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# shRNAfoldChange, v6

Calculate the fold change of each sample in a gct file, based on the appropriate DNA reference value (present in a gct file of the same dimension).

**Author:** Barbara Weir;The Broad Institute

**Contact:** bweir@broadinstitute.org

**Algorithm Version:**

## Introduction

shRNAfoldChange is a GenePattern module that calculates the fold change values of all shRNAs for each sample in a GCT file. The fold change is calculated by subtracting the starting DNA reference matrix in the user-uploaded DNA reference file from the shRNA value matrix in the user-uploaded DNA reference file from the shRNA value matrix in the user-uploaded gct file (both matrices should have the same dimensions). The module outputs a GCT file containing the fold change of each sample, for each shRNA in the dataset.

## Parameters

Name	Description
gct file *	The input gct data file.
DNA reference file *	The values of the DNA pool reference per sample/shRNA in a gct file (same dimension as input gct file).
prefix *	The file name prefix.

\* - required

## Input Files

1. gct file
  - Data file containing shRNA data, with cell lines as columns and shRNAs as rows.
2. DNA reference file

- A GCT file containing the values of the DNA pool reference per sample/shRNA (same dimensions as input GCT file).

## Output Files

1. Data file with fold change values `[prefix]_FC.rnai.gct`
  - A GCT file containing the fold change values of each sample in the user-inputted dataset.

## Platform Dependencies

**Task Type:**

RNAi

**CPU Type:**

any

**Operating System:**

any

**Language:**

R

## Version Comments

Version	Release Date	Description
6	2014-09-16	updated command line
5	2013-03-20	



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