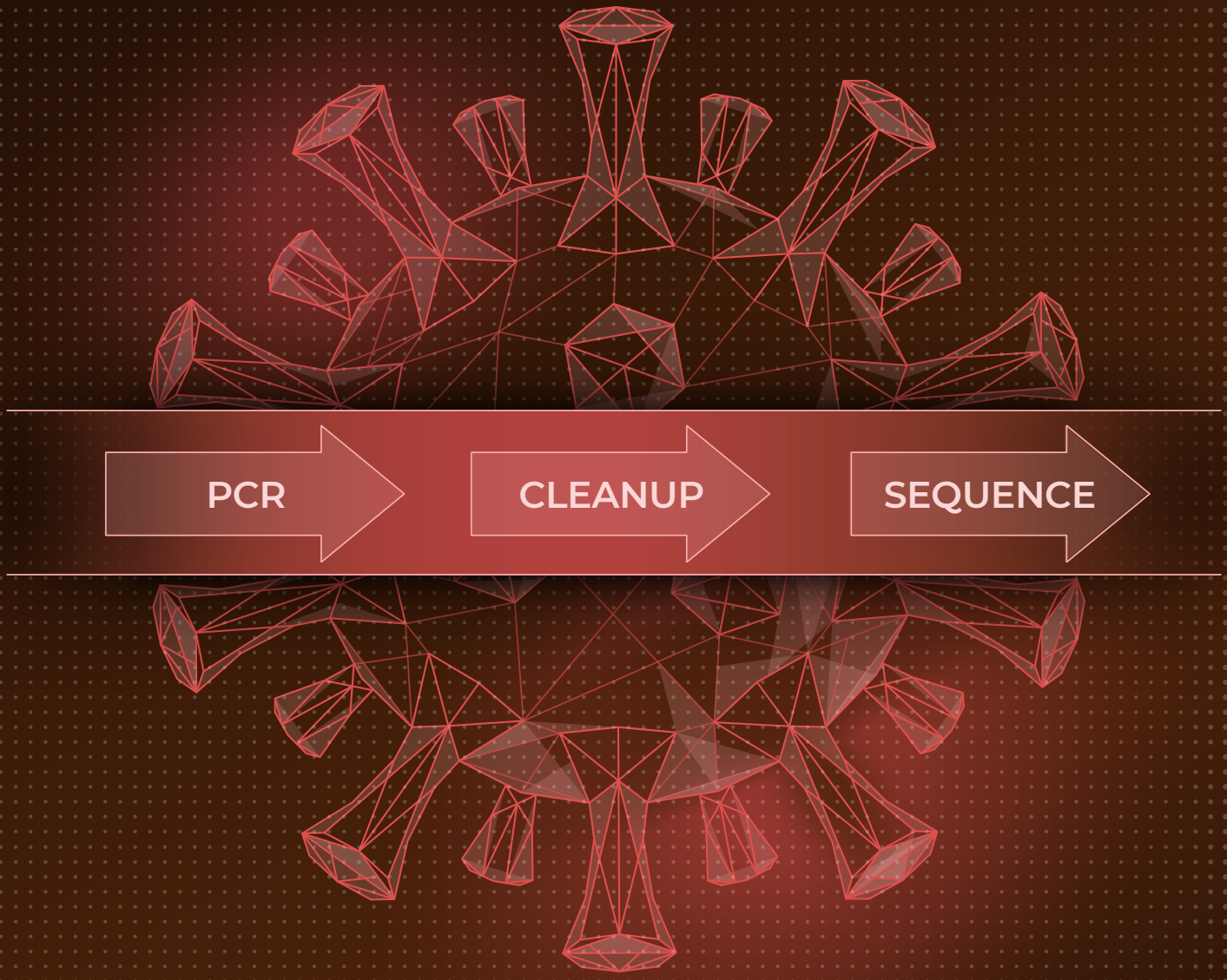
Keep it simple and safe:

EasySeq™

SARS-CoV-2

Whole Genome Sequencing Library Prep by Reverse Complement PCR



- More efficient library prep: Up to 80% less hands-on time
- Combined Amplification and Indexing with RC-PCR
- Less Handling Less Risk, Greater Sample Safety
- Easily adapted for Automation
- Single Click Analysis with virSEAK (JSI Medical Systems)

NimaGen.

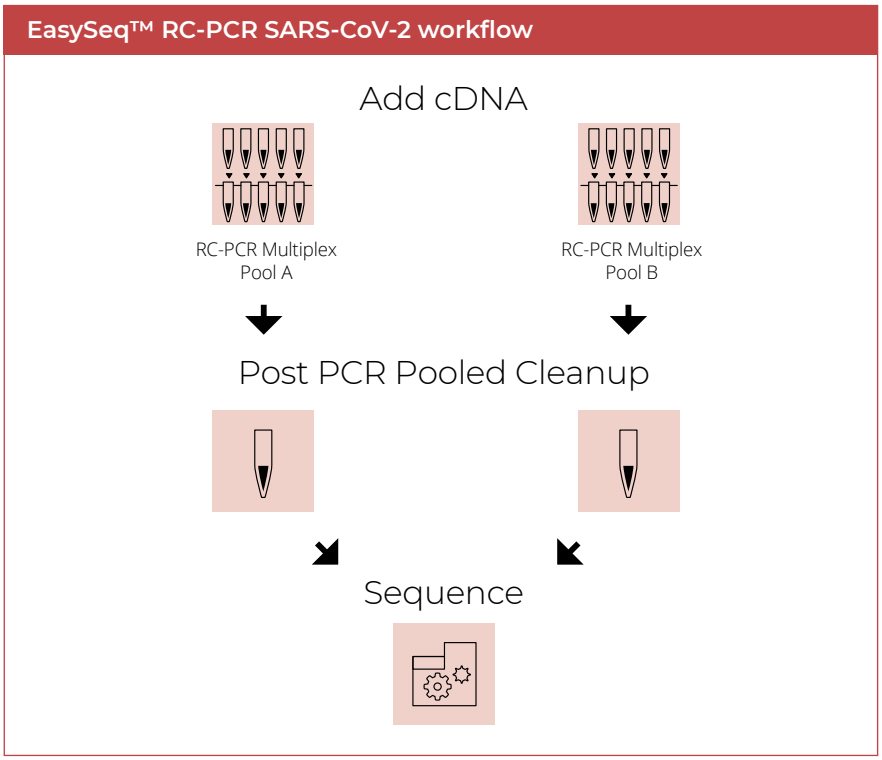
Innovators in DNA tech

Introduction

The analysis and study of viral genomes is an essential epidemiological requirement to track the evolution of a virus, the origin of strains and their transmission during any epidemic or pandemic. Targeted Next Generation Sequencing (NGS) is a valuable tool for both detection and classification of viral genomes.

The 2019 outbreak of the novel Coronavirus strain (SARS-CoV-2) is obviously unprecedented with over 26 million confirmed cases of the disease associated with SARS-CoV-2 (COVID-19) and sadly approaching 1 million of of lost lives in a relatively short period of time.

Therefore, the ability for public health professionals and researchers to monitor situations in the most efficient and streamlined manner possible is essential. As is the reassurance that testing methods are secure, and results are accurate.



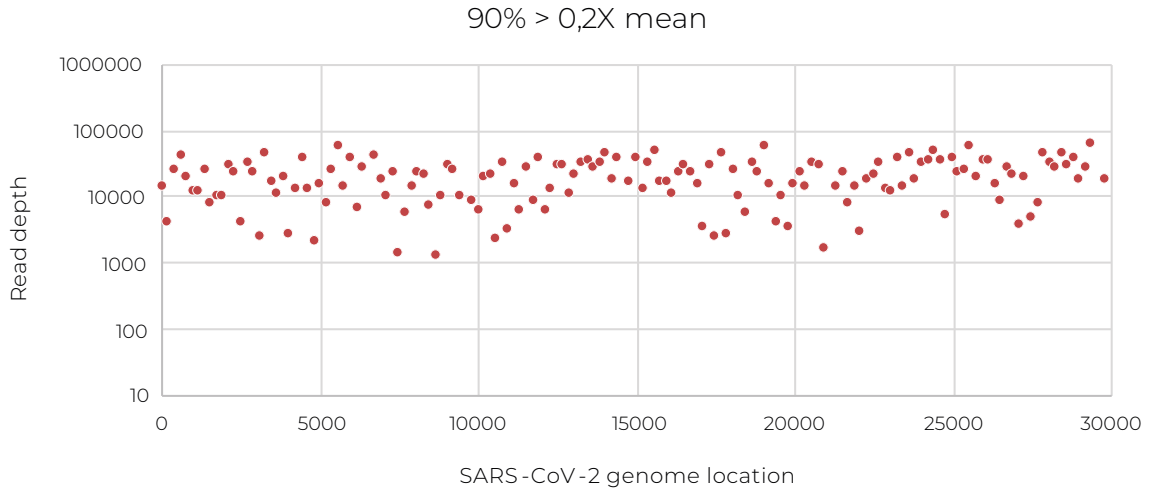
RC-PCR, the next revolution in NGS Library Prep

With the NimaGen EasySeq™ RC-PCR Library Preparation method the implementation of an NGS driven viral surveillance strategy could not be simpler or safer.

Utilising patented RC-PCR technology, sequence ready libraries are generated from cDNA covering the entire 29.9Kb SARS-CoV-2 Genome with minimal hands-on time and just a single PCR for both amplification and indexing.

RC-PCR probe mixes are provided in two tubes, as well as two breakable 96 well plates which include UDI Indexes. Just add cDNA and the RC-PCR mastermix provided in the kit and load on to your PCR instrument. Post PCR all samples can be combined for pooled cleanup with the included Ampliclean Magnetic Bead Cleanup Kit and following standard quantification and QC checks your libraries are ready to sequence.

Uniformity RC-PCR SARS-CoV-2



Performance

Thanks to the improved reaction kinetics, intrinsic in the RC-PCR method, in combination with the well designed and balanced probe pools, the kit delivers clean data. Also, this allows for well balanced read distributions in order to make efficient use of the sequencer's capacity. The method delivers a coverage of ~99% of the Covid Genome, and an on-target percentage of >90%. Thanks to the easy workflow, with just a few pipetting steps, this kit is the ideal solution for any virology lab, even without NGS experience. Our support team will get you up and running in no time.

NimaGen EasySeq™ RC-PCR SARS-CoV-2

- The simplicity and security of RC-PCR
- Single pre-PCR reaction setup - Just add cDNA and Mastermix to UDI index plates and go. Post-PCR pool all samples, perform single clean-up reaction, QC, quantify and sequence.
- Ideal for HTP automation
- Less handling steps, less risk of contamination or sample mix up, greater safety and reassurance

Sample Numbers per run:

Instrument	Samples per run*
iSeq™	32
MiniSeq™ (mid-output)	96
MiniSeq™ (high-output)	288
MiSeq™ (chemistry Micro)	32
MiSeq™ (v2 chemistry)	192
MiSeq™ (V3 chemistry)	288
NextSeq Mid	480*
NovaSeq™ SP (one lane):	480*
NovaSeq™ SP (two lanes):	960*

* Maximum UDI Indexes available is currently 480

Kit content

- RC-PCR SARS-CoV-2 probe pool A
- RC-PCR SARS-CoV-2 probe pool B
- RC-PCR Taq Mastermix, HiFi – Hotstart
- 96 x 10bp UDI indexes (additional sets of 96 UDI combinations available shortly)
- AmpliClean Bead Clean-up

Ordering Information

Part Number	Description
RC-COV096	EasySeqTM RC-PCR SARS-CoV-2 Kit (96 samples)
MMHS-25	HiFi 2x Hotstart PCR Mastermix (for 96 samples)
IDX96-U01D	2 x Index Primer Plate U01 (for 96 samples)
IDX96-U02D	2 x Index Primer Plate U02 (for 96 samples)
IDX96-U03D	2 x Index Primer Plate U03 (for 96 samples)
IDX96-U05D	2 x Index Primer Plate U05 (for 96 samples)
IDX96-U06D	2 x Index Primer Plate U06 (for 96 samples)

SARS-CoV-2 WGS analysis software virSEAK by JSI

VirSEAK Analysis software
JSI medical systems GmbH in Germany developed a dedicated software tool for analyzing NGS data from the SARS-CoV-2 virus.

Global GISAID data integrated
After the sequencing run ends, the generated fastq files can be imported into the JSI virSEAK software tool. virSEAK will automatically create a consensus sequence and alignment to the reference genome.

virSEAK calls mutations and assigns a type to the sample by comparing to the GISAID database. You will be shown the type frequencies and distribution per country, as well as the evolution of the strain.

Results can be uploaded to the GISAID database with a single mouse-click to share the results with the global Covid community. It also provides an exportable consensus sequence in fasta format for a more detailed analysis in local healthcare systems, or detailed lineage analysis for example in Pangolin COVID-19 Lineage Assigner and phylogenetic analysis.

JSI medical systems

Greater simplicity, less risk

NimaGen.

Product and Company Information

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Product name
EasySeq™ RC-PCR SARS CoV-2 kit

Product use
For Research Use Only

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