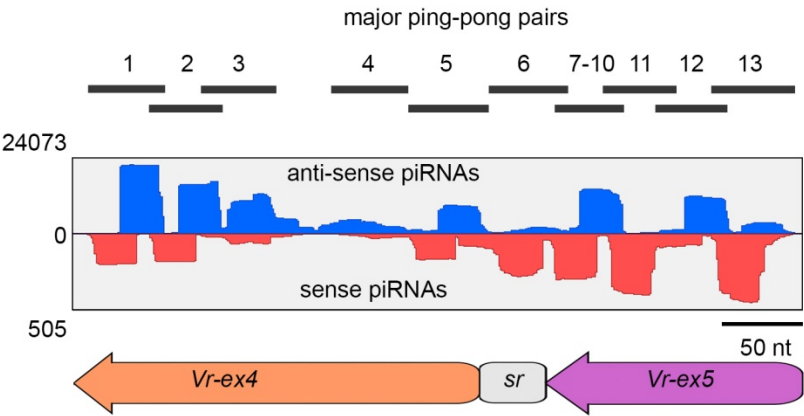


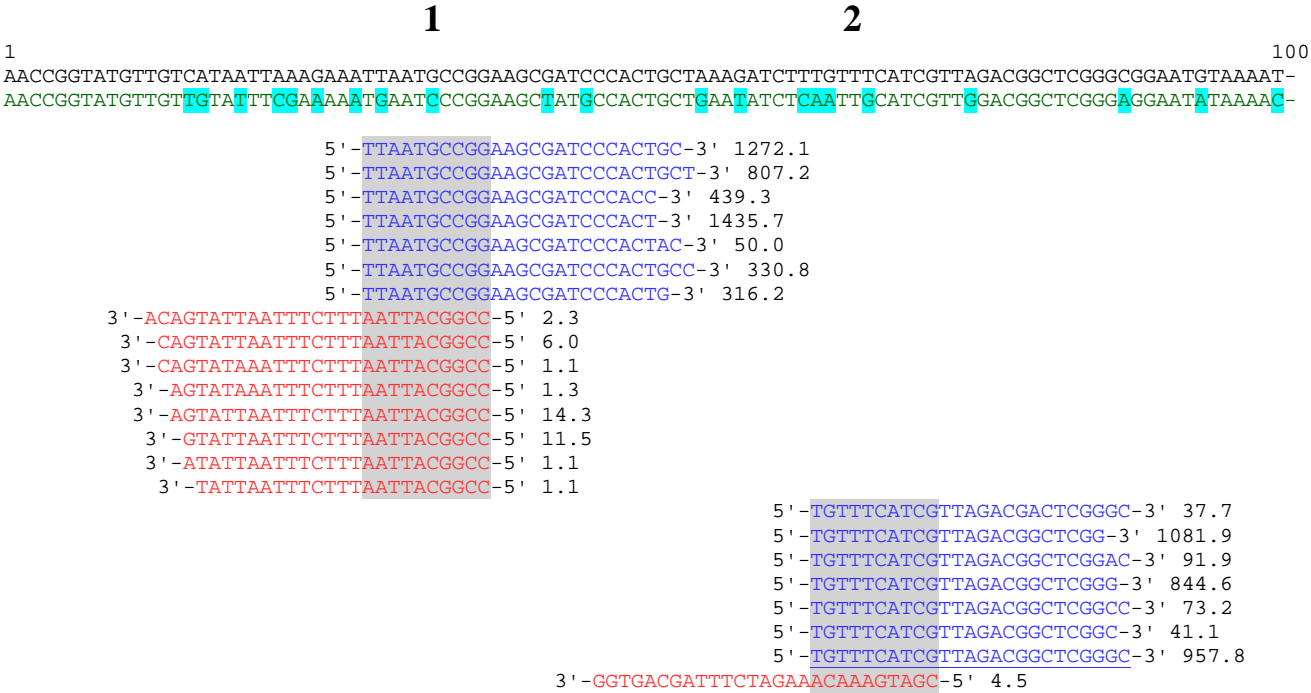
Supplementary Figure S3
A

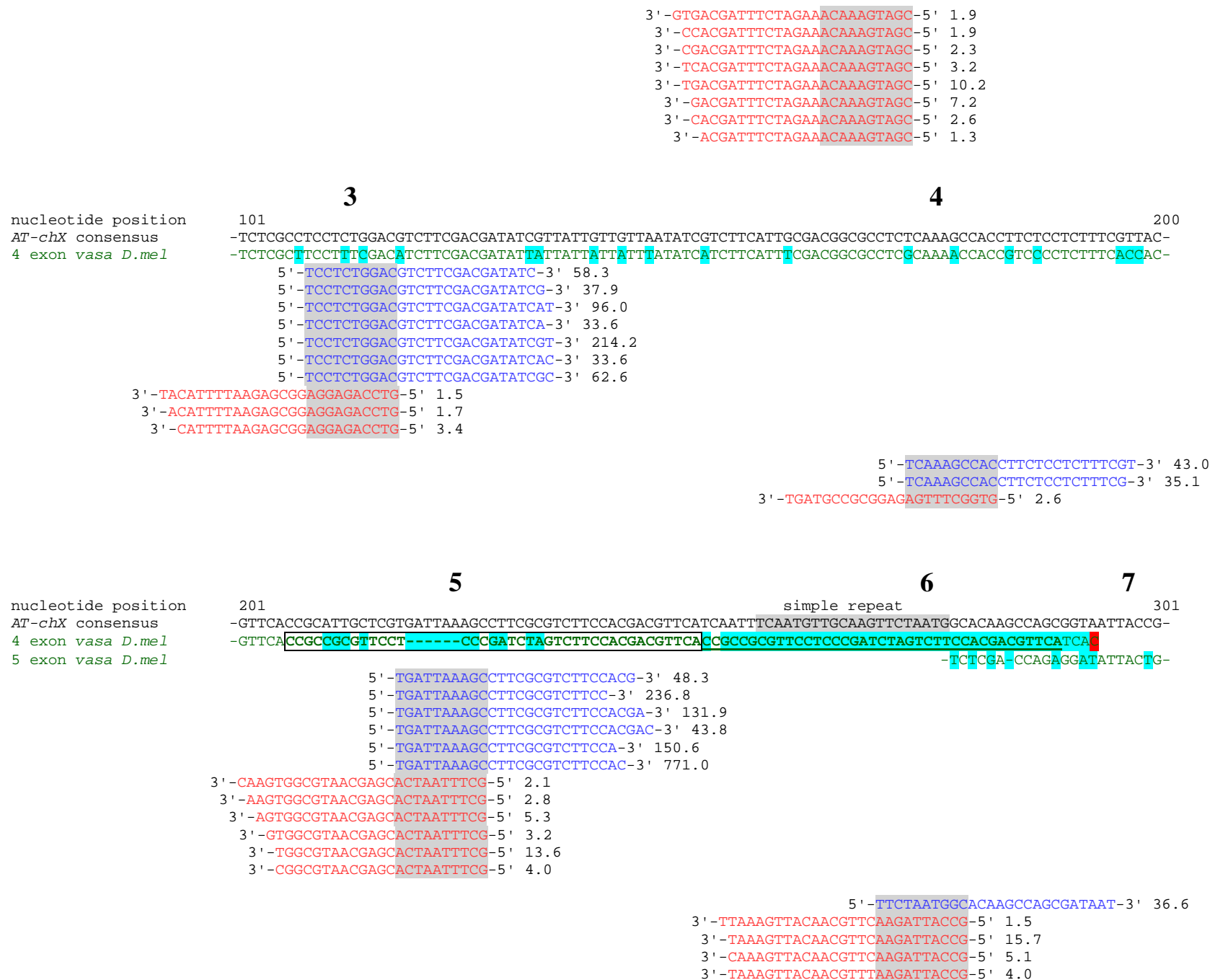


B

pair number

nucleotide position
AT-chX consensus
4 exon vasa D.mel





3'-AAAGTTACAACGTTCAAGATTACCG-5' 6.2
3'-AAAGTTACAACGTTTAAGATTACCG-5' 2.1
3'-AGTTACAACGTTCAAGATTACCG-5' 3.6

5'-TACCGGTATAGCACACTTTTGTA-3' 52.3
5'-TACCGGTATAGCACACTTTTGATC-3' 96.4
5'-TACTGGTATAGCACACTTTTGATC-3' 39.1
5'-TACCGGTATAGCACACTTTTGTA-3' 87.7
5'-TACTGGTATAGCACACTTTTGATCGG-3' 36.2
3'-TCGGTCGCCATTAAATGGCCATAT-5' 1.1

8 9 10

11

12

13

nucleotide position
AT-chX consensus
5 exon vasa D.mel

301
-GTATAGCACACGTTTGTATCGGCGTCGATACCTAGTATCCAGATTTCGTCACATTTTCCACAATAATGTCCTTTAATCAGCACTCGTAAAGTTTTTATGCGTGTGGAACGTCGTTGCCGGTCACCTTTTATTT
-GTATGCAACACTTTTGAATGGTGTGCGGTATTTGTATCCAGATTGTTTACATTGTCTATAATAATATCTCTCAATCAGCGCTCGTAAATGTTGTATAGGTGTGGAACATCGCTGCCGGTCA

5'-GTATAGCACACTTTTGTATCGGCGTC-3' 72.8
5'-GTATAGCACACTTTTGTATCGGCG-3' 48.3

3'-TCGCCATTAAATGGCCATATCGTGT-5' 4.3

5'-TATAGCACACTTTTGTATCGGCG-3' 360.8
5'-TATAGCACACTTTTGTATCGGCGTC-3' 1794.6
5'-TATAGCACACTTTTGTATCGGCGTCG-3' 58.9
5'-TATAGCACACTTTTGTATCGGCGT-3' 265.7
5'-TATAGCACACTTTTGTATCGGCGC-3' 53.8
5'-TATAGCACACTTTTGTATCGGCGTCGA-3' 71.1
5'-TATAGCACACTTTTGTATCGGCGGAC-3' 98.7

3'-GGTCGCCATTAAATGGCCATATCGTGTG-5' 3.6
3'-TCGCCATTAAATGGCCATATCGTGTG-5' 1.1
3'-GTCGCCATTAAATGGCCATATCGTGTG-5' 1.5
3'-TCGCCATTAAATGGCCATATCGTGTG-5' 24.9
3'-TCGCCATTTATGGCCATATCGTGTG-5' 1.5
3'-CCGCCATTAAATGGCCATATCGTGTG-5' 6.2
3'-CGCCATTAAATGGACATATCGTGTG-5' 1.1
3'-CGCCATTAAATGGCCATATCGTGTG-5' 8.5
3'-GCCATTAAATGGCCATATCGTGTG-5' 1.1

5'-ATAGCACACTTTTGTATCGGCGTC-3' 74.7
3'-TCGCCATTAAATGGCCATATCGTGTG-5' 1.3

5'-TCCAGATTTCCTTACATTTTCCACAA-3' 37.2
3'-CCGCAGCTATGGATCATAGGTCTAAAG-5' 3.4
3'-CGCAGCTATGGATCATAGGTCTAAAG-5' 1.1

5'-TAATGTCCCTTAAATCAGCACTCG-3' 752.1
5'-TAATGTCCCTTAAATCAGCACTCGTAAA-3' 126.6
5'-TAATGTCCCTTAAATCAGCACTCGTA-3' 750.4
5'-TAATGTCCCTTAAATCAGCACTCGT-3' 501.0
5'-TAATGTCCCTTAAATCAGCACTCC-3' 44.7
5'-TAATGTCCCTTAAATCAGCACTCGC-3' 129.6
5'-TAATGTCCCTTAAATCAGCACTC-3' 123.0
5'-TAATGTCCCTTAAATCAGCACTCGTAA-3' 110.0
3'-TCAGTGTAAGGTGTTATTACAGGGA-5' 1.3
3'-GCAGTGTAAGGTGTTATTACAGGGA-5' 1.3

3' - CCAGTGTAAGGTGTTATTACAGGGA - 5' 1.1
 3' - CAGTGTAAGGTGTTATTACAGGGA - 5' 5.5
 3' - AGTGTAAGGTGTTATTACAGGGA - 5' 2.8

5' - TATTGCTTGTGGAACGTCGTTGCCG - 3' 42.6
 5' - TATTGCTTGTGGAACGTCGTTGCCG - 3' 50.0
 5' - TATTGCTTGTGGAACGTCGTTGC - 3' 87.2
 5' - TATTGCTTGTGGAACGTCGTTGCC - 3' 288.5

3' - TCGTGAGCATTTCAAAAATAACGCACA - 5' 2.6
 3' - CGAGCATTTCAAAAATAACGCACA - 5' 6.0
 3' - TGAGCATTTCAAAAATAACGCACA - 5' 14.3
 3' - CAGCATTTCAAAAATAACGCACA - 5' 1.1
 3' - GAGCATTTCAAAAATAACGCACA - 5' 6.0
 3' - AGCATTTCAAAAATAACGCACA - 5' 4.5

Figure S3. Distribution of *AT-chX* piRNA ping-pong pairs from *yw* testis library.

(A) The distribution of *AT-chX* piRNAs along *AT-chX* consensus permitting 0-3 mm using bowtie1 soft. Antisense read density graphs are shown in blue color; sense read graphs are shown in red (scales indicates read number per nucleotide position). Black bars on the top indicate positions of major ping-pong pairs with corresponding numbers. (B) Alignment of major ping-pong pairs under consensus *AT-chX* sequence and homologous *D. melanogaster vasa* sequences of fourth and fifth exons (in antisense orientation, green letters). Sense piRNAs are marked by red color, antisense piRNAs are marked by blue color. Overlapped 10-nt regions of piRNAs are boxed in grey. Read numbers of corresponding piRNAs in the *yw* testis library are shown on the right as rpm. Only antisense reads with more than 30 rpm and sense reads with more than 1 rpm are presented. First nucleotide positions of the *vasa* exons are marked by red boxes. Nucleotide substitutions in *vasa* sequences which distinguished from *AT-chX* consensus are marked by cyan color. Start of fourth *vasa* exon bears twice repeated 39 nt sequences (both in bold letters, one repeat – in the box, and other one is underlined). This region is not perfectly match to *Vr-ex4* part of consensus. Simple repeat spacer that connects *Vr-ex4* and *Vr-ex5* parts of the *AT-chX* consensus is shown in light grey bar. Numbers of major ping-pong regions as in (A) are indicated above *AT-chX* consensus. Note that antisense *AT-chX-1* piRNA previously published as abundant (12) is mapped in region #2 (underlined) and has sense ping-pong partners. Antisense *AT-chX-2* piRNA is found in the library as minor one (0.2 rpm) and is not shown in the figure.