

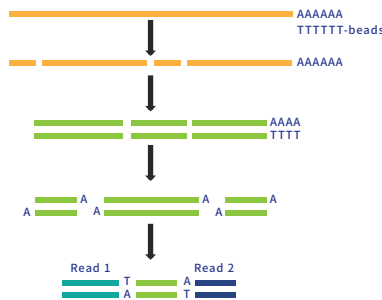
# Eukaryotic mRNA Sequencing (NGS)

Unlock the secrets of eukaryotic mRNA with the next-generation sequencing (NGS) technology. Gain invaluable insights into gene transcription and expression levels under specific space-time. This information is crucial for advancing gene functionality research, understanding cellular signaling, and development, and improving disease diagnosis and treatment. With BMKGENE's extensive expertise in eukaryotic mRNA sequencing, we have successfully processed over 500,000 diverse samples, completing over 80,000 mRNA-seq projects.

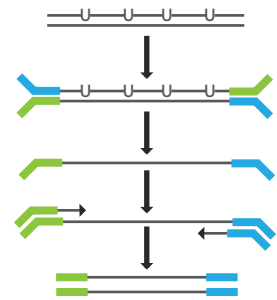
## Technical Features



### Non-stranded library construction



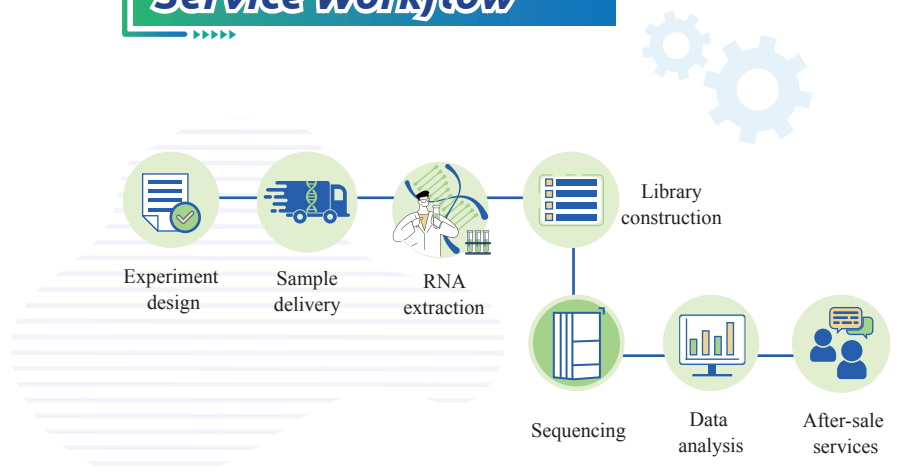
### Stranded library construction



## Bioinformatics

- ▶ Gene structure analysis;
- ▶ Gene expression quantification;
- ▶ Differential expression analysis;
- ▶ Function annotation and enrichment on DEGs;
- ▶ Novel gene identification and function annotation;
- ▶ DEG protein-protein interaction.

## Service Workflow



## Service Advantages

- Reveal differences and regulation of gene expression, and study the mechanisms of gene regulation and cell fate determination.
- Discover new genes and transcripts, which helps to reveal the integrity and complexity of the genome.
- Strict quality control system:** Core quality control points through all steps including sample preparation, library construction, sequencing and bioinformatics are under close monitoring in order to deliver high-quality results.
- Multiple databases available for function annotation and enrichment studies to fulfill diverse research goals.
- After-sale services:** After-sale services are valid for 3 months upon project completion, including project follow-up, trouble-shooting, results Q&A, etc.

## Service Specifications

Library	Platform	Recommended Data	Data Quality
PolyA enriched	Illumina/DNBSEQ	6 /10 /15 Gb	Q30 ≥ 85%

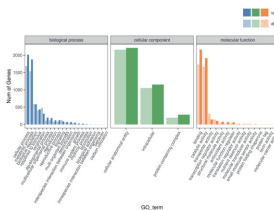
## Sample Requirements

Amount	Purity	Integrity
Conc. ≥ 20 ng/μL; Volume ≥ 10 μL; Total ≥ 0.5 μg	OD260/280=1.7-2.5 OD260/230=0.5-2.5 Limited or no protein or DNA contamination shown on gel.	For plants: RIN ≥ 6.0; For animals: RIN ≥ 6.5; 5.0 ≥ 28S/18S ≥ 1.0; limited or no baseline elevation

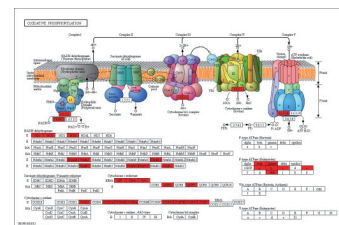
## Demo Results



1. Differential expression analysis-Volcano plot



2. GO classification on DEGs



3. KEGG annotation on DEGs

## Featured Publications

Year	Journal	Article	Applications	DOI
2023	Cell Host & Microbe	Aspergillus fumigatus hijacks human p11 to redirect fungal-containing phagosomes to non-degradative pathway	Disease prevention	10.1016/j.chom.2023.02.002
2023	Water Research	Triclosan and triclocarban weaken the olfactory capacity of goldfish by constraining odorant recognition, disrupting olfactory signal transduction, and disturbing olfactory information processing	Environmental adaptation	10.1016/j.watres.2023.119736
2023	nanotoday	A cascade nanoreactor for enhancing sonodynamic therapy on colorectal cancer via synergistic ROS augment and autophagy blockage	Disease treatment	10.1016/j.nantod.2023.101798



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