

# Package ‘BeadSorted.Saliva.EPIC’

November 18, 2025

**Title** Illumina EPIC data on BeadSorted child saliva cells

**Version** 1.19.0

**Description** Raw data objects used to estimate saliva cell proportion estimates in ewastools. The FlowSorted.Saliva.EPIC object is constructed from samples assayed by Lauren Middleton et. al. (2021).

**Depends** R (>= 4.1), minfi(>= 1.36.0), ExperimentHub

**biocViews** ExperimentData, Homo\_sapiens\_Data, MicroarrayData, Genome, MethylationArrayData, ExperimentHub

**License** GPL-3

**Encoding** UTF-8

**LazyData** true

**VignetteBuilder** knitr

**RoxygenNote** 7.1.1

**Suggests** knitr, rmarkdown

**git\_url** <https://git.bioconductor.org/packages/BeadSorted.Saliva.EPIC>

**git\_branch** devel

**git\_last\_commit** 56a3301

**git\_last\_commit\_date** 2025-10-29

**Repository** Bioconductor 3.23

**Date/Publication** 2025-11-18

**Author** Jonah Fisher [aut, cre],  
Kelly Bakulski [aut],  
Lauren Middleton [aut]

**Maintainer** Jonah Fisher <jazzfish@umich.edu>

## Contents

|                                            |   |
|--------------------------------------------|---|
| BeadSorted.Saliva.EPIC . . . . .           | 2 |
| BeadSorted.Saliva.EPIC.compTable . . . . . | 3 |
| BeadSorted.Saliva.EPIC.estimates . . . . . | 4 |

**Index****5**

---

BeadSorted.Saliva.EPIC*DNA Methylation RGChannelSet*

---

**Description**

Illumina Human Methylation data from EPIC on cell-sorted child saliva cell populations. The BeadSorted.Saliva.EPIC package contains Illumina HumanMethylationEPIC (“EPIC”) DNA methylation microarray data from Middleton and colleagues, consisting of 38 magnetic bead sorted saliva cell references from 22 samples, formatted as an RGChannelSet object for easy integration with other bioconductor packages.

This package contains data similar to other data packages for cell-type deconvolution, such as FlowSorted.Blood.450k and FlowSorted.Blood.EPIC. However, this package provides novel data from saliva biosamples.

Researchers may find this package useful as these samples represent cell populations (immune and epithelial cells) from cell-sorted saliva.

Implementation of cell-type estimation using these data can be performed using the **ewastools** package’s function `estimateLC`.

**Format**

An RGChannelSet, dimensions: 1051815 60

**Source**

<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE147318> The BeadSorted.Saliva.EPIC object is based on samples assayed by Lauren Middleton et al. (2021).

**See Also****References**

1. Lauren Y. M. Middleton, John Dou, Jonah Fisher, Jonathan A. Heiss, Vy K. Nguyen, Allan C. Just, Jessica Faul, Erin B. Ware, Colter Mitchell, Justin A. Colacino & Kelly M. Bakulski (2021) *Saliva cell type DNA methylation reference panel for epidemiological studies in children*, Epigenetics, DOI: 10.1080/15592294.2021.1890874
2. EA Houseman et al. (2012) *DNA methylation arrays as surrogate measures of cell mixture distribution*. BMC Bioinformatics 13, 86. doi:10.1186/1471-2105-13-86.
3. **ewastools** package with implementation for estimating cell type proportions in saliva using these data

<https://github.com/hhhh5/ewastools>

**Examples**

```
library(ExperimentHub)
query(ExperimentHub(), "BeadSorted.Saliva.EPIC")

BeadSorted.Saliva.EPIC <- ExperimentHub()[["EH4539"]]
BeadSorted.Saliva.EPIC
```

---

```
BeadSorted.Saliva.EPIC.compTable
```

*Cell Proportion Association Table*

---

**Description**

Association of each probe in the Illumina EPIC array with saliva cell type composition.

**Format**

A data frame with 795694 rows and 7 columns

**probeName** CpG identifier

**t-statistic** test statistic for the t-test between immune and epithelial compositions

**p-value** p-value for the t-test between immune and epithelial compositions

**averageMethylationImmune** average methylation beta value across immune cell samples

**averageMethylationEpithelial** average methylation beta value across epithelial cell samples

**low** minimum methylation beta across all samples

**high** maximum methylation beta across all samples

**Examples**

```
library(ExperimentHub)
query(ExperimentHub(), "BeadSorted.Saliva.EPIC.compTable")

BeadSorted.Saliva.EPIC.compTable <- ExperimentHub()[["EH4540"]]
BeadSorted.Saliva.EPIC.compTable
```

---

`BeadSorted.Saliva.EPIC.estimated`*Estimated cell proportion for samples*

---

**Description**

Cell-type proportion estimates for each of 60 samples from 22 children. Proportions were estimated using the `estimateLC` function from the **ewastools** package.

**Usage**`BeadSorted.Saliva.EPIC.estimated`**Format**

A data frame with 60 rows and 4 columns

**sampid** Sample identifier

**immuneCells** Estimated proportion of immune cells in sample

**epithelialCells** Estimate proportion of epithelial cells in sample

**See Also**

## References

1. EA Houseman et al. (2012) *DNA methylation arrays as surrogate measures of cell mixture distribution*. BMC Bioinformatics 13, 86. doi:10.1186/1471-2105-13-86.
2. **ewastools** package with implementation for estimating cell-type proportion in saliva using these data

<https://github.com/hhhh5/ewastools>

# Index

## \* **datasets**

BeadSorted.Saliva.EPIC.estimates,  
[4](#)

BeadSorted.Saliva.EPIC, [2](#)

BeadSorted.Saliva.EPIC.compTable, [3](#)

BeadSorted.Saliva.EPIC.estimates, [4](#)