



Technical overview **Vega system v1.2** **+ SPRQ-Nx chemistry** **and SMRT Link v26.2**

Vega system ICS v1.2
SMRT Link v26.2

PN 103-902-600 Rev 01 | August 2026

Technical overview

Vega system ICS v1.2 + SPRQ-Nx chemistry and SMRT Link v26.2

§ Part 1: Vega system v1.2 + SPRQ-Nx chemistry

1. Vega system v1.2 key features & benefits
2. New Vega SPRQ-Nx consumables and instrument control software
3. 21 CFR Part 11 compliance support overview
4. Vega system v1.2 applications & protocol updates
5. Vega system v1.2 user experience improvements
6. Vega system v1.2 example sequencing performance

§ Part 2: SMRT Link v26.2 + SMRT Link Cloud v26.2

1. SMRT Link v26.2 key features & benefits
2. New Vega SPRQ-Nx chemistry support
3. SMRT Link v26.2 21 CFR Part 11 support
4. SMRT Link v26.2 user experience improvements

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§ Part 1:

Vega system v1.2 + SPRQ-Nx

1. Vega system v1.2 key features & benefits
2. New Vega SPRQ-Nx consumables and instrument control software
3. Vega system 21 CFR Part 11 support
4. Vega system v1.2 applications & protocol updates
5. Vega system v1.2 user experience improvements
6. Vega system v1.2 example sequencing performance





Vega system v1.2

key features and benefits

What is staying the same in Vega system v1.2?

No major changes to core HiFi library prep kits and Vega instrument hardware / data file formats



HiFi library prep kits

Continue to use existing SMRTbell prep kit 3.0 / HiFi prep kit 96 / HiFi plex prep kit 96 / Kinnex / PureTarget 2.0 products



Vega SMRT Cell

Single-use SMRT Cell



Vega instrument hardware and run setup

1 SMRT Cell per run; no changes to work deck loading steps



Vega data file formats

No changes to hifi_reads.bam + fail_reads.bam file structures



What is new in Vega system v1.2?

New Vega system v1.2 with SPRQ-Nx chemistry makes HiFi sequencing more accessible and more cost-effective



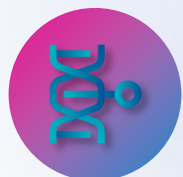
Increased HiFi data yield

90 Gb per Vega SMRT Cell acquisition (50% higher)
[15 – 20 kb library insert sizes]



Shorter run times

2- and 4-hour movie time options for shorter (0.5 – 2 kb)
library insert sizes enable faster time to results



Richer multiomic data

New 5hmC caller expands Vega system on-instrument
methylation detection capabilities beyond 5mC and 6mA



More accessible sample types

4× reduction in DNA input (500 ng input requirement) enables
analysis of more precious sample types



Regulatory compliance support

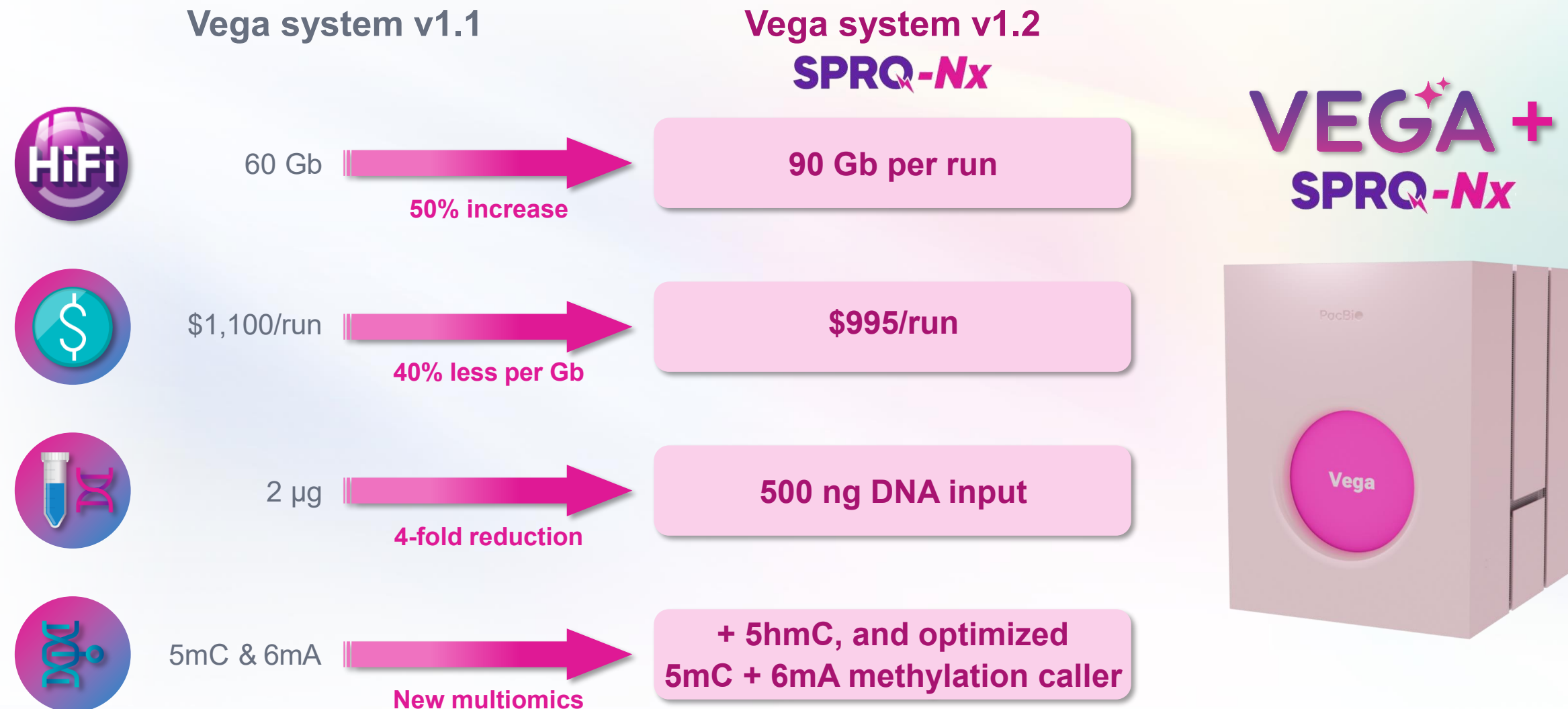
New Vega system ICS v1.2 + SMRT Link v26.2 software login mode
provides support for 21 CFR Part 11 compliance¹

VEGA+
SPRQ-Nx



Vega system v1.1 versus v1.2 feature comparison summary

New Vega system v1.2 with SPRQ-Nx chemistry supercharges your research where it counts



Vega system v1.2 key workflow updates

Vega workflow step	What's new		What stays the same
DNA sample extraction		N/A	- Existing Nanobind HMW DNA extraction workflows - Existing Nanobind kits
SMRTbell library preparation		Reduced genomic DNA input requirements for HiFi WGS library preparation (500 ng)	- Core SMRTbell library construction workflow - Existing HiFi library preparation kits - Existing applications support
Sample setup (ABC)		- Updated sample setup ABC (annealing / binding / complex cleanup) cleanup volumes in Proc. & checklists to support new Vega SPRQ polymerase kit - SMRT Link v26.2 Loading Calculator support for new Vega SPRQ polymerase kit	- Core sample setup ABC workflow - Existing applications support
Run design		SMRT Link v26.2 run design support for new Vega SPRQ sequencing plate-Nx	- Overall Vega run design workflow - Existing applications support
Sequencing		- Vega ICS v1.2 support for new login mode - Vega ICS v1.2 support for new Vega SPRQ sequencing plate-Nx chemistry - Vega ICS v1.2 support for new on-instrument 5hmC calling	- Overall Vega run setup workflow - Existing Vega SMRT Cell - Existing Vega on-instrument analysis features

Vega system v1.2 key software updates

New ICS and SMRT Link software enable support for Vega SPRQ-Nx chemistry



Vega system supported software					
 Vega ICS v1.2 ¹			 SMRT Link v26.2 ²		
Instrument control	- New Vega system login mode to support 21 CFR Part 11 enablement - Minor ICS software bug fixes		 Instruments	No major changes	
Primary analysis	Added support for new Vega SPRQ-Nx sequencing chemistry³		 Sample Setup	Loading Calculator support for new Vega SPRQ polymerase kit	
On-instrument CCS analysis	Updated consensus basecalling model to support new Vega SPRQ-Nx sequencing chemistry³		 Runs	Run design support for new Vega SPRQ sequencing plate – Nx³ and shorter movie acquisition times (2, 4 hours)	
On-instrument methylation calling	- Improved accuracy and increased confidence of 5mCpG calling - Added on-instrument 5hmC caller		 Data Management	No major changes	
On-instrument barcode demux	No major changes		 SMRT Analysis	New Redo Demultiplexing data utility	

New instrument login mode setup option to support 21 CFR103-902-600 Part 11 enablement

¹ See Vega system v1.2 release notes ([103-892-200](#)) for latest ICS software update details.

² SMRT Link v26.2 supports Revio system ICS v13.5 and Vega system ICS v1.2. SMRT Link v26.2 does not support Sequel II/Ile systems.

³ Vega ICS v1.2 retains support for original Vega sequencing chemistry (v1).



New Vega SPRQ-Nx consumables & instrument control software

Vega system v1.2 release includes new SPRQ-Nx consumables & ICS

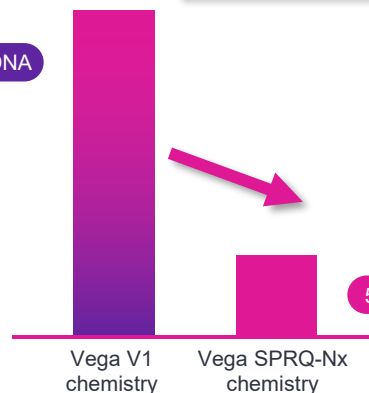
New consumables and instrument control software enable an improved user experience for HiFi sequencing

Vega SPRQ sequencing plate – Nx PN 103-726-600



SPRQ-Nx chemistry upgrade
4× lower DNA input for library prep¹

2000 ng DNA



Vega V1 chemistry

Vega SPRQ-Nx chemistry

500 ng DNA

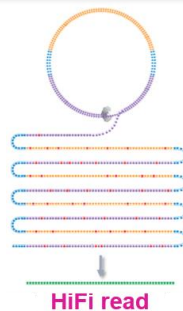
Vega SPRQ polymerase kit 8 rxn – PN 103-794-300



New polymerase enzyme
Improved raw read length performance²



Increased HiFi data yield
90 Gb per Vega SMRT Cell



HiFi read

60

Vega V1 chemistry and v1.1 ICS

90

Vega SPRQ-Nx chemistry and v1.2 ICS

HiFi data (Gb)

Vega ICS v1.2



Improved compute efficiency
Supports increased data output



Shorter run times

2- and 4-hour movie time options



Regulatory compliance support

21 CFR Part 11 compliant-capable



Richer multiomic data

5hmC along with 5mC and 6mA³

¹ Vega SPRQ-Nx chemistry formulation improves sample loading efficiency on Vega SMRT Cells and supports all existing HiFi applications.

² Vega SPRQ polymerase features improved processivity that reduces number of early-terminating reads and produces a higher proportion of reads that are long enough to generate a HiFi (≥Q20) read. 11

³ Vega ICS v1.2 improves 5mC + 6mA calling accuracy and features new on-instrument 5hmC calling.

New Vega SPRQ-Nx consumables packaging and kit configurations

New Vega SPRQ-Nx consumables product packaging features white-colored boxes with magenta trim to easily distinguish them from old v1 Vega consumables

	On-market Vega v1 consumables ¹	NEW Vega SPRQ-Nx consumables
Polymerase kit	 Vega polymerase kit 103-517-600	 NEW Vega SPRQ polymerase kit 103-794-300 <i>No change to new Vega SPRQ polymerase kit packaging color</i>
Sequencing plate	 Vega sequencing plate 103-274-300	 NEW Vega SPRQ sequencing plate – Nx ² 103-726-600 <i>New Vega SPRQ-Nx seq. plate packaging is white-colored with magenta trim</i>
SMRT Cell tray	 Vega SMRT Cell tray 103-406-700	 Vega SMRT Cell tray 103-406-700 <i>No change to Vega SMRT Cell tray product part or packaging → Continue to use with new SPRQ-Nx consumables</i>
24-pack reagent kit	 Vega SPRQ reagent kit, 8-pack 103-535-700 (8 acquisitions) Contains: (1) Vega SPRQ polymerase kit, (8) Vega SPRQ sequencing plate (8) Vega SMRT Cell tray (1) SMRTbell cleanup beads (10 mL)	 NEW Vega SPRQ-Nx reagent kit, 8-pack 103-885-900 (8 acquisitions) Contains: (1) Vega SPRQ polymerase kit, (8) Vega SPRQ sequencing plate – Nx, (8) Vega SMRT Cell tray (1) SMRTbell cleanup beads (10 mL) <i>Updated to include new Vega SPRQ-Nx seq. plate and new Vega SPRQ pol. kit</i>



¹ On-market Vega v1 consumables will remain available for purchase.

² Vega SPRQ-Nx sequencing reagent plate thawing procedure remains unchanged (see *Vega system operations guide* ([103-526-600](#)) for detailed sequencing plate thawing instructions).

Vega polymerase kit vs. Vega SPRQ polymerase kit configuration and layout

New Vega SPRQ polymerase kit contains updated chemistry formulations sample setup ABC¹ step

Vega SPRQ polymerase kit

103-794-300

(Supports up to 8 binding Rxs / 8 Vega SMRT Cells)

#	Component	Part number	Qty	Color	Volume
1	Annealing buffer	103-829-600	1	light blue	120 µL
2	Standard sequencing primer	103-829-700	1	light green	120 µL
3	Kinnex sequencing primer	103-829-800	1	light purple	120 µL
4	Polymerase buffer	103-829-900	1	yellow	450 uL
5	Sequencing polymerase	103-830-200	1	purple	29 µL
6	Dilution buffer	103-830-000	1	blue	575 uL
7	Sequencing control	103-830-100	1	red	9.6 µL
8	Loading buffer	103-830-300	1	green	480 uL

Note: Vega SPRQ polymerase kit contains **new** reagents with **new** part numbers – but **existing** tube labels (tube names) stay the same

NEW SPRQ polymerase enzyme

NEW SPRQ DNA control complex

NEW loading buffer

8 tubes



Same number of tubes and package configuration

Vega polymerase kit

103-517-600

(Supports up to 8 binding Rxs / 8 Vega SMRT Cells)

#	Component	Part number	Qty	Color	Volume
1	Annealing buffer	103-517-900	1	light blue	177 µL
2	Standard sequencing primer	103-518-000	1	light green	177 µL
3	Kinnex sequencing primer	103-518-100	1	light purple	177 µL
4	Polymerase buffer	103-518-200	1	yellow	800 µL
5	Sequencing polymerase	103-518-300	1	purple	34 µL
6	Dilution buffer	103-518-400	1	blue	1.7 mL
7	Sequencing control	103-518-500	1	red	9 µL
8	Loading buffer	103-518-600	1	green	800 µL

8 tubes



Vega system v1.2 DNA sequencing control performance

Vega DNA sequencing control is bound to new Vega SPRQ polymerase enzyme

Metric	Expected control performance ¹				
	Vega v1.1 DNA control [24 hrs]	Vega v1.2 SPRQ DNA control [2 hrs]	Vega v1.2 SPRQ DNA control [4 hrs]	Vega v1.2 SPRQ DNA control [12 hrs]	Vega v1.2 SPRQ DNA control [24 hrs]
Control read count	≥500	≥500	≥500	≥500	≥500
Control polymerase read length (Mean)	≥40 kb	≥1 kb	≥5 kb	≥20 kb	≥50 kb
Control concordance (Mean)	≥0.88	≥0.88	≥0.88	≥0.88	≥0.88

¹ Expected control performance metrics shown for Vega system v1.2 are based on the use of Vega SPRQ-Nx chemistry.

DNA internal control metrics are useful to help assess the performance of a sequencing run

- If control read count or control read length is **lower than expected**
 - Focus troubleshooting on **PacBio system and/or consumables**
- If control performance appears **normal**,
 - Focus troubleshooting on investigating **DNA sample quality and/or library prep QC metrics**



Vega v1 *versus* Vega SPRQ-Nx consumable cross-compatibility

Vega SPRQ-Nx sequencing plate chemistry is compatible with Vega SPRQ polymerase kit and not compatible with Vega (v1) polymerase kit

	Vega sequencing plate 103-274-300 	Vega SPRQ sequencing plate – Nx 103-726-600 
Vega polymerase kit 103-517-600 		
Vega SPRQ polymerase kit 103-794-300 		

Vega v1 *versus* Vega SPRQ-Nx consumable cross-compatibility

Vega SPRQ polymerase kit & Vega SPRQ sequencing plate must be used together and cannot be combined with older Vega polymerase kit & Vega sequencing plate consumables

V1.1 ICS



Compatible

Not compatible



Vega polymerase kit
Vega sequencing plate



~~Vega SPRQ polymerase kit
Vega SPRQ sequencing plate – Nx~~

V1.2 ICS



Compatible

Not compatible

Cannot mix and match
SPRQ and non-SPRQ
reagents in the same run



Vega polymerase kit
Vega sequencing plate



~~Vega SPRQ polymerase kit
Vega sequencing plate~~



Vega SPRQ polymerase kit
Vega SPRQ sequencing plate – Nx



~~Vega polymerase kit
Vega SPRQ sequencing plate – Nx~~

Vega SPRQ-Nx sequencing plate chemistry supports all existing applications

Vega SPRQ-Nx chemistry supports all applications, sample types, and library types currently supported by Vega v1 chemistry¹

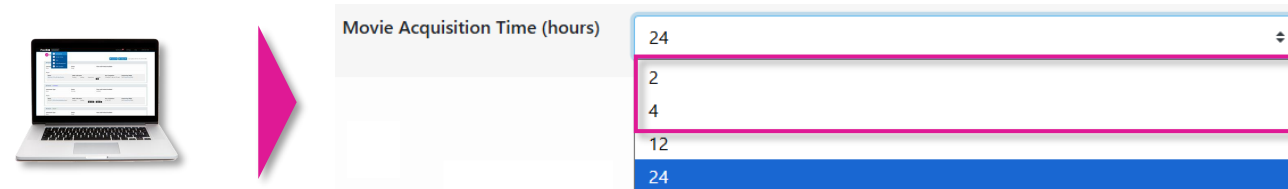
HiFi sequencing application	Compatible Polymerase kit	Compatible Sequencing plate	Compatible SMRT Cell tray
WGS (15 – 20 kb)	Vega SPRQ polymerase kit 103-794-300	Vega SPRQ sequencing plate – Nx 103-726-600	Vega SMRT Cell tray 103-406-700
Kinnex full-length RNA / single-cell RNA / 16s rRNA (15 – 20 kb)			
Microbial genomes (5 – 10 kb)			
Shotgun metagenomics (7 – 20 kb)			
PureTarget (5 – 10 kb)			
Amplicon sequencing (≥ 5kb)			
Amplicon sequencing (< 5kb) ²			

¹ Data quality of Vega SPRQ-Nx is consistent with SPRQ-Nx chemistry on Revio and improved relative to Vega v1 chemistry. Both data types are compatible.

² Vega system v1.2 + SPRQ-Nx chemistry supports amplicon library insert sizes down to 0.5 kb. (Refer to [Vega system specification sheet \(102-326-625\)](#) for the latest supported library insert sizes and system specifications.

Vega system v1.2 enables shorter 2- and 4-hour movie acquisition times

In SMRT Link v26.2 Run Design, Vega movie acquisition time can be optionally set to 2, 4, 12 or 24 hours for increased flexibility when running different library insert sizes



Shorter

2 hrs ~500 bp – 1 kb

4 hrs ~1 kb – 2 kb

Example:
Shorter amplicons ≤2 kb

New 2-hour and 4-hour “fast movie” options enable quick-turnaround work like synthetic DNA QC and small plasmid sequencing²

12 hrs ~2 kb – 5 kb

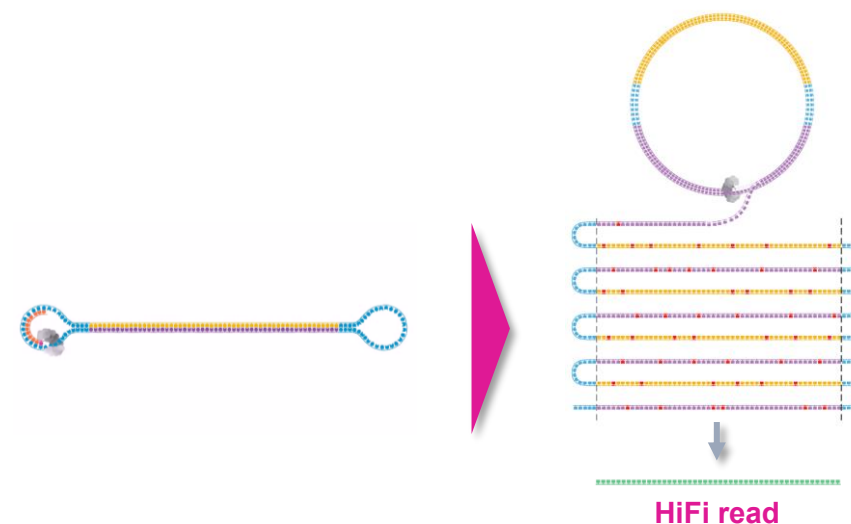
24 hrs ~5 – 20 kb

Example:
Longer amplicons >2 kb

Example:
WGS, Kinnex, PureTarget
and most other applications

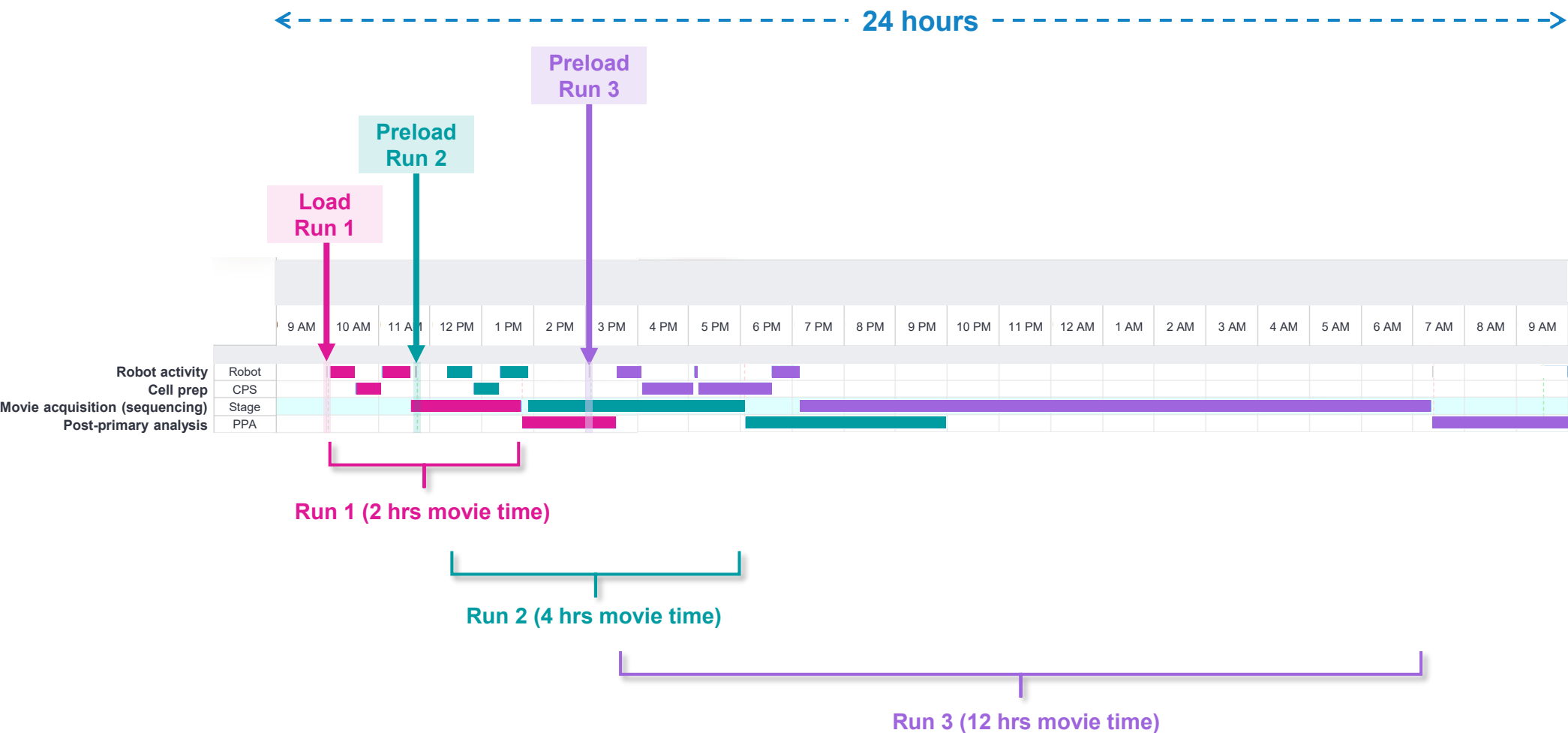
Vega system specifications¹

Library	Run time ¹	Q30+ bases	HiFi yield per Vega SMRT Cell ²	Methylation detection
0.5-1 kb	2 hours	95%	6-8 million reads	5mC and 5hmC at CpG sites and 6mA for native DNA ³
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	



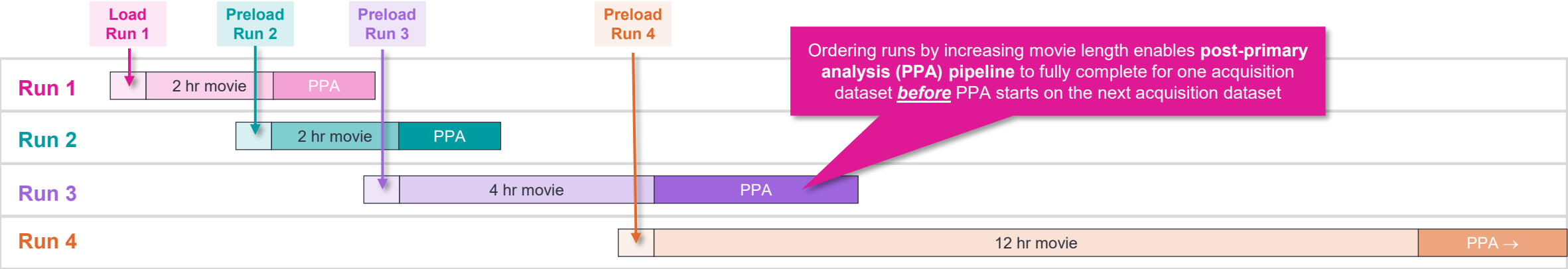
With Vega system v1.2, shorter movie acquisition times allow for multiple runs to be completed within 1 day

Using a mixed workflow schedule can enable 3 sequencing runs to be completed per day on 1 Vega instrument



For optimal data throughput, schedule consecutive (back-to-back) Vega sequencing runs by increasing movie length

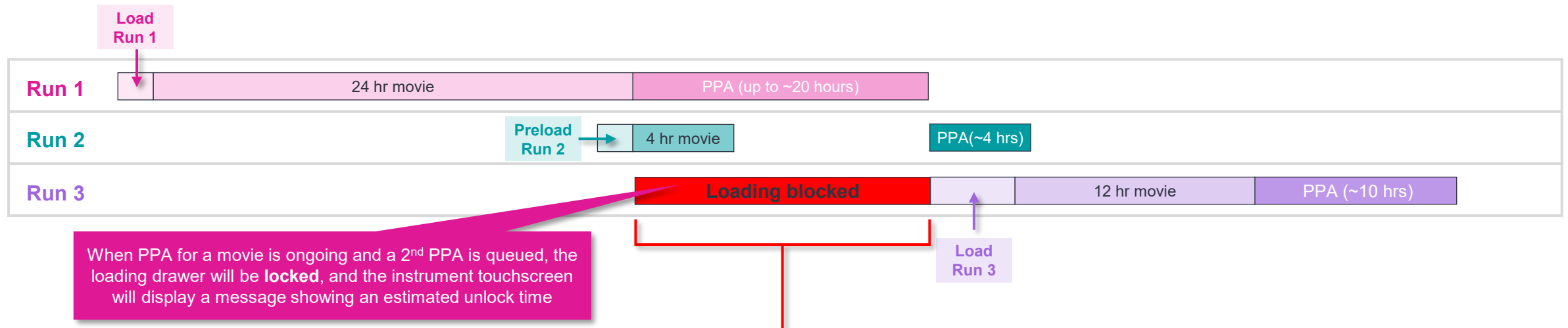
Runs should be ordered in increasing movie time to avoid delays due to lack of compute storage availability



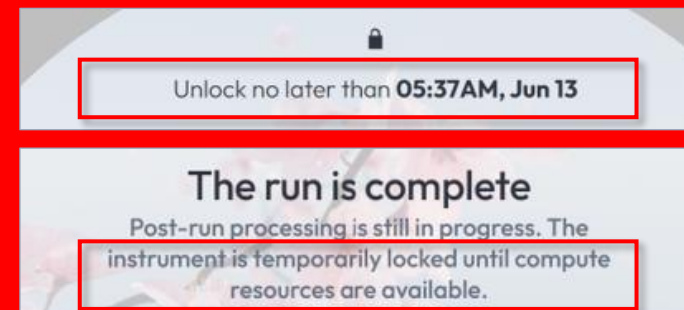
IMPORTANT! To enable optimal data throughput when running back-to-back acquisitions, **Vega system runs with shorter movie times should be scheduled before runs with longer movie times** to give post-primary analysis (PPA) pipeline enough time to complete

For optimal data throughput, schedule consecutive (back-to-back) Vega sequencing runs by increasing movie length (cont.)

A long Vega sequencing run (≥ 12 -hour acquisition) followed by a short run (2- or 4-hour acquisition) can result in a lockout period due to lack of compute storage availability that prevents users from preloading their next run



- Post-primary analysis (PPA) working on Run 1 (24-hr) movie with **all available compute resources fully utilized**
- Vega instrument drawer is **locked** → User is **unable** to preload Run 3 during a period of **up to 20 hours** (for 24 hr movie)¹
- After PPA completes for the 24-hr movie, the instrument is **unlocked** and the user can proceed to preload fresh consumables for Run 3



Vega system v1.2 improves methylation detection capabilities

Updated methylation analysis software supports 5hmC calling

Vega on-instrument methylation analysis Jasmine v26.2



Available in
GitHub

<https://github.com/PacificBiosciences/jasmine>

- New models for SPRQ-Nx chemistry (Vega & Revio systems)
- 5-methylcytosine (5mC in CpG) calls more strongly match bisulfite data
- Improved 6mA strand calling annotation¹
- New 5-Hydroxymethylcytosine (5hmC in CpG) caller

Off-instrument methylation analysis MethBat v1.1.0



Available in
GitHub

<https://github.com/PacificBiosciences/methbat>

- MethBat secondary analysis tool aggregates and analyzes CpG methylation calls made from PacBio HiFi datasets²
 - Now includes 5mC, 6mA, and 5hmC pileup functionality
- **Note:** pb-CpG-tools is **deprecated** and will not undergo further development³
- If using Jasmine version $\geq 26.x$
 - Recommend to use **MethBat tool** since it supports analysis of all methylation types
- If using Jasmine version $< 26.x$
 - Can continue to use **pb-CpG-tools**

¹ Methylation analysis pipeline now keeps separate forward/reverse 6mA probabilities instead of treating 6mA as one un-stranded value → 6mA strand shown in BAM modification tags and inspection output now matches the strand of the called modification.

² See [MethBat GitHub](#) page for more details about methylation secondary analysis features, including: Creation of a methylation profile for a collection of genomic regions (e.g., CpG islands) Creation of cohort / background profiles from a collection of methylation profiles.

³ pb-CpG-tools will remain available for at least the remainder of 2026.

21 CFR Part 11 compliance support overview

How to set up and enable Vega system login mode – Overview

Login mode setup and configuration workflow overview for SMRT Link Administrators:

- A. SMRT Link user status and role settings
- B. Login mode user, configuration and instrument settings

Login mode setup and authentication workflow overview for SMRT Link Users:

- A. Set Instrument Login settings
- B. Vega user identification and authentication procedure

Vega system v1.2 and SMRT Link v26.2 support FDA 21 CFR Part 11¹

What is 21 CFR Part 11 and how does the Vega system support 21 CFR part 11?

What is 21 CFR part 11?

- 21 CFR Part 11 is a U.S. Food and Drug Administration (FDA) regulation outlining how regulated organizations should maintain electronic records



Validation

- Systems must be validated to perform as intended



Audit trails

- All actions must be recorded with date and time stamps



Record retention

- Records must be retained in a secure environment



Security

- Access to records must be restricted to authorized users



Electronic signatures

- Signatures must be unique and linked to their respective records



Training

- Personnel must be trained on 21 CFR Part 11 requirements

How do PacBio systems support 21 CFR part 11?

- Vega system v1.2 user login mode feature can be enabled per instrument
- SMRT Link v26.1 audit trail logging feature provides tamper-resistant logging with centralized visibility and exportable records for SMRT Link servers connected to Revio and Vega systems



User authentication with login mode

- If enabled, login mode requires users to log in with their SMRT Link username and a personal identification code (PIC)
 - Ensures actions are tied to a specific user
 - Extends user accountability to on-instrument activity
 - User management limited to Admins



Traceability with audit trails

- SMRT Link captures audit trails across both software and instrument activity
- **Each record includes:**
 - Who performed the action
 - What action was performed
 - When the action occurred
- **Audit trails are:**
 - Tamper-evident
 - Accessible to Admins
 - Exportable for inspection and documentation

Vega system v1.2 and SMRT Link v26.2 support FDA 21 CFR part 11¹ (cont.)

Key requirements and customer responsibilities for enabling 21 CFR Part 11 compliance

PacBio provides

- Authentication via login mode
- Secure, timestamped audit trails
- Attributions of actions to users
- Configurable access controls
- Audit log export

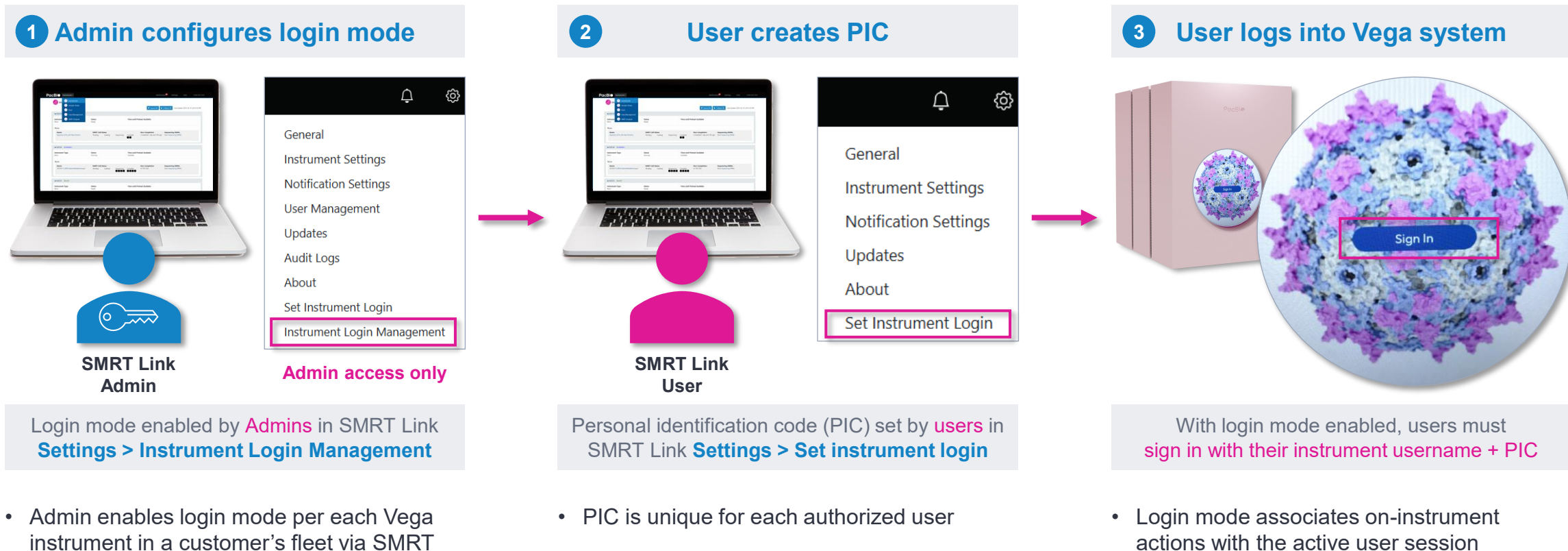
Customer is responsible for

- Enabling and enforcing login mode
- Defining access/password policies
- Routine audit trail review
- Standard operating procedures for audit review, deviations, and Corrective and Preventative Action and Standard Operating Procedure
- System validation within their environment



How to set up Vega system v1.2 login mode: Overview

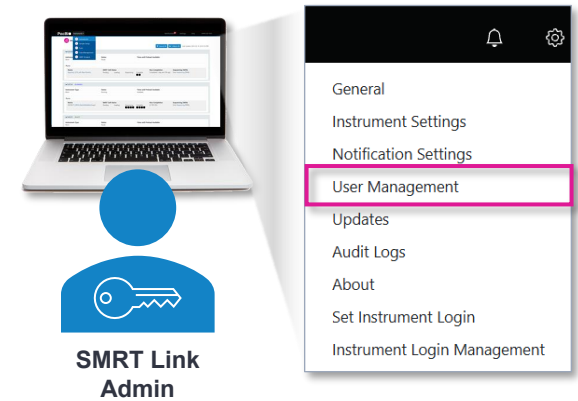
Login mode is configured by SMRT Link Administrator, and then authorized users create a unique personal identification code (PIC) to log into a Vega instrument



Login mode setup and configuration workflow overview for SMRT Link

Administrators: A. SMRT Link user status and role settings

Before enabling login mode, SMRT Link Administrator must first configure SMRT Link user status and role settings



Navigate to SMRT Link Settings
> User Management

1 Manage SMRT Link user Status settings

2 Manage SMRT Link user Role settings

PacBio

Select module ▾

Settings

Sections

General

Instrument Settings

Notification Settings

User Management

Updates

Audit Logs

About

Set Instrument Login

Instrument Login Management

User Management

Display All Enabled Users

Search By Name

1

Displaying rows 1 to 678 out of 678

User Name IT	Status IT	Role IT
Admin_Username	Enabled	Admin
Username_01	Enabled	Lab Tech
Username_02	Enabled	Lab Tech
Username_03	Enabled	Lab Tech
Username_04	Enabled	Lab Tech
Username_05	Enabled	Lab Tech
Username_06	Enabled	Lab Tech
Username_07	Enabled	Lab Tech

User Details

User ID

aalibakhshi

User Name

Amin Alibakhshi

Status

ENABLED

DISABLED

Role

Lab Tech

Contact Information

Email Address

aalibakhshi@pacificbiosciences.com

Phone Number

Phone

Cancel

Save Changes

SMRT Link user status

Enabled = User has access to SMRT Link
Disabled = User cannot access SMRT Link

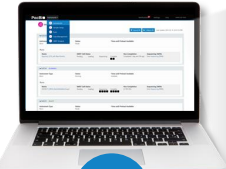
Login mode setup and configuration workflow overview for SMRT Link

Administrators: A. SMRT Link user status and role settings

Before enabling login mode, SMRT Link Administrator must first configure SMRT Link user status and role settings



SMRT Link Admin



- General
- Instrument Settings
- Notification Settings
- User Management
- Updates
- Audit Logs
- About
- Set Instrument Login
- Instrument Login Management

Navigate to SMRT Link Settings > User Management

- 1 Manage SMRT Link user Status settings
- 2 Manage SMRT Link user Role settings

User Management

Display All Enabled Users

Search By Name

2

Displaying rows 1 - 8 out of 678

User Name	Status	Role
Admin_Username	Enabled	Admin
Username_01	Enabled	Lab Tech
Username_02	Enabled	Lab Tech
Username_03	Enabled	Lab Tech
Username_04	Enabled	Lab Tech
Username_05	Enabled	Lab Tech
Username_06	Enabled	Lab Tech
Username_07	Enabled	Lab Tech

User Details

User ID

aalibakhshi

User Name

Amin Alibakhshi

Status

ENABLED

DISABLED

Role

Lab Tech

SMRT Link user roles

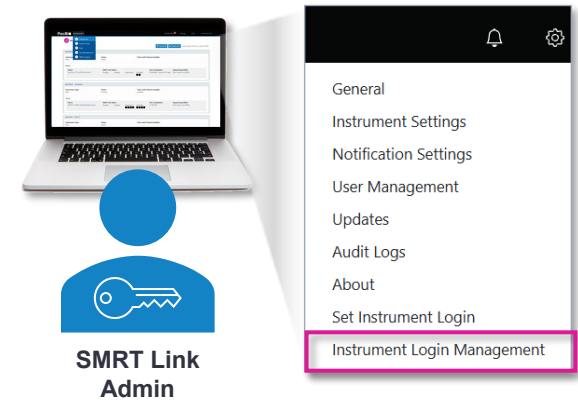
- SMRT Link supports three user roles: Admin, Lab Tech, and Bioinformatician
- Roles define which SMRT Link modules a user can access
- Table below lists privileges associated with the three user roles

Tasks or privileges	Admin	Lab Tech	Bioinformatician
Add/delete SMRT Link users	Y	N	N
Assign roles to SMRT Link users	Y	N	N
Update SMRT Link software	Y	N	N
Add/update instruments	Y	N	N
Access Instruments module	Y	Y	N
Access Sample Setup module	Y	Y	N
Access Runs module	Y	Y	N
Access Data Management module	Y	Y	Y
Access SMRT Analysis module	Y	Y	Y

Login mode setup and configuration workflow overview for SMRT Link

Administrators: B. Login mode user, configuration and instrument settings

To set up login mode, SMRT Link Administrator manages login mode user, configuration and instrument settings



Navigate to SMRT Link Settings
> Instrument Login Management

- 1 Manage login mode
User settings
- 2 Manage login mode
Configuration settings
- 3 Manage login mode
Instrument settings

Instrument Login Management

1 Users Configuration Instruments

Status	Username	Instrument user name	PIC Expires	Failed Attempts	Actions
Active	john.doe@example.com	john.doe	3/26/2026	0	Unlock Force PIC Reset Remove
Locked Out	jane.smith@example.com	jane.smith	3/11/2026	5	Unlock Force PIC Reset Remove
Active	bob.jones@example.com	bob.jones	4/25/2026	2	Unlock Force PIC Reset Remove
Locked Out	alice.brown@example.com	alice.brown	Expired	6	Unlock Force PIC Reset Remove
Active	charlie.wilson@example.com	charlie.wilson	Not set	0	Unlock Force PIC Reset Remove

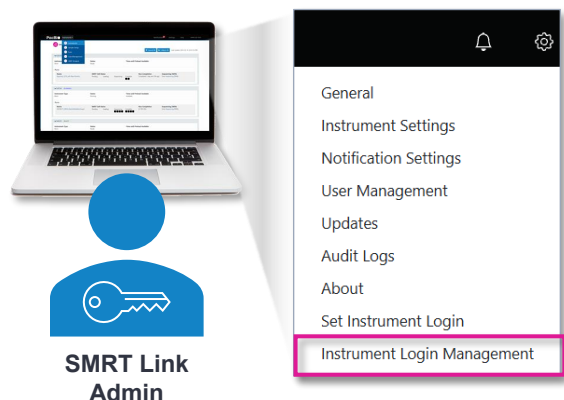
Instrument Login Management – User management tab

- Display list of users with their instrument login status
- Allow administrators to **unlock** locked-out users
- Allow administrators to **force PIC reset** for one or more users
- Allow administrators to **remove** users from instrument login (if applicable)

Login mode setup and configuration workflow overview for SMRT Link

Administrators: B. Login mode user, configuration and instrument settings

To set up login mode, SMRT Link Administrator manages login mode user, configuration and instrument settings



Navigate to **SMRT Link Settings**
> **Instrument Login Management**

- 1 Manage login mode **User** settings
- 2 Manage login mode **Configuration** settings
- 3 Manage login mode **Instrument** settings

Instrument Login Management

2

Users	Configuration	Instruments
PIC Minimum Length:	8	characters
PIC Expiration:	180	days
Max Failed Attempts:	5	attempts
Observation Window:	15	minutes
Instrument Session Timeout:	30	minutes

Save Configuration

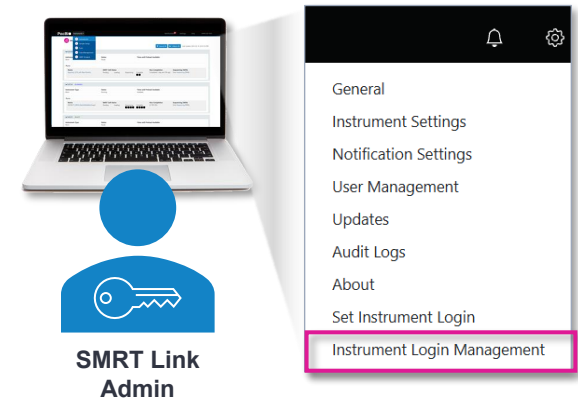
Instrument Login Management – Configuration tab

- Display and allow editing of login policy configuration
- **PIC Minimum Length** – Min. number of characters required for a PIC. PICs can be alphanumeric.
- **PIC Expiration** – Number of days after which a PIC will expire and need to be reset.
- **Max Failed Attempts** – Maximum number of failed login attempts allowed before an account is locked out.
- **Observation Window** – Time window in minutes during which failed login attempts are counted toward lockout.
- **Instrument Session Timeout** – Number of minutes of inactivity before an instrument session times out.

Login mode setup and configuration workflow overview for SMRT Link

Administrators: B. Login mode user, configuration and instrument settings

To set up login mode, SMRT Link Administrator manages login mode user, configuration and instrument settings



Navigate to SMRT Link Settings
> Instrument Login Management

- 1 Manage login mode
User settings
- 2 Manage login mode
Configuration settings
- 3 Manage login mode
Instrument settings

Instrument Login Management

Instrument Login Management				
3				
Users Configuration Instruments				
Instrument Name	Serial	Instrument Type	Connected	Login Mode Enabled
21044	21044	Vega	Disconnected	☐
21033	21033	Vega	Connected	☐
21039	21039	Vega	Connected	☐
21026	21026	Vega	Connected	☒

Instrument Login Management – Instruments tab

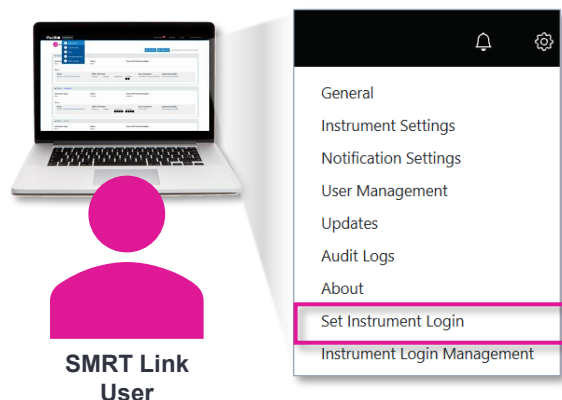
- Displays a list of instruments **connected** to the SMRT Link server
- Allow administrators to **enable or disable login mode** for each instrument¹
 - Show current login mode status for each instrument
 - Provide visual indicators for login mode state

¹ Administrators can toggle login mode on or off for individual PacBio instruments, and the system will then notify the instrument to require authenticated user access or allow unauthenticated access accordingly.

Login mode setup and authentication workflow overview for SMRT Link Users:

A. Set Instrument Login settings

Before using login mode, users must first create a unique Personal Identification Code (PIC)¹



Navigate to **SMRT Link Settings**
> **Set Instrument Login**

- 1 **Create Personal Identification Code (PIC)**
- 2 **Confirm PIC and click Save PIC**
- 3 **Review PIC status info**

Set Instrument Login

Please enter the instrument Personal Identification Code (PIC) you will use to log in to instruments connected to SMRT Link.

1

PIC:

Enter alphanumeric PIC

Enter an alphanumeric PIC (minimum 8 characters)

Confirm PIC:

Re-enter your PIC

Save PIC

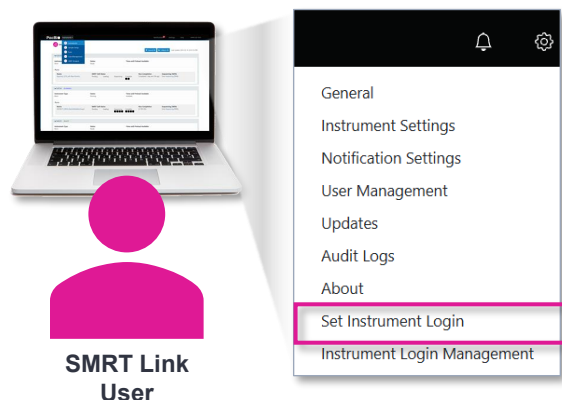
Set Instrument Login – Instruments tab

- Allows SMRT Link users to set, change, or reset their own PIC for instrument authentication
- Displays PIC criteria and requirements
- Provides feedback on PIC validation
- Informs the user if their PIC has expired or if their login is locked

Login mode setup and authentication workflow overview for SMRT Link Users:

A. Set Instrument Login settings

Before using login mode, users must first create a unique Personal Identification Code (PIC)¹



Navigate to SMRT Link Settings
> Set Instrument Login

- 1 Create Personal Identification Code (PIC)
- 2 Confirm PIC and click Save PIC
- 3 Review PIC status info

Set Instrument Login

Please enter the instrument Personal Identification Code (PIC) you will use to log in to instruments connected to SMRT Link.

PIC:

Enter alphanumeric PIC

Enter an alphanumeric PIC (minimum 8 characters)

2

Confirm PIC:

Re-enter your PIC

Save PIC

Important: Once an instrument PIC is set, it cannot be retrieved. You can only change it. Make sure to remember your PIC or store it securely.

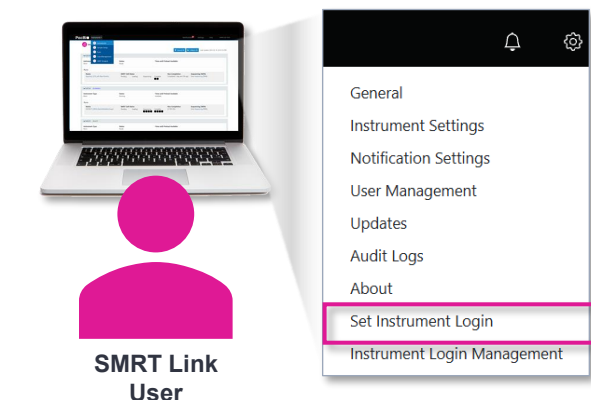
Set Instrument Login – Instruments tab

- Allows SMRT Link users to set, change, or reset their own PIC for instrument authentication
- Displays PIC criteria and requirements
- Provides feedback on PIC validation
- Informs the user if their PIC has expired or if their login is locked

Login mode setup and authentication workflow overview for SMRT Link Users:

A. Set Instrument Login settings

Before using login mode, users must first create a unique Personal Identification Code (PIC)¹



Navigate to SMRT Link Settings
> Set Instrument Login

- 1 Create Personal Identification Code (PIC)
- 2 Confirm PIC and click Save PIC
- 3 Review PIC status info

Set Instrument Login

Instrument user name:  john.doe

By default, Instrument username
= SMRT Link username

Current PIC: 



PIC Status: Expires on 08/18/2027

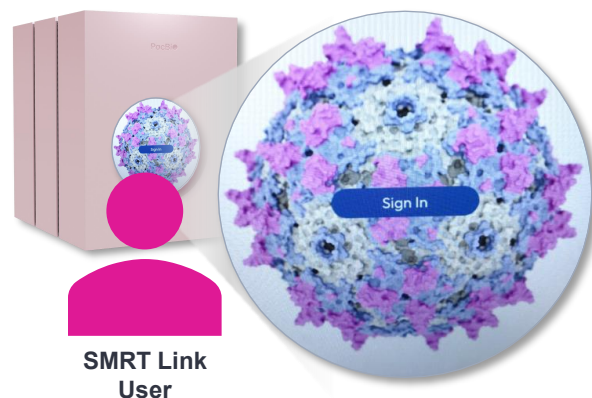
New PIC

Optional: Change your PIC by
clicking on New PIC

Login mode setup and authentication workflow overview for SMRT Link Users:

B. Vega user identification and authentication procedure

To use login mode, users must sign into Vega system using their instrument username and PIC

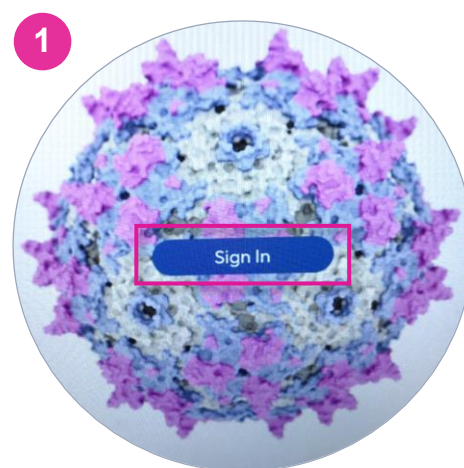


Start from Vega system login screen

1 Click **Sign In** button

2 Enter **username + PIC** and click **Apply to authenticate**

3 Operate Vega system within **authenticated session**



Click **Sign In** on Vega system login screen

- If login mode is enabled, users **must log in** prior to operating a Vega instrument



Enter instrument **Username¹** + **PIC** (Personal identification code)

- PIC should be **unique** for each authorized user



Operate Vega system within **authenticated session**

- Upon successful login, on-instrument events enter the **audit trail** and can be attributed to specific users¹

Note: If there are multiple failed login attempts, then an **Account Locked Out** message will appear in **SMRT Link Settings > Set Instrument Login** page

Account Locked Out

Your account has been locked due to multiple failed login attempts. Please contact an administrator of SMRT Link to unlock your account.

¹ Upon successful login, username will appear below the Vega instrument name on the main touchscreen display.

² **Note:** In Vega system v1.2 and SMRT Link v26.2, by default a user's instrument username is the same as their SMRT Link username.



Vega system v1.2 applications & protocol updates

HiFi library prep protocols are updated to support reduced DNA input mass requirements for Vega SPRQ-Nx chemistry

DNA input requirements for WGS library prep are reduced from 2 µg to 500 ng per acquisition for Vega SPRQ-Nx chemistry¹



Prior Procedure & checklist protocol documentation (Vega v1 chemistry)



gDNA input mass into library prep	Sequel II® and Sequel IIe	Vega	Revio SPRQ™-Nx chemistry)
Total DNA per SMRT® Cell**	1 µg	2 µg	500 ng
**If multiplexing, the total mass must be equivalent to the numbers indicated above. If using SRE, 500 ng per sample must be used. If bypassing SRE, no less than 20 ng should be used for an individual sample going into library preparation.			
DNA quality recommendation		Femto Pulse genome quality number (GQN)	
DNA size distribution (Femto Pulse system)	70% ≥10 kb (GQN _{10 kb} ≥7.0) & 50% ≥30 kb (GQN _{30 kb} ≥5.0)	Lower quality DNA may be used with the expectation of lower sequencing yields	
DNA fragment size recommendations			
DNA shearing	Automated pipette-tip shearing (preferred DNA shearing method)		
Target fragment lengths	15–20 kb		

Updated Procedure & checklist protocol documentation (Vega SPRQ-Nx chemistry)



Genomic DNA input	Sequel II® and Sequel IIe	SPRQ™ /SPRQ-Nx chemistry
Minimum DNA mass*	1 µg per SMRT Cell	500 ng per acquisition
*Multiplexing samples can lower per sample genomic DNA input requirements <i>if excluding</i> SRE treatment. The total mass of all multiplexed samples must be equivalent to the numbers indicated above (e.g. 500 ng for SPRQ chemistries).		
Library prep with SMRTbell prep kit 3.0		
Number of libraries supported per kit		24
Workflow time for manual preparation of 8 samples or fewer**		
• Short read eliminator (optional, size-selection)		2.5 hours
• Library prep with SMRTbell prep kit 3.0		3.5 hours

DNA input requirements for HiFi library prep are the **same** for Vega and Revio systems with **SPRQ-Nx chemistry**

HiFi library prep protocols are updated to support reduced DNA input mass requirements for Vega SPRQ-Nx chemistry (cont.)

For sample setup ABC¹ post-binding cleanup step, purified Vega SPRQ polymerase-bound SMRTbell complexes are eluted in a reduced volume of Loading buffer (25 µL instead of 50 µL)



Prior Procedure & checklist protocol documentation (Vega v1 chemistry)



Post-binding cleanup with 1X SMRTbell cleanup beads			
5.13	Add 100 µL of resuspended, room-temperature SMRTbell cleanup beads to each sample		
5.14	Pipette-mix the beads until evenly distributed and quick-spin if necessary to collect all liquid from the sides of the tube.		
5.15	Incubate at room temperature for 10 minutes to allow DNA to bind beads		
5.16	Place sample on an appropriate magnet and allow beads to separate fully from the solution		
5.17	Slowly remove the cleared supernatant without disturbing the beads. Discard the supernatant. DO NOT USE EtOH. Proceed immediately to the elution. It is important not to let the beads dry out.		
5.18	Remove sample from the magnet and immediately add Loading buffer to each tube and resuspend the beads by pipette mixing.		
	Revio SPRQ polymerase kit	Vega polymerase kit	
	Loading buffer	25 µL	50 µL
5.19	Quick-spin the samples to collect any liquid from the sides of the tube.		

Updated Procedure & checklist protocol documentation (Vega SPRQ-Nx chemistry)



Post-binding cleanup with 1X SMRTbell cleanup beads			
5.13	Add 100 µL of resuspended, room-temperature SMRTbell cleanup beads to each sample		
5.14	Pipette-mix the beads until evenly distributed and quick-spin if necessary to collect all liquid from the sides of the tube.		
5.15	Incubate at room temperature for 10 minutes to allow DNA to bind beads		
5.16	Place sample on an appropriate magnet and allow beads to separate fully from the solution		
5.17	Slowly remove the cleared supernatant without disturbing the beads. Discard the supernatant. DO NOT USE EtOH. Proceed immediately to the elution. It is important not to let the beads dry out.		
5.18	Remove sample from the magnet and immediately add Loading buffer to each tube and resuspend the beads by pipette mixing.		
	Revio/Vega SPRQ polymerase kit	Vega polymerase kit (non-SPRQ)	
	Loading buffer	25 µL	50 µL
5.19	Quick-spin the samples to collect any liquid from the sides of the tube.		

For Vega SPRQ polymerase and Revio SPRQ polymerase, elute cleaned complex in 25 µL of Loading buffer

¹ ABC = Annealing / binding / cleanup sample setup steps for preparing SMRTbell library of sequencing on PacBio long-read systems.
² Refer to latest PacBio Procedure & checklist protocol [documentation](#) for up-to-date guidance on application-specific sequencing preparation instructions.

Vega system sequencing prep core workflows remain the same for SPRQ-Nx chemistry (cont.)

No changes to Vega run setup and on-instrument/off-instrument data analysis procedures



Follow **existing** Vega run setup and HiFi data analysis procedures



Vega system v1.2 on-plate loading concentration (OPLC) recommendations

Updated OPLC recommendations¹ for 1 – 2 kb inserts sizes to achieve SMRT Cell target loading ranges

Application	Application subtype	Library insert size	OPLC	Run time	Target Loading level	HiFi reads or yield per acquisition
Whole genome sequencing	Human WGS	15 – 20 kb	200 – 300 pM	24 hours	50 – 75%	80 – 90 Gb
	Microbial assembly	15 – 20 kb	200 – 300 pM	24 hours	50 – 75%	80 – 90 Gb
	Other WGS	10 – 15 kb	200 – 300 pM	24 hours	50 – 75%	70 – 80 Gb
		15 – 20 kb	200 – 300 pM	24 hours	50 – 75%	80 – 90 Gb
Low DNA input	Ampli-Fi sequencing	5 – 10 kb	100 – 140 pM	24 hours	50 – 75%	35 – 70 Gb
RNA sequencing	Kinnex single-cell RNA	15 – 20 kb	80 – 130 pM	24 hours	50 – 75%	80 – 90 Gb
	Kinnex full-length RNA	15 – 20 kb	80 – 130 pM	24 hours	50 – 75%	80 – 90 Gb
Viral sequencing	AAV sequencing	2 – 5 kb	200 – 300 pM	24 hours	50 – 75%	6 – 8 M reads
Metagenomics	Kinnex 16S rRNA	15 – 20 kb	80 – 130 pM	24 hours	50 – 75%	80 – 90 Gb
	Shotgun metagenomic profiling or assembly	7 – 10 kb	200 – 300 pM	24 hours	50 – 75%	35 – 70 Gb
Targeted sequencing	500 bp – 1 kb amplicons	500 bp – 1 kb	400 – 600 pM	2 hours	55 – 70%	6 – 8 M reads
	1 – 2 kb amplicons	1 – 2 kb	100 – 200 pM	4 hours	55 – 70%	6 – 8 M reads
	2 – 5 kb amplicons	2 – 5 kb	100 pM	12 hours	50 – 75%	6 – 8 M reads
	≥5 kb amplicons	5 – 10 kb	200 – 300 pM	24 hours	50 – 75%	35 – 70 Gb
	Hybrid capture	5 – 10 kb	200 – 300 pM	24 hours	50 – 75%	35 – 70 Gb

Kinnex SC RNA, FL RNA and 16S target OPLC was previously 130 – 160 pM

Previously, target OPLC was 400 pM for <1 kb amplicons and 200 – 300 pM for 1 – 5 kb amplicons

For 0.5 – 2 kb amplicons, recommended target loading level is 55 – 70% to minimize chances of overloading



Vega system v1.2 user experience improvements

Vega system v1.2 release notes (103-892-200)

Refer to Vega system release notes for summary of new features & updates, fixed issues, and known issues¹

Vega™ system instrument software release notes (v1.2)

PacBio

Supported SMRT® Link versions

Vega instrument software v1.2 is compatible with SMRT Link v26.2 and SMRT Link Cloud.

New features and updates

The Vega system instrument software v1.2 introduces support for the new SPRQ™-Nx chemistry, shorter runtimes, higher yields, and 21 CFR Part 11 compliance.

- Support for 4- and 2-hour runs to enable single-shift sequencing of 0.5–2 kb inserts.
- New SPRQ-Nx chemistry support unlocks lower input requirements and higher yields. Note, multi-use SMRT® Cells are not supported.
- New login mode for Vega allows users to optionally trace on-instrument actions to an individual user.
- Updated DeepConsensus model trained on SPRQ-Nx data improves HiFi sequencing accuracy. For optimal variant calling performance at 20x coverage, use DeepVariant v1.10.0.
- Updated on-instrument methylation calling using jasmine v26.2 including models for SPRQ-Nx chemistry and a model for strand-specific ShmC detection at CpG sites. See jasmine changelog for additional details: <https://github.com/PacificBiosciences/jasmine#changelog>.

System safeguards

- Added a touchscreen warning when a user attempts to restart or shut down the instrument while post-primary analysis is in progress, to help prevent accidental data loss. Restarting or shutting down the instrument while a network transfer is in progress may interrupt the transfer and cause data loss. Please confirm no data transfer is in progress before restarting or shutting down the instrument.
- The instrument no longer allows the connected SMRT Link server to be changed while a user is logged in or a run is in progress.

BAM output improvements

- **Feature Request:** Output BAM files now include LIBRARYTYPE=<LibraryType> in the header. This enables clear identification if a collection was processed for a specific library type. LibraryType options are Standard, AAV, and masSeq.
- The unused 0x4 "single-stranded" fail_flag bit is no longer included in BAM outputs. Single-strand reads generated in STRAND consensus mode will continue to be output in hifi_reads.bam without the fail_flag bit set.

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PN 103-892-200 REV 01 (August 2026)

PacBio

New Features and Updates



Fixed Issues



Known Issues



Vega system v1.2 new features and updates – Examples

New Features and Updates



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BAM output improvements

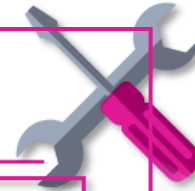
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Vega system v1.2 fixed issues – Examples

Fixed Issues

- Fixed an issue where the Q30+ bases statistic is missing in SMRT Link Run Details for runs that use STRAND consensus mode.
- On-instrument 6mA calling is now supported for runs that use STRAND consensus mode. Note, *jasmine* 5mC CpG methylation models require both strands; therefore, 5mC CpG calls are not reported when using STRAND consensus mode.
- Fixed an issue where if a user aborted a run within the first three minutes of data acquisition, a subsequent run could fail if the instrument is not first restarted.
- Added support for configuring a non-standard SSH port when setting up a data transfer scheme. Previously, transfers were limited to the standard port 22.
- Fixed an issue where some SSH (srs) data transfers could fail with a checksum mismatch error, even though the file had been transferred successfully.
- Fixed an issue where selecting "Export logs" from IUI resulted in a network error.



Vega system v1.2 known issues – Examples



Known Issues

- If login mode is enabled, when editing the PIC and Username fields on the instrument sign-in screen, the text cursor will insert a new character when typed and then move to the end of the field.
- When a cloud storage bucket (e.g. AWS S3) is configured to require server-side encryption (SSE), the transfer may fail or the transferred file may be corrupted (checksum mismatch). Support for configuring server-side encryption within the transfer scheme is not yet available in this release. Please contact PacBio Support to apply a custom transfer configuration enabling server-side encryption.

Known Issues





Vega system v1.2 example sequencing performance

Vega system v1.2 + SPRQ-Nx chemistry example performance

SPRQ-Nx chemistry shows excellent HiFi sequencing performance that meets or exceeds Vega system specifications¹

Application								
Whole genome sequencing ²	HiFi yield (Gb)	HiFi Reads (M)	HiFi Length (kb)	HiFi Read QV	Loading level	SNV F1	INDEL F1	SV F1
HG002 17 kb Run 1	99.9	5.7	17.4	35	63	0.9986	0.9898	0.9706
HG002 17 kb Run 2	99.9	5.8	17.1	36	64	0.9986	0.9886	0.9693
HG002 17 kb Run 3	99.9	5.8	17.2	35	67	0.9986	0.9891	0.9695

Application						
Targeted amplicon sequencing ³	Run time (hours)	HiFi reads (M)	HiFi length (kb)	HiFi read QV	Loading level	Product specifications
0.5 kb amplicon	2 hours	8.6	0.54	72	68%	6 – 8 M HiFi reads
1 kb amplicon	2 hours	7.7	1.04	56	65%	6 – 8 M HiFi reads
2 kb amplicon	4 hours	9.1	2.22	45	70%	6 – 8 M HiFi reads

¹ See [Vega specifications sheet \(102-326-625\)](#) for expected HiFi yield performance range for different library insert sizes and applications. For 15 – 20 kb library insert sizes run using a 24-hour movie time, the specified HiFi yield range is 80 – 90 Gb of HiFi data per acquisition when using Vega SPRQ-Nx chemistry. For 0.5 – 2 kb library insert sizes run using movie (run) times shown in the above table, the specified HiFi yield range is 6 – 8 million HiFi reads per acquisition. **Note:** HiFi yield is dependent on library quality and sequencing preparation procedures. Specified yields are based on high-quality samples prepared following best practices.

² Example data shown are for the same HG002 17 kb WGS library run on a Vega system with SPRQ-Nx chemistry (24-hour acquisition time; 200 pM on-plate loading concentration) on three different Vega SMRT Cells. Variant calling performed using [PacBio WGS variant pipeline](#) WDL v3.2.1 [DeepVariant 1.10 [GIAB v4.2.1 small variant benchmark; GIAB T2TQ100 v1.1 SV benchmark]].

³ Example data shown are for amplicon libraries run on a Vega system with SPRQ-Nx chemistry (**500 bp amplicon:** 2-hour acquisition time; 500 pM OPLC; **1 kb amplicon:** 2-hour acquisition time; 200 pM OPLC; **2 kb amplicon:** 4-hour acquisition time; 150 pM OPLC;).

Vega system v1.2 + SPRQ-Nx chemistry example performance (cont.)

SPRQ-Nx chemistry shows excellent HiFi sequencing performance that meets or exceeds Vega system specifications¹

Application							
RNA sequencing	HiFi yield (Gb)	HiFi reads (M)	HiFi length (kb)	HiFi read QV	Loading level	Segmented reads ⁵ per acquisition	Product specifications
Kinnex full-length RNA, UHRR ²	99.9	6.5	15.3	34	63%	47.9 M	≥40 M S-reads per acquisition
16S sequencing	HiFi yield (Gb)	HiFi reads (M)	HiFi length (kb)	HiFi read QV	Loading level	Segmented reads ⁵ per acquisition	Product specifications
Kinnex full-length 16S rRNA, 384-plex ATCC MSA1001, 1003 ³	99.9	5.2	19.3	34	67%	60.6 M	≥40 M S-reads per acquisition
PureTarget sequencing	HiFi yield (Gb)	HiFi reads (M)	HiFi length (kb)	HiFi read QV	Loading level	Target coverage per sample	Product specifications
PureTarget 2.0 repeat expansion panel 2.0, 24-plex whole blood / Coriell cell line ⁴	8.7	1.5	5.8	45	22%	469	Mean target coverage 100-fold or greater per 1 ug DNA per sample Min. target coverage 20-fold per sample

¹ See **Vega specifications sheet** ([102-326-625](#)) for expected HiFi yield performance range for different library insert sizes and applications. For 15 – 20 kb library insert sizes run using a 24-hour movie time, the specified HiFi yield range is 80 – 90 Gb of HiFi data per acquisition when using Vega SPRQ-Nx chemistry. **Note:** HiFi yield is dependent on library quality and sequencing preparation procedures. Specified yields are based on high-quality samples prepared following best practices.

² Kinnex full-length RNA UHRR libraries were run on a Vega system with SPRQ-Nx chemistry (24-hour acquisition time; 100 pM on-plate loading concentration).

³ Kinnex full-length 16S rRNA, ATCC MSA1001 + MSA 1003 libraries were run on a Vega system with SPRQ-Nx chemistry (24-hour acquisition time; 80 pM on-plate loading concentration).

⁴ PureTarget 2.0 repeat expansion panel 24-plex whole blood/Coriell cell line libraries (2 µg of input DNA per sample) were run on a Vega system with SPRQ-Nx chemistry (24-hour acquisition time).

⁵ Segmented reads ("S-reads") are generated from bioinformatically splitting Kinnex concatenated HiFi reads using the SMRT Link read segmentation data processing utility.

Vega system v1.2 key specifications with SPRQ-Nx chemistry

Vega system v1.2 data throughput

Library	Run time ¹	Q30+ bases	HiFi yield per acquisition ²	Methylation
0.5–1 kb	2 hours	95%	6 – 8 Million reads	5mC + 5hmC at CpG sites and 6mA ³ 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 Cell acquisitions.

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.

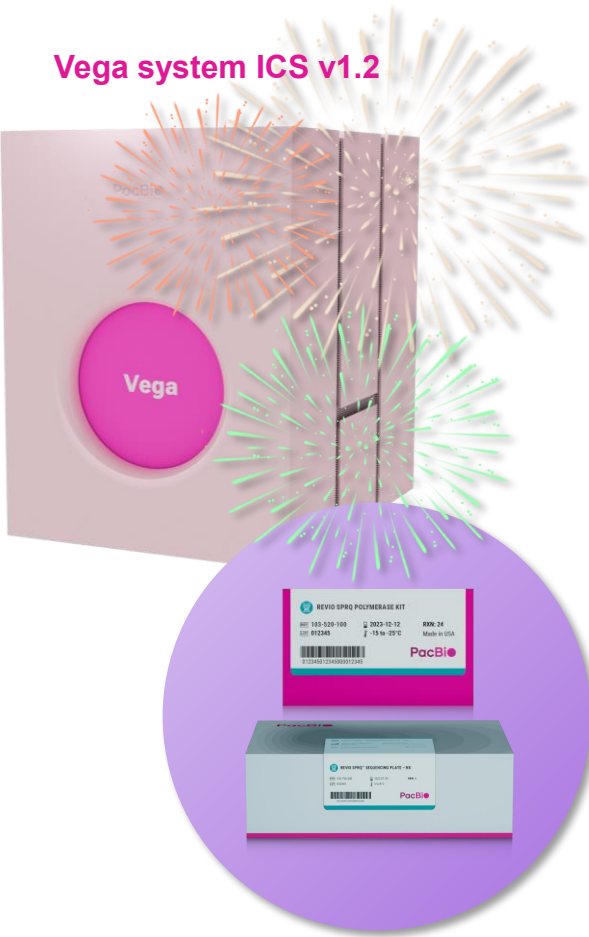
Vega system v1.2 key applications and sample throughput

Library	Sample	Expected coverage ⁴	Samples per acquisition	Samples per year ⁵
0.5–5 kb	Amplicon	50×	>1,000	200,000
5–10 kb	Microbial genome	30×	384	76,800
5 -10 kb	PureTarget	200×	96	19,200
15–20 kb	Human genome	20×	1.5	300
15–20 kb	Human Methylation profiling	5×	6	1,200
15–20 kb	Transcriptome with Kinnex full-length RNA kit	10 million reads	4	800

⁴ Expected coverages are estimates.

⁵ Annual throughput is estimated and based on 200 Vega SMRT Cell acquisitions.

Vega system ICS v1.2



Vega system v1.2
+
SPRQ-Nx chemistry



Vega system v1.2 summary

Vega system v1.2 + SPRQ-Nx chemistry enables a richer and cost-effective HiFi workflow on a benchtop platform

VEGA

v1.1

HiFi within reach

65 Gb per run

2000 ng DNA input

12 or 24-hour run times

5mC and 6mA methylation calling

\$1,100 per run

VEGA

v1.2 + SPRQ-Nx chemistry

Benchtop HiFi supercharged

90 Gb per run

500 ng DNA input

2, 4, 12 or 24-hour run times

5mC, 5hmC and 6mA methylation calling

\$995 per run

Vega system v1.2 + SPRQ-Nx chemistry enables a richer and cost-effective HiFi workflow on a benchtop platform

VEGA
SPRQ-Nx



More data per run
(90 Gb) and 40%
lower cost per Gb

More affordable
long-read genome



5hmC in
every run

Built-in multiomic
insights



4x lower DNA
input

More accessible sample types



Stronger
compliance support

User authentication, audit
trails, and access management

VEGA

+ *SPRQ-Nx chemistry*

HiFi within reach

Benchtop

1 SMRT Cell per run

90 Gb per run

500 ng DNA input

2, 4, 12 or 24-hour run times

5mC, 5hmC and 6mA methylation calling

\$995 per run with SPRQ-Nx chemistry¹

Revio

+ *SPRQ-Nx chemistry*

HiFi at scale

Production

Up to 3 acquisitions per SMRT cell
and 4 acquisitions per run

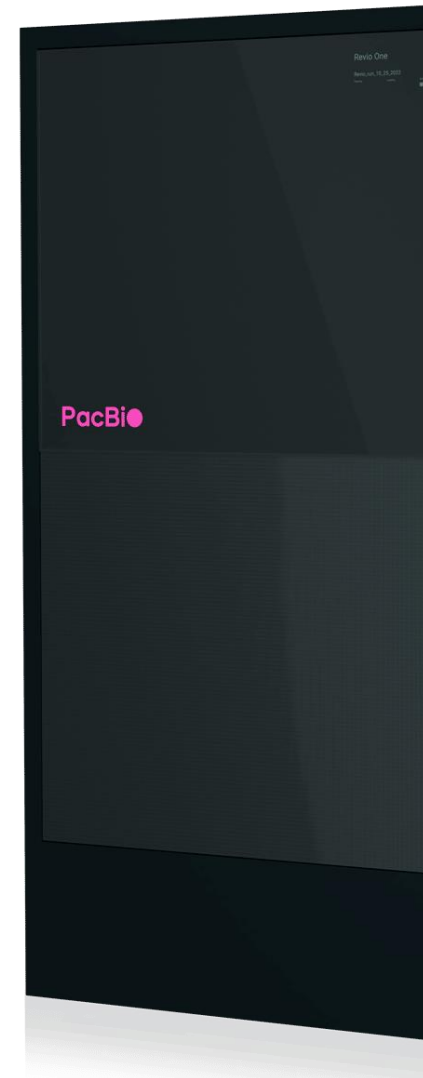
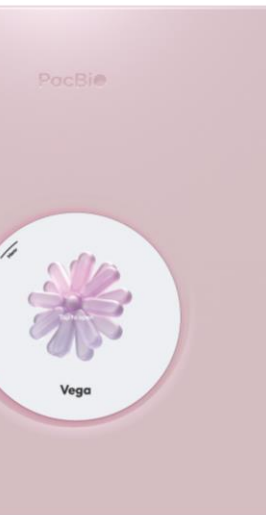
480 Gb per run (4 acquisitions)

500 ng DNA input

12, 24, or 30-hour run times

5mC, 5hmC and 6mA methylation calling

\$690 per acquisition with SPRQ-Nx chemistry¹



Vega system v1.2 vs. Revio system v13.5 sample throughput comparison

See *What can you do with one HiFi run?* ([102-326-578](tel:102-326-578))



Vega + SPRQ-Nx
HiFi within reach



Revio + SPRQ-Nx
HiFi at scale

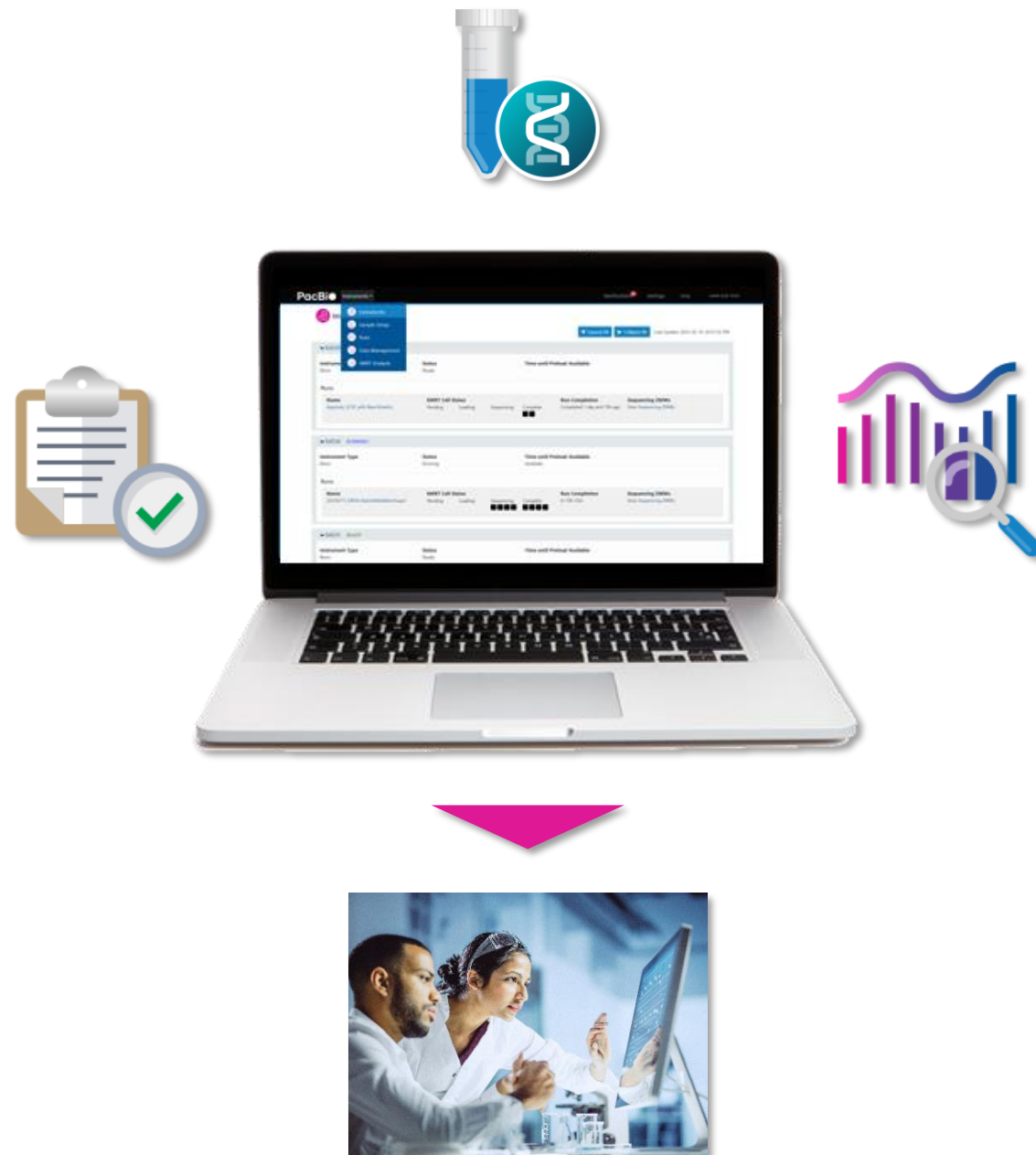
Application	Samples per run		
	1 acquisition	1 acquisition	4 acquisitions
Whole genome sequencing			
Human genome (20× coverage)	1.5	2	8
Human methylation profiling (5× coverage)	6	8	32
De novo assembly (1 Gb genome)	3	4	16
Microbial de novo assembly (2 Gb total sum of genomes)	384	384	1,536
Targeted panels			
Amplicon sequencing	>1,000	>1,000	>4,000
Target enrichment			
20 Mb panel	12	16	64
2 Mb panel	72	96	384
PureTarget panel	96	96	384
RNA sequencing			
Kinnex single-cell RNA sequencing	1 (up to 10,000 cells)	1 (6,000 – 10,000 cells)	4 (6,000 – 10,000 cells)
Kinnex full-length RNA sequencing			
5M reads	8	12	48
10M reads	4	6	24
Microbial			
Shotgun metagenomic profiling	96 communities	128 communities	512 communities
Shotgun metagenomic assembly	12 communities	16 communities	64 communities
Kinnex 16S rRNA	1,536 communities	1,536 communities	6,144 communities

All sample throughputs are estimates for either the Vega system with 1 acquisition or the Revio system using SPRQ or SPRQ-Nx chemistry with both 1 or 4 acquisitions. 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. PureTarget panel assumes >100× mean per target and Revio throughput assumes automated library prep.

§ Part 2:

SMRT Link v26.2 + SMRT Link Cloud v26.2

1. SMRT Link v26.3 key features & benefits
2. New SPRQ-Nx chemistry support
3. SMRT Link v26.2 21 CFR Part 11 support
4. SMRT Link v26.2 user experience improvements
 - Redo Demux





SMRT Link v26.2 key features & benefits

SMRT Link v26.2 key features and updates

SMRT Link v26.2 makes HiFi sequencing easier with Vega SPRQ-Nx chemistry support, stronger compliance support and data analysis workflow usability improvements



SPRQ-Nx chemistry support

- Support for new Vega SPRQ-Nx chemistry and consumables



21 CFR Part 11 support

- New Instrument Login Management feature to support 21 CFR Part 11 compliance by customer end users



Data analysis workflow usability improvements

- New Redo Demultiplexing data utility performs undo step from Undo Demultiplexing followed by the full Demultiplex Barcodes workflow





SMRT Link v26.2 SPRQ-Nx chemistry support

SMRT Link v26.2 Run Design page includes support for Vega SPRQ-Nx consumables

Plate field dropdown selection menu includes new Vega SPRQ sequencing plate – Nx¹

PacBio Select module ▾

Runs / Create New

New Run Design

Run Information

Instrument Type

☐ Revo ☒ Vega

Run Name

Run 07.21.2026 18:02

Plate 1 Required ⓘ

Vega sequencing plate

Vega SPRQ sequencing plate - Nx

Transfer Subdirectory ⓘ

Sample Information

▼ Plate 1, Well A01:

Import from Sample Setup [Select Sample](#)

Application Required

Well Name ⓘ Required

Well Comment

Library Type Required Standard

Insert Size (bp) Required

Library Concentration (pM) Required

Movie Acquisition Time (hours) 24

Samples

Sample is indexed ☒ YES ☐ NO

Indexes Required SMRTbell adapter indexes

Biosample names ⓘ Required Interactively From a File

No cha Run



SMRT Link v26.2 21 CFR Part 11 support

How to access SMRT Link audit logs

Admin users can access audit logs through SMRT Link Settings menu¹

How to access audit logs

- 1. Log into SMRT Link using a user profile with Admin privileges.
- 2. Click **Settings** button.
- 3. Select **Audit Logs**.

Access to Audit Logs page is restricted to users with the Admin role

The screenshot shows the PacBio SMRT Link web interface. The top navigation bar includes the PacBio logo, a 'Select module' dropdown, a notification bell, a settings gear icon (labeled with a blue circle '2'), a 'User Guide' link, and a user profile dropdown (labeled with a blue circle '1') showing 'admin (Admin)'. The settings menu is open, showing options: General, Instrument Settings, Notification Settings, User Management (labeled with a blue circle '3'), Updates, Audit Logs (highlighted with a pink box), and About. The main content area shows an 'Instruments' section with a card for instrument '84006' in 'RUNNING' status. Below this is a 'Runs' table with columns for Name, SMRT Cell Status, and Run Completion. The table contains one row for 'Revio_example_run_name'.

Instrument Type	Status	Time until preload available
Revio	Running	Available

Runs	SMRT Cell Status	Run Completion			
Name	Pending	Loading	Sequencing	Complete	In
Revio_example_run_name			■	■ ■ ■	In 1h 52m

Audit Logs page displays a table of recorded activity across all connected instruments

Each entry includes: Entry Number, Date and Time (UTC), User ID, Source, Event Name, Description, and Software Version

PacBio

Select module ▾

🔔

⚙️

User Guide

👤 admin (Admin)

Settings

Sections

General

Instrument Settings

Notification Settings

User Management

Updates

Audit Logs

About

Audit Logs

Can view all activities recorded in SMRT Link sorted by, for example, timestamp

Audit table information can be filtered by applying column-specific filter settings

Download ⓘ

Displaying rows 1 to 11 out of 101 (scroll to load more)

Entry Number	Date and Time (UTC) ⬆️ ▾	User ID ⬆️ ▾	Source ⬆️ ▾	Event Name ⬆️ ▾	Description ⬆️ ▾
1	2026-04-04, 12:53:29 AM	pbinstrument	SMRT Link	Run Data Updated	The XML data for run 20260
2	2026-04-04, 12:53:29 AM	pbinstrument	SMRT Link	Run Data Updated	The XML data for run 20260
3	2026-04-04, 12:51:56 AM	pbinstrument	SMRT Link	Run Data Updated	The XML data for run 20260
4	2026-04-04, 12:51:56 AM	pbinstrument	SMRT Link	Run Data Updated	The XML data for run 20260
5	2026-04-04, 12:48:38 AM	pbinstrument	SMRT Link	Run Completed	Run '20260402_84030_SMB_

Audit logs capture system and user actions performed in SMRT Link and on connected instruments, including who performed the action, what action was performed, where it occurred, and when it occurred.

Audit log entries include both system-generated and user-performed actions

User ID field identifies whether an action was performed by a PacBio user or by the PacBio system ICS

Action generated by	User ID type	Example event or activity
PacBio system ICS	SYSTEM ¹	• Actions that affect instrument status • E.g., "run state changed" or "data transfer initiated"
	pbinstrument ¹	• Actions that affect SMRT Link status • E.g., "run data updated"
PacBio (human) end-user	Instrument user (e.g., "Jane_Doe") ²	• On-instrument user actions • E.g., electing to start a run with expired consumables
	SMRT Link user (e.g., "John_Smith")	• In-SMRT Link user actions • E.g., creating a new run design or a new analysis job

Displaying rows 901 to 912 out of 1701 (scroll to load)					
Entry Number	Date and Time (UTC)	User ID	Source	Event Name	Description
901	2026-04-17, 09:...	SYSTEM	Vega 21016	Run State Changed	Run state changed from Idl...
902	2026-04-17, 09:...	Jane_Doe	Vega 21016	Expired consumable	User 'Jane_Doe' has elected...
903	2026-04-17, 09:...	Jane_Doe	Vega 21016	Expired consumable	User 'Jane_Doe' has elected...
904	2026-04-17, 09:...	Jane_Doe	Vega 21016	Expired consumable	User 'Jane_Doe' has elected...
905	2026-04-17, 09:...	Jane_Doe	Vega 21016	Humidity low	User 'Jane_Doe' has elected...
906	2026-04-17, 09:...	pbinstrument	SMRT Link	Run Data Updated	The XML data for run 2026...
907	2026-04-17, 09:...	pbinstrument	SMRT Link	Run Data Updated	The XML data for run 2026...
908	2026-04-17, 09:...	pbinstrument	SMRT Link	Run Data Updated	The XML data for run 2026...
909	2026-04-17, 09:...	pbinstrument	SMRT Link	Run Data Updated	The XML data for run 2026...
910	2026-04-17, 09:...	pbinstrument	SMRT Link	Run Data Updated	The XML data for run 2026...
911	2026-04-17, 09:...	pbinstrument	SMRT Link	Run Data Updated	The XML data for run 2026...
912	2026-04-17, 09:...	John_Smith	SMRT Link	Run Design Created	Run 2026_0417_84025_10...

¹ For actions taken by the PacBio system ICS that affect the instrument status, the User ID type ("SYSTEM") is taken from literal strings used in the system logs.
² In Revio system ICS v13.5 + SMRT Link v26.2, on-instrument actions performed by a human end-user are recorded in audit logs with User ID = "instrument_user". In future software versions, the User ID will reflect the (human) end-user's actual ID username.

How to download SMRT Link audit report

Admin users can download audit report through SMRT Link Audit Logs page

How to download audit report PDF

1. Click **Download** on Audit Logs page and wait for Audit Report PDF to be generated. This may take up to a few minutes.

PacBio

Select module ▾

User Guide

admin (Admin)

Settings

Sections

General

Instrument Settings

Notification Settings

User Management

Updates

Audit Logs

About

Audit Logs

Displaying rows 1 to 11 out of 101 (scroll to load more)

Entry Number	Date and Time (UTC) ▴ ▾	User ID ▴ ▾	Source ▴ ▾	Event Name ▴ ▾	Description ▴ ▾
1	2026-04-04, 12:53:29 AM	pbinstrument	SMRT Link	Run Data Updated	The XML data for run 20260
2	2026-04-04, 12:53:29 AM	pbinstrument	SMRT Link	Run Data Updated	The XML data for run 20260
3	2026-04-04, 12:51:56 AM	pbinstrument	SMRT Link	Run Data Updated	The XML data for run 20260
4	2026-04-04, 12:51:56 AM	pbinstrument	SMRT Link	Run Data Updated	The XML data for run 20260
5	2026-04-04, 12:48:38 AM	pbinstrument	SMRT Link	Run Completed	Run '20260402_84030_SMB_

Download ⓘ

Sections

General

Instrument Settings

Audit Logs

Preparing Audit Report. This may take up to a few minutes. Please do not close this page.

Example Audit Report

PDF report reflects the filters that were applied to the SMRT Link audit table at the time of export.



Server: smrtlink-sms.nanofluidics.com
System ID: 5da74fe3-2183-461a-ae12-e870f7070032

Exported by: admin
Exported on: 2026-04-04 00:57:35 UTC

This PDF reflects the filters that were applied to the SMRT Link audit table at the time of export.

Entry Number	Date & Time (UTC)	User ID	Source	Event Name	Description	Software Version
1	2026-04-04 00:56:15 UTC	pbinstrument	SMRT Link	Run Data Updated	The XML data for run 2026_0403_84015_SID_Pack_testing_HG_3use_use1and2 (484e2025-7620-4c3e-a997-de76149208a1) was updated.	26.1.0.283967
2	2026-04-04 00:56:14 UTC	pbinstrument	SMRT Link	Run Data Updated	The XML data for run 2026_0403_84015_SID_Pack_testing_HG_3use_use1and2 (484e2025-7620-4c3e-a997-de76149208a1) was updated.	26.1.0.283967
3	2026-04-04 00:53:29 UTC	pbinstrument	SMRT Link	Run Data Updated	The XML data for run 20260304_84028_Hg002_RavenTroubleshooting_PkmidFloor (00aa0abc-b17a-4370-b7ce-4e2bd6656e96) was updated.	26.1.0.283967
4	2026-04-04 00:53:29 UTC	pbinstrument	SMRT Link	Run Data Updated	The XML data for run 20260304_84028_Hg002_RavenTroubleshooting_PkmidFloor (00aa0abc-b17a-4370-b7ce-4e2bd6656e96) was updated.	26.1.0.283967
5	2026-04-04 00:51:56 UTC	pbinstrument	SMRT Link	Run Data Updated	The XML data for run 20260304_84026_Hg002_RavenTroubleshooting_PkmidFloor (71ab16f7-62ed-43b3-aae4-d95c3491e5fc) was updated.	26.1.0.283967

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	Software Version
g002_RavenTrou loor 3-aae4-d95c3491	26.1.0.283967
30_SMB_dyeball- D5A2-dC_YY954 '302296_Take3' f-bac6-4a356d6a d on REV10	26.1.0.283967
rom Completing	13.5.0.284573
MB_dyeball-dG_Y 2-dC_YY954-167_ 96_Take3 f-bac6-4a356d6a	26.1.0.283967
MB_dyeball-dG_Y 2-dC_YY954-167_ 96_Take3 f-bac6-4a356d6a	26.1.0.283967
MB_dyeball-dG_Y 2-dC_YY954-167_ 96_Take3 f-bac6-4a356d6a	26.1.0.283967
MB_dyeball-dG_Y 2-dC_YY954-167_ 96_Take3 f-bac6-4a356d6a	26.1.0.283967

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	Software Version
h MB_dyeball-dG_Y 2-dC_YY954-167_ 96_Take3 f-bac6-4a356d6a	26.1.0.283967
h MB_dyeball-dG_Y 2-dC_YY954-167_ 96_Take3 f-bac6-4a356d6a	26.1.0.283967
0110_s1 in 83820 failed with after placement fter 2 cell resear or chip not 1":"Sensor chip st", "2":"Sensor chip not detected or chip not 5":"Sensor chip st", "6":"Sensor chip not detected or chip not - (Col: 4)	13.5.0.284573
h G2_21206_formul -435e-82ea-b34c ited.	26.1.0.283967
h G2_21206_formul -435e-82ea-b34c ited.	26.1.0.283967

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SMRT Link v26.2 user experience improvements

New SMRT Link v26.2 Redo Demultiplexing data utility allows easier re-analysis of multiplexed samples (cont.)

Redo Demultiplexing workflow (cont.)

SMRT Analysis / Create New Analysis

1. Select Data 2. Select Analysis

3 Job Name Required

Redo Demultiplexing Demo

Datasets

	Name	Demultiplexed Subsets
☐	HG002_Lib5-Cell1 (all samples)	2
☒	HG002_Lib2-Cell1 (all samples)	4 (all selected)

4 Analysis Application Required

Redo Demultiplexing

Import Analysis Settings Export

Associated Inputs

Barcode Set Required

SMRTbell adapter indexes

Assign Bio Sample Names to Barcodes Required

Interactively From a File

Demultiplexed Output Data Set Name Required

HG002_Lib2-Cell1 (all samples) (demux)

Same Barcodes on Both Ends of Sequence

YES NO

Advanced Parameters

5 Start

3. Specify **Job Name**.
4. Specify **Analysis Application** (→ 'Redo Demultiplexing') and **Barcode Set**. **Assign Bio Sample Names to Barcodes** and specify **Demultiplexed Output Data Set Name**. Optionally edit **Advanced Parameters**.

5. Click **Start**.

SMRT Link v26.2 release notes (103-891-800)

Refer to SMRT Link release notes for summary of new features & updates, fixed issues, and known issues¹

SMRT® Link release notes (v26.2)

PacBio

Supported instruments and chemistries

SMRT Link 26.2 supports the following:

Instruments	Instrument software
Revio® system	Instrument software v13.5, SPRQ™ and SPRQ-Nx chemistries
Vega™ system	Instrument software v1.2.0, all chemistries

The Sequel® II and IIe systems are not supported by SMRT Link v25+. An installation of SMRT Link v13.1 is required. See <https://www.pacb.com/support/software-downloads/> for details on earlier SMRT Link versions.

Refer to the SMRT Link installation guide v26.2 for detailed hardware and software requirements and installation instructions.

Users upgrading from 25.3 or earlier should also review the SMRT Link v26.1 release notes, which include changes not reflected in this document.

Supported data transfer options

- Direct transfers to network storage over an encrypted connection provided by SSH.
- Direct file transfer to cloud storage for: Amazon S3, Google Cloud Storage, and Microsoft Azure Blob Storage, and S3-compatible storage (including Oracle Cloud Object Storage and Cloudflare R2).

Notice: As of SMRT Link v26.1 unencrypted rsync daemon transfer schemes for Revio are no longer supported. File transfers using this option will fail. Transitioning to a supported transfer option such as SSH (srs) or direct to cloud is required.

New features and updates

SMRT Link v26.2 introduces support for the new SPRQ-Nx chemistry, shorter runtimes, and 21 CFR Part 11 compliance features.

- Added SMRT Link support for the Vega SPRQ-Nx reagents for use with the Vega SMRT® Cell tray. Multi-use SMRT Cells remain Revio-only.
- Added support for 2-hour and 4-hour movie times on Vega, enabling faster turnaround for shorter-insert libraries.
- SMRT Link now includes ShmC methylation reports for Vega. ShmC calls and per-read modification-probability distributions, introduced in SMRT Link 26.1 for Revio, are now available for Vega collections.
- Added on-instrument login mode for Vega, supporting 21 CFR Part 11 compliance. When enabled, users must set a Personal Identification Code (PIC) before performing on-instrument actions, and login and logout events are recorded in the instrument's audit trail. See the SMRT Link user guide for configuration details.
- New tamper detection for audit logs. SMRT Link admins can reset the audit trail once tampering has been detected and resolved.

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PN 103-891-800 REV 01 (August 2026)

PacBio



SMRT Link v26.2 new features and updates – Examples

New Features and Updates



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- New tamper detection for audit logs. SMRT Link admins can reset the audit trail once tampering has been detected and resolved.

Sample Setup and Run Design

- Removed Revio v1 chemistry from Run Design and Sample Setup, including the ABC Calculator. Historical runs and ABC Calculator records that use v1 chemistry remain viewable.

SMRT® Analysis

- **Feature Request:** Added the Redo Demultiplexing workflow, allowing users to re-run demultiplexing on an already demultiplexed parent dataset without having to run Undo demultiplexing first. The new workflow is packaged in the wdl-v2.zip. Direct execution requires `cromwell` and workflow-specific JSON input file.
- Legacy analysis workflow versions (previous implementations of Demultiplex Barcodes, Undo Demultiplexing, Read Segmentation, and Export Reads) are no longer shown in the standard SMRT Analysis application list, to reduce confusion between current and legacy pipeline versions.



SMRT Link v26.2 fixed issues – Examples

Fixed Issues

Page 3

- **Run Design:** Fixed an issue where duplicating a run carried over consumable metadata (plate lot, serial number, and expiry), which could cause unused wells on a new plate to be incorrectly labeled as “Used.”
- **Run Design:** Fixed an issue where SMRT Link could crash when creating a new run design using the “Kinnex 16S rRNA” Application together with the Export FASTQ analysis workflow.
- **Run Design:** Fixed an issue where a crash sometimes occurred when an invalid expiry date (for example, an out-of-range month) was entered for a plate or reagent kit.
- **Run Design:** Fixed an issue where viewing or editing the run design for a previously completed run intermittently displayed an error page instead of the read-only run design.
- **Run Design:** Fixed an issue where a PureTarget repeat expansion run design could be saved without a reference genome selected, instead of being blocked with a missing entry point error.
- **Run Details:** Fixed an issue where Run QC report PDF timestamps were always displayed in UTC; timestamps are now localized to the configured time zone.
- **Run Details:** Fixed an issue where a run name exceeding 255 characters could fail to import or crash the SMRT Link UI. Run names are now validated and limited to 255 characters in Run Design.
- **Data Management:** Fixed an issue where exporting a parent dataset (all samples in a collection) could fail because the export used the local file path instead of the dataset’s canonical location; this also affected the dataset merge and create functions.
- **SMRT Analysis:** Fixed an issue where Demultiplexing Barcodes (1ima) could fail to trim one base present in the barcode when demultiplexing with asymmetric barcodes in some cases.
- **SMRT Analysis:** Increased the default memory allocation for the Variant Calling workflow to reduce out-of-memory failures, particularly for SPRQ-Nx datasets.
- **SMRT Analysis:** Fixed an issue in the Demultiplex Barcodes workflow where users could not rename the



SMRT Link v26.2 known issues – Examples



Known Issues

- **Run Design:** When setting up a Run Design with auto-analysis using Read Segmentation, the Segmentation Adapter Set is not automatically set based on the selected application. Workaround: manually set the Segmentation Adapter Set to the appropriate value before saving the run design.
- **Run Design:** When duplicating a sample with incomplete fields, Plate 1 Well A01 may be assigned twice. Workaround: delete the duplicate entry before saving the run design.
- **Run Design:** Run Design may prompt about unsaved changes even when no changes were made or after the design has already been saved. Workaround: click OK on the prompt; the run design has been saved correctly.
- **Run Details:** In Revio runs that use Adaptive Loading, SMRT Link may underreport the displayed loading time for collections where loading extends beyond the configured default time of two hours. Sequencing results, run execution, instrument performance, and actual run duration are not affected.
- **Data Management:** In the Target Regions view, sorting by some columns may not sort correctly.
- **Data Management:** Sorting the Barcodes page by Barcode Type may fail.
- **SMRT Analysis:** Some fields in job reports are sorted alphabetically rather than numerically, including Demultiplexing's HiFi Reads values in the Barcode Data table, Target Enrichment's Mean Target Coverage values, and PureTarget repeat expansion's Number of Reads values.
- **SMRT Analysis:** When demultiplexing more than one dataset with shared barcoded samples, merging datasets prior to demultiplexing is not supported. Per-sample datasets should be merged after demultiplexing.
- **SMRT Analysis:** The PureTarget repeat expansion workflow may report per-target coverage values in `/call-pbreports_target_enrichment_puretarget/execution/target_cov_by_sample.csv` that are too high. Please use the recommended per-allele, per-sample coverage from the `puretarget.repeat_expansion_genotypes.csv` in the job `/outputs` or the Target Enrichment workflow.
- **SMRT Analysis:** Target Enrichment analyses may fail when BED files contain quotation marks. Workaround: remove quotes from column 4, or validate the BED file using `trgt validate`.



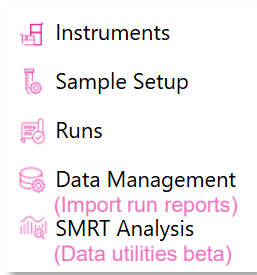
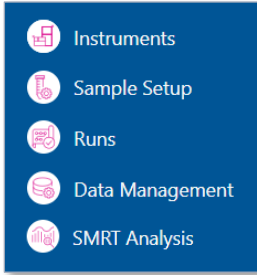
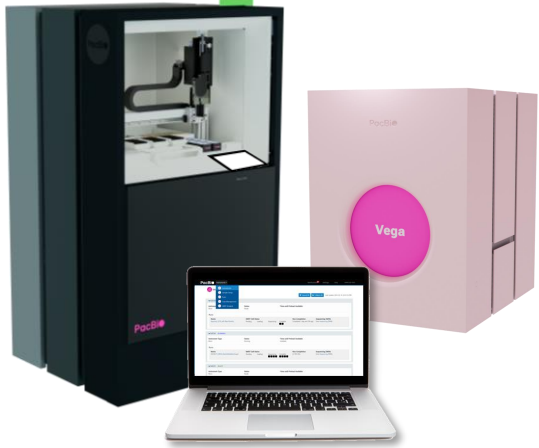


SMRT Link Cloud v26.2 SMRT Analysis support (Beta feature)

SMRT Link Cloud v26.2 SMRT Analysis support (Beta feature)

Vega system customers can optionally connect an existing cloud account (e.g., AWS) to SMRT Link Cloud to enable running core SMRT Analysis workflows in their own cloud computing environment^{1,2,3}

- Enables PacBio users to **start analysis jobs on a connected AWS account** using the SMRT Link Cloud interface
- SMRT Link Cloud v26.2 analysis support is limited to the following **data utility** workflows:
 - Demultiplex Barcodes
 - Export FASTQ
 - Read segmentation
 - Undo Demultiplexing
 - **Redo Demultiplexing (NEW)**
- SMRT Link Cloud v26.2 analysis support (beta) is enabled for Revio and Vega systems



Feature	SMRT Link	SMRT Link Cloud
Instrument management	Y	Y
Run setup, run monitoring, run QC	Y	Y
Push-button secondary analysis (SMRT Analysis)	Y	N
Data utilities (e.g., Demultiplex Barcodes)	Y	Beta ²
3 rd party and PacBio Compatible Partner analysis	Y	Y
API access	Y	Y

Beta feature

¹ SMRT Link Cloud is a PacBio-hosted and managed private workspace that provides support for instrument management, run setup, run monitoring, and run QC.

² SMRT Link Cloud v26.2 software includes the option to enable SMRT Analysis data utility features by configuring a connection to third-party cloud computing resources (BYOC; Bring Your Own Compute). **Note:** This BYOC capability to support data utilities is a **beta feature** in SMRT Link v26.2.

³ **Note:** SMRT Link Cloud v26.2 Data Management Import Data feature only supports importing Run Reports (*.reports.zip) files and does not support importing of other data types (e.g., HiFi reads, barcodes, references, or target regions (BED)).



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§ Part 3: Technical documentation & applications support resources



Revio and Vega system supported applications & protocols

Refer to PacBio Documentation website for the latest application-specific HiFi library preparation procedures

Sequencing method	Application	Protocol or Guide
Whole genome sequencing	Large genome & small (microbial) genome WGS ¹	Preparing whole genome and metagenome libraries using SPK 3.0 [102-166-600]
		Short Read Eliminator (SRE), DNA shearing, and cleanup for the Hamilton Microlab Prep system [103-424-100]
		Preparing whole genome libraries using the HiFi prep kit 96 [103-420-700]
		Automated HiFi prep 96 and HiFi ABC for the Hamilton NGS STAR MOA system [103-425-700]
		Preparing multiplexed whole genome and amplicon libraries using the HiFi plex prep kit 96 [103-418-800]
		Automated HiFi plex prep 96 for the Hamilton NGS STAR MOA system [103-425-800]
Low-DNA input sequencing	Ampli-Fi sequencing	Amplifying genomic DNA for SMRTbell library preparation and HiFi sequencing [103-648-000]
RNA sequencing	Kinnex full-length RNA	Preparing Kinnex libraries using Kinnex single-cell RNA kit [103-254-300]
	Kinnex single-cell RNA	Preparing Kinnex libraries using Kinnex full-length RNA kit [103-238-700]
Targeted sequencing	Amplicon sequencing	Preparing multiplexed amplicon libraries using SMRTbell prep kit 3.0 [102-359-000]
		Preparing multiplexed whole genome and amplicon libraries using the HiFi plex prep kit 96 [103-418-800]
	HiFi target enrichment sequencing	Preparing multiplexed amplicon libraries using SMRTbell prep kit 3.0 [102-359-000]
	PureTarget sequencing	Generating PureTarget libraries with PureTarget kit 24 manual protocol [103-740-700]
		Generating PureTarget libraries with PureTarget kit 96 automation protocol [103-740-800]
		Automated PureTarget kit 96 for the Hamilton NGS STAR MOA system [103-740-900]
Viral sequencing	Adeno-associated virus (AAV)	Preparing multiplexed AAV SMRTbell libraries using SPK 3.0 [102-126-400]
Metagenomics	Shotgun metagenomic assembly	Preparing whole genome and metagenome libraries using SPK 3.0 [102-166-600]
	Shotgun metagenomic profiling	Preparing multiplexed whole genome and amplicon libraries using the HiFi plex prep kit 96 [103-418-800]
	Kinnex full-length 16S	Preparing Kinnex libraries from 16s rRNA amplicons [103-238-800]

PacBio system and SMRT Link documentation

Revio system documentation

- Revio system brochure ([102-326-543](#))
- Revio system instrument control software release notes ([103-854-800](#))
- Revio system operations guide ([102-962-600](#))
- Revio system specifications sheet ([102-326-552](#))

Vega system documentation

- Vega system brochure ([102-326-627](#))
- Vega system instrument control software release notes ([103-892-200](#))
- Vega system operations guide ([103-526-600](#))
- Vega system specifications sheet ([102-326-625](#))

SMRT Link and other data analysis documentation

- Brief primer and lexicon for PacBio SMRT sequencing webpage ([v13.1](#))
- Overview – Analysis options for HiFi data ([103-796-000](#))
- PacBio bioinformatics file formats documentation webpage ([v13.1](#))
- SMRT Link Cloud v26.2 release notes ([103-892-100](#))
- SMRT Link Cloud v26.2 user guide ([103-892-000](#))
- SMRT Link v26.2 release notes ([103-891-800](#))
- SMRT Link v26.2 software installation guide ([103-891-700](#))
- SMRT Link v26.2 user guide ([103-891-900](#))
- SMRT Link API use cases ([103-720-500](#))



DNA sample extraction documentation

Application, product, and technical notes

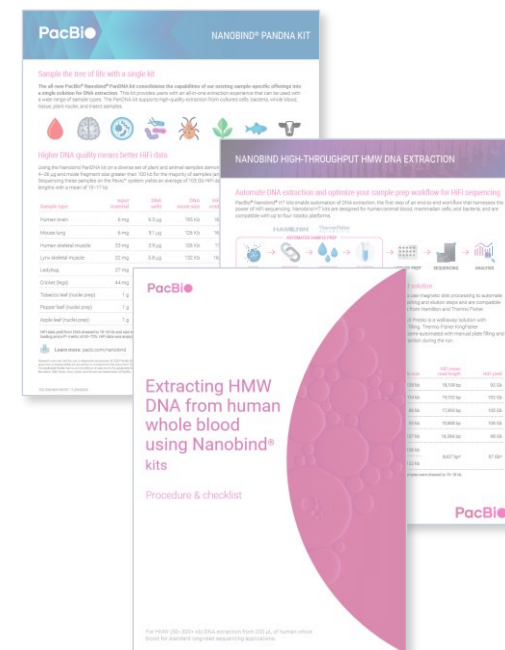
- Application note – HMW DNA extraction from human blood and saliva using Nanobind kits for HiFi long-read sequencing ([102-326-656](#))
- Technical note – Nanobind high-throughput HMW DNA extraction ([102-326-565](#))
- Technical note – Insect DNA extraction ([102-326-612](#))
- Technical note – Preparing DNA for PacBio HiFi sequencing – Extraction and quality control ([102-193-651](#))

Nanobind kit protocols and Guides & overviews

- Guide & overview – Nanobind CBB kit ([102-572-200](#))
- Guide & overview – Nanobind PanDNA kit ([103-394-800](#))
- Nanobind Procedures & checklists – see PacBio [Documentation](#)
- Overview – Nanobind CBB HMW DNA extraction protocols ([103-515-700](#))
- Overview – Nanobind HT HMW DNA extraction robotic procedures ([103-032-000](#))
- Overview – Nanobind PanDNA HMW DNA extraction protocols ([103-510-000](#))
- Technical overview – HMW DNA sample preparation for PacBio long-read sequencing using Nanobind PanDNA and SRE kits ([103-401-100](#))

Nanobind high-throughput (HT) automation kit protocols and Guides & overviews

- Guide & overview – Nanobind HT kits ([103-028-100](#))
- Nanobind HT Procedures & checklists – see PacBio [Documentation](#)
- Technical overview – Automated high-throughput HMW DNA extraction for PacBio long-read sequencing using Nanobind HT kits ([103-401-700](#))



SMRTbell library preparation documentation & other resources

SMRTbell library preparation literature

- Overview – HiFi application options ([101-851-300](#))
- Procedure & checklist – Amplifying genomic DNA for SMRTbell library preparation and HiFi sequencing ([103-648-000](#))
- Procedure & checklist – Generating PureTarget libraries with PureTarget kit 24 – Manual protocol ([103-740-700](#))
- Procedure & checklist – Generating PureTarget libraries with PureTarget kit 96 – Automation protocol ([103-740-800](#))
- Procedure & checklist – Preparing Kinnex libraries using Kinnex single-cell RNA kit ([103-254-300](#))
- Procedure & checklist – Preparing Kinnex libraries using Kinnex full-length RNA kit ([103-238-700](#))
- Procedure & checklist – Preparing Kinnex libraries from 16s rRNA amplicons ([103-238-800](#))
- Procedure & checklist – Preparing multiplexed AAV SMRTbell libraries using SMRTbell prep kit 3.0 ([102-126-400](#))
- Procedure & checklist – Preparing multiplexed amplicon libraries using PacBio barcoded M13 primers and SMRTbell prep kit 3.0 ([101-921-300](#))
- Procedure & checklist – Preparing multiplexed amplicon libraries using SMRTbell prep kit 3.0 ([102-359-000](#))
- Procedure & checklist – Preparing whole genome and metagenome sequencing libraries using SMRTbell prep kit 3.0 ([102-166-600](#))



Hybrid capture library preparation literature

- Agilent protocol – Target Capture Long-Read Sequencing Using the Agilent SureSelect XT HS2 Target Enrichment System ([5994-7612EN](#))
- QIAGEN protocol – QIAseq xHYB Long Read Panel Handbook ([HB-3695-001](#))
- Twist protocol – Long read library preparation and standard hyb v2 enrichment ([DOC-001320](#))

PacBio system applications support documentation

Application notes & best practices guides

Whole genome sequencing applications

- Application brief – Whole genome sequencing for de novo assembly – Best Practices ([102-193-627](#))
- Application brief – Variant detection using whole genome sequencing with HiFi reads – Best Practices ([102-193-604](#))
- Application brief – Microbial whole genome sequencing – Best Practices ([102-193-601](#))

Viral sequencing applications

- Application brief – AAV sequencing – Best Practices ([102-193-502](#))
- Application brief – Highly-accurate HiFi reads for AAV-research ([102-326-594](#))

RNA sequencing applications

- Application note – Kinnex full-length RNA kit for isoform sequencing ([102-326-591](#))
- Application note – Kinnex single-cell RNA kit for single-cell isoform sequencing ([102-326-549](#))

Metagenomics applications

- Application note – Kinnex 16S rRNA kit for full-length 16S sequencing ([102-326-601](#))
- Application brief – Metagenomic sequencing with HiFi reads – Best Practices ([102-193-684](#))

Targeted sequencing applications

- Application brief – Target enrichment using hybrid capture for HiFi sequencing ([102-326-515](#))
- Application brief – Targeted sequencing for amplicons – Best Practices ([102-193-603](#))
- Application note – Comprehensive genotyping with the PureTarget repeat expansion panel and HiFi sequencing ([102-326-614](#))
- Application note – Consolidate challenging genes with PureTarget carrier screen panel



PacBio system applications support documentation (cont.)

Application technical overviews

- Technical overview – Adeno-associated virus (AAV) library preparation using SMRTbell prep kit 3.0 ([102-390-400](#))
- Technical overview – Amplifying genomic DNA for SMRTbell library preparation and HiFi sequencing ([103-648-000](#))
- Technical overview – HiFi library preparation using HiFi prep kits for high-throughput sequencing on PacBio long-read systems ([103-424-600](#))
- Technical overview – Kinnex kits for single-cell RNA and full-length RNA and 16S rRNA sequencing ([103-343-700](#))
- Technical overview – Kinnex library preparation for full-length 16S rRNA sequencing ([103-344-800](#))
- Technical overview – Kinnex library preparation using Kinnex full-length RNA kit ([103-344-700](#))
- Technical overview – Kinnex library preparation using Kinnex single-cell RNA kit ([103-344-600](#))
- Technical overview – Multiplexed amplicon and hybrid capture library preparation using SMRTbell prep kit 3.0 ([103-705-200](#))
- Technical overview – PureTarget library preparation using PureTarget kit 2.0 ([103-742-600](#))
- Technical overview – Whole genome and metagenome library preparation using SMRTbell prep kit 3.0 ([102-390-900](#))



PacBio HiFi sequencing project getting started guides

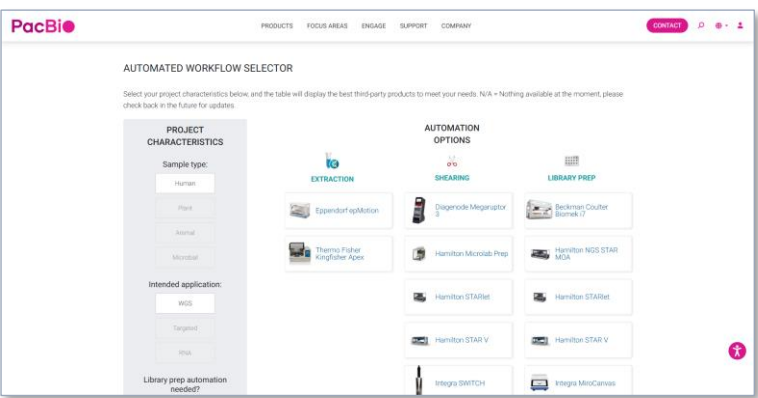
Equipment and materials checklists

- Get started with HiFi sequencing – Checklist ([102-326-639](#))
- Buyer's guide with automation platforms ([102-326-638](#))
- Getting started with long-read sequencing ([102-326-640](#))



PacBio HiFi sequencing getting started guides & project builder tools

- Personalized HiFi Fit kit bundle [[Link](#)]
- Getting started with long-read sequencing ([102-326-640](#))
- Getting started with targeted long-read sequencing ([102-326-674](#))
- Getting started with long-read sequencing for Biopharma ([102-326-675](#))
- Getting started with long-read sequencing: Microbial genomics ([102-326-640](#))
- Automated workflow selector tool [[Link](#)]



Sample prep

Nanobind DNA kits enable extraction of HMW gDNA from a variety of samples: saliva, cultured cells, bacteria, whole blood, tissue, plant nuclei, and insect.

Library prep

Automated-friendly and manual library prep kits for WGS, full-length RNA-seq, targeted panels, and many more.

Sequencing

Simple, load-and-go consumable reagents makes sequencing runs effortless.

Analysis

Advanced algorithms from Google Health and cutting-edge NVIDIA GPUs allow for on-board processing of sequencing data, all with reduced output file sizes to facilitate downstream analysis.

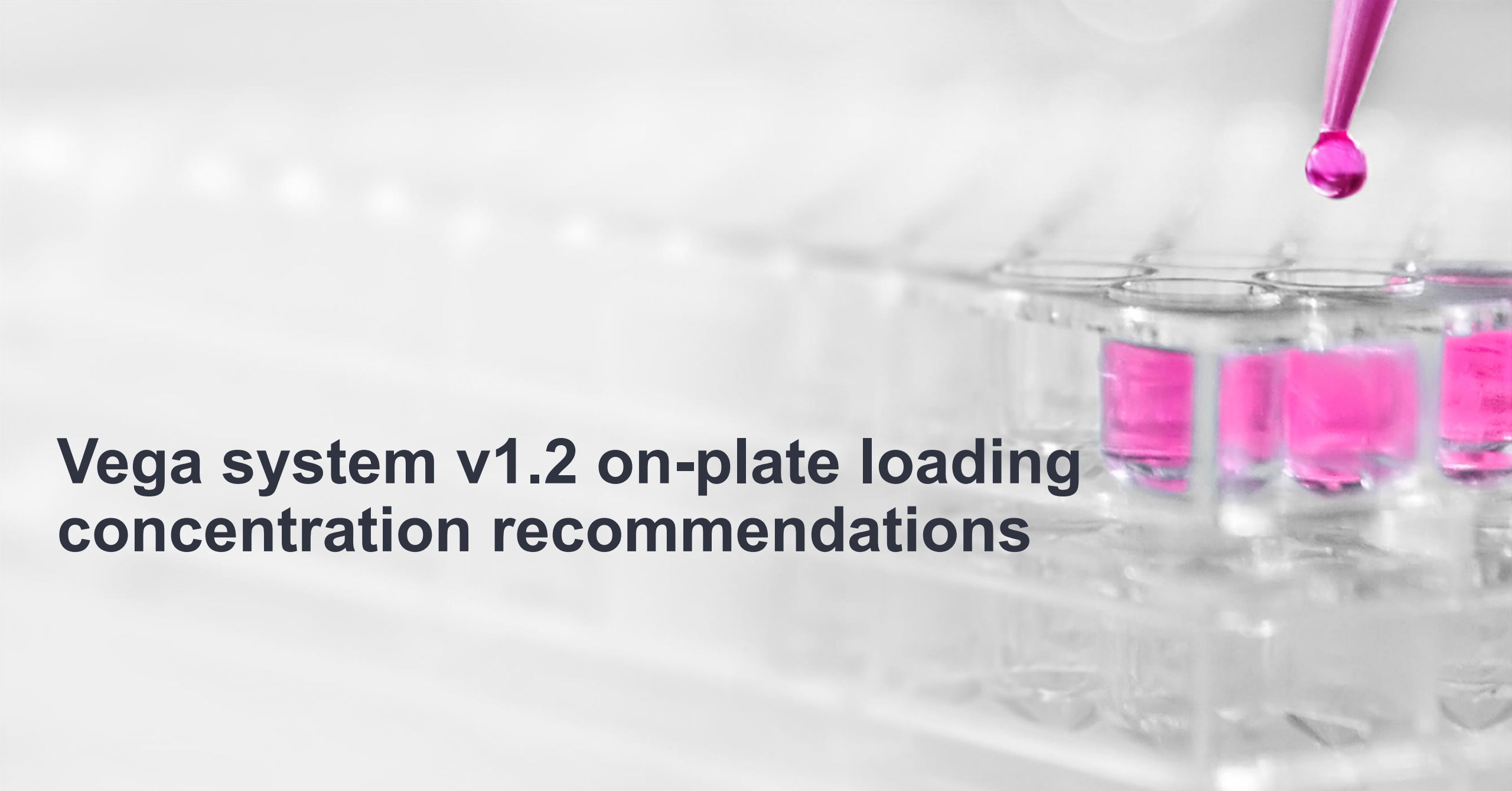


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§ Part 4: Appendix



Vega system v1.2 on-plate loading concentration recommendations

Vega system v1.2 on-plate loading concentration (OPLC) recommendations

Updated OPLC recommendations¹ for 1 – 2 kb inserts sizes to achieve SMRT Cell target loading ranges

Application	Application subtype	Library insert size	OPLC	Run time	Target Loading level	HiFi reads or yield per acquisition
Whole genome sequencing	Human WGS	15 – 20 kb	200 – 300 pM	24 hours	50 – 75%	80 – 90 Gb
	Microbial assembly	15 – 20 kb	200 – 300 pM	24 hours	50 – 75%	80 – 90 Gb
	Other WGS	10 – 15 kb	200 – 300 pM	24 hours	50 – 75%	70 – 80 Gb
		15 – 20 kb	200 – 300 pM	24 hours	50 – 75%	80 – 90 Gb
Low DNA input	Ampli-Fi sequencing	5 – 10 kb	100 – 140 pM	24 hours	50 – 75%	35 – 70 Gb
RNA sequencing	Kinnex single-cell RNA	15 – 20 kb	80 – 130 pM	24 hours	50 – 75%	80 – 90 Gb
	Kinnex full-length RNA	15 – 20 kb	80 – 130 pM	24 hours	50 – 75%	80 – 90 Gb
Viral sequencing	AAV sequencing	2 – 5 kb	200 – 300 pM	24 hours	50 – 75%	6 – 8 M reads
Metagenomics	Kinnex 16S rRNA	15 – 20 kb	80 – 130 pM	24 hours	50 – 75%	80 – 90 Gb
	Shotgun metagenomic profiling or assembly	7 – 10 kb	200 – 300 pM	24 hours	50 – 75%	35 – 70 Gb
Targeted sequencing	500 bp – 1 kb amplicons	500 bp – 1 kb	400 – 600 pM	2 hours	55 – 70%	6 – 8 M reads
	1 – 2 kb amplicons	1 – 2 kb	100 – 200 pM	4 hours	55 – 70%	6 – 8 M reads
	2 – 5 kb amplicons	2 – 5 kb	100 pM	12 hours	50 – 75%	6 – 8 M reads
	≥5 kb amplicons	5 – 10 kb	200 – 300 pM	24 hours	50 – 75%	35 – 70 Gb
	Hybrid capture	5 – 10 kb	200 – 300 pM	24 hours	50 – 75%	35 – 70 Gb