Novogene

Whole Transcriptome Sequencing

Whole Transcriptome Sequencing service equips the researcher with cutting-edge NGS solutions that provide in-depth bioinformatic analysis on all transcripts, including mRNAs and non-coding RNAs.

This competitive approach investigates and explores potential transcriptional and regulatory network mechanisms while providing key insights into interaction and intersection functionality from a comprehensive transcriptomic perspective.

Applications:
· Co-localization and co-expression of ncRNA and mRNA detection
· miRNA sponge and target regulatory elements detection
· Regulatory network investigation: ceRNA regulatory
· Network set up based on lncRNA/circRNA-miRNA-gene pairs, taking lncRNA/circRNA as decoy, miRNA as core and mRNA as target.

Our Key Features & Advantages

Extensive Experience
We have extensive records of sequencing projects that have been published in journals.
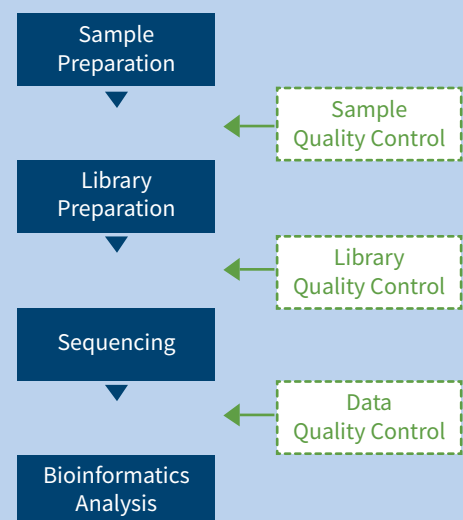
Comprehensive Analysis
Utlizing mainstream software and mature in-house pipeline to meet multiple bioinformatic requests.

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

Sample Requirements

Library Type	Sample Type	Amount	Volume	RNA Integrity Number (Agilent 2100)	Purity Nanopore
lncRNA library & Small RNA library	Total RNA	⩾ 3 μg	⩾ 30 μL	Animal ⩾ 7.5, Plant ⩾ 7 with smooth baseline	OD260/280 = 1.8-2.2; OD260/230 ⩾ 1.8;
lncRNA library, Small RNA library & CircRNA library	Total RNA	⩾ 5 μg	⩾ 50 μL		

Standard Analysis Content

Platform	Illumina Novaseq 6000
Read Length	Paired-end 150 & Single-end 50
Recommended Sequencing Depth	⩾ 40 million read pair per sample (lncRNA library); ⩾ 20 million read pair per sample (small RNA library);
Association Analysis of Transcriptome	• Interaction of lncRNA and miRNA • Interaction of mRNA and miRNA • Interaction of circRNA and miRNA • Regulatory Network of lncRNA, miRNA and mRNA • Regulatory Network of circRNA, miRNA and mRNA

Package 1 (lncRNA+sRNA): lncRNA standard analysis, small RNA standard analysis; interaction of lncRNA and miRNA, interaction of mRNA and miRNA, regulatory network of lncRNA, miRNA and mRNA.

Package 2 (lncRNA+sRNA+circRNA): lncRNA standard analysis, small RNA standard analysis, circRNA standard analysis, interaction of lncRNA and miRNA, interaction of mRNA and miRNA, interaction of circRNA and miRNA, regulatory network of lncRNA, miRNA and mRNA and regulatory network of circRNA, miRNA and mRNA.

Publications

Listed below are some publications that were supported by Novogene solutions.

Journal	IF	Title
International Journal of Genomics	2.326	Analysis of lncRNA, miRNA, and mRNA Expression Profiling in Type I IFN and Type II IFN Overexpressed in Porcine Alveolar Macrophages (2021.06)
Genomics	6.025	Identifying circRNA- and lncRNA-associated-ceRNA networks in the hippocampi of rats exposed to PM2.5 using RNA-seq analysis(2020.12)
J Hematol Oncol	11.059	Transcriptional factor six2 promotes the competitive endogenous RNA network between CYP4Z1 and pseudogene CYP4Z2P responsible for maintaining the stemness of breast cancer cells (2019.12)