

Note: SMRT Link v11.1 is for use with Sequel[®] II and Sequel IIe systems **only**. Customers running Sequel systems, or those with mixed fleets running Sequel and Sequel II/IIe systems, should continue using SMRT Link v10.2.

SMRT Link server installation

SMRT Link server software is supported on:

- English-language CentOS 7.x, supported until end-of-life 6/30/2024.
- English-language Rocky Linux 8.x supported until end-of-life 5/31/2029.
- Ubuntu 18.04 and 20.04 64-bit Linux[®] distributions.
- These supported versions **also** apply to SMRT Link compute nodes.
- **Note:** PacBio[®] advises **against** new installations of CentOS for use with SMRT Link.
- SMRT Link is **not** guaranteed to work on Linux versions that are no longer supported by the operating systems' vendors.
- SMRT Link server software **cannot** be installed on systems running other versions of UNIX, macOS[®] or Windows[®].
- Several SMRT Link v11.1 features are computationally-intensive and require adherence to the computational and storage hardware requirements listed in the document **SMRT Link software installation guide (v11.1)**.

To install **only** command-line SMRT[®] Tools, use the `--smrttools-only` option with the installation command, whether for a new installation or an upgrade. See **SMRT Link software installation guide (v11.1)** for complete instructions.

Supported chemistry

- SMRT Link v11.1 supports all chemistry versions for Sequel II and Sequel IIe systems.

SMRT Link database note

- SMRT Link v11.1 no longer includes weekly automatic database backups. A database backup is still automatically performed once, during installation or upgrade. Failure to back up the SMRT Link database on a regular schedule risks losing all records in SMRT Link (including users, Data Sets, analyses, barcodes, and references) if a file system or reconfiguration error occurs. The underlying sequencing or analysis files, such as BAM files, are **not** affected. We **strongly** recommend asking your local Linux system administrator to schedule regular weekly backups of the SMRT Link database using standard Linux utilities. For additional details, please contact PacBio Technical Support.

New Features

SMRT[®] Analysis support for new MAS-Seq for 10x Single Cell 3' kit

- New **Single-cell Iso-Seq[®] Analysis** application enables easy analysis and functional characterization of full-length transcript isoforms with additional single-cell information, including single-cell barcodes and unique molecular identifiers (UMIs).
- New **Read Segmentation** data utility splits arrayed HiFi reads at concatenation adapter positions, generating segmented reads (S-reads) which are the comprising fragments.

- New **Read Segmentation and Single-cell Iso-Seq Analysis** application combines the functionality of the **Read Segmentation** data utility and the **Single-cell Iso-Seq Analysis** application. This application is for use with concatenation-based library preparations such as the MAS-Seq libraries.

SMRT Tools support for new MAS-Seq for 10x Single Cell 3' kit

- New `skera` deconcatenation tool splits arrayed HiFi reads at adapter positions, generating segmented reads (S-reads) which are the individual fragments.
- New `pigeon` PacBio transcript toolkit contains tools to classify and filter full-length transcript isoforms into categories against a reference annotation.
- Updated `isoseq3`: Added support for the new single-cell Iso-Seq workflow.

Run Design support for new MAS-Seq for 10x Single Cell 3' kit

- New **MAS-Seq single-cell** Run Design application choice to support the new MAS-Seq for 10x Single Cell 3' kit.

Sample Setup support for new MAS-Seq for 10x Single Cell 3' kit

- New **MAS-Seq single-cell** Sample Setup application choice to support the new MAS-Seq for 10x Single Cell 3' kit.

SMRT Analysis

- New **Summarize Jobs** functionality generates summary information on multiple selected **Microbial Genome Analysis** jobs. (In this release, only the **Microbial Genome Analysis** workflow is supported. Future releases will include support for summarizing additional workflows.)
- The **Minor Variants Analysis** pipeline was deprecated in this release.

Known Issues

- Reference download fails if the `curl` command is not installed on the server operating system.
- Large runs POST updates are sometimes rejected by the API gateway.
- The AWS Datasync Lambda function python runtime should be upgraded to v3.9 as the current v3.8 is no longer supported.
- **Single-cell Iso-Seq**: The Read Statistics reports FL-tagged reads with a misleading title.
- **Single-cell Iso-Seq**: When uploading a custom 10x barcode in the **Advanced Parameters** dialog, the workflow should block users from doing anything until the upload is completed.
- **Single-cell Iso-Seq**: When an uncompressed 10X barcodes file is uploaded using the **Advanced Parameters** dialog, the upload is rejected, but the GUI still shows the upload as being successful.
- **Single-cell Iso-Seq**: The input of `isoseq3 bcstats` should be the output of `isoseq3 correct`.
- **Sample Setup**: Creating a new high-throughput calculation without specifying an application displays an erroneous error message.
- **Sample Setup**: Sometimes cell and volume validation messages are inconsistent.
- **Run Design**: Run Designs that specify both **Include Low Quality Reads** and **Include Kinetics Information** generate a server error.
- **Run Design**: When creating a new Run Design and selecting an application, sometimes incorrect values are entered into the Run Design fields.

- **Run Design:** When saving a new Run Design, an error message is sometimes displayed.
- **Run Design:** The Run design Auto Analysis GUI doesn't display the expected Data Set members.
- **Run Design:** It is possible to import a Run Design .CSV file that specifies too many reaction plates. The Run Design will load on an instrument, but then fail the inventory scan.
- Windows line endings from demultiplexing jobs are inserted into the @RG SM field of BAM file headers. Such line endings can cause unexpected issues with downstream tools that parse BAM file headers.
- The *skera* tool only processes the first BAM file in a multi-cell Data Set.
- Multi-job submissions using the GUI are run on the head node instead of using distributed processing.
- When clicking **Start and Create Next** for multiple-Data Set custom parameters, the demultiplexed output Data Set name is not updated to reflect the newly selected Data Set.
- When creating an Auto Analysis, selecting a Run, then clicking **Back** enables workflow choice.

Fixed Issues

- Fixed an issue where the `$SMRT_ROOT/admin/bin/keytool` symlink pointed to a non-existing file.
- Fixed an issue that caused the Trim Ultra-Low Adapters data utility to fail.
- Fixed an issue that caused a Microbial Genome Analysis job to fail.
- Fixed an issue where a Microbial Assembly job with two combined Data Sets produced a single, small contig.
- Fixed an issue where the imported .CSV setting was not retained when the run was modified in the GUI.
- Fixed an issue where the SMRT Analysis Iso-Seq report primer data table displayed the same numbers for different multiplexed samples.
- Fixed an issue where using **Data > File Downloads > Edit Output File Name Prefix** to add a Data Set name prefix did not work.

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