

New Zealand Wastewater Surveillance Programme COVID-19

Monthly Report April 2023

Weeks ending 2 April to 30 April 2023, weeks 13 to 17

Report prepared 10 May 2023

Key Trends & Insights

Nationally, SARS-CoV-2 levels in wastewater increased from an average of 2.46 million genome copies per person per day (gc/p/d) at the end of March to a peak of 4.37 million gc/p/d in week ending 16 April 2023, followed by a decrease to 3.07 million gc/p/d by the end of April.

100%

Sites (87/87) where SARS-CoV-2 was detected.

70%

NZ population covered by wastewater testing

XBB

Most prevalent variant detected (~60-65%)

- In total, 464 wastewater samples were collected across Aotearoa. SARS-CoV-2 RNA was detected in 457/464 (98%) samples from 87/87 (100%) of sites.
- Wastewater levels trended upwards during the first two weeks of April, peaking in the week ending 16 April 2023 (week 15, 4.37M gc/p/d), followed by a steady decline, such that levels at the end of April (week 17, ending 30 April 2023, 3.07M gc/p/d) were nearing levels observed at the end of March (week 12, ending 26 March, 2.46M gc/p/d).
- The SARS-CoV-2 peak in week 15 (week ending 16 April 2023) was the highest level observed in wastewater since week 1 (week ending 8 January 2023, 5.72M gc/p/d).
- XBB (includes XBB.1.5 and XBB.1.16) was the most common variant detected in April (~60-65% of national reads per week), with CH.1.1 (includes FK.1.1) also common (~24-35% of national reads per week). Other variants remained rare.

National Results

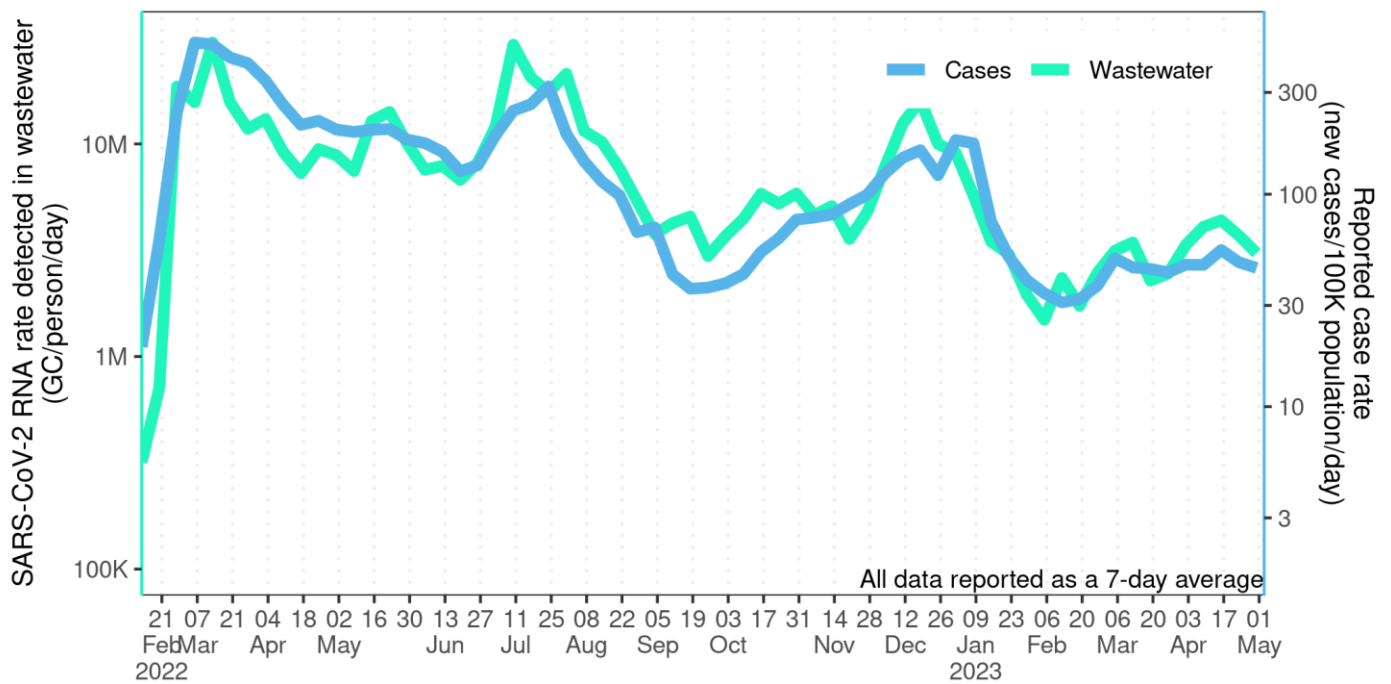


Figure 1. National timeseries of estimated SARS-CoV-2 genome copies (GC) in wastewater rate (GC/person/day, green line) and reported case rate (new cases/100,000 population/day, blue line) on a log₁₀ scale.

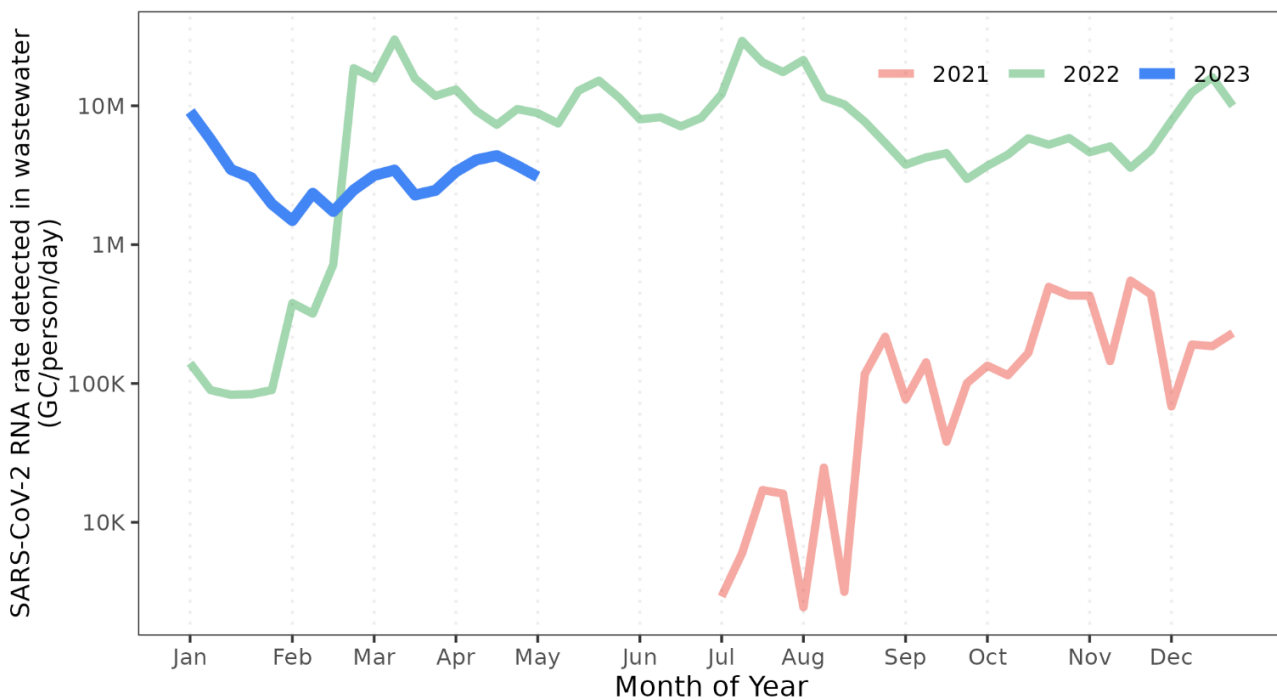


Figure 2. National timeseries of estimated SARS-CoV-2 genome copies (GC) in wastewater rate (GC/person/day) from July 2021 to April 2023 on a log₁₀ scale..

Change in SARS-CoV-2 levels per site

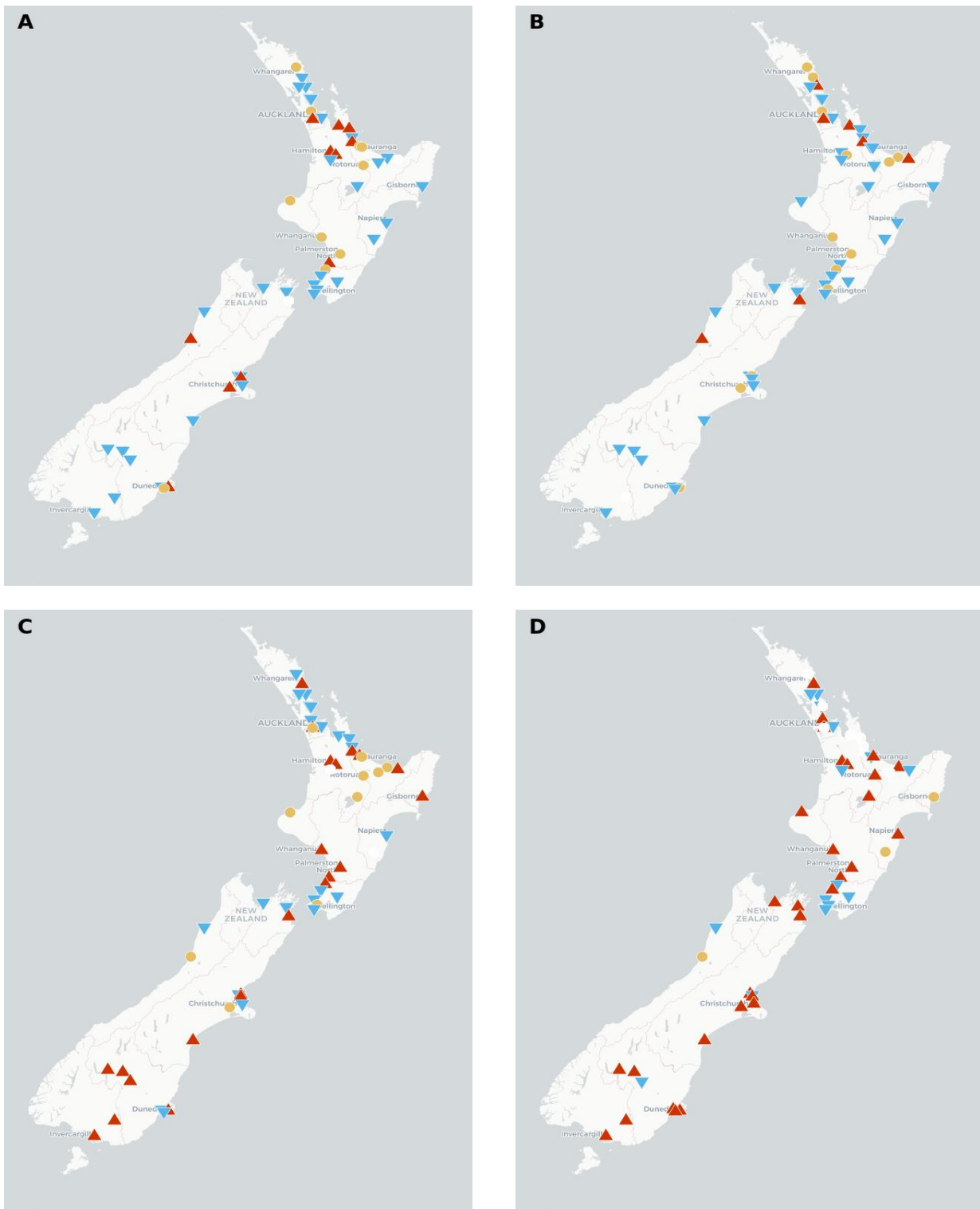


Figure 3. Comparison of SARS-CoV-2 levels for the week ending 30 April 2023 (week 17), compared to levels measured: A) 1 week ago; B) 2 weeks ago; C) 4 weeks ago; D) 12 weeks ago. Only sites with results for both time points are included. When the viral quantity is 30% or more higher this is labelled as increased (red up arrow on map). When the viral quantity is 30% or more lower, this is labelled as decreased (blue down arrow on map). If viral levels have changed less than this in the compared weeks, this is labelled as no change (yellow circle on map). Interactive map of weekly results available publicly at <https://www.poops.nz/>

Variant Analysis

In collaboration with Wilderlab, ESR generated the variant analysis results from sentinel sites in April 2023 (Table 1 and Figure 4). Note that wastewater variant analysis is based on sequencing a short fragment of the spike gene and therefore provides less resolution than whole genome sequencing from clinical cases. Consistent with the WGS of clinical cases, BQ.1.1 will now be reported with BA.4/BA.5. FK.1.1 cannot be distinguished from its parental CH.1.1 lineage using the Wilderlab assay, so is placed in this group.

Results for April 2023

XBB (includes **XBB.1.5** and **XBB.1.16**) was frequently detected, comprising ~65% of reads nationally in week 13 (16/19 sites), ~63% of reads nationally in week 14 (17/20 sites), ~63% of reads nationally in week 15 (18/20 sites), and ~60% of reads nationally in week 16 (16/20 sites).

CH.1.1 (includes **FK.1.1**) was also frequently detected in weeks 13 (9/19 sites), 14 (13/20 sites), 15 (16/20 sites) and 16 (12/20 sites). CH.1.1 comprised ~24-35% of sequencing reads nationally in April. Other subvariants in the **BA.2.75*** group (including BM.4, BR.2, XBF and BA.2.75) have declined significantly in wastewater, accounting for only ~4% of reads in week 13 (5/19 sites), ~1% of reads in weeks 14 (2/20 sites) and 15 (4/20 sites), and ~6% of reads in week 16 (6/20 sites).

BA.4/BA.5 (now includes **BQ.1.1**) was only detected in Porirua in week 13 (accounting for ~6% of national sequence reads) and in Hutt Valley in week 16 (accounting for ~3% of national sequence reads). This variant group was not detected in weeks 14 or 15.

XBC was detected in week 13 (North Shore only, ~1% of national sequence reads), week 14 (Tauranga only, ~1% of national sequencing reads), and week 15 (3/20 sites, ~2% of sequencing reads nationally). It was not detected in week 16.

Collectively, wastewater results suggest that XBB (including XBB.1.5 and XBB.1.16), and to a lesser extent CH.1.1, continued to circulate widely in the community in April, with minor contributions from other variants, in agreement with clinical WGS results.

	Week 13					Week 14					Week 15					Week 16					
	BA.4/BA.5	BA.2.75*	CH.1.1	XBB	XBC	BA.4/BA.5	BA.2.75*	CH.1.1	XBB	XBC	BA.4/BA.5	BA.2.75*	CH.1.1	XBB	XBC	BA.4/BA.5	BA.2.75*	CH.1.1	XBB	XBC	
Whangarei																					
North Shore																					
Auckland East																					
Auckland Southwest																					
Auckland West																					
Mt Maunganui																					
Tauranga																					
Rotorua																					
Taupo																					
Gisborne																					
New Plymouth																					
Palmerston North																					
Porirua																					
Hutt Valley																					
Wellington (Moa Point)																					
Nelson																					
Christchurch																					
Queenstown																					
Dunedin (Tahuna)																					
Dunedin (Mosgiel)																					
All Sites (national)	6	4	24	65	1	0	1	35	63	0.5	0	1	34	63	2	3	6	31	60	0	

Table 1. Data from 20 wastewater sentinel sites sampled in week 13 (ending 2 April 2023), week 14 (ending 9 April 2023), week 15 (ending 16 April 2023) and week 16 (ending 23 April 2023) using a S-gene (spike) barcoding assay able to assign BA.4/BA.5 (includes BQ.1.1), BA2.75* (includes BA.2.75/XBF/BR.2), CH.1.1 (includes FK.1.1), XBB (includes XBB.1.5 and XBB.1.16) and XBC (sub)variants. Coloured box denotes that the variant was detected at that site that week, white box denotes that the variant was not detected, and grey box denotes site was not sampled that week. Numbers in the bottom row denote the estimated percentage of each variant at the national scale.

Variant Timeline - National

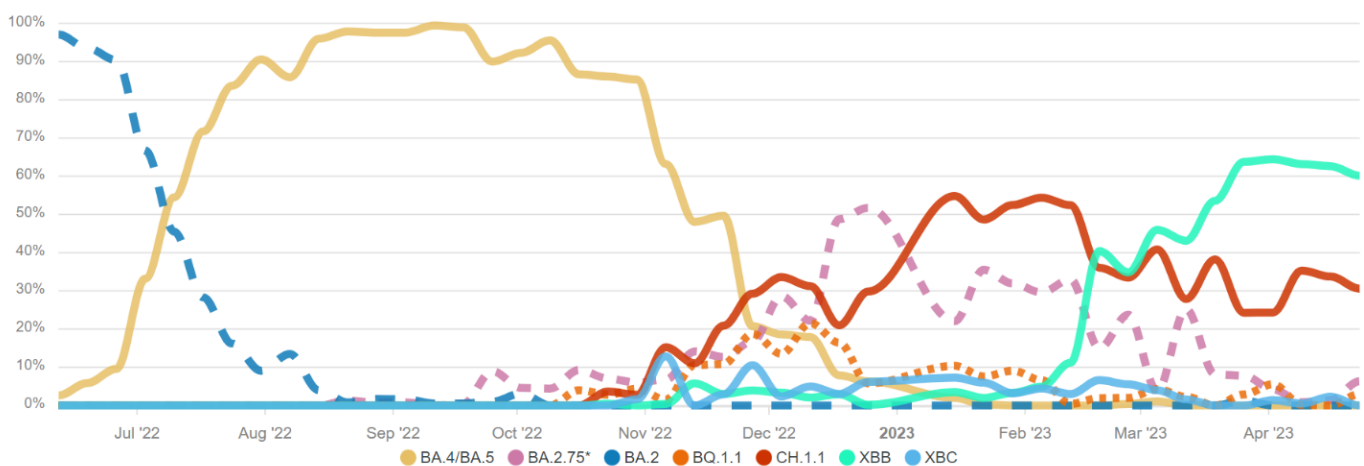


Figure 4. Variant prevalence over time at a national scale (average). Data are collected from up to 20 sentinel sites each week.

Wastewater Trends in Ministry of Health Regions

Regional analysis of the wastewater data (Figure 5) indicates an increasing trend in SARS-CoV-2 levels in most regions in the early weeks of April, but this plateaued in the latter half of the month.

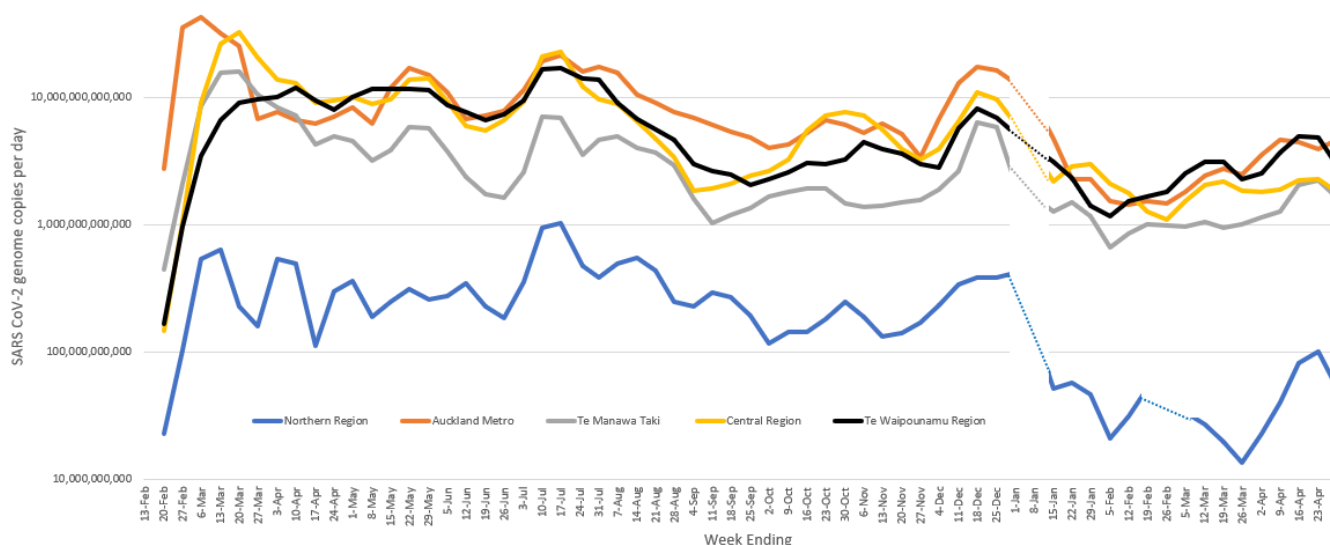


Figure 5. Total SARS-CoV-2 genome copies detected per day in the five Ministry of Health regions. Dashed lines are inferred levels during periods when samples were either not collected (Christmas period) or insufficient numbers collected (due to weather impacts) for the region.

Note: Regional trend analysis for week 52 (2022) and week 1 (2023) was only possible for Auckland Metro, as there were limited samples collected during the holiday period. Viral quantitation for the other regions was therefore not available during this period (denoted by dashed line). Due to the weather-related impacts in February 2023, fewer samples were collected in some regions. The Central regional summary excludes Hawke’s Bay samples in weeks 8-10, and analysis for the Northern region was not possible in between weeks 7-9 due to too few samples being received from this region.

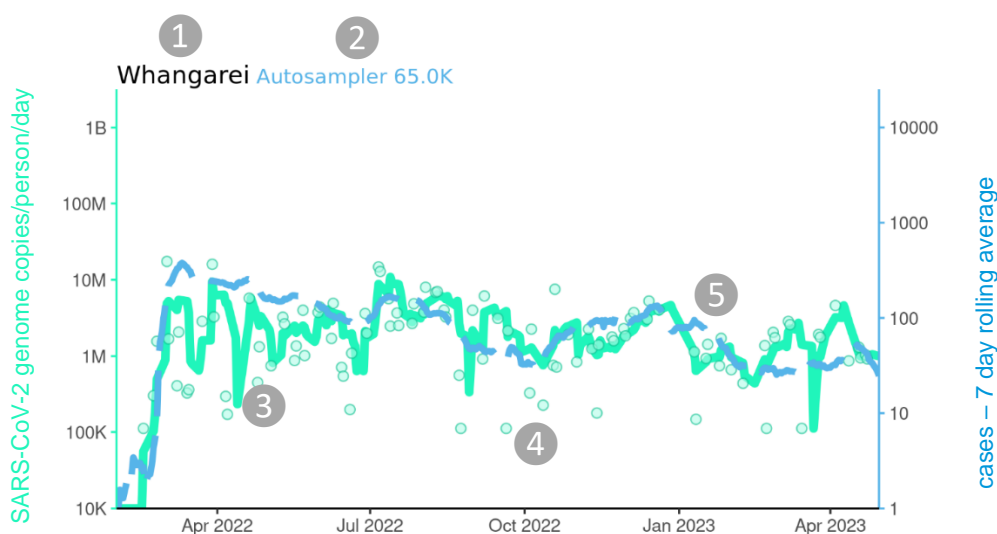
The following pages include summaries for 12 regions of New Zealand, based on all the sites within each region. Graphs shown are for the larger catchment sites within each of these regions, with results for the smaller catchments shown in *Appendix C*.

The coloured symbols on each of the maps illustrate changes in wastewater viral quantity (GC/person/day) for that site in comparison to **4 weeks prior to the current end of week date**. These graphs use the same thresholds as Figure 3. When the viral quantity is 30% or more higher in the current week than it was 4 weeks ago, this is labelled as increased (red up arrow on map). When the viral quantity is 30% or more lower in the current week than it was 4 weeks ago, this is labelled as decreased (blue down arrow on map). If viral levels have changed less than either of these values in the two compared weeks, this is labelled as no change (yellow circle on map). If a site was not tested in the current week, or 4 weeks previously, no symbol will appear on the map for that site.

Regional Trend Time Series

Regional time series graphs for the last 12 months are presented. The raw data (genome copies per litre of wastewater) is converted to a viral load of genome copies/person/day (GC/person/day). This conversion considers flow of wastewater entering the treatment plant and the population serviced in each wastewater catchment. An average value of all samples collected within a week from a site is calculated. For regions an average GC/person/day from all sites in that region is calculated for that given week. The cases are a reported case rate (new cases/100,000 population/day).

Site Graphs

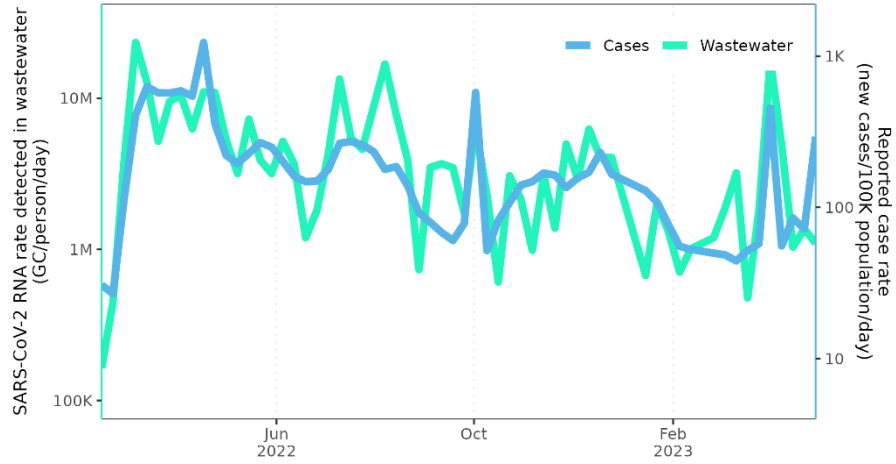


- 1 Site Name
- 2 Sample collection method and population. Results based on autosampler may be more representative than grab sample-based results.
- 3 Wastewater results shown as solid line (green line) | 14-day average of genome copies/person/day on a log₁₀ scale.
- 4 Individual results samples shown as circles | Rolling 14-day average of genome copies/person/day on a log₁₀ scale.
- 5 Rolling 7-day average of new cases shown as dashed line (blue 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.

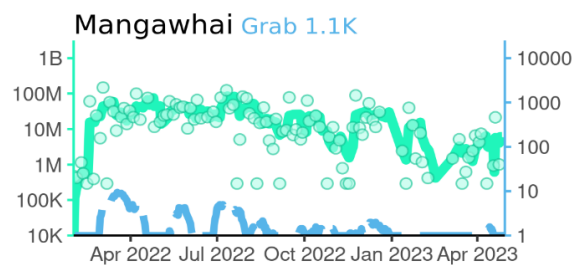
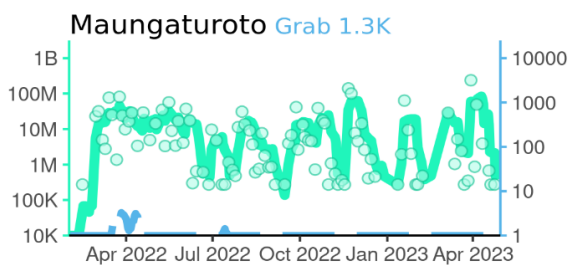
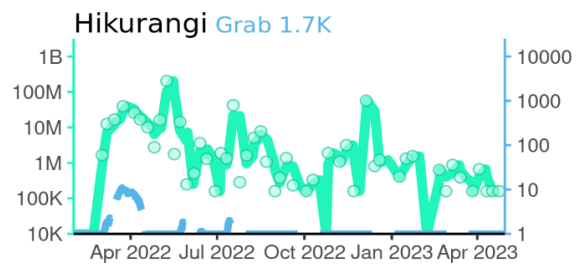
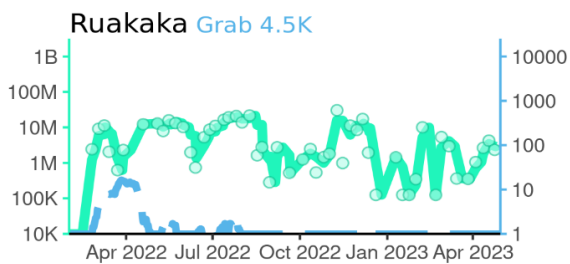
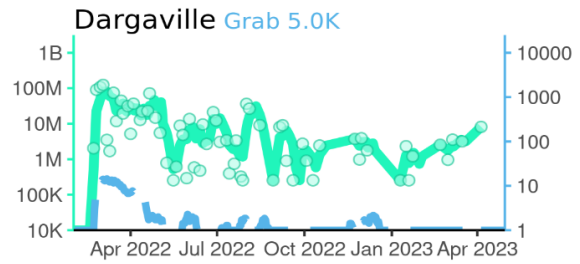
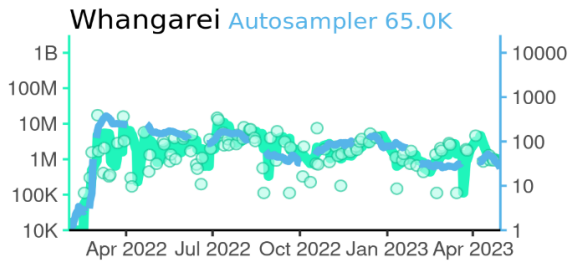
Note: Wastewater and cases data are on a log₁₀ scale. Scales on all graphs have been normalized to cover the same scale on every graph. Care should be taken when interpreting the data.

Northland

The overall average levels of SARS-CoV-2 in wastewater in Northland were lower in the most recent week than they were 4 weeks ago.



▲ Increased ▼ Decreased ● No Change



SARS-CoV-2 genome copies/person/day

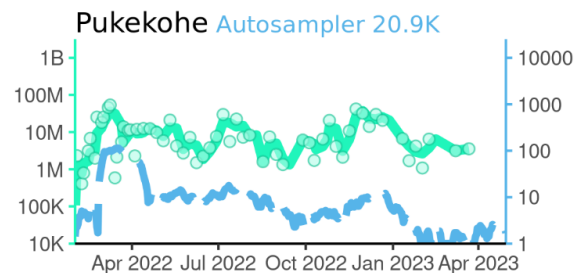
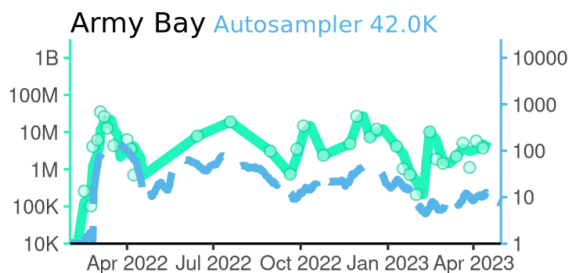
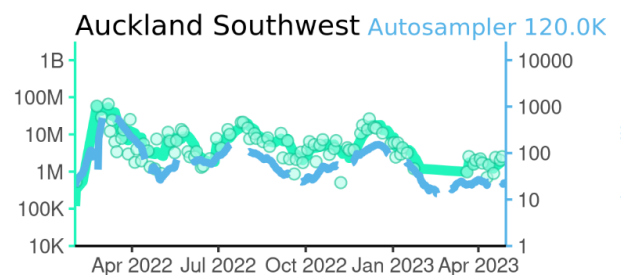
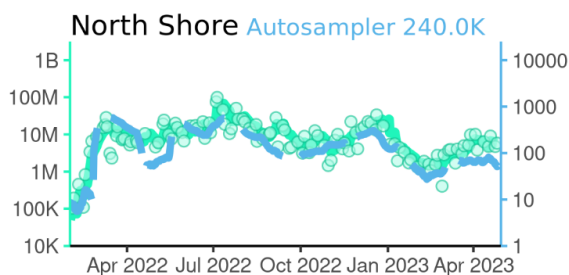
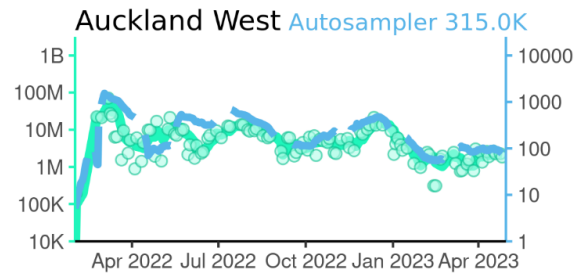
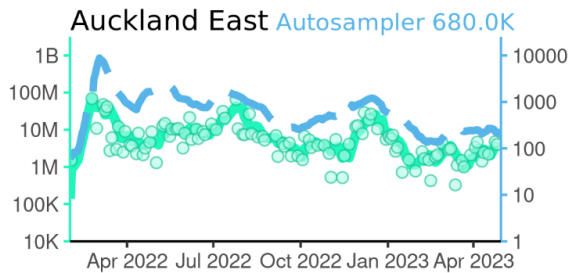
Cases – 7 day rolling average

Auckland

The overall average levels of SARS-CoV-2 in wastewater in Auckland were higher in the most recent week than they were 4 weeks ago.



▲ Increased ▼ Decreased ● No Change

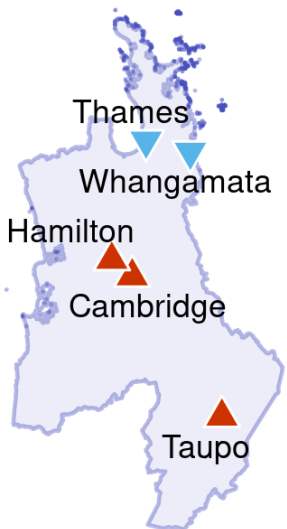


SARS-CoV-2 genome copies/person/day

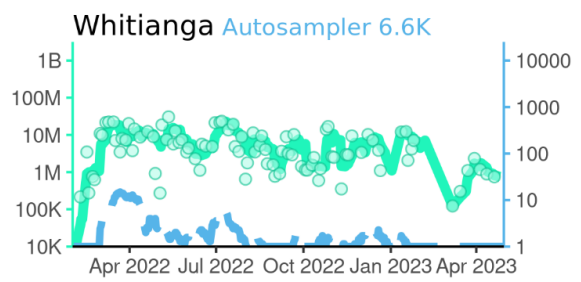
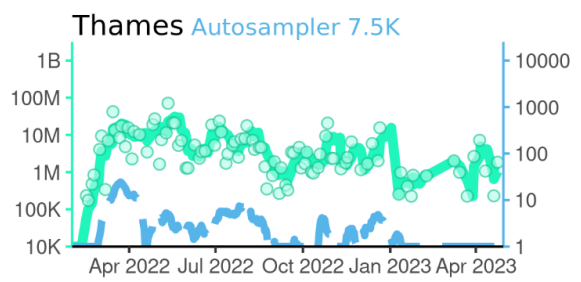
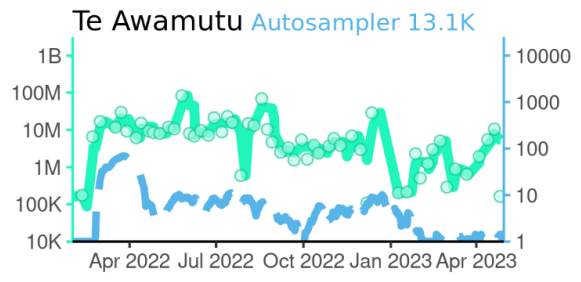
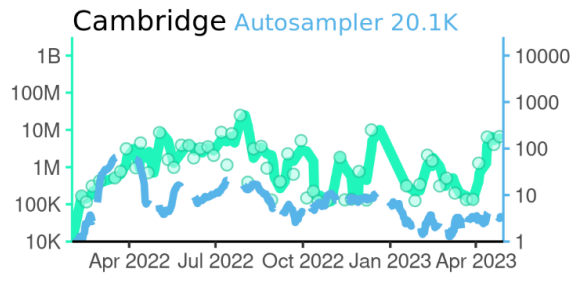
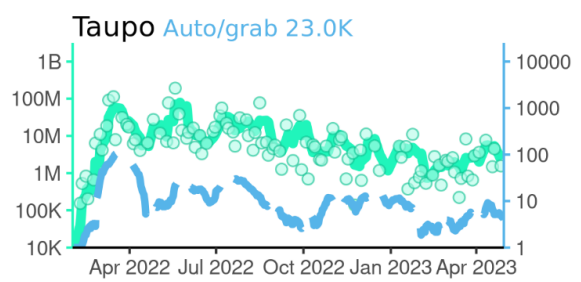
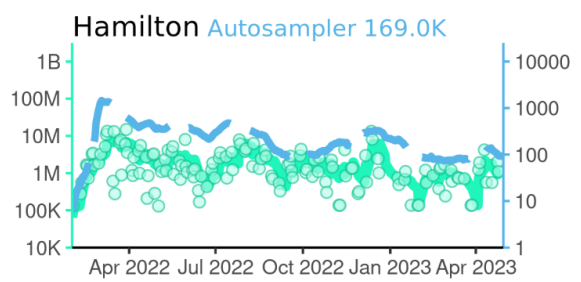
Cases – 7 day rolling average

Waikato

The overall average levels of SARS-CoV-2 in wastewater in Waikato were higher in the most recent week than they were 4 weeks ago.



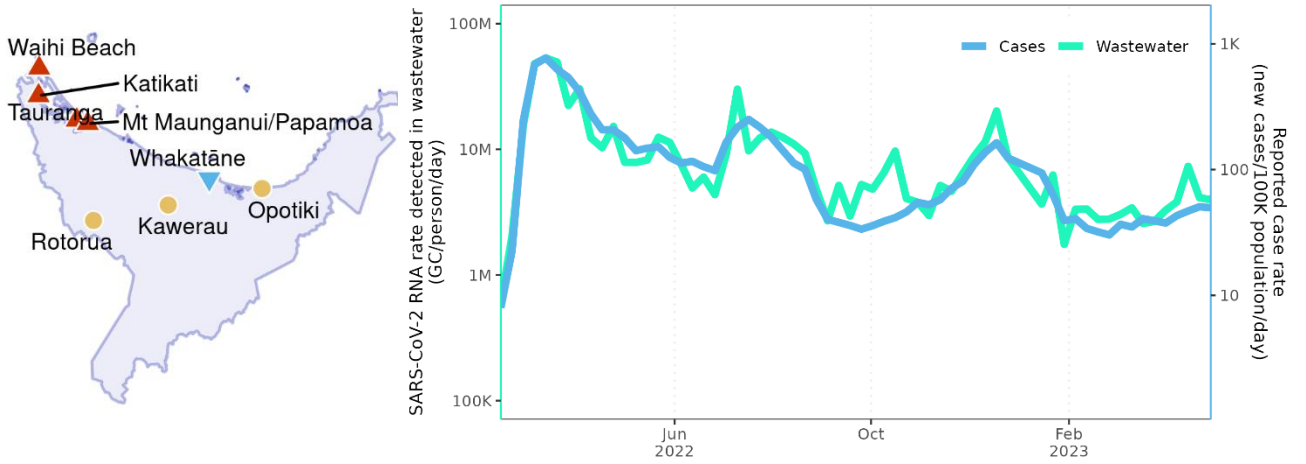
▲ Increased ▼ Decreased ● No Change



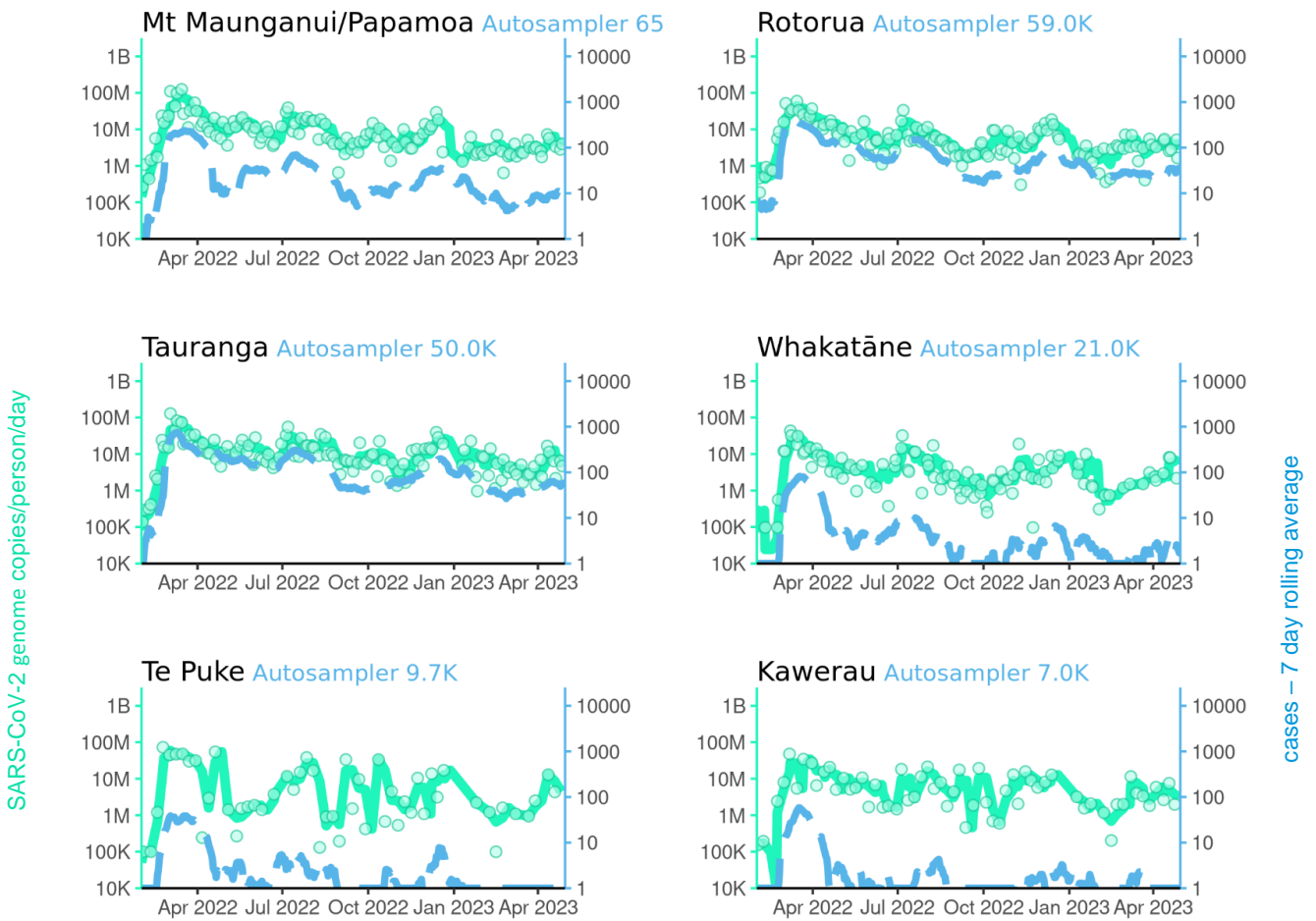
April 2023 (Weeks ending 2 April to 30 April)

Bay of Plenty

The overall average levels of SARS-CoV-2 in wastewater in Bay of Plenty were lower in the most recent week than they were 4 weeks ago.



▲ Increased ▼ Decreased ● No Change

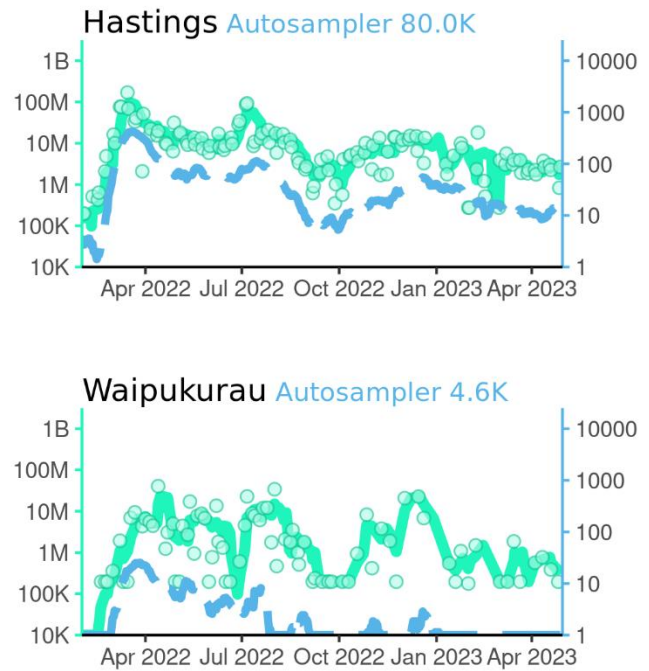
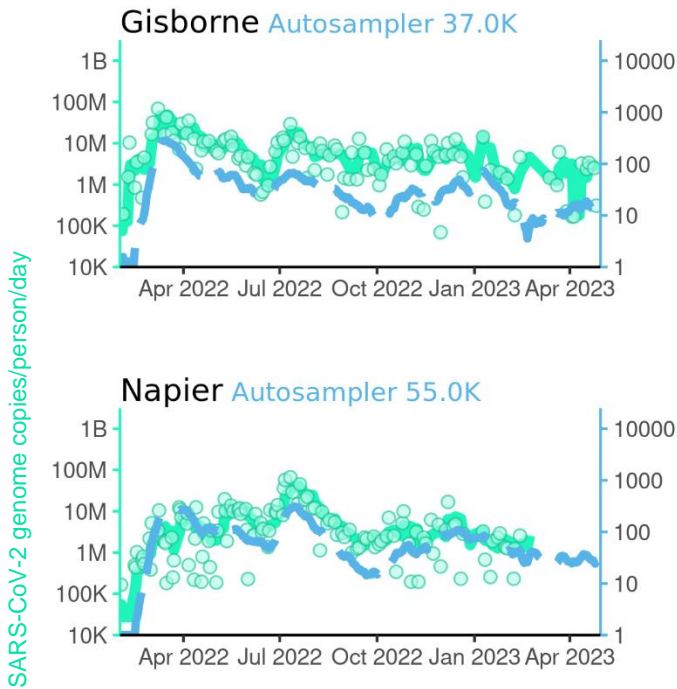


Hawke's Bay & Gisborne

The overall average levels of SARS-CoV-2 in wastewater in Hawke's Bay and Gisborne were lower in the most recent week than they were 4 weeks ago.

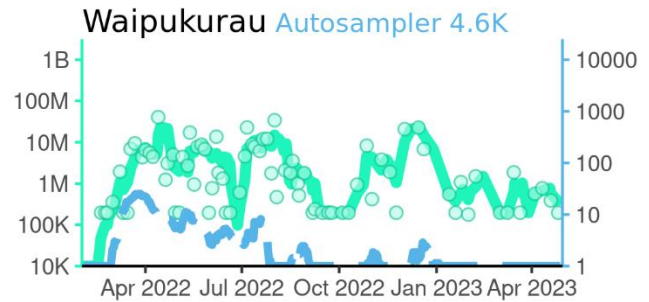
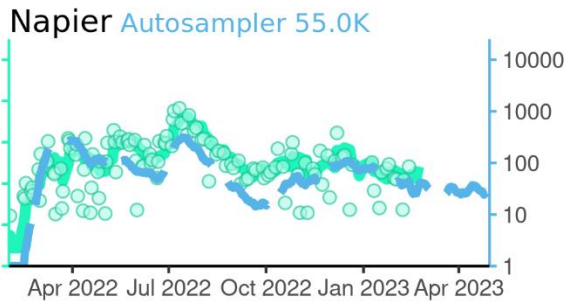


▲ Increased ▼ Decreased ● No Change



cases — 7 day rolling average

SARS-CoV-2 genome copies/person/day

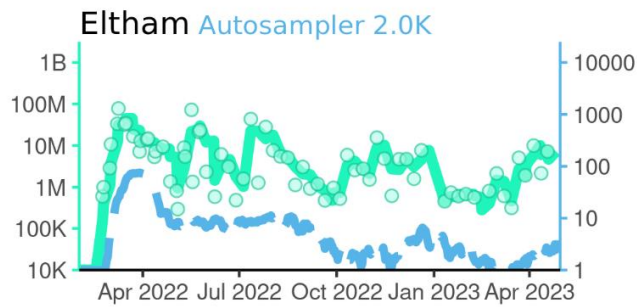
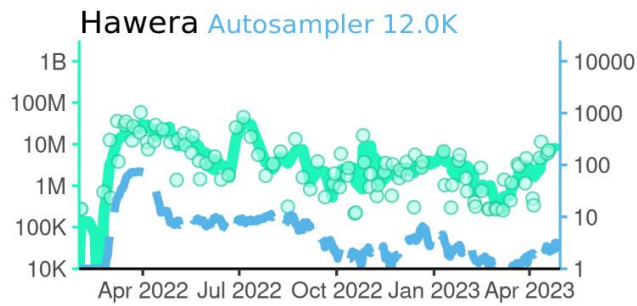
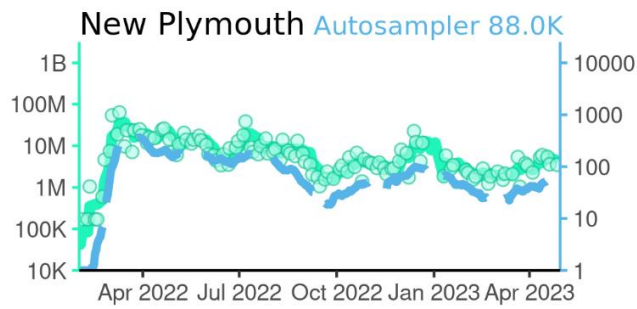
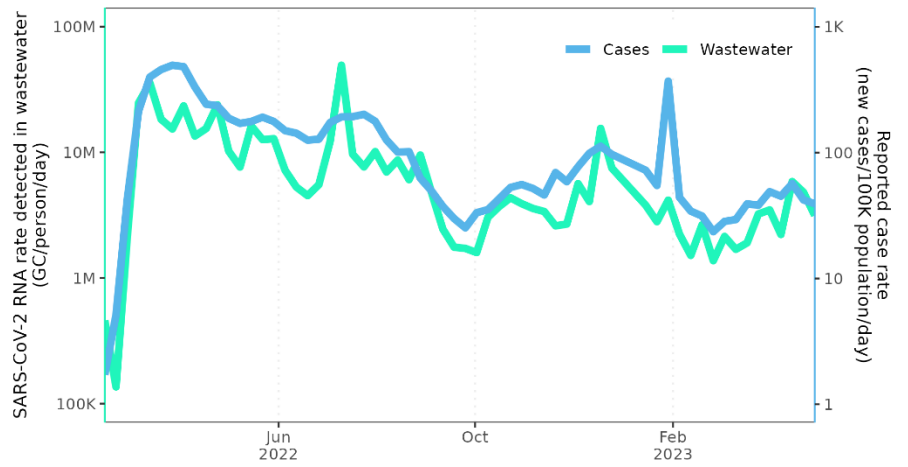


Taranaki

The overall average levels of SARS-CoV-2 in wastewater in Taranaki were lower in the most recent week than they were 4 weeks ago.



▲ Increased ▼ Decreased ● No Change



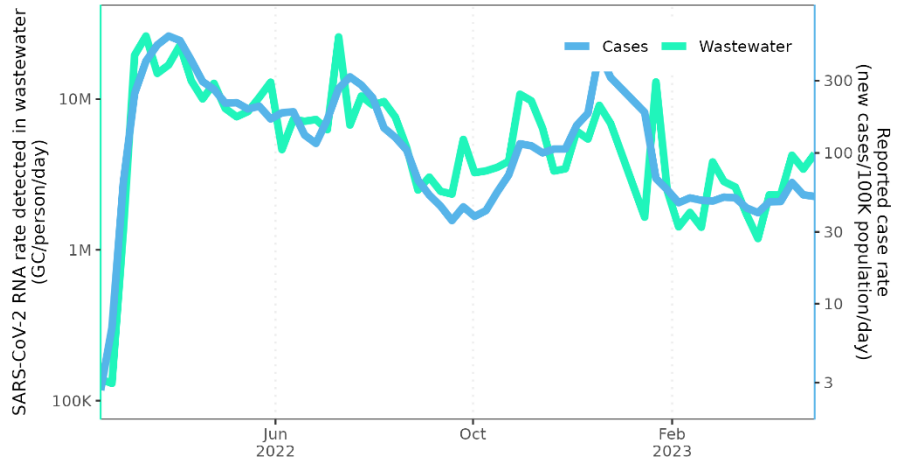
SARS-CoV-2 genome copies/person/day

cases – 7 day rolling average

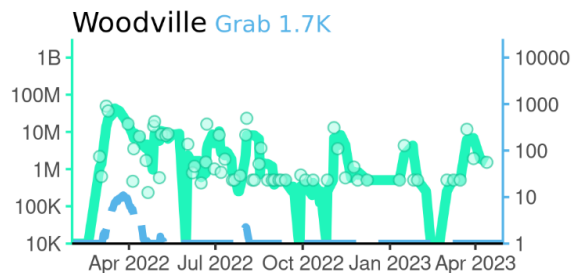
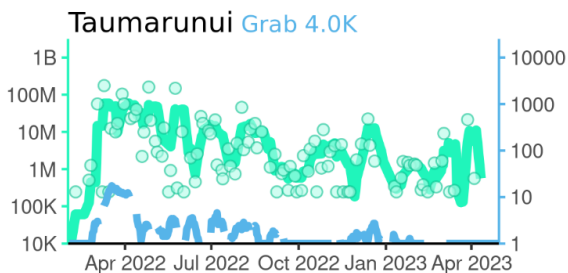
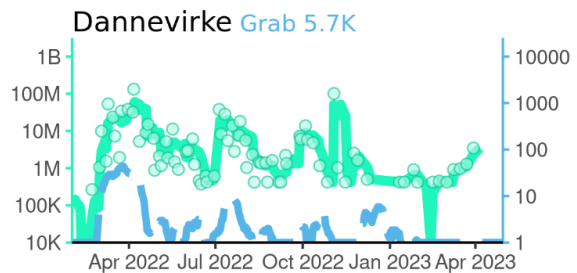
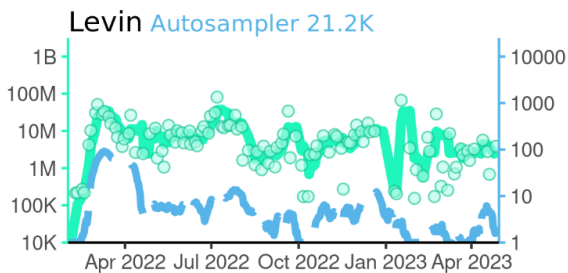
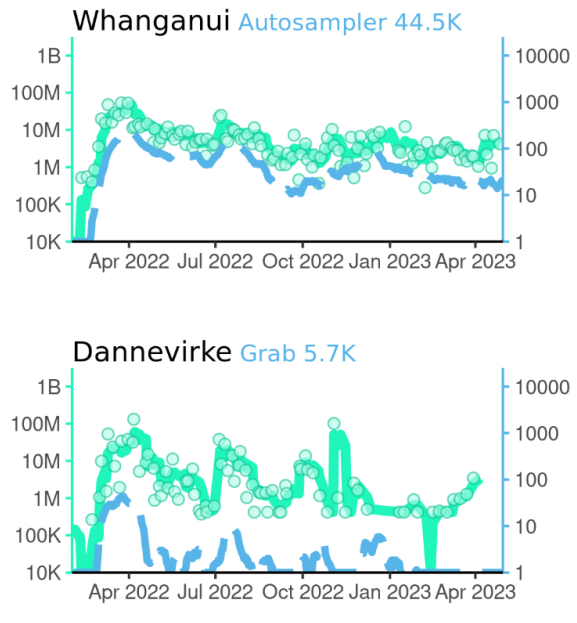
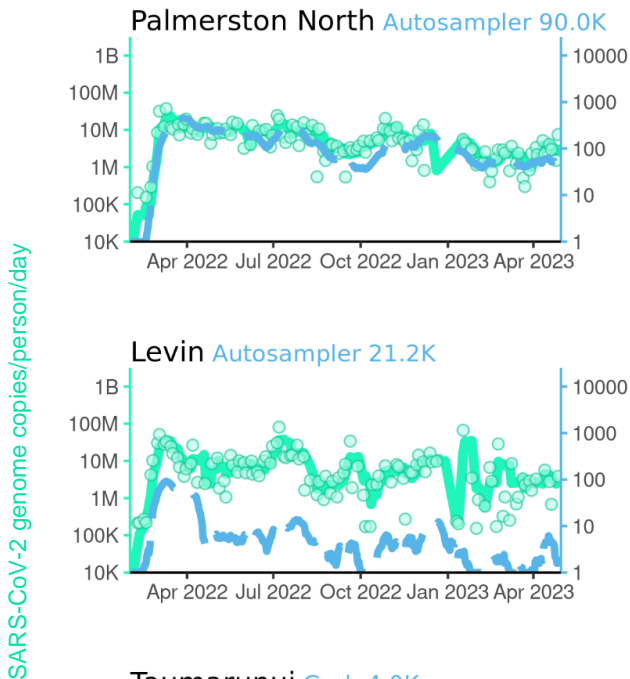
April 2023 (Weeks ending 2 April to 30 April)

Manawatu-Whanganui

The overall average levels of SARS-CoV-2 in wastewater in Manawatu-Whanganui were higher in the most recent week than they were 4 weeks ago.

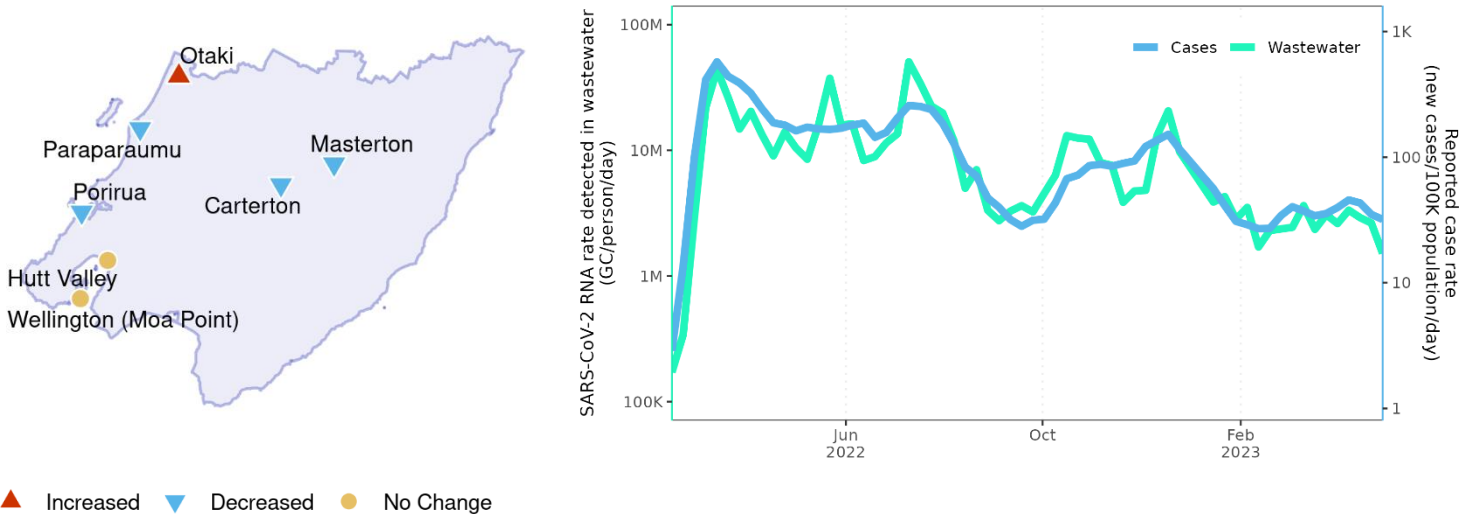


▲ Increased ▼ Decreased ● No Change



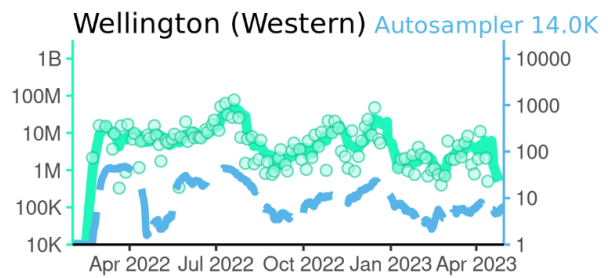
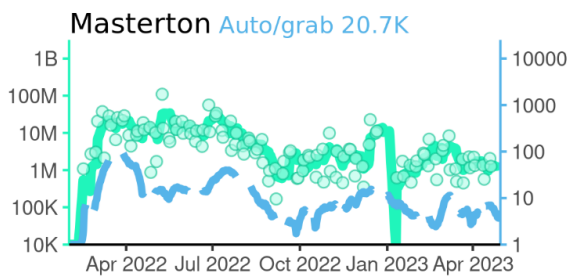
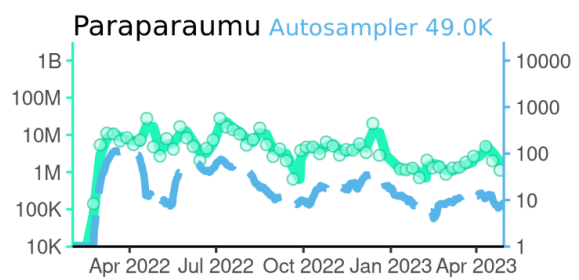
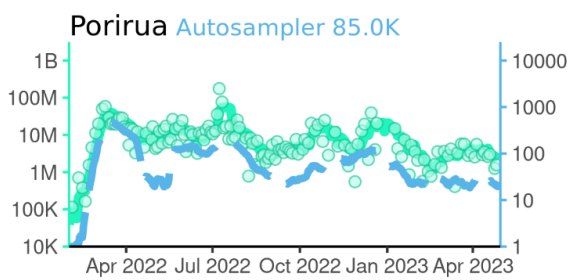
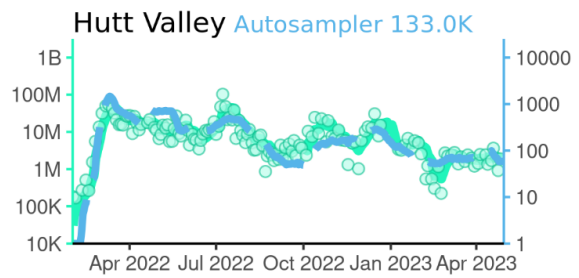
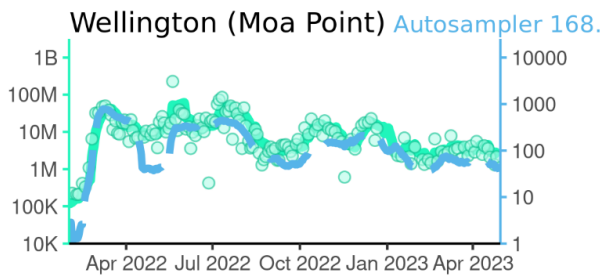
Wellington

The overall average levels of SARS-CoV-2 in wastewater in Wellington Northland were lower in the most recent week than they were 4 weeks ago.



▲ Increased ▼ Decreased ● No Change

SARS-CoV-2 genome copies/person/day



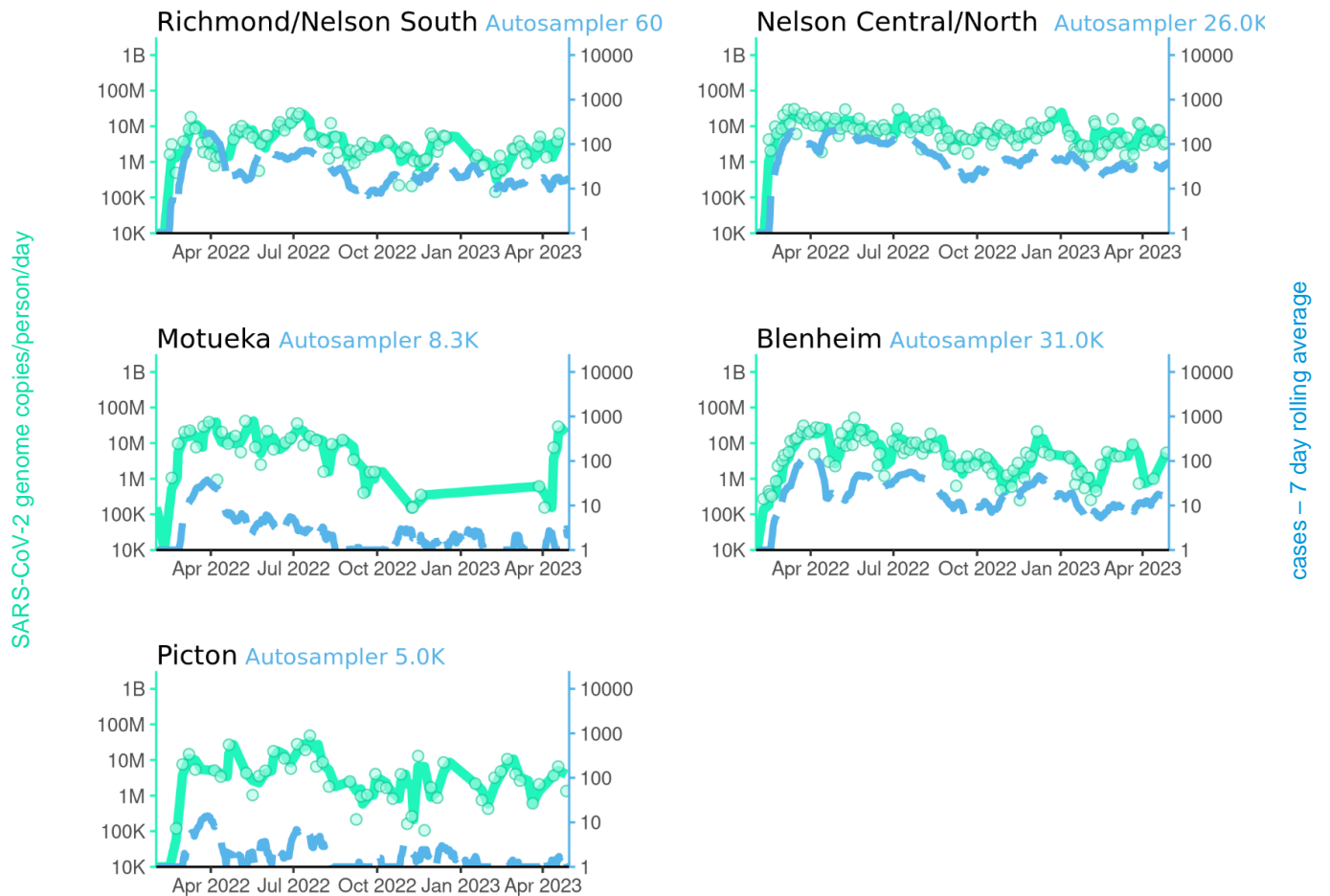
cases - 7 day rolling average

Tasman, Nelson & Marlborough

The overall average levels of SARS-CoV-2 in wastewater in combined Tasman, Nelson and Marlborough were lower in the most recent week than they were 4 weeks ago.



▲ Increased ▼ Decreased ● No Change



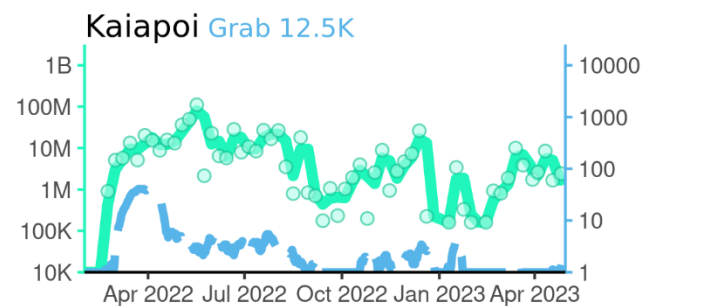
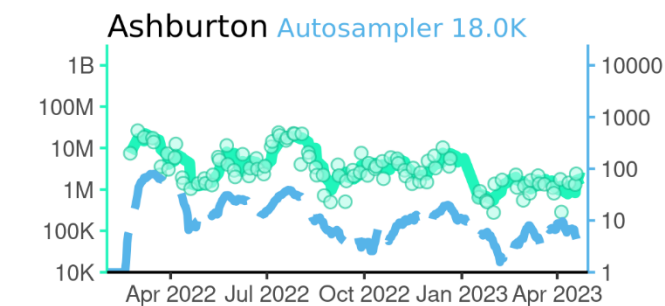
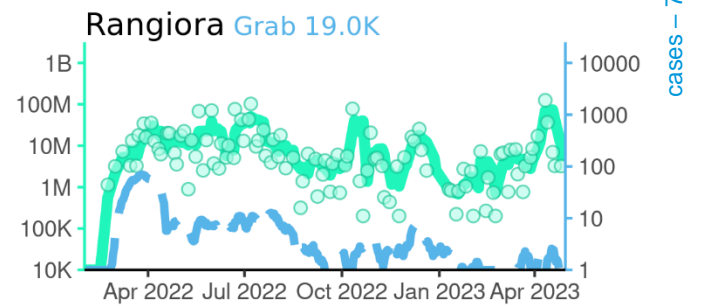
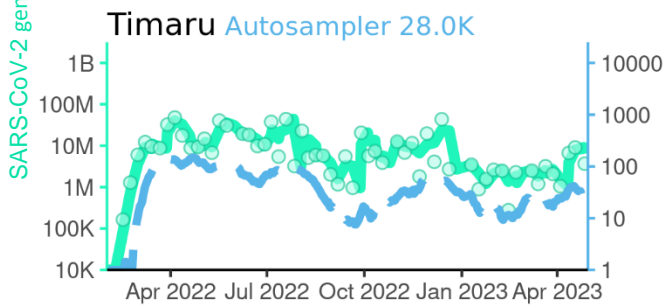
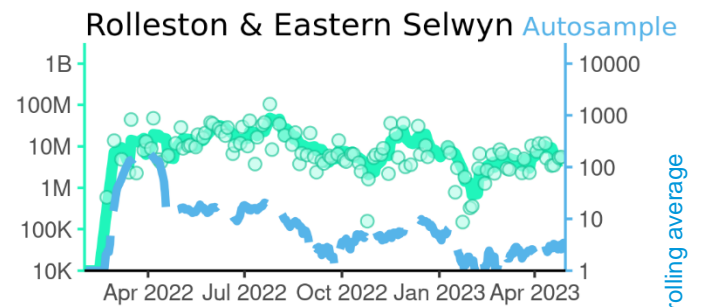
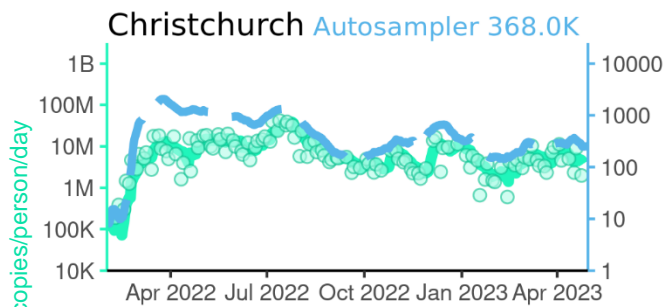
April 2023 (Weeks ending 2 April to 30 April)

Canterbury

The overall average levels of SARS-CoV-2 in wastewater in Canterbury were lower in the most recent week than they were 4 weeks ago.



▲ Increased ▼ Decreased ● No Change



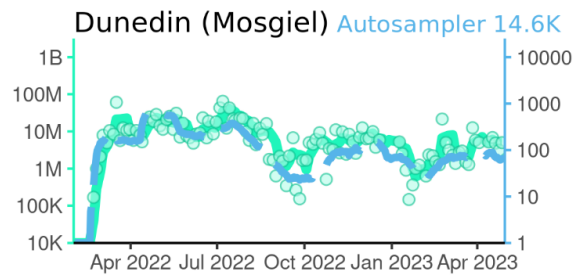
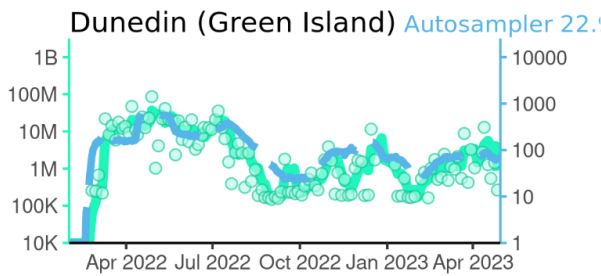
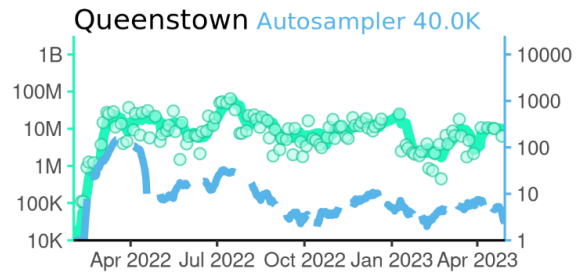
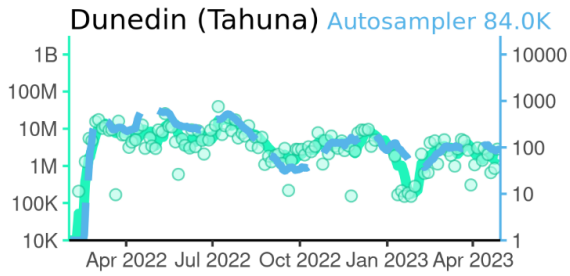
April 2023 (Weeks ending 2 April to 30 April)

Otago

The overall average levels of SARS-CoV-2 in wastewater in Otago were lower in the most recent week than they were 4 weeks ago.

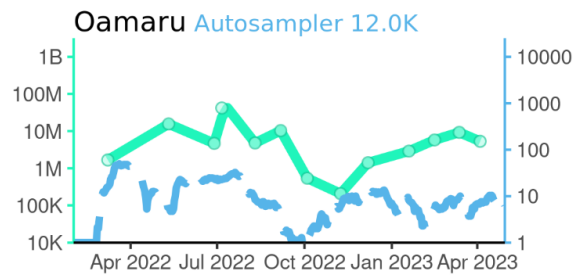
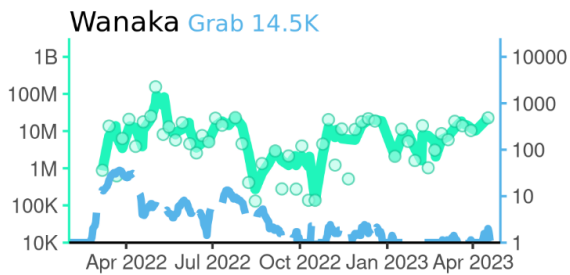


▲ Increased ▼ Decreased ● No Change



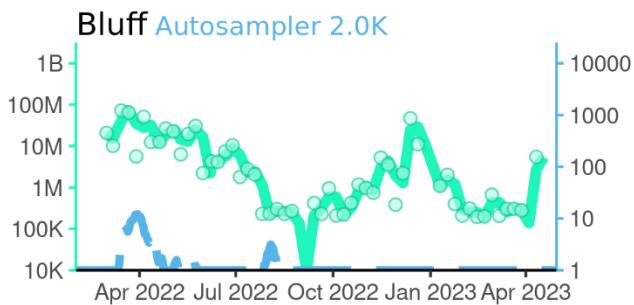
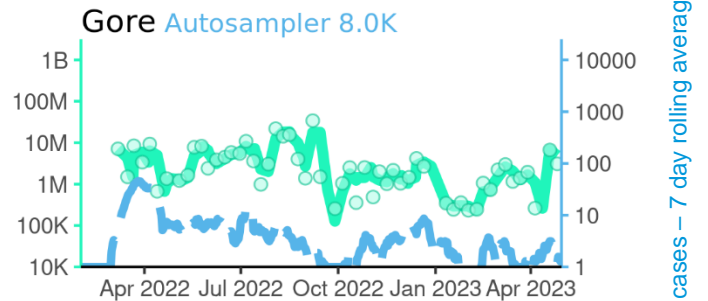
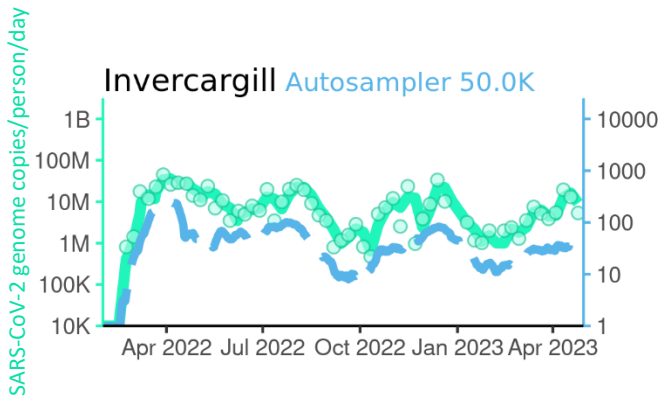
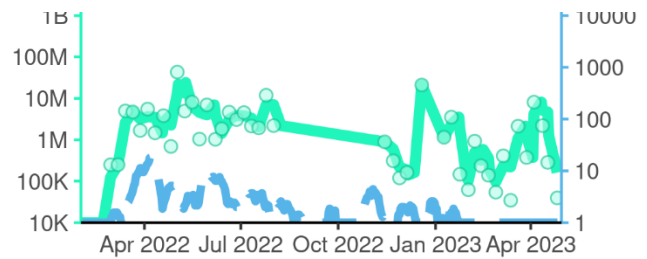
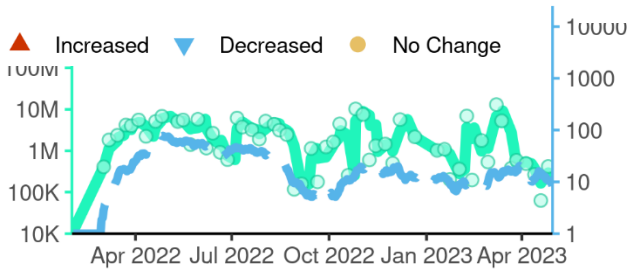
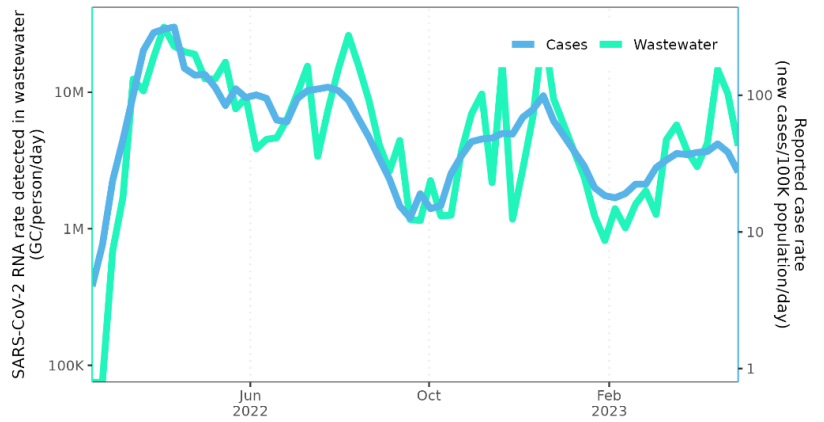
SARS-CoV-2 genome copies/person/day

cases - 7 day rolling average



West Coast & Southland

The overall average levels of SARS-CoV-2 in wastewater in combined West Coast and Southland were lower in the most recent week than they were 4 weeks ago.



Glossary of Terms

Autosampler – an automatic water sampling machine that automatically collects water typically based on time or flow parameters.

Coronavirus disease 19 (COVID-19) – a respiratory illness caused by the virus SARS-CoV-2.

Grab sampler (Grab) – a grab sample is a sample physically taken from a sampler and consists of either a single discrete sample or multiple samples collected over a period.

Genome – The entire genetic code of an organism. In the case of SARS-CoV-2, the genome is ~30,000 nucleotides (or base pairs) in length. The process of obtaining the entire genome is called whole-genome-sequencing (WGS). It is achieved by sequencing SARS-CoV-2 in overlapping pieces and then ‘stitching’ them together (genome assembly). Sometimes genomes are tagged as *failed* or *partial*.

Genome copies per person per day – The raw data (genome copies per litre) is converted to a viral load of genome copies/person/day). This conversion considers the flow of wastewater entering the treatment plant and the population in the wastewater catchment (please note that this will not necessarily be the same as the population of the town/city). At the site level, GC/person/day is the average value of all samples collected within that week. When a site is sampled only once per week, the value of that sample is shown (as there is no average for the week). This approach allows for the aggregation at regional and national levels, and avoids small catchments being over-represented and large catchments being under-represented. This dashboard provides linear and log₁₀ unit options for data presentation.

Receptor binding domain (RBD) – a small part of the Spike protein that is instrumental in the virus attaching to the ACE2 receptor, a protein found on the outside of many human cells. Several key mutations have been identified here which determine a variant’s transmissibility and ability to evade immunity.

Ribonucleic acid (RNA) – is a nucleic acid, typically single-stranded – aids in cellular protein synthesis. In some viruses replace DNA as the primary source of genetic information such as SARS-CoV-2.

Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) – the virus that causes the disease coronavirus disease 19 (COVID-19). SARS-CoV-2 is a single stranded RNA virus.

Subvariant – a sub-branch of a formally recognized variant. For example, BA.1 and BA.2 are classified as subvariants of Omicron; while BA.2.75 is a subvariant of BA.2. A sub-branch of a variant will remain unless the World health organization (WHO) elevates it to a distinct *variant status*.

Spike protein – a protein location on the outside of the SARS-CoV-2 virus that allows the virus to attach to, penetrate and infect cells. The spike protein is targeted by most vaccines. Changes to the spike protein can result in immune evasion.

Variant or Lineage – these are interchangeable terms that refer to a group of closely related viruses with a common ancestor. Several systematic methods of naming and classifying SARS-CoV-2 variants include the Pango (names like B.1.617.2) and Nextstrain (names like 21A) systems. The World health organization (WHO) also names various lineages of particular interest to public health.

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 Javed, Ashley McDonald, Andrew Ng, Fatiha Sulthana and Michelle Sutherland. Data science analysis, visualisation and reporting is the result of team effort from: Franco Andrews, Bridget Armstrong, Raewyn Campbell, Joanne Chapman, Lei Chen, Gerhard de Beer, Richard Dean, Brent Gilpin, Joanne Hewitt, Dawen Li, Jonathan Marshall, Helen Morris and Leighton Watson. Ongoing support for this work from the Ministry of Health and ESR management is appreciated.

Notes

Sites and frequency of sample collection: The catchment population sites selected for the surveillance range from approximately 400 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 2023, the wastewater catchment areas cover over 75% 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.

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

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

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

Method sensitivity: The protocol used to concentrate SARS-CoV-2 from wastewater allows for the sensitive detection of SARS-CoV-2 by RT-qPCR. ESR has shown that when 10 individuals are actively

shedding SARS-CoV-2 RNA in a catchment of 100,000 individuals, there was a high likelihood of detecting viral RNA in wastewater (<https://doi.org/10.1016/j.watres.2021.118032>). Shedding by one individual may be detected in wastewater, but it does depend on many factors including the amount and duration of shedding. Very low levels in wastewater may be not able to be quantified (i.e., less than the limit of quantification- see below).

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

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

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

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

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

Data not shown: Results from certain samples may not be shown, as the result was either deemed invalid, or the sample could not be tested (e.g., leaked in transit, not labelled).

For further information please contact:

Joanne Hewitt

Science Leader

Joanne.hewitt@esr.cri.nz

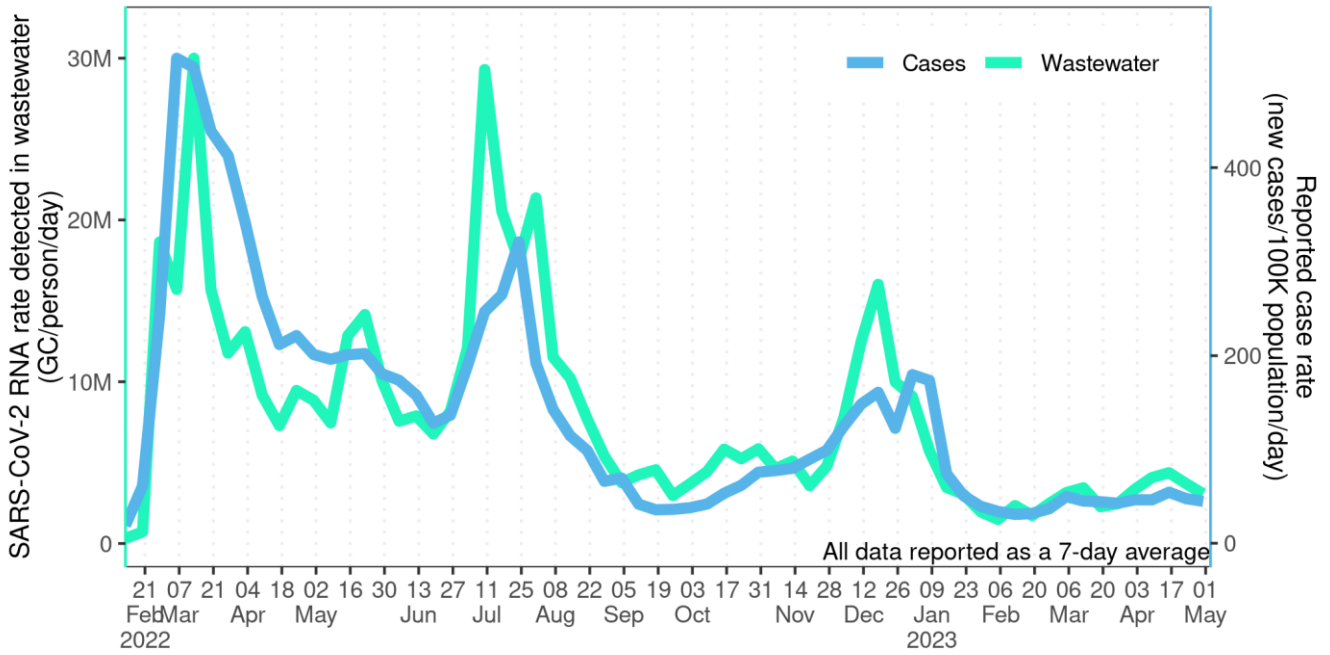
Jo Chapman

Senior Scientist

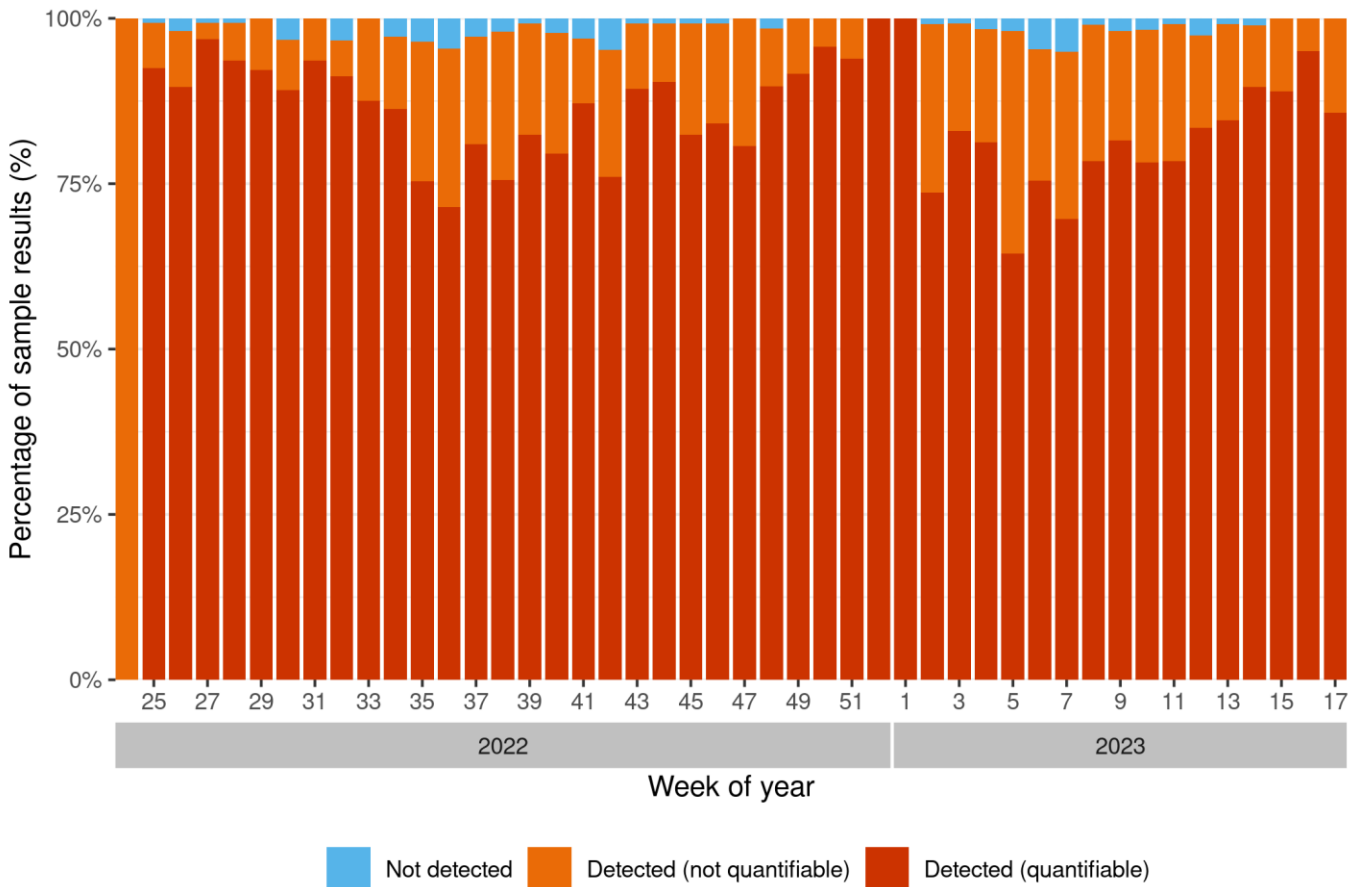
Joanne.chapman@esr.cri.nz

Appendix A. National Results

Time series plotted on linear scale



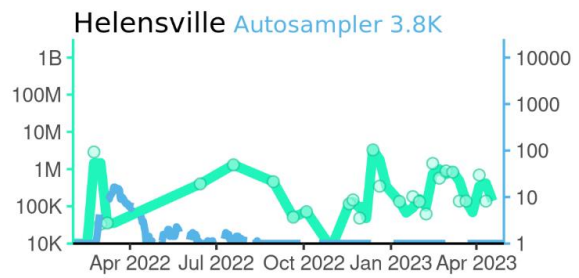
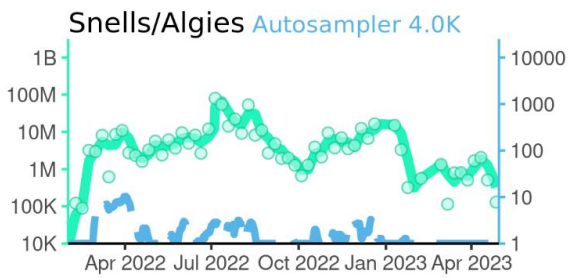
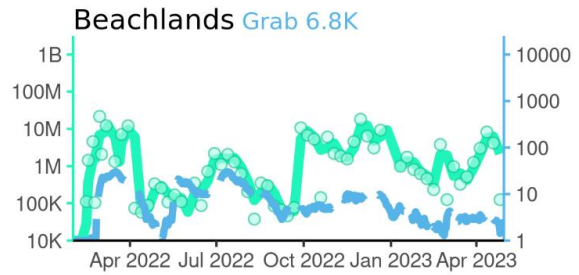
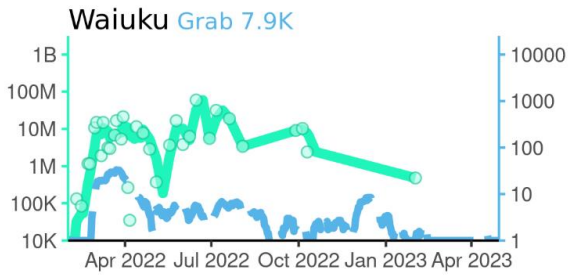
Detections for the past 52 weeks



Appendix C

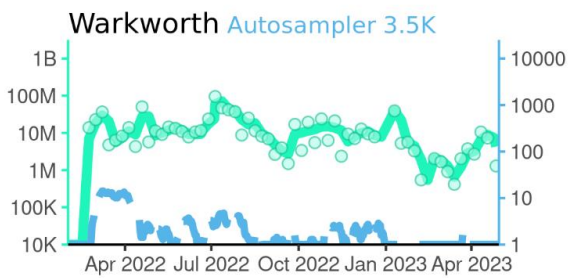
Additional Site Graphs

Auckland

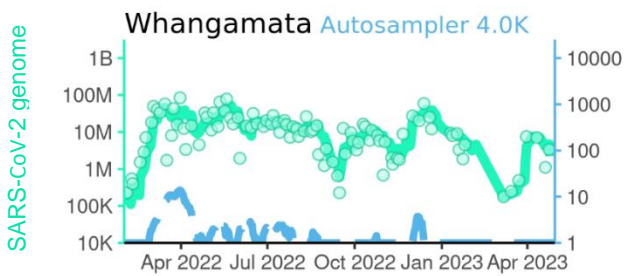


SARS-CoV-2 genome copies/person/day

Cases – 7 day rolling average



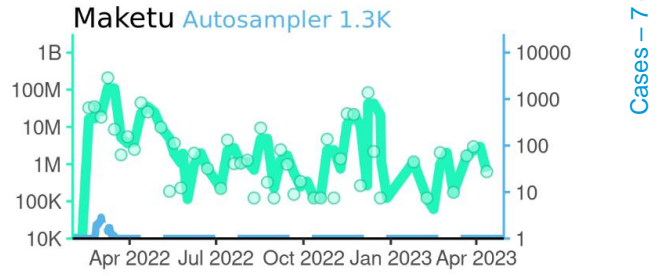
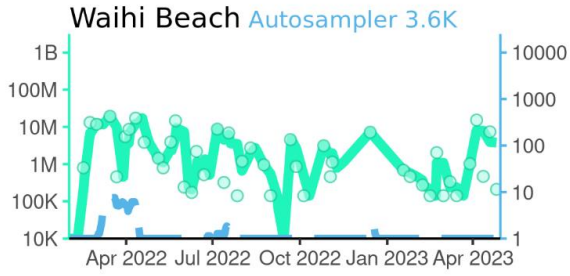
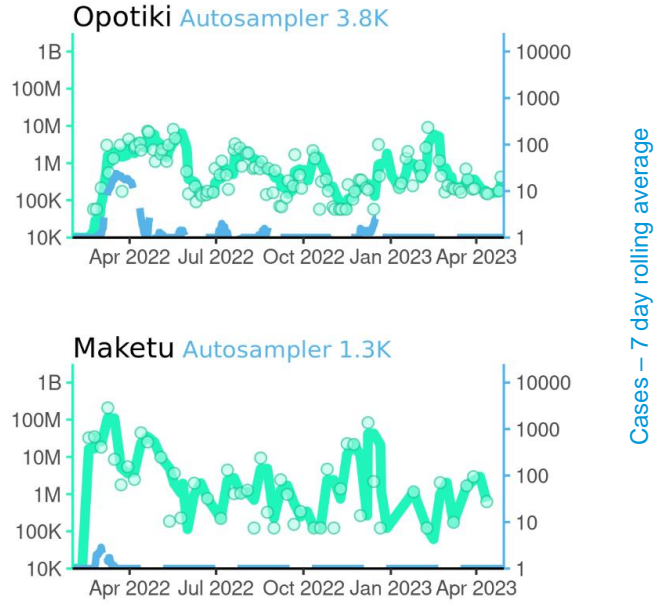
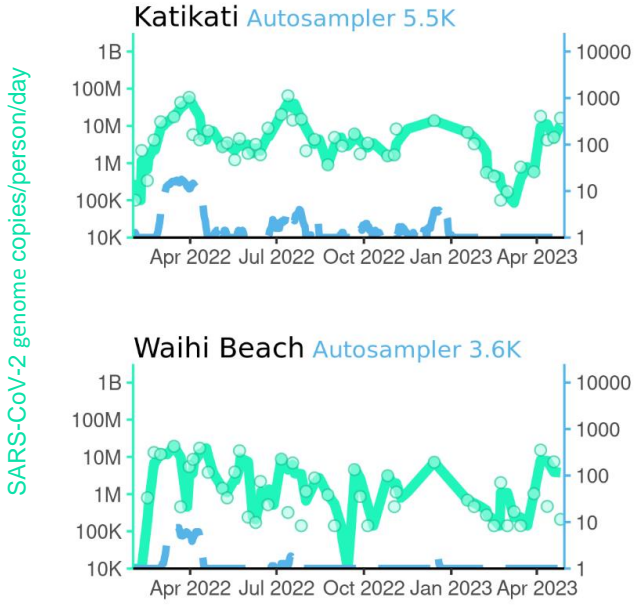
Waikato



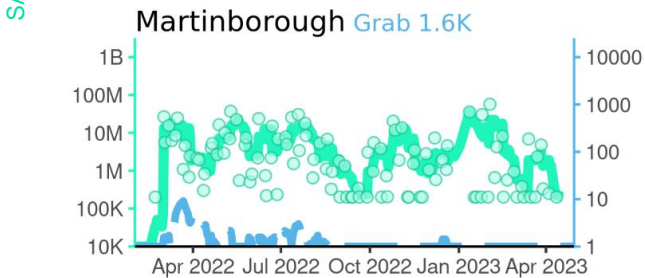
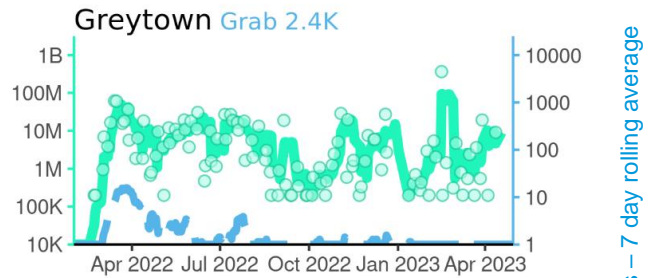
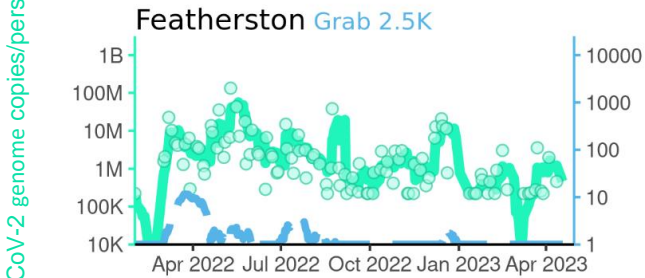
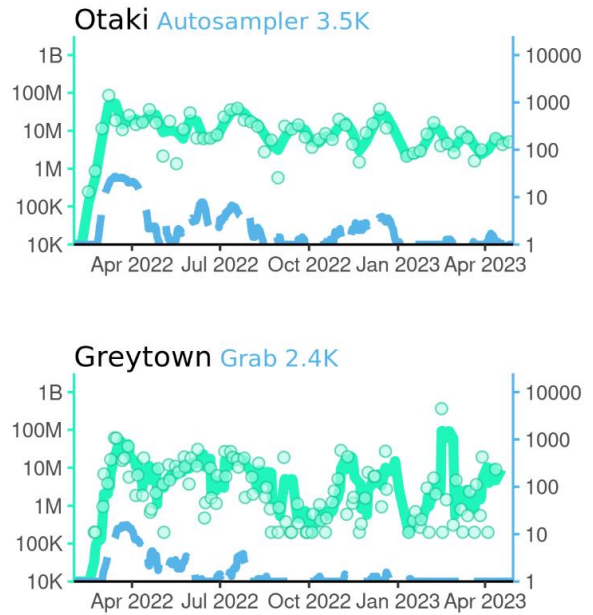
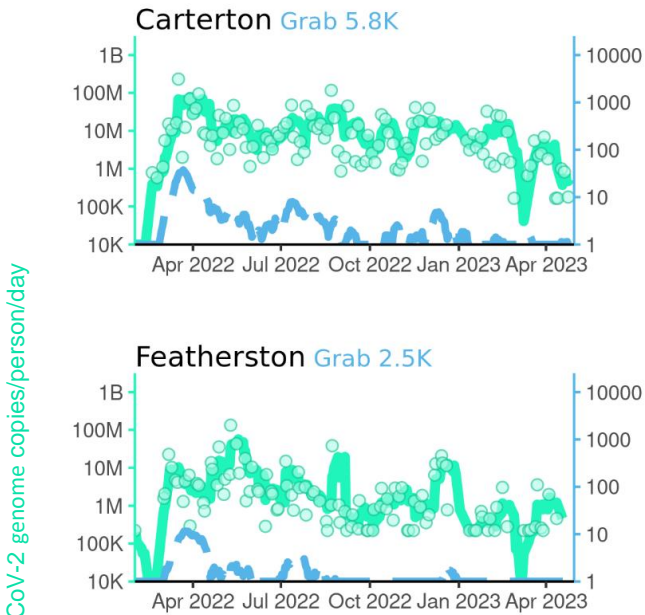
Cases – 7 day rolling average

Monthly Wastewater Surveillance Report COVID-19

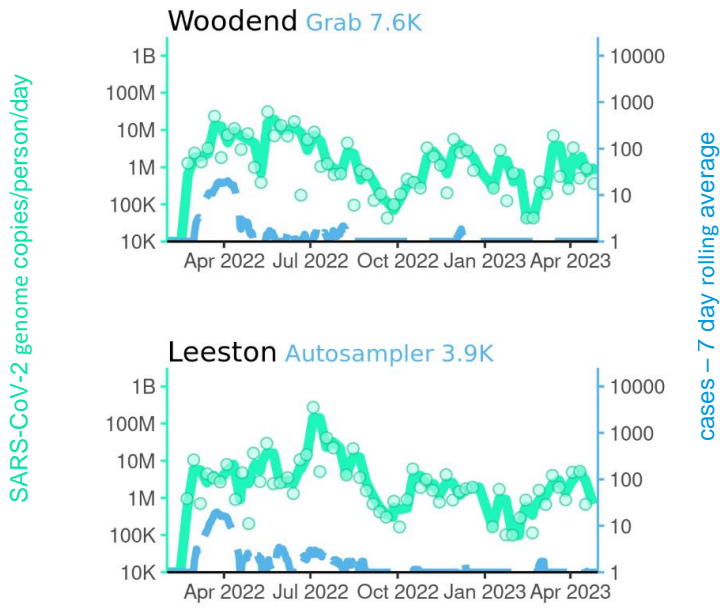
Bay of Plenty



Wellington



Canterbury



Otago

