

Isoform Sequencing Solutions



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

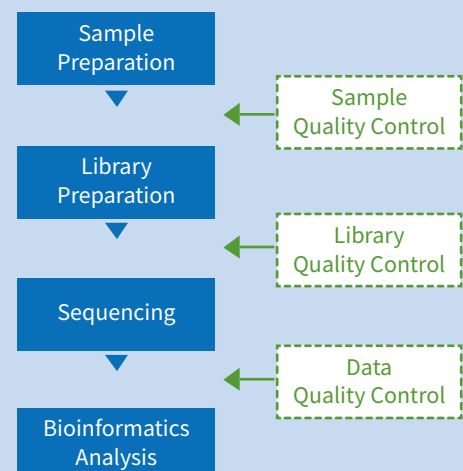
We have the largest Illumina and PacBio sequencing capacity globally, allowing us to provide high-quality data and faster turnaround time at affordable prices.



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 | RNA Integrity Number (Agilent 2100) | Purity NanoDrop |
|------------------|-------------|-----------------------------------------------------------|---------------------------------------------|------------------------------------------|
| SMRTbell Library | Total RNA | ≥ 2 µg (Concentration ≥ 30 ng / µl, Volume ≥ 50 µl) | ≥ 7, with smooth baseline; 28S/18S ≥ 1.5 | OD260/280 = 1.8-2.2; OD260/230 ≥ 1.8; |

Standard Analysis Content

| Platform | PacBio Sequel II System | |
|------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| Recommended Sequencing Depth | ≥ 20 G bases pair per sample | |
| Standard Data Analysis | For Species with Reference | For Species without Reference |
| | <ul style="list-style-type: none"> · 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) | <ul style="list-style-type: none"> · 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 <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) |

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