



COMPLETE BIOLOGICAL INSIGHTS FOR CONFIDENT DECISIONS

Unlock greater value with HiFi long-read sequencing systems



Genomes

Complete + accurate genomes



Transcriptomes

Ful-length RNA isoforms



Epigenomes

Directly phased methylomes



Metagenomics

Species-level resolution for profiling and assembly



Targeted sequencing

Comprehensive variant calling for regions of interest

HiFi sequencing is SMRT[®] business

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



HiFi sequencing is the only known 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, the PacBio portfolio of reliable and established sequencing systems includes both the production-scale Revio[®] and the Vega[™] benchtop system.

The benefits of HiFi reads



Long read lengths



Easy library preparation



Low coverage requirements



Small file sizes to minimize compute time



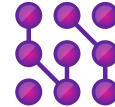
Supported analysis tools consolidated into a single pipeline



High read accuracy



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



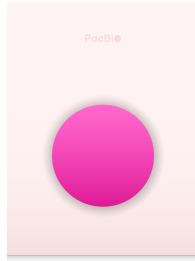
A single technology solution



Data shown is for a single Revio or Vega SMRT[®] Cell.

Two systems, one gold standard

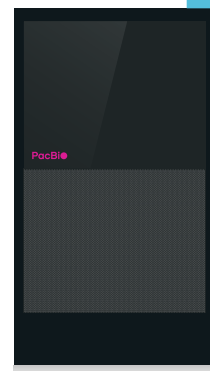
Vega and Revio systems deliver the same high-standard HiFi sequencing, ensuring consistent, accurate data. HiFi reads cover all regions of the genome, providing the most complete and precise assemblies and variant calls. Unlike short reads, which can miss complex regions, HiFi captures full-length transcripts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



VEGA

HiFi within reach

Built on Revio technology, the Vega **benchtop system** brings HiFi sequencing into any lab, giving you full control to produce complete genomes, full-length isoforms, and directly-phased methylomes.



Revio

+ *SPRQ chemistry*

HiFi at scale

The Revio system revolutionized HiFi sequencing with **production-scale power**. Now with SPRQ chemistry, Revio requires less DNA input, expands multiomic applications, decreases costs, and includes on-board 6mA methylation calling.

1 SMRT® Cell per run

Up to 4 SMRT Cells per run

60 Gb per run

480 Gb per run (4 SMRT Cells)

2 µg DNA input

500 ng DNA input

12 or 24-hour run times

12, 24, or 30-hour run times

5mC and 6mA methylation calling

5mC and 6mA methylation calling

Seamless workflow

Revio and Vega systems feature powerful NVIDIA GPUs for accurate, ready-to-use data directly from the sequencer.

With streamlined consumables and flexible software, both systems simplify the sequencing workflow – for any genome center, service provider, or research lab.



Boost your efficiency

Fully automated sequencing with loading under a minute

Run preview and the capability to pre-stage consumables for the next run keeps you one step ahead

On-board primary analysis including Google DeepConsensus, methylation calling, and demultiplexing in every run



Sequencing, simplified

Universal HiFi workflow from extraction to analysis across all HiFi systems

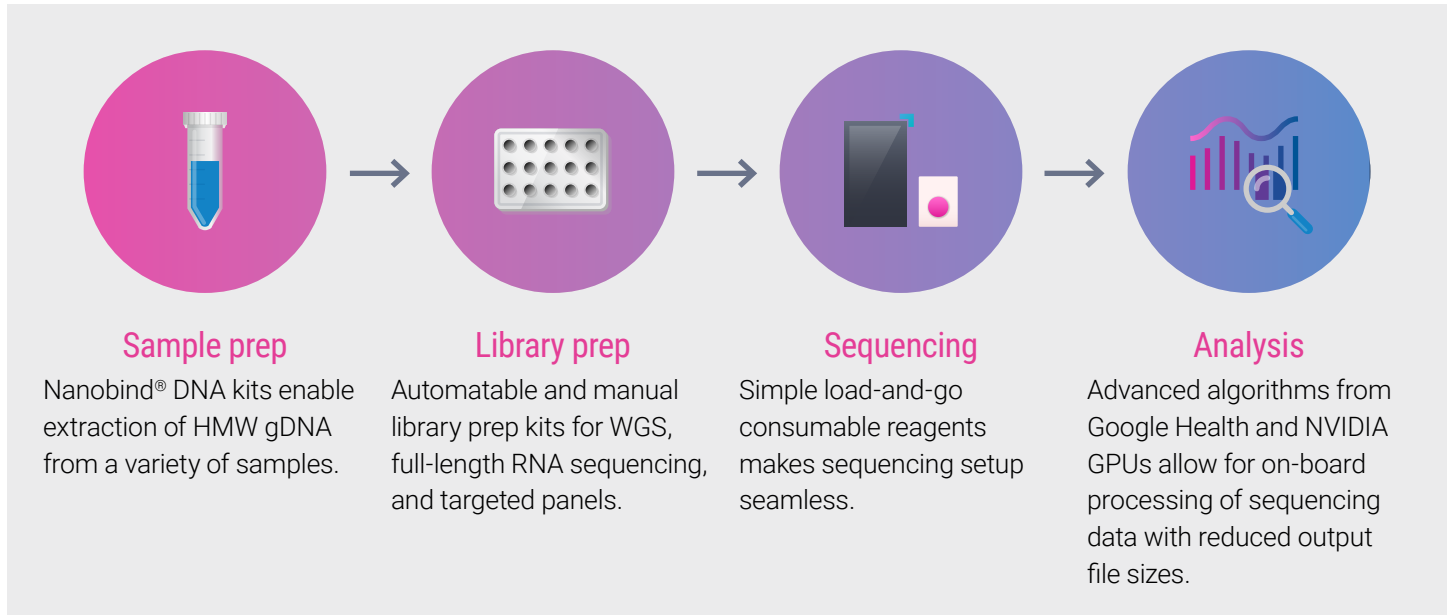
Intuitive user interface with simple, NFC tagged consumables

Standard BAM file format with direct-to-cloud upload

Web-based **SMRT® Link** software supports sequencing prep, run design, and data analysis in a single interface across a wide range of applications.

SMRT® Analysis provides fast, easy, and powerful computational tools and workflows to achieve a complete view of the genome or region of interest.

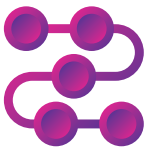
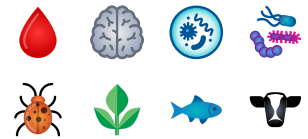
Universal HiFi workflow from sample prep to analysis



Our 30+ **PacBio Compatible partners** integrate products optimized for HiFi sequencing at every step of the workflow, from sample prep to analysis.



Nanobind extraction kits employ proprietary Nanobind disks for the extraction of DNA from diverse sample types, including saliva, blood, cell, and tissue samples. With Nanobind, researchers can extract longer fragments from high-quality DNA in less than two hours, with minimal sample input and without the use of harmful chemicals or mechanical homogenization.



Whether you are doing full-length RNA sequencing, single-cell RNA sequencing, or 16S rRNA, **Kinnex™** offers full-length isoform discovery and abundance information, cell type-specific isoform characterization, and species-level metagenomics community identification that are difficult to capture with short reads.



PureTarget™ generates targeted native DNA libraries with an amplification-free approach which retains epigenetic signals and has no PCR artifacts or errors. Now you can screen the most challenging genomic regions at scale. The PureTarget product line includes a panel of the most important repeat expansions for human health in genes like *FMR1*, *C9orf72*, and *RFC1*.



SMRTbell® library generation using **HiFi prep kit 96** and **HiFi plex prep kit 96** offers automation-friendly and scalable library prep solutions for projects and genomes sizes from microbial to human.

What can you do with 1 SMRT Cell?

PacBio is the only sequencing technology to offer HiFi reads that provide accuracy of 99.9%. With one SMRT Cell on either the Vega or Revio system, you can sequence a human genome at 20x coverage, multiplex up to 384 microbial genomes, or analyze full-length RNA isoforms—all with the accuracy and completeness of HiFi sequencing. This flexibility allows you to scale your research across whole genomes, targeted regions, or transcriptomes with ease.



Vega™ system
HiFi within reach

1 SMRT® Cell



**Revio® system with
SPRQ™ chemistry**
HiFi at scale

1 SMRT Cell

4 SMRT Cells

Application

Samples per run

Application	1 SMRT® Cell	1 SMRT Cell	4 SMRT Cells
Whole genome sequencing			
Human genome (20x coverage)	1	2	8
Human methylation profiling (5x)	4	8	32
<i>De novo</i> assembly (1 Gb genome)	2	4	16
Microbial <i>de novo</i> assembly (2 Gb total)	384	384	1,536
Targeted panels			
PureTarget™ panels	48	96	384
Amplicon sequencing	>1,000	>1,000	>4,000
Hybrid capture			
20 Mb panel	12	16	64
2 Mb panel	72	96	384
100 kb panel	288	384	1,536
RNA sequencing			
Kinnex™ single-cell RNA sequencing	1 (3,000–6,000 cells)	1 (6,000–10,000 cells)	4 (6,000–10,000 cells)
Kinnex full-length RNA sequencing			
5M reads	6	12	48
10M reads	3	6	24
Microbial			
Shotgun metagenomic profiling	64 communities	128 communities	512 communities
Shotgun metagenomic assembly	8 communities	16 communities	64 communities
Kinnex 16S rRNA	1,024 communities	1,536 communities	6,144 communities

All sample throughputs are estimates for either the Vega system with 1 SMRT Cell or the Revio system using SPRQ chemistry with both 1 or 4 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. 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 >50x per sample. PureTarget panel assumes >100x mean per target and Revio throughput assumes automated library prep.

Go further with HiFi long-reads



Annual throughput

200 Vega SMRT Cells

1,250 Revio SMRT Cells

Est samples
per year

Est samples
per year

Whole genomes		
Human genome (20x)	200	2,500
Human methylation profiling (5x)	800	10,000
<i>de novo</i> assembly (1 Gb genome)	400	5,000
Microbial <i>de novo</i> assembly (2 Gb total)	76,800	480,000
Targeted panels		
Amplicons	>200,000	1.2M
PureTarget panels	9,600	96,000
RNA sequencing		
Kinnex single-cell RNA sequencing	200 (3,000–6,000 cells each)	1,250 (6,000–10,000 cells each)
Kinnex full-length RNA sequencing	5M reads: 1,200 10M reads: 600	5M reads: 15,000 10M reads: 7,500
Microbial		
Shotgun metagenomic profiling	12,800 communities	160,000 communities
Shotgun metagenomic assembly	1,600 communities	20,000 communities
Kinnex 16S rRNA	200,000 communities	1.9M communities

All sample throughputs are estimates for either the Vega system with 1 SMRT Cell or the Revio system using SPRQ chemistry with 4 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. 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 >50x per sample. PureTarget panels assume >100x per target, PureTarget kit 24 for Vega, and PureTarget kit 96 for Revio.



World-class service + support teams

With our dedicated support teams by your side and the **Customer Hub** as your one-stop online solution, managing orders and getting assistance has never been easier.



Financing available

PacBio Capital enhances accessibility by eliminating the up-front capital expenditure barrier. This financing program offers highly competitive rates, six-month same-as-cash financing option, and a streamlined credit and funding process to fast-track your purchase.



An ecosystem to support you

The PacBio Compatible program integrates products optimized for HiFi sequencing at every step of the workflow for a highly efficient experience. This includes seamless sample prep and library prep workflows and integrated automation products.

Ordering information

Part number	Product
103-525-500	Vega system
103-517-600	Vega polymerase kit
103-274-300	Vega sequencing plate
103-406-700	Vega SMRT Cell tray
102-090-600	Revio system
103-520-100	Revio SPRQ polymerase kit
103-504-900	Revio SPRQ sequencing plate
102-202-200	Revio SMRT Cell tray



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pacb.com/applications



Learn more about the Vega system
pacb.com/vega



Learn more about the Revio system
pacb.com/revio