Prokaryotic RNA sequencing

Sequencing Strategy: HiSeq PE150, 250~300bp insertion library

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

Standard Analysis	Software
Data Quality Control: filtering reads containing adapter or with low quality	
Evaluation of Data Quality	
Mapping Reads to Reference Genome	Bowtie
Gene Expression Analysis	HTSeq
Novel Transcript Prediction	Rockhopper
Differential Expression Analysis (two or more groups of samples)	DEGSeq/DESeq/edgeR
GO Enrichment Analysis of Differentially Expressed Genes (DEGs) (two or more groups of samples)	GOSeq,topGO,hmmscan
KEGG Pathway Enrichment Analysis of Differentially Expressed Genes (DEGs) (two or more groups of samples)	KOBAS
Operon and TSS/TTS Prediction	Rockhopper
SD Sequence prediction	RBSfinder
Rho-independent Terminator Sequence Prediction	TranstermHP
sRNA Secondary Structure Prediction	RNAfold
sRNA Targeted Gene Prediction	IntaRNA