

# Your Title Here

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## 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.

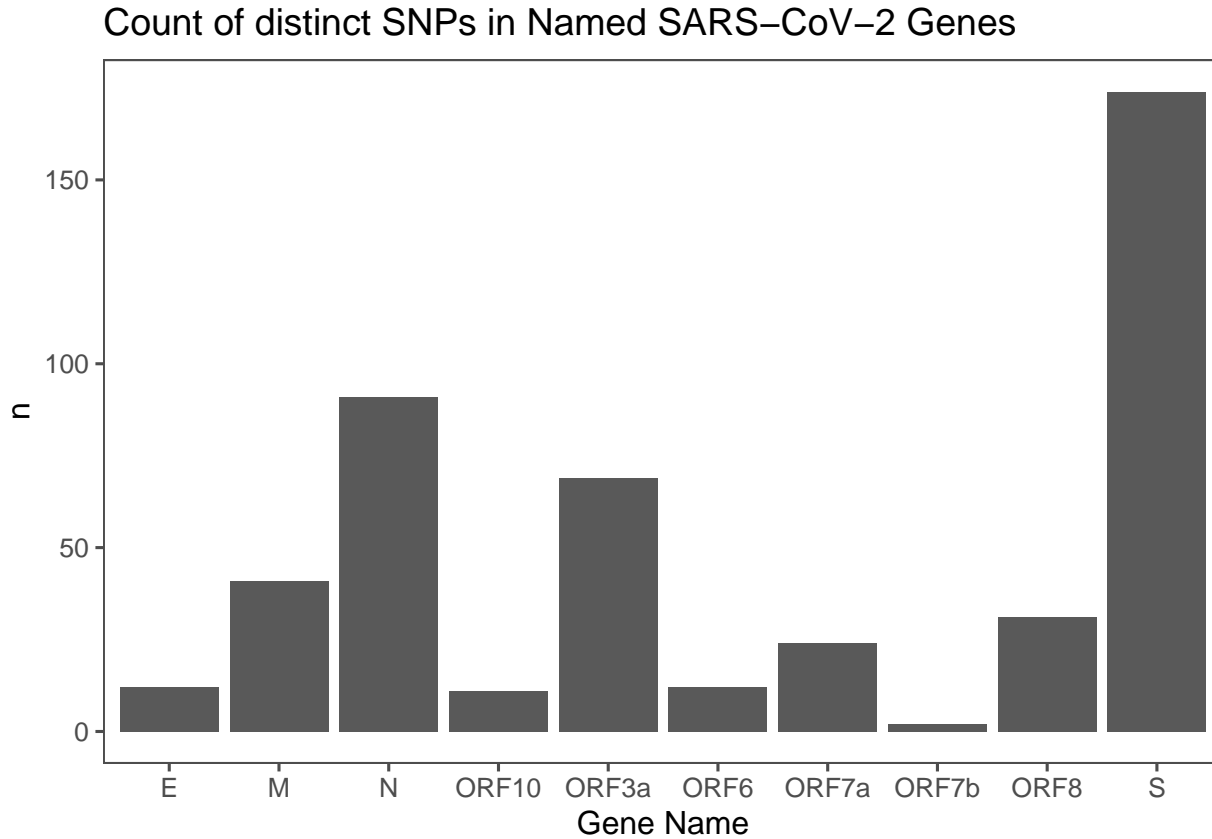
You may also want to use any of a range of different COVID data packages and data sources:

- <https://kjhealy.github.io/covdata/>
- <https://github.com/como-ph/oxcovid19>
- <https://ropensci.org/blog/2020/10/20/searching-medrxiv-and-biorxiv-preprint-data/>
- <https://covidtracking.com/data/api>
  - `readr::read_csv("https://api.covidtracking.com/v1/states/daily.csv")`
- <https://rt.live/>
  - `readr::read_csv("https://d14wlfuexuxgcm.cloudfront.net/covid/rt.csv")`

Subsections are ok too

## Results and Discussion

### Figures



**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.