

Package 'FlowSorted.CordTissueAndBlood.EPIC'

May 4, 2018

Version 1.0.1

Date 2018-05-04

Title Illumina EPIC methylation data on isolated cord tissue and cord blood cells

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Description

Raw data objects to be used for cord tissue/blood cell-type composition estimation in minfi.

License GPL (>= 2.0)

Depends R (>= 3.2.0), minfi (>= 1.19.16),
IlluminaHumanMethylationEPICanno.ilm10b2.hg19 (>= 0.6.0),
IlluminaHumanMethylationEPICmanifest (>= 0.3.0)

LazyData yes

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

NeedsCompilation no

R topics documented:

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FlowSorted.CordBlood.EPIC.compTable

ANOVA F-test results for testing the association between methylation and cord blood isolated cell-types.

Description

Association of CpGs on the EPIC array with cord blood isolated cell-types. Please see manuscript for CpG filtering criteria.

Usage

```
data(FlowSorted.CordBlood.EPIC.compTable)
```

Format

A data frame with with 618,485 CpGs/rows and 11 variables/columns. See rowFtests in gene-filter/minfi for more information on the output.

Fstat F-statistic for association between methylation and cord blood isolated cell-types.

p.value p-value corresponding to F-statistic.

Bcell mean methylation level across 13 B cell samples.

CD4T mean methylation level across 14 CD4 T-cell samples.

CD8T mean methylation level across 14 CD8 T-cell samples.

Gran mean methylation level across 14 granulocyte samples.

Mono mean methylation level across 14 monocyte samples.

NK mean methylation level across 14 natural killer cell samples.

low minimum value of methylation across all samples.

high maximum value of methylation across all samples.

range range of methylation values across all samples.

Details

This dataset is similar to those given in the (adult) blood package, FlowSorted.Blood.450k. It can be used to evaluate the potential for confounding by cell-type heterogeneity at various EPIC probes in an epigenome-wide association study.

Value

A data frame with 618,485 CpGs/rows and 11 variables/columns.

Author(s)

Xinyi (Cindy) Lin

References

TBA

Examples

```
data(FlowSorted.CordBlood.EPIC.compTable)
dim(FlowSorted.CordBlood.EPIC.compTable)
head(FlowSorted.CordBlood.EPIC.compTable)
```

```
FlowSorted.CordTissue.EPIC.compTable
```

ANOVA F-test results for testing the association between methylation and cord tissue isolated cell-types.

Description

Association of CpGs on the EPIC array with cord tissue isolated cell-types. Please see manuscript for CpG filtering criteria.

Usage

```
data(FlowSorted.CordBlood.EPIC.compTable)
```

Format

A data frame with with 618,485 CpGs/rows and 8 variables/columns. See rowFtests in gene-filter/minfi for more information on the output.

Fstat F-statistic for association between methylation and cord tissue isolated cell-types.

p.value p-value corresponding to F-test statistic.

Stromal mean methylation level across 14 Stromal samples.

Endothelial mean methylation level across 11 Endothelial samples.

Epithelial mean methylation level across 13 Epithelial samples.

low minimum value of methylation across all samples.

high maximum value of methylation across all samples.

range range of methylation values across all samples.

Details

This dataset is similar to those given in the (adult) blood package, FlowSorted.Blood.450k. It can be used to evaluate the potential for confounding by cell-type heterogeneity at various EPIC probes in an epigenome-wide association study.

Value

A data frame with 618,485 CpGs/rows and 8 variables/columns.

References

TBA

Examples

```
data(FlowSorted.CordTissue.EPIC.compTable)
dim(FlowSorted.CordTissue.EPIC.compTable)
head(FlowSorted.CordTissue.EPIC.compTable)
```

FlowSorted.CordTissueAndBlood.EPIC

Illumina EPIC methylation data on isolated cord tissue and cord blood cells

Description

This RGChannelSet contains Illumina EPIC methylation measurements of isolated cells from cord tissue/cord blood from 14 infants. The 3 cell populations from cord tissue are: stromal, endothelial, epithelial. The 6 cell populations from cord blood are: B cells, CD4 T cells, CD8 T cells, granulocytes, monocytes, natural killer cells.

Usage

```
data(FlowSorted.CordTissueAndBlood.EPIC)
```

Details

Please see manuscript for additional details on samples.

Value

An RGChannelSet.

References

TBA

Examples

```
data(FlowSorted.CordTissueAndBlood.EPIC)
dim(FlowSorted.CordTissueAndBlood.EPIC)
head(FlowSorted.CordTissueAndBlood.EPIC)
pData(FlowSorted.CordTissueAndBlood.EPIC)
attributes(FlowSorted.CordTissueAndBlood.EPIC)
```

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