

## **ExpressionFileCreator Documentation**

**Module name:** ExpressionFileCreator

**Description:** Creates a gct or res file from a set of cel files

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**Summary**: Creates a res or gct file from a set of cel files. The cel files are given in one zip file.

**Usage/Example:** efc.out <- ExpressionFileCreator (input.filename='my.cel.files.zip')

Parameters:

Name Description

input filename A zip file containing CEL files or zipped CEL files

output file The base name of the output file

method The method to use

quantile normalization (RMA only) Whether to normalize data using quantile normalization background correct using RMA background

correction

scale value (MAS5 only) Value at which all arrays will be scaled to compute present absent calls (MAS5 only) Whether to compute Present/Absent calls

normalization The normalization method to apply after expression values are computed sample index: (mean or median scaling only) The sample index (starting at 1) to be

used as a reference for normalization

class filename tab-delimitted text file containing one scan and class per line

**Return Value:** An R list with components:

1. gct or res file

## Platform dependencies:

Task type: Preprocess&Utility

CPU type: any
OS: any
Language: R
Support files: expr.R

**Native command line:** <R> libdir>expr.R create.expression.file -i<input.filename> -o<output.file> -m<method> -q<quantile.normalization> -b<br/>c<compute.present.absent.calls> -n<normalization> -x<sample.index> -f<class.filename> -llibdir>