bcl2fastq2 Software

Release Notes

bcl2fastq2 2.19.0

March 7, 2017

Introduction

These Release Notes detail the key changes to the bcl2fastq2 converter since the release of bcl2fastq2 v2.18. This new version updates and replaces the version listed below.

This is a required software update for customers currently using bcl2fastq2 v2.18, as this release includes important features and bug fixes outlined below. The changes outlined here are changes to bcl2fastq2 since the release of v2.18.

Version 2.19.0 is used to convert bcl files to FASTQ, and is compatible with MiniSeq, MiSeq, NextSeq 500, all HiSeq (2000, 2500, 3000, 4000, and HiSeqX), and NovaSeq 5000/6000 systems running RTA version 1.18.54 and above. Installers and the software User Guide, which includes installation instructions, are available for download from illumina.com

For FASTQ conversion of bcl files generated on Illumina GAIIx and HiScan-SQ sequencing instruments, or any other type of sequencer running earlier versions of RTA, use bcl2fastq v1.18.4, available on illumina.com

NEW FEATURES:

- Added compatibility support for NovaSeq 5000/6000 systems.

DEFECT REPAIRS:

- Corrupted *.bcl or *.bcl.gz files no longer stalls bcl2fastq software indefinitely
- The HTML report, Stats.json, and ConversionStats.xml files now correctly report the % ≥ $Q30$ metric.
- Fixed an issue where adapter sequences could fail to be fully masked when using the default trimming method.
- Improved robustness for handling corrupt or missing input files to prevent bcl2fastq from stalling.
- Fixed an issue where the number of barcode mismatches was incorrectly reported in the Stats.json file
- Fixed an issue where the total yield was incorrectly reported in the Stats.json file
- Fixed an issue where the User Guide incorrectly spelled a sample sheet setting as "FindAdapterWithIndels" instead of "FindAdapter**s**WithIndels." The User Guide has been corrected with the appropriate spelling and bcl2fastq now accepts both spellings of the setting. However, "FindAdapterWithIndels" may be deprecated in future versions.

KNOWN ISSUES:

- No index sequences are included in the header for each read in the resulting FASTQ files if bcl2fastq is run without providing a sample sheet file.
- The HTML report files will not display statistics for samples named "default", "all", "unknown", and "undetermined".

- "N" is incorrectly not treated as a wildcard when provided as an index sequence character in the sample sheet. When used, this will cause a mismatch for any sequence character other than "N".
- 5' adapter trimming is not supported.
- NovaSeq runs with a corrupted *.cbcl file for cycle 1 in a given lane will prevent FASTQ files from being generated for all data in that lane.

OTHER:

- The --ignore-missing-controls command-line option has been deprecated. Control files are now always ignored by the bcl2fastq software.