

Erratum to: The Phylogenetic Distribution of Non-CTCF Insulator Proteins Is Limited to Insects and Reveals that BEAF-32 Is *Drosophila* Lineage Specific

Todd A. Schoborg · Mariano Labrador

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Figure 5a of the original published article erroneously published.

The x-axis labels for Figure 5a were not present in the final version. The labels should have read (from left to right): <1 kb from TSS; >1 kb from TSS; Inside Gene; Downstream.

The correct Figure 5 follows.

(A)
Localization of CGATA Motif Clusters in Relation to Gene Position

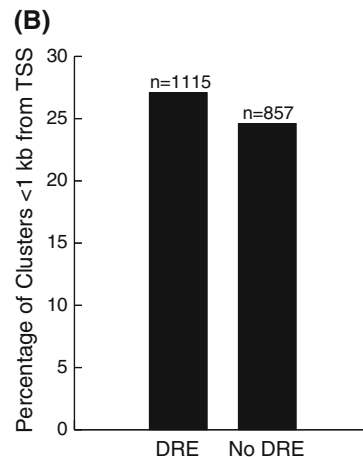
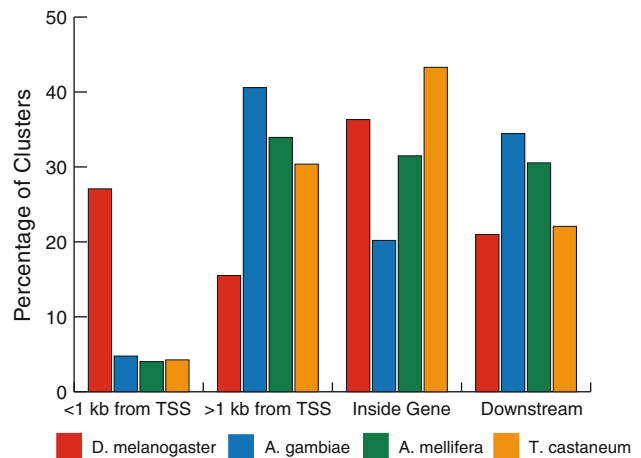


Fig. 5 BEAF-32-binding sites show a general bias near the transcription start sites (TSS) of genes only in *Drosophila*. **a** Clusters were obtained using the motif searching program Fly Enhancer (Markstein et al. 2002) using 7 CGATA motifs within a 1,000-bp window as the search parameter (*D. melanogaster*: $n = 1,115$; *A. gambiae*: $n = 2,035$; *A. mellifera*: $n = 36,184$; *T. castaneum*: $n = 1,409$). **b** Inclusion or removal of the DREF-binding site (DRE) during motif searching did not significantly alter the percentage of clusters <1 kb from the TSS in *D. melanogaster*

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T. A. Schoborg · M. Labrador (✉)
Department of Biochemistry and Cellular and Molecular Biology, The University of Tennessee, M407 Walters Life Sciences, 1414 Cumberland Ave, Knoxville, TN 37996, USA
e-mail: labrador@utk.edu