File 3A: The **146 Ahab** module predictions were examined for the presence of neighboring genes with blastoderm expression based on the BDGP/Celera genome annotation (Release 2) and the existing literature. The four genes closest to the module were examined, and the position of the module relative to the patterned gene is noted, including whether other genes are more proximal (up = upstream, down = downstream, intra = intragenic, 1 = closest gene, 2 = 2nd closest gene etc). The list also includes genes/regions that were hit more than once. The columns give the rank and score of each module, and indicate whether the module was recovered with any of the other methods (File 3A = Ahab 146, File 3B = Ahab – Tll, File 3C = Ahab window 700, File 5 = Gibbs on hairy + Ahab). Modules whose annotated binding sites were used to construct weight matrices are marked by a star.

Rank	Score	Gene	Genomic organization	Comments	Rank in File				References
					3A	3B	3C	5	
1 *	37.82	hairy	up / 9.2 kb / 1		1	1	3	2	(1)
2 *	28.29	knirps	up / 1.6 kb / 1		2	5	26	-	(2)
3 *	27.24	tailless	up / 2.6 kb / 1		3	2	1	-	(3)
5 *	25.32	knirps	up / 1.1 kb / 1		5	-	2	-	(2)
6	23.97	Cyp6V1	down / 1.6 kb / 1		6	4	16	-	double hit, see module 14
8	20.80	runt	up / 3.2 kb / 1		8	10	10	-	(4)
9	19.89	optix = six3	down / 11 kb / 2	1: down 3.7 kb (CG12769)	9	-	68	-	(5)
10	19.75	Dichaete	down / 2.3 kb / 1		10	11	11	-	(6, 7)
11	19.66	CG13595?	down / 4.5 kb / 2	1: up 1.2 kb (CG4871)	11	59	19	-	double hit, see module 137
14	19.32	Cyp6V1	up / 6 kb / 1		14	41	28	-	double hit, see module 6
17	18.88	Tenascin-m	up / 110 kb /	neighboring CGs very small ORFs	17	-	33	-	(8)
18	18.87	giant	down / 14.5 kb / 2	1: up 1.3 kb (CG12469)	18	13	-	-	(9)
20 *	18.76	Krüppel	up /4.1 kb/ 1		20	12	5	-	(10, 11)
23	18.30	ken	intra		23	19	48	-	(12)
24	18.29	giant	up / 2.1 kb / 1		24	62	36	-	(9)
25	18.29	hairy	up / 4.7 kb / 1		25	8	8	-	(1)
27	18.06	hairy	up / 5.4 kb / 1		27	8	8	-	(1)
34	17.36	hairy	up / 10.4 kb / 1		34	30	193	1+4	(1)
36 *	17.25	even skipped	up / 3.5 kb / 1		36	26	9	-	(13, 14)
37	17.15	knirps-like	intra		37	-	117	-	(15)
41 *	17.02	hairy	up / 6.2 kb / 1		41	49	-	3	(1)
43	16.94	brinker	up / 10.9 kb / 2	1: up 5.6 kb (unc 119)	43	-	41	-	(16)
45	16.83	pipsqueak	intra		45	-	20	-	(17)
46	16.82	teashirt	intra		46	-	29	-	(18)
48 *	16.80	short gastrulation	intra		48	7	25	-	(19)
51	16.76	abdominal-A	up / 17 kb / 1		51	-	122	-	(20)
54	16.65	Abdominal-B	up / 15.3 kb / 2	1: down 11.7 kb (CG11648)	54	33	-	-	(21)
55	16.62	echinoid	up / 58 kb / 2	1: down 11.8 kb (CG 10039 / small ORF)	55	-	111	-	double hit, see module 93
58	16.34	CG2118/Acf1/faf	intra	2: up 2.4 kb Acf1 3: 1.5 kb down (faf)	58	-	-	-	double hit, see module 69
61	16.20	vnd	intra		61	9	30	-	(22)
69	16.01	faf/Acf1/CG2118	intra	2: up 5.2 kb Acf1 3: down 2 kb CG2118	69	-	-	-	double hit, see module 58
75	15.90	cap n' collar	up / 4.3 kb / 1		75	63	-	-	(23)
76 *	15.89	even skipped	up / 1.7 kb / 1		76	42	283	-	(13, 14)
91	15.69	runt	up / 9.67 / 1		91	45	112	-	(4)
93	15.66	echinoid	intra		93	-	47	-	double hit, see module 55
105	15.51	bruno 3	up / 95 kb / 2	1: down 89 kb	105	48	236	-	double hit, see module 130
117	15.37	CG5060	up / 31.1 kb	uncertain which locus but good evidence for control region	117	54	195	-	double hit, see module 132
120 *	15.34	tailless	up / -.64 kb / 1		120	24	-	-	(3)
124	15.32	proboscopedia	intra		124	-	284	-	(24)
126	15.29	runt	up / 17.2 kb / 3	1: 3.7 kb up (CG1338) 2: 6.6 kb down (CG1835)	126	57	57	-	(4)
129 *	15.24	hunchback	up / 3.34 kb / 1		129	-	37	5	(25)
130	15.22	bruno 3	up / 25.1 kb /		130	-	-	-	double hit, see module 105
132	15.18	CG5060	up / 30.1 kb		132	-	-	-	double hit, see module 117

References for File 3A

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2. Nauber, U., Pankratz, M. J., Kienlin, A., Seifert, E., Klemm, U. & Jackle, H. (1988) *Nature* **336,** 489-492.
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20. Karch, F., Bender, W. & Weiffenbach, B. (1990) *Genes Dev* **4,** 1573-1587.
21. Celniker, S. E., Keelan, D. J. & Lewis, E. B. (1989) *Genes Dev* **3,** 1424-1436.
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File 3B: 67 modules predicted by **Ahab after the removal of the least specific matrix (Tailless)** were examined for the presence of neighboring genes with blastoderm expression based on the BDGP/Celera genome annotation (Release 2) and the existing literature. The four genes closest to the module were examined, and the position of the module relative to the patterned gene is noted, including whether other genes are more proximal (up = upstream, down = downstream, intra = intragenic, 1 = closest gene, 2 = 2nd closest gene etc). The list also includes genes/regions that were hit more than once. The columns give the rank and score of each module, and indicate whether the module was recovered with any of the other methods (File 3A = Ahab 146, File 3B = Ahab – Tll, File 3C = Ahab window 700, File 5 = Gibbs on hairy + Ahab). Modules whose annotated binding sites were used to construct weight matrices are marked by a star.

Rank	Score	Gene	Genomic organization	Comments	Rank in File				References
					3A	3B	3C	5	
1 *	35.02	hairy	up / 9.2 kb / 1		1	1	3	2	(1)
2 *	26.71	tailless	up / 2.7 kb / 1		3	2	1	-	(2)
4	23.97	Cyp6V1	down / 1.6 kb / 1		6	4	16	-	double hit, see module 41
5 *	23.31	knirps	up / 1.6 kb / 1		2	5	2	-	(3)
7 *	20.64	short gastrulation	intra		48	7	25	-	(4)
8	20.13	hairy	up / 5.2 kb / 1		27+25	8	8	-	(1)
9	20.09	vnd	intra		61	9	30	-	(5)
10	19.98	runt	up / 3.2 kb / 1		8	10	10	-	(6)
11	19.75	Dichaete	down / 2.3 kb / 1	2: up 41kb (CG6419)	10	11	11	-	(7, 8)
12 *	19.73	Krüppel	up / 4.3 kb / 1		20	12	5	-	(9, 10)
13	18.87	giant	down / 14.5 kb / 2	1: up 1.3 kb (CG12496)	18	13	-	-	(11)
19	18.23	ken	intra		23	19	48	-	(12)
24 *	17.46	tailless	up / -.5 kb / 1		120	24	-	-	(2)
26 *	17.25	even skipped	up / 3.5 kb / 1		36	26	9	-	(13, 14)
30	16.52	hairy	up / 10.5 kb / 1		34	30	193	1+4	(1)
33	16.27	Abdominal-B	up / 15.3 kb / 2	1: down 11.7 kb (CG11648)	54	33	-	-	(15)
41	15.85	Cyp6V1	up / 6 kb / 1		14	41	28	-	double hit, see module 4
42	15.79	even skipped	up / 1.4 kb / 1		76	42	283	-	(13, 14)
45	15.69	runt	up / 9.6 kb / 1		91	45	112	-	(6)
48	15.51	bruno 3	up / 95 kb / 2	1: down 89 kb (CG8757)	105	48	236	-	double hit in File 3A (105 + 130)
49 *	15.48	hairy	up / 6.2 kb / 1		41	49	-	3	(1)
54	15.37	CG5060	up / 31 kb / 4	1: 2: 3: down	117	54	195	-	double hit in File 3A (117 + 132)
57	15.25	runt	up / 17 kb / 3	1: up 3.8 kb (CG1338) 2: down 8 kb (CG1835)	126	57	57	-	(6)
62	15.17	giant	up / 2 kb / 1		24	62	36	-	(11)
63	15.08	cap n' collar	up / 4.3 kb / 1		75	63	-	-	(16)

References for File 3B

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File 3C: 290 modules predicted by **Ahab after the window size had been increased to 700 bp** were examined for the presence of neighboring genes with blastoderm expression based on the BDGP/Celera genome annotation (Release 2) and the existing literature. The four genes closest to the module were examined, and the position of the module relative to the patterned gene is noted, including whether other genes are more proximal (up = upstream, down = downstream, intra = intragenic, 1 = closest gene, 2 = 2nd closest gene etc). The list also includes genes/regions that were hit more than once. The columns give the rank and score of each module, and indicate whether the module was recovered with any of the other methods (File 3A = Ahab 146, File 3B = Ahab – Tll, File 3C = Ahab window 700, File 5 = Gibbs on hairy + Ahab). Modules whose annotated binding sites were used to construct weight matrices are marked by a star.

Rank	Score	Gene	Genomic organization	Comments	Rank in File				References
					3A	3B	3C	5	
1 *	38.96	tailless	up / 2.8 kb / 1		3	2	1	-	(1)
2 *	34.48	knirps	up / 1.1 kb / 1		2+5	5	2	-	(2)
3 *	33.99	hairy	up / 9.2 kb / 1		1	1	3	2	(3)
5 *	26.64	Krüppel	up / 4.3 kb / 1		20	12	5	-	(4, 5)
8	25.42	hairy	up / 5 kb / 1		25	8	8	-	(3)
9 *	23.21	even skipped	up / 3.7 kb / 2	1: down 2.7 kb (CG12134)	36	26	9	-	(6, 7)
10	22.86	runt	up / 3.4 kb / 1		8	10	10	-	(8)
11	22.70	Dichaete	down / 2.3 kb/ 1		10	11	11	-	(9, 10)
16	22.13	Cyp6v1	down / 1.5 kb / 1	2: up 5.5 kb (CG1835 - vsmall ORF)	6	4	16	-	Double hit (16 + 28), also in File 3A (6 + 16)
20	21.37	pipsqueak	intra		45	-	20	-	(11)
24	20.96	Krüppel	up / 1kb / 1		-	-	24	-	(4, 5)
25 *	20.94	short gastrulation	intra		48	7	25	-	(12)
26	20.86	knirps	up / 1.8 kb / 1		2	5	26	-	(2)
28	20.51	Cyp6v1	up / 6 kb / 1		14	41	28	-	double hit (16 + 28), also in File 3A (6+16)
29	20.48	teashirt	intra		46	-	29	-	(13)
30	20.47	vnd	intra		61	9	30	-	(14)
33	20.01	Tenascin-m	up / 94 kb / 4	neighboring CGs v small ORFs	17	-	36	-	(15)
36	19.87	giant	up / 1.9 kb / 1		24	62	36	-	(16)
37	19.86	hunchback	up / 3.2 kb / 1		129	-	37	5	(17)
40	19.75	grainyhead	intra		-	-	40	-	(18)
41	19.66	brinker	up / 10.8 kb / 2	1: up 5.7 kb (CG1659)	43	-	41	-	(19)
42	19.66	hephaestus	intra		-	-	42	-	(20)
47	19.36	echinoid	intra		93	-	47	-	double hit in File 3A (55+93)
48	19.33	ken	up / -.1 kb / 1		23	19	48	-	(21)
52	19.05	Furin 1	up / 60 kb / 3		-	-	52	-	quadrupel hit, see modules 74, 131, 201
54	18.99	dachsous	intra		-	-	54	-	(22)
57	18.78	runt	up / 17 kb / 3	1: up 3.8 kb (CG1338) 2: down 6.7 kb (1835)	126	57	57	-	(8)
58	18.70	Antennapedia	up / 6.9 kb / 1		-	-	58	-	(23)
63	18.65	tailless	up / 1.5 kb / 1		-	-	63	-	(1)
68	18.44	Optix	down / 11 kb / 2	1: down 2.2. kb (CG12769)	9	-	68	-	(24)
74	18.27	Fur1	up / 21 kb / 1		56	-	74	-	quadrupel hit, see modules 52, 131, 201
85	17.91	ushaped	up / 12.7 kb / 1		-	-	85	-	(25)
86	17.91	paired	down / 2.5 kb / 1	2: up 12.9 kb (CG 5325)	-	-	86	-	(26)
92	17.70	CG14678	up / 71 kb/ 2	1: down 2 kb (CG11373	52	-	92	-	double hit, see module 151
94	17.66	CG1573	up / 11 kb / 2	1: down 3.7 kb (CG1733)	-	-	94	-	double hit, see module 228
99	17.46	caudal	down / 2.3 kb / 1	2: up 3.1 kb (CG9324 -small ORF)	-	-	99	-	(27)
103	17.40	CG13034	down / -.7 kb / 1	2: up 24.7 kb (CG4541)	-	-	103	-	double hit, see module 187
112	17.16	runt	up / 9.8 kb / 1		91	45	112	-	(8)
117	17.09	knirps-like	intra		37	-	117	-	(28, 29)

120	17.05	Abdominal-B	down / 40 kb / 2	1: down 1.6 kb (CG10349) 3: up 57 kb abd-A	-	-	120	-	(30)
122	17.04	abdominal-A	up / 17 kb /1		51	-	122	-	(31)
131	16.95	Furin1	up / 43 kb / 3	1: up 31 kb (CG5127) 2: down 34 kb (CG4553)	-	-	131	-	quadruple hit, see modules 52, 74, 201
136	16.89	knirps	intra		-	-	136	37	(2)
137	16.88	CG8965	up / 11 kb / 3	1: down 1.5 kb (CG9024) 2: down 4.3 kb (CG9029)	-	-	137	-	double hit, see module 198
151	16.75	CG14678	up / 30 kb / 1		-	-	151	-	double hit, see module 92
156	16.65	sloppy paired 2	up / 3.5 kb / 1	2: down 6.1 kb (slp1)	-	-	156	-	(32)
167	16.57	runt ?	down / 38 kb / 4	1: up 29 bp (CG1324) 2: down 9 kb (CG15452) 3: down 35 kb (shakB)	-	-	167	-	(8)
174	16.52	odd skipped	up / 4.3 kb / 1		-	-	174	-	(33)
179	16.44	irre C	up / 144 kb / 2	1: up 13 kb (kirre)	-	-	179	-	(34)
193	16.35	hairy	up / 10.5 kb / 1		34	30	193	1+4	(3)
195	16.34	CG5060	up / 31 kb / 3	1: down 12.3 kb (CG15683) 2: down 21 kb (CG17201)	117	54	195	-	double hit in File 3A (117 + 132)
201	16.28	Furin1	up / 17 kb / 1		-	-	201	-	quadruple hit, see modules 52, 74, 131
202	16.27	Hr38	intra		-	-	202	-	(35)
203	16.27	Goosecoid	up / 2.5 kb / 1		-	-	203	-	(36)
204	16.26	no ocelli	down / 29 kb / 2	1: down 24 kb (CG4218) 3: up 72 kb (CG15283)	-	-	204	-	(37)
228	16.07	CG1573	intra		-	-	228	-	double hit, see module 94
232	16.03	AlstR	up / 16 kb / 1		-	-	232	-	double hit, see module 260
235	15.99	TepIV	up / 2.5 kb / 2	1: up -.4 kb (CG10337)	-	-	235	-	double hit, see module 268
236	15.99	bruno 3	up / 95 / 2	1: down 89 kb (CG8757)	105	48	236	-	double hit in File 3A (105 + 130)
260	15.84	AlstR	up / 16 kb / 1		-	-	260	-	double hit, see module 232
268	15.80	TepIV	intra		-	-	268	-	double hit, see module 235
269	15.79	spalt-m	up / 31 kb/ 3	1: up 9.6 kb (sala) 2: down 20 kb (CG6488)	-	-	269	-	(38)
277	15.75	abdominal-A	up / 35 kb / 2	1: up 15 kb (CG10349)	-	-	277	21	(31)
283	15.72	even skipped	up / 1.5 kb / 1		76	42	283	-	(6, 7)
284	15.71	proboscipedia	intra		124	-	284	-	(39)

References for File 3C

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