

# Your Title Here

Don Francisco

26 April, 2021

## Background and Overview

This is a report on SARS-CoV-2, including some variant analysis (Koyama *et al.*, 2020).

## Methods

See the set of tutorials on the vcfR package website.

You may also want to use any of a range of different COVID data packages and data sources:

- <https://kjhealy.github.io/covdata/>
- <https://github.com/como-ph/oxcovid19>
- <https://ropensci.org/blog/2020/10/20/searching-medrxivr-and-biorxiv-preprint-data/>
- <https://covidtracking.com/data/api>
  - `readr::read_csv("https://api.covidtracking.com/v1/states/daily.csv")`

Subsections are ok too

## Results and Discussion

```
## Error in library("vcfR"): there is no package called 'vcfR'
## Error in library("ggthemes"): there is no package called 'ggthemes'
## Error in loadNamespace(name): there is no package called 'vcfR'
## Error in is.data.frame(stacked_vcf): object 'stacked_vcfs' not found
```

## Figures

```
## Error in eval(lhs, parent, parent): object 'vcf_with_metadata' not found
```

**Figure 1:** N and S genes have more unique SNPs in the set of samples analyzed.

## Tables

| Gene Name | Start | End   | Length |
|-----------|-------|-------|--------|
| S         | 21563 | 25384 | 3821   |
| ORF3a     | 25393 | 26220 | 827    |
| E         | 26245 | 26472 | 227    |
| M         | 26523 | 27191 | 668    |
| ORF6      | 27202 | 27387 | 185    |
| ORF7a     | 27394 | 27759 | 365    |
| ORF7b     | 27756 | 27887 | 131    |
| ORF8      | 27894 | 28259 | 365    |
| N         | 28274 | 29533 | 1259   |
| ORF10     | 29558 | 29674 | 116    |

**Table 1:** Gene names, locations, and lengths in the SARS-CoV-2 genome. Higher SNP counts in the S and N genes may be related to the larger size of these genes.

## Sources Cited

Koyama,T. *et al.* (2020) Variant analysis of sars-cov-2 genomes. *Bulletin of the World Health Organization*, **98**, 495.