Package 'mAPKLData'

April 11, 2023

Type Package

Title Gene expression data for testing of the package mAPKL.

Version 1.30.0

Date 2014-12-14

Description Gene expression data from a breast cancer study published
by Turashvili et al. in 2007, provided as an eSet.

biocViews ExperimentData, ExpressionData, Cancer, Breast

Author Argiris Sakellariou

Maintainer Argiris Sakellariou <a.sakellariou@gonkhosp.gr>

Depends R (>= 3.2.0)

Suggests Biobase

LazyLoad yes

License Artistic-2.0

git_url https://git.bioconductor.org/packages/mAPKLData

git_branch RELEASE_3_16

git_last_commit 988de37

git_last_commit_date 2022-11-01

Date/Publication 2023-04-11

R topics documented:

---

mAPKLData   *Gene expression data from Turashvili et al. in 2007*

Description

This dataset contains the gene expression and clinical data as published in Turashvili et al. 2007.

Usage

    data(mAPKLData)

Format

ExpressionSet with 54675 features and 30 samples, containing:

- exprs(mAPKLData): Matrix containing gene expressions as measured by Affymetrix hgu133plus2 technology.

- pData(mAPKLData): AnnotatedDataFrame containing Clinical information of the invasive lobular and ductal breast carcinomas.

- annotation(mAPKLData): Name of the affy chip.

Details

This dataset represent the study published by Turashvili et al. 2007.

- BACKGROUND: Invasive ductal and lobular carcinomas (IDC and ILC) are the most common histological types of breast cancer. Clinical follow-up data and metastatic patterns suggest that the development and progression of these tumors are different. The aim of our study was to identify gene expression profiles of IDC and ILC in relation to normal breast epithelial cells.

- METHODS: We examined 30 samples (normal ductal and lobular cells from 10 patients, IDC cells from 5 patients, ILC cells from 5 patients) microdissected from cryosections of ten mastectomy specimens from postmenopausal patients. Fifty nanograms of total RNA were amplified and labeled by PCR and in vitro transcription. Samples were analysed upon Affymetrix U133 Plus 2.0 Arrays. The expression of seven differentially expressed genes (CDH1, EMP1, DDR1, DVL1, KRT5, KRT6, KRT17) was verified by immunohistochemistry on tissue microarrays. Expression of ASPN mRNA was validated by in situ hybridization on frozen sections, and CTHRC1, ASPN and COL3A1 were tested by PCR.

- RESULTS: Using GCOS pairwise comparison algorithm and rank products we have identified 84 named genes common to ILC versus normal cell types, 74 named genes common to IDC versus normal cell types, 78 named genes differentially expressed between normal ductal and lobular cells, and 28 named genes between IDC and ILC. Genes distinguishing between IDC and ILC are involved in epithelial-mesenchymal transition, TGF-beta and Wnt signaling. These changes were present in both tumor types but appeared to be more prominent in ILC. Immunohistochemistry for several novel markers (EMP1, DVL1, DDR1) distinguished large sets of IDC from ILC.

- CONCLUSION: IDC and ILC can be differentiated both at the gene and protein levels. In this study we report two candidate genes, asporin (ASPN) and collagen triple helix repeat containing 1 (CTHRC1) which might be significant in breast carcinogenesis. Besides E-cadherin, the proteins validated on tissue microarrays (EMP1, DVL1, DDR1) may represent novel immunohistochemical markers helpful in distinguishing between IDC and ILC. Further studies with larger sets of patients are needed to verify the gene expression profiles of various histological types of breast cancer in order to determine molecular subclassifications, prognosis and the optimum treatment strategies.

Source

http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE5764

References

Turashvili G, Bouchal J, Baumforth K, Wei W, Dziechciarkova M, Ehrmann J, Klein J, Fridman E, Skarda J, Srovnal J et al: **Novel markers for differentiation of lobular and ductal invasive breast carcinomas by laser microdissection and microarray analysis.** *BMC cancer* 2007, **7**:55.

Examples

```
## load Biobase package
library(Biobase)
## load the dataset
data(mAPKLData)
## show the first 5 rows and columns of the expression data
exprs(mAPKLData)[1:5,1:5]
## show the first 6 rows of the phenotype data
head(pData(mAPKLData))
## show first 20 featuren names
featureNames(mAPKLData)[1:20]
## show the experiment data summary
experimentData(mAPKLData)
```

Index