De Novo Genome Sequencing

Novogene is always at the forefront of ***de novo*** genome sequencing. Novogene's founder, Dr. Ruiqiang Li, is a leading genomics expert and a primary developer of the SOAPdenovo software package for genome assembly. Together with Dr. Li, Novogene teams have contributed to critical publications on novel genome assembly and annotation, and can provide you with the high level of expertise required for your ***de novo*** genome sequencing projects.

With the development of next-generation sequencing technology, ***de novo*** genome sequencing has become more rapid and affordable. With ***de novo*** genome sequencing, the first genome map for a species is generated, providing a valuable reference sequence for phylogenetic studies, analysis of species diversity, mapping of specific traits and genetic markers, and other genomics research.

The Novogene Advantage

- **Highly experienced:** We have completed critical ***de novo*** genome sequencing projects, and our data have been published in top-tier journals including Nature, Science and Nature Genetics.
- **Leader in NGS services:** We provide high-quality sequencing, an efficient standard workflow, fast turnaround time, and bioinformatics analyses at a cost-effective price.
- **Bioinformatics expertise:** The SOAPdenovoII software and the NovoHeter software developed by Novogene scientists as well as other prevalent softwares are used for complex genome assembly.

Project Types

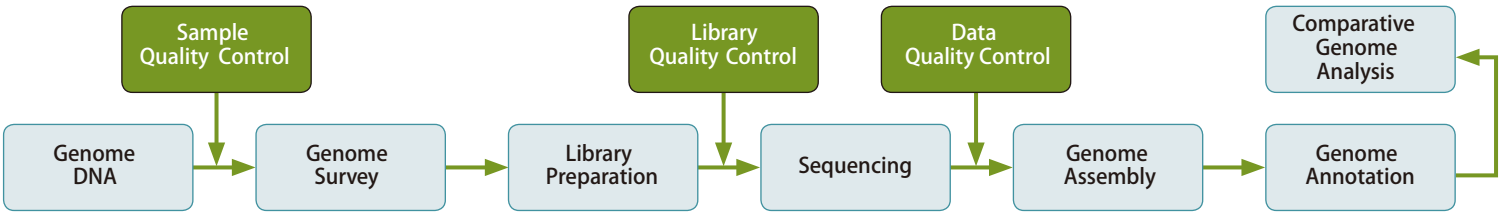
Simple Genome

A simple genome refers to a haploid or diploid genome with a low repeat content (<50%) and a low rate of heterozygosity (<0.5%), such as most mammals, birds, and cultivated crops.

Complex Genome

A complex genome refers to a diploid or polyploid genome with a high repeat content (higher than 50%) or a high rate of heterozygosity (higher than 0.5%), such as many species of plants, aquatics, and insects.

Project Workflow



SEQUENCING STRATEGY

- Illumina platform, paired-end 150 bp
- Pacbio/Nanopore platforms
- 10X Genomics/Bionano/Hi-C/Chicago

SAMPLE REQUIREMENTS

- DNA amount for survey: ⩾ 10 μg (Illumina platform, quantified by Qubit 2.0)
- DNA amount for genome de novo sequencing: ⩾ 40 μg, ⩾ 50Kb (Pacbio platform, quantified by Qubit 2.0 and electrophoresis)
- DNA concentration: ⩾ 40 ng/μl
- Purity: OD260/280 = 1.8 - 2.0 without degradation and RNA contamination

DATA QUALITY GUARANTEE

- Simple genome: Contig N50 ⩾ 500 Kb
- Mammal or bird genome (Quick de novo): Contig N50 ⩾ 1 Mb
- Complex genome: Contig N50 ⩾ 200 Kb

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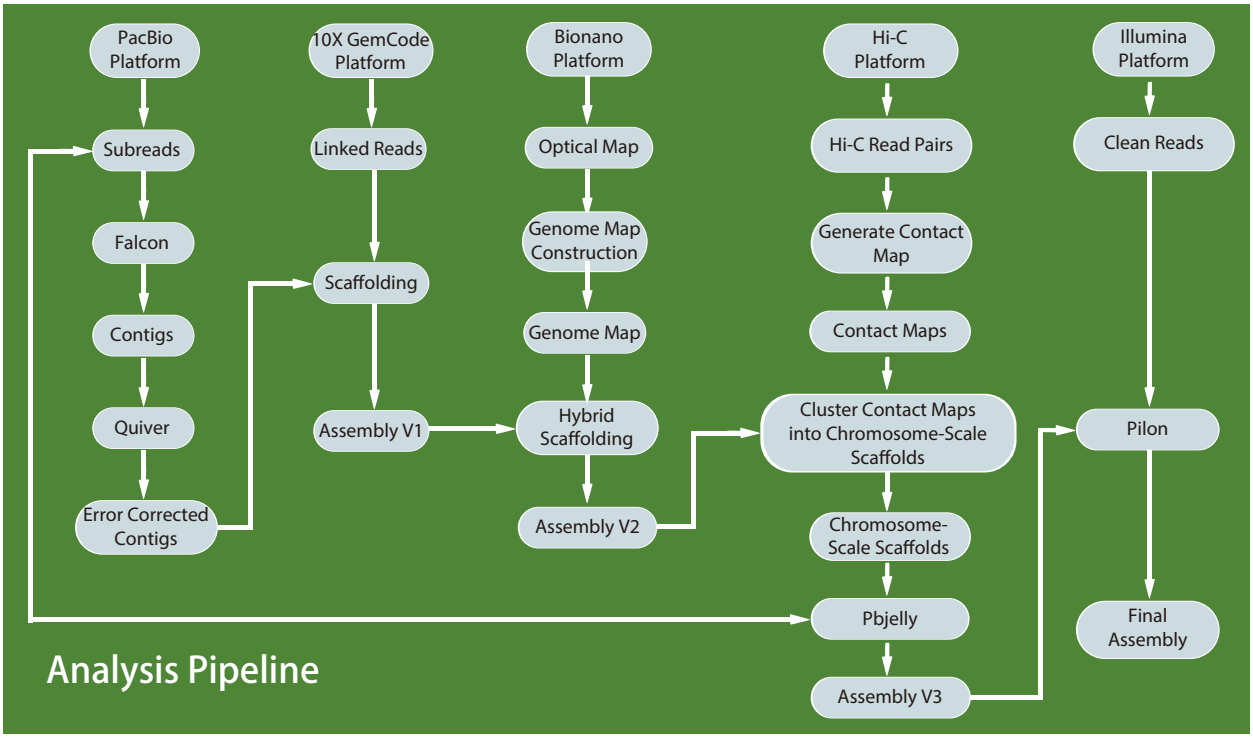
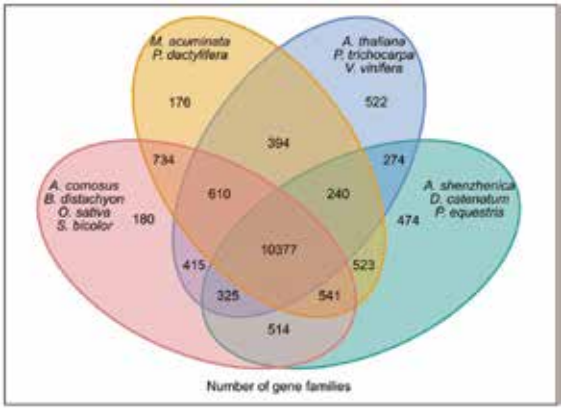


TECHNICAL PARAMETERS

Procedures	Library Preparation	Sequencing Depth	Turnaround Time
Survey Analysis	Illumina: 350 bp insert	50X	30 Days
Genome de novo Sequencing	PacBio: SMRT library	⩾80X	Simple genome 6 months
	Illumina: 350 bp insert	100X	Mammal or bird genome (Quick de novo) 3 Months
	10X Genomics/Hi-C/ Bionano/Chicago	100X	Complex genome 8-10 months



Venn diagram showing unique and shared gene families among members of Orchidaceae, dicots, and Poaceae, and M. acuminata and P. dactylifera.

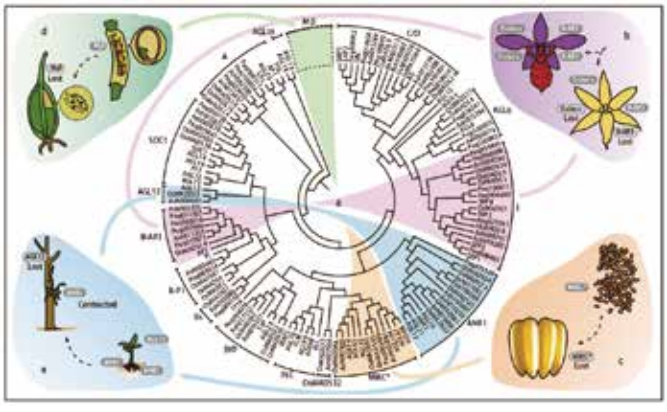
Project Case

The following study utilized Novogene's sequencing expertise.

The Apostasia Genome and the Evolution of Orchids

Nature, 549.7672 (2017): 379

Researchers from Novogene and The Orchid Conservation and Research Center of Shenzhen together with other research teams collaborated on the whole-genome sequencing of *A. shenzhenica*, a self-pollinating orchid found in Shenzhen, China. Sequencing of *A. shenzhenica* were conducted on the Illumina platform, and preliminary assembly were improved using PacBio and 10X Genomics. Together with the genome and transcriptome data of other related species, this research enlightened genetic mechanisms of orchids' habits and critical evolutionary milestones.



The phylogenetic tree of MADS-box genes among A. shenzhenica, P. equestris, O. sativa and Arabidopsis.

NOVOGENE'S PUBLICATIONS

Year	Journal	Ariticle
2018	Nature Plants	A genome for gnetophytes and early evolution of seed plants
2017	Nature	The Apostasia genome and the evolution of orchids
2017	Nature Genetics	The Aegilops tauschiigenome reveals multipleimpacts of transposons
2015	Nature Biotechnology	sequencing of allotetraploid cotton (Gossypium hirsutum l. acc. tM-1) provides a resource for fiber improvement
2014	Nature Biotechnology	De novo assembly of soybean wild relatives for pan-genome analysis of diversity and agronomic traits
2014	Nature Genetics	Whole-genome sequencing of the snub-nosed monkey provides insights into folivory and evolutionary history