

Table S3. Comparison Between PWMs

	This work	Berman <i>et al.</i> [1]	Segal <i>et al.</i> [2]
Bcd	79% (38/48)	100% (48/48)	58% (28/48)
	8% (3/35)	42% (15/35)	14% (5/35)
Cad	76% (10/13)	100% (13/13)	69% (9/13)
	15% (4/26)	100% (26/26)	19% (5/26)
D-STAT	100% (3/3)	N/A	0% (0/3)
	17% (3/17)	N/A	17%(3/17)
Dichaete	100% (4/4)	N/A	N/A
	22% (4/18)	N/A	N/A
Hb	87% (90/103)	98% (101/103)	86% (89/103)
	3% (1/26)	19% (5/26)	0% (0/26)
Kr	75% (34/45)	86% (39/45)	86% (39/45)
	6% (1/15)	26% (4/15)	40% (6/15)
Kni	75% (25/33)	84% (28/33)	42% (14/33)
	21% (9/42)	59% (25/42)	28% (12/42)
Gt	75% (6/8)	N/A	62% (5/8)
	6% (1/15)	N/A	20% (3/15)
Tll	94% (35/37)	N/A	70% (26/37)
	63% (23/26)	N/A	52% (19/36)

For each TF, the top row is the recovery rate of footprint sites and the bottom row is the rate of false positives.

References

1. Berman BP, Nibu Y, Pfeiffer BD, Tomancak P, Celniker SE, et al. (2002) Exploiting transcription factor binding site clustering to identify cis-regulatory modules involved in pattern formation in the *Drosophila* genome. *Proceedings of the National Academy of Sciences USA* 99: 757-762.
2. Segal E, Raveh-Sadka T, Schroeder M, Unnerstall U, Gaul U (2008) Predicting expression patterns from regulatory sequence in *Drosophila* segmentation. *Nature* 451: 535-540.