



Supplementary Figure S1: Conserved and newly-evolved *D. melanogaster* miRNAs recovered at varied read depth thresholds using *in silico* simulated libraries. These libraries are composed of randomly sampled reads across all *D. melanogaster* sRNA-seq male-body, female-body, head, and mixed embryo libraries used within this study. miRNA recovery rates are computed per read-depth sample at various miR or miR* read thresholds. Error bars depict the standard error of the recovery rate across 100 simulations.