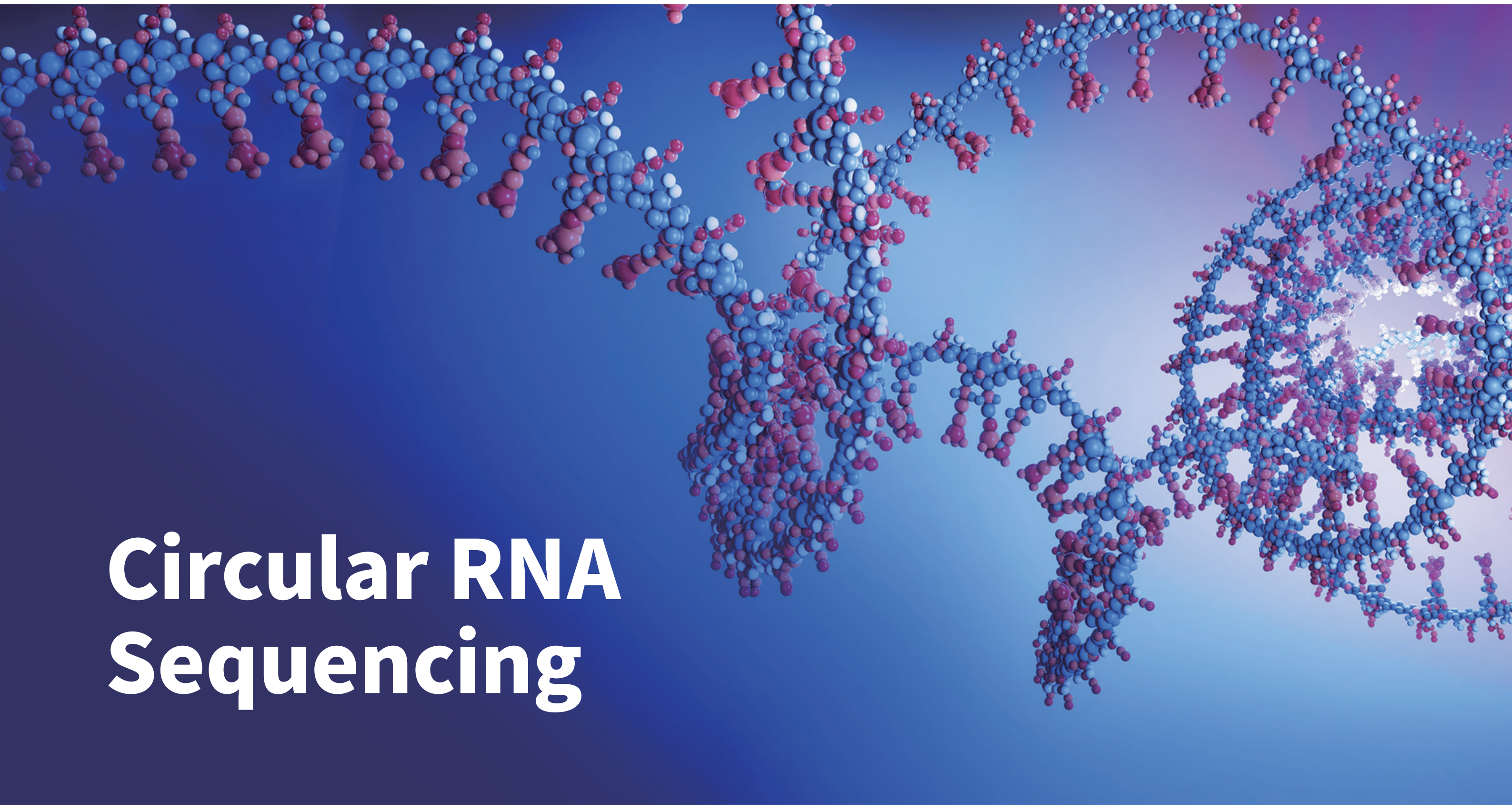
Novogene



Circular RNA Sequencing

Circular RNA (circRNA) molecules are a novel type of non-coding transcripts equipped with a covalently closed loop lacking 5’ end caps and 3’ poly(A) tails. The stable structure enables the circular transcripts resistant to exonuclease digestion. It provides a mechanism for library construction with linear transcripts digested by RNase R.

Our circRNA sequencing service (circRNA-seq) supports the investigation of miRNA sponges and fulfills the regulatory function in gene expression.

Applications:

- Expression quantification of circRNA transcripts.
- Cellular function verification and animal mode test, such as cell proliferation and apoptosis.
- Function verification, such as gene knockout, over-expression of circRNA genes.
- Competing endogenous RNA (ceRNA) investigation.

Our Key Features & Advantages

Extensive Experience

We have extensive records of sequencing projects that have been published in journals.

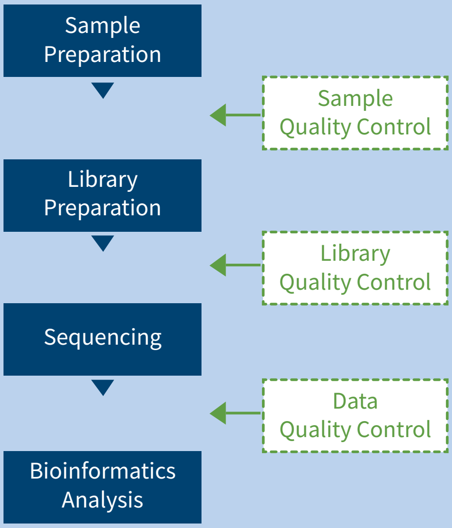
Comprehensive Analysis

Comprehensive analysis using mainstream software and mature in-house pipeline to meet multiple bioinformatic requests.

Unsurpassed Data Quality

We guarantee that ⩾ 80% of bases have a sequencing quality score ⩾ Q30, exceeding Illumina’s official guarantee of ⩾ 75%.

Project Workflow



Sample Preparation

Sample Quality Control

Library Preparation

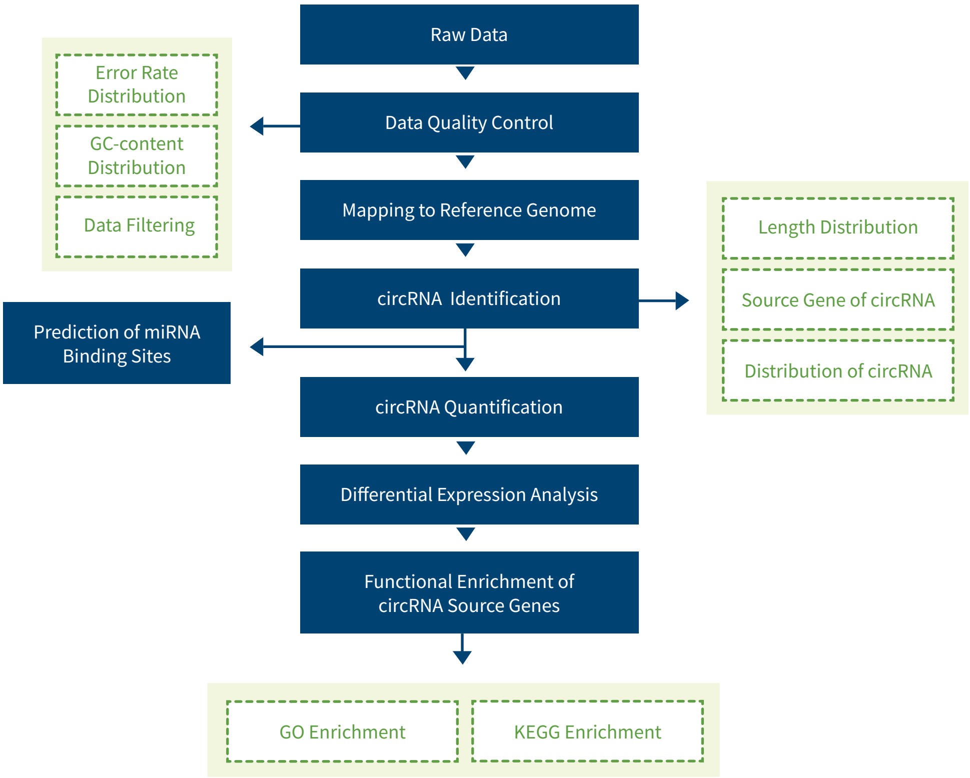
Library Quality Control

Sequencing

Data Quality Control

Bioinformatics Analysis

Standard Analysis Pipeline



Raw Data

Data Quality Control

Error Rate Distribution

GC-content Distribution

Data Filtering

Mapping to Reference Genome

circRNA Identification

Length Distribution

Source Gene of circRNA

Distribution of circRNA

Prediction of miRNA Binding Sites

circRNA Quantification

Differential Expression Analysis

Functional Enrichment of circRNA Source Genes

GO Enrichment

KEGG Enrichment

Sample Requirements

Library Type	Sample Type	Amount	RNA Integrity Number (Agilent 2100)	Purity Nanopore
circRNA Library	Total RNA	⩾ 2 μg	Animal ⩾ 7, Plant ⩾ 6.5 with smooth baseline	OD260/280 = 1.8-2.2; OD260/230 ⩾1.8;

Publications

Listed below are some publications that were supported by Novogene solutions, and more at our website.

Journal	IF	Title
Neural Regeneration Research	3.171	Novel circular RNAs expressed in brain microvascular endothelial cells after oxygen-glucose deprivation/ recovery (2019.11)
Frontiers in Genetics	3.65	miRNA and circRNA expression patterns in mouse brain during toxoplasmosis development (2020)

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