

New Project / Load Input Data dialog

Load Input Data for Current Project

Project Information

Name:

Single series time course

Annotation Data

Species:

Mus musculus

☐ Use application's annotation features file - requires download first time used

Select annotation features file

☒ Specify annotation features file's location

/Users/hdelrisco/Documents/tappas_files/Downloads/pacbioMixCurated_timeCourse_funcAnno

...

Experiment Design and Data

Experiment Type:

Single Series Time-Course

Design File:

/Users/hdelrisco/Documents/tappas_files/Downloads/Single4Times.tsv

...

Matrix Data File:

/Users/hdelrisco/Documents/tappas_files/Downloads/expressionMatrix.txt

...

Note: First group in design file must be the control and expression matrix MUST contain raw counts - see Help

☒ Expression Values Filter (recommended):

Low count values cutoff:

1

CPM

Coefficient of variation cutoff:

100

%

Transcripts Filter:

Do not filter transcripts

Use button on right or type in full file path and name

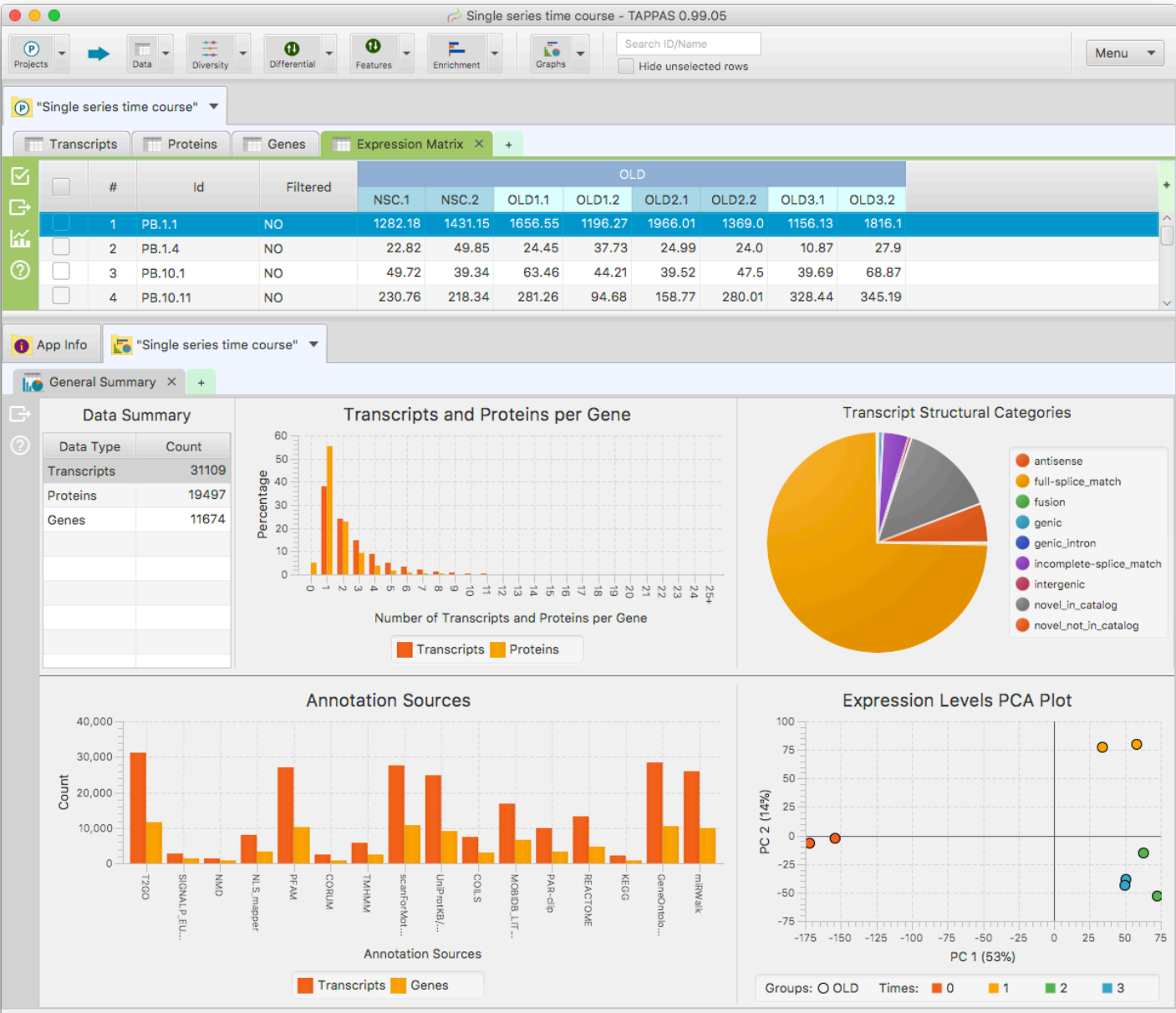
...

Help

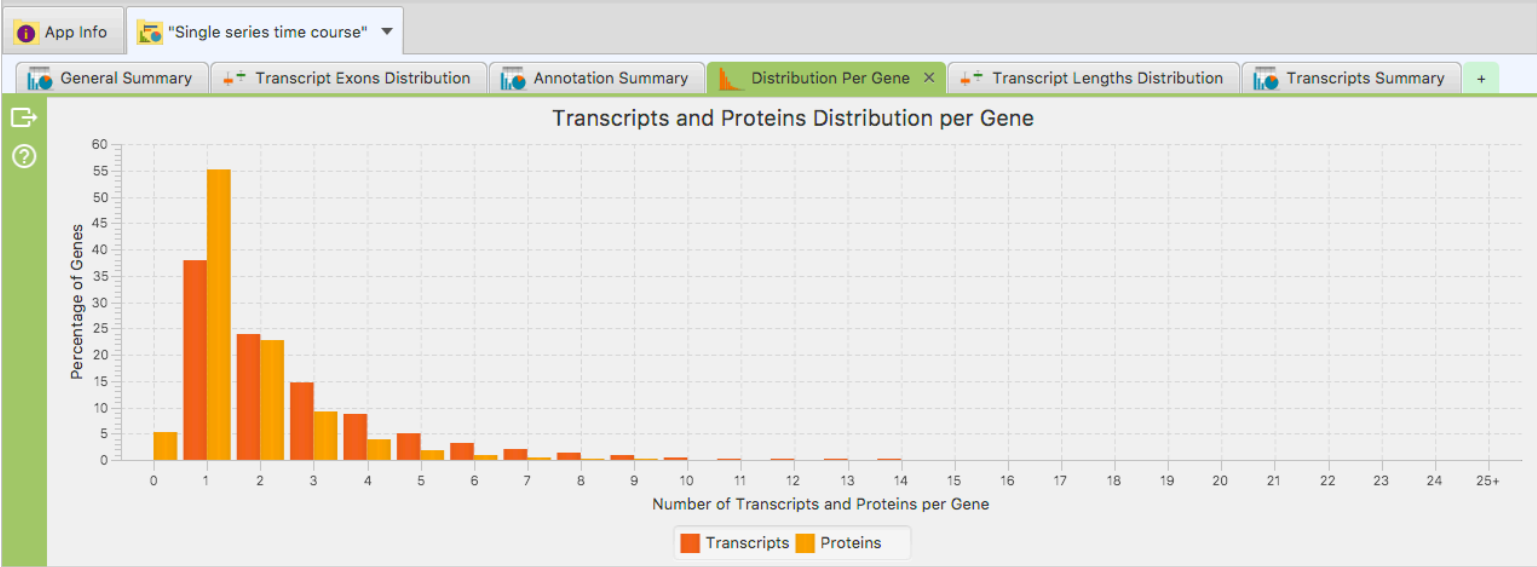
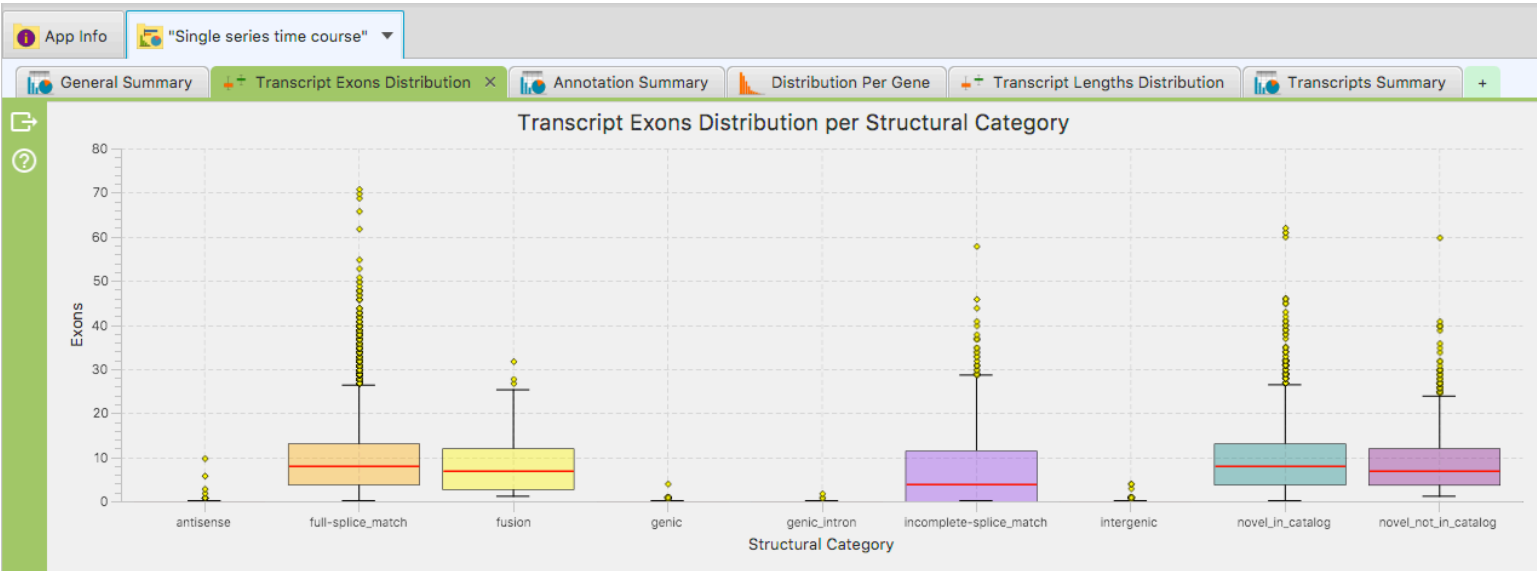
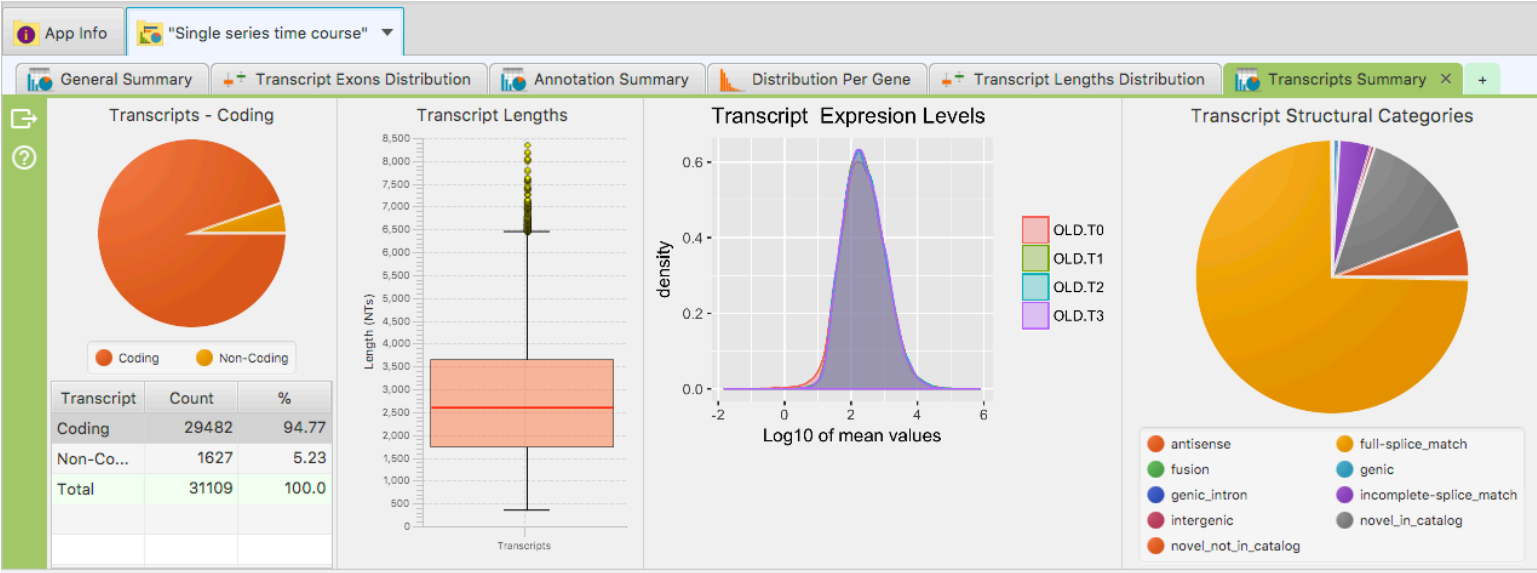
Cancel

OK

Main Application Window - Data and General Summary sub tabs



Additional Data Visualization sub tabs



Application Info Tab and sub tabs

App Info

"Single series time course"

OverviewLogTechnical Information

Application Tips

Here are some tips to help you get the most out of the application:

Use context-sensitive menus - don't be afraid to right-click on any display control and see what pops up

"New Annotation"

Genes

	#	Gene	Name/Description	OPC
	6044	Tfb2m	transcription factor B2, mitochondrial	
	6045	Tfdp1	transcription factor Dp 1	
	6046	Tfdp2		
	6047	Tfe3		
	6048	Tfg		
	6049	Tfip11	turtein interacting protein 11	

Show gene data visualization

Show gene online references in web browser

Export table data...

Take advantage of mouseover functionality - hover over buttons and visual display areas to see tooltips with additional information

5' UTR

PB.1000.1 (-) NM_001110211 full-splice_match

DE

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Data Drill Down

Export Data and Images

Ad Hoc Query

Differential Expression Analysis

Differential Splicing Analysis

Annotation Features Analysis

Enrichment Analysis

Gene Data Visualization Tab and sub tabs

App Info

"Single series time course"

"Tardbp"

TranscriptsProteinsGenomicGene OntologyExpression ChartsAnnotation Features DiversityAnnotation File Data

PB.9289.4 (-) NM_145556.4 full-splice_match 2,886nt

PB.9289.5 (-) NR_027864.1 full-splice_match 1,232nt

PB.9289.6 (-) novel_not_in_catalog 1,328nt

PB.9289.7 (-) XR_390742.3 full-splice_match 2,162nt

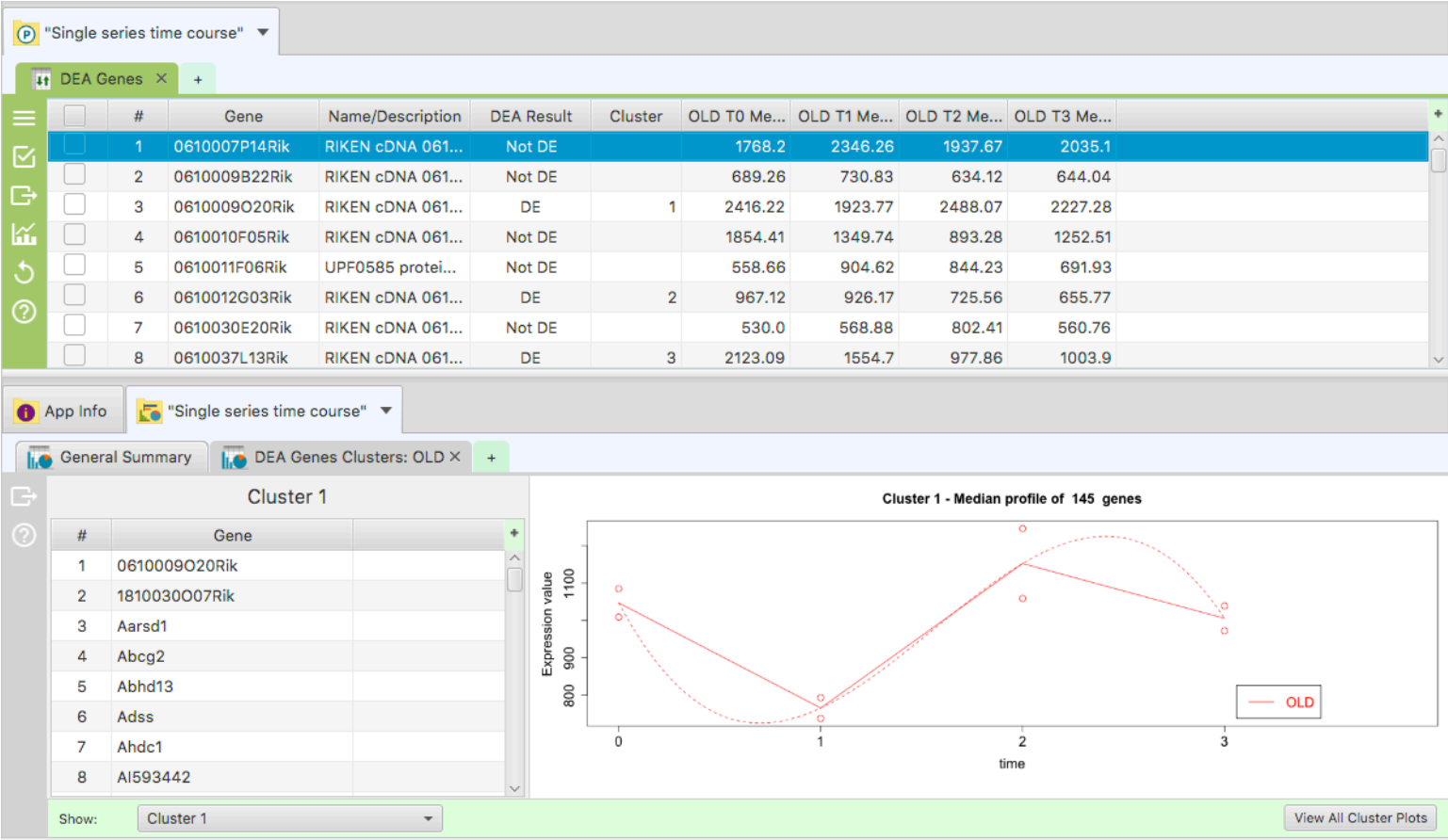
PAR-clip : RNA_binding_129Brain

scanForMotifs : 3UTRmotif

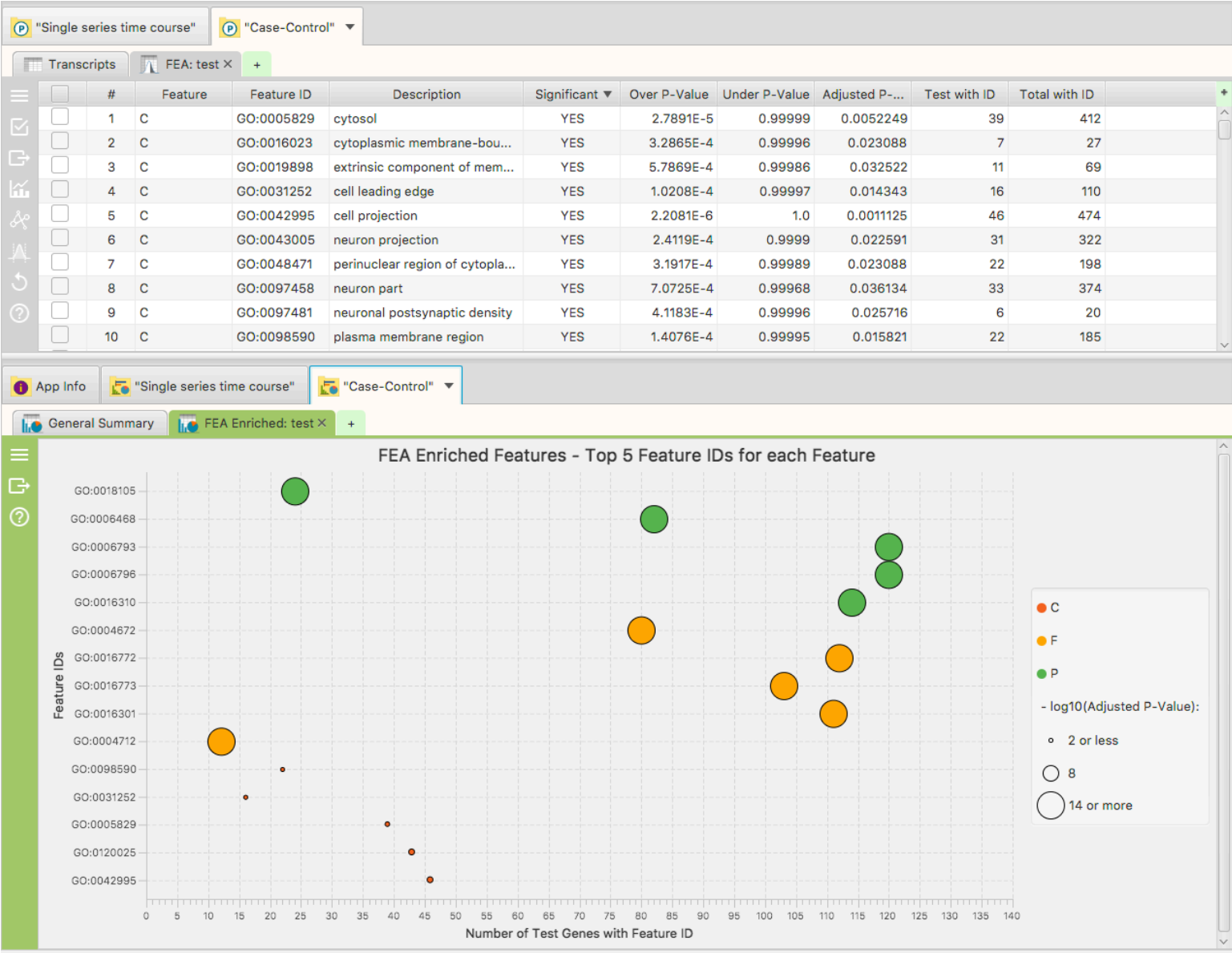
miRWalk : miRNA

Annotation (symbol within) located in intron region

Differential Expression Analysis Data and Cluster Visualization



Functional Enrichment Analysis Data and Enriched Features Visualization



Gene Set Enrichment Analysis Data and Summary

