Kruskal-Wallis

- Running the task
- Report

The Kruskal-Wallis and Dunn's tests (Non-parametric ANOVA) task is used to identify deferentially 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).



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 <u>Home</u> > <u>Prostate Cancer RNASeq</u> > Non-parametric ANOVA > Model	or at a time
Select factor for analysis	
Cell Line	
Treatment	
Back Next	

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.

<u>Home</u> > <u>XYZ-17-002</u> > Normalize counts									
Read count normalization									
Transform on O Samples Features									
Normalization methods		Normalization order							
Absolute value		1. Rank							
Add									
Antilog									
Divide by									
Log									
Logit									
Lower bound	Drag								
Multiply by	and drop								
Quantile normalization	\rightarrow								
Rank 🚺 🕂 🕂									
Subtract									
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).

<u>Home</u> > <u>Prostate Cancer RN</u>	ASeq > Non-parametric ANOVA > Comparisons
Define comparisons	
Factor Treatment ▼	
Drug Vehicle	
Add comparison Reset	comparison
Comparisons	
Comparison Delete	
Drug vs. Vehicle 🗙	
Advanced options	
Option set Default	Configure
	▼ Configure
Back	

Figure 9. Set-up desired comparisons

Report

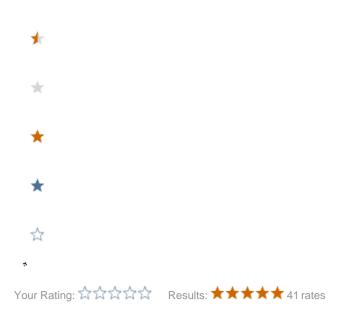
The results of the analysis will appear similar to other differential expression analysis results. However, the column to indicate mean expression levels for each group will display the median instead (Figure 5).

ne list												
Results: 12379	Optio	nal columns										
ilter	1			Drug vs Vehicle								
	-	View	Gene ID	Total counts	 P-value 	♦ FDR step up	Ratio		≎ Median(Drug)	Median(Vehicle)		♦ FDR step up
Gene ID 4	1	チ .:: 🗉		984.52	3.95E-3	0.08	0.90	-1.12	A-84	86.97	3.95E-3	0.08
Total counts	2	チ.:: 🗉		883.45	3.95E-3	0.08	0.83	-1.21	66.69	80.56	3.95E-3	0.08
P-value	3	チュ: 🗉		79.26	3.95E-3	0.08	0.48	-2.10	4.41	9.26	3.95E-3	0.08
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
Ratio	5	チ .: 🗉		38.77	3.95E-3	0.08	1.20	1.20	3.42	2.84	3.95E-3	0.08
	6	チ .: 🗉	GNS	1,331.05	3.95E-3	0.08	1.20	1.20	123.55	102.77	3.95E-3	0.08
- Told change	7	チ.:: 🗉	HNF4G	24.66	3.95E-3	0.08	1.59	1.59	2.45	1.54	3.95E-3	0.08
Median 4	8	チ.:: 🗉	IRF2BPL	772.34	3.95E-3	0.08	1.24	1.24	70.74	57.25	3.95E-3	0.08
Low expressed	9	チ .: 🗉	HADHB	813.28	3.95E-3	0.08	1.21	1.21	75.50	62.14	3.95E-3	0.08
Save filter Clear filter	10	チ .: 🗉	PRPSAP2	256.32	3.95E-3	0.08	1.10	1.10	22.67	20.69	3.95E-3	0.08
aved filters 🔅 🔻	11	チ := 🗉	DPY19L3	320.33	3.95E-3	0.08	1.13	1.13	28.57	25.38	3.95E-3	0.08
saved inters byr	12	チュ: 🗉	MAN1C1	37.51	3.95E-3	0.08	1.51	1.51	3.77	2.50	3.95E-3	0.08
No saved filters available)	13	チ.!: 🗉	HNRNPUL1	2,004.31	3.95E-3	0.08	0.95	-1.05	160.36	167.97	3.95E-3	0.08
Generate filtered node	14	チ.:: 🗉	STBD1	210.74	3.95E-3	0.08	1.44	1.44	20.21	14.03	3.95E-3	0.08
	15	チュ: 🗉	TRAM1	1,470.82	3.95E-3	0.08	0.91	-1.10	116.66	128.54	3.95E-3	0.08
	16	チュ: 🗉	THRAP3	3,424.40	3.95E-3	0.08	0.82	-1.21	261.29	316.95	3.95E-3	0.08
	17	チュ: 🗉	PLGRKT	160.16	3.95E-3	0.08	1.22	1.22	15.06	12.30	3.95E-3	0.08
	18	チュ: 🗉	KCNMA1	496.20	3.95E-3	0.08	0.48	-2.10	26.35	55.32	3.95E-3	0.08
	19	チ.:: 目	KLHL29	237.39	3.95E-3	0.08	0.69	-1.45	15.93	23.09	3.95E-3	0.08
	20	チ.:: 目	RBBP7	1,826.62	3.95E-3	0.08	0.89	-1.12	143.21	160.19	3.95E-3	0.08
	21	チ.:: 目	SH3GL1	815.84	3.95E-3	0.08	0.91	-1.09	64.07	70.14	3.95E-3	0.08
	22	チ.: =	SAFB2	690.07	3.95E-3	0.08	0.82	-1.22	51.48	62.58	3.95E-3	0.08
	23	チュ 目	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	f. :=		2,394.17	3.95E-3	0.08	0.89	-1.12	186.04	209.20	3.95E-3	0.08
		,			Rows per	page 25 V	4	1 of 496) 🕟	E.			Download

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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