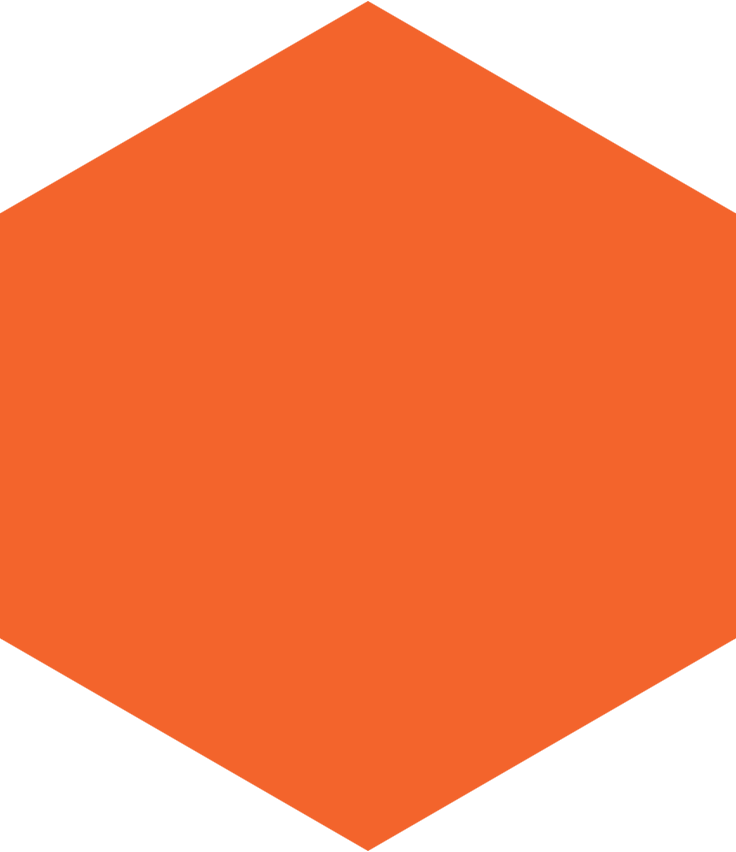


|  |
| --- |
| **metagenomic Next Generation Sequencing Report** |
| 六边形 1 |



**Basic Information**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Name: | xingming | Gender: | xingbie | Age: | nianling |
| Sampling Day: | CYRQ | Test Day: | jieyangriqi | Tel: | dianhua |
| Requesting physician: | songjianyisheng | Sample Type: | BBLX | Sample Status: | yangbenzhuangtai |
| Requesting apartment: | songjiankeshi | Requesting hospital: | songjianyiyuan | | |
| Clinical information (medical history, chief complaint, symptoms, diagnosis, medication, etc.) | | | | | |
| Symptoms: zhusu  Concerning pathogens: bingyuanleixing  Pretreatment: kangganran | | | | | |
| Test items | | | | | |
| Nucleic acid（DNA+RNA） | | | | | |

**Summary of Test Results**

|  |
| --- |
| **Bacteria:** No suspected pathogens are detected. Common commensal bacteria found in humans (see the suspected microbiome list for details). |
| **Fungi:** No suspected pathogens are detected. common commensal fungi found in humans (see the suspected microbiome list for details). |
| **Viruses:** No viruses are detected. |
| **Parasites:** No parasites are detected. |
|  |

**List of Detected Results**

**> list of detected bacteria**

| Species | Types | Reads | Coverage |
| --- | --- | --- | --- |
| Undetected | | | |

**> list of detected Mycobacterium complex species**

| Species | Types | Reads | Coverage |
| --- | --- | --- | --- |
| Undetected | | | |

**> list of detected fungi**

| Species | Types | Reads | Coverage |
| --- | --- | --- | --- |
| Undetected | | | |

**> list of detected viruses**

| Species | Types | Reads | Coverage |
| --- | --- | --- | --- |
| Undetected | | | |

**> list of detected parasites**

| Species | Types | Reads | Coverage |
| --- | --- | --- | --- |
| Undetected | | | |

**> Suspected microbiome list**

\* 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) | HSND |
| Library Concentration | WKND |
| Negative Control | Qualified |
| Host Removal Status | No |
| Data Quality Control | Total Number of Sequences | ZXLS |
| Non-Human Sequences | FRYXL |
| Q30 | QSLB |

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Tester: |  | Reviewer: |  | Report Date: | 2023/06/15 |

**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.