

# CleanPlex® for MGI 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 over 99% coverage
- Ultra-sensitive Detection**  
 Detect down to one copy per reaction for degraded or limited sample input
- Fast, Streamlined Workflow**  
 Generate libraries for DNBSEQ™ in just 5 hours using a simple, three-step protocol, compatible with automation.
- 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 is an assay platform for ultra-sensitive and highly-multiplexed PCR-based targeted sequencing tests. 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® for MGI 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 DNBSEQ™. 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 for MGI SARS-CoV-2 Research and Surveillance Panel Specifications

| Parameter                | Specification  |
|--------------------------|--|
| Enrichment Method        | Multiplex PCR  |
| Platform                 | DNBSEQ™  |
| Strain Compatibility     | Complete coverage of major strains: MN908947 and MT007544  |
| Cumulative Target Size   | 29,903 bp  |
| Number of Amplicons      | 343  |
| Amplicon Size            | 116 - 196 bp, Median 149bp   |
| Number of Primer Pools   | 2  |
| Sample Input Requirement | 5-11 µL of extracted total RNA or ~50ng purified total RNA   |
| Sample Types             | Sputum, nasopharyngeal and oropharyngeal swabs and aspirate, tissue samples, and other methods for viral RNA sampling. |
| Total Assay Time         | 5 hours  |
| Hand on Time             | Less than 1 hour   |
| Design Coverage          | Complete coverage (except 92 bp at the ends of the genome)   |
| Amplicon Coverage (≥50x) | >95% with 300 copies viral input at 0.2M PE Reads per sample   |
| On-Target Aligned Reads  | >98% with 300 copies viral input at 0.2M PE Reads per sample   |
| Total Reads per sample   | 0.2 to 0.3 M PE per sample with 2 x 150 PE reads   |

## CleanPlex Streamlined Targeted Sequencing Workflow

CleanPlex for MGI 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.



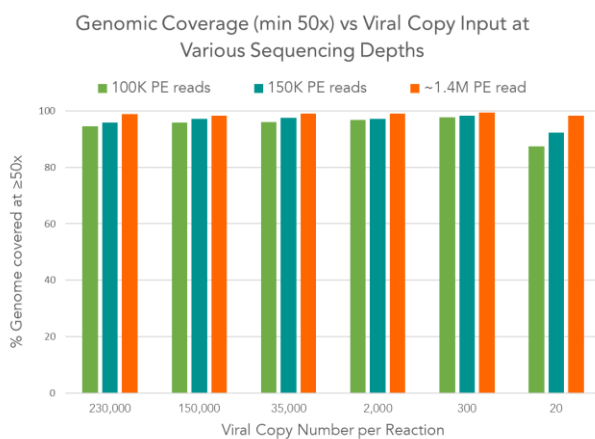
### CleanPlex Target Enrichment and Library Preparation

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

## High Performance Translates to Cost-Effective Sequencing and Confident Analysis

| Specifications           | 20 copies | 300 copies |
|--------------------------|-----------|------------|
| % Uniformity (0.2x Mean) | 87%       | 97%        |
| % Mapping Rate           | 84%       | 98%        |
| % On-Target Rate         | 93%       | 99%        |

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 pooled per chip for higher throughput.



Using nasopharyngeal swab samples from COVID-19 patients spanning 4 to 40,000 copies/μL (5.5 μL input/reaction) libraries were prepared and sequenced at ~0.7 million cluster reads per sample. The plot above shows *in silico* down sampling data indicating high coverage even at low reads and copy numbers. At the original sequencing depth, >98% of the amplicons are covered at >50X, more than sufficient for mutation monitoring and phylogenetic analysis. For strain confirmation of samples with as little as 4 copies/uL of viral RNA, just 0.1M PE reads is sufficient.

| Base Position | Reference base | Alternative Base | Call Frequency |
|---------------|----------------|------------------|----------------|
| 19065         | T              | C                | 99.4%          |
| 22303         | T              | G                | 99.0%          |
| 26144         | G              | T                | 99.3%          |
| 29749         | ACGATCGAGTG    | A                | 99.5%          |

CleanPlex Libraries were created using Twist's control synthetic SARS-CoV-2 MT007544 strain RNA, and variant calling was performed against reference genome NC\_045512.2 (MN908947). As shown in the table above, all four expected variants (3 SNVs and 1 deletion) were confidently detected with 99% calling frequency.

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## Sequencing suggestions for SARS-CoV-2 Panel on DNBSEQ

CleanPlex for MGI panels are specifically designed for 100bp PE reads on the DNBSEQ platforms. Suggested average read per amplicon is 75x or 50,000 cluster reads per sample with 2-pool workflow. More reads might be needed to achieve deeper coverage per amplicon and higher genome coverage for low viral copy number detection or low percentage variant calling.

### MGISP-960 Automated Liquid Handling System Compatible

|                      |  |
|----------------------|--|
| User-defined         | 24-position board supporting multiple combinations                                       |
| Efficient & Accurate | 96-channel pipettor with a robotic gripper to ensure high precision and reproducibility. |
| Hands-Free           | Complete CleanPlex SARS-CoV-2 Panel workflow fully integrated.                           |

## Ordering Information

The CleanPlex for MGI SARS-CoV-2 Research and Surveillance Panel contains panel mPCR 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. visit [paragongenomics.com/store\\_mgi/](http://paragongenomics.com/store_mgi/)

| Product   | SKU              |
|---|------------------|
| CleanPlex for MGI SARS-CoV-2 Panel (8 reactions)                                  | 918001           |
| CleanPlex for MGI SARS-CoV-2 Panel (96 reactions)                                 | 918002           |
| CleanPlex for MGI Single-Indexed PCR Primers, Set A (16 indexes, 32/96 reactions) | 318001<br>318007 |
| CleanPlex for MGI Single-Indexed PCR Primers, Set B (16 indexes, 32/96 reactions) | 318002<br>318008 |
| CleanPlex for MGI Single-Indexed PCR Primers, Set C (16 indexes, 32/96 reactions) | 318003<br>318009 |
| CleanPlex for MGI Single-Indexed PCR Primers, Set D (16 indexes, 32/96 reactions) | 318004<br>318010 |
| CleanPlex for MGI Single-Indexed PCR Primers, Set E (16 indexes, 32/96 reactions) | 318005<br>318011 |
| CleanPlex for MGI Single-Indexed PCR Primers, Set F (16 indexes, 32/96 reactions) | 318006<br>318012 |
| CleanMag Magnetic Beads (5 mL)  | 718002           |
| CleanMag Magnetic Beads (60 mL)   | 718003           |
| MGISP-960 Automated Sample Preparation System                                     | Variable         |

## Learn More

To learn more about NGS applications for Infectious Diseases, visit [www.paragongenomics.com/applications/infectious\\_disease/](http://www.paragongenomics.com/applications/infectious_disease/)

To learn more about CleanPlex Technology, visit [www.paragongenomics.com/cleanplex\\_technology/](http://www.paragongenomics.com/cleanplex_technology/)