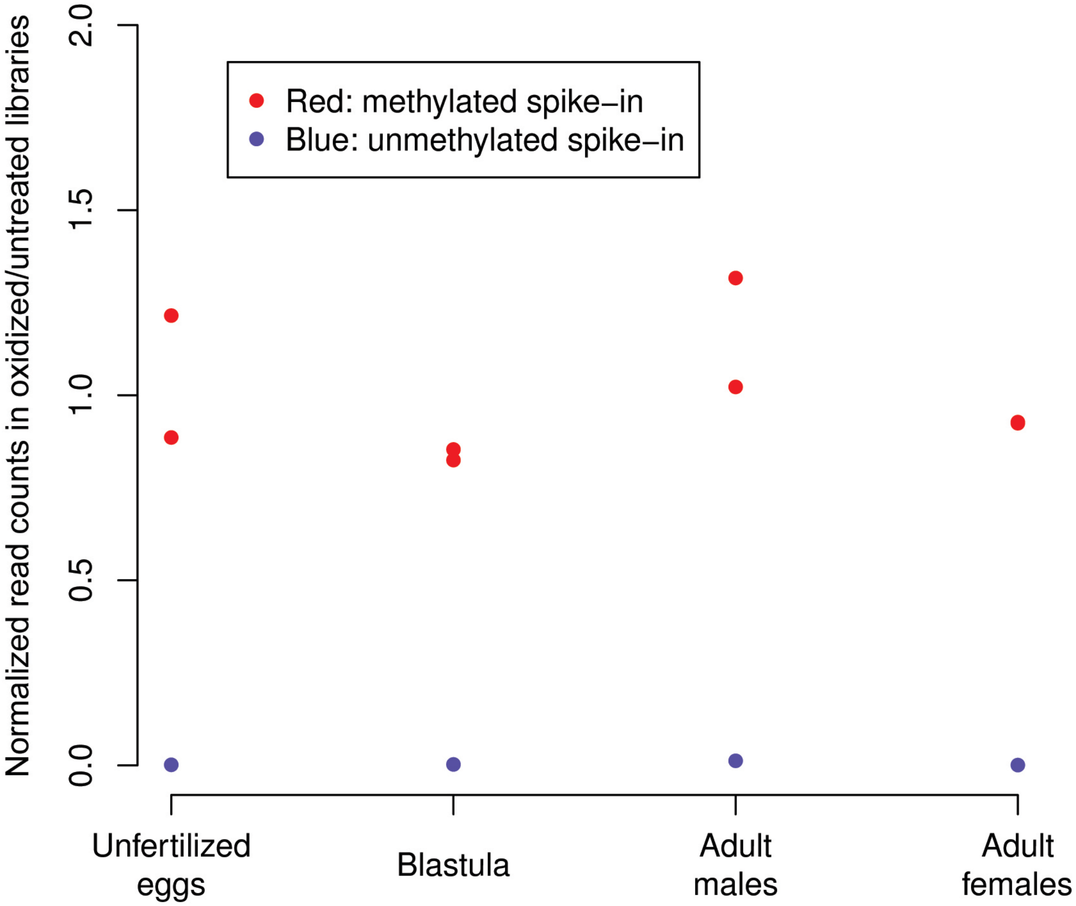
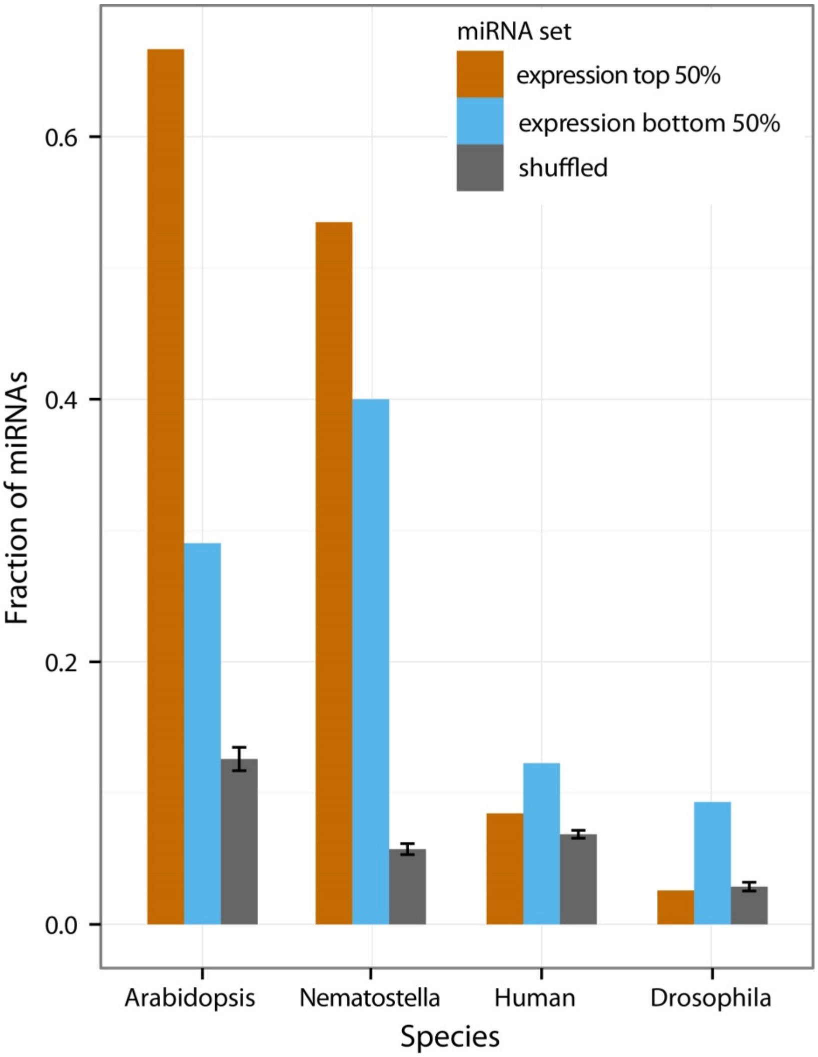
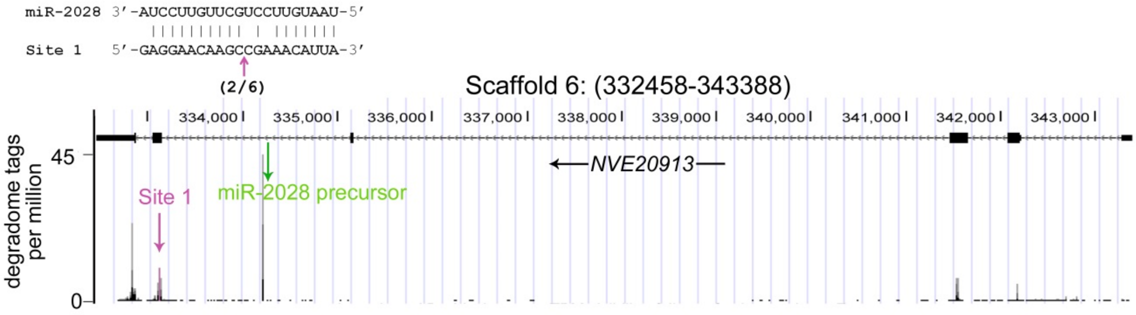
Supplemental Figure S3. Methylated and unmethylated spike-ins in *Nematostella* libraries. Unmethylated synthetic RNA spike-ins were lost in oxidized libraries, whereas methylated ones exhibited similar read numbers in oxidized and untreated libraries. Read counts in each library were normalized to library depth.





Supplemental Figure S4. The fraction of mRNA alignment mismatch scores lower than 2.5 for the 50% most expressed and 50% least expressed miRNAs of *Nematostella vectensis*, *Homo sapiens, Drosophila melanogaster* and *Arabidopsis thaliana.* The background noise levels are shown by matches of shuffled miRNAs.

Supplemental Figure S5. miR-2028 and the gene *NVE20913*, which is both the intronic host of the miRNA and its regulatory target, create an incoherent regulatory circuit.



Supplemental Figure S6. Enrichment of observed cleavage sites among predicted sites. Predicted sites were required to exhibit a perfect match to a subsequence of the miRNA, with varying starting and ending positions for the perfectly-matched subsequence.