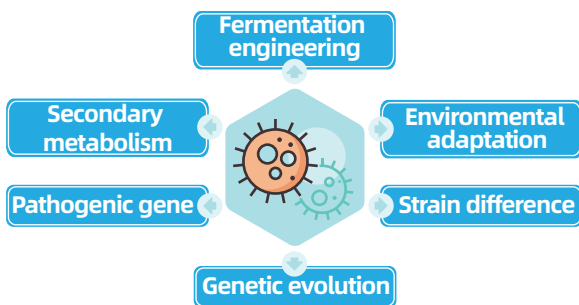


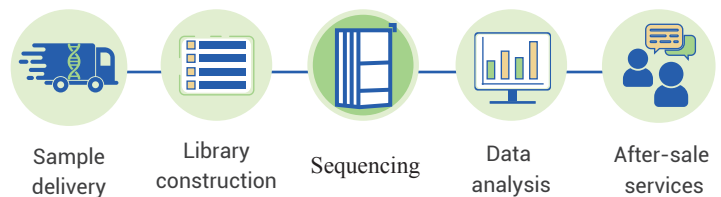
Bacterial Genome Sequencing

Tailored to meet various research goals, BMKGENE offers genome sequencing and assembly services for bacteria, including whole genome, draft genome, and complete genome. By combining next-generation sequencing with third-generation sequencing data, to achieve high-quality genome assembly and accurate functional annotation. For complete bacterial genome assembly, BMKGENE guarantees 0 gap, providing researchers with a comprehensive understanding of their target bacteria.

Application



Service Workflow



Bacterial Genome Solutions

Option 1 Genome re-sequencing:

- Bacterial whole genome sequencing(WGS): SNP calling.

Option 2 Genome assembly:

- Bacterial Draft Genome (NGS): Genome component analysis and function annotation.
- Bacterial Complete Genome (TGS+NGS): Genome component analysis, function annotation, and circos of genome.

Service Advantages

- Multiple sequencing strategies are available for different bacterial genome research goals.
- The species identification and classification of bacteria are conducted to study their evolutionary relationships and more.
- Bacteria complete genome sequencing by PacBio or ONT platform with 0 Gap guaranteed.
- Highly experienced in bacterial genome assembly with over 20,000 microbial genomes assembled.
- Professional after-sale technical support team fulfilling more specific research needs.

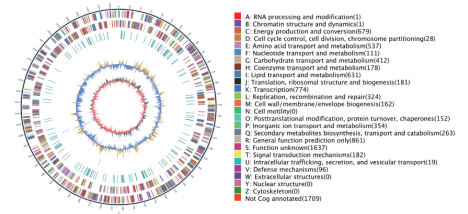
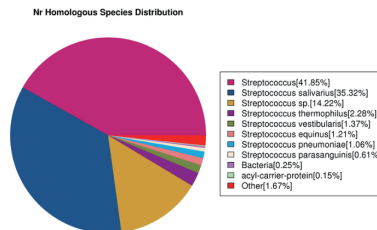
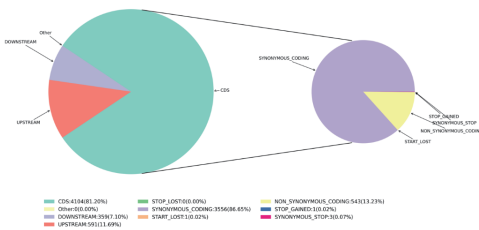
Service Specifications

Library	Read Length	Recommended Strategy	Assembly
Illumina	PE150	100X NGS	Draft map
PacBio	HiFi-10 Kb	30X HiFi	Complete map 0-Gap
Nanopore	20 Kb	100X ONT + 100X NGS	Complete map 0-Gap

Sample Requirements

Platform	Conc. (ng/μL)	Amount (μg)	Volume (μL)
Illumina	1	0.06	20
PacBio	20	1.2	20
Nanopore	40	2	20

Demo Results



1. SNP classification and annotation

2. Coding gene annotation

3. Genome visualization

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	Nature Microbiology	Non-canonical start codons confer context-dependent advantages in carbohydrate utilization for commensal E. coli in the murine gut	Metabolic competition	10.1038/s41564-024-01775-x
2024	Journal of Infection	Pandrug-resistant Klebsiella pneumoniae isolated from Ukrainian war victims are hypervirulent	Pathogenic bacteria	10.1016/j.jinf.2024.106312



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