

Microbiome Sequencing

Understanding the microbiome using genomic sequencing and analysis

Microbiome sequencing is a valuable tool in drug discovery, providing insights into complex microbial communities. Choose our microbiome sequencing services for:

- **Diverse service options:** We offer multiple methods for comprehensive microbiome sequencing analysis.
- **Superior data quality and advanced technology platforms:** Our services utilize Illumina NovaSeq and PacBio platforms, ensuring accurate and high-quality sequencing for comprehensive microbiome analysis.
- **Expert data analysis:** Our experienced bioinformatics team provides in-depth data interpretation and analysis.
- **In vivo service integration:** Gain valuable insights into host-microbiome interactions through access to our *in vivo* service.

Acceptable Sample Types:

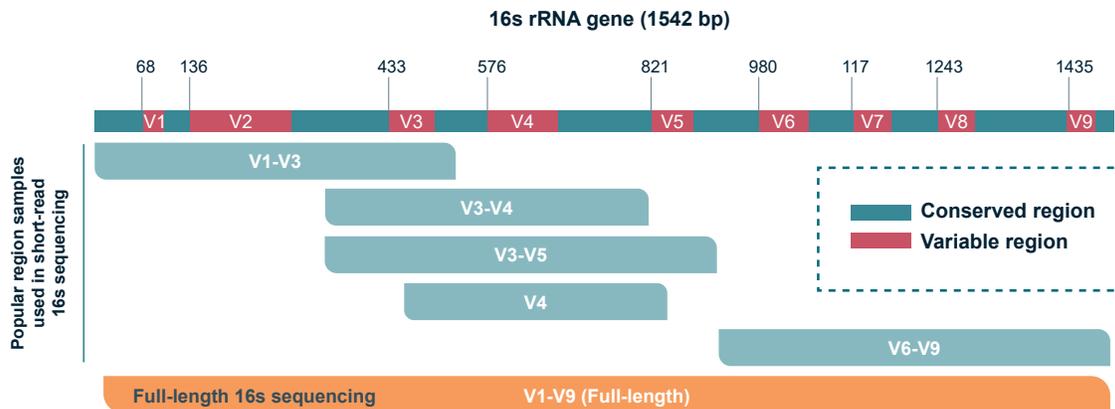
- Feces
- Intestine Solution
- DNA
- Tissue (snap frozen or fresh)

Full-length 16s rRNA Sequencing

Crown Bioscience leads in comprehensive and cost-effective full-length 16S rRNA analysis using PacBio’s long-read third-generation sequencing. Our approach offers distinct advantages over short-read sequencing. By capturing the entire 16S rRNA gene, we provide unparalleled insights into bacterial diversity and ensure precise taxonomic classification. Overcoming limitations of short-read methods, such as primer bias and reduced taxonomic resolution, our full-length sequencing delivers a comprehensive and unbiased view of the microbial community. This empowers the identification of potential drug targets and deepens understanding of their functional roles.

	Traditional 16S Sequencing	Full-length 16S Sequencing
Sequencing Platform	Short-Read Sequencing	Long Read Sequencing
Targeted Region	Short Hypervariable Region	Entire 16S rRNA gene
Taxonomic Resolution	Moderate	Higher
Primer Bias	Yes	Reduced
Secondary Structure	Not Captured	Captured

Fig. Commonly used DNA regions in short-read and long-read 16S rRNA sequencing



Full Length 16S rRNA Sequencing



PacBio Sequel II Platform

Highly Accurate Long Read Sequencing

Primer	Sequence	Product Size	Reference
PB_F	AGRGTTYGATYMTGGCTCAG	1510bp	PacBio
PB_R	RGYTACCTGTACGACTT	1510bp	PacBio



Shotgun Metagenomic Sequencing

Metagenomic sequencing provides a significant advantage over 16S rRNA sequencing by capturing comprehensive genomic information. This empowers higher taxonomic resolution, direct functional profiling, and the identification of novel or rare species. While it comes at a higher cost and requires specialized bioinformatics expertise, shotgun sequencing is an ideal choice for researchers looking to delve into a smaller number of samples with greater depth compared to amplicon sequencing. Embrace the power of metagenomic sequencing to unlock a wealth of valuable insights about microbial communities and their functional potential.

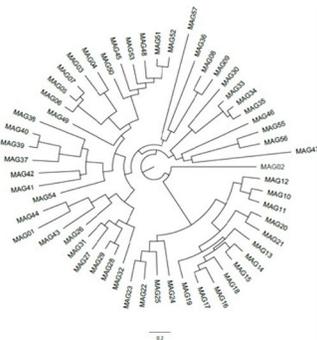
Metatranscriptomic Sequencing

Metatranscriptomic sequencing studies gene expression profiles of microbial communities, providing insights into their functional activities and responses to the environment. By analyzing RNA molecules, researchers can identify actively expressed genes, revealing the metabolic pathways and biological processes within the microbiome. This approach enhances our understanding of how microbes interact with their surroundings and contribute to ecosystem functions and host-associated processes.

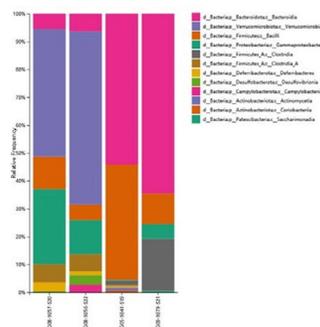
Methods	Applications	Advantages	Limitations
Full-length 16S rRNA Sequencing	Identification, classification, and quantification of microbes (bacteria) within complex biological mixtures Microbial contamination detection	Cost-effective Established pipeline for data analysis Well-developed database	Potential PCR amplification bias Relatively low taxonomic resolution (genus-species) Focuses on bacterial microbes only
Shotgun Metagenomic Sequencing	Comprehensive sequencing of all genes in all organisms (bacteria, fungi, etc.) present in a given complex sample	High taxonomic resolution (species-strains) Improved sequencing depth and accuracy Increased detection of microbial diversity Functional profiling	Relatively higher cost Longer sequencing period Challenges with database completeness and reference availability
Metatranscriptomic Sequencing	Capturing and studying the expressed transcripts within a microbiome at a specific time and environmental condition	Whole gene expression profiling Functional enrichment analysis Insight into active members of the microbiome Study of microbiome-host and microbiome-environment interactions	Relatively higher cost Longer sequencing period Limited availability of reference genomes

Shotgun Metagenomic Sequencing

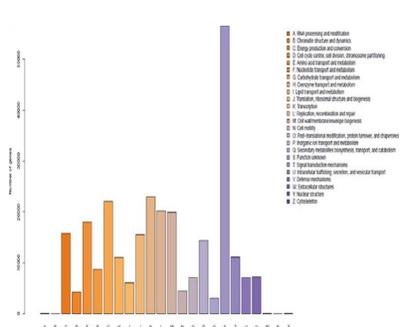
Metagenome Assembled Genome



Taxonomy Abundance



Unigene Function Description



Get in touch



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