

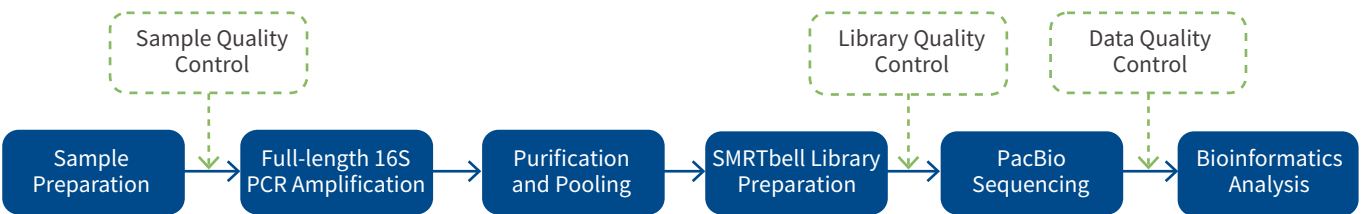
Full-length 16S Amplicon Metagenomic Sequencing

Full-length 16S Amplicon Metagenomic Sequencing is frequently used to identify and differentiate microbial species. PacBio Sequel Systems are powered by Single Molecule Real-Time (SMRT) sequencing technology and deliver highly accurate long reads. Using the PacBio Sequel, full-length 16S amplicon sequencing resolves the limitations of short read lengths (e.g. shattered gene distribution and minor hypervariable region coverage) in next generation sequencing (NGS), and improves the resolution of the strain.

Advantages and Highlights

- Long Read Lengths**
 No fragmentation enables easy reading of full-length 16S rRNA, with PacBio SMRT sequencing technology to avoid GC bias compared to short read sequencing
- High Resolution**
 Guaranteed >99.9% single-molecule sequencing accuracy enables more accurate species classification and more low-abundant species discovery
- Clean Reads Delivery In WBI Option***
 Our advanced filters help you get rid of 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 with bioinformatics (WBI) projects)
- Updated Analysis Software**
 Amplicon Sequence Variants (ASV) generated from QIIME 2 software infer the biological sequences in the sample prior to the introduction of amplification, can distinguish as little as one nucleotide difference

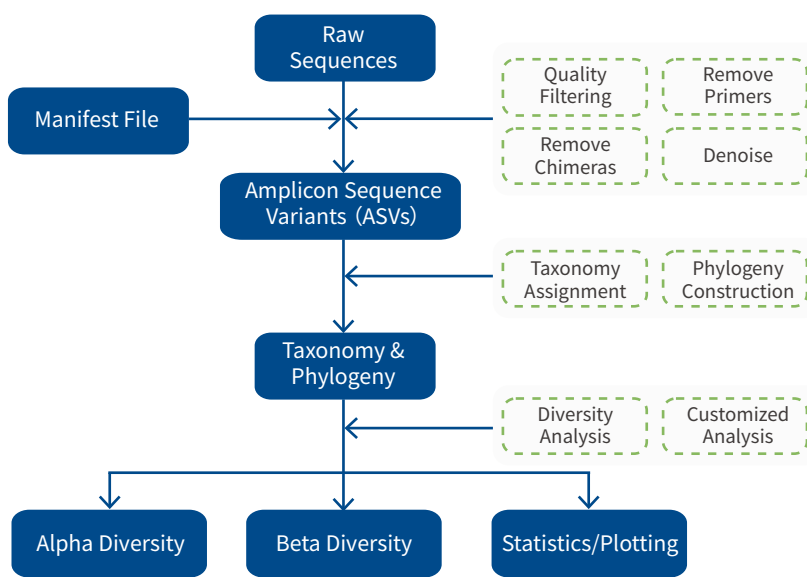
Project Workflow



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



Related Papers

Year	Journal	Title
2020	<i>Water Research</i>	Superior resolution characterisation of microbial diversity in anaerobic digesters using full-length 16S rRNA gene amplicon sequencing
2019	<i>Nucleic Acids Research</i>	High-throughput amplicon sequencing of the full-length 16S rRNA gene with single-nucleotide resolution
2018	<i>Nature Biotechnology</i>	Retrieval of a million high-quality, full-length microbial 16S and 18S rRNA gene sequences without primer bias
2018	<i>Emerging Infectious Disease</i>	Diagnosis of Haemophilus influenzae Pneumonia by Nanopore 16S Amplicon Sequencing of Sputum
2018	<i>Scientific Data</i>	The effects of sequencing platforms on phylogenetic resolution in 16 S rRNA gene profiling of human feces

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