

[← Go Back \(/\)](#)

# keepSamples, v5

Filters out samples not in keeplist file

**Author:** Barbara Weir, Broad Institute

**Contact:** AchillesTeamArchive@gmail.com

**Algorithm Version:**

## Introduction

[Why use this module? What does it do? If this is one of a set of modules, how does this module fit in the set?]

## Algorithm

[if applicable: a short overview of the algorithm in normal prose, followed by any details; write overview as if you are explaining to a novice]

## References

[appropriate papers cited]

## Parameters

| Name        | Description             |
|-------------|-------------------------|
| gct file *  | data file to filter     |
| keeplist *  | list of samples to keep |
| extension * | filename prefix         |

\* - required

## Input Files

1. [parameter name]

[Description. For example: The segmentation file contains the segmented data for all the samples identified by GLAD, CBS, or some other segmentation algorithm. (See GLAD file format in the GenePattern file formats documentation.) It is a six column, tab-delimited file with an optional first line identifying the columns. Positions are in base pair units.

## Output Files

1. [File name]

[Description of the content, file format, and how to interpret the results.]

## Example Data

[provide example data, including input files and parameter settings]. (we'll put the input files on the ftp site and link to them from the doc)

## Requirements

[any software requirements for running this, e.g., version of R, licensing]

## Platform Dependencies

**Task Type:**

RNAi

**CPU Type:**

any

**Operating System:**

any

**Language:**

R

## Version Comments

| Version | Release |   |
|---------|---------|---|
|         | Date    | Description   |
| 5       |         | Keeps only samples from a gct file that are in a txt file (one sample per line - must match name exactly) and writes out a new gct file |



(<http://www.broadinstitute.org>)©2021

Broad Institute of MIT & Harvard (<http://www.broadinstitute.org>)