Obc2fastq release notes (v6.1)

New features

- Output FASTQ files now use the following file naming convention to improve compatibility with downstream secondary analysis tools:

  `<Sample Name>_S<Sample Number>_L00<Lane Number>_R<Read Number>_001.fastq.gz`

Note: Contact your FSE (Field Service Engineer) or PacBio Technical Support to perform the Instrument Control Software installation.