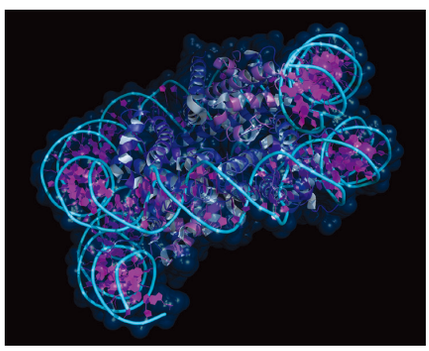
Novogene

Chromatin Immunoprecipitation Sequencing



ChIP-Seq provides genome-wide profiling of DNA targets for histone modification, transcription factors, and other DNA-associated proteins. It combines the selectivity of chromatin immuno-precipitation (ChIP) to recover specific protein-DNA complexes, with the power of next-generation sequencing (NGS) for high-throughput sequencing of the recovered DNA. Additionally, because the protein-DNA complexes are recovered from living cells, binding sites can be compared in different cell types and tissues, or under different conditions. Applications range from transcriptional regulation to developmental pathways to disease mechanisms and beyond.

At Novogene, we provide high-quality sequencing and comprehensive bioinformatics solutions for your ChIP-Seq projects.

Novogene Advantages

Cost-Effective and Quick Turnaround:

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

Extensive Experience:

Over 2000 projects successfully completed.

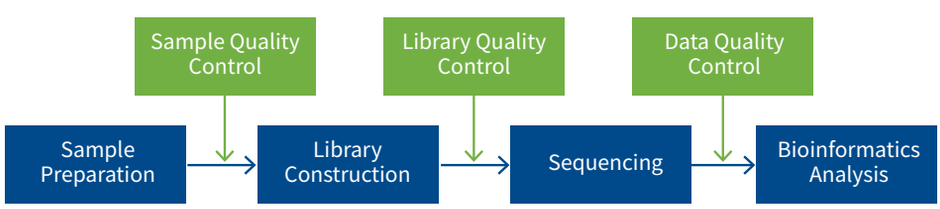
Comprehensive Analysis:

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

SEQUENCING STRATEGY

- 100-500 bp insert DNA library (depending on peak distribution)
- NovaSeq platform, paired-end 150 bp

TURNAROUND TIME

- 22 business days for 20 or fewer samples, from the time sample quality is verified*

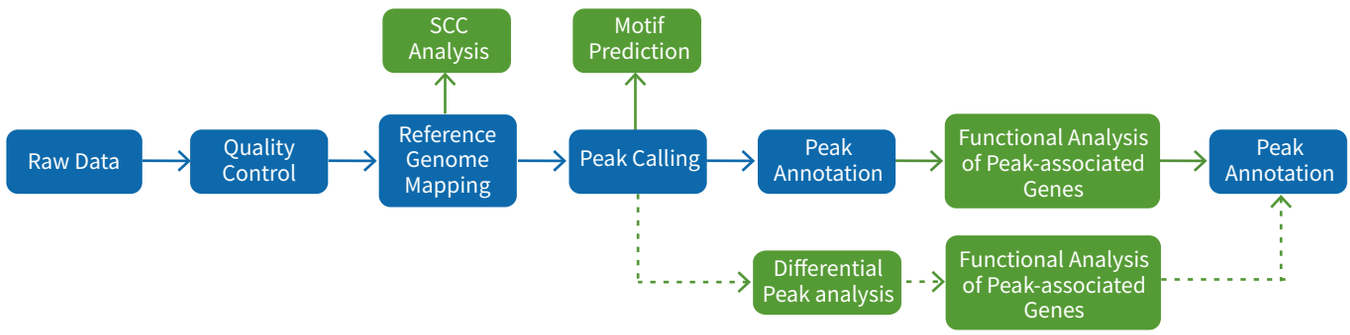
SAMPLE REQUIREMENTS

- DNA quantity: ⩾ 50 ng, main peak locates between 100 to 500 bp
- Sample volume: ⩾ 10 µl
- OD260/280 = 1.8 to 2.0 without degradation or RNA contamination

RECOMMENDED DATA OUTPUT

- ⩾6 Gb per sample

Analysis Pipeline



Only applicable for projects with comparable experimental groups.

Novogene Client Publication

Targeting Epigenetic Crosstalk as a Therapeutic Strategy for EZH2-Aberrant Solid Tumors (Huang *et al,* 2018)

Mutations or aberrant upregulation of EZH2 occur frequently in human cancers. In this study, the results of H3K27ac ChIP-seq, RNA-seq, and proteomics analysis demonstrated that H3K27ac upregulation, due to EZH2 inhibition, results in the transcriptional activation of multiple onco-pathways in a cell-context-dependent manner. This may also underline the resistance to EZH2i.

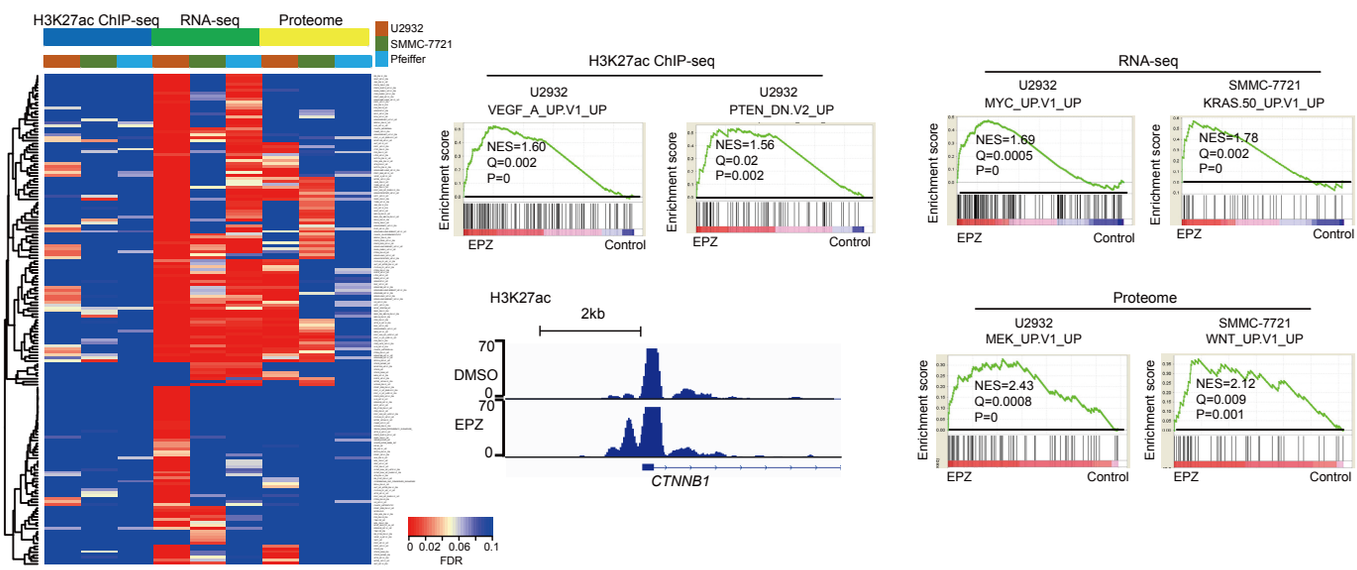


Figure 1. Feedback H3K27 Acetylation Change Drives Oncogenic Transcriptional Reprogramming.

Reference: Huang X, Yan J, Zhang M, *et al*. Targeting Epigenetic Crosstalk as a Therapeutic Strategy for EZH2-Aberrant Solid Tumors[J]. *Cell*, 2018, 175(1): 186-199.

* For projects without data analysis.

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