

Figure S1 - page 1

Eudicots

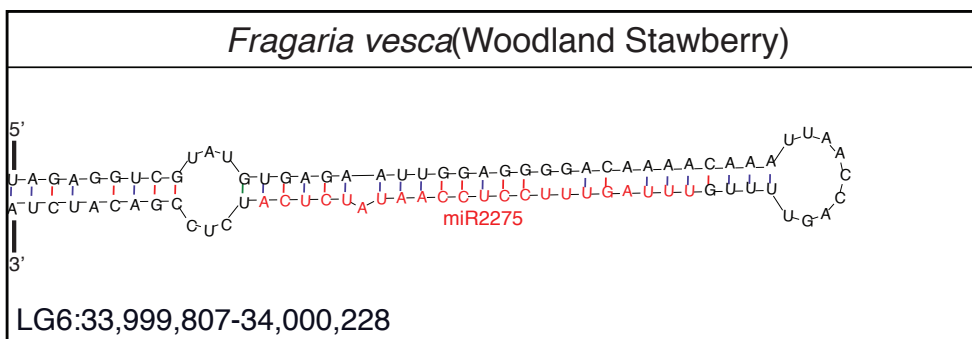
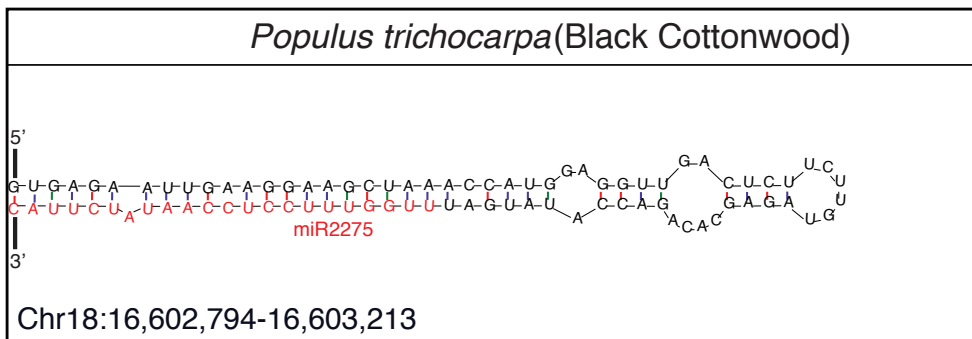
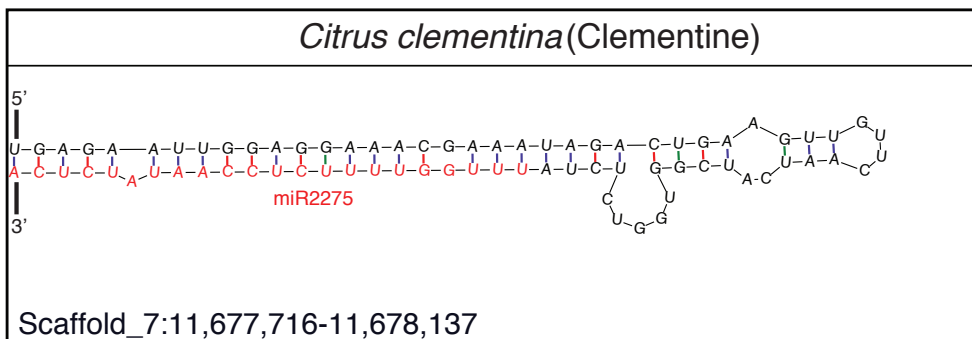
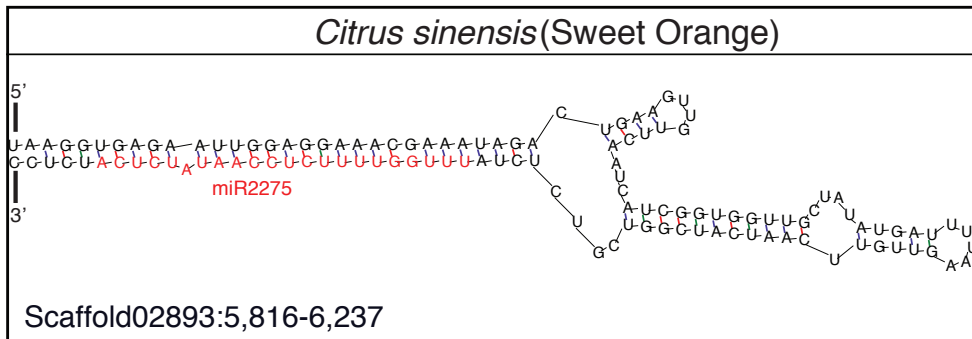


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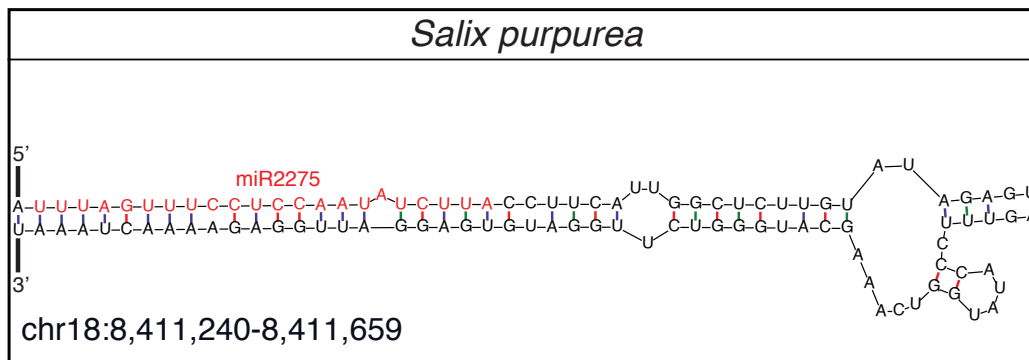
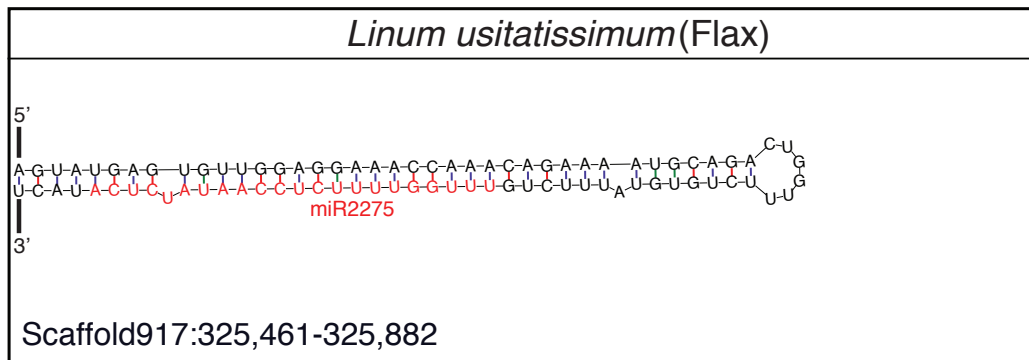
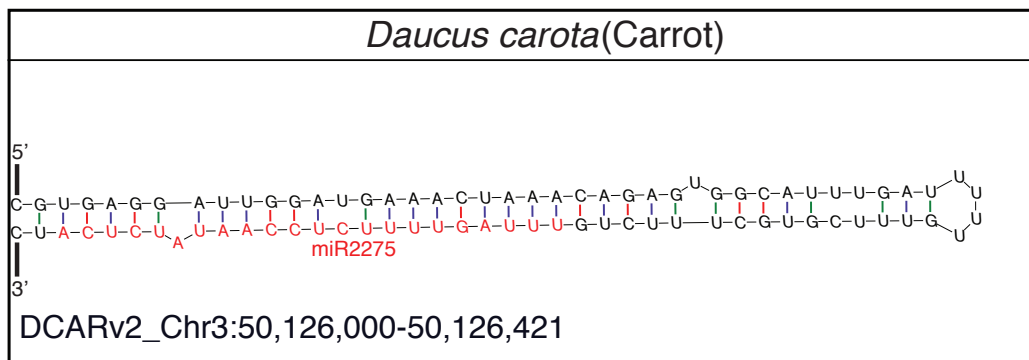
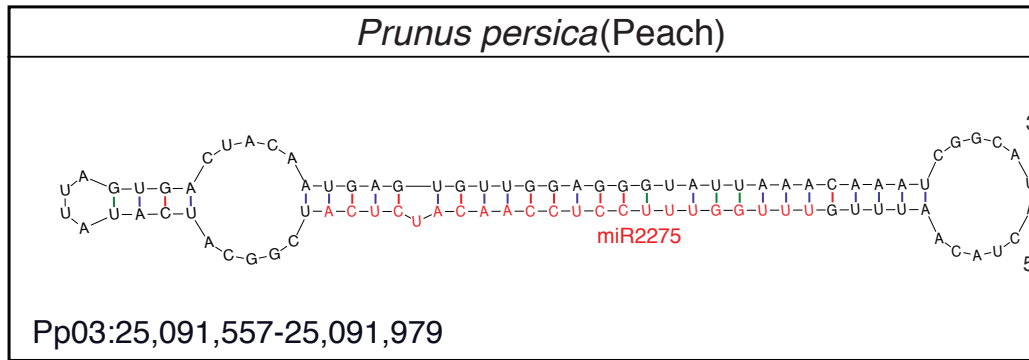


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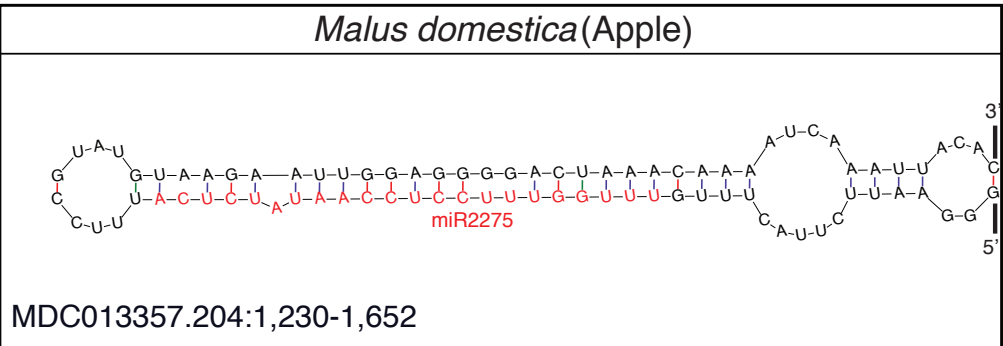
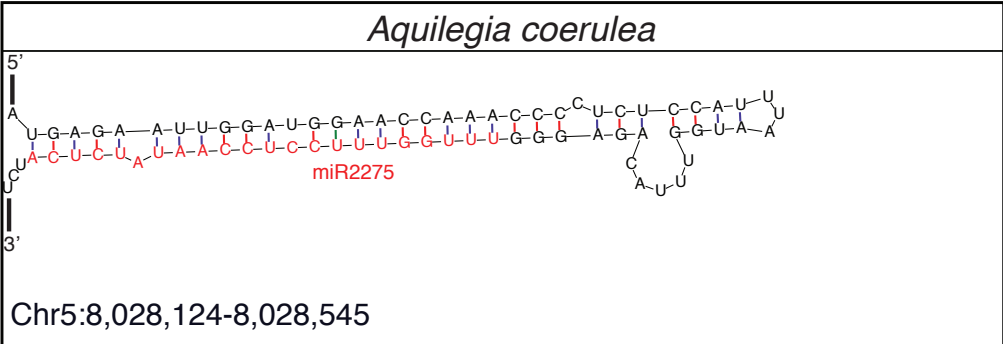
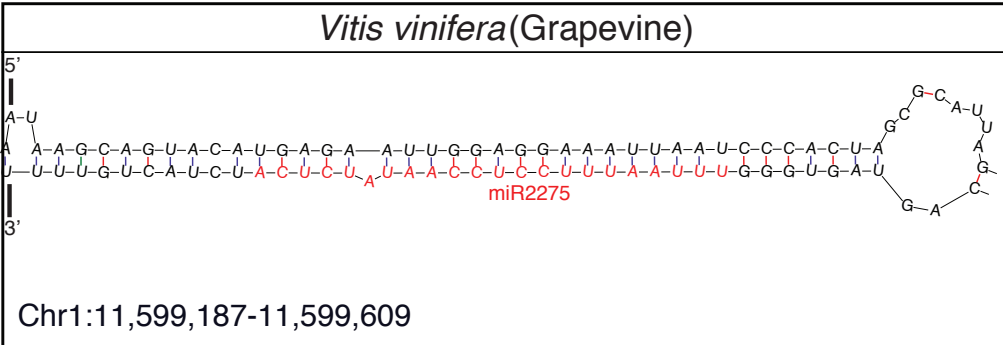
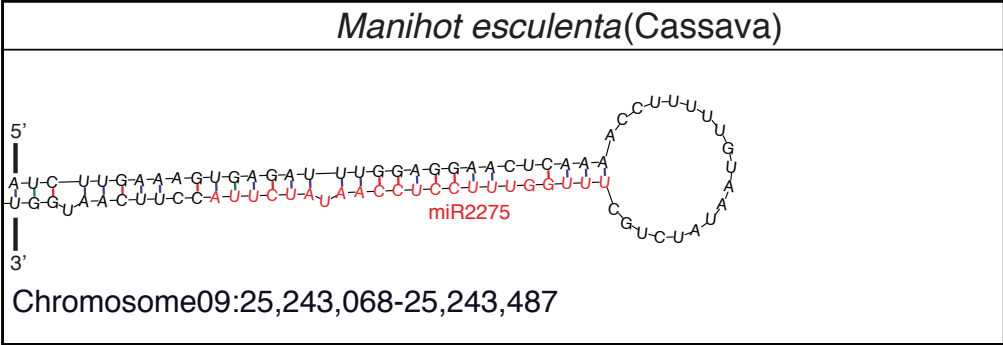


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Monocots

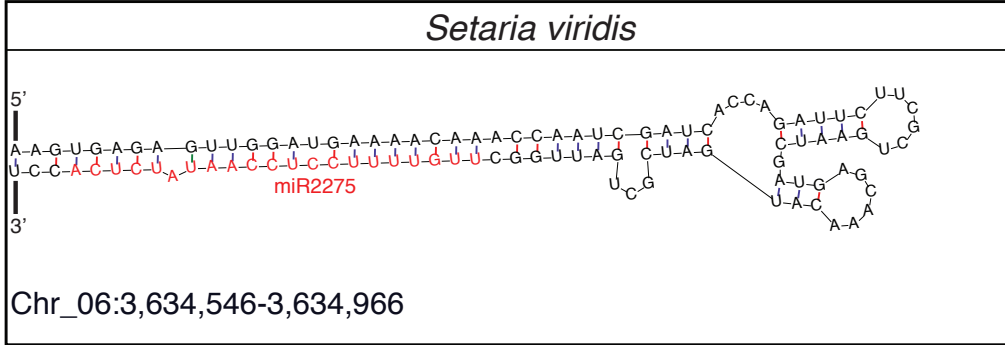
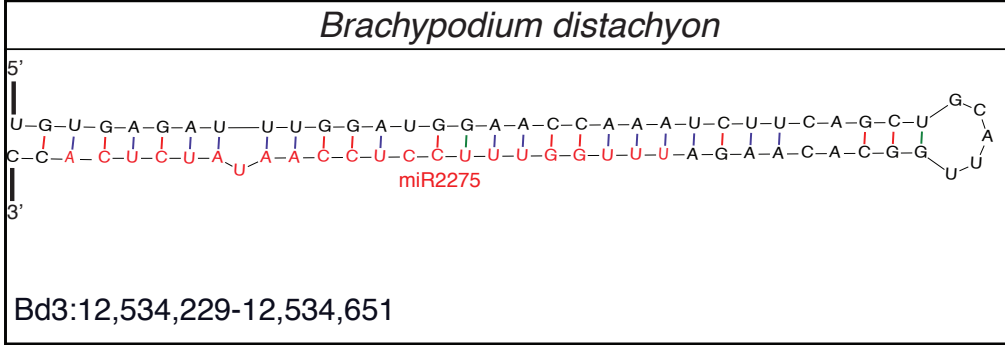
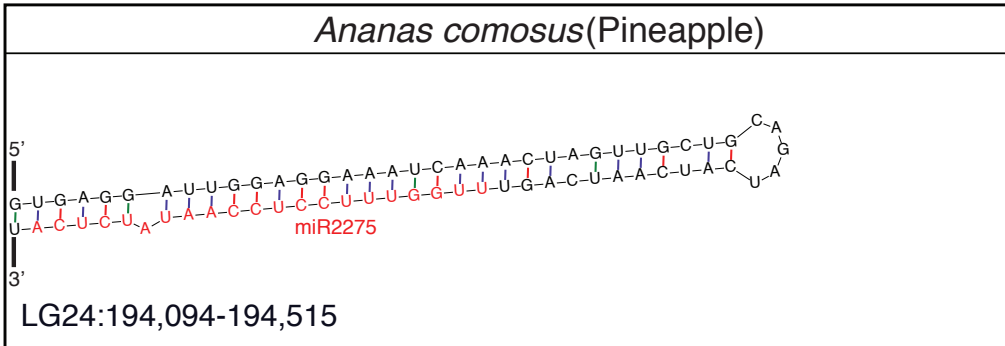
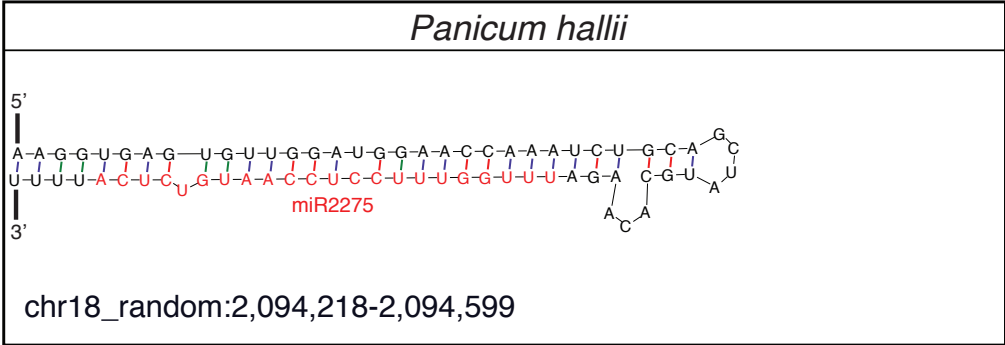


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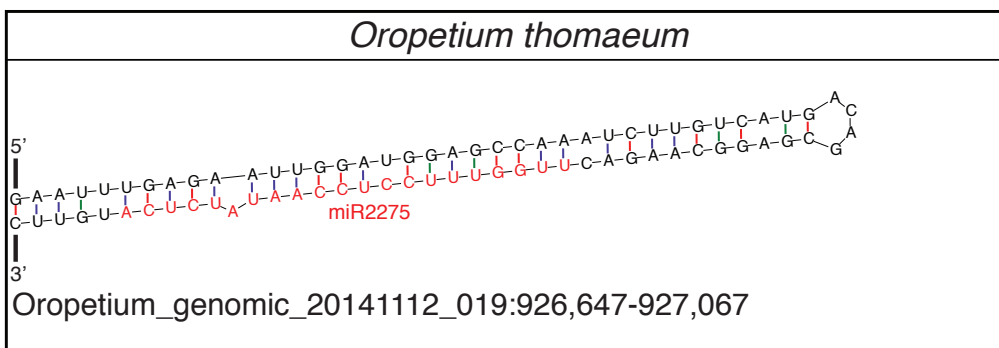
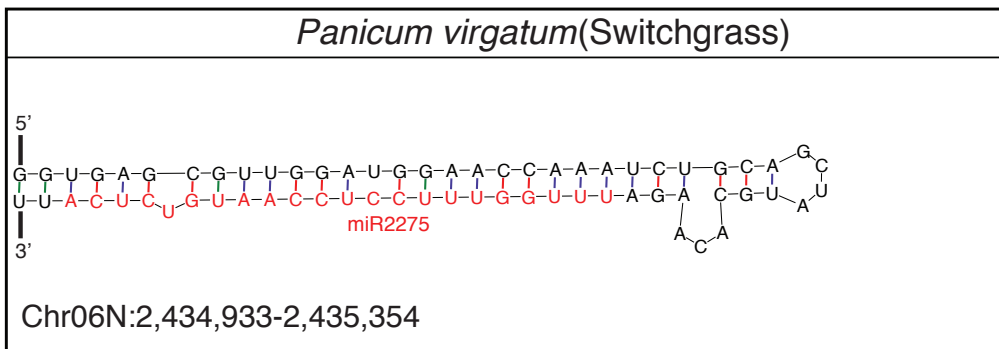
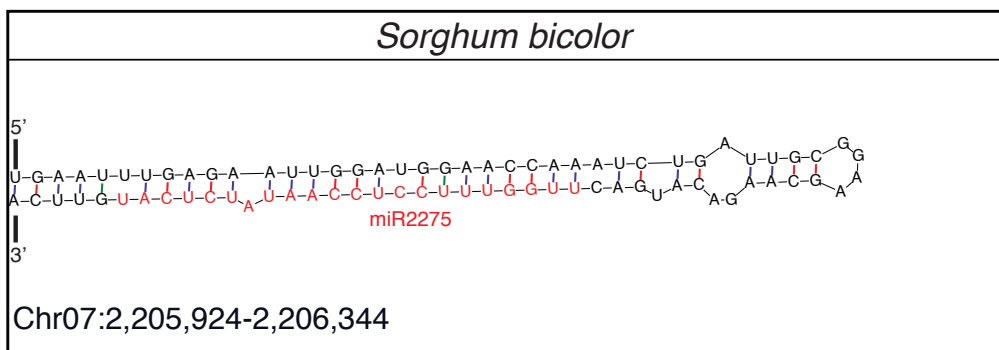
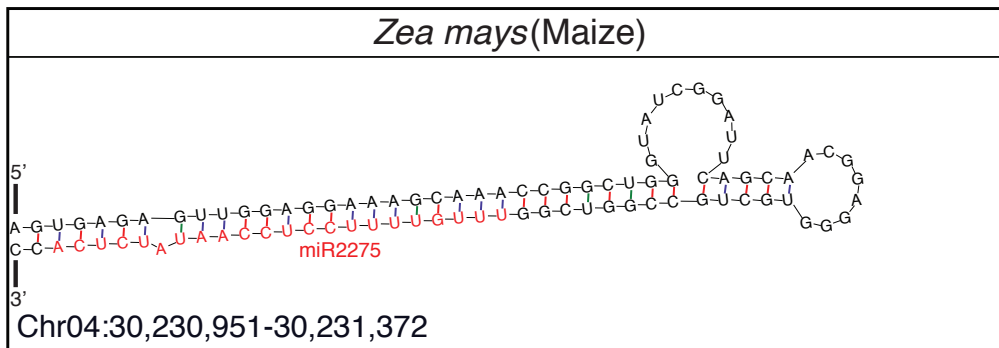


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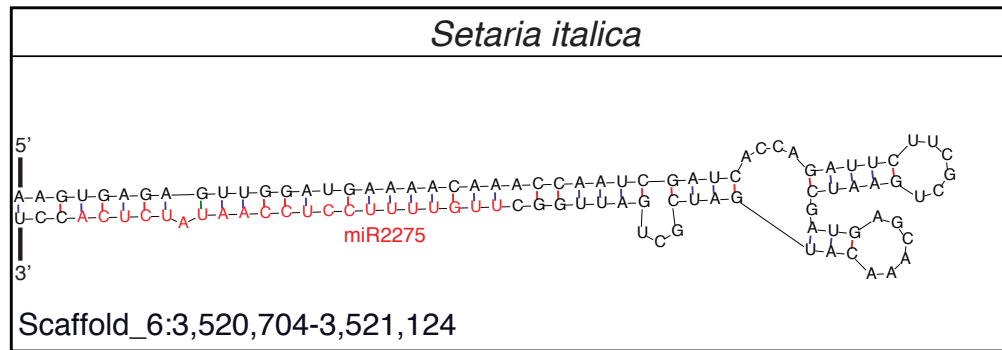


Figure S1. The RNA secondary structure of Bowtie-validated MIR2275 homologs. Secondary structures of loci were predicted via mFOLD. If the potential MIR2275 homolog formed a stem-and-loop structure, it is shown above. The red nucleotides denote the mature MIR2275 homolog in the secondary structure.

<i>Phalli</i>	AGTAGGCATGGCCATTGCAGA- - ATCAAA TTGGTACGGTGACTTAGCTTAGGTAGCATCAGAAATTCAGAAACCAAAA CTT	78
<i>Oropetium</i>	AGTAGGCATGACAAATGCAGATCATATAGTAGGTGTGAGGAATTAAGCTGCATACCATGAAAA CAAA TTAGCCGAAA CTC	80
<i>Osativa</i>	TGCAG - - - - TGACTGTAAAT - - - - GTGTGGAGTGGTAGCTTAGCTA - - - - GGCATCAGAAAA CCAAT AATCTT	59
<i>Bdistachyon</i>	GCTGA - - - - ATGCTGCAAGT - - - - AGTGGAGCTGGATGAACAGCTG - - - - AAATTTCTCAGGAACCT	57
<i>Pvirgatum</i>	- - CAG - - - - ATGATGGGTA - - - - GTCAA GTAGTGCAGATAGACACT - - - - AGACTTCTCTGAAGAATT	55
<i>Acoerulea</i>	TTCAGATACITTAATAA TAGAGAA - - - - GCATAAATGCCTTATTTAGTAGT - - - - TCATAGCTAAGCATAGAGTT	66
<i>Sitalica</i>	TCCATA - - - - CTGTTATGACC - - - - AGCTAA - - - - TTT CAGGCACTGAAA - - - - GTGAGAGTTGGATGAAAA CA	58
<i>Sviridis</i>	TCCATA - - - - CTGTTATGACC - - - - AGCTAA - - - - TTT CAGGCACTGAAA - - - - GTGAGAGTTGGATGAAAA CA	58
<i>Zmays</i>	TCCACC - - - - CTGTTAAGAAA - - - - AGCTAGAAAA GTGTCAGGCACTGAAA - - - - GTGAGAGTTGGAGGAAA GCA	63
<i>Acomosus</i>	TCTACT - - - - TAGCTGAATGT - - - - AGAGTA - - - - TTGAGATAGAGAGA - - - - GATAGGGAGAGAGAGAGT	57
<i>Mdomestica</i>	TTGCTCCA - - - - ACATCTCATCT - - - - AC - CACTGGCTCTC AAA TCAAT - - - T - - - CAACATTTTATTGTTT	61
<i>Fvesca</i>	TTTCTCCA - - - - ATATCTCATTT - - - - CCAGCATCTAAA TTTCAA GTAATAGCT - - - - ATAAATATTTTCTGTTT	66
<i>Ppersica</i>	TTCTCCA - - - - ATATCTCATTT - - - - CCGACATCTAAA CTGAAAA TTAAT - - - - GGTTATTTCT - - - - CAATT	58
<i>Lusitatissimum</i>	TTCTCCA - - - - ATATCTTATAT - - - - TCGCAGCTCTACTAGAGAT - CT - - - - GGTTAGTGGTGGCCAGCT	61
<i>Clemantina</i>	ATTTTA - - - - CGTCCACTTTTCTT - - - - GTTT - ATACATCTGAAACTT - - - - TT - - - - GTGATAA TAGTGC AAC	61
<i>Csinesis</i>	ATGGTAAAGAAA TTTTGTGATA - - - - AATAGATGCAACTTAAGGTGAGAAAT - - - - GGAGGAAA CCAAA TAGAC	67
<i>Trichocarpa</i>	AGTATCAA - - - - ATAATACAAAT - - - - - - - - GATTCTAGAAAA T - - - - - - - - GCAGTCAATGGATCT	51
<i>Mesculenta</i>	ATTTTATTGGGAAAGTGGCTGTTGTGTCTGCTCTCTCTTATAGTATCTGCTTAAAGCTGGCCAAATGGCCACC	70
<i>Spurpurea</i>	ACTCTTTGCAC - TCAATGGTCT - - - - TTGATGTTTTACCAATGTGGATGGCTTTT - TGAATATTTTGAATTTT	83
<i>Vinifera</i>	ACATGCCAAA TTTTCTGATAGT -	69
<i>Dcarota</i>	TATCTTACAAAGAAAA GGGGAAATAGTATAATTTCCCTGATATTACATCTATTCTACAAGGAAA CGCATACATCGG	80
	100.....110.....120.....130.....140.....150.....160.....170.....18	



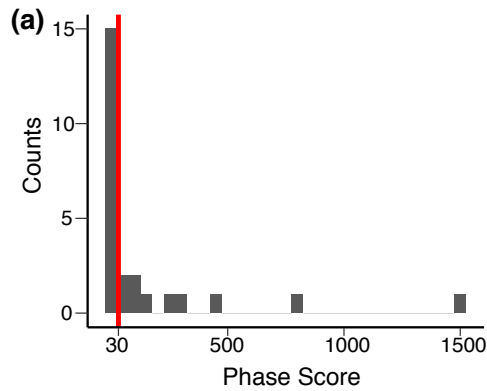
<i>Phalli</i>	GGGGG - TTGAATTTGAGAAATGGATGGAA CCAAA TCTG - - - TTTGCGAA - - - - AGCGAGG - - - - CAAGACTT	140
<i>Oropetium</i>	TGGCAG - TTGAATTTGAGAAATGGATGGAGCCAAA TCTG - - - TC - ATGAC - - - - AGCGAGG - - - - CAAGACTT	141
<i>Osativa</i>	TGGCAG - TTGAATTTGAGAGTTGGATGGGACCAAA TCTA - - - CTGCAGACTTGCAGATTAAGG - - - - CAAGATTT	127
<i>Bdistachyon</i>	GGGAG - CTGAATGTGAGATTTGGATGGAA CCAAA TCTT - - - - CAAGCTGC - - - - ATTGGCA - - - - CAAGATTT	117
<i>Pvirgatum</i>	TGGAG - CTGAAGGTGAGCGTTGGATGGAA CCAAA TCTG - - - - CAAGCTAT - - - - GCA - - - - CAAGATTT	111
<i>Acoerulea</i>	- -	131
<i>Sitalica</i>	AACCAA - - - - TOGATCACCAGATTCTTCTGCTGAATCGATGAG - - - - CAAA CAT - - - - GATCGCTG - - - - ATTTGCTT	119
<i>Sviridis</i>	AACCAA - - - - TOGATCACCAGATTCTTCTGCTGAATCGATGAG - - - - CAAA CAT - - - - GATCGCTG - - - - ATTTGCTT	119
<i>Zmays</i>	AACCGG - CTGGGATCGGATTCAGC -	112
<i>Acomosus</i>	TGAGCA - CTGAATGTGAGGATTTGGATGGAA CCAAA CCGC - - - - TCTCCATTTAATGGTTTACA - - - - GAGGCTT	119
<i>Mdomestica</i>	TAAAA G - - - - CGTATGTAGAAATGGAGGGACTAAA CAAA TCAAATACACGGGGAAATCTTA - - - - CTTTCTT	132
<i>Fvesca</i>	TAGAGG - TOGATGTGAGAAATGGAGGGACAAA CA -	120
<i>Ppersica</i>	TAAAG - - - - TOGATATGAGTGTGGAGGGTATAAA CA -	127
<i>Lusitatissimum</i>	TGGCAGAGTCAGTATGAGTGTGGAGGAAA CCAAA CA -	133
<i>Clemantina</i>	CGGAGG - - - - TG - - - - AGAATTTGGAGGAAA CCAAA TAA -	125
<i>Csinesis</i>	TGAAGT - - - - TGTTCATCATCGGTGGTGCATATGATT - - - - TTAAGTGTTCATCATCGGTGCT - - - - CTCTATTT	135
<i>Trichocarpa</i>	TGAAA G -	122
<i>Mesculenta</i>	CACATATCTTGAAA GTGAGATTTGGAGGAACTCAAAA CTTT - - - - TTTGATA -	138
<i>Spurpurea</i>	TACAAC - - - - AAGTAAACATACAAGTTGCTCATCTTTGAGTGCAGGCA -	129
<i>Vinifera</i>	AATAAG - CAGTACATGAGAAATGGAGGAAATTAATCCCA -	135
<i>Dcarota</i>	TAATGT - - - - TGAACGTGAGGATTTGGATGAAA CTA AAA CA -	151
	0.....190.....200.....210.....220.....230.....240.....250.....26	



<i>Phalli</i>	GGTTTCTCCAAATATCTCA GTTCAGCTG - - - - - AGCTGATCAGATGGATGCGTA - GTGCAAGTAGTGCAGAT - GTAC	211
<i>Oropetium</i>	GGTTTCTCCAAATATCTCA GTTCACATGTT CAGA - AAA TGGTGGTTCAGTT CACCCTT CAGGTAGTGTAGCTAGCAC	220
<i>Osativa</i>	GGTTTCTCCAAATATCTCA GTTCAGTTGTC - - - - AGACAGTGAAT - - - - AATG - - - - GTGCAATTAGTG - AGCT - - - -	189
<i>Bdistachyon</i>	GGTTTCTCCAAATATCTCA CTTCAACTGCCG - - - - AGATGAGCCCAACACATCCTCGGTCAAGCAATC - AGTGACCCT	193
<i>Pvirgatum</i>	GGTTTCTCCAAATGTCCTA TTTCAACTGTCCAA - - - - ATGCAACATTGA - GGOGTTTT CAGGGTATTAATCATTCAATGAT	189
<i>Acoerulea</i>	GGTTTCTCCAAATATCTCA CTTCAACAA TTTTC - - - - AACTACAGTATATATTTTCAA TTAATAATCCATTC - - - -	202
<i>Sitalica</i>	GI TTTCTCCAAATATCTCA CTTTCAGTGCATC - - - - GCCTGGTACTACGCATTACGAGAACAGATATGCTAGGG - - - -	190
<i>Sviridis</i>	GI TTTCTCCAAATATCTCA CTTTCAGTGCATC - - - - GCCTGGTACTACGCATTACGAGAACAGATATGCTAGGG - - - -	190
<i>Zmays</i>	GI TTTCTCCAAATATCTCA CTTTCAGTGCATA - - - - GTCTGATGAAGATGTACACTACCAACA -	171
<i>Acomosus</i>	GGTTTCTCCAAATATCTCA CTTCACTTGCITTT - - - - GGCTATTGGCTATTACTGTTGTTATTAATTTCTTC - - - - - - - - - - - -	186
<i>Mdomestica</i>	GGTTTCTCCAAATATCTCA TTTCCGGCTTTAAA - - - - AGCCATATTTGAGAA TACGAGAGGGCTAAA CAAA TTAATCTCCC	209
<i>Fvesca</i>	AGTTTCTCCAAATATCTCA TCTCCGACTCTAA - - - - AGTGTAACTTTTATCTATAGC - - - - TTTAAAA GTTGGATGTAAG	193
<i>Ppersica</i>	GGTTTCTCCAAATATCTCA TCTCCGACTCTGA - - - - AGTGTAACTTTTATCTATAGC - - - - TTTAAAA GTTGGATGTAAG	197
<i>Lusitatissimum</i>	GGTTTCTCCAAATATCTCA TCTCCGGC -	198
<i>Clemantina</i>	GGTTTCTCCAAATATCTCA CTTCAAGTTTGTACTC - - - - AGATTCTGTCT - CACCACAGTAA TTAATAGACTTGTCT - - - -	198
<i>Csinesis</i>	GGTTTCTCCAAATATCTCA CTTCAAGTTTGTACTC - - - - AGATTCTGTCT - TACCGTAGTAA TTAATAGACTTGTCT - - - -	208
<i>Trichocarpa</i>	GGTTTCTCCAAATATCTCA CTTTCAATGGCATTAA - - - - GAAA GCAA CAGAGGAA GATCTAGTCTTTGTTGACCATAT - - - -	196
<i>Mesculenta</i>	GGTTTCTCCAAATATCTCA CTTTCAATGGTGTGT - - - - GAAAA TCACTGTAGCATTTGTTTCTGAGAAA GATGAGGT - - - -	210
<i>Spurpurea</i>	AGTTTCTCCAAATATCTCA CTTTCAATGGTGTGTATAGAGTAGTGAAGTAGTAAAA GAACTGTCTTCTTTAGCT	209
<i>Vinifera</i>	AA TTTCTCCAAATATCTCA CTTACTGTTTCACTCTACATGTCAAATTTTCTGGTCT - ATCAGATGAAA TTTGTGTTG	214
<i>Dcarota</i>	AGTTTCTCCAAATATCTCA CTTCAAACCTTACTC - TTTTAGTACAGTAAA TAGAATCTTGCATTAAGCAGCACA - - - -	225
	0.....270.....280.....290.....300.....310.....320.....330.....34	

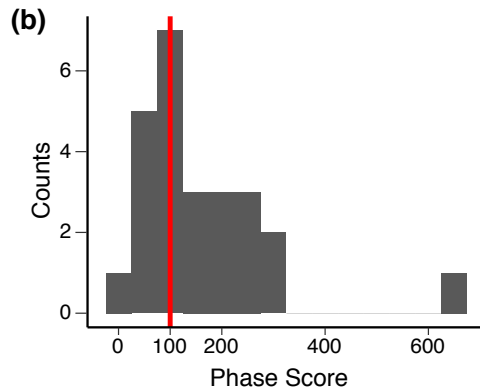


Figure S2. Alignment of MIR2275 homologs. Sequences corresponding to miR2275 with flanking 200 bp islands were extracted from genomes of the above-listed genomes and aligned via ClustalX2. Only the 100th to 340th nucleotide of each sequence (including gaps) are shown. miR2275 and miR2275* in each species are shown.



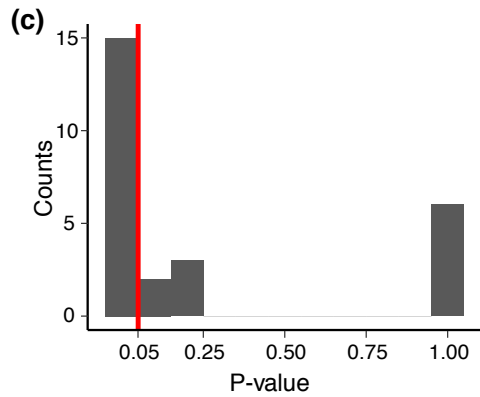
$$S = PR * PN * \ln(1+PARpm)$$

S is the Phase Score.
 PR is the Phase Ratio.
 PN is the number of distinct, "in-phase" reads.
 PARpm is the accumulation of "in-phase" reads (in Reads Per Million).



$$S = \ln \left[\left(1 + C * \frac{\sum_{i=1}^C P_i}{\sum U} \right)^{n-2} \right], n > 4$$

S is the Phase Score.
 C is the number of 21 nt or 24 nt Phase Cycles that fits into the PHAS locus.
 P is the number of "in-phase" reads.
 U is the number of "out-of-phase" reads.
 n is the number of phase cycles with at least one read.



$$P\text{-val} (X=k) = \sum_{X=k}^m \frac{\binom{(H-1)m}{n-k} \binom{m}{k}}{\binom{Hm}{n}}$$

P-val= p-value with null hypothesis that a locus is a true PHAS.
 k is the number of unique 21 nt or 24 nt "in phase" reads.
 m is the number of phase cycles.
 H is 21 or 24.
 n is the number of unique 21 nt or 24 nt reads in a particular locus.

Figure S3. Determination of phase score cutoffs using three different algorithms
 (a) Small RNA accumulation at 27 known 21 nt PHAS loci (Table S1) was analyzed using the PHAS-Test algorithm from Guo et al. (2015), which is used by ShortStack. Variables and formula are shown. Red line represents the cut-off used in this study to determine if a locus was phased or not; scores above the red line were considered 'phased'.
 (b) Same as in panel a except for the PHAS-Test algorithm from Dotto et al. (2014).
 (c) Same as in panel a except for the PHAS-Test algorithm from Zheng et al. (2014); scores below the red-line were considered 'phased'.

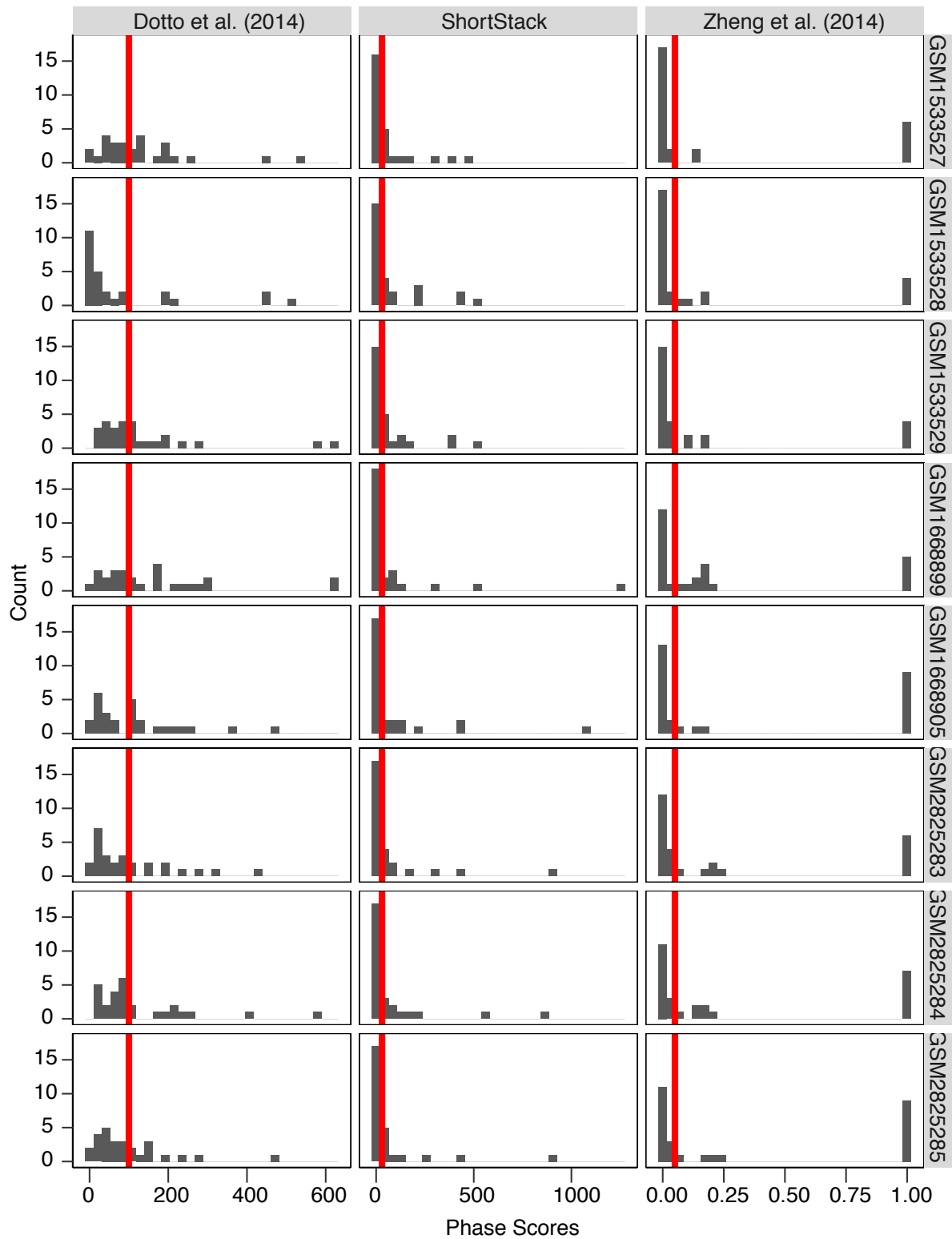


Figure S4. Phase scores of 27 previously known *A. thaliana* phased siRNA loci from the indicated algorithms. Cutoff values for called 'phasing' in our study are shown in red.

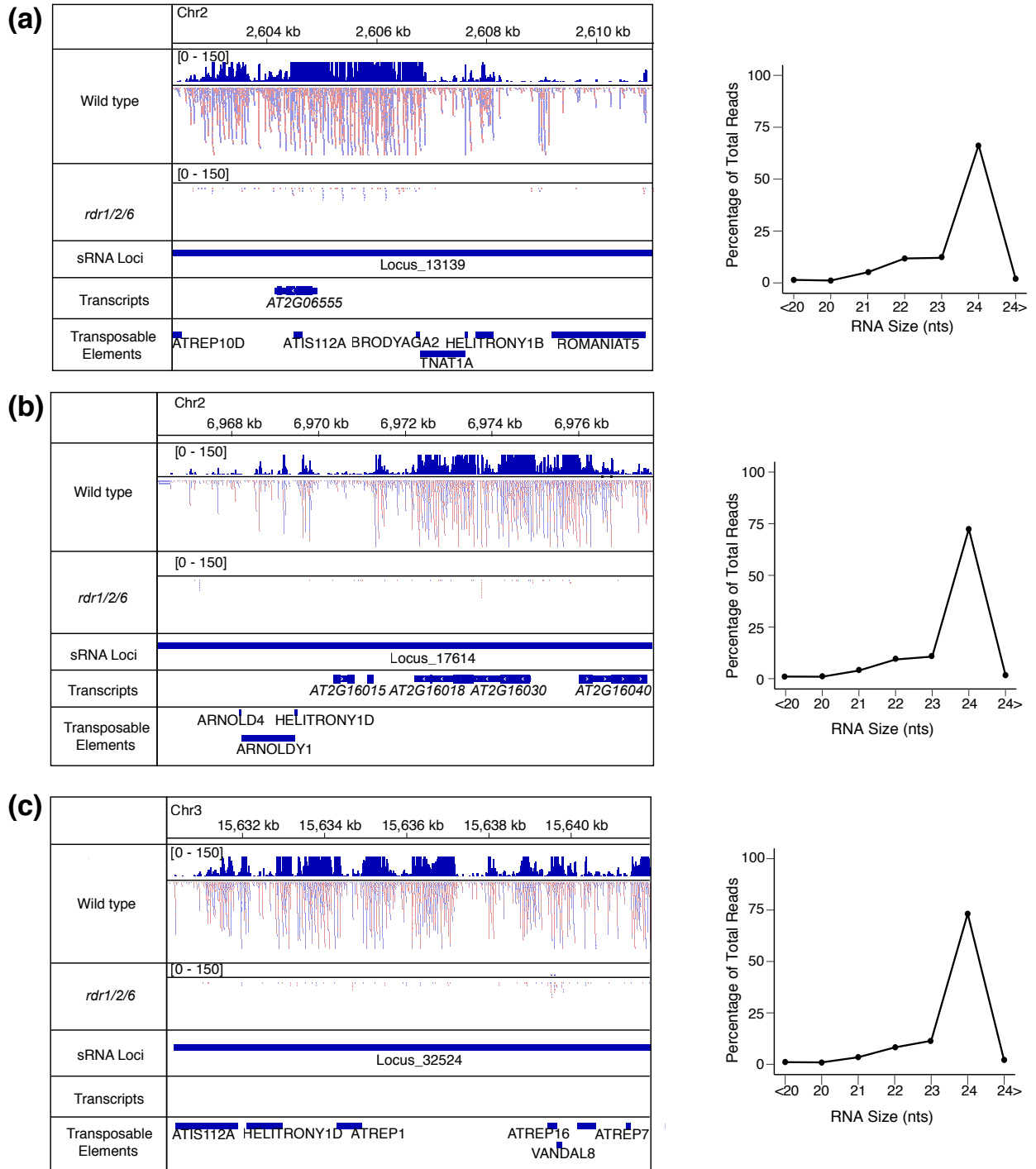


Figure S5. Genome browser snapshots of the three *Arabidopsis thaliana* PHAS-Test passing loci.

(a) Alignments and read size distribution of Locus_13139. Red reads represent positive-strand mapped genes, while blue reads are those that mapped to the negative strand. Numbers in the brackets are the range of coverage shown in Reads per Million.

(b) Same as a, except for Locus_17614.

(c) Same as a, except for Locus_32524.

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Locus_32524

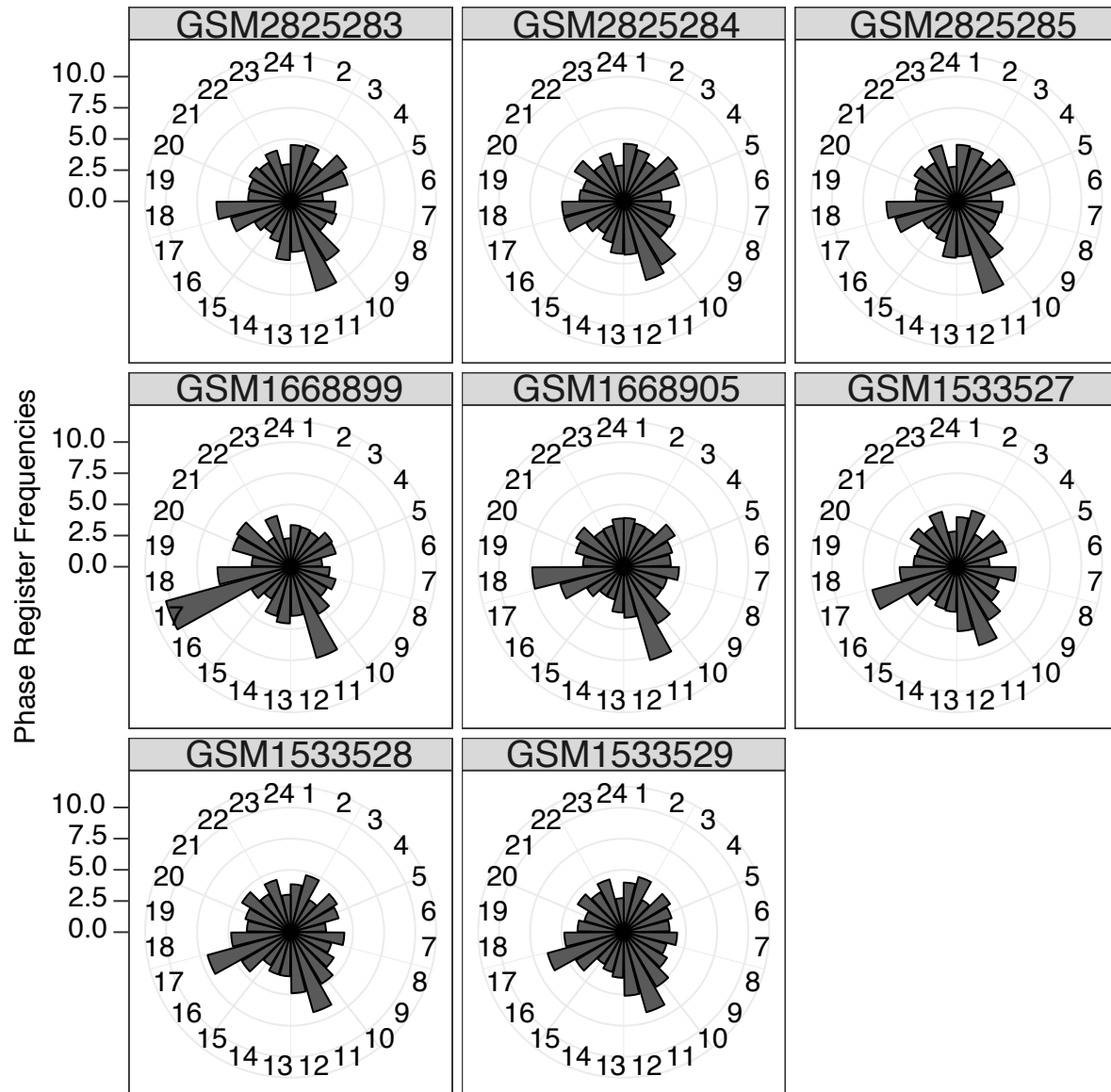


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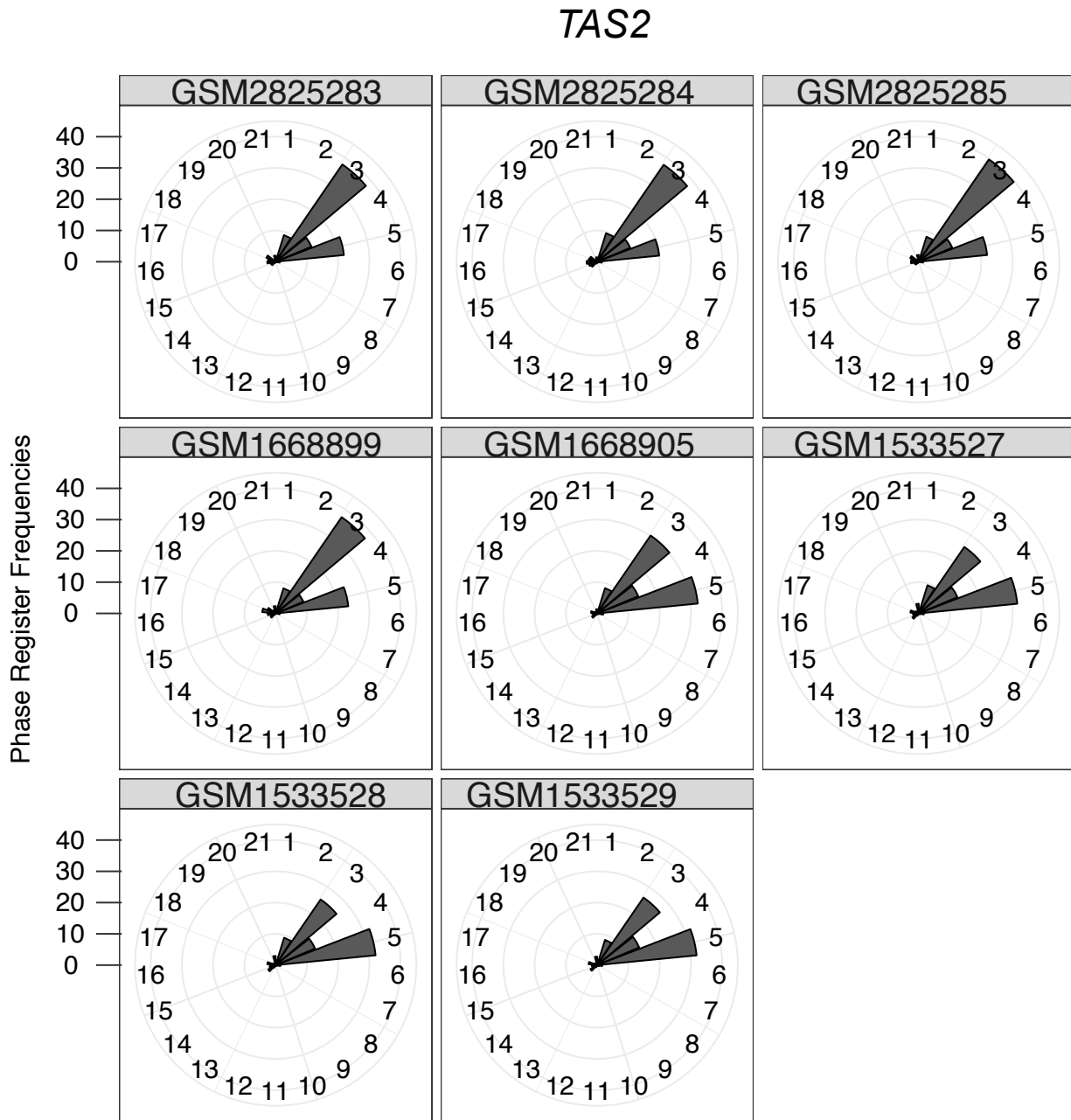


Figure S6. The three PHAS-Test passing loci have inconsistent phase register frequencies. Frequencies of phase registers were calculated in eight publicly available wild-type inflorescence libraries from *A. thaliana* (the accession numbers are listed in the grey boxes). TAS2 is shown for comparison. Phase register frequencies are calculated via the following formula: (number of reads “in phase”/ total number of reads at locus)*100.

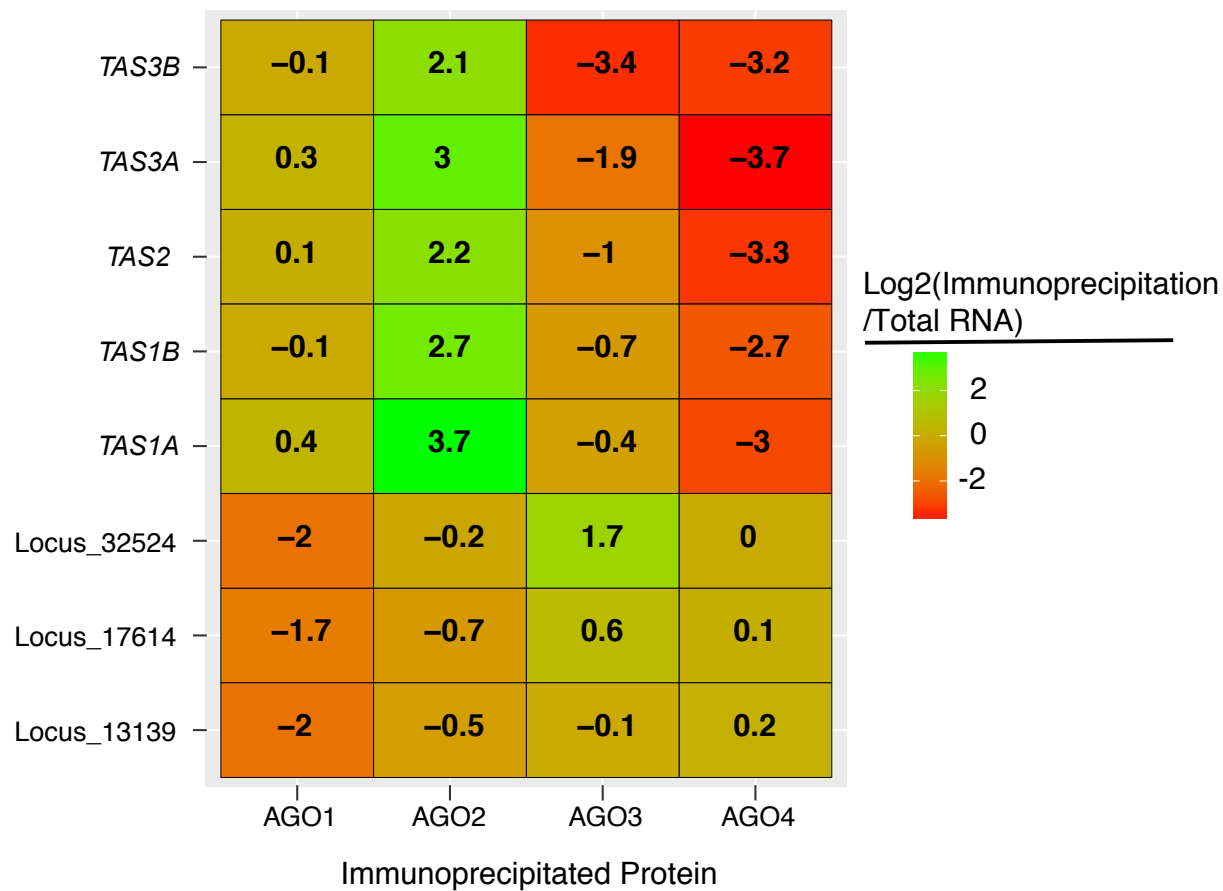


Figure S7. The three putative 24 nt PHAS loci show AGO-loading profiles that are distinct from TAS loci.

Small RNAs from immunoprecipitation protein were aligned to the *A. thaliana* (TAIR10) genome. Numbers indicate the ratio of sRNA accumulation between immunoprecipitated and total libraries (in RPMs).

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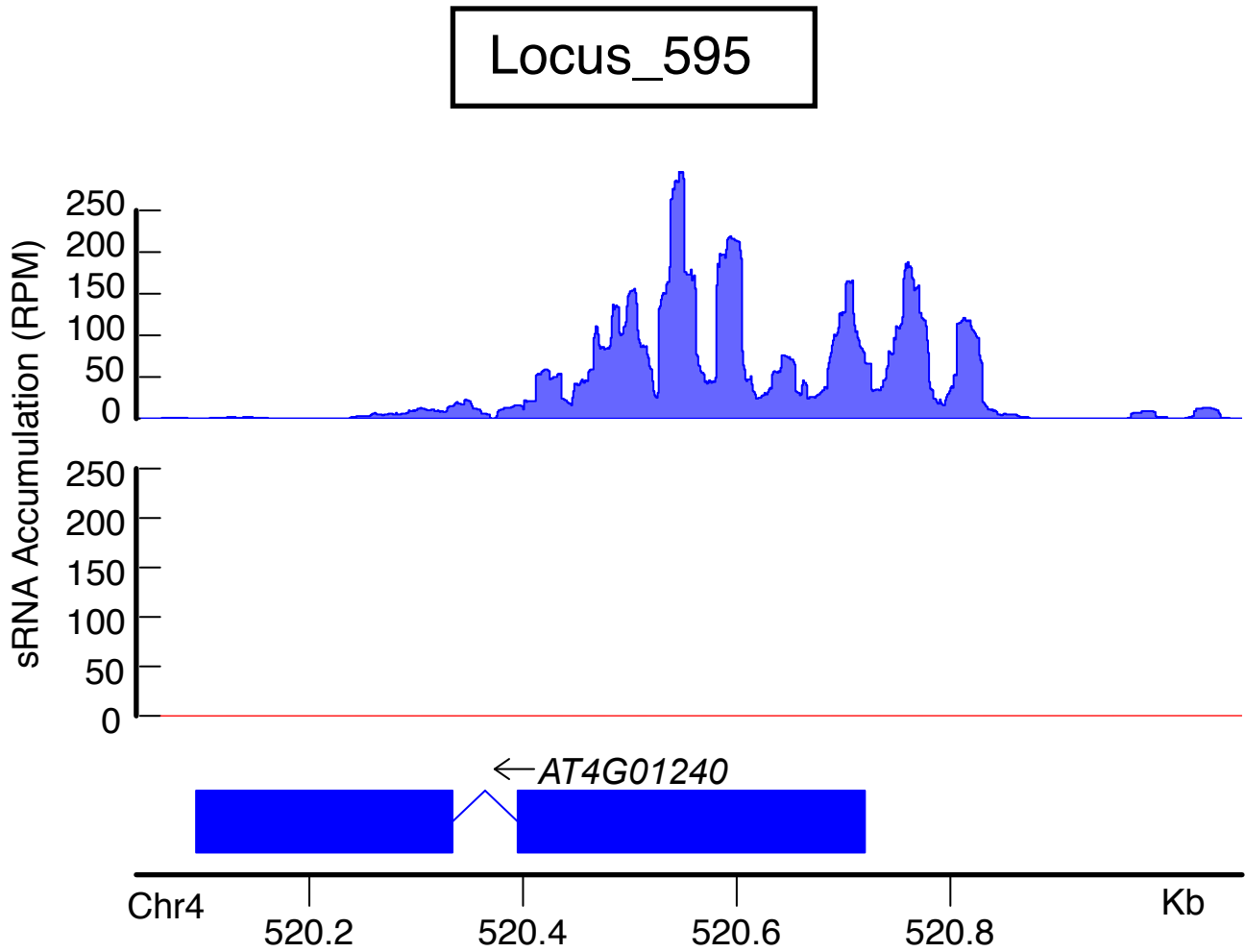


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Locus_12303

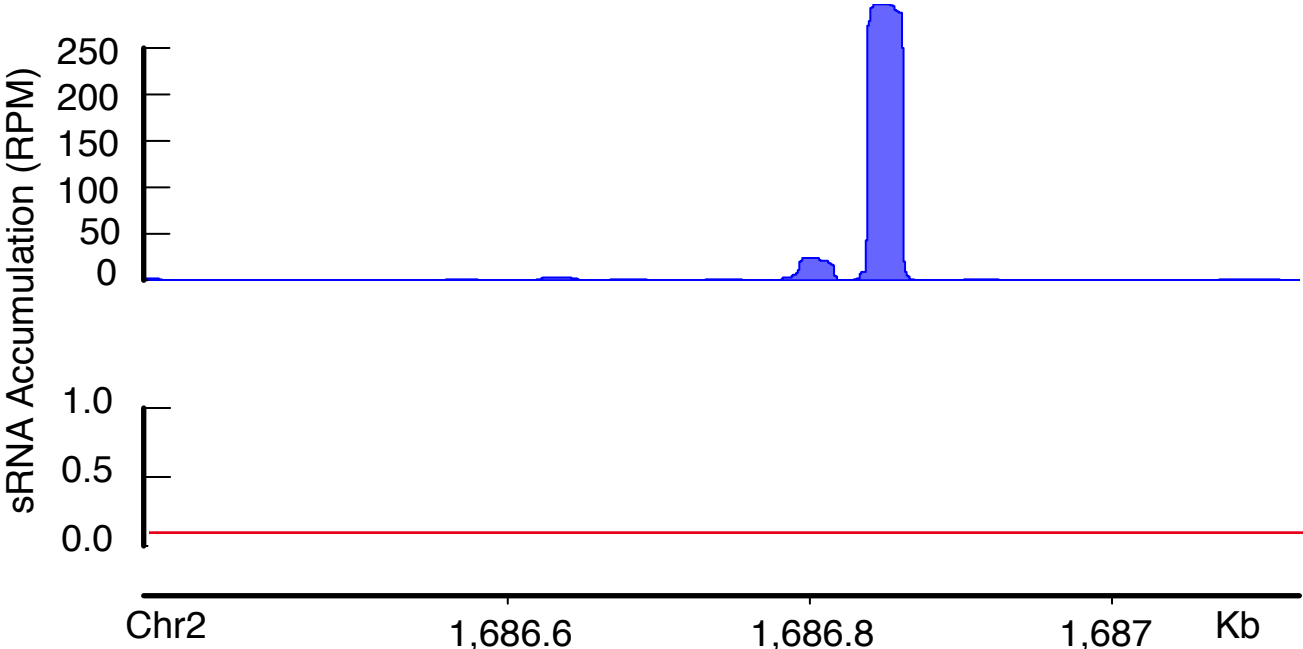


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Locus_17665

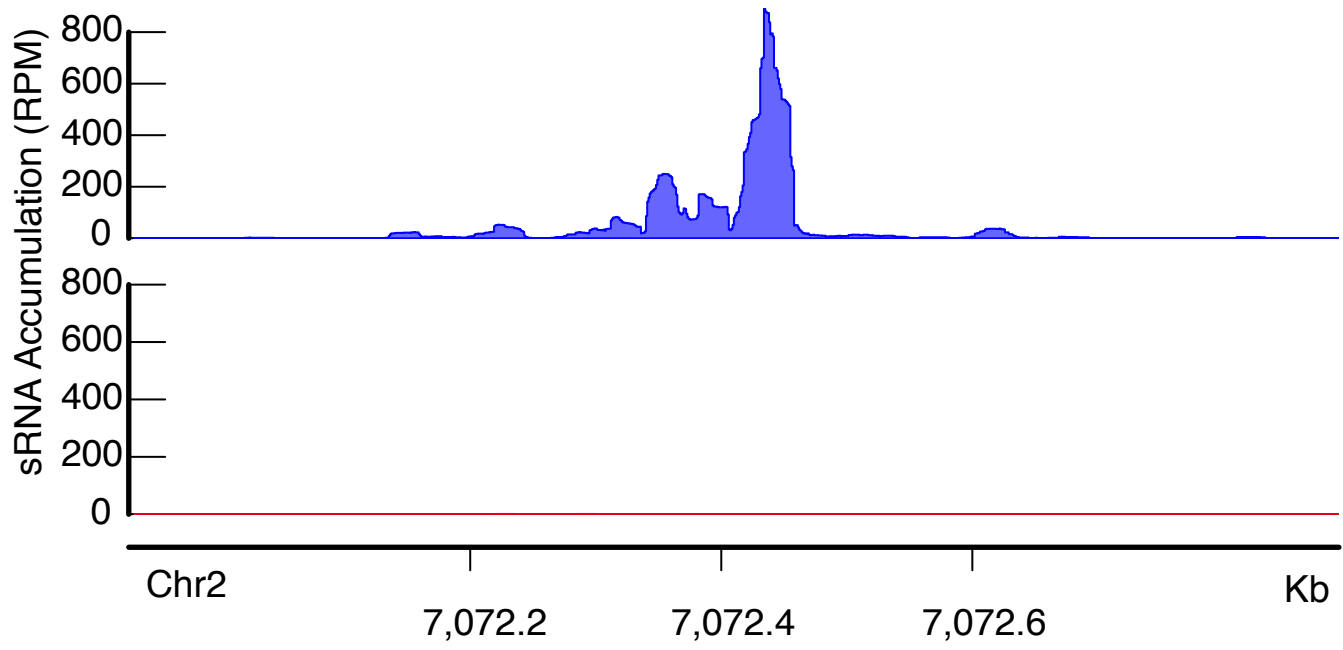


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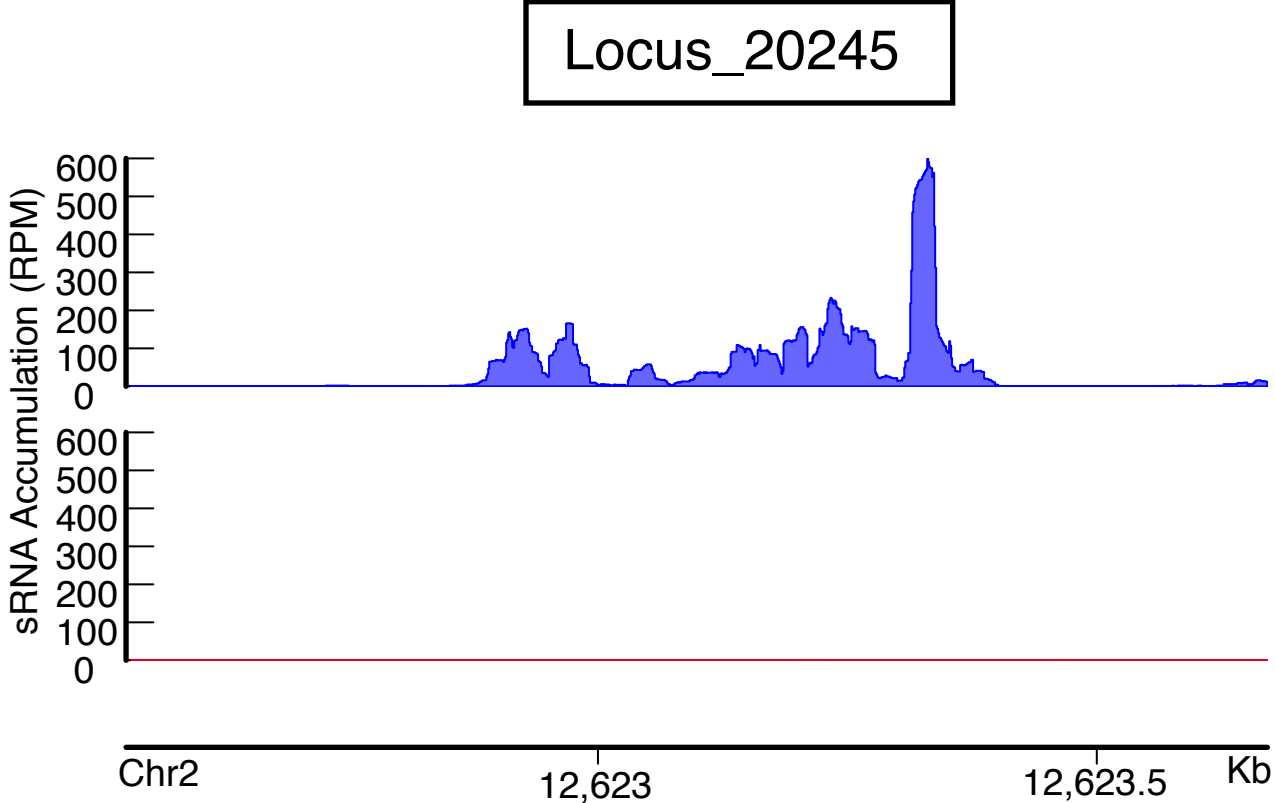


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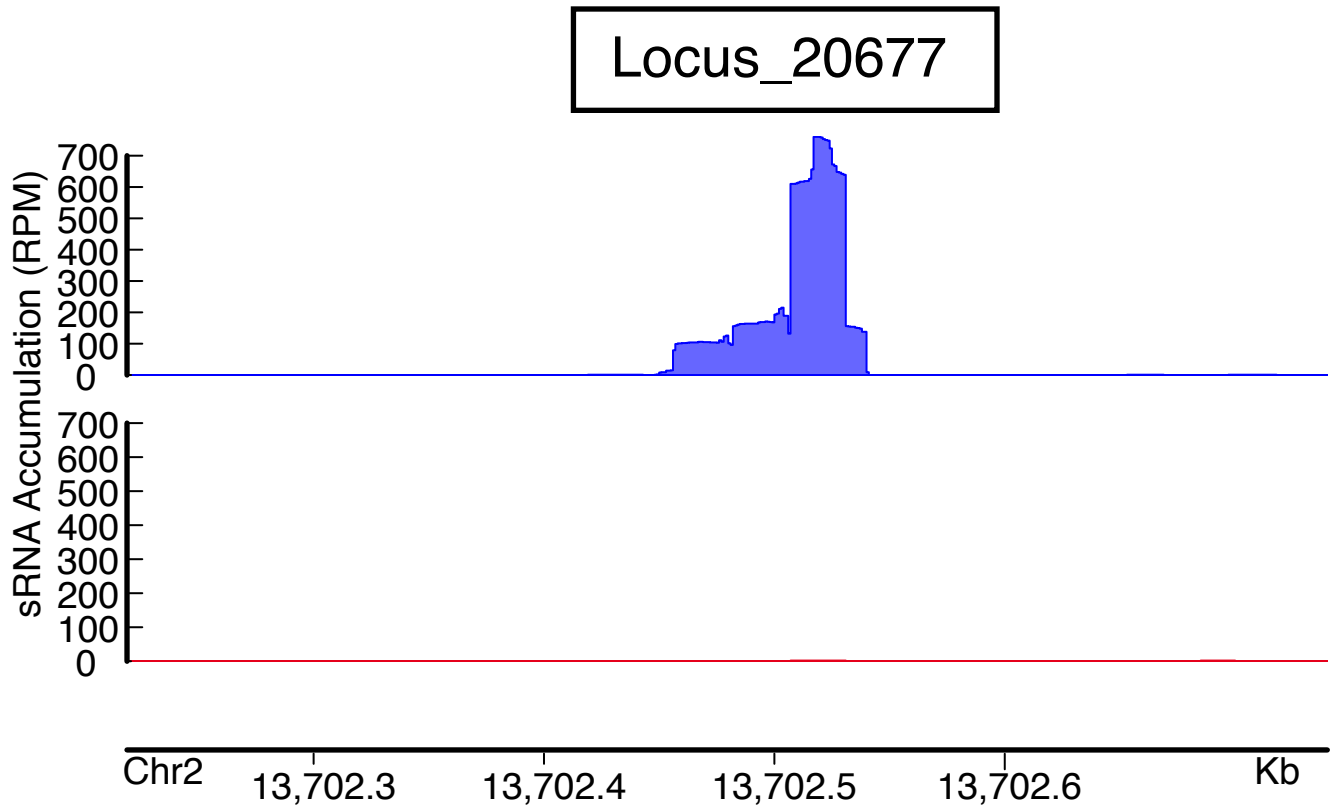


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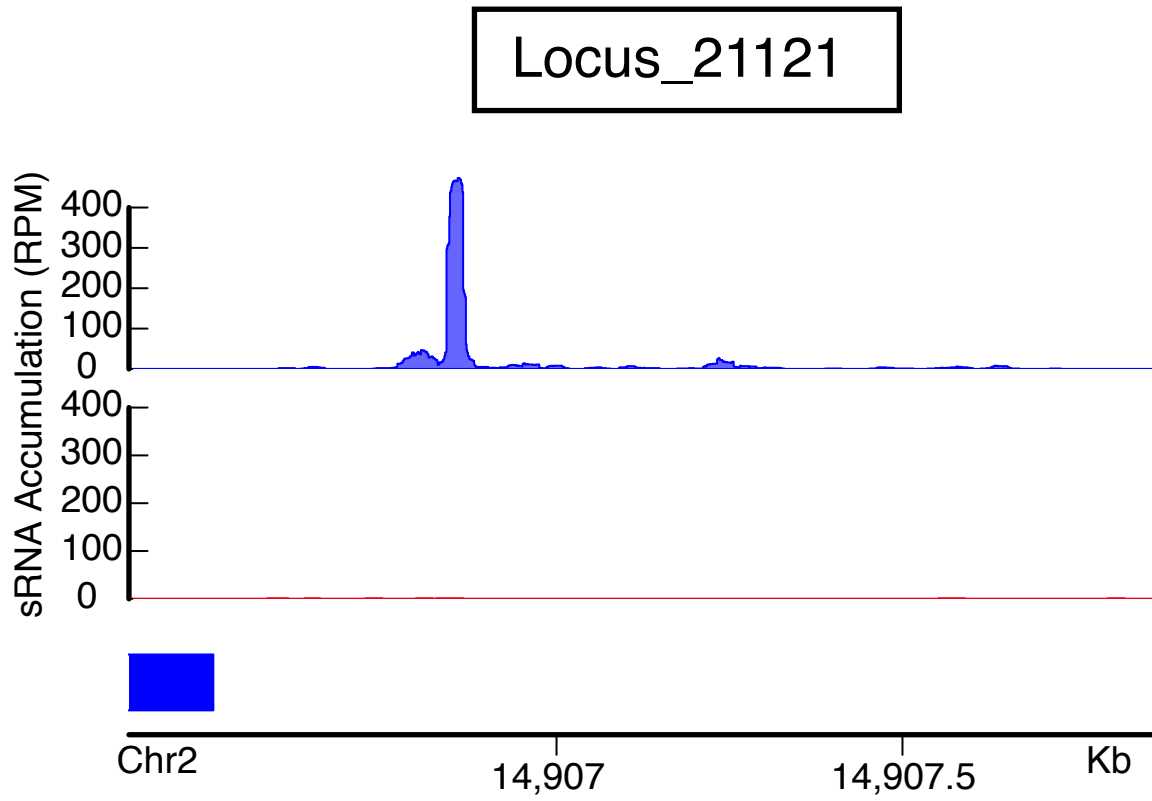


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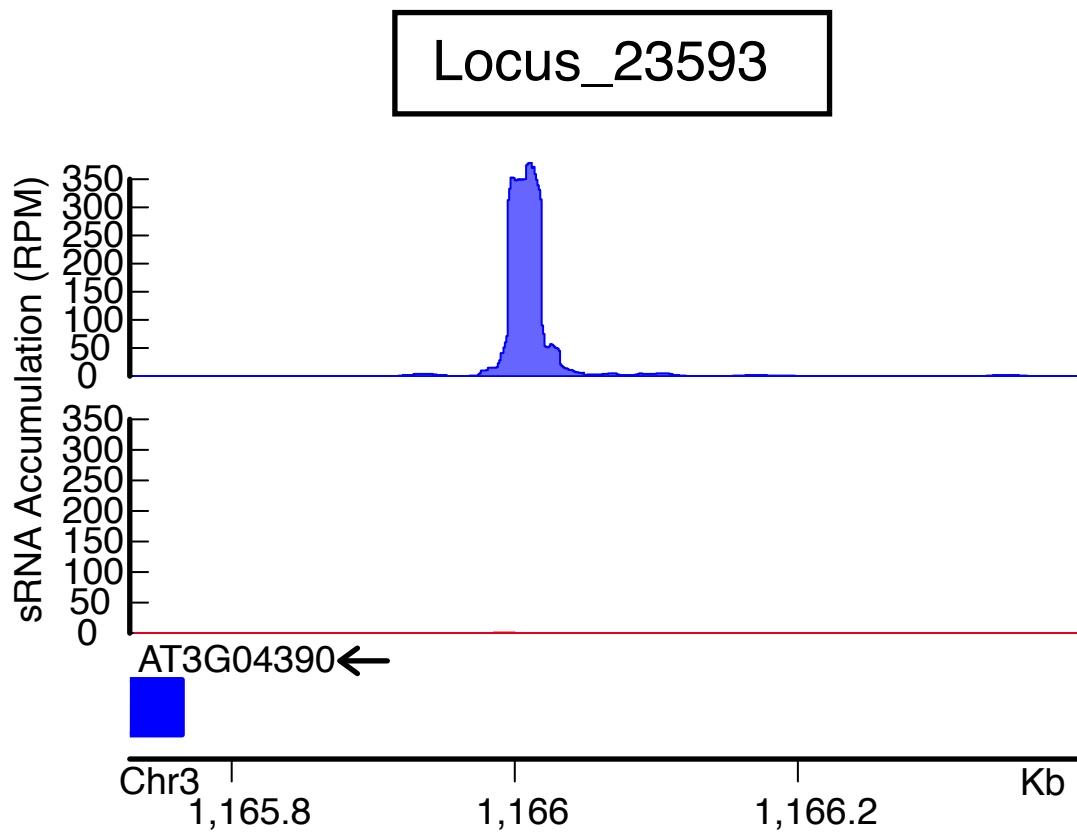


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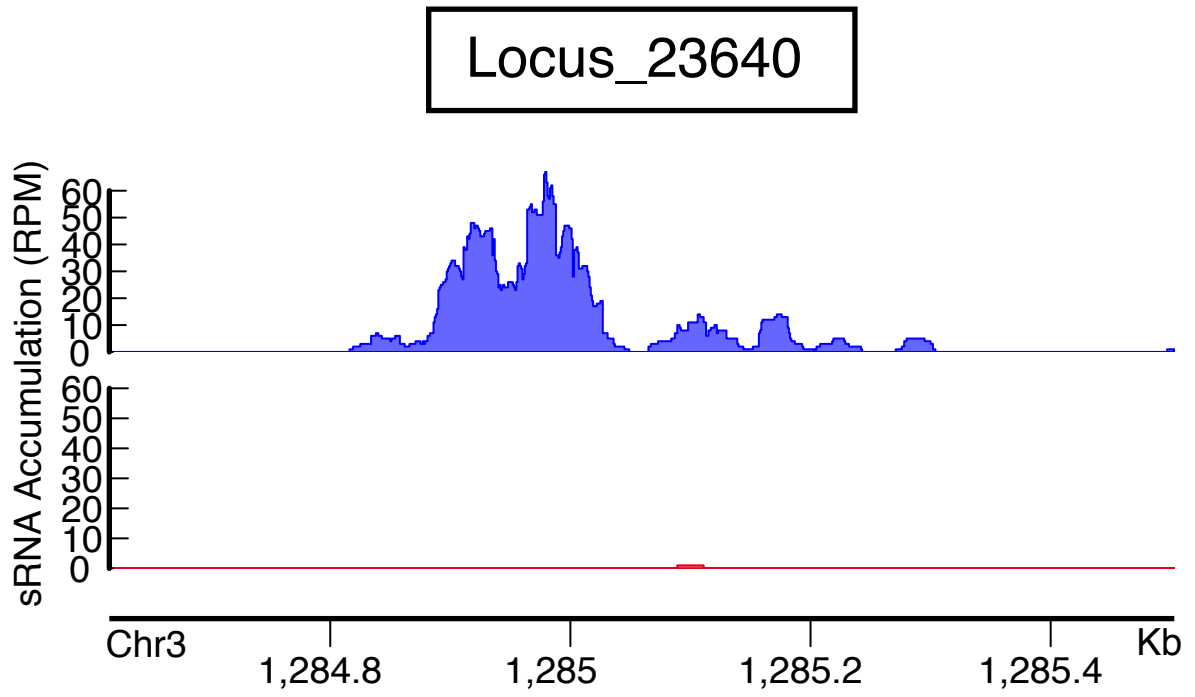


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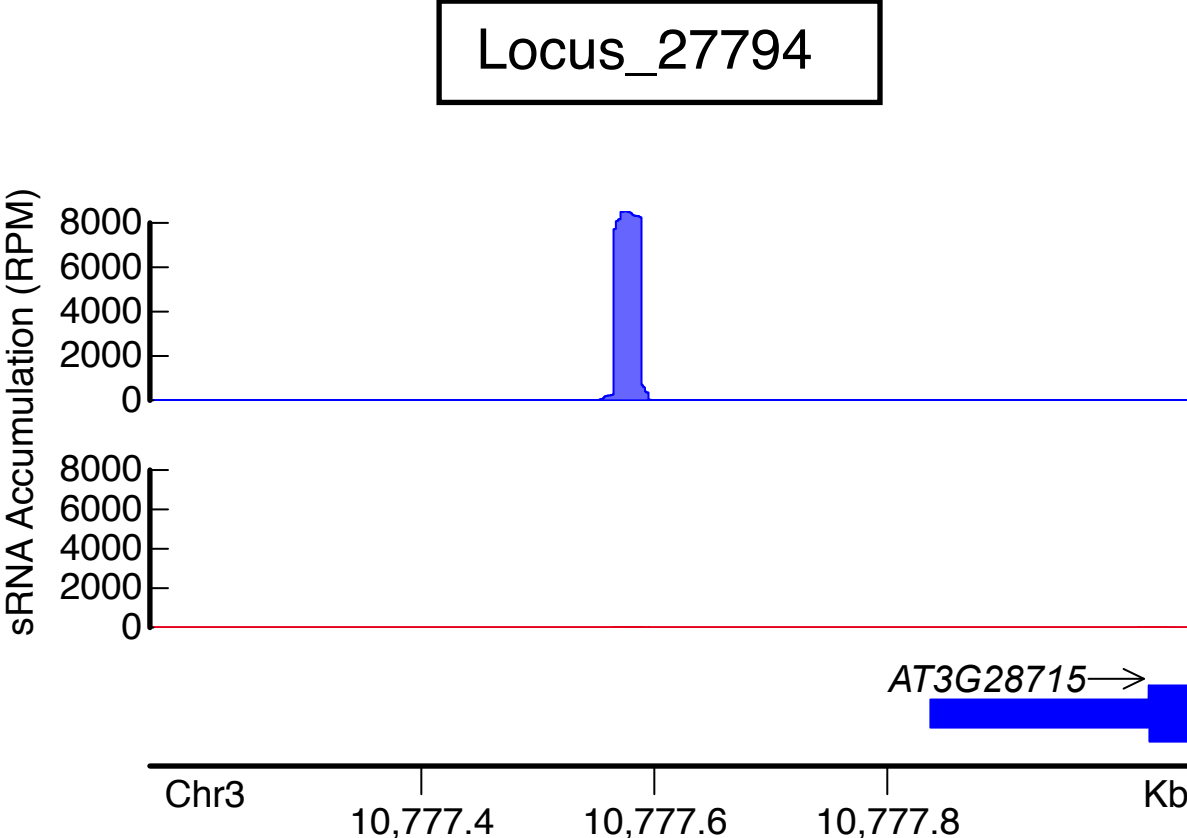


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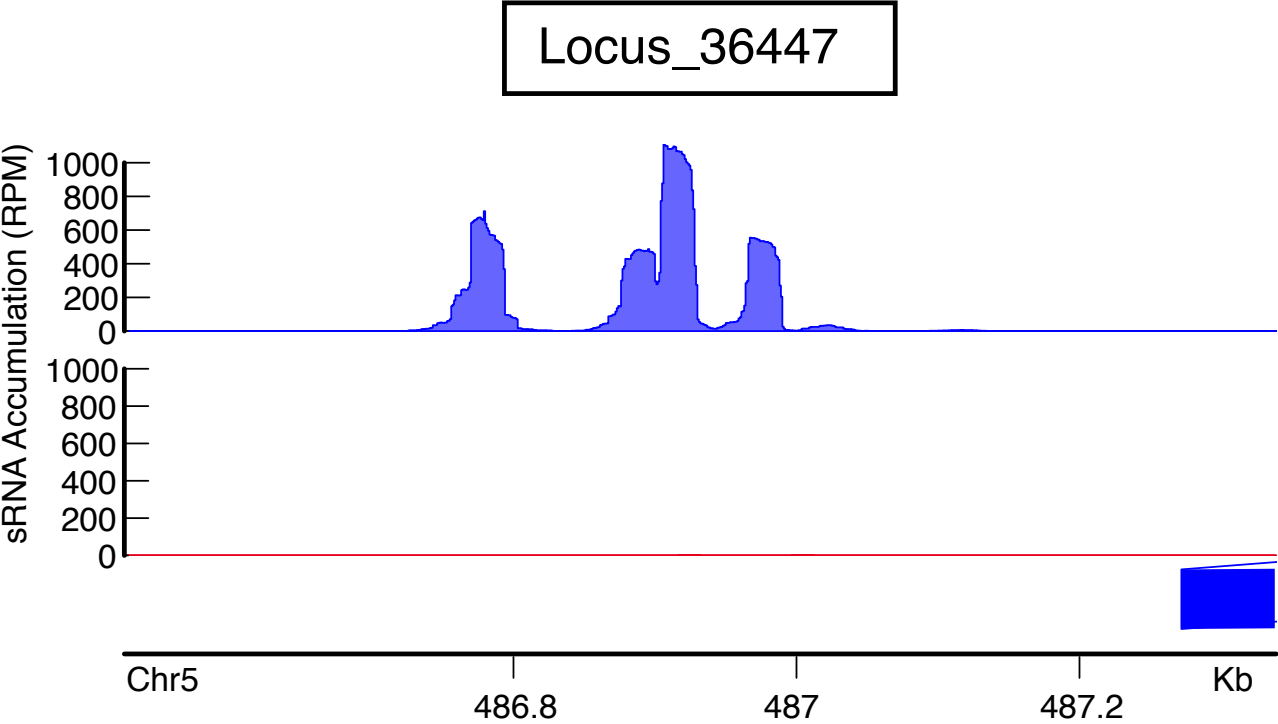
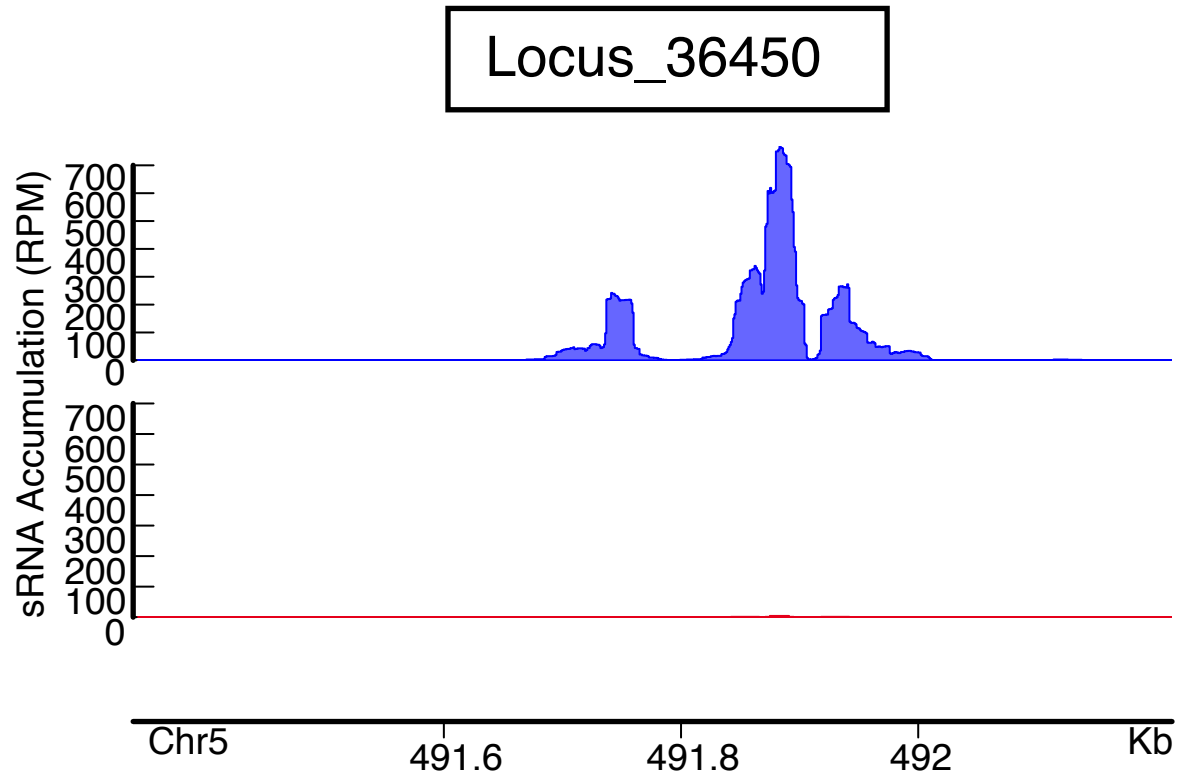


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Locus_45036

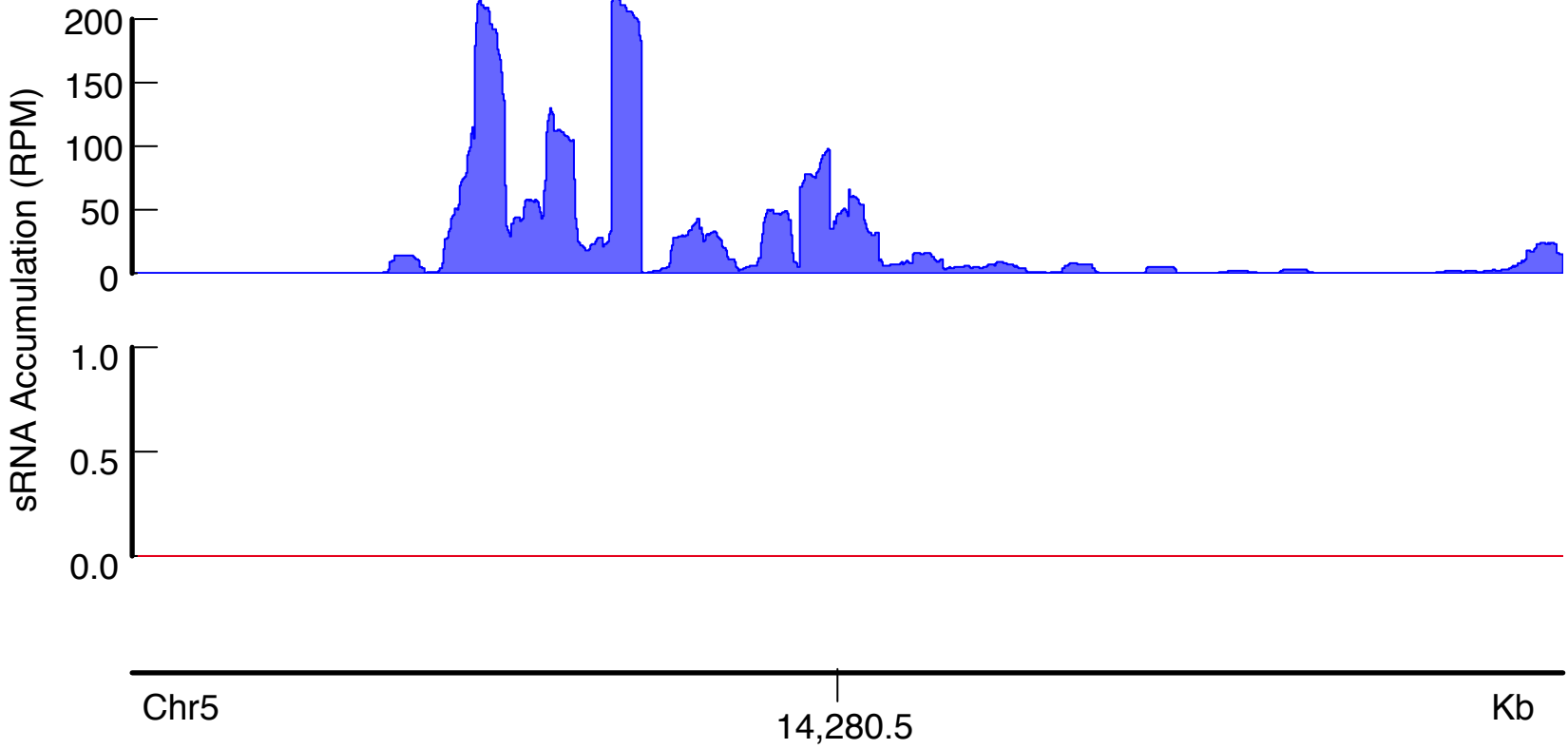


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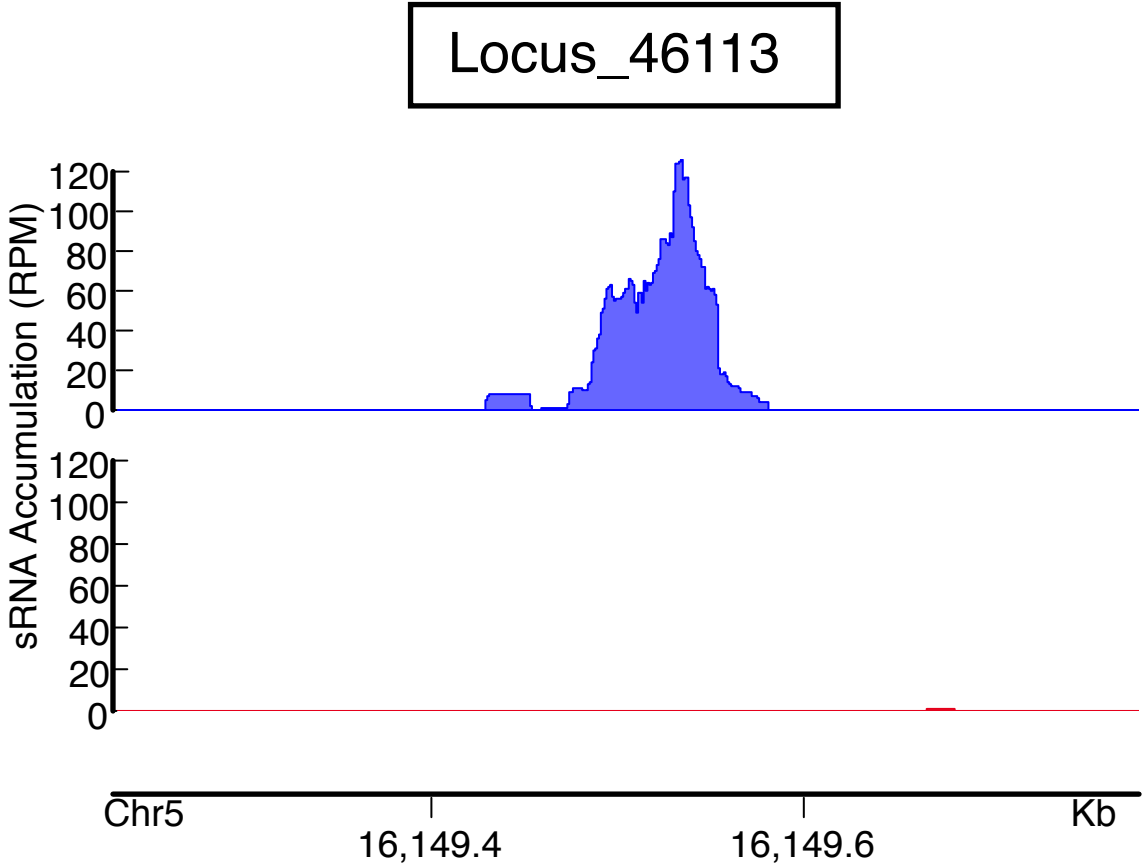


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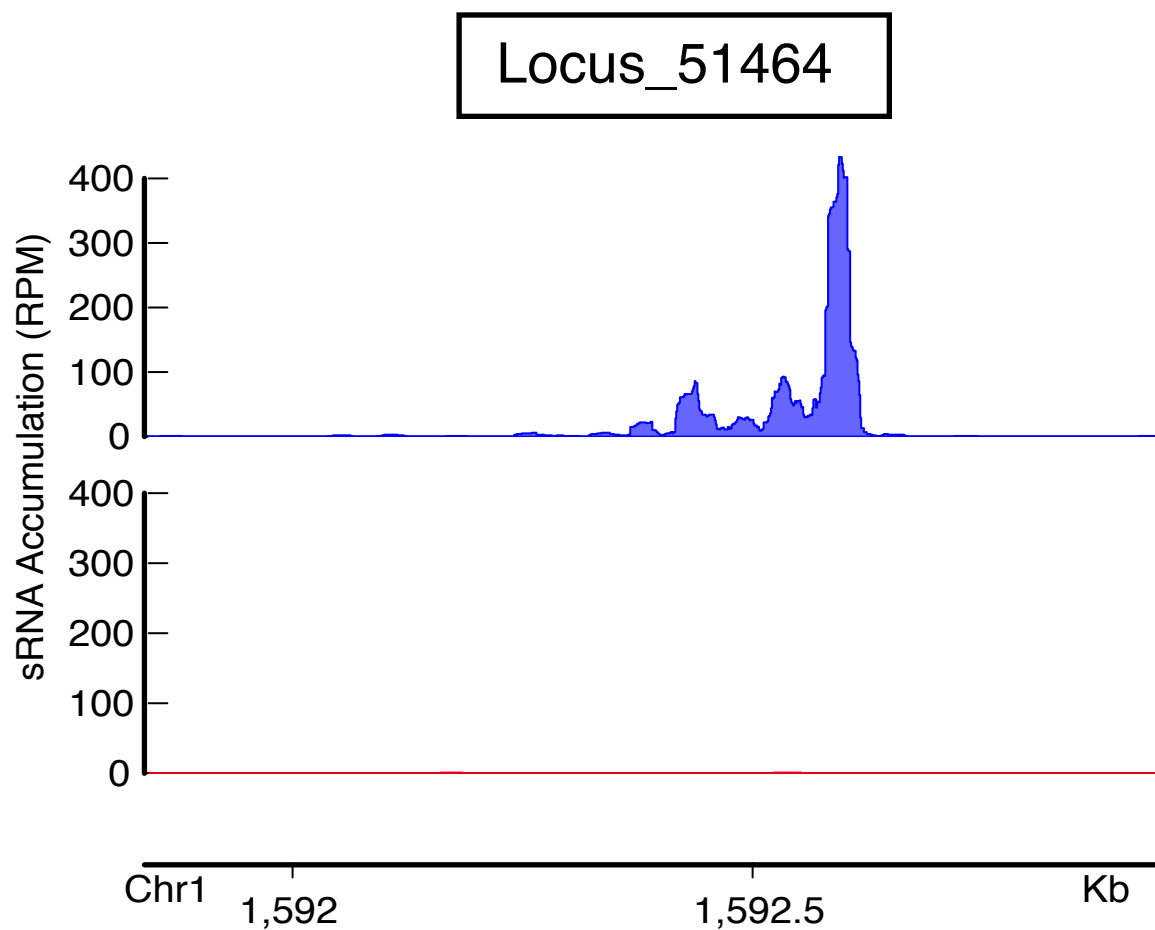
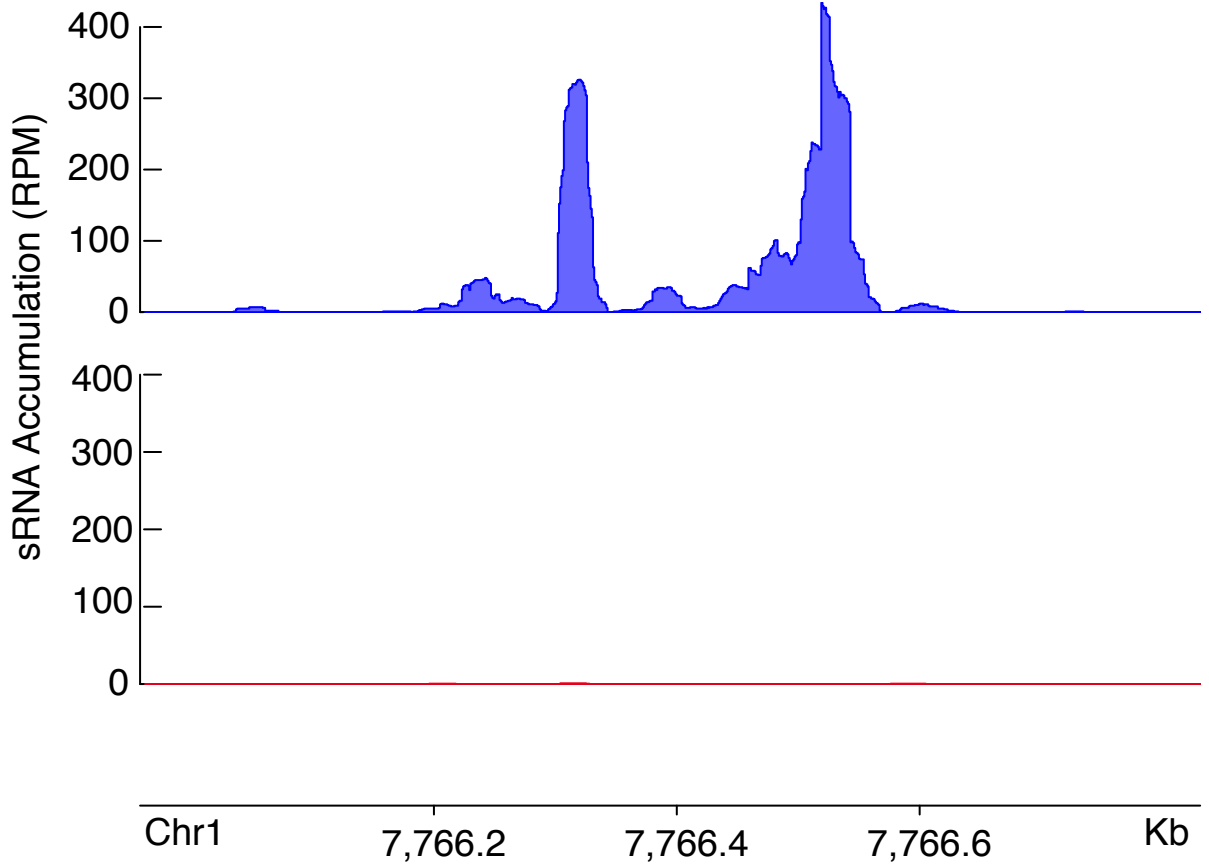


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Locus_54003



Locus_59879

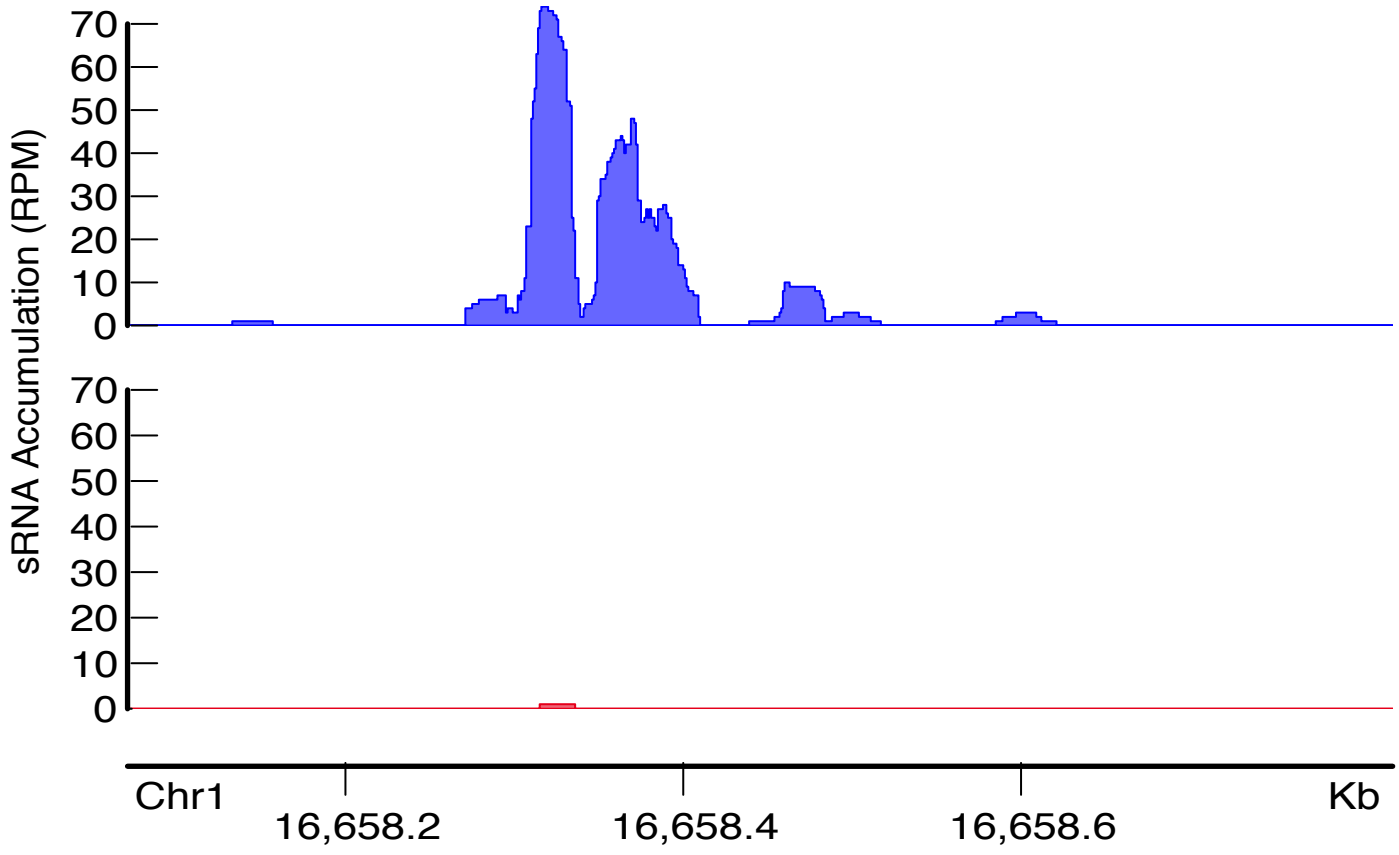


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Locus_62375

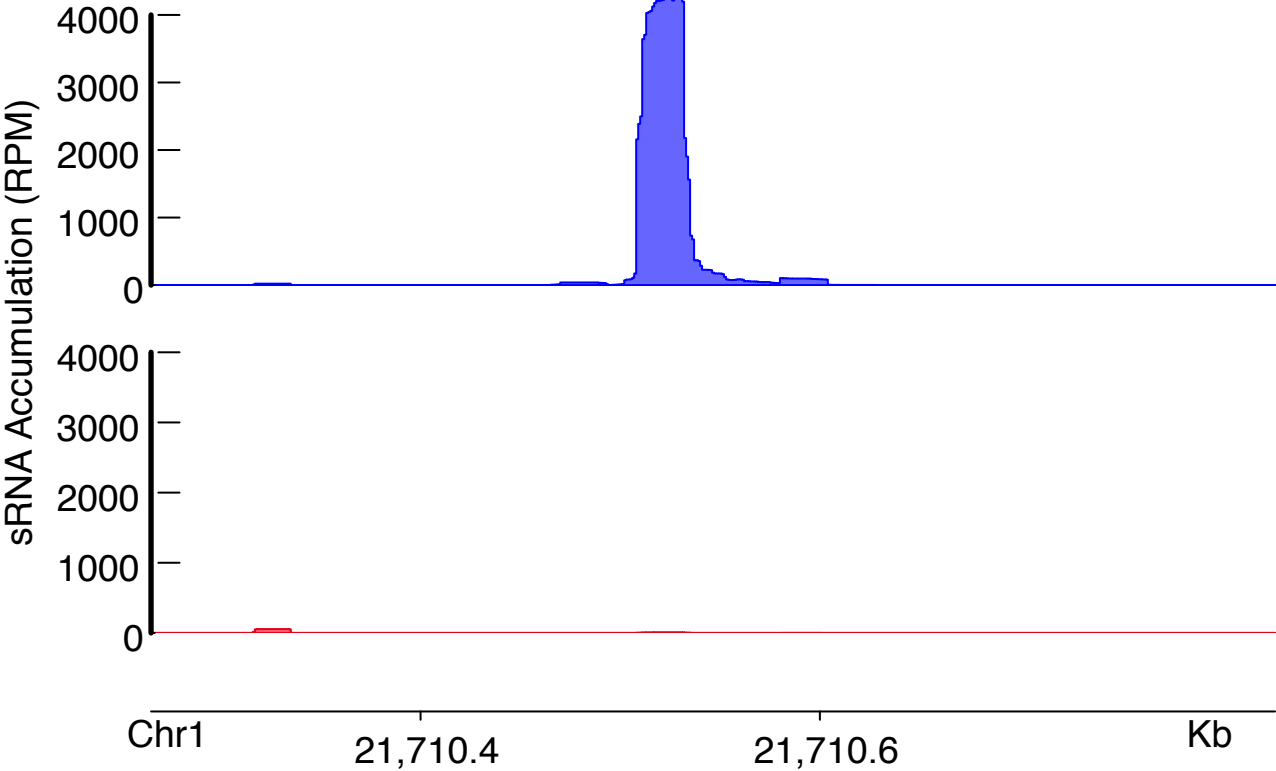
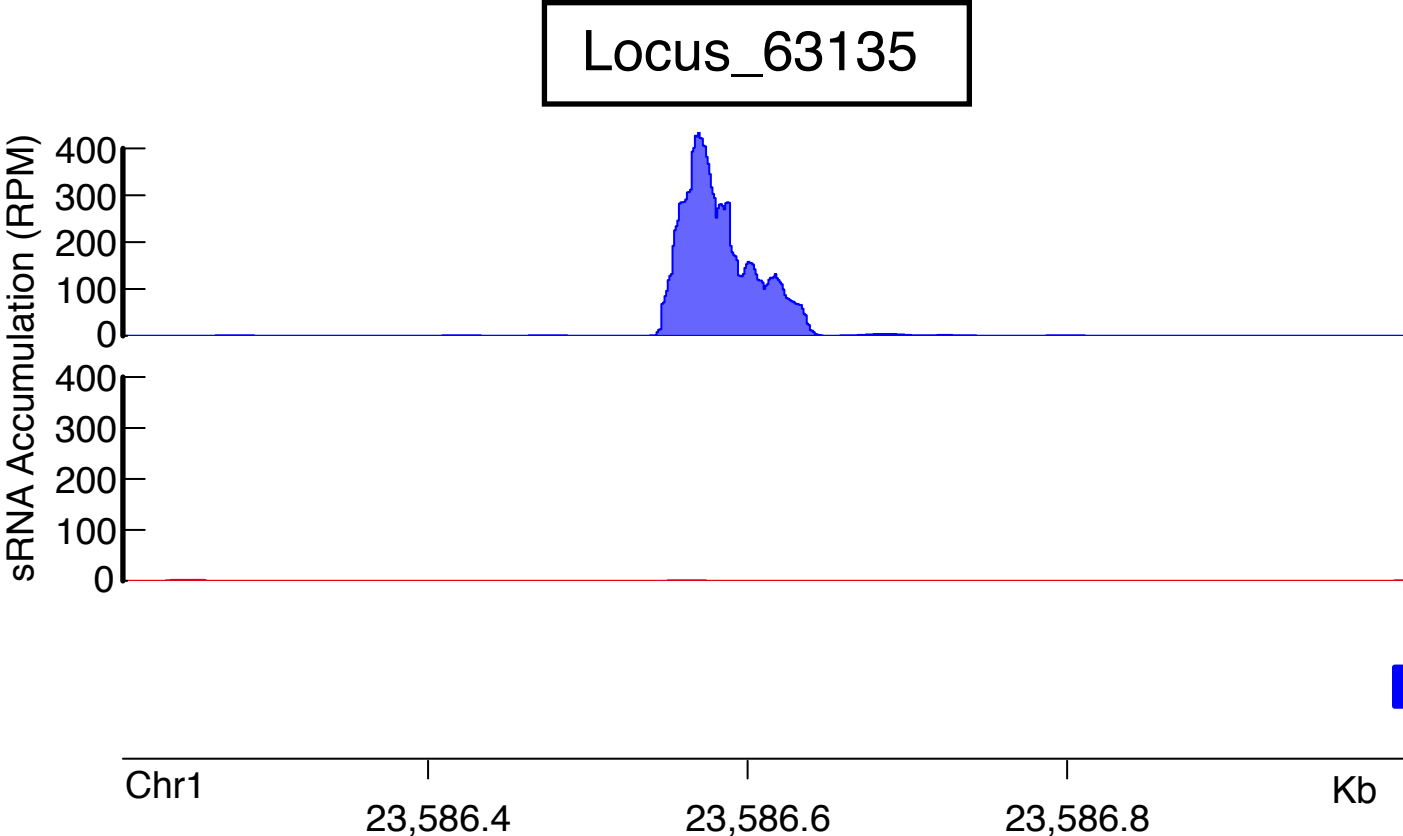


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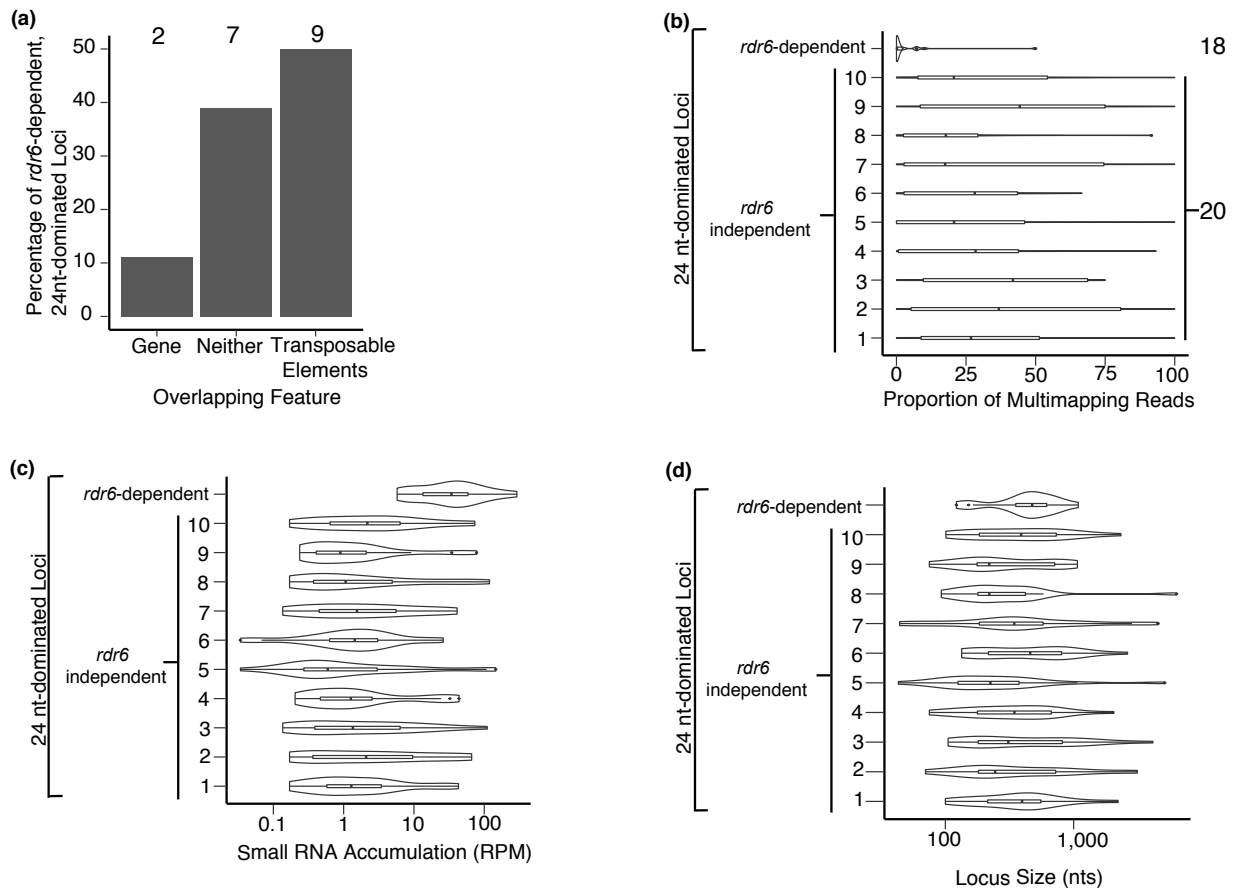


Figure S9. *rdr6*-dependent, 24 nt-dominated loci' characteristics compared to other 24nt-dominated loci.

(a) The overlap between *rdr6*-dependent, 24 nt-dominated loci with genes and transposons was calculated as in Figure 3a. Numbers at the top indicate the count in each category.

(b) The proportion of multi-mapping reads produced at *rdr6*-dependent, 24 nt-dominated loci compared to other 24 nt-dominated loci. Numbers at the top indicate the count in each category.

(c) Same as panel b except showing small RNA accumulation (in RPM). Amount in each category is the same as panel b.

(d) Same as panel b except showing length (in nts). Amount in each category is the same as panel b.

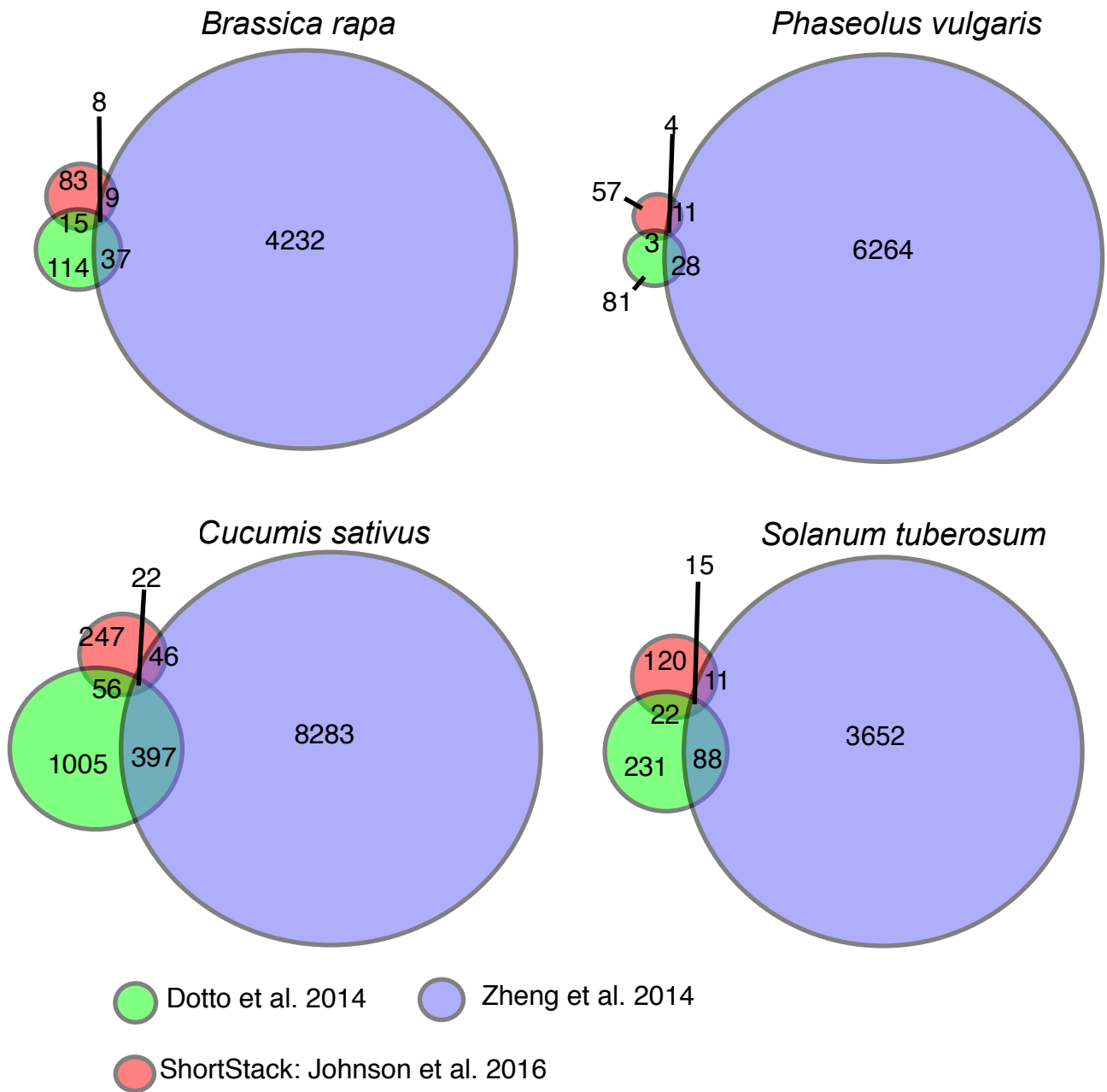


Figure S10. Several 24 nt-dominated small RNA loci pass PHAS-detection algorithms in four other eudicots.

Venn diagram shows numbers of 24 nt-dominated loci that were called 'phased' by the indicated algorithms. Species examined is shown above the graphs.

Table S1. List of 25 known 21 nt *PHAS* loci in *A. thaliana*.

Chr.	Start	Stop	Locus Name	Source
Chr2	11721539	11722468	<i>TAS1a</i>	(Vazquez et al., 2004)
Chr1	18549204	18550042	<i>TAS1b</i>	(Allen et al., 2005)
Chr2	16537288	16538277	<i>TAS1c</i>	(Allen et al., 2005)
Chr2	16539384	16540417	<i>TAS2</i>	(Allen et al., 2005)
Chr3	5861491	5862437	<i>TAS3a</i>	(Montgomery et al., 2008)
Chr5	20134200	20134786	<i>TAS3b</i>	(Howell et al., 2007)
Chr5	23394005	23394500	<i>TAS3c</i>	(Howell et al., 2007)
Chr3	9415004	9422587	<i>TAS4</i>	(Rajagopalan et al., 2006)
Chr1	23299057	23300958	<i>PPR-At1g62910</i>	(Ronemus et al., 2006)
Chr1	23412730	23415149	<i>PPR-At1g63130</i>	(Ronemus et al., 2006)
Chr1	23306534	23308683	<i>PPR-At1g62930</i>	(Ronemus et al., 2006)
Chr1	23387631	23390816	<i>PPR-At1g63080</i>	(Ronemus et al., 2006)
Chr1	23507320	23509053	<i>PPR-At1g63400</i>	(Ronemus et al., 2006)
Chr1	23419396	23421579	<i>PPR-At1g63150</i>	(Ronemus et al., 2006)
Chr1	23385324	23387167	<i>PPR-At1g63070</i>	(Ronemus et al., 2006)
Chr1	23489840	23491519	<i>PPR-At1g63330</i>	(Ronemus et al., 2006)
Chr1	23176930	23179248	<i>PPR-At1g62590</i>	(Ronemus et al., 2006)
Chr5	15555156	15558732	<i>TIR-NBS-LRR-At5g38850</i>	(Howell et al., 2007)
Chr1	4368760	4371293	<i>AFB3</i>	(Si-Ammour et al., 2011)
Chr5	16638370	16641728	<i>ATCHX18</i>	(Howell et al., 2007)
Chr1	17886098	17892586	<i>AGO1</i>	(Axtell et al., 2006)
Chr3	23273116	23276375	<i>TIR1</i>	(Si-Ammour et al., 2011)
Chr4	1404887	1407139	<i>AFB1</i>	(Si-Ammour et al., 2011)
Chr3	9867845	9870640	<i>AFB2</i>	(Si-Ammour et al., 2011)
Chr5	15757717	15758109	<i>SLG</i>	(Chen et al., 2007)
Chr4	8380848	8383496	<i>CC-NBS-LRR-At4g14610</i>	(Zhai et al., 2011)
Chr4	8146345	8152131	<i>MET2</i>	(Chen et al., 2010)

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Table S2. *A. thaliana* small RNA libraries used in this study

Accession Number	Genotype	3' Adapter (First 8 nts)	Source
GSM2825283	Wild-type Replicate 1	TGGAATTC	(Polydore & Axtell, 2018)
GSM2825284	Wild-type Replicate 2	TGGAATTC	(Polydore & Axtell, 2018)
GSM2825285	Wild-type Replicate 3	TGGAATTC	(Polydore & Axtell, 2018)
GSM2825286	<i>rdr1-1/2-1/6-15</i> Replicate 1	TGGAATTC	(Polydore & Axtell, 2018)
GSM2825287	<i>rdr1-1/2-1/6-15</i> Replicate 2	TGGAATTC	(Polydore & Axtell, 2018)
GSM2825288	<i>rdr1-1/2-1/6-15</i> Replicate 3	TGGAATTC	(Polydore & Axtell, 2018)
GSM1533527	Wild-type Replicate 1	TGGAATTC	(Groth et al., 2014)
GSM1533528	Wild-type Replicate 2	TGGAATTC	(Groth et al., 2014)
GSM1533529	Wild-type Replicate 3	TGGAATTC	(Groth et al., 2014)
GSM1533542	<i>dcl3</i> Replicate 1	TGGAATTC	(Groth et al., 2014)
GSM1533543	<i>dcl3</i> Replicate 2	TGGAATTC	(Groth et al., 2014)
GSM1533544	<i>dcl3</i> Replicate 3	TGGAATTC	(Groth et al., 2014)
GSM1845210	Wild-type Replicate 1	AGATCGGA	(Elvira-Matelot et al., 2016)
GSM1845211	Wild-type Replicate 2	AGATCGGA	(Elvira-Matelot et al., 2016)
GSM1845212	Wild-type Replicate 3	AGATCGGA	(Elvira-Matelot et al., 2016)
GSM1845222	<i>dcl2-1/3-1/4-2t</i> Replicate 1	AGATCGGA	(Elvira-Matelot et al., 2016)
GSM1845223	<i>dcl2-1/3-1/4-2t</i> Replicate 2	AGATCGGA	(Elvira-Matelot et al., 2016)
GSM1845224	<i>dcl2-1/3-1/4-2t</i> Replicate 3	AGATCGGA	(Elvira-Matelot et al., 2016)
GSM1087973	Wild-type Replicate 1	TCGTATGC	(Jeong et al., 2013)
GSM1087974	Wild-type Replicate 2	TCGTATGC	(Jeong et al., 2013)
GSM1087975	<i>dcl1-7</i> Replicate 1	TCGTATGC	(Jeong et al., 2013)
GSM1087976	<i>dcl1-7</i> Replicate 2	TCGTATGC	(Jeong et al., 2013)
GSM1377370	Wild-type Replicate 1	TGGAATTC	(Li et al., 2014)
GSM1377371	Wild-type Replicate 2	TGGAATTC	(Li et al., 2014)
GSM1377372	<i>nrpd1-3</i> Replicate 1	TGGAATTC	(Li et al., 2014)
GSM1377373	<i>nrpd1-3</i> Replicate 2	TGGAATTC	(Li et al., 2014)
GSM1377376	<i>rdr2-1</i> Replicate 1	TGGAATTC	(Li et al., 2014)

GSM1377377	<i>rdr2-1</i> Replicate 2	TGGAATTC	(Li et al., 2014)
GSM2102962	Wild-type Replicate 1	TGGAATTC	(Panda et al., 2016)
GSM2102963	Wild-type Replicate 2	TGGAATTC	(Panda et al., 2016)
GSM2102965	<i>rdr6-15</i> Replicate 1	TGGAATTC	(Panda et al., 2016)
GSM2102462	<i>rdr6-15</i> Replicate 2	TGGAATTC	(Panda et al., 2016)
GSM893112	Wild-type Replicate 1	CACTCGGG	(Lee et al., 2012)
GSM893113	Wild-type Replicate 2	CACTCGGG	(Lee et al., 2012)
GSM893114	Wild-type Replicate 3	CACTCGGG	(Lee et al., 2012)
GSM893115	<i>nrbp1-1 (nrpe)</i> Replicate 1	CACTCGGG	(Lee et al., 2012)
GSM893116	<i>nrbp1-1 (nrpe)</i> Replicate 2	CACTCGGG	(Lee et al., 2012)
GSM893117	<i>nrbp1-1 (nrpe)</i> Replicate 3	CACTCGGG	(Lee et al., 2012)
GSM1668899	Wild-type Replicate 1	TGGAATTC	(Zhai et al., 2015)
GSM1668905	Wild-type Replicate 2	TGGAATTC	(Zhai et al., 2015)

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