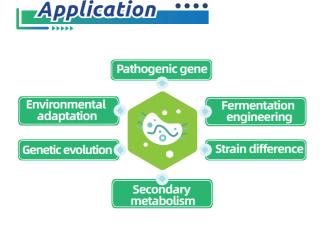


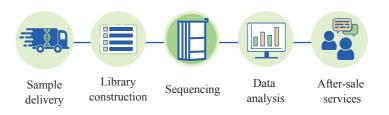
# **Fungal Genome Sequencing**

#### Product Introduction

Biomarker Technologies provides whole genome, genome survey, draft genome and fine genome sequencing of fungi depending on specific research goal. Genome sequencing, assembly and functional annotation can be achieved by combining Next-generation sequencing + Third-generation sequencing to achieve high-level genome assembly.









#### Genome sequencing:

1 Fungal whole genome sequencing-Illumina

#### Genome assembly:

- 2 Fungal whole genome sequencing-Illumina
- **3** Draft fungal genome-Illumina
- **4** Hi-C based fungal genome
- **5** Fungal fine genome-Nanopore
- **6** Fungal fine genome-PacBio

#### 

### Service,Advantages....

- Multiple sequencing strategies are available for different fungal genome research goals.
- In pathogenicity, resistance, environmental adaptability, metabolic pathways and other multi-angle to dig deeper into functional genes.
- Provide a variety of fungal genome analyses, interpret the detai -led information of fungi, and have a comprehensive understanding of genomic information.
- Highly experienced in fungi genome assembly with over 10,000 microbial genomes assembled.
- Professional after-sale technical support team fulfilling more s -pecific research needs.

Service Specifications ....

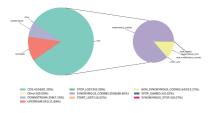
| Library  | Sequencing | Recommended data                  | Turnaround Time |
|----------|------------|-----------------------------------|-----------------|
| Illumina | PE150      | GS≤60M;100X NGS (Survey: 50X NGS) | 30              |
| PacBio   | ZMW        | GS≤60M; 30X HIFI+50X NGS          | 33              |
| Nanopore | ONT        | GS≤60M; 100X ONT +50X NGS         | 33              |

## Sample Requirements

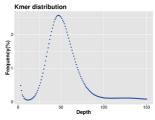
| Platform | Qubit Conc. (ng/µL) | Amount (µg)      | Volume (µL) | Purity   |  |
|----------|---------------------|------------------|-------------|--|--|
| Illumina | 1                   | 0.06             | 20          | OD260/280: 1.7-2.2;<br>OD260/230: ≥1.6;<br>Nanodrop/Qubit: 0.8-2.5 |  |
| PacBio   | 20                  | 1 μg/1 G<br>≥2.0 | 20          |  |  |
| Nanopore | 40                  | 2                | 20          |  |  |



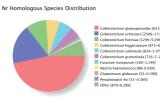
1.Fungal whole genome sequencing -SNP annotation result statistics



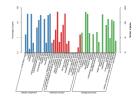
2.Fungal genome survey -K-mer depth distribution



3.Draft fungal genome -Nr database annotation



4.Fungal fine genome -GO database annotation



## Featured Publications

| Year | Journal          | Paper  | Article              | DOI                        |
|------|------------------|--|----------------------|----------------------------|
| 2023 | Scientific Data  | Gapless genome assembly of Fusarium verticillioides, a filamentous fungus threatening plant and human health | Genome evolution     | 10.1038/s41597-023-02145-8 |
| 2023 | Journal of Fungi | Genetic and Molecular Evidence of a Tetrapolar Mating System<br>in the Edible Mushroom Grifola frondosa      | Genetics and hybrid  | 10.3390/jof9100959         |
| 2022 | Plant disease    | Genome Resources for Four Clarireedia Species Causing Dollar<br>Spot on Diverse Turfgrasses                  | Disease<br>treatment | 10.1094/PDIS-08-22-1921-A  |

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