Table S8 DREME analysis of Yan bound regions. Motifs identified by DREME analysis are indicated along with the p-value, e-value and number of sites they were found at. TomTom was used to match enriched motifs to the PWM databases: FlyReg (based on Flyreg Drosophila DNAse I Footprint Database v2.0); idmmpmm2009 and dmmpmm2009 {Kulakovskii, 2009 #106;Kulakovskiy, 2009 #110}.

DREME motif	TomTom ID	p-value	E-value	sites
Top 600 peaks associated with HDRs				
GARAGRGA	Trl	9.64E-05	0.00722792	173
DACAACAA	Aef1	0.000418125	0.0313594	164
CTCKCTY	Trl	3.72E-05	0.00279222	229
KGGAAAW	dl	0.0012355	0.0926621	333
CAGGTAG	sna	0.000531537	0.0398653	65
CGRCAGC	Adf1	0.000816332	0.0612249	92
CACTCGM	z	0.000766762	0.0575072	97
CACTCGM	tin	0.00120053	0.0900398	97
TTAATTR	Dfd	3.91E-05	0.00293183	131
TTAATTR	en	0.000104947	0.007871	131
TTAATTR	ara	0.000701701	0.0526276	131
CASTTGAG	tin	5.07E-06	0.000380059	44
CASTTGAG	vnd	1.33E-05	0.000995676	44
TOP 600 Isolated peaks				
DREME motif	**TomTom ID**	**p-value**	**E-value**	**sites**
CBCTCTCY	Trl	1.29E-05	0.000965534	159
CARCARCA	Aef1	1.61E-05	0.00120872	185
AAHAAYAA	bab1	0.000985128	0.0738846	243
CACTCRCW	z	4.80E-05	0.00360071	112
CACTCRCW	ey	0.000539699	0.0404774	112
CACTCRCW	toy	0.00106265	0.0796985	112
AHATAAA	zen	0.000889086	0.0666815	193
GGCDGCCA	shn	0.000443008	0.0332256	38

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