



Supplementary information, Figure S1 Prediction of piRNA targets by computational approaches.

(A) MIWI associated small RNAs in elongating spermatids. Top, size distribution for MIWI-associated small RNAs. Middle, nucleotide distribution for MIWI-associated small RNAs. Right, Genome annotation for MIWI-associated small RNAs.

(B) The number of predicted targets for each MIWI-associated piRNA with reads $\geq 1,000$. X axis shows individual MIWI-associated 2861 piRNAs containing in predicted mRNA:piRNA interactions. Y axis represents the predicted target numbers for each MIWI-associated piRNA, with miRanda

alignscore >150.

(C) Distributions of filtered piRNA target genes. Left, the plots were distributions of mRNAs with fold-change > 1.5 and FDR<0.05 in anti-MIWI RIP relative to IgG RIP (Y axis), against the read number (log2) for piRNAs that were predicted to target the mRNAs (X axis). Right, X axis shows the reads of piRNAs, while Y axis represents the targets numbers for cognate piRNAs. Four piRNAs that were confirmed to regulate their targets by reporter assays were indicated in red.