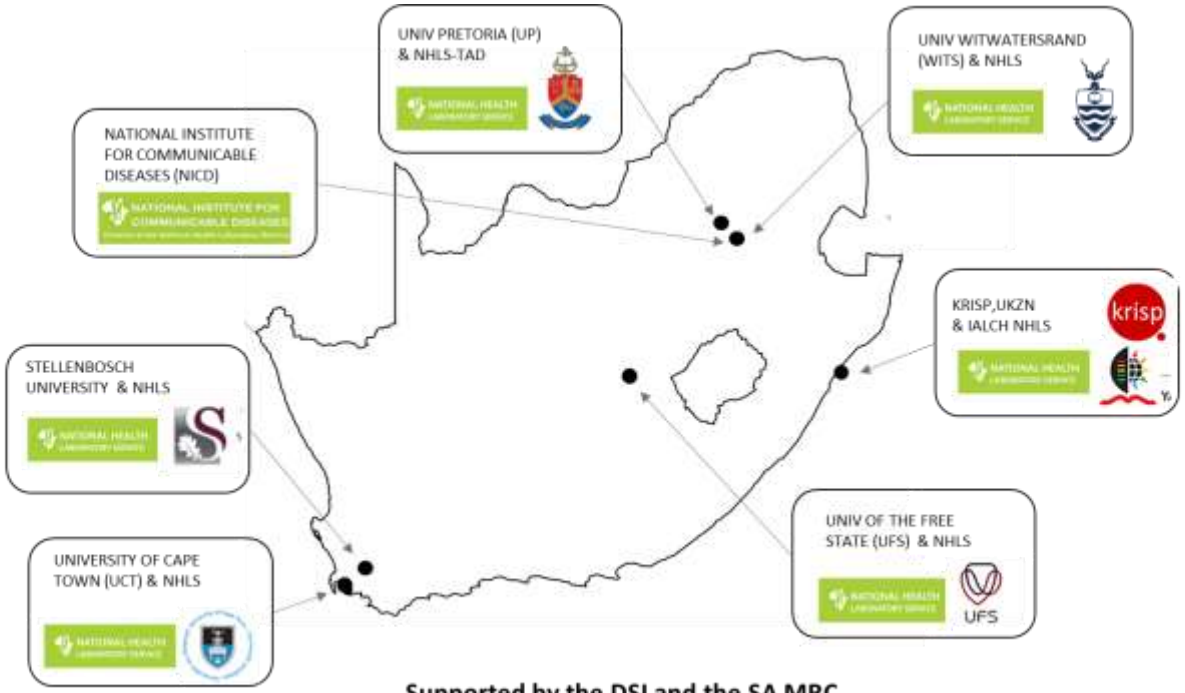
Network for Genomic Surveillance in South Africa (NGS-SA)

SARS-CoV-2 Sequencing Update
10 December 2021



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 10 December at 07h45

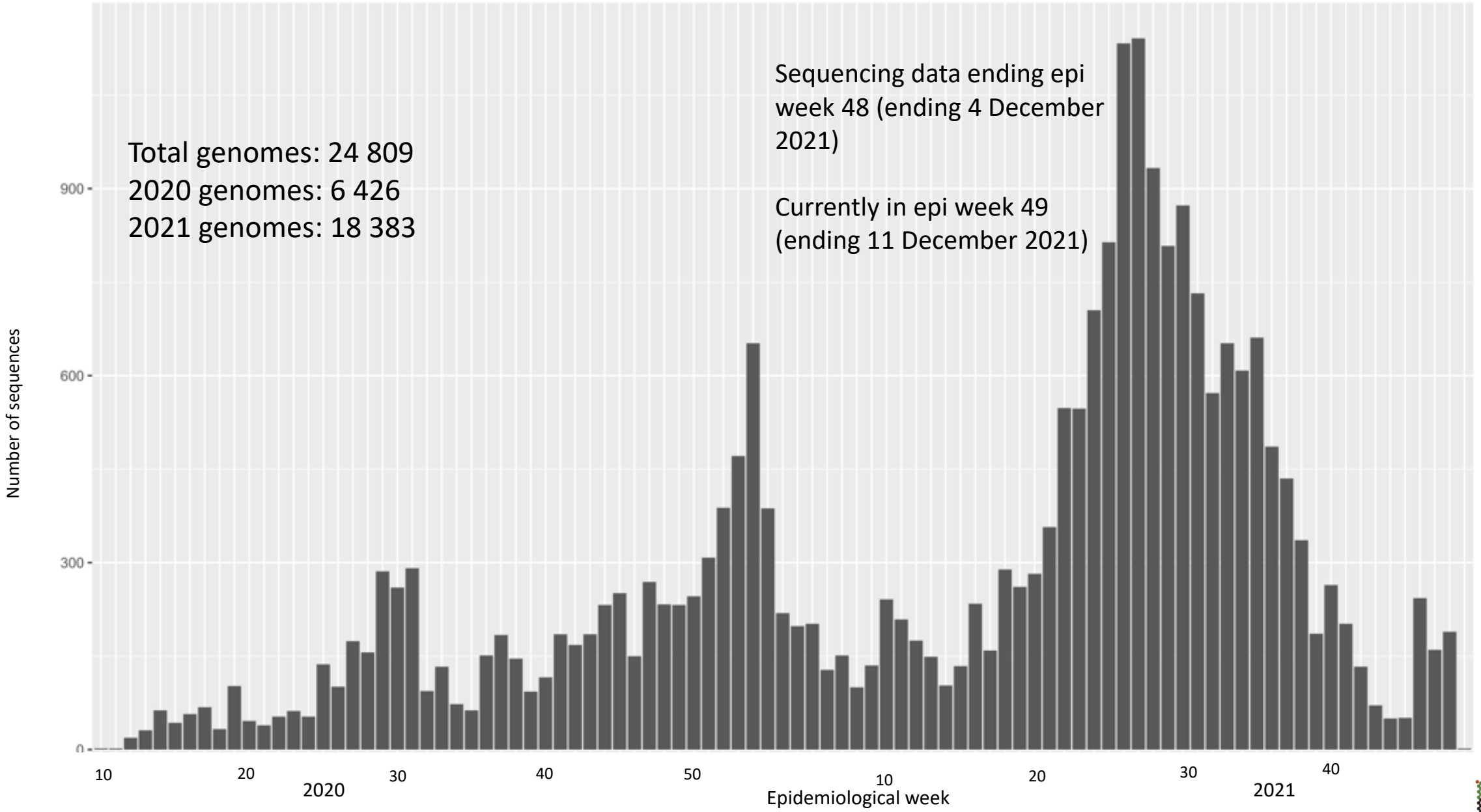
Data license: https://www.gisaid.org/registration/terms-of-use/

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

Case data is based on specimen collection date. Cases from https://www.nicd.ac.za/diseases-a-z-index/disease-index-covid-19/surveillance-reports/weekly-epidemiological-brief/ Test data from https://www.nicd.ac.za/diseases-a-z-index/disease-index-covid-19/surveillance-reports/weekly-testing-summary/

Number of South African genomes deposited on GISAID, by specimen collection week, 2020 and 2021 (N=24 809*)



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

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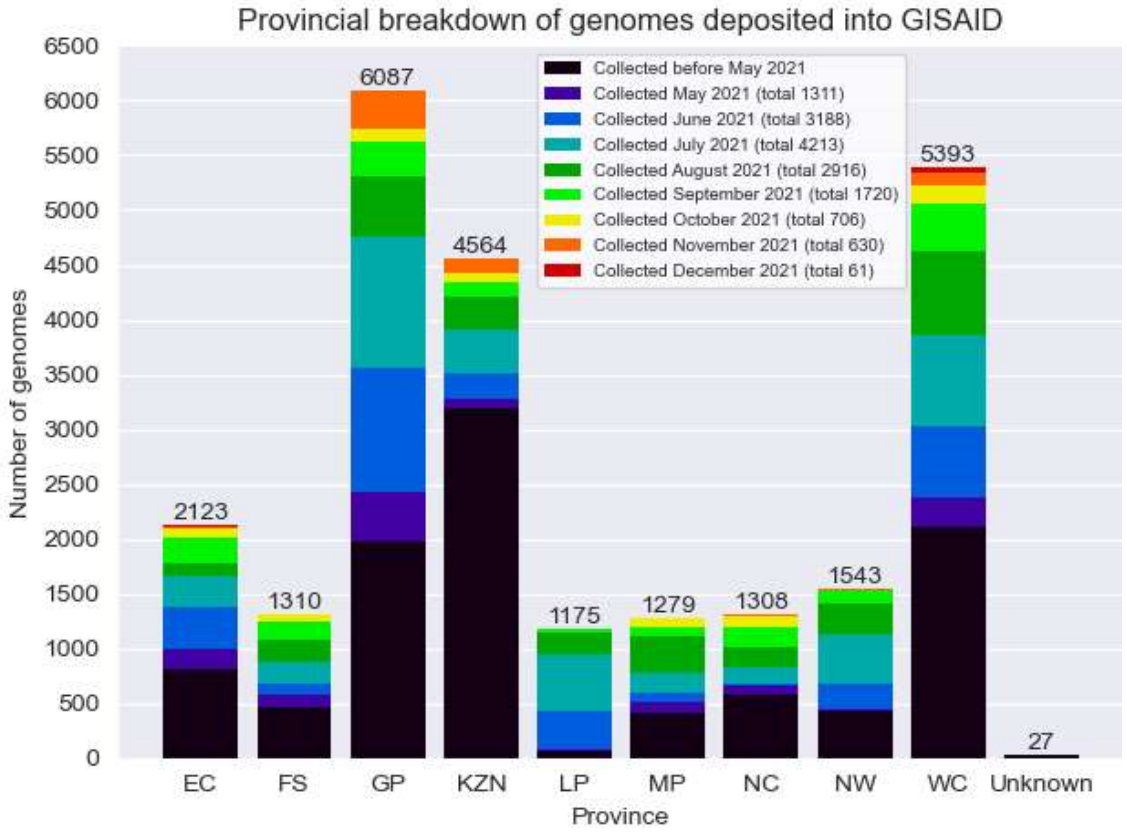
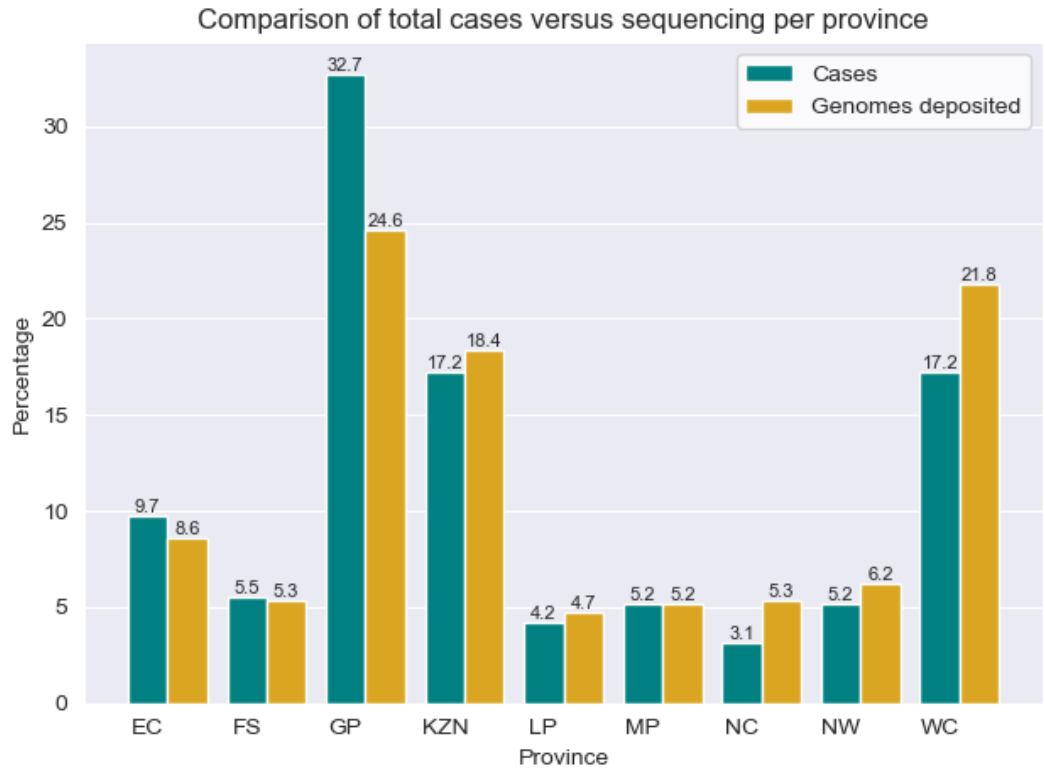
GISAID genomes vs total cases, 2020 and 2021 (N=24 809)





All provinces, apart from GP, KZN, NC and WC, have comparable percentage of overall cases and overall sequenced genomes. The majority of November sequencing data is from Gauteng.

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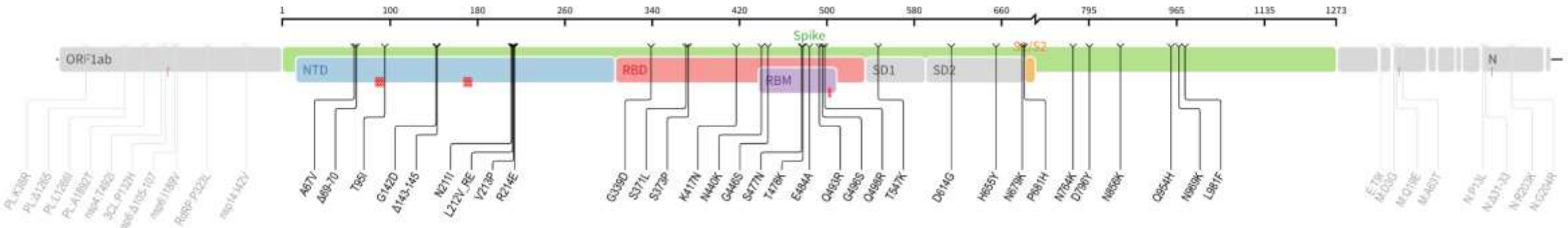
Omicron lineage mutation profile



- 45-52 amino acid changes (including deletions) across the whole GENOME
  - 26-32 changes in SPIKE

- Does <u>not possess</u> the RdRp G671S change associated with a decrease in Ct value for Delta variants
- Does possess the Δ69-70, which causes the S-Gene Target Failure (SGTF) and was previously seen in the Alpha VOC

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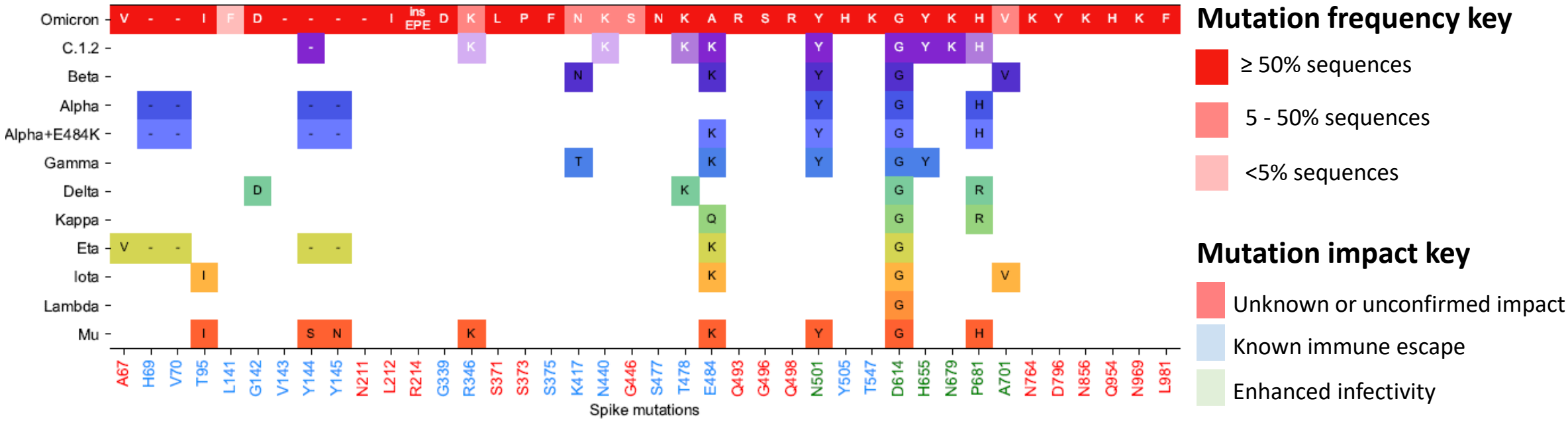
Omicron spike mutations compared to other VOC/VOIs



- 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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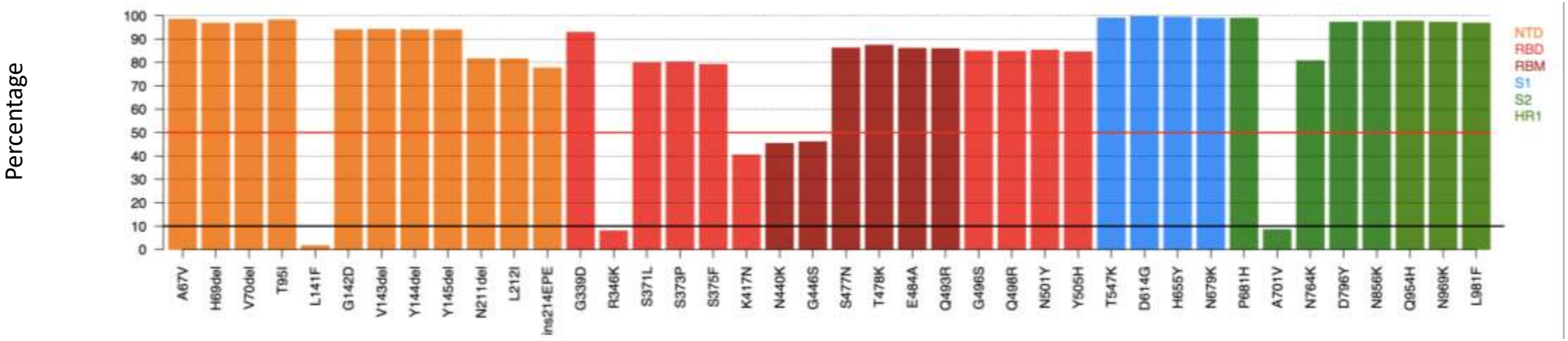
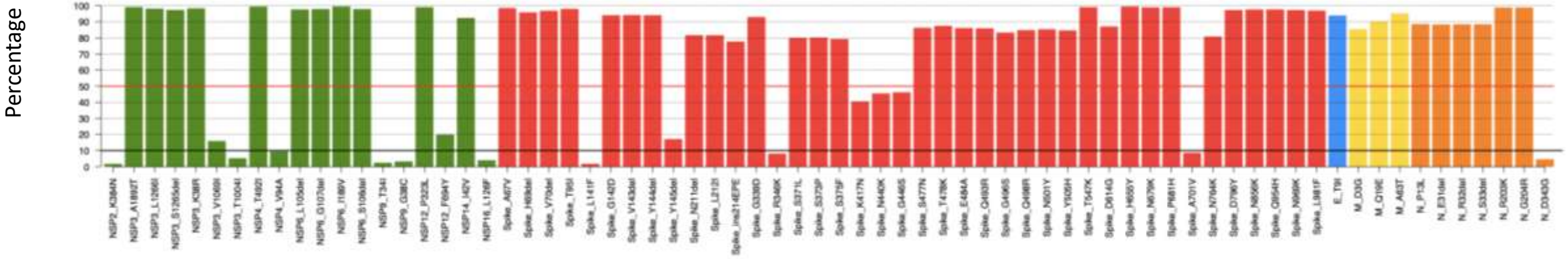
Mutational profile of Omicron sequences

Frequency of Spike SNVs for Omicron (n = 1522)



Frequency of whole genome SNVs for Omicron (n = 1522)



Mutational profile of Omicron is largely shared amongst all sequences. Low mutation frequencies for N417N, N440K, G446S and N764K are most likely a result of poor coverage due to primer drop off.

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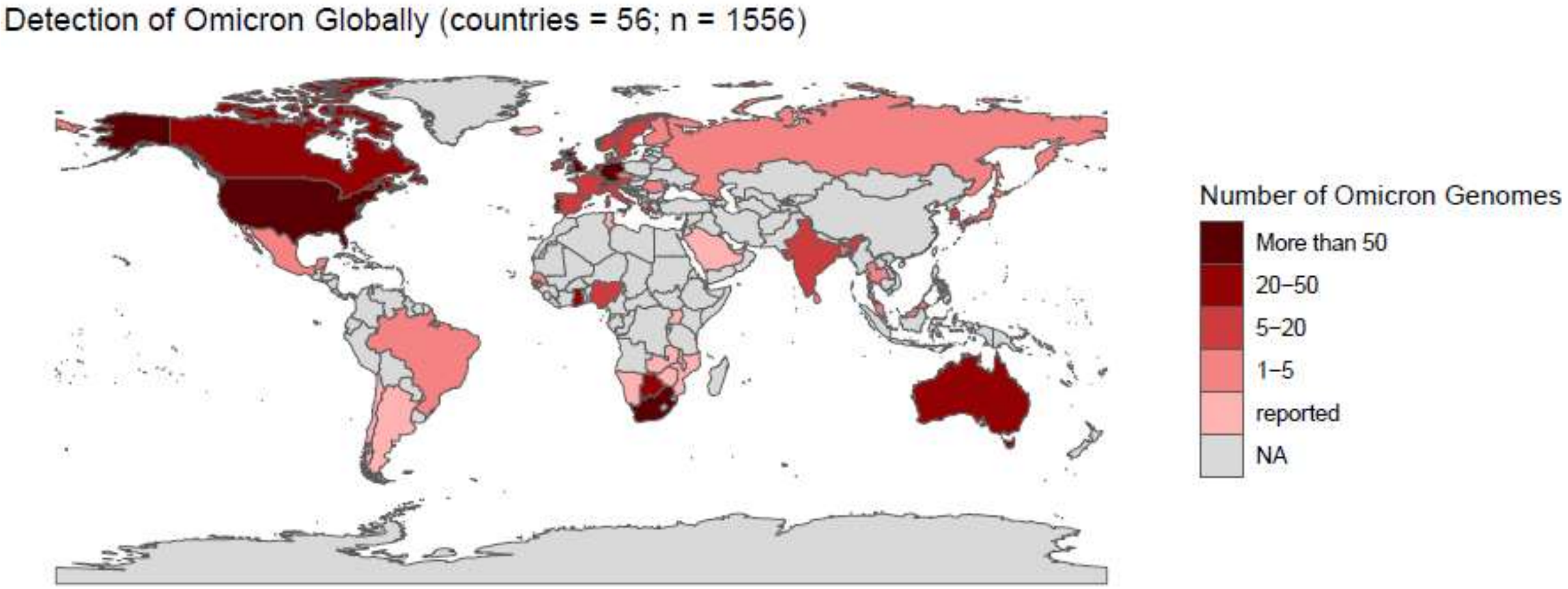
Omicron global prevalence



Omicron has been detected in 56 countries across the globe (detections based on GISAID).

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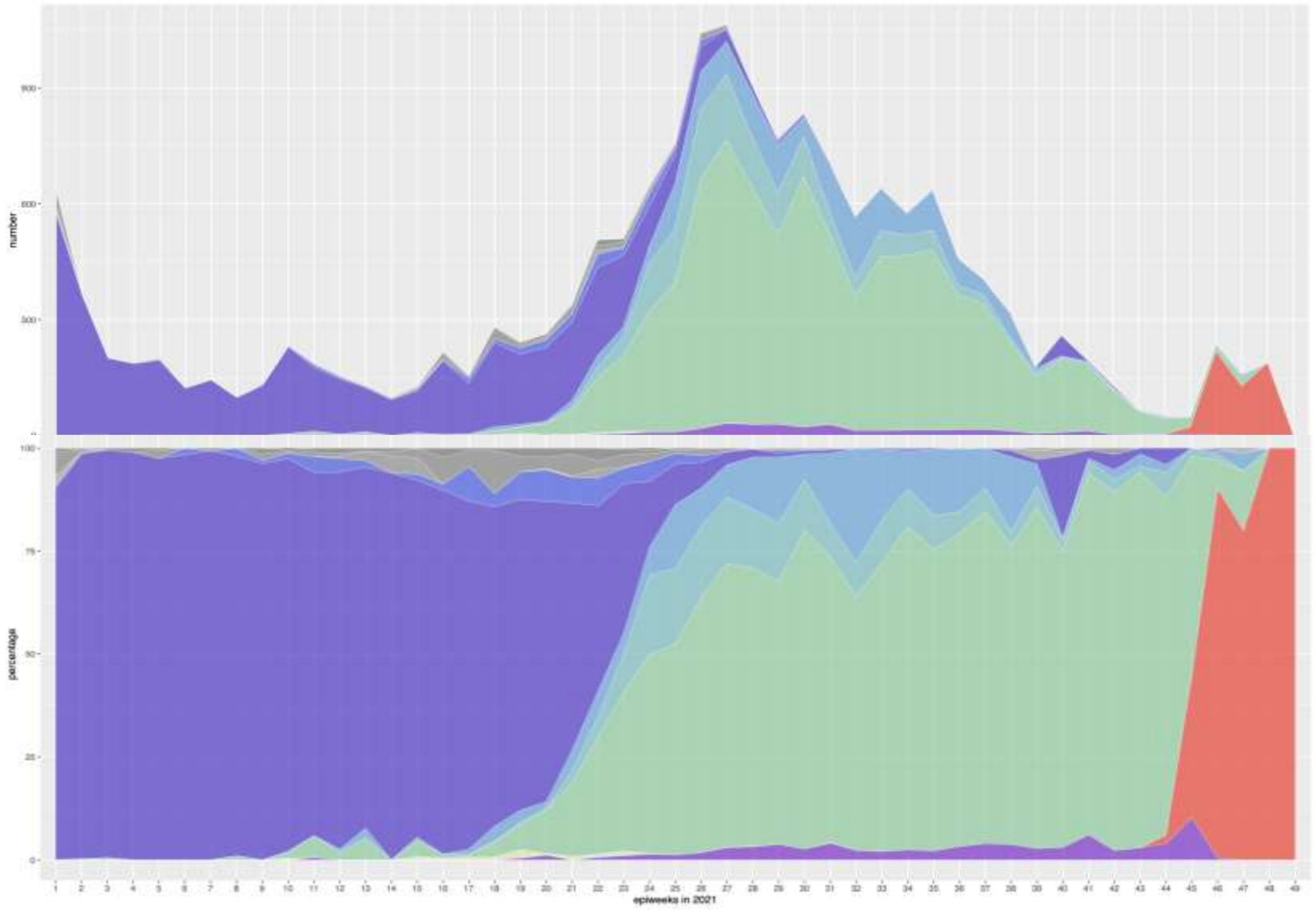
Proportion and number of clades by epiweek in South Africa, 2021 (N= 18 383)



Sequencing data ending epi week 48 (ending 4 December 2021)

Currently in epi week 49 (ending 11 December 2021)

Delta dominated South Africa's third wave with >80% frequency in October, with C.1.2 detection remaining <4%. Omicron appears to dominate November sequencing data but sequencing is ongoing to determine its prevalence.

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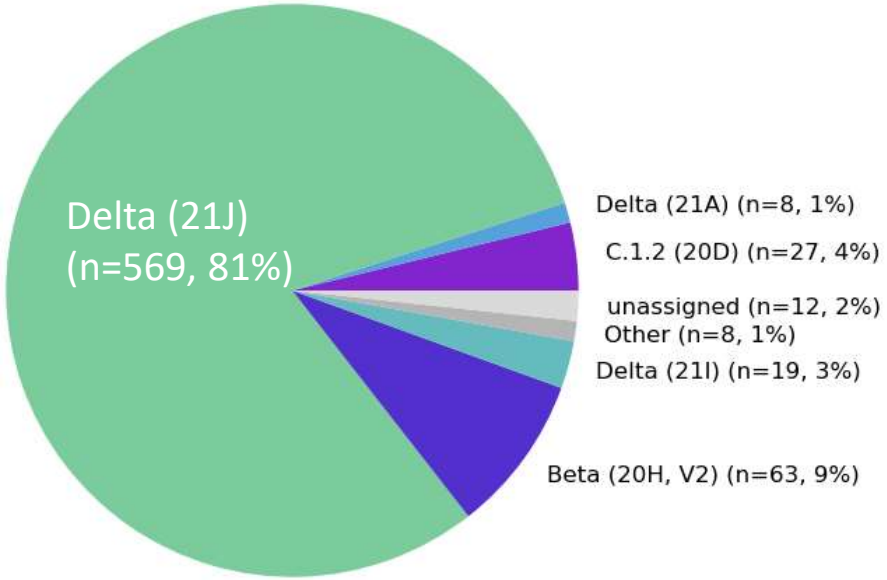
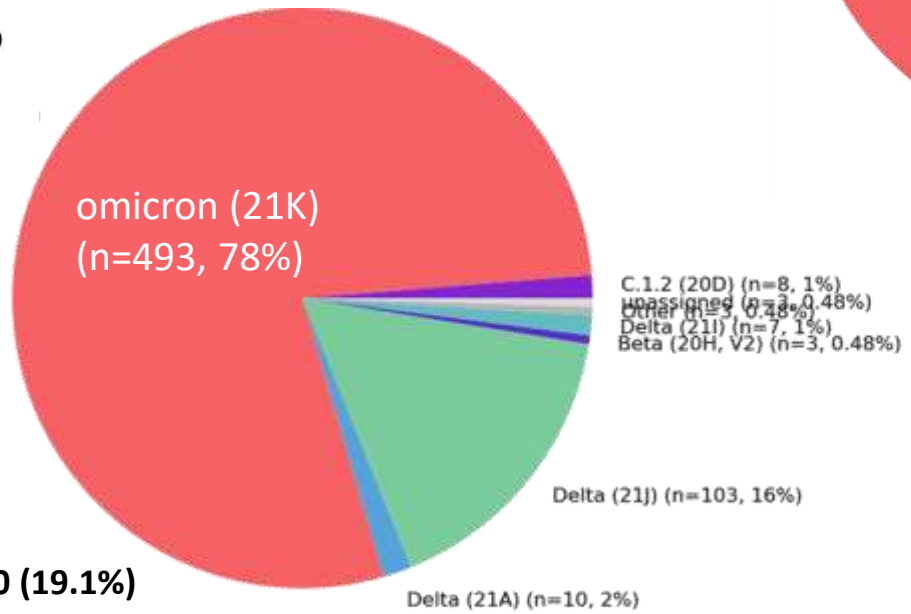
Prevalence of Variants of Concern (VOC) and Variants of Interest (VOI) in October – December 2021

October (N=706)



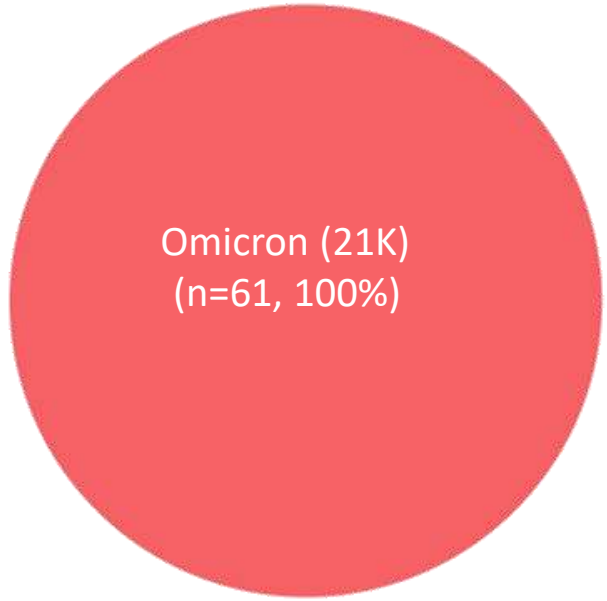
Total Delta in Oct: 596 (84.4%)

November (N=630)



Total Delta in Nov: 120 (19.1%)

December (N=61)



Total omicron in Dec: 61 (100%)

Omicron (21K) | C.1.2 (20D) | Beta (20H, V2) | Alpha (20I, V1) | Delta (21A) | Delta (21I) | Delta (21J) | Kappa (21B) | Eta (21D) | Other | unassigned

The Delta variant dominated in October in South Africa with >80% frequency.
Omicron was first detected in South Africa in November comprising 78% (493/630) of sequences.

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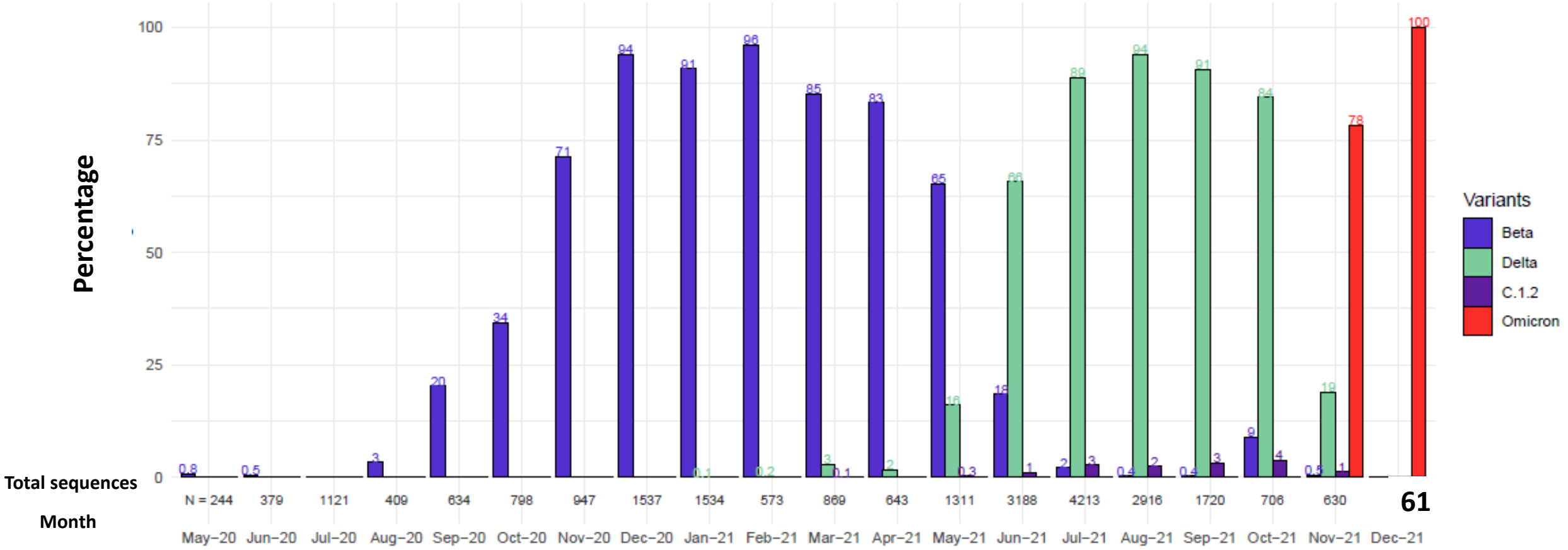
Detection Rates: Beta, Delta, C.1.2 and Omicron

Detection rates of variants being monitored in South Africa



C.1.2 has been detected at ≤ 4% of sequences monthly.
Beta prevalence increased slightly in October and has also been detected in November.
Omicron first detected in South Africa on November 8th, accounting for 78% (n=493/630) genomes.

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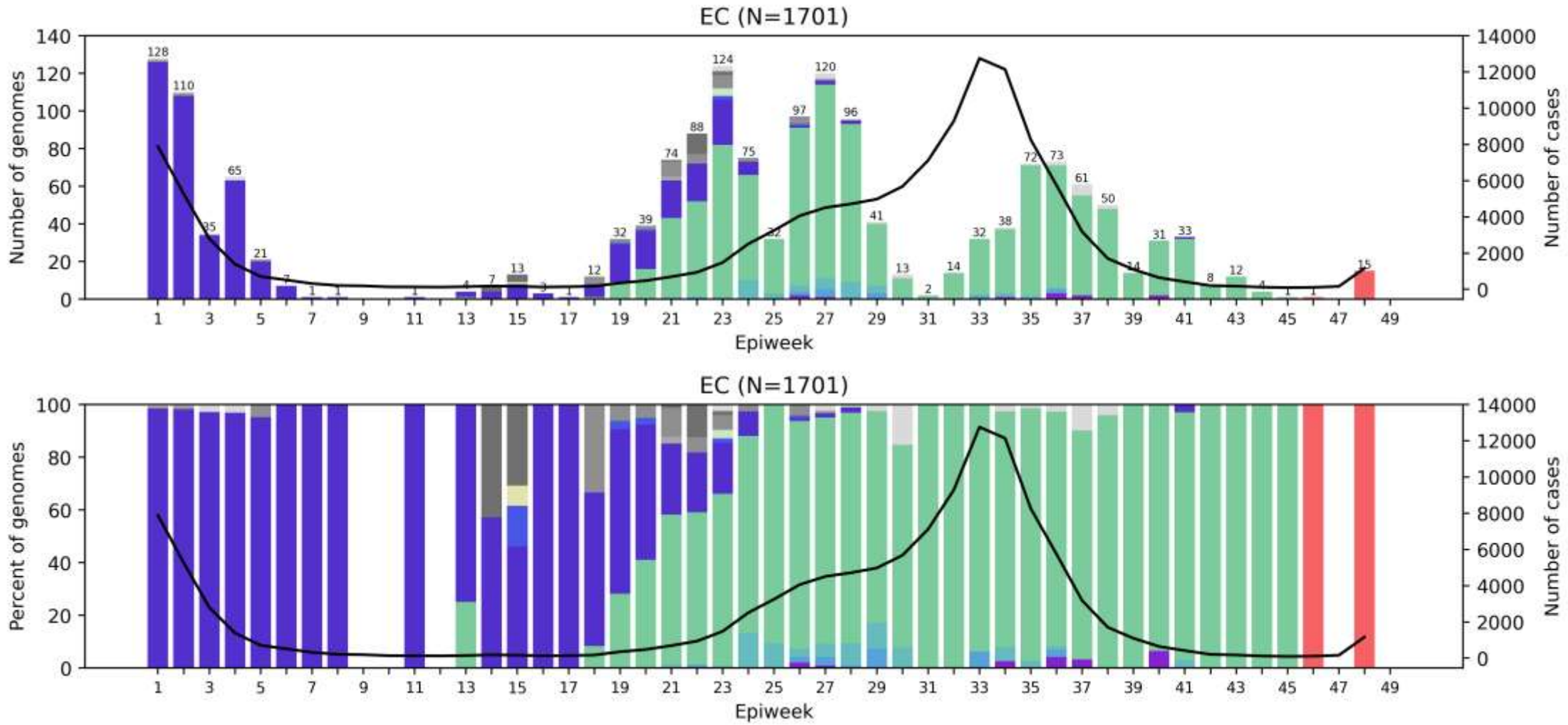
Eastern Cape Province, 2021, n =1701



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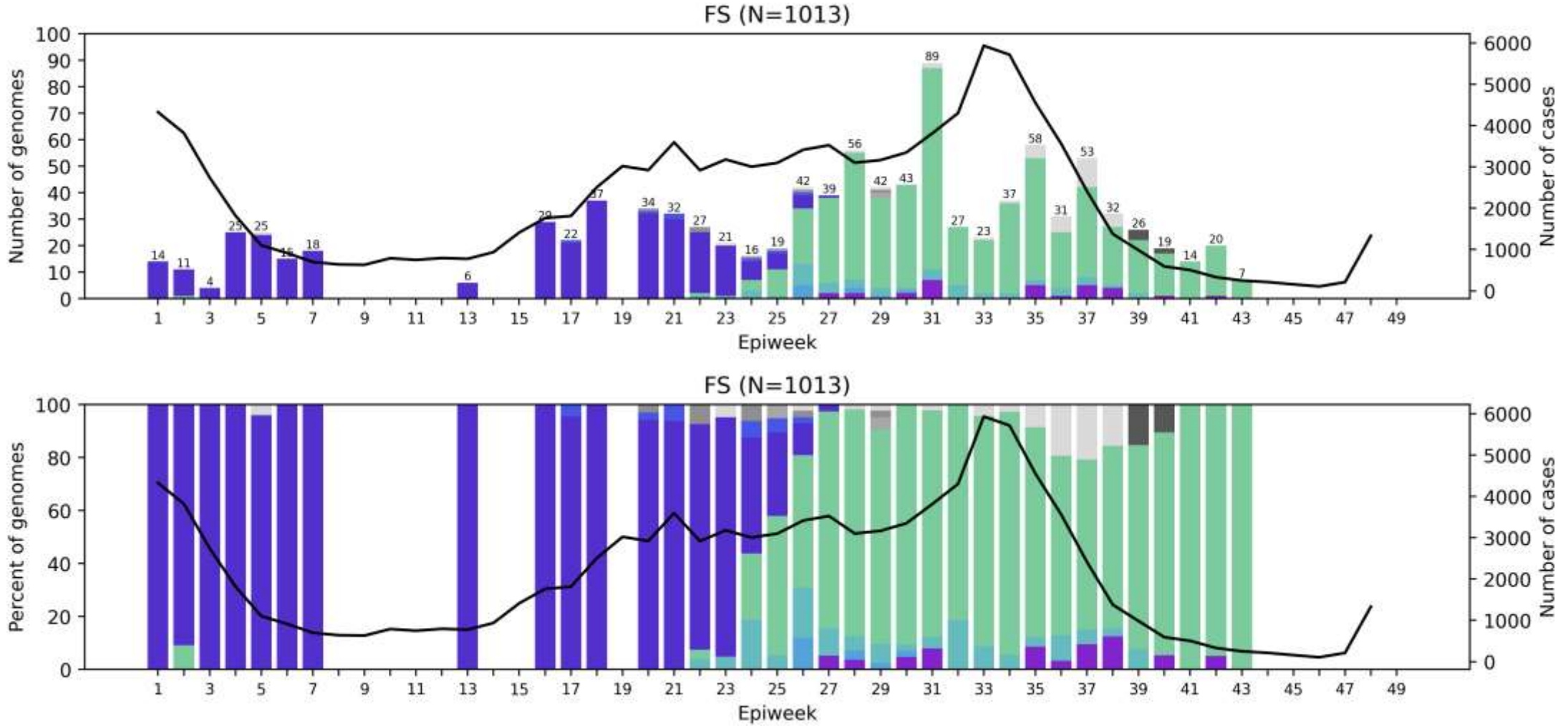
Free State Province, 2021, n = 1013



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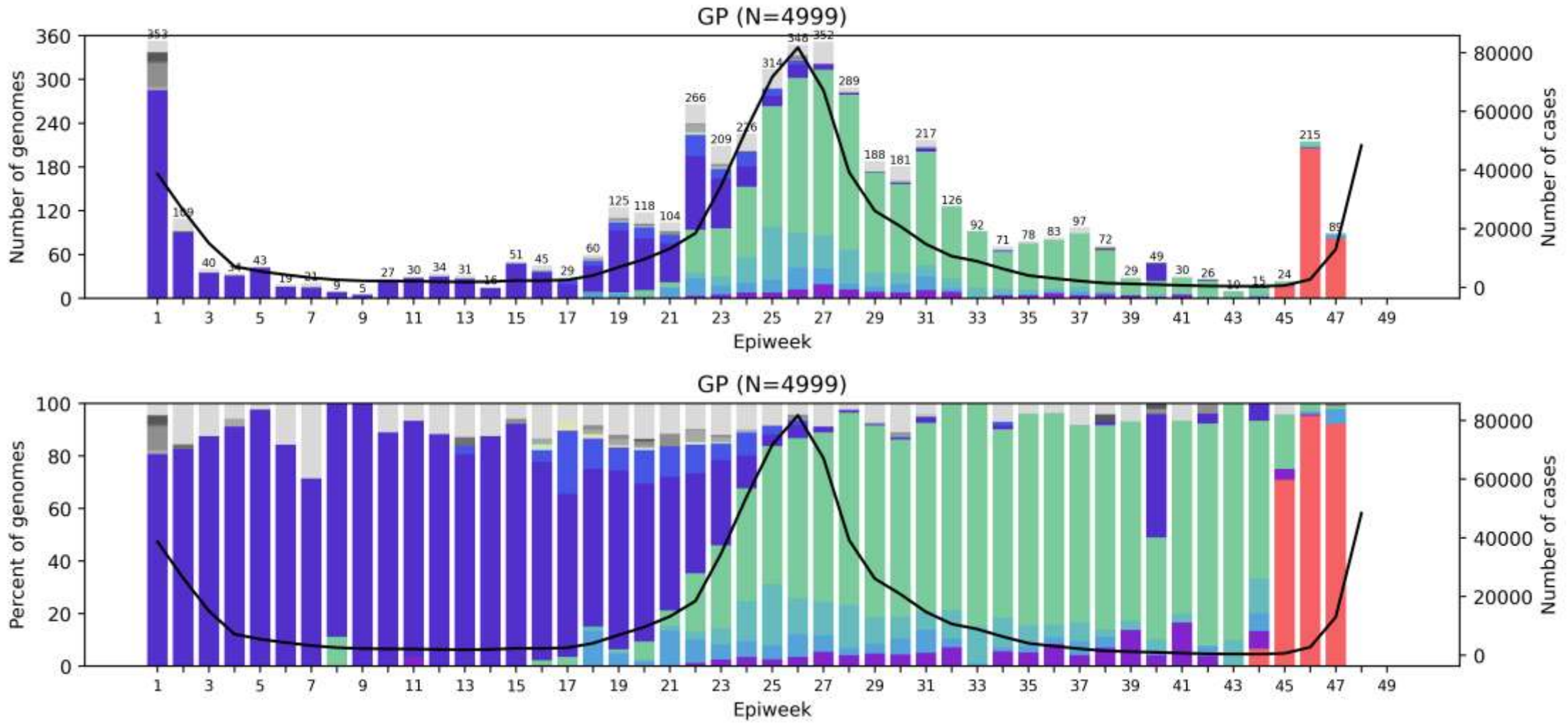
Gauteng Province, 2021, n = 4999



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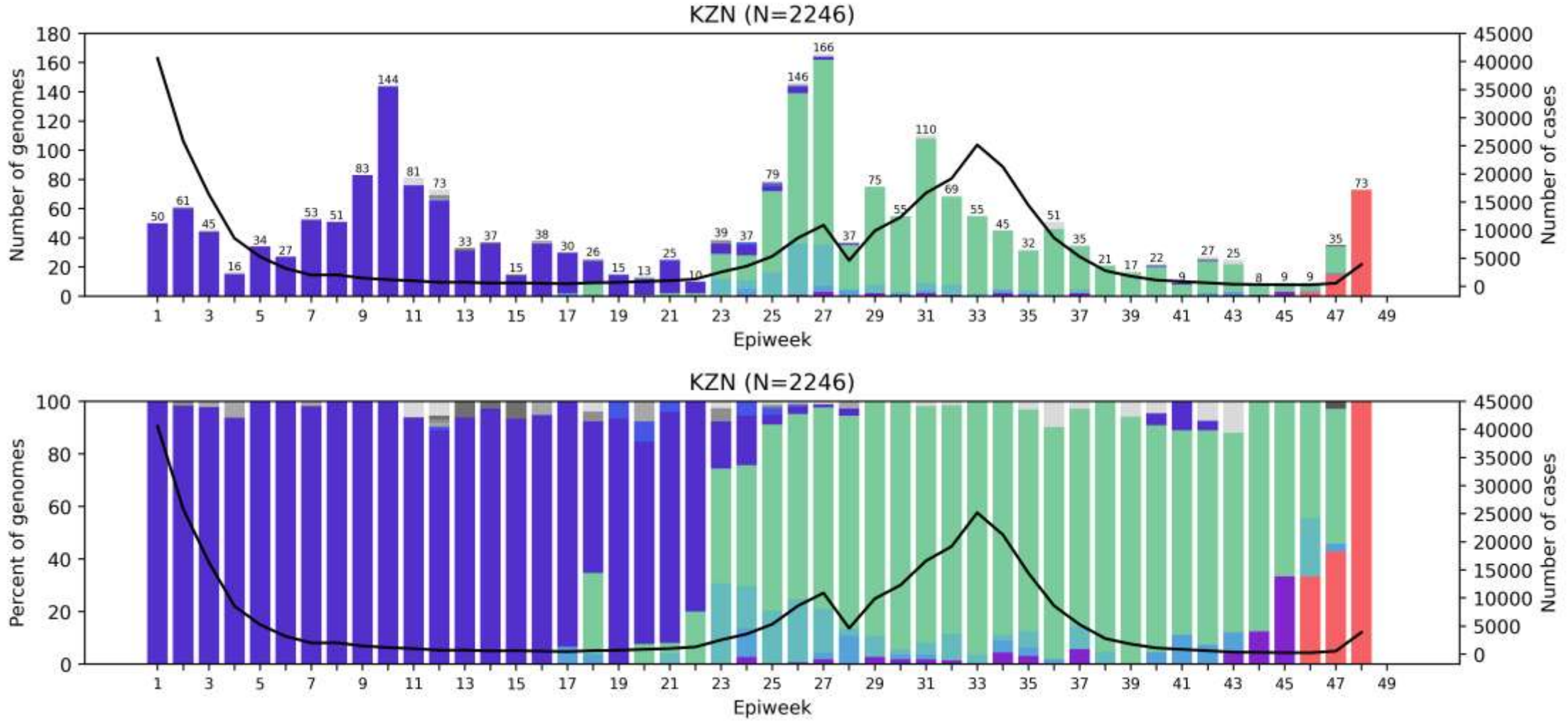
KwaZulu-Natal Province, 2021, n = 2246



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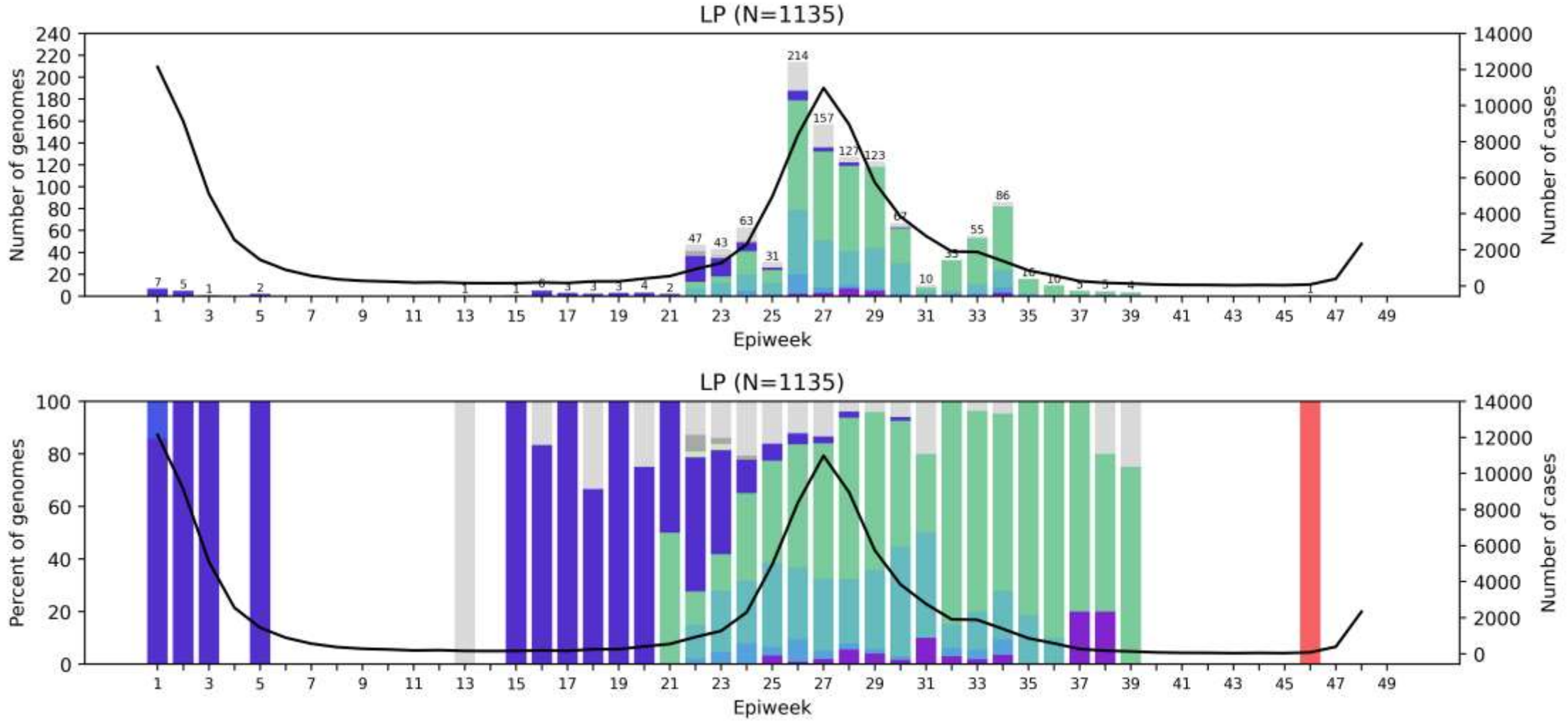
Limpopo Province, 2021, n = 1135



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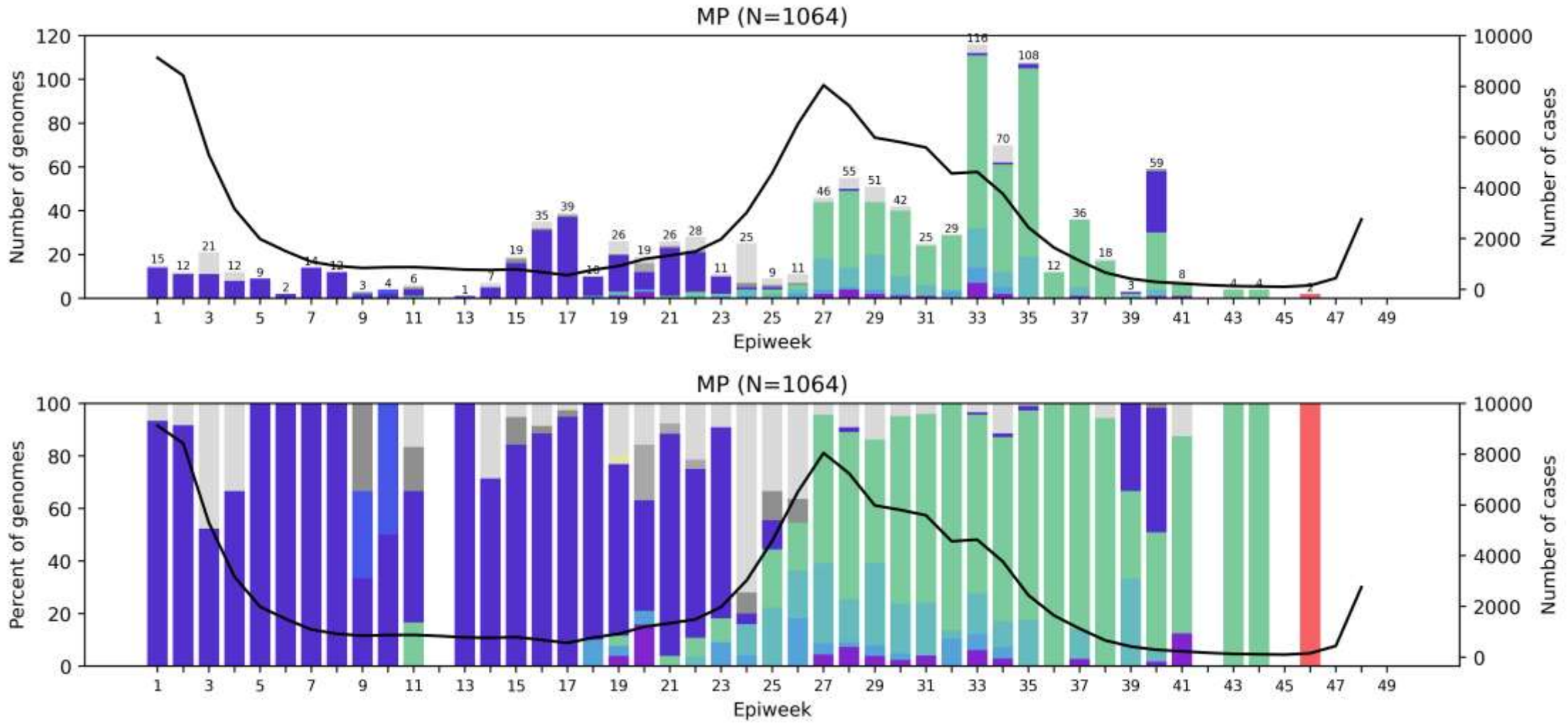
Mpumalanga Province, 2021, n = 1064



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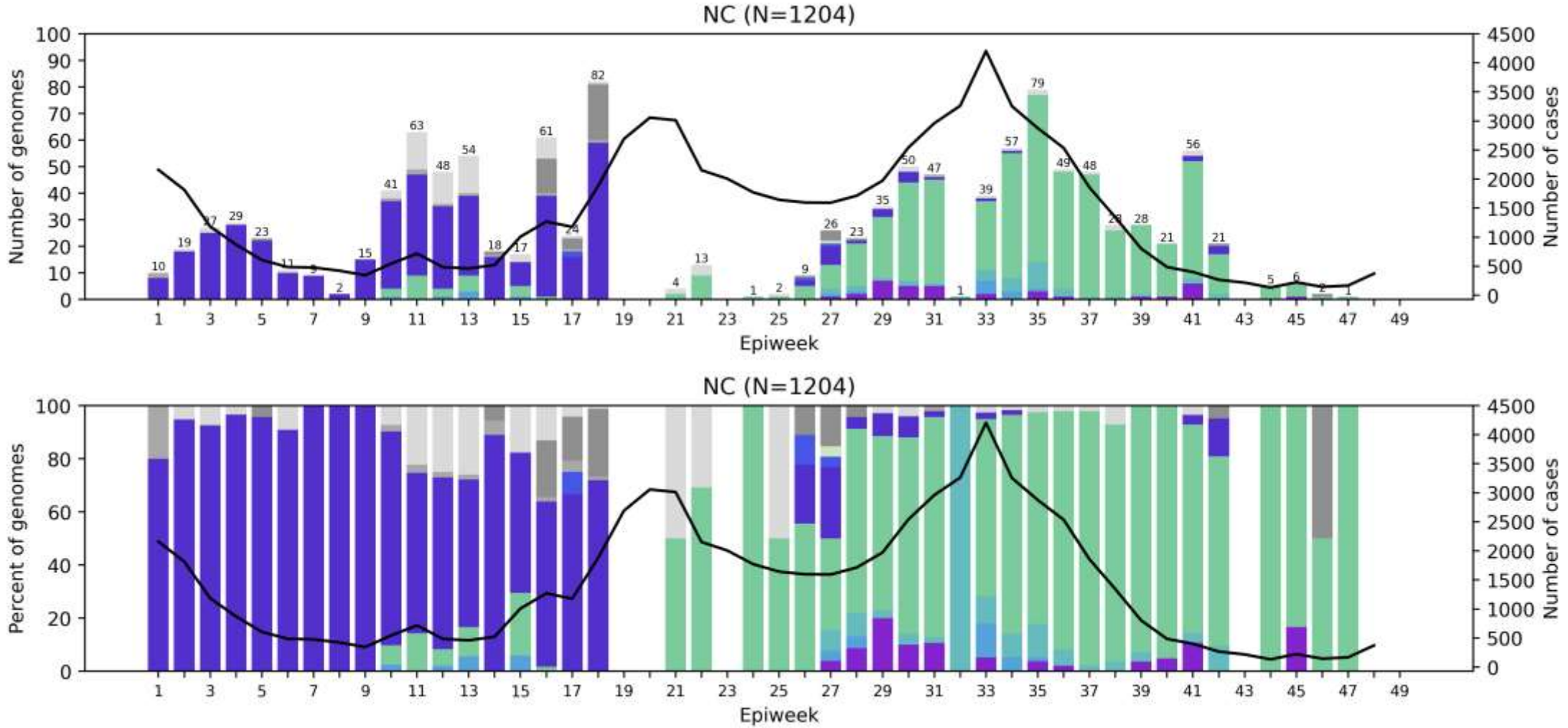
Northern Cape Province, 2021, n = 1204



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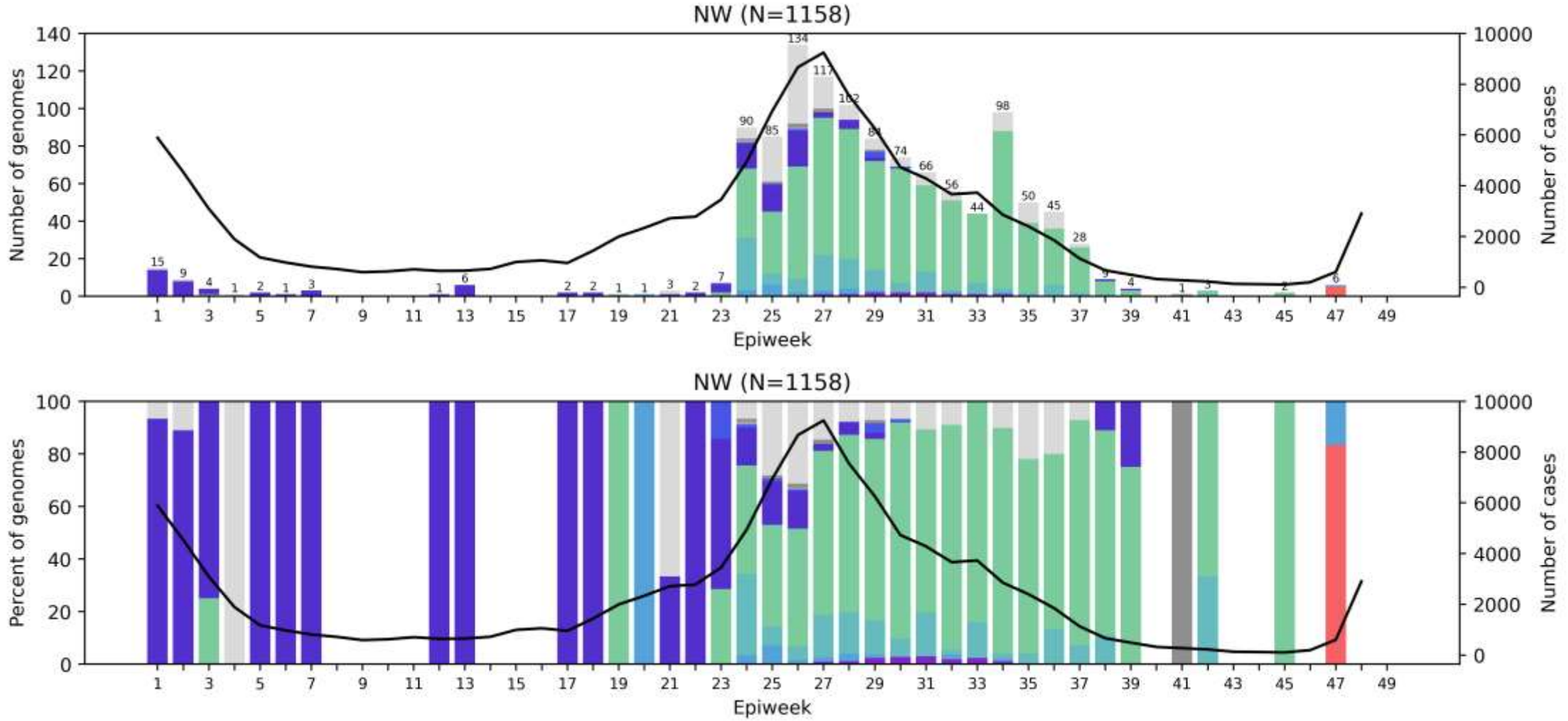
North West Province, 2021, n = 1158



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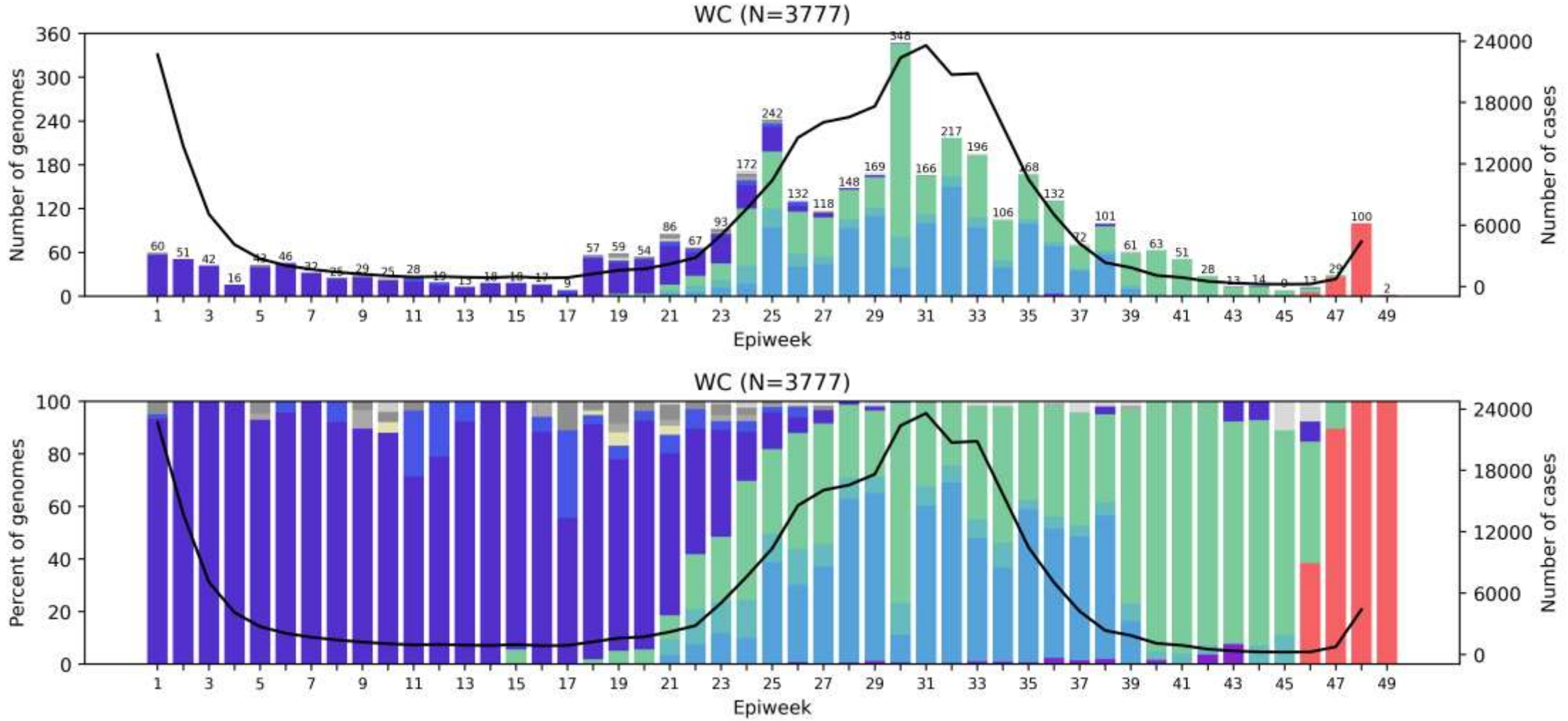
Western Cape Province, 2021, n =3777



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Summary

- New B.1.1.529 (21K) lineage has been designated Variant of Concern Omicron
  - Current earliest detection in South Africa: 8 November, Gauteng
  - Omicron dominates November sequencing data at 78% of genomes (n=493/630). Sequencing is ongoing to determine prevalence of Omicron in other provinces.
  - Omicron has now been detected in 56 countries worldwide
- Delta variant dominated in all provinces until end October
  - The Delta sub-lineages varied by province
- C.1.2 lineage detected in all provinces of South Africa with prevalence of <4% of genomes per month

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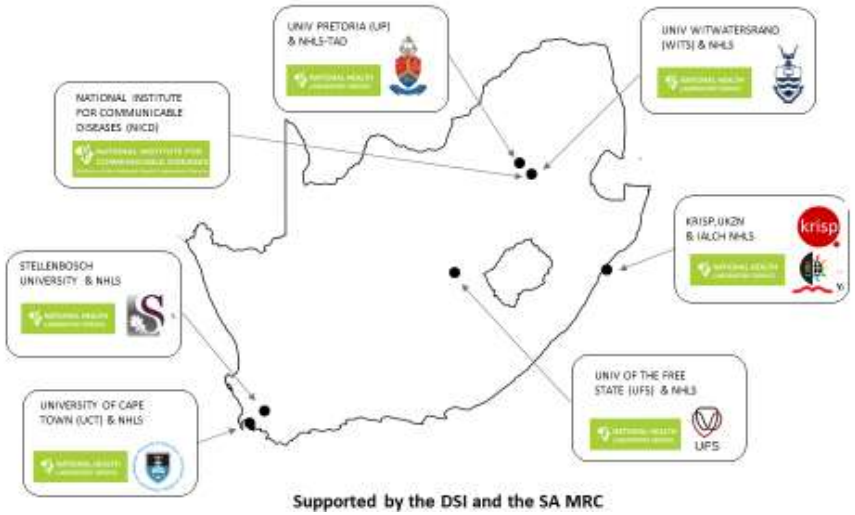

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Division of the National Health Laboratory Service

EDCTP

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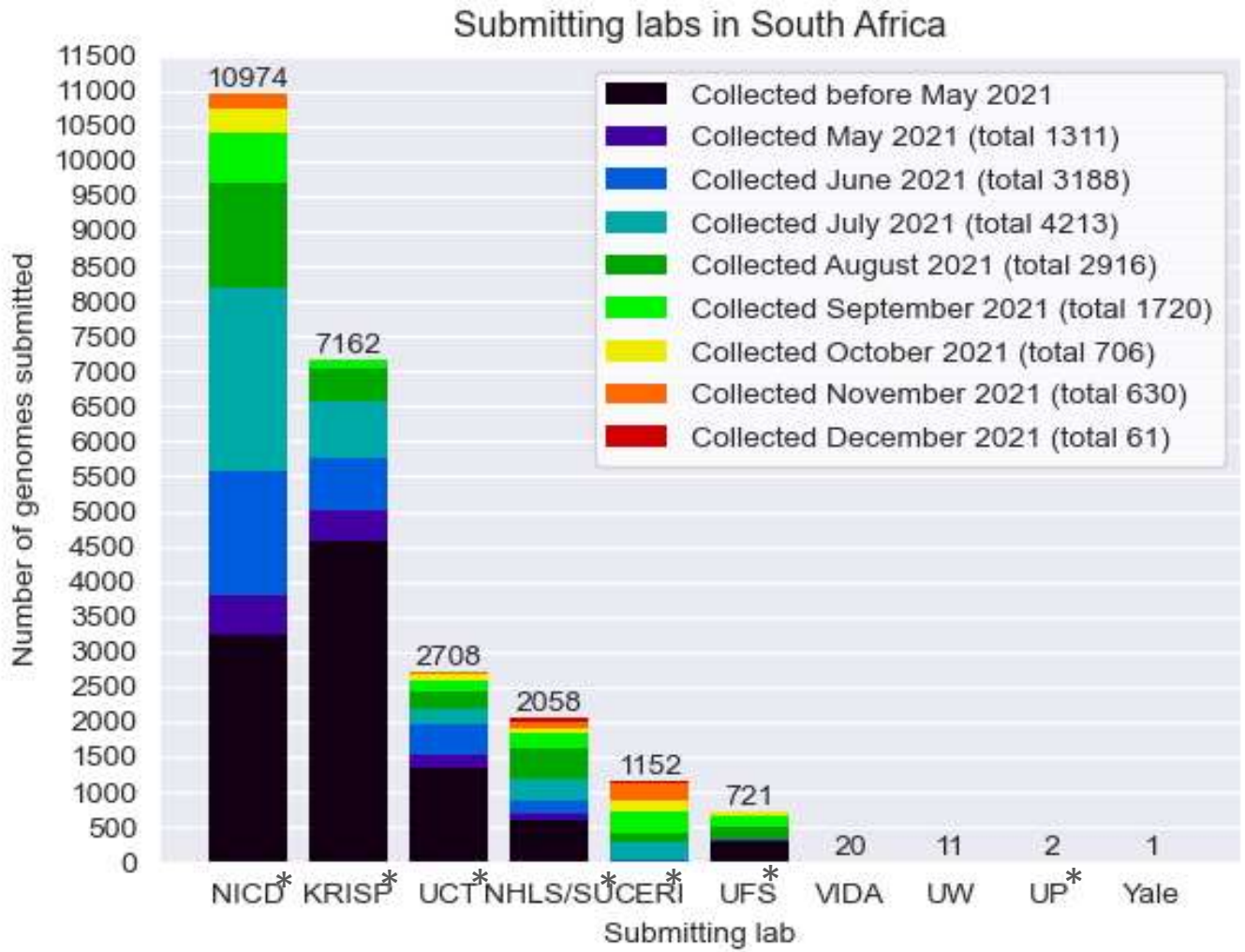
Funders:
GIZ/BMBF: African Network for Improved diagnostics and epidemiology of common and emerging infectious agents (ANDEMIA)
G7 Global Health fund, Robert Koch Institute, Dr Fabian Leendertz

South African genomes submitted per submitting lab, 2020 and 2021 (N=24 809)



NGS-SA Labs

CERI: Centre for Epidemic Response and Innovation
KRISP: KZN Research Innovation and Sequencing Platform
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

*NGS-SA laboratories

Multiple labs from NGS-SA and collaborating private laboratories are contributing to the sequencing effort.

NGS-SA
Network for Genomic Surveillance in South Africa

Variants of Concern (VOC)

WHO label	Pango lineages[+]	GISAID clade	Nextstrain clade	Additional amino acid changes monitored*	Earliest documented samples	Date of designation
Alpha	B.1.1.7[#]	GRY	20I (V1)	+S:484K +S:452R	United Kingdom, Sep-2020	18-Dec-2020
Beta	B.1.351	GH/501Y.V2	20H (V2)	+S:L18F	South Africa, May-2020	18-Dec-2020
Gamma	P.1	GR/501Y.V3	20J (V3)	+S:681H	Brazil, Nov-2020	11-Jan-2021
Delta	B.1.617.2[§]	G/478K.V1	21A	+S:417N	India, Oct-2020	VOI: 4-Apr-2021 VOC: 11-May-2021
Omicron*	B.1.1.529	GR/484A	21K	-	Multiple countries, Nov-2021	VUM: 24-Nov-2021 VOC: 26-Nov-2021

https://www.who.int/en/activities/tracking-SARS-CoV-2-variants/ accessed 10 December 2021

*Notable spike (S) amino acid changes under monitoring, which are currently reported in a minority of sequenced samples

[+]Includes all descendant lineages.

[#]Includes all Q.* lineages in the PANGO nomenclature system.

[§]Includes all AY.* lineages in the PANGO nomenclature system.

Currently designated Variants of Interest (VOI)

WHO label	Pango* lineages	GISAID clade	Nextstrain clade	Earliest documented samples	Date of designation
Lambda	C.37	GR/452Q.V1	21G	Peru, Dec-2020	14-Jun-2021
Mu	B.1.631	GH	21H	Colombia, Jan-2021	30-Aug-2021

https://www.who.int/en/activities/tracking-SARS-CoV-2-variants/ accessed 10 December 2021

*Includes all descendant lineages.

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.)