

Plant and Animal Whole Genome Sequencing



With advancements in next-generation sequencing technology, whole genome resequencing (WGS) has become the most rapid and effective method to unravel the underlying mechanisms of species origin, development, growth, and evolution at the genomic level. Utilizing WGS, complete genomic data from one or more variants can be aligned with known genomic sequences for the species. Applications of WGS include detection of genetic differences between variants, transposon fingerprinting for assessing germplasm diversity and lineages, and mapping loci associated with specific traits such as disease resistance.

The Novogene Advantage



Extensive experience:

Over 4000 re-sequencing projects completed, with associated data published in several high impact journals.



Unsurpassed data quality:

Guaranteed Q30 \geq 80%, exceeding Illumina's official guarantee of \geq 75%.



Cost-effective service:

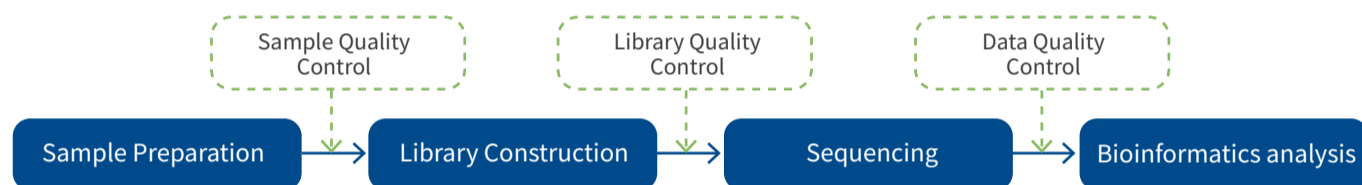
Rapid and efficient genome-wide profiling of multiple samples at a competitive price.



High verification rate:

SNP verification rate of $>$ 95% guaranteed.

Analysis Pipeline



Specifications

01

SAMPLE REQUIREMENTS

- Genomic DNA quantity: \geq 200 ng
- Sample volume: \geq 20 μ l
- OD260/280 = 1.8 to 2.0 without degradation or RNA contamination

02

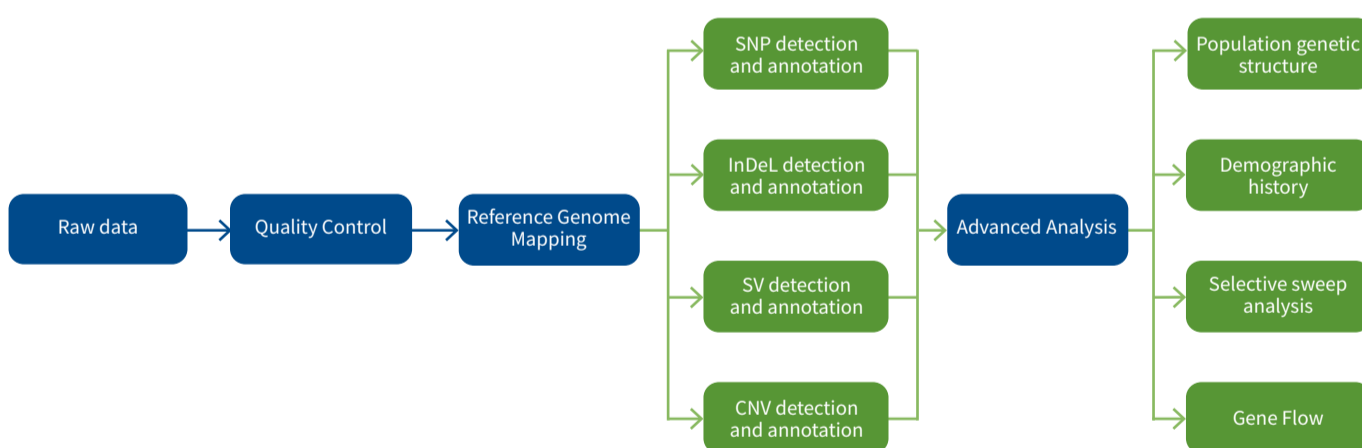
SEQUENCING STRATEGY

- 350 bp insert DNA library
- NovaSeq platform, paired-end 150 bp

03

TURNAROUND TIME

- 20 business days from verification of sample quality (without data analysis)



Novogene Powered Literature

Year	Journal	Title
2020	<i>Nature communications</i>	Whole-genome resequencing of wild and domestic sheep identifies genes associated with morphological and agronomic traits
2020	<i>Plant biotechnology journal</i>	Genome-wide expression quantitative trait locus analysis in a recombinant inbred line population for trait dissection in peanut
2019	<i>Molecular Biology and Evolution</i>	Phylogenomics reveals an ancient hybrid origin of the persian walnut
2018	<i>Nature communications</i>	Genome re-sequencing reveals the evolutionary history of peach fruit edibility
2018	<i>Nature Genetics</i>	Resequencing a core collection of upland cotton identifies genomic variation and loci influencing fiber quality and yield
2018	<i>Nature communications</i>	Genetic variation in <i>PTPNI</i> contributes to metabolic adaptation to high-altitude hypoxia in Tibetan migratory locusts

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