

**Table 3 (EXTENDED).** Evaluation of the induced rules using annotations from the three parts of Gene Ontology. A rule is said to be significant if at least one Gene Ontology term used to annotate the matching genes obtained a Bonferroni corrected P-value less than 0.01. The table gives the fraction of significant rules for each dataset and each part of Gene Ontology, 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).

Expression data	Gene Ontology evaluation (significant fractions P < 0.01)											
	Rule (P-values)			Random tests (std. dev.) Similar expression   Common motifs   Random								
	Molecular function	Biological Process	Cellular component	Molecular Function			Biological Process			Cellular component		
<b>Cell cycle</b>	0.308 (0.000)	0.462 (0.000)	0.410 (0.000)	0.049 (0.033)	0.037 (0.028)	0.011 (0.017)	0.132 (0.053)	0.180 (0.061)	0.027 (0.025)	0.027 (0.025)	0.042 (0.031)	0.002 (0.007)
<b>Sporulation</b>	0.262 (0.000)	0.535 (0.000)	0.442 (0.000)	0.077 (0.040)	0.043 (0.031)	0.013 (0.016)	0.188 (0.058)	0.170 (0.052)	0.023 (0.023)	0.050 (0.034)	0.025 (0.023)	0.002 (0.006)
<b>Diauxic Shift</b>	0.302 (0.000)	0.429 (0.000)	0.444 (0.000)	0.043 (0.017)	0.052 (0.019)	0.017 (0.010)	0.113 (0.027)	0.172 (0.032)	0.028 (0.014)	0.024 (0.013)	0.030 (0.015)	0.004 (0.005)
<b>Heat and cold shock</b>	0.538 (0.000)	0.635 (0.006)	0.596 (0.000)	0.238 (0.059)	0.059 (0.032)	0.033 (0.025)	<b>0.461</b> <b>(0.068)</b>	0.242 (0.060)	0.054 (0.031)	0.165 (0.052)	0.036 (0.025)	0.006 (0.011)
<b>Pheromone</b>	0.512 (0.000)	0.667 (0.000)	0.600 (0.000)	0.103 (0.043)	0.051 (0.031)	0.013 (0.016)	0.249 (0.064)	0.164 (0.056)	0.024 (0.022)	0.081 (0.038)	0.026 (0.021)	0.002 (0.006)
<b>DNA-damaging agents</b>	0.386 (0.000)	0.638 (0.000)	0.614 (0.000)	0.089 (0.037)	0.045 (0.027)	0.014 (0.015)	0.189 (0.050)	0.174 (0.048)	0.029 (0.022)	0.072 (0.034)	0.039 (0.024)	0.003 (0.007)