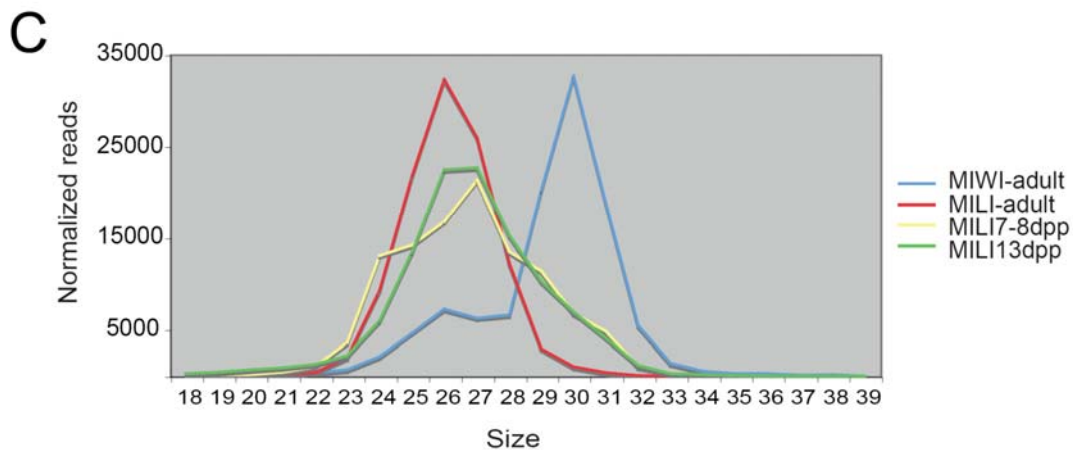


B

<i>piRNA Library</i>	<i>Clone #</i>	<i>Read #</i>
MILI 7-8dpp	35078	262458
MILI 13dpp	61759	119361
MILI Adult	34218	108570
MIWI Adult	35286	55430



Supplementary information, Figure S1 Overall profiles of MILI- and MIWI-associated piRNAs.

A, The percentages of the sequence reads from each library that are clipped, selected, and mapped. Preliminary processing of the four libraries yielded more than 90% successfully clipped sequences. More than 80% of the total clones were clippable with a size range of 18-35nt for MILI-associated piRNAs and 20-39nt for MIWI-associated piRNAs, that were selected for further analysis. Over 70% of the total clones could be mapped on the genome. B, Total read of the libraries. C, Size distribution of piRNAs from each of the four libraries. The MILI- and MIWI-associated piRNA libraries are abundant with piRNAs of 26-27nt and 30nt, respectively. The small RNA abundance is normalized to the sequencing depth.