1. Sample Requirements

Library Type	Sample Type	Amount	Volume	Concentration	RNA Integrity Number (Agilent 2100)	Purity (NanoDrop)
Eukaryotic RNA-Seq (cDNA library)	Total RNA	≥ 0.4 μg	≥ 20 μL	≥ 20 ng/μL	≥ 6.8 (Animal), with smooth base line ≥ 6.3 (Plant and Fungus), with smooth base line	OD260/280 = 1.8-2.2; OD260/230 ≥ 1.8; No degradation, No contamination
	Total RNA (Blood)	≥ 0.8 μg				
	Total RNA (Single Cell)	≥ 100ng	≥ 20 μL	≥ 10 ng/μL		
	Amplified cDNA (double-stranded)	≥ 100ng	≥ 20 μL	≥ 20 ng/μL	Fragments between 400bp and 5000bp with main peak at ~2000bp	
Eukaryotic RNA-Seq (strand specific library)	Total RNA	≥ 0.8 μg	≥ 20 μL	≥ 20 ng/μL	≥ 6.8 (Animal), with smooth base line ≥ 6.3 (Plant and Fungus), with smooth base line	

For total RNA less than 100ng, please consult us for ultra-low input library solutions.

2. Sequencing Parameters

Platform	Illumina NovaSeq 6000
Read length	Pair-end 150
Recommended Sequencing Depth	≥20 million read pair per sample for species with reference genome; ≥50 million read pairs per sample for species without reference genome (de novo transcriptome assembly projects)
Data quality	Guaranteed Q30≥80%, exceeding Illumina's official benchmark of ≥75%
Turnaround time	Within 2-3 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
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)