ChIP-seq

Sequencing Strategy: HiSeq SE50, 100~350bp insert DNA library (depends on peak distribution)

Turnaround Time:(≤30 samples)
Without standard bioinformatics analysis: 15 working days
With standard bioinformatics analysis: 33 working days

Standard Analysis	Software
Data quality control (get rid of reads containing adapter or with low quality; Q20, Q30, error rate distribution, GC distribution, total bases)	FastQC
Mapping onto reference genome (mapping rate, reads distribution)	BWA
Peak calling	MACS2
Motif prediction	MEME
Peak annotation (downstream or overlapping gene, TSS)	PeakAnalyzer
Functional analysis of peak-associated genes (Gene Ontology, pathway)	
Visualization of ChIP_seq data	R