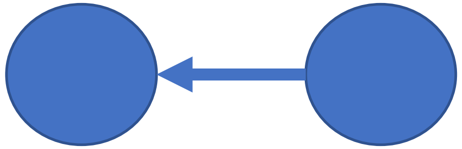
Cytoscape for Visualisation

Cytoscape

- Analysing and visualising networks
    - Protein-Protein interactions
    - Gene coexpression
    - Functional Enrichments

- https://github.com/cytoscape/cytoscape-tutorials/wiki

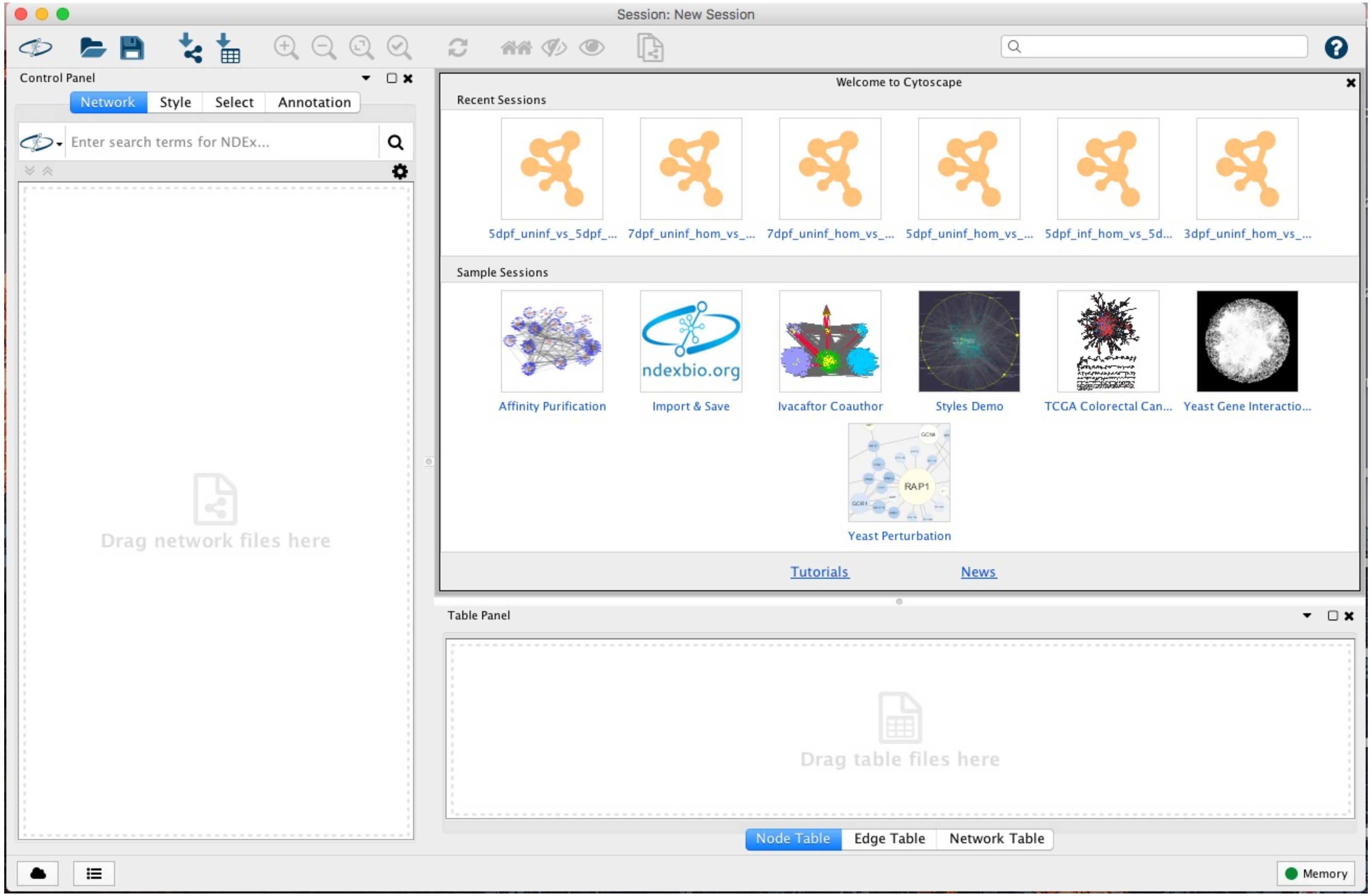
Graphs/Networks

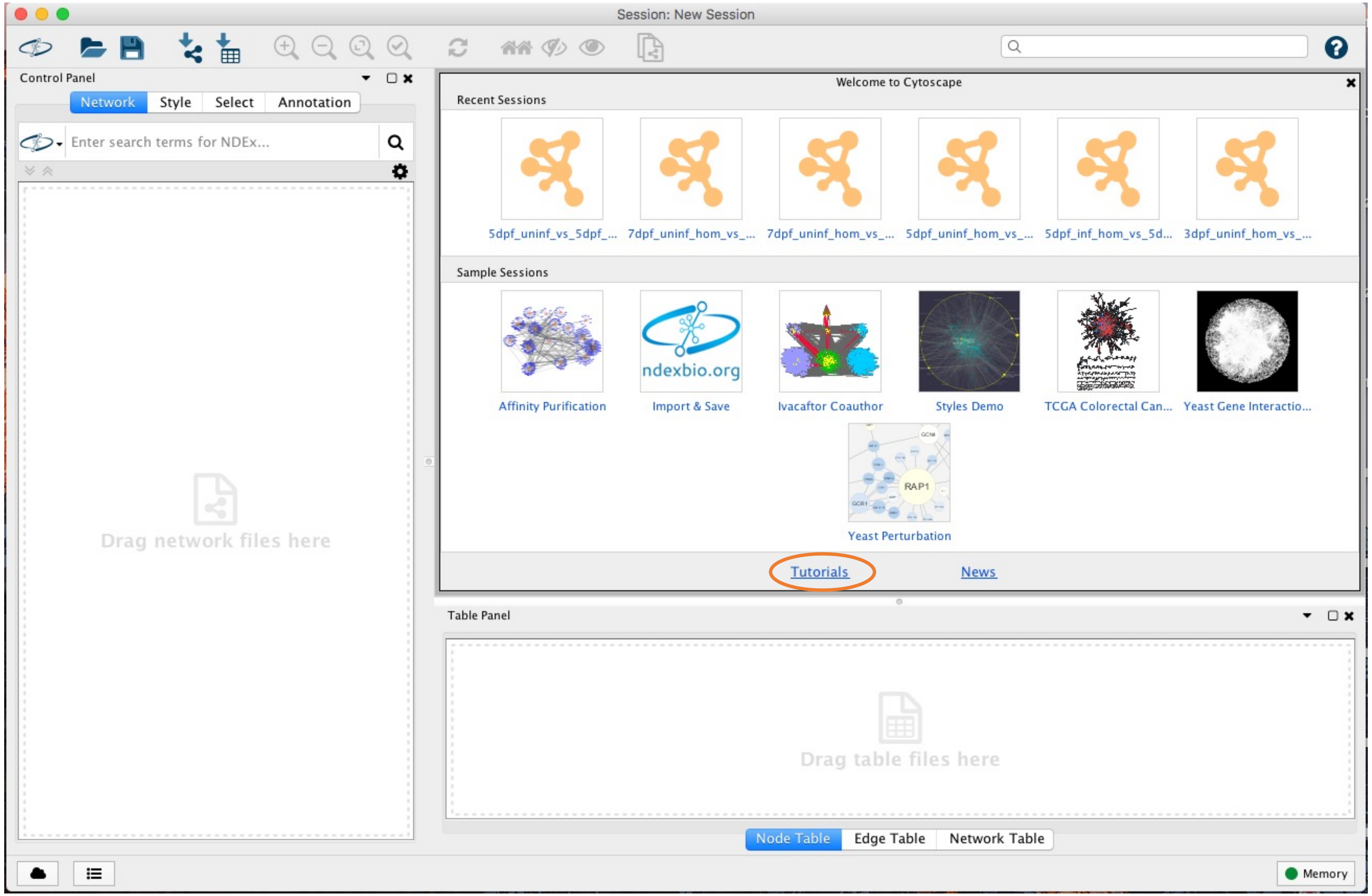


- Nodes connected by edges
- Nodes represent entities (genes, proteins, GO terms, nucelotides)
- Edges represent connections between the nodes (Pearson correlation, protein-protein interactions, the next base in a sequence)
- Can be directed or not

Cytoscape

- Load networks in various graph formats (sif, graphML, GML, BioPax)


Session: New Session
Control Panel
Network
Style
Select
Annotation
Enter search terms for NDEx...
Drag network files here
Welcome to Cytoscape
Recent Sessions
5dpf_uninf_vs_5dpf_...
7dpf_uninf_hom_vs_...
7dpf_uninf_hom_vs_...
5dpf_uninf_hom_vs_...
5dpf_inf_hom_vs_5d...
3dpf_uninf_hom_vs_...
Sample Sessions
Affinity Purification
ndexbio.org
Import & Save
Ivacaftor Coauthor
Styles Demo
TCGA Colorectal Can...
Yeast Gene Interactio...
RAP1
Yeast Perturbation
Tutorials
News
Table Panel
Drag table files here
Node Table
Edge Table
Network Table
Memory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5dpf_uninf_hom_vs_...
5dpf_inf_hom_vs_5d...
3dpf_uninf_hom_vs_...
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Drag table files here
Node Table
Edge Table
Network Table
Memory

Loading Networks

- Simplest format is Simple interaction file (.sif)
- columns are:
  - Source Node
  - relationship type
  - Target Node

ENSDARG00000099966	geneExprCor	ENSDARG00000095904
ENSDARG00000099966	geneExprCor	ENSDARG00000086425
ENSDARG00000099966	geneExprCor	ENSDARG00000104899
ENSDARG00000070656	geneExprCor	ENSDARG00000038066
ENSDARG00000070656	geneExprCor	ENSDARG00000019339
ENSDARG00000070656	geneExprCor	ENSDARG00000095743

Loading Networks

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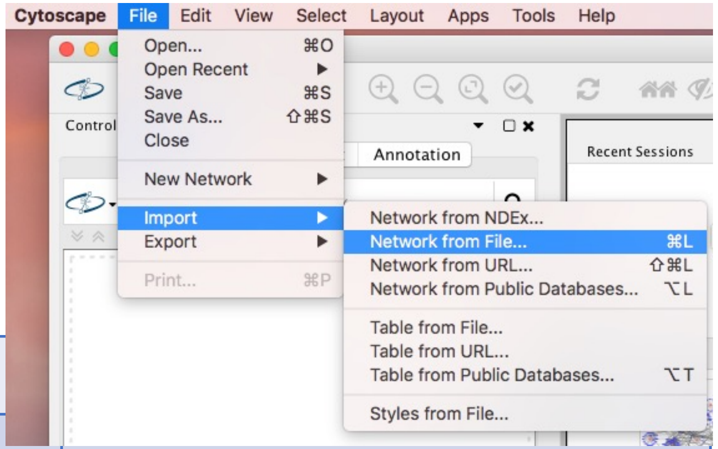
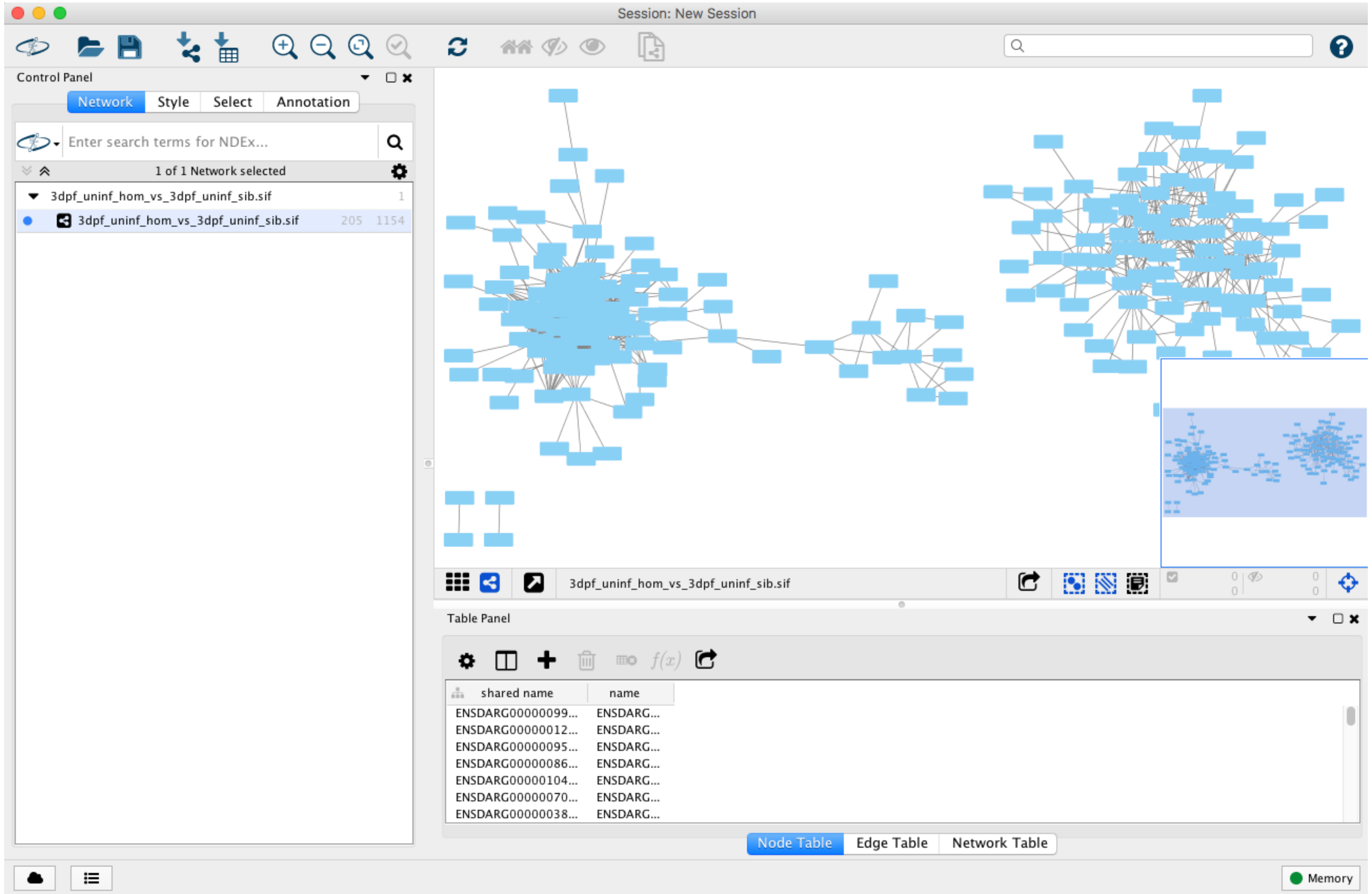


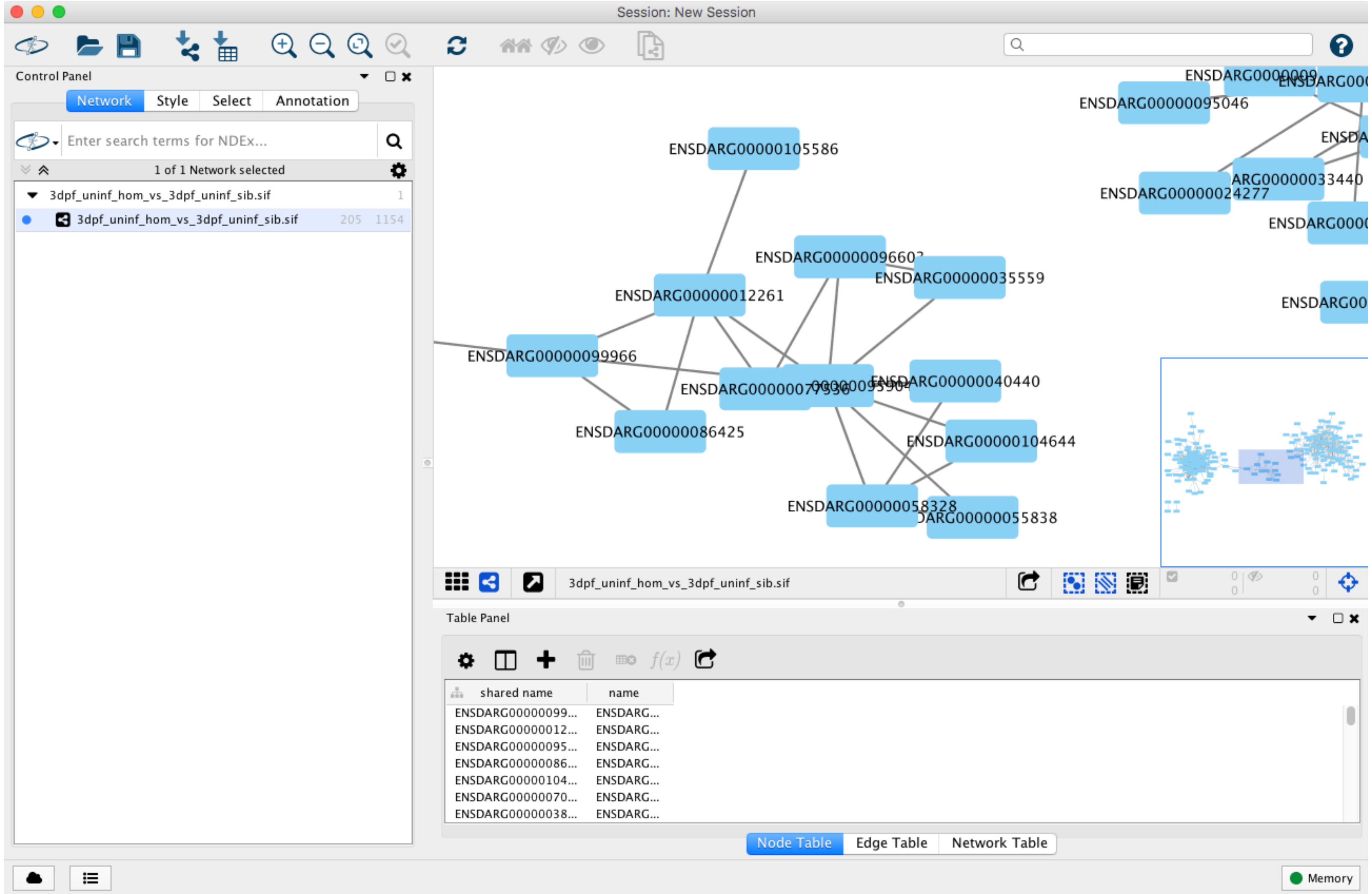
ENSDARG00000099966	geneExprCor	
ENSDARG00000099966	geneExprCor	ENSDARG00000086425
ENSDARG00000099966	geneExprCor	ENSDARG00000104899
ENSDARG00000070656	geneExprCor	ENSDARG00000038066
ENSDARG00000070656	geneExprCor	ENSDARG00000019339
ENSDARG00000070656	geneExprCor	ENSDARG00000095743

Loading Networks



shared name	name
ENSDARG00000099...	ENSDARG...
ENSDARG00000012...	ENSDARG...
ENSDARG00000095...	ENSDARG...
ENSDARG00000086...	ENSDARG...
ENSDARG00000104...	ENSDARG...
ENSDARG00000070...	ENSDARG...
ENSDARG00000038...	ENSDARG...

Loading Networks



Session: New Session

1 of 1 Network selected

3dpf_uninf_hom_vs_3dpf_uninf_sib.sif		1
3dpf_uninf_hom_vs_3dpf_uninf_sib.sif	205	1154

3dpf_uninf_hom_vs_3dpf_uninf_sib.sif

shared name	name
ENSDARG00000099...	ENSDARG...
ENSDARG00000012...	ENSDARG...
ENSDARG00000095...	ENSDARG...
ENSDARG00000086...	ENSDARG...
ENSDARG00000104...	ENSDARG...
ENSDARG00000070...	ENSDARG...
ENSDARG00000038...	ENSDARG...

Add extra node/edge information

- Extra node information can be imported from a file containing a column that matches the node names

Gene ID	GeneName	log2fc	adjp
ENSDARG00000099966	polr2a	0.773509255	1.32E-49
ENSDARG00000070656	si:ch211-69g19.2	-0.583759051	2.25E-15
ENSDARG00000038066	kpna2	-0.520683514	5.79E-14
ENSDARG00000037551	pm20d1.1	2.334699018	6.79E-11

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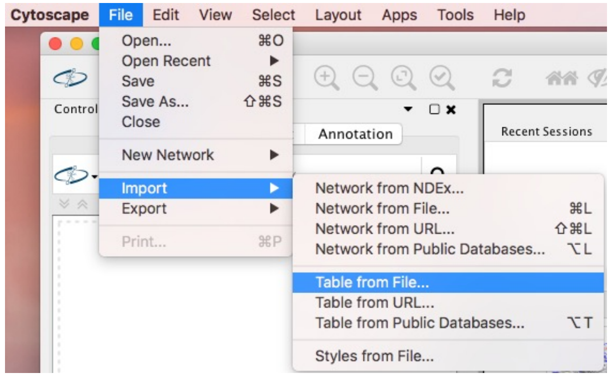
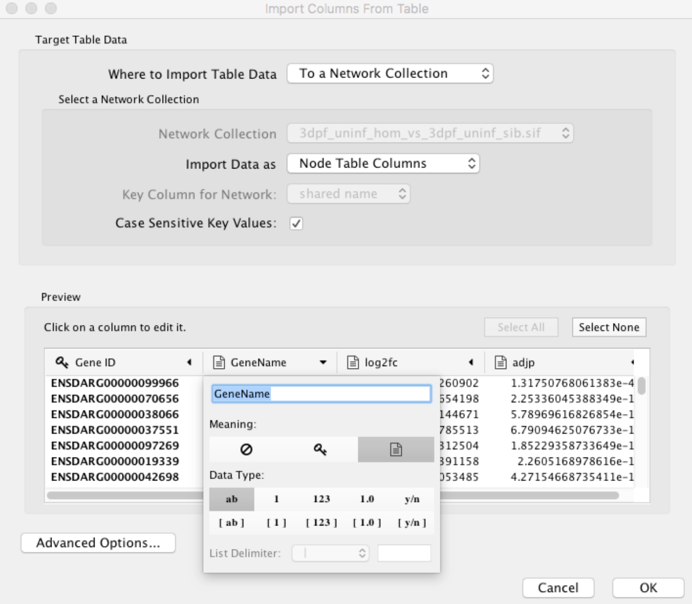
Gene ID	GeneName	log2fc	adjp
ENSDARG00000099966	polr2a	0.773509255	1.32E-49
ENSDARG00000070656	si:ch211-69g19.2		2.25E-15
ENSDARG00000038066	kpna2		5.79E-14
ENSDARG00000037551	pm20d1.1		6.79E-11




Import Columns From Table

Target Table Data

Where to Import Table Data: To a Network Collection

Select a Network Collection

Network Collection: 3dpf_uninf_hom_vs_3dpf_uninf_sib.sif

Import Data as: Node Table Columns

Key Column for Network: shared name

Case Sensitive Key Values: ☑

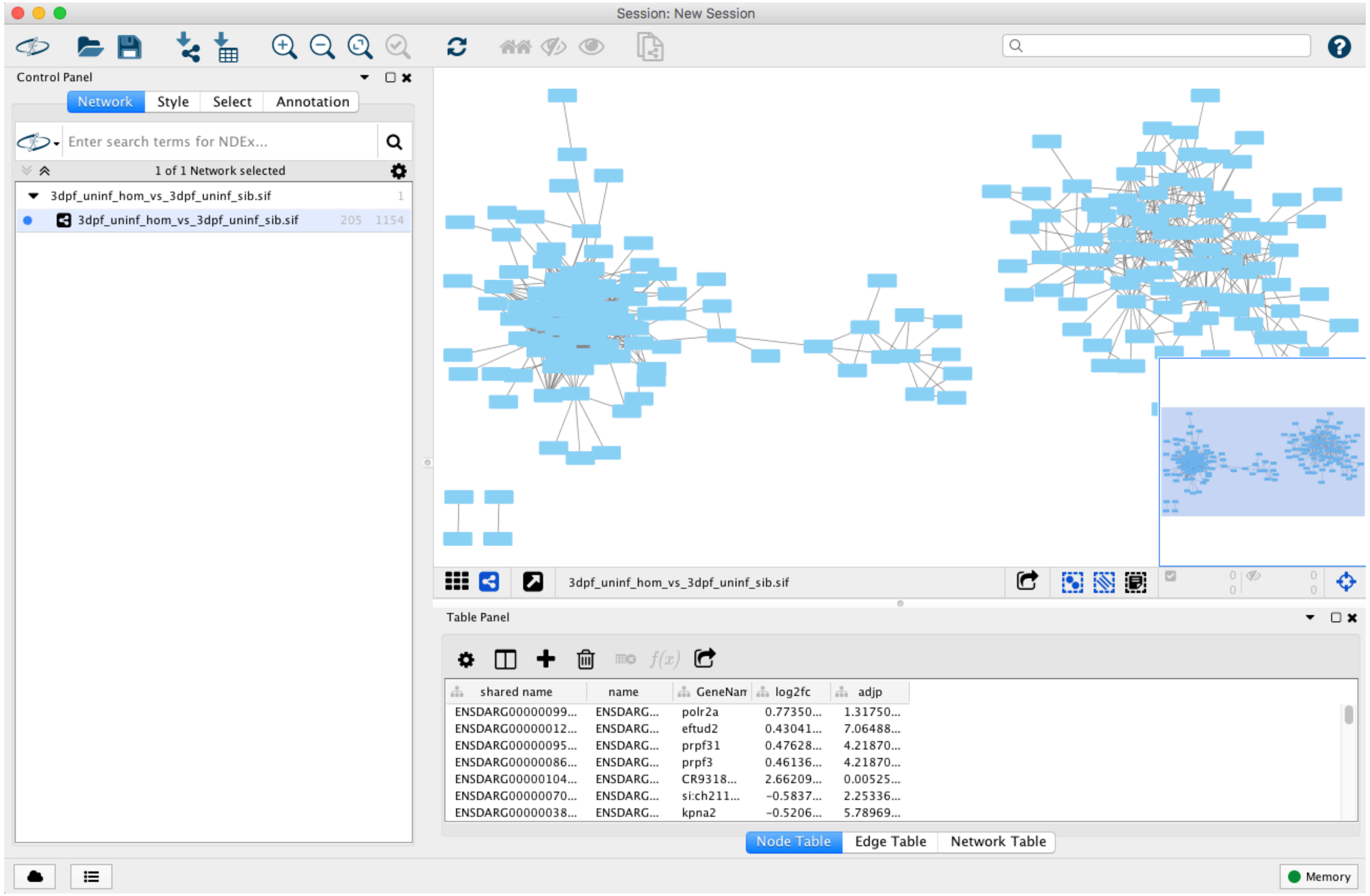
Preview

Click on a column to edit it.

Gene ID	GeneName	log2fc	adjp
ENSDARG00000099966		260902	1.31750768061383e-4
ENSDARG00000070656		554198	2.25336045388349e-1
ENSDARG00000038066		144671	5.78969616826854e-1
ENSDARG00000037551		785513	6.79094625076733e-1
ENSDARG00000097269		312504	1.85229358733649e-1
ENSDARG00000019339		391158	2.2605168978616e-1
ENSDARG00000042698		053485	4.27154668735411e-1

GeneName

Add extra node/edge information



shared name	name	GeneNan	log2fc	adjp
ENSDARG00000099...	ENSDARG...	polr2a	0.77350...	1.31750...
ENSDARG00000012...	ENSDARG...	eftud2	0.43041...	7.06488...
ENSDARG00000095...	ENSDARG...	prpf31	0.47628...	4.21870...
ENSDARG00000086...	ENSDARG...	prpf3	0.46136...	4.21870...
ENSDARG00000104...	ENSDARG...	CR9318...	2.66209...	0.00525...
ENSDARG00000070...	ENSDARG...	si:ch211...	-0.5837...	2.25336...
ENSDARG00000038...	ENSDARG...	kpna2	-0.5206...	5.78969...

Add extra node/edge information

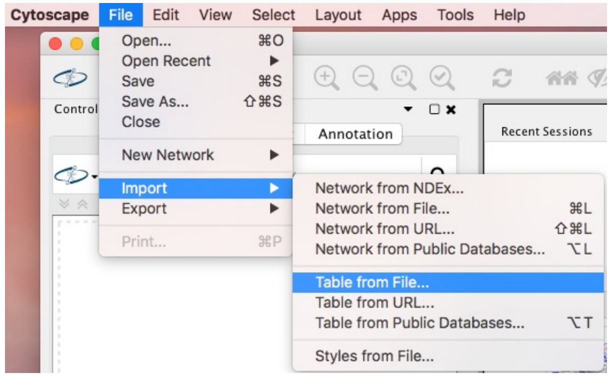
- Extra edge information can be imported in the same way

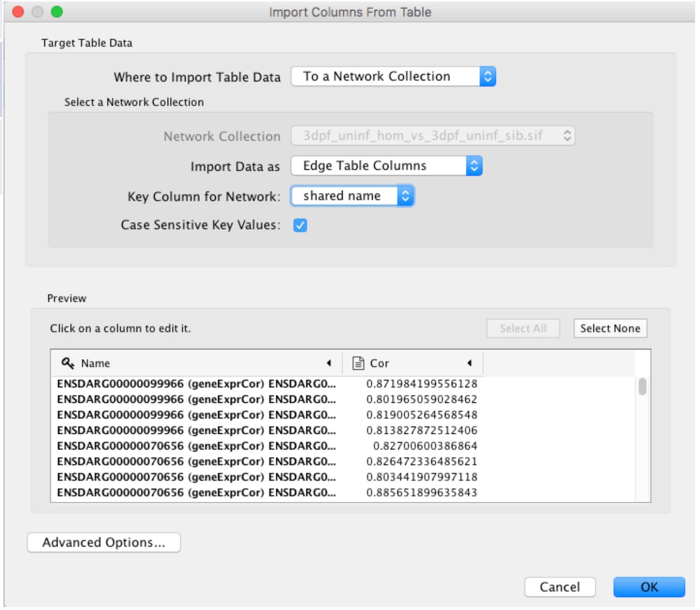
Name	Cor
ENSDARG00000099966 (geneExprCor) ENSDARG00000012261	0.8719842
ENSDARG00000099966 (geneExprCor) ENSDARG00000095904	0.801965059
ENSDARG00000099966 (geneExprCor) ENSDARG00000086425	0.819005265
ENSDARG00000099966 (geneExprCor) ENSDARG00000104899	0.813827873

Add extra node/edge information

- Extra edge information can be imported in the same way

Name	Cor
ENSDARG00000099966 (geneExprCor) ENSDARG00000012261	0.8719842
ENSDARG00000099966 (geneExprCor) ENSDARG00000095904	0.801965059
ENSDARG00000099966 (geneExprCor) ENSDARG00000086425	0.819005265
ENSDARG00000099966 (geneExprCor) ENSDARG00000104899	0.813827873





Target Table Data

Where to Import Table Data: To a Network Collection

Select a Network Collection

Network Collection: 3dpf_uninf_hom_vs_3dpf_uninf_sib.sif

Import Data as: Edge Table Columns

Key Column for Network: shared name

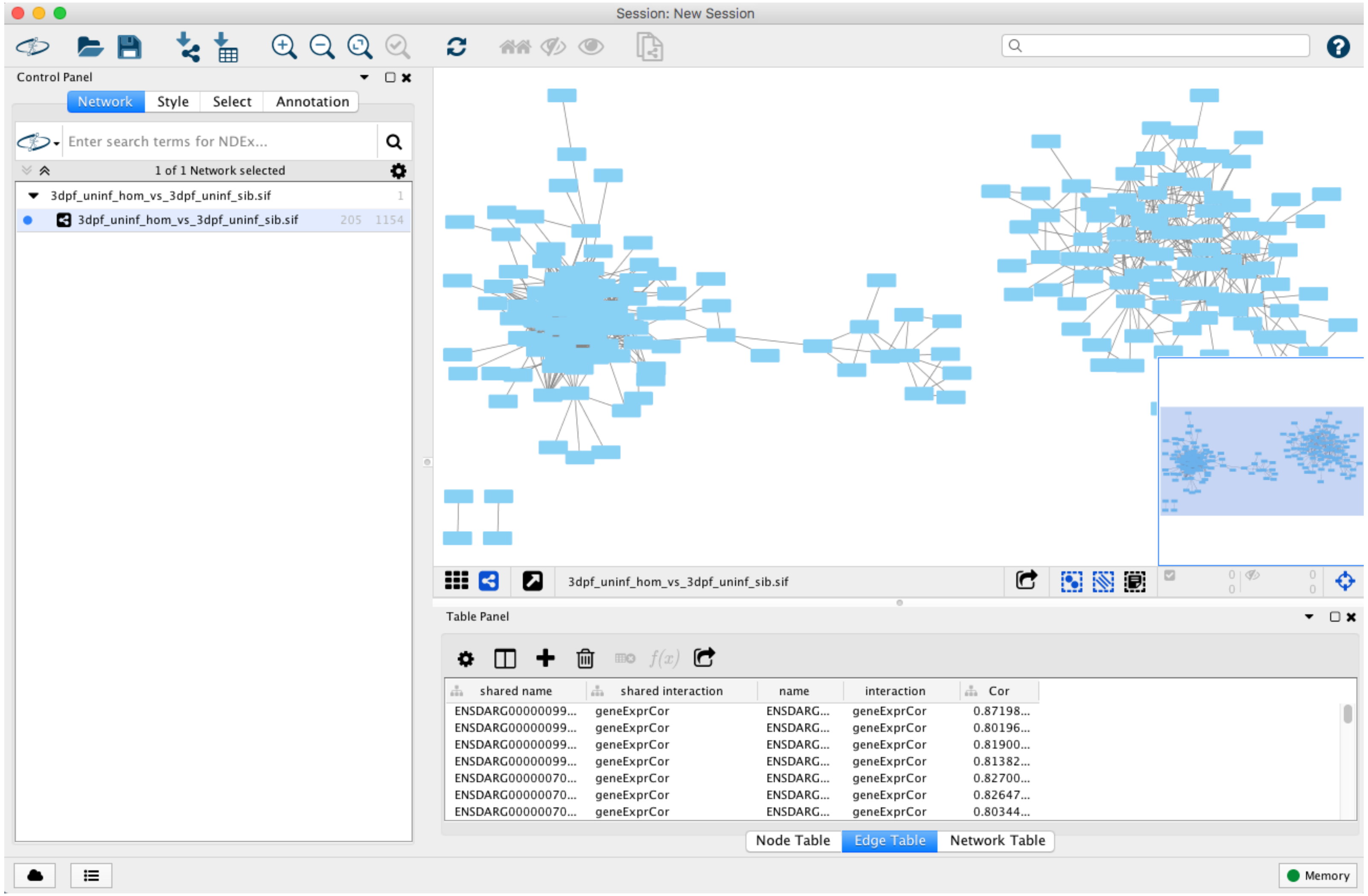
Case Sensitive Key Values: ☑

Preview

Click on a column to edit it.

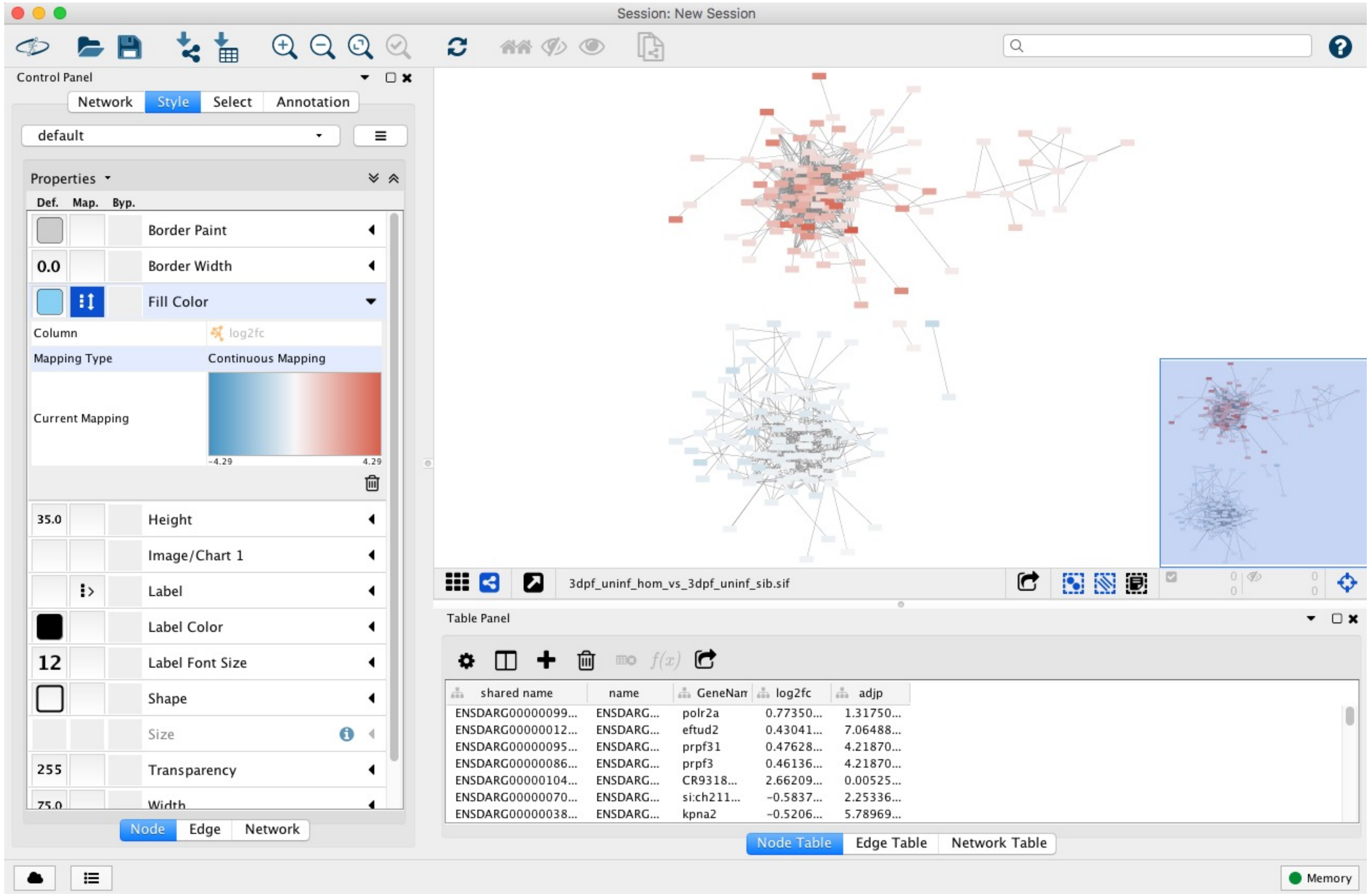
Name	Cor
ENSDARG00000099966 (geneExprCor) ENSDARG0...	0.871984199556128
ENSDARG00000099966 (geneExprCor) ENSDARG0...	0.801965059028462
ENSDARG00000099966 (geneExprCor) ENSDARG0...	0.819005264568548
ENSDARG00000099966 (geneExprCor) ENSDARG0...	0.813827872512406
ENSDARG00000070656 (geneExprCor) ENSDARG0...	0.82700600386864
ENSDARG00000070656 (geneExprCor) ENSDARG0...	0.826472336485621
ENSDARG00000070656 (geneExprCor) ENSDARG0...	0.803441907997118
ENSDARG00000070656 (geneExprCor) ENSDARG0...	0.885651899635843

Add extra node/edge information



shared name	shared interaction	name	interaction	Cor
ENSDARG00000099...	geneExprCor	ENSDARG...	geneExprCor	0.87198...
ENSDARG00000099...	geneExprCor	ENSDARG...	geneExprCor	0.80196...
ENSDARG00000099...	geneExprCor	ENSDARG...	geneExprCor	0.81900...
ENSDARG00000099...	geneExprCor	ENSDARG...	geneExprCor	0.81382...
ENSDARG00000070...	geneExprCor	ENSDARG...	geneExprCor	0.82700...
ENSDARG00000070...	geneExprCor	ENSDARG...	geneExprCor	0.82647...
ENSDARG00000070...	geneExprCor	ENSDARG...	geneExprCor	0.80344...

Add styles to nodes

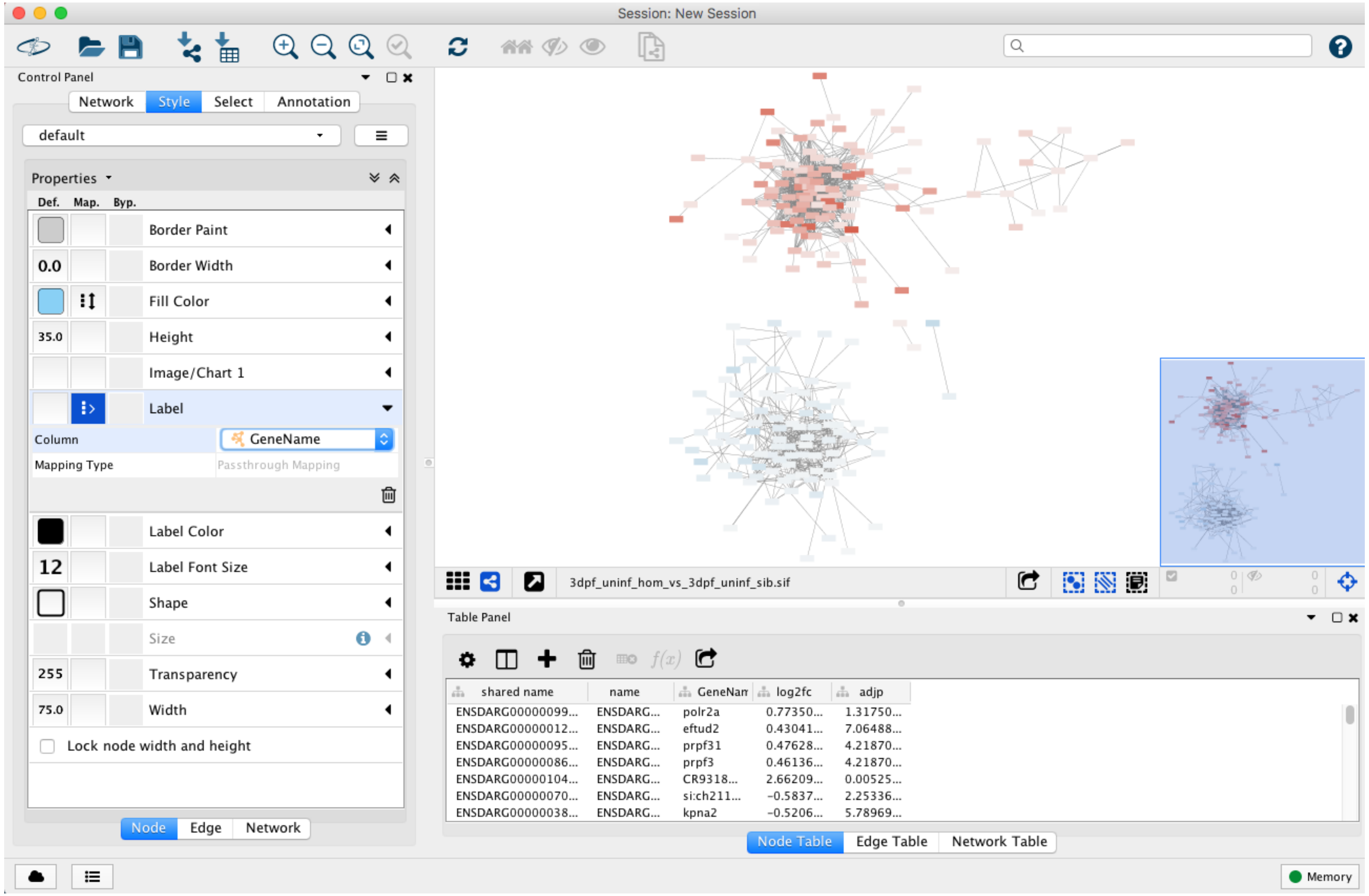


Border Paint
0.0 Border Width
Fill Color
Column log2fc
Mapping Type Continuous Mapping
Current Mapping -4.29 4.29
35.0 Height
Image/Chart 1
Label
Label Color
12 Label Font Size
Shape
Size
255 Transparency
75.0 Width

3dpf_uninf_hom_vs_3dpf_uninf_sib.sif

shared name	name	GeneNam	log2fc	adjp
ENSDARG00000099...	ENSDARG...	polr2a	0.77350...	1.31750...
ENSDARG00000012...	ENSDARG...	eftud2	0.43041...	7.06488...
ENSDARG00000095...	ENSDARG...	prpf31	0.47628...	4.21870...
ENSDARG00000086...	ENSDARG...	prpf3	0.46136...	4.21870...
ENSDARG00000104...	ENSDARG...	CR9318...	2.66209...	0.00525...
ENSDARG00000070...	ENSDARG...	si:ch211...	-0.5837...	2.25336...
ENSDARG00000038...	ENSDARG...	kpna2	-0.5206...	5.78969...

Add styles to nodes



default

Def.	Property
	Border Paint
0.0	Border Width
	Fill Color
35.0	Height
	Image/Chart 1
	Label
	Label Color
12	Label Font Size
	Shape
	Size
255	Transparency
75.0	Width

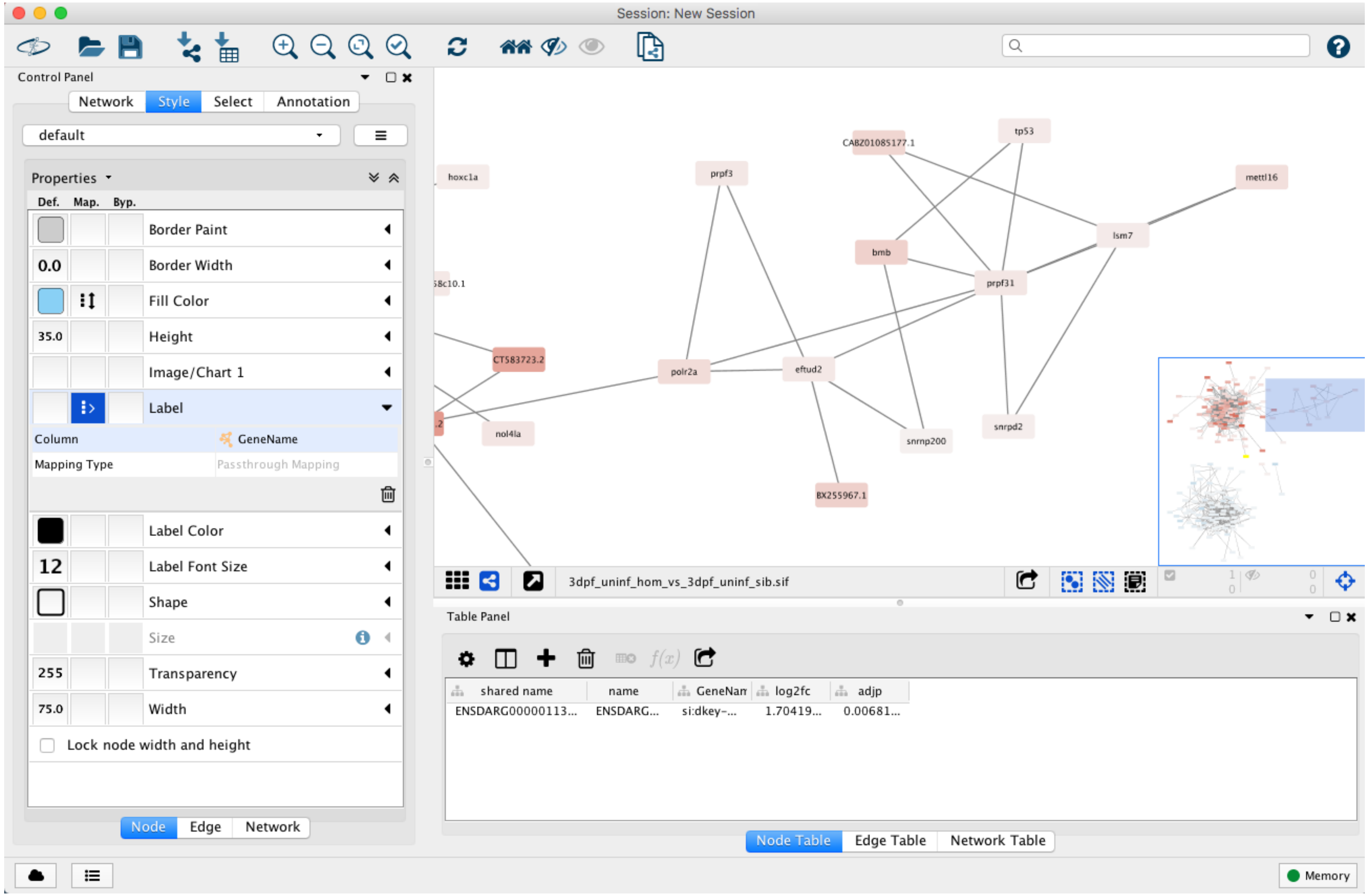
Label
Column: GeneName
Mapping Type: Passthrough Mapping

☐ Lock node width and height

3dpf_uninf_hom_vs_3dpf_uninf_sib.sif

shared name	name	GeneNam	log2fc	adjp
ENSDARG00000099...	ENSDARG...	polr2a	0.77350...	1.31750...
ENSDARG00000012...	ENSDARG...	eftud2	0.43041...	7.06488...
ENSDARG00000095...	ENSDARG...	prpf31	0.47628...	4.21870...
ENSDARG00000086...	ENSDARG...	prpf3	0.46136...	4.21870...
ENSDARG00000104...	ENSDARG...	CR9318...	2.66209...	0.00525...
ENSDARG00000070...	ENSDARG...	si:ch211...	−0.5837...	2.25336...
ENSDARG00000038...	ENSDARG...	kpna2	−0.5206...	5.78969...

Add styles to nodes



Session: New Session

Control Panel

Network | Style | Select | Annotation

default

Properties

Def.	Map.	Byp.	
			Border Paint
0.0			Border Width
			Fill Color
35.0			Height
			Image/Chart 1
			Label
12			Label Font Size
			Label Color
			Shape
			Size
255			Transparency
75.0			Width

Label: Column: GeneName; Mapping Type: Passthrough Mapping

☐ Lock node width and height

Node | Edge | Network

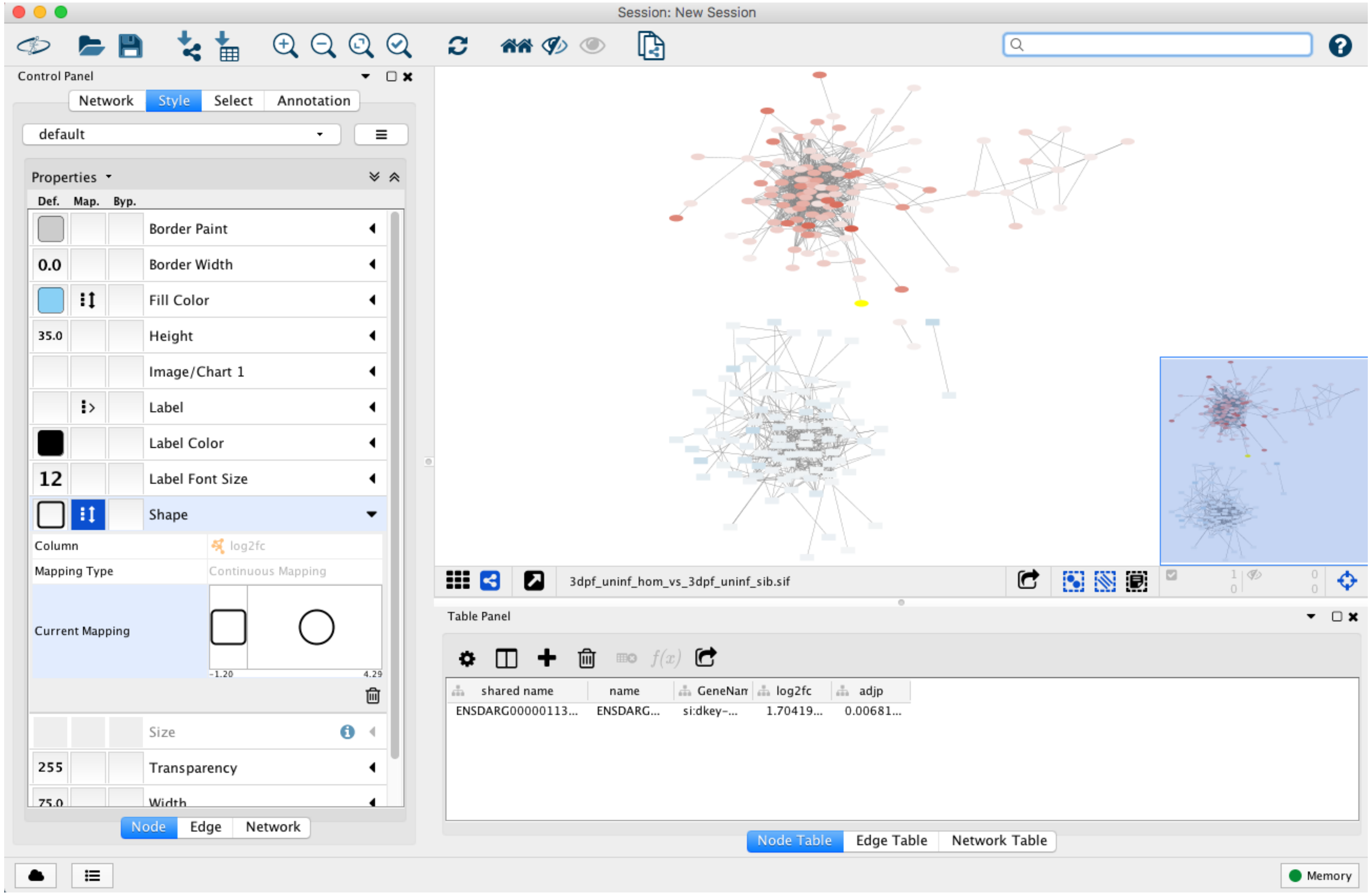
3dpf_uninf_hom_vs_3dpf_uninf_sib.sif

Table Panel

shared name	name	GeneNam	log2fc	adjp
ENSDARG00000113...	ENSDARG...	si:dkey-...	1.70419...	0.00681...

Node Table | Edge Table | Network Table

Add styles to nodes



Border Width 0.0

Height 35.0

Label Font Size 12

Shape

Column: log2fc

Mapping Type: Continuous Mapping

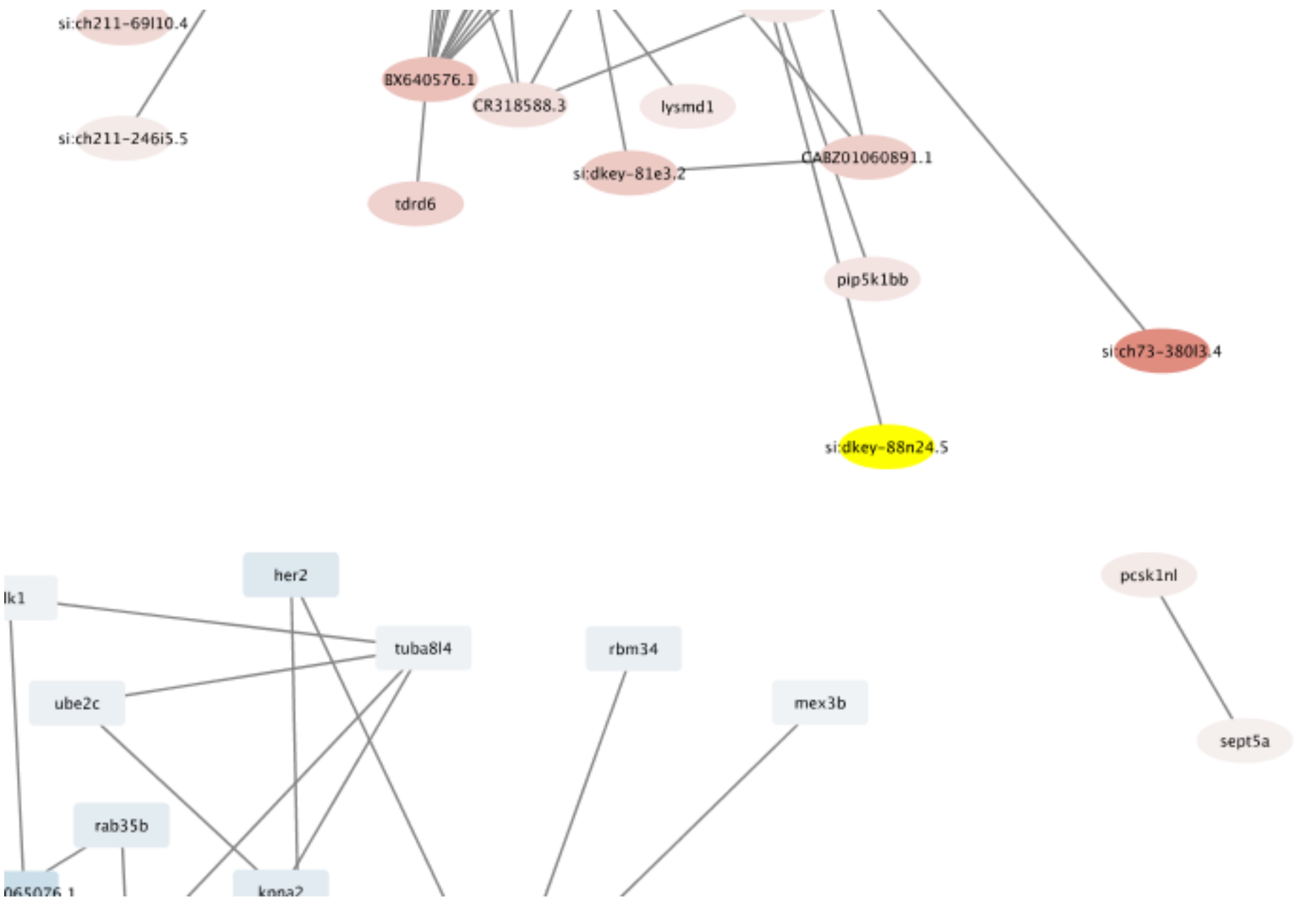
Current Mapping: -1.20 … 4.29

Transparency 255

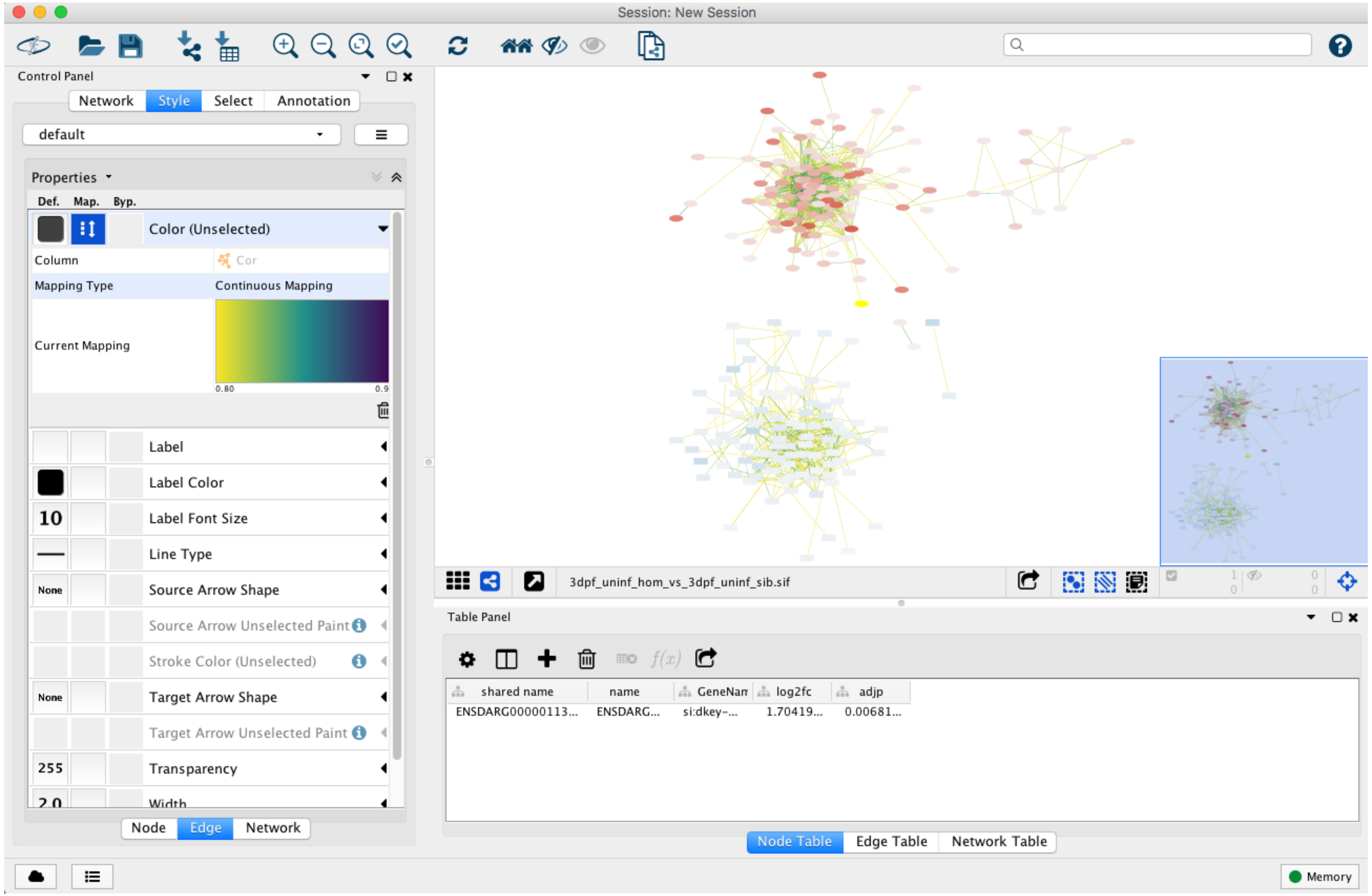
Width 75.0

shared name	name	GeneNan	log2fc	adjp
ENSDARG00000113...	ENSDARG...	si:dkey-...	1.70419...	0.00681...

Add styles to nodes



Add styles to edges



3dpf_uninf_hom_vs_3dpf_uninf_sib.sif

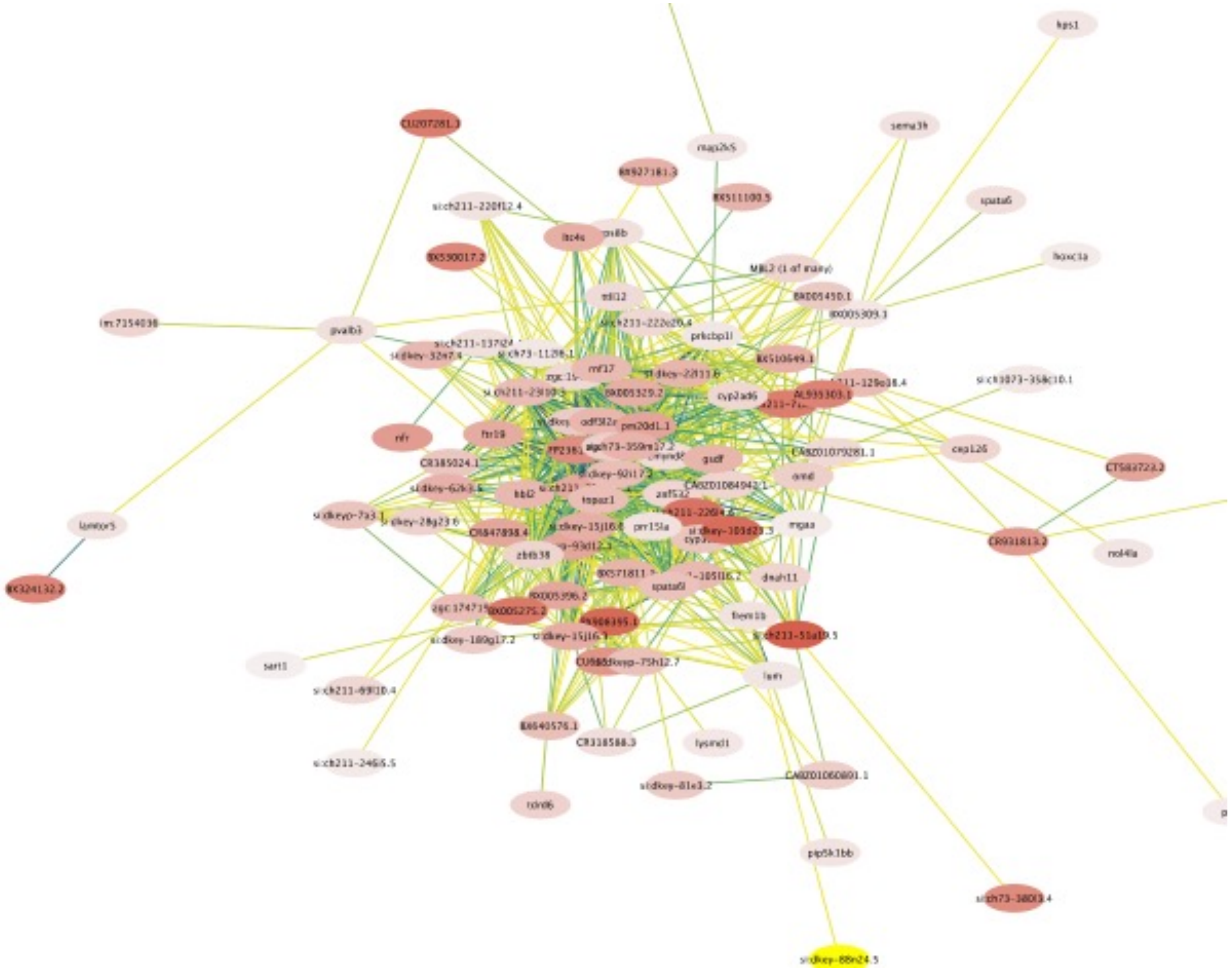
Color (Unselected)

Column	Cor
Mapping Type	Continuous Mapping
Current Mapping	0.80 – 0.9

Def.	Property
	Label
■	Label Color
10	Label Font Size
—	Line Type
None	Source Arrow Shape
	Source Arrow Unselected Paint
	Stroke Color (Unselected)
None	Target Arrow Shape
	Target Arrow Unselected Paint
255	Transparency
2.0	Width

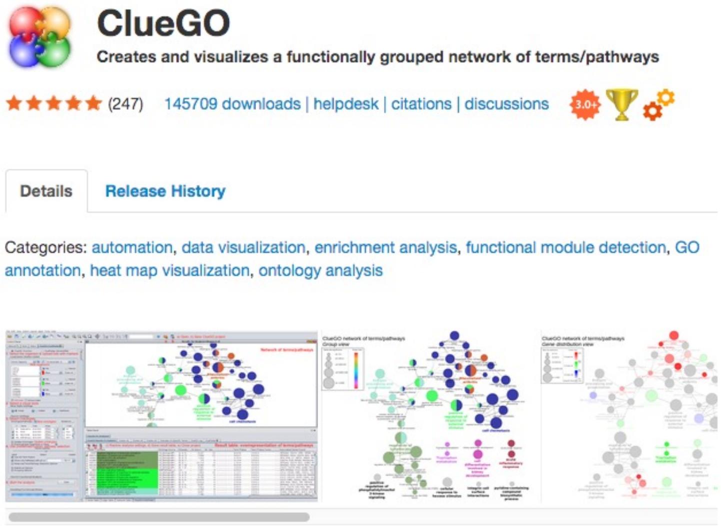
shared name	name	GeneNam	log2fc	adjp
ENSDARG00000113...	ENSDARG...	si:dkey-...	1.70419...	0.00681...

Add styles to edges



ClueGO

- Cytoscape App for visualising functional enrichments
  - GO/KEGG/Reactome etc.
  - http://www.ici.upmc.fr/cluego/cluegoDocumentation.shtml
- Groups terms to identify non-redundant terms



ClueGO

Creates and visualizes a functionally grouped network of terms/pathways

★★★★★ (247) 145709 downloads | helpdesk | citations | discussions

Details | Release History

Categories: automation, data visualization, enrichment analysis, functional module detection, GO annotation, heat map visualization, ontology analysis

Bindea et al. 2009

ClueGO

- Cytoscape App for visualising functional enrichments
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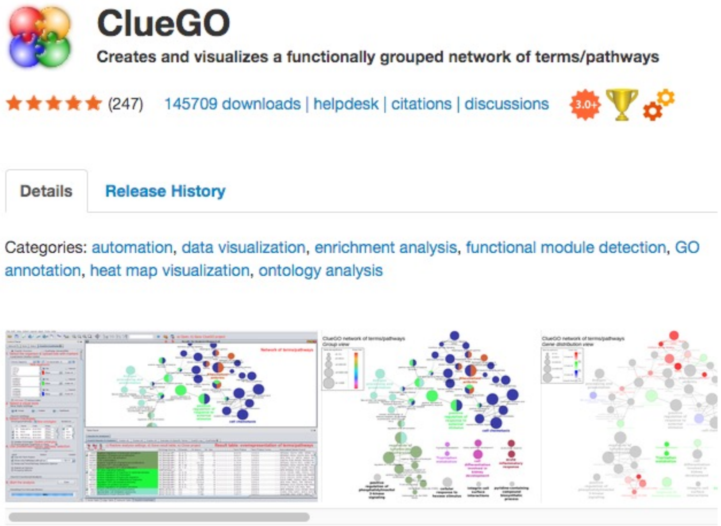

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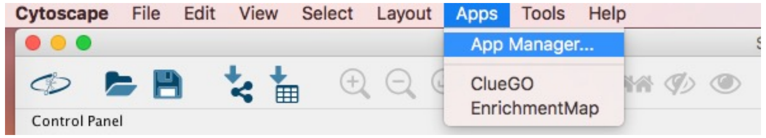

Bindea et al. 2009

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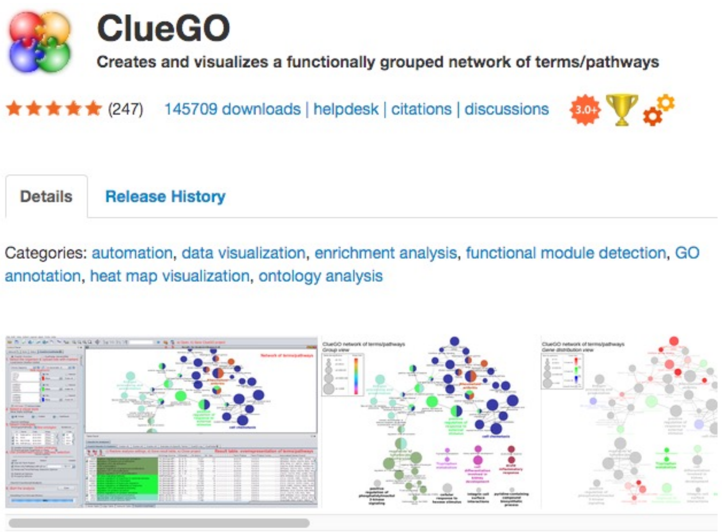

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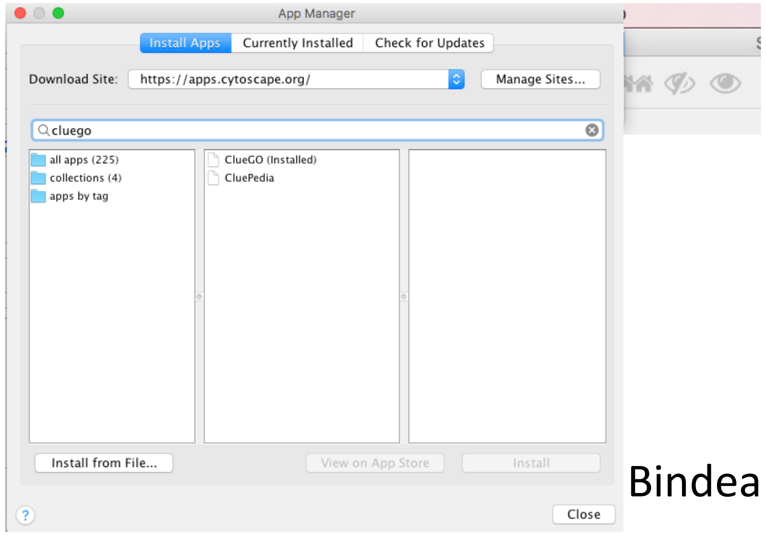


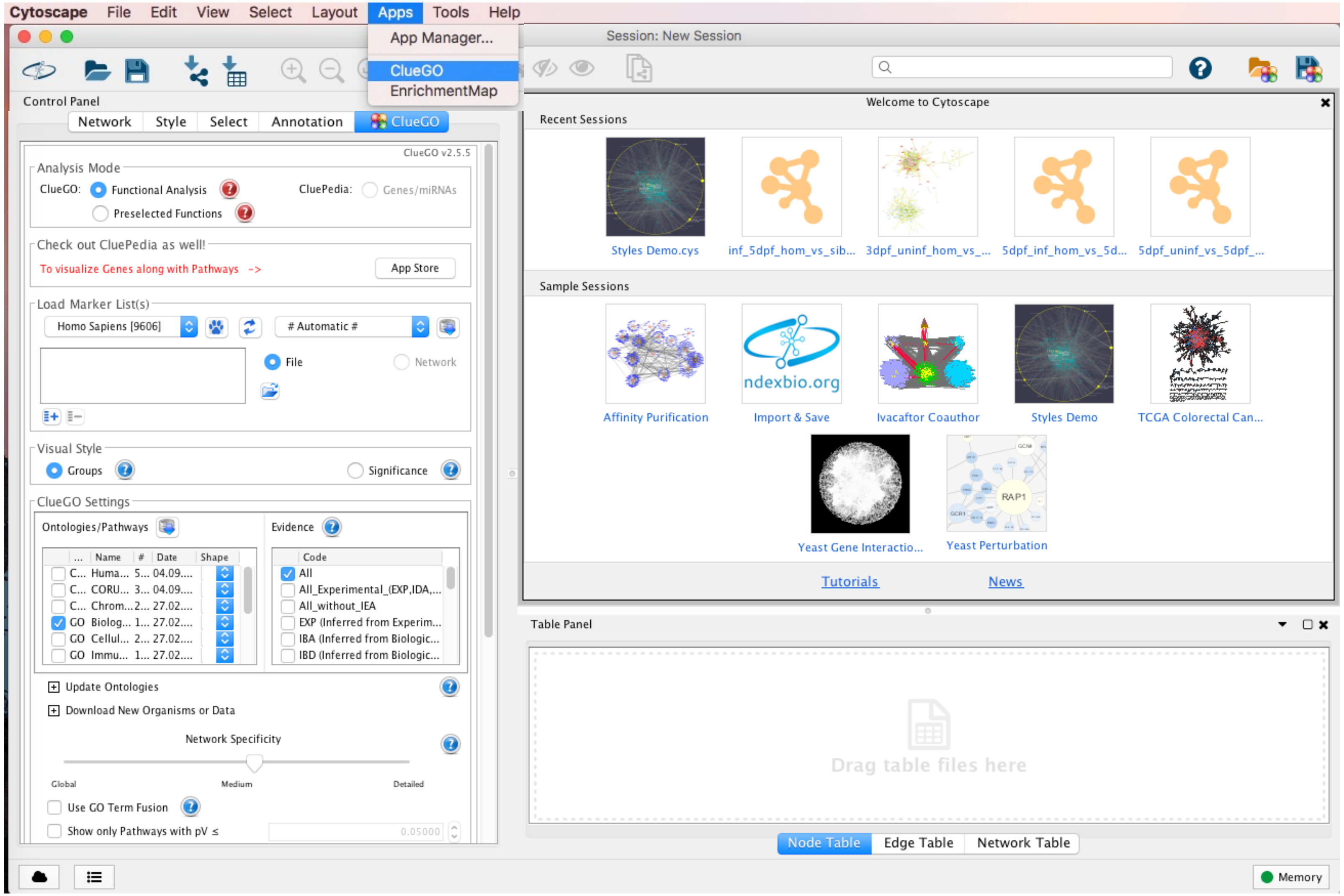
App Manager

Download Site: https://apps.cytoscape.org/

cluego

Bindea et al. 2009

ClueGO



Analysis Mode

ClueGO: ● Functional Analysis
○ Preselected Functions

CluePedia: ○ Genes/miRNAs

Check out CluePedia as well!

To visualize Genes along with Pathways -> App Store

Load Marker List(s)

Homo Sapiens [9606]

Automatic

● File ○ Network

Visual Style

● Groups ○ Significance

ClueGO Settings

Ontologies/Pathways

	...	Name	#	Date	Shape
☐	C...	Huma...	5...	04.09....	
☐	C...	CORU...	3...	04.09....	
☐	C...	Chrom...	2...	27.02....	
☑	GO	Biolog...	1...	27.02....	
☐	GO	Cellul...	2...	27.02....	
☐	GO	Immu...	1...	27.02....	

Evidence

	Code
☑	All
☐	All_Experimental_(EXP,IDA,...
☐	All_without_IEA
☐	EXP (Inferred from Experim...
☐	IBA (Inferred from Biologic...
☐	IBD (Inferred from Biologic...

⊞ Update Ontologies

⊞ Download New Organisms or Data

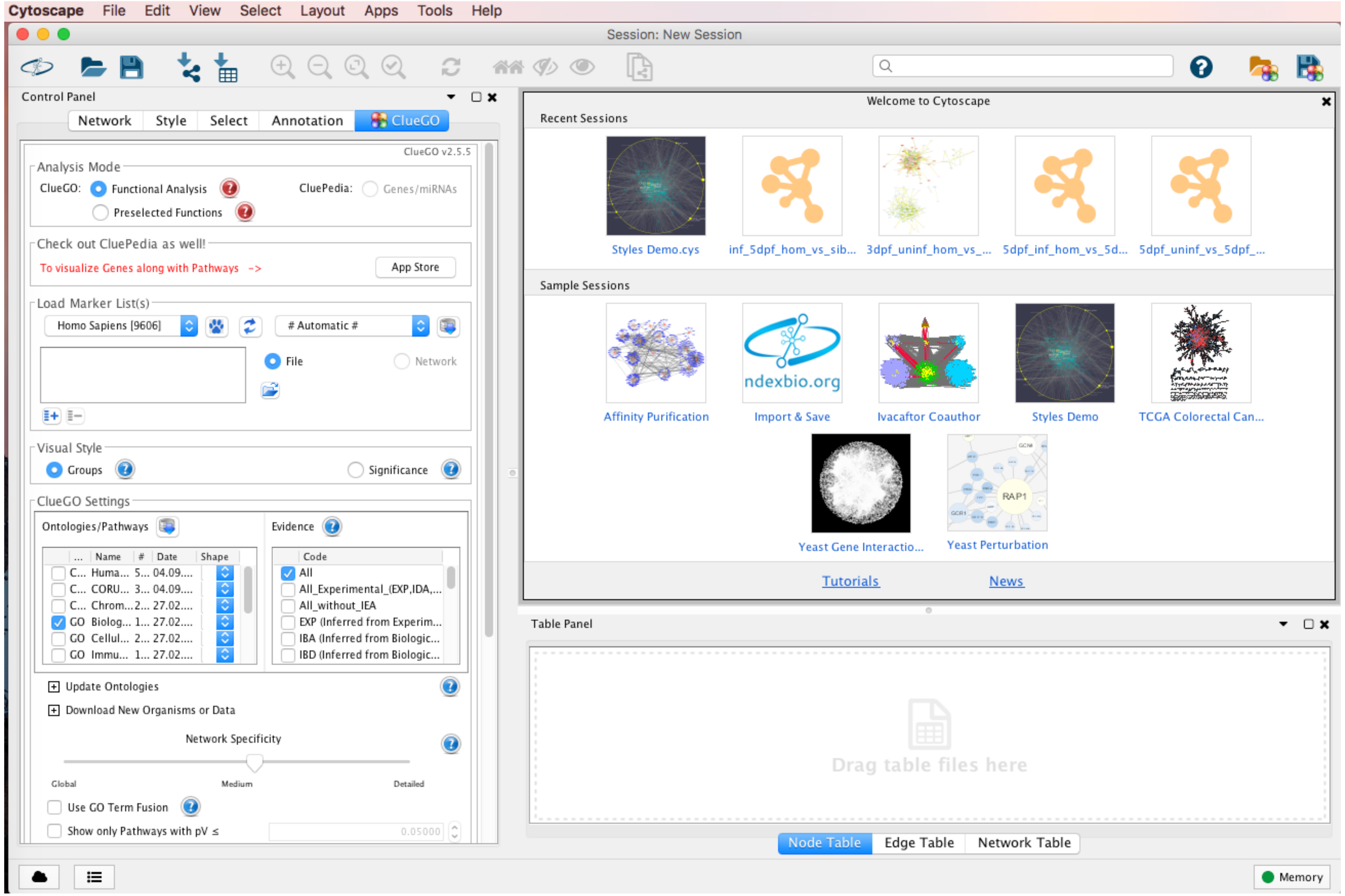
Network Specificity

Global Medium Detailed

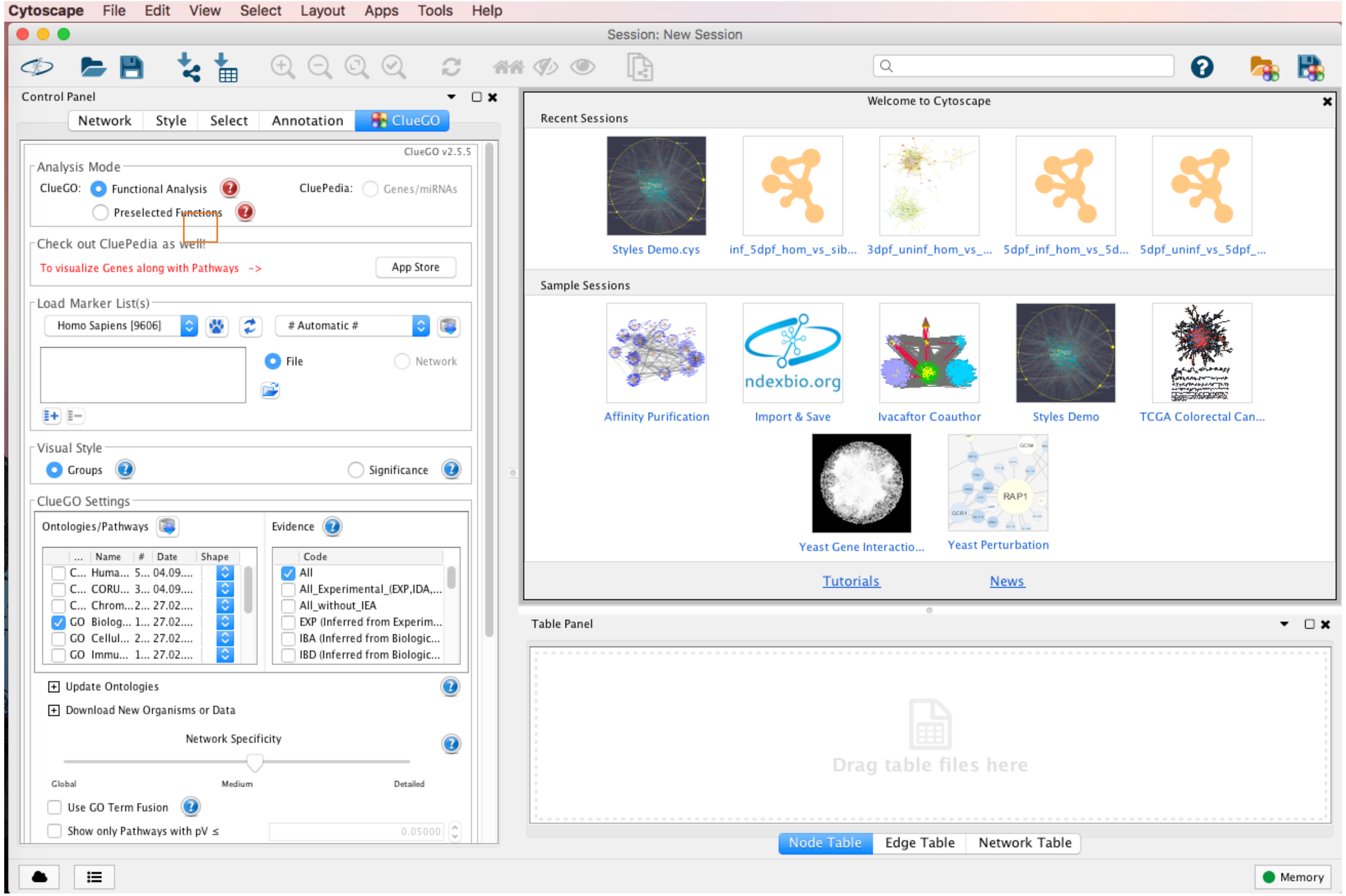
☐ Use GO Term Fusion

☐ Show only Pathways with pV ≤ 0.05000

ClueGO


Cytoscape File Edit View Select Layout Apps Tools Help
Session: New Session
Control Panel
Network Style Select Annotation ClueGO
ClueGO v2.5.5
Analysis Mode
ClueGO: ● Functional Analysis
○ Preselected Functions
CluePedia: ○ Genes/miRNAs
Check out CluePedia as well!
To visualize Genes along with Pathways ->
App Store
Load Marker List(s)
Homo Sapiens [9606]
Automatic
● File
○ Network
Visual Style
● Groups
○ Significance
ClueGO Settings
Ontologies/Pathways
... Name # Date Shape
☐ C... Huma... 5... 04.09....
☐ C... CORU... 3... 04.09....
☐ C... Chrom... 2... 27.02....
☑ GO Biolog... 1... 27.02....
☐ GO Cellul... 2... 27.02....
☐ GO Immu... 1... 27.02....
Evidence
Code
☑ All
☐ All_Experimental_(EXP,IDA,...
☐ All_without_IEA
☐ EXP (Inferred from Experim...
☐ IBA (Inferred from Biologic...
☐ IBD (Inferred from Biologic...
Update Ontologies
Download New Organisms or Data
Network Specificity
Global
Medium
Detailed
☐ Use GO Term Fusion
☐ Show only Pathways with pV ≤
0.05000
Welcome to Cytoscape
Recent Sessions
Styles Demo.cys
inf_5dpf_hom_vs_sib...
3dpf_uninf_hom_vs_...
5dpf_inf_hom_vs_5d...
5dpf_uninf_vs_5dpf_...
Sample Sessions
Affinity Purification
ndexbio.org
Import & Save
Ivacaftor Coauthor
Styles Demo
TCGA Colorectal Can...
Yeast Gene Interactio...
Yeast Perturbation
RAP1
Tutorials
News
Table Panel
Drag table files here
Node Table
Edge Table
Network Table
Memory

ClueGO


Cytoscape File Edit View Select Layout Apps Tools Help
Session: New Session
Control Panel
Network Style Select Annotation ClueGO
ClueGO v2.5.5
Analysis Mode
ClueGO: ● Functional Analysis
○ Preselected Functions
CluePedia: ○ Genes/miRNAs
Check out CluePedia as well!
To visualize Genes along with Pathways ->
App Store
Load Marker List(s)
Homo Sapiens [9606]
Automatic
● File ○ Network
Visual Style
● Groups ○ Significance
ClueGO Settings
Ontologies/Pathways
... Name # Date Shape
☐ C... Huma... 5... 04.09....
☐ C... CORU... 3... 04.09....
☐ C... Chrom... 2... 27.02....
☑ GO Biolog... 1... 27.02....
☐ GO Cellul... 2... 27.02....
☐ GO Immu... 1... 27.02....
Evidence
Code
☑ All
☐ All_Experimental_(EXP,IDA,...
☐ All_without_IEA
☐ EXP (Inferred from Experim...
☐ IBA (Inferred from Biologic...
☐ IBD (Inferred from Biologic...
Update Ontologies
Download New Organisms or Data
Network Specificity
Global Medium Detailed
☐ Use GO Term Fusion
☐ Show only Pathways with pV ≤ 0.05000
Welcome to Cytoscape
Recent Sessions
Styles Demo.cys
inf_5dpf_hom_vs_sib...
3dpf_uninf_hom_vs_...
5dpf_inf_hom_vs_5d...
5dpf_uninf_vs_5dpf_...
Sample Sessions
Affinity Purification
ndexbio.org
Import & Save
Ivacaftor Coauthor
Styles Demo
TCGA Colorectal Can...
Yeast Gene Interactio...
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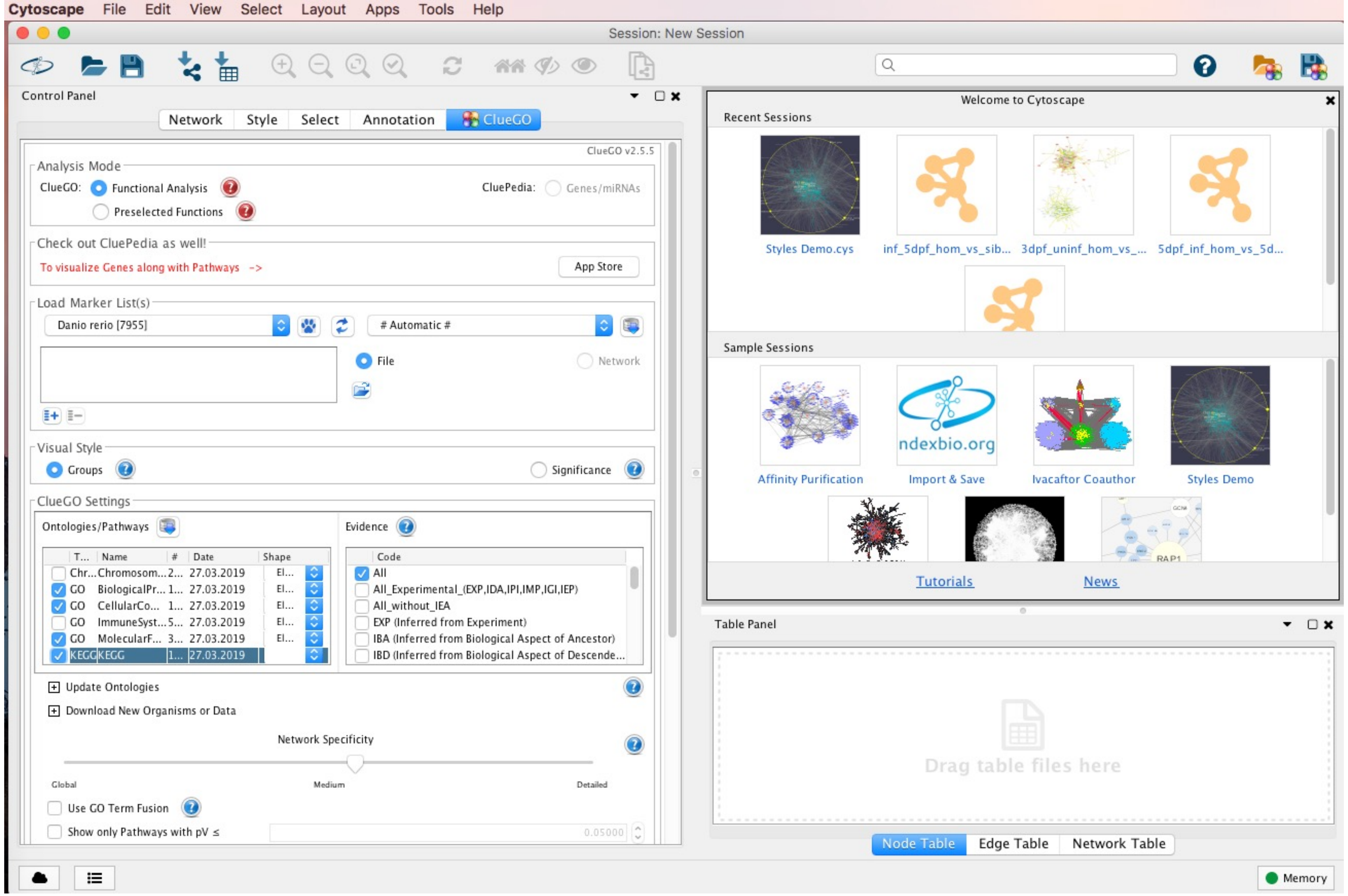
Tutorials
News
Table Panel
Drag table files here
Node Table Edge Table Network Table
Memory

ClueGO



ClueGO: ● Functional Analysis ○ Preselected Functions

CluePedia: ○ Genes/miRNAs

Danio rerio [7955]

Automatic

● File ○ Network

● Groups ○ Significance

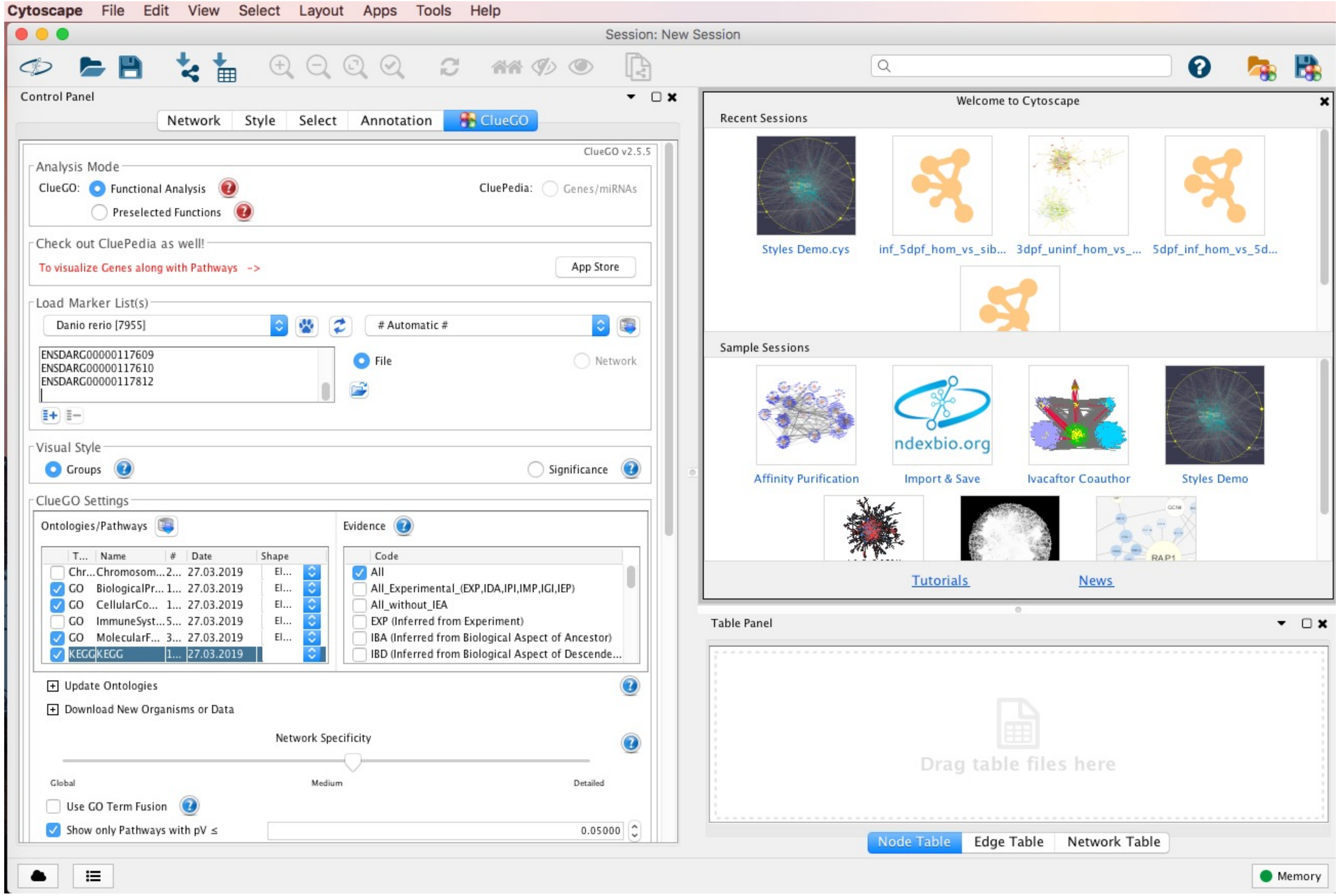
	T...	Name	#	Date	Shape
☐	Chr...	Chromosom...	2...	27.03.2019	El...
☑	GO	BiologicalPr...	1...	27.03.2019	El...
☑	GO	CellularCo...	1...	27.03.2019	El...
☐	GO	ImmuneSyst...	5...	27.03.2019	El...
☑	GO	MolecularF...	3...	27.03.2019	El...
☑	KEGG	KEGG	1...	27.03.2019	

	Code
☑	All
☐	All_Experimental_(EXP,IDA,IPI,IMP,IGI,IEP)
☐	All_without_IEA
☐	EXP (Inferred from Experiment)
☐	IBA (Inferred from Biological Aspect of Ancestor)
☐	IBD (Inferred from Biological Aspect of Descende...

☐ Use GO Term Fusion

☐ Show only Pathways with pV ≤ 0.05000

ClueGO



Analysis Mode

ClueGO: ● Functional Analysis

○ Preselected Functions

CluePedia: ○ Genes/miRNAs

Check out CluePedia as well!

To visualize Genes along with Pathways ->

App Store

Load Marker List(s)

Danio rerio [7955]

Automatic

ENSDARG00000117609
ENSDARG00000117610
ENSDARG00000117812

● File ○ Network

Visual Style

● Groups ○ Significance

ClueGO Settings

Ontologies/Pathways

	T...	Name	#	Date	Shape
☐	Chr...	Chromosom...	2...	27.03.2019	El...
☑	GO	BiologicalPr...	1...	27.03.2019	El...
☑	GO	CellularCo...	1...	27.03.2019	El...
☐	GO	ImmuneSyst...	5...	27.03.2019	El...
☑	GO	MolecularF...	3...	27.03.2019	El...
☑	KEGG	KEGG	1...	27.03.2019	

Evidence

	Code
☑	All
☐	All_Experimental_(EXP,IDA,IPI,IMP,IGI,IEP)
☐	All_without_IEA
☐	EXP (Inferred from Experiment)
☐	IBA (Inferred from Biological Aspect of Ancestor)
☐	IBD (Inferred from Biological Aspect of Descende...

⊞ Update Ontologies

⊞ Download New Organisms or Data

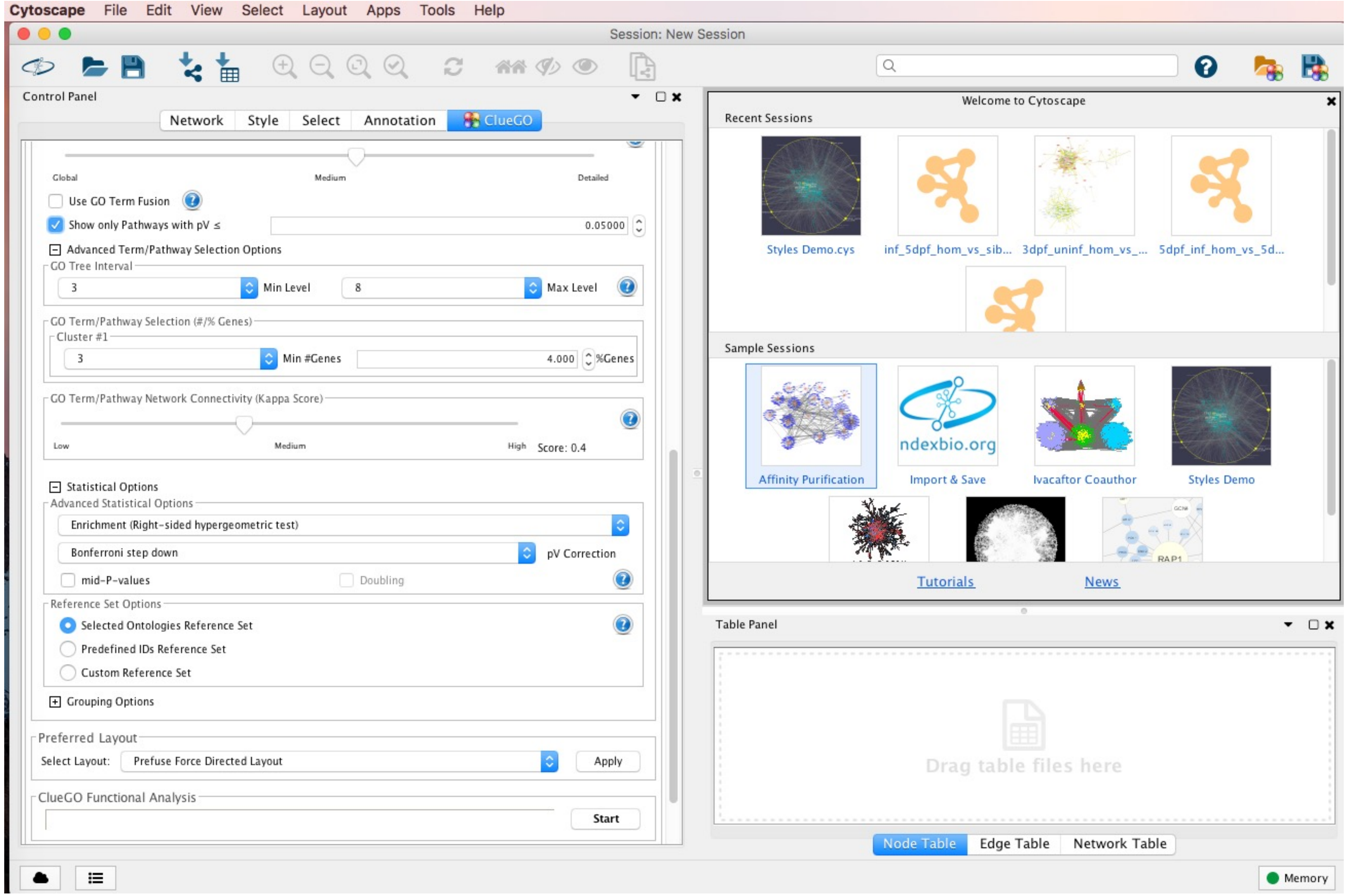
Network Specificity

Global — Medium — Detailed

☐ Use GO Term Fusion

☑ Show only Pathways with pV ≤ 0.05000

ClueGO



☐ Use GO Term Fusion

☑ Show only Pathways with pV ≤ 0.05000

⊟ Advanced Term/Pathway Selection Options

GO Tree Interval: 3 Min Level, 8 Max Level

GO Term/Pathway Selection (#/% Genes)
Cluster #1: 3 Min #Genes, 4.000 %Genes

GO Term/Pathway Network Connectivity (Kappa Score): Score: 0.4

⊟ Statistical Options

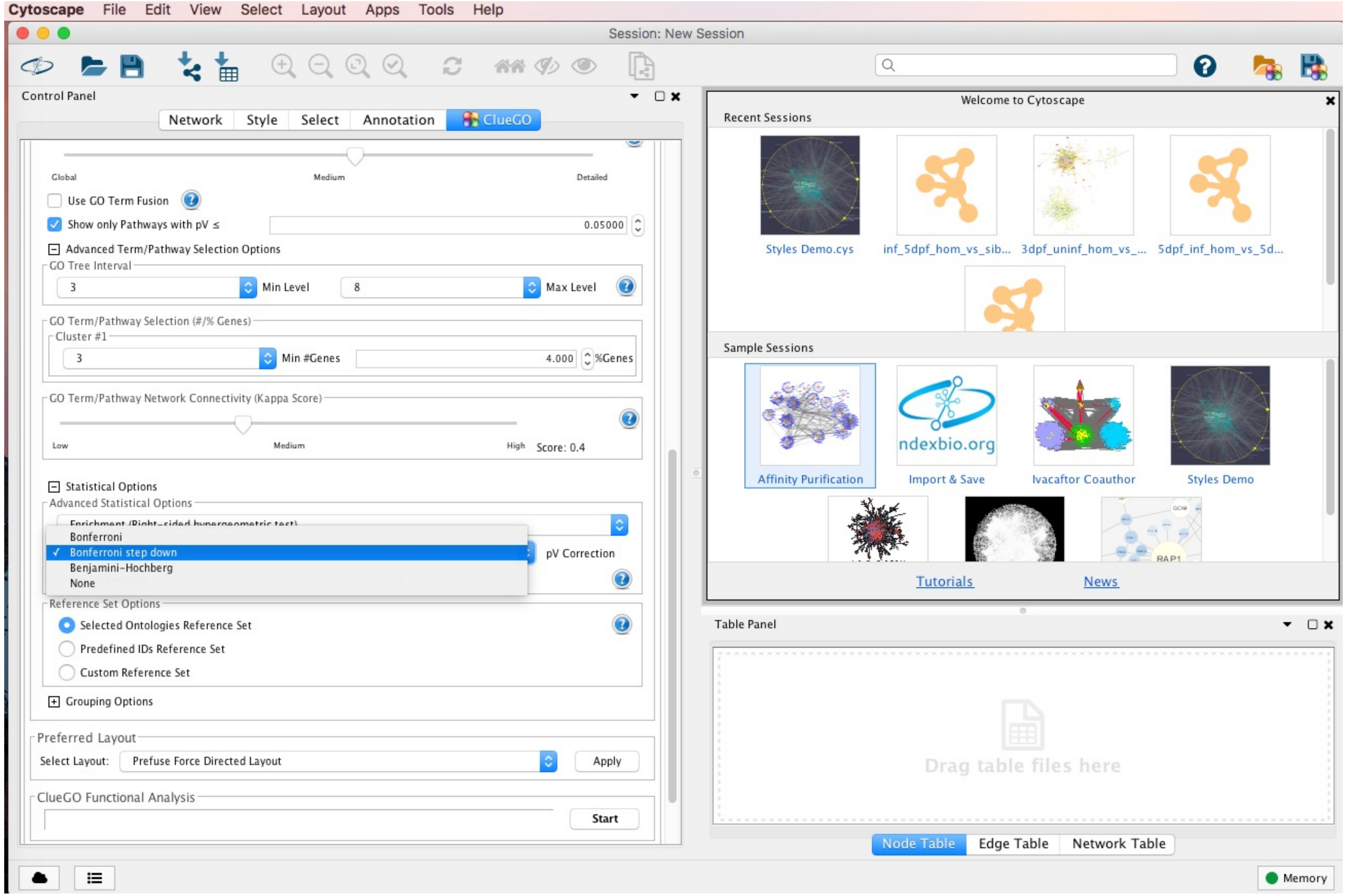
Advanced Statistical Options:
Enrichment (Right-sided hypergeometric test)
Bonferroni step down pV Correction
☐ mid-P-values ☐ Doubling

Reference Set Options:
● Selected Ontologies Reference Set
○ Predefined IDs Reference Set
○ Custom Reference Set

⊞ Grouping Options

Preferred Layout
Select Layout: Prefuse Force Directed Layout

ClueGO



☐ Use GO Term Fusion

☑ Show only Pathways with pV ≤ 0.05000

Advanced Term/Pathway Selection Options

GO Tree Interval: 3 Min Level, 8 Max Level

GO Term/Pathway Selection (#/% Genes)

Cluster #1: 3 Min #Genes, 4.000 %Genes

GO Term/Pathway Network Connectivity (Kappa Score): Low – Medium – High, Score: 0.4

Statistical Options

Advanced Statistical Options: Enrichment (Right-sided hypergeometric test)

pV Correction:
- Bonferroni
- ✓ Bonferroni step down
- Benjamini-Hochberg
- None

Reference Set Options
- ● Selected Ontologies Reference Set
- ○ Predefined IDs Reference Set
- ○ Custom Reference Set

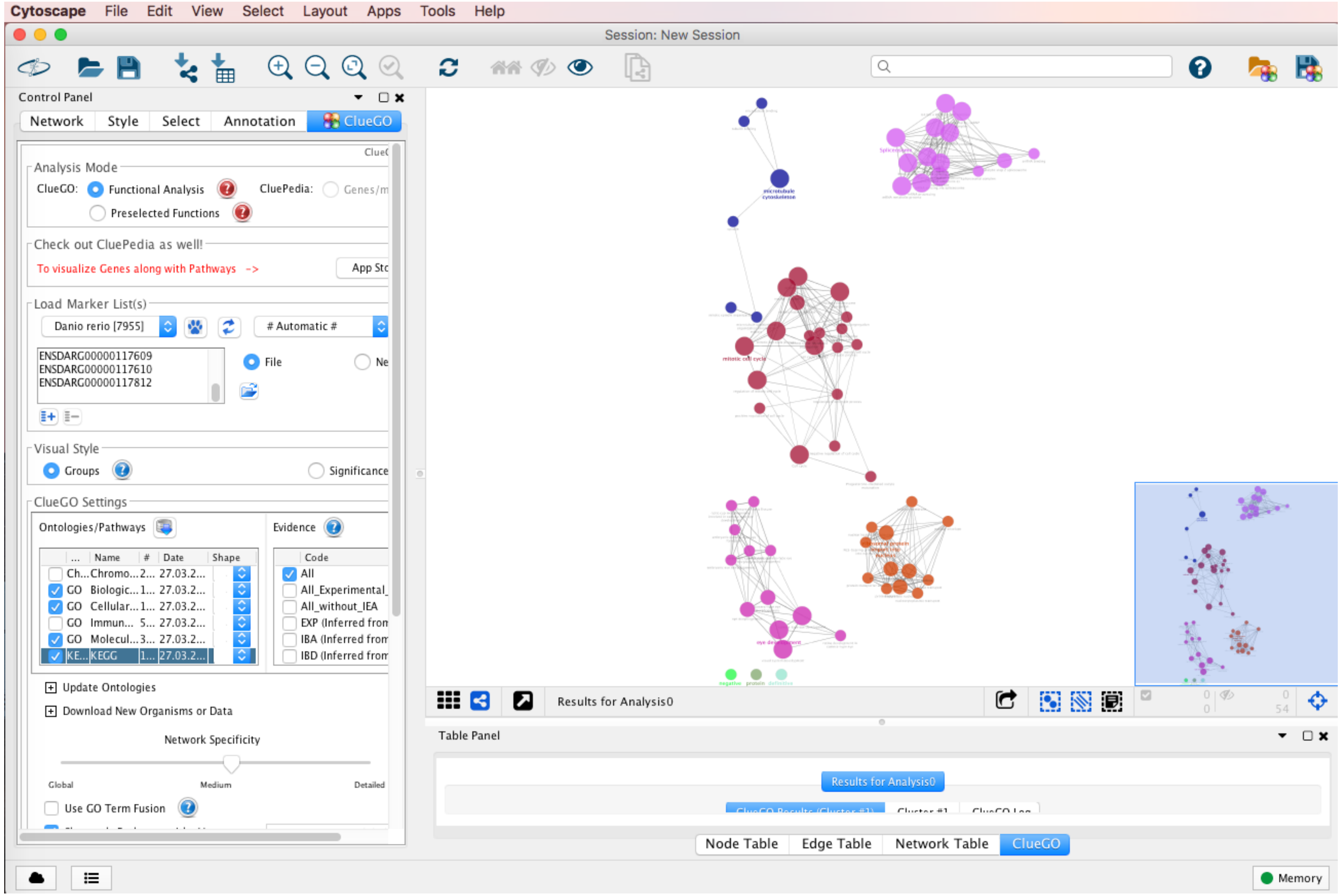
Grouping Options

Preferred Layout

Select Layout: Prefuse Force Directed Layout — Apply

ClueGO Functional Analysis — Start

ClueGO



Analysis Mode

ClueGO: ● Functional Analysis ○ Preselected Functions

CluePedia: ○ Genes/m

Check out CluePedia as well!

To visualize Genes along with Pathways ->

App Stc

Load Marker List(s)

Danio rerio [7955]

Automatic

ENSDARG00000117609
ENSDARG00000117610
ENSDARG00000117812

● File ○ Ne

Visual Style

● Groups ○ Significance

ClueGO Settings

Ontologies/Pathways

	...	Name	#	Date	Shape
☐	Ch...	Chromo...	2...	27.03.2...	
☑	GO	Biologic...	1...	27.03.2...	
☑	GO	Cellular...	1...	27.03.2...	
☐	GO	Immun...	5...	27.03.2...	
☑	GO	Molecul...	3...	27.03.2...	
☑	KE...	KEGG	1...	27.03.2...	

Evidence

	Code
☑	All
☐	All_Experimental_
☐	All_without_IEA
☐	EXP (Inferred from
☐	IBA (Inferred from
☐	IBD (Inferred from

⊞ Update Ontologies

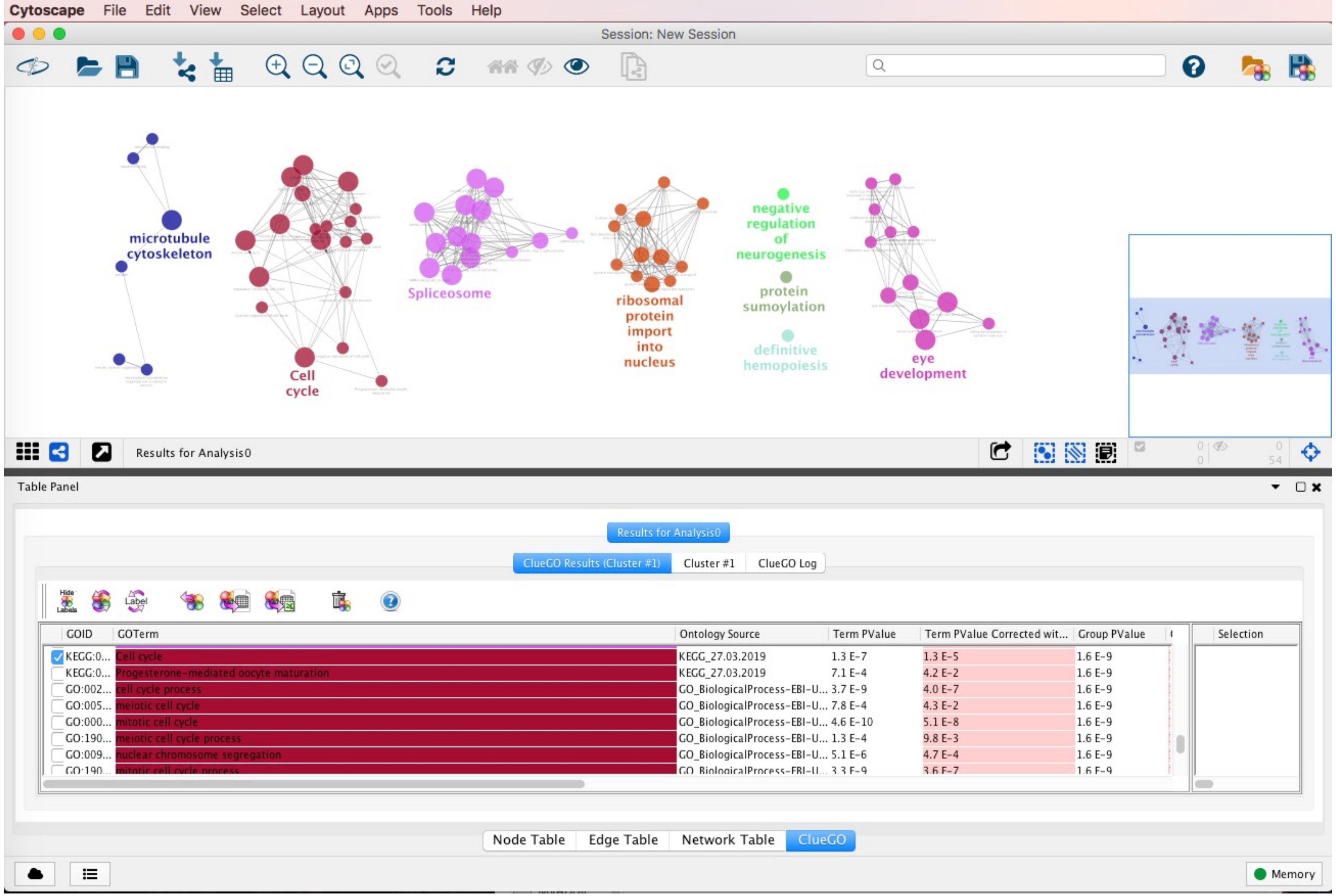
⊞ Download New Organisms or Data

Network Specificity

Global — Medium — Detailed

☐ Use GO Term Fusion

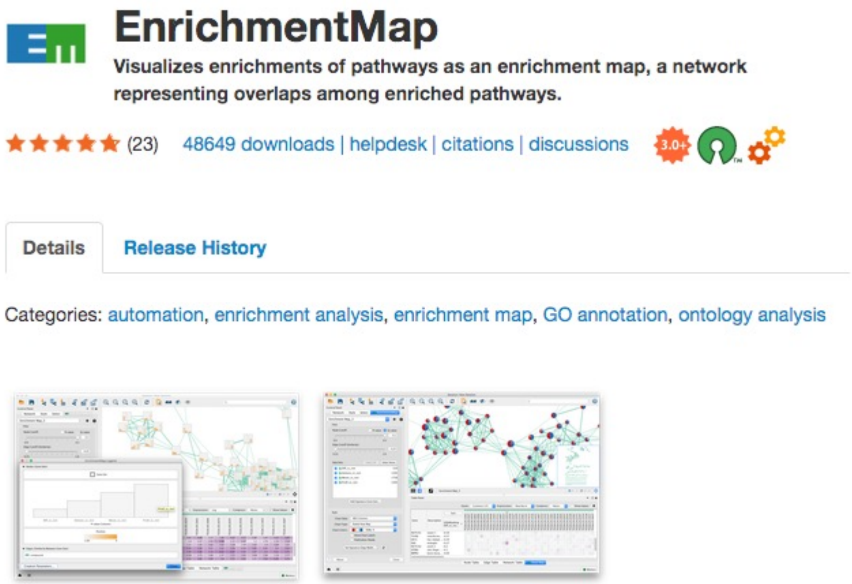
ClueGO



	GOID	GOTerm	Ontology Source	Term PValue	Term PValue Corrected wit...	Group PValue
☑	KEGG:0...	Cell cycle	KEGG_27.03.2019	1.3 E-7	1.3 E-5	1.6 E-9
☐	KEGG:0...	Progesterone-mediated oocyte maturation	KEGG_27.03.2019	7.1 E-4	4.2 E-2	1.6 E-9
☐	GO:002...	cell cycle process	GO_BiologicalProcess-EBI-U...	3.7 E-9	4.0 E-7	1.6 E-9
☐	GO:005...	meiotic cell cycle	GO_BiologicalProcess-EBI-U...	7.8 E-4	4.3 E-2	1.6 E-9
☐	GO:000...	mitotic cell cycle	GO_BiologicalProcess-EBI-U...	4.6 E-10	5.1 E-8	1.6 E-9
☐	GO:190...	meiotic cell cycle process	GO_BiologicalProcess-EBI-U...	1.3 E-4	9.8 E-3	1.6 E-9
☐	GO:009...	nuclear chromosome segregation	GO_BiologicalProcess-EBI-U...	5.1 E-6	4.7 E-4	1.6 E-9
☐	GO:190...	mitotic cell cycle process	GO_BiologicalProcess-EBI-U...	3.3 E-9	3.6 E-7	1.6 E-9

Enrichment Map

- https://enrichmentmap.readthedocs.io/en/latest
- Inputs:
  - GSEA
  - DAVID/BINGO/Great
  - Generic



EnrichmentMap

Visualizes enrichments of pathways as an enrichment map, a network representing overlaps among enriched pathways.

★★★★★ (23) 48649 downloads | helpdesk | citations | discussions

Details Release History

Categories: automation, enrichment analysis, enrichment map, GO annotation, ontology analysis

Merico et al. 2010

Generic Input Files

Enrichments

GeneSetID	Description	p.Val	FDR	Phenotype
GO:0000070	mitotic sister chromatid segregation	6.83E-04	0.04165	1.38041
GO:0000278	mitotic cell cycle	4.64E-10	5.10E-08	7.29235
GO:0000280	NA	3.62E-07	NA	4.43731

GeneSets

GeneSetID	Description	Genes					
GO:0000070	mitotic sister chromatid segregation	bub1	incenp	nusap1	pds5a	ran	
GO:0000278	mitotic cell cycle	aspm	atoh7	bmb	bub1	ccna2	…
GO:0000280	NA	bub1	ccna2	ccnd1	ccne2	incenp	…

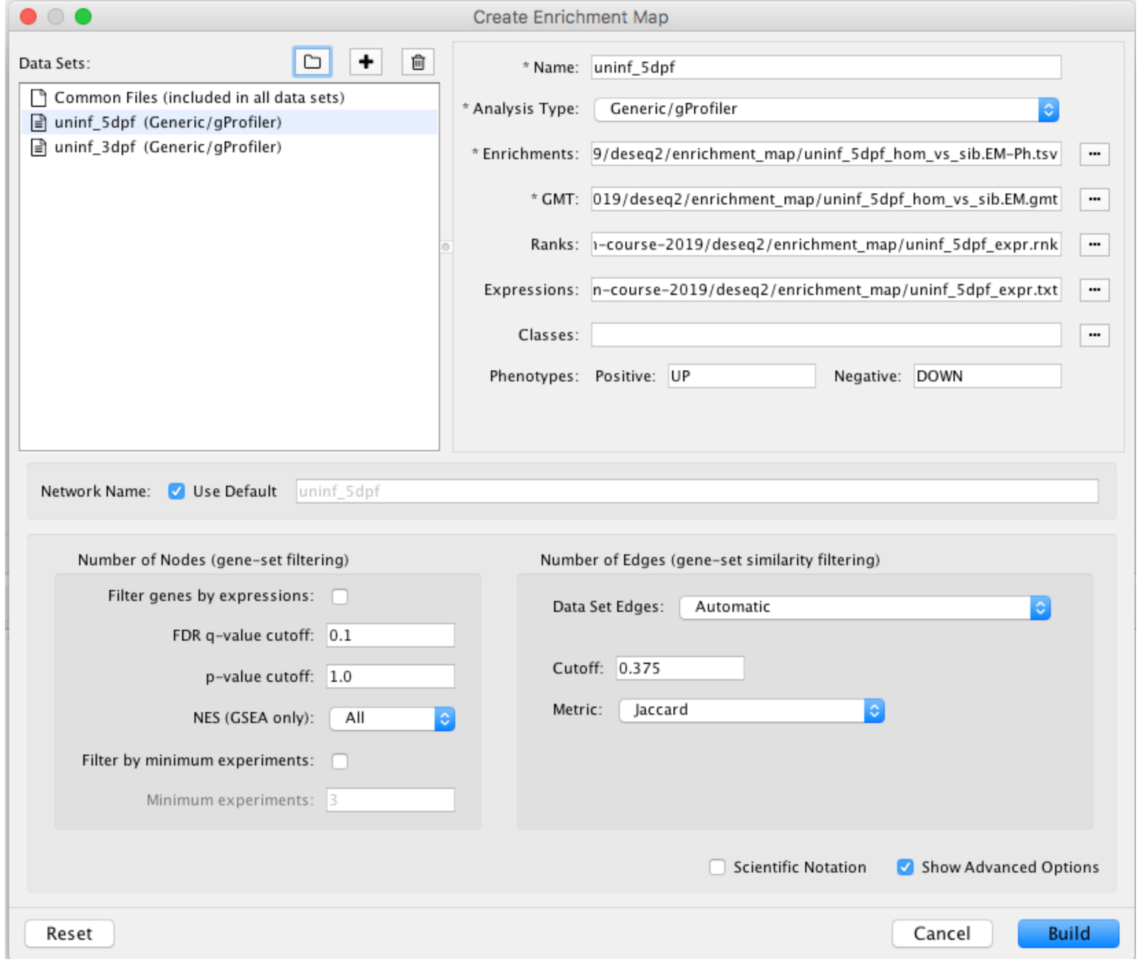
Expression

name	description	uninf_3dpf_wt_rep1	uninf_3dpf_wt_rep2
slc35a5	ENSDARG00000000001	36.28229146	33.4323
ccdc80	ENSDARG00000000002	75.50639034	113.155
nrf1	ENSDARG00000000018	305.9479712	281.174

Ranks

name	rank
slc35a5	0.946000588
ccdc80	0.987509859
nrf1	0.646467578

Enrichment Map



Data Sets:
- Common Files (included in all data sets)
- uninf_5dpf (Generic/gProfiler)
- uninf_3dpf (Generic/gProfiler)

* Name: uninf_5dpf

* Analysis Type: Generic/gProfiler

* Enrichments: 9/deseq2/enrichment_map/uninf_5dpf_hom_vs_sib.EM-Ph.tsv

* GMT: 019/deseq2/enrichment_map/uninf_5dpf_hom_vs_sib.EM.gmt

Ranks: ı-course-2019/deseq2/enrichment_map/uninf_5dpf_expr.rnk

Expressions: n-course-2019/deseq2/enrichment_map/uninf_5dpf_expr.txt

Classes:

Phenotypes: Positive: UP Negative: DOWN

Network Name: ☑ Use Default uninf_5dpf

Number of Nodes (gene-set filtering)

Filter genes by expressions: ☐

FDR q-value cutoff: 0.1

p-value cutoff: 1.0

NES (GSEA only): All

Filter by minimum experiments: ☐

Minimum experiments: 3

Number of Edges (gene-set similarity filtering)

Data Set Edges: Automatic

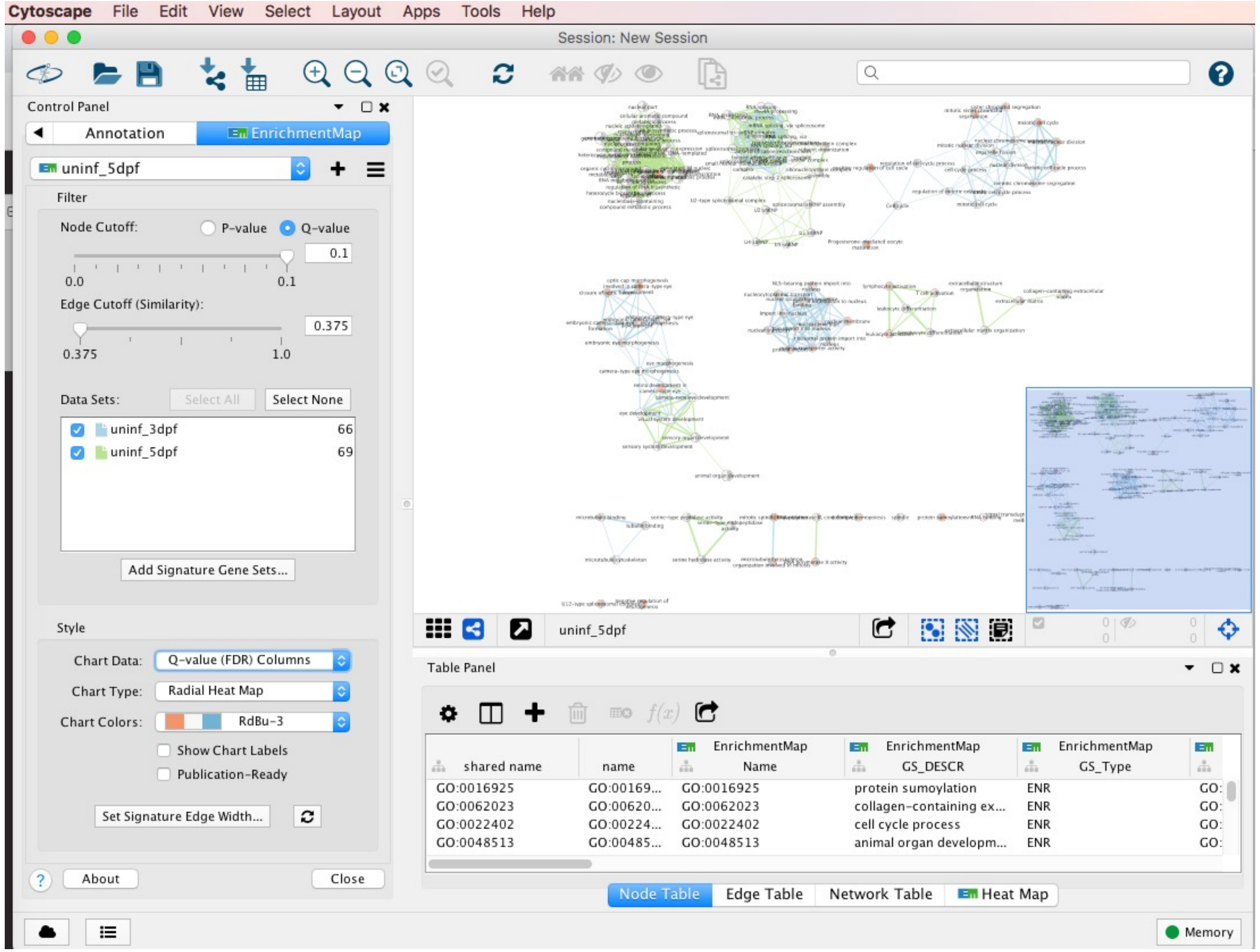
Cutoff: 0.375

Metric: Jaccard

☐ Scientific Notation ☑ Show Advanced Options

https://enrichmentmap.readthedocs.io/en/latest/Parameters.html

Enrichment Map



uninf_5dpf

Filter

Node Cutoff: ○ P-value ● Q-value 0.1

0.0 0.1

Edge Cutoff (Similarity): 0.375

0.375 1.0

Data Sets:

☑	uninf_3dpf	66
☑	uninf_5dpf	69

Style

Chart Data: Q-value (FDR) Columns

Chart Type: Radial Heat Map

Chart Colors: RdBu-3

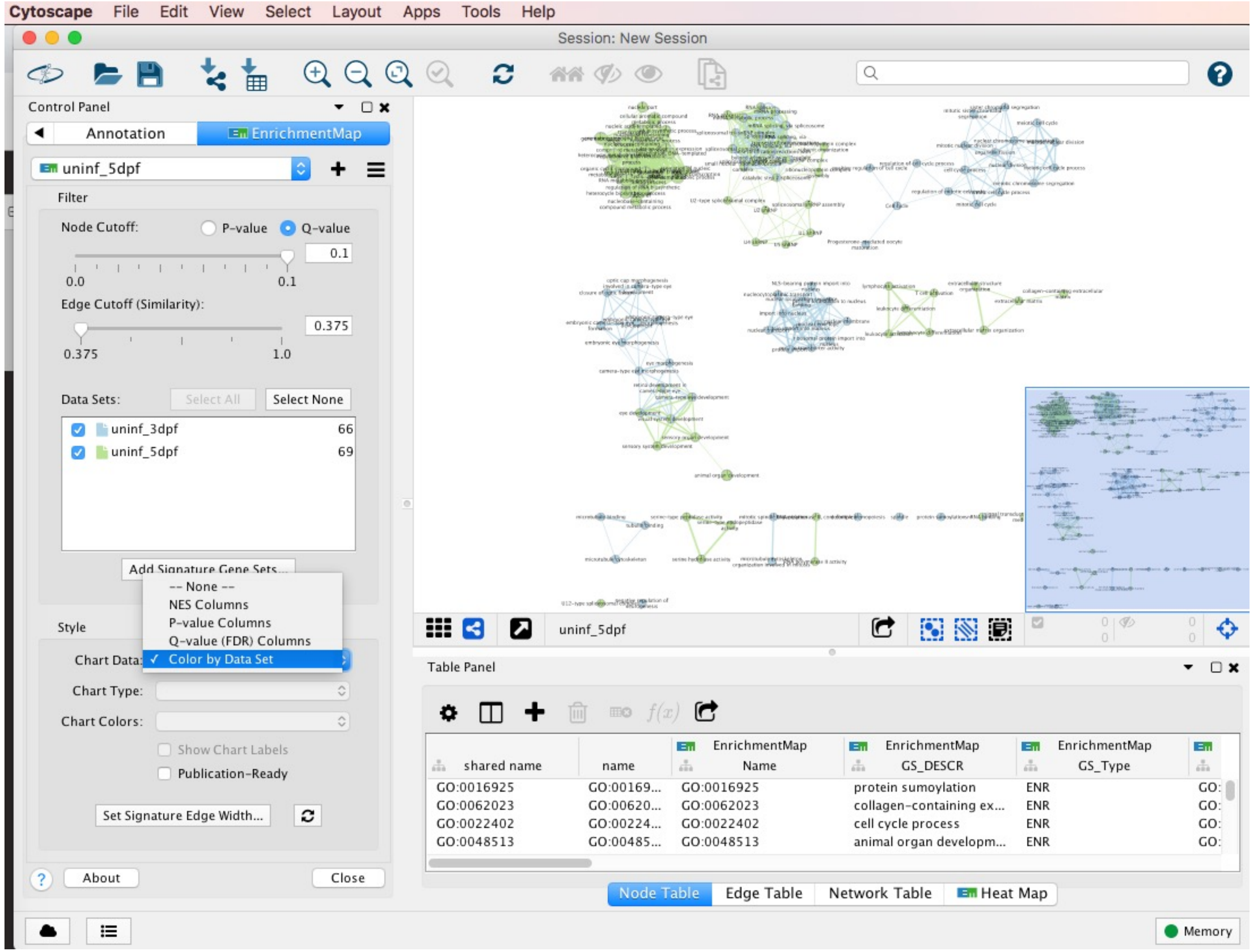
☐ Show Chart Labels

☐ Publication-Ready

uninf_5dpf

shared name	name	EnrichmentMap Name	EnrichmentMap GS_DESCR	EnrichmentMap GS_Type	
GO:0016925	GO:00169...	GO:0016925	protein sumoylation	ENR	GO:
GO:0062023	GO:00620...	GO:0062023	collagen-containing ex...	ENR	GO:
GO:0022402	GO:00224...	GO:0022402	cell cycle process	ENR	GO:
GO:0048513	GO:00485...	GO:0048513	animal organ developm...	ENR	GO:

Enrichment Map



uninf_5dpf

Node Cutoff: ○ P-value ● Q-value 0.1

0.0 0.1

Edge Cutoff (Similarity): 0.375

0.375 1.0

Data Sets: Select All Select None

☑	uninf_3dpf	66
☑	uninf_5dpf	69

Chart Data: ✓ Color by Data Set

Chart Type:

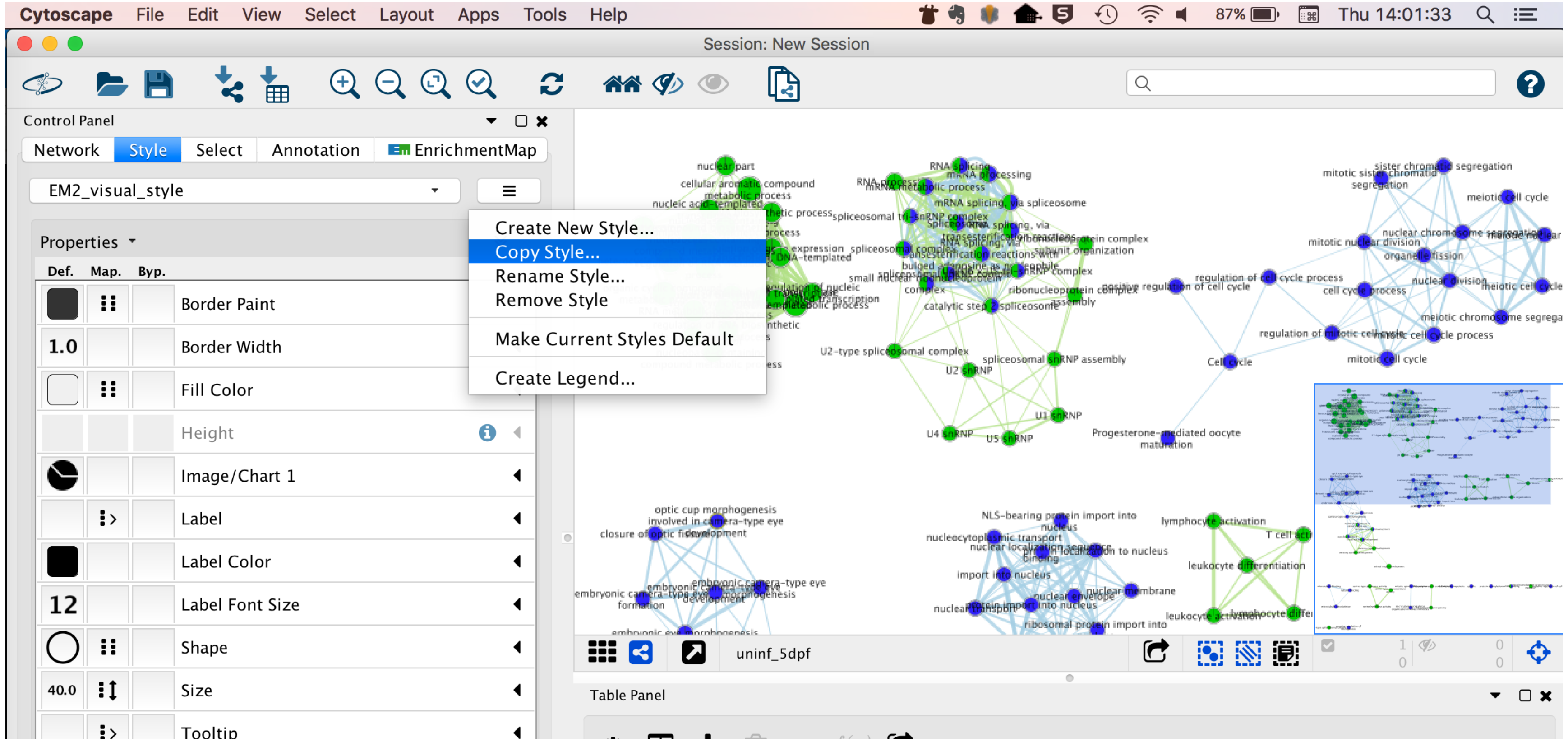
Chart Colors:

☐ Show Chart Labels

☐ Publication-Ready

shared name	name	EnrichmentMap Name	EnrichmentMap GS_DESCR	EnrichmentMap GS_Type	
GO:0016925	GO:00169...	GO:0016925	protein sumoylation	ENR	GO:
GO:0062023	GO:00620...	GO:0062023	collagen-containing ex...	ENR	GO:
GO:0022402	GO:00224...	GO:0022402	cell cycle process	ENR	GO:
GO:0048513	GO:00485...	GO:0048513	animal organ developm...	ENR	GO:

Enrichment Map



EM2_visual_style

Def.	Map.	Byp.	
■	⠿		Border Paint
1.0			Border Width
□	⠿		Fill Color
			Height
◕			Image/Chart 1
	⠿>		Label
■			Label Color
12			Label Font Size
○	⠿		Shape
40.0	⠿↕		Size
	⠿>		Tooltip