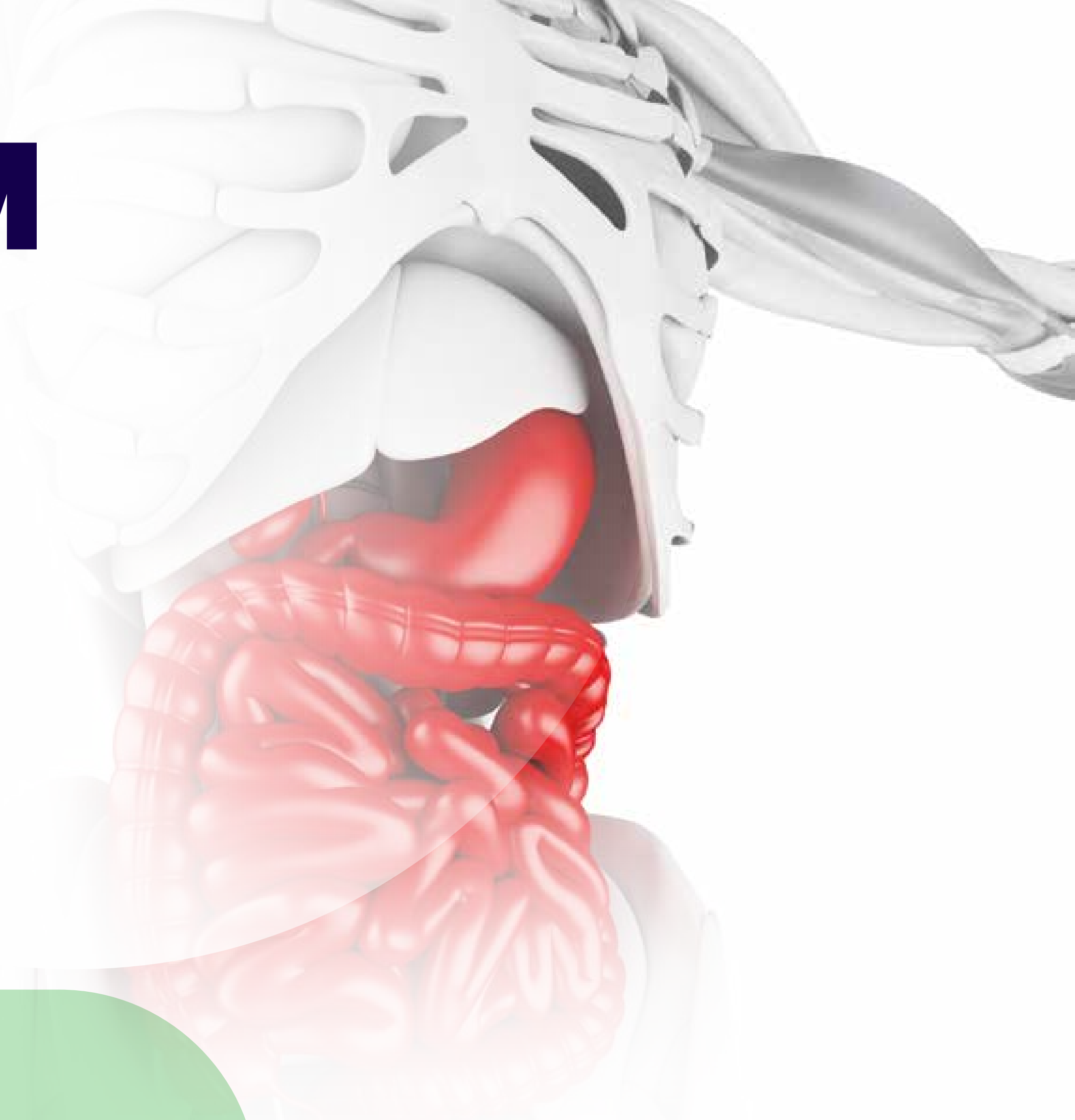
G2M

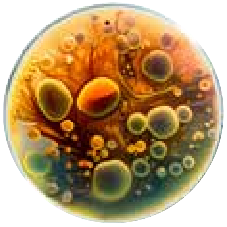


Covering more than

7000

Pathogens

PAN Pathogen Panel



Simplifies complexity and reconstructs **a new method for rapid detection of ultra-broad spectrum pathogens**

Pan Pathogen Panel

Genes2Me PAN Pathogen Panel uses hybridization based enrichment technology and second-generation high-throughput sequencing technology for high-precision detection of trace pathogenic microbial nucleic acids in samples, and can quickly identify viruses, bacteria, fungi, parasites and other pathogenic microorganisms, and also can detect multiple drug resistance genes, which can help the rapid identification and detection of pathogenic microorganisms.

Covers 7000+ Pathogenic Micro-organisms

Bacteria	Fungus	Parasite	Virus	Other Categories
Abiotrophia defectiva, Actinobacillus ureae, Actinomadura, Actinomyces israelii, Bacillus, Brevibacterium, Clostridioides difficile, Clostridium, Corynebacterium, Cutibacterium acnes, Enterococcus, Erysipelothrix, Gardnerella vaginalis, gemella, Gordonia, Granulicatella, Kocuria, Leuconostoc mesenteroides, Listeri monocytogenes, Micrococcus luteus, Mycobacteria	*Alternaria, Aspergillus, Blastomyces dermatitidis, Candida, Cladophialophora, Clavispora lusitaniae, Coccidioides, Cryptococcus, Exophiala dermatitidis, Fonsecaea, Fusarium, Histoplasma capsulatum, Lichtheimia corymbifera, Magnusiomyces capitatus, Malassezia furfur, Meyerozyma guilliermondii, Microsporum*	*Acanthamoeba, Angiostrongylus cantonensis, Anisakis, Ascaris lumbricoides, Babesia, Brugia malayi, Clonorchis sinensis, Cryptosporidium, Cyclospora cayetanensis, Echinococcus, Encephalitozoon, Entamoeba histolytica*	*Adenovirus, Anelloviridae, Herpesviridae,Parvovirus, Polyomavirus,Poxviridae,TTV, Alphavirus, Astrovirus, Bunyavirales, Coronavirus,Deltaretrovirus, Flavivirus, Influenza, Lyssavirus, Norovirus, Orthoreovirus, Paramyxoviridae, Picornavirus, Pneumoviridae, Rotavirus, Sapovirus*	*Borrelia, Leptospira, Treponema pallidum, Anaplasma phagocytophilum*

Key Features

Ultra-Broad Spectrum

One test covers more than 95% of common clinical pathogen infections

High detection rate of fungi and intracellular bacteria

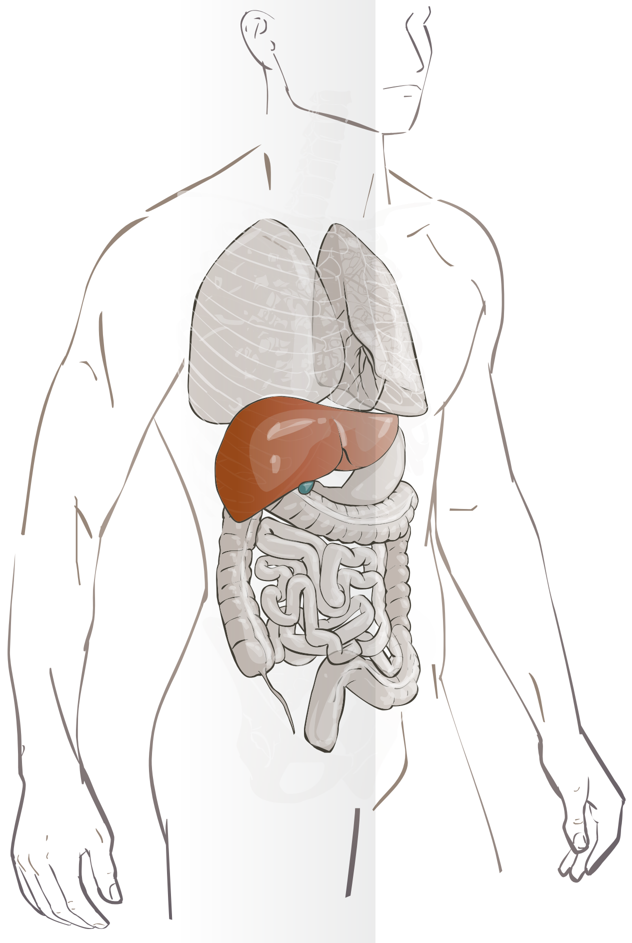
Significantly improved the detection rate of fungi and intracellular bacteria

High Sensitivity

High-throughput targeted sequencing, no host DNA interference, trace pathogens can be accurately detected

Fast Detection

Rapid test for rapid identification of critical infection



Workflow

01 Extraction of nucleic acids

02 Library construction

03 Quality testing

04 High-throughput sequencing

05 Reporting

Detection of Drug Resistant Genes

The analysis of a range of drug resistance genes for Anti-microbial drug resistance is done using databases like CARD as reference database. It spans over 4,000 genes linked to drug resistance. For categorisation, we use the SARG database as reference which categorizes resistance genes into four levels: Level I, includes mobile resistance genes and families associated with humans, carried by ESKAPE pathogens (*Enterococcus faecium*, *Staphylococcus aureus*, *Klebsiella pneumoniae*, *Acinetobacter baumannii*, *Pseudomonas aeruginosa*, and *Enterobacter spp*); Level II comprises mobile resistance genes and families linked to humans but not carried by ESKAPE pathogens; Level III encompasses resistance genes and families associated with humans but not carried by ESKAPE pathogens. Additionally, the MGEs database lists non-mobile resistance genes and families. Level IV identifies resistance genes or families that are prevalent in the human environment and connected to human health.

Clinical Applications

- Central nervous system infections
- Cardiogenic infections
- Reproductive system infections
- Skin infections
- Respiratory infections
- Urinary tract infection
- Bloodstream infection
- Other infections

Specifications

Number of Organism:- 7000 +	**Target Size**: ~8000 probes	**Target Regions**:- 16S and internal transcribed spacer (ITS)	**Sample Type**:- Blood, Sputum, Saliva, Stool, Swab, Fresh tissue, Body fluid	**Genes**:- Housekeeping genes, drug-resistant related genes	**Data Required**: 1 Million reads
Bacteria - ~88	Fungus - ~ 31	Parasites - ~ 27	Viruses - ~ 22	Obligate Intracellular Parasite - ~8	Spirochete - ~ 3

** Minimum data output from sequencing depends on the content of pathogenic microorganism in clinical specimen. Whether a particular pathogen is detected in the report depends on the number of supporting reads detected for the pathogen, and not solely on the total amount of data obtained from sequencing.

Scan for Pathogen List

ORDERING INFORMATION

Commercial Name	Cat No.
LeoNext PP LibraryPrep Kit for PAN Pathogen	NGS3104-01; NGS3104-02

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