



PLANT AND ANIMAL BIOLOGY

Accurate and actionable data for biodiversity

Unravel the complexity of plant and animal biology for any species with HiFi sequencing. Discover more about species and populations with more accurate genomes, transcriptomes, and epigenomes.

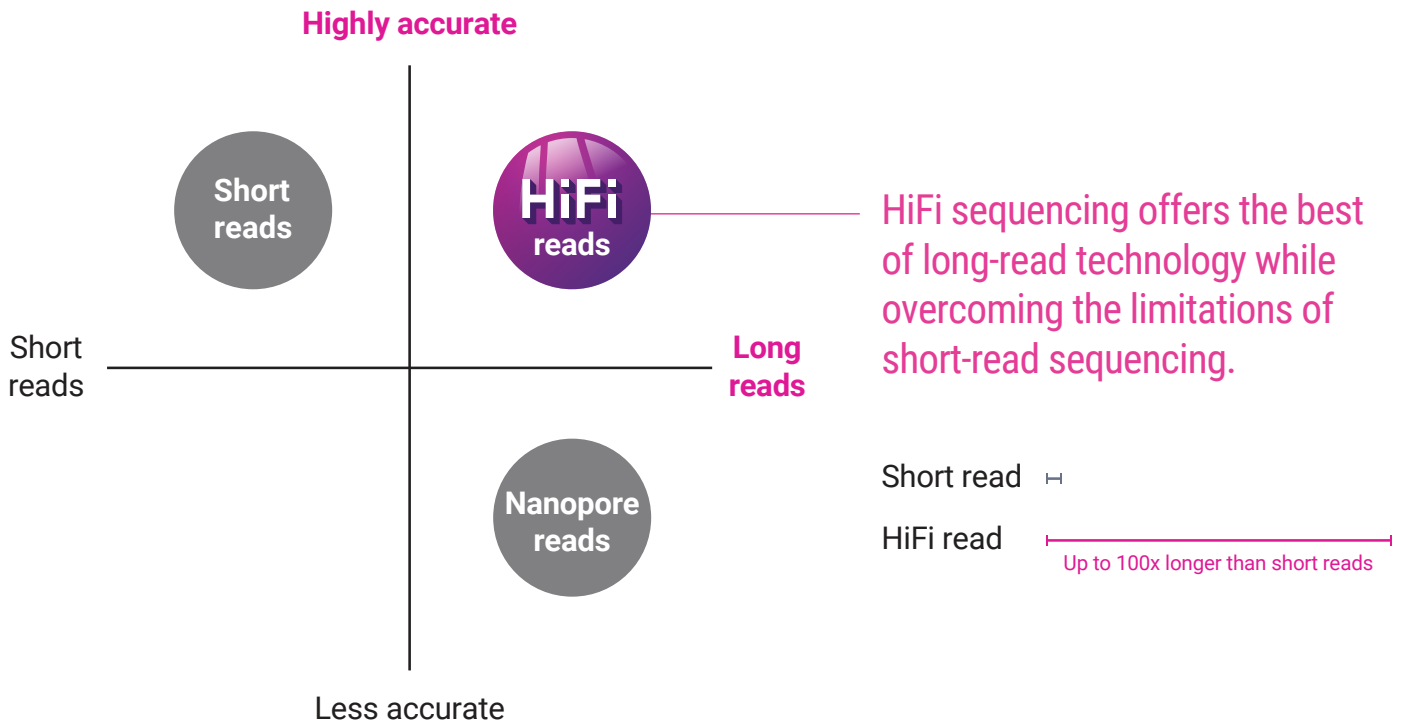
Sequencing to understand and protect species, populations, and ecosystems

As climate patterns change and ecosystems shift, scientists are turning to modern genomics technology to better understand and protect the species and populations with whom we share our world. PacBio® provides cutting-edge sequencing solutions that enable plant and animal biologists to discover and harness biological information for all organisms — big or small. From sea to sky, and everything in between, researchers are using genomic data that more accurately represents the complex biology of plants and animals to drive conservation efforts, capture biodiversity, and dive deeper into the unique biology of all organisms.



What is HiFi sequencing?

PacBio HiFi sequencing unites long reads and accuracy, giving you the highest quality genomic data for any species. When it comes to protecting biodiversity, why compromise with draft genomes that provide limited information?



The benefits of HiFi reads



Long read lengths



Low DNA input requirements and easy library prep



Low coverage requirements



Small file sizes to minimize compute time



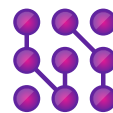
Supported analysis tools consolidated into a single pipeline



High read accuracy



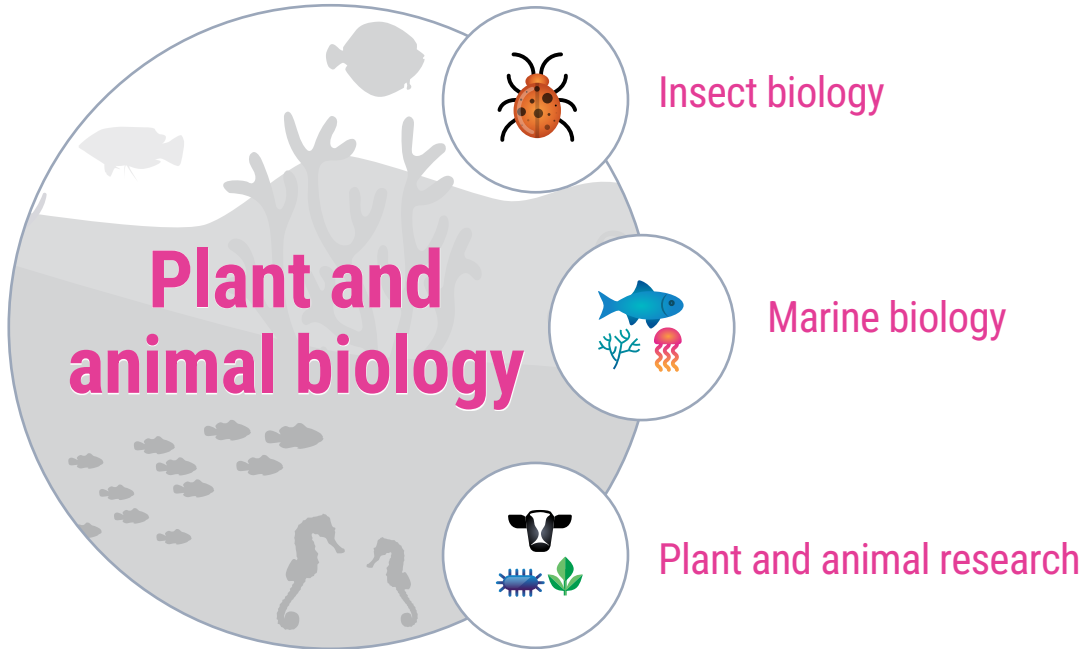
Compatible ecosystem partners to enable an end-to-end workflow



A single technology solution



Plant and animal biology in action



Applications to power plant + animal sciences



Whole genome sequencing

Produce reference-quality, haplotype-phased genomes for any organism.



RNA sequencing

Generate high-quality genome annotation by accessing full-length cDNA sequences and identifying novel genes and isoforms.



Structural variant calling

Use high-sensitivity variant calling with low false discovery rate to gain actionable insights across populations.



Metagenome sequencing

Comprehensively characterize metagenomes with long, highly accurate single-molecule reads — no assembly required.



Epigenetics

Capture simultaneous methylation modifications (5mC at CpG sites and 6mA) in standard sequencing runs without any additional library preparation.



Targeted sequencing

Choose from flexible options to target genes in even the most complex regions with access to a majority of variant types

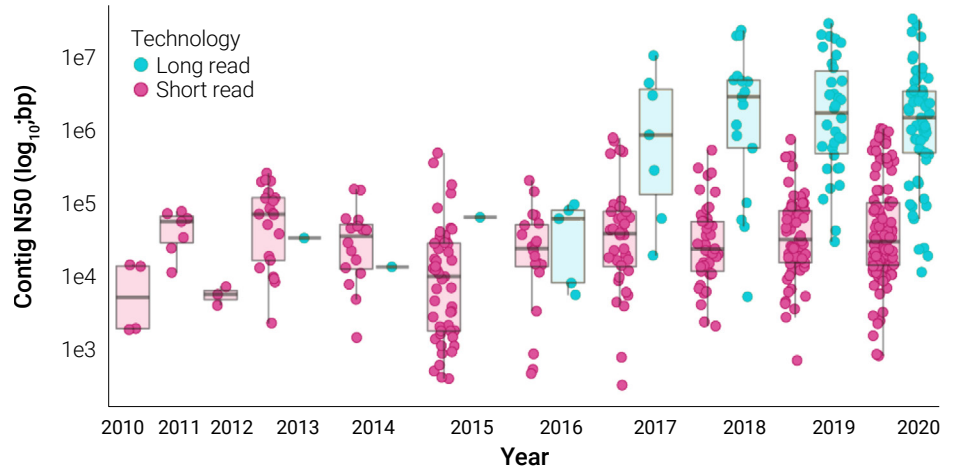


Insect biology

Develop disease prevention methods, understand basic biology, and improve pest control using a population or a single individual.

Genomes to capture the vast diversity of insects

Over two decades ago, the first insect genome assembly was published in *Science* for *Drosophila melanogaster*, and since then, the insect biology scientific community has sequenced hundreds of genomes for insects, arthropods, and pests all over the world. Even though these genomes only represent 0.06% of the million different insect species on earth, scientists are quickly sequencing more insect genomes than ever before, because long-read sequencing allows scientists to efficiently assemble, phase, and capture genomic diversity from single-nucleotide polymorphisms to complex structural variants.

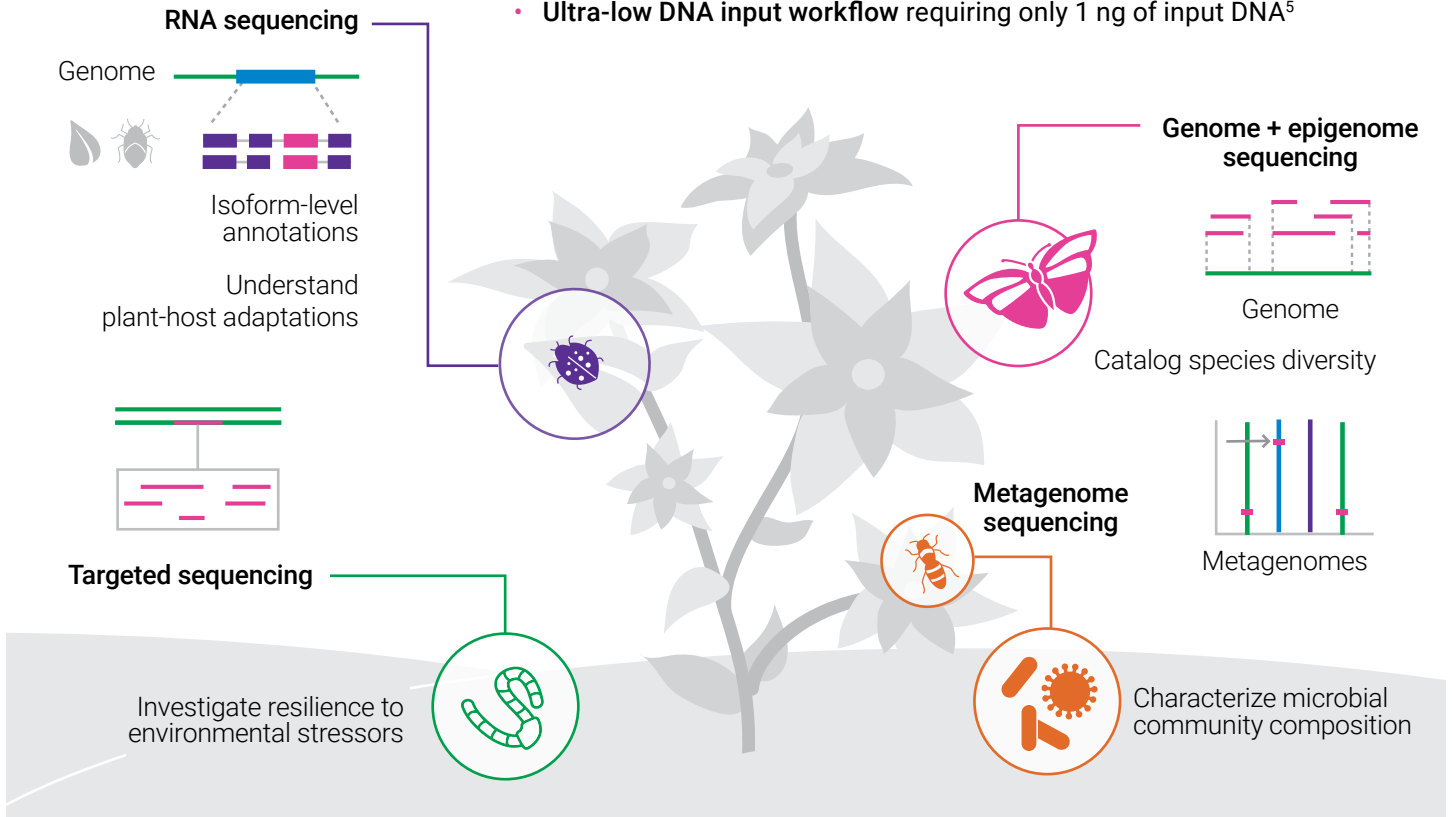


Insect genome assembly contiguity by year⁴
Image adapted from *Long Reads Are Revolutionizing 20 Years of Insect Genome Sequencing*

Sequence even the smallest organisms

Overcome DNA input barriers to sequencing small-bodied organisms

- **Dedicated insect DNA extraction protocol** for a seamless workflow and high-quality sequencing data
- **Ultra-low DNA input workflow** requiring only 1 ng of input DNA⁵





Marine biology

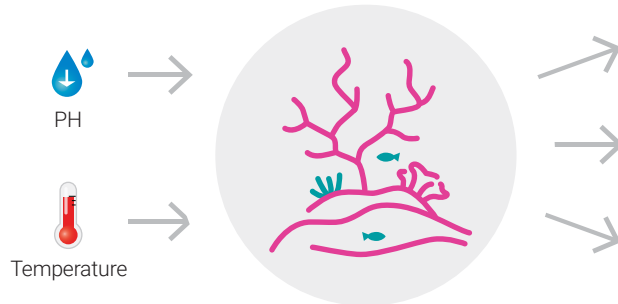
Dive into the depths of marine ecosystems to study evolution, reveal insights into developmental biology, and address the challenges of climate change.

Genomes to protect marine biodiversity

Science may, at times, seem like a fishing expedition. But for those who are charting the depths of the 321 trillion gallons of water that make up Earth's seas and oceans, the endeavor to collect genetic information is particularly difficult. The magnitude of global marine species diversity is immense, with thousands of species yet to be discovered and described. Luckily, the process of comprehensively characterizing the genetics of marine species is well underway. Many scientists are employing the exceptional accuracy of HiFi sequencing to explore the genomes, transcriptomes, and epigenomes of a wide variety of marine species and ecosystems. These studies are already adding to our understanding of how marine species adapt and evolve, shedding light on efforts to protect life in our lakes, rivers, oceans, and seas.

- **Genome + epigenome sequencing**
Assemble high-quality genomes to better understand complex genotypes such as bioluminescence⁶
- Understand how fish adapt to harsh environments with full-length transcriptome sequencing⁷
- **Metagenome sequencing** Dive into aquatic ecosystems by deconvoluting microbial life and understanding symbiosis⁸
- Identify, sequence, and multiplex genomic regions of interest without compromising amplicon size

Environmental stressors



Detect effects with HiFi sequencing

- **DNA sequencing**
Population variation
- **RNA sequencing**
Transcriptional compensation mechanisms
- **Metagenomic sequencing**
Shifting microbial communities

Sequencing applications for marine ecosystems⁹

Obtaining high-molecular weight DNA from difficult-to-sequence species

It is no deep secret that isolating DNA from mollusks, corals, and other marine species is difficult. However, solutions from PacBio Nanobind[®] technology make it easier than ever to obtain high-quality DNA from marine specimens.



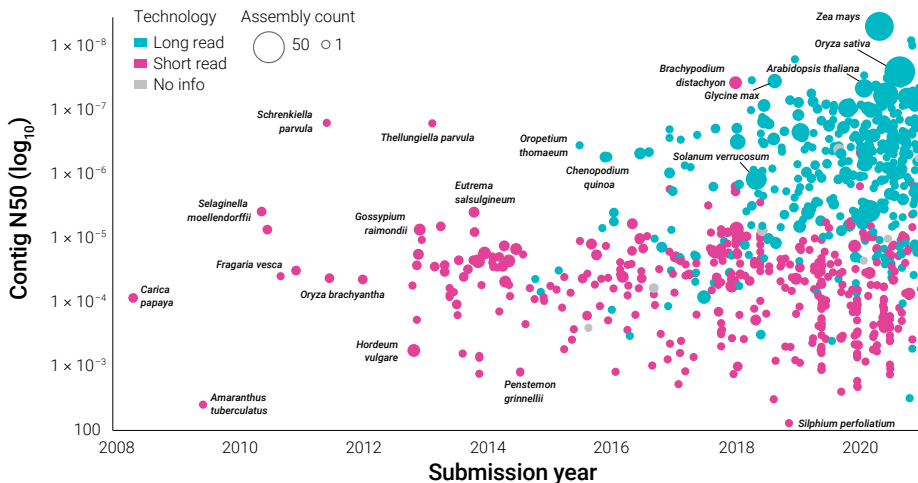
Overview of PacBio Nanobind technology¹⁰



Plant and animal biology

The blossoming possibilities with plant and animal genomics

Over the past two decades, plant and animal researchers have tackled the world's most complex genomes, ranging in size, ploidy, repetitive elements, and GC content. Despite these challenges, plant and animal genomics is reaching new heights with the help of highly accurate long-read sequencing, with genomes resulting in a 32-fold increase in contig N50 compared to short-read assemblies and the ability to resolve complex haplotypes. As scientists continue to sequence the *Tree of Life*, the currently published genomes — only representing a small fraction of the eukaryotic species on our planet — have transformed our collective knowledge of biodiversity and are being used to better preserve it.

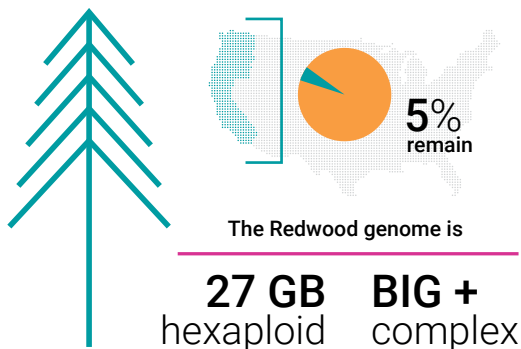


Changes in land plant genome assembly quality and availability over time¹⁵
Image adapted from *Representation and participation across 20 years of plant genome sequencing*

- **Genome + epigenome sequencing**
Build haplotype-resolved *de novo* assemblies for even the largest, most complex of genomes¹¹
- **RNA sequencing**
Generate isoform-level transcriptomes for individuals or at single-cell resolution^{12,13}
- **Metagenome sequencing**
Obtain a complete picture of complex populations with high-quality metagenomes¹⁴
- **Targeted sequencing**
Identify, sequence, and multiplex genomic regions of interest without compromising amplicon size

A genome fit for a giant: the California redwood

Sequoia sempervirens is one of the world's fastest-growing conifers that live for hundreds of years. Once ubiquitous throughout the Northern Hemisphere, now only 5% of the original old-growth coastal redwood forest remains.



Technology matters

PacBio HiFi sequencing gets complex genomes right



Short reads



Long reads



HiFi reads

Efficiency matters

HiFi sequencing produces high-quality results quickly and affordably



Contig N50



Coverage



Project time

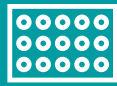
Workflow

With easy-to-use, high throughput sequencing, you can get the accuracy you need at an affordable cost



Sample prep

Efficient extraction of a diverse range of sample types and flexible DNA input requirements down to 1 ng



Library prep

Adjustable multiplexing options to maximize throughput



HiFi sequencing

Highly accurate multiomic solutions for genomes, transcriptomes, and epigenomes



Data analysis

Supported analysis tools consolidated into a single pipeline

This scalable workflow allows for sequencing 1,000s to 10,000s of genomes per year





We have offices in countries around the world.

Visit pacb.com/contact for contact info.

Headquarters

1305 O'Brien Drive
Menlo Park, CA 94025
United States
Phone: 1.650.521.8000

Customer service

1.877.920.PACB (7222), option 1
Fax: 1.650.618.2699
orders@pacb.com

Technical support

1.877.920.PACB (7222), option 2
support@pacb.com

Connect with PacBio for more info:

North America: nasales@pacb.com

South America: sasales@pacb.com

EMEA: emea@pacb.com

Asia Pacific: apsales@pacb.com

Ready to get started with HiFi sequencing?



Learn more about HiFi sequencing:
pacb.com/hifi



Learn more about plant + animal genetics:
pacb.com/plant-animal-sciences



Connect with a PacBio scientist to get started:
pacb.com/scientist

REFERENCES

1. Main, B.J., et al (2021) Whole-genome assembly of *Culex tarsalis* G3 Genes|Genomes|Genetics 11, 2 jkaa063
2. Yang, H., et al. (2020) SMRT sequencing of the full-length transcriptome of the *rhyncophorus ferrugineus* (coleoptera: *curculionidae*) *PeerJ* 8:e9133
3. PacBio application brief (2019) Targeted sequencing for amplicons
4. Hotaling, S. et al. (2021) Long reads are revolutionizing 20 years of insect genome sequencing. *Biology and Evolution* 13, 8, evab138
5. PacBio (2020) Application note – considerations for using the low and ultra-low DNA input workflows for whole genome sequencing
6. Gould A., et al. (2021) Chromosomal-level genome assembly of the bioluminescent cardinalfish *siphania* tubifer, an emerging model for symbiosis research bioRxiv 2021.09.03.458932
7. Luo, H., et al. (2020) Full-length transcript sequencing accelerates the transcriptome research of *gymnocypris namensis*, an iconic fish of the Tibetan plateau *SciRep* 10, 9668
8. Shumaker, A., et al. (2019) Genome analysis of the rice coral *Montipora capitata* *Sci Rep* 9, 2571
9. PacBio (2019) Case study: Diving deep – Revealing the mysteries of marine life with SMRT sequencing
10. Circulomics Nanobind technology, website
11. Kazuhiro, S., et al. (2021) Chromosome-scale genome assembly of the transformation-amenable common wheat cultivar 'Fielder.' *DNA Research* 28, 3, dsab008
12. Ali, A., et al. (2021) PacBio Iso-Seq improves the rainbow trout genome annotation and identifies alternative splicing associated with economically important phenotypes *Front. Genet* 12, 683408
13. Shields, E., et al. (2021) Genome annotation with long RNA reads reveals new patterns of gene expression and improves single-cell analyses in an ant brain *BMC Biol* 19, 254
14. Dirks, A.C., et al. (2020) Community structure of arbuscular mycorrhizal fungi in soils of switchgrass harvested for bioenergy appl *Environ Microbiol* 86, 19, e00880-20
15. Marks, R.A., et al. (2021) Representation and participation across 20 years of plant genome sequencing *Nat. Plants*
16. Tseng, L. (2020) A genome fit for a giant – sequencing the California Redwood. Medium, blog