Package 'FlowSorted.DLPFC.450k'

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Version 1.14.0

Title Illumina HumanMethylation data on sorted frontal cortex cell
populations

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

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License Artistic-2.0

Depends R (>= 2.13.0), minfi (>= 1.21.2)

LazyData yes

biocViews ExperimentData, Homo_sapiens_Data, Tissue, MicroarrayData,
TissueMicroarrayData, MethylationArrayData

NeedsCompilation no

R topics documented:

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

Description

This `RGChannelSet` 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 types. 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 RGChannelSet.

Details

The FlowSorted.DLPFC.450k objects is based an samples assayed as part of Guintivano et al (2013). Please cite this paper, if the data is used. If you're using this data together with the minfi package, please see the package vignette for details on how to cite that package.

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), 8(3):290-302. doi: 10.4161/epi.23924.

Examples

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

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