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shRNAmappingGenes, v8

Maps shRNAs in a gct data file to genes based on a mapping file.

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Algorithm Version:

Introduction

shRNAmappingGenes is a GenePattern module that maps shRNAs in a user-uploaded dataset to genes based on an 'shRNA to gene' mapping file. The module outputs a GCT file containing the original dataset with the name of the gene appended to the shRNA sequence in the name column, as well as the name of the gene in the description column. If an shRNA maps to more than one gene, that row of data is duplicated so that both shRNA/gene combinations occur in the final data matrix.

Parameters

Name	Description
gct file *	The input gct data file.
mapping *	The shRNA to gene mapping file.
prefix *	The file name prefix.

* - required

Input Files

1. gct file
 - Data file containing shRNA data (GCT file format). The shRNA identifier (usually the sequence) should exist in the first (Name) column.
2. mapping file
 - The shRNA to gene mapping file

Output Files

1. Data file with shRNAs mapped to genes [prefix]_mapped.rnai.gct
 - A GCT file containing the original dataset with the shRNAs mapped to genes. The first column (Name) will contain the shRNA sequence with the gene name appended to it and the second column (Description) will contain the gene name.

Platform Dependencies

Task Type:

RNAi

CPU Type:

any

Operating System:

any

Language:

R

Version Comments

Version	Release	
	Date	Description
8	2014-09-16	Does some additional cleanup (remove rows with all NaN, removes all but 1 of duplicated control shRNA mappings like LacZ, lacZ, etc.) and updated command line
7	2013-03-20	Does some additional cleanup (remove rows with all NaN, removes all but 1 of duplicated control shRNA mappings like LacZ, lacZ, etc.)



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