

# Package ‘kangoo’

October 16, 2014

**Type** Package

**Title** Analyse qRT-PCR data with a special focus on differential splicing detection

**Version** 1.0

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**Description** Especially designed for ABI output.

**License** GPL-3

**Depends** R (>= 3.0.0),ggplot2, reshape2, scales, plyr, tcltk

**Imports**

**Suggests** RSVGTipsDevice

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analyzeInclIndex	<i>analyzeInclIndex</i>
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### Description

This function takes the output of the ABI SDS programm and calculates the alternative isoform fraction (AIF), which describes the proportion of the alternative isoform compared to the constitutive expression as defined by the conservative primer pair.

Combines the loadExp and calculateInclIndex function into one call.

### Usage

```
analyzeInclIndex(plate.setup = "splicing", plate.format = "96-well")
```

### Arguments

plate.setup	Specify the sample setup on the plate. Default is "splicing".
plate.format	Specify the plate format of the RT-PCR cycler. Default is "96-well".

### Details

This function outputs 3 plots: 1. plot of the raw CT values for quality control 2. plot of the AIF without p-value 3. plot of the AIF including the p-value for each gene

Also it outputs a table describing the results and showing the dAIF. This output is also appended to the general output file in the e-book. In addition a small txt file is written giving the session info.

### Examples

```
{
}
```

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analyzeInclIndexKD	<i>analyzeInclIndexKD</i>
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### Description

This function takes the output of the ABI SDS programm and calculates the alternative isoform fraction (AIF), which describes the proportion of the alternative isoform compared to the constitutive expression as defined by the conservative primer pair.

Combines the loadExp and calculateInclIndex function into one call.

This version is adapted to incorporate different knockdown experiments by siRNAs. Sample information is needed in form AGS\_SESN1\_SRPK2-7\_con\_NI

**Usage**

```
analyzeInclIndexKD(plate.setup="splicing",plate.format="96-well")
```

**Arguments**

plate.setup	Specify the sample setup on the plate. Default is "splicing" ("Cells_Gene_Primer_Treatment"). Alternatively you can use "splicing_knockdown", which needs a sample description in the form "Cells_Gene_Knockdown_Primer_Treatment".
plate.format	Specify the plate format of the RT-PCR cyclers. Default is "96-well".

**Details**

This function outputs 3 plots: 1. plot of the raw CT values for quality control 2. plot of the AIF without p-value 3. plot of the AIF including the p-value for each gene

Also it outputs a table describing the results and showing the dAIF. This output is also appended to the general output file in the e-book. In addition a small txt file is written giving the session info.

**Examples**

```
{  
}
```

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