BCL Convert Standalone v4.1.23 Software Release Notes

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

- Combined index collision checking remains enabled by default for all lanes.

DRAGEN™ version	Index collision check behavior
3.9.x	Relaxed by default. No option to change. Matches bcl2fastq2
3.10.x and 4.0.x	Strict by default. No option to change.
4.1.5	Strict by default. New option `CombinedIndexCollisionCheck` introduced to optionally relax the strictness
4.1.7, 4.1.23 and 4.2.x	Relaxed by default. Remove `CombinedIndexCollisionCheck` option, add new `IndependentIndexCollisionCheck` option to allow optional strict checking. Default matches bcl2fastq2

RESOLVED ISSUES

- Fixed behavior so that BCL does not output Undetermined FASTQs when `--bcl-only-matched-reads` is enabled.
- Fixed issue where the ORA outputs were generated in the root output directory, instead of inside the Sample_Project and Sample_Name directories like FASTQ.gz files.
- Prevent using `--no-sample-sheet` option and the `--fastq-compression-format=dragen` (or dragen-interleaved) option together.
- Fixed an ORA error when FASTQ.gz files for a sample-read were not generated if the whole read was masked out as N or U.
- Fixed a performance issue with very high sample counts, such as 150K samples.
- Fixed an issue where customers with high CPU core count systems have reduced BCL performance due to a thread limit, since v3.10.
- Fix for BCL crash when `--no-sample-sheet true` and 0 indexes supplied.
- Fixed an issue where a large number of demultiplex cycles (~26) caused a hang and crash
- Fixed an issue where specifying an invalid lane in 'bcl-only-lane' parameter errored out without providing an error message.
- Support for values 'true' and 'false' for sample sheet settings 'TrimUMI' and 'CreateFastqForIndexReads', in addition to '1' and '0'
- Fixed an issue that failed to catch an invalid integer parameter for TrimUMI (must be 0 or 1 if an integer)
- Fixed a crash issue with i5 index lengths greater than 18

KNOWN ISSUES

Component	Issue ID	Summary	Remedy/Workaround
BCL	DRAGEN-18920	bcl-convert outputs different PF cluster YieldQ30 and QualityScoreSum metrics in the legacy stats file ConversionStats.xml as compared to bcl2fastq2.	No workaround. Fix planned for future version
BCL	DRAGEN-19103	BCL crashes in Robust mode when converting a single lane of an aggregated (bgzf) format, and the lane's filter file is missing or corrupted.	No conversion can be done without some P/F data from the filter file. Because the filter file is for the entire lane, the lane cannot be converted.
BCL	DRAGEN-26220	When using mixed indexing strategies, the index hopping counts metrics for Undetermined reads may differ slightly between bcl-convert and NovaSeq-X on-instrument	No workaround. Fix planned for future version
BCL	DRAGEN-26294	Bcl-convert fails to catch the error case where per-sample-settings is used and the same Sample_ID has multiple entries with a different set of expected output files for each entry due to fully masked reads. In this case, the set of files will be inconsistent and incomplete.	Rare corner case where the same Sample_ID may be used with, e.g. R1 masked out in one entry but not in another, in the same lane. Error will be caught in future versions.

RELEASE HISTORY

Revision	Release Reference	Originator	Description of Change
00	1092698	Daniel Tracy	Initial release