# Package 'antiProfilesData'

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**Version** 1.48.0

**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'

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

## 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://cbcb.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

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

## 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)

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## 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., Sabunciyan, 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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