



CD Genomics

The Genomics Services Company

Microbiome 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

Sequencing Platforms

CD Genomics stands at the forefront of advancing microbiome research through its globally recognized innovative sequencing and bioinformatics services. CD Genomics is committed to providing novel NGS services enabling researchers to explore the structure and function of the microbial community in a high-resolution and culture-independent manner using technology from short-read and long-read sequencing platforms.

CD Genomics offers diverse microbiome sequencing solutions utilizing PacBio SMRT and Nanopore sequencing platforms. These solutions directly provide full-length gene sequences, enhancing the accuracy of species-level annotations by eliminating errors introduced by amplification preferences in different regions. This enables a more precise characterization of microbial species-level compositions.

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

Service Advantages

- **Expert Team:** Our team of professionals specializes in microbiome sequencing, with expertise in analyzing microbial communities. We are well-versed in interpreting complex microbiome data, ensuring accurate and insightful analysis.
- **Cutting-edge Technology:** We utilize sequencing technology and analysis tools, ensuring comprehensive profiling of microbial communities, and enabling in-depth exploration of microbiome dynamics.
- **Customized Analytical Approaches:** We tailor our analytical approaches to meet the specific needs of microbiome research projects. Whether investigating microbial diversity, community structure, or functional potential, our customized solutions provide precise insights into the microbiome ecosystem.
- **Comprehensive Data Interpretation:** Our detailed analysis reports offer a comprehensive interpretation of microbiome data, highlighting key findings and trends. We provide clear and actionable insights to aid in understanding microbial community composition and function.
- **Data Security and Confidentiality:** Your microbiome sequencing data is treated with the utmost confidentiality and security. We employ robust data protection measures to safeguard sensitive information throughout the sequencing and analysis process.
- **Efficient Turnaround Time:** With streamlined workflows and efficient processes, we ensure rapid delivery of microbiome sequencing results. Our quick turnaround time allows researchers to promptly access valuable microbiome insights for their studies.

Comprehensive Microbiome Sequencing Solutions

- 16s/18s/ITS Amplicon Sequencing
- Metagenomic Shotgun Sequencing
- Viral Metagenomic Sequencing
- Metatranscriptomic Sequencing
- Microbial Whole Genome Sequencing
- Absolute Quantitative 16s/18s/ITS Amplicon Sequencing
- Microbial Identification

CD Genomics Microbiome Sequencing Solutions

Microorganisms permeate every aspect of our lives, exhibiting a vast array of forms including bacteria, fungi, viruses, and various small protists, algae, and beyond. This rich diversity offers numerous avenues for microbial research exploration. When delving into the study of a single strain, we can unravel the intricacies of microorganisms at the genomic level through methods such as fungal/bacterial de novo sequencing or resequencing. On the other hand, for investigations into community-level dynamics, a plethora of techniques exist, such as amplicon sequencing, which sheds light on community diversity and compositional structure, and metagenome analysis, illuminating community functions and evolutionary relationships. The selection of these techniques depends on the specific research objectives at hand.

CD Genomics stands ready to support microbial research endeavors with cutting-edge sequencing-based technologies and comprehensive bioinformatic data analysis services.

16s/18s/ITS Amplicon Sequencing

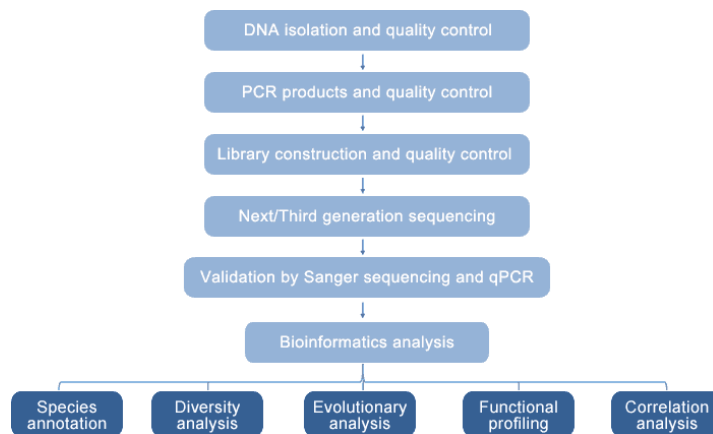
Amplicon sequencing serves as a primary method for scrutinizing PCR products of specific lengths through sequencing. In the realm of environmental studies, the utilization of 16S/18S/ITS amplicon sequencing holds particular significance, enabling researchers to probe into the diversity of environmental microorganisms and discern discrepancies in community composition. Presently, 16S sequencing stands out as a dependable tool for community analysis, species composition determination, and diversity assessment, among other applications.

CD Genomics offers a comprehensive suite of amplicon sequencing technologies by using both Illumina and PacBio sequencing tailored to diverse research objectives and requirements, including 16S rDNA sequencing, 18S rDNA sequencing, ITS sequencing, and target region amplicon sequencing.

Key Application Areas

- Environmental microbiology
- Microbial diversity analysis
- Colony structure examination

- Species composition variation
- Environmental factor influence
- Functional prediction



Metagenomic Shotgun Sequencing

Metagenome analysis encompasses the comprehensive study of all microbial genomes within an environment, facilitating in-depth exploration of microbial species, functions, and their interactions within samples. This approach enables the discovery and examination of genes with practical applications, the structural dynamics of microbial communities, and the intricate relationships between microorganisms and their environments or hosts. Notably, metagenomes offer precise species-level annotation, greatly enhancing species identification capabilities, and can be seamlessly integrated with other genomic technologies like amplicon sequencing and metagenomics.

We present two distinct analysis pathways for educators to select from:

- i. Assembly analysis involves gene prediction based on assembly outcomes, followed by species and functional annotation, along with differential analysis at the gene level.
- ii. In cases of substantial host contamination, the Reads mapping process provides a direct analysis of species and functions based on reads without the need for assembly.

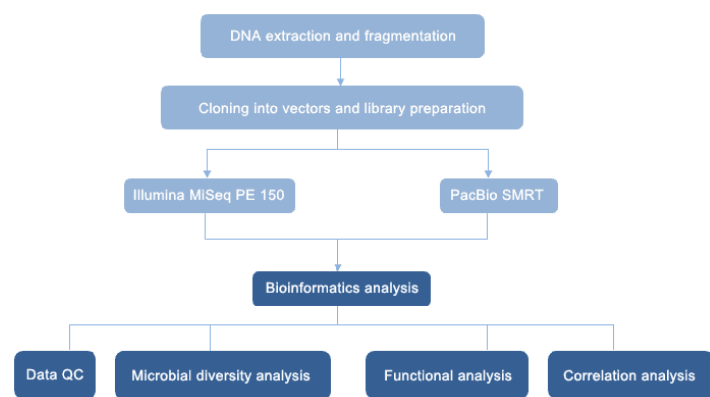
How to Choose: 16S/18S/ITS Amplicon Sequencing vs. Metagenome Sequencing

- Functional Annotation: Metagenomics sequencing reigns supreme in functional annotation, offering unparalleled depth.
- Sequencing Mode Distinction: 16S/18S/ITS amplicon sequencing employs the PE250 sequencing mode, whereas macro-genome sequencing utilizes PE150 mode.

- **Variation in Sequencing Regions:** In 16S amplicon sequencing, emphasis is placed on detecting the V3-V4 region within the 16S gene, whereas metagenome sequencing covers the entirety of genomic DNA.
- **Differential Species Identification Precision:** While 16S amplicon sequencing provides identification up to the genus level, metagenome sequencing offers species-level identification for microorganisms.

Key Application Areas

- Exploration of microbial species and functional disparities
- Investigation into the correlation between microbiota and disease
- Environmental management initiatives
- Screening for functional genes
- Probing microbial-host interactions in research
- Conducting studies on industrial fermentation processes



Metatranscriptomic Sequencing

Metatranscriptome sequencing represents a distinct approach from both conventional transcriptome sequencing and metagenome sequencing. It focuses on elucidating the entire repertoire of microbial mRNA within specific samples, delving into the active strains' composition and gene expression at a transcriptional level. This methodology unveils not only the adaptability of these strains but also sheds light on the potential regulatory mechanisms governing gene expression under specific environmental conditions.

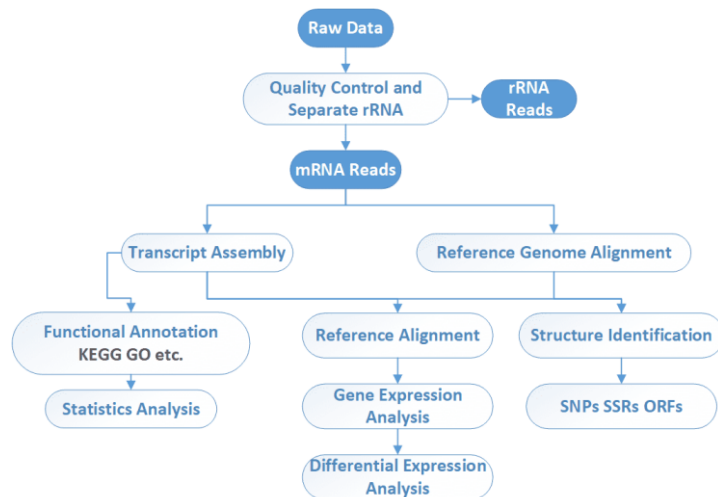
In contrast to metagenome sequencing, metatranscriptome analysis enables the exploration of active strains' composition and the identification of highly expressed genes, offering insights into species delineation and unveiling strain adaptability amidst environmental influences and potential regulatory pathways. It's

important to note that while metatranscriptome sequencing captures expressed genes, metagenome sequencing encompasses the entire genomic content of environmental microorganisms, thus presenting a more comprehensive dataset.

Therefore, our metagenome sequencing service serves as a valuable source of "reference gene information" for metatranscriptome analysis, enhancing our ability to discern species composition and differential gene expression patterns.

Advantages

- A culture-free method to reveal the true extent of microbial diversity
- Permitting function-based activity screens
- More targeted than shotgun random sequencing
- Cost-efficient and time-effective
- A wide range of applications, including basic research, ecological applications, clinical applications, industrial applications

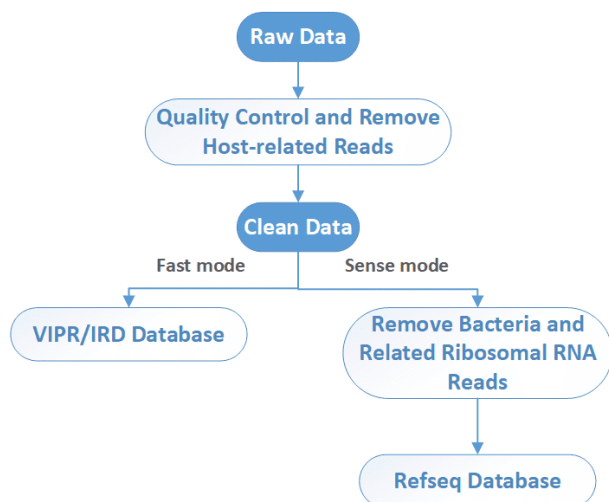


Viral Metagenomic Sequencing

Meta-virome analysis directly targets the genetic material of all viruses present in the environment. This approach enables rapid and accurate identification of viral compositions, thereby playing a crucial role in virus discovery, tracing viral origins, early microbial detection, and other related research endeavors. Viral metagenomic sequencing studies can be applied across various samples, detecting both DNA and RNA viruses, including human or animal intestinal and blood samples, oceans, soils, etc., to assess potential risks to both human health and the environment.

Advantages

- Efficient enrichment of viral particles from samples, facilitating the isolation of viral groups even from trace amounts.
- Preservation of phage integrity, maximizing viral activity and suitability for downstream research, such as functional virome transcriptomics (FVT).
- Superior homogeneity and reduced phage bias compared to conventional methods like PEG and CsCl.
- Implementation of a comprehensive data analysis strategy, including customized multi-omics data mining, for a deeper understanding of viral dynamics.



Microbial Whole Genome Sequencing

Single-organism studies delve deeply into individual strains of bacteria or fungi that are isolable and cultivable at the genetic level. Whole-genome sequencing of microorganisms plays a pivotal role in precise microbial identification, generating complete reference genomes (ab initio sequencing), conducting comparative genomic analyses (ressequencing), and advancing genome development.

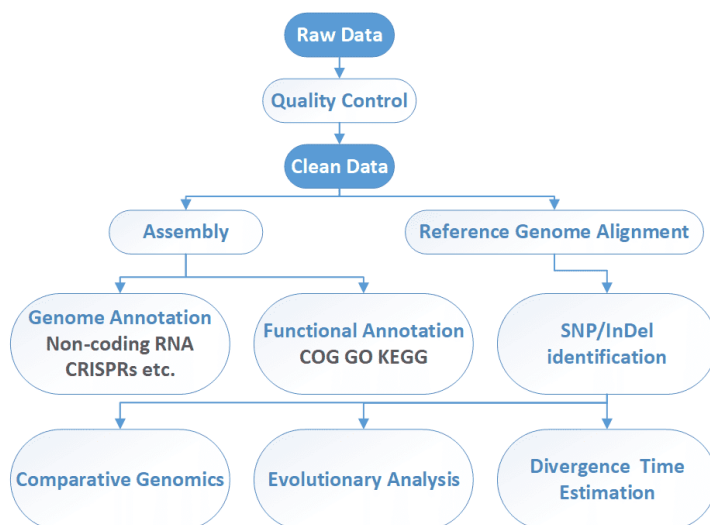
Microbial de novo sequencing, also known as whole genome de novo sequencing, constructs genomes from scratch using high-throughput sequencing data. This approach allows us to predict the genes within the genome and extract functional insights by comparing them against databases of known functions.

Whole-genome resequencing of a single bacterium entails variant detection using high-throughput sequencing data and comparison with a closely related reference genome. Through resequencing, a plethora of variant information such as SNPs, InDels, SVs, CNVs, etc., can be gleaned, facilitating the resolution

of trait disparities between genomes or serving as targets for large-scale evolutionary analyses.

Applications

- A time-effective and cost-efficient approach
- Broad applications: de novo sequencing, gene annotations, comparative genomic studies, evolutionary studies of microorganisms, etc.
- Drug discovery and development: assess the contribution of DNA on pathogenesis, and understand the role of mobile elements in drug resistance and transmission



Absolute Quantitative 16s/18s/ITS Amplicon Sequencing

In recent years, high-throughput sequencing technology has gained significant traction in studying microbial community composition and functionality. However, it has encountered challenges when it comes to quantitatively analyzing microorganisms. Traditional amplicon sequencing, due to factors such as amplification efficiency, nucleic acid extraction, and sequencing depth, typically provides only relative abundance information of bacteria, making it difficult to accurately determine the absolute abundance of various bacterial species within a sample.

To solve the challenge of PCR amplification, CD Genomics has introduced absolute quantitative amplicon sequencing technology. This technology utilizes a unique internal standard that combines 16S amplicon sequencing technology and qPCR absolute quantification technology into one, giving full play to the advantages of the 16S amplicon's wide range of applicability, avoiding bias caused by factors such as PCR efficiency and

different library construction methods, and improving the accuracy and comparability of data. In a single sequencing, the abundance and absolute copy number of each bacterium in the sample can be obtained.

Applications

- **Precision:** It provides precise quantification of microbial populations, offering exact counts rather than relative proportions, and enhancing accuracy in microbial community analysis.
- **Elimination of Bias:** By integrating absolute quantification techniques, biases arising from PCR amplification and sequencing variations are minimized, ensuring more reliable results across different samples.
- **Comprehensive Insight:** This method offers a comprehensive understanding of microbial community composition and structure by accurately determining the exact number of each species present in a sample.
- **Simplicity:** It employs universal primers, simplifying experimental procedures and reducing the need for laborious primer design and optimization.
- **High-throughput Capability:** Despite its quantitative nature, Absolute Quantitative Amplicon Sequencing retains the high-throughput capacity characteristic of traditional amplicon sequencing methods, enabling efficient analysis of large sample sets.
- **Accuracy:** By constructing standard curves for each sample, this technique provides accurate microorganism counts, avoiding biases from factors such as PCR efficiency and sequencing depth.
- **Enhanced Sensitivity:** It offers higher precision and sensitivity compared to traditional methods like colony counting, enabling more detailed and reliable analysis of microbial communities.

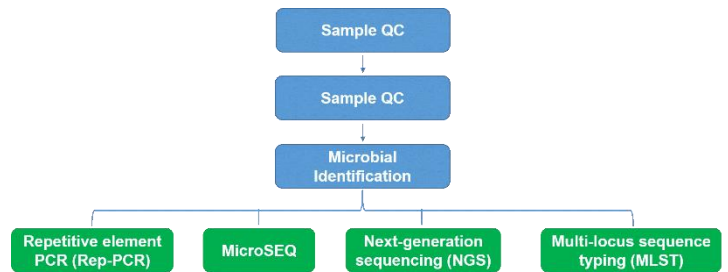
Microbial Identification Solution

Microbial identification involves determining the characteristics of unknown microorganisms, distinguishing between bacteria, yeasts, and molds, and pinpointing their genus, species, and strain levels. Methods for microbial identification encompass both phenotypic and genotypic approaches, or a combination thereof.

The level of microbial identification needed depends on product characteristics, colony diversity, and the intended use of the data. Genotypic microbial identification, typically independent of

growth medium or isolate activity, requires only pure colonies for analysis.

Our microbial identification solutions leverage various techniques including PCR, RNA sequencing, 16S/ITS/18S amplicon sequencing, and whole genome sequencing. By analyzing highly conserved nucleic acid sequence fragments, our aim is to achieve accurate microbial identification across diverse samples.



How to Choose Your Microbiome Research Solution

Microorganisms, though tiny, wield immense influence across ecosystems, impacting human health, animal well-being, and plant growth. In microbiome research, we explore microbial dynamics at three levels: microbial, DNA, and mRNA.

Choosing the right method depends on your goals. Use amplicon sequencing to assess microbial diversity and community composition.

- For deeper insights into species and their genes/functions, opt for metagenome sequencing.
- For a comprehensive view, combine amplicon and metagenome analyses. Screen multiple samples with amplicon sequencing, then delve deeper with metagenome sequencing on well-replicated samples.
- For a holistic perspective, integrate amplicon, metagenome, and metatranscriptome analyses. This multi-omics approach reveals the community's composition, capabilities, and activities, providing insights into "who's there, what they can do, and what they're actually doing."

Our Results

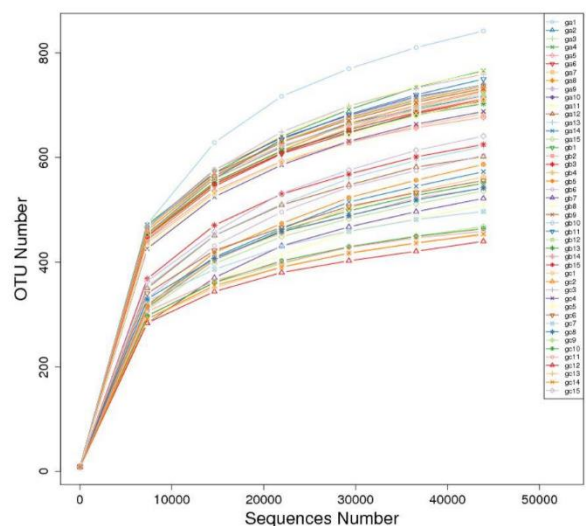
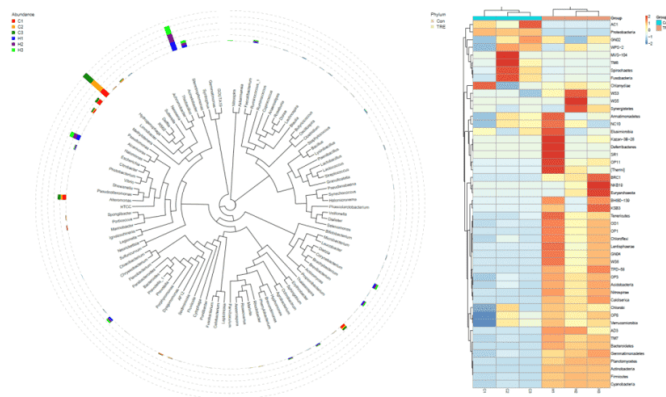
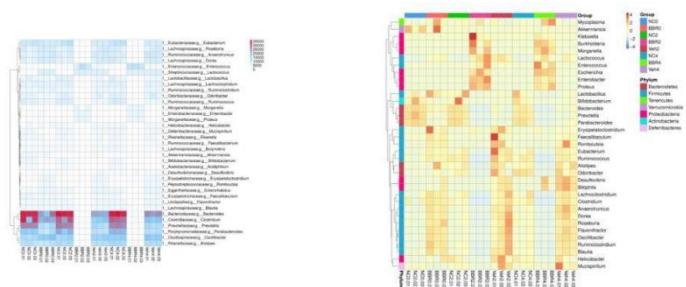
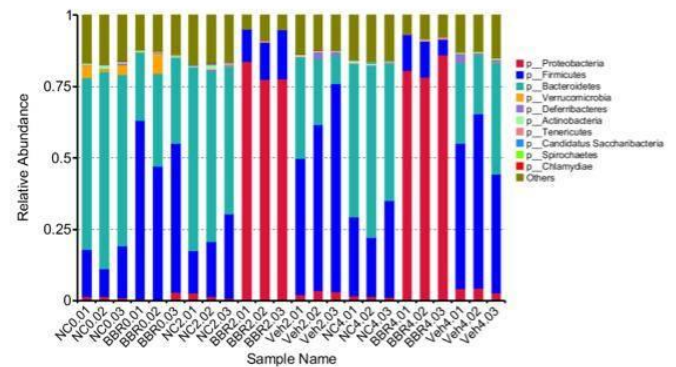
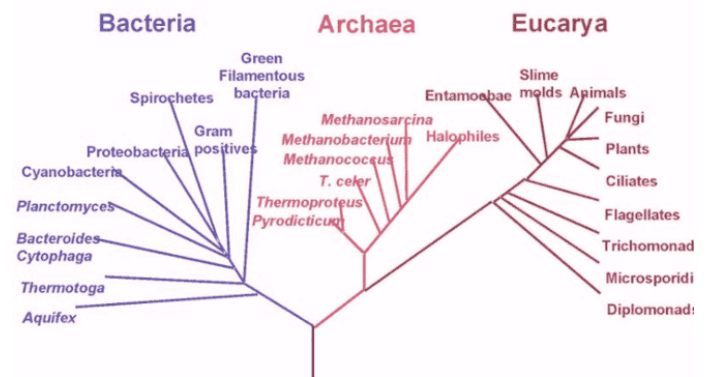
We effortlessly remove low-quality sequences from the raw data while generating clean reads and qualified data. The process commences at the DNA/RNA level, where we compare the sample sequencing information to an extensive database encompassing animal, plant, human, and microbial genomes. This comparison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

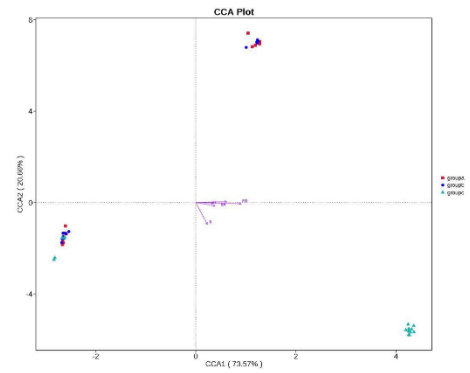
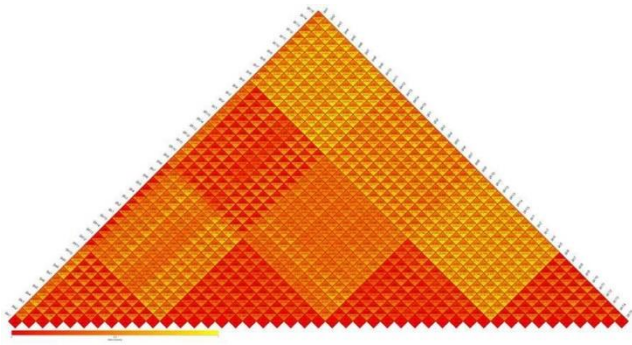
General information

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

Custom bioinformatic analysis result

- Assembly
- Metaphlan species annotation
- Taxonomy distribution histogram of all samples
- Functional database annotation
- Alpha diversity analysis
- Beta diversity analysis
- Data binning





Applications

- **Medical Research:** Microbiome sequencing plays a crucial role in investigating metabolic diseases and cancer. It offers insights into microbial influences on metabolism and tumor development, paving the way for targeted treatments and personalized medicine.
- **Animal Health and Husbandry:** In animal husbandry, microbiome sequencing aids in understanding gut and rumen microbiota, impacting animal health, nutrition, and digestion. It guides research on methane-producing bacteria and informs strategies for optimizing animal feed and health management.
- **Agricultural Studies:** Microbiome studies contributes to research on microbial-plant interactions, agricultural practices, and soil health. By studying soil microbial communities, it informs decisions on tillage methods, fertilizer treatments, and sustainable agriculture practices.
- **Environmental Applications:** Microbiome sequencing informs environmental remediation efforts in areas such as air pollution control, wastewater treatment, oil spill cleanup, and restoration of acid mine drainage sites. It also aids in understanding microbial dynamics in marine ecosystems, contributing to marine conservation efforts.
- **Bioenergy Development:** Microbiome sequencing facilitates the discovery of specialized microbial strains and genes relevant to bioenergy production. It supports gene mining efforts, development of engineered bacteria for biofuel production, and optimization of bioreactor systems.
- **Extreme Environments Research:** Microbiome sequencing is instrumental in studying microbial taxa thriving in extreme environments such as hot springs, deep-sea vents, and polar regions. Understanding their adaptations provides insights into microbial diversity and evolution under extreme conditions.