

Table V. Enrichment for Genes with Promoters Containing
Adr1 and Pip2-Oaf1 Binding Sites

<u>Binding Site Consensus</u>	<u>% <i>ADR1</i>-dependent Promoters</u>	<u>% Promoters from Genome</u>
Adr1BS	90	79
UAS1-perfect	18	4
UAS1-imperfect	70	51
CSRE	17	17
ORE	25	11

All promoter sequences from -600 bp to the translation start site of the *ADR1*-dependent genes listed in Table III and all yeast nuclear gene promoter sequences of the same length were searched for matches to each binding site consensus sequence. The consensus sequences were as follows: Adr1BS, DYGGRG; UAS1, CYCCRHN{2,36}DYGGRG; ORE, CGGN{15,18}CCG; CSRE, CCDNHN{3}CCG. The UAS1-perfect consensus required an exact match to the consensus while the UAS1-imperfect allowed for a single mismatch at any position within the consensus. Promoters with one or more matches to each consensus were counted and divided by the total number of promoters searched, 108 for *ADR1*-dependent genes and 6182 for the entire yeast genome (RSA Tools Sequence Database), to calculate the percentage of promoters containing each binding site.