

Release Notes

BCL Convert v3.8.2

INTRODUCTION

These Release Notes detail the latest release of BCL Convert, including known issues.

BCL Convert converts per cycle binary data output by Illumina sequencers containing basecall files and quality scores to per read FASTQ files.

FEATURES

Support for No Lane Splitting defined in sample sheets:

- Users can enable No Lane Splitting in the settings section of the Sample Sheet
- This setting is supported for both V1 and V2 Sample Sheets.
- This setting cannot be in conflict with the command line setting, or the software will error.
- The output fastq_list.csv will contain one entry per lane, where all Reads will list the same files. When the file is used as input to DRAGEN, the sample files will only be read once and read-group distinctions between lanes will be lost.

RESOLVED ISSUES

- BCL Convert will be robust to corrupt cbcl input files.

KNOWN ISSUES

- BCL Convert does not validate when “Logs” or “Reports” is provided for a Sample_Project, and the software will be unable to create the subdirectories if these strings are provided.
- BCL Convert will not provide a warning or error when a corrupt bcl lane file is found in strict or robust mode
- BCL Convert does not support output of multiple, non-contiguous base regions to FASTQ files, such as may occur in the following OverrideCycles setting for a read: Y50N10Y50. This omission of a middle portion of the bases sequence within a single read is not supported. The new support for TrimUMI,0 (do not trim UMI sequences from FASTQ sequence bases) in bcl-convert 3.7 created new conditions where such gaps are being specified, and bcl-convert failed to detect this as an error before conversion. An example is specifying the following OverrideCycles setting for a read: U50N10Y101. If TrimUMI,0 (do not trim) is specified, then this is equivalent to Y50N10Y101 for the sequence bases line in the FASTQ output. When this kind of OverrideCycles setting was used, the output FASTQ represented the wrong set of cycles, and so did not output the correct data as the operator specified. bcl-convert now detects this condition for both index and genomic reads, aborting conversion with an error rather than outputting incorrect data.
- BCL Convert does not support the –first-tile-only option being specified for SP flow cells