

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 support for 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 20× 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 5hmC 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.

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.

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.
- In rare cases, if a required component (such as a SMRT Cell tray) is missing when a run is unload, the unload process can time out and the instrument displays an error. Workaround: power-cycle the instrument to recover.

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