

Release Notes

This document describes the new features and updates to the bcl2fastq version 1.8.4 software described below. This software can be used to convert zipped or non-zipped bcl files, generated by Illumina HiSeq sequencers, to fastq files, and perform simultaneous demultiplexing of the data according to a sample sheet. For additional information and the bcl2fastq User Guide, please go to Illumina's website.

1. Bcl2fastq 1.8.4

FEATURES

- 1.1 Added ability to mask multiple adapter sequences per read.
- 1.2 Standard Illumina adapter sequences are now included in the bcl2fastq installation in the /share directory. These files can optionally be specified for use in adapter masking with the `--adapter-sequence` option. Please see the bcl2fastq User Guide for additional information.
- 1.3 The stringency to be applied by the adapter masking feature is now configurable with the `--adapter-stringency` option. If a stringency is not specified by the user, the default value of 0.9 is applied. Please note that Illumina recommends using an adapter stringency setting of greater than 0.5. Internal testing has shown that at values of 0.5 or less, many false positive matches to the adapter sequence may occur.

FIXES

- 1.4 A fix was made so that the `--adapter-sequence` option is now fully enabled and functional.

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