

ClickTech Single Strain Mutation Mapping Kit For SARS-CoV-2

The coronavirus
is mutating –
does it matter?
We say YES!

FACTS of SARS-CoV-2

SARS-CoV-2 is an RNA virus with a genomic length of around 30,000 nucleotides. Researchers have catalogued more than 12,000 mutations in SARS-CoV-2 genomes [1]. This virus continuously accumulates genomic mutations during its replication in humans. Most mutations will be either be deleterious, or have little to no consequence for the virus's ability to spread or cause disease.

Because they do not alter the amino acid sequence in particular of the 4 structural proteins the Spike, Envelope, Membrane and Nucleocapsid 'S-E-M-N'. Of interest are mutations that reshape these proteins and are therefore far more likely to affect infectivity and/or pathogenicity.

[1] E. Callaway, Nature 585, 174-177 (2020)

The most pressing questions in the COVID-19 crisis are:

“How and in which direction will the SARS-CoV-2 Virus evolve”. This is important for the so-called herd immunity and vaccine development. The biological question is: “Is the evolution of the SARS-CoV-2 Virus horizontal, from human to human, or also vertical within a patient.”

Today, Amplicon Technology

is used for mapping such mutations – but this leads to ambiguous assemblies and limit biological interpretation by using index primer and short read technologies.

Our Kit promises a lot more information!

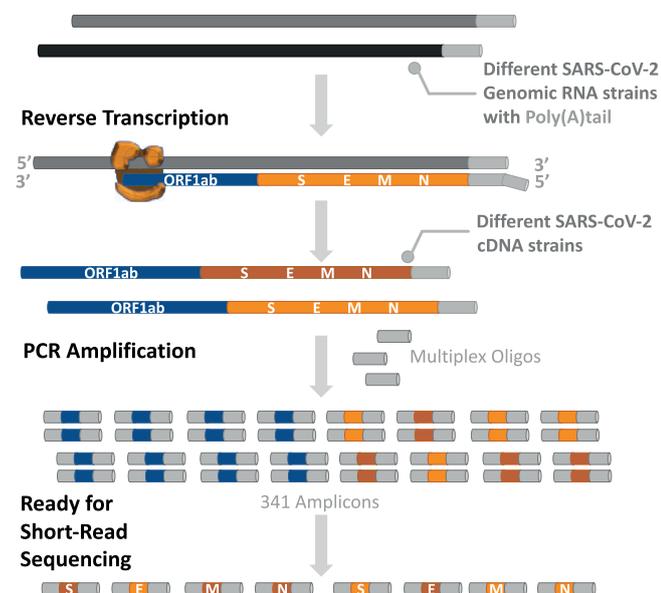
Let's work together to accelerate the fight against Covid-19 pandemic.

The Proof: Why the ClickTech Single Strain Mutation Mapping Kit has advantages over other commercially available amplification!

We offer a kit that generate first a 1:1 cDNA copy of the entire 30,000 base-long SARS-CoV-2 mRNA genome, irrespective of the strain involved. Secondly, overlapping genomic fragments up to 4,2kb are amplified of critical S-E-M-N coding genome part. When coupled with existing long-read NGS technologies, these long DNA fragments can even be used to precisely distinguish and characterize multiple SARS-CoV-2 variants. This can be used to predict e.g. genome plasticity, presents of multiple strains in a patient, mutation accumulation during infection in patient etc.

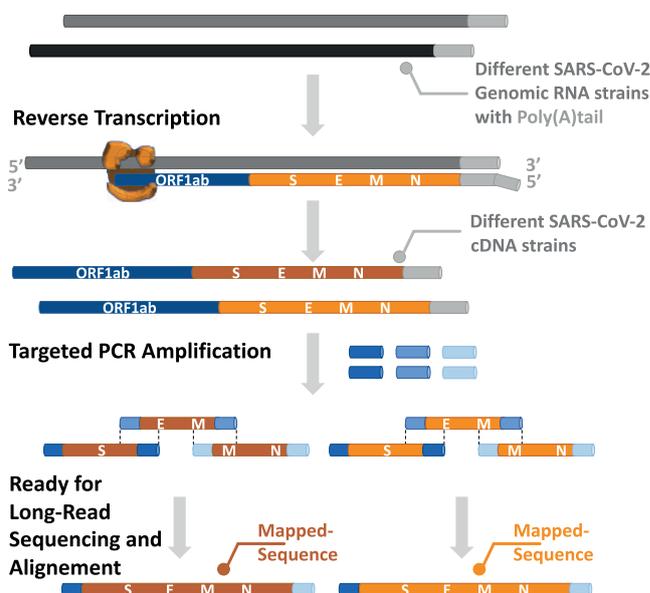
This sequencing kit could be the tool to help you with all the above questions and more.

Amplicon Technology



- 98% of SARS-CoV-2 genome covered computationally
- 341 Amplicons with size range of 116-255bp
- Information might get lost on genetic diversity by Index primers (8 i5 x 12 i7)

baseclick's Solution



- 100% cDNA SARS-CoV-2 genome covered
- 3' genome (S-E-M-N gene) covered by three amplicons with a size of 4200bp, 3000bp and 2,700bp
- Straight forward alignment due to overlapping long PCR fragments

Product Name	Product Number	Application	Price
ClickTech SARS-CoV-2 Single Strain Mutation Mapping Kit	BCK-COV-MM	For discrete mutation detection in new viral strains.	630 €

If you are interested in the possibilities of these kits, please talk to a sequencing lab which has PacBio® Sequencers in operation or contact us to find these laboratories in your area. Only these sequencers together with our kit are able to give the correct and complete information you would be looking for.

Order at www.baseclick.eu