General Motif Characteristics:

Top Similar Looking Motifs:

```
HTSELEX.JDP2.bZIP.full.dimeric.wm2        0.000
HTSELEX.Jdp2.bZIP.DBD.dimeric.wm2         0.001
HTSELEX.JDP2.bZIP.DBD.dimeric.wm2         0.003
HTSELEX.Creb5.bZIP.DBD.dimeric.wm1        0.008
HTSELEX.XBP1.bZIP.DBD.dimeric.wm1         0.023
HTSELEX.ATF7.bZIP.DBD.dimeric.wm1         0.036
HTSELEX.CREB3.bZIP.full.dimeric.wm1       0.059
ENCODE.v-JUN      0.066
HOMER.c-Jun-CRE(bZIP).K562-cJun-ChIP-Seq          0.067
UNIPROBE.Jundm2_primary.wm        0.074
```

Statistics:

```
- Motif name: HTSELEX.JDP2.bZIP.full.dimeric.wm2
- Enrichment: 12.5112170232
- log-Likelihood Ratio: 1263.31280189
- Area under precision recall curve: 0.1046
```

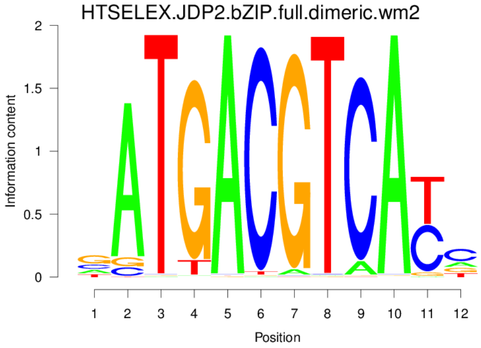

Figure 1: Logo of Weight Matrix

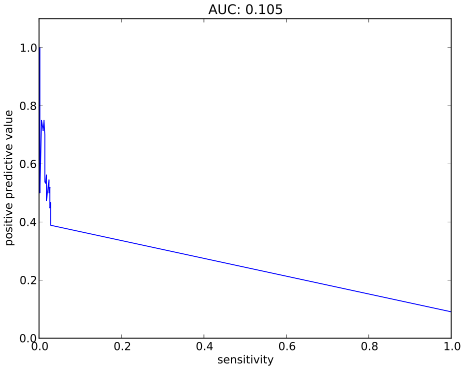

Figure 2: Precision and Recall curve

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: 257/37435
        - 0.69 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: 3.3069
Correlation between peak Z-score and number of binding sites at peak: 0.0441
```

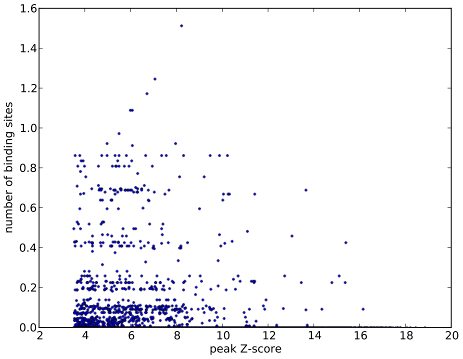

Figure 3: Scatter plot of peak Z-score versus number of binding sites at peak

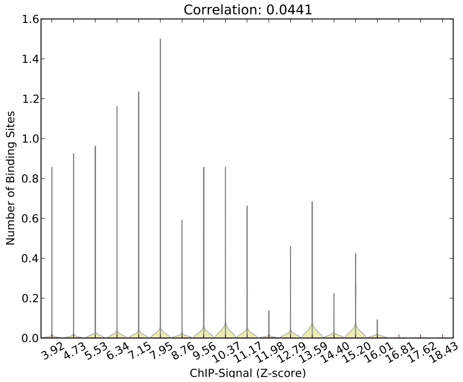

Figure 4: Violin plot of peak Z-score versus number of binding sites at peak

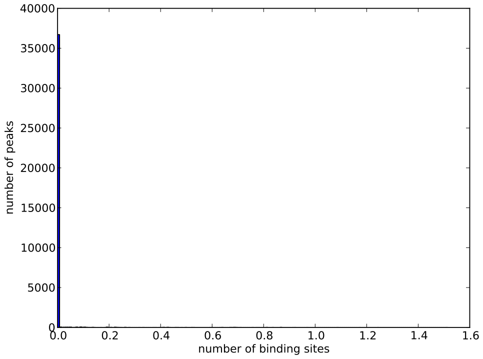

Figure 5: Histogram of number of binding sites at peaks

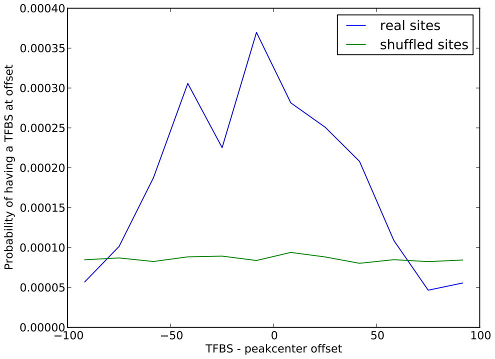

Figure 6: Histogram of distances of TFBS to its nearest peak center

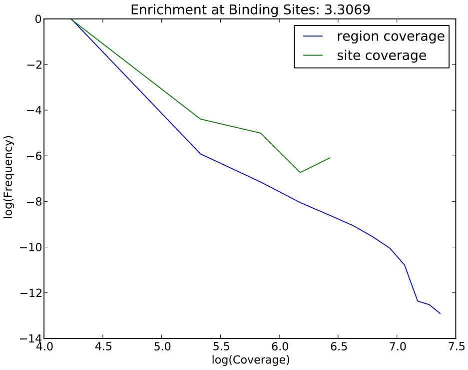

Figure 7: Histograms of coverage at sites and in total regions