

Metagenomic Sequencing



Metagenomics 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

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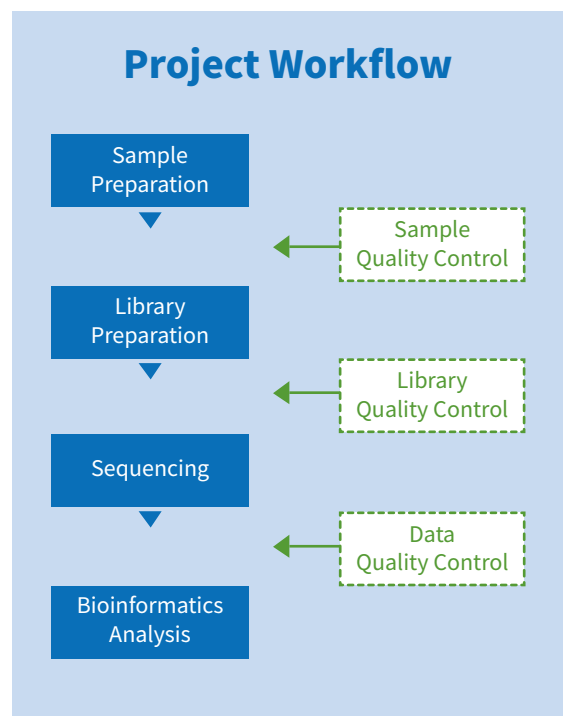
Comprehensive Analysis
Expert bioinformatics analysis with three databases (KEGG, eggNOG, CAZy) provides comprehensive data on annotated genes and metabolic pathways.
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Extensive Experience
We have completed numerous metagenomic sequencing projects for our customers, and have published multiple metagenomic studies.
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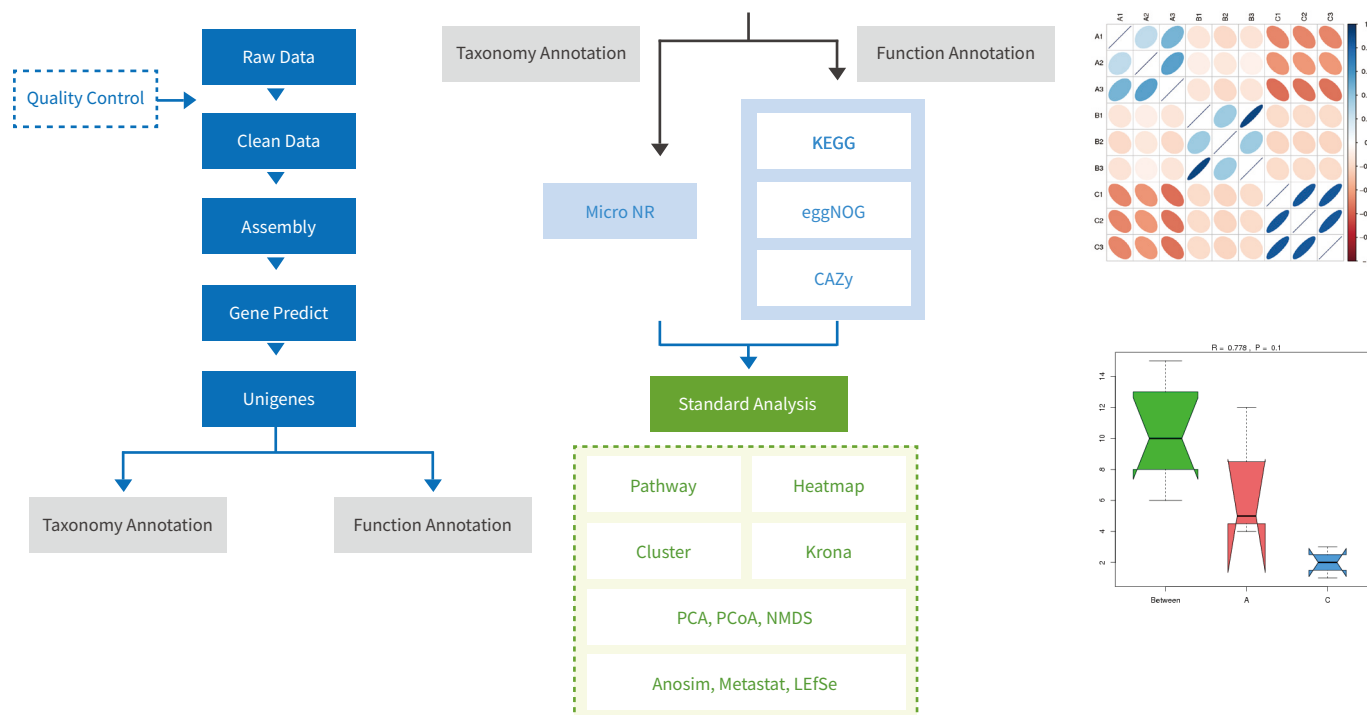
Effective Methodology
Our techniques enhance the generation of data from low-abundance species.
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Unsurpassed Data Quality
We provide high-quality sequencing (with Q30 score $\geq 80\%$), an efficient standard workflow, and cost-effective bioinformatics analysis.
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Reliable & Faster Turnaround Time
The strategic locations of our labs across Asia and our extensive NGS system can provide faster turnaround time.



Standard Analysis Pipeline



Sample Requirements

Sample Type	Amount	Volume	Concentration	Purity
Genomic DNA	$\geq 0.2 \mu\text{g}$	$\geq 20 \mu\text{L}$	$\geq 10 \text{ ng} / \mu\text{L}$	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	7.832	Effects of spaceflight on the composition and function of the human gut microbiota (2020)
Nature Communications	11.878	Marine biofilms constitute a bank of hidden microbial diversity and functional potential (2019)
Microbiome	10.465	Mobile antibiotic resistome in wastewater treatment plants revealed by Nanopore metagenomic sequencing (2019)

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