New Zealand Wastewater Surveillance Programme COVID-19

Monthly Report May 2023

Weeks ending 7 May to 4 June 2023, weeks 18 to 22

Report prepared 14 June 2023

Key Trends & Insights

At the end of April, national SARS-CoV-2 levels averaged 3.07 million genome copies per person per day (GC/p/d). During May, this reduced to a low of 2.16 million GC/p/d in the week ending 14 May 2023, this remained steady for two weeks, before increasing to 3.21 million GC/p/d by the end of the month (week ending 4 June 2023).

100%	70%	XBB
Sites (71/71) where SARS-CoV-2 was detected	NZ population covered by wastewater testing	Most prevalent variant detected (52% in week 22)

- In May 2023, 463 samples were collected across Aotearoa. SARS-CoV-2 RNA was detected in 462/463 (99.7%) samples from 71/71 (100%) of sites.
- The average wastewater SARS-CoV-2 viral load was 803,557 GC/person/day in May, compared to 2,438,981 GC/person/day in April. This equates to a month on month decrease of 67%.
- XBB (includes XBB.1.5 and XBB.1.16) was the most common variant detected in May (~52-71% of national reads per week), with CH.1.1 (includes FK.1.1) also common (~23-34% of national reads per week). Other variants remained rare, although XBC did show an increase in week 22.

National Results

Trends over time

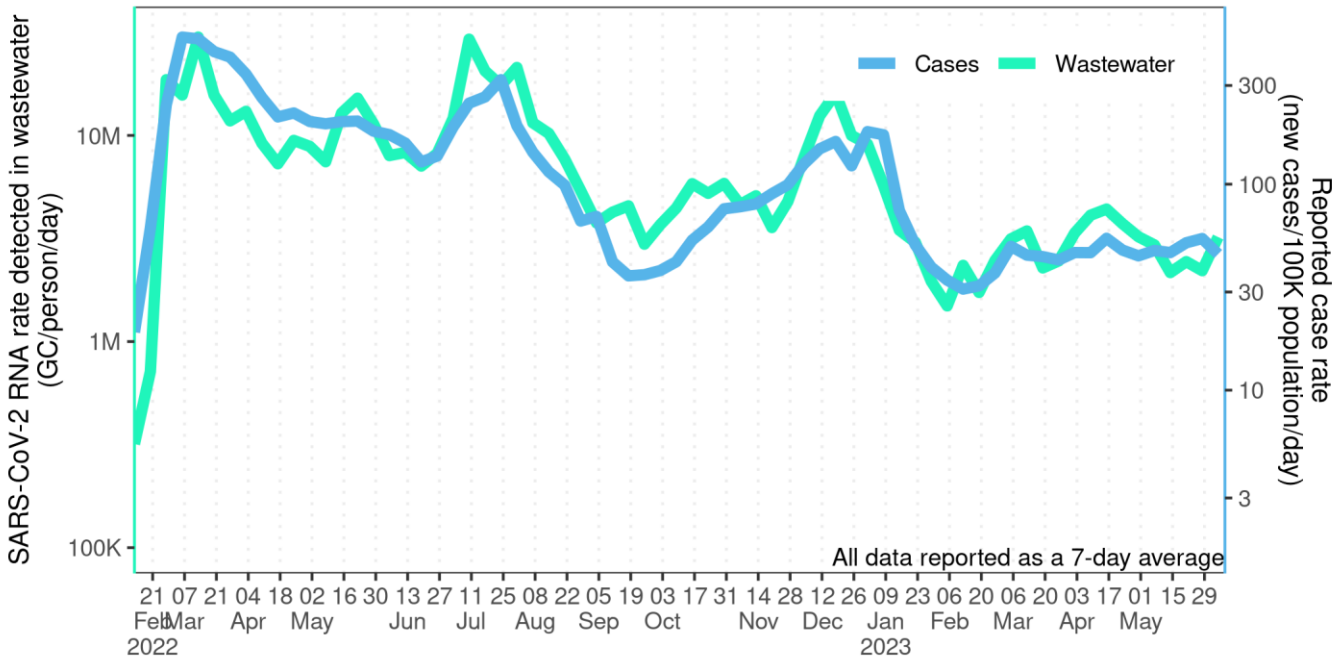


Figure 1. National timeseries of estimated SARS-CoV-2 wastewater rate (GC/person/day, green line) and reported case rate (new cases/100,000 population/day, blue line) on a $\log_{10}$ scale.

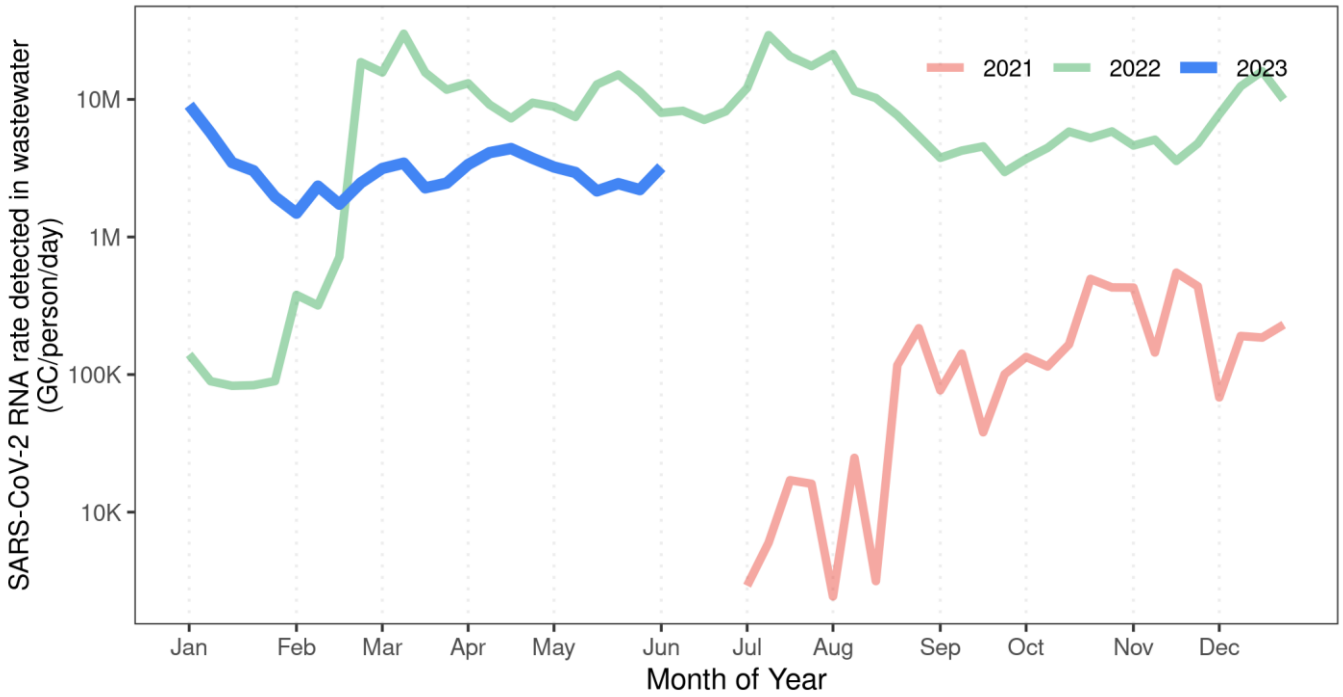


Figure 2. National timeseries of estimated SARS-CoV-2 wastewater rate (GC/person/day) from July 2021 to May 2023 on a $\log_{10}$ scale.

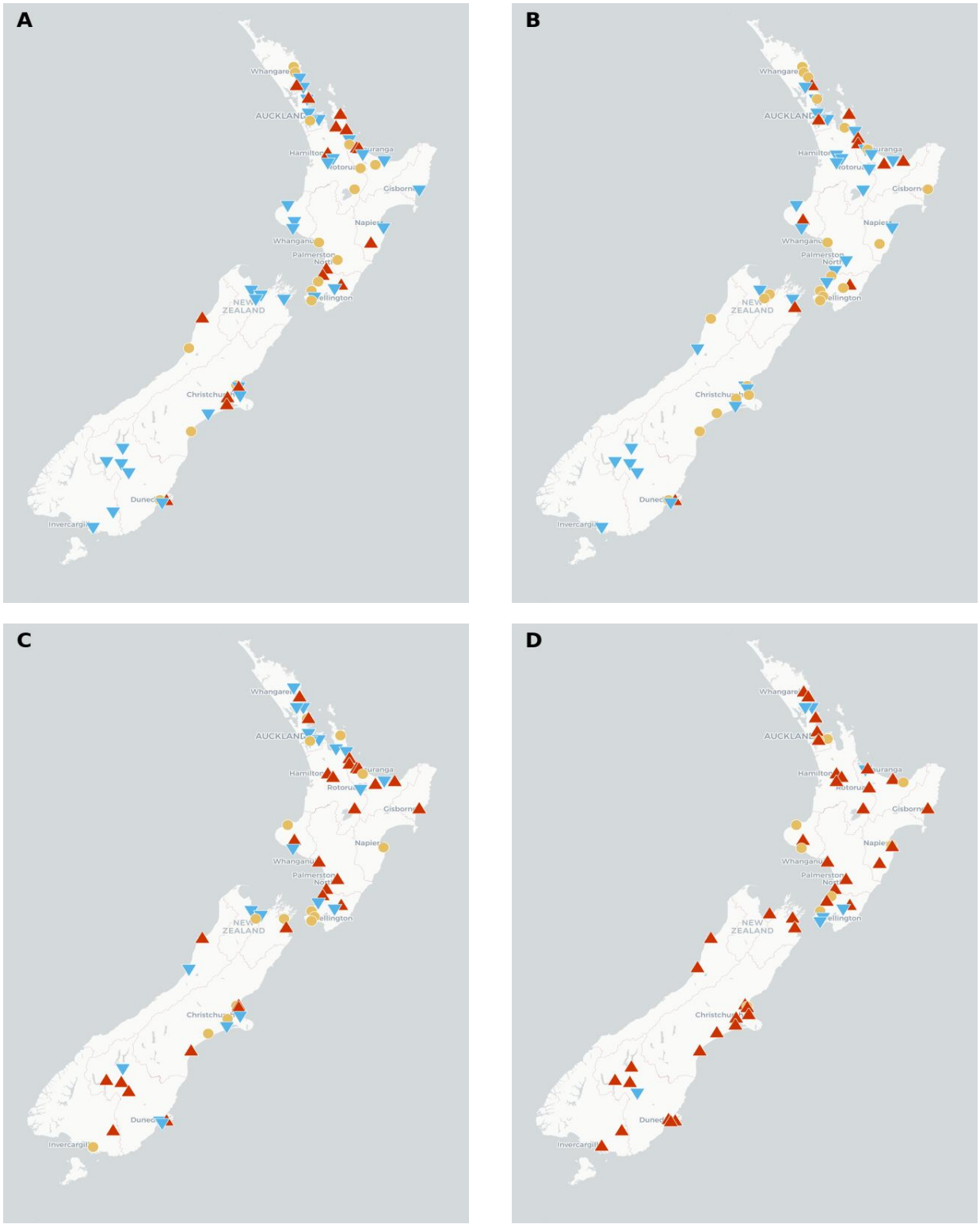


Figure 3. Comparison of SARS-CoV-2 levels for the week ending 4 June 2023 (week 22), compared to levels measured: A) 1 week ago; B) 2 weeks ago; C) 4 weeks ago; D) 12 weeks ago. Only sites with results for both time points are included. When the viral quantity is 30% or more higher this is labelled as 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 May 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 May 2023

XBB (includes **XBB.1.5** and **XBB.1.16**) was frequently detected, comprising ~76% of reads nationally in week (w) 17 (17/19 sites), ~63% of reads nationally in w18 (14/20 sites), ~71% of reads nationally in w19 (15/20 sites), ~67% of reads nationally in w20 (16/20 sites), ~65% of reads nationally in w21 (16/20 sites) and ~52% of reads nationally in w22 (16/19 sites).

CH.1.1 (includes **FK.1.1**) was also frequently detected in week 17 (10/19 sites), w18 (14/20 sites), w19 (8/20 sites), w20 (13/20 sites), w21 (15/20 sites) and w22 (14/19 sites). CH.1.1 comprised ~22-34% of sequencing reads nationally across these four weeks. 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 ~2% of reads in weeks 17, 18 and 20 (2-3 sites per week) and not being detected in weeks 19, 21 and 22.

BA.4/BA.5 (now includes **BQ.1.1**) was only detected in weeks 19, 20 and 22 at a single site (Tauranga in w19, Rotorua in w20 and Auckland West in w22) and accounted for only ~1-3% of national sequence reads in these three weeks.

XBC was relatively steady in weeks 18-21 being detected in week 18 (~1% of national sequencing reads, 1/20 sites), w19 (~5% of reads, 2/20 sites) and w21 (~4% of reads, 4/20 sites). It was not detected in w17 or w20. In week 22, this variant showed an increase to ~16% of national sequencing reads (8/20 sites).

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 May, with minor contributions from other variants, in agreement with clinical WGS results.

	Week 17					Week 18					Week 19					Week 20					Week 21					Week 22				
	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	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)		2	22	76			2	34	63	1	1		23	71	5	1	2	30	67				31	65	4	3		29	52	16

Table 1. Data from 20 wastewater sentinel sites sampled in week 17 (ending 30 April 2023)*, week 18 (ending 7 May 2023), week 19 (ending 14 May 2023), week 20 (ending 21 May 2023), week 21 (ending 28 May 2023) and week 22 (ending 4 June 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.

*week 17 variant data not included in the April report

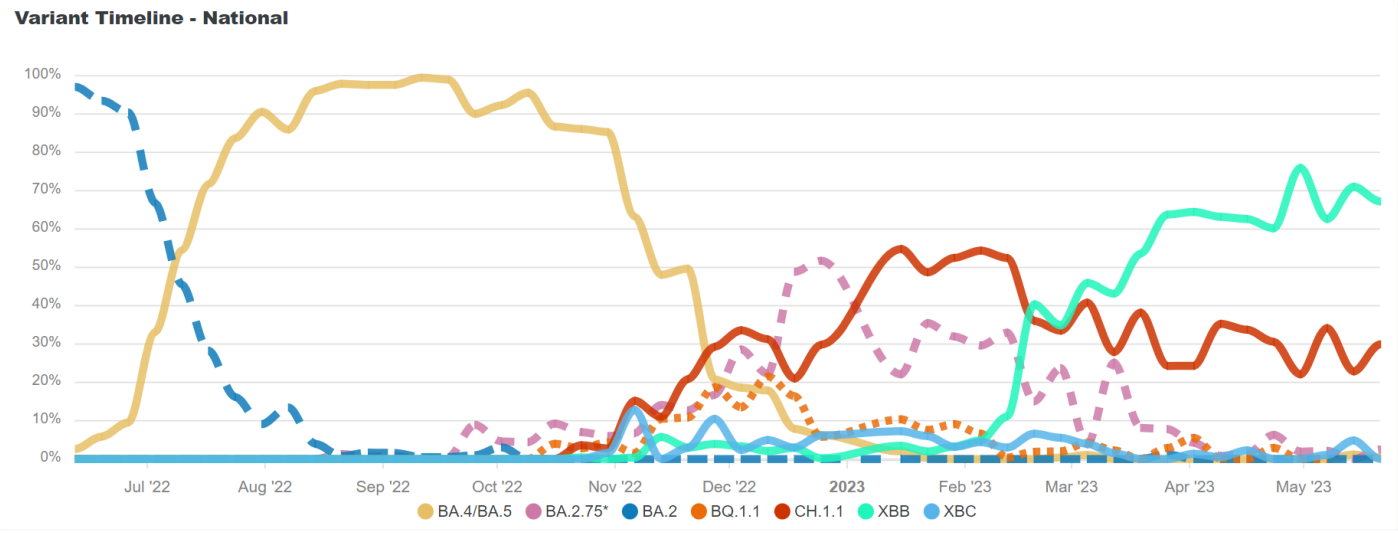


Figure 4. Variant prevalence over time at a national scale (average). Data are collected from up to 20 sentinel sites each week.

Trends in Ministry of Health Regions

Regional analysis of the wastewater data (Figure 7) indicates relatively stable SARS-CoV-2 levels in most regions in the early weeks of May, but this has increased in the last week of the month.

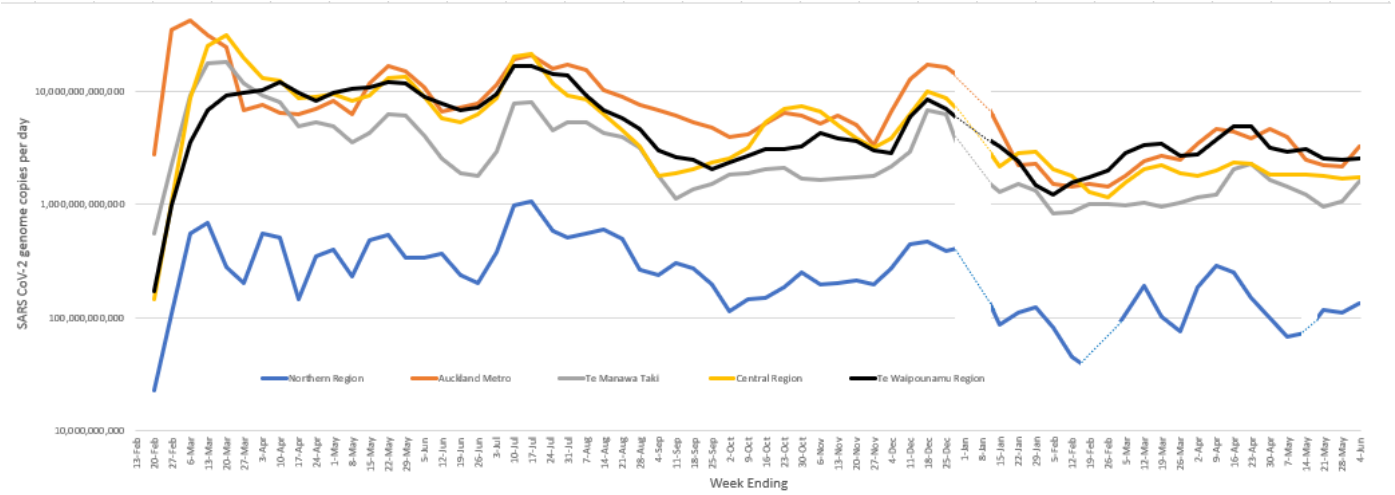


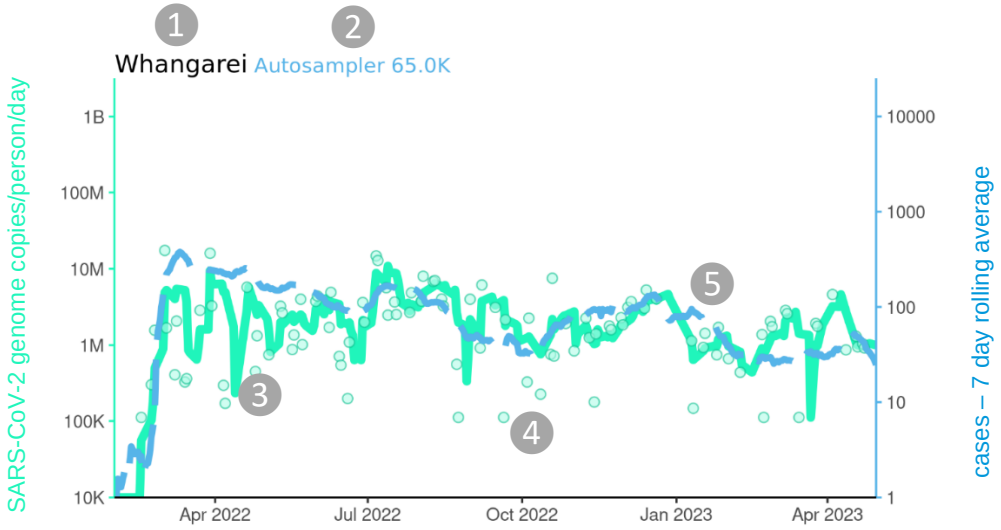
Figure 5. Two week rolling average of total SARS-CoV-2 genome copies detected per day in the five Ministry of Health regions. Dashed lines are inferred levels during periods when samples were either not collected (Christmas period) or insufficient numbers collected (due to weather impacts) for the region.

Regional Trend Time Series

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).

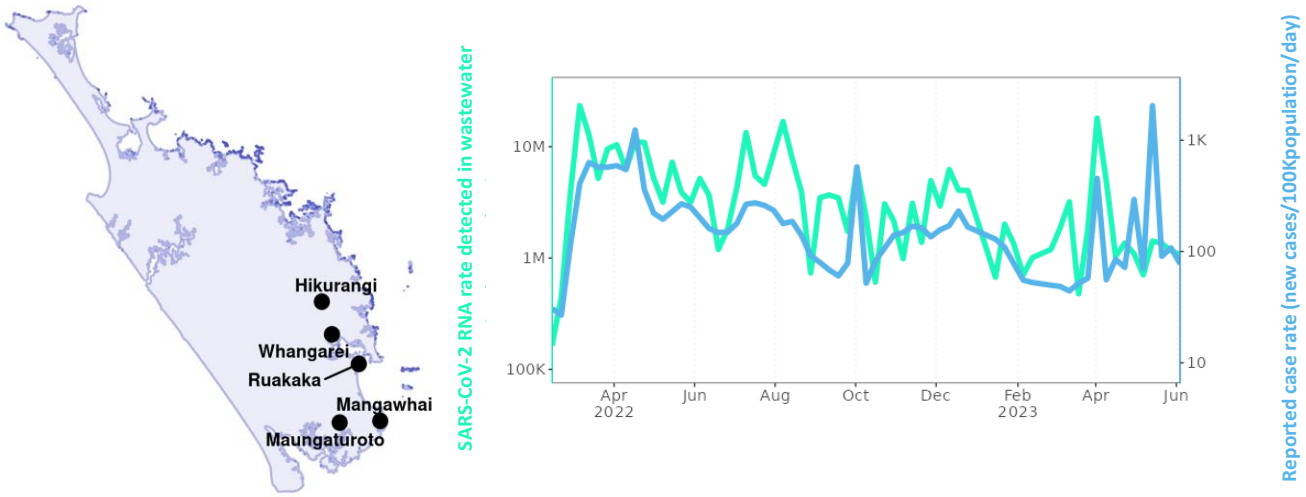
Interpreting Site Graphs

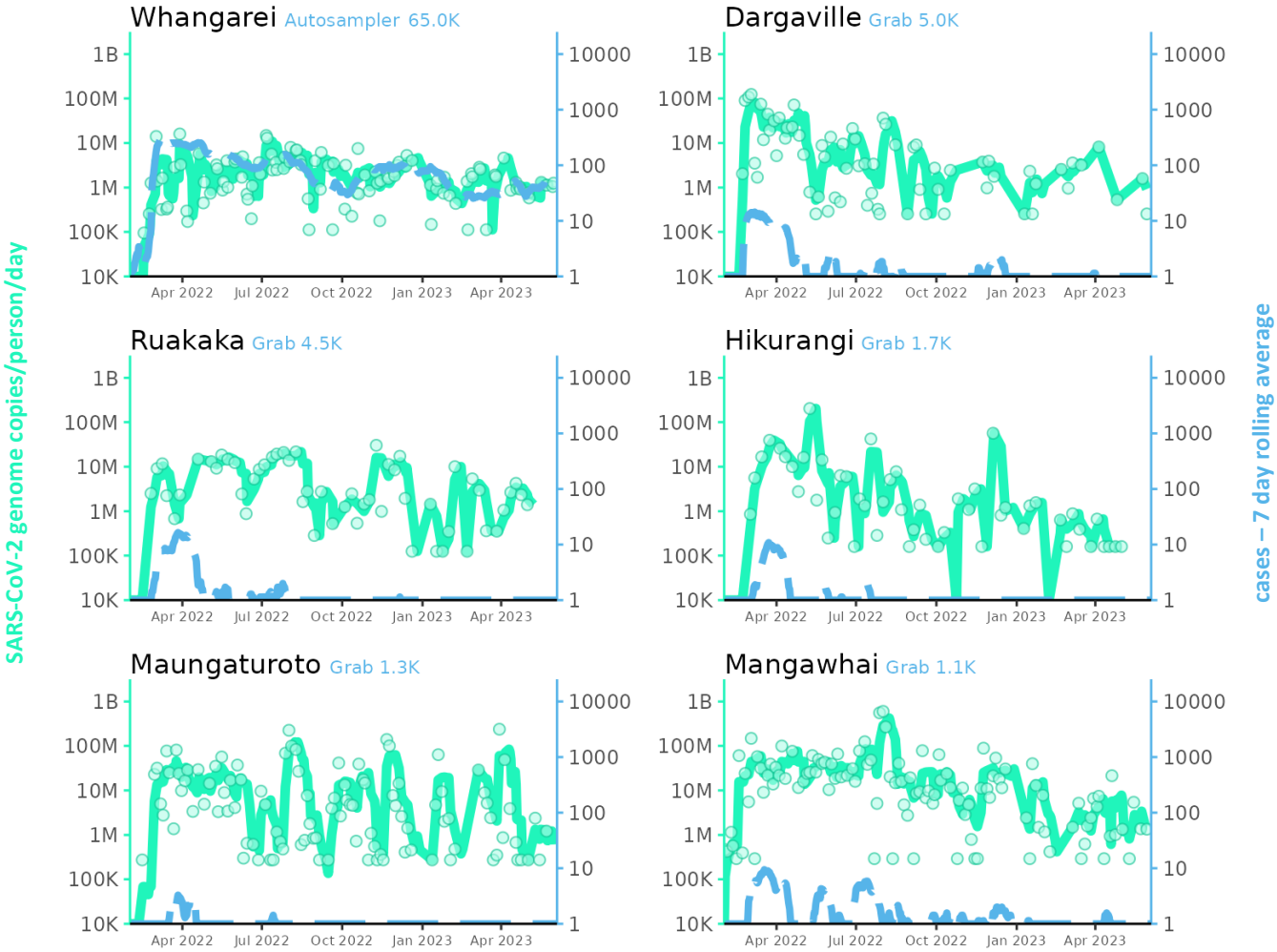


1. Site Name
2. Sample collection method and population. Results based on autosampler may be more representative than grab sample-based results.
3. **Wastewater** results shown as solid line (**green line**) | 14-day average of genome copies/person/day on a $\log_{10}$ scale.
4. Individual results samples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

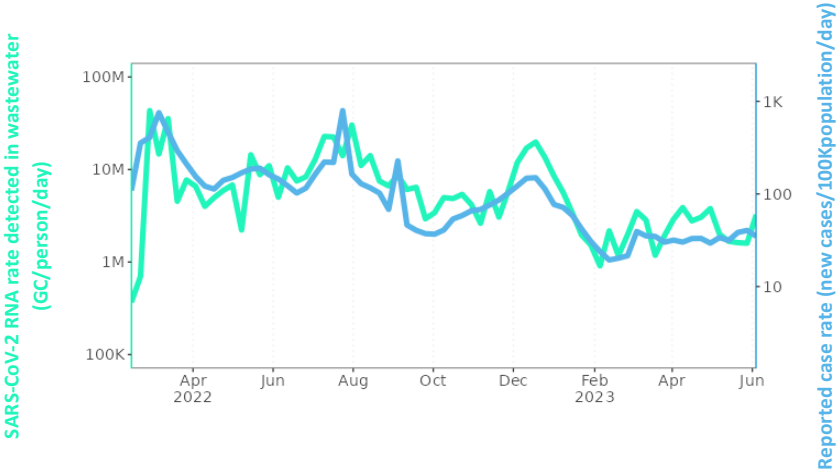
Northland

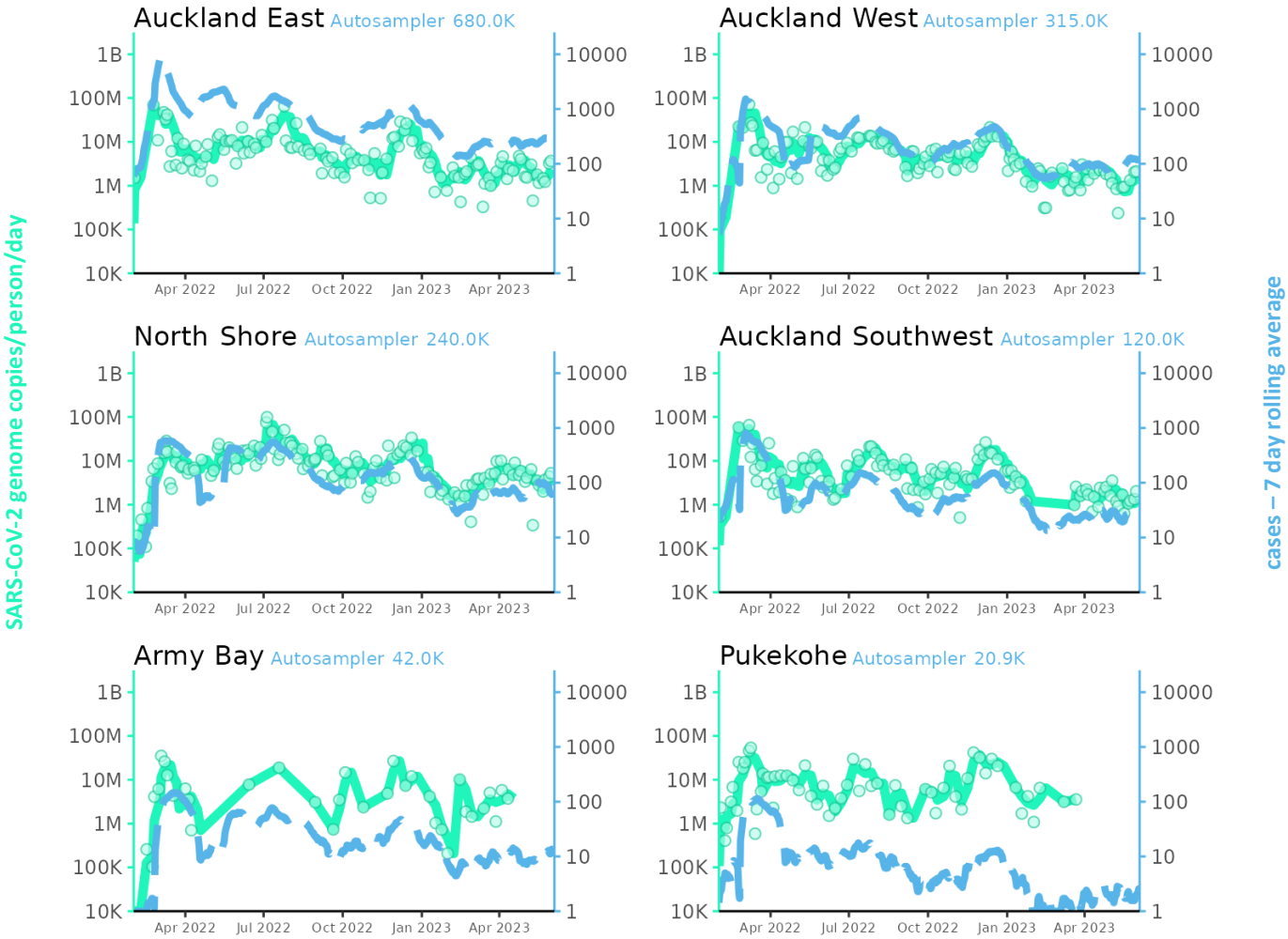

Hikurangi
Whangarei
Ruakaka
Mangawhai
Maungaturoto
SARS-CoV-2 RNA rate detected in wastewater
10M
1M
100K
1K
100
10
Apr 2022
Jun
Aug
Oct
Dec
Feb 2023
Apr
Jun
Reported case rate (new cases/100Kpopulation/day)


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

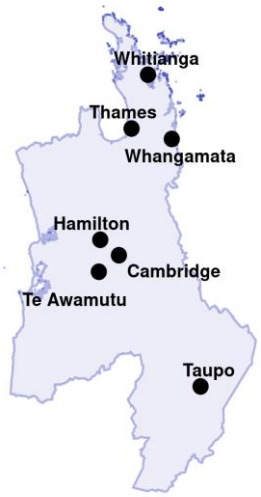
Auckland

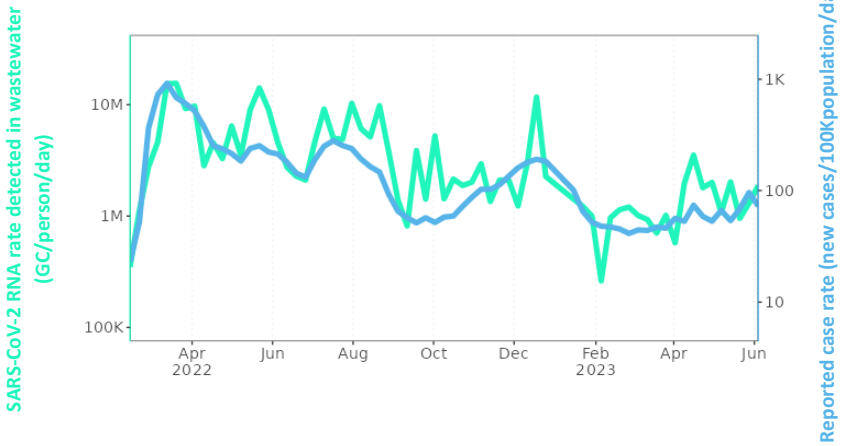

Warkworth
Snells/Algies
North Shore
Auckland West
Beachlands
Auckland East
Auckland Southwest

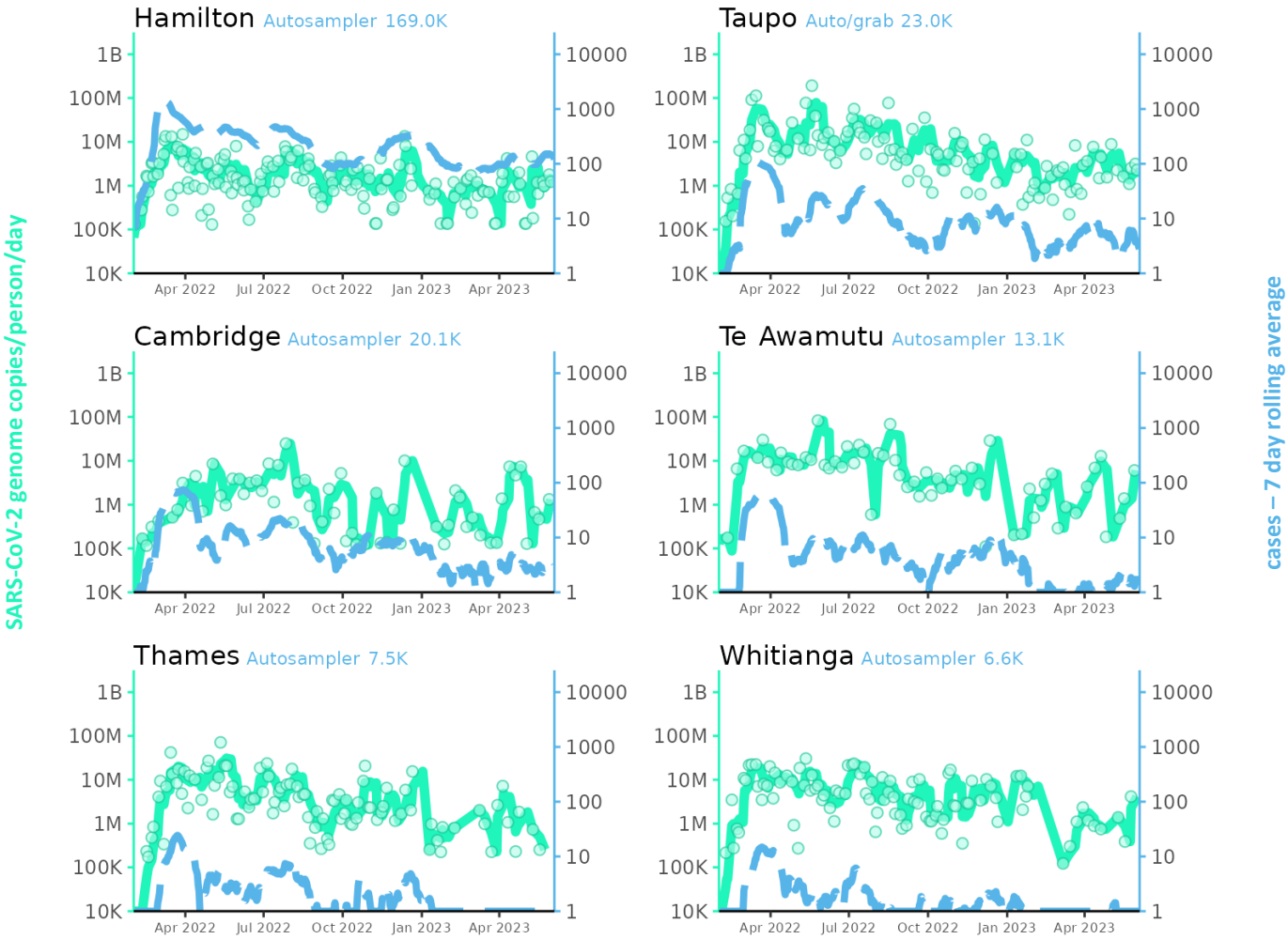

SARS-CoV-2 RNA rate detected in wastewater (GC/person/day)
100M
10M
1M
100K
Apr 2022
Jun
Aug
Oct
Dec
Feb 2023
Apr
Jun
1K
100
10
Reported case rate (new cases/100Kpopulation/day)


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
Army Bay Autosampler 42.0K
Pukekohe Autosampler 20.9K
1B
100M
10M
1M
100K
10K
10000
1000
100
10
1
Apr 2022
Jul 2022
Oct 2022
Jan 2023
Apr 2023
cases – 7 day rolling average

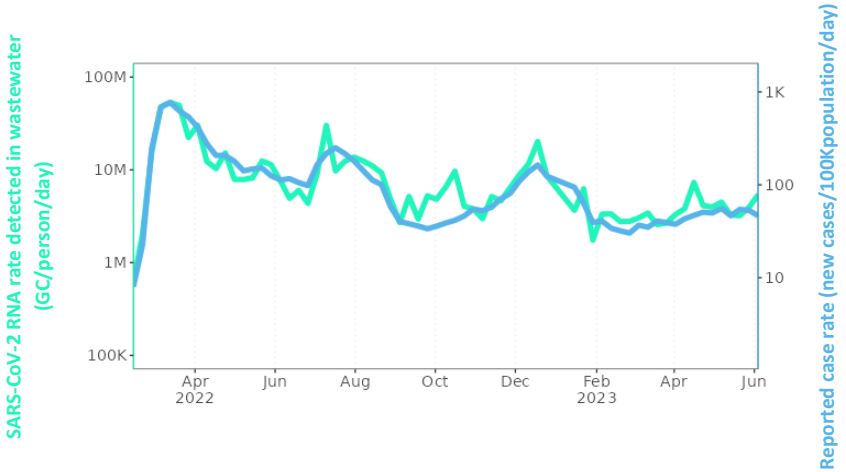
Waikato

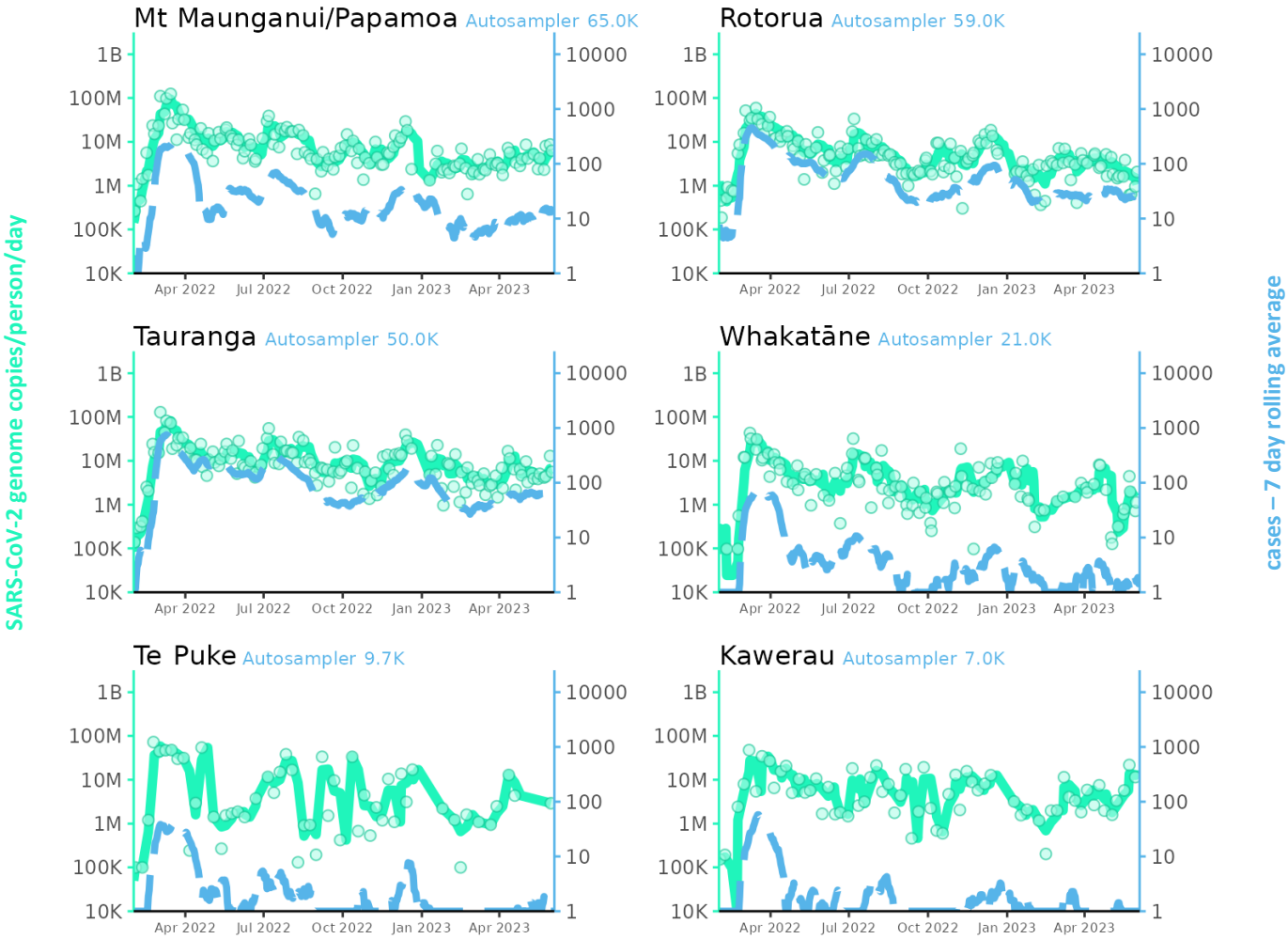

Whitianga
Thames
Whangamata
Hamilton
Cambridge
Te Awamutu
Taupo


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

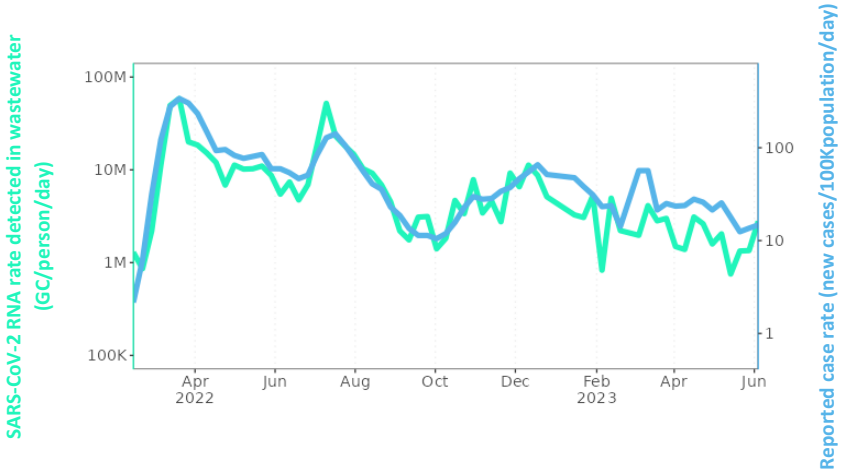

SARS-CoV-2 genome copies/person/day
Hamilton Autosampler 169.0K
Taupo Auto/grab 23.0K
Cambridge Autosampler 20.1K
Te Awamutu Autosampler 13.1K
Thames Autosampler 7.5K
Whitianga Autosampler 6.6K
1B
100M
10M
1M
100K
10K
10000
1000
100
10
1
Apr 2022
Jul 2022
Oct 2022
Jan 2023
Apr 2023
cases – 7 day rolling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

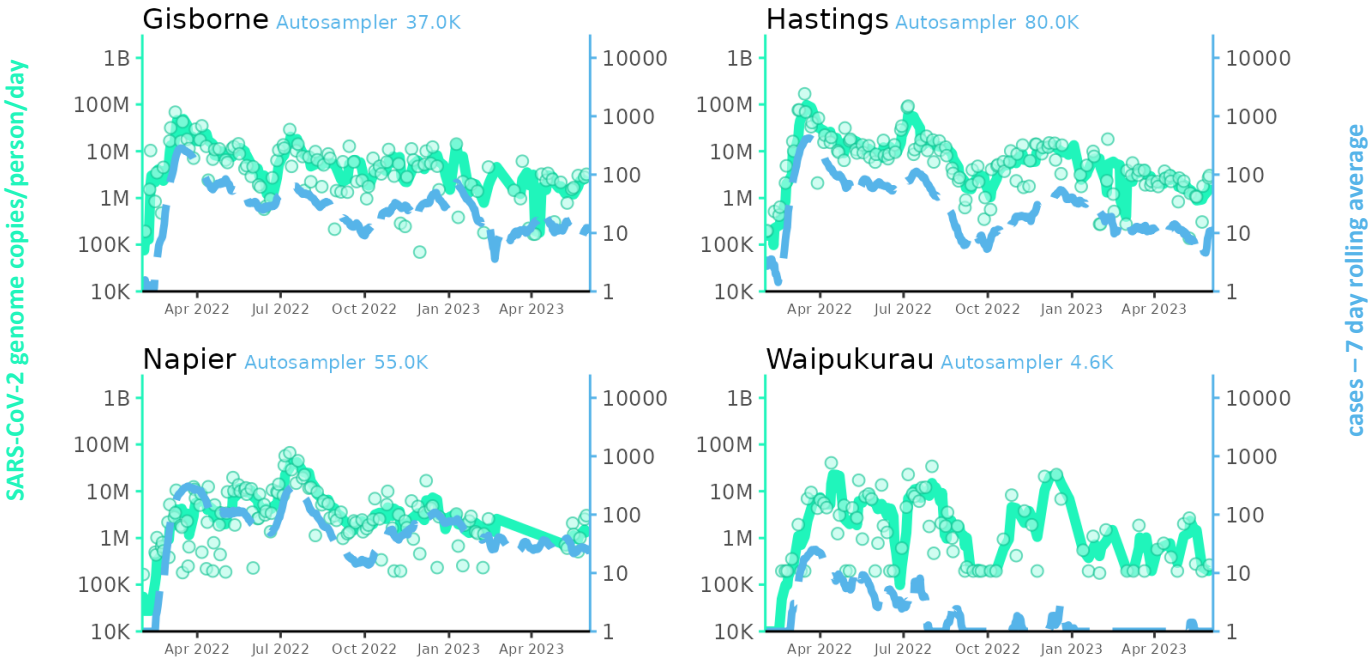
Bay of Plenty





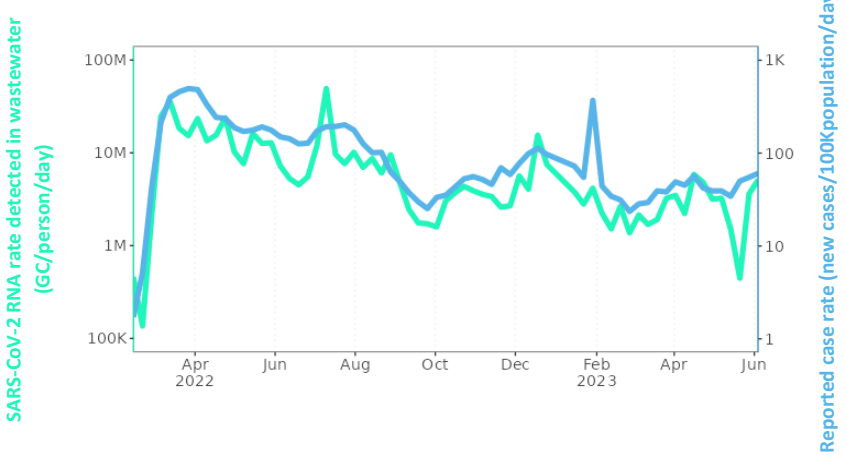
Hawke's Bay & Gisborne

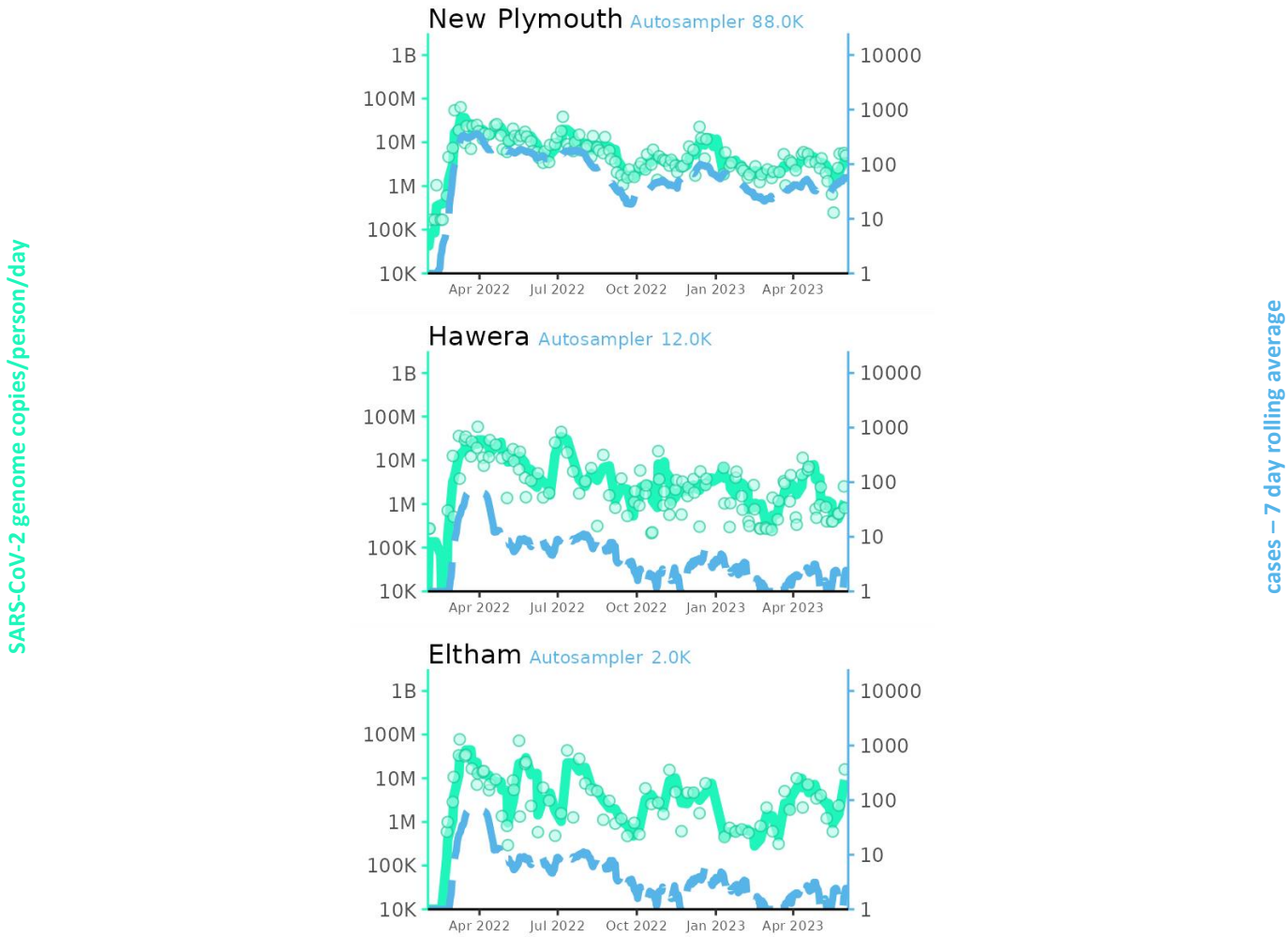




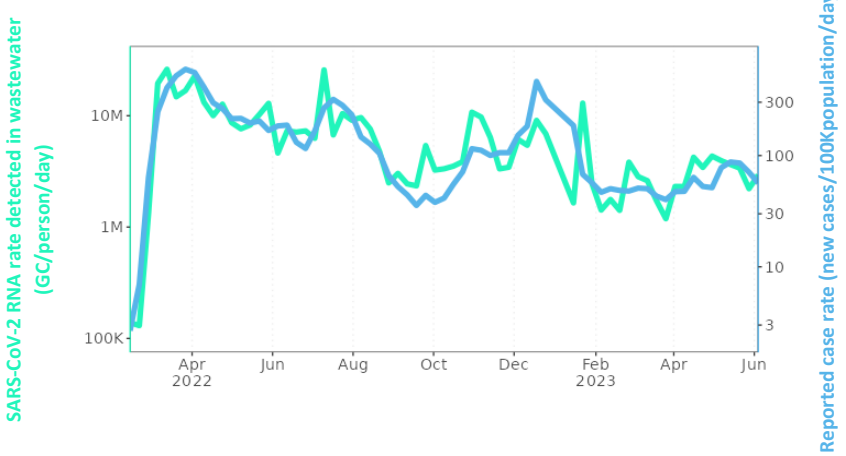
Taranaki

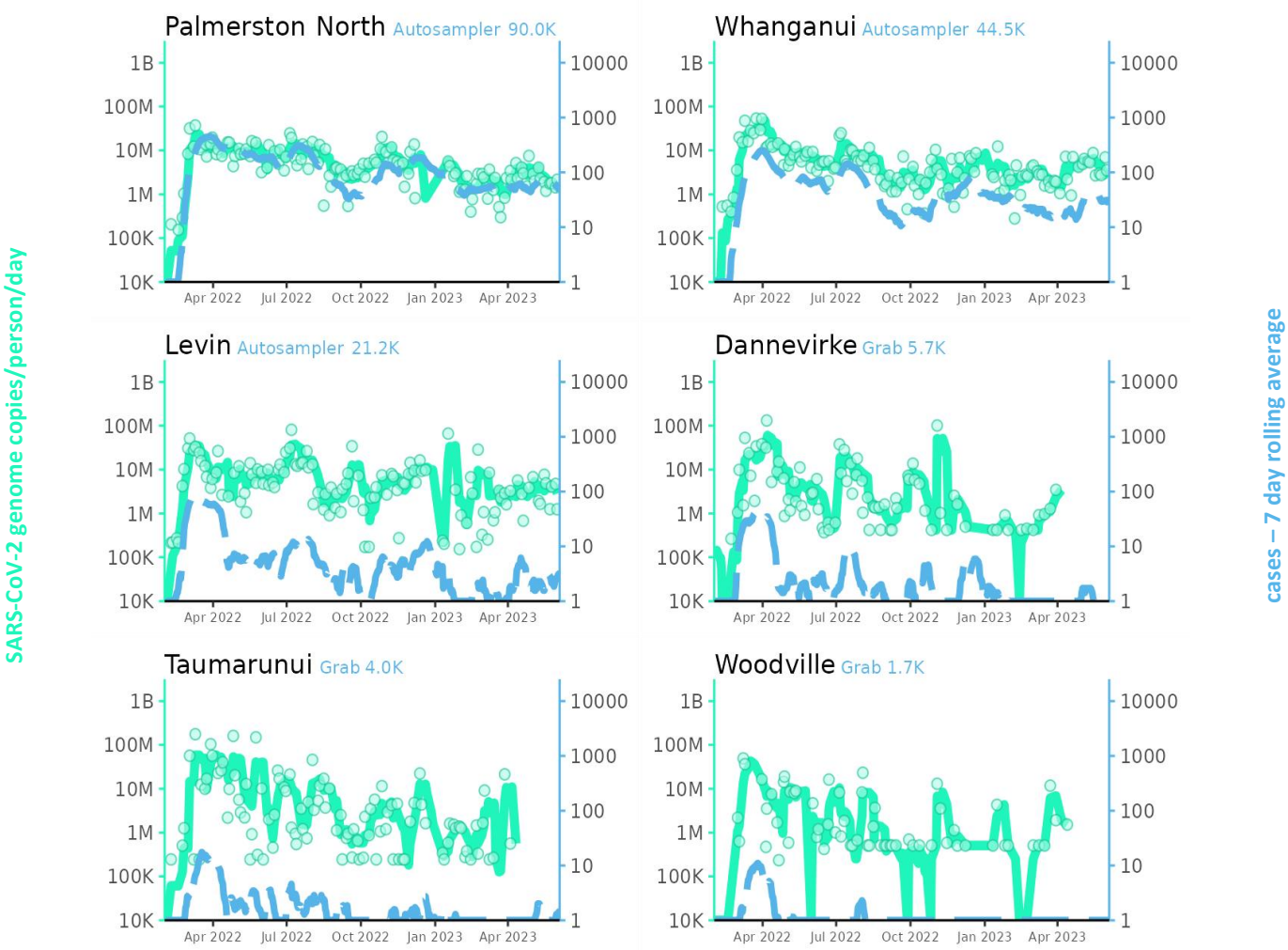

New Plymouth
Eltham
Hawera


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

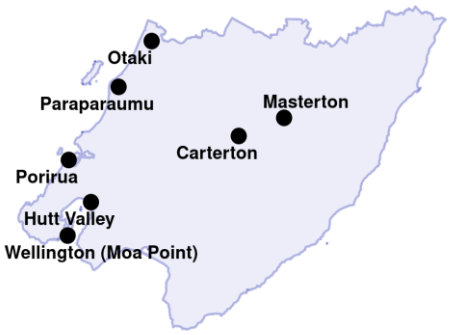

SARS-CoV-2 genome copies/person/day
New Plymouth Autosampler 88.0K
Hawera Autosampler 12.0K
Eltham Autosampler 2.0K
1B
100M
10M
1M
100K
10K
10000
1000
100
10
1
Apr 2022
Jul 2022
Oct 2022
Jan 2023
Apr 2023
cases – 7 day rolling average

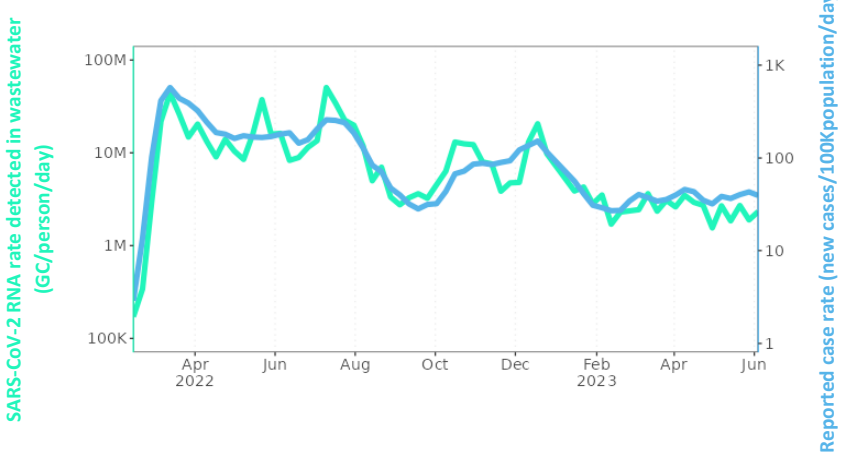
Manawatu-Whanganui





Wellington


Otaki
Paraparaumu
Masterton
Carterton
Porirua
Hutt Valley
Wellington (Moa Point)


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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Apr 2022
Jun
Aug
Oct
Dec
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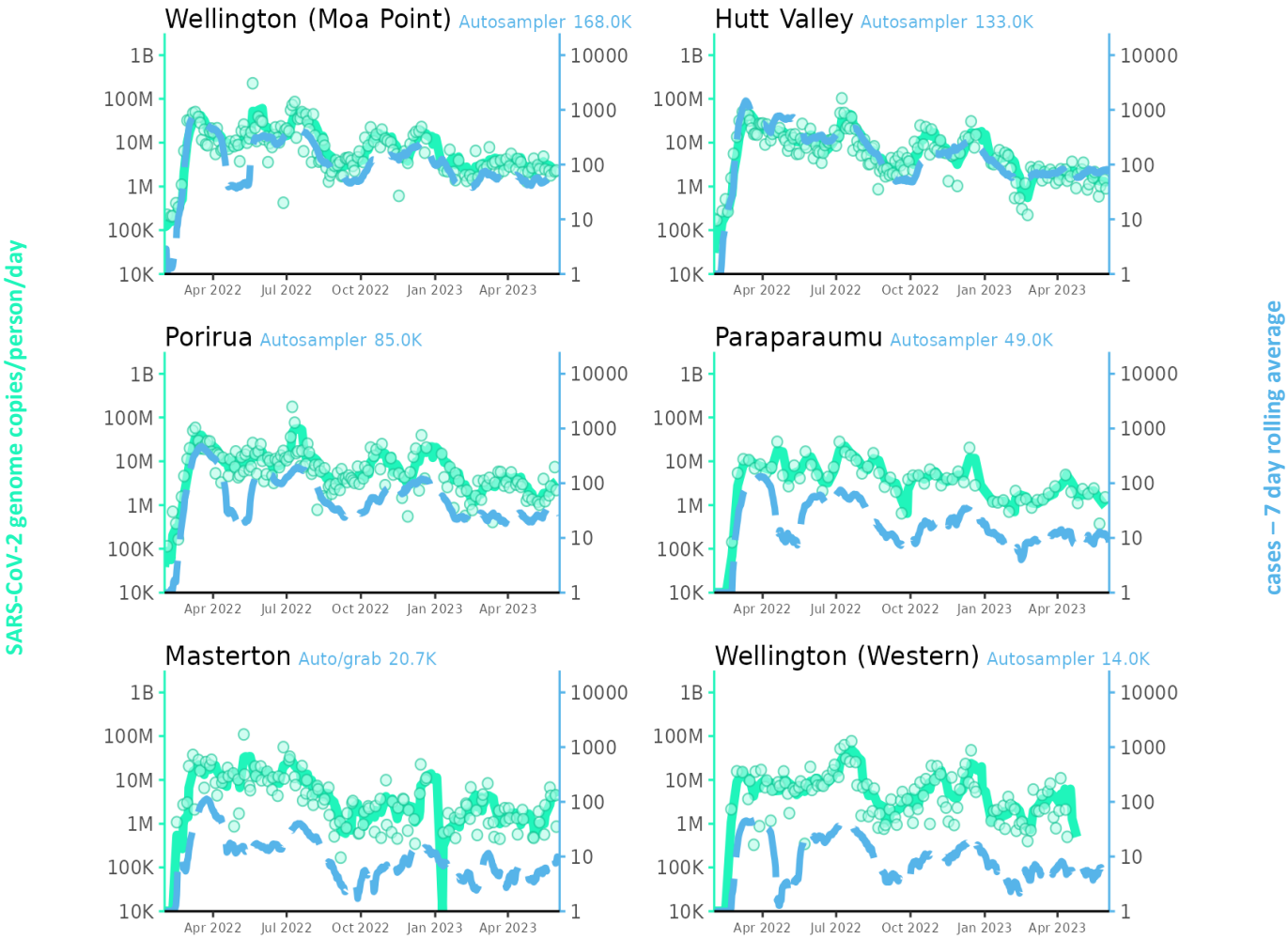
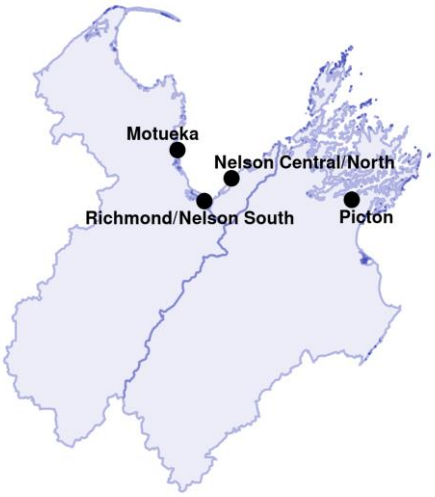
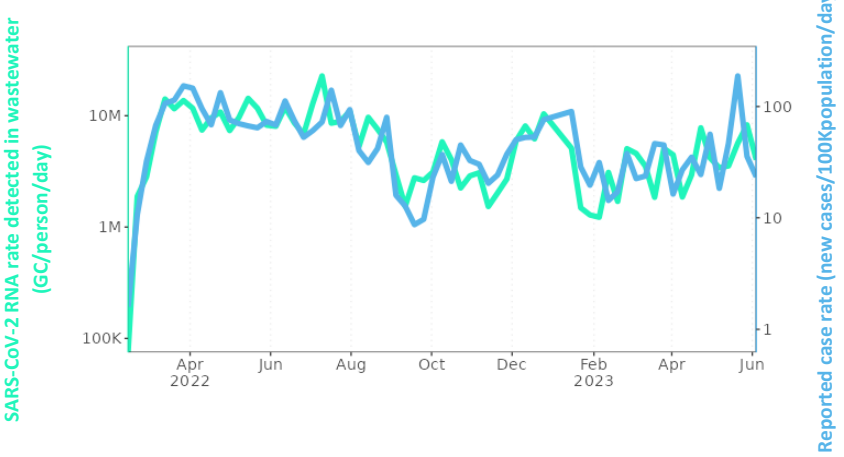
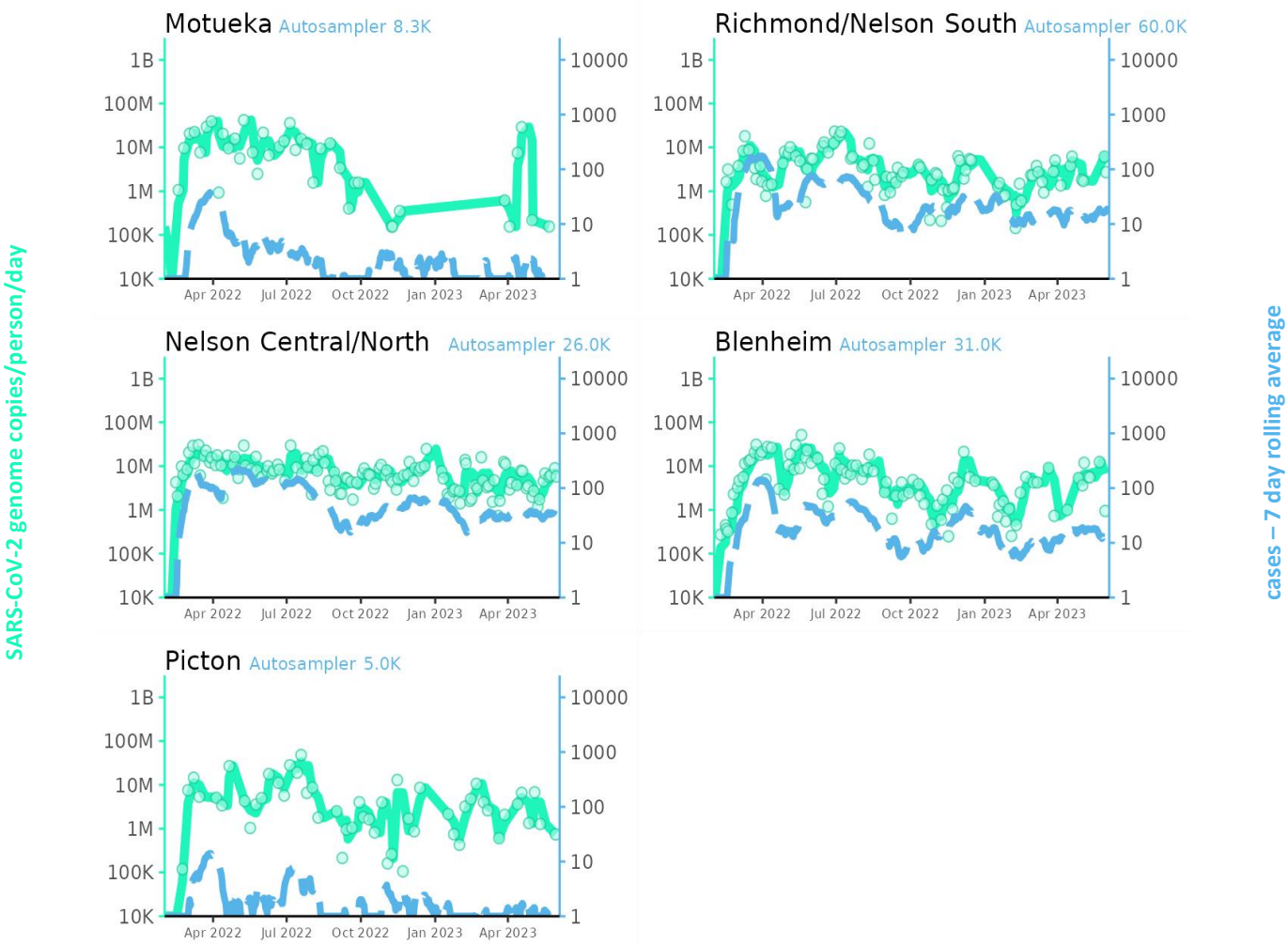
Reported case rate (new cases/100Kpopulation/day)


SARS-CoV-2 genome copies/person/day
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
1B
100M
10M
1M
100K
10K
10000
1000
100
10
1
Apr 2022
Jul 2022
Oct 2022
Jan 2023
Apr 2023
cases – 7 day rolling average

Tasman, Nelson & Marlborough

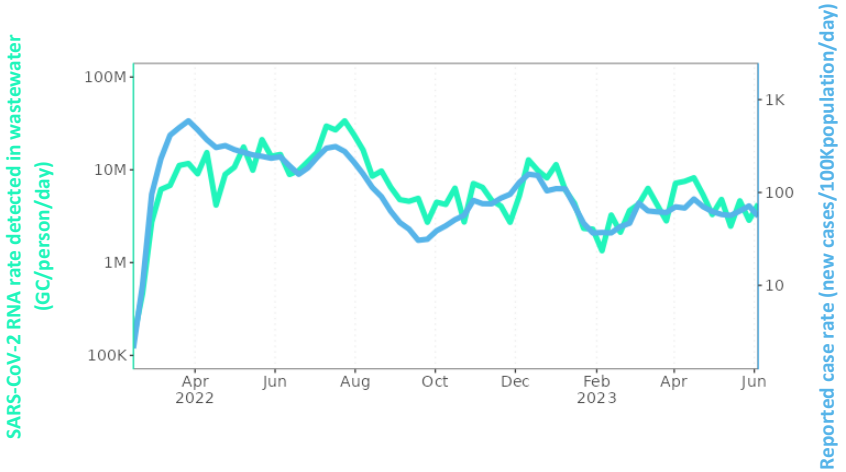






Canterbury


Rangiora
Woodend
Rolleston & Eastern Selwyn
Kaiapoi
Christchurch
Leeston
Ashburton
Timaru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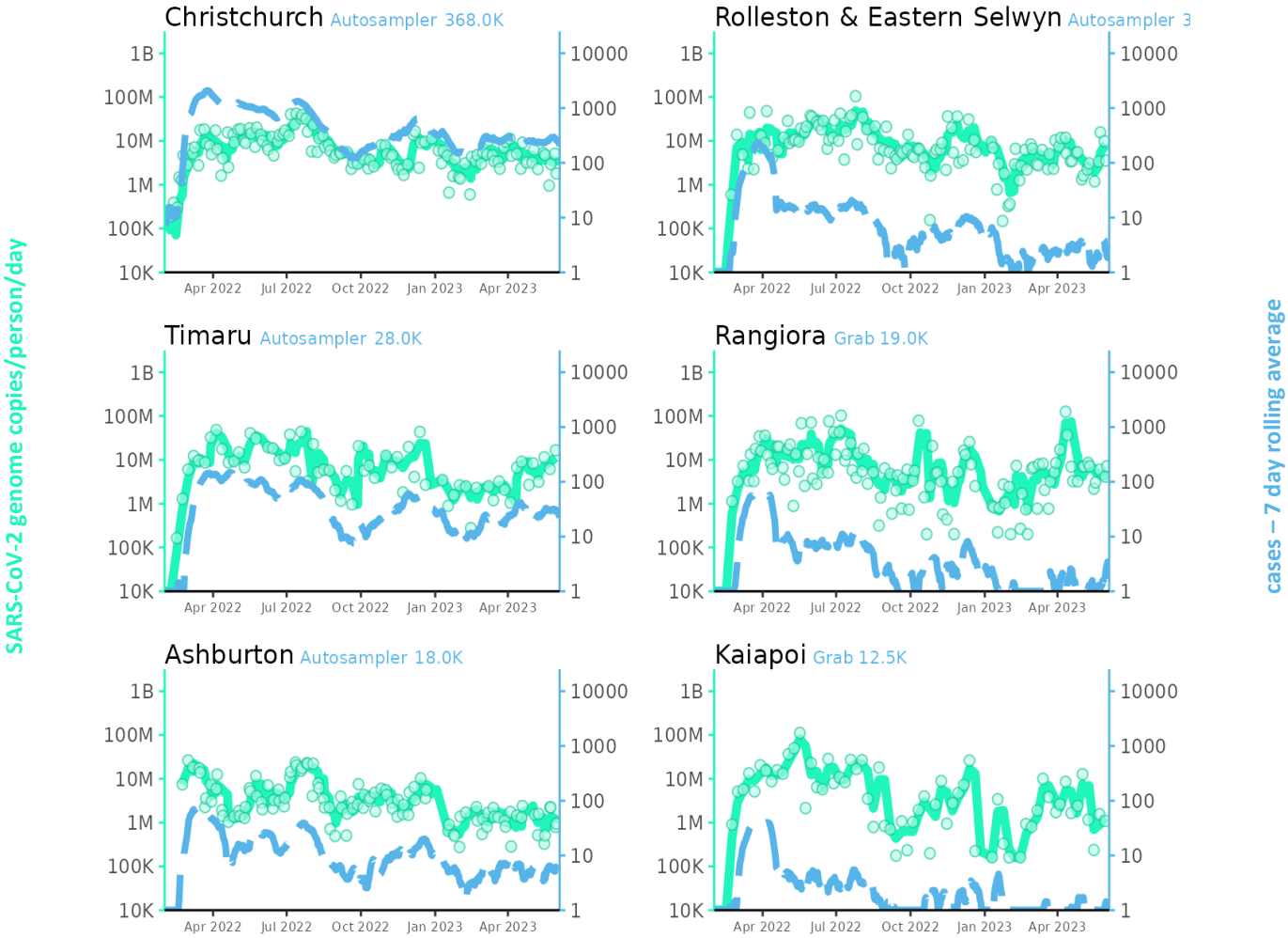
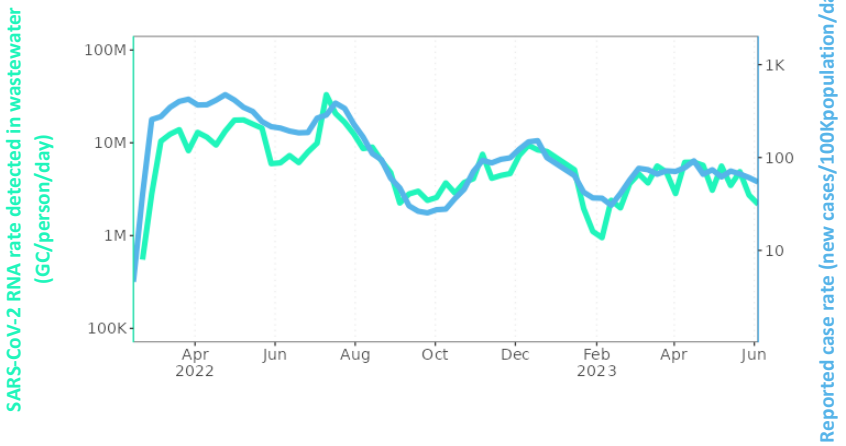
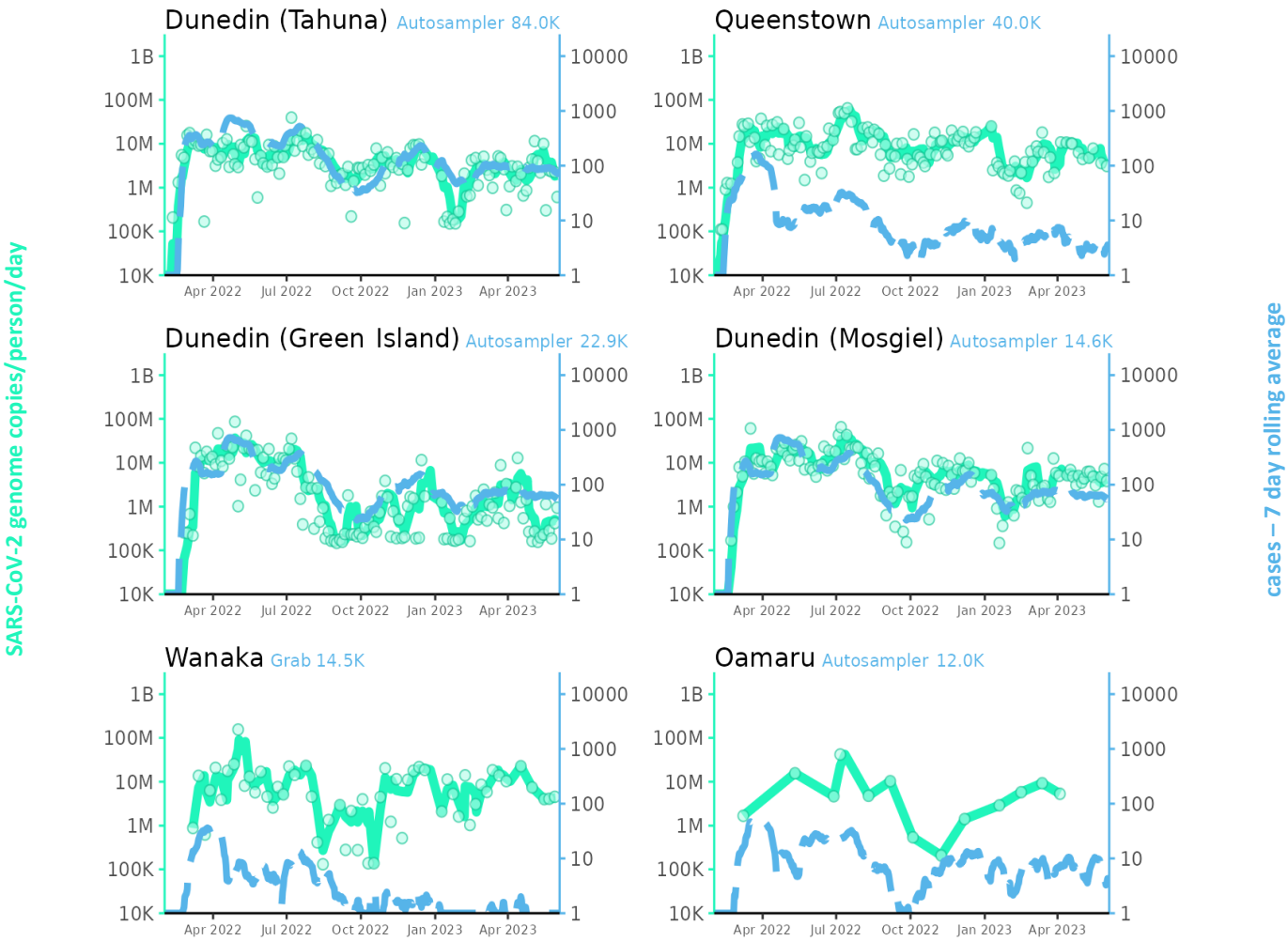
100M
10M
1M
100K
1K
100
10
Apr 2022
Jun
Aug
Oct
Dec
Feb 2023
Apr
Jun
Reported case rate (new cases/100Kpopulation/day)


SARS-CoV-2 genome copies/person/day
Christchurch Autosampler 368.0K
Rolleston & Eastern Selwyn Autosampler 3
Timaru Autosampler 28.0K
Rangiora Grab 19.0K
Ashburton Autosampler 18.0K
Kaiapoi Grab 12.5K
1B
100M
10M
1M
100K
10K
10000
1000
100
10
1
Apr 2022
Jul 2022
Oct 2022
Jan 2023
Apr 2023
cases – 7 day rolling average

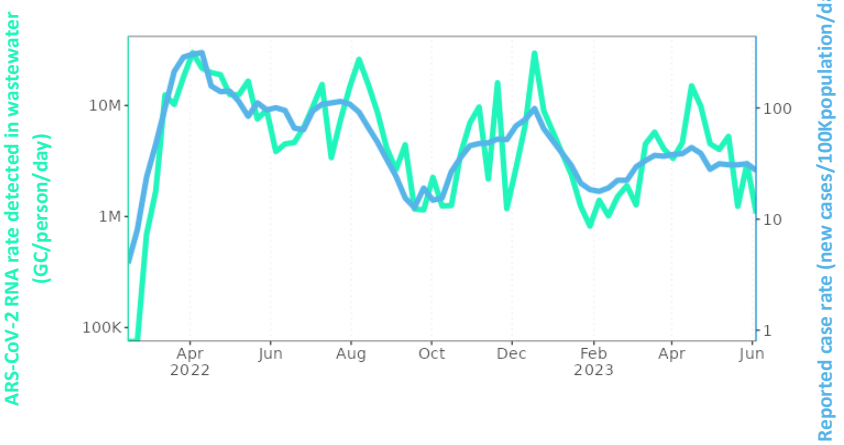
Otago

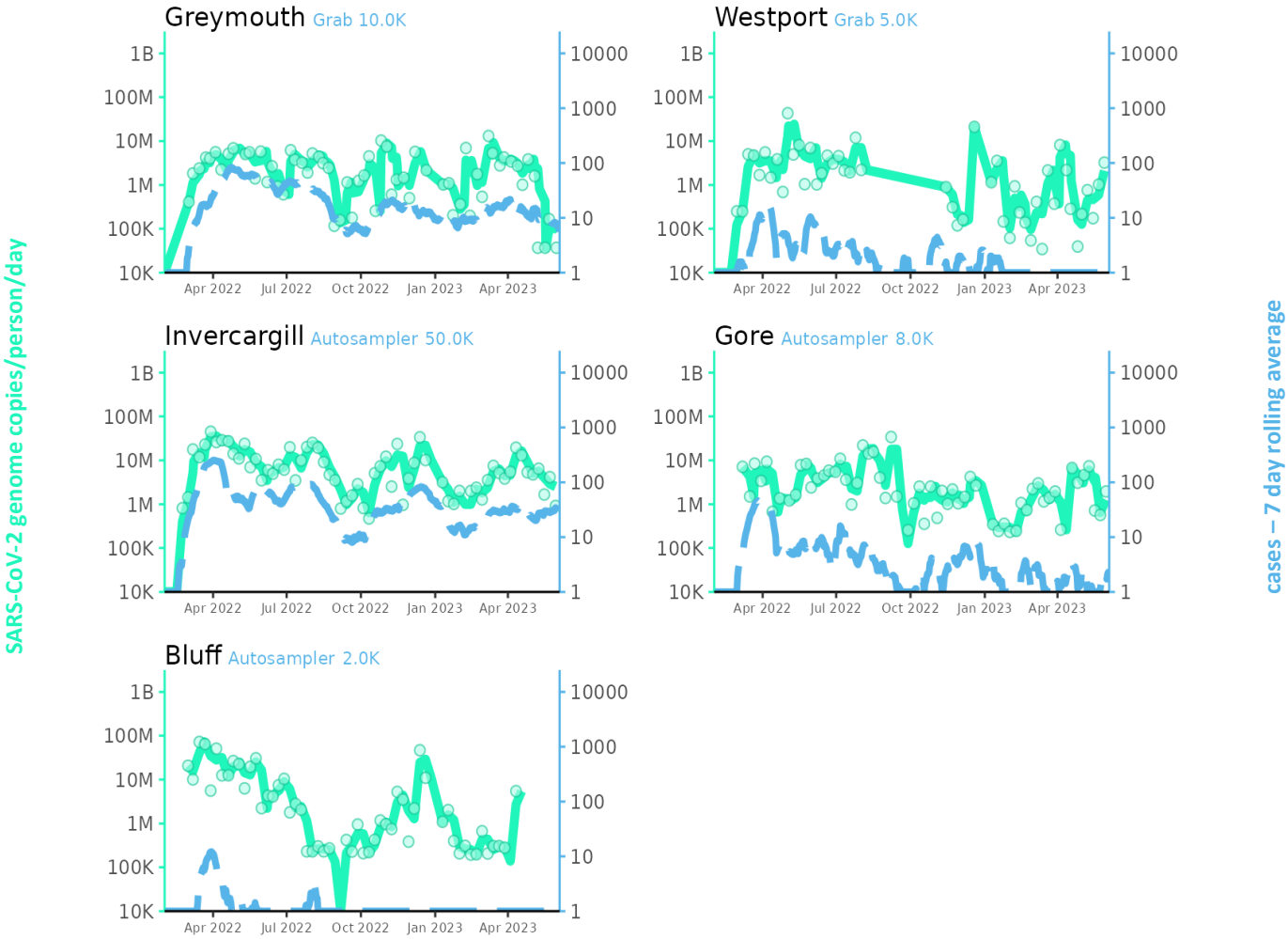

Wanaka
Queenstown
Cromwell
Alexandra
Dunedin (Mosgiel)
Dunedin (Tahuna)
Dunedin (Green Island)


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


SARS-CoV-2 genome copies/person/day
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
1B
100M
10M
1M
100K
10K
10000
1000
100
10
1
Apr 2022
Jul 2022
Oct 2022
Jan 2023
Apr 2023
cases – 7 day rolling average

West Coast & Southland





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 which may on any given week include contributions from Joanne Chapman, Dawn Croucher, Joanne Hewitt, Joycelyn Ho, Anower Jabed, Laurel Julian, Ashley McDonald, Andrew Ng, and Fatiha Sulthana. 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, Alvaro Orsi, Leighton Watson and Jiawei Zhao. 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 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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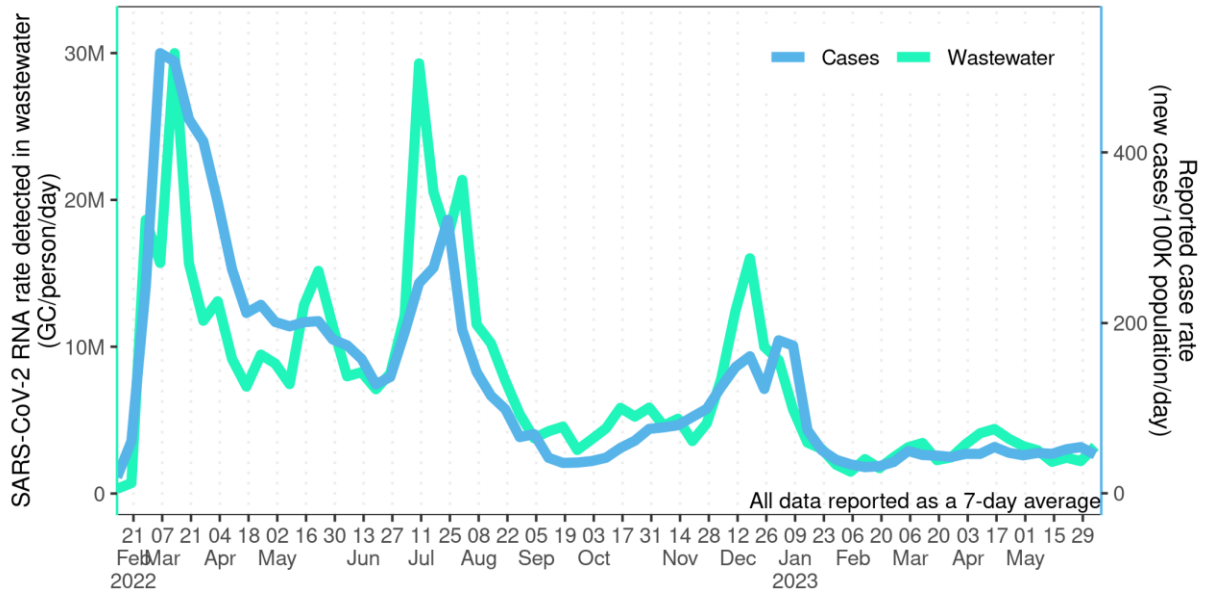
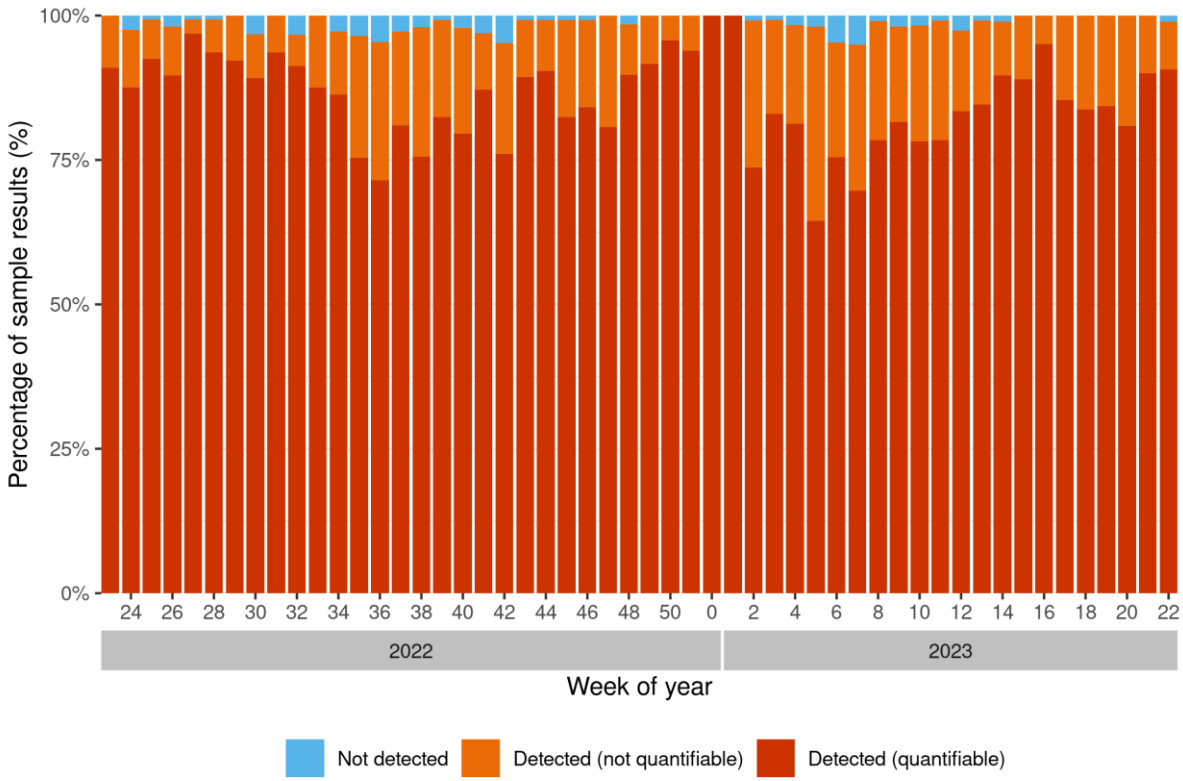
Appendix A. National Results

Time series plotted on linear scale

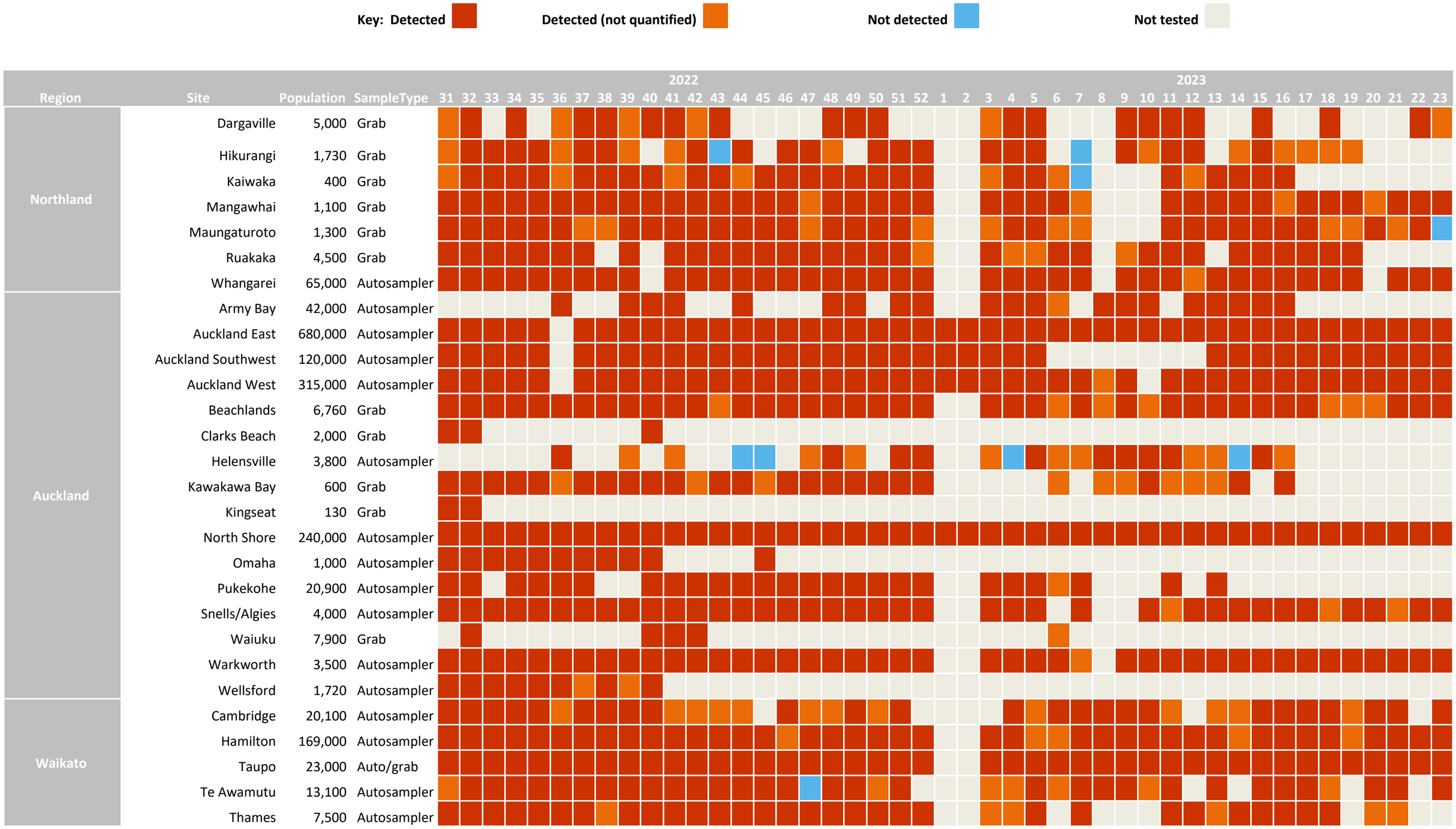


Detections for the past 52 weeks

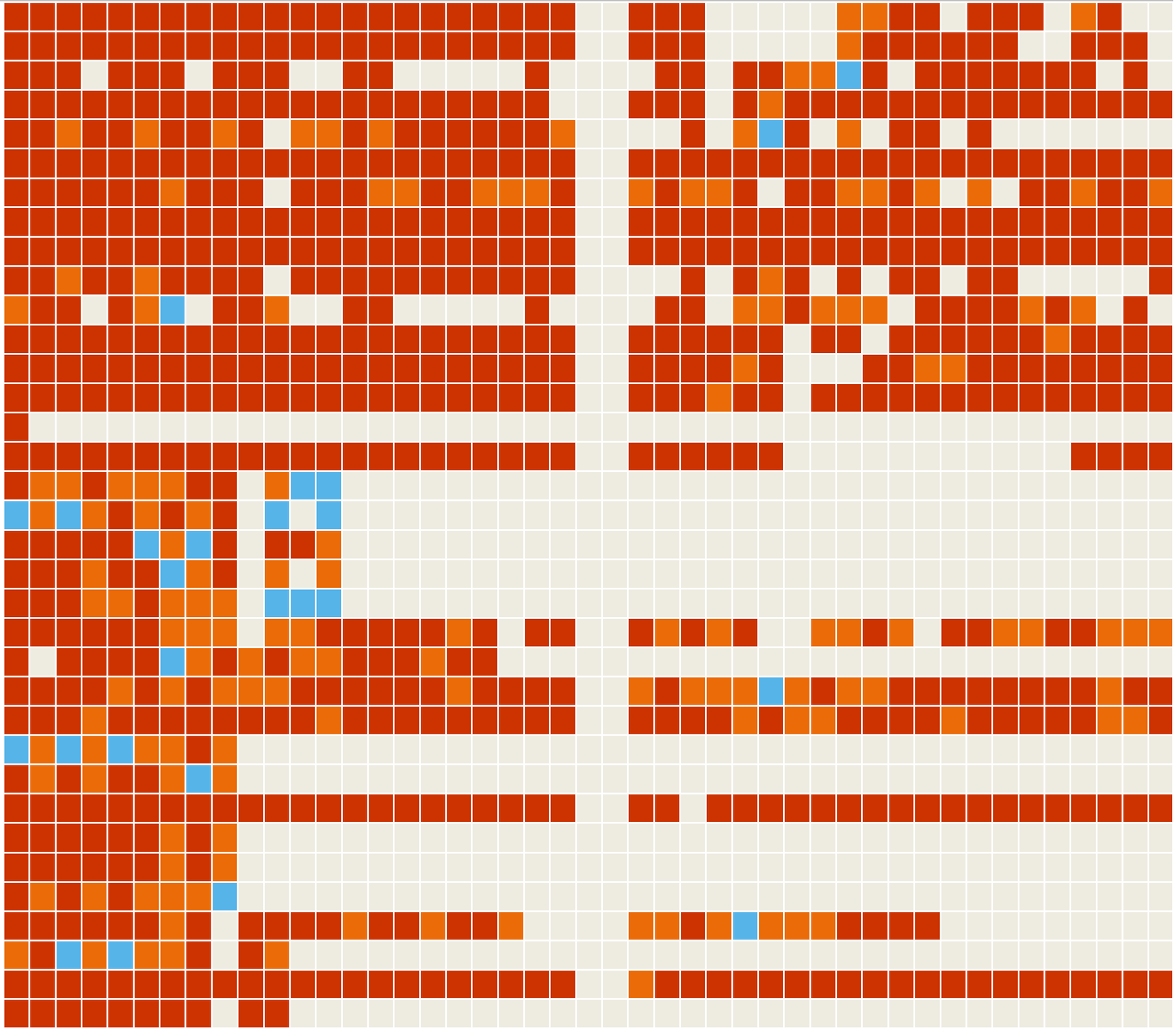


Appendix B. Site Results, Weekly Summary

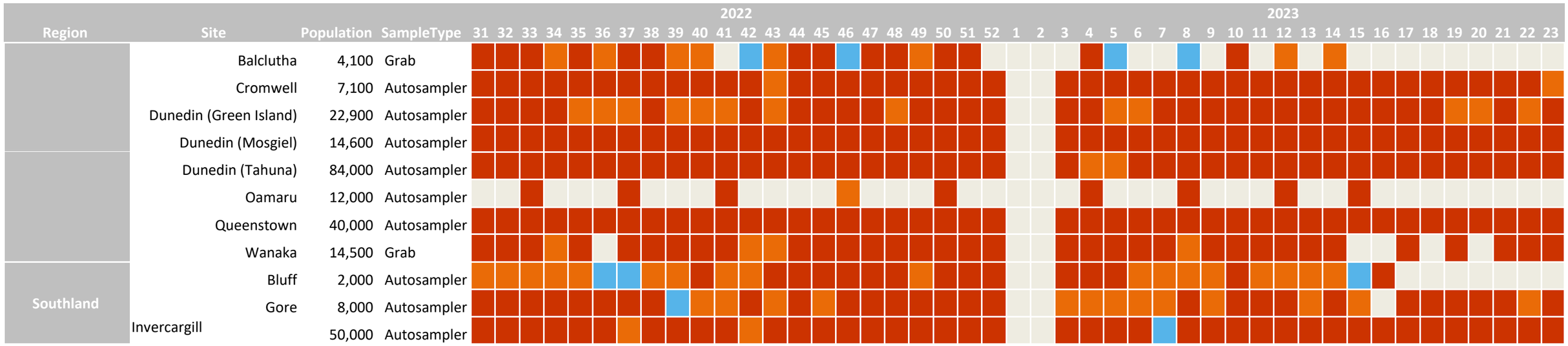
Table 2: Weekly Summary of Wastewater Sampling Results for SARS-CoV-2



Region	Site	Population	SampleType
	Whangamata	4,000	Autosampler
	Whitianga	6,600	Autosampler
Bay of Plenty	Katikati	5,500	Autosampler
	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
	Mahia	1,100	Grab
	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
	Kaponga	400	Grab
	Manaia	950	Grab
	New Plymouth	88,000	Autosampler
	Opunake	1,400	Autosampler
	Patea	1,200	Autosampler
	Waverley	900	Grab
Manawatu-Whanganui	Dannevirke	5,697	Grab
	Eketahuna	1,630	Grab
	Levin	21,200	Autosampler
	Pahiatua	2,797	Grab



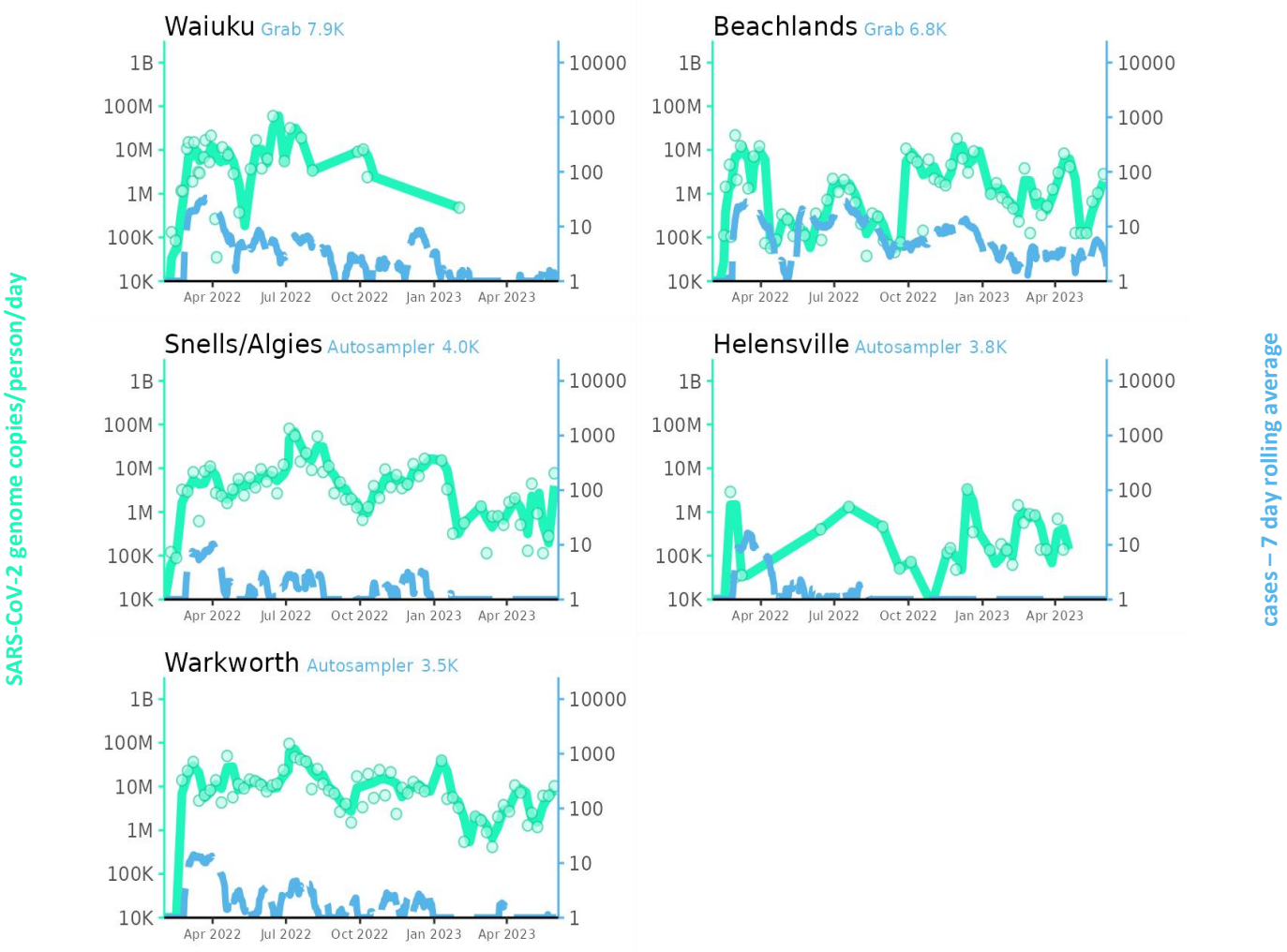
Region	Site	Population	SampleType	2022 31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	2023 1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23
Wellington	Palmerston North	90,000	Autosampler																																												
	Taumarunui	4,000	Grab																																												
	Whanganui	44,500	Autosampler																																											
	Woodville	1,657	Grab																																											
	Carterton	5,800	Grab																																											
	Featherston	2,500	Grab																																											
	Greytown	2,438	Grab																																											
	Hutt Valley	133,000	Autosampler																																												
	Martinborough	1,641	Grab																																											
	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	Amberley	1,800	Grab																																											
	Ashburton	18,000	Autosampler																																												
	Christchurch	368,000	Autosampler																																											
	Hanmer Springs	900	Grab																																											
	Kaiapoi	12,500	Grab																																												
	Leeston	3,900	Autosampler																																												
	Rangiora	19,000	Grab																																											
	Rolleston & East Selwyn	35,000	Autosampler																																											
	Timaru	28,000	Autosampler																																											
	Woodend	7,600	Grab																																											
Otago	Alexandra	6,200	Autosampler																																											


Region
Site
Population
SampleType
2022
31 32 33 34 35 36 37 38 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
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

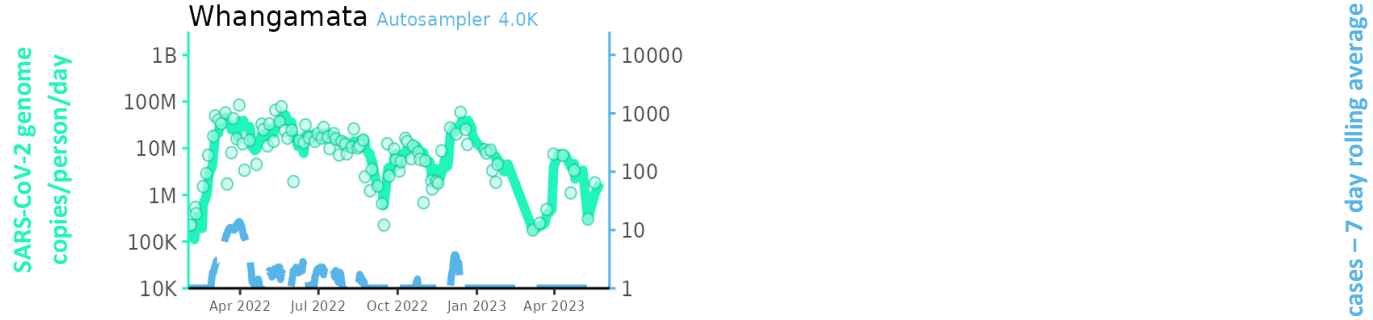
Appendix C

Additional Site Graphs

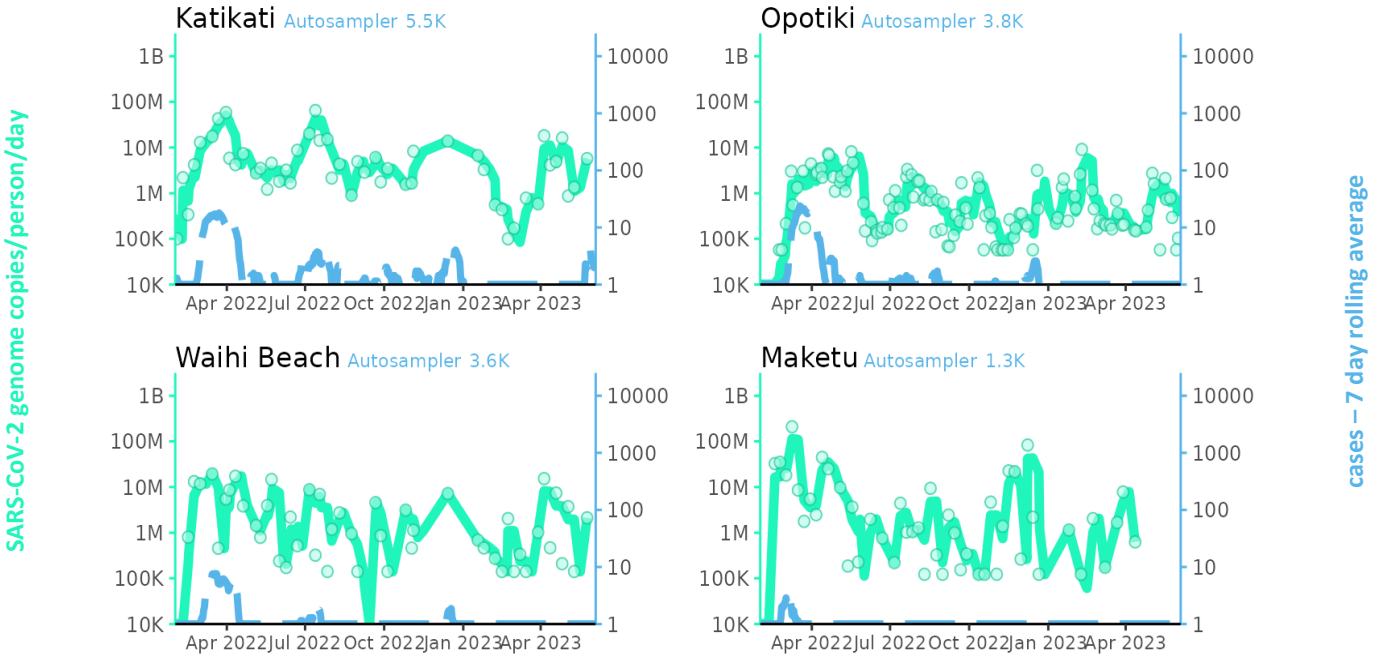
Auckland



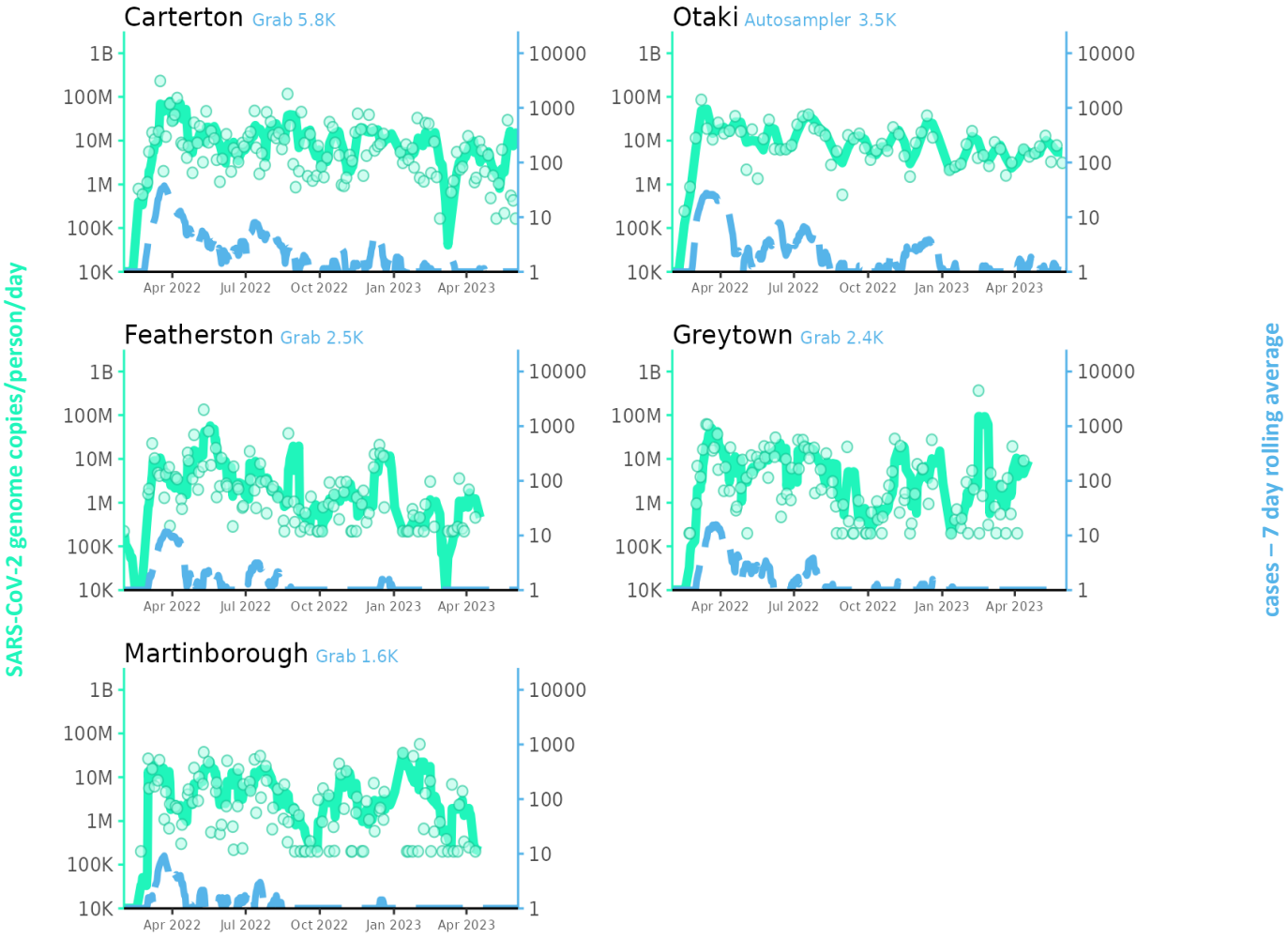
Waikato



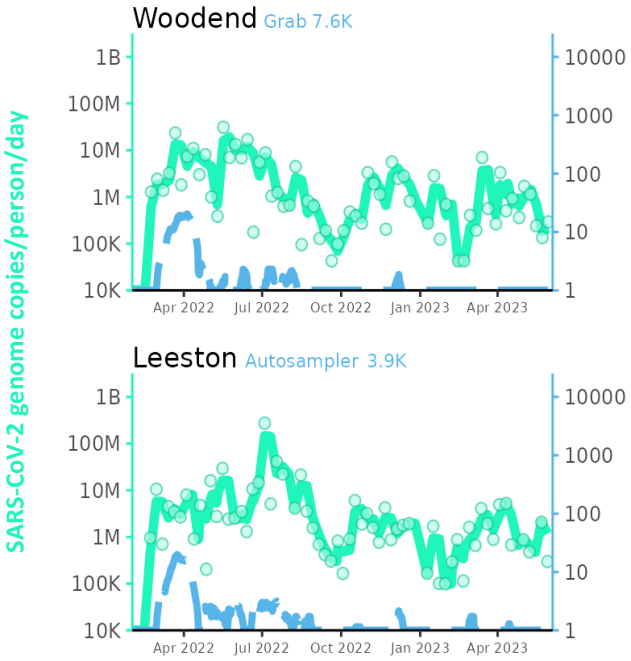
Bay of Plenty



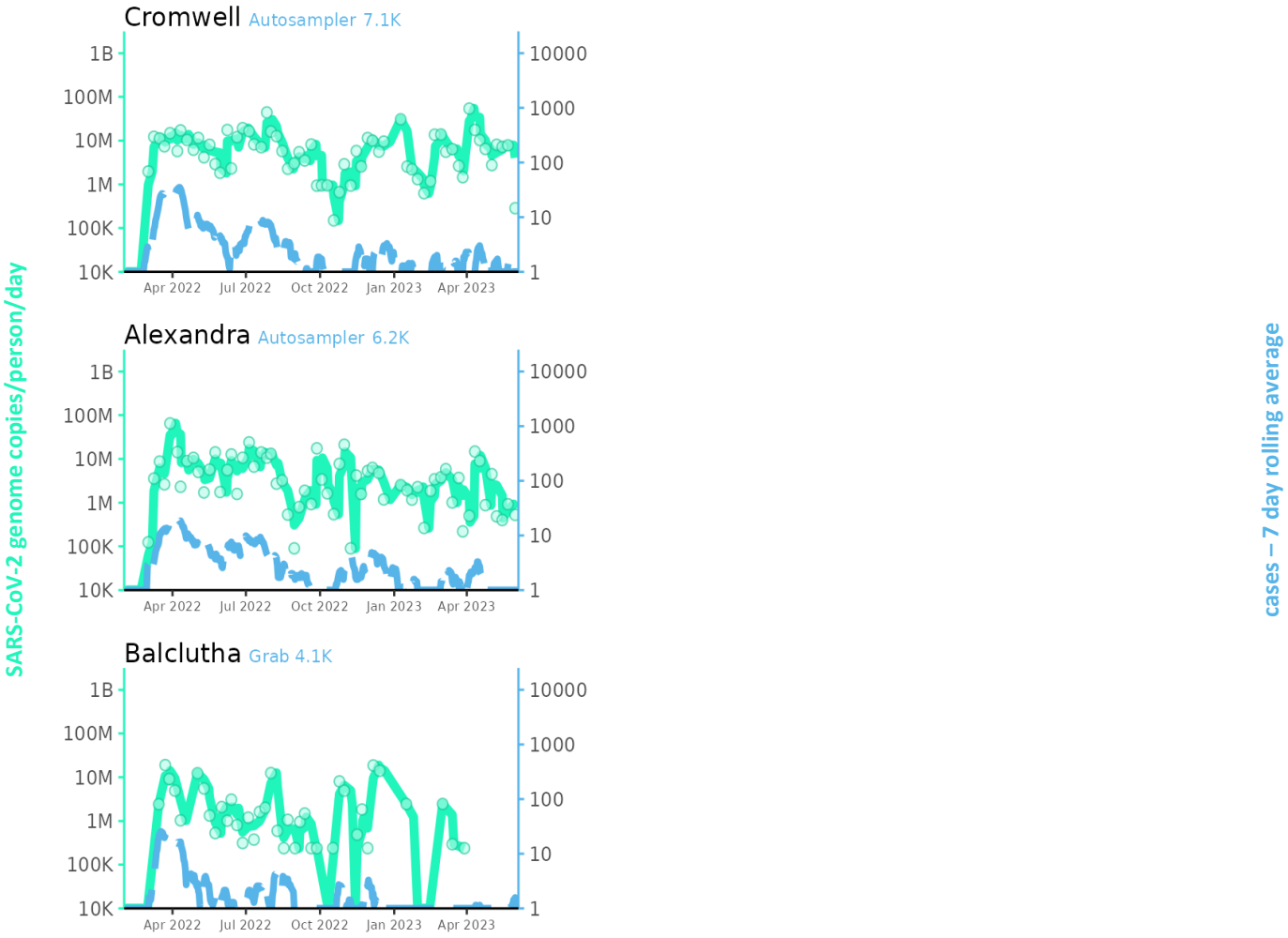
Wellington


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

Canterbury


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

Otago


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