General Motif Characteristics:

Top Similar Looking Motifs:

```
JASPAR.Myf.wm     0.000
MYFfamily.p2      0.031
HCMC.MYOG_f1.wm  0.106
HOMER.MyoD(HLH).Myotube-MyoD-ChIP-Seq       0.143
HOMER.Tcf12(HLH).GM12878-Tcf12-ChIP-Seq  0.144
HCMC.TFAP4_si.wm                 0.153
HTSELEX.Ascl2.bHLH.DBD.dimeric.wml         0.155
NHLH1,2.p2        0.160
ENCODE.TCF12      0.162
LMO2.p2  0.166
```

Statistics:

```
- Motif name: JASPAR.Myf.wm
- Enrichment: 3.1219432186
- log-Likelihood Ratio: 566.950905941
- Area under precision recall curve: 0.1827
```

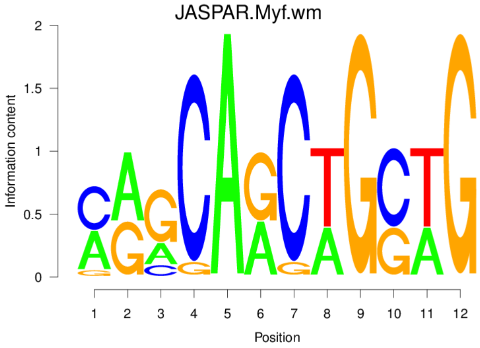

Figure 1: Logo of Weight Matrix

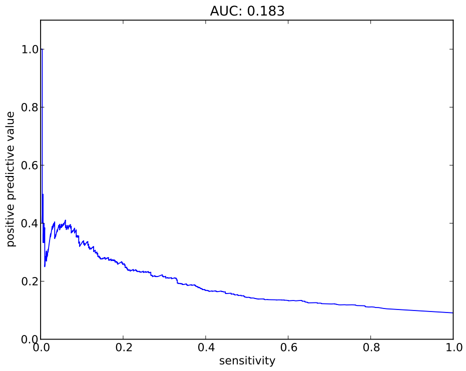

Figure 2: Precision and Recall curve

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: 3830/19318
        - 19.83 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: 1.2066
Correlation between peak Z-score and number of binding sites at peak: -0.0098
```

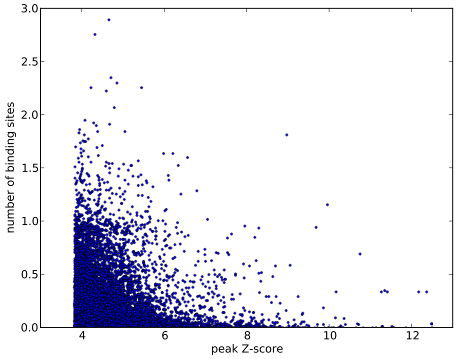

Figure 3: Scatter plot of peak Z-score versus number of binding sites at peak

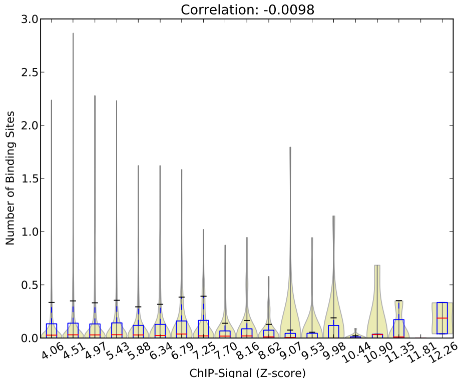

Figure 4: Violin plot of peak Z-score versus number of binding sites at peak

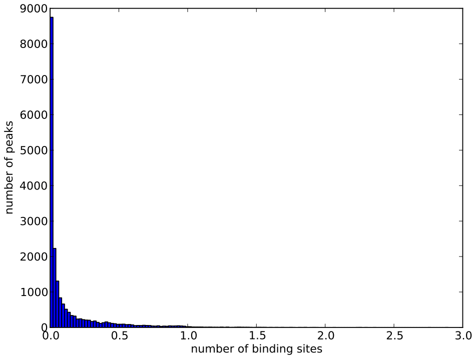

Figure 5: Histogram of number of binding sites at peaks

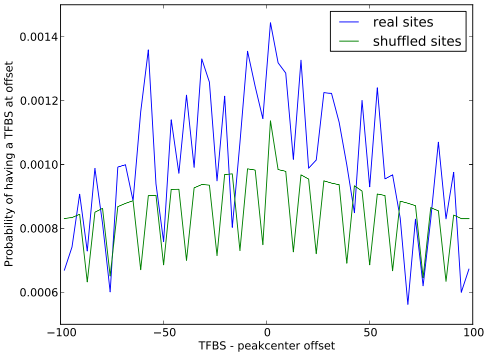

Figure 6: Histogram of distances of TFBS to its nearest peak center

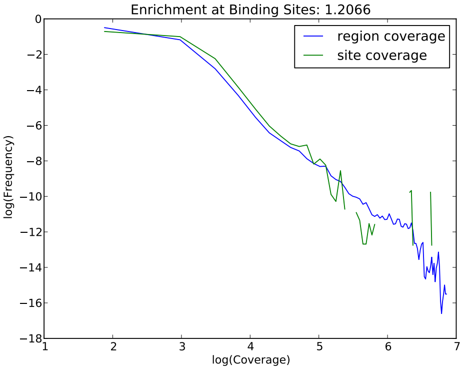

Figure 7: Histograms of coverage at sites and in total regions