

National Wastewater Surveillance Programme - COVID-19

Week 29 (Week ending 24 July 2022)

Report prepared on 27 July 2022

Key highlights:

SARS-CoV-2 RNA detected at 100% (104/104) sites tested

51% of NZ population covered by wastewater testing

Most prevalent variant detected Omicron BA.4/5 (~81%)

Overall, SARS-CoV-2 levels in wastewater have plateaued. Omicron BA.4/5 levels continue to increase relative to BA.2.

SARS-CoV-2 in Wastewater and Reported COVID-19 Case Numbers
 National, last 12 months, on log₁₀ scale



- Week ending **24 July 2022**, **34%** of sites have **increased** SARS-CoV-2 levels compared to the previous week, and **30%** **decreased** levels. However, levels at **66%** of sites are still **higher** than that observed a month ago.

Results:

In the week ending 24 July 2022, 155 samples were collected from 104 locations in New Zealand. Analysis of six samples is still in progress due to late arrival of samples from Auckland (Mangere (2 samples), Army Bay, Helensville, Pukekohe, Waiuku).

This week COVID-19 impacted on the ability to collect and courier samples from four of the regular sites across Auckland. Therefore, three central Auckland interceptor samples (Eastern, Western and Southwestern) were not collected due to staff illness. The two Mangere samples, which are in progress, combine the three interceptors.

Heavy rainfall at some locations in New Zealand may have resulted in lower viral levels detected at some sites. Flow adjustment calculations are in progress and results will be updated when these are available.

SARS CoV-2 RNA was detected at all sites tested. While levels at most sites have decreased compared with 2 weeks ago, 66% of sites remains higher than levels measured one month ago (Figure 1, Figure 2, Table 1).

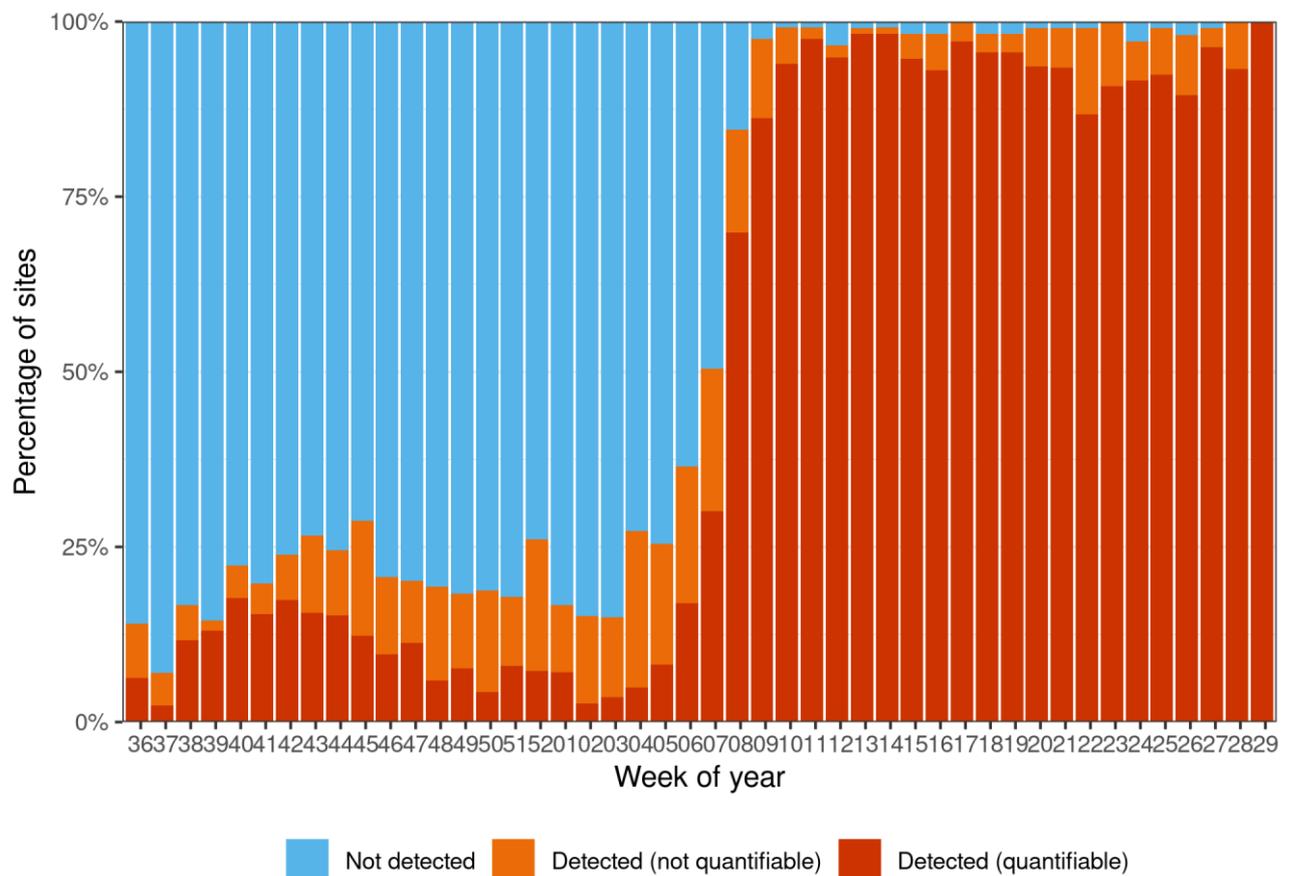


Figure 1. Results for SARS-CoV-2 RNA in wastewater collected across New Zealand.

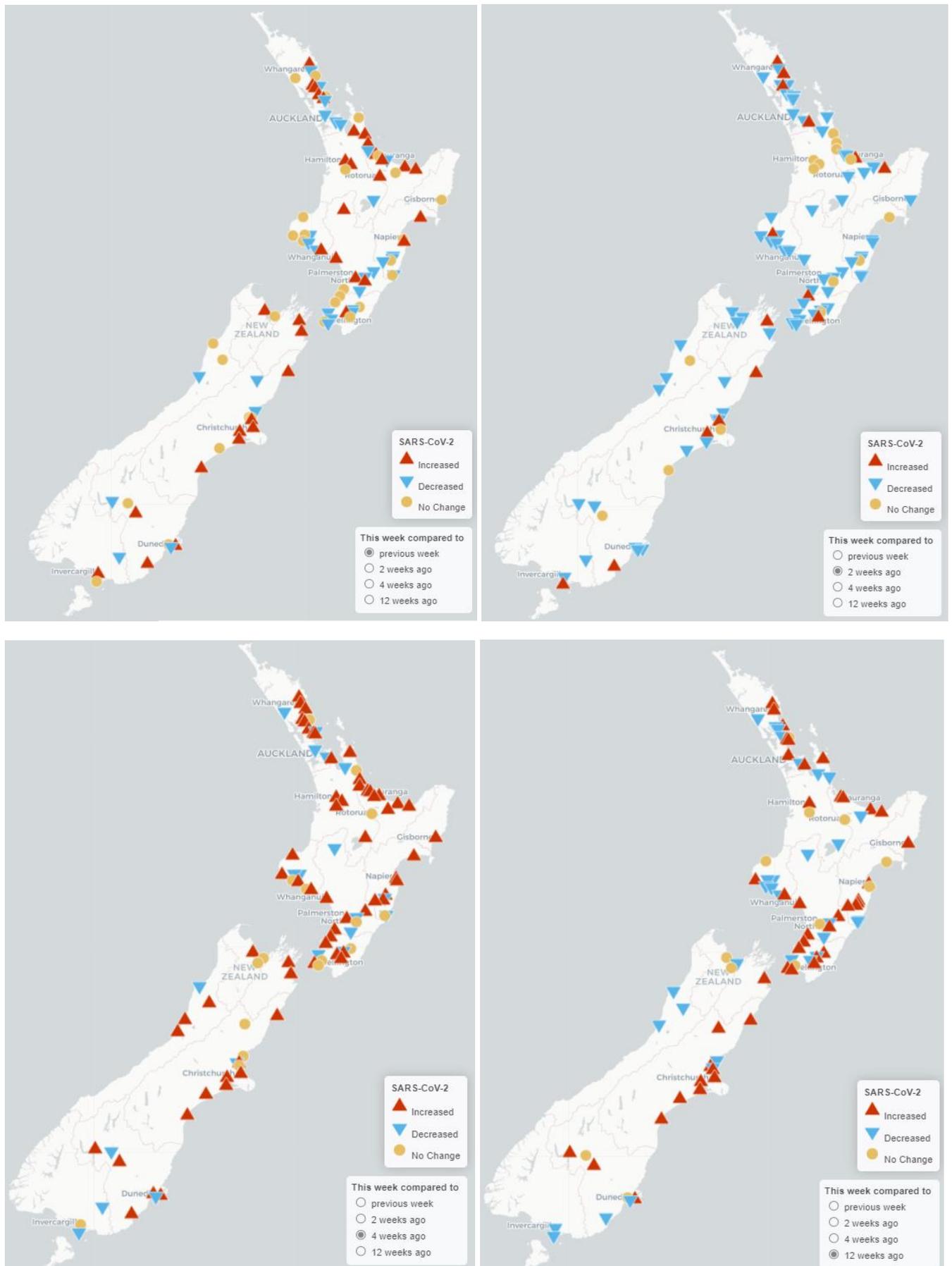
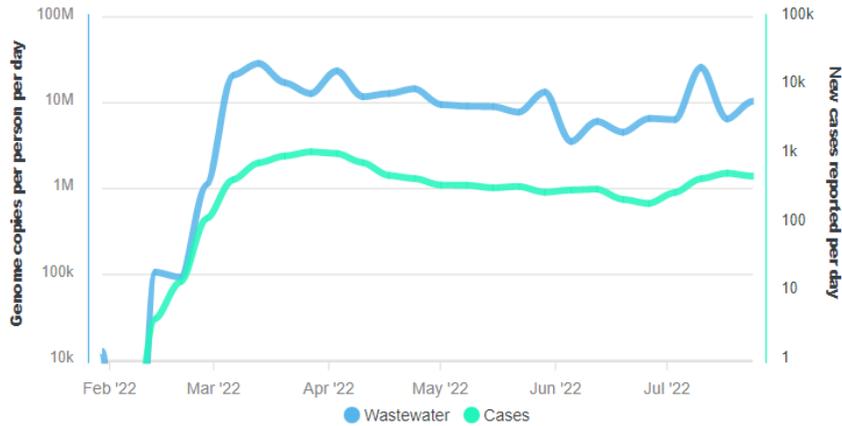


Figure 2. Comparison of SARS-CoV-2 levels for the week ending 24 July 2022, compared with the levels measured **1 week, 2 weeks, 4 weeks, or 12 weeks previously**. Only sites with results for both time points are included. When the viral quantity is 30% or more higher this is labelled as increased (red 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).

Regional summaries are available at <https://esr-cri.shinyapps.io/wastewater/>. Examples are shown below which illustrate increases in some regions (top panel), a plateau in some regions (middle panel) and decreases in others (bottom panel). These regional summaries are population weighted, so the largest catchments dominate the trends.

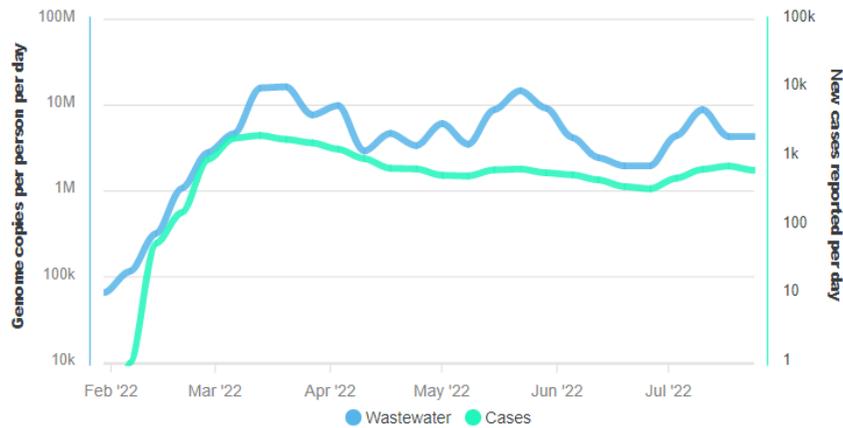
SARS-CoV-2 in Wastewater and Reported COVID-19 Case Numbers
Manawatu-Whanganui, last 6 months, on log₁₀ scale



SARS-CoV-2 in Wastewater and Reported COVID-19 Case Numbers
Canterbury, last 6 months, on log₁₀ scale



SARS-CoV-2 in Wastewater and Reported COVID-19 Case Numbers
Waikato, last 6 months, on log₁₀ scale



SARS-CoV-2 in Wastewater and Reported COVID-19 Case Numbers
Hawke's Bay, last 6 months, on log₁₀ scale



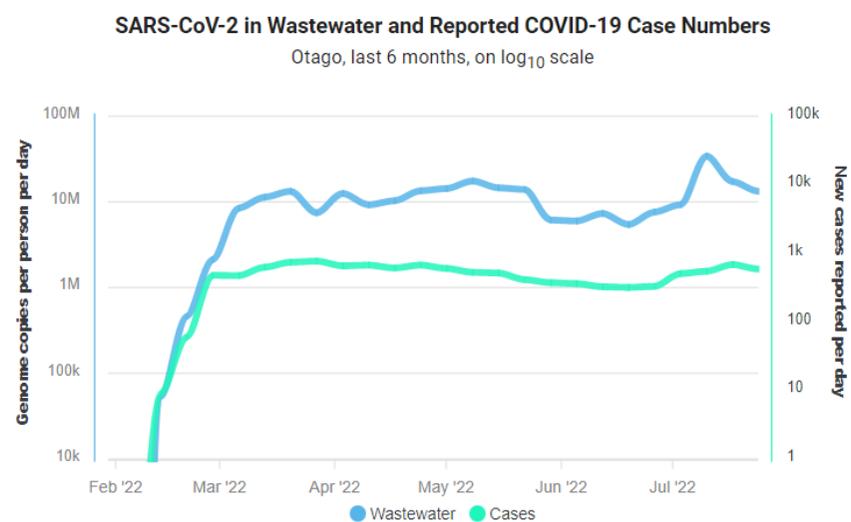
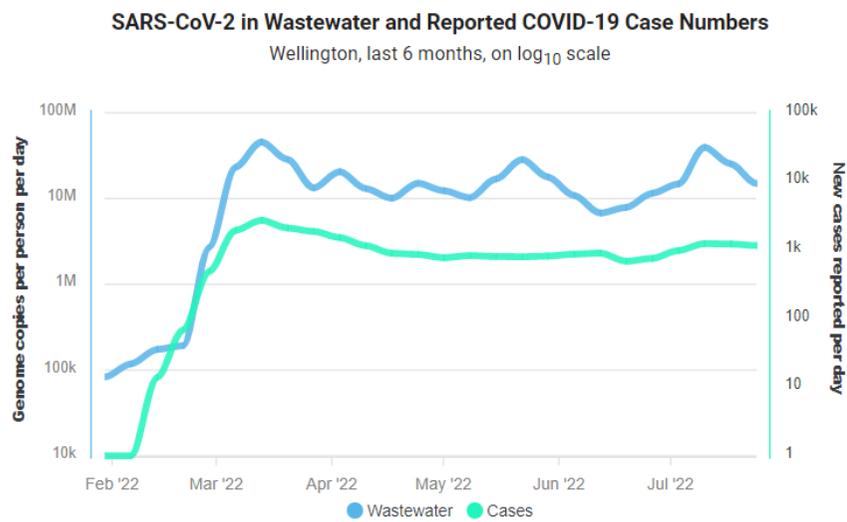


Figure 3. Examples of regional summaries to illustrate increases in some regions (top panel), a plateau in some regions (middle panel) and decreases in others (bottom panel).

Consistent with results from sequencing of clinical cases, **Omicron BA.4/5 levels continue to increase relative to BA.2** (national average of ~81%). The BA.2.75 (sub)variant was not detected. The change in variant prevalence in wastewater over the past 7 weeks nationally (aggregated across all 21 sentinel sites) is shown in Figure 4. Note that level of precision and sensitivity in the percentage estimates can be uncertain.

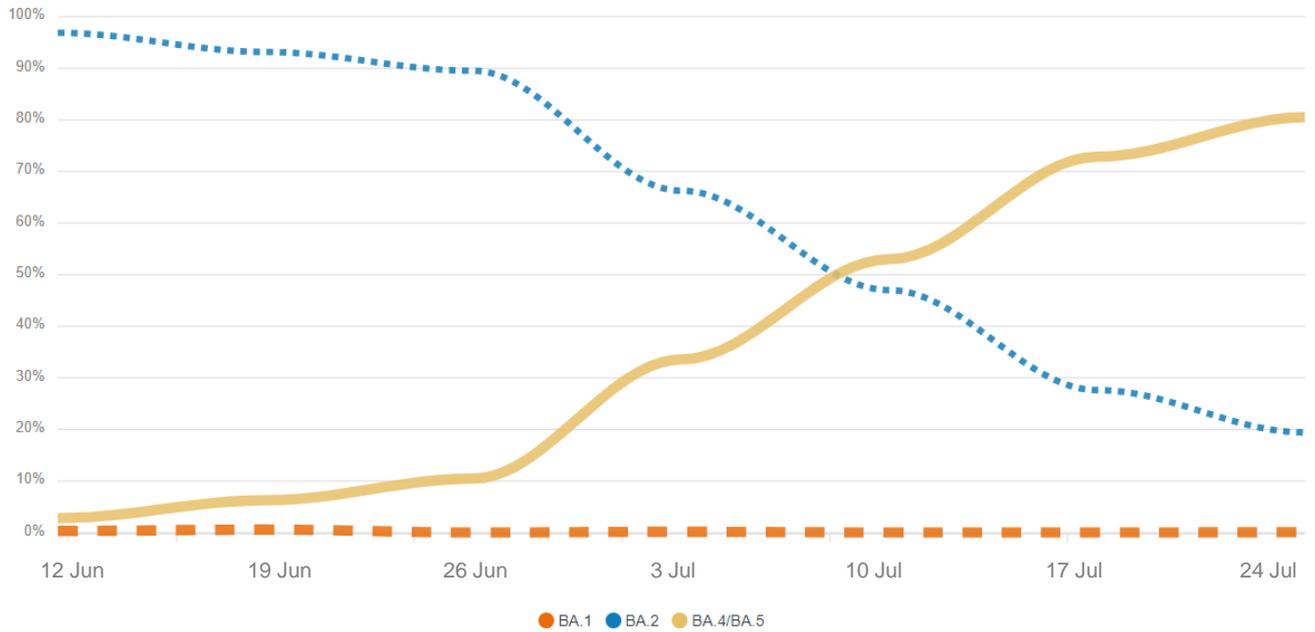
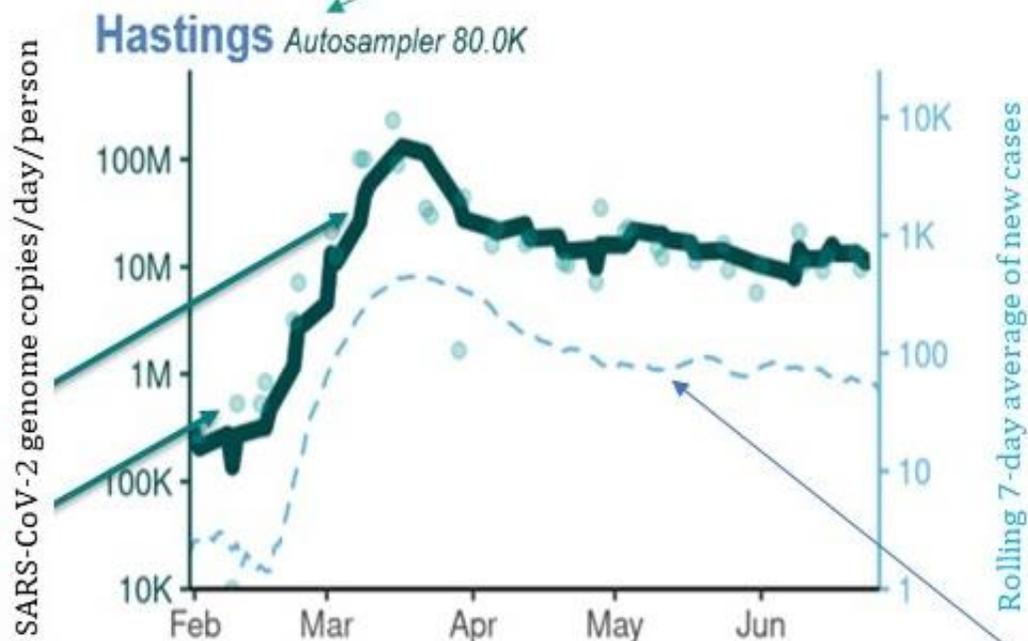


Figure 4. Variants present in New Zealand wastewater between 12 June and 24 July 2022, based on data from up to 22 sentinel sites surveyed each week. Data for week ending 24 July 2022 excludes Auckland metro sites.

Interpreting site graphs

Site, sample collection method and population. Results based on autosampler may be more representative than grab sample-based results.



Wastewater Results

Rolling 14-day average of genome copies/day/person shown as **solid line**

Individual wastewater sample results are shown as **circles**

Log₁₀ scale

Rolling 7-day average **new cases** in the catchment based on **reported date** of illness

Dotted line

Log₁₀ scale

This data is not available for all sites, and subject to change

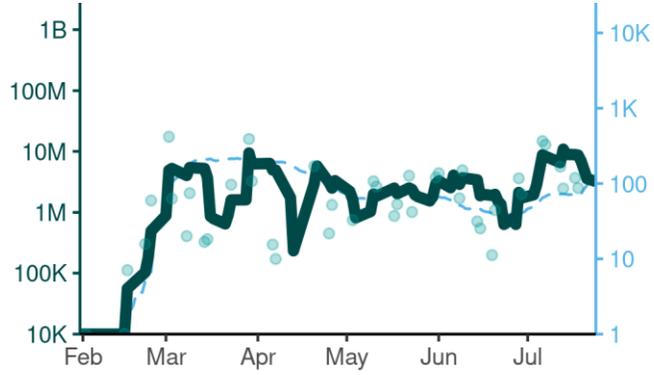
Both wastewater and cases data are on a **log₁₀ scale**.

Scales on all graphs have been normalised to cover the same scale on every graph.

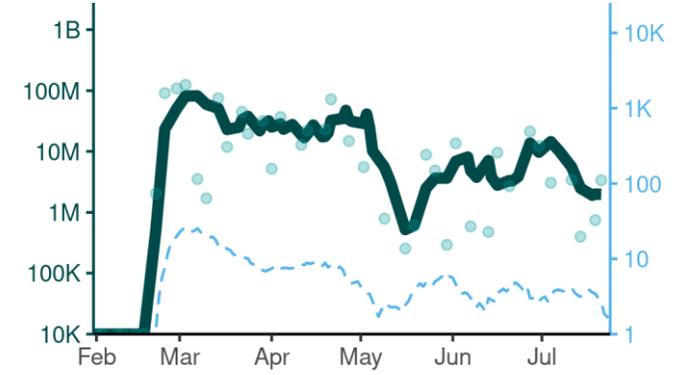
Care should be taken when interpreting the data.

Northland

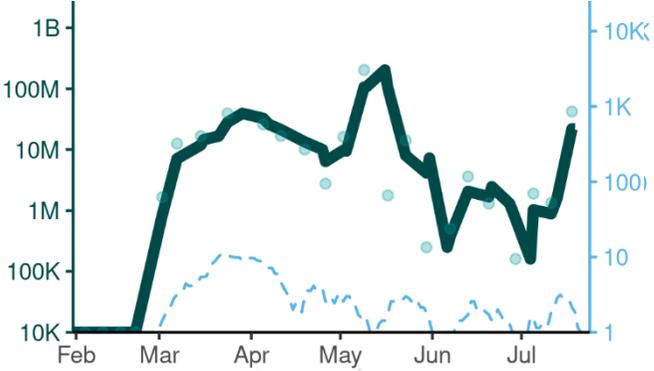
Whangarei Autosampler 65.0K



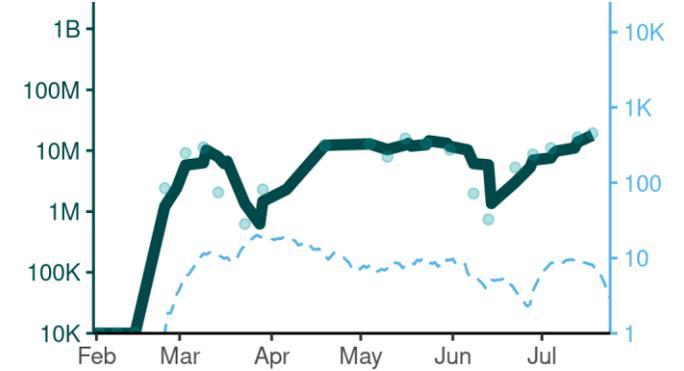
Dargaville Grab 5.0K



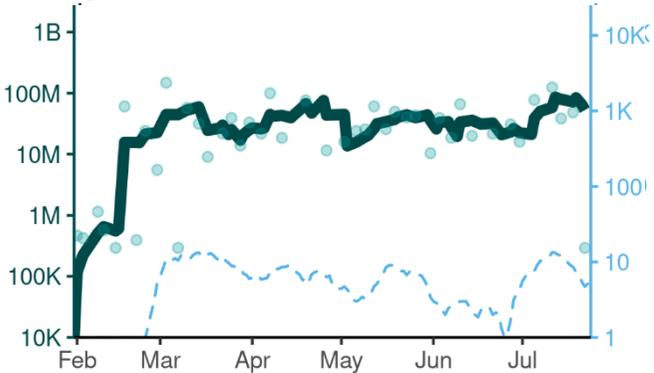
Hikurangi Grab 1.7K



Ruakaka Grab 4.5K



Mangawhai Grab 1.1K

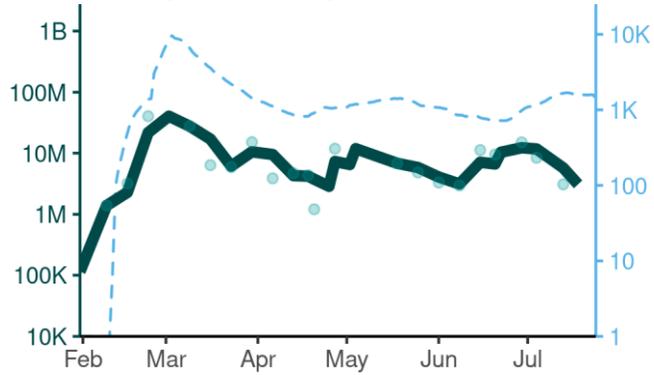


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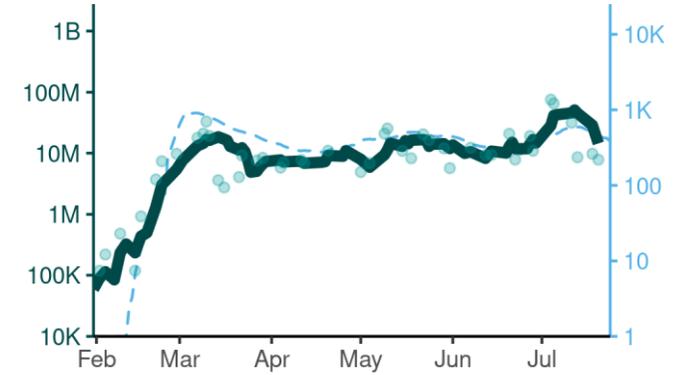
Cases - 7 day rolling average

Auckland

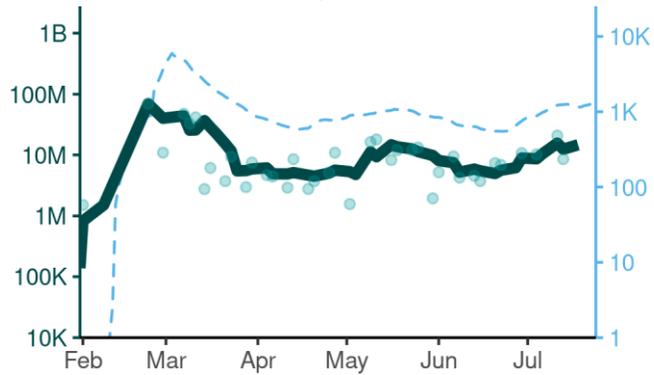
Auckland (Combined) Autosampler 1.1M



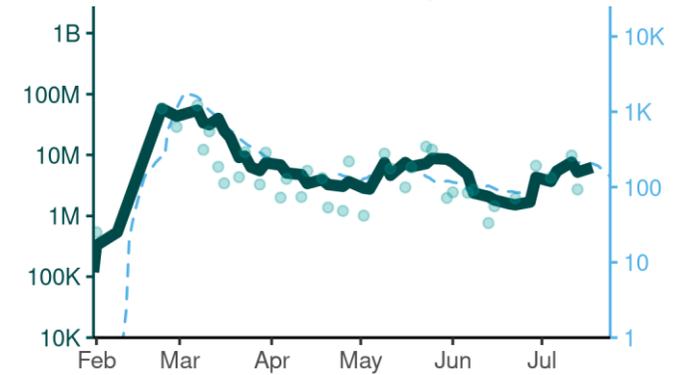
North Shore Autosampler 240.0K



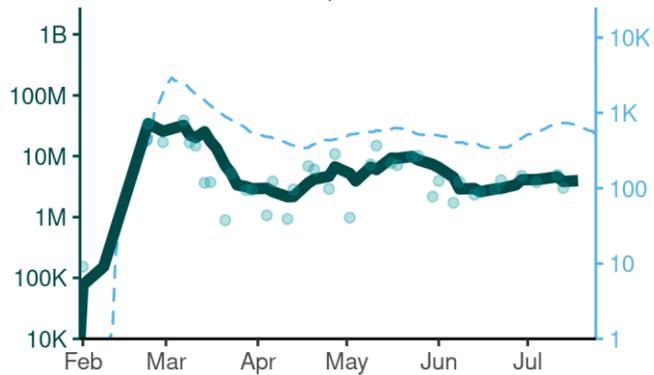
Auckland East Autosampler 680.0K



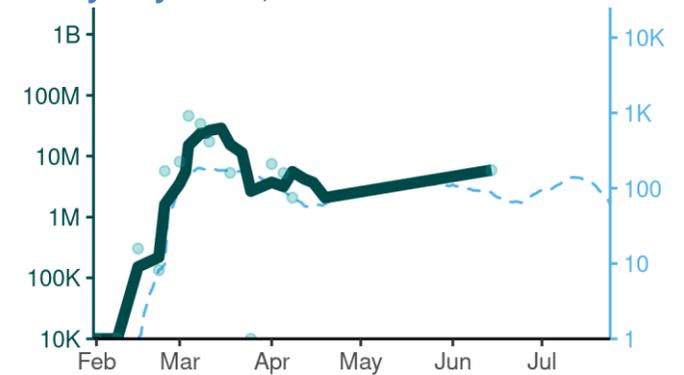
Auckland Southwest Autosampler 120.0K



Auckland West Autosampler 315.0K



Army Bay Autosampler 42.0K



Status ● Detected ● Not detected

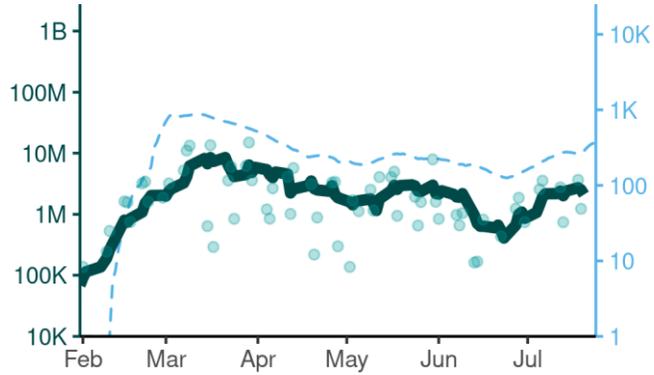
SARS-CoV-2 genome copies per person per day

Cases - 7 day rolling average

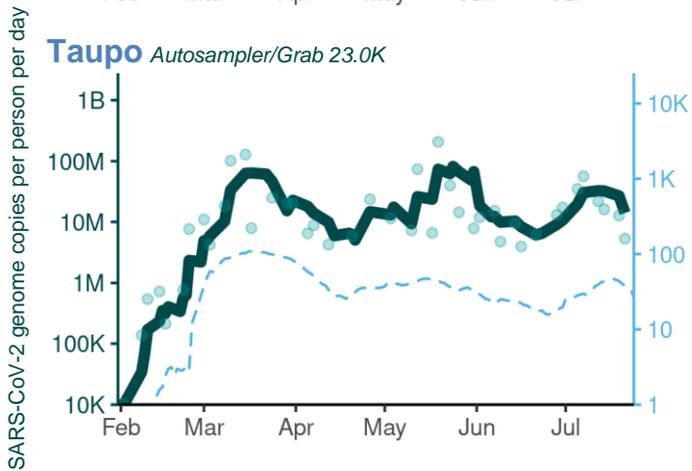


Waikato

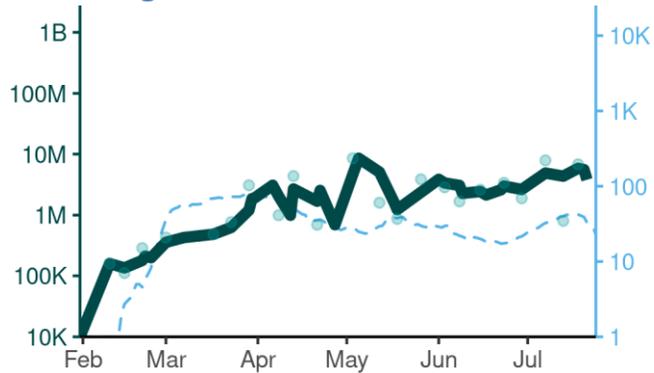
Hamilton Autosampler 169.0K



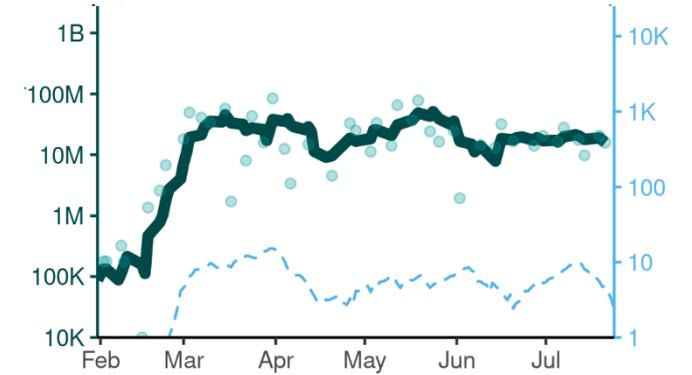
Taupo Autosampler/Grab 23.0K



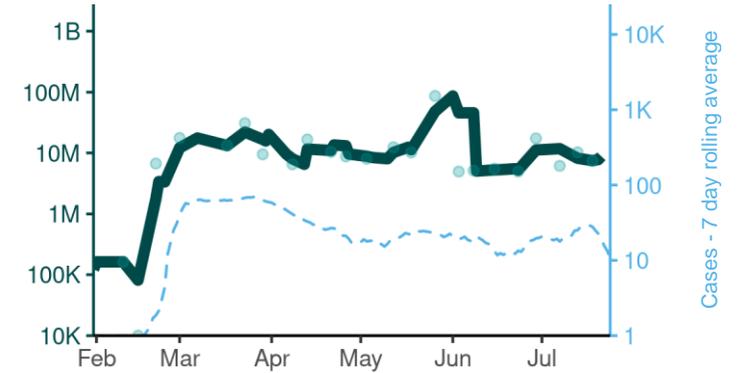
Cambridge Autosampler 20.1K



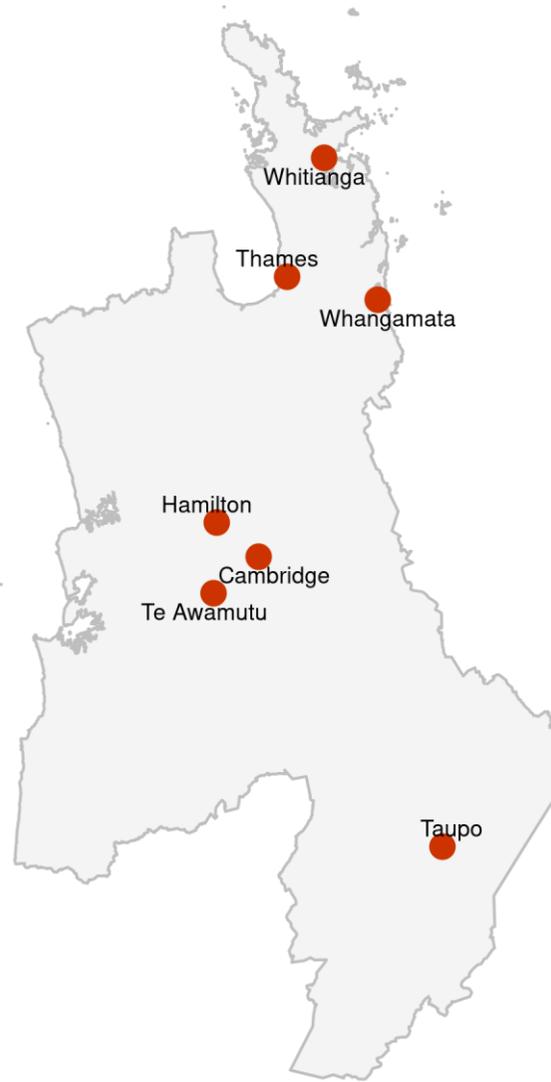
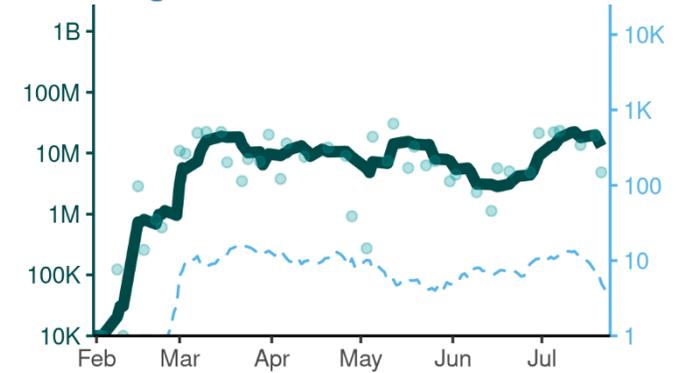
Whangamata Autosampler 4.0K



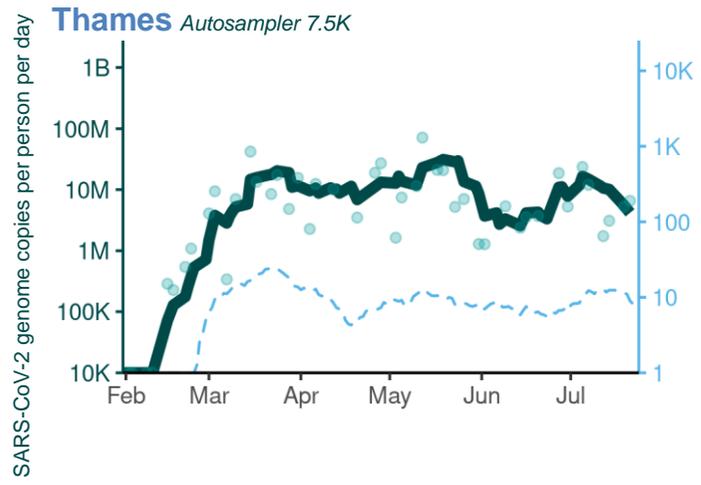
Te Awamutu Autosampler 13.1K



Whitianga Autosampler 6.6K

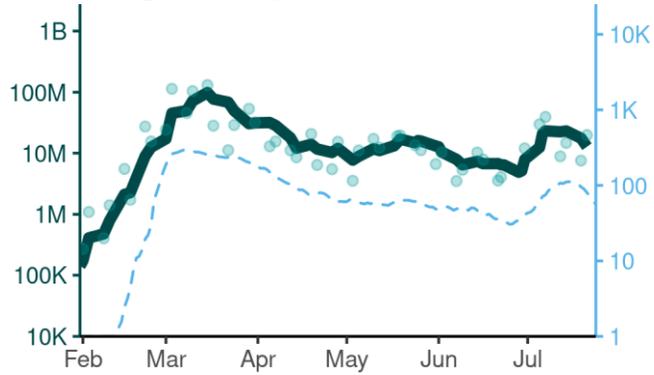


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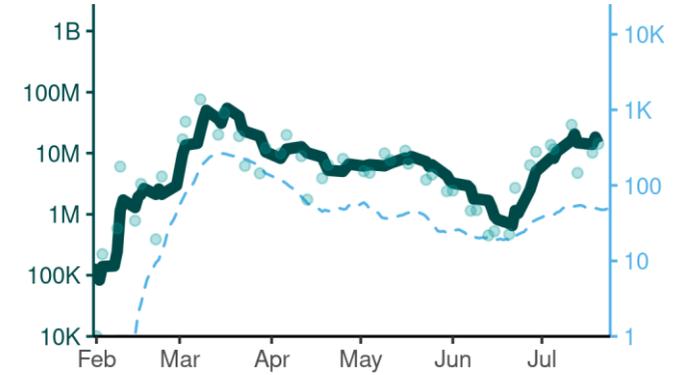


Bay of Plenty and Gisborne

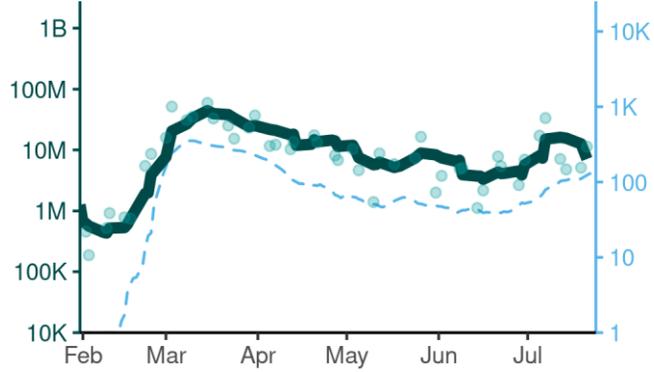
Mt Maunganui/Papamoa Autosampler 65.0K



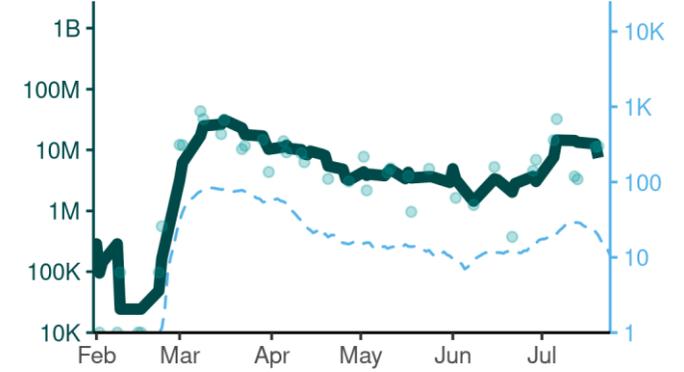
Gisborne Autosampler 37.0K



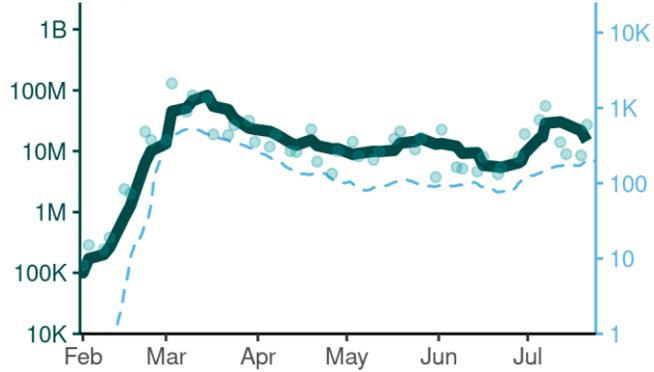
Rotorua Autosampler 59.0K



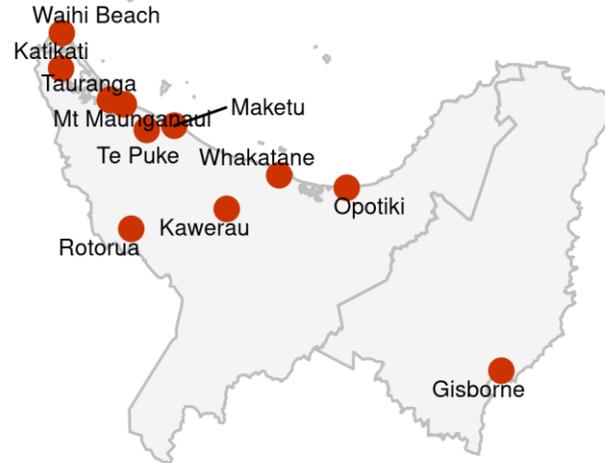
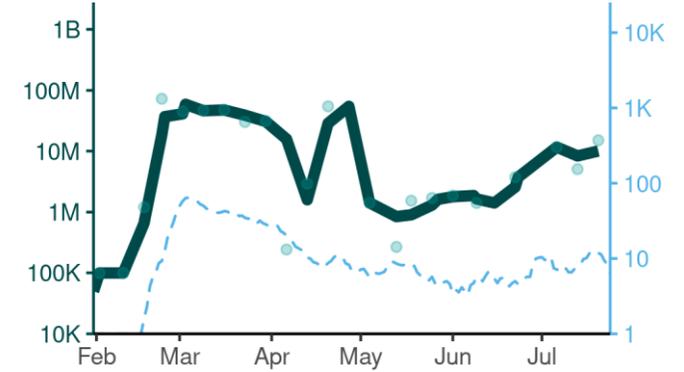
Whakatane Autosampler 21.0K



Tauranga Autosampler 50.0K



Te Puke Autosampler 9.7K

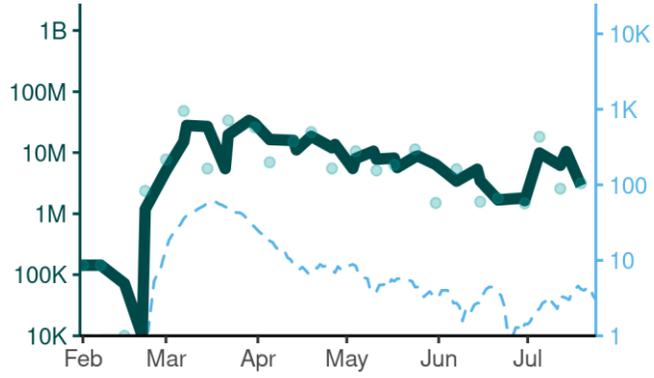


Status ● Detected ● Not detected

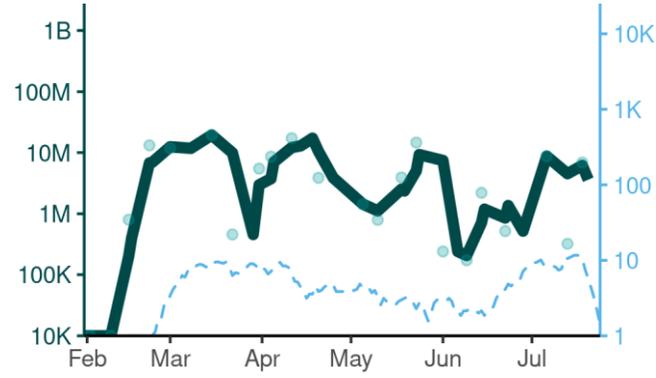
SARS-CoV-2 genome copies per person per day

Cases - 7 day rolling average

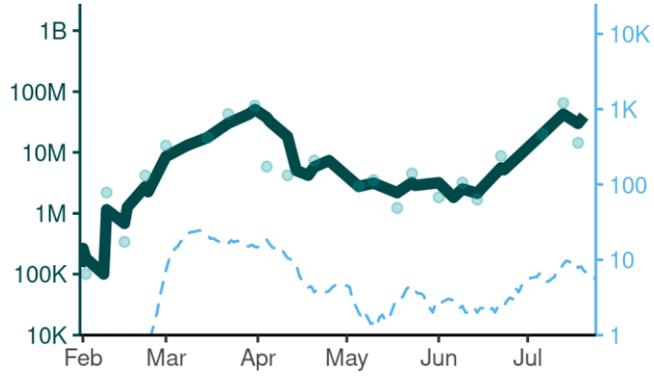
Kawerau Autosampler 7.0K



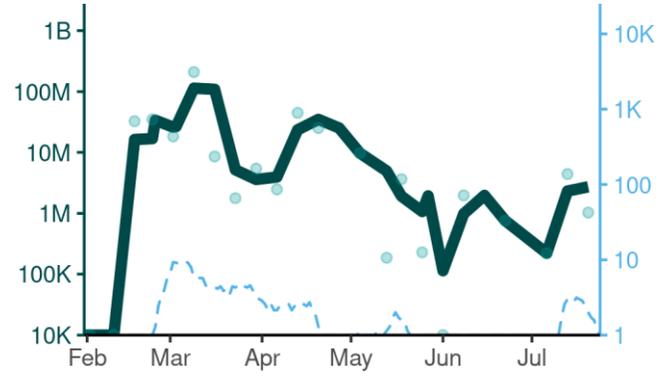
Waihi Beach Autosampler 3.6K



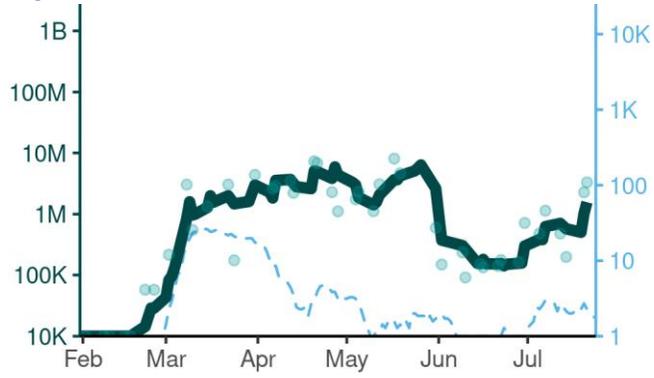
Katikati Autosampler 5.5K



Maketu Autosampler 1.3K



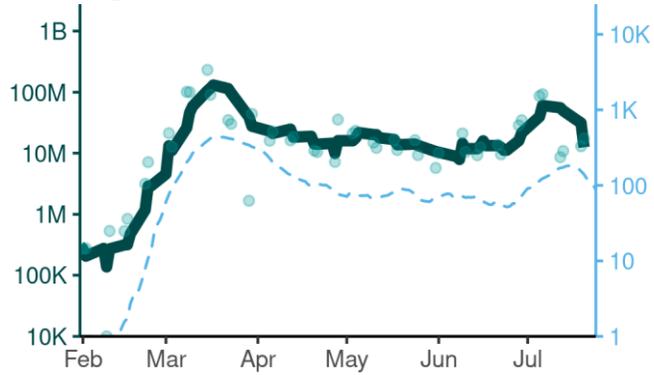
Opotiki Grab 3.8K



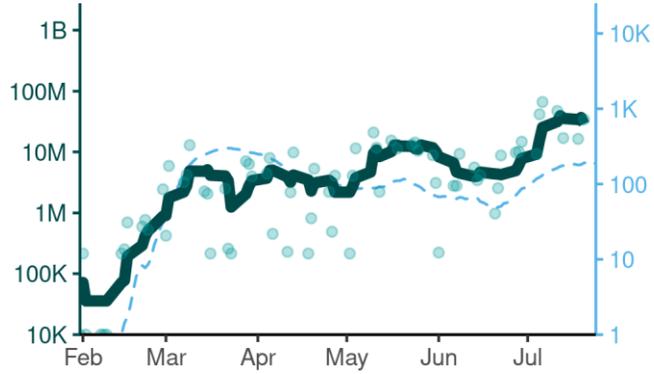
SARS-CoV-2 genome copies per person per day

Hawke's Bay

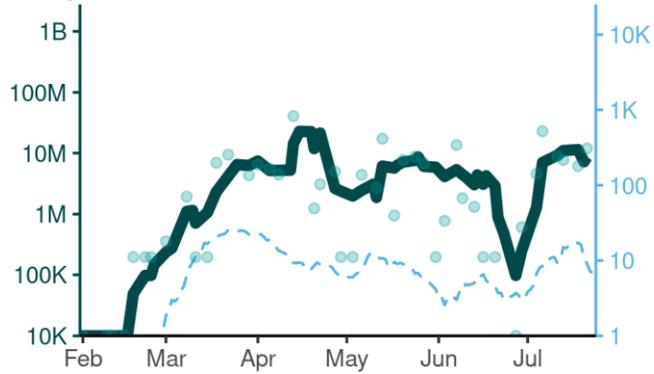
Hastings Autosampler 80.0K



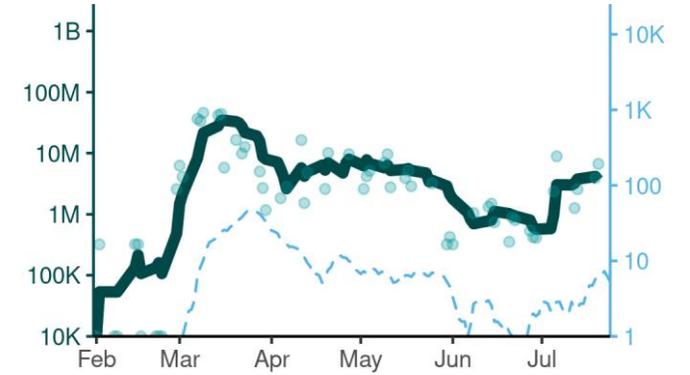
Napier Autosampler 55.0K



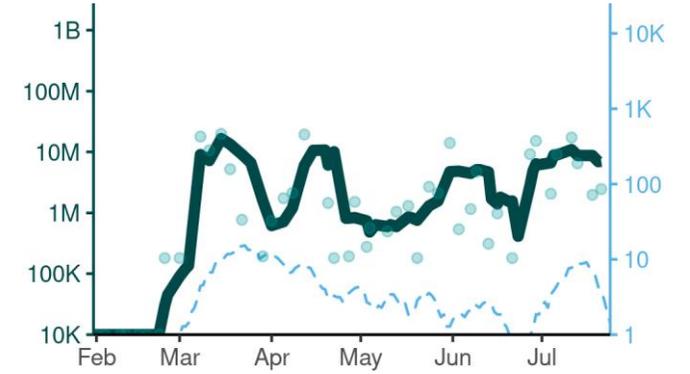
Waipukurau Autosampler 4.6K



Wairoa Grab 4.4K



Waipawa Autosampler 2.2K



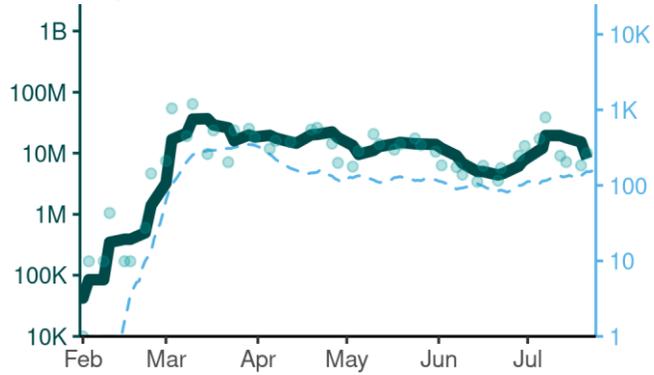
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SARS-CoV-2 genome copies per person per day

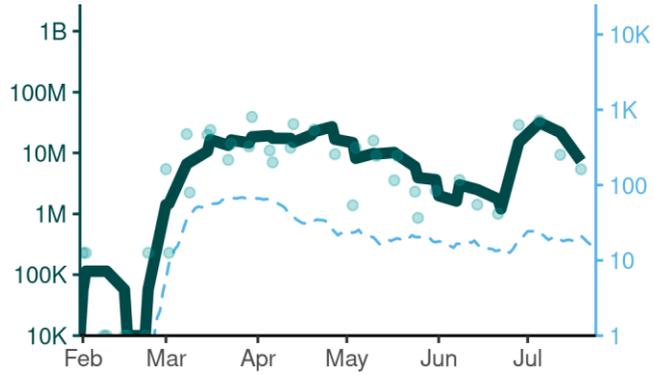
Cases - 7 day rolling average

Taranaki

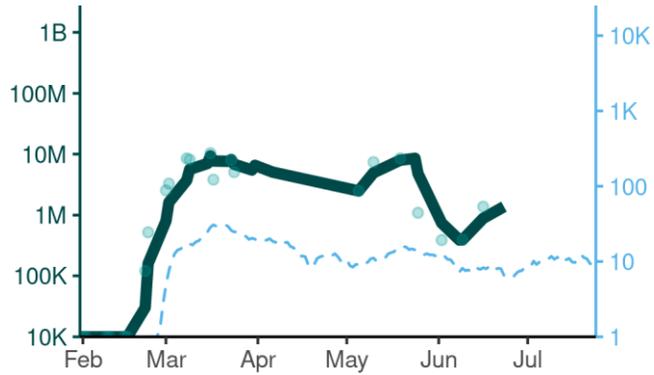
New Plymouth Autosampler 88.0K



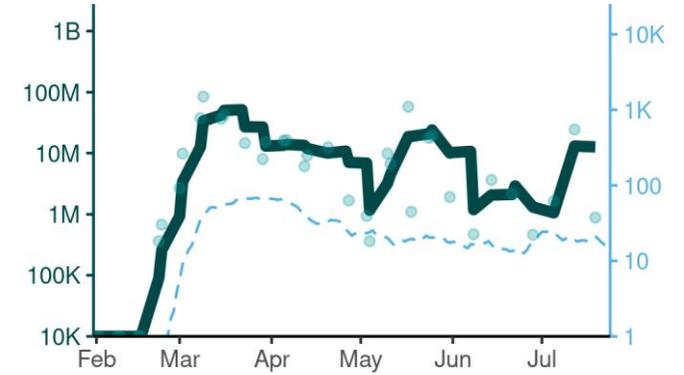
Hawera Autosampler 12.0K



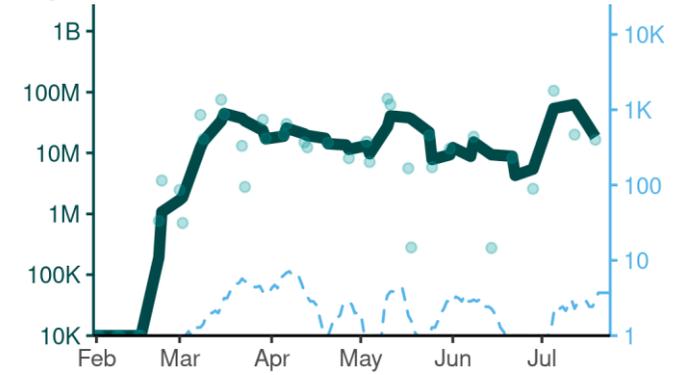
Stratford Autosampler 9.9K



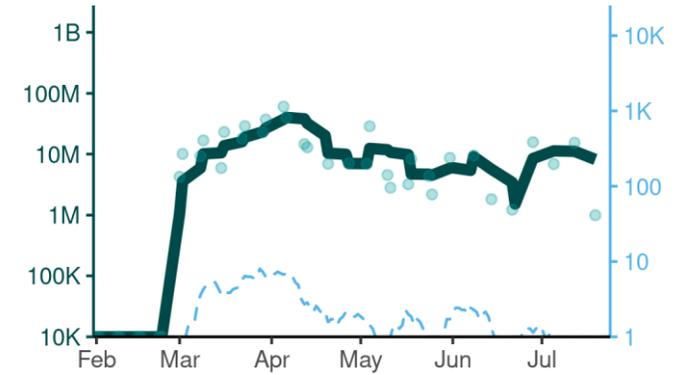
Eltham Autosampler 2.0K



Opunake Autosampler 1.4K



Patea Autosampler 1.2K



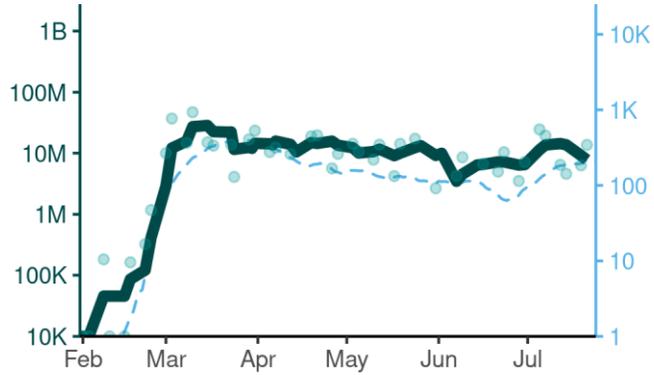
Status ● Detected ● Not detected

SARS-CoV-2 genome copies per person per day

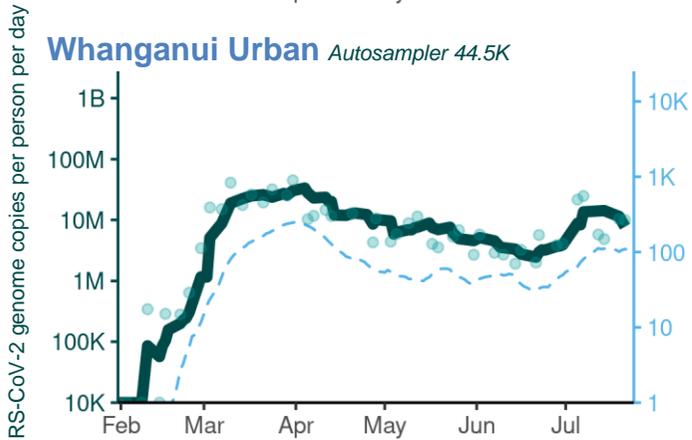
Cases - 7 day rolling average

Manawatu-Whanganui

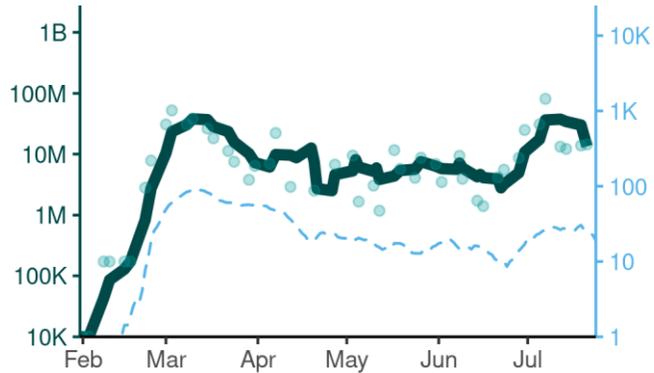
Palmerston North Autosampler 90.0K



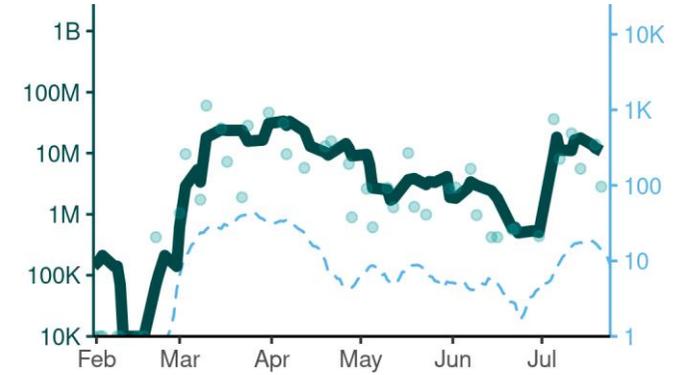
Whanganui Urban Autosampler 44.5K



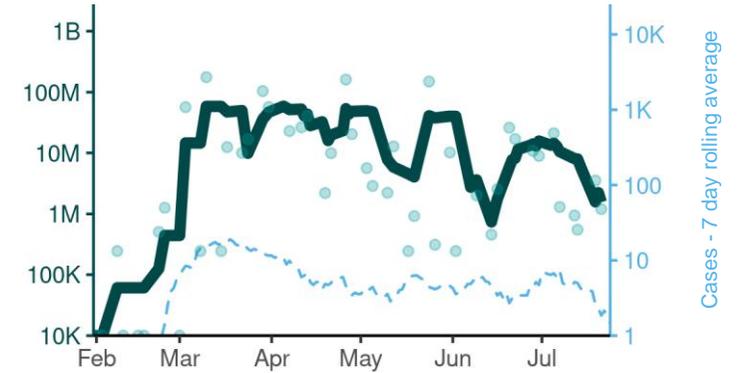
Levin Autosampler 21.2K



Dannevirke Grab 5.7K

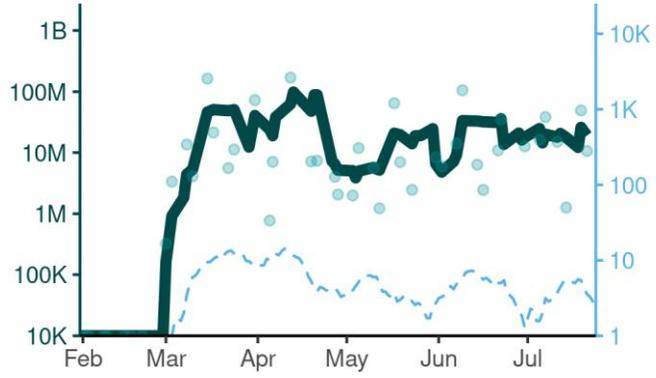


Taumarunui Grab 4.0K

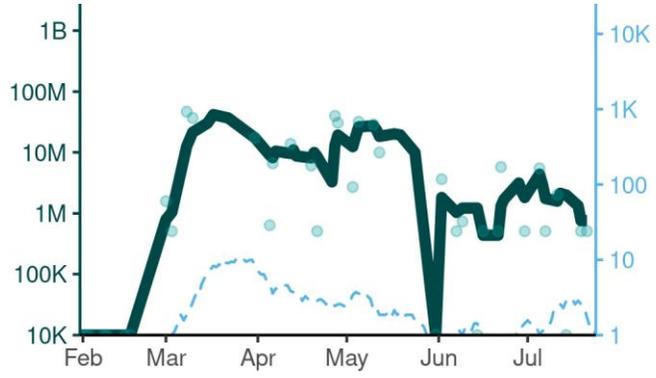


Status ● Detected ● Not detected

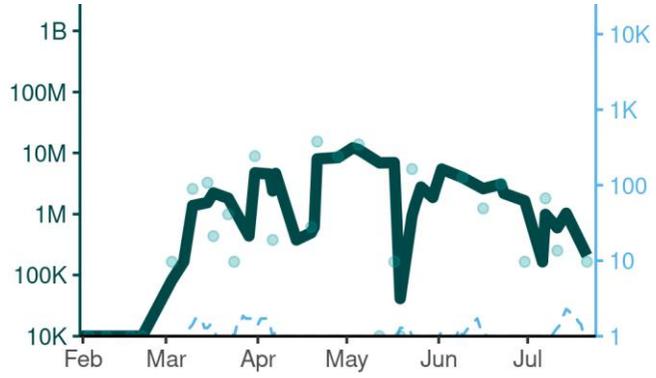
Pahiatua Grab 2.8K



Woodville Grab 1.7K

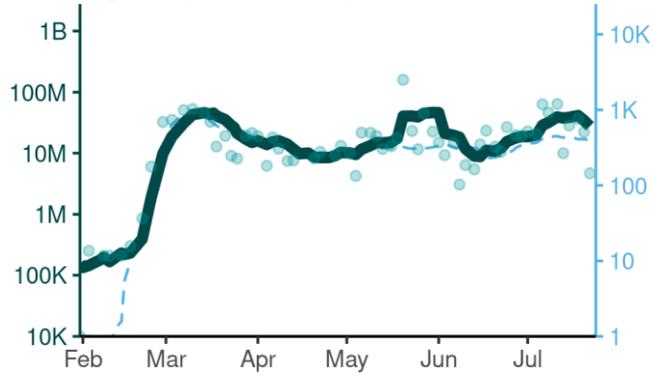


Eketahuna Grab 1.6K

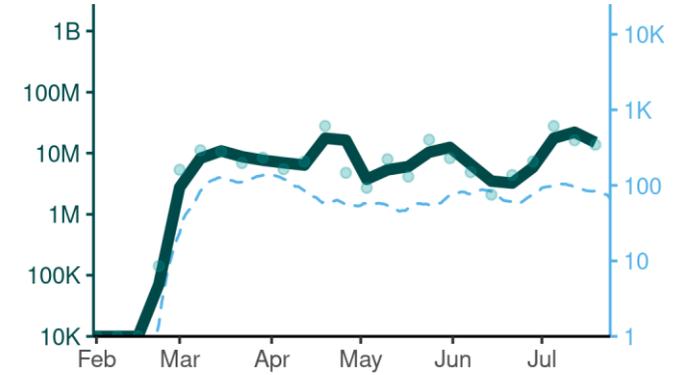


Wellington

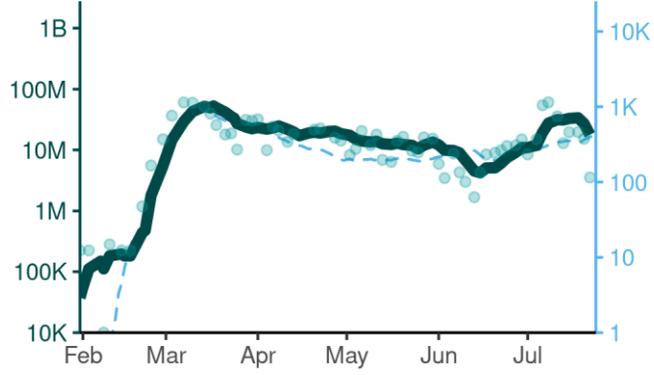
Wellington (Moa Point) Autosampler 168.0K



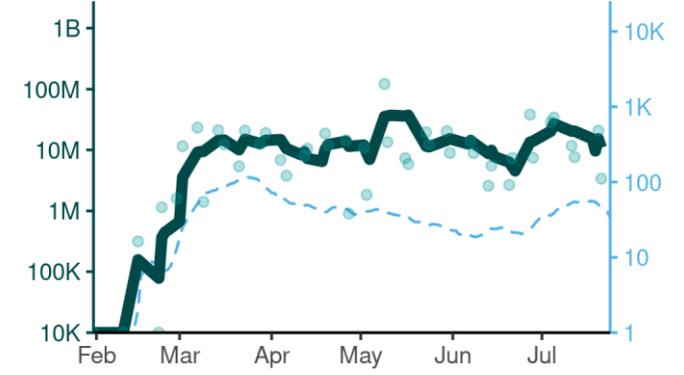
Paraparaumu Autosampler 49.0K



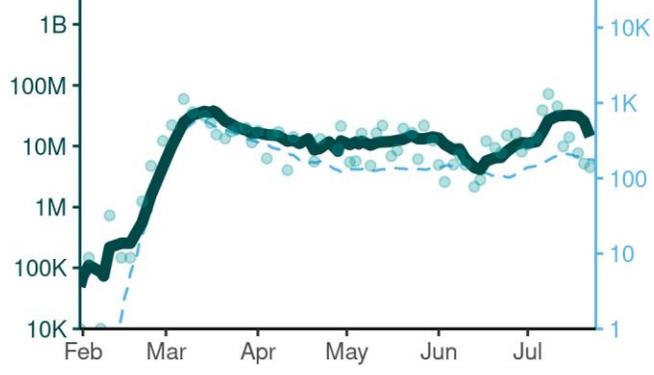
Hutt Valley Autosampler 133.0K



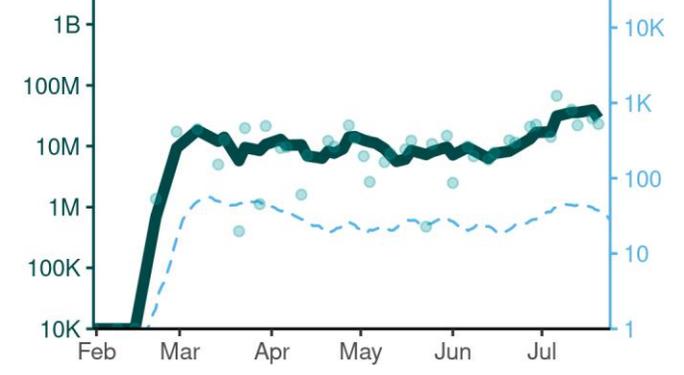
Masterton Grab 20.7K



Porirua Autosampler 85.0K



Wellington (Western) Autosampler 14.0K

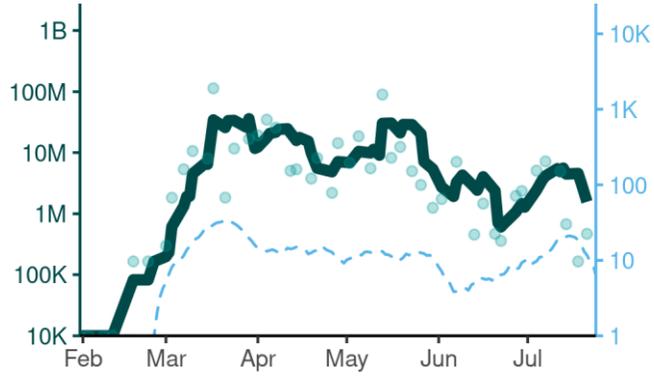


Status ● Detected ● Not detected

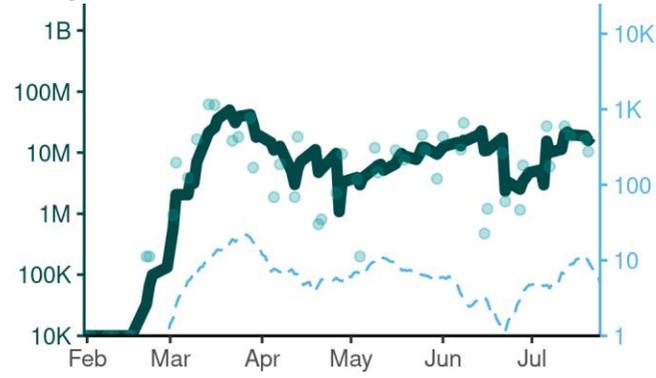
SARS-CoV-2 genome copies per person per day

Cases - 7 day rolling average

Carterton *Grab 5.8K*

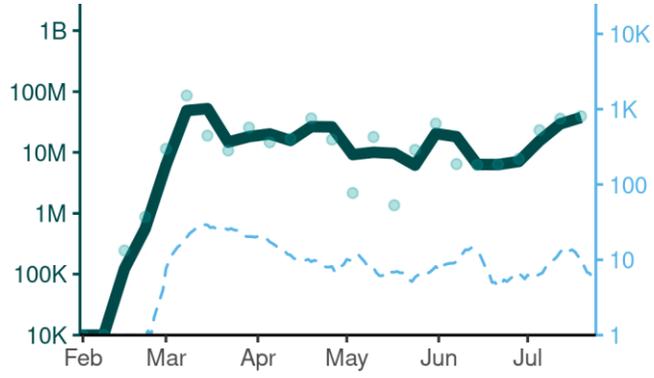


Greytown *Grab 2.4K*

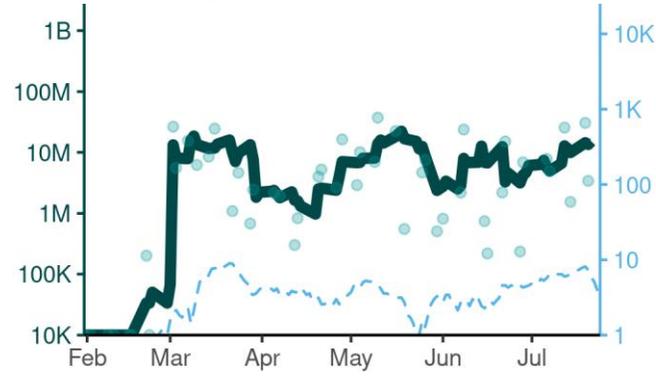


SARS-CoV-2 genome copies per person per day

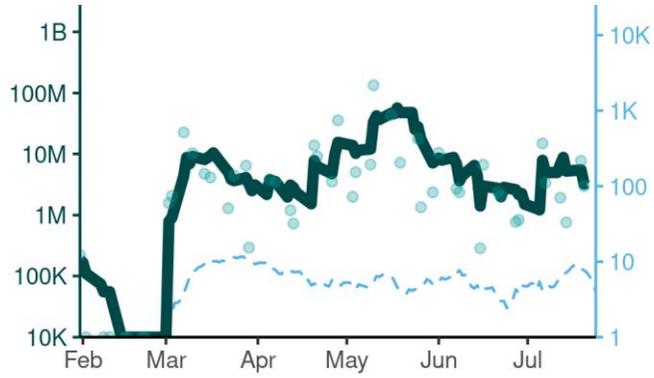
Otaki *Grab 3.5K*



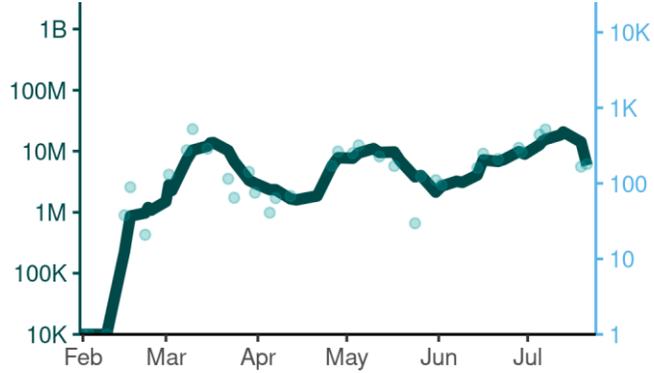
Martinborough *Autosampler/grab 1.6K*



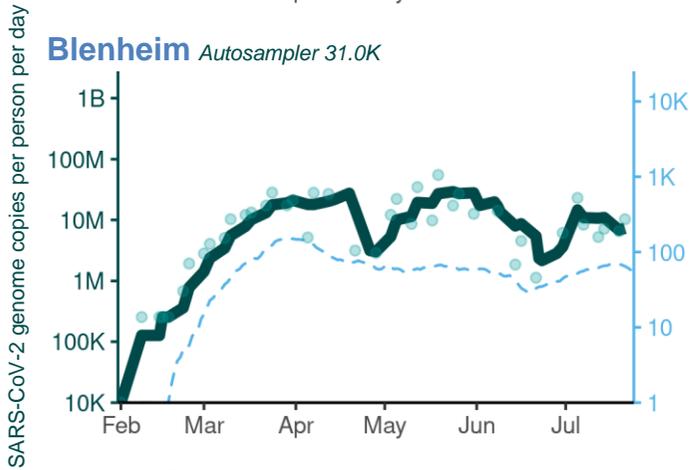
Featherston *Grab 2.5K*



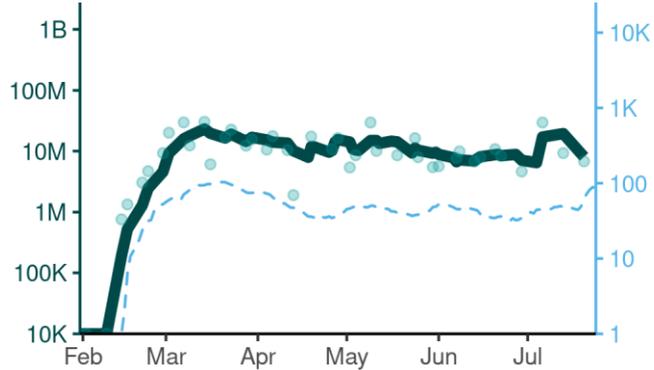
Tasman, Nelson, and Marlborough
Richmond/Nelson South Autosampler 60.0K



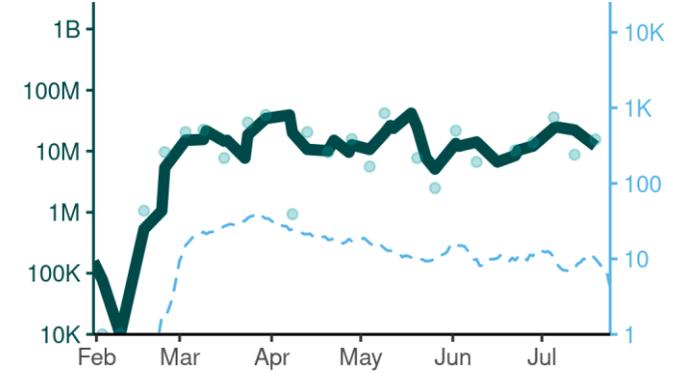
Blenheim Autosampler 31.0K



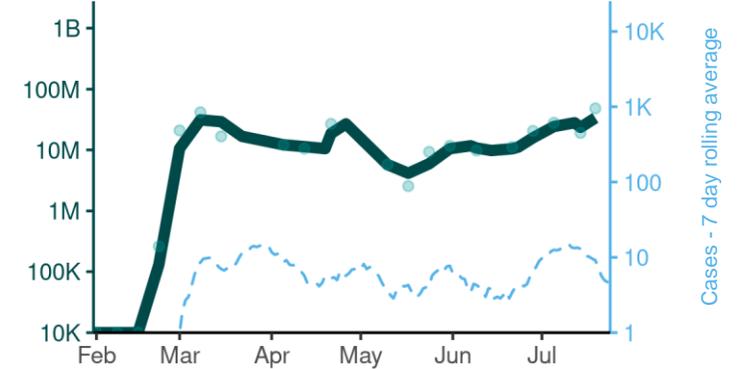
Nelson Central/North Autosampler 26.0K



Motueka Autosampler 8.3K



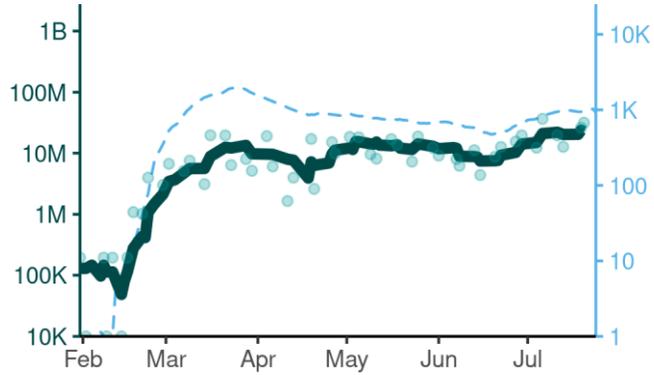
Picton Autosampler 5.0K



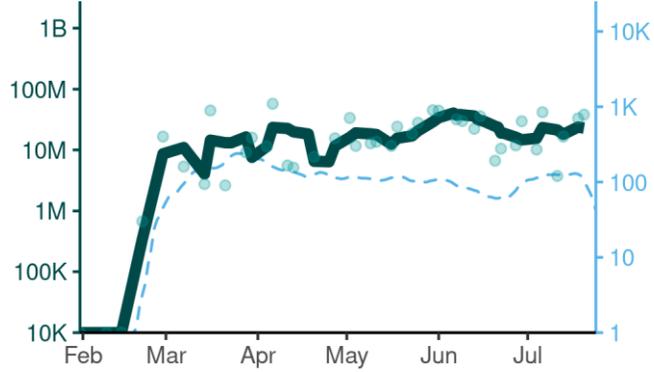
Status ● Detected ● Not detected

West Coast and Canterbury

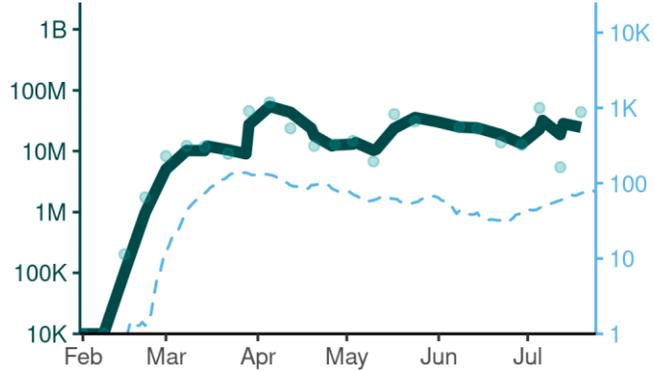
Christchurch Autosampler 368.0K



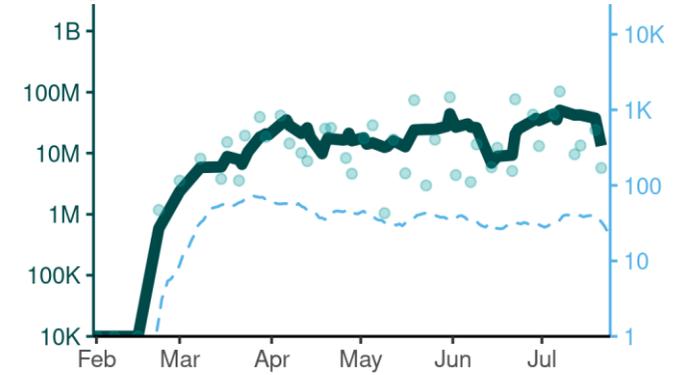
Rolleston & Eastern Selwyn Autosampler 35.0K



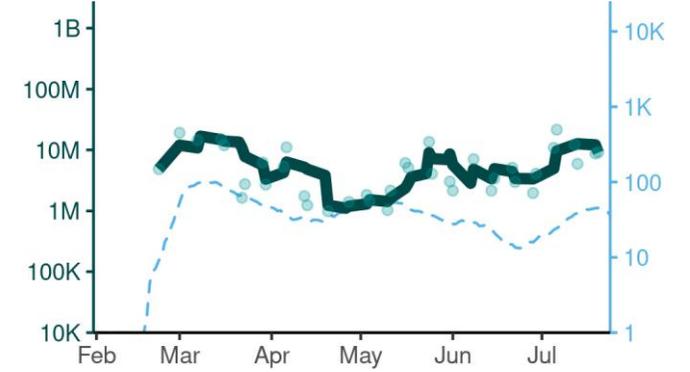
Timaru Autosampler 28.0K



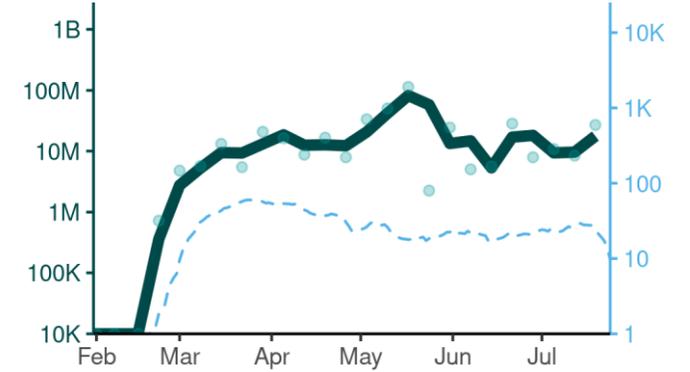
Rangiora Grab 19.0K



Ashburton Autosampler 18.0K



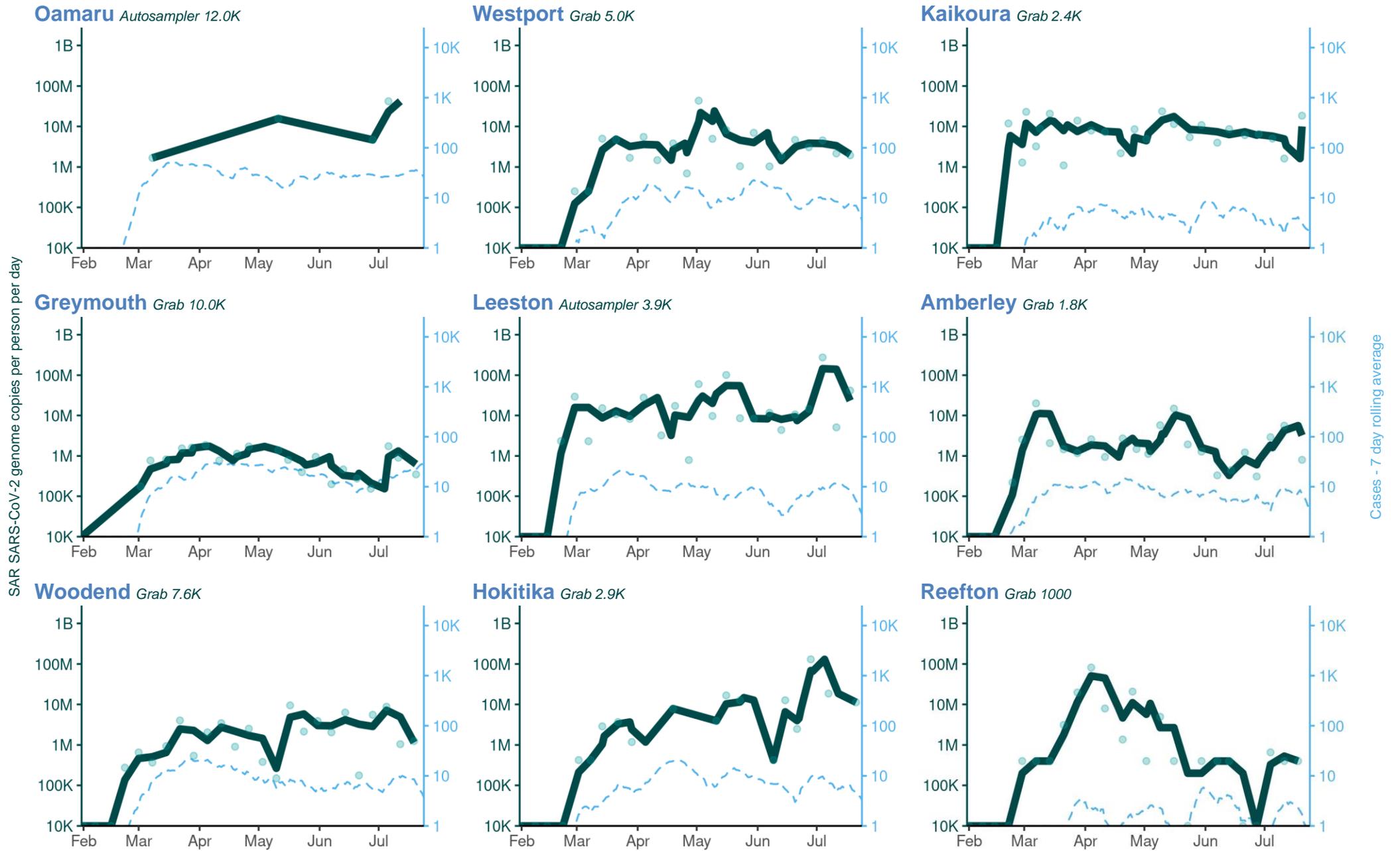
Kaipoi Grab 12.5K



Status ● Detected ● Not detected

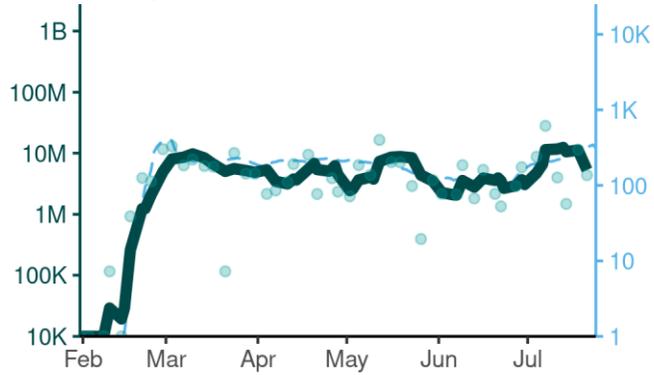
SARS-CoV-2 genome copies per person per day

Cases - 7 day rolling average

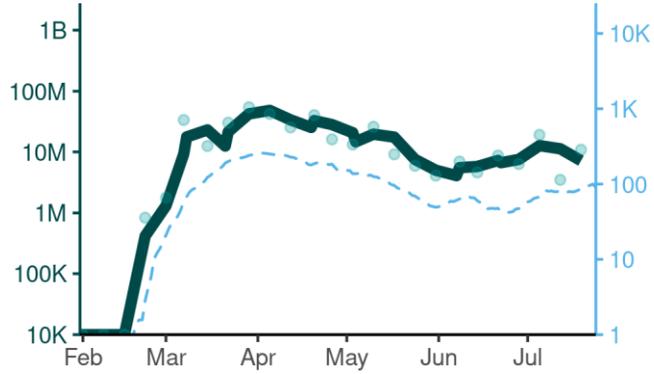


Otago and Southland

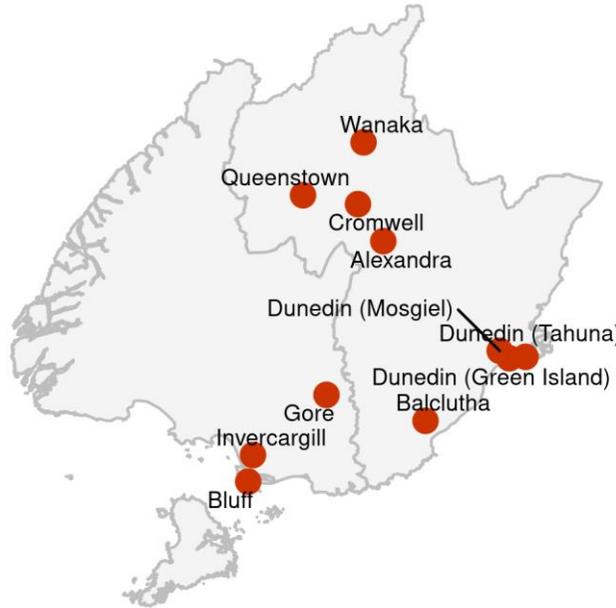
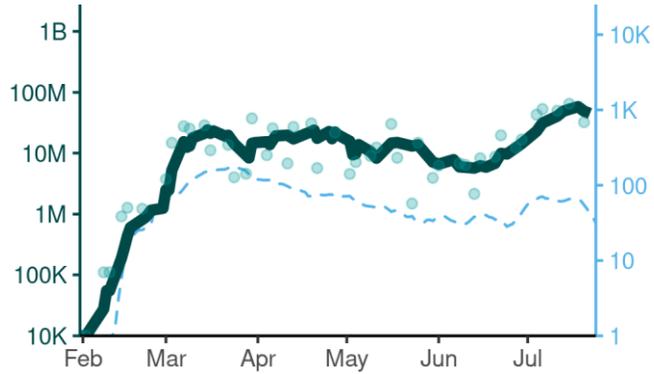
Dunedin (Tahuna) Autosampler 84.0K



Invercargill Autosampler 50.0K

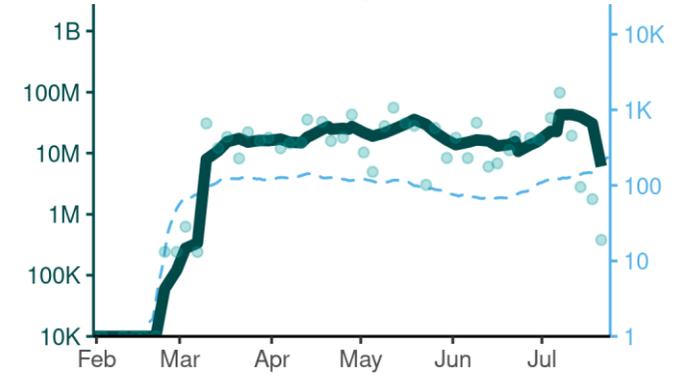


Queenstown Autosampler 40.0K

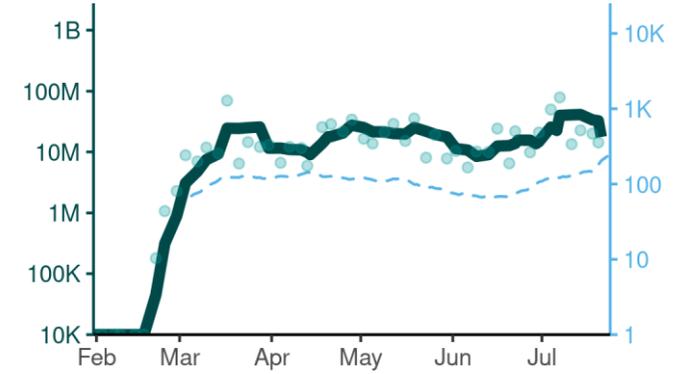


Status ● Detected ● Not detected

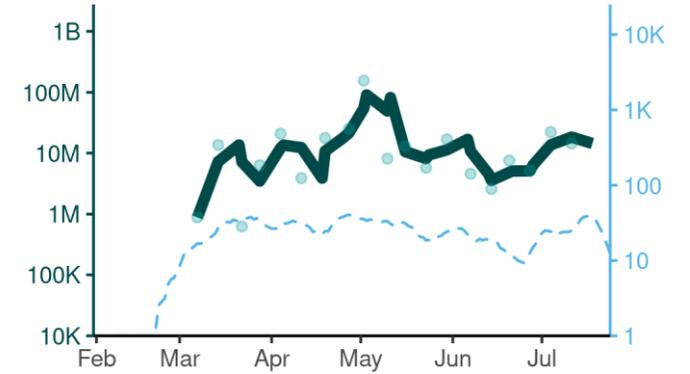
Dunedin (Green Island) Autosampler 22.9K



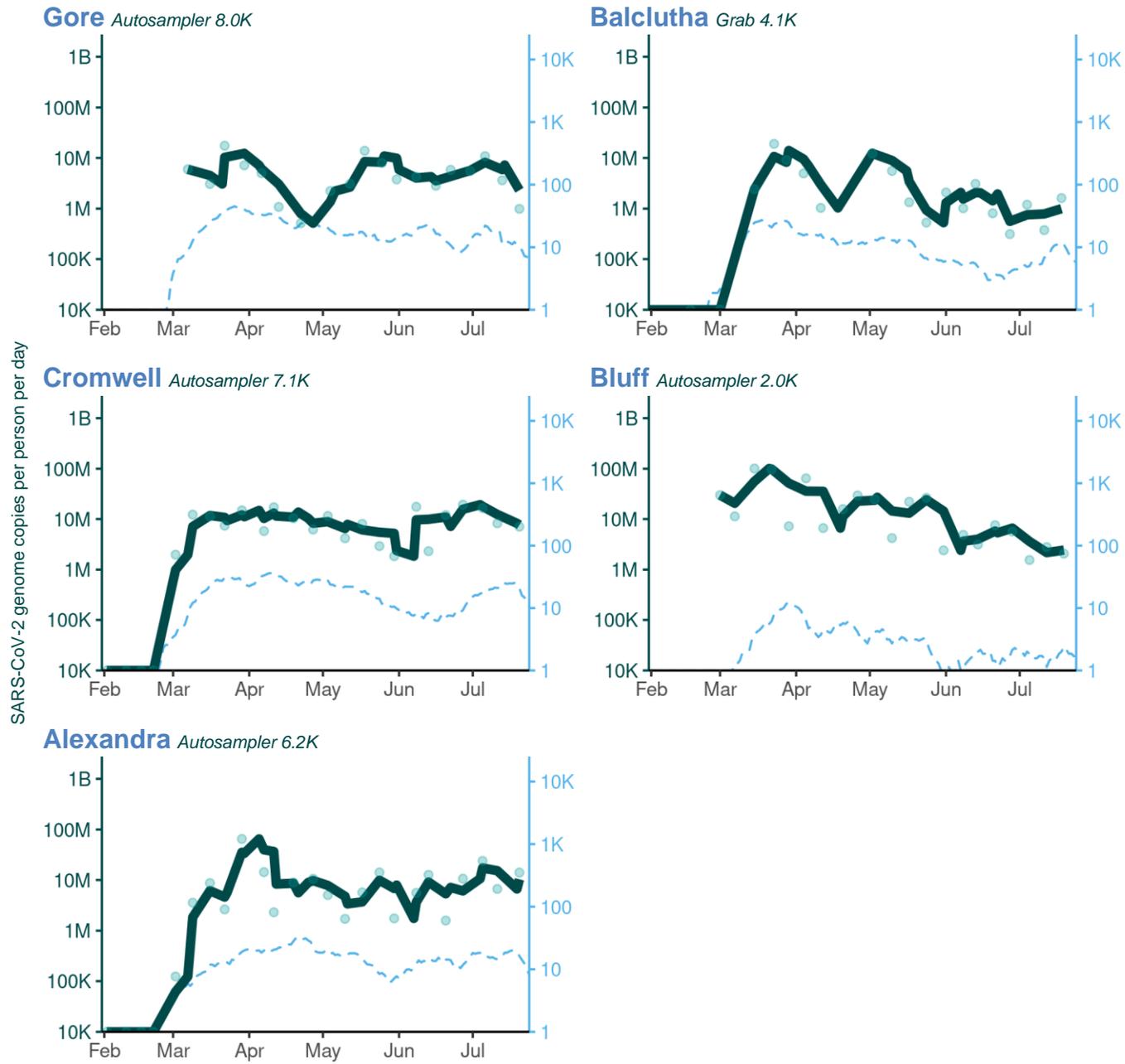
Dunedin (Mosgiel) Autosampler 14.6K



Wanaka Grab 14.5K



Cases - 7 day rolling average



Acknowledgements

This work represents the combined efforts of many 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 the ESR by a team which may, on any given week, include contributions from: Joanne Chapman, Dawn Croucher, Joanne Hewitt, Joycelyn Ho, Anower Javed, Susan Lin, Olivia Macrae, Ashley McDonald, Andrew Ng, Ashley Orton, Paula Scholes and Fatiha Sulthana. Data science analysis, visualisation and reporting is the result of team effort from: Franco Andrews, Bridget Armstrong, Michael Bunce, Raewyn Campbell, Joanne Chapman, Gerhard de Beer, Richard Dean, Brent Gilpin, Joanne Hewitt, Dawen Li, Lillian Lu, Helen Morris and Bindu Priya. Ongoing support for this work from the Ministry of Health and ESR management is appreciated.

Notes

Overview

SARS-CoV-2, the virus that causes COVID-19 disease, is shed in the faeces of people that are infected and so the viral RNA can be detected in wastewater. As such, testing wastewater for SARS-CoV-2 RNA is an efficient population-based COVID-19 surveillance tool. Based on national and international data, this method has been shown to be an indicator of increasing and decreasing cases (i.e., early warning system) and complements other surveillance tools. A national wastewater COVID-19 surveillance programme was established in 2021 by the Institute of Environmental Science and Research (ESR). This work is funded by the New Zealand Ministry of Health and is part of New Zealand's COVID-19 response.

Wastewater samples are collected from wastewater treatment plants across both the North and South Island of New Zealand. Most sites are sampled at least weekly between Monday and Thursday of any given week. The number of sites and frequency of collection varies over time.

Approach

Samples are sent from each wastewater treatment plant to one of the ESR laboratories (Porirua or Christchurch). Processing involves the concentration of virus and extraction of viral RNA. The presence of SARS-CoV-2 RNA in the sample is then determined using RT-qPCR.

A result of 'not detected' means that SARS-CoV-2 RNA is either absent from the sample, or at a level too low to be detected. When SARS-CoV-2 RNA is 'detected', the concentration in the sample can be calculated. Low amounts of SARS-CoV-2 RNA in a sample may not be able to be accurately quantified and is recorded as 'less than the limit of quantitation'. For quantitation, the raw concentration data (i.e., genome copies per L) is converted to a viral load of genome copies per person per day. This calculation considers the flow rate of wastewater entering the wastewater treatment plant and the population in the catchment. This is the population-normalised viral load.

Sites and frequency of sample collection: The catchment population sites selected for 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 covered 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 varies 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 an autosampler. 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 one of the ESR laboratories (Porirua or Christchurch). 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) is used to convert RNA to complementary DNA (cDNA), followed by quantitative PCR (qPCR) to amplify and quantify the cDNA. RT-qPCR is the standard method 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 be 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, a 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 litre (L) of wastewater. This is then converted to a viral load of **genome copies/person/day**. This conversion considers 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 the **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 viral lower concentrations or a false negative result).

In future, SARS-CoV-2 RNA concentrations will also be normalised by testing for the presence of pepper mild mottled virus (PMMoV). PMMoV is a virus that infects peppers but not humans. Consumption of peppers (capsicum) or pepper products, such as chilli sauce, means that PMMoV is detected in wastewater – normally at very high concentrations. Therefore, PMMoV has been found to be a useful proxy for the amount of faecal material in a wastewater sample. For normalisation, the concentration of SARS-CoV-2 RNA is divided by that of PMMoV in each sample. Different normalisation methods may result in changes to some data points, but trends are unlikely to change significantly.

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).

Key Points & Limitations

- Day to day variability in SARS-CoV-2 RNA concentrations, especially in smaller catchments, is to be expected. Greater variability is expected with grab samples, and with samples collected from sites with small populations.
- Generally, increasing viral loads are associated with increasing numbers of people with SARS-CoV-2 infection and vice versa (decreasing concentrations indicating decreasing cases). However, there are a number of factors that affect the amount of viral RNA detected. Thus, data from wastewater surveillance cannot indicate the exact number of COVID-19 cases in a catchment area.
- The number of COVID-19 cases reported via individual testing are reported for each region to provide a comparison to the wastewater results. The cases in each catchment area are an estimate of the number of people in that wastewater catchment that have reported a positive test. However, because the wastewater catchments do not exactly align with regional boundaries, the number of cases estimated by region and by water catchment area may be different.
- Data are provisional and may be subject to change by location.
- As septic tank systems are not connected to wastewater treatment plants, the wastewater from these households will not be represented in the data.

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END OF REPORT