Release Notes

BCL Convert v3.8.9

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

No new features introduced in v3.8.9 patch.

Resolved Issues

- Fix for the wrong index length in 'Top_Unknown_Barcodes.csv' when demultiplexing using bcl-convert
- Fix a crash when --bcl-only-read 1 is specified and UMI ranges are specified in OverrideCycles
- Fix an issue where non-contiguous bases are output to fastq, introduced by new TrimUMI,0 and CreateFastqForIndexReads,1 options. Cases are sequences of YNU, UNY or UNU in a genomic read when TrimUMI is disabled, and INU, UNI, and UNU in an index read when TrimUMI is disabled and CreateFastqForIndexReads is enabled.
- Fix for bcl-convert producing incorrect data when Read 1 size is less than 25 cycles
- Fix crash when config.xml is present in BaseCalls on aggregated-bcl input (HiSeq/MiSeq)

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 string are provided.
- BCL Convert will not provided a warning or error when a corrupt bci lane file is found in strict or robust mode
- BCL Convert does not support the –first-tile-only option being specified for SP flow cells

Release History

Revision	Release Reference	Originator	Description of Change
00	1083775	Daniel Tracy	Initial release