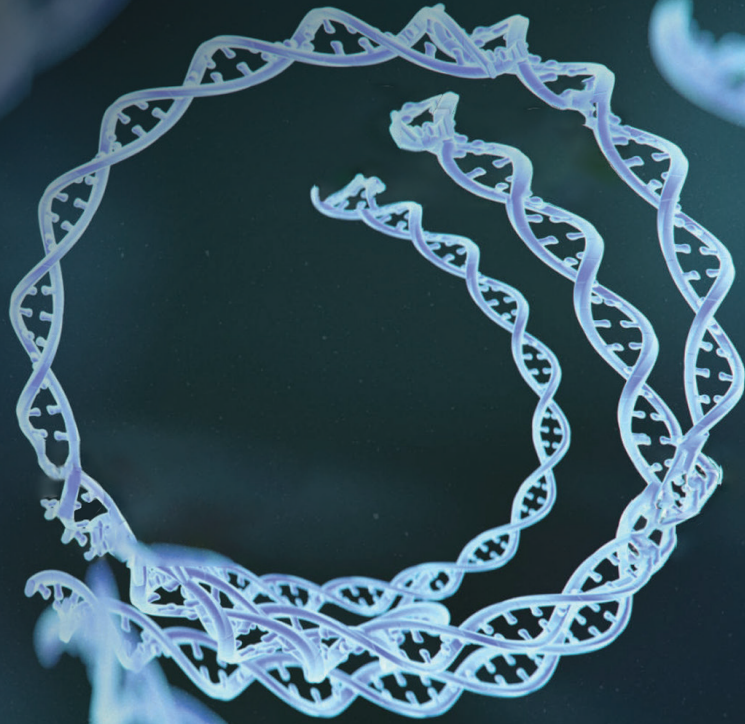


## Isoform Sequencing



**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 isoforms from 5' UTR to 3' polyadenylation without assembly required.

Iso-seq is an ultra-high-throughput method for characterizing gene fusion, alternative splicing, and gene fusion events, and improving annotations for genomes, and discovering novel transcripts by complementing the potential error by the short reads.

### Applications

**Medical Research:** Transcript annotation; Fusion gene exploration; Disease mechanism investigation

**Agricultural Research:** Functional study; Fusion gene exploration, Development and stress study, Collaboration for gene prediction and genome annotation

### Our Key Features & Advantages



#### Largest Sequencing Capacity

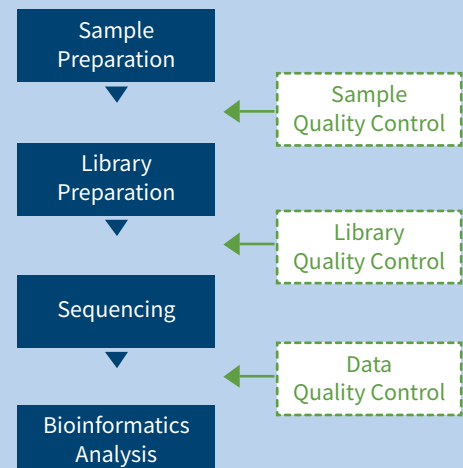
We have the largest Illumina and PacBio sequencing capacity globally, allowing us to provide high-quality data and faster turnaround time at affordable prices.



#### Comprehensive Data Analysis

We use industry-standard software and a mature in-house pipeline to discover novel transcripts, differential expressions, and function annotations.

### Project Workflow



## Sample Requirements

Library Type	Sample Type	Amount	Volume	Concentration	RNA Integrity Number (Agilent 2100)	Purity NanoDrop
PacBio Sequel II/IIe RNA Library	Total RNA	≥ 600 ng	≥ 20 µl	≥ 40 ng/µl	≥ 6.5, smooth baseline	OD260/280 = 1.8-2.2; OD260/230 = 1.3-2.5

## Standard Analysis Content

Platform	PacBio Sequel II(e) System	
Recommended Sequencing Depth	≥ 20 Gb subreads per sample	
Standard Data Analysis	For Species with Reference Genome	For Species without Reference Genome
	<ul style="list-style-type: none"> <li>· Data quality control</li> <li>· Identification, clustering and correction of full-length transcripts</li> <li>· Alternative splicing analysis</li> <li>· Prediction and annotation of novel gene and novel genes and novel transcripts</li> <li>· Fusion transcript analysis</li> <li>· Alternative Polyadenylation</li> <li>· lncRNA prediction</li> <li>· Quantification and differential expression analysis (base NGS data)</li> <li>· Functional enrichment analysis (base NGS data)</li> </ul>	<ul style="list-style-type: none"> <li>· Data quality control</li> <li>· Identification, clustering and correction of full-length transcripts</li> <li>· Simple Sequence Repeat (SSR) analysis</li> <li>· Functional annotation of transcripts</li> <li>· Quantification and differential expression Analysis (base NGS data)</li> <li>· Functional enrichment analysis (base NGS data)</li> </ul>

## Publications

Listed below are some publications that were supported by Novogene solutions.

Journal	IF	Title
BMC Genomics	3.65	PacBio single molecule long-read sequencing provides insight into the complexity and diversity of the <i>Pinctada fucata martensii</i> transcriptome (2020.07)
Frontiers in Genetics	3.258	Isoform Sequencing Provides Insight Into Freezing Response of Common Wheat ( <i>Triticum aestivum</i> L.) (2020.06)
International Journal of Molecular Sciences	4.65	Full-Length Transcriptome Assembly of Italian Ryegrass Root Integrated with RNA-Seq to Identify Genes in Response to Plant Cadmium Stress (2020.02)
Frontiers in Genetics	3.258	Third-Generation Sequencing Reveals lncRNA-Regulated HSP Genes in the <i>Populus x canadensis</i> Moench Heat Stress Response (2020.07)

### NovogeneAIT Genomics Singapore Pte. Ltd.

(Regional office for Asia Pacific, Middle-East & Africa)

[novogene.com/amea-en](https://www.novogene.com/amea-en)    [marketing\\_amea@novogeneait.sg](mailto:marketing_amea@novogeneait.sg)

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