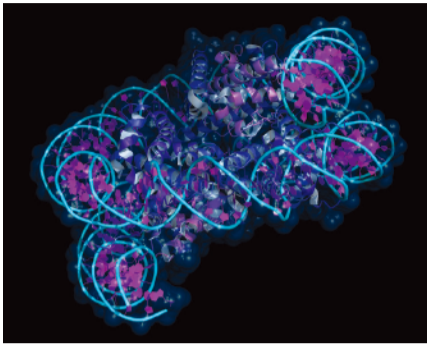


Chromatin Immunoprecipitation Sequencing



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 a very competitive price.



Extensive Experience:

Over 2000 projects successfully completed.



Comprehensive Analysis:

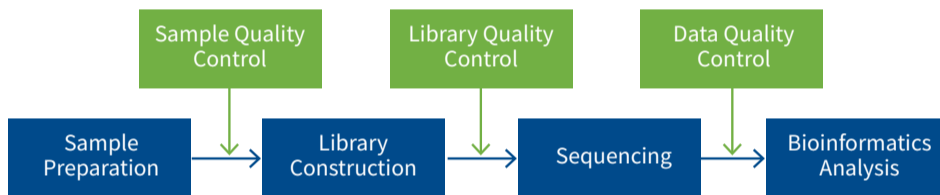
Using the widely accepted MACS2 software and the latest programs for peak annotation, motif prediction, functional analysis and data visualization, we offer analysis solutions to meet your project needs.



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

✓ SAMPLE REQUIREMENTS

- DNA quantity: ≥ 50 ng, main peak of 100 to 500 bp
- Sample volume: ≥ 10 μ l
- OD260/280 = 1.8 to 2.0 without degradation or RNA contamination

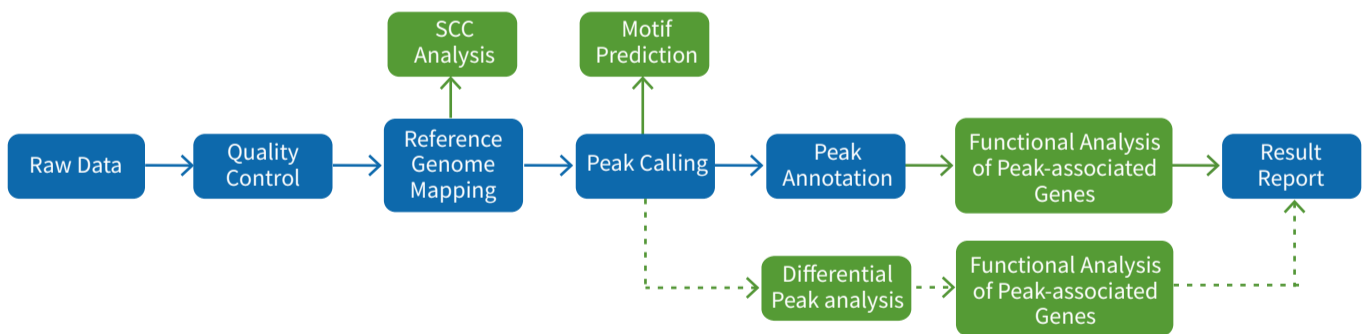
✓ TURNAROUND TIME

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

✓ RECOMMENDED DATA OUTPUT

- ≥ 6 Gb per sample

Analysis Pipeline



-----> Only applicable for projects with comparable experimental groups.

Novogene Powered Publications

Year	Journal	Title
2019	<i>Nucleic acids research</i>	Zscan4c Activates Endogenous Retrovirus MERVL and Cleavage Embryo Genes
2019	<i>Nature communications</i>	Hematopoietic PBX-interacting Protein Mediates Cartilage Degeneration During the Pathogenesis of Osteoarthritis
2019	<i>Cancer Research</i>	SET Domain-Containing Protein 4 Epigenetically Controls Breast Cancer Stem Cell Quiescence
2018	<i>Cell</i>	Targeting Epigenetic Crosstalk as a Therapeutic Strategy for EZH2-Aberrant Solid Tumors
2018	<i>Cancer Research</i>	E6 Protein Expressed by High-Risk HPV Activates Super-Enhancers of the EGFR and c-MET Oncogenes by Destabilizing the Histone Demethylase KDM5C

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