New Zealand Wastewater Surveillance Programme COVID-19

Monthly Report July 2023

Weeks ending 9 July to 30 July 2023, weeks 27 to 30

Report prepared 7 August 2023

Key Trends & Insights

For the month of July, national SARS-CoV-2 levels averaged 1.25 million genome copies per person per day (GC/p/d). During this period, SARS-CoV-2 levels declined steadily, and were lowest (0.85 million GC/p/d) in the week ending 30 July 2023.

Month overview

100%	68%	XBB
Sites (56/56) where SARS-CoV-2 was detected	NZ population covered by wastewater testing	Most prevalent variant detected (40 - 63%)

- In July 2023, 293 samples were collected across Aotearoa. SARS-CoV-2 RNA was detected in 291/293 (99.3%) of samples from 56/56 sites (100%).
- SARS-CoV-2 levels in week 30, ending 30 July 2023, were the lowest observed since 2022 week 7, ending 20 February 2022.
- The XBB family of lineages was predominant in July (estimated percentage between 41% (week 27) and 64% (week 28) of national sequence reads this month).

National Results

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

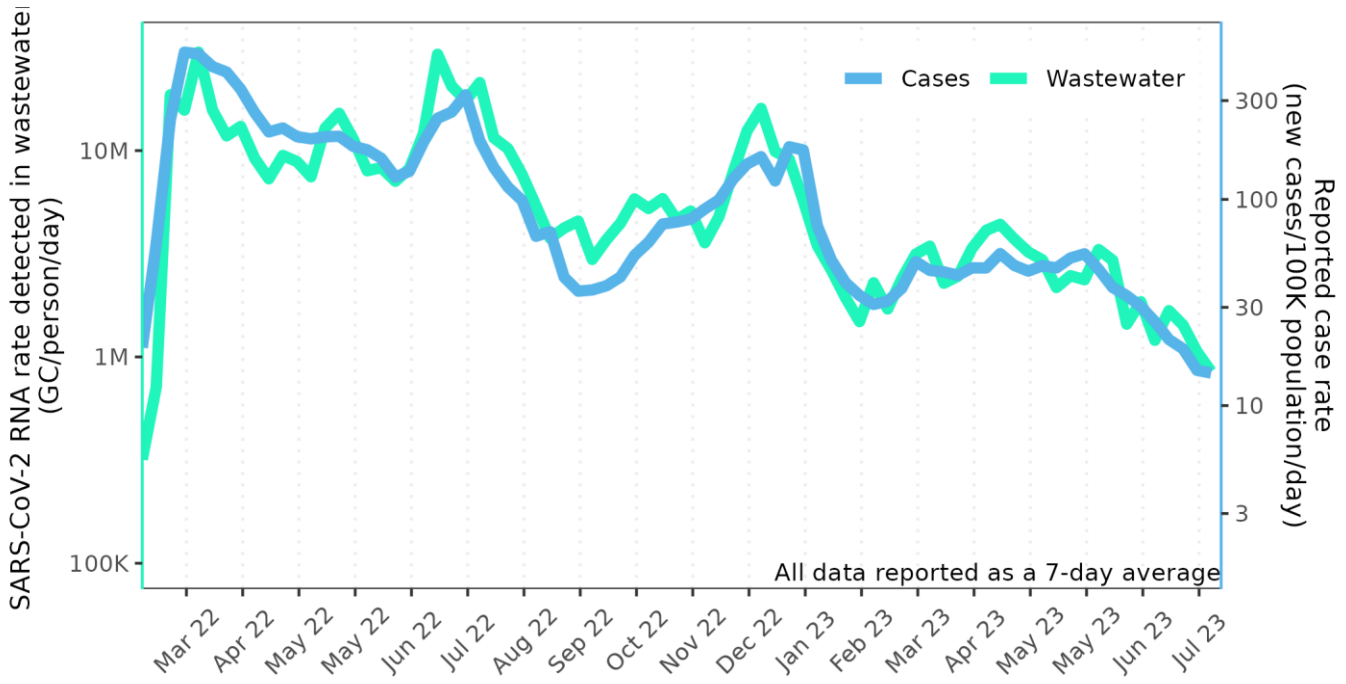


Figure 1. National timeseries of estimated SARS-CoV-2 wastewater rate (GC/person/day, green line) and reported case rate (new cases/100,000 population/day, blue line) on a $\log_{10}$ scale.

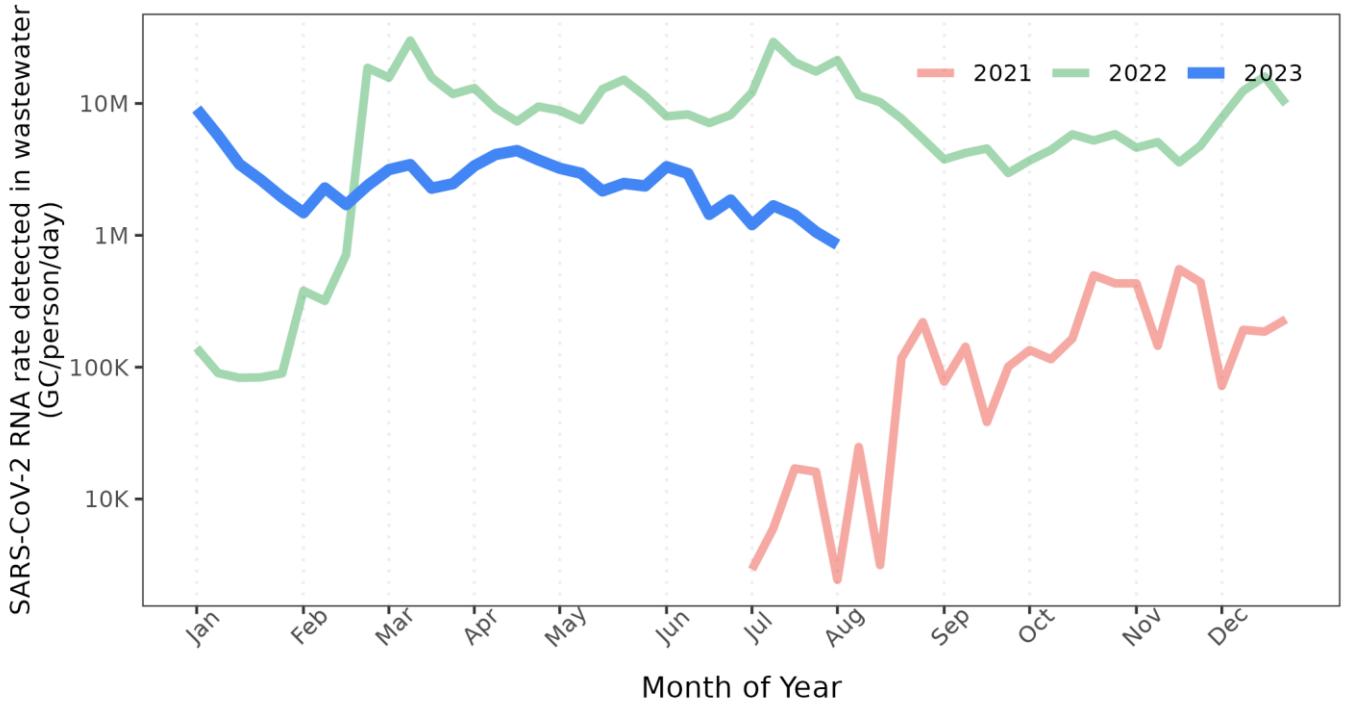


Figure 2. National timeseries of estimated SARS-CoV-2 wastewater rate (GC/person/day) from July 2021 to May 2023 on a $\log_{10}$ scale.

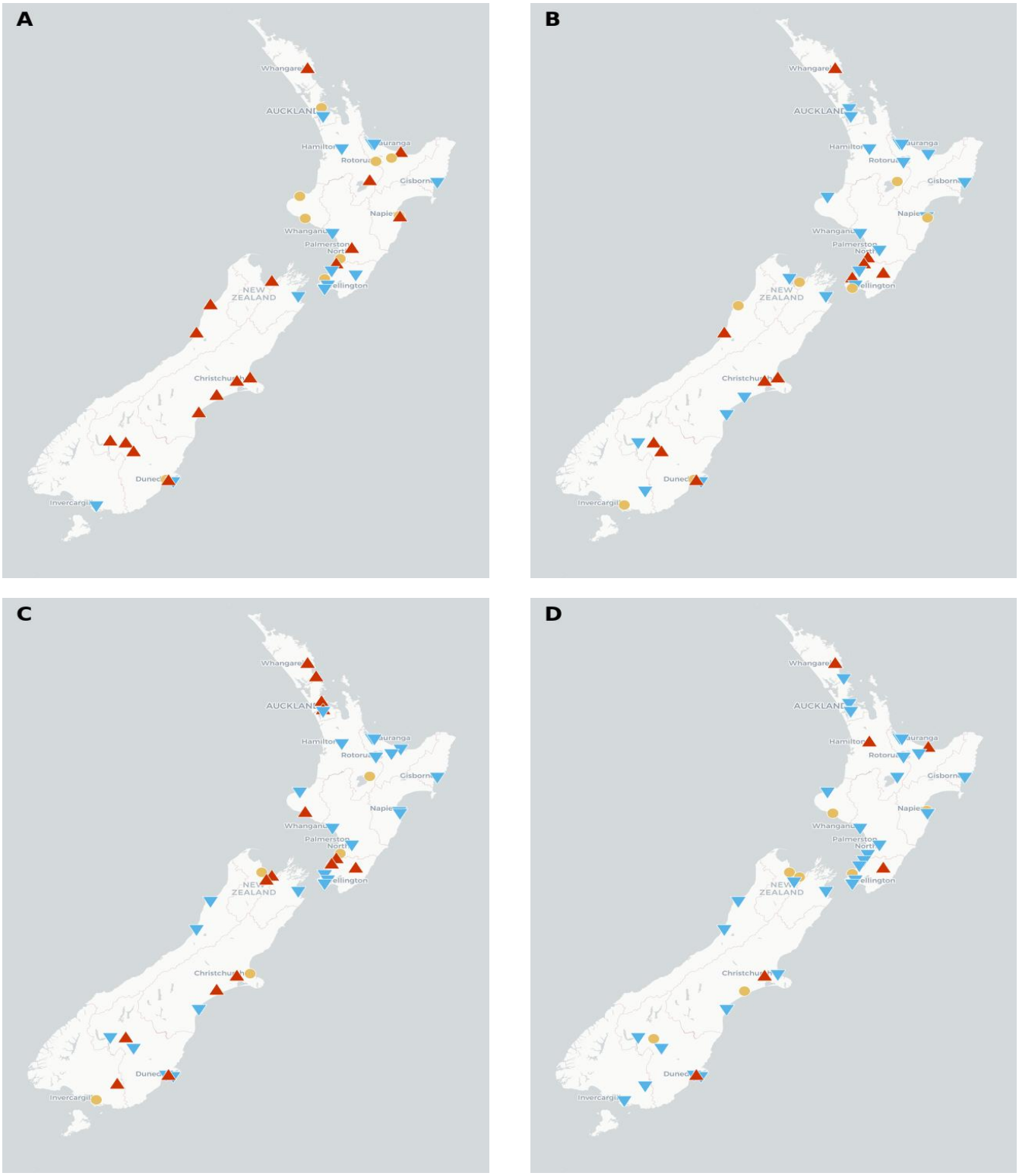


Figure 3. Comparison of SARS-CoV-2 levels for the week ending 30 July 2023, compared to levels measured: A) 1 week ago; B) 2 weeks ago; C) 4 weeks ago; D) 12 weeks ago. Only sites with results for both time points are included. When the viral quantity is 30% or more higher this is labelled as increased (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

ESR has recently validated a new assay ('CoVarSeq') for SARS-CoV-2 variant analysis from wastewater, replacing the Wilderlab S-gene barcoding assay. This assay allows considerably finer resolution of variants, such as the detection of specific XBB sublineages and improves alignment of the wastewater and clinical reporting.

The CoVarSeq method was retrospectively applied to samples from February 2023 to present.

Results from the four weeks of sampling up to week 28 from twenty sentinel wastewater sites (Table 1) across New Zealand show that the XBB family of lineages were detected most frequently (estimated percentage between 41% and 64%, with XBB predominant at 24-38%) across this period (Figures 4 and 5, Table 1). CH.1.1 (including the descendant lineage FK.1.1) was the next most common variant (21-38%) followed by XBC (9-25%). BA.2.75 and non-XBC recombinants (including XBF) were detected at low levels (approx. 2- 5% and 0-2% respectively).

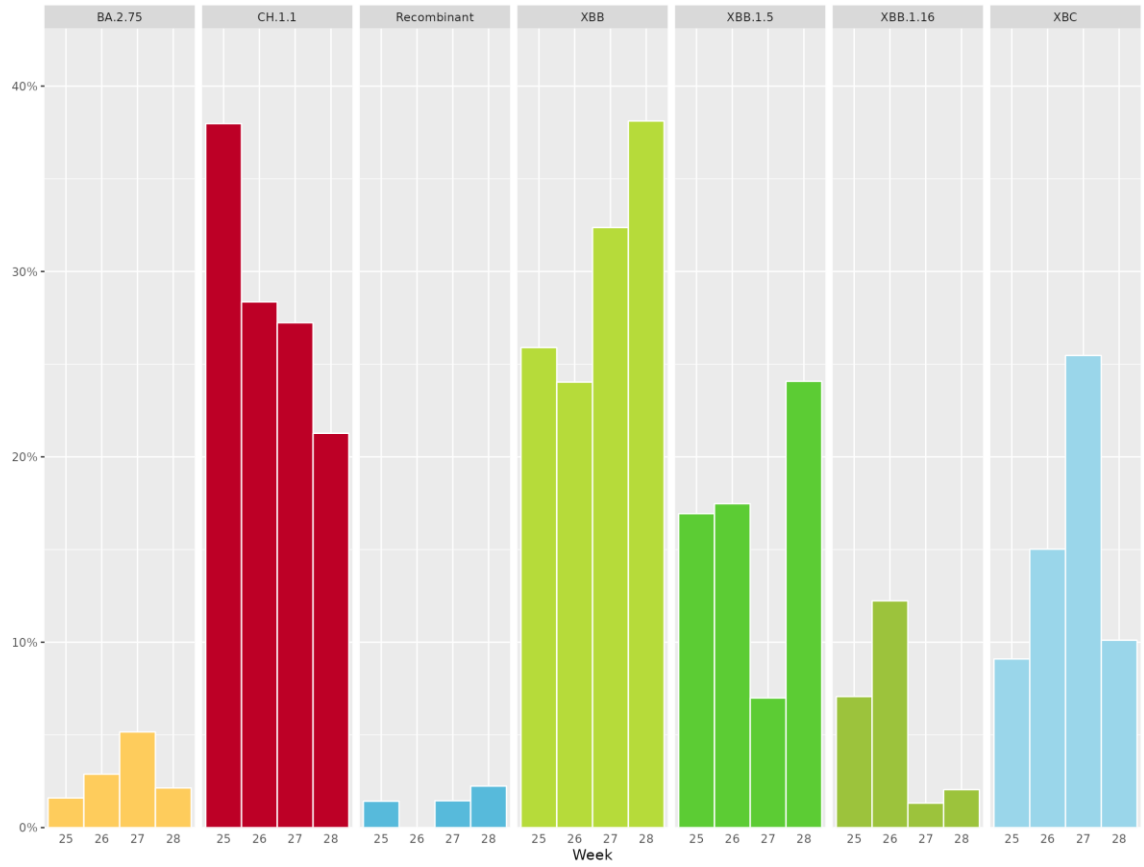


Figure 4. National percentage of each variant from week 25 to 28 (week ending 16 July 2023).

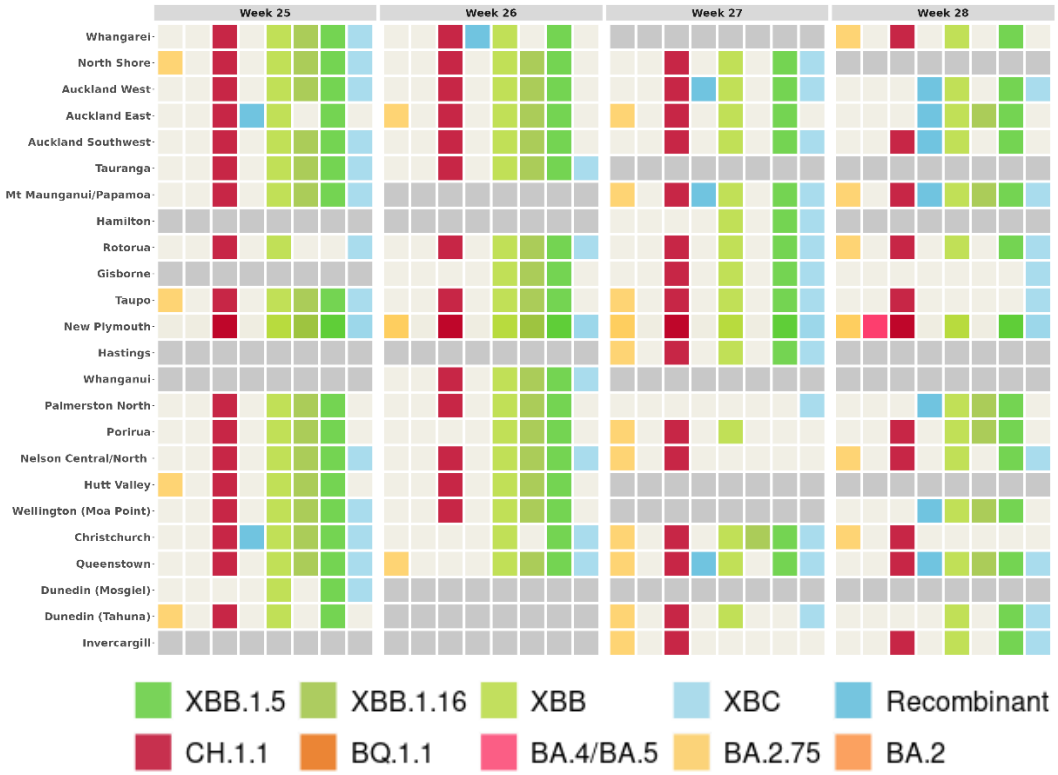


Table 1. Data from 20 wastewater sentinel sites sampled from week 25 to 28. Coloured box denotes that the variant was detected at that site that week, cream box denotes that the variant was not detected, and grey box denotes that no data is available for that site, either due to the sample not being collected or no valid sequence output (e.g., due to low virus concentration).

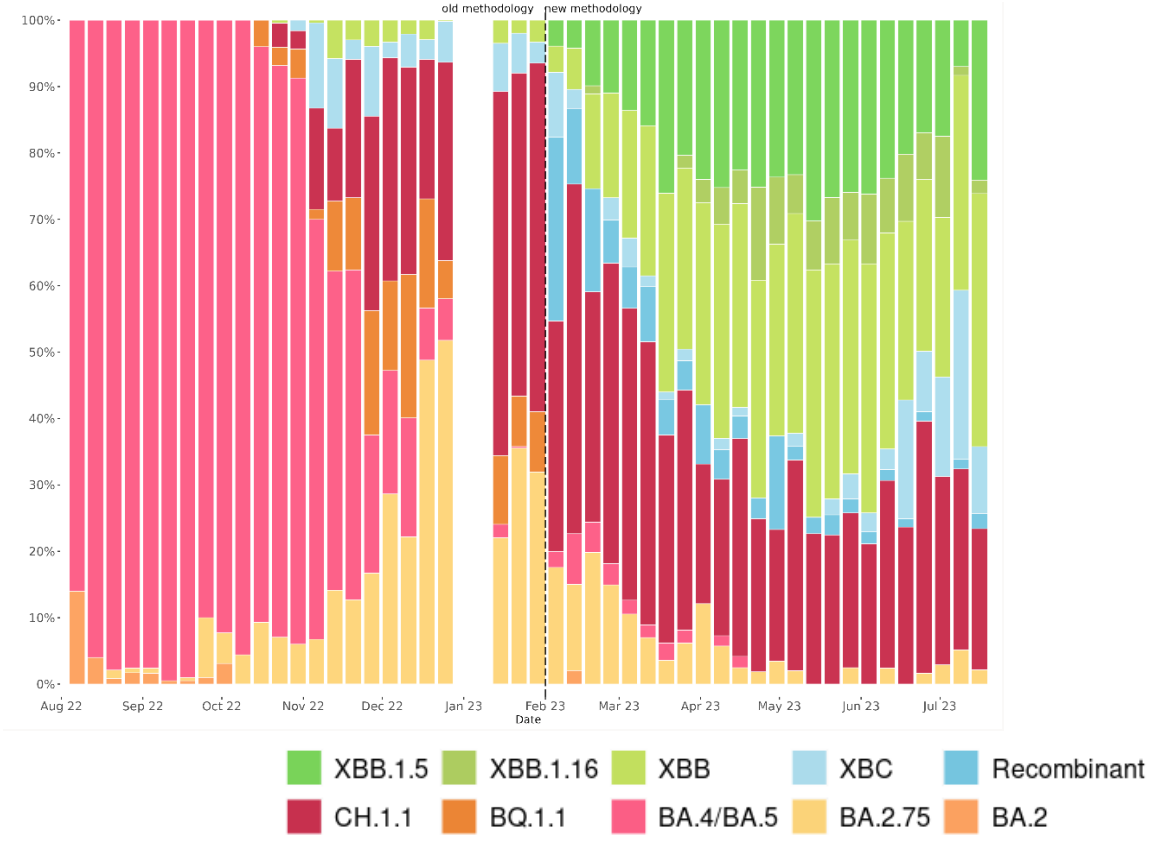


Figure 5. Estimated variant percentage over time at a national scale (average). Data are collected from up to 20 sentinel sites each week.

Trends in Ministry of Health Regions

Regional analysis of the wastewater data is shown in Figure 6. During July, there was a general decreasing trend in the SARS-CoV-2 genome copies detected per day in each of the regions.

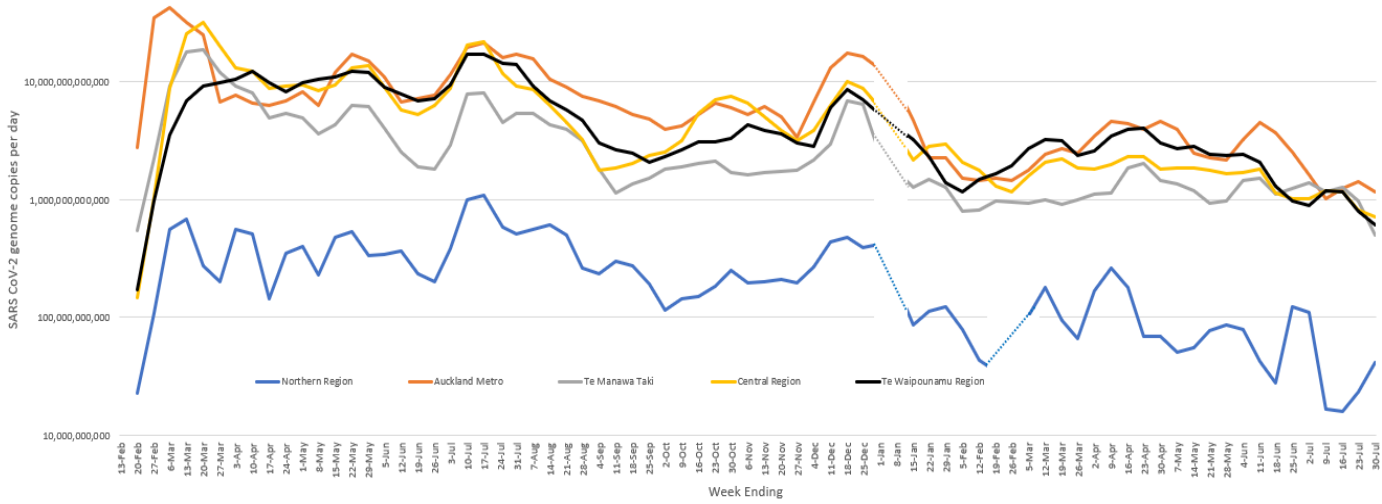


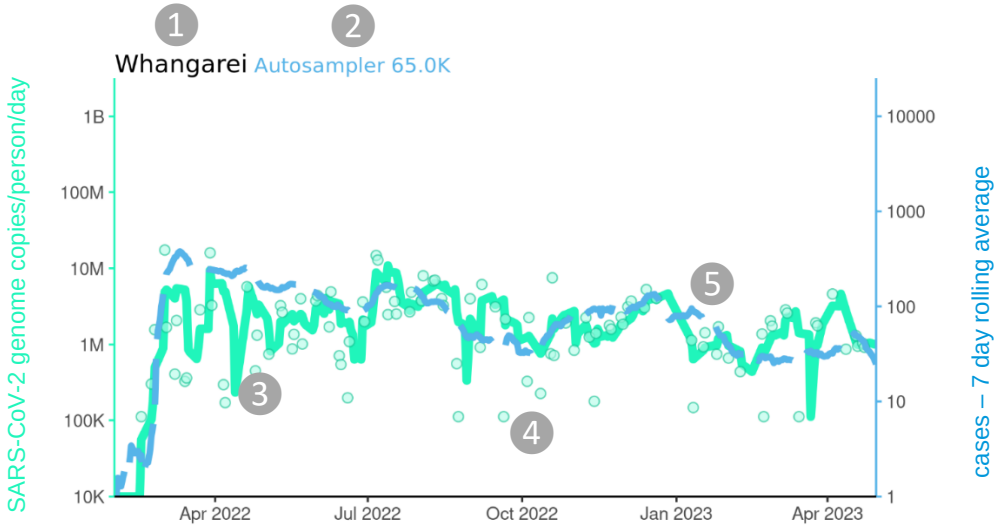
Figure 6. Two-week rolling average of total SARS-CoV-2 genome copies detected per day in the five Ministry of Health regions. Dashed lines are inferred levels during periods when samples were either not collected (Christmas period) or insufficient numbers collected (due to weather impacts) for the region.

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).

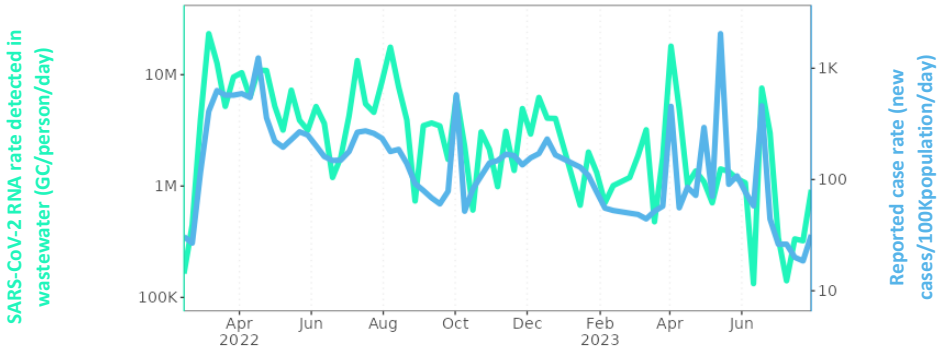
Interpreting Site Graphs

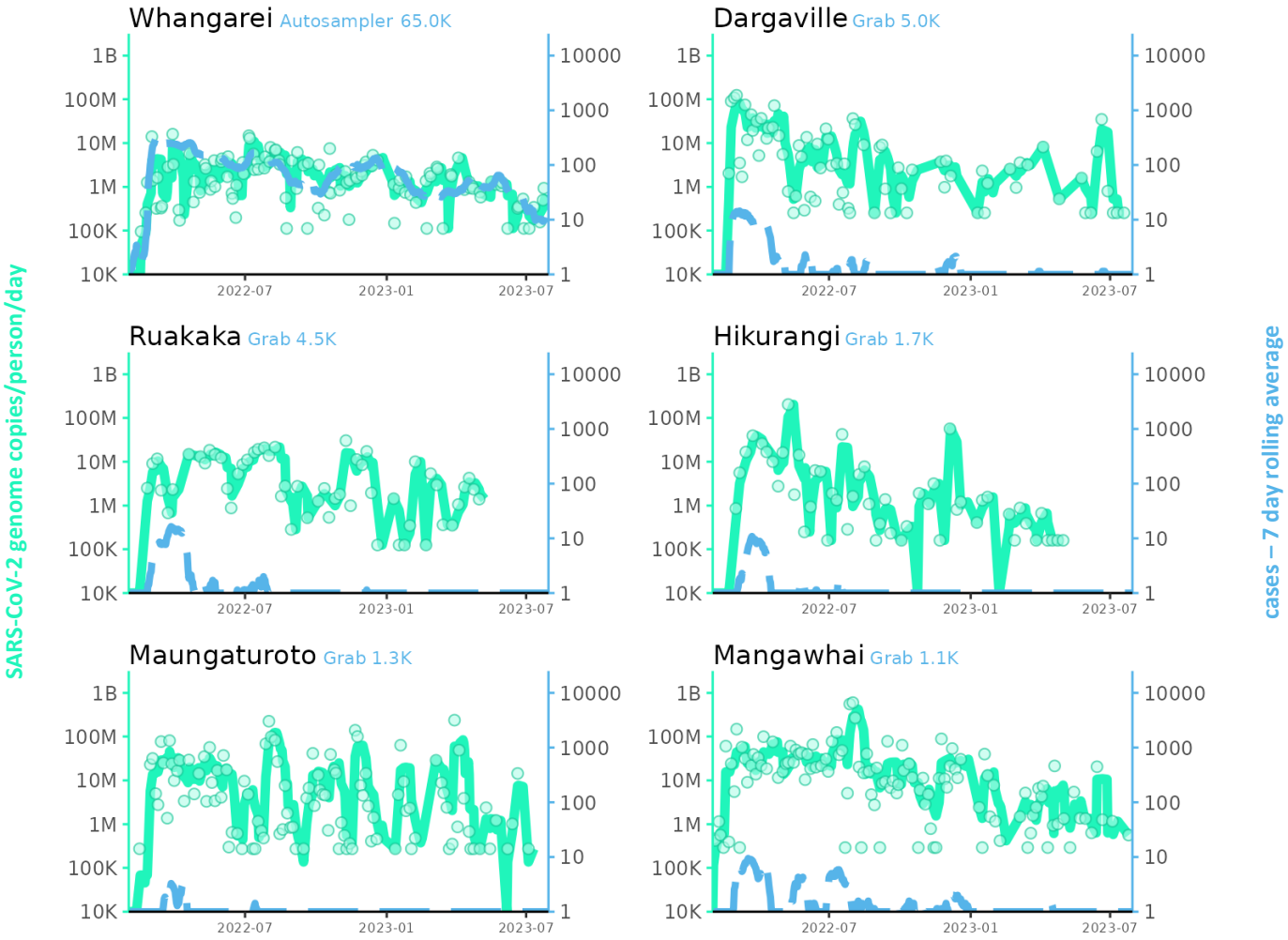


1. Site Name
2. Sample collection method and population of wastewater catchment. Results based on autosampler may be more representative than grab sample-based results.
3. **Wastewater** results shown as solid **green** line | 14-day rolling average of genome copies/person/day on a $\log_{10}$ scale.
4. Individual sample results 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 **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 is subject to change.

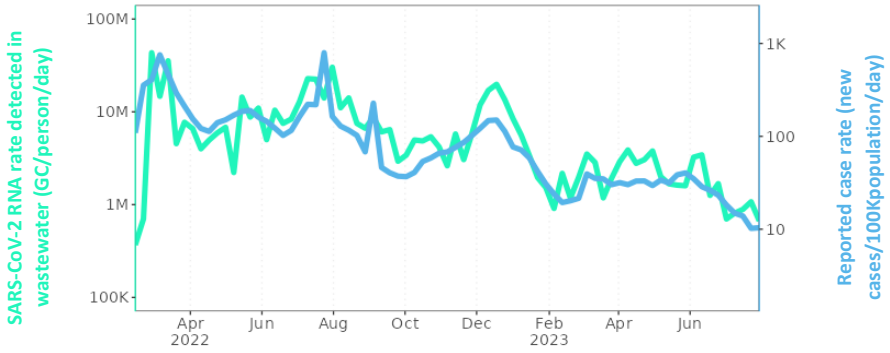
Note: Wastewater and cases data are on a $\log_{10}$ scale. Scales on all graphs have been normalized to cover the same scale on every graph. Care should be taken when interpreting the data.

Northland


SARS-CoV-2 RNA rate detected in wastewater (GC/person/day)
10M
1M
100K
1K
100
10
Reported case rate (new cases/100K population/day)
Apr 2022
Jun
Aug
Oct
Dec
Feb 2023
Apr
Jun


Whangarei Autosampler 65.0K
Dargaville Grab 5.0K
Ruakaka Grab 4.5K
Hikurangi Grab 1.7K
Maungaturoto Grab 1.3K
Mangawhai Grab 1.1K
SARS-CoV-2 genome copies/person/day
cases – 7 day rolling average
1B
100M
10M
1M
100K
10K
10000
1000
100
10
1
2022-07
2023-01
2023-07

Auckland


SARS-CoV-2 RNA rate detected in wastewater (GC/person/day)
100M
10M
1M
100K
1K
100
10
Reported case rate (new cases/100K population/day)
Apr 2022
Jun
Aug
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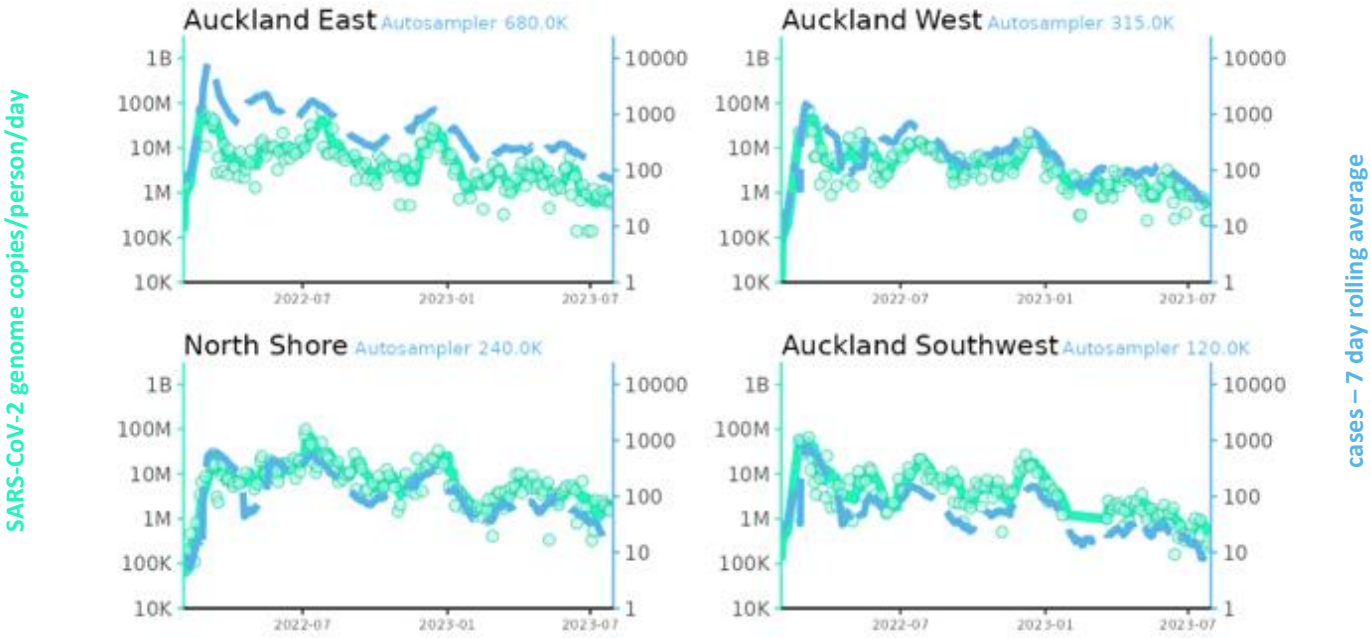
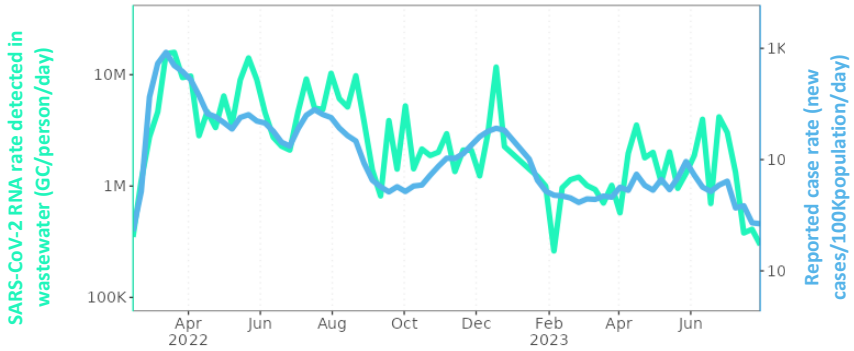
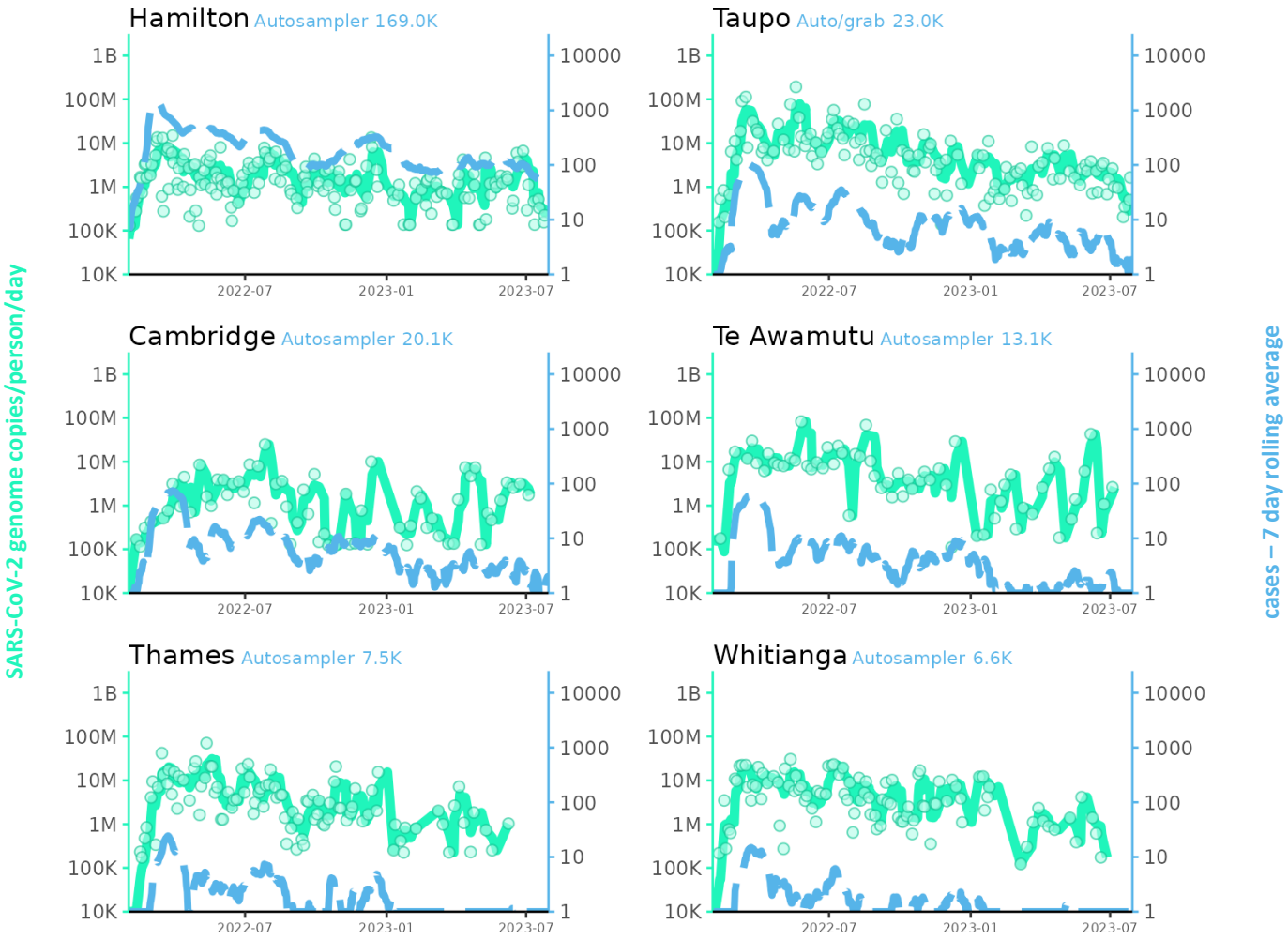
Dec
Feb 2023
Apr
Jun

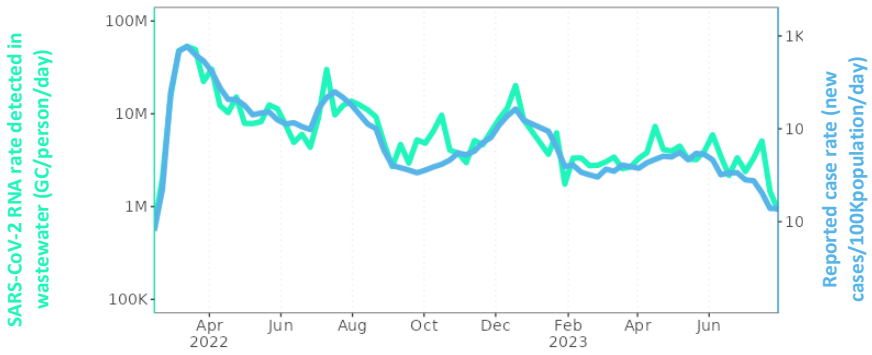

SARS-CoV-2 genome copies/person/day
Auckland East Autosampler 680.0K
Auckland West Autosampler 315.0K
North Shore Autosampler 240.0K
Auckland Southwest Autosampler 120.0K
1B
100M
10M
1M
100K
10K
10000
1000
100
10
1
2022-07
2023-01
2023-07
cases – 7 day rolling average

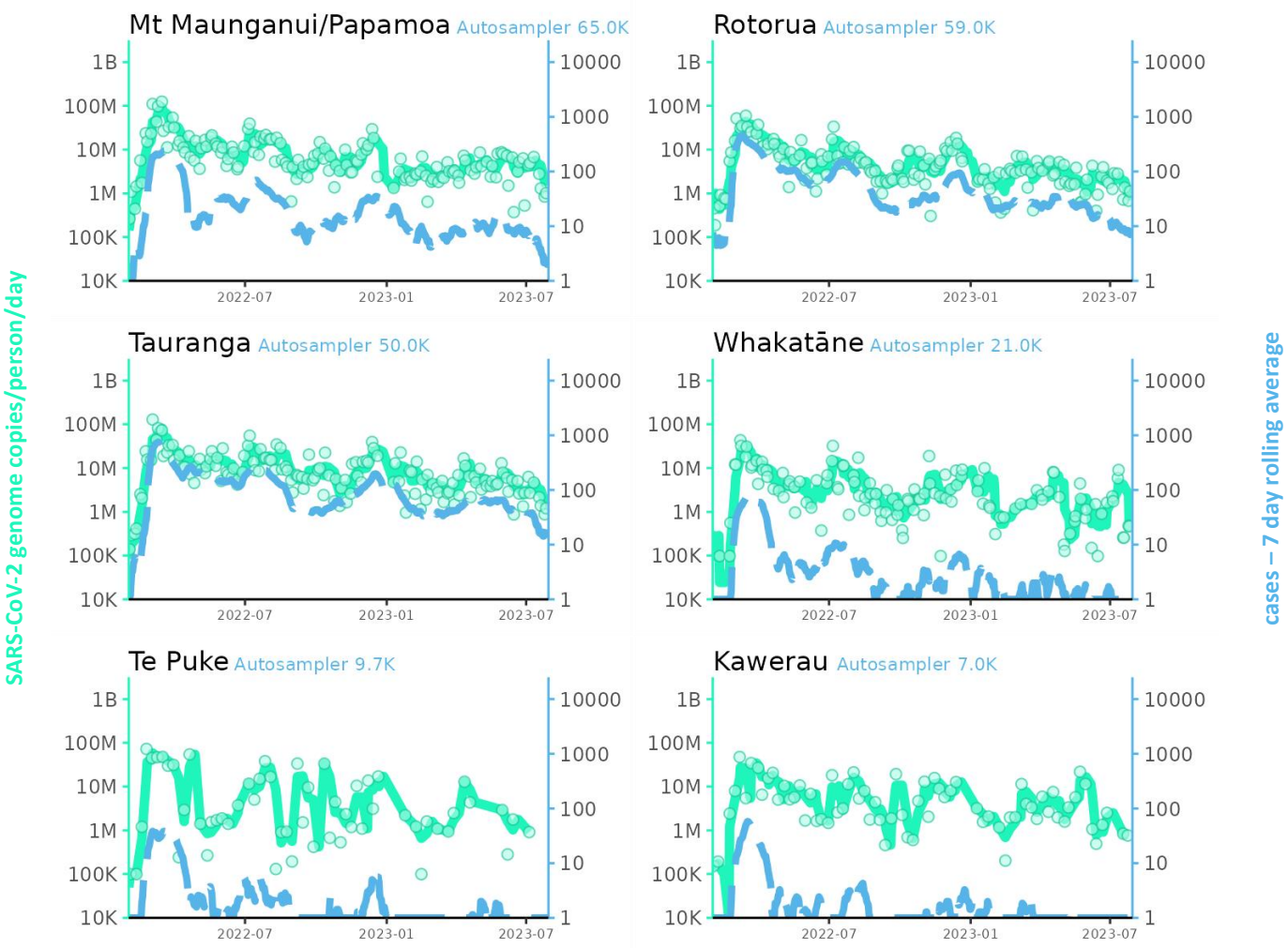
Waikato


SARS-CoV-2 RNA rate detected in wastewater (GC/person/day)
10M
1M
100K
1K
10
10
Reported case rate (new cases/100Kpopulation/day)
Apr 2022
Jun
Aug
Oct
Dec
Feb 2023
Apr
Jun

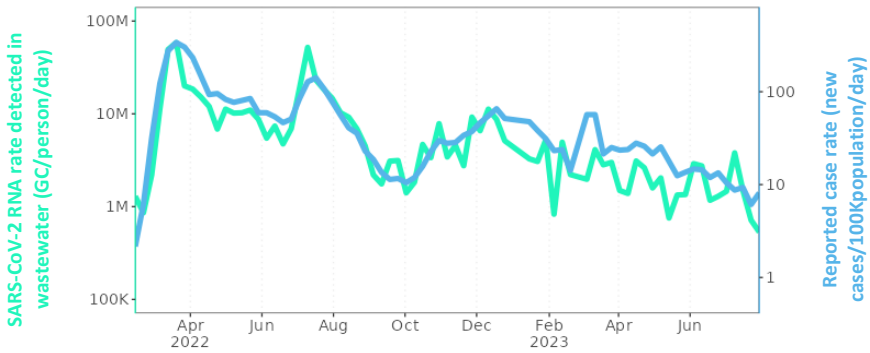

Hamilton Autosampler 169.0K
Taupo Auto/grab 23.0K
Cambridge Autosampler 20.1K
Te Awamutu Autosampler 13.1K
Thames Autosampler 7.5K
Whitianga Autosampler 6.6K
SARS-CoV-2 genome copies/person/day
cases – 7 day rolling average
1B
100M
10M
1M
100K
10K
10000
1000
100
10
1
2022-07
2023-01
2023-07

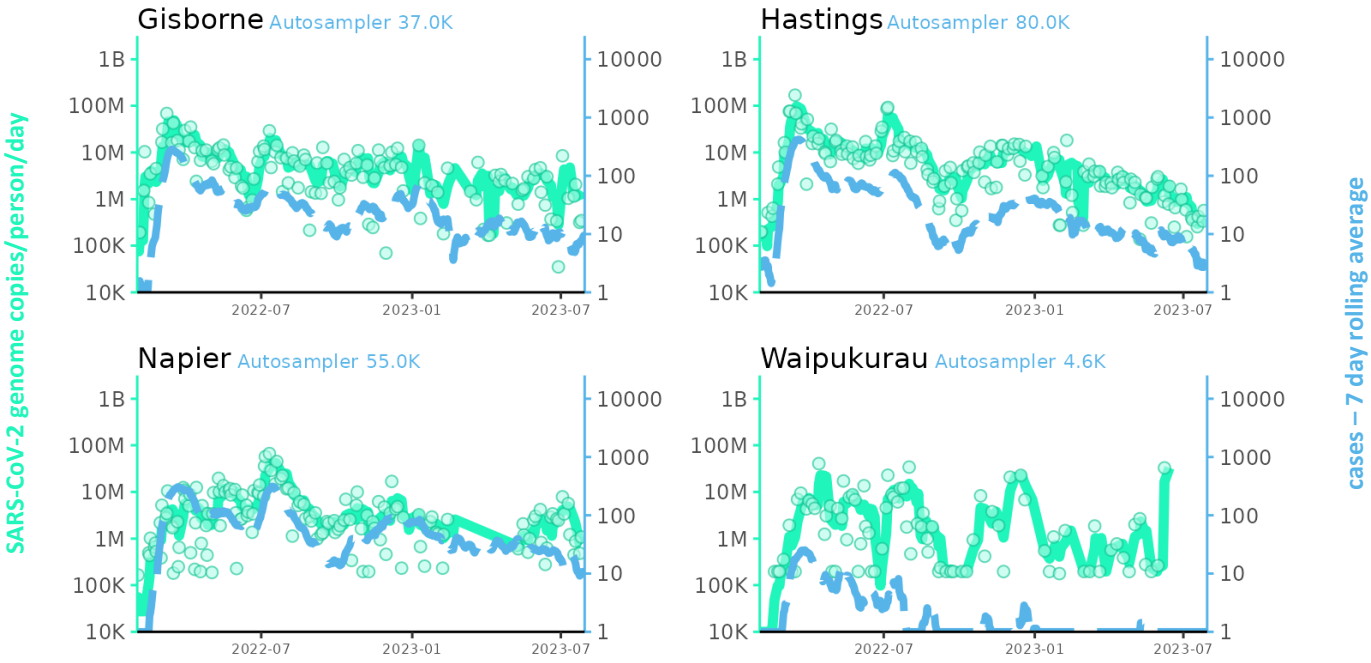
Bay of Plenty



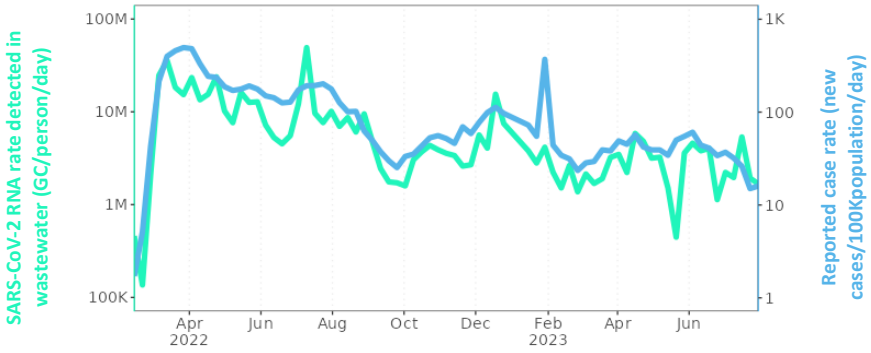


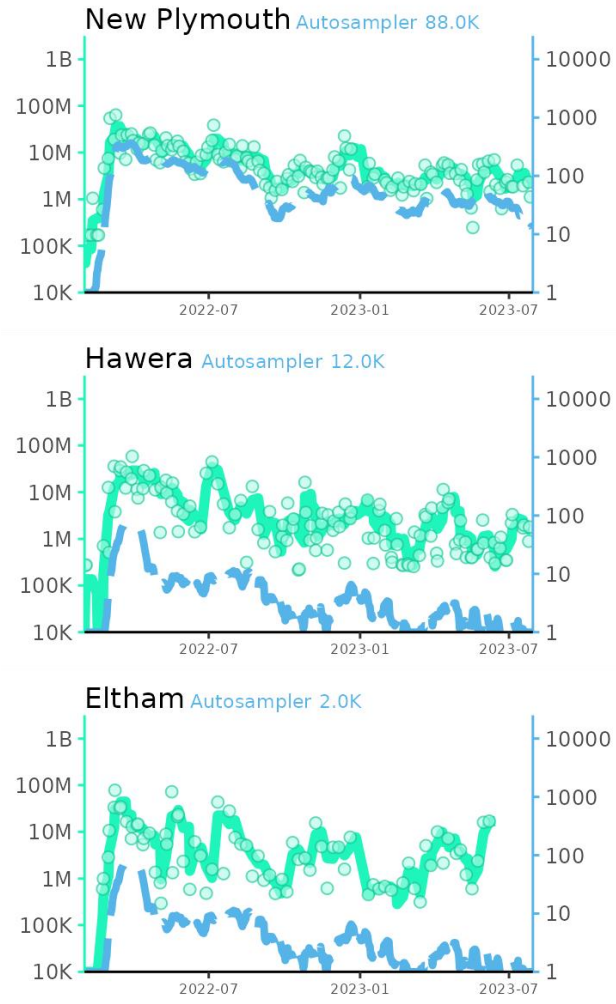
Hawke's Bay & Gisborne



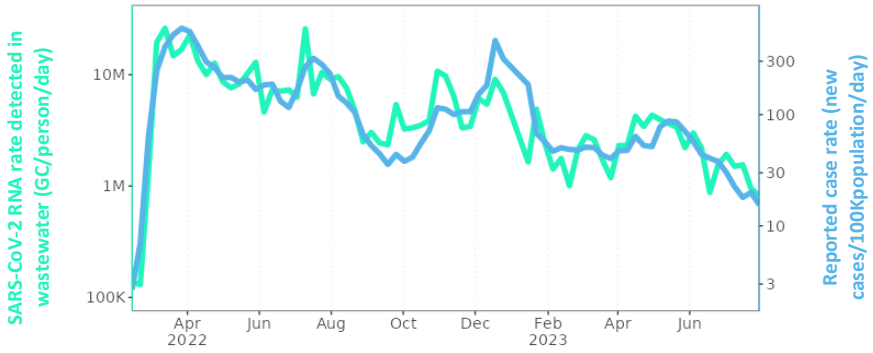


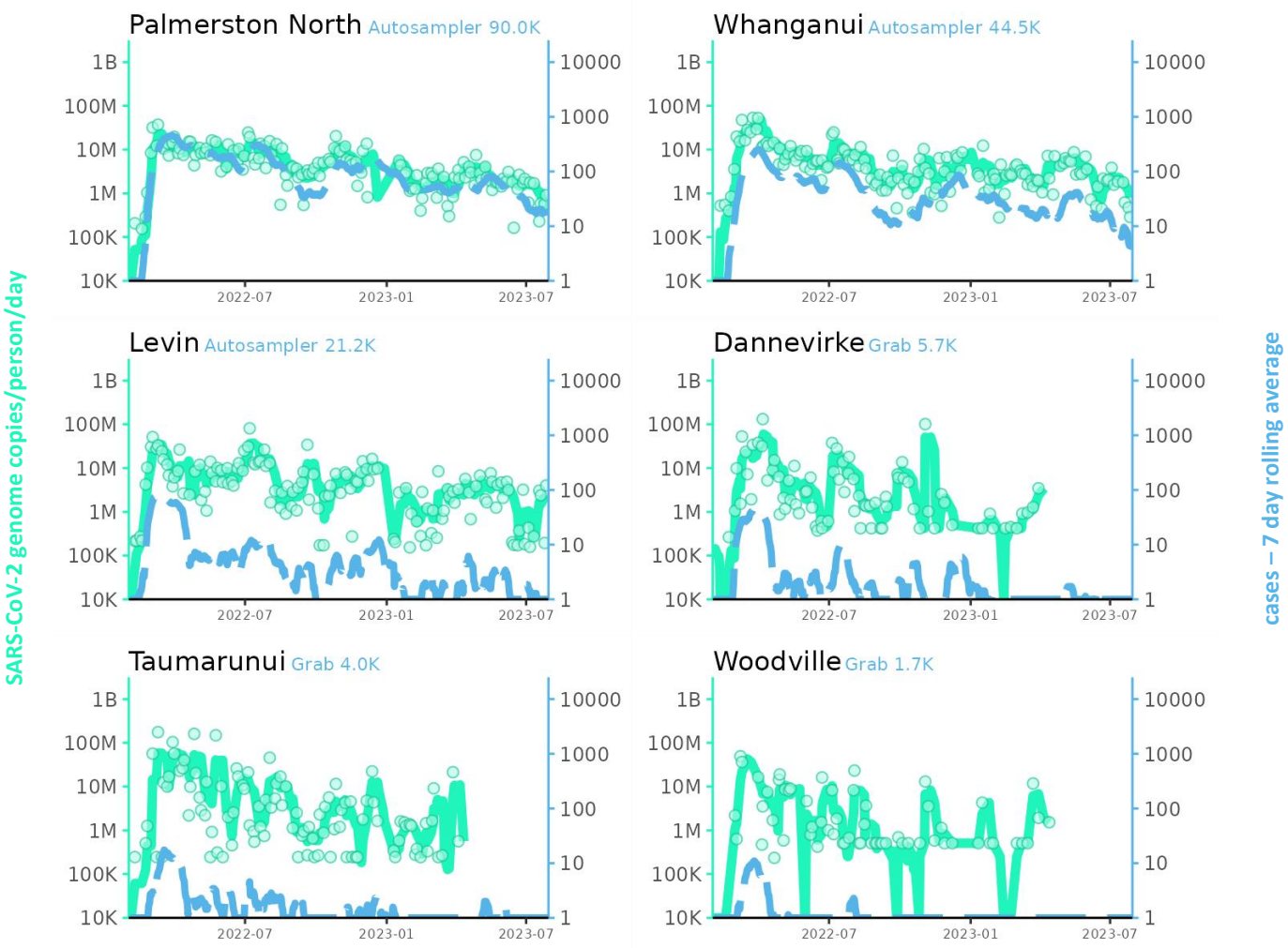
Taranaki


SARS-CoV-2 RNA rate detected in wastewater (GC/person/day)
100M
10M
1M
100K
1K
100
10
1
Reported case rate (new cases/100Kpopulation/day)
Apr 2022
Jun
Aug
Oct
Dec
Feb 2023
Apr
Jun

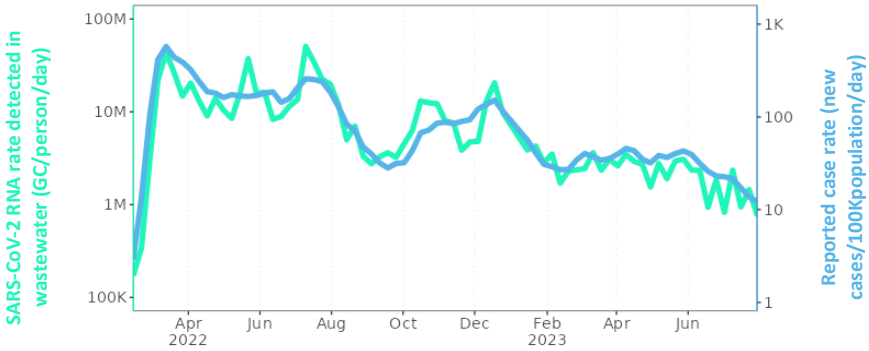

New Plymouth Autosampler 88.0K
Hawera Autosampler 12.0K
Eltham Autosampler 2.0K
SARS-CoV-2 genome copies/person/day
cases – 7 day rolling average
1B
100M
10M
1M
100K
10K
10000
1000
100
10
1
2022-07
2023-01
2023-07

Manawatu & Whanganui





Wellington


SARS-CoV-2 RNA rate detected in wastewater (GC/person/day)
100M
10M
1M
100K
1K
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10
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Reported case rate (new cases/100K population/day)
Apr 2022
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Feb 2023
Apr
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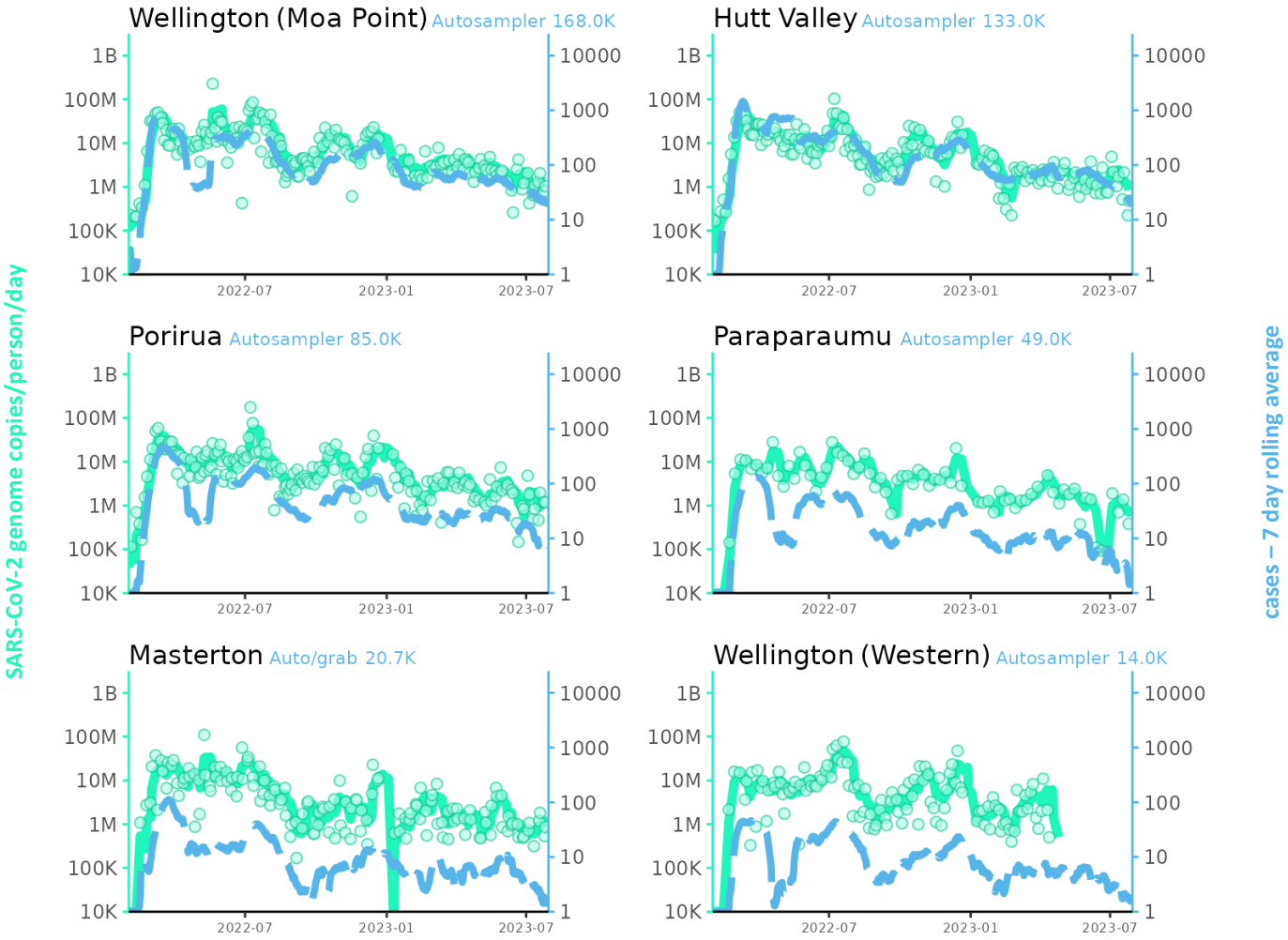
Wellington (Moa Point) Autosampler 168.0K
Hutt Valley Autosampler 133.0K
Porirua Autosampler 85.0K
Paraparaumu Autosampler 49.0K
Masterton Auto/grab 20.7K
Wellington (Western) Autosampler 14.0K
SARS-CoV-2 genome copies/person/day
cases – 7 day rolling average
1B
100M
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1M
100K
10K
10000
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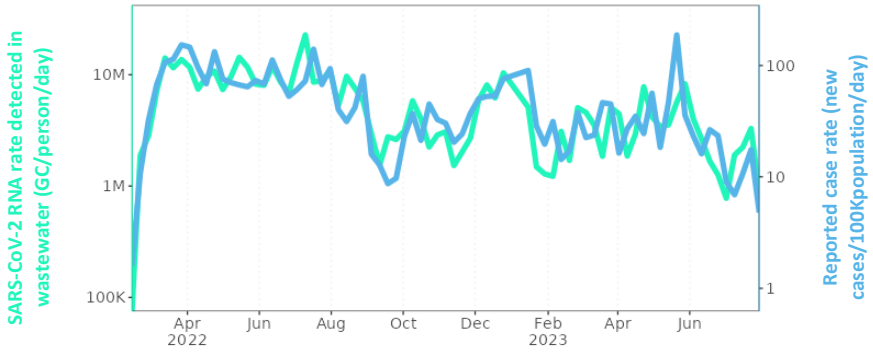
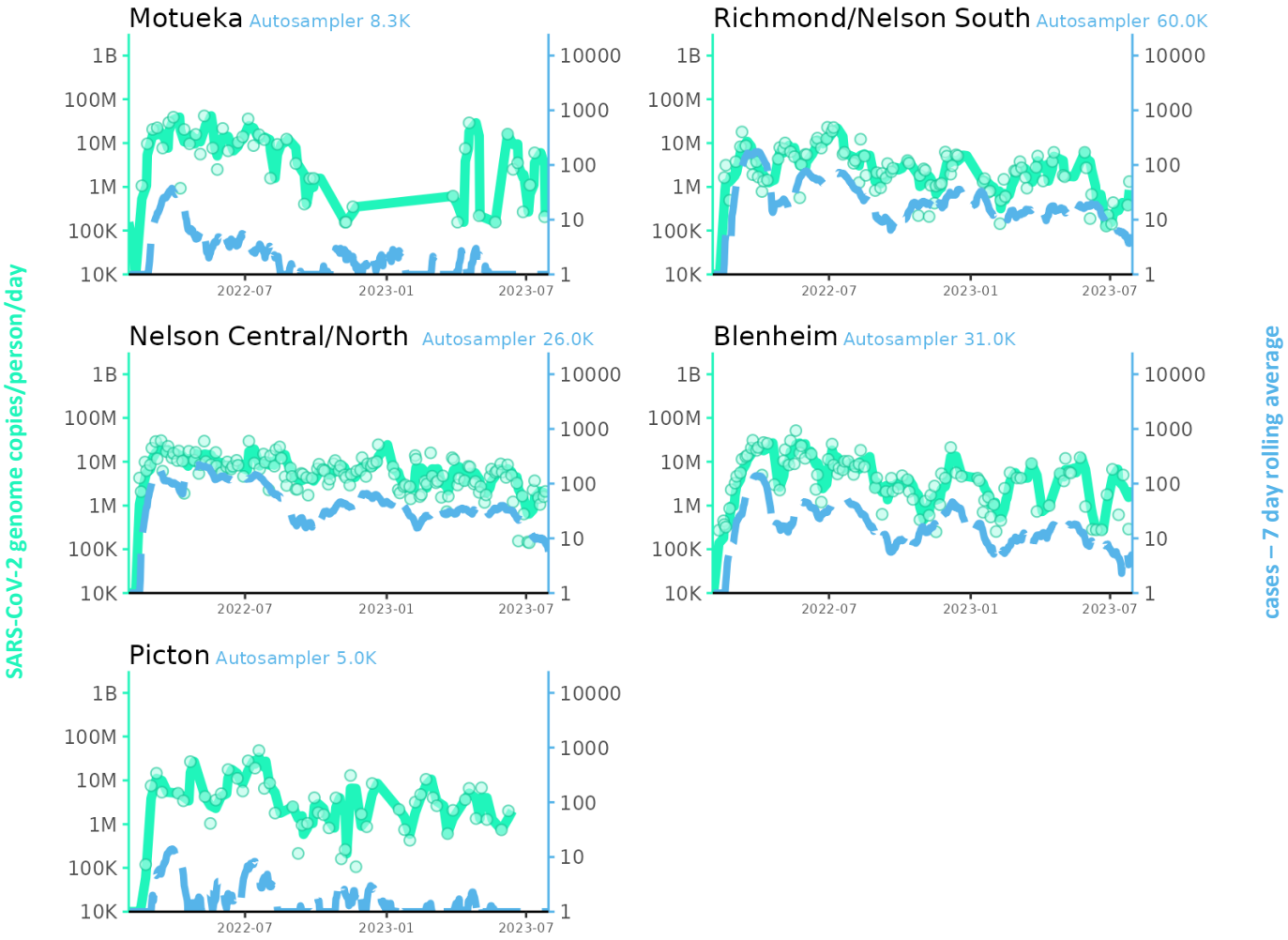
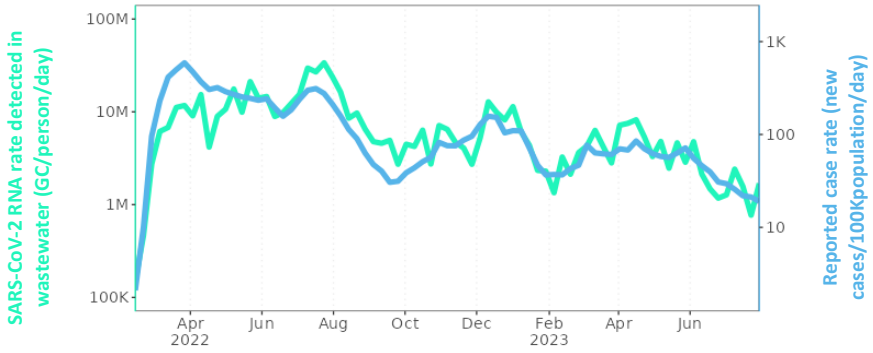
100
10
1
2022-07
2023-01
2023-07

Tasman, Nelson & Marlborough





Canterbury


SARS-CoV-2 RNA rate detected in wastewater (GC/person/day)
100M
10M
1M
100K
1K
100
10
Reported case rate (new cases/100Kpopulation/day)
Apr 2022
Jun
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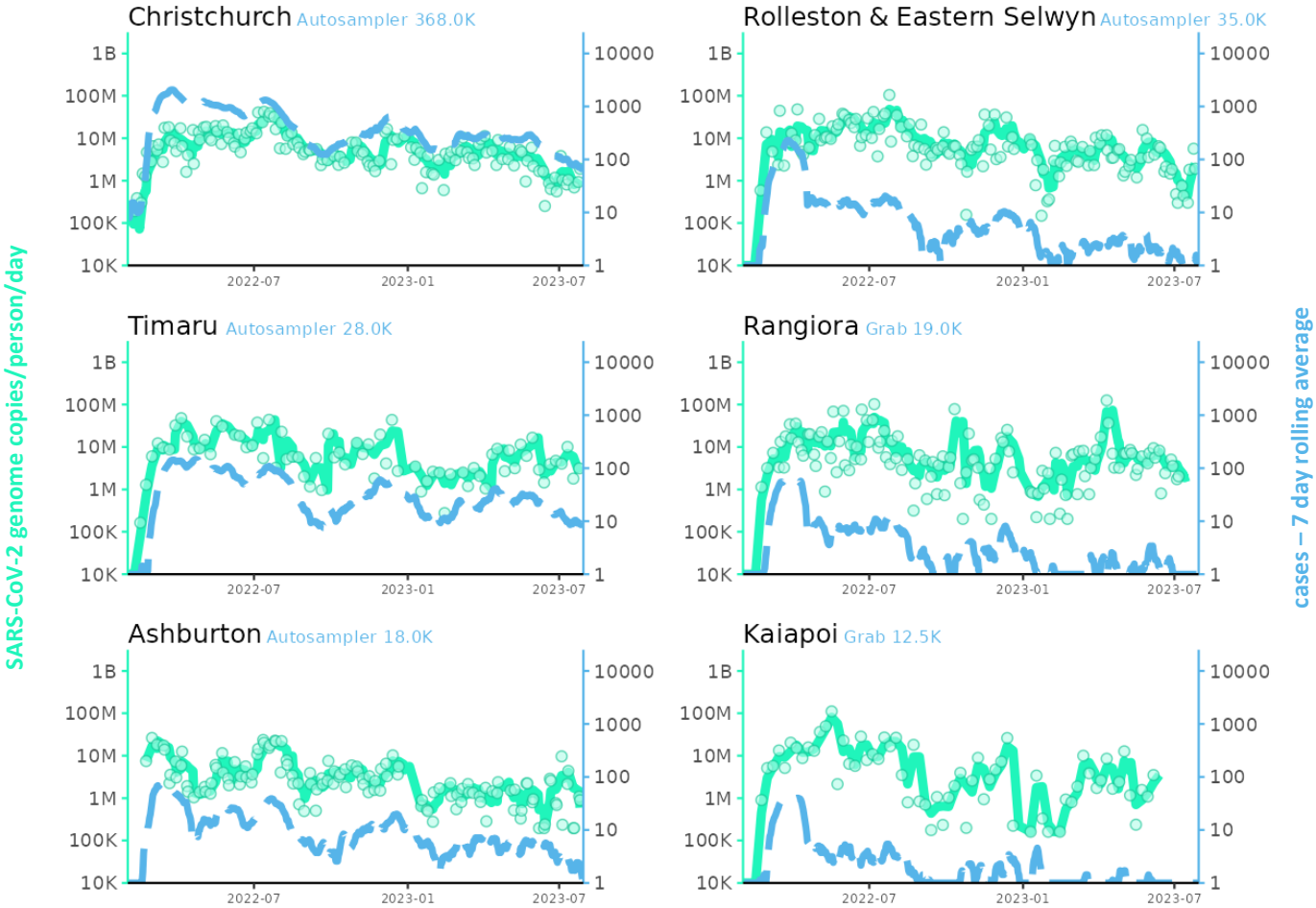
Feb 2023
Apr
Jun


SARS-CoV-2 genome copies/person/day
cases – 7 day rolling average
Christchurch Autosampler 368.0K
Rolleston & Eastern Selwyn Autosampler 35.0K
Timaru Autosampler 28.0K
Rangiora Grab 19.0K
Ashburton Autosampler 18.0K
Kaiapoi Grab 12.5K
1B
100M
10M
1M
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10K
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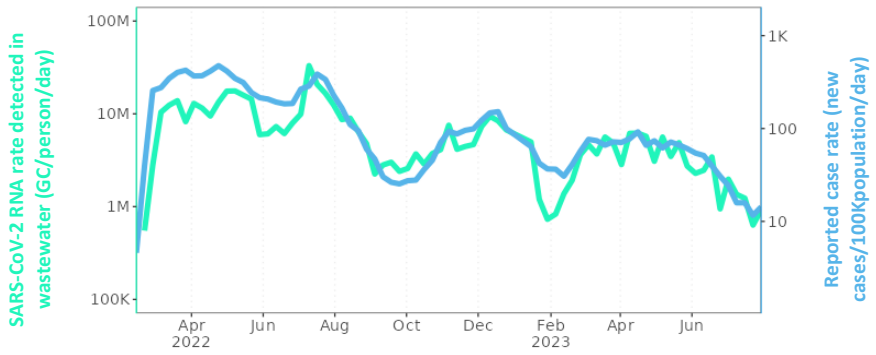
1
2022-07
2023-01
2023-07

Otago


SARS-CoV-2 RNA rate detected in wastewater (GC/person/day)
100M
10M
1M
100K
1K
100
10
Reported case rate (new cases/100Kpopulation/day)
Apr 2022
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Feb 2023
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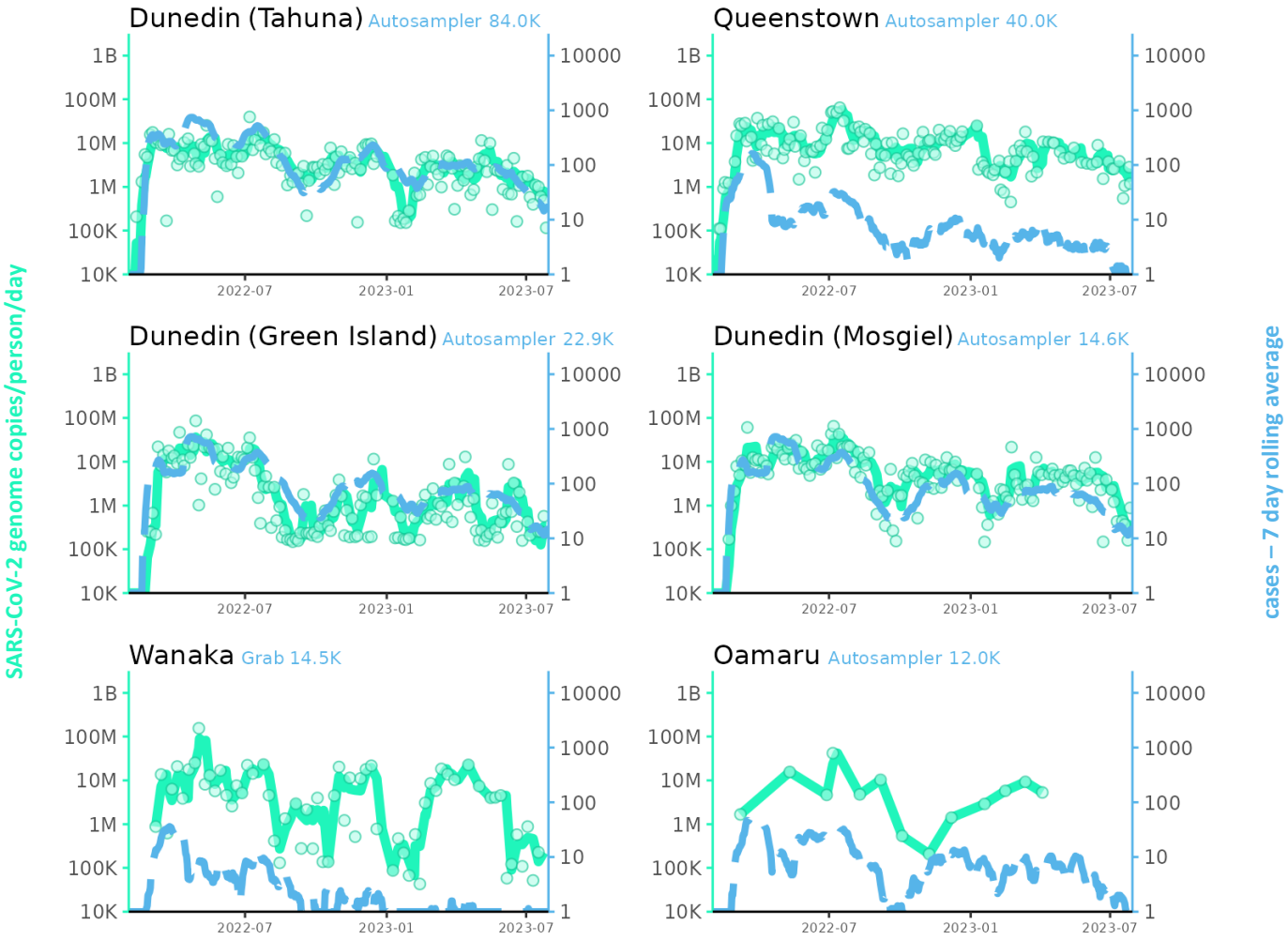
Jun


Dunedin (Tahuna) Autosampler 84.0K
Queenstown Autosampler 40.0K
Dunedin (Green Island) Autosampler 22.9K
Dunedin (Mosgiel) Autosampler 14.6K
Wanaka Grab 14.5K
Oamaru Autosampler 12.0K
SARS-CoV-2 genome copies/person/day
cases – 7 day rolling average
1B
100M
10M
1M
100K
10K
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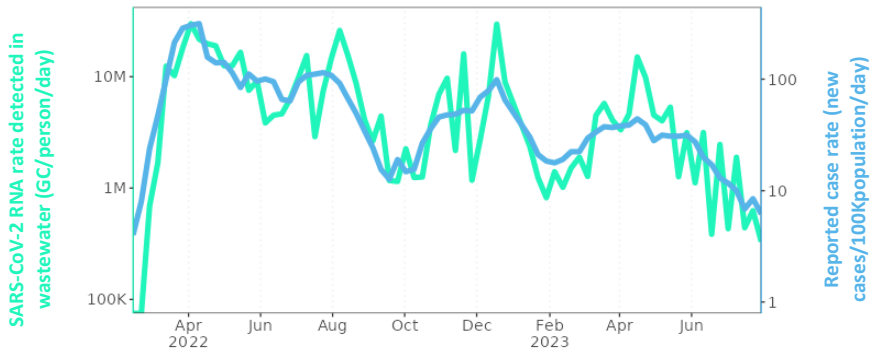
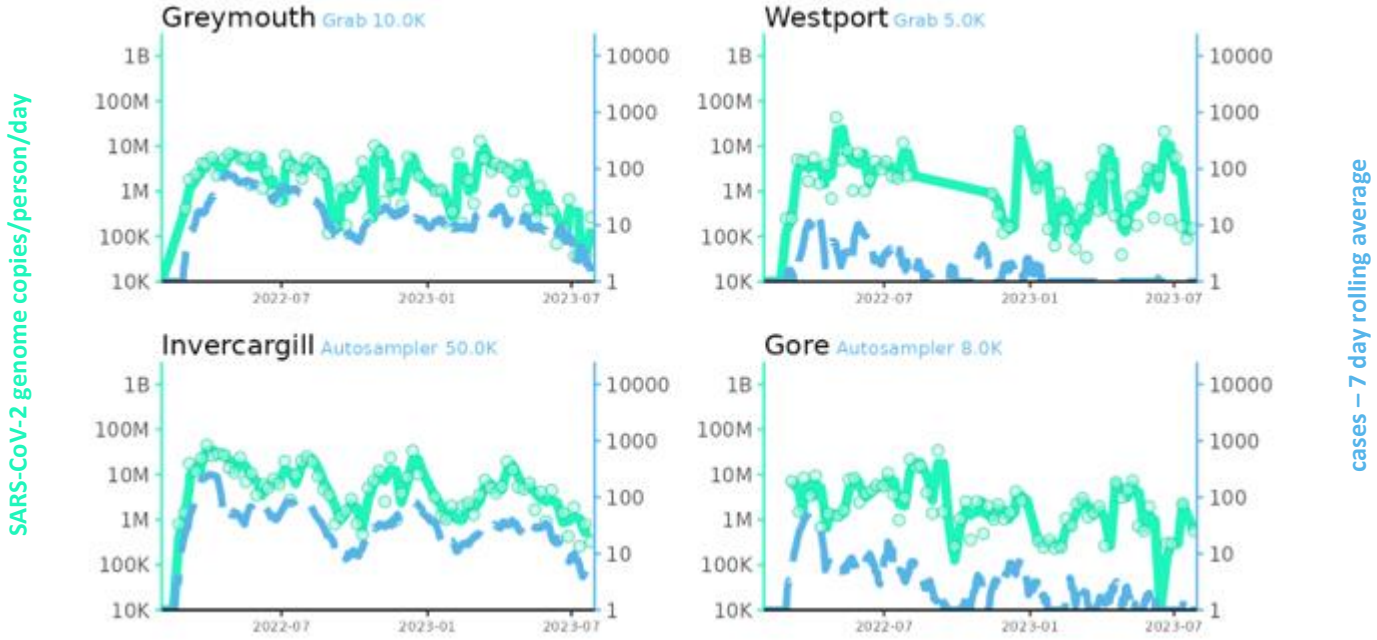
10
1
2022-07
2023-01
2023-07

Southland & West Coast





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 $\log_{10}$ 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.

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:

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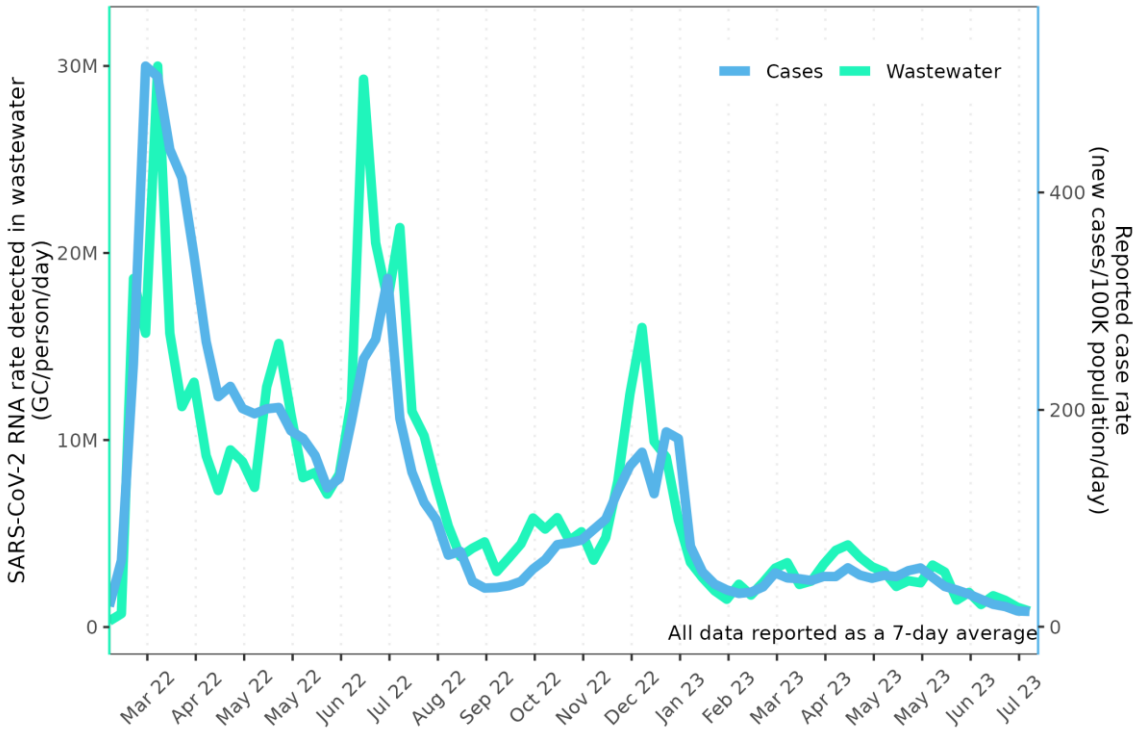
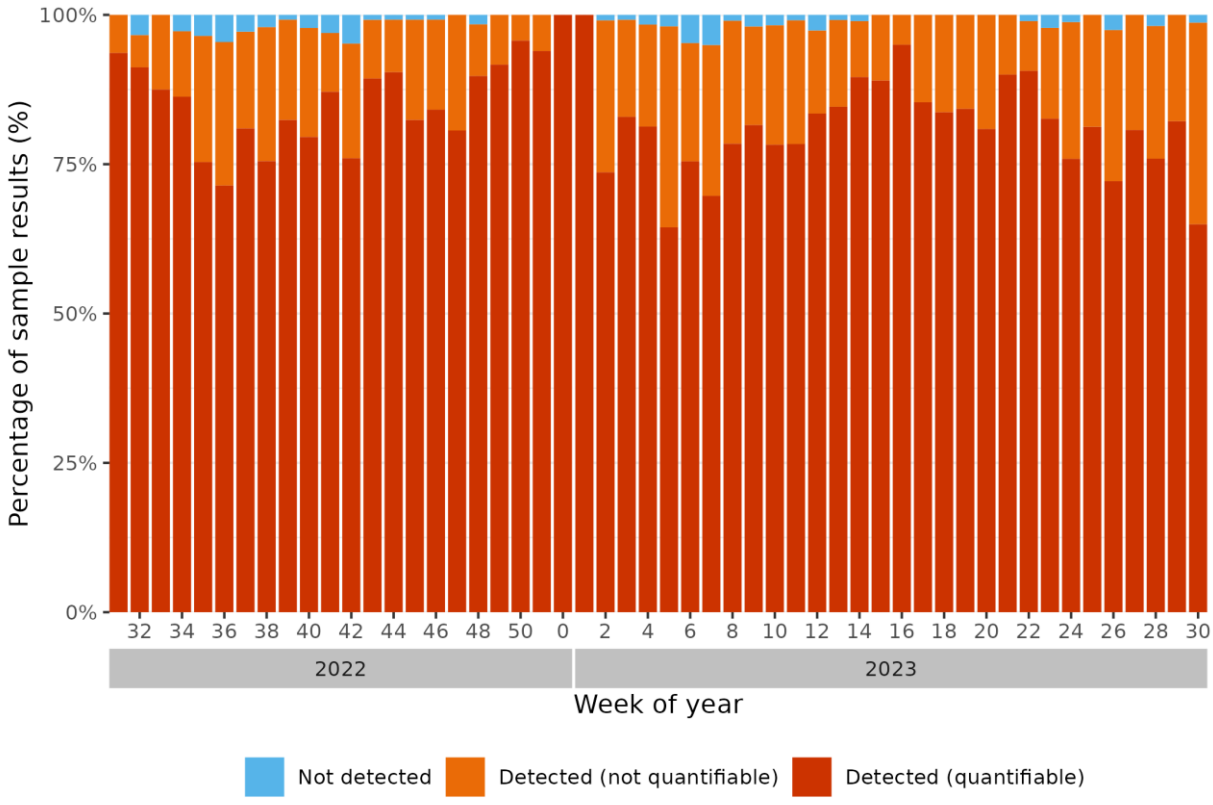
Appendix A. National Results

Time series plotted on linear scale



Detections for the past 52 weeks



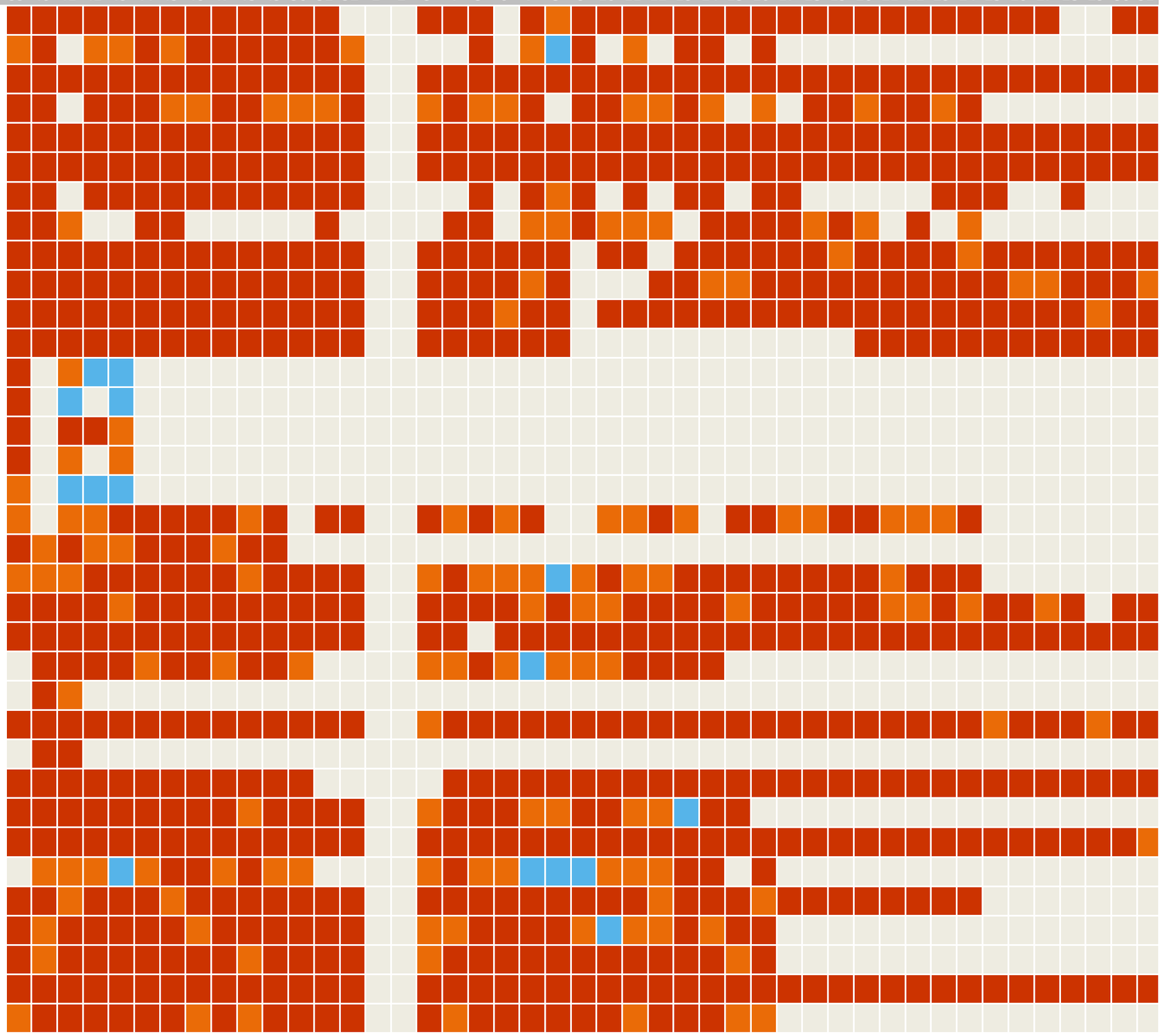
Appendix B. Site Results Weekly Summary

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

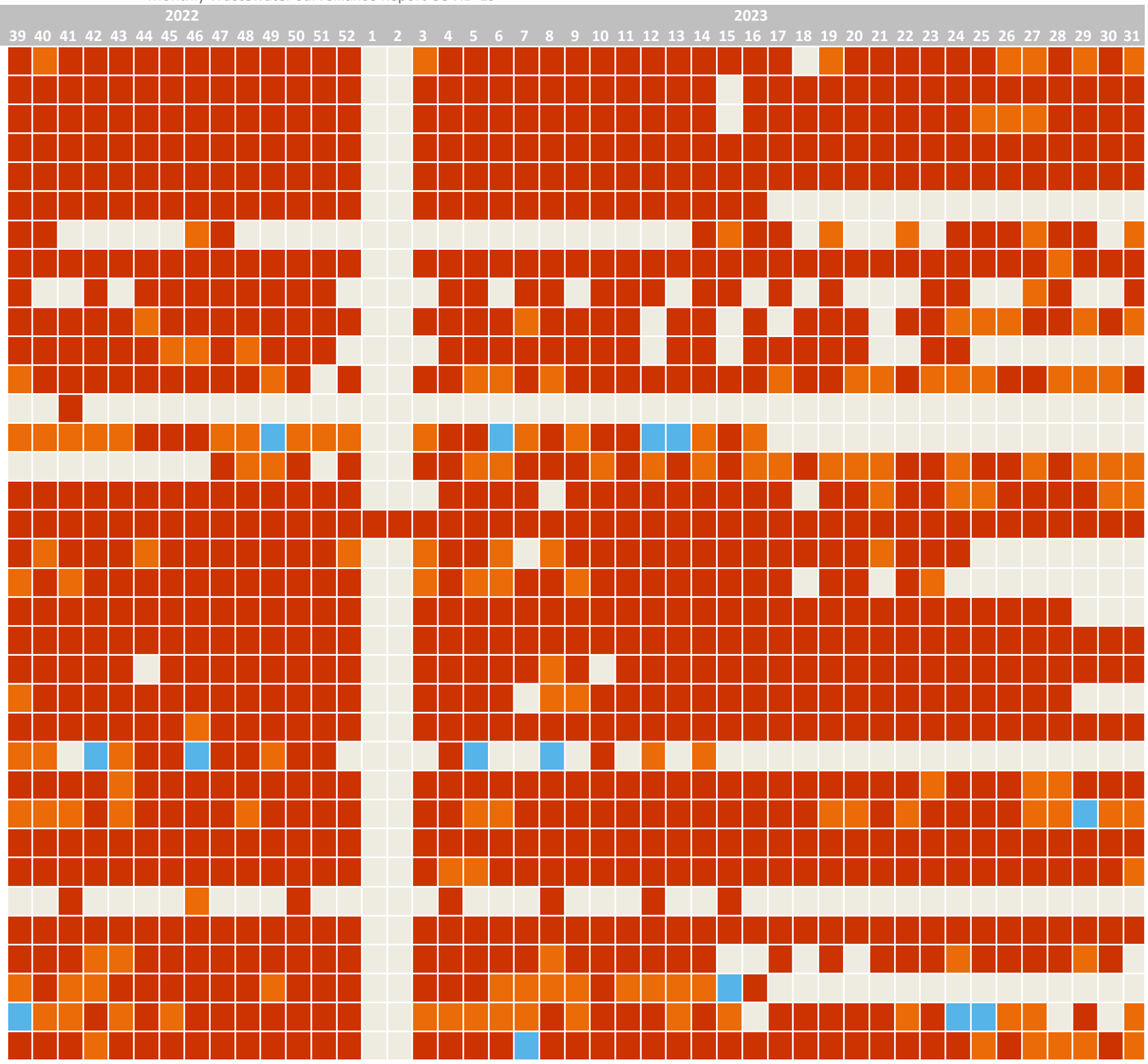
Key: Detected **Detected (not quantified)** **Not detected** **Not tested**

region	Site	Population	SampleType	2022 39	40	41	42	43	44	45	46	47	48	49	50	51	52	2023 1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31
Northland	Dargaville	5,000	Grab																																												
	Hikurangi	1,730	Grab																																												
	Kaiwaka	400	Grab																																											
	Mangawhai	1,100	Grab																																											
	Maungaturoto	1,300	Grab																																										
	Ruakaka	4,500	Grab																																										
	Whangarei	65,000	Autosampler																																											
Auckland	Army Bay	42,000	Autosampler																																											
	Auckland East	680,000	Autosampler																																										
	Auckland Southwest	120,000	Autosampler																																										
	Auckland West	315,000	Autosampler																																											
	Beachlands	6,760	Grab																																										
	Clarks Beach	2,000	Grab																																											
	Helensville	3,800	Autosampler																																											
	Kawakawa Bay	600	Grab																																										
	North Shore	240,000	Autosampler																																												
	Omaha	1,000	Autosampler																																										
	Pukekohe	20,900	Autosampler																																										
	Snells/Algies	4,000	Autosampler																																											
	Waiuku	7,900	Grab																																										
	Warkworth	3,500	Autosampler																																											
	Wellsford	1,720	Autosampler																																										
Waikato	Cambridge	20,100	Autosampler																																											
	Hamilton	169,000	Autosampler																																										
	Taupo	23,000	Auto/grab																																											
	Te Awamutu	13,100	Autosampler																																										
	Thames	7,500	Autosampler																																										
	Whangamata	4,000	Autosampler																																										
	Whitianga	6,600	Autosampler																																										
Bay of Plenty	Katikati	5,500	Autosampler																																										

region	Site	Population	SampleType
	Kawerau	7,000	Autosampler
	Maketu	1,300	Autosampler
	Mt	65,000	Autosampler
	Opotiki	3,800	Autosampler
	Rotorua	59,000	Autosampler
	Tauranga	50,000	Autosampler
	Te Puke	9,700	Autosampler
	Waihi Beach	3,600	Autosampler
	Whakatāne	21,020	Autosampler
Gisborne	Gisborne	37,000	Autosampler
Hawke's Bay	Hastings	80,000	Autosampler
	Napier	55,000	Autosampler
	Otane	640	Autosampler
	Porangahau	317	Grab
	Takapau	534	Autosampler
	Te Paerahi	106	Grab
	Waipawa	2,250	Autosampler
	Waipukurau	4,610	Autosampler
	Wairoa	4,400	Grab
Taranaki	Eltham	2,007	Autosampler
	Hawera	12,000	Autosampler
	New Plymouth	88,000	Autosampler
Manawatu-Whanganui	Dannevirke	5,697	Grab
	Eketahuna	1,630	Grab
	Levin	21,200	Autosampler
	Pahiatua	2,797	Grab
	Palmerston North	90,000	Autosampler
	Taumarunui	4,000	Grab
	Whanganui	44,500	Autosampler
	Woodville	1,657	Grab
Wellington	Carterton	5,800	Grab
	Featherston	2,500	Grab
	Greytown	2,438	Grab
	Hutt Valley	133,000	Autosampler
	Martinborough	1,641	Grab



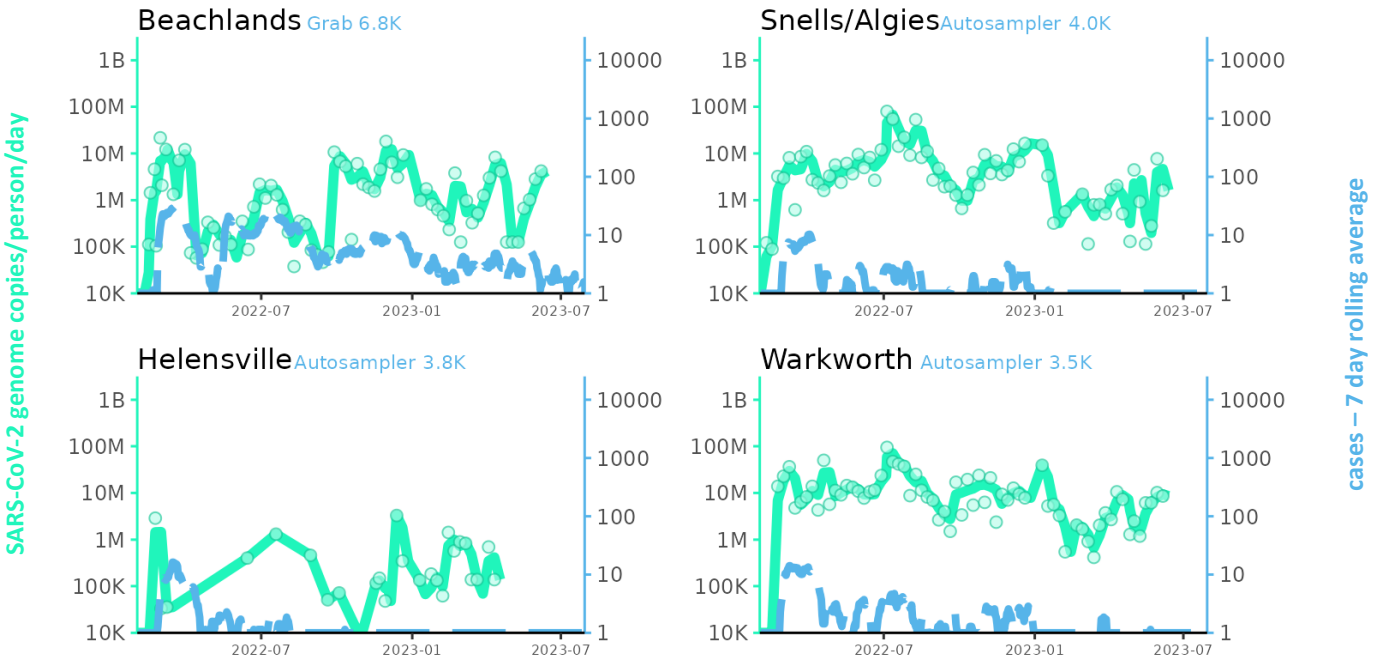
region	Site	Population	SampleType
	Masterton	20,700	Auto/grab
	Otaki	3,500	Autosampler
	Paraparaumu	49,000	Autosampler
	Porirua	85,000	Autosampler
	Wellington (Moa Point)	168,000	Autosampler
	Wellington (Western)	14,000	Autosampler
Tasman	Motueka	8,300	Autosampler
Nelson	Nelson Central/North	26,000	Autosampler
	Richmond/Nelson South	60,000	Autosampler
Marlborough	Blenheim	31,000	Autosampler
	Picton	5,000	Autosampler
West Coast	Greymouth	10,000	Grab
	Hokitika	2,900	Grab
	Reefton	1,000	Grab
	Westport	5,000	Grab
Canterbury	Ashburton	18,000	Autosampler
	Christchurch	368,000	Autosampler
	Kaiapoi	12,500	Grab
	Leeston	3,900	Autosampler
	Rangiora	19,000	Grab
	Rolleston & Eastern	35,000	Autosampler
	Timaru	28,000	Autosampler
	Woodend	7,600	Grab
Otago	Alexandra	6,200	Autosampler
	Balclutha	4,100	Grab
	Cromwell	7,100	Autosampler
	Dunedin (Green Island)	22,900	Autosampler
	Dunedin (Mosgiel)	14,600	Autosampler
	Dunedin (Tahuna)	84,000	Autosampler
	Oamaru	12,000	Autosampler
	Queenstown	40,000	Autosampler
	Wanaka	14,500	Grab
Southland	Bluff	2,000	Autosampler
	Gore	8,000	Autosampler
	Invercargill	50,000	Autosampler



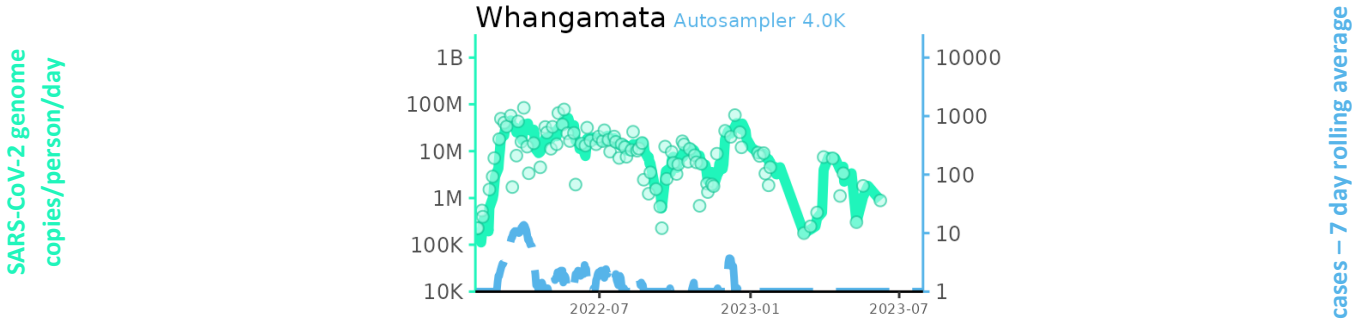
Appendix C

Additional Site Graphs

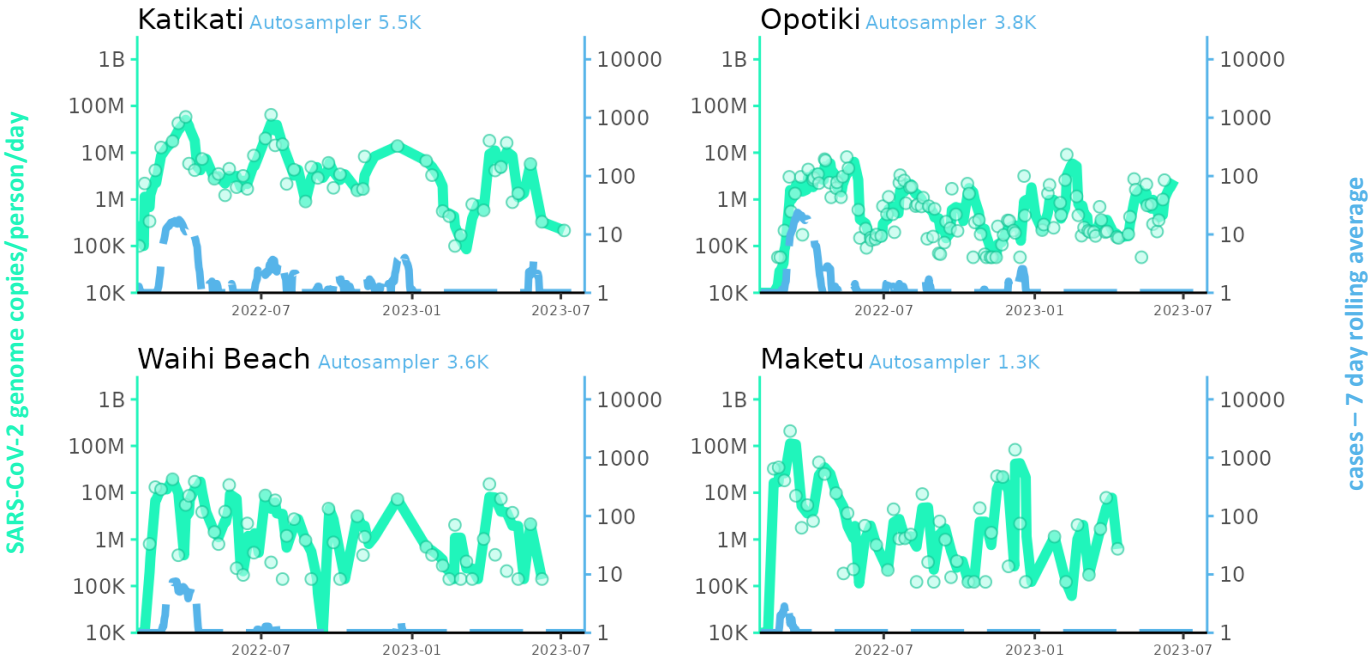
Auckland



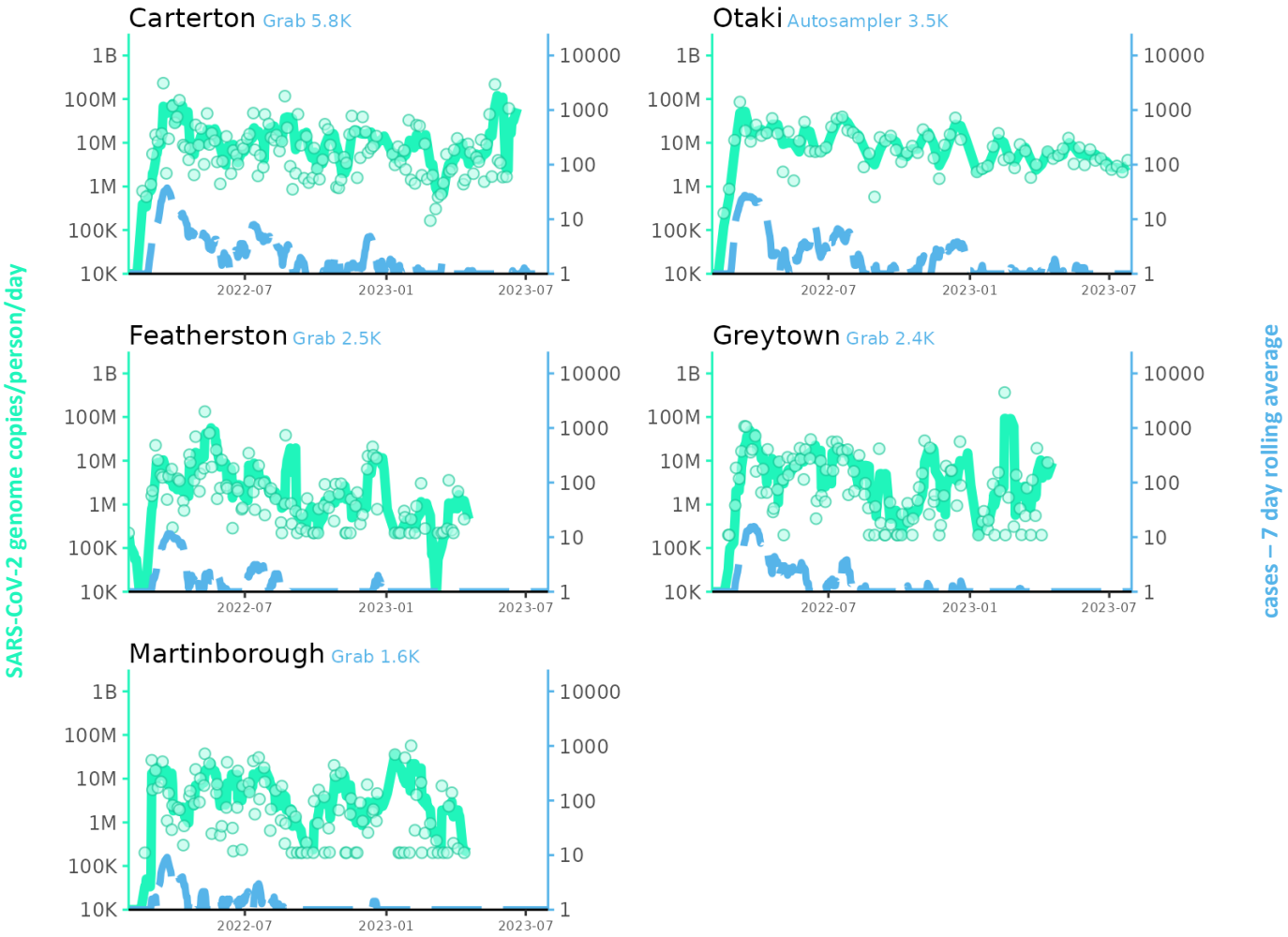
Waikato



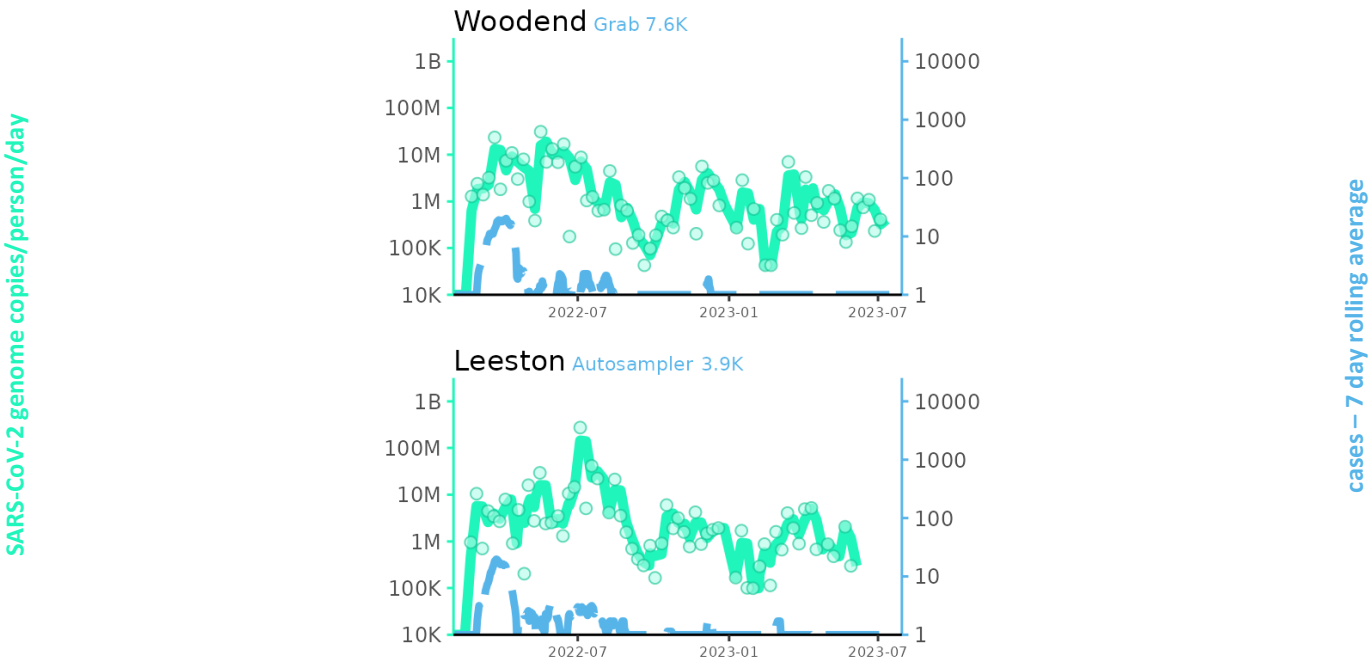
Bay of Plenty



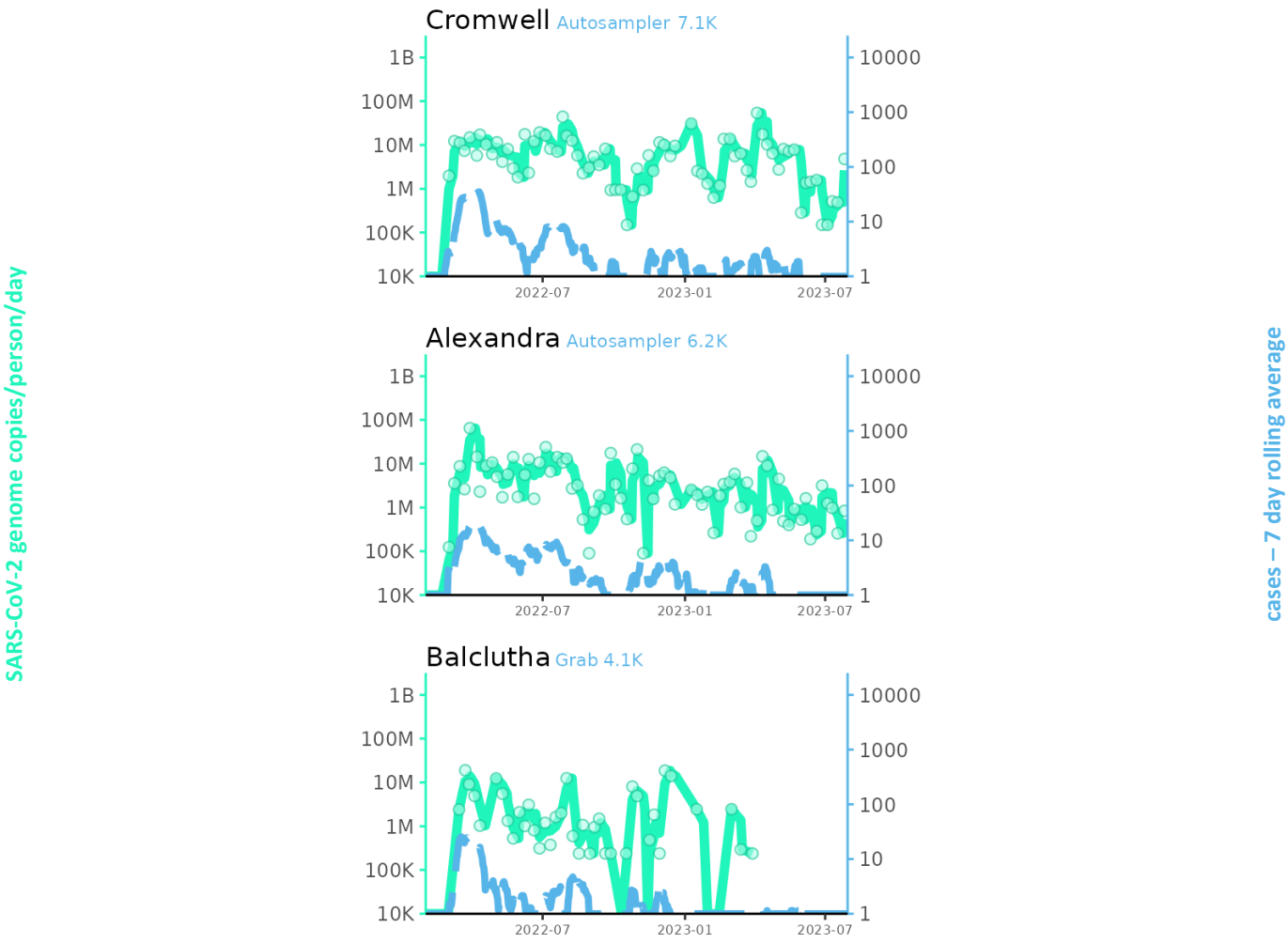
Wellington


Carterton Grab 5.8K
Otaki Autosampler 3.5K
Featherston Grab 2.5K
Greytown Grab 2.4K
Martinborough Grab 1.6K
SARS-CoV-2 genome copies/person/day
cases – 7 day rolling average
1B
100M
10M
1M
100K
10K
10000
1000
100
10
1
2022-07
2023-01
2023-07

Canterbury


Woodend Grab 7.6K
1B
100M
10M
1M
100K
10K
10000
1000
100
10
1
2022-07
2023-01
2023-07
Leeston Autosampler 3.9K
1B
100M
10M
1M
100K
10K
10000
1000
100
10
1
2022-07
2023-01
2023-07
SARS-CoV-2 genome copies/person/day
cases – 7 day rolling average

Otago


Cromwell Autosampler 7.1K
Alexandra Autosampler 6.2K
Balclutha Grab 4.1K
1B
100M
10M
1M
100K
10K
10000
1000
100
10
1
2022-07
2023-01
2023-07
SARS-CoV-2 genome copies/person/day
cases – 7 day rolling average