

PLANT AND ANIMAL BIOLOGY

Accurate and actionable data for conservation, biodiversity, and biodiscovery

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

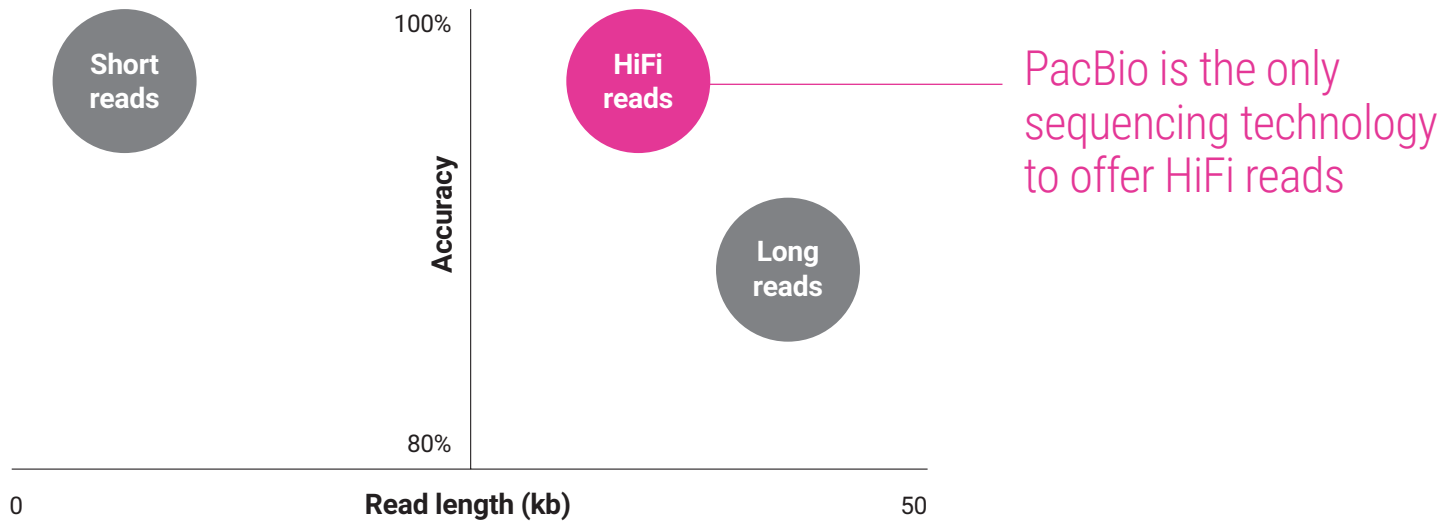
Sequencing to understand and protect species, populations, and ecosystems

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.



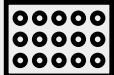





HiFi sequencing for the best of long *and* short reads

With PacBio HiFi sequencing, you no longer have to compromise between long read lengths and high accuracy.



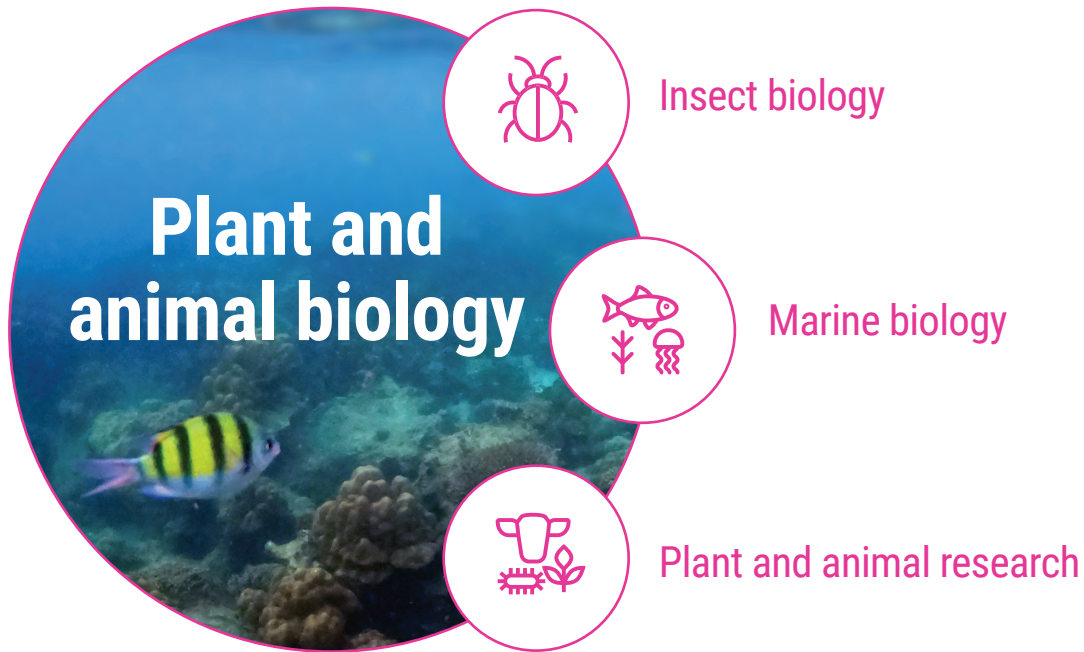
The benefits of HiFi reads

| | | | | | |
|---|---|---|---|---|---|
|  |  |  |  |  |  |
| 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 |

A typical 20,000 bp HiFi read has ~ **8 incorrect bases**



Plant and animal biology in action



Applications to fuel plant and animal biology



Whole genome sequencing

Produce reference-quality genomes with phased haplotypes from even small-bodied organisms



RNA sequencing

Access full-length transcript sequences to identify novel genes and transcripts and improve genome annotation



Structural variant calling

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



Complex populations

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



Targeted sequencing

Choose from flexible options to target regions to access to all variants – even in the most complex regions

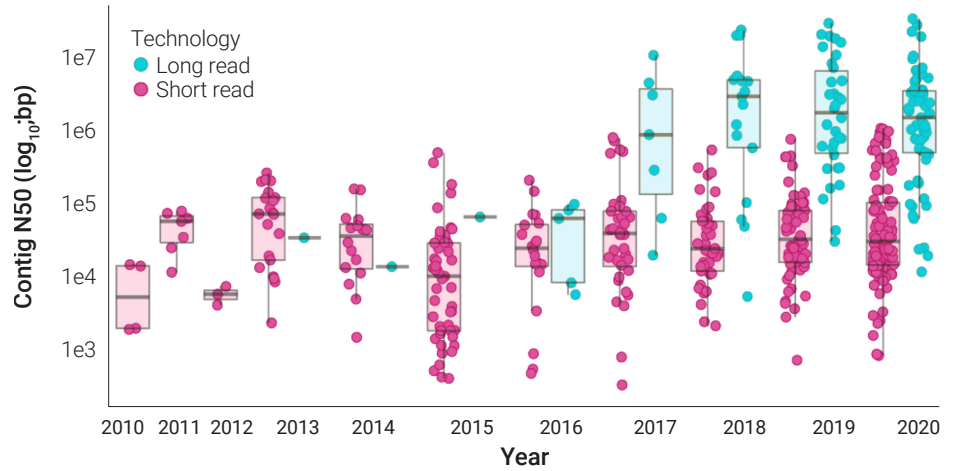


Insect biology

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.

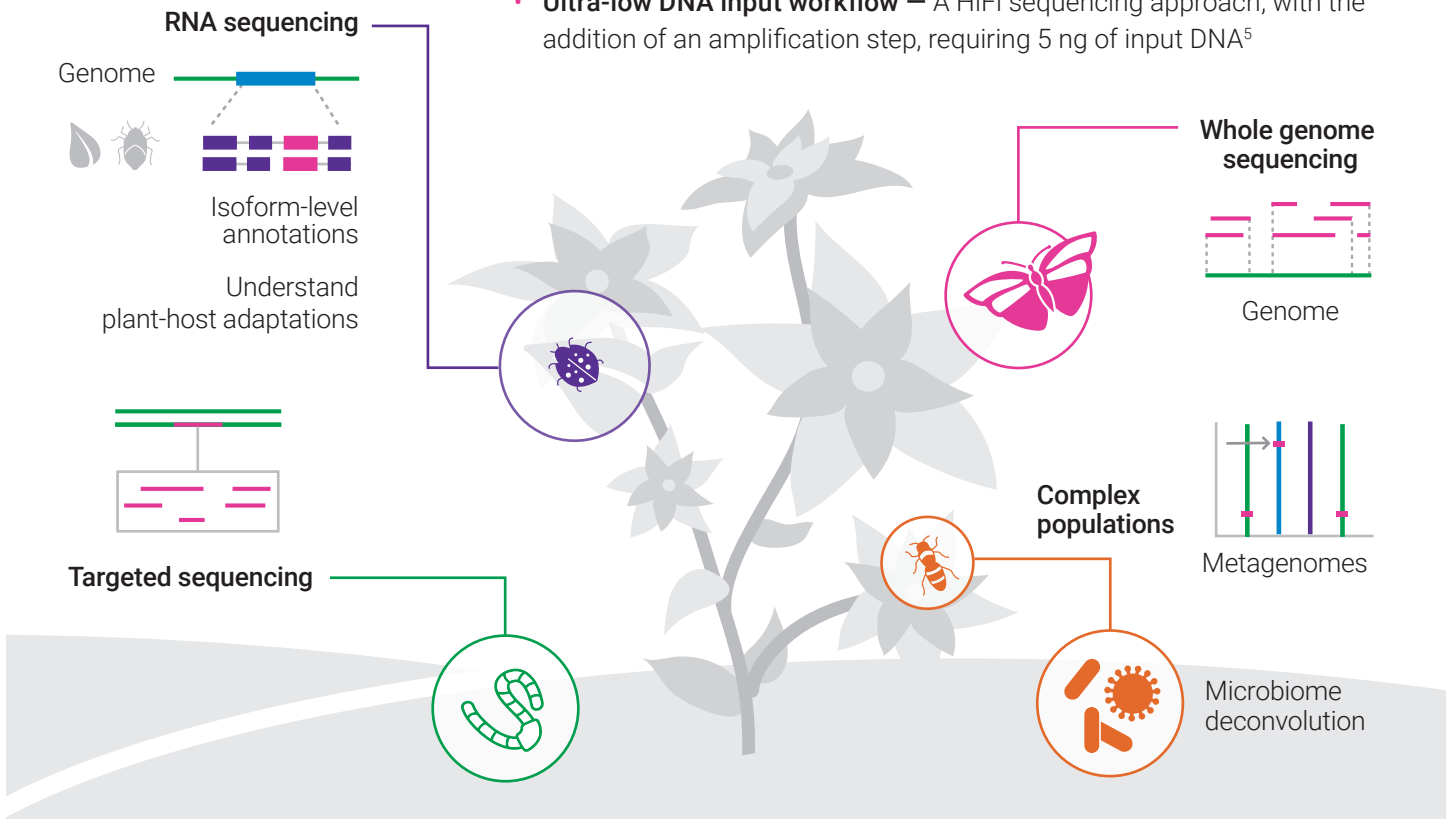


Insect genome assembly contiguity by year⁴
Image adapted from *Long Reads Are Revolutionizing 20 Years of Insect Genome Sequencing*

Sequence even the smallest organisms

Overcome DNA input barriers to sequencing small-bodied organisms

- **Standard HiFi workflow** – A HiFi sequencing approach requiring >300 ng input DNA
- **Ultra-low DNA input workflow** – A HiFi sequencing approach, with the addition of an amplification step, requiring 5 ng of input DNA⁵



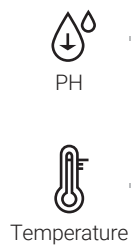
Dive into the depths of marine ecosystems to study evolution, reveal insights into developmental biology, and address the challenges of climate change.

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 using HiFi sequencing to explore the genomes and transcriptomes 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.

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

Environmental stressors



Detect effects with SMRT® 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 the “hardest” organisms

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



Overview of Circulomics Nanobind technology¹⁰

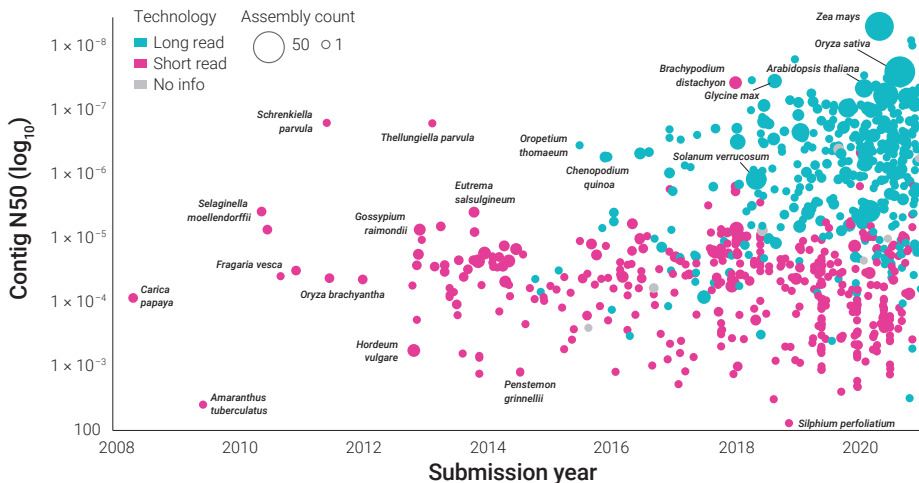


Plant and animal biology

Find answers hidden in the complexity of plant and animal genomes to better understand their evolution, unravel complex traits, and capture biodiversity on a population scale.

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.

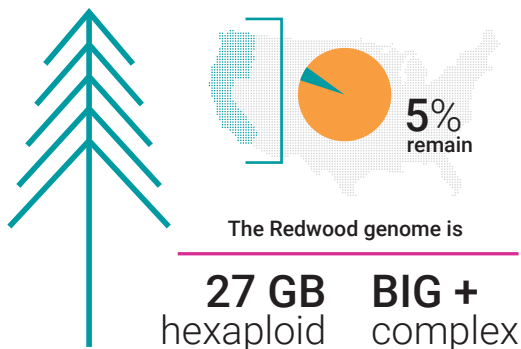


Changes in land plant genome assembly quality and availability over time¹⁵
Image adapted from *Representation and participation across 20 years of plant genome sequencing*

- **Whole genome 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}
- **Complex populations**
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 |

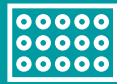
Workflow

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



Sample prep

Flexible DNA input requirements down to 5 ng



Library prep

Adjustable multiplexing options to maximize throughput



SMRT[®] sequencing

Run up to four SMRT[®] Cells 25M at a time with the option to load the next run while the current one is sequencing



Data analysis

Use SMRT[®] Link, or open-source tools to analyze your HiFi data

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





Headquarters

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

Customer service

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

Technical support

Phone: 1.877.920.PACB (7222);
option 2
support@pacb.com



We have offices in countries around the world. Visit pacb.com/contact for contact info.

READY TO GET STARTED WITH HIFI SEQUENCING?



Learn more about HiFi sequencing pacb.com/hifi



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



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 *rhynchophorus 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

Research use only. Not for use in diagnostic procedures. © 2023 Pacific Biosciences of California, Inc. ("PacBio"). All rights reserved. Information in this document is subject to change without notice. PacBio assumes no responsibility for any errors or omissions in this document. Certain notices, terms, conditions and/or use restrictions may pertain to your use of PacBio products and/or third-party products. Refer to the applicable PacBio terms and conditions of sale and to the applicable license terms at pacb.com/license. Pacific Biosciences, the PacBio logo, PacBio, Circulomics, Omniome, SMRT, SMRTbell, Iso-Seq, Sequel, Nanobind, SBB, Revio, and Onso are trademarks of PacBio.