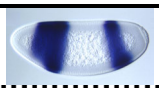
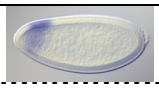
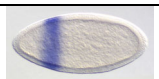
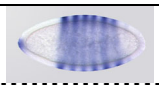
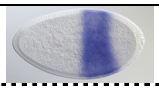
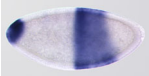
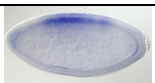
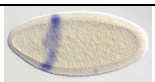
Table 2: Novel binding site clusters identified in genome-wide searches and their flanking genes. For 23 clusters located in intergenic regions, both adjacent genes are shown. For 5 clusters located in introns, only containing gene is shown.

Cluster number	*Cyto-logical position*	*Flanking gene(s)*	*Cluster start position**	*Cluster end position**	*Annotated molecular function*	*Whole mount in-situ hybridization hour 0-4*[†]	*Embryonic DNA microarray*[‡]	*Known Regulators*	*References*
1	3A	gt	-2,759	-1,815	RNA Polymerase II Transcription Factor		+	*bcd, cad, hb, Kr*	(1-6)
		tko	+12,310	+13,254	structural protein of the ribosome	not available	+		
2	4B	CG12688	+2,033	+3,039	none	not available	-		
3,4	5C	CG3011	-1,966	-1,341	glycine hydroxymethyltransferase	not available	-		
		CG3726	-4,038	-3,344	none	ubiquitous	+		
5	7A	CG9650	+23,470	+24,018	transcription factor	ubiquitous	+		
		CG1958	-11,100	-10,552	none	no staining	-		
6	7B	CG11368	+46,957	+47,595	none	no staining	-		
		CG11369	-75,488	-74,850	none	not available	inconclusive		
7	7F	otd	+37,924	+38,583	RNA Polymerase II Transcription Factor		+	*bcd, hb*	(7-9)
		Caf1-180	-6,195	-5,536	nucleosome assembly chaperone	ubiquitous	+		
8	8F	btd	+23, 975	+24,716	RNA Polymerase II Transcription Factor		+	*bcd, hb*	(10, 11)
		Sp1	-34,117	-33,376	RNA Polymerase II Transcription Factor	not available	+		
9	12E	CG5291	-9,253	-8,590	Immunoglobulin and major histocompatibility complex	not available	-		
		CG18313	+34,741	+35,404	none	not available	-		
10	24A	odd	-3,394	-2,634	RNA Polymerase II Transcription Factor		+		(12)
		Dot	-10,102	-9,342	UDP glucuronosyl transferase	not available	inconclusive		
11	33E	pdm1	-2,519	-1,825	RNA Polymerase II Transcription Factor		+	*hb, kni*	(13)

		CG15488	+2,688	+3,382	None	not available	-		
12	33F	pdm2	-3,596	-2,873	RNA Polymerase II Transcription Factor		+	*hb*	(13)
		CG15486	+2,085	+2,808	None	not available	inconclusive		
13	34E	bgm	-6,635	-5,785	long-chain-fatty-acid-CoA-ligase	patterned (early gastrulation)	+		
		rk	-14,492	-13,642	G-protein coupled receptor	no staining	-		
14	36F	Fas3	+39,849	+40,550	cell adhesion	not available	-		
		RpS26	+19,831	+20,532	structural protein of ribosome	not available	+		
15	47A	psq	+45,838	+46,493	Transcription Factor		+		(14)
16	55C	sbb	-2,637	-1,934	Zinc-finger C2H2	ubiquitous	+		
		CG14502	-3,199	-2,496	none	no staining	+		
17	56B	CG7097	+24,150	+24,783	protein serine/threonine kinase	not available	+		
18	59B	CG13534	+5,589	+6,305	none	not available	+		
		CG9898	+32,094	+32,810	serine-type peptidase	no staining	-		
19	67B	CG14178	+19,239	+19,905	none	no staining	-		
		CG17357	-8,941	-8,275	none	not available	-		
20	70F	CG17705	+10,471	+11,181	none	no staining	inconclusive		
		CG13473	-12,244	-11,534	electron transfer/thioredoxin	no staining	-		
21	75C	rpr	+6,616	+7,368	unknown		+		
		grim	-87,688	-86,936	unknown	not available	inconclusive		
22	76C	CG8786	-2,356	-1,652	none	ubiquitous	+		
		CG8782	+4,833	+5,537	ornithine-oxo-acid aminotransferase	no staining	-		
23	84A	Dfd	-22,070	-21,370	RNA Polymerase II Transcription Factor		+	*bcd, hb*	(15-17)

		Ama	+6,089	+6,789	Cell Adhesion	patterned	+		
24	84B	Antp	+131,348	+132,041	RNA Polymerase II Transcription Factor		+	*hb, kr, kni*	(17, 18)
		ftz	+3,696	+4,389	RNA Polymerase II Transcription Factor		+	*cad*	(19-21)
25	85C	pum	+117,980	+118,817	RNA binding	ubiquitous	+		
26	88F-89A	CG18516	-46,483	-45,810	none	not available	-		
		CG5302	-35,010	-34,328	serine-type endopeptidase	not available	-		
27	91F	sqz	+10,124	+10,933	transcription factor	no staining	-		
		CG14282	-2,691	-1,882	none	not available	not available		
28	95C	Gdh	+937	+1,560	glutamate dehydrogenase	ubiquitous	+		

* Sequence coordinates are based on BDGP/Celera Release 1 genomic sequence and are relative to the annotated start of the transcript.

† Whole mount *in situ* images are available on the Berkeley Drosophila Genome Project website, http://www.fruitfly.org.

‡ DNA microarray expression levels for 0-3 hour old embryos were examined and categorized as either indicating expression during these stages (+), not indicating expression during these stages (-), or as inconclusive.

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