General Motif Characteristics:

Top Similar Looking Motifs:

CTCF.p2 0.000 JASPAR.CTCF.wm 0.018 $HCMC.\ CTCF_f2.wm\ 0.022$ HOMER.CTCF(Zf).CD4+-CTCF-ChIP-Seq0.028 $\operatorname{\mathsf{HO\!ME\!R}}.\operatorname{\mathsf{BORIS}}(\operatorname{Zf})$. K
562–CTCFL–ChIP–Seq 0.091 ENCODE.CTCF 0.092HTSELEX.CTCF.C2H2.full.monomeric.wm1 0.124UNIPROBE.UW. Motif.0003.wm $\operatorname{HTSELEX}$. $\operatorname{Hic1}$. $\operatorname{C2H2}$. DBD . $\operatorname{dimeric}$. $\operatorname{wm1}$ 0.278TFAP4.p20.279

Statistics:

- Motif name: CTCF.p2

- Enrichment: 4.90125727717

- log-Likelihood Ratio: 791.566896171

- Area under precision recall curve: 0.1348

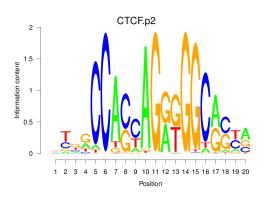


Figure 1: Logo of Weight Matrix

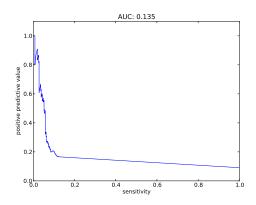


Figure 2: Precision and Recall curve

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: 2143/33576
- 6.38 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: 1.8867

Correlation between peak Z-score and number of binding sites at peak: -0.0198

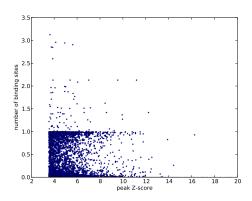


Figure 3: Scatter plot of peak Z-score versus number of binding sites at peak

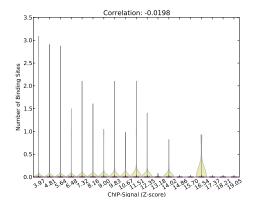


Figure 4: Violin plot of peak Z-score versus number of binding sites at peak

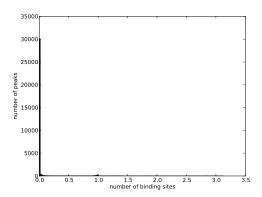


Figure 5: Histogram of number of binding sites at peaks

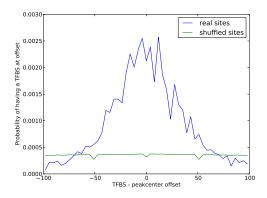


Figure 6: Histogram of distances of TFBS to its nearest peak center $\,$

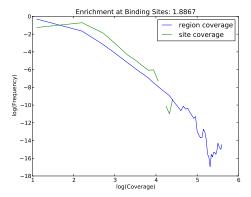


Figure 7: Histograms of coverage at sites and in total regions $\,$