

FilterLowshRNAs, v31

Removes shRNAs with low read counts in original DNA plasmid pool. Outputs a GCT file containing filtered shRNA data and a GCT file containing the mean read count for each shRNA in the original DNA plasmid pool.

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Algorithm Version:

Introduction

FilterLowshRNAs is a GenePattern module that implements a quality control step during the analysis of shRNA pooled screen data. The user inputs at least one and up to three GCT files containing shRNA data, with each file containing data from a separate batch. The cell lines where the shRNAs have low read counts in the original DNA plasmid pool are defined as NaN in each file and shRNAs where the read counts in the original DNA plasmid pool were low in all files are removed from the dataset entirely.

References

Contact author for more information

Parameters

Name	Description
shRNA data file(s) *	Format is a GCT file where each row corresponds to a unique shRNA sequence. At least one file is required and up to three files can be uploaded.
File Prefix *	User-defined prefix of output file names.

^{* -} required

Input Files

- 1. shRNA data file(s)
 - The shRNA data file(s) are GCT files where each row corresponds to a unique shRNA sequence.

Output Files

- 1. Achilles file with shRNAs filtered out [File Prefix]_Achilles_filtered.rnai.gct
 - A GCT file containing the shRNA data with the shRNA sequences containing low read counts in the original DNA plasmid pool.
- 2. DNA references file with shRNAs filtered out [File Prefix]_DNAreferences_filtered.rnai.gct
 - A GCT file containing all of the cell lines and their corresponding ready counts for the original DNA plasmid pool, based on the separate batch files.

Example Data

Coming Soon

Requirements

Memory Requirements on the GenePattern Server: 8G

Platform Dependencies

Task	Type:

RNAi

CPU Type:

any

Operating System:

any

Language:

R

Version Comments

Version	Release Date	Description
31	2014-10-08	
30	2014-09-16	updated command line
29	2014-04-11	Converted documentation from pdf to html

