1. Sample Requirements

Sample Type	Remarks	Amount	RIN	Volume	Concentration	Purity
			(Agilent 2100TM)			(NanoDropTM/Agarose gel)
Total RNA	Strongly Recommended	≥ 10 μg	Animal ≥ 7, Plant ≥ 6.5, with smooth baseline	≥ 20 μL	≥ 50 ng/μL	OD260/280≥2.0;
	Required	≥ 5 μg				No degradation or DNA contamination

2. Sequencing Parameters

Platform	Illumina Novaseq 6000
Read length	Paired-end 150
Recommended Sequencing Depth	≥40 million read pair per sample
Data quality	Guaranteed ≥80% bases with Q30 or higher
Turnaround time	Within 24 working days from project verification to data releasing without bioinformatic analysis

Note: For sequencing depth, the sequencing depth could be customized according to the project needs. Please contact us for more detail information.

3. Data Analysis Contents

Standard Analysis (for Species with Reference)	
Data Quality Control: Filtering reads containing adapter or uncertain nucleotides or of low quality, and statistic summary of data quality	
Mapping Clean Reads to Reference Genome	
circRNA Identification	Length Distribution of circRNAs
	Sources of circRNAs
	Distribution of circRNA on the Chromosomes

Transcript Expression Quantification	
Correlation Analysis Between Groups (Only for Samples with biological replicates)	
Differential Expression Analysis (Only for Compared Groupings)	
Functional Analysis of Differentially Expressed circRNA Source Genes (Only for Compared Groupings)	Gene Ontology (GO) Enrichment Analysis
	Kyoto Encyclopedia of Genes and Genomes (KEGG) Pathway Enrichment Analysis
CircRNA Target Gene Prediction	