Genotyping Sequencing 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

Genotyping Platforms

CD Genomics has global recognition for providing innovative and bespoke genotyping sequencing and microarray services and products to the life science industries and academic research institutions. At CD Genomics, we have a comprehensive range of sequencing and bioanalytical platforms dedicated to meeting the experimental scale and breadth of functional analysis of our partners, advancing disease research, drug development and molecular test development.

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

Comprehensive Genotyping Services

- Genotyping by Sequencing (GBS)
- 2b-RAD sequencing
- ddRAD-seq
- Whole Genome Sequencing
- SNP Microarray
- MassARRAY SNP Genotyping
- SNaPshot Multiplex System for SNP Genotyping
- TaqMan SNP Genotyping
- CNV Genotyping
- CGH Microarray Service
- Microsatellite Genotyping Service
- Microsatellite Instability Analysis
- Microsatellite Development
- Hi-SSRseq

CD Genomics Genotyping Solutions

CD Genomics delivers a comprehensive and adaptable genotyping service tailored to suit projects of any scale or complexity, be it small, large, standard, or entirely customized – extending our expertise to both humans and various other species. Our robust portfolio encompasses cutting-edge arrays, high-quality reagents, advanced instruments, and state-of-the-art bioinformatics tools, empowering you to identify both common and rare single nucleotide polymorphisms (SNPs), copy number variations (CNVs), and other genetic variations with precision.

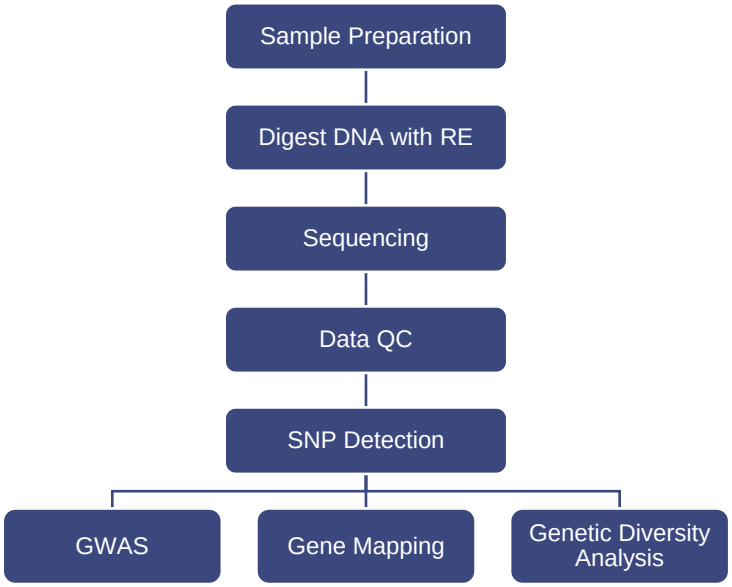
At CD Genomics, our genotyping services and products are designed to cater to a diverse array of projects, offering unparalleled flexibility and versatility. With over a decade of dedicated service, we bring forth a highly reliable, flexible, and skilled approach, maintaining the highest industry standards and scalable capacity.

Genotyping by Sequencing (GBS)

Genotyping by Sequencing (GBS), also known as reduced-representative sequencing (RRS), is a strategy for generating whole-genome high-throughput sequencing data by sequencing only a small portion of the genome, effectively reducing the cost of analysis. GBS is simple, quick, specific, highly reproducible and rapid due to the simultaneous detection of SNPs and genotypes, and may reach important regions of the genome that are inaccessible to capture sequencing approaches. Thus, the key components of this system have the advantages of lower cost, reduced sample handling, fewer PCR and purification steps, no size fractionation, no reference sequence limits, and efficient barcoding, and the system is easy to scale up.

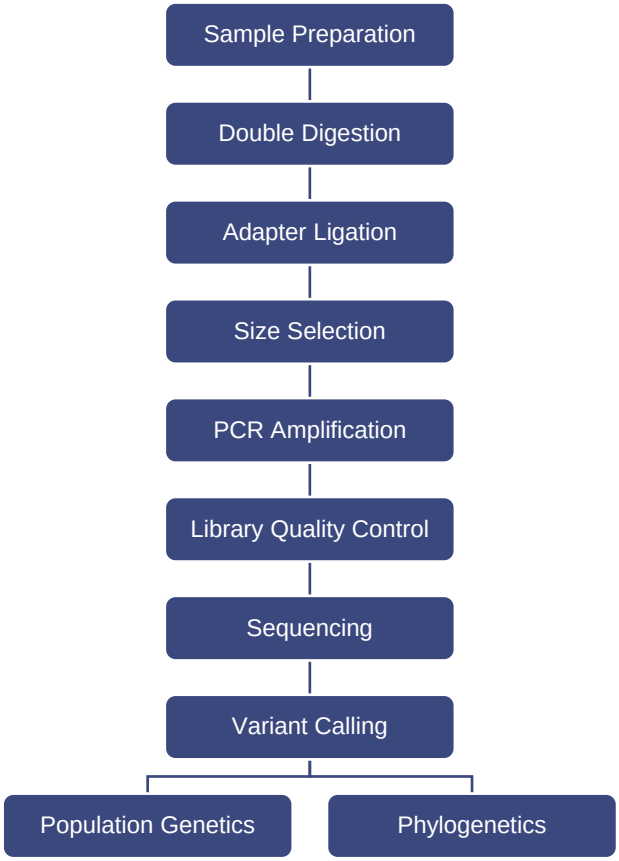
Our Features

- Reaching important genome regions
- Simultaneous detection of SNPs and genotypes
- More flexibility in targeting specific areas of interest
- Simplicity and quick turnaround
- Available for GWAS, genetic linkage analyses, molecular marker discovery, *etc.*



ddRAD-Seq

ddRADSeq (Double digest restriction-site associated DNA sequencing) is a variant of RAD sequencing that treats genomic DNA with double restriction enzymes to eliminate random shearing. The detection area and coverage can be flexibly adjusted without the need for a reference genome.



Our Features

- No reference genome required
- A cost-effective alternative to whole-genome sequencing
- Scalability of markers yield from thousands to hundreds of thousands
- Select from a variety of restriction enzymes tailored to the specific genome under investigation

2b-RADSeq

2b-RADSeq is similar to ddRAD-Seq, but uses type IIB restriction enzymes and requires a reference genome. It targets all restriction sites and requires highly reduced library sequencing, further reducing losses and processing time.

Our Features

- Flexible tag number
- Consistent label length
- High density of markers
- No interim purification steps
- Low DNA input and degraded DNA compatibility
- Highly reduced libraries for efficient sequencing

Whole Genome Sequencing

Whole genome (re)sequencing stands out for its advanced applications, enabling the identification of the largest number of SNP calls. It efficiently detects SNP motifs closely linked or overlapping with potential phenotypic variants. This makes it particularly well-suited for analyzing highly heterozygous populations and conducting Genome-Wide Association Studies (GWAS).

Our Features

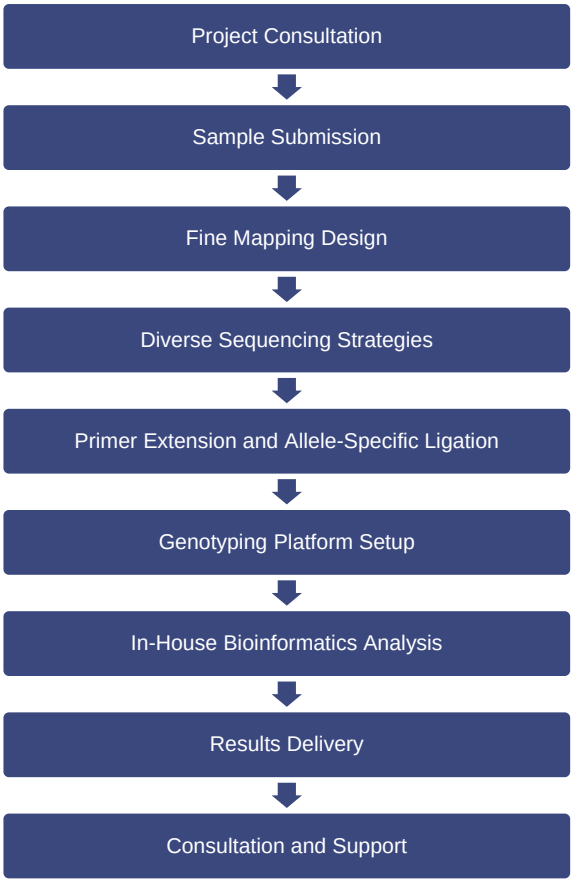
- Single base-pair precision providing a comprehensive view of the genome
- Enabling the detection of rare and novel SNPs
- The annotation of functional elements within the genome, providing insights into the potential functional consequences of identified SNPs.
- Beyond SNPs, enabling the identification of long-range SV and CNV
- Integration of WGS with epigenomic data enhancing the understanding of the functional consequences of genetic variations

SNP Genotyping

CD genomics provides SNP genotyping service for large SNP number and high volume of samples to help you validate and confirm the SNP loci of interest based on a subset of the detected SNPs, based on **Sanger sequencing**, **MassARRAY**, **TaqMan**, **SNaPshot**, **and targeted NGS**. SNP fine mapping often follows large-scale whole-genome SNP genotyping studies to zoom into potential genes associated with the phenotypes of interest.

Our Features

- Comprehensive SNP validation
- Tailored for high sample volume
- Fine mapping service for broad-scale SNP genotyping
- A high call rate for selected SNPs with our in-house bioinformatics platform
- Diverse sequencing strategies, including Sanger sequencing, MassARRAY, TaqMan, SNaPshot, multiplex PCR-based NGS, and probe panel-based NGS.



SNP Microarray

High-throughput DNA microarrays can analyze hundreds of thousands of SNPs simultaneously with probes designed for known sequences, enabling the screening of rare variants at the genome-wide level. The advantage of our SNP microarrays is that they can be precisely designed for different purposes, such as susceptibility gene mutations, disease-associated mutations, complex trait studies, and the construction of SNP-based DNA fingerprints.

Our Features

- Custom, scalable, and flexible.
- Exceed 99% with pinpoint accuracy, ensuring reliable results.
- Cost-effective and high-throughput
- Targeted or whole-genome coverage for confident SNP identification
- Beyond SNPs
- Versatile applications

Microsatellite Analysis

Microsatellites, also known as simple sequence repeats (SSRs) or short tandem repeats (STRs), have been popular markers due to their high polymorphism. Genotyping is an accurate, cost-effective, and fast approach to distinguish microsatellite alleles, boosted by successive technical advances, including multiplexing PCR and next-generation sequencing technologies.

Our Features

- **Microsatellite Genotyping Service**: Benefit from our sequencing-based service, delivering accurate and insightful results for diverse research applications.
- **Microsatellite Instability Analysis**: Engage in microsatellite instability analysis to unveil potential genetic aberrations and gain insights into genomic stability.
- **Microsatellite Development**: designed to identify and characterize novel microsatellite loci tailored to your specific research needs.
- **Hi-SSRseq**: providing high-throughput and in-depth microsatellite analysis for large-scale genomic studies.

CNV Genotyping

Copy number variations refer to the presence of extra or missing copies of a particular DNA segment compared to the reference genome. Based on sequencing and CGH microarray technologies, we offer end-to-end **CNV typing services**, encompassing every stage from meticulous sample processing to advanced sequencing and thorough data analysis.

Our Features

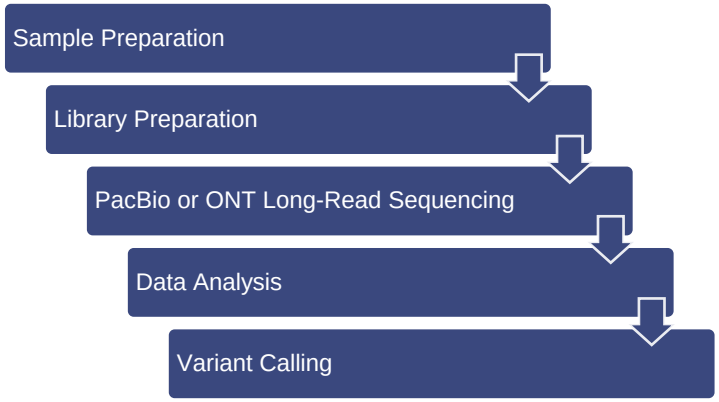
- High-resolution CNV detection
- Flexible and tailor-made solutions
- Comprehensive annotation and interpretation of the detected CNVs

Long Read Sequencing for Genotyping

Despite the high accuracy of short-read sequencing, obtaining accurate genotypes for long insertion or deletion and highly repetitive genomes remains problematic. Long-read sequencing systems, including the Oxford Nanopore Technologies (ONT) and the PacBio SMRT technology, have become popular *de novo* choices for genome assembly and structural variant characterization, which are expected to be used for routine genotyping.

Our Features

- Long-read precision (over 10 kb)
- PCR amplification-free approach
- Direct sequencing of repeat expansions and regions with extreme GC content
- Variant phasing and distinguishing genes of interest from their pseudogene



Our Results

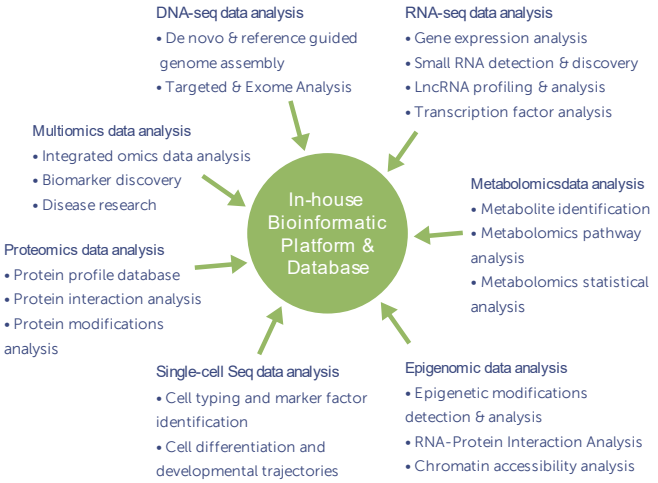
The report is organized into two main sections:

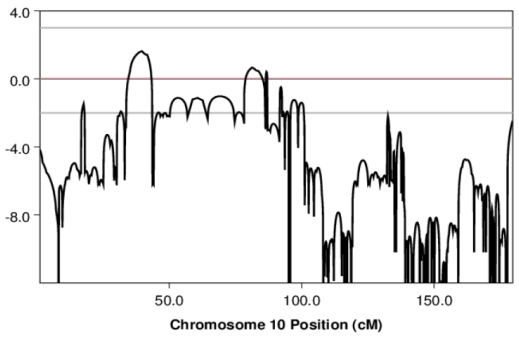
General information

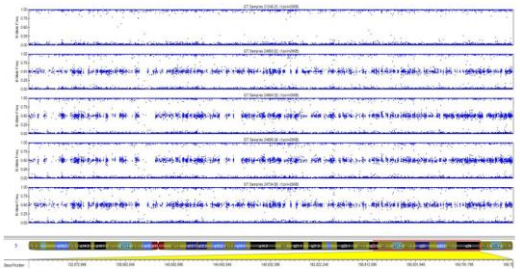
- Experimental procedure
- Data quality control
- Reference data alignment
- Data annotation
- Variant calling (SNP/Indels/CNV/SV)

Custom bioinformatic analysis result

- Purity and hybrid authenticity identification
- Authenticity and variety identification
- Genetic evaluation of breeding parents/germplasm resources
- Marker validation
- Genetic diversity analysis
- GWAS
- Genetic map construction
- QTL localization and population analysis
- Targeted improvement in desired traits
- Molecular marker-assisted breeding
- Genomic selection (GS) breeding
- Germplasm genebank construction
- Custom analysis







Applications

Single-nucleotide polymorphisms (SNPs) are found in both coding and non-coding regions of genes, one of the most common types of variation; single nucleotide variants (SNVs) are characterized by changes in a single position within the DNA sequence, including conversions, reversals, insertions or deletions, with a variable frequency of >1%. In humans, approximately 3 × 106 SNPs were found, with an average of 1 in 500-1000 base pairs.

Studies of population-specific SNP datasets are useful for predicting individual responses to certain drugs, sensitivity to the environment, and risk for disease development. Alternatively, SNPs can be used to track the inheritance of genetic disorders within families and provide insight into SNP linkage.

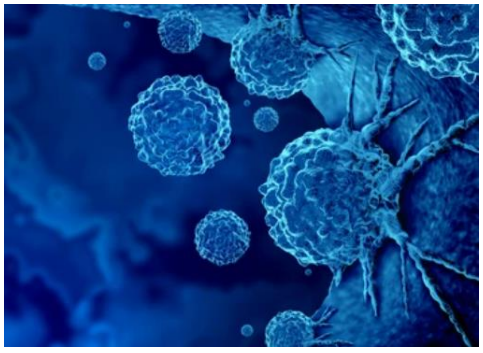
CD Genomics, as an advanced genomics service provider, has equipped sequencing-based genotyping technologies as well as SNP array services for our global customers. We deliver SNP and CNV discovery, genotype screening, and subsequent association analysis results, dedicated to facilitating research in pharmacogenomics, molecular breeding, genetics, and more.

Agrigenomics

High-throughput genotyping stands as a beacon in agrigenomics, spotlighting SNPs linked to economically pivotal factors such as yield, resistance to environmental stresses, and product quality on a genome-wide scale. This comprehensive approach serves as a beacon for screening and discovery tools, guiding breeding decisions and elevating the value of crops and herds.

Pharmacogenomics

In pharmacogenomics, the exploration of gene variants and their associations with drug responses takes center stage. This nuanced understanding holds the promise of improved outcomes for individuals and healthcare providers alike, enhancing drug safety, efficacy, and ultimately reducing healthcare costs.



Oncology

In the realm of oncology, high-throughput genotyping, particularly through SNP markers, emerges as a cornerstone for assessing cancer polygenic risk, progression, and treatment response. By utilizing advanced sequencing and association analysis, the genetic underpinnings of cancers, including breast and lung cancers, are unveiled. This knowledge not only identifies the genetic basis but also steers the trajectory toward precision prevention, promising tailored strategies for the future of cancer care.