

Supplemental Data File 7:

Genes Regulated by Caloric Restriction Have Unique Roles within Transcriptional Networks

William R. Swindell

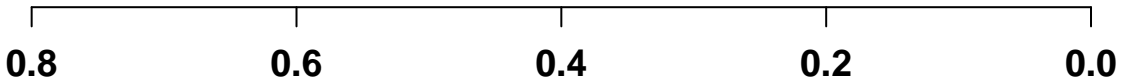
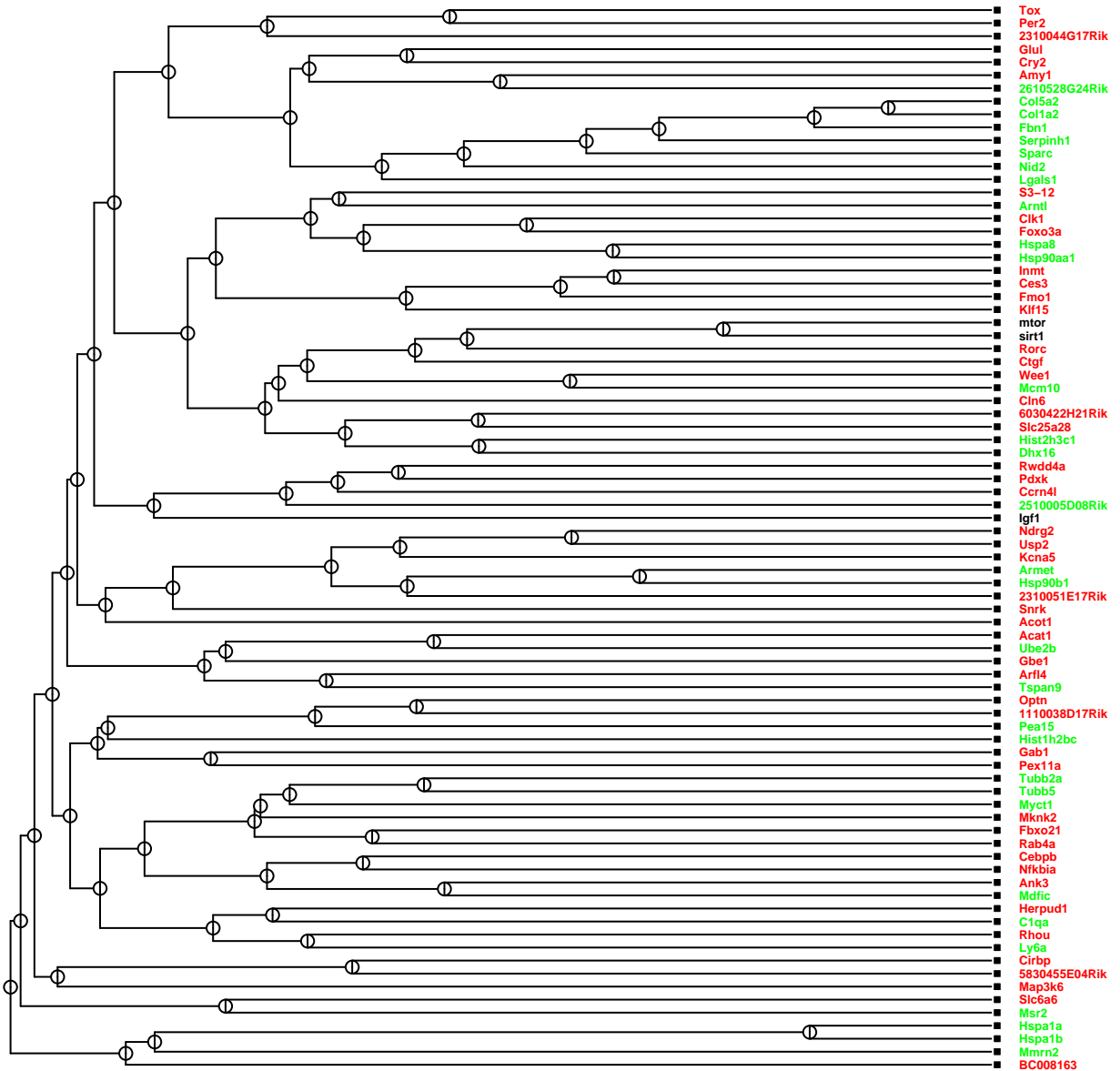
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This file provides analyses of 79 genes that were upregulated or downregulated by CR with respect to four different types of tissues. All other analyses focus on genes upregulated or downregulated by CR with respect to five or more tissues. An overall cluster analysis of the 79 genes is provided in Section 1 (pgs 2–3). Section 2 provides an analysis of the local connectivity properties of the 79 genes (pgs 4–8). Section 3 provides an analysis of the non–local connectivity properties of the 79 genes (pgs 9–13). The 79 genes analysed in this file correspond to 83 transcripts represented on the Affymetrix Mouse 430 2.0 microarray

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Section I: Cluster Analysis

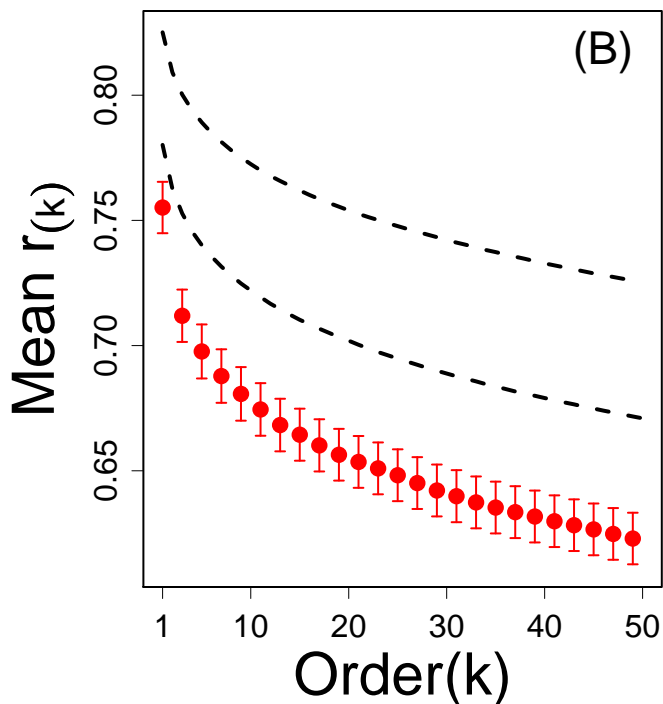
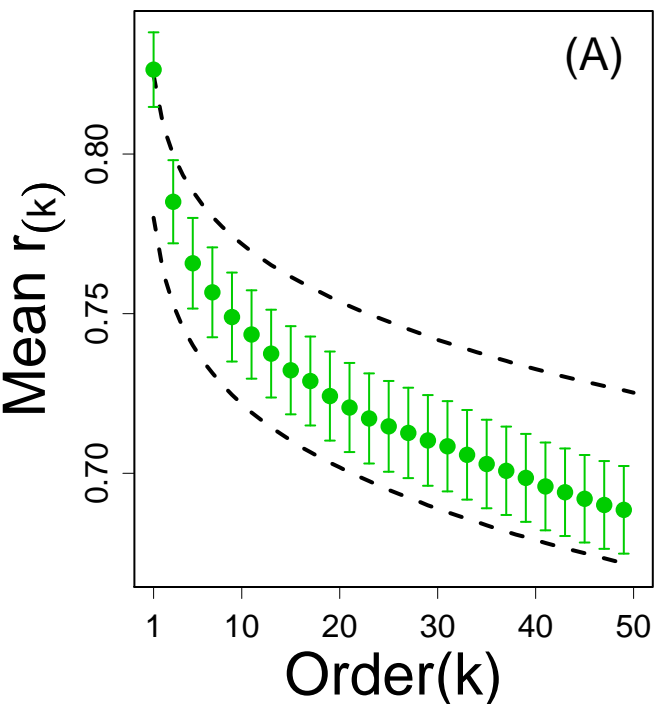
The next page shows a dendrogram generated by clustering of the 78 genes upregulated or downregulated by CR across four tissue types. Hierarchical clustering was performed using the average linkage method, with distance among expression profiles based upon absolute pearson correlation. To generate distance matrices upon which clustering was based, absolute pearson correlations were averaged across the four independent datasets analysed in this study (Tissue, Developmental, Treatment and Mutation Series). 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. For genes represented by more than one of the 83 CR-associated transcripts, expression values were averaged among transcripts prior to cluster analysis. To magnify the image, use the 'zoom' option under the 'view' menu.



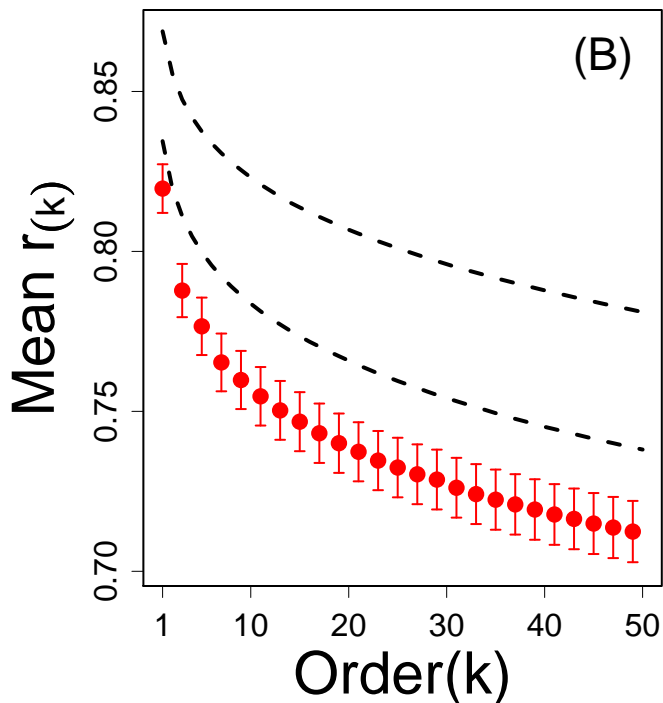
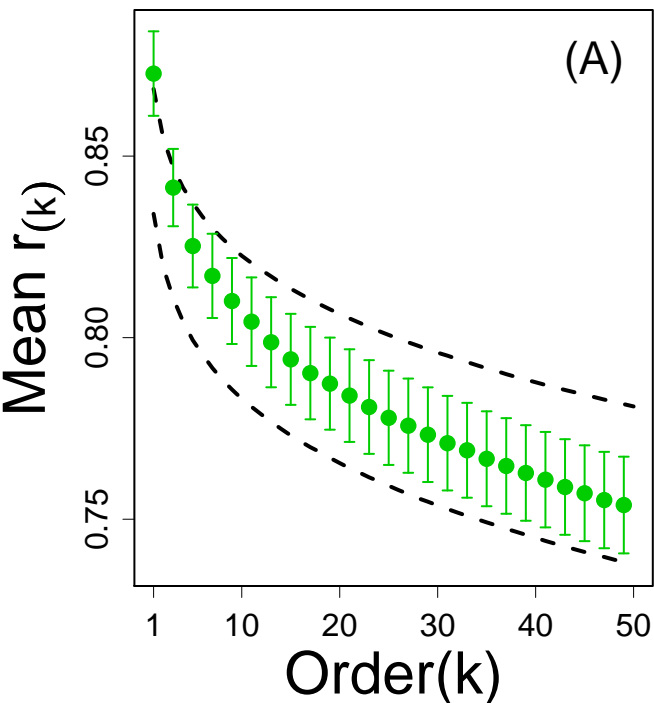
Section II: Local Connectivity

The next pages show plots of correlation order statistics for genes regulated by CR across four tissue types (compare with Figure 4 and Supplemental Data File 5). In each plot, the vertical axis represents the average k th correlation order statistic (among n genes) and the horizontal axis corresponds to k . For a given gene, the k th correlation order statistic equals the k th largest correlation between that gene and all other transcripts represented on the Affymetrix Mouse 430 2.0 microarray. Highly connected genes should have a larger correlation order statistic for a given value of k . In part (A), green points represent the average k th correlation order statistic among the $n = 31$ CR–downregulated genes. In part (B), red points represent the average k th correlation order statistic among the $n = 49$ CR–upregulated genes. In both (A) and (B), dashed black lines outline a 95% confidence interval for the average k th 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 k th correlation order statistic within the dashed lines.

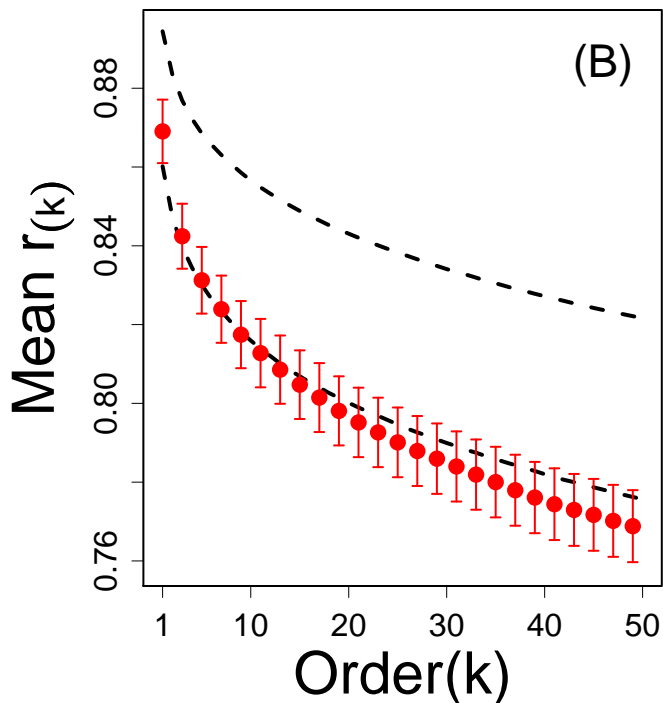
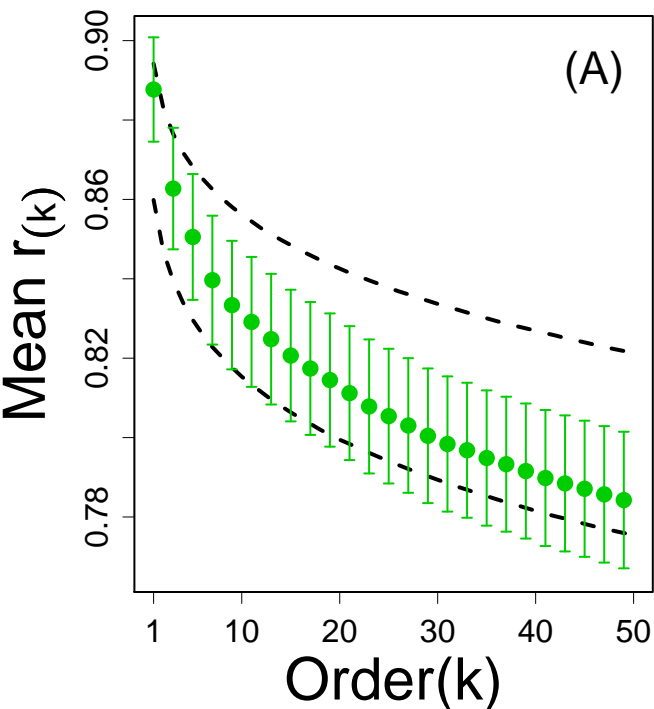
Tissue Series



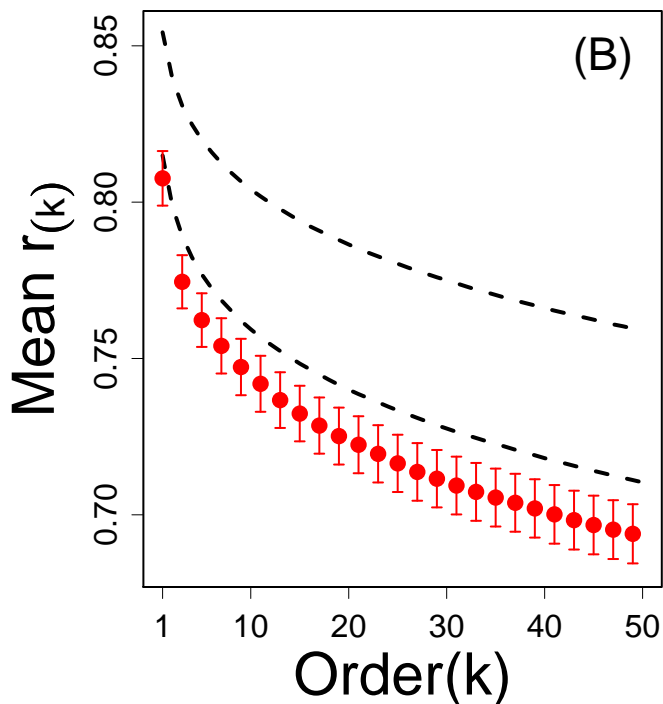
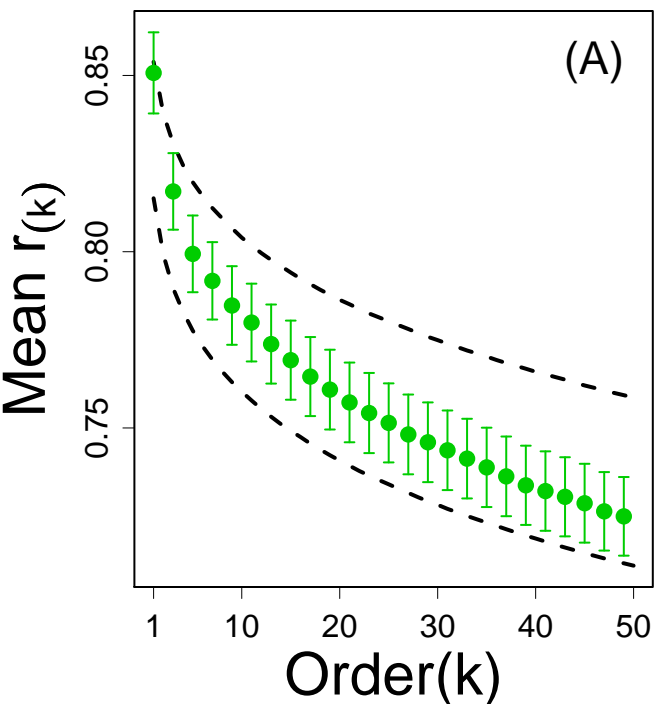
Developmental Series



Treatment Series



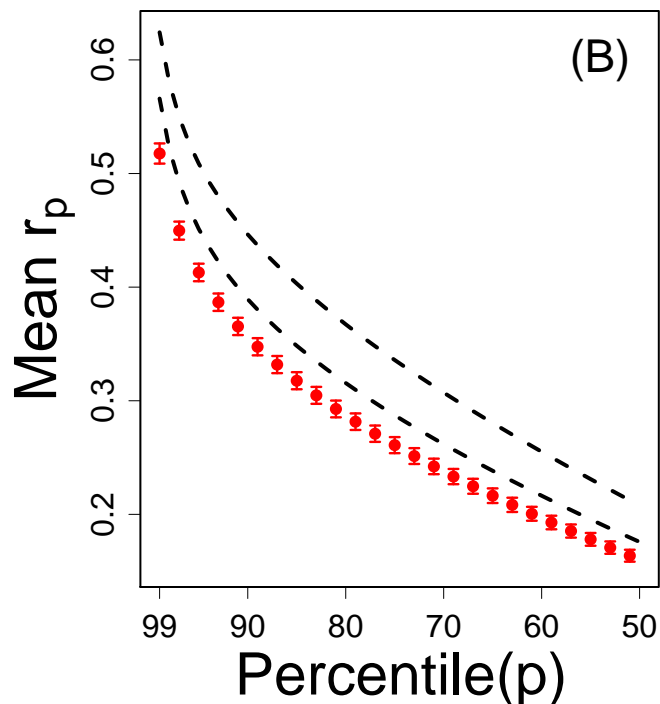
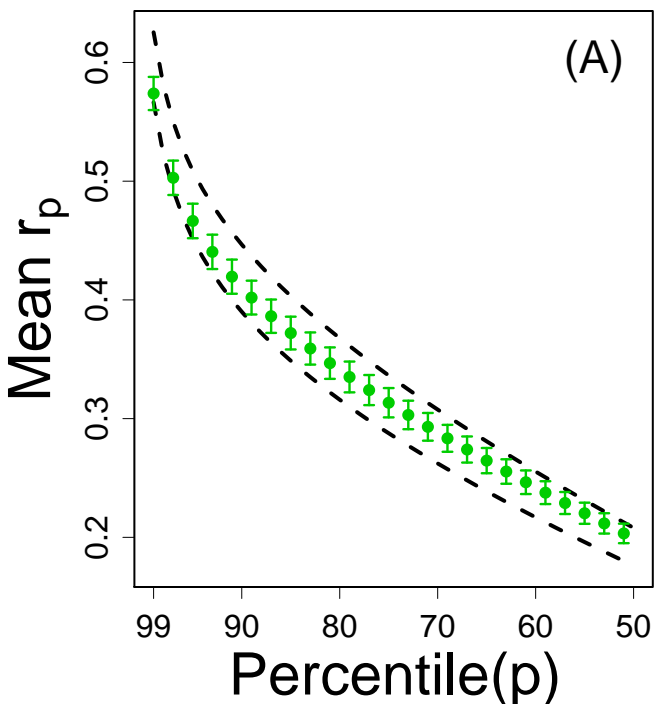
Mutation Series



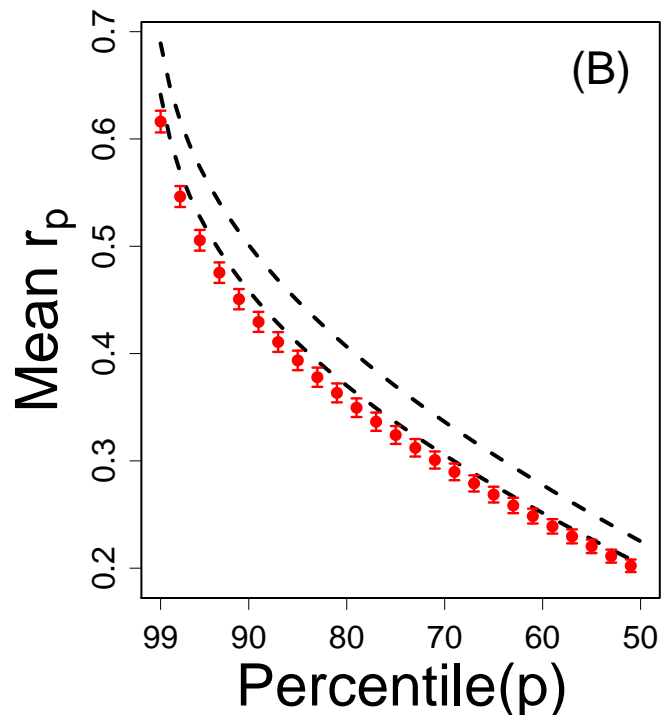
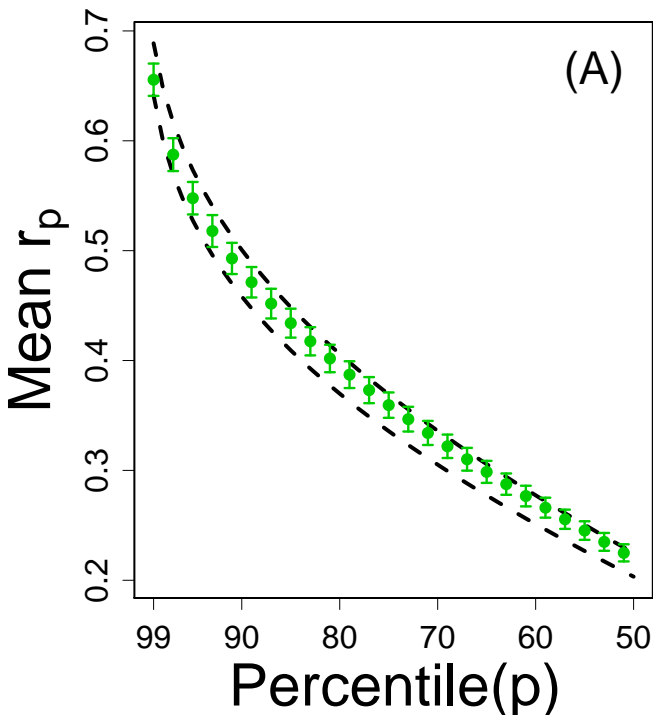
Section III: Non-local Connectivity

The next pages show plots of correlation percentiles for genes regulated by CR across four tissue types (compare with Figure 7 and Supplemental Data File 6). In each plot, the vertical axis represents the average p th 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 p th 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 p th correlation percentile among the $n = 31$ CR-downregulated genes. In part (B), red points represent the average p th correlation percentile among the $n = 49$ CR-upregulated genes. In both (A) and (B), dashed black lines outline a 95% confidence interval for the average p th 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 p th correlation percentile within the dashed lines.

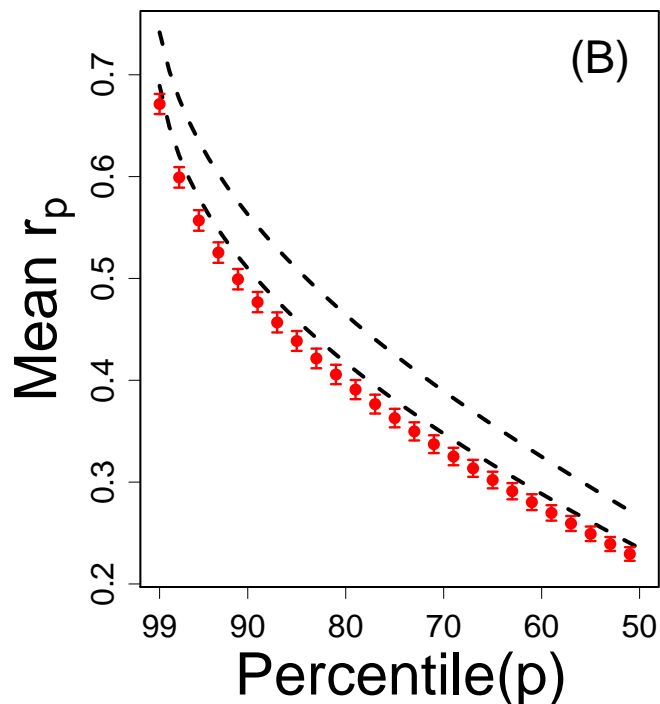
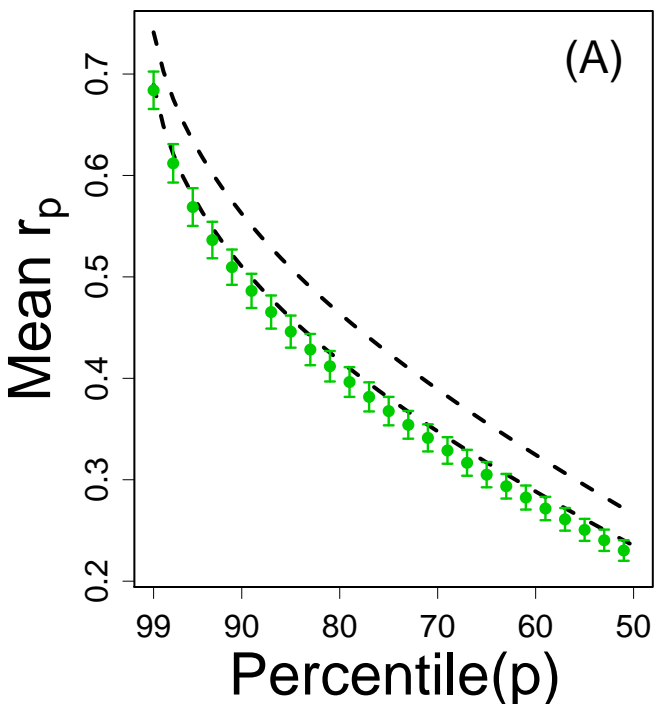
Tissue Series



Developmental Series



Treatment Series



Mutation Series

