

Shotgun Metagenomic Sequencing takes the entire microbial community in a specific habitat as the research object via directly recovering environmental genetic materials for sequencing without prior microbial isolation and culture.

It involves studies of the community structure, species classification, systematic evolution, gene function, and metabolic network of environmental microorganisms.

Our Key Features & Advantages



Comprehensive Analysis

Expert bioinformatics analysis with five databases (microNR/NR, KEGG, eggNOG, CAZy and ARDB) provides comprehensive data on annotated genes, function profiling, metabolic pathways and antibiotic resistance genes.



Effective Methodology

Our techniques enhance the generation of data from low-abundance species.



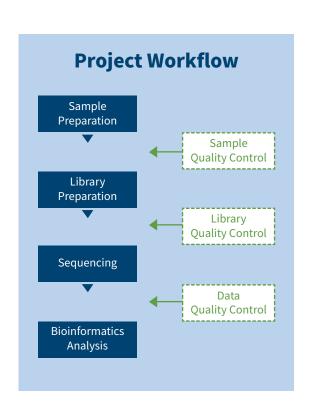
Unsurpassed Data Quality

We provide high-quality sequencing (with Q30 score ≥85%), an efficient standard workflow, fast turnaround time and cost-effective bioinformatics analysis.



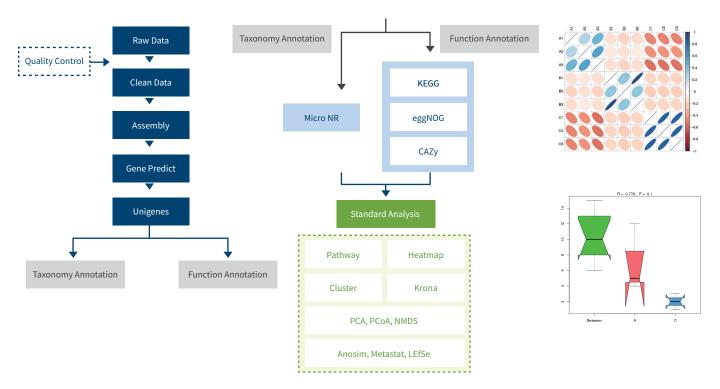
Real-time Project Management

Our Customer Service System (CSS) online platform allows for real-time project tracking 24/7, collaboration with your team and other helpful information.





Standard Analysis Pipeline



Sample Requirements

Sample Type	Amount	Volume	Concentration	Purity
Genomic DNA	≥ 200 ng	≥ 20 μL	\geqslant 10 ng / μ L	OD260/280 = 1.8-2.0 No degradation, no contamination, no color

Publications

Listed below are some recent publications that were supported by Novogene solutions. We have successfully sequenced more than 70,000 samples, including soil, water, feces, sludge, etc.

Journal	IF	Title	
Gut Microbes	23. 059	Cigarette smoke promotes colorectal cancer through modulation of gut microbiota and related metabolites (2022)	
Frontiers in Medicine 9.927		Clinical evaluation of metagenomic next-generation sequencing for detecting pathogens in bronchoalveolar lavage fluid collected from children with community-acquired pneumonia (2022)	

