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.

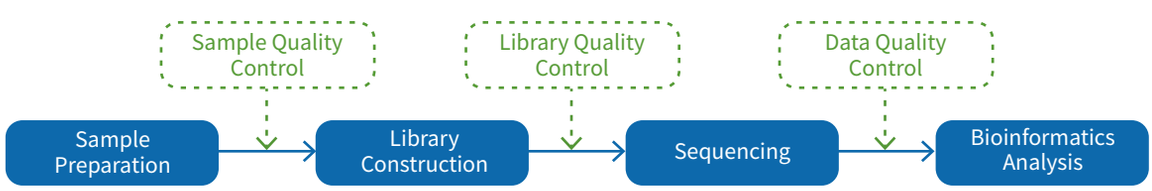
Comprehensive Analysis:

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

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

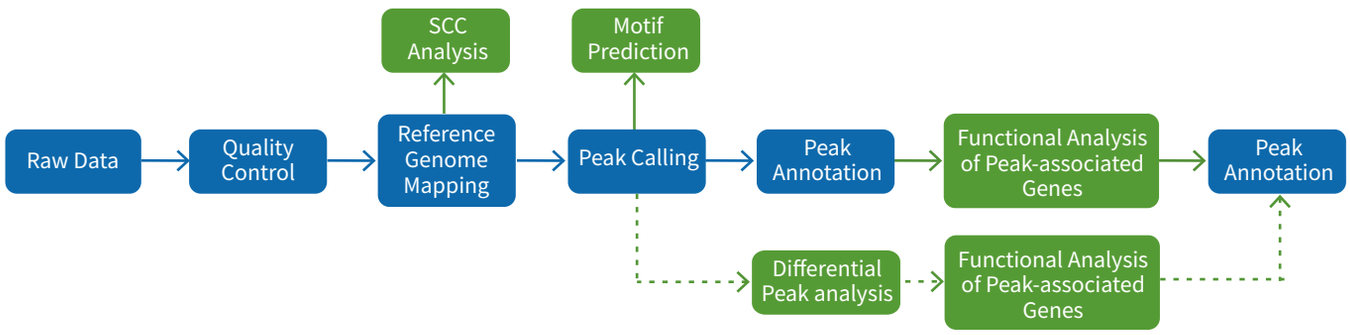
SEQUENCING STRATEGY

- 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



Novogene Client Publication

The RNA binding protein SORBS2 suppresses metastatic colonization of ovarian cancer by stabilizing tumor-suppressive immunomodulatory transcripts (Zhao *et al,* 2018)

Ovarian cancer constitutes one of the most lethal gynecologic malignancies for females. In this study, the RBP sorbin and SH3 domain containing 2 (SORBS2) is identified as a potent suppressor of ovarian cancer metastatic colonization. Mechanistic studies show that SORBS2 binds the 3′-untranslated regions (UTRs) of WFDC1 (WAP four-disulfide core domain 1) and IL-17D (Interleukin-17D), two secreted molecules that are shown to act as metastasis suppressors (Fig. 1). By enhancing the stability of these gene transcripts, SORBS2 suppresses ovarian cancer invasiveness and affects monocyte to myeloid-derived suppressor cell and M2-like macrophage polarization, eliciting a tumor-suppressive immune microenvironment.

This study takes advantage of RNA-seq and RIP-seq technology to illustrate a novel post-transcriptional network that links cancer progression and immunomodulation within the tumor microenvironment through SORBS2-mediated transcript stabilization.

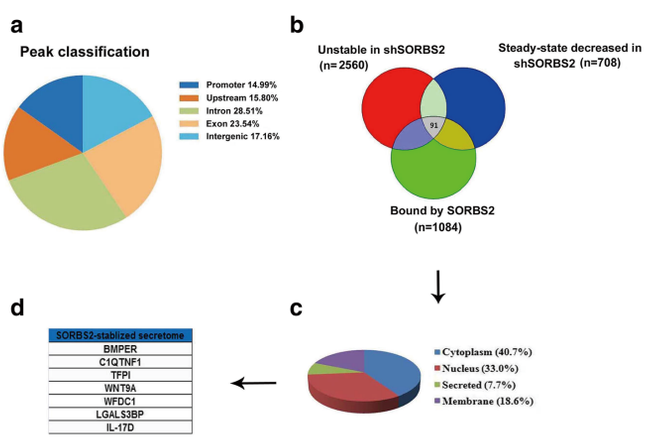


Figure. 1 SORBS2 depletion affects the stability of transcripts directly bound by SORBS2.

Reference: Zhao L, Wang W, Huang S, *et al.* The RNA binding protein SORBS2 suppresses metastatic colonization of ovarian cancer by stabilizing tumor-suppressive immunomodulatory transcripts.[J]. *Genome Biology,* 2018, 19(1):35.

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