

Small RNA sequencing

Sequencing Strategy: HiSeq SE50, 18~40bp insert sRNA 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	
Summarize the length distribution of small RNA	
Analyze common and specific sequences between two samples	
Align small RNA to reference genome	Bowtie
Identify known miRNA	miREvo
Identify rRNA, tRNA, snRNA, snoRNA and Non-coding RNA	
Identify repeat associated small RNAs (repeat annotation information of the reference genome should be provided)	RepeatMasker
Align small RNA to mRNA, exon and intron	
Predict novel miRNAs and their secondary structures by Mireap from unannotated small RNAs	mirdeep2/ViennaRNA
Analyze the expression pattern of known miRNAs	
Analyze the base bias of miRNA	
Classify and annotate of small RNAs	
Advanced Analysis of Small RNA Sequencing	
Analyze correlation of miRNA expression among samples (≥2 samples)	
Analyze differentially expressed miRNA and cluster analysis among samples (≥2 samples)	
Predict target gene of miRNA	miRanda/psRobot
Gene ontology analysis of DEGs and pathway enrichment analysis of DEGs	

Standard Analysis of conjunction analysis between mRNA and miRNA	Software
Cluster analysis of the common gene between Differential Expression mRNA and Differential Expression miRNA downstream target mRNA.	
GO enrichment analysis of the common gene between Differential Expression mRNA and Differential Expression miRNA downstream target mRNA.	GOSeq/topGO
KEGG enrichment analysis of the common gene between Differential Expression mRNA and Differential Expression miRNA downstream target mRNA.	KOBAS
Interaction analysis between Differential Expression mRNA and Differential Expression miRNA.	