

[← Go Back \(/\)](#)

# removeSamples, v12

Remove samples in dataset (.gct), using a list of samples provided

**Author:** Barbara Weir;Broad Institute

**Contact:** bweir@broadinstitute.org

**Algorithm Version:**

## Introduction

removeSamples is a GenePattern module that removes user-defined samples from a dataset. The user inputs their dataset as a GCT file, along with a text file containing the list of samples to be removed. The module outputs a GCT file containing the dataset with the user-defined samples removed.

## Parameters

Name	Description
gct file *	Data file containing samples to be removed in a GCT file format.
removelist *	Text file containing the list of samples to remove. Each sample should be on a separate line and must match a sample name in the file exactly.
extension *	User defined prefix for the output file.

\* - required

## Input Files

1. gct file  
Data file containing samplese to be removed in a GCT file format.
2. removelist  
Text file containing the list of samples to remove. Each sample should be on a separate line and must match a sample name in the file exactly.

# Output Files

1. Data file with samples removed *[extension].gct*

A GCT file containing the user-inputted dataset with the samples in the removelist text file removed from the dataset.

# Platform Dependencies

**Task Type:**

RNAi

**CPU Type:**

any

**Operating System:**


any

**Language:**

R

# Version Comments

Version	Release Date	Description
12		

 **BROAD**  
INSTITUTE (http://www.broadinstitute.org)©2021  
Broad Institute of MIT & Harvard (http://www.broadinstitute.org)