Product Advantages

1.High Data Volume

High-throughput sequencing technology boosts data output, ensuring ultra-sensitive pathogen detection and robust support for precise diagnosis of complex infections.

2.Comprehensive Testing

One-time detection of 36,000 pathogens, including drug-resistant and virulence genes (e.g., Mycobacterium tuberculosis resistance mutations), for full-spectrum pathogen analysis in complex infections.

3. Precision processing

Targeted sample pretreatment and optimized workflows enhance testing sensitivity, delivering accurate, reliable results for clinical decisions.

4. Clinical-level Database

Powered by a clinical-grade database and intelligent algorithms, ensuring precise report outcomes to guide diagnosis and treatment of complex infections.

5. Fully Qualified

End-to-end process—from nucleic acid extraction to analysis software—holds clinical certifications, guaranteeing quality, authority, and credibility of results.

6. Reliable Performance

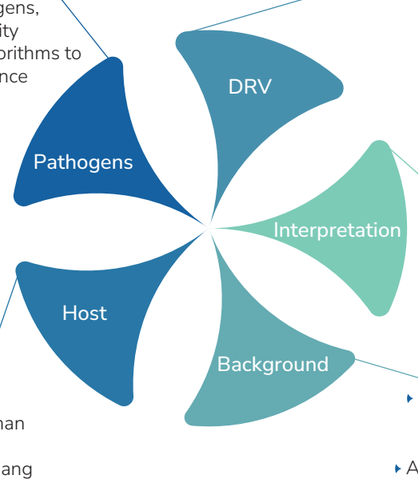
Standardized quality management ensures stable, consistent testing. Years of passing NHC's mNGS external quality assessments validate the accuracy and reliability.

PMseq Database

Clinical-level database and core intelligent algorithm ensure accurate results.

Pathogen Database

- Over 36,000 kinds of pathogens, strictly control genome quality
- Independently integrate algorithms to screen representative reference sequences
- Comprehensive evaluation



Drug Resistance and Virulence Database

- 32 representative drug resistance genes. Include CTX-M, KPC, OXA, MecA, NDM, etc. (CARD database).
- 281 representative virulence genes. Include rmpA, rmpA2, iutA of Klebsiella pneumoniae, hly of Listeria monocytogenes, and ctxA/ctxB of Vibrio cholerae (VFDB database).

Interpretation Database

- Comprehensive and meticulous literature research
- Precisely extract pathogen interpretation information

Detection Background Database

- Diversified background library for large-sample data analysis
- Constructed from 300,000 real samples
- Accumulated over many years of clinical practice

Host Database

- Internationally common human reference genome
- BGI's self-assembled Yanhuang genome

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@BGI Genomics

PMseq™

Pathogen Metagenomic Sequencing

PMseq™ Pathogen Metagenomic Sequencing is based on metagenomics, which allows for the simultaneous detection of major microorganisms in a sample using next-generation sequencing without the need for prior knowledge of their identities. PMseq™ can detect more than 36,000 types of pathogens, including bacteria, fungi, viruses, parasites, etc., as well as representative drug resistance and virulence genes without bias. By using PMseq™, the positive rate of pathogen diagnosis can be significantly increased, guiding the clinical targeted use of antibiotics and assisting in the precise diagnosis and treatment of infections.

Applicable Population

Complicated or unexplained infectious patients

Severe Infectious Patients

Immunocompromised Patients

Detection Scope

PMseq™ Pathogen Metagenomic Sequencing – Detects over 36,000 pathogens and their representative resistance and virulence genes in a single test, and also supports analysis of human chromosomal copy number variations (CNV).

Bacteria:	16,343	(Including 226 Mycobacteria and 179 Mycoplasma/Chlamydia/Rickettsia)
Fungi:	2,431	
Viruses:	16,679	(Including 11,545 DNA viruses, 5,134 RNA viruses)
Parasites:	718	
Drug resistant Gene:	33	(Detects 67 types of antibiotic-resistant bacteria, including genes/sites such as ***CTX-M, KPC, OXA, MecA, NDM, and 23S rRNA***.)
Virulence Genes:	281	(***Including rmpA, rmpA2, iutA, hly, ctxA/ctxB, etc.***)

Sample Types

Clinical Presentations	Sample Types
Bloodstream infections, sepsis	Peripheral blood
Encephalitis, meningitis, myelitis	Cerebrospinal fluid, brain abscess aspirate, spinal fluid, brain tissue
Upper respiratory tract infections	Nasopharyngeal swabs > oropharyngeal swabs
Lower respiratory tract infections	Protected brush samples > bronchoalveolar lavage fluid, lung tissue > endotracheal aspirates > deep sputum
Pleuritis	Pleural fluid, ascites
Joint infections, prosthetic infections	Synovial fluid, prosthetic sonicate fluid
Ocular infections	Vitreous humor, aqueous humor, corneal tissue, ocular discharge
Skin and soft tissue infections	Wound swabs, wound tissue (at the junction of normal and necrotic tissue), abscesses
Urinary tract infections	Urine (first morning urine), bladder aspirate
Genitourinary infections	Urethral/vaginal/cervical/endometrial secretions, pelvic abscess; prostatic fluid, semen, ulcer discharge, etc.
Deep and superficial abscesses	Purulent fluid, aspirate fluid
Tissue infection	Fresh tissue, biopsy tissue, paraffin-embedded tissue
Fever of unknown origin	Peripheral blood + focal site samples
Intolerant to invasive surgery patients	Peripheral blood

One-stop Localization Solutions for Different Scenarios

1. Flexible and combinable localization solution

MGISP-100

Automated sample preparation system

(16 samples/run)

Sample Preparation~2.5h
Library Construction~4h

DNBSEQ-G400/G50/G99

High-throughput sequencer

Sequencing~3.5-14h

HALOS

All-in-one bioinformatic analyzer

Bioinformatic Analysis + Result Interpreting~0.5h-2h

Multiple sequencing platforms can flexibly meet different clinical needs

	DNBSEQ-G400	DNBSEQ-G50	DNBSEQ-G99
			
Max. Flow Cell/Run	2	1	2
Effective Reads	1500-1800M/FCL	500M/FCL	80M/Flow Cell
Number of Samples per Flow Cell	16-48 Samples/FCL	4-12 Samples/FCL	1-4 Samples/Flow Cell
Sequencing Time	FCL SE50: 12-14h	FCL SE50: 7h	FCL SE50: 3.5h

Mixed sequencing of PMseq and PTseq samples based on DNBSEQ-G400/G50/G99 are available!

2. Highly integrated and fully automated localized solution: GenSIRO-16

Nucleic Acid Extraction → Library Construction → Sequencing → Bioinformatics Analysis → Interpretation Analysis → Report Review

Integrates, Intelligence, Simplicity, Accuracy