



PLANT AND ANIMAL SCIENCES: AGRIGENOMICS

Accurate and actionable data to power agriculture

Unravel the complexity of plant and animal genomes with HiFi sequencing to harness agrigenomics insights for breeding, crop protection, and genome engineering workflows to feed a growing population.

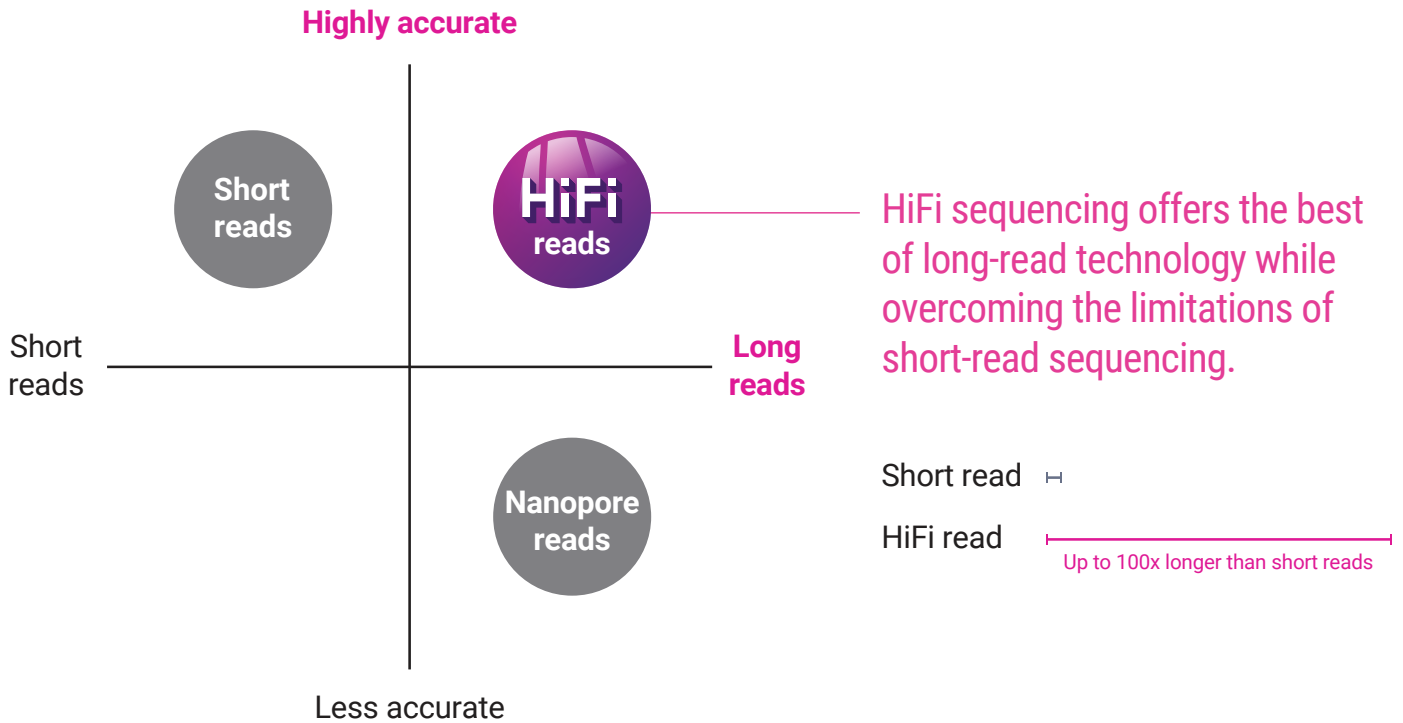
Utilizing agrigenomics to tackle global challenges

Amongst a growing population and a changing climate, scientists are increasingly turning to genome sequencing technology to address mounting demands for sustainable food production. PacBio delivers cutting-edge sequencing solutions that empower agricultural researchers to solve these global challenges. Scientists can use these biological insights to enhance breeding programs, facilitate the production of more nutritious food, protect crop and livestock health, and increase agricultural yield.



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 agricultural 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



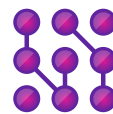
Supported analysis tools consolidated into a single pipeline



High read accuracy



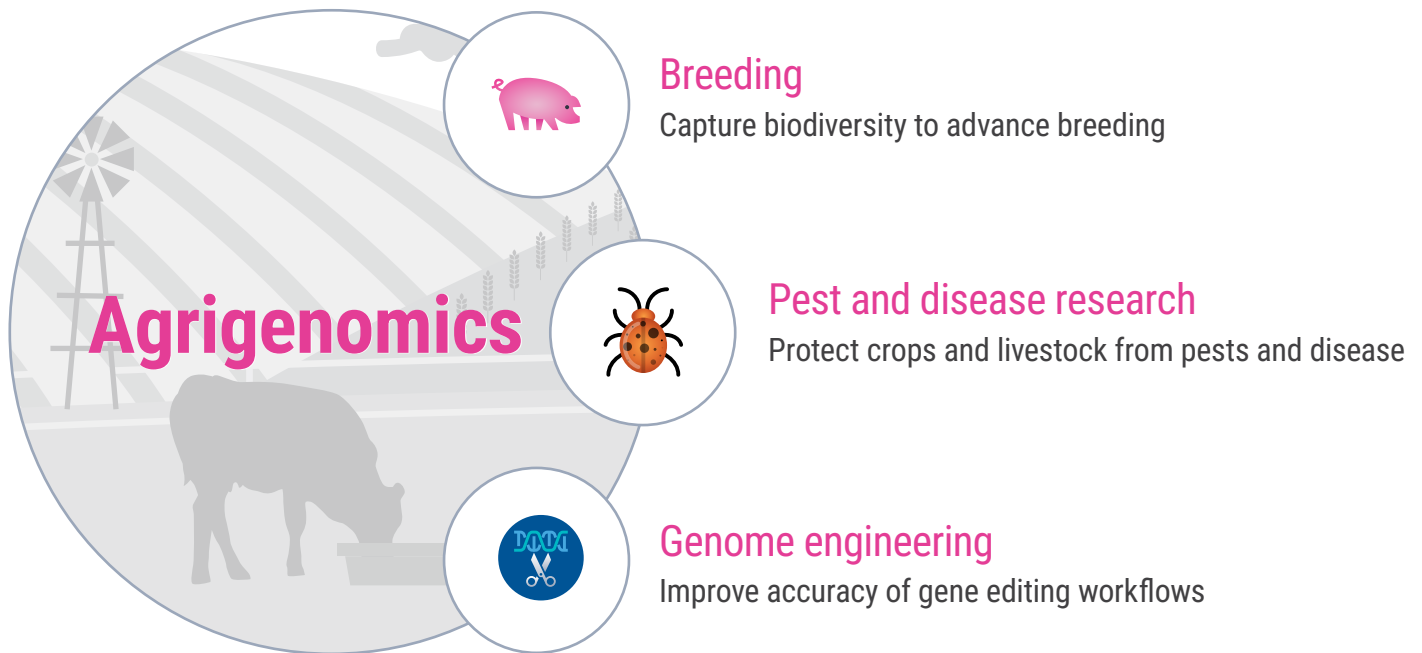
Compatible ecosystem partners to enable an end-to-end workflow



A single technology solution



Agrigenomics data in action



Applications to fuel agrigenomics



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



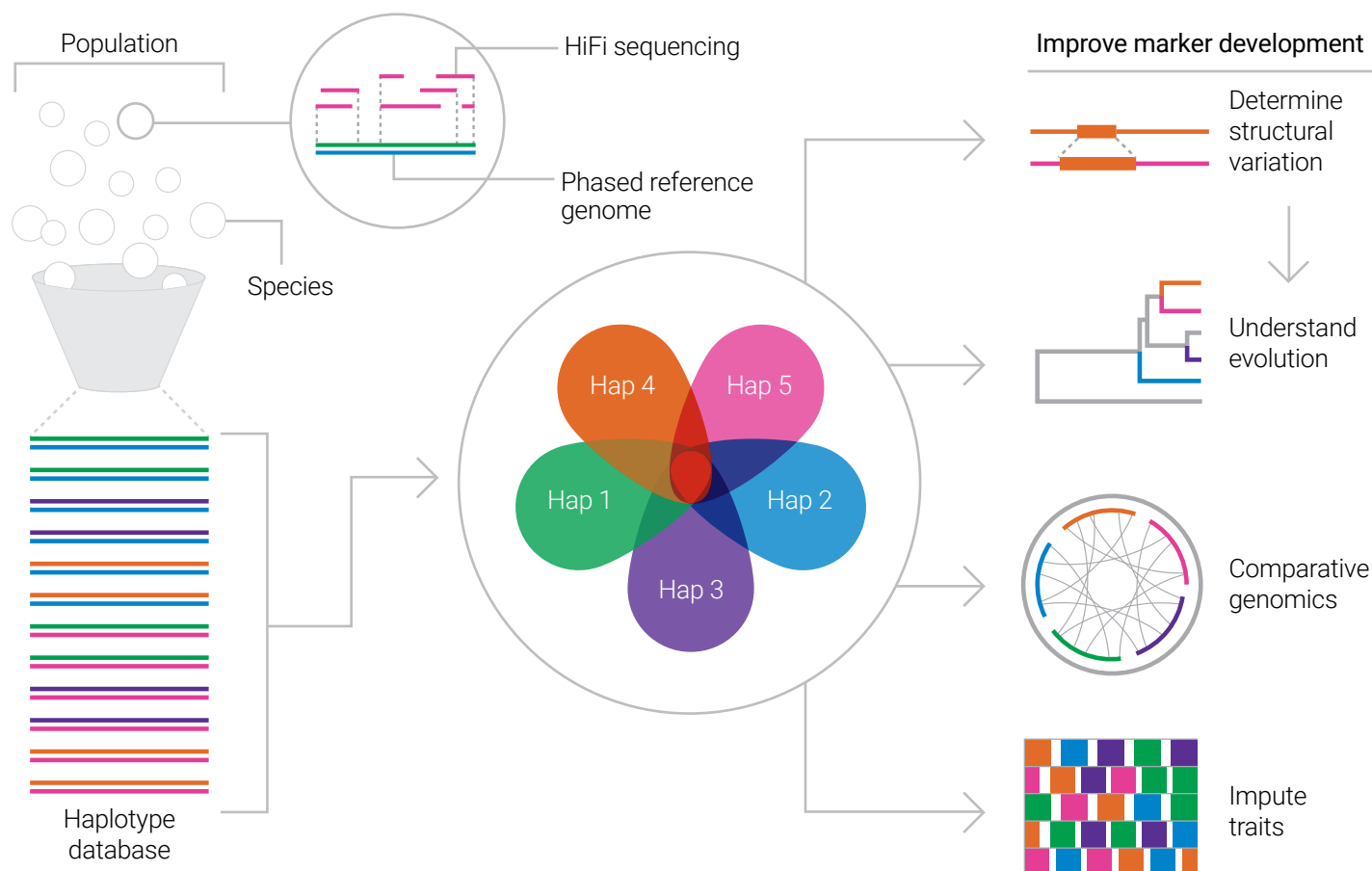
Agrigenomics for breeding programs

Build haplotype-resolved pangenomes to drive marker development, trait discovery, and germplasm characterization

- Build reference-quality, haplotype-resolved pangenomes for breeding
- Impute desirable traits to SNPs, structural variants, and complex genotypes
- Capture genomic variants on a genome-wide scale for outbreds, inbreds, and populations

Because HiFi sequencing is single molecule in nature, highly accurate, and capable of spanning many kilobases, researchers can now assemble phased, reference-quality genomes for even the most complex plant and animal species. This third-generation long-read sequencing technology has enabled more reliable imputation of traits related to climate adaptation, pest and pathogen resistance, and overall species health.

Whole genome sequencing has provided breeders with data-driven strategies for marker-assisted selection, yet many key traits originate from structural variation that short-read sequencing or genotyping arrays cannot fully resolve. HiFi reads are long enough to span complex structural variants and accurate enough to resolve SNPs and indels in complicated regions of the genome. This level of resolution allows breeding programs to map and impute traits at the appropriate haplotype scale, supporting more confident and effective selection decisions.





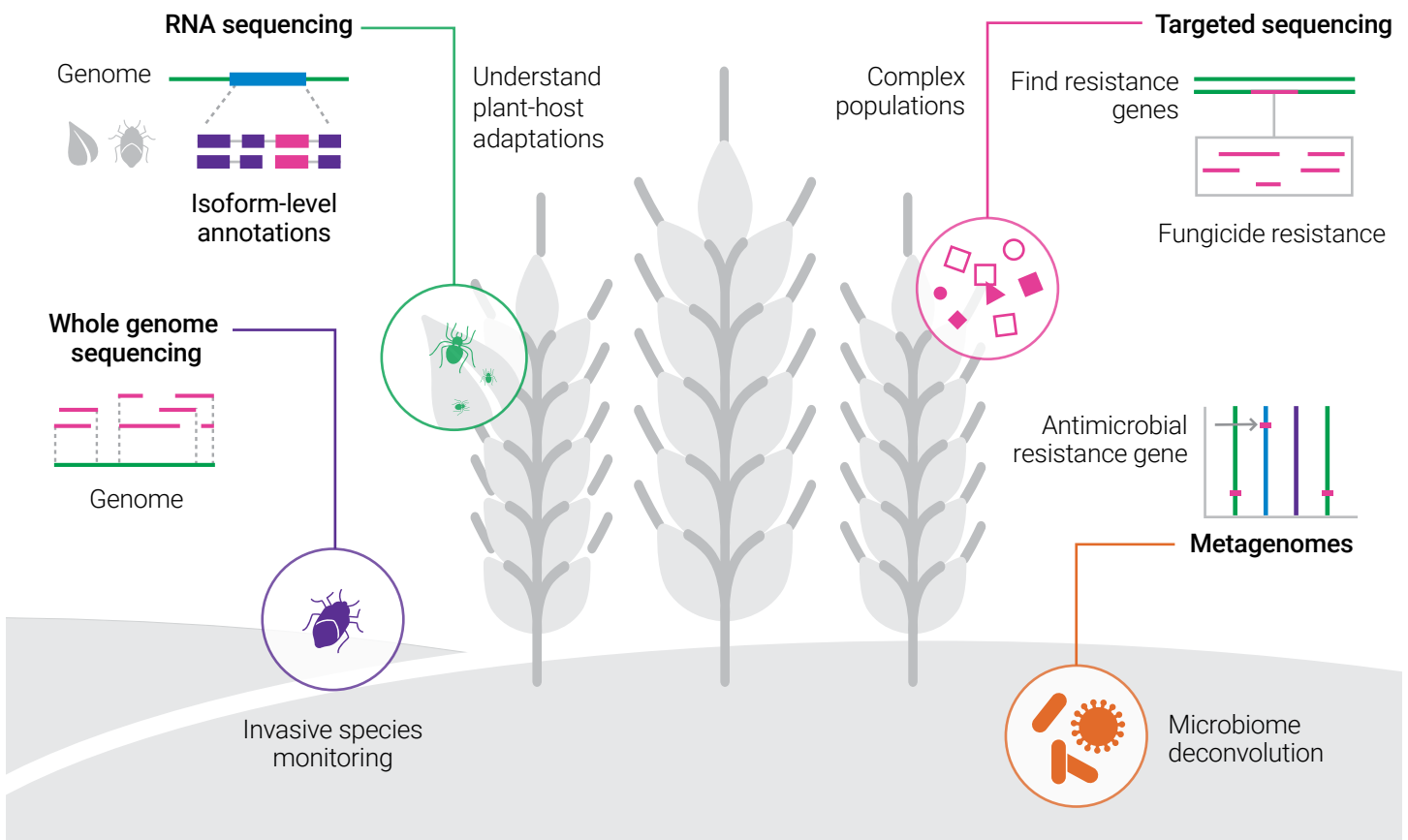
Agrigenomics for pest and disease research

Identify genomic strategies to protect crop and livestock health

- Capture pest diversity on the molecular level
- Generate complete genome assemblies from just 1 ng of DNA input
- Build annotations to better understand gene function
- Optimize data quality through efficient DNA extraction from insect, plant, and bacterial samples with the Nanobind PanDNA kit

Combat threats to agricultural yield on a molecular level by using HiFi sequencing to resolve the complex genetics of harmful organisms such as insects, weeds, fungi, and microbial communities. Many of these invasive species have short life cycles and reproduce rapidly, resulting in highly variable genetics within single populations.

HiFi sequencing equips researchers with multiomic tools to characterize these organisms and communities with high precision. Its long, accurate reads enable complete genome assembly, resolution of complex structural variants, and confident haplotype phasing that underlie virulence and resistance traits. HiFi data also strengthens metagenomic and transcriptomic analyses, revealing genes involved in immunity, metabolic detoxification, pathogenicity, and pesticide resistance. This comprehensive view of genetic diversity and function supports more effective strategies for protecting agricultural productivity.





Agrigenomics for genome engineering programs

Sequencing tools for a new paradigm in agriculture

- Speed up design workflows with accurate reference genomes
- Find splice variants within the transcriptome
- Validate edited sites
- Accurately capture structural rearrangements across chromosomes

Discover, design, and validate genome engineering workflows with confidence, ease, and sensitivity.

Agriscientists know that in order to feed an estimated 10 billion people by 2050,⁹ a variety of different programmable molecular techniques are needed to increase our food supply. Whether you need a better reference genome to design your editing experiment, or accurate sequence data to validate constructs, confirm edits, and evaluate off-target effects, HiFi sequencing provides a fast, reliable solution.



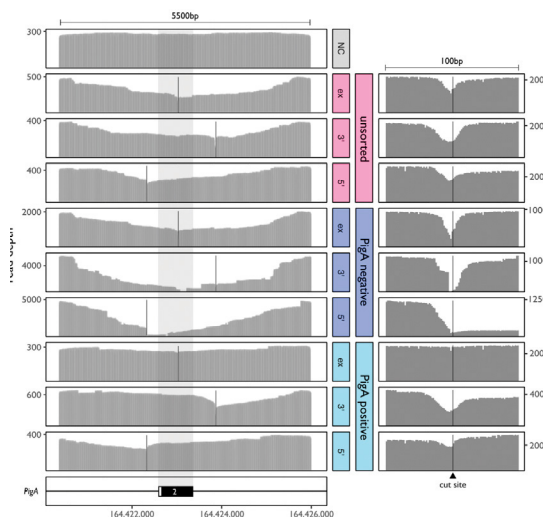
Better reference genomes for better editing

Owen et al. (2021) used HiFi whole genome sequencing to assess on-target and off-target integration of donor template effects in a CRISPR edited calf,¹⁰ demonstrating the impact of PacBio WGS on the precision and safety of agricultural genome editing programs.

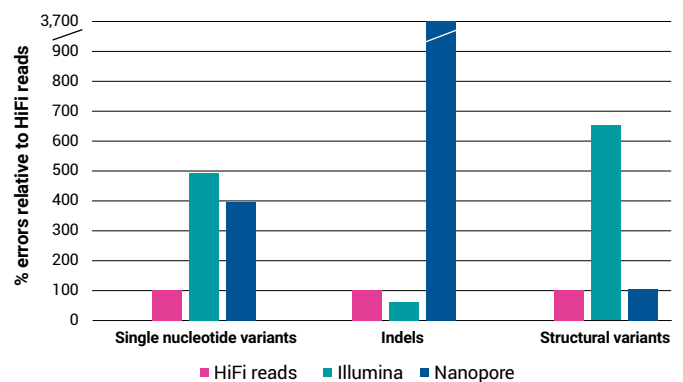
Sequence beyond your target

Understanding the extent of CRISPR-Cas9 editing requires long read lengths and high accuracy to capture both on- and off-target effects to fully evaluate editing outcomes on a targeted and genome-wide scale.

Targeted validation



Comprehensive variant detection



Variant calling performance against *Genome in a Bottle* benchmarks for PacBio HiFi reads (35-fold, Sequel II system, 2.0 chemistry); Illumina (35-fold, NovaSeq); Oxford Nanopore (60-fold, PromethION R9.4.1.)

Analysis of the *PigA* locus edited with the CRISPR-Cas9 method using selected gRNAs. SMRT® sequencing of a 5.5 kb amplicon around gRNA cut sites (vertical lines) enabled detection of large-scale deletions and structural changes missed by other methods¹¹



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





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Ready to get started with HiFi sequencing?



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