Normalized to non-coding RNAs (including rRNA)

A

Change in abundance vs. \( w^{1118} \), by transposon family

\[ \frac{qin^1}{Df} \quad \frac{qin^2}{Df} \quad \frac{qinkum^{\text{TM3}}}{Df} \]

\( f.c. > 2 & FDR < 0.05 \)

B

Normalized piRNA (ppm)

C

Normalized piRNA (ppm)
Figure S5. Relative piRNA abundance, normalized to non-coding RNA (ncRNA) abundance, including 2S ribosomal RNA. (A) piRNA length distribution. The normalization procedure failed for the Anand et al., 2012 dataset because > 89% of its sequence reads are 2S rRNA. Blue, sense piRNAs; red, antisense. (B) Box plots reporting the change in abundance of all piRNAs mapping to transposons. (C) qin\textsuperscript{1}/Df, qin\textsuperscript{2}/Df and qin\textsuperscript{kumo}/Df, but not qin\textsuperscript{kumo}/qin\textsuperscript{kumo}, affect piRNA production similarly. Transposons were grouped as Figure S3A.