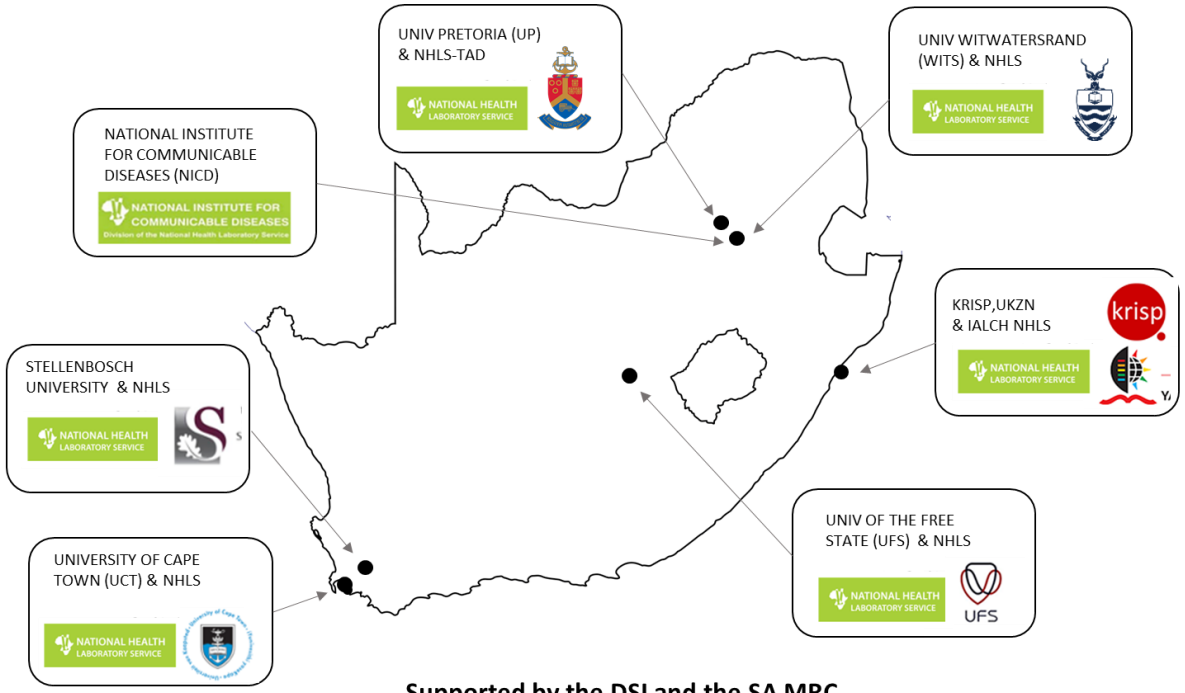
Network for Genomic Surveillance in South Africa (NGS-SA)

SARS-CoV-2 Sequencing Update
7 January 2022



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 7 January at 16h27

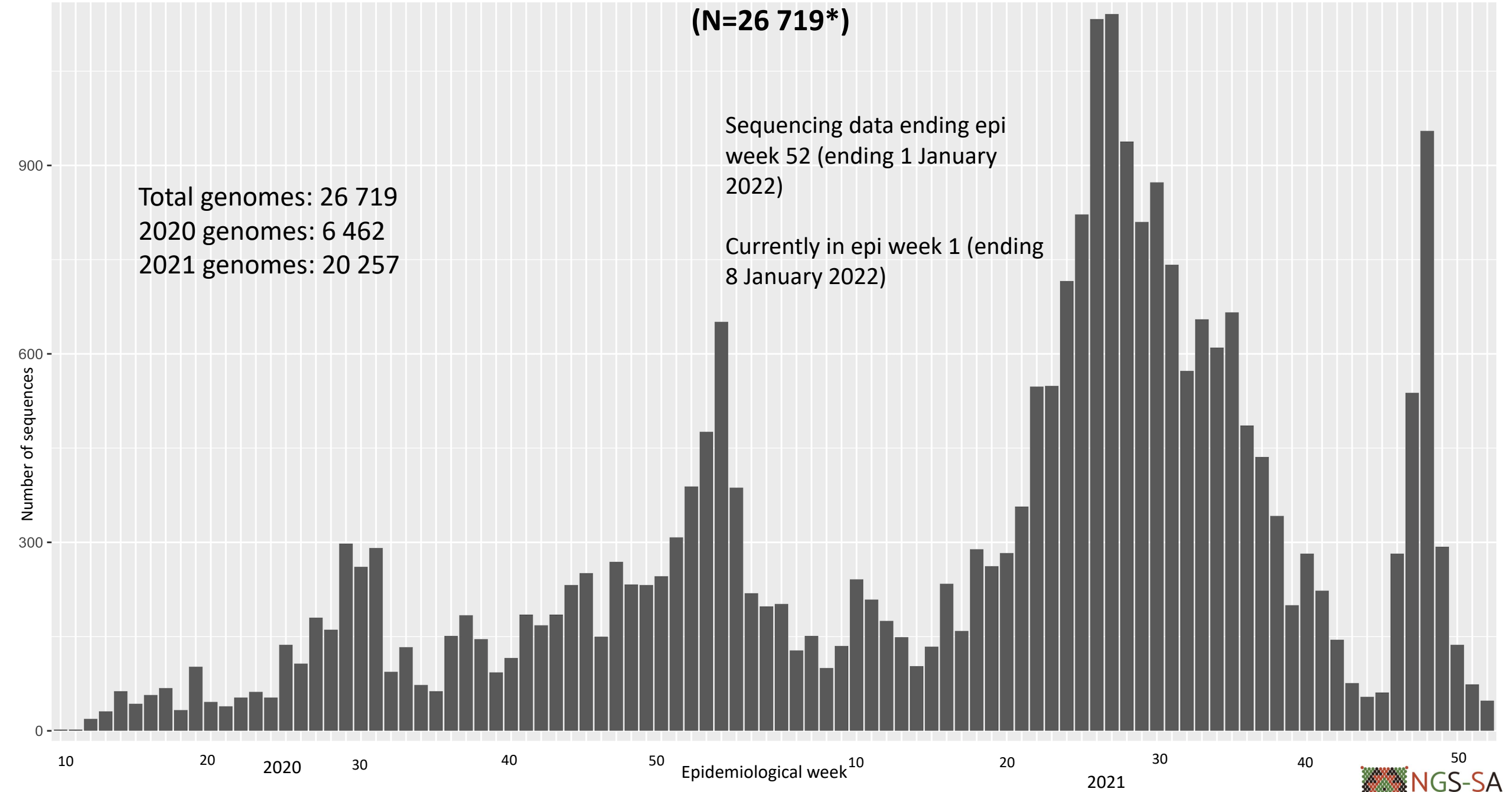
Data license: https://www.gisaid.org/registration/terms-of-use/

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 – 2022 (N=26 719*)



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

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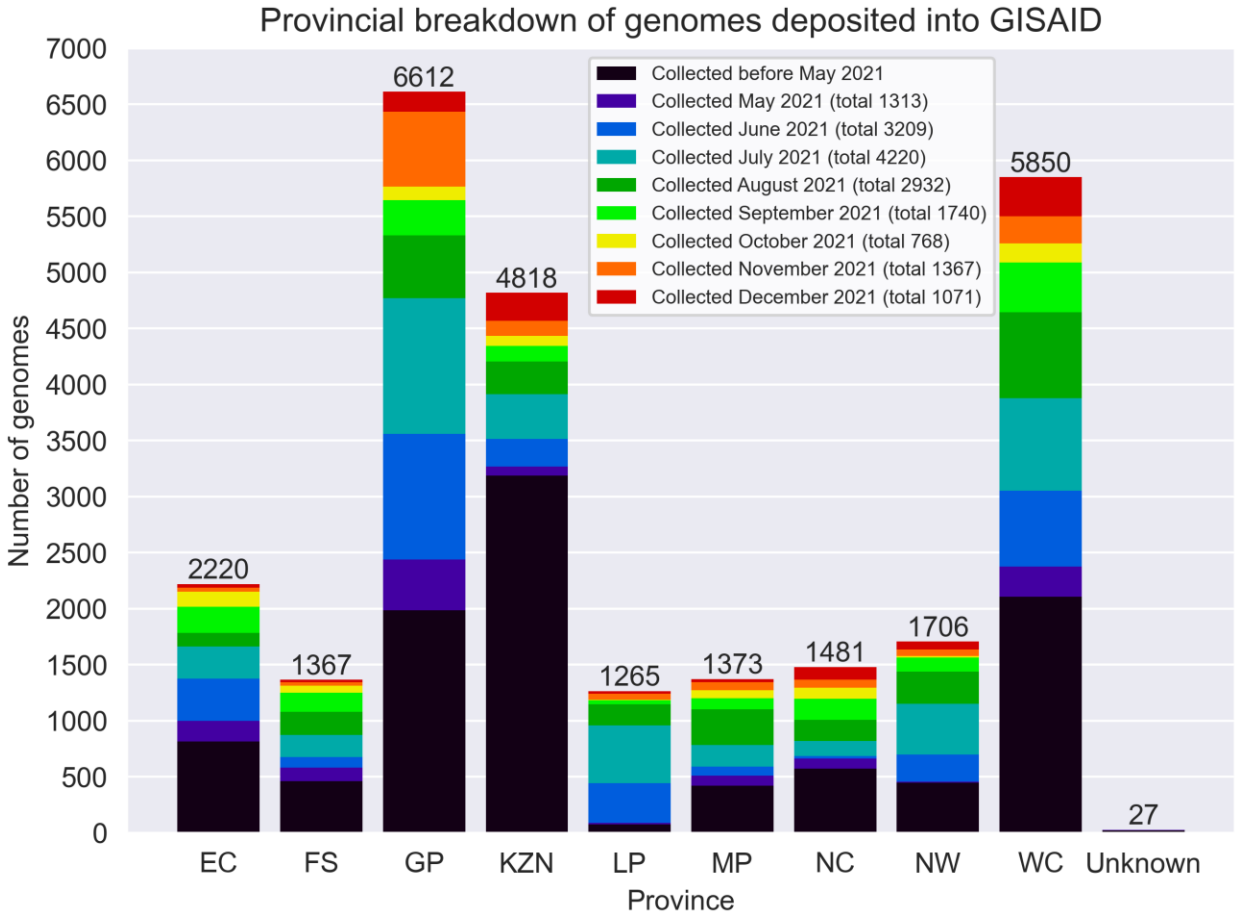
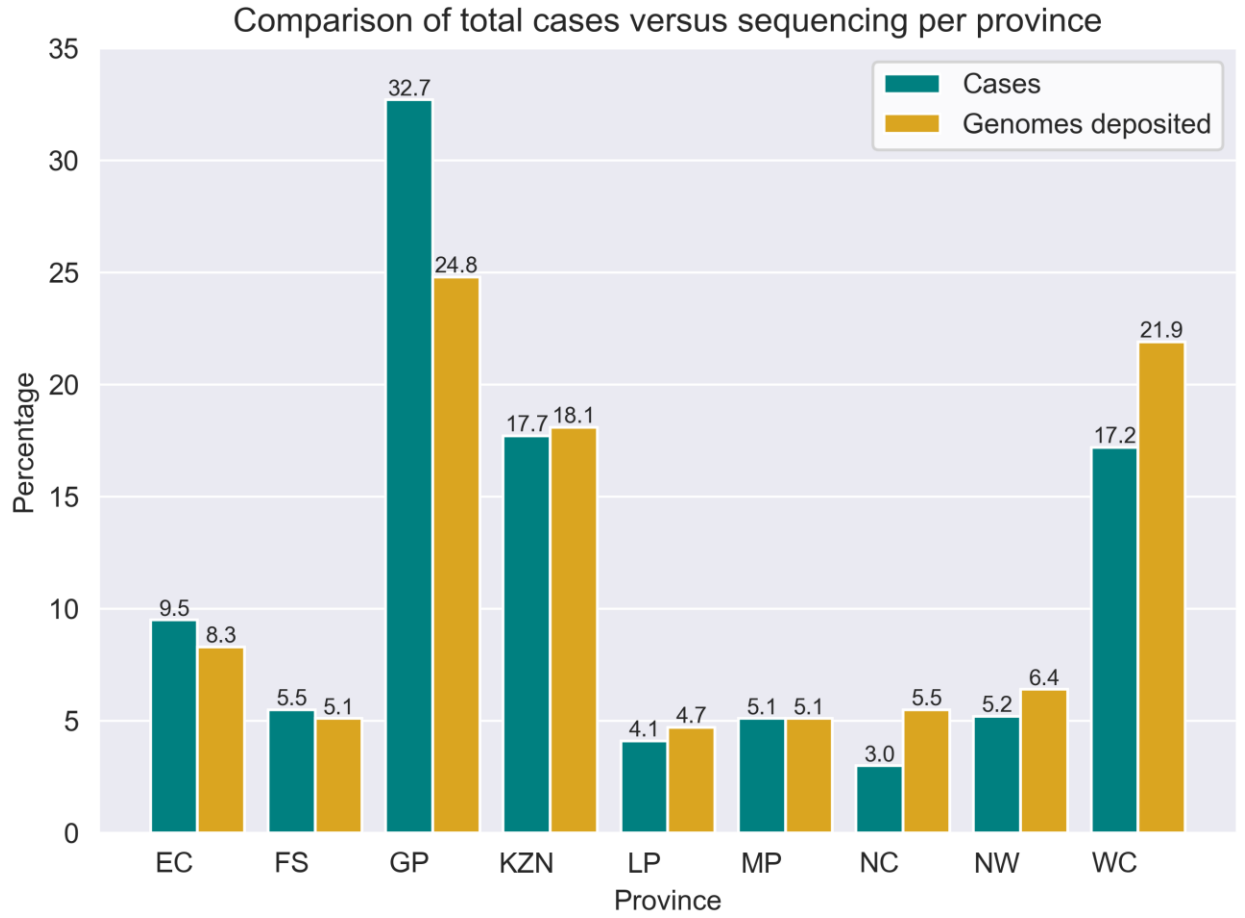
GISAID genomes vs total cases, 2020 and 2021 (N=26 719)





All provinces, apart from GP, NC and WC, have comparable percentages of overall cases and overall sequenced genomes.

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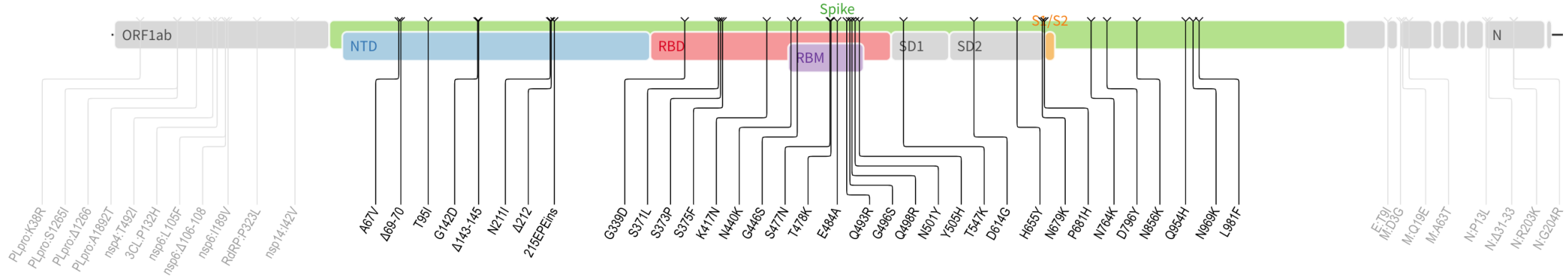
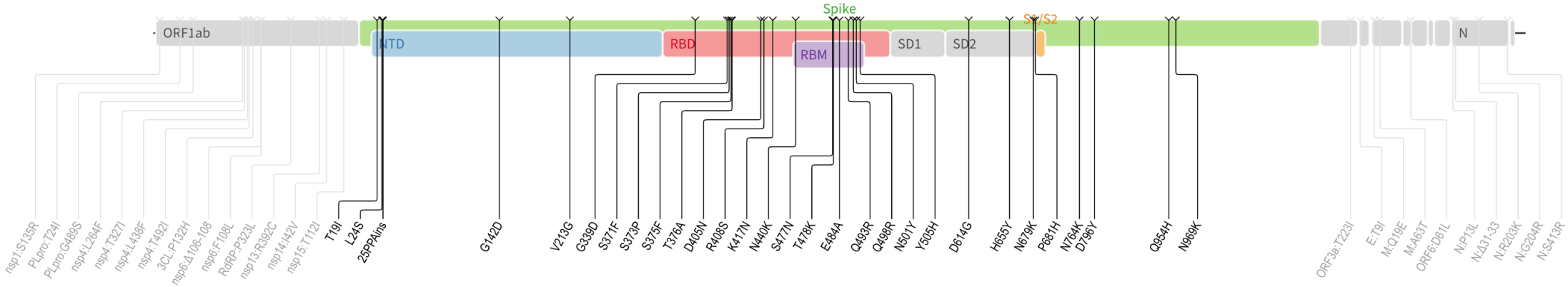
Omicron sub-lineage spike mutation profiles

BA.1
21K

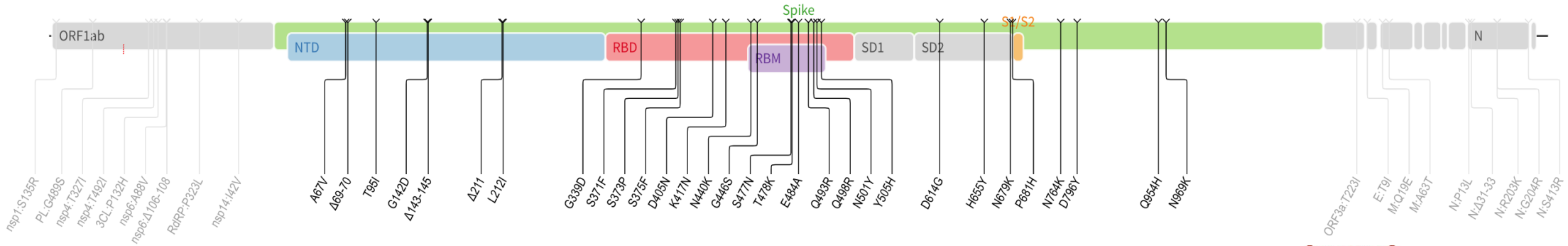


BA.2
21L

Lacks 69-70del
Not detectable by
S-Gene Target
Failure



BA.3
21M



Lineage definitions based on https://github.com/cov-lineages/pango-designation/issues/367
Images from https://covdb.stanford.edu/page/mutation-viewer/

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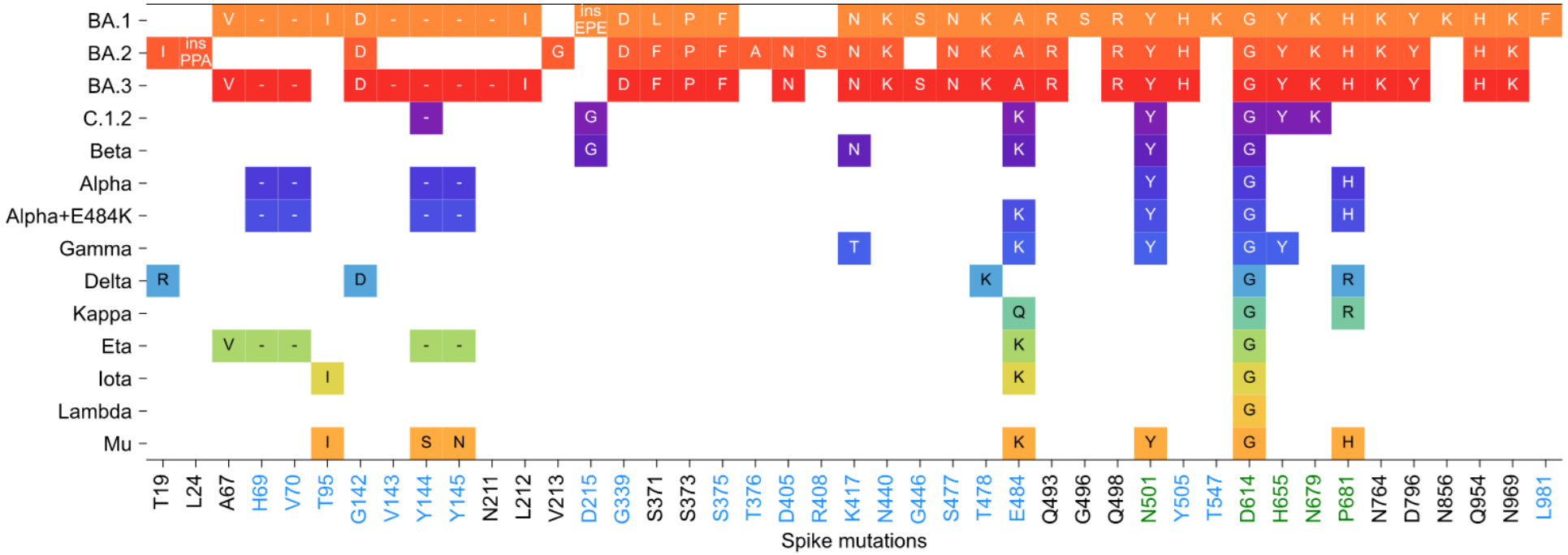
Omicron spike mutations compared to other VOC/VOIs



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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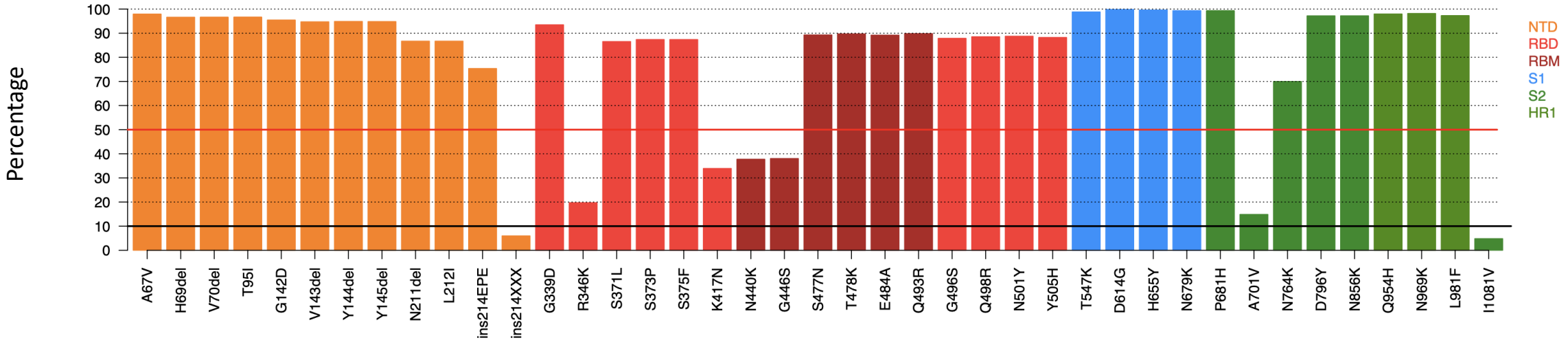
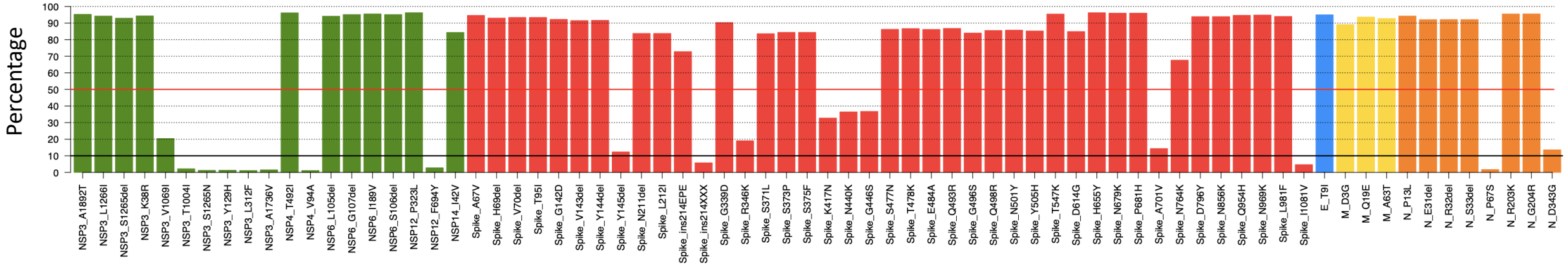
Mutational profile of Omicron sequences

Frequency of Spike SNVs for Omicron (n = 187 801)



Frequency of whole genome SNVs for Omicron (n = 194 413)



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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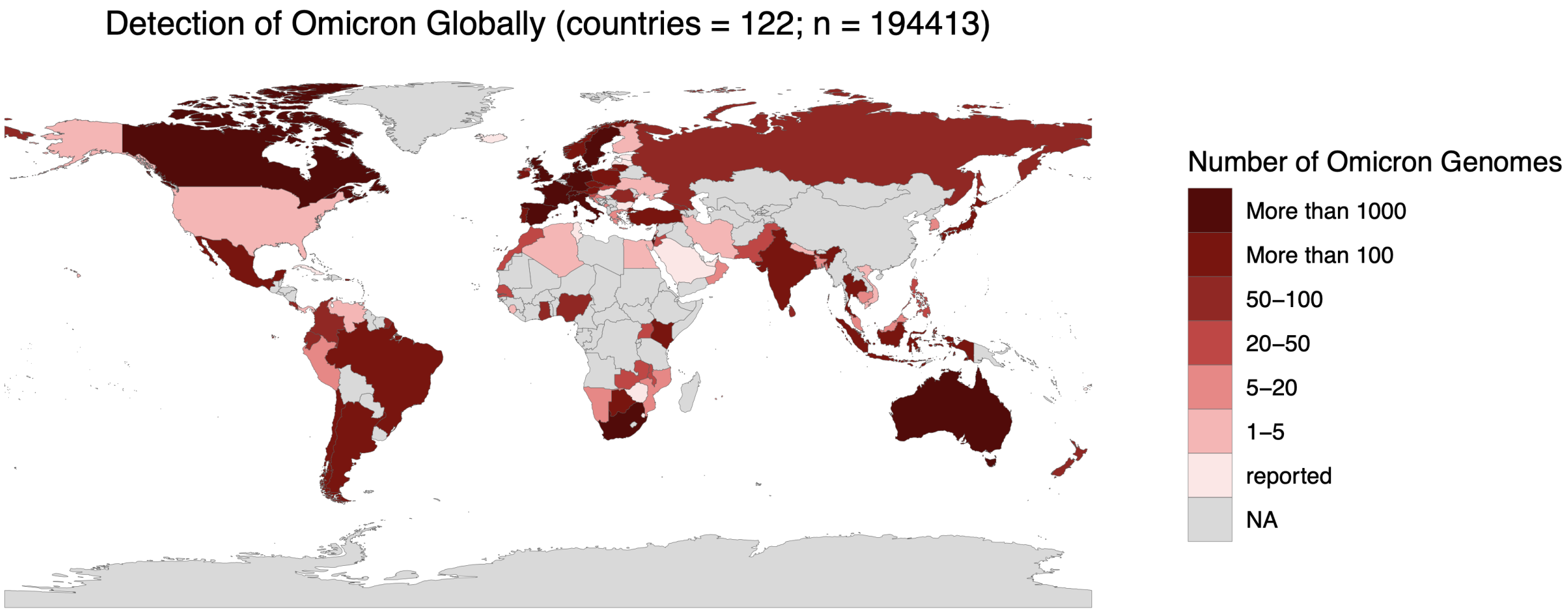
Omicron global prevalence



Omicron has been detected in 122 countries across the globe (detections based on GISAID).

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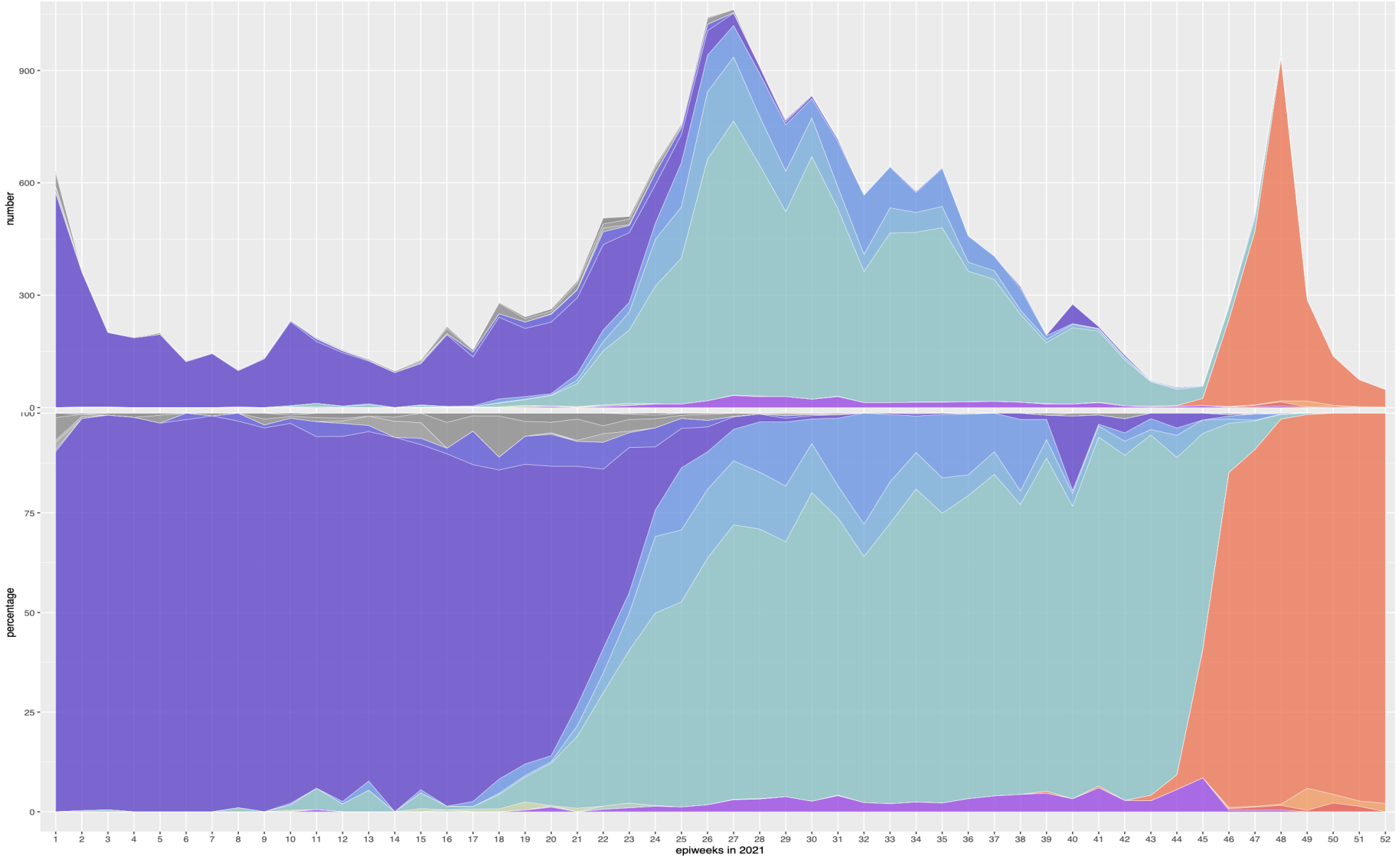
Proportion and number of clades by epiweek in South Africa, 2021 (N=20 257)



Sequencing data ending epi week 52 (ending 1 January 2022)

Currently in epi week 1 (ending 8 January 2022)

Delta dominated in South Africa until October at >80%. Omicron dominated November and early December at >95%.

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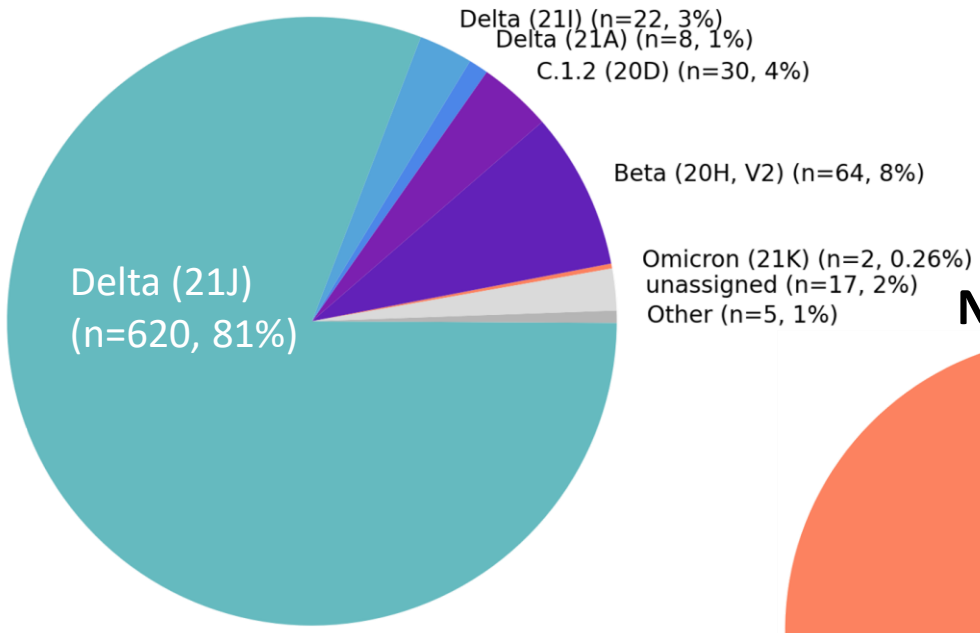
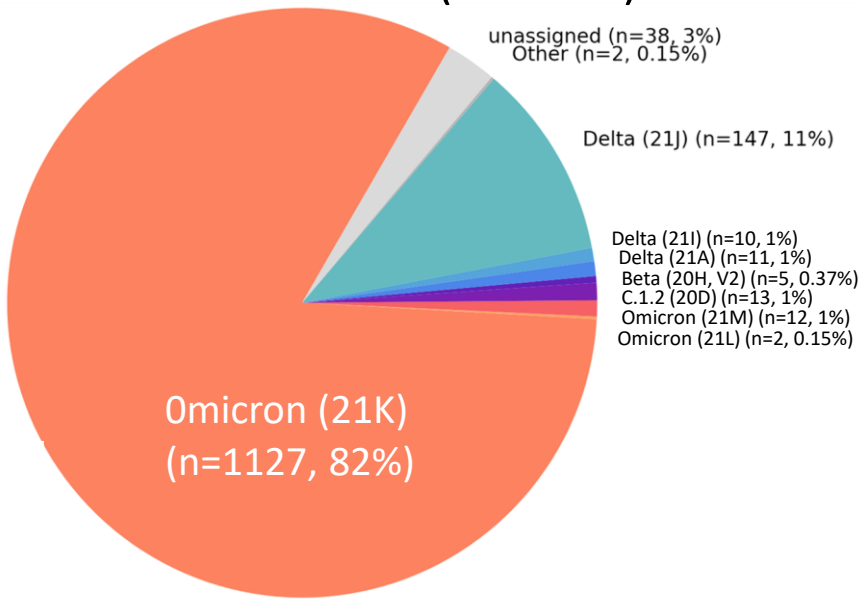
Prevalence of Variants of Concern (VOC) and Variants of Interest (VOI) in October – December 2021

October (N=768)



Total Delta in Oct: 650 (84.6%)

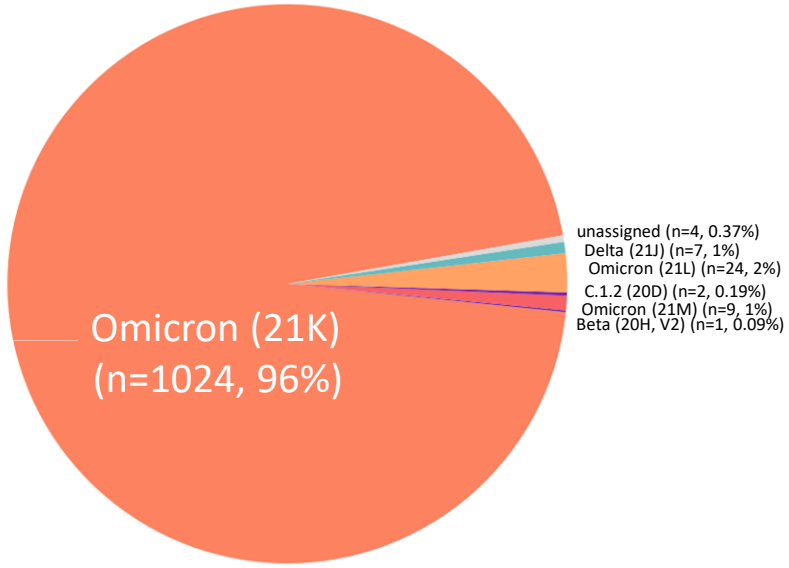
November (N=1367)



Total Delta in Nov: 168 (12.3%)

Total Omicron in Nov: 1141 (83.5%)

December (N=1071)



Total Omicron in Dec: 1057 (98.7%)

The Delta variant dominated at >80% in October in South Africa, while Omicron was detected at 0.3% (2/768)
Omicron dominated in November, at 84% (1141/1367) and continues to dominate in December (99%, 1057/1071)

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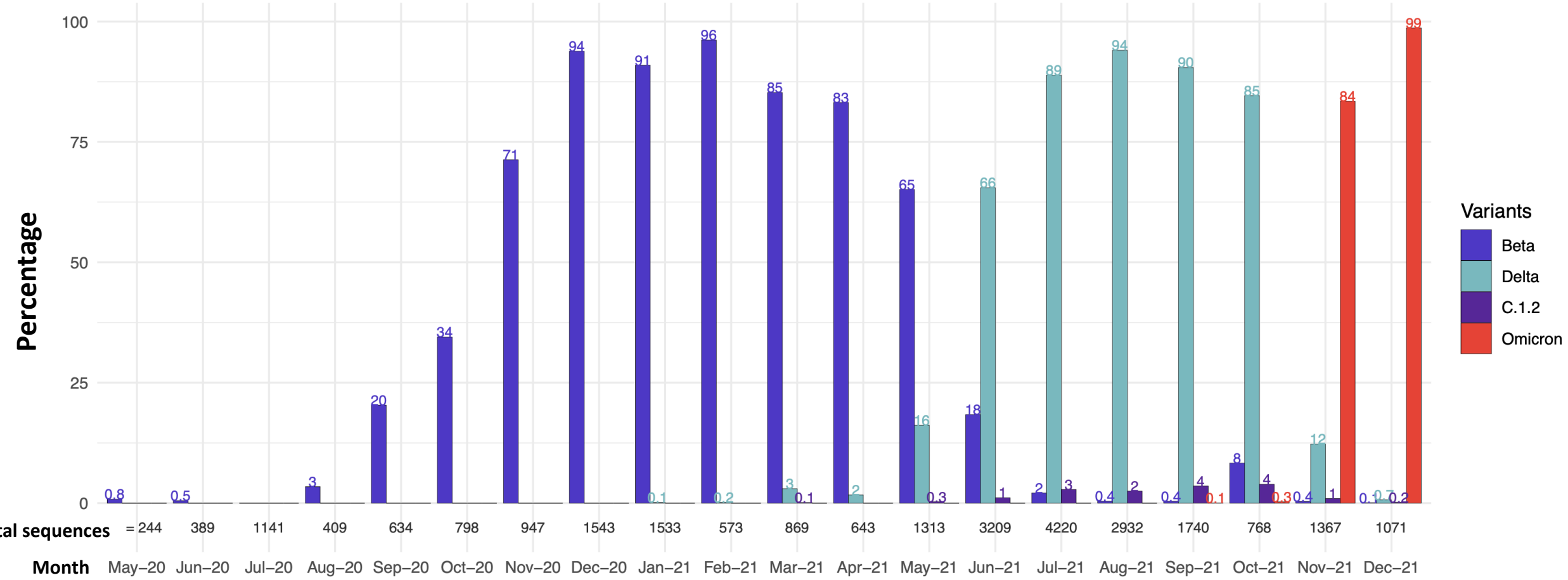
Detection Rates: Beta, Delta, C.1.2 and Omicron

Detection rates of variants being monitored in South Africa



C.1.2 has been detected at ≤ 4% of sequences monthly since May 2021.
Beta prevalence increased slightly in October but has since remained at low levels in November and December.
Omicron has been dominant since November (>80% in November, >98% in December).

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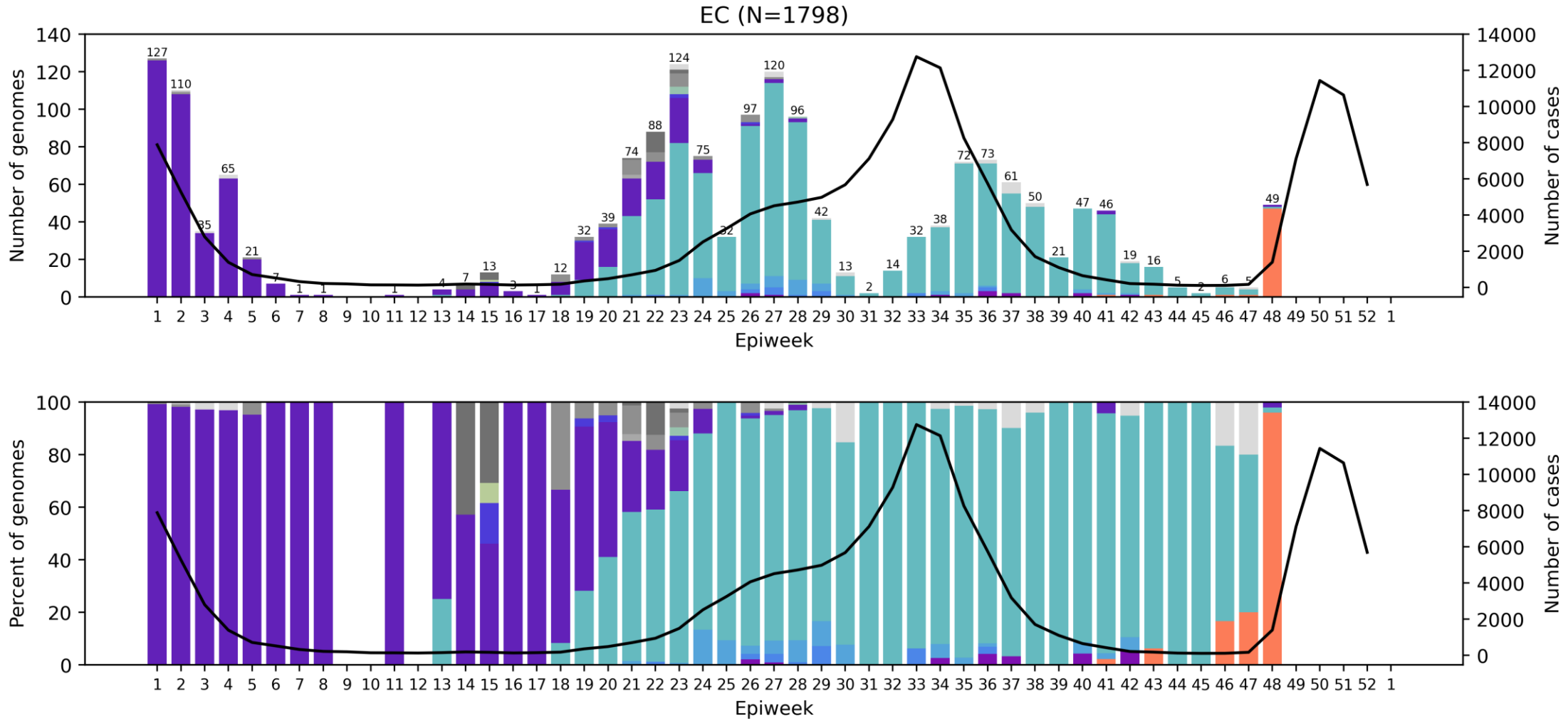
Eastern Cape Province, 2021-2022, n =1798



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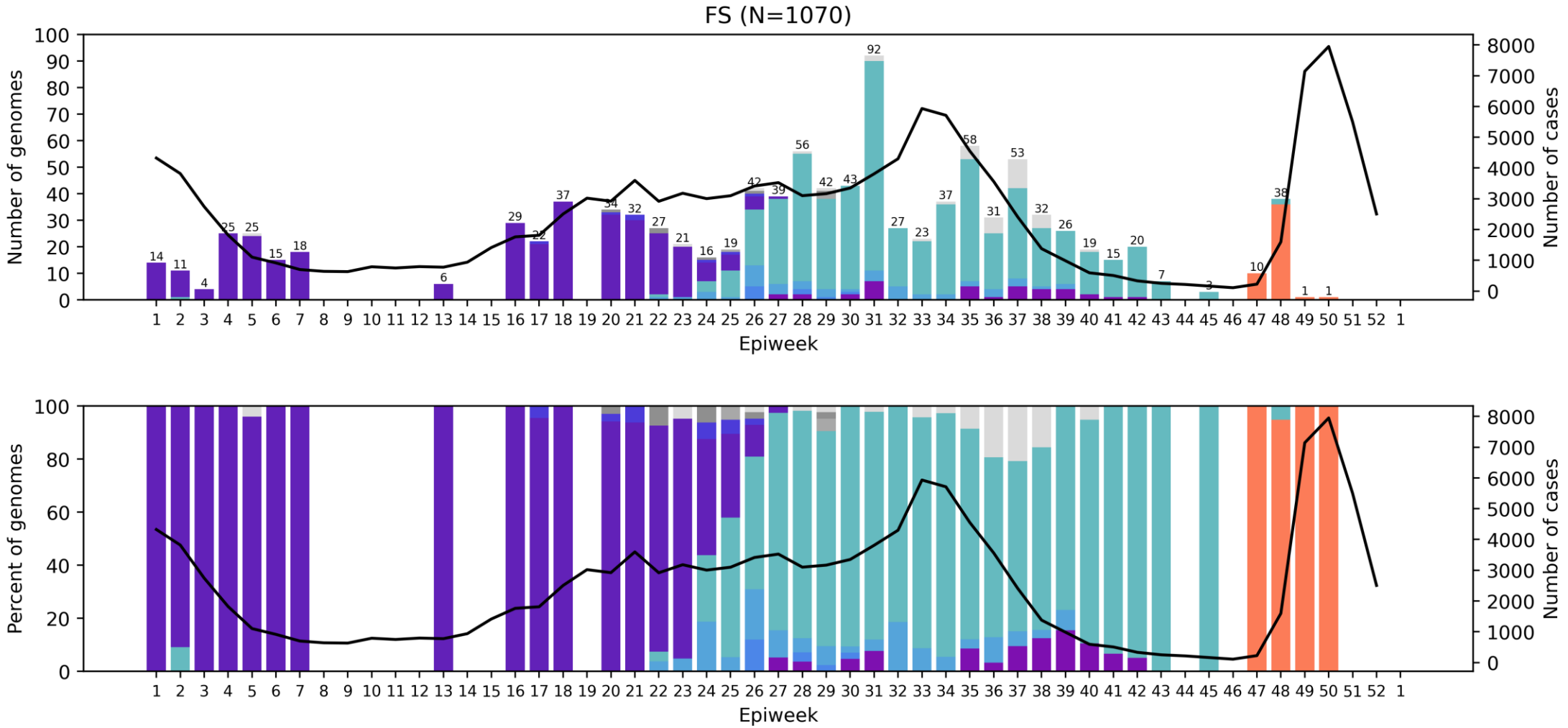
Free State Province, 2021-2022, n = 1070



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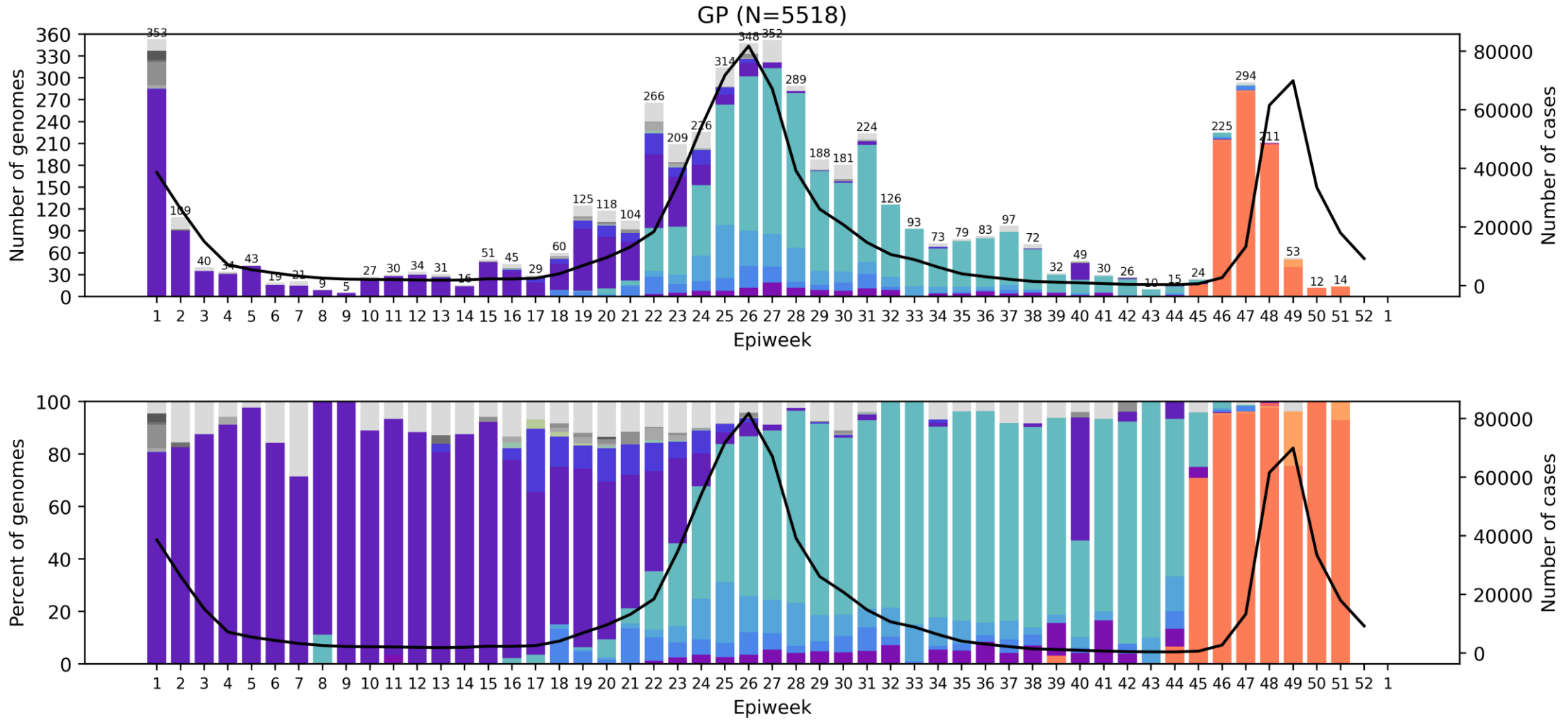
Gauteng Province, 2021-2022, n = 5518



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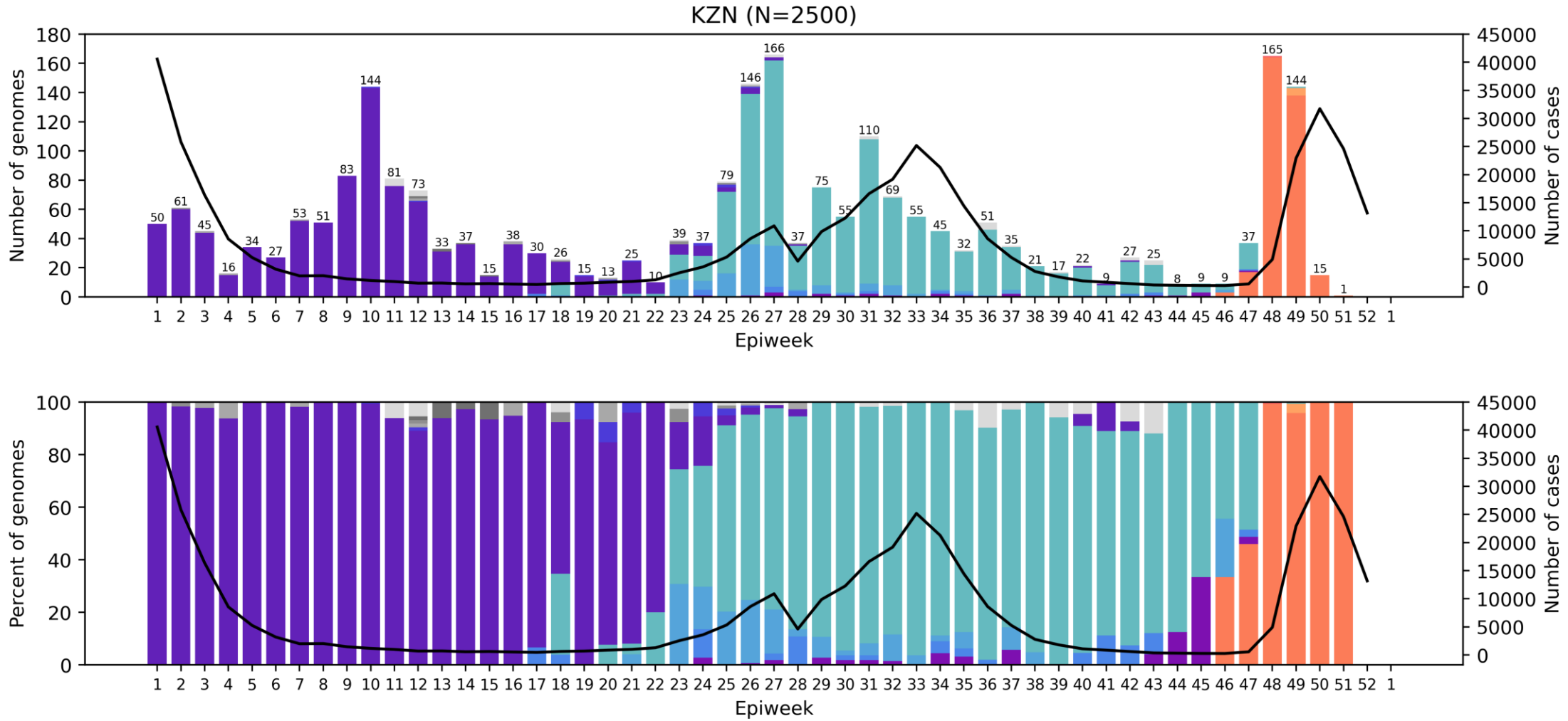
KwaZulu-Natal Province, 2021-2022, n = 2500



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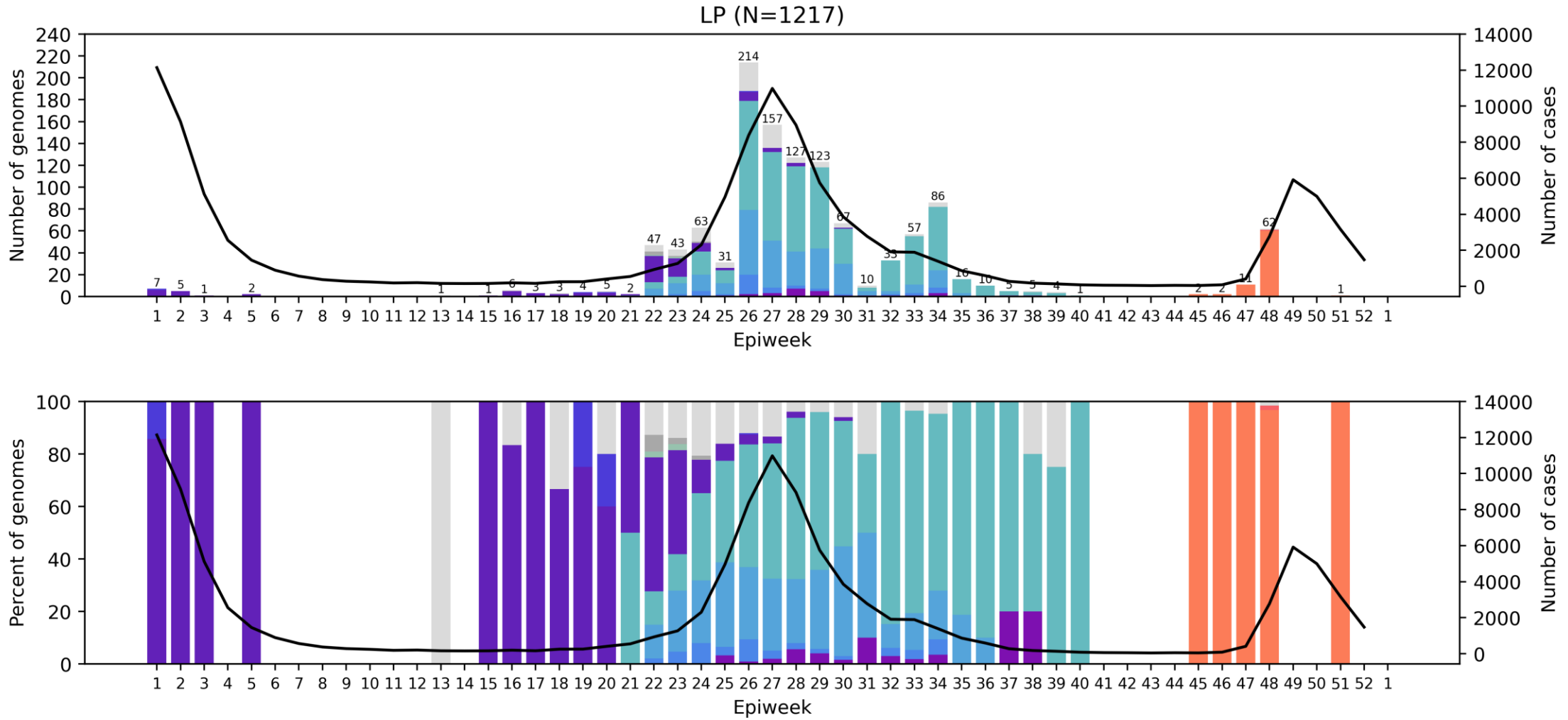
Limpopo Province, 2021-2022, n = 1217



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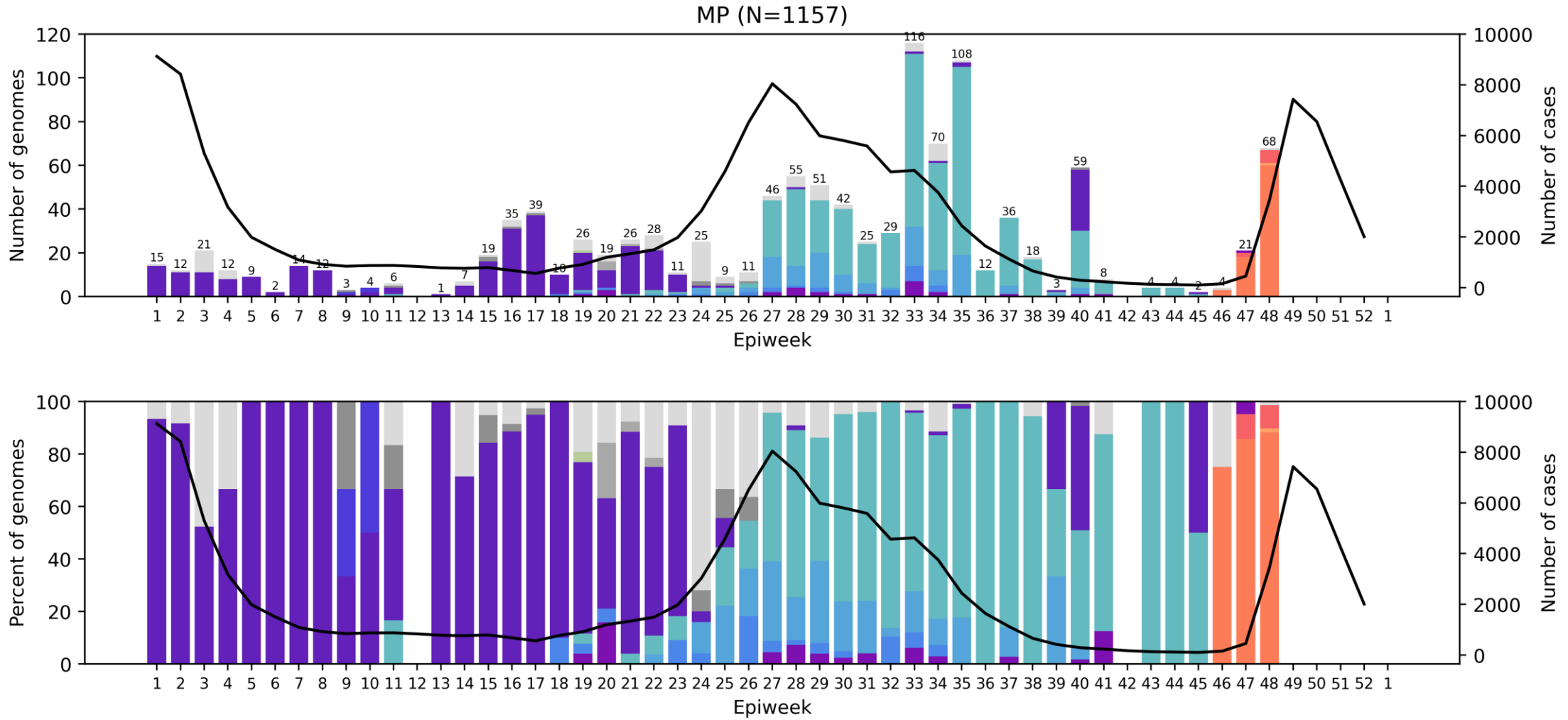
Mpumalanga Province, 2021-2022, n = 1157



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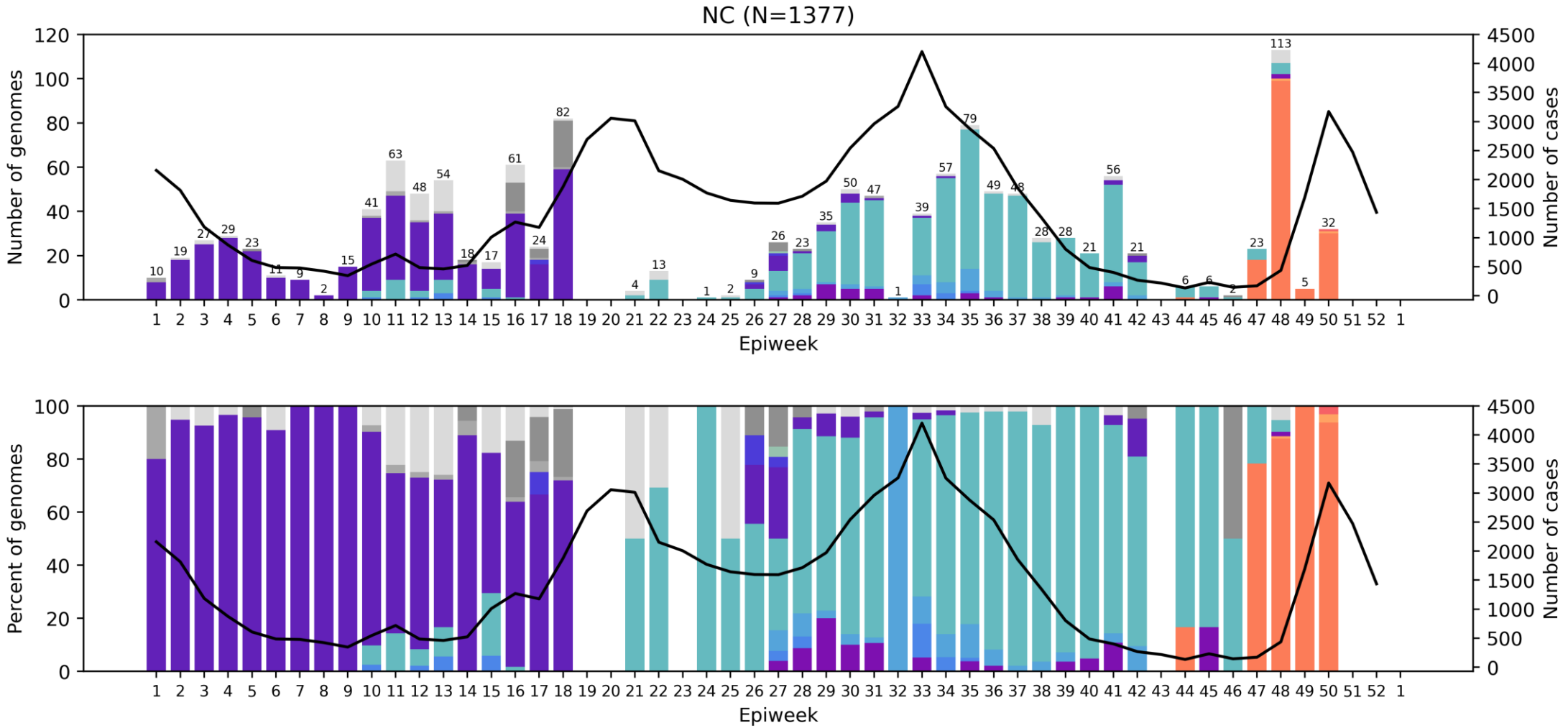
Northern Cape Province, 2021-2022, n = 1377



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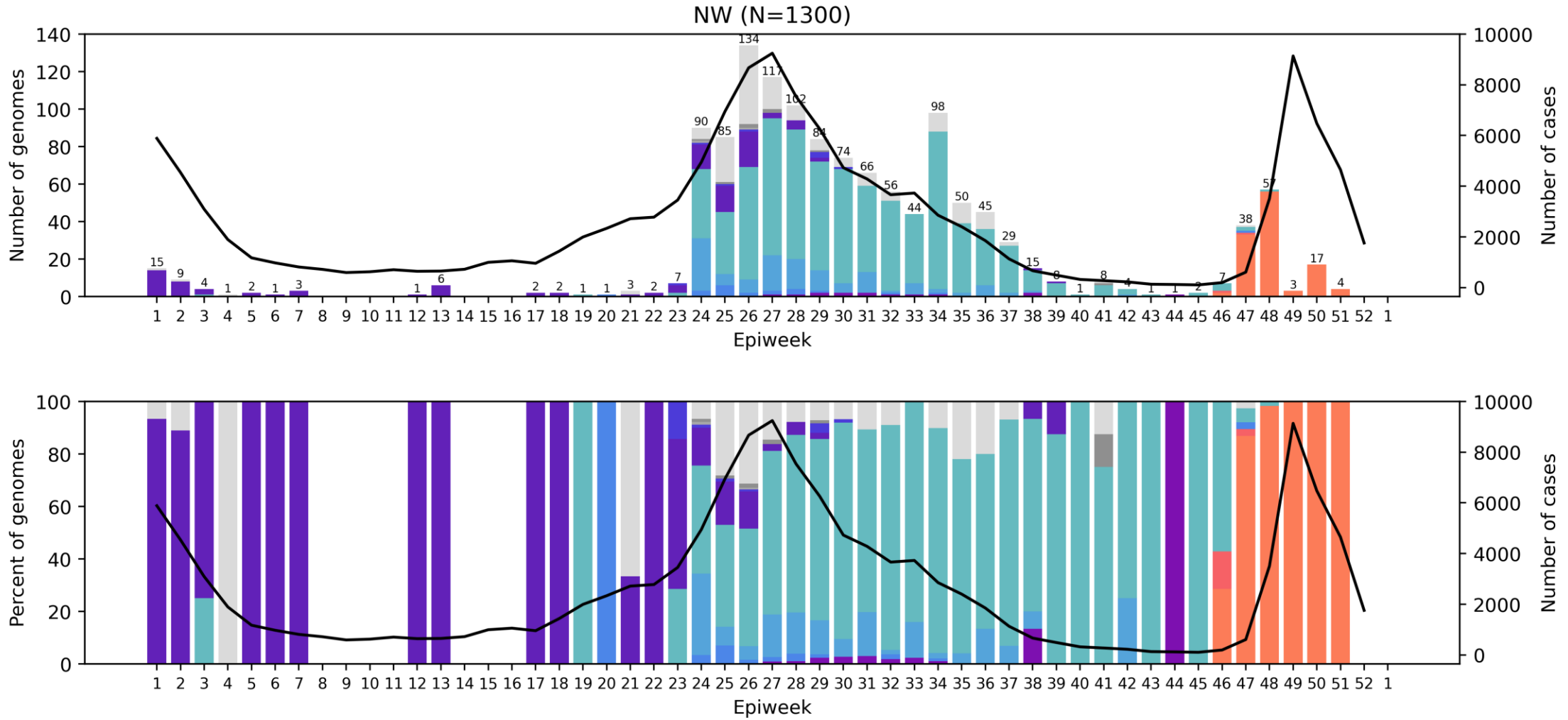
North West Province, 2021, n = 1300



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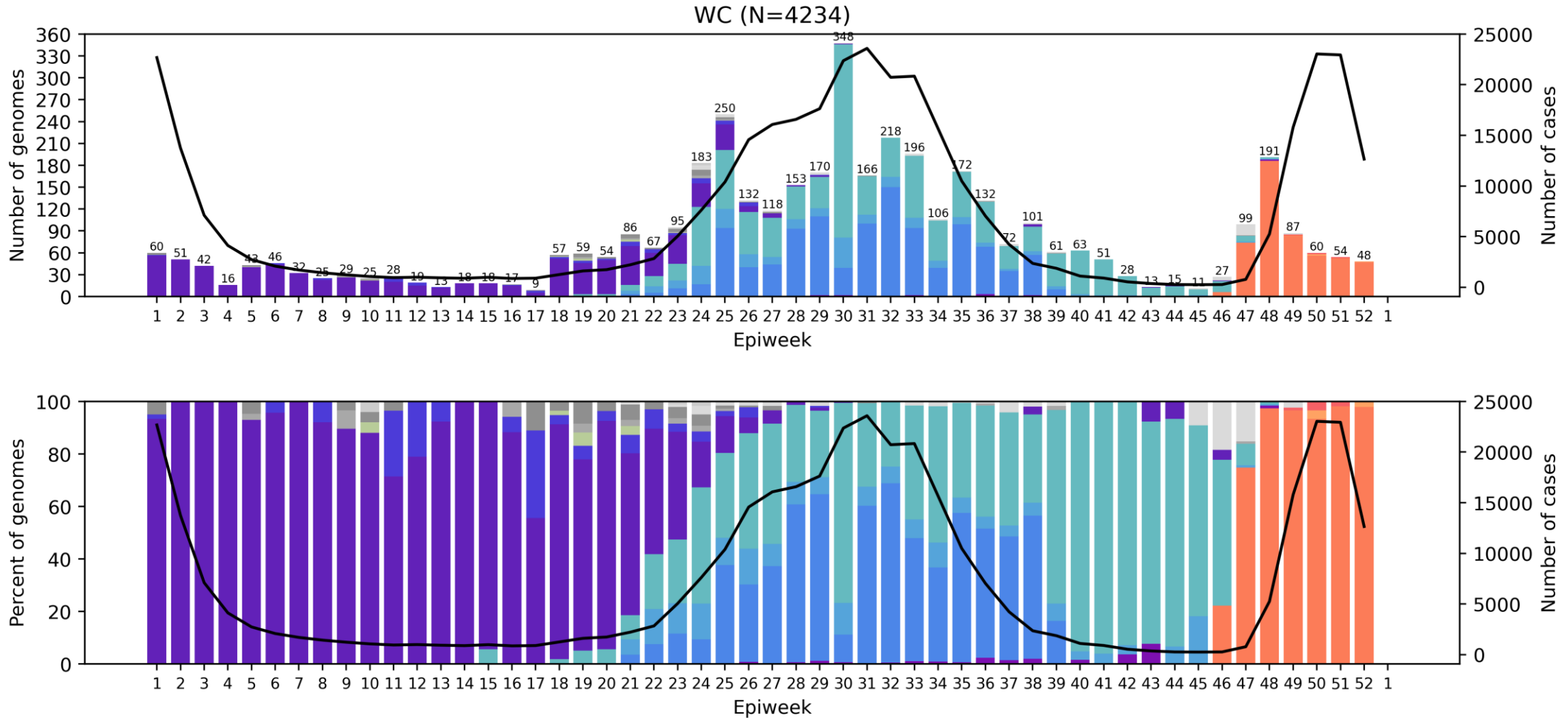
Western Cape Province, 2021-2022, n = 4234



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Summary

- **Variant of Concern Omicron**
  - South Africa:
    - Dominated November sequencing data at 83.5% of genomes (n=1141/1367) and December sequencing data at 98.7% of genomes (n=1057/1071)
    - Detected in all provinces
    - BA.1 is dominant in South Africa. BA.2 has been detected at low levels since November 2021 and does not appear to be increasing; however, more sequencing data from recent weeks are needed to confirm this
  - Global:
    - Detected in 122 countries worldwide
    - Split into three lineages based on different mutational profiles: BA.1 (21K), BA.2 (21L), BA.3 (remains in 21M with parent lineage B.1.1.529 as does not meet requirements for new clade)
- Delta variant dominated in all provinces until end October
  - 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 and continues to be detected at low frequency

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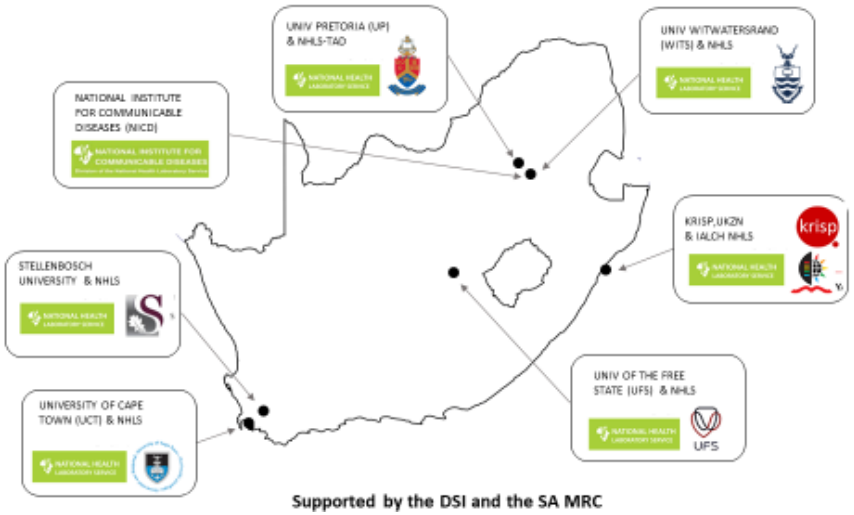

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Division of the National Health Laboratory Service

EDCTP

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REPUBLIC OF SOUTH AFRICA

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wellcome

CDC
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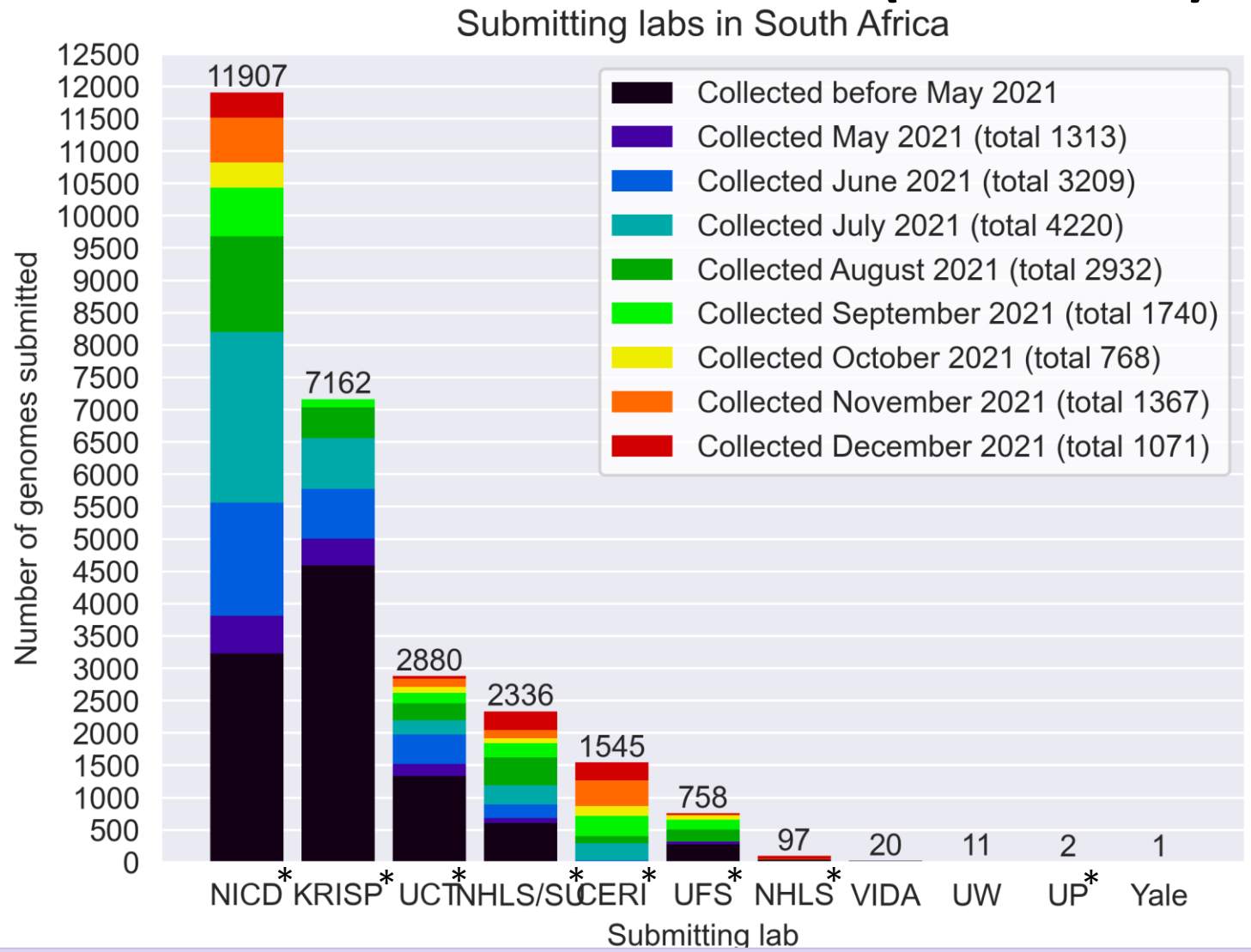
G7 Global Health fund, Robert Koch Institute, Dr Fabian Leendertz

NGS-SA
Network for Genomic Surveillance in South Africa

South African genomes submitted per submitting lab, 2020 and 2021 (N=26 719)



***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

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

Variants of Concern (VOC)

WHO label	Pango lineage•	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 +S:E484K	India, Oct-2020	VOI: 4-Apr-2021 VOC: 11-May-2021
Omicron*	B.1.1.529	GRA	21K, 21L	+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 17 December 2021

•Includes all descendant lineages. See the cov-lineages.org and the Pango network websites for further details.

* See TAG-VE statement issued on 26 November 2021

° Only found in a subset of sequences

Currently designated Variants of Interest (VOI)

WHO label	Pango lineage*	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 17 December 2021

*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.)