

Package ‘tcgaWGBSData.hg19’

April 9, 2019

Type Package

Title Data

Version 1.0.0

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Depends R (>= 3.5.0), ExperimentHub

Imports bsseq, knitr

Suggests

Description Data package for WGBS Data in TCGA.

Data is stored as SummarizedExperiment Format.

See vignette on how to extract the data and perform differential methylation analysis.

biocViews Genome, SequencingData, ExperimentData, Homo_sapiens_Data, CancerData

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RoxygenNote 6.0.1

VignetteBuilder knitr

git_url <https://git.bioconductor.org/packages/tcgaWGBSData.hg19>

git_branch RELEASE_3_8

git_last_commit caf3bb2

git_last_commit_date 2018-11-19

Date/Publication 2019-04-09

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tcgaWGBSData.hg19-package

TCGA Whole Genome Bisulfite Sequencing (WGBS) data available as bsseq object.

Description

TCGA re-processed Whole Genome Bisulfite Sequencing (WGBS) data with 39 tumor samples and 8 normal samples. Publicly available BED file for these 47 samples can be found here. (<https://portal.gdc.cancer.gov/legacy-archive/search/f?filters=>

5D format These data have been processed and aligned to hg19 genome and are available as SummarizedExperiment objects and are available in ExperimentHub.

Details

See the vignette for examples of using these data to calculate mean methylation and conduct differential methylation analysis.

browseVignettes("tcgaWGBSData.hg19") Details of how these data were created are in the scripts/ directory of the source package.

Examples

```
library(ExperimentHub)
hub <- ExperimentHub()
x <- query(hub, "tcgaWGBSData.hg19")
## Not run:
## download resource
tcga_data <- x[["EH1661"]]
TCGA_bs <- x[["EH1662"]]
file.rename(from=tcga_data,to=paste0(dirname(tcga_data), '/assays.h5'))

## End(Not run)
```

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