Supplementary Figures and Tables.

Supplementary Figure 1. PDFs of published fly mirtrons

Supplementary Figure 2. PDFs of novel fly mirtrons

Supplementary Figure 3. PDFs of candidate fly mirtrons

Supplementary Figure 4. PDFs of published worm mirtrons

Supplementary Figure 5. PDFs of novel worm mirtrons

Supplementary Table 1. Summary of *D. melanogaster* short RNA libraries analyzed in this study.

Supplementary Table 2. Summary of *C. elegans* short RNA libraries analyzed in this study.

Supplementary Table 3. Summary of *D. melanogaster* computational mirtron rankings and experimental evidence.

Supplementary Table 4. Summary of *C. elegans* computational mirtron rankings and experimental evidence.

Supplementary HTML documents on *D. melanogaster* and *C. elegans* introns:

http://cbio.mskcc.org/leslielab/mirtrons/

The summary pages for the *D. melanogaster* and *C. elegans* summaries combine the top 1000 introns ranked according to their mirtron-like features, combined with all introns with more than 5 mapped reads. This combination allows one to inspect poorly-ranked loci with read evidence (including, for example tailed 3' mirtrons, highlighted pink). Loci currently annotated at miRBase are highlighted blue, novel mirtrons with confident read evidence annotated in this study are highlighted green, and candidate loci with compelling structures and limited read evidence are highlighted yellow. The summary pages are sortable by various column headers, including by mirtron score or by read number. Each intron is linked to its genomic position in the UCSC Genome Browser (http://genome.ucsc.edu/) and to an individual gene page containing its optimal mirtron-like secondary structure, a schematic of the read density along the intron, and alignments of all the small RNA reads mapped to the intron and/or to 25 nt of flanking exons (separated by individual library). These read alignments are sortable according to sequence or read number.

This page also contains download links for the mirtron-SVM scripts, which are executable in Matlab, as well as a detailed description of how to run the SVM, how to retrain it on user-defined datasets, and how to visualize the results.