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 (≤-30 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.