

Whole Transcriptome Sequencing

Whole Transcriptome Sequencing (WTS), which includes RNA-Seq with rRNA removal and small RNA-Seq, is used to reveal the complete picture of mRNAs, lncRNAs, circRNAs, as well as microRNA (miRNA), in a biological sample under specific conditions. WTS enables exploration of a complicated post-transcriptional regulation mechanism referred to as a competitive endogenous RNA (ceRNA) network. These ceRNAs such as mRNAs, lncRNAs, circRNAs act as molecular sponges for a miRNA through their miRNA binding sites, thereby de-repressing all target genes of the respective miRNA family.

Applications



Study of mRNA and ncRNA interactions



miRNA sponge and target regulatory elements detection



ceRNA regulation network investigation

Our Features & Advantages



Comprehensive Analysis of RNA

the lncRNA library and the small RNA library are constructed to detect miRNAs, mRNAs, lncRNAs and circRNAs, providing a more comprehensive analysis of transcriptional regulatory networks.



Extensive Experience

We were one of the first companies to provide whole transcriptome sequencing and RNA comprehensive analysis services (since 2008).



Specialist Team

We have experienced experts to assist you with experimental design and data interpretation.



Reliable & Fast Turnaround Time

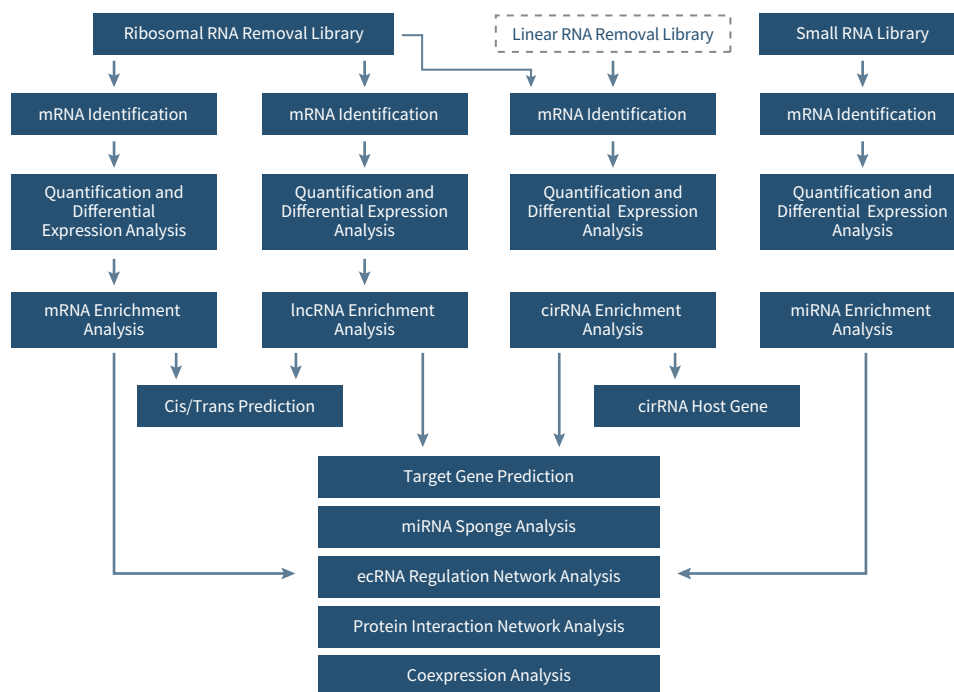
A dedicated project manager will be provided and the results will be given to you within 20 business days after sample quality verification.

Project Workflow



Sequencing Strategy: illumina Novaseq platform, PE150 bp and 12 Gb for lncRNA library, SE50 bp and 10M reads for small RNA library

Bioinformatics Analysis Pipeline




Sample Requirements

Sample Type	Amount	RIN	Purity (Nanodrop)
Total RNA	≥ 1 µg	≥ 20 ng/µl	260/280=1.8~2.0


Recent Publications

Journal	IF	Title	Year
Bioactive Materials	18.9	MicroRNA-122-functionalized DNA tetrahedron stimulate hepatic differentiation of human mesenchymal stem cells for acute liver failure therapy	2023
Molecular Cancer	37.3	Characterization of distinct circular RNA signatures in solid tumors	2022
Nature Cancer	22.7	The cancer-testis lncRNA lnc-CTHCC promotes hepatocellular carcinogenesis by binding hnRNP K and activating YAP1 transcription	2022

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