











	Joint Binding Deconvolution		Enrichment Ratios		Literature Specificity
	positional prior	no positional prior	positional prior	no positional prior	
Gcn4					
Mig2					

Figure 3: Motif discovery output. Motif discovery using JBD for sequence selection and positional priors recovers motifs consistent with the known binding specificities of Gcn4 and Mig2. We evaluated our motif discovery accuracy results along two dimensions: DNA sequence region selection method and positional prior use. In this comparison, input sequences were selected using either the JBD predicted binding strengths or IP enrichment ratios. Similarly, positional priors were derived either from JBD posterior probabilities or using interpolated IP enrichment ratios (see the Methods section for details). Also shown is the expected motif obtained from the TRANSFAC database for Gcn4 and as described by Lutfiyya *et al.* for Mig2. The log-odds weight matrices for Gcn4 and Mig2 are shown in Supplementary Table 2