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# shRNACollapseReps, v10

Collapses replicate samples in a gct data file, based on a sample information file

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**Algorithm Version:**

## Introduction

shRNACollapseReps is a GenePattern module that collapses replicate samples in a user-inputted shRNA dataset. The module outputs a GCT file containing the user-inputted dataset with the replicate cell line samples collapsed by taking the mean value per shRNA. It also returns a text file containing the sample info of the cell lines in the dataset, based on the provided sample info file.

## Parameters

Name	Description
gct file *	The input gct data file.
sample info file *	The cell line (sample) information file.
prefix *	The file name prefix.

\* - required

## Input Files

1. gct file
  - The gct file contains shRNA data, with columns as cell line samples and rows as shRNAs.

## Output Files

1. Data file with replicate samples collapsed *[prefix]\_meanrep.rnai.gct*
  - A GCT file containing the user-inputted dataset with the replicate cell line samples collapsed.

**2. Sample info file** *[prefix]\_SampleInfo.txt*

- A text file containing the sample information contained in the user provided sample info file, subsetting to only cell lines in the dataset.

## Platform Dependencies

**Task Type:**

RNAi

**CPU Type:**

any

**Operating System:**

any

**Language:**

R

## Version Comments

Version	Release Date	Description
10	2014-09-16	updated command line
9	2013-03-20	



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