

Full-Length 16S Metagenomic Sequencing

Introducing our **Full-Length 16S Metagenomics sequencing** using the Single Molecule Real-Time (SMRT) technology for your microbiome analysis. This method overcomes the limitations associated with short reads (e.g., shattered gene distribution and minor hypervariable region coverage). It enables the strain level resolution to have data with greater accuracy at higher throughput to characterize your microbiome communities.

Our Key Features & Advantages



Longest Average Read Lengths

Fragmentation free amplification enables easy reading of full-length 16S genes, erasing GC bias associated with short read sequencing.



Highest Consensus Accuracy

Guaranteed >99.9% single-molecule sequencing accuracy enables more accurate species classification and less abundant species discovery.



Updated Analysis Software

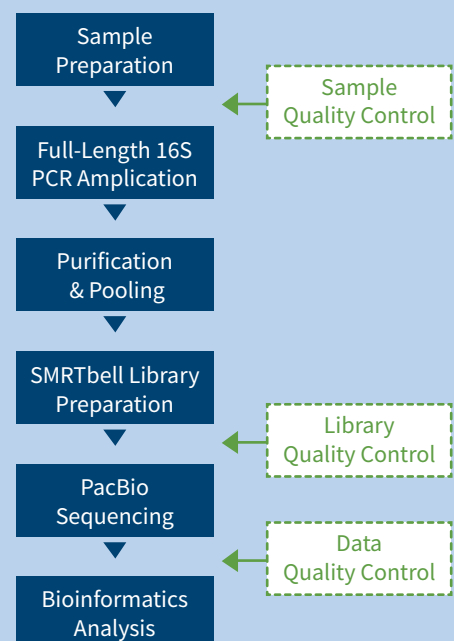
Amplicon Sequence Variants (ASV) generated from QIIME 2 can infer the biological sequences in the sample prior to the introduction of amplification and distinguish sequence variants differing by as little as one nucleotide.



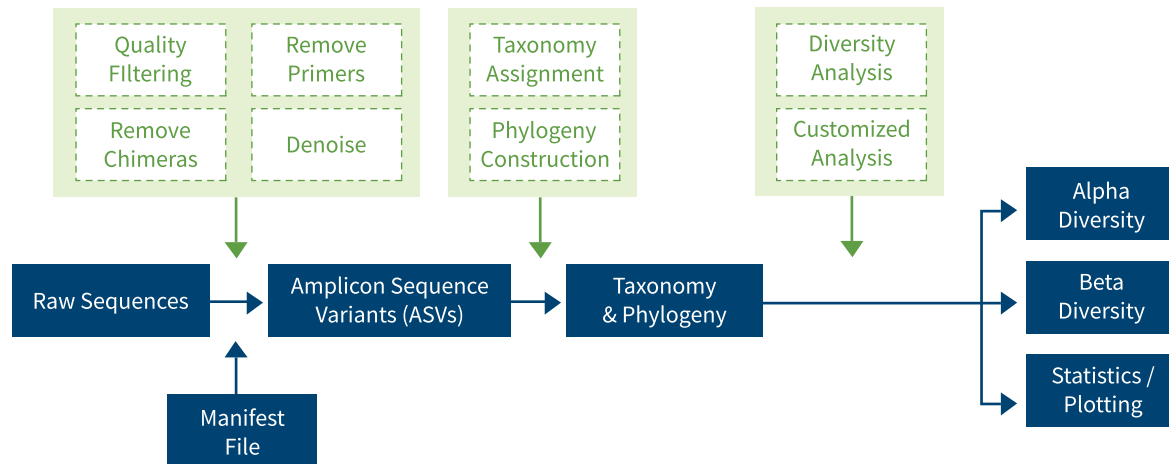
Real-Time Project Management

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

Project Workflow



Standard Analysis Pipeline



Sample Requirements

Sample Type	Amount	Volume	Concentration	Purity
Genomic DNA	≥ 150 ng	≥ 20 µL	≥ 10 ng/µL	OD260/280 = 1.8-2.0, No degradation, no RNA or protein contamination

Publications

Listed below are some recent publications that were supported by Novogene solutions to provide full-length 16S rRNA metagenomics sequencing.

Journal	IF	Title
Genes	4.141	Microbial Richness of Marine Biofilms Revealed by Sequencing Full-Length 16S rRNA Genes (2022)
Microbiome	14.35	A simplified synthetic community rescues Astragalus mongholicus from root rot disease by activating plant-induced systemic resistance (2021)

NovogeneAIT Genomics Singapore Pte. Ltd.

(Regional office for Asia Pacific, Middle-East & Africa)

novogene.com/amea-en marketing_amea@novogeneait.sg

[NovogeneAIT](#) [NovogeneAMEA](#)

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