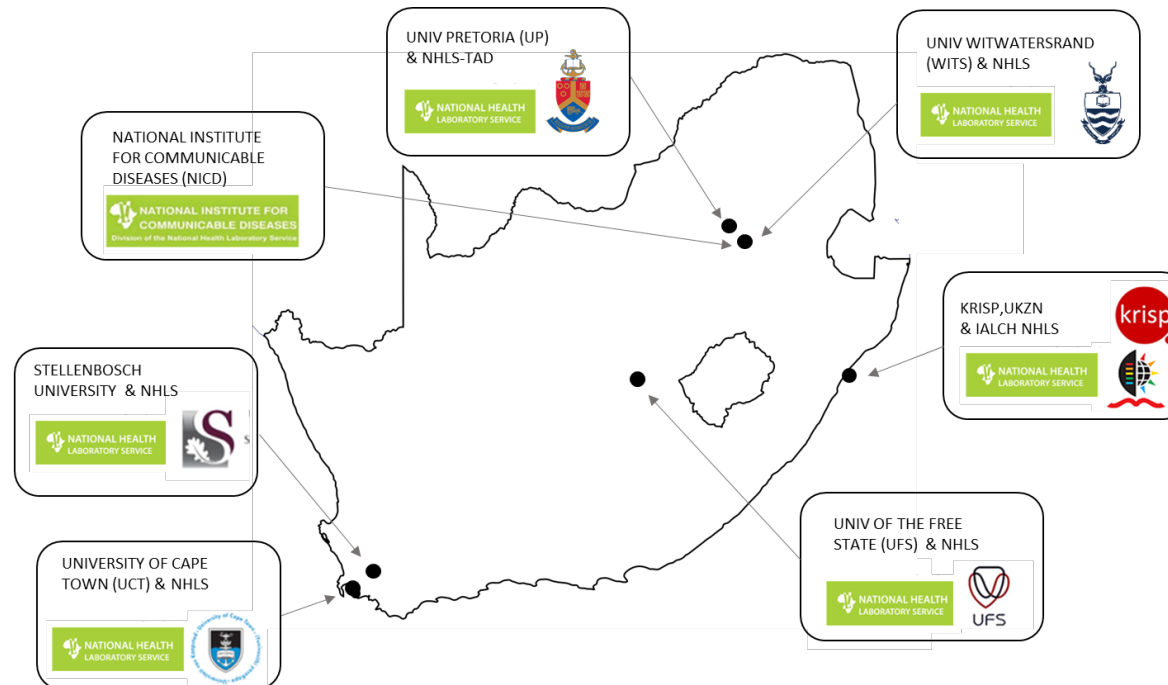


SARS-CoV-2 Sequencing Update 1 December 2021



Supported by the DSI and the SA MRC

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

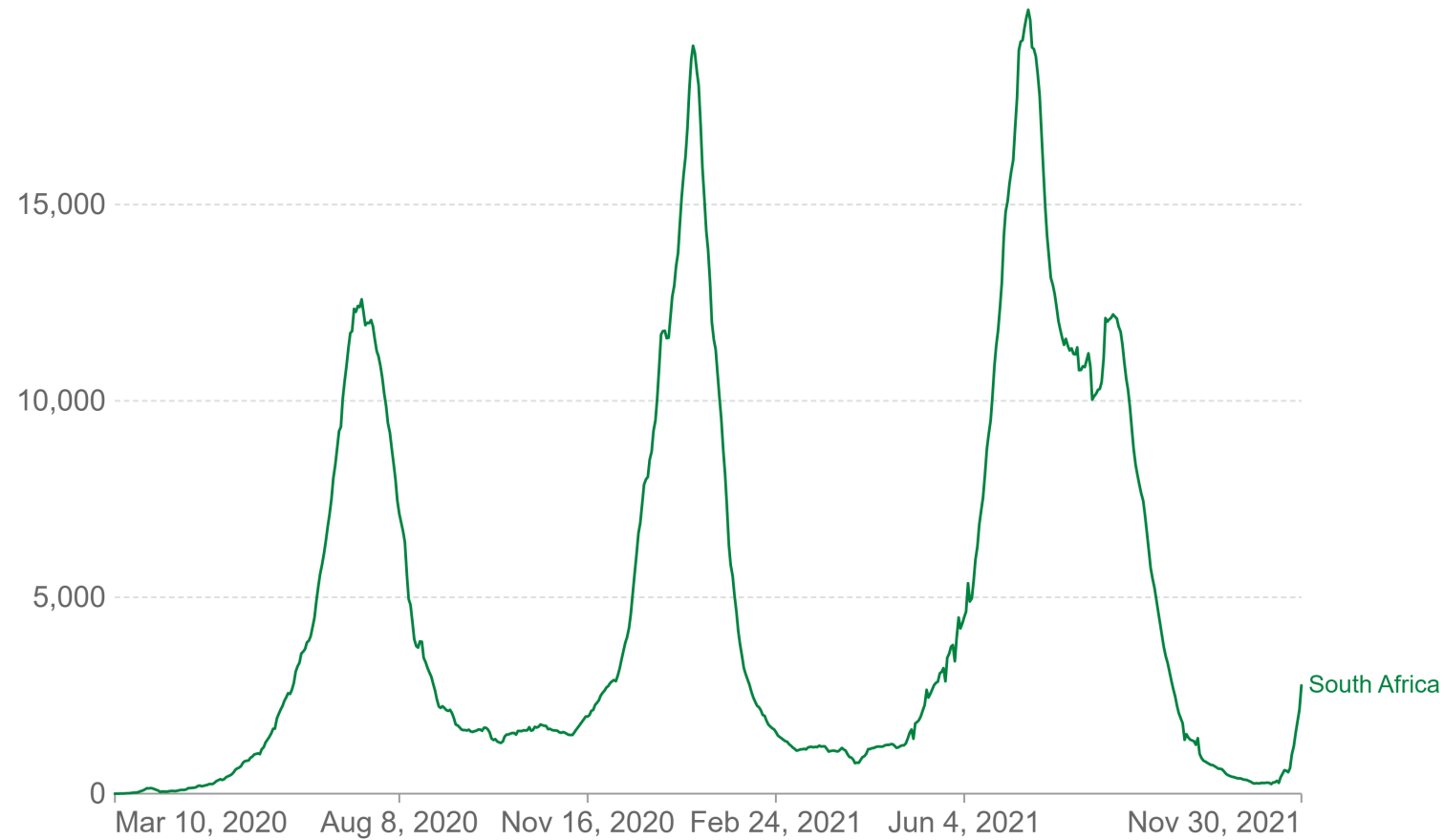
Summary of new variant

- **New variant** detected in South Africa (**Omicron, B.1.1.529**)
- **215 Omicron genomes** in public database (GISAID) from samples collected since 11 Nov including **128 from South Africa (GP, KZN and WC)**, and 19 from Botswana (n=19)
- Now detected in multiple other locations around the world
- Signs from diagnostic laboratories that Omicron is **likely to be present in all provinces**
- We can make some predictions about the properties of this variant based on the genetic mutations, but **more work is needed to fully understand**
- **Vaccination remains the critical tool to prevent severe disease, hospitalisation and death**

Epidemic curve – South Africa

Daily new confirmed COVID-19 cases

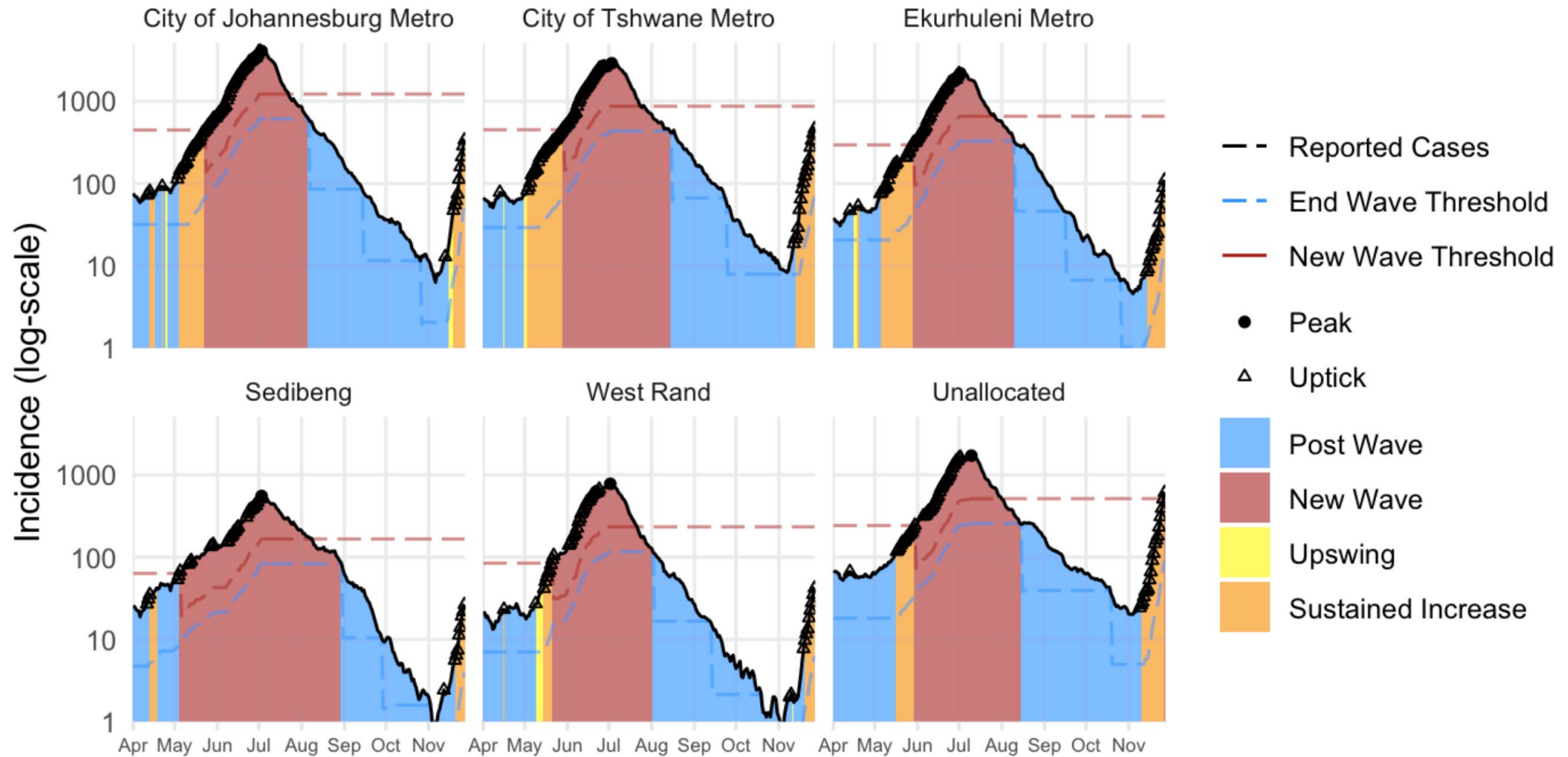
7-day rolling average. Due to limited testing, the number of confirmed cases is lower than the true number of infections.



Source: Johns Hopkins University CSSE COVID-19 Data

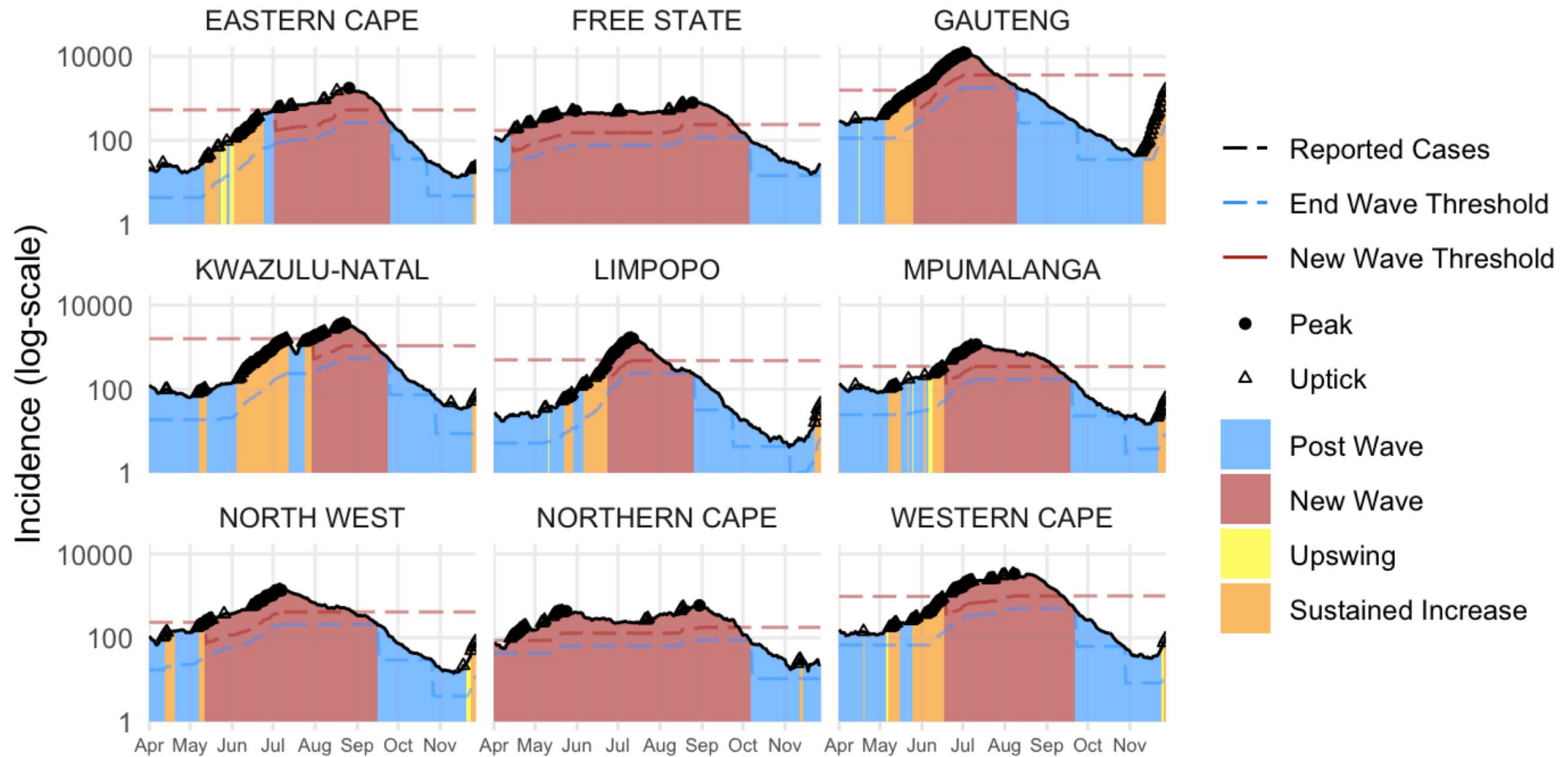
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Sustained Increase Monitoring Gauteng - SACMC



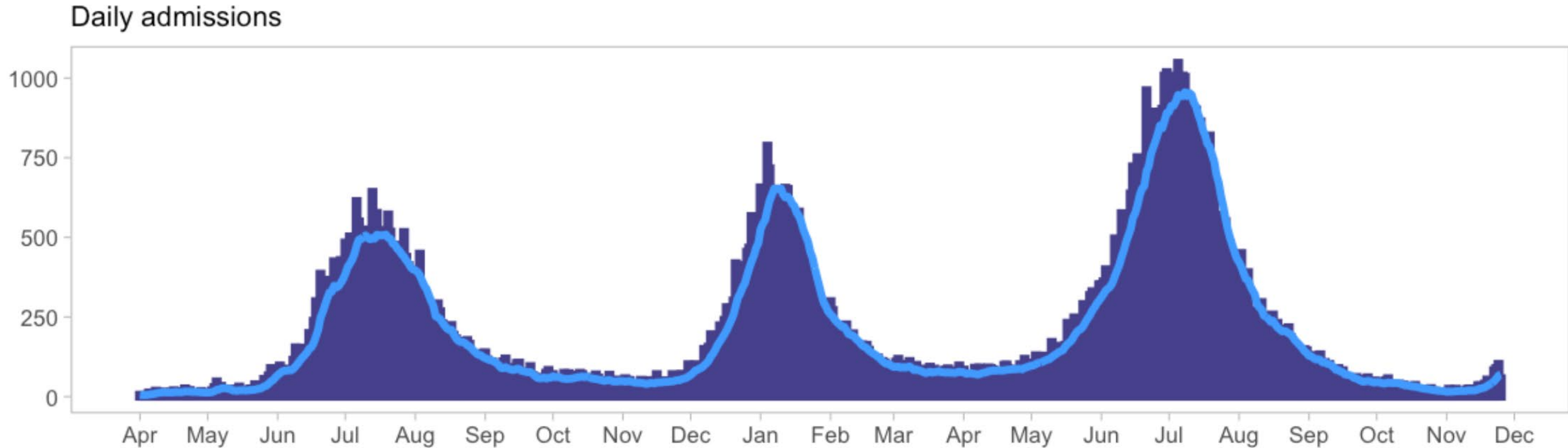
Sustained increase in incidence across all Gauteng municipalities

Sustained Increase Monitoring – all provinces



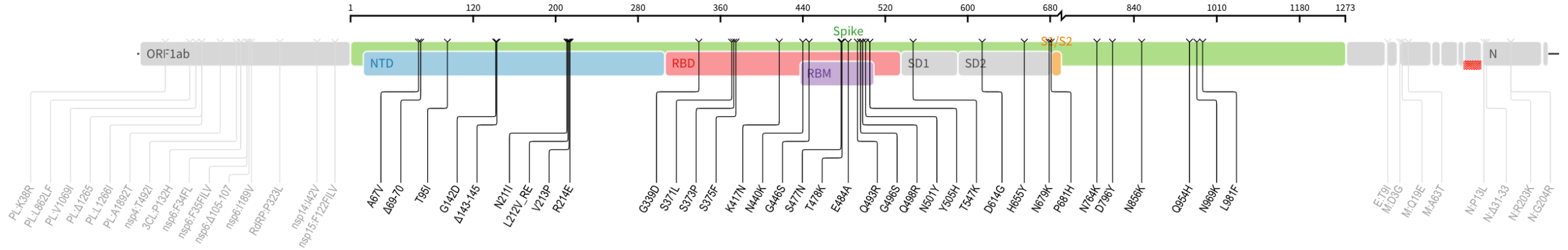
Sustained increase in incidence now in most other provinces

Hospital admissions - Gauteng



Increase in hospital admissions in Gauteng but very early

Omicron – mutation profile



Very unusual constellation of mutations - multiple mutations across the SARS-CoV-2 genome, with >30 mutations in spike protein

In the phylogenetic tree (family tree) this variant is distinct from other circulating VOCs/VOIs – not a direct descendent of Delta or Beta

Some mutations well characterized with known known impact (affecting transmissibility or immune escape), but many others rarely observed until now and not well characterized – so full significance uncertain

Omicron can be presumptively detected by PCR test

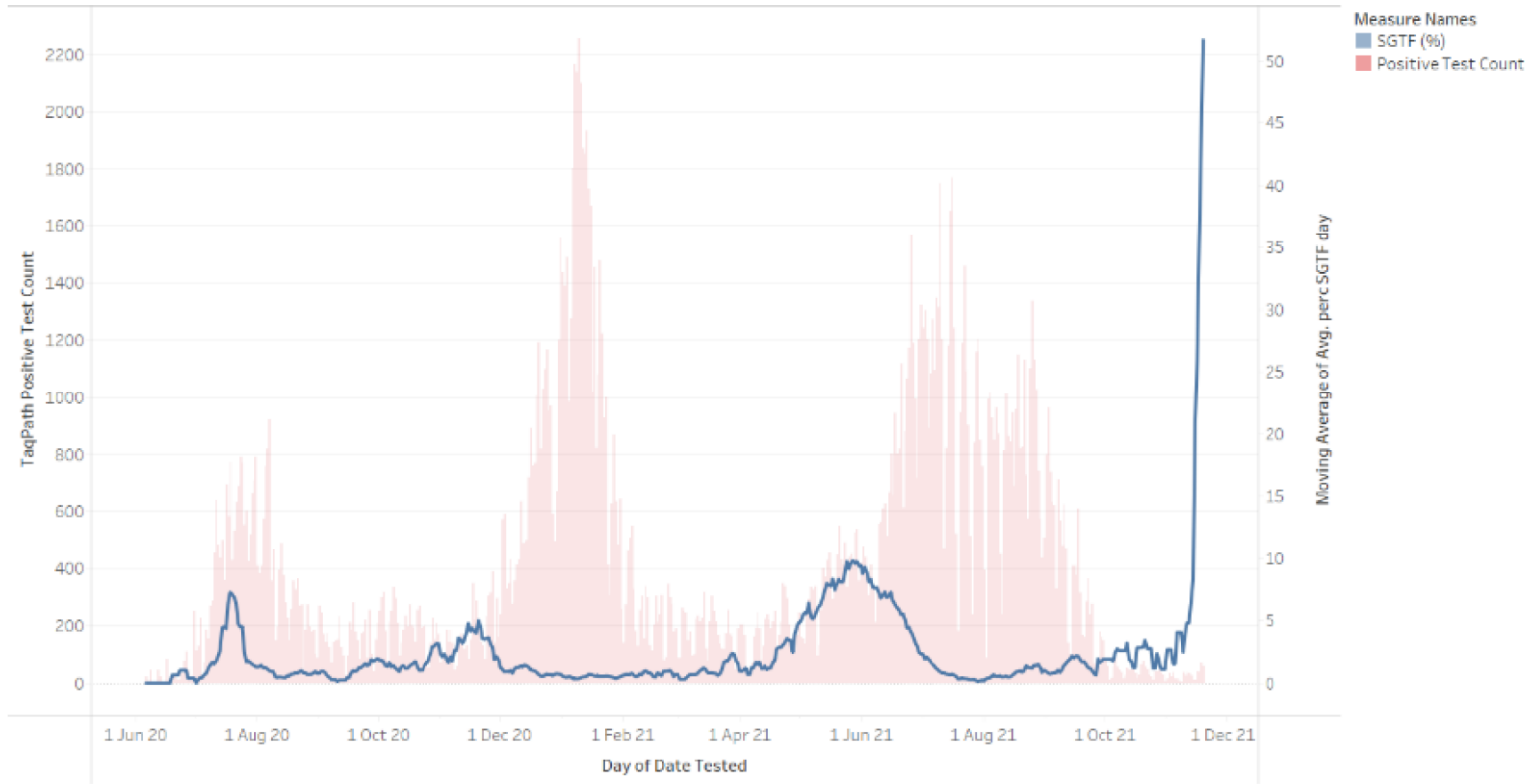
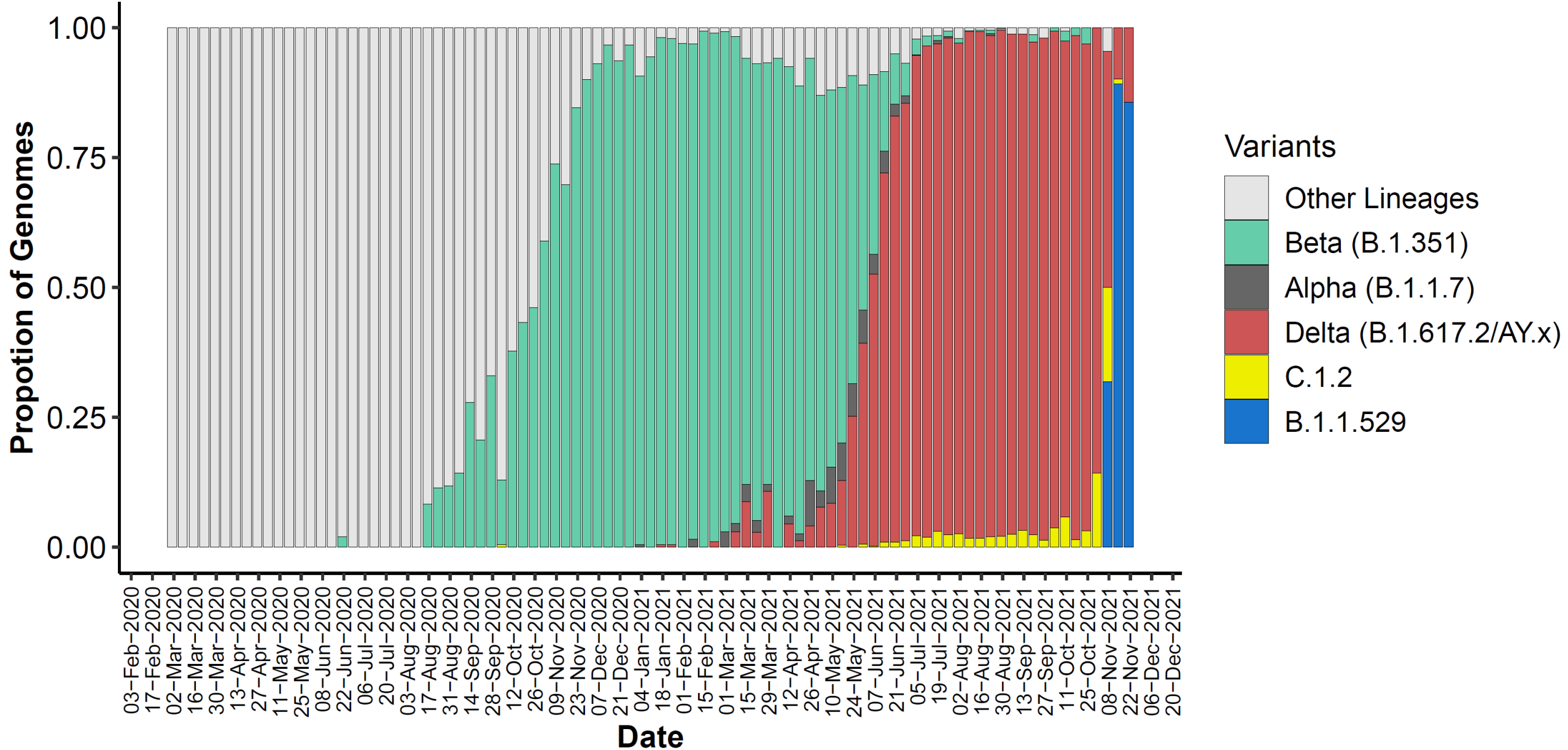


Figure 9: S-gene dropout (%) of cases with high VL (Ct value<30 for ORF or N gene). The red bars are the number of tests reporting the presence of SARS-CoV-2 (daily) on the TaqPath assay. The solid blue line is the moving median of S-gene dropout (%).

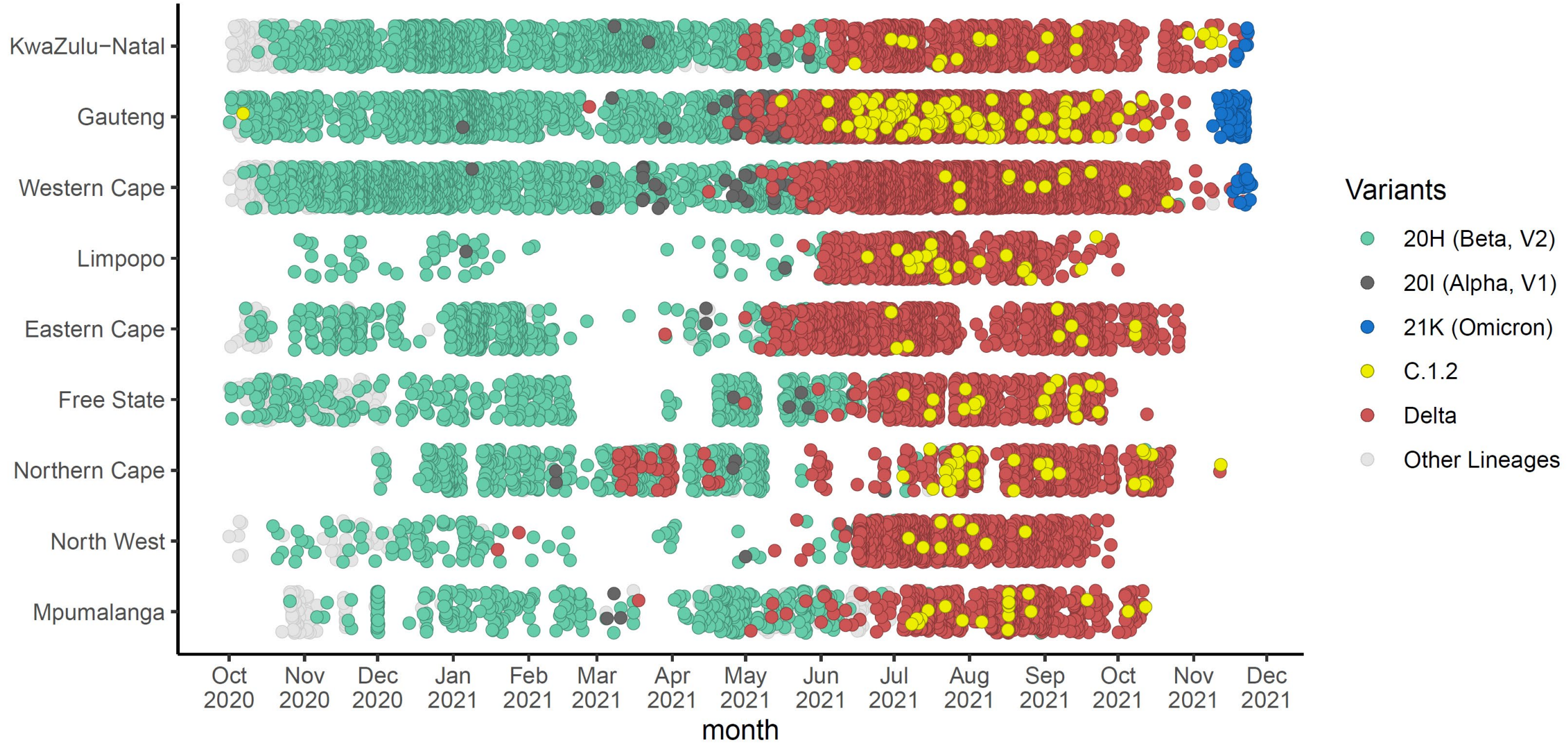
*Current (end of Nov '21) dramatically increasing trend in the proportion of SGTF (Ct value<30 for ORF or N gene)

- Variant can be detected presumptively by qPCR assay (before whole genome sequencing)
- New increase in S-gene dropout noted by NHLS and private labs very recently - from mid-November
- Now rapidly increasing in most provinces

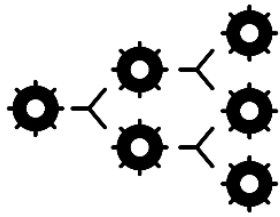
Omicron rapidly becoming dominant variant



Omicron rapidly becoming dominant variant



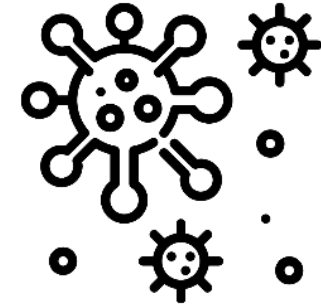
Work underway to understand impact



Transmissibility



Effect on vaccine protection



Risk of reinfection



Effect on therapeutics



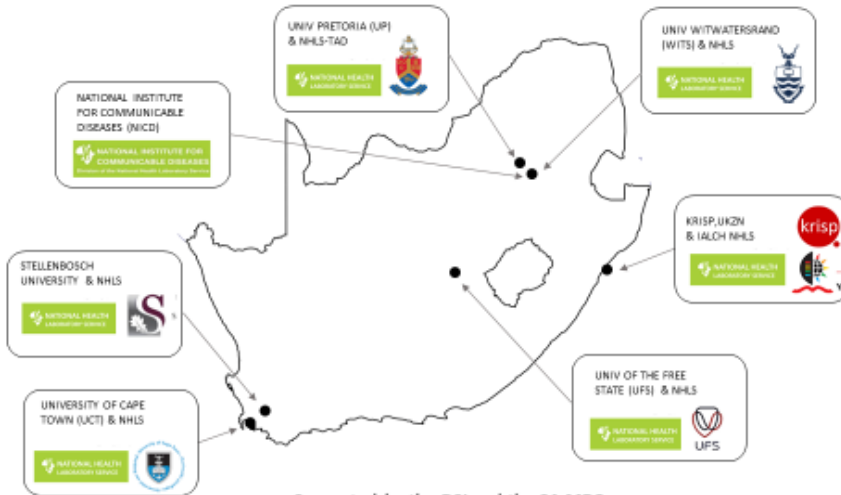
Disease severity



Diagnostics

Summary

- Epidemiological data suggest **sustained increase in COVID-19 incidence** initially across Gauteng, and now across most provinces
- New variant (**Omicron**, B.1.1.529) detected in multiple samples from multiple locations and PCR signal suggests already widespread across the country
- Mutation profile and epidemiological picture suggests Omicron is able to get around some of our immune protection (to cause infection) but the protection against severe disease and death from vaccines should be less affected
- **Vaccination remains the critical tool to prevent severe disease and death** and public health and social measures remain critical to slow the spread



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