

Package ‘RnaSeqSampleSizeData’

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Type Package

Title RnaSeqSampleSizeData

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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

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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/

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/illuminahtseq_rnaseqv2/rnaseqv2/unc.edu_BRCA.IlluminaHiSeq_RNASeqV2.Level_3.1.10.0/

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/illuminahtseq_rnaseqv2/rnaseqv2/

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/illuminahisec_rnaseqv2/rnaseqv2/unc.edu_COAD.IlluminaHiSeq_RNASeqV2.Level_3.1.9.0/

TCGA_HNSC

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

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/illuminahisec_rnaseqv2/rnaseqv2/unc.edu_HNSC.IlluminaHiSeq_RNASeqV2.Level_3.1.7.0/

TCGA_KIRC

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

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/illuminahisec_rnaseqv2/rnaseqv2/unc.edu_KIRC.IlluminaHiSeq_RNASeqV2.Level_3.1.5.0/

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

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/illuminaHiSeq_rnaseqv2/rnaseqv2/unc.edu_LGG.IlluminaHiSeq_RNASeqV2.Level3.1.12.0/

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

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/illuminaHiSeq_rnaseqv2/rnaseqv2/unc.edu_LUAD.IlluminaHiSeq_RNASeqV2.Level3.1.13.0/

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/

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/

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/

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/

TCGA_UCEC	<i>Read counts and dispersion distribution for genes in TCGA UCEC data.</i>
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Description

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

Usage

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TCGA_UCEC
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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/illuminahtseq_rnaseqv2/rnaseqv2/unc.edu_UCEC.IlluminaHiSeq_RNASeqV2.Level_3.1.10.0/

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