

General Motif Characteristics:

Top Similar Looking Motifs:

JASPAR.RUNX1.wm	0.000	
HCMC.RUNX1_f1.wm	0.050	
HCMC.PEBB_f1.wm	0.073	
HOMER.RUNX(Runt).HPC7-Runx1-ChIP-Seq	0.074	
RUNX1..3.p2	0.081	
ENCODE.RUNX1	0.082	
HTSELEX.RUNX3.RUNX.full.monomeric.wm1	0.089	
HTSELEX.RUNX3.RUNX.DBD.monomeric.wm1	0.099	
HCMC.RUNX2_f1.wm	0.108	
HTSELEX.RUNX2.RUNX.DBD.monomeric.wm1	0.128	

Statistics:

- Motif name: JASPAR.RUNX1.wm
- Enrichment: 3.15656581119
- log-Likelihood Ratio: 505.773253931
- Area under precision recall curve: 0.3715

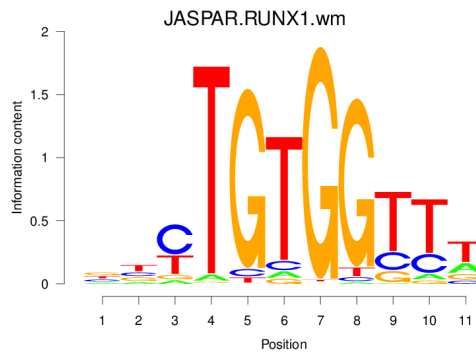


Figure 1: Logo of Weight Matrix

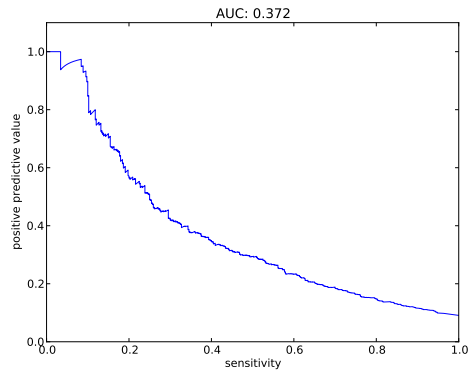


Figure 2: Precision and Recall curve

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: 794/1200
- 66.17 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: 1.2952

Correlation between peak Z-score and number of binding sites at peak: -0.0112

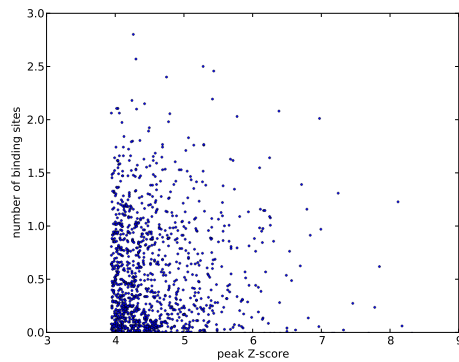


Figure 3: Scatter plot of peak Z-score versus number of binding sites at peak

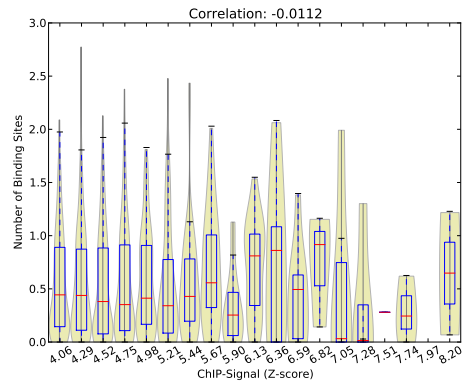


Figure 4: Violin plot of peak Z-score versus number of binding sites at peak

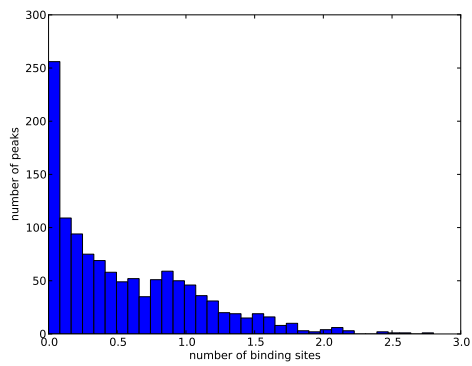


Figure 5: Histogram of number of binding sites at peaks

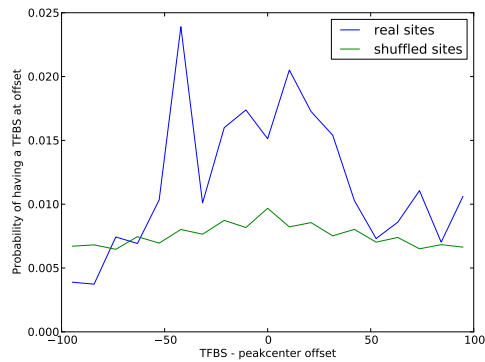


Figure 6: Histogram of distances of TFBS to its nearest peak center

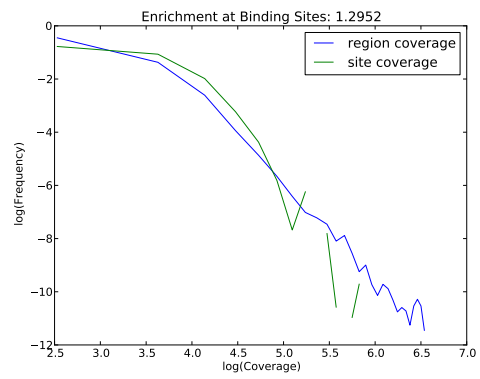


Figure 7: Histograms of coverage at sites and in total regions