

Package ‘FlowSorted.DLPFC.450k’

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Version 1.6.0

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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Depends R (>= 2.13.0), minfi

LazyData yes

biocViews Homo_sapiens_Data, MicroarrayData

NeedsCompilation no

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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)
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*Topic **datasets**

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