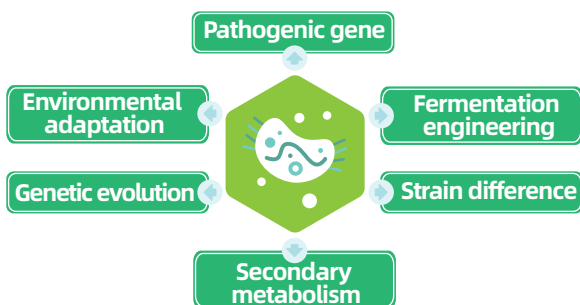


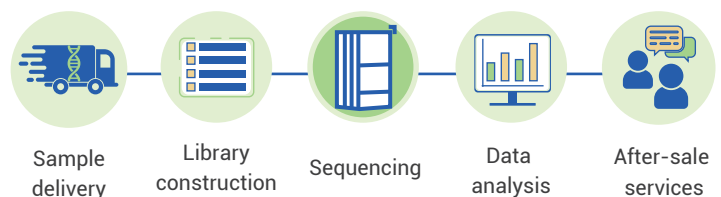
Fungal Genome Sequencing

In order to study the structure, function, and evolution of fungal genomes, BMKGENE provides whole genome resequencing, genome survey, draft genome, and fine genome sequencing and assembly services. To achieve more accurate genome assembly and functional annotation, next-generation sequencing data is combined with third-generation sequencing data for analysis, to help gain a deep insight into fungal biology.

Application



Service Workflow



Fungal Genome Solutions

Option 1 Genome re-sequencing:

- Fungal whole genome sequencing (WGS): SNP calling

Option 2 Genome assembly:

- Fungal Genome Survey (NGS): Genome estimation.
- Fungal Draft Genome (NGS): Genome component analysis and function annotation.
- Fungal Fine Genome (TGS+NGS): Genome component analysis and function annotation.

Service Advantages

- Unlock the power of fungal genomes with our diverse sequencing strategies.
- Delve into the depths of functional genes: uncover pathogenicity, resistance, adaptability, and more.
- Gain comprehensive insights into fungal genomes: explore detailed information and unravel their mysteries.
- Extensive experience: over 12,000 microbial genomes assembled with precision in fungal genome assembly.
- Professional after-sale technical support team fulfilling more specific research needs.

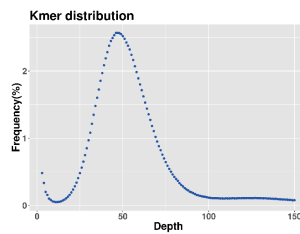
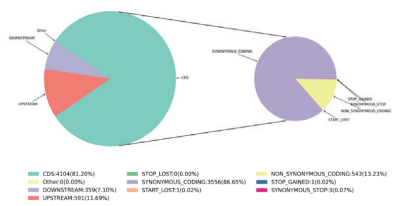
Service Specifications

Library	Read Length	Recommended Data
Illumina	PE150	100X NGS (Survey: 50X NGS)
PacBio	HiFi-10 Kb	30X HiFi + 50X NGS
Nanopore	20 Kb	100X ONT + 50X NGS

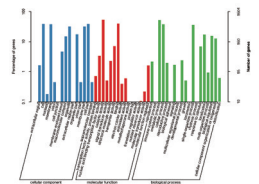
Sample Requirements

Platform	Conc. (ng/μL)	Amount (μg)	Volume (μL)
Illumina	1	0.06	20
PacBio	20	2	20
Nanopore	40	2	20

Demo Results



Nr Homologous Species Distribution



1. SNP classification and annotation

2. K-mer depth distribution

3. Coding gene annotation

4. GO database annotation

Featured Publications

Year	Journal	Article	Applications	DOI
2024	Nature	Inducing novel endosymbioses by implanting bacteria in fungi	Endosymbioses	10.1038/s41586-024-08010-x
2024	Advanced Science	Adaptation of fusarium head blight pathogens to changes in agricultural practices and human migration	Pathogen evolution	10.1002/adv.202401899
2024	Journal of Fungi	Integrated genome sequencing and transcriptome analysis identifies candidate pathogenicity genes from Ustilago crameri	Crop disease	10.3390/jof10010082



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Global Locations

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