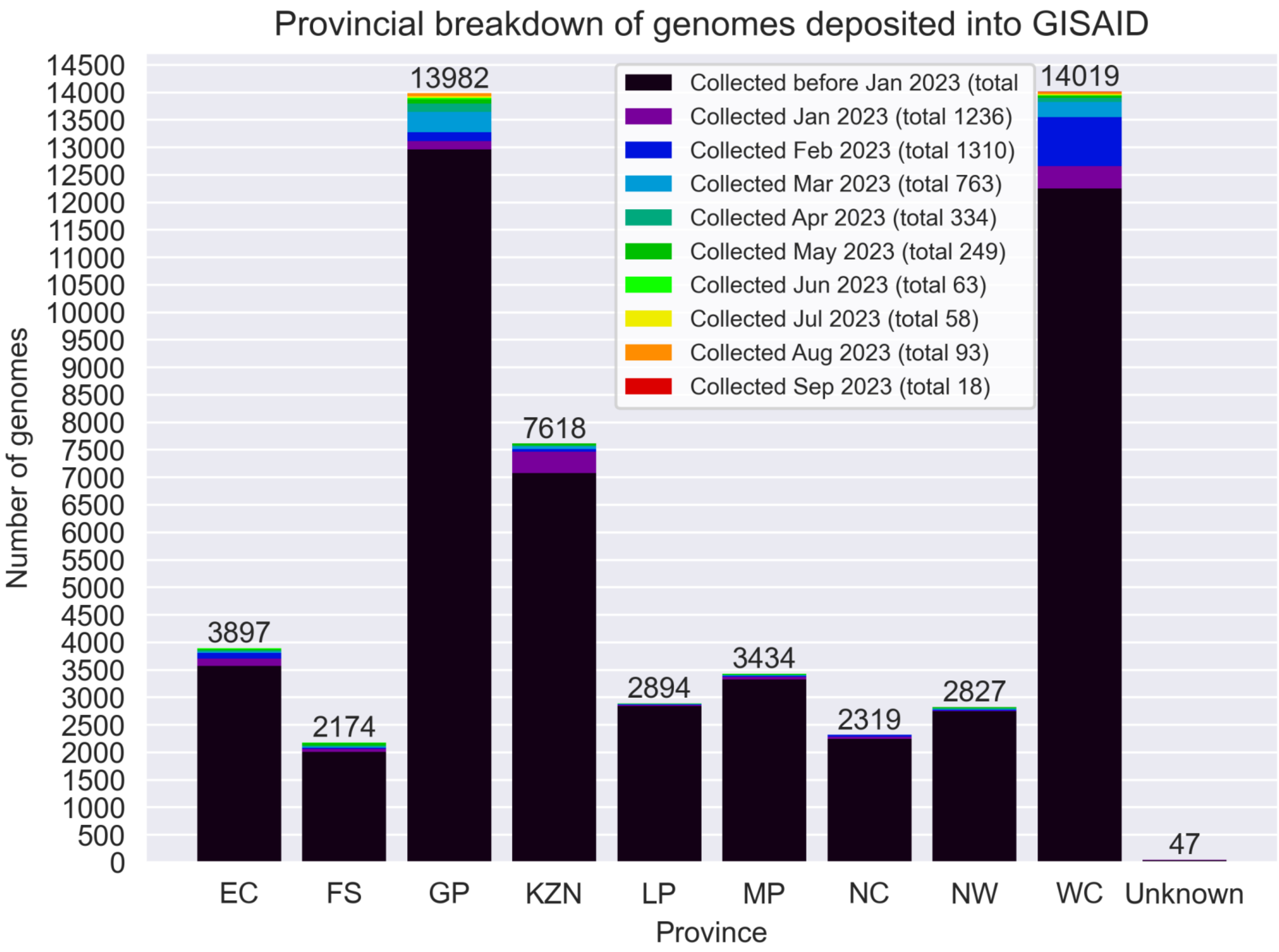
GISAID genomes vs total cases, 2020 – 2023 (N= 53 211)



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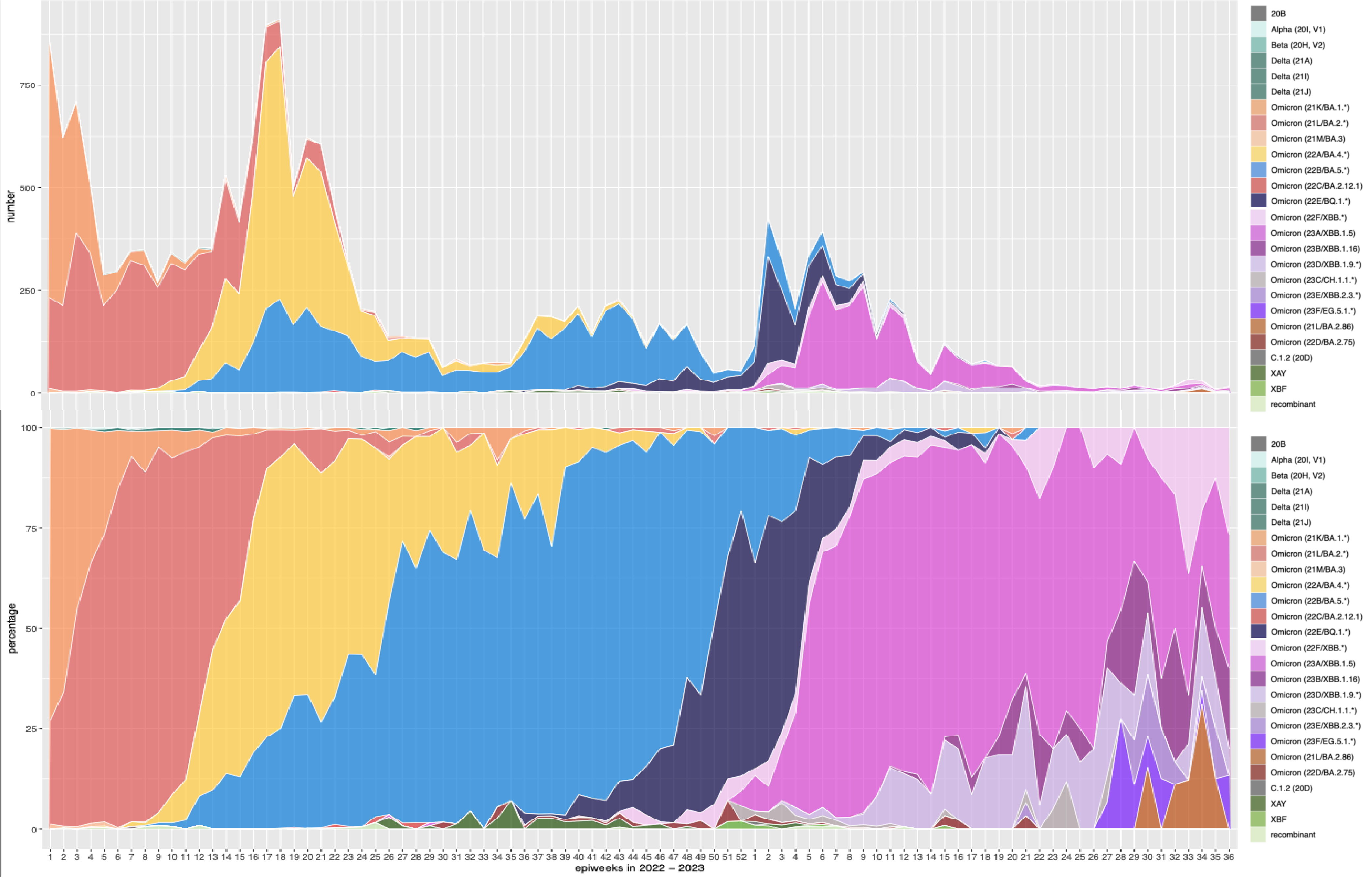
Number and percentage of clades by epiweek in South Africa, 2022-2023 (19 604*)



Sequencing data ending epi week 36 (ending 09 Sep 2023)

Currently in epi week 38 (ending 23 Sep 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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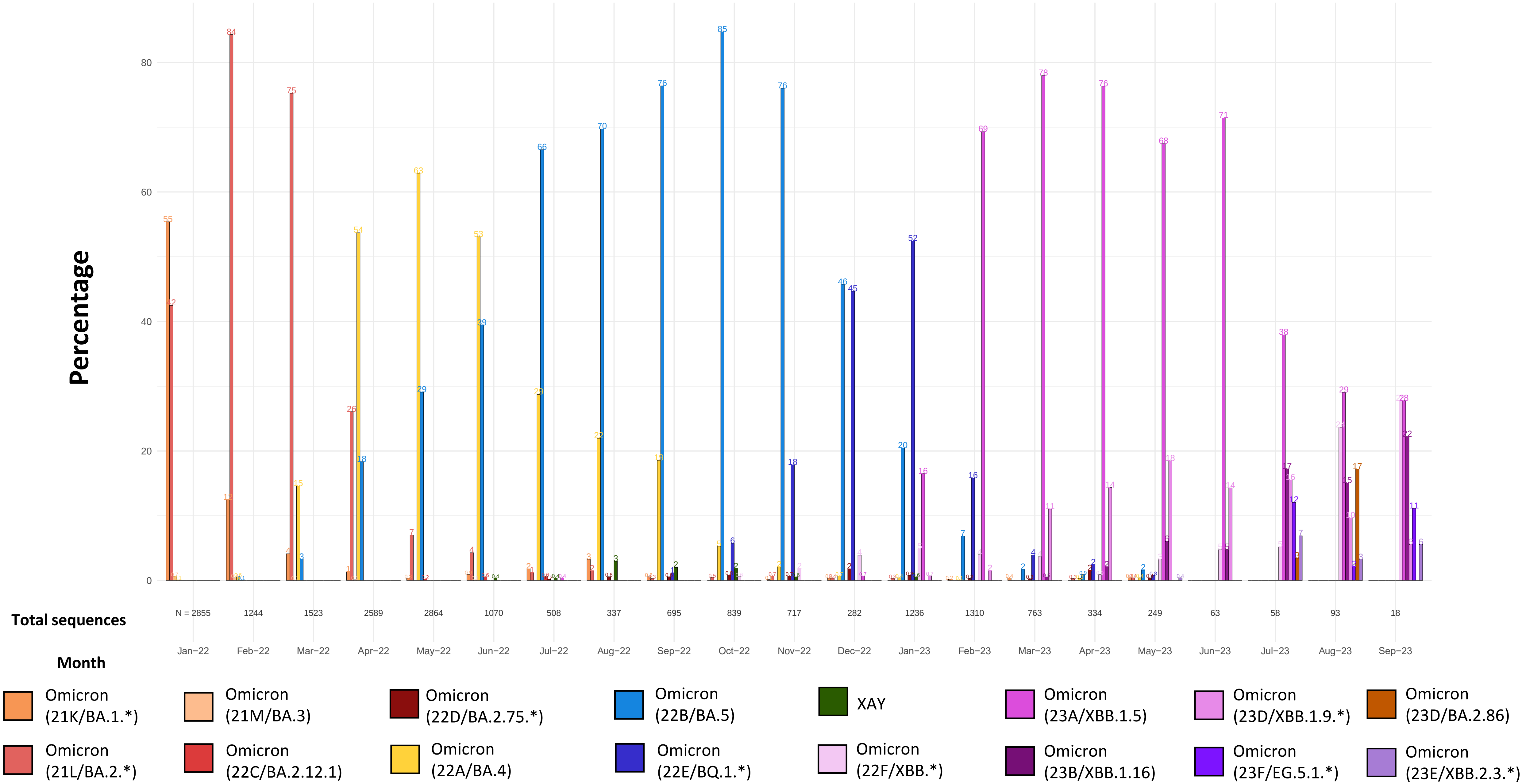
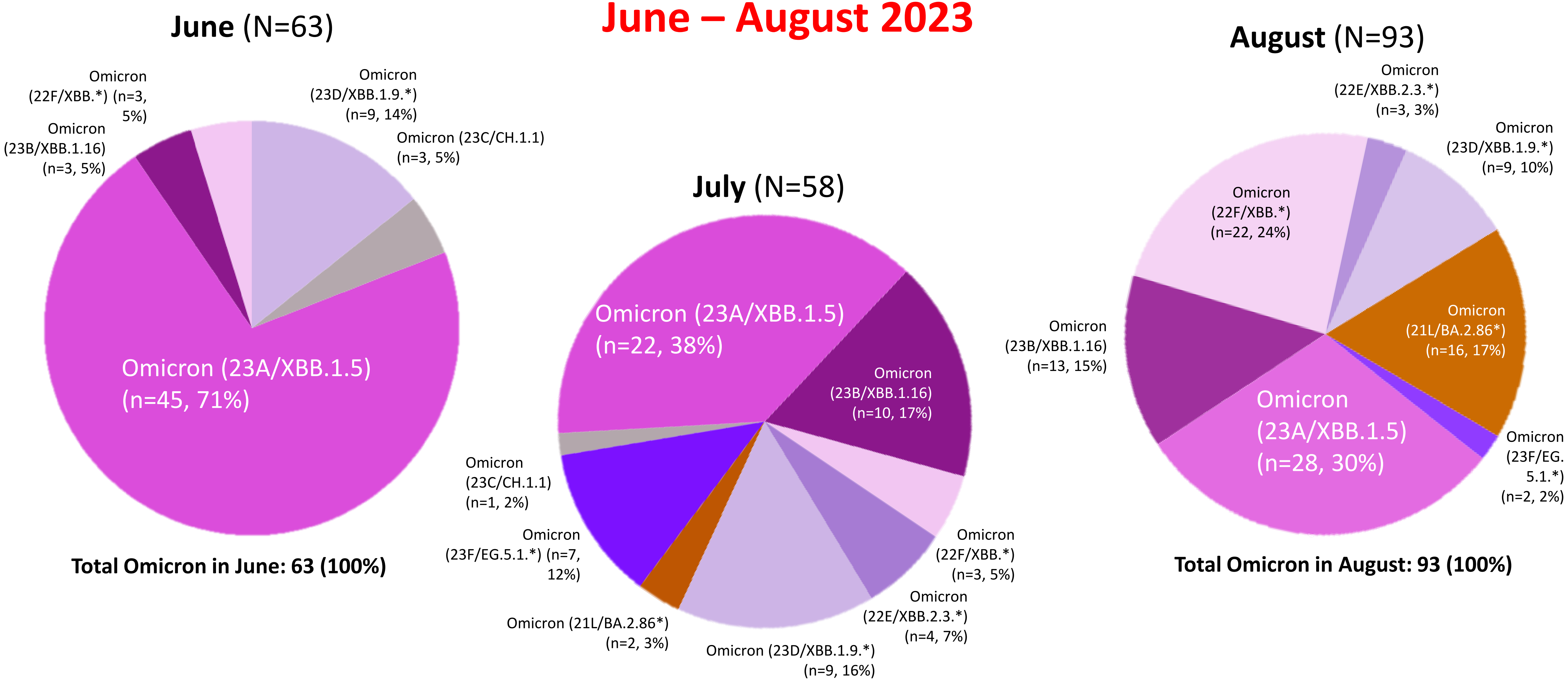
Detection Rates: Omicron and recombinants



*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 June – August 2023



Total Omicron in June: 63 (100%)

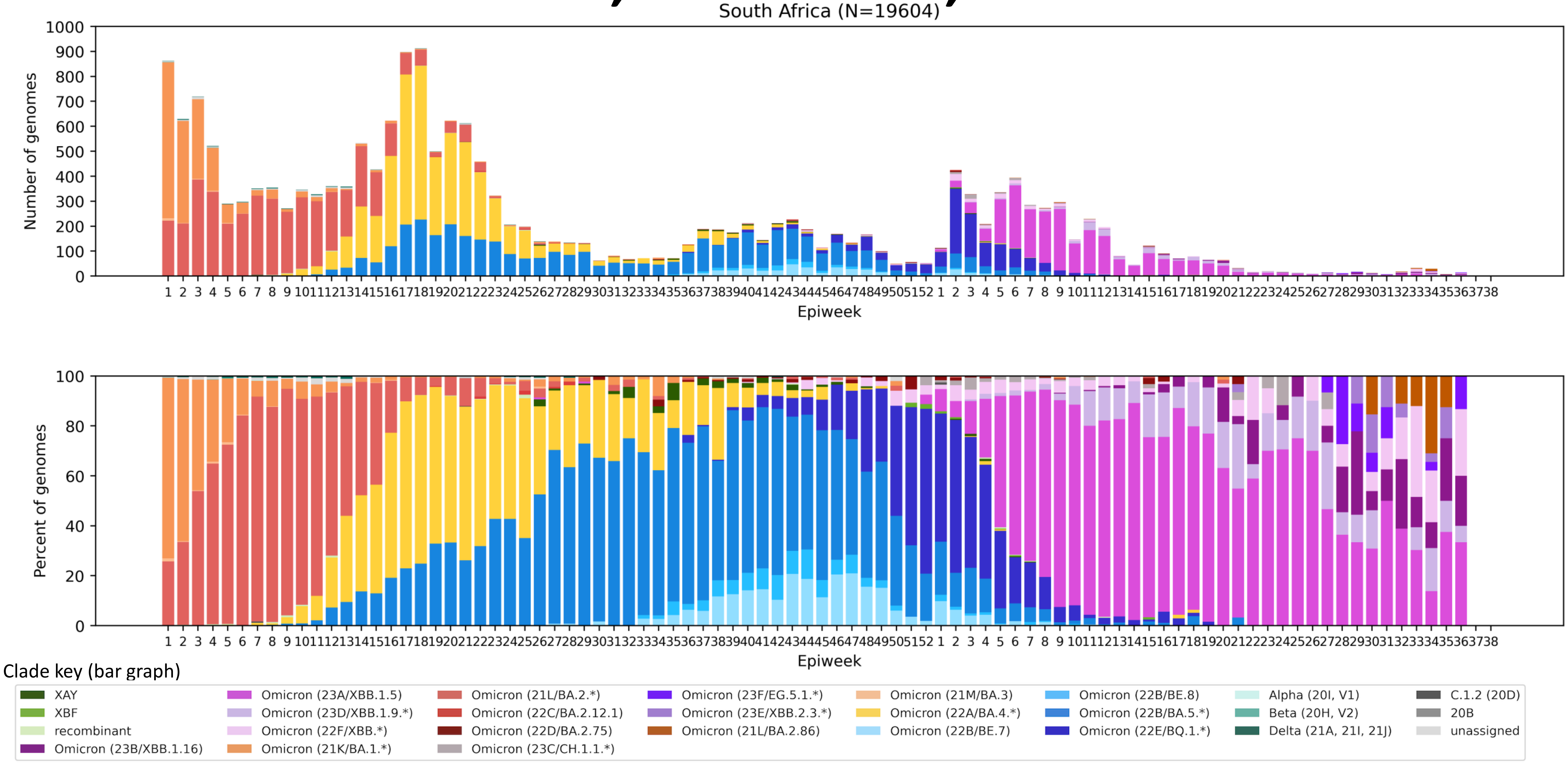
Total Omicron in July: 58 (100%)

Total Omicron in August: 93 (100%)

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

South Africa, 2022-2023, n = 19 604*



*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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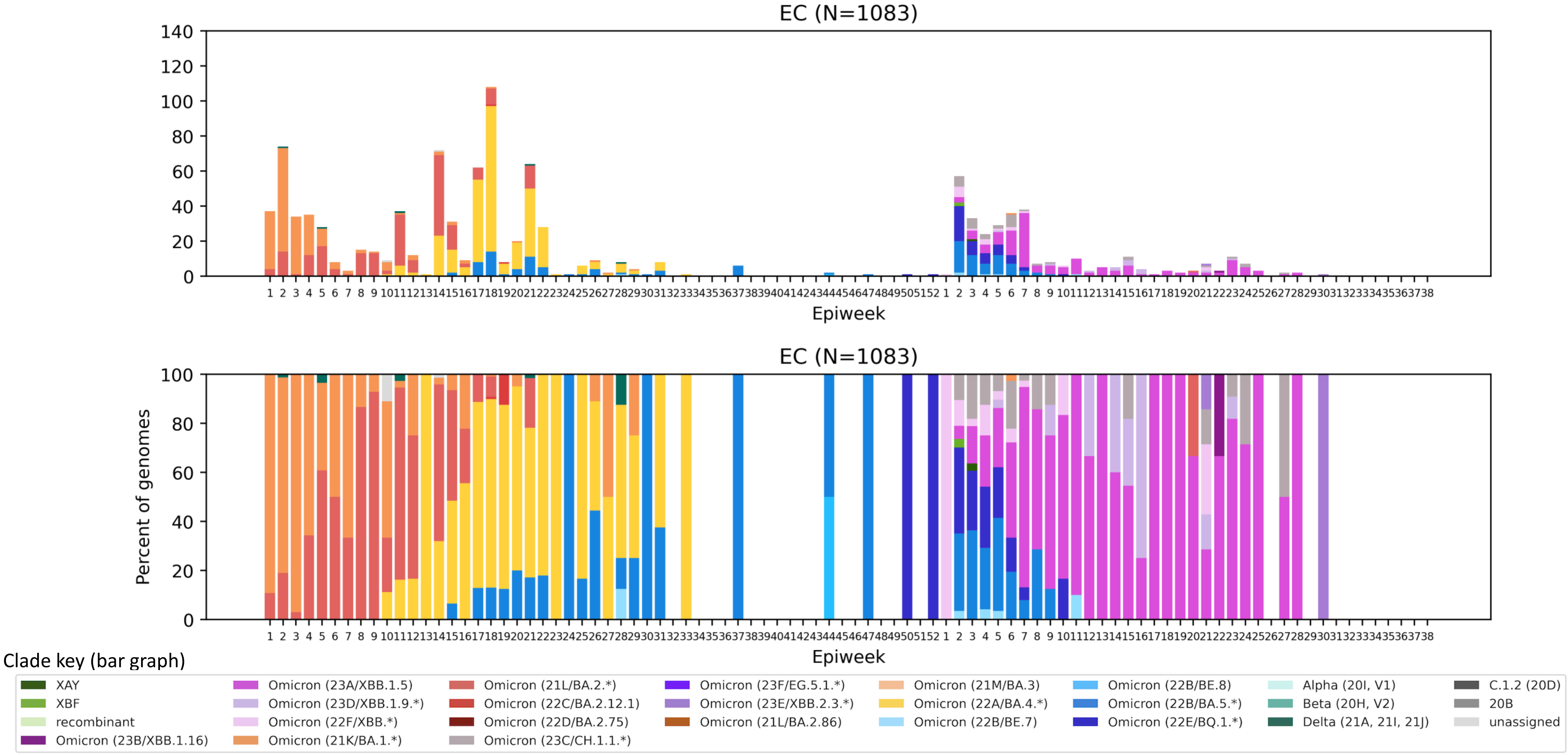
Eastern Cape Province, 2022-2023, n = 1083

Genomes added since last report: 0*



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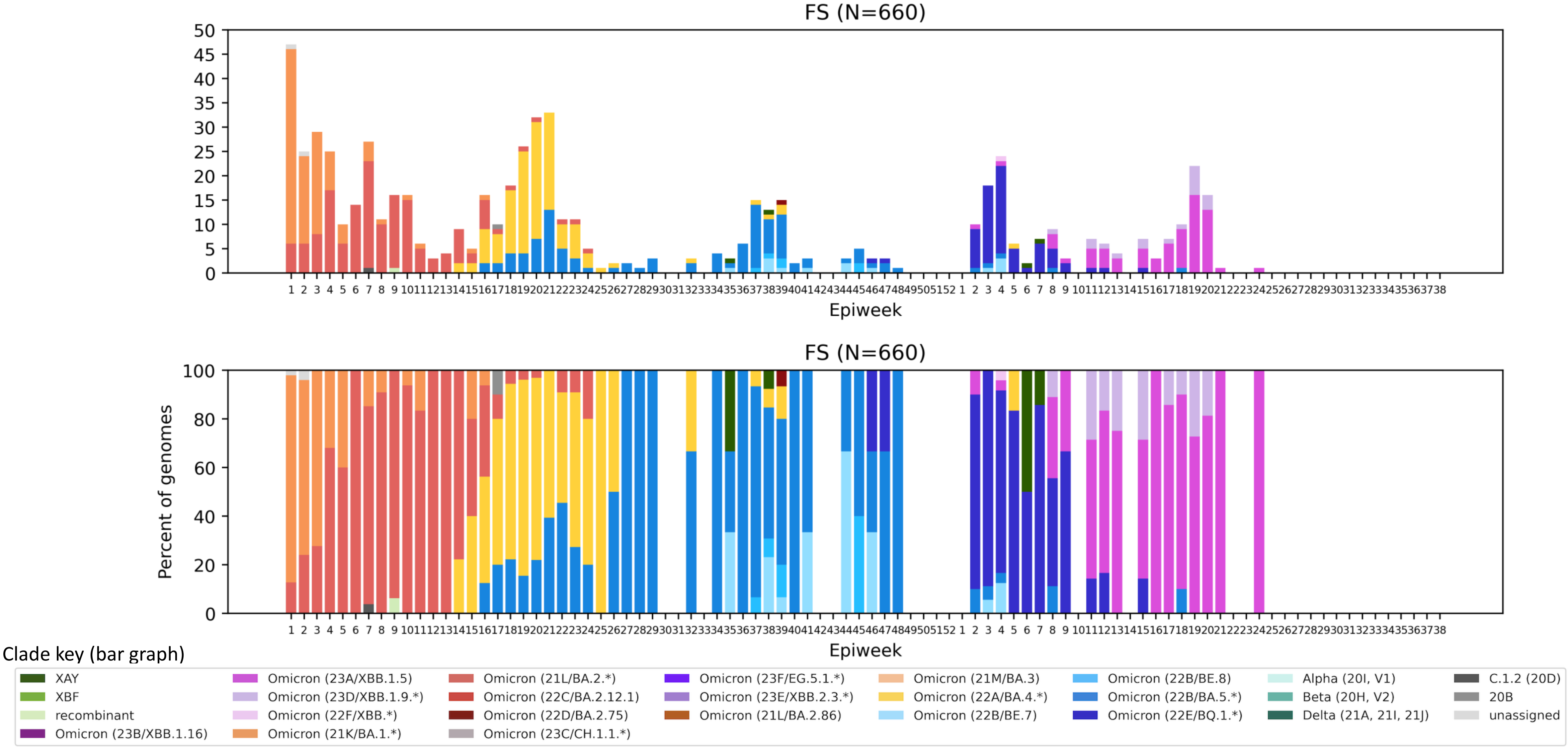
*May include genomes from 2020 and 2021 which are not pictured here and are not included in the slide total.

Free State Province, 2022-2023, n = 660

Genomes added since last report: 0*



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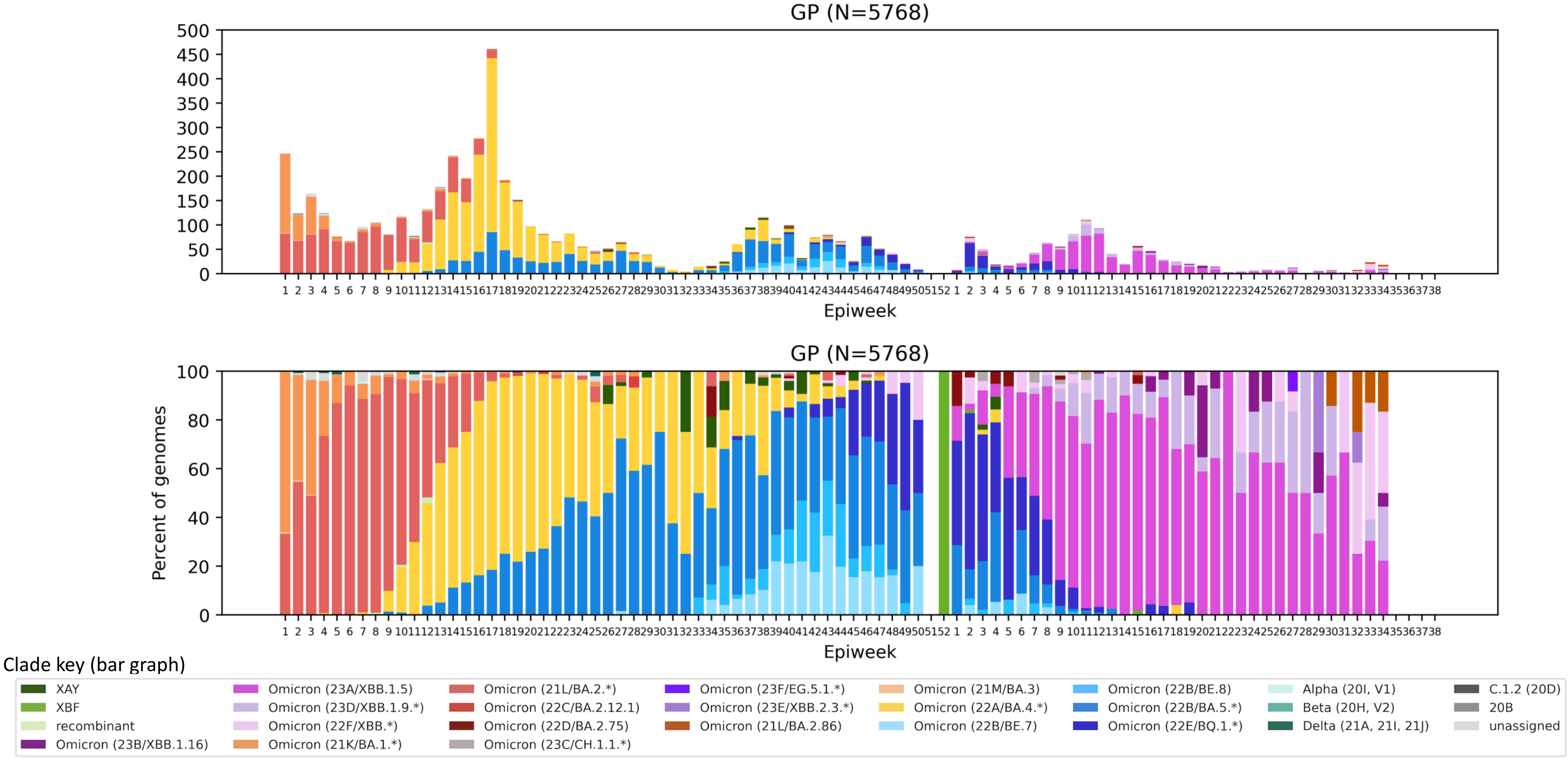
*May include genomes from 2020 and 2021 which are not pictured here and are not included in the slide total.

Gauteng Province, 2022-2023, n = 5768

Genomes added since last report: 1*



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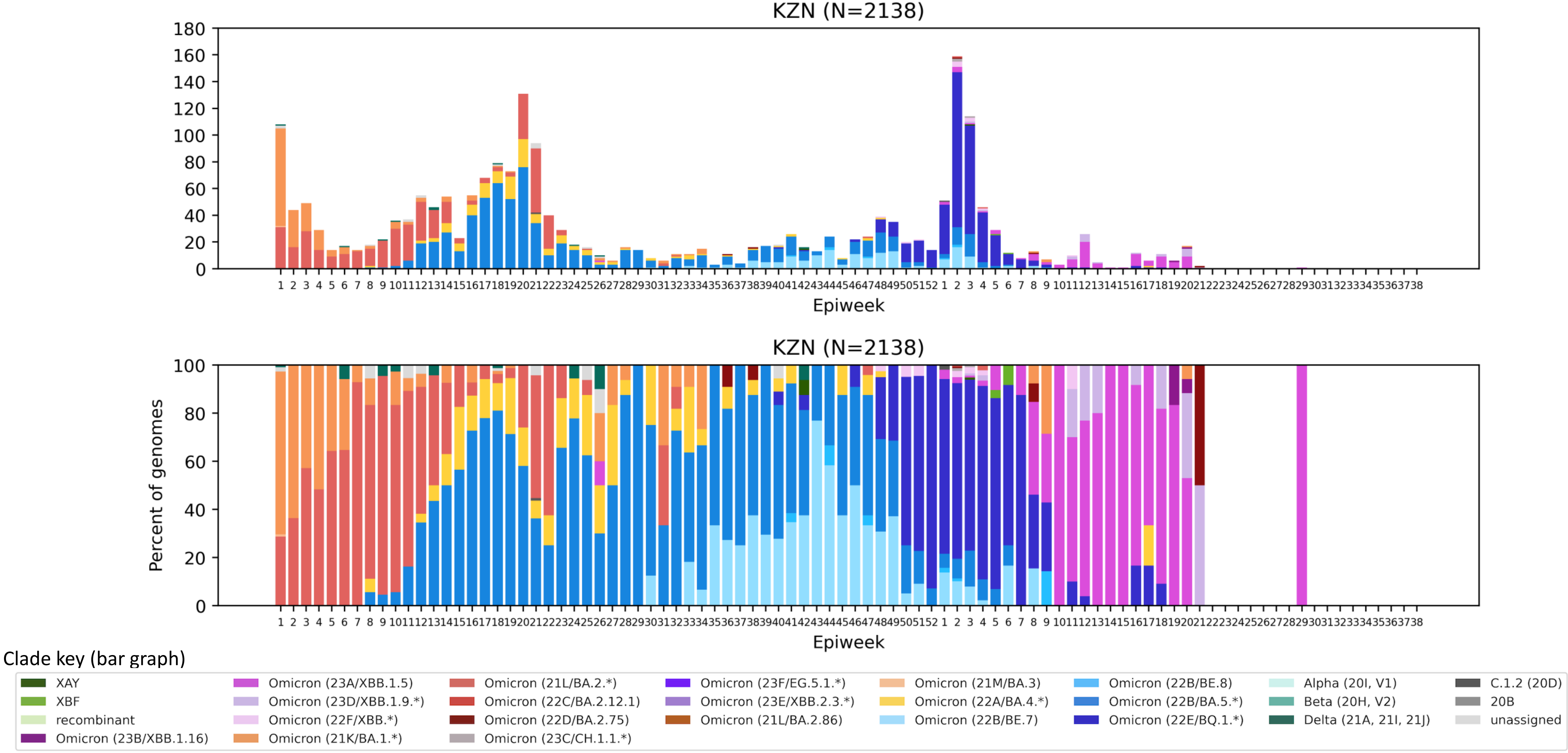
*May include genomes from 2020 and 2021 which are not pictured here and are not included in the slide total.

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

Genomes added since last report: 0*



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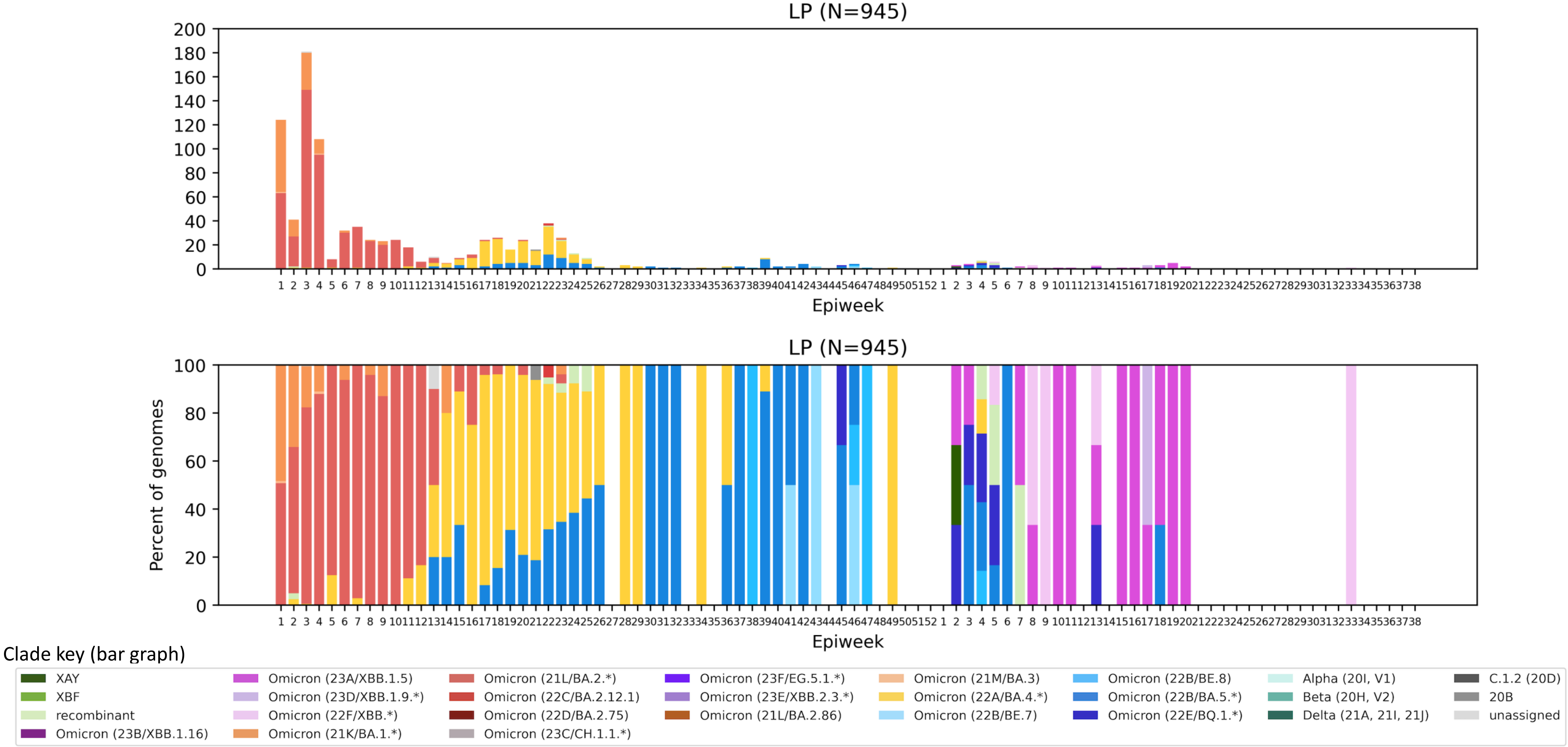
*May include genomes from 2020 and 2021 which are not pictured here and are not included in the slide total.

Limpopo Province, 2022-2023, n = 945

Genomes added since last report: 0*



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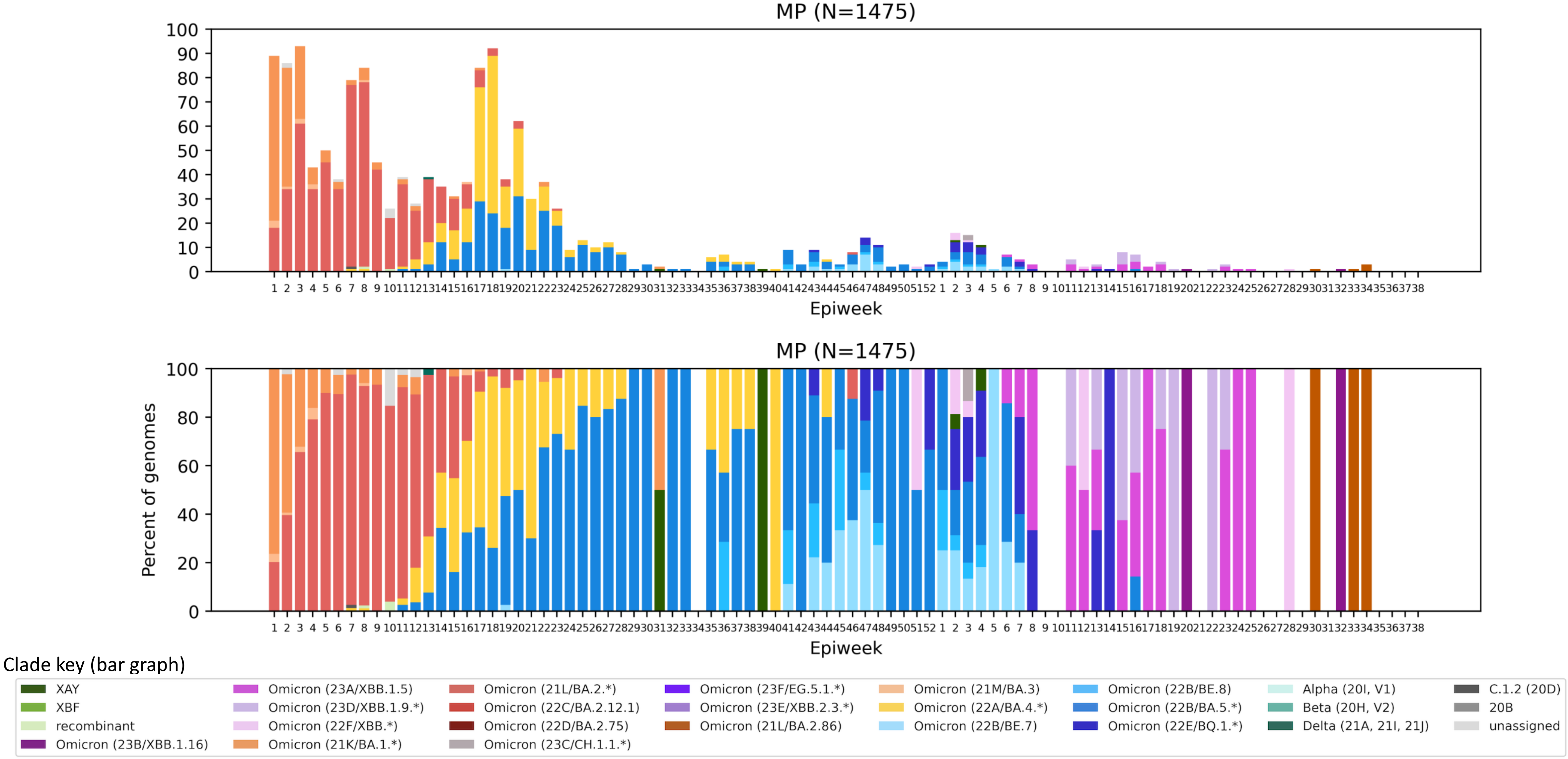
*May include genomes from 2020 and 2021 which are not pictured here and are not included in the slide total.

Mpumalanga Province, 2022-2023, n = 1475

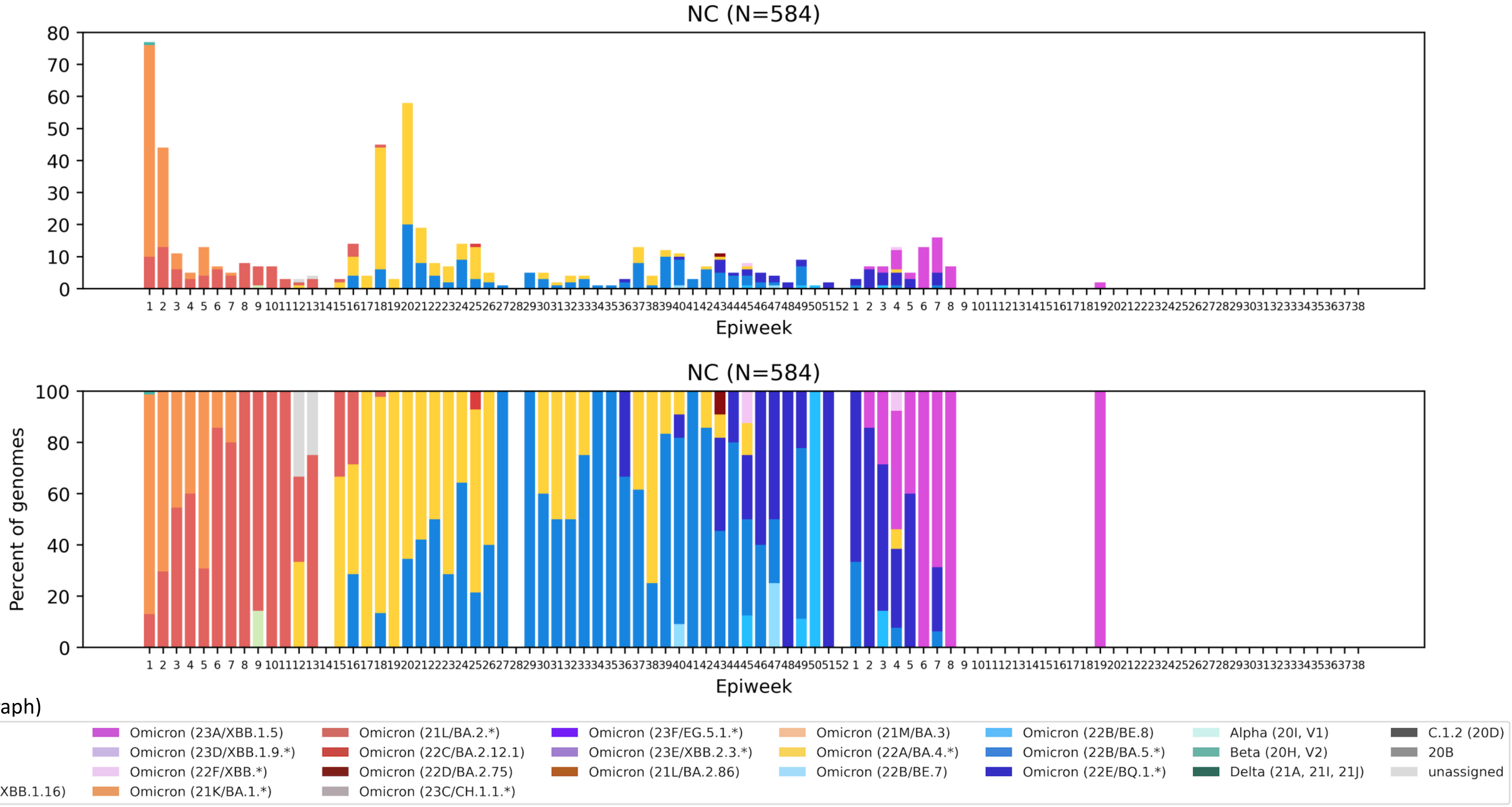
Genomes added since last report: 0*



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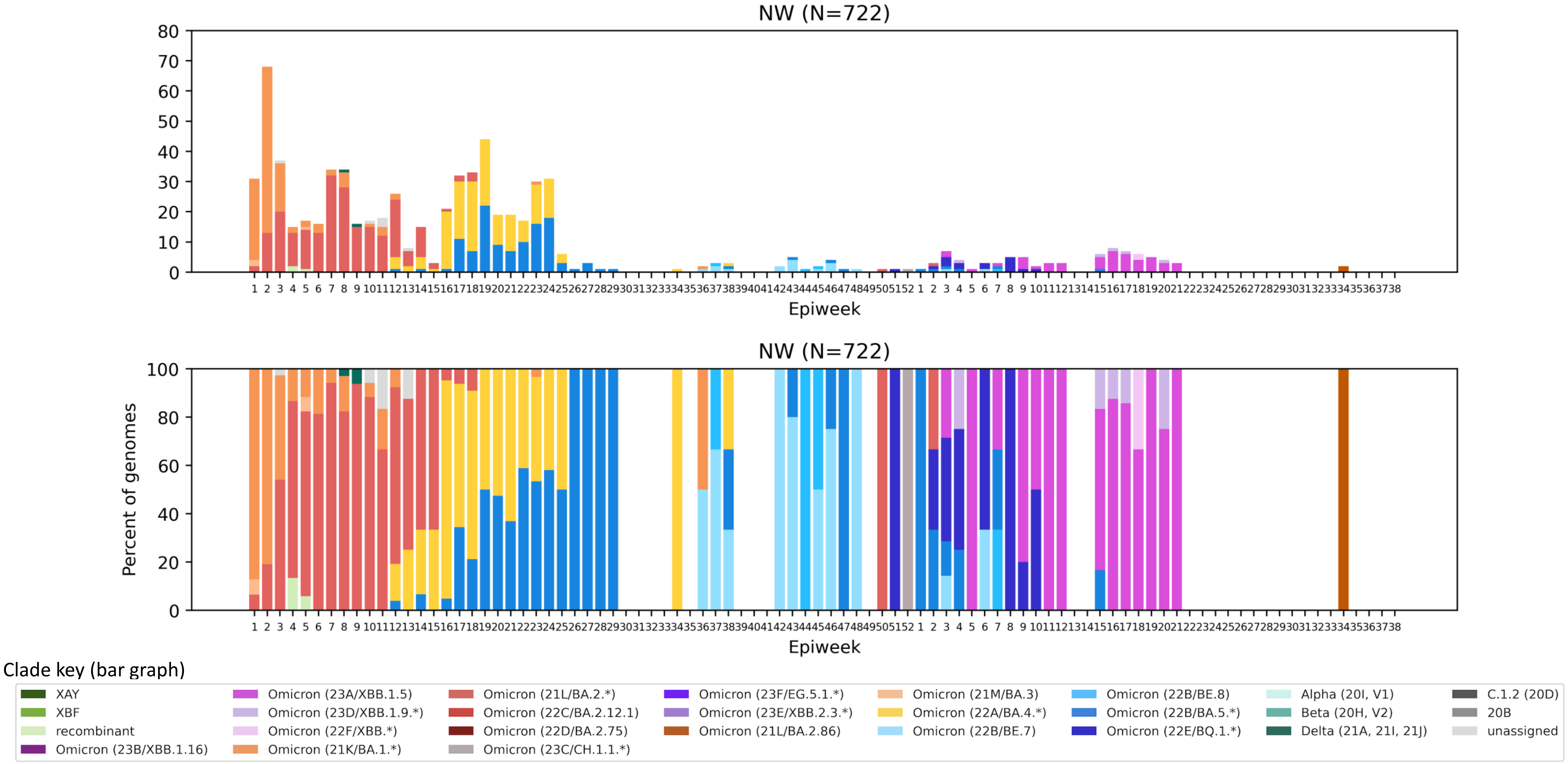
*May include genomes from 2020 and 2021 which are not pictured here and are not included in the slide total.

North West Province, 2022-2023, n = 722

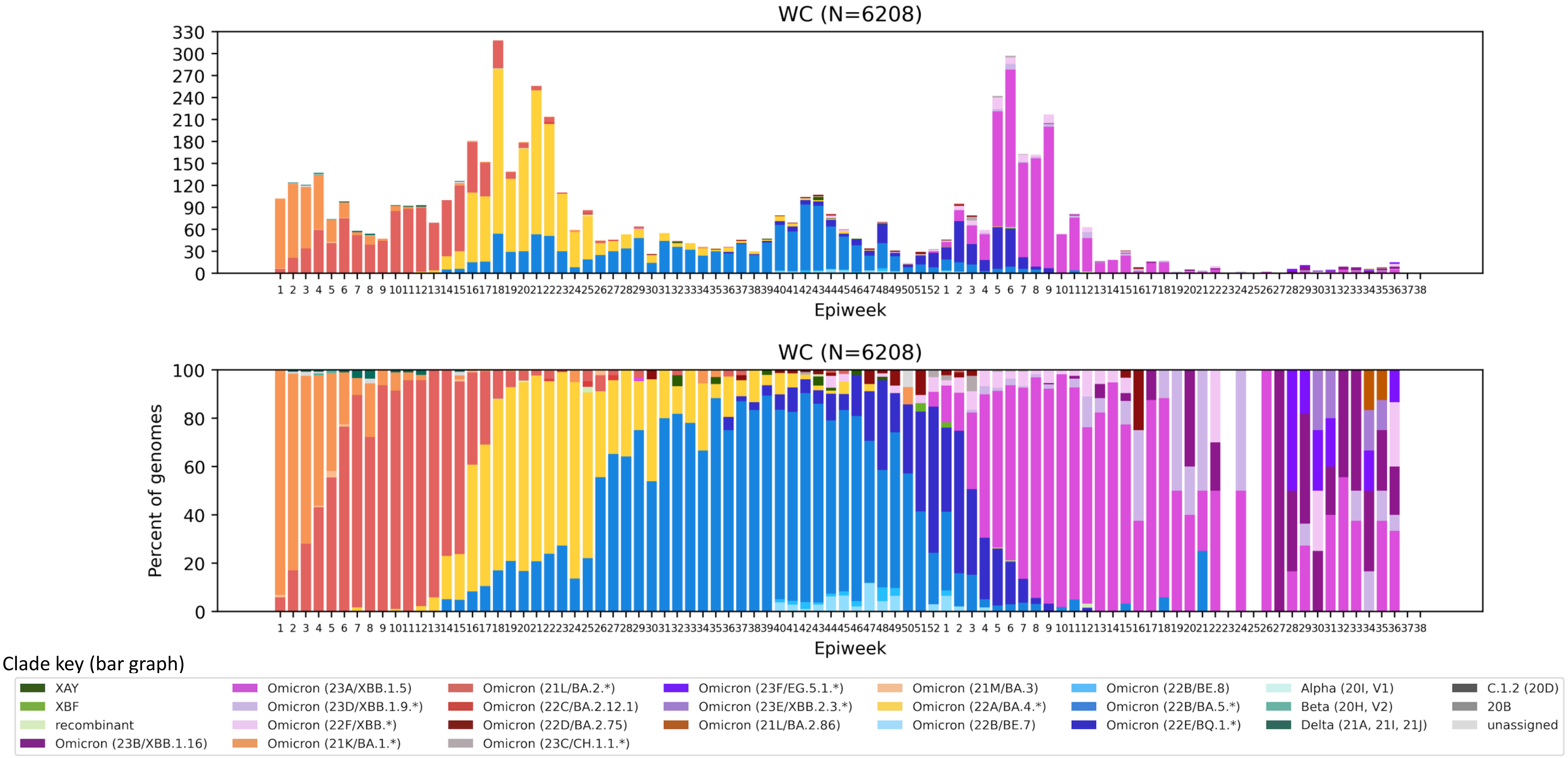
Genomes added since last report: 0*



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

Western Cape Province, 2022-2023, n = 6208

Genomes added since last report: 32*



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

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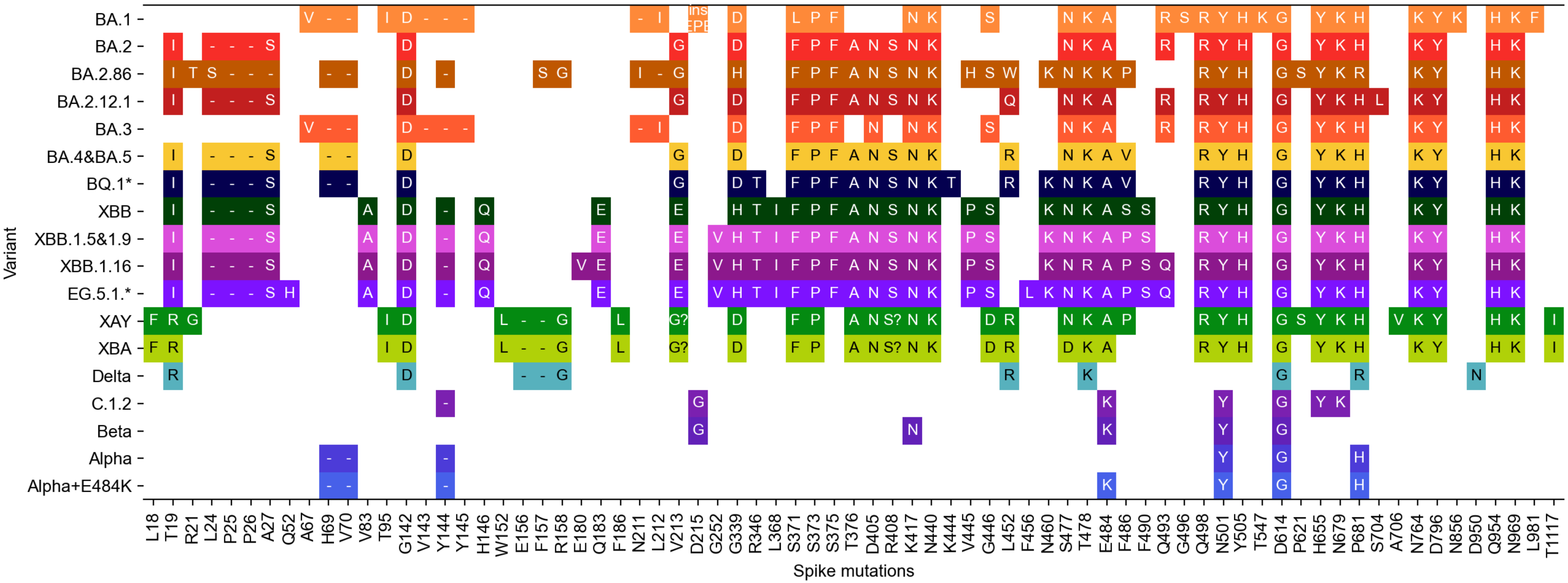
Summary

- **Sequencing update**
  - July sequences (n=58) are from the Eastern Cape, KwaZulu-Natal, Gauteng, Mpumalanga, and the Western Cape. August sequences (n=93) are from Gauteng, Limpopo, Mpumalanga, North West and the Western Cape. September sequences (n=18) are from the Western Cape

- **Variant of Concern Omicron in South Africa**
  - Omicron dominated in July (100%), August (100%), and September (100%), although the number of sequences from September are small (n=18)
  - XBB.1.5 constituted 38% of July, 30% of August and 28% of September sequences
  - XBB.1.16 has been detected in July (17%), August (15%), and September (22%)
  - XBB.1.9.* (newly designated clade 23D) was detected in sequences from July (16%), August (10%) and September (6%)
  - Eleven sequences of the EG.5.1.* lineage (newly designated clade 23F) have been detected in Gauteng (n=1) and the Western Cape (n=10) in July (n=7), August (n=2), and September (n=2)
  - Eighteen sequences of the BA.2.86 lineage have been detected in Gauteng (n=9), Mpumalanga (n=5), Western Cape (n=2) and North West (n=2), in July (n=2) and August (n=16)

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
BA.1									V	-	-		I	D	-	-	-	
BA.2		I		-	-	-	S							D				
BA.2.86		I	T	S	-	-	-			-	-			D		-		
BA.2.12.1		I		-	-	-	S							D				
BA.3									V	-	-			D	-	-	-	
BA.4&BA.5		I		-	-	-	S			-	-			D				
BQ.1*		I		-	-	-	S			-	-			D				
XBB		I		-	-	-	S					A		D		-		Q
XBB.1.5&1.9		I		-	-	-	S					A		D		-		Q
XBB.1.16		I		-	-	-	S					A		D		-		Q
EG.5.1.*		I		-	-	-	S	H				A		D		-		Q
XAY	F	R	G										I	D				
XBA	F	R											I	D				
Delta		R												D				
C.1.2																-		
Beta																		
Alpha										-	-					-		
Alpha+E484K										-	-					-		

Variant	W152	E156	F157	R158	E180	Q183	F186	N211	L212	V213	D215	G252	G339	R346	L368	S371	S373	S375
BA.1								-	I		ins EPE		D			L	P	F
BA.2										G			D			F	P	F
BA.2.86			S	G				I	-	G			H			F	P	F
BA.2.12.1										G			D			F	P	F
BA.3								-	I				D			F	P	F
BA.4&BA.5										G			D			F	P	F
BQ.1*										G			D	T		F	P	F
XBB						E				E			H	T	I	F	P	F
XBB.1.5&1.9						E				E		V	H	T	I	F	P	F
XBB.1.16					V	E				E		V	H	T	I	F	P	F
EG.5.1.*						E				E		V	H	T	I	F	P	F
XAY	L	-	-	G			L			G?			D			F	P	
XBA	L	-	-	G			L			G?			D			F	P	
Delta		-	-	G														
C.1.2											G							
Beta											G							
Alpha																		
Alpha+E484K																		

Variant	T376	D405	R408	K417	N440	K444	V445	G446	L452	F456	N460	S477	T478	E484	F486	F490	Q493	G496	Q498
BA.1				N	K			S				N	K	A			R	S	R
BA.2	A	N	S	N	K							N	K	A			R		R
BA.2.86	A	N	S	N	K		H	S	W		K	N	K	K	P				R
BA.2.12.1	A	N	S	N	K				Q			N	K	A			R		R
BA.3		N		N	K			S				N	K	A			R		R
BA.4&BA.5	A	N	S	N	K				R			N	K	A	V				R
BQ.1*	A	N	S	N	K	T			R		K	N	K	A	V				R
XBB	A	N	S	N	K		P	S			K	N	K	A	S	S			R
XBB.1.5&1.9	A	N	S	N	K		P	S			K	N	K	A	P	S			R
XBB.1.16	A	N	S	N	K		P	S			K	N	R	A	P	S	Q		R
EG.5.1.*	A	N	S	N	K		P	S		L	K	N	K	A	P	S	Q		R
XAY	A	N	S?	N	K			D	R			N	K	A	P				R
XBA	A	N	S?	N	K			D	R			D	K	A					R
Delta									R				K						
C.1.2														K					
Beta				N										K					
Alpha																			
Alpha+E484K														K					

Variant	N501	Y505	T547	D614	P621	H655	N679	P681	S704	A706	N764	D796	N856	D950	Q954	N969	L981	T1117
BA.1	Y	H	K	G		Y	K	H			K	Y	K		H	K	F	
BA.2	Y	H		G		Y	K	H			K	Y			H	K		
BA.2.86	Y	H		G	S	Y	K	R			K	Y			H	K		
BA.2.12.1	Y	H		G		Y	K	H	L		K	Y			H	K		
BA.3	Y	H		G		Y	K	H			K	Y			H	K		
BA.4&BA.5	Y	H		G		Y	K	H			K	Y			H	K		
BQ.1*	Y	H		G		Y	K	H			K	Y			H	K		
XBB	Y	H		G		Y	K	H			K	Y			H	K		
XBB.1.5&1.9	Y	H		G		Y	K	H			K	Y			H	K		
XBB.1.16	Y	H		G		Y	K	H			K	Y			H	K		
EG.5.1.*	Y	H		G		Y	K	H			K	Y			H	K		
XAY	Y	H		G	S	Y	K	H		V	K	Y			H	K		I
XBA	Y	H		G		Y	K	H			K	Y			H	K		I
Delta				G				R						N				
C.1.2	Y			G		Y	K											
Beta	Y			G														
Alpha	Y			G				H										
Alpha+E484K	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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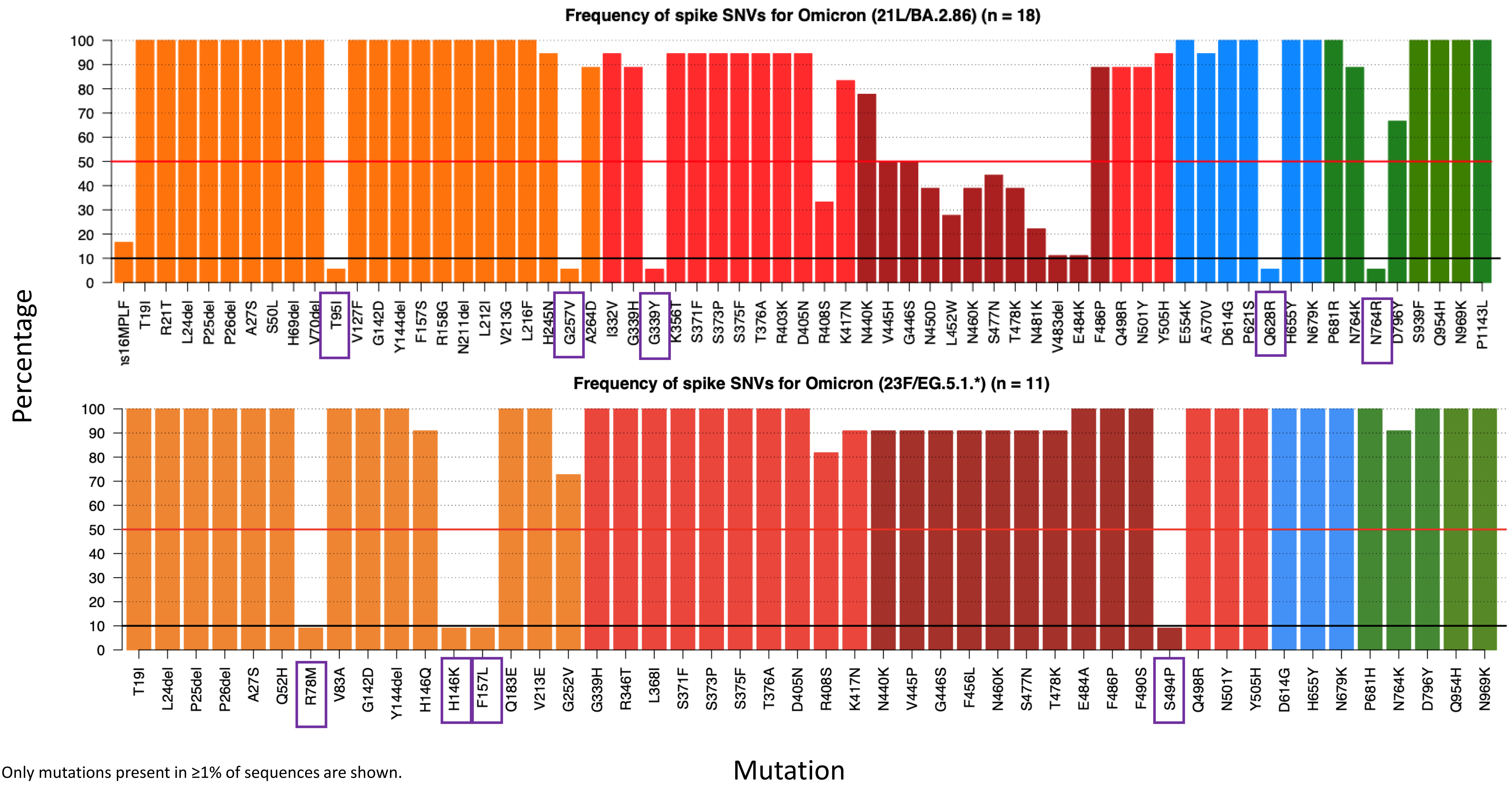
BA.2.86 and EG.5.1 spike mutations*


Frequency of spike SNVs for Omicron (21L/BA.2.86) (n = 18)

Frequency of spike SNVs for Omicron (23F/EG.5.1.*) (n = 11)

*Only mutations present in ≥1% of sequences are shown.

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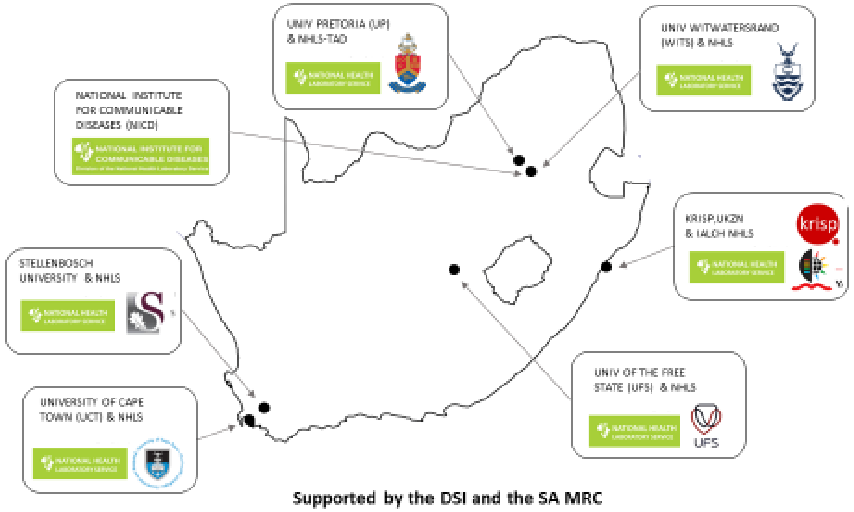
NGS-SA

Network for Genomic Surveillance in South Africa



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Division of the National Health Laboratory Service

EDCTP

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

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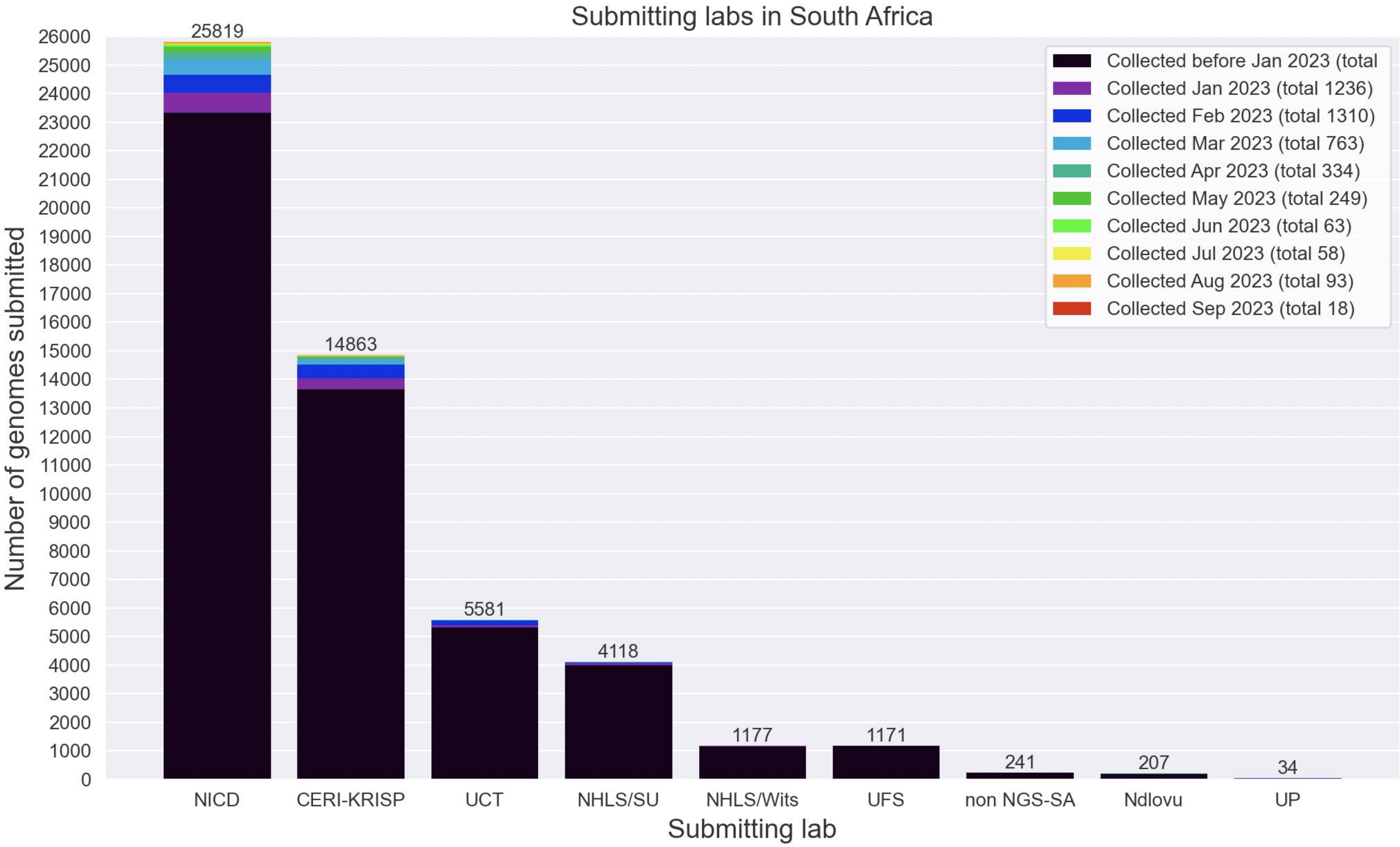
NATIONAL HEALTH
LABORATORY SERVICE

South African genomes submitted per submitting lab, 2020 - 2023 (N= 53 211)



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.)