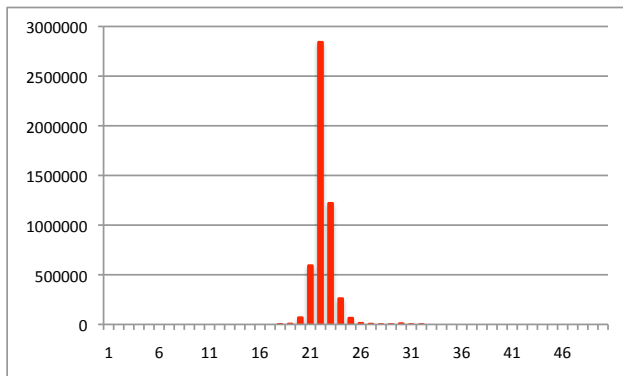


Supplementary Figure 6. Distribution of reads in original sequence data and predicted small RNA transcripts.

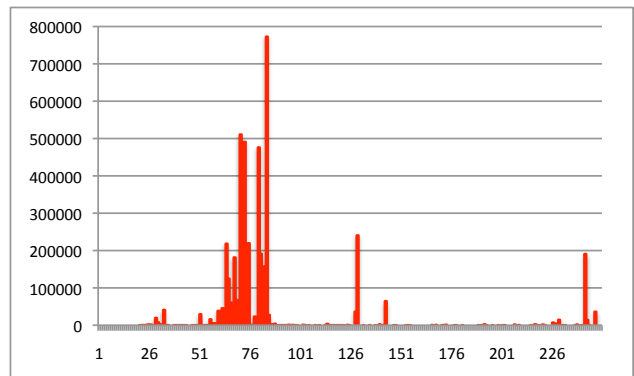
The total number of reads (y-axis) found in specific nucleotide length reads/predicted transcripts (x-axis): A) sequence reads and B) predicted transcripts in brain sample, C) sequence reads and D) predicted transcripts in muscle sample, E) sequence reads and F) predicted transcripts in testes sample, and G) sequence reads and H) predicted transcripts in ovary sample.

Brain

A

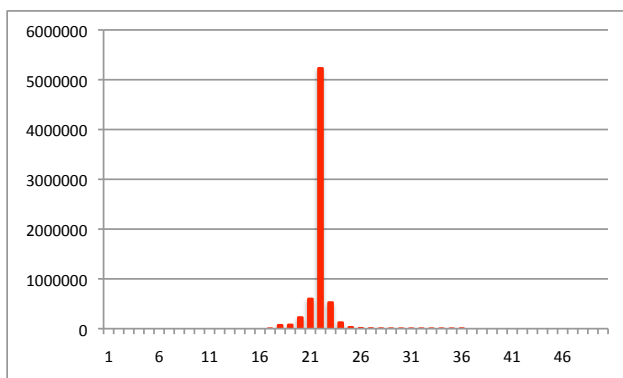


B

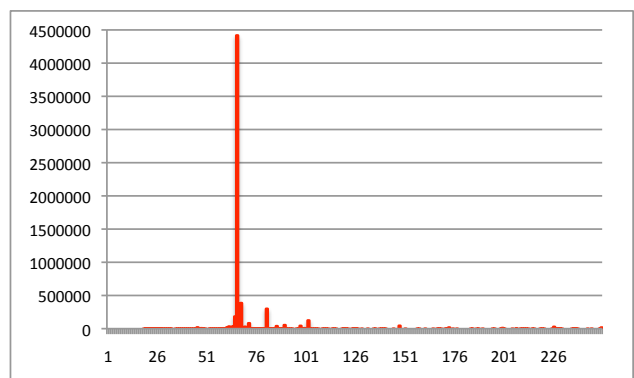


Skeletal muscle

C

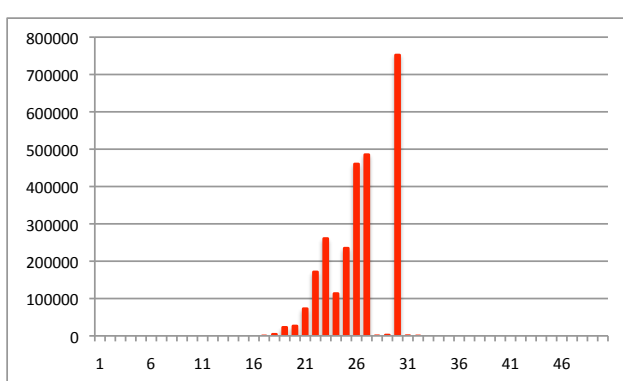


D

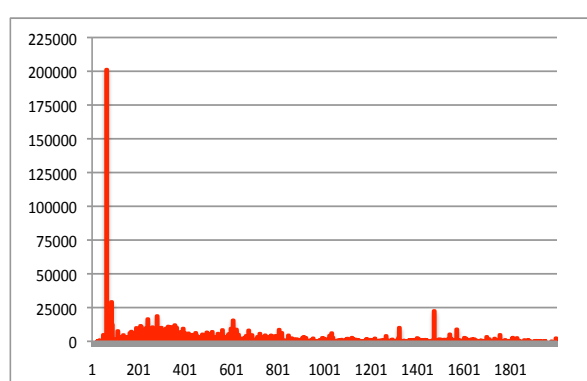


Testes

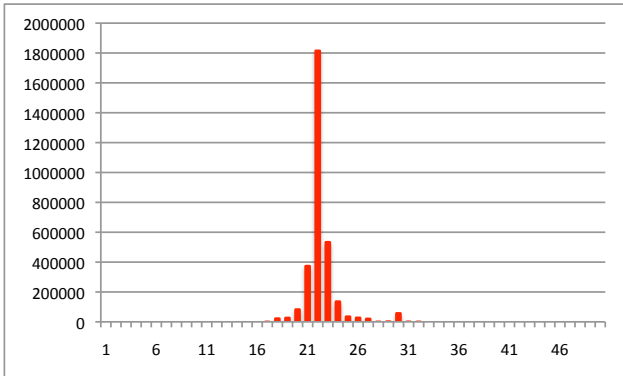
E



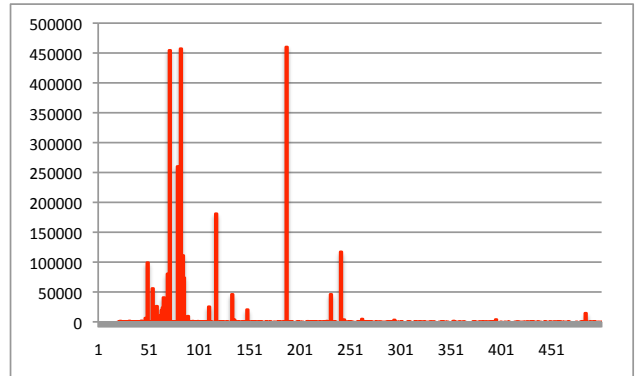
F



Ovary
G

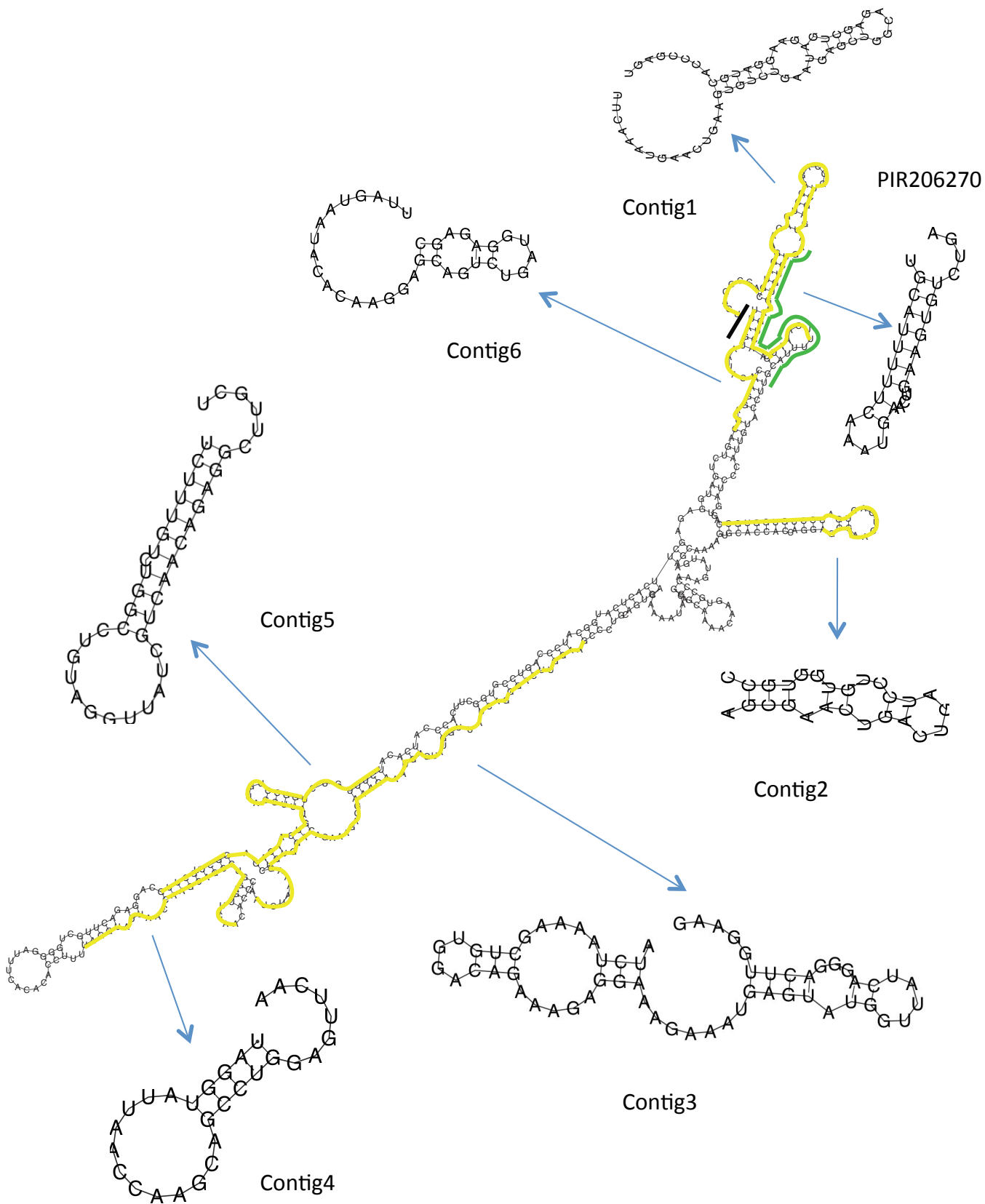


H



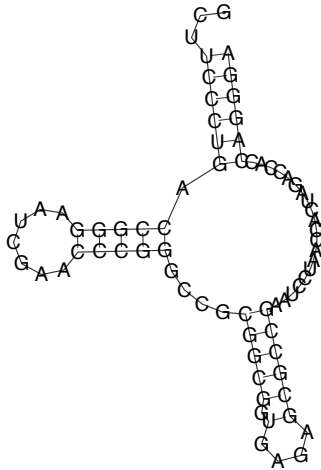
Note: The length distributions 1-50 nt in graphs A, C, E and G cover 100% of total reads and the variable length distributions 250-2000 nt in graphs B, D, F and H cover >98% of total reads.

Supplementary Figure 7. Predicted structures of un-annotated contigs in a piRNA transcripts from chr6:128121896-128122316 (- strand).

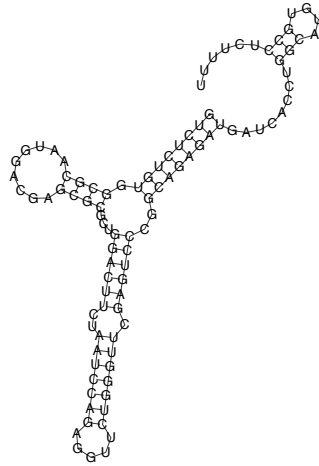


Supplementary Figure 8. The structures of predicted novel small ncRNAs in brain. A – G) 7 out of 8 transcripts are overlapped with tRNAscan-SE predictions (Schattner *et al.* 2005), and H) one remaining transcript.

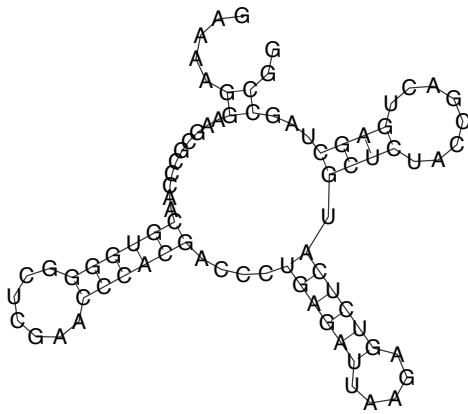
A) chr1:173,001,920-173,001,994 -28.2 kcal/mol



B) chr1:175,320,459-175,320,556 -37.5 kcal/mol



C) chr3:96303424-96303505 -22.3 kcal/mol



D) chr4:10801209-10801294 -25.7 kcal/mol

