

SARS-CoV-2 Genome Sequencing

The COVID 19 pandemic has had an unprecedented impact on society. It has also highlighted the incredible collaborative work by the global scientific community in developing vaccines so quickly. Now with multiple vaccination programmes underway there is light at the end of the tunnel. However, there is a risk of new vaccine-resistant variants of the novel Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) emerging.

With this specific challenge in mind we have developed a SARS-CoV-2 genome sequencing service to enable researchers to identify variants for further phylogenetic analysis of related strains. This research can then be used to inform and optimise pandemic management strategies. The service is available from our Cambridge Sequencing Centre. The centre is equipped with the latest NovaSeq 6000 sequencers and supported by our expert and friendly team.

SARS-CoV-2 Sequencing Solution

High data quality

- Industry leading Q30 guarantee

Fast turn around time

- Ten calendar days

Cost-efficient sequencing solution

- Multiplex PCR amplification

Sequence SARS-Cov-2 positive samples and identify variants

- SNP and InDel identification

Standard analysis included

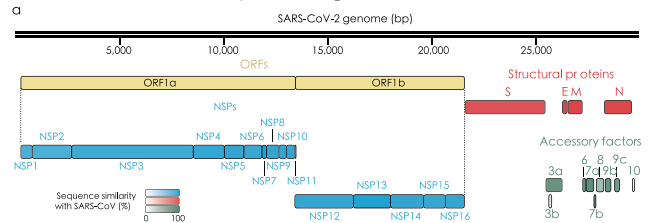
- Lineage analysis and variant calling

Optional customized analysis available

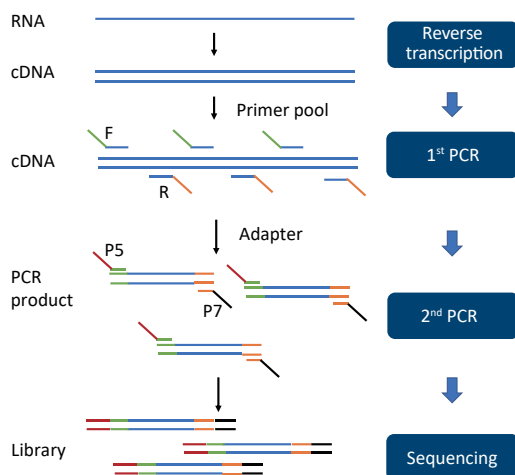
- For example, Phylogenetic tree

SARS-CoV-2 is an enveloped virus consisting of a positive-sense, single-stranded RNA genome of around 30kb. Two overlapping ORFs, ORF1a and ORF1b, are translated from the positive-strand genomic RNA and translated into continuous polypeptides, which are cleaved into a total of 16 nonstructural proteins^[1].

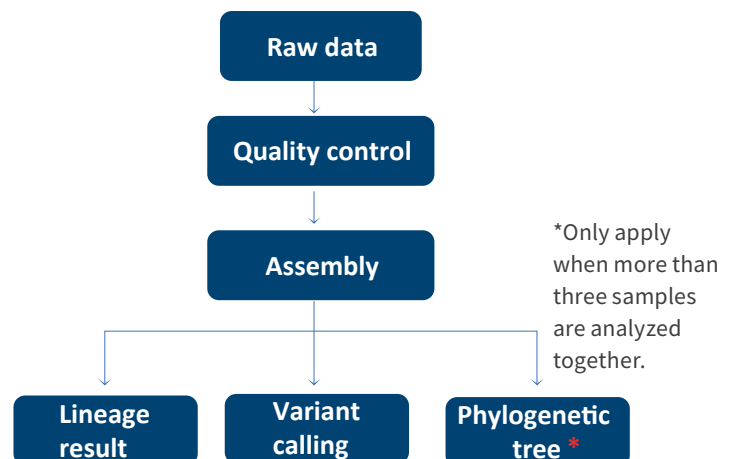
1: Gordon, D.E., Jang, G.M., Bouhaddou, M. et al. A SARS-CoV-2 protein interaction map reveals targets for drug repurposing. Nature 583, 459–468 (2020). <https://doi.org/10.1038/s41586-020-2286-9>



Library preparation



Bioinformatics analysis pipeline



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