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PertMapGenes, v15

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

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Algorithm Version:

Introduction

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

Parameters

Name	Description
gct file *	Data file containing reagent data (GCT file format). The reagent identifier (usually the sequence) should be located in the first (Name) column.
mapping *	The reagent to gene mapping file.
prefix *	The output file name prefix.

* - required

Input Files

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

Output Files

1. Data file with reagents mapped to genes `[prefix]_mapped.gct`

A GCT file containing the original dataset with the reagents mapped to genes. The first column (Name) will contain the reagent 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
15	2013-03-20	Updated from shRNAmmapGenes



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