

New Zealand Wastewater Surveillance Programme COVID-19

Monthly Report August 2023

Weeks ending 6 August to 3 September 2023, weeks 31 to 35

Report prepared 11 September 2023

Key Trends & Insights

For the month of August, national SARS-CoV-2 levels averaged 1.98 million genome copies per person per day (GC/p/d). During this period, SARS-CoV-2 levels were lowest (1.60 million GC/p/d) in the week ending 3 September 2023

100%

Sites (49/49) where SARS-CoV-2 was detected.

68%

NZ population covered by wastewater testing

XBC

Most prevalent variant detected (18 - 39%)

- In August 2023, 374 samples were collected across Aotearoa. SARS-CoV-2 RNA was detected in 369/374 (98.6%) of samples from 49/49 sites (100%).
- SARS-CoV-2 levels remained relatively low in August 2023.
- XBC recombinant lineage was the most prevalent nationally in wastewater throughout August, with percentages ranging from 17 to 39%. However, as a group, the XBB family of lineages was predominant in August (estimated national percentage of XBB, XBB.1.5, XBB.1.16 and EG.5 collectively was between 56% and 72% of sequences this month). The proportion of EG.5 increased notably (to 33%) in late August.

National Results

National SARS-CoV-2 levels in wastewater and reported cases

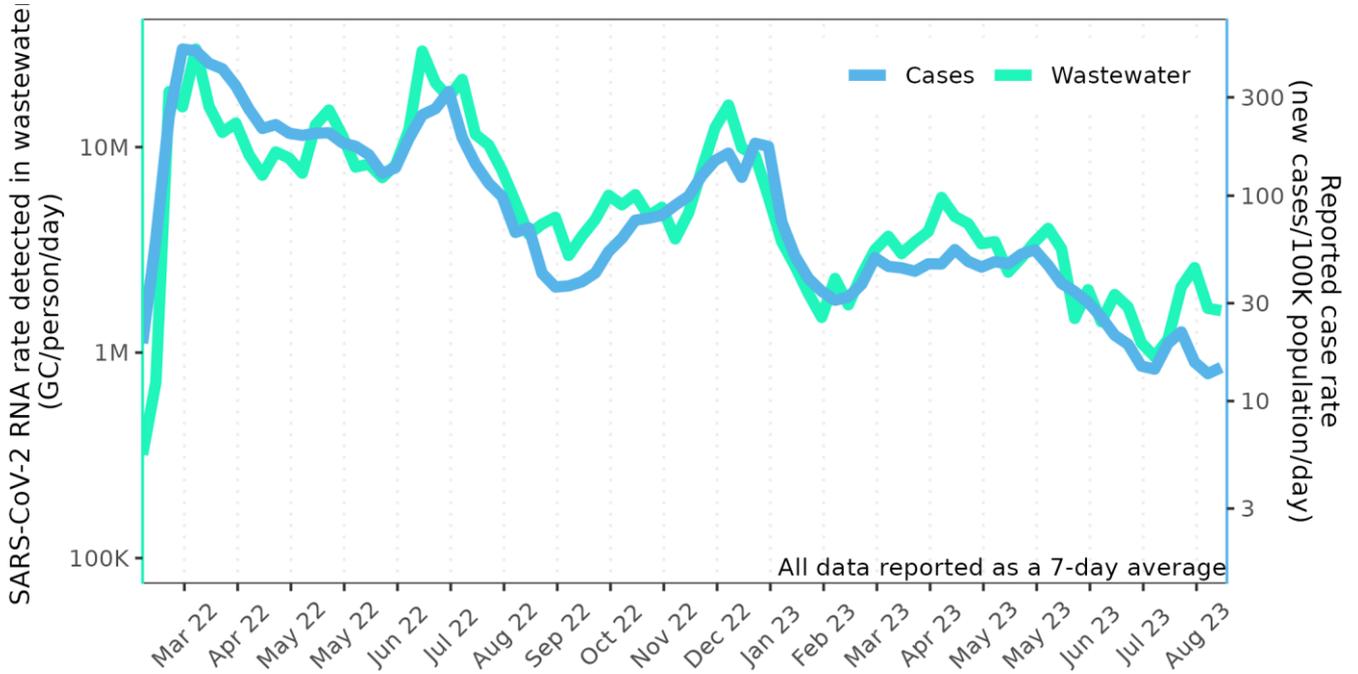


Figure 1. National timeseries of estimated SARS-CoV-2 wastewater rate (GC/person/day, green line) and reported case rate (new cases/100,000 population/day, blue line) on a log₁₀ scale.

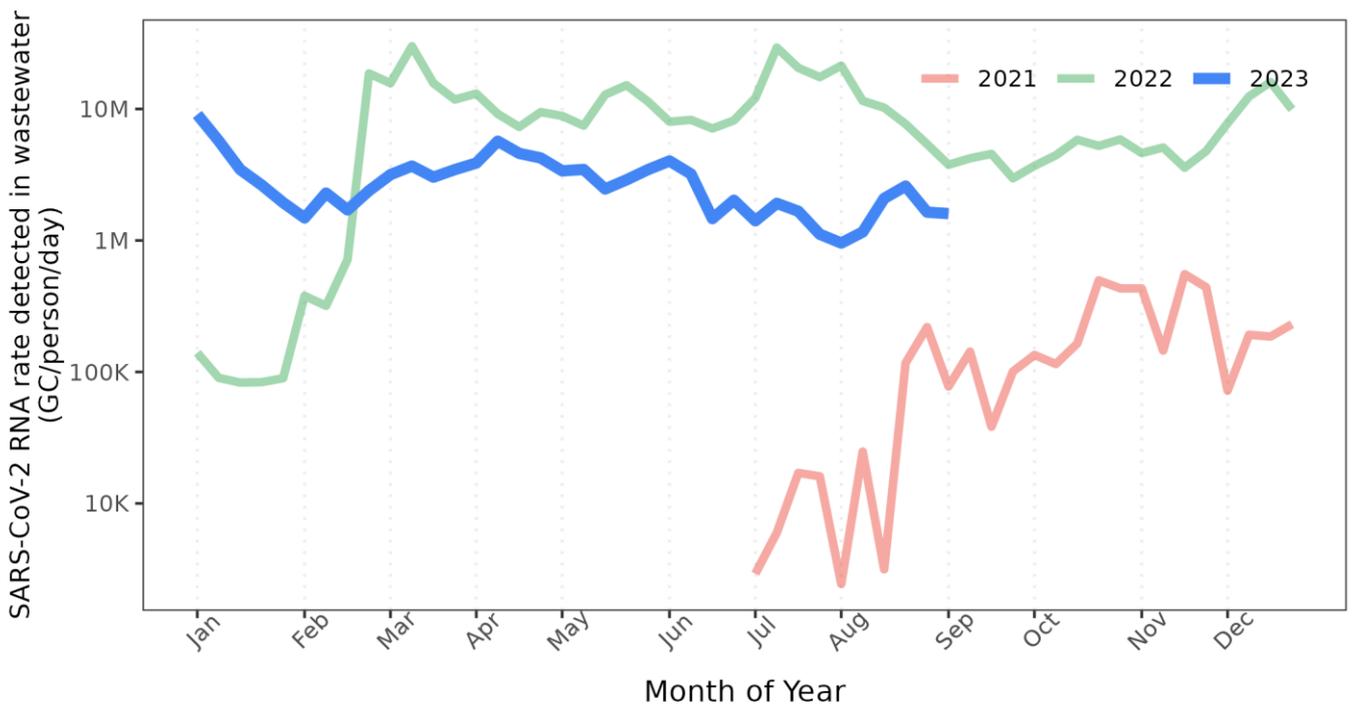


Figure 2. National timeseries of estimated SARS-CoV-2 wastewater rate (GC/person/day) from July 2021, on a log₁₀ scale.

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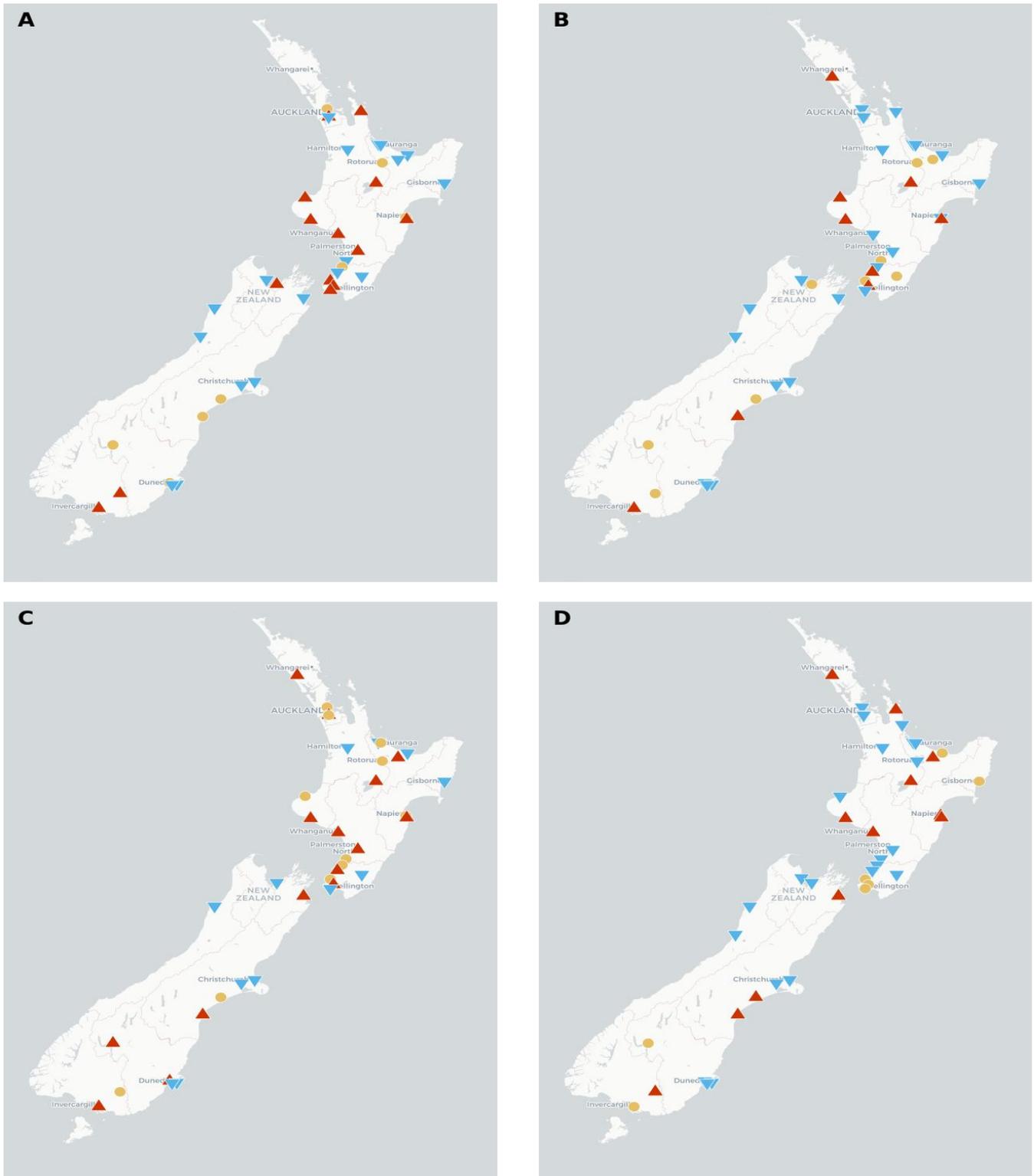


Figure 3. Comparison of SARS-CoV-2 levels for the week ending 3 September 2023, compared to levels measured: A) 1 week ago; B) 2 weeks ago; C) 4 weeks ago; D) 12 weeks ago. Only sites with results for both time points are included. When the viral quantity is 30% or more higher this is labelled as increased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

Variant Analysis

Results from the six weeks of sampling (week 29 to week 34) from twenty sentinel wastewater sites (Table 1) across Aotearoa New Zealand are reported (noting that the July report reported to week 28).

The results show that the XBC recombinant lineage was the most prevalent nationally in wastewater throughout August, with percentages ranging from 17 to 39% (Figures 4 and 5).

The XBB family of lineages was also common across this period. EG.5, XBB.1.5 and XBB.1.16 were at similar levels from weeks 29 to 33 (generally ranging from ~10% to ~20% each week per variant). However, the proportion of EG.5 increased to 33% for the week ending 27 August, with a reduction in the other XBB lineages. The increase in EG.5 in August was also reported in clinical samples which increased to 32% from 4% cases in July.

CH.1.1 (including the descendant lineage FK.1.1) proportions have dropped from ~10-24% in July to ~5-9% in August.

BA.2.86 was not detected in either wastewater (or clinical samples) in this period.

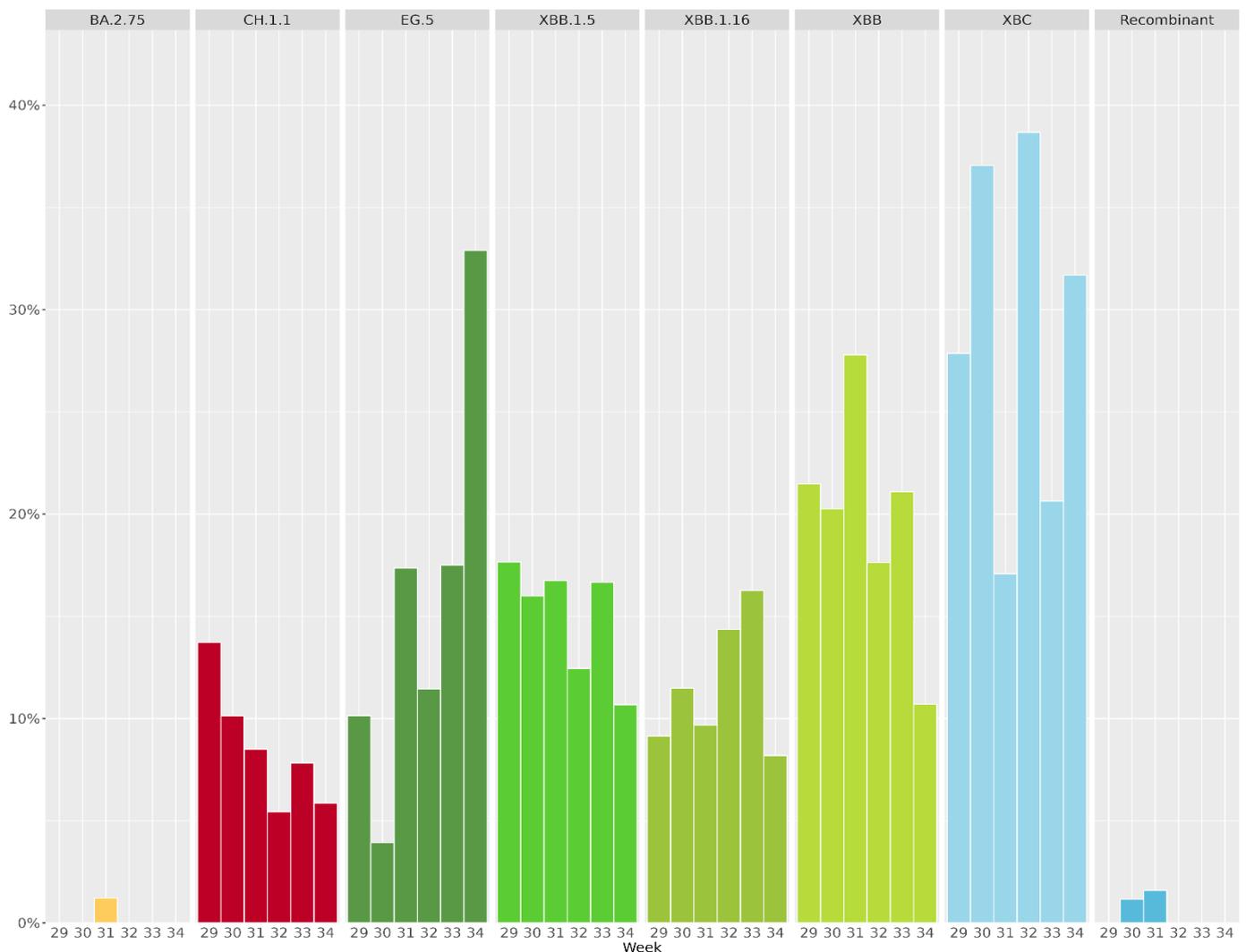


Figure 4. National percentage of each variant for week 29 (ending 23 July 2023) to week 34 (ending 27 August 2023).

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Table 1. Data from 20 wastewater sentinel sites sampled in weeks 29 (ending 23 July 2023) to 34 (ending 27 August 2023). Coloured box denotes that the variant was detected at that site that week, cream box denotes that the variant was not detected, and grey box denotes that no data is available for that site, either due to the sample not being collected or no valid sequence output (e.g., due to low virus concentration).

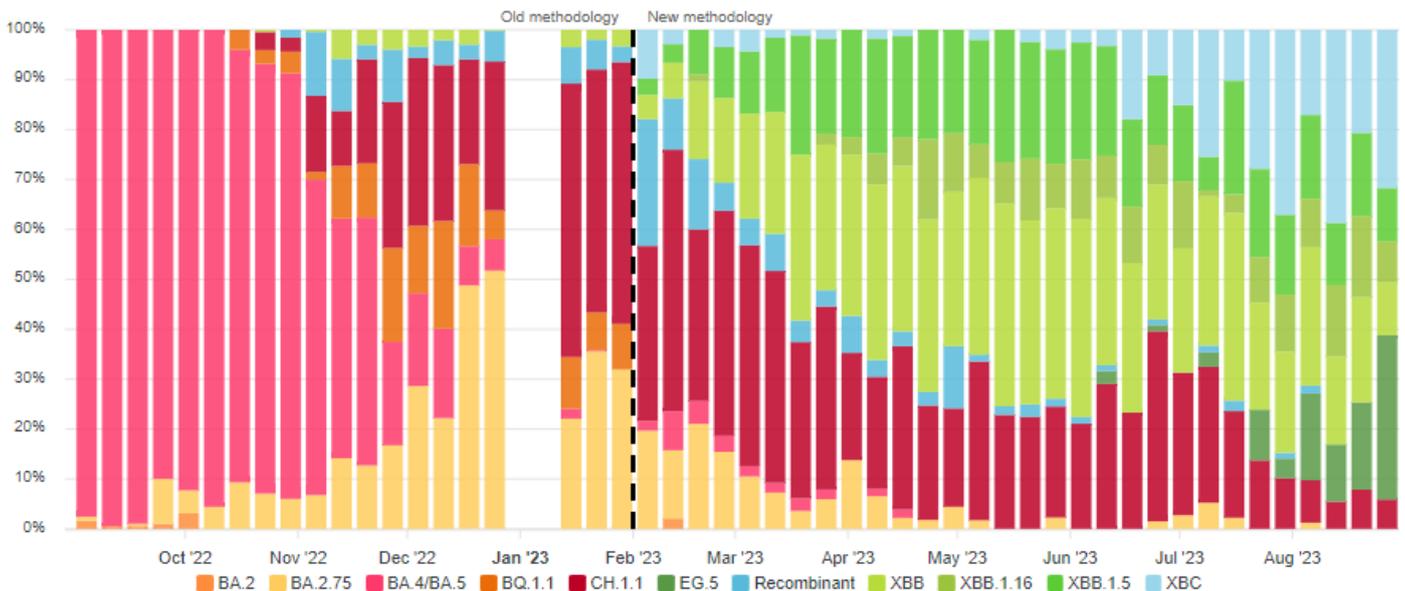


Figure 5. Estimated variant percentage over time at a national scale (average). Data are collected from up to 20 sentinel sites each week.

Instantaneous Reproduction Number Modelling

Wastewater and case data up to the 3 September 2023 (week 35) was used for the modelling. However, to account for the delay between infections and people reporting as cases, a lag of three days is used. As such the modelled results are up to the 31 August 2023. The uncertainty in these measures is denoted with 90% uncertainty intervals (shown in orange in Figure 6).

Instantaneous reproduction number: The estimate of the instantaneous reproduction number for 31 August 2023 (in week 35) was 0.97 (90% uncertainty interval 0.85 - 1.13, Figure 6A and 6B).

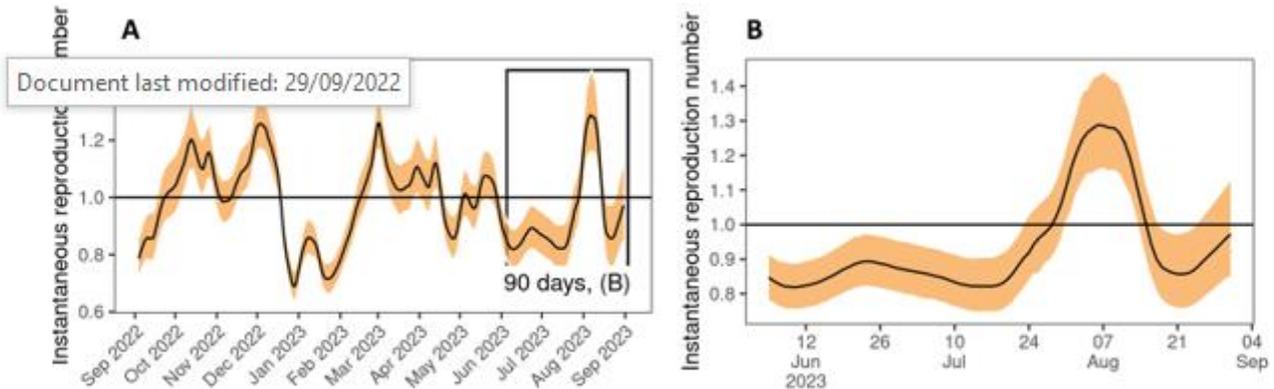


Figure 6. Estimates of (A) reproduction number (B) reproduction number for the past 90 days. These results are from a semi-mechanistic model and are fitted to 7-day national averages of reported cases and viral levels (GC/person/day) in wastewater. The figures show the mean (solid black line) and 90% uncertainty intervals (orange shading) of the simulation results with tighter uncertainty intervals indicating more confidence in the estimate.

Trends in Ministry of Health Regions

Regional analysis of the wastewater data is shown in Figure 7. Regional wastewater levels have been relatively steady through August 2023.

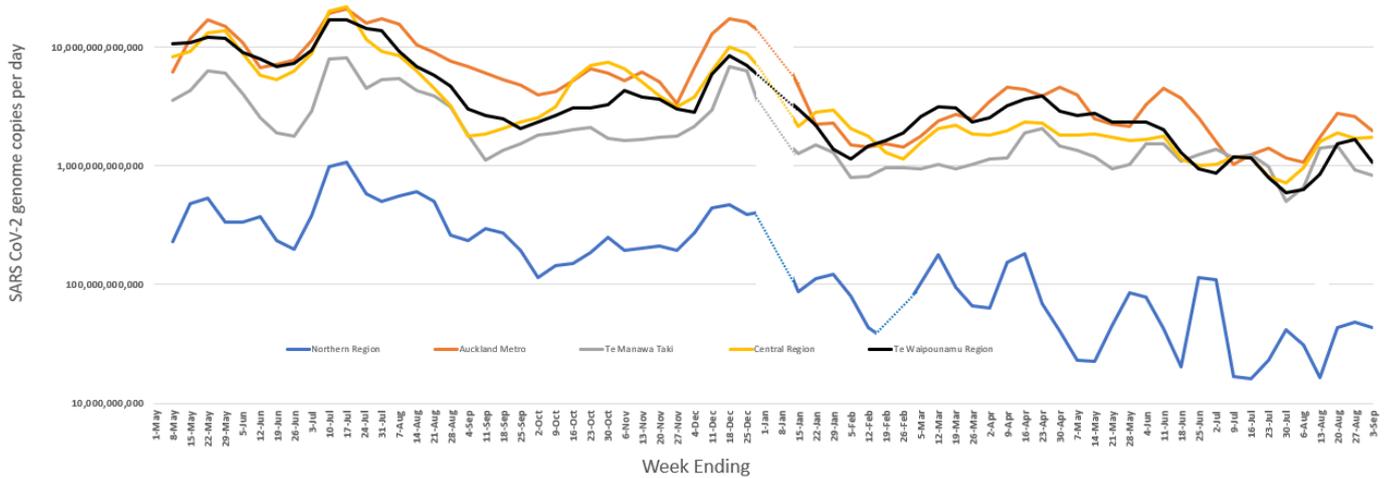


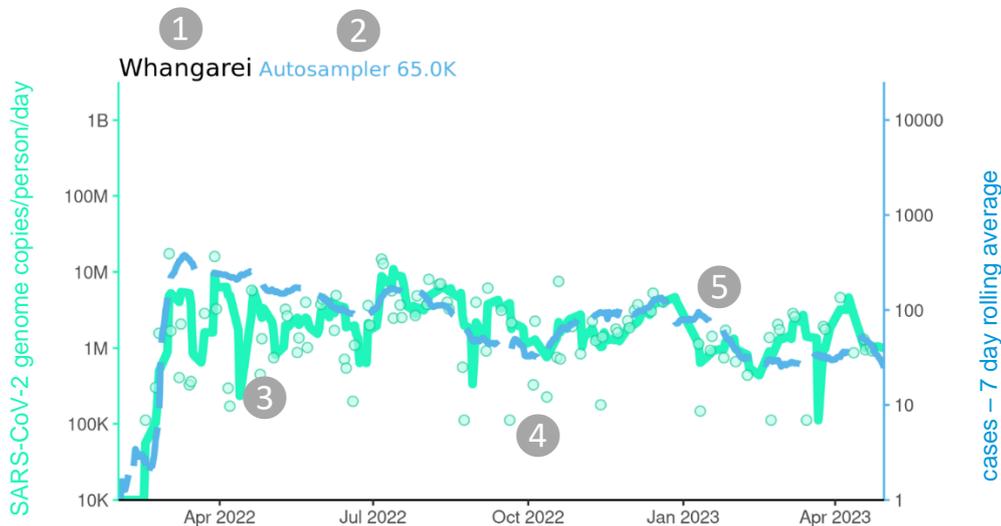
Figure 7. Two week rolling average of total SARS-CoV-2 genome copies detected per day in the five Ministry of Health regions since week 17, 2022. Dashed lines are inferred levels during periods when samples were either not collected (Christmas period) or insufficient numbers collected (due to weather impacts) for the region.

SARS-CoV-2 levels in wastewater and reported cases, per site, in each 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*.

Regional and site-specific time series graphs for the last 12 months are presented. The raw data (GC/L wastewater) is converted to a viral load of GC/person/day. This conversion considers flow of wastewater entering the treatment plant and the population serviced in each wastewater catchment. An average of 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).

Interpreting Site Graphs



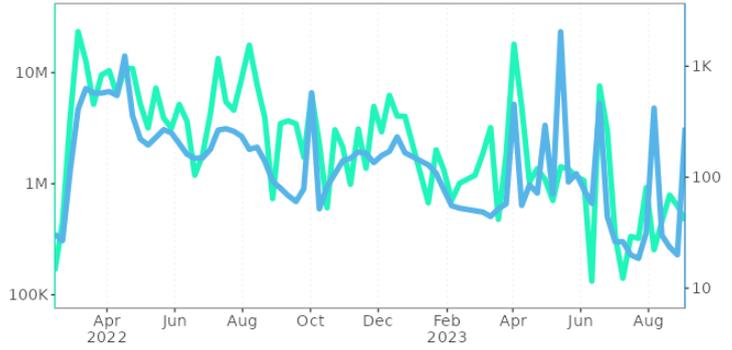
- ① Site Name
- ② Sample collection method and population. Results based on autosampler may be more representative than grab sample-based results.
- ③ **Wastewater** results shown as solid line (**green line**) | 14-day average of genome copies/person/day on a \log_{10} scale.
- ④ Individual results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

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

Northland

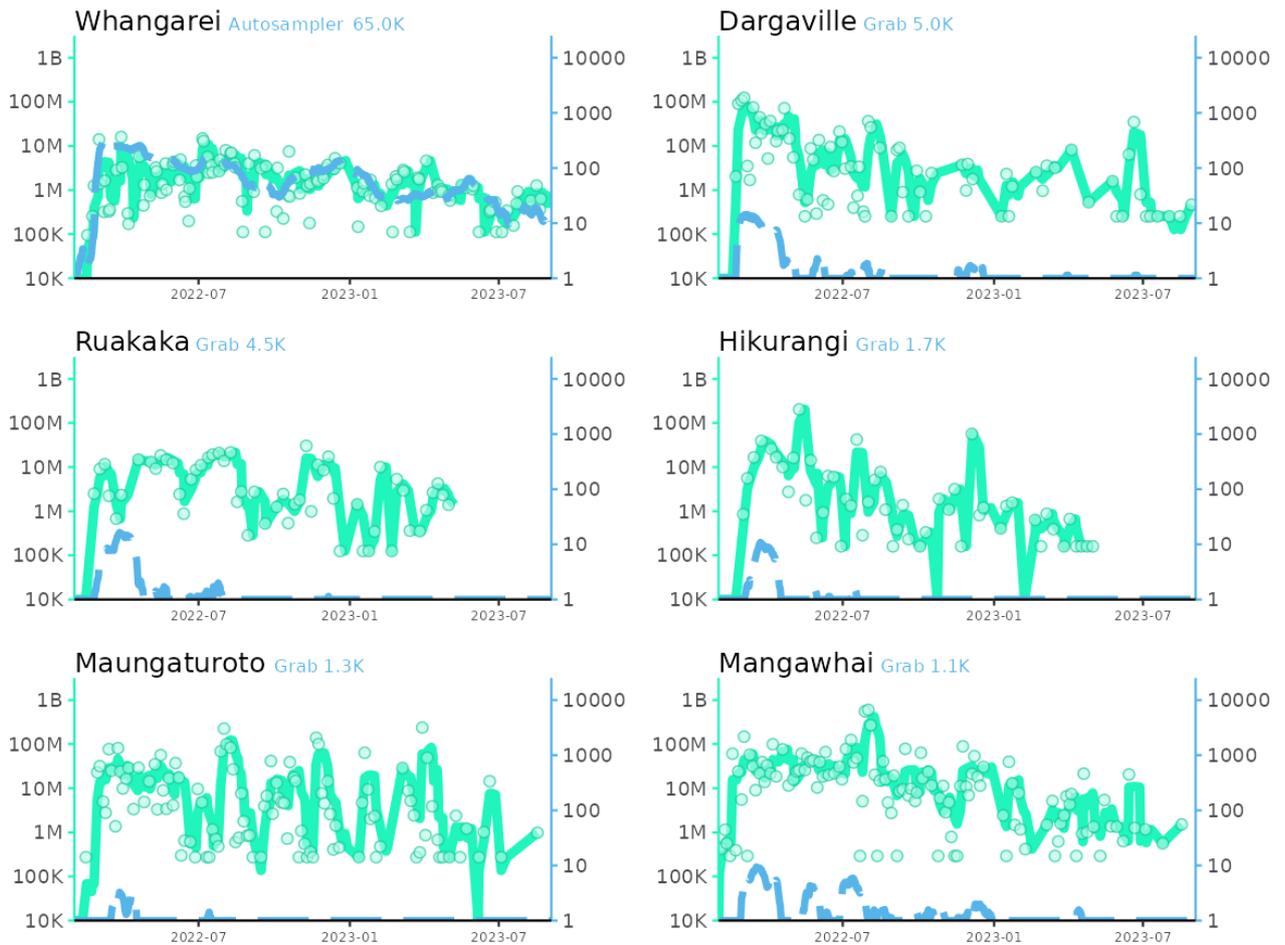


SARS-CoV-2 RNA rate detected in wastewater (GC/person/day)



Reported case rate (new cases/100k population/day)

SARS-CoV-2 genome copies/person/day

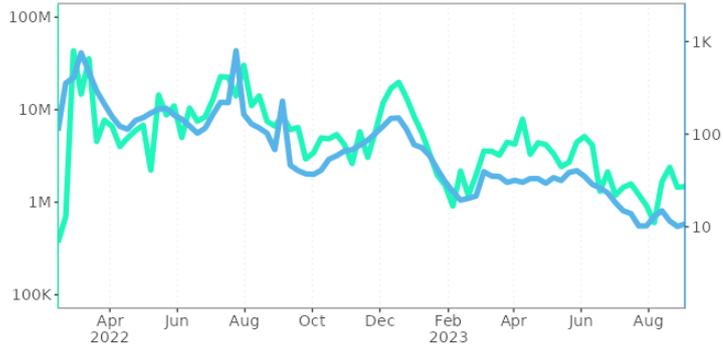


cases - 7 day rolling average

Auckland

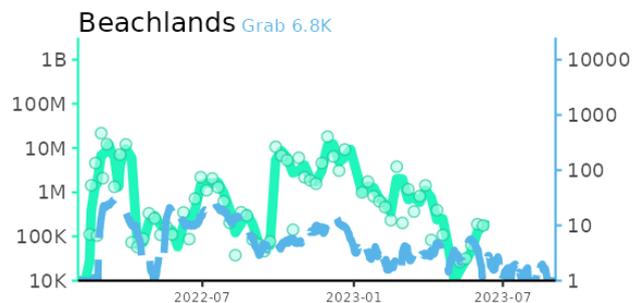
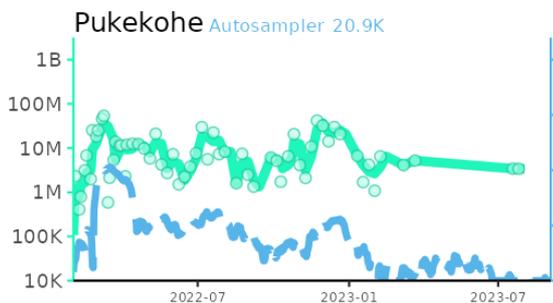
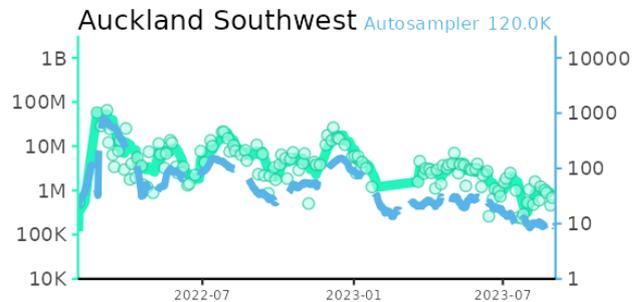
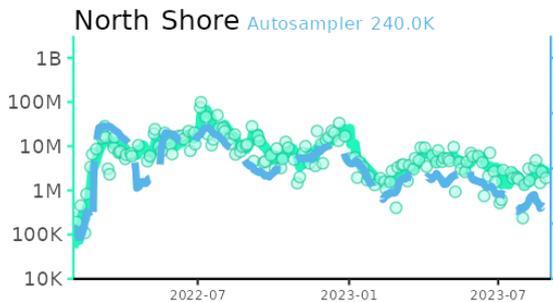
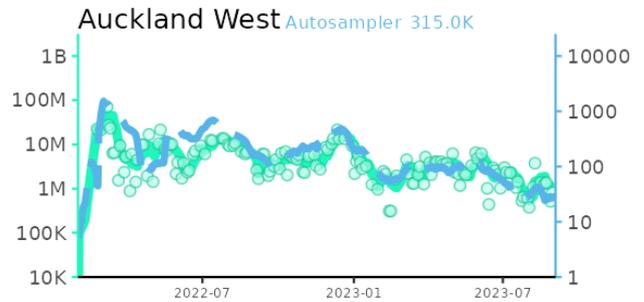
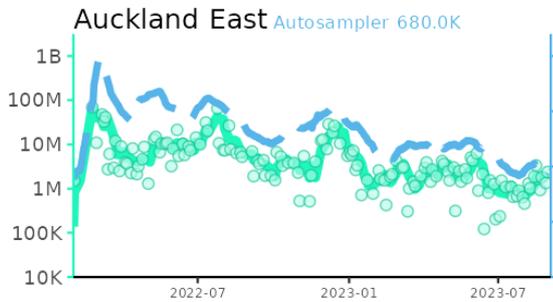


SARS-CoV-2 RNA rate detected in wastewater (GC/person/day)



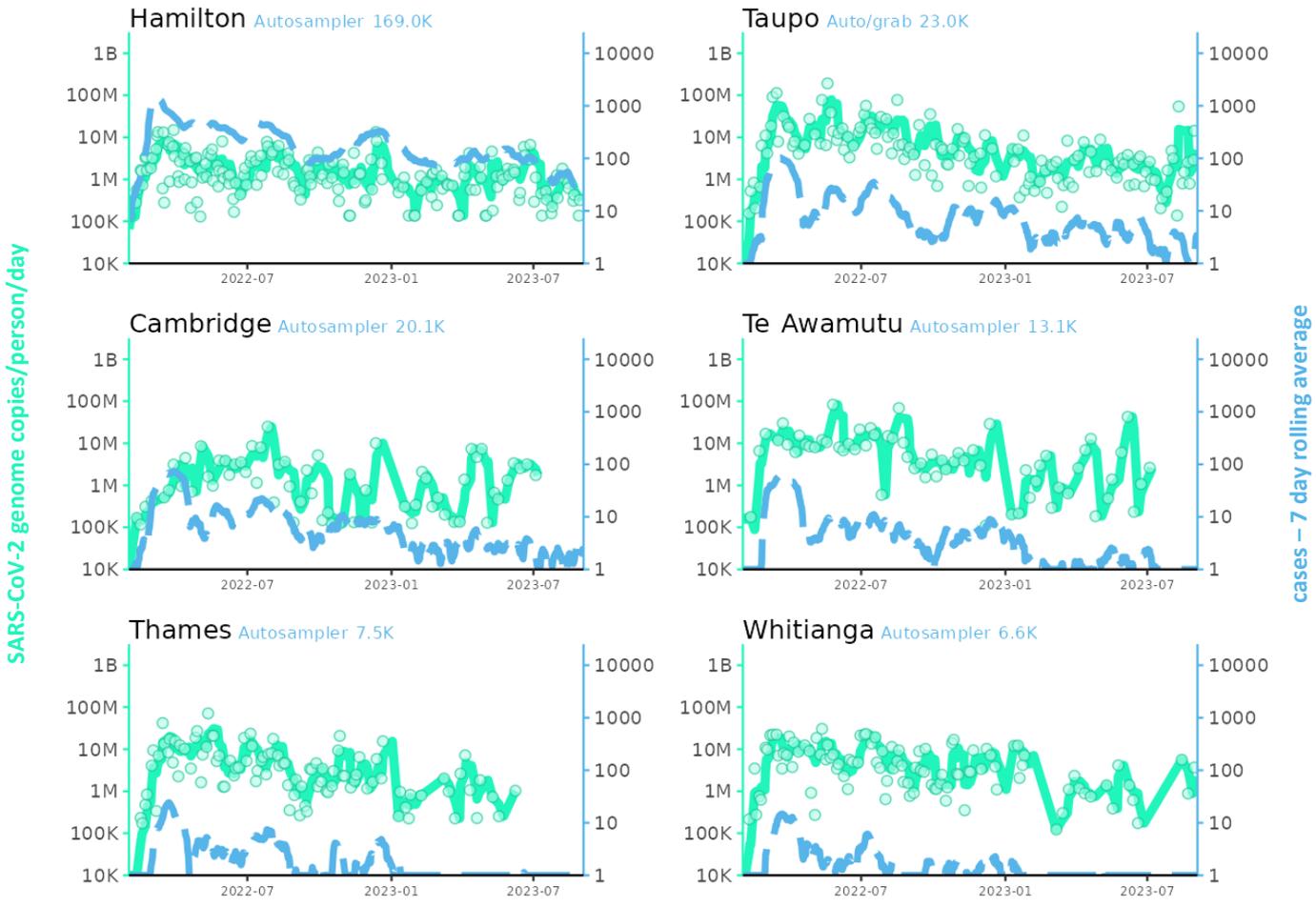
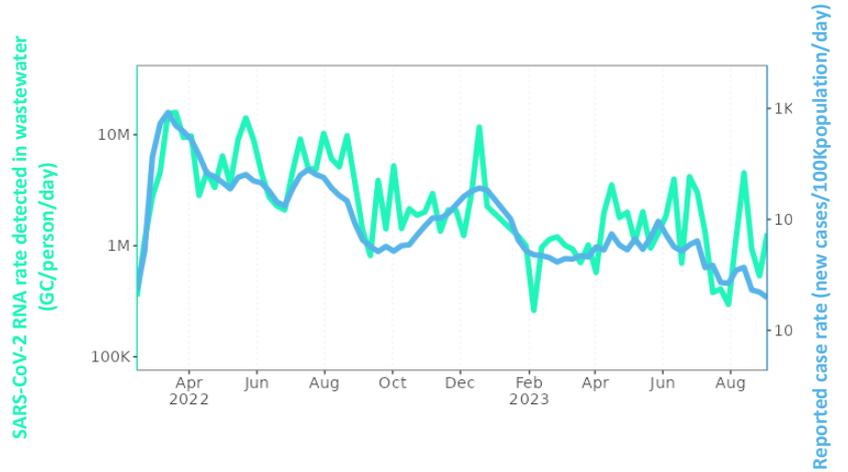
Reported case rate (new cases/100k population/day)

SARS-CoV-2 genome copies/person/day



cases – 7 day rolling average

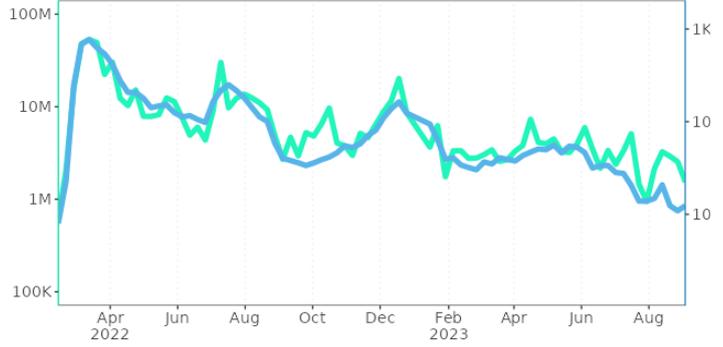
Waikato



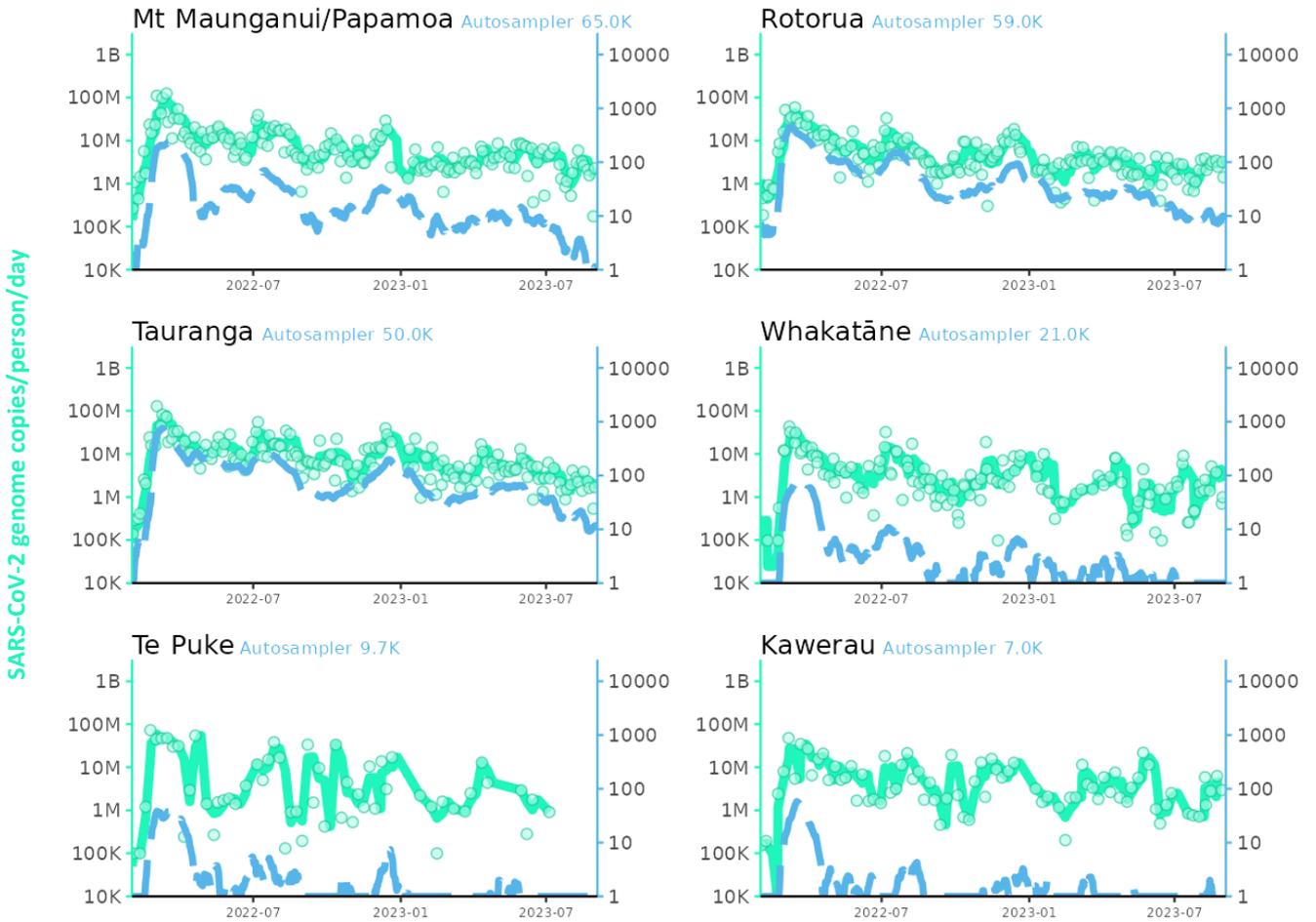
Bay of Plenty



SARS-CoV-2 RNA rate detected in wastewater (GC/person/day)



Reported case rate (new cases/100k population/day)



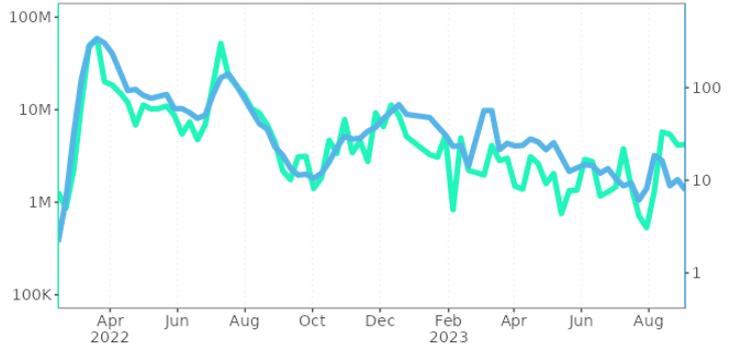
SARS-CoV-2 genome copies/person/day

cases - 7 day rolling average

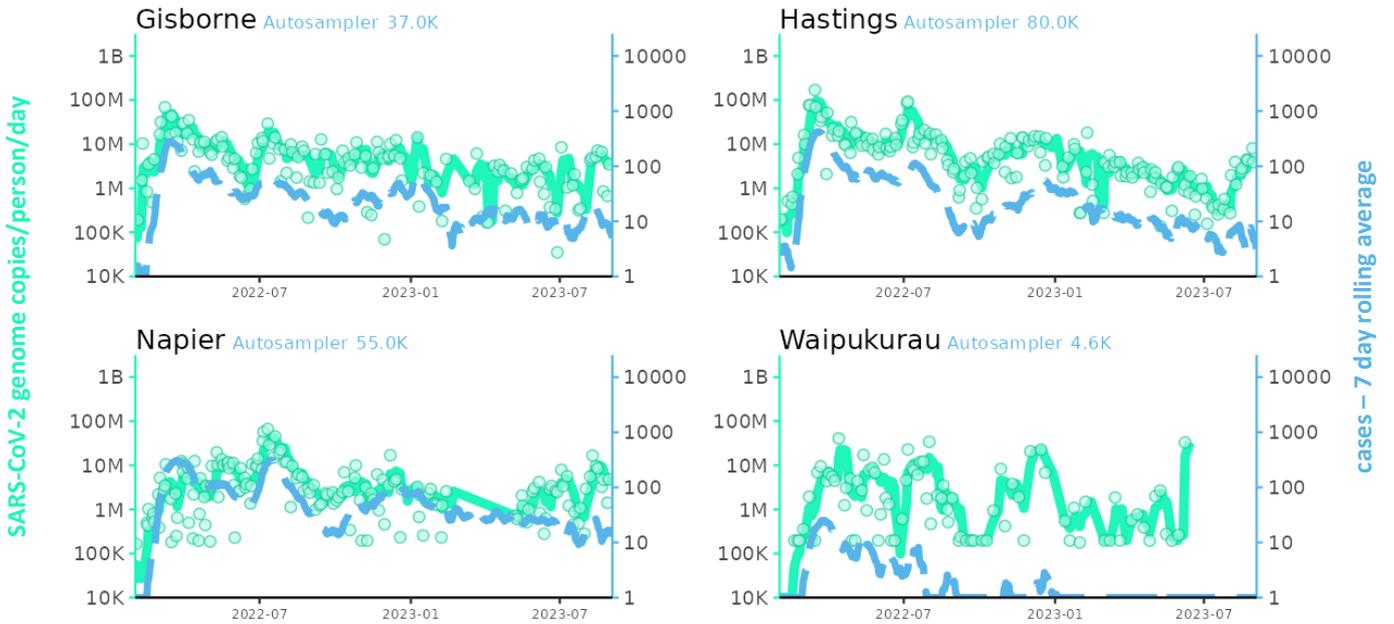
Hawke's Bay & Gisborne



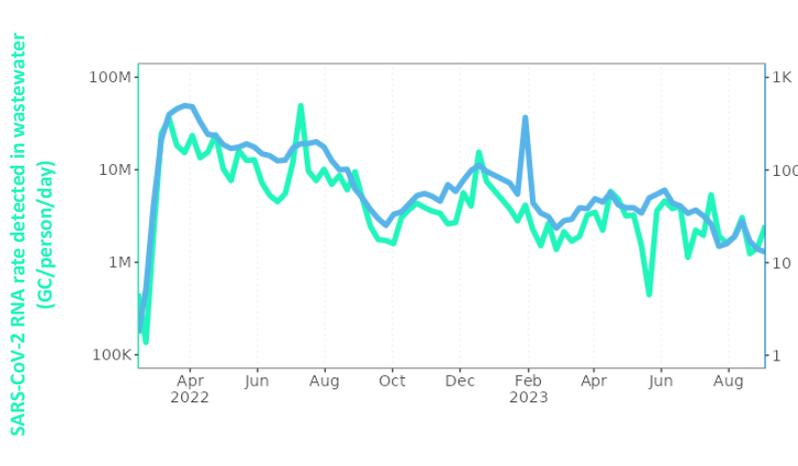
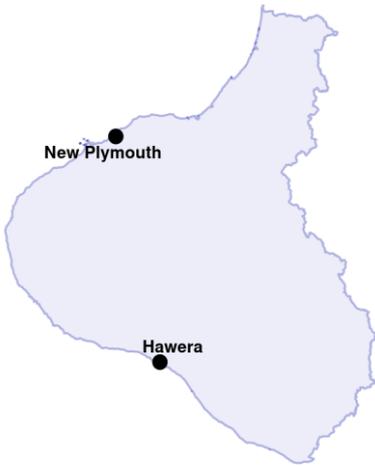
SARS-CoV-2 RNA rate detected in wastewater (GC/person/day)



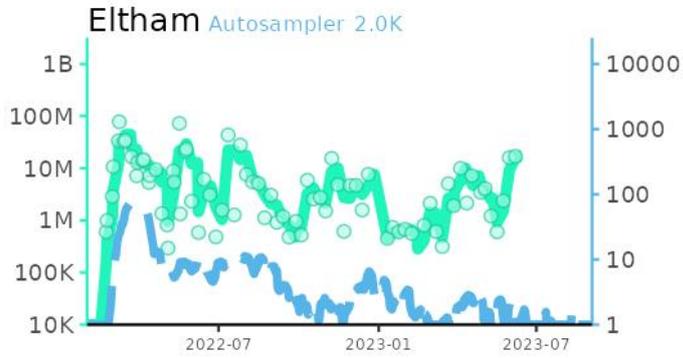
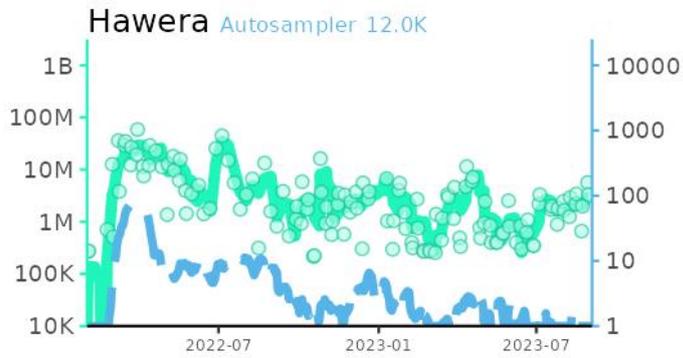
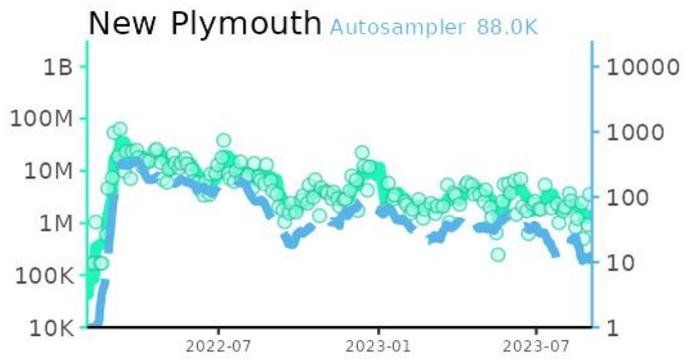
Reported case rate (new cases/100k population/day)



Taranaki



SARS-CoV-2 genome copies/person/day

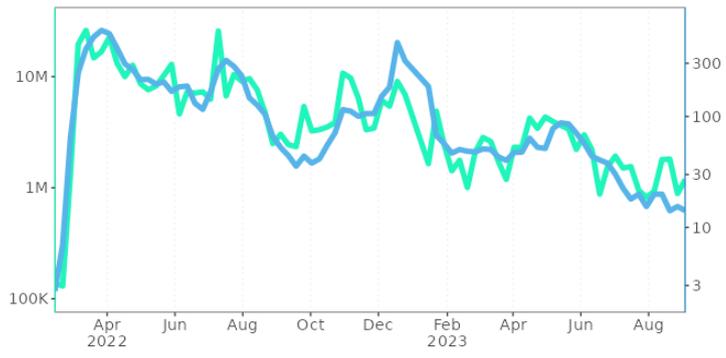


cases - 7 day rolling average

Manawatu & Whanganui

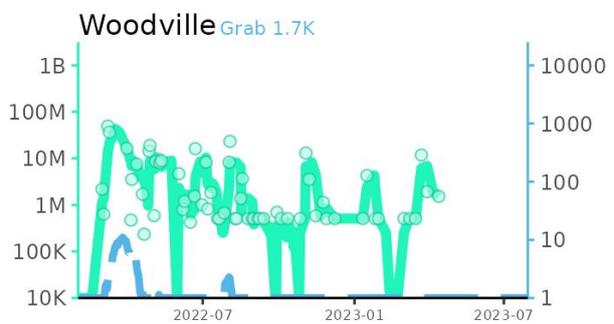
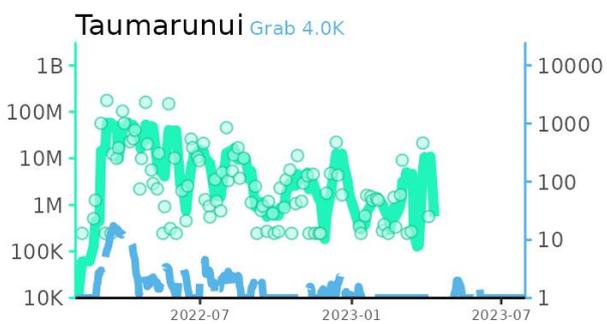
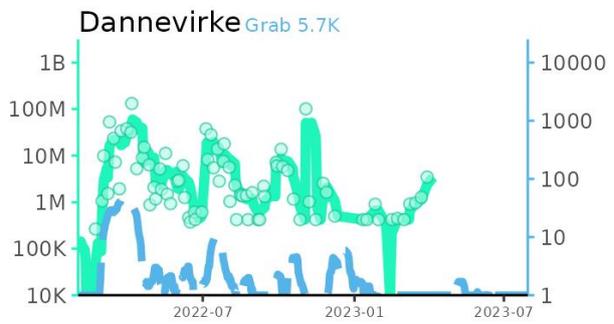
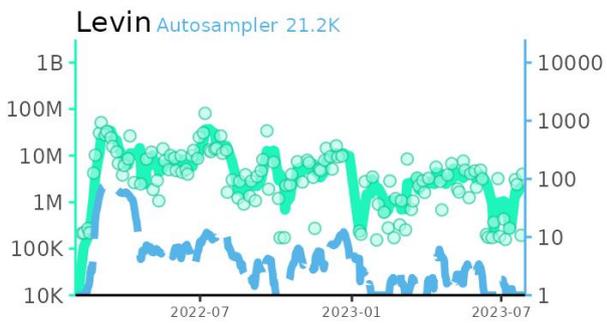
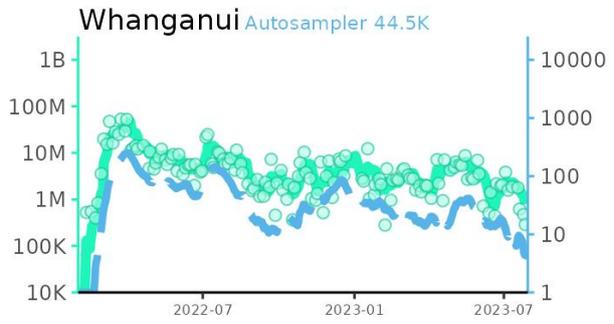
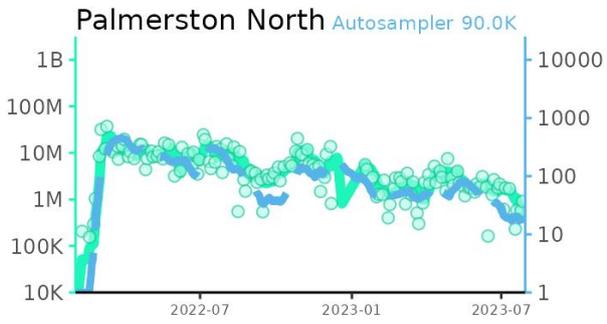


SARS-CoV-2 RNA rate detected in wastewater (GC/person/day)



Reported case rate (new cases/100k population/day)

SARS-CoV-2 genome copies/person/day

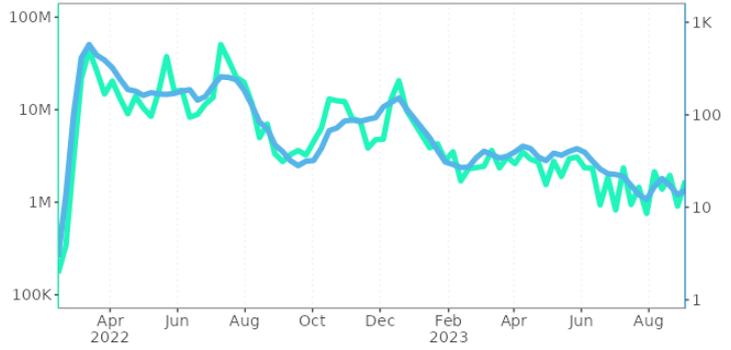


cases - 7 day rolling average

Wellington

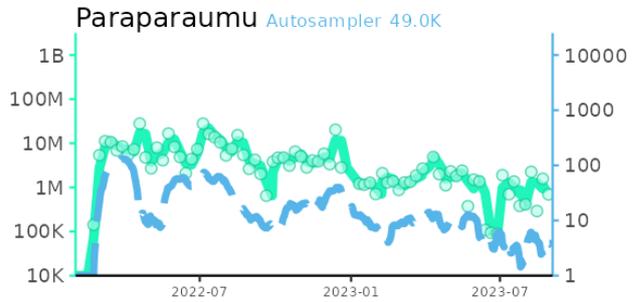
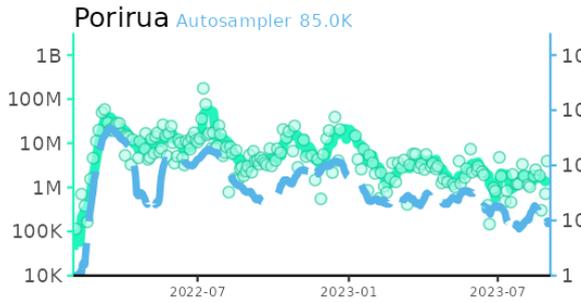
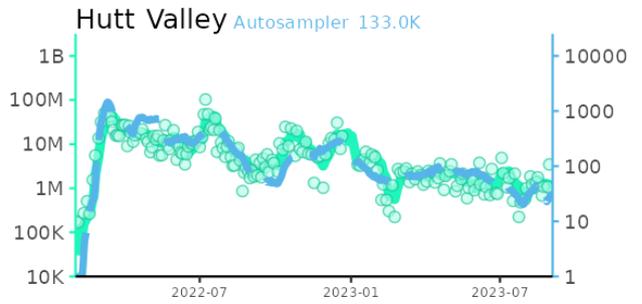
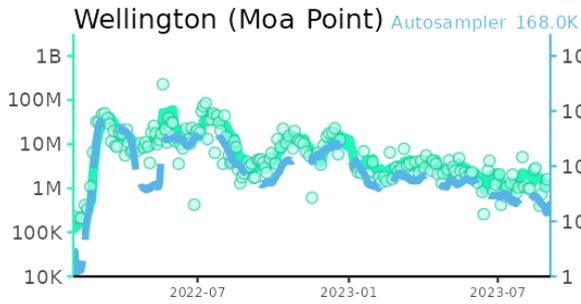


SARS-CoV-2 RNA rate detected in wastewater (GC/person/day)

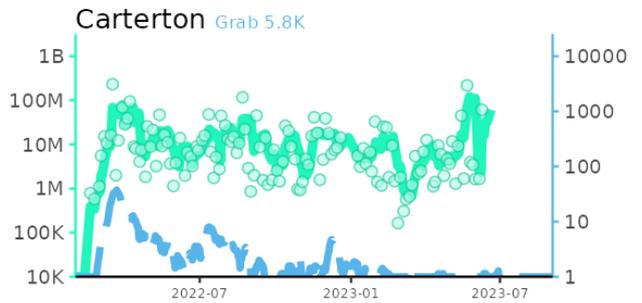
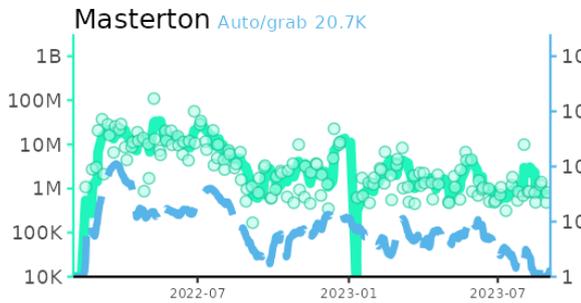


Reported case rate (new cases/100k population/day)

SARS-CoV-2 genome copies/person/day



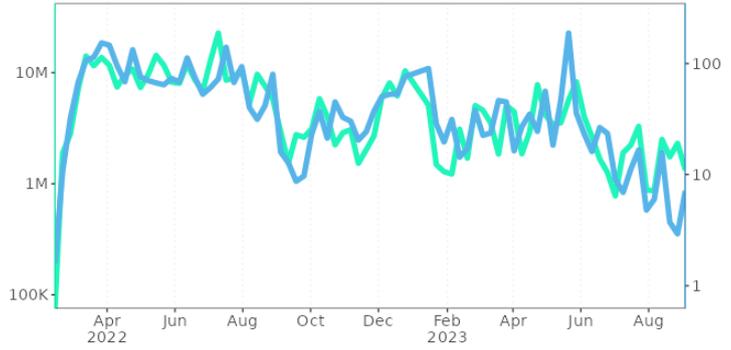
cases - 7 day rolling average



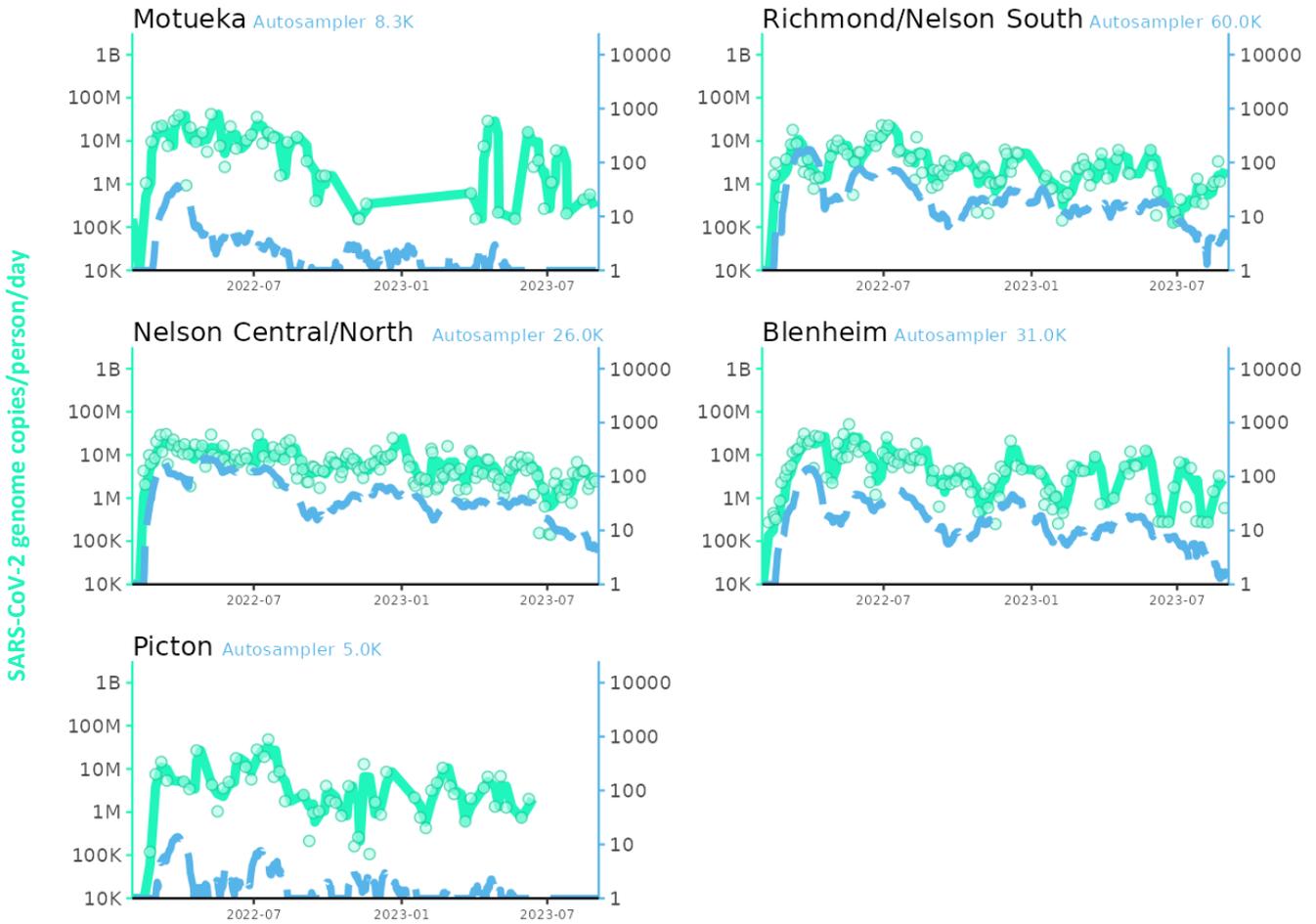
Tasman, Nelson & Marlborough



SARS-CoV-2 RNA rate detected in wastewater (GC/person/day)



Reported case rate (new cases/100k population/day)



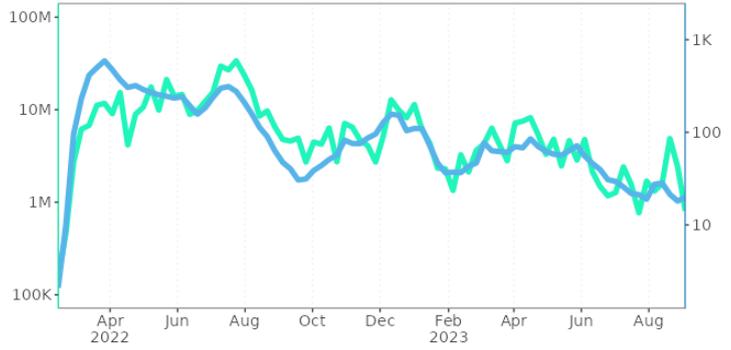
SARS-CoV-2 genome copies/person/day

cases - 7 day rolling average

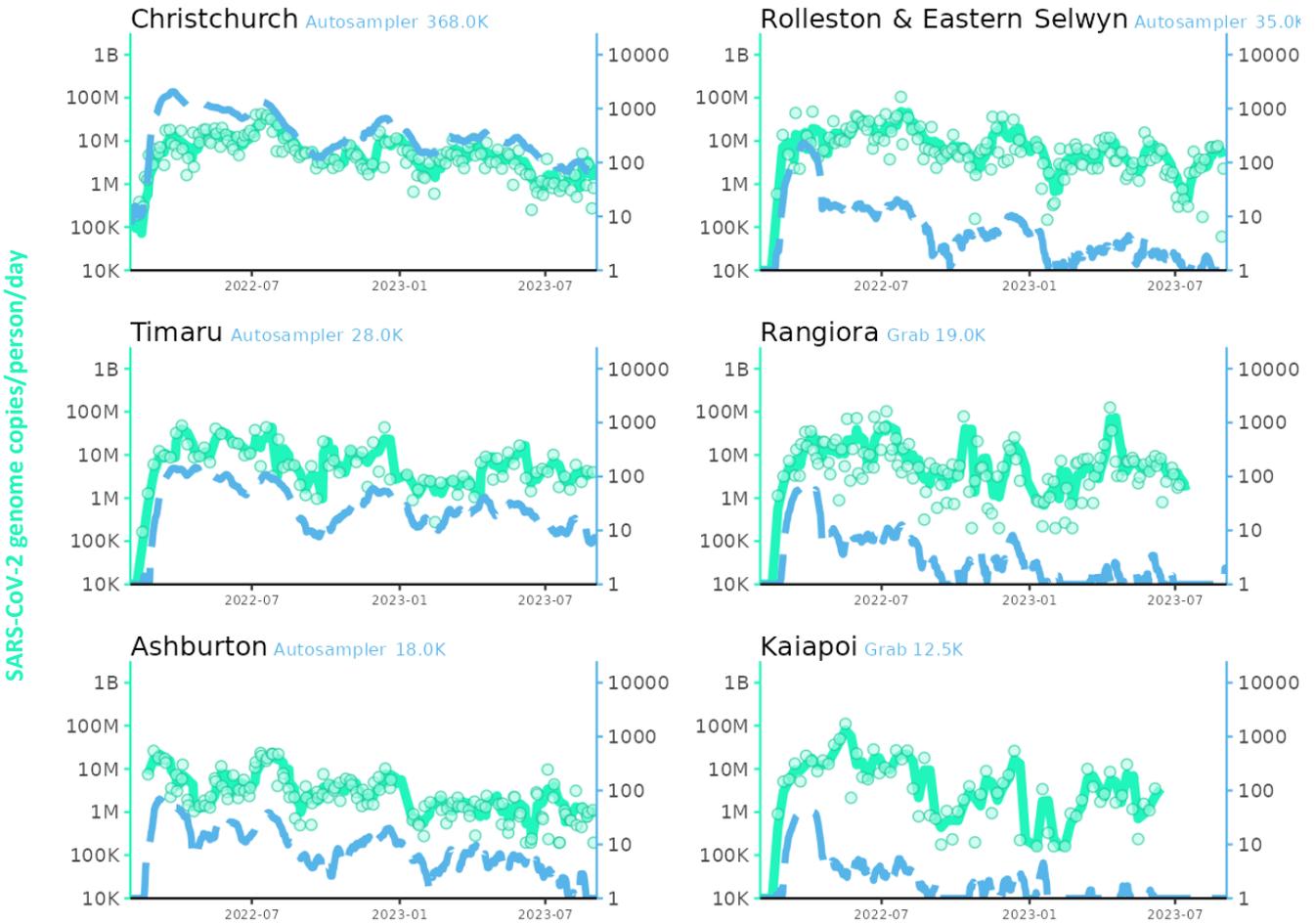
Canterbury



SARS-CoV-2 RNA rate detected in wastewater (GC/person/day)



Reported case rate (new cases/100k population/day)



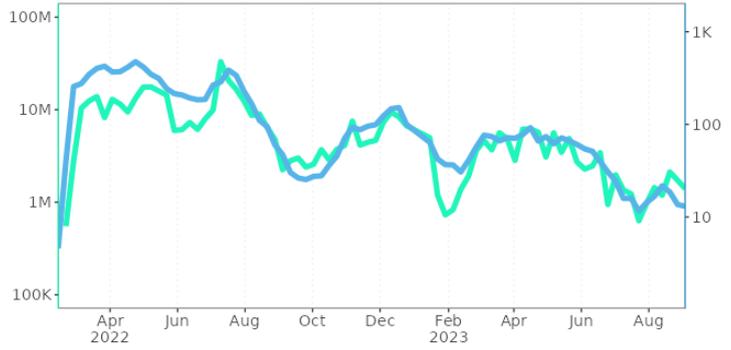
SARS-CoV-2 genome copies/person/day

cases - 7 day rolling average

Otago

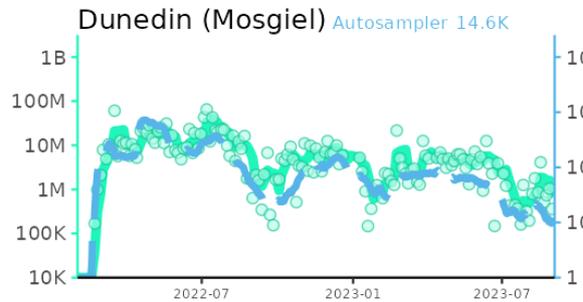
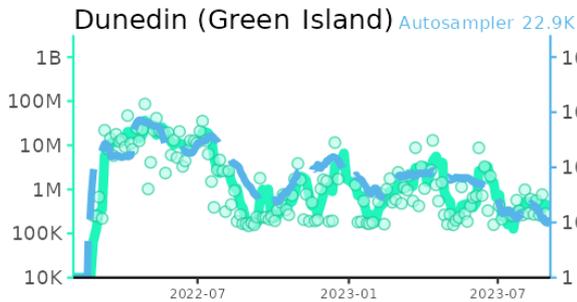
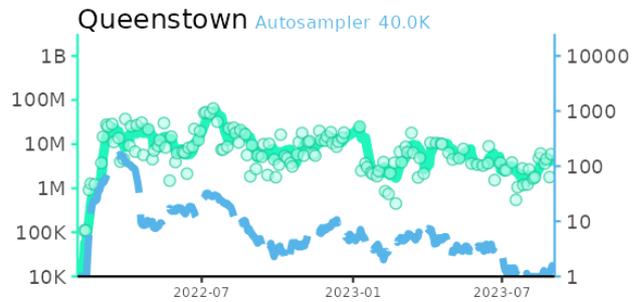
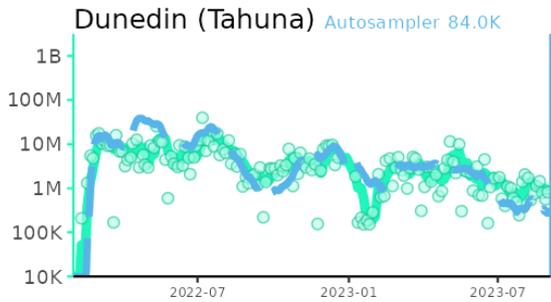


SARS-CoV-2 RNA rate detected in wastewater (GC/person/day)

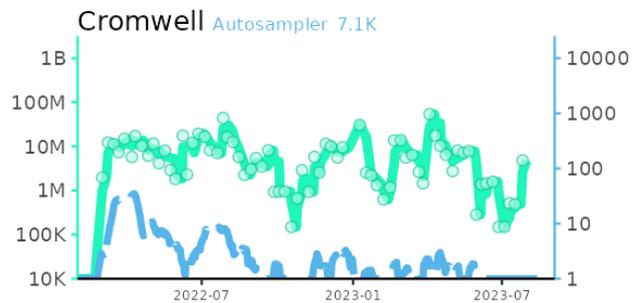
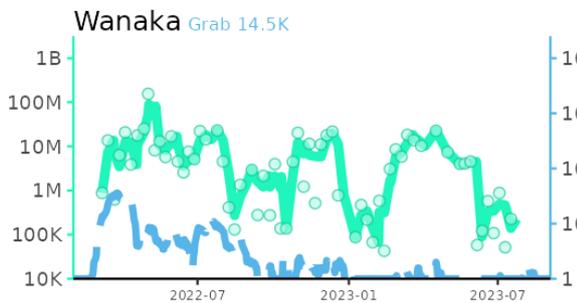


Reported case rate (new cases/100k population/day)

SARS-CoV-2 genome copies/person/day



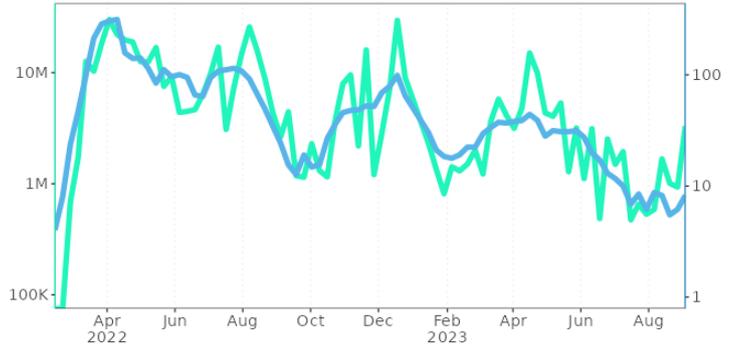
cases - 7 day rolling average



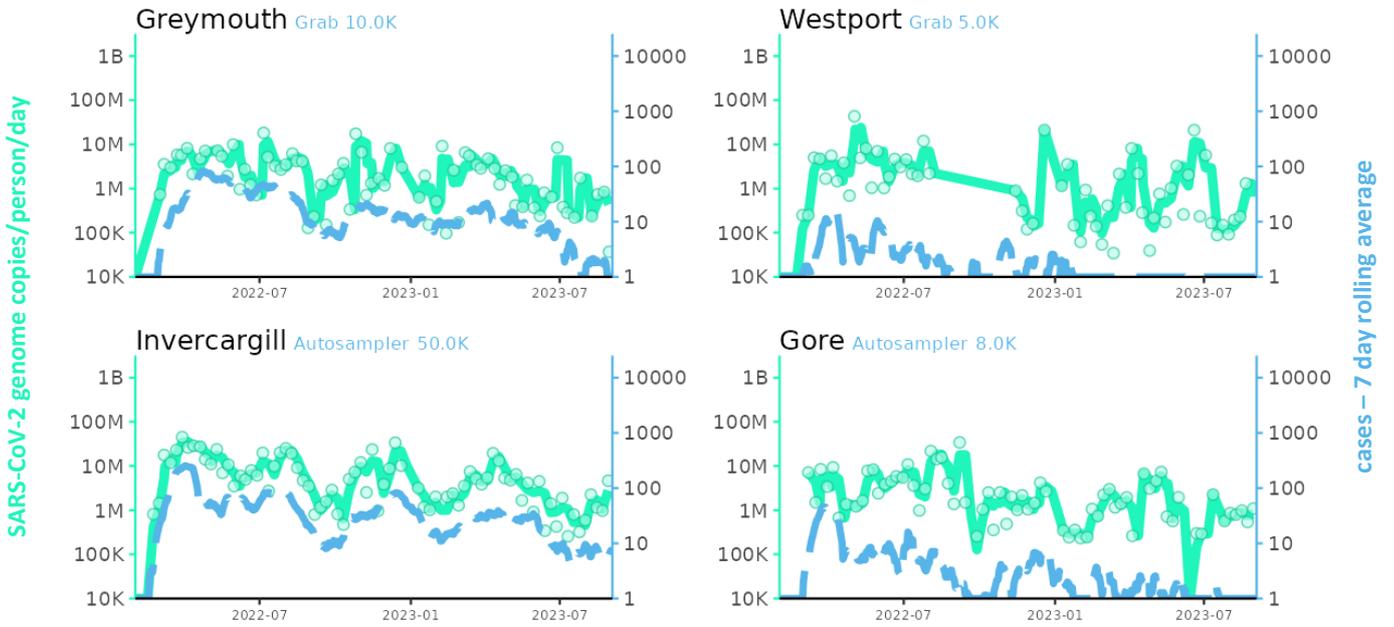
Southland & West Coast



SARS-CoV-2 RNA rate detected in wastewater (GC/person/day)



Reported case rate (new cases/100k population/day)



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 thank 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 including laboratory staff, data scientists, bioinformaticians, and other staff. 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 considers the flow rate of wastewater entering the treatment plant (the influent) and the population in the catchment. The flow rate is the total volume (m³ per day) recorded at the inlet of the wastewater treatment plant over 24 hours. This is 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.

Wastewater Data Modelling: *Instantaneous reproduction number (R_t)*: The instantaneous reproduction number (R_{eff}) represents the average number of secondary cases that will arise per primary infectious case. The effective reproduction number can be measured as either the instantaneous reproduction number (R_t), which measures transmission at a specific point in time; or the case reproductive number, which measures transmission for a specific cohort of individuals. The models described measure the instantaneous reproduction number (R_t). In general terms, an R_t above 1 would typically indicate an increasing number of infections in the population. The instantaneous reproduction number is calculated using a semi-mechanistic model that is fitted to (i) case numbers and (ii) wastewater quantitation, and incorporates information about shedding rates, infection generation times, and case ascertainment. Instantaneous reproduction number is estimated take into account any delays in self-reporting of cases. It should be noted that there is uncertainty in this measure, which is denoted with the 90% uncertainty intervals.

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 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

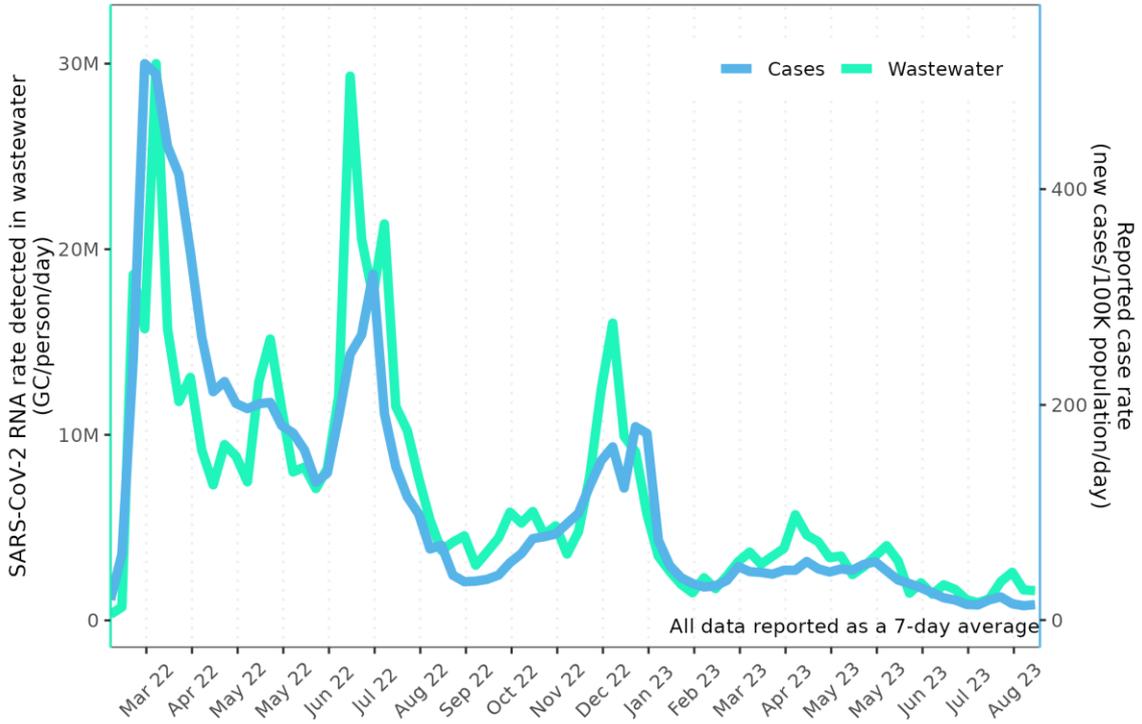
Jo Chapman

Senior Scientist

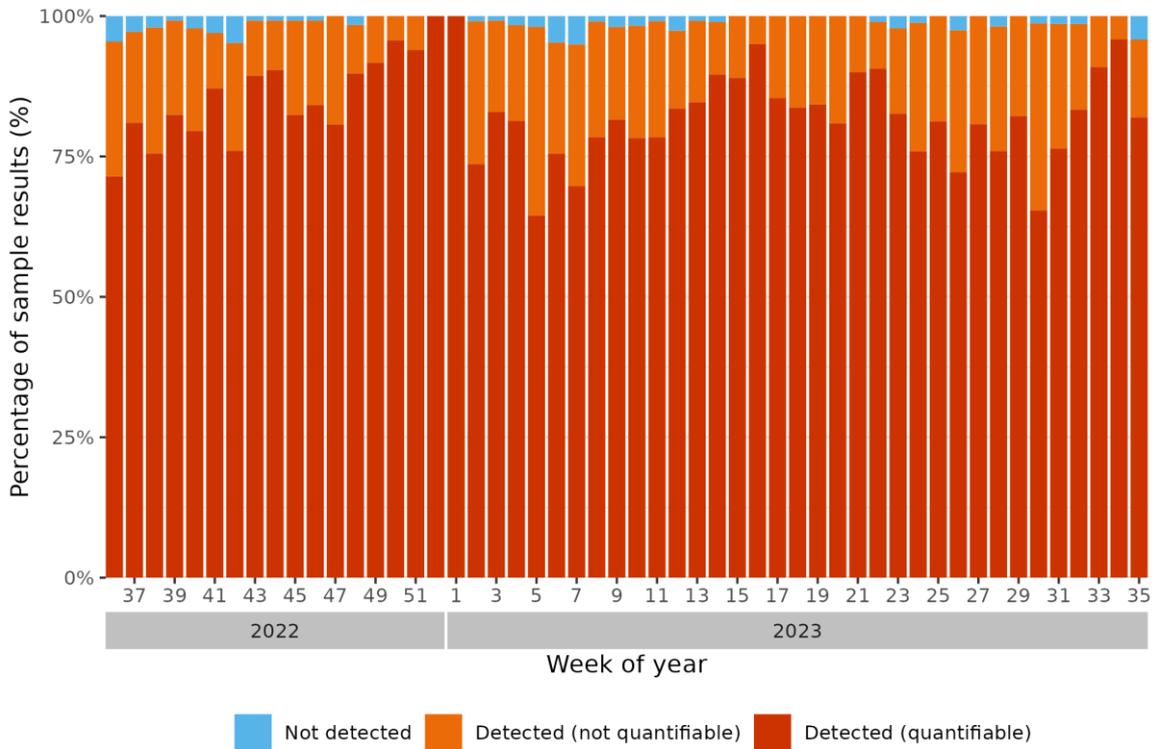
Joanne.chapman@esr.cri.nz

Appendix A. National Results

Time series plotted on linear scale



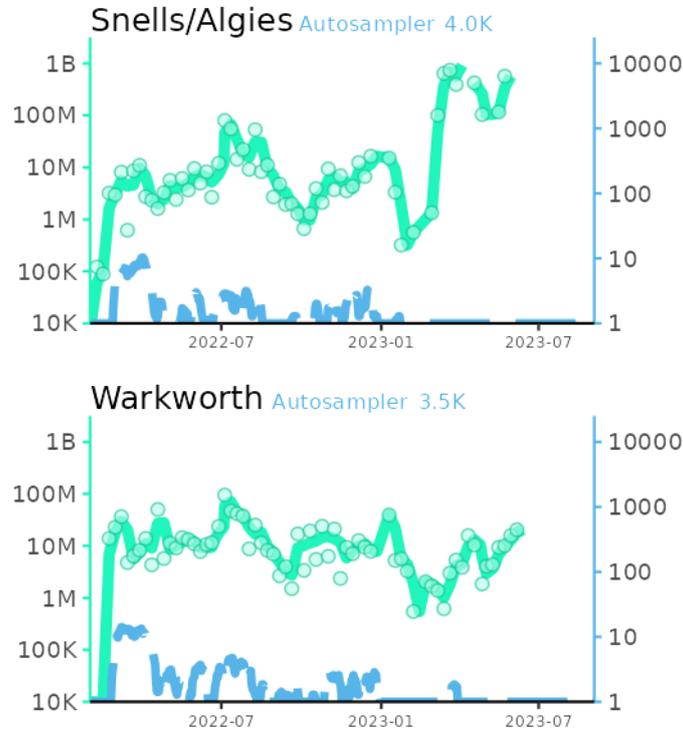
Detections for the past 52 weeks



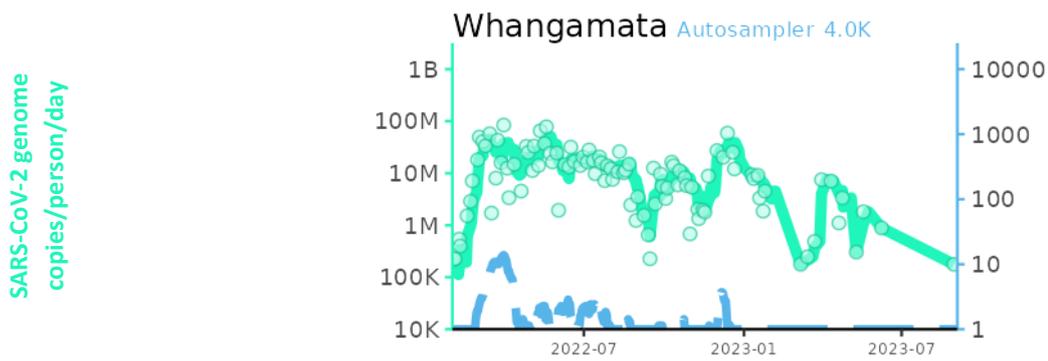
Appendix C

Additional Site Graphs

Auckland

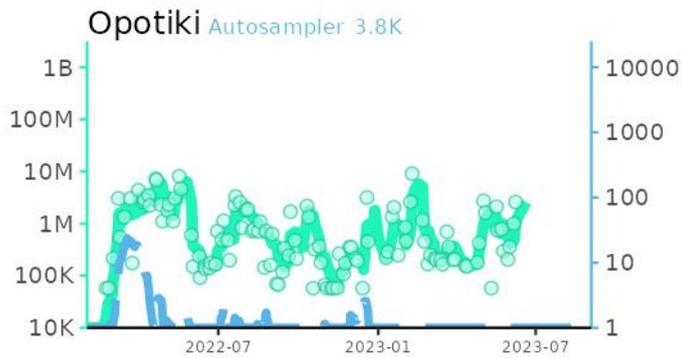
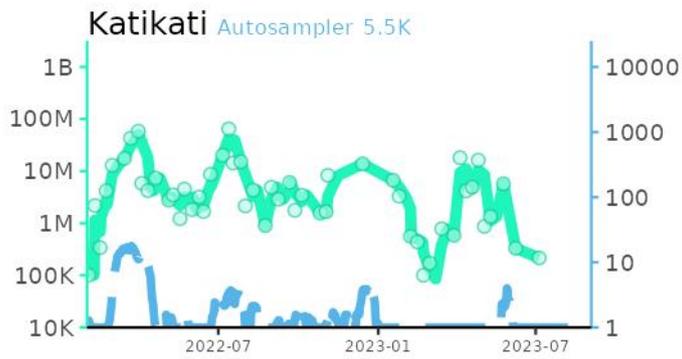


Waikato

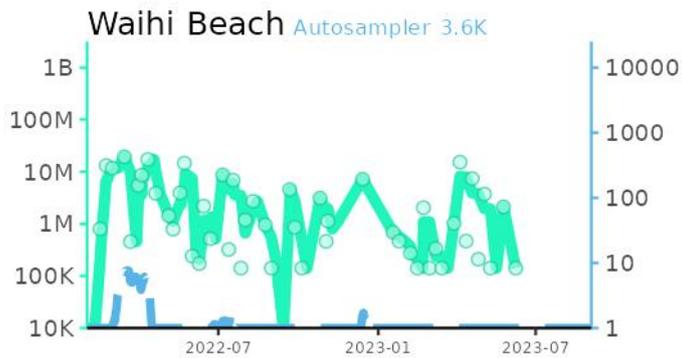


Bay of Plenty

SARS-CoV-2 genome copies/person/day

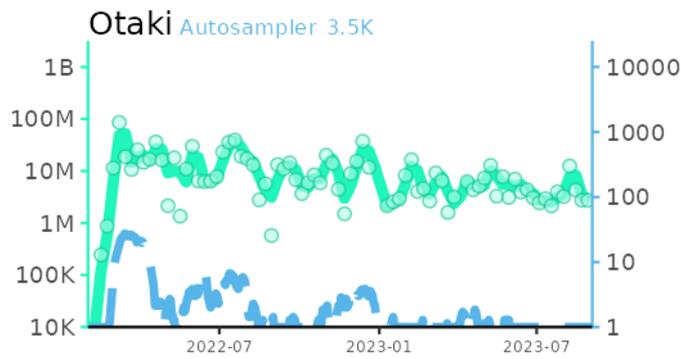


cases – 7 day rolling average



Wellington

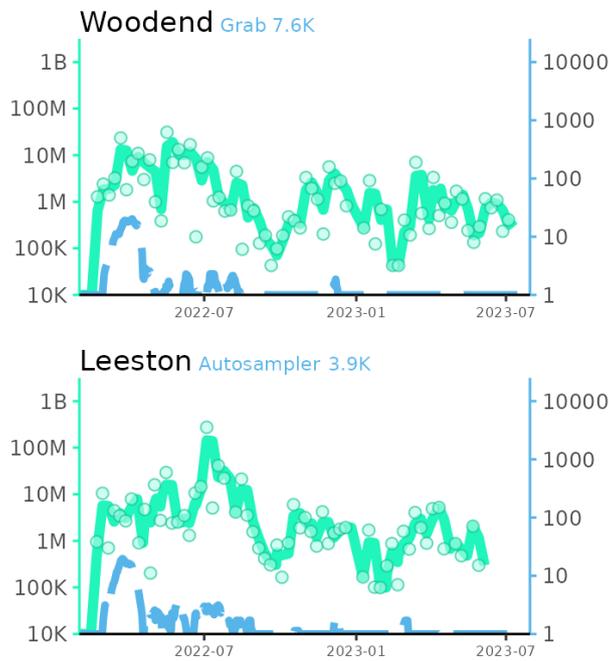
SARS-CoV-2 genome



cases – 7 day rolling average

Canterbury

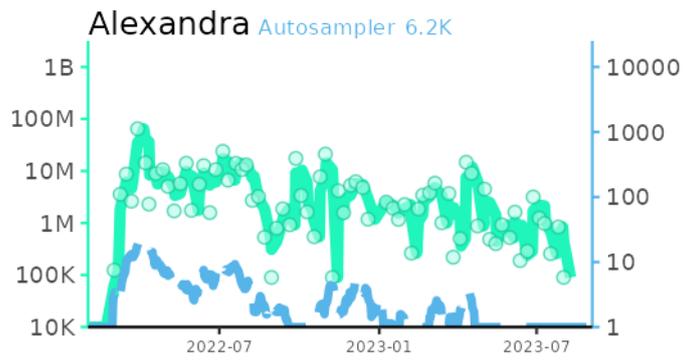
SARS-CoV-2 genome copies/person/day



cases – 7 day rolling average

Otago

SARS-CoV-2 genome



cases – 7 day rolling average