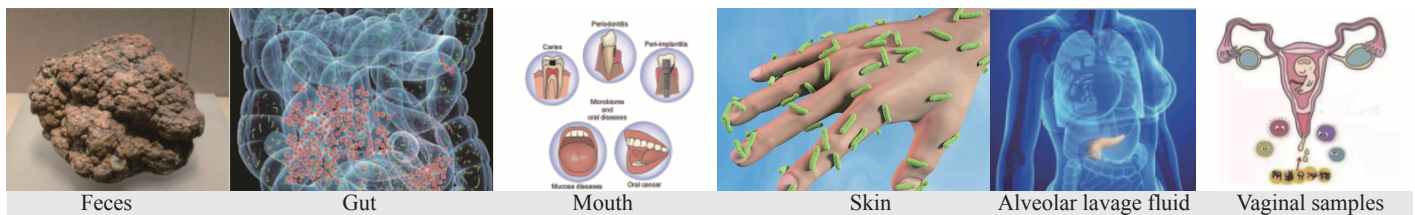


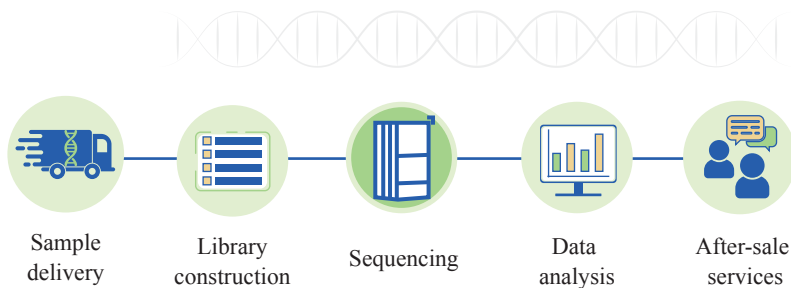
# Metagenomics Sequencing

Dive into the hidden world of genetic diversity with cutting-edge metagenomic sequencing technology. Analyze complex environmental samples to uncover species diversity, population structure, functional genes, and more. With 700+ global research collaborations, BMKGENE has processed over 100,000 samples from soil, water, air, and beyond. Our expertise extends to feces, biofilm, insects, and other fascinating realms. Witness BMKGENE's impact through 500+ published articles.

## Application



## Service Workflow



## Bioinformatics

- ▶ Metagenome assembly;
- ▶ Function annotation: Nr, GO, KEGG, eggNOG, Pfam, SwissProt, CAZy, CARD, VFDB, PHI-base, CYPED, QS, BacMet;
- ▶ **Diversity analysis -function level and species level:**
  1. Components and relative abundance;
  2. Alpha and Beta diversity analysis;
  3. Intergroup differential analysis;
  4. Correlation and association analysis.

## Service Advantages

- High-quality assembly-Enhancing accuracy of species identification and functional gene prediction.
- More powerful and reliable application in diverse areas, e.g. detection of pathogenic microorganisms or antibiotic resistance-related genes.
- Multi-platforms to meet the needs of scientific research: Illumina NovaSeq X; DNBSEQ-T7; Nanopore PromethION 48.
- Bacterial genome isolation; Comparative metagenome analysis.
- Decades of metagenomics expertise, diverse sample coverage, and an exceptional analysis team.

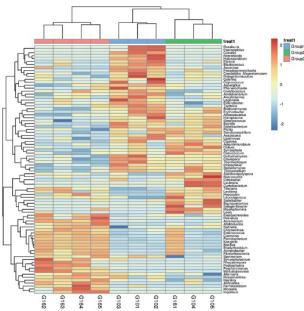
## Service Specifications

Platform	Read Length	Recommended Data
Illumina/DNBSEQ	PE150	6 G/10 G/20 G
Nanopore	8 kb	6 G/10 G

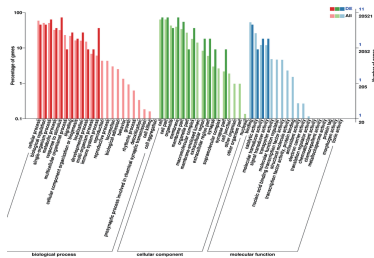
## Sample Requirements

Platform	Qubit Conc. (ng/μL)	Amount (μg)	Volume (μL)	OD260/280
Illumina/DNBSEQ	1	0.03	20	1.6-2.5
Nanopore	40	2	20	1.7-2.2

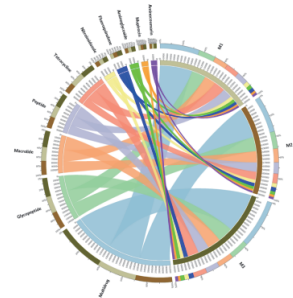
## Demo Results



1. Heatmap: Species abundance clustering



2. Functional genes annotated to GO database



3. Circos of CARD antibiotic resistance genes

## Featured Publications

Year	Journal	Article	Applications	DOI
2023	The Innovation	Obese Ningxiang pig-derived microbiota rewires carnitine metabolism to promote muscle fatty acid deposition in lean DLY pigs	Gut microbiota	10.1016/j.xinn.2023.100486
2023	Nature Microbiology	A high-quality genome compendium of the human gut microbiome of Inner Mongolians	Human gut microbiota	10.1038/s41564-022-01270-1
2023	Journal of Cleaner Production	Low-level cadmium alleviates the disturbance of doxycycline on nitrogen removal and N2O emissions in ditch wetlands by altering microbial community and enzymatic activity	Environmental pollution control	10.1016/j.jclepro.2022.135807



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