General Motif Characteristics:

Top Similar Looking Motifs:

HOMER.NFAT_AP1.Jurkat−NFATC1−ChIP−Seq   0.000
HOMER.GATA−DR8(Zf).iTreg−Gata3−ChIP−Seq(GSE20898)   0.085
HOMER.Pax7−longest(Paired.Homeobox)   0.089
HOMER.Tcfcp2l1(CP2).mES−Tcfcp2l1−ChIP−Seq   0.090
HOMER.GATA−IR3(Zf).iTreg−Gata3−ChIP−Seq(GSE20898)   0.096
HOMER.p53(p53).Saos−p53−ChIP−Seq   0.097
HOMER.p63(p53).Keratinocyte−p63−ChIP−Seq   0.102
HOMER.GATA_SCL.Ter119−SCL−ChIP−Seq   0.102
HOMER.p53(p53).p53−ChIP−Chip   0.117
HOMER.FOXA1_AR.LNCAP−AR−ChIP−Seq(GSE27824)   0.123

Statistics:

− Motif name: HOMER.NFAT_AP1.Jurkat−NFATC1−ChIP−Seq
− Enrichment: 4.55052129333
− log−Likelihood Ratio: 239.408203825
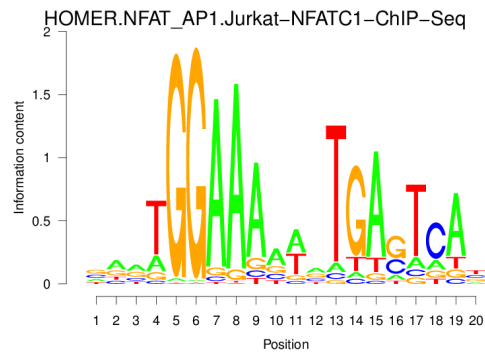− Area under precision recall curve: 0.2064
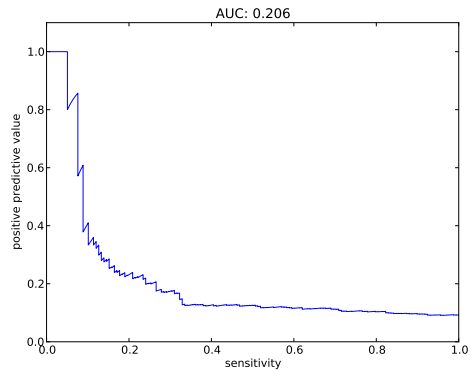

Figure 1: Logo of Weight Matrix

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:  427/542
        − 78.78  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:  1.1005
Correlation  between  peak  Z−score  and  number  of  binding  sites  at  peak:  −0.1684
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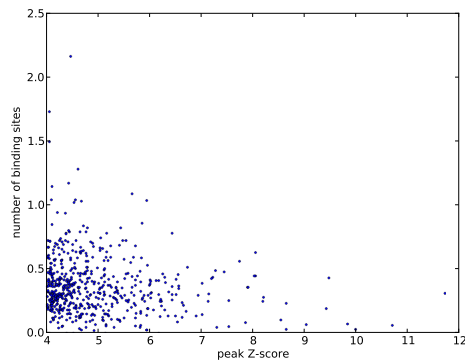

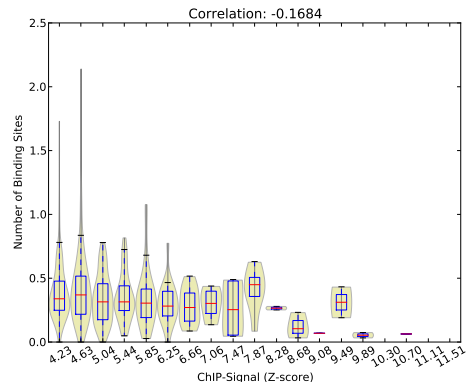Figure 3: Scatter plot of peak Z-score versus number of binding sites at peak

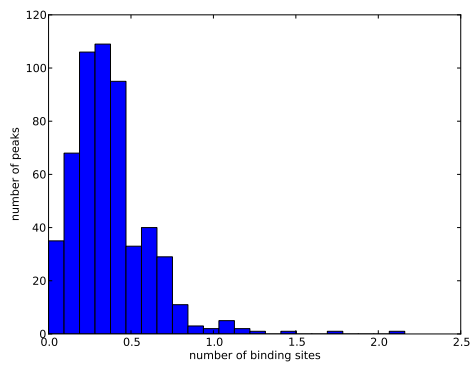Figure 4: Violin plot of peak Z-score versus number of binding sites at peak

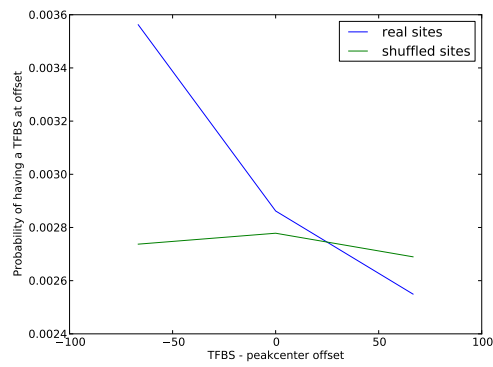Figure 5: Histogram of number of binding sites at peaks

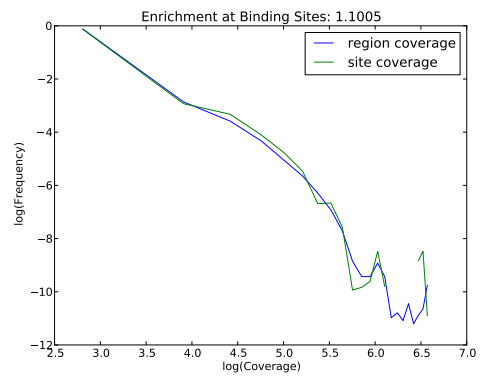Figure 6: Histogram of distances of TFBS to its nearest peak center

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