

Whole Genome Sequencing

Whole genome sequencing (WGS) enables researchers to describe the full genetic composition of individuals and characterize entire genomes of human, animals and plants. It is ideal for discovery applications, such as identifying causative variants and novel genome assembly. Whole-genome sequencing can detect single nucleotide variants (SNPs), insertions/deletions (InDels), copy number changes (CNVs), and large structural variants (SVs).

Applications



Identify genetic variations among populations



Explore the molecular mechanisms of cancers



Reveal the pathogenesis of diseases



Investigate the origin and evolution of species

Our Features & Advantages



supercomputing capability

We have a big datacomputing center of over 150 square meters, more than 300 computenodes, and over 50 petabytes of distributed storage system.



Extensive Experience

We have served clients in more than 100 countries and regions around the world, and have assisted them in publishing more than 4,000 SCI papers, including more than 300 CNS.



Multiple sequencing platforms available

We have a variety of next-generation sequencing instruments, suitable for sequencing and analyzing all kinds of human gene libraries, with stable technology and reliable data.



Reliable & Fast Turnaround Time

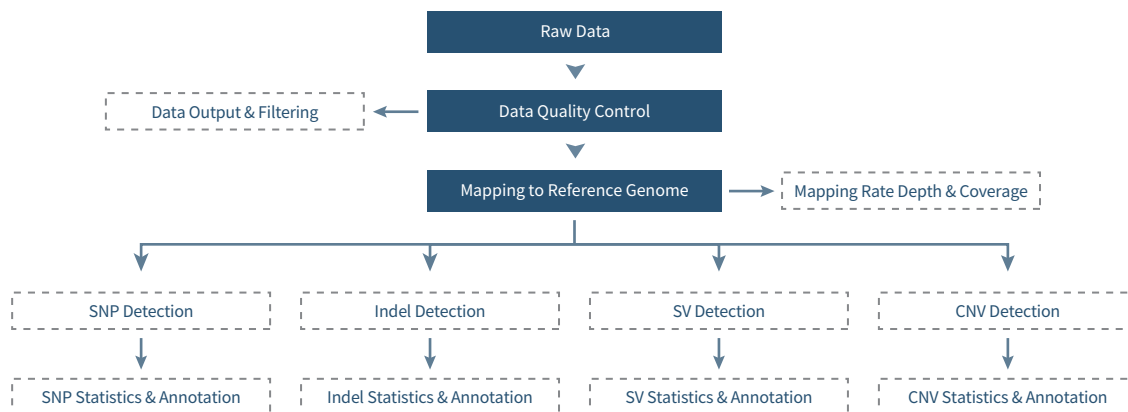
A dedicated project manager will be provided and the results will be given to you within 20 business days after sample quality verification.

Project Workflow



Sequencing Strategy: illumina Novaseq platform, PE150 bp, 90 Gb raw data/sample

⚡ Bioinformatics Analysis Pipeline



⚡ Sample Requirements

Library Preparation	Sample Type	Amount	RIN	Purity
Illumina-compatible PCR-based 300-450 bp insert DNA Library	Genomic DNA	≥2 µg	≥20 ng/µl	260/280=1.8~2.0

⚡ Next Generation Sequencing Platform



Illumina Novaseq™ 6000



Illumina Novaseq™ X Plus



MGI DNBSEQ-T7

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