General Motif Characteristics:

Top Similar Looking Motifs:

```
CTCF.p2  0.000
JASPAR.CTCF.wm    0.018
HCMC.CTCF_f2.wm  0.022
HOMER.CTCF(Zf).CD4+-CTCF-ChIP-Seq          0.028
HOMER.BORIS(Zf).K562-CTCFL-ChIP-Seq        0.091
ENCODE.CTCF         0.092
HTSELEX.CTCF.C2H2.full.monomeric.wm1       0.124
UNIPROBE.UW.Motif.0003.wm           0.186
HTSELEX.Hic1.C2H2.DBD.dimeric.wm1          0.278
TFAP4.p2            0.279
```

Statistics:

```
- Motif name: CTCF.p2
- Enrichment: 81.3976335485
- log-Likelihood Ratio: 2199.67310035
- Area under precision recall curve: 0.9491
```

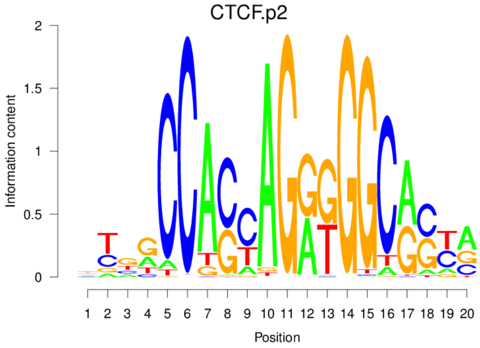

Figure 1: Logo of Weight Matrix

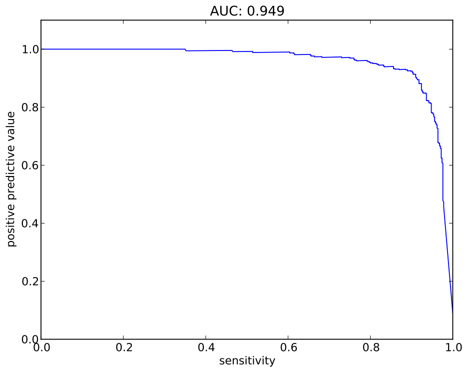

Figure 2: Precision and Recall curve

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: 25428/44017
        − 57.77 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: 5.2811
Correlation between peak Z−score and number of binding sites at peak: 0.4879
```

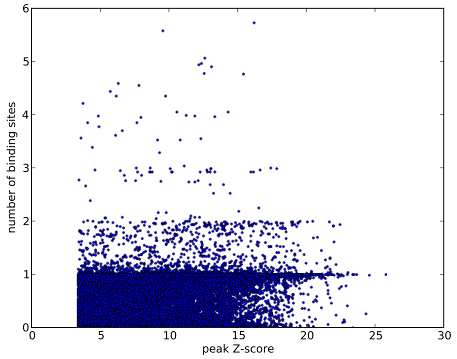

Figure 3: Scatter plot of peak Z-score versus number of binding sites at peak

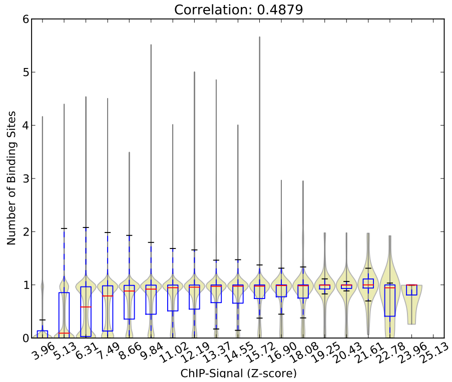

Figure 4: Violin plot of peak Z-score versus number of binding sites at peak

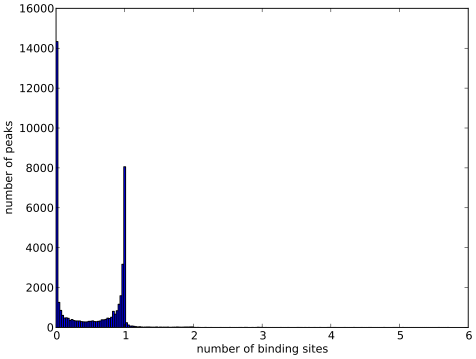

Figure 5: Histogram of number of binding sites at peaks

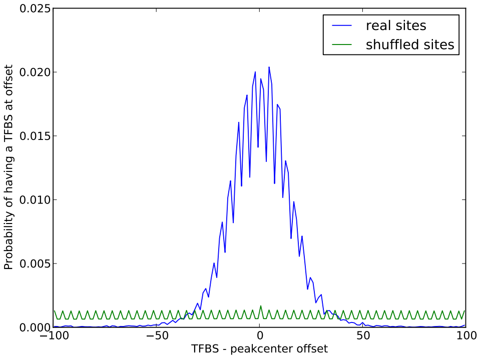

Figure 6: Histogram of distances of TFBS to its nearest peak center

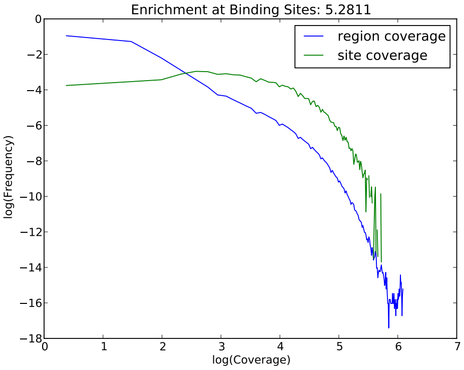

Figure 7: Histograms of coverage at sites and in total regions