# ONEOMICS

Pioneer in Genomics Services

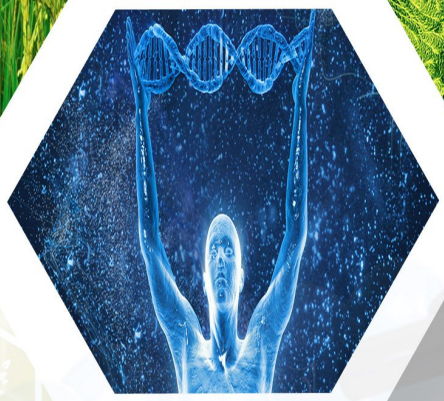
sales@oneomics.in

# About Oneomics

ONEOMICS is a privately owned company headquartered in Trichy, Tamil Nadu, India focused on Genomics cum bioinformatics. Oneomics is a team of highly qualified specialists has detailed knowledge of Genomics. Our founding team recognized that the life sciences were turning into a data-intensive field, creating and commercially offering an increasing range and scale of omics measurements. While the experiments were easily available to all researchers in the life sciences, analysis of the produced broad biological data sets has become critical. It was a logical step to assemble a team of the best bioinformaticians, data scientists, software developers and molecular biologists, and start providing professional support to the front line of life science researchers and businesses. We are in process of developing new softwares which could be commercially viable and can complement in data analysis. Over the years, our laboratory has developed into a diverse team of bioinformatics experts to provide a fully customizable service for all omics-intensive investigations. We offer our services to anyone interested in these technologies. Our goal is to provide high added value services . In accordance with the current technical developments, our laboratory department deals with the complicated processing of your samples and their analysis. Our service team manages your sophisticated genomic samples and offers quality services.

# Table of Contents

ONEOMICS



# ONEOMICS'S NEXT GENERATION SEQUENCING AND BIOINFORMATICS ANALYSIS

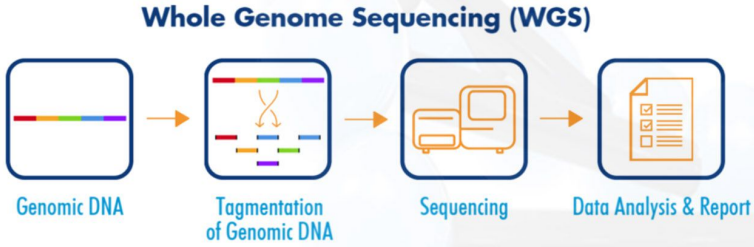
## Whole Genome Sequencing

The whole genome sequence of the genome means the entire genome is read and analysed, providing the most detailed genetic variation information. The first household genome map was completed by Oneomics and various fauna-flora genomes were successfully decrypted.



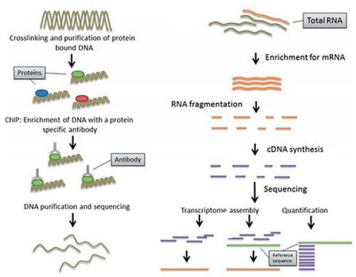
## Denovo Sequencing

*De novo* sequencing is commonly achieved without prior knowledge of the sequencing. De novo sequencing has proven successful in confirming and expanding upon consequences from database searches, providing splendid assets for knowledge of species. Some of the most important information obtained through the re-sequencing of the genome DNA of an organism are the human genetic variations, such as single nucleotide polymorphism (SNP), copy number variation(CNV), and structural variation(SV)




## Resequencing

Resequencing is one of the most common applications of next generation sequencing, particularly with human samples. It is used to evaluate a sample's genomic variations against a specific reference sequence. The created sequence for SNPs and CNVs as well as genomic rearrangements and indels is aligned with the reference sequence and mined.





**Sequencing Platform**
HiSeq X / NovaSeq 6000
NextSeq 500, MiSeq
PacBio RS II, PacBio Sequel

**Service Overview**
**WGRS**
SNV/Indels
- Structure Variantion
- Copy Number Variantion
- Trio Analysis

**Data Analysis**
**De novo Sequencing**
**Standard Data Analysis**
- Genome Assembly
- Genome Annotation
- Consensus sequence assembled into contigs

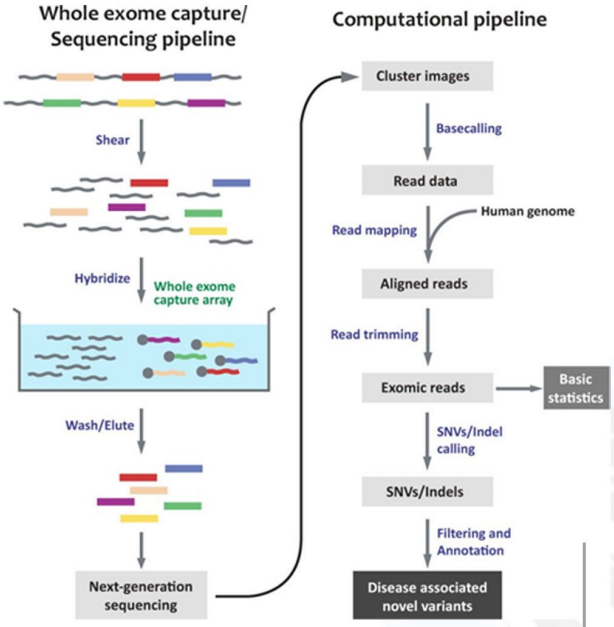
**Advanced data analysis**
- Gene Prediction &Annotation

**Main Capture Kit**
- TruSeq Nano DNA Sample Prep Kit

**Standard Data Analysis**
- Mapping Statistics
- Gene Expression Profile
- SNPs and InDels calling by mapping the reference genome (Human, Mouse, Rat)
- Novel Transcripts
- Alternative Spliced Transcripts
- Fusion Gene (Human, Mouse, Rat)

**Advanced Data Analysis**
- Customized Analysis
- Differentially Expressed Genes (DEGs)
- Gene Ontology Analysis

## Exome/Targeted Sequencing




Human exome sequencing is selective sequencing of human genome coding areas, after the exome has been identified effectively.Although the exome region is only 1% (30 Mb) of the entire genome, its biofunctions are very significant. Exome sequencing is a technology which controls the region of the exome and is very economical in comparison to the sequencing of the entire genome. It is mostly used in clinical research, as it can be widely used for cancer and chronic disease genetic recognition.

**Enrichment Methods**

- Agilent SureSelect Human All Exon Kit
- Illumina Nextera / TruSeq Exome Enrichment Kit
- ThermoFisher / Ion AmpliSeq Exome RDY Kit

**Main Capture Kit**

- SureSelect XT All Exon V5 Kit
- SureSelect XT All Exon V6 Kit
- SureSelect XT custom Teir 1

**Sequencing Platforms**

- HiSeq X, NovaSeq 6000 NextSeq 500, Miseq

**Service overview**

- SNV/Indels
- Copy Number Variantion
- Trio Analysis

**Data Analysis**

**Standard Data Analysis**

-Variant Calling (SNPs/InDels) & Annotation

**Advanced Data Analysis**

-CNV (Copy Number Variation)
-Various Variant Calling Pipeling
-Cancer Analysis/ Family Analysis / Population Analysis

**Custom Sequencing**

- Standard Data Analysis

-Variant Calling (SNPs/InDels) & Annotation

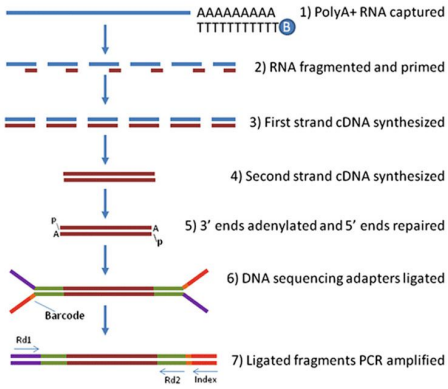
- Advanced Data Analysis

-Various Variant Calling Pipeling
- Population Analysis

| Sequencing System | iSeq™ | MiniSeq™ | MiSeq® | NextSeq® | HiSeq® | HiSeq® X | NovaSeq® |
|---|---|---|---|---|---|---|---|
| | | | | | 4000 | Five/Ten | 6000 |
| **Output per run** | 1.2 Gb | 7.5 Gb | 15 Gb | 120 Gb | 1.5 Tb | 1.8 Tb | 1 Tb - 6 Tb[1] |
| **Instrument price** | $19.9K | $49.5K | $99K | $275K | $900K | $6M[2]/$10M[2] | $985K |
| **Installed base**[3] | NA | ~600 | ~6,000 | ~2,400 | ~2,300[4] | | ~285 |

## RNA Sequencing

Transcriptome sequencing by using Next Generation Sequencing is a fast and reliable tool for genomic knowledge identification. Oneomics provides the complete analysis of mRNA transcript expression, allowing the discovery of novel genes, identification of novel SNP and InDel, discovery of novel splice variants and chromosomal rearrangements, and identification of fusion genes. Differences in the value of the transcriptome of each sample can be verified with transcriptome sequence.All living organisms are transcribed in an intermediate called mRNA from DNA sequences to generate protein based on their own genetic data. If such mRNA is analyzed, you can get information on the genes that have been activated at certain points.




**Service overview**

Reference Based

- Gene Expression
- DEG
- Splicing Variants
- Gene Fusions

De novo Based

- Transcript Assembly
- Gene Expression
- DEG

**Main Capture Kit**

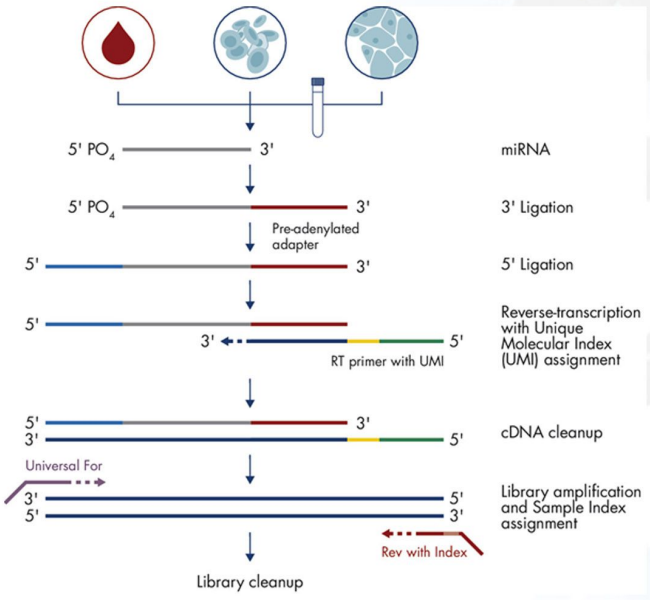
- TruSeq Stranded mRNA Sample Prep Kit
- TruSeq Stranded Total RNA Sample Prep Kit
- NEXTflex Small RNA-Seq Kit v3

**Data Analysis**

- De Novo Sequencing Standard Data Analysis
- De novo Assembly Statistics
- Gene Expression Profile Advanced Data Analysis
- Blastnt or Blastnr
- Gene Annotations & Ontology Analysis
- Differentially Expressed Genes (DEG)

## Small RNA Sequencing

Small genome- encoded RNA molecules are particularly responsible for regulating the gene expression. Oneomics's NGS technology allows all the small RNA families to be sequenced and quantified in a sample, and miRNA, siRNA, miRNA and other non-coding RNAs profiled. Single cell sequencing recognizes cell diversity and can be applied to a number of research fields such as cell therapy screening, stem cell research, anticancer development, and fundamental structure growth research. In each of the cells manufactured using NGS technology, existing data and amplifying capabilities combine characteristics and various methods for analyzing data.. Different biological interpretations are possible by examining the cell type, cell type or tissue by clustering the transcriptome genome if single cells are used




**Service overview**

- Gene Expression
- Cell Type Signature
- Tumor Heterogeneity
- Tumor Microenvironment
- Single Cell Immune Profiling

**Data Analysis**

**Small RNA Sequencing**

**Standard Data Analysis**

- Expression Profiles
- Novel miRNA
- Differentially Expressed miRNA Advanced Data Analysis
- Identified and Novel miRNA
- Gene Set Analysis
- Comparative Data Analysis

## Epigenome Sequencing
## WGBS(Whole Genome Bisulfite) Sequencing
## MBD(Methyl-CpG Binding Domain) Sequencing
## Methylation Sequencing

Methylation is one of the main mechanisms for controlling gene expression in chromosomal DNA. Hence, to describe base methylation is to understand gene regulation.Comparison of the sequence obtained from the bisulfate-treated library to the reported sequence allows for differential methylation recognition.The methylation condition can be quantitatively defined on the target regions (e.g., CpG islands).

**Sequencing Platforms**

- HiSeq X
- HiSeq 2500/4000, NovaSeq6000
- MiSeq System

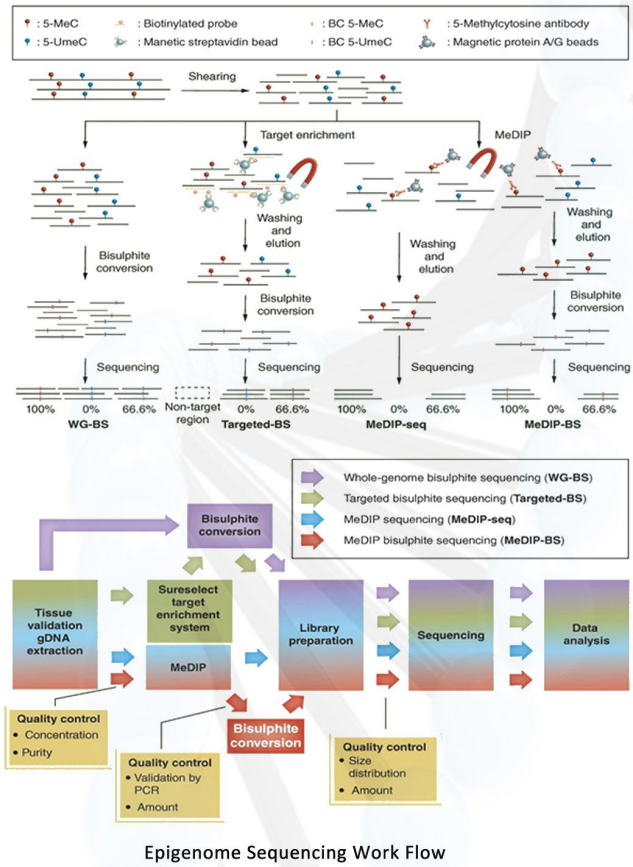
**Data Analysis**

Standard Data Analysis

- Universal Methylation Profiles
- Specific Methylation Profiles
- CpG Islands
- Differentially Methylation Regions (DMRs)

**Advanced Data Analysis**

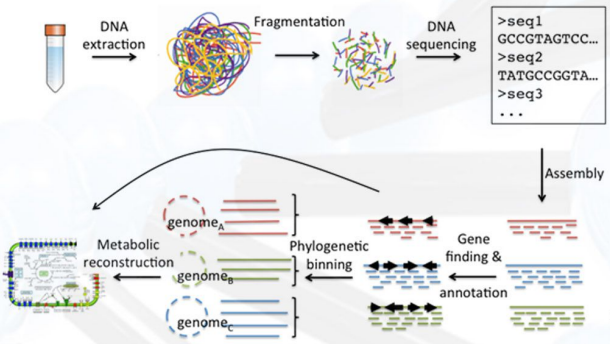
- DMR-Associated Genes
- Gene Set Analysis
- Comparative Analysis




Epigenome Sequencing Work Flow

## Metagenome Sequencing

NGS emerges as an effective instrument for profiling complex microbial communities. New technology dramatically reduces both the time and the expense of DNA sequencing, allowing a small laboratory to sequence the genome of its preferred bacterium entirely .Different strains have been sequenced for several bacterial species of interest. Such reference strains are attractive subjects in genetic engineering, since derived strains can be easily compared with the parental strain at the genomic level using NGS methods of Oneomics




Metagenomics Sequencing Work Flow

## Amplicon Metagenomic Sequencing

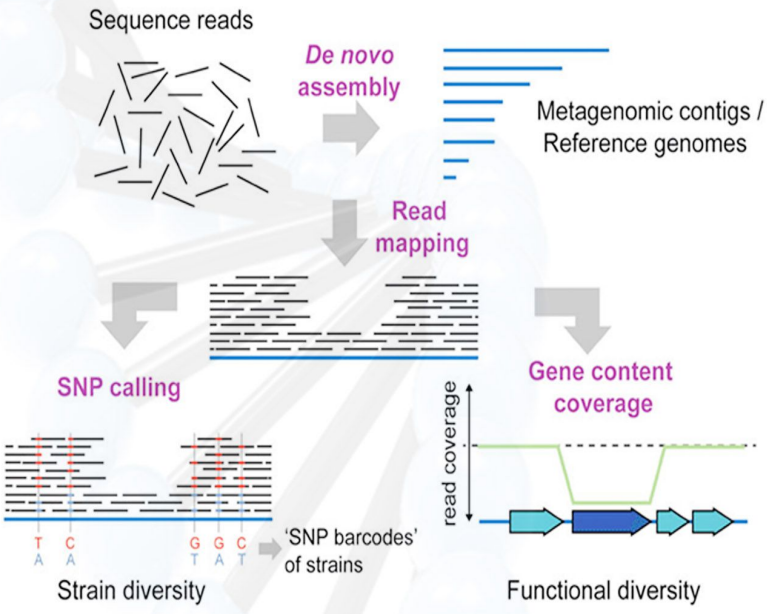
Metagenomic sequencing allows accurate detection of the diversity of micro-organisms in a particular environment.

Sequencing Types & Platforms

- 16S rDNA sequencing MiSeq system
  -V3 to V4 Regions
  -Cutomized Regions
- Full-length 16s rRNA sequencing on PacBio RS II or Sequel
- 18S rDNA/ITS sequencing

## Shotgun Metagenomic Sequencing

Shotgun metagenomic sequencing is a comprehensive method of sampling all the genes in all the species present in a given mixed sample. The method enables evaluation of the microbial diversity and identification of species abundance under different conditions. DNA is prepared for shotgun sequencing and uniformly shaved into smaller fragments prior to sequencing. Shotgun metagenomic sequencing offers knowledge about both which species are present in the population and what metabolic processes are possible.




Data Analysis

Amplicon Metagenome Sequencing

Standard Data Analysis

- Community Diversity Analysis (OUT)
- Probiotics Analysis

Advanced Data Analysis

- Phylogenetic Tree
- Hierarchical Taxonomy Graph
- Heatmap
- PCA biplot

Amplicon Shotgun Sequencing

- Standard Data Analysis
- Assembly
- Gene Prediction & Annotation
- Taxonomy Analysis

## Long Read Sequencing

Researchers continue to face challenges in finishing the genomes, characterizing variants, and recognizing the role of key biological markers given the dramatic progress of NGS technology. In many areas of research, accurate read lengths of 1,000 base pairs (bp) or longer in a single sequencing reaction are important for -investigators. Oneomics implements PacBio RS II / Sequel sequencer technology to overcome the DNA strand's long reads (up to 10 kb), enabling structural and cell type variability not explained by other sequencing technologies to be observed. The versatility of long read sequencing systems in Oneomics allows you to easily switch between platforms and applications as the changing research environment changes research needs.

Sequencing Platforms

- PacBio RS II / PacBIo Sequel

Applications

Genome Finishing & De novo Assembly

- Support of multiple applications: genome ending, metagenomics, de novo assembly, meta-assembly with long & short reads
- High-quality reads of up to 20kb

Whole Human Genome Phasing

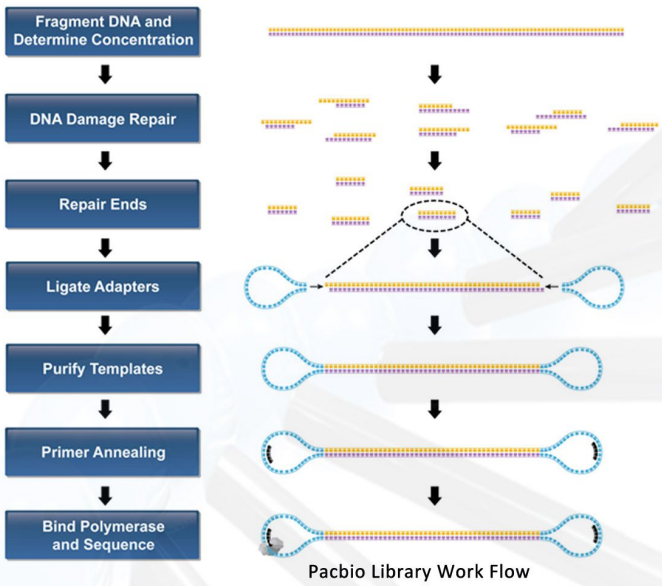
- Explores the distinct halotype quality of two homologous chromosomes
- One assay to process over 94 per cent of heterozygous SNPs and InDEIs
- Easy push-button analysis within one day

Pacbio Sequel

## Pacbio Sequencing

Single Molecular Real-Time (SMRT) sequencing employs a specialized flow cell with several thousand individual picolitre wells with transparent bottoms— zero-mode waveguides (ZMW). The polymerase is fixed to the well's bottom and enables the DNA strand to advance through the ZMW. As a result, a single molecular could be the focus of the system. SMRT sequencing allows real-time visualization of fluorescently tagged nucleotides that are synthesized along individual molecules of the DNA template. When the template and polymerase dissociate, the sequencing reaction terminates. The PacBio instrument's average read length is about 2 kb, and some reads may be more than 20 kb. Longer readings are particularly useful for assembling new genomes de novo

Highly repetitive elements present in eukaryotic and prokaryotic genomes pose a challenge to the assembly of genomes and make it difficult to study repetitive sequences in detail. Long-read sequencing offers reads spanning hundreds or thousands of kilobases (kbs), which can cover complex or repetitive regions with a single continuous reading, allowing these broad structural features to be solved. Besides significantly longer and highly accurate DNA sequences from individual unamplified molecules, it can also exhibit where methylated bases exist, thereby supplying functional information about the genome encoded DNA methyltransferases. PacBio SMRT sequencing has unique advantages in the genomics, metagenomics, transcriptomics and epigenetics of de novo studies.




Pacbio Library Work Flow

### Advantages of PacBio SMRT Sequencing

- Longest average read lengths
- Highest consensus accuracy
- Uniform coverage
- Simultaneous epigenetic characterization
- Single-molecule resolution
- Rapid and affordable

### Our PacBio SMRT Sequencing services

- Long-Read metagenomic sequencing
- Bacterial whole genome de novo sequencing
- Fungal whole genome de novo sequencing
- Full-length transcripts sequencing (Iso-Seq)
- Human genome PacBio SMRT sequencing
- Full-length 16S/18S/ITS rRNA sequencing

The bioinformatics pipeline involves *de novo* assembly, identification of specific modifications, generation of consensus between single molecules, transcript analysis, amplicon analysis, sequence alignment with variant detection. And there's more data mining available according to your specific needs.

## Nanopore sequencing

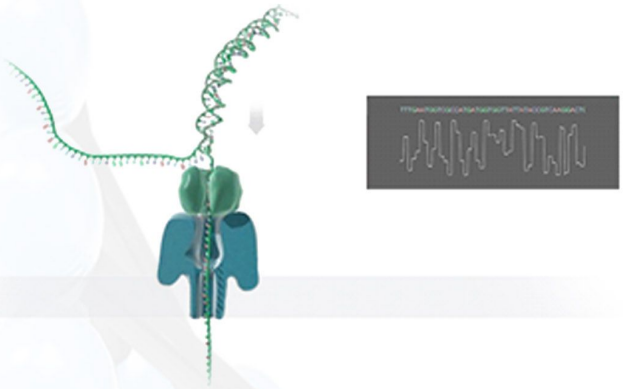
The nanopore based DNA and RNA sequencing technology was developed by Oxford Nanopore Technologies. The Nanopore sequencer is known to be compatible with a range of input materials, including genomic DNA, DNA amplified, cDNA, and RNA. Nanopore biomolecular sequencing technology has wide applications in the life sciences, Identification of pathogens, monitoring of food safety, genomic analysis, monitoring of the metagenomic environment and bacterial antibiotic resistance characterisation.

The Nanopore sequencer has some highlighted advantages when opposed to the conventional workflow.

• Ultra-long reading lengths of several hundred kb may be sequenced in a single continuous reading for high molecular weight samples of DNA (HMW-DNA) The data on nanopore sequencing boost de novo genome assemblies and structural genomic variant and transcriptome studies considerably.

• The nanopore is holes of a nano-scale creating gateways through membranes in nature. A nanopore moves through nanopores an ionic current, and tests the current changes. We cause disruption in the current when molecules such as DNA or RNA pass through the nanopores. You can use the knowledge about the current change to classify the molecule. The native strand of interest is sequenced directly, without optics or amplification. Different kinds of library preparation protocols allow the direct sequencing of DNA / RNA with epigenetic information.

• The streaming of sequence data in real time allows quick insight into samples, on-demand sequencing, and complex workflows.



Oxford Nanopore Technology

## Genotyping

For small, big, regular or personalized projects, on humans and many other species, Oneomics offers a completely versatile genotyping service. Our powerful portfolio includes clusters, reagents, instruments, and bioinformatics tools that allow you to detect common and rare single nucleotide polymorphisms (SNPs), variations in copy numbers (CNVs), and other genetic variations. Oneomics genotyping services accommodate projects with a broad range of applications. We deliver a highly trustworthy, versatile and knowledgeable service combined with high industry standards and scalable ability, and have been recognized as the premium SNP genotyping option.
Depending on the application and species, the intent of the experiment, the number of SNPs per sample (from just a few to five million), and the number of samples in the test, We offer various genotyping technologies. Our comprehensive SNP genotyping services include both full-genome SNP screening testing and fine SNP validation testing based on 5 platforms — Affymetrix, Illumina, Sequenom MassARRAY, ABI TaqMan, and ABI 3730XL.

## Whole Genome SNP Genotyping

Oneomics provides full- genome SNP genotyping for the overview of the entire genome by using both microarray technologies and next-generation high-throughput sequencing (NGS), enabling genome-wide discovery and screening of the SNP loci. Genome-wide association studies with SNP markers are expected to allow identification of genetic variation that underlie complex disorders.

For SNP Genotyping, we provide genotyping by sequencing and dd-RAD. 2b-RAD is a reduced genome representation sequencing or restriction site associated DNA sequencing strategy, to discover and genotype genetic variants in a cost effective manner, which are applicable to both mode l organisms with known genomes and non-model organisms with unknown genomes.

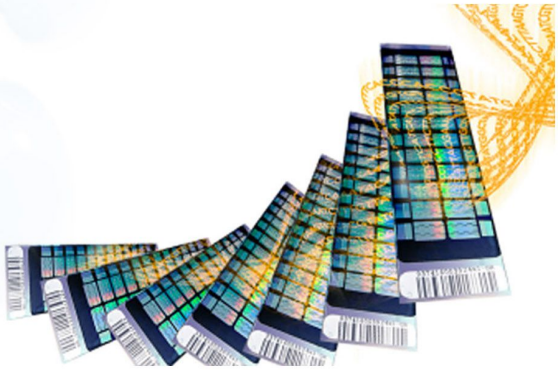
## Genotyping by Sequencing (GBS)

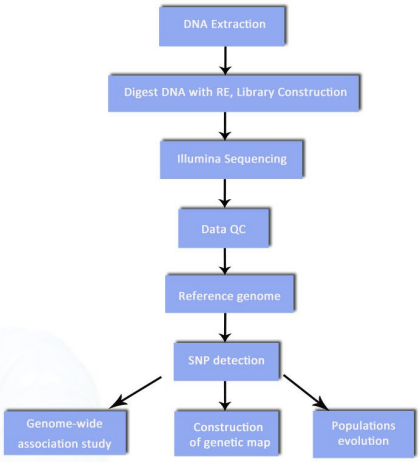
Genotyping by Sequencing (GBS), which belongs to one of the techniques of reduced-representation genome sequencing, is a tool for discovering single nucleotide polymorphisms (SNP) to conduct genotyping trials. By using restriction enzymes to cleave the DNA combined with DNA-barcoded adapters, GBS greatly reduces the genome size. GBS can provide high SNP coverage in gene-rich regions of the genome in a highly cost-effective manner by selecting suitable restriction enzymes, and increase the number of tags in the assay. The sequenced portion of the genome within a population is highly consistent, as restriction sites are typically conserved across organisms.

As a consequence, GBS is easy, quick, accurate, highly reproducible and rapid due to the simultaneous detection of SNPs and genotypes, and can reach important genome regions that are inaccessible to capture sequencing approaches. The key components of this system therefore have the benefits of lower cost, reduced sample handling, less PCR and purification steps, no fractionation of the samples, no reference sequence limits and effective barcoding, and the system is easy to scale up. Such features make GBS a powerful tool for implementing study of genome-wide association (GWAS), study of genomic diversity, analysis of genetic correlation, discovery of molecular markers and selection of genomics in large scale plant breeding programmes.

### Key Features and Advantages

- Reduced sample handling
- Few PCR & purification steps
- No DNA size fractionation
- Efficient barcoding system
- Simultaneous marker discovery & genotyping
- Large scales






GBS Work Flow

## SNP Microarray

Oneomics offers various genotyping services fuelled by state- of - the-art variant detection and SNP genotyping technologies, providing high quality data at low cost per sample. Microarray is a valuable tool for researchers to investigate genetic variants from discovery applications to routine screening, such as single nucleotide polymorphisms (SNPs), and significant structural changes. Affymetrix and Illumina genotyping microarrays both offer positive performance in precision medicine programs, clinical and translational testing, pharmacology, customer screening, and agricultural applications. Multiple genotyping strategies are possible, based on the species and selection of SNPs.

### Advantages of SNP Microarray

- Custom, flexible, and scalable
- High call rates (> 99%) and high accuracy
- Cost-effectiveness and high-throughput
- Identifies SNPs in a targeted or whole genome scale
- In addition to SNPs, other genetic differences, such as copy number variations, can be measured
- Applied in biomarker discovery and validation, clinical testing, GWAS, pharmacogenomics, forensics, and breed discrimination


SNP Microarray Work Flow

### Bioinformatics Analysis

We provide tailored bioinformatics analyses including:

- SNP identification
- GWAS
- Linkage map construction
- Genomic selection
- Population structure analysis

## dd-RAD Sequencing

dd-RAD method uses Type IIB restriction enzymes (REs), which share the genomic DNA cutting feature on both sides of the recognition to create a fixed-size dsDNA fragment, resulting in protruding, non-cohesive ends. Subsequently, a biotinylated adaptor similar to the initial enzyme catches DNA fragments of interest. Different approaches such as restriction-site associated DNA (RAD) and genotyping-by-sequencing (GBS) technologies, compared to dd-RAD, lack geographic precision and generate many sequences from non-informative and repetitive regions.

Sequencing of these short and standardized tags offers many advantages, including targeting all restriction sites, even sequencing depth across sites, high reproducibility for quantitative analysis, low cost of sequencing per tag and low sensitivity to DNA degradation.

### Applications

- Bin Map construction and QTL location
- Population genetic study
- Population evolution analysis
- Genome-wide association study
- Genome phylogeny
- Genomic selection
- Linkage and association mapping
- Discrimination of microbial strains
- Detection of somatic mutations

### Advantages of dd-RAD

- Accurate and affordable
- Flexible tag number
- Consistent label length
- High density of markers
- Not requiring interim purification steps
- Allowing low DNA input and degraded DNA
- Highly reduced 2b-RAD libraries require much less sequencing for accurate genotyping


dd – Rad Sequencing Work Flow

### Bioinformatics Analysis

- Raw data quality control
- Statistical analysis
- SNP genotyping
- Annotation of SNP locus
- Construction of genetic linkage map
- Population studies

## Bioinformatics Analysis

Data analysis is an inherent part of our Sequencing Services for Next Generation. Skilled bioinformaticians explore with your research priorities and evaluate the results whether or not they have been collected in our Next-Gen sequencing lab. You can also tailor the standard research pipelines to your needs as well as to the performance of a pilot experiment that we can run on your dataset.

## DNA SEQUENCING DATA ANALYSIS

Our DNA Sequencing Data Processing workflow also adapts for assembly of non-model organism genomes. We generate assemblies of genomes based on WGS data, which are then computationally post-processed to achieve the best quality possible. The assembled genomes are then annotated using prediction of genes, automated searches of homology using genome databases and transfer of gene annotation from closely related organisms. Thorough novel genome annotation ensures the best possible starting point for transcriptome studies of these organisms.

### Variant calling

Deliverables:

- Full lists of variants for all samples with data-based evidence
- Filtered lists of variants based on any criteria (e.g. germ line control for mutations)
- Low-coverage regions where variants can not be called

### Variant annotation

- Functional and location annotation for every variant
- Minor allele frequencies in relevant databases
- Database identifiers for known variants
- Pathogenicity predictions

### Copy number analysis

### Genomic rearrangements

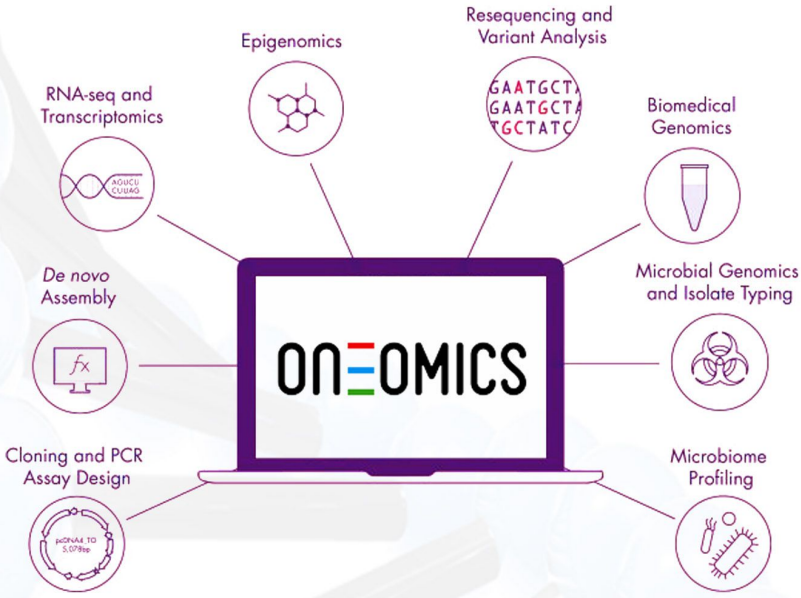
Deliverables:

- List of potential fusion genes
- List of all rearrangements

### Genome assembly and refinement

Deliverables:

- Assembled contigs in FASTA format
- Computationally-refined genome assembly
- Quality estimation scores




### Genome annotation

Deliverables:

- Loci of predicted genes
- Fully annotated genes based on homology searches
- Validated genes based on RNA-seq data

### Cell-free DNA biomarker discovery

- List of biomarker candidates from cell-free DNA
- Sensitivity and specificity estimates for each candidate Identified
- Database identifiers for identified mutations and predicted pathogenicity.

## METAGENOMICS DATA ANALYSIS

Metagenomics offers an unbiased insight into the microbial diversity of ecological niches, including host organism and soil samples. We assemble the sequence reads into contigs using whole-genome or, alternatively, 16S sequencing data, and assign them to species or operational taxonomic units (OTUs). Afterwards we measure each taxon's abundance. In the case of multiple samples, we compare and correlate the relative abundances with host phenotype or environmental factors. We recognize and annotate genes for whole- genome studies using both sequence homology and prediction of computational genes.

Deliverables:

- Quantitative characterization of microbial diversity
- Association of species/OTU with host phenotype or other environmental factors
- Identified and predicted genes with custom annotations

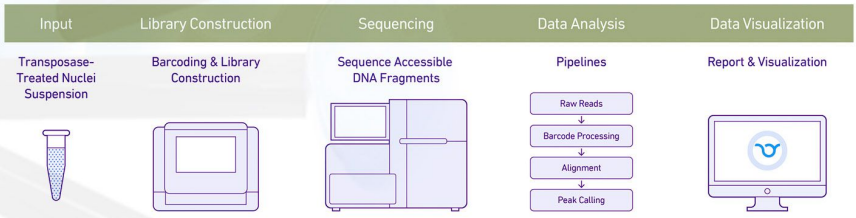
## RNA SEQUENCING DATA ANALYSIS

RNA sequencing data analysis shows complex gene regulation mechanisms Gene expression Transcriptome wide analysis are now extremely popular among researchers studying gene regulation in biological systems ranging from single cells to tissues and complex microbiomas. Our customers are usually interested in differential gene expression based on RNA sequencing, single cell RNA sequencing or microRNA sequencing steps, followed by pathway analysis and integration with other omics modalities such as epigenomics.

Although gene expression analysis is the core of the data analysis of RNA sequencing, it must not end there. We do prefer investigating some of the less obvious regulatory mechanisms and transcriptomic markers, including

- Alternative splicing and alternative polyadenylation events
- Allele-specific expression
- Long non-coding RNA expression
- Transposable element expression
- Genetic variants
- Post-transcriptional A-to-I editing events
- TCR and antibody sequences
- Fusion genes
- Novel transcripts

RNA-seq data analysis workflow

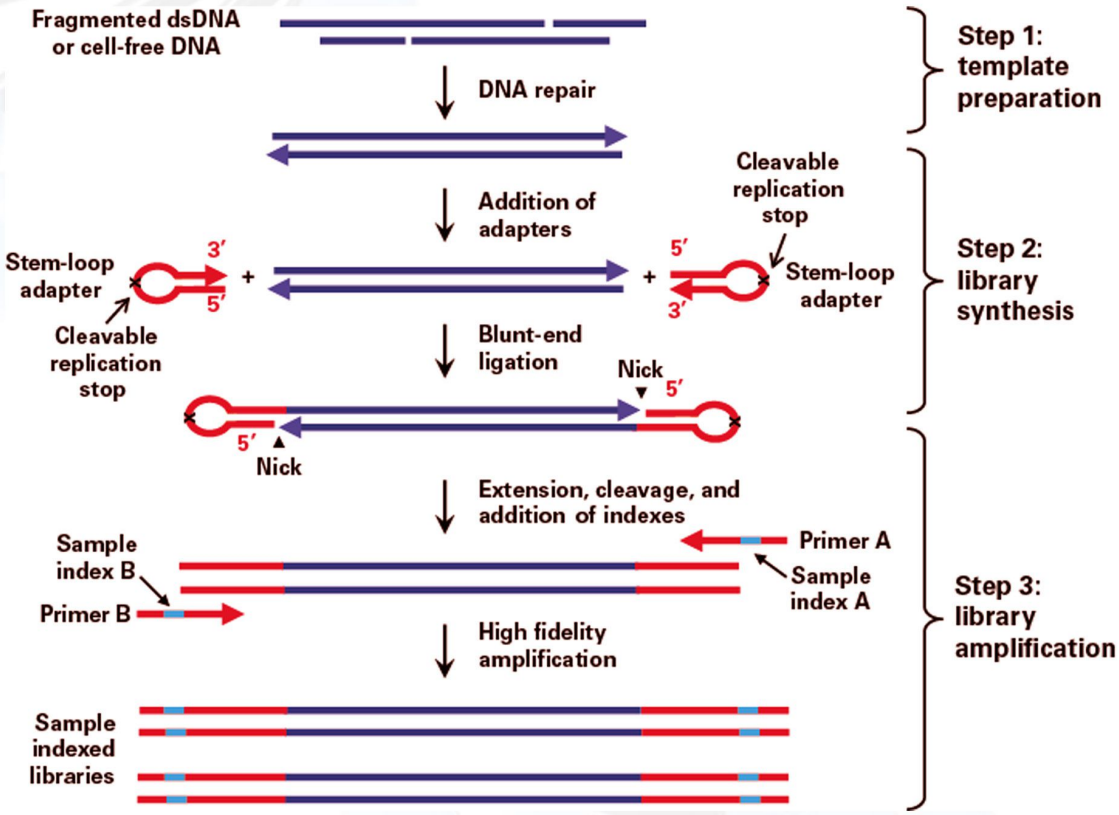



Project Workflow

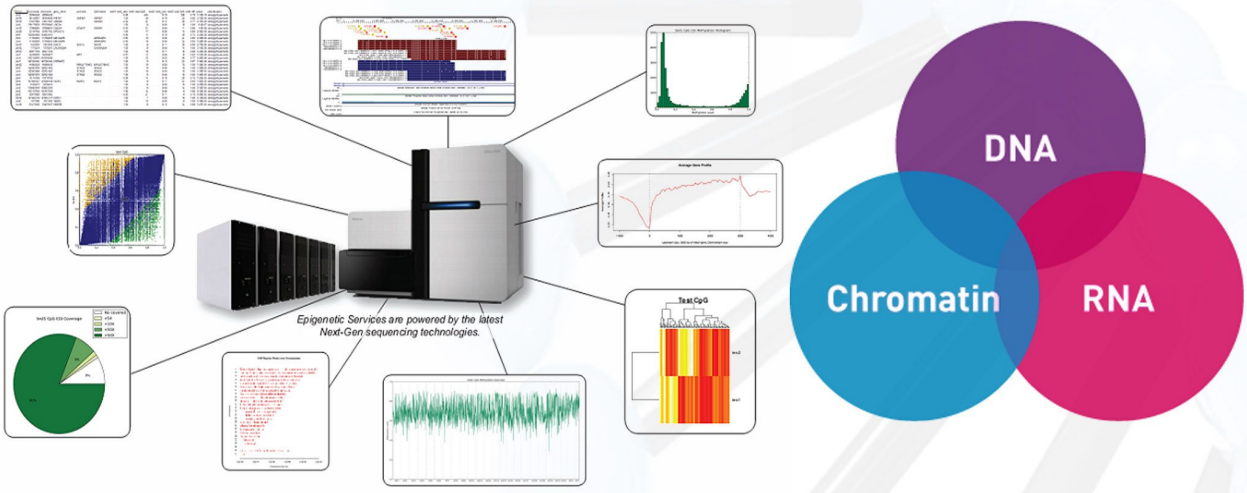
- Project Inititation
- Data Pre-processing
- Differential expression analysis
- Sequence analyses
- Predictive modeling
- Reporting and documentation

## EPIGENOMICS DATA ANALYSIS

Researchers Venturing into epigenomics also seek to map the complex state of DNA to clarify anomalies found through studies of gene expression. Our data analysis pipeline for the ChIP sequencing has been designed to classify both narrow binding sites for transcription factor and broader binding sites for histones. Customers interested in binding motives can opt for our motif discovery research, based on sequences where these molecules bind together. with our epigentics data analysis pipelines, methylated CpG islands can be identified using both bisulfite sequencing data (Bis-seq or RRBS) and DNA methylation sequencing data (MeDIP-seq) based on enrichment. To help understand the biological significance of these events, the methylated regions are then annotated with information such as the overlapping of identified promoters or enhancer regions. Linking these data back to data on expressions helps you to classify functional methylation events in your experiments.




Epigenetics



### DNA binding sites (ChIP-seq)

Chromatin immunoprecipitation of a DNA-binding protein, coupled with next-generation sequencing (ChIP-seq), is one of the most widely used methods for measuring high-throughput epigenomics. From these data, we can identify protein binding sites across the genome. We provide a list of significant peaks that are annotated with the genomic position and statistical information, such as duration, number of reads, meaning p-values, location relative to the nearest genes (distance to TSS), location within genes (exon, intron, UTR), and the binding motif contained within peak. The binding sites are often analyzed in tandem with transcriptomics data in order to identify the genes that the DNA-binding protein is likely to be of interest under control. If there are data on expression, expression of the nearest gene will also be included to promote the correlation.

Deliverables:

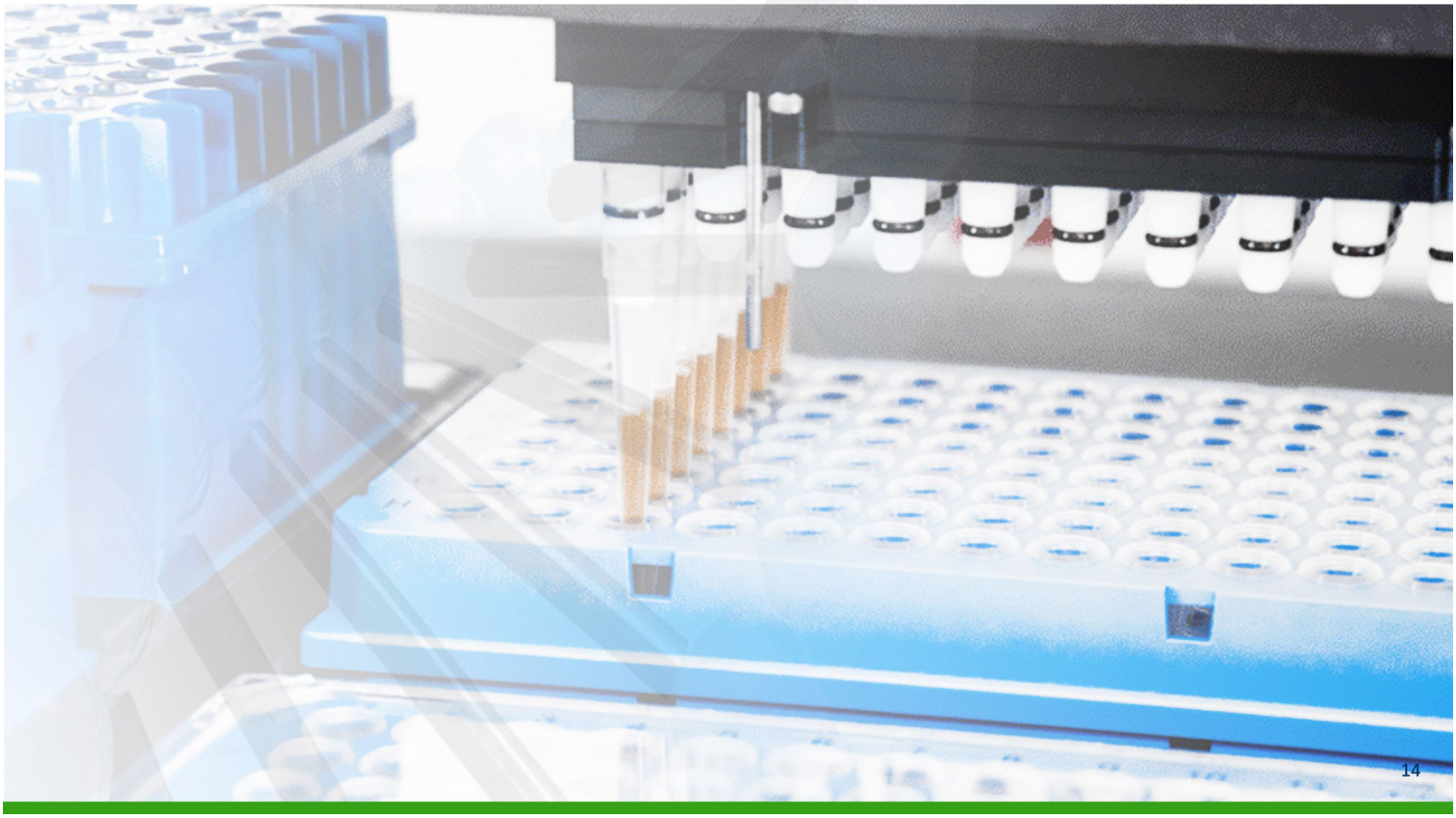
- Statistically significant binding locations
- Functional annotation of the binding loci
- Comparison of binding events between samples

### Chromatin state (ChIP-seq)

Then pulling down and sequencing the DNA results in genome-wide epigenomics data indicating the positions of modified histones by using antibodies that target specific histone modifications. Targeting multiple different markers and integrating the data can reveal a map of chromatin state indicating promoters, active and inactive enhancers and actively transcribed genes. Besides the completely annotated histone positions with different modifications, we can also provide an explanation of the chromatin state, given sufficient measurements of various modifications.

Deliverables:

- Statistically significant binding locations with functional annotation
- Comparison of binding events between samples
- Chromatin state interpretation based on combinations of histone modifications



## DNA-methylation (BS-seq, RRBS-seq, MeDIP-seq)

Adding methyl groups to cytosines in DNA shifts nearby gene expression rates. You can either pull down and sequence methylated DNA (MeDIP-seq) or convert unmethylated cytosines to uracil and sequenced (bisulphite sequencing). We will map, annotate and compare the methylated CpG islands using a variety of protocols to make analysis of your findings simpler for you. Methylation profiles can also be integratively analyzed using other epigenomics or transcriptomics measurements

Deliverables:

- Quantification of methylation for all CpG islands
- Functional annotation for differentially methylated CpG islands
- Methylated individual cytosines (for BS- and RRBS-seq)

## Open chromatin sequencing (ATAC-seq)

Chromatin's complex state is a central focus of epigenomics, and can be analyzed throughout the genome by testing the chromatin's openness. Genome segments that aren't densely packed can be traced using ATAC sequncing. Open chromatine is linked to active regions in terms of gene expression or expression regulation. Transcriptomics data are therefore normally integrated with open chromatin information. Our analysis will indicate regions of open chromatin, with annotations about what genes are within that region and how the regions between your samples may have changed.

Deliverables:

- Loci of open chromatin
- Differentially open chromatin between samples
- Functional annotation of open chromatin loci

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Oneomics Private Limited
F12, Bharathidasan University Technology Park,
Khajamalai Campus,
Tiruchirapalli,
Tamil Nadu 620023, India
www.oneomics.in
sales@oneomics.in