

Table S2 Position weight matrix used to scan the SAM and ORE genomes for SD binding sites, derived from a MEME (Bailey et al. 2009) scan of 23 known SD binding sites.

	A	C	G	T
1	0	5	14	4
2	8	1	14	0
3	18	4	0	1
4	22	0	1	0
5	0	0	0	23
6	3	0	14	6
7	3	3	3	14