

Package ‘FlowSorted.DLPFC.450k’

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Version 1.18.0

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 (>= 1.21.2)

LazyData yes

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

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R topics documented:

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

Description

This RChannelSet 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 on 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](https://doi.org/10.4161/epi.23924).

Examples

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

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*Topic **datasets**

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