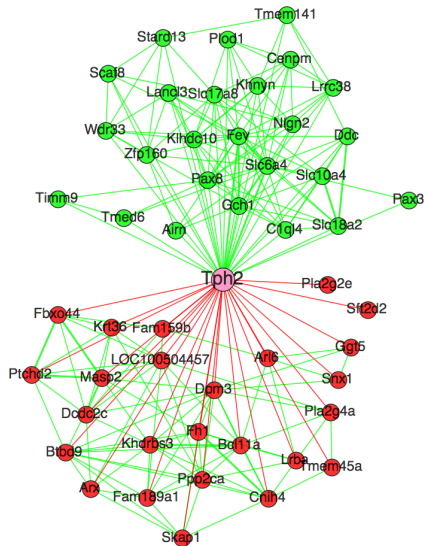


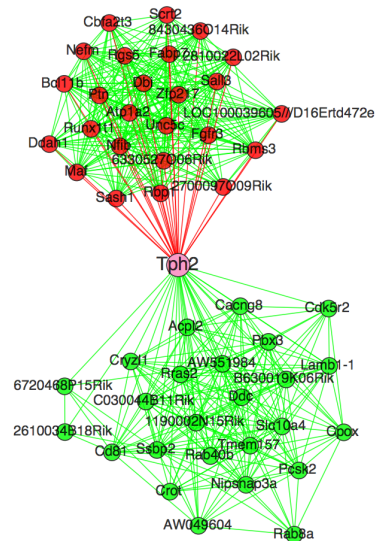
Introduction to Gene2Net (<http://contegene2net.zhang-lab.org>)

Gene2Net is a web application that expands a gene of interest into a gene co-expression network based on a gene expression data set selected from the underlying database. The current version of Gene2Net includes 16 data sets.

A user may use a probe set ID or a gene symbol as query input. In the latter case, all probe sets corresponding to the gene will be retrieved, and relevant statistics for each probe set including average expression, standard deviation (SD), and interquartile range (IQR) will be presented. Typically, the probe set with higher average expression or larger expression variation (SD or IQR) can be selected to represent the gene. For the selected probe set, the top n probe sets with the strongest positive and negative correlation in the data set will be identified respectively and reported in a table. Pair-wise correlation is computed by the Spearman's correlation coefficient. The default value of n is 25, which can be adjusted by the user between 1 and 100. Based on the table, Gene2Net creates a network in which each node represents a probe set in the table, and two nodes are connected by an edge if their correlation is above a user defined threshold r . In the network diagrams, green and red nodes/edges denote positive and negative correlations, respectively. The default value of r is 0.5, which can be adjusted by the user between 0 and 1. Both the correlation table and the network can be downloaded. Using Tph2 as an example, the networks constructed based on the two data sets are shown below.



Tph2 network I
BXD_male_midbrain_microarray, $n=25$, $r=0.5$



Tph2 network II
Serotonin_neuron_e14_microarray, $n=25$, $r=0.9$