

Supplementary information, Table S3 Deep sequencing of MIWI CLIPed RNAs

| MIWI CLIPed tags | >33 nt reads | | All reads | |
|--------------------|--------------|-------|------------|--------|
| Unique reads | 5,091,165 | | 23,928,416 | |
| miRNA | 1,165 | 0.02% | 13,788 | 0.06% |
| ncRNA | 161,542 | 3.2% | 409,674 | 1.71% |
| 5'UTR+CDS+3'UTR | 856,430 | 16.8% | 2,089,628 | 8.74% |
| Intron | 1,399,027 | 27.5% | 4,006,540 | 16.74% |
| TE | 1,214,070 | 23.8% | 5,140,664 | 21.48% |
| Intergenic regions | 1,458,928 | 28.7% | 12,268,122 | 51.27% |