

# Package ‘receptLoss’

November 21, 2024

**Type** Package

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

**Version** 1.18.0

**Author** Daniel Pique, John Greally, Jessica Mar

**Maintainer** Daniel Pique <daniel.pique@med.einstein.yu.edu>

**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.

**License** GPL-3 + file LICENSE

**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

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

**git\_branch** RELEASE\_3\_20

**git\_last\_commit** f0b251d

**git\_last\_commit\_date** 2024-10-29

**Repository** Bioconductor 3.20

**Date/Publication** 2024-11-20

## Contents

nhrs . . . . .	2
nSdBelowMean . . . . .	3
plotReceptLoss . . . . .	3
receptLoss . . . . .	4
toMatrix . . . . .	5
<b>Index</b>	<b>6</b>

---

 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/>

---

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'

---

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

---

**Description**

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

**Usage**

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

**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.
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 exprMatrNml 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**

```

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 <- receptLoss(exprMatrNm1, exprMatrTum, nSdBelow, minPropPerGroup)
clrs <- c("#E78AC3", "#8DA0CB")
plotReceptLoss(exprMatrNm1, exprMatrTum, r1, geneName="g7", clrs=clrs)

```

receptLoss

*Identify genes with expression loss***Description**

This function allows you to identify genes with loss of expression

**Usage**

```
receptLoss(exprMatrNm1, exprMatrTum, nSdBelow, minPropPerGroup)
```

**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.
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)
```

---

**toMatrix***Convert SummarizedExperiment or Dataframe to Matrix*

---

**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, rownms = NA)
```

**Arguments**

<b>m</b>	Can be a matrix, a data.frame, a DataFrame, or SummarizedExperiment object.
<b>rownms</b>	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)
```

# Index

- \* **datasets**
    - nhrs, [2](#)
  - \* **expression,**
    - plotReceptLoss, [3](#)
    - receptLoss, [4](#)
  - \* **gene**
    - plotReceptLoss, [3](#)
    - receptLoss, [4](#)
  - \* **internal**
    - nSdBelowMean, [3](#)
    - toMatrix, [5](#)
  - \* **subgroups,**
    - plotReceptLoss, [3](#)
  - \* **subgroups**
    - receptLoss, [4](#)
  - \* **visualization**
    - plotReceptLoss, [3](#)
- nhrs, [2](#)  
nSdBelowMean, [3](#)  
  
plotReceptLoss, [3](#)  
  
receptLoss, [4](#)  
  
toMatrix, [5](#)