

Supplementary information, Table 1 Deep sequencing analysis of MIWI RIPed RNAs.

Libraries	Small RNAs		Long Transcripts	
Unique reads	715,144		1,499,244	
Total reads	25,697,817		19,174,539	
miRNA	74,520	0.29%	352	0.003%
ncRNA	127,897	0.50%	272,597	2.49%
mRNA	749,596	2.92%	2,269,940	20.75%
Intron	496,710	1.93%	644,688	5.88%
TE	5,273,641	20.52%	7,357,553	67.2%
Intergenic regions	18,975,453	73.84%	410,289	3.7%