

New Zealand Wastewater Surveillance Programme COVID-19

Monthly Report: December 2023

Weeks ending 10 December to 31 December 2023

Report prepared 18 January 2024

Key Trends & Insights

For December, SARS-CoV-2 levels in wastewater averaged 5.81 million genome copies per person per day (GC/p/d) compared to 5.77 GC/p/d in November. During this period SARS-CoV-2 levels were highest in the week ending 17 December at 7.63 million GC/p/d.

100%

Sites (45/45) where SARS-CoV-2 was detected

53% – 68%

NZ population covered by wastewater testing in December

JN.1

Most prevalent variant detected (49%)

- In December 2023, 192 samples were collected across Aotearoa. SARS-CoV-2 RNA was detected in 192/192 (100%) samples from 45/45 (100%) sites.
- Due to the holiday period, samples were only collected from a few sites in the week ending 31 December 2023, resulting on population coverage dropping to 53% that week.
- While there were notable fluctuations evident in December 2023, the overall trend shows that following a sustained increase in SARS-CoV-2 RNA quantities in wastewater since August 2023, this has levelled off at a moderately high level this month.
- By the end of December, the JN.1 variant, detected in NZ at the beginning of November 2023, replaced the XBB family of lineages as the predominant circulating variant in NZ wastewater. The estimated national percentage of JN.1 steadily increased through December from 17% in week 48 to 49% in week 51.

National Results

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

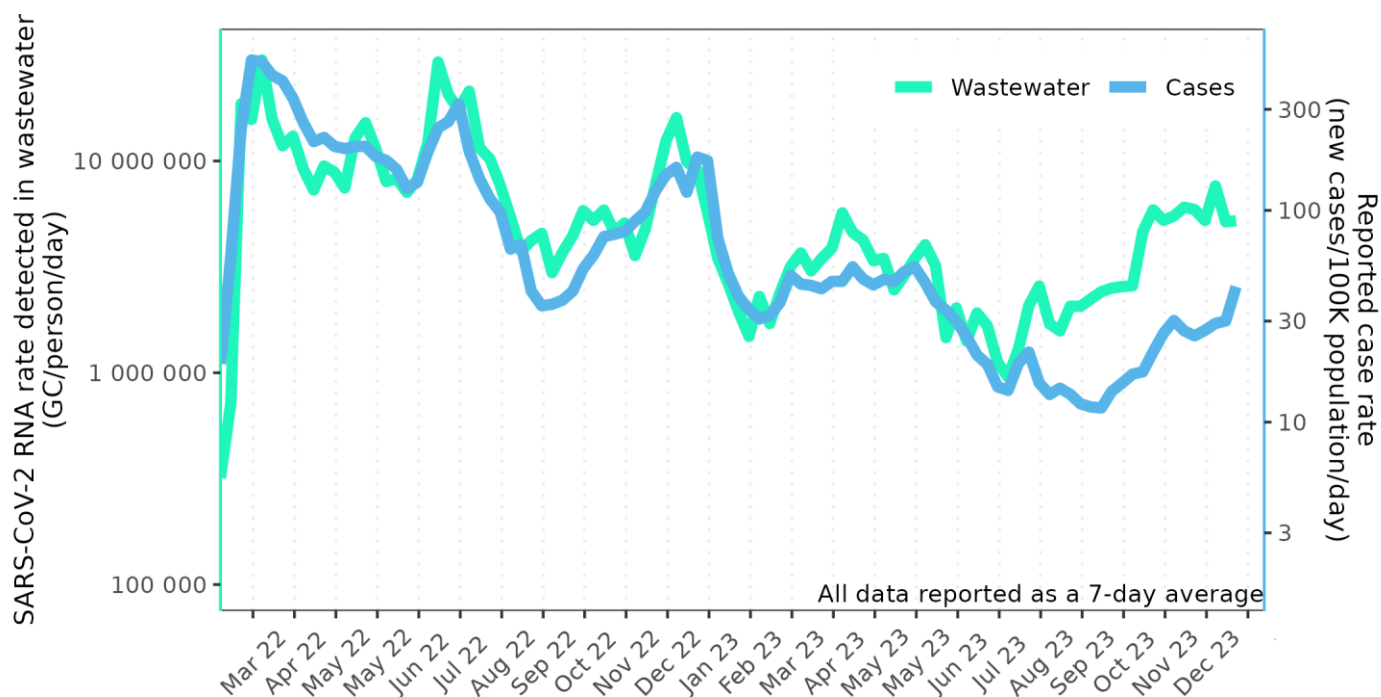


Figure 1. National timeseries of estimated SARS-CoV-2 wastewater rate (GC/person/day, green line) and reported case rate (new cases/100,000 population/day, blue line) on a log₁₀ scale.

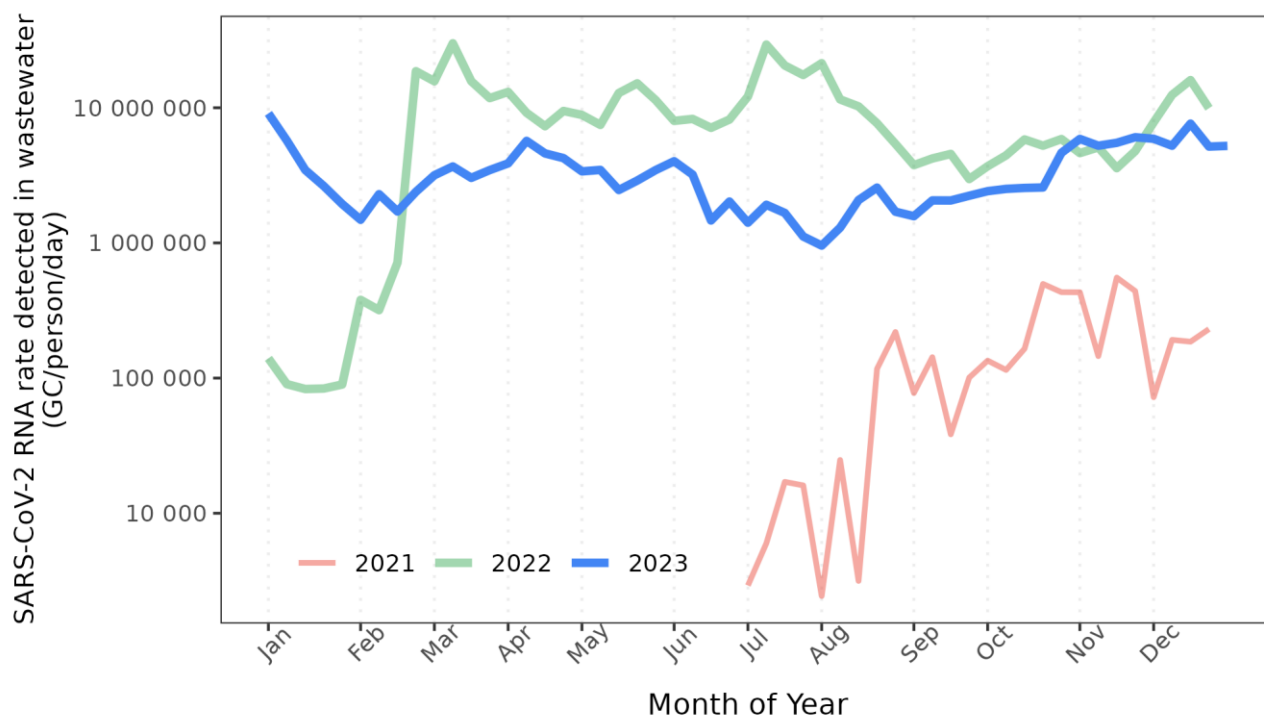


Figure 2. National timeseries of estimated SARS-CoV-2 wastewater rate (GC/person/day)

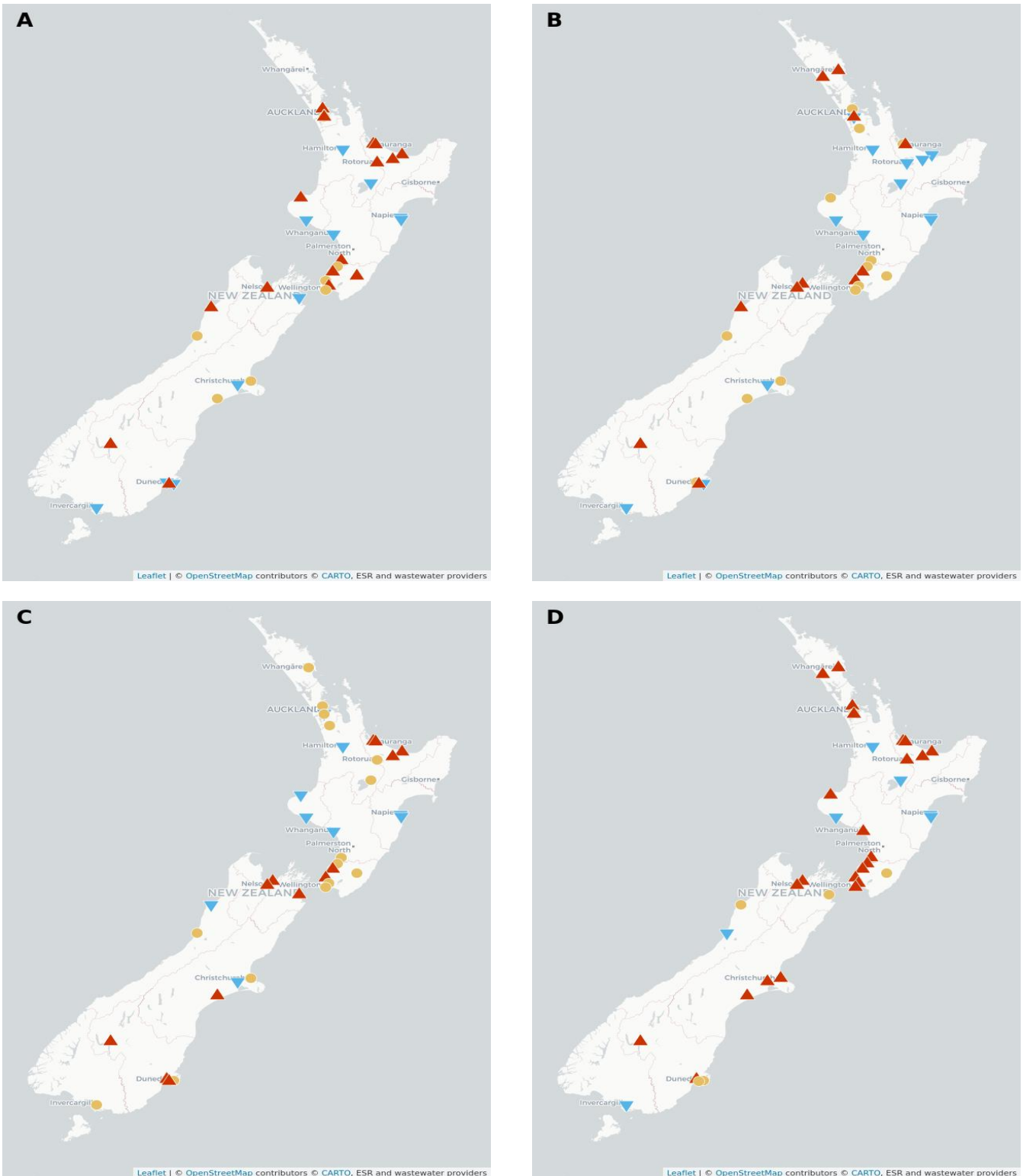


Figure 3. Comparison of SARS-CoV-2 levels for the week ending 24 December 2023 compared to levels measured: A) 1 week ago; B) 2 weeks ago; C) 4 weeks ago; D) 12 weeks ago. Only sites with results for both time points are included. When the viral quantity is 30% or more higher this is labelled as increased (red up arrow on map). When the viral quantity is 30% or more lower, this is labelled as decreased (blue down arrow on map). If viral levels have changed less than this in the compared weeks, this is labelled as no change (yellow circle on map). Interactive map of weekly results available publicly at <https://www.poops.nz/>

Variant Analysis

Results from four weeks of sampling (weeks 48 to 51) from up to 20 sentinel wastewater sites (Table 1) across New Zealand are reported.

The XBB family of lineages (which includes EG.5, HK.1.2, HK.3 and JD.1.1) was the predominant lineage group at the beginning December but decreased as a percentage throughout the month. The estimated national percentage of this group collectively was 69% in week 48, 64% in week 49, 53% in week 50 and 39% in week 51 (variants shown in shades of green, Figures 4 and 5, Table 1).

The percentage of JN.1 (a descendant lineage of BA.2.86) increased from weeks 48 to week 51. The estimated national percentage was this variant was 17% in week 48, 26% in week 49, 34% in week 50 and 49% in week 51 (shown in purple in Figures 4 and 5, Table 1).

The percentage of BA.2.86 increased slightly across the month, from 6% in week 48 to 10% in week 51.

XBC and other recombinant lineages decreased as a percentage of the national total over December, being at low levels by the end of the month.

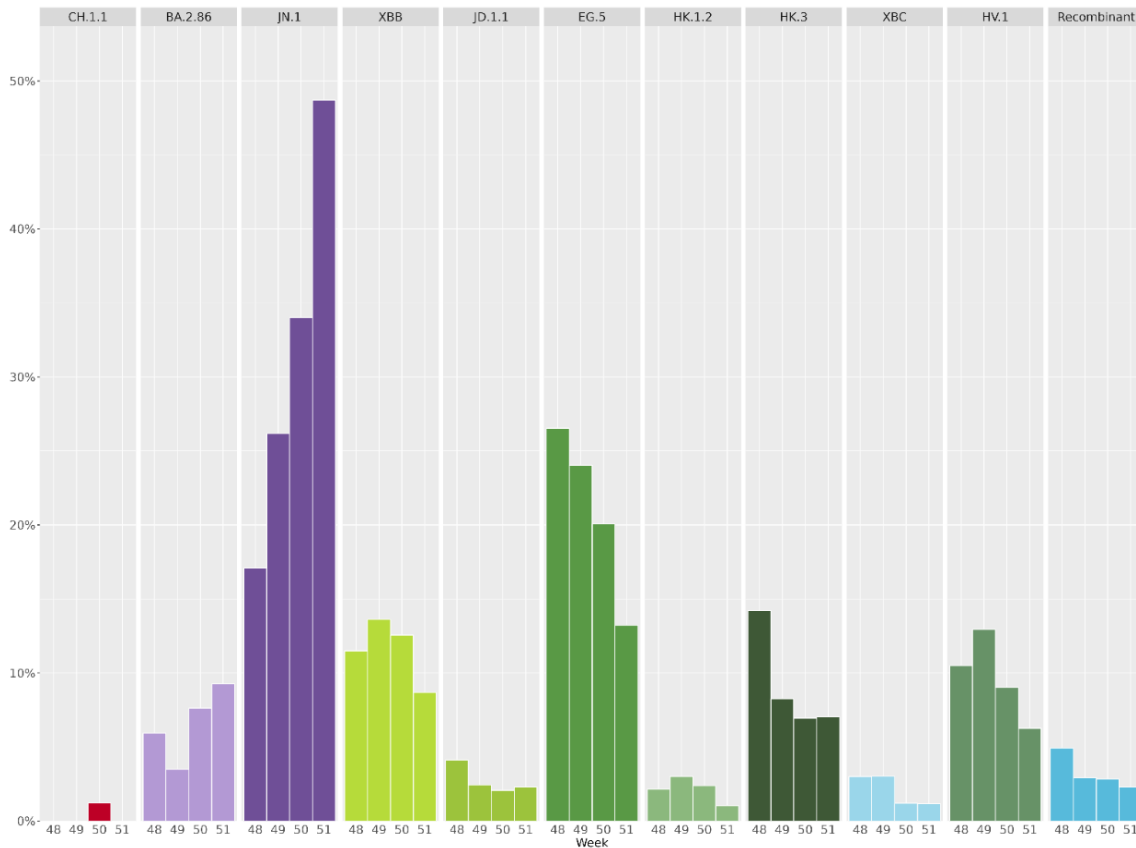


Figure 4. National percentage of each variant for week 48 (ending 03 December 2023) to week 51 (ending 24 December 2023).

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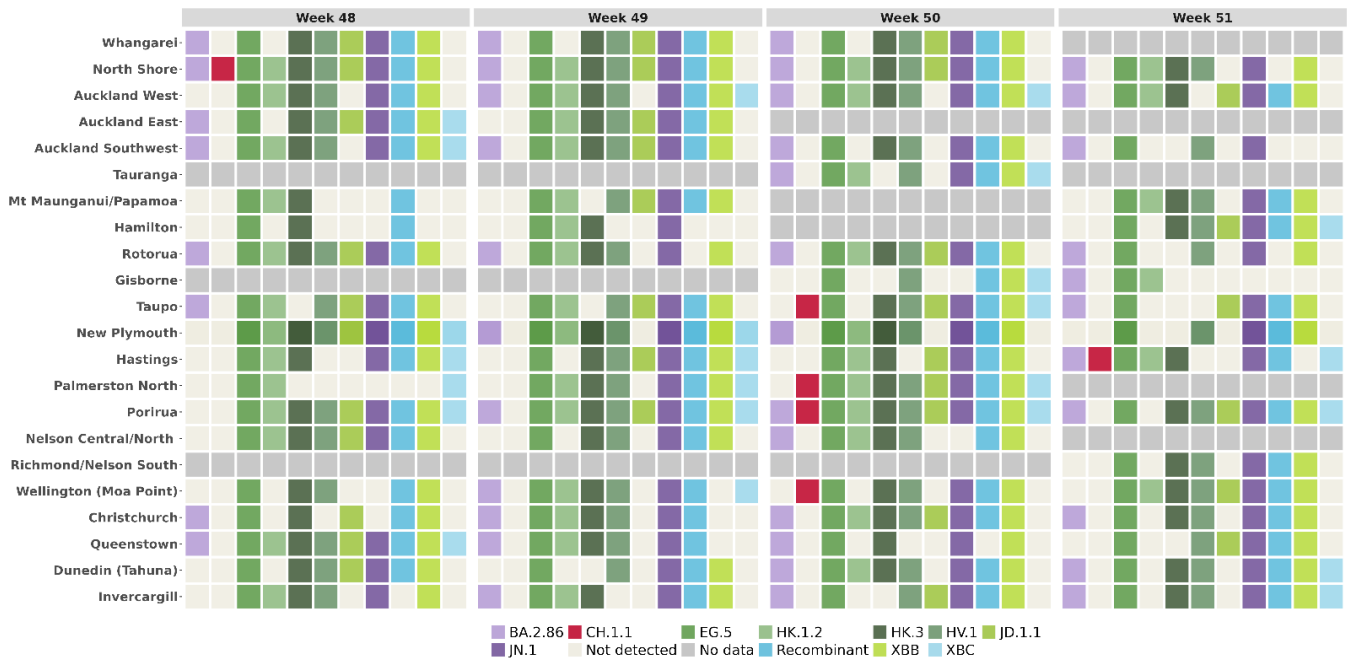


Table 1. Data from ~20 wastewater sentinel sites sampled from week 48 (ending 3 December 2023) to week 51 (ending 24 December 2023). Coloured box denotes that the variant was detected at that site that week, cream box denotes that the variant was not detected, and grey box denotes site was not sampled that week.

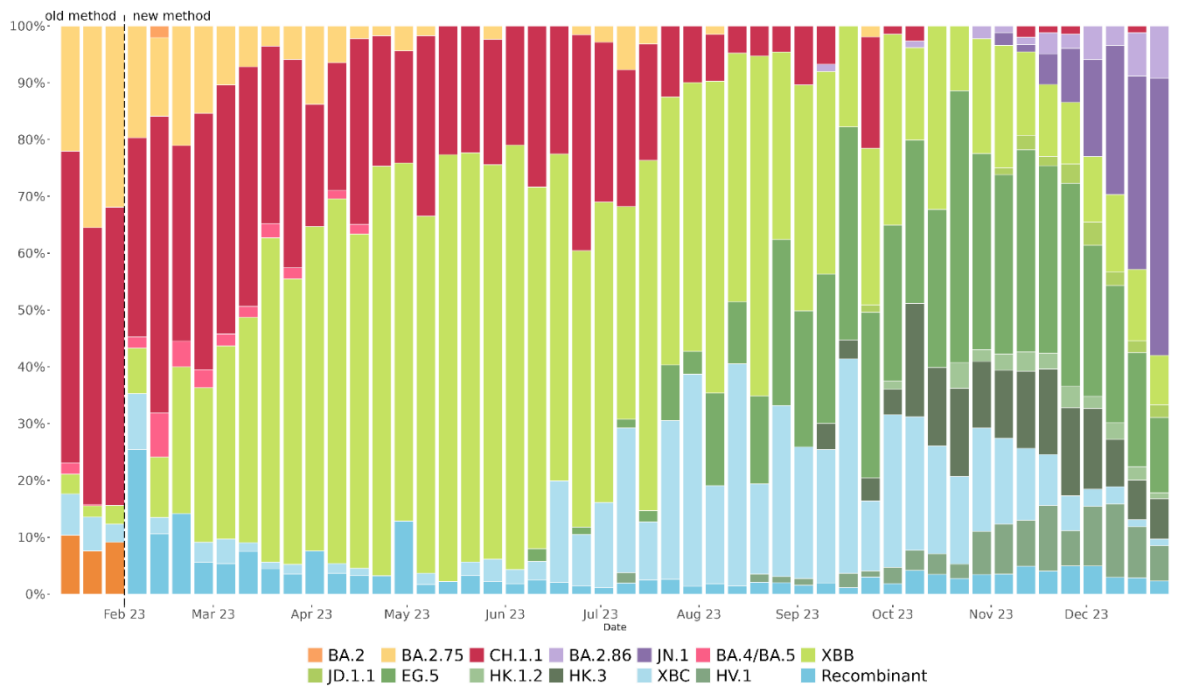


Figure 5. Estimated variant percentage over time at a national scale (average). Data are collected from ~20 sentinel sites each week.

Instantaneous Reproduction Number

Daily wastewater and case data up to 31 December 2023 was used. The uncertainty in these measures is denoted with 95% credible intervals (shown in green in Figure 6).

The estimate of the instantaneous reproduction number for 31 December 2023 (in week 52) was 0.94 (95% credible interval 0.67 – 1.31, Figure 6).

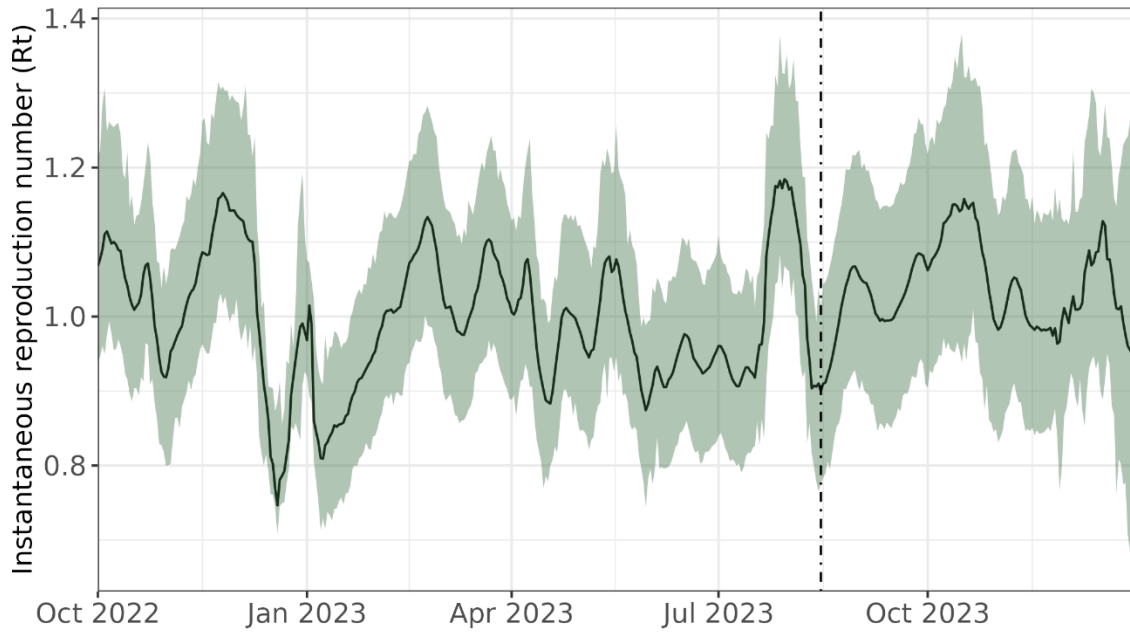


Figure 6. Estimates of instantaneous reproduction number. Black vertical lines represent when COVID-19 restrictions were lifted on 15 August 2023. Results assume the average total shedding per infection does not vary over time ($\alpha = 3 \times 10^9$). Black solid lines represent central estimates. Shaded regions show 95% credible intervals on the value of the hidden states.

Trends in Ministry of Health Regions

Regional analysis of the wastewater data is shown in Figure 7. Regional estimates could not be calculated for week 52 (ending 31 December 2023) due to a limited sampling schedule being operated over the holiday break.

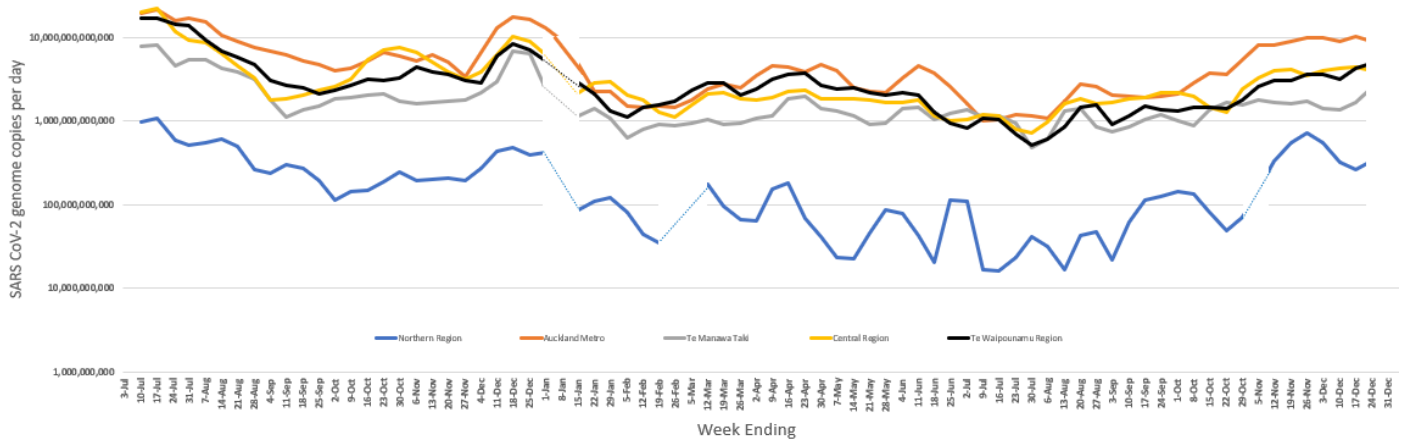


Figure 7. Two week rolling average of total SARS-CoV-2 genome copies detected per day in the five Ministry of Health regions. Dashed lines are inferred levels during periods when samples were either not collected (Christmas period) or insufficient numbers collected (due to weather impacts) for the region.

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 (GC/p/d). 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/p/d 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.

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 recognised 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*.

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

Acknowledgements

This work represents the combined efforts of many individuals and organisations.

We thank the teams across the country who are collecting the wastewater that underpins this work.

The wastewater analysis has been undertaken at ESR by a team including laboratory staff, data scientists, bioinformaticians, and other staff. Ongoing support for this work from the Ministry of Health and ESR management is appreciated.

Notes

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

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

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

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

Method sensitivity: The protocol used to concentrate SARS-CoV-2 from wastewater allows for the sensitive detection of SARS-CoV-2 by RT-qPCR. ESR has shown that when 10 individuals are actively shedding SARS-CoV-2 RNA in a catchment of 100,000 individuals, there was a high likelihood of detecting viral RNA in wastewater (<https://doi.org/10.1016/j.watres.2021.118032>). Shedding by one individual may be detected in wastewater, but it does depend on many factors including the amount and duration of

shedding. Very low levels in wastewater may be not able to be quantified (i.e., less than the limit of quantification- see below).

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

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

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

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

Wastewater Data Modelling

COVID-19 surveillance in Aotearoa, based on self-reported tests, can be problematic due to decreased testing and reporting. This difficulty is further amplified by increasing numbers of asymptomatic infections and reinfections. Accordingly, there is a need to use additional tools to monitor the rates/trends of infection within the community and to explore what information, predictive potential, and uncertainty, lies within the wastewater data. ESR has partnered with Auckland, Massey and Canterbury Universities (including the COVID-19 Modelling Aotearoa group; CMA) to address these issues. Modelling infection dynamics using wastewater data has challenges. There are many confounding factors that can influence the levels of SARS-CoV-2 in a wastewater catchment - from rainfall effects and shedding rates through to differences in RNA concentrations between variants. Current modelling reports on three key metrics (i) an estimate of the instantaneous reproduction number ' R_t ' based on both case data and wastewater quantitation and (ii) an estimate of the relative case ascertainment rate (rCAR).

Instantaneous reproduction number (R_t): The instantaneous reproduction number (R_t) represents the average number of secondary cases that will arise per primary infectious case. The effective reproduction (R_{eff}) number can be measured as either the instantaneous reproduction number (R_t),

which measures transmission at a specific point in time; or the case reproductive number, which measures transmission for a specific cohort of individuals. The models described measure the instantaneous reproduction number (R_t). In general terms, an R_t above 1 would typically indicate an increasing number of infections in the population. The instantaneous reproduction number is calculated using a semi-mechanistic model that is fitted to (i) case numbers and (ii) wastewater quantitation, and incorporates information about shedding rates, infection generation times, and case ascertainment. Instantaneous reproduction number is estimated take into account any delays in self-reporting of cases. It should be noted that there is uncertainty in this measure, which is denoted with the 95% credible intervals.

Case Ascertainment Rate (CAR) modelling: The case ascertainment rate (CAR) is the ratio of detected cases to the true number of cases, and therefore provides an estimate of how many unreported cases there are in a population. Estimating, and accounting for, the rate at which COVID-19 cases are under reported in the community is changing over time and is complicated by a variety of confounding factors. In particular, in the absence of any other evidence, we assume that the average total shedding per infection does not vary over time ($\alpha = 3 \times 10^9$). There are a variety of methods used to estimate CAR, from surveys to inpatient positivity. The wastewater-based estimate of CAR is an alternative approach. In the absence of a seroprevalence survey to 'ground-truth' the population infection rate, the case ascertainment rate is unknown. Instead, we model the relative case ascertainment rate (rCAR) relative to 1 April 2022 (with CAR on this date being arbitrarily set to 1). rCAR provides a measure of how CAR has varied since this time. There is a need to be cautious about the precision of this model and its underlying assumptions, but we consider, currently, that this is the best available estimate of the CAR.

Data subject to change: Data generated for the New Zealand Wastewater COVID-19 Surveillance Programme should be considered provisional and may be subject to change.

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

For further information please contact:

Joanne Hewitt

Science Leader

Joanne.hewitt@esr.cri.nz

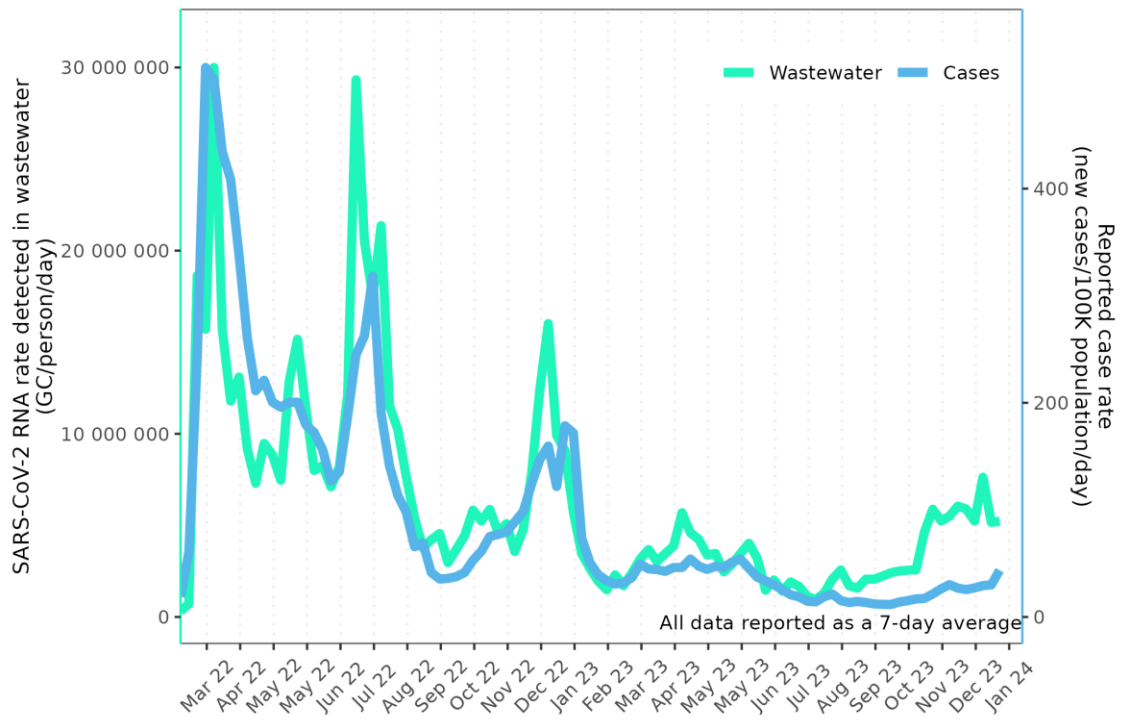
Jo Chapman

Senior Scientist

Joanne.chapman@esr.cri.nz

Appendix A. National Results

Time series plotted on linear scale



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	Sample Type	2023																																																			
				8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52							
Northland	Dargaville	5,000	Grab	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■						
	Mangawhai	1,100	Grab	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■					
	Maungaturoto	1,300	Grab	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■				
Auckland	Whangarei	65,000	Autosampler	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■				
	Army Bay	42,000	Autosampler	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■			
	Auckland East	680,000	Autosampler	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■			
	Auckland Southwest	120,000	Autosampler	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■			
	Auckland West	315,000	Autosampler	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■		
	Beachlands	6,760	Grab	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■			
	North Shore	240,000	Autosampler	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■		
	Pukekohe	20,900	Autosampler	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■		
	Snells/Algies	4,000	Autosampler	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■		
	Warkworth	3,500	Autosampler	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	
	Waikato	Cambridge	20,100	Autosampler	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	
Hamilton		169,000	Autosampler	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	
Taupo		23,000	Auto/grab	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	
Te Awamutu		13,100	Autosampler	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	
Whitianga		6,600	Autosampler	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	
Bay of Plenty	Katikati	5,500	Autosampler	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■		
	Kawerau	7,000	Autosampler	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	
	Mt Maunganui/Papamoa	65,000	Autosampler	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■
	Rotorua	59,000	Autosampler	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■
	Tauranga	50,000	Autosampler	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■
Gisborne	Whakatāne	21,020	Autosampler	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	
	Gisborne	37,000	Autosampler	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■
Hawke's Bay	Hastings	80,000	Autosampler	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■
	Napier	55,000	Autosampler	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■
Taranaki	Waipukurau	4,610	Autosampler	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■
	Eltham	2,007	Autosampler	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■

