Table 2 (EXTENDED). Evaluation of the induced rules using the binding data from Lee et al. (2002) and Harbison et al (2004). A rule is said to be significant if at least one transcription factor binding any of the matching genes obtained a Bonferroni corrected P-value less than 0.01 (only bindings at P < 0.01 from Lee et al. (2002) were considered). The table gives the fraction of significant rules for each dataset, and compares these values to what is observed when randomly selecting corresponding sets of genes with only similar expression, common binding sites or neither. The P-value given for each dataset is the highest probability of observing a higher value than the one observed for the rules in any of the random tests (in fact all three tests produce one P-value each, but only the highest P-value is shown and indicated in bold). The table also gives the Euclidean distance threshold (normalized with a number of measurement points) used to define similar expression profiles and the number of rules induced for each expression dataset.

Expression data	Expression similarity thresholds	No. rules unique/all	Binding data evaluation (significant fractions P < 0.01) Lee et al./Harbison et al.			
			Rules (P-value)	**Random tests (std. dev.)**		
				Similar expression	**Common motifs**	**Random**
Cell cycle	0.250	39/109	0.538/0.487 (0.000)	0.109 (0.049)	0.171 (0.062)	0.019 (0.020)
Sporulation	0.250	45/81	0.133/0.178 (0.708)	0.085 (0.041)	**0.179 (0.057)**	0.015 (0.018)
Diauxic shift	0.200	150/428	0.291/0.315 (0.000)	0.061 (0.029)	0.183 (0.029)	0.016 (0.010)
Heat and cold shock	0.125	52/123	0.520/0.529 (0.000)	0.180 (0.053)	0.175 (0.053)	0.017 (0.018)
Pheromone	0.150	53/91	0.388/0.365 (0.001)	0.135 (0.048)	**0.170 (0.055)**	0.017 (0.018)
DNA-damaging agents	0.200	59/116	0.351/0.345 (0.000)	0.101 (0.040)	0.165 (0.049)	0.018 (0.018)