Picard.AddOrReplaceReadGroups Documentation

Description: Replaces all read groups in the input file with a new read group and assigns all reads to this read group in the output.

Author: Picard team, gp-help@broadinstitute.org

Summary

This module replaces all read groups in the input file with a new read group provided by the user and assigns all reads to this read group in the output. The input file must be in either BAM or SAM format. For more details on the SAM/BAM format, see the specification here: http://samtools.sourceforge.net/SAM1.pdf

Parameters

Name	Description
input.file (required)	Input file (BAM or SAM).
read.group.id (required)	Read Group ID.
read.group. library (required)	DNA preparation library. Note that this field is required by the module Picard.MarkDuplicates. It is used to determine which read groups may contain molecular duplicates, in the case where the same DNA library was sequenced on multiple lanes.
read.group. platform (required)	Read Group platform (e.g., Illumina, SOLID).
read.group. platform.unit (required)	Read Group platform unit (e.g., run barcode).
read.group. sample.name (required)	Read Group sample name.

read.group. sequencing. center.name	Read Group sequencing center name.
read.group. description	Read Group description.
output.prefix (required)	The prefix of the output SAM or BAM file.

Output Files

1. SAM/BAM file

   A SAM or BAM file (depending on the input format) with the given read group added/replaced. For more details on the SAM/BAM format, see the specification here: http://samtools.sourceforge.net/SAM1.pdf

Platform Dependencies

Module type:	Preprocess & Utilities
CPU type:	any
OS:	any
Language:	Java (minimum version 1.6)

GenePattern Module Version Notes

Date	Version	Description
3/19/13	3	Read Group ID now a required parameter