

Web Table H: Potential regulatory motifs.

The upstream sequences of all ORFs (500 bp) were scanned for the presence of short oligomers over-represented in a cluster with respect to the whole genome. The identified sequences were similar to previously known binding sites (related motif column). The frequencies of motif occurrence both within the clusters and in random genomic sequences are indicated. The p values indicate the probabilities that the observed results are due to chance. The last column shows the percentage of genes containing more than one copy of the motif in their upstream sequences.

Cluster	Sequence	Related Motif (Reference)	Orientation	Frequency (cluster)	Frequency (genome)	p value	>1 copy
Starvation/ pheromone (delayed)	TCTTTGT	TR box (19)	forward	40% (16/40)	9.5%	0.036	52%
			reverse	45% (18/40)	4.8%	1.0e-8	
Early	ACGCGT	MluI box (20)	palindrome	32% (30/94)	4.1%	0.013	25%
Middle	GTAAACA	FLEX (8)	forward	22.6% (122/540)	9.12%	9.6e-16	30%
			reverse	35.0% (189/540)	12.3%	4.2e-37	
Late	TGACGGT (0/1 mismatch)	ARE (21)	forward	44% (58/129)	21.06%	2.8e-4	22%