Supplementary Figures S1-S4

for

Analysis of the hierarchical structure of the *B. subtilis* transcriptional regulatory network

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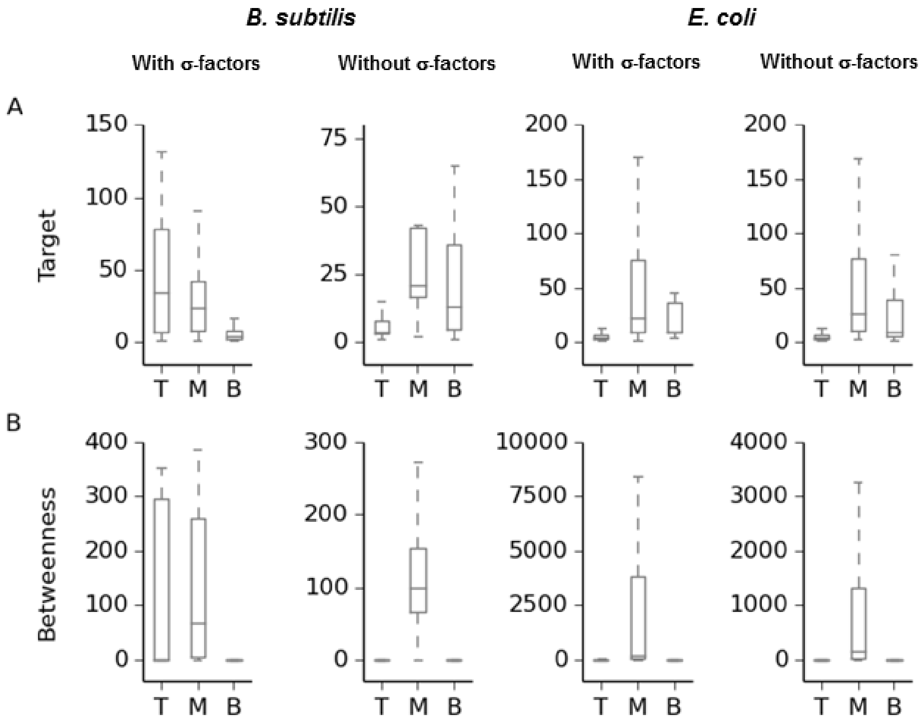
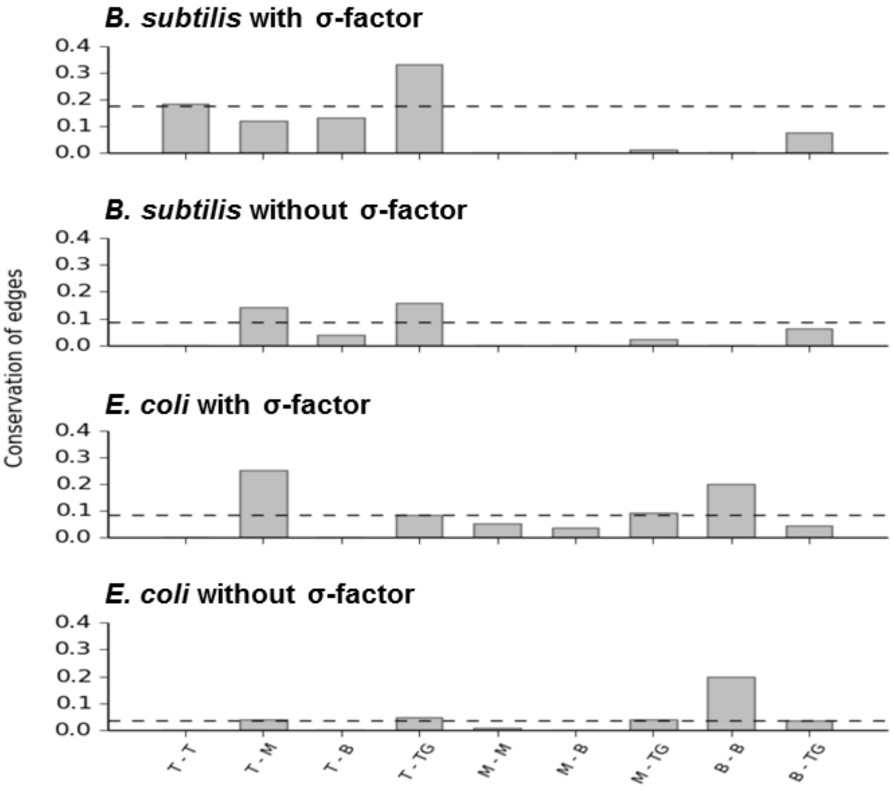
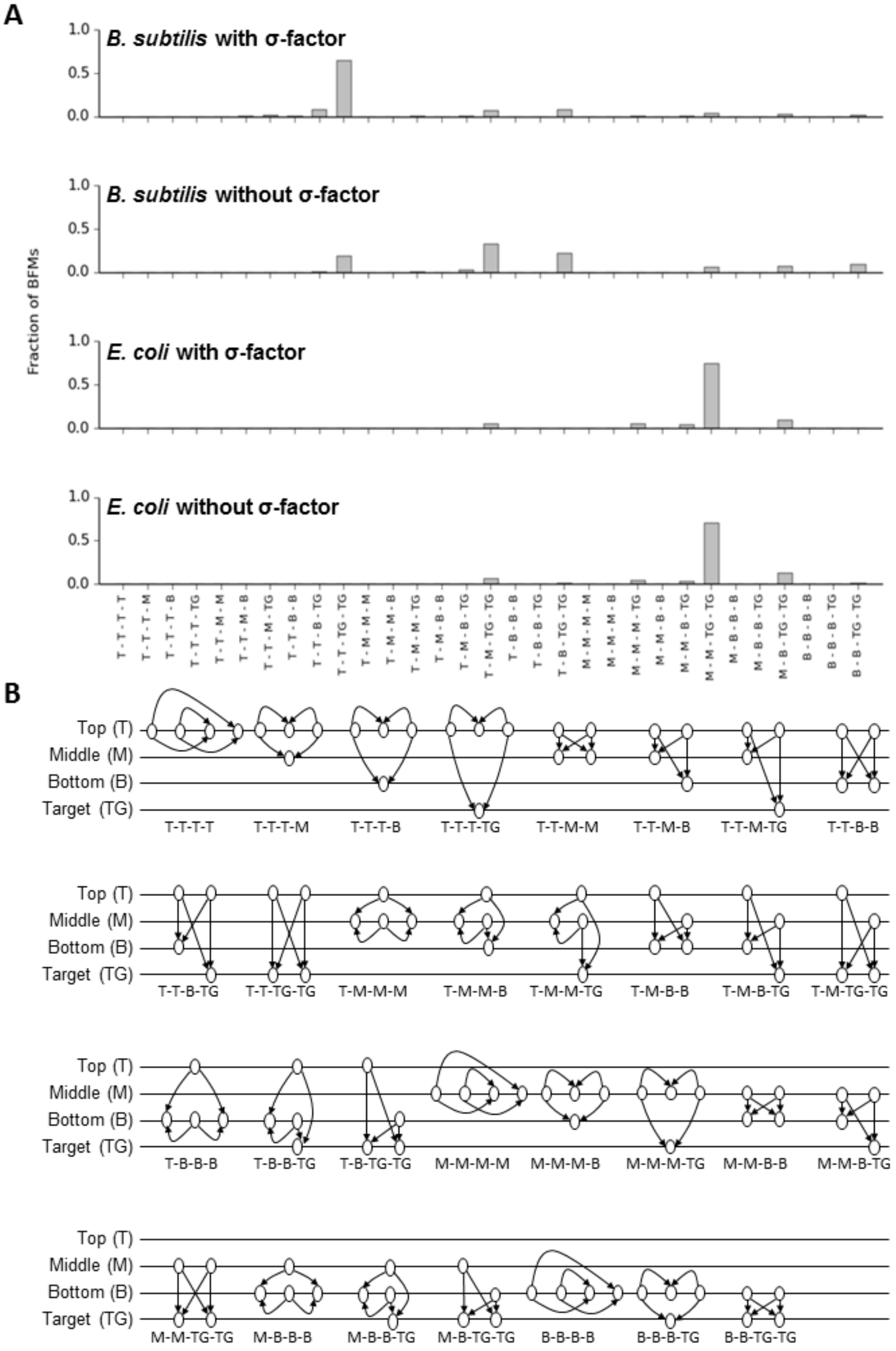


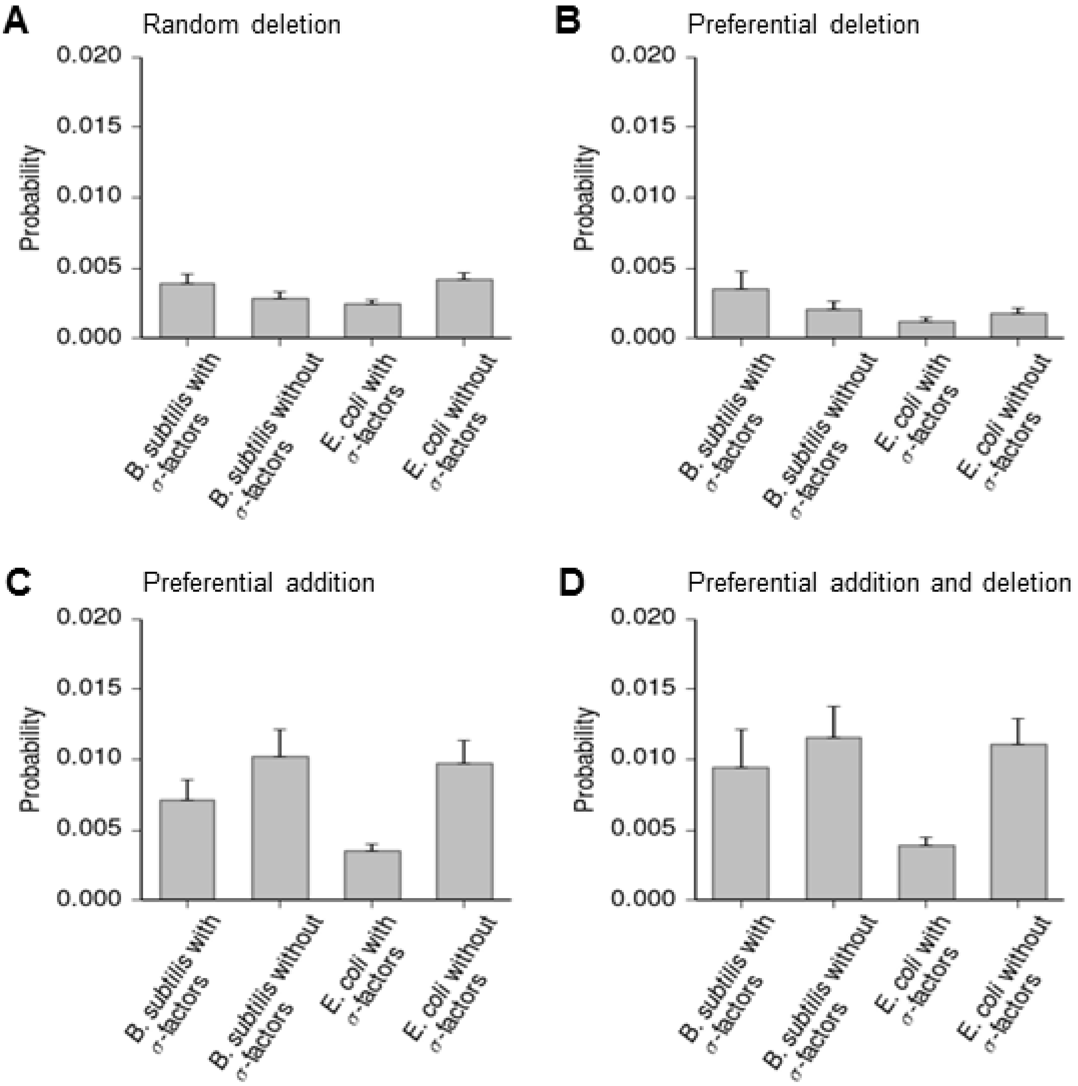
Supplementary Figure S1: Distribution of number of targets and betweenness centrality of transcriptional regulators in the different levels of hierarchy in the TRNs of *B. subtilis* and *E. coli*. (A) Number of targets (out-degree) and (B) Betweenness centrality. Box plots show the median and inter quartile range for investigated properties of transcriptional regulators in different levels of hierarchy.



Supplementary Figure S2: Evolutionary conservation of intra- and inter-level transcriptional interactions of and between different levels of hierarchy in the TRNs of *B. subtilis* and *E. coli*. The expected values of conservation of transcriptional interactions for randomized networks are shown as dashed black lines.



Supplementary Figure S3: Composition of Bi-fan motifs (BFMs) for genes from different levels of hierarchy in the TRNs of *B. subtilis* and *E. coli*. Top level regulators appear more often in BFMs in the TRN of *B. subtilis* while Middle level regulators appear more often in BFMs in the TRN of *E. coli*.



Supplementary Figure S4: Robustness of the hierarchical decomposition of transcriptional regulatory networks to incomplete information. The figure shows the probability that the assigned level of a gene in the hierarchical decomposition of the TRNs of *B. subtilis* and *E. coli* changes under 4 different perturbations: (A) Random deletion of 10% of existing edges. (B) Preferential deletion (based on out-degree of the regulatory node) of 10% of existing edges. (C) Preferential addition (based on out-degree of the regulatory node) of new edges equal to 10% of existing edges. (D) Preferential addition of new edges equal to 10% of existing edges and simultaneous preferential deletion of 10% of existing edges.