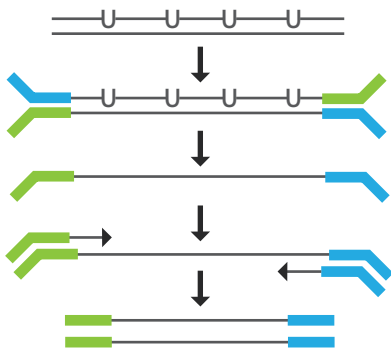


Prokaryotic mRNA Sequencing (NGS)

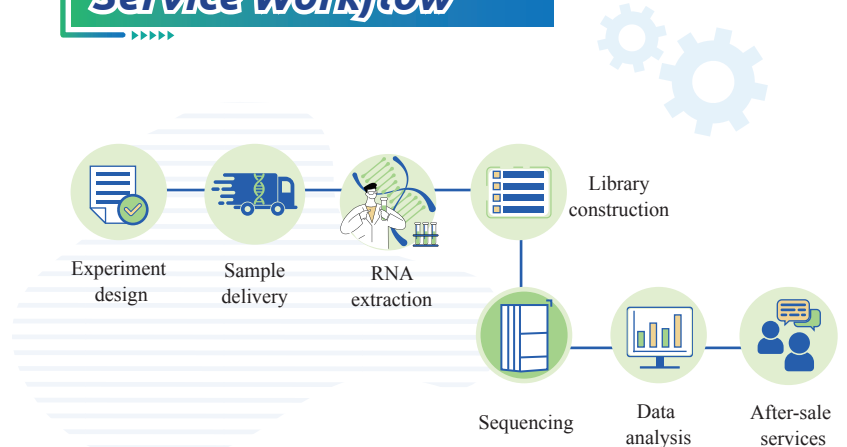
Prokaryotic RNA sequencing harnesses the power of next-generation sequencing (NGS) to unlock dynamic cellular transcriptomes. BMKGENE's cutting-edge technology is tailored for prokaryotes with a reference genome, providing comprehensive transcriptome analysis, gene structure analysis, and more. Widely applied in basic scientific research, drug development, and other fields, it helps unravel the mysteries of prokaryotic gene expression.

Technical Features

Stranded library construction



Service Workflow



Bioinformatics

- Gene expression analysis;
- Differential expression analysis;
- Function annotation and enrichment analysis;
- sRNA prediction and annotation;
- Transcript structure analysis.



Service Advantages

- Unlock comprehensive and high-resolution insights into gene expression and regulation in prokaryotes.
- The reference genome based prokaryotic transcriptome can be more accurate.
- Dig deep into gene structure and SNP/InDel information to discover new genes or gene expression elements.
- Nine interactive analysis modules, including advanced analysis, to realize the comprehensive analysis of transcriptome data.
- After-sale services: After-sale services are valid for 3 months upon project completion, including project follow-up, trouble-shooting, results Q&A, etc.

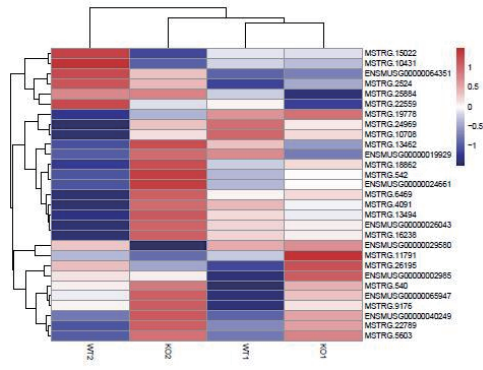
Service Specifications

Library	Read Length	Recommended Data	Data Quality
rRNA depletion	PE150	2 Gb	Q30 ≥ 85%

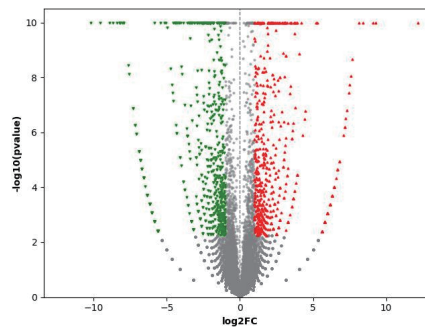
Sample Requirements

Amount	Purity	Integrity
Conc. ≥ 50 ng/μL; Volume ≥ 10 μL; Total ≥ 1 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

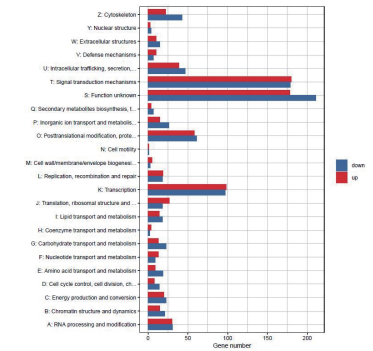
Demo Results



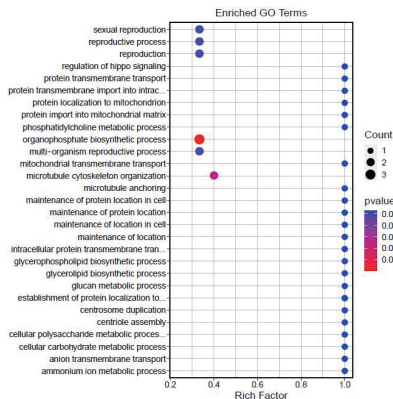
1. Sample expression heatmap



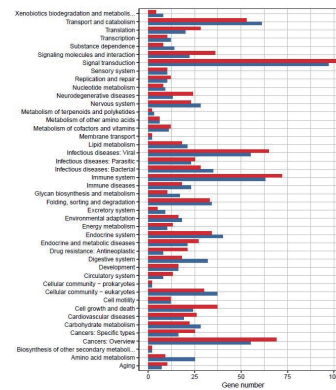
2. Differential expression analysis



3. eggnog annotation on DEGs



4. GO annotation on DEGs



5. KEGG annotation on DEGs



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