



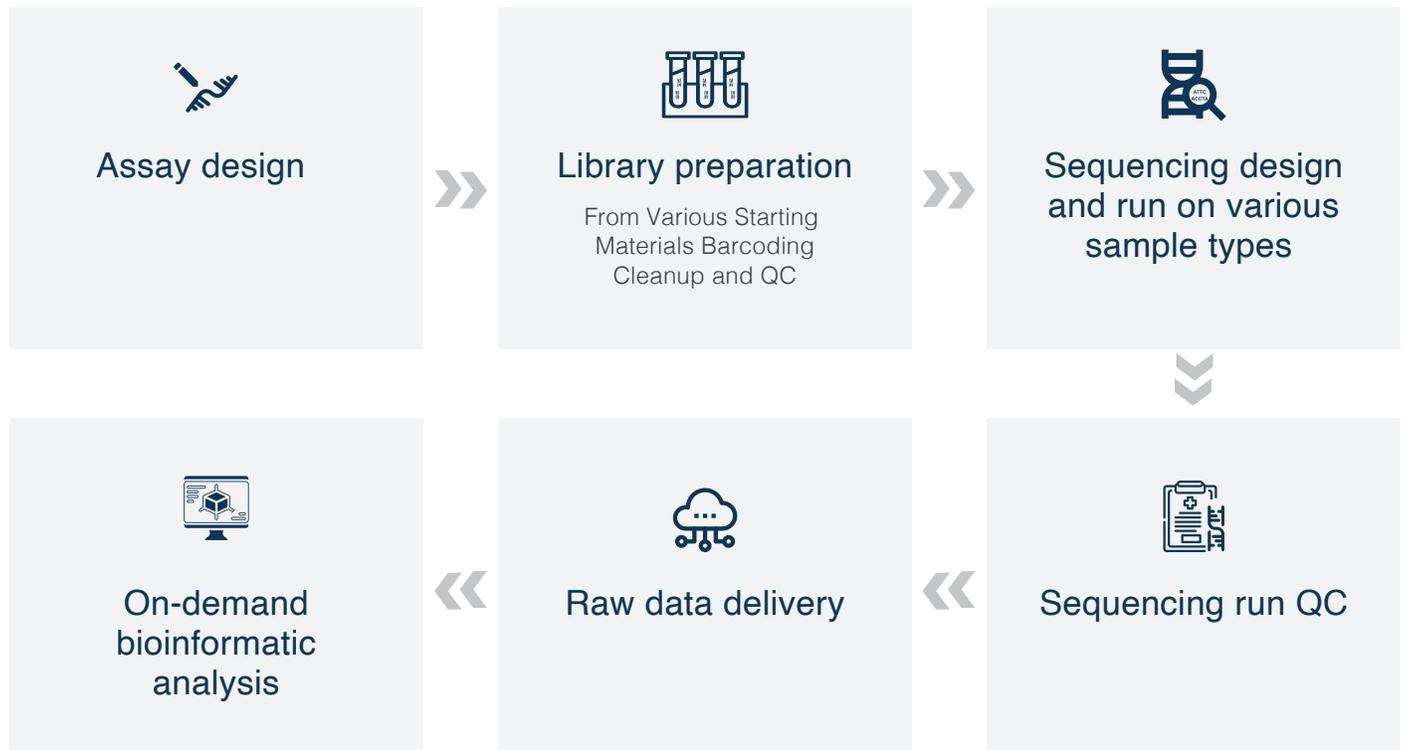
Single-Molecule, Real-Time (SMRT) Sequencing

# PacBio Sequencing Service

*A complete solution with fast turn-around time  
& comprehensive technical support*

## Services at-a-glance

Quintara offers a complete package of PacBio sequencing services, from assay design and library prep to sequencing reactions and data analysis. We are aiming to provide a solution to facilitate biomedical research.

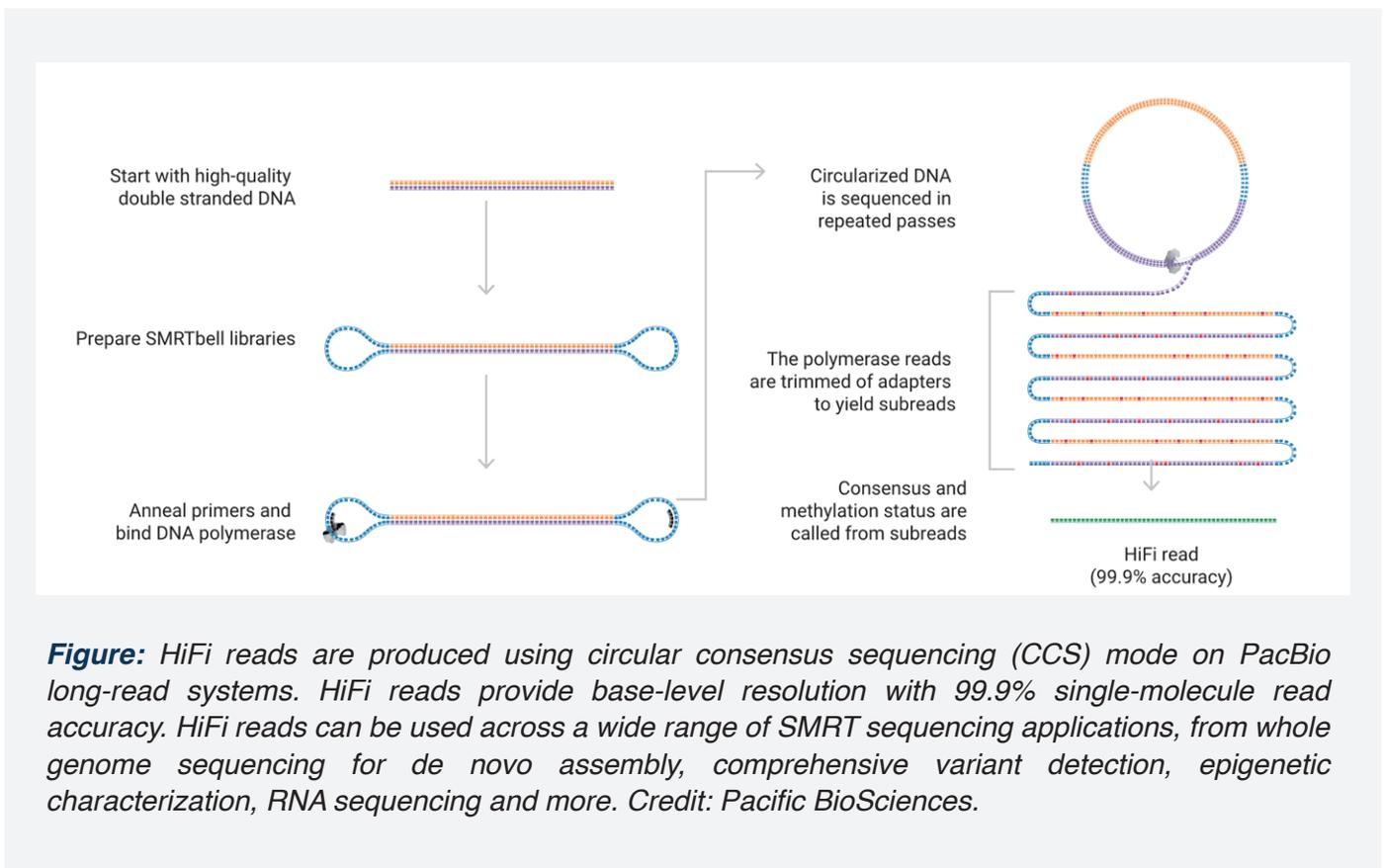


## Introducing PacBio sequencing method

Single-molecule, real-time (SMRT) sequencing developed by Pacific BioSciences has become a trending new member of the NGS family. Nicknamed “PacBio,” the new method outputs highly accurate long reads, as much as tens of kilobases, making it a powerful tool for investigating many unanswered questions in biomedicine.

PacBio sequencing provides long reads that span large structural variants and repetitive regions that are poorly covered by short-reads methods. Its low GC bias enables through-reading in extreme GC- or AT-rich regions. DNA methylations can also be accurately detected.

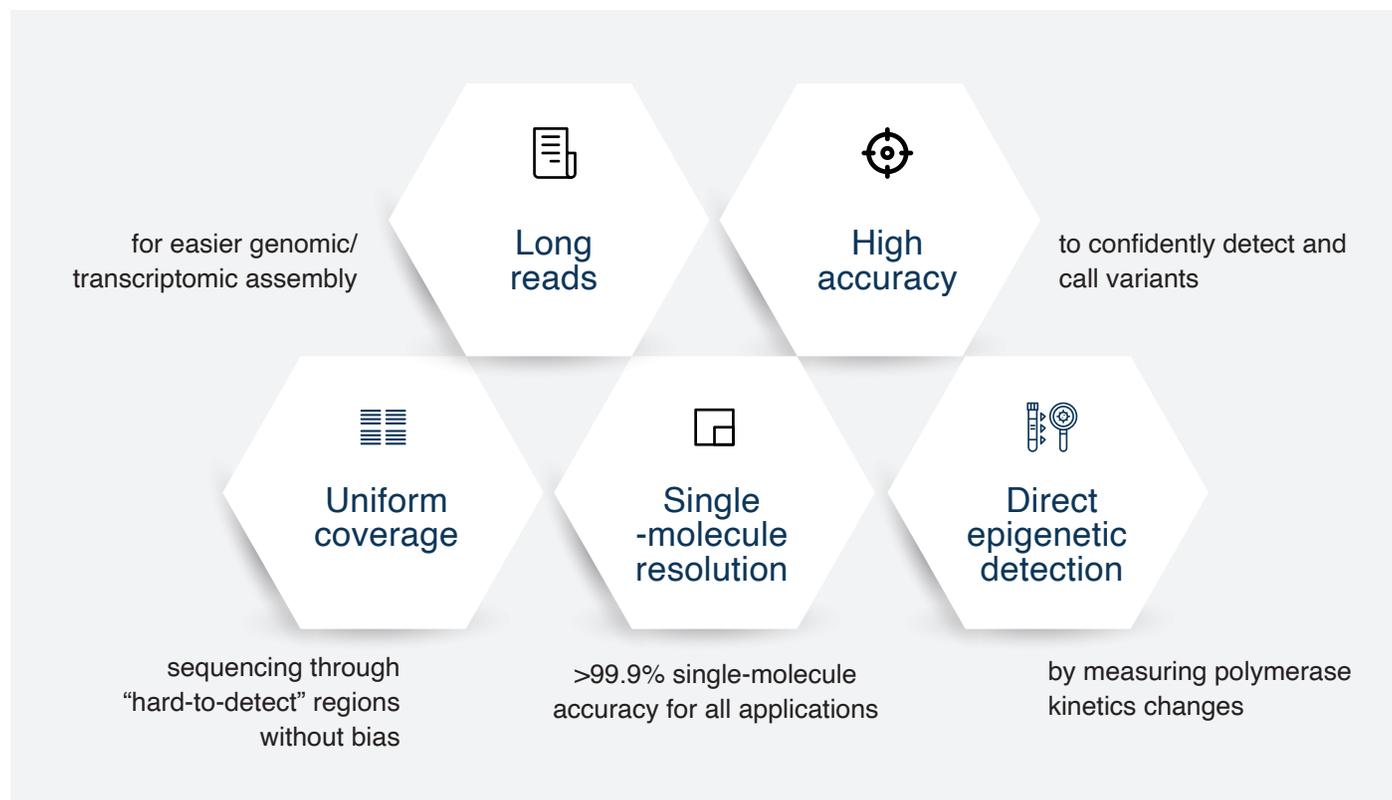
Since its inauguration, PacBio has seen growing applications in de novo genome sequencing, phasing, structural variants detection, epigenetic characterization, transcriptomics, metagenomics, etc.



**Figure:** HiFi reads are produced using circular consensus sequencing (CCS) mode on PacBio long-read systems. HiFi reads provide base-level resolution with 99.9% single-molecule read accuracy. HiFi reads can be used across a wide range of SMRT sequencing applications, from whole genome sequencing for de novo assembly, comprehensive variant detection, epigenetic characterization, RNA sequencing and more. Credit: Pacific BioSciences.



## Advantages of PacBio sequencing




## PacBio sequencing applications

Category	Application	PacBio solution
Whole genome sequencing with methylation	De novo assembly (2 Gb)	Complete, contiguous, and correct assemblies with base-level methylation
	Variant detection (3 Gb)	High precision and recall for all variant types with base-level methylation
Iso-Seq® method	Full-length RNA sequencing	High-quality comprehensive genome annotation
		Novel isoform discovery differential analysis
Targeted sequencing	Amplicon (1-20 kb)	Haplotype phasing while detecting all variant types
	HiFiViral SARS-CoV-2 sequencing	Unique MIPs solution is simple and robust to novel variants
Microbial sequencing	De novo assembly	Closed genomes and plasmids
	Metagenome assembly	Generation of complete or near-complete genome assemblies from microbial populations
	Metagenome profiling	Recovery of 8-10 full-length genes per HiFi read, without assembly
	Full-length 16S rRNA sequencing	Unambiguous species or strain-level resolution



## The Quintara PacBio sequencing solution

■ We are devoted to providing a complete solution with fast turn-around time & comprehensive technical support.

- **Sequel® IIe system:** fast and high throughput SMRT sequencing
- **Extensive customer care:** thorough discussion of sequencing projects with expert suggestions. No project is too small or too hard.
- **Expert technical support:** Comprehensive support from a team of experienced scientists from raw material extraction to library prep and sample loading.



■ **Sample requirement (amplicon)**

PCR-barcoded samples		Adapter-barcoded samples	
Mean size	Minimum pooled amount per SMRT Cell 8M*	Mean size	Minimum per sample amount per SMRT Cell 8M
< 5 kb	150 ng	< 5 kb	150 ng
5-7kb	200 na	5-7kb	200 na
> 7 kb	300 ng	> 7 kb	300 ng

■ **Price and timeline (pilot program)**

- Our goal is to provide high-quality service at a fair and honest price.
- The project timeline depends on shipping arrangement, sample prep complexity, and sequencing time per sample.

 **ABOUT QUINTARA**

Quintara stands as a nationwide gene sequencing leader, spanning California, Massachusetts, Colorado, Connecticut, Maryland, and beyond. We are committed to delivering the best service to the life science community and ensuring the fastest turnarounds so your research can move forward faster.

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|--|--|---|
| <input checked="" type="checkbox"/> Sanger Sequencing          | <input checked="" type="checkbox"/> Whole Plasmid Sequencing | <input checked="" type="checkbox"/> Single-Stranded DNA Synthesis |
| <input checked="" type="checkbox"/> Amplicon NGS Sequencing    | <input checked="" type="checkbox"/> Oligo Synthesis          | <input checked="" type="checkbox"/> DNA Prep                      |
| <input checked="" type="checkbox"/> NGS Service                | <input checked="" type="checkbox"/> <b>PacBio Sequencing</b> | <input checked="" type="checkbox"/> Cell Line Engineering         |
| <input checked="" type="checkbox"/> Gene Synthesis and Cloning | <input checked="" type="checkbox"/> Virus Packaging          |   |