

Customer Release Notes

BCL Convert Standalone v4.1.5

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.

NEW FEATURES

- Per-sample settings supported
 - Specify OverrideCycles, mismatch tolerance, & adapter settings per sample in Data section
- Support combined-mode (relaxed) index validation
 - Enabled per lane
 - Matches bcl2fastq2 behavior when enabled
 - Allows some samples to mask an index for per-sample-settings (mixing single-index and dual-index demux)

RESOLVED ISSUES

- Fixed issue where undetermined fastq files were being created when `--bcl-only-matched-reads` is set to true
- BCL will abort when ORA compression and `--no-sample-sheet` are used together
- Fixed a crash caused by too many open files for high sample counts
- Fixed a performance issue that occurs with high sample counts
- Fixed: BCL convert aborted with an empty [BCLConvert_Settings] section in v2 sample sheets
- Fixed: When R1 or R2 is masked out, it should not produce empty fastq.gz files- no FASTQ file will be output when the entire read is set to be trimmed using OverrideCycles
- Fixed: RTA3 has a version that outputs cbcl w/ 0qual+non0base for 0/"N#". Output differed from bcl2fastq2
 - ported to earlier versions (3.10.11, e.g.)
- Fixed a robustness failure on truncated cbcl files
- Fixed: BCL produced no files for fully-masked-as-U reads even when TrimUMI is disabled
- BCL crashed with threading error on very high sample dataset (150k per lane)

KNOWN ISSUES

- If a directory is specified as input to `--sample-sheet`, BCL Convert will hang at the beginning of a run while trying to copy that path as a file to `<outdir>/Reports/SampleSheet.csv`
- 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 string are provided.
- BCL Convert does not support the `--first-tile-only` option being specified for SP flow cells, but the new `--tiles` option can be used as a substitute.
- Does not error when no tile list exists in the RunInfo.xml file and `--tile` or `--exclude-tiles` is specified in the command line
- BCL will abort with an exit code of 1 if a .filter file is missing from a single lane dataset
- There will be many duplicate adapters error for all sampleIDs, and also for any cbcl errors

RELEASE HISTORY

Revision	Release Reference	Originator	Description of Change
00	1082864	Daniel Tracy	Initial release