

A

Run quality check tools
Choose the quality checks you want to include in your analysis and click Next to continue.

If you don't want any quality checking you can skip this step.

Info
Boxplots and MA plots
The boxplots visualize the distribution of unprocessed log scale probe intensities. Generally in a perfect experiment all the plots should be in agreement with each other. Chips that show a strongly deviating probe intensity distribution might be problematic.

In the MA plots, the normalized log scale probe intensities are plotted against the log fold change in expression when compared to a synthetic chip that was created by taking probe-wise medians of all chips in the input set. A lowess curve is fitted to the scatter plot and the deviation of the data from the theoretically expected zero-line is estimated via the integral of the lowess curve over the zero-line. In addition to this the amount of probes that show a more than 2 fold change in expression are recorded and a warning is issued if the amount exceeds 5% of the genes.

Box plot and MA plots Include? [more](#)

PLM – Fitting probe level models to the data Include? [more](#)

RNA digestion – Uses ordered probes in probeset to detect possible RNA degradation Include? [more](#)

Histogram – Shows density plots of the signal intensity for each chip Include? [more](#)

Scatterplot – The data will be normalised before plotting the log₂-fold expression values of all possible combinations of two chips against each other Include? [more](#)

PCA and hierarchical clustering Include? [more](#)

NUSE and RLE – Normalized unscaled standard errors and relative logarithmic expression Include? [more](#)

Select all

Edit expert options
The chosen default values will be suitable in most cases. They should only be changed by an expert.

Expert settings

Normalisation method: rma [?](#)

P value correction method: BH [?](#)

Multiple testing strategy: nestedF [?](#)

Analysis strategy: Linear models (package limma) [?](#)

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B

Design your experiment
You can arrange groups by dragging them around. Define which group shall be compared by holding down the **CONTROL** key when click-dragging from the **first group** to the **second group**. Right-click and choose delete to delete connections. To combine several groups into one "metagroup" select all groups you want to combine (by left-clicking and drawing a selection rectangle around them) and click "Create Metagroup".

Show expert settings

Expert settings

Normalisation: rma [?](#)

P value correction: BH [?](#)

Multiple testing strategy: nestedF [?](#)

Write out normalized raw data

Preview R script

Log-fold change min=1

p-value cutoff: 0.05 [?](#)

wildtype

wildtype stressed

mutant

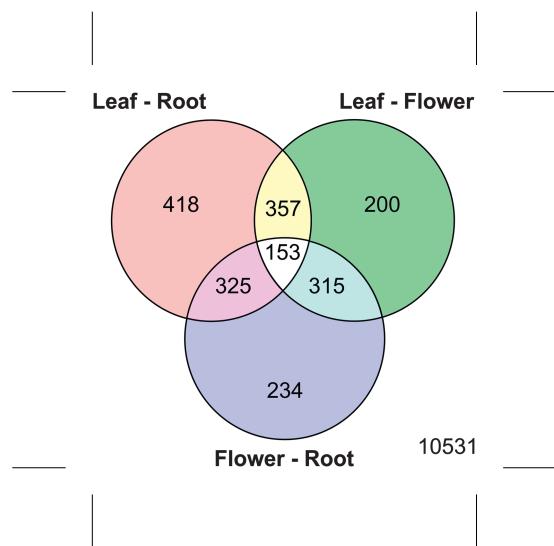
mutant stressed

wildtype-wildtype stressed → mutant-mutant stressed

Reset design **Create Metagroup** **Delete Metagroup**

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pp152553F02_CMYK.tif



pp152553F03_CMYK.tif

