

ATOplex SARS-CoV-2 Full Length Genome Panel for Research



Accurate, fast, cost-efficient, sensitive and simple for SARS-CoV-2 detection and full length genome analysis

Highlight

Fast, Simple, Streamlined Workflow

- Three-step workflow converts viral RNA into sequencing-ready libraries in just 5 hours, all amplicons in one tube

Ultra-Sensitive Detection

- Analyze samples with as low as 10 copies/ml viral load

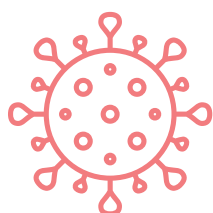
Accurate Quantification

- Ability to accurately quantify viral load based on spike-in control

Ultra-Sensitive Detection

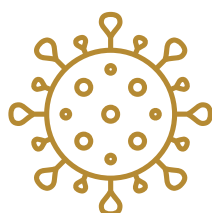
- It covers >99% of the viral genome and variants in challenging sample

Multiple variants of SARS-CoV-2, including all five VOCs (Variant of Concern) currently designated by WHO, can be effectively detected by ATOplex SARS-CoV-2 Full Length Genome Panel.



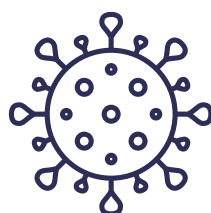
Alpha

B.1.1.7



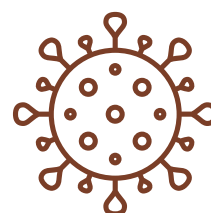
Beta

B.1.351



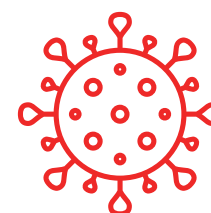
Gamma

P.1



Delta

B.1.617.2



Omicron

B.1.1.529

Ordering Information

Cat. No.	Product Name	Product Name
1000027431	ATOplex RNA Library Prep Set	96preps

Learn more

To learn more about MGI please visit: <https://www.mgitech.cn/>

To learn more about ATOplex platform please visit: <https://www.mgitech.cn/products/atoplex/>

 <https://www.linkedin.com/company/mgi-bgi>

 https://twitter.com/MGI_BGI

 **Telephone**
4000-688-114

 **Website**
www.mgitech.cn

 **Service**
MGI-service@genomics.cn



website

Performance

1 ng of Human gDNA and an artificial DNA with known copy number were added to 6 serial dilutions of a cultured isolate and subjected to direct mPCR-based MPS and RT-PCR (Figure 1).

According to the results (Table 2), mPCR-based MPS can detect samples with 10^{-6} gradient dilutions (about ~10copies/ml).

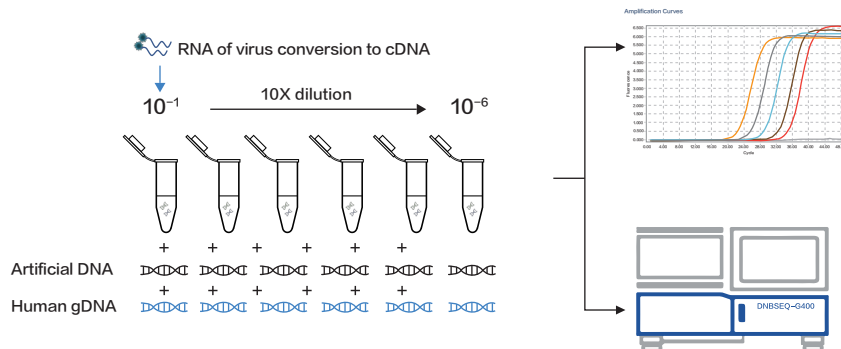


Figure 1. The overview of the study design

Table 2 Comparison of mPCR-based MPS and RT-PCR results

ID	Raw Reads	MPS			qPCR
		SARS-CoV-2 reads	SARS-CoV-2 depth	1XCoverage%	qPCR-Ct Value
Dilution 10^{-1}	3,841,506	3,413,916	36054.7	99.7	21.8
Dilution 10^{-2}	2,836,864	2,454,959	25698.0	99.8	25.5
Dilution 10^{-3}	4,640,806	3,178,230	33132.2	99.7	29.7
Dilution 10^{-4}	10,321,121	2,183,454	22796.5	99.7	32.8
Dilution 10^{-5}	10,132,009	312,440	3242.5	99.5	36
Dilution 10^{-6}	8,960,529	30,928	319.5	95.2	No CT

According to the results (Figure 2), Left, Basic performance statistics, >98% mapped rate (red), >97% targeted rate to three targeted regions (green), >92% 0.2X uniformity(yellow); Right, reproductivity of two repeat tests. x, y-axis are normalized depth of each amplicon in two separate experiments ($R^2=0.97$).

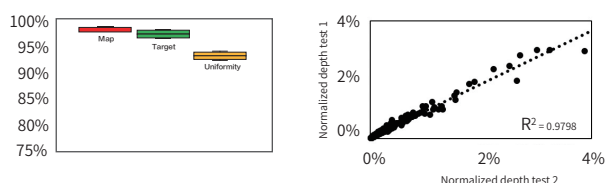


Figure 2 .Performance of mPCR-based MPS