MEDIKONIA
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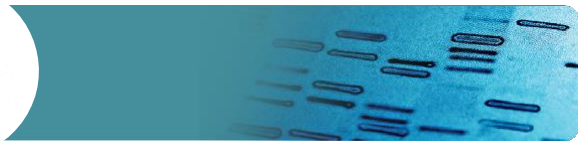
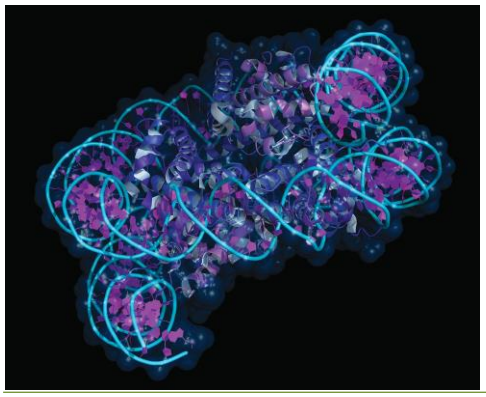
Genomic Services & Solutions



ChIP-Seq



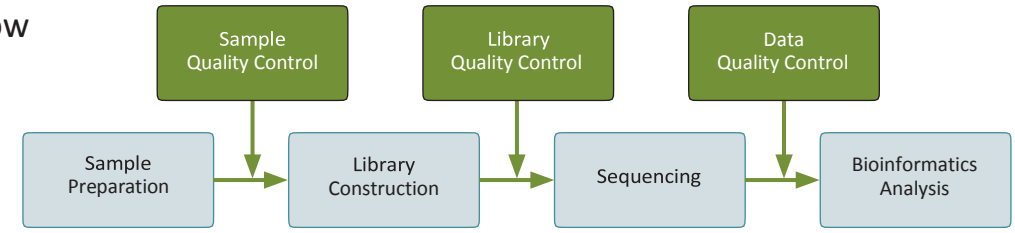
ChIP-Seq provides genome-wide profiling of DNA targets for histone modification, transcription factors, and other DNA-associated proteins; it combines the selectivity of chromatin immuno-precipitation (ChIP) for recovering specific protein-DNA complexes with the power of NGS for high-throughput sequencing 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 Medikonia, we can provide you with high quality sequencing and comprehensive bioinformatics analysis for your ChIP-Seq project.

The 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: all PhD team for ChIP-Seq data analysis.

Project Workflow



SEQUENCING STRATEGY

- 100~350 bp insert DNA library
- HiSeq platform, single-end 50 bp

SAMPLE REQUIREMENTS

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

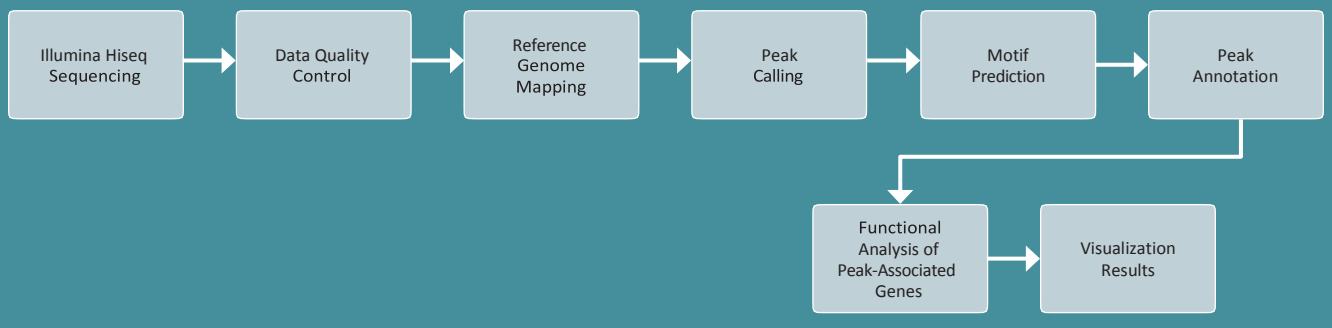
TURNAROUND TIME

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

RECOMMENDED SEQUENCING DEPTH

- ≥ 20 M reads

Analysis Pipeline

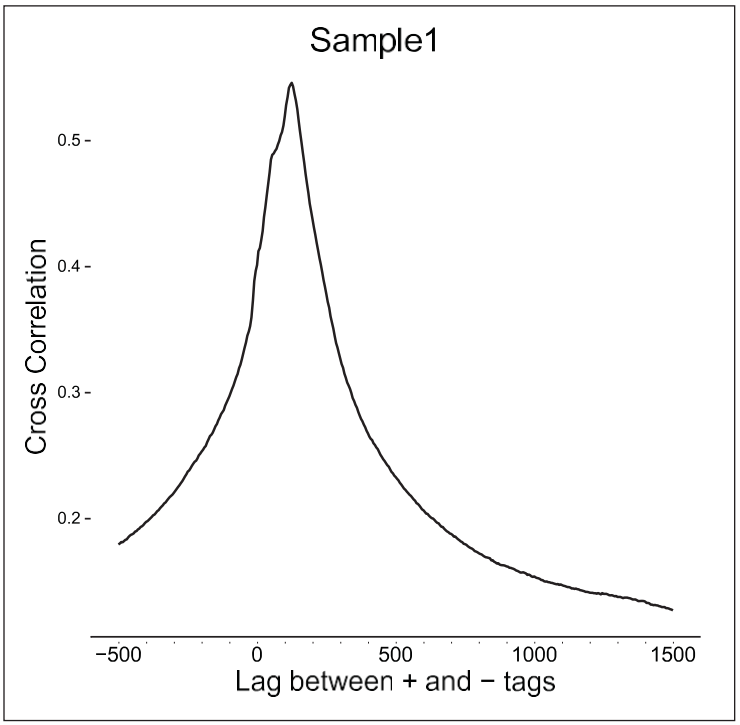


Medikonia Data

QUALITY CONTROL RESULTS

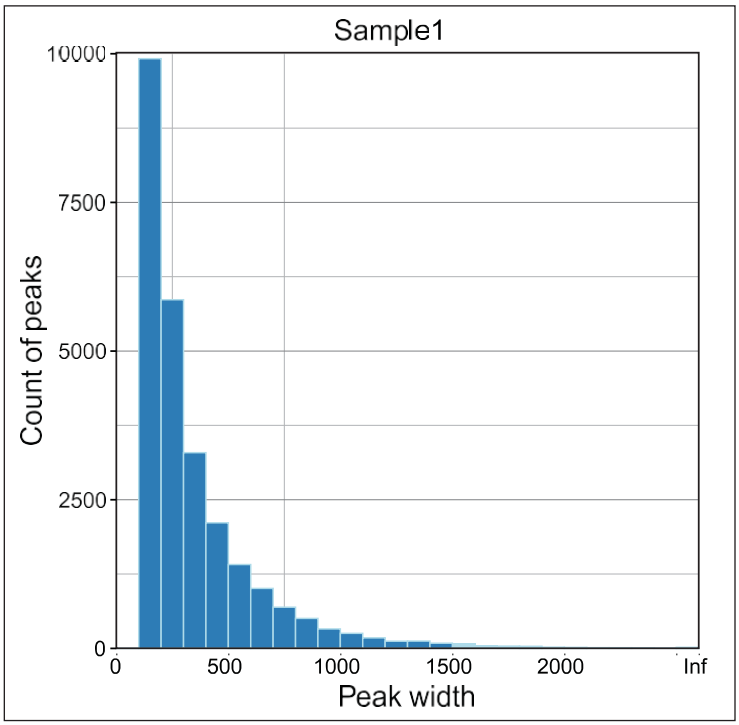
Sample	RAW_Reads	Low_Quality	Degeneratives	Empty	Too_Short	Trimmed	Untrimmed	Clean_Reads	Clean_Rate
Sample1	21618631	43220	768	2079	1420	703080	20868064	21571144	99.78%
Control Input	30300790	21692	1038	3255	888	869766	29404161	30273927	99.91%

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



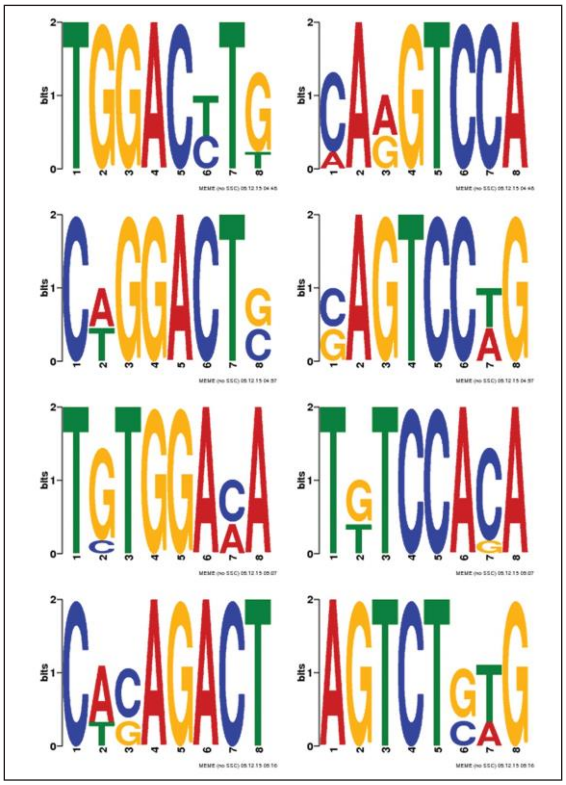
Strand cross-correlation evaluation curve

The x-axis represents the distance (nt) between forward strand and reverse strand and the y-axis represents the Pearson Correlation Coefficient.



Peak width distribution

The x-axis represents the Peak width and y-axis represents the peak count.



Motif prediction results

The base calls as predicted by motif search software. The base calls on the right were the reverse-complementary strands.