

## Whole Transcriptome Sequencing

### 1. Sample Requirements

Library Type	Sample Type	Amount	Volume	Concentration	RNA Integrity Number (Agilent 2100)	Purity (NanoDrop™)
lncRNA library & Small RNA library	Total RNA	≥ 3 µg	≥ 30 µL	≥ 50 ng/µL	Animal ≥ 7.5, Plant ≥ 7, with smooth baseline	OD260/280 ≥ 2.0; OD260/230 ≥ 2.0; no degradation, no contamination
lncRNA library & Small RNA library & CircRNA library	Total RNA	≥ 5 µg	≥ 50 µL	≥ 50 ng/µL		

### 2. Sequencing Parameters

Platform	Illumina NovaSeq 6000
Read length	Paired-end 150 & Single-end 50
Recommended Sequencing Depth	≥ 40 million read pair per sample (lncRNA library); ≥ 20 million read pair per sample (small RNA library);
Data quality	Guaranteed ≥ 85% bases with Q30 or higher
Turnaround time	Within 10 weeks from project verification to data releasing without bioinformatic analysis

### 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