

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

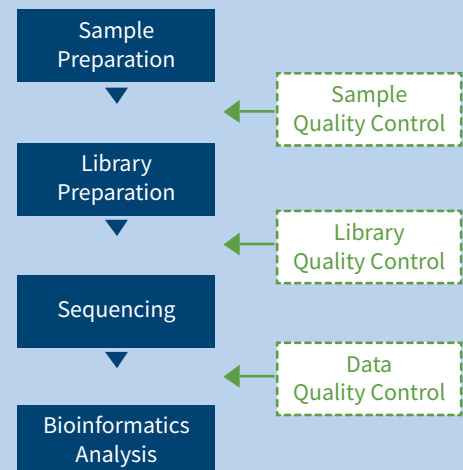
We have a diverse and complete line-up of sequencing systems (>10 units of PacBio Sequel II/IIe and Oxford Nanopore PromethION Sequencers, >20 units of Illumina Novaseq) and protocols to deliver the best possible results to support our customers' research.



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
PacBio DNA HiFi Library	HMW* Genomic DNA	≥ 9 µg (Additional 8 µg per sample per Cell)	≥ 50 µL	≥ 70 ng/µL	OD260/280=1.75~2.0; OD260/230=1.5~2.6; NC/QC**=1.00~2.20 Fragments should be ≥ 30K
PacBio DNA CLR library	HMW* Genomic DNA	≥ 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
Nanopore	HMW* Genomic DNA	≥ 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
Hi-C***	Plant/ Animal Tissue***	≥ 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 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
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, and more at our website.

Journal	IF	Title
Science	47.728	Horizontal gene transfer of Fhb7 from fungus underlies Fusarium head blight resistance in wheat
Nature Genetics	38.33	Genomic insights into the origin, domestication and diversification of Brassica juncea
Molecular Plant	21.949	The genomes of medicinal skullcaps reveal the polyphyletic origins of clerodane diterpene biosynthesis in the family Lamiaceae

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