General Motif Characteristics:

Top Similar Looking Motifs:

JASPAR.CTCF.wm   0.000
HCMC.CTCF_f2.wm 0.005
CTCF.p2 0.018
HOMER.CTCF(Zf).CD4+—CTCF—ChIP−Seq   0.022
ENCODE.CTCF   0.072
HOMER.BORIS(Zf).K562—CTCFL—ChIP−Seq   0.076
HTSELEX.CTCF.C2H2.full.monomeric.wm1   0.092
UNIPROBE.UW.Motif.0003.wm   0.173
UNIPROBE.Sp4_primary.wm 0.285
TFAP4.p2   0.288

Statistics:

− Motif name: JASPAR.CTCF.wm
− Enrichment: 36.2417526756
− log−Likelihood Ratio: 1795.10592151
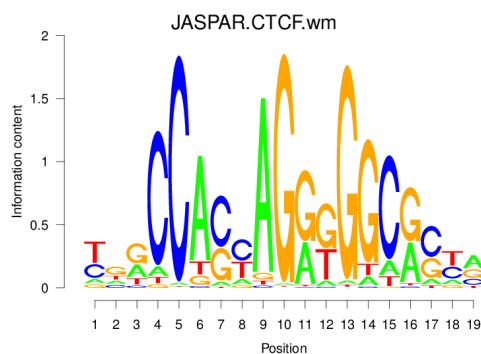− Area under precision recall curve: 0.9505
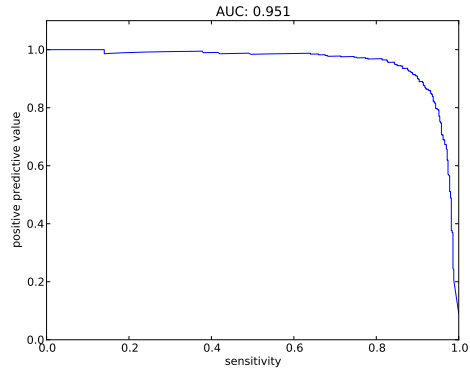

Figure 1: Logo of Weight Matrix

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: 30151/44017
 – 68.50 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: 4.7093
Correlation between peak Z−score and number of binding sites at peak: 0.4939
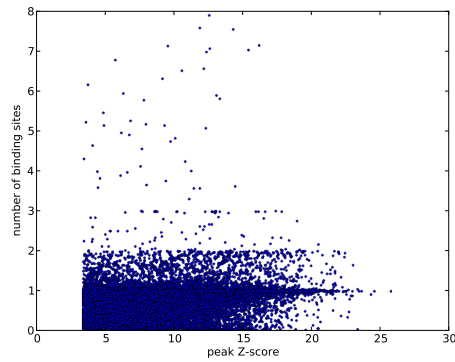

Figure 3: Scatter plot of peak Z-score versus number of binding sites at peak
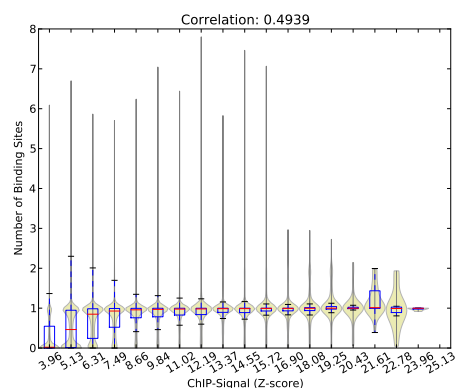
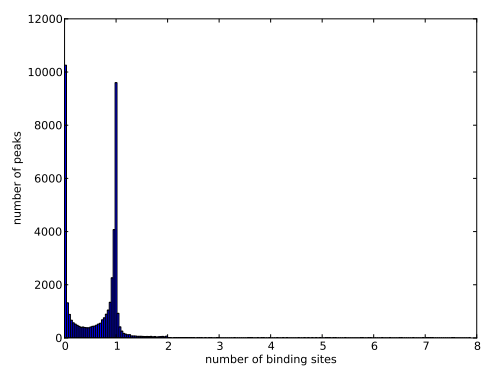Figure 4: Violin plot of peak Z-score versus number of binding sites at peak

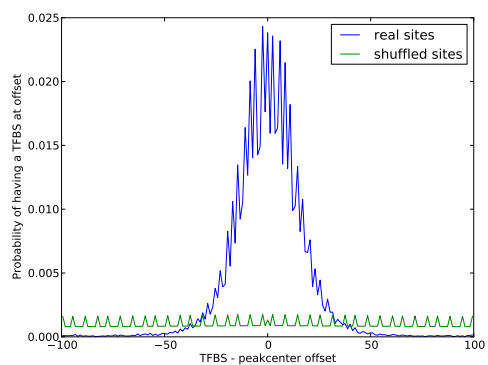Figure 5: Histogram of number of binding sites at peaks

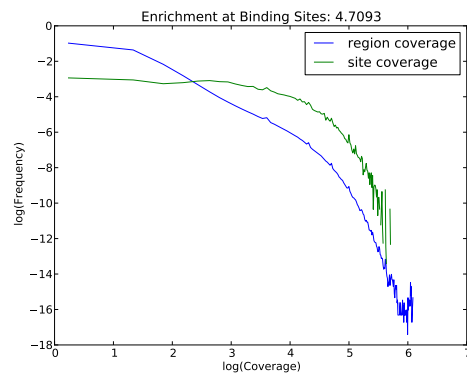Figure 6: Histogram of distances of TFBS to its nearest peak center

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