Novogene

Solve the Mysteries of Life Sciences with PacBio Sequel II/IIe/Revio Sequencing Service

Highly Accurate Long Reads, Single Molecule, Real-Time (SMRT) Sequencing Technology

Advancing Genomics, Improving Life

About Novogene

Novogene Corporation Inc.

Founded in 2011, Novogene is a leading provider of genomic services and solutions with cutting edge next-generation sequencing (NGS) and bioinformatics expertise. The company has become a world-leader in NGS services, with 2,000+ employees and multiple locations (China, US, UK, and Singapore) across the globe.

The UC Davis location of Novogene Corporation Inc. was opened in early 2016. We utilize Illumina platform to serve customers in North and South America, and we also offer PacBio and Nanopore services. Novogene Corporation Inc. is proud to have collaborated with scientists from the USA, Canada, Brazil, Colombia, Mexico, and so many more. We are excited to see this global collaboration and partnership growing.

13 Years	6,950+	20,000+	120,000+
of careful work	global customers	SCI articles*	cumulative impact factor*

*Include publications powered by Novogene and published in collaboration with Novogene.

2014 Novogene
2016 UC Davis Lab

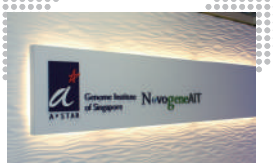
2011 Beijing HQ

Novogene Netherlands

2022 San Jose Lab

2014 Tianjin research and CAP lab

2014 Novogene UK
2018 Cambridge Lab



2016 NovogeneAIT
2016 Singapore Lab

2013 Novogene
Hong Kong

2017 Nanjing

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Exclusive for Clients in North and South America.

Services at a glance

What Can Novogene Provide?

Novogene offers a range of NGS-based and TGS-based* services for human, plant, animal, and microbial DNA and RNA analysis at highly competitive prices. (*NGS: Next Generation Sequencing; TGS: Third Generation Sequencing)

Whole Genome Sequencing

- Re-Sequencing
  -Variation Calling of SNV, InDel, CNV and SV
  -Good Coverage of High Repetitive and Complex Area
  -NO GC or Amplification Bias

De novo Genome Assembly

- Generate Gold-Standard Reference Genomes as Genetic Underpinning
- Improve Current Reference Version
  -Bacteria Complete or Fungi Fine Map
  - High Contiguity, Integrity and Accuracy

Full-length Isoform Sequencing

- Full-Length transcript from 5'UTR to 3'UTR with poly(A) tail
  -Genome Annotation
  -Complete review of Transcript Isoform Diversity

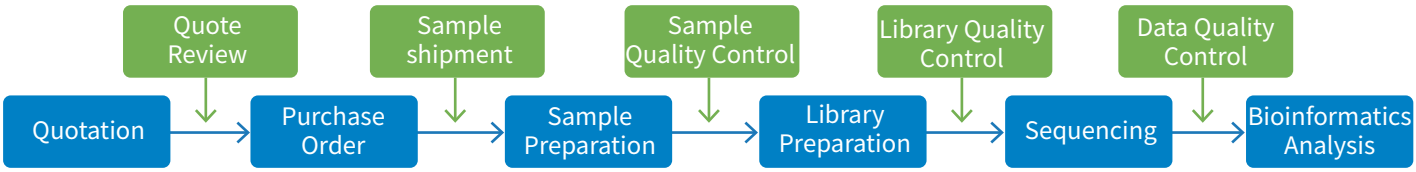
Full-Length 16S Amplicon Metagenomic Sequencing

- Full-length 16S sequences (V1–V9)
  -Reveal Microbial Diversity with highly accurate, strain-level resolution

Epigenetics

- Simultaneous Epigenetic Characterization
  - CpG, CHH, CHG, 6mA, 4mC, 5hmC
  - Direct 5mC Calling with HIFI reads with SMRT LINK V11

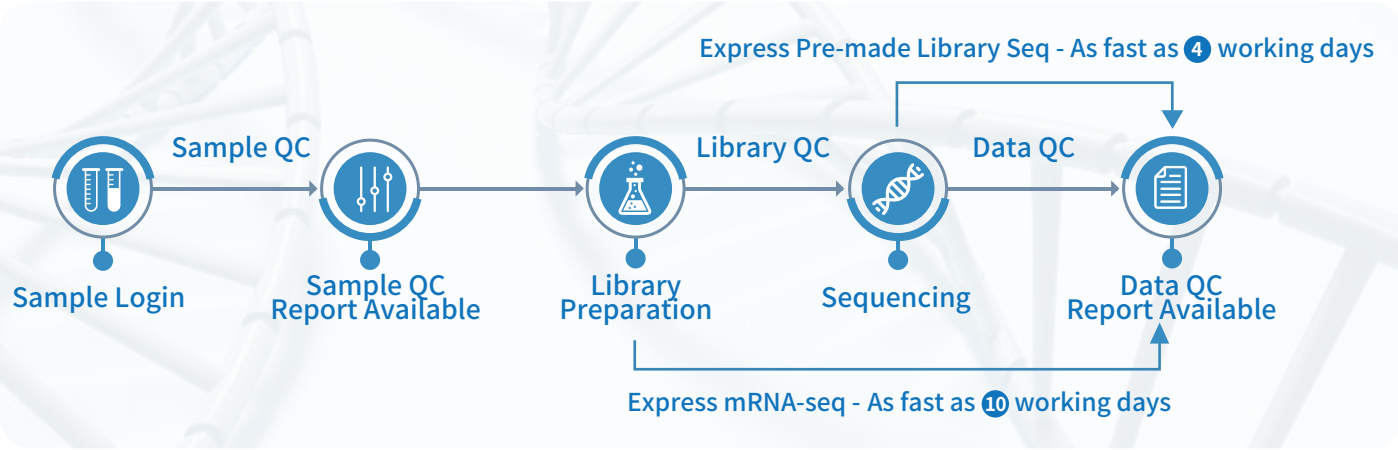
Project Workflow



Core Capability

An Intelligent and Flexible NGS Delivery Platform - Falcon II

Leveraging years of sequencing expertise and technology accumulation, Novogene will continue to propel the digitalization and intelligentization of genomic sequencing industry, and strive for revolutionary breakthroughs in delivery time, data quality, and production stability.



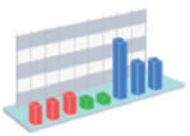
Novogene NovoMagic
Your Totally-Free Aftersales Analysis Assistant

Products Included

"Human mRNA-seq" projects and "Plant and Animal Eukaryotic mRNA-seq with reference" projects. In the future, Novogene will gradually launch other products on NovoMagic.

Analysis Contents Included

NovoMagic can support you to select specific group of genes, analyze gene expression, identify differentially expressed genes and perform gene function analysis. Overall, 17 small tool kits are offered In the Toolkit item.
In the future, Novogene will gradually launch more toolkits on NovoMagic.

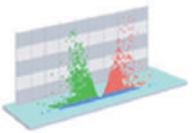


GO Plot

Gene Ontology enrichment based on the customized parameters

Venn Diagram

Plot Venn diagram based on gene ID list or gene expression quantity table



Volcano Plot

Make Volcano plot based on customized threshold

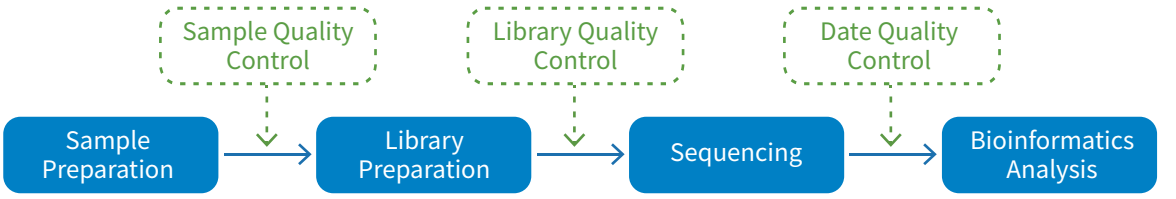
And more…

Novogene PacBio Sequel II/IIe/Revio Sequencing Service

Novogene provides Sequel II/IIe/Revio Sequencing Service which is powered by Single Molecule, Real-Time (SMRT) Sequencing technology and generating longer reads with greater accuracy. The PacBio Sequel II/IIe/Revio Systems and their cost-effective sequencing applications make it more affordable for all scientists to drive discovery with comprehensive views of genomes, transcriptomes, and epigenomes.

Applications

Project Workflow



Service Highlights

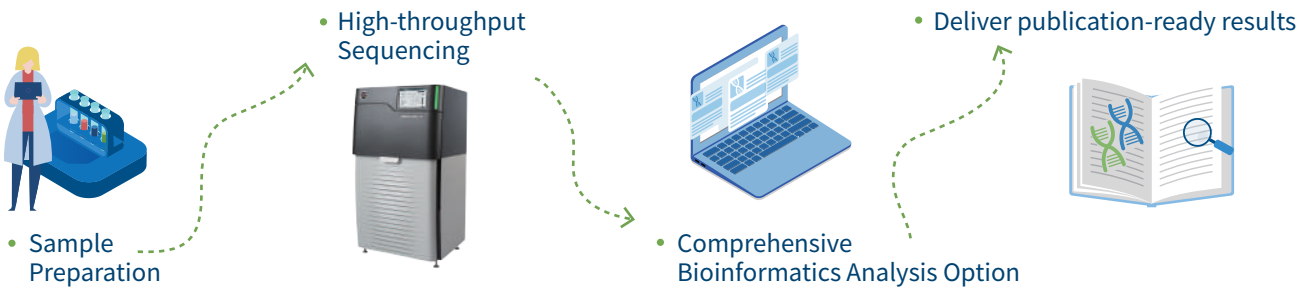
Long Read Length
- Direct access to High-fidelity (HiFi) Long Reads and Continuous Long Reads (CLRs)

Single-Molecule Resolution
- Sequence DNA or RNA

Highly accurate
- Achieves ⩾99.9% (Q30) consensus accuracy (HiFi)

Uniform Coverage
- No DNA amplification
  Least GC content and sequence complexity bias

One-stop service



Plant and Animal Whole Genome Resequencing

SMRT Sequencing provides comprehensive detection of variants in a genome including single nucleotide variants (SNVs), InDel, structural variants (SVs), and copy number variants (CNVs), even in difficult-to-map repetitive regions. PacBio highly accurate long reads let you generate complete and phased human genome assemblies of diverse populations to better understand the complexity of health and disease.

Sample Requirements

Sample Type	Amount	Volume	Concentration	DNA size	Purity / Size (NanoDrop Purity TM/Agarose Gel)
HMW Genomic DNA (HiFi library)	⩾5 μg	⩾50 μL	⩾70 ng/μL	Fragments should be ⩾ 30K	OD260/280=1.75~2.0; OD260/230=1.5~2.6; NC/QC=1.00~2.20 no degradation, no contamination
HMW Genomic DNA (CLR library)	⩾5 μg	⩾50 μL	⩾70 ng/μL	Fragments should be ⩾ 30K	OD260/280=1.75~2.0; OD260/230=1.5~2.6; NC/QC=0.95~3.00 no degradation, no contamination

Specifications

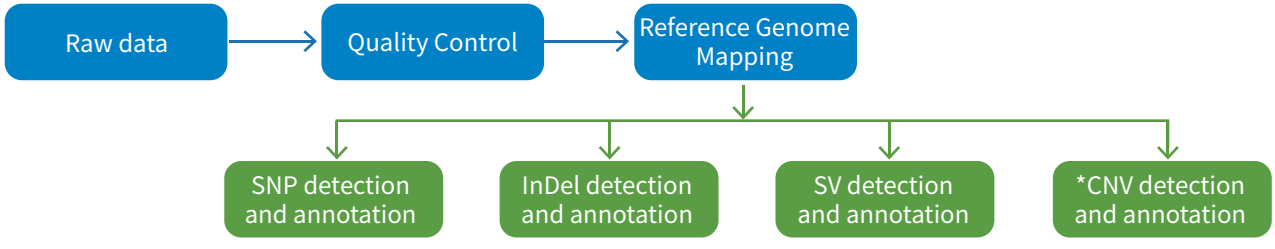
Library type: HiFi library >15 kb
Data output: ~25Gb/90Gb HiFi reads/cell

Recommended sequencing depth:
SNV, SV, CNVs detection: ⩾ 15x
SNP/InDel detection: ⩾ 30×
Data accuracy: Q30

Library type: CLR library >25 kb
Data output: 75Gb~100Gb subreads/cell

Recommended sequencing depth:
SNV, SV, CNVs detection: ⩾ 15x
Data accuracy: Q20

Analysis Pipeline



* CNV detection and annotation is only for human sample

DE NOVO Genome Assembly

With de novo sequencing, the first genome map for a species is generated, providing a valuable reference sequence for phylo-genetic studies, analysis of species diversity, mapping of specific traits and genetic markers, and any other genomics research. Large and complex genomes present unique challenges such as polyploidy and high levels of heterozygosity. PacBio offers the long reads with high accuracy necessary to overcome these challenges and help researchers to generate gold-standard reference genomes.

Specifications

- Microbial *De Novo* Assembly

  Library type: microbial CLR library >12kb
  Recommended sequencing depth: ⩾ 100x
  Data accuracy: Q20

- Plant and Animal *De Novo* Assembly

  Library type: HiFi library >15kb
  Recommended sequencing depth: ⩾ 30x
  Data output: ~25Gb/90Gb HiFi reads/cell
  Data accuracy: Q30

Advantages and Highlights

- **Highly experienced**

  Over 1000 *de novo* genome sequencing projects completed, with associated data published in hight impact journals.

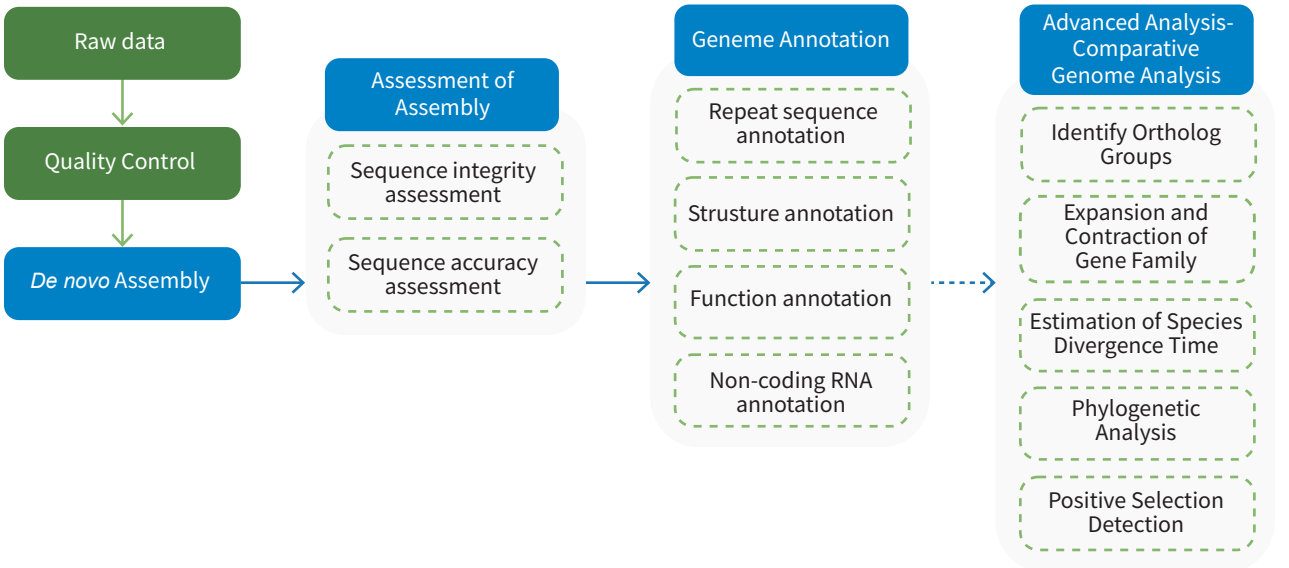
- **Bioinformatics expertise**

  Best-in-class and widely recognized software, such as Hifiasm, Hificanu and Falcon, used for De novo assembly bioinformatic analysis.

- **Diversification strategies**

  We incorporate sequencing results from various platforms including Illumina Novaseq, Sequel II/IIe/Revio and Nanopore to offer the best assembly solution tailored towards each unique genome.

Analysis Pipeline



Full-length 16S Amplicon Metagenomic Sequencing

Full-length 16S Amplicon Metagenomic Sequencing is frequently used to identify and differentiate microbial species. Pacbio Sequel Systems are powered by Single Molecule Real-Time (SMRT) sequencing technology and deliver highly accurate long reads. Using the PacBio Sequel, full-length 16S amplicon sequencing resolves the limitations of short read lengths (e.g. shattered gene distribution and minor hypervariable region coverage) in next generation sequencing (NGS), and improves the resolution of the strain.

Advantages and Highlights

- **High Resolution**

  Guaranteed >99.9% single-molecule sequencing accuracy enables more accurate species classification and more low-abundant species discovery

- **Clean Reads Delivery In WBI Option***

  Our advanced filters help you get rid of primers and chimeras in raw reads. 5,000 or 10,000 clean CCS reads per sample enables more efficient data analysis (*Clean reads are delivered only for with bioinformatics (WBI) projects)

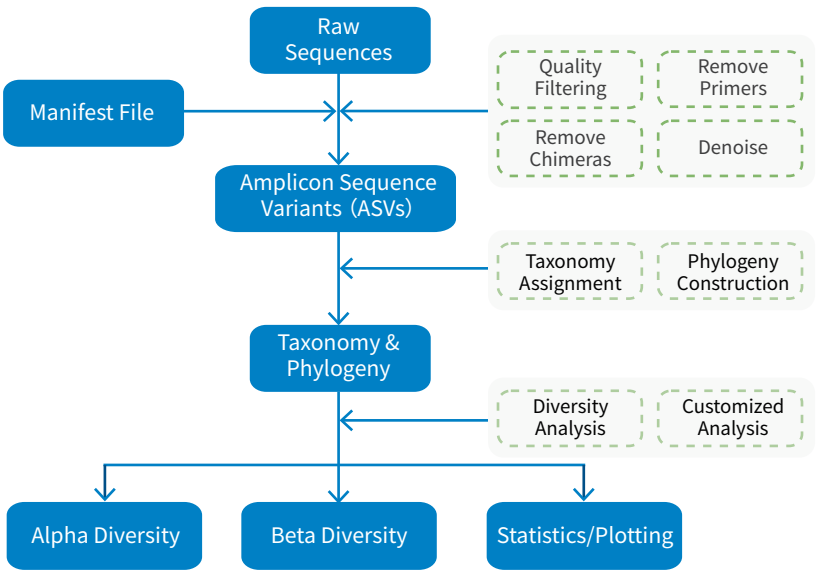
- **Updated Analysis Software**

  Amplicon Sequence Variants (ASV) generated from QIIME 2 software infer the biological sequences in the sample prior to the introduction of amplification, can distinguish as little as one nucleotide difference

Sample Requirements

SAMPLE TYPE	AMOUNT	CONCENTRATION	VOLUME	PURITY
Environmental gDNA	⩾ 200 ng	⩾10 ng/μL	⩾ 20 μL	OD260/280=1.8-2.0, no degradation, no RNA or protein contamination

Analysis Pipeline



Full-length 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 discovery of novel transcripts by complementing for the potential error by the short reads.

Sample Requirements

AMOUNT (QUBIT®)	CONCENTRATION (QUBIT®)	A260/280	A260/230	NC/QC	RNA INTEGRITY NUMBER (AGILENT 2100)	PURITY (NANODROP™/ AGAROSE GEL)
⩾ 600 ng	⩾ 40 ng/uL	1.8~2.2	1.3-2.5	⩽ 2.0	⩾6.5, with the smooth baseline	No degradation, no contamination

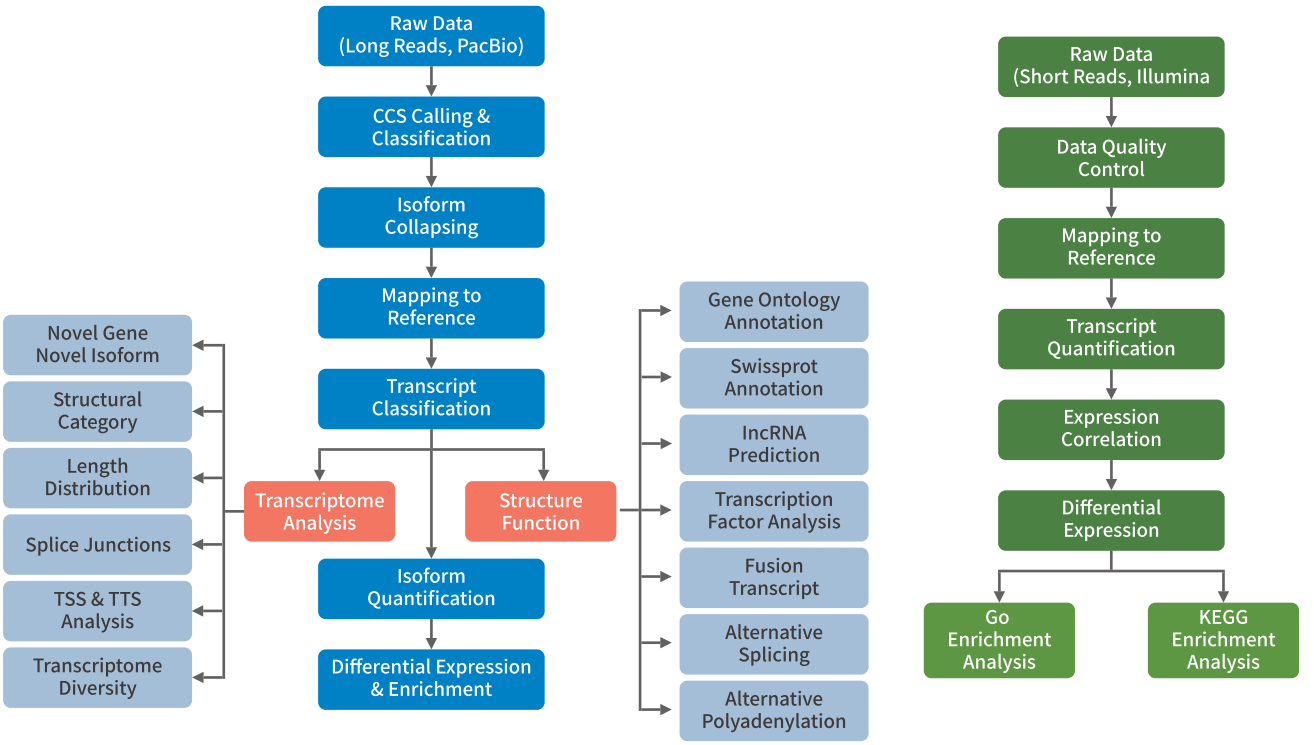
Specifications

LIBRARY TYPE: Full-length cDNA library

SEQUENCING PLATFORM: PacBio Sequel II/IIe and Revio platforms

RECOMMENDED DATA OUTPUT: ⩾ 30G Raw Data / Sample

Analysis Pipeline



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