General Motif Characteristics:

Top Similar Looking Motifs:

HCMC.CTCF_f2.wm	0.000
JASPAR.CTCF.wm	0.005
CTCF.p2	0.022
HOMER.CTCF(Zf).CD4+−CTCF−ChIP−Seq	0.026
ENCODE.CTCF	0.068
HOMER.BORIS(Zf).K562−CTCFL−ChIP−Seq	0.072
HTSELEX.CTCF.C2H2.full.monomeric.wm1	0.098
UNIPROBE.UW.Motif.0003.wm	0.175
UNIPROBE.Sp4_primary.wm	0.266
TFAP2B.p2	0.270

Statistics:

- Motif name: HCMC.CTCF_f2.wm
- Enrichment: 18.6613728459
- log−Likelihood Ratio: 1463.22788215
- Area under precision recall curve: 0.9403

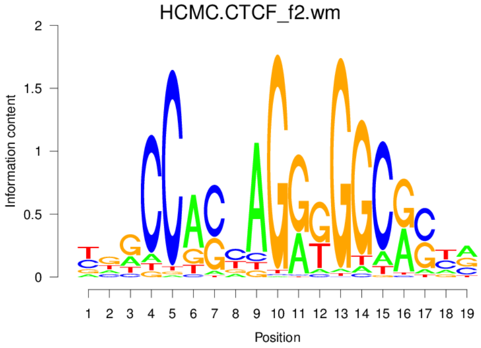

Figure 1: Logo of Weight Matrix

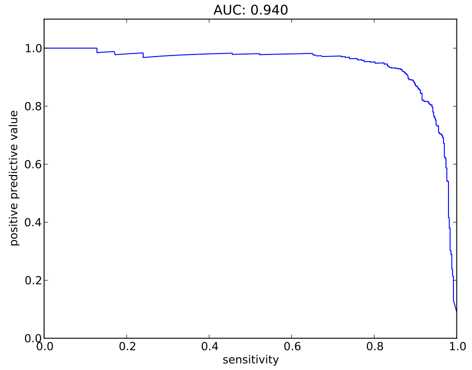

Figure 2: Precision and Recall curve

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: 32154/44017
        - 73.05 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: 4.218
Correlation between peak Z-score and number of binding sites at peak: 0.4756
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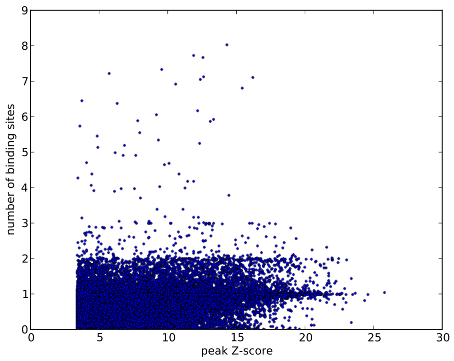

Figure 3: Scatter plot of peak Z-score versus number of binding sites at peak

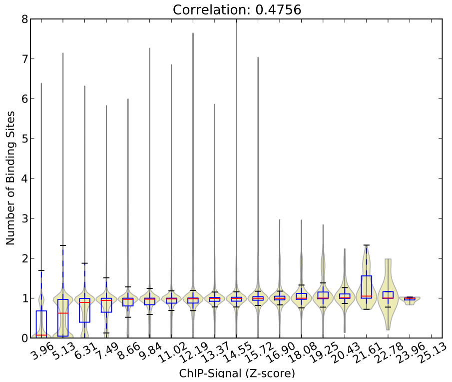

Figure 4: Violin plot of peak Z-score versus number of binding sites at peak

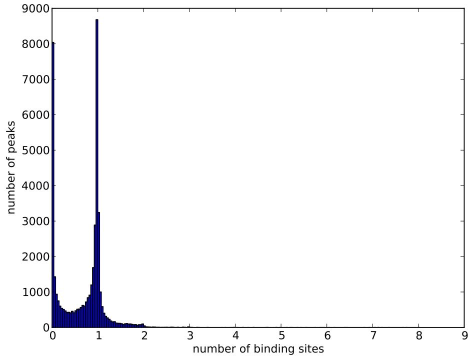

Figure 5: Histogram of number of binding sites at peaks

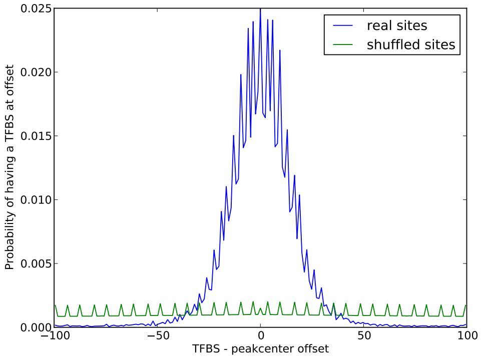

Figure 6: Histogram of distances of TFBS to its nearest peak center

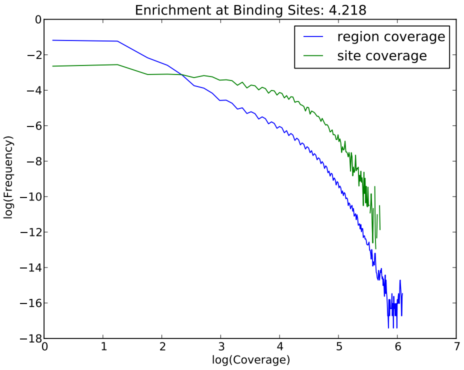

Figure 7: Histograms of coverage at sites and in total regions