Eukaryotic RNA Sequencing

1.Sample Requirements

Library Type	Sample Type	Amount	Volume	Concentration	RNA Integrity Number (Agilent 2100™)	Purity (NanoDrop™)
Eukaryotic RNA-Seq (cDNA library)	Total RNA	⩾ 400ng	⩾ 20 μL	⩾ 20 ng/μL	⩾ 6.3 (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)	⩾ 800ng				
	Total RNA (Single Cell)	⩾ 100 ng	⩾ 20 μL	⩾ 10 ng/μL		
	Amplified cDNA (double-stranded)	⩾ 100 ng	⩾ 10 μL	⩾ 10 ng/μL	Fragments should be distributed between 400bp - 5000bp with main peak at ~2000 bp	OD260/280 ⩾ 2.0 OD260/230 ⩾ 2.0; No degradation, no contamination
Eukaryotic RNA-Seq (strand specific library)	Total RNA	⩾ 800ng	⩾ 20 μL	⩾ 20 ng/μL	⩾ 6.3 (Animal), ⩾ 6.3 (Plant and Fungus), with smooth base line	OD260/280 ⩾ 2.0; OD260/230 ⩾ 2.0; No degradation, no contamination

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
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

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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)