

Overview

The Revio system instrument software v13.3 includes support for the Revio SPRQ™ sequencing chemistry, a new 6mA caller, improved 5mC calling, direct cloud file transfer capabilities, and various bug fixes and performance improvements.

Supported SMRT[®] Link versions

Revio instrument software v13.3 is compatible with SMRT Link v25.1, SMRT Link v25.2, SMRT Link v25.3, and SMRT Link Cloud.

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 API, including Oracle Cloud Object Storage and Cloudflare R2.

Notice: The rsync daemon file transfer scheme will be disabled through a future software update in favor of more secure alternatives. Once disabled, file transfers will fail. PacBio strongly recommends transitioning to a supported transfer option.

New Features

- Added support for Revio SPRQ sequencing chemistry, including basecalling, consensus, and methylation-calling models. Revio (non-SPRQ) chemistry remains supported.
- Updated 5mCpG methylation caller, which increases accuracy of single CpG sites in individual reads.
- Added a new 6mA caller to support the Fiber-seq chromatin accessibility assay.
- Enabled direct file transfer to cloud storage buckets for Amazon S3, Google Cloud Storage, and Microsoft Azure Blob Storage.
- Added ability to connect to SMRT Link Cloud.
- Enabled generation of dataset report PDFs directly on the instrument, saved in the statistics directory.

Fixed Issues

- Resolved condensation buildup on instrument chillers.
- Fixed flickering of the "Continue" button when an environmental warning was present during run loading.
- Improved HiFi yields in strand consensus mode, including for AAV libraries.
- Now use "UNASSIGNED" rather than an arbitrary sample name in the read group header for the unassigned.bam.
- No longer copy duplicate ".xml.bak" files to transfer output directory.

Known Issues

- Run Design: For runs that use STRAND consensus mode, on-instrument methylation calling is not supported. Currently `jasmine` 5mC CpG methylation models require both strands: therefore, 5mC CpG calls are not reported when using STRAND consensus mode. To generate 6mA calls, set "Include Base Kinetics" to YES in Run Design and, post-sequencing, run `jasmine v2.799` using the unaligned BAM files with kinetics retained as input. Please reference the [jasmine GitHub documentation](#) for more details.
- Run Details: The Q30+ bases statistic is missing in runs that use STRAND consensus mode.

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