### Supplemental Data File 4:

Genes Regulated by Caloric Restriction Have Unique Roles within Transcriptional Networks

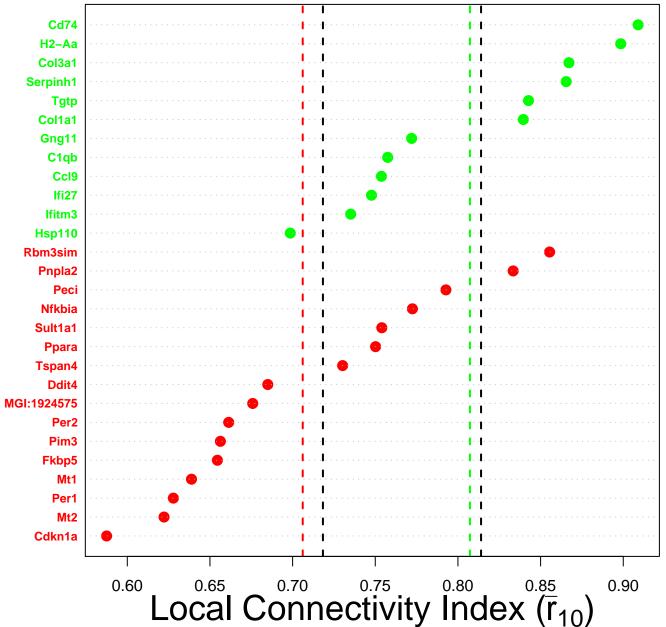
William R. Swindell

University of Michigan, Departments of Pathology and Geriatrics

This file shows plots of the local connectivity index for CR-regulated genes with respect to each of four independent datasets (Tissue, Developmental, Treatment and Mutation Series). The local connectivity index is directly related to the density of the local region immediately surrounding a given gene within the transcriptional network. Green symbols correspond to genes downregulated by CR, while red symbols correspond to genes upregulated by CR. The dashed green line represents the average local connectivity index among the n = 12 CR-downregulated genes, while the dashed red line represents the average local connectivity index among the n = 16 CR-upregulated genes. Dashed black lines were generated by sampling n transcripts at random and calculating the average local connectivity index within each sample. Among 10,000 simulations, 95% of trials yielded an average local connectivity index within the range indicated by the dashed black lines (see Figure 3).

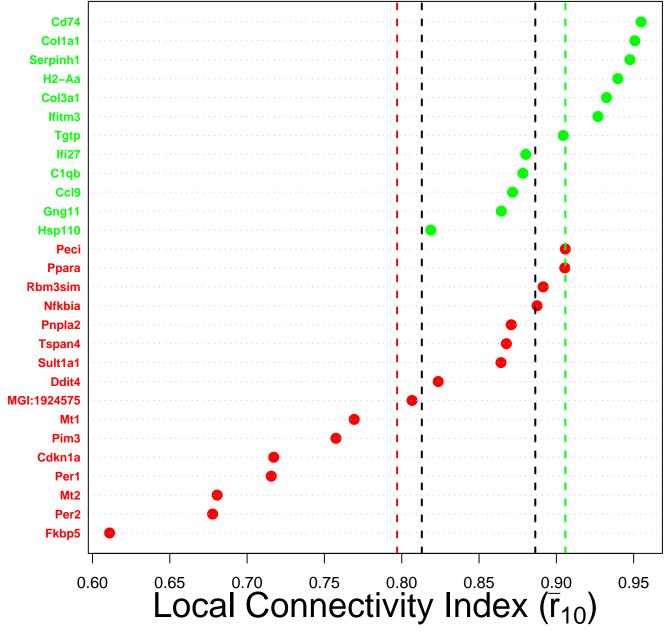
Contact: William R. Swindell, wswindel@umich.edu

## **Tissue Series**



#### **Developmental Series Cd74** H2-Aa Col3a1 Serpinh1 Gng11 **Tgtp** Col1a1 **Hsp110** C1qb Ccl9 lfi27 Ifitm3 Pnpla2 **Ppara** Per2 Rbm3sim Ddit4 Nfkbia Peci Mt2 Mt1 Sult1a1 Tspan4 Fkbp5 Per1 Pim3 MGI:1924575 Cdkn1a 0.65 0.70 0.75 0.80 0.85 Local Connectivity Index (r<sub>10</sub>)

# **Treatment Series**



#### **Mutation Series Cd74** H2-Aa Col3a1 C1qb Serpinh1 Ifi27 Col1a1 **Tgtp** lfitm3 **Hsp110** Gng11 Ccl9 Pnpla2 Sult1a1 Rbm3sim **Ppara** Nfkbia Tspan4 Mt1 MGI:1924575 **Peci** Fkbp5 Mt2 Per1 Cdkn1a Pim3 Per2 Ddit4 0.65 0.70 0.75 0.80 0.85 0.90

Local Connectivity Index  $(\bar{r}_{10})$