

Supplementary Figure 3

Pairwise analysis of motifs at different cutoff scores.

PSSM motif scans for ERE, Forkhead, AP-1, Oct and C/EBP were performed and overlapping sites were processed as follows: PSSM cutoff scores were chosen to be 100% of relative entropy (RE), except for C/EBP for which 5.0 cutoff was used because of its very low RE. The PSSM scores were then normalized as $(\text{Score} - \text{RE})/\text{length}$ and when two motifs overlapped, only the motif with higher normalized score was kept. A 5-dimensional contingency table was thus obtained for the distribution of the 5 motifs in the ER CHIP regions. Using MIM graphical modeling software, conditional independence graphical models were then constructed in order to understand the association of the five transcription factors. Unrestricted bidirectional selection was used with the chi-square test, and the same model in the Figure was produced for all critical levels in the range 0.01-0.05; exact tests using Monte Carlo sampling also yielded the same model. Fisher's exact test was used to determine whether a given association in the model was positive (Black) or negative (Red). At these levels of significance there is a 3-way interaction between Forkhead, C/EBP and Oct motifs; and ERE and AP-1 are negatively associated.

