

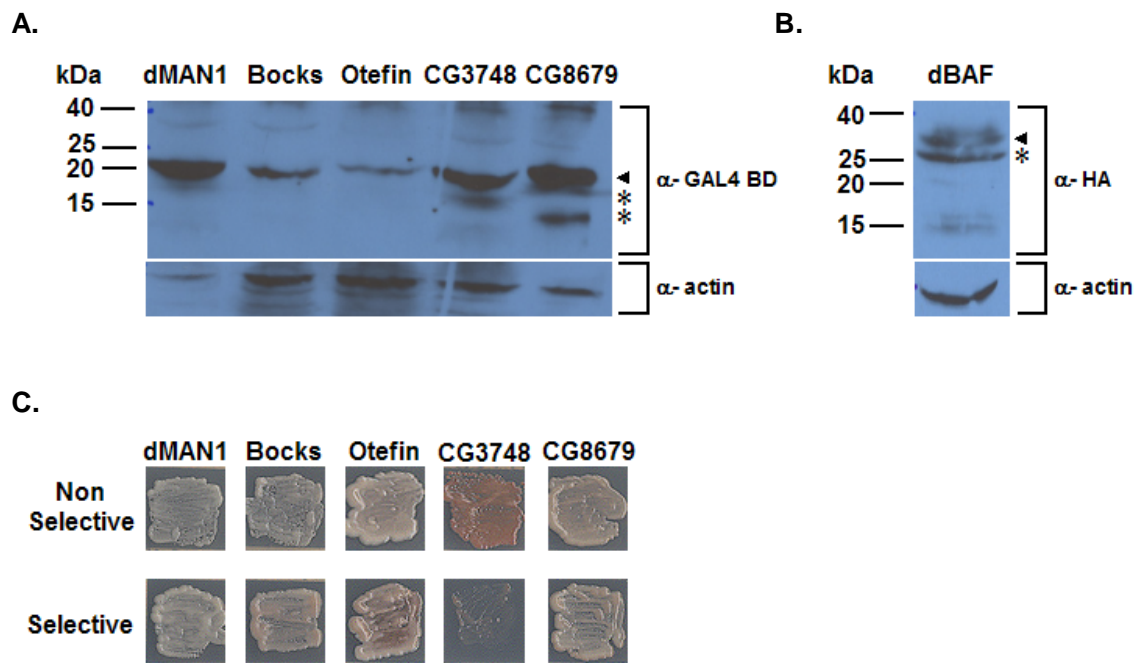
Sup Table I. Conservation of dMAN1 domains.

Species	Evolutionary distance from <i>D. melanogaster</i> (mya)	dMAN1 domains ^a			
		LEM	BTM ^b	MSC	UHM
<i>D. pseudoobscura</i>	20-46	85 (92)	64 (85)	71 (87)	88 (96)
<i>D. virilis</i>	40-60	52 (78)	46 (71)	61 (82)	78 (90)
<i>A. gambiae</i>	250	48 (70)	28 (53)	36 (65)	71 (85)
<i>D. rerio</i>	800-1,200	39 (61)	11 (39)	18 (48)	44 (64)
<i>X. laevis</i>		37 (63)	13 (38)	23 (53)	44 (63)
<i>M. musculus</i>		36 (60)	14 (37)	21 (48)	44 (64)
<i>H. sapiens</i> MAN1		37 (61)	12 (29)	23 (50)	44 (64)
<i>H. sapiens</i> LEM2		30 (43)	11 (39)	25 (54)	NA

^a Numbers indicate % identity (% similarity).

^b BTM, Region Between the Transmembrane domains.

NA, Not Applicable.



Supplemental Figure 1

Sup. Fig. 1. Yeast two hybrid analysis of interactions between the *Drosophila* LEM homology domains and dBAF. (A) Western analysis of the bait proteins representing fusions between the GAL4 BD and the five LEM homology domains. Proteins were detected using antibodies against the GAL4 BD. An arrowhead shows the position of the full-length fusion protein, with breakdown products shown by an asterisk. Actin represents the loading control. (B) Western analysis of the prey protein representing the fusion between the GAL4 AD and dBAF. Proteins were detected using antibodies against the HA tag, which is fused to the GAL4 AD. An arrowhead marks the position of the full-length protein, while the asterisk marks positions of breakdown proteins. Actin represents the loading control. (C) Yeast two hybrid plates testing protein interactions. Yeast carrying the indicated bait expression vector were co-transformed with the dBAF prey expression vector and plated onto non-selective and selective media. Growth on selective media indicates a positive protein interaction.