

Unlock Advanced Metagenomic Solutions for Your Microbiome Research Today!

Microbes play a crucial role in health, industry, and the environment, contributing to innovations in biotechnology, sustainable materials, and pharmaceuticals. The rise of antimicrobial resistance, infectious diseases, and food safety concerns highlights the need for advanced microbial genomics.

Introduction

Metagenomics is a powerful approach for studying microorganisms through functional gene screening and sequencing. It examines microbial diversity, community composition, genetic relationships, and environmental interactions. At Novogene, we offer shotgun metagenomic sequencing and 16S/18S/ITS amplicon sequencing using NGS and third-generation technologies, including PacBio and Oxford Nanopore. By combining these methods, we provide deeper insights into microbial ecology, addressing key questions on community composition and functional roles within multiomics research.

	Shotgun Metagenomic Sequencing Assembly-Based (SRS)	Shotgun Metagenomic Sequencing Mapping-Based (SRS)	16S/18S/ITS Amplicon Sequencing (SRS)
Taxonomic Resolution	Species/sub-species level	Species level	Genus Level
Taxonomy	All taxa , including viruses, protists etc.	Bacteria, Archaea, Fungi, (Viruses and protists with Kraken2)	Specific to primer
Genome Reconstruction	Yes	No	No
Benefits	• Applicable to all sample types (microbiome and environmental) • Provides species and functional insights and correlation through predicted genes • Includes antibiotic resistance gene annotation and analysis	• Ideal for complex samples (microbiome and environmental) • Delivers species and functional profiling results	• Suitable for all sample types, particularly those with high host contamination • Enables taxonomic identification using distinct metabarcoding primers

Applications



Comprehensive microbial profiling

Identify and classify complex microbial communities without culturing.



Marker identification

Discover genetic markers for virulence, antibiotic resistance, or microbial functions.



Novel species discovery

Identify and characterize previously unrecognized species, including genome assembly.



Enzyme and metabolite discovery

Explore new enzymes and metabolic pathways for industrial or medical use.

Citations

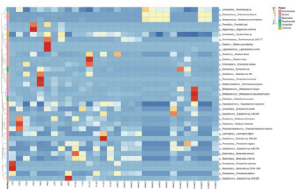
- 1) Alves, L. F., Westmann, C. A., Lovate, G. L., de Siqueira, G. M. V., Borelli, T. C., & Guazzaroni, M. E. (2018). Metagenomic Approaches for Understanding New Concepts in Microbial Science. *International journal of genomics*, 2018, 2312987. <https://doi.org/10.1155/2018/2312987>
- 2) Simon, C., & Daniel, R. (2011). Metagenomic analyses: past and future trends. *Applied and environmental microbiology*, 77(4), 1153–1161. <https://doi.org/10.1128/AEM.02345-10>
- 3) Zhang, L., Chen, F., Zeng, Z., Xu, M., Sun, F., Yang, L., Bi, X., Lin, Y., Gao, Y., Hao, H., Yi, W., Li, M., & Xie, Y. (2021). Advances in Metagenomics and Its Application in Environmental Microorganisms. *Frontiers in Microbiology*, 12(1). <https://doi.org/10.3389/fmicb.2021.766364>

Shotgun Metagenomic Sequencing (Short-Reads)

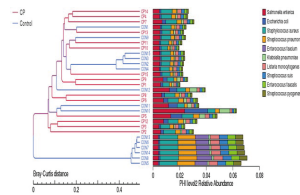
Metagenomic sequencing facilitates the comprehensive analysis of microorganisms in their natural environments, eliminating the need for culturing and providing valuable insights into microbial diversity, functional activity, and environmental interactions. Specifically, shotgun metagenomic sequencing enables the detailed identification and characterization of the entire microbiome, elucidating community structure, species classification, gene function, metabolic pathways, and antibiotic resistance. This method is advancing rapidly across disciplines such as medicine, agriculture, and environmental science.

At Novogene, we provide a variety of sequencing platforms, including the Illumina NovaSeq for shotgun metagenomic sequencing and the PacBio and Oxford Nanopore systems for long-read sequencing, tailored to meet diverse research requirements. In addition, we offer extensive analytical capabilities to further support your research needs.

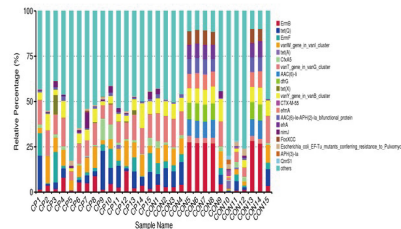
Demo Results



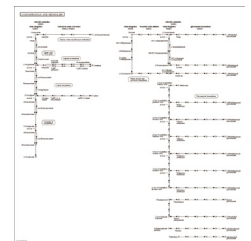
Taxonomic Abundance
Heatmap at Species Level



Pathogen-Host Interaction
Clustering Tree based
on Bray-Curtis Distance



Relative Abundance of
Antibiotic Resistance Gene

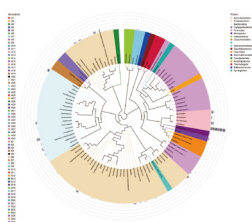


Metabolic
Pathway Analysis

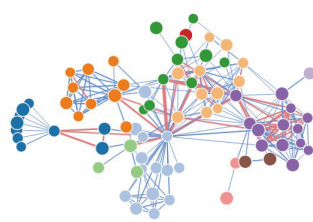
16S/18S/ITS Amplicon Sequencing (Short-Reads)

16S/18S/ITS amplicon sequencing identifies and differentiates microbial species by amplifying hypervariable regions of conserved genes (16S for bacteria/archaea, ITS for fungi, 18S for fungi/protists) and analyzing them via next-generation sequencing (NGS). At Novogene, we leverage this strategy to enhance microbial ecology insights, addressing community composition and functional roles. We offer 16S/18S/ITS amplicon sequencing on Illumina NovaSeq for short-reads and PacBio Revio for full-length 16S sequencing.

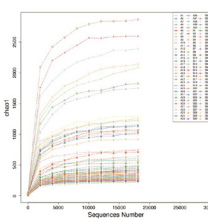
Demo Results



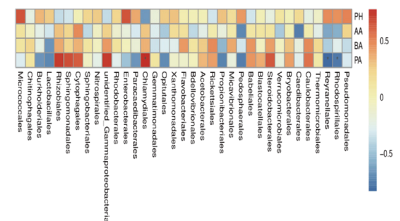
Taxonomy Annotation:
Evolutionary Tree in Genus



3D Network Analysis

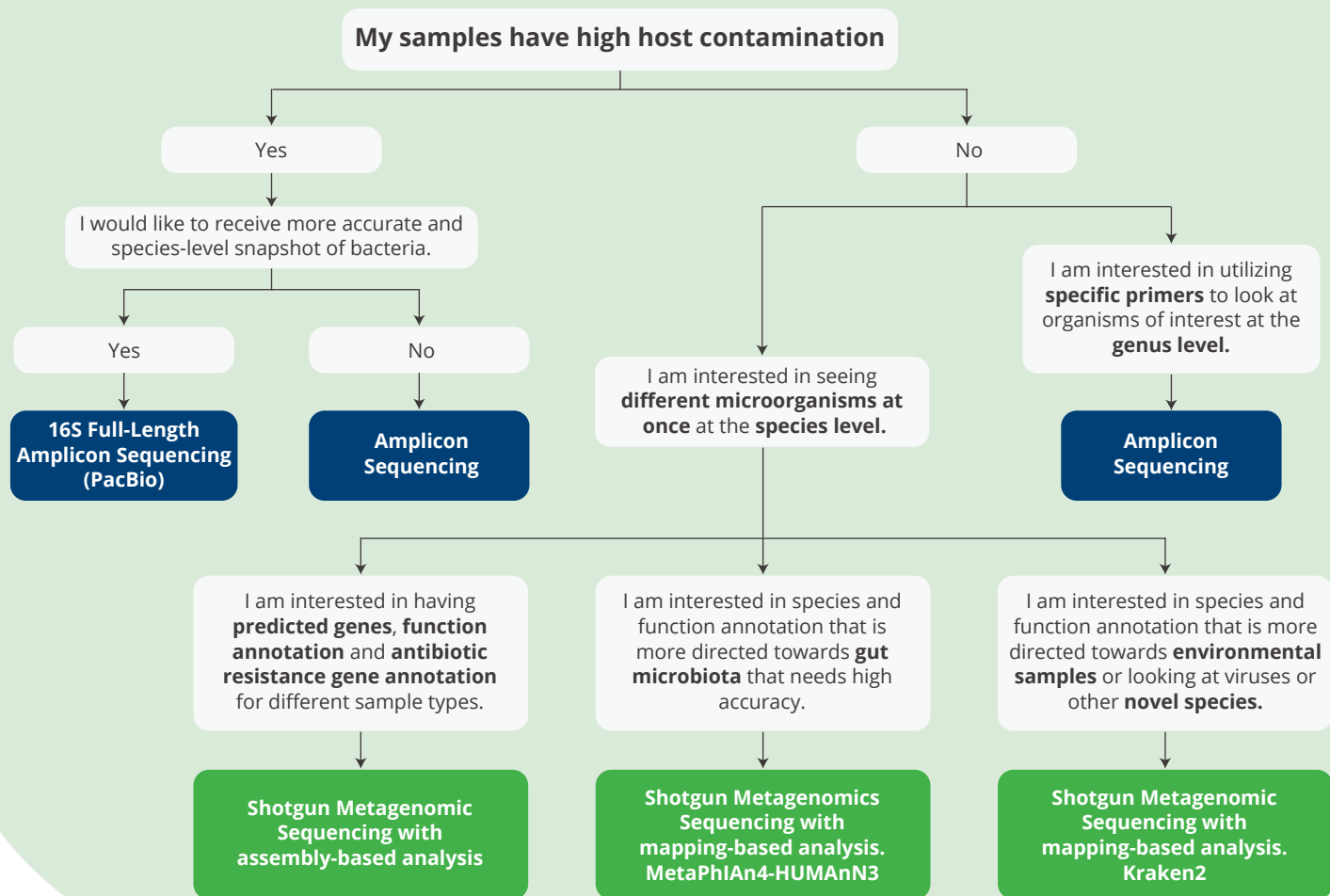


Alpha Diversity
Rarefaction Curves



Spearman Correlation Analysis

Discover Your Ideal Metagenomic Solution Now!



Novogene is committed to be Your Trusted Genomics Partner

- Trusted International Corporation
- Trusted Comprehensive Experience
- Trusted Expertise & Technology
- Trusted Service & Standardized Procedures
- Trusted Delivery Quality & Efficiency

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