

# Package ‘signifinder’

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**Type** Package

**Title** Collection and implementation of public transcriptional cancer signatures

**Version** 1.7.0

**Description** signifinder is an R package for computing and exploring a compendium of tumor signatures. It allows to compute a variety of signatures, based on gene expression values, and return single-sample scores. Currently, signifinder contains more than 60 distinct signatures collected from the literature, relating to multiple tumors and multiple cancer processes.

**License** AGPL-3

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**Imports** AnnotationDbi, BiocGenerics, ComplexHeatmap, consensusOV, cowplot, DGEobj.utils, dplyr, ensemblDb, ggplot2, ggridges, GSVA, IRanges, magrittr, matrixStats, maxstat, methods, openair, org.Hs.eg.db, patchwork, RColorBrewer, TxDb.Hsapiens.UCSC.hg19.knownGene, TxDb.Hsapiens.UCSC.hg38.knownGene, sparrow, SpatialExperiment, stats, SummarizedExperiment, survival, survminer, viridis

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signifinder-package	<i>signifinder: Collection and implementation of public transcriptional cancer signatures</i>
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## Description

signifinder is an R package for computing and exploring a compendium of tumor signatures. It allows to compute a variety of signatures, based on gene expression values, and return single-sample scores. Currently, signifinder contains more than 60 distinct signatures collected from the literature, relating to multiple tumors and multiple cancer processes.

## Author(s)

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## See Also

Useful links:

- <https://github.com/CaluraLab/signifinder>
- Report bugs at <https://github.com/CaluraLab/signifinder/issues>

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ADOSign

*Adenosine Signaling Signature*


---

### Description

This signature is computed accordingly to the reference paper, to have more details explore the function [availableSignatures](#).

### Usage

```
ADOSign(dataset, nametype = "SYMBOL", whichAssay = "norm_expr", ...)
```

### Arguments

dataset	Normalized expression values. A data frame or a matrix where rows correspond to genes and columns correspond to samples. Alternatively, an object of type <a href="#">SummarizedExperiment</a> , <a href="#">SingleCellExperiment</a> or <a href="#">SpatialExperiment</a> where the normalized expression values should be in an assay called 'norm_expr'.
nametype	character string saying the type of gene name ID (row names in dataset). Either one of "SYMBOL", "ENTREZID" or "ENSEMBL".
whichAssay	integer scalar or string indicating which assay of dataset to use.
...	other arguments passed on to the <a href="#">gsvaParam</a> function.

### Value

If dataset is a [SummarizedExperiment](#) object, then scores are added in the [colData](#) section. If dataset is a data frame or a matrix, then a [SummarizedExperiment](#) object is created in which scores are added in the [colData](#) section.

### Examples

```
data(ovse)
ADOSign(dataset = ovse)
```

---

APMSign

*Antigen Processing Machinery Signature*


---

### Description

This signature is computed accordingly to the reference paper, to have more details explore the function [availableSignatures](#).

**Usage**

```
APMSign(
  dataset,
  nametype = "SYMBOL",
  inputType = "microarray",
  author = "Wang",
  whichAssay = "norm_expr",
  hgReference = "hg38",
  ...
)
```

**Arguments**

dataset	Normalized expression values. A data frame or a matrix where rows correspond to genes and columns correspond to samples. Alternatively, an object of type <a href="#">SummarizedExperiment</a> , <a href="#">SingleCellExperiment</a> or <a href="#">SpatialExperiment</a> where the normalized expression values should be in an assay called 'norm_expr'.
nametype	character string saying the type of gene name ID (row names in dataset). Either one of "SYMBOL", "ENTREZID" or "ENSEMBL".
inputType	character string saying the type of data you are using. Either one of "microarray" or "rnaseq".
author	character string saying the first author of the signature publication. Check it in <a href="#">availableSignatures</a> .
whichAssay	integer scalar or string indicating which assay of dataset to use.
hgReference	character string saying the human reference genome. Either one of "hg19" or "hg38".
...	other arguments passed on to the <a href="#">gsvaParam</a> function.

**Value**

If dataset is a [SummarizedExperiment](#) object, then scores are added in the [colData](#) section. If dataset is a data frame or a matrix, then a [SummarizedExperiment](#) object is created in which scores are added in the [colData](#) section.

**Examples**

```
data(ovse)
APMSign(dataset = ovse)
```

---

ASCSign

*Adult Stem Cell Signature*


---

**Description**

This signature is computed accordingly to the reference paper, to have more details explore the function [availableSignatures](#).

**Usage**

```
ASCSign(dataset, nametype = "SYMBOL", whichAssay = "norm_expr")
```

**Arguments**

dataset	Normalized expression values. A data frame or a matrix where rows correspond to genes and columns correspond to samples. Alternatively, an object of type <a href="#">SummarizedExperiment</a> , <a href="#">SingleCellExperiment</a> or <a href="#">SpatialExperiment</a> where the normalized expression values should be in an assay called 'norm_expr'.
nametype	character string saying the type of gene name ID (row names in dataset). Either one of "SYMBOL", "ENTREZID" or "ENSEMBL".
whichAssay	integer scalar or string indicating which assay of dataset to use.

**Value**

If dataset is a [SummarizedExperiment](#) object, then scores are added in the [colData](#) section. If dataset is a data frame or a matrix, then a [SummarizedExperiment](#) object is created in which scores are added in the [colData](#) section.

**Examples**

```
data(ovse)
ASCSign(dataset = ovse)
```

---

autophagySign	<i>Autophagy Signature</i>
---------------	----------------------------

---

**Description**

This signature is computed accordingly to the reference paper, to have more details explore the function [availableSignatures](#).

**Usage**

```
autophagySign(
  dataset,
  nametype = "SYMBOL",
  author = "Xu",
  whichAssay = "norm_expr",
  hgReference = "hg38"
)
```

**Arguments**

dataset	Normalized expression values. A data frame or a matrix where rows correspond to genes and columns correspond to samples. Alternatively, an object of type <a href="#">SummarizedExperiment</a> , <a href="#">SingleCellExperiment</a> or <a href="#">SpatialExperiment</a> where the normalized expression values should be in an assay called 'norm_expr'.
nametype	character string saying the type of gene name ID (row names in dataset). Either one of "SYMBOL", "ENTREZID" or "ENSEMBL".

author	character string saying the first author of the signature publication. Check it in <a href="#">availableSignatures</a> .
whichAssay	integer scalar or string indicating which assay of dataset to use.
hgReference	character string saying the human reference genome. Either one of "hg19" or "hg38".

### Value

If dataset is a [SummarizedExperiment](#) object, then scores are added in the [colData](#) section. If dataset is a data frame or a matrix, then a [SummarizedExperiment](#) object is created in which scores are added in the [colData](#) section.

### Examples

```
data(ovse)
autophagySign(dataset = ovse)
```

---

availableSignatures      *Show Available Signatures*

---

### Description

It returns a table with all the information of the signatures collected in signifinder.

### Usage

```
availableSignatures(
  tumor = NULL,
  tissue = NULL,
  topic = NULL,
  requiredInput = NULL,
  description = TRUE
)
```

### Arguments

tumor	character vector saying the type of tumors for which signatures are developed. Used to filter the signatures in the table.
tissue	character vector saying the type of tissues for which signatures are developed. Used to filter the signatures in the table.
topic	character vector saying the signature topics. Used to filter the signatures in the table.
requiredInput	character string saying the type of data required in input by the signature. Either one of "microarray", "rnaseq" or "sc". Used to filter the signatures in the table.
description	logical. If TRUE it shows the signature's description.

**Value**

A data frame with 12 variables:

**signature** name of the signature

**scoreLabel** label of the signature when added inside colData section

**functionName** name of the function to use to compute the signature

**topic** main cancer topic of the signature

**tumor** tumor type for which the signature was developed

**tissue** tumor tissue for which the signature was developed

**cellType** cell type for which the signature was developed

**requiredInput** type of data with which the signature was developed

**transformationStep** data transformation step performed inside the function starting from the user's 'normArray' or 'normCounts' data

**author** first author of the work in which the signature is described

**reference** reference of the work

**description** signature description and how to evaluate its score ...

**Examples**

```
availableSignatures()
```

---

breastStateSign	<i>Breast Cancer Cellular States Signature</i>
-----------------	--

---

**Description**

This signature is computed accordingly to the reference paper, to have more details explore the function [availableSignatures](#).

**Usage**

```
breastStateSign(
  dataset,
  nametype = "SYMBOL",
  whichAssay = "norm_expr",
  isMalignant = NULL,
  hgReference = "hg38"
)
```

**Arguments**

dataset	Normalized expression values. A data frame or a matrix where rows correspond to genes and columns correspond to samples. Alternatively, an object of type <a href="#">SummarizedExperiment</a> , <a href="#">SingleCellExperiment</a> or <a href="#">SpatialExperiment</a> where the normalized expression values should be in an assay called 'norm_expr'.
nametype	character string saying the type of gene name ID (row names in dataset). Either one of "SYMBOL", "ENTREZID" or "ENSEMBL".



whichAssay	integer scalar or string indicating which assay of dataset to use.
isMalignant	logical vector of the same length of ncol(dataset), where TRUE states malignant cells and FALSE states non-malignant cells.
hgReference	character string saying the human reference genome. Either one of "hg19" or "hg38".

### Value

If dataset is a [SummarizedExperiment](#) object, then scores are added in the [colData](#) section. If dataset is a data frame or a matrix, then a [SummarizedExperiment](#) object is created in which scores are added in the [colData](#) section.

### Examples

```
data(ovse)
```

---

cellCycleSign	<i>Cell-cycle Signature classifier</i>
---------------	--

---

### Description

This signature is computed accordingly to the reference paper, to have more details explore the function [availableSignatures](#).

### Usage

```
cellCycleSign(
  dataset,
  nametype = "SYMBOL",
  author = "Lundberg",
  inputType = "microarray",
  whichAssay = "norm_expr"
)
```

### Arguments

dataset	Normalized expression values. A data frame or a matrix where rows correspond to genes and columns correspond to samples. Alternatively, an object of type <a href="#">SummarizedExperiment</a> , <a href="#">SingleCellExperiment</a> or <a href="#">SpatialExperiment</a> where the normalized expression values should be in an assay called 'norm_expr'.
nametype	character string saying the type of gene name ID (row names in dataset). Either one of "SYMBOL", "ENTREZID" or "ENSEMBL".
author	character string saying the first author of the signature publication. Check it in <a href="#">availableSignatures</a> .
inputType	character string saying the type of data you are using. Either one of "microarray" or "rnaseq".
whichAssay	integer scalar or string indicating which assay of dataset to use.

**Value**

If dataset is a [SummarizedExperiment](#) object, then scores are added in the [colData](#) section. If dataset is a data frame or a matrix, then a [SummarizedExperiment](#) object is created in which scores are added in the [colData](#) section.

**Examples**

```
data(ovse)
cellCycleSign(dataset = ovse, inputType = "rnaseq")
```

---

chemokineSign	<i>Chemokine Signature</i>
---------------	----------------------------

---

**Description**

This signature is computed accordingly to the reference paper, to have more details explore the function [availableSignatures](#).

**Usage**

```
chemokineSign(
  dataset,
  nametype = "SYMBOL",
  inputType = "microarray",
  whichAssay = "norm_expr"
)
```

**Arguments**

dataset	Normalized expression values. A data frame or a matrix where rows correspond to genes and columns correspond to samples. Alternatively, an object of type <a href="#">SummarizedExperiment</a> , <a href="#">SingleCellExperiment</a> or <a href="#">SpatialExperiment</a> where the normalized expression values should be in an assay called 'norm_expr'.
nametype	character string saying the type of gene name ID (row names in dataset). Either one of "SYMBOL", "ENTREZID" or "ENSEMBL".
inputType	character string saying the type of data you are using. Either one of "microarray" or "rnaseq".
whichAssay	integer scalar or string indicating which assay of dataset to use.

**Value**

If dataset is a [SummarizedExperiment](#) object, then scores are added in the [colData](#) section. If dataset is a data frame or a matrix, then a [SummarizedExperiment](#) object is created in which scores are added in the [colData](#) section.

**Examples**

```
data(ovse)
chemokineSign(dataset = ovse, inputType = "rnaseq")
```

---

CINSign*Chromosomal instability Signature*

---

## Description

This signature is computed accordingly to the reference paper, to have more details explore the function [availableSignatures](#).

## Usage

```
CINSign(  
  dataset,  
  nametype = "SYMBOL",  
  inputType = "microarray",  
  whichAssay = "norm_expr"  
)
```

## Arguments

dataset	Normalized expression values. A data frame or a matrix where rows correspond to genes and columns correspond to samples. Alternatively, an object of type <a href="#">SummarizedExperiment</a> , <a href="#">SingleCellExperiment</a> or <a href="#">SpatialExperiment</a> where the normalized expression values should be in an assay called 'norm_expr'.
nametype	character string saying the type of gene name ID (row names in dataset). Either one of "SYMBOL", "ENTREZID" or "ENSEMBL".
inputType	character string saying the type of data you are using. Either one of "microarray" or "rnaseq".
whichAssay	integer scalar or string indicating which assay of dataset to use.

## Value

If dataset is a [SummarizedExperiment](#) object, then scores are added in the [colData](#) section. If dataset is a data frame or a matrix, then a [SummarizedExperiment](#) object is created in which scores are added in the [colData](#) section.

## Examples

```
data(ovse)  
CINSign(dataset = ovse, inputType = "rnaseq")
```

---

CISSign	<i>CIS (carcinoma-in situ) Signature</i>
---------	--

---

### Description

This signature is computed accordingly to the reference paper, to have more details explore the function [availableSignatures](#).

### Usage

```
CISSign(dataset, nametype = "SYMBOL", whichAssay = "norm_expr")
```

### Arguments

dataset	Normalized expression values. A data frame or a matrix where rows correspond to genes and columns correspond to samples. Alternatively, an object of type <a href="#">SummarizedExperiment</a> , <a href="#">SingleCellExperiment</a> or <a href="#">SpatialExperiment</a> where the normalized expression values should be in an assay called 'norm_expr'.
nametype	character string saying the type of gene name ID (row names in dataset). Either one of "SYMBOL", "ENTREZID" or "ENSEMBL".
whichAssay	integer scalar or string indicating which assay of dataset to use.

### Value

If dataset is a [SummarizedExperiment](#) object, then scores are added in the [colData](#) section. If dataset is a data frame or a matrix, then a [SummarizedExperiment](#) object is created in which scores are added in the [colData](#) section.

### Examples

```
data(ovse)
CISSign(dataset = ovse)
```

---

CombinedSign	<i>EMT-Inflammation Combined Signature</i>
--------------	--

---

### Description

This signature is computed accordingly to the reference paper, to have more details explore the function [availableSignatures](#).

### Usage

```
CombinedSign(
  dataset,
  nametype = "SYMBOL",
  whichAssay = "norm_expr",
  hgReference = "hg38",
  weighted = FALSE
)
```

**Arguments**

dataset	Normalized expression values. A data frame or a matrix where rows correspond to genes and columns correspond to samples. Alternatively, an object of type <a href="#">SummarizedExperiment</a> , <a href="#">SingleCellExperiment</a> or <a href="#">SpatialExperiment</a> where the normalized expression values should be in an assay called 'norm_expr'.
nametype	character string saying the type of gene name ID (row names in dataset). Either one of "SYMBOL", "ENTREZID" or "ENSEMBL".
whichAssay	integer scalar or string indicating which assay of dataset to use.
hgReference	character string saying the human reference genome. Either one of "hg19" or "hg38".
weighted	logical value, saying whether the score should be calculated with or without weights.

**Value**

If dataset is a [SummarizedExperiment](#) object, then scores are added in the `colData` section. If dataset is a data frame or a matrix, then a [SummarizedExperiment](#) object is created in which scores are added in the `colData` section.

**Examples**

```
data(ovse)
CombinedSign(dataset = ovse)
```

---

consensusOVSign	<i>ConsensusOV Signature</i>
-----------------	------------------------------

---

**Description**

This signature is computed accordingly to the reference paper, to have more details explore the function [availableSignatures](#).

**Usage**

```
consensusOVSign(dataset, nametype = "SYMBOL", whichAssay = "norm_expr", ...)
```

**Arguments**

dataset	Normalized expression values. A data frame or a matrix where rows correspond to genes and columns correspond to samples. Alternatively, an object of type <a href="#">SummarizedExperiment</a> , <a href="#">SingleCellExperiment</a> or <a href="#">SpatialExperiment</a> where the normalized expression values should be in an assay called 'norm_expr'.
nametype	character string saying the type of gene name ID (row names in dataset). Either one of "SYMBOL", "ENTREZID" or "ENSEMBL".
whichAssay	integer scalar or string indicating which assay of dataset to use.
...	optional parameters to be passed to <a href="#">get.subtypes</a> .

**Value**

If dataset is a [SummarizedExperiment](#) object, then scores are added in the [colData](#) section. If dataset is a data frame or a matrix, then a [SummarizedExperiment](#) object is created in which scores are added in the [colData](#) section.

**Examples**

```
data(ovse)
consensusOVSign(dataset = ovse)
```

---

correlationSignPlot	<i>Correlation Plot</i>
---------------------	-------------------------

---

**Description**

Given multiple signatures, the function plots signatures correlations.

**Usage**

```
correlationSignPlot(
  data,
  whichSign = NULL,
  sampleAnnot = NULL,
  selectByAnnot = NULL
)
```

**Arguments**

data	an object of type <a href="#">SummarizedExperiment</a> . Output of the signatures functions.
whichSign	character vector saying the signatures to plot. If not specified, all the signatures inside data will be plotted. Other signatures not computed with signifinder can be added in the vector if they are also included in the colData section of data.
sampleAnnot	character vector containing samples' annotations.
selectByAnnot	character string saying the subgroup from 'sampleAnnot' used to compute the correlation plot.

**Value**

An object of class "openair".

**Examples**

```
data(ovse)
correlationSignPlot(data = ovse)
```

COXISSign

*COX-2-associated Inflammatory Signature***Description**

This signature is computed accordingly to the reference paper, to have more details explore the function [availableSignatures](#).

**Usage**

```
COXISSign(dataset, nametype = "SYMBOL", whichAssay = "norm_expr")
```

**Arguments**

dataset	Normalized expression values. A data frame or a matrix where rows correspond to genes and columns correspond to samples. Alternatively, an object of type <a href="#">SummarizedExperiment</a> , <a href="#">SingleCellExperiment</a> or <a href="#">SpatialExperiment</a> where the normalized expression values should be in an assay called 'norm_expr'.
nametype	character string saying the type of gene name ID (row names in dataset). Either one of "SYMBOL", "ENTREZID" or "ENSEMBL".
whichAssay	integer scalar or string indicating which assay of dataset to use.

**Value**

If dataset is a [SummarizedExperiment](#) object, then scores are added in the [colData](#) section. If dataset is a data frame or a matrix, then a [SummarizedExperiment](#) object is created in which scores are added in the [colData](#) section.

**Examples**

```
data(ovse)
COXISSign(dataset = ovse)
```

DNArepSign

*DNA Repair Signature***Description**

This signature is computed accordingly to the reference paper, to have more details explore the function [availableSignatures](#).

**Usage**

```
DNArepSign(
  dataset,
  nametype = "SYMBOL",
  inputType = "microarray",
  whichAssay = "norm_expr"
)
```

**Arguments**

dataset	Normalized expression values. A data frame or a matrix where rows correspond to genes and columns correspond to samples. Alternatively, an object of type <a href="#">SummarizedExperiment</a> , <a href="#">SingleCellExperiment</a> or <a href="#">SpatialExperiment</a> where the normalized expression values should be in an assay called 'norm_expr'.
nametype	character string saying the type of gene name ID (row names in dataset). Either one of "SYMBOL", "ENTREZID" or "ENSEMBL".
inputType	character string saying the type of data you are using. Either one of "microarray" or "rnaseq".
whichAssay	integer scalar or string indicating which assay of dataset to use.

**Value**

If dataset is a [SummarizedExperiment](#) object, then scores are added in the [colData](#) section. If dataset is a data frame or a matrix, then a [SummarizedExperiment](#) object is created in which scores are added in the [colData](#) section.

**Examples**

```
data(ovse)
DNArepSign(dataset = ovse, inputType = "rnaseq")
```

ECMSign

*Extracellular Matrix Signature***Description**

This signature is computed accordingly to the reference paper, to have more details explore the function [availableSignatures](#).

**Usage**

```
ECMSign(dataset, nametype = "SYMBOL", whichAssay = "norm_expr", ...)
```

**Arguments**

dataset	Normalized expression values. A data frame or a matrix where rows correspond to genes and columns correspond to samples. Alternatively, an object of type <a href="#">SummarizedExperiment</a> , <a href="#">SingleCellExperiment</a> or <a href="#">SpatialExperiment</a> where the normalized expression values should be in an assay called 'norm_expr'.
nametype	character string saying the type of gene name ID (row names in dataset). Either one of "SYMBOL", "ENTREZID" or "ENSEMBL".
whichAssay	integer scalar or string indicating which assay of dataset to use.
...	other arguments passed on to the <a href="#">ssgseaParam</a> function.

**Value**

If dataset is a [SummarizedExperiment](#) object, then scores are added in the [colData](#) section. If dataset is a data frame or a matrix, then a [SummarizedExperiment](#) object is created in which scores are added in the [colData](#) section.



**Examples**

```
data(ovse)
ECMSign(dataset = ovse)
```

EMTSign

*Epithelial-Mesenchymal Transition Signature***Description**

This signature is computed accordingly to the reference paper, to have more details explore the function [availableSignatures](#).

**Usage**

```
EMTSign(
  dataset,
  nametype = "SYMBOL",
  inputType = "microarray",
  author = "Miow",
  whichAssay = "norm_expr",
  hgReference = "hg38",
  ...
)
```

**Arguments**

dataset	Normalized expression values. A data frame or a matrix where rows correspond to genes and columns correspond to samples. Alternatively, an object of type <a href="#">SummarizedExperiment</a> , <a href="#">SingleCellExperiment</a> or <a href="#">SpatialExperiment</a> where the normalized expression values should be in an assay called 'norm_expr'.
nametype	character string saying the type of gene name ID (row names in dataset). Either one of "SYMBOL", "ENTREZID" or "ENSEMBL".
inputType	character string saying the type of data you are using. Either one of "microarray" or "rnaseq".
author	character string saying the first author of the signature publication. Check it in <a href="#">availableSignatures</a> .
whichAssay	integer scalar or string indicating which assay of dataset to use.
hgReference	character string saying the human reference genome. Either one of "hg19" or "hg38".
...	other arguments passed on to the <a href="#">ssgseaParam</a> function.

**Value**

If dataset is a [SummarizedExperiment](#) object, then scores are added in the [colData](#) section. If dataset is a data frame or a matrix, then a [SummarizedExperiment](#) object is created in which scores are added in the [colData](#) section.

**Examples**

```
data(ovse)
EMTSig(dataset = ovse, inputType = "rnaseq")
```

---

evaluationSignPlot	<i>Evaluation Plot</i>
--------------------	------------------------

---

**Description**

A multipanel plot that shows: (i) a value of the goodness of a signature for the user's dataset. This is a combination of the parameters shown in the other pannels; (ii) the percentage of genes from the signature gene list that are actually available in the dataset; (iii) the percentage of zero values in the signature genes, for each sample; (iv) the correlation between signature scores and the sample total read counts; (v) the correlation between signature scores and the percentage of the sample total zero values.

**Usage**

```
evaluationSignPlot(
  data,
  nametype = "SYMBOL",
  whichSign = NULL,
  whichAssay = "norm_expr",
  sampleAnnot = NULL,
  selectByAnnot = NULL
)
```

**Arguments**

data	an object of type <a href="#">SummarizedExperiment</a> . Output of the signatures functions.
nametype	character string saying the type of gene name ID (row names in data). Either one of "SYMBOL", "ENTREZID" or "ENSEMBL".
whichSign	character vector saying the signatures to plot. These must be signatures computed with signifinder. If not specified, all the signatures inside data will be plotted.
whichAssay	integer scalar or string indicating which assay of data to use.
sampleAnnot	character vector containing samples' annotations.
selectByAnnot	character string saying the subgroup from 'sampleAnnot' used to compute the evaluation plot.

**Value**

A [ggplot](#) object.

**Examples**

```
data(ovse)
evaluationSignPlot(data = ovse)
```

---

expandedImmuneSign	<i>ExpandedImmune Signature</i>
--------------------	---------------------------------

---

### Description

This signature is computed accordingly to the reference paper, to have more details explore the function [availableSignatures](#).

### Usage

```
expandedImmuneSign(dataset, nametype = "SYMBOL", whichAssay = "norm_expr")
```

### Arguments

dataset	Normalized expression values. A data frame or a matrix where rows correspond to genes and columns correspond to samples. Alternatively, an object of type <a href="#">SummarizedExperiment</a> , <a href="#">SingleCellExperiment</a> or <a href="#">SpatialExperiment</a> where the normalized expression values should be in an assay called 'norm_expr'.
nametype	character string saying the type of gene name ID (row names in dataset). Either one of "SYMBOL", "ENTREZID" or "ENSEMBL".
whichAssay	integer scalar or string indicating which assay of dataset to use.

### Value

If dataset is a [SummarizedExperiment](#) object, then scores are added in the [colData](#) section. If dataset is a data frame or a matrix, then a [SummarizedExperiment](#) object is created in which scores are added in the [colData](#) section.

### Examples

```
data(ovse)
expandedImmuneSign(dataset = ovse)
```

---

ferroptosisSign	<i>Ferroptosis Signature</i>
-----------------	------------------------------

---

### Description

This signature is computed accordingly to the reference paper, to have more details explore the function [availableSignatures](#).

### Usage

```
ferroptosisSign(
  dataset,
  nametype = "SYMBOL",
  inputType = "rnaseq",
  author = "Ye",
  whichAssay = "norm_expr",
  hgReference = "hg38"
)
```

**Arguments**

dataset	Normalized expression values. A data frame or a matrix where rows correspond to genes and columns correspond to samples. Alternatively, an object of type <a href="#">SummarizedExperiment</a> , <a href="#">SingleCellExperiment</a> or <a href="#">SpatialExperiment</a> where the normalized expression values should be in an assay called 'norm_expr'.
nametype	character string saying the type of gene name ID (row names in dataset). Either one of "SYMBOL", "ENTREZID" or "ENSEMBL".
inputType	character string saying the type of data you are using. Either one of "microarray" or "rnaseq".
author	character string saying the first author of the signature publication. Check it in <a href="#">availableSignatures</a> .
whichAssay	integer scalar or string indicating which assay of dataset to use.
hgReference	character string saying the human reference genome. Either one of "hg19" or "hg38".

**Value**

If dataset is a [SummarizedExperiment](#) object, then scores are added in the `colData` section. If dataset is a data frame or a matrix, then a [SummarizedExperiment](#) object is created in which scores are added in the `colData` section.

**Examples**

```
data(ovse)
ferroptosisSign(dataset = ovse)
```

---

geneHeatmapSignPlot     *Genes' Signatures' Heatmap*

---

**Description**

Given one or multiple signatures, the function returns a heatmap of the expression values of the genes included in each of them.

**Usage**

```
geneHeatmapSignPlot(
  data,
  nametype = "SYMBOL",
  whichSign,
  logCount = FALSE,
  whichAssay = "norm_expr",
  splitBySign = FALSE,
  sampleAnnot = NULL,
  splitBySampleAnnot = FALSE,
  ...
)
```

**Arguments**

data	an object of type <a href="#">SummarizedExperiment</a> . Output of the signatures functions.
nametype	character string saying the type of gene name ID (row names in data). Either one of "SYMBOL", "ENTREZID" or "ENSEMBL".
whichSign	character vector saying the signatures to plot. These must be signatures computed with signifinder.
logCount	logical. If TRUE it shows logarithms of expression values.
whichAssay	integer scalar or string indicating which assay of data to use.
splitBySign	logical. If TRUE it splits rows by signatures.
sampleAnnot	vector containing samples' annotations.
splitBySampleAnnot	logical. If TRUE it splits columns by samples' annotations.
...	other parameters specific of the function <a href="#">Heatmap</a> .

**Value**

A [Heatmap-class](#) object.

**Examples**

```
data(ovse)
geneHeatmapSignPlot(data = ovse, whichSign = "Ferroptosis_Ye")
```

---

getSignGenes	<i>Get Signature Gene List</i>
--------------	--------------------------------

---

**Description**

This function returns the list of genes of a signature.

**Usage**

```
getSignGenes(whichSign)
```

**Arguments**

whichSign	name of the signature. The names are those in column 'signature' from the table which is obtained by <a href="#">availableSignatures</a> .
-----------	--

**Value**

A dataframe object with "SYMBOL" in the first column. Some signatures have also additional columns: "coeff" for coefficients that weigh the gene contributions; "class" for a classification that divides the signature in two or more groups. Few signatures have other specific columns.

**Examples**

```
getSignGenes("EMT_Miow")
```

---

glioCellStateSign	<i>Glioblastoma Cellular States Signature</i>
-------------------	---

---

## Description

This signature is computed accordingly to the reference paper, to have more details explore the function [availableSignatures](#).

## Usage

```
glioCellStateSign(
  dataset,
  nametype = "SYMBOL",
  whichAssay = "norm_expr",
  isMalignant = NULL,
  hgReference = "hg38"
)
```

## Arguments

dataset	Normalized expression values. A data frame or a matrix where rows correspond to genes and columns correspond to samples. Alternatively, an object of type <a href="#">SummarizedExperiment</a> , <a href="#">SingleCellExperiment</a> or <a href="#">SpatialExperiment</a> where the normalized expression values should be in an assay called 'norm_expr'.
nametype	character string saying the type of gene name ID (row names in dataset). Either one of "SYMBOL", "ENTREZID" or "ENSEMBL".
whichAssay	integer scalar or string indicating which assay of dataset to use.
isMalignant	logical vector of the same length of ncol(dataset), where TRUE states malignant cells and FALSE states non-malignant cells.
hgReference	character string saying the human reference genome. Either one of "hg19" or "hg38".

## Value

If dataset is a [SummarizedExperiment](#) object, then scores are added in the [colData](#) section. If dataset is a data frame or a matrix, then a [SummarizedExperiment](#) object is created in which scores are added in the [colData](#) section.

## Examples

```
data(ovse)
```

---

glycolysisSign	<i>Glycolysis Signature</i>
----------------	-----------------------------

---

## Description

This signature is computed accordingly to the reference paper, to have more details explore the function [availableSignatures](#).

## Usage

```
glycolysisSign(  
  dataset,  
  nametype = "SYMBOL",  
  author = "Zhang",  
  whichAssay = "norm_expr"  
)
```

## Arguments

dataset	Normalized expression values. A data frame or a matrix where rows correspond to genes and columns correspond to samples. Alternatively, an object of type <a href="#">SummarizedExperiment</a> , <a href="#">SingleCellExperiment</a> or <a href="#">SpatialExperiment</a> where the normalized expression values should be in an assay called 'norm_expr'.
nametype	character string saying the type of gene name ID (row names in dataset). Either one of "SYMBOL", "ENTREZID" or "ENSEMBL".
author	character string saying the first author of the signature publication. Check it in <a href="#">availableSignatures</a> .
whichAssay	integer scalar or string indicating which assay of dataset to use.

## Value

If dataset is a [SummarizedExperiment](#) object, then scores are added in the [colData](#) section. If dataset is a data frame or a matrix, then a [SummarizedExperiment](#) object is created in which scores are added in the [colData](#) section.

## Examples

```
data(ovse)  
glycolysisSign(dataset = ovse)
```

---

heatmapSignPlot	<i>Global Heatmap of Signatures' scores.</i>
-----------------	--

---

## Description

Given one or multiple signatures, the function returns a heatmap of scores. Since each signature has its own method to compute the score then to plot several signatures together the scores are transformed into z-score, individually for each signature.

## Usage

```
heatmapSignPlot(
  data,
  whichSign = NULL,
  clusterBySign = NULL,
  sampleAnnot = NULL,
  signAnnot = NULL,
  splitBySampleAnnot = FALSE,
  ...
)
```

## Arguments

data	an object of type <a href="#">SummarizedExperiment</a> . Output of the signatures functions.
whichSign	character vector saying the signatures to plot. If not specified, all the signatures inside data will be plotted. Other signatures not computed with signifinder can be added in the vector if they are also included in the colData section of data.
clusterBySign	character vector saying one or more signatures to use to cluster columns.
sampleAnnot	vector containing samples' annotations.
signAnnot	character vector of signature's annotations. One or more between: "signature", "topic", "tumor", "tissue".
splitBySampleAnnot	logical. If TRUE it splits columns by samples' annotations.
...	other parameters specific of the function <a href="#">Heatmap</a> .

## Value

A [Heatmap-class](#) object.

## Examples

```
data(ovse)
heatmapSignPlot(data = ovse)
```



HRDSSign

*Homologous Recombination Deficiency Signature***Description**

This signature is computed accordingly to the reference paper, to have more details explore the function [availableSignatures](#).

**Usage**

```
HRDSSign(dataset, nametype = "SYMBOL", whichAssay = "norm_expr")
```

**Arguments**

dataset	Normalized expression values. A data frame or a matrix where rows correspond to genes and columns correspond to samples. Alternatively, an object of type <a href="#">SummarizedExperiment</a> , <a href="#">SingleCellExperiment</a> or <a href="#">SpatialExperiment</a> where the normalized expression values should be in an assay called 'norm_expr'.
nametype	character string saying the type of gene name ID (row names in dataset). Either one of "SYMBOL", "ENTREZID" or "ENSEMBL".
whichAssay	integer scalar or string indicating which assay of dataset to use.

**Value**

If dataset is a [SummarizedExperiment](#) object, then scores are added in the [colData](#) section. If dataset is a data frame or a matrix, then a [SummarizedExperiment](#) object is created in which scores are added in the [colData](#) section.

**Examples**

```
data(ovse)
HRDSSign(dataset = ovse)
```

hypoxiaSign

*Hypoxia Signature***Description**

This signature is computed accordingly to the reference paper, to have more details explore the function [availableSignatures](#).

**Usage**

```
hypoxiaSign(
  dataset,
  nametype = "SYMBOL",
  inputType = "microarray",
  whichAssay = "norm_expr"
)
```

**Arguments**

dataset	Normalized expression values. A data frame or a matrix where rows correspond to genes and columns correspond to samples. Alternatively, an object of type <a href="#">SummarizedExperiment</a> , <a href="#">SingleCellExperiment</a> or <a href="#">SpatialExperiment</a> where the normalized expression values should be in an assay called 'norm_expr'.
nametype	character string saying the type of gene name ID (row names in dataset). Either one of "SYMBOL", "ENTREZID" or "ENSEMBL".
inputType	character string saying the type of data you are using. Either one of "microarray" or "rnaseq".
whichAssay	integer scalar or string indicating which assay of dataset to use.

**Value**

If dataset is a [SummarizedExperiment](#) object, then scores are added in the [colData](#) section. If dataset is a data frame or a matrix, then a [SummarizedExperiment](#) object is created in which scores are added in the [colData](#) section.

**Examples**

```
data(ovse)
hypoxiaSign(dataset = ovse, inputType = "rnaseq")
```

---

ICBResponseSign	<i>ICB Response Signature</i>
-----------------	-------------------------------

---

**Description**

This signature is computed accordingly to the reference paper, to have more details explore the function [availableSignatures](#).

**Usage**

```
ICBResponseSign(dataset, nametype = "SYMBOL", whichAssay = "norm_expr")
```

**Arguments**

dataset	Normalized expression values. A data frame or a matrix where rows correspond to genes and columns correspond to samples. Alternatively, an object of type <a href="#">SummarizedExperiment</a> , <a href="#">SingleCellExperiment</a> or <a href="#">SpatialExperiment</a> where the normalized expression values should be in an assay called 'norm_expr'.
nametype	character string saying the type of gene name ID (row names in dataset). Either one of "SYMBOL", "ENTREZID" or "ENSEMBL".
whichAssay	integer scalar or string indicating which assay of dataset to use.

**Value**

If dataset is a [SummarizedExperiment](#) object, then scores are added in the [colData](#) section. If dataset is a data frame or a matrix, then a [SummarizedExperiment](#) object is created in which scores are added in the [colData](#) section.

**Examples**

```
data(ovse)
ICBResponseSign(dataset = ovse)
```

---

IFNSign	<i>IFN-gamma Signature</i>
---------	----------------------------

---

**Description**

This signature is computed accordingly to the reference paper, to have more details explore the function [availableSignatures](#).

**Usage**

```
IFNSign(dataset, nametype = "SYMBOL", whichAssay = "norm_expr")
```

**Arguments**

dataset	Normalized expression values. A data frame or a matrix where rows correspond to genes and columns correspond to samples. Alternatively, an object of type <a href="#">SummarizedExperiment</a> , <a href="#">SingleCellExperiment</a> or <a href="#">SpatialExperiment</a> where the normalized expression values should be in an assay called 'norm_expr'.
nametype	character string saying the type of gene name ID (row names in dataset). Either one of "SYMBOL", "ENTREZID" or "ENSEMBL".
whichAssay	integer scalar or string indicating which assay of dataset to use.

**Value**

If dataset is a [SummarizedExperiment](#) object, then scores are added in the [colData](#) section. If dataset is a data frame or a matrix, then a [SummarizedExperiment](#) object is created in which scores are added in the [colData](#) section.

**Examples**

```
data(ovse)
IFNSign(dataset = ovse)
```

immuneCytSign

*Immune Cytolytic Activity Signature***Description**

This signature is computed accordingly to the reference paper, to have more details explore the function [availableSignatures](#).

**Usage**

```
immuneCytSign(
  dataset,
  nametype = "SYMBOL",
  inputType = "microarray",
  author = "Rooney",
  whichAssay = "norm_expr",
  hgReference = "hg38"
)
```

**Arguments**

dataset	Normalized expression values. A data frame or a matrix where rows correspond to genes and columns correspond to samples. Alternatively, an object of type <a href="#">SummarizedExperiment</a> , <a href="#">SingleCellExperiment</a> or <a href="#">SpatialExperiment</a> where the normalized expression values should be in an assay called 'norm_expr'.
nametype	character string saying the type of gene name ID (row names in dataset). Either one of "SYMBOL", "ENTREZID" or "ENSEMBL".
inputType	character string saying the type of data you are using. Either one of "microarray" or "rnaseq".
author	character string saying the first author of the signature publication. Check it in <a href="#">availableSignatures</a> .
whichAssay	integer scalar or string indicating which assay of dataset to use.
hgReference	character string saying the human reference genome. Either one of "hg19" or "hg38".

**Value**

If dataset is a [SummarizedExperiment](#) object, then scores are added in the [colData](#) section. If dataset is a data frame or a matrix, then a [SummarizedExperiment](#) object is created in which scores are added in the [colData](#) section.

**Examples**

```
data(ovse)
immuneCytSign(dataset = ovse, inputType = "rnaseq")
```

---

immunoScoreSign	<i>Immunogenic Signature</i>
-----------------	------------------------------

---

## Description

This signature is computed accordingly to the reference paper, to have more details explore the function [availableSignatures](#).

## Usage

```
immunoScoreSign(
  dataset,
  nametype = "SYMBOL",
  author = "Hao",
  inputType = "rnaseq",
  whichAssay = "norm_expr",
  hgReference = "hg38"
)
```

## Arguments

dataset	Normalized expression values. A data frame or a matrix where rows correspond to genes and columns correspond to samples. Alternatively, an object of type <a href="#">SummarizedExperiment</a> , <a href="#">SingleCellExperiment</a> or <a href="#">SpatialExperiment</a> where the normalized expression values should be in an assay called 'norm_expr'.
nametype	character string saying the type of gene name ID (row names in dataset). Either one of "SYMBOL", "ENTREZID" or "ENSEMBL".
author	character string saying the first author of the signature publication. Check it in <a href="#">availableSignatures</a> .
inputType	character string saying the type of data you are using. Either one of "microarray" or "rnaseq".
whichAssay	integer scalar or string indicating which assay of dataset to use.
hgReference	character string saying the human reference genome. Either one of "hg19" or "hg38".

## Value

If dataset is a [SummarizedExperiment](#) object, then scores are added in the [colData](#) section. If dataset is a data frame or a matrix, then a [SummarizedExperiment](#) object is created in which scores are added in the [colData](#) section.

## Examples

```
data(ovse)
immunoScoreSign(dataset = ovse)
```

---

IPRESSign	<i>IPRES Signature</i>
-----------	------------------------

---

## Description

This signature is computed accordingly to the reference paper, to have more details explore the function [availableSignatures](#).

## Usage

```
IPRESSign(
  dataset,
  nametype = "SYMBOL",
  whichAssay = "norm_expr",
  hgReference = "hg38",
  ...
)
```

## Arguments

dataset	Normalized expression values. A data frame or a matrix where rows correspond to genes and columns correspond to samples. Alternatively, an object of type <a href="#">SummarizedExperiment</a> , <a href="#">SingleCellExperiment</a> or <a href="#">SpatialExperiment</a> where the normalized expression values should be in an assay called 'norm_expr'.
nametype	character string saying the type of gene name ID (row names in dataset). Either one of "SYMBOL", "ENTREZID" or "ENSEMBL".
whichAssay	integer scalar or string indicating which assay of dataset to use.
hgReference	character string saying the human reference genome. Either one of "hg19" or "hg38".
...	other arguments passed on to the <a href="#">ssgseaParam</a> function.

## Value

If dataset is a [SummarizedExperiment](#) object, then scores are added in the [colData](#) section. If dataset is a data frame or a matrix, then a [SummarizedExperiment](#) object is created in which scores are added in the [colData](#) section.

## Examples

```
data(ovse)
IPRESSign(dataset = ovse)
```

---

IPSOVSign	<i>IPSOV Signature</i>
-----------	------------------------

---

## Description

This signature is computed accordingly to the reference paper, to have more details explore the function [availableSignatures](#).

## Usage

```
IPSOVSign(
  dataset,
  nametype = "SYMBOL",
  inputType = "microarray",
  whichAssay = "norm_expr",
  ...
)
```

## Arguments

dataset	Normalized expression values. A data frame or a matrix where rows correspond to genes and columns correspond to samples. Alternatively, an object of type <a href="#">SummarizedExperiment</a> , <a href="#">SingleCellExperiment</a> or <a href="#">SpatialExperiment</a> where the normalized expression values should be in an assay called 'norm_expr'.
nametype	character string saying the type of gene name ID (row names in dataset). Either one of "SYMBOL", "ENTREZID" or "ENSEMBL".
inputType	character string saying the type of data you are using. Either one of "microarray" or "rnaseq".
whichAssay	integer scalar or string indicating which assay of dataset to use.
...	other arguments passed on to the <a href="#">ssgseaParam</a> function.

## Value

If dataset is a [SummarizedExperiment](#) object, then scores are added in the [colData](#) section. If dataset is a data frame or a matrix, then a [SummarizedExperiment](#) object is created in which scores are added in the [colData](#) section.

## Examples

```
data(ovse)
IPSOVSign(dataset = ovse)
```

IPSSign

*ImmunoPhenoScore Signature***Description**

This signature is computed accordingly to the reference paper, to have more details explore the function [availableSignatures](#).

**Usage**

```
IPSSign(
  dataset,
  nametype = "SYMBOL",
  whichAssay = "norm_expr",
  hgReference = "hg38"
)
```

**Arguments**

dataset	Normalized expression values. A data frame or a matrix where rows correspond to genes and columns correspond to samples. Alternatively, an object of type <a href="#">SummarizedExperiment</a> , <a href="#">SingleCellExperiment</a> or <a href="#">SpatialExperiment</a> where the normalized expression values should be in an assay called 'norm_expr'.
nametype	character string saying the type of gene name ID (row names in dataset). Either one of "SYMBOL", "ENTREZID" or "ENSEMBL".
whichAssay	integer scalar or string indicating which assay of dataset to use.
hgReference	character string saying the human reference genome. Either one of "hg19" or "hg38".

**Value**

If dataset is a [SummarizedExperiment](#) object, then scores are added in the [colData](#) section. If dataset is a data frame or a matrix, then a [SummarizedExperiment](#) object is created in which scores are added in the [colData](#) section.

**Examples**

```
data(ovse)
IPSSign(dataset = ovse)
```



IRGSign

*Immune-Related Genes Signature***Description**

This signature is computed accordingly to the reference paper, to have more details explore the function [availableSignatures](#).

**Usage**

```
IRGSign(dataset, nametype = "SYMBOL", whichAssay = "norm_expr")
```

**Arguments**

dataset	Normalized expression values. A data frame or a matrix where rows correspond to genes and columns correspond to samples. Alternatively, an object of type <a href="#">SummarizedExperiment</a> , <a href="#">SingleCellExperiment</a> or <a href="#">SpatialExperiment</a> where the normalized expression values should be in an assay called 'norm_expr'.
nametype	character string saying the type of gene name ID (row names in dataset). Either one of "SYMBOL", "ENTREZID" or "ENSEMBL".
whichAssay	integer scalar or string indicating which assay of dataset to use.

**Value**

If dataset is a [SummarizedExperiment](#) object, then scores are added in the [colData](#) section. If dataset is a data frame or a matrix, then a [SummarizedExperiment](#) object is created in which scores are added in the [colData](#) section.

**Examples**

```
data(ovse)
IRGSign(dataset = ovse)
```

ISCSign

*Adult Intestinal Stem Cell Signature***Description**

This signature is computed accordingly to the reference paper, to have more details explore the function [availableSignatures](#).

**Usage**

```
ISCSign(
  dataset,
  nametype = "SYMBOL",
  inputType = "microarray",
  whichAssay = "norm_expr"
)
```

**Arguments**

dataset	Normalized expression values. A data frame or a matrix where rows correspond to genes and columns correspond to samples. Alternatively, an object of type <a href="#">SummarizedExperiment</a> , <a href="#">SingleCellExperiment</a> or <a href="#">SpatialExperiment</a> where the normalized expression values should be in an assay called 'norm_expr'.
nametype	character string saying the type of gene name ID (row names in dataset). Either one of "SYMBOL", "ENTREZID" or "ENSEMBL".
inputType	character string saying the type of data you are using. Either one of "microarray" or "rnaseq".
whichAssay	integer scalar or string indicating which assay of dataset to use.

**Value**

If dataset is a [SummarizedExperiment](#) object, then scores are added in the [colData](#) section. If dataset is a data frame or a matrix, then a [SummarizedExperiment](#) object is created in which scores are added in the [colData](#) section.

**Examples**

```
data(ovse)
ISCSign(dataset = ovse, inputType = "rnaseq")
```

---

lipidMetabolismSign	<i>Lipid Metabolism Signature</i>
---------------------	-----------------------------------

---

**Description**

This signature is computed accordingly to the reference paper, to have more details explore the function [availableSignatures](#).

**Usage**

```
lipidMetabolismSign(dataset, nametype = "SYMBOL", whichAssay = "norm_expr")
```

**Arguments**

dataset	Normalized expression values. A data frame or a matrix where rows correspond to genes and columns correspond to samples. Alternatively, an object of type <a href="#">SummarizedExperiment</a> , <a href="#">SingleCellExperiment</a> or <a href="#">SpatialExperiment</a> where the normalized expression values should be in an assay called 'norm_expr'.
nametype	character string saying the type of gene name ID (row names in dataset). Either one of "SYMBOL", "ENTREZID" or "ENSEMBL".
whichAssay	integer scalar or string indicating which assay of dataset to use.

**Value**

If dataset is a [SummarizedExperiment](#) object, then scores are added in the [colData](#) section. If dataset is a data frame or a matrix, then a [SummarizedExperiment](#) object is created in which scores are added in the [colData](#) section.

**Examples**

```
data(ovse)
lipidMetabolismSign(dataset = ovse)
```

---

LRRC15CAFSign	<i>LRRC15 CAF Signature</i>
---------------	-----------------------------

---

**Description**

This signature is computed accordingly to the reference paper, to have more details explore the function [availableSignatures](#).

**Usage**

```
LRRC15CAFSign(dataset, nametype = "SYMBOL", whichAssay = "norm_expr")
```

**Arguments**

dataset	Normalized expression values. A data frame or a matrix where rows correspond to genes and columns correspond to samples. Alternatively, an object of type <a href="#">SummarizedExperiment</a> , <a href="#">SingleCellExperiment</a> or <a href="#">SpatialExperiment</a> where the normalized expression values should be in an assay called 'norm_expr'.
nametype	character string saying the type of gene name ID (row names in dataset). Either one of "SYMBOL", "ENTREZID" or "ENSEMBL".
whichAssay	integer scalar or string indicating which assay of dataset to use.

**Value**

If dataset is a [SummarizedExperiment](#) object, then scores are added in the [colData](#) section. If dataset is a data frame or a matrix, then a [SummarizedExperiment](#) object is created in which scores are added in the [colData](#) section.

**Examples**

```
data(ovse)
LRRC15CAFSign(dataset = ovse)
```

---

matrisomeSign	<i>Core Matrisome Gene signature</i>
---------------	--------------------------------------

---

### Description

This signature is computed accordingly to the reference paper, to have more details explore the function [availableSignatures](#).

### Usage

```
matrisomeSign(dataset, nametype = "SYMBOL", whichAssay = "norm_expr")
```

### Arguments

dataset	Normalized expression values. A data frame or a matrix where rows correspond to genes and columns correspond to samples. Alternatively, an object of type <a href="#">SummarizedExperiment</a> , <a href="#">SingleCellExperiment</a> or <a href="#">SpatialExperiment</a> where the normalized expression values should be in an assay called 'norm_expr'.
nametype	character string saying the type of gene name ID (row names in dataset). Either one of "SYMBOL", "ENTREZID" or "ENSEMBL".
whichAssay	integer scalar or string indicating which assay of dataset to use.

### Value

If dataset is a [SummarizedExperiment](#) object, then scores are added in the [colData](#) section. If dataset is a data frame or a matrix, then a [SummarizedExperiment](#) object is created in which scores are added in the [colData](#) section.

### Examples

```
data(ovse)
matrisomeSign(dataset = ovse)
```

---

melStateSign	<i>Metastatic Melanoma Cellular States Signature</i>
--------------	--

---

### Description

This signature is computed accordingly to the reference paper, to have more details explore the function [availableSignatures](#).

### Usage

```
melStateSign(
  dataset,
  nametype = "SYMBOL",
  whichAssay = "norm_expr",
  isMalignant = NULL,
  hgReference = "hg38"
)
```

**Arguments**

dataset	Normalized expression values. A data frame or a matrix where rows correspond to genes and columns correspond to samples. Alternatively, an object of type <a href="#">SummarizedExperiment</a> , <a href="#">SingleCellExperiment</a> or <a href="#">SpatialExperiment</a> where the normalized expression values should be in an assay called 'norm_expr'.
nametype	character string saying the type of gene name ID (row names in dataset). Either one of "SYMBOL", "ENTREZID" or "ENSEMBL".
whichAssay	integer scalar or string indicating which assay of dataset to use.
isMalignant	logical vector of the same length of ncol(dataset), where TRUE states malignant cells and FALSE states non-malignant cells.
hgReference	character string saying the human reference genome. Either one of "hg19" or "hg38".

**Value**

If dataset is a [SummarizedExperiment](#) object, then scores are added in the `colData` section. If dataset is a data frame or a matrix, then a [SummarizedExperiment](#) object is created in which scores are added in the `colData` section.

**Examples**

```
data(ovse)
```

---

MITFlowPTENnegSign	<i>MITFlow/PTENneg Signature</i>
--------------------	----------------------------------

---

**Description**

This signature is computed accordingly to the reference paper, to have more details explore the function [availableSignatures](#).

**Usage**

```
MITFlowPTENnegSign(dataset, nametype = "SYMBOL", whichAssay = "norm_expr")
```

**Arguments**

dataset	Normalized expression values. A data frame or a matrix where rows correspond to genes and columns correspond to samples. Alternatively, an object of type <a href="#">SummarizedExperiment</a> , <a href="#">SingleCellExperiment</a> or <a href="#">SpatialExperiment</a> where the normalized expression values should be in an assay called 'norm_expr'.
nametype	character string saying the type of gene name ID (row names in dataset). Either one of "SYMBOL", "ENTREZID" or "ENSEMBL".
whichAssay	integer scalar or string indicating which assay of dataset to use.

**Value**

If dataset is a [SummarizedExperiment](#) object, then scores are added in the `colData` section. If dataset is a data frame or a matrix, then a [SummarizedExperiment](#) object is created in which scores are added in the `colData` section.

**Examples**

```
data(ovse)
MITFlowPTENnegSign(dataset = ovse)
```

---

mitoticIndexSign	<i>Mitotic Index</i>
------------------	----------------------

---

**Description**

This signature is computed accordingly to the reference paper, to have more details explore the function [availableSignatures](#).

**Usage**

```
mitoticIndexSign(dataset, nametype = "SYMBOL", whichAssay = "norm_expr")
```

**Arguments**

dataset	Normalized expression values. A data frame or a matrix where rows correspond to genes and columns correspond to samples. Alternatively, an object of type <a href="#">SummarizedExperiment</a> , <a href="#">SingleCellExperiment</a> or <a href="#">SpatialExperiment</a> where the normalized expression values should be in an assay called 'norm_expr'.
nametype	character string saying the type of gene name ID (row names in dataset). Either one of "SYMBOL", "ENTREZID" or "ENSEMBL".
whichAssay	integer scalar or string indicating which assay of dataset to use.

**Value**

If dataset is a [SummarizedExperiment](#) object, then scores are added in the [colData](#) section. If dataset is a data frame or a matrix, then a [SummarizedExperiment](#) object is created in which scores are added in the [colData](#) section.

**Examples**

```
data(ovse)
mitoticIndexSign(dataset = ovse)
```

---

MPSSign*Melanocytic Plasticity Signature*

---

## Description

This signature is computed accordingly to the reference paper, to have more details explore the function [availableSignatures](#).

## Usage

```
MPSSign(  
  dataset,  
  nametype = "SYMBOL",  
  whichAssay = "norm_expr",  
  hgReference = "hg38"  
)
```

## Arguments

dataset	Normalized expression values. A data frame or a matrix where rows correspond to genes and columns correspond to samples. Alternatively, an object of type <a href="#">SummarizedExperiment</a> , <a href="#">SingleCellExperiment</a> or <a href="#">SpatialExperiment</a> where the normalized expression values should be in an assay called 'norm_expr'.
nametype	character string saying the type of gene name ID (row names in dataset). Either one of "SYMBOL", "ENTREZID" or "ENSEMBL".
whichAssay	integer scalar or string indicating which assay of dataset to use.
hgReference	character string saying the human reference genome. Either one of "hg19" or "hg38".

## Value

If dataset is a [SummarizedExperiment](#) object, then scores are added in the [colData](#) section. If dataset is a data frame or a matrix, then a [SummarizedExperiment](#) object is created in which scores are added in the [colData](#) section.

## Examples

```
data(ovse)  
MPSSign(dataset = ovse)
```

multipleSign

*Multiple Signatures Computation***Description**

This function computes all the signatures for a specific 'inputType'. Further, it is possible to select specific signatures setting the 'tumor', the 'tissue' and/or the 'topic'.

**Usage**

```
multipleSign(
  dataset,
  nametype = "SYMBOL",
  inputType = "rnaseq",
  whichAssay = "norm_expr",
  whichSign = NULL,
  tumor = NULL,
  tissue = NULL,
  topic = NULL,
  ...
)
```

**Arguments**

dataset	Expression values. A data frame or a matrix where rows correspond to genes and columns correspond to samples. Alternatively, an object of type <a href="#">SummarizedExperiment</a> , <a href="#">SingleCellExperiment</a> or <a href="#">SpatialExperiment</a> .
nametype	character string saying the type of gene name ID (row names in dataset). Either one of "SYMBOL", "ENTREZID" or "ENSEMBL".
inputType	character vector saying the type of data you are using. When working with bulk data this should be either one of "microarray" or "rnaseq". When working with single-cell data and spatial transcriptomics data this could be "sc" to compute only signatures developed by single-cell data or c("rnaseq", "sc") to compute all the signatures.
whichAssay	integer scalar or string indicating which assay of dataset to use.
whichSign	character vector saying the signatures to compute.
tumor	character vector saying the tumor types. Signatures from that tumors will be computed (this can also be "pan-cancer").
tissue	character vector saying the tumor tissues. Signatures from that tissues will be computed (this can also be "pan-tissue").
topic	character vector saying signatures topics. Signatures having that topics will be computed.
...	other arguments passed on to the signature functions.

**Value**

A SummarizedExperiment object in which the signatures' scores are added in the [colData](#) section.



**Examples**

```
data(ovse)
multipleSign(dataset = ovse)
multipleSign(dataset = ovse, tissue = "ovary")
```

---

oneSignPlot	<i>Scatterplot for a single signature</i>
-------------	---

---

**Description**

Given signatures' scores, it returns a scatterplot of samples' scores and a barplot of the density distribution of samples' scores.

**Usage**

```
oneSignPlot(data, whichSign, statistics = NULL)
```

**Arguments**

data	an object of type <a href="#">SummarizedExperiment</a> . Output of the signatures functions.
whichSign	character string saying the signature to plot. This must be a signature computed with signifinder.
statistics	character string saying the statistics to be plotted in the graph. Either one of "mean", "median" or "quantiles".

**Value**

A [ggplot](#) object.

**Examples**

```
data(ovse)
oneSignPlot(data = ovse, whichSign = "Ferroptosis_Ye")
```

---

ovse	<i>Example expression data.</i>
------	---------------------------------

---

**Description**

This is an example dataset containing gene expression values (in normalized counts, TPM, CPM, and FPKM) of 40 ovarian cancer (OVC) patients extracted from the Cancer Genome Atlas (TCGA) database. This dataset should be used only with example purpose. RNA sequencing OVC data were retrieved using [curatedTCGAData](#) package. Data were then normalized with the [betweenLaneNormalization](#) function. To lighten the dataset, the [consensusOVSign](#) function was computed, which return 4 different scores, one for each OVC subtype (Chen et al, 2018, Clinical Cancer Research) and the 10 samples with the highest scores were selected for each subgroup. Further, only the genes used for the signatures computation were kept. Finally, all the signatures available in signifinder for OVC plus all the pan-cancer signatures were computed. Further details in `signifinder/inst/scripts/howToGenerateOvse.Rmd`.

**Usage**

```
data(ovse)
```

**Format**

An object of class SummarizedExperiment with 3180 rows and 40 columns.

---

PassONSign	<i>passON Signature</i>
------------	-------------------------

---

**Description**

This signature is computed accordingly to the reference paper, to have more details explore the function [availableSignatures](#).

**Usage**

```
PassONSign(
  dataset,
  nametype = "SYMBOL",
  whichAssay = "norm_expr",
  hgReference = "hg38",
  ...
)
```

**Arguments**

dataset	Normalized expression values. A data frame or a matrix where rows correspond to genes and columns correspond to samples. Alternatively, an object of type <a href="#">SummarizedExperiment</a> , <a href="#">SingleCellExperiment</a> or <a href="#">SpatialExperiment</a> where the normalized expression values should be in an assay called 'norm_expr'.
nametype	character string saying the type of gene name ID (row names in dataset). Either one of "SYMBOL", "ENTREZID" or "ENSEMBL".
whichAssay	integer scalar or string indicating which assay of dataset to use.
hgReference	character string saying the human reference genome. Either one of "hg19" or "hg38".
...	other arguments passed on to the <a href="#">ssgseaParam</a> function.

**Value**

If dataset is a [SummarizedExperiment](#) object, then scores are added in the [colData](#) section. If dataset is a data frame or a matrix, then a [SummarizedExperiment](#) object is created in which scores are added in the [colData](#) section.

**Examples**

```
data(ovse)
PassONSign(dataset = ovse)
```

---

pyroptosisSign	<i>Pyroptosis Signature</i>
----------------	-----------------------------

---

## Description

This signature is computed accordingly to the reference paper, to have more details explore the function [availableSignatures](#).

## Usage

```
pyroptosisSign(  
  dataset,  
  nametype = "SYMBOL",  
  inputType = "rnaseq",  
  author = "Ye",  
  whichAssay = "norm_expr",  
  hgReference = "hg38"  
)
```

## Arguments

dataset	Normalized expression values. A data frame or a matrix where rows correspond to genes and columns correspond to samples. Alternatively, an object of type <a href="#">SummarizedExperiment</a> , <a href="#">SingleCellExperiment</a> or <a href="#">SpatialExperiment</a> where the normalized expression values should be in an assay called 'norm_expr'.
nametype	character string saying the type of gene name ID (row names in dataset). Either one of "SYMBOL", "ENTREZID" or "ENSEMBL".
inputType	character string saying the type of data you are using. Either one of "microarray" or "rnaseq".
author	character string saying the first author of the signature publication. Check it in <a href="#">availableSignatures</a> .
whichAssay	integer scalar or string indicating which assay of dataset to use.
hgReference	character string saying the human reference genome. Either one of "hg19" or "hg38".

## Value

If dataset is a [SummarizedExperiment](#) object, then scores are added in the [colData](#) section. If dataset is a data frame or a matrix, then a [SummarizedExperiment](#) object is created in which scores are added in the [colData](#) section.

## Examples

```
data(ovse)  
pyroptosisSign(dataset = ovse)
```

---

ridgelineSignPlot	<i>Ridgeline Plot</i>
-------------------	-----------------------

---

### Description

Given multiple signatures, the function plots scores density distribution.

### Usage

```
ridgelineSignPlot(
  data,
  whichSign = NULL,
  groupByAnnot = NULL,
  selectByAnnot = NULL,
  ...
)
```

### Arguments

data	an object of type <a href="#">SummarizedExperiment</a> . Output of the signatures functions.
whichSign	character vector saying the signatures to plot. If not specified, all the signatures inside data will be plotted. Other signatures not computed with signfinder can be added in the vector if they are also included in the colData section of data.
groupByAnnot	character vector containing samples' annotations.
selectByAnnot	character string saying the subgroup from 'groupByAnnot' used to compute the ridgeline plot.
...	other parameters specific of the functions <a href="#">geom_density_ridges</a> and <a href="#">geom_density_ridges_gradient</a> .

### Value

A [ggplot](#) object.

### Examples

```
data(ovse)
ridgelineSignPlot(data = ovse)
```

---

stemCellCD49fSign	<i>CD49fHi Basal Stem Cell Signature</i>
-------------------	--

---

### Description

This signature is computed accordingly to the reference paper, to have more details explore the function [availableSignatures](#).

### Usage

```
stemCellCD49fSign(dataset, nametype = "SYMBOL", whichAssay = "norm_expr")
```

**Arguments**

dataset	Normalized expression values. A data frame or a matrix where rows correspond to genes and columns correspond to samples. Alternatively, an object of type <a href="#">SummarizedExperiment</a> , <a href="#">SingleCellExperiment</a> or <a href="#">SpatialExperiment</a> where the normalized expression values should be in an assay called 'norm_expr'.
nametype	character string saying the type of gene name ID (row names in dataset). Either one of "SYMBOL", "ENTREZID" or "ENSEMBL".
whichAssay	integer scalar or string indicating which assay of dataset to use.

**Value**

If dataset is a [SummarizedExperiment](#) object, then scores are added in the `colData` section. If dataset is a data frame or a matrix, then a [SummarizedExperiment](#) object is created in which scores are added in the `colData` section.

**Examples**

```
data(ovse)
stemCellCD49fSign(dataset = ovse)
```

---

survivalSignPlot	<i>Survival Plot</i>
------------------	----------------------

---

**Description**

Given a signature and samples' survival data, the function plots survival curves for that signature. This is a wrapper around [survfit](#), that creates survival curves from a model formula. Here, the response variable in the formula is a survival object created by [Surv](#). Survival curves are then passed to the [ggsurvplot](#) function. For details about the statistics see [survfit](#) and [Surv](#).

**Usage**

```
survivalSignPlot(
  data,
  survData,
  whichSign,
  cutpoint = "mean",
  sampleAnnot = NULL,
  selectByAnnot = NULL
)
```

**Arguments**

data	an object of type <a href="#">SummarizedExperiment</a> . Output of the signatures functions.
survData	a dataframe with samples on rows and two columns. The first column holds survival data of time, indicating the follow up times; the second holds data of the survival status, normally 0=alive and 1=dead. For further details check <a href="#">Surv</a> function.

whichSign	character string saying the signature to plot. This must be a signature computed with signifinder.
cutpoint	a character string (one of: "median", "mean" and "optimal") or a numeric value, which divide samples between high scores and low scores. The function computes the threshold with the method indicated or employs the values directly supplied by the user. Based on that number, it divides samples. In case of "optimal" the <code>maxstat.test</code> function will be used to estimate the cutpoint which separates samples best.
sampleAnnot	a categorical vector containing samples' annotations named with samples names equal to the row names used in 'survData'.
selectByAnnot	character string saying the subgroup from 'sampleAnnot' used to compute the survival analysis.

### Value

A `ggplot` object.

### Examples

```
data(ovse)
mysurvData <- cbind(ovse$os, ovse$status)
rownames(mysurvData) <- rownames(SummarizedExperiment::colData(ovse))
survivalSignPlot(
  data = ovse,
  survData = mysurvData,
  whichSign = "Ferroptosis_Ye"
)
```

---

TGFBSign

*Pan-Fibroblast TGFB Response Signature*

---

### Description

This signature is computed accordingly to the reference paper, to have more details explore the function [availableSignatures](#).

### Usage

```
TGFBSign(dataset, nametype = "SYMBOL", whichAssay = "norm_expr")
```

### Arguments

dataset	Normalized expression values. A data frame or a matrix where rows correspond to genes and columns correspond to samples. Alternatively, an object of type <a href="#">SummarizedExperiment</a> , <a href="#">SingleCellExperiment</a> or <a href="#">SpatialExperiment</a> where the normalized expression values should be in an assay called 'norm_expr'.
nametype	character string saying the type of gene name ID (row names in dataset). Either one of "SYMBOL", "ENTREZID" or "ENSEMBL".
whichAssay	integer scalar or string indicating which assay of dataset to use.

**Value**

If dataset is a [SummarizedExperiment](#) object, then scores are added in the [colData](#) section. If dataset is a data frame or a matrix, then a [SummarizedExperiment](#) object is created in which scores are added in the [colData](#) section.

**Examples**

```
data(ovse)
TGFBSign(dataset = ovse)
```

---

TinflamSign	<i>TinflamSign Signature</i>
-------------	------------------------------

---

**Description**

This signature is computed accordingly to the reference paper, to have more details explore the function [availableSignatures](#).

**Usage**

```
TinflamSign(
  dataset,
  nametype = "SYMBOL",
  author = "Ayers",
  whichAssay = "norm_expr",
  hgReference = "hg38"
)
```

**Arguments**

dataset	Normalized expression values. A data frame or a matrix where rows correspond to genes and columns correspond to samples. Alternatively, an object of type <a href="#">SummarizedExperiment</a> , <a href="#">SingleCellExperiment</a> or <a href="#">SpatialExperiment</a> where the normalized expression values should be in an assay called 'norm_expr'.
nametype	character string saying the type of gene name ID (row names in dataset). Either one of "SYMBOL", "ENTREZID" or "ENSEMBL".
author	character string saying the first author of the signature publication. Check it in <a href="#">availableSignatures</a> .
whichAssay	integer scalar or string indicating which assay of dataset to use.
hgReference	character string saying the human reference genome. Either one of "hg19" or "hg38".

**Value**

If dataset is a [SummarizedExperiment](#) object, then scores are added in the [colData](#) section. If dataset is a data frame or a matrix, then a [SummarizedExperiment](#) object is created in which scores are added in the [colData](#) section.

## Examples

```
data(ovse)
TinflamSign(dataset = ovse)
```

---

TLSSign

*Tertiary Lymphoid Structures (TLS) Signature*

---

## Description

This signature is computed accordingly to the reference paper, to have more details explore the function [availableSignatures](#).

## Usage

```
TLSSign(
  dataset,
  nametype = "SYMBOL",
  inputType = "rnaseq",
  whichAssay = "norm_expr"
)
```

## Arguments

dataset	Normalized expression values. A data frame or a matrix where rows correspond to genes and columns correspond to samples. Alternatively, an object of type <a href="#">SummarizedExperiment</a> , <a href="#">SingleCellExperiment</a> or <a href="#">SpatialExperiment</a> where the normalized expression values should be in an assay called 'norm_expr'.
nametype	character string saying the type of gene name ID (row names in dataset). Either one of "SYMBOL", "ENTREZID" or "ENSEMBL".
inputType	character string saying the type of data you are using. Either one of "microarray" or "rnaseq".
whichAssay	integer scalar or string indicating which assay of dataset to use.

## Value

If dataset is a [SummarizedExperiment](#) object, then scores are added in the [colData](#) section. If dataset is a data frame or a matrix, then a [SummarizedExperiment](#) object is created in which scores are added in the [colData](#) section.

## Examples

```
data(ovse)
TLSSign(dataset = ovse)
```



---

VEGFSign

---

*VEGF Signature*

---

**Description**

This signature is computed accordingly to the reference paper, to have more details explore the function [availableSignatures](#).

**Usage**

```
VEGFSign(dataset, nametype = "SYMBOL", whichAssay = "norm_expr")
```

**Arguments**

dataset	Normalized expression values. A data frame or a matrix where rows correspond to genes and columns correspond to samples. Alternatively, an object of type <a href="#">SummarizedExperiment</a> , <a href="#">SingleCellExperiment</a> or <a href="#">SpatialExperiment</a> where the normalized expression values should be in an assay called 'norm_expr'.
nametype	character string saying the type of gene name ID (row names in dataset). Either one of "SYMBOL", "ENTREZID" or "ENSEMBL".
whichAssay	integer scalar or string indicating which assay of dataset to use.

**Value**

If dataset is a [SummarizedExperiment](#) object, then scores are added in the [colData](#) section. If dataset is a data frame or a matrix, then a [SummarizedExperiment](#) object is created in which scores are added in the [colData](#) section.

**Examples**

```
data(ovse)
VEGFSign(dataset = ovse)
```

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