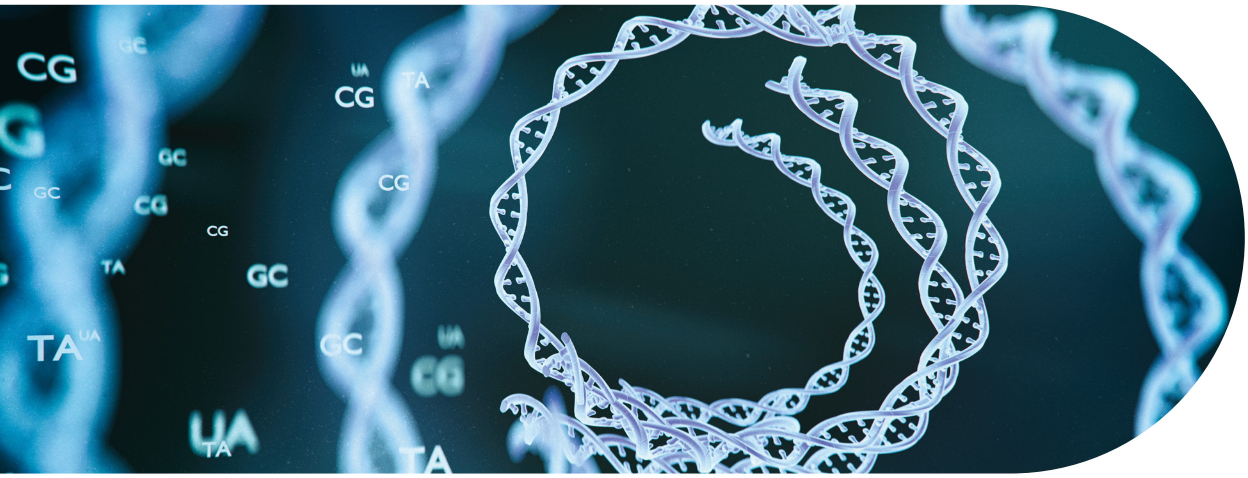
Isoform Sequencing



Isoform Sequencing Service (Iso-Seq), based on cutting-edge PacBio SMRT (Single Molecule, Real-Time) technology, enables full-length reads being sequenced of entire transcript from 5’ UTR to 3’ polyadenylation without assembly required. The isoform sequencing offers precise detection of native transcript structures, allowing for comprehensive analysis, such as characterizing fusion genes, identifying alternative splicing, annotating genomes, and discovering novel transcripts.

Kinnex full-length RNA Kit provides an ultra-high-throughput solution compared to the original Iso-Seq method. It employs the MAS-Seq technique, which concatenates smaller amplicons into larger fragment libraries, significantly enhancing throughput. Combined with the PacBio Revio system, Novogene offers a highly cost-effective service for your transcriptome research.

Our Key Features & Advantages

PacBio HiFi Long-Read Sequencing

- HiFi data with base accuracy >99.9%.
- Accurate characterization of full-length transcript isoforms.

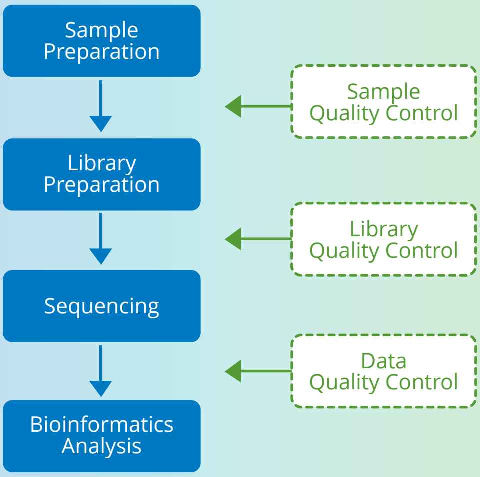
Comprehensive Analysis Pipeline

- Tailored analysis available for species with or without a reference genome.

Real-time Project Management

- 24/7 real-time Customer Service System (CSS).

Project Workflow



Sample Requirements

Library Type	Sample Type	Amount	Volume	Concentration	RIN (Agilent 2100)	Purity (NanoDrop™)
PacBio Kinnex full-length RNA library	Total RNA	≥ 1.2 ug	≥ 30 μL	≥ 40 ng/μL	≥ 6.5 with flat baseline	OD260/280=1.8-2.2; OD260/230=1.3-2.5; NC/QC* ≤ 2

*NC/QC: NanoDrop concentration/Qubit concentration

Analysis Content

<table>
<tr><th>Standard Analysis
Eukaryotic species with reference genome</th><th>Standard Analysis
Eukaryotic species without reference genome</th></tr>
<tr><td colspan="2">Recommended data volume:
· 5M HiFi reads/ sample: Isoform discovery of highly expressed transcripts; comprehensive transcript annotation in a species.
· 10M HiFi reads/ sample: Isoform discovery and quantification of moderate-to-rare transcripts.</td></tr>
<tr><td>1. Alternative splicing
2. Alternative polyadenylation
3. Novel gene/ Novel transcript prediction and annotation
4. Transcription factor analysis
5. LncRNA prediction
6. Fusion transcript analysis
7. Gene/ Transcript expression level analysis
8. Differentially expressed gene/ transcript analysis</td><td>1. Prediction of coding sequences
2. Transcription factor analysis
3. SSR analysis
4. LncRNA prediction
5. Gene expression level analysis
6. Differentially expressed gene analysis</td></tr>
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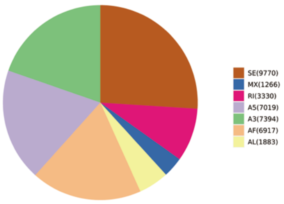
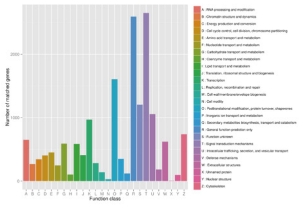
Demo Analysis Result

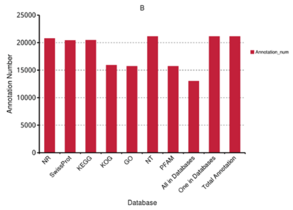


Alternative splicing detection

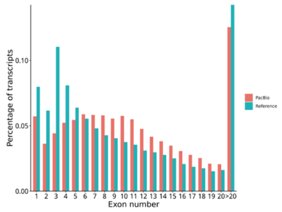
Circos plot of fusion genes



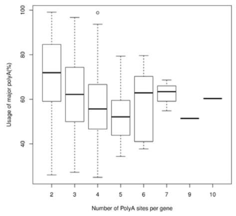
KOG function annotation



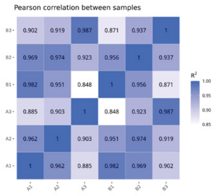
Function annotation summary



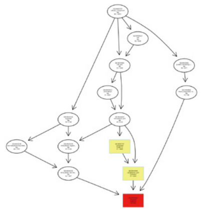
Exon number distribution of each transcript



Poly(A) site analysis



Correlation analysis of gene expression level



Directed Acyclic Graph of GO enrichment analysis

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