

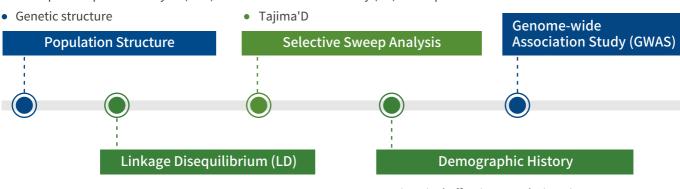


Advanced Analysis for Plant and Animal Whole Genome Sequencing

With advancements in next-generation sequencing technology, whole genome re-sequencing (WGS) has become the most rapid and effective method to identify the genetic variations in individuals of the same species or between related species. The variation information such as single nucleotide polymorphism (SNP), insertion and deletion (InDel), copy number variation (CNV), and structural variation (SV) obtained through re-sequencing is used in population genetics research and genome-wide association studies (GWAS). These powerful tools are used to investigate the causes of diseases, to select plants and animals in agricultural breeding programs, and to identify common genetic variations among populations.

Advanced Analysis – Population Genetics Research and GWAS analysis

- Phylogenetic tree
- Principal component analysis (PCA)
- Fixation statistics (Fst) Comparison
- Nucleotide diversity $(\theta \pi)$ Comparison



- Historical effective population size
- Divergence time estimation
- Historical relationships among populations

Novogene Advantages

- Scalable Sequencing Capacity
- **Competitive Pricing**
- Extensive In-House Bioinformatics Expertise

Service Highlights

- Comprehensive standard and advanced analysis pipeline
- Customized analysis to meet your research needs
- Best-in-class and widely recognized software

Novogene Powered Literature

Year	Journal	Title
2020	Nature communications	Whole-genome resequencing of wild and domestic sheep identifies genes associated with morphological and agronomic traits
2020	Plant biotechnology journal	Genome-wide expression quantitative trait locus analysis in a recombinant inbred line population for trait dissection in peanut
2019	Molecular Biology and Evolution	Phylogenomics reveals an ancient hybrid origin of the persian walnut
2018	Nature communications	Genome re-sequencing reveals the evolutionary history of peach fruit edibility
2018	Nature Genetics	Resequencing a core collection of upland cotton identifies genomic variation and loci influencing fiber quality and yield
2018	Nature communications	Genetic variation in <i>PTPN1</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.





Novogene Corporation Inc.

- 9 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.