

# Package ‘antiProfilesData’

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**Version** 1.28.0

**License** Artistic-2.0

**Title** Normal colon and cancer preprocessed affy data for antiProfile building.

**Description** Colon normal tissue and cancer samples used in Corrada Bravo, et al. gene expression anti-profiles paper: BMC Bioinformatics 2012, 13:272 doi:10.1186/1471-2105-13-272. Measurements are z-scores obtained from the GeneExpression Barcode in the 'frma' package

**LazyData** yes

**Depends** Biobase,

**Suggests** frma, GEOquery, GEOmetadb

**biocViews** ExperimentData, MicroarrayData, Tissue, CancerData, ColonCancerData

**Collate** 'antiProfilesData-package.r' 'apColonData.r'

**git\_url** <https://git.bioconductor.org/packages/antiProfilesData>

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antiProfilesData-package

*Curated dataset of normal and cancer samples on Affymetrix hgu133plus2 expression arrays.*

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### Description

Data used in Corrada Bravo, et al. gene expression anti-profiles paper: BMC Bioinformatics 2012, 13:272 doi:10.1186/1471-2105-13-272. Measurements are z-scores obtained from the GeneExpression Barcode in the 'frma' package. The full curated dataset in the same format containing many normal and cancer samples is available for download <http://cpcb.umd.edu/~hcorrada/antiProfiles>

### Author(s)

Hector Corrada Bravo

### References

Corrada Bravo, H., Pihur, V., McCall, M., Irizarry, R.A., Leek, J.T. (2012). "Gene expression anti-profiles as a basis for accurate universal cancer signatures" BMC Bioinformatics, 13:272

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apColonData

*Curated dataset of many colon normal and cancer samples on Affymetrix hgu133plus2 expression arrays.*

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### Description

Data used in Corrada Bravo, et al. gene expression anti-profiles paper: BMC Bioinformatics 2012, 13:272 doi:10.1186/1471-2105-13-272. Measurements are z-scores obtained from the GeneExpression Barcode in the 'frma' package. Only probes mapped to genes within colon cancer hypomethylation blocks defined in Hansen et al. are included.

### format

Data is an `ExpressionSet` object. The `exprs` slot contains gene expression barcode z-scores from frma preprocessed data. The `phenoData` slot contains a data frame with the following columns:

`filename`: The CEL filename in the Gene Expression Omnibus (GEO)

`DB_ID`: The GSM sample id in GEO

`ExperimentID`: The GSE experiment id in GEO

`Tissue`: Tissue type, obtained from the gene expression barcode annotation

`SubType`: Sample sub-type, obtained from the gene expression barcode annotation

`ClinicalGroup`: Clinical sample annotation, obtained from the gene expression barcode annotation

`Status`: Normal (0) or Cancer (1) indicator

**Author(s)**

Hector Corrada Bravo

**References**

Corrada Bravo, H., Pihur, V., McCall, M., Irizarry, R.A., Leek, J.T. (2012). "Gene expression anti-profiles as a basis for accurate universal cancer signatures" *BMC Bioinformatics*, 13:272

Hansen, K. D., Timp, W., Bravo, H. C., Sabunciyar, S., Langmead, B., McDonald, O. G., Wen, B., et al. (2011). "Increased methylation variation in epigenetic domains across cancer types." *Nature Genetics*, 43(8), 768

**See Also**

[ExpressionSet](#) for the class definition, [frma](#) for the preprocessing method used, [barcode](#) for the function to obtain the z-score definition.

**Examples**

```
data(apColonData)
pData(apColonData)
```

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