

Raw data File suffix	File information
*.adapters.fasta	File of SMRTbell adaptor sequences removed from data
*.baz2bam_1.log	Log file during BAM file generation
*.scraps.bam	The scraps arising from cutting out adapter and barcode sequences, to enable reconstruction of HQ regions of the ZMW reads, in case the customer needs to rerun barcode finding with a different option
*.scraps.bam.pbi	PacBio BAM index file (bam.pbi) for scraps.bam
*.sts.xml	An XML file representing data about the SMRTcell statistics
*.subreads.bam	Unaligned BAM files representing the subreads produced natively by the PacBio instrument. The subreads.bam will be the starting point for secondary analysis
*.subreads.bam.pbi	PacBio BAM index file (bam.pbi) for subreads.bam
*.subreadset.xml	A PacBio DataSet is an XML file representing a set of a particular sequence data type such as subreads, references or aligned subreads. The actual data elements contained in a DataSet are stored in files referred to by the XML, usually in FASTA or BAM files. The DataSet can optionally filter these files or store metadata about their contents.
*.transferdone	Manifest of files transferred from instrument to server
tmp-file-*.txt	Temporary file generated during data transfer from instrument to server

Useful files for downstream analysis

*.subreads.bam
 *.subreads.bam.pbi
 *.subreadset.xml

Additional information on formats

.bam.pbi information <https://pacbiofileformats.readthedocs.io/en/5.1/PacBioBamIndex.html>
 .bam info <https://pacbiofileformats.readthedocs.io/en/5.1/BAM.html>
 .xml info <https://pacbiofileformats.readthedocs.io/en/5.1/DataSet.html>