	Number of Sites				
	1	2	3	4	5
Number of Genes					
Operons	76	18	9	7	2
Non-Operons	79	17	2	0	3

Supplementary Table 1: Phylogenetic footprints in B. subtilis correlate with operons. We show the distribution of the number of predicted regulatory sites (from Terai *et al.* 2001) upstream of predicted operons and upstream of predicted single-gene transcripts. As discussed in the text, operons have a significantly larger average number of sites. More specifically, operons are significantly more likely to have three or more sites ($p = 0.01$, Fisher exact test).