Table S2. New gap factor PWMs used in this study

GT (12)			
3	0	2	11
9	2	3	2
1	0	0	15
0	1	2	13
9	1	5	1
2	9	2	3
3	2	9	2
1	5	1	9
13	2	1	0
15	0	0	1
2	3	2	9
11	2	0	3
KNI (12)			
31	7	4	11
43	1	3	6
32	2	3	16
9	16	11	17
3	9	10	31
37	5	11	0
0	1	52	0
33	1	10	9
8	4	25	16
0	52	0	1
45	2	5	1
12	21	17	3
TLL (10)			
34	10	9	12
47	1	10	7
55	5	5	0
54	4	7	0
5	0	60	0
2	2	2	59
1	53	2	9
60	0	3	2
53	3	5	4
35	14	6	10

For some participating transcription factors, our original PWMs were either overly specific (GT) or too unspecific (KNI, TLL) (Schroeder et al., 2004). We therefore generated new PWMs, utilizing the results of a recent bacterial one-hybrid study of segmentation factor binding preferences (Noyes et al., 2008b). The PWMs reported in that paper are too specific and miss known footprinted sites, but we found that superior PWMs could be generated by realigning the footprinted binding sites from literature we used previously (Rajewsky et al., 2002; Schroeder et al., 2004) and combining them with the aligned sites from the bacterial one-hybrid data. For GT, which has only a few footprinted sites, the combined PWM remains overly specific; we therefore generated a new PWM using only the known sites, but aligned in both orientations to reflect the palindromic nature of the bacterial one-hybrid PWM. PWMs are shown in Stubb format, with each row representing a position and each column a base in the order ACGT.