General Motif Characteristics:

Top Similar Looking Motifs:

HTSELEX.ERG.ETS.full.monomeric.wm1	0.000
HTSELEX.ELK4.ETS.DBD.monomeric.wm1	0.001
HTSELEX.ERG.ETS.DBD.monomeric.wm1	0.002
HTSELEX.FLI1.ETS.full.monomeric.wm1	0.002
HTSELEX.ETS1.ETS.DBD.monomeric.wm1	0.003
HTSELEX.FEV.ETS.DBD.monomeric.wm1	0.004
HTSELEX.FLI1.ETS.DBD.monomeric.wm1	0.004
HTSELEX.ERF.ETS.DBD.monomeric.wm1	0.007
HTSELEX.ETS1.ETS.full.monomeric.wm1	0.007
HTSELEX.ETV1.ETS.DBD.monomeric.wm1	0.009

Statistics:

- Motif name: HTSELEX.ERG.ETS.full.monomeric.wm1
- Enrichment: 14.3772161007
- log−Likelihood Ratio: 1332.82236916
- Area under precision recall curve: 0.8480

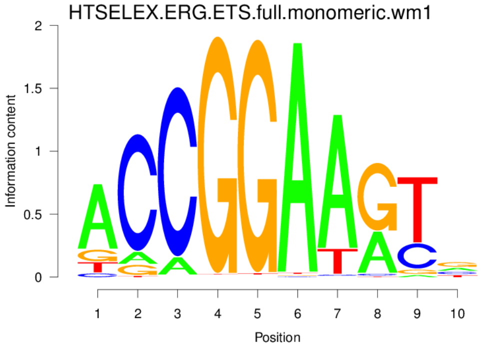

Figure 1: Logo of Weight Matrix

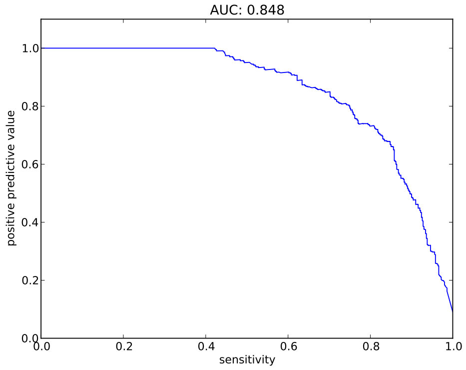

Figure 2: Precision and Recall curve

Statistics for TFBS - Peak Centering and Peak Posterior - Peak Height Correlation:

0.1

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Overall statistics:
        - Number of true peaks out of total number of peaks: 3843/5538
        - 69.39 percent are true.
        - Cut-off: minimum summed posterior of 0.20
        - Peak plots contain TFBS of posterior >= 0.20
Statistic for centering of TFBSs at peak centers:
        - Enrichment at binding sites: 5.27
Correlation between peak Z-score and number of binding sites at peak: 0.4258
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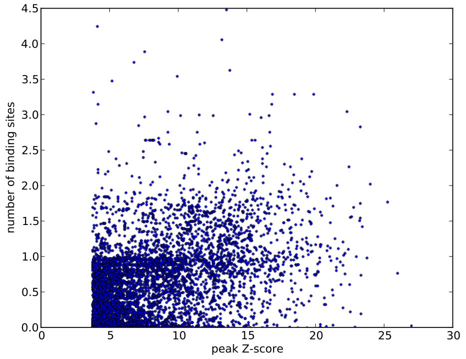

Figure 3: Scatter plot of peak Z-score versus number of binding sites at peak

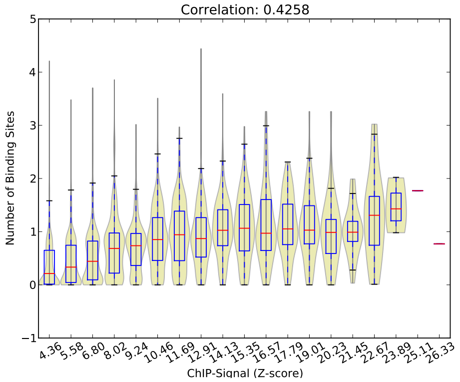

Figure 4: Violin plot of peak Z-score versus number of binding sites at peak

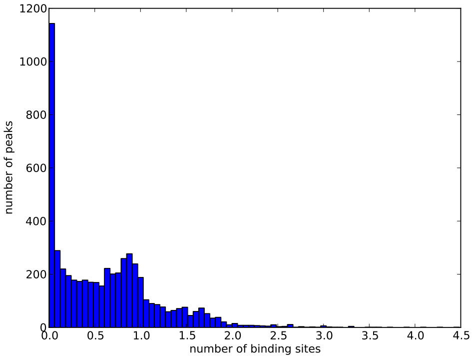

Figure 5: Histogram of number of binding sites at peaks

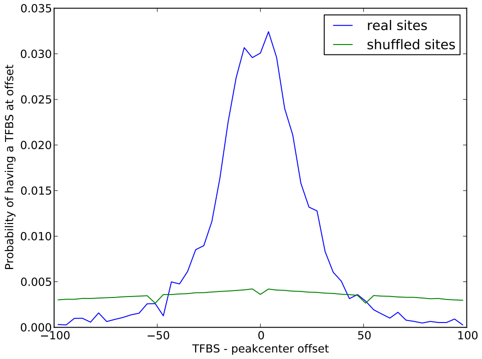

Figure 6: Histogram of distances of TFBS to its nearest peak center

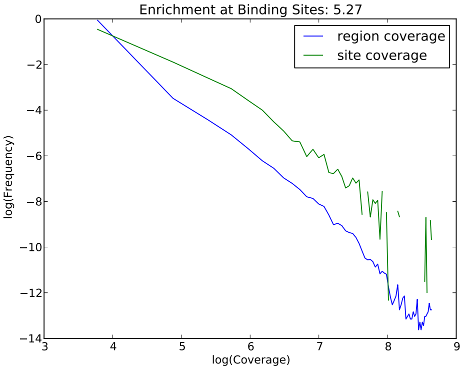

Figure 7: Histograms of coverage at sites and in total regions