

## General Motif Characteristics:

### Top Similar Looking Motifs:

HTSELEX.CTCF.C2H2.full.monomeric.wm1	0.000
JASPAR.CTCF.wm	0.092
ENCODE.CTCF	0.093
HCMC.CTCF_f2.wm	0.098
HOMER.CTCF(Zf).CD4+CTCF-ChIP-Seq	0.114
CTCF.p2	0.124
HOMER.BORIS(Zf).K562-CTCFL-ChIP-Seq	0.129
UNIPROBE.UW.Motif.0003.wm	0.216
UNIPROBE.Gcm1_secondary.wm	0.274
UNIPROBE.Sp4_primary.wm	0.289

### Statistics:

- Motif name: HTSELEX.CTCF.C2H2.full.monomeric.wm1
- Enrichment: 22.9510730718
- log-Likelihood Ratio: 1566.68234618
- Area under precision recall curve: 0.8098

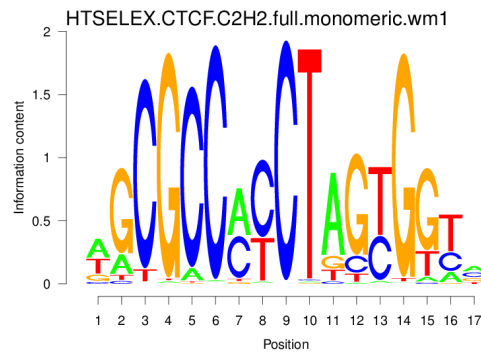


Figure 1: Logo of Weight Matrix

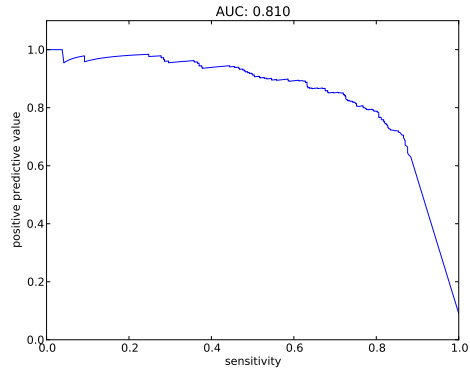


Figure 2: Precision and Recall curve

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

### 0.1

Overall statistics:

- Number of true peaks out of total number of peaks: 13757/44017
- 31.25 percent are true.
- Cut-off: minimum summed posterior of 0.20
- Peak plots contain TFBS of posterior  $\geq 0.20$

Statistic for centering of TFBSs at peak centers:

- Enrichment at binding sites: 5.8104

Correlation between peak Z-score and number of binding sites at peak: 0.3488

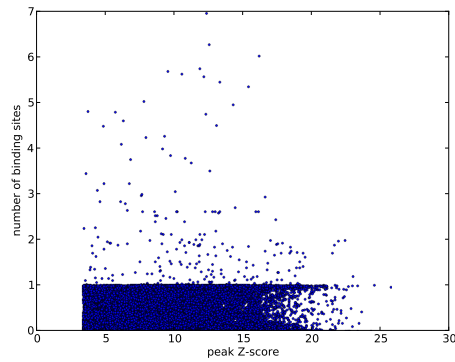


Figure 3: Scatter plot of peak Z-score versus number of binding sites at peak

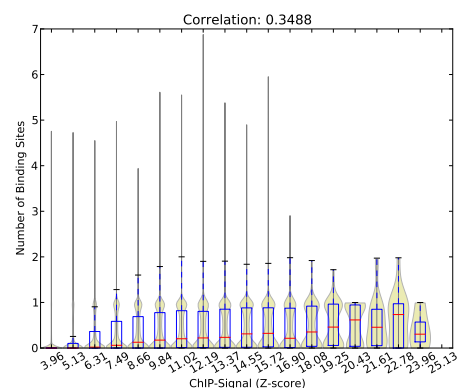


Figure 4: Violin plot of peak Z-score versus number of binding sites at peak

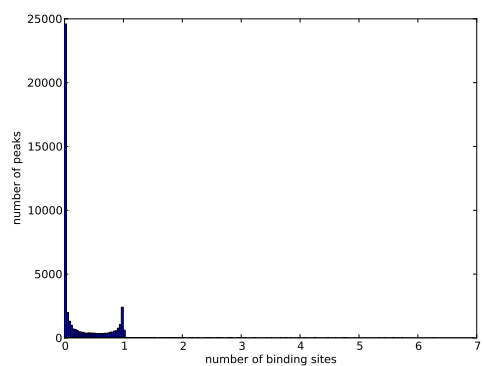


Figure 5: Histogram of number of binding sites at peaks

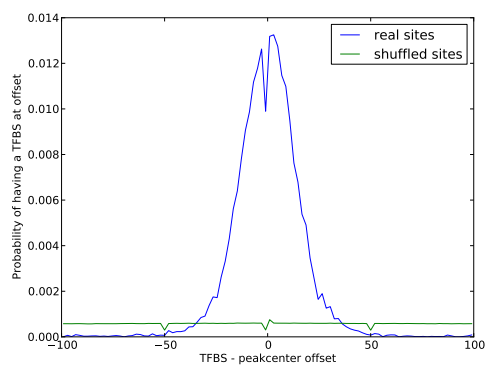


Figure 6: Histogram of distances of TFBS to its nearest peak center

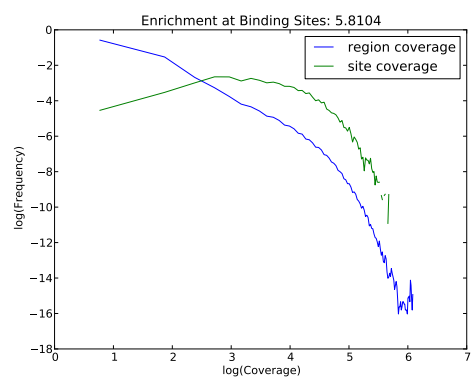


Figure 7: Histograms of coverage at sites and in total regions