



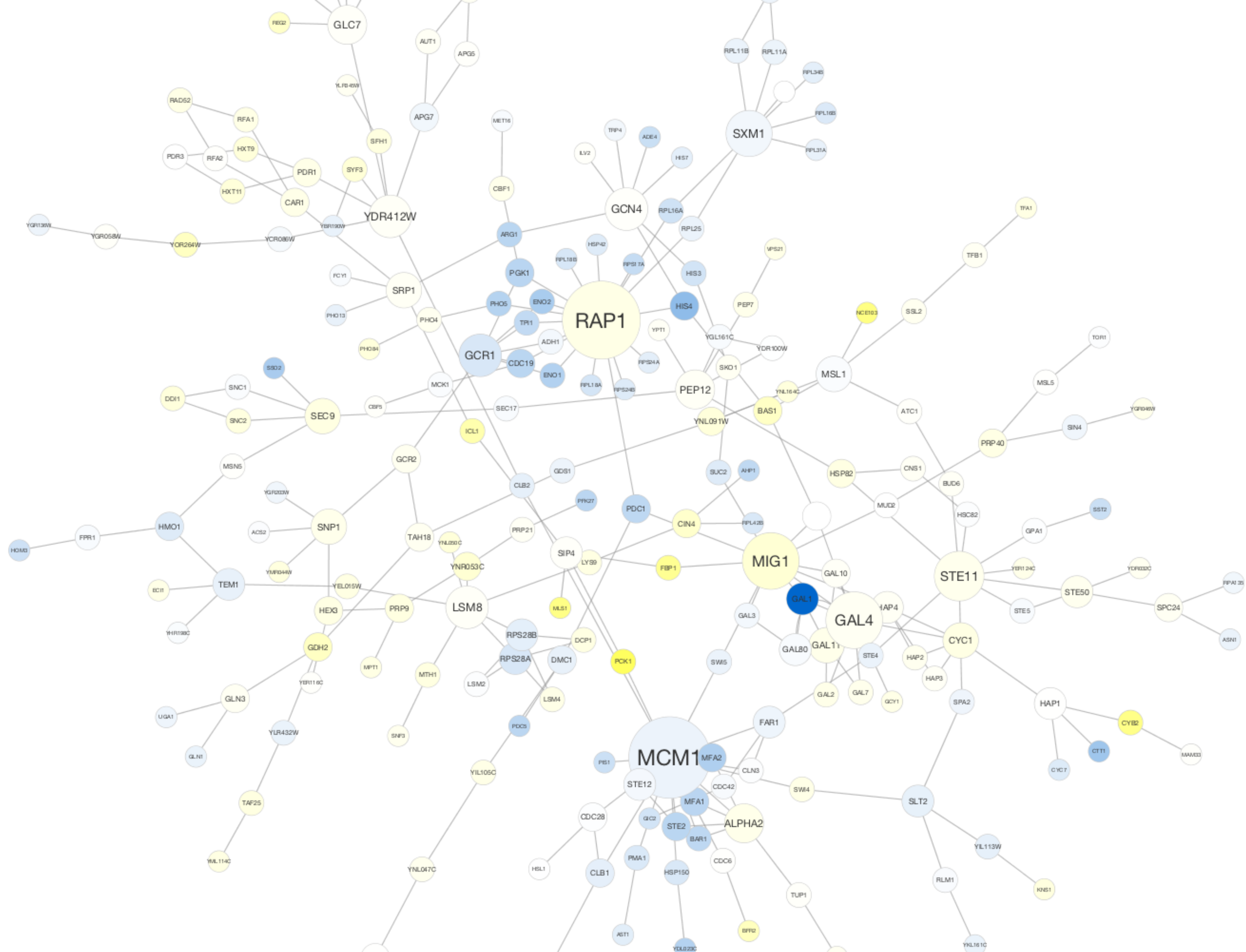
**Weill Cornell Medicine**

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Biomedical Information Center

# Cytoscape for Analysis and Visualization of Gene Networks

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B I O - I N F O R M A T I C S  
S E R V I C E - - - - -



[cytoscape.org](http://cytoscape.org)

## Requirements

Mac OS X, Windows (64 bit), Linux  
Java 8



# Built-in functions

## Network analysis

Node count  
Density  
Heterogeneity  
Path length  
Node degree

## ID mapping

HGNC  
Ensemble  
Entrez Gene  
KEGG  
miRBase  
Unigene  
Uniprot - TrEMBL

## Merging

Networks  
Tables (eg. Node info)

## Complex selection

Filter on columns,  
or network properties  
  
Chain filters together

# All visual aspects of a network can be mapped to values of the nodes or edges

galFiltered Style

Properties

Def.	Map.	Byp.	
			Border Paint
2.0			Border Width
			Fill Color

Column: gal1RGexp

Mapping Type: Continuous Mapping

Current Mapping:

Height:

Image/Chart 1:

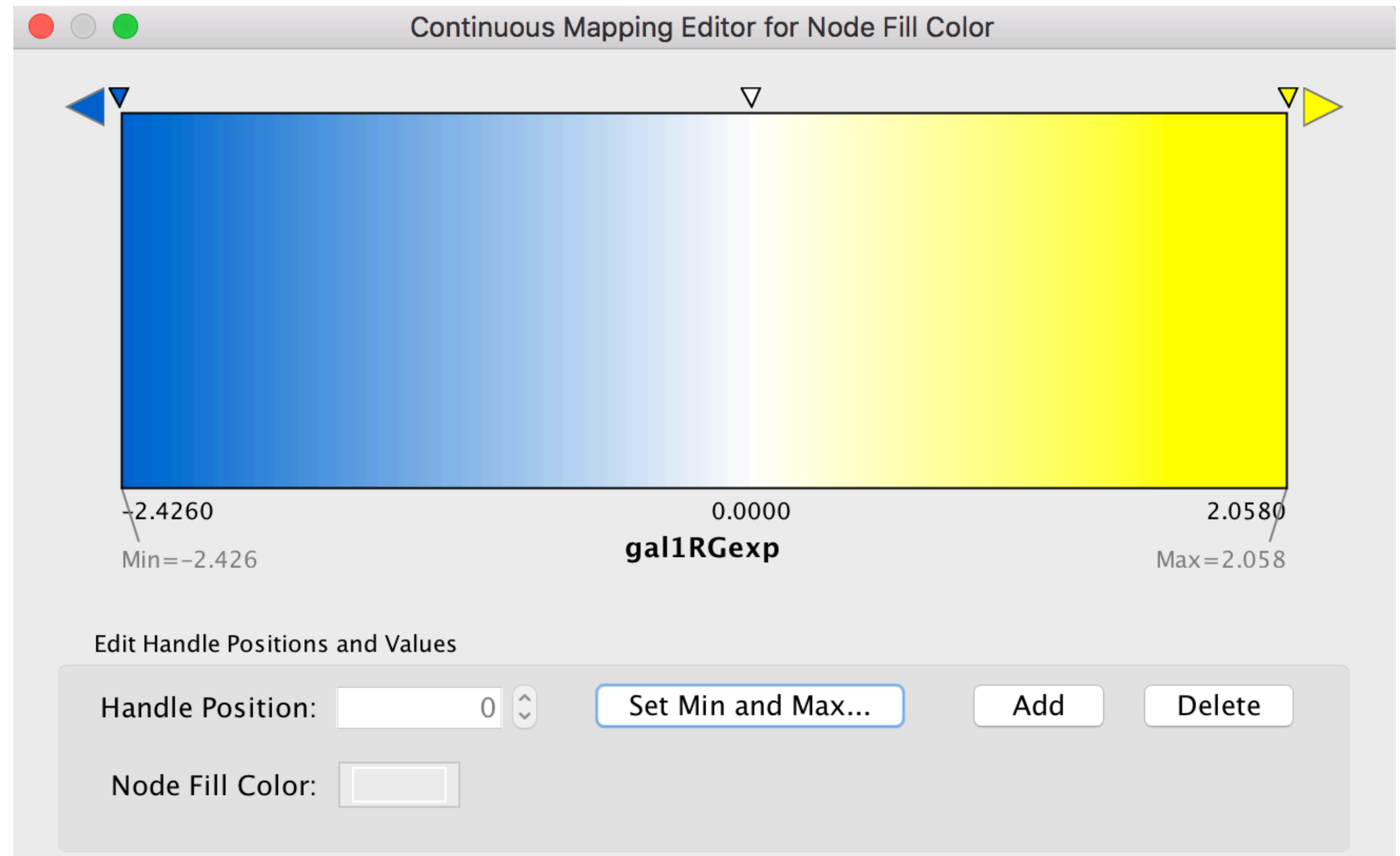
Label:

Label Color:

Label Font Size: 12

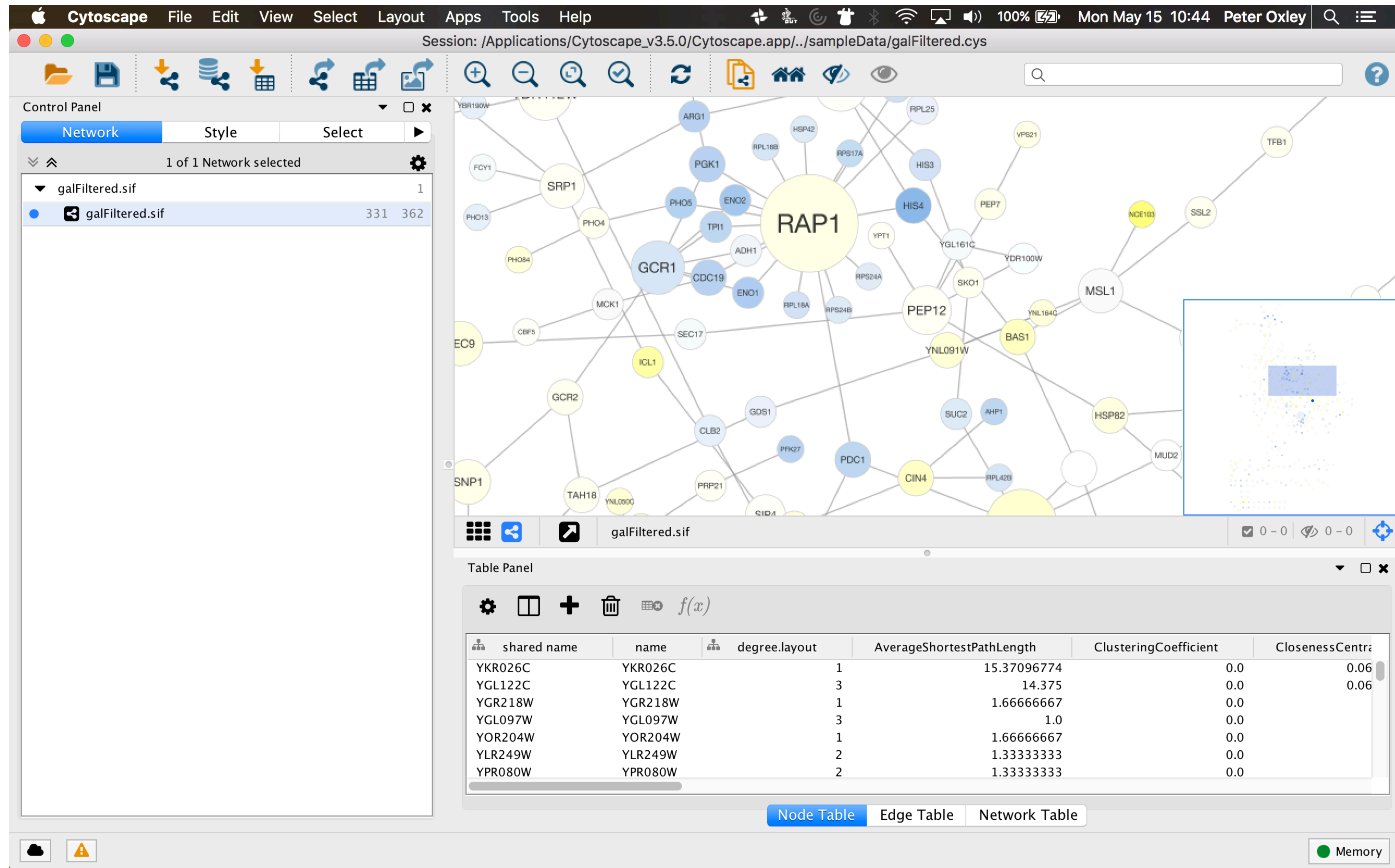
Shape:

Node Edge Network





# Cytoscape layout



# Network and expression data can be merged and displayed

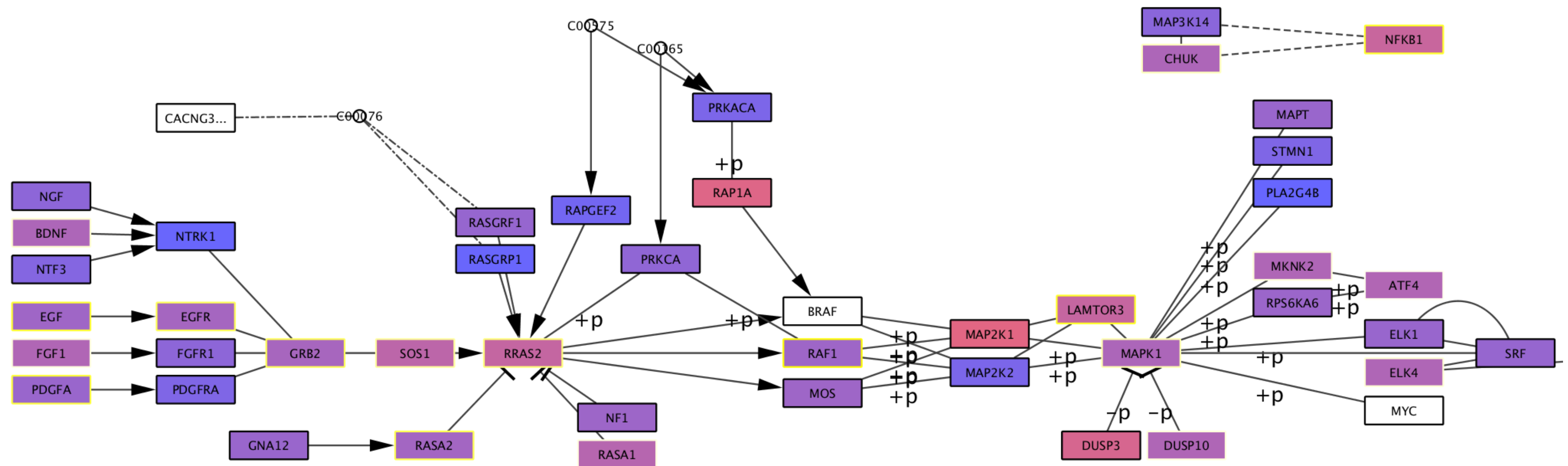
Download network data (eg, KEGG pathway)

Download gene data (eg. gene expression fold change)

Map gene ids to each other

Merge tables on gene ids

Visualize gene expression differences



# Gene enrichment tools allow easy analysis and visualization

GO over-representation analysis directly from network  
Results can be overlayed on existing network  
Relationships between GO terms can also be viewed

