Pacbio Long-Read Whole Genome Sequencing

PacBio High Fidelity (HiFi) Sequencing utilizes Single Molecule, Real-Time (SMRT) technology to deliver long reads (10-25kb) with unparalleled accuracy ≥99.9%, or Q30). HiFi sequencing provides the most complete and accurate view of the genome, transcriptome, and epigenome, taking research to the next level.

Unlock complete, accurate, and highly contiguous genomes with PacBio Revio long-read sequencing. Designed for complex genomes and challenging samples, our Revio WGS services deliver the clarity and confidence researchers need for discovery, assembly, and variant analysis.

DNA Quality Requirements

HMW DNA for PacBio Sequencing

Sample Type	Amount	Volume	Concentration	Purity	Fragment Size
Human, animal, plant	15 µg (recommended) 5 µg (minimum)	> 20 µL	> 100 ng/µL	OD260/280 = 1.7–1.9 OD260/230 = 2.0	≥ 30 kb
Bacteria & Fungi	8 µg (recommended) 2 µg (minimum)	> 20 µL	> 100 ng/µL	OD260/280 = 1.7–1.9 OD260/230 = 2.0	≥ 20 kb

Contact Us
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126 Corporate Boulevard, South Plainfield, New Jersey 07080

PACBIO LONG-READ WGS

Workflow

Genomic DNA QC & shearing

HMW DNA is extracted & QC'ed
Input: ≥1 µg gDNA per SMRT Cell 8M
DNA is sheared to ~15–20 kb for WGS

Library Construction

Libraries are prepared and indexed for multiplexed sequencing. Library prep is optimized for coverage & accuracy

Sequencing on the PacBio Revio

Libraries are sequenced for high-fidelity (HiFi), long-read WGS data

Data Analysis: SMRT Link

Comprehensive bioinformatics: genome assembly, variant detection, structural variation

Applications & Deliverables

Variant Discovery

- QC + Mapping + Duplicate Detection + Variant Detection + annotation (if available) + Structural Variation + insertion site analysis

Assembly Small genome Bacterial and yeast

- genome fasta files + reference-based gene annotation + online genome browser

Assembly Large Genome Human, hamster, CHO, etc

- genome fasta files + reference-based gene annotation + online genome browser + haplotype sequences for mammalian genomes

Special Service Benefits

- **Fast TAT:** 4-6 weeks; expedited 3 weeks upon request
- **Tailored Solutions:** 1:1 support from our PhD-level scientists, customized workflows available

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