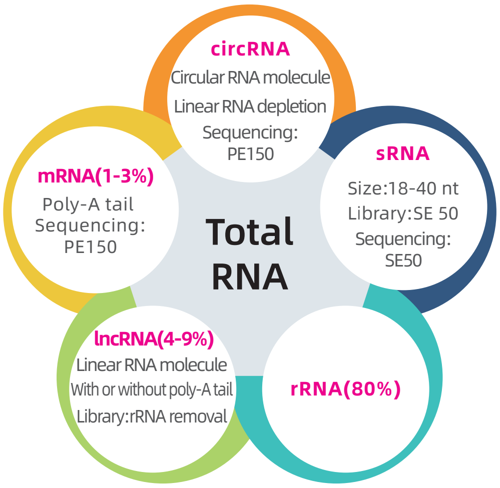
BMKGENE

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



Total RNA

circRNA
Circular RNA molecule
Linear RNA depletion
Sequencing: PE150

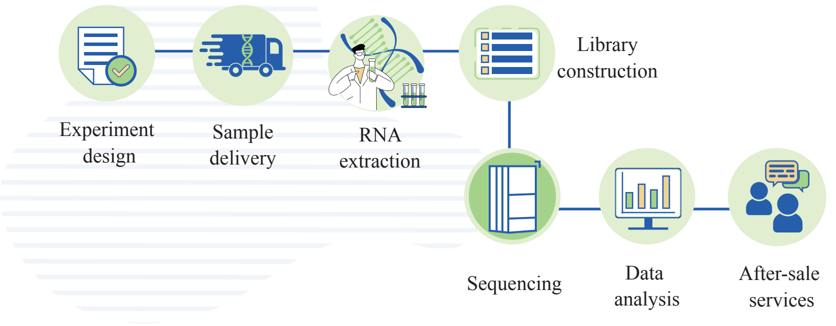
sRNA
Size:18-40 nt
Library:SE 50
Sequencing: SE50

mRNA(1-3%)
Poly-A tail
Sequencing: PE150

lncRNA(4-9%)
Linear RNA molecule
With or without poly-A tail
Library:rRNA removal

rRNA(80%)

Service Workflow



Experiment design → Sample delivery → RNA extraction → Library construction → Sequencing → Data analysis → After-sale services

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.

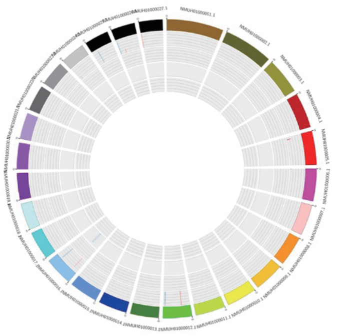
Service Specifications

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

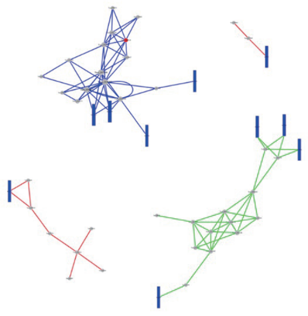
Sample Requirements

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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Biomarker Technologies (BMK) GmbH

BioZ, Johann-Krane Weg
42, 48149 Münster, Germany
tech@bmkcloud.com
www.bmkgene.com