

# Package ‘iScreen’

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**Title** image-based High-Throughput RNAi Screening Analysis Tool

**Description** image-based high-throughput RNAi screening tools for data analysis and visualization

**Version** 1.0

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autophagy	<i>Data set for autophagy study.</i>
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### Description

Data set used to fit a Poisson regression from an autophagy study.

### Usage

```
data(autophagy)
```

### Format

The format is: chr "autophagy"

### Examples

```
data(autophagy)
## maybe str(autophagy) ; plot(autophagy) ...
```

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colocalization	<i>Data set for autophagy study.</i>
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### Description

Data set used to fit a customized function from an autophagy study.

### Usage

```
data(colocalization)
```

### Format

The format is: chr "colocalization"

### Examples

```
data(colocalization)
## maybe str(colocalization) ; plot(colocalization) ...
```

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fun.iScreen	<i>Custom analysis of image-based HTS</i>
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**Description**

Perform custom analysis of image-based HTS data.

**Usage**

```
fun.iScreen(data, FUN)
```

**Arguments**

data	A data frame containing the variables in the model with the first column as Well ID. For details of the Well ID format, see <a href="#">WellCheck</a> . If not found, an error will be reported.
FUN	A user-provided function for analysis

**Details**

For argument FUN, user has to provide a custom function. Function argument has to be from data. Return value can be a single value or a vector. For vector return, the first value has to be estimate for each Well ID.

**Value**

A list of two components, fit and coefficients.

fit	NULL
coefficients	Estimations of coefficients for each Well ID

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glm.iScreen	<i>Generalized linear model for image-based HTS</i>
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**Description**

Perform generalized linear model for image-based HTS data analysis.

**Usage**

```
glm.iScreen(data, formula, control = NULL, ...)
```

**Arguments**

data	A data frame containing the variables in the model with the first column as Well ID. For details of the Well ID format, see <a href="#">WellCheck</a> . If not found, an error will be reported.
formula	An object of class <a href="#">formula</a> or one that can be coerced to that class. a symbolic description of the model to be fitted. The details of model specification are given under 'Details' from <a href="#">glm</a> .
control	A optional vector of the length as the number of rows in data indicating which row or rows from data should be used as control when fitting generalized linear model.
...	Arguments to be passed to method. For details also see <a href="#">formula</a> .

**Value**

A list of two components, fit and coefficients.

fit	A fitted generalized linear model object from <a href="#">glm</a>
coefficients	Estimations of coefficients for each Well ID

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iPlate	<i>image-based HTS Plate</i>
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**Description**

image-based HTS Plate object to be used for analysis and visualization

**Usage**

```
iPlate(data, column, log = FALSE, FUN = mean, ...)
```

**Arguments**

data	A data frame containing the variables in the model with the first column as Well ID. For details of the Well ID format, see <a href="#">WellCheck</a> . If not found, an error will be reported.
column	Specify the column to be used for analysis and visualization.
log	Specify if data need be logarithm transformed.
FUN	A function to compute the summary statistics which can be applied to all data subsets.
...	Further arguments passed to or used by methods. See <a href="#">aggregate</a> for further information.

**Value**

A object "iPlate" list of 4 elements.

z	A data frame containing Well ID and summary statistics for each Well ID
loc	A list of coordinate information returned by <a href="#">WellToLoc</a>
log	A logical value indicating if data is logarithm transformed
FUN	the function to compute the summary statistics

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iPlateBoxplot	<i>Plotting iPlate boxplot</i>
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**Description**

Function for box plotting object returned by iPlate. For more details about the graphical parameter arguments, see [boxplot](#) and [par](#).

**Usage**

```
iPlateBoxplot(object, by = "row", ...)
```

**Arguments**

object	A iPlate object.
by	Default is "row" and can also be "column".
...	Arguments to be passed to methods. See <a href="#">boxplot</a> and <a href="#">par</a> .

**Examples**

```
data(autophagy)
p1 <- iPlate(autophagy, "dot.number", log=TRUE, FUN=mean)
iPlateBoxplot(p1)
```

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iPlateLegend	<i>Plotting iPlate legend</i>
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**Description**

Function for plotting legend for object returned by iPlate. For more details about the graphical parameter arguments, see [image](#) and [par](#).

**Usage**

```
iPlateLegend(object, ...)
```

**Arguments**

object            A iPlate object.  
 ...              Arguments to be passed to methods. See [image](#) and [par](#).

**Examples**

```
data(autophagy)
p1 <- iPlate(autophagy, "dot.number", log=TRUE, FUN=mean)
iPlateLegend(p1)
```

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iPlatePlot                      *Plotting iPlate object*

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**Description**

Function for plotting object returned by iPlate. For more details about the graphical parameter arguments, see [par](#).

**Usage**

```
iPlatePlot(object, ...)
```

**Arguments**

object            A iPlate object.  
 ...              Arguments to be passed to methods. See [plot](#) and [par](#)

**Examples**

```
data(autophagy)
p1 <- iPlate(autophagy, "dot.number", log=TRUE, FUN=mean)
iPlatePlot(p1)
```

---

iScreen                              *image-based HTS analysis*

---

**Description**

Analysis of image-based high-throughput RNAi screen via either generalized linear model or customized user function.

**Usage**

```
iScreen(data = NULL, formula = NULL, control = NULL,
        FUN = NULL, ...)
```

**Arguments**

data	A data frame containing the variables in the model with the first column as Well ID. For details of the Well ID format, see <a href="#">WellCheck</a> . If not found, an error will be reported.
formula	An object of class " <a href="#">formula</a> " (or one that can be coerced to that class): a symbolic description of the model to be fitted. The details of model specification are given under 'Details' from <a href="#">glm</a> .
control	A optional vector of the length as the number of rows in data indicating which row or rows from data should be used as control when fitting generalized linear model.
FUN	A user-provided function for analysis
...	Arguments to be passed to method. For details also see <a href="#">formula</a> .

**Details**

For argument FUN, user has to provide a custom function. Function argument has to be from data. Return value can be a single value or a vector. For vector return, the first value has to be estimate for each Well ID.

**Value**

A "iScreen" list of two components, fit and coefficients.

fit	A fitted generalized linear model object from <a href="#">glm</a> or NULL if FUN is used
coefficients	Estimations of coefficients for each Well ID

**Examples**

```
data(autophagy)
fit.auto <- iScreen(autophagy, dot.number~WellID, family=poisson, control=(autophagy$control == 1))
head(fit.auto$coefficients)
```

---

iScreenBoxplot	<i>Plotting iScreen boxplot</i>
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**Description**

Function for box plotting object returned by iScreen. For more details about the graphical parameter arguments, see [boxplot](#) and [par](#).

**Usage**

```
iScreenBoxplot(object, by = "row", ...)
```

**Arguments**

object	A iScreen object.
by	Default is "row" and can also be "column".
...	Arguments to be passed to methods. See <a href="#">boxplot</a> and <a href="#">par</a> .

**Examples**

```
data(autophagy)
fit.auto <- iScreen(autophagy, dot.number~WellID, family=poisson, control=(autophagy$control == 1))
iScreenBoxplot(fit.auto)
```

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iScreenInBatch	<i>Batch process of image-based HTS</i>
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**Description**

Batch processing of image-based high-throughput RNAi screen via either generalized linear model or customized user function.

**Usage**

```
iScreenInBatch(data = NULL, formula = NULL,
               control = NULL, FUN = NULL, ...)
```

**Arguments**

data	A data frame containing the variables in the model with the first two column as Well ID and Plate ID. For details of the Well ID format, see <a href="#">WellCheck</a> . If not found, an error will be reported.
formula	An object of class " <a href="#">formula</a> " (or one that can be coerced to that class): a symbolic description of the model to be fitted. The details of model specification are given under 'Details' from <a href="#">glm</a> .
control	A optional vector of the length as the number of rows in data indicating which row or rows from data should be used as control when fitting generalized linear model.
FUN	A user-provided function for analysis.
...	Arguments to be passed to method. For details also see <a href="#">formula</a> .

**Details**

For argument FUN, user has to provide a custom function. Function argument has to be from data. Return value can be a single value or a vector. For vector return, the first value has to be estimate for each Well ID.

**Value**

A "iScreenInBatch" data frame containing summary coefficients.

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iScreenInBatchBoxplot *Plotting iScreenInBatch boxplot*

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### Description

Function for plotting object returned by iScreenInBatch. For more details about the graphical parameter arguments, see [par](#).

### Usage

```
iScreenInBatchBoxplot(object, ...)
```

### Arguments

object	A iScreenInBatch object.
...	Arguments to be passed to methods. See <a href="#">boxplot</a> and <a href="#">par</a>

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iScreenLegend *Plotting iScreen legend*

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### Description

Function for plotting legend for object returned by iScreen. For more details about the graphical parameter arguments, see [image](#) and [par](#).

### Usage

```
iScreenLegend(object, ...)
```

### Arguments

object	A iScreen object.
...	Arguments to be passed to methods. See <a href="#">image</a> and <a href="#">par</a> .

### Examples

```
data(autophagy)
fit.auto <- iScreen(autophagy, dot.number~WellID, family=poisson, control=(autophagy$control == 1))
iScreenLegend(fit.auto)
```

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iScreenPlot	<i>Plotting iScreen</i>
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---

**Description**

Function for plotting object returned by iScreen. For more details about the graphical parameter arguments, see [par](#).

**Usage**

```
iScreenPlot(object, xlab = "Column", ylab = "Row", ...)
```

**Arguments**

object	A iScreen object.
xlab	Default is "Column".
ylab	Default is "Row".
...	Arguments to be passed to methods. See <a href="#">plot</a> and <a href="#">par</a>

**Examples**

```
data(autophagy)
fit.auto <- iScreen(autophagy, dot.number~WellID, family=poisson, control=(autophagy$control == 1))
iScreenPlot(fit.auto)
```

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iWell	<i>image-based HTS Well object</i>
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**Description**

image-based HTS Well object to be used for visualization

**Usage**

```
iWell(x, y, d, c, n = 4, angle = 0, type = 1)
```

**Arguments**

x	A vector containing X coordinate of each plot unit.
y	A vector containing Y coordinate of each plot unit.
d	A vector containing diameter of each plot unit.
c	A vector containing plot colore of each plot unit.
n	A numeric or vector containing number of sides for each plot unit.
angle	A numeric or vector containing rotation angle of each plot unit, in degrees.
type	A numeric or vector containing plotting type type=1 => interior filled, type=2 => edge, type=3 => both.

**Details**

For details also see [ngon](#).

**Value**

A object "iWell".

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iWellPlot	<i>Plotting iWell</i>
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**Description**

Function for plotting object returned by iPlate. For more details about the graphical parameter arguments, see [par](#).

**Usage**

```
iWellPlot(object, xlab = "X", ylab = "Y", ...)
```

**Arguments**

object	A iScreen object.
xlab	Default is "X".
ylab	Default is "Y".
...	Arguments to be passed to methods. See <a href="#">plot</a> and <a href="#">par</a>

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WellCheck	<i>Check WellID format</i>
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**Description**

Examination of variable WellID format

**Usage**

```
WellCheck(x)
```

**Arguments**

x	A character or a vector of characters as variable WellID
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**Value**

The value is logical of length one. Return TRUE if and only if all elements in x accord with WELLID requirement, otherwise return FALSE.

**Examples**

```
#WellID format should be "A01", "B02", "C03", ..."J12", ...
WellCheck(c("A01"))
WellCheck(c("A1"))
WellCheck(c("A01", "B02", "C03"))
WellCheck(c("A01", "B2", "C03"))
```

---

WellToLoc

*Convert WellID*


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**Description**

Convert Well ID into plot coordinate and label

**Usage**

```
WellToLoc(WellNO)
```

**Arguments**

WellNO            A character or a vector of characters as variable WellID to converted

**Value**

A list consisting of 4 vectors.

x.loc	A vector of the length of WellNO indicating x coordinate of each WellNO upon plot
y.loc	A vector of the length of WellNO indicating y coordinate of each WellNO upon plot
x.label	A vector of names to be used as label on X axis upon plot
y.label	A vector of names to be used as label on Y axis upon plot

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