General Motif Characteristics:

Top Similar Looking Motifs:

```
HOMER.RLR1?.SacCer-Promoters        0.000
HOMER.IRF2(IRF).Erythroblas-IRF2-ChIP-Seq(GSE36985)         0.042
HOMER.ISRE(IRF).ThioMac-LPS-exp(GSE23622)           0.055
HOMER.T1ISRE(IRF).Ifnb-Exp          0.067
HOMER.Foxa2(Forkhead).Liver-Foxa2-ChIP-Seq          0.107
HOMER.Foxh1(Forkhead).hESC-FOXH1-ChIP-Seq(GSE29422)         0.108
HOMER.PU.1-IRF(ETS_IRF).Bcell-PU.1-ChIP-Seq(GSE21512)       0.109
HOMER.REB1.SacCer-Promoters         0.113
HOMER.RUNX2(Runt).PCa-RUNX2-ChIP-Seq(GSE33889)      0.118
HOMER.SFP1.SacCer-Promoters         0.121
```

Statistics:

```
- Motif name: HOMER.RLR1?.SacCer-Promoters
- Enrichment: 13.3254249484
- log-Likelihood Ratio: 1294.8369303
- Area under precision recall curve: 0.2597
```

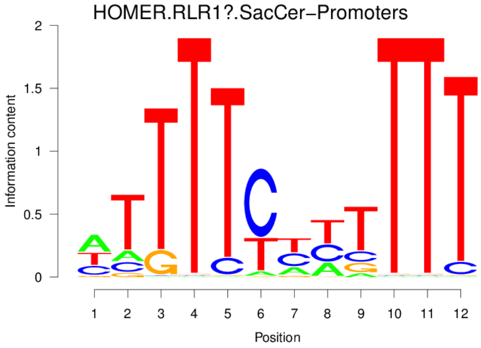

Figure 1: Logo of Weight Matrix

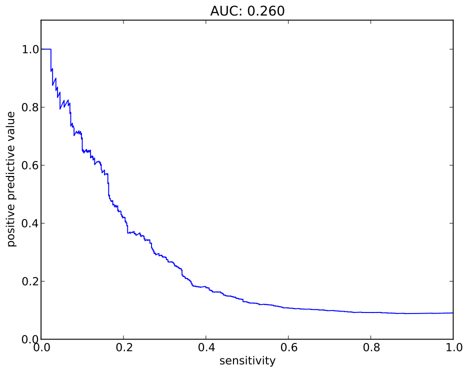

Figure 2: Precision and Recall curve

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: 3801/37435
        - 10.15 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: 0.6335
Correlation between peak Z-score and number of binding sites at peak: -0.105
```

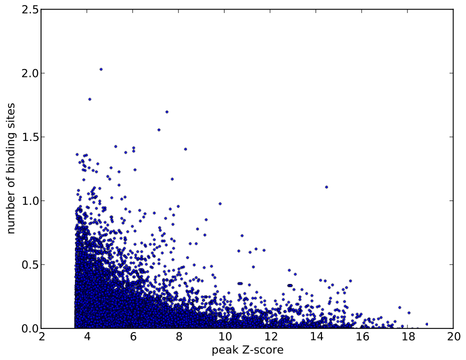

Figure 3: Scatter plot of peak Z-score versus number of binding sites at peak

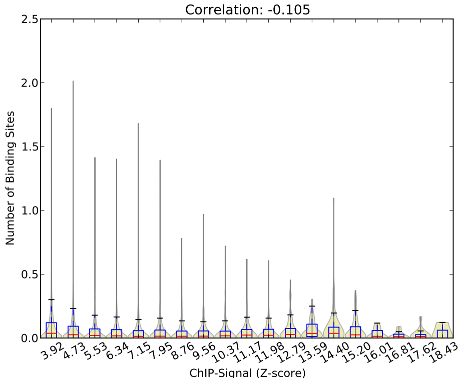

Figure 4: Violin plot of peak Z-score versus number of binding sites at peak

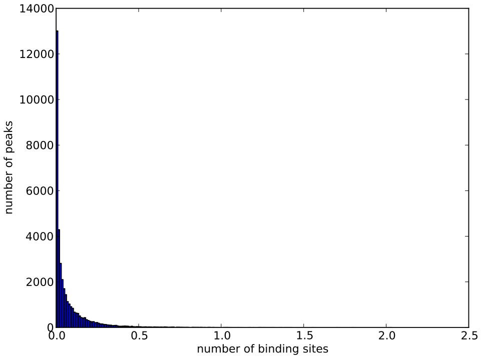

Figure 5: Histogram of number of binding sites at peaks

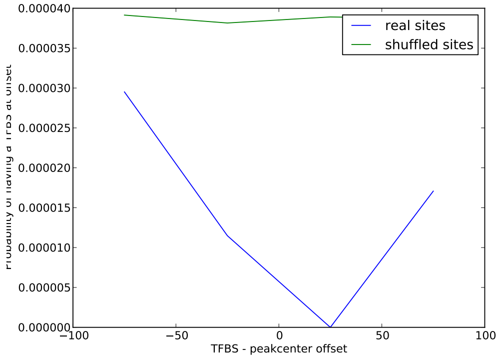

Figure 6: Histogram of distances of TFBS to its nearest peak center

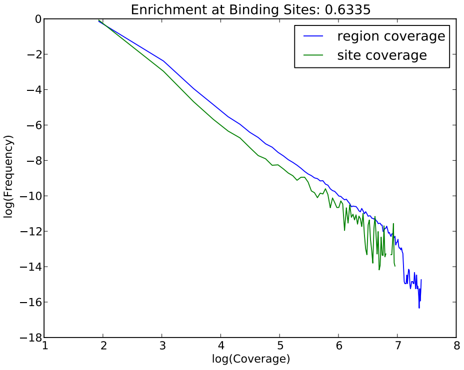

Figure 7: Histograms of coverage at sites and in total regions