**Table S6. Oligonucleotides and siRNAs used in this study.**

|  |  |  |  |
| --- | --- | --- | --- |
| **siRNA** | **Target name** | **Sense** | **Antisense** |
| siGFP | rGrGrCrArArGrCrUrGrArCrCrCrUrGrArArGrUTT | rArCrUrUrCrArGrGrGrUrCrArGrCrUrUrGrCrCTT |
| siPIWI | rGrCrUrCrCrCrArGrGrCrGrUrGrArArGrGrUrGTT | rCrArCrCrUrUrCrArCrGrCrCrUrGrGrGrArGrCTT |
| **Oligos for libraries construction** | 3’ Adaptor | pCGTCGTATGCCGTCTTCTGCTTGT/3AmMO/ | |
| 5‘ adaptor | GTTCAGAGTTCTACAGTCCGACGATCNNNrXrXrXrArA  (XXX –barcode trinucleotide sequence) | |
| 18.206 (RT and PCR primer) | CAAGCAGAAGACGGCATA | |
| 44.45 (forward PCR primer) | AATGATACGGCGACCACCGACAGGTTCAGAGTTCTACAGTCCGA | |
| **Oligos for gDNA libraries construction** | PE\_Tdot\_common\_C\* linker | AATGATACGGCGACCACCGAGATCTACACTCTTTCCCTACACGACGCTCTTCCGATC\*T | |
| Barcoded linker PE\_tdot\_CAGCACTA | /5Phos/GATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGcagcactaATCTCGTATGCCGTCTTCTGCTTG | |
| Barcode linker PE\_tdot\_AGAGATGC | /5Phos/GATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGagagatgcATCTCGTATGCCGTCTTCTGCTTG | |
| Barcode linker  PE\_tdot\_TCACGTGT | /5Phos/GATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGtcacgtgtATCTCGTATGCCGTCTTCTGCTTG | |
| PE-POSTPCR\_1 | AATGATACGGCGACCACCGAGA | |
| PE-POSTPCR\_2 | CAAGCAGAAGACGGCATACGAG | |
| **Oligos for EMSA** | T7DNA\_Bantam\_anti | CGTCGCAACCGCtgagatcattgtgaaagctaatCAGCTCCATTCCCTATAGTGAGTCGTATTA  (T7 transcription DNA template, transcribed sequence marked in lower case) | |
| Akap200 | rArGrArArTrGrGrCrArCrCrArArTrGrG**rCrArCrCrArCrCrA**rCrG  rCrCrCrCrCrGrCrCrCrArCrTrCrC  (CA-rich motif shown in bold) | |
| piR-142847-2Ome3' | prUrGrGrGrArUrUrArCrArArGrUrGrUrGrCrArCrArArCrUrUrUrCrCrUrGmrC | |

**Table S6 continued.**

|  |  |  |  |
| --- | --- | --- | --- |
| **Primers for detection of TE insertions** | **Sequence** | **Oligodeoxynucleotide** | |
| **Forward** | **Reverse** |
| 297 near Mec2 | CCCCTTTTTCGAAACAACAA | CAGTTCTGCTTTGGGGTCAC |
| ZAM LTR at Fau | GCATGGCACACAGAAAGTGT | CAACGGTGATGCTTTGAATG |
| 297 at Chas | TGCCCATTGTTCGTCTATATG | ATGAAGTGGTTGACTGCCCT |
| MDG3 at CG3679 | AACCGTGGCTCAGGTAACAT | GTGGCATGCAACCTAACCTT |
| 17.6 LTR at Btk29a | GGAAAGTGCATTCCCACATT | AAATTCGGTTGGTTTTCAGC |
| Gypsy at Ex | TCGTGGAAGTGGAAGAGGTC | GACGTCAGTGCTCAATCGAA |
| MDG1 at CG15278 | TAGTCCGTTCCGTTCCATTC | ATAGGAGGAGTTGCGTGTGC |
| ZAM insertion #1 at Trim9 | GGCTTTTTCCACATTGCTCT | TGAACATGTGCGACGAATTT |
| ZAM insertion #2 at Trim9 | GCAAGCCAGGCAGAAAACT | CCATTCATAACCAGCGCTTT |
| Springer near RpL37b | CGCCTGTCCCTTTCATTTTA | TTTGTGTTTGCTTTTCGGACT |
| ZAM near RpL37b | CGCTTGAAATTCTCTAAGCCACT | TTTCCCCACATTTTTCCAAG |
| Springer at Chr2L:5.4 | CGCGCAATTTTTCAGCATA | ACTGACTCGACCGAAAATCG |
| Copia at Cyp4p2 | TTTTCCCCTTGGTCTATTCG | GTGCCATTTCTTTTCTGCAA |
| Springer at CG4983 | TCTAGGAAGCGGGAGTCATT | AAACGAACTGACACAAAAATCAG |
| Stalker4 at KCNQ | GCCATTTTCATTGCATGCTT | GACCGGGAAACGACACTTTA |
| Springer at Prosap | TGACTGCCGATAAAATGTCAA | TGAAAACTCGATCCCCTTTC |
| Juan at cni | TCCTCGGATCTCAAATCACA | AGCCTCAATCCGGTCAGTAA |
| Roo at Dlp | ACCAAAAGCTACCGGAAACC | TTCCTATACCACCGGGTTCA |
| **Primers for qPCR** | Akap200 | GCTGAAAAGCCAGCTGAGA | GGGCTTCTCATCCTTGGAC |
| Ef1alfa48D | CGTTGGTGTGAACAAGATGG | ACCAGGGCATGTTGGTAGAG |
| Ef2b | GCCGATCTGCGCTCTAATAC | AGCTGCACTTGGATGTTGTG |
| Larp | GCCTCCTTGATGCTGTTAGC | CCCGACTTATCGCATACCAC |
| Mec2 | GTCATTTCCGCCAGTCCAT | GGCCAGATACGGAGTAAGCA |
| TJ | GCAAAAATTCCAATCCTTCAGT | CGCTTCGATCCAGTTTCACT |
| Not1 | TTTGTGTGTGCTGTTGCTGA | TTCTGCCTGGAGGTCTGC |
| Osa | ACCGTCACAGCAGTACAGGA | GGCGGATAGGGTGACTGAC |
| Rp49 (RpL32) | ATGACCATCCGCCCAGCATAC | CTGCATGAGCAGGACCTCCAG |

**Table S6 continued.**

|  |  |  |  |
| --- | --- | --- | --- |
| **Primers for qPCR** | **Sequence** | **Oligodeoxynucleotide** | |
| **Forward** | **Reverse** |
| lncRNA-NL-RpL37b | CCGTTCCAGCTTCCCATA | AGGCCATGACACTGCTCTG |
| lncRNA-NL-Trim9 | GAATCGCACCCACTCACTTC | GGCTGCTCTGGTGAAATGTT |
| lncRNA-NL-CG4168 | TGGCTACCTTTTGGCTACCTT | CGCCGCAGTGTCTATTAGTG |
| lncRNA-NL-CG4983 | AGTGGCAGGATGAGGCTAAG | CTGGGAGGACAGCTCTCAAG |
| lncRNA-NL-Cyp4p2R | GGCCATACTTGTGGTCATCC | TGATCATGGGCACTAAGCTG |
| lncRNA-NL-Chr2L:5.47M | TCCGAGACCTTCGCAGAG | GATCGCCCAATTCCAATG |
| RpL37b\_#1 | CATGGCACATAAAGCTCGTG | TCCCGGCGAATATATCATGT |
| RpL37b\_#2 | CGTGTGTAGCCTTCAGAGCA | CGCATTCCCTTAAGTTCTGC |
| MDG1(Vagin, Sigova et al. 2006) | AACAGAAACGCCAGCAACAGC | CGTTCCCATGTCCGTTGTGAT |
| 297(Saito, Ishizu et al. 2010) | CTGGCAAAGGGATTTCATCA | TGCATTCCTAAGGCCAAATG |
| ZAM | ACTTGACCTGGATACACTCACAAC | GAGTATTACGGCGACTAGGGATAC |
| DM412(Wang and Elgin 2011) | CACCGGTTTGGTCGAAAG | GGACATGCCTGGTATTTTGG |
| HeT-A | CGCGCGGAACCCATCTTCAGA | CGCCGCAGTCGTTTGGTGAGT |
| Copia | TCAAAGTATAAAGTCAAGTGTCACCA | CGTGTGATGTTGCAGTTTGAA |
| Roo | CGTCTGCAATGTACTGGCTCT | CGGCACTCCACTAACTTCTCC |
| Gypsy | GTTGAGGCAAGGATTGGAAA | TAAGCAGGTCAGCACCCTCT |
| **Primers for hybrid TE-lncRNA transcripts** | Springer-RpL37b | CTGCCTCCCAGTGACAGAG | CGCATTCCCTTAAGTTCTGC |
| ZAM-Trim9 | ACTTGACCTGGATACACTCAC  AAC | CGTTGTTTTGCTTTCCCTTC |
| ZAM-Mlc2 | ACTTGACCTGGATACACTCAC  AAC | TACCTAGGCTGATCGGAGGA |
| Springer-Chr2L:5.47M | CTGCCTCCCAGTGACAGAG | GATCGCCCAATTCCAATG |
| Springer-CG4168 | CTGCCTCCCAGTGACAGAG | CGCCGCAGTGTCTATTAGTG |