

# Whole-genome sequencing of SARS-CoV-2 for Canada's COVID-19 genomic surveillance

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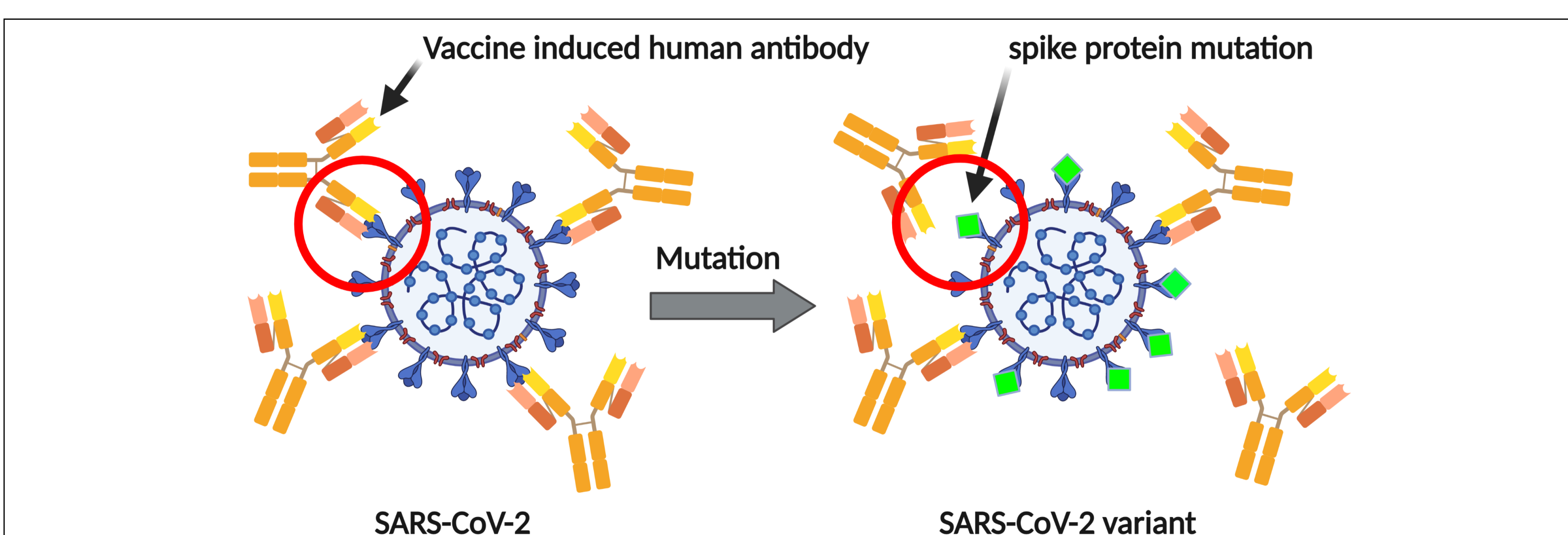
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## Background

Whole-genome sequencing (WGS) technology is a powerful tool used to determine the complete genome of an organism allowing for the detection of mutations. Genomic surveillance, which is the continuous monitoring of genomic variations over time, is made possible by WGS. Through genomic surveillance, mutations in SARS-CoV-2 can be used to identify novel variants of concern (VOC) that are known to:

1. Enhance transmission of SARS-CoV-2
2. Decrease COVID-19 vaccine effectiveness



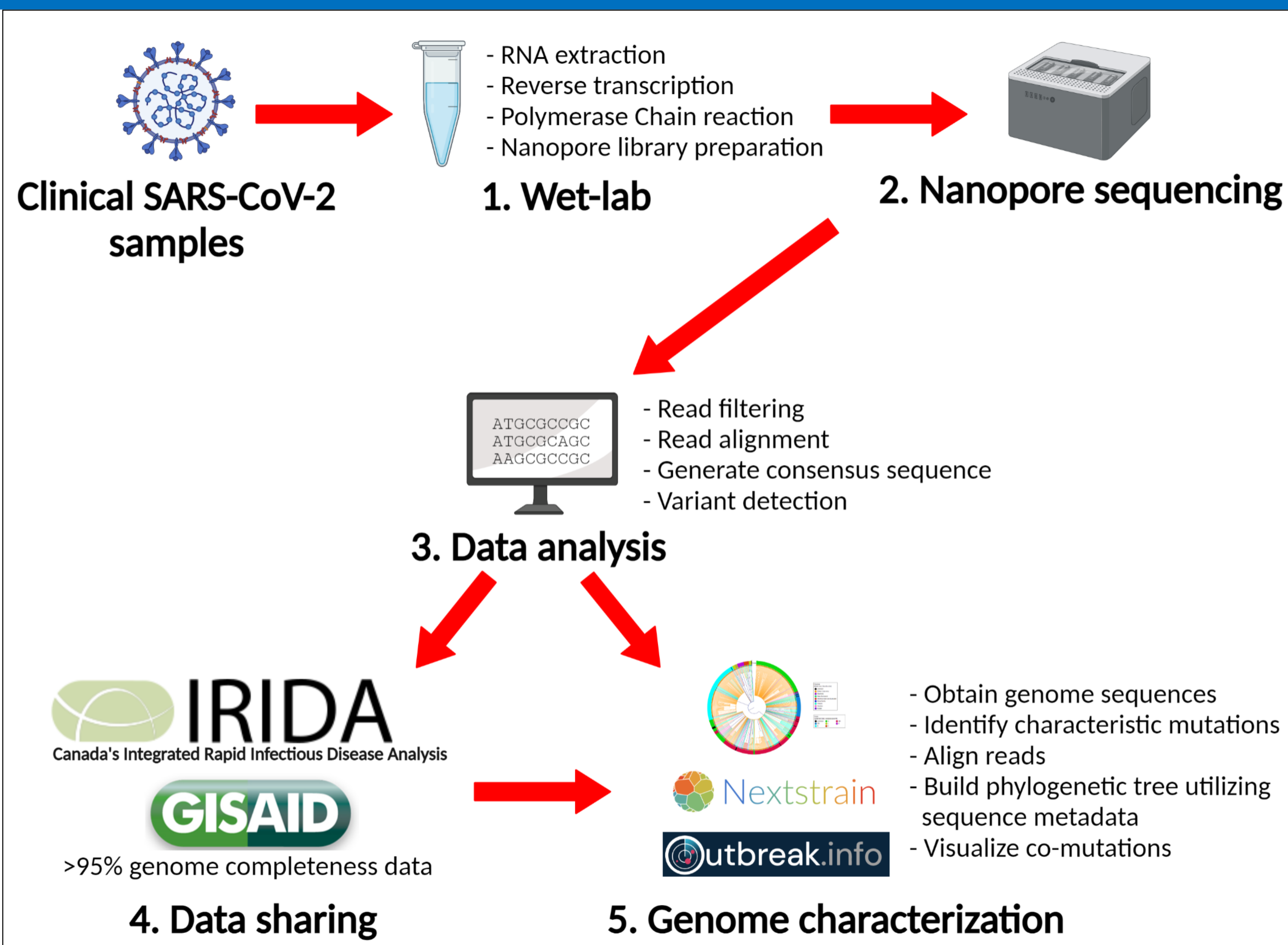
**Figure 1.** Potential mutation in SARS-CoV-2 spike protein could lead to virus escaping human immune response induced by vaccine.

In Canada, prior to COVID-19, large-scale standardized genomic surveillance of viral pathogens was not available. In this study, we standardized SARS-CoV-2 WGS protocol and established genomic surveillance infrastructure. We have been using genomic surveillance to monitor circulating SARS-CoV-2 strains in Canada to ensure diagnostic tests, treatments, and vaccines for COVID-19 remain effective.

## Objectives

1. Standardize WGS protocols and sequence clinical SARS-CoV-2 samples received from various Canadian jurisdictions.
2. Characterize SARS-CoV-2 lineages circulating within Canada for the purpose of genomic surveillance.

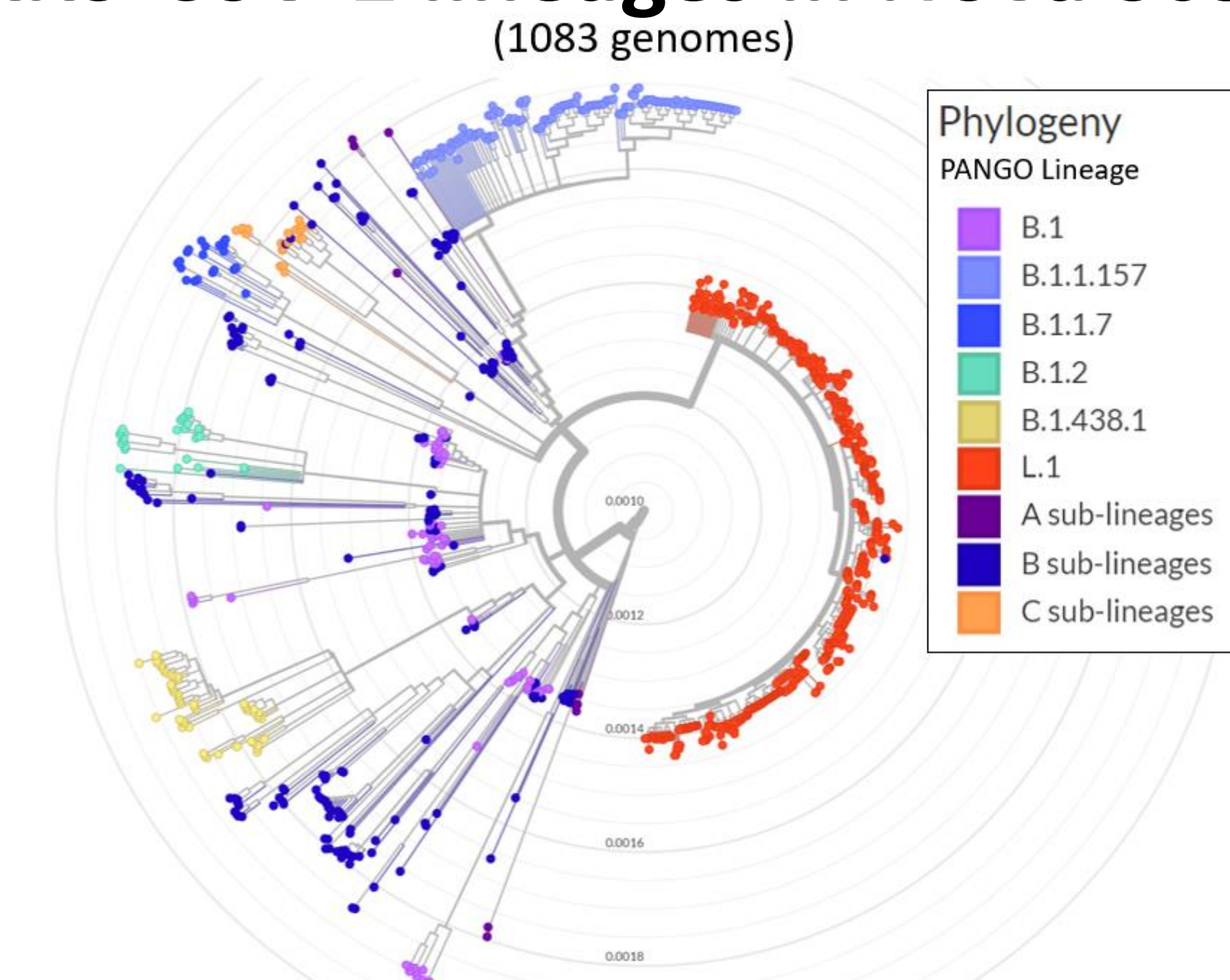
## Methods



**Figure 2.** SARS-CoV-2 genomic surveillance workflow.

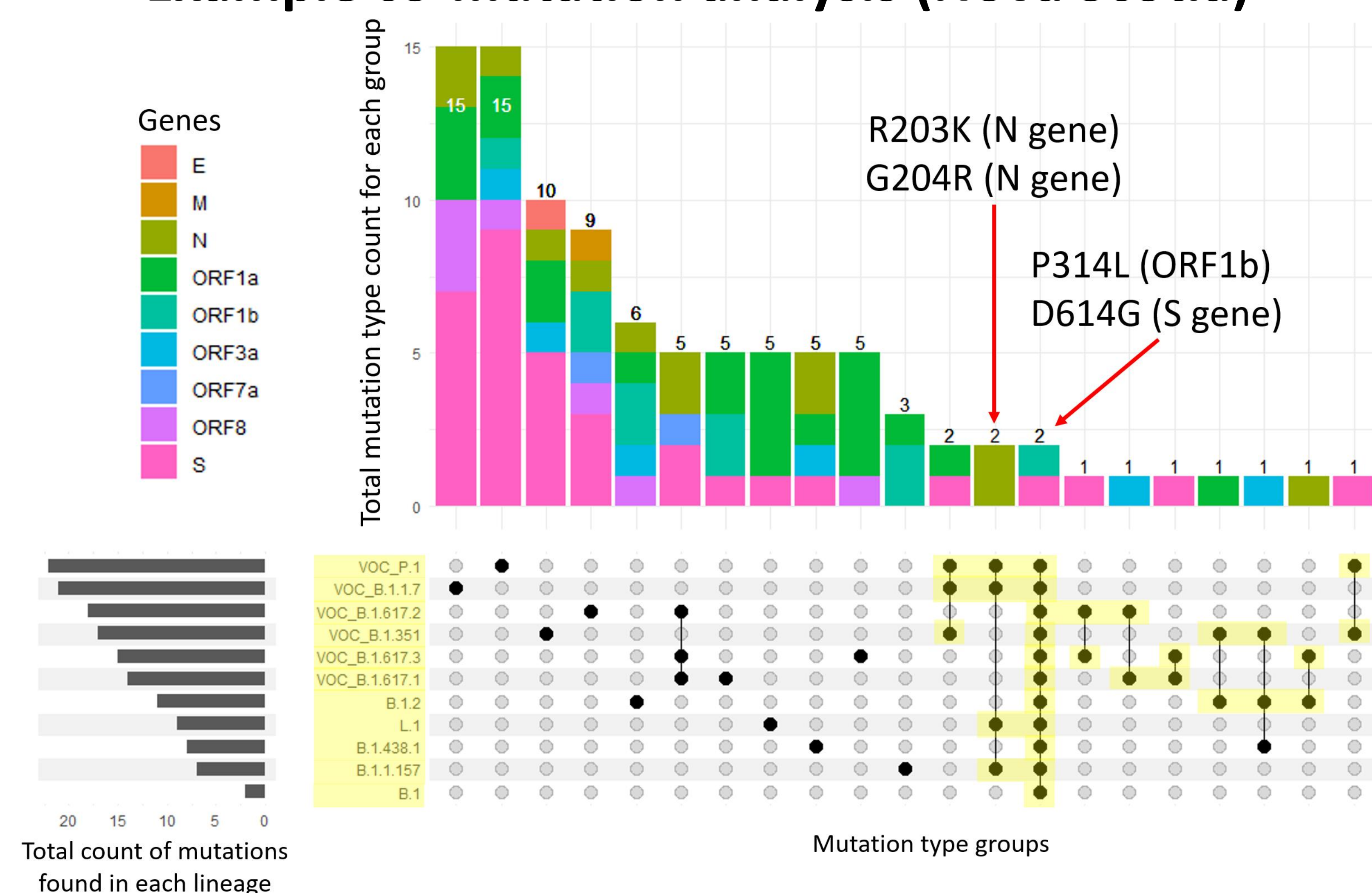
## Results

### SARS-CoV-2 lineages in Nova Scotia



**Figure 3.** SARS-CoV-2 phylogenetic tree representation of circulating lineages in Nova Scotia based on 1083 complete genomes over time since the start of COVID-19 pandemic in Nova Scotia from March 2020 to March 28, 2021.

### Example co-mutation analysis (Nova Scotia)



**Figure 4.** UpSet plot representing co-occurring characteristic mutations (>75% occurrence within lineages) found in significant SARS-CoV-2 lineages of Nova Scotia that circulated from March 2020 to March 28, 2021 and characteristic mutations found in VOCs circulating in Canada. Only most co-occurring mutations were labelled. Mutation profiles are from <https://outbreak.info/>.

## Conclusions

A standardized protocol for WGS, data analysis, and visualization of SARS-CoV-2 data enabled the establishment of the first national genomic surveillance program for viral pathogens in Canada. Although WGS is limited to SARS-CoV-2 clinical samples with sufficient viral load, genomic surveillance is serving a crucial role by monitoring for VOCs that may render vaccines ineffective and providing data to influence important public health decisions thereby protecting Canadians during the COVID-19 pandemic.

## Acknowledgements

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