



# NCCID Report

2024-11-25

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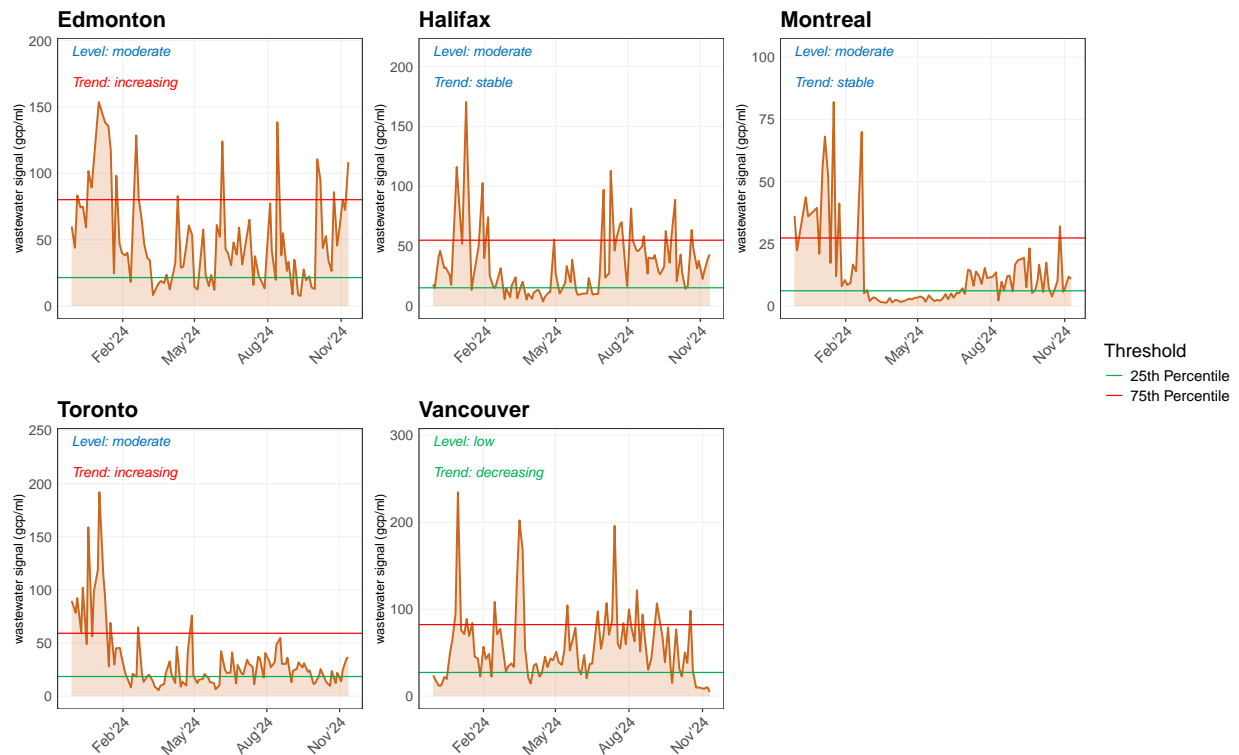
## Introduction

This document shows the current level of SARS-CoV-2 in the wastewater in cities across the country. In the plots below, the horizontal axis displays the month, and the vertical displays the wastewater signal as SARS-CoV-2 genome copies per ml (gcp/ml). The green and orange threshold lines display the historical 25th and 75th percentile, respectively. Information on how these values are calculated can be seen in Appendix 2: Technical Documentation. The current level compared to historical data and trends for each city are shown in the top left corner of each plot, and the key messages highlight recent important changes in the data.

## Current Data

### Key messages:

Current levels of SARS-CoV-2 in the wastewater are low or medium for all reporting cities. The monthly trends in most reporting cities are either stable or increasing, except Vancouver which is decreasing. Current  $R_t$  values are at or above one for most cities, except for Vancouver, which is below 1.



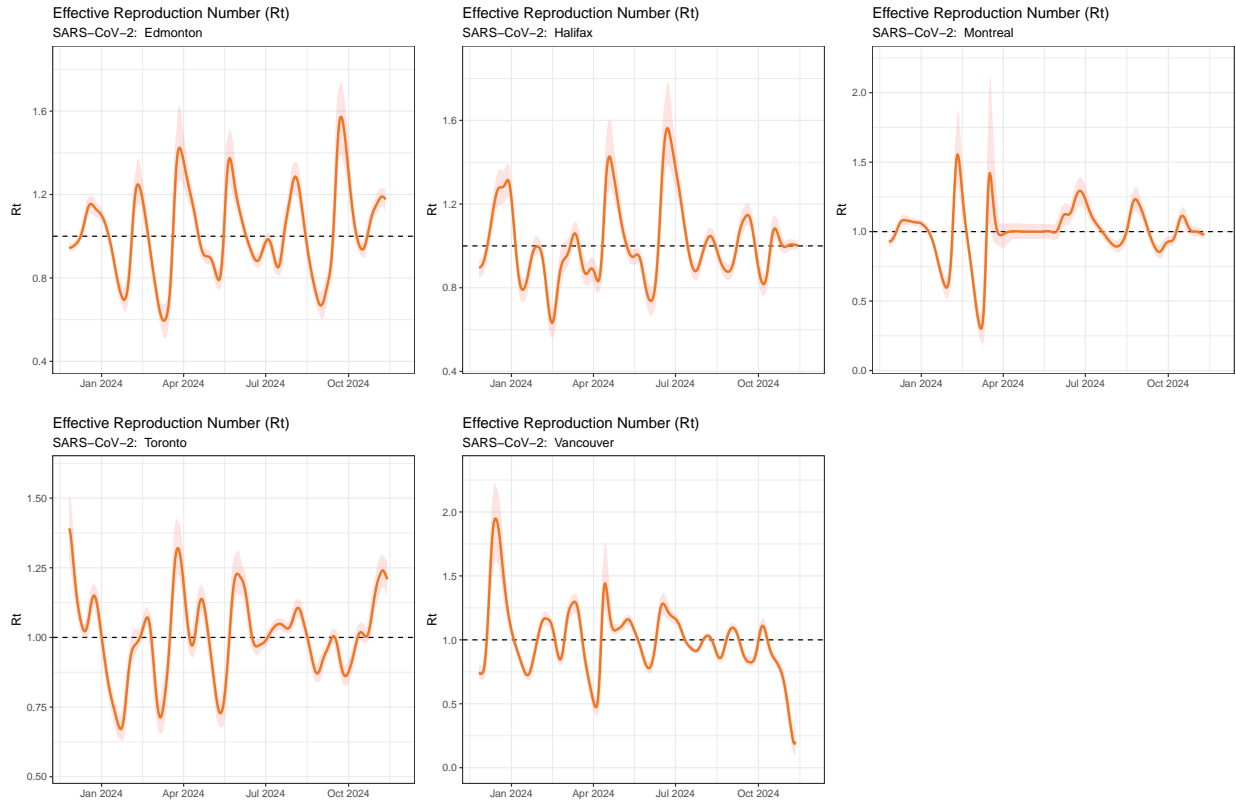
Threshold lines are calculated based on historical wastewater concentrations since the Omicron wave. Levels are based on the last 4 reported values. Any asterisks denoted on trends indicate uncertainty in data due to variability and continued monitoring is required.

## Previous Report Data

City	Previous Month Level	Previous Month Trend
Toronto	Low	Stable
Vancouver	Medium	Increasing
Edmonton	Medium	Decreasing
Montreal	Medium	Decreasing
Halifax	Medium	Decreasing

## $R_t$ Values

Effective reproduction number, or  $R_t$ , is estimated from the concentration of SARS-CoV-2 genome in the wastewater.  $R_t$  indicates how rapidly a disease is spreading; a value greater than 1 indicates the number of new infections is increasing, and a value less than 1 indicates the number of new infections is decreasing. The plots below show the estimated  $R_t$  (y-axis) over time, and the dashed line represents an  $R_t$  value of 1.



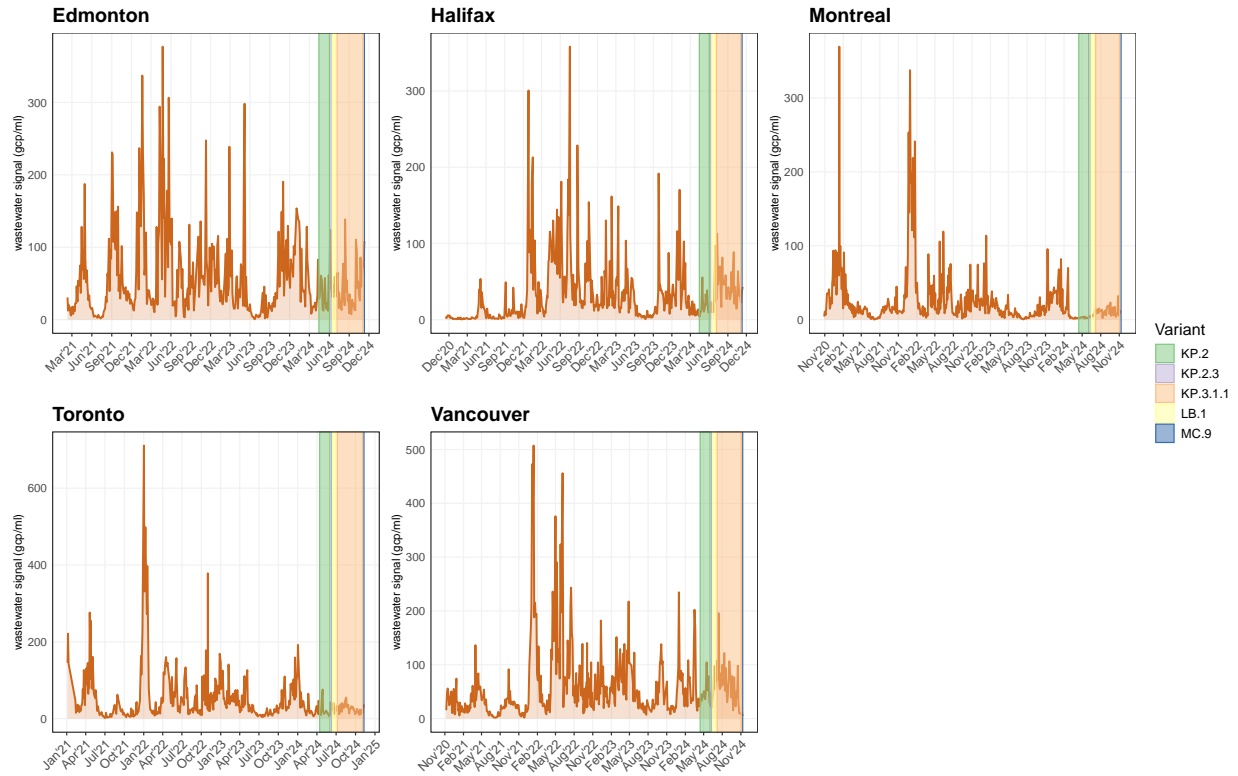
## Latest Observation Dates

This document contains wastewater data collected for each city up to the following dates:

City	Date
Edmonton	2024-11-10
Halifax	2024-11-13
Montreal	2024-11-09
Toronto	2024-11-12
Vancouver	2024-11-10

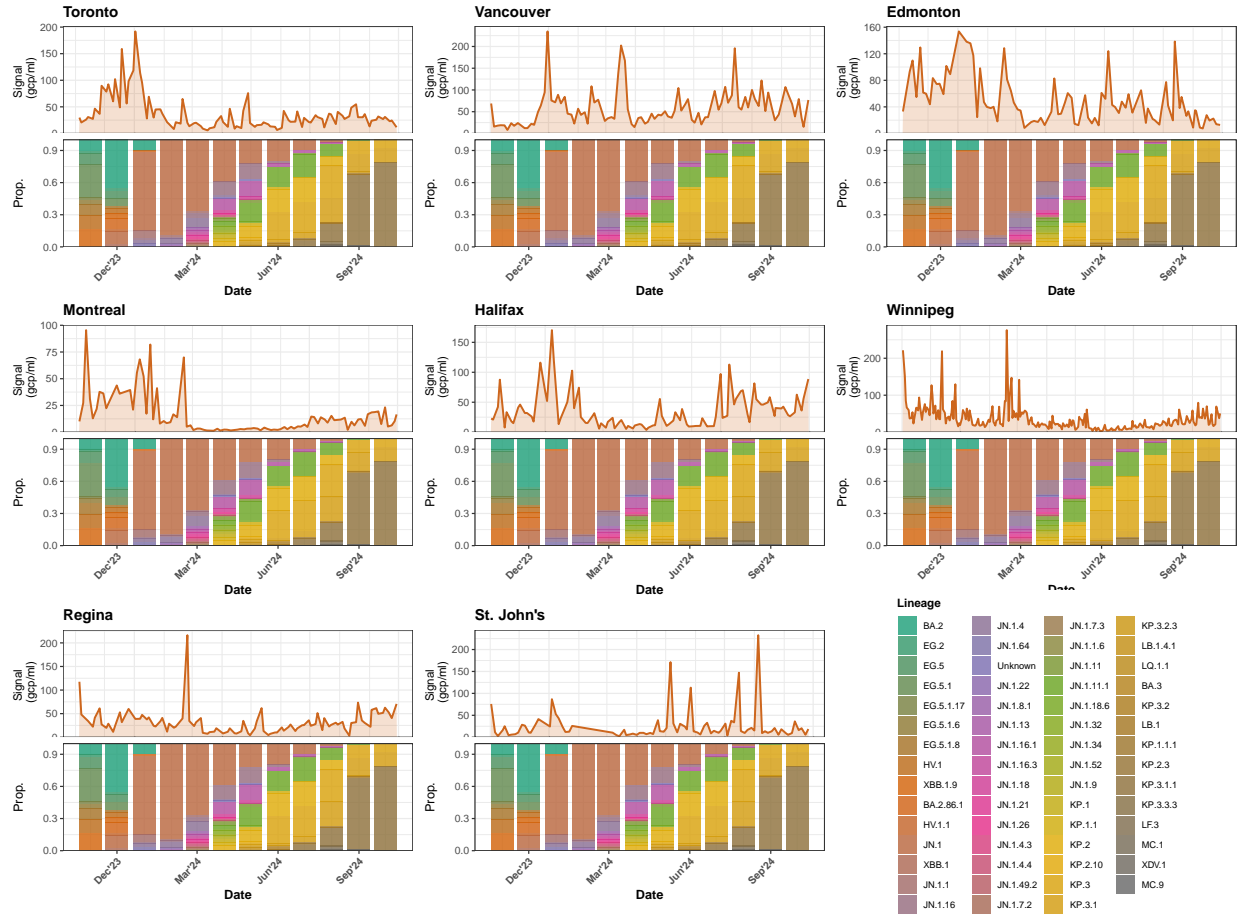
# Appendices

## Appendix 1: Historical Data with SARS-CoV-2 Variants



Most common circulating variant. Periods where there was competing dominance between multiple variants are not shaded.

## Appendix 2: SARS-CoV-2 Wastewater Signal and Sequenced Lineages



### Appendix 3: Technical Documentation

This document serves to provide background information on the Monthly NCCID wastewater report. Here we outline the steps to produce wastewater data, model the levels and trends of SARS-CoV-2, and report the information.

**Sample Collection:** Wastewater is sampled from numerous sites in cities across the country. Each city has a different number of sites the samples are collected from (Table 1). Moreover, each site has a different sampling and shipping schedule; for example, Winnipeg sites are sampled more frequently than those in other cities (Table 1). Table 1 shows the percentage of the city and province that is sampled by the wastewater sites. The values in this table are based off 2021 Canadian Census values.

Table 1: Region Sampling Characteristics

	Number of Sites	Average samples per week	% Coverage (City)	% Coverage (Province)
Toronto	4	2.38	100.00	19.84
Vancouver	5	2.43	99.73	52.70
Edmonton	1	2.29	90.71	21.51
Montreal	2	2.65	100.00	24.14
Halifax	3	2.38	51.19	23.23
Winnipeg	3	5.86	79.79	49.62
Regina	1	2.15	97.17	19.43
St. John's	1	2.28	61.15	25.46

**Data Generation:** Samples are processed by the National Microbiology Laboratory in Winnipeg. Reverse Transcriptase quantitative Polymerase Chain Reaction (RT-qPCR) assays are used to quantify the amount of SARS-CoV-2 genome present in the samples, measured in genome copies per ml (gcp/ml; y-axis above). All samples are completed in duplicate to ensure stability of measurements. However, wastewater is a complex sample; inhibited PCR reactions, rapid changes in genome quantities, and temporal aberrations are common which can cause uncertainty in the data. We work with the NML to identify these inconsistencies and report them with the monthly updates.

#### Modelling the Data:

**Levels:** Data from the RT-qPCR are collected weekly and added to our database of historical data. Thresholds are calculated from this data to determine low, medium, and high gcp/ml for each region. Low values are defined as below the historical 25th percentile since emergence of Omicron; high values are defined as above the historical 75th percentile since omicron; values between the 25th and 75th percentiles are considered medium.

**Trends:** Trends are calculated using polynomial functions fit to the data from the previous six months. The average slope (rate of change) of the functions over the previous month provides a trend index which corresponds (roughly) to the change in levels reported (Increasing, Stable, or Decreasing). However, the index requires some interpretation before reporting. The modelling team, along with the NML, observe recent data, trend indices, and the polynomial plots to determine the recent trends reported in our monthly updates.