

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	≥ 3 µg	≥ 20 µL	≥ 50 ng/µL	≥ 6.0, smooth base line	OD260/280 ≥ 2.0, OD260/230 ≥ 2.0, No degradation, No contamination

Remark: This sample requirement is for reference only. If you have any questions, please consult your local sales or Novogene support for detailed information.

2. Sequencing Parameters

Platform	Illumina NovaSeq 6000
Read length	Paired-end 150
Sequencing depth	2 G raw data per sample for the species with reference genome
Data quality	Guaranteed Q30 ≥ 80%, exceeding Illumina's official benchmark of ≥ 75%

Remark: Detailed sequencing parameters can be consulted with your local sales or Novogene support.

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

Remark: Detailed analysis contents can be consulted with your local sales or Novogene support.