

GPSTTM

Super-multiplex targeted Next Generation Sequencing (tNGS)
for Common Pathogens in Pan-infection Scenarios

Coverage of 476 pathogens in one test

217 drug resistance genes/mutations



GPSTTM

Gastrointestinal Infection (GI)

Bone and Joint Infection

Respiratory Tract Infection (RTI)

Skin and Soft Tissue Infection (SSTI)

Bloodstream Infection (BSI)

Central Nervous System Infection (CNSI)

Urogenital Tract Infection

Fever of Unknown Origin (FUO)

Introduction to GPS™

Based on super-multiplex targeted amplification and NGS technology, GPS™ can be used for the detection of pathogens in general scenarios, including 476 pathogens, 192 drug resistance genes/mutations and 25 hypervirulence genes, as well as co-detection of DNA and RNA Pathogens. It is suitable for various clinical scenarios, such as moderate or severe infections, mixed infections, and suspected drug resistant infections.

Product Advantages

› Comprehensive coverage

476 pathogens, completely covering general clinical scenarios including respiratory system, central nervous system, and focal infections.
Drug resistance genes and hypervirulence genes detection.

› High sensitivity

In-house super-multiplex targeted amplification and primer-dimer removal technology, achieving >90% effective data rate.
Expanded targets still with superb performance, with LoD as low as 50 copies/mL.

› User-friendly operation

Single-tube amplification system simplifies experimental operation with a fast TAT time of 10.5 hours for the whole workflow.
DNA& RNA pathogen Co-detection.

› Semiquantitative analysis of pathogens

Internal control and in-house tNGS quantitative algorithm.
Correction of PCR amplification bias to achieve accurate pathogen quantification.

Sample Requirements

Respiratory Tract System	Central Nervous System	Bloodstream System	Urogenital Tract	Other Focal Infections
Bronchoalveolar lavage fluid (BALF) ≥5 mL; Sputum ≥2 mL; Nasopharyngeal swabs ≥2	Cerebrospinal fluid (CSF) ≥2 mL	Peripheral blood: Adult ≥5 mL Child ≥2 mL	Urine ≥5 mL; Vaginal secretion swabs ≥2	Hydrothorax or ascite ≥5 mL; Pus or joint aspirate ≥2 mL; Puncture specimen/ Tissue 0.2-2 g

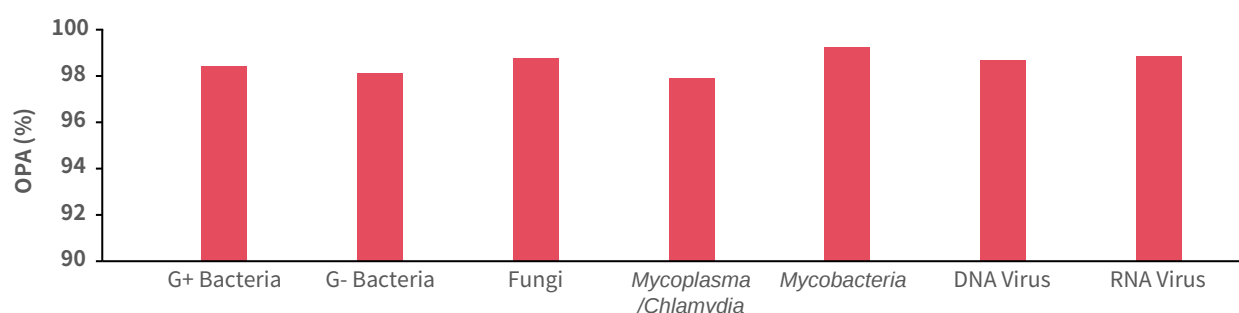
Detection Performance

» LoD as low as 50 copies/mL

G+&G- Bacteria (CFU/mL)	MTBC (Copies/mL)	NTM (Copies/mL)	Fungi (CFU/mL)	DNA&RNA Viruses (Copies/mL)
100	50	100	100	100

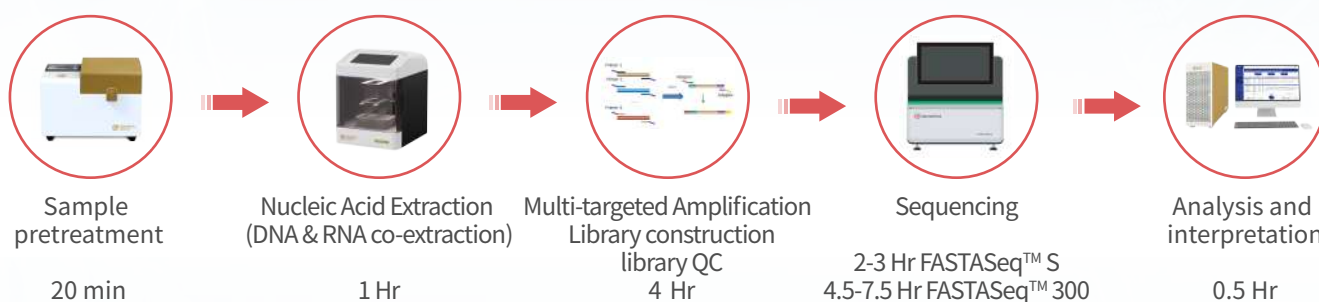
“G+” indicates Gram-positive bacteria, “G-” indicates Gram-negative bacteria, MTBC means *Mycobacterium tuberculosis* complex, and NTM means Non-tuberculous *Mycobacteria*.

» >95% OPA between GPS™ and mNGS+qPCR composite results



OPA indicates Overall Percentage Agreement.

Solution workflow



The entire process takes ~10.5 hours for tNGS in actual operation.
The processing time for each step depends on the sample type and quantity.

PARAMETERS		
Method	multiplex PCR and NGS	
Reads requirement/sample	0.5 M for SE50	
Sequencing platform	FASTASeq™ S	FASTASeq™ 300
Number of samples/run	1 FCL: 24 1 FCM: 48 1 FCH: 96	1 FCL: 50 1 FCM: 125 1 FCH: 280 1 FCP: 500
Turnaround time ¹	10.5-11.5 h	13-16 h
Report generation	Local analysis and report system	

1. Please note that the turn-around-time shown in the table is validated in GeneMind's lab, just for reference. It may be different due to the local situation, such as the sample volumes, lab equipment and the proficiency of operator.

Scope of Detection (partial)

Indications	Representative Pathogens / Genes
Respiratory Tract Infection	<i>Klebsiella pneumoniae</i> , <i>Staphylococcus aureus</i> , <i>Moraxella catarrhalis</i> , <i>Mycoplasmoides pneumoniae</i> , <i>Mycobacterium tuberculosis</i> , <i>Aspergillus</i> , Influenza A virus H1N1/H3N2, Influenza B virus, Human respiratory syncytial virus A/B, Human parainfluenza viruses 1-4, Adenoviridae, Coronavirus, Bocavirus, Human metapneumovirus
Central Nervous System Infection	<i>Streptococcus pyogenes</i> , <i>Listeria monocytogenes</i> , <i>Cryptococcus neoformans</i> , <i>Streptococcus agalactiae</i> , <i>Mycobacterium tuberculosis</i> , Coxsackievirus, VZV, HSV1, Enterovirus,
Fever of Unknown Origin	<i>Brucella</i> , <i>Leptospira</i> , Bandavirus dabieense, Dengue virus, Coxiella burnetii, Hantaan orthohantavirus, Yellow fever virus, Chikungunya virus, Orientia tsutsugamushi
Bloodstream System Infection	<i>Escherichia coli</i> , <i>Klebsiella pneumoniae</i> , <i>Staphylococcus aureus</i> , <i>Candida</i> , <i>Pseudomonas aeruginosa</i> , <i>Enterococcus faecium</i> , <i>Enterococcus faecalis</i> , <i>Stenotrophomonas maltophilia</i> , Coagulase negative staphylococci, <i>Enterobacter cloacae</i> ,
Gastrointestinal Infection	<i>Escherichia coli</i> , <i>Klebsiella pneumoniae</i> , <i>Pseudomonas aeruginosa</i> , <i>Enterococcus faecalis</i> , Rotavirus, <i>Enterococcus faecium</i> , <i>Bacteroides fragilis</i> , Norwalk virus, <i>Salmonella enterica</i>
Urogenital Tract infection	<i>Escherichia coli</i> , <i>Klebsiella pneumoniae</i> , <i>Enterococcus</i> , <i>Pseudomonas aeruginosa</i> , <i>Proteus</i> , <i>Candida</i> , Betapolyomavirus hominis (BKV), HPV, <i>Mycoplasmoides genitalium</i> , <i>Neisseria gonorrhoeae</i>
Bone and Joint Infection	<i>Staphylococcus aureus</i> , <i>Streptococcus pyogenes</i> , <i>Bacteroides fragilis</i> , <i>Mycobacterium tuberculosis</i> , <i>Pseudomonas aeruginosa</i> , <i>Enterococcus</i>
Drug Resistance Genes	KPC, CTX-M, NDM, <i>vanA</i> , <i>GES</i> , <i>mcr-1</i> , <i>mecA</i> , <i>rpoB</i> , MP_23S rRNA, Bp_23S rRNA
Hypervirulence Genes	<i>Klebsiella pneumoniae</i> (<i>rmpA</i> , <i>rmpA2</i> , <i>iucA</i> , <i>rpoB</i> , <i>peg-344</i>), <i>Acinetobacter baumannii</i> (<i>gtr100</i>), <i>Staphylococcus aureus</i> (LukS-PV, LukF-PV), <i>Haemophilus Influenzae</i> (<i>bexA</i>)

✖ Disclaimer

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