Population Genetics Solutions

An expert in sequencing & bioinformatics, delivering high-quality genomics results and advanced data analysis

CD Genomics At A Glance

Solution

- End-to-end solutions for sequencing, from sample preparation to data analysis.
- Comprehensive range of sequencing services, including whole-genome sequencing, transcriptome sequencing, metagenomics sequencing, epigenetics sequencing, and more.
- Commitment to quality, reliability, and exceptional customer service

Capacity

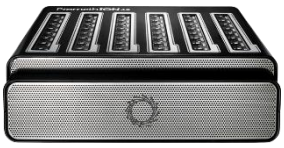
- Headquarters located in New York, USA, and operations in Europe and Asia
- Expertise in all mainstream sequencing technologies, including Illumina, MGI, SMRT sequencing, and nanopore sequencing
- Dedicated to advancing scientific research and promoting innovation in the field of genomics
- Licensed technologies with de novo variant detection capability in target SNP region

Experience

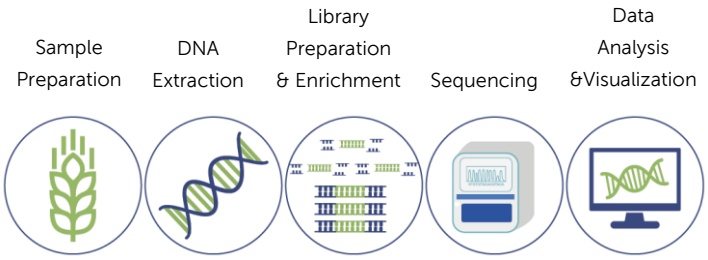
- Worked with numerous pharmaceutical, biotech companies, academic institutions, and government agencies around the world
- Applied genomics technologies to various research areas, including disease research, microbiology, food and agriculture, biomarkers, and drug discovery

Sequencing Platforms

CD Genomics stands at the forefront of advancing population genetics research through its globally recognized innovative genome sequencing and microarray services and products. With a commitment to excellence, we have meticulously developed a comprehensive range of sequencing and bioanalytical platforms. These platforms are not only tailored to meet the experimental scale and functional analysis needs of our partners but also play a crucial role in pushing the boundaries of population genetics research. By leveraging our services and platforms, researchers can make significant strides in unraveling the complexities of genetic diversity, contributing to the forefront of population genetics advancement.

PacBio Sequel II	NovaSeq 6000
	
MiSeq	**NextSeq 500**
	
Oxford Nanopore MinION	**Oxford Nanopore PromethION**
	
PacBio Revio	
	

CD Genomics Sequencing Solution Workflow



Service Advantages

- **Expert Team:** Our team of professionals specializes in population genetics, bringing expertise in bioinformatics and genetics. This ensures the delivery of precise and high-quality analysis.
- **Cutting-edge Technology:** We utilize sequencing technology and analysis tools, emphasizing accuracy and reliability in both data generation and analysis.
- **Customized Solutions:** Recognizing the uniqueness of each research project, we offer tailored solutions aligned with your specific research objectives.
- **Comprehensive Reporting:** Receive detailed reports presenting complex analysis results in a clear and understandable format. Our reports facilitate better comprehension, supporting meaningful scientific decisions.
- **Data Security and Confidentiality:** Your data's security and confidentiality are our top priorities. We implement stringent measures to protect your research data.
- **Efficient Delivery:** Experience an efficient workflow and rapid delivery, ensuring timely access to your desired results.

Comprehensive Population Genetics Solutions

- Whole Genome Sequencing and Resequencing
- Reduced-Representation Genome Sequencing (RRGS)
- Target Region Sequencing
- SNP Microarray
- Genome-wide association study (GWAS)
- Pan Genome
- Variant Calling
- Population Evolution
- Genetic Linkage Map
- Bulk Segregant Analysis (BSA)

CD Genomics Population Genetics Solutions

At CD Genomics, we leverage advanced genomic techniques, including whole-genome resequencing and reduced-representation genome sequencing technology. Our approach involves capturing comprehensive genomic information from diverse subgroups within a species' natural population. By comparing this data with reference genomes or utilizing cluster analysis, we extract a wealth of variant information. This process forms the basis for exploring critical biological insights such as population genetic structure, gene exchange patterns, species formation mechanisms, and the dynamic evolution of populations. Our cutting-edge methods empower in-depth discussions on the intricate genetic dynamics shaping natural populations.

Through the application of genome sequencing technology, we delve into the genomic intricacies of diverse subgroups within a species' natural population. This process yields a wealth of variant information, including SNPs, InDel, SV, and CNV. Building upon the identification of SNPs, our exploration extends to critical biological inquiries, encompassing the genetic structure of the population, patterns of gene exchange, mechanisms driving species formation, and the dynamic evolution of the population. Our approach unlocks a comprehensive understanding of the genetic landscape, fostering insightful discussions on the complex biological aspects that shape natural populations.

Whole Genome Sequencing and Resequencing

Whole genome sequencing services use NGS and long-read sequencing platforms that allow for the de novo sequencing and resequencing of a wide range of animals, plants, humans, and microorganisms. Our services unveil comprehensive genome maps, unraveling genetic mysteries in areas such as disease etiology, growth and development, evolutionary analysis, and beyond. With a rich history of successfully completed genome sequencing projects, we stand as your trusted partner in genomics exploration.

Whole genome resequencing involves sequencing the genome of a species in comparison to a known reference genome sequence, enabling differential analysis among individuals or populations. This process utilizes sequencing libraries with varied insertion fragment sizes combined with short sequences, double ends (Paired-End), uncovering numerous single nucleotide polymorphism sites (SNPs), copy number variations (CNV), insertion/deletions (InDel), and structural variations (SV). The versatility of whole-genome resequencing extends to diverse fields, including clinical medicine research, population genetics research, association analysis, evolutionary studies, and more.

Our Features

- Single base-pair resolution
- *De novo* sequencing and genome-wide mutation characterization
- Population evolution and phylogenetic studies
- Disease research, drug discovery and development, and personalized medicine

Reduced-Representation Genome Sequencing (RRGS)

Reduced-Representation Genome Sequencing (RRGS) is a cutting-edge technology that strategically utilizes specific restriction endonucleases to digest genomic DNA, selectively choosing characteristic target fragments. By employing next-generation sequencing and advanced bioinformatics analysis, it acquires sequence information from these target fragments, independent of reliance on a reference genome.

After a thorough comparison of various genome sequencing technologies (e.g., RAD-seq, GBS, etc.), we highly recommend 2b-RAD, ddRAD-seq and GBS. Drawing from our experience in current projects, these two technologies effectively complement each other, addressing the unique requirements of diverse species.

2b-RAD and ddRAD-seq

2b-RAD and ddRAD-seq utilize restriction endonucleases (e.g., BsaXI) to cleave genomic DNA, generating equal 33 bp tags flanked by cleavage sites. These tags are enriched and subjected to high-throughput sequencing, followed by bioinformatic analysis. This approach enables comprehensive SNP screening and typing analysis across the entire genome.

Genotyping-by-Sequencing (GBS)

GBS is a simplified method of genome sequencing. It involves enzymatically cleaving genomic DNA using restriction endonucleases, followed by high-throughput sequencing of the cleaved segments. The obtained data is then analyzed to extract SNP information and perform genotyping. GBS stands out as a swift, straightforward, and cost-effective genotyping method.

Advantages

- Streamlined Library Construction: Our process boasts a simple and rapid library construction, ensuring efficiency and reducing time constraints in your research.
- Abundant Markers for Diverse Species: We provide a high marker output suitable for a wide range of species, offering versatility and adaptability to different genetic contexts.
- Polyploid Species Study Facilitation: Our technology excels in facilitating the study of polyploid species, allowing for comprehensive analysis and insights into complex genetic structures.
- Genome Size-Independent Data Volume: The volume of sequencing data remains consistent and unaffected by genome size, providing reliability and consistency in your research outcomes.
- Effective Repetitive Sequence Avoidance: We efficiently avoid issues related to repetitive sequences, ensuring the accuracy and precision of your genetic analyses.

Target Region Sequencing

Targeted region sequencing involves conducting large-scale sequencing after selectively enriching a specific region of interest. Researchers have the capability to sequence hundreds or even thousands of samples for a chromosomal or candidate gene region. Its adaptability in target selection, coupled with high sequencing depth, and cost-effectiveness, has led to its widespread application in population studies, often in conjunction with other technologies.

In the realm of animal and plant research, including genetic map construction, QTL localization, GWAS, population evolution, and molecular marker development, these fields heavily rely on whole gene resequencing and simplified genome sequencing. However, both these approaches generate substantial data, and as data volume increases, the sequencing depth naturally decreases. Consequently, a reduction in depth limits the identification of high-frequency SNPs. Targeted region sequencing addresses these challenges effectively, offering solutions in terms of methodology and cost.

Advantages

- Identification of variants at low allele frequencies (down to 1%)
- A smaller data set for bioinformatics analysis
- Much lower cost with a large number of samples
- High depth, allowing identification of rare variants

SNP Microarray

Single nucleotide polymorphisms (SNPs) are distributed densely across the entire genomes of animals and humans, occurring in both coding and non-coding regions. While their probability of occurrence in coding regions is relatively lower, the potential impact on gene function can lead to significant changes in biological traits.

SNP Microarray technology has emerged as a powerful tool in population genetic studies. These microarrays enable the simultaneous analysis of thousands to millions of SNPs across the genome, providing researchers with a comprehensive view of genetic variations within and among populations. The high-density coverage of SNPs on microarrays facilitates the identification of population-specific markers, aiding in the characterization of genetic diversity, population structure, and evolutionary dynamics.

Applications

- Fine-scale population structure
- Ancestry and migration patterns
- Natural selection and adaptation
- Association studies

Genome-wide Association Study (GWAS)

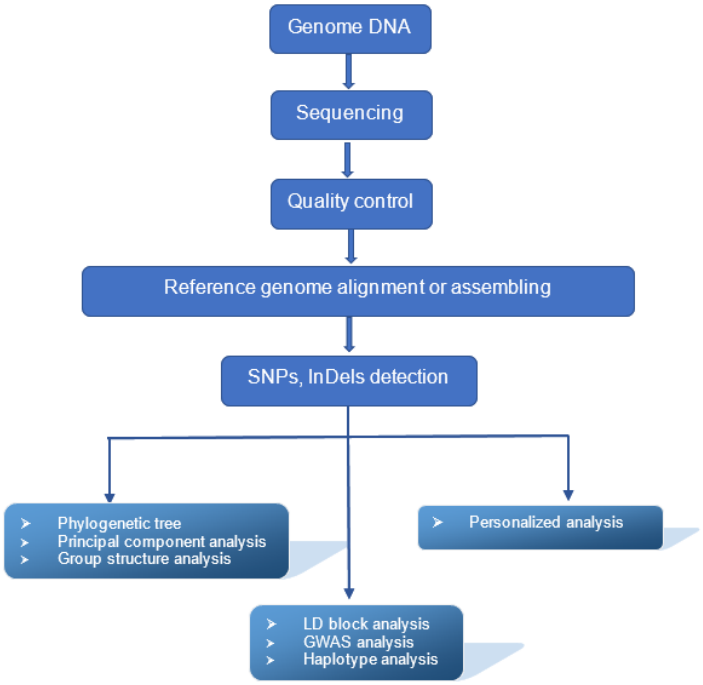
Our GWAS service meticulously analyzes genes for genome-wide associations with common genetic variants, including single nucleotide polymorphisms and copy number variants. Focused on natural populations, this method leverages linkage disequilibrium (LD) among genes (loci) that persist after prolonged recombination.

By examining the diversity of target trait phenotypes in correlation with gene polymorphisms (or marker loci), our approach allows for the direct identification of gene loci or marker loci closely associated with phenotypic variations. This enables the pinpointing of specific functions linked to these genetic elements.

Our genome-wide study offers a comprehensive overview of desirable traits in a single analysis. This approach is particularly well-suited for the exploration and identification of valuable traits, providing a robust foundation for trait mining research.

Our Features

- Whole genome-wide investigation
- High resolution, based on single base
- Wide range of research materials and rich variations available



Pan Genome

Pan-genome sequencing represents the cutting-edge application of high-throughput sequencing and bioinformatic analysis, aiming to sequence and pan-assemble various but related individual materials at varying depths. This process constructs a comprehensive pan-genome map, enriching the genetic information of the targeted species.

As research trends shift towards exploring the evolutionary relationships of larger taxonomic orders, our approach involves sequencing species from different genera or families with intrinsic correlations. This not only yields multiple genomes to complete the species' gene set but also provides DNA sequences and functional genes specific to populations or individuals. This rich dataset contributes to understanding the molecular evolutionary mechanisms behind species formation and their relationship with natural selection.

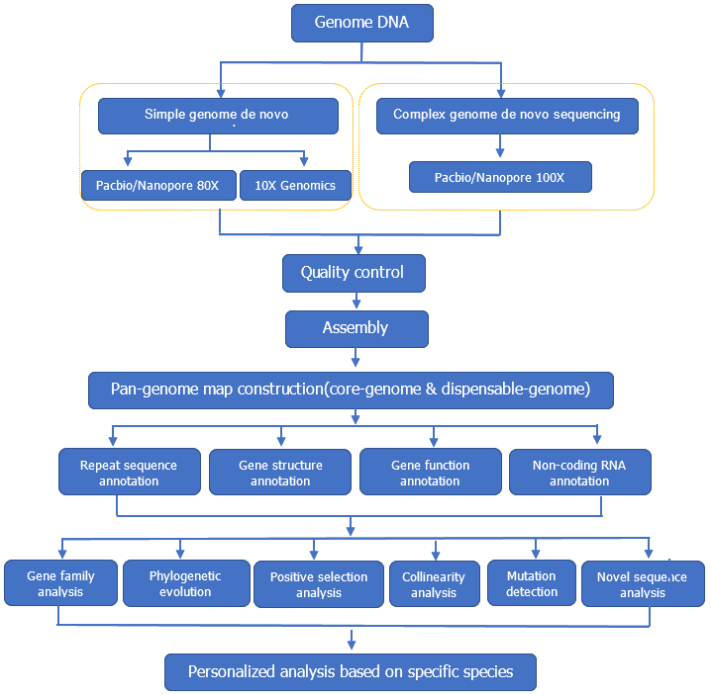
Our pan-genome serves as an invaluable research tool for disciplines like molecular ecology, offering new insights and possibilities for scientific exploration.

Our Features

- Enrich genome information of the species through sequencing the subspecies and individuals
- Quickly find genes or structural variations of genes related to important traits based on study of variable genome
- Study the differences within species from the perspective of unique gene sequences
- Small population, cost and time efficient

Applications

- Species origin and evolution
- Identify trait-related genetic resources for scientific breeding guidance
- Research adaptive evolution
- Invasive alien species



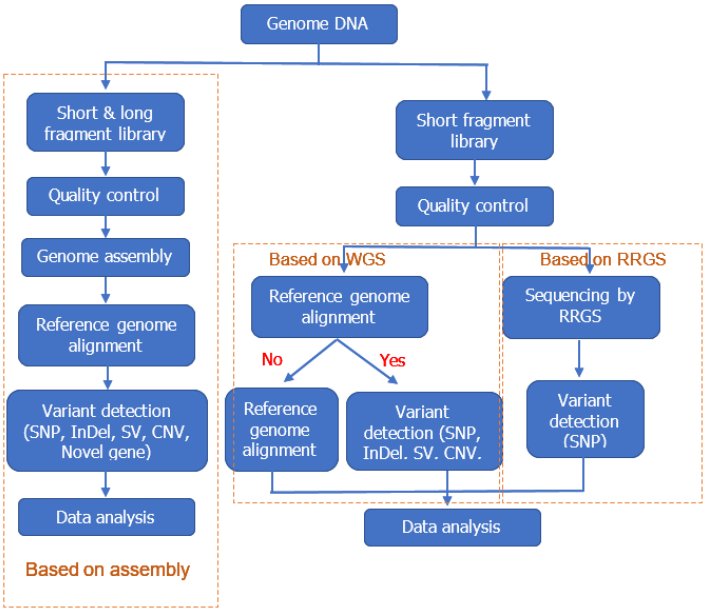
Variant Calling

Variant calling refers to the use of high-throughput sequencing technology to sequence and analyze the differences in the entire genome of an individual or population of a species, to obtain a large amount of genetic variation information, such as Single Nucleotide Polymorphism (SNP), Insertion and deletion sites (InDel) and structural variation sites (SV), copy number variation (CNV) and other information. Variant calling can provide the most basic and comprehensive data foundation for subsequent functional gene fine mapping and quickly, accurately and efficiently analyze the differences between genomes, analyze

each base of the whole genome, and obtain the most extensive molecular markers.

Our Features

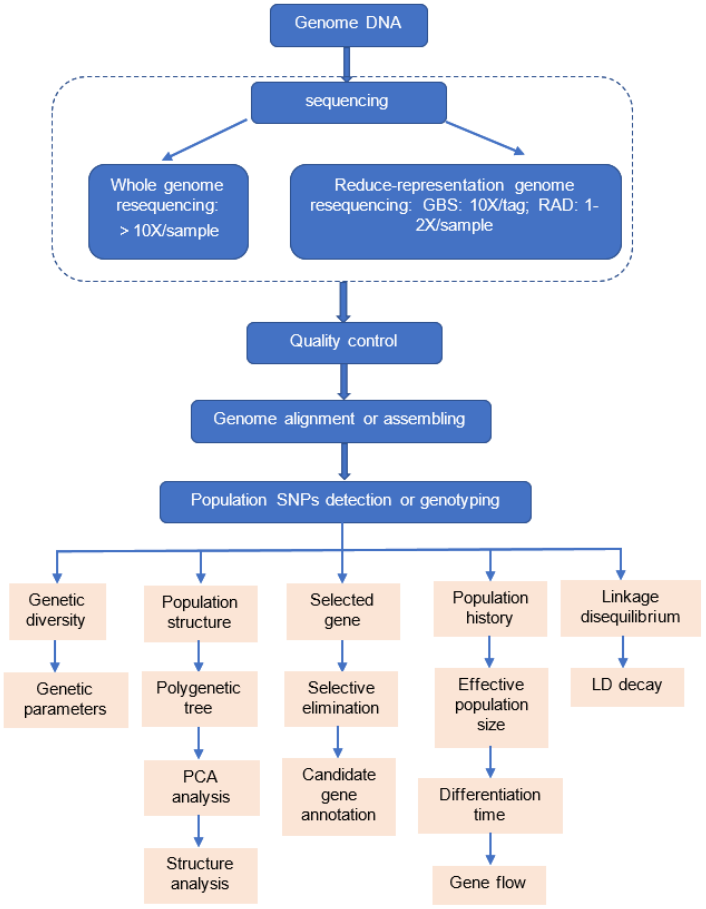
- Variant detection analysis is suitable for many species and does not need reference genome
- The detection of variation is more comprehensive
- New mutations can be detected.



Population Evolution

The survival conditions a species encounter can lead to the formation of distinct subspecies or subgroups through mechanisms like natural selection, artificial domestication, and genetic drift. The study of population evolution serves as a crucial method to trace and analyze this dynamic process.

Our population evolution study relies on cutting-edge whole-genome resequencing technology. By obtaining comprehensive genomic information from each subgroup within a species' natural population, we extract a multitude of genetic variations, including SNPs, InDel, SV, and CNV. This extensive data allows us to delve into the genetic structure of the population, patterns of gene exchange, mechanisms driving species formation, and the dynamic evolution of the population. This method serves as a powerful tool for exploring and understanding complex biological issues related to population genetics and evolution.

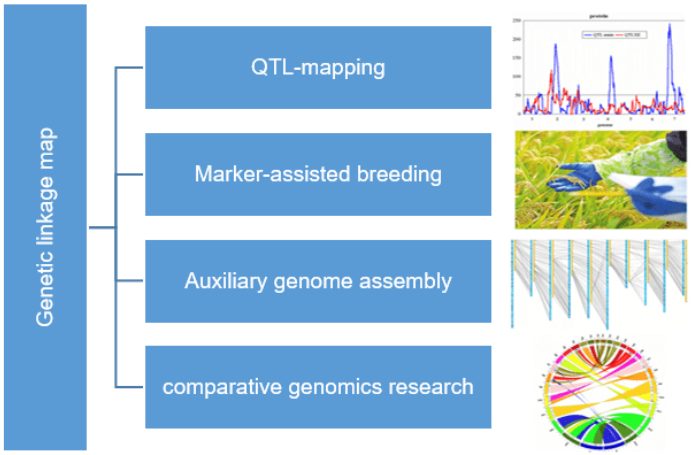


Genetic Linkage Map

A genetic linkage map represents a linear depiction of molecular marker sequences and their relative distances on chromosomes.

CD Genomics addresses the evolving demands of research communities by offering a cost-effective and reliable Genetic Linkage Map service. Leveraging high-throughput sequencing, our service rapidly generates an abundance of molecular markers, resulting in an ultra-high-density genetic map. This map not only provides precise and comprehensive information on the number and location of Quantitative Trait Loci (QTLs) but also identifies loci co-segregating with the phenotype.

Our commitment to delivering top-notch services extends to professional data analysis, ensuring researchers receive a high-quality genetic linkage map tailored to their specific needs.



Bulked Segregant Analysis

Bulked Segregation Analysis (BSA), also known as segregation grouping analysis, is a methodology focused on constructing segregation groups by utilizing two parents with extreme phenotypic differences in target traits. In the offspring segregation groups, individuals showcasing extreme phenotypic differences are selected to form a mixed pool. This mixed pool is then subjected to sequencing, employing high-throughput sequencing technology.

The sequencing of mixed samples involves a thorough comparison of allele frequencies (AF) at polymorphic loci (SNPs) between the two extreme phenotype groups, followed by annotation of any identified differences. This process allows for the identification and annotation of loci associated with the target traits. The ultimate goal is to delve into the genes controlling the target traits and understand their molecular mechanisms.

A standout feature of BSA lies in its efficiency—it doesn't necessitate genotyping of all individuals in a population. Instead, it involves analyzing a mixture of selected individuals based on traits. This approach significantly reduces the workload and cost of the study, making BSA a powerful and resource-efficient tool for trait-associated genetic research.

Our Results

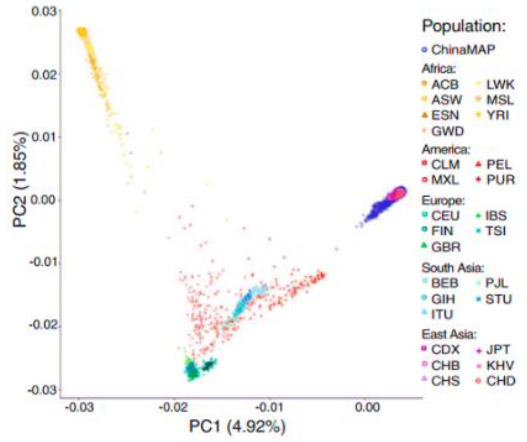
We effortlessly remove low-quality sequences from the raw data while generating clean reads and qualified data. The process commences at the DNA/RNA level, where we compare the sample sequencing information to an extensive database encompassing animal, plant, human, and microbial genomes. This comparison leads to the generation of a results report tailored to your specific analysis. The report is organized into two main sections:

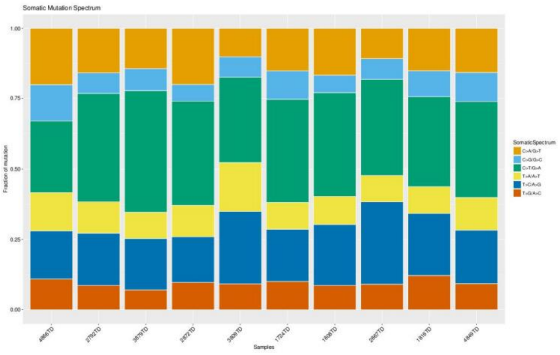
General information

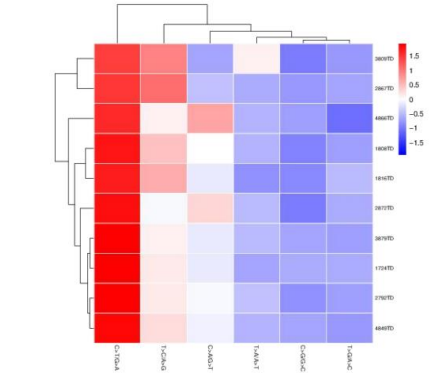
- Experimental procedure
- Data quality control
- Reference data alignment
- Data annotation

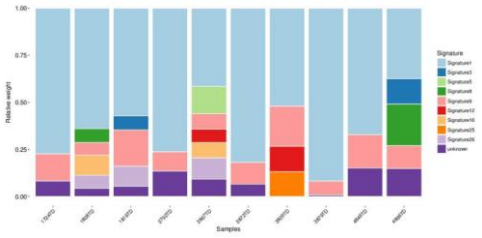
Custom bioinformatic analysis result

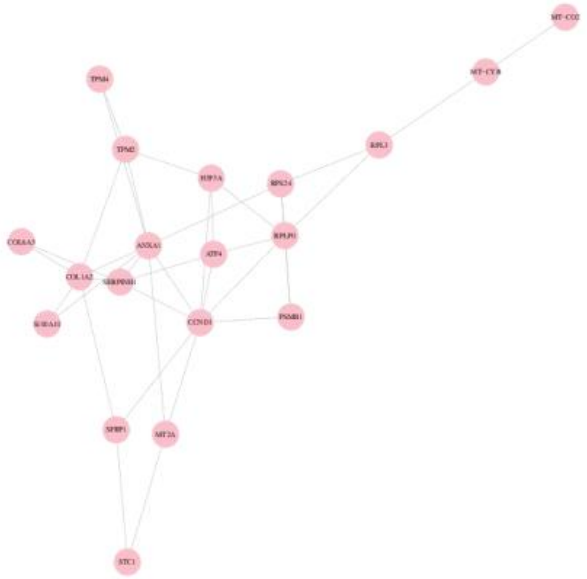
- Principal component analysis
- Ancestry component analysis
- Genetic differentiation
- Population structure analysis
- Gene flow analysis
- Ancient DNA analysis
- Ancestral lineage tracing
- MtDNA and Y chromosome analysis
- ROHs analysis











Applications

Population genetics delves into the genetic structure and dynamic patterns within a population, focusing on natural populations, often various groups within a species (e.g., different varieties, geographic locations). Initially, research employed SSR markers or specific genes (e.g., COI). Our high-throughput sequencing technology services streamline population genetics research. By generating a multitude of SNP markers across the entire genome through simplified genome sequencing, we enable exploration in population genetic evolution, phylogeny, germplasm resource identification, molecular marker development, DNA fingerprinting, and other genomic analyses. Simplified genome technology is currently widespread in population analysis, offering advantages such as genome non-restriction, reduced complexity, low data volume, ease of operation, cost-effectiveness, and particular suitability for extensive sample size studies.

- **Population Genetic Structure Study**

  Conduct sequencing and phylogenetic analysis of SNPs across diverse populations. This aids in classifying population structures and identifying species pivotal to evolutionary processes.

- **Study of Artificial Domestication Mechanism**

  Investigate wild-type and domesticated populations to infer kinship relationships. Uncover genes selected under artificial domestication, guiding the breeding of plants and animals.

- **Research on the Mechanism of Natural Selection**

  Explore populations in different geographic environments to identify genes subject to selection during adaptive evolution. Provide high-quality genetic resources for breeding purposes.

- **Research on Population History**

  Analyze the potential origin of species and genetic variation across populations in various distribution areas. Explore the evolutionary process, considering gene exchange, effective population size, and differentiation time. Our applications extend to understanding and leveraging genetic information for diverse research goals.