

**Table S3. Binding site predictions (Stubb integrated profile values) for pair-rule gene cis-elements**

cis-element	Length	Bcd	Cad	Stat	Gt	Hb	Hkb	Kni	Kr	Tll	Slp1
eve_stripe1	801	1.2		0.8			1.9		1.6	0.9	0.9
eve_stripe2	663	1.4			0.4	1.1		0.5	1.5	0.5	
eve_stripe3_7	511		0.9	1.8		3.1		4.3			0.4
eve_stripe4_6	602		2.8	1.0		2.6		0.4		0.5	
eve_stripe5	800	0.5	0.7	0.4	0.4	1.0	0.5		1.7	1.0	
eve_late	1288	0.6				0.9		0.7			
ftz_+3	1745	0.9	1.8	1.3	1.0	1.4			2.1	2.7	1.0
ftz_-1	1075		1.6	1.2	0.6	1.6					1.8
ftz_-6	1240	0.8	1.1	0.9	1.8	2.4		2.7	0.7		
ftz_-7	1618	0.8	1.7			3.3		1.4		1.0	
ftz_zebra	1118		1.3	1.2		1.5					1.3
ftz_autoreg	2241		1.2		1.3	1.7					
ftz_LacC	6489		4.1	3.4	3.8	6.0		2.8			4.1
h_stripe1+5	2971	2.3	2.6	2.3		3.6	2.3		5.8	3.7	
h_stripe1	1286	0.9	1.2	0.9		1.2	2.0		4.5	2.7	
h_stripe2+6	1081		4.0	2.1		2.5			3.5	1.7	
h_stripe3+4	912		1.6		1.0	2.8	0.8	1.6			0.6
h_stripe5	1674	1.4	1.4	1.4		2.3			1.3	0.9	
h_stripe7	1474		1.9	1.1		4.6		3.1	2.5	1.2	0.7
odd_-1	1510		1.2		1.0	1.2			1.4	1.2	
odd_-3	1650		2.1	1.5		3.4		1.8	0.9	1.1	1.0
odd_-5	1384		0.8			0.7	0.9		2.4	0.9	1.1
odd_-10	5102			2.9		2.7	2.9			2.4	4.3
odd_basal-1	2431		1.7		1.1	1.4			1.9	1.6	
run_-41_42	2323		3.8	1.2		5.8		1.2	2.7	4.0	
run_-31	2524		1.7	1.3		3.4			2.1		1.3
run_-16	2519	1.2		1.1		1.9		1.2	3.9	3.7	2.4
run_-17	997		2.7	0.9	0.9	4.6				0.5	0.8
run_+19	2261		1.9			3.1	1.0	2.0	1.8	2.2	1.5
run_+30	2709		1.6	2.3	1.9	3.5	1.8	1.5	4.5	1.5	2.5
run_-3	1371	2.6	1.9	1.1	0.7	1.4	1.2		1.2	0.7	
run_-3_Kr-	1371	2.6	1.8	1.1	0.8	1.4	1.2			0.7	
run_-10	862		1.8	0.8	0.9	4.3	0.6	2.9			
run_7stripes	5092	3.8	4.5		2.4	6.4	3.1		2.6		2.7
run_stripe1	1617	1.9		0.9		1.1	0.8		2.2	2.0	1.3
run_stripe3	2315		2.5	0.9	1.3	5.4		2.9			1.8
run_stripe5	1336		1.2		0.7	1.8			0.7	1.2	

When predicting binding site strength, the use of a local background model and the adjustment of the probability of site occurrence for each factor by the Stubb optimization procedure means that an identical DNA sequence can score differently in different cis-elements. To ensure maximum comparability of binding site predictions across different elements, we therefore ran Stubb as follows: each cis-element was analyzed as a single window with only one transcription factor at a time; in each case, the probability of site occurrence was fixed at the same low value (0.0005), and the same zero order background model, generated from the pooled genomic sequence of all segmentation genes, was used. Stubb assigns each potential binding site in the sequence a probability from 0 to 1, and the integrated profile value is the sum over all sites, thus representing a robust predictor of the total strength of input.