

Prokaryotic RNA Sequencing

1. Sample Requirements

Library Type	Sample Type	Required Amount	Volume	Concentration	RNA Integrity Number (Agilent 2100TM)	Purity (NanoDropTM)
Prokaryotic RNA Library	Total RNA	≥ 500 ng	≥ 10 μL	≥ 50 ng/μL	≥ 6.0, smooth base line	OD260/280 ≥ 2.0, OD260/230 ≥ 2.0, No degradation, No contamination

2. Sequencing Parameters

Platform	Illumina NovaSeq 6000
Read length	Paired-end 150
Recommended Sequencing Depth	2 G raw data per sample for the species with reference genome
Data quality	Guaranteed ≥ 85% bases with Q30 or higher
Turnaround time	Within 4-5 working weeks from library construction verification to data releasing without bioinformatic analysis. (depending on the sample size)

3. Data Analysis Contents

Standard analysis
Data filtering
Mapping to reference genome/assembled genome
Novel Transcript Prediction
Gene expression quantification & Differential expressed genes profiling & Functional analysis
Operon Analysis
SNP and InDel
UTR Analysis
Antisense Transcript Prediction
sRNA Analysis