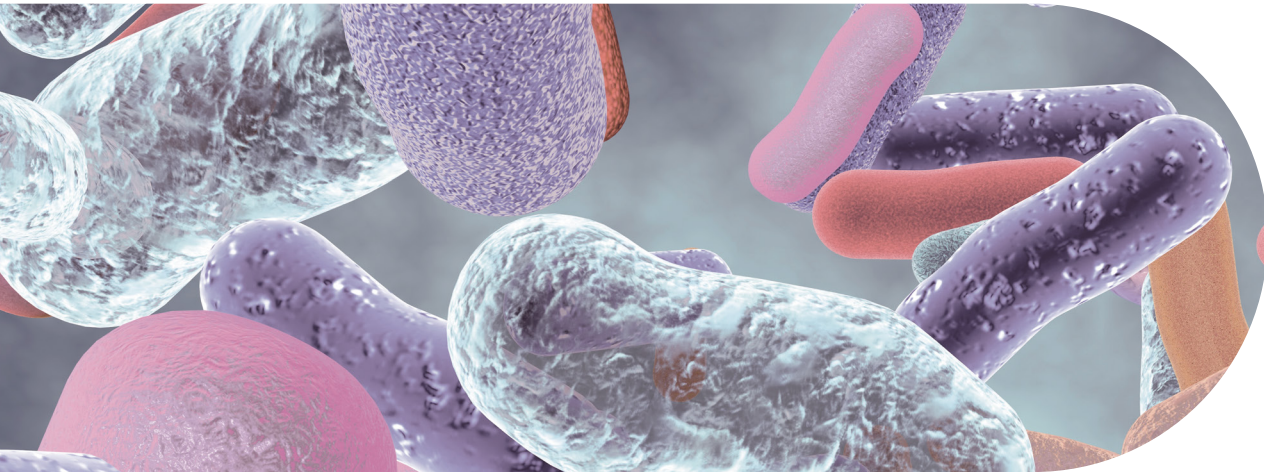


Shotgun Metagenomic Sequencing

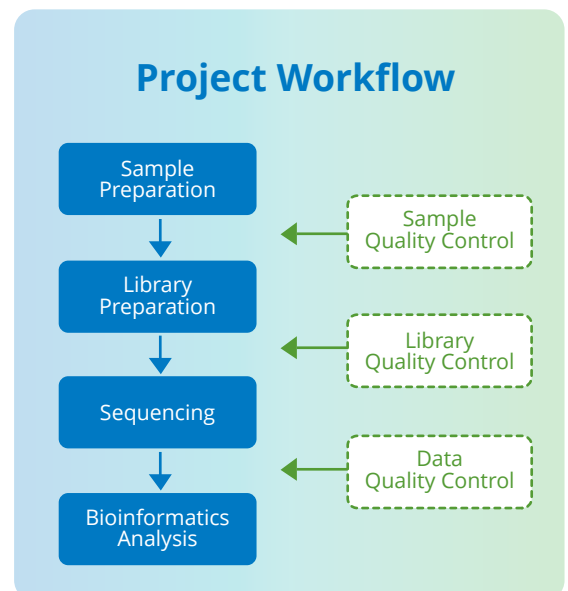


Shotgun Metagenomic Sequencing offers an approach to identify and characterize the entire microbiome in a specific environment without the need for microbial isolation or culturing. It can elucidate the community structure, species classification and provide insights into systemic evolution, gene function, metabolic network, and antibiotic resistance gene information for multidisciplinary research.

At Novogene, a diverse range of sequencing platforms and strategies is available to meet your needs. We offer the NovaSeq X Plus and NovaSeq 6000 sequencing platforms for our shotgun metagenomic sequencing service, while we offer both the PacBio and Nanopore PromethION systems for our metagenomic sequencing with long reads sequencing.

Our Key Features & Advantages

- 
Comprehensive microbial profiling and functional annotation
- 
Publication-ready data results
- 
DNA extraction services
- 
Real-time project management on our Customer Service System



Sample Requirements

Library Type	Sample Type	Amount	Volume	Concentration	Purity
Shotgun Metagenomic Library (350bp)	Total DNA	≥ 200 ng	≥ 20 µL	≥ 10 ng/µL	OD260/280= 1.8-2.0; No degradation, No contamination, No color

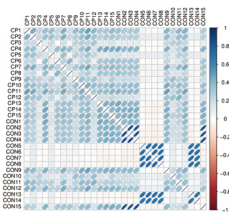
Analysis Content

Standard Analysis

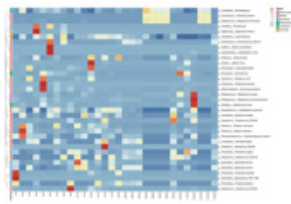
1. Data quality control (host contamination removal if required)
2. Metagenome Assembly
3. Gene Prediction
4. Taxonomy Annotation
5. Function Annotation (KEGG, eggNOG, CAZY...etc)
6. Alpha and Beta Diversity Analyses
7. Antibiotic Resistance Gene and Mobile Genetic Elements Annotation and Analyses

Note: Anticipate additional updates to our analysis pipeline in the near future!

Demo Analysis Results



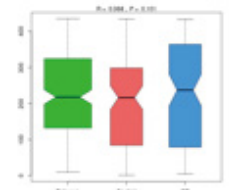
Correlation Analysis between Samples



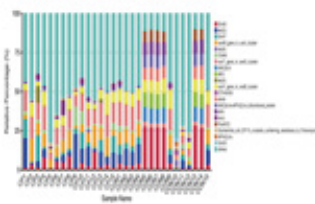
Taxonomic Abundance Heatmap at Species Level



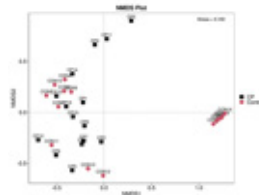
KEGG Pathway Annotation Cartogram



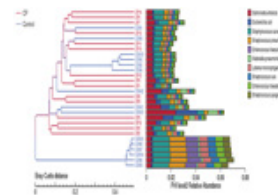
Anosim of CAZY



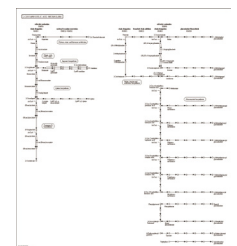
Relative Abundance of Antibiotic Resistance Gene



NMDS of Plasmid Annotation



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



Metabolic Pathway Analysis

If you are interested to explore long read sequencing possibilities with PacBio and Nanopore platforms, please contact us for more details.

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