

# Package ‘Neve2006’

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**Title** expression and CGH data on breast cancer cell lines

**Version** 0.44.0

**Author** M. Neve et al. in Gray Lab at LBL

**Description** Experimental organization of combined expression and CGH data

**Depends** R (>= 2.14.0), tools, methods, utils, Biobase (>= 1.14.0),  
hgu133a.db, annotate

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**License** Artistic-2.0

**LazyLoad** yes

**biocViews** ExperimentData, CancerData, BreastCancerData

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## Contents

cghExSet-class	1
logRatios	3
neveCGHmatch	4
<b>Index</b>	<b>5</b>

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cghExSet-class	<i>Class "cghExSet" for combining CGH and expression data</i>
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## Description

combination of an ExpressionSet and CGH assay results

## Usage

```
make_cghExSet(exprs, logRatios, cloneMeta, pd, mi, anno) # pd is AnnotatedDataFrame, mi is MIAME
```

**Arguments**

<code>exprs</code>	matrix of expression assay results
<code>logRatios</code>	matrix of aCGH assay results
<code>cloneMeta</code>	AnnotatedDataFrame for aCGH clone descriptions
<code>pd</code>	AnnotatedDataFrame for sample level data
<code>mi</code>	MIAME instance for experiment documentation
<code>anno</code>	character string with annotation platform descriptor for expression data

**Objects from the Class**

Objects can be created by calls of the form `new("cghExSet", phenoData, experimentData, annotation, exprs, logRatios, cloneMeta)`.

**Slots**

`cghAssays`: Object of class "AssayData" rectangular representation of logRatio data from CGH  
`cloneMeta`: Object of class "AnnotatedDataFrame" information on chromosome and offset of clones  
`assayData`: Object of class "AssayData" expression assay results  
`phenoData`: Object of class "AnnotatedDataFrame" sample level data  
`featureData`: Object of class "AnnotatedDataFrame" reporter level metadata for expression assay results  
`experimentData`: Object of class "MIAME" container for experiment documentation  
`annotation`: Object of class "character" identifiers for expression and CGH platforms, as a named vector with elements named 'exprs' and 'logRatios'  
`.__classVersion__`: Object of class "Versions"

**Extends**

Class `eSet-class`, directly. Class `VersionedBiobase-class`, by class "eSet", distance 2. Class `Versioned-class`, by class "eSet", distance 3.

**Methods**

**cloneMeta** signature(`cghSet = "cghExSet"`): extract annotated data frame on clone locations for CGH component  
**cloneNames** signature(`cghSet = "cghExSet"`): extract character vector of clone IDs for CGH component  
**exprs** signature(`object = "cghExSet"`): extract expression assay results  
**initialize** signature(`.Object = "cghExSet"`): infrastructure  
**logRatios** signature(`cghSet = "cghExSet"`): extract CGH assay results  
**show** signature(`object = "cghExSet"`): display object in concise form  
**"["** signature(`object = "cghExSet"`): when first index is set, subset expression features; when second, subset samples

**Author(s)**

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## References

R. M. Neve Cancer Cell Dec 2006

## Examples

```
showClass("cghExSet")
data(neveExCGH)
logRatios(neveExCGH)[1:4,]
exprs(neveExCGH)[1:4,]
```

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logRatios	<i>extractor for cghSet assay data</i>
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## Description

extractor for cghSet assay data

## Usage

```
logRatios(cghSet)
```

## Arguments

cghSet            instance of [cghSet](#) class

## Details

gets the AssayData element

## Value

matrix

## Author(s)

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## Examples

```
data(neveCGHmatch)
logRatios(neveCGHmatch)[1:4,1:4]
```

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`neveCGHmatch`*Neve Cancer Cell 2006 expression plus CGH data*

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**Description**

ExpressionSet and cghSet

**Usage**

```
data(neveCGHmatch)
data(neveRMAMatch)
data(neveExCGH)
```

**Format**

The individual datasets (aCGH and expression assays) take the form of a cghSet for neveCGHmatch and an ExpressionSet for neveRMAMatch. There are only 50 samples because only 50 could be aligned on the given sample name tokens in the caArrayDB data as of June 9 2007. Those sample name tokens are very mangled in the CEL files.

The combined data structure neveExCGH has a special container class [cghExSet](#).

**Source**

links are provided in the pdf of the Cancer Cell paper; see the PMID of `experimentData(neveCGHmatch)`

**References**

PMID 17157791

**Examples**

```
data(neveCGHmatch)
neveCGHmatch
logRatios(neveCGHmatch)[1:4,1:4]
data(neveRMAMatch)
neveRMAMatch
```

# Index

- \* **classes**
  - cghExSet-class, 1
- \* **datasets**
  - neveCGHmatch, 4
- \* **models**
  - logRatios, 3

[, cghExSet-method (cghExSet-class), 1

cghExSet, 4

cghExSet-class, 1

cghSet, 3

cghSet-class (logRatios), 3

cloneMeta (cghExSet-class), 1

cloneMeta, cghExSet-method  
(cghExSet-class), 1

cloneNames (cghExSet-class), 1

cloneNames, cghExSet-method  
(cghExSet-class), 1

exprs, cghExSet-method (cghExSet-class),  
1

initialize, cghExSet-method  
(cghExSet-class), 1

logRatios, 3

logRatios, cghExSet-method  
(cghExSet-class), 1

logRatios, cghSet-method (logRatios), 3

make\_cghExSet (cghExSet-class), 1

MIAME, 2

neveCGHmatch, 4

neveExCGH (neveCGHmatch), 4

neveRMAmatch (neveCGHmatch), 4

show, cghExSet-method (cghExSet-class), 1