Supporting Information

Spradling et al. 10.1073/pnas.1112960108

Table S1. *P* element hotpoints have a normal consensus sequence

Gene	Site	N (+,–)	Sequence
Rapgap1	2L:7576630	66,30	GTCTGGCC
cpo	3R13769792	61,24	GTTCAGGC
CG14709	3R:7394886	28,7	ACCTGGCA
Hsromega	3R:17122251	11,4	CTCCAACC
Hsromega	3R: 17122251	11,4	CTCCAACC
Men	3R:8545692	5,19	GCCGCGAC
emc	3L: 749335	29,10	ACTCCGCC
emc	3L:749314	7,3	CTCCAGCC
CG32529	X:19781153	6,13	GCCCAAAC
fw	X:11898003	11,8	GTCTGCAC
apt	2R:19468319	11,4	AATCAGCC
CG11033	3R:4878202	10,7	GTGTTGGC
No gene	3R:4076136	5,13	GTTTGGCG
kis	2L: 249358	5,3	GTCCAAGC
CG17646	2L: 1737432	9,0	GTCTTATA
CG2201	2L: 21618795	7,32	ACCCAGAC
sra	3R: 12015331	6,18	GGCTATAC
l(2)01289	2R: 2628194	17,26	CTCGGTGC
heph	3R: 27811472	4,23	CGCTGGAT
mir-282	3L: 3250542	12,13	GCACAAAC
wech	2R: 337745	15,9	GTTCAGGG
Gli	2L: 15762777	14,13	CCCAAACG
Myo31D	2L: 10506779	6,8	GGTCAGAC
CG3624	2R: 18289592	7,15	GGTTGGAT
Tm1	3R: 11117373	12,3	GTCCAGCG
PQBP-1	3R: 4303341	2,14	CTTGGAAC
RhoL	3R: 5328296	4,9	AACTGAAC
No gene	2L: 7423926	6,8	GTCTGGGC
Thor	2L: 3478324	4,13	AGCCGACC
Consensus			G(T/G/C)CYPuPu(A/G/C)C

Sites with at least eight *P* element insertions into the same nucleotide ("hotpoints") are listed by gene and sequence coordinate. The number of insertions in the + and – orientation [N (+,–)] are given along with the eight-base pair duplication associated with the insertions. An imperfect consensus is shown that agrees closely with a similar consensus for all *P* target sites (1).

1. Liao GC, Rehm EJ, Rubin GM (2000) Insertion site preferences of the *P* transposable element in *Drosophila melanogaster*. *Proc Natl Acad Sci USA* 97:3347–3351.

Table S2. *P* element hotspots are often associated with ORC-binding sites

N	Gene	P hits	ORC site(s)	P	enr	Pig	enr	Mi	enr
1	*Rapgap1*	114	317_Kc, 298_BG, **281_S2**	113	3,520	0	0	0	0
2	*cpo*	94	3370_Kc, **2900_S2**	88	3,790	0	0	0	0
3	*CG14709*	83	**3107_Kc**, 2881_BG, 2641_S2	71	2,040	1	42	1	51
4	*Hsromega*	81	**3274_BG**, 3043_S2, 3516_Kc	70	2,830	0	0	0	0
5	*l(2)01289*	81		0	0	0	0	0	0
6	*Men*	73	2923_BG, **3146_Kc**, 2680_S2	69	728	0	0	0	0
7	*GstS1*	70	**1308_BG**, 1454_Kc, 1230_S2	36	1,100	0	0	0	0
8	*emc*	66	1698_BG, **1580_S2**, 1861_Kc	65	1,480	0	0	0	0
9	*amn*	59	**4180_S2**, 4429_BG, 5083_Kc	56	338	0	0	0	0
10	*CG11033*	58	2536_S2, 2994_Kc, **2782_BG**	20	1,020	0	0	0	0
11	*pum*	53	2999_Kc, 2787_BG, **2541_S2**	28	861	0	0	0	0
12	*apt*	53	1455_S2, 1739_Kc, **1558_BG**	47	1,190	1	21	0	0
13	*CG33960*	53	**1291_BG**	30	1,360	0	0	0	0
14	*jing*	52	811_BG, **907_Kc**, 786_S2	35	472	0	0	0	0
15	*bin3*	51	**782_S2**	3	154	0	0	0	0
16	*CG5555*	51		0	0	0	0	0	0
17	*3L:1586000-1587000*	51	**1746_BG**, 1624_S2	42	1,390	0	0	0	0
18	*Ten-m*	51	**2736_Kc**, 2565_BG	36	605	0	0	0	0
19	*sca*	47		0	0	0	0	0	0
20	*bun*	47	447_S2, **498_Kc**, 465_BG	4	129	0	0	0	0
21	*Sema-5c*	47	2314_Kc, 2140_BG, **1999_S2**	38	1,470	0	0	0	0
22	*tara*	47	3297_Kc, **2834_S2**, 3068_BG	14	67	0	0	0	0
23	*Indy*	46	2580_Kc, 2424_BG, **2244_S2**	27	635	0	0	0	0
24	*3R:23731000-2000*	45		0	0	0	0	0	0
25	*Gli*	45	591_Kc, 529_S2, **553_BG**	42	1,610	0	0	0	0
26	*hts*	45	**1413_BG**, 1574_Kc	19	1,060	0	0	0	0
27	*Crc*	45	2812_BG, 3032_Kc, **2573_S2**	42	970	0	0	0	0
28	*heph*	45	3940_Kc, **3430_S2**, 3662_BG	29	1,160	0	0	0	0
29	*alpha-Est10*	45	2731_BG, **2484_S2**	28	932	0	0	0	0
30	*Gdh*	44	3652_Kc, **3382_BG**, 3142_S2	43	780	0	0	0	0
31	*LanA*	44	2081_Kc, **1930_BG**, 2082_Kc	23	438	0	0	0	0
32	*Tm1*	44	2784_S2, **3017_BG**, 3236_Kc	6	156	0	0	0	0
33	*2L:7423430-7424130*	43	309_Kc, **288_BG**, 274_S2	42	490	0	0	0	0
34	*kis*	43	**16_S2**, 20_BG, 17_BG, 11_Kc,	13	330	0	0	0	0
35	*sra*	42	**2815_S2**, 3275_Kc, 3049_BG	2	46	0	0	0	0
36	*CG2201*	41	**726_S2**	2	66	0	0	0	0
37	*mir-282*	41	1979_Kc, **1692_S2**	55	992	2	54	0	0
38	*RhoGAP18B*	40	**4137_S2**, 5029_Kc, 4384_BG	35	293	0	0	0	0
39	*corto*	39	**2649_BG**, 2825_Kc, 2305_S2	33	614	0	0	0	0
40	*mub*	39	**2331_S2**, 2724_Kc, 2554_BG,	26	481	0	0	0	0
41	*Thor*	39	**172_Kc**, 147_S2, 146_BG	39	541	0	0	0	0
42	*CG31522*	39	**2800_Kc**, 2624_BG, 2382_S2	34	341	0	0	0	0
43	*RhoL*	38	3016_Kc, **2801_BG**, 2562_S2	36	1,220	0	0	0	0
44	*CG9894*	38	130_Kc, 114_S2, 111_BG, **115_S2**	18	433	2	98	0	0
45	*for*	37	149_S2, **176_Kc**, 150_BG	30	584	0	0	0	0
46	*lama*	37	1749_S2, 1904_BG, **2056_Kc**	32	1,400	0	0	0	0
47	*CG13928*	37	**1909_Kc**	14	301	0	0	0	0
48	*spin*	37	**1408_Kc**, 1279_BG, 1191_S2	18	210	0	0	0	0
49	*trx*	36	**2967_BG**, 2736_S2, 3191_Kc	3	40	0	0	0	0
50	*HmgD*	36	**1495_BG**, 1671_Kc, 1672_Kc,	13	525	0	0	0	0
51	*wech*	36	858_BG, 953_Kc, **820_S2**	29	1,130	0	0	0	0
52	*crol*	35	**423_S2**, 470_Kc, 438_BG	18	169	1	15	0	0
53	*Fkbp13*	35	1648_Kc, 1478_BG, **1385_S2**	20	746	0	0	0	0
54	*hiw*	35	**4814_Kc**	23	1,180	0	0	0	0
55	*LanA upstream*	34	**2082_Kc**	15	830	0	0	0	0
56	*Hr39*	34	718_S2, 820_Kc, **743_BG**	18	291	0	0	0	0
57	*SNF4Agamma*	34	**3265_BG**	24	607	0	0	0	0
58	*CG8920*	34	**1604_Kc**, 1343_S2, 1442_BG	24	161	0	0	0	0
59	*CG30115*	34	1534_Kc, **1378_BG**, 1288_S2	11	390	0	0	0	0
60	*stg*	33	**3834_Kc**, 3552_BG, 3307_S2	29	260	0	0	0	0
61	*grp*	33	637_Kc, **585_BG**	8	264	0	0	0	0
62	*l(2)44DEa*	32	913_BG, **1022_Kc**, 863_S2	5	139	0	0	0	0
63	*bnl*	32	3439_Kc, 2970_S2, **3199_BG**	22	494	0	0	0	0

Table S2. Cont.

N	Gene	P hits	ORC site(s)	P	enr	Pig	enr	Mi	enr
64	*Lk6*	32	3119_Kc, 2658_S2, **2892_BG**	16	274	0	0	0	0
65	*CG17646*	32	**76_BG3**	26	861	0	0	1	59
66	*ttk*	31	**3653_BG**, 3420_S2, 3932_Kc	14	233	0	0	0	0
67	*oaf*	31	107_BG, 124_Kc, **110_S2**	8	395	0	0	0	0
68	*CG11367*	31	2738_Kc, 2560_BG, **2339_S2**	24	1,360	0	0	0	0
69	*exba*	31	2668_BG, **2860_Kc**, 2429_S2	17	317	1	28	0	0
70	*CG30015*	31	**956_S2**, 1138_Kc, 1032_BG	24	629	0	0	0	0
71	*PQBP-1*	31	**2967_Kc**	28	705	0	0	0	0
72	*Eip75B*	29	**2535_Kc**, 2208_S2, 2372_BG	16	144	0	0	0	0
73	*stwl*	29	2206_BG, 2385_Kc, **2063_S2**	26	298	0	0	0	0
74	*inx2*	29	**3975_BG**, 4377_Kc, 3702_S2	23	459	0	0	0	0
75	*Mocs1*	29	2267_Kc, 1962_S2, **2101_BG**	27	1,290	0	0	0	0
76	*CG9674*	29	**2317_BG**, 2472_Kc, 2152_S2	4	59	0	0	0	0
77	*shep*	29	2051_Kc, **1747_S2**, 1903_BG	8	184	0	0	0	0
78	*rdx*	29	3183_Kc, **2955_BG**, 2724_S2	8	245	0	0	0	0
79	*tlk*	29	**3594_S2**, 4212_Kc, 3851_BG	6	98	0	0	0	0
80	*melt*	28		0	0	0	0	0	0
81	*CG3036*	28	173_S2, 202_Kc, **179_BG**	26	780	0	0	0	0
82	*EcR*	27	801_BG, 777_S2, **897_Kc**	14	304	0	0	0	0
83	*eff*	27	3216_Kc, 2997_BG, **2766_S2**	20	522	0	0	0	0
84	*B4*	27	**496_BG**, 543_Kc, 486_S2	11	84	0	0	0	0
85	*tou*	27	**1069_BG**, 996_S2, 1173_Kc	7	119	0	0	0	0
86	*CG2185*	27	2675_BG, 2866_Kc, **2435_S2**	26	831	0	0	0	0
87	*tai*	27	349_S2, **384_Kc**, 350_S2	15	389	0	0	0	0
88	*mbl*	27	1313_BG3, 1234_S2	0	0	0	0	0	0
89	*TyrR*	26		0	0	0	0	0	0
90	*brat*	26	721_Kc, **632_S2**, 659_BG	14	81	0	0	0	0
91	*sgl*	26	1794_S2, **2099_Kc**, 1950_BG	24	249	0	0	0	0
92	*Trl*	26	**2224_BG**, 2073_S2	9	115	0	0	0	0
93	*wun2*	26	1057_Kc, **886_S2**, 942_BG	14	864	0	0	0	0
94	*dpr*	26		0	0	0	0	0	0
95	*trbl*	26	2489_BG, **2284**_S2, 2649_Kc	17	624	0	0	0	0
96	*elav*	26	4030_Kc, 3716_BG, **4031_Kc**	3	350	0	0	0	0
97	*Pfrx*	26	**5051_Kc**, 4155_S2	20	306	0	0	0	0
98	*chic*	25	**236_Kc**, 209_S2, 220_BG	23	127	0	0	0	0
99	*Myo31D-f*	25	441_Kc, 399_S2, **408_BG**	25	578	0	0	0	0
100	*Df31*	25	728_S2, **753_BG**, 831_Kc	11	447	0	0	0	0

The 100 top *P* element hotspots are listed along with the number of *P* element insertions observed (*P* hits). One or more sites of ORC-binding (1) are listed if they overlap genic insertions. The number of *P* element (P), *piggyBac* (Pig), and *Minos* element (Mi) insertions within the specific ORC site shown in boldface, and the corresponding enrichment values (enr) are listed.

1. Eaton ML, et al. (2011) Chromatin signatures of the Drosophila replication program. *Genome Res* 21:164–174.