

# Package ‘receptLoss’

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**Type** Package

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

**Version** 1.2.0

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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.

**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>

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nhrs	<i>Table of Nuclear Hormone Receptors (NHRs)</i>
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**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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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(exprMatrNml, exprMatrTum, rldf, geneName, addToTitle = "", clrs)
```

**Arguments**

<code>exprMatrNml</code>	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 <code>exprMatrTum</code> .
<code>exprMatrTum</code>	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 <code>exprMatrNml</code> .
<code>r1df</code>	The dataframe output from running the <code>receptLoss</code> function
<code>geneName</code>	The name of the gene to plot. The name of the gene should correspond to a row name in both <code>exprMatrNml</code> and <code>exprMatrTum</code> matrices.
<code>addToTitle</code>	A string that can be added to the title, which includes the gene name.
<code>clrs</code>	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*


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**Description**

This function allows you to identify genes with loss of expression

**Usage**

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

**Arguments**

<code>exprMatrNml</code>	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 <code>exprMatrTum</code> .
<code>exprMatrTum</code>	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 <code>exprMatrNml</code> .
<code>nSdBelow</code>	The number of SD below the mean of the adjacent normal tissue to set the boundary between tumor subgroups.
<code>minPropPerGroup</code>	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 <code>nSdBelow</code> ) for a particular gene.

**Value**

a  $n \times 7$  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 <- receptLoss(exprMatrNm1, exprMatrTum, nSdBelow, minPropPerGroup)
head(r1)
```

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