Package ‘FlowSorted.CordBlood.450k’

February 1, 2017

Type Package
Title Illumina 450k data on sorted cord blood cells
Version 1.2.0
Date 2016-01-21
Maintainer Shan V. Andrews <sandre17@jhu.edu>
Description Raw data objects to be used for cord blood cell proportion estimation in minfi.
License Artistic-2.0
Depends R (>= 3.2.0), minfi (>= 1.15.0)
LazyData yes
biocViews ExperimentData, Homo_sapiens_Data, MethylationArrayData, MicroarrayData
NeedsCompilation no
Author Shan V. Andrews [cre, aut], Kelly M. Bakulski [aut]

R topics documented:

FlowSorted.CordBlood.450k .............................................. 1
FlowSorted.CordBlood.450k.compTable .................................. 2

Index

FlowSorted.CordBlood.450k

*Illumina 450k data on sorted cord blood cell populations*

Description

This RGset contains Illumina 450k measurements on 17 cord blood samples, each of which contribute between 4 and 7 sorted cell populations. These 7 cell populations are: B cells, CD4 T cells, CD8 T cells, granulocytes, monocytes, natural killer cells, and nucleated red blood cells.

Usage
data(FlowSorted.CordBlood.450k)
Details

Please see manuscript for additional details on cord blood samples and prediction pipeline.

Value

An RGset.

References


Examples

data(FlowSorted.CordBlood.450k)

---

FlowSorted.CordBlood.450k.compTable

Cell composition association table

Description

Association of probes on the 450k with cord blood cell composition. Please see manuscript for probe filtering criteria.

Usage

data(FlowSorted.CordBlood.450k.compTable)

Format

A data frame with 429794 observations on the following 12 variables.

Fstat f-statistic for composition from ANOVA. See estimateCellCounts in minfi.
p.value p-value corresponding to f-statistic.
Bcell mean methylation level across 15 B cell replicates.
CD4T mean methylation level across 15 CD4 T-cell replicates.
CD8T mean methylation level across 14 CD8 T-cell replicates.
Gran mean methylation level across 12 granulocyte replicates.
Mono mean methylation level across 15 monocyte replicates.
NKT mean methylation level across 14 natural killer cell replicates.
NnRBC mean methylation level across 4 nucleated red blood cell replicates.
low low value of methylation across all samples.
high high value of methylation across all samples.
range range of methylation values across all samples.
Details

Our recommendations for this object parallel those given in the (adult) blood companion package, FlowSorted.Blood.450k. Briefly, this object can be used to evaluate the potential for confounding by cell-type heterogeneity at 450k probes following an association study.

Value

A data frame with 429794 observations and 12 variables.

References


Examples

data(FlowSorted.CordBlood.450k.compTable)

data(FlowSorted.CordBlood.450k.ModelPars)

Description

This object is generated during the course of cord blood cell proportion estimation in the minfi estimateCellCounts function.

Usage

data(FlowSorted.CordBlood.450k.ModelPars)

Details

A matrix of 700 rows and 7 columns, the latter corresponding to 7 cell types. 100 probes were selected as being differentially methylated by each cell type from the reference RGset contained herein (FlowSorted.CordBlood.450k). In the implementation of the estimateCellCounts function, probes are selected based on a combined RGset of user and reference data. Please see manuscript for details on the probe selection process.

Value

A matrix with 700 rows and 7 columns.

References


Examples

data(FlowSorted.CordBlood.450k.ModelPars)
Index

FlowSorted.CordBlood.450k, 1
FlowSorted.CordBlood.450k.compTable, 2