Supplemental Data File 5:

Genes Regulated by Caloric Restriction Have Unique Roles within Transcriptional Networks

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This file shows plots of correlation order statistics for CR−regulated genes, with respect to each of the four mouse profiling datasets examined in this study (see Figure 4). In each plot, the vertical axis represents the average kth correlation order statistic (among n genes) and the horizontal axis corresponds to k. For a given gene, the kth correlation order statistic equals the kth largest correlation between that gene and all other transcripts represented on the Affymetrix Mouse 430 2.0 microarray. Highly connected genes should have a large correlation order statistic for a given value of k. In part (A), green points represent the average kth correlation order statistic among the n = 12 CR−downregulated genes. In part (B), red points represent the average kth correlation order statistic among the n = 16 CR−upregulated genes. In both (A) and (B), dashed black lines outline a 95% confidence region for the average kth correlation order statistic 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 kth correlation order statistic within the dashed lines.

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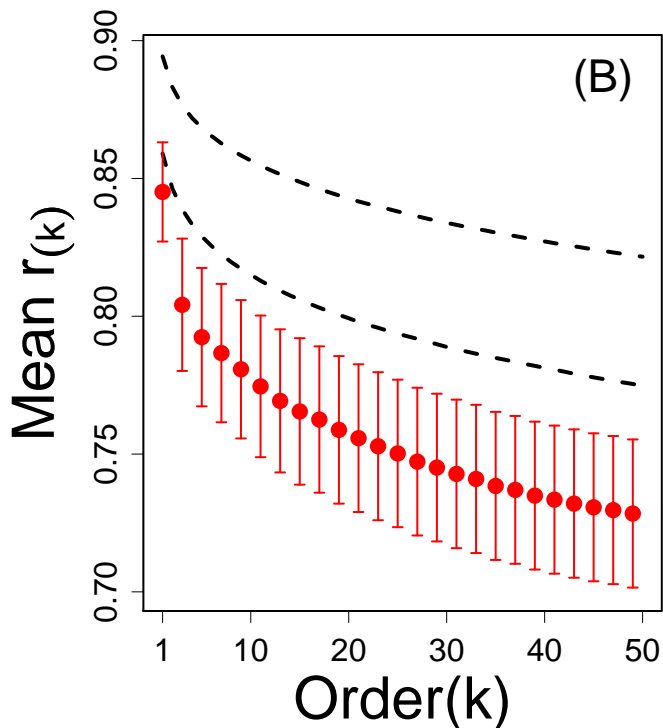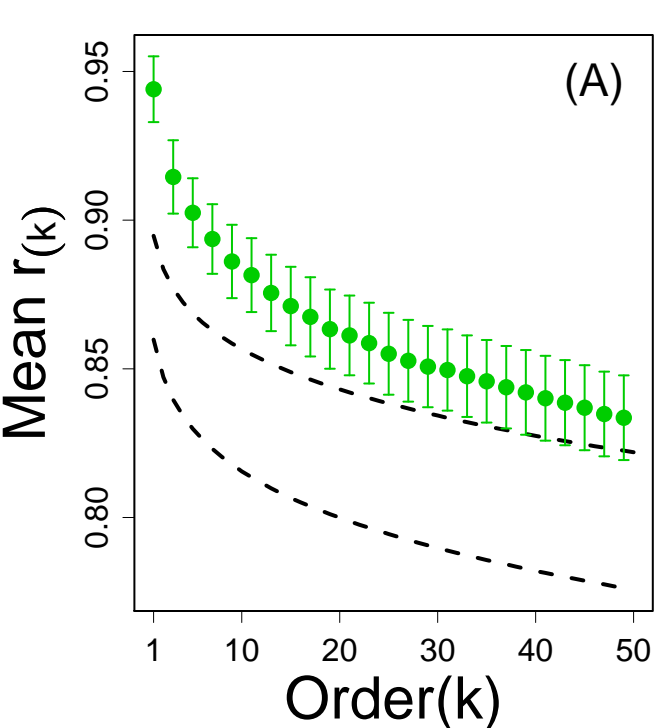
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Tissue Series
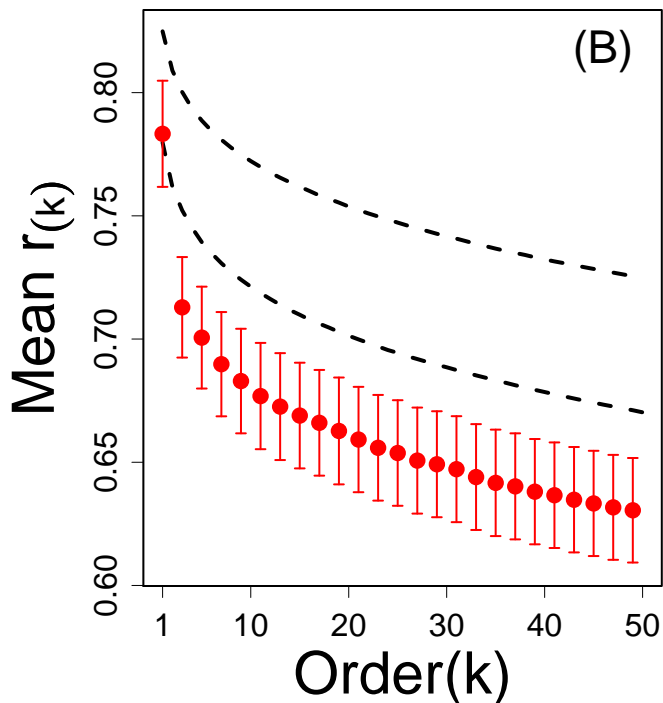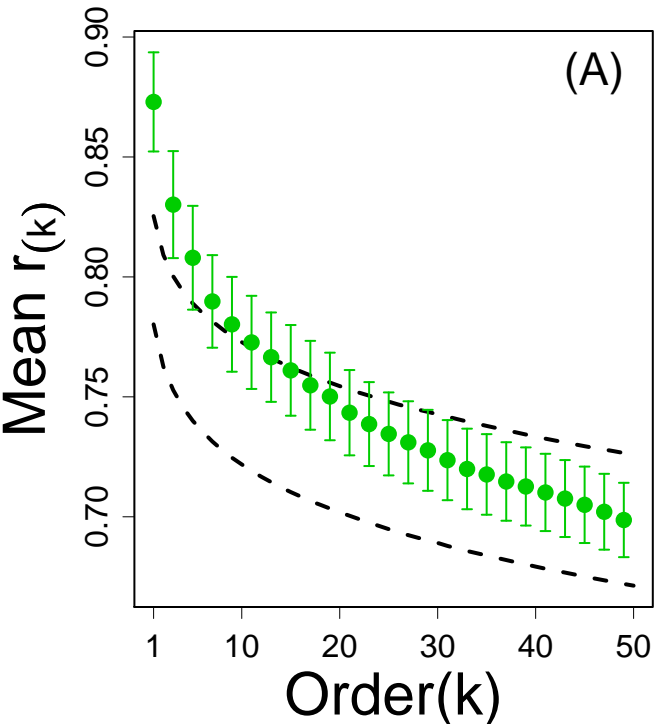
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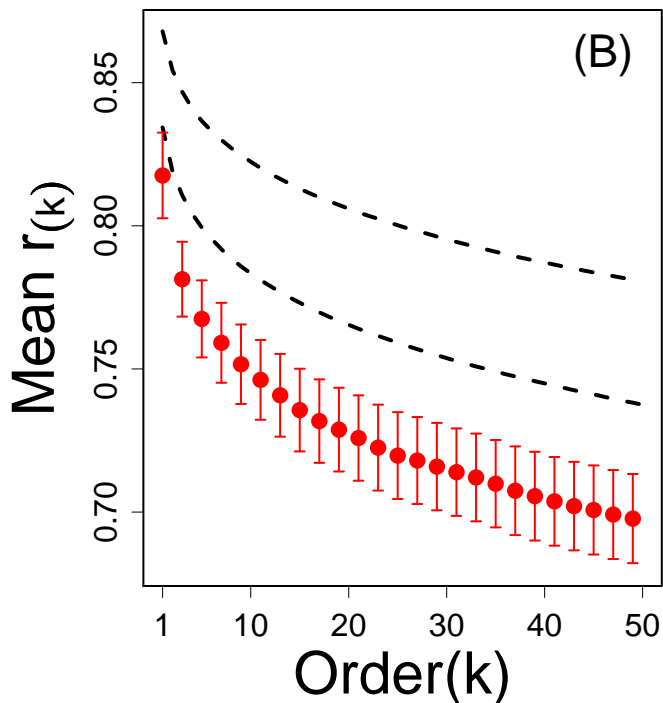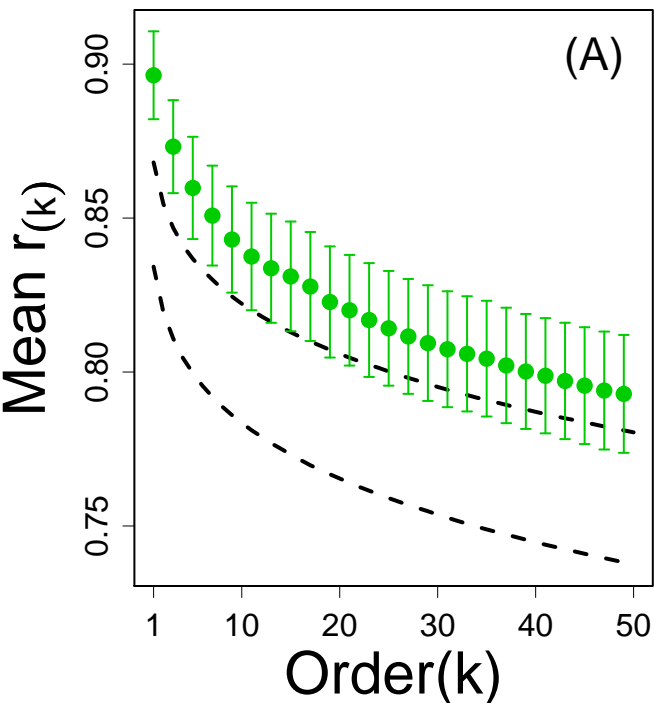
Treatment Series

Mutation Series