## Sup Table I. Conservation of dMAN1 domains.

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

<sup>a</sup> Numbers indicate % identity (% similarity).

<sup>b</sup> 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.