General Motif Characteristics:

Top Similar Looking Motifs:

```
HTSELEX.TCF4.bHLH.DBD.dimeric.wm1          0.000
HTSELEX.TCF3.bHLH.DBD.dimeric.wm1          0.005
HTSELEX.ID4.bHLH.DBD.dimeric.wm1           0.013
HOMER.E2A-nearPU.1(HLH).Bcell-PU.1-ChIP-Seq(GSE21512)      0.013
HTSELEX.MESP1.bHLH.DBD.dimeric.wm1         0.016
HCMC.ITF2_f1.wm 0.026
HTSELEX.FIGLA.bHLH.DBD.dimeric.wm1         0.042
HTSELEX.TCF4.bHLH.full.dimeric.wm1         0.046
ENCODE.ZEB1        0.050
HTSELEX.SNAI2.C2H2.DBD.monomeric.wm1       0.051
```

Statistics:

```
- Motif name: HTSELEX.TCF4.bHLH.DBD.dimeric.wm1
- Enrichment: 4.25040048752
- log-Likelihood Ratio: 723.506605428
- Area under precision recall curve: 0.6326
```

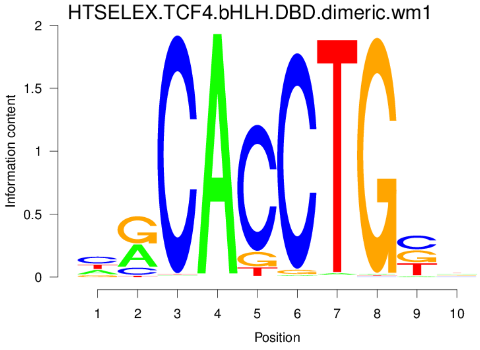

Figure 1: Logo of Weight Matrix

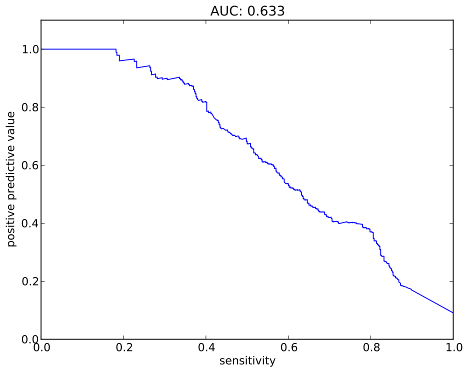

Figure 2: Precision and Recall curve

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: 4891/7427
        - 65.85 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: 2.2538
Correlation between peak Z-score and number of binding sites at peak: 0.3737
```

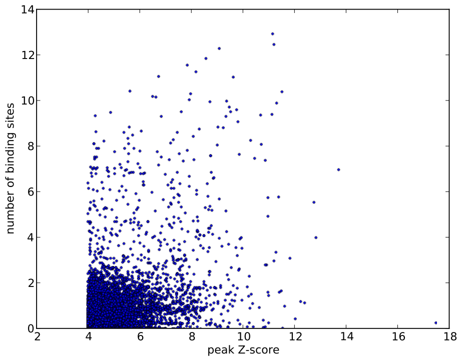

Figure 3: Scatter plot of peak Z-score versus number of binding sites at peak

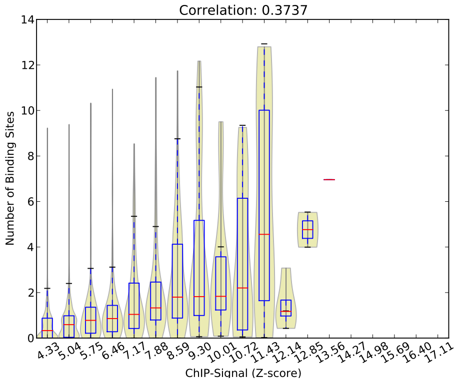

Figure 4: Violin plot of peak Z-score versus number of binding sites at peak

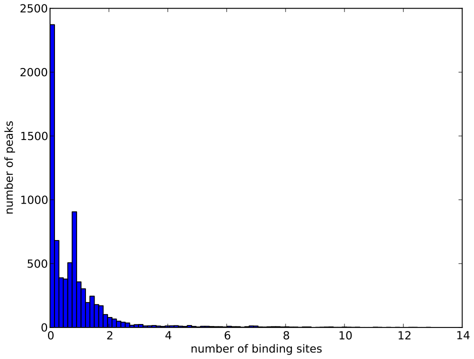

Figure 5: Histogram of number of binding sites at peaks

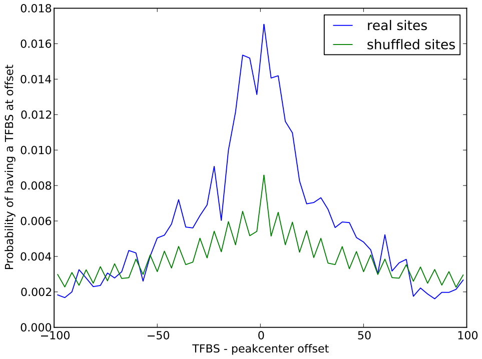

Figure 6: Histogram of distances of TFBS to its nearest peak center

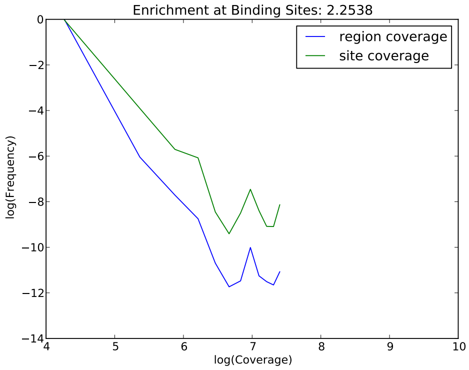

Figure 7: Histograms of coverage at sites and in total regions