National Wastewater Surveillance Programme - COVID-19

Weeks 40 & 41 (Weeks Ending 09 October & 16 October 2022)

Report prepared on 19 October 2022

96%	76%	Omicron BA.4/5 (>91%)
sites tested in the last 2 weeks had SARS-CoV-2 detected (92/96 sites)	NZ population covered by wastewater testing	Most prevalent variant detected

Nationally, SARS-CoV-2 levels in wastewater have been trending upwards since week 38. This is reflected by an increase in reported cases in recent weeks.

In the previous fortnight (weeks 40 and 41, ending 16 October 2022), SARS-CoV-2 RNA was detected in 96% of sites tested. Many sites, particularly those across the central regions of New Zealand, showed marked increases in viral levels. Overall, 17% of sites have levels of SARS-CoV-2 that were either below the limit of quantitation or not detected. In week 41 compared to Week 40, **56%** of sites showed **increased** SARS-CoV-2 levels and **23%** of sites showed a **decrease**. For week 41 compared to a month ago (week 37, ending 18 September 2022), **56%** of sites showed **increased** levels and **22%** of sites showed a **decrease**. The results for weeks 40 and 41 suggest that case rates are **31% and 43%** lower than would be expected based on the SARS-CoV-2 levels in wastewater, respectively.

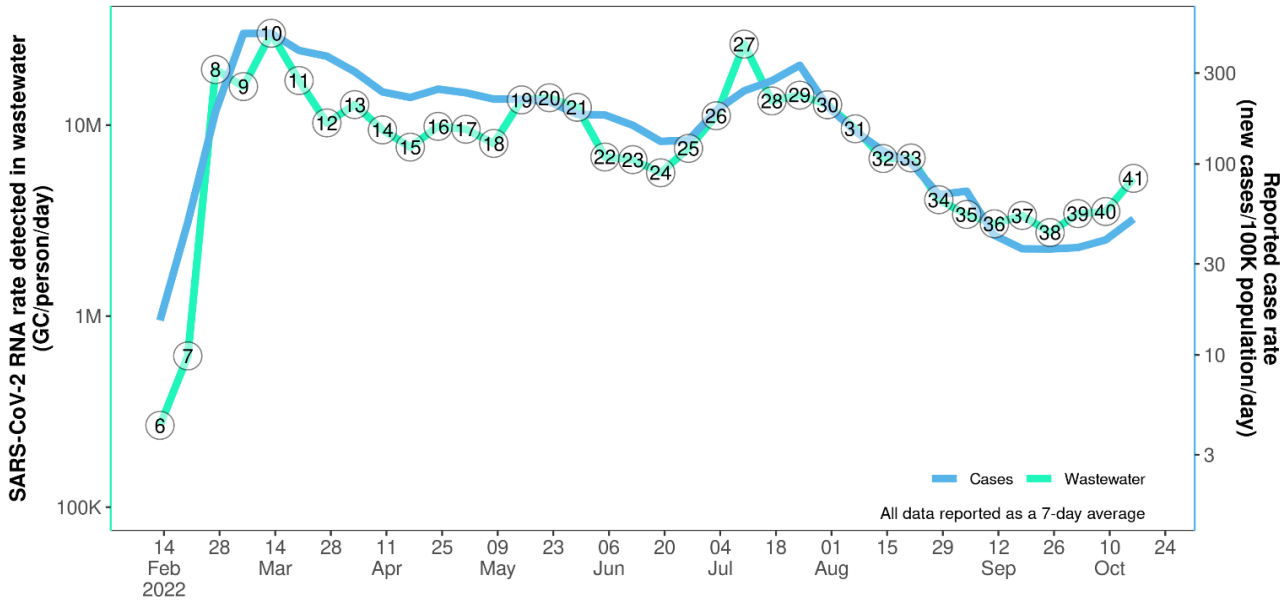


Figure 1a. National timeseries of estimated SARS-CoV-2 genome copies (GC) in wastewater rate (GC/person/day, green line) and reported case rate (new cases/100,000 population/day, blue line). Numbers in the points are the week of the year. **Log_{10} scale**. Data reported as 7-day average.

Combined Results for Weeks 40 & 41 (Weeks ending 09 October & 16 October 2022)

In the two weeks ending 16 October 2022, 266 samples were collected from 96 locations across New Zealand.

SARS-CoV-2 RNA was detected in 259 samples from 92/96 (96%) of sites tested during this period (Figure 2, Table 1). SARS-CoV-2 was not detected in three samples in week 40 (Porangahau, Waipawa and Woodville but detected in another Woodville sample collected that week) and four samples in week 41 (Otane, Waipawa, Balclutha and Mangawhai but detected in another Managawhai sample collected that week).

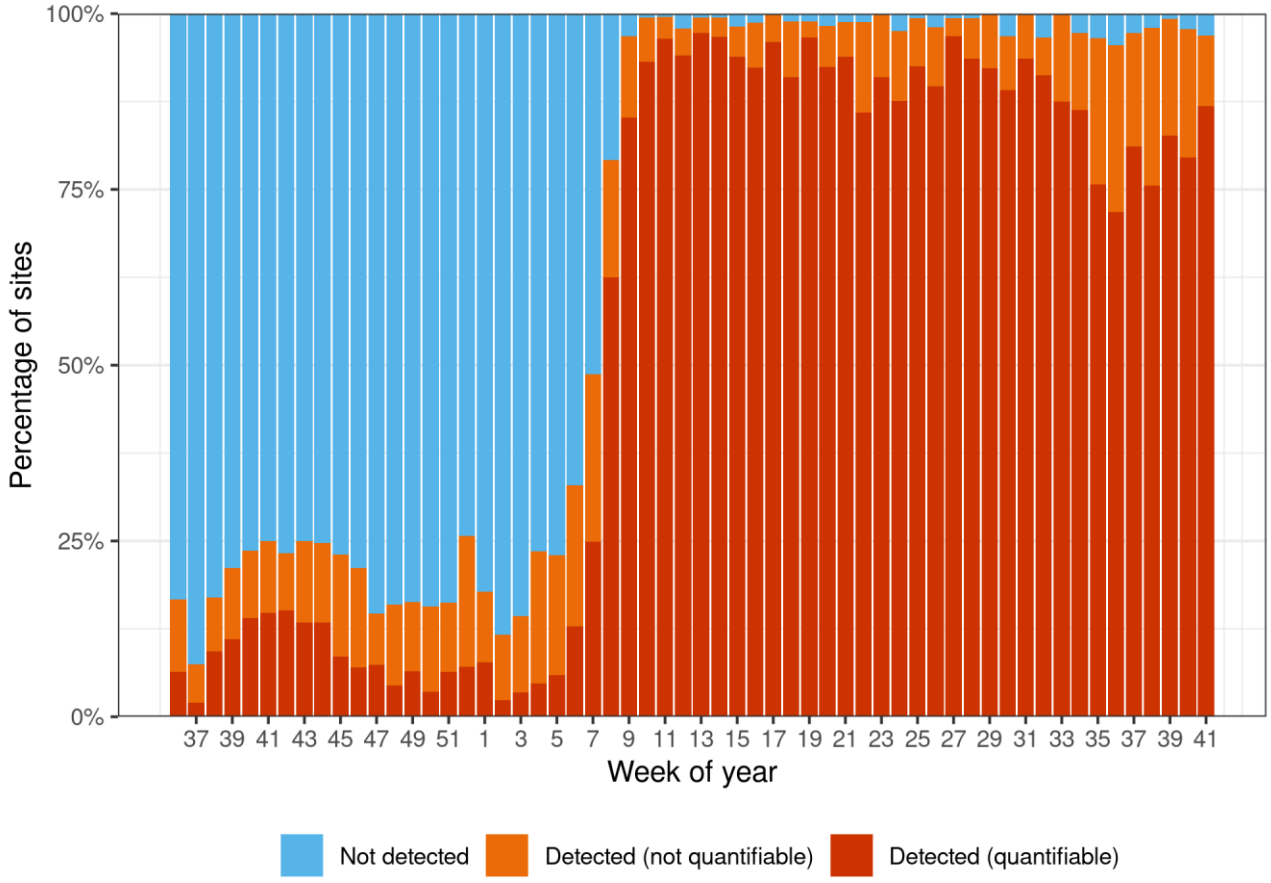


Figure 2. Results for SARS-CoV-2 RNA in wastewater collected across New Zealand.

Regional Trends

Regional summaries (Figure 3) of the wastewater data indicates increasing viral levels in the Central and Te Waipounamu regions. In other regions, viral levels are generally steady.

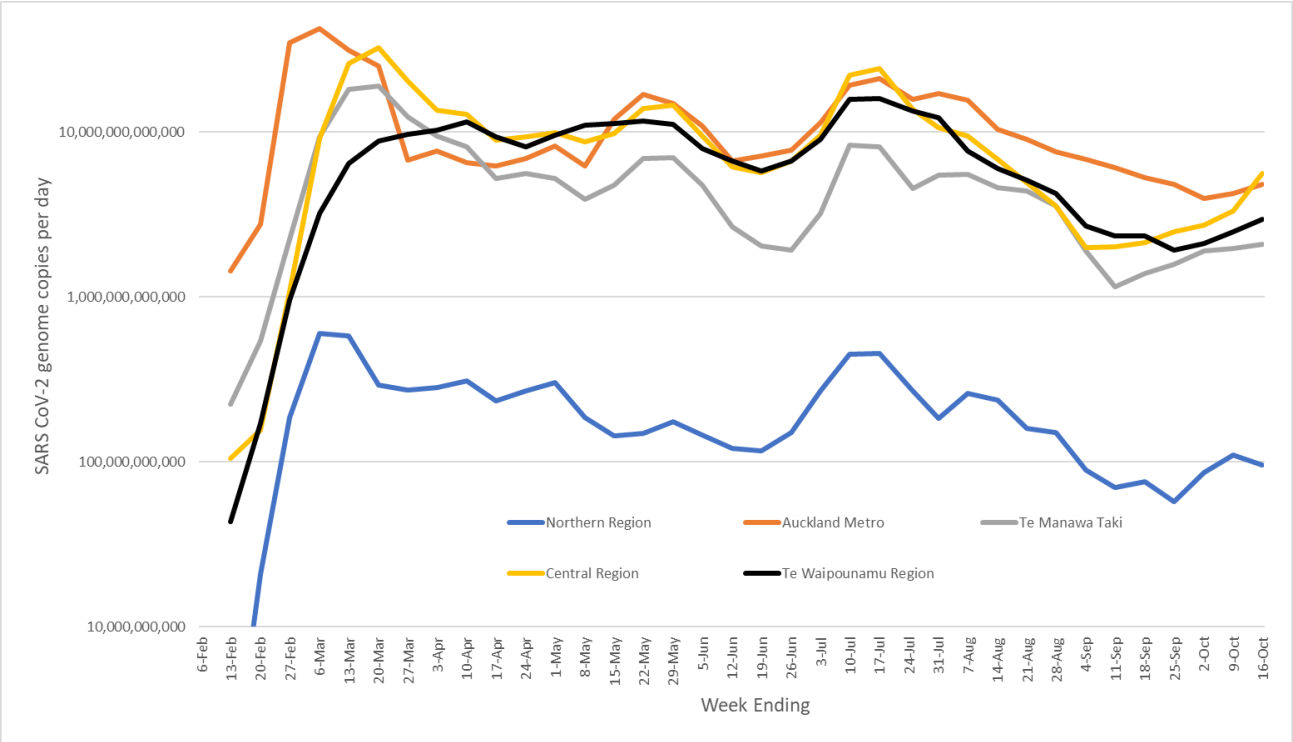


Figure 3. Total SARS-CoV-2 genome copies detected per day in the five Ministry of Health regions (Rolling two-week average).

There is however site to site variation as illustrated in Figure 4 and the individual site plots. In week 41 compared to Week 40, **56%** of sites showed **increased** SARS-CoV-2 levels and **23%** of sites showed a **decrease** (

4A). For week 41 compared to a month ago (Week 37), **56%** of sites showed **increased** levels and **22%** of sites showed a **decrease** (Figure 4C)**.**

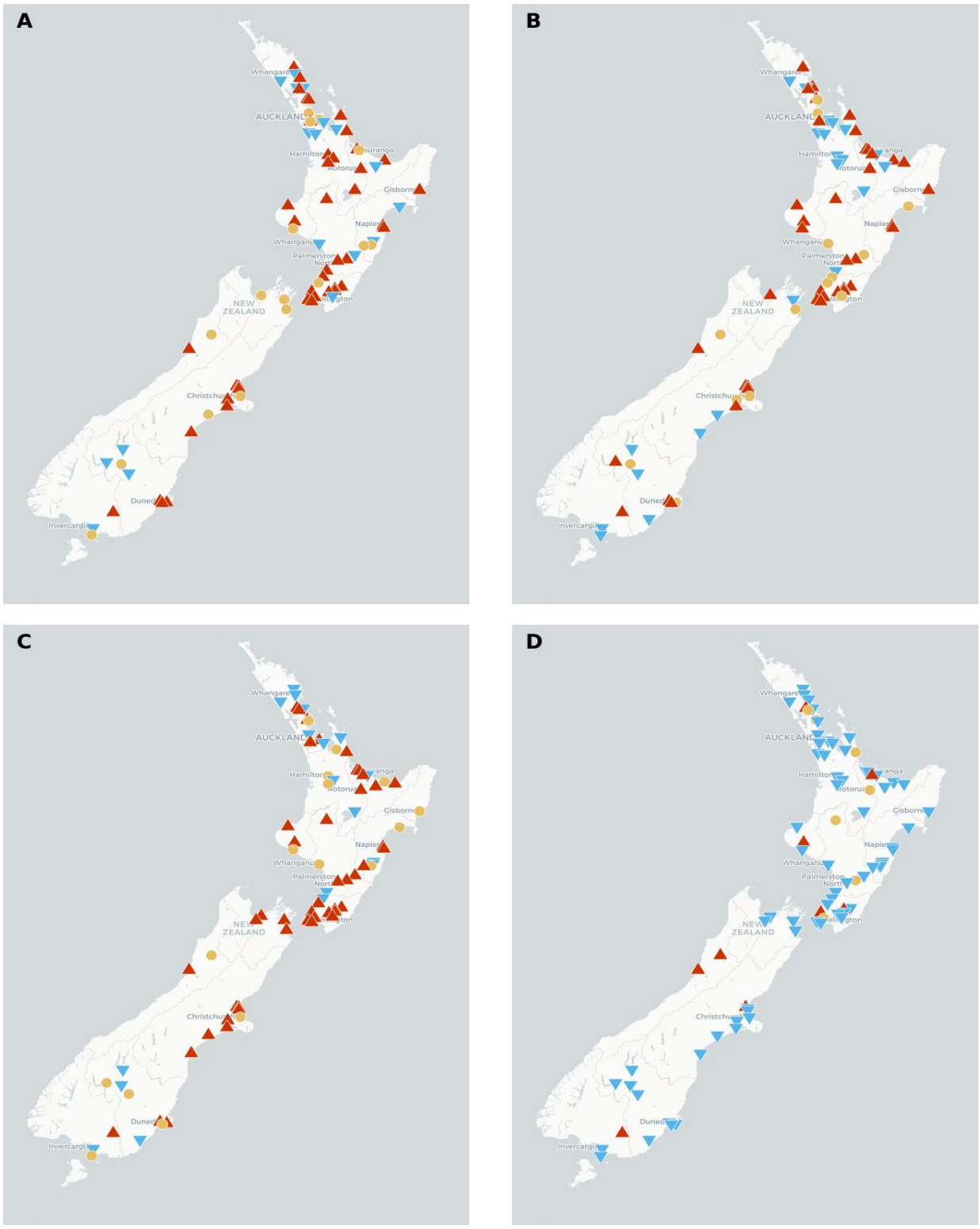


Figure 4. Comparison of SARS-CoV-2 levels for the week ending 16 October 2022, compared to levels measured: A) 1 week ago; B) 2 weeks ago; C) 4 weeks ago; D) 12 weeks ago. Only sites with results for both time points are included. When the viral quantity is 30% or more higher this is labelled as increased (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.esr.cri.nz/our-expertise/covid-19-response/wastewater-testing-results.

Wastewater Variant Analysis

In collaboration with Wilderlab, ESR generated the variant analysis results (Figure 5, Figure 6) from a set of nationwide sentinel sites in: Week 40 (ending 9 October 2022) and Week 41 (ending 16 October 2022).

Consistent with the WGS of clinical cases, the BA.4/5 variants continue to be the dominant circulating SARS-CoV-2 circulating variants across Aotearoa (national average of 91%). In the past fortnight, 40% of monitored sites were 100% BA.4/5 (i.e., other variants could not be detected in these sites as they were either not present, or below the limit of detection). This is down from 81% of sites being 100% BA.4/5 in the previous fortnight (weeks 38 & 39).

Across both weeks, BA.2.75 lineages have been identified in sites across the country. This is consistent with WGS of clinical cases in recent weeks. Additionally, in Week 41 signals of BQ.1.1 were detected in wastewater collected from Auckland (Western), Rotorua and Porirua. BQ.1.1 was not detected in week 40 at any site.

The level of precision and sensitivity of variant percentages can be uncertain.

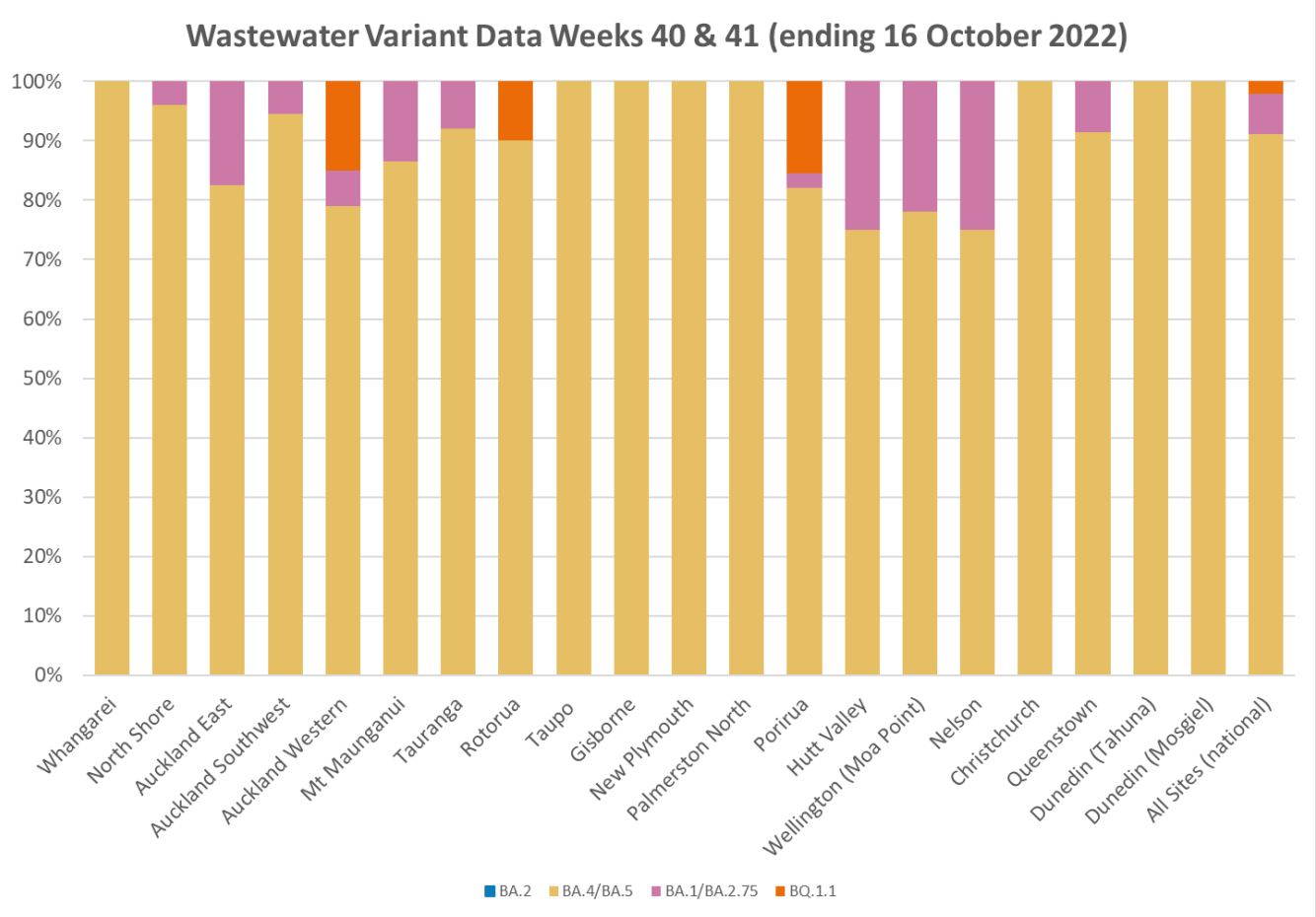


Figure 5. Data from sentinel wastewater sites across NZ using a S-gene (spike) barcoding assay able to 'call' the BA.2 (including BA.2.12.1), BA.4/BA.5, BA.1/BA.2.75 and BQ.1.1 (sub)variants. Wastewater samples were collected from up to 20 sentinel sites. The level of precision and sensitivity in these percentage estimates can be uncertain.

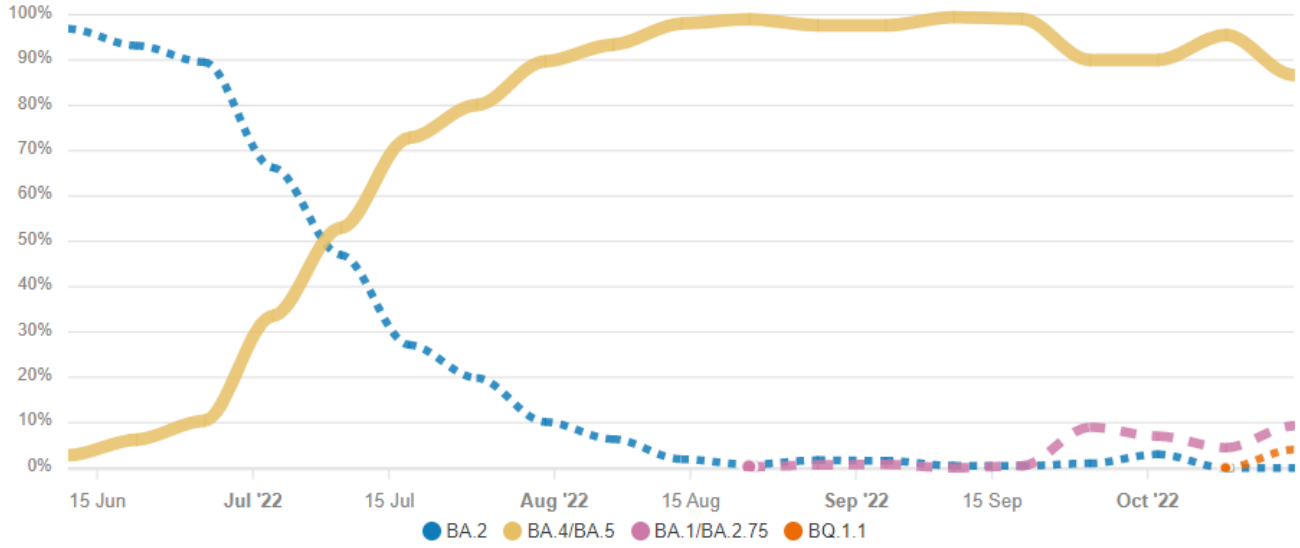
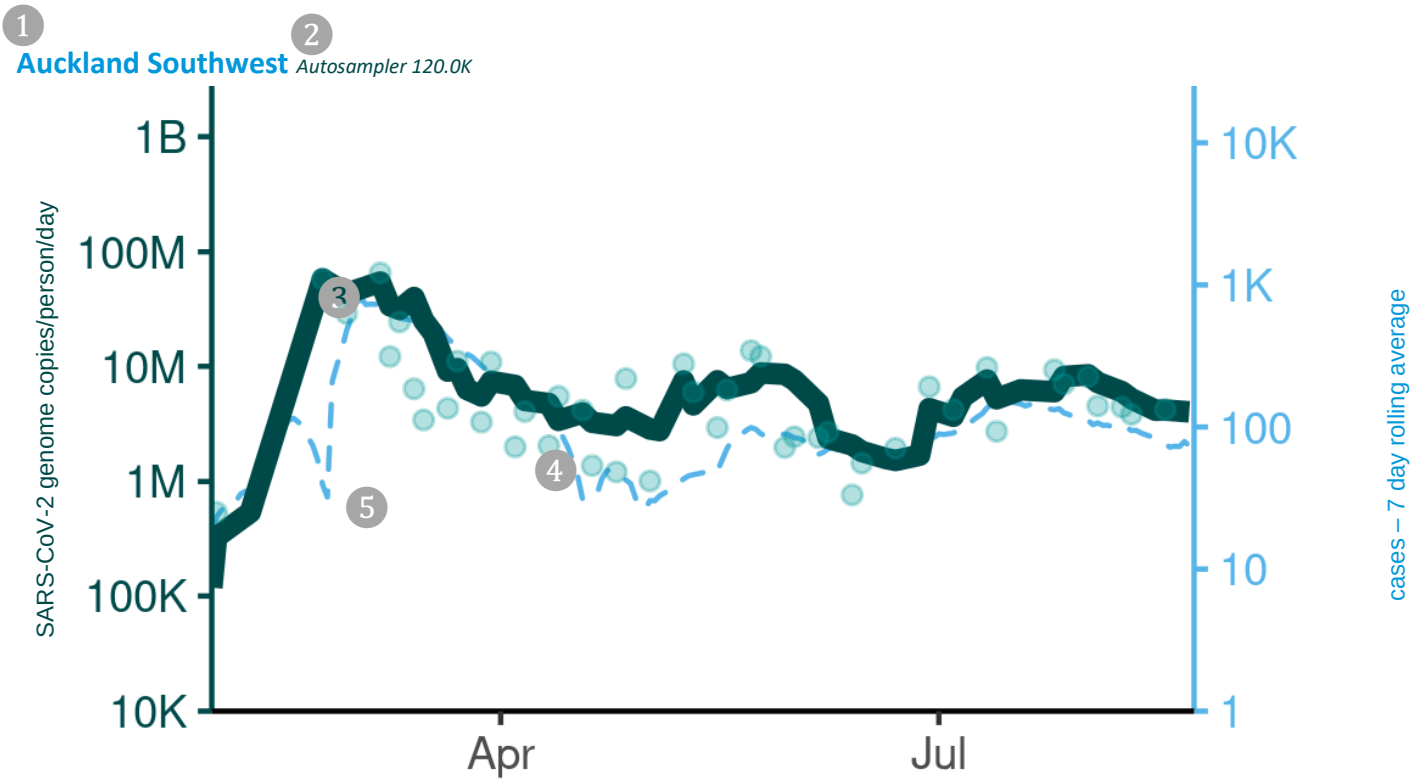


Figure 6. Change in variant prevalence over time at a national scale. Data are collected from up to 20 sentinel sites each week

Interpreting Sites Graphs

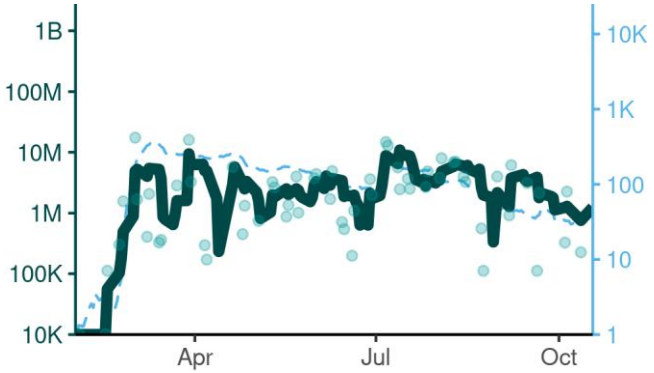


1. Site Name
2. Sample collection method and population. Results based on autosampler may be more representative than grab sample-based results.
3. Wastewater results shown as solid line. 14-day average of genome copies/person/day on a $\log_{10}$ scale.
4. Individual results samples shown as circles. 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. Data are not available for all sites and subject to change.

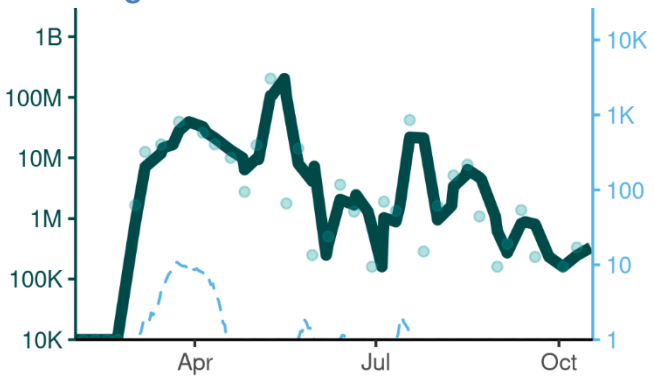
Note: Scales on all graphs have been normalised to cover the same scale on every graph. Care should be taken when interpreting the data.

Northland

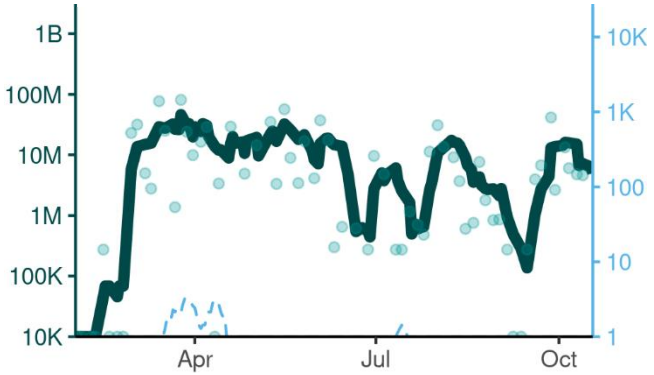
Whangarei *Autosampler 65.0K*



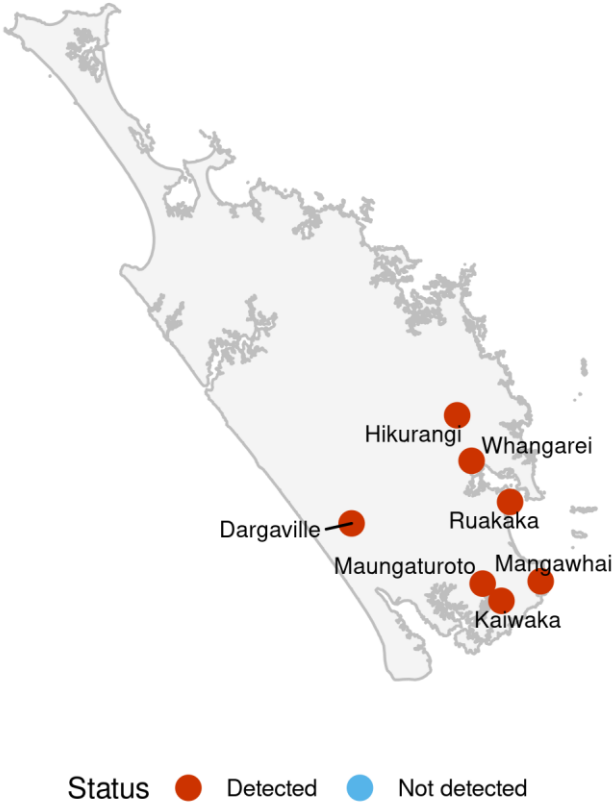
Hikurangi *Grab 1.7K*



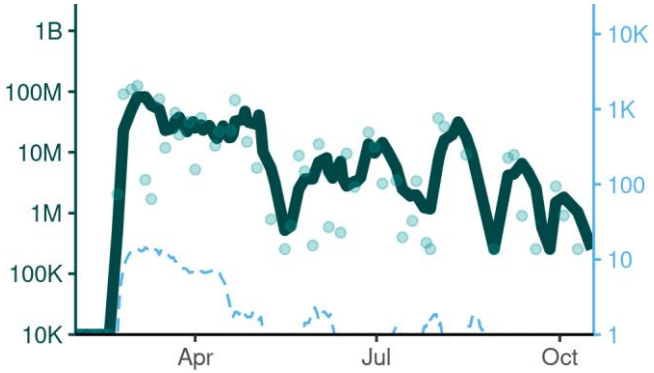
Maungaturoto *Grab 1.3K*



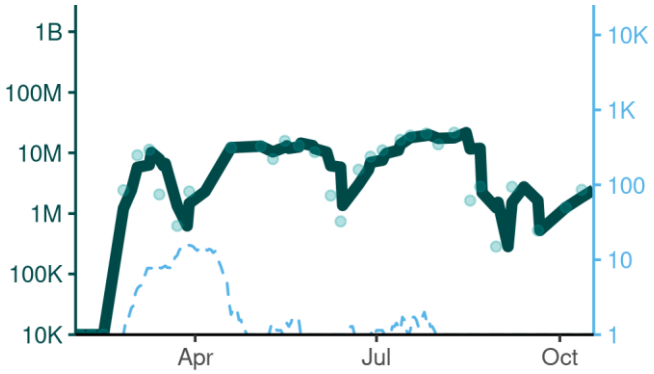
SARS-CoV-2 genome copies / day / person



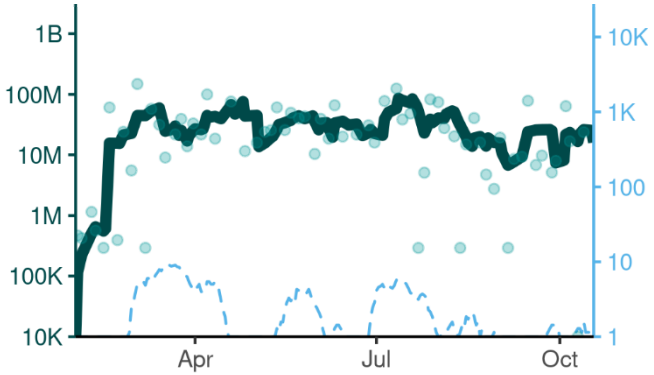
Dargaville *Grab 5.0K*



Ruakaka *Grab 4.5K*



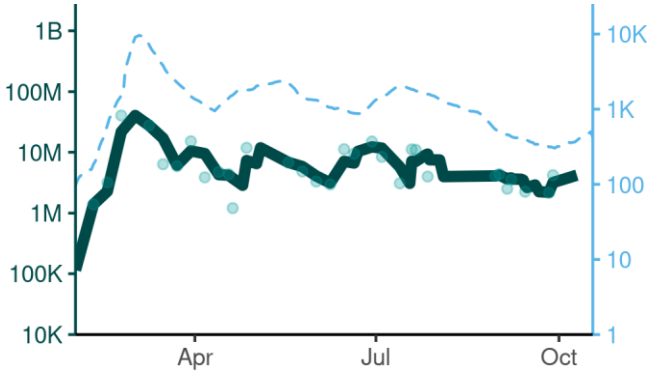
Mangawhai *Grab 1.1K*



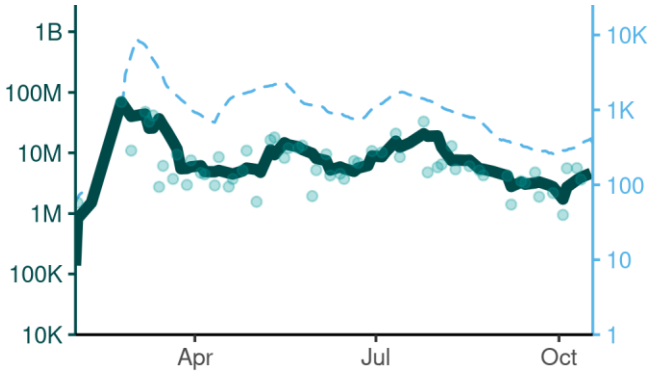
Cases - 7 day rolling average

Auckland

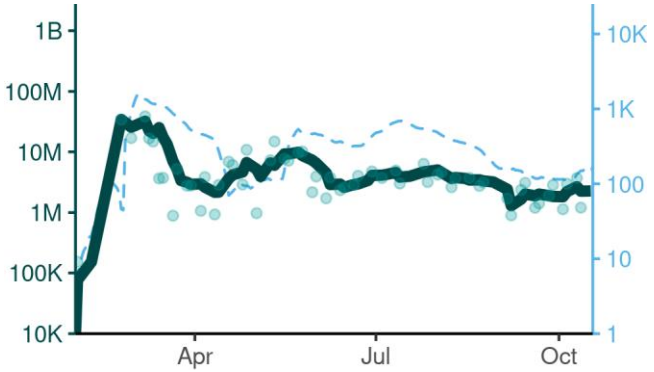
Auckland (Combined) *Autosampler 1.1M*



Auckland East *Autosampler 680.0K*

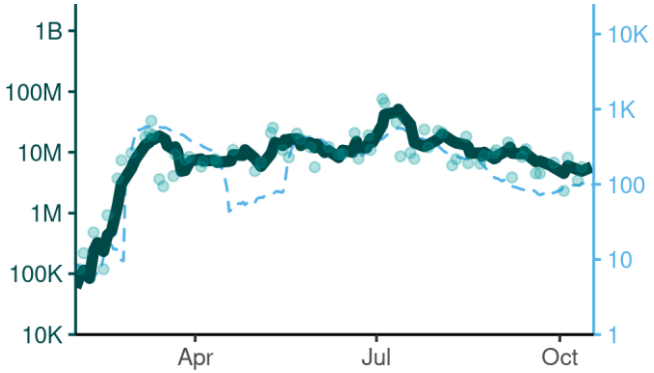


Auckland West *Autosampler 315.0K*

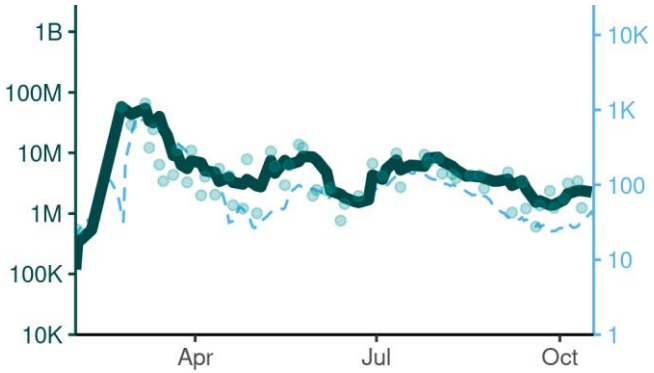


SARS-CoV-2 genome copies / day / person

North Shore *Autosampler 240.0K*

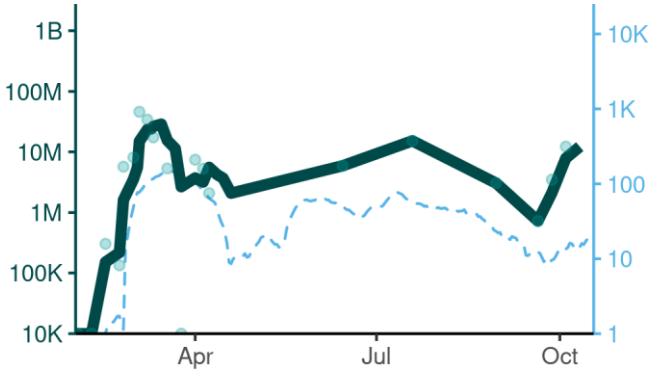


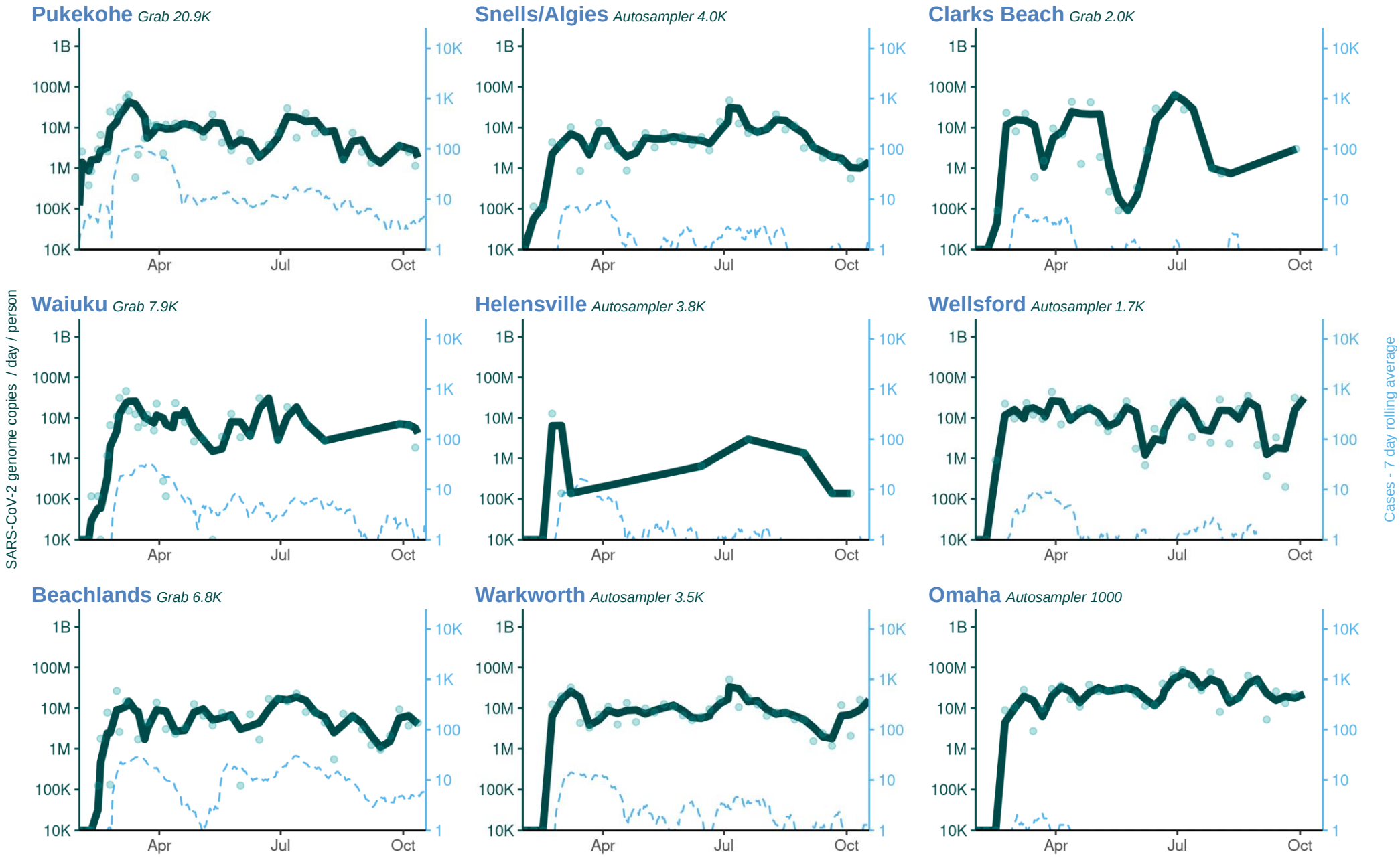
Auckland Southwest *Autosampler 120.0K*



Cases - 7 day rolling average

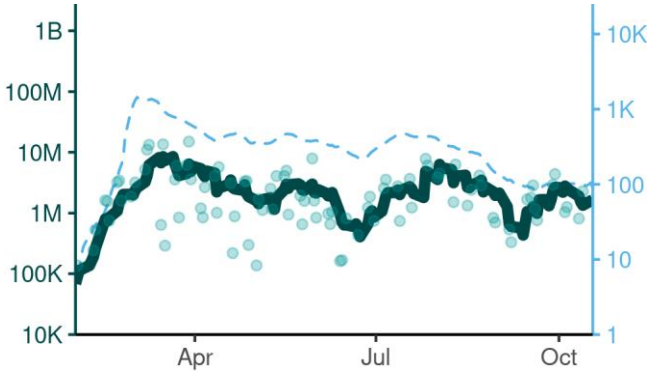
Army Bay *Autosampler 42.0K*



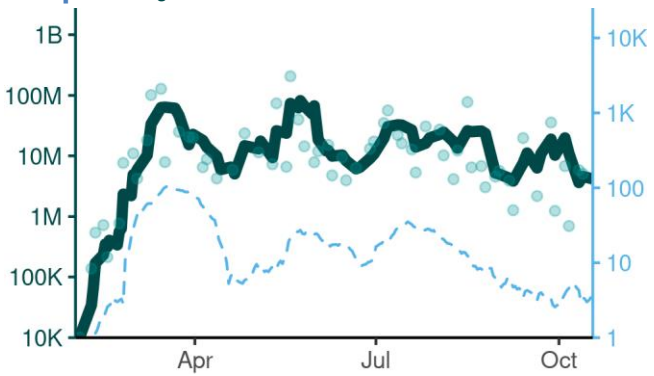

Pukekohe Grab 20.9K
Snells/Algies Autosampler 4.0K
Clarks Beach Grab 2.0K
Waiuku Grab 7.9K
Helensville Autosampler 3.8K
Wellsford Autosampler 1.7K
Beachlands Grab 6.8K
Warkworth Autosampler 3.5K
Omaha Autosampler 1000
SARS-CoV-2 genome copies / day / person
Cases - 7 day rolling average
1B
100M
10M
1M
100K
10K
1K
100
10
1
Apr
Jul
Oct

Waikato

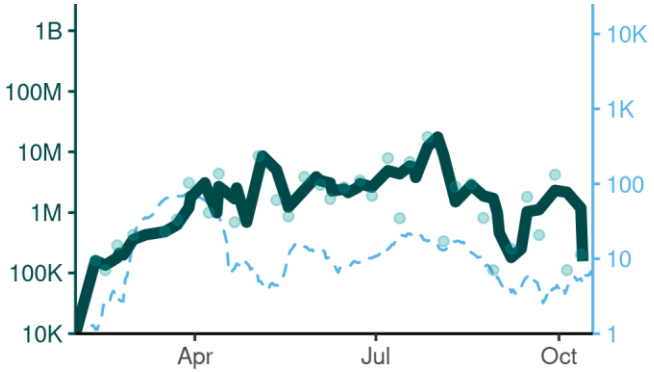
Hamilton *Autosampler 169.0K*



Taupo *Auto/grab 23.0K*

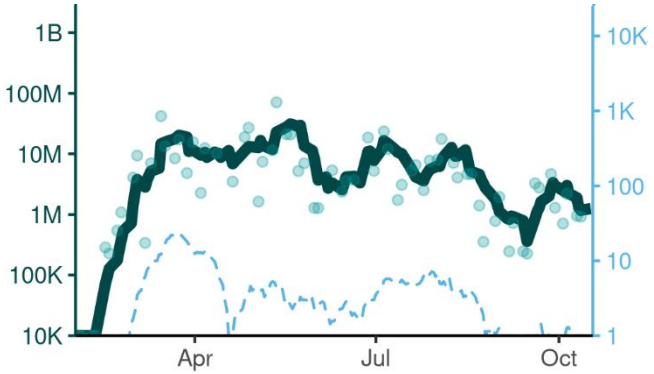


Cambridge *Autosampler 20.1K*

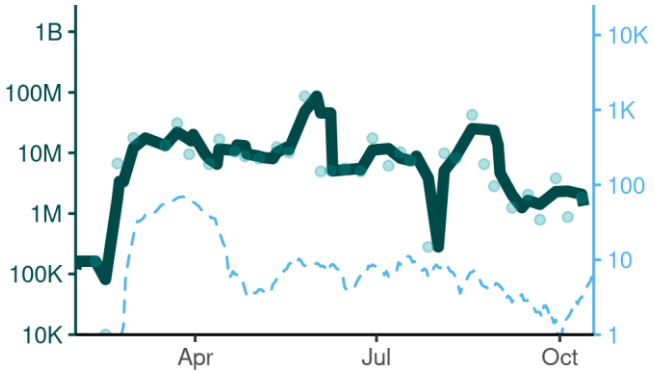


SARS-CoV-2 genome copies / day / person

Thames *Autosampler 7.5K*

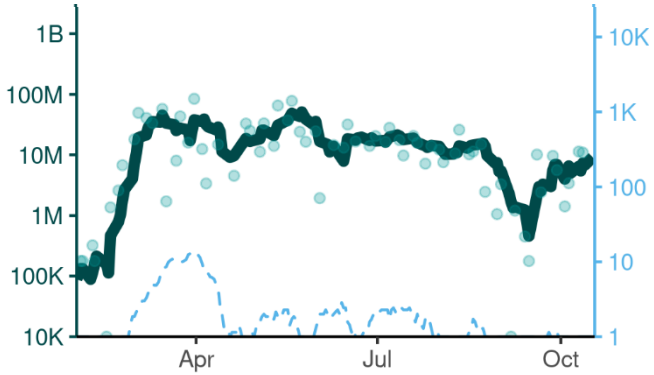


Te Awamutu *Autosampler 13.1K*

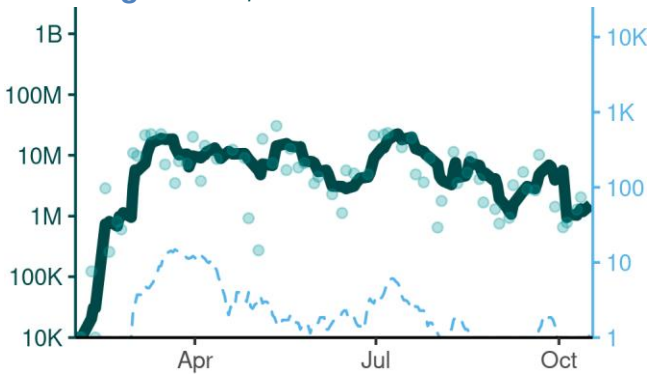


Cases - 7 day rolling average

Whangamata *Autosampler 4.0K*



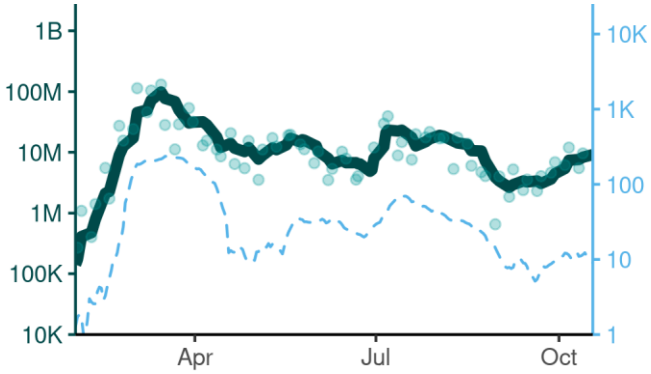
Whitianga *Autosampler 6.6K*



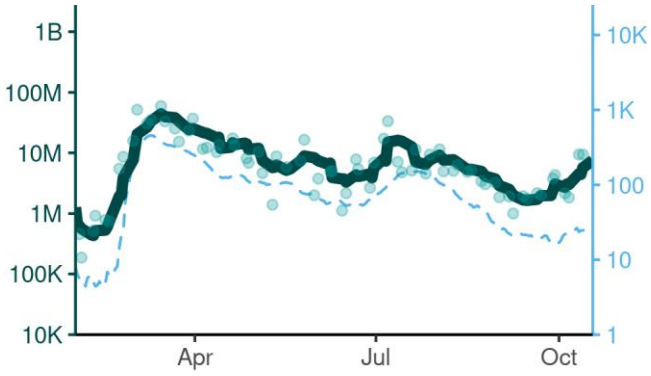
SARS-CoV-2 genome copies / day / person

Bay of Plenty and Gisborne

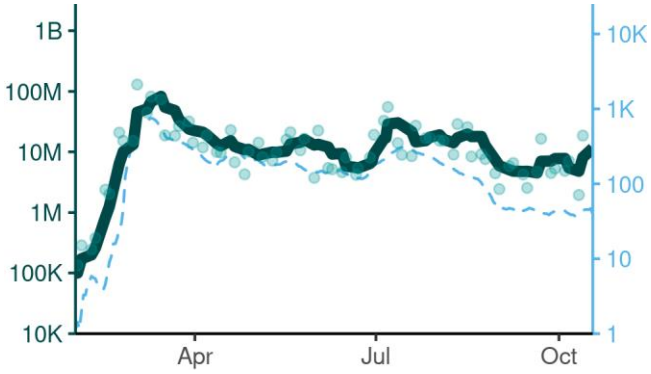
Mt Maunganui/Papamoa *Autosampler 65.0K*



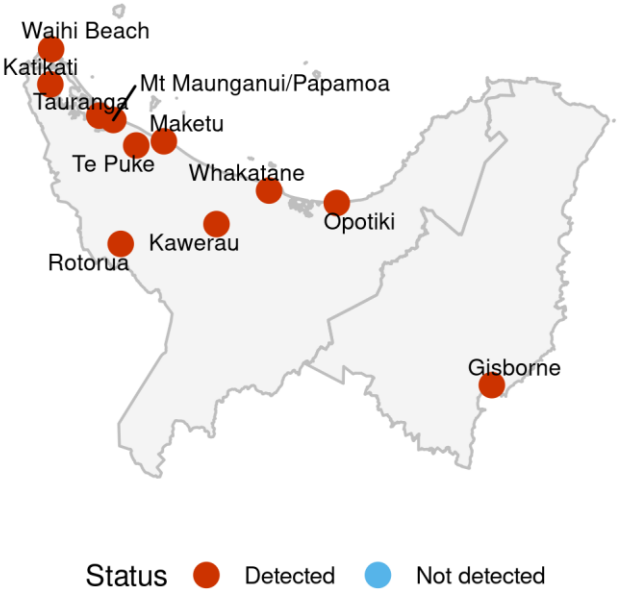
Rotorua *Autosampler 59.0K*



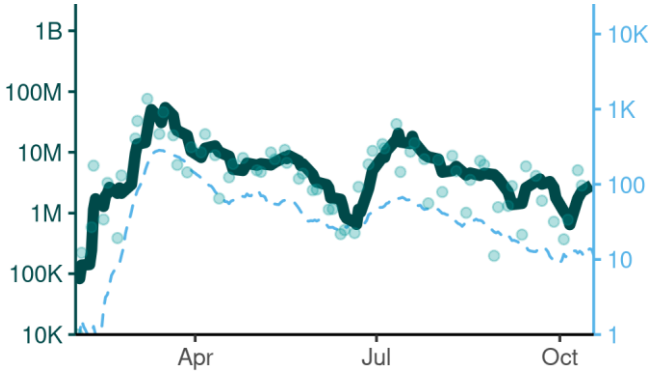
Tauranga *Autosampler 50.0K*



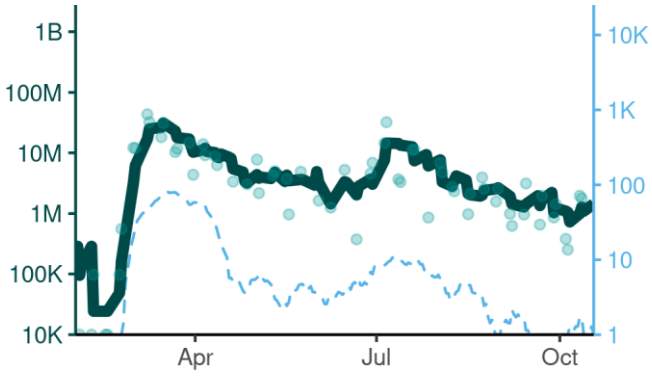
SARS-CoV-2 genome copies / day / person



Gisborne *Autosampler 37.0K*

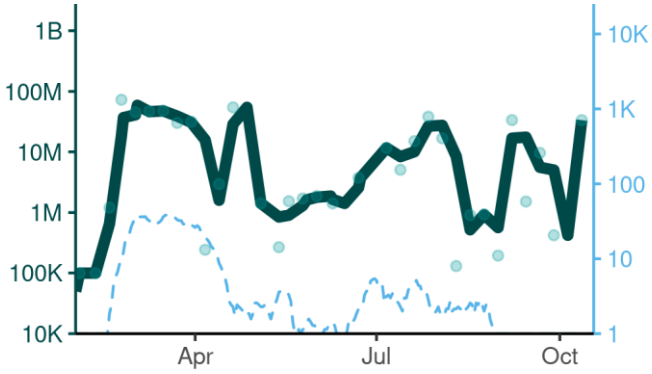


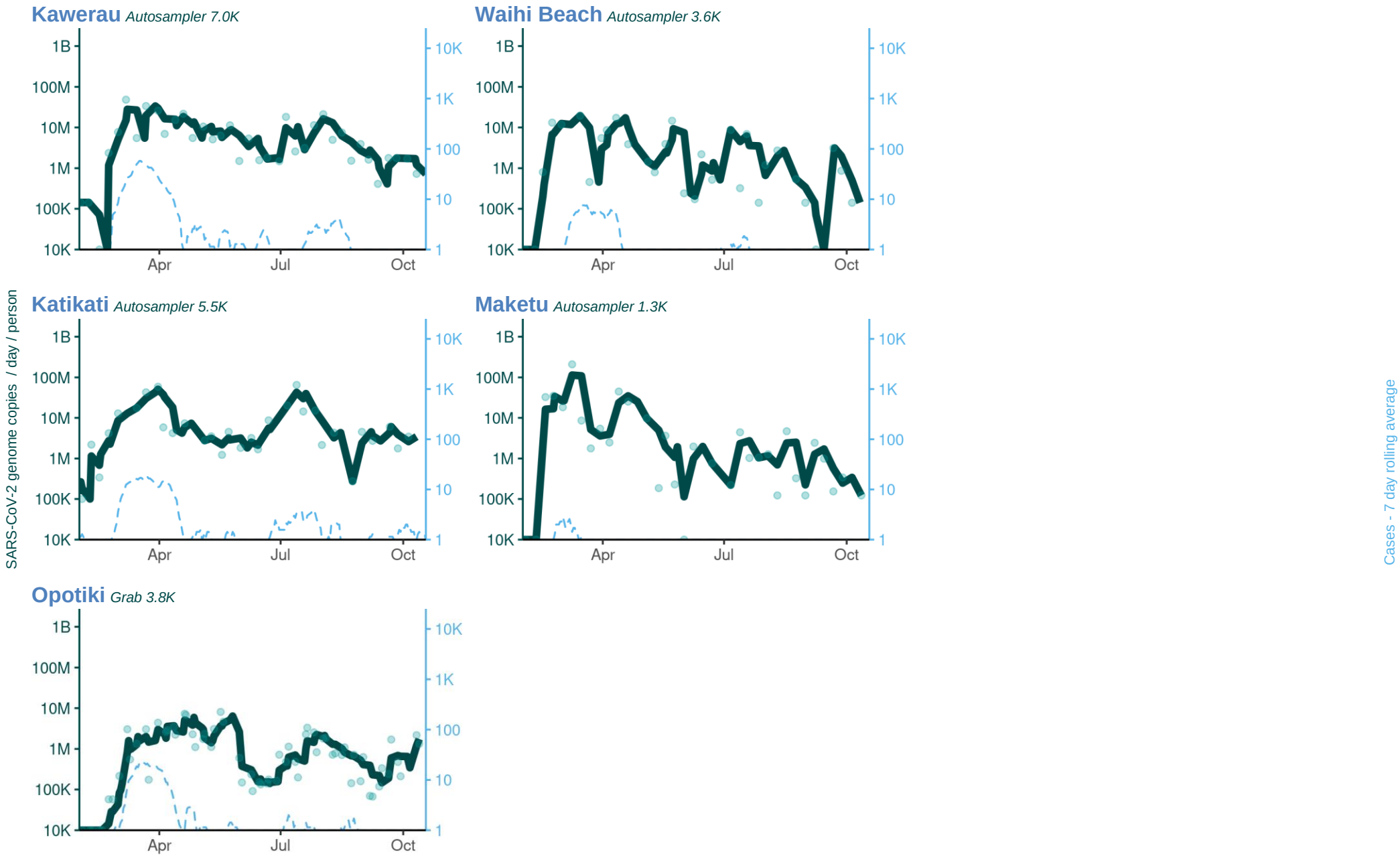
Whakatane *Autosampler 21.0K*



Cases - 7 day rolling average

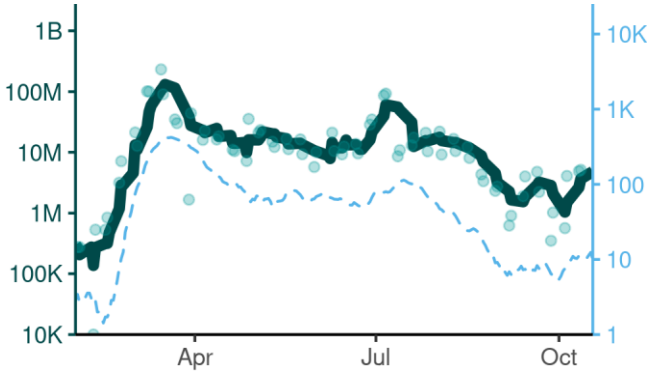
Te Puke *Autosampler 9.7K*



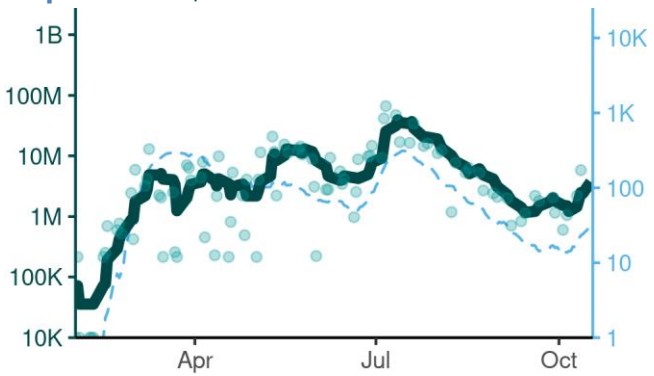

Kawerau Autosampler 7.0K
Waihi Beach Autosampler 3.6K
Katikati Autosampler 5.5K
Maketu Autosampler 1.3K
Opotiki Grab 3.8K
SARS-CoV-2 genome copies / day / person
Cases - 7 day rolling average
1B
100M
10M
1M
100K
10K
10K
1K
100
10
1
Apr
Jul
Oct

Hawke's Bay

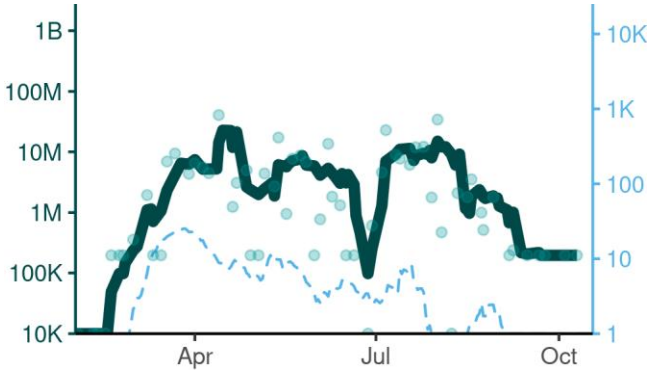
Hastings *Autosampler 80.0K*



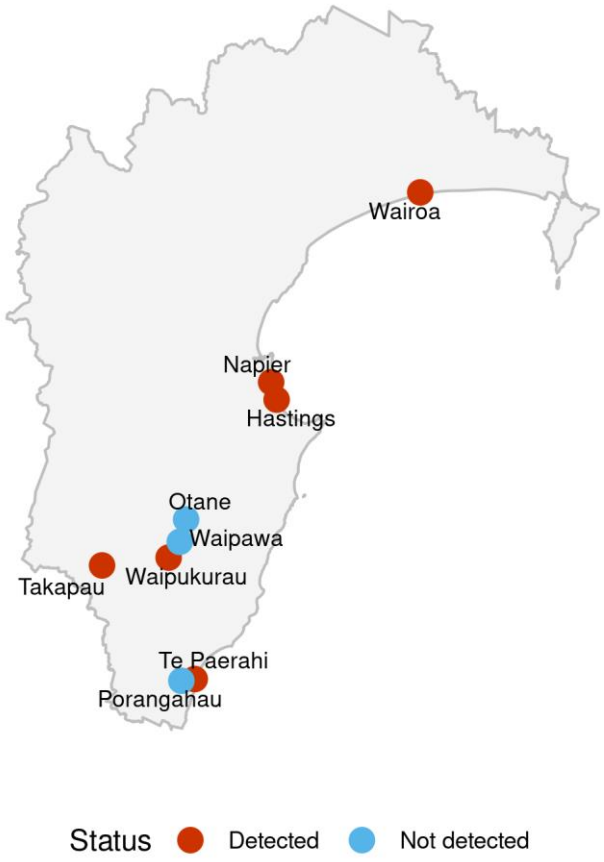
Napier *Autosampler 55.0K*



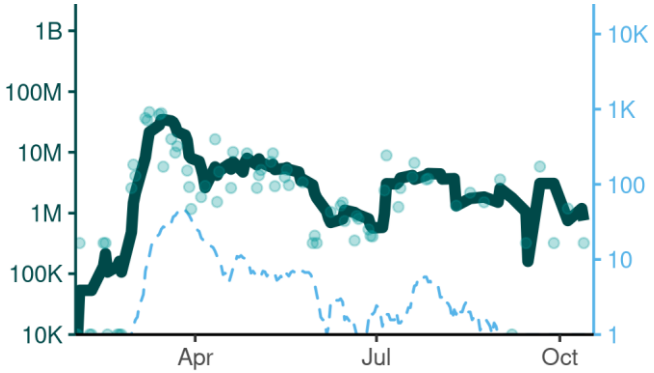
Waipukurau *Autosampler 4.6K*



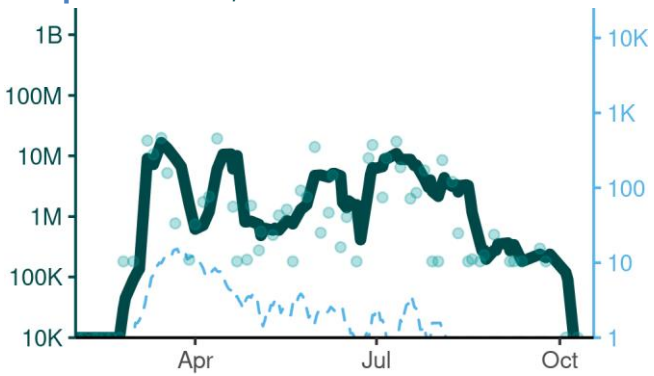
SARS-CoV-2 genome copies / day / person



Wairoa *Grab 4.4K*



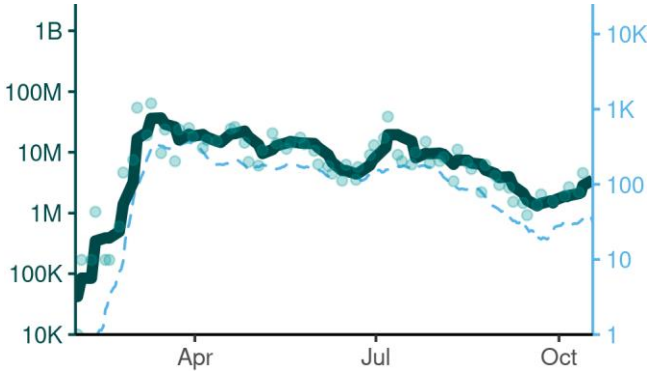
Waipawa *Autosampler 2.2K*



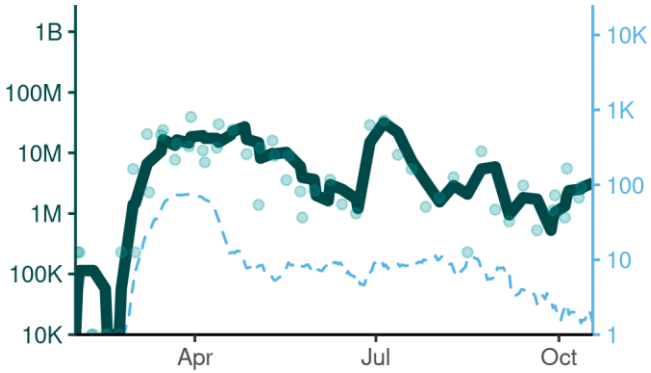
Cases - 7 day rolling average

Taranaki

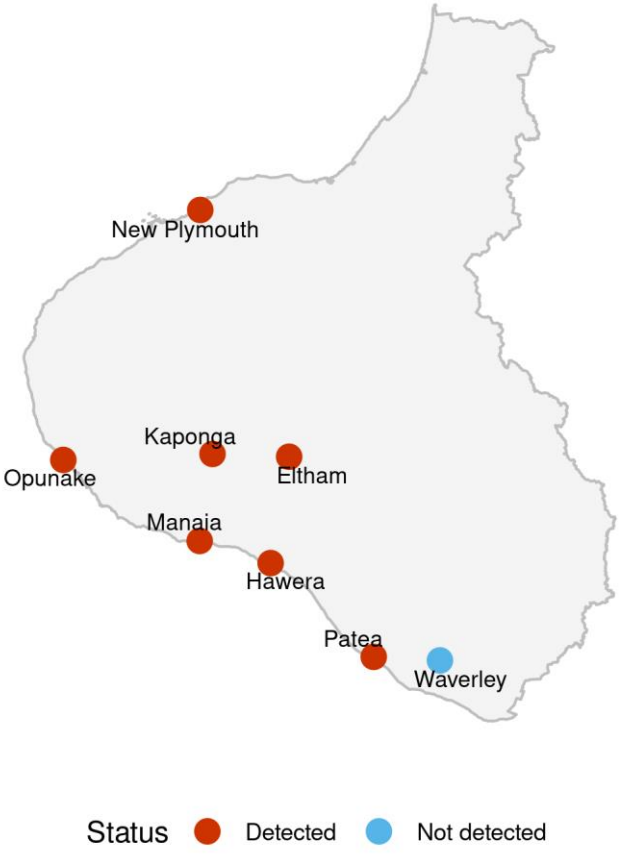
New Plymouth *Autosampler 88.0K*



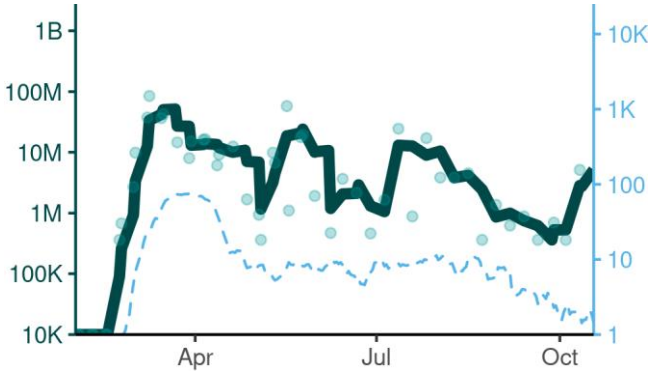
Hawera *Autosampler 12.0K*



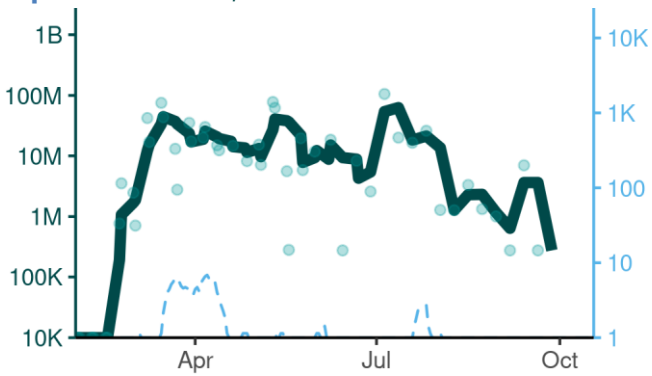
SARS-CoV-2 genome copies / day / person



Eltham *Autosampler 2.0K*

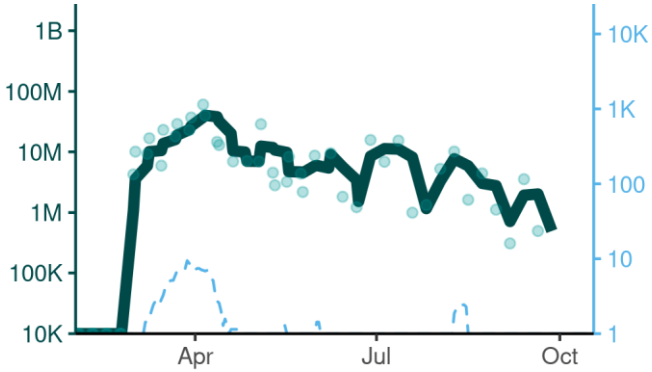


Opunake *Autosampler 1.4K*



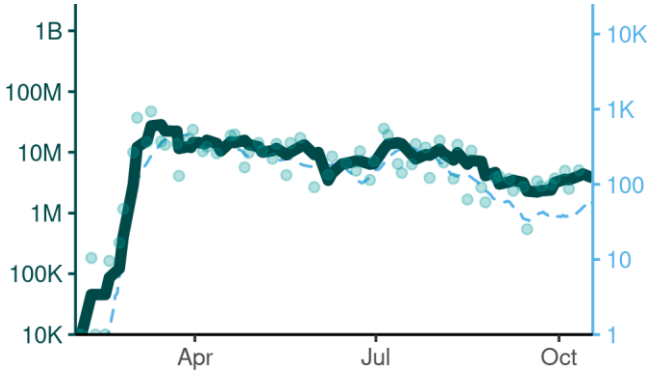
Cases - 7 day rolling average

Patea *Autosampler 1.2K*

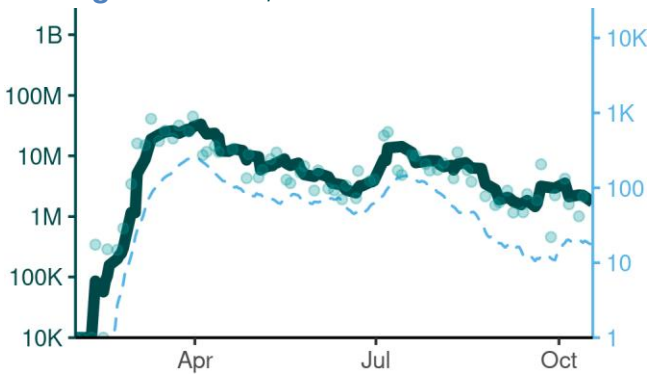


Manawatu-Whanganui

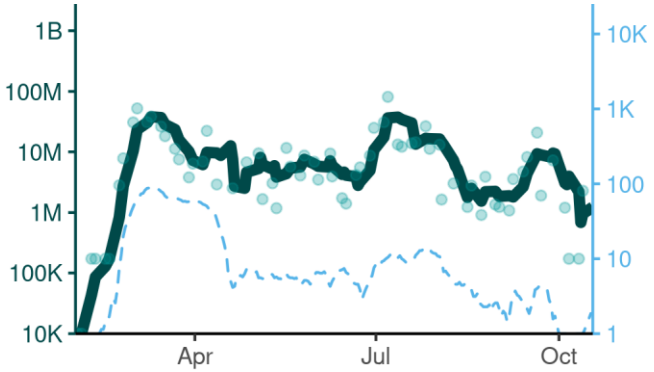
Palmerston North *Autosampler 90.0K*



Whanganui *Autosampler 44.5K*

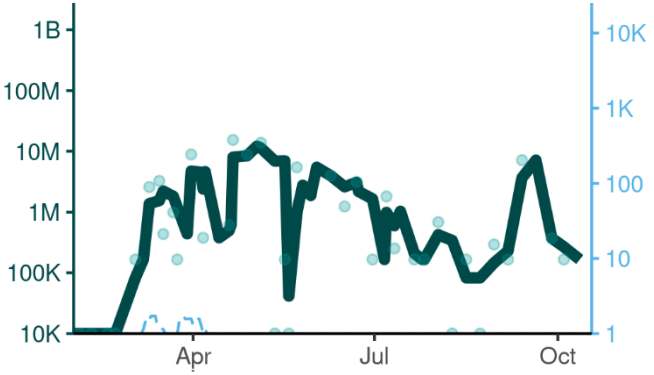


Levin *Autosampler 21.2K*

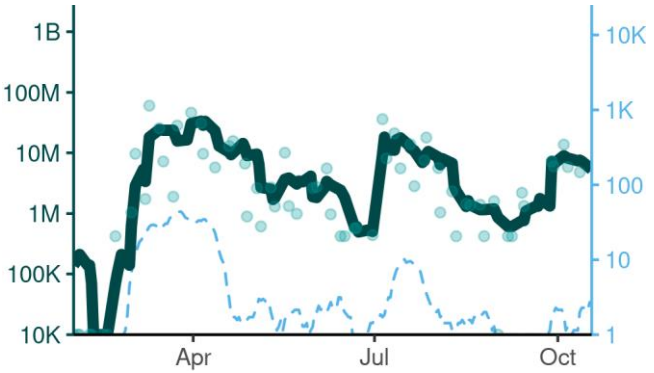


SARS-CoV-2 genome copies / day / person

Eketahuna *Grab 1.6K*

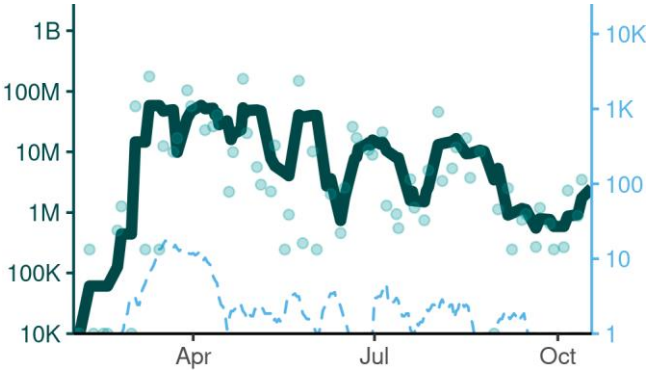


Dannevirke *Grab 5.7K*

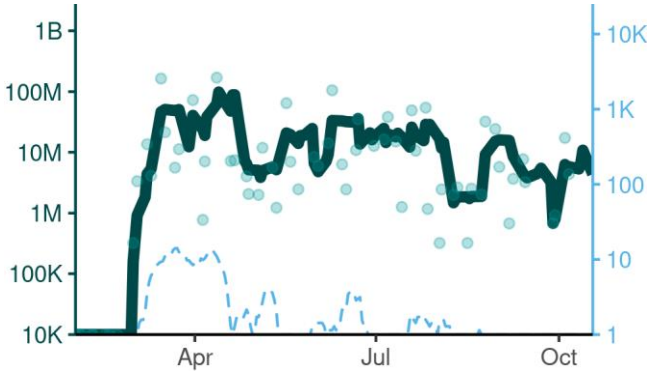


Cases - 7 day rolling average

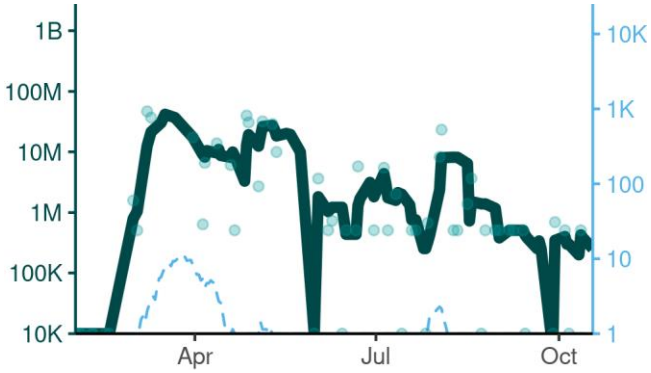
Taumarunui *Grab 4.0K*



Pahiatua *Grab 2.8K*



Woodville *Grab 1.7K*

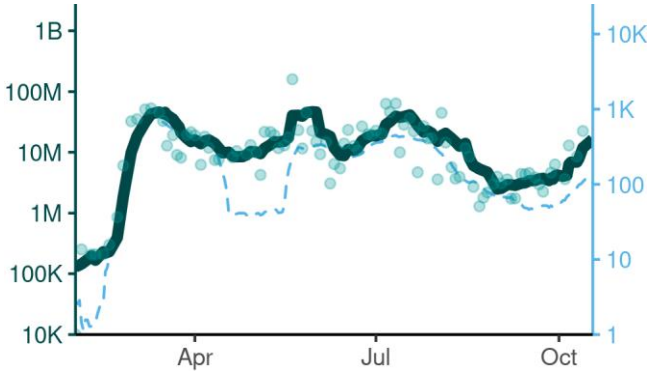


SARS-CoV-2 genome copies / day / person

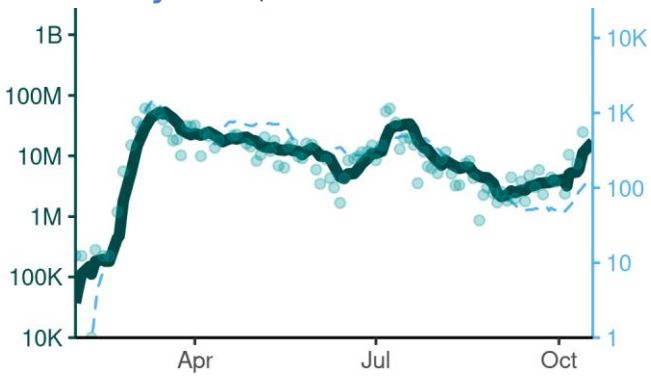
Cases - 7 day rolling average

Wellington

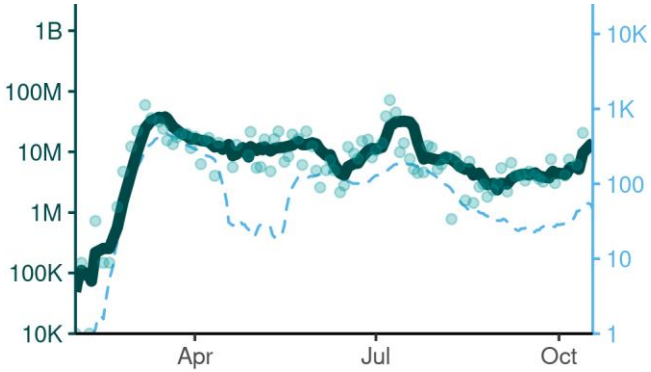
Wellington (Moa Point) *Autosampler 168.0K*



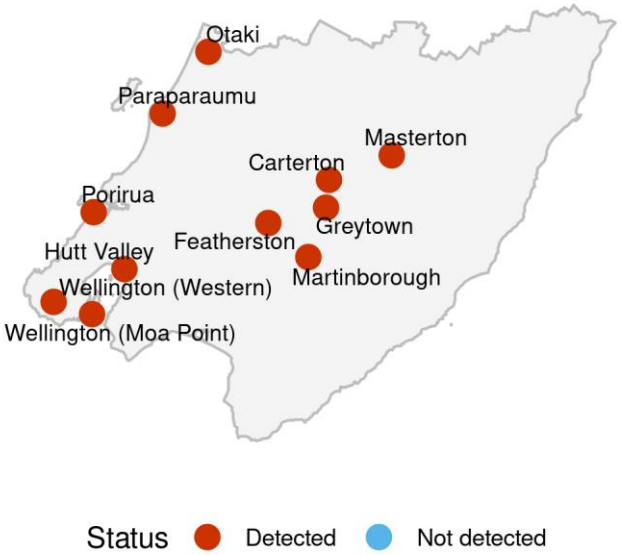
Hutt Valley *Autosampler 133.0K*



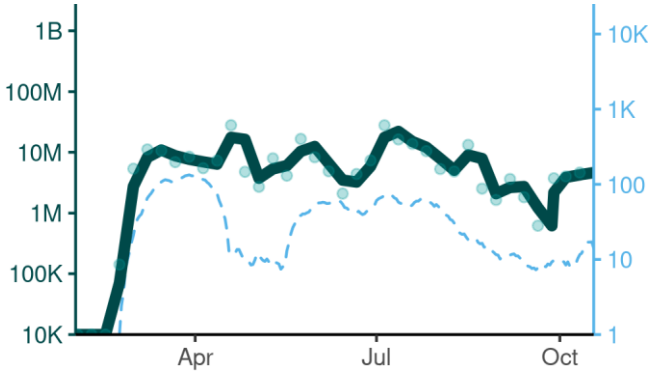
Porirua *Autosampler 85.0K*



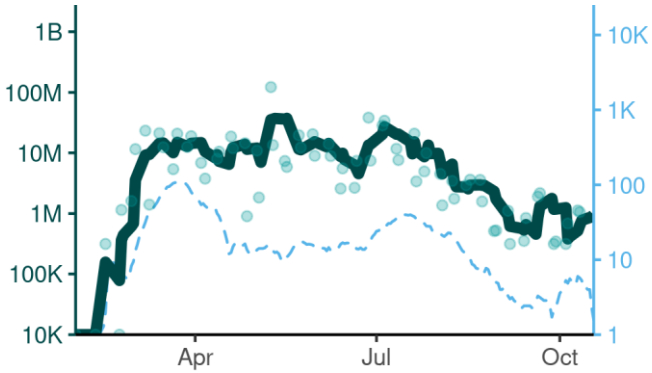
SARS-CoV-2 genome copies / day / person



Paraparaumu *Autosampler 49.0K*

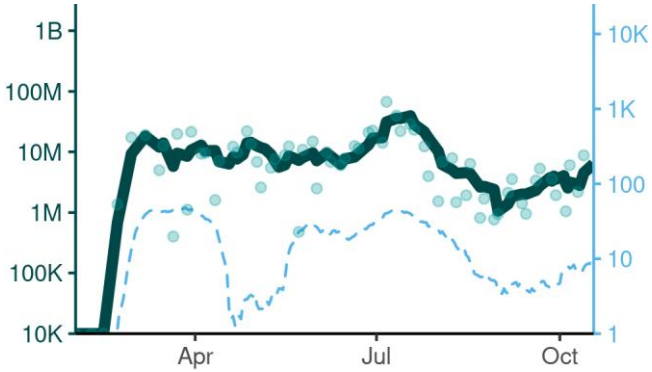


Masterton *Grab 20.7K*

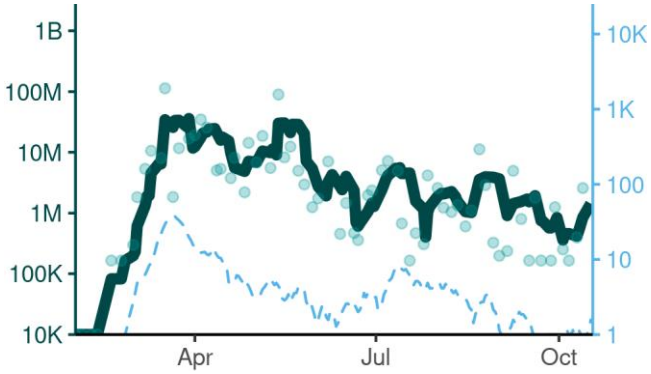


Cases - 7 day rolling average

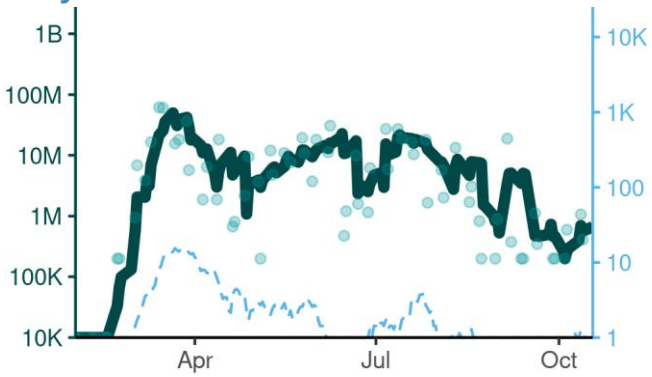
Wellington (Western) *Autosampler 14.0K*



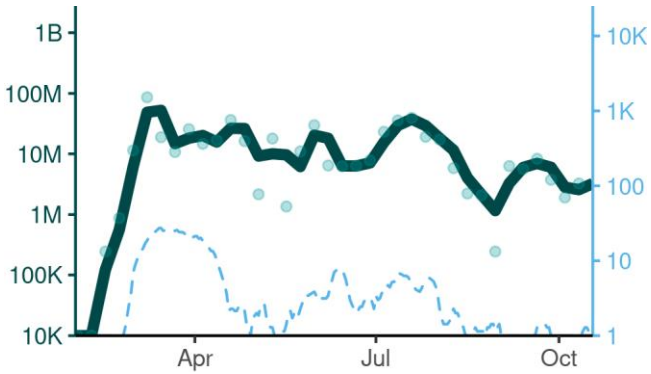
Carterton *Grab 5.8K*



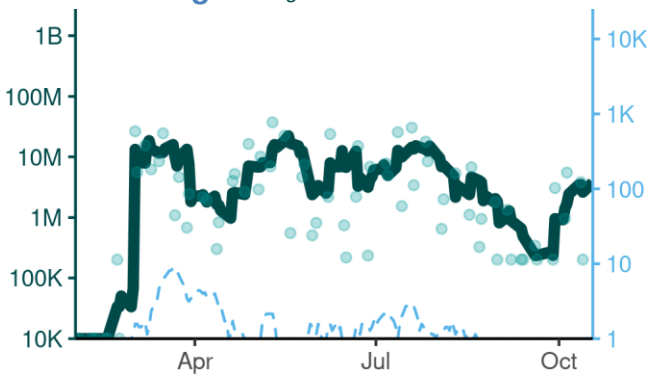
Greytown *Grab 2.4K*



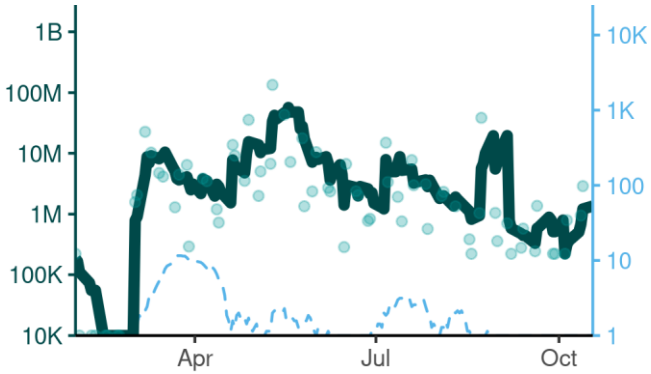
Otaki *Grab 3.5K*



Martinborough *Auto/grab 1.6K*



Featherston *Grab 2.5K*

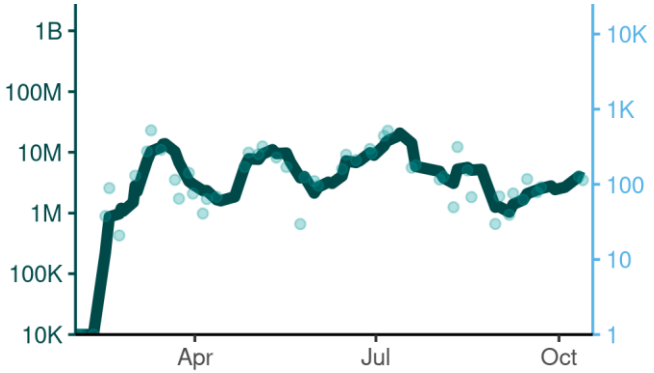


SARS-CoV-2 genome copies / day / person

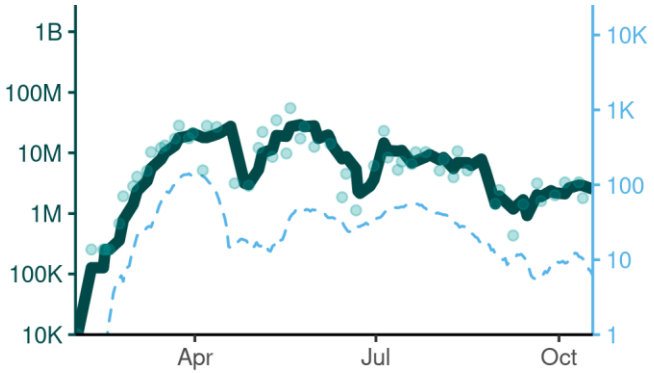
Cases - 7 day rolling average

Tasman, Nelson, and Marlborough

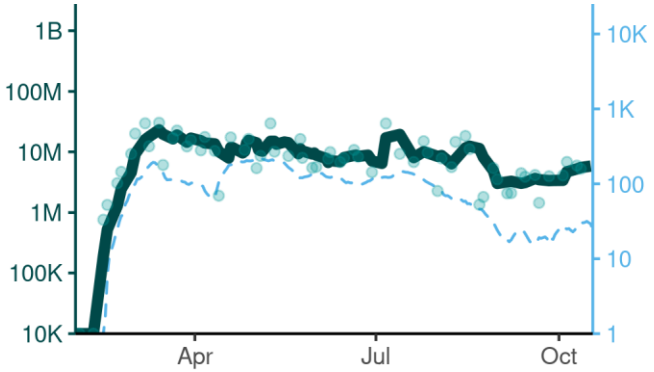
Richmond/Nelson South *Autosampler 60.0K*



Blenheim *Autosampler 31.0K*

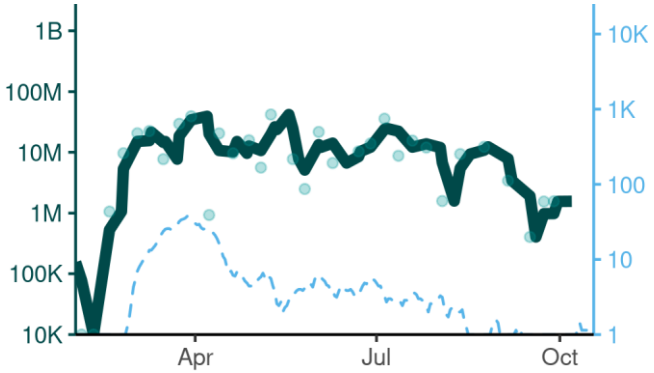


Nelson Central/North *Autosampler 26.0K*

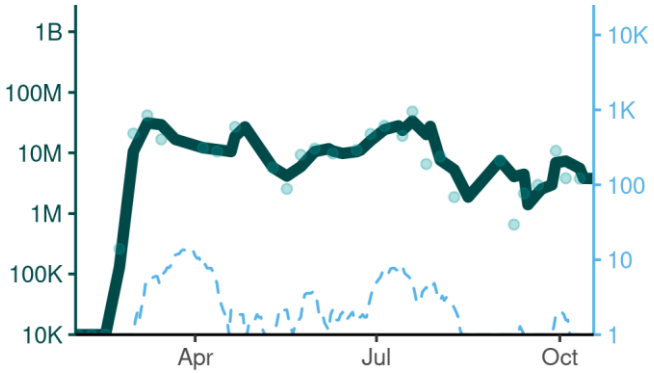


SARS-CoV-2 genome copies / day / person

Motueka *Autosampler 8.3K*



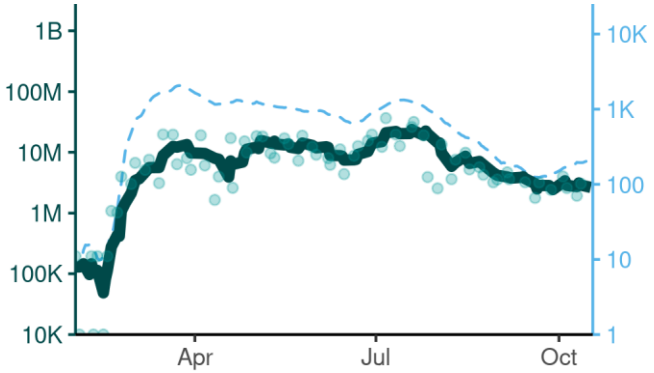
Picton *Autosampler 5.0K*



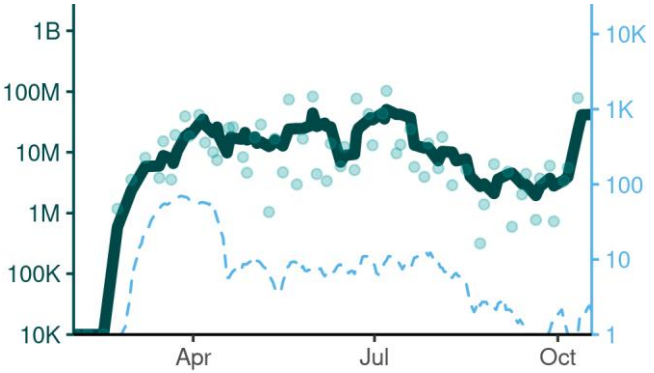
Cases - 7 day rolling average

West Coast and Canterbury

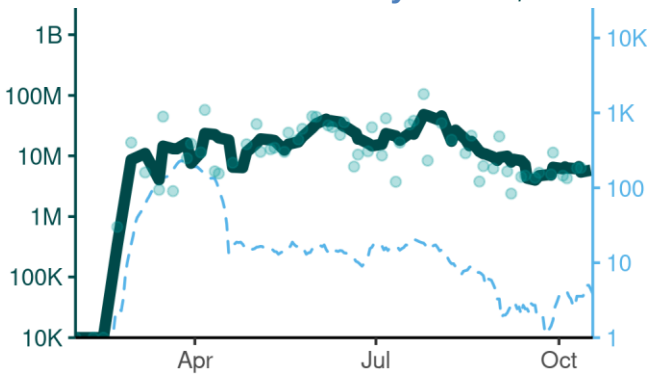
Christchurch *Autosampler 368.0K*



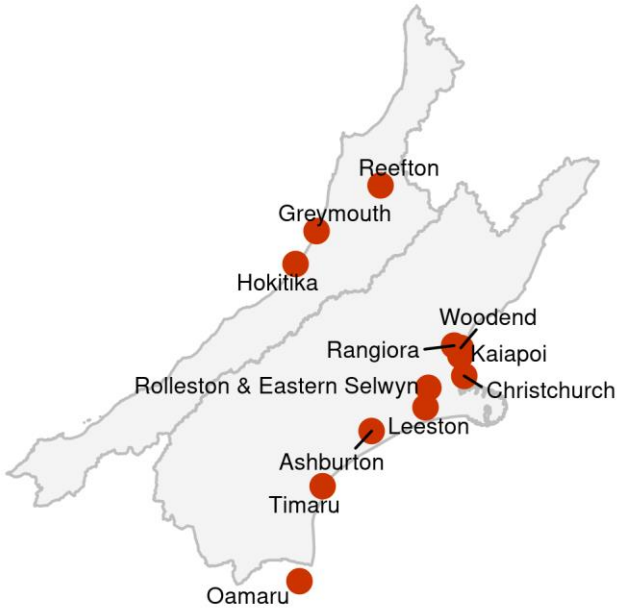
Rangiora *Grab 19.0K*



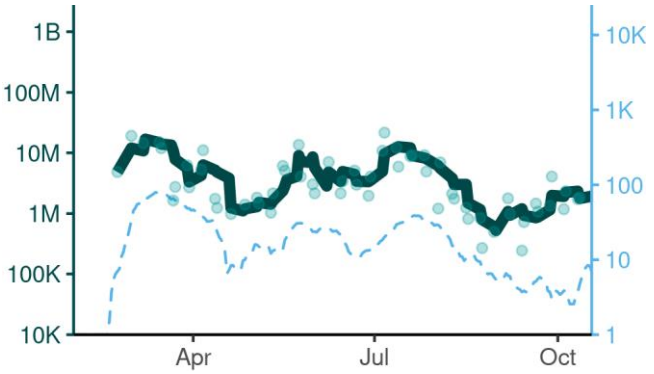
Rolleston & Eastern Selwyn *Autosampler 35.0K*



SARS-CoV-2 genome copies / day / person

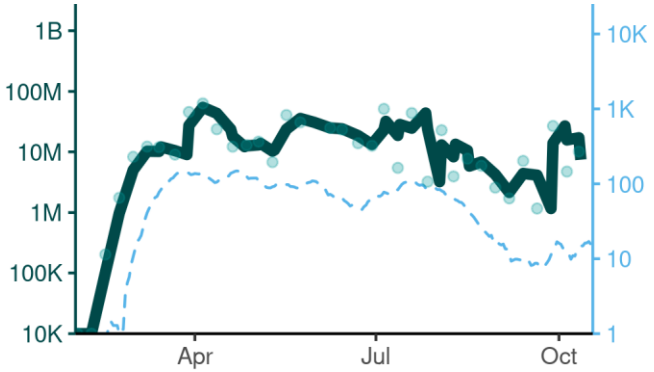


Ashburton *Autosampler 18.0K*

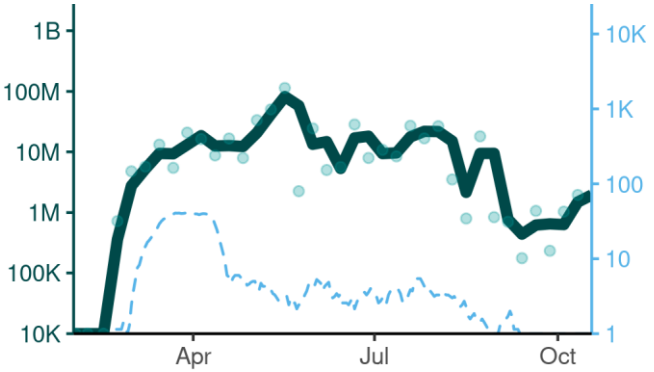


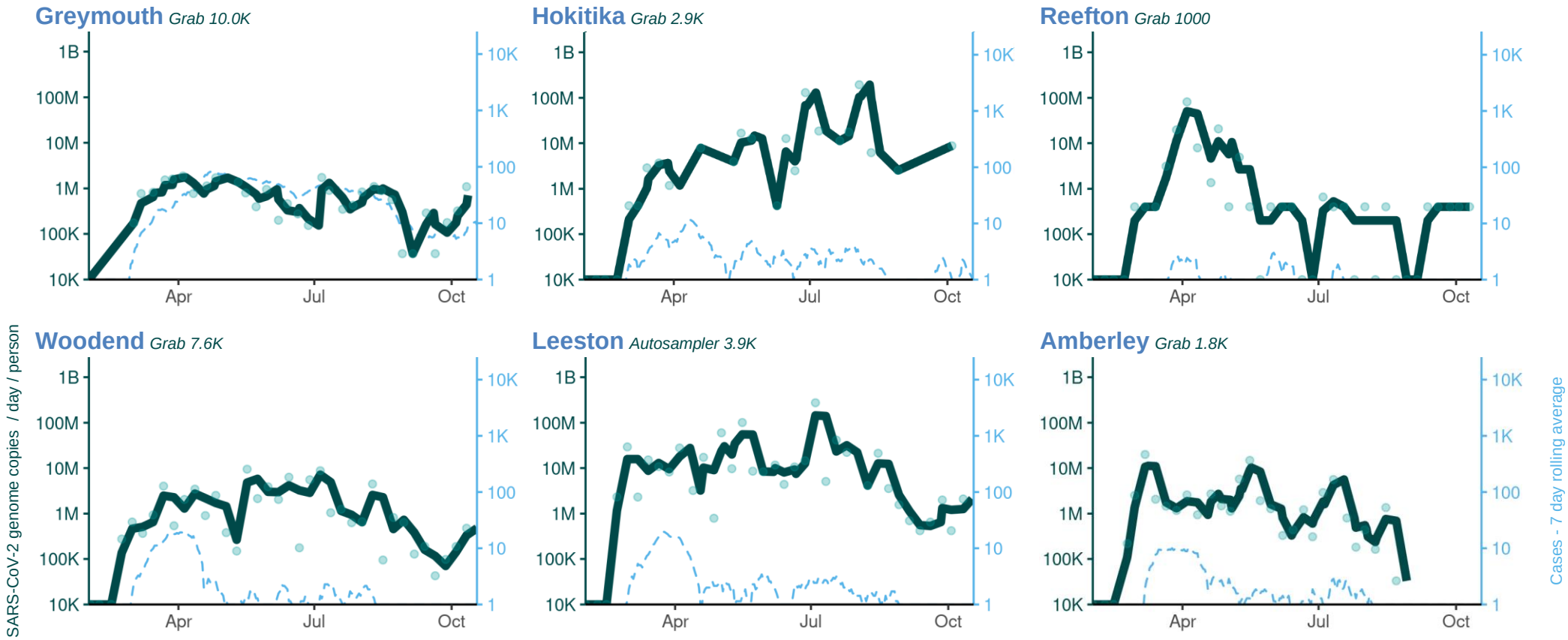
Cases - 7 day rolling average

Timaru *Autosampler 28.0K*



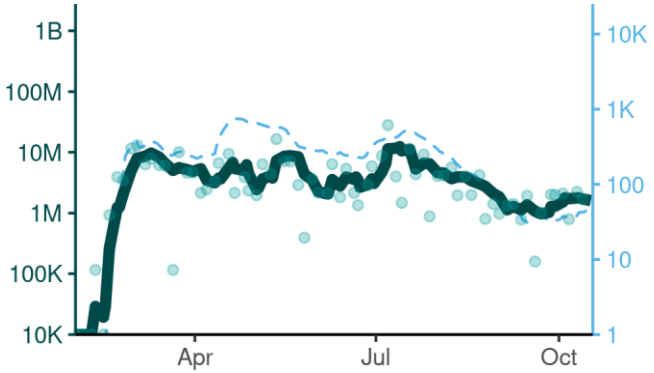
Kaiapoi *Grab 12.5K*



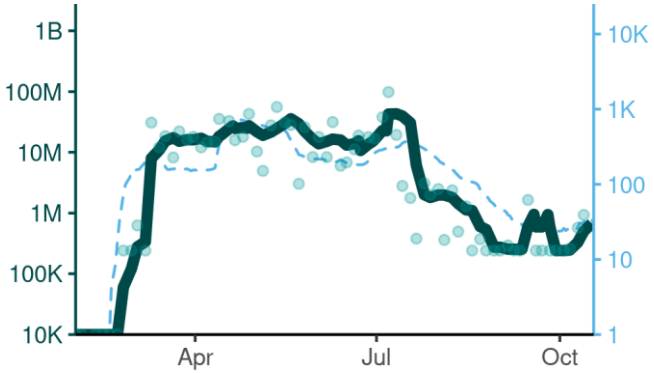

Greymouth Grab 10.0K
Hokitika Grab 2.9K
Reefton Grab 1000
Woodend Grab 7.6K
Leeston Autosampler 3.9K
Amberley Grab 1.8K
SARS-CoV-2 genome copies / day / person
Cases - 7 day rolling average
1B
100M
10M
1M
100K
10K
1K
100
10
1
Apr
Jul
Oct

Otago and Southland

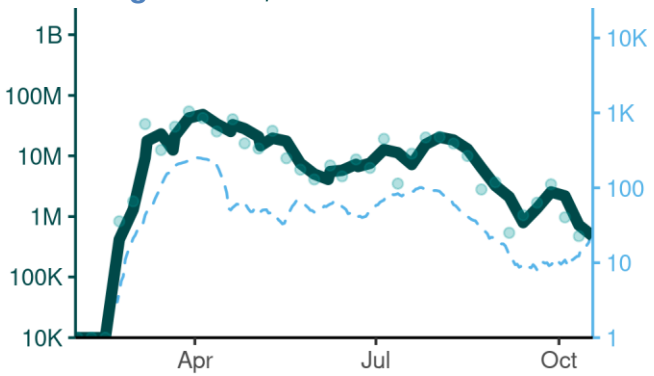
Dunedin (Tahuna) *Autosampler 84.0K*



Dunedin (Green Island) *Autosampler 22.9K*

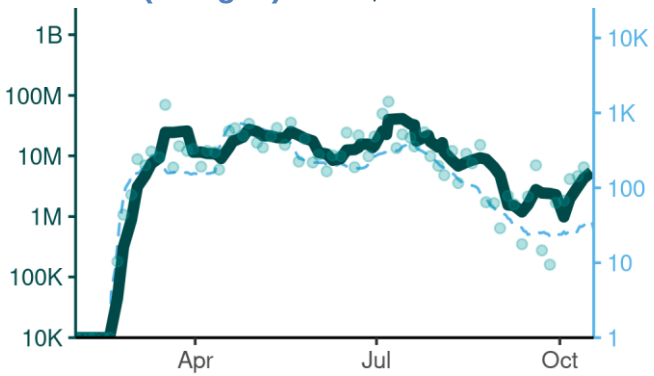


Invercargill *Autosampler 50.0K*



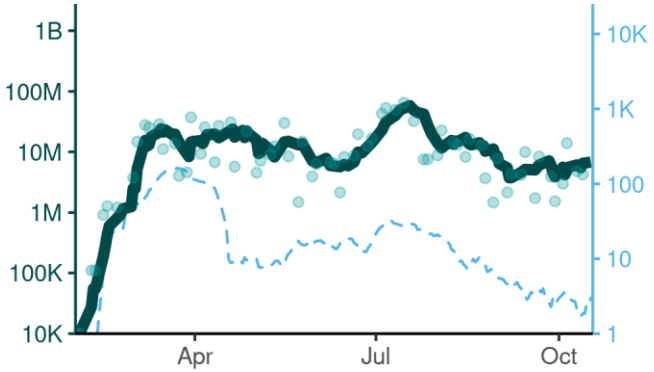
SARS-CoV-2 genome copies / day / person

Dunedin (Mosgiel) *Autosampler 14.6K*

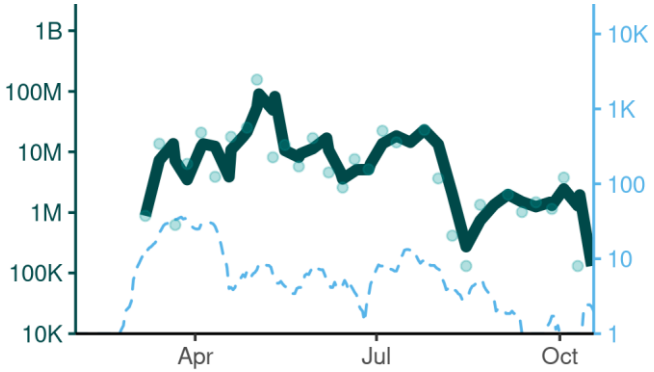


Cases - 7 day rolling average

Queenstown *Autosampler 40.0K*

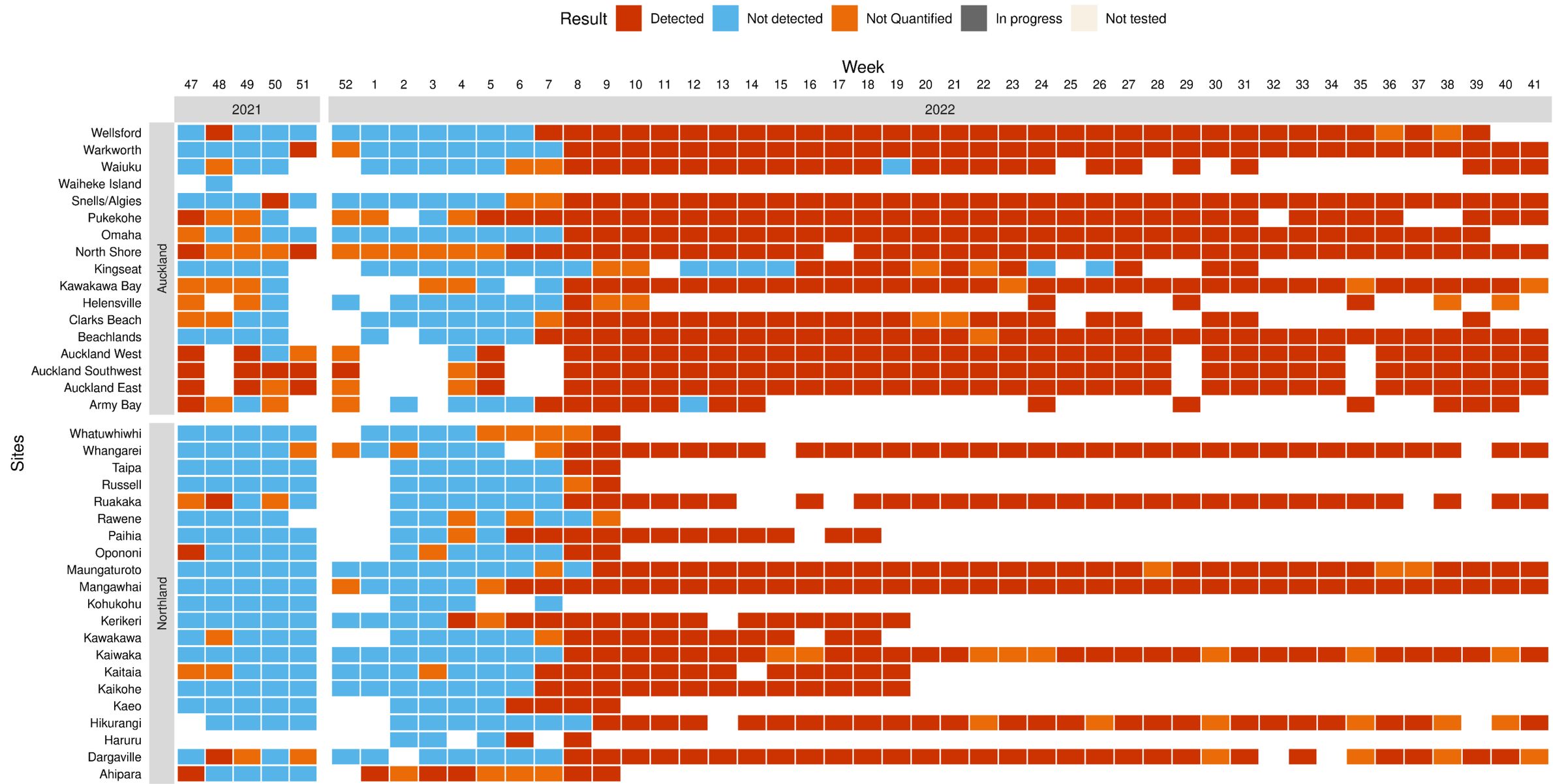


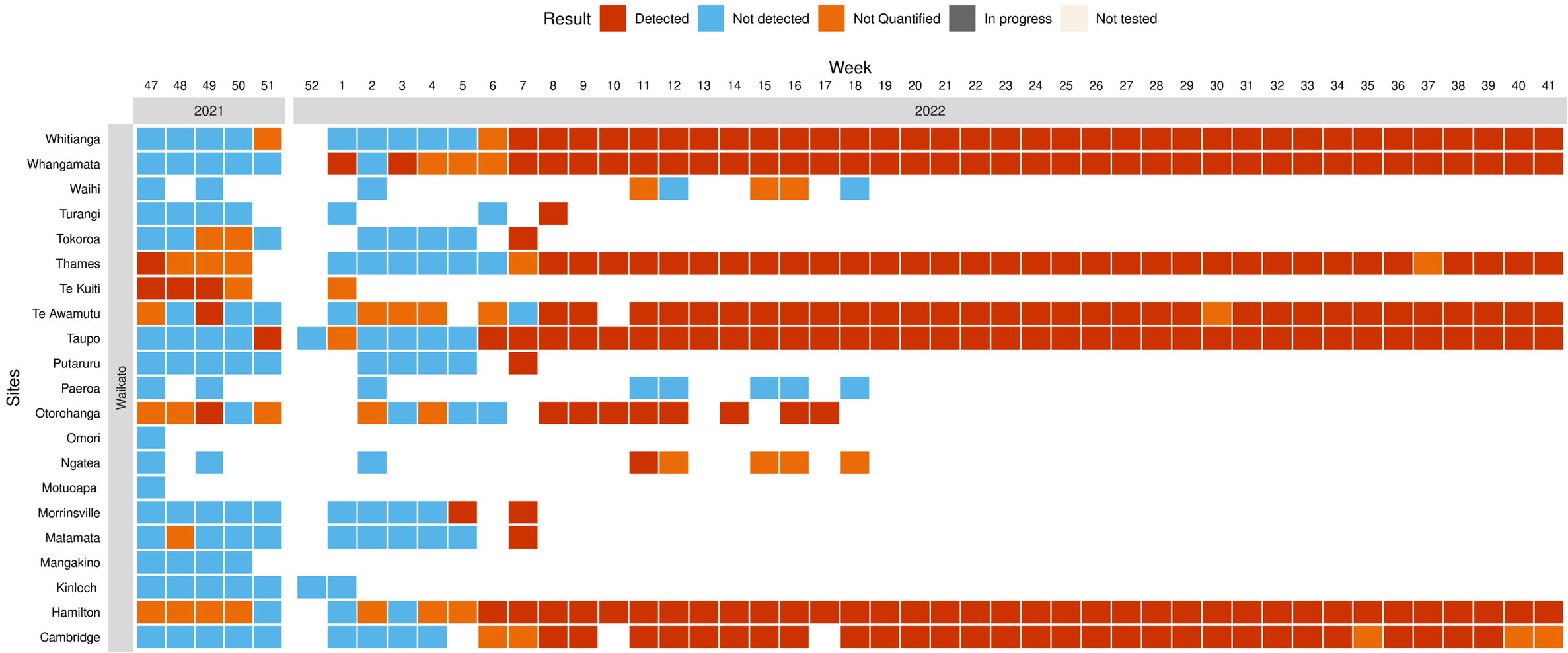
Wanaka *Grab 14.5K*

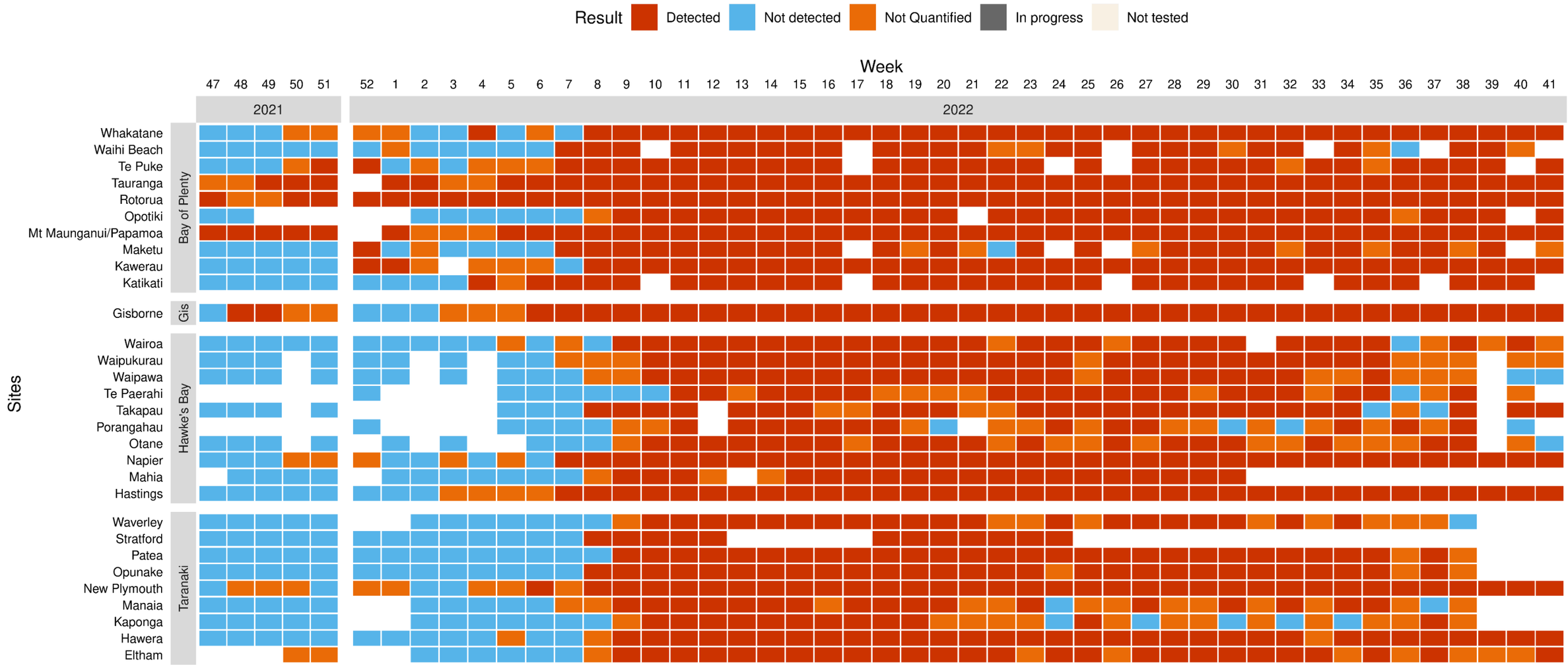


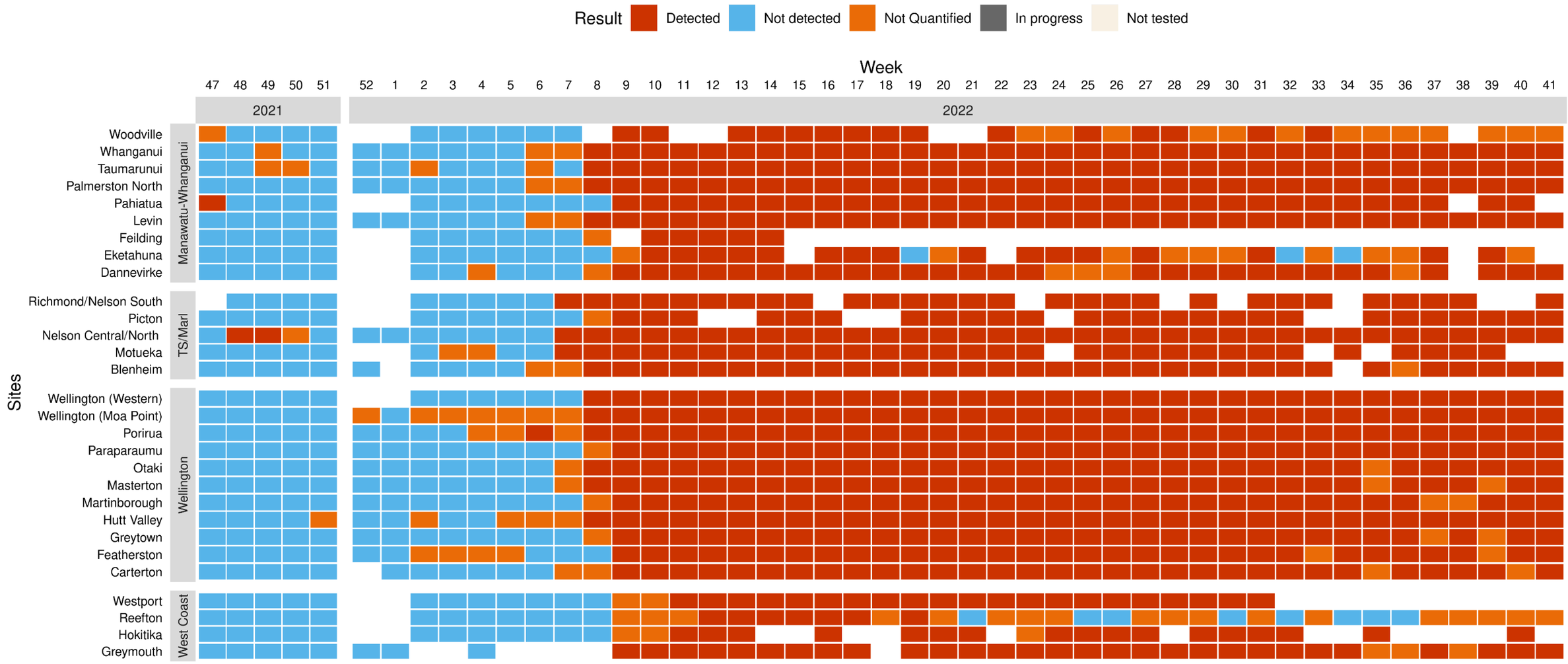

Gore Autosampler 8.0K
Balclutha Grab 4.1K
Cromwell Autosampler 7.1K
Bluff Autosampler 2.0K
Alexandra Autosampler 6.2K
Oamaru Autosampler 12.0K
1B
100M
10M
1M
100K
10K
Apr
Jul
Oct
10K
1K
100
10
1
SARS-CoV-2 genome copies / day / person
Cases - 7 day rolling average

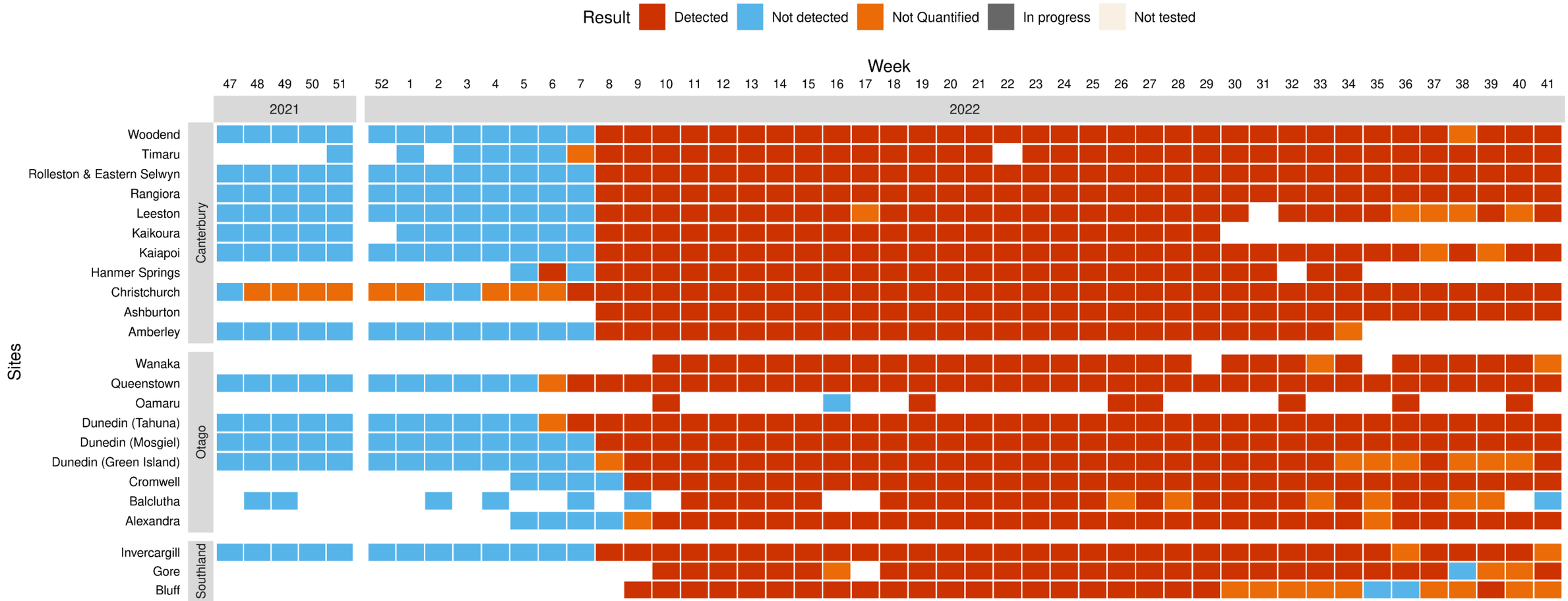
Table 1: Weekly summary of wastewater sampling results for SARS-CoV-2




Result
Detected
Not detected
Not Quantified
In progress
Not tested
Week
47 48 49 50 51 52 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41
2021
2022
Sites
Waikato
Whitianga
Whangamata
Waihi
Turangi
Tokoroa
Thames
Te Kuiti
Te Awamutu
Taupo
Putaruru
Paeroa
Otorohanga
Omori
Ngatea
Motuoapa
Morrinsville
Matamata
Mangakino
Kinloch
Hamilton
Cambridge


Result
Detected
Not detected
Not Quantified
In progress
Not tested
Week
47 48 49 50 51 52 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41
2021
2022
Sites
Bay of Plenty
Whakatane
Waihi Beach
Te Puke
Tauranga
Rotorua
Opotiki
Mt Maunganui/Papamoa
Maketu
Kawerau
Katikati
Gis
Gisborne
Hawke's Bay
Wairoa
Waipukurau
Waipawa
Te Paerahi
Takapau
Porangahau
Otane
Napier
Mahia
Hastings
Taranaki
Waverley
Stratford
Patea
Opunake
New Plymouth
Manaia
Kaponga
Hawera
Eltham


Result
Detected
Not detected
Not Quantified
In progress
Not tested
Week
47 48 49 50 51 52 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41
2021
2022
Sites
Manawatu-Whanganui
Woodville
Whanganui
Taumarunui
Palmerston North
Pahiatua
Levin
Feilding
Eketahuna
Dannevirke
TS/Marl
Richmond/Nelson South
Picton
Nelson Central/North
Motueka
Blenheim
Wellington
Wellington (Western)
Wellington (Moa Point)
Porirua
Paraparaumu
Otaki
Masterton
Martinborough
Hutt Valley
Greytown
Featherston
Carterton
West Coast
Westport
Reefton
Hokitika
Greymouth


Result
Detected
Not detected
Not Quantified
In progress
Not tested
Week
47 48 49 50 51 52 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41
2021
2022
Sites
Canterbury
Woodend
Timaru
Rolleston & Eastern Selwyn
Rangiora
Leeston
Kaikoura
Kaiapoi
Hanmer Springs
Christchurch
Ashburton
Amberley
Otago
Wanaka
Queenstown
Oamaru
Dunedin (Tahuna)
Dunedin (Mosgiel)
Dunedin (Green Island)
Cromwell
Balclutha
Alexandra
Southland
Invercargill
Gore
Bluff

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. Grab or 24 hr composite sample s are collected. 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. Greater variability is expected with grab samples.

Approach

Samples are sent from each wastewater treatment plant to ESR. 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 are recorded as less than the limit of quantitation. For quantitation, the raw concentration data (i.e., genome copies/L) is converted to a viral load of **genome copies per day per person**. 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.

Key Points & Limitations

- SARS-CoV-2 RNA concentrations should not be compared between wastewater catchments.
- 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.
- 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 and so data from wastewater surveillance cannot indicate the exact number of COVID-19 cases in the 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 area 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.

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 ESR by a team which may on any given week include contributions from Joanne Chapman, Dawn Croucher, Joanne Hewitt, Joycelyn Ho, Anower Jabed, Susan Lin, Olivia Macrae, Ashley McDonald, Andrew Ng, Ashley Orton, Andri Rachmadi, Daniel Rexin, Paula Scholes and Fatiha Sulthana. Data science analysis, visualisation and reporting is the result of team effort from: Franco Andrews, Bridget Armstrong, Raewyn Campbell, Joanne Chapman, Gerhard de Beer, Richard Dean, Brent Gilpin, Joanne Hewitt, Dawen Li, Helen Morris and Michael Bunce. 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: 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).

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 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).

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