bcl2fastq2 Software v2.19.1

Release Notes

For MiniSeq, MiSeq, NextSeq, HiSeq, and NovaSeq Systems

June 12, 2017

Introduction

These Release Notes detail the key changes to the bcl2fastq converter since the release of bcl2fastq v2.19.0. This new version updates and replaces the version listed below.

Software Application	**Prior Version**	**New Version**
bcl2fastq	2.19.0	2.19.1

This is a required software update for customers currently using bcl2fastq v2.19.0, as this release includes important features and bug fixes outlined below. The changes outlined here are changes to bcl2fastq since the release of v2.19.0.

bcl2fastq version 2.19.1 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

DEFECT REPAIRS:

- Fixed an issue where some NextSeq and MiniSeq runs were incorrectly reported as containing corrupt data, causing the software to abort before all data was processed.
- Fixed an issue where some NextSeq and MiniSeq runs could be incorrectly reported as contaning .bcl files with 0 clusters.
- Fixed an issue where the FastqSummaryF1L#.txt stats file could incorrectly assign non-PF clusters to the non-PF pool for a sample, rather than to the non-PF pool of Undetermined reads.

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.