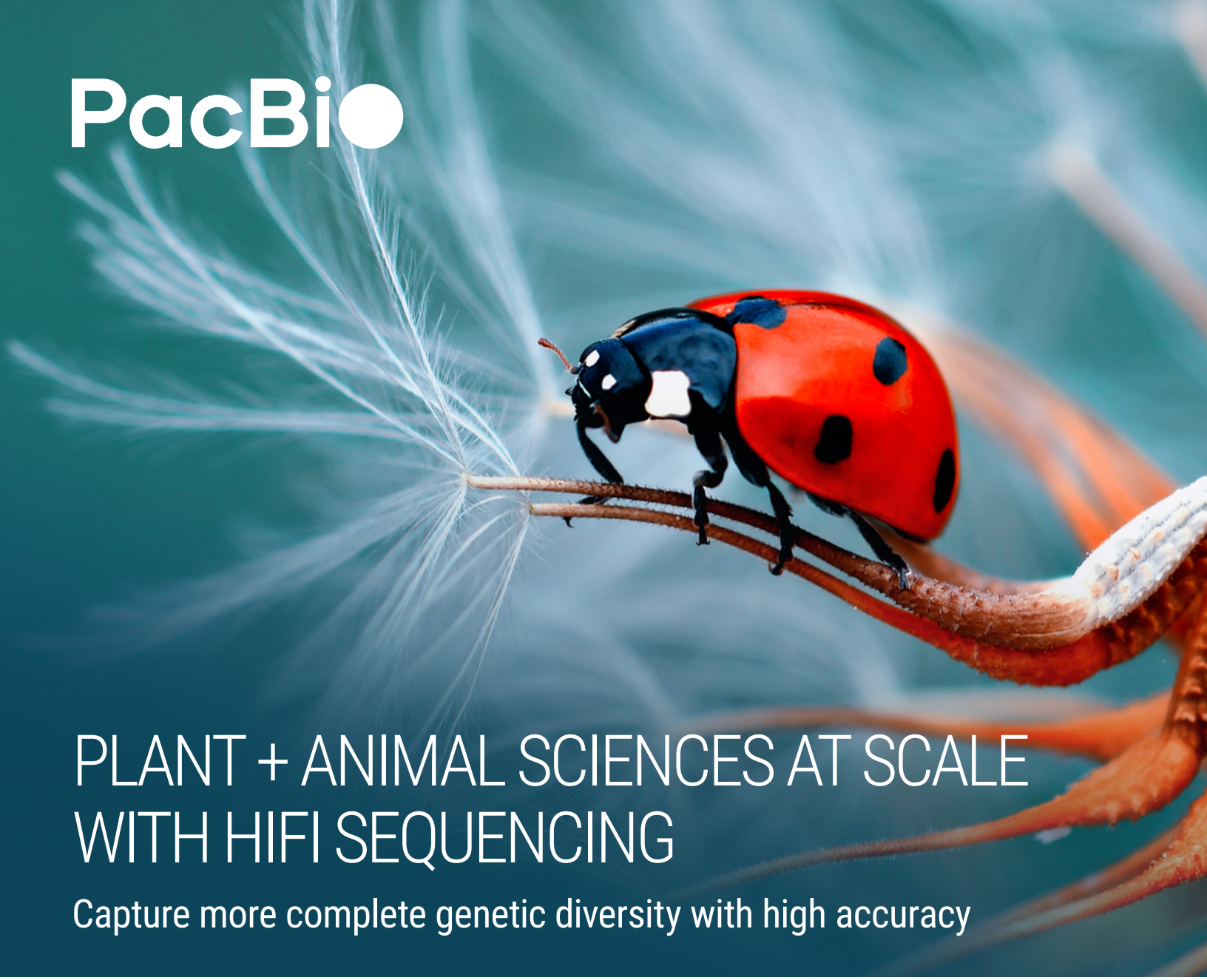


PLANT + ANIMAL SCIENCES AT SCALE WITH HIFI SEQUENCING

Capture more complete genetic diversity with high accuracy

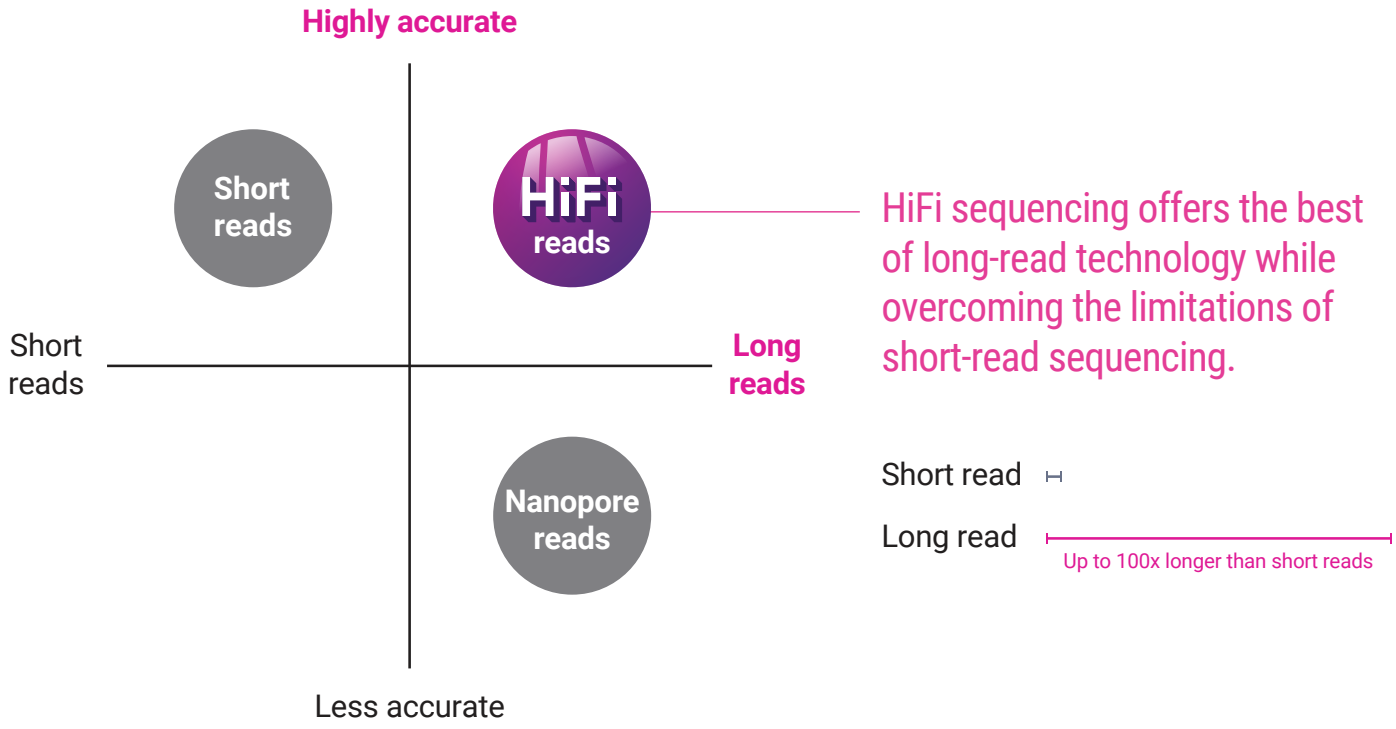
Sequencing life, sustaining futures

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?



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

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

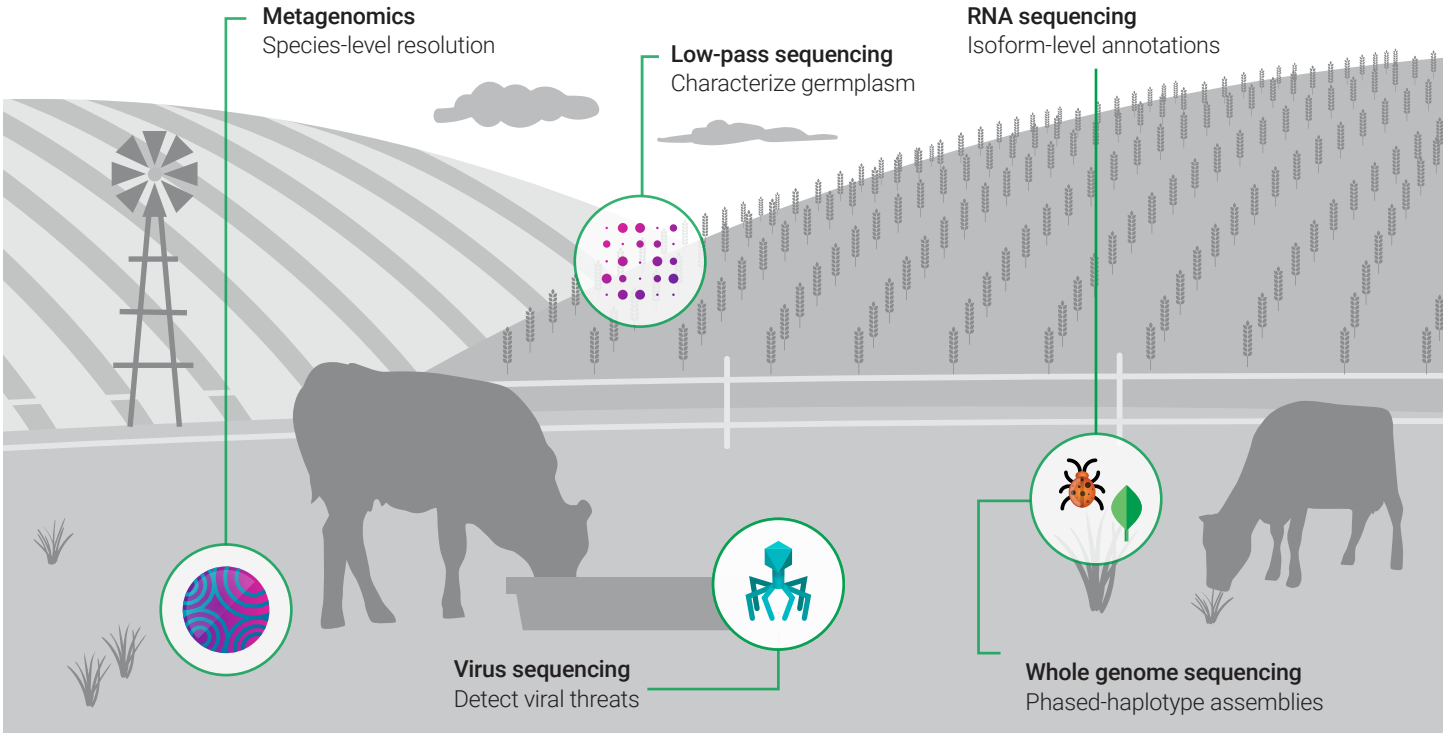
- **Resolve** complex regions of the genome to improve understanding of traits missed by short-read sequencing
- **Capture** SNPs, indels, and larger structural variants to impute desirable traits for any organism
- **Generate** more complete annotated genes and isoforms

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

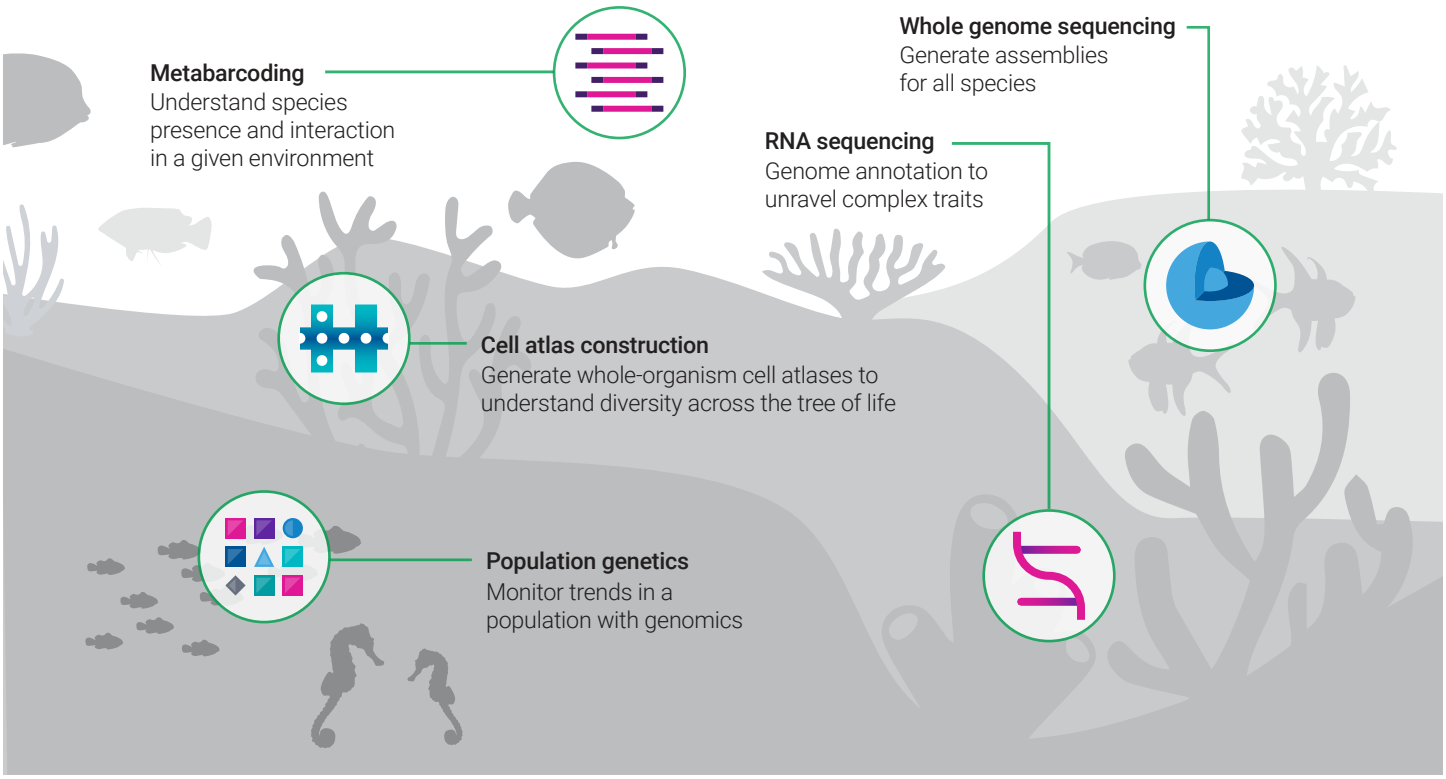
- **Assemble**, phase, and capture genomic diversity from SNPs to complex structural variants
- **Generate** more complete genome assemblies from as little as 5 ng of DNA input
- **Identify** more complete annotated genes and isoforms
- **Target** larger regions (>500 bp) for metabarcoding to improve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

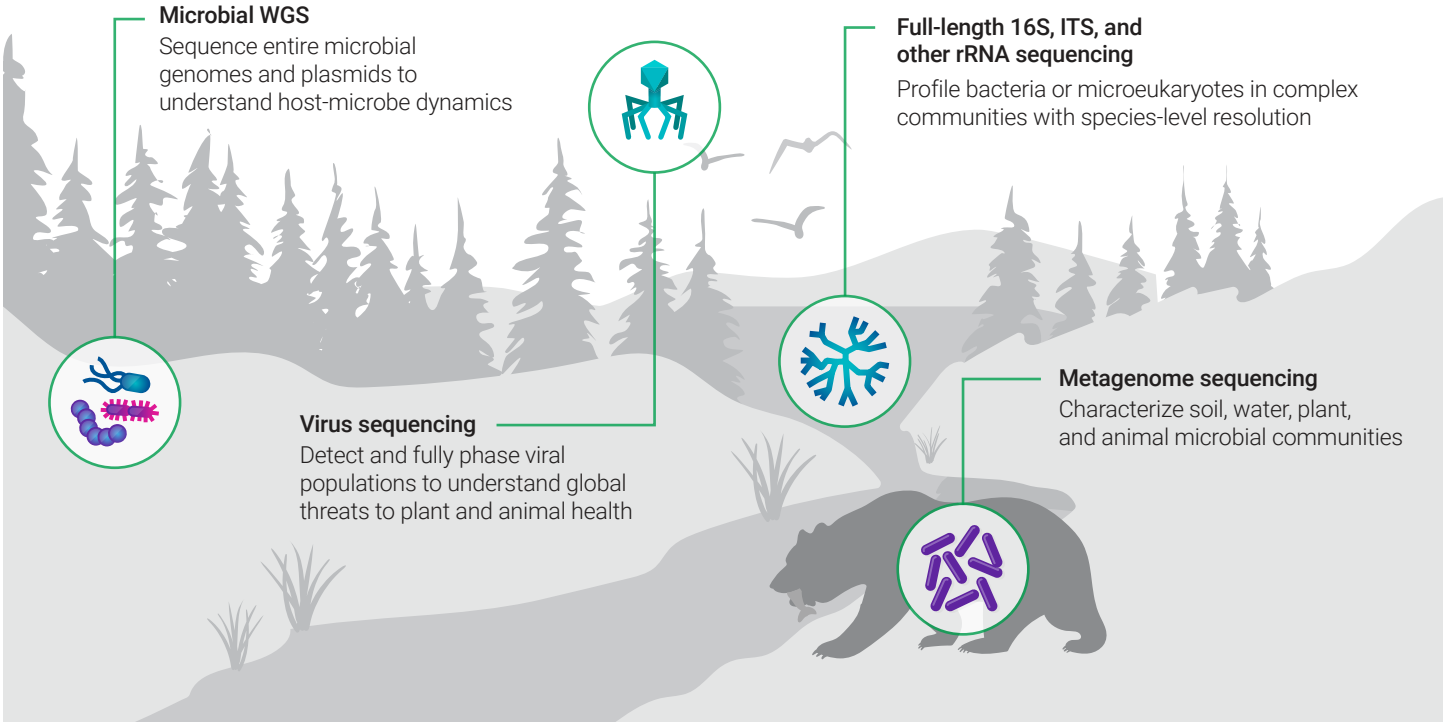
- **Reveal** virulence and resistance potentials for pathogens with more complete whole genome information
- **Achieve** species- and strain-level resolution to profile bacteria, fungi, and other eukaryotes
- **Generate** among the highest quality and most complete MAGs per Gb of other sequencing technologies

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 any scale with the Vega™ and Revio® systems

HiFi sequencing now with flexible throughput options for all plant and animal applications

- **Multiple instrument options** to match your throughput needs
- **Simultaneous** 5mC/6mA epigenetic information from native DNA sequencing applications
- **Revio system** has four independent sequencing stages generating **120 Gb each**

Vega™ system
HiFi within reach

60 Gb per SMRT Cell

Revio® system with SPRQ™ chemistry
HiFi at scale

120 Gb per SMRT Cell

Application	Samples per Vega SMRT Cell	Samples per Revio SMRT Cell
Whole genome sequencing		
***De novo* assembly (2 Gbs genome)**	1	2
Variant detection (2 Gbs genome)	Structural variants: 3 All variants: 1	Structural variants: 6 All variants: 2
Microbial *de novo* assembly (2 Gb total)	384	384
RNA sequencing		
Kinnex™ single-cell RNA sequencing	1 (3,000–6,000 cells)	1 (6,000–10,000 cells)
Kinnex full-length RNA sequencing		
5M reads	6	12
10M reads	3	6
Targeted sequencing		
Amplicon sequencing	>1,000	>1,000
Microbial		
Shotgun metagenomic profiling	64 communities	128 communities
Shotgun metagenomic assembly	8 communities	16 communities
Kinnex 16S rRNA	1,024 communities	1,536 communities

All sample throughputs are estimates for either the Vega system with 1 SMRT Cell or the Revio system using SPRQ chemistry with 1 SMRT Cell. Coverage may vary based on sample quality, library quality, and fragment lengths. Currently available SMRTbell® adapter index plates 96A-96D contain a total of 384 SMRTbell barcoded adapters. Microbial de novo assembly assumes microbes with 2 Gb of total genome size at 30x per sample. Single-cell transcriptomics assumes ≥80 million reads per library on the Revio system and ~50-60 million reads per library on the Vega system. Full-length RNA sequencing assumes a total of 60M reads for Revio SPRQ and 30M reads for Vega, regardless of plexity. Amplicon sequencing assumes a 12-hour movie time for 1–5 kb, 24-hour movie time for 5+ kb, and >50× per sample. Target enrichment assumes >50× per sample.

PacBio

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Ready to get started with HiFi sequencing?

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Connect with a PacBio scientist to get started:
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