Convert.10xBAM.To.FASTQ Documentation

Description: Tool for converting 10x BAMs produced by Cell Ranger, Space Ranger, Cell Ranger ATAC, Cell Ranger DNA, and Long Ranger back to FASTQ files that can be used as inputs to re-run analysis. See: 10x Genomics bamtofastq Documentation for detailed usage guidelines.

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Summary: Extract FASTQ files from BAM files produced by the 10x Genomics pipeline. Can be used directly on SRA deposited "_OriginalRef.bam.1" files.

Parameters:

Name	Description
BAM File	BAM produced by cellranger, cellranger-atac, cellrange-dna or longranger. Supports URLs to SRA deposited "Original Format" BAM files.
Output Name	By default, output files will be named for the base name of the input BAM file along with any path and read information extracted. Specifying the output name replaces the BAM file base name but does not change additional information parsed from the internal bam structure.
mode	Specific mode options for non-standard 10x pipelines.
Reads per FASTQ	The number of reads to be included in each FASTQ

Output File(s): One or more _R1 and _R2 FASTQ files for each input BAM file.

Module Language: Python
Source Repository: https://github.com/genepattern/Convert.10xBAM.To.FASTQ/releases/tag/v1
Docker image: rust:1.50-buster

Version	Comment
1	Initial release.