Package ‘antiProfilesData’

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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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