

Circular RNA Sequencing Solutions

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

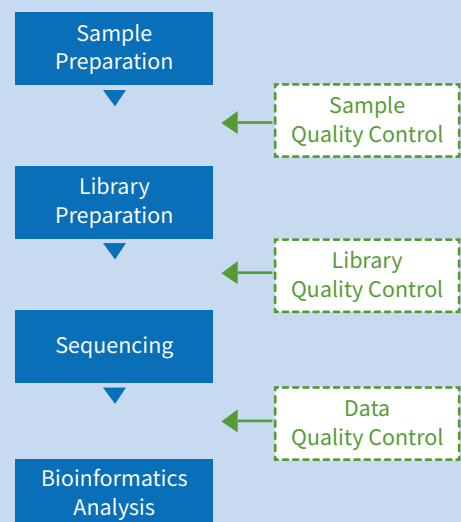
Comprehensive analysis using mainstream software and mature in-house pipeline to meet multiple bioinformatic requests.



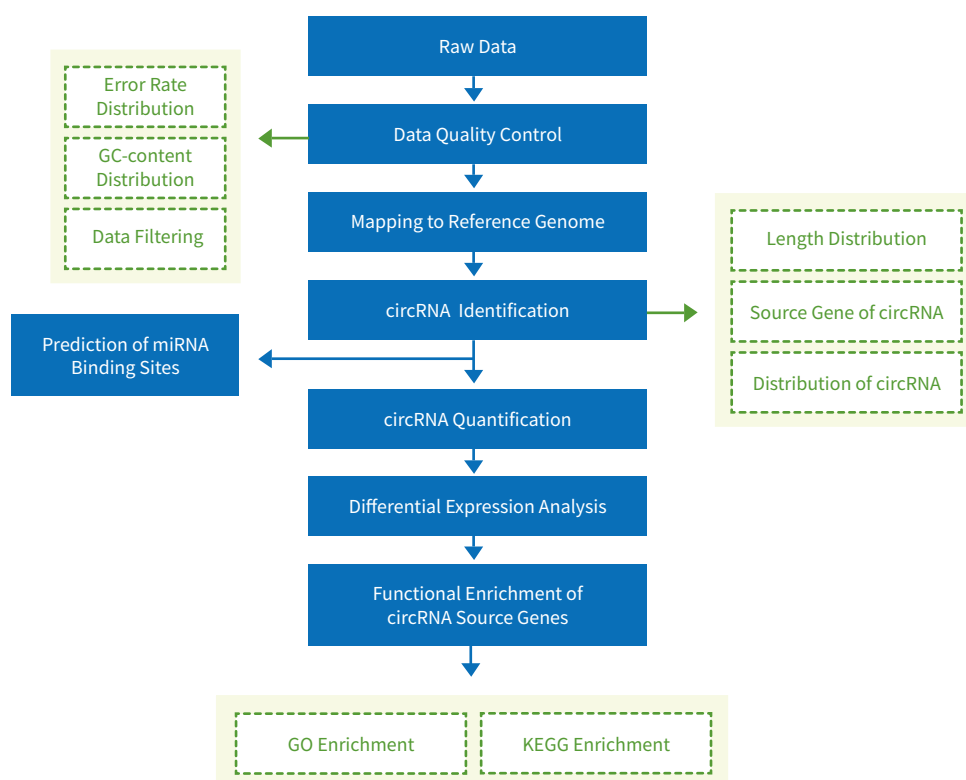
Unsurpassed Data Quality

We guarantee that $\geq 80\%$ of bases have a sequencing quality score $\geq Q30$, exceeding Illumina's official guarantee of $\geq 75\%$.

Project Workflow



Standard Analysis Pipeline



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.

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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NovogeneAIT Genomics Singapore Pte. Ltd.
(Joint Venture & Sequencing Centre)

Novogene International Pte. Ltd.
25 Pandan Crescent #05-15 TIC Tech Centre, Singapore 128477

T: +65-8823-3182
e: marketing_amea@novogeneait.sg

en.novogene.com