

# Supplemental Data File 9:

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

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This file provides analyses of the connectivity patterns of CR-regulated and dauer-regulated genes from invertebrate models (see Figure 8). On page 2, results are shown based upon the *Drosophila* and *Caenorhabditis elegans* Series A datasets. On page 3, results are shown based upon the *Drosophila* and *Caenorhabditis elegans* Series B datasets. On each page, parts (A) and (B) show mean correlation order statistics for *Drosophila* CR-downregulated and CR-upregulated genes, respectively, based upon microarray data from Pletcher et al. (2001). Parts (C) and (D) show mean correlation order statistics for CR-downregulated and CR-upregulated genes, respectively, based upon microarray data from Szewczyk et al. (2006). Parts (E) and (F) show mean correlation order statistics for *C. elegans* nondauer-specific and dauer-specific, respectively, based upon microarray data from Jones et al. (2001) and Wang and Kim (2003). In each plot, the vertical axis represents the average  $k$ th correlation order statistic (among  $n$  transcripts) and the horizontal axis corresponds to  $k$ . Dashed black lines outline a 95% confidence region for the average  $k$ th correlation order statistic among  $n$  transcripts sampled at random (based upon simulation).

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