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

Accurate Quantification

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

Ultra-Sensitive Detection

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

Ultra-Sensitive Detection

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

Introduction

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.

Table 1 the Parameter of the ATOPlex SARS-CoV-2 Full Length Genome Panel

Parameter	Specification
Product Name	ATOPlex RNA Library Prep Set
Configuration	96 preps/kit
Sample Types	Throat swabs, BALF, saliva, urine, etc
Automatic Platform Compatibility	MGISP-100, MGISP-960
Application	surveillance, variation and evolution analysis of SARS-CoV-2
Region	SARS-CoV-2 Full length
Amplicons Size	159-199bp(average 189bp)
Amplicons	296 amplicons in one tube
cDNA Input	>10copies genome for full length，10copies/ml for detection
Variant Types	SNP, InDel
Sample Type	Total nucleic acid from throat swab, BALF, etc
Total time	5.0 hours (sample to library)
Hands-on time	1 hour (sample to library)
Uniformity(0.1X)	95%
On Target Aligned Reads	≥95%
Sequence type	SE200, PE100 for full length genome
Total reads	5-10 Mreads

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).

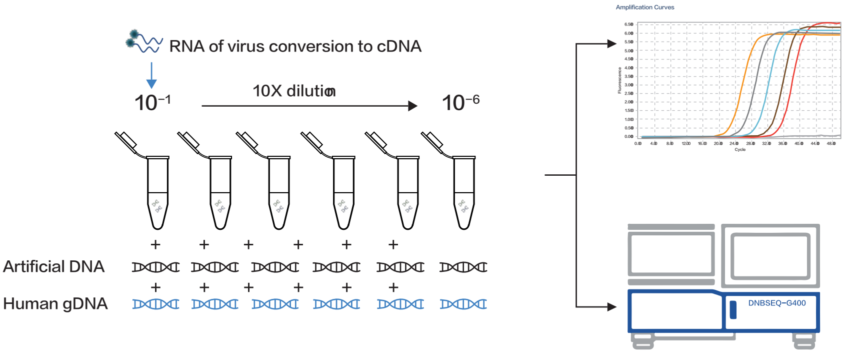

Figure 1. The overview of the study design

Table2 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 (R2=0.97).

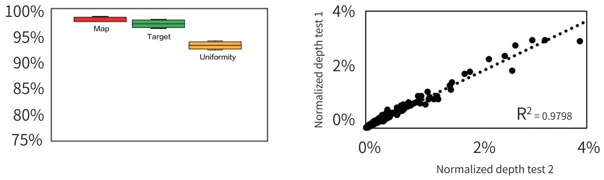

Figure 2 .Performance of mPCR-based MPS

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/

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