Supplemental Data File 2:

Genes Regulated by Caloric Restriction Have Unique Roles within Transcriptional Networks

William R. Swindell University of Michigan, Departments of Pathology and Geriatrics

This file displays dendrograms obtained by clustering CR-regulated genes with respect to the tissue series, developmental series, treatment series and mutation series. Hierarchical clustering was performed using the average linkage method, with distance among expression profiles based upon absolute pearson correlation. Labels of transcripts upregulated by CR are displayed in red, while labels of transcripts downregulated by CR are displayed in green. The horizontal axis below each dendrogram indicates the average distance at which two clusters (or transcripts) were joined. The dashed vertical line indicates the lowest distance expected to arise by chance between any two transcripts (given the total number of transcripts clustered in each dendrogram).

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







