

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:

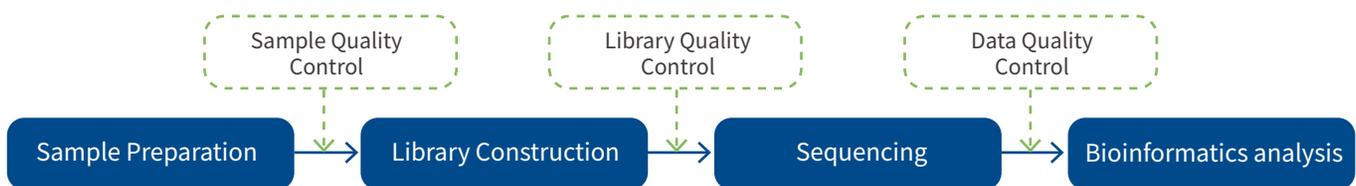
Rapid and efficient genome-wide profiling of multiple samples at a competitive price.



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

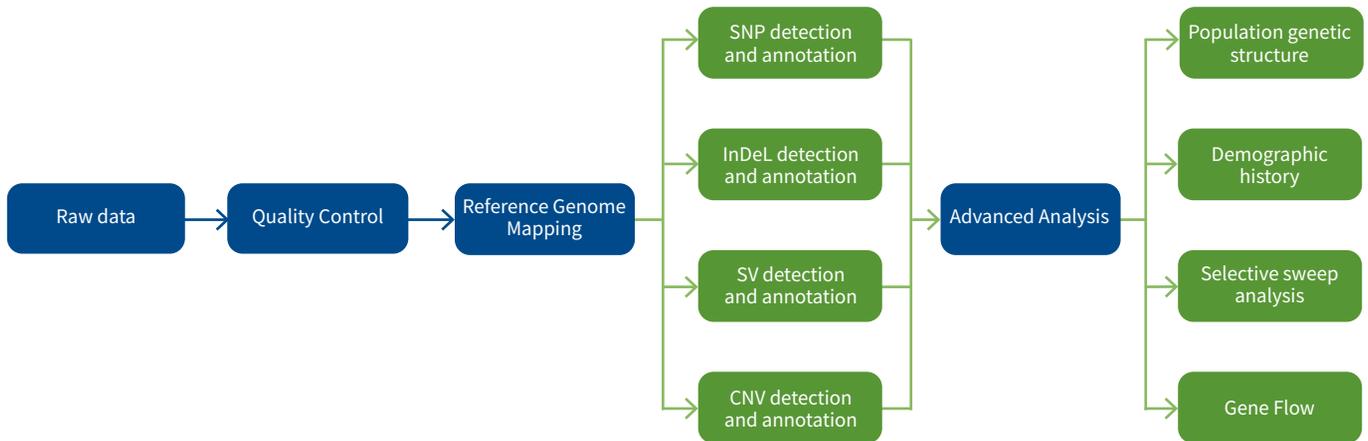
03

TURNAROUND TIME

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



Analysis Pipeline



Novogene Powered Research

▶ Genome re-sequencing reveals the evolutionary history of peach fruit edibility

Peach is an economically important fruit crop and a well-characterized model for studying the *Prunus* species. This study suggests that peach originated about 2.47 Mya in southwest China in glacial refugia generated by the uplift of the Tibetan plateau (Fig.1). The copy number of four fruit texture or taste associated candidate genes (*EXPA16*, Pectin lyase-like, *CAD9*, and *PMT5*) increased in *P. persica* during the course of domestication and/or subsequent selection (Fig.2). Our exploration of genomic selection signatures and demographic history supports the hypothesis that frugivore-mediated selection occurred several million years before the eventual human-mediated domestication of peach.

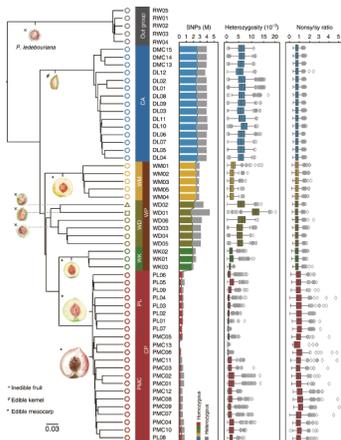


Fig.1 Neighbor-joining phylogenetic tree of the 51 *Amygdalus* accessions.

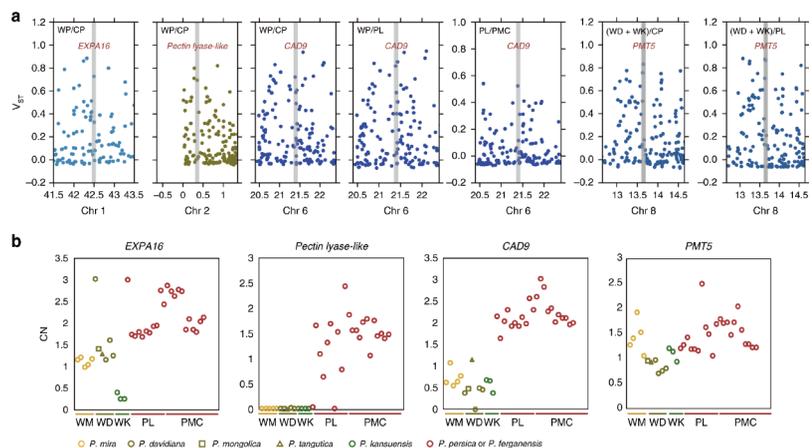


Fig.2 CNVs involved in fruit texture and taste during peach domestication and improvement.

Reference

Yang Yu, Jun Fu, Yaoguang Xu, *et al.* Genome re-sequencing reveals the evolutionary history of peach fruit edibility[J]. Nature Communications, 2019

* Only for research use in North and South America.



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