

Introducing Longer Reads with greater accuracy for your microbiome analyses

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.



Clean Reads Delivery in WBI Option*

Our advanced filters are capable of removing primers and chimeras in raw reads. 5,000 or 10,000 clean CCS reads per sample enables more efficient data analysis.

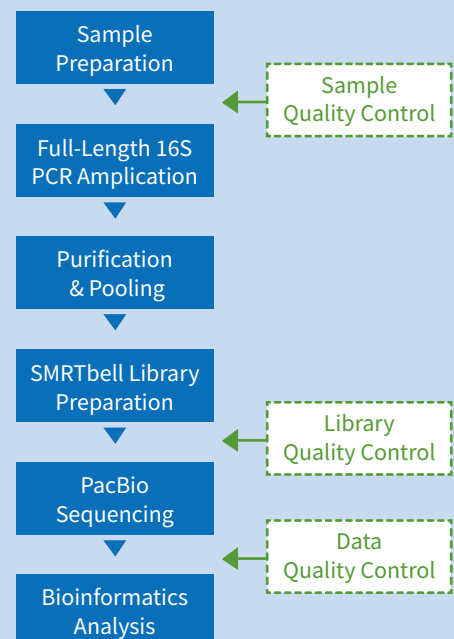
(*Clean reads are delivered only for WBI projects).



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.

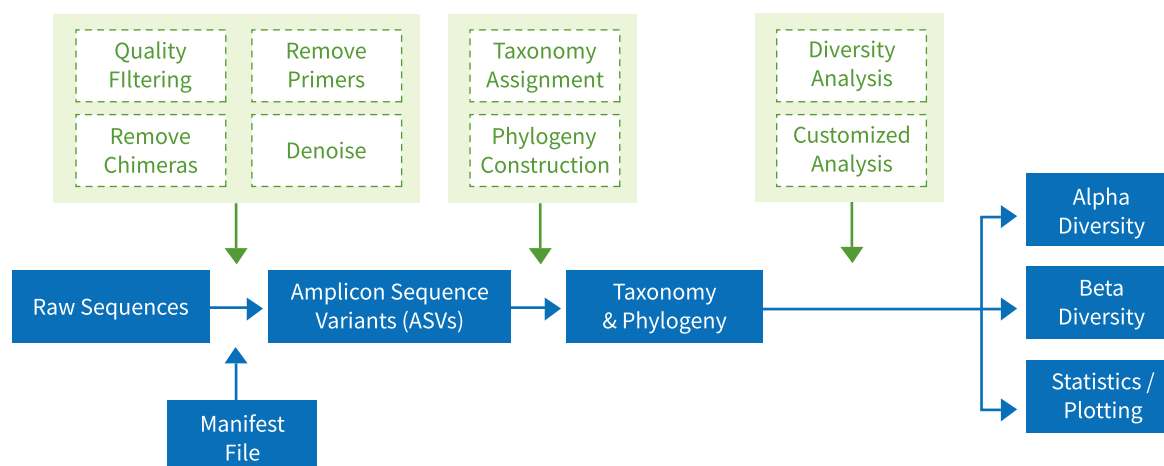
Project Workflow



Sample Requirements

Sample Type	Amount	Concentration	Volume	Purity
Genomic DNA	≥ 150 ng	≥ 10 ng/μl	≥ 15 μl	OD260/280= 1.8-2.0, no degradation, no RNA or protein contamination

Standard Analysis Pipeline



Publications

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

Journal	IF	Title
Nucleic Acids Research	11.147	High-throughput amplicon sequencing of the full-length 16S rRNA gene with single-nucleotide resolution.
Microbiome	10.465	Species-level bacterial community profiling of the healthy sinonasal microbiome using Pacific Biosciences sequencing of full-length 16S rRNA genes.

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