

# TRACKING COVID-19 MUTATIONS ACROSS THE WORLD

## MUTATIONS OF CONCERN

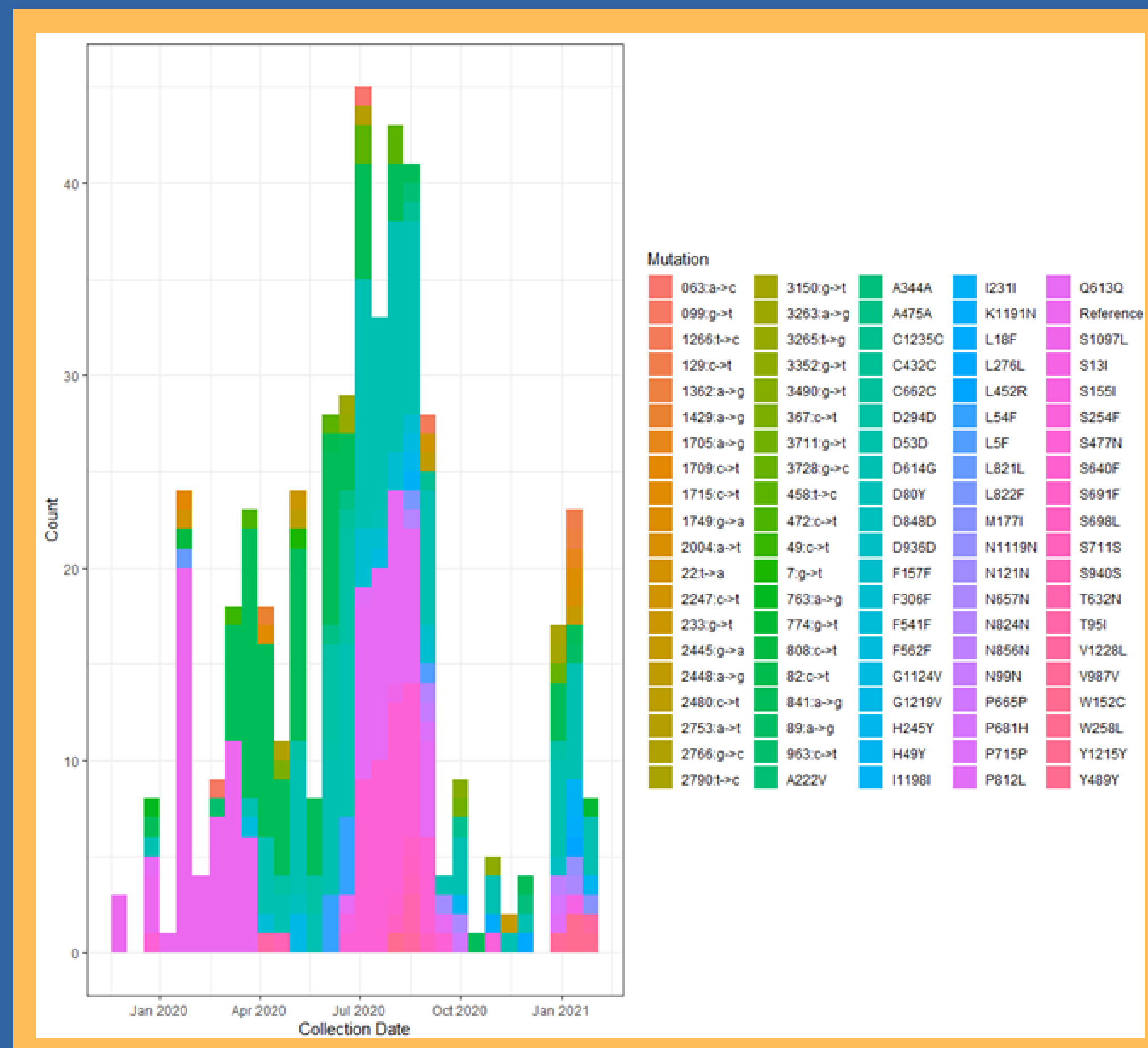


Table 1. Frequency of mutations

Mutation	Total Mutated
D614G	107
841A>G	78
Reference	55
Q613Q	45
S477N	45
D294D	16
F306F	8
L54F	7
458L>C	5
S698L	3

## BIOLOGICAL QUESTIONS

1. Which regions are producing the greatest variety of strains?
2. How are some clinically significant mutations distributed and what are the implications?

## MAP OF MUTATIONS

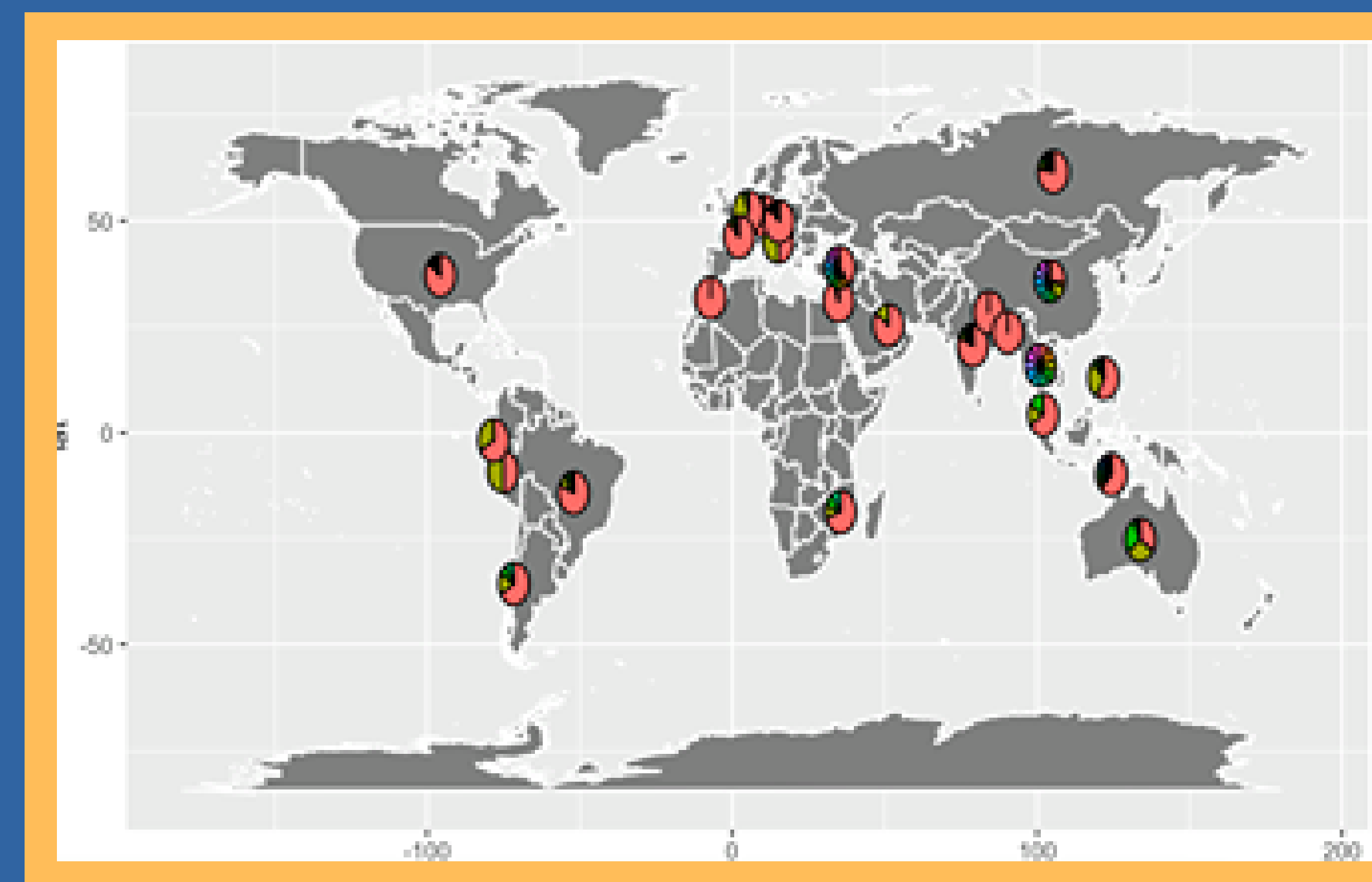


Figure 6. Geographical representation of the frequency of mutations by country.

## COVID-19 DATASET

- 46,000 Sequences
- 5 Countries: Australia, China, India, Japan, USA
- 50 sequences sampled per country

Table 2. Summary table of mutation by country

Country	Unique Mutations	Mutated Sequences	Avg Mutations per Sequence
AUS	21	48	3.50
CHN	9	11	1.09
IND	28	50	1.92
JPN	10	39	1.33
USA	40	48	1.83

## CONCLUSIONS

- Australia is the country producing the greatest variety of strains
- The mutations map shows the diversity and distribution of mutations across the world
- the most clinically significant mutation in our data is D614G

## FUTURE RESEARCH

- Tracking the evolution of new mutations is crucial for informing public health officials on preventative measures like quarantines and lockdowns.
- Australia was linked with high mutation accumulation which could be the result of tight COVID-19 regulations that isolated these mutations within the country.
- Further research contributes to the growing COVID-19 database and allows researchers to predict future rate of infections.

## PHYLOGENY

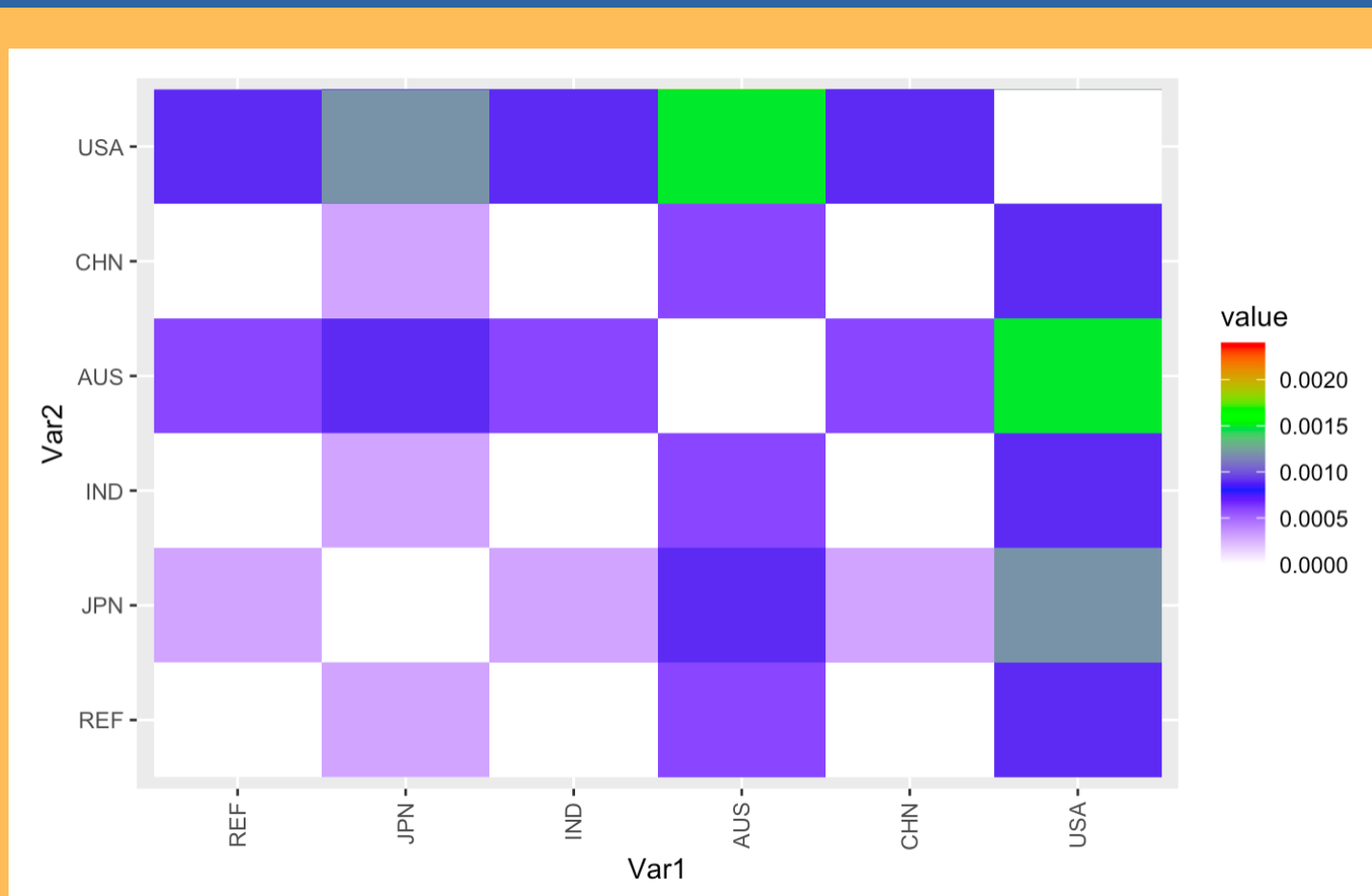


Figure 2. Countries distance matrix.

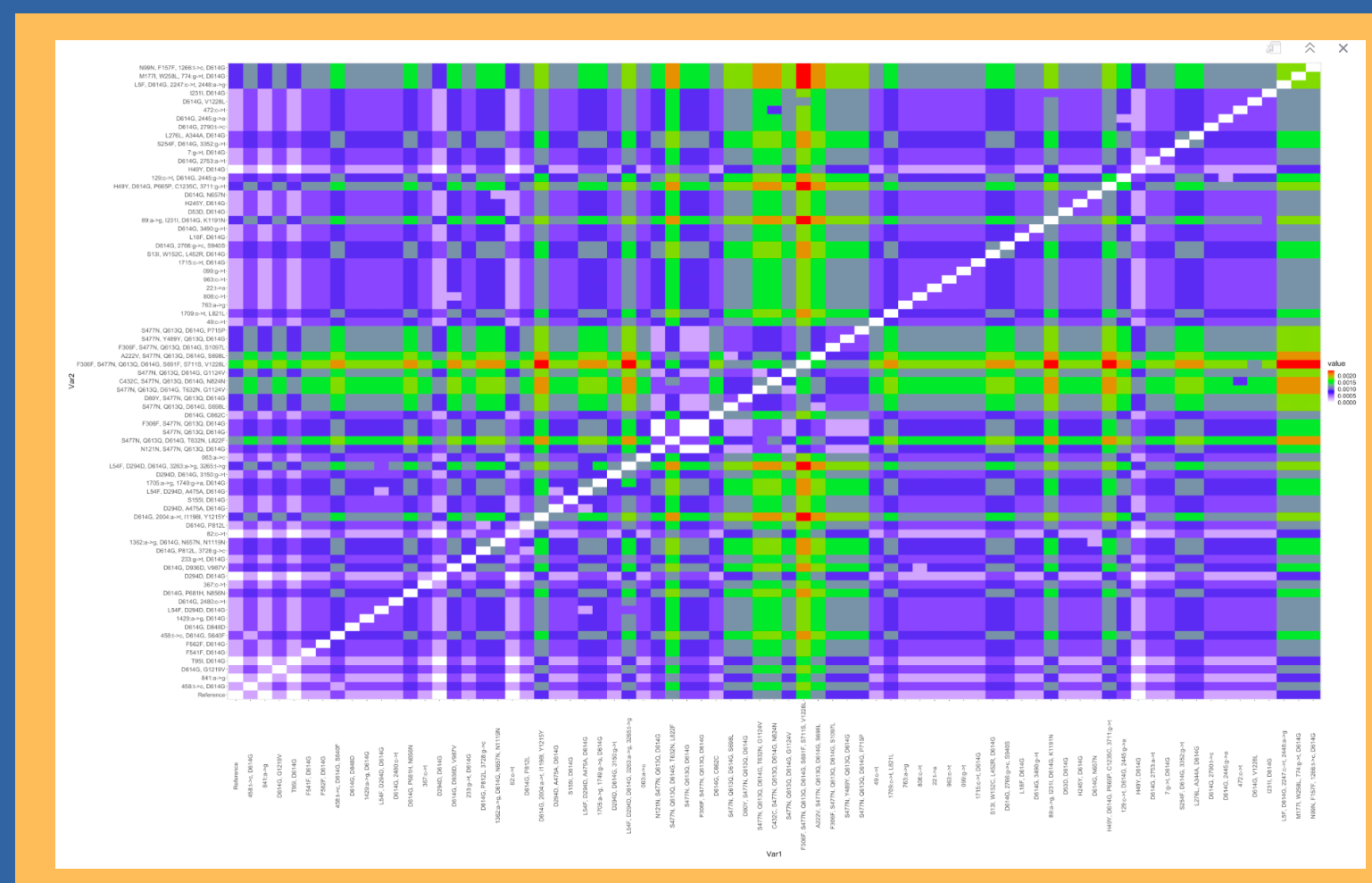


Figure 3. Mutations distance matrix.

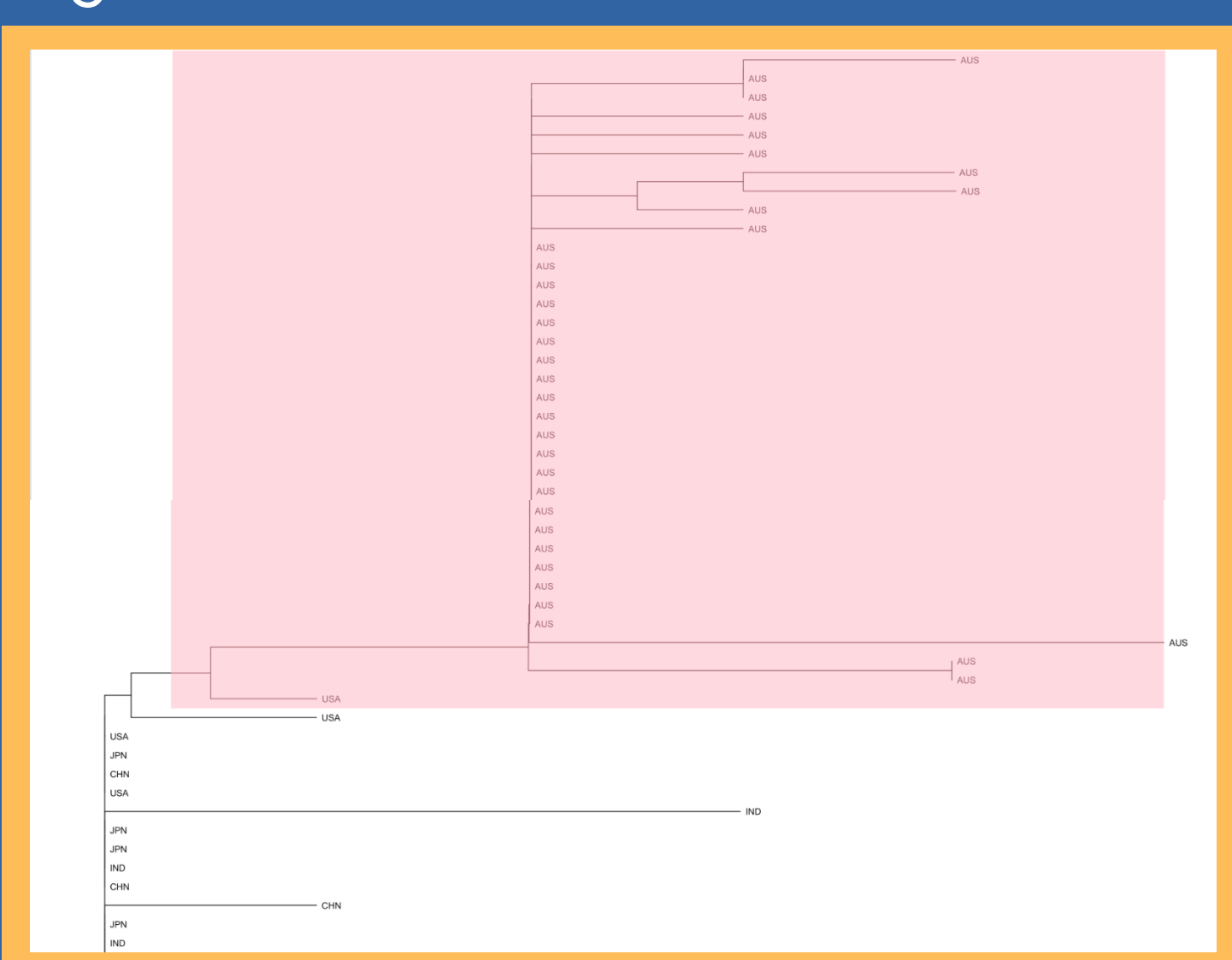


Figure 4. Phylogeny showing the evolutionary relationship between COVID-19 strains grouped by country

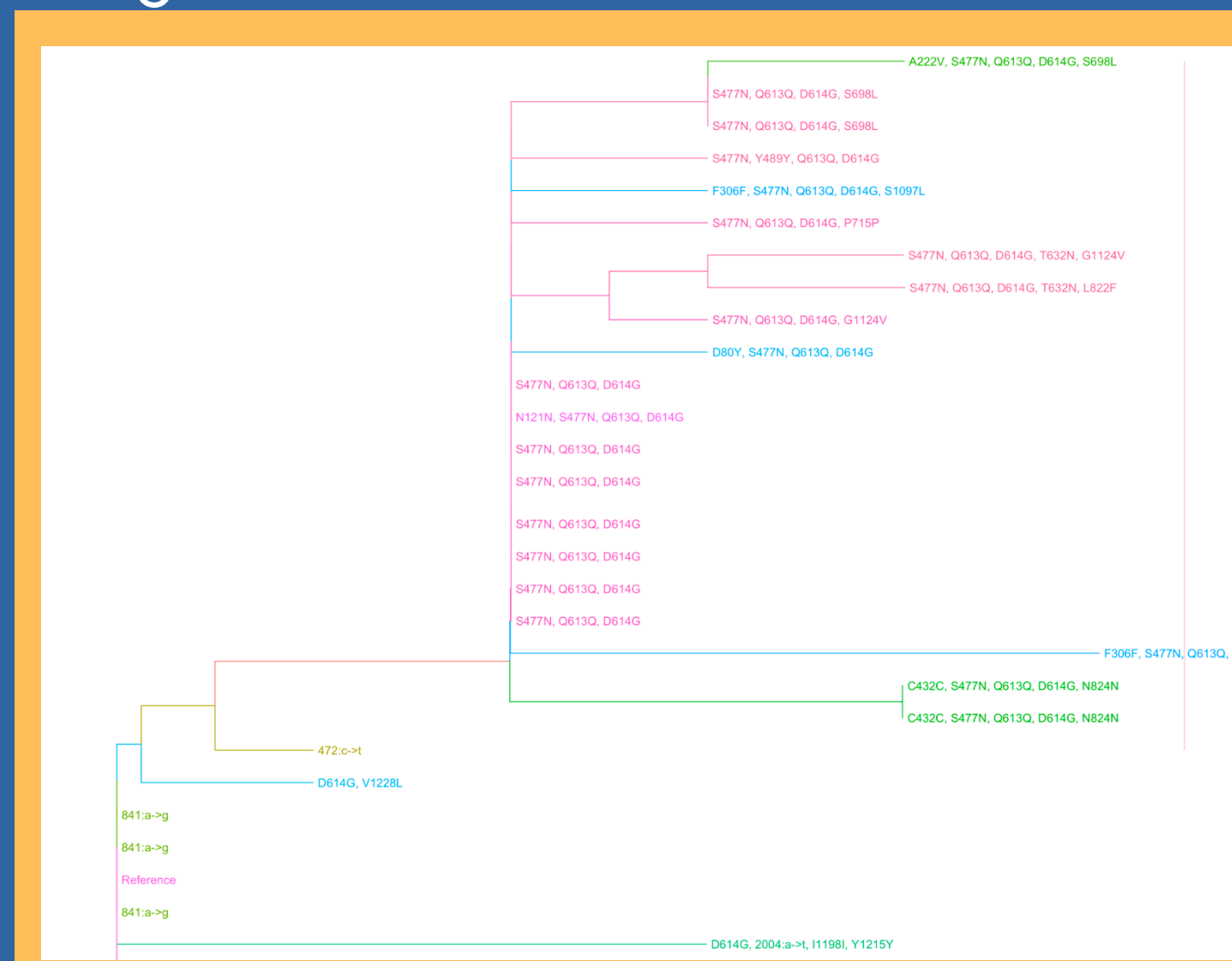


Figure 5. Phylogeny showing the evolutionary relationship between COVID-19 strains grouped by mutation

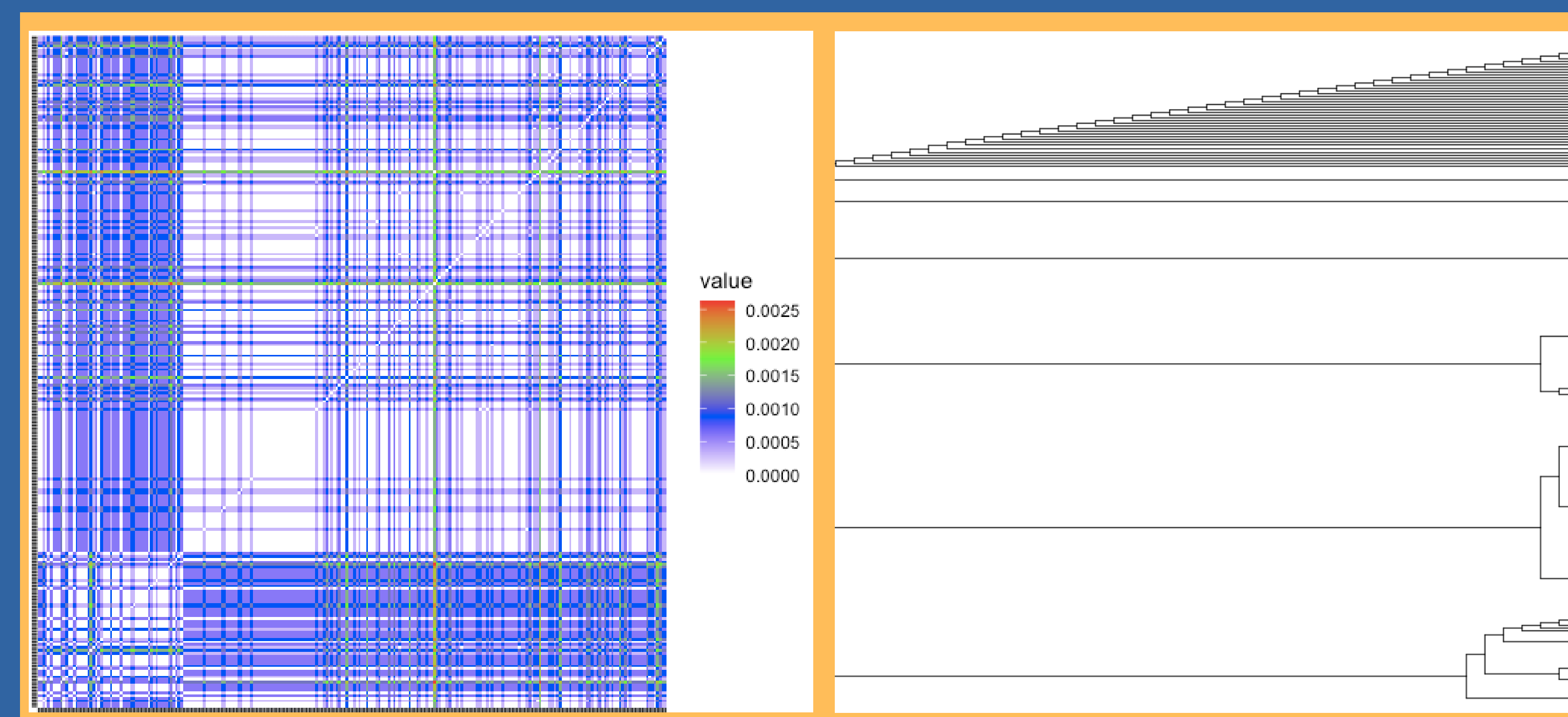


Figure 6. Distance matrix of full sequences of the SARS-Cov-2 genome

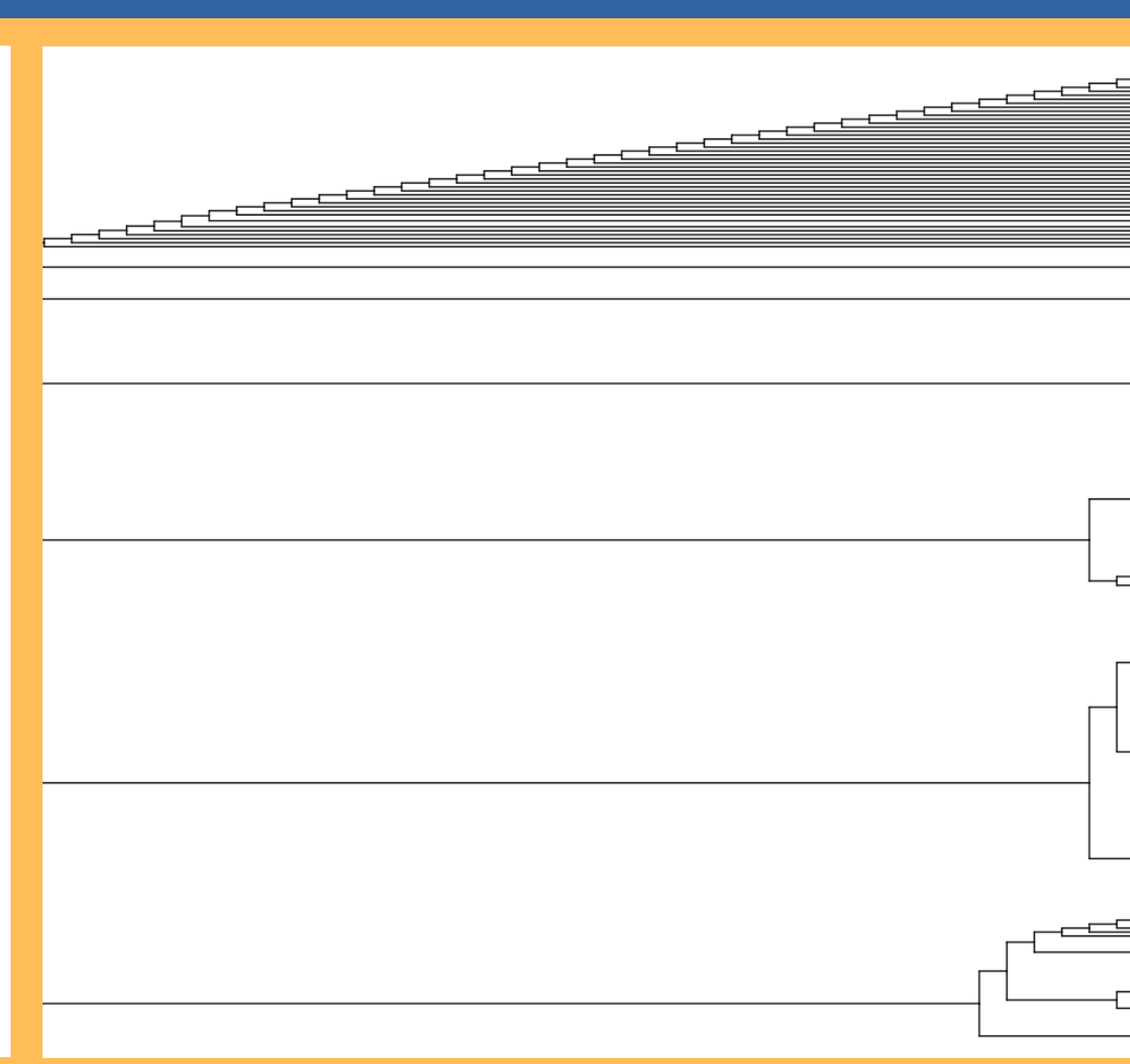


Figure 7. Phylogeny of the full sequences from the dataset

- two distance matrices showing relation between mutations and countries
- created two phylogenies for countries and mutations
- demonstrated that Australia was producing the greatest variety of strains