

# Package ‘FlowSorted.CordBlood.450k’

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**Type** Package

**Title** Illumina 450k data on sorted cord blood cells

**Version** 1.9.0

**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 (>= 1.21.2)

**LazyData** yes

**biocViews** ExperimentData, Homo\_sapiens\_Data, Tissue, MicroarrayData, TissueMicroarrayData, MethylationArrayData

**git\_url** <https://git.bioconductor.org/packages/FlowSorted.CordBlood.450k>

**git\_branch** master

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**git\_last\_commit\_date** 2018-04-30

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FlowSorted.CordBlood.450k

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

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### Description

This RGChannelSet 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 RGChannelSet.

### References

Bakulski KM, Feinberg JI, Yang J, Brown S, Andrews SV, McKenney S, Witter F, Walston J, Feinberg AP, Fallin MD. *DNA methylation of cord blood cell types: Applications for mixed cell birth studies*. Epigenetics (2016), 11:354-362. doi: [10.1080/15592294.2016.1161875](https://doi.org/10.1080/15592294.2016.1161875).

### Examples

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

---

FlowSorted.CordBlood.450k.compTable

*Cell composition association table*

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### 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.

`NK` mean methylation level across 14 natural killer cell replicates.

`nRBC` 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**

Bakulski KM, Feinberg JI, Yang J, Brown S, Andrews SV, McKenney S, Witter F, Walston J, Feinberg AP, Fallin MD. *DNA methylation of cord blood cell types: Applications for mixed cell birth studies*. Manuscript in review.

**Examples**

```
data(FlowSorted.CordBlood.450k.compTable)
```

---

```
FlowSorted.CordBlood.450k.ModelPars
```

*Model parameters for cord blood cell type estimation*

---

**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**

Bakulski KM, Feinberg JI, Yang J, Brown S, Andrews SV, McKenney S, Witter F, Walston J, Feinberg AP, Fallin MD. *DNA methylation of cord blood cell types: Applications for mixed cell birth studies*. Manuscript in review.

**Examples**

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

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