

Kruskal-Wallis

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The Kruskal-Wallis and Dunn's tests (Non-parametric ANOVA) task is used to identify differentially expressed genes among two or more groups. Note that such rank-based tests are generally advised for use with larger sample sizes.

Running the task

To invoke the Kruskal-Wallis test, select any count-based data nodes, these include:

- Gene counts
- Transcript counts
- Normalized counts

Select *Statistics > Differential analysis* in the context-sensitive menu, then select *Kruskal-Wallis* (Figure 1).

Method to use for differential analysis Choose one method then proceed with model setup. See [documentation](#) for more details.

☐ DESeq2 ⁱ ☐ Hurdle model ⁱ ☐ ANOVA ⁱ ☐ Limma-trend ⁱ ☐ Welch's ANOVA ⁱ ☒ Kruskal-Wallis ⁱ

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Kruskal-Wallis and Dunn's tests (non-parametric ANOVA) can identify differentially expressed genes among two or more groups. It is recommended for larger sample sizes ($n \geq 20$) and does not assume equal variance or normal distribution. Estimated feature expression, ratio, and fold change are reported in median terms

Figure 6. Select any count node to invoke the Non-parametric ANOVA task

Select a specific factor for analysis and click the **Next** button (Figure 2). Note that this task can only take into account one factor at a time.

[Home](#) > [Prostate Cancer RNASeq](#) > [Non-parametric ANOVA](#) > [Model](#)

Select factor for analysis

☐ Cell Line

☒ Treatment

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Figure 7. Select one factor for analysis

For more complicated experimental designs, go back to the original count data that will be used as input and perform **Rank normalization** at the *Features* level (Figure 3). The resulting *Normalized counts* data node can then be analyzed using the **Detect differential expression (ANOVA)** task, which can take into account multiple factors as well as interactions.

[Home](#) > [XYZ-17-002](#) > [Normalize counts](#)

Read count normalization

Transform on ☐ Samples ☒ Features

Normalization methods

Absolute value

Add

Antilog

Divide by




Log

Logit

Lower bound

Multiply by


Quantile normalization

Rank   

Subtract

Normalization order

1. Rank

Drag and drop 

Back

Finish

Figure 8. Normalize your count data by rank to do non-parametric testing on more complicated experimental designs

Define the desired comparisons between groups and click the **Finish** button (Figure 4). Note that comparisons can only be added between single group (i.e. one group per box).

[Home](#) > [Prostate Cancer RNASeq](#) > [Non-parametric ANOVA](#) > [Comparisons](#)

Define comparisons

Factor Treatment ▼

Drug
Vehicle

>
<

Vs

>
<

Add comparison

Reset comparison

Comparisons

Comparison	Delete
Drug vs. Vehicle	✖

Advanced options

Option set -- Default -- ▼ [Configure](#)

Back

Finish

Figure 9. Set-up desired comparisons

Report

The results of the analysis will appear similar to other differential expression analysis results. However, the column to indicate mean expression levels for each group will display the median instead (Figure 5).

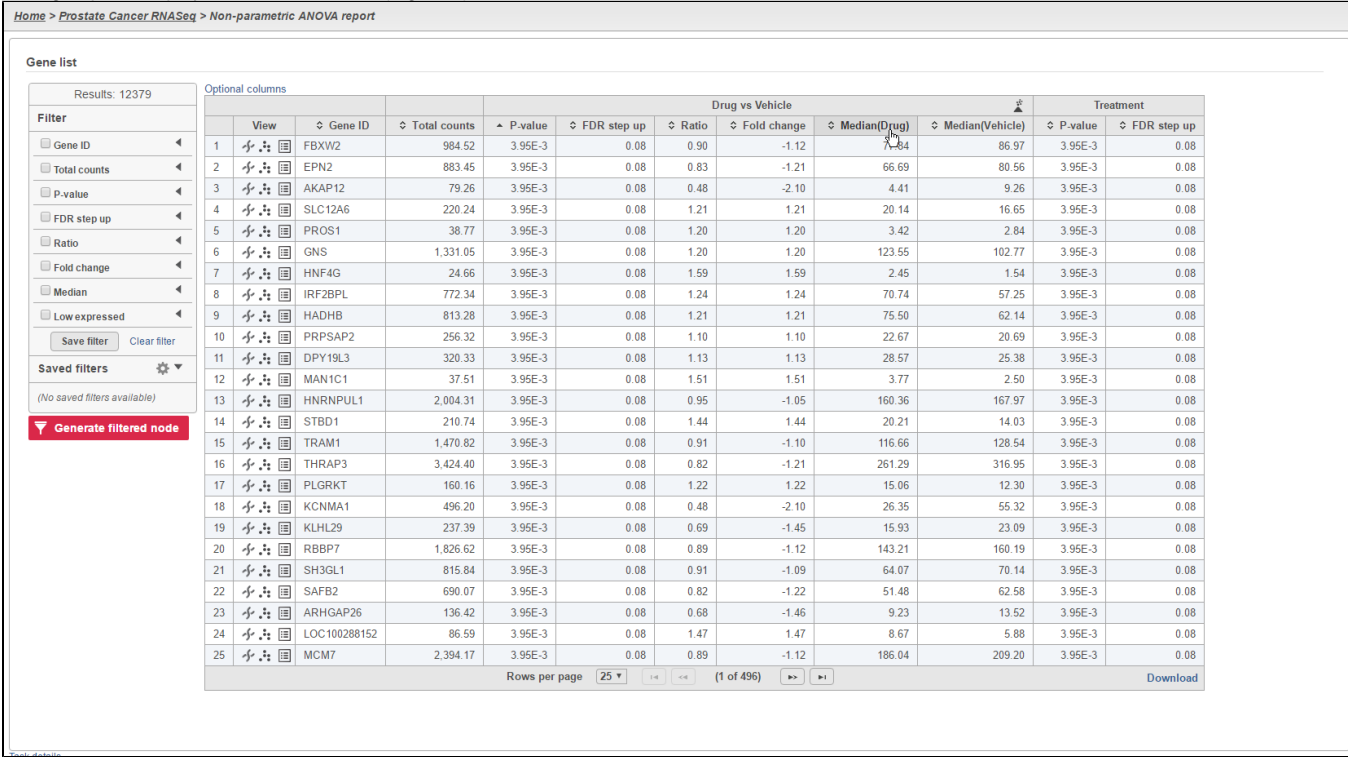


Figure 10. The task's ANOVA report will display the median instead of the LSmean

Additional Assistance

If you need additional assistance, please visit our support page to submit a help ticket or find phone numbers for regional support.

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Your Rating: ★★★★★

Results: ★★★★★ 41 rates

