

Whole Transcriptome Sequencing Solutions

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

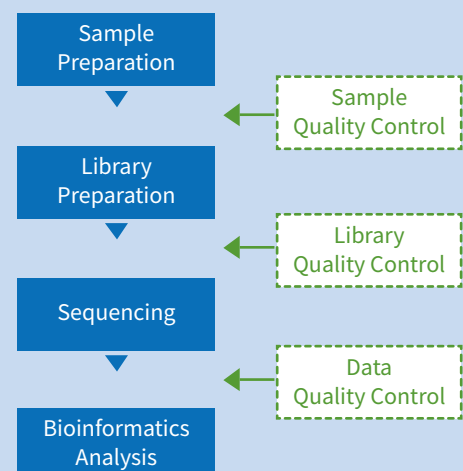
Utilizing mainstream software and mature in-house pipeline to meet multiple bioinformatic requests.



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



Sample Requirements

Library Type	Sample Type	Amount	RNA Integrity Number (Agilent 2100)	Purity Nanopore
lncRNA library & small RNA Library	Total RNA	≥ 3 µg	Animal ≥ 7.5, Plant ≥ 7 with smooth baseline	OD260/280 = 1.8-2.2; OD260/230 ≥ 1.8;

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	<ul style="list-style-type: none"> • 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

Publications

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

Journal	IF	Title
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)
Frontiers in Genetics	3.517	Identification of Potential Immune-Related circRNA-miRNA-mRNA Regulatory Network in Intestine of Paralichthys olivaceus During Edwardsiella tarda Infection (2019.08)

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