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Accelerate your genomic research with long-read sequencing technology

The development of long-read sequencing technologies has revolutionised genomic studies in fields such as evolution, cancer research, rare disease studies and population analysis. Many genes involved in these areas of research are located in genomic regions of high structural variation, making them difficult to sequence due to the presence of tandem repeats or high GC content. Long-read technology can unravel the sequence of these hypervariable regions, facilitating the investigation of disease and drug resistance mechanisms and the discovery of regulatory and structural elements. Long-read platforms also facilitate the detection of alternative splicing isoforms and direct detection of epigenetic modifications.

Novogene's long-read sequencing services are powered by the latest PacBio and Oxford Nanopore platforms. With the **PacBio Sequel II, IIe, and Revio** at our disposal, along with the **Oxford Nanopore PromethION,** we utilise our deep scientific knowledge, first-class customer service and unsurpassed data quality to provide a full range of long-read sequencing services.

ADVANCING GENOMICS
IMPROVING LIFE

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PacBio Sequencing Solutions

PacBio sequencing platforms use single-molecule real-time (SMRT) sequencing to produce accurate long reads of DNA molecules or full-length RNA molecules. A SMRT cell is a sequencing chip that contains many small pores called zero-mode waveguides (ZMWs) in which a DNA polymerase is immobilised to read sequences of libraries. The **PacBio sequel II and IIe** systems contains 8 million ZMWs per SMRTcell. The **latest Revio platform** contains 25 million ZMWs with optimised base calling. This cutting-edge technology offers a historically high throughput of 360 Gb of HiFi reads per day, a 15x increase compared to the Sequel IIe system.

Sample requirements

Service	Sample type	Amount (Qubit)	Volume	Concentration	Purity
PacBio Sequel II DNA CLR library	HMW genomic DNA (Bacteria & Fungus)	≥ 2 μg	≥ 50 μL	≥ 70 ng/μL	OD260/280 = 1.7-2.2; OD260/230 = 1.3-2.6; NC/QC = 0.95-3.00 Fragments should be ≥ 20K
PacBio Sequel II/ IIe/Revio DNA HiFi library	HMW genomic DNA (Plant & Animal)	≥ 5 μg	≥ 50 μL	≥ 70 ng/μL	OD260/280 = 1.75-2.0; OD260/230 = 1.5-2.6; NC/QC = 0.95-3.00 Fragments should be ≥ 30K
	HMW genomic DNA (Bacteria & Fungus)	≥ 5 μg	≥ 50 μL	≥ 70 ng/μL	OD260/280 = 1.7-2.2; OD260/230 = 1.3-2.6; NC/QC = 0.95-3.00 Fragments should be ≥ 20K
Pacbio Full-Length 16S/18S/ITS	Isolated DNA	≥ 300 ng	≥ 30 μL	≥ 10 ng/μL	OD260/280 = 1.8-2.0; no degradation, no contamination
PacBio Iso-Seq (Poly-A enrichment)	Total RNA	≥ 600 ng	≥ 15 μL	≥ 40 ng/μL	OD260/280 = 1.8-2.2 OD260/230 = 1.3-2.5 NC/QC = ≤ 2 RIN value ≥ 6.5 with flat baseline

Applications

- Microbial *de novo* sequencing services
- Human, plant, and animal whole genome sequencing
- DNA methylation information available in WGS raw data
- 16S/18S/ITS full-length amplicon sequencing
- Full-length transcriptome sequencing – detect alternative splicing and fusion genes
- Premade library sequencing available on the Revio platform

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Oxford Nanopore Sequencing Solutions

Oxford Nanopore Technology (ONT) reads sequences by detecting the changes in electric signal when a single-stranded nucleic acid passes through a protein nanopore. Novogene features the PromethION, ONT's industrial scale production unit, which utilises the latest Q20+ chemistry to provide data with high accuracy and yield. It generates 50–100 Gb of long-read data per flow cell. Using this platform, Novogene has achieved reads as long as 18.2 kb.

Sample requirements

Service	Sample type	Amount (Qubit)	Volume	Concentration	Purity
Nanopore PromethION DNA library	HMW genomic DNA (Plant & Animal)	≥ 8 μg	≥ 50 μL	≥ 100 ng/μL	OD260/280 = 1.75-2.0 OD260/230 = 1.4-2.6 NC/QC = 0.95-3.00 Fragments should be ≥ 30K
	HMW genomic DNA (Bacteria & Fungus)	≥ 6 μg	≥ 50 μL	≥ 60 ng/μL	OD260/280 = 1.7-2.2 OD260/230 = 1.3-2.6 NC/QC = 0.95-3.00 Fragments should be ≥ 20K
Nanopore RNA (polyA enrichment)	Total RNA	≥ 100 ng	≥ 10 μL	≥ 10 ng/μL	OD260/280 = 1.8-2.2 OD260/230 = 1.3-2.5 NC/QC ≤ 2

Applications

- Human, plant, animal, and microbial whole genome sequencing
- DNA methylation information available in WGS raw data
- Full-length transcriptome sequencing

Extraction services

We offer DNA and RNA extraction services in collaboration with our specialist partner BioEcho. This includes the extraction of high molecular weight (HMW) genomic DNA for use on PacBio and Oxford Nanopore platforms. Please contact us for further information.

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About Novogene

Novogene is a leading provider of genomic services and solutions with cutting edge NGS and bioinformatics expertise. With one of the largest sequencing capacities in the world, we utilise our deep scientific knowledge, first-class customer service and unsurpassed data quality to help clients realise their research goals in the rapidly evolving world of genomics.

With almost 2,000 employees, multiple locations around the world, 69 NGS related patents and over 16,000 publications in top tier journals such as Nature and Science, we have rapidly become a world-leader in NGS services.

Our Sequencing Centre on the Cambridge Science Park offers our customers an unrivalled NGS service with a quick turn-around, exceptional data quality and expert PhD level advice and support throughout your project.

PacBio

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