

CleanPlex® SARS-CoV-2 Research and Surveillance Panel

Targeted Sequencing NGS Panels to Support SARS-CoV-2 Research and Surveillance

Highlights

- Complete Coverage and Comprehensive Data**
 Sequence the entire SARS-CoV-2 genome with 99% coverage
- Ultra-sensitive Detection**
 Detect down to one copy per reaction for degraded or limited sample input
- Fast, Streamlined Workflow**
 Generate libraries for Illumina® platforms in just 5.5 hours using a simple, four - step protocol
- Superb Performance**
 Prepare high-quality NGS libraries with excellent coverage uniformity and on-target performance to enable efficient use of sequencing reads and reduce costs

Real Time RT-PCR and antibody-based methods are the main tools for detecting infectious agents, however, such methods can only focus on a limited number of targets and can at times suffer from low assay sensitivity and false negatives results. These methods also do not provide additional information other than a positive or negative diagnosis. The CleanPlex technology specializes in highly-multiplexed PCR-based targeted sequencing assays. This technology provides an easy to use, fast, and-comprehensive solution for detection, identification, and mutation analysis of infectious pathogens all via a quick and easy workflow.

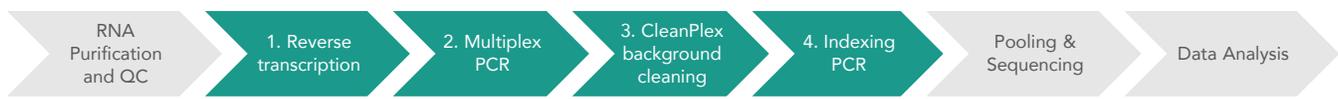
The CleanPlex® SARS-CoV-2 Research and Surveillance Panel was expertly designed from reference sequence MN908947 (NC_045512.2) using a proprietary design pipeline to cover the entire genome. For additional flexibility, the panel is available on two major sequencing platforms including Illumina®. The NGS panel not only allows high sensitivity detection and confirmation of questionable qPCR results, but also enables mutation analysis, tracking, surveillance, and informed infection control through comprehensive sequence information generated.

CleanPlex SARS-CoV-2 Research and Surveillance Panel Specifications for Illumina Platforms

Parameter	Specification
Enrichment Method	Multiplex PCR
Platform	Illumina®
Strain Compatibility	Above 97% coverage of over 107 known strains
Cumulative Target Size	29,903 bp
Number of Amplicons	343
Amplicon Size	116 - 196 bp, Median 149bp
Number of Primer Pools	2
Input DNA Requirement	~50ng purified total RNA
Sample Types	Bronchoalveolar lavage, tracheal aspirate, Sputum, NP/OP swab, Nasopharyngeal wash/aspirate or nasal aspirate
Total Assay Time	5.5 hours for Illumina
Hands on time	Less than 1 hour
Design Coverage	complete coverage (except 92 bp at the end of the genome)
Coverage Uniformity (targets with > 0.2X mean coverage)	whole genome sequencing metrics coming soon
On-Target Aligned Reads	whole genome sequencing metrics coming soon
Total Reads per sample	0.2 to 0.3 M per sample for complete genome sequencing with 2x 150 PE reads

CleanPlex Streamlined Targeted Sequencing Workflow

CleanPlex SARS-CoV-2 Panels offer a simple and streamlined workflow. Starting from purified RNA, the protocol can be completed to generate target-enriched NGS libraries in just 5 hours, with less than 1hr of hands-on time, using a three-step workflow with minimal tube-to-tube transfers. Libraries generated for Illumina sequencing contain an additional 15min background cleaning step that involves enzymatic digestion of non-specific products for cleaner and higher quality libraries.



CleanPlex Target Enrichment and Library Preparation

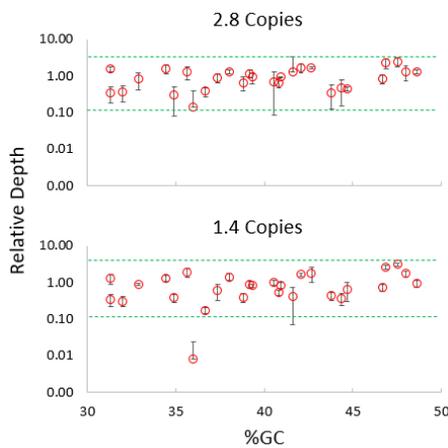
5.5 hours of total assay time, with less than 1 hour of hands-on time.

FOR RESEARCH USE ONLY. NOT FOR USE IN DIAGNOSTIC PROCEDURES.

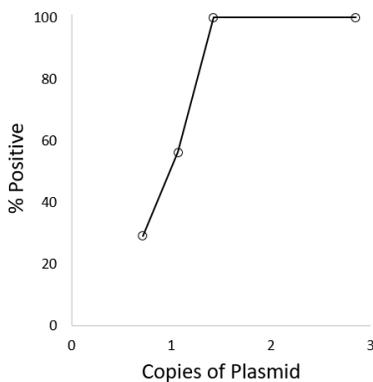
High Performance Translates to Cost-Effective Sequencing and Confident Analysis

CleanPlex Panels exhibit highly uniform coverage even with low template input and ultra high multiplexing. Without the need for deep sequencing to capture all targets, high sequencing performance allows for more cost-effective sequencing with more samples run per chip for higher throughput. With as little as 0.2M reads per sample, one can confidently capture the entire genome for mutation monitoring and phylogenetic analysis.

Using plasmids containing the N and S genes of SARS-CoV-2 with a single pool workflow for detection, the panel was able to on average capture all targets within 10 fold read depth range for 2.8 viral copies, and similarly for all but one target for 1.4 viral copies. All targets were also uniformly distributed across the GC range.



Using only one out of the two primer pools included in the panel, the detection rate was shown to be 56% at 1.1 copies and 100% when more than 2 copies were present. With the use of both pools to cover the entire viral genome, the sensitivity is expected to only further increase.



Recommended Sample Multiplexing for CleanPlex SARS-CoV-2 Research and Surveillance Panel

Instrument	Samples per Run ^A
iSeq™ 100 System	11
MiniSeq™ System (mid-output)	23
MiniSeq System (high-output)	72
MiSeq® System (v2 chemistry Nano)	3
MiSeq System (v2 chemistry Micro)	11
MiSeq System (v2 chemistry)	43
NextSeq™ 550 System (mid-output)	379
NextSeq™ 550 System (high-output)	1166

A. Samples per run at an intended average read depth of 1000x

Ordering Information

The CleanPlex SARS-CoV-2 Research and Surveillance Panels contain CleanPlex Multiplex PCR Primers and CleanPlex Targeted Library Kit with RT reagents. CleanPlex Indexed PCR Primers and CleanMag® Magnetic Beads are ordered separately to complete the workflow from input RNA to sequencing-ready NGS libraries. For more indexing options and additional product configurations, please visit www.paragongenomics.com/store/

Product	SKU
CleanPlex SARS-CoV-2 Panel (8 reactions)	918010
CleanPlex SARS-CoV-2 Panel (96 reactions)	918011
CleanPlex Dual-Indexed PCR Primers for Illumina® Set A (96 indexes, 96 reactions)	716006
CleanMag Magnetic Beads (1 mL)	718001
CleanMag Magnetic Beads (5 mL)	718002
CleanMag Magnetic Beads (60 mL)	718003

Learn More

To learn more about NGS applications for Infectious Diseases, please visit

www.paragongenomics.com/applications/infectious_disease/

To learn more about CleanPlex Technology, please visit

www.paragongenomics.com/cleanplex_technology/