Long-Read Sequencing
With PacBio Revio

Redefining Comprehensive Genomic Analysis

Genomic sequencing has long been characterized by a trade-off between read length and accuracy. Traditional next-generation sequencing (NGS) provides high-accuracy short reads but may struggle to resolve long repeats and complex structural variants (SVs), while older long-read methods offered length but suffered from high error rates.

Feature	HiFi Sequencing Technology	Primary Advantage
Accuracy	≥99.95% (Q33) accuracy in a single read, achieved via Circular Consensus Sequencing (CCS).	Highest-quality data for all variant types (SNVs, indels, SVs), eliminating the need to "polish" long reads with short-read data.
Completeness	Long reads resolve structural variants (SVs) and tandem repeats in a single read; sequencing uses native DNA.	Enables the generation of gapless, Telomere-to-Telomere (T2T) genome assemblies, providing the most complete view of all genetic variation.
Mappability	Ultra-long reads (typically 10–25 kb) are generated with uniform coverage (low GC bias).	High confidence mapping into complex, repetitive, and GC-rich "dark regions" of the genome, which are often inaccessible to short reads.
Phasing	Long, accurate reads span multiple heterozygous variants on a single DNA molecule.	Streamlined, accurate haplotype phasing (determining which variants are on the maternal vs. paternal chromosome) over long distances, often without parent-child trio data.

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Technology Advantages

PacBio High Fidelity (HiFi) Sequencing resolves this fundamental challenge. Utilizing Single Molecule, Real-Time (SMRT®) technology, HiFi reads deliver an optimal combination: long reads (~10–25 kb) with unparalleled accuracy (≥99.9%, or Q30).

HiFi sequencing, therefore, provides the most complete and accurate view of the genome, transcriptome, and epigenome, driving research to the different level.

Superior Support for Your Research

- Best Pricing
- 3-4 Week Turnaround
- US Operations

PacBio HiFi Advantages	
Sequencing Only	Highly accurate long HiFi reads, perfectly suited for bioinformatics pipelines.
Full-Length RNA-seq	Full-length reads span transcripts, eliminating assembly and accurately identifying alternative splicing, novel isoforms, and gene fusions.
Whole Genome Sequencing (WGS)	Accurately resolves structural variants (SVs) and repetitive elements for the most contiguous and correctly phased (de novo) assemblies.
Metagenomics	Long, accurate reads assemble closed, high-quality MAGs and provide full-length marker genes (e.g., 16S) for deep, strain-level classification.
Amplicon Sequencing	Single reads span the full amplicon (up to 20 kb), enabling direct phasing of multiple variants and resolving complex gene families (like HLA) and tandem repeat expansions.
Epigenetics	Simultaneous detection of 5mC (and microbial m6A, m4C) alongside sequence data, with no bisulfite conversion required.

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