Novogene

Oxford Nanopore DNA Sequencing Service

Long-read, Real-time Nanopore Sequencing Technology

Advancing Genomics, Improving Life

Oxford Nanopore DNA Sequencing Service

Novogene's real-time nanopore sequencing service offers advantages in all areas of research by providing long read lengths, comprehensive analysis, and insights into *de novo* assembly, large structural variations, repetitive regions, haplotype phasing, and more.

Novogene Advantages

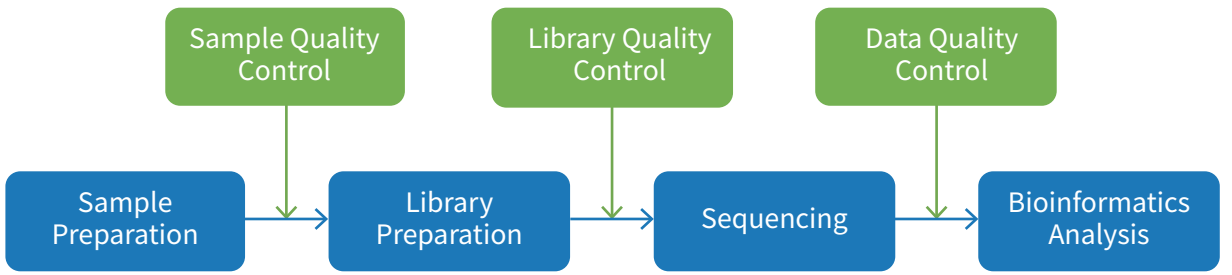
Extensive experience in Nanopore sequencing with over 100 species sequenced

High quality data, delivered as FASTQ files at a competitive price

Service Highlights

- Sequencing : PromethION
- Direct DNA sequencing: without PCR amplification and GC bias
- Long read length: N50 > 25 kb, with some reads > 1 Mb
- Turnaround time: 28 working days, after sample passing QC

Project Workflow



Applications

- Human Whole Genome Resequencing
- Plant and Animal Whole Genome Resequencing

A

Human Whole Genome Resequencing

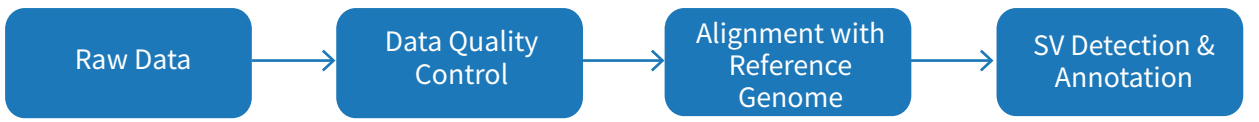
Novogene offers human whole genome sequencing (WGS) service with Nanopore PromethION at multiple coverage levels, accurately resolving structural variants, breakpoints, and repeat regions, and providing comprehensive solutions for disease mechanism studies, cancer research, and haplotype studies.

Specifications

Sample Requirements *	
Sample Type: HMW DNA	DNA Amount: ⩾ 8 μg
DNA Concentration: ⩾ 100 ng/μL	Purity: no degradation and no contamination (RNA or protein)
* For tissue samples, please contact us for more information.	

Recommended Sequencing Depth	
For Genetic Diseases: ⩾10×	For Tumor: ⩾20×

Analysis Pipeline

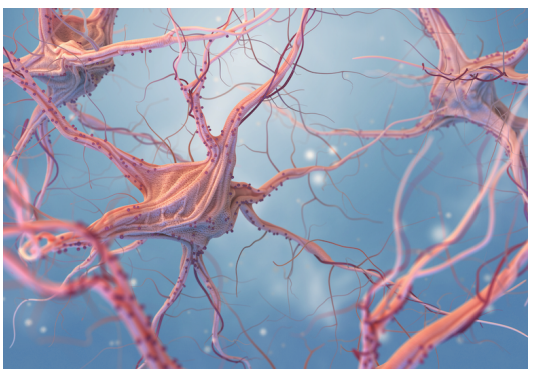


Case Study

Expansions of intronic TTTCA and TTTTA repeats in benign adult familial myoclonic epilepsy (Ishiura *et al,* 2018)

Sequencing Strategy:

- Nanopore long-read sequencing by MinION
- SMRT sequencing by PacBio RSII
- Illumina sequencing by HiSeq platform



Conclusions:

By using the third-generation sequencing on Nanopore and PacBio platform, the results revealed that expansions of noncoding TTTCA repeats in SAMD12, TNRC6A and RAPGEF2 cause BAFME, which should extend insights into the molecular bases of epilepsies and lead to the development of efficacious therapeutic measures for BAFME based on the elucidated molecular mechanisms of the diseases.

Reference : Ishiura H, Doi K, Mitsui J, *et al.* Expansions of intronic TTTCA and TTTTA repeats in benign adult familial myoclonic epilepsy[J]. *Nature Genetics*, 2018, 50: 581–590.

B

Plant and Animal Whole Genome Resequencing

Novogene is highly experienced (over 1200 projects in 2019) in applications of WGS for characterizing plant and animal variants. With the Oxford Nanopore platform and our expert bioinformatics analysis, we provide comprehensive detection of structural variants in a genome. Increased variant detection improves the ability to link genetics to phenotypes of interests for the novel discovery of genes, causative variants, and mapping loci associated with specific traits.

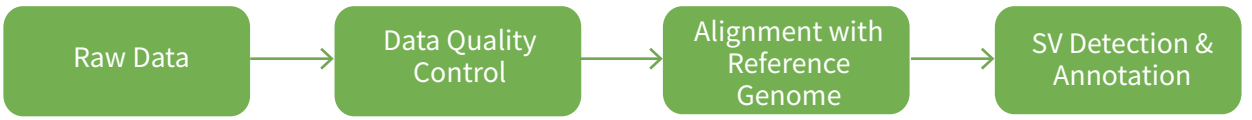
Specifications

Sample Requirements *	
Sample Type: HMW DNA	DNA Amount: ⩾ 8 μg
DNA Concentration: ⩾ 100 ng/μL	Purity: no degradation and no contamination (RNA or protein)

* For tissue samples, please contact us for more information.

Recommended Sequencing Depth
⩾ 10×

Analysis Pipeline



Case Study

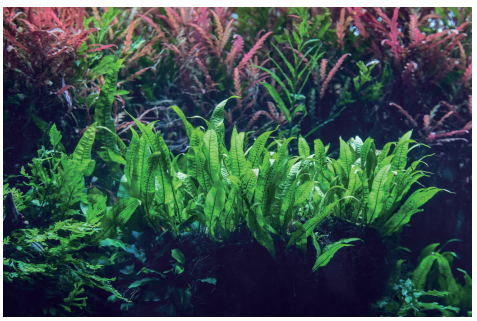
Promising prospects of nanopore sequencing for algal hologenomics and structural variation discovery (Sauvage *et al,* 2019)

Sequencing Strategy:

- Nanopore long-read sequencing by MinION
- Illumina sequencing by HiSeq platform

Conclusions:

This findings relying on a very modest number of nanopore R9 reads as compared to current output with newer chemistries demonstrate the promising prospects of the technology for the assembly and profiling of an algal hologenome and resolution of structural variation.



Reference : Sauvage T, Schmidt WE, Yoon HS,*et al.* Promising prospects of nanopore sequencing for algal hologenomics and structural variation discovery[J]. *BMC Genomics*, 2019, 20: 850.

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