

Supplemental information for “Characterization of piRNAs across postnatal development in mouse brain”.

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Supplemental Figures

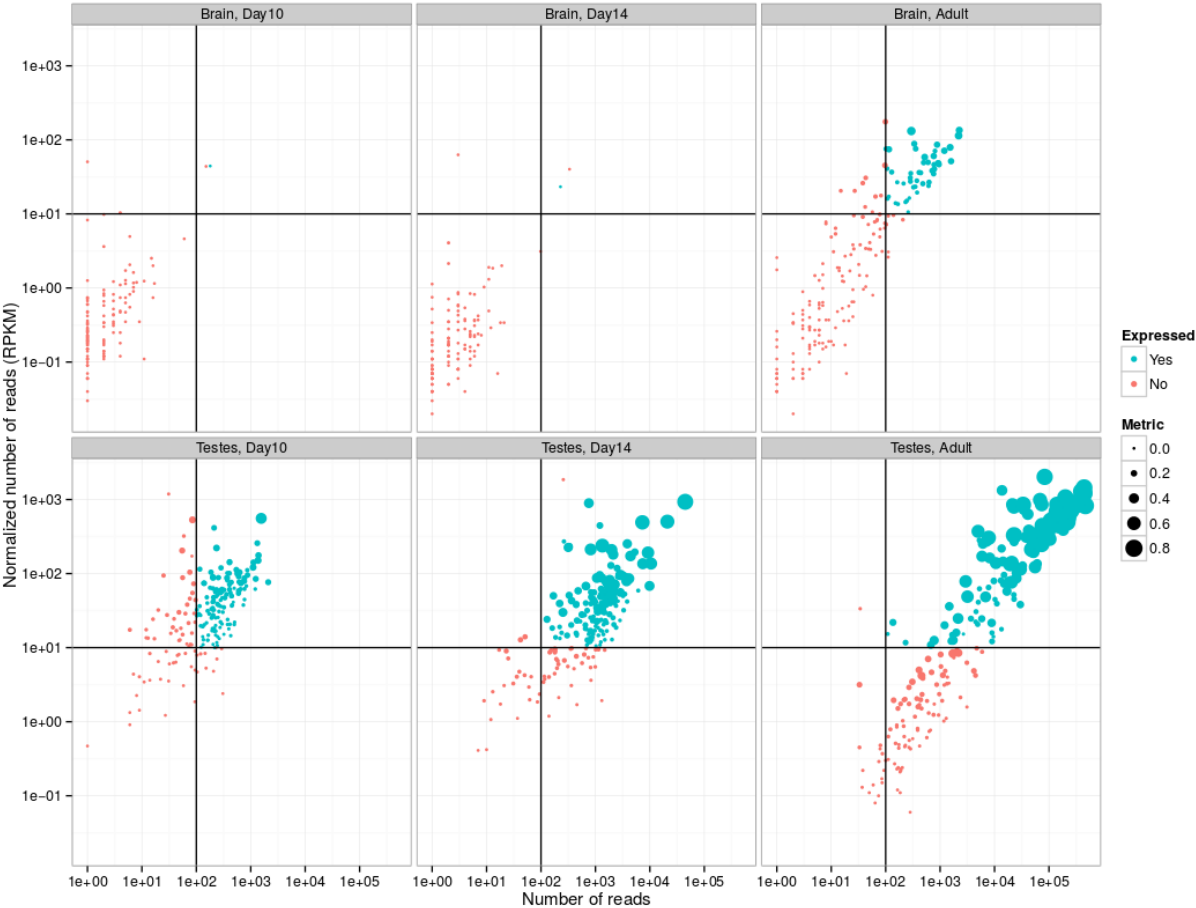


Figure S1. Filtering non-expressed piRNA clusters. scatter point shows expressed piRNA clusters (blue): pass threshold of 10 rpkM (horizontal); 100 reads (vertical); have more uniform-like coverage of reads (metric; see methods).

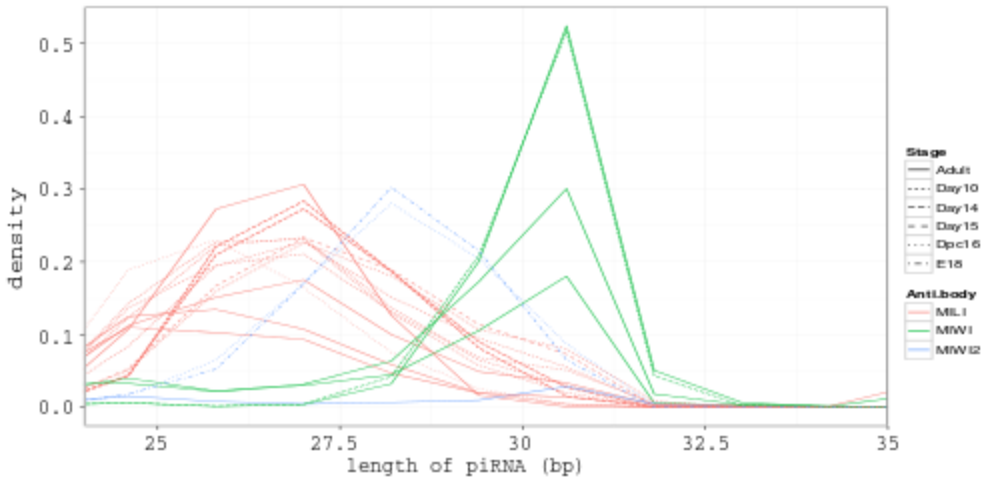


Figure S2. Piwi-like genes bind piRNAs of specific sequence lengths. lineplot shows sequence length distribution of piRNAs obtained from publicly available PIWI-like proteins IP datasets. piRNAs of lengths 26~27bp, 28~29bp and 29~31bp associate to MILI, MIWI2 and to MIWI. These data sets were obtained from the following NCBI GEO series: GSE7414, GSE12757, GSE16023, GSE18825, GSE19172, GSE26251, GSE27623, GSE32184, GSE39203.

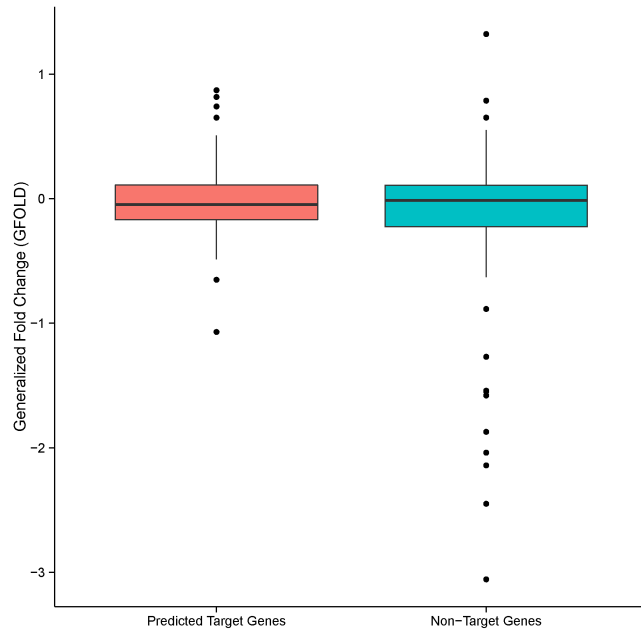


Figure S3: miRanda-predicted target genes do not exhibit more down regulation than non-target genes (p-value 0. 5122). The similarity between the two distributions suggests that piRNAs in adult brain may not be implicated in massive mRNA deadenylation.

Supplementary Tables

Motif	Over-representation	Over-represented Motif E-value	TF Match P-value	TF
	BT Clusters' Promoters	4.9e-003	0.00497752	Eomes
	Non BT Clusters' Promoters	2.0e-002	0.00858316	Meis1
	Non BT Clusters' Promoters	4.5e-002	0.014478	Sox4
	BT Clusters' Promoters	3.7e-008	0.00616759	Zic1
		1.4e-004	0.0152929	
	BT Clusters' Promoters	3.7e-008	0.00909189	Zic2

Supplementary Table S1: Discriminatory motifs that distinguish between BT clusters' promoters and non-BT clusters' promoters. These motifs were compared against

JASPAR vertebrate and UniPROBE mouse to find their associated candidate TFs.
These TFs may regulate the transcription of BT piRNA clusters.