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FilterLowPert, v15

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

Author: Barbara Weir, Sara Howell;The Broad Institute

Contact: bweir@broadinstitute.org

Algorithm Version:

Introduction

FilterLowPert is a GenePattern module that implements a quality control step during the analysis of pooled screen data. The user inputs at least one and up to three GCT files containing reagent data, with each file containing data from a separate batch. The cell lines where the reagents have low read counts in the original DNA plasmid pool are defined as NaN in each file and reagents where the read counts in the original DNA plasmid pool were low in all files are marked for complete removal (see removeSamples module).

Parameters

Name	Description
GCT Files *	Format is a GCT file where each row corresponds to a unique sequence. At least one file is required and up to seven files can be uploaded.
File Prefix *	User defined prefix for output file names.

* - required

Input Files

1. GCT File(s)

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

Output Files

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

Platform Dependencies

Task Type:

RNAi

CPU Type:

any

Operating System:

any

Language:

R

Version Comments

Version	Release Date	Description
15		



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