

# Package ‘zFPKM’

April 10, 2025

**Title** A suite of functions to facilitate zFPKM transformations

**Version** 1.29.0

**Description** Perform the zFPKM transform on RNA-seq FPKM data. This algorithm is based on the publication by Hart et al., 2013 (Pubmed ID 24215113). Reference recommends using zFPKM > -3 to select expressed genes. Validated with encode open/closed chromosome data. Works well for gene level data using FPKM or TPM. Does not appear to calibrate well for transcript level data.

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**URL** <https://github.com/ronammar/zFPKM/>

**BugReports** <https://github.com/ronammar/zFPKM/issues>

**Imports** checkmate, dplyr, ggplot2, tidyr, SummarizedExperiment

**Suggests** knitr, limma, edgeR, GEOquery, stringr, printr, rmarkdown

**VignetteBuilder** knitr

**biocViews** ImmunoOncology, RNASeq, FeatureExtraction, Software, GeneExpression

**Depends** R (>= 3.4.0)

**LazyData** true

**RoxygenNote** 6.0.1

**git\_url** <https://git.bioconductor.org/packages/zFPKM>

**git\_branch** devel

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## Contents

zFPKM . . . . .	2
zFPKMPlot . . . . .	3
<b>Index</b>	<b>5</b>

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zFPKM	<i>zFPKM Transformation</i>
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### Description

Perform the zFPKM transform on RNA-seq FPKM data. This algorithm is based on the publication by Hart et al., 2013 (Pubmed ID 24215113). Reference recommends using zFPKM > -3 to select expressed genes. Validated with encode open/closed promoter chromatin structure epigenetic data on six of the ENCODE cell lines. Works well for gene level data using FPKM or TPM. Does not appear to calibrate well for transcript level data.

### Usage

```
zFPKM(fpkmDF, assayName = "fpkm")
```

### Arguments

fpkmDF	A SummarizedExperiment or data frame containing raw FPKM (or TPM) values. Each row corresponds to a gene/transcript and each column corresponds to a sample. NOTE: these are NOT log <sub>2</sub> transformed. Also, the rownames are gene/transcript names and NOT included as a separate column
assayName	When input is a SummarizedExperiment, names the specific assay. Typically one of "fpkm" or "tpm" [default = "fpkm"]

### Value

zFPKM data frame

### Author(s)

Ron Ammar, <ron.ammar@bms.com>

### References

<http://www.ncbi.nlm.nih.gov/pubmed/24215113>

**Examples**

```

library(dplyr)
gse94802 <- "ftp://ftp.ncbi.nlm.nih.gov/geo/series/GSE94nnn/GSE94802/suppl/GSE94802_Minkina_etal_normalized_FPKM"
temp <- tempfile()
download.file(gse94802, temp)
fpkm <- read.csv(gzfile(temp), row.names=1)
MyFPKMdf <- select(fpkm, -MGI_Symbol)

zfpkm <- zFPKM(MyFPKMdf)

```

zFPKMPlot

*zFPKM Transformation***Description**

Perform the zFPKM transform on RNA-seq FPKM data. This algorithm is based on the publication by Hart et al., 2013 (Pubmed ID 24215113). Reference recommends using zFPKM > -3 to select expressed genes. Validated with encode open/closed promoter chromatin structure epigenetic data on six of the ENCODE cell lines. Works well for gene level data using FPKM or TPM. Does not appear to calibrate well for transcript level data.

**Usage**

```

zFPKMPlot(fpkmDF, assayName = "fpkm", FacetTitles = FALSE,
          PlotXfloor = -20)

```

**Arguments**

fpkmDF	A SummarizedExperiment or data frame containing raw FPKM (or TPM) values. Each row corresponds to a gene/transcript and each column corresponds to a sample. NOTE: these are NOT log <sub>2</sub> transformed. Also, the rownames are gene/transcript names and NOT included as a separate column
assayName	When input is a SummarizedExperiment, names the specific assay. Typically one of "fpkm" or "tpm" [default = "fpkm"]
FacetTitles	use to label each facet with the sample name [default = FALSE]
PlotXfloor	Lower limit for X axis (log <sub>2</sub> FPKM units) [default = -20] set to NULL to disable

**Value**

Displays plots of zFPKM distributions

**Author(s)**

Ron Ammar, <ron.ammar@bms.com>

**References**

<http://www.ncbi.nlm.nih.gov/pubmed/24215113>

**Examples**

```
library(dplyr)
gse94802 <- "ftp://ftp.ncbi.nlm.nih.gov/geo/series/GSE94nnn/GSE94802/suppl/GSE94802_Minkina_etal_normalized_FPKM.txt.gz"
temp <- tempfile()
download.file(gse94802, temp)
fpkm <- read.csv(gzfile(temp), row.names=1)
MyFPKMdf <- select(fpkm, -MGI_Symbol)

zFPKMPlot(MyFPKMdf)
```

# Index

\* **zFPKM**

zFPKM, 2

zFPKMPlot, 3

zFPKM, 2

zFPKMPlot, 3