Prokaryotic RNA Sequencing

1.Sample Requirements

Library Type	Sample Type	Amount	Volume	Concentration	*RIN (Agilent 2100™)	Purity (NanoDrop™)
Prokaryotic RNA Library	Total RNA	⩾ 3 μg	⩾ 20 μL	⩾ 50 ng/μL	⩾ 6.0, smooth base line	OD260/280 ⩾ 2.0, OD260/230 ⩾ 2.0, no degradation, no contamination

*RIN: RNA Integrity Number

2.Sequencing Parameters

Platform	Illumina NovaSeq 6000
Read length	Paired-end 150 bp
Recommended sequencing depth	2 G raw data per sample
Data quality	Q30 ⩾ 80%, exceeding Illumina's official benchmark of ⩾ 75%
**Turnaround time	4~5 working weeks from library construction verification to data releasing without bioinformatic analysis.

**Turnaround time varies depending on the project volume.

3.Data Analysis Contents

Standard analysis for species with reference genome
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 analysis
UTR analysis
Antisense transcript prediction
sRNA Analysis