

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

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Home > Prostate Cancer RNAseq > Non-parametric ANOVA

Gene list

Results: 12379	Optional columns		Drug vs Vehicle										Treatment	
Filter		View	Gene ID	Total counts	P-value	FDR step up	Ratio	Fold change	Median(Drug)	Median(Vehicle)	P-value	FDR step up		
<input type="checkbox"/> Gene ID	1		FBXW2	984.52	3.95E-3	0.08	0.90	-1.12	7.84	86.97	3.95E-3	0.08		
<input type="checkbox"/> Total counts	2		EPN2	883.45	3.95E-3	0.08	0.83	-1.21	66.69	80.56	3.95E-3	0.08		
<input type="checkbox"/> P-value	3		AKAP12	79.26	3.95E-3	0.08	0.48	-2.10	4.41	9.26	3.95E-3	0.08		
<input type="checkbox"/> FDR step up	4		SLC12A6	220.24	3.95E-3	0.08	1.21	1.21	20.14	16.65	3.95E-3	0.08		
<input type="checkbox"/> Ratio	5		PROS1	38.77	3.95E-3	0.08	1.20	1.20	3.42	2.84	3.95E-3	0.08		
<input type="checkbox"/> Fold change	6		GNS	1,331.05	3.95E-3	0.08	1.20	1.20	123.55	102.77	3.95E-3	0.08		
<input type="checkbox"/> Median	7		HNF4G	24.66	3.95E-3	0.08	1.59	1.59	2.45	1.54	3.95E-3	0.08		
<input type="checkbox"/> Low expressed	8		IRF2BPL	772.34	3.95E-3	0.08	1.24	1.24	70.74	57.25	3.95E-3	0.08		
<input type="button" value="Save filter"/> <input type="button" value="Clear filter"/>	9		HADHB	813.28	3.95E-3	0.08	1.21	1.21	75.50	62.14	3.95E-3	0.08		
Saved filters	10		PRPSAP2	256.32	3.95E-3	0.08	1.10	1.10	22.67	20.69	3.95E-3	0.08		
(No saved filters available)	11		DPY19L3	320.33	3.95E-3	0.08	1.13	1.13	28.57	25.38	3.95E-3	0.08		
<input type="button" value="Generate filtered node"/>	12		MAN1C1	37.51	3.95E-3	0.08	1.51	1.51	3.77	2.50	3.95E-3	0.08		
	13		HNRNPUL1	2,004.31	3.95E-3	0.08	0.95	-1.05	160.36	167.97	3.95E-3	0.08		
	14		STBD1	210.74	3.95E-3	0.08	1.44	1.44	20.21	14.03	3.95E-3	0.08		
	15		TRAM1	1,470.82	3.95E-3	0.08	0.91	-1.10	116.66	128.54	3.95E-3	0.08		
	16		THRAP3	3,424.40	3.95E-3	0.08	0.82	-1.21	261.29	316.95	3.95E-3	0.08		
	17		PLGRKT	160.16	3.95E-3	0.08	1.22	1.22	15.06	12.30	3.95E-3	0.08		
	18		KCNMA1	496.20	3.95E-3	0.08	0.48	-2.10	26.35	55.32	3.95E-3	0.08		
	19		KLHL29	237.39	3.95E-3	0.08	0.69	-1.45	15.93	23.09	3.95E-3	0.08		
	20		RBBP7	1,826.62	3.95E-3	0.08	0.89	-1.12	143.21	160.19	3.95E-3	0.08		
	21		SH3GL1	815.84	3.95E-3	0.08	0.91	-1.09	64.07	70.14	3.95E-3	0.08		
	22		SAFB2	690.07	3.95E-3	0.08	0.82	-1.22	51.48	62.58	3.95E-3	0.08		
	23		ARHGAP26	136.42	3.95E-3	0.08	0.68	-1.46	9.23	13.52	3.95E-3	0.08		
	24		LOC100288152	86.59	3.95E-3	0.08	1.47	1.47	8.67	5.88	3.95E-3	0.08		
	25		MCM7	2,394.17	3.95E-3	0.08	0.89	-1.12	186.04	209.20	3.95E-3	0.08		
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