Supplementary data for online-only publication

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            492                                                                                                548
DmBAB1      1 SLADDLEIKPGIAEMIREEERAKMMENSHAWMG-------------ATGSTLAADSYQYQLQSMWQKCWN
DmBAB2      1 SHHDDMEIKPEIAEMIREEERAKMIESGGHGGWMGAAAAATG------AASVAADSYQYQLQSMWQKCWN
AgBAB       1 NHPDDMEIKPGIAEMIREEERGNRTNTARAALMGERFTSLIQPPDDRLVWKVFAESYQYQLQSMWQKCWN
DvBAB       1                                                      ADSYQYQLQSMWQKCWN
AmBAB       1                                                 GGRKLADSYQYQLQSMWQKCWN

            549                                                                                                617
DmBAB1     58 TN-QNLMHHMRFRERGPLKSWRPETMAEAIFSVLKEGLSLSQAARKYDIPYPTFVLYANRVHNMLGPSID
DmBAB2     65 TNQQNLVQQLRFRERGPLKSWRPEAMAEAIFSVLKEGLSLSQAARKFDIPYPTFVLYANRVHNMLGPSLD
AgBAB      71 S--QNLIHHLRFRERGPLKSWRPETMAEAIFSVLKEGLSLSQAARKYDIPYPTFVLYANRVHNMLGPSID
DvBAB      18 TN-QNLMHHMRFRERGPLKSWRPETMAEAIFSVLKEGLSLSQAARKYDIPYPTFVLYANRVHNMLGPSID
AmBAB      23 TN-QSLVHNLRFRERGPLKSWRPETMAEAIFSVLKEGLSLSQAARKYDIPYPTFVLYANRVHNMLGPSAD
```

psq motif

```
            618                                                                                    674
DmBAB1    127 GGPDLRPKGRGRPQRILLGIWPDEHIKGVIKTVVFRDTKDIKDESLAAHMPPYGRHS
DmBAB2    135 GGADPRPKARGRPQRILLGMWPEELIRSVIKAVVFRDYREIKEDMSAHQYANGQGHG
AgBAB     139 GGTDLRPKGRGRPQRILLGIWPDDHIKGVIKSVVFRDAKDMKEE-----PMMYGRHS
DvBAB      87 GGPDLRPKGRGRPQRILLGIWPDEHIKGVIKTVVFRDTKDLKDDSLGAHLPPYGRHS
AmBAB      92 GGADLRPKGRGRPQRILLGVWPDEHIRGVIRAVVFRD--------------------
```

AT-hook motif

Multiple sequence alignment of BabCD motifs.

Amino acid sequences of the BabCD of the BAB proteins of *D. melanogaster* Bab1 (AJ252082.1), *D. melanogaster* Bab2 (AJ252173.1), *D. virilis* (AJ544785), *A gambiae* (AAAB01008960.1) and *A. mellifera* (BB170013A10G09) have been aligned. Amino acid residues that are identical in all the sequences are shaded black. Amino acid positions with conservative changes are shaded gray. The position of the psq and the AT-Hook domains is indicated. Numbers above the sequence indicate the amino acid positions respective to the BAB1 protein.

Supplemental data