Patterns of subnet usage reveal distinct scales of regulation in the transcriptional regulatory network of *Escherichia coli*

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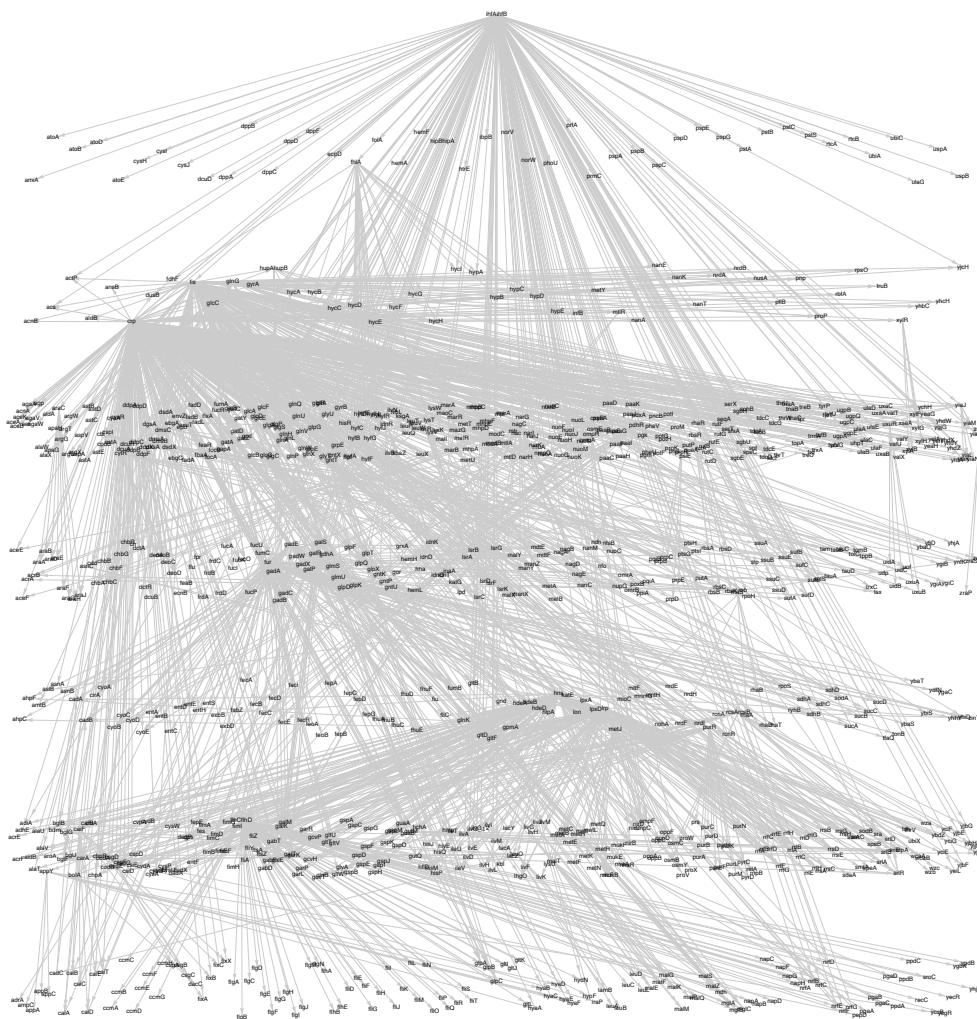
Text S1: Supplementary figures

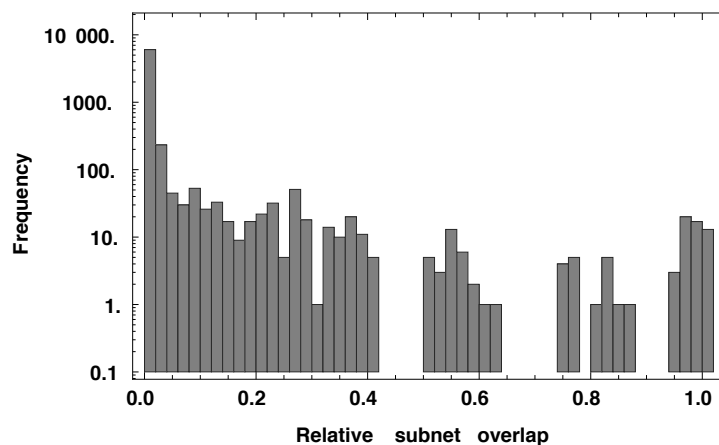**Figure 1. A highly resolved version of the ihfAihfB subnet.**

Figure 2. Histogram of the relative overlap of all pairs of subnets. We plot the frequency distribution of the relative overlap (Intersection/Maximum) calcluated for all $117 \times 116/2$ pairs of subnets. Interestingly, apart from a peak at 0, the subnet overlap is a fairly equally distributed quantity.
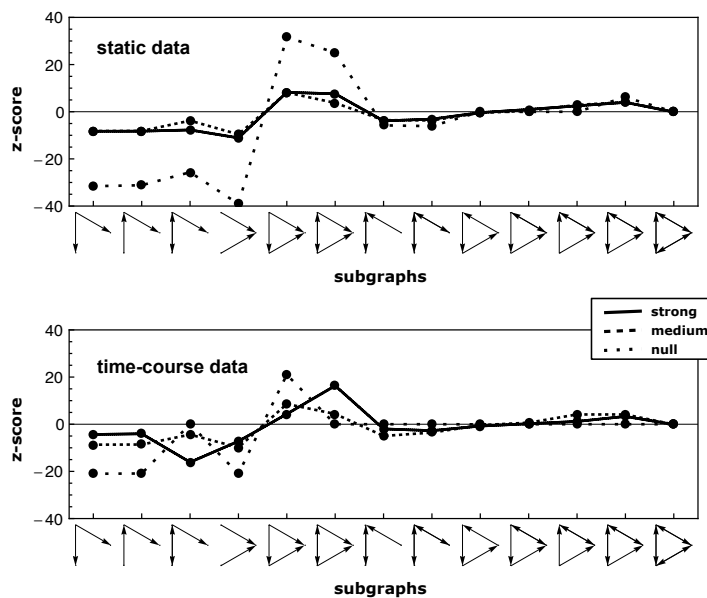

Figure 3. z-score profiles of all 13 possible directed triads. For the two expression data sets (top: static data, bottom: time-course data) we calcluate the z-score profiles for all identified clusters of different subnet usage. In both data sets, we find the feed-forward loop (5th triad) to be overrepresented in the 'null' cluster, in contrast to other cluster.
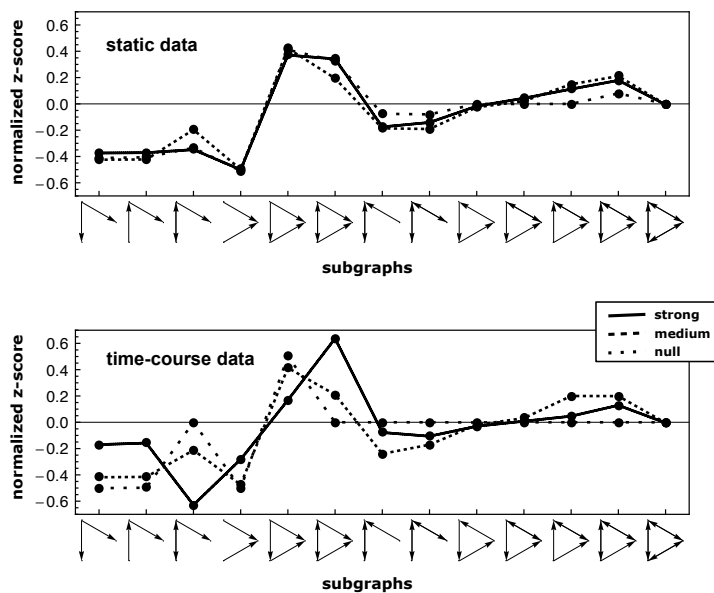
Figure 4. Normalized z-score profiles of all 13 possible directed triads. For the two expression data sets (top: static data, bottom: time-course data) we calcluate the normalized z-score profiles for all identified clusters of different subnet usage. The networks of all cluster show the triad significance profile of bacterial regulatory networks (compare with [12]).
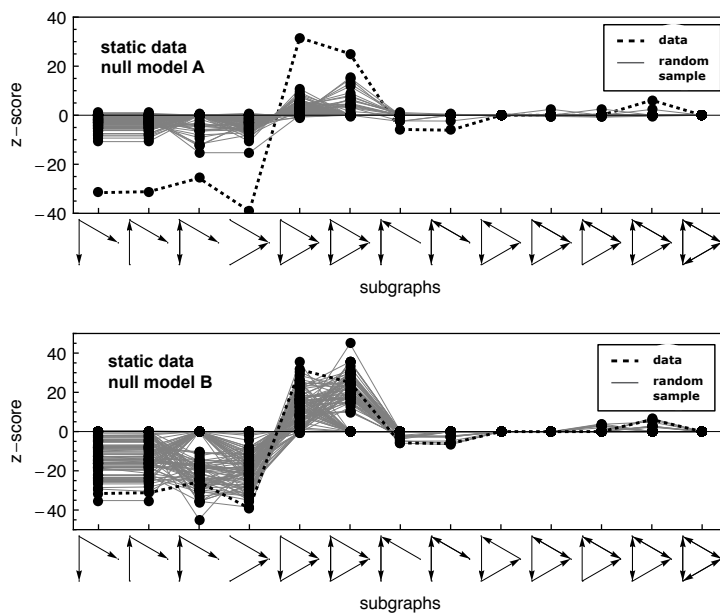

Figure 5. Comparison with null model z-score profiles. For both null models (see main text for details) we find that the feed-forward loop z-score of the 'null' cluster exceeds both null model averages.
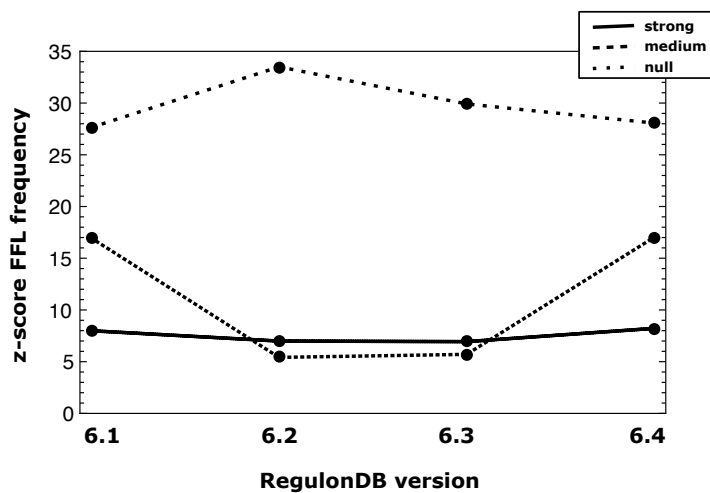
Figure 6. FFL enrichment in the time-course data, using the last four version of RegulonDB (6.1 - 6.4). We find that irrespective of the RegulonDB version used in our analysis, a prominent FFL enrichment in the 'null' cluster appears.
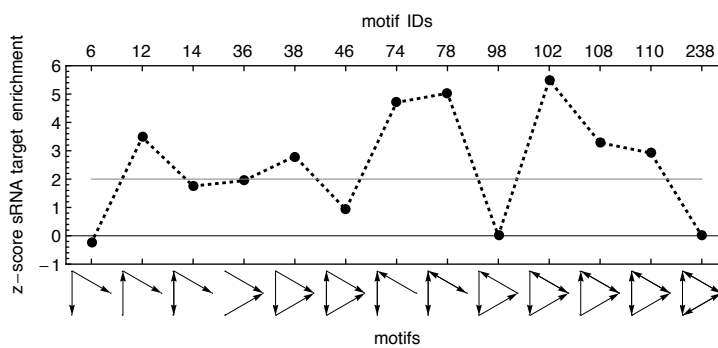

Figure 7. sRNA mediated control on network motifs. Comparing the number of 3-node motifs with at least one sRNA target with randomly sampled sets of targets of the same size, we identify seven motifs with significantly ($z - score \geq 2$) enriched occurrence of sRNA targets.