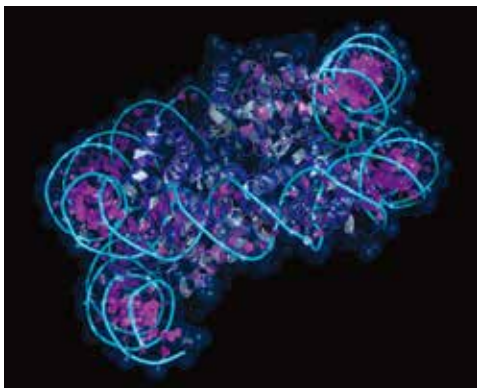
ChIP-Seq



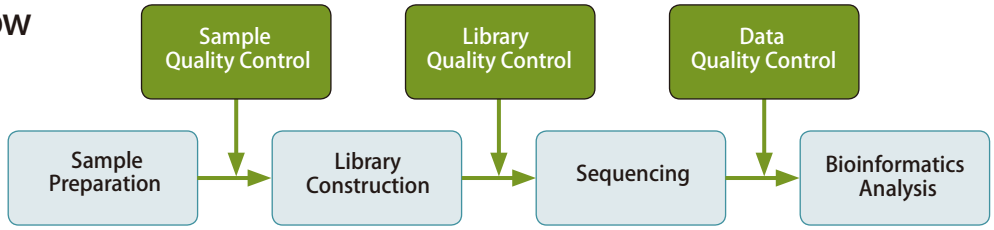
ChIP-Seq provides genome-wide profiling of DNA targets for histone modification, transcription factors, and other DNA-associated proteins; it combines the selectivity of chromatin immuno-precipitation (ChIP) for recovering specific protein-DNA complexes with the power of NGS for high-throughput sequencing of the recovered DNA. Additionally, because the protein-DNA complexes are recovered from living cells, binding sites can be compared in different cell types or tissues, or under different conditions.

In ChIP-Seq, enriched DNA regions (protein binding sites) are detected as peaks above background reads, and bioinformatics analyses of these regions can reveal binding motifs. Applications include studies on gene regulation, transcription complex assembly, histone modification, developmental mechanisms, and disease processes. At Novogene, we can provide you with high quality sequencing and comprehensive bioinformatics analysis for your ChIP-Seq project.

The Novogene Advantage

- Cost-effective: rapid and efficient genome-wide profiling of multiple samples, using only 1/100 of the amount of DNA required for ChIP-chip.
- Comprehensive analysis: expert bioinformatics analyses utilizing widely accepted MACS2 software and latest programs for motif prediction, peak annotation, functional analysis and data visualization.
- Professional bioinformatics: for ChIP-Seq data analysis.

Project Workflow



SEQUENCING STRATEGY

- 250~300 bp insert DNA library
- Illumina platform, Paired-end 150 bp

SAMPLE REQUIREMENTS

- DNA amount ⩾ 50 ng, main peak in 100~500 bp

TURNAROUND TIME

- 15 working days from verification of sample quality without data analysis

RECOMMENDED SEQUENCING DEPTH

- Minimum: 6G per sample
- Recommendation: 12G per sample

Novogene Data

QUALITY CONTROL RESULTS

Sample	RAW_Reads	Low_Quality	Degeneratives	Empty	Too_Short	Trimmed	Untrimmed	Clean_Reads	Clean_Rate
Sample1	21618631	43220	768	2079	1420	703080	20868064	21571144	99.78%
Control Input	30300790	21692	1038	3255	888	869766	29404161	30273927	99.91%

Quality control result of the project: including raw reads, trimmed reads and the raw-to-clean rate.

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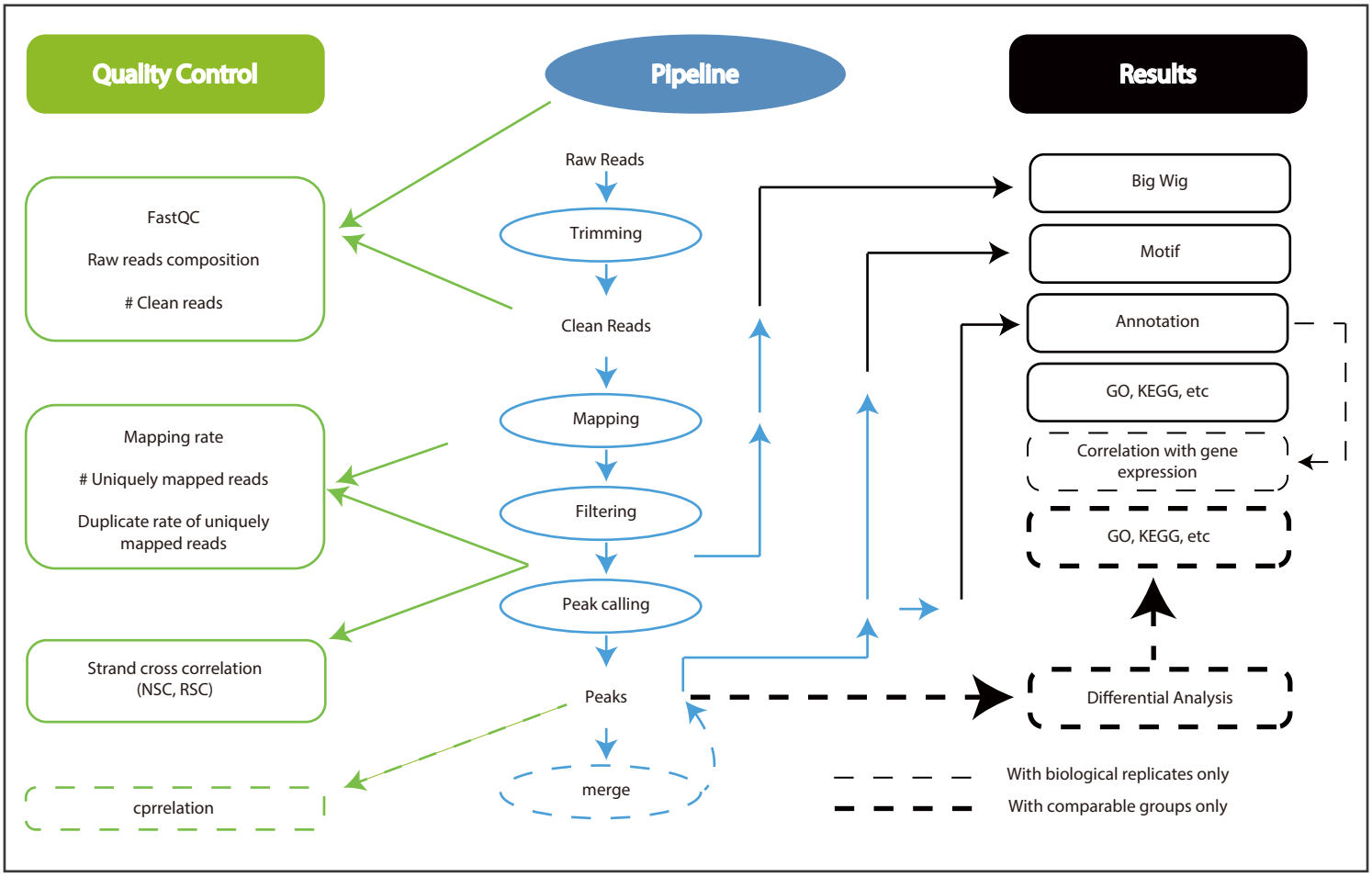


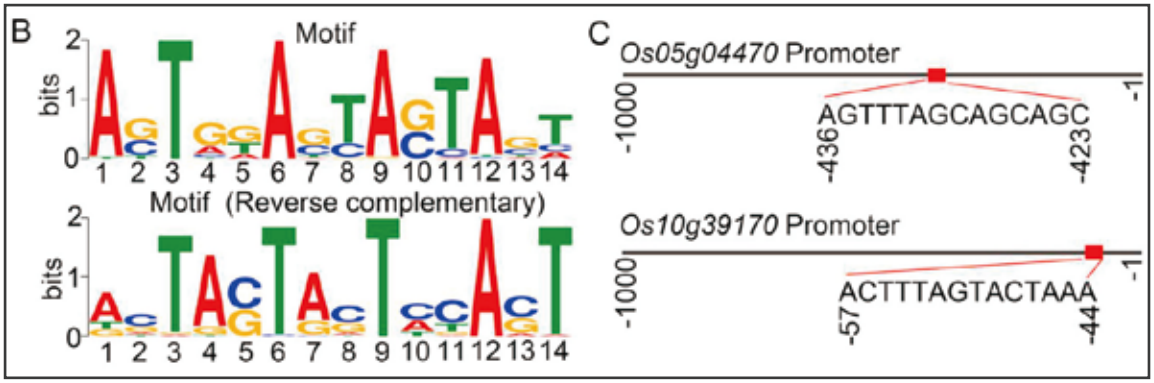
Project Example

The following study utilized Novogene's sequencing and analysis expertise.

A Natural Allele of a Transcription Factor in Rice Confers Broad-Spectrum Blast Resistance

Li W, Zhu Z, Chern M, et al. Cell, 2017, 170(1): 114-126.

Rice is a major grain in the whole world. Rice blast caused by Magnaporthe oryzae (M. oryzae) races leads to great destruction to its yield and quality. Compared with race-specific resistance, non-race-specific resistance cope with a broader spectrum with higher durability and thus makes it more effective to fight against diseases. Digu is a rice variety carrying durable and high-level resistance to a broad-spectrum of M. oryzae races. In this study, researchers identified a critical SNP in the Bsr-d1 promoter in Digu, and found the new allele indispensable in the broad-spectrum and durable resistance to M. oryzae. Bsr-d1 encodes a C2H2-type transcription factor, and this novel allele reduced expression of itself by binding to the repressive MYB transcription factor. Low Bsr-d1 levels led to reduced expression of H2O2 degredation enzymes, and thus caused further H2O2 accumulation to enhance resistance to M. oryzae. Results also indicate that this favorable trait has been selected through breeding. This study offers a potential novel strategy for breeding non-race-specific durable resistance in rice.



(1) A Bsr-d1 binding motif found in the promoters of two peroxidase genes based on ChIP-seq in the overlapping BSR-D1 binding peaks.
(2) BSR-D1 binding sequences in the promoters of two peroxidase genes (Red rectangle: peak summits; numbers: positions of bases).

Year	Journal	Article
2017	Cell	A Natural Allele of a Transcription Factor in Rice Confers Broad-Spectrum Blast Resistance