



Figure S6 Predicted miRNA seed sequences in the *yar* gene. Show is the UCSC Genome Browser view of *yar* genomic region with predicted seed sequences corresponding to the experimentally identified (black) and predicted (blue) *D. melanogaster* miRNAs (miRBase release 17). Boxes representing seed sequences are colored based on free energy of miRNA-*yar* interaction, with strongest seeds (<math>< -30</math> kcal/mol) colored black and weaker seeds colored in lighter gray. High free energy cutoff for these analyses was set at -25 kcal/mol. The position of the Dorsocentral enhancer of AS-C complex genes is indicated by light blue bar.