Novogene

RNA Immunoprecipitation Sequencing

Protein-RNA interactions play important roles in multiple post-transcriptional regulation processes such as RNA cleavage, transport, sequence editing, intracellular localization and translational control. RNA immunoprecipitation (RIP) can be used to detect the association of individual proteins with specific nucleic acids. RNA immunoprecipitation sequencing (RIP-Seq) is a revolutionary technology that reveals the interaction of RNA and RNA-binding proteins at the genome-wide level. RIP-Seq maps the sites at which proteins are bound to the RNA and provides single-base resolution of protein-bound RNA.

The Novogene Advantages

Cost-effective and Quick Turnaround:

Rapid and efficient transcriptome-wide profiling of multiple samples at a very competitive prices.

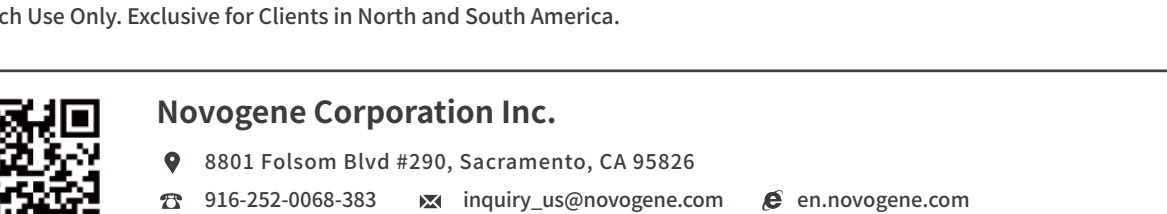
Comprehensive Analysis:

Using the widely accepted MACS2 software and the latest programs for peak annotation, motif prediction, functional analysis and data visualization, we offer analysis solutions to meet your project needs.

Data and Analysis Guarantee:

Our team of experienced scientists ensure the data and analysis quality to be publication ready.

Project Workflow



Specifications

SAMPLE REQUIREMENTS

- Sample type : RNA sample after RIP assay without fragmentation
- RNA amount : ⩾ 100 ng
- Concentration : ⩾ 3 ng/μL, main peak ⩾ 1000 bp
- Sample volume : ⩾ 20 μl
- OD260/280 ⩾ 2.0, no degradation or DNA contamination

TURNAROUND TIME

- 22 working days for 20 or fewer samples from verification of sample quality without data analysis

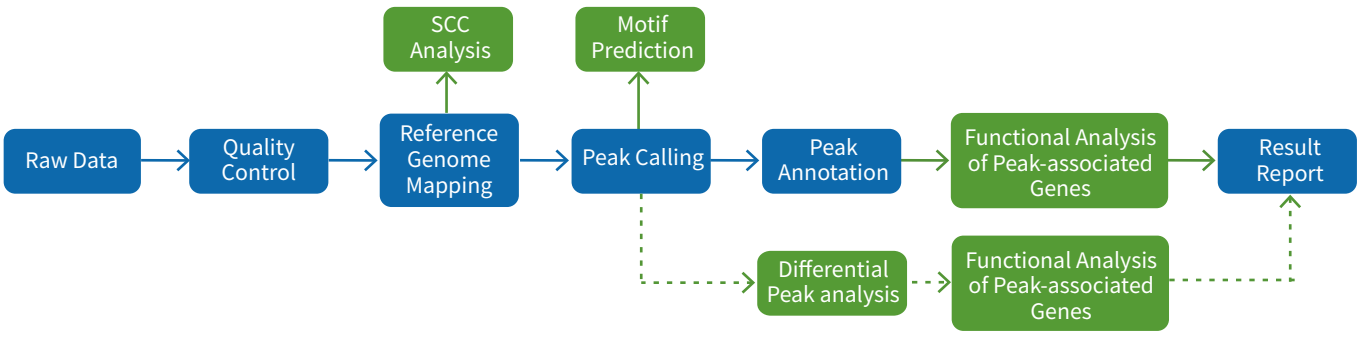
SEQUENCING STRATEGY

- Library type : 250-300 bp insert cDNA library
- Sequencing platform : NovaSeq 6000
- Sequencing strategy : pair-end 150 bp

RECOMMENDED DATA OUTPUT

- ⩾ 6 Gb per sample

Standard Analysis Pipeline



Only applicable for projects with comparable experimental groups.

Novogene Powered Publications

Year	Journal	Title
2020	*Nature Communications*	METTL3 is essential for postnatal development of brown adipose tissue and energy expenditure in mice
2020	*Nucleic Acids Research*	The m6A reader YTHDF1 promotes ovarian cancer progression via augmenting EIF3C translation
2020	*Cell Death and Disease*	CPEB3-mediated MTDH mRNA translational suppression restrains hepatocellular carcinoma progression
2018	*Hepatology*	RNA N6 - methyladenosine methyltransferase - like 3 promotes liver cancer progression through YTHDF2 - dependent posttranscriptional silencing of SOCS2

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