



Genome-wide association study (GWAS) with Whole Genome Resequencing

Genome-wide association study (GWAS) is a method used to detect associations between genetic variants and traits in specific population samples. Employing a GWAS has also become a widely accepted strategy for decoding genotype-phenotype associations in many species. At the genome-wide scale, association studies typically focus on statistical relationships between single-nucleotide polymorphisms (SNPs) and specific traits.

Service Highlights



Extensive experience

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



Comprehensive bioinformatics analysis

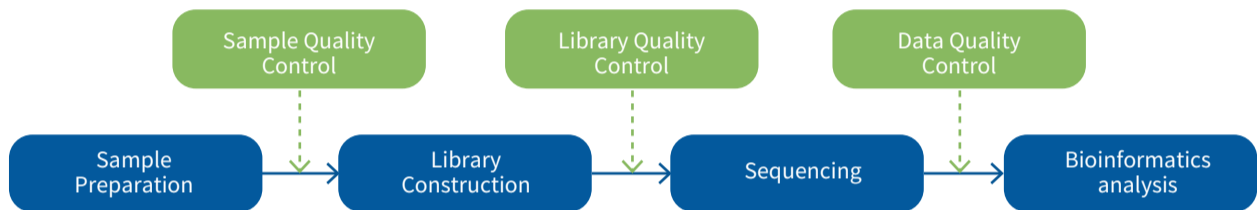
Multiple analysis solutions with widely accepted mainstream software to meet your project needs.



Unsurpassed data quality

Illumina Novaseq PE150, Guaranteed Q30 \geq 80%, exceeding Illumina's official guarantee of \geq 75%.

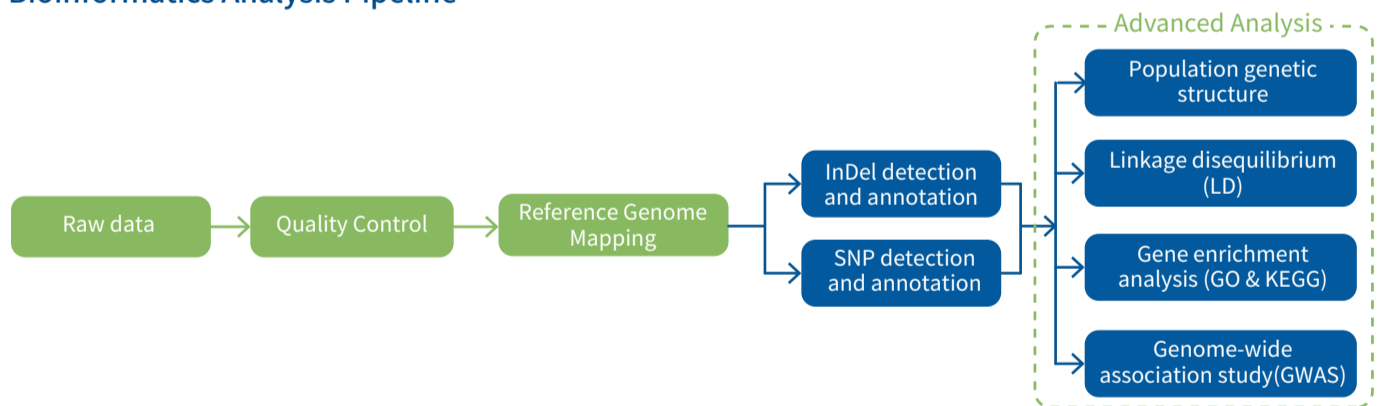
Project Workflow



Sample Requirement

Sample Type	Amount (Qubit®)	Volume	Concentration	Purity (NanoDrop™/Agarose Gel)
Genomic DNA	\geq 0.2 μ g	\geq 20 μ L	\geq 20 ng/ μ L	OD260/280 = 1.8 - 2.0, no degradation, no contamination
Genomic DNA (PCR-free low input-350bp)	\geq 1.5 μ g	\geq 20 μ L	\geq 20 ng/ μ L	

Bioinformatics Analysis Pipeline



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

For Research Use Only. Exclusive for Clients in North and South America.



Follow us on LinkedIn

Novogene Corporation Inc.

8801 Folsom Blvd #290, Sacramento, CA 95826

916-252-0068-383 inquiry_us@novogene.com en.novogene.com

Copyright©2011-2021 Novogene Corporation.

All Rights Reserved. Information and specifications are subject to change at any time without notice.