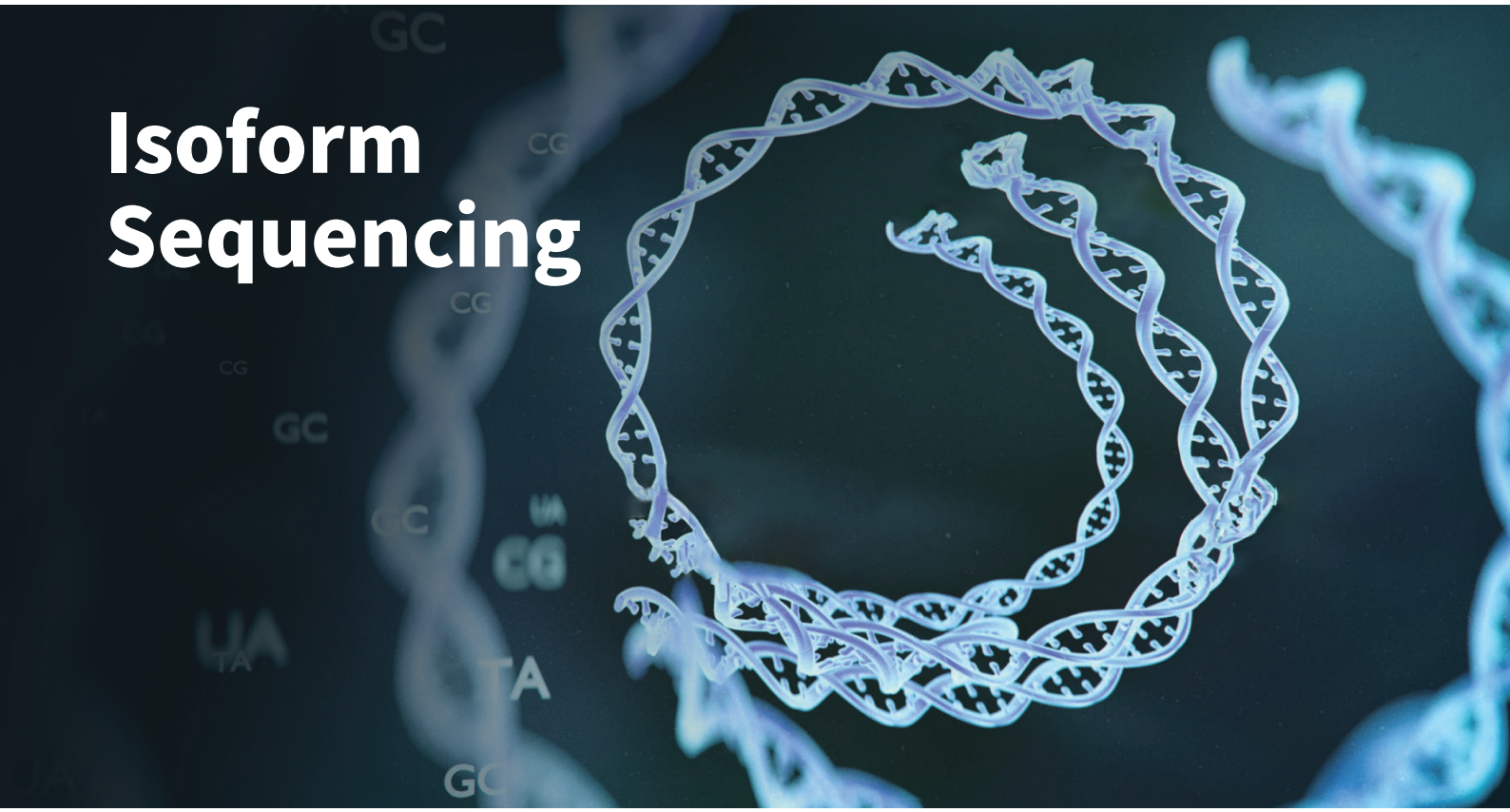
Novogene

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.

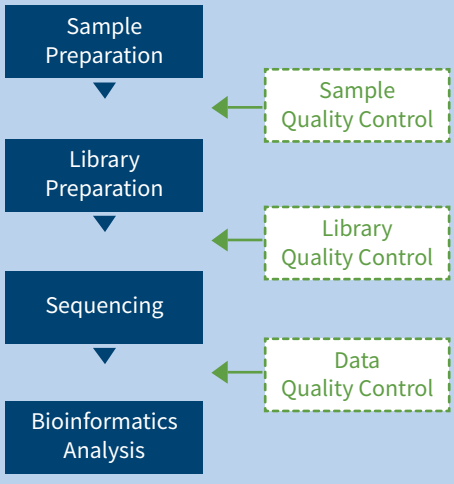
Iso-seq is an ultra-high-throughput method for characterizing gene fusion, alternative splicing, and gene fusion events, and improving annotations for genomes, and discovering novel transcripts by complementing the potential error by the short reads.

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

Project Workflow



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.

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**
	· Data quality control · Identification, clustering and correction of full-length transcripts · Alternative splicing analysis · Prediction and annotation of novel gene and novel genes and novel transcripts · Fusion transcript analysis · Alternative Polyadenylation · lncRNA prediction · Quantification and differential expression analysis (base NGS data) · Functional enrichment analysis (base NGS data)	· Data quality control · Identification, clustering and correction of full-length transcripts · Simple Sequence Repeat (SSR) analysis · Functional annotation of transcripts · Quantification and differential expression Analysis (base NGS data) · Functional enrichment analysis (base NGS data)

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 Pinctada fucata martensii transcriptome (2020.07)
Frontiers in Genetics	3.258	Isoform Sequencing Provides Insight Into Freezing Response of Common Wheat (Triticum aestivum 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 Populus x canadensis Moench Heat Stress Response (2020.07)

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