PTseq™

Pathogen Targeted Sequencing

Product Introduction

PTseq™ Pathogen Targeted Sequencing is based on ultra-multiplex PCR and targeted next-generation sequencing technology (tNGS). It specifically amplifies target genes and performs sequencing on a high-throughput sequencing platform. Through database comparison and bioinformatics algorithm analysis, it can identify suspected pathogenic microorganisms, resistance genes, and virulence gene information, thereby significantly improving the positive rate of pathogen diagnosis, assisting clinicians in formulating personalized anti-infection treatment regimens, reducing the risk of drug resistance, and aiding in precise diagnosis and treatment of infections.

Sample Types

This product is applicable to various types of respiratory samples:

BALF, sputum, swab, and other respiratory fluid samples such as pulmonary fluid and endotrache al aspirated fluids, etc.

Applicable Population

Patients with respiratory infections, including upper respiratory tract infections, lower respiratory tract infections, tuberculosis infections, chronic respiratory infections, etc.

Detection Content

PTseq™ Pathogen Targeted Sequencing – Comprehensive coverage of 274 targets, including 232 common pathogens associated with respiratory infection syndromes and 42 clinically representative antibiotic resistance genes and virulence genes.

Bacterial Species	Viral Species	Fungal Species
72	95	50

Other Pathogens	Resistance Genes	Virulence Genes
15	31	11

Data volume ≥100K Reads, TAT as fast as 10h, LoD can reach to 50 copies/mL

Localized Solution

MGISP-100
Automated sample preparation system

(16 samples/run)

Sample preparation~2.5h
Library construction~4h

DNBSEQ-G99/E25
High-throughput sequencer

Sequencing~3.5-4h

HALOS
All-in-one bioinformatic analyzer

Data analysis~0.5h

Portability + Modularity + Automation + Comprehensive Localized Tech-transfer Service

DNBSEQ-G99 | Multifunctional and rapid

- Contains double chips, data volume ≥ 80M Reads/Chip
- Sequencing time: 3.5h
- tNGS supports up to 96 samples (including quality control) / dual chips
- mNGS supports up to 8 samples (including quality control) / dual chips
- Compatible with tNGS and mNGS mixed sample detection

DNBSEQ-E25 | Portable and economical

- Contains single chip, data volume ≥ 20M Reads/Chip
- Sequencing time: 4h
- tNGS supports up to 16 samples (including quality control) / chip
- Occupying only 0.1m^2 of space

Product Advantages

High specificity
No background interference, positive enrichment, and species-specific sequences, greatly improving the target detection rate

High sensitivity
No background interference + positive enrichment

Wide coverage
Covering more than 95% of respiratory tract infection pathogens

No lab culture required
Direct extraction of nucleic acid, microbial culture not required

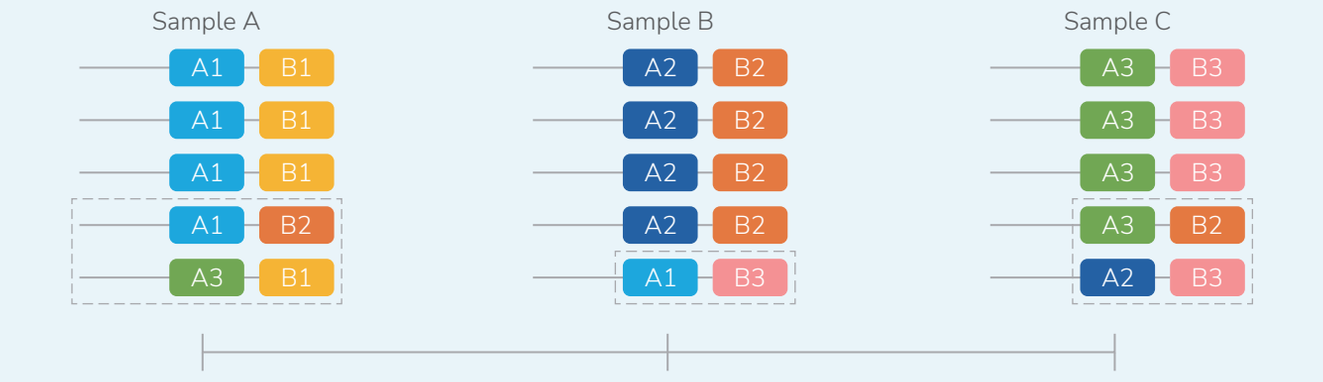
Fast and convenient
Simultaneous DNA and RNA pathogen detection for quick results

High cost effectiveness
Significantly lower cost and higher clinical applicability compared with mNGS (metagenomics next-generation sequencing)

Comprehensive Anti-pollution System

Intra-batch Contamination Risk Prevention and Control

The dual barcode technology is adopted, where the sample is marked with a unique label in each round of PCR marks, accurately identifying and correcting the bioinformatics process, and strictly controlling the risk of cross-contamination within a single batch.

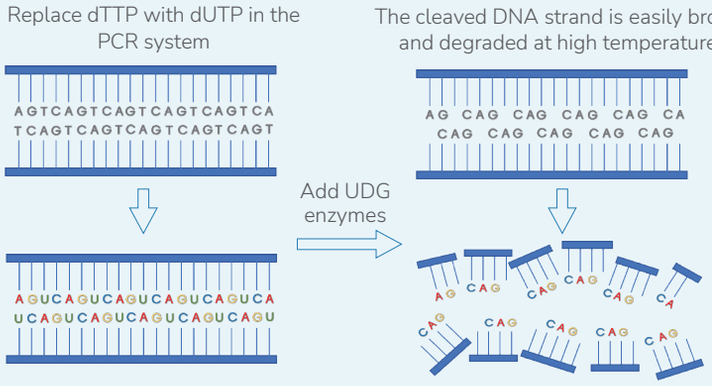


- Sample A is marked with the label pair A1 and B1
- Sample B is marked with the label pair A2 and B2
- Sample C is marked with the label pair A3 and B3
- If a sample's sequencing results show the label of another sample, it is considered contaminated

The bioinformatics process automatically identifies and filters contaminated sequences to reduce the false positive rate of detection results.

Batch-to-batch Contamination Risk Prevention and Control

The thermosensitive UDG enzyme anti-contamination technology is adopted to remove PCR residual products and prevent batch-to-batch contamination in the first place.



Residual PCR products from the previous batch:

Replace dTTP with dUTP in the PCR system to generate amplification products.

Before the next PCR is initiated:

UDG enzymes degrades the amplification products, avoiding the contamination of the previous batch of products with the current batch of samples.

Patented Primer Design System

Core Primer Design System for Efficient Amplification of Pathogens

Database

Based on the clinical-level microbial sequence database PTDB of BGI, the precise selection of pathogen-specific regions is ensured.

Primer Design Algorithm

An efficient primer design algorithm ensures that the primer sequence is highly common within a single pathogen species and highly specific to differentiate different pathogen species.

Multi-Target Primer Design

A multi-target primer design strategy is adopted to ensure efficient amplification of pathogen targets and avoid off-target detection, so that the positive rate and minimum detection limit can be greatly improved.

List of 274 Detectable Pathogen Targets

Bacteria (72 types)	Gram-positive bacteria (34 types)	Streptococcus pneumoniae, Streptococcus pyogenes, Streptococcus agalactiae, Streptococcus constellatus, Streptococcus dysgalactiae, Staphylococcus aureus, Mycobacterium tuberculosis complex, Mycobacterium avium complex (MAC), Mycobacterium kansasii, Mycobacteroides abscessus, Mycobacteroides chelonae, Mycolicibacterium fortuitum, Enterococcus faecalis, Enterococcus faecium, Corynebacterium diphtheriae, Corynebacterium striatum, Rhodococcus equi, Listeria monocytogenes, Erysipelothrix rhusiopathiae, Clostridium perfringens, Bacillus anthracis, Nocardia abscessus, Nocardia asteroides, Nocardia cyriacigeorgica, Nocardia farcinica, Nocardia brasiliensis, Nocardia nova, Nocardia otitidiscaviarum, Nocardia paucivorans, Nocardia pseudobrasiliensis, Nocardia veterana, Nocardia wallacei, Nocardia concava, Tropheryma whipplei
	Gram-negative bacteria (38 types)	Yersinia pestis, Pseudomonas aeruginosa, Haemophilus influenzae, Legionella pneumophila, Legionella bozemanae, Legionella_micdadei, Klebsiella pneumoniae, Klebsiella aerogenes, Klebsiella oxytoca, Acinetobacter baumannii, Escherichia coli, Enterobacter cloacae, Proteus mirabilis, Proteus vulgaris, Proteus penneri, Streptobacillus moniliformis, Bordetella pertussis, Bordetella parapertussis, Bordetella avium, Bordetella bronchiseptica, Bordetella holmesii, Burkholderia mallei, Burkholderia pseudomallei, Burkholderia cepacia, Stenotrophomonas maltophilia, Morganella morganii, Salmonella enterica, Pasteurella multocida, Neisseria meningitidis, Moraxella catarrhalis, Bacteroides fragilis, Serratia marcescens, Fluoribacter dumoffii, Brucella, Francisella tularensis, Citrobacter freundii, Elizabethkingia meningoseptica, Achromobacter xylosoxidans
Virus (95 types)	DNA virus (33 types)	Monkeypox virus, Human bocavirus 1, Human bocavirus 2, Human bocavirus 3, Human bocavirus 4, Human adenovirus , Human mastadenovirus A, Human mastadenovirus B, Human adenovirus B3, Human adenovirus 7, Human adenovirus 11, Human adenovirus 14, Human adenovirus 21, Human adenovirus 34, Human adenovirus 35, Human adenovirus 56, Human mastadenovirus C, Human adenovirus 1, Human adenovirus 2, Human adenovirus 5, Human adenovirus 6, Human mastadenovirus D, Human mastadenovirus E, Human adenovirus E4 , Human alphaherpesvirus 1 (Herpes simplex virus type 1), Human alphaherpesvirus 2, Human alphaherpesvirus 3 (Varicella-zoster virus) , Human betaherpesvirus 5 , Human betaherpesvirus 6A, Human betaherpesvirus 6B, Human gammaherpesvirus 4 (Epstein-Barr virus), BK polyomavirus, JC polyomavirus
	RNA virus (62 types)	Influenza A virus, Influenza A virus H1N1, Influenza A virus H3N2, Influenza A virus H5N1, Influenza A virus H5N6, Influenza A virus H7N9, Influenza B virus, Influenza C virus, Human orthopneumovirus, Human respiratory syncytial virus A, Human respiratory syncytial virus B, Human coronavirus OC43, Human coronavirus 229E, Human coronavirus HKU1, Human coronavirus NL63, 2019-nCoV (SARS-CoV-2), Middle East respiratory syndrome-related coronavirus, Mumps rubulavirus, Human respirovirus 1, Human rubulavirus 2, Human respirovirus 3, Human rubulavirus 4, Measles morbillivirus, Human metapneumovirus, Rhinovirus, Rhinovirus A, Rhinovirus B, Rhinovirus C, Enterovirus, Enterovirus A, Enterovirus A71, Enterovirus B, Enterovirus C, Enterovirus D, enterovirus D68, Coxsackievirus A2, Coxsackievirus A5, Coxsackievirus A6, Coxsackievirus A8, Coxsackievirus A9, Coxsackievirus A10, Coxsackievirus A12, Coxsackievirus A16, Coxsackievirus A19, Coxsackievirus B1, Coxsackievirus B2, Coxsackievirus B3, Coxsackievirus B4, Coxsackievirus B5, Coxsackievirus B6, Echovirus E4, Echovirus E11, Echovirus E17, Echovirus E18, Echovirus E19, Echovirus E20, Echovirus E24, Echovirus E25, Echovirus E33, Human poliovirus 1, Parechovirus A, Rubella virus
Fungi(50 types)		Candida albicans, Candida orthopsilosis, Candida parapsilosis, Candida glabrata, Candida tropicalis, Pichia kudriavzevii, Cryptococcus neoformans, Cryptococcus gattii, Cryptococcus deuterogattii, Cryptococcus bacillisporus, Cryptococcus tetragattii, Histoplasma capsulatum, Talaromyces marneffei, Aspergillus niger, Aspergillus fumigatus, Aspergillus flavus, Aspergillus lentulus, Aspergillus nidulans, Aspergillus oryzae, Aspergillus terreus, Lichtheimia corymbifera, Lichtheimia ramosa, Rhizopus oryzae (Rhizopus arrhizus), Rhizopus microsporus, Rhizomucor pusillus, Actinomucor elegans, Mucor circinelloides, Mucor indicus, Mucor irregularis, Mucor racemosus, Pneumocystis jirovecii, Coccidioides immitis, Coccidioides posadasii, Magnusiomyces capitatus, Trichosporon asahii, Scedosporium apiospermum, Clavispora lusitaniae, Blastomyces dermatitidis, Blastomyces gilchristii, Blastomyces parvus, Cunninghamella bertholletiae, Cunninghamella elegans, Apophysomyces elegans, Emergomyces orientalis, Emergomyces pasteurianus, Fusarium solani, Geotrichum candidum, Sporothrix brasiliensis, Sporothrix schenckii, Syncephalastrum racemosum
Other pathogens (15 types)		Mycoplasma pneumoniae, Chlamydia pneumoniae, Chlamydia psittaci, Chlamydia trachomatis, Bartonella bacilliformis, Bartonella henselae, Bartonella quintana, Rickettsia rickettsii, Rickettsia prowazekii, Rickettsia typhi, Orientia tsutsugamushi, Coxiella burnetii, Ureaplasma parvum, Ureaplasma urealyticum, Paragonimus westermani
Drug resistance genes (31 types)		*IMP, NDM, SPM, KPC, PER, VIM, SIM, DIM, OXA, ACT, GIM, CTX-M, GES, VEB, CMY, OKP, TLA, ACC, MOX, MIR, QnrA, QnrB, mecA, MCR, vanA, vanB, vanC, SHV, FOX, sul, 23S rRNA*
Virulence genes (11 types)		*rmpA, fyuA, fepA, iroN, iutA, cnf1, sat, eta, etb, tox, MPN372*

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