

National Wastewater Surveillance Programme - COVID-19

Weeks 3 & 4 (Weeks Ending 22 January & 29 January 2023)

Report prepared on 02 February 2023

100%

sites tested in week 2 had SARS-CoV-2 detected (75/75 sites)

70%

NZ population covered by wastewater testing

**Omicron
CH.1.1 (53%)**

Most prevalent variant detected

Nationally, SARS-CoV-2 levels are low and continue to decline. Variant analysis suggests that XBB.1.5 has not yet spread widely in the community.

- Comparing week ending 29 January to week ending 22 January 2023, 20% of sites show an increase in SARS-CoV-2 levels while 46% sites showed a decrease in SARS-CoV-2.
- The main variants detected in wastewater in the week ending 29 January 2023 (week 4) were CH.1.1 (~53%), BA.2.75* (~32%). Minor contributions of BQ.1.1 (~9%), XBB (includes XBB.1.5, ~3%) and XBC (~3%). BA.4/BA.5 not detected in week 4.

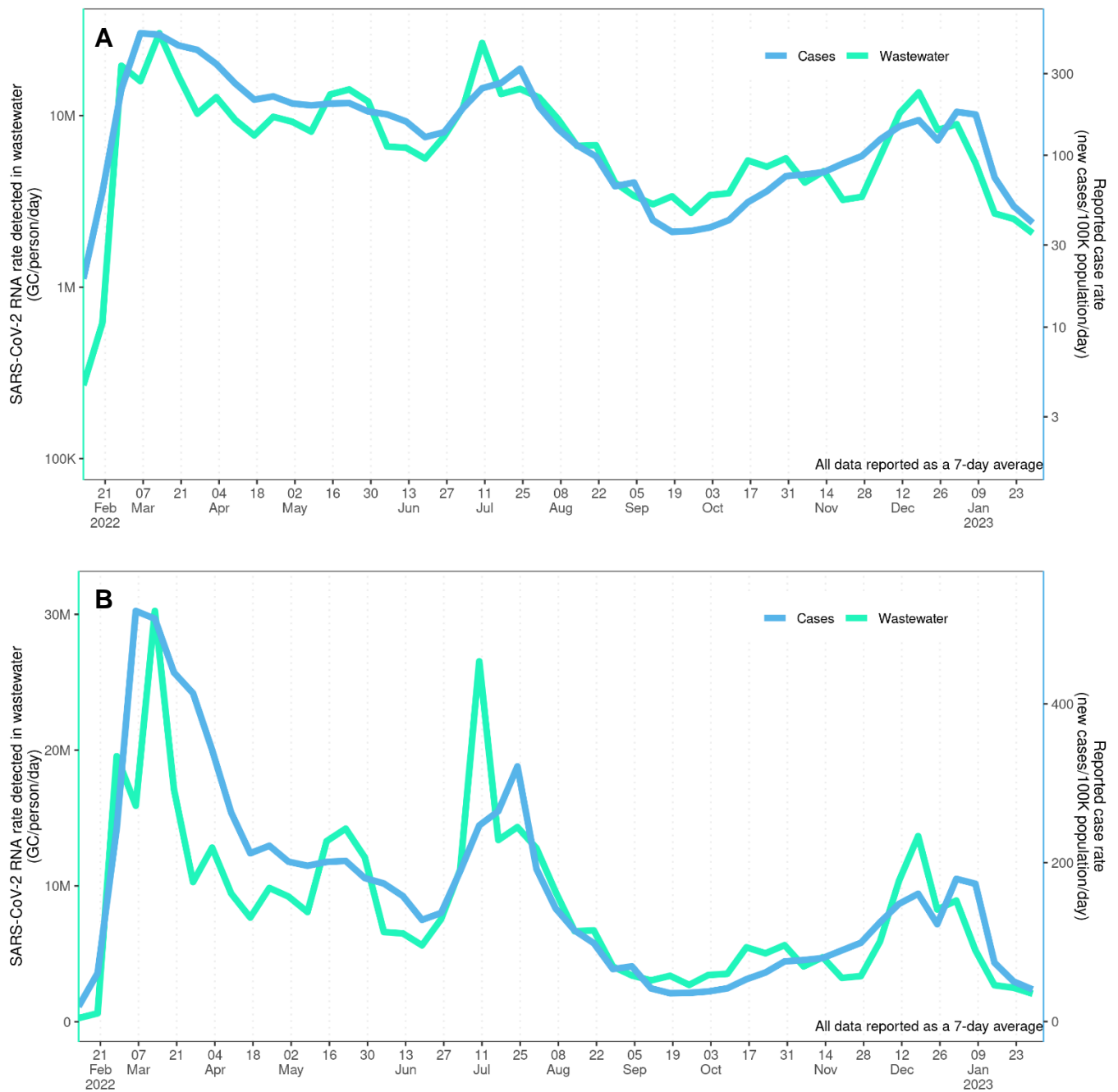


Figure 1. National timeseries of estimated SARS-CoV-2 genome copies (GC) in wastewater rate (GC/person/day, green line) and reported case rate (new cases/100,000 population/day, blue line) on a Log₁₀ scale (A) and linear scale (B). Data reported as 7-day average.

Results for Weeks 3 & 4 (Weeks ending 22 January & 29 January 23)

In the two weeks ending 29 January 2023, 242 samples were collected from 86 locations across New Zealand.

SARS CoV-2 RNA was **detected** in 240/242 (99%) of tested samples from 86/86 (100%) of sites.

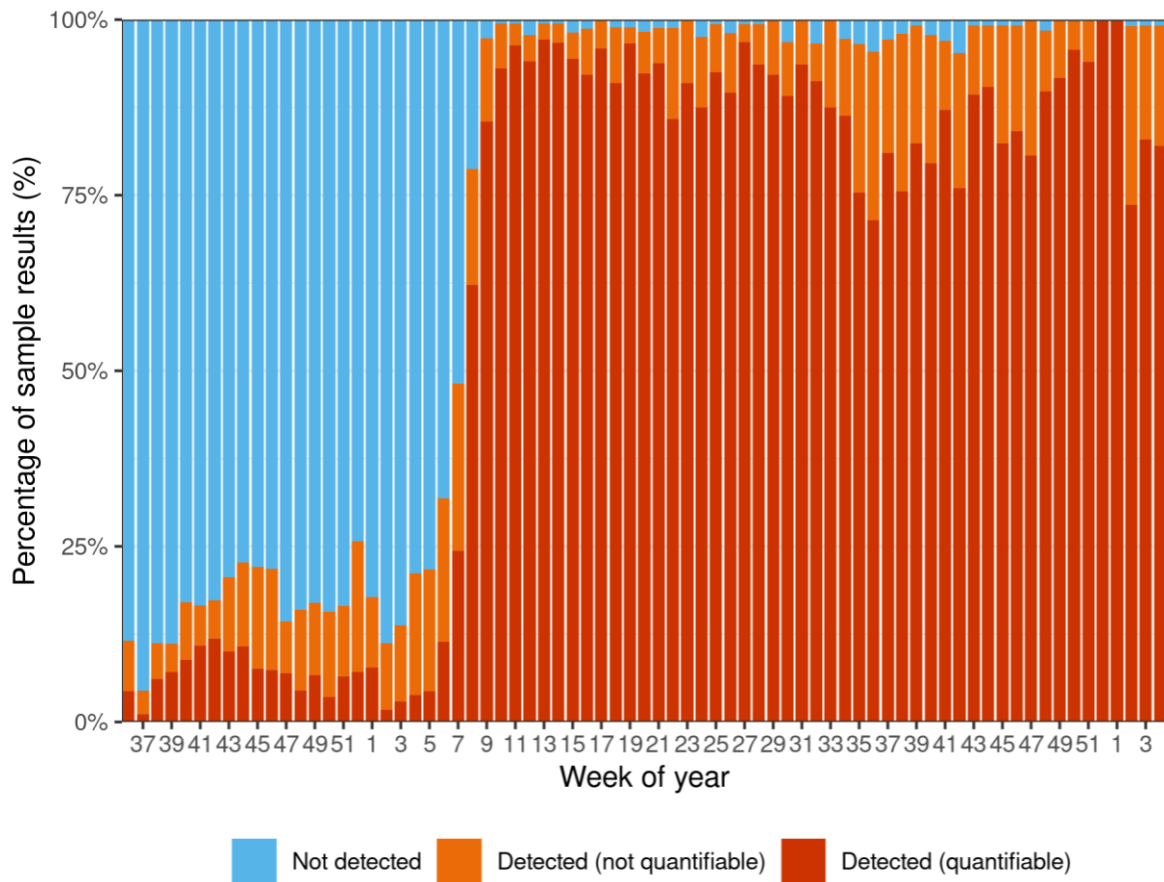


Figure 2. Results for SARS-CoV-2 RNA in wastewater collected across New Zealand.

Regional Trends

Regional summaries (Figure 3) of the wastewater data indicates generally steady (and low) viral levels across all regions except Te Manawa Taki, which shows declining (and low) viral levels in week 4. Note that regional trend analysis for week 52 (2022) and week 1 (2023) was only possible for Auckland Metro, as there were limited samples collected during the holiday period. Viral quantitation for the other regions were therefore not available during this period (denoted by dashed line).

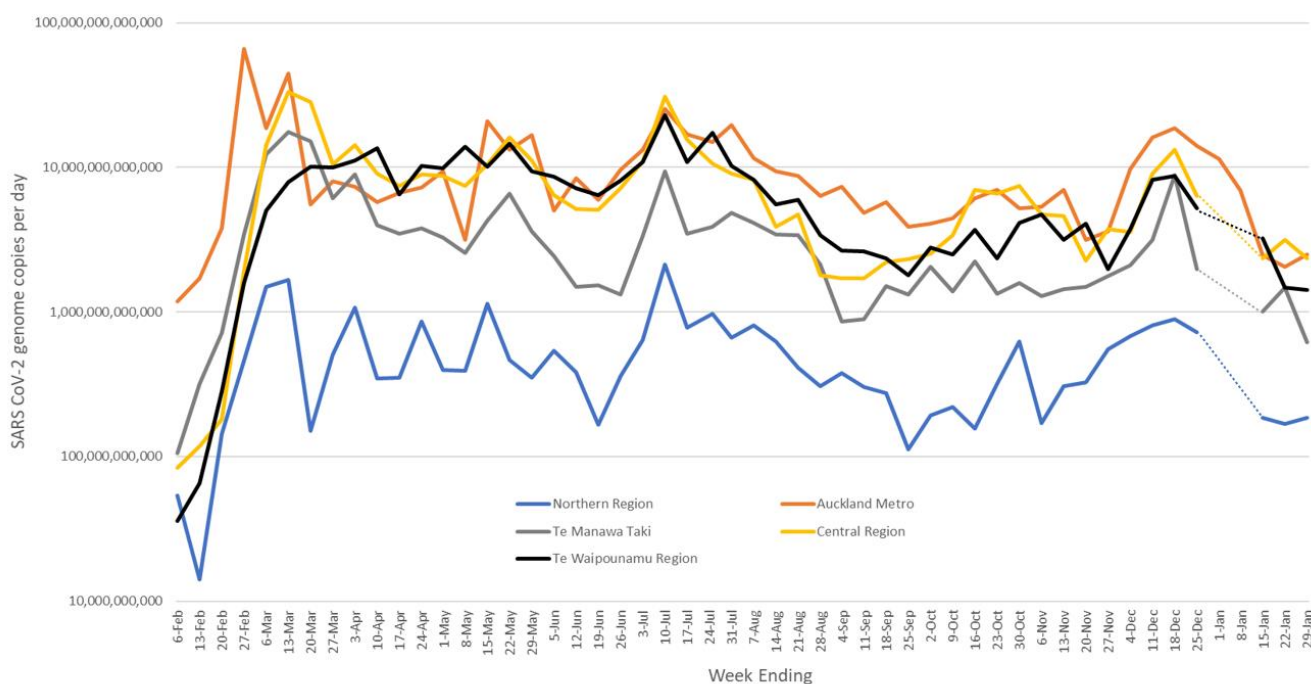


Figure 3. Total SARS-CoV-2 genome copies detected per day in the five Ministry of Health regions.

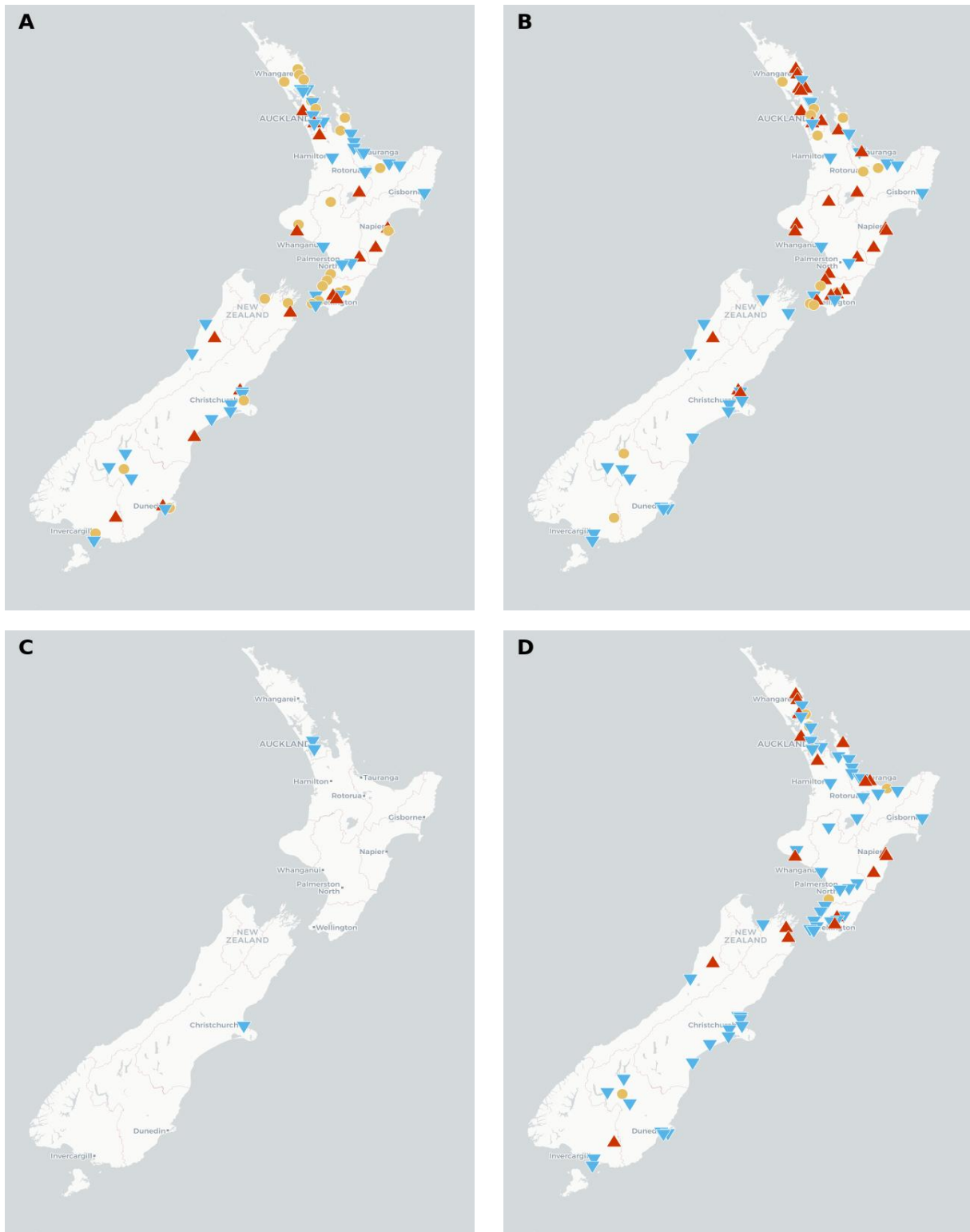


Figure 4. Comparison of SARS-CoV-2 levels for the week ending 29 January 2023, compared to levels measured: **A)** 1 week ago; **B)** 2 weeks ago; **C)** 4 weeks ago; **D)** 12 weeks ago. Only sites with results for both time points are included. When the viral quantity is 30% or more higher this is labelled as increased (red up arrow on map). When the viral quantity is 30% or more lower, this is labelled as decreased (blue down arrow on map). If viral levels have changed less than this in the compared weeks, this is labelled as no change (yellow circle on map). Interactive map of weekly results available publicly at <https://www.poops.nz/>

Note that due to limited sampling over holiday period, only Auckland metro and Christchurch sites have data plotted in Figure 4C.

Wastewater Variant Analysis

In collaboration with Wilderlab, ESR generated the variant analysis results from sentinel sites in week 3 (ending 22 January 2023) and week 4 (ending 29 January 2023). Note that the generally low viral levels in wastewater in weeks 3 and 4 mean that variant detection may be less reliable.

Wastewater variant analysis is based on sequencing a short fragment of the spike gene and therefore provides less resolution than WGS from clinical cases. As such, some specific lineages cannot be distinguished from each other, and are reported as variant groups. The following variants/groups are reported: BA.4/BA.5, BA.2.75* (includes BA.2.75/XBF/BR.2 subvariants), CH.1.1, BQ.1.1, XBB (includes XBB.1.5) and XBC.

Consistent with the WGS of clinical cases, the **CH.1.1 subvariant** will now be reported separately from other BA.2.75* subvariants.

CH.1.1 was the most widespread and common variant in wastewater in weeks 3 and 4, being detected at 16/20 and 17/19 sites respectively, and comprising ~49% (week 3) to ~53% (week 4) of sequencing reads nationally. Other subvariants in the BA.2.75* group (includes BM.4, BR.2, XBF and BA.2.75) accounted for another ~36% (week 3) to ~32% (week 4) of sequencing reads nationally, being detected at 16/20 (week 3) and 14/19 (week 4) sites. Thus, as a whole, the BA.2.75* constellation represented ~84% of sequencing reads nationally in both weeks.

The BA.4/BA.5 variant group (includes **BF.7**) continued to decline, being detected only in Queenstown wastewater in week 3 (accounting for only ~0.3% of sequences nationally) and not being detected at any site in week 4.

Levels of BQ.1.1 in wastewater at the start of 2023 have remained steady: ~8-9% of reads nationally in weeks 3 and 4. However, locations where this variant was detected varied somewhat between weeks 3 and 4 (Figure 5).

The XBB variant (includes XBB.1.5) accounted for ~2-3% of reads nationally in weeks 3 and 4 (~3% in week 2). The wastewater assay cannot distinguish XBB.1.5 from other XBB variants. XBB detections remain steady and at low levels, suggesting that XBB.1.5 has not yet spread widely in the community.

The XBC variant also remains at relatively low levels. In week 3, it accounted for ~6% of sequence reads and ~3% of reads in week 4 (~7% in week 2).

Due to the increasing complexity of variants in the population, each at relatively low levels, the current approach for sequencing wastewater samples needs to be more precise to report percentages for each variant at the sentinel site level. Instead, the presence of each lineage will currently be reported. ESR is actively testing and developing methods to address the current uncertainty and increase the resolution to identify variants in wastewater.

	Week 3						Week 4					
	BA.4/BA.5	BA.2.75*	CH.1.1	BQ.1.1	XBB	XBC	BA.4/BA.5	BA.2.75*	CH.1.1	BQ.1.1	XBB	XBC
Whangarei												
North Shore												
Auckland East												
Auckland Southwest												
Auckland West												
Mt Maunganui												
Tauranga												
Rotorua												
Taupo												
Gisborne												
New Plymouth												
Palmerston North												
Porirua												
Hutt Valley												
Wellington (Moa Point)												
Nelson												
Christchurch												
Queenstown												
Dunedin (Tahuna)												
Dunedin (Mosgiel)												
All Sites (national)	0.3	36	49	8	2	6	0	32	53	9	3	3

Table 1. Data from up to 20 wastewater sentinel sites sampled in week 3 (ending 22 January 2022) and week 4 (ending 29 January 2023) using a S-gene (spike) barcoding assay able to ‘call’ the BA.4/BA.5, the BA2.75* constellation (includes BA.2.75/XBF/BR.2 subvariants), CH.1.1, BQ.1.1, XBB (includes XBB.1.5) and XBC (sub)variants. Coloured box denotes that the variant was detected at that site that week, and white box denotes that the variant was not detected. Grey box denotes site was not sequenced/no sample. Numbers in the bottom row denote the estimated percentage of each variant at the national scale. No sequence reads mapped to variants for Whangarei and Dunedin Tahuna in week 3.

Variant Timeline - National

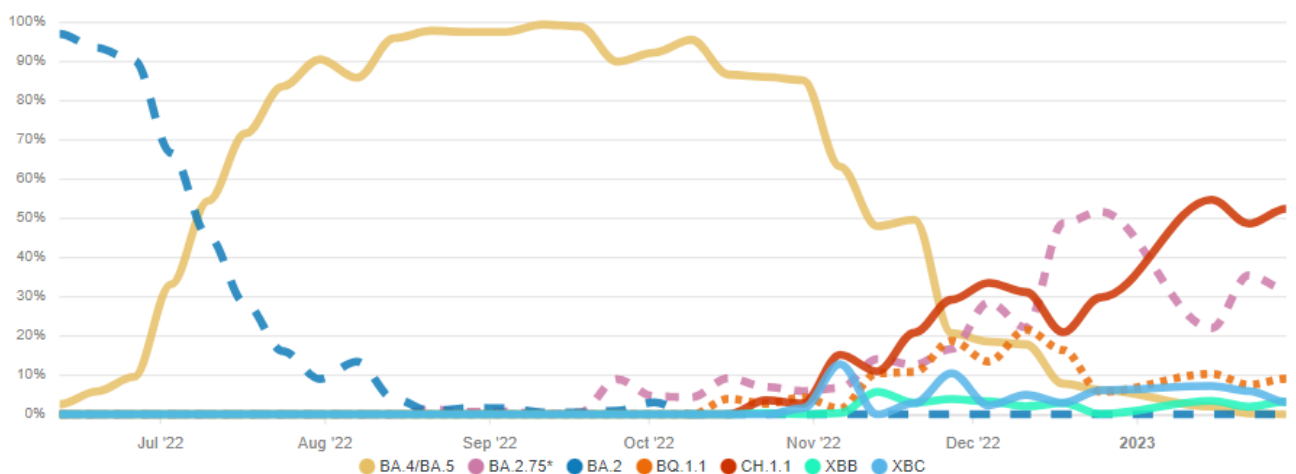
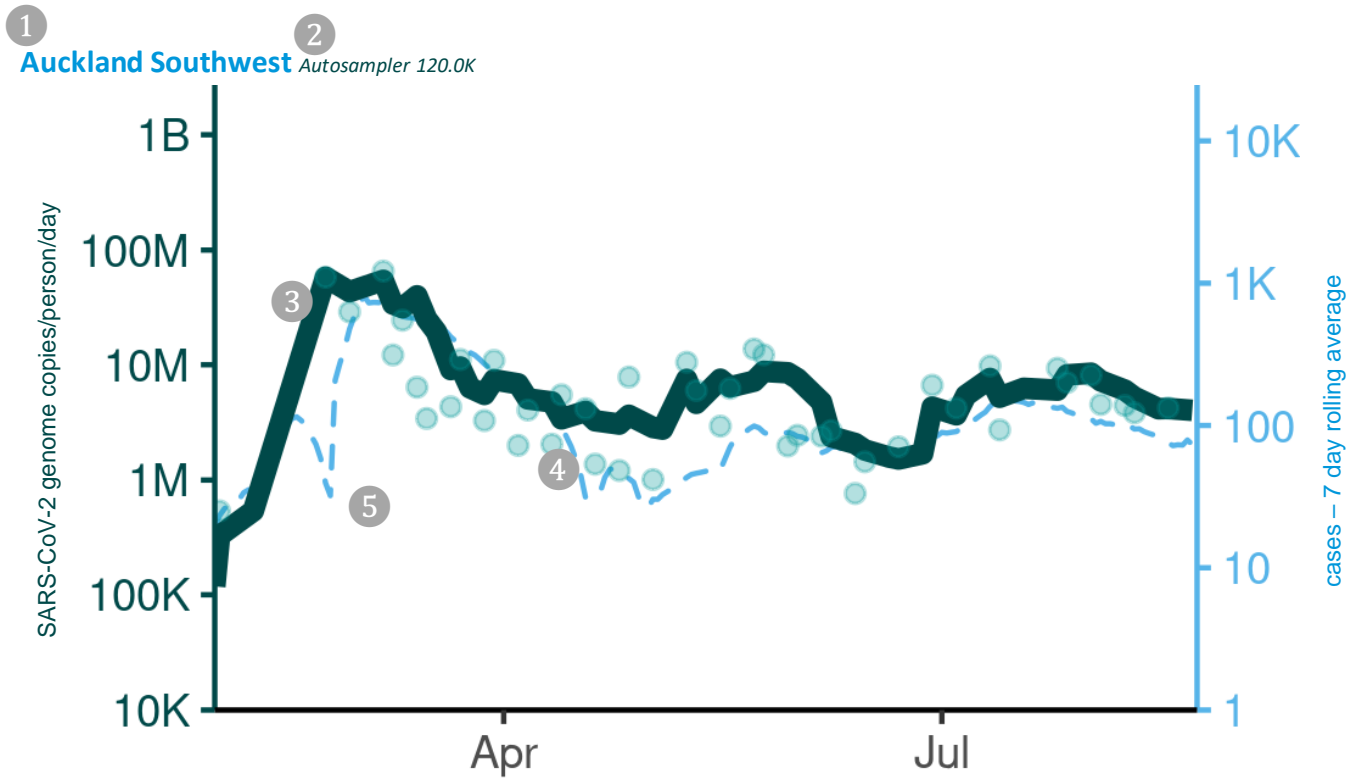


Figure 5 Change in variant prevalence over time at a national scale. Data are collected from up to 20 sentinel sites each week.

Interpreting Sites Graphs

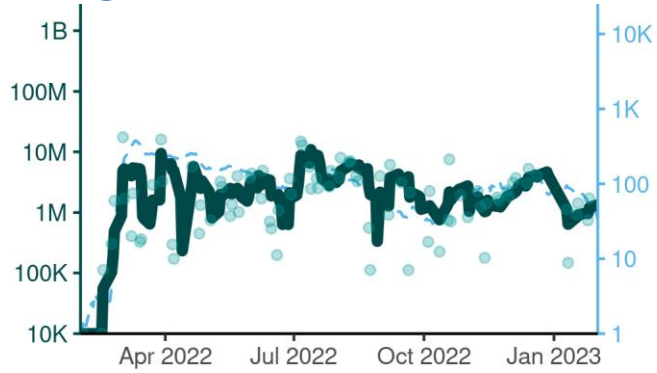


- 1 Site Name
- 2 Sample collection method and population. Results based on autosampler may be more representative than grab sample-based results.
- 3 Wastewater results shown as solid line | 14-day average of genome copies/person/day on a \log_{10} scale.
- 4 Individual results samples shown as circles | Rolling 14-day average of genome copies/person/day on a \log_{10} scale.
- 5 Rolling 7-day average of new cases shown as dashed line | New cases reported in a catchment based on reported date of illness on a \log_{10} scale. This data is not available for all sites and subject to change.

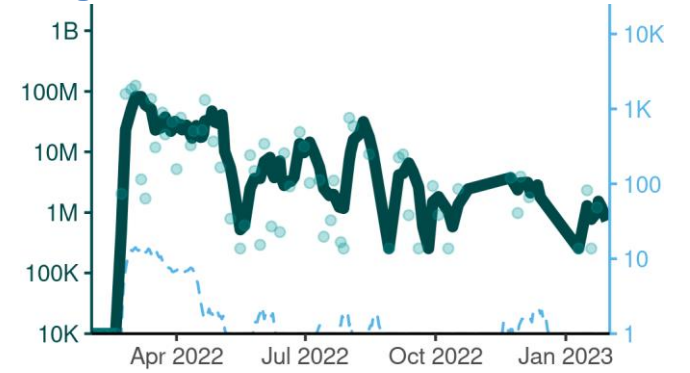
Note: Wastewater and cases data are on a \log_{10} scale. Scales on all graphs have been normalized to cover the same scale on every graph. Care should be taken when interpreting the data.

Northland

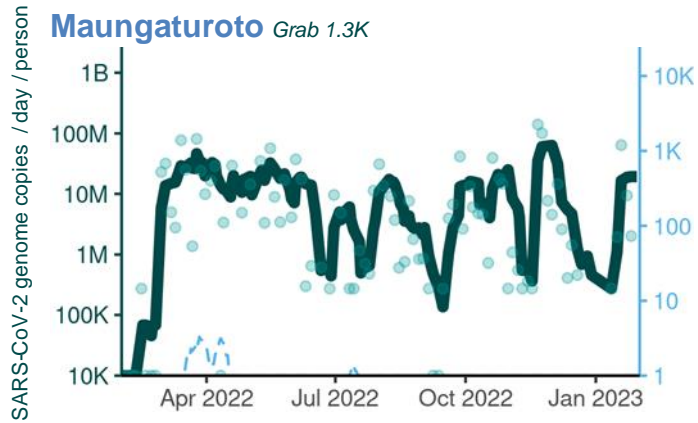
Whangarei Autosampler 65.0K



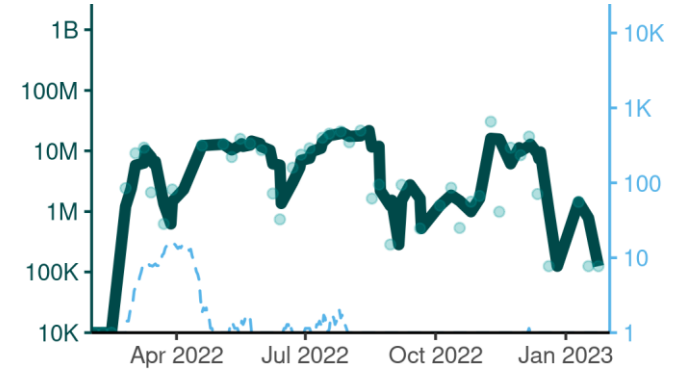
Dargaville Grab 5.0K



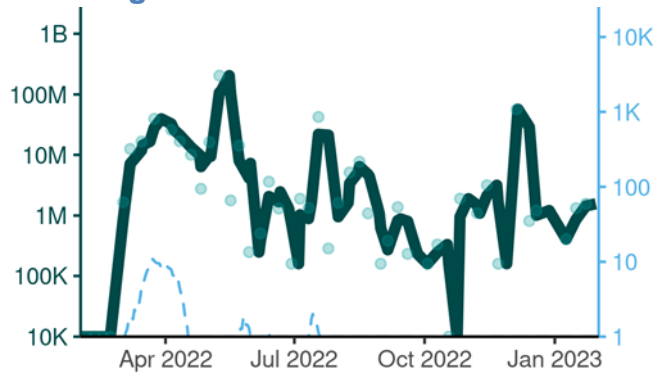
Maungaturoto Grab 1.3K



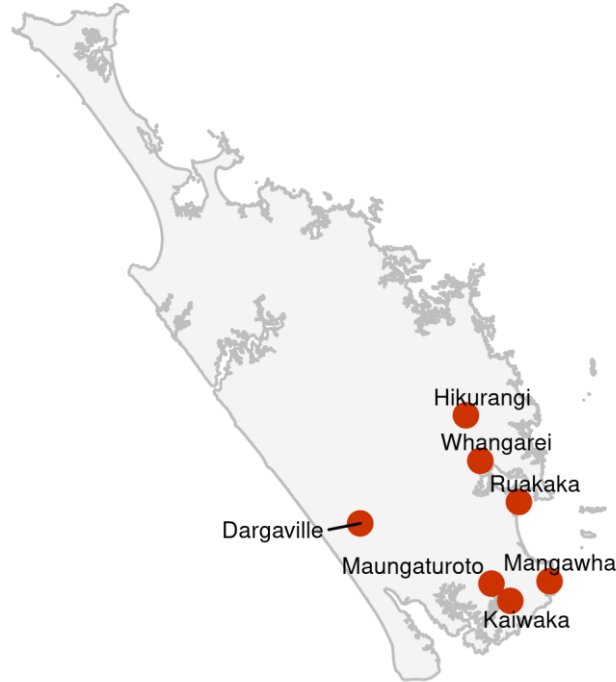
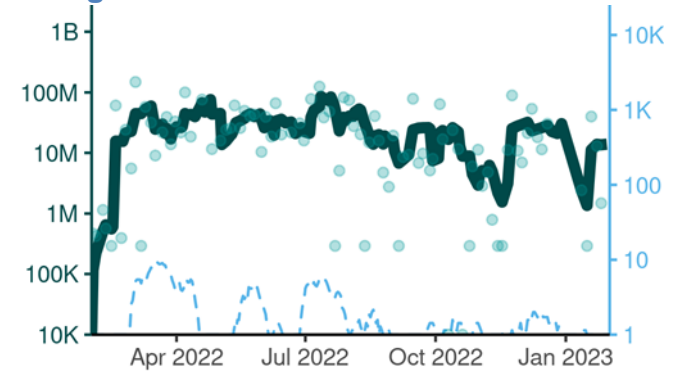
Ruakaka Grab 4.5K



Hikurangi Grab 1.7K



Mangawhai Grab 1.1K

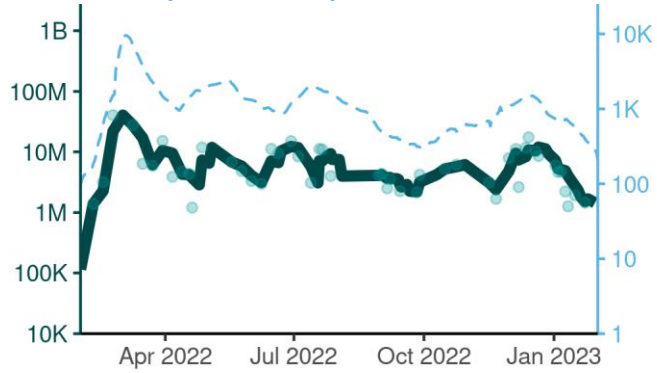


Status ● Detected ● Not detected

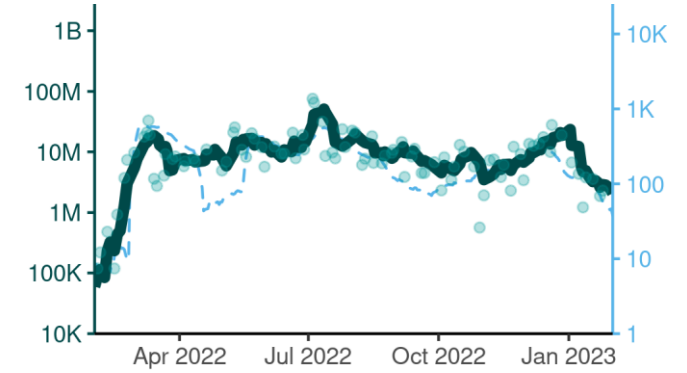
Cases - 7 day rolling average

Auckland

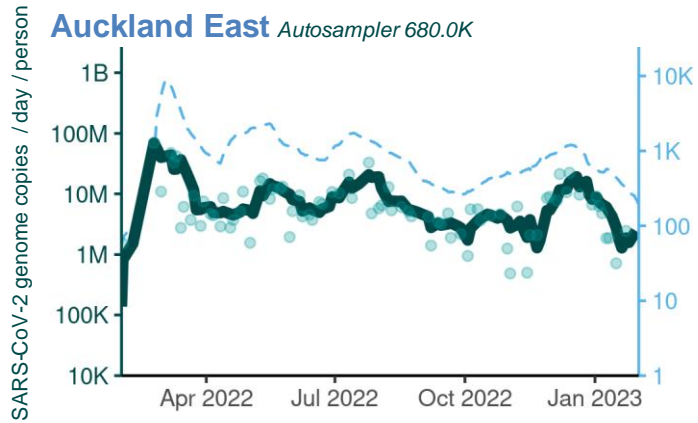
Auckland (Combined) Autosampler 1.1M



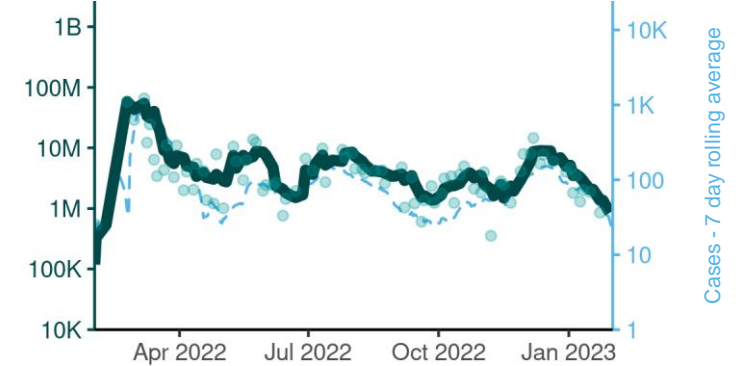
North Shore Autosampler 240.0K



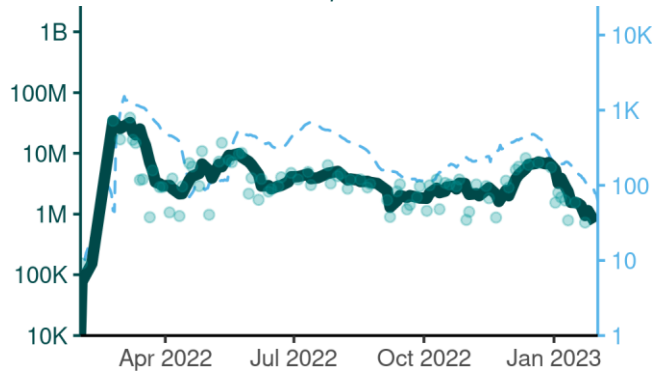
Auckland East Autosampler 680.0K



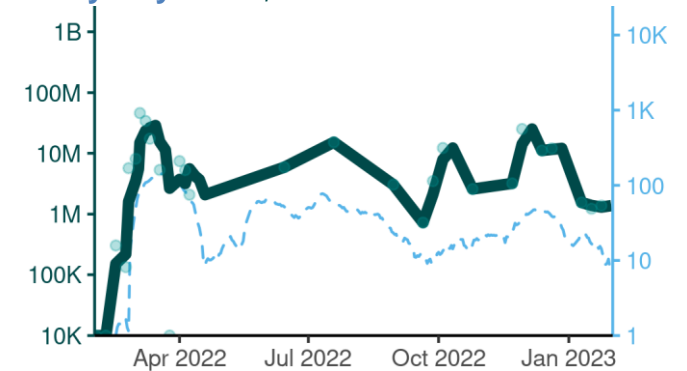
Auckland Southwest Autosampler 120.0K



Auckland West Autosampler 315.0K

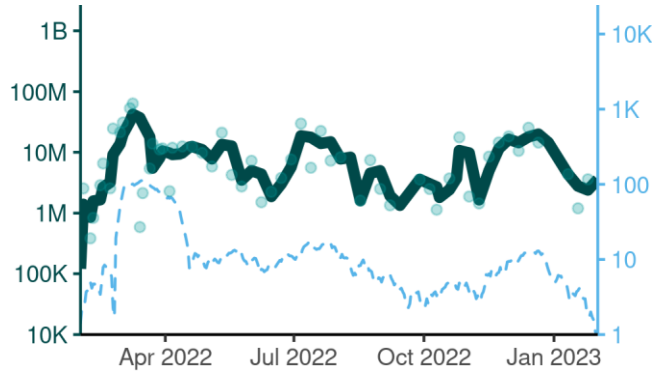


Army Bay Autosampler 42.0K

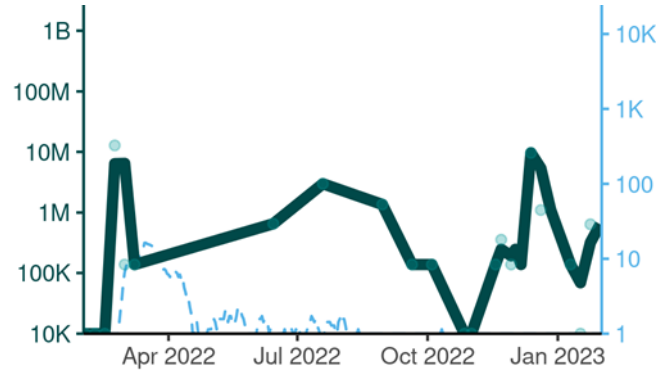


Status ● Detected ● Not detected

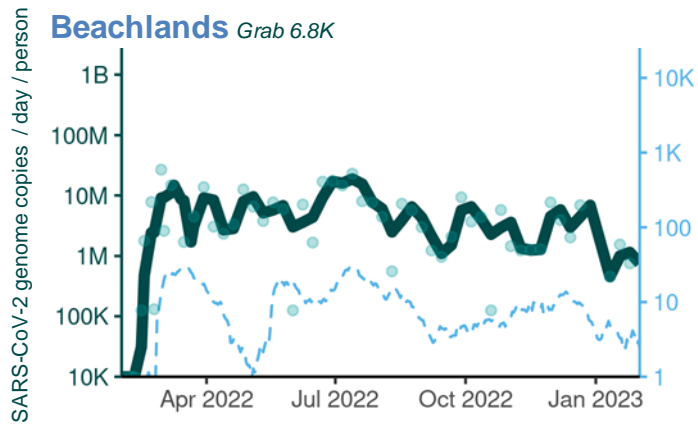
Pukekohe Autosampler 20.9K



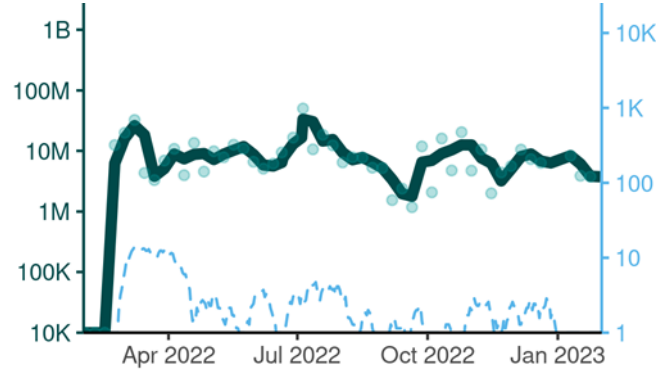
Helensville Autosampler 3.8K



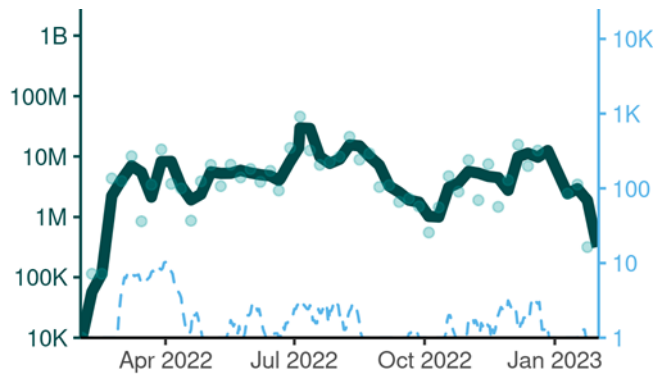
Beachlands Grab 6.8K



Warkworth Autosampler 3.5K



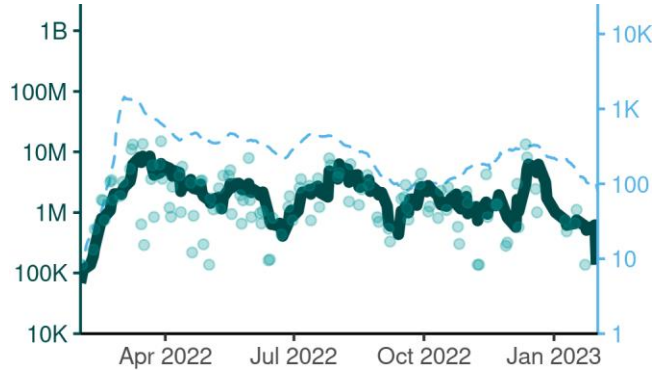
Snells/Algies Autosampler 4.0K



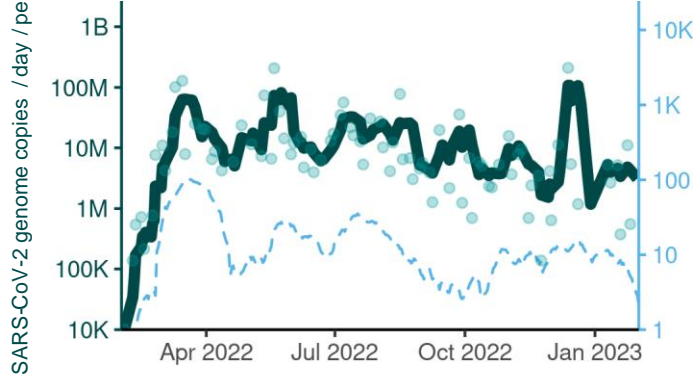
Cases - 7 day rolling average

Waikato

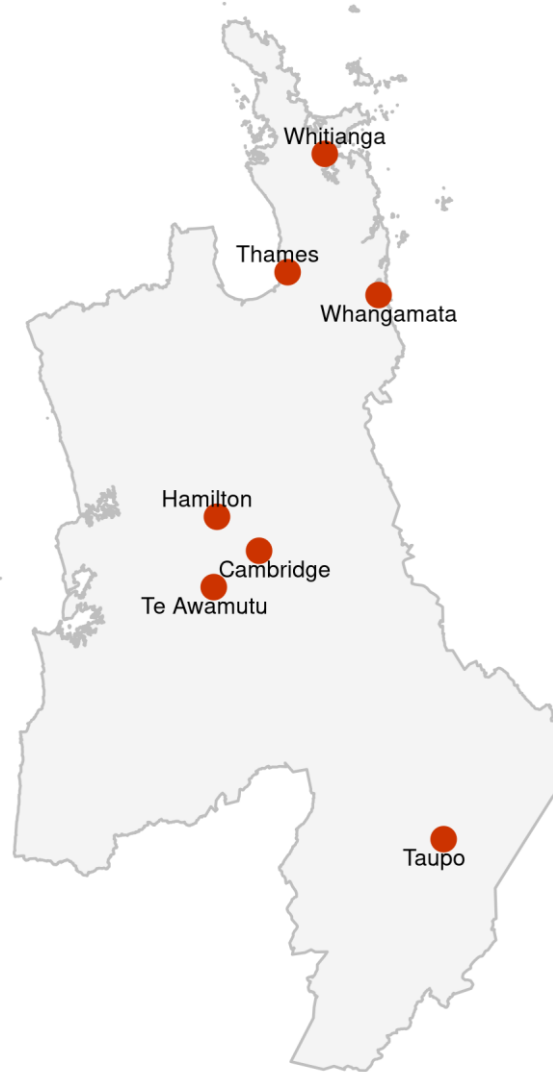
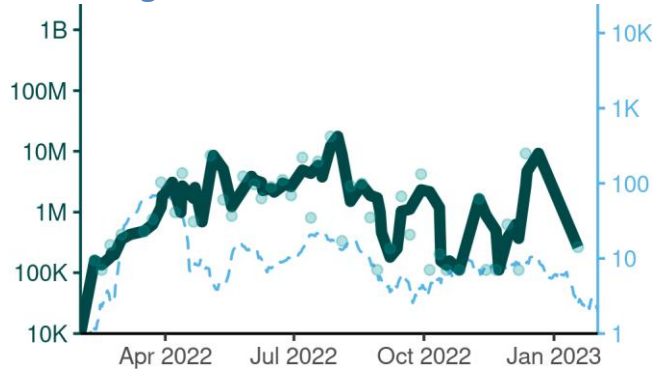
Hamilton Autosampler 169.0K



Taupo Auto/grab 23.0K

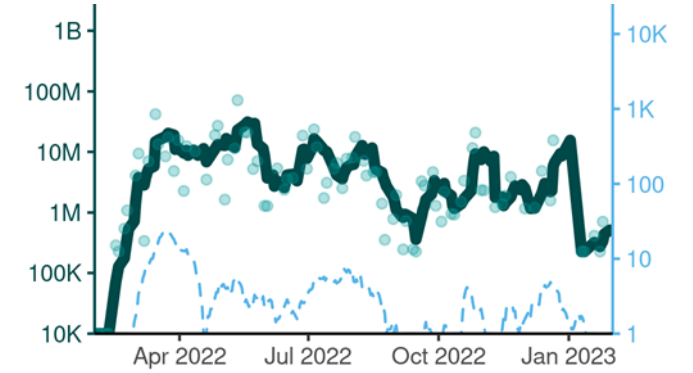


Cambridge Autosampler 20.1K

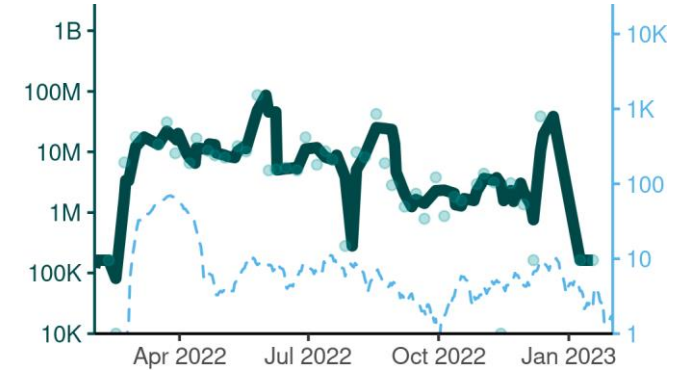


Status ● Detected ● Not detected

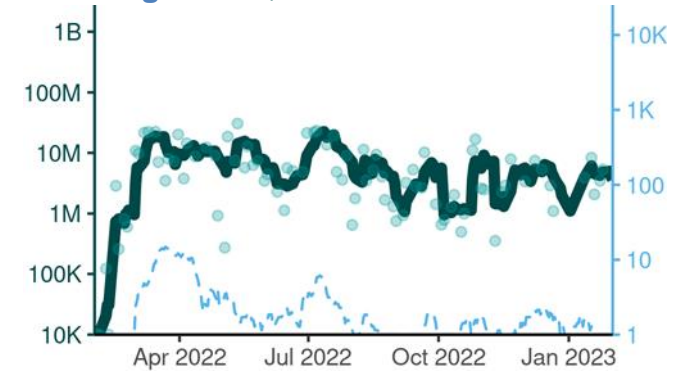
Thames Autosampler 7.5K



Te Awamutu Autosampler 13.1K

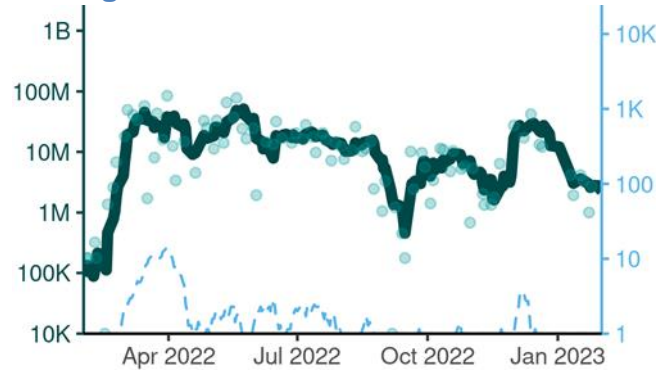


Whitianga Autosampler 6.6K



Cases - 7 day rolling average

Whangamata Autosampler 4.0K

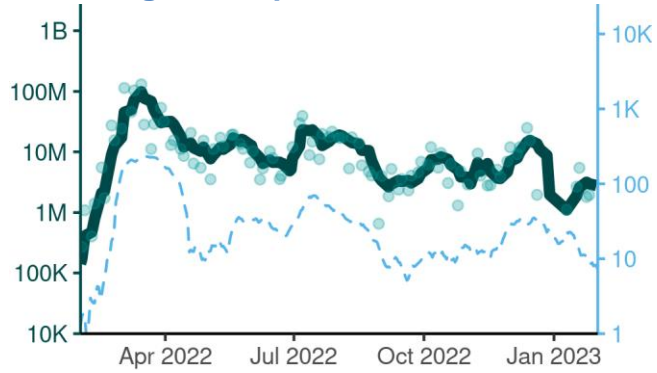


SARS-CoV-2 genome copies / day / person

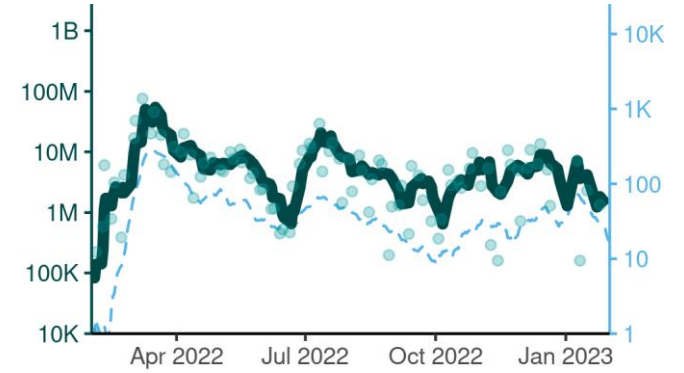
Cases - 7 day rolling average

Bay of Plenty and Gisborne

Mt Maunganui/Papamoa Autosampler 65.0K

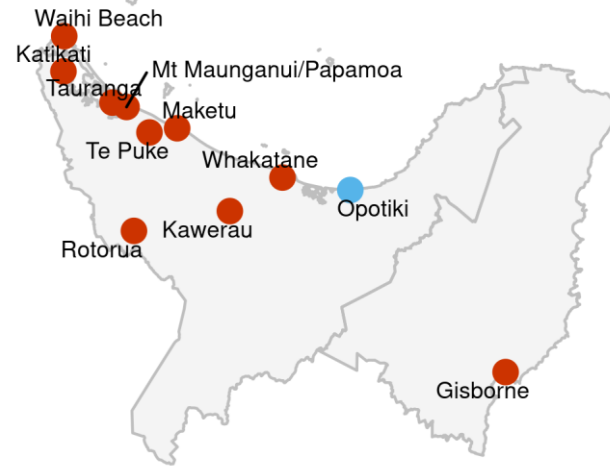
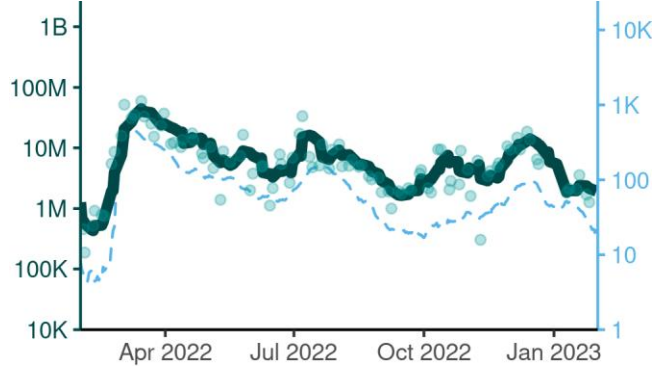


Gisborne Autosampler 37.0K

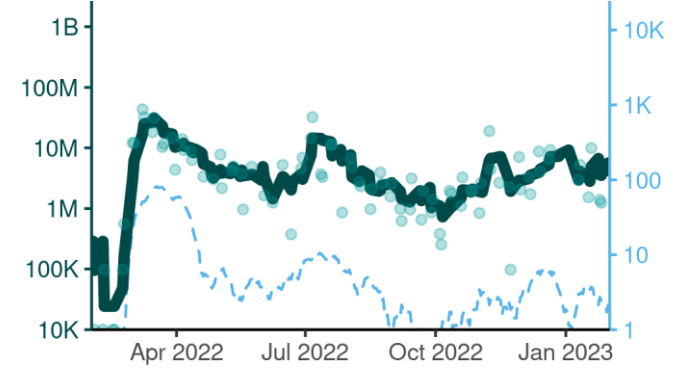


SARS-CoV-2 genome copies / day / person

Rotorua Autosampler 59.0K

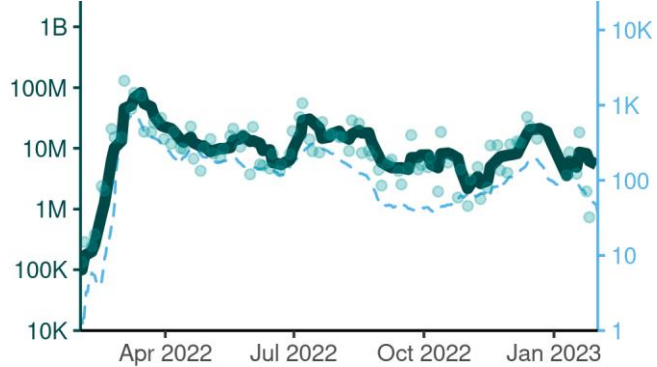


Whakatane Autosampler 21.0K



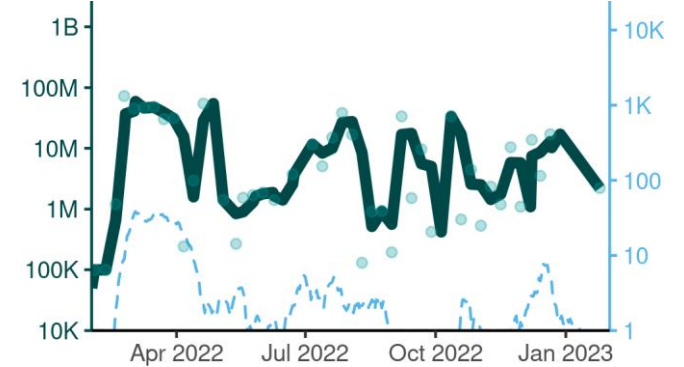
Cases - 7 day rolling average

Tauranga Autosampler 50.0K

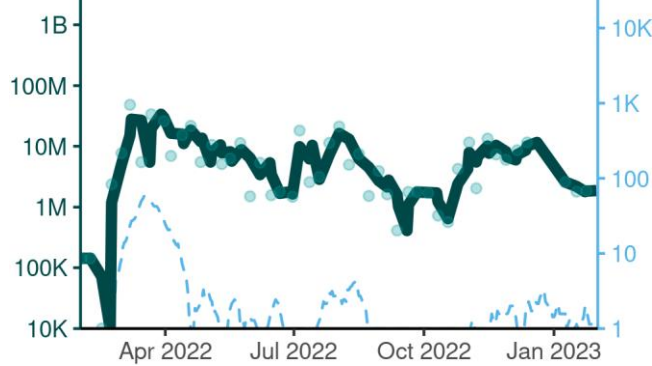


Status ● Detected ● Not detected

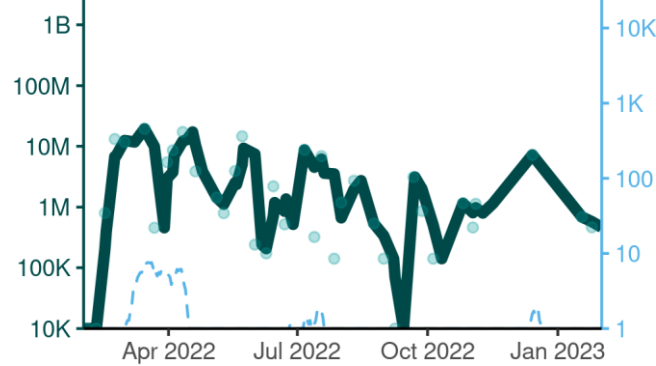
Te Puke Autosampler 9.7K



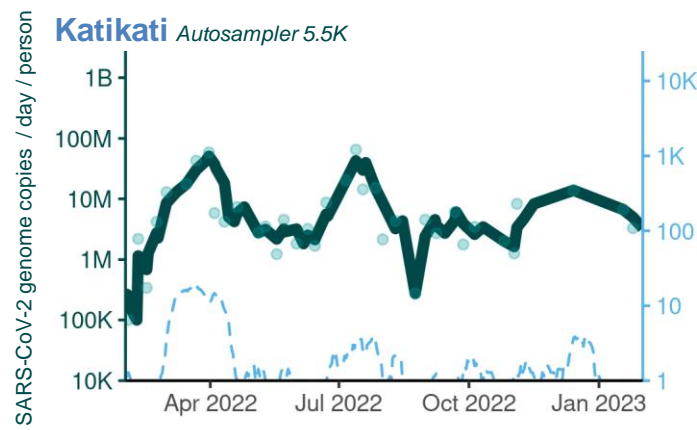
Kawerau Autosampler 7.0K



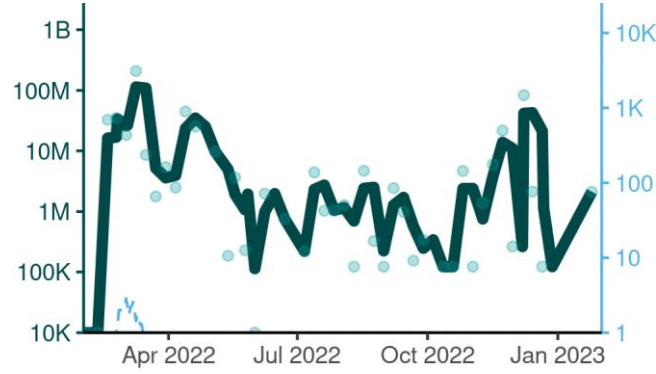
Waihi Beach Autosampler 3.6K



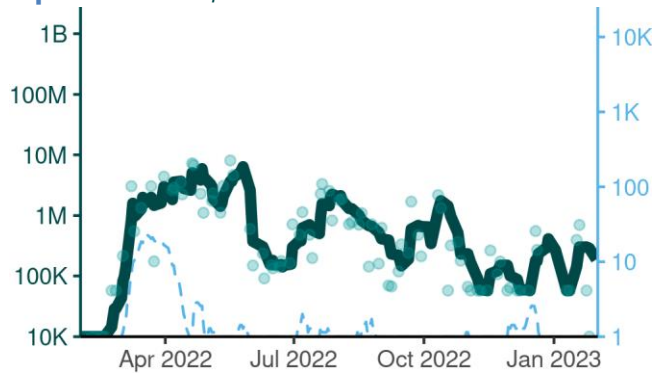
Katikati Autosampler 5.5K



Maketu Autosampler 1.3K



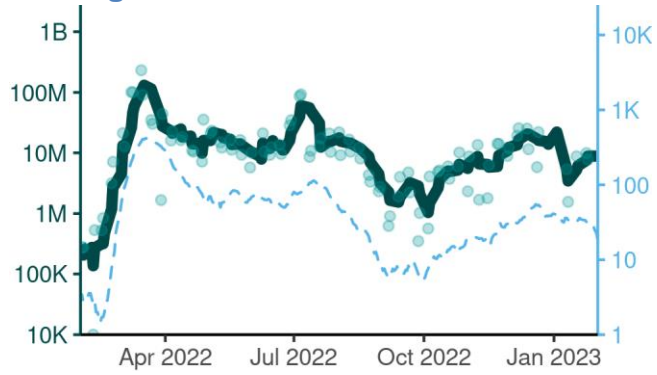
Opotiki Autosampler 3.8K



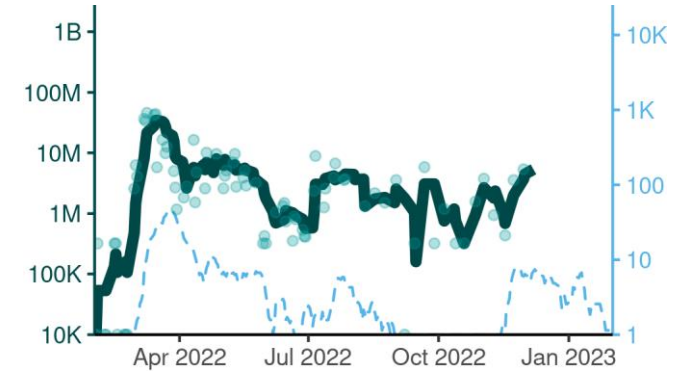
Cases - 7 day rolling average

Hawke's Bay

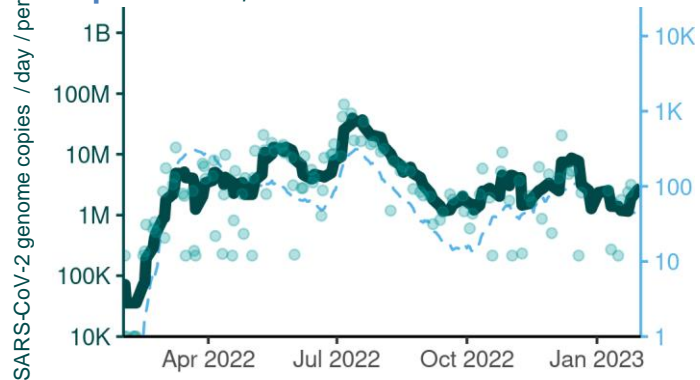
Hastings Autosampler 80.0K



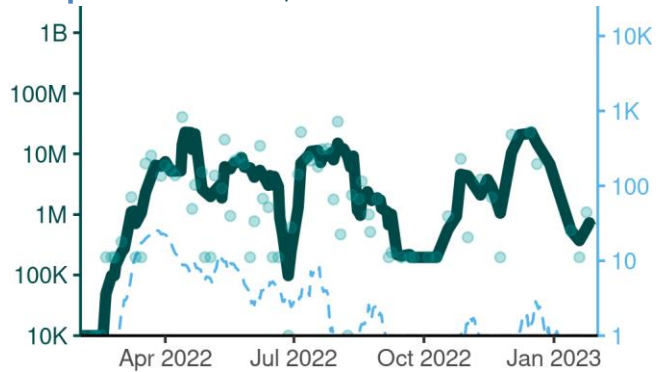
Wairoa Grab 4.4K



Napier Autosampler 55.0K



Waipukurau Autosampler 4.6K

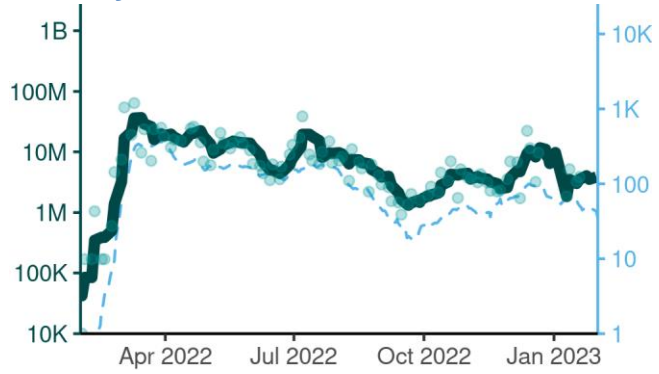


Status ● Detected ● Not detected

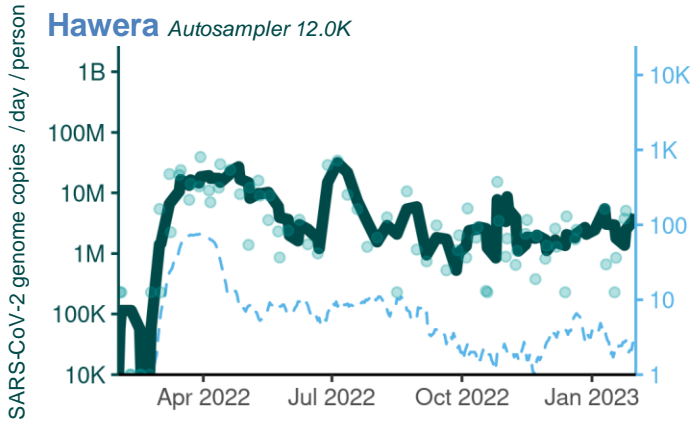
Cases - 7 day rolling average

Taranaki

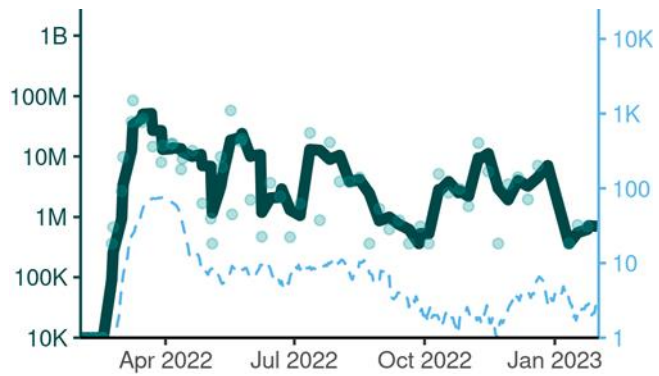
New Plymouth Autosampler 88.0K



Hawera Autosampler 12.0K



Eltham Autosampler 2.0K

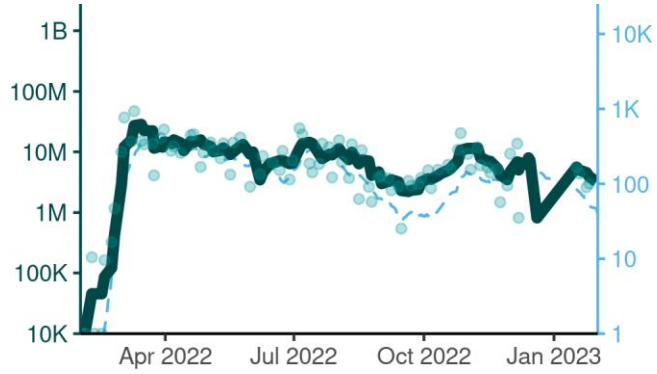


Status ● Detected ● Not detected

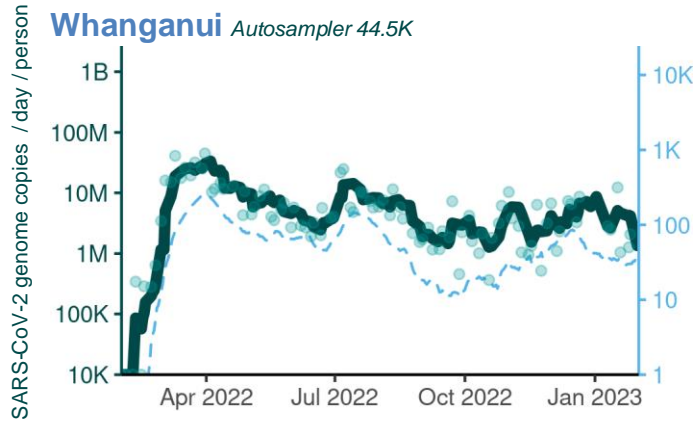
Cases - 7 day rolling average

Manawatu-Whanganui

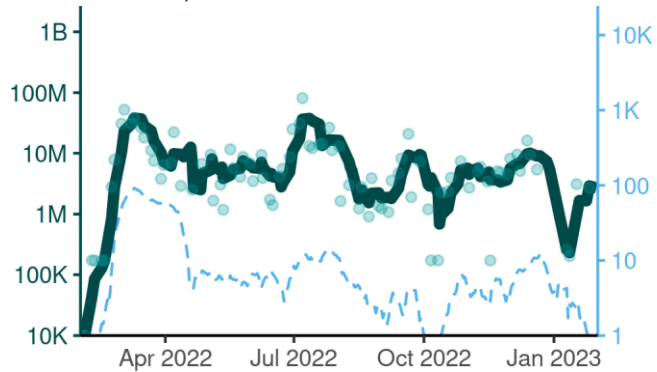
Palmerston North Autosampler 90.0K



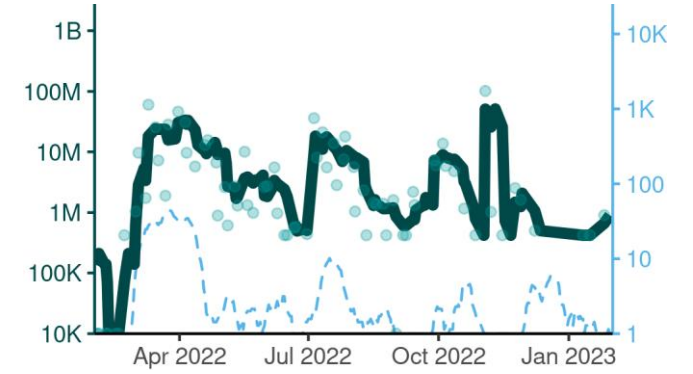
Whanganui Autosampler 44.5K



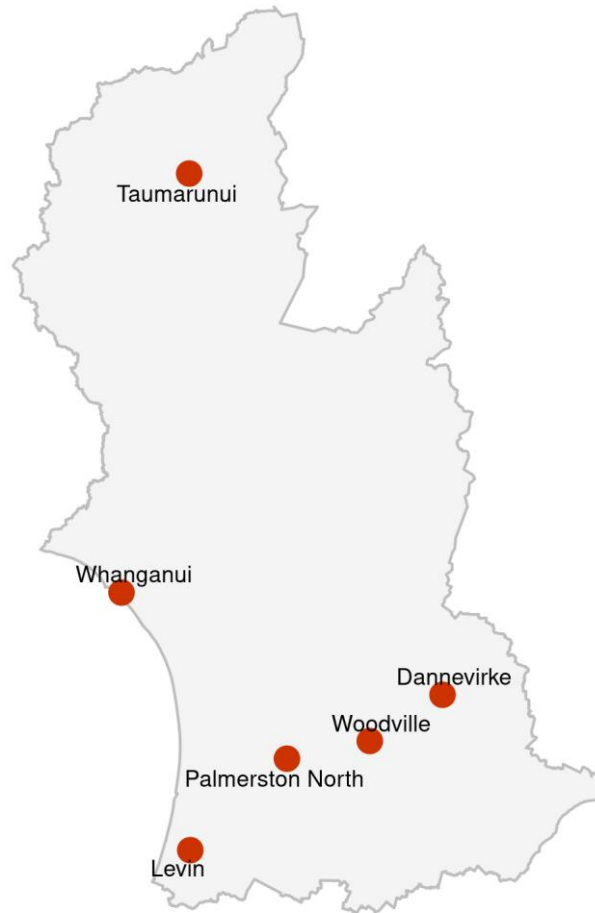
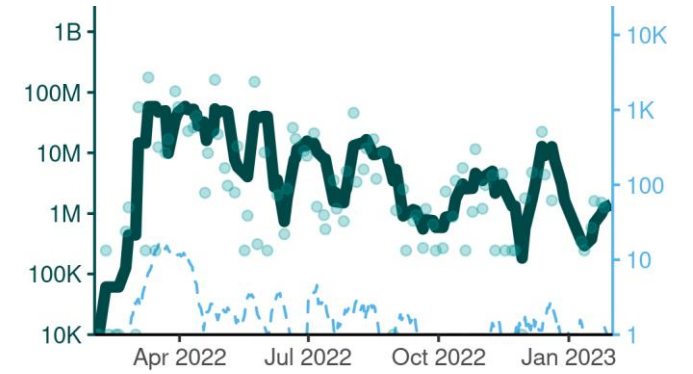
Levin Autosampler 21.2K



Dannevirke Grab 5.7K



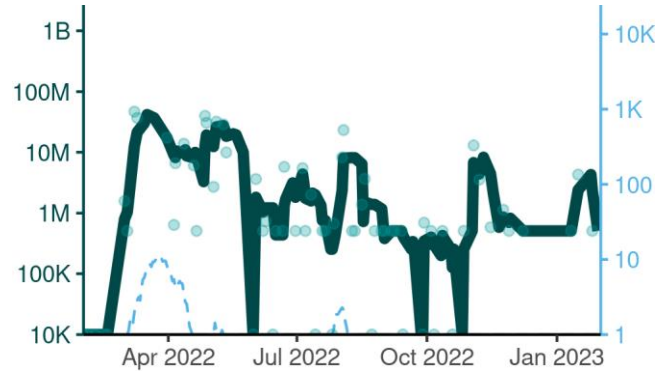
Taumarunui Grab 4.0K



Status ● Detected ● Not detected

Cases - 7 day rolling average

Woodville *Grab 1.7K*

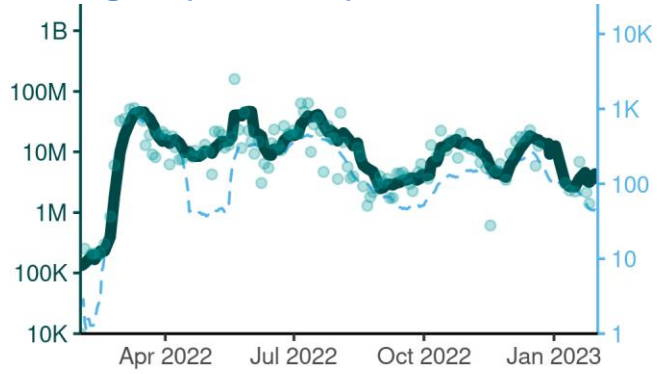


SARS-CoV-2 genome copies / day / person

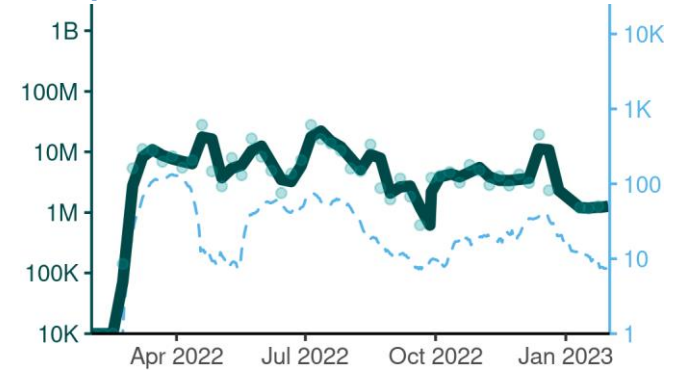
Cases - 7 day rolling average

Wellington

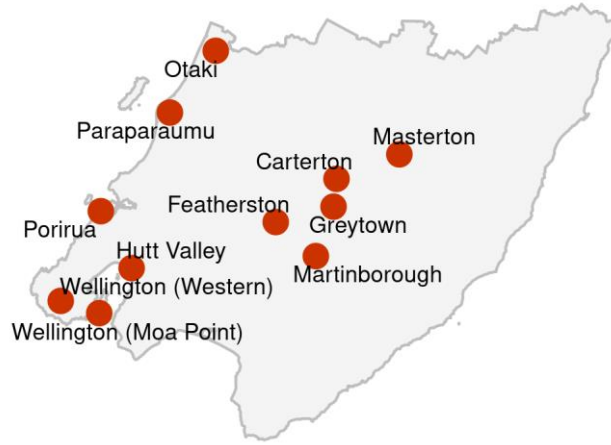
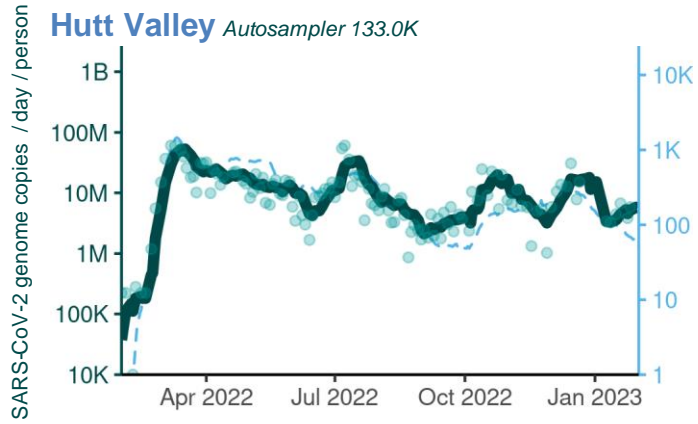
Wellington (Moa Point) Autosampler 168.0K



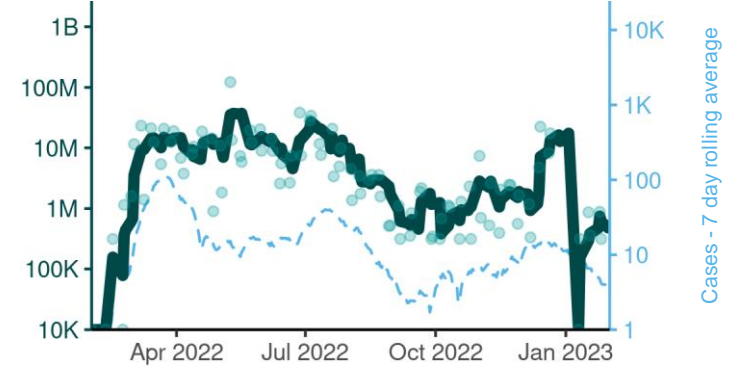
Paraparaumu Autosampler 49.0K



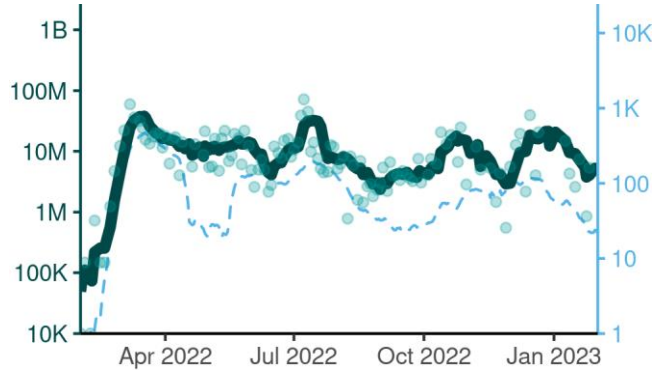
Hutt Valley Autosampler 133.0K



Masterton Auto/grab 20.7K

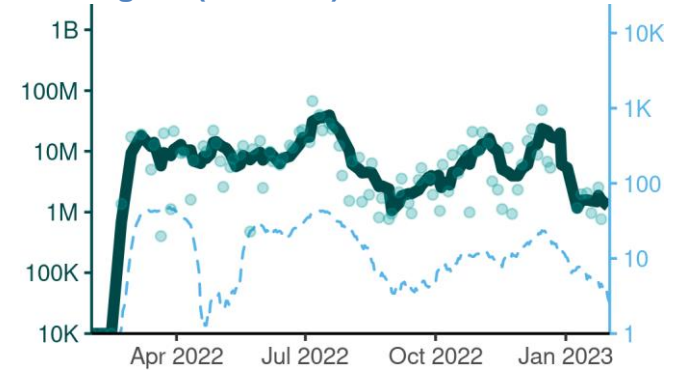


Porirua Autosampler 85.0K

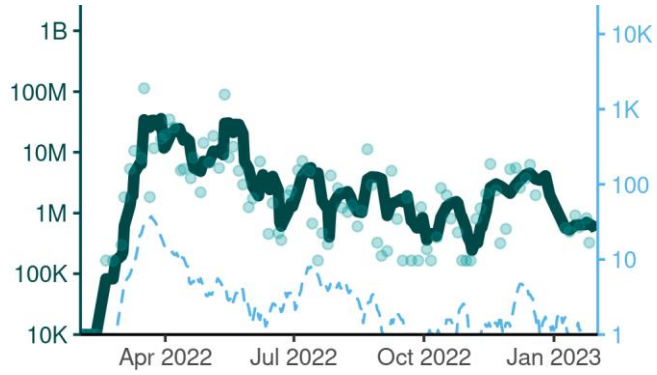


Status ● Detected ● Not detected

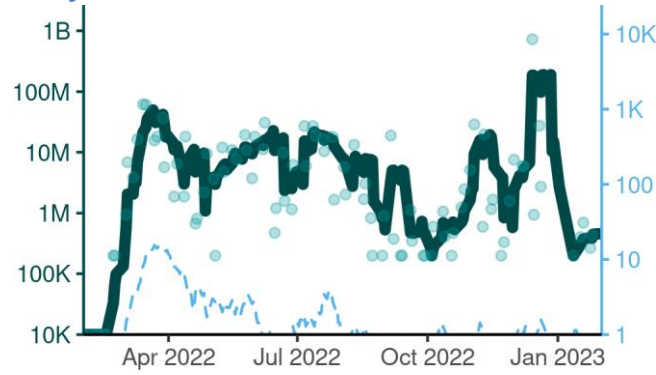
Wellington (Western) Autosampler 14.0K



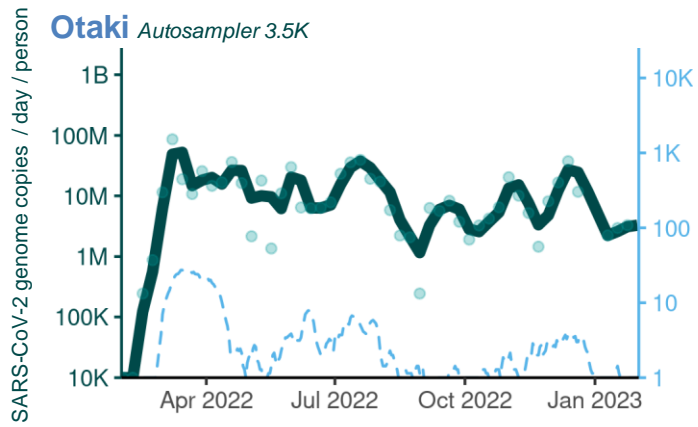
Carterton *Grab 5.8K*



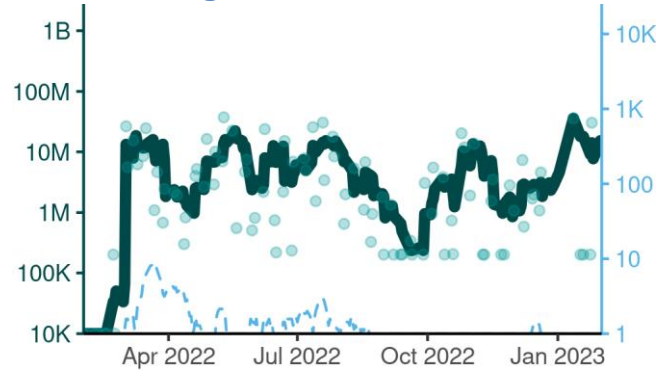
Greytown *Grab 2.4K*



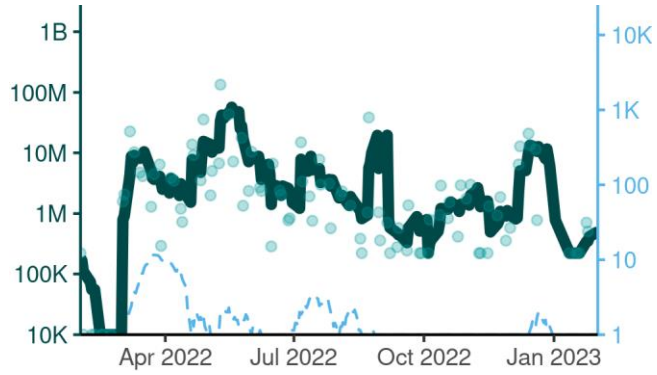
Otaki *Autosampler 3.5K*



Martinborough *Auto/grab 1.6K*

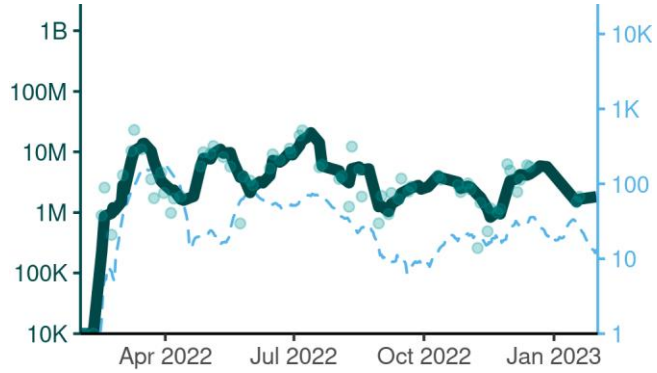


Featherston *Grab 2.5K*

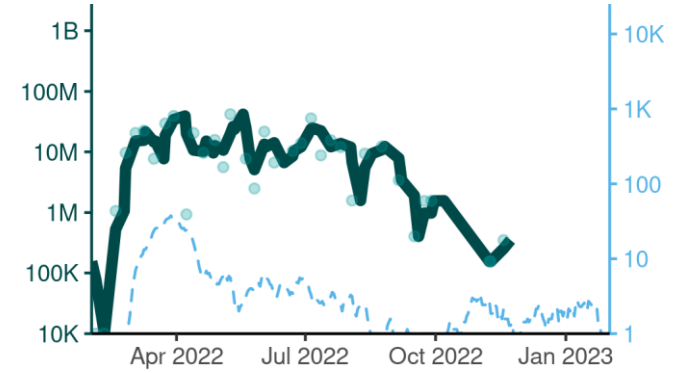


Cases - 7 day rolling average

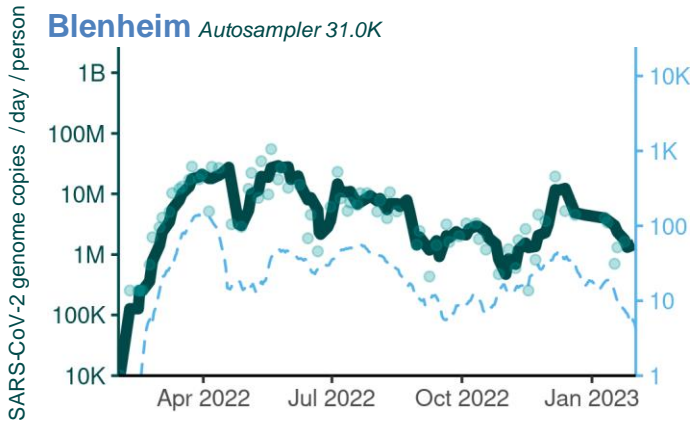
Tasman, Nelson, and Marlborough
Richmond/Nelson South Autosampler 60.0K



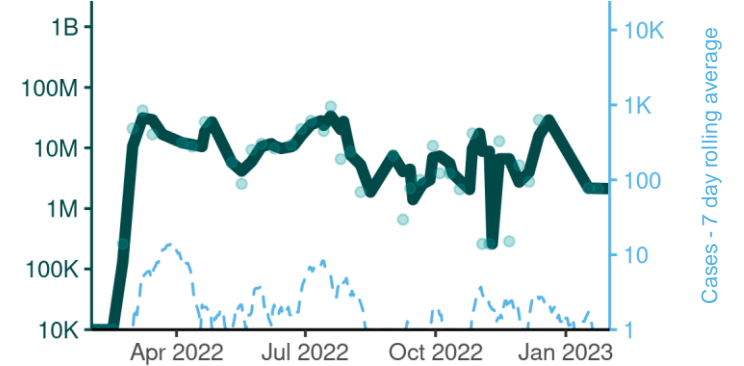
Motueka Autosampler 8.3K



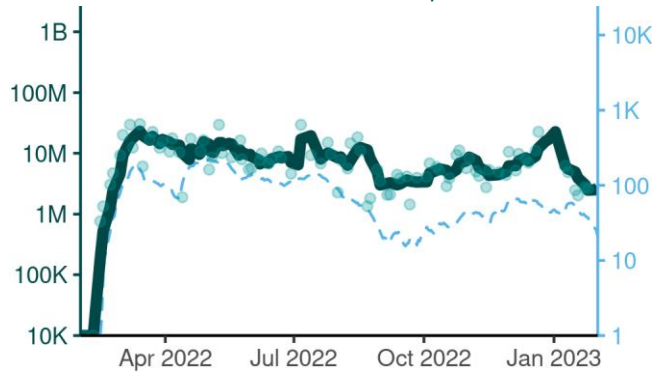
Blenheim Autosampler 31.0K



Picton Autosampler 5.0K



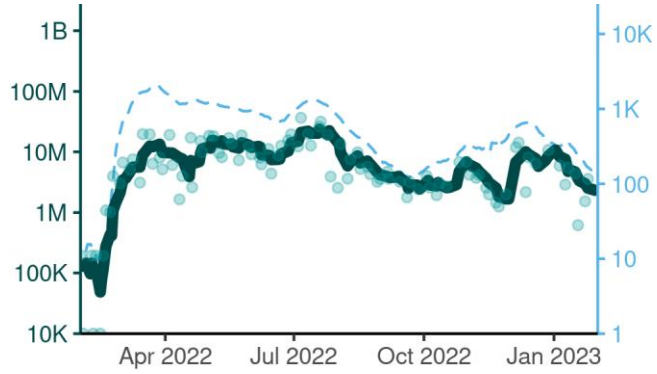
Nelson Central/North Autosampler 26.0K



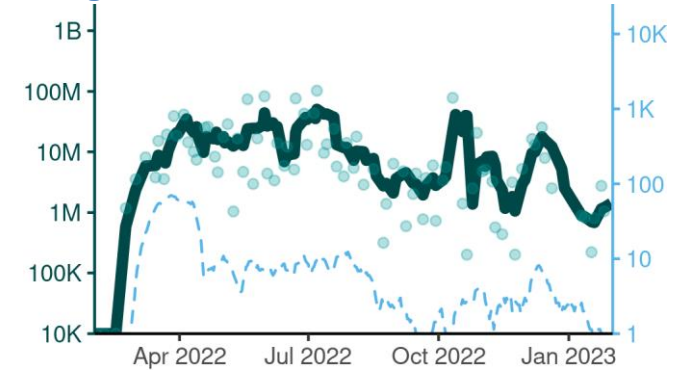
Status ● Detected ● Not detected

West Coast and Canterbury

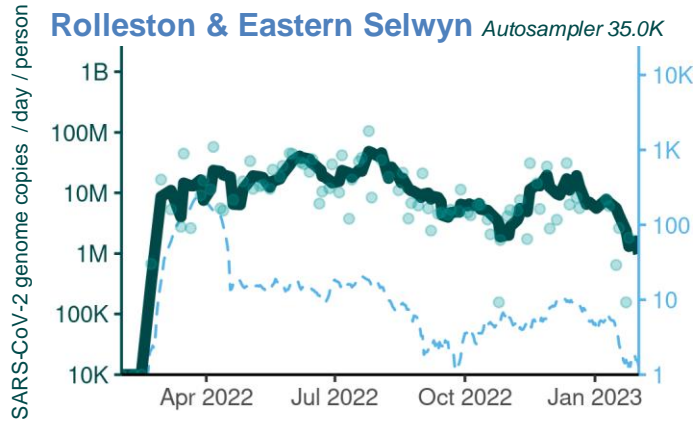
Christchurch Autosampler 368.0K



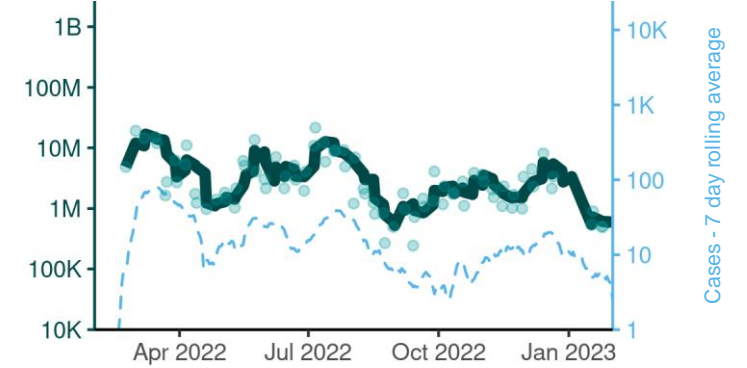
Rangiora Grab 19.0K



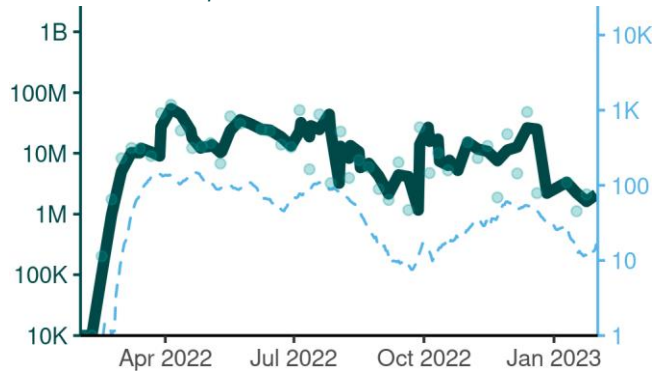
Rolleston & Eastern Selwyn Autosampler 35.0K



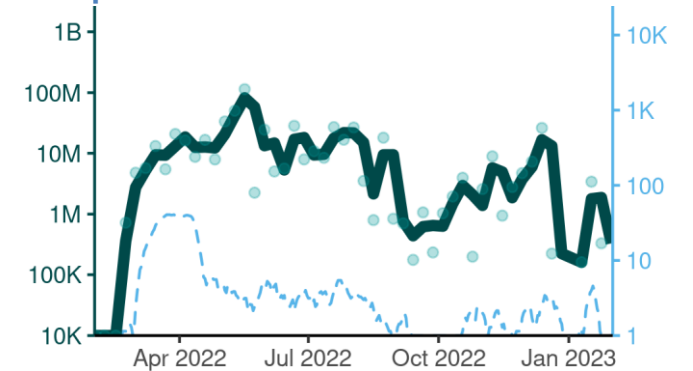
Ashburton Autosampler 18.0K



Timaru Autosampler 28.0K



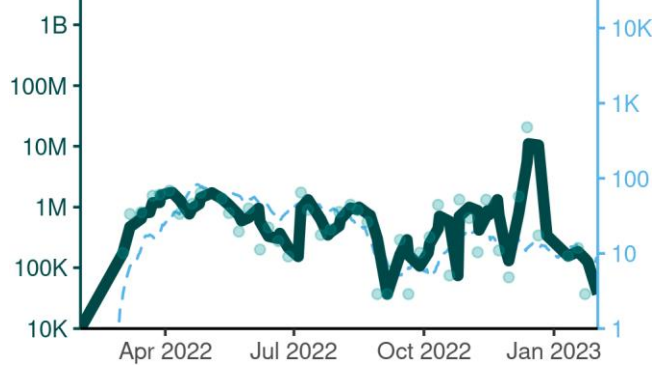
Kaiapoi Grab 12.5K



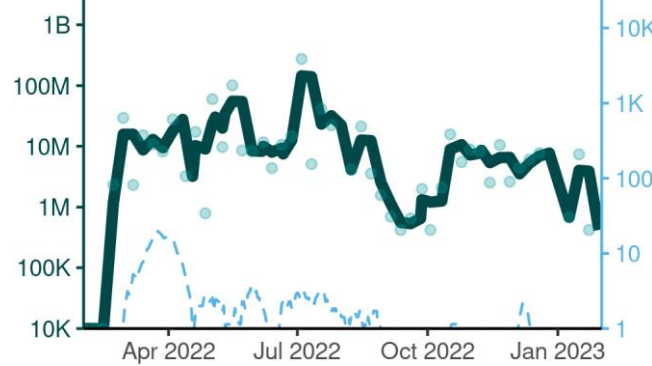
Status ● Detected ● Not detected

Cases - 7 day rolling average

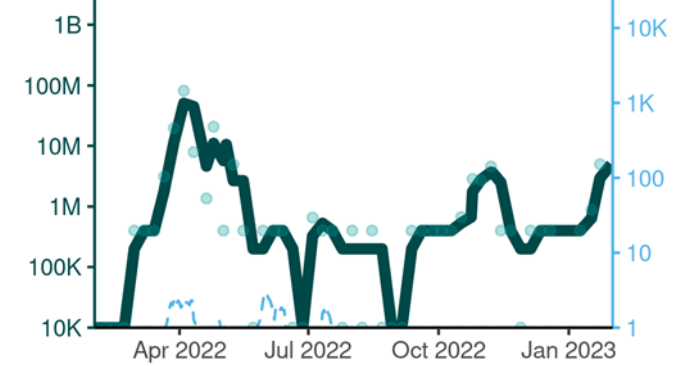
Greymouth *Grab 10.0K*



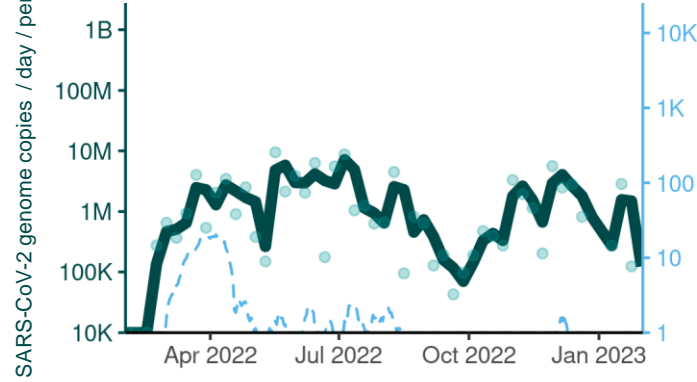
Leeston *Autosampler 3.9K*



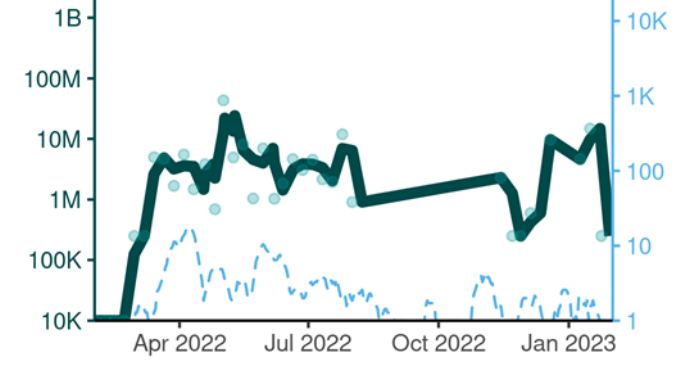
Reefton *Grab 1000*



Woodend *Grab 7.6K*



Westport *Grab 5.0K*

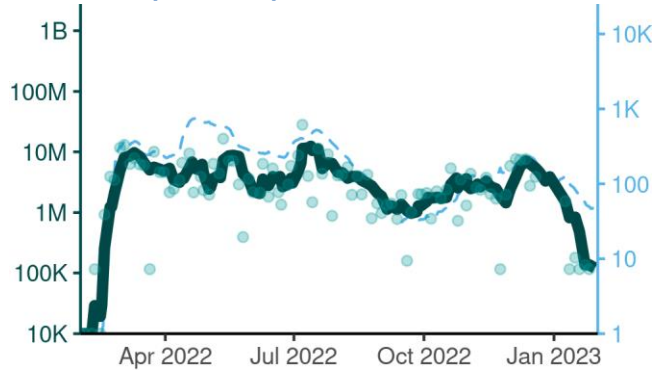


Cases - 7 day rolling average

Otago and Southland

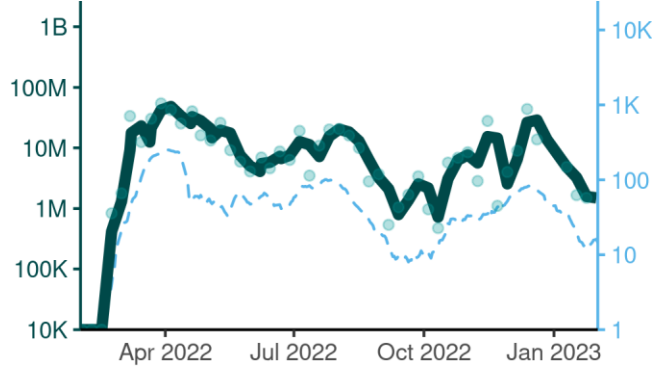
Otago and Southland

Dunedin (Tahuna) Autosampler 84.0K

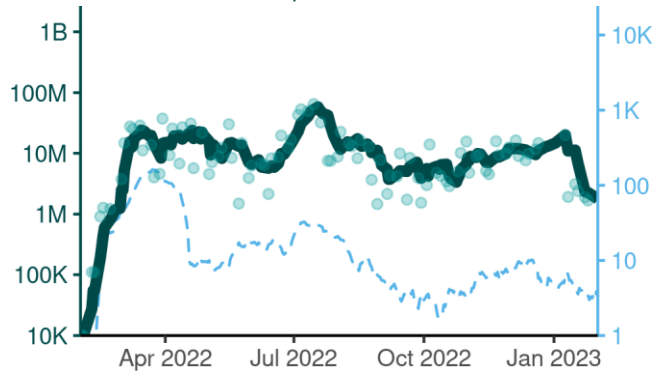


SARS-CoV-2 genome copies / day / person

Invercargill Autosampler 50.0K

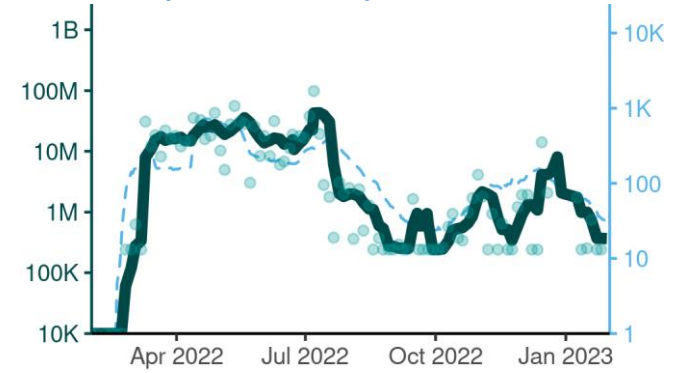


Queenstown Autosampler 40.0K

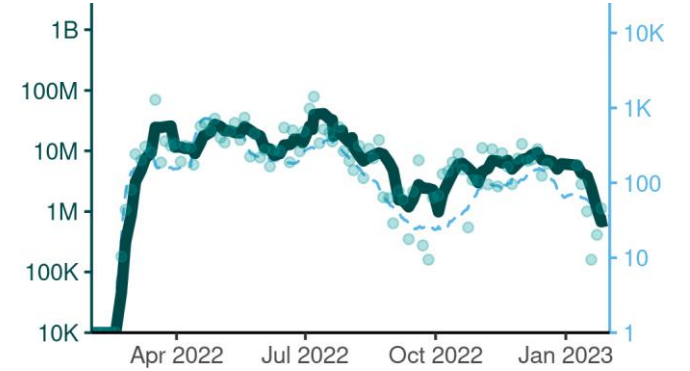


Status ● Detected ● Not detected

Dunedin (Green Island) Autosampler 22.9K

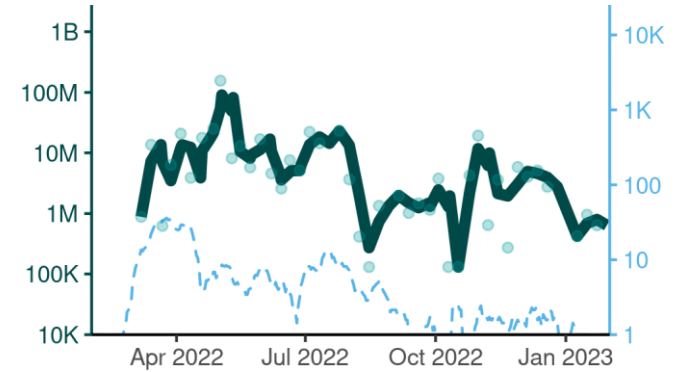


Dunedin (Mosgiel) Autosampler 14.6K

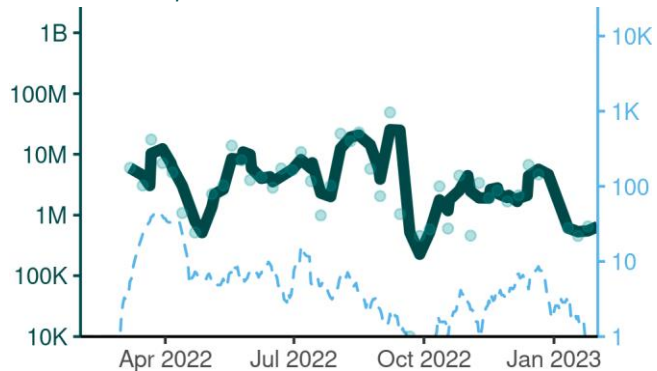


Cases - 7 day rolling average

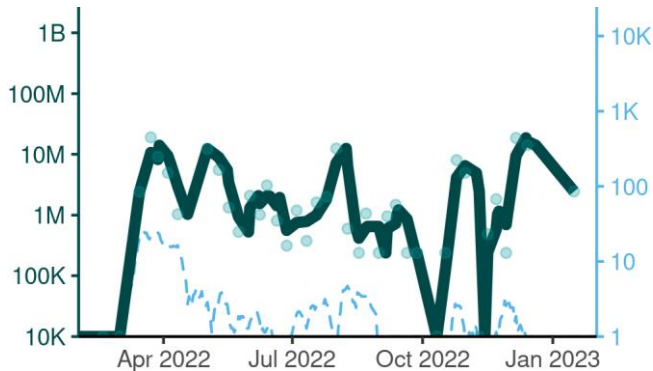
Wanaka Grab 14.5K



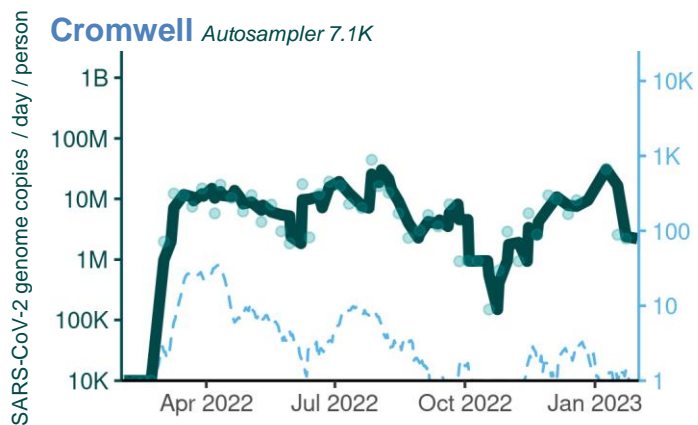
Gore Autosampler 8.0K



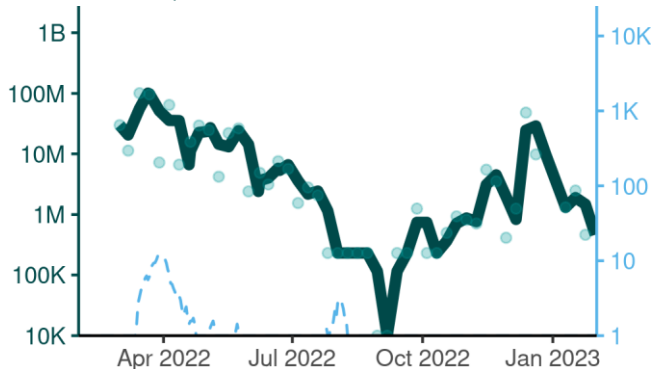
Balclutha Grab 4.1K



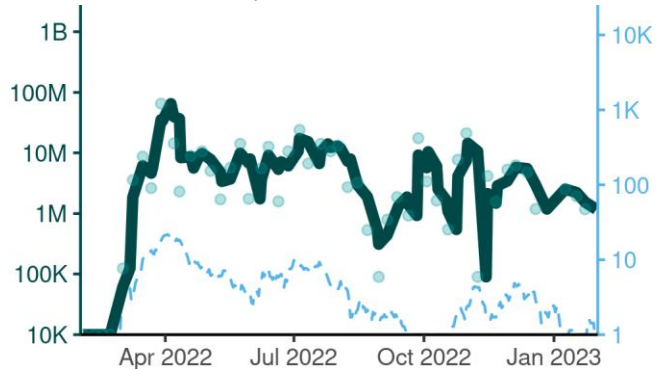
Cromwell Autosampler 7.1K



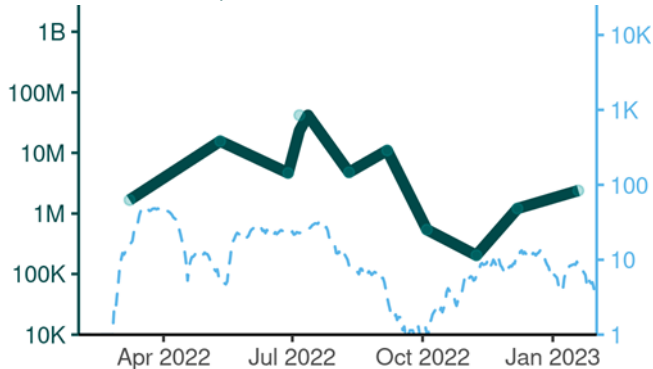
Bluff Autosampler 2.0K



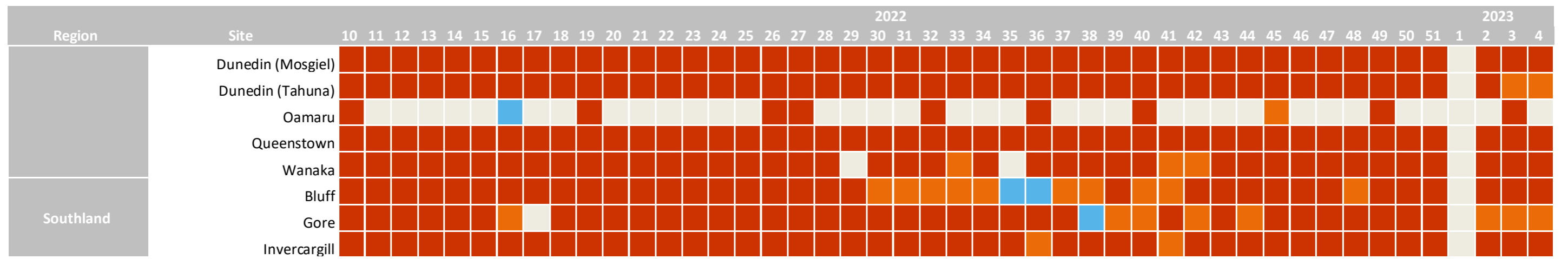
Alexandra Autosampler 6.2K



Oamaru Autosampler 12.0K



Cases - 7 day rolling average



Acknowledgements

This work represents the combined efforts of a large number of individuals and organisations.

We continue to be indebted to the teams across the country who are collecting the wastewater that underpins this work.

The wastewater analysis has been undertaken at ESR by a team which may on any given week include contributions from Joanne Chapman, Dawn Croucher, Joanne Hewitt, Joycelyn Ho, Anower Javed, Olivia Macrae, Ashley McDonald, Andrew Ng, Ashley Orton, and Fatiha Sulthana. Data science analysis, visualisation and reporting is the result of team effort from: Franco Andrews, Bridget Armstrong, Raewyn Campbell, Joanne Chapman, Lei Chen, Gerhard de Beer, Richard Dean, Brent Gilpin, Joanne Hewitt, Dawen Li, Jonathan Marshall, Helen Morris and Leighton Watson. Ongoing support for this work from the Ministry of Health and ESR management is appreciated.

Notes

Sites and frequency of sample collection: The catchment population sites selected for the surveillance range from approximately 100 to over 1,000,000 individuals. The sites cover all regions of the country. Most major towns and all cities, as well as many smaller communities, are included. In early 2022, the wastewater catchment areas cover over 80% of the population connected to wastewater treatment plants. The sites from which samples have been collected have varied over the last 12 months. New sites may be added over time, and/or sampling may reduce in frequency or cease for other sites. The selection and frequency of sampling vary depending on the local population, access to wastewater collection points, staff availability to collect samples and risk factors. When included, samples are collected at least weekly, with twice weekly sampling being common. A number of samples have also been collected from non-WWTP sites (manholes and pump stations- mostly in Auckland).

Sampling method: The preferred option is to automatically collect a 24 hour 'composite' sample. This is where a pump automatically collects a small volume of wastewater every 15 minutes over 24 hours using a composite sampler. These samplers are available in some wastewater treatment plants. When composite samplers are not available, 'grab' samples are collected. These range from a sample being taken at a single point in time, to 3 samples taken over 30 minutes, to samples collected over a day. Grab samples represent only the composition of the source at that time of collection and may not be as representative as a 24-hour composite sampler. More variation may be expected with grab samples.

Laboratory analysis of wastewater samples: Samples are sent from each wastewater treatment plant to ESR. Processing of each sample commences within an hour or two of receipt. Processing involves the concentration of virus from 250 mL sample to approx. 1 mL using centrifugation and polyethylene glycol. Viral RNA is then extracted from a small volume of 0.2 mL concentrate to give a final volume of 0.05 mL. The presence of SARS-CoV-2 RNA is determined using RT-qPCR. SARS-CoV-2 is considered detected when any of the RT-qPCR replicates are positive.

RT-qPCR: Reverse transcription (RT) to convert RNA to complementary DNA (cDNA), followed by quantitative PCR (qPCR). RT-qPCR is used for detection and quantification of viral RNA.

Method sensitivity: The protocol used to concentrate SARS-CoV-2 from wastewater allows for the sensitive detection of SARS-CoV-2 by RT-qPCR. ESR has shown that when 10 individuals are actively shedding SARS-CoV-2 RNA in a catchment of 100,000 individuals, there was a high likelihood of detecting viral RNA in wastewater (<https://doi.org/10.1016/j.watres.2021.118032>). Shedding by one individual may be detected in wastewater, but it does depend on many factors including the amount and duration of shedding. Very low levels in wastewater may be not able to be quantified (i.e., less than the limit of quantification- see below).

SARS-CoV-2 RNA detected (positive result): A positive detection in the wastewater indicates that at least one person has been shedding SARS-CoV-2 into the wastewater at some point during the time period that the sample was being collected. In some cases, detections could also be due to the shedding of low levels of SARS-CoV-2 RNA by a recently recovered case. The detection of SARS-CoV-2 RNA does not indicate that infectious virus is present.

SARS-CoV-2 RNA not detected (negative result): A negative result can occur because there are no active 'shedding' cases in the catchment or because the SARS-CoV-2 RNA concentration is too low to be detected, most likely because there are a very low number of cases in the wastewater catchment. Therefore, negative finding does not necessarily guarantee the absence of COVID-19 in the community.

Viral loads and normalisation: When detected, the SARS-CoV-2 RNA concentration is calculated as genome copies per L of wastewater. This is then converted to a viral load of **genome copies/day/person**. This conversion takes into account the flow rate of wastewater entering the treatment plant (the influent) and the population in the catchment. The **flow rate** is the total volume (m³ per day) recorded at the inlet of the wastewater treatment plant over 24 hours. This is a **population-normalised viral load**. Currently, the flow rate is the average annual flow rate, but will be replaced with daily flow rate when available (note that rainfall may significantly increase the flow rate at the inlet, diluting the sample, and may result in lower concentrations and a false negative result).

Limit of quantification: The lowest concentration of the target that can be reliably quantified is referred to as the limit of quantification. For those samples where SARS-CoV-2 is detected but cannot be quantified, a value of 5 genome copies/mL wastewater is used. While a standard method is being used, virus recovery can vary from sample to sample, and this may affect the quantitation.

Data subject to change: Data generated for the New Zealand Wastewater COVID-19 Surveillance Programme should be considered provisional and may be subject to change. Data may be incomplete for the most recent 2-week period due to processing, testing and reporting delays.

Data not shown:

- Data from 'ad hoc' sampling locations including from individual facilities/building (e.g., workplaces, prisons, MIQs) are not included.
- Results from certain samples may not be shown, as the result was either deemed invalid, or the sample could not be tested (e.g., leaked in transit, not labelled).

For further information please contact

Joanne Hewitt

Science Leader

Joanne.hewitt@esr.cri.nz

Jo Chapman

Senior Scientist

Joanne.chapman@esr.cri.nz