

# MiSeq Software Release Notes

**MCS 2.5**

**RTA v1.18.54**

**MiSeq Reporter 2.5**

**BaseSpace Broker v2.1**

**MiSeq Recipes 3.1.0**

*For MiSeq Systems*

**September 2014**

## Introduction

These Release Notes detail the key changes to software components for the MiSeq since the package containing MCS v2.4, MiSeq Reporter v2.4, RTA v.1.18.54, BaseSpace Broker v2.1, and MiSeq Recipes v3.0. All of these pieces are contained within a new MiSeq Updater 2.5.0.

For VeriSeq PGS workflow users, this release is required. For all other users, this release is optional, but highly recommended due to the features and bug fixes described in these Release Notes. Please review these changes before updating your software.

If you are upgrading from version 2.3 or earlier, please review the release notes for v2.4 for a list of features and bug fixes introduced in that version.

For more information about the MiSeq system and how to use the software included with it, please see the product and support pages at [illumina.com](http://www.illumina.com)

<http://www.illumina.com/systems/miseq.ilmn>

[http://support.illumina.com/sequencing/sequencing\\_instruments/miseq.ilmn](http://support.illumina.com/sequencing/sequencing_instruments/miseq.ilmn)

To update this software suite, your MiSeq must already be running MiSeq versions 2.1, 2.2 or 2.3. If you have an earlier MiSeq software version, you can update your software using the MiSeq Updater 2.1, which can be found on the Illumina website.

The software package includes:

- MiSeq Control Software (MCS) v2.5
- RTA v1.18.54 -- no change in this release
- MiSeq Reporter v2.5
- BaseSpace Broker v2.1 -- no change in this release
- MiSeq Recipes 3.1.0

## I. MiSeq Control Software (MCS) v2.5

### NEW FEATURES:

- Enabled VeriSeq PGS workflow. This workflow only proceeds with a VeriSeq PGS reagent cartridge and components.
- The system no longer checks for a BaseSpace connection if instrument health data and BaseSpace analysis are disabled. Previously, MCS checked for a BaseSpace connection before starting every run.
- Added a new template line wash option to the post-run wash and manual wash. This option is unselected by default, except in the case of a post-run wash for a VeriSeq workflow run, where it is selected.
  - MCS now tracks whether a template line wash was included in the most recent post-run or manual wash.
  - If a user attempts to run a VeriSeq workflow run, and a template line wash was not performed at the last wash, the user is warned and prompted to

perform a template line wash. This warning does not apply to other workflows.

**DEFECT REPAIRS:**

- A fix was made to ensure that run folder names are synchronized with run count values.

**KNOWN ISSUES:**

- None

**II. RTA v1.18.54**

- No changes were made to this application in this release.

**III. MiSeq Reporter v2.5****NEW FEATURES:**

- None

**DEFECT REPAIRS:**

- 16S Metagenomics Workflow:
  - A fix was made to a bug that could lead to suboptimal classification of reads at the species level. This bug impacts the assignment of some reads to species-level classification, in cases where there is little difference in the probability scoring of the first and second most likely species classification. This fix improves the accuracy of read classification at the species level.
- Amplicon-DS Workflow:
  - A fix was made to resolve an out of memory error occurring when the somatic variant caller identifies a large number of indels. This issue has been resolved and the out of memory condition no longer occurs in these situations.
- Enrichment:
  - A fix was made to resolve an error reporting gaps when there are no actual gaps, and the gaps.csv file is empty. This issue has been resolved.
- All Workflows:
  - A fix was made to prevent application crashes in the event of index duplications on a given sample sheet. If a sample sheet with duplicate indexes is used, MiSeq Reporter now displays an error message to the user.
  - MiSeq Reporter no longer performs read stitching on index reads.
  - The Somatic Variant Caller now calculates coverage of insertions & deletions more accurately than previous versions of MSR in regions with extremely high read depth. In this new MSR 2.5 version, unless the indel is on the edge of a coverage region, the reported depth will be the average of the coverage of the base before and after the indel. If the indel is at an edge (so coverage is missing for either the base before or after) then the reported coverage will be for whichever one exists.

**KNOWN ISSUES:**

- None

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**CURRENT ALGORITHM VERSIONS:**

| Algorithms      | Versions  | Workflows   |
|-----------------|---|---|
| Aligners        | BWA 0.6.1-r104-tpx<br>(no change in this release)                             | Default for Enrichment, Library QC, PCR Amplicon, Resequencing                      |
|                 | Banded Smith Waterman 2.5.1.3<br>(was 2.4.60.8 in MiSeq Reporter 2.4 release) | Targeted RNA, TruSeq Amplicon, Amplicon-DS  |
|                 | Isaac 01.13.10.21<br>(no change in this release)                              | Optional for Resequencing   |
| Variant Callers | Somatic 3.5.2.1<br>(was 3.2.3.0 in MiSeq Reporter 2.4 release)                | Optional for PCR Amplicon, Resequencing, TruSeq Amplicon<br>Default for Amplicon-DS |
|                 | GATK 1.6-22-g3ec78bd<br>(no change in this release)                           | Default for Enrichment, PCR Amplicon, Resequencing, TruSeq Amplicon                 |
|                 | Starling 2.0.3<br>(no change in this release)                                 | Optional for Resequencing   |
| Other           | Samtools 0.1.18<br>Tabix 0.2.5<br>Zlib 1.25                                   |   |

**IV. BaseSpace Broker v2.1**

- No changes were made to this application in this release.

**V. MiSeq Recipes v3.1.0****NEW FEATURES:**

- Updated the standard MiSeq post-run wash and manual wash recipes to perform an optional a template line wash if selected by the user.
- Added VeriSeq workflow recipes.

**DEFECT REPAIRS:**

- None

**KNOWN ISSUES:**

- None