Table S2 – Bcd binding strengths

Model *Experiment*	1A[a] *pThb3*	3A *pThb10*	3X *pThb12*	4A *pThb11*	4X *pThb13*	3A3X[b] *hb[14F]*	2x(3X)[c] *pThb15*	3x(3X)[d] *pThb16*
Position of boundary (%EL)	35	35	21	42	23	42	28	30
Sharpness (degrees)	43	54	57	63	64	72	62	63
1st Bcd binding (k_{11}, $M^{-1}\,s^{-1}$)	2.8e7	2.8e7	1.09e7	2.8e7	1.09e7	2.8e7	1.09e7	1.09e7
2nd Bcd (k_{14})		3.6e7	1.67e7	3.6e7	1.67e7	3.6e7	1.67e7	1.67e7
3rd Bcd (k_{17})		4.18e7	1.94e7	4.18e7	1.94e7	4.18e7	3e8	4e8
4th Bcd (k_{20})				4.25e8	1.4e8	1.4e8		
5th Bcd (k_{23})						1.4e8		
6th Bcd (k_{26})						1.4e8		

These values are relative to unbinding rates (k_{12}, k_{15}, k_{18}, k_{21}, k_{24}, k_{27}) of 1/s. The model Bcd gradient was determined by k_8=3.5e-3 and k_9=2e-3, set to match the experimentally measured shape [3], and by a Bcd diffusivity D_{Bcd}=20μm²/s (embryo-scale value measured in [57]).
[a] **A** strong site, **X** weak site (see Figure 2A).
[b] The core Bcd sites of the proximal promoter, no Hb self-binding.
[c] 2 copies of the 3X sequence; the 3rd site of the 3X segment was strengthened to match experimental position.
[d] 3 copies of the 3X sequence; the 3rd site of the 3X segment was strengthened to match experimental position.