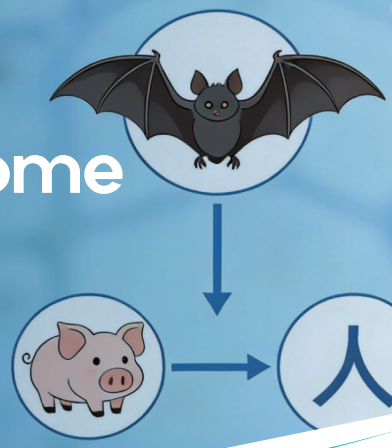
CycloneSEQ | MGI

# ATOPlex Fast NiV Whole-Genome Targeted Sequencing Package (for DNBSEQ/CycloneSEQ)



## Highlights

### Convenient and quick library preparation

NiV primer pool combined with ATOPlex Fast series kits eliminates end-repair and A-tailing. 5-min rapid adapter ligation, and only 4 steps from RNA to library, completion in 3.5 h. It' s also compatible with MGI automated system.

### High detection sensitivity

This method requires no sample culture and can directly detect RNA extracted from human serum, cerebrospinal fluid, tissue, swab samples, as well as environmental and food samples. It can also obtain high-coverage whole-genome sequencing data for samples with low viral loads.

### Supports both long and short-read sequencing

Amplicons can be compatible with both CycloneSEQ and DNBSEQ platforms. The short-read sequencing solution is cost-effective. The long-read sequencing solution enables real-time sequencing. Samples can be processed immediately upon arrival without batching, significantly reducing turnaround time, meeting the needs of different application scenario.

## Product Parameter

| | DNBSEQ solution | CycloneSEQ solution |
|---|---|---|
| Sample type | RNA extracted from serum, cerebrospinal fluid, tissue, swabs, or the environment, etc. | |
| Amplicon region | Nipah virus whole genome ( Malaysian strain (NiV-M) and Bangladeshi strain (NiV-B)) | |
| Amplicon length | 200~300 bp | 200~300 bp or 600~800 bp are available |
| Amplicon count | 90 pairs | 90 or 30 pairs are available |
| Number of amplification tubes | 1 tube | 1 tube |
| Recommended RNA input | 10 μL | 10 μL |
| Automation | SP-100 | SP-100 |
| Library-prep time | 4.2 h (Including make DNB) | 3.5 h |
| Recommended sequencing platforms | E25, G99 | G100-ER |
| Sequencing read | PE150+10+10 | / |
| Recommended sample size | Ct≤28: : E25(8 samples/FC); G99 (32 samples/FC)<br>Ct>28 /Unkown Ct value: E25(4 samples/FC); G99 (16 samples/FC) | Ct≤28: G100-ER (8 samples/FC)<br>Ct>28 /Unkown Ct value: G100-ER (4 samples/FC) |
| Bioinformatics analysis software | ATOPlex MMRS | ATOPlex MMRS |
| Recommended analysis data volume per sample | Ct≤28: 2.5M reads/sample<br>Ct>28 /Unkown Ct value: 5M reads/sample | Ct≤28: 1 Gb/sample<br>Ct>28 /Unkown Ct value: 2 Gb/sample |
| Variant types | SNV, INDEL | SNV, INDEL |
| Key advantages | Cost-effective | Real-time sequencing for faster turnaround |

# Total solution introduction

This sequencing package is based on MGI's independently developed reagents, automated sample preparation system, sequencing platform, and data processing system, covering the entire process from sample to result output.

The ATOPlex Fast NiV Library Prep Set is developed based on the ATOPlex multiplex PCR library preparation platform. It enables efficient amplification of the entire NiV genome in a single tube without the need for sample culture, and features advantages such as simple operation and low sample requirement.

The library is compatible with DNBSEQ and CycloneSEQ platforms, meeting the diverse needs of different application scenarios. The short-read protocols (DNBSEQ-E25/G99, etc.) offer both high cost-effectiveness and accuracy, processing large numbers of samples in a single run, suitable for large-scale epidemiological surveys and routine surveillance. The long-read protocols (G100-ER, etc.) can sequence a single sample in as little as 1 hour, with the entire process from sample to report completed in as little as 6 hours, supporting immediate sample testing upon receipt, perfectly suited for rapid pathogen screening and emergency tracing needs.

The ATOPlex MultiPCR Microbiome Research Software (ATOPlex MMRS) is designed for ATOPlex targeted sequencing data analysis and can analyze both long-read and short-read data, enabling the identification and characterization of microorganism. It includes reference genomes and primer sequences for SARS-CoV-2, monkeypox virus, dengue virus, respiratory syncytial virus and Chikungunya virus, with modules for data quality control, sequence alignment, variant detection, and closely related genome analysis. Meanwhile, the software supports custom input of reference genome information and primer sequences for species to complete the above analyses for specific species.

This sequencing package has been proven to perform rapid, accurate, and comprehensive short/ long-read sequencing of NiV samples, providing crucial references for variant detection, gene annotation of variant sites, lineage identification, and phylogenetic analysis of NiV.

**Nucleic acid extraction ( ~0.5 h )**

- MGIEasy Nucleic Acid Extraction
- MGIEasy Microbiome DNA&RNA Extraction Kit

- SP-NE32

**Library Preparation ( ~3.5 h )**

- ATOPlex Fast NiV Library Prep Set ( for DNBSEQ )
- ATOPlex Fast NiV Library Prep Set (for CycloneSEQ)

- SP-100

**Sequencing ( 1-24 h )**

- DNBSEQ short-read sequencing

- G99 (PE150, 12h )
- E25 (PE150, 20h )

or

- CycloneSEQ long-read sequencing

- G100-ER（1~24 h）

**Bioinformatics analysis ( ~0.2-0.5h )**

- ATOPlex MultiPCR Microbiome Research Software( ATOPlex MMRS )

- OmicsNest

# Order information

## Short-read sequencing solution

| Category | Product Name | Product number |
|---|---|---|
| Genetic Sequencers | DNBSEQ-E25RS Genetic Sequencer | 900-000537-00 |
| | DNBSEQ-G99RS Genetic Sequencer | 900-000607-00 |
| | DNBSEQ-G99ARS Genetic Sequencer | 900-000609-00 |
| Automation Instruments | Automated Nucleic Acid Extractor MGISP-NE32RS | 950-000020-00 |
| | DNA Sequencing Library Preparation System MGISP-100RS | 900-000206-00 |
| Nucleic acid extraction reagents | MGIEasy Nucleic Acid Extraction Kit OP02-32 (32 RXN) | 1000023774 |
| | MGIEasy Nucleic Acid Extraction Kit T-96 (96RXN) | 1000020471 |
| | MGIEasy Microbiome DNA&RNA Extraction Kit PMT-48 48Preps/Kit (48RXN) | 940-002223-00 |
| | MGIEasy Microbiome DNA&RNA Extraction Kit (96RXN) | 940-002222-00 |
| Library preparation reagents | ATOPlex Fast NiV Library Prep Set (for DNBSEQ) (16 RXN) | 940-003133-00 |
| | ATOPlex Fast NiV Library Prep Set (for DNBSEQ) (96 RXN) | 940-003132-00 |
| Sequencing reagents | DNBSEQ OneStep DNB Make Reagent Kit V4.0 (OS-Dual Barcode) (4 RXN) | 940-001654-00 |
| | DNBSEQ-G99 High-throughput Sequencing Set (G99 FCL PE150) | 940-001269-00 |
| | DNBSEQ-E25RS High-throughput Sequencing Set (FCL PE150) | 940-000567-00 |
| Data analysis | ATOPlex MultiPCR Microbiome Research Software Analysis Package (16 reports) | 970-000528-00 |
| | ATOPlex MultiPCR Microbiome Research Software (ATOPlex MMRS) | 970-000518-00 |
| | OmicsNest Bioinformatics Platform | 900-001195-00 |

## Long-read sequencing solution

| Category | Product Name | Product number |
|---|---|---|
| Genetic Sequencers | Nanopore Genetic Sequencer G100-ER | H900-000048 |
| | Nanopore Genetic Sequencer Bundle 2( G100-ER sequencer+work-station+Keyboard & Mouse+Display Screen) | H910-000022 |
| Automation Instruments | Automated Nucleic Acid Extractor MGISP-NE32RS | 950-000020-00 |
| | DNA sequencing Library Preparation System MGISP-100RS | 900-000206-00 |
| Nucleic acid extraction reagents | MGIEasy Nucleic Acid Extraction Kit OP02-32 (32 RXN) | 1000023774 |
| | MGIEasy Nucleic Acid Extraction Kit T-96 (96RXN) | 1000020471 |
| | MGIEasy Microbiome DNA&RNA Extraction Kit PMT-48 48Preps/Kit (48RXN) | 940-002223-00 |
| | MGIEasy Microbiome DNA&RNA Extraction Kit (96RXN) | 940-002222-00 |
| Library preparation reagents | ATOPlex Fast NiV Library Prep Set (for CycloneSEQ) (24RXN) | 940-003130-00 |
| | ATOPlex Fast NiV Library Prep Set (for CycloneSEQ) (96RXN) | 940-003131-00 |
| Sequencing reagents | WT Sequencing Flow Cell (2 pcs/set) | H930-000002-00 |
| | CycloneSEQ WT Sequencing Kit (6 T) | H940-000016 |
| Data analysis | ATOPlex MultiPCR Microbiome Research Software Analysis Package (16 reports) | 970-000528-00 |
| | ATOPlex MultiPCR Microbiome Research Software (ATOPlex MMRS) | 970-000518-00 |
| | OmicsNest Bioinformatics Platform | 900-001195-00 |

**MGI Tech Co., Ltd.**
Building 11, Beishan Industrial Zone, Yantian District, Shenzhen, CHINA, 518083
4000-688-114
global-mgitech.com
MGI-service@mgi-tech.com
Version: 202608