

Whole Transcriptome Sequencing

1. Sample Requirements

Sample Type	Amount	Volume	Concentration	*RIN (Agilent 2100™)	Purity (NanoDrop™)
Total RNA	≥ 5 µg	≥ 20 µL	≥ 50 ng/µL	Animal ≥ 7.5, Plant/Fungus ≥ 7, with smooth baseline	OD260/280 = 1.8~2.2; OD260/230 ≥ 1.8; no degradation or contamination

*RIN: RNA Integrity Number

2. Sequencing Parameters

Platform	Illumina NovaSeq 6000
Read length	Paired-end 150 bp & Single-end 50 bp
Recommended sequencing depth	≥ 40 million read pair per sample (lncRNA library); ≥ 20 million read pair per sample (small RNA library);
Data quality	Guaranteed ≥ 80% bases with Q30 or higher
**Turnaround time	Within 10 weeks from project verification to data releasing without bioinformatic analysis

**Turnaround time varies depending on the project volume.

3. Data Analysis Contents

*WTS service provides standard analysis for lncRNA, mRNA, circRNA and small RNA transcripts. Detailed contents can be referred to the service introduction pages separately. Please contact us for more information.

Advanced Association Analysis	
LncRNA vs miRNA	Homology analysis of lncRNA and pro-miRNA
	Targeting relation analysis between lncRNA and mRNA
	Interaction analysis of differential miRNA and its targeted lncRNA
miRNA vs mRNA	Interaction relation analysis between differential mRNA and miRNA
	Interaction analysis of differential miRNA and its targeted mRNA
circRNA vs mRNA	Interaction analysis of circRNA and its source gene
circRNA vs miRNA	Targeting relation analysis of differential circRNA and miRNA Interaction analysis of miRNA, lncRNA and mRNA
lncRNA vs miRNA vs mRNA	Interaction analysis of miRNA, lncRNA and mRNA
circRNA vs miRNA vs mRNA	Interaction analysis of circRNA, lncRNA and mRNA