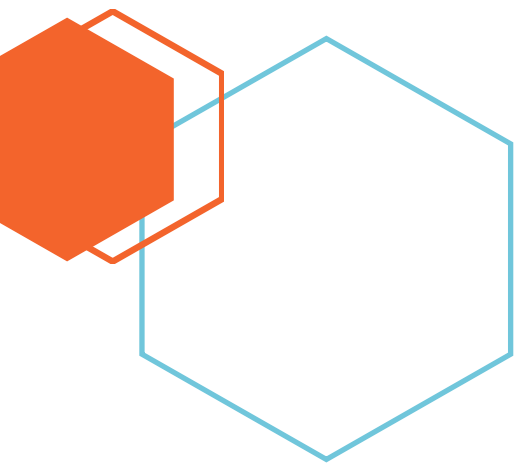


metagenomic Next Generation Sequencing Report



Basic Information

Name:	ww	Gender:	F	Age:	1
Sampling Day:	2024-10-04	Test Day:	2024-10-05	Tel:	13234345678
Requesting physician:	respiratory tract infections	Sample Type:	zs	Sample Status:	PUS
Requesting apartment:	Yellow	Requesting hospital:	Department of respiration		
Clinical information (medical history, chief complaint, symptoms, diagnosis, medication, etc.)					
Symptoms: Xi'an No.1 hospital					
Concerning pathogens: Xi'an					
Pretreatment: Decreased appetite, headache					
Test items					
Nucleic acid （DNA+RNA）					

Summary of Test Results

Bacteria: Streptococcus pneumoniae 175 reads
Eukaryota: Candida albicans 164 reads; Toxoplasma gondii 11 reads
Viruses: Human mastadenovirus C 2 reads

List of Detected Results

> list of detected bacteria

Species	Types	Reads	Coverage
肺炎链球菌 <i>Streptococcus pneumoniae</i>	G+	175	97.70%

> list of detected Mycobacterium complex species

Species	Types	Reads	Coverage
Undetected			

> list of detected fungi

Species	Types	Reads	Coverage
白色念珠菌 <i>Candida albicans</i>	fun	164	

> list of detected viruses

Species	Types	Reads	Coverage
人类哺乳动物腺病毒 <i>Human mastadenovirus C</i>	vir	2	

> list of detected parasites

Species	Types	Reads	Coverage
弓形虫 <i>Toxoplasma gondii</i>	par	11	

> Suspected microbiome list

Species	Types	Reads
齿垢密螺旋体 <i>Treponema denticola</i>	G-	65
曲形弯曲菌 <i>Campylobacter curvus</i>	G-	11
牙龈卟啉单胞菌 <i>Porphyromonas gingivalis</i>	G-	16,296
具核梭杆菌 <i>Fusobacterium nucleatum</i>	G-	173
坏死梭杆菌 <i>Fusobacterium necrophorum</i>	G-	19
咽峡炎链球菌 <i>Streptococcus anginosus</i>	G+	103
福赛斯坦纳菌 <i>Tannerella forsythia</i>	G-	40,373
中间普雷沃菌 <i>Prevotella intermedia</i>	G-	43
产黑素普雷沃菌 <i>Prevotella melaninogenica</i>	G-	36
微小微单胞菌 <i>Parvimonas micra</i>	G+	63
纹带棒状杆菌 <i>Corynebacterium striatum</i>	G+	20
<i>Treponema vincentii</i>		29

* The pathogens in this list are microbial communities from the human skin, respiratory tract, intestines, reproductive tract, and the environment. The determination of colonization, contamination, or infection should be considered in conjunction with clinical symptoms and other relevant diagnostic methods.

Definition of terms:

- ❖ **Number of Reads:** The number of reads matching the pathogen. This number is related to the pathogen load in the sample, the amount of nucleic acid extracted, and the proportion of human reads. A higher number of reads indicates higher confidence in detecting the pathogen in the sample.
- ❖ **Relative Abundance:** The proportion of this microorganism among all detected microorganisms of the same type in the sample. The higher the abundance, the greater the proportion of this microorganism relative to other microorganisms of the same type.
- ❖ **Coverage:** The ratio of the detected nucleic acid sequences of this microorganism to the entire genomic sequence of the microorganism. Higher coverage indicates a higher proportion of the microorganism’s genome being detected.

Sequencing Quality

Quality Control Parameters		Sample Data
Experimental Quality Control	Internal Control	Qualified
	Nucleic Acid Extraction Concentration (ng/μL)	NA
	Library Concentration	NA
	Negative Control	Qualified
	Host Removal Status	No
Data Quality Control	Total Number of Sequences	16. 034314 M
	Non-Human Sequences	5123008
	Q30	94. 19%

Tester:	Reviewer:	Report Date:	2023/06/15
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Statement: This report is only responsible for the submitted sample. The results are for the doctor’ s reference only. Microorganisms below the detection limit cannot be guaranteed to be detected.