



Vega benchtop system

HiFi sequencing within reach



**Premium HiFi data,
accessibly priced**

Vega price
\$169k system
\$1,100 per run

Vega Access
\$79k system
\$1,750 per run



**Built on proven
HiFi technology**

Compatible with
HiFi library prep and
analysis workflows



**Sequence
your way**

Take control of your
data and streamline
project timelines



**Diverse
applications**

Full-length RNA, whole
genomes, targeted
panels 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 1,000 peer-reviewed publications in 2023 alone and over 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



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



Data shown is for a single Revio SMRT Cell for HG002 at 20x coverage.

Two systems, one gold standard

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



Comprehensive variant calling with phasing + 5mC

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 amplification.



Microbial genomics

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

"HiFi long read sequencing can now produce the most comprehensive variant dataset obtainable by a single technology in a single laboratory, allowing accurate calling of substitutions, indels, STRs and SVs."

Kucuk et al. Genome Med 2023

One SMRT® Cell per run with 60 Gb output generates...

Application	Expected coverage	Samples per Vega SMRT Cell	Samples per year
Amplicon	50×	>1,000	200,000
Microbial genome	30×	384	75,000
PureTarget repeat expansion panel	200×	48	9,600
Transcriptome with Kinnex™ full-length RNA kit	10 million reads	3	600
Human genome	20×	1	200
Human methylation profiling	5×	4	800

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 per sample. Full-length RNA sequencing assumes a total of 30M reads for Vega.

Small *and* mighty



Innovative Revio technology, reimagined in a benchtop solution

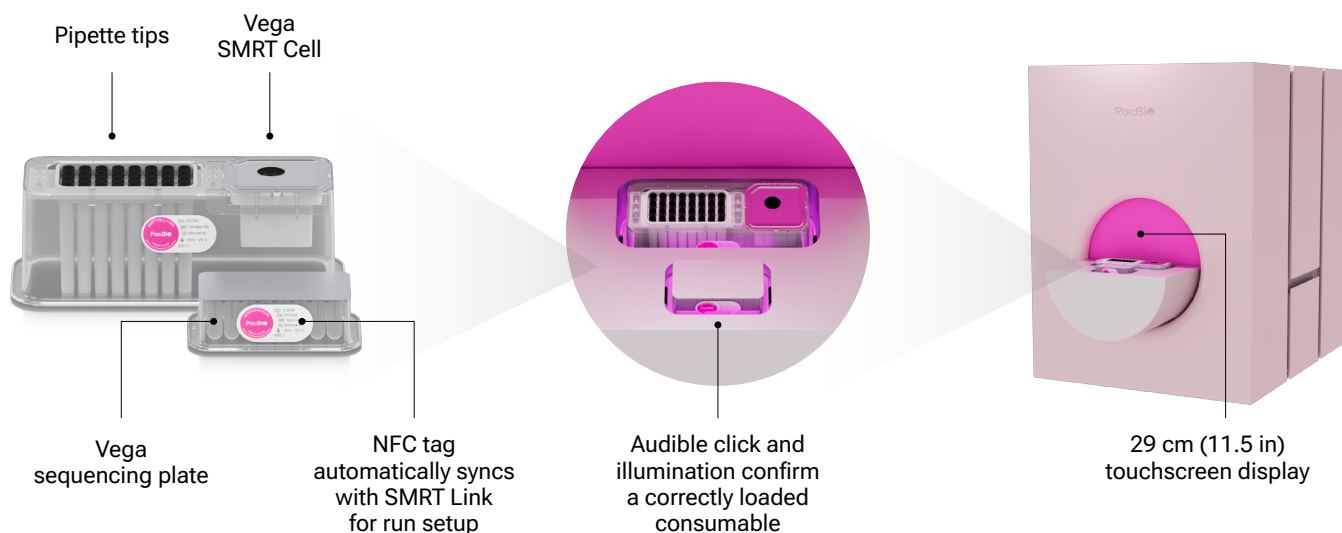


Seamless integration with HiFi library prep workflows and SMRT® Link run management software



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

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



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.



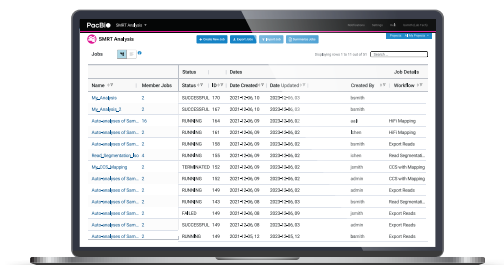
Data management

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 bits per base – 20× smaller than for other long-read technologies.

	On instrument	Off instrument	Typical output file format and size
 Vega system	<ul style="list-style-type: none"> Base calling HiFi read generation with DeepConsensus Methylation calling Barcode demultiplexing BAM file generation 	<ul style="list-style-type: none"> Variant calling Genome assembly 	hifi_reads.bam Vega: 30 GB
 Other long-read technologies	<ul style="list-style-type: none"> Signal collection Initial base calling 	<ul style="list-style-type: none"> Additional base calling Methylation calling Barcode demultiplexing BAM file generation Variant calling Genome assembly 	Fast5/pod5 1,300 GB

Sequence your way



vs.



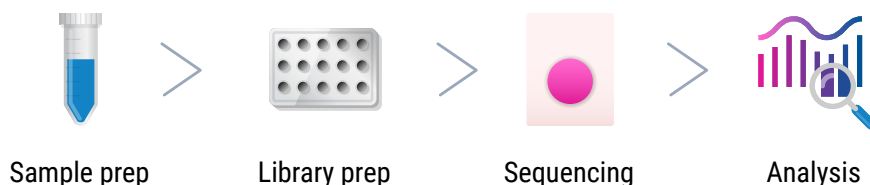
A single SMRT Cell per run means no waiting.

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.

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.



Ready, set, sequence - we're here for you







Our world-class service & support teams, and PacBio Compatible program will get your experiments up and running faster by integrating industry-leading third-party products optimized for HiFi sequencing at every step.

The Customer Hub is your one-stop shop for seamless online ordering, order management, and streamlined support. Designed to make your life easier, it puts everything you need in a centralized location.

With over 30 trusted partners qualified by PacBio scientists, you can confidently streamline your workflow knowing these steps work seamlessly to deliver the answers you need.

Premium HiFi data, accessibly priced

For the first time, you can generate reference-grade microbial genomes, shine a light on repeat expansion regions, characterize full-length isoforms, and produce a comprehensive and phased human genome right from the bench, transforming your lab into a true hub for discovery. The Vega system makes HiFi data accessible, offering accuracy and quality that were once out of reach.

Key applications (coverage ¹)	Samples ¹ per SMRT Cell	Est. total cost per sample ² (USD)
 Microbial genome ³ (30×)	384	\$40
 PureTarget repeat expansion panel ⁴ (200×)	48	\$240
 Transcriptome with Kinnex full-length RNA kit ⁵ (10M reads)	3	\$645
 Human genome ⁶ (20×)	1	\$1,150

1. All sample throughputs are estimates for the Vega system with one SMRT Cell per run, up to 60 Gb per 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.
2. USD list price as of Nov 2024. Total cost per sample includes extraction, library prep, adapter indexes, and sequencing costs.
3. Microbial genome assumes 2 Gb of total genome size per SMRT Cell at >30× per sample and use of the HiFi plex prep kit 96 (103-381-300).
4. PureTarget repeat expansion kit (103-390-400)
5. Kinnex full-length RNA kit (103-072-000) assumes a total of 30M reads.
6. Human genome at 20X coverage uses SMRTbell prep 3.0 (102-182-700).

Shrink your costs, grow your ambitions

With a reagent commitment, Vega Access offers an affordable purchasing option.

Flexible options	Vega price	Vega Access
Instrument price ¹	\$169,000	\$79,000
Reagent price per run ²	\$1,100	\$1,750 for first 152 runs; \$1,100 thereafter

1. Vega system (103-525-500)
2. Reagents include one reaction of Vega polymerase kit (103-517-600), Vega sequencing plate (103-274-300), and Vega SMRT Cell tray (103-406-700).

Vega system specifications

Library	Run time ¹	Q30+ bases	HiFi yield per Vega SMRT Cell ²	Methylation detection
0.5–5 kb	12 hours	95%	6–8M reads	5mC at CpG sites and 6mA for native DNA
5–10 kb	24 hours	90%	25–50 Gb	
10–15 kb			50–60 Gb	
15–20 kb			50–60 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.



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

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
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Compute

Network connection	1 GbE
Instrument operating system	Rocky Linux 9.4
Output file format	hifi_reads.bam; ~30 GB each, up to 6 TB per year



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