Regulator	Logo of Identified Motif	TRANSFAC Logo	Enrichment	Group Specificity Scores	
			ChIP-chip	Test Set	Matched Randoms
Ungapped Binding Site					
Gcn4	TGAGTCAT	TGACTCA	5.00×10^{-39}	2.10×10^{-38}	7.91×10^{-4} (7.50×10^{-1} - 6.00×10^{-22})
Pho4	Not Found	CACGTG	1.00×10^{-1}	1.00×10^{-20}	4.92×10^{-4} (8.50×10^{-1} - 6.90×10^{-21})
Reb1	cCGGGTAAc	CGGGTAA	6.00×10^{-54}	3.30×10^{-70}	1.04×10^{-3} (6.40×10^{-1} - 2.00×10^{-20})
Swi4	GACGCGAAA	CGCG	2.00×10^{-9}	1.90×10^{-29}	4.88×10^{-4} (7.40×10^{-1} - 5.10×10^{-22})
Yap1	cTTAcTAAT	GaTTAcTAAT [†]	9.00×10^{-11}	2.70×10^{-22}	2.17×10^{-2} (8.80×10^{-1} - 9.70×10^{-6})
Gapped Binding Site					
Abf1	CGT...AGTGAT	CGT...AATGAT	8.00×10^{-101}	2.50×10^{-124}	6.04×10^{-4} (5.80×10^{-1} - 5.30×10^{-43})
Gal4	Not Found	CGG...ACT..T...CCGAA	1.00×10^{-3}	2.20×10^{-15}	7.77×10^{-4} (6.30×10^{-1} - 2.00×10^{-19})
HSF1	GAAc.TTCTAGAAc	GAA	6.00×10^{-21}	6.70×10^{-32}	2.63×10^{-4} (7.30×10^{-1} - 4.90×10^{-23})
Mcm1	CC..AT..GGAAA	..TAAT..GGTAA	3.00×10^{-18}	1.20×10^{-51}	3.05×10^{-4} (8.90×10^{-1} - 9.20×10^{-20})
Rap1	aTGTAtGGGTg	aTGTaTGGGTtt	3.00×10^{-24}	7.70×10^{-84}	1.99×10^{-4} (7.10×10^{-1} - 1.00×10^{-21})

Additional Figure 1

Performance of MultiFinder with yeast ChIP-chip input sets. The logo for the highest scoring motif for each TF ("regulator") is shown next to the corresponding TRANSFAC [1,2] logo. The motif enrichment scores as determined by Lee *et al.* [3] are listed next to the corresponding motif. In order to determine the statistical significance of the motifs found by MultiFinder, 10 size-matched randomly selected sequence sets were generated for each of the 10 TFs and submitted to MultiFinder (see **Materials and methods**). The group specificity score for the best scoring motif in the test set is shown next to the geometric mean and range of scores for all of the motifs from 10 randomly generated size-matched sequence sets. [†] The Yap1 motif was not found in TRANSFAC; instead, the depicted motif was obtained from Cohen *et al.* [4]. Note that HSF1 binds as a trimer and that the TRANSFAC HSF motif corresponds to the binding site for just one monomer.

References for Additional Figure 1:

1. Matys V, Fricke E, Geffers R, Gossling E, Haubrock M, Hehl R, Hornischer K, Karas D, Kel A, Kel-Margoulis O, et al.: **TRANSFAC: transcriptional regulation, from patterns to profiles**. *Nucleic Acids Res.* 2003, **31**:374-378.
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3. Lee T, Rinaldi N, Robert R, Odom D, Bar-Joseph Z, Gerber G, Hannett N, Harbison C, Thompson C, Simon I, et al.: **Transcriptional regulatory networks in *Saccharomyces cerevisiae***. *Science* 2002, **298**:799-804.
4. Cohen BA, Pilpel Y, Mitra RD, Church GM: **Discrimination between Paralogs using Microarray Analysis: Application to the Yap1p and Yap2p Transcriptional Networks**. *Mol. Biol. Cell* 2002, **13**:1608-1614.