Novogene

Animal and Plant Re-sequencing

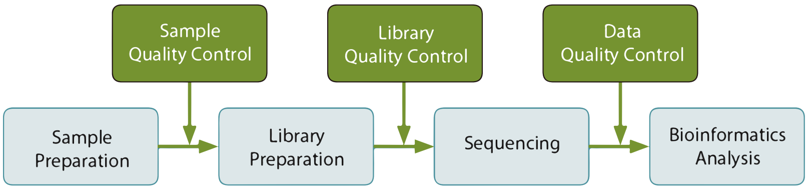
With advancements in next-generation sequencing technology, whole genome re-sequencing (WGS) has become a more rapid and effective method to unravel, at the genomic level, the underlying mechanisms of species origin, development, growth and evolution. Using WGS, the complete genome data from one or more variants can be aligned to 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.

Novogene is highly experienced in the applications of WGS for characterizing plant and animal variants. With cutting-edge Illumina platforms and our expert bioinformatics analysis, we provide researchers with high quality data in a highly cost-effective manner. Bioinformatics analyses includes but are not limited to detecting SNPs, InDels, structure variations, and copy number variations with high accuracy and verification rates.

The Novogene Advantage

- Extensive experience: We have completed thousands of re-sequencing projects, and our data has been published in top-tier journals continuously.
- Unsurpassed data quality: We guarantee a Q30 score ≥ 80%, exceeding Illumina's official guarantee of ≥ 75%.
- Cost-effective service: By employing state-of-the-art Illumina platforms that have enabled the $1000 human genome, we provide higher data output, faster turnaround time, and lower prices possible for plant and animal re-sequencing projects of any size.
- High verification rate: We promise that the verification rate of SNPs is higher than 95%.

Project Workflow



Sample Quality Control

Library Quality Control

Data Quality Control

Sample Preparation

Library Preparation

Sequencing

Bioinformatics Analysis

SEQUENCING STRATEGY

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

DATA QUALITY GUARANTEE

- Novogene guarantees its data output. The quality of our data, as measured by the percentage of bases with a sequencing quality score above Q30 (PE150, ≥ 80%), exceeding Illumina's official guideline (PE150, ≥ 75%).

TURNAROUND TIME

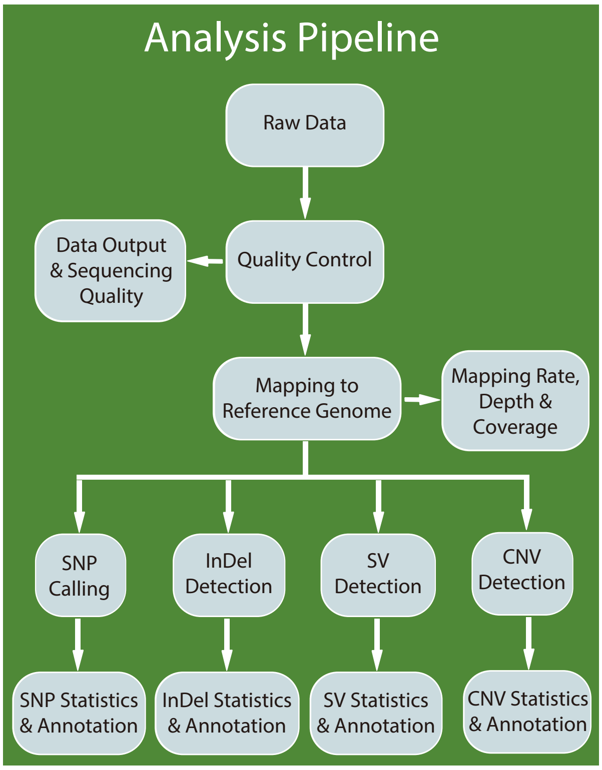
- Within 15 working days from verification of sample quality (without data analysis)
- Additional 10 working days for data analysis

RECOMMENDED SEQUENCING DEPTH

- SNP and InDel: ≥ 10X
- SV: ≥ 20X
- CNV: ≥ 30X

SAMPLE REQUIREMENTS

- DNA amount: ≥ 0.6 μg
- Total volume: ≥ 20 μl
- OD260/280 = 1.8-2.0 without degradation or contamination
  Concentration ≥ 30 ng/μl



Analysis Pipeline

Raw Data

Quality Control

Data Output & Sequencing Quality

Mapping to Reference Genome

Mapping Rate, Depth & Coverage

SNP Calling

InDel Detection

SV Detection

CNV Detection

SNP Statistics & Annotation

InDel Statistics & Annotation

SV Statistics & Annotation

CNV Statistics & Annotation

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Project Example

The following study utillized Novogene's sequencing services

Genomic Analyses Yield Markers for Identifying Agronomically Important Genes in Potato

Molecular Plant 11.3(2018).

Wild potato species have substantial phenotypic and physiological diversity. Here, the genomes of 201 accessions of Solanum section Petota were sequenced to have a comprehensive assessment of wild and cultivated potato species.

1. 6,487,006 high-quality SNPs were identified from 167 accessions in clade 4 of Solanum section Petota, including 146 wild and 21 cultivated diploid potato accessions with a broad geographic distribution.
2. By exploiting information about known quantitative trait loci (QTL), 609 genes were identified under selection, including those correlated with the loss of bitterness in tubers and those involved in tuberization, two major domesticated traits of potato.
3. 529 genes were lost in cultivated potato according to the genome analysis results of S. candolleanum.

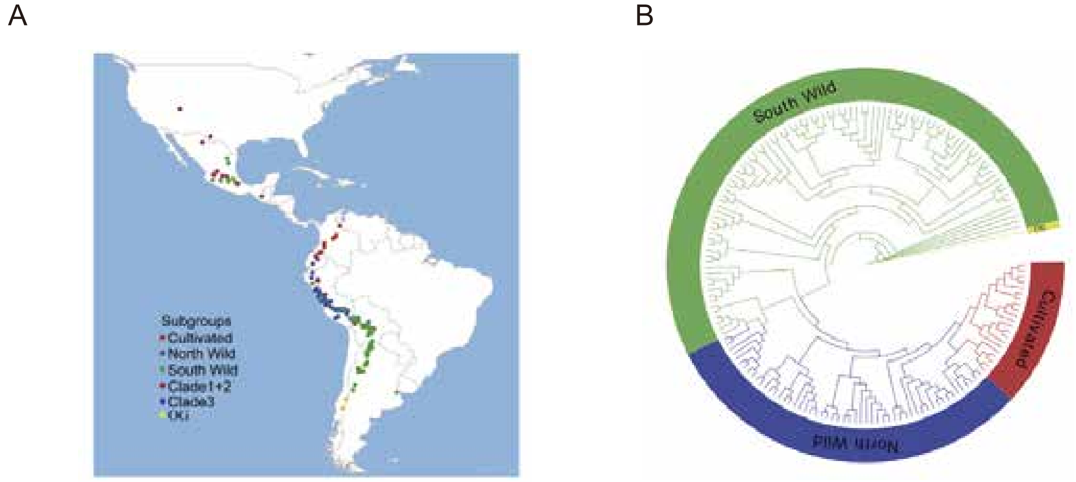

Figure 1. Geographic Distribution and Population Structure of 167 Potato Accessions.

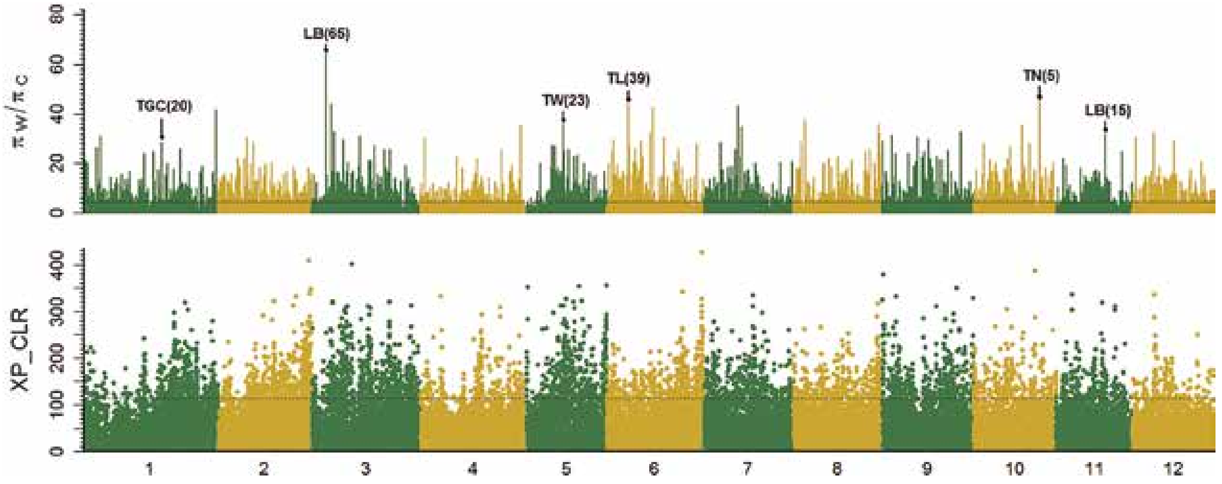

Figure 2. Whole-Genome Screening and Functional Annotation of Selective Sweeps.

SELECTED PUBLICATIONS USING NOVOGENE'S EXPERTISE

Year	Journal	Article
2018	Nature Genetics	Resequencing a core collection of upland cottonidentifies genomic variation and loci influencing fiber quality and yield
2017	Cell Research	The genetics of tiger pelage color variations
2016	Molecular Biology & Evolution	Population genomics reveals low genetic diversity and adaptation to hypoxia in snub-nosed monkeys
2013	Nature Genetics	Genomic analyses identify distinct patterns of selection in domesticated pigs and Tibetan wild boars
2011	Nature	Mapping copy number variation by population-scale genome sequeancing
2009	Science	Complete resequencing of 40 genomes reveals domestication events and genes in silkworm