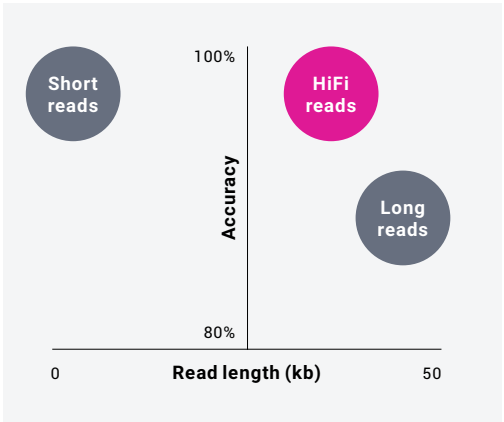
A NEW PARADIGM:

HiFi reads for highly accurate long-read sequencing



With PacBio® HiFi reads, you no longer need to compromise between long read lengths and high-accuracy sequencing.

The benefits of HiFi reads:

- Long read lengths up to 25 kb
- High read accuracy >99.9%
- Easy library preparation
- Low coverage requirements
- Small file sizes to minimize compute time
- A single technology solution for a range of applications

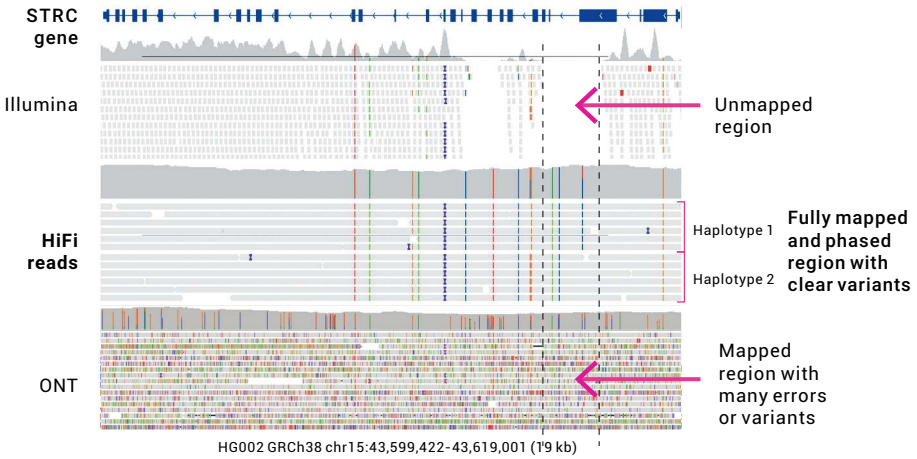
PacBio is the only sequencing technology to offer highly accurate long reads.
A typical 20,000 bp HiFi read has ~8 incorrect bases

PacBio 伯森生技

Achieve comprehensive variant detection

HiFi reads let you accurately detect all types of variants with high precision and recall and phase haplotypes, even in hard-to-sequence regions of the genome missed by other technologies.

> "HiFi reads really allow us to call accurate structural variations and other types of variations that you can't actually see with short-read sequencing."
>
> Jeremy Schmutz, *Faculty Investigator, HudsonAlpha Institute of Biotechnology*



STRC gene alignments from *Genome in a Bottle* (GIAB), HG002_NA24385_son.

Precision | Recall (%)

	Illumina	ONT	HiFi reads
SNVs	99.8 | 99.4	99.7 | 99.5	**99.9 | 99.9**
Indels	99.7 | 99.5	86.6 | 63.6	**99.4 | 99.4**
SVs	94.7 | 62.4	95.7 | 95.8	**96.1 | 96.0**

Detect all variant types with high precision and recall

SNVs, indels: *PrecisionFDA Truth Challenge V2* HG003 DeepVariant callsets evaluated against GIAB v4.2 benchmark using hap.py. SVs: HG002 callsets evaluated against GIAB v0.6 SV benchmark using Truvari, Illumina: DRAGEN 3.5, ONT: Sniffles at 30×, PacBio: pbsv 2.1.0 at 30×

Produce reference-quality *de novo* assemblies

HiFi reads generate complete, contiguous, and correct *de novo* assemblies of any genome, including the large and highly complex California Redwood.

> "If your genome isn't HiFi, it's no longer reference grade."
>
> Kevin McKernan, *Medicinal Genomics*

California Redwood genome (27 Gb hexaploid)

	OONT 23-fold + short reads 122-fold	HiFi reads 22-fold
Assembly size (Gb)	26.5	**47.7**
Contig N50 (Mb)	0.11	**1.92**
Average alignment of *A. thaliana* genes*	80.80%	**87.70%**
Assembly time	5–6 months	**6 days**

Haplotype resolution

More complete genes

HiFi sequencing produces high-quality results quickly and affordably

*Completeness of alignments of 458 *Arabidopsis thaliana* genes, measured by how much of each gene was covered in the alignment averaged over all the genes. Learn more at **pacb.com/redwood**. ONT data: Sequencing and assembling mega-genomes of mega-trees.

Explore metagenomes in high resolution

HiFi reads enable direct error-free gene discovery in heterogeneous samples, even in low-abundance species with too little coverage for assembly.

Human fecal sample	Number of predicted genes	Mean length (bp)	Clustered genes (99% id)	Mean predicted genes / read
HF 1	19,639,322	1,005	1,012,982	7.9
HF 2	22,064,417	1,001	1,141,123	8.4
HF 3	18,059,181	1,024	1,154,341	7.6
HF 4	19,844,033	978	1,250,711	9.3
HF 5	18,396,237	970	1,087,015	9

Human fecal samples sequenced on the Sequel® II system. Learn more at **pacb.com/microbial-genomics**.

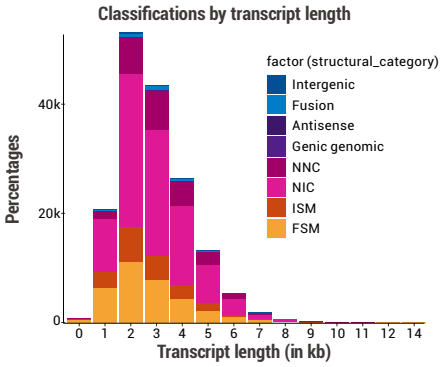
Did You Know?

30–70% of short-read data do not map to a metagenome assembly and are not useful for identifying genes

Each individual HiFi read contains complete genes even for low-abundance species

Characterize and annotate whole transcriptomes

Access full-length transcripts to identify novel genes and complex alternative splicing events with HiFi reads.



- **162,290 transcripts**
- **Min: 80 bp**
- **Max: 14,288 bp**
- **Mean: 3,347 bp**

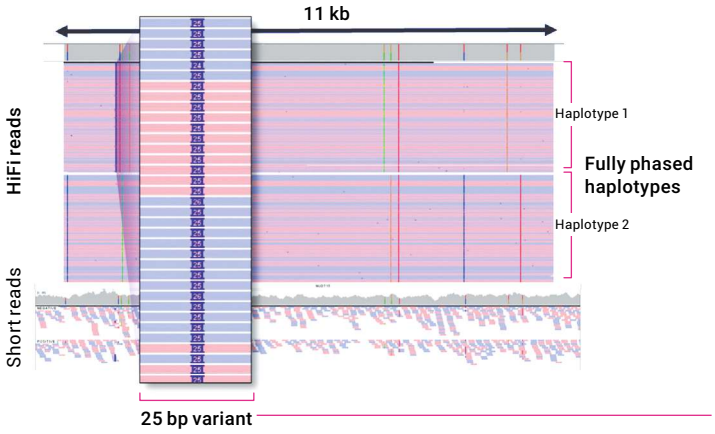
Detect full-length transcripts up to 14 kb

Alzheimer brain sample

	Known	Novel	Total
Genes	17,051	619	17,670
Isoforms	51,660	110,630	162,290

Sequencing of an Alzheimer brain sample using the Iso-Seq® method on the Sequel II system, learn more at **pacb.com/alzheimer**.

Target even difficult-to-sequence genes or regions



HiFi reads let you obtain Sanger-quality accuracy and detect novel variants missed by other technologies.

An 11 kb amplicon of a clinically-actionable gene sequenced on the Sequel system. Learn more at **pacb.com/ASHGworkshop**.

Detect variants missed by short reads

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SEQUENCE WITH CONFIDENCE

Achieve comprehensive variant detection

Explore the applications:
pacb.com/applications

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