Southern Ontario Wastewater Analysis Report

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Background

On

Analysis of Omicron mutations

We had the following objectives:

1. identify common mutations in lineage B.1.1.529 (Omicron) relative to the SARS-CoV-2 reference genome sequence (WH1);
2. determine which of these common mutations are unique to B.1.1.529, in comparison to all other defined lineages;
3. retrospectively screen all available wastewater sample data sets for the presence of these mutations.

Prevalence of Omicron Mutations

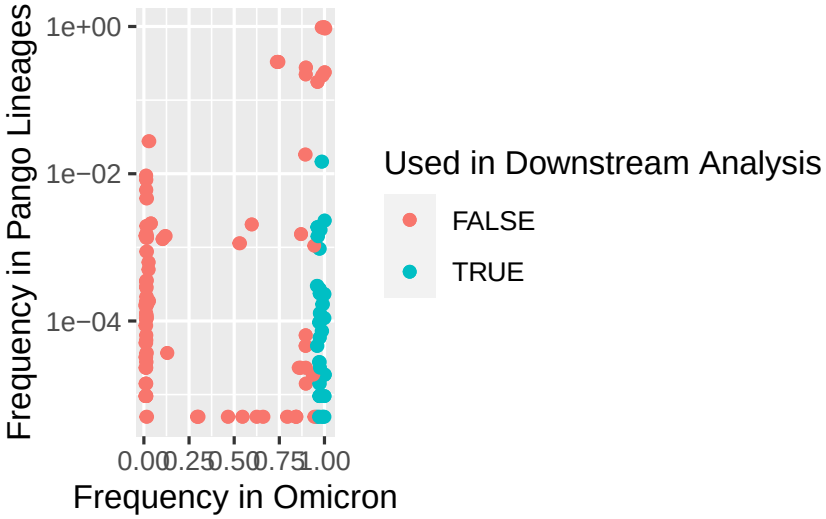

Figure 1 Illustration of 111 mutations found throughout 77 Omicron genomes. Mutations used in downstream analysis were present in >95% of Omicron genomes and <5% of all other Pango lineages.

From the 111 mutations, we selected mutations present in >95% of Omicron genomes and <5% of all other Pango lineages for further downstream analysis (n=29) on existing data files. These mutations are shown in Table 1.

Table 1 Mutations selected from Omicron mutations for downstream analysis of fastq files.

Mutation	Frequency in Omicron	Frequency in Pango Lineages
~8392A	1.000000	0.0000000
~18162G	1.000000	0.0000045
~2831G	1.000000	0.0000136
~10448A	1.000000	0.0000136
~13194C	1.000000	0.0001044
~11536G	1.000000	0.0002270
~15239T	1.000000	0.0023066
~5385G	0.987013	0.0000000
~23201A	0.987013	0.0000681
~23598G	0.987013	0.0001635
~23524T	0.987013	0.0145930
~26576G	0.974026	0.0000000
~22673T	0.974026	0.0000045
~24468A	0.974026	0.0000045
~27258C	0.974026	0.0000091
~22672C	0.974026	0.0000182
~22678C	0.974026	0.0000227
~22897A	0.974026	0.0000545
~26708A	0.974026	0.0000908
~22577A	0.974026	0.0001226
~27806T	0.974026	0.0002316
~22881G	0.974026	0.0002679
~26529G	0.974026	0.0009535
~24999T	0.974026	0.0017254
~24129A	0.961039	0.0000000
~23853A	0.961039	0.0000409
~23947T	0.961039	0.0002951
~26269T	0.961039	0.0014075
~22812T	0.961039	0.0018798

Omicron Mutations in Wastewater Samples

Omicron Mutation Coverage

Omicron Mutations Discovered