

Isoform Sequencing (Full-length Transcript Sequencing)

1. Sample Requirements

Sample Type	Amount	Volume	Concentration	*RIN (Agilent 2100™)	Purity (NanoDrop™)
Total RNA	≥ 5 µg	≥ 20 µL	≥ 300 ng/µL	≥ 9, with smooth baseline; 28S/18S ≥ 1.5	OD260/280 = 1.8-2.2; OD260/230 ≥ 1.8; no degradation or contamination

Remark: This sample requirement is for reference only. If you have any questions, please consult your local sales or Novogene support for detailed information.

2. Sequencing Parameters

Platform	PacBio Sequel system
Sequencing depth	≥ 15 G bases pair per sample

Remark: Detailed sequencing parameters can be consulted with your local sales or Novogene support.

3. Data Analysis Contents

Standard Analysis (for Species with Reference)	
(1) Data quality control	
(2) Identification, clustering and correction of full-length transcripts	
(3) Mapping reads to reference genome	
(4) Prediction and annotation (GO, Swiss-Prot) of novel transcripts	
(5) Structural Analysis of Isoforms	Fusion transcript analysis
	Alternative splicing
	Alternative polyadenylation
	TTS & TSS prediction
(6) Transcription factor analysis	
(7) lncRNA prediction	
(8) Differential expression analysis (Only for Compared Groupings)	Isoform quantification and differential expression analysis
	GO enrichment
	KEGG enrichment

Standard Analysis (for Species without Reference)	
(1) Data quality control	
(2) Identification, cluster and correction of full-length transcripts	
(3) Simple Sequence Repeat (SSR) analysis	
(4) Functional annotation (via Nr, Nt, KEGG, GO, KOG, Swiss-Prot and Pfam databases)	
(5) Transcription factor analysis (only for plants and animals species)	
(6) Differential expression analysis (Only for Compared Groupings)	Isoform quantification and differential expression analysis
	GO enrichment
	KEGG enrichment

Remark: Detailed analysis contents can be consulted with your local sales or Novogene support.