

# Supplemental Data File 6:

## Genes Regulated by Caloric Restriction Have Unique Roles within Transcriptional Networks

*William R. Swindell*

*University of Michigan, Departments of Pathology and Geriatrics*

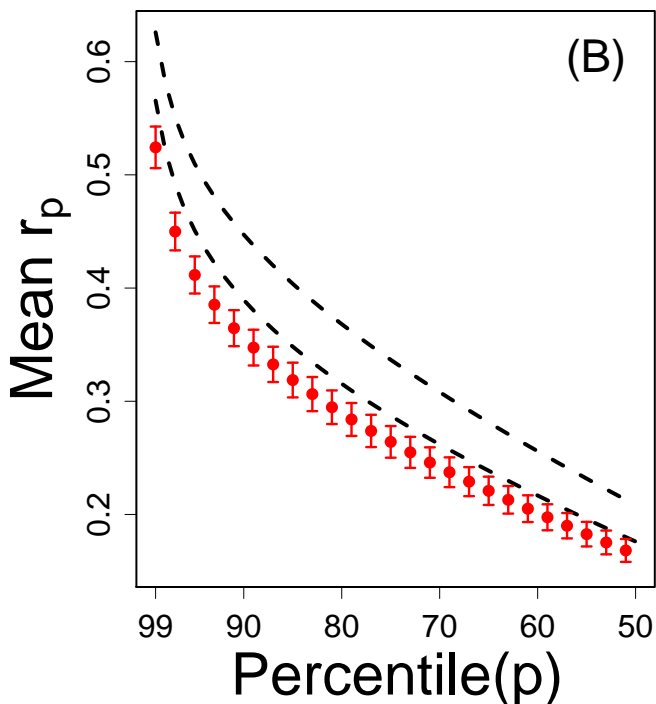
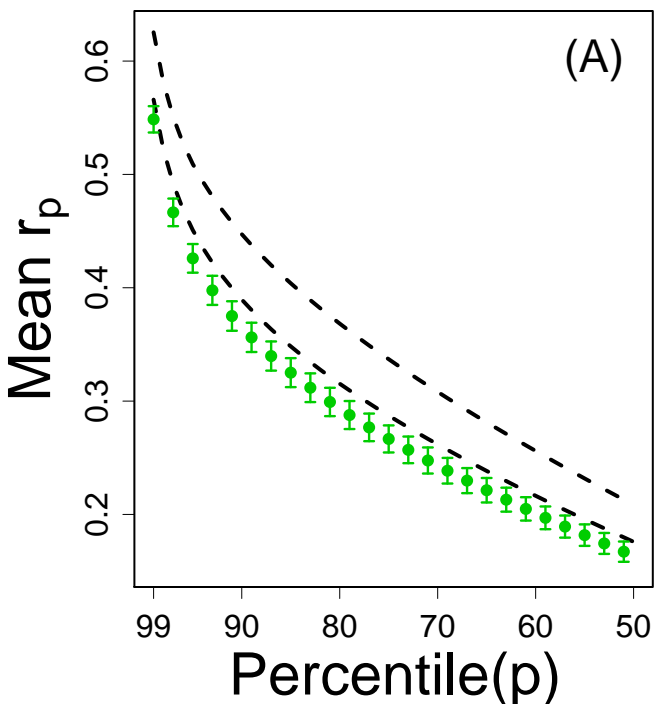
-----

This file shows plots of correlation percentiles for CR-regulated genes, with respect to each of the four mouse expression profiling datasets considered in this study (see Figure 7). In each plot, the vertical axis represents the average pth correlation percentile among  $n$  genes, and the horizontal axis corresponds to  $p$ . For a given gene, correlations with all other transcripts on the Affymetrix Mouse 430 2.0 array were determined, and the pth correlation percentile is the correlation value that is larger than  $p$  percent of these correlations. Genes that have strong “distant” connections should have large correlation percentiles. In part (A), green points represent the average pth correlation percentile among the  $n = 12$  CR-downregulated genes. In part (B), red points represent the average pth correlation percentile among the  $n = 16$  CR-upregulated genes. In both (A) and (B), dashed black lines outline a 95% confidence region for the average pth correlation percentile among  $n$  genes sampled at random (based upon simulation). In 95% of 10,000 simulation trials, random samples of  $n$  genes from the Affymetrix Mouse 430 2.0 array yielded an average pth correlation percentile within the dashed lines.

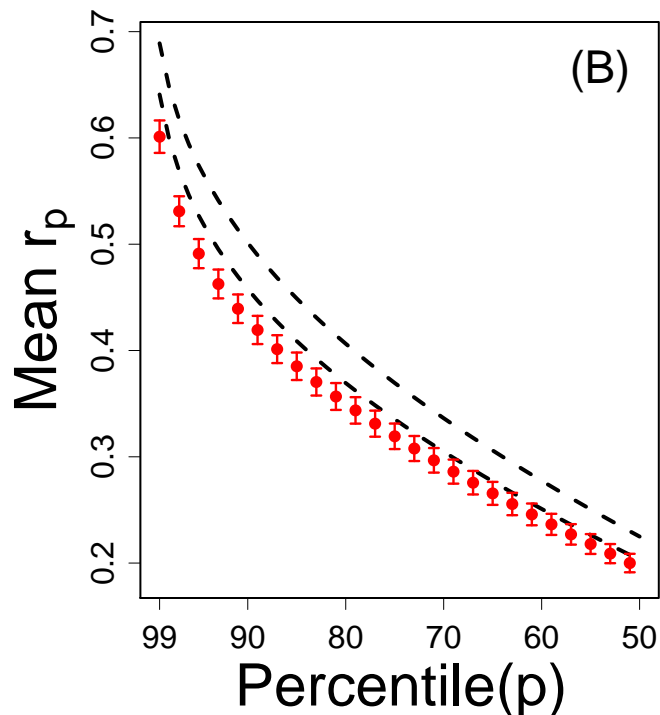
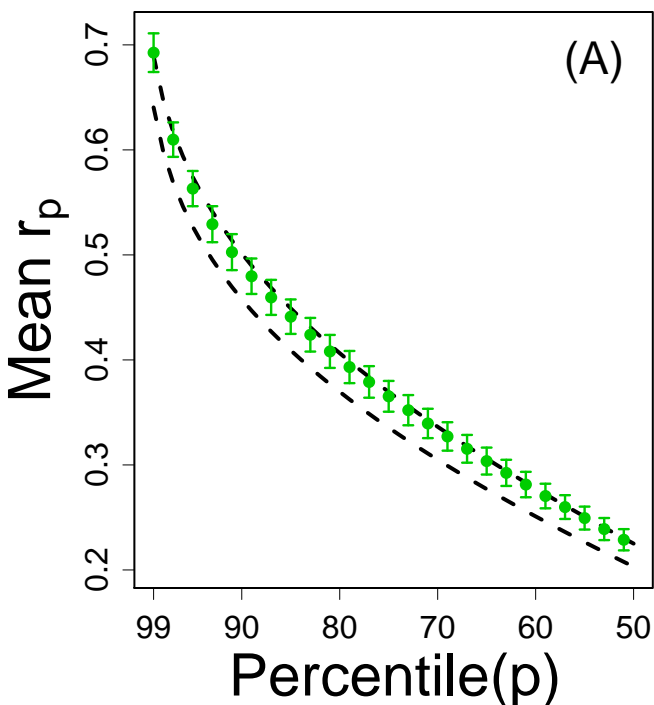
-----

Contact: William R. Swindell, [wswindel@umich.edu](mailto:wswindel@umich.edu)

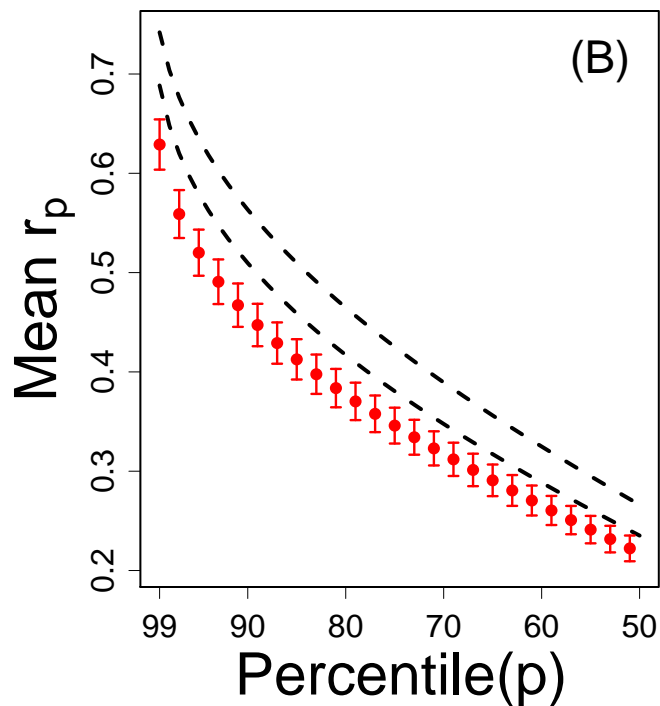
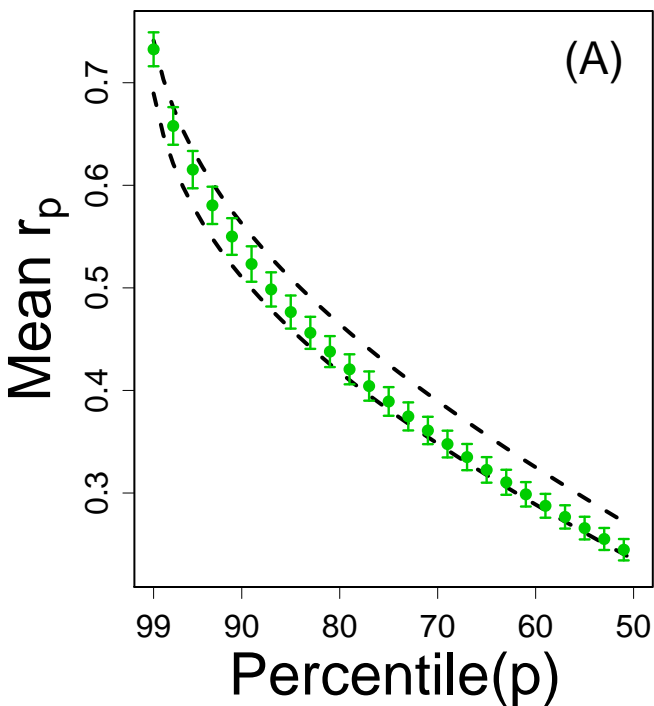
# Tissue Series



# Developmental Series



# Treatment Series



# Mutation Series

