

One year of SARS-CoV-2: Genomic characterization of a COVID-19 outbreak in Qatar

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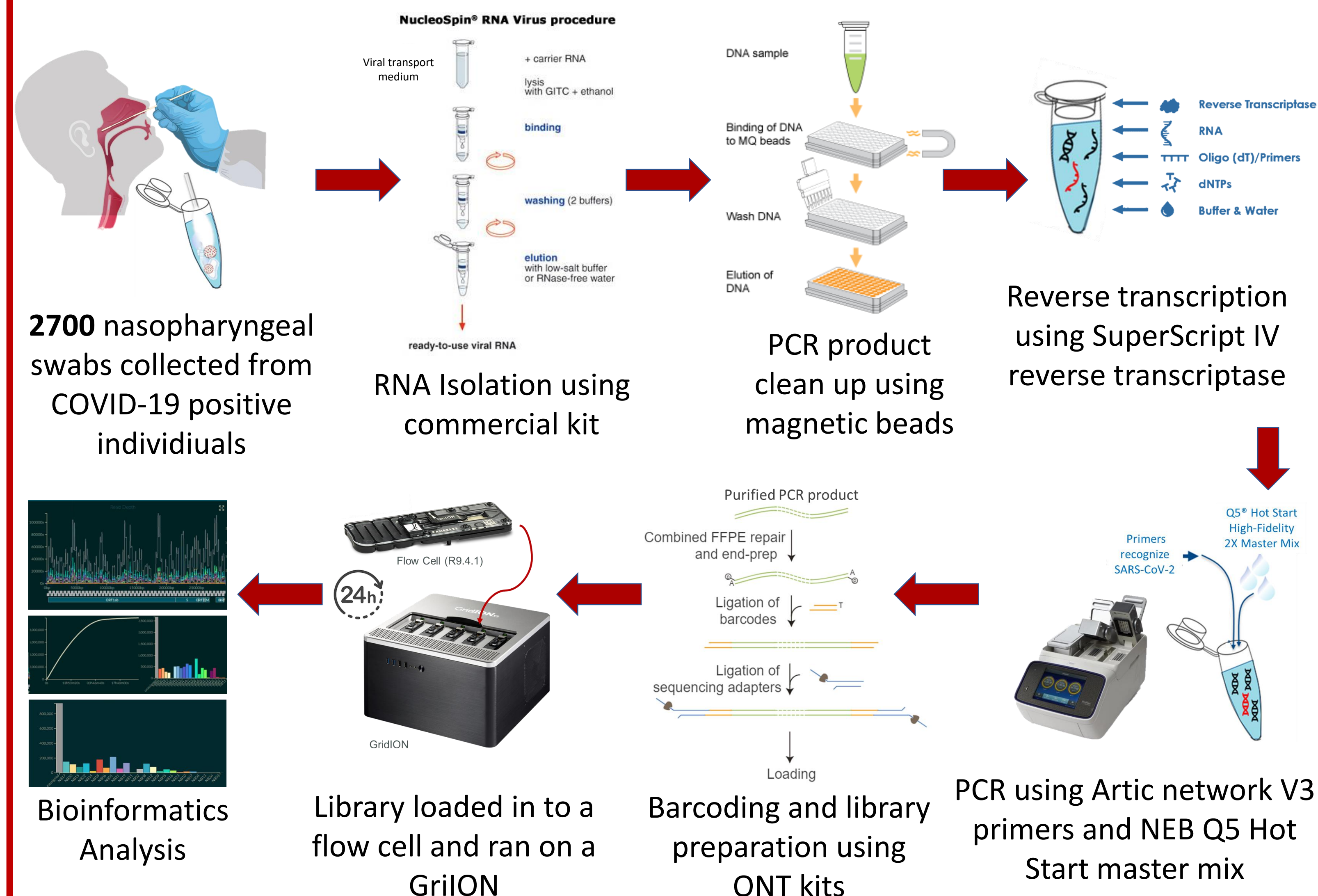
BACKGROUND

The current pandemic, Coronaviruses Disease (COVID-19), is caused by an RNA coronavirus that was recently identified as Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2). RNA viruses tend to have a high mutation rate; the rate is around a million times greater than that of their hosts. The mutagenic potential of the virus depends on many factors, including the fidelity of nucleic acid-replicating viral enzymes, such as SARS-CoV-2 RNA dependent RNA polymerase (RdRp). The rate of mutation drives viral evolution and genome variability, consequently allowing viruses to escape the immunity of the host and develop resistance to drugs. Therefore, the characterization of SARS-CoV-2 variants might lead to implement better therapeutics treatments, vaccines design and identify new diagnostics approaches.

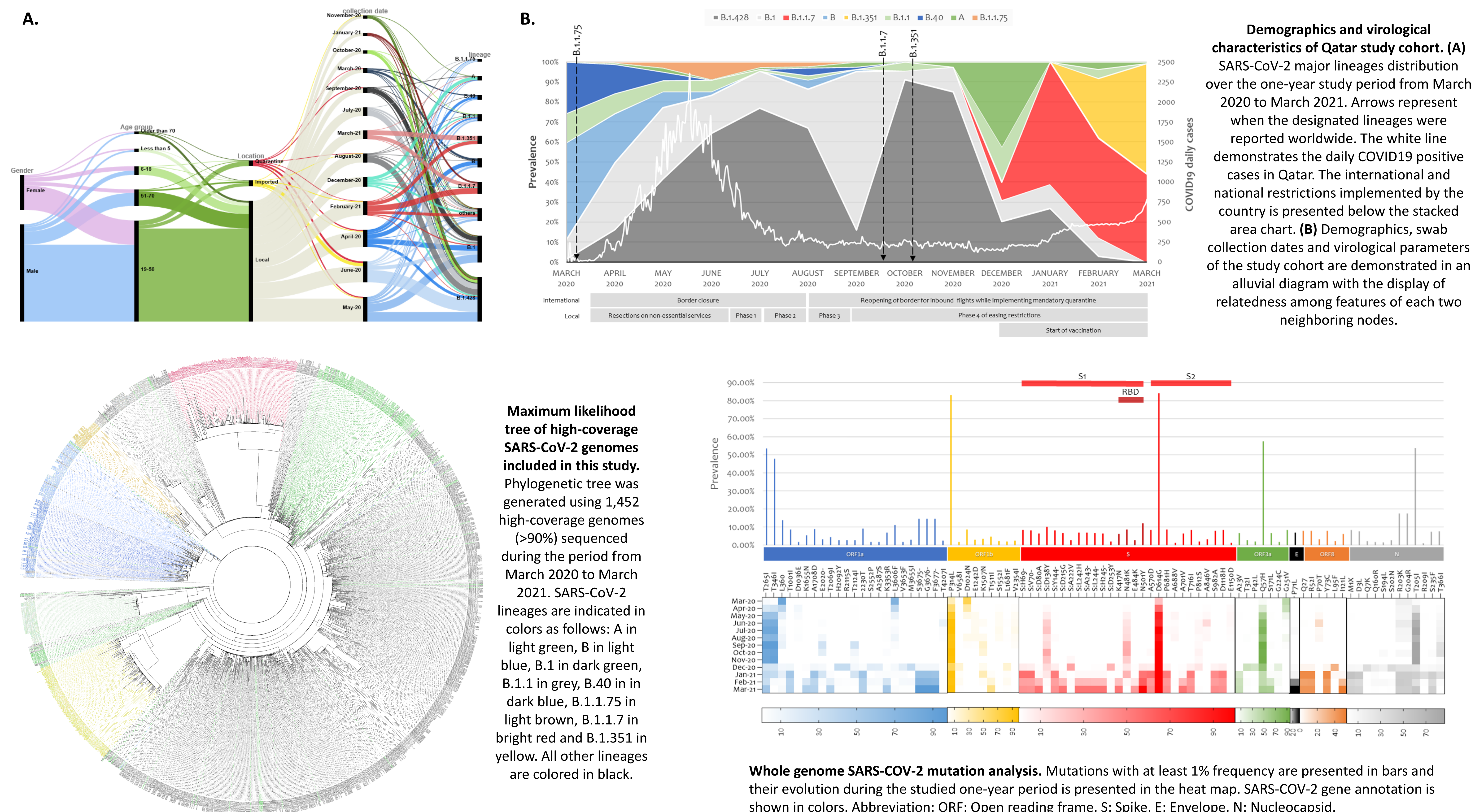
AIM

The aim of this study was to detect, monitor, and evaluate the spread of the virus, including the variants of concern in order to give science based evidence to ease or implement COVID19 restrictions.

METHODS



RESULTS



CONCLUSION

In conclusion, this study identified SARS-CoV-2 lineages and their circulation pattern in Qatar, a highly diverse region that was heavily impacted by COVID-19. Regardless of the implementation of restriction measure, particularly on international movements, 61 SARS-COV-2 lineages were detected. Nine were widely represented including two VOCs. We identified a number of novel mutations that are likely to have originated in Qatar including N481K located in the spike protein. We also reported an increased number in the mutations and deletions in the backbone of the VOCs, B.1.1.7 and B.1.351, in a short period. This raises the imperative need to continue the ongoing genomic surveillance that has been an integral part of the national response to monitor any SARS-CoV-2 re-emergence in Qatar.

ACKNOWLEDGEMENT

This work was supported by Qatar Petroleum under Qatar University external grant number (QUEX-BRC-GH-18/19) and Qatar Genome Project. We acknowledge the support from the Ministry of Public Health, Doha, Qatar, the virology laboratory in Hamad Medical Corporation, Doha, Qatar, and Qatar BioBank, Doha, Qatar, for their efforts in the preparation of nasopharyngeal samples and collection of clinical data.

REFERENCES

- <https://artic.network/ncov-2019>
- Benslimane, F.M., AlKhatib, H.A., Al-Jamal, O., Albatesh, D., Boughattas, S., Ahmed, A.A., Bensaad, M., Younuskunju, S., Mohamoud, Y.A., Al Badr, M. and Mohamed, A.A., 2021. One year of SARS-CoV-2: Genomic characterization of COVID-19 outbreak in Qatar. medRxiv.