ChIP-Seq

1. Sample Requirements

Sample Type	Amount	Volume	Concentration	Fragment size	Purity
Enriched DNA Sample	⩾ 50 ng	⩾ 10 µL	⩾ 2 ng/µL	Main peak should be 100 bp~500 bp.	OD260/280=1.8-2.0 no degradation, no contamination

2. Sequencing Parameters

Platform	**Illumina NovaSeq 6000**
Read length	Paired-end 150 bp
Recommended sequencing depth	⩾ 20 million read pairs per sample for the species with reference genome
Data quality	Guaranteed ⩾ 80% bases with Q30 or higher
Turnaround time	Typical 4~5 weeks for 20 or fewer samples from project verification to data releasing

3. Data Analysis Contents

Standard analysis
Data quality control (get rid of reads containing adapter or with low quality; Q20, Q30, error rate distribution, GC distribution, total bases)
Mapping onto reference genome (mapping rate, reads distribution)
Peak calling
Motif prediction
Peak annotation (downstream or overlapping gene, TSS) and functional analysis of peak-associated genes (Gene Ontology, pathway)
Summary of differential peaks and functional analysis of differential peak related genes
Visualization of ChIP-seq data