

General Motif Characteristics:

Top Similar Looking Motifs:

HOMER.GFY-Staf.Promoters	0.000	
HOMER.Tcfcp211(CP2).mES-Tcfcp211-ChIP-Seq	0.122	
HOMER.Pax7-longest(Paired.Homeobox)	0.123	
HOMER.p63(p53).Keratinocyte-p63-ChIP-Seq	0.128	
HOMER.p53(p53).Saos-p53-ChIP-Seq	0.129	
HOMER.GATA-IR3(Zf).iTreg-Gata3-ChIP-Seq(GSE20898)	0.130	
HOMER.GATA-DR8(Zf).iTreg-Gata3-ChIP-Seq(GSE20898)	0.134	
HOMER.p53(p53).p53-ChIP-Chip	0.141	
HOMER.Mouse_Recombination_Hotspot.Testis-DMC1-ChIP-Seq	0.145	
HOMER.GATA-SCL.Ter119-SCL-ChIP-Seq	0.162	

Statistics:

- Motif name: HOMER.GFY-Staf.Promoters
- Enrichment: 10.3930184682
- log-Likelihood Ratio: 1170.56713979
- Area under precision recall curve: 0.1891

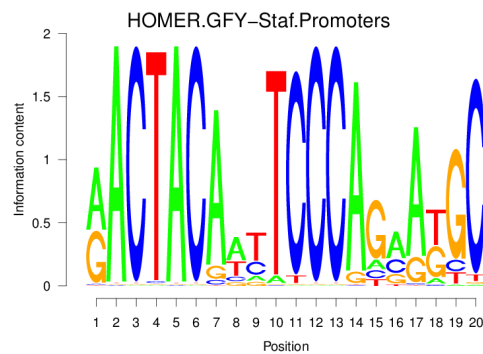


Figure 1: Logo of Weight Matrix

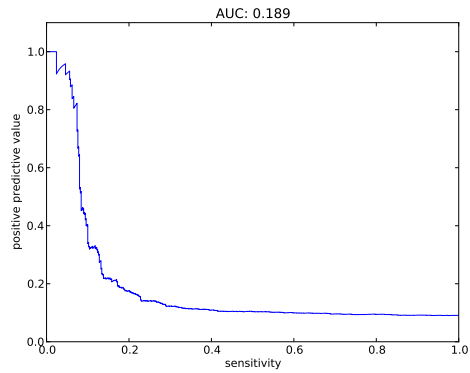


Figure 2: Precision and Recall curve

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: 1334/1348
- 98.96 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: 1.2423

Correlation between peak Z-score and number of binding sites at peak: -0.021

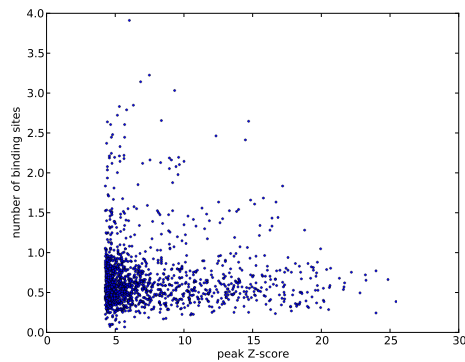


Figure 3: Scatter plot of peak Z-score versus number of binding sites at peak

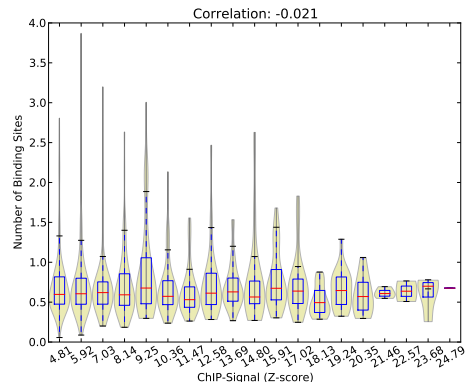


Figure 4: Violin plot of peak Z-score versus number of binding sites at peak

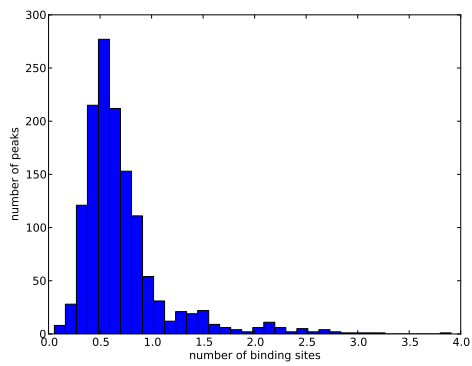


Figure 5: Histogram of number of binding sites at peaks

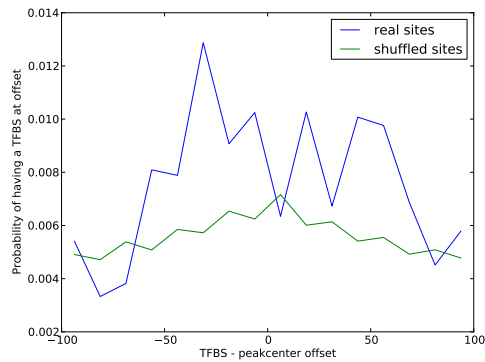


Figure 6: Histogram of distances of TFBS to its nearest peak center

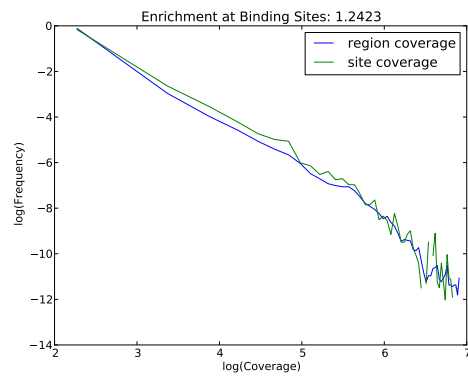


Figure 7: Histograms of coverage at sites and in total regions