

# Package ‘tcgaWGBSDData.hg19’

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**Type** Package

**Title** Data

**Version** 1.6.0

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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

**BugReports** <https://github.com/aryeelab/tcgaWGBSDData.hg19/issues>

**License** GPL-2

**RoxygenNote** 6.0.1

**VignetteBuilder** knitr

**git\_url** <https://git.bioconductor.org/packages/tcgaWGBSDData.hg19>

**git\_branch** RELEASE\_3\_11

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tcgaWGBSData.hg19-package

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

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## 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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## \* **utilities**

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