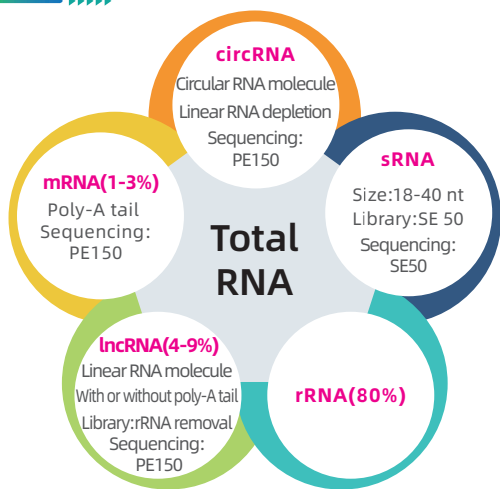


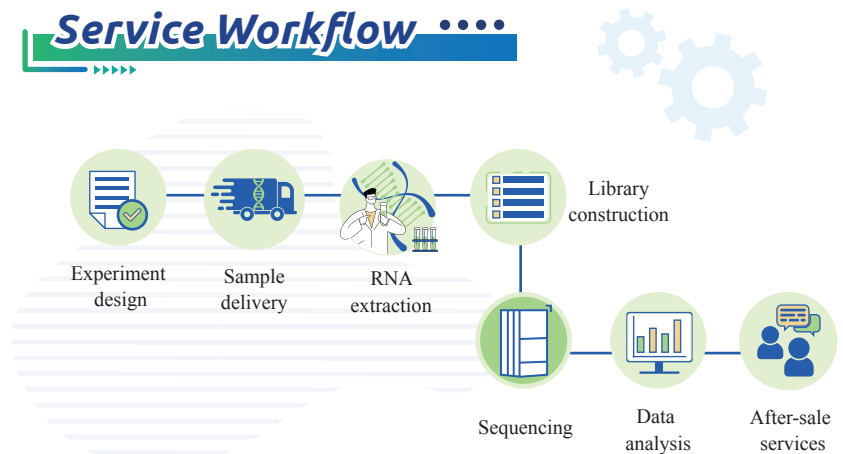
# Whole Transcriptome Sequencing

Whole transcriptome sequencing is a method of studying the expression profiles of all transcripts, including both coding (mRNA) and non-coding (lncRNA, circRNA, and sRNA) RNAs, in cells or tissues through high-throughput sequencing technology. Providing a snapshot of gene expression at any given moment. Leveraging the capabilities of NGS, BMKGENE's whole transcriptome sequencing uncovers intricate regulatory networks, including circRNA-miRNA-mRNA ceRNA interactions, enabling comprehensive RNA analysis.

## Technical Features



## Service Workflow



## Bioinformatics

- ▶ **RNA expression overview:**  
mRNA, lncRNA, sRNA and circRNA;
- ▶ Differential expression overview;
- ▶ Co-expression analysis;
- ▶ Competing endogenous RNA(ceRNA) network;
- ▶ Integrated pathway analysis on key genes;
- ▶ Targeting relations between differential RNAs.

## Service Advantages

- ▶ Estimation of all types of RNAs in terms of counts, expression, and chromosome-based relative expression.
- ▶ Identification of differentially expressed RNAs and corresponding expression.
- ▶ Gene co-expression analysis and ceRNA network analysis.
- ▶ Extensive experience: Has completed 2000+ whole transcriptome sequencing projects.
- ▶ After-sale services: After-sale services are valid for 3 months upon project completion, including project follow-up, trouble-shooting, results Q&A, etc.

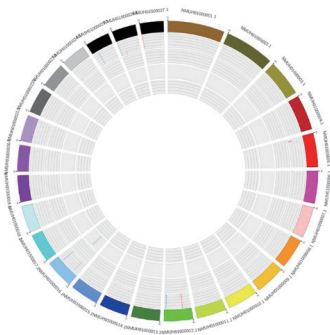
## Service Specifications

Library	Platform	Recommended Data	Data Quality
Total RNA	Illumina PE150&SE50	Circ/lnc/mRNA: 16G; miRNA: 10M reads	Q30 ≥ 85%

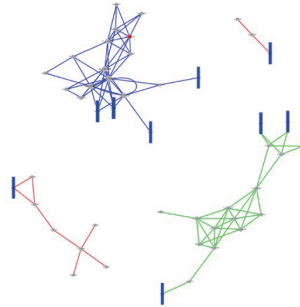
## Sample Requirements

Amount	Qubit Conc. (ng/μL)	Integrity
Conc. ≥ 100 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 ≥ 6.5; For animals: RIN ≥ 7.0; 5.0 ≥ 28S/18S ≥ 1.0; limited or no baseline elevation

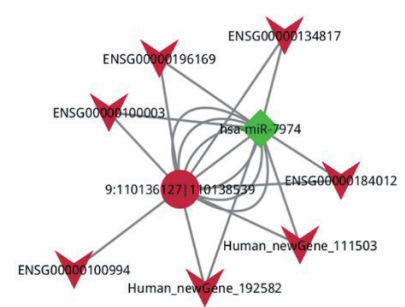
## Demo Results



1. Estimation on all types of RNAs based relative expression



2. Integrated KEGG pathway network



3. ceRNA network analysis

## Featured Publications

Year	Journal	Article	Applications	DOI
2023	Pharmacological Research	Targeting hnRNPC suppresses thyroid follicular epithelial cell apoptosis and necroptosis through m6A-modified ATF4 in autoimmune thyroid disease	Disease treatment	10.1016/j.phrs.2023.106933
2023	Aging	Whole-transcriptome sequencing analysis reveal mechanisms of Yiqi Huoxue Yangyin (YHY) decoction in ameliorating D-gal-induced cardiac aging	Disease treatment	10.18632/aging.204532
2022	Frontiers in Plant Science	Identification and validation of coding and non-coding RNAs involved in high-temperature-mediated seed dormancy in common wheat	Environmental adaptation	10.3389/fpls.2023.1107277



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