

Supporting Information

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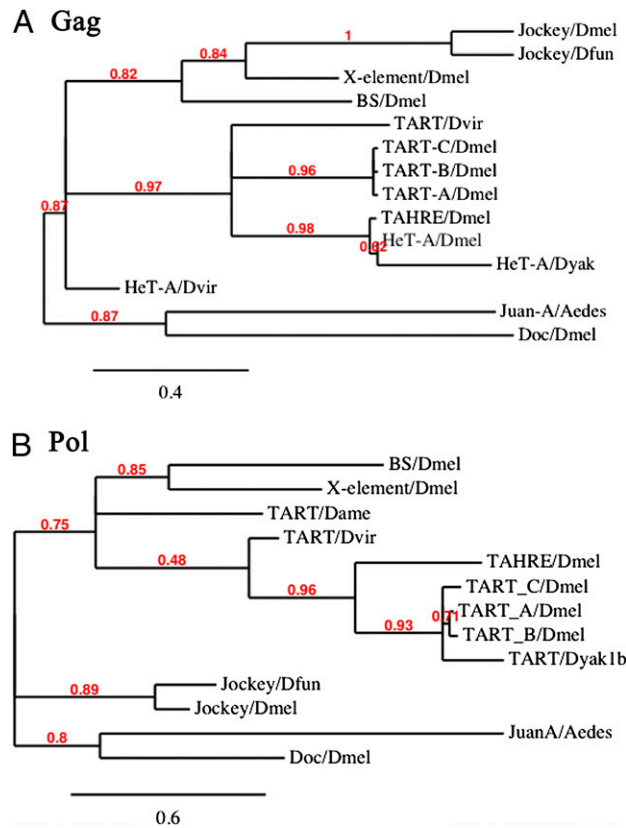


Fig. S1. Phylogenetic relationships of Gag (A) and Pol (B) amino acid sequences of non-LTR elements in the jockey clade. Elements are from several *Drosophila* species as well as *Juan-1* from *Aedes aegypti*. Analysis by One Click Phylogeny Analysis package available at http://www.phylogeny.fr/version2.cgi/simple_phylogeny.cgi; alignment was done by MUSCLE with curation by G blocks, phylogeny determination by PhyML, and tree rendering by TreeDYN (1). Branch support values in red are the expectation values that a branch is a realistic description; support values less than 0.1 have been collapsed. (A) Gag proteins. (B) Pol proteins. Elements shown are those elements listed in Fig. 1 plus *HeT-A^{yak}*, AF043258 (*D. yakuba*); *jockey^{mel}*, M22874; *Doc^{mel}*, X17551; *jockey^{fun}*, M38437 (*D. funebris*); *BS^{mel}*, Flybase FBgn0000224; *X^{mel}*, AF237761; *TART^{yak1b}*, AP468024; *TART^{ame}*, AY219710 (*D. americana*); and *Juan-A^{Aedes}*, M95171.

1. Dereeper A, et al. (2008) Phylogeny.fr: robust phylogenetic analysis for the non-specialist. *Nucleic Acids Res* 36:W465-9.