

# Package ‘RnaSeqSampleSizeData’

May 15, 2025

**Type** Package

**Title** RnaSeqSampleSizeData

**Version** 1.40.0

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**Description** RnaSeqSampleSizeData package provides the read counts and dispersion distribution from real RNA-seq experiments. It can be used by RnaSeqSampleSize package to estimate sample size and power for RNA-seq experiment design.

**License** GPL (>= 2)

**LazyLoad** yes

**LazyData** false

**Depends** edgeR,R (>= 2.10)

**VignetteBuilder** knitr

**Suggests** BiocStyle, knitr

**biocViews** ExperimentData, CancerData, RNASeqData

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

**git\_branch** RELEASE\_3\_21

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**Repository** Bioconductor 3.21

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|           |   |
|-----------|---|
| TCGA_BLCA | <i>Read counts and dispersion distribution for genes in TCGA BLCA data.</i> |
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### Description

Read counts and dispersion distribution for genes in TCGA BLCA data.

### Usage

TCGA\_BLCA

### Value

A class 'DGEList' from edgeR package.

### Source

[https://tcga-data.nci.nih.gov/tcgafiles/ftp\\_auth/distro\\_ftpusers/anonymous/tumor/blca/cgcc/unc.edu/illuminaHiSeq\\_rnaseqv2/rnaseqv2/unc.edu\\_BLCA.IlluminaHiSeq\\_RNASeqV2.Level\\_3.1.17.0/](https://tcga-data.nci.nih.gov/tcgafiles/ftp_auth/distro_ftpusers/anonymous/tumor/blca/cgcc/unc.edu/illuminaHiSeq_rnaseqv2/rnaseqv2/unc.edu_BLCA.IlluminaHiSeq_RNASeqV2.Level_3.1.17.0/)

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|           |   |
|-----------|---|
| TCGA_BRCA | <i>Read counts and dispersion distribution for genes in TCGA BRCA data.</i> |
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### Description

Read counts and dispersion distribution for genes in TCGA BRCA data.

### Usage

TCGA\_BRCA

**Value**

A class 'DGEList' from edgeR package.

**Source**

[https://tcga-data.nci.nih.gov/tcgafiles/ftp\\_auth/distro\\_ftpusers/anonymous/tumor/brca/cgcc/unc.edu/illuminaHiSeq\\_rnaseqv2/rnaseqv2/unc.edu\\_BRCA.IlluminaHiSeq\\_RNASeqV2.Level\\_3.1.10.0/](https://tcga-data.nci.nih.gov/tcgafiles/ftp_auth/distro_ftpusers/anonymous/tumor/brca/cgcc/unc.edu/illuminaHiSeq_rnaseqv2/rnaseqv2/unc.edu_BRCA.IlluminaHiSeq_RNASeqV2.Level_3.1.10.0/)

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|           |   |
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| TCGA_CESC | <i>Read counts and dispersion distribution for genes in TCGA CESC data.</i> |
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**Description**

Read counts and dispersion distribution for genes in TCGA CESC data.

**Usage**

TCGA\_CESC

**Value**

A class 'DGEList' from edgeR package.

**Source**

[https://tcga-data.nci.nih.gov/tcgafiles/ftp\\_auth/distro\\_ftpusers/anonymous/tumor/cesc/cgcc/unc.edu/illuminaHiSeq\\_rnaseqv2/rnaseqv2/](https://tcga-data.nci.nih.gov/tcgafiles/ftp_auth/distro_ftpusers/anonymous/tumor/cesc/cgcc/unc.edu/illuminaHiSeq_rnaseqv2/rnaseqv2/)

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|           |   |
|-----------|---|
| TCGA_COAD | <i>Read counts and dispersion distribution for genes in TCGA COAD data.</i> |
|-----------|---|

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**Description**

Read counts and dispersion distribution for genes in TCGA COAD data.

**Usage**

TCGA\_COAD

**Value**

A class 'DGEList' from edgeR package.

**Source**

[https://tcga-data.nci.nih.gov/tcgafiles/ftp\\_auth/distro\\_ftpusers/anonymous/tumor/coad/cgcc/unc.edu/illuminahiseq\\_rnaseqv2/rnaseqv2/unc.edu\\_COAD.IlluminaHiSeq\\_RNASeqV2.Level\\_3.1.9.0/](https://tcga-data.nci.nih.gov/tcgafiles/ftp_auth/distro_ftpusers/anonymous/tumor/coad/cgcc/unc.edu/illuminahiseq_rnaseqv2/rnaseqv2/unc.edu_COAD.IlluminaHiSeq_RNASeqV2.Level_3.1.9.0/)

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|           |   |
|-----------|---|
| TCGA_HNSC | <i>Read counts and dispersion distribution for genes in TCGA HNSC data.</i> |
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**Description**

Read counts and dispersion distribution for genes in TCGA HNSC data.

**Usage**

TCGA\_HNSC

**Value**

A class 'DGEList' from edgeR package.

**Source**

[https://tcga-data.nci.nih.gov/tcgafiles/ftp\\_auth/distro\\_ftpusers/anonymous/tumor/hnsc/cgcc/unc.edu/illuminahiseq\\_rnaseqv2/rnaseqv2/unc.edu\\_HNSC.IlluminaHiSeq\\_RNASeqV2.Level\\_3.1.7.0/](https://tcga-data.nci.nih.gov/tcgafiles/ftp_auth/distro_ftpusers/anonymous/tumor/hnsc/cgcc/unc.edu/illuminahiseq_rnaseqv2/rnaseqv2/unc.edu_HNSC.IlluminaHiSeq_RNASeqV2.Level_3.1.7.0/)

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|           |   |
|-----------|---|
| TCGA_KIRC | <i>Read counts and dispersion distribution for genes in TCGA KIRC data.</i> |
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**Description**

Read counts and dispersion distribution for genes in TCGA KIRC data.

**Usage**

TCGA\_KIRC

**Value**

A class 'DGEList' from edgeR package.

**Source**

[https://tcga-data.nci.nih.gov/tcgafiles/ftp\\_auth/distro\\_ftpusers/anonymous/tumor/kirc/cgcc/unc.edu/illuminahiseq\\_rnaseqv2/rnaseqv2/unc.edu\\_KIRC.IlluminaHiSeq\\_RNASeqV2.Level\\_3.1.5.0/](https://tcga-data.nci.nih.gov/tcgafiles/ftp_auth/distro_ftpusers/anonymous/tumor/kirc/cgcc/unc.edu/illuminahiseq_rnaseqv2/rnaseqv2/unc.edu_KIRC.IlluminaHiSeq_RNASeqV2.Level_3.1.5.0/)

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TCGA\_LGG

*Read counts and dispersion distribution for genes in TCGA LGG data.*

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**Description**

Read counts and dispersion distribution for genes in TCGA LGG data.

**Usage**

TCGA\_LGG

**Value**

A class 'DGEList' from edgeR package.

**Source**

[https://tcga-data.nci.nih.gov/tcgafiles/ftp\\_auth/distro\\_ftpusers/anonymous/tumor/lgg/cgcc/unc.edu/illuminahisec\\_rnaseqv2/rnaseqv2/unc.edu\\_LGG.IlluminaHiSeq\\_RNASeqV2.Level\\_3.1.12.0/](https://tcga-data.nci.nih.gov/tcgafiles/ftp_auth/distro_ftpusers/anonymous/tumor/lgg/cgcc/unc.edu/illuminahisec_rnaseqv2/rnaseqv2/unc.edu_LGG.IlluminaHiSeq_RNASeqV2.Level_3.1.12.0/)

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TCGA\_LUAD

*Read counts and dispersion distribution for genes in TCGA LUAD data.*

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**Description**

Read counts and dispersion distribution for genes in TCGA LUAD data.

**Usage**

TCGA\_LUAD

**Value**

A class 'DGEList' from edgeR package.

**Source**

[https://tcga-data.nci.nih.gov/tcgafiles/ftp\\_auth/distro\\_ftpusers/anonymous/tumor/luad/cgcc/unc.edu/illuminahisec\\_rnaseqv2/rnaseqv2/unc.edu\\_LUAD.IlluminaHiSeq\\_RNASeqV2.Level\\_3.1.13.0/](https://tcga-data.nci.nih.gov/tcgafiles/ftp_auth/distro_ftpusers/anonymous/tumor/luad/cgcc/unc.edu/illuminahisec_rnaseqv2/rnaseqv2/unc.edu_LUAD.IlluminaHiSeq_RNASeqV2.Level_3.1.13.0/)

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|           |   |
|-----------|---|
| TCGA_LUSC | <i>Read counts and dispersion distribution for genes in TCGA LUSC data.</i> |
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**Description**

Read counts and dispersion distribution for genes in TCGA LUSC data.

**Usage**

TCGA\_LUSC

**Value**

A class 'DGEList' from edgeR package.

**Source**

[https://tcga-data.nci.nih.gov/tcgafiles/ftp\\_auth/distro\\_ftpusers/anonymous/tumor/lusc/cgcc/unc.edu/illuminahiseq\\_rnaseqv2/rnaseqv2/unc.edu\\_LUSC.IlluminaHiSeq\\_RNASeqV2.Level\\_3.1.9.0/](https://tcga-data.nci.nih.gov/tcgafiles/ftp_auth/distro_ftpusers/anonymous/tumor/lusc/cgcc/unc.edu/illuminahiseq_rnaseqv2/rnaseqv2/unc.edu_LUSC.IlluminaHiSeq_RNASeqV2.Level_3.1.9.0/)

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|           |   |
|-----------|---|
| TCGA_PRAD | <i>Read counts and dispersion distribution for genes in TCGA PRAD data.</i> |
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**Description**

Read counts and dispersion distribution for genes in TCGA PRAD data.

**Usage**

TCGA\_PRAD

**Value**

A class 'DGEList' from edgeR package.

**Source**

[https://tcga-data.nci.nih.gov/tcgafiles/ftp\\_auth/distro\\_ftpusers/anonymous/tumor/prad/cgcc/unc.edu/illuminahiseq\\_rnaseqv2/rnaseqv2/unc.edu\\_PRAD.IlluminaHiSeq\\_RNASeqV2.Level\\_3.1.12.0/](https://tcga-data.nci.nih.gov/tcgafiles/ftp_auth/distro_ftpusers/anonymous/tumor/prad/cgcc/unc.edu/illuminahiseq_rnaseqv2/rnaseqv2/unc.edu_PRAD.IlluminaHiSeq_RNASeqV2.Level_3.1.12.0/)

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|           |   |
|-----------|---|
| TCGA_READ | <i>Read counts and dispersion distribution for genes in TCGA READ data.</i> |
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**Description**

Read counts and dispersion distribution for genes in TCGA READ data.

**Usage**

TCGA\_READ

**Value**

A class 'DGEList' from edgeR package.

**Source**

[https://tcga-data.nci.nih.gov/tcgafiles/ftp\\_auth/distro\\_ftpusers/anonymous/tumor/read/cgcc/unc.edu/illuminahiseq\\_rnaseqv2/rnaseqv2/unc.edu\\_READ.IlluminaHiSeq\\_RNASeqV2.Level\\_3.1.8.0/](https://tcga-data.nci.nih.gov/tcgafiles/ftp_auth/distro_ftpusers/anonymous/tumor/read/cgcc/unc.edu/illuminahiseq_rnaseqv2/rnaseqv2/unc.edu_READ.IlluminaHiSeq_RNASeqV2.Level_3.1.8.0/)

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|           |   |
|-----------|---|
| TCGA_THCA | <i>Read counts and dispersion distribution for genes in TCGA THCA data.</i> |
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**Description**

Read counts and dispersion distribution for genes in TCGA THCA data.

**Usage**

TCGA\_THCA

**Value**

A class 'DGEList' from edgeR package.

**Source**

[https://tcga-data.nci.nih.gov/tcgafiles/ftp\\_auth/distro\\_ftpusers/anonymous/tumor/thca/cgcc/unc.edu/illuminahiseq\\_rnaseqv2/rnaseqv2/unc.edu\\_THCA.IlluminaHiSeq\\_RNASeqV2.Level\\_3.1.12.0/](https://tcga-data.nci.nih.gov/tcgafiles/ftp_auth/distro_ftpusers/anonymous/tumor/thca/cgcc/unc.edu/illuminahiseq_rnaseqv2/rnaseqv2/unc.edu_THCA.IlluminaHiSeq_RNASeqV2.Level_3.1.12.0/)

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TCGA\_UCEC

*Read counts and dispersion distribution for genes in TCGA UCEC data.*

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**Description**

Read counts and dispersion distribution for genes in TCGA UCEC data.

**Usage**

TCGA\_UCEC

**Value**

A class 'DGEList' from edgeR package.

**Source**

[https://tcga-data.nci.nih.gov/tcgafiles/ftp\\_auth/distro\\_ftpusers/anonymous/tumor/ucec/cgcc/unc.edu/illuminahisec\\_rnaseqv2/rnaseqv2/unc.edu\\_UCEC.IlluminaHiSeq\\_RNASeqV2.Level\\_3.1.10.0/](https://tcga-data.nci.nih.gov/tcgafiles/ftp_auth/distro_ftpusers/anonymous/tumor/ucec/cgcc/unc.edu/illuminahisec_rnaseqv2/rnaseqv2/unc.edu_UCEC.IlluminaHiSeq_RNASeqV2.Level_3.1.10.0/)



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