Package ‘FlowSorted.DLPFC.450k’

April 13, 2017

Version 1.10.0

Title Illumina HumanMethylation data on sorted frontal cortex cell populations

Description Raw data objects for the Illumina 450k DNA methylation microarrays.

Author Andrew E Jaffe, Zachary A. Kaminsky

Maintainer Andrew E Jaffe `<andrew.jaffe@libd.org>`

License Artistic-2.0

Depends R (>= 2.13.0), minfi

LazyData yes

biocViews Homo_sapiens_Data, MicroarrayData

NeedsCompilation no

R topics documented:

`FlowSorted.DLPFC.450k` *Illumina Human Methylation data from 450k on sorted frontal cortex cell populations*

Description

This `RGset` contains Illumina 450k DNA methylation measurements on 58 flow-sorted dorsolateral prefrontal cortex samples from non-psychiatric controls from Guintivano et al. 2013. These samples were separated into neuronal (NeuN+) and non-neuronal (NeuN-) cell type. These data can be used by the minfi package to estimate cellular composition from bulk frontal cortex samples. This data may also be useful to individuals as example Illumina 450k data for trying preprocessing methods across a variety of Bioconductor packages.

Usage

```
data(FlowSorted.DLPFC.450k)
```

Format

An object of class `RGset`.

Details

The `FlowSorted.DLPFC.450k` objects is based an samples assayed as part of Guintivano et al (2013).

References

Guintivano J., Aryee M.J., Kaminsky Z.A. *A cell epigenotype specific model for the correction of brain cellular heterogeneity bias and its application to age, brain region and major depression.* Epigenetics. 2013 Mar;8(3):290-302. `http://www.landesbioscience.com/journals/epi/abstract.php?id=23924`

Examples

```
data(FlowSorted.DLPFC.450k)
```

Index