

Package ‘SH’

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Type Package

Title Advises the user on the quality of Seahorse data

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Description The main function sh_full() gives an overview of how often each well within the dataset deviates from the mean +/- sd of the measurement.

License file LICENSE

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`sh_full`*Seahorse Full function*

Description

Gives an overview of how often each well within each group of the dataset deviates from the mean \pm sd of the measurement.

Usage

```
sh_full(input, check.min=T, assay="ms", save.out=F, custom=NULL, save.name="output.txt")
```

Arguments

<code>input</code>	A .csv file containing all measurements for all wells of the groups to analyze.
<code>check.min</code>	A logical value indicating whether columns containing NA values should be removed. Default TRUE
<code>assay</code>	Either 'ms' for mitrostress or 'gs' for glycolysis stress. Default 'ms' but is overwritten by 'custom' argument.
<code>save.out</code>	Saves the output of the analysis to a .txt document. New results will be appended to the file. Default FALSE
<code>custom</code>	Please use for custom well priority. Has to be a numeric vector (e.g. <code>custom = c(1:2,5:8)</code>)
<code>save.name</code>	A string to a .txt file to which the output should be appended. The default saves the output in the project folder, this can however be changes by adding other destinations. Default "output.txt"

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