Supplementary Table 3

Search results using a PWM for Odd built in Target Explorer. Segments in the *D. melanogaster* genome were required to contain two Odd sites within a window of 300 bp and a PWM score threshold of ≥ 7.5 for each site. This search identified a list of 1789 segments throughout the genome. This list was refined by requiring the presence of two Odd sites above the same PWM threshold in corresponding segments of the *D. pseudoobscura* genome. Finally binding sites within exons or more than 20 kb from the nearest gene were removed from the list. 130 segments met these criteria. The score of the Odd sites is the sum of the score of the best pair of sites in each segment divided by the maximum possible score (10.16). Position corresponds to the *Drosophila melanogaster* genome sequence release 3.

odd is a primary pair-rule gene that is required for segmentation, head development and central nervous system (CNS) development during embryogenesis[1-4]. This list includes genes required for segmentation (*nkd, gsb, slp1, prd, h*), head development (*Gsc, ems, lab, oc*), and CNS development (*sc, ac, SoxN*). Based on genetic analysis, at least five of these genes are likely to be directly regulated by Odd[3-5]: three pair rule genes (*h*, *prd*, and *slp1*) and two proneural genes (*sc* and *ac*). Some previously identified genetic targets of Odd[3,6], including *engrailed* and *wingless*, were not recovered in our genomic search using the Odd PWM. These omissions may reflect our stringent search parameters. Both *engrailed* and *wingless* have individual Odd binding sites within 5 kb of their transcriptional start sites that are conserved between the *D. melanogaster* and *D. pseudoobscura* (*data not shown*). More accurate CRM predictions should be possible using a combination of PWMs for multiple factors involved in a common regulatory network, such as the pair-rule genes[7,8].

Score of Odd sites	Chr.	Position of first Odd site	Gene A	Segment position relative to A	Distance to Transcription Start Site (bp)	Gene B	Segment position relative to B	Distance to Transcription Start Site (bp)
1.97	X	17073340	*B-H2*	3'	27800			
1.97	2R	20109481	*gsb*	3'	3763	*gol*	3'	18409/11762
1.97	3R	4157251	*CG7443*	3'	7179	*CG9603*	3'	9527
1.97	3R	12227143	*ss*	intron	2280			
1.96	3R	2493214	*lab*	intron	11099			
1.96	X	8530931	*Lim1*	intron	13843			
1.96	3L	18187778	*CheA75a*	5'	13198			
1.95	2R	4127672	*CG8197*	5'	5001	*ana*	5'	2176
1.95	3L	18970954	*nkd*	intron	23256			
1.95	X	13643881	*CG11072*	5'	11599	*CG32606*	3'	1882
1.95	X	18282867	*Bx*	intron	17243/14429			
1.95	3L	11327535	*CG6163*	5'	5118			
1.95	3R	6480770	*hth*	5'	16366			
1.95	3R	3152555	*CG10029*	5'	9645	*CG31496*	5'	18399
1.95	2L	14418526	*CG3474*	5'	11243	*CG15283*	3'	14442
1.95	X	7287275	*CG32720*	5'	10009			

1.95	X	8384268	*oc*	intron	5328			
1.94	2R	13626166	*CG30115*	5'	811			
1.93	X	160065	*sc*	3'	6567	*l(1)sc*	5'	7096
1.92	3R	21907920	*dys*	intron	3712			
1.92	2R	4770073	*CG10459*	3'	1802	*dap*	5'	2883
1.92	2R	9499021	*phyl*	5'	2960	*CG17388*	5'	6944
1.92	2L	15262288	*CG15261*	5'	9175	*CG15263*	5'	824
1.92	3L	553243	*CG17090*	intron	29544/26543			
1.89	3R	9716184	*E5*	5'	16264	*ems*	5'	11416
1.82	2L	16388914	*CG5888*	intron	37635			
1.81	2L	8810494	*SoxN*	5'	7362			
1.8	2R	17198073	*a*	intron	17531/17089			
1.8	3L	710829	*CG13896*	5'	18626	*CG13897*	3'	8920
1.8	3R	20789396	*CG13647*	3'	2555	*CG31422*	3'	25147
1.79	3L	16437084	*CG33158*	intron	68411			
1.79	X	8406035	*oc*	5'	16439	*CG12772*	5'	10025
1.79	3L	20601963	*CG32431*	5'	4317			
1.79	2L	15326224	*esg*	3'	14275	*CG15258*	3'	13449
1.78	3R	12019746	*sra*	intron	7072			
1.78	2R	2256768	*pk*	intron	45164/8604			
1.78	3R	21836710	*m2*	5'	4153	*HLHm3*	5'	92
1.78	X	17065733	*B-H2*	3'	20193			
1.78	X	124671	*y*	3'	10724	*ac*	5'	2798
1.78	X	1321046	*CG14796*	5'	6102			
1.78	3R	5114769	*CG8454*	3'	21999	*CG8861*	3'	39474/5015
1.78	2L	5450620	*CG31647*	5'	9203	*CG6634*	5'	3236
1.77	3L	12387146	*toe*	intron	3069			
1.77	2L	15077733	*CG15270*	3'	24003	*CG15269*	5'	9937
1.77	3L	2522454	*Spn*	intron	12452			
1.76	3L	22533345	*CG6914*	3'	9698			
1.76	2L	4350753	*CG15429*	3'	5209	*Traf1*	5'	13806
1.76	2R	4126236	*CG8197*	5'	3565	*ana*	5'	3612
1.76	2L	12070805	*CG14947*	3'	5111	*prd*	3'	4522/3444
1.76	3R	13330528	*CG31190*	intron	876			
1.76	3R	11056313	*mRpS10*	3'	906/820	*CG6535*	3'	11570
1.75	3R	19142388	*pnt*	intron	20153/11914			
1.75	2L	14432503	*CG15283*	intron	465			
1.75	2L	17491891	*Dhc36C*	intron	12341			
1.75	3R	27835883	*CG2053*	5'	17578			
1.75	3R	24372095	*CG14063*	3'	2644			
1.75	2L	8907731	*CG15867*	5'	335			
1.75	3R	17655621	*Gr93a*	3'	6432	*CG13416*	5'	1970
1.75	X	8409695	*CG12772*	5'	6365			
1.75	3R	22717622	*T48*	intron	20801			
1.74	2R	10946734	*sli*	intron	7845			
1.74	3R	13983718	*CG14316*	3'	5861	*CG14315*	5'	789

1.74	X	15278472	*CG32584*	3'	28205			
1.74	2R	16008812	*hbn*	5'	4359	*CG15649*	3'	8663
1.74	2L	5254918	*tkv*	intron	9006			
1.74	2L	15299975	*nht*	5'	1984	*esg*	5'	11974
1.73	2L	14372370	*elB*	intron	17540			
1.73	3R	25321433	*Trc8*	5'	2548	*CG2014*	5'	9500
1.73	3L	13907610	*CG32137*	intron	19478/19477			
1.73	2R	14873689	*Obp56h*	5'	5601			
1.73	3L	6734508	*CG32392*	5'	11733	*vvl*	5'	15181/8148
1.72	3L	8630244	*h*	5'	4425			
1.72	2R	9989803	*CG10249*	5'	13860	*CG10253*	3'	7223
1.72	X	6932312	*CG32729*	3'	2207	*CG9650*	5'	1140
1.72	2L	591812	*Gsc*	intron	4540			
1.72	X	20232340	*CG15455*	3'	18661	*CG15454*	5'	5229
1.72	3L	15122159	*CG7011*	5'	9656			
1.72	2R	848020	*ap*	intron	17681			
1.72	2L	12624482	*nub*	3'	17264			
1.72	2R	2470747	*CG1701*	intron	2235			
1.71	2R	18683619	*retn*	intron	7439			
1.71	3L	20591496	*CG32431*	5'	14784			
1.71	3L	7922305	*exex*	3'	14584	*RNaseX25*	5'	7819
1.71	X	11513842	*dy*	5'	4509	*Karl*	5'	5661
1.71	3L	13265462	*Acp70A*	3'	6259			
1.7	2L	8848506	*CG32986*	5'	6532			
1.7	2L	3826483	*slp1*	3'	8234	*slp2*	5'	2928
1.69	2R	1690306	*Vha16*	intron	3724/2977			
1.64	3R	17248719	*lbl*	intron	2090			
1.62	3L	16713314	*Nrt*	5'	1640			
1.6	3L	19613099	*CG8780*	intron	521			
1.6	3L	8981081	*Doc2*	5'	3131	*Doc1*	5'	19006
1.6	2L	7356176	*Wnt6*	3'	13047	*Wnt10*	5'	10817
1.59	3R	4152688	*CG7443*	3'	2616	*CG9603*	3'	14090
1.59	3L	12437330	*CG10663*	5'	1694	*CG10660*	3'	10305
1.58	2R	10887316	*tun*	5'	8678	*Poxn*	3'	11184
1.58	3L	502848	*klar*	intron	18370			
1.57	3R	3154983	*CG10029*	5'	12073	*CG31496*	5'	15971
1.57	2R	15184841	*18w*	3'	9618			
1.57	2L	8852440	*CG32986*	5'	2598			
1.57	X	14689532	*CG9030*	5'	3418	*eag*	5'	12738
1.57	3R	16845088	*Rlip*	intron	1645			
1.57	3R	12562470	*Ubx*	5'	2104		3'	14659/9656
1.56	3R	24381227	*CG14063*	3'	11776	*fkh*	3'	18944
1.56	2L	20346069	*Ugt37a1*	5'	2360	*CG16798*	3'	6028
1.55	3L	7897471	*CG8268*	3'	1567	*exex*	5'	10250
1.55	2R	873539	*ap*	5'	7838	*l(2)09851*	5'	19860/4490
1.55	2L	10795834	*CG31869*	5'	2340	*CG6508*	5'	15698

1.55	3R	15490545	*ort*	3'	5058	*CG7432*	5'	2934
1.55	3R	17253878	*lbl*	5'	3069	*lbe*	3'	9128
1.55	3L	12394551	*toe*	5'	4336			
1.55	3R	10421211	*stumps*	intron	3008/1395			
1.54	X	7282988	*CG32720*	5'	5722			
1.54	3L	16890459	*CG9665*	intron	60			
1.54	3L	12889583	*CG32115*	5'	18390			
1.53	X	2154224	*CG14045*	5'	9788	*CG12496*	3'	13447/2441
1.52	3R	17775673	*Eip93F*	5'	16639			
1.52	3R	21607770	*CG31093*	5'	2212	*CG5024*	5'	18413
1.52	2L	15999265	*beat-Ic*	intron	20644			
1.52	X	7874749	*CG2120*	intron	108			
1.51	3R	6871365	*CG4695*	intron	1653			
1.51	2L	11442500	*salm*	5'	8026			
1.51	X	20387452	*run*	3'	20596	*CG1324*	3'	20923
1.51	X	19988339	*CG1504*	5'	3868	*CG1631*	5'	11953
1.51	2L	16479848	*Tpr2*	intron	10222/4998			
1.5	3L	13450203	*CG10741*	intron	5831/2992			
1.5	2L	702374	*ds*	intron	14259			
1.49	3R	13904260	*CG14317*	5'	2598			
1.49	2R	3091987	*CG14762*	5'	17332	*Optix*	5'	393
1.49	2R	13765541	*CG15071*	3'	5187	*CG18604*	5'	138

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