Figure S1  Defining the analysis regions for *D. melanogaster*, *D. erecta*, *D. mojavensis*, and *D. grimshawi* based on changes in repeat density. The bar in the "Region" track corresponds to the region analyzed in this study. The grayscale in the "Repeat Density" track corresponds to the results of sliding window analysis (1 kb window and 0.5 kb step size) of total transposon density using a species-specific repeat library. Darker regions in this track correspond to regions with higher repeat density. One of the characteristics of heterochromatin is its high repeat density and the selections of the euchromatic reference regions at the base of the D element correspond to regions with mostly uniform low repeat density juxtaposed with regions with high repeat density. The Genome Browser screenshots of the base of the D elements show the region that spans from the start of the analysis region to the end of the assembled scaffold.