Mapping NTD of S protein utilising DMS to predict the evolution of SARS-CoV-2

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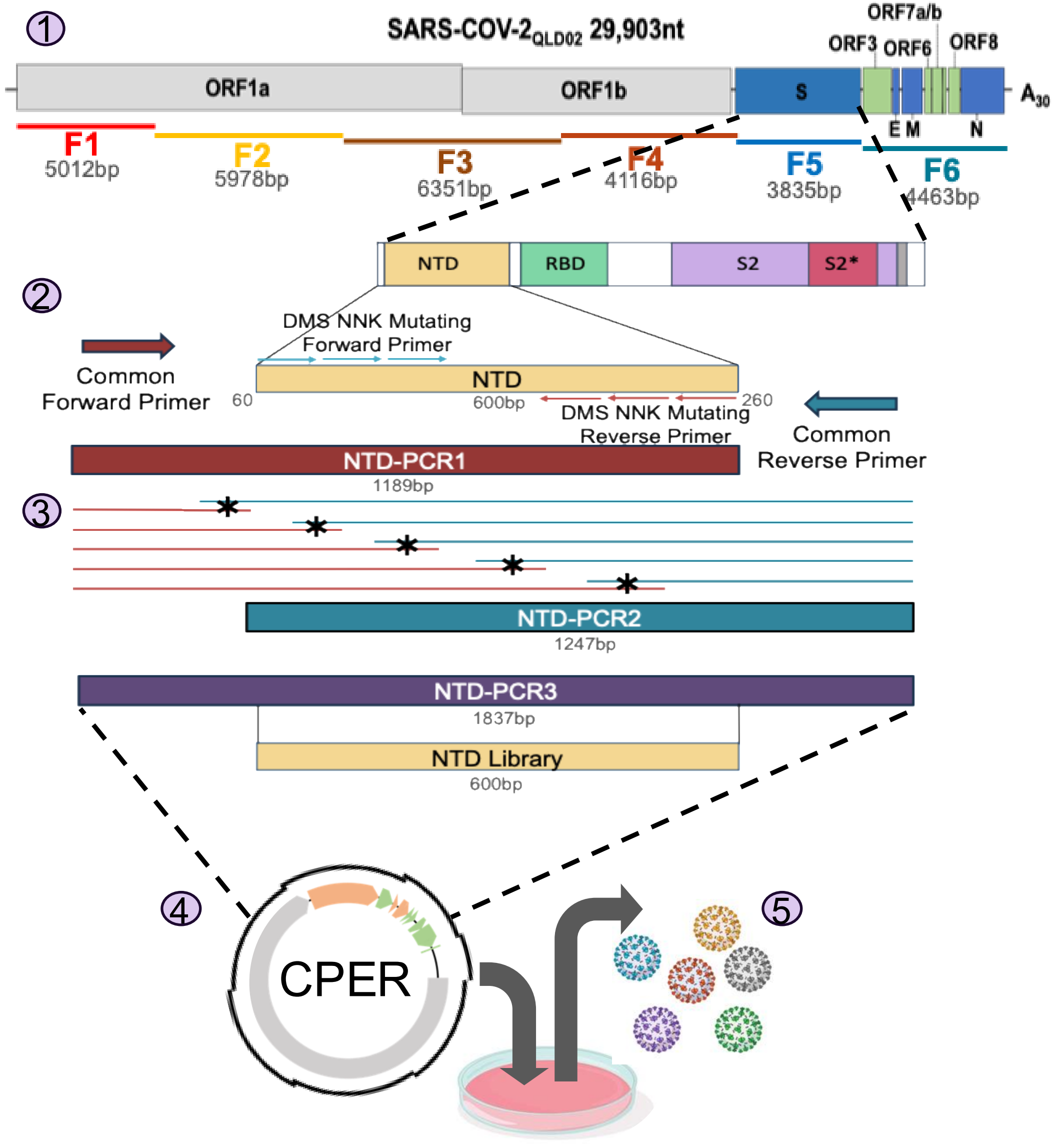

SARS-CoV-2 undergoes evolutionary changes to evade neutralising antibodies from vaccinations or infections.

The NTD within the Spike protein undergoes indels, which allow the virus to escape current vaccinations

This study aims to generate and analyse the NTD viral library using DMS to identify potential changes responsible for viral escape to unfold the evolution of SARS-COV-2

Method:

1. Amplification of Fragments spanning the SARS-CoV-2 genome
2. Creating a diverse mutant library (NNK) of a protein region (PCR mutagenesis)
3. Assemble the pooled fragments
4. Assembling library fragment into a reverse genetics backbone (CPER).
5. Recovering a diverse library.
6. Characterise with deep sequencing.

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