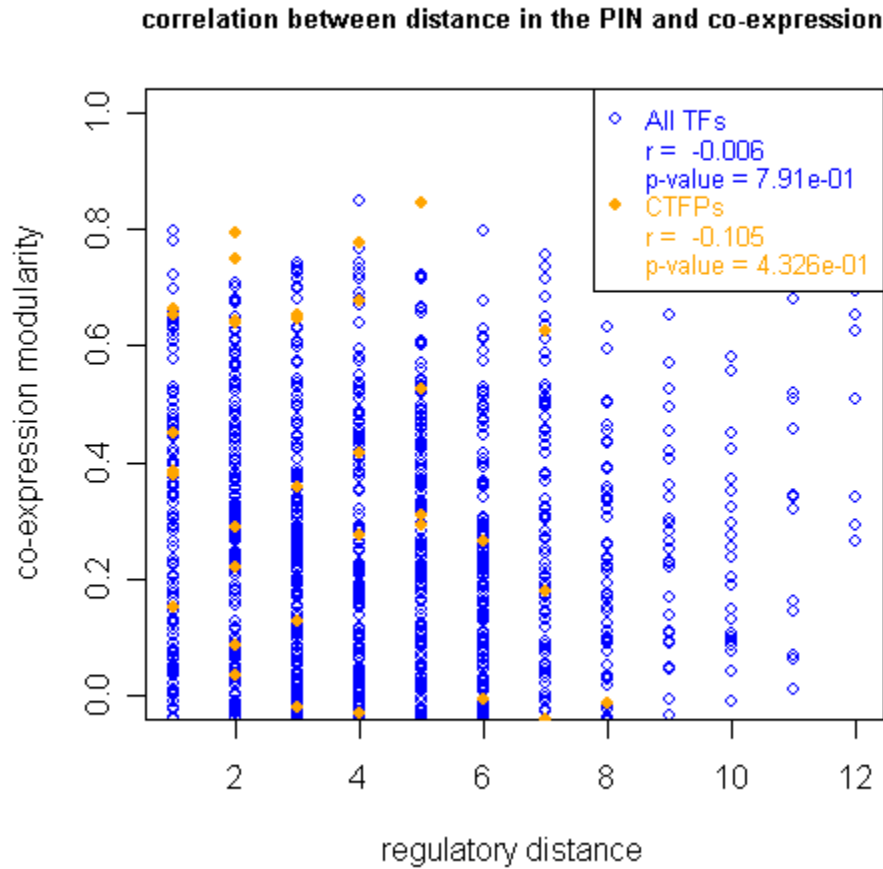




Additional file 5. Correlation between the path length in the regulatory network and the co-expression of TF pairs. Co-expression was calculated by means of the Pearson correlation coefficient of cell-cycle-based expression data (see *Methods*). Blue dots represent values derived from all TFs. Orange dots represent values derived from CTFPs only. Correlation was calculated by means of a Spearman test. Correlations for each set of CTFPs are as follows: $\rho = -0.059$ ($p\text{-value} = 0.775$) for CTFPs predicted by method N, $\rho = -0.319$ ($p\text{-value} = 0.148$) for CTFPs predicted by method B, $\rho = 0.391$ ($p\text{-value} = 0.186$) for CTFPs predicted by method T, $\rho = -0.019$ ($p\text{-value} = 0.918$) for CTFPs predicted by method C.