



## 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.

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### 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	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.

# GenePattern

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

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