



# Release Notes

## BCL Convert v3.7.5



## 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.

## FEATURES

Support for Sample Project in V1 and V2 sample sheets:

- Support for `--no-lane-splitting` option which is enabled as a command line setting. When used, the software will output a single fastq file across all lanes per sample per read
- Support for `CreateFastqsForIndexReads` Sample Sheet setting. When set to 1, the software will output fastqs for index reads when provided, and if index reads are defined as a UMI then fastqs for the UMI will be output (if `TrimUMI` is also set to 0). These fastq files will not be affected by the `MaskShortReads` or `MinimumTrimmedReadLength` settings. The default is 0.
- Support for `TrimUMI` Sample Sheet setting. When set to 1, the software will exclude UMI cycles from the fastq files. The default is 1.
- Support for `--bcl-num-parallel-tiles` command line option which defines the number of tiles being converted to fastq files in parallel. The value provided must be between 1 and the number of available hardware threads.
- Support for `--bcl-conversion-threads` command line option which defines the number of threads used for conversion per tile. The value provided must be between 1 and the number of available hardware threads.
- Support for `--bcl-num-compression-threads` command line option which defined the number of CPU threads used for compression of output fastq files. The value must be between 1 and the number of available hardware threads.
- Support for `--bcl-num-decompression-threads` command line option which defines the number of CPU threads used for decompression of input basecall files. The value must be between 1 and the number of available hardware threads.
- Support for `--shared-thread-odirect-output` which uses experimental shared thread file output code, which requires `O_DIRECT` mode. The value must be true or false.
- Support for up to 100,000 samples provided in the sample sheet

## RESOLVED ISSUES

- Duplicate `Sample_ID` entries in the same lane in the sample sheet no longer result in duplicate entries in the output `fastq_list.csv` file

## KNOWN ISSUES

- `bcl-convert 3.7` uses more memory than `bcl-convert 3.6`. If you experience an error in which the WatchDog terminates `bcl-convert 3.7` due to low system memory, try increasing memory on the host machine.
- Use of `--no-lane-splitting` requires no 'Lane' column in the sample sheet.
- Use of `'bcl-num-decompression-threads'` has no effect for NextSeq inputs.
- Use of `'shared-thread-odirect-output'` might hang or have poor performance when writing directly to a distributed file system (e.g. GPFS or Lustre).
- Use of 10000 or more samples automatically enables and requires `'shared-thread-odirect-output'` mode.



- A sample count below 10000 samples does not automatically enable 'shared-thread-odirect-output' mode, but may still encounter "resource not available" errors (Linux user thread exhaustion) if 'ulimit -u' is not sufficiently high to support the sample count without this mode. Operators may wish to enable 'shared-thread-odirect-output' mode for sample counts above a few thousand, depending upon their ulimit settings.
- Recommended ulimit settings are 32768 processes (-u) and 720000 file descriptors (-n), though higher user process settings may help alleviate issues with higher sample counts. If you encounter a "resource temporarily unavailable" error or are demultiplexing thousands of samples, increase the Linux user processes limit (ulimit -u) to 32768 instead.