

**Figure S1. Related to Figures 1 and 2.**  
**Assembly issues of *Nmy* and *Tmy* regions in available *D. simulans* genome versions.**

(A) *Nmy* is genetically known to localize to chromosome 3R, but it is misplaced onto 2R in the mosaic *D. simulans* genome assembly r1.3. This version also contains a gap, so that only one hairpin arm of *Nmy* is contained in the assembly. Since we have biochemically shown that these siRNAs are produced from a hpRNA precursor, and that a *nmy* mutant deleted for one of hpRNA arms cannot produce siRNAs, we know that this represents an assembly artifact. In the updated assembly r2.02 from the w501 strain, *Nmy* is correctly placed at the known location on chromosome 3R, but it still contains a gap, such that only one hairpin arm is present in the assembly. (B) *Tmy* is genetically delimited by introgressions to an ~80 kb region on chromosome 3R. We recognized a small RNA producing locus in this region that includes perfect matches to some *Nmy* siRNAs. This region is gapped in Dsim r1.3, and the small RNA producing regions are missing from the r2.02. However, PacBio assembly (Figure 2) resolves both of these regions within a full contig, showing that both *Nmy* and *Tmy* are hpRNAs.

Dox TCGTTACTTGGCACAGTTGTAAGACACATCACATTATTTAAATCTTACACGGCAAAAGCCGTGTTCCAAATTCGTACATTAATAATACGGTTTTTTT

Tmy GCCTGAATTTGGAATGTTATACCTTGTGAGCGTCATGCGTTGCAACCCTGATGGCCACTCTGCGCCACCATGTCTCTTG

Dox TGCCTTAACTATAAAAAATAAAAGCCTGAATTTGGAATGTTATACCTTGTGAGCGTCATGCGTTGCCCTGAGGCTTCTGCGCCACCATGTCTCTTG

Tmy TCCGCCGATGAACACGATGATCAAGCAGGGCGCCCTGCCCTTCAACACCTCCTCTGCTACGTCAATGCTACCAAGAAAGGTAGTCGACGGCTGCAA

Dox TCCGCCGATGAACACGATGATCAAGCAGGGCGCCCTGCCCTTCAACACCTCCTCTGCTACGTCAATGCTACCAAGA-GGTAGTCGACGGCTGCAA

Tmy CGCCTTCGTGCCAACATCAATACCTGCATCGCCAGCATGACATAAGCGCTTCCAAAAATGGTAATAAAACATTTGAAATTTATAAGCAAGCAGATGCTG

Dox CGCCTTCGTGCCAACATCAATACCTGCATCGCCAGCATGACATAAGCGCTTCCAAAAATGGTAATAAAACATTTGAAATTTATAAGCAAGCAGATGCTG

Tmy TTTTATTAAAGAAACATACTGCTCTAGCAGTATCAATGGGGTGGACACCAACAAAACAAAAAGTAGAATCTGAAGTGAAGGATTGCAGATCACTGCA

Dox TTTTATCAAGAAACATACTGCTCTAGCAGTATCAATGGGGTGGACACCAACAAAACAAAAAGTAGAATCTGAAGTGAAGGATTGCAGATCACTGCA

Tmy ACCAACACCCATTTTGTCCAAGTTAGTAGTCAACAACAGTAGTTAAACACGTTACTCTGAGACTAAAAGGGTATACTAGATTCTGTTGAAATGATGTA

Dox ACCAACACCCATTTTGTCCAAGT-----CACAACCTAGTTAAGCACGTTACTCTGAGACTAAAAGGGTATACTAGATTCTGTTGAAATGATGTA

Tmy CTTAGTCTCCGACCATAAAAGTGTACAACACGTCGATACGATTGACCAAAAATTTCTTTGCCACACCGAATTAATAGCGCGGGGGTAGAAATTTAAA

Dox CTTAGTCTCCGACCATAAAAGTGTACAACACGTCGATACGATTGACCAAAAATTTCTTTAGCCACACCGAGTTAATAGCGCGGGGGTAGAAATTTAAA

MDox AGCGCGGGCTAGAAATTTAAA

Tmy TAAGCT-AATTAATTAATTTAATTTAATATGATGAACCTACCACACCGCCAAACGGCAAAGGAAACATGGGG-CGTACCACCTAACAGAAAGGATGTTT

Dox TAAGCTGAAT-ATTAATATTTAATTTAATATGATGAACCTACCACACCGCCAAACGGCAAAGGAAACATGGGGCGGTACCACCTAACAGAAAGGATGTTT

MDox TAAGCTGAAT-ATTAATATTTAATTTAATATGATGAACCTACCACACCGCCAAACGGCAAAGGAAACATGGGG-----

Tmy CGCAGGATGCGAATCCGCGAGCGTCGTTTGTGATCAAACTAACTTTATCCATCTAGTTGGCGTGGGGTTGCGTACACGTATACAGCTAGCAATTCGG

Nmy CATCTAGTTGGCGTGGGGTTGCGCTACACGTATACAGCTAGCAATTCGG

Dox CCCAGGATGCGAATCCGCGGGGTCGTTTGTGATCAAACTAACTTTATCCATCTAGTTGGCGTGGGGTTGCGCTACACGTATACAGCTAGCAATTCGG

mDox ----GATGCGAATCCGCGGGTCGTTTGTGATCAAACTAACTTTATCCATCTAGTTGGCGTGGGGTTGCGCTACACGTATACAGCTAGCAATTCGG

Tmy TTATTCGAACCCCATTCGTTACTTGGTACAGTTGTAAGACACATCAAATAAAAAAAGAAAAATTTACTGTTATCATACAACAAATAATACCATATT

Nmy TTTTTCGAACCCCATTCGTTACTTGGGACAGCTGTAAGACACATCAA-----

Dox TTTTTCGAACCCCATTCGTTACTTGGGACAGCTGTAAGACACATCAA-----

mDox TTTTTCGAACCCCATTCGTTACTTGGGACAGCTGTAAGACACATCAA-----

Tmy AAATCCCTCTCCTTTTCTTTTTCAGAAATTTGATACAGAAATCTACAATTTCTATA-GAA-AAAAGGAAATGCCTTCGATCAATCCATTTTGAATA

Nmy -----TTGATAAAATAAATCTAAAATAATCTATC-GAA-AAAAA-AAAATGCCCTCAATAAACCCATTTTTCATA

Dox -----TTGATAAAATAAATCTAAAATAATCTATCTAAAACAAAAAAATGCAATTCAGTAAATCCGTTTTCATA

mDox -----TTGATAAAATAAATCTACAACAATCTATA-GAA-AAAAATAATGCGCTTCGGTAAATCCCTTTTTCATA

exon1

Tmy TGTGGCTAAATACCGTAGAGAATCCAGACCT-AAAACACAAACCGCTTATCGTATCAAGAGCTGCGGAT----GAATATAAT-GCTTT-A-T-CG

Nmy TGTAGCTACATTCGTAAGGAACATCAAGAGCTTAAAAA-CAAAGTGTATCGCACAAAGAGCTAGGGATTCATGGAAT-----GTCTTAACATACACA

Dox TGTAGCTACATTCGTAAGGAACATCAAGAACTTAAAAAT-CAAAGTGTATCGCACAAAGAGCTAGGGATTCATGGAAT-----CTTTTAACATACACA

mDox TGTAGCTAAATTCGTAGGAGCATCGAGAGCTAAGAGAT-CAACGCTTATCGCAAAAAGAGCTAGGGATTCATGGAAT-----TCCCTAATACACA

exon1 exon2 Dox/MDox forward qPCR primers

Nmy AGAGAAAAATATCTACCGGAACAG-----CGCGCGATGAACAAAATCGGCGTCGGAGAGTG

Dox AGAGAAAAATATCTACCGGAACAGGCGCGCATGAACAAAATCGGCGTCGGAGAGTGGCAGTACAGGCGCGGATGAACAAAATCGGCGTCGGAGAGTG

mDox GGAGAAAAATATCTACCGGAACAGGCGCGCATGAACAAAATCGGCGTCGGAGAGTGGCAGTACAGGCGCGGATGAACAAAATCGGCGTCGGAGAGTG

exon1 exon2 Dox/MDox reverse qPCR primers exon3

Nmy GCAGTAATGCCAGCGATGCCGTGCCAAG

Dox GCAGTAATGCCAGCGATGCCGTGCCAACAATGCCGTTATTACAATTTG

Dox CATCTATGTTATCCCAATCGAAAACCGGGAAAACCGATAATGGCAGTAATGCCGGCAACGATGCCGTTATACCAAAATAGCATTTTCTGCACTGCT

mDox -----GCATTTCTGCACTGCT

exon3

Dox TTTGTTGGTGTGTTTTTTTGGTTTGGAAATATCATCCTATGCTTTTAAAGTGAACAAAATAATCAGTTTTTTGTCAGAACA-TTGCAAATTTGAAAG

mDox TTTGTTGGTGTGTTTTT-----GGTTGG-----TTTGTCTTTAAGTGAACAAAATAATCAGTTTTTTGTCAGAACAGTTACCATAGTTGAAAG

exon3

Dox TTATCCCACAAAATATGCGAAAAATACCCAAAATTAATTTCCATAAATCTTTAAAAAATGATAGGGATCGTTATTCGTTTAGGGCTGAACACTTTTA

mDox TTATCCCACAAAATATGCGAAAAATACCCAAAATTAATTTCCATAAATCTTTAAAAAATGATAGGGATCGTTATTCGTTTAGGGCTGAACACTTTTA

Dox TTGTCGGTTGATTAAAACCTAAAATCTGAACTAATCTTGACAGAATTATAGACATCTTGATCTTTAAAGGTGAGAAGTTGCTTACTTAGATGATTTTA

mDox TTGTCGGTTGATTAAAACCTAAAATCTGAACTAATCTTGACAGAATTATAGACATCTTGATCTTTAAAGGTGAGAAGTTGCTTACTTAGATGATTTTA

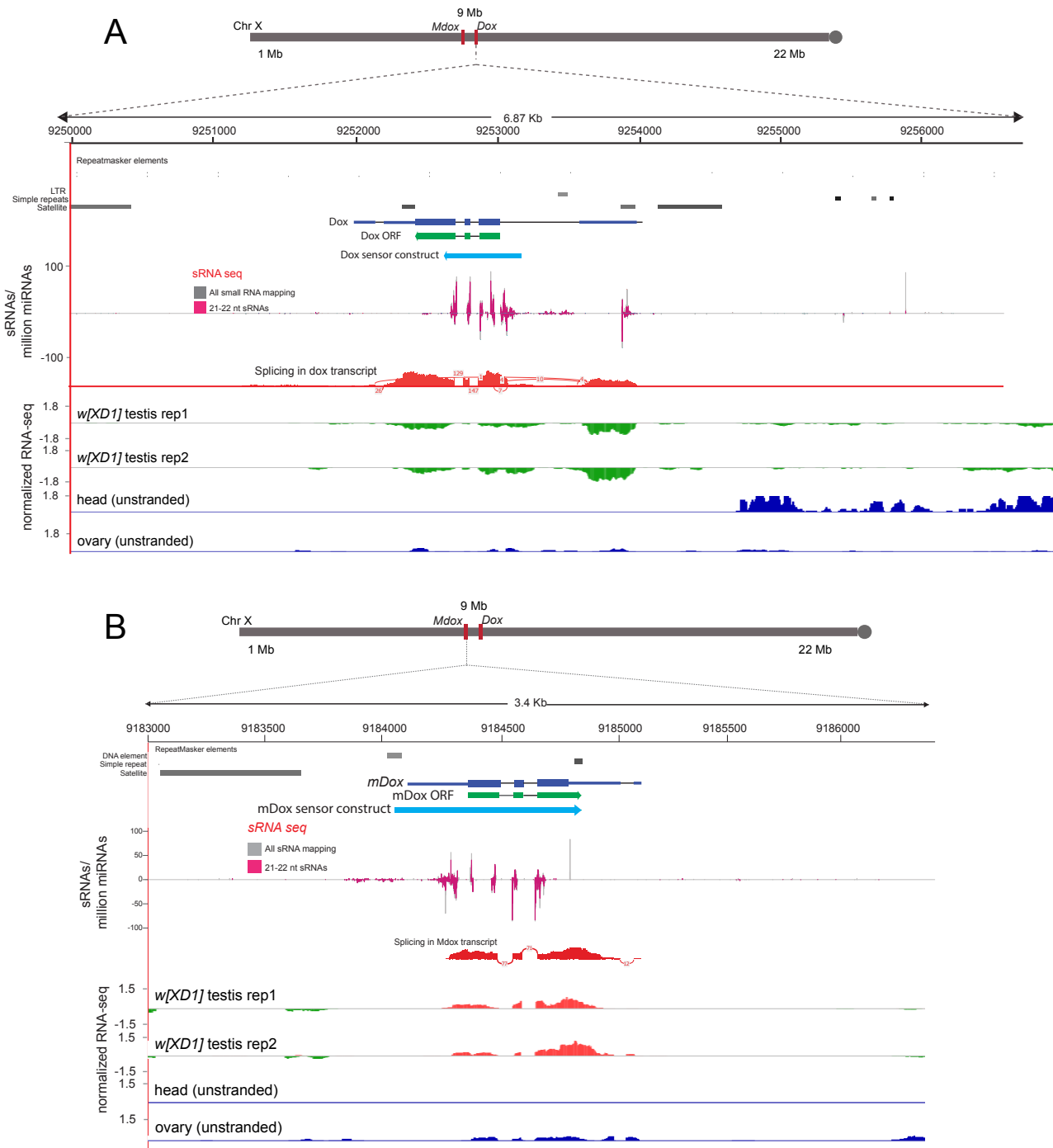
Dox TTGCAATAAAAATGATTTAATTTTAGGAATTTGATTTCAGCTTCTTAATACCAGTGGCGGCTGAAGAGGAGAGCGGTTAGGAACCGCTCAACAGGTAT

mDox TTGCAATAAAAATGATTTAATTTTAGGAATTTGATTTCAGCTTCTTAATACCAGTGGCGGCT

Dox CTGGGTATCTGATGGTGGAGTAGACACCGCAAGCGGATCACCCAACCGATACCGTCTAGTTGACGGCTTTGTGGAAGCGGACGAGCACCT

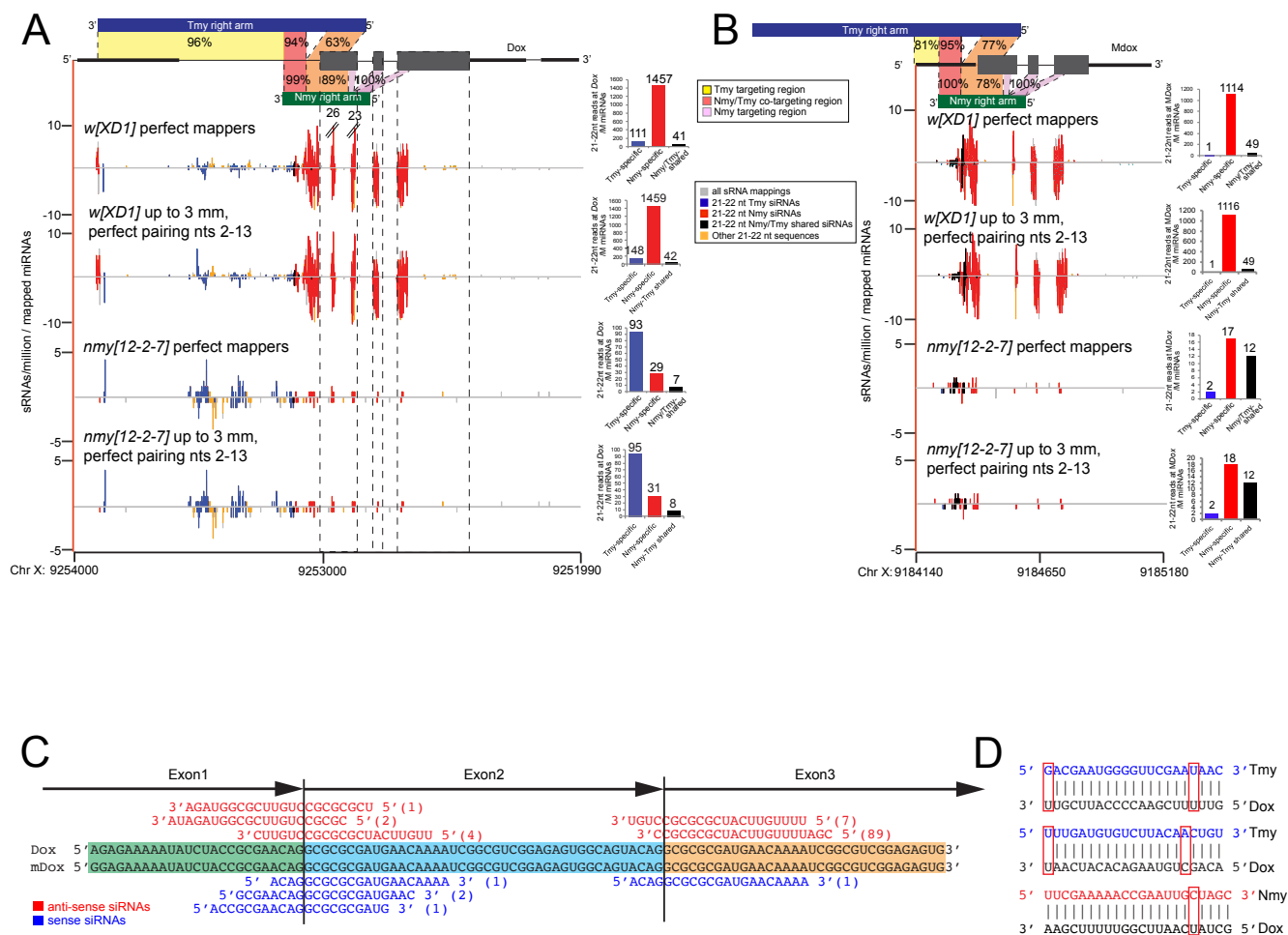
**Figure S2, Related to Figures 2-4.**  
**Alignment of the complementary hairpin arms of *Tmy* and *Nmy* with the transcribed strands of *Dox* and *MDox*.**

Regions are color-coded as in Figure 4, according to whether there is pairing only between *Tmy* and *Dox* (yellow), pairing amongst all four (orange) or pairing between *Nmy* and *Dox/MDox* (purple). The positions of *Dox/MDox* qPCR primers are noted in boxes. We were able to design primers in exon 1 with at least 6 mismatches between *Dox* and *mDox*, and especially that exhibit at least two mismatches within the last 5 nt of the primers. In addition, there is a mismatched nucleotide within the amplicon that we used to verify on-target amplification of qPCR products by sequencing.



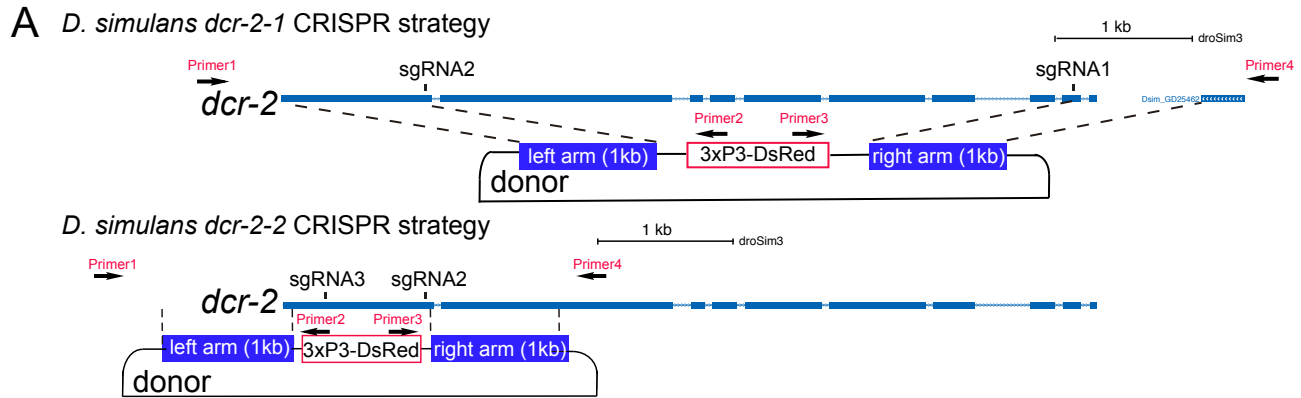
**Figure S3, Related to Figure 4.**  
**Genomics of the Dox and MDox loci, which are closely linked on the X chromosome.**

(A) Summary of RNA-seq and *Nmy/Tmy* small RNA matching to the *Dox* locus. *Dox* is much higher expressed in testis compared to ovary, and is not detected in head. The *Dox* transcript is extensively targeted by siRNAs. The region used in the *Dox* sensor is indicated. (B) Summary of RNA-seq and *Nmy/Tmy* small RNA matching to the *MDox* locus. *MDox* is much higher expressed in testis compared to ovary, and is not detected in head. The *MDox* transcript is extensively targeted by siRNAs. The region used in the *MDox* sensor is indicated.



**Figure S4. Related to Figure 4.**  
**Comparison of perfect and imperfect Nmy/Tmy siRNA matching to *Dox/MDox* targets.**

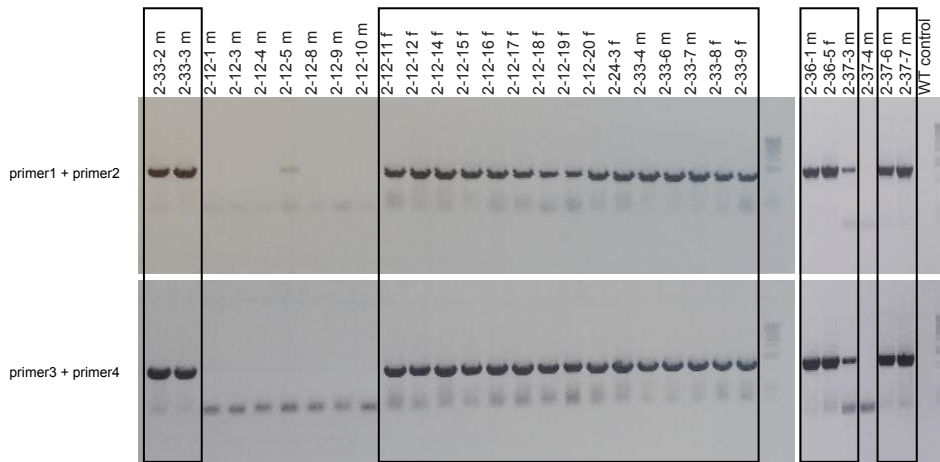
(A) Allowing restricted mismatches, with required perfect pairing in an extended seed region (from siRNA nts 2-13) recovered modest increase in siRNA mapping to the *Dox* and (B) *MDox* loci for *w[XD1]* and *nmy[12-2-7]*, indicating that a strong majority of siRNAs match perfectly to *Dox* and *MDox*. (C) siRNA mapping to *Dox* and *MDox* splice junctions reveal target complementary siRNAs at exon junctions, which are omitted when mapped to *Dox/MDox* DNA sequence. However, mapping to *Dox/MDox* DNA sequence highlights a preponderance of siRNAs mapping only to exons, evident from the homology relationship that *Nmy* hpRNA loci contains a retroposed copy of the *Dox/MDox* target. (D) Examples of siRNA complementary targeting with restricted mismatches allowed at nts 1 and 14 and above, preserving and extended siRNA seed pairing through nts 2-13.



**Validation of *D. simulans* *dcr-2-1* replacements**

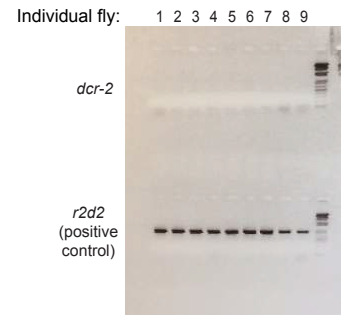
**B**

- PCR to verify integration site



**C**

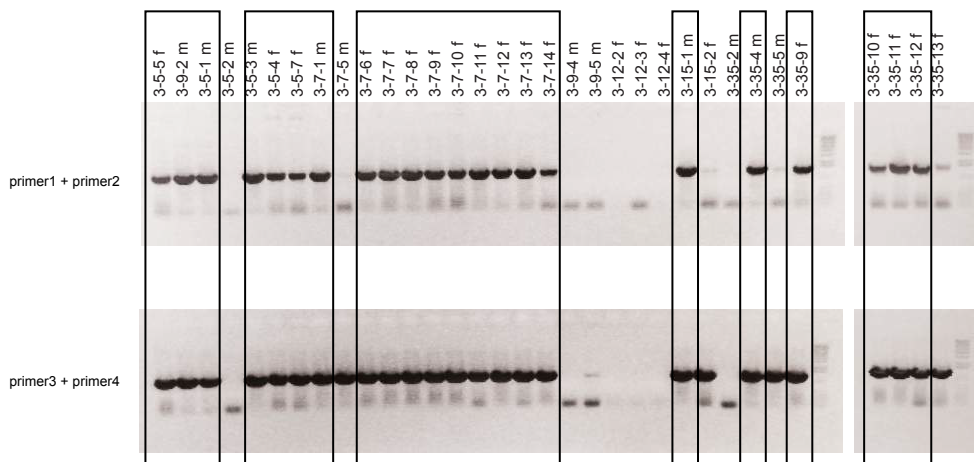
- PCR to validate individual homozygous *dcr-2-1* mutant flies picked based on DsRed fluorescence



**Validation of *D. simulans* *dcr-2-2* replacements**

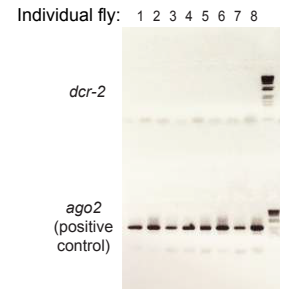
**D**

- PCR to verify integration site



**E**

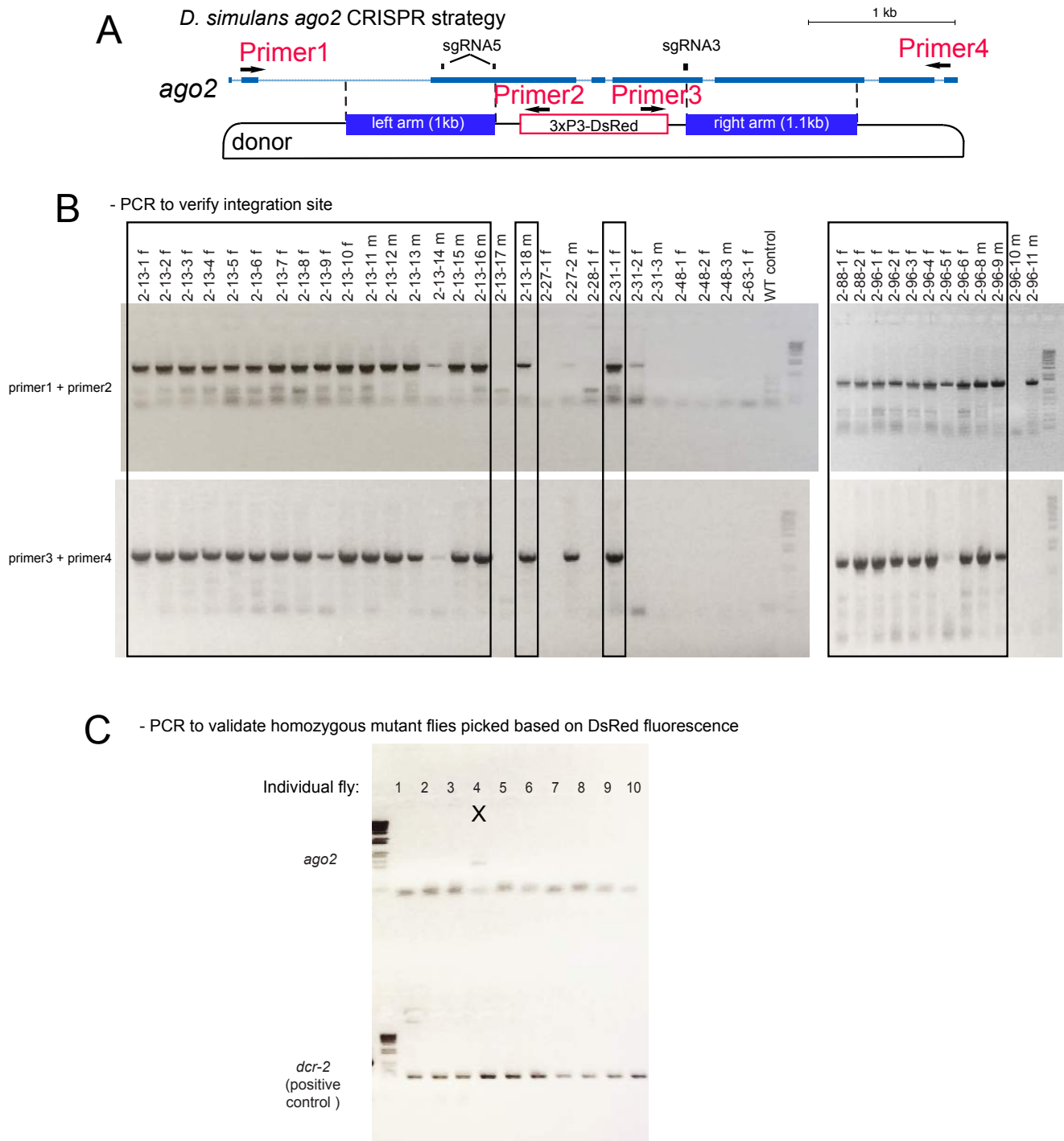
- PCR to validate individual homozygous *dcr-2-2* mutant flies picked based on DsRed fluorescence



**Figure S5. Related to Figure 4. *Dcr-2* CRISPR mutagenesis strategy and validation.**

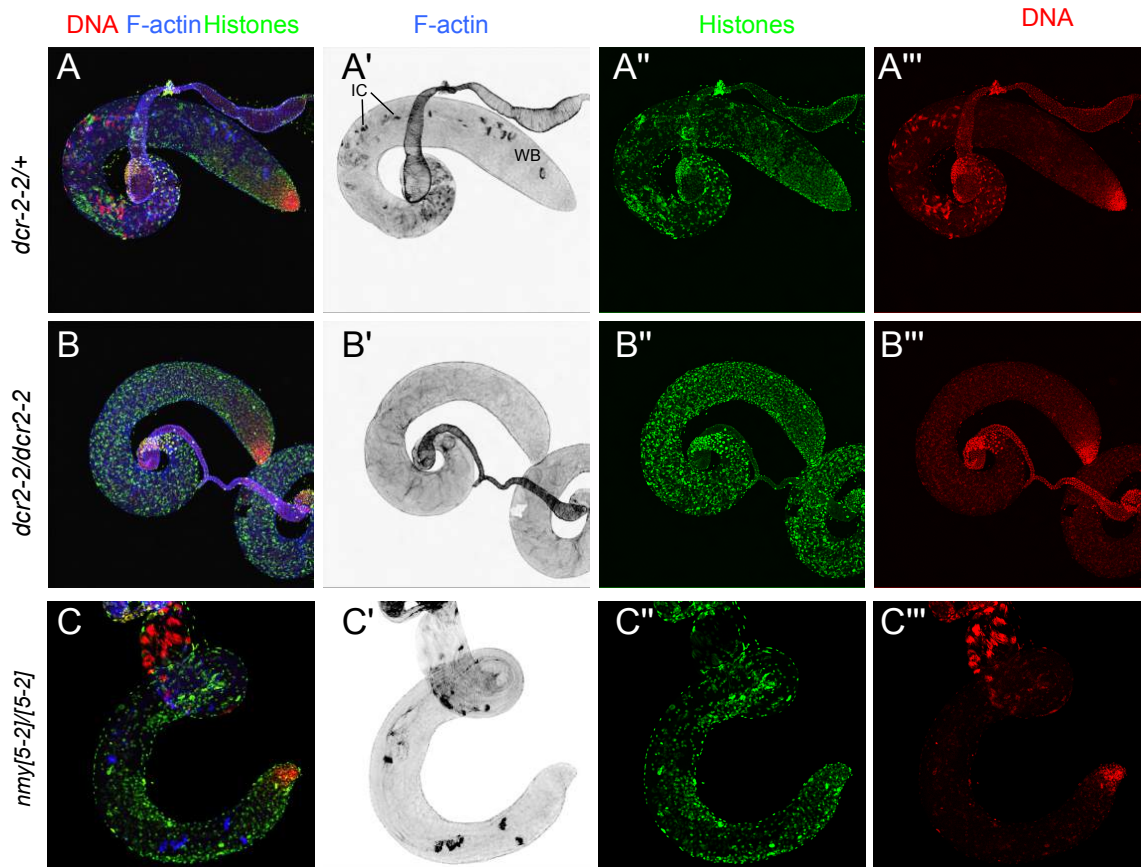
(A) Location of *dcr-2* sgRNAs, homology donor arms and 3xP3-DsRed reporter used for mutant selection to generate two different deletion alleles of *dcr-2* (*dcr-2-1* and *dcr-2-2*). (B-C) Selection and validation of *dcr-2-1* mutants. (B) Candidate DsRed positive flies were genotyped for marker integration at the *dcr2* locus. Boxed PCR tests indicate positive hybrid amplification on both left and right flanks. (C) Genotyping of individual candidate homozygous *dcr-2* mutant animals for deletion of *dcr-2* DNA; amplification of *r2d2* DNA serves as a positive control. (D-E) Selection and validation of *dcr-2-2* mutants. (D) Candidate DsRed founders were genotyped for marker integration at the *dcr-2* locus. Boxed PCR tests indicate positive hybrid amplification on both left and right flanks. Note that some animals only validated on one flank and were not considered further, although they likely contained a disruption of the *dcr-2* gene. (E) Genotyping of individual candidate homozygous *dcr-2* mutant animals for deletion of *dcr-2* DNA; amplification of *ago2* DNA serves as a positive control. All primer sequences are listed in Table S2.

*D. simulans* AGO2 CRISPR strategy



**Figure S6. Related to Figure 4.**  
***Ago2* CRISPR mutagenesis strategy and validation.**

(A) Location of *ago2* sgRNAs, homology donor arms and 3xP3-DsRed reporter used for mutant selection. (B) Candidate DsRed positive mutants were genotyped for marker integration at the *ago2* locus. Boxed PCR tests indicate positive hybrid amplification on both left and right flanks. Note that some animals only validated on one flank and were not considered further, although they likely contained a disruption of the *ago2* gene. (C) Genotyping of individual candidate homozygous *ago2* mutant animals for deletion of *ago2* DNA; amplification of *dcr-2* DNA serves as a positive control. Note that fluorescence is not entirely reliable for genotyping, since lane 4 indicates a false positive (X) heterozygote with detection of wildtype *ago2* DNA. All primer sequences are listed in Table S2.



**Figure S7. Related to Figure 6.**  
**Cytological analysis of *dcr-2-2* mutants and *nmy[5-2]* mutants.**

(A-C) Whole testes stained for DNA (red), histones (green) and F-actin (blue), showing that the normal pattern of spermatogenesis in control (A, *dcr-2-2* heterozygote) is severely disrupted in *dcr-2-2* homozygote (B) but not in *nmy[5-2]* homozygote (C) that exhibits severe sex ratio bias. F-actin staining highlights individualization complexes (IC) that separate spermatids into individual cells to form wastebags (WB). These actin structures found in control (A') are completely absent in *dcr-2-2* mutant (B') but are present in *nmy[5-2]* mutant (C') testis. In addition, the histone-to-protamine transition of post-meiotic spermatid nuclei is evident in control testis (A''), but histones remain associated throughout in *dcr-2-2* testis (B''). This transition occurs normally in *nmy* mutant testis (C'').

**Table S1, Related to Figure 1, 2, 3, S3 and S4.**  
**Small RNA and RNA-seq libraries used in this study.**  
 This table depicts the details of public and new small RNA and RNA-seq datasets analyzed in this study.  
 For each dataset, its tissue origin and mapping statistics are provided.

Sample	Tissue	Total reads	mapped reads	type	map %	Non paired	Unmapped	non-unique	Unique	Read 1	Read 2	Reads map	Reads map	Non-splice	Splice junction	Proport ratio
accSRA_acc	tissue		total mapped reads													
M023	head		38990369													
SRR1205790	male_body		37988067													
M025	embryo		79194312													
M053	female_body		123490687													
V044	embryo		117360240													
SRR653485	ovary		394537604	Chicharo, 3 day-old Ovaries												
SRR653486	ovary		474328738	Malindu, 3 day-old Ovaries												
SRR653487	egg		254889630	NRT_0-2 hours_egg98												
SRR653488	egg		203161228	RT_0-2 hours_egg98												
SRR618934	ovary		278925212	dsm_W901_ovaries												
SRR618935	body		141315165	F_1dmeI-dsm1_interspecies_body												
SRR902008	ovary		196907535	ovary												
SRR902009	testis		100562829	testis												
small RNA datasets produced for this study																
wXD1_1_sRNA	testes		19079372	testes - wildtype												
wXD1_2_sRNA	testes		5869386	testes - wildtype												
12-2-7_1_sRNA	testes		17694739	testes - rmy mutant												
12-2-7_2_sRNA	testes		11226479	testes - rmy mutant												
<b>Mapping statistics for RNA-seq libraries used in this study.</b>																
SRR1107945	Head	6130129	5416328	Paired, unstr	88.36	347285	713801	124082	4944961	2529102	2416859	2479528	2465433	4651085	293876	4338926
SRR330570	Ovary	81046293	65750134	Paired, unstr	81.13	27035605	15296159	12070538	26543991	13521221	13122770	13241693	13402298	18726432	7918559	22865244
wXD1_1	testis	29917669	29240366	Paired, stran	97.74	3998809	677303	2245876	22995681	11510649	114885032	11503335	11492346	20533691	2441990	22621452
wXD1_2	testis	33177913	32393175	Paired, stran	97.63	4274447	784738	2400445	25718283	12882002	12836281	12869703	12849580	22983207	2735076	241724214



<b>Table S2. Related to STAR methods. Oligonucleotides used in this study.</b>		
This table lists all primers used for cloning and for generating RNA-seq libraries, and oligos used as probes.		
<b>Primers for pDCC6-sgRNA construct</b>		
ago2 sgRNA3:GTAGTTGCGACTGTGGAAGT (AGG)	Fwd	cttcGTAGTTGCGACTGTGGAAGT
	Rev	aaacACTTCCACAGTCGAACTAC
ago2 sgRNA4:GCTCATTGGTAGCTGCTCG (CGG)	Fwd	cttcGCTCAITTTGGTAGCTGCTCG
	Rev	aaacCGAGCAGTACCAAATGAGC
ago2 sgRNA5:GAAACACAAGGCCAGGCTC (GGG)	Fwd	cttcGAAACACAAGGCCAGGCTC
	Rev	aaacGAGCCTGGCCTTGTGTTTTTC
dcr-2 sgRNA1:GGCATTGTATACCTGCCAC (AGG)	Fwd	cttcGGCATTGTATACCTGCCAC
	Rev	aaacGTGGGCGGTATACAATGCC
dcr-2 sgRNA2:GGTGATAGCCGATACCCCTTG (AGG)	Fwd	cttcGGTGATAGCCGATACCCCTTG
	Rev	aaacCAAGGGTATCGGCTATCACC
dcr-2 sgRNA3:GACGTTGGGGATGTTCTGG (AGG)	Fwd	cttcGACGTTGGGGATGTTCTGG
	Rev	aaacCCAGAACATCCCCAACGTC
<b>Primers for pH-DsRed HRD construct</b>		
ago2 sgRNA3 and sgRNA5	Left arm Fwd	GAGGAATTCGACGTGGTTGTATAGAACCTATG
	Left arm Rev	GACCCGGCGCTGGCCTGTGTTTTCTGTCC
	Right arm Fwd	GAGGGCGCGCTCCACAGTCGCAACTACCATTG
	Right arm Rev	GAACCTGAGCCAAAGTTACTGTGATCATGTC
dcr-2 sgRNA1 and sgRNA2	Left arm Fwd	GAGGAATTCGCTTGGCCTGGTCTTATTCG
	Left arm Rev	GACCCGGCGTTGAGGCGTATTGGCGTG
	Right arm Fwd	GAGACTAGTGGCAGGTATACAATGCCATTGC
	Right arm Rev	GAAGGCGCGCCAGCCAGCAGTGTATGATGC
dcr-2 sgRNA2 and sgRNA3	Left arm Fwd	GAGGAATTCGGGGTAACCCAAATGTTAC
	Left arm Rev	GACCCGGCGCCAAAGAGCTTGGGGGATGTC
	Right arm Fwd	GAGACTAGTGGGTATCGGCTATCACCCTTG
	Right arm Rev	GAAGGCGCGCGGTATCGAGGAGCCGAAATC
<b>Primers for genotyping</b>		
Checking deletion		
ago2(DsRed)	ago2 sgRNA3 target Fwd	ggaatctcgcgacgtctcttg
	ago2 sgRNA3 target Rev	gatgctggatccaggttgac
	ago2 sgRNA5 target Fwd	gagatacaaatatttctatcg
	ago2 sgRNA5 target Rev	ggattggccttgctctggg
dcr-2(DsRed)	dcr2 sgRNA1 target Fwd	cagtaaacatgcaagagcc
	dcr2 sgRNA1 target Rev	cgatttcaactcactcttc
	dcr2 sgRNA2 target Fwd	ccgcttctggaaggatgctc
	dcr2 sgRNA2 target Rev	atcgctctcagcagaatg
	dcr2 sgRNA3 target Fwd	gttcgctcagcccgctggac
	dcr2 sgRNA3 target Rev	ttaggcctgcaattcttagc
Checking insertion of DsRed		
Primers on 3XP3-DsRed	3xP3 Rev	ATTGTCGCTCCGTAGACGAGC
	UniSV40 seq fwd	GTTAACTTGTTTATGACAGTTATAATGG
ago2(DsRed)	AGO2 insertion site left fwd	CATTCTCGGCTATGTAAAAAAC
	AGO2 insertion site right rev	GGCCGTGGCTCACGCCATCTCGG
dcr-2(DsRed)-1	Dcr2-1 insertion site left fwd	GGAACTCGAATGGAATCTAG
	Dcr2-1 insertion site right rev	CTTCTACTCTCTTCTCTCGTC
dcr-2(DsRed)-2	Dcr2-2 insertion site left fwd	CGACAGCGCATCAATAAGCC
	Dcr2-2 insertion site right rev	GCTGCCTTCAATGGAACG
<b>Primers for cloning hpRNA constructs</b>		
Nmy/mmy_F	ATAAGAATCGGGCCGACACACCTCTGCCAAGTAG	
Nmy/mmy_R	CTAGTCTAGAATTTTAGTTCAATTTTATAACCAATATAC	
Tmy_F	ATAAGAATCGGGCCGCTCAATTTGGAATGTTATACC	
Tmy_Loop_R	CCGCTCGAGACGGTATAACGGCATCTTG	
Tmy_Loop_F	CCGCTCGAGTAGTTCATCATATTAGCGGTAGCGATTTCTGA	
Tmy_R	GCTCTAGAGCCTGAATTTGGAATGTTATACC	
<b>Primers for cloning sensor constructs.</b>		
Dox-sensor-F	AAAAGGAAAAGCGGCCCATCTAGTTGGCGTGGGTT	
Dox-sensor-R	CCGCTCGAGGTTGGCAGCGCATCGCTGG	
mDox-sensor-F	CGGGCCGCACTTAGTCTCCGACCATATA	
mDox-sensor-R	GGACTAGTAAAAGACAAACCAACCAAA	
<b>qPCR primers</b>		
Dox-qPCR-F	CTAGGGATTCTTGAATCTTTTA	
mDox-qPCR-F	CTAGCGATTATGGTATCCCTA	
Dox/mDox-qPCR-R	CATCGCGCCTGTACT	
Rpl32 fw	CCGCTTCAAGGGACAGTATC	
Rpl32 rev	ACGTTGTGCACAGGAACCT	
<b>probes for Northern blotting_Nmy</b>		
Nmy_5388	ATGTGCTTACAGCTGTCCCA	
Nmy_2307	GTGTCTACAGCTGTCCCAAG	
Nmy_2210	CTCTCGACGCCGATTTTGT	
Nmy_2065	TTGATGTGTCTTACAGCTGTG	
Nmy_1829	CTCTCGACGCCGATTTGT	
Nmy_1684	TGTGTCTTACAGCTGTCCAA	
Nmy_630	GCTGTATACGTGTACGGCAAC	
Nmy/Tmy_551	ACACGTATACAGTAGCAATT	
Nmy/Tmy_444	GTACACGTATACAGTAGCAA	
<b>probes for Northern blotting_Tmy specific</b>		
Tmy_989	GTTATCGAACCCATTCTGCA	
Tmy_514	ATGTGCTTACAACGTACCA	
Tmy_13081	ATGCCTTCGATCAATCCATT	
Tmy_13070	ATACCGTAGAGAACATCCAGA	
Tmy_528	AACTCCCTCTCTTTCTTT	
<b>oligos for small RNA library cloning</b>		
illumina_RT_primer	GCCTTGGCACCCGAGAATTCCA	
illumina_PCR_FW	AATGATACGGGACCCAGGATCTACAGTTCAGAGTTCAGTCCGA	
illumina_PCR_REV	CAAGCAGAAGACGGCATAACGATCGTATGTACTGGAGTTCCTGGCACCCGAGAATTCCA	
3' linker	5' phos-TGGAATTCCTGGGTGCAAGG-ddC 3'	
5' linker	5' ddT- rGrUrCrArGrArGrUrUrCrArCrArGrUrCrCrGrArUrC 3'	
	standard illumina barcode primers were used for multiplexing	