Supplemental Table 2. Existence of SLIM1/EIL3 Binding Site, AYGWAYCT, in the Upstream Regions.

Gene classification	Number of genes		Frequencies of AYGWAYCT (%)			single-P
	all	AYGWAYCT observed	specific gene class	other genes	random rate	
All genes	16,731	1,598	9.6	9.0	13.1	1.000
└ -S-responsive in parental line	469	54	11.5	9.4	13.1	0.854
├ SLIM1-dependent, S15>S1500 in parental line	52	13	25.0	9.4	12.9	0.013
├ SLIM1-dependent, S1500>S15 in parental line	27	3	11.1	9.4	13.0	0.698
└ SLIM1-dependency not significant	390	38	9.7	9.4	13.1	0.982

Classifications of SLIM1-dependent genes correspond to those in Figure 5A and Supplemental Table1. AYGWAYCT sequences were searched on the 10 bp to 800 bp upstream regions of all genes. Frequencies of the binding sequence in other genes on the Affymetrix ATH-1 GeneChip, those with random base distributions (random rates), and single-P values showing the probability that this particular sequence is that common due to chance, were calculated using GeneSpring 7.2 (Silicon Genetics).