Supplementary Table 1(a): Complete list of promoter elements in the un-pruned model for yeast α-arrest experiment, listed in order from the last to be pruned from the model to the first. “Putative site” is the assignment of known binding site names to the elements. If the element does not match exactly to any known motif, it is labeled new\(_x\), where \(x\) is the order of appearance in the list. Many of the “new” motifs are similar to and may be variations of known motifs. “Phase” is the phase of the cell cycle at which the effect of the promoter element is strongest. The columns \(n\) and \(m\) are the number of genes in the training set and in Spellman’s 800 list, respectively, that contain the element. The column “p-value” contains the p-values for \((n, m)\) computed using Fisher’s exact test.

<table>
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<tr>
<th>Rank</th>
<th>Motif</th>
<th>Putative Site</th>
<th>Phase</th>
<th>(n)</th>
<th>(m)</th>
<th>P-value</th>
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<td>d-MCB</td>
<td>G1</td>
<td>582</td>
<td>380</td>
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<td>new1, new2, d-MCB</td>
<td>S</td>
<td>5</td>
<td>5</td>
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<td>mixed</td>
<td>160</td>
<td>123</td>
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<td>S (?)</td>
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<td>G2/M/G1</td>
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<td>ROX1, SFF</td>
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Supplementary Table 1(b): Information content $I_{seq}$ and corresponding $p$-values for the 20 base flanking sequences of promoter elements found for yeast α-reassort experiment.

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<th>Promoter element ($p$)</th>
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<th>$N(p, w)$</th>
<th>$I_{seq}$</th>
<th>$p$-value</th>
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<tr>
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<tr>
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<tr>
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</tr>
<tr>
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<td>TTGGTT</td>
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<tr>
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<tr>
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<tr>
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<td>TTGGCGG</td>
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<td>$1 \times 10^{-3}$</td>
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<tr>
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<td>TTGGTTT</td>
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Supplementary Table 2 (a,b): Gene list enrichment, annotation, and flanking sequence analysis for promoter elements identified in Wildermuth et al. (2007) Arabidopsis powdery mildew infection experiment.

Supplementary Table 2(a): Promoter elements in the unpruned model for Arabidopsis powdery mildew infection experiment, listed in order from the last to be pruned from the model to the first. “Putative site” is the assignment of known binding site names to the elements. Putative sites listed in Table 4 are specified by name as is the NFkB-like motif identified by Lebel et al. (1998) and associated with innate immunity. All other identified motifs are listed as new though some of these exhibit significant overlap with known motifs (Higo et al., 1999).

“Component” is the principal component with which the element has a strong effect, and “none” if no principal component significantly dominates the other. The columns n and m are the number of genes in the training set and in the top 1500-list, respectively, that contain the element. The column “p-value” contains the p-values for (n, m) computed using Fisher’s exact test.

<table>
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<th>Rank</th>
<th>Motif</th>
<th>Putative site</th>
<th>Component</th>
<th>n</th>
<th>m</th>
<th>P-value</th>
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<td>909</td>
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<tr>
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<td>W-box</td>
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<td>914</td>
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</tr>
<tr>
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<tr>
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**Supplementary Table 2(b):** Information content $I_{seq}$ and corresponding p-values for the 20 base flanking sequences of promoter elements found for arabidopsis mildew infection experiment.

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<th>Rank</th>
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<th>Word(w)</th>
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<th>$I_{seq}$</th>
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Supplementary Figures 1 and 2: Principal component analysis of Spellman et al. yeast cell cycle data.

Supplementary Figure 1: Principal components of the yeast α-arrest experiment.
Supplementary Figure 2: Scree plot for principal components of the yeast