

National Wastewater Surveillance Programme - COVID-19

Weeks 46 & 47 (Weeks Ending 20 November & 27 November 2022)

Report prepared on 30 November 2022

100%

sites tested in the last 2 weeks had SARS-CoV-2 detected (86/86 sites)

74%

NZ population covered by wastewater testing

Omicron BA.4/5 & BA.2.75*

Most prevalent variants detected

Nationally, SARS-CoV-2 levels in wastewater have been plateauing in November (weeks 44-47)

- In week 47 compared to week 46, 46% of sites showed an increase in SARS-CoV-2 levels while 38% of sites showed a decrease.
- Compared to a month ago (week 43, week ending 30 October 2022), 33% of sites show an increase in SARS-CoV-2 levels while 51% sites showed a decrease in SARS-CoV-2.
- BA.4/BA.5 (~40%) and BA.2.75* (~39%) are the main variants in wastewater for weeks 46 and 47. Detections of BQ.1.1 (~12%) and XBB (~3%) were steady, while XBC (~7%) was detected for the first time.

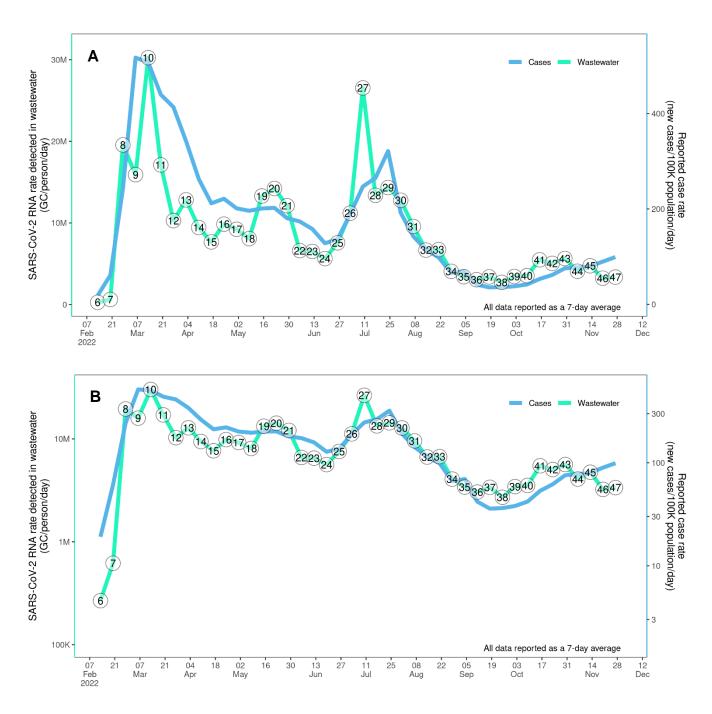


Figure 1. National timeseries of estimated SARS-CoV-2 genome copies (GC) in wastewater rate (GC/person/day, green line) and reported case rate (new cases/100,000 population/day, blue line). Numbers in the points are the week of the year. A. Linear scale. B. Log₁₀ scale. Data reported as 7-day average.

Results for Weeks 46 & 47 (Weeks ending 20 November & 27 November 22)

In the two weeks ending 27 November 2022, 252 samples were collected from 86 locations across New Zealand.

SARS CoV-2 RNA was **detected/detected (not quantified)** in 251/252 samples from 86 (100%) sites tested during this period (Figure 2, Table 2). SARS-CoV-2 was **not detected** in one sample collected from Te Awamutu (week 46) and subsequently was **detected** in week 47.

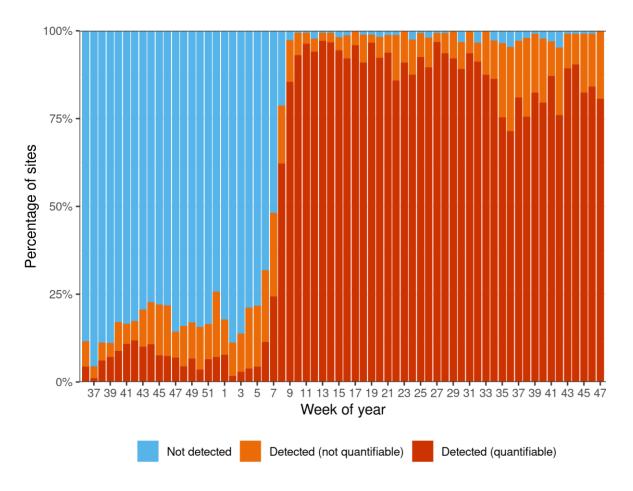


Figure 2. Results for SARS-CoV-2 RNA in wastewater collected across New Zealand.

Regional Trends

Regional summaries (Figure 3) of the wastewater data indicates generally steady or marginally declining viral levels across all regions except Northern, which shows an increase in weeks 46 and 47.

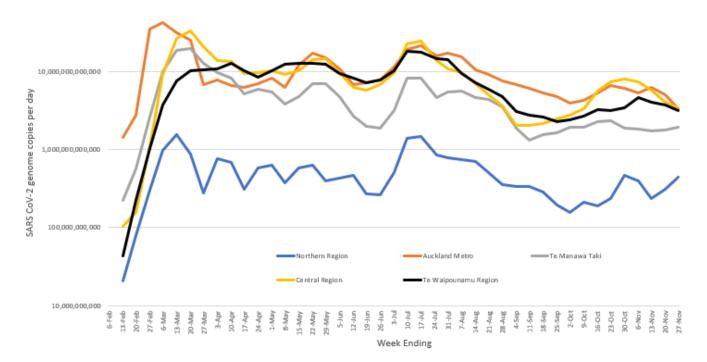


Figure 3. Total SARS-CoV-2 genome copies detected per day in the five Ministry of Health regions (Rolling two-week average).

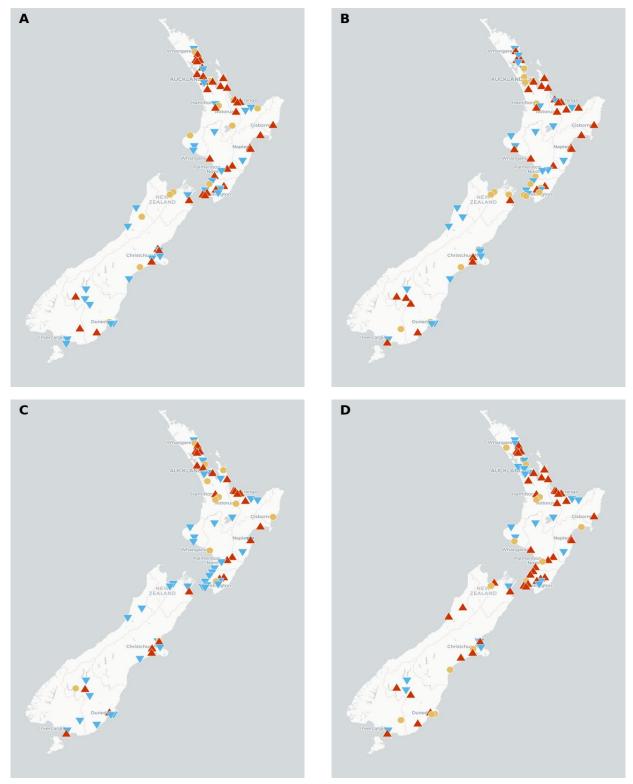


Figure 4. Comparison of SARS-CoV-2 levels for the week ending 27 November 2022, compared to levels measured: A) 1 week ago; B) 2 weeks ago; C) 4 weeks ago; D) 12 weeks ago. Only sites with results for both time points are included. When the viral quantity is 30% or more higher this is labelled as increased (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 (Table 1, Figure 5) from a set of nationwide sentinel sites in: Week 46 (ending 20 November 2022) and Week 47 (ending 27 November 2022).

Consistent with the WGS of clinical cases, the wastewater results represent a complex picture with BA.4/BA.5 declining and being replaced with a mixture of different variants. The BA.4/5 variants are still present at all sites across Aotearoa, with a national average estimated prevalence of ~40%. However, in weeks 46 and 47, the BA.2.75* constellation of variants is at a similar proportion nationally (~39%). BQ.1.1 levels in wastewater were relatively steady, from a national average of ~10% of sequences last fortnight to ~12% of sequences this fortnight.

The XBB variant was detected in five sites this fortnight but only comprised ~3% of sequences nationally. For the first time, the XBC variant was detected in wastewater in week 46 (2 sites) and week 47 (5 sites), comprising ~7% of sequences nationally.

Due to the increasing complexity of variants in the population, each at relatively low levels, the current approach for sequencing wastewater samples is no longer precise enough to report as percentages for each variant at the sentinel site level. Instead, the presence of each lineage is reported (Table 1). ESR are actively testing and developing methods to address the current uncertainty and increase the resolution at which variants can be identified in wastewater.

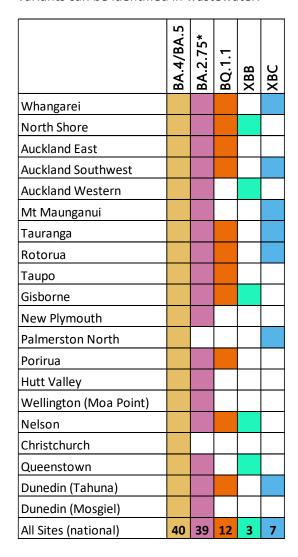


Table 1. Data from 20 sentinel wastewater sites across NZ using a S-gene (spike) barcoding assay able to 'call' the BA.4/BA.5, the BA.1/BA.2.75/CH.1.1/BR.2 constellation (denoted BA.2.75*), BQ.1.1, XBB and XBC (sub)variants. Coloured box denotes that the variant was detected at that site this fortnight, white box denotes that it was not detected. Numbers in the bottom row denote the estimated percentage of each variant at the national scale for weeks 46 and 47 combined.

Variant Timeline - National

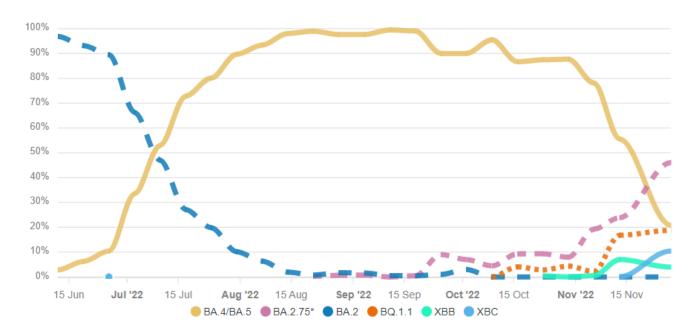
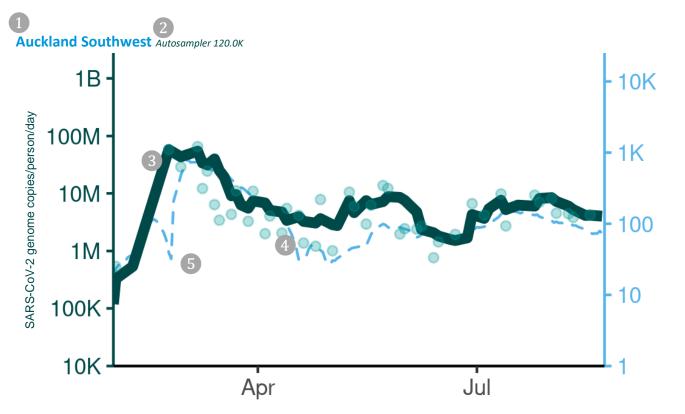


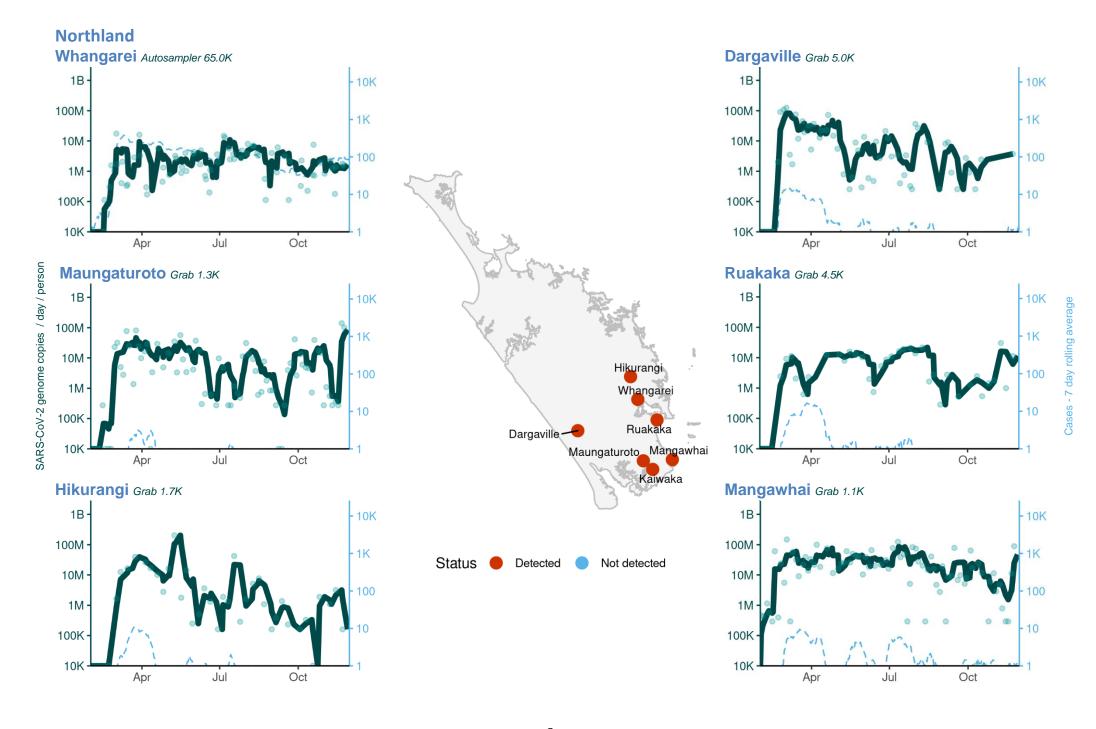
Figure 5. Change in variant prevalence over time at a national scale. Data are collected from up to 20 sentinel sites each week

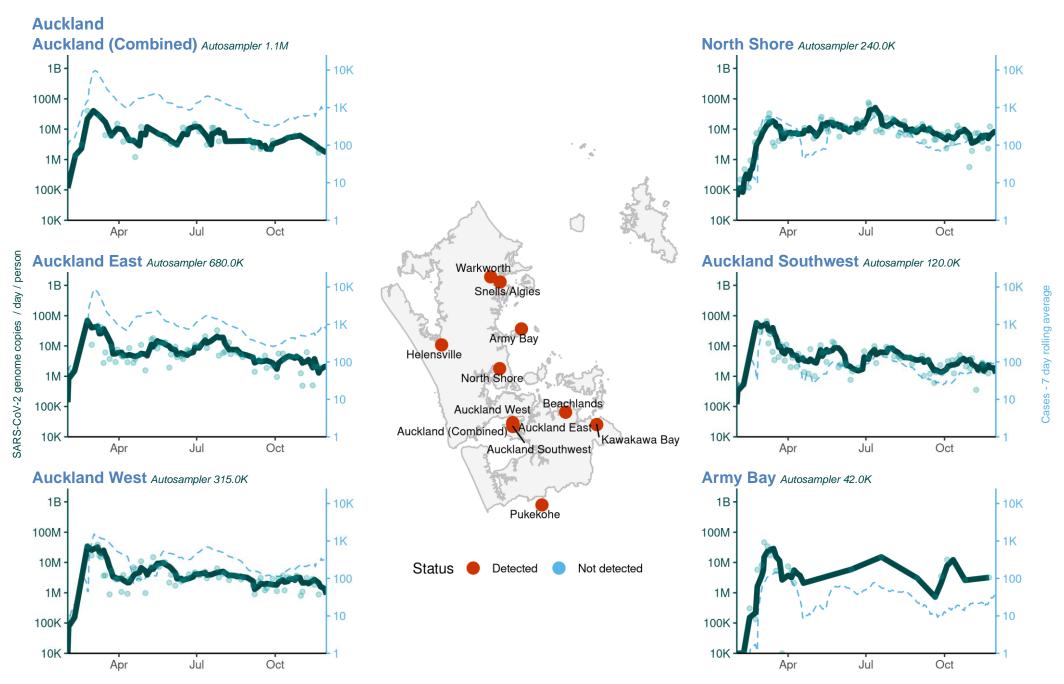
Interpreting Sites Graphs

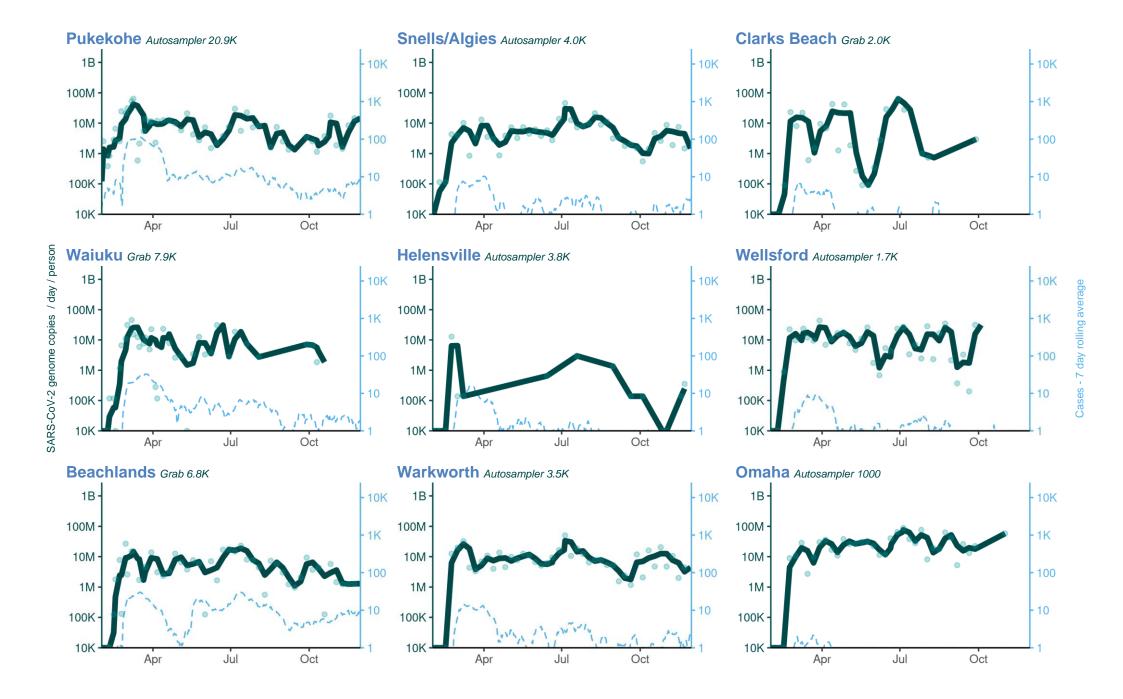


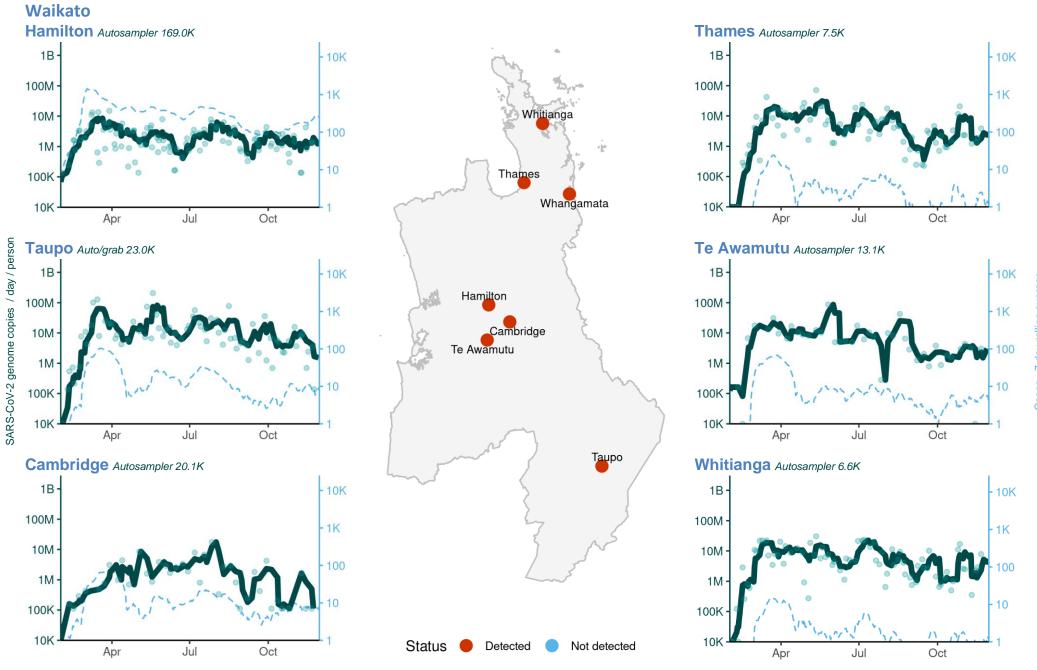
- Site Name
- 2 Sample collection method and population. Results based on autosampler may be more representative than grab sample-based results.
- 3 Wastewater results shown as solid line | 14-day average of genome copies/person/day on a log₁₀ scale.
- 4 Individual results samples shown as circles | Rolling 14-day average of genome copies/person/day on a log₁₀ scale.
- 6 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 log₁₀ 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.

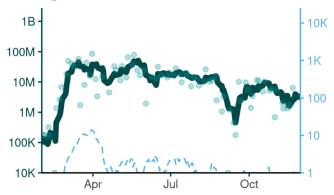


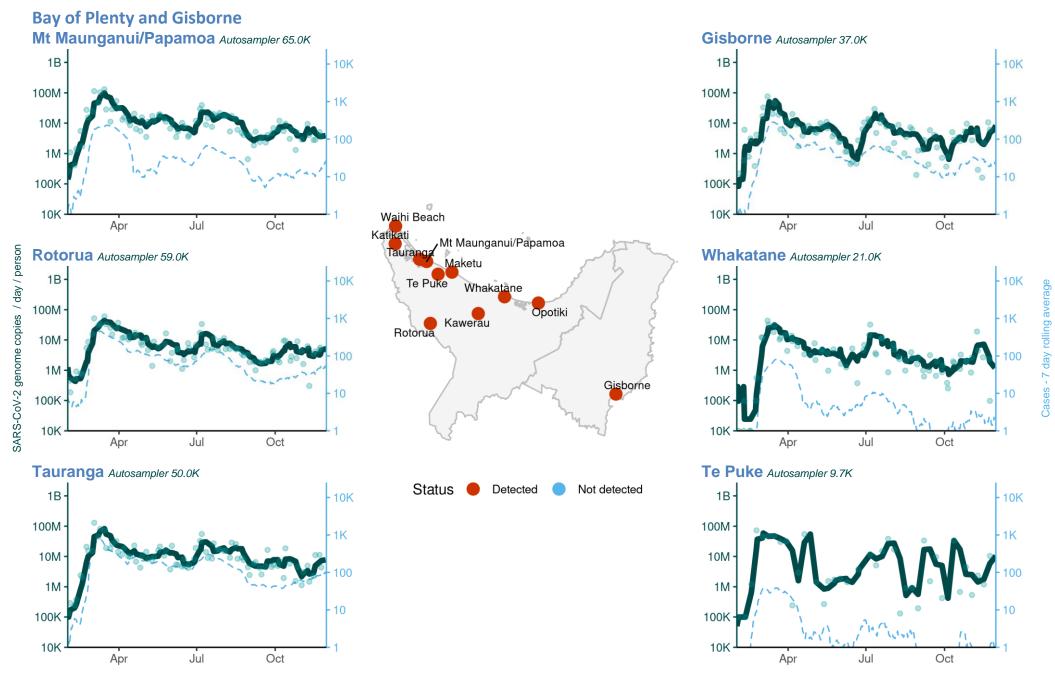


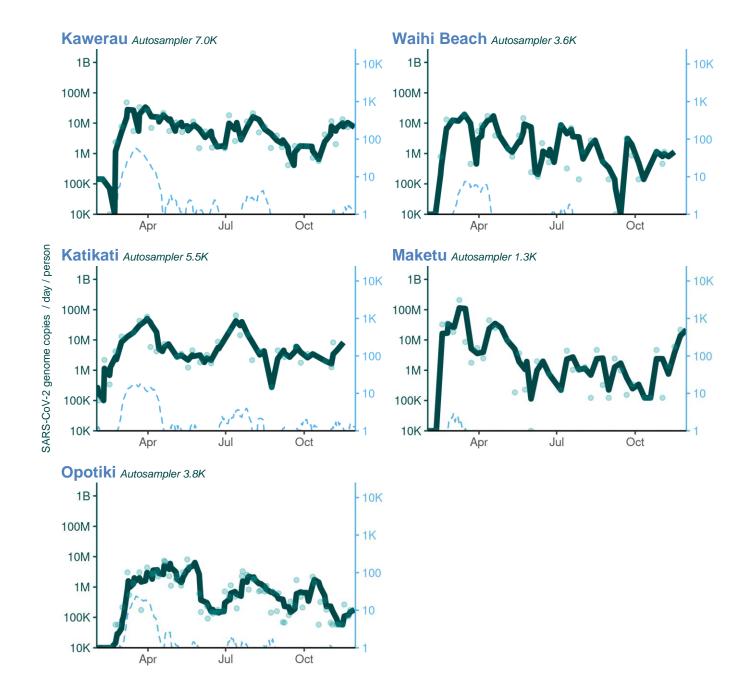


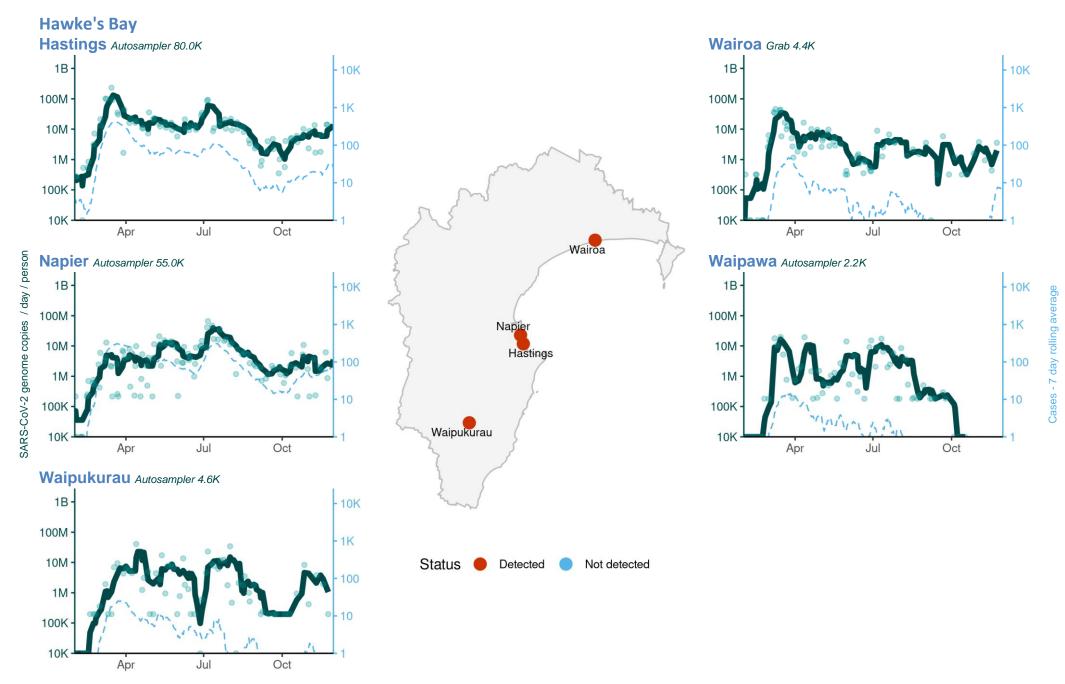


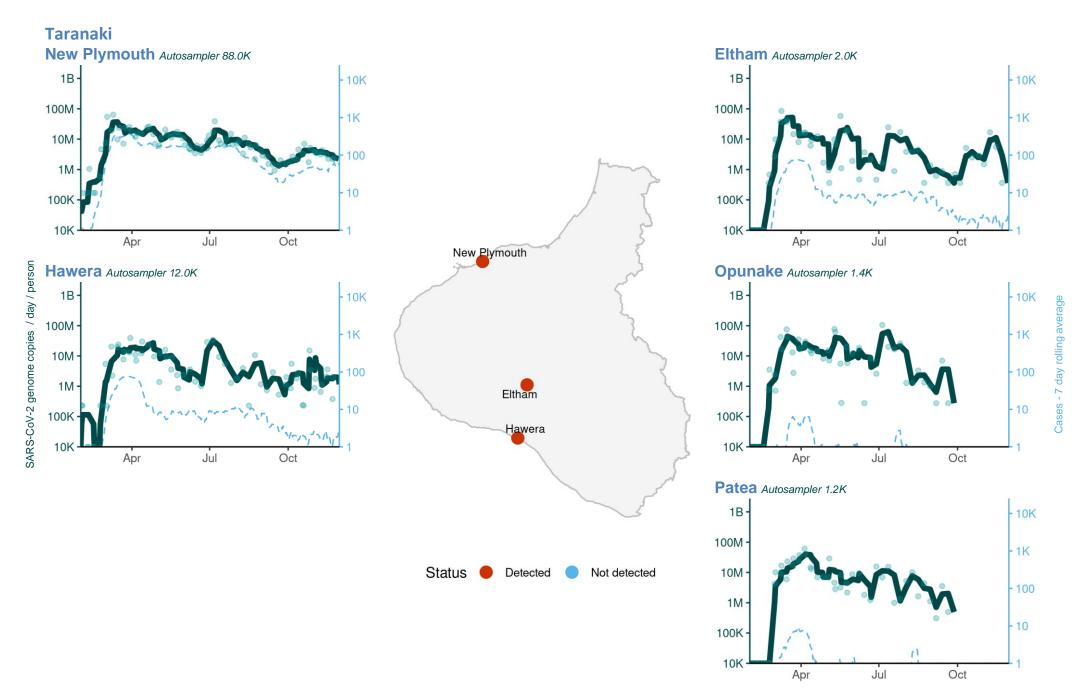


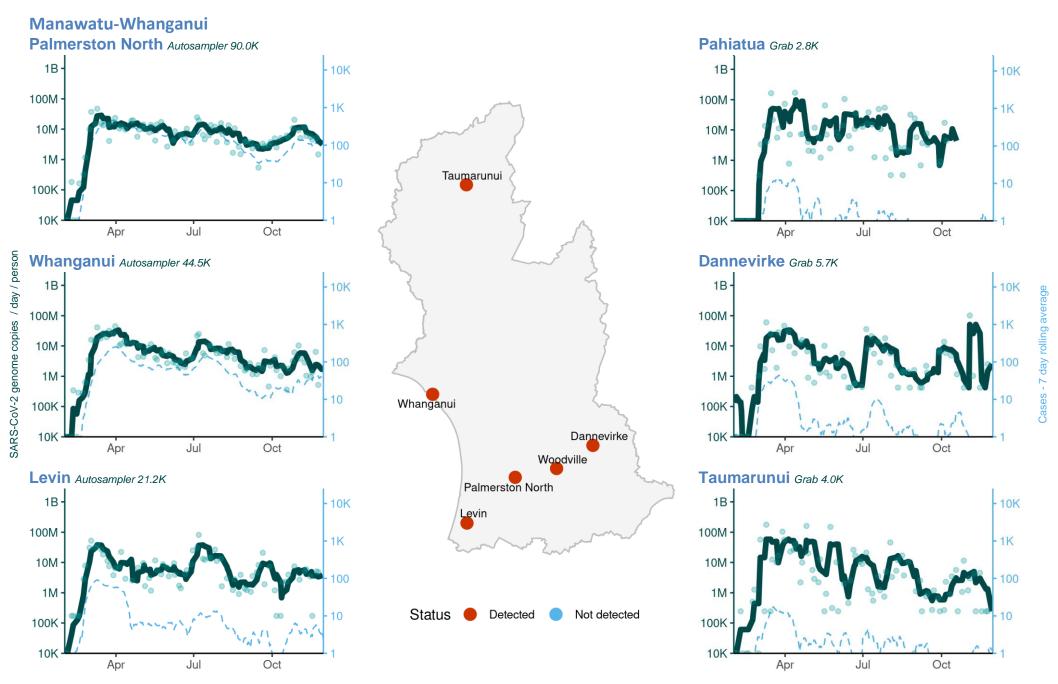


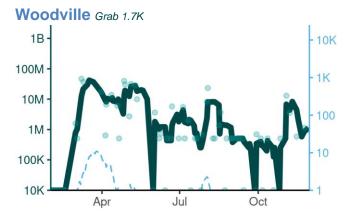


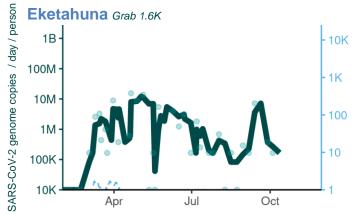


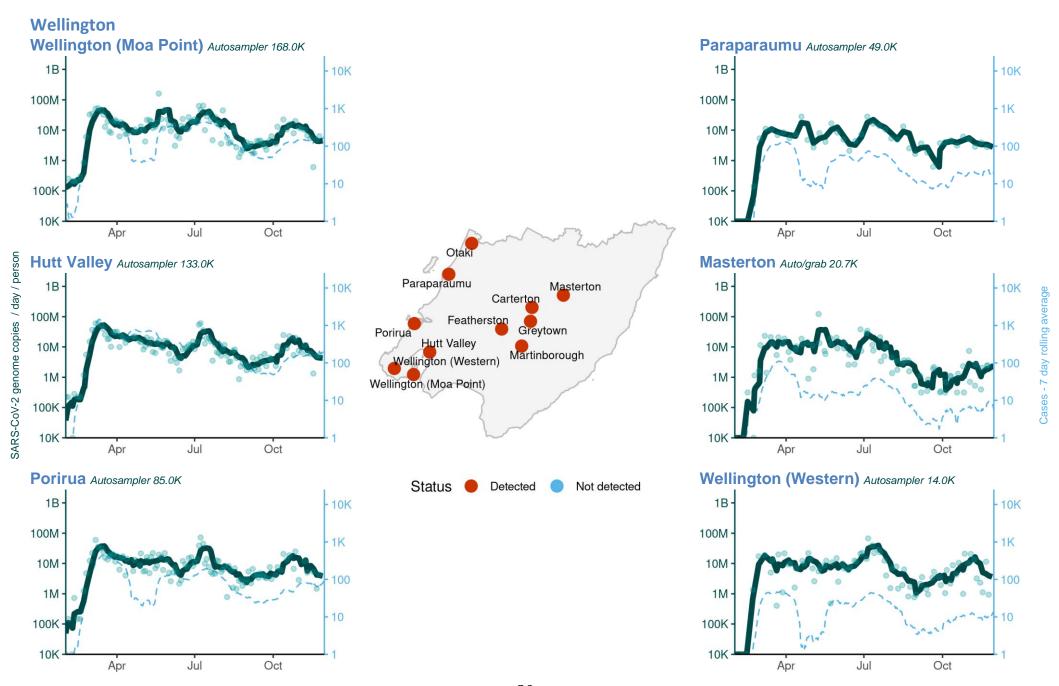


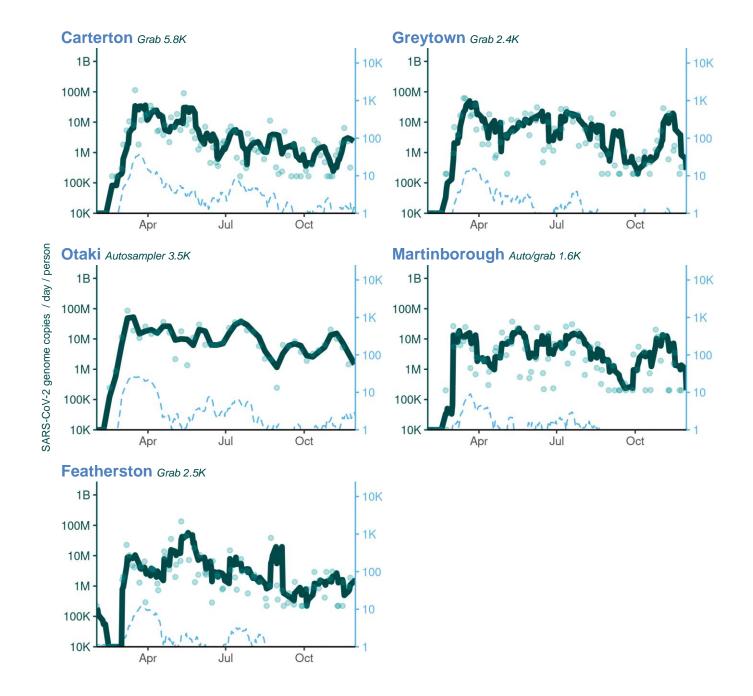


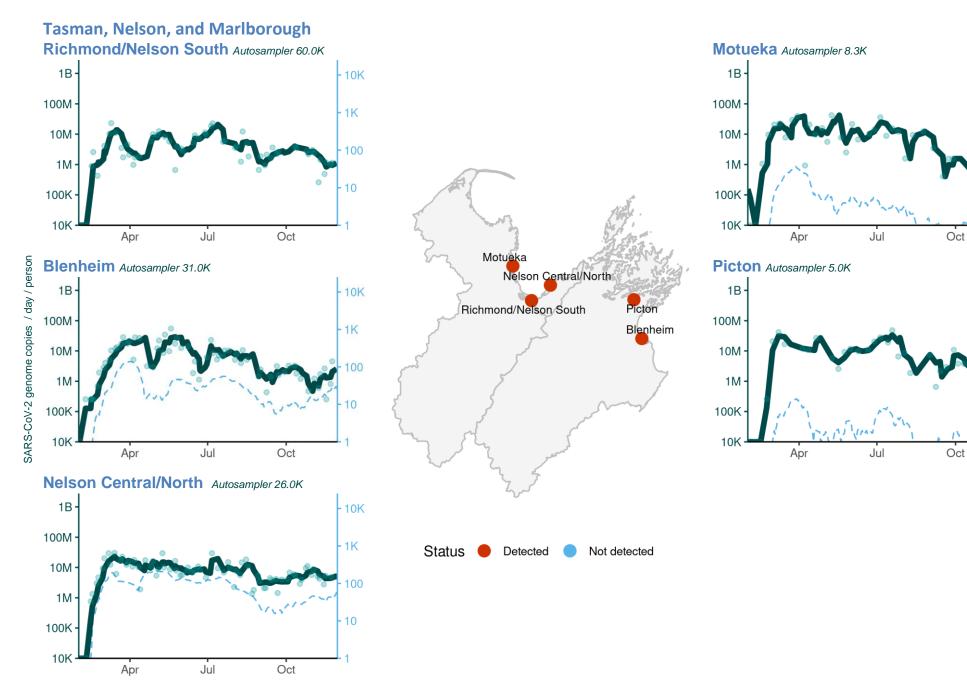












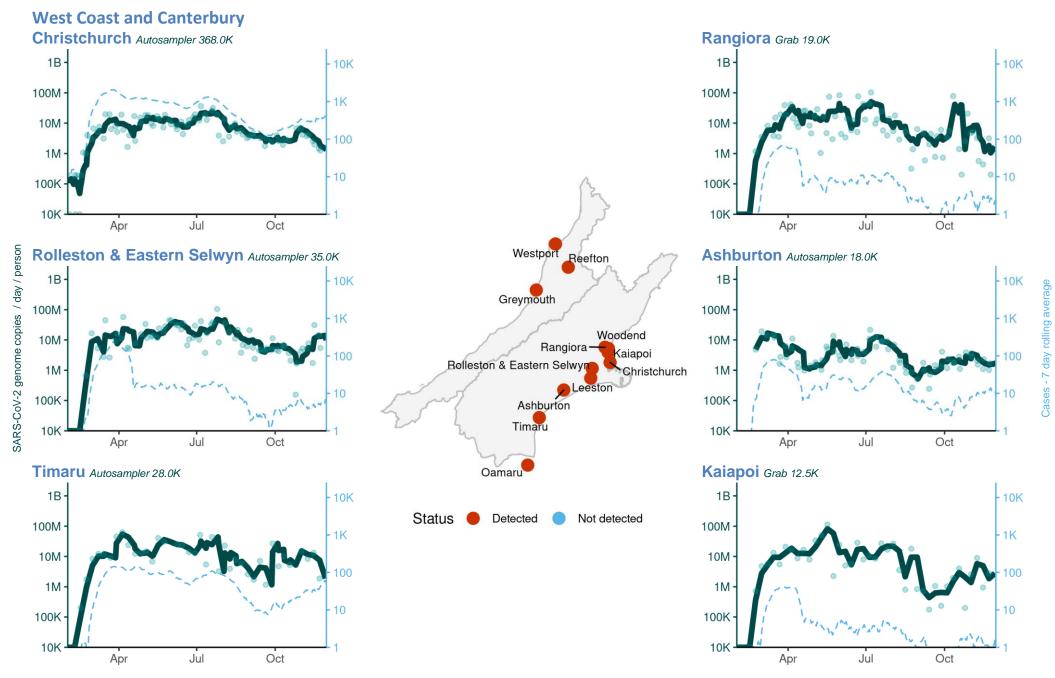
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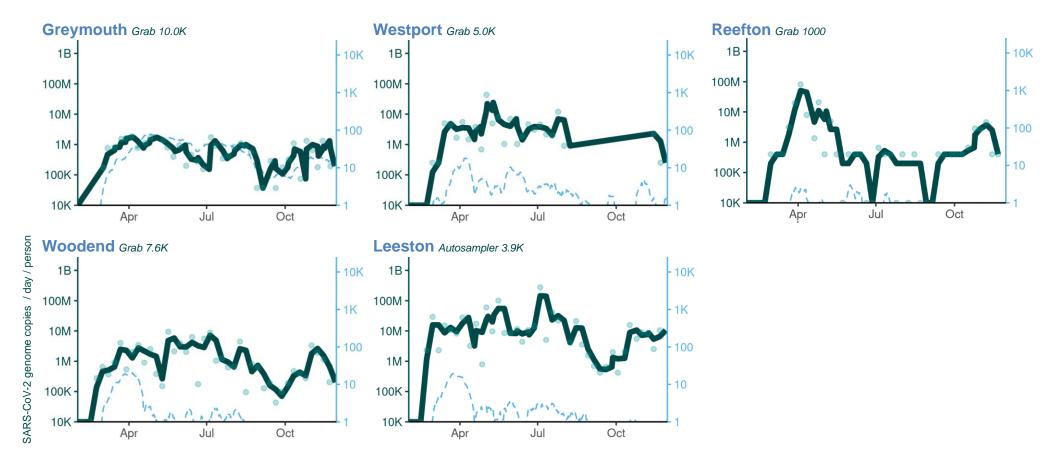
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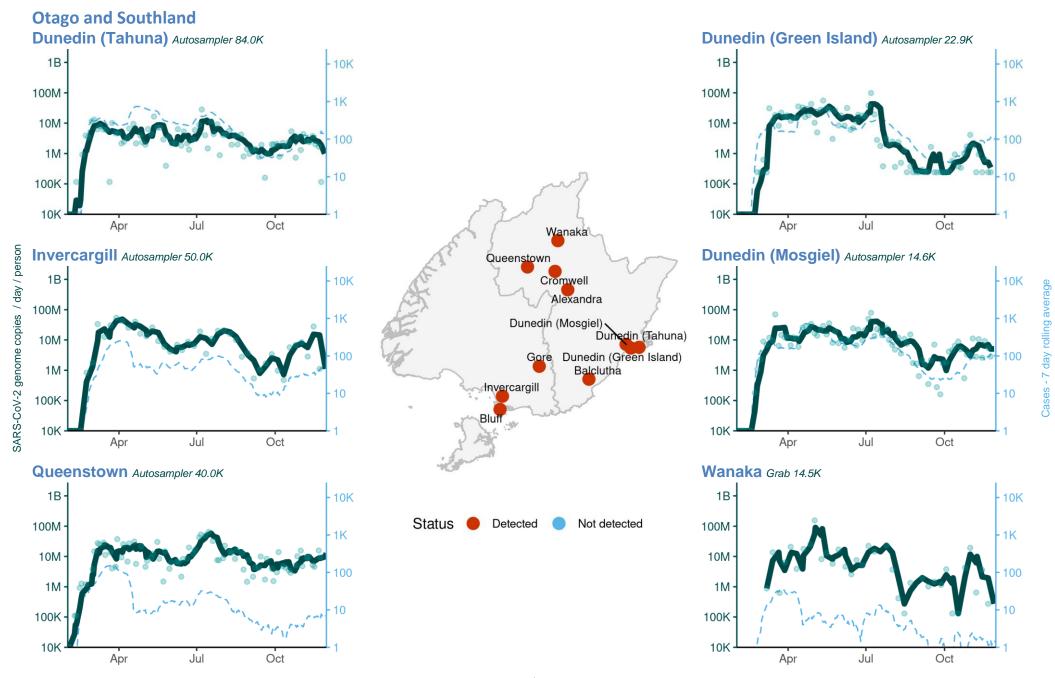
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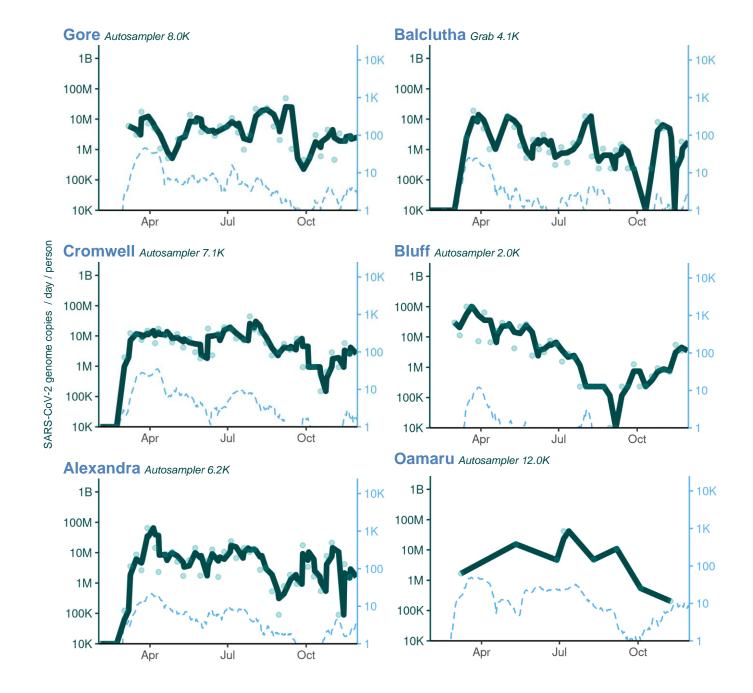
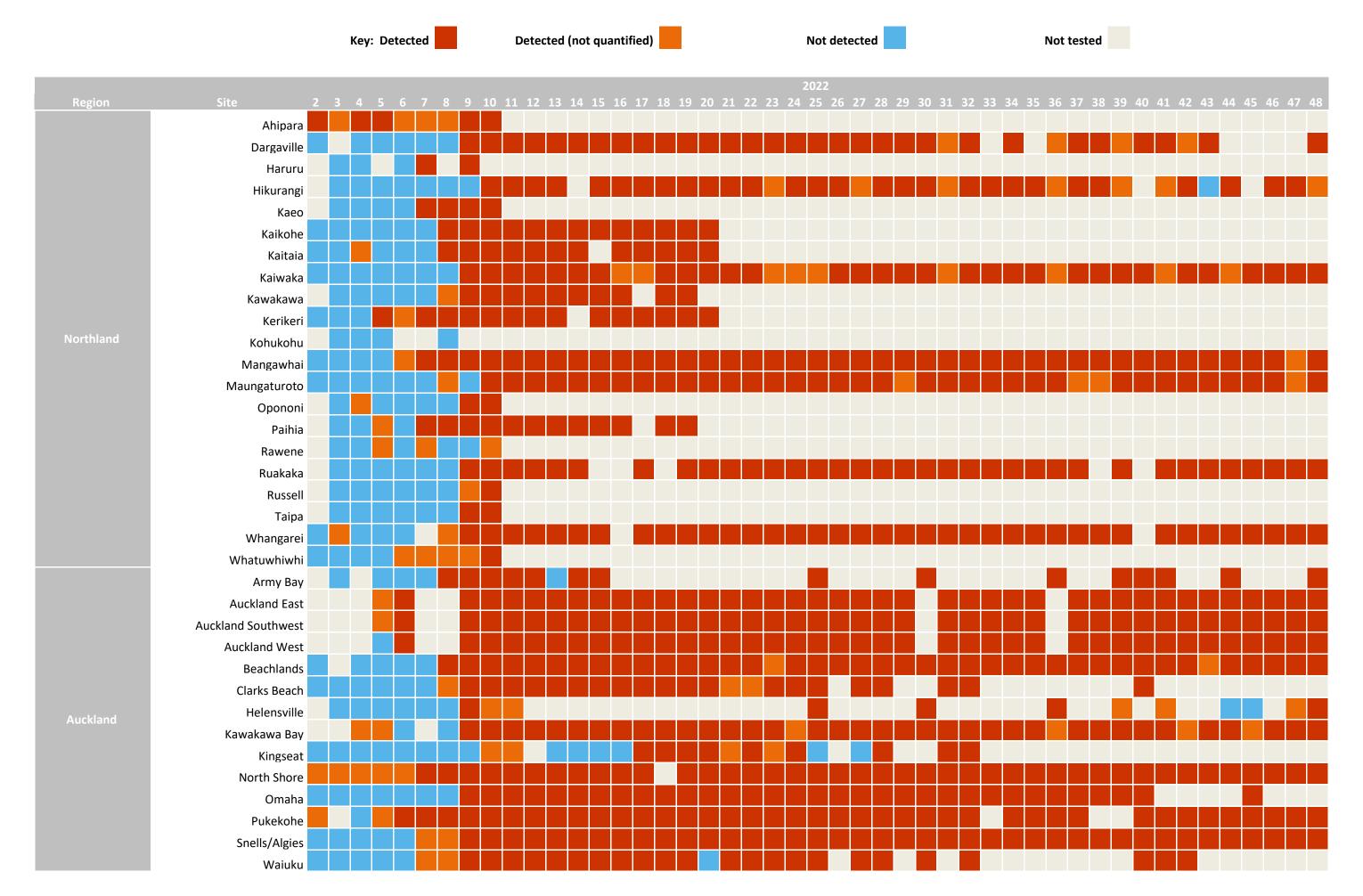
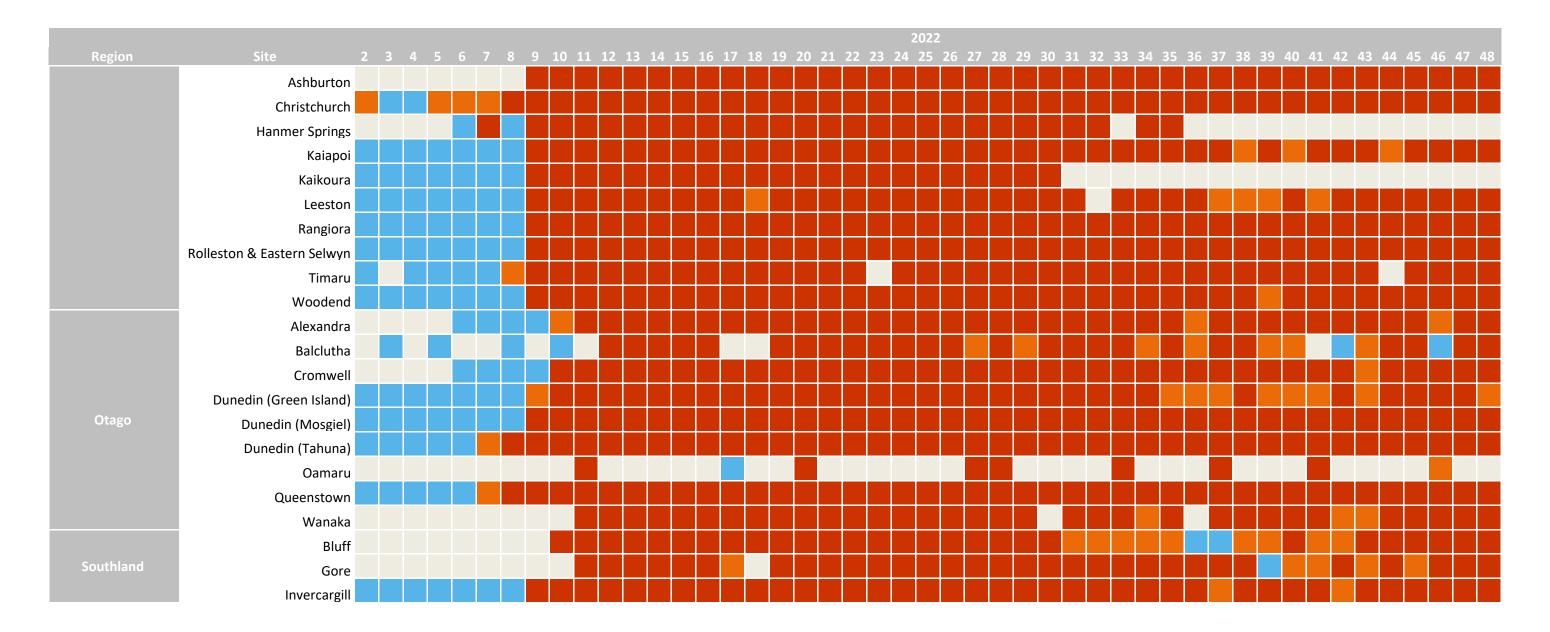


Table 2: Weekly Summary of Wastewater Sampling Results for SARS-CoV-2





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, Paula Scholes and Fatiha Sulthana. Data science analysis, visualisation and reporting is the result of team effort from: Franco Andrews, Bridget Armstrong, Raewyn Campbell, Gerhard de Beer, Richard Dean, Brent Gilpin, Joanne Hewitt, Dawen Li, Helen Morris, Alvaro Orsi, Niki Stefanogiannis, 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 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) 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).

For further information please contact

Brent Gilpin Joanne Hewitt

Science Leader Senior Scientist, Environmental & Food Virology