



BCL Convert Standalone v4.1.7 Software Release Notes



Introduction

These release notes detail the key changes to BCL Convert v4.1.7 relative to the previous release v4.1.5, including known issues.

BCL Convert Installers, User Guide and Release Notes are available here:
https://support.illumina.com/sequencing/sequencing_software/bcl-convert.html

The following RPM packages are available:

- BCL Convert for x86 Centos 7 - bcl-convert-4.1.7-2.el7.x86_64.rpm
- BCL Convert for x86 Oracle 8 - bcl-convert-4.1.7-2.el8.x86_64.rpm

New Features and Changes

- Make the combined index collision checking default to enabled for all lanes. Implement a new `IndependentIndexCollisionCheck` option to replace `CombinedIndexCollisionCheck`
 - This important change reverts a strict check on dual index collisions added to BCL based on customer feedback. With this change, the default behavior matches `bcl2fastq2` and adds an option to change the behavior.

DRAGEN™ version	Index collision check behavior
3.9.x	Relaxed by default. No option to change. Matches <code>bcl2fastq2</code>
3.10.x and 4.0.x	Strict by default. No option to change.
4.1.5	Strict by default. New option <code>CombinedIndexCollisionCheck</code> introduced to optionally relax the strictness
4.1.7 and 4.2.x	Relaxed by default. Remove <code>CombinedIndexCollisionCheck</code> option, add new <code>IndependentIndexCollisionCheck</code> option to allow optional strict checking. Default matches <code>bcl2fastq2</code>

- Fix for index sequences missing from fastq headers when using `--no-sample-sheet` setting.
- Fix for BCL behavior being different than `bcl2fastq2` with respect to "Sample_Name" and "Sample_Project". In the special case of "Sample_Name" == "Sample_ID", `bcl2fastq2` does not create a "Sample_ID" subdirectory. This change makes `bcl-convert` behavior the same.
- Fix for false barcode collision reports when one sample's index is entirely trimmed out and another sample's index exists.
- Fix for BCL not aborting when single-index datasets have barcode collisions.
- Fix for incorrect `yieldQ30/qscoresum` stats when there is UMI in the first part of a read and `TrimUMI` is enabled (true by default).
- Fix for a false error when using global `BarcodeMismatchesIndex2` and a sample does not use index `BarcodeMismatchesIndex1`, when the sample sheet contains both single & dual-index samples.
- Fix for BCL failing with a "vector::reserve" message for mixed index strategies.
- Fix for BCL outputting many duplicate error messages for missing CBCL files.
- Fixes related to the **Per-Sample Settings** feature introduced with the NovaSeq-X instrument:
 - Fix for extra metrics being output when running with Per-Sample Settings on a `NextSeq550` dataset.
 - Fix a validation bug where Per-Sample Settings incorrectly flags errors when any read (genomic or index) is fully masked in one or more samples, but not in all samples. For example, an inconsistently fully-masked genomic read can cause a spurious error message indicating that `AdapterRead{1,2}` must be specified or not specified for a sample. An inconsistently fully-masked index read can cause a spurious error message indicating that `BarcodeMismatchesIndex{1,2}` must be specified or not specified. This error can be wrong and prevents conversion from continuing and exits with an error code.



- Fix for mixed single & dual-index samples with combinatorial inputs in a lane via Per-Sample Settings, to cause some collisions to go undetected.
- Fix for mixed single & dual-index samples in a lane using Per-Sample Settings not working properly, sometimes resulting in missing output for the single-index sample.
- Fix for too-long-index-reads error "No more than 27 total bases can be used as index bases" when using fewer than 27 consecutive bases.
- Fix for Top Unknown Barcodes output listed cycles being based upon the first sample listed, and not necessarily including all bases being used for indexing, when Per-Sample Settings are used.
- Fix for Per-Sample Settings not isolating lanes when determining index cycles.
- Fix for Per-Sample vs Global Settings in BCL producing different FASTQs and Demux Metrics when variety of reads are fully masked.

Known Issues

Known issues of the BCL Convert v4.1.7 release.

Issue	Resolution / Workaround
When sample sheet has same sampleID in the same lane multiple times, but with different output files (e.g. R1 fully masked out in one entry, but not in another), the validator fails to detect this case and does not error out. Subsequent on-instrument secondary analysis fails in fastqc generation	No workaround, except to change sample sheet to make output files match. Handling of this case planned for future version.
When using mixed indexing strategies, the index hopping counts .csv metrics for Undetermined reads may differ slightly between bcl-convert and NovaSeq-X on-instrument	No workaround. Fix planned for future version
BCL omits lines with zero reads in Demux tile stats and Quality tile stats .csv metrics	No workaround. Fix planned for future version
BCL will crash when "--no-sample-sheet true" & 0 indexes supplied	No workaround. Fix planned for future version
Customers with high CPU core count systems have reduced BCL performance due to a thread limit, since v3.10	No workaround. Fix planned for future version
BCL does not abort when Combined Index Collision Check is enabled on a dual index run with one index removed	Uncaught user input error. Operation proceeds normally.
Filenames for interleaved FASTQs that are Ora compressed, are not the same as the original file names. For original filenames ending in "R1_001.fastq", "R2_001.fastq" the decompressed file names are "R_1.fastq", "R_2.fastq", dropping the identifier "001". This could potentially lead to duplicate file name conflicts	No workaround. Fix planned for future version



BCL crashes in Robust mode when *.filter file is missing for single lane dataset	No workaround. Fix planned for future version
bcl-convert outputs different PF cluster YieldQ30 and QualityScoreSum stats in the legacy stats file ConversionStats.xml as compared to bcl2fastq2.	No workaround. Fix planned for future version
A crash during bcl error checks can lead to hang, due to timing race condition	No workaround. Fix planned for future version

Release History

Revision	Release Reference	Originator	Description of Change
00	1087776	Cobus De Beer	Initial release