General Motif Characteristics:

Top Similar Looking Motifs:

STAT5{A,B}.p2	0.000
JASPAR.STAT1.wm	0.236
ENCODE.STAT1	0.238
HCMC.STAT1_f2.wm	0.239
STAT1,3.p3	0.254
HCMC.STA5B_f1.wm	0.261
ENCODE.ZNF143−ext	0.277
HOMER.Bcl6(Zf).Liver−Bcl6−ChIP−Seq(GSE31578)	0.278
HOMER.STAT5(Stat).mCD4+−Stat5a|b−ChIP−Seq	0.282
HCMC.STA5A_do.wm	0.284

Statistics:

- Motif name: STAT5{A,B}.p2
- Enrichment: 58.6401849032
- log−Likelihood Ratio: 2035.71010538
- Area under precision recall curve: 0.5297

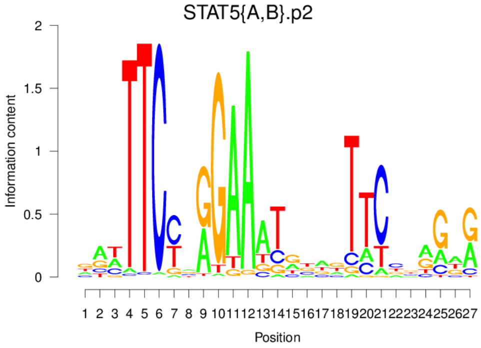

Figure 1: Logo of Weight Matrix

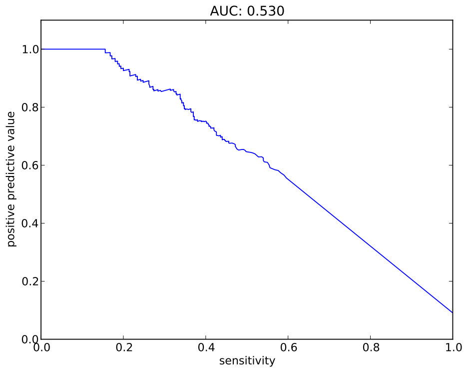

Figure 2: Precision and Recall curve

Statistics for TFBS - Peak Centering and Peak Posterior - Peak Height Correlation:

0.1

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Overall statistics:
        - Number of true peaks out of total number of peaks: 1039/36955
        - 2.81 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: 8.2143
Correlation between peak Z-score and number of binding sites at peak: 0.2175
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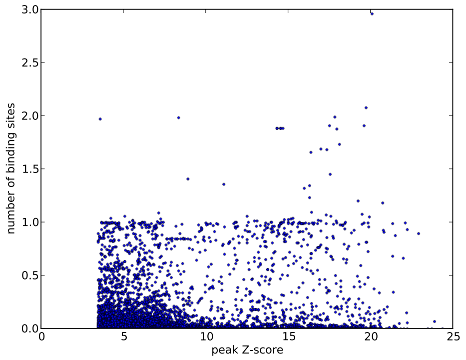

Figure 3: Scatter plot of peak Z-score versus number of binding sites at peak

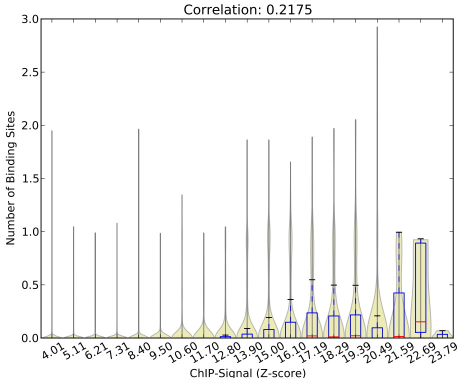

Figure 4: Violin plot of peak Z-score versus number of binding sites at peak

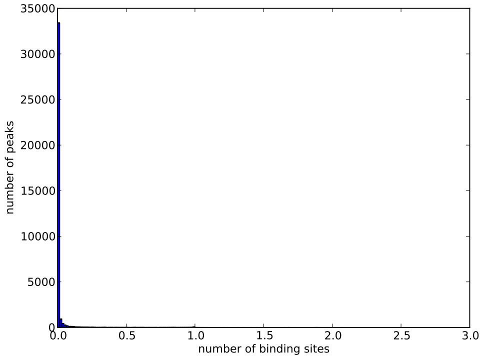

Figure 5: Histogram of number of binding sites at peaks

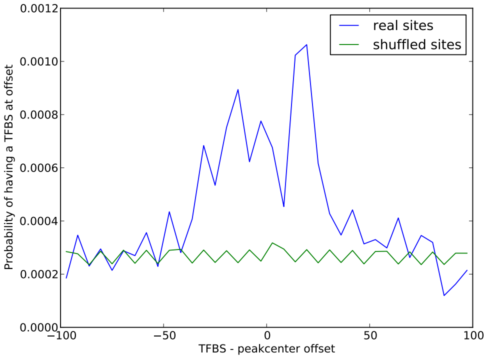

Figure 6: Histogram of distances of TFBS to its nearest peak center

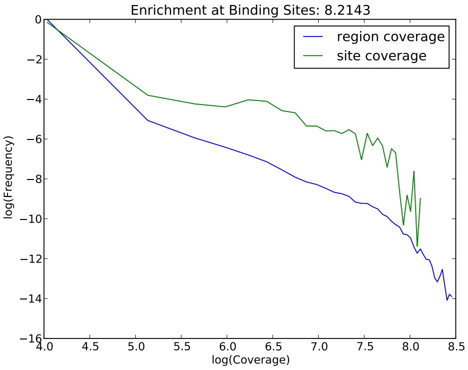

Figure 7: Histograms of coverage at sites and in total regions