

Table S2. Alignment Matrices Used in the Model

Bicoid														
A	83	74	108	48	6	381	379	5	0	6	72	61	65	68
C	114	159	127	149	1	0	0	0	383	340	136	174	166	158
G	106	72	114	11	0	2	4	4	0	3	132	60	52	49
T	80	78	34	175	376	0	0	374	0	34	43	88	100	108
Caudal														
A	9	12	3	4	12	38	0	4	22	1				
C	10	6	3	0	0	0	0	0	0	8				
G	4	4	3	0	2	0	0	7	15	10				
T	11	16	29	34	24	0	38	27	1	1				
D-STAT														
A	1	1	2	1	1	5	3	0	24	28	27	5		
C	0	0	1	27	20	16	3	2	3	0	1	8		
G	0	1	0	1	6	8	22	27	1	1	0	6		
T	29	28	27	1	3	1	2	1	2	1	2	1		
Dichaete														
A	1	0	0	20	0	0	2	0	1	4	6			
C	8	25	17	0	0	0	0	0	2	10	1			
G	7	0	0	0	0	3	27	0	4	6	1			
T	13	4	12	9	29	26	0	29	22	9	21			
Hunchback														
A	53	2	0	2	0	0	0	281	31	20				
C	6	6	2	0	2	3	2	0	43	100				
G	224	3	0	0	0	0	0	3	78	109				
T	7	279	288	288	288	287	288	6	138	61				
Kruppel														
A	17	187	158	0	1	0	8	0	2	44				
C	73	5	39	194	194	197	22	2	34	109				
G	6	0	0	1	0	0	6	0	2	15				
T	101	5	0	2	2	0	161	195	159	29				
Knirps														
A	19	25	16	5	0	21	0	17	1	0	25	5		
C	1	1	0	9	4	0	0	0	3	26	0	12		
G	2	0	0	6	1	5	26	8	18	0	1	7		
T	4	0	10	6	21	0	0	1	4	0	0	2		
Giant														
A	86	12	776	8	83	0	1020	1106	15					
C	62	108	25	762	19	556	88	0	378					
G	19	359	275	65	996	0	1	0	85					
T	942	630	33	274	11	553	0	3	631					
Tailless														
A	12	1	1	5	2	11	1	0	0					
C	8	2	2	1	3	1	17	2	3					
G	0	2	1	0	15	5	0	1	2					
T	0	15	16	14	0	3	2	17	15					

For each PWM, the left most column indicates DNA bases. The remaining columns show the number of observed bases at each position in the binding site.