

## New features

- Added trimming of low quality bases at the ends of reads. This is configured using the following new sample sheet settings. See **Obc2fastq reference guide (v6.0)** for details.
  - `TrimLowScores`
  - `TrimQ`
  - `TrimWindow`
- Added new command-line parameters. See **Obc2fastq reference guide (v6.0)** for details.
  - `--n-padding`
  - `--save-sample-tag`
  - `--logutctime`
- Reduced memory usage.
- Significantly faster time to results.

## Fixed issues

- Fixed an issue where empty fields and extra commas at the ends of lines in sample sheet files caused the sample sheet settings to be ignored.

Research use only. Not for use in diagnostic procedures. © 2024 Pacific Biosciences of California, Inc. ("PacBio"). All rights reserved. Information in this document is subject to change without notice. PacBio assumes no responsibility for any errors or omissions in this document. Certain notices, terms, conditions and/or use restrictions may pertain to your use of PacBio products and/or third-party products. Refer to the applicable PacBio terms and conditions of sale and to the applicable license terms at [pacb.com/license](https://pacb.com/license).

Pacific Biosciences, the PacBio logo, PacBio, Circulomics, Omniome, SMRT, SMRTbell, Iso-Seq, Sequel, Nanobind, SBB, Revio, Onso, Apton, Kinnex, and PureTarget are trademarks of PacBio.