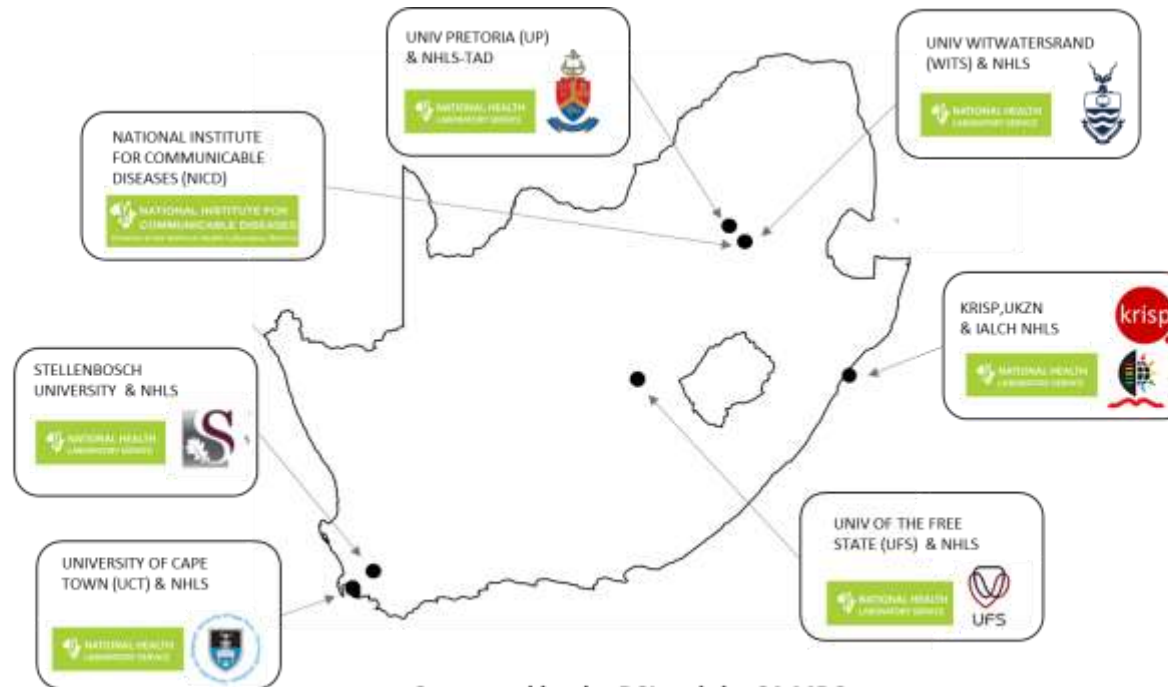


## SARS-CoV-2 Sequencing Update 3 December 2021



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](http://www.gisaid.org)) on 3 December at 08h30

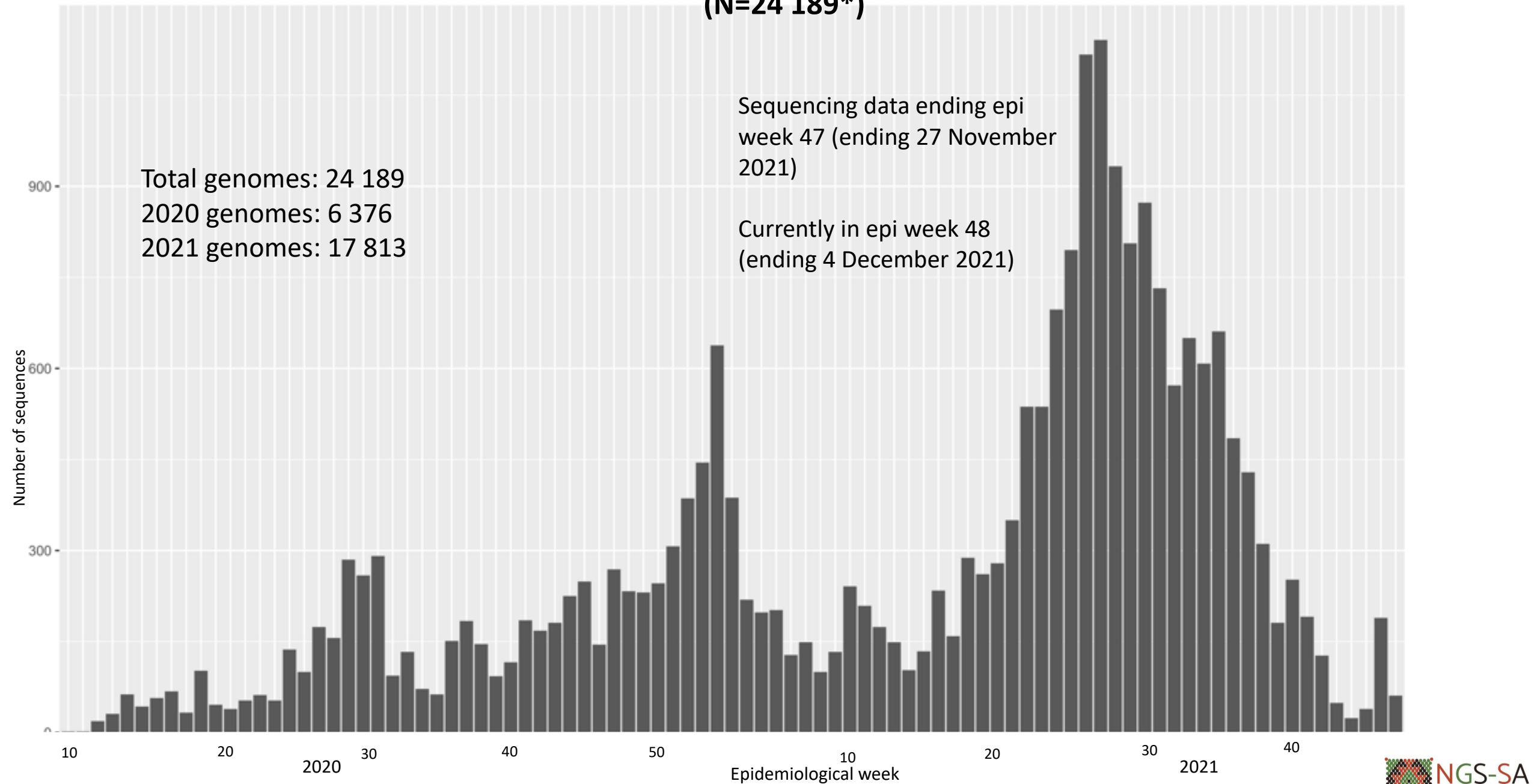


Data license: <https://www.gisaid.org/registration/terms-of-use/>

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

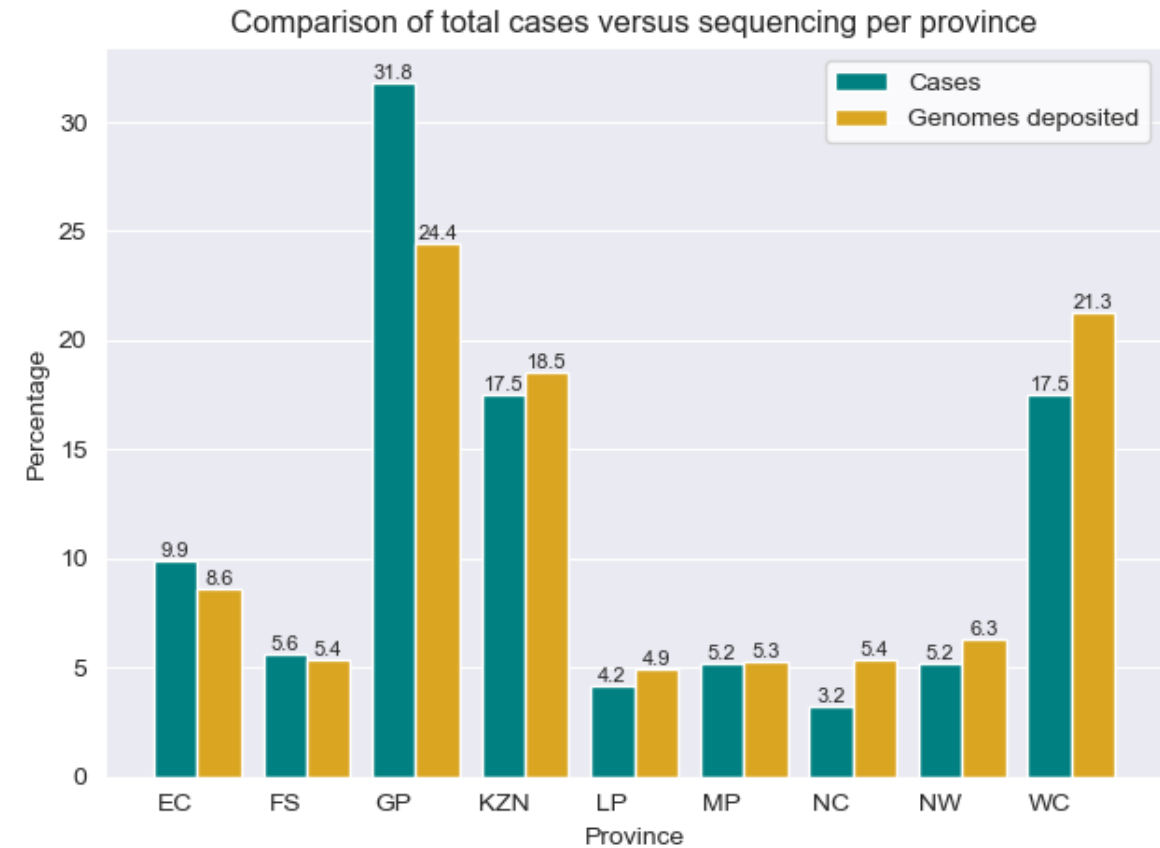
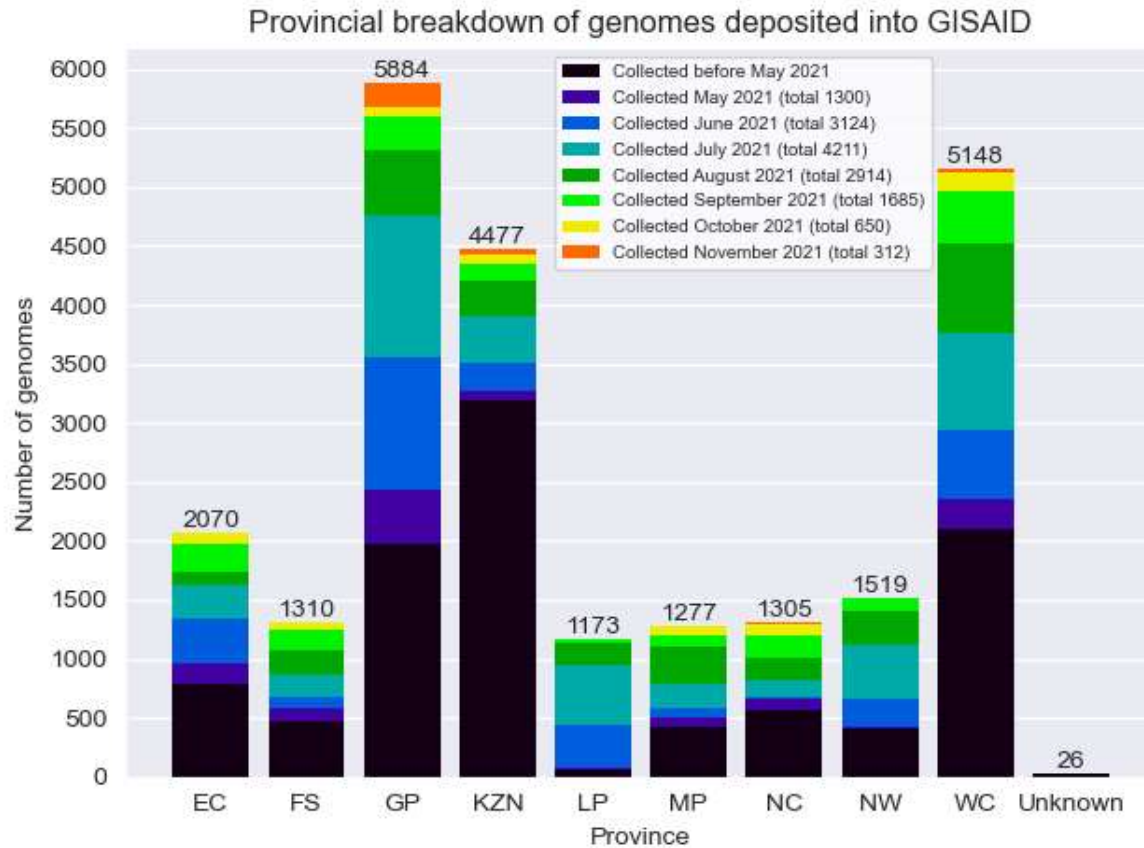
Shu, Y., McCauley, J. (2017) GISAID: Global initiative on sharing all influenza data – from vision to reality. EuroSurveillance, 22(13) DOI: 10.2807/1560-7917.ES.2017.22.13.30494 PMID: PMC5388101

# Number of South African genomes deposited on GISAID, by specimen collection week, 2020 and 2021 (N=24 189\*)



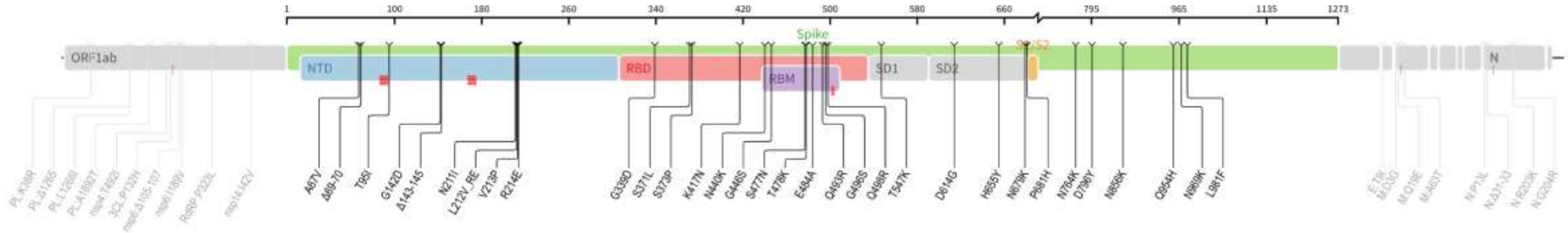
\*This represents the cleaned, de-duplicated dataset of unique sequences. This dataset will be used for all further figures.

# GISAID genomes vs total cases, 2020 and 2021 (N=24 189)



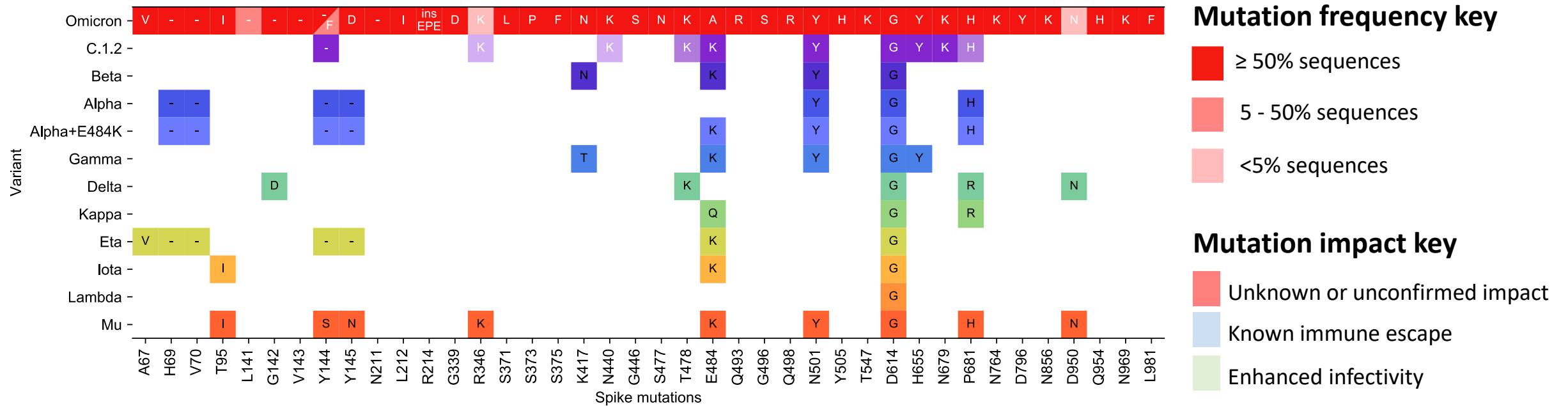
All provinces, apart from GP, KZN, NC and WC, have comparable percentage of overall cases and overall sequenced genomes. The majority of November sequencing data is from Gauteng.

# Omicron lineage mutation profile



- 45-52 amino acid changes (including deletions) across the whole GENOME
  - 26-32 changes in SPIKE
- Does not possess 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

# Omicron spike mutations compared to other VOC/VOIs

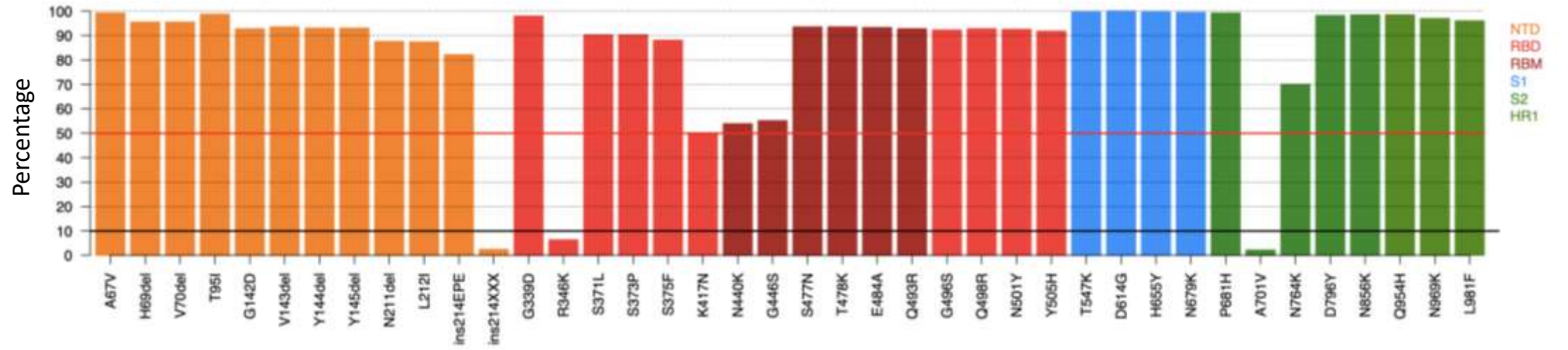


- Multiple changes within the two immunogenic regions in S1 (NTD and RBD)
  - including a three amino acid insertion
- Accumulation of mutations surrounding the furin cleavage site
  - Including combination of N679K and P681H
- Effect of most spike S2 subunit changes have not been defined, but may be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

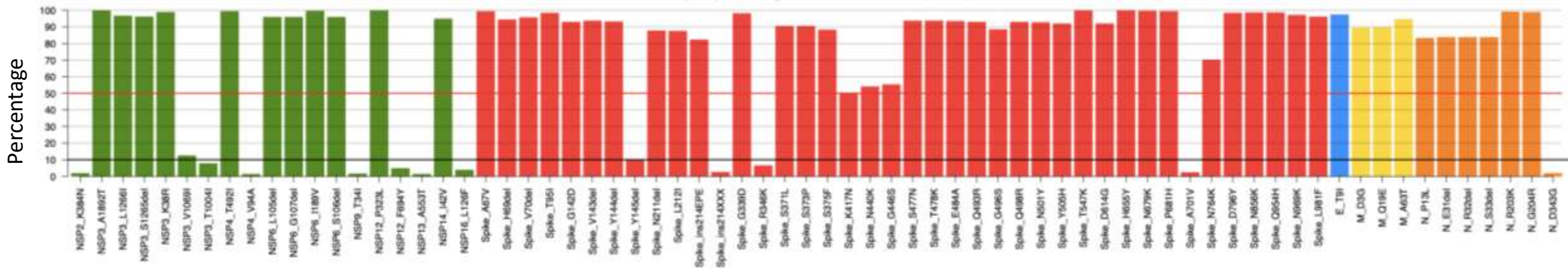


# Mutational profile of Omicron sequences

Frequency of Spike SNVs for Omicron (n = 404)



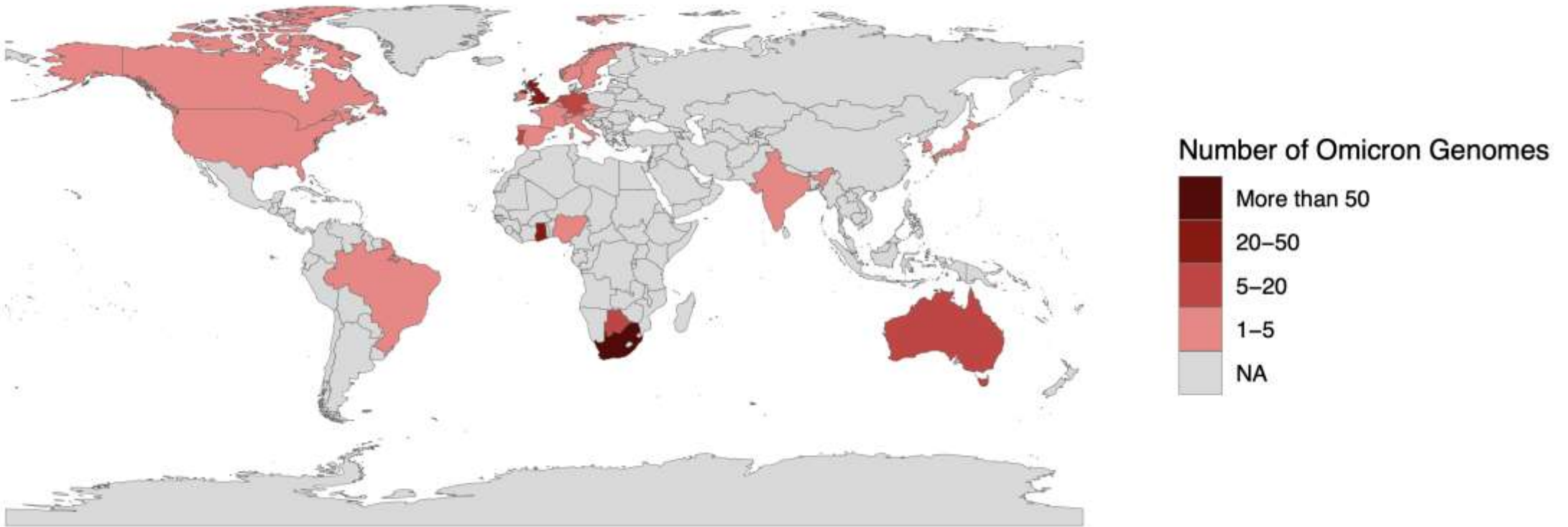
Frequency of whole genome SNVs for Omicron (n = 404)



Mutational profile of Omicron is largely shared amongst all sequences

# Omicron global prevalence

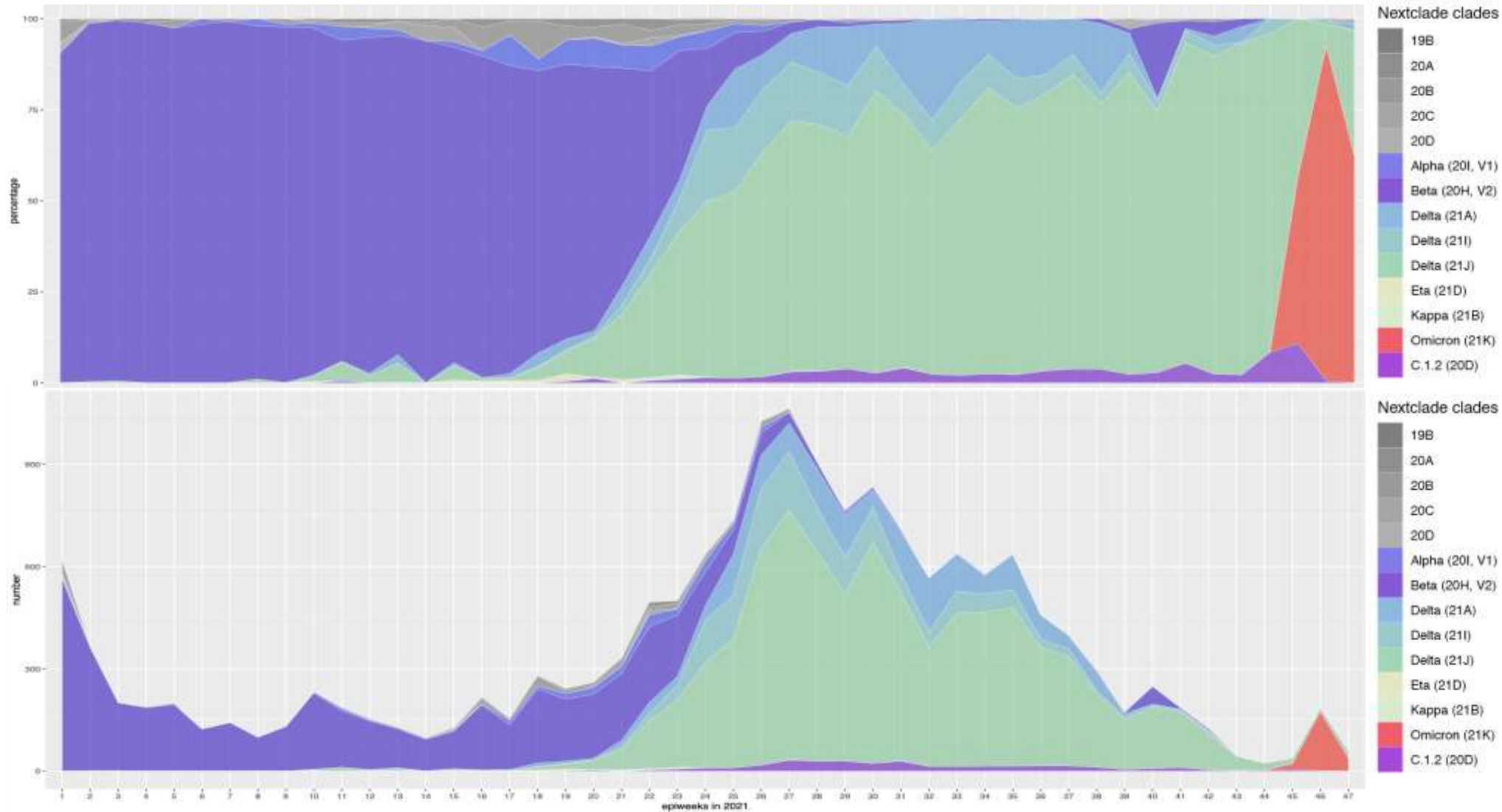
Detection of Omicron Globally (countries = 28; n = 404)



Omicron has been detected in 28 countries across the globe (detections based on GISAID).



# Proportion and number of clades by epiweek in South Africa, 2021 (N= 17 813)



Sequencing data  
ending epi week 47  
(ending 27  
November 2021)

Currently in epi  
week 48 (ending 4  
December 2021)

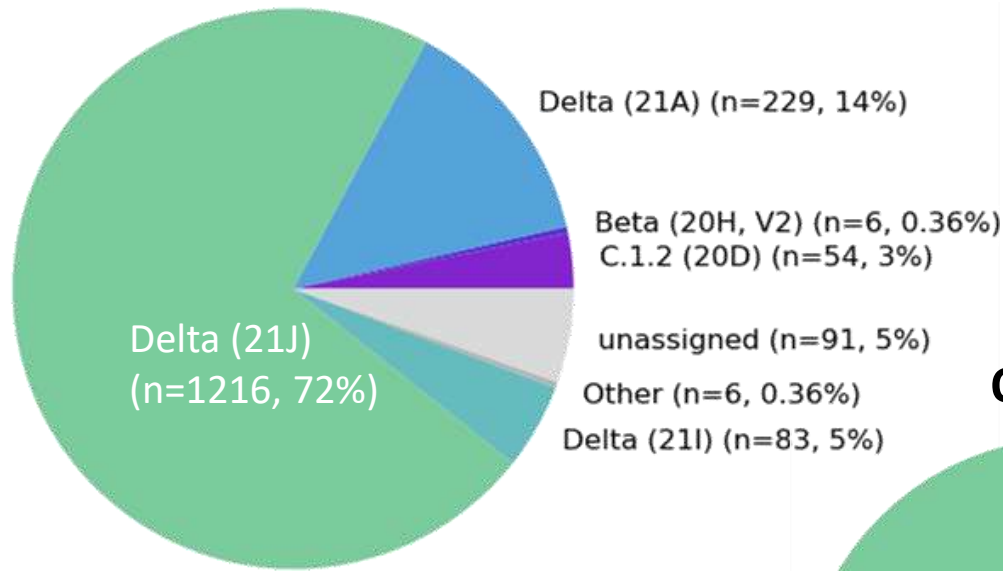
Delta dominated South Africa's third wave with >80% frequency in October, with C.1.2 detection remaining <4%.  
Omicron appears to dominate November sequencing data but sequencing is ongoing to determine its true prevalence.

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

September (N=1685)

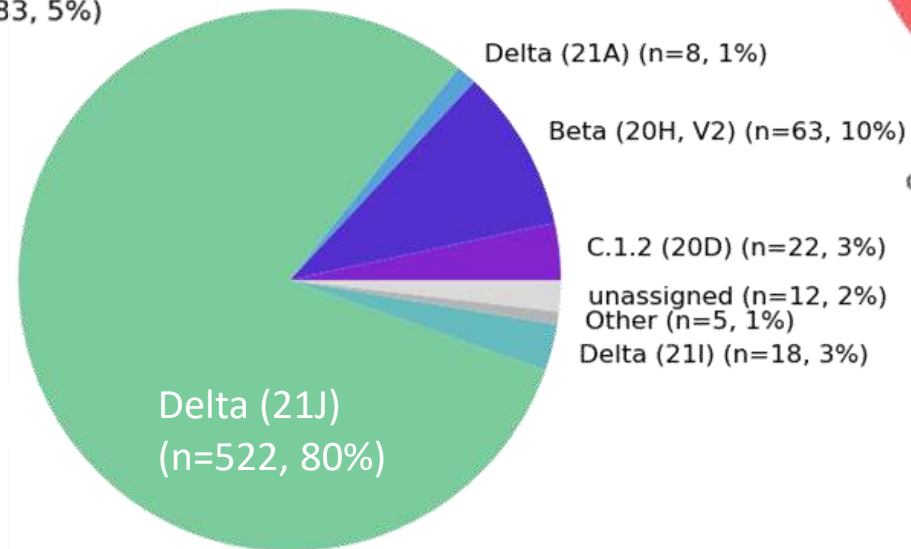
**September – November 2021**

November (N=312)

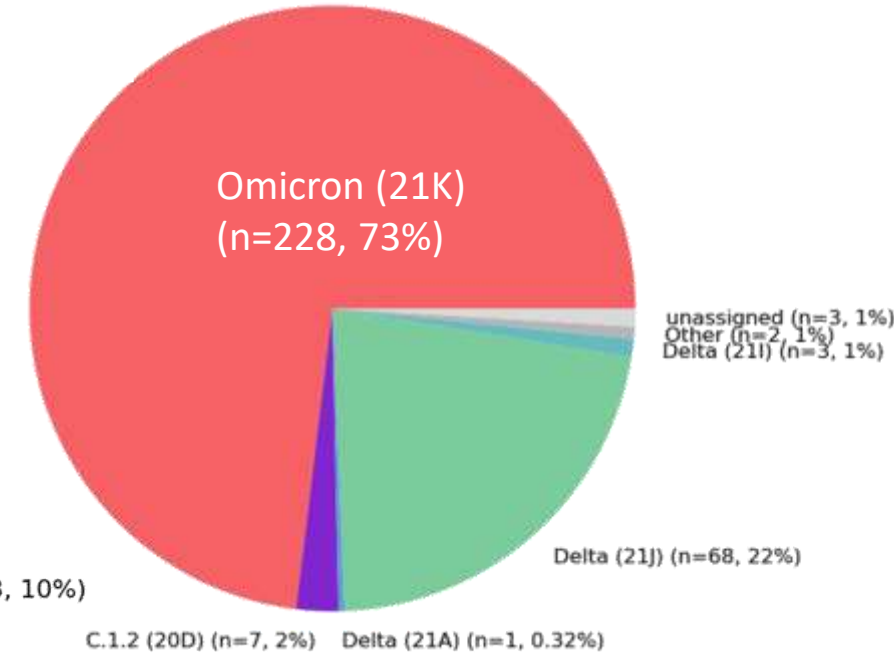


**Total Delta in Sep: 1528 (91%)**

**October (N=650)**



**Total Delta in Oct: 548 (84.3%)**



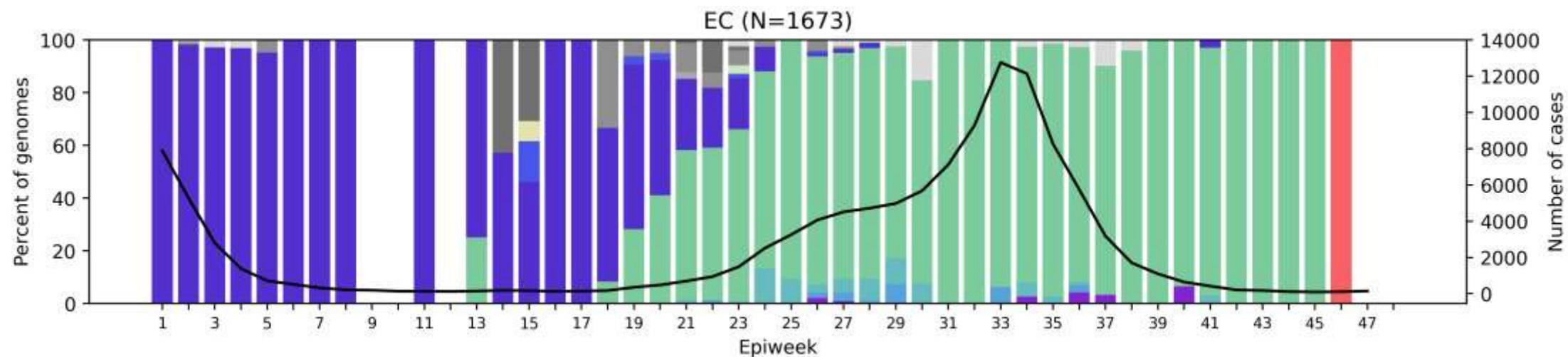
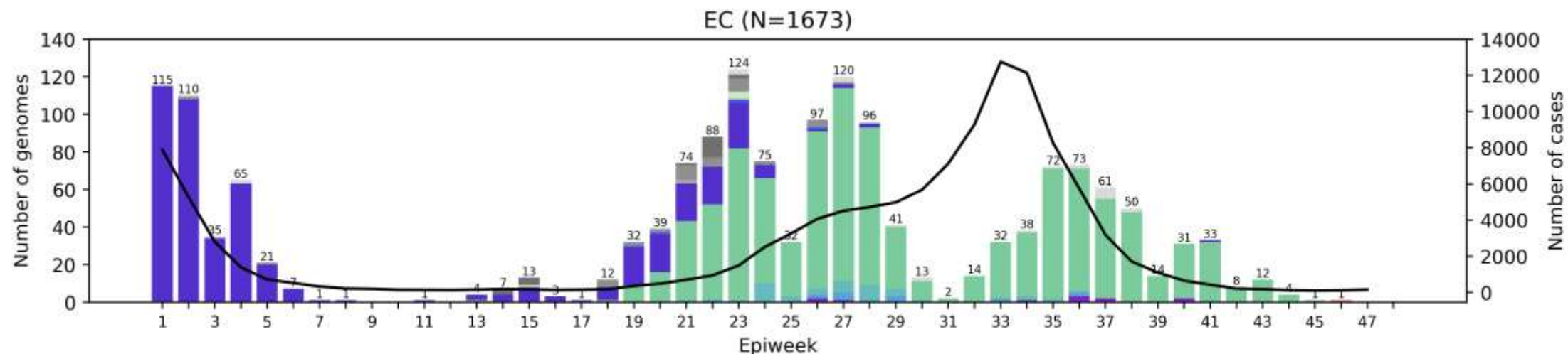
**Total Delta in Nov: 72 (23%)**

Legend: 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 September and October in South Africa.  
Omicron was first detected in South Africa in November, comprising 73% (228/312) of sequences.**



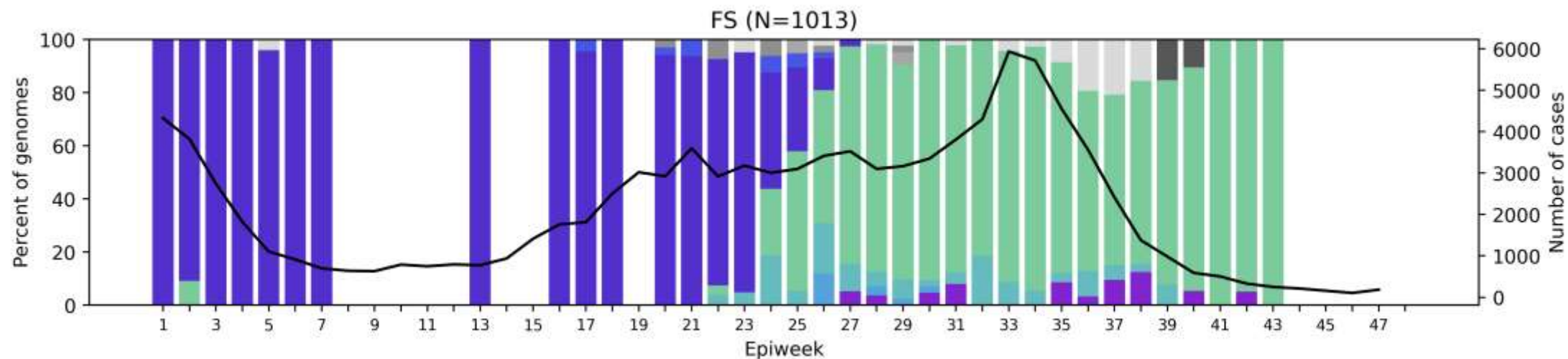
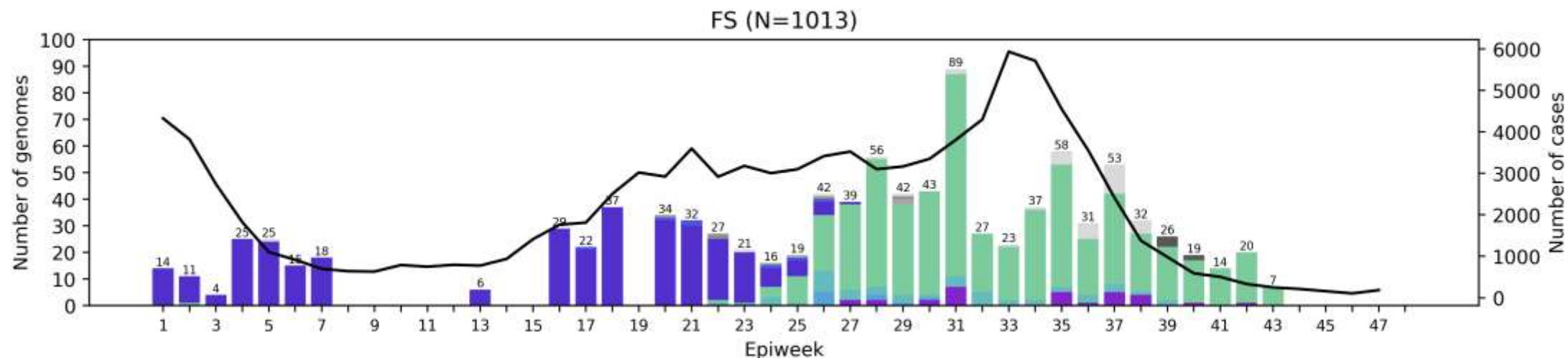
# Eastern Cape Province, 2021, n =1673



— cases — Omicron (21K) — C.1.2 (20D) — Delta (21A) — Delta (21I) — Delta (21J) — Beta (20H, V2) — Alpha (20I, V1) — Kappa (21B) — Eta (21D) — 20A — 20B — 20C — 20D — unassigned — 19B



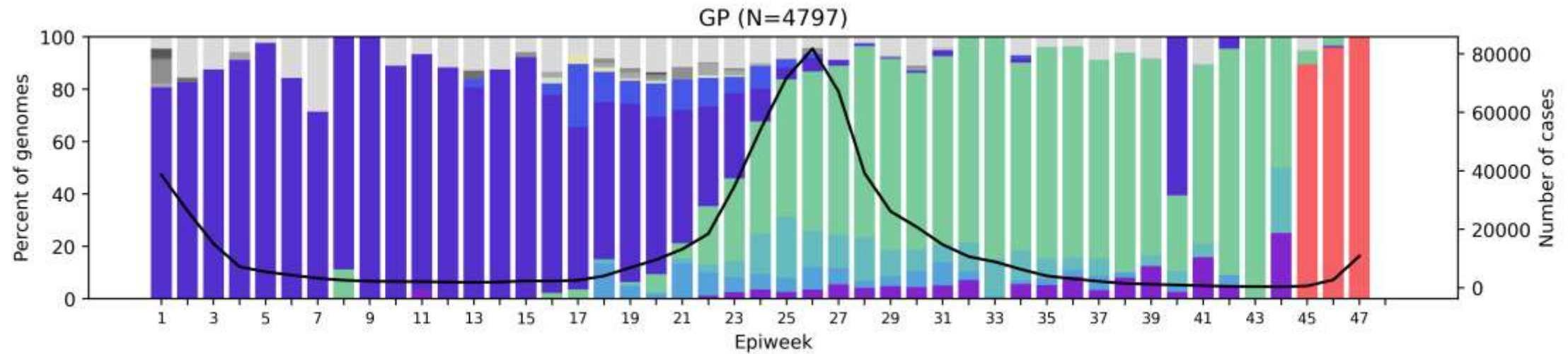
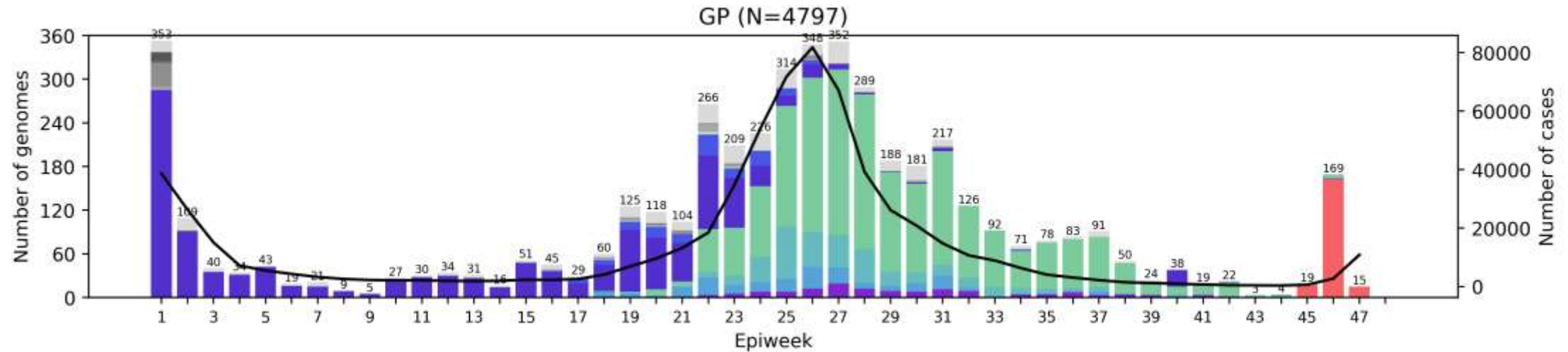
# Free State Province, 2021, n = 1013



— cases    Omicron (21K)    C.1.2 (20D)    Delta (21A)    Delta (21I)    Delta (21J)    Beta (20H, V2)    Alpha (20I, V1)    Kappa (21B)    Eta (21D)    20A    20B    20C    20D    unassigned    19B

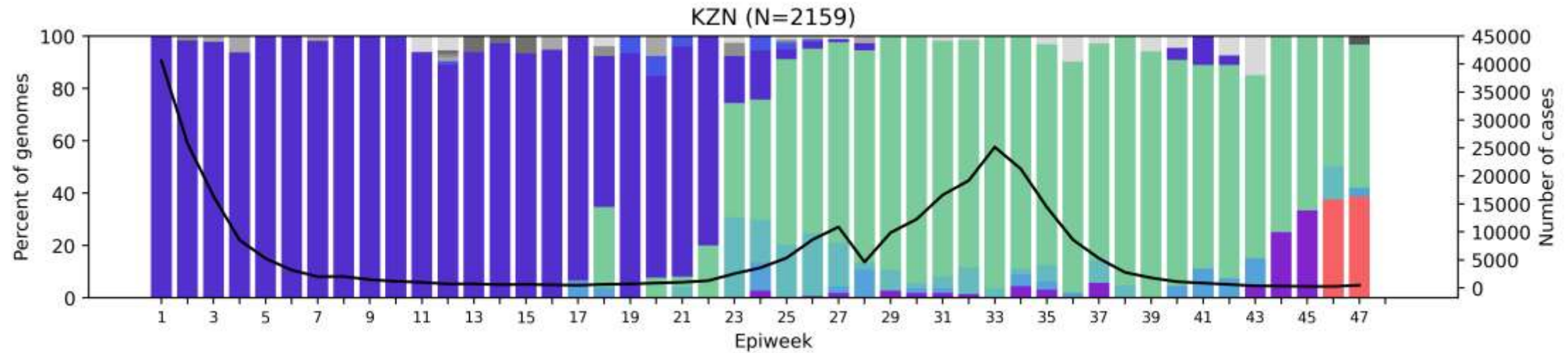
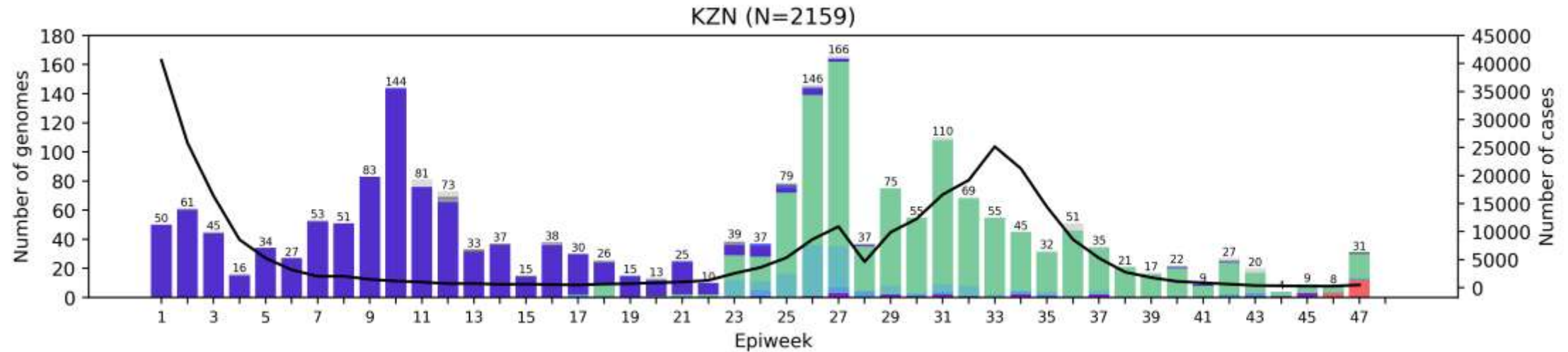


# Gauteng Province, 2021, n = 4797



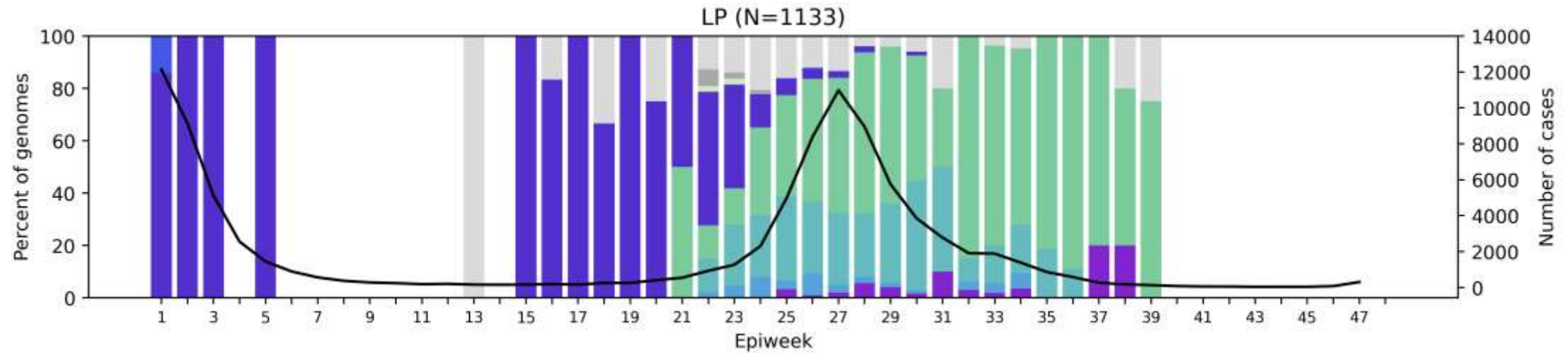
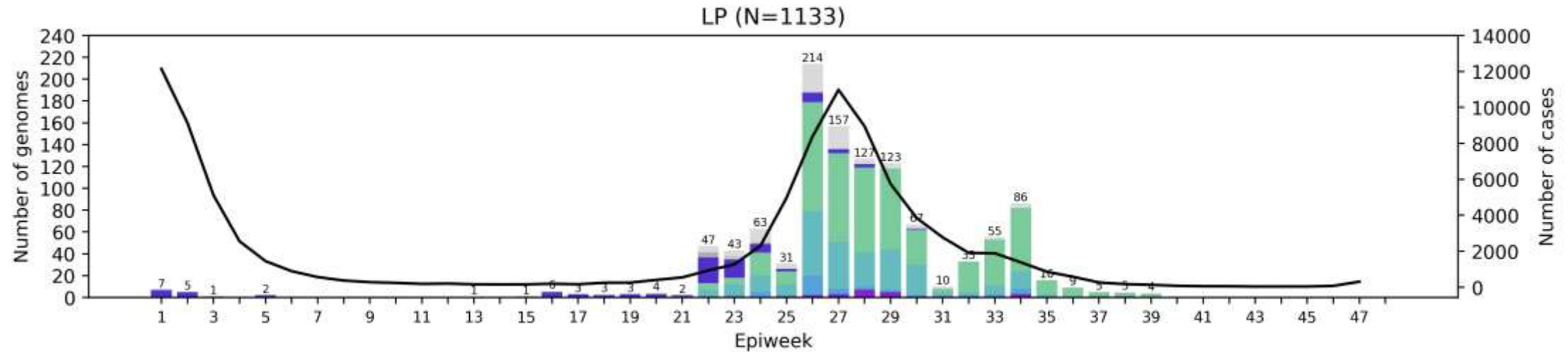
— cases — Omicron (21K) — C.1.2 (20D) — Delta (21A) — Delta (21I) — Delta (21J) — Beta (20H, V2) — Alpha (20I, V1) — Kappa (21B) — Eta (21D) — 20A — 20B — 20C — 20D — unassigned — 19B

# KwaZulu-Natal Province, 2021, n = 2159



— cases    Omicron (21K)    C.1.2 (20D)    Delta (21A)    Delta (21I)    Delta (21J)    Beta (20H, V2)    Alpha (20I, V1)    Kappa (21B)    Eta (21D)    20A    20B    20C    20D    unassigned    19B

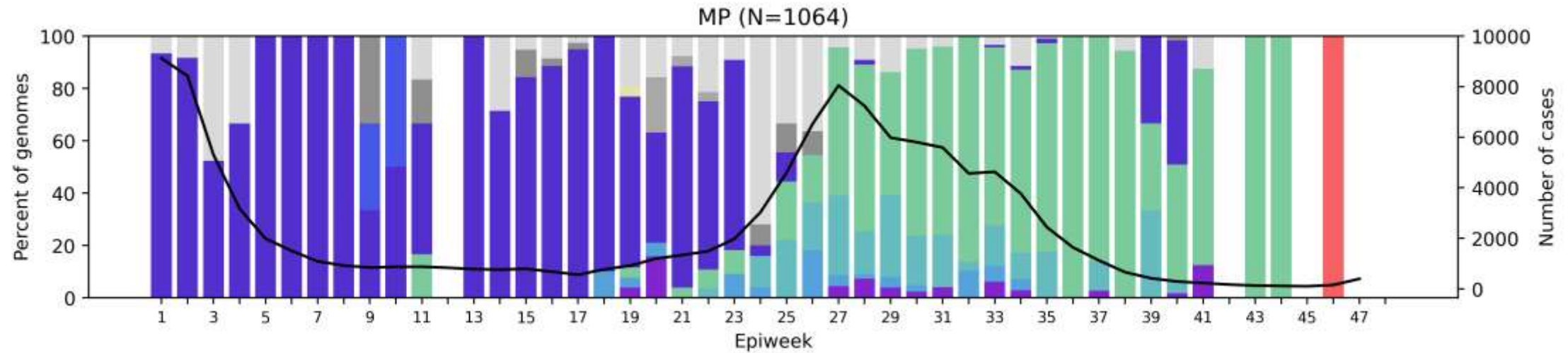
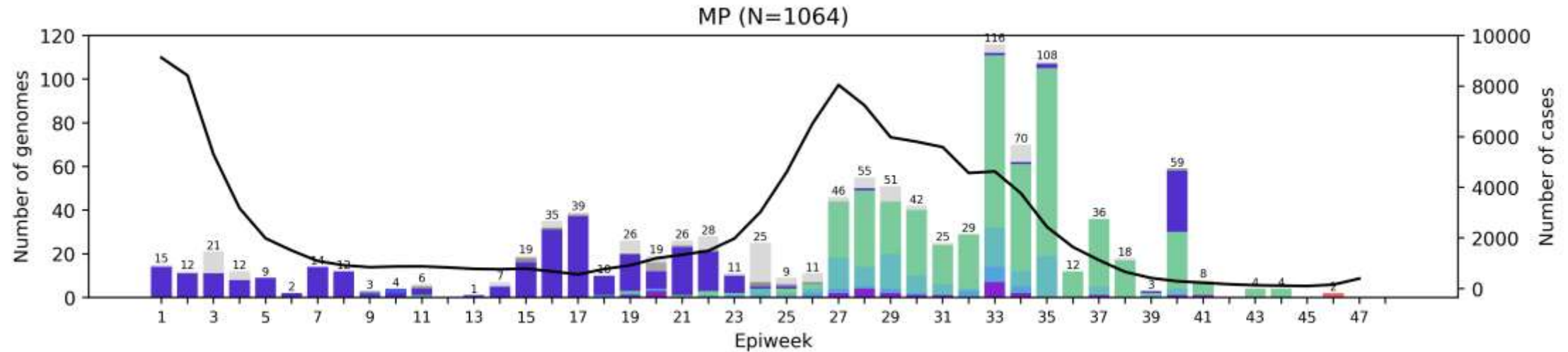
# Limpopo Province, 2021, n = 1133



— cases — Omicron (21K) — C.1.2 (20D) — Delta (21A) — Delta (21I) — Delta (21J) — Beta (20H, V2) — Alpha (20I, V1) — Kappa (21B) — Eta (21D) — 20A — 20B — 20C — 20D — unassigned — 19B

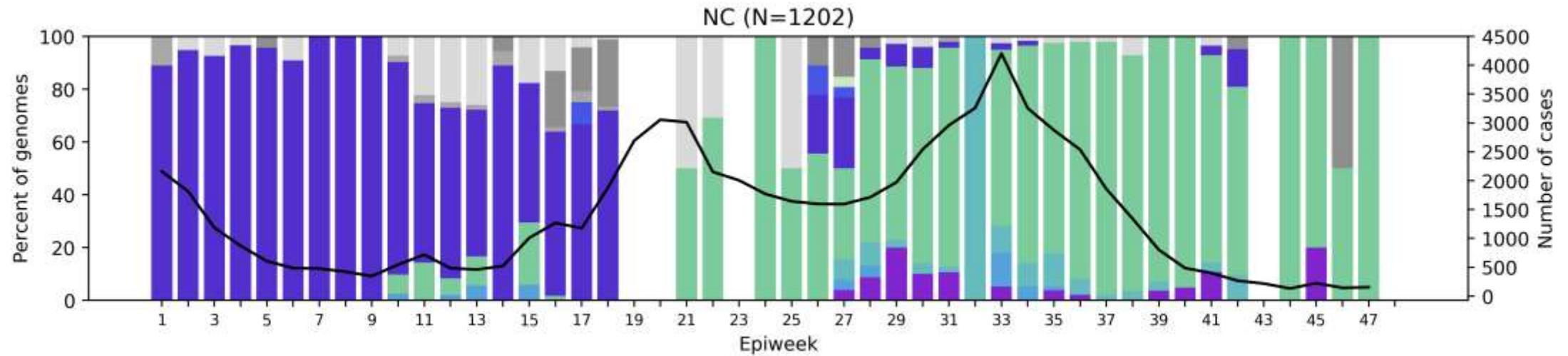
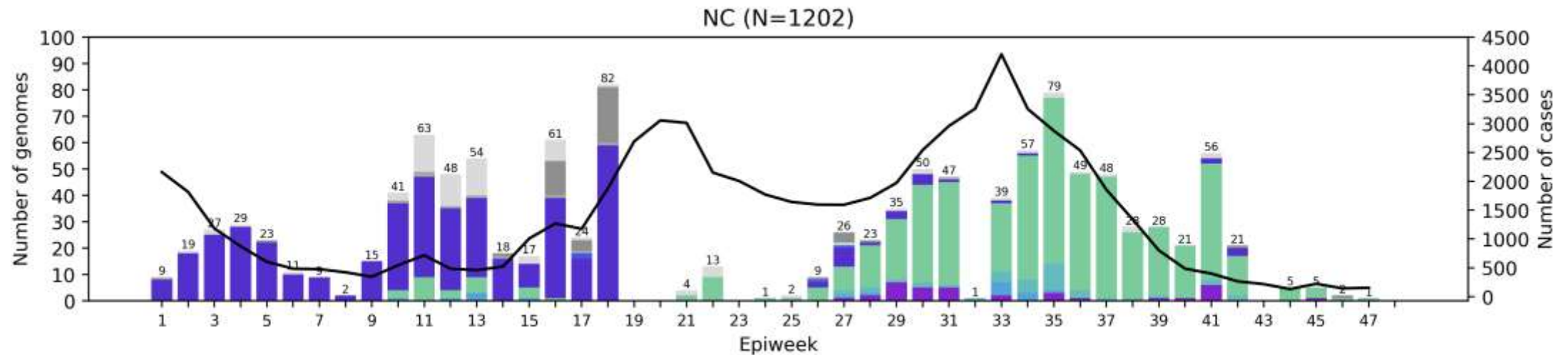


# Mpumalanga Province, 2021, n = 1064



— cases    Omicron (21K)    C.1.2 (20D)    Delta (21A)    Delta (21I)    Delta (21J)    Beta (20H, V2)    Alpha (20I, V1)    Kappa (21B)    Eta (21D)    20A    20B    20C    20D    unassigned    19B

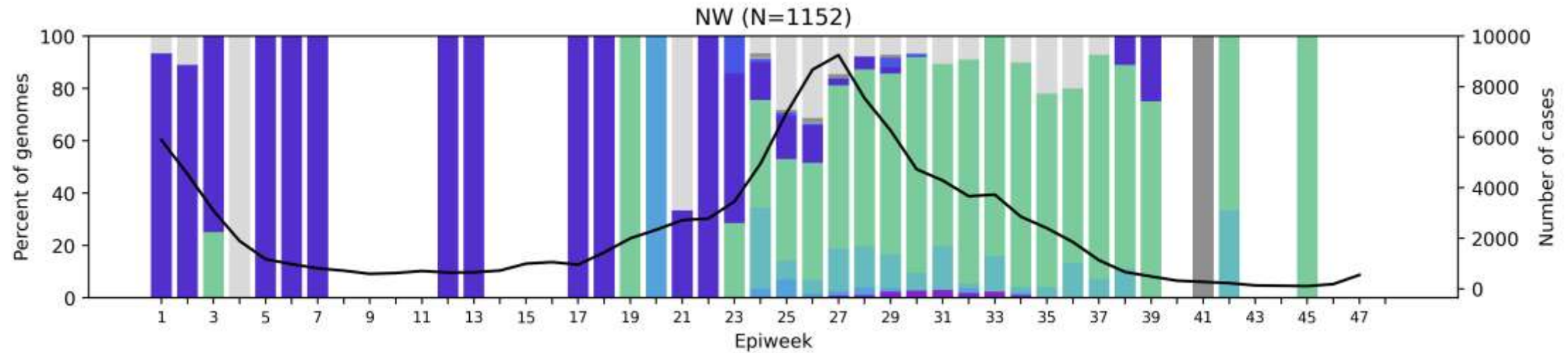
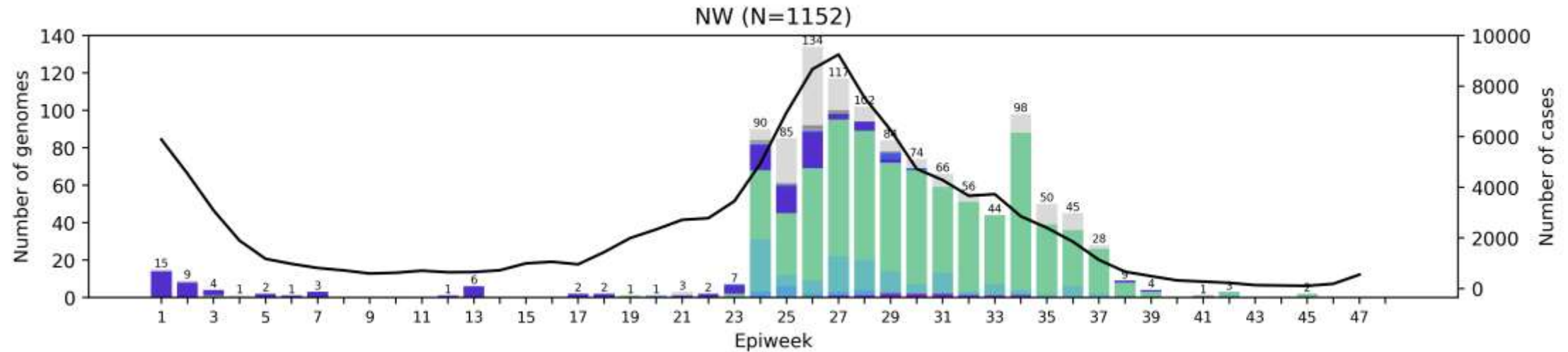
# Northern Cape Province, 2021, n = 1202



— cases    Omicron (21K)    C.1.2 (20D)    Delta (21A)    Delta (21I)    Delta (21J)    Beta (20H, V2)    Alpha (20I, V1)    Kappa (21B)    Eta (21D)    20A    20B    20C    20D    unassigned    19B

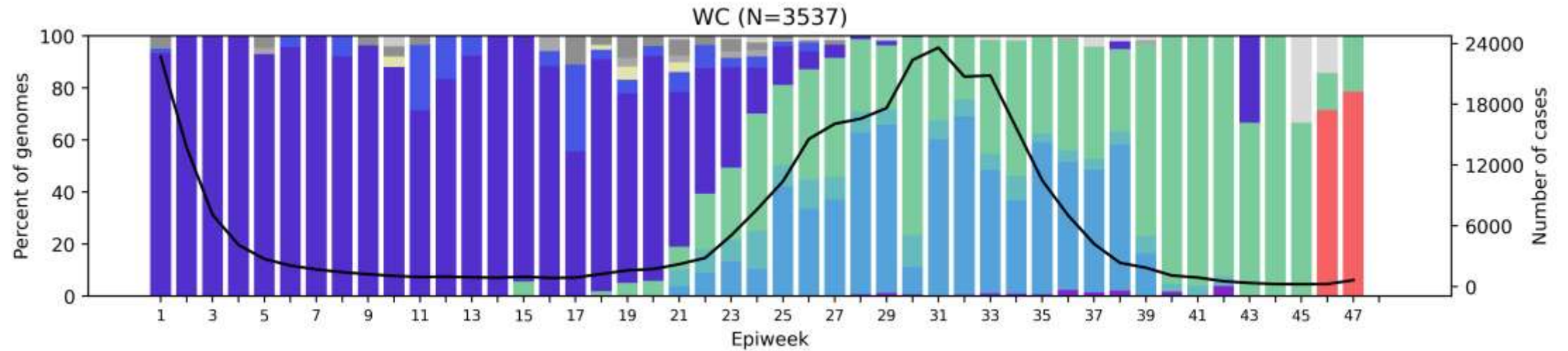
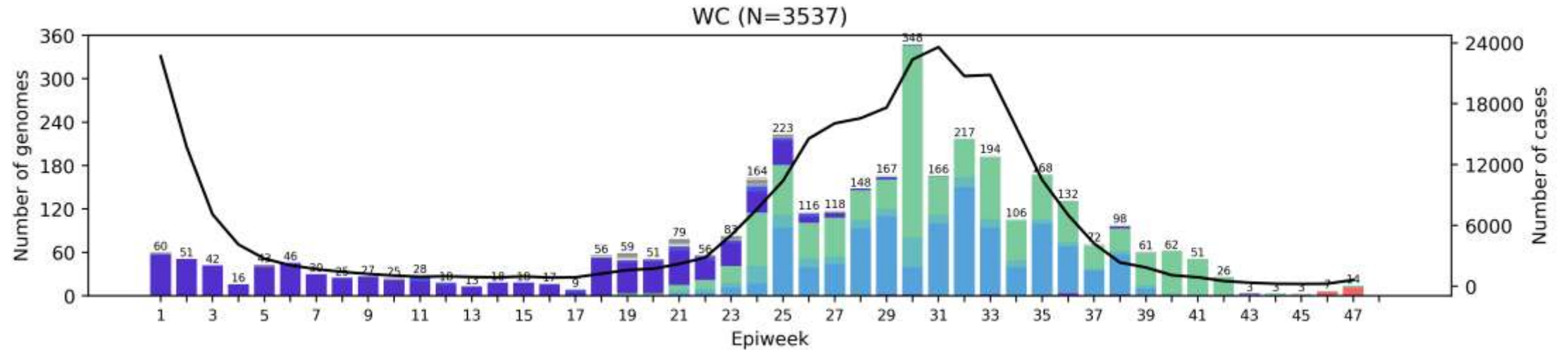


# North West Province, 2021, n = 1152



— cases    Omicron (21K)    C.1.2 (20D)    Delta (21A)    Delta (21I)    Delta (21J)    Beta (20H, V2)    Alpha (20I, V1)    Kappa (21B)    Eta (21D)    20A    20B    20C    20D    unassigned    19B

# Western Cape Province, 2021, n =3537

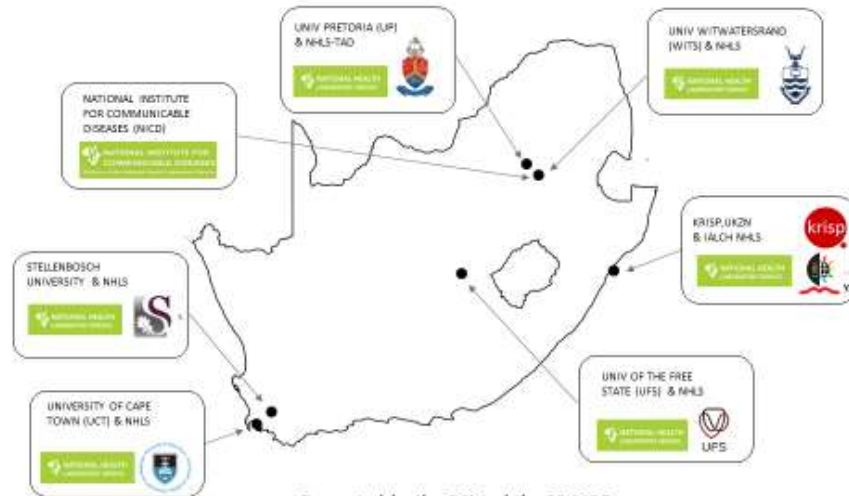


— cases    Omicron (21K)    C.1.2 (20D)    Delta (21A)    Delta (21I)    Delta (21J)    Beta (20H, V2)    Alpha (20I, V1)    Kappa (21B)    Eta (21D)    20A    20B    20C    20D    unassigned    19B

# 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 73% of genomes (n=228/312). Sequencing is ongoing to determine prevalence of Omicron in other provinces.
  - Omicron has now been detected in 28 countries worldwide
  - More information can be found at <https://www.nicd.ac.za/frequently-asked-questions-for-the-b-1-1-529-mutated-sars-cov-2-lineage-in-south-africa/>
- Delta variant dominated in all provinces until end October
  - The Delta sub-lineages vary 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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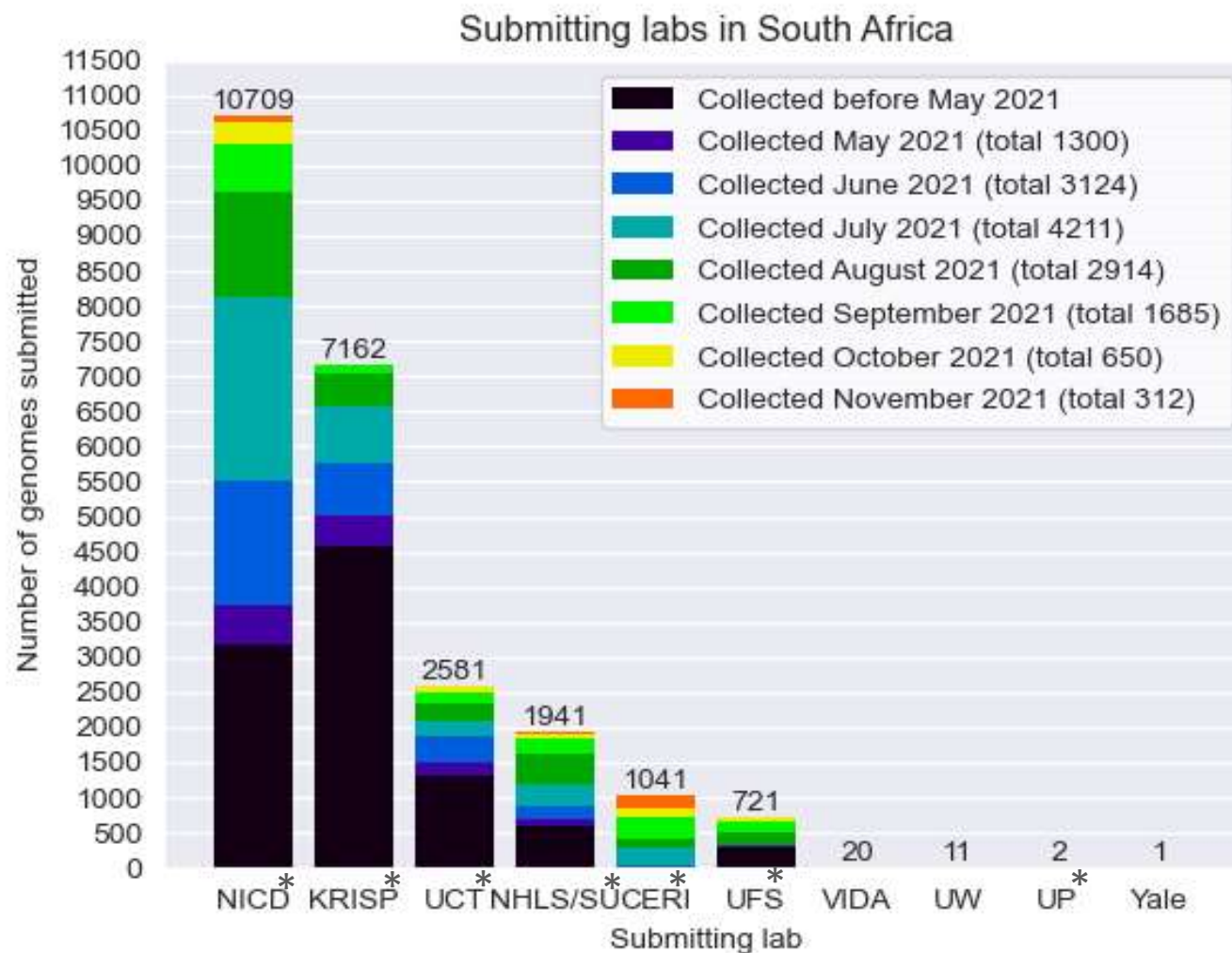
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# South African genomes submitted per submitting lab, 2020 and 2021 (N=24 189)



## 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.

# Variants of Concern (VOC)

WHO label	Pango lineages <sup>+</sup>	GISAID clade	Nextstrain clade	Additional amino acid changes monitored*	Earliest documented samples	Date of designation
Alpha	B.1.1.7 <sup>#</sup>	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 <sup>§</sup>	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 3 December 2021

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

<sup>+</sup>Includes all descendant lineages.

<sup>#</sup>Includes all Q.\* lineages in the PANGO nomenclature system.

<sup>§</sup>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 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 ( $\geq 14$  days after vaccine), especially if hospitalised and clinically severe
- Suspected re-infection ( $\geq 90$  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.)