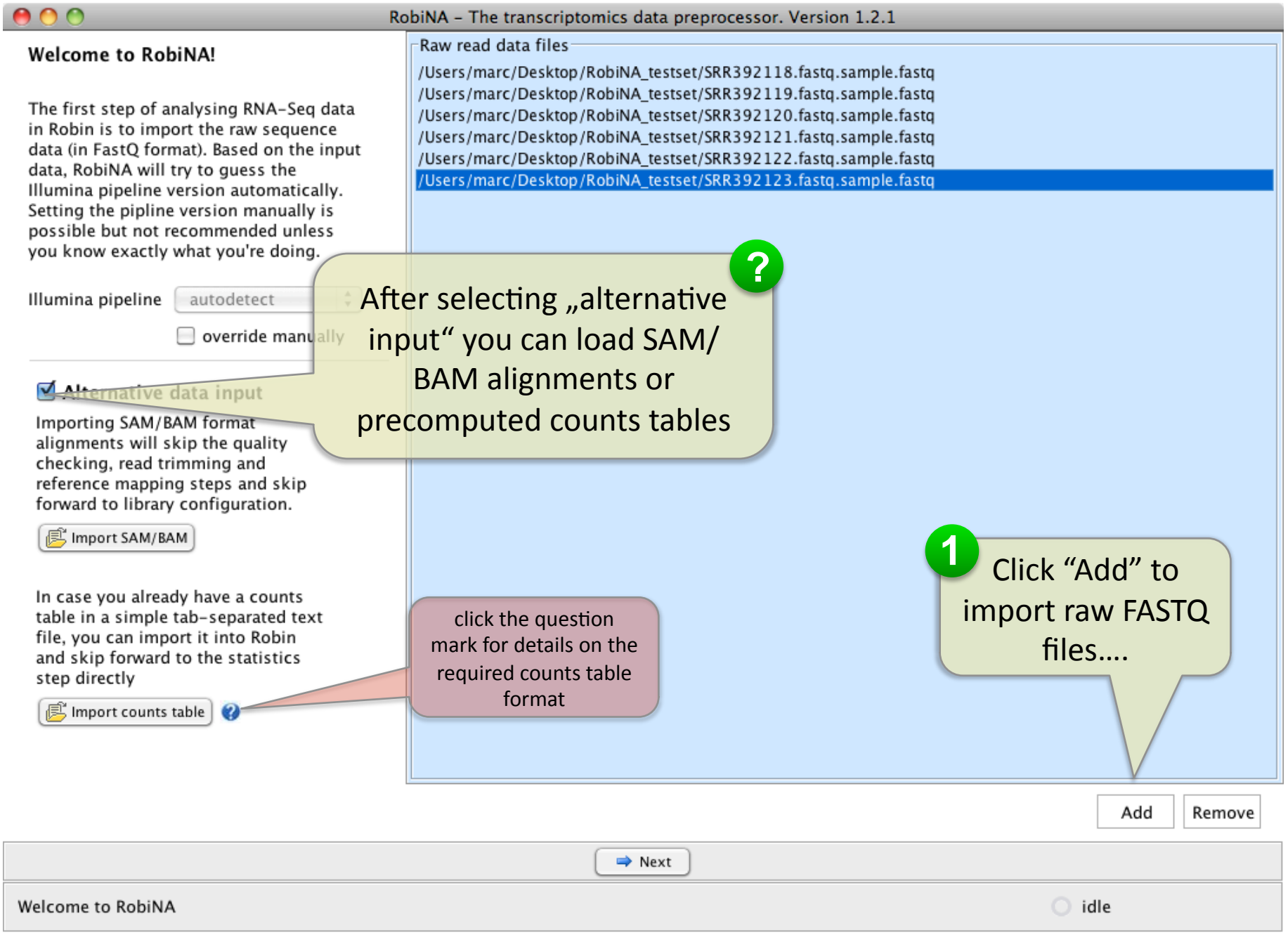
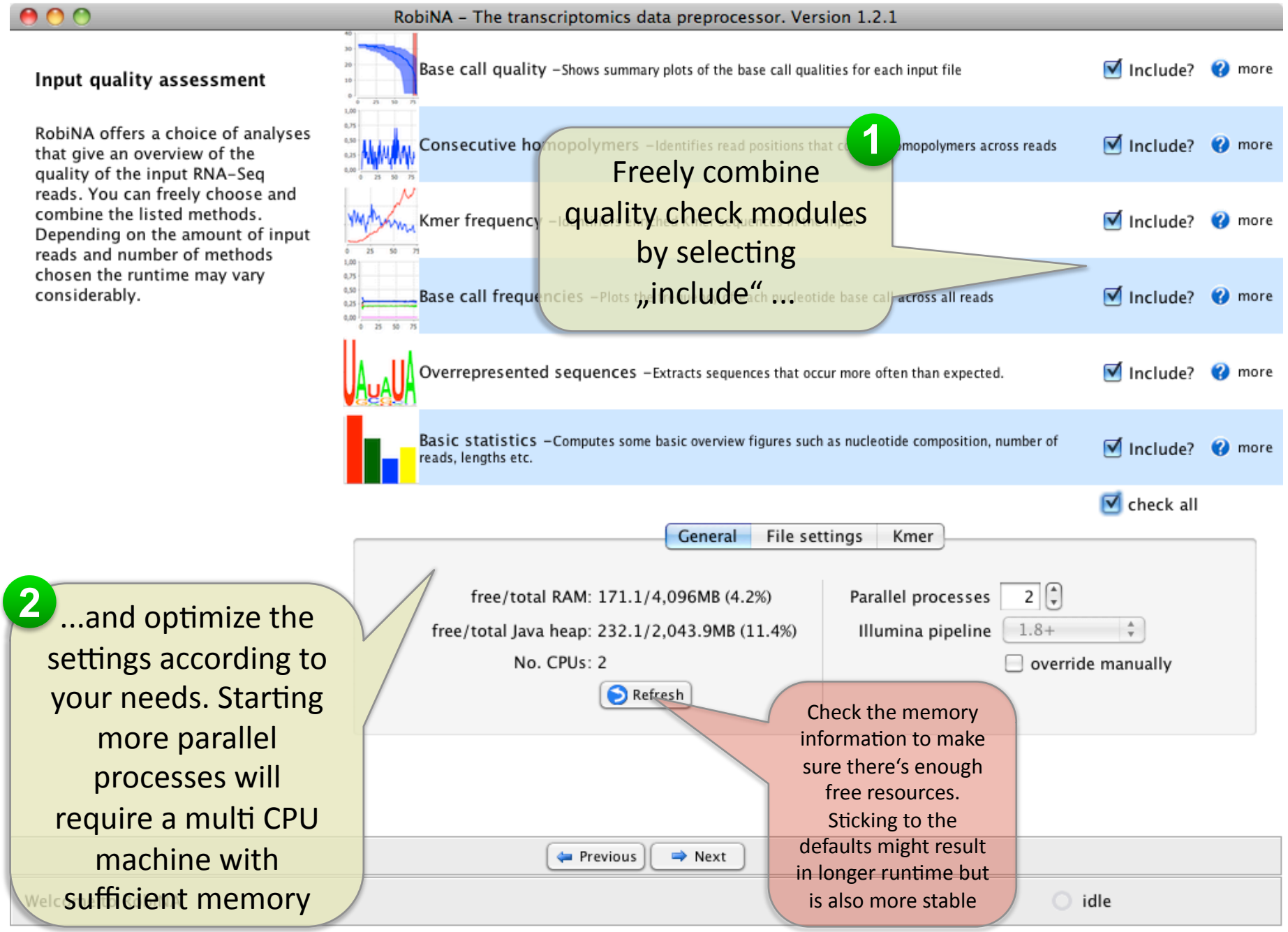
RNA-Seq based analysis of differential gene expression
Using RobiNA – a quick guide

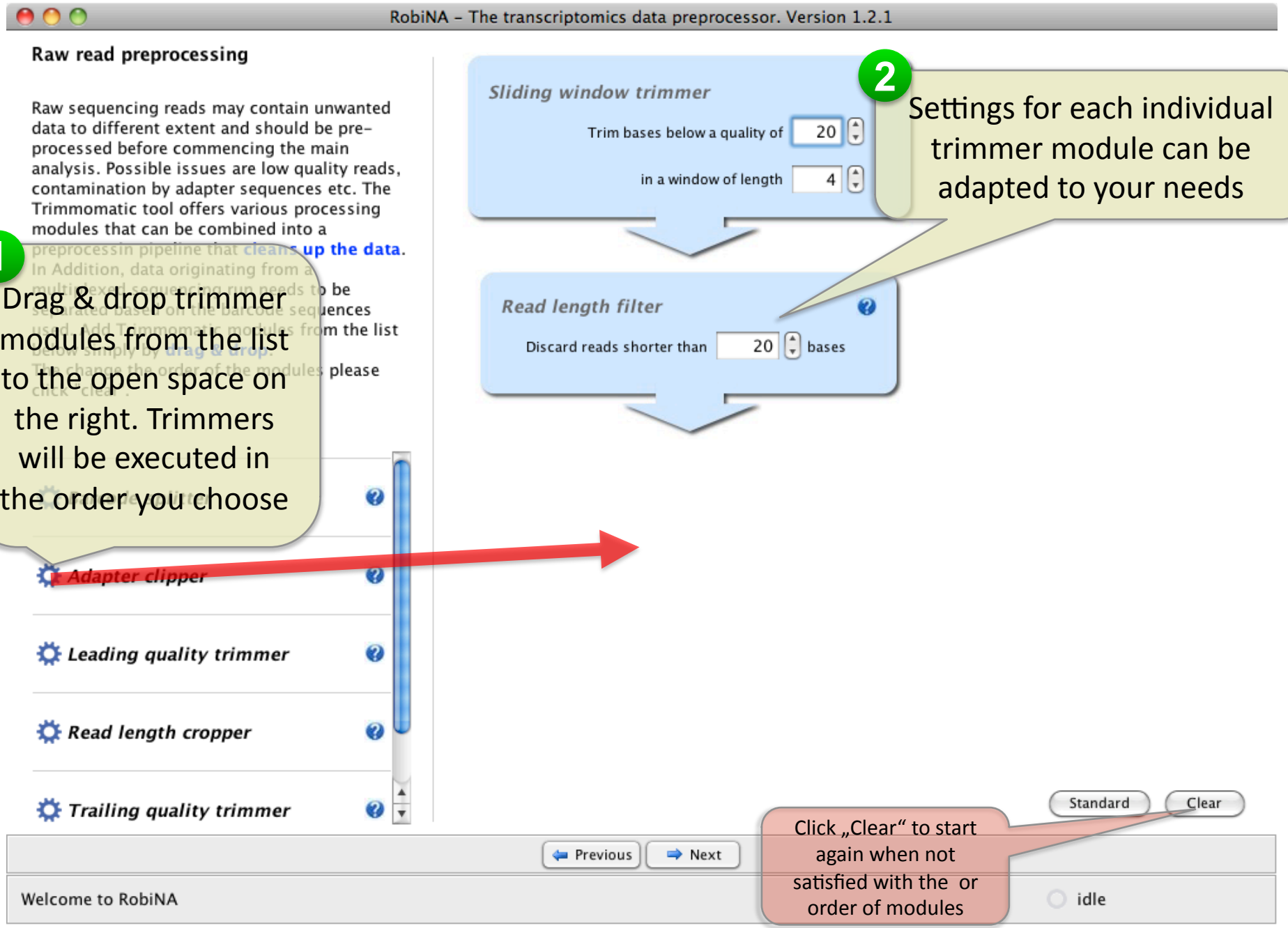
Step 1: Data import



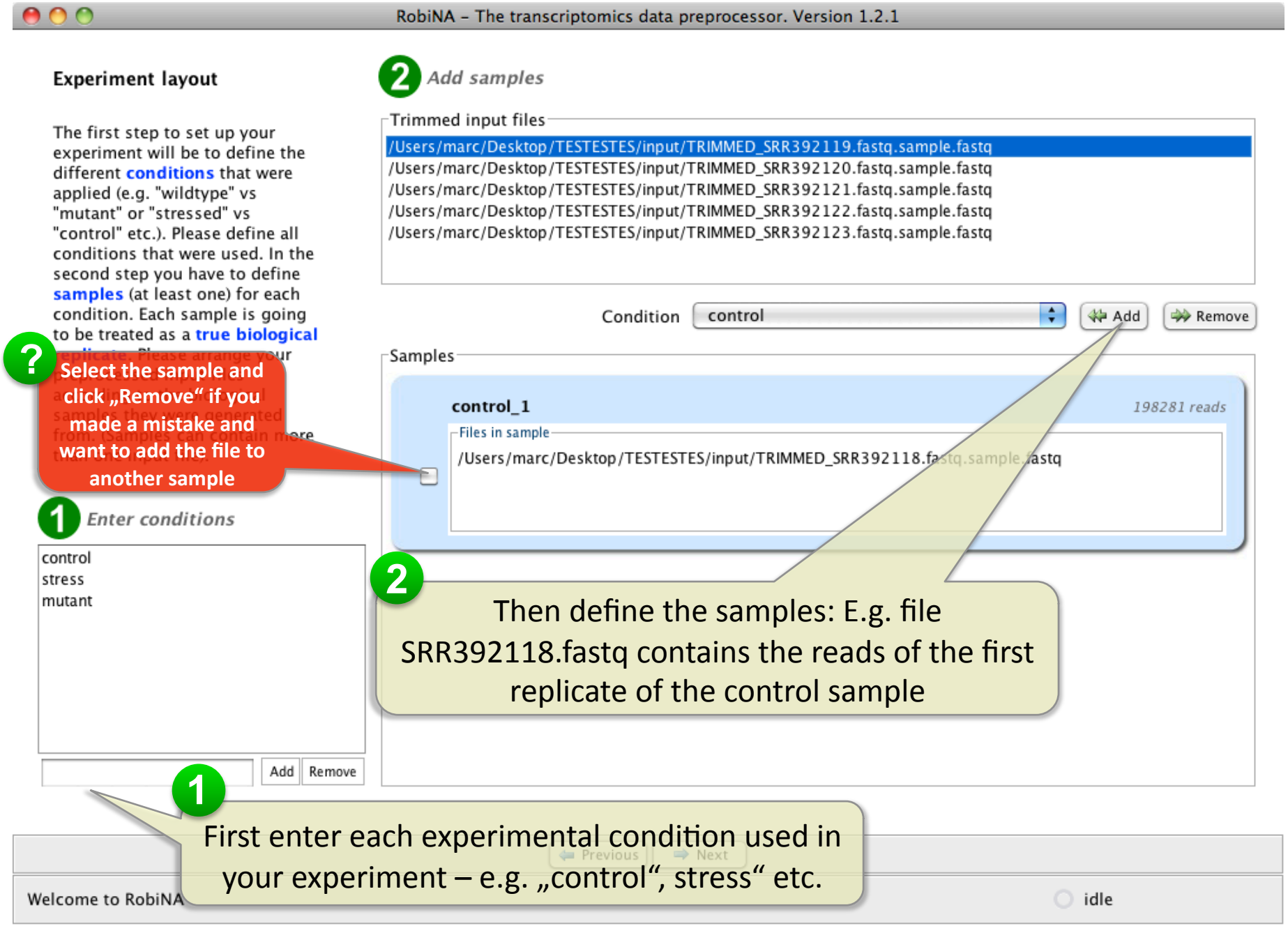
Step 2: Quality checking



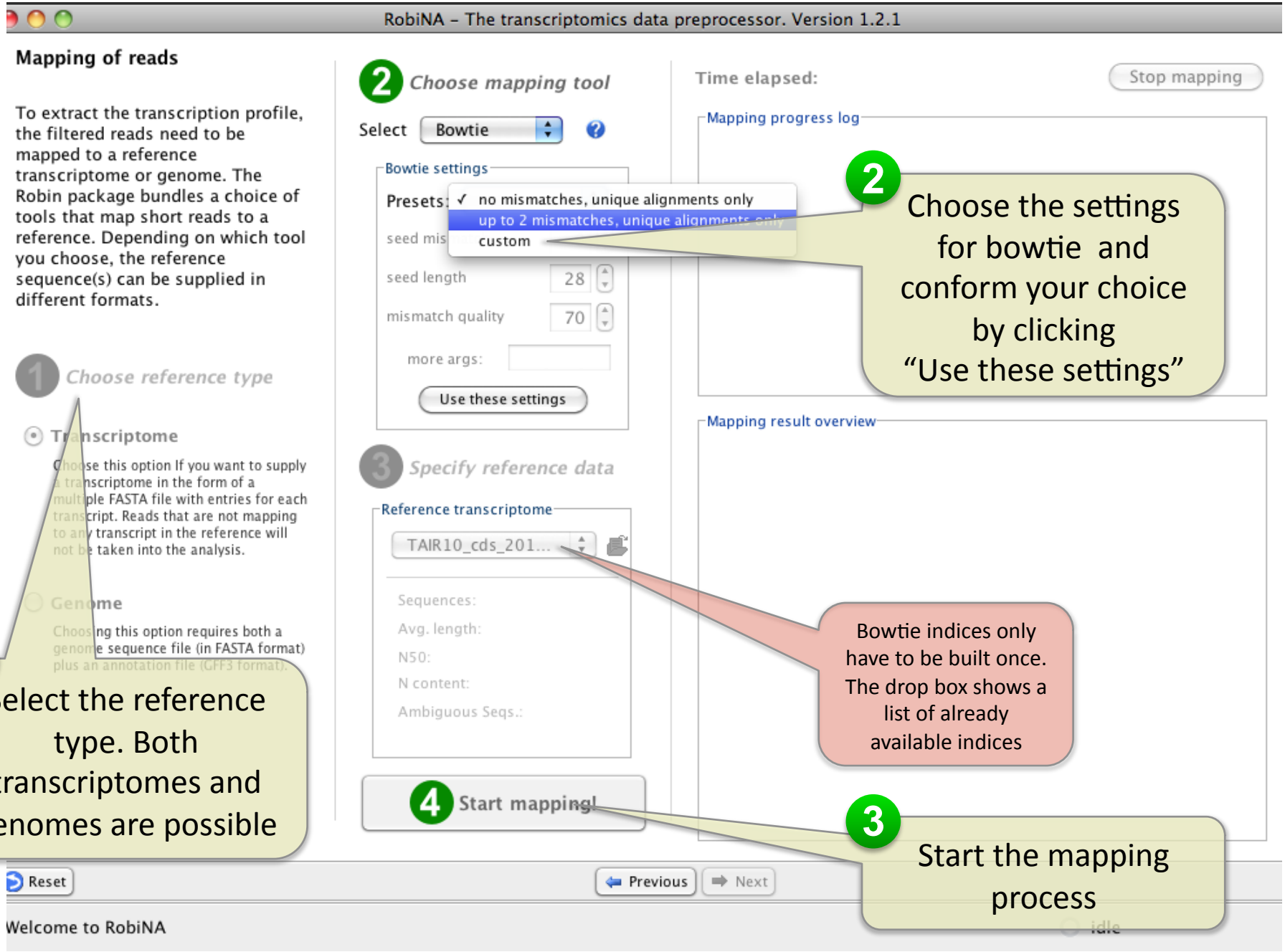
Step 3: Raw read trimming to remove low quality data



Step 4: Experiment layout



Step 5: Mapping of the reads to a reference -> Generate counts table



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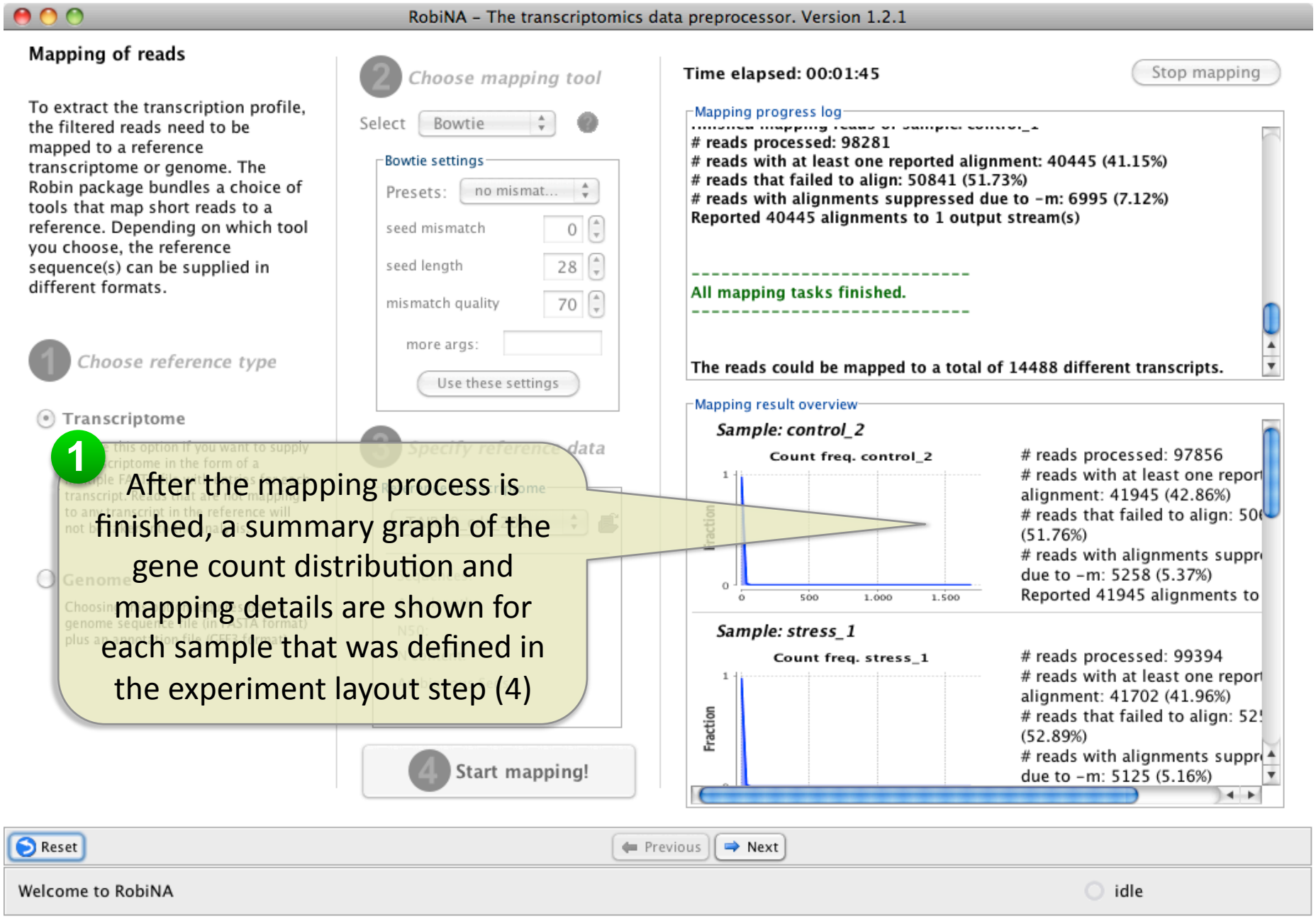
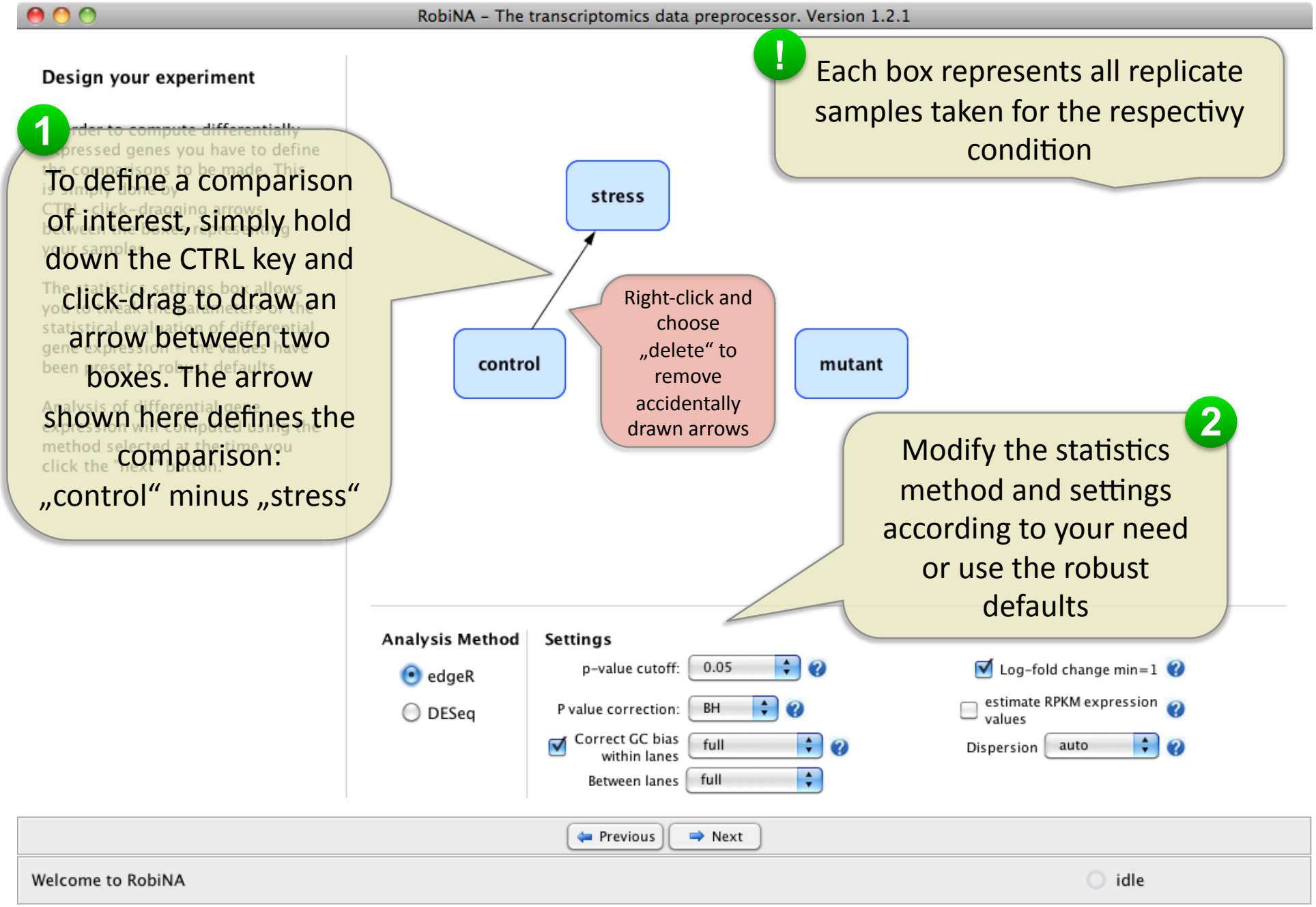
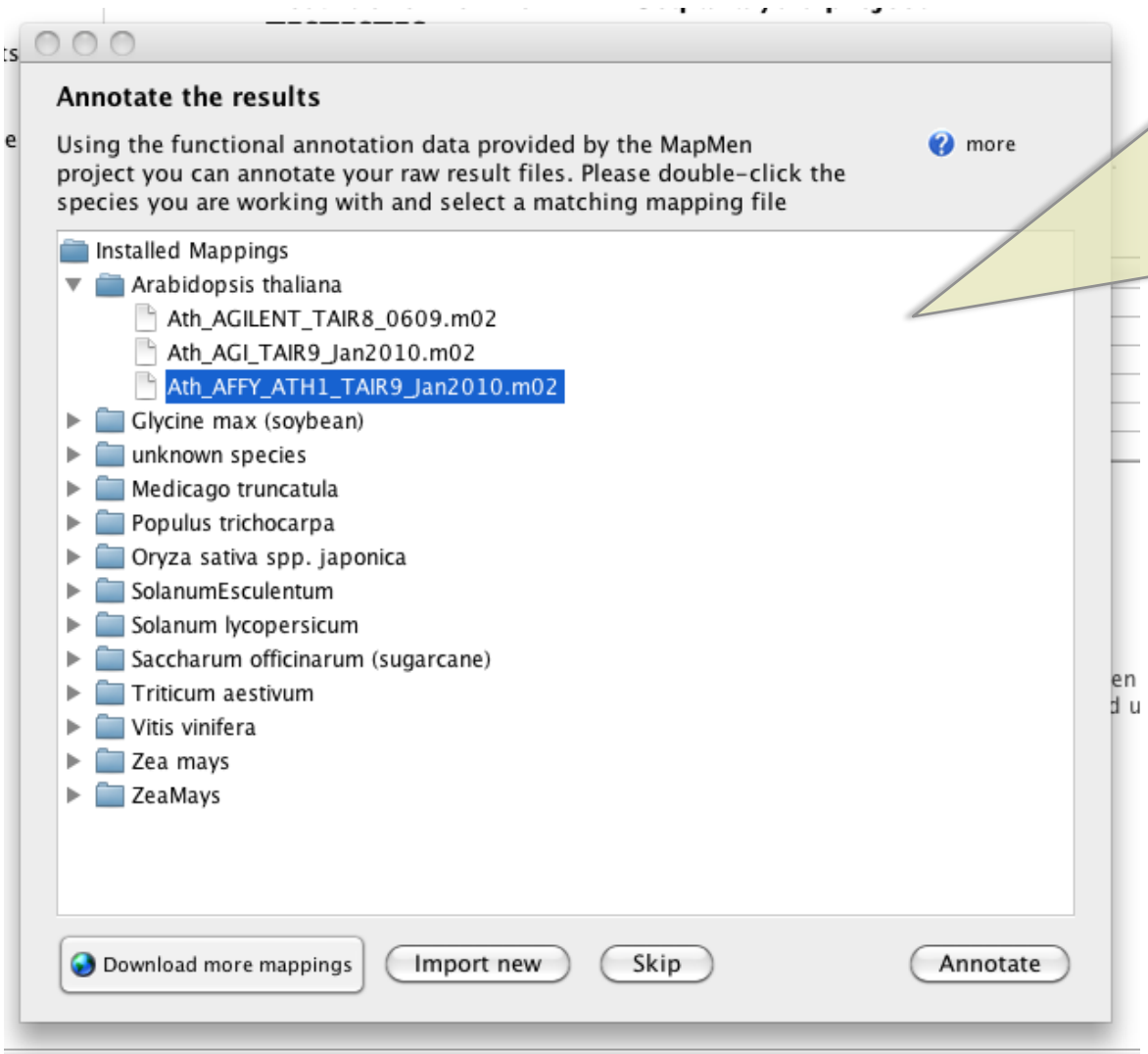


1 After the mapping process is finished, a summary graph of the gene count distribution and mapping details are shown for each sample that was defined in the experiment layout step (4)

Step 6: Analysis setup



Optional step 6.2: Annotate the results with functional MapMan Bins



In case you are working with an organism for which a MapMan mapping is available you can choose to create an additional result table in which all genes are annotated with functional terms (named „Bins“).

Step 7: Analysis finished - browse results

RobiNA – The transcriptomics data preprocessor. Version 1.2.1

Browse your results

You can now browse the results of the analysis.

All results will be written to the project folder when you close Robin.

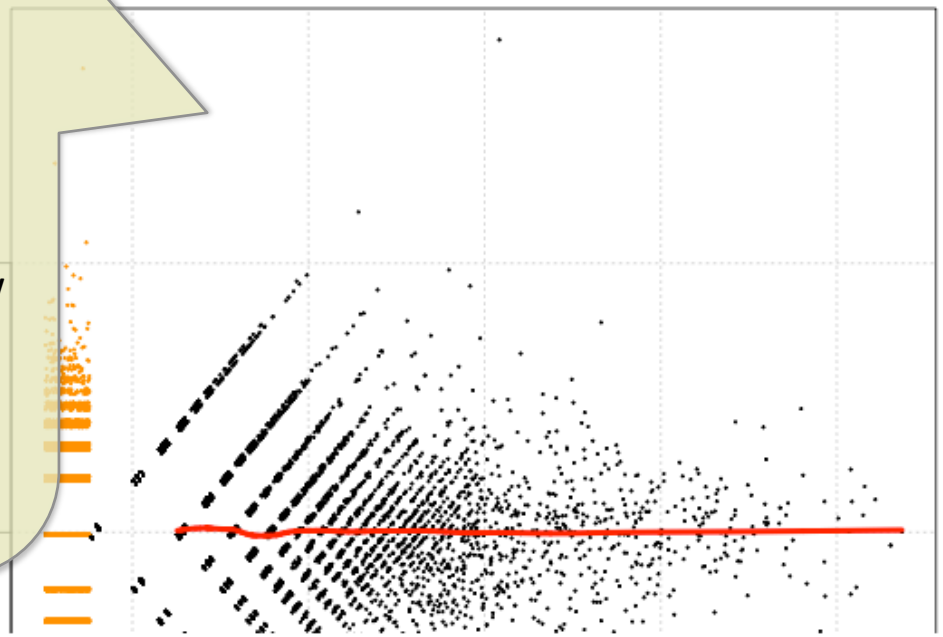
The analysis is done – You can browse the results directly within RobiNA. A PDF file with the same content is automatically saved in the project directory for documentation and review (plus, of course, all result tables and plots, quality check results, trimming details etc.)

MA plots of each comparison

The MA plots show the log2 fold change (M; logFC) plotted versus the average expression strength (A; LogConc) for each of the comparisons that was computed. Usually, these scatter plots show a trumpet-like shape which is attributed to the fact that genes with a lower expression signal strength are more strongly affected by noise than strongly expressed genes.

According to the assumption that under most experimental conditions the bulk of the genes of an organism are not responding differentially, the cloud of points should be centered around a log fold change of 0.
Genes that were called significantly differentially expressed are shown in red.

MA plot of contrast control-stress



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