PacBio



Vega benchtop system

HiFi sequencing within reach

Premium HiFi data, accessibly priced

Bring best-in-class sequencing to your benchtop

Built on proven HiFi technology

Consistent HiFi library prep, 500 ng input, and analysis workflows

Sequence your way

Take control of your data and support regulated workflows

Diverse applications

Full-length RNA, whole genomes, targeted sequencing and more

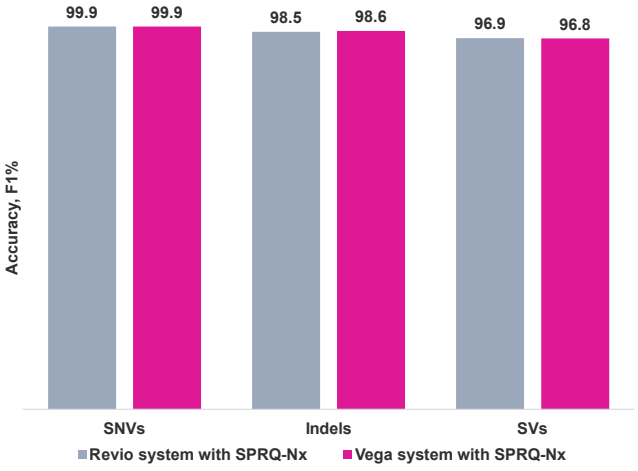
The HiFi accuracy you love, at the price and throughput you need

HiFi sequencing is the only long-read technology to provide 99.9% or better accuracy in every run. HiFi reads eliminate the tradeoff between read length and accuracy, allowing you to address your most complex biological questions.

With over 1,350+ peer-reviewed publications in 2025 alone and 1,200+ HiFi sequencers globally, Vega™ joins the PacBio® portfolio of reliable and established sequencing systems.

The benefits of HiFi reads

- Long read lengths
- Easy library preparation
- SPRQ-Nx chemistry enables lower cost per run, 90 Gb yield, single-shift movies, and supports 21 CFR Part 11 compliance
- 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



Data shown is for HG002 at 20x coverage.

Two systems, one gold standard

Now with SPRQ-Nx chemistry, Vega and Revio systems deliver the same high-standard HiFi sequencing, ensuring consistent, accurate data. HiFi reads cover all regions of the genome, providing the most complete and precise assemblies and variant calls. Unlike short reads, which can miss complex regions, HiFi captures full-length transcripts and difficult areas. With either HiFi system, you get the best possible genome with low coverage requirements.

Get a more complete view of biology with HiFi reads

Variant calling with phasing + methylation

Access high accuracy for all variant types — SNVs, indels, structural variants, tandem repeat expansions, and methylation — including in challenging regions.

Full-length RNA sequencing

Characterize full-length isoforms, complex alternative splicing events, and fusion transcripts.

Targeted sequencing to study genes

Focus the power of HiFi variant calling by enriching for regions of interest using PureTarget™, hybrid capture or PCR amplicons.

Microbial genomics

Characterize microbiomes and metagenomes to gain a better understanding of microbial communities.

> ***"These Vega systems are a great fit for us because the smaller benchtop footprint and throughput is ideal for our targeted single-gene assays and our expansion into panels and whole-genome sequencing as well.***

> ***"Overall, I think Vega is a perfect and promising benchtop sequencer for clinical genomics with its long HiFi reads, efficient turn-around-time, and easy operation."***

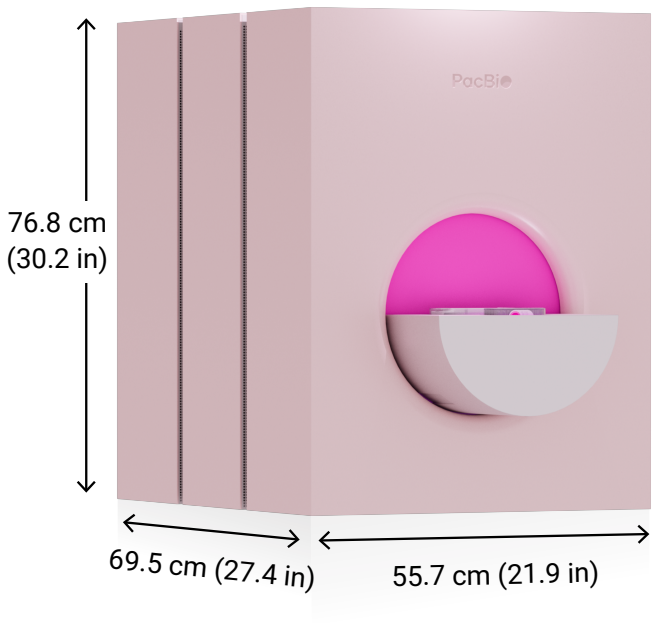
Dr. Aiping Mao, Vice Director of R&D at Berry Genomics

SPRQ-Nx chemistry generates 90 Gb per run across applications

Application	Expected coverage	Samples per Vega SMRT Cell	Samples per year
Amplicon	50×	>1,000	200,000
Microbial genome	30×	384	76,800
PureTarget panels	> 100× mean per target	96	19,200
Transcriptome with Kinnex™ full-length RNA kit	10 million reads	4	800
Human genome	20×	1.5	300
Human methylation profiling	5×	6	1,200

All sample throughputs are estimates for the Vega system with 1 SMRT Cell per run. Annual throughput on Vega is based on 200 Vega SMRT Cells. 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 coverage. Full-length RNA sequencing assumes a total of 40M reads for Vega.

Small *and* mighty



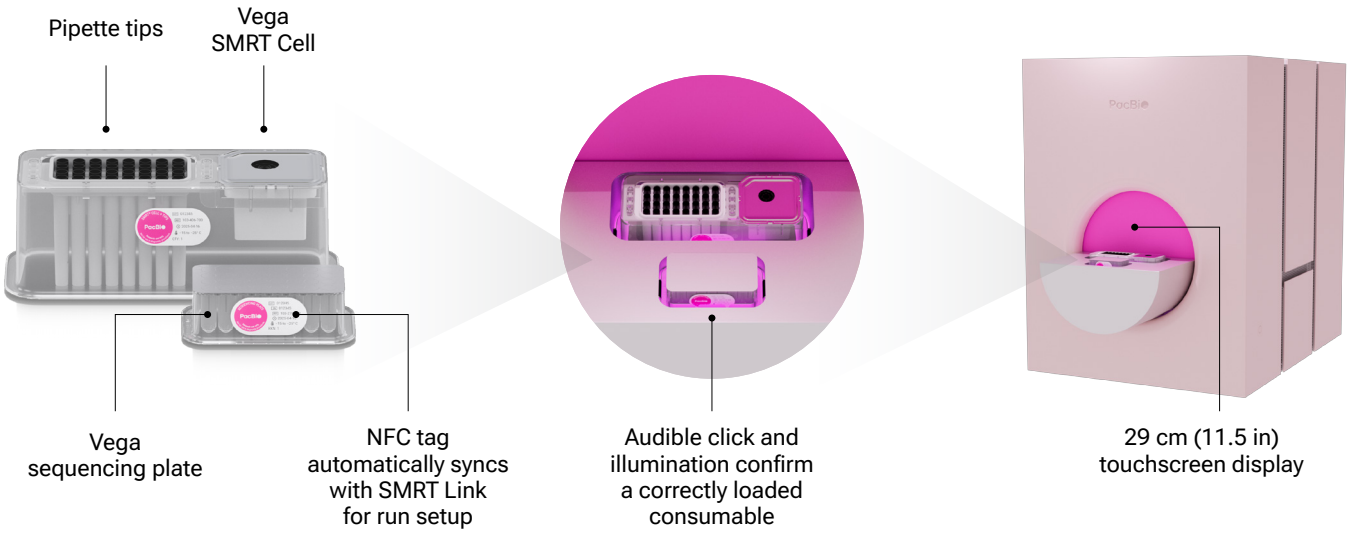
Innovative Revio technology, reimagined in a benchtop solution

Seamless integration with HiFi library prep workflows and SMRT® Link run management software

On-instrument primary analysis, including DeepConsensus, methylation calling, and optional barcode demultiplexing in every run

Audit tracking and instrument login to help support regulated environments

Two consumables, too easy



The Vega SMRT Cell is the heart of HiFi sequencing and is powered by a semiconductor device to deliver single-molecule insights in real time.

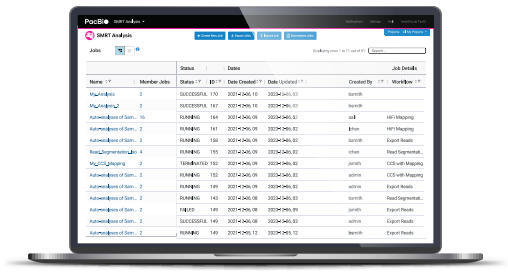
The Vega sequencing plate holds everything you need – sample and reagents – ready to power your next game-changing insight.

A push-button run setup links the Vega sequencing plate to SMRT Link run design. Intuitive design and tactile confirmations reduce errors and steps to get to results.

Design + control experiments with SMRT Link software

An end-to-end workflow manager available for local installation or the cloud.

Built-in features to help support 21 CFR 11 compliance in regulated environments, including system login and audit tracking.



Sample setup

Calculate binding and annealing reactions for preparing libraries for use on all HiFi systems.

Runs

View information about sequencing runs, monitor run progress, and create run designs.

Instruments

View information about instruments, including sequencing status, remaining run time, and pre-load availability for the next run.

Data management

Create projects and data sets; generate QC reports; view, import, or delete sequence, reference, and barcode files.

SMRT Analysis

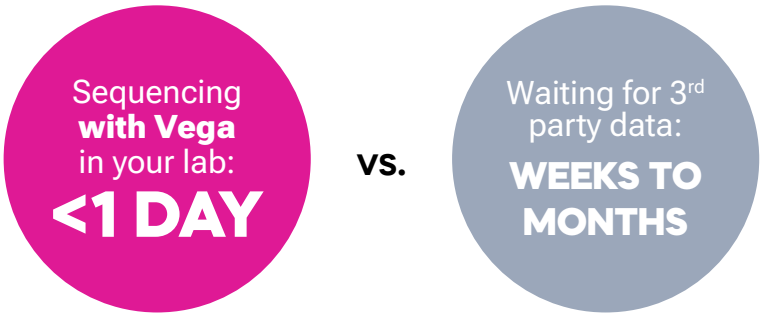
Perform secondary analysis, including sequence alignment, variant detection, structural variant calling, and RNA analysis.

Save on compute and storage costs

The Vega system goes beyond basecalling – every run also measures DNA methylation status, calculated with a deep learning algorithm. On-instrument primary analysis includes barcode demultiplexing and conversion to the standard BAM format, so you can make meaningful insights faster. Efficient data representation encodes sequence, quality values, and methylation in about 0.5 bytes per base — 20× smaller than for other long-read technologies.

	On instrument	Off instrument	Typical output file format and size
Vega system	• Base calling • HiFi read generation with DeepConsensus • Methylation calling • Barcode demultiplexing • BAM file generation	• Variant calling • Genome assembly	hifi_reads.bam 45 Gb each, up to 9 TB per year
Other long-read technologies	• Signal collection • Initial base calling	• Additional base calling • Methylation calling • Barcode demultiplexing • BAM file generation • Variant calling • Genome assembly	Fast5/pod5 1,300 GB

Sequence your way



A single SMRT Cell per run means no waiting.

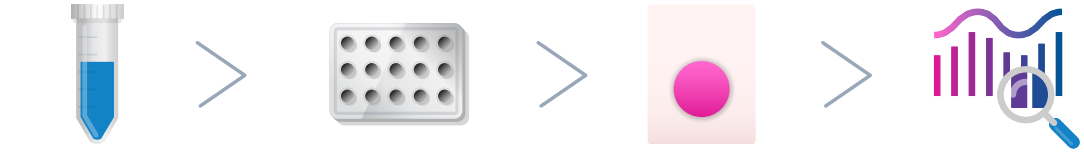
Take control of your data, timelines, and budget by bringing sequencing in-house for more effective project management.

Continuous productivity: Vega lets you pre-stage consumables for the next run, keeping you one step ahead and boosting efficiency.

Short movie times: Single-shift workflows, improving lab efficiency and turnaround time.

Effortless HiFi workflow from sample prep to results

Adopting HiFi reads is simpler than ever with the PacBio universal HiFi workflow—from extraction to data analysis. This seamless experience, paired with the Vega system's intuitive, load-and-go setup and fully automated sequencing, ensures less than 1 min hands-on loading time and reliable results for an effortless experience.



Sample prep | Library prep | Sequencing | Analysis

21 CFR Part 11 on Vega + SMRT Link

21 CFR Part 11 is the U.S. Food and Drug Administration regulation that requires electronic records to be trustworthy, traceable, and attributable to individuals. **Vega SMRT Link software provides** the core technical controls needed to help support these requirements, including user authentication, audit trails, and access management.

- **User authentication:** Optional login mode requires users to authenticate with their SMRT Link credentials, extending accountability to on-instrument activity.
- **Audit trails:** Comprehensive, tamper-evident audit trails record who performed each action, what was done and when, with administrator access and export capabilities for documentation and review.

Vega system specifications

Library	Run time[1]	Q30+ bases	HiFi yield per Vega SMRT Cell[2]	Methylation detection[3]
0.5–1 kb	2 hours	95%	6–8M reads	5mC and 5hmC at CpG sites and 6mA for native DNA
1–2 kb	4 hours			
2–5 kb	12 hours			
5–10 kb	24 hours	90%	35–70 Gb	
10–15 kb			70–80 Gb	
15–20 kb			80–90 Gb	

1. Run time refers to the data collection step, which determines the time between processing SMRT Cells.
2. HiFi yield is dependent on library quality and sequencing preparation procedures. Specified yield is based on high-quality samples prepared following best practices.
3. The 6mA caller is designed to detect methylation in the context of the Fiber-seq chromatin assay

Instrument operating environment	
Temperature	19–25°C (66–77°F)
Humidity	20–80% relative humidity, non-condensing
Ventilation	4,250 BTU/hr (1,250 W)
Noise output	<70 dBA
Dimensions	
W × D × H	55.7 cm × 69.5cm × 76.8cm
Weight	125 kg (276 lb)
Electrical power	
Power requirements	100-120 VAC at 50-60 Hz
Compute	
Network connection	1 GbE
Instrument operating system	Rocky Linux 9.4
Output file format	hifi_reads.bam; 45 Gb each, up to 9 TB per year

What will you discover with Vega?

Whether you are purchasing your first PacBio sequencer or scaling up your fleet, contact a sales rep to see what Vega can bring to your lab.

Learn more about the Vega system:
pacb.com/vega

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

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