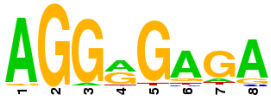
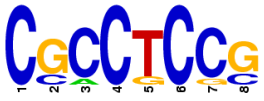
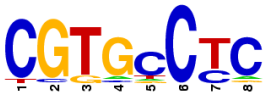
Supplement D - Promoter binding site motif search results

For the set of genes in each module, 500bp bases upstream of the transcription start site in each gene were tested for enriched motifs. Motifs were identified by the Amadeus de-novo motif finder (Halperin et al. 2006). Amadeus computes an enrichment score for each motif found, and indicates if the motif is similar to some known motif in TRANSFAC v8.3 database. In that case the motif name and the name of the TRANSFAC matrix are included.

Crz1 module	 enrichment = 1.6E-11	 enrichment = 4.2E-10	
Msn2/4 module	 enrichment = 1.1E-18 STRE[M00154] STRE[M00308]	 enrichment = 2.1E-11 STRE[M00308]	 enrichment = 8.3E-11 ETF[M00695]
Ste12 module	 enrichment = 1.7E-12 STE12[M00664]		
Hot1/Msn1 module	 enrichment = 1.8E-9		
Hog1B module	 enrichment = 2.5E-10		

Hog1/Ca module	 enrichment = 4.9E-9 GCR1[YP00022] GCR1[M00046]
Hog1A module	 enrichment = 3.3E-14

Y. Halperin, C. Linhart, G. Weber, R. Shamir. (2006) The AMADEUS motif discovery tool. RECOMB poster session. www.cs.tau.ac.il/~rshamir/Amadeus/