

# Package ‘receptLoss’

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**Type** Package

**Title** Unsupervised Identification of Genes with Expression Loss in Subsets of Tumors

**Version** 1.20.0

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**Description** receptLoss identifies genes whose expression is lost in subsets of tumors relative to normal tissue. It is particularly well-suited in cases where the number of normal tissue samples is small, as the distribution of gene expression in normal tissue samples is approximated by a Gaussian. Originally designed for identifying nuclear hormone receptor expression loss but can be applied transcriptome wide as well.

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**Encoding** UTF-8

**LazyData** true

**Depends** R (>= 3.6.0)

**RoxygenNote** 7.1.0

**Imports** dplyr, ggplot2, magrittr, tidyr, SummarizedExperiment

**Suggests** knitr, rmarkdown, testthat (>= 2.1.0), here

**VignetteBuilder** knitr

**biocViews** GeneExpression, StatisticalMethod

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nhrs

*Table of Nuclear Hormone Receptors (NHRs)*

## Description

This object contains a table of all known NHRs and was adapted from the 'guidetopharmacology' website (see references). It was joined with a bioMart table to include ensemble gene ids, which are commonly used gene symbols.

## Usage

nhrs

## Format

A tibble with 54 rows and 6 variables:

**hgnc\_symbol** the HUGO gene nomenclature committee (HGNC) symbol (letters and numbers, ex. THRB)

**hgnc\_id** the HUGO gene nomenclature committee (HGNC) symbol (a number, ex. 11799)

**hgnc\_name** the HUGO gene nomenclature committee (HGNC) gene name (ex. "Thyroid hormone receptor beta")

**entrez\_gene\_id** the entrez gene id (a number, ex. 7068)

**ensembl\_gene\_id** the ensembl gene id (ex. ENSG00000151090, always starts with ENSG)

**synonyms** words or gene symbols in the literature that refer to the same gene

## Source

[http://www.guidetopharmacology.org/DATA/targets\\_and\\_families.csv](http://www.guidetopharmacology.org/DATA/targets_and_families.csv)

<http://www.biomart.org/>

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|              |                                                 |
|--------------|-------------------------------------------------|
| nSdBelowMean | <i>Calculate value N std dev away from mean</i> |
|--------------|-------------------------------------------------|

---

**Description**

This function allows you to identify genes with loss of expression

**Usage**

```
nSdBelowMean(mn, stdv, n)
```

**Arguments**

|      |                                           |
|------|-------------------------------------------|
| mn   | Mean of distribution                      |
| stdv | std dev of distribution                   |
| n    | number of std dev below mean to calculate |

**Value**

the value 'n' standard deviations below the mean 'mn'

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|                |                                                     |
|----------------|-----------------------------------------------------|
| plotReceptLoss | <i>Plot histogram of genes with expression loss</i> |
|----------------|-----------------------------------------------------|

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**Description**

This function allows you to plot histograms of tumor and adj normal data

**Usage**

```
plotReceptLoss(exprMatrNm1, exprMatrTum, rldf, geneName, addToTitle = "", clr)
```

**Arguments**

|             |                                                                                                                                                             |
|-------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------|
| exprMatrNm1 | A matrix of expression values from normal tissue. Each row is a gene, and each column is a patient or sample. Genes should be in same order as exprMatrTum. |
| exprMatrTum | A matrix of expression values from tumor tissue. Each row is a gene, and each column is a patient or sample. Genes should be in same order as exprMatrNm1.  |
| rldf        | The dataframe output from running the receptLoss function                                                                                                   |
| geneName    | The name of the gene to plot. The name of the gene should correspond to a row name in both exprMatrNm1 and exprMatrTum matrices.                            |
| addToTitle  | A string that can be added to the title, which includes the gene name.                                                                                      |
| clr         | Vector of length 2 containing colors to use for plot                                                                                                        |

**Value**

returns an object of class 'ggplot'

**Examples**

```
exprMatrNml <- matrix(abs(rnorm(100, mean=2))), nrow=10)
exprMatrTum <- matrix(abs(rnorm(100))), nrow=10)
geneNames <- paste0(letters[seq_len(nrow(exprMatrNml))],
  seq_len(nrow(exprMatrNml)))
rownames(exprMatrNml) <- rownames(exprMatrTum) <- geneNames
nSdBelow <- 2
minPropPerGroup <- .2
r1 <- receptLoss(exprMatrNml, exprMatrTum, nSdBelow, minPropPerGroup)
clrs <- c("#E78AC3", "#8DA0CB")
plotReceptLoss(exprMatrNml, exprMatrTum, r1, geneName="g7", clrs=clrs)
```

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receptLoss

*Identify genes with expression loss*


---

**Description**

This function allows you to identify genes with loss of expression

**Usage**

```
receptLoss(exprMatrNml, exprMatrTum, nSdBelow, minPropPerGroup)
```

**Arguments**

|                 |                                                                                                                                                                                            |
|-----------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| exprMatrNml     | A matrix of expression values from normal tissue. Each row is a gene, and each column is a patient or sample. Genes should be in same order as exprMatrTum.                                |
| exprMatrTum     | A matrix of expression values from tumor tissue. Each row is a gene, and each column is a patient or sample. Genes should be in same order as exprMatrNml.                                 |
| nSdBelow        | The number of SD below the mean of the adjacent normal tissue to set the boundary between tumor subgroups.                                                                                 |
| minPropPerGroup | A value between 0-1 that represents the minimum proportion of samples that should be present in each of the two subgroups (defined by the boundary set by nSdBelow) for a particular gene. |

**Value**

a nx7 matrix, with n equaling the number of genes. The columns are as follows:

- geneNm - the gene name
- lowerBound - the lower bound, or the value 'nSdBelow' the mean of the normal tissue expression data.

- `propTumLessThBound` - the proportion of tumor samples with expression levels less than `'lowerBound'`
- `muAb` - "mu above", the mean expression value of tumors greater than (ie above) the `'lowerBound'`.
- `'muBl'` - "mu below", the mean expression value of tumors less than (ie below) the `'lowerBound'`.
- `'deltaMu'` - the difference between `'muAb'` and `'muBl'`.
- `meetsMinPropPerGrp` - a logical indicating whether the proportion of samples in each group is greater than that set by `'minPropPerGroup'`.

### Examples

```
exprMatrNm1 <- matrix(abs(rnorm(100, mean=2)), nrow=10)
exprMatrTum <- matrix(abs(rnorm(100)), nrow=10)
geneNames <- paste0(letters[seq_len(nrow(exprMatrNm1))],
  seq_len(nrow(exprMatrNm1)))
rownames(exprMatrNm1) <- rownames(exprMatrTum) <- geneNames
nSdBelow <- 2
minPropPerGroup <- .2
r1 <- receiptLoss(exprMatrNm1, exprMatrTum, nSdBelow, minPropPerGroup)
head(r1)
```

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toMatrix

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*Convert SummarizedExperiment or Dataframe to Matrix*


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### Description

This function converts `SummarizedExperiment` objects and dataframes (both S3 and S4) to matrices of expression values. Used within `receiptLoss` functions to convert all matrix-like objects to the matrix class.

### Usage

```
toMatrix(m, rwnms = NA)
```

### Arguments

|                    |                                                                                                                                                                      |
|--------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>m</code>     | Can be a matrix, a data.frame, a <code>DataFrame</code> , or <code>SummarizedExperiment</code> object.                                                               |
| <code>rwnms</code> | the rownames of the object. If NA (the default), assumes that the matrix-like object already has rownames, which in this case do not need to be supplied separately. |

### Value

A matrix of expression values

**Examples**

```
m <- as.data.frame(matrix(data=rgamma(n=100, shape=3, rate=2),  
  nrow=10, ncol=10))  
m <- toMatrix(m)
```

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