

## Eukaryotic RNA Sequencing

### 1. Sample Requirements

Library Type	Sample Type	Amount	Volume	Concentration	*RIN (Agilent 2100™)	Purity (NanoDrop™)
Eukaryotic cDNA Library	Total RNA	** ≥ 0.4 µg	≥ 20 µL	≥ 20 ng/µL	≥ 6.8 (Animal), ≥ 6.3 (Plant and Fungus), with smooth base line	OD260/280 ≥ 2.0; OD260/230 ≥ 2.0; no degradation, no contamination
	Total RNA (Blood)	≥ 0.8 µg				
	Total rRNA (Single cell)	≥ 100 ng	≥ 10 µL	≥ 10 ng/µL		
	Amplified cDNA (double-stranded)	≥ 100 ng	≥ 10 µL	≥ 10 ng/µL		
Eukaryotic Strand Specific Library	Total RNA	≥ 0.8 µg	≥ 20 µL	≥ 20 ng/µL	≥ 6.8 (Animal), ≥ 6.3 (Plant and Fungus), with smooth base line	OD260/280 ≥ 2.0; OD260/230 ≥ 2.0; no degradation, no contamination

\*RIN: RNA Integrity Number

\*\*For total RNA less than 100 ng, please contact us for ultra-low input solutions.

### 2. Sequencing Parameters

Platform	Illumina NovaSeq 6000
Read length	Paired-end 150 bp
Recommended sequencing depth	≥ 20 million read pairs per sample for species with reference genome; ≥ 50 million read pairs per sample for species without reference genome (de novo transcriptome assembly)
Data quality	Q30 ≥ 80%, exceeding Illumina's official benchmark of ≥ 75%
**Turnaround time	2~3 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
Data filtering
Transcriptome assembly & Gene functional annotation (only for species without reference genome)
Mapping to reference genome/assembled genome
Gene expression quantification & Differential expressed genes profiling & Enrichment analysis
Protein-protein Interaction (PPI) analysis
Transcription factors functional annotation analysis
Oncogene functional annotation analysis
SNP & InDel analysis
Alternative splicing analysis
Fusion gene prediction (Only for tumor sample and cancer cell line)

