

# De novo Sequencing

**De novo sequencing** performs genome sequencing and assembly of a species without a reference genome. A complete and accurate genome sequence is essential to the genomics study of new species and the investigation of complex structural genomic changes in wild relatives compared to published cultivar genome sequences.

Genome sequencing also lay the foundation for subsequent studies on the origin, evolution and specific environments adaptation. According to the complexity of the genome, it can be divided into a simple genome and a complex genome.

## Applications

Forestry/ Horticultural/ Livestock/ Bird/ Fishery Genome Research

## Our Key Features & Advantages



### Leading Sequencing Capacity

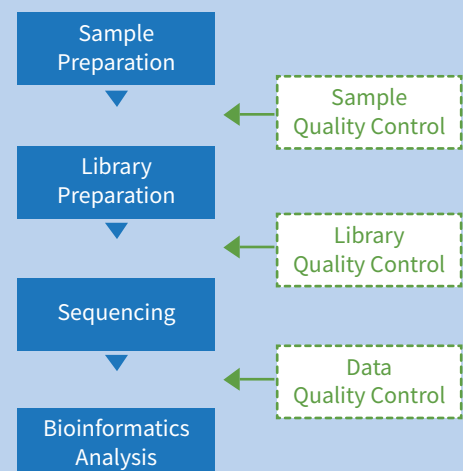
We have a diverse and complete line-up of sequencing systems (>10 units of PacBio Sequel II/IIe and Oxford Nanopore PromethION Sequencers, >20 units of Illumina Novaseq) and protocols to deliver the best possible results to support our customers' research.



### Comprehensive Analysis

Our founding leader Dr. Ruiqiang Li is known for developing the software SOAP for ultra-fast sequence mapping, variation detection, and *de novo* genome assembly. We have been in a leading position, working with scientists on *de novo* genome research in academia and have published numerous articles in top-tier journals.

## Project Workflow



## Sample Requirements

Library Type	Sample Type	Amount		Volume	Concentration	Purity
		Strongly Recommended	Required/ Lib			(Qubit/Agarose Gel)
PacBio CLR	*HMW Genomic DNA	≥ 16 µg	≥ 8 µg	≥ 50 µL	≥ 80 ng/µL	Fragment size: most of DNA fragment is above 40k; A260/ 280 = 1.8~2.0; A260/ 230 = 1.5~2.6; ** Nc/ Qc = 0.95~3.00
PacBio HiFi	*HMW Genomic DNA	≥ 30 µg	≥ 15 µg	≥ 50 µL	≥ 80 ng/µL	
Nanopore	*HMW Genomic DNA	≥ 16 µg	≥ 8 µg	≥ 50 µL	≥ 100 ng/µL	Fragment size: most of DNA fragment is above 40k; A260/ 280 = 1.8~2.0; A260/ 230 = 1.5~2.6
Hi-C ****	Plant/ Animal Tissue ****	≥ 2 µg	≥ 1 g	-	-	Plant: fresh and tender tissue sample Animal: blood or muscle tissue sample

\* HMW: High Molecular Weight

\*\* Nc/Qc: NanoDrop concentration/Qubit concentration

\*\*\* For ultra-long library prep requirement, please enquiry from APM team for price and species experience.

\*\*\*\* For Hi-C, tissue is required.

To obtain best results, data used for all analysis of this project should be generated from the same sample.

## Standard Analysis Content

Genome Survey	▶	K-mer analysis (genome size, heterozygosity, repeats) / Primary assembly (GC contents)
Genome Assembly	▶	Assembly and assessment
Genome Annotation	▶	Repeats/ Gene structure and function/ ncRNA
Comparative Analysis	▶	Gene family clustering/ Phylogenetic tree/ Time of divergence/ Gene family expansion and contraction/ Positive selection/ WGD/ Synteny

## Publications

Listed below are some publications that were supported by Novogene solutions.

Journal	IF	Title
Science	47.728	Horizontal gene transfer of <i>Fhb7</i> from fungus underlies <i>Fusarium</i> head blight resistance in wheat
Nature Genetics	38.33	Genomic insights into the origin, domestication and diversification of <i>Brassica juncea</i>
Nature Communications	14.919	Genome of <i>Tripterygium wilfordii</i> and identification of cytochrome P450 involved in triptolide biosynthesis
Genome Biology	13.583	The chromosome-level wintersweet ( <i>Chimonanthus praecox</i> ) genome provides insights into floral scent biosynthesis and flowering in winter
Molecular Plant	13.164	Gapless <i>indica</i> rice genome reveals synergistic contributions of active transposable elements and segmental duplications to rice genome evolution.

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