

National Wastewater Surveillance Programme - COVID-19

Weeks 7 & 8 (Weeks Ending 19 February & 26 February 2023)

Report prepared on 01 March 2023

97%

Sites tested in weeks 7 & 8 had SARS-CoV-2 detected (75/77 sites)

67%

NZ population covered by wastewater testing

Omicron XBB (35%) & CH.1.1 (33%)

Most prevalent variants detected

Nationally, SARS-CoV-2 levels remain low. Variant analysis suggests that XBB and CH.1.1 are the most common variants detected in wastewater.

- Comparing week 8 (ending 26 February 2023) to week 7 (ending 19 February 2023), 54% of sites show an increase in SARS-CoV-2 levels while 30% sites showed a decrease in SARS-CoV-2 levels.
- Comparing week 8 (ending 26 February 2023) to one month ago (week 4, ending 29 January 2023), 48% of sites show an increase in SARS-CoV-2 levels while 31% of sites showed a decrease in SARS-CoV-2 levels.
- The main variants detected in wastewater in the week ending 26 February 2023 (week 8) were XBB (includes XBB.1.5, ~35%), CH.1.1 (~33%), and BA.2.75* (~24%). Minor contributions of BQ.1.1 (~2%), BA.4/BA.5 (0.5%) and XBC (~5%).

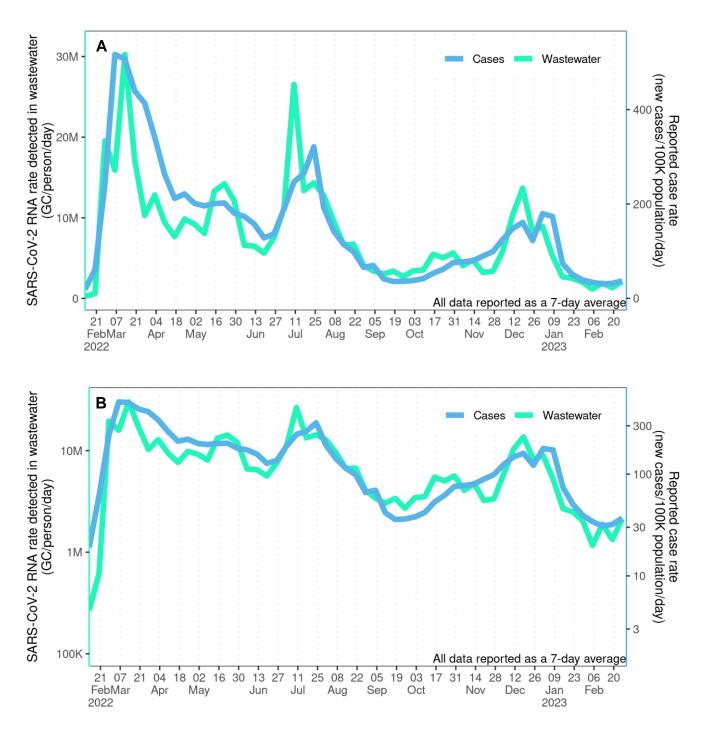


Figure 1. National timeseries of estimated SARS-CoV-2 genome copies (GC) in wastewater rate (GC/person/day, green line) and reported case rate (new cases/100,000 population/day, blue line) on a linear scale (**A**) and Log₁₀ scale (**B**). Data reported as 7-day average.

Results for Weeks 7 & 8 (Weeks ending 19 February & 26 February 2023)

In the two weeks ending 26 February 2023, 204 samples were collected from 77 locations across New Zealand. SARS CoV-2 RNA was **detected** in 198/204 samples from 75/77 (97%) sites.

In the week ending 19 February 2023, no samples were collected from any of the seven regular Northland sites. In the week ending 26 February 2023, no samples were collected from the four regular sites in Hawkes Bay or from Gisborne. Samples from three of the seven Northland sites were also not collected in that week.

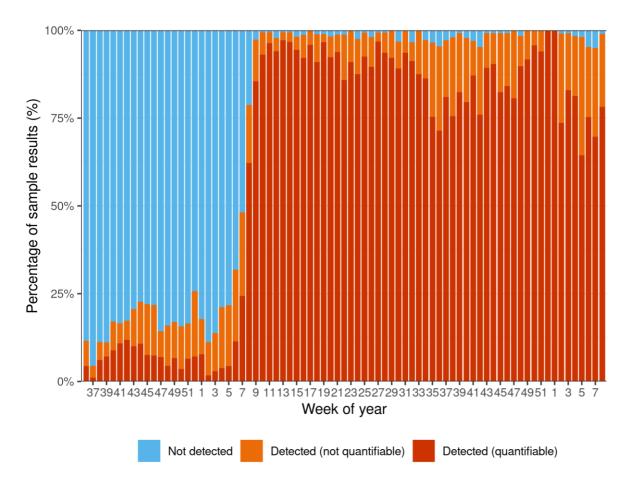


Figure 2. Results for SARS-CoV-2 RNA in wastewater collected across New Zealand.

Regional Trends

Regional summaries (Figure 3) of the wastewater data indicate increasing SARS-CoV-2 levels in most regions. Note that Northern regional trend analysis (blue line) is not available for weeks 7 and 8 due to few samples being received from this region over the last fortnight. Additionally, no samples were received from Hawkes Bay in week 8, so the trend line for the Central region (yellow line) excludes Hawkes Bay in this report (Figure 3). Sample collection for week 52 (2022) and week 1 (2023) was only possible for Auckland Metro, as there were limited samples collected during the holiday period. Viral quantitation for the other regions were therefore not available during this period.

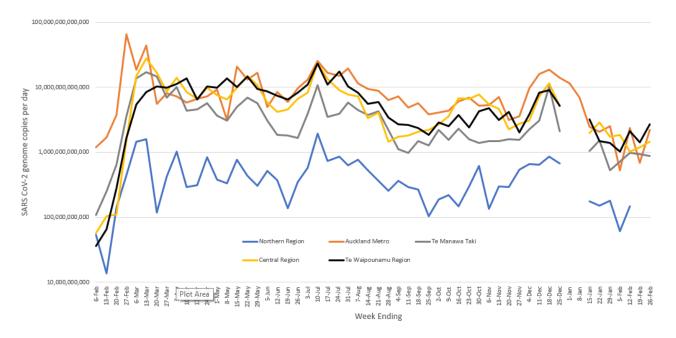


Figure 3. Total SARS-CoV-2 genome copies detected per day in the five Ministry of Health regions.

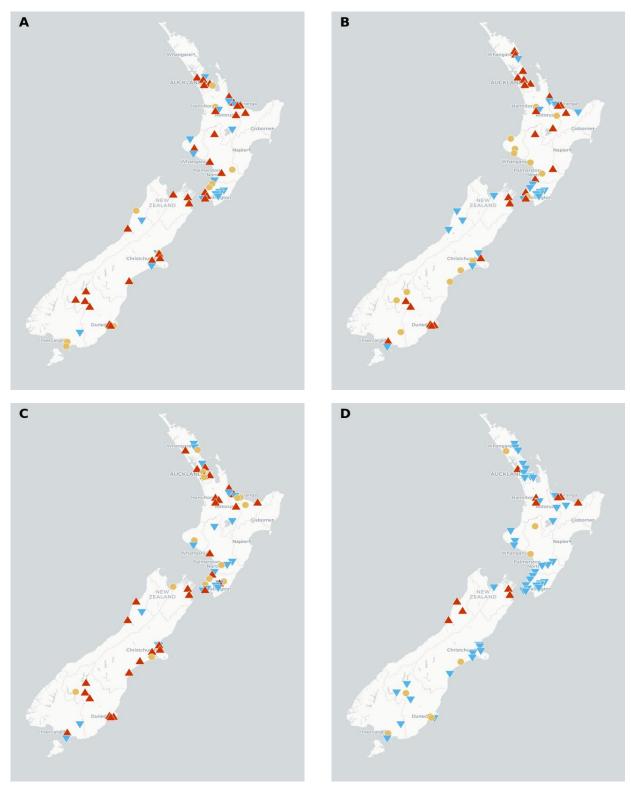


Figure 4. Comparison of SARS-CoV-2 levels for the week ending 26 February 2023, compared to levels measured: A) 1 week ago; B) 2 weeks ago; C) 4 weeks ago; D) 12 weeks ago. Only sites with results for both time points are included. When the viral quantity is 30% or more higher this is labelled as increased (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/

Wastewater Variant Analysis

In collaboration with Wilderlab, ESR generated the variant analysis results from sentinel sites in week 7 (ending 19 February 2023) and week 8 (ending 26 February 2023).

Wastewater variant analysis is based on sequencing a short fragment of the spike gene and therefore provides less resolution than WGS from clinical cases. As such, some specific lineages cannot be distinguished from each other, and are reported as variant groups. The following variants/groups are reported: BA.4/BA.5, BA2.75* (includes BA.2.75/XBF/BR.2 subvariants), CH.1.1, BQ.1.1, XBB (includes XBB.1.5) and XBC. Consistent with the WGS of clinical cases, the CH.1.1 subvariant will now be reported separately from other BA.2.75* subvariants.

CH.1.1 has declined in weeks 7 and 8 respective to XBB (see below). CH.1.1 was detected in 12/17 (week 7) and 11/18 (week 8) sites, comprising ~36% (week 7) and ~33% (week 8) of sequencing reads nationally. Other subvariants in the BA.2.75* group (includes BM.4, BR.2, XBF and BA.2.75) accounted for another ~15% (week 7) and ~24% (week 8) of sequencing reads nationally. Thus, as a whole, the BA.2.75* constellation represented ~51-57% sequences in weeks 7-8, compared to ~84-85% of sequencing reads nationally in weeks 5-6.

The XBB variant (includes XBB.1.5) has been steadily increasing in wastewater samples. This variant accounted for ~5% of reads nationally in week 5 (4/19 sites), ~11% of reads nationally in week 6 (4/19 sites), ~40% of reads nationally in week 7 (10/17 sites), and ~35% of reads nationally in week 8 (15/18 sites). The wastewater assay cannot distinguish XBB.1.5 from other XBB variants. This suggests that XBB.1.5 has started to circulate more widely in the community, in agreement with clinical WGS results.

The BA.4/BA.5 variant group (including BF.7) continued to decline, only being detected in Queenstown wastewater in week 8 (accounting for only ~0.4% of sequences nationally) and not being detected at any site in week 7. Note that BA.4/BA.5 was previously detected, in Queenstown only, in week 3.

BQ.1.1 in wastewater is only being detected intermittently, accounting for ~2% of reads in weeks 7 and 8, but with low consistency in which sites had BQ.1.1 detections between weeks (Table 1).

The XBC variant also remains at relatively low levels, comprising ~7% (week 7) and ~5% (week 8) of sequencing reads nationally.

Due to the increasing complexity of variants in the population, each at relatively low levels, the current approach for sequencing wastewater samples needs to be more precise to report percentages for each variant at the sentinel site level. Instead, the presence of each lineage will currently be reported. ESR is actively testing and developing methods to address the current uncertainty and increase the resolution to identify variants in wastewater.

			We	ek 7					We	ek 8		
	BA.4/BA.5	BA.2.75*	CH.1.1	BQ.1.1	XBB	XBC	BA.4/BA.5	BA.2.75*	CH.1.1	BQ.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)		15	36	2	40	7	1	24	33	2	35	5

Table 1. Data from 17 wastewater sentinel sites sampled in week 7 (ending 19 February 2023) and 18 sentinel sites sampled in week 8 (ending 26 February 2023) using a S-gene (spike) barcoding assay able to 'call' the BA.4/BA.5, the BA2.75* constellation (includes BA.2.75/XBF/BR.2 subvariants), CH.1.1, BQ.1.1, XBB (includes XBB.1.5) and XBC (sub)variants. Coloured box denotes that the variant was detected at that site that week, white box denotes that the variant was not detected, and grey box denotes site was not sampled that week. Numbers in the bottom row denote the estimated percentage of each variant at the national scale.

Variant Timeline - National

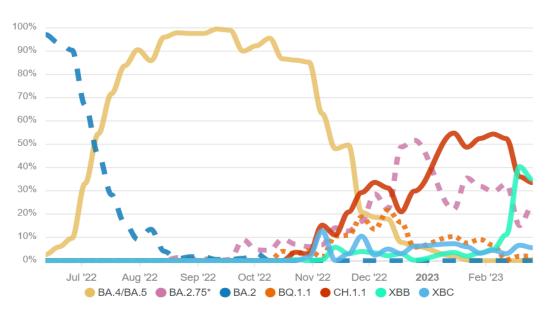
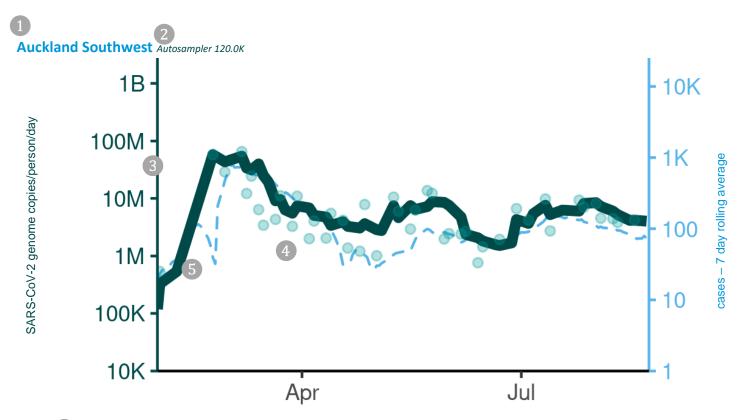


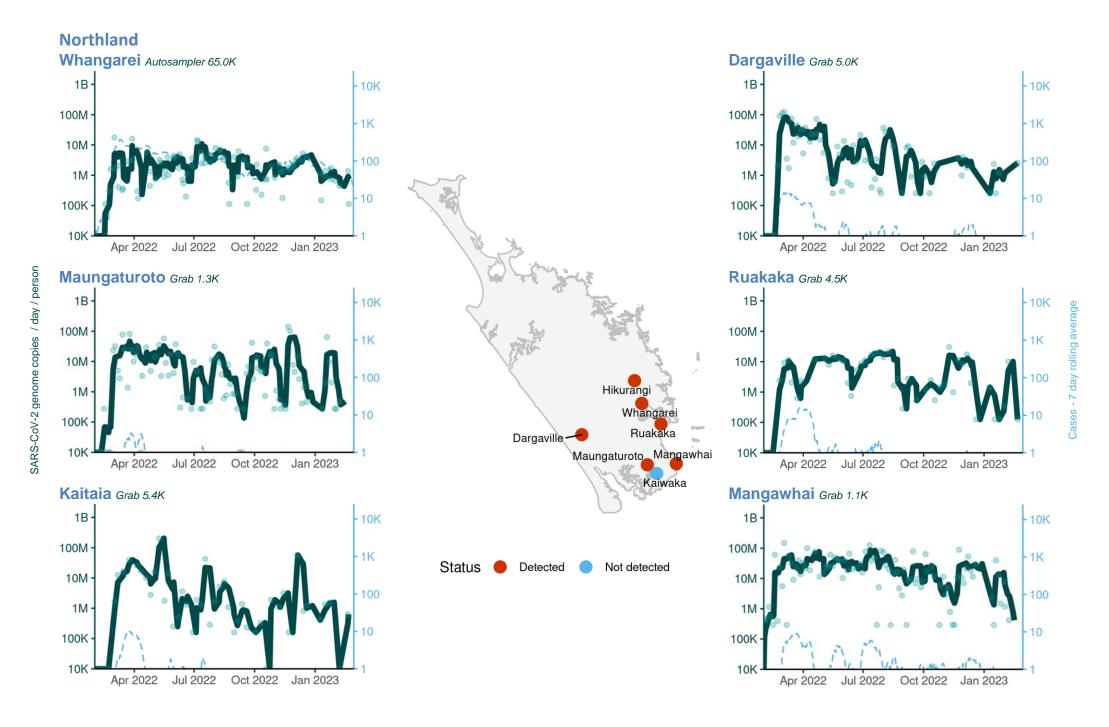
Figure 5. Change in variant prevalence over time at a national scale. Data are collected from up to 20 sentinel sites each week.

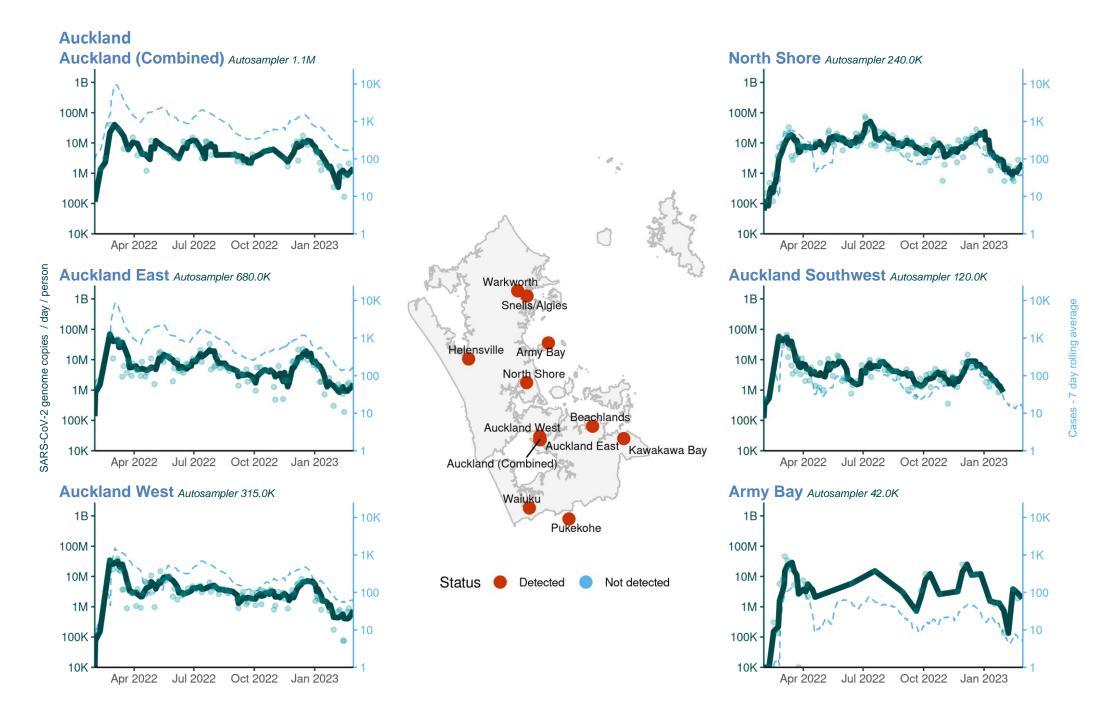
Interpreting Sites Graphs

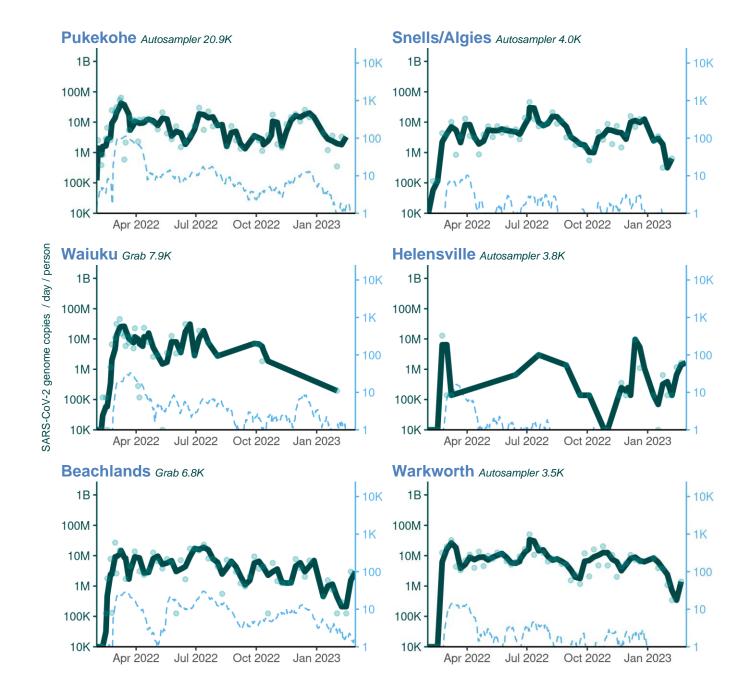


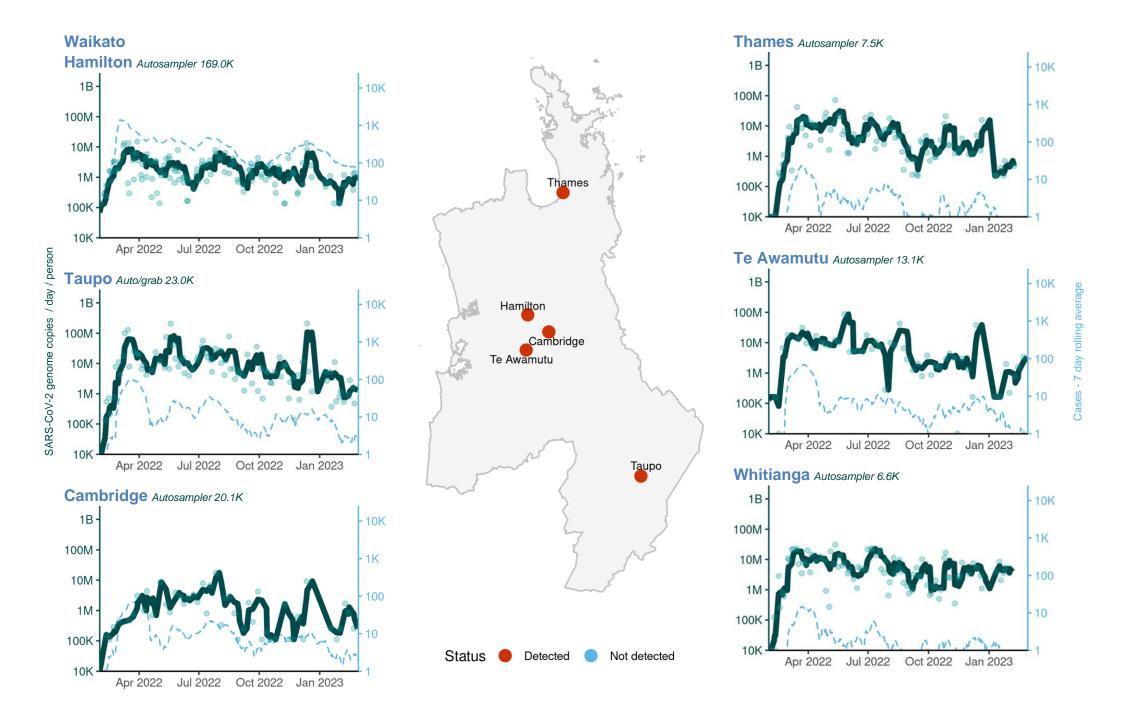
- Site Name
- 2 Sample collection method and population. Results based on autosampler may be more representative than grab sample-based results.
- 3 Wastewater results shown as solid line | 14-day average of genome copies/person/day on a log₁₀ scale.
- 4 Individual results samples shown as circles | Rolling 14-day average of genome copies/person/day on a log₁₀ scale.
- Solling 7-day average of new cases shown as dashed 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 log₁₀ scale. Scales on all graphs have been normalised to cover the same scale on every graph. Care should be taken when interpreting the data.

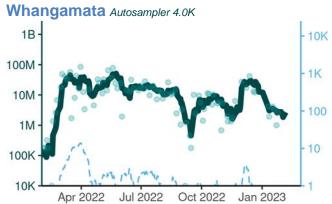


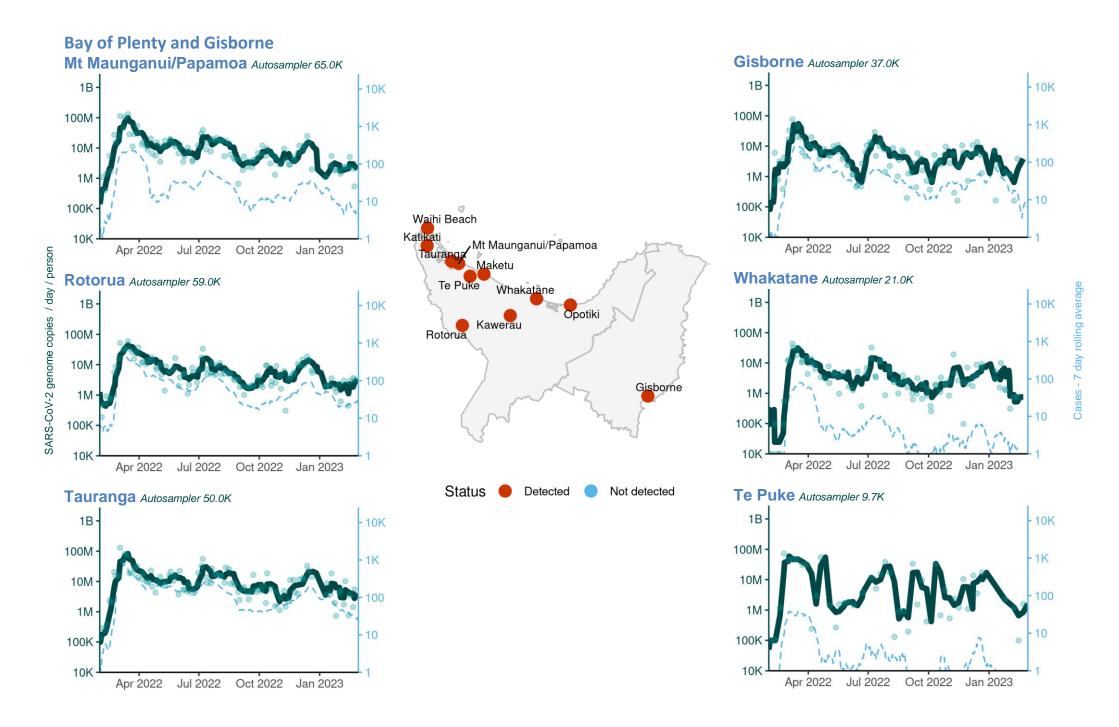


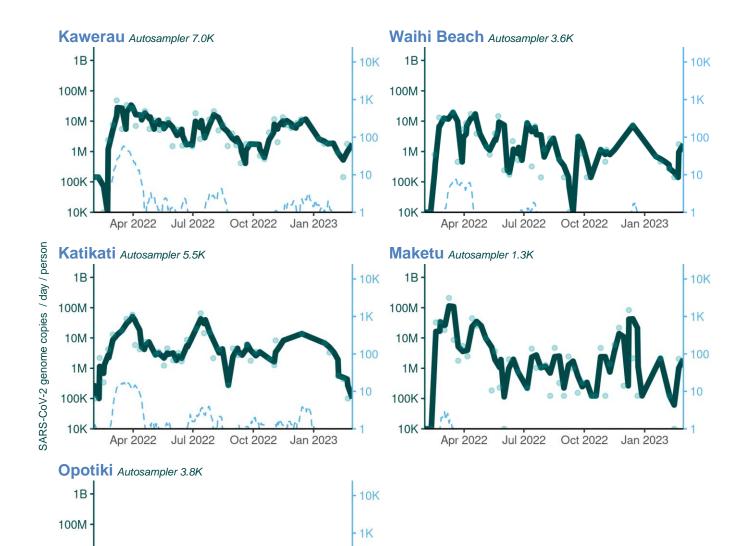








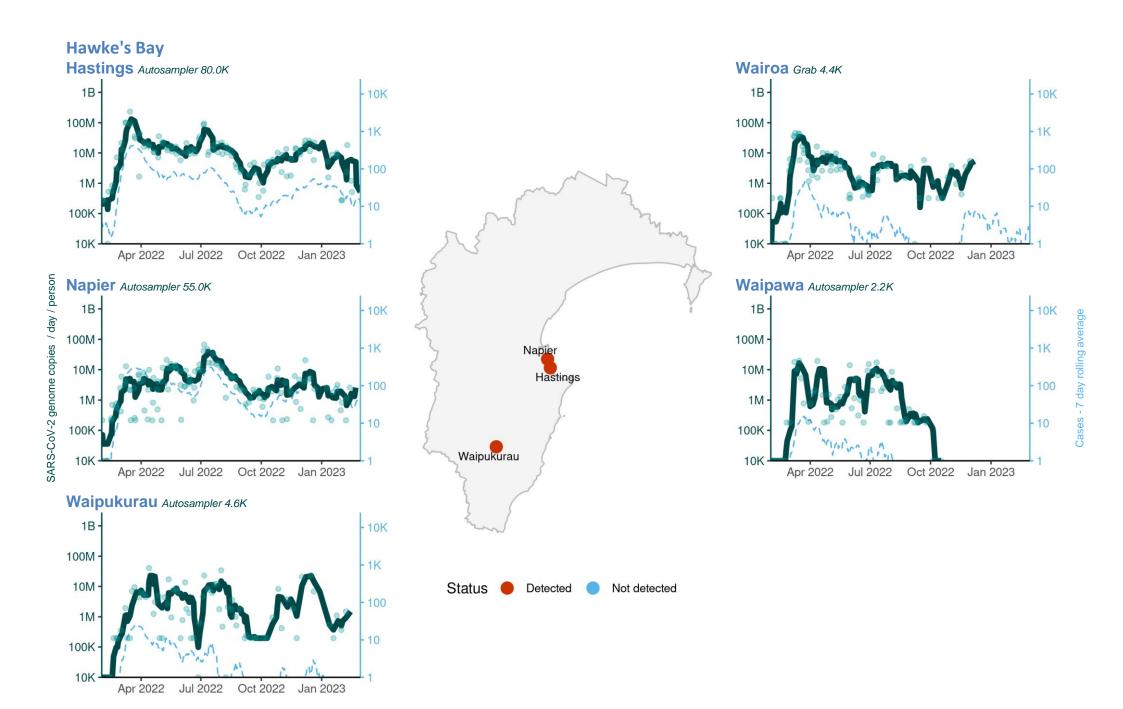


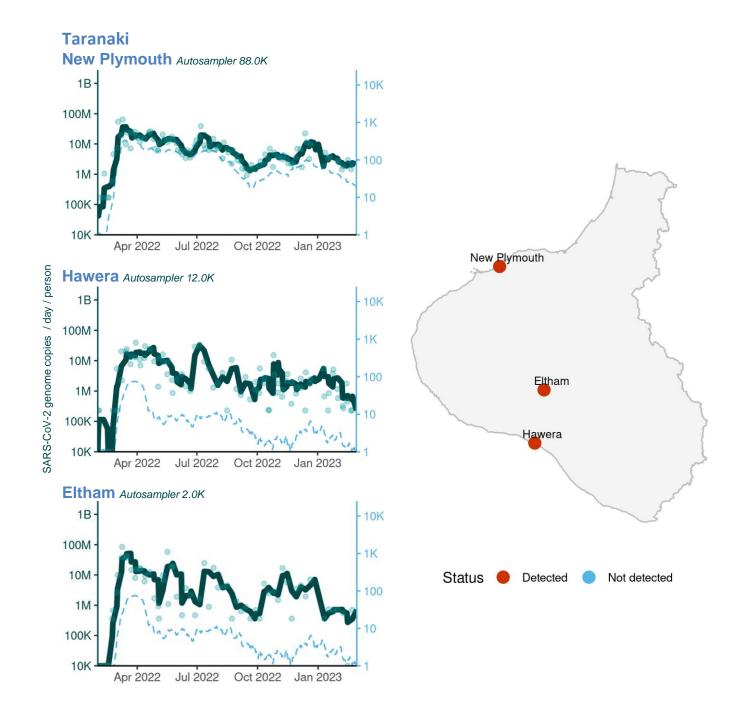


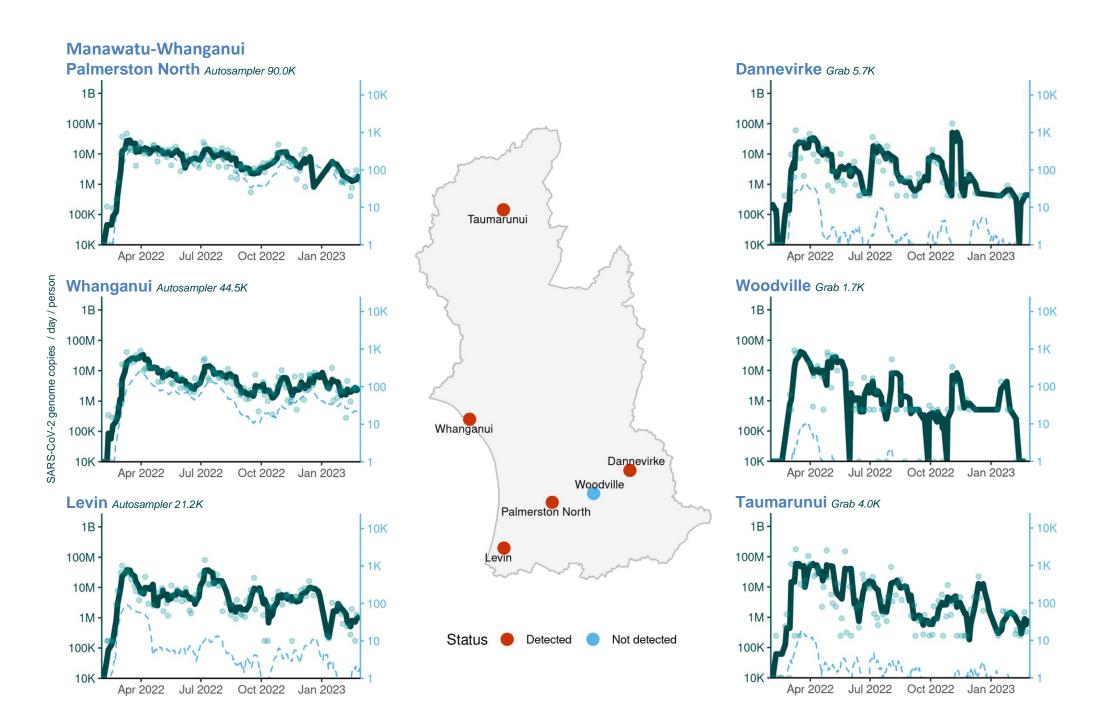
10M

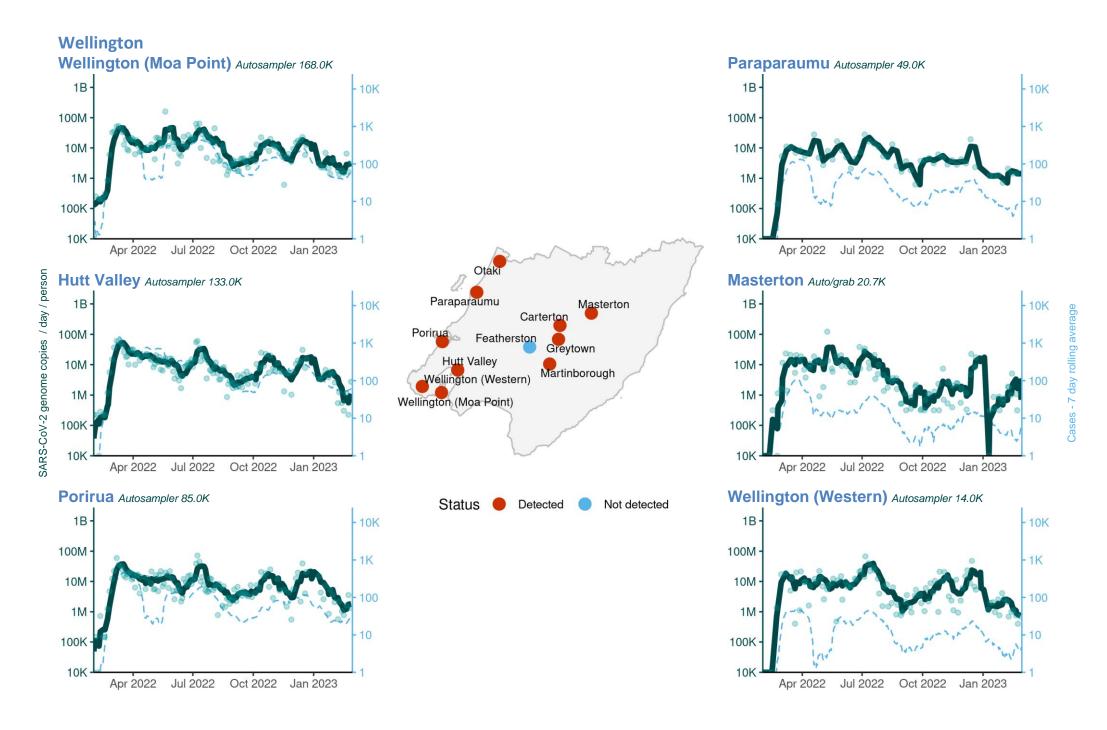
1M

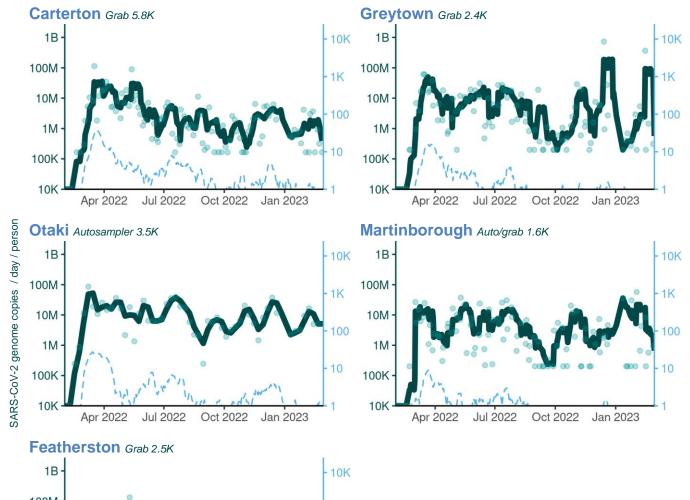
100K

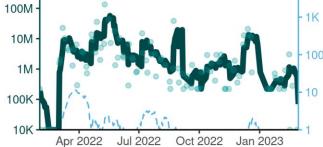


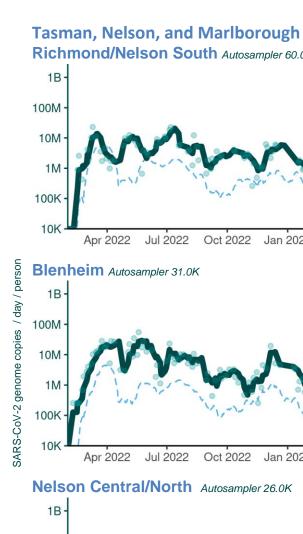


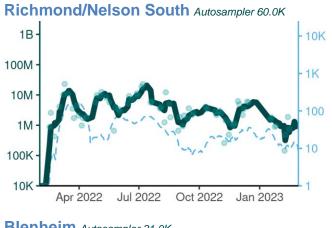


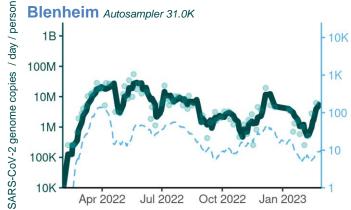


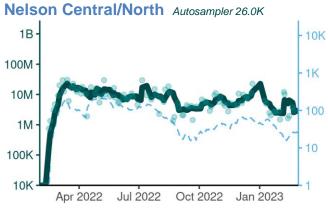




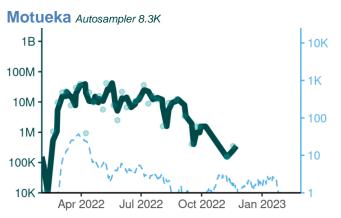


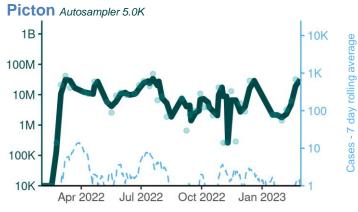


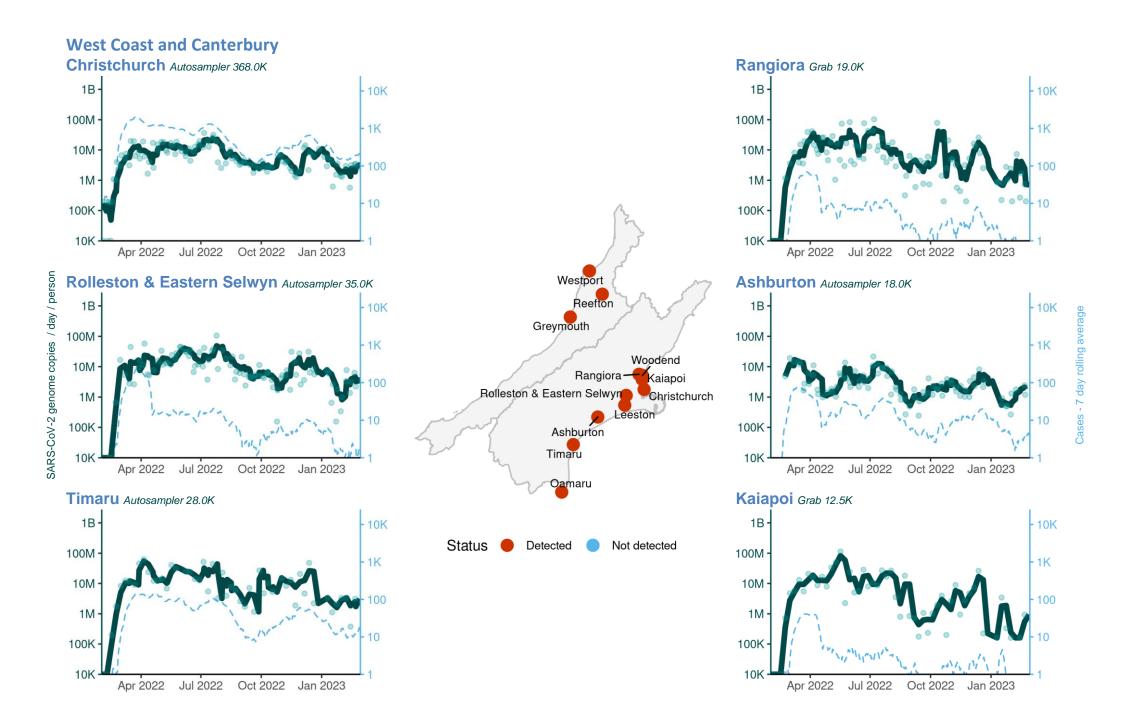


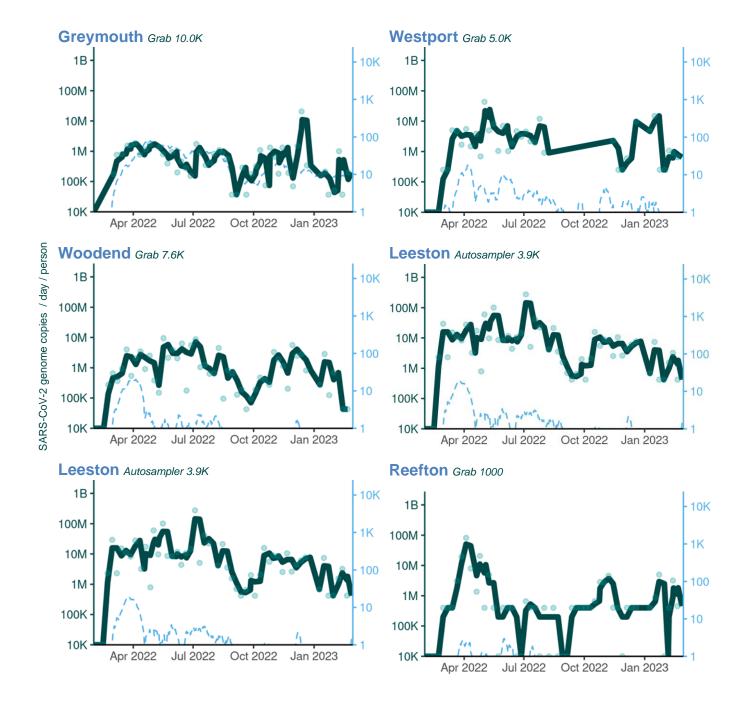


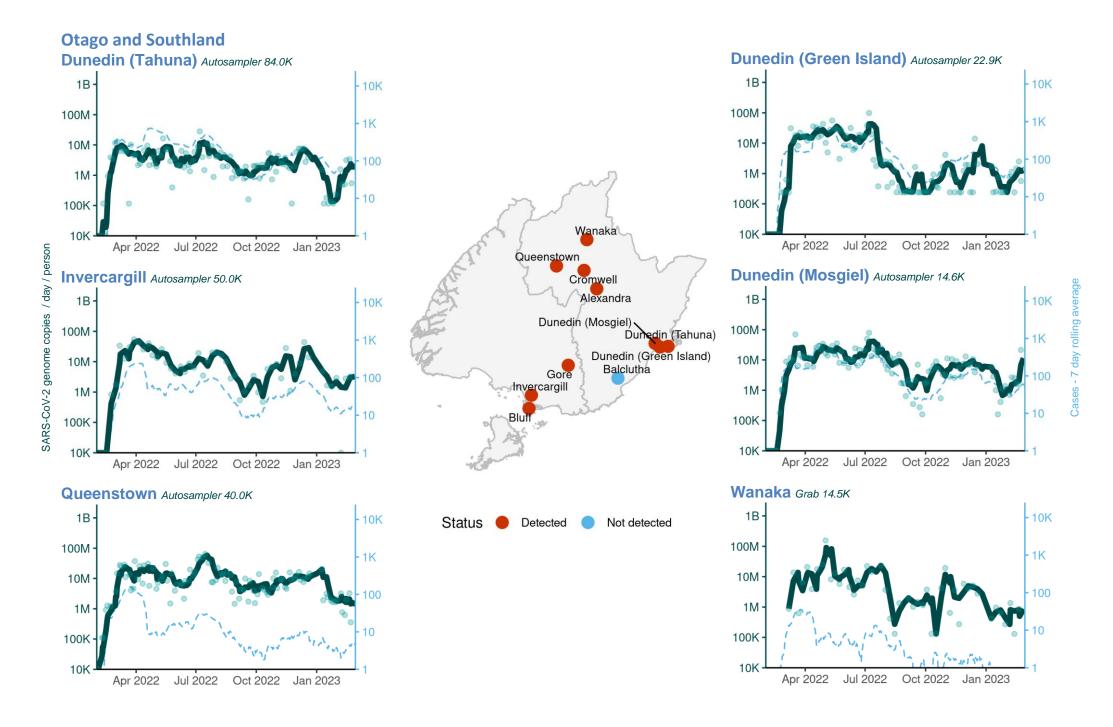












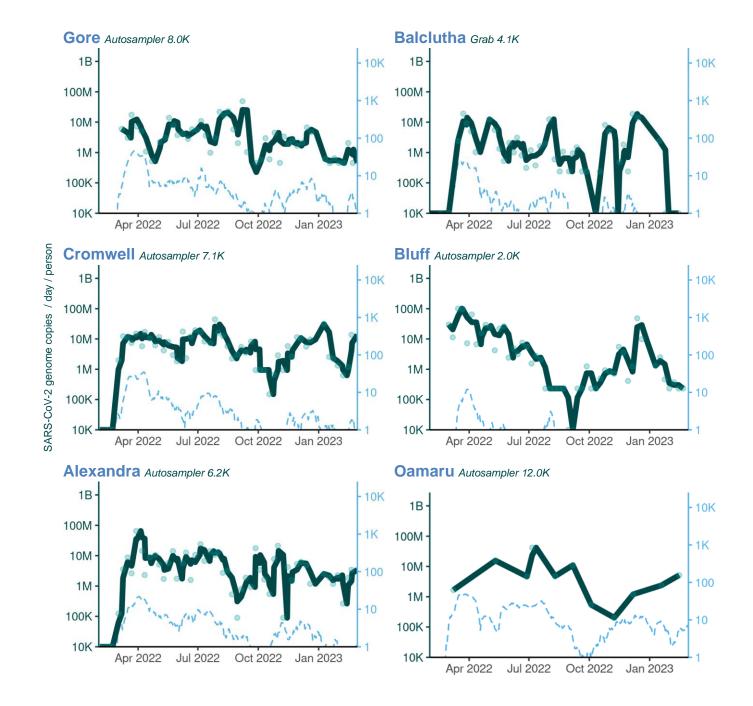


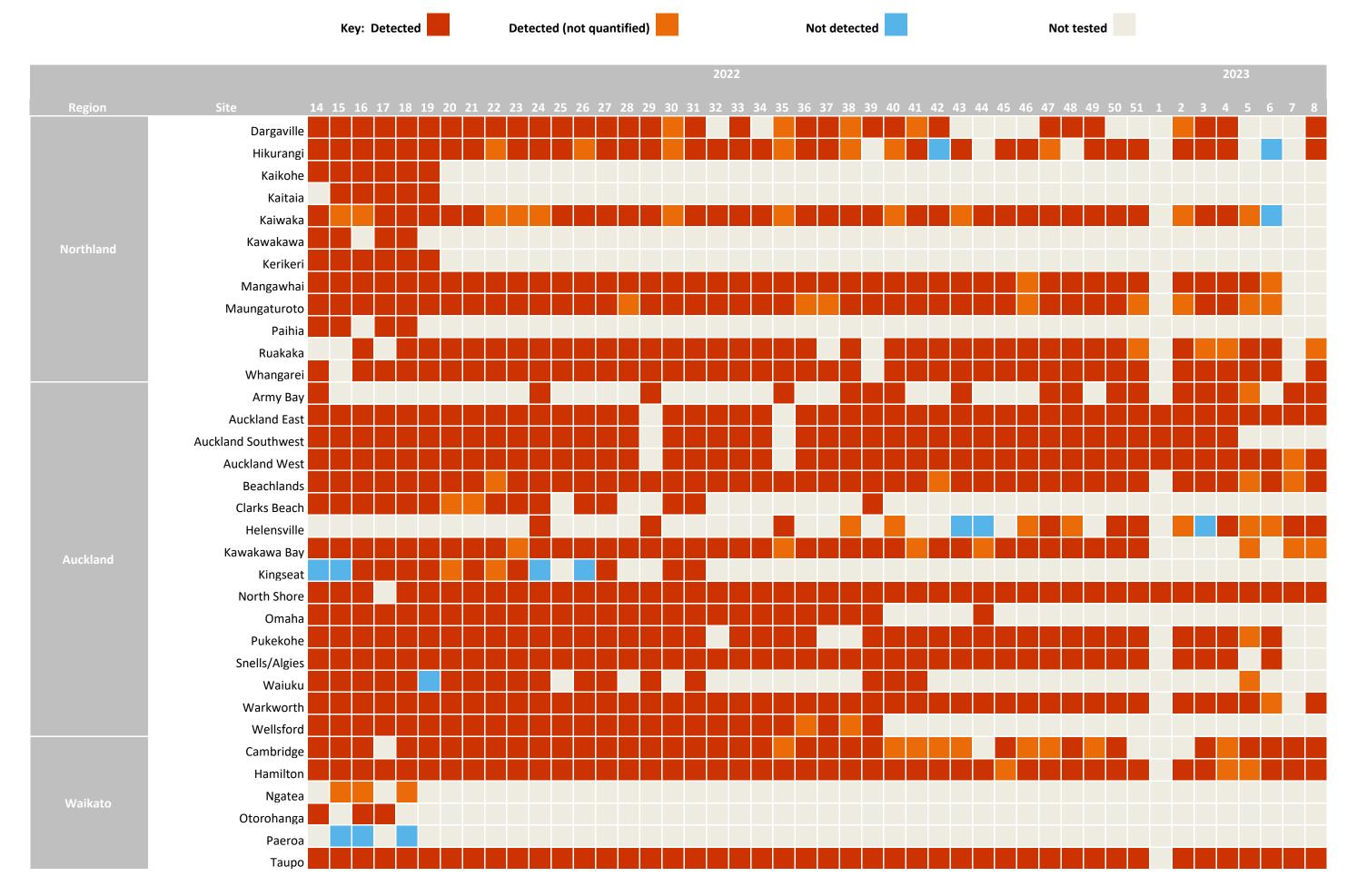
Table 2: Results for weeks 7 & 8 (ending 19 February and 26 February 2023)

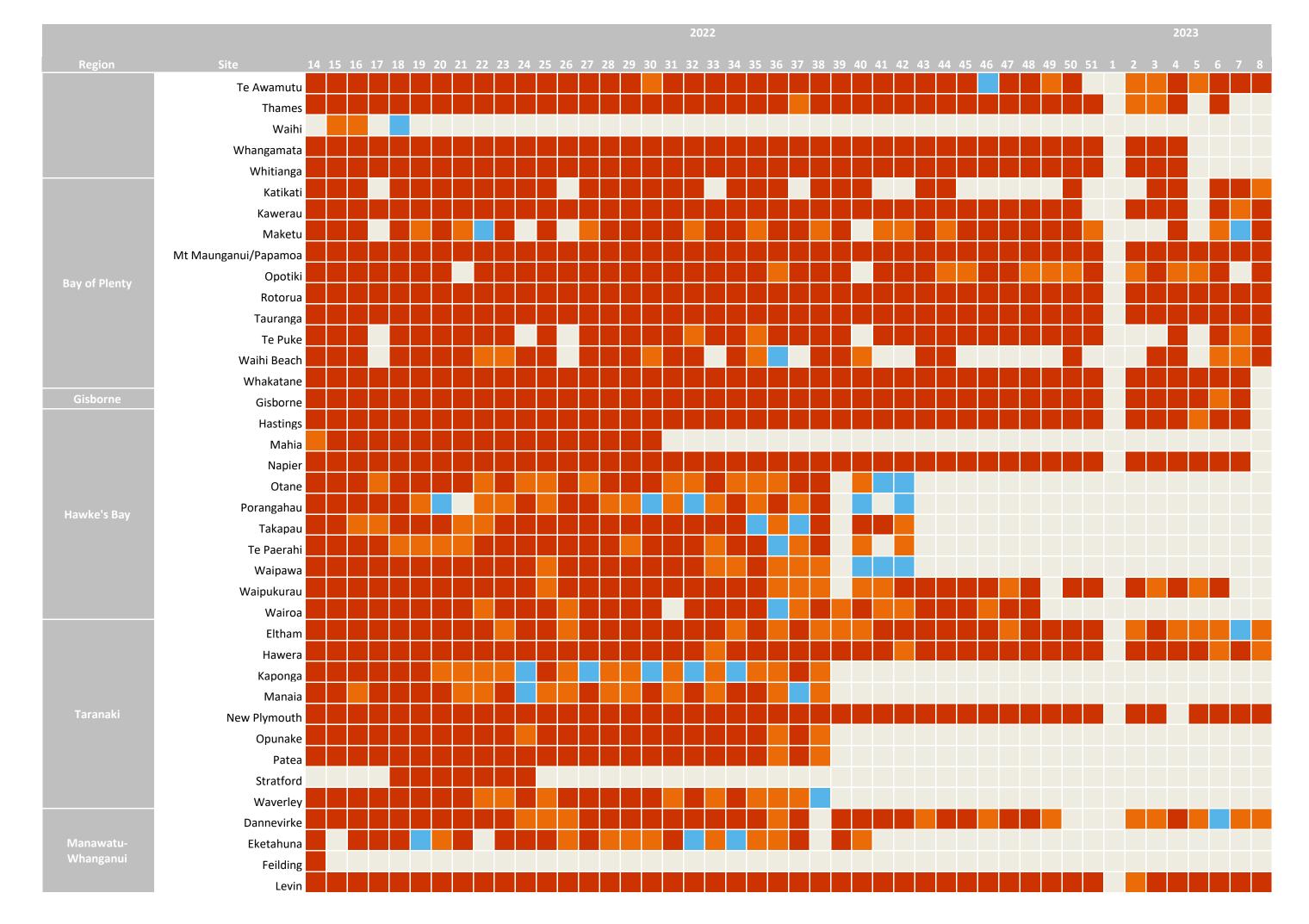
Wastewater testing results. Grab samples are collected usually over 15-30 minutes. Autosampler are 24-hour composites.

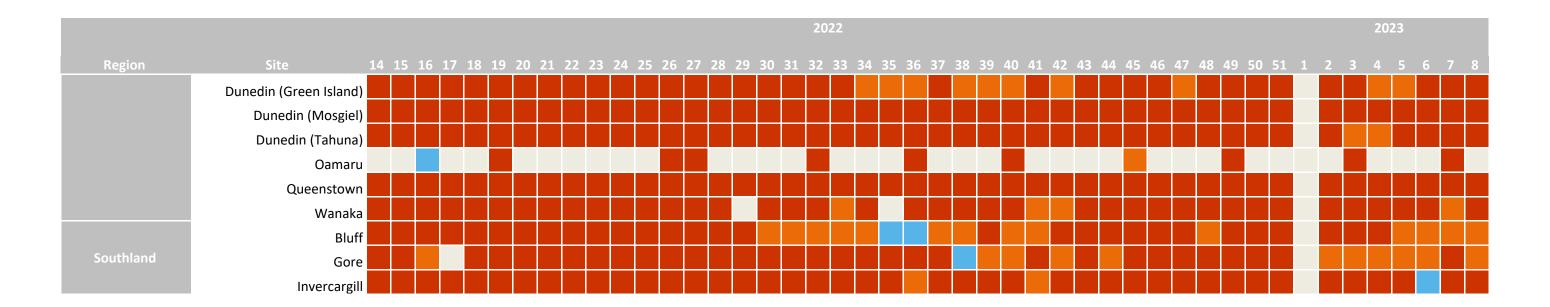
							Februa	ry 2023			
Region	Site	Population	Sample Type	Mon 13	Tue 14	Wed 15	Thu 16	, Mon 20	Tue 21	Wed 22	Thu 23
Northland	Dargaville	5,000	Grab						Detected		
	Hikurangi	1,730	Grab					Detected			
	Ruakaka	4,500	Grab						Detected		
	Whangarei	65,000	Autosampler						Detected	Detected	
Auckland	Army Bay	42,000	Autosampler		Detected				Detected		
	Auckland East	680,000	Autosampler	Detected		Detected		Detected		Detected	
	Auckland West	315,000	Autosampler	Detected		Detected		Detected		Detected	
	Beachlands	6,760	Grab			Detected				Detected	
	Helensville	3,800	Autosampler		Detected				Detected		
	Kawakawa Bay	600	Grab			Detected				Detected	
	North Shore	240,000	Autosampler	Detected		Detected		Detected		Detected	
	Warkworth	3,500	Autosampler						Detected		
Waikato	Cambridge	20,100	Autosampler		Detected					Detected	
	Hamilton	169,000	Autosampler			Detected			Detected	Detected	Detected
	Taupo	23,000	Auto/grab		Detected		Detected		Detected		Detected
	Te Awamutu	13,100	Autosampler		Detected					Detected	
Bay of Plenty	Katikati	5,500	Autosampler			Detected				Detected	
	Kawerau	7,000	Autosampler			Detected			Detected		
	Maketu	1,300	Autosampler			Not detected				Detected	
	Mt Maunganui/Papamoa	65,000	Autosampler		Detected		Detected		Detected	Detected Detected Detected Detected Detected Detected Detected Detected Detected Detected	Detected
	Opotiki	3,800	Autosampler						Detected		Detected
	Rotorua	59,000	Autosampler		Detected		Detected		Detected		Detected
	Tauranga	50,000	Autosampler		Detected		Detected		Detected		Detected
	Te Puke	9,700	Autosampler			Detected				Detected	
	Waihi Beach	3,600	Autosampler			Detected				Detected	
	Whakatane	21,020	Autosampler	Detected							
Gisborne	Gisborne	37,000	Autosampler	Detected							
Hawke's Bay	Hastings	80,000	Autosampler			Detected	Detected				
	Napier	55,000	Autosampler	Detected							
Taranaki	Eltham	2,006	Autosampler			Not detected				Detected	
	Hawera	12,000	Autosampler		Detected	Detected			Detected	Detected	
	New Plymouth	88,000	Autosampler				Detected		Detected		Detected
Manawatu-	Dannevirke	5,696	Grab			Detected				Detected	
Whanganui	Levin	21,200	Autosampler		Detected		Detected		Detected		Detected
	Palmerston North	90,000	Autosampler		Detected		Detected		Detected		Detected
	Taumarunui	4,000	Grab		Detected				Detected		Detected
	Whanganui	44,500	Autosampler		Detected		Detected		Detected		Detected
	Woodville	1,657	Grab			Not detected				Not detected	
Wellington	Carterton	5,800		Detected			Detected	Detected		Detected Detected Detected Not detected	Detected
	Featherston	2,500	Grab			Detected	Not detected	Detected			
	Greytown	2,438	Grab			Detected	Detected	Detected			
	Hutt Valley	133,000	Autosampler	Detected			Detected	Detected			Detected
	Martinborough	1,641	Auto/grab			Detected	Detected	Detected			
	Masterton	20,700	Auto/grab	Detected	Detected				Detected	Detected Detected Detected Not detected	
	Otaki	3,500	Autosampler		Detected				Detected		

				February 2023								
Region	Site	Population	Sample Type	Mon 13	Tue 14	Wed 15	Thu 16	Mon 20	Tue 21	Wed 22	Thu 23	
	Paraparaumu	49,000	Autosampler		Detected				Detected			
	Porirua	85,000	Autosampler	Detected			Detected	Detected			Detected	
	Wellington (Moa Point)	168,000	Autosampler	Detected			Detected	Detected			Detected	
	Wellington (Western)	14,000	Autosampler	Detected			Detected	Detected			Detected	
Nelson	Nelson Central/North	26,000	Autosampler	Detected		Detected		Detected		Detected		
	Richmond/Nelson South	60,000	Autosampler	Detected		Detected						
Marlborough	Blenheim	31,000	Autosampler		Detected				Detected			
	Picton	5,000	Autosampler		Detected				Detected			
West Coast	Greymouth	10,000	Grab	Detected						Detected		
	Reefton	1,000	Grab	Detected				Detected				
	Westport	5,000	Grab	Detected				Detected				
Canterbury	Ashburton	18,000	Autosampler						Detected	Detected		
•	Christchurch	368,000	Autosampler	Detected		Detected		Detected		Detected		
	Kaiapoi	12,500	Grab		Detected				Detected			
	Leeston	3,900	Autosampler	Detected				Detected				
	Rangiora	19,000	Grab		Detected		Detected		Detected		Detected	
	Rolleston & Eastern Selwyn	35,000	Autosampler	Detected		Detected		Detected		Detected		
	Timaru	28,000	Autosampler		Detected				Detected			
	Woodend	7,600	Grab		Detected				Detected			
Otago	Alexandra	6,200	Autosampler			Detected		Detected				
	Balclutha	4,100	Grab		Not detected							
	Cromwell	7,100	Autosampler			Detected		Detected				
	Dunedin (Green Island)	22,900	Autosampler	Detected			Detected	Detected			Detected	
	Dunedin (Mosgiel)	14,600	Autosampler	Detected			Detected	Detected			Detected	
	Dunedin (Tahuna)	84,000	Autosampler	Detected		Detected		Detected			Detected	
	Oamaru	12,000	Autosampler			Detected						
	Queenstown	40,000	Autosampler	Detected		Detected		Detected		Detected		
	Wanaka	14,500	Grab	Detected				Detected				
Southland	Bluff	2,000	Autosampler		Detected				Detected			
	Gore	8,000	Autosampler			Detected				Detected		
	Invercargill	50,000	Autosampler		Detected				Detected			

Table 3: Weekly Summary of Wastewater Sampling Results for SARS-CoV-2







Acknowledgements

This work represents the combined efforts of a large number of individuals and organisations.

We continue to be indebted to the teams across the country who are collecting the wastewater that underpins this work.

The wastewater analysis has been undertaken at ESR by a team which may on any given week include contributions from Joanne Chapman, Dawn Croucher, Joanne Hewitt, Joycelyn Ho, Anower Jabed, Olivia Macrae, Ashley McDonald, Andrew Ng, Ashley Orton, 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 and Leighton Watson. Ongoing support for this work from the Ministry of Health and ESR management is appreciated.

Notes

Sites and frequency of sample collection: The catchment population sites selected for the surveillance range from approximately 400 to over 1,000,000 individuals. The sites cover all regions of the country. Most major towns and all cities, as well as many smaller communities, are included. In early 2023, the wastewater catchment areas cover over 75% of the population connected to wastewater treatment plants. The sites from which samples have been collected have varied over the last 12 months. New sites may be added over time, and/or sampling may reduce in frequency or cease for other sites. The selection and frequency of sampling vary depending on the local population, access to wastewater collection points, staff availability to collect samples and risk factors. When included, samples are collected at least weekly, with twice weekly sampling being common.

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

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

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

Method sensitivity: The protocol used to concentrate SARS-CoV-2 from wastewater allows for the sensitive detection of SARS-CoV-2 by RT-qPCR. ESR has shown that when 10 individuals are actively shedding SARS-CoV-2 RNA in a catchment of 100,000 individuals, there was a high likelihood of detecting viral RNA in wastewater (https://doi.org/10.1016/j.watres.2021.118032). Shedding by one individual may be detected in wastewater, but it does depend on many factors including the amount and duration of shedding. Very low levels in wastewater may be not able to be quantified (i.e., less than the limit of quantification- see below).

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

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

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

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

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

Data not shown:

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

For further information please contact:

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