bcl2fastq2 Software

Release Notes

bcl2fastq2 2.18.0

August 10th, 2016

Introduction

These Release Notes detail the key changes to the bcl2fastq2 converter since the release of bcl2fastq2 v2.17.1. This new version updates and replaces the version listed below.

Software Application	Prior Version	New Version
bcl2fastq	2.17.1	2.18.0

This is a required software update for customers currently using bcl2fastq2 v2.17.1, as this release includes important features and bug fixes outlined below. The changes outlined here are changes to bcl2fastq2 since the release of v2.17.1.

Version 2.18.0 is used to convert bcl files to FASTQ, and is compatible with MiniSeq, MiSeq, NextSeq 500, and all HiSeq (2000, 2500, 3000, 4000, and HiSeqX) 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 v1.8.4, available on illumina.com

NEW FEATURES:

- A new JSON formatted file (Stats.json) is generated to provide consolidated run and sample statistics.
- Multiple index sequences can now be assigned to the same Sample ID within the same lane
- UMI sequences are no longer removed from the read by default. This behavior can be toggled using the new TrimUMI sample sheet setting.
- Added new Read1UMIStartFromCycle and Read2UMIStartFromCycle Sample Sheet settings to be used in conjunction with the Read1UMILength and Read2UMILength settings for supporting UMI sequences that do not start at the beginning of a read.

DEFECT REPAIRS:

- IndexMetricsOut.bin files are now correctly formatted, allowing dual index sequences to be displayed correctly in the Sequence Analysis Viewer software and BaseSpace
- Sample numbers in FASTQ file names are now correctly assigned purely based on order in the the [Data] section of the sample sheet file.
- Masking i5 indexes works correctly for NextSeq runs
- FASTQ files can now be generated for samples occupying an entire lane with empty strings assigned for the index sequences in the sample sheet
- Space characters in file or folder paths supplied as command-line options do not throw exceptions
- Fixed issue where ConversionStats.xml was malformed in cases where the sample sheet has two non-index reads

KNOWN ISSUES:

- Corrupted *.bcl or *.bcl.gz files may cause bcl2fastq to stall indefinitely.
- 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 and projects named "default", "all", "unknown", and "undetermined".
- The HTML report, Stats.json, and ConversionStats.xml files incorrectly reports the $\% \geq Q30$ metric by excluding bases with quality score 30 (i.e. the number reported is actually % > Q30).
- 5' adapter trimming is not supported.
- "N" is incorrectly allowed as an index sequence character in the sample sheet. When used, this will cause a mismatch for any sequence character other than "N".
- No warnings or errors are displayed when bcl2fastq is used to process run folders that are missing control files.
- Sample sheet files generated from Illumina Experiment Manager may cause bcl2fastq to abort if they contain non-ASCII characters. Only alphanumeric characters dashes, and underscores are allowed in the sample sheet.