

**Table S7.  $K_{\text{miR}}$  /  $K_s$  of the older miRNAs (60-250 Myrs) that have been evolving rapidly between *D. melanogaster* and *D. simulans*.** The common ancestral sequences of *D. melanogaster* and *D. simulans* are inferred from *D. yakuba* and *D. erecta*.

miRNA	$K_{\text{miR}}$ / $K_s$ ( <i>D. mel</i> vs the common ancestor of <i>D. mel</i> and <i>D. sim</i> )	$K_{\text{miR}}$ / $K_s$ ( <i>D. sim</i> vs the common ancestor of <i>D. mel</i> and <i>D. sim</i> )
dme-mir-311	0.814	0.194
dme-mir-313	0.475	1.231
dme-mir-964	0.680	0.140
dme-mir-973	0.511	1.676
dme-mir-974	0.676	0.862
dme-mir-975	0.184	0.943
dme-mir-976	0.346	0.743
dme-mir-977	0.687	1.290