



ATOplex RNA library preparation set for SARS-CoV-2

ATOplex RNA Multiplex PCR-based Library Preparation Set V3.1 can complete the full process of variant identification and genetic typing of SARS-CoV-2, with MGI's extraction kits, sequencing platform and data analysis, fastest in 17.2 hours.



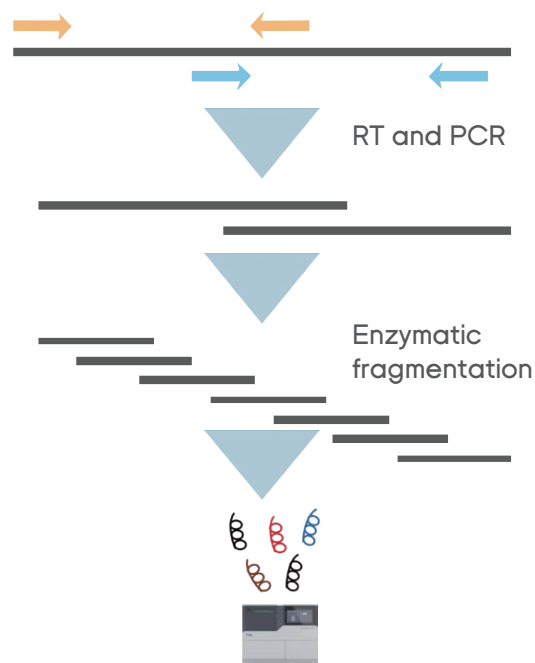
Highlights

- **Identify Quickly**
The whole process can be completed in 17.2 h*
- **Comprehensive Information**
The report covers genome-wide alignment, mutation information, and variants of SARS-CoV-2
- **High Sensitivity**
Whole-genome can be obtained from a minimum of 40 copies
- **Wide Samples Type**
It can be used for various samples, such as pharyngeal swabs, alveolar lavage fluid, environmental samples and so on
- **Accurate Quantitative**
The copy number of virus can be quantified by adding synthetic DNA into the sample



Technologies

ATOplex V3.1

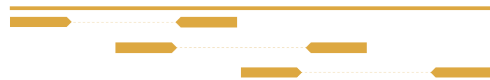


*The whole process time measured when the RNA library was prepared manually with DNBSEQ-G50RS **(FCS) for sequencing.



ATOPlex Unique Primers

SARS-CoV-2 genome



Spike-in control DNA



GAPDH gene (Human)



1

SARS-CoV-2 primer pool ~328 pairs

Primers targeting at the whole genome are designed to obtain the full-length sequence of nCoV virus

2

Spike-in control primer pool ~4 pairs

A known amount of synthetic DNA is inserted into the sample for the relative quantification of the virus and the quality control of library process

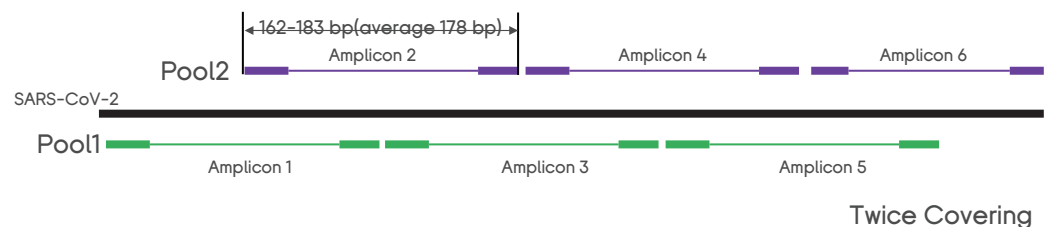
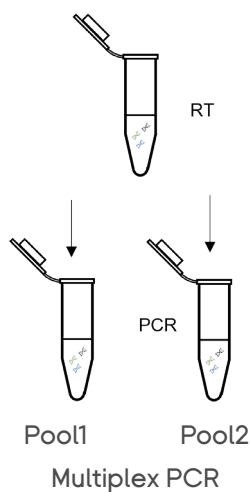
2

GAPDH gene primer pool ~2 pairs

As the quality control of extraction process



Two Tubes with Twice Coverage



Pool1: 164 pairs*178=29704bp

Pool2: 164 pairs*178=29704bp



Parameters

Target region	SARS-CoV-2 whole genome
Amplicon size	162-183 bp(average 178 bp)
Amplicon number	334 pairs (328 SARS-CoV-2,4 external control,2 Internal control)
Tube	2 tubes
RNA input	10 µL
Detection type	SNV, indel
Sample type	Swab, BLAF, environmental samples, and so on
TAT	6 h library preparation+1 h DNB making
Hand-on time	2.5 hours
Uniformity	≥99%
Sequencing strategy	SE100+10+10
Reads recommended	1-5 M reads

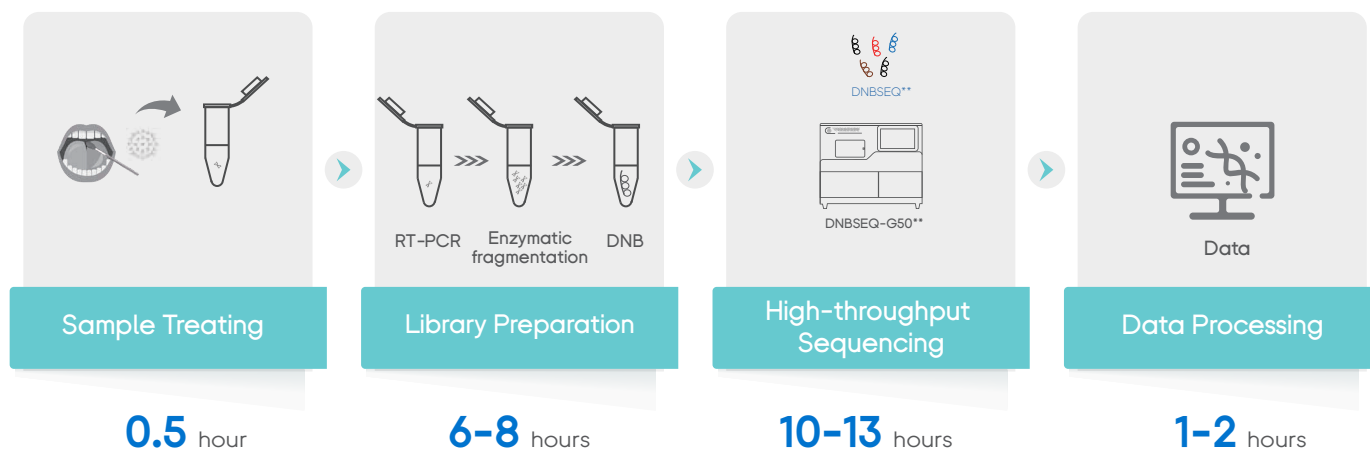


Excellent Performance

Sample	CT Value	Copies	Reads *	SARS-CoV-2 (%)	Identification	Coverage (1X)	Coverage (100X)	Average depth
S1	20.85	400000	3,191,323	98.94%	Positive	99.75%	99.73%	8591.49
S2	24.58	40000	3,765,741	98.07%	Positive	99.75%	99.73%	9954.79
S3	28.96	4000	3,192,686	97.02%	Positive	99.75%	99.74%	8329.67
S4	32.88	400	2,057,541	87.81%	Positive	99.75%	99.61%	3948.87
S5	36.7	40	3,402,272	76.68%	Positive	99.75%	99.65%	3551.67
Negative	NOCT	0	1,475,376	0.02%	Negative	0.00%	0.00%	0

*data per sample on DNBSEQ-G50RS**

Workflow



Ordering Information

Product Name	Specification	Product Number
ATOPlex RNA Multiplex PCR-based Library Preparation Set V3.1	96RXN	940-000133-00

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