

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

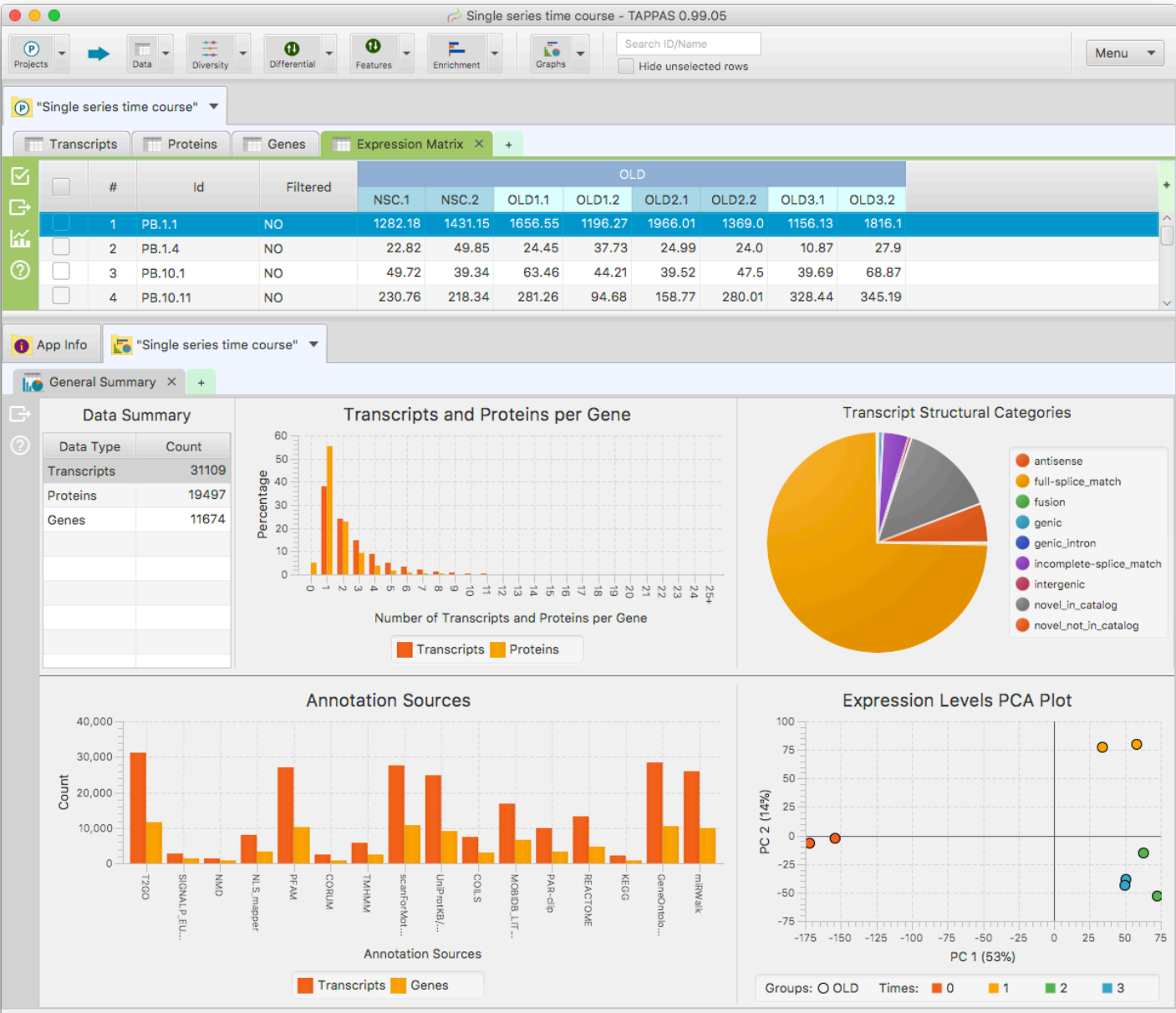
...

Help

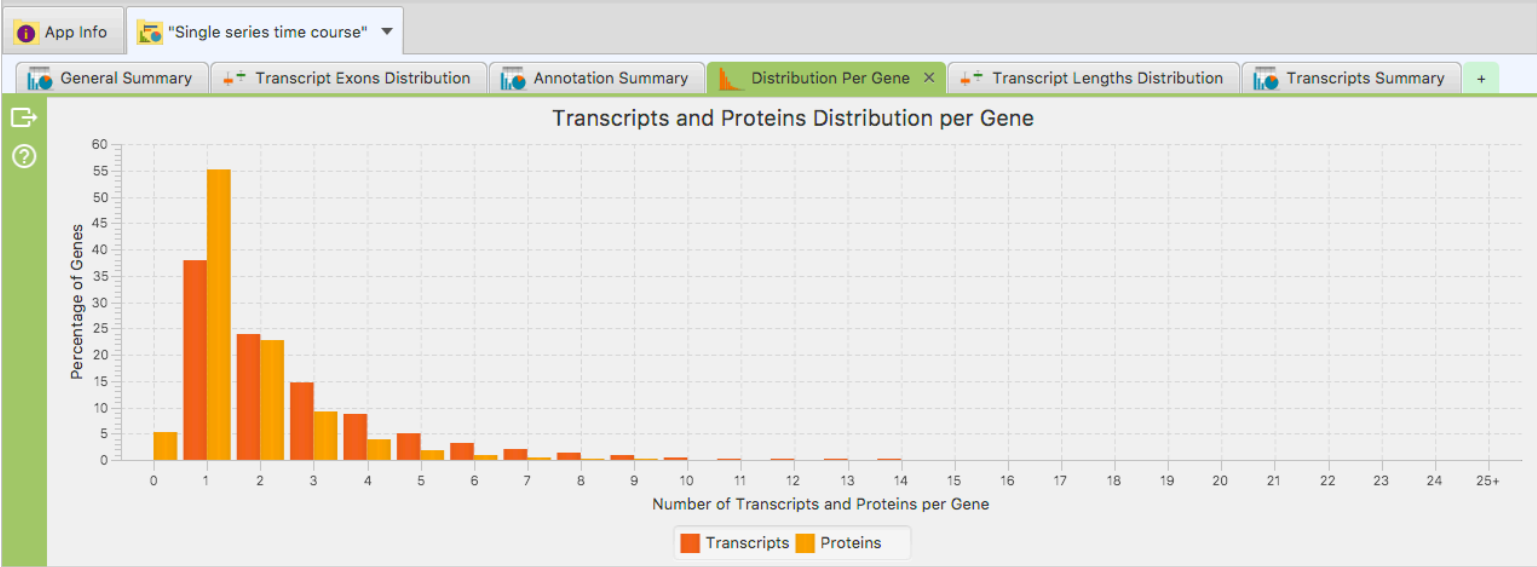
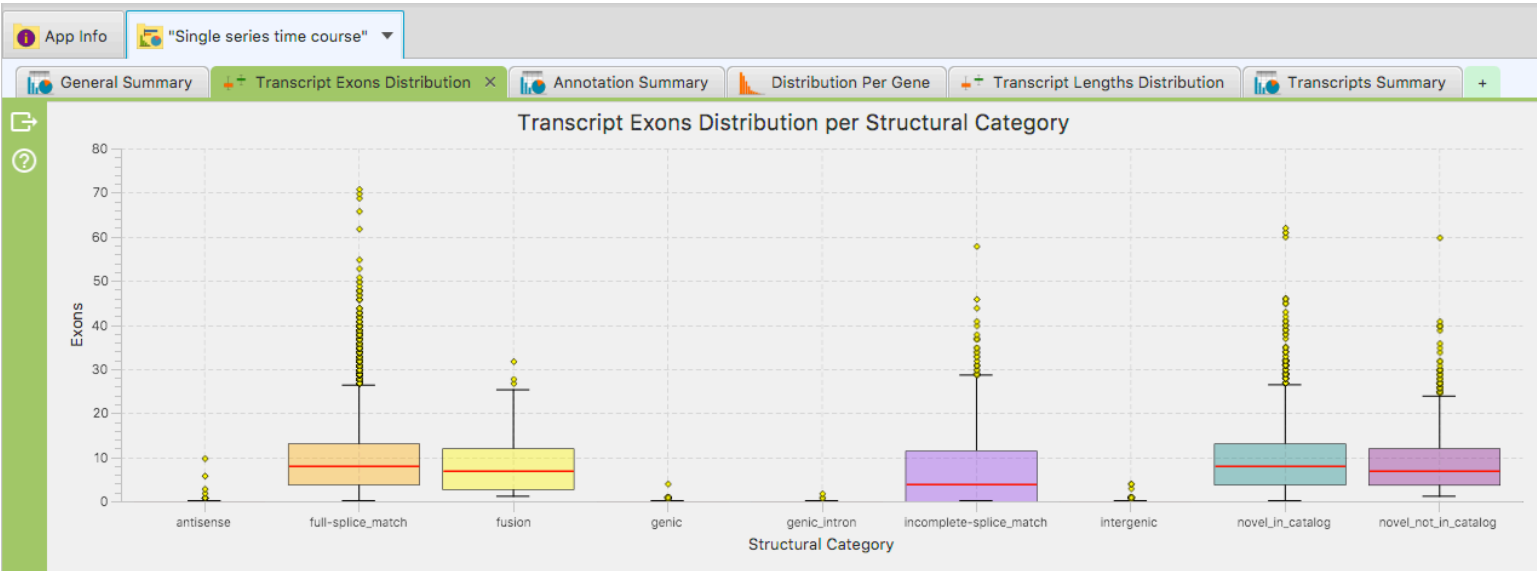
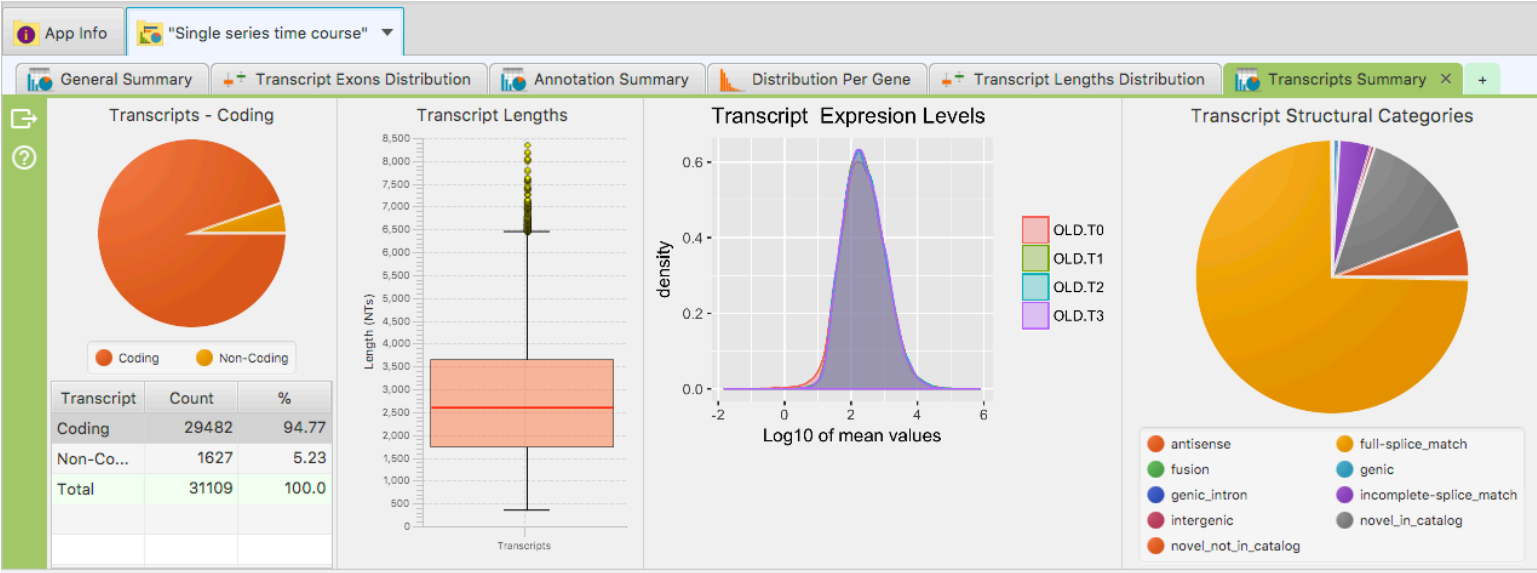
Cancel

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	

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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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

PB.9289.5 (-) NR_027864.1 full-splice_match

PB.9289.6 (-) novel_not_in_catalog

PB.9289.7 (-) XR_390742.3 full-splice_match

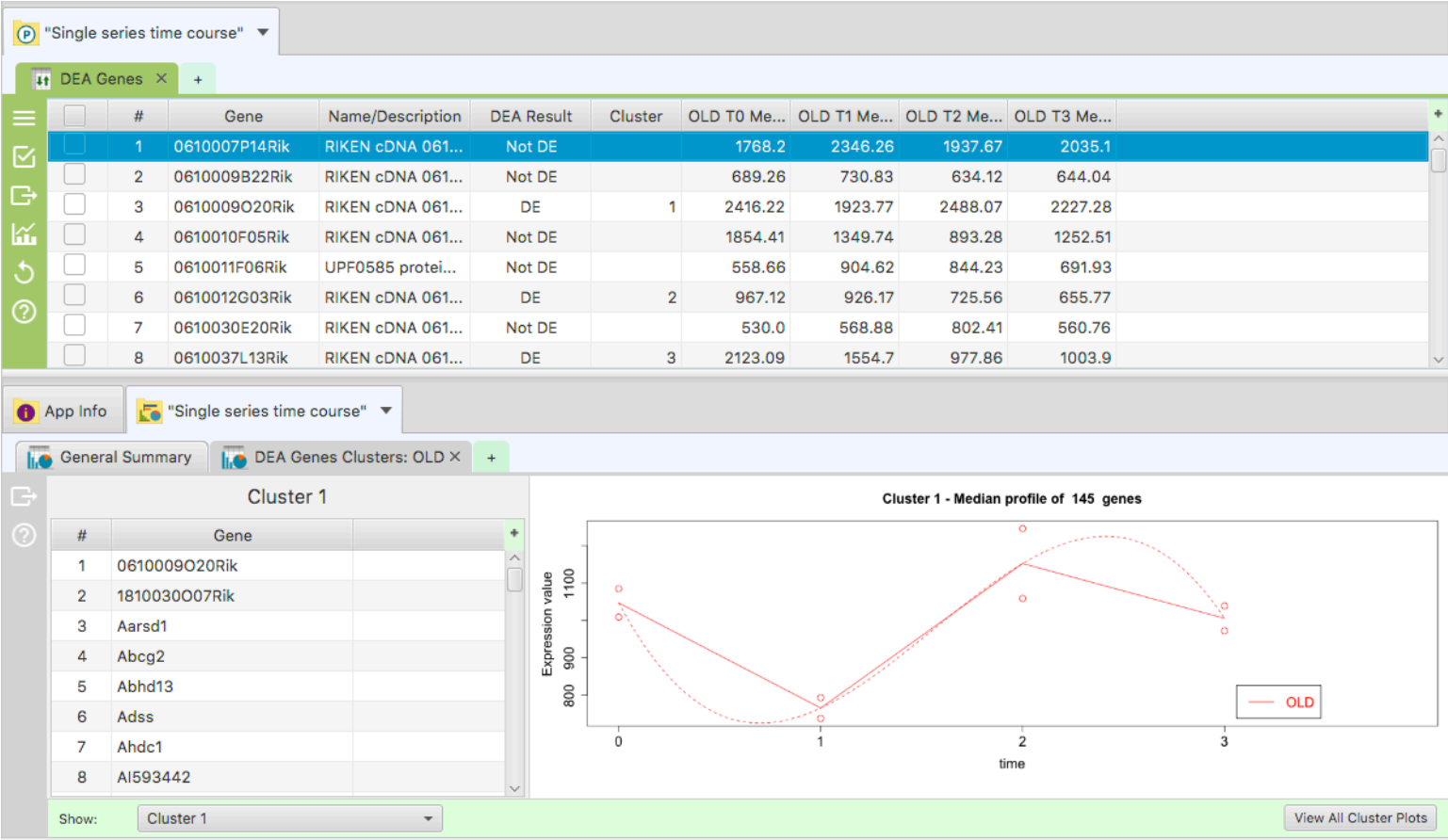
PAR-clip : RNA_binding_129Brain

miRWalk : miRNA

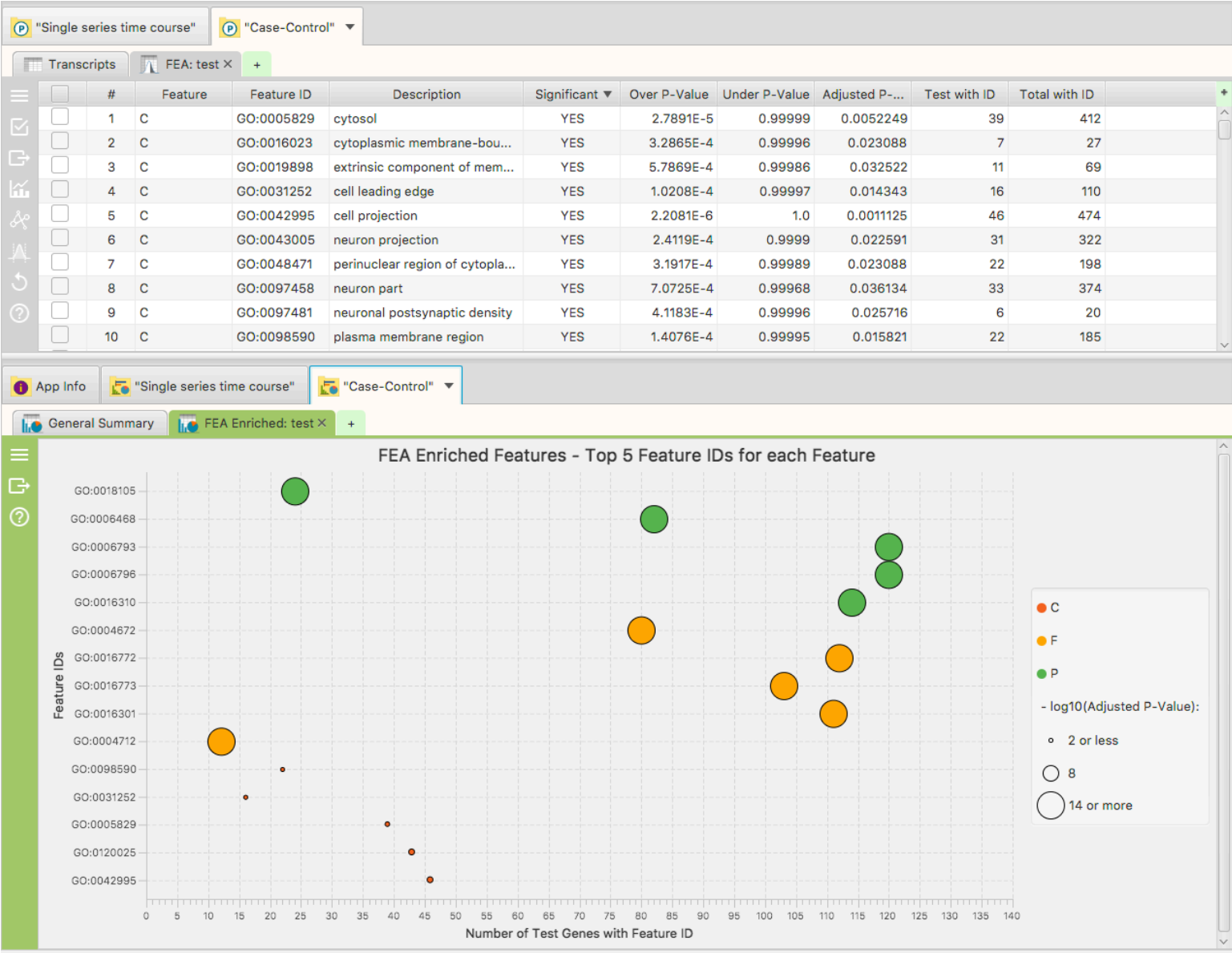
Annotation (symbol within) located in intron region

scanForMotifs : 3UTRmotif

Differential Expression Analysis Data and Cluster Visualization



Functional Enrichment Analysis Data and Enriched Features Visualization



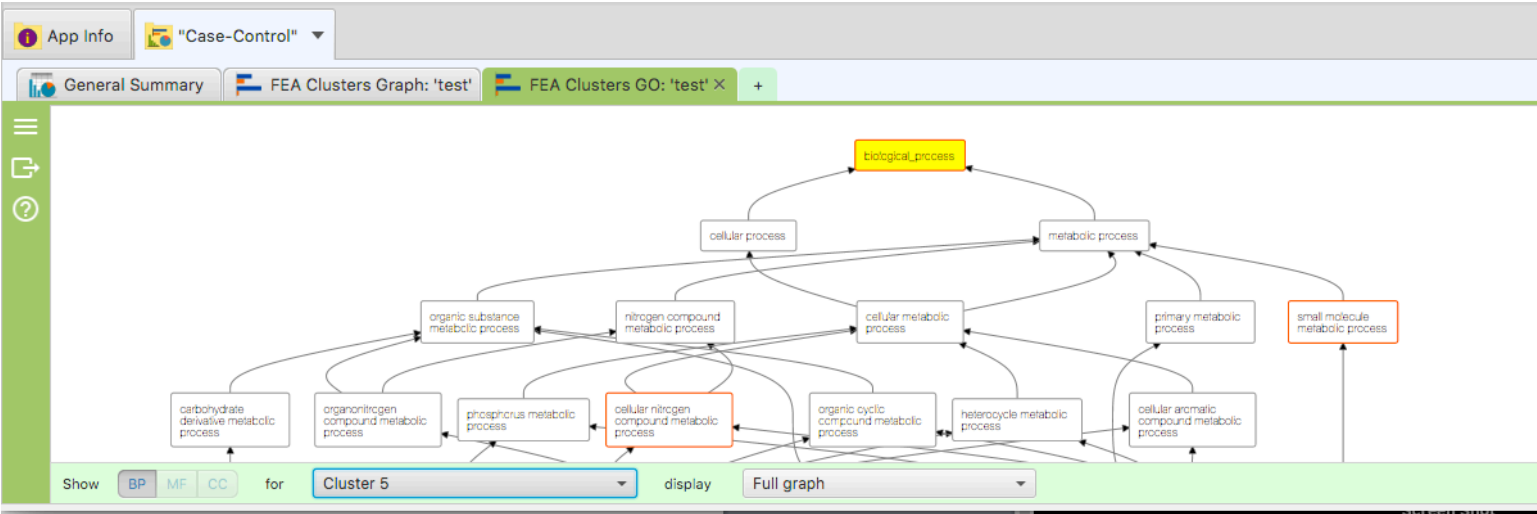
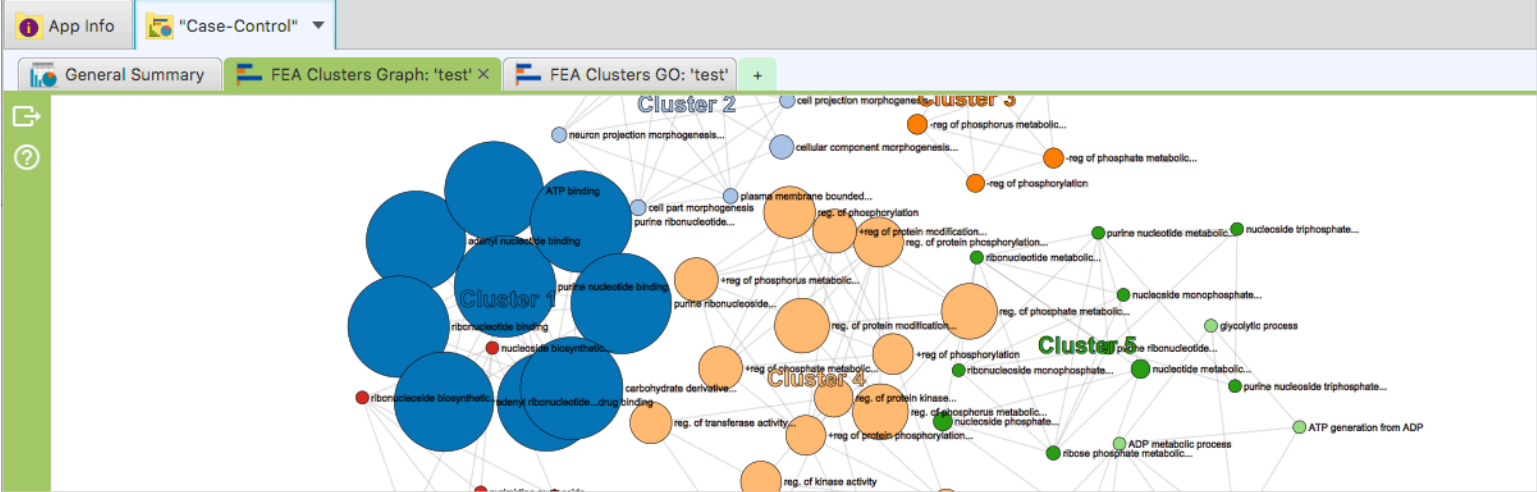
FEA Clusters and GO terms

"Case-Control"

TranscriptsFEA: testFEA Clusters: 'test' ×

#	Cl...	Name	No...	%
4	4	Cluster 4	16	3.67
5	5	Cluster 5	11	2.52
6	6	Cluster 6	9	2.06
7	7	Cluster 7	17	3.9
8	8	Cluster 8	11	2.52
9	9	Cluster 9	11	2.52

#	Cluster ID	Node (Featu...	Name	Feature	Adjusted P-Va...	Test Genes
1	1	GO:0005524	ATP binding	F	1.2257E-51	99
2	1	GO:0008144	drug binding	F	3.7719E-46	99
3	1	GO:0017076	purine nucleotide binding	F	4.6822E-43	102
4	1	GO:0030554	adenyl nucleotide binding	F	5.1892E-51	100
5	1	GO:0032553	ribonucleotide binding	F	1.623E-43	102
6	1	GO:0032555	purine ribonucleotide binding	F	1.1102E-43	102



Gene Set Enrichment Analysis Data and Summary

