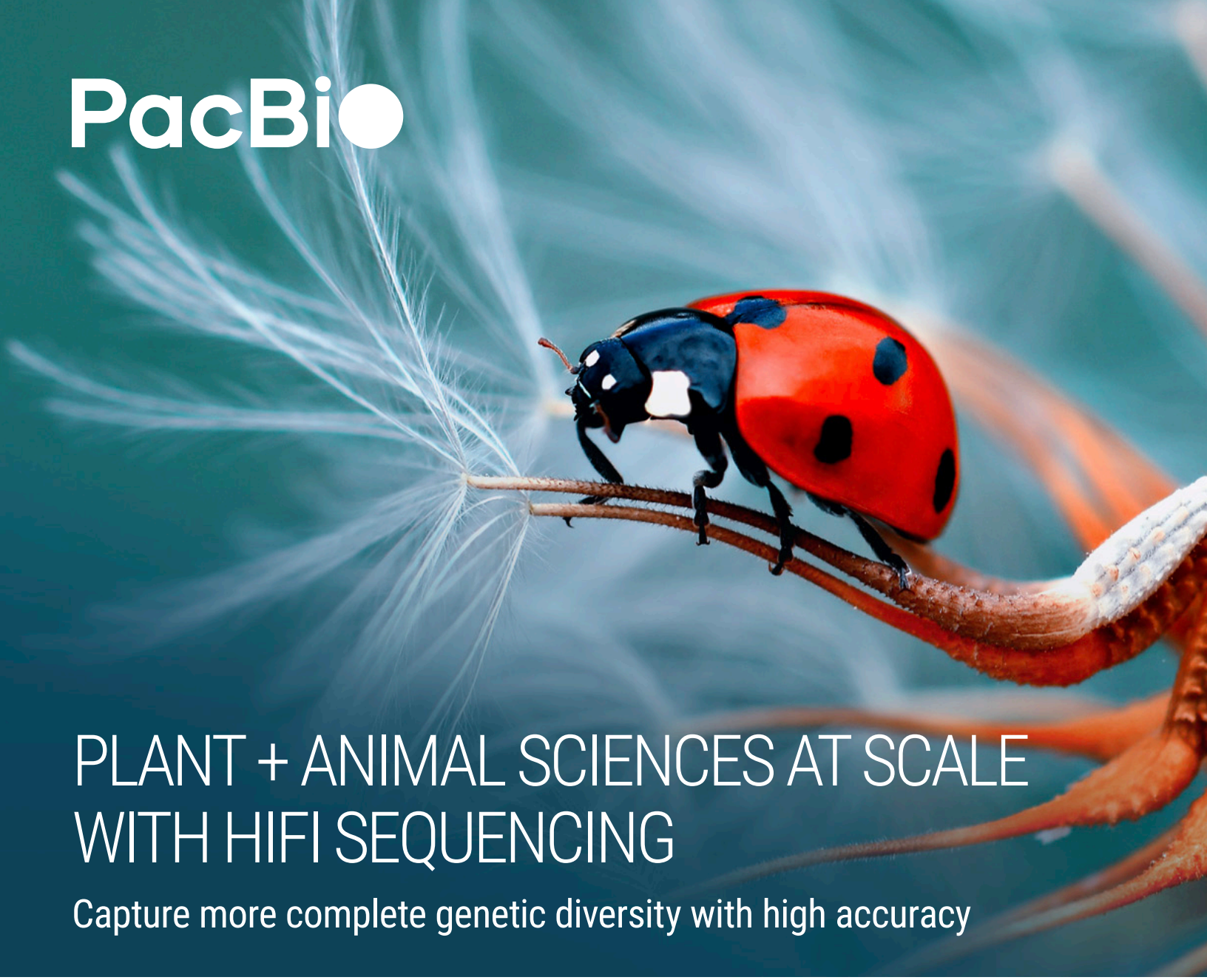


# PLANT + ANIMAL SCIENCES AT SCALE WITH HIFI SEQUENCING

## Capture more complete genetic diversity with high accuracy

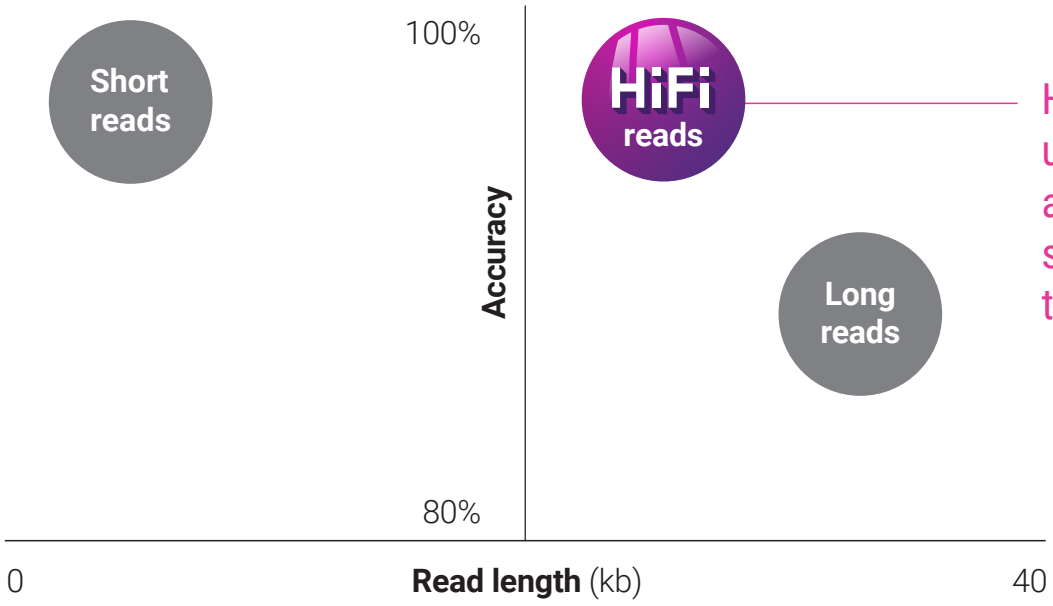
Sequencing life, sustaining futures

## Creating a sustainable future through sequencing

**Genomics has quickly become a vital tool to address global challenges like climate change and biodiversity loss.** This technology enables the development of sustainable solutions to feed growing populations and protect global health. PacBio® provides cutting-edge sequencing that allows scientists to unlock the genetic diversity of all species on earth. These tools can fuel discoveries in agriculture, biodiversity, and environmental health, and build toward a sustainable future.

# 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 meeting global health concerns, why compromise with draft genomes that provide limited information?




HiFi sequencing unites the advantages of short- and long-read technologies

## The benefits of HiFi reads

| | | | | | |
|---|---|---|---|---|---|
| Long read lengths up to 20 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**

# HiFi data in action

PacBio HiFi sequencing is uniquely suited to solve problems in these fields of global study.

## Agrigenomics

Accelerate breeding programs to increase crop + livestock resilience to pests, disease, and climate challenges

## Biodiversity

Explore the biodiversity of populations, species, and ecosystems through genomics for conservation initiatives

## Environmental health

Answer questions through genomics to study the biology of plants, animals, and ecology to sustain environmental health

## 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.

### Complex populations

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

### Epigenetics

Capture simultaneous 5mC detection at CpG sites 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

# Agrigenomics to sustain global food demands

## Employ haplotype-resolved databases to develop world-class breeding, crop protection, and animal health programs

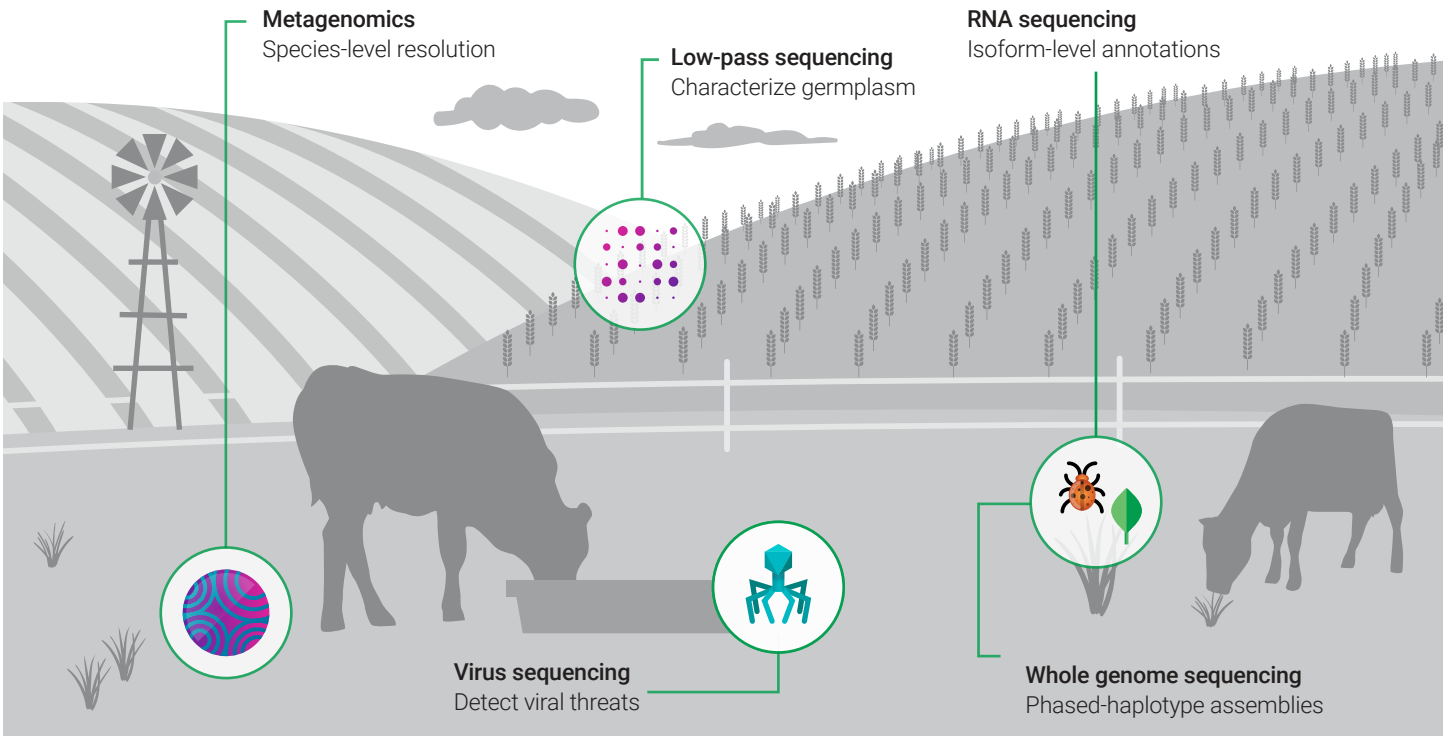
- **Resolve** complex regions of the genome to improve understanding of traits missed by short-read sequencing
- **Capture** SNPs, indels, and larger structural variants to impute desirable traits for any organism
- **Generate** more complete annotated genes and isoforms

### The power of high-quality assemblies

Whole genome sequencing has provided agrigenomics researchers with the ability to generate haplotype-resolved assemblies and identify genome-wide structural variations (SVs) that can be tracked back to traits of interest. Often times, these SVs are larger than single nucleotide polymorphisms (SNPs) and small insertions and deletions (indels) and are in complex regions of the genome that cannot be resolved by short reads. HiFi reads are not only able to phase haplotypes but can also identify SVs in complex regions of the genome, such as transposable elements. This more comprehensive view of variants identifies more candidates for quantitative trait loci (QTL) mapping, allowing for improved molecular phenotyping for any organism.

### What can you do with a HiFi assembly?

Generating an assembly is an important milestone, but HiFi sequencing unlocks additional applications for researchers. HiFi reads can be used to annotate assemblies at the gene and isoform level and confirm gene-editing events and constructs. Together, these assemblies can be used to build pangenomes, providing vital information for improving crop productivity and resilience in a changing world.



# Biodiversity for conservation and ecosystem balance

## Reveal the complexity of plant and animal biology to better understand evolution, unravel complex traits, and capture genetic diversity

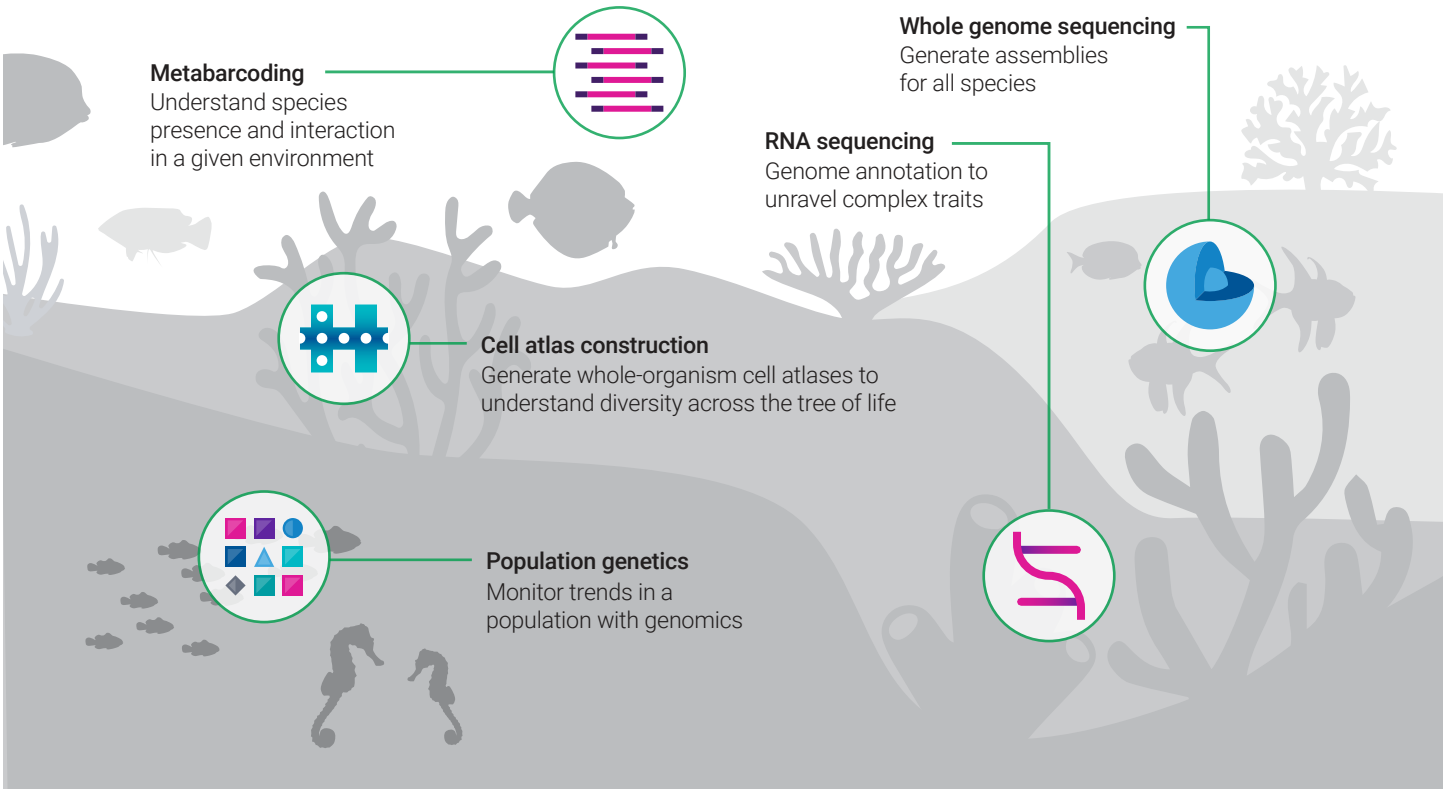
- **Assemble**, phase, and capture genomic diversity from SNPs to complex structural variants
- **Generate** more complete genome assemblies from as little as 5 ng of DNA input
- **Identify** more complete annotated genes and isoforms
- **Target** larger regions (>500 bp) for metabarcoding to improve species identification

### Why is biodiversity important?

Our planet is home to millions of species that contain multitudes of diverse adaptations. Global biodiversity consortia are tasked with the lofty goal of sequencing these species to reveal the underlying mechanisms of genetic expression, complex biological traits, and to build a genetic database that can be used for conservation efforts. These discoveries can be applied to species management, environmental monitoring, and biomedical research.

### How HiFi sequencing supports biodiversity

HiFi sequencing is the backbone technology for most major global conservation genomics efforts happening today. HiFi reads contribute long and accurate sequences, enabling nearly complete genome assemblies for the majority of sequenced species. These annotated genomes are being used to explore whole-organism cell atlases to understand species evolution, and for conservation strategies like genetic rescue and biodiversity monitoring using population genetics or metabarcoding. Genomics is a vital resource to preserve Earth's biodiversity and unlock additional areas of study.



# Environmental health to cultivate growth and prevent disease

## Monitor microbes to improve crop yield and protect the environment from pest and disease

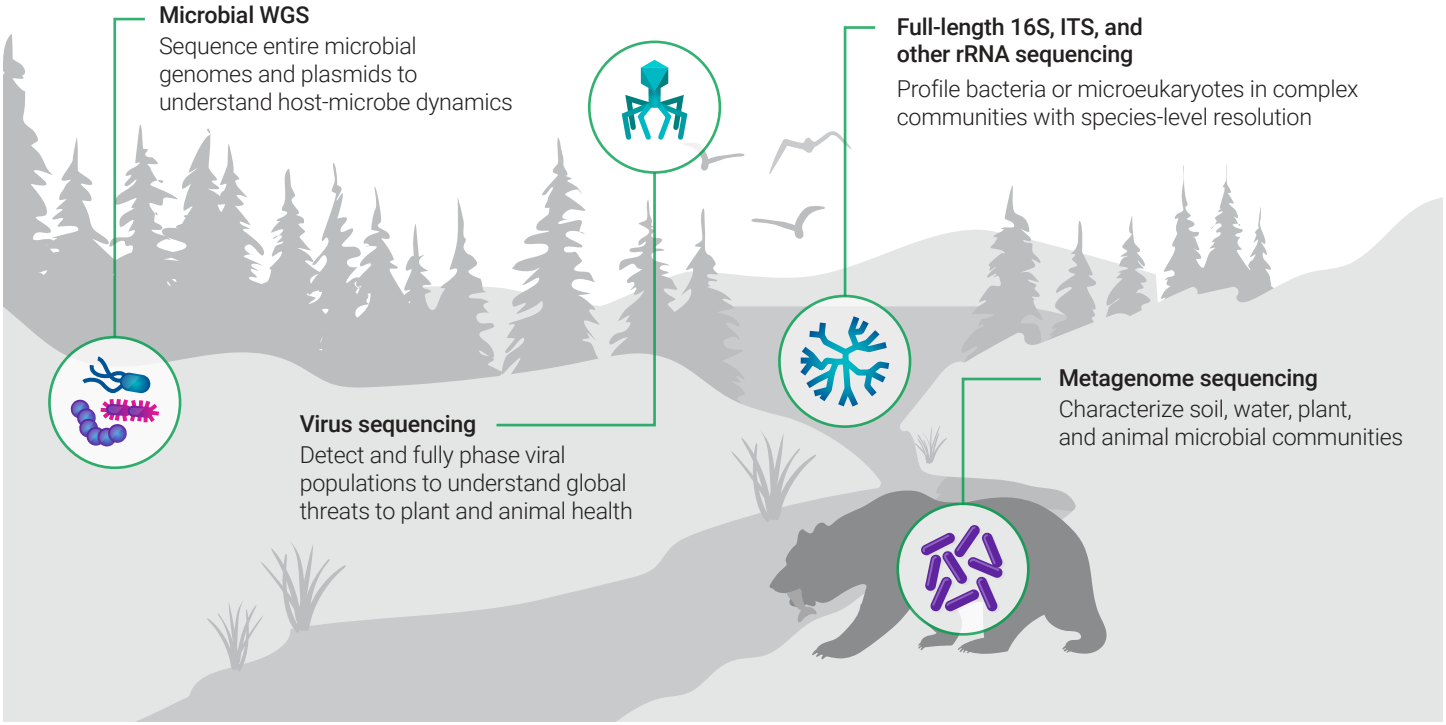
- **Reveal** virulence and resistance potentials for pathogens with more complete whole genome information
- **Achieve** species- and strain-level resolution to profile bacteria, fungi, and other eukaryotes
- **Generate** among the highest quality and most complete MAGs per Gb of other sequencing technologies

### How do microbial communities influence environmental health and disease?

Addressing global biodiversity and food supply challenges requires an in-depth look at the individual species that contribute to their larger communities. Crucial to these communities are the trillions of microbes that play critical roles in soil, water, and living organism populations. Genomics provides a high-resolution view of the influence these microscopic organisms have on the larger ecosystem and the potential impact on health, disease, phenotype, fitness, and ecology.

### HiFi sequencing for environmental health

To understand these complex microbial communities, researchers can harness HiFi sequencing to achieve species-level identification. This information is vital for characterizing microbiomes and phytobiomes, identifying commensal vs pathogenic organisms, and investigating host-pathogen dynamics. These interactions are critical for understanding community ecology interactions and protecting vital ecosystem health.



# Plant and animal genomics at scale enabled by the Revio™ system

## HiFi sequencing on the Revio system brings higher throughput to plant and animal applications

- **$1,000 USD complete, phased genome per SMRT® Cell** (3 Gb or less genome size)[1]
- **Simultaneous** epigenetic information from native DNA sequencing applications
- **Four independent** sequencing stages generating 90 Gb per SMRT Cell for multi-experiment runs

| SMRT Cell 1 | SMRT Cell 2 | SMRT Cell 3 | SMRT Cell 4 |
|---|---|---|---|
|  |  |  |  |
| 3 Gb plant genome with 5mC calling | Kinnex™ full-length transcriptome of 3 Gb plant (40 M cDNA reads) | Soil metagenome assembly at 30× coverage | Kinnex 16S rRNA of river sample (30 k reads per sample) |

| Application | Samples per SMRT Cell | Samples per Revio run using 4 SMRT Cells | Estimated samples per year[2] |
|---|---|---|---|
| **Whole genome sequencing** | | | |
| ***De novo* assembly**[3] | 1 | 4 | ~1,300 |
| **Variant detection**[3] | Structural variants: 3<br>All variants: 1 | Structural variants: 12<br>All variants: 4 | Structural variants: ~3,900<br>All variants: ~1,300 |
| **Microbial *de novo* assembly**[4] | 96 | 384 | ~124,800 |
| **RNA sequencing** | | | |
| **Kinnex single-cell RNA**[5] | 1 | 4 | ~1,300 |
| **Kinnex full-length RNA**[6] | 4 | 16 | ~5,200 |
| **Targeted sequencing** | | | |
| **Amplicon sequencing**[7] | ≥1,000 | ≥4,000 | ~2.6M for 1–5 kb<br>~1.3M for 5+ kb |
| **Metagenomics** | | | |
| **Shotgun metagenomic profiling** | 96 communities | 384 communities | ~124,800 communities |
| **Shotgun metagenomic assembly** | 12 communities | 48 communities | ~15,600 communities |
| **Kinnex 16S rRNA** | 1,536 communities | 6,144 communities | ~2M communities |

1. US list price is $995 for sequencing reagents for one Revio SMRT Cell, which has an expected yield of 90 Gb, equivalent to a 30× human genome. 2. Estimated samples per year calculated by assuming 1,300 samples per year for each Revio system run using 4 SMRT Cells, 365 days in a year, and 90% utilization. Annual throughput is based on 1,300 Revio SMRT Cells. All sample throughputs are estimates per Revio run using 1 or 4 SMRT Cells. Coverage may vary based on sample quality, library quality, and fragment lengths. 3. Currently available SMRTbell® barcoded adapter plate 3.0 contains 96 SMRTbell barcoded adapters. Whole genome sequencing for a 3 Gb human-like genome at >15× per haplotype for *de novo* assembly, >10× coverage for structural variants, and >30× coverage to detect more variants. 4. Microbial *de novo* assembly assumes microbes with ~1.2 Gb of total genome size per SMRT Cell at >50× per sample. 5. Single-cell transcriptomics assumes ≥80 million reads per library. 6. Full-length RNA assumes a total of 40M reads regardless of plexity. 7. Amplicon sequencing assumes 12-hour movie time for 1–5 kb, 24-hour movie time for 5+ kb, and >50× per sample.

PacBio

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# Ready to get started with HiFi sequencing?

Learn more about HiFi sequencing:
**pacb.com/hifi**

Learn more about plant + animal genetics:
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