

# Package ‘DealGPL570’

November 12, 2019

**Title** Dealing GPL570 RAW.tar file

**Version** 0.0.1

**Description** Dealing GPL570 (Affymetrix Human Genome U133 Plus 2.0 Array) RAW.tar file using the robust multi-array average expression measure and returning expression profile.

**Depends** R (>= 3.5.0)

**License** Artistic-2.0

**Encoding** UTF-8

**LazyData** true

**Imports** dplyr, stringr, GEOquery, affy, tibble

**Suggests** BiocGenerics, knitr, rmarkdown, spelling

**RoxygenNote** 6.1.1

**VignetteBuilder** knitr

**Language** en-US

**NeedsCompilation** no

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**Repository** CRAN

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DealGPL570	<i>Dealing GPL570 (Affymetrix Human Genome U133 Plus 2.0 Array) RAW.tar file using the robust multi-array average expression measure</i>
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**Description**

Dealing GPL570 (Affymetrix Human Genome U133 Plus 2.0 Array) RAW.tar file using the robust multi-array average expression measure

**Usage**

```
DealGPL570(file, type = "probeIDAndGeneSymbol")
```

**Arguments**

file	a file name specified by either a variable of mode character, or a double-quoted string, which is of 'GSE*_RAW.tar' which is of platform GPL570.
type	a character string indicating which type of data frame is to be outputted. One of 'probeIDAndGeneSymbol'(default), 'probeID', or 'geneSymbol'.

**Value**

a expression profile.

**Examples**

```
# You can put your own `GSE*_RAW.tar` under the working directory,  
# now we download one online and have a test.  
# Next step would run for about 30s, so you can try it yourself or view the vignettes  
  
GEOquery::getGEOSuppFiles("GSE104683", makeDirectory = FALSE, baseDir = tempdir())  
file <- list.files(path = tempdir(), pattern = "GSE104683_RAW.tar", full.names = TRUE)  
file  
result <- DealGPL570(file = file)
```

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