bcl2fastq2 Software v2.20.0

Release Notes

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

Introduction

These Release Notes detail the key changes to the bcl2fastq converter since the release of bcl2fastq v2.19.1. This new version updates and replaces the version listed below.

Software Application	**Prior Version**	**New Version**
bcl2fastq	2.19.1	2.20.0

This is a required software update for customers currently using bcl2fastq v2.19.1, as this release includes important features and bug fixes outlined below. The changes outlined here are changes to bcl2fastq since the release of v2.19.1.

bcl2fastq version 2.20.0 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 v1.8.4, available on illumina.com

NEW FEATURES:

- Added support for sequencing data generated from NovaSeq S4 flowcells.

DEFECT REPAIRS:

- Fixed an issue that could cause bcl2fastq to hang indefinitely in rare cases.
- Fixed an issue where a corrupted cBCL file in the first cycle of a lane in NovaSeq data would cause loss of all data for the affected lane. bcl2fastq can now skip over the first cycle of corrupted cBCL data when the --ignore-missing-bcls flag is provided.

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.