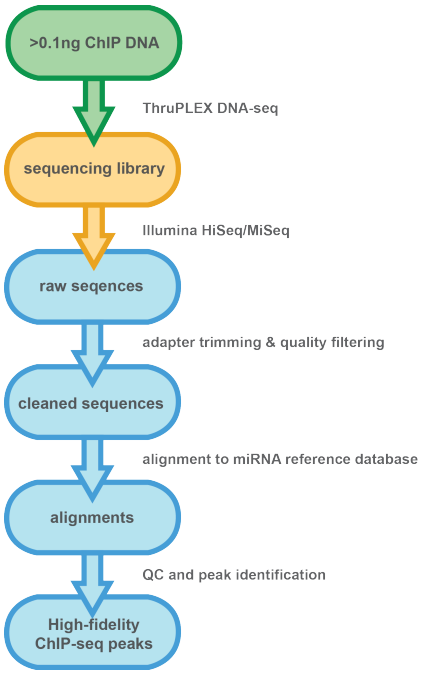
ChIP-seq

Introduction

Chromatin immunoprecipitation followed by high-throughput sequencing (ChIP-seq) has been widely used in studying histone modification, transcriptional regulation, chromatin organization, and other types of epigenetic regulations. NGI Stockholm has set up cost-effective protocols for sequencing libraries constructed from ChIP DNA, as well as an automated ChIP-seq data analysis pipeline.

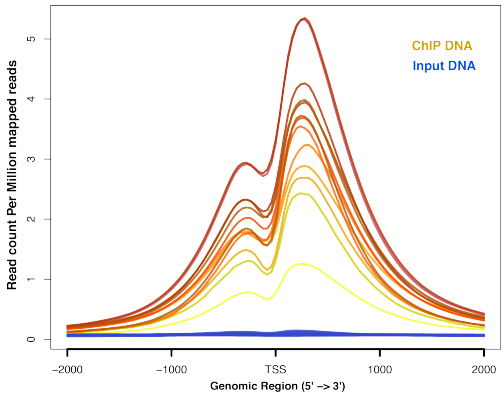
Workflow

Libraries can be constructed with as little as 0.1 ng ChIP DNA using the ThruPLEX DNA-seq protocol. Sequencing is done on the Illumina HiSeq or MiSeq Platform. The required sequencing depth depends on the application. Typically 10-40 million uniquely aligned reads (~100× coverage) are required for reliable ChIP-seq peak identification for transcription factors or histone modification markers in human and mouse. The data analysis pipeline is structured according to the ENCODE Consortia Guidelines. Raw sequences, processed sequences, alignment results, ChIP-seq peaks with annotations, and QC results will be provided for the user.

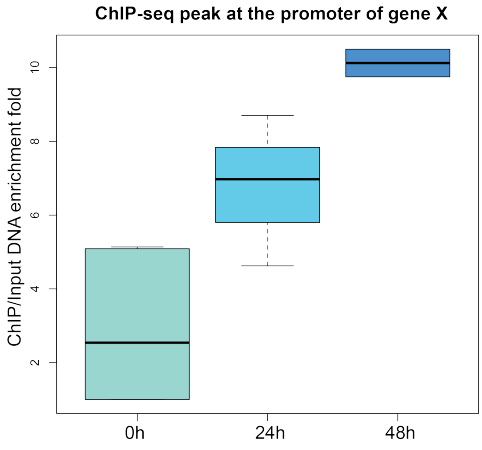


Example study

This ChIP-seq study focused on the dynamic changes of one histone modification marker for active promoters. Clear enrichment of sequence reads around transcription start site (TSS) could be observed from all ChIP samples compared with input DNA samples.



Using the fold enrichment of sequence reads of ChIP sample and matched input DNA, we could identify genes with significant changes in transcriptional regulation at three time points.



More information

NGI Order Portal: https://ngisweden.scilifelab.se

ChIP-seq data analysis pipeline:

https://github.com/SciLifeLab/NGI-ChIPseq