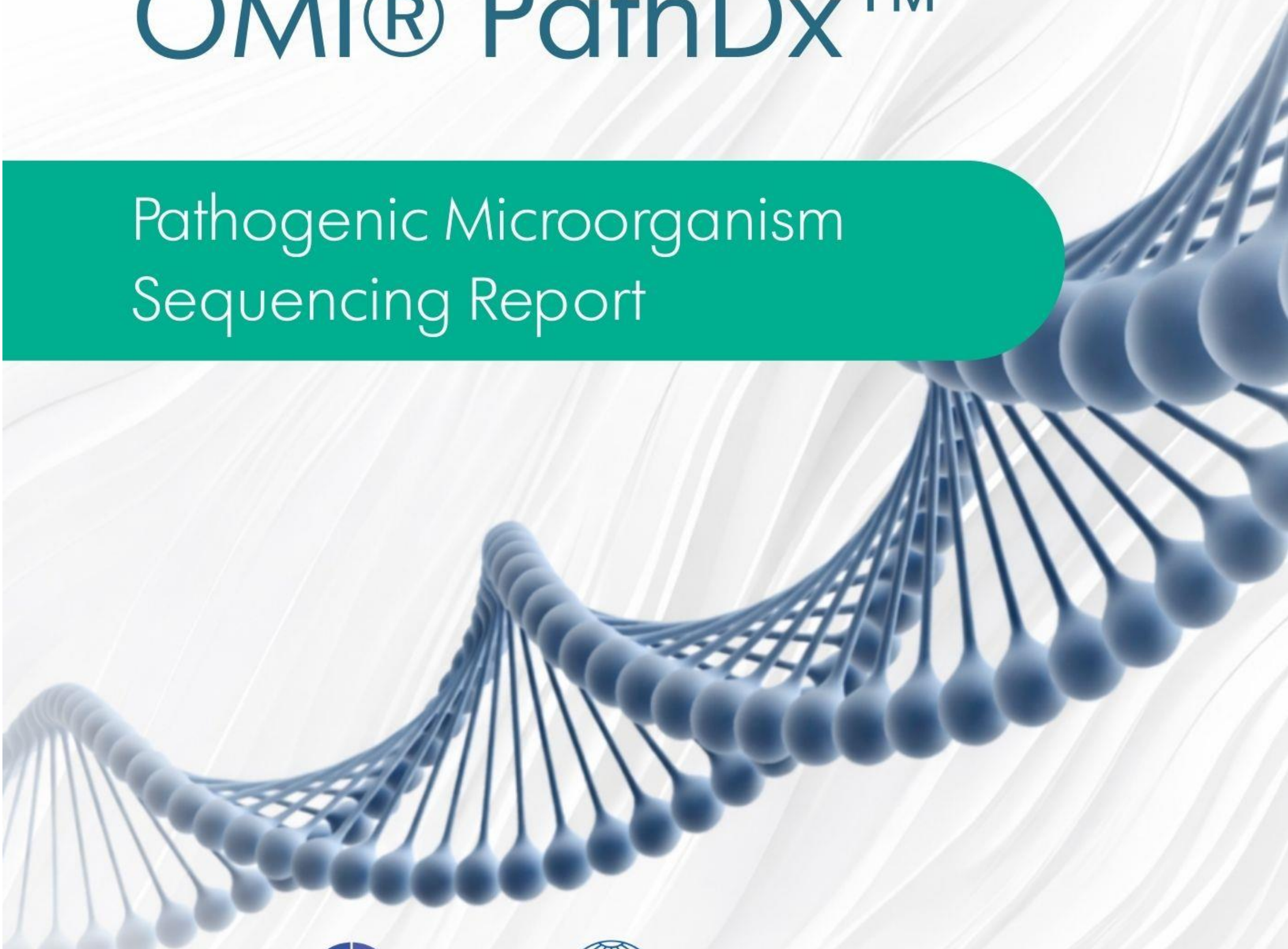
OMI® PathDx™

Pathogenic Microorganism Sequencing Report



This test is performed in contractor laboratories accredited to internationally recognized quality standards, including CAP, CLIA, and ISO 15189, depending on laboratory location.

OMI ® PathDx™ Pathogenic Microorganism Sequencing Report

1. Basic Information

Patient Information			
Name:	________________	Gender:	________________
Age:	________________	Admission No.:	________________
Bed No.:	________________	Original Sample ID:	________________

Clinical Information	
Clinical Symptoms:	________________
Clinical Diagnosis:	________________
Suggestive Pathogenic Agents:	________________
Anti-infection Agents History:	________________

Sample Information			
Hospital/Clinic:	________-__________	Department:	_______-__________
Clinician:	_______-___________	Sampling Date:	08/19/2021
Received Date:	08/20/2021	Reported Date:	05/23/2023 09:35
Sample ID:	19S0489210	Sample Type:	Bronchoalveolar lavage fluid (BALF)
Sample Status:	Qualified	Lab workflow:	DR
Test Item:	Nucleic acid detection for respiratory pathogenic microorganism		

2. Sample sequencing data and theoretical sensitivity of pathogens

Total Reads	Human (6GB) Cell Content (cells/mL)	Bacteria (4MB) theoretical sensitivity (copies/mL)	Fungi (100MB) theoretical sensitivity (copies/mL)	Virus (10KB) theoretical sensitivity (copies/mL)	Parasites (1GB) theoretical sensitivity (copies/mL)	Internal Control (YES/NO)
101,593,291	1.8E+04	1.0E+00	1.0E+00	1.1E+02	1.0E+00	DNA: YES RNA: YES

Notes:

Total reads: The total number of reads sequenced.

Human cells content (cells/mL): The theoretical numbers of human cells detected through quantitative of human genomic DNA.

Theoretical sensitivity: The number of microorganisms in the unit volume is required when one sequence of pathogenic microorganisms was detected and interpreted as positive.

* The number of pathogenic microorganisms = (human cell content x human genome size) / (total reads x mi- crobial genome size).

* The human genome (diploid) size was about 6GB, assumed about 4 MB for the bacteria genome, about 100MB for fungi genome, 10KB for the virus genome, and 1 GB for the parasite genome, respectively. Note: The pathogen genome was determined using the common pathogen size of the Pathogen Microbial Public Database rather than

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actual size.

Detection sensitivity: The detection sensitivity was correlated positively with the total reads and negatively corre- lated with the human cells content per volume of specimen. Due to sequence homology among species, the actual sensitivity is slightly lower than theoretical sensitivity.

Internal control: The sequence of internal control added to testing sample.

3. Sequencing Results

3.1. List of Detected Bacteria

Type	Genus		Species		Relative abundance
	Name	SMRN	Name	SMRN	
Undetected					

3.2. List of Detected Fungi

Genus		Species		Relative abundance
Name	SMRN	Name	SMRN	
Candida	17	*Candida albicans*	10	42.52%

3.3. List of Detected DNA Viruses

Type	Genus		Species		Relative abundance
	Name	SMRN	Name	SMRN	
Undetected					

3.4. List of Detected RNA Viruses

Type	Genus		Species		Relative abundance
	Name	SMRN	Name	SMRN	
Undetected					

3.5. List of Detected Parasites

Genus		Species		Relative abundance
Name	SMRN	Name	SMRN	
Undetected				

3.6. List of Detected Mycobacterium tuberculosis complex

Species Complex		Species		Relative abundance
Name	SMRN	Name	SMRN	
Undetected				

3.7. List of Detected Mycoplasma/Chlamydia/Rickettsia

Genus		Species		Relative abundance
Name	SMRN	Name	SMRN	
Undetected				

3.8. List of Suspected Background Microorganisms

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Type	Genus		Species		Relative abundance
	Name	SMRN	Name	SMRN	
Undetected					

Notes:

1) **Type:** Refers to the type of pathogenic microorganism detected including bacteria, viruses, fungi and parasites. The type of bacteria includes G+ (gram-positive bacteria), G- (gram-negative bacteria) and Gram-variable (gram-variable bacteria). The type of viruses includes single-stranded DNA virus (ssDNA), double-stranded DNA virus (dsDNA), single-stranded RNA virus (ssRNA), double-stranded RNA virus (dsRNA) and so on.
2) **-:** Unknown.
3) **SMRN:** Stringently mapped reads number of a specific microorganism at the taxonomic rank listed in the test result.
4) **Relative abundance:** Refers to the percentage of microorganisms at the lowest level detected in same type of microorganisms (bacteria/ fungi/ viruses/ parasites).
5) **Suspected background microorganism:** Refers to the normal commensal/colonizing microorganism present in the human body, or the microorganism by contamination, the possibility of infection is not ruled out.

4. Results Interpretation

The pathogenic microorganisms detected in the delivered sample was listed by bacteria, viruses, fungi, parasites, mycobacterium tuberculosis complex, mycoplasma/chlamydia/rickettsia and suspected background microorganisms in order of the number of unique reads from high to low. The interpretation of testing results in clinical practice should be made by the clinician integrating the patients' clinical situation and other examination results.

The following was brief information of the detected microorganisms (excluding suspected background microorganisms) listed in the tables. (If no microorganism was listed in above table, the following will be empty):

References

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5. Detection Technology

5.1. Methods

PMseq^{TM} Pathogenic Microorganism High-Throughput Sequencing is based on metagenomics technology. The nucleic acids of all microorganisms in the testing samples are extracted and se- quenced unbiasedly on BGI's high-throughput sequencing platform. The generated data was ana- lyzed using dedicated bioinformatic pipelines with curated high-quality and high-standard pathogen database PMDB to detect the pathogens in testing specimens. The curated database PMDB includes about 17,500 pathogens composed of bacteria, fungi, viruses, and parasites. The technology signifi- cantly improves the positive rate of pathogen intending to provide information for clinical diagnosis, infection control and management and precise treatment of infections.

5.2. Assay Procedures

The detection process includes sample collection, sample reception, nucleic acid extraction, DNA enzyme hydrolysis + bead-milling / RNA enrichment, library construction, high-

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