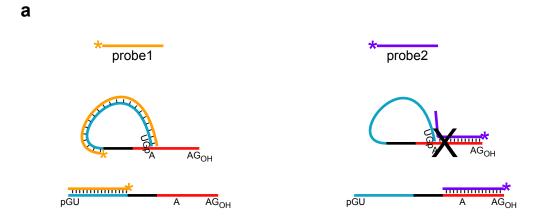
# **Intronic microRNA precursors that bypass Drosha processing**

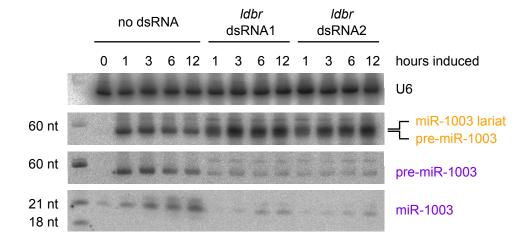
J. Graham Ruby\*, Calvin H. Jan\*, David P. Bartel

\*these authors contributed equally to this work

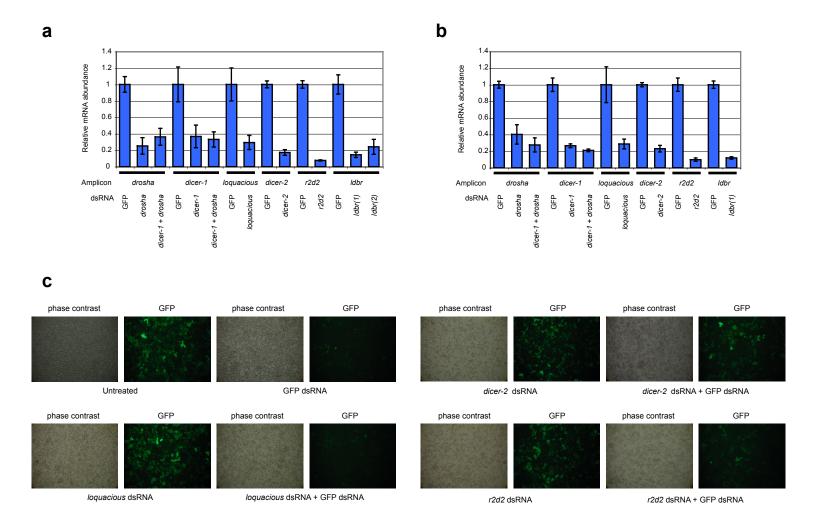
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**Figure S1. Mirtrons accumulate as lariats after splicing and require debranching enzyme (Ldbr) for conversion into functional pre-miRNAs. a,** Left, hybridization of probe1 to miR-1003 intron lariat or linear pre-miR-1003. Right, stable hybridization of probe2 occurs only with linear pre-miR-1003, and is inhibited by the presence of the branch-point adenosine in the lariat. **b,** Northern blotting was used to analyze miR-1003 maturation in a time course after induction of mini-gene expression. Prior to induction, cells were soaked with either of two dsRNAs targeting *ldbr* (CG7942) or left untreated. RNA was resolved on a denaturing 15% acrylamide gel. Under these conditions, the lariat runs slightly above the pre-miRNA hairpin. In DBR dsRNA lanes, the major band detected by probe1 is absent when the blot is hybridized to probe2, indicating the presence of a lariat in these samples. When separated on a 17% gel, the lariat runs significantly higher (Fig. 2c). Changes in relative mobility in gels with different polyacrylamide densities are characteristic of non-linear RNA species.



**Figure S2.** Confirmation of RNAi knockdowns. a, Quantitative RT-PCR analysis of samples from Fig. 2c. Relative abundance was measured using the  $\Delta\Delta$ Ct method, normalizing to *actin 5c* ( $\Delta$ Ct), and then to samples soaked in GFP dsRNA ( $\Delta\Delta$ Ct). Values are reported as geometric mean  $\pm$  s.d. (n=3). b, Analysis as in (a), using samples from Fig. 2d. c, Functional analysis of *dicer-2* and *r2d2* knockdown by fluorescence microscopy. Cells stably expressing GFP were soaked in dsRNAs targeting *loquacious*, *dicer-2*, or *r2d2*. After 4 days, dsRNA targeting GFP was added. Depletion of Dicer-2 or R2D2 reduces the ability of GFP dsRNA to silence GFP. Depletion of Loquacious serves as a negative control. Functional efficacy of the other dsRNAs was assessed by northern blot analysis of miRNA or intron processing (Fig. 2).

## mir-1003

# reads: 352

Most abundant read: UCUCACAUUUACAUAUUCACAG
Host gene: CG6695-RA, CG6695-RB

**Intron coordinates:** chr3R:20484326-20484382(+)

	# reads	<u># loci</u>
GUGGGUAUCUGGAUGUGGCUCUGGCGGUCCUCUCACAUUUACAUAUUCACAG		
(((((((((((((((((((((((((((((((((((((((		
GUGGGUAUCUGGAUGUGGUUG	6	1
GUGGGUAUCUGGAUGUGGUUGG	9	1
GUGGGUAUCUGGAUGUGGC	1	1
UCUCACAUUUACAUAUUCA	3	1
	15	1
	84	1
UCUCACAUUUACAUAUUCACAG	233	1
	1	1

## mir-1004

# **reads:** 50

Most abundant read: UCUCACAUCACUUCCCUCACAG

Host gene: CG31772-RA

**Intron coordinates:** chr2L:3767620-3767688(+)

			# reads	# loci	
GUUGGGGGACAUU	GAUCUCGGAGACGCCGUUUAACUGAUCCAUUCUCUCACAUCAC	UUCCCUCACAG			
(((((((	(((.(.((((((((()))))))))).	.))))))			
		JUCCCUCACA.	4	1	
		UUCCCUCACAG	46	1	
D.melanogaster	GT-TGGGGGACATTGATCT	rcggagacggcgg	TTTAACTGATCCAT1	CTCTCACATC-ACTTC	CCTCACAG
D.simulans	GT-TGGGGGACATTGATCT	[CGGAGACGGCGG	TTTAACTGATCCATT	CTCTCACATC-ACTTC	CCTCACAG
D.yakuba	GT-TGGGGGACATTGATCT	rcggagacggcgg	TTTAACTGATCCATT	CTCTCACATC-ACTTC	CCTCACAG
D.ananassae	GT-GAGATAACACGTTCTAACCAACTGATATGAAACTACGAATGTTT	l'TATCGCTGTCGA	ATTCGAACGA	CTCTCA <mark>T</mark> AT <mark>A</mark> -AC <mark>CGTAC</mark> C	TATTACAG
D.pseudoobscur	a GTGTGTGGGATACTGATT	rtagag <mark>aaaaaaaaaacca</mark>	ATTAACGTGAGGCTTCGT	TTCTCACATC-ATTTT-CC	CCTCACAG
D.virilis	GT-TGGGGCACATTGATCT	PTCAAGAAACTCACAGCCA	AGCTCATTTACTCAC7	CTCTCTCTCTTCTCTC	CCTCACAG
D.mojavensis	GTTGATC	ACTCcta	tatatgtatatat	ttctc <mark>tttctg</mark> actctctc	ccactctttATTTGTAG

## mir-1005

# **reads:** 8

Most abundant read: UCUGGAAUCUUUAAUUCGCAG
Host gene: CG2969-RA CG2969-RB
Intron coordinates: chr2L:4343695-4343756(+)

		# reads	# loci	
GUGAGUUGAUCGAU	UUCGAGGUUUUGGCACACGAAUAUAAUCUGGAAUCUUUAAUUCGCAG			
(((((((((	(((.(((((((()))))))))))))))))))			
		1	1	
		7	1	
D.melanogaster	GTGAGTTGATCGATTTCGAGGTTTTGGCA	CACG	AATATAATCTGGAA	TCTTTAATTCGCAG
D.simulans	GTGAGTTGATCGATTTCGAGTTTTTGGC	CAC <mark>A</mark>	AATATAATCTGGAA	TCTTTAATTCGCAG
D.yakuba	GTGAGTTGATCGATTTCGAGGTTTTGGCA	GCCA	AA <mark>A</mark> ATAATCTGGAA	TCTTTAATTCGCAG
D.ananassae	GTAAGTACATTGTGGATATTGTTTATAC		TACAGCCTCTAA	TCTTATACTATATTTTTGCAG
D.pseudoobscur	a GTAAGTGTCCATATCCTCGAGGCTCctgcaatgcactgcaat	gcactgcaatgaccgca	atgcTGACGTATTATTTATGT	TCTCCGATCCCCAG
D.virilis	GTAAGGGCTGAATTTTAAAATTG-AATTT	<b>A</b> AC <b>A</b>	AGTATACAACAATATTATAAT	CCCACACAG
D.mojavensis	GTAAGCATAGAGCAGATCAGATTTATGATTT	CAC <mark>A</mark>	TATTCTCAATACTGCTTCGAT	CCTCCACAG

# mir-1006

# reads: 57

Most abundant read: UAAAUUCGAUUUCUUAUUCAUAG

Host gene: CG17332-RA CG17332-RB CG17332-RD

**Intron coordinates:** chr2L:16720723-16720787(-)

	# reads	# loci
GUGAGUUUGAAAUUGAAAUGCGUAAAUUGUUUGGUACAAUUUAAAUUCGAUUUCUUAUUCAUAG		
(((((((((((((()))))))))))))))))))))		
	1	1
	12	1
	8	1
	35	1
	1	1
_		

## mir-1007

# **reads:** 9

Most abundant read: UAAGCUCAAUUAACUGUUUGCA

Host gene: CG1718-RA

**Intron coordinates:** chrX:21107060-21107125(-)

		# reads	# loci
GUAAGCAGUGUUUG	AACUCGAUCUUGGUUCUUGGACUCUUGAUAAGCUCAAUUAACUGUUUGCAG		
(((((((((	(.(((((((())).)))).))))))))))		
	UAAGCUCAAUUAACUGUUUGC	2	1
	UAAGCUCAAUUAACUGUUUGCA.	6	1
	UAAGCUCAAUUAACUGUUUGCAG	1	1
D.melanogaster	GTAAGCAGTGTTTGAACTCGATCTTGGTTCTTGGACTCT	TGATAAGCTCAATT	AACTGTTTGCAG
D.simulans	GTAAGCAGTGTTTGAACTCGATCTTGGTTCTTGGACTCT	TGATAAGCTCAATT	AACTGTTTGCAG
D.yakuba	GTAAGCAGTGTTTGAACTCGATCTAGGATCTTGGACTCT	TGATAAGCTCAATT.	AACTGTTTGCAG
D.ananassae	GTAAGCAGTGTTTGAACTCGATCTTGGAATAGCTCC	CGATAAGCTCAATT	AACTGTTTGCAG
D.pseudoobscur	a GTAAGCAG <mark>CGATTGA</mark> TC <mark>A</mark> ATC <mark>aa</mark> ttgaatcgaatcgaat	cgaatGATAA <mark>A</mark> CTC <mark>C</mark> ATT	AACTGTTTGCAG
D.virilis	GTAAGCAGTGCTTGAGCTTATTCTCTGGCTTCATTTGACCATTTTC	TGATAAGCTCAATT	AACTGTTTGCAG
D.mojavensis	GTAAGCAGTGTTTGAACT <mark>AA</mark> ATCT <mark>CTGGCT</mark> <mark>AC</mark> TTGGCCGTATAT	TGATAAGCTCAA <mark>C</mark> T	AACTGTTTGCAG

# mir-1008

# **reads:** 46

Most abundant read:UCACAGCUUUUUGUGUUUACAHost gene:CG18004-RA CG18004-RBIntron coordinates:chr2R:6401439-6401496(+)

		# reads	# loci
GUAAAUAUCUAAAGU	JUGAACUUGGCCAAUGGCAAGUCACAGCUUUUUGUGUUUACAG		
(((((((((	(((.((((().)))))))))))))))		
GUAAAUAUCUAAAGU	JUGAACU	1	1
	UCACAGCUUUUUGUGU	1	1
	UCACAGCUUUUUGUGUUU	1	1
	UCACAGCUUUUUGUGUUUAC	6	1
	UCACAGCUUUUUGUGUUUACA.	22	1
	UCACAGCUUUUUGUGUUUACAG	14	1
	CAGCUUUUUGUGUUUACAG	1	1
D.melanogaster	GTAAATATCTAAAGTTGAACTTGGCCAATGGCAAGTCACA	GCTTTTTGTC	STTTACAG
D.simulans	GTAAATATCTAAAGTTGAACTTGGCCAACGGCAAGTCACA	GCTTTTTGTC	STTTACAG
D.yakuba	GTAAATATCTAAAGTTGAACTTGGCCAACGGCAAGTCACA	GCTTTTTGTG	STTTACAG
D.ananassae	GTAAGGAACTCAATTTTTACATTAAACCGAAGCAATTTAAC	ACGTTTCTT	ATTT-CAG
D.pseudoobscura	GTAAGGGATCGGCGAGAGTTTTTCCCACGGAATATCATTATATATA	<mark>TTG</mark> TTATGTO	GCCTGCAG
D.virilis	GTAAGTGATGATGCGTCCATTGGGAATATCATTTAATT	TGTC	GTT <mark>GGT</mark> AG
D.mojavensis	GTAAGTAGTAATAGGTGTTTGTAGACATATTCAGTTAATT	TTCGCATTTGTGT#	ATTGGCAG

## mir-1009

# reads: 14

Most abundant read: UCUCAAAAAUUGUUACAUUUCAG

Host gene: CG3860-RA

**Intron coordinates:** chr2R:19500653-19500714(-)

		# reads	# loci
GUAAGUGUAAGACUU	JUCUUGAGUUACCCGCGAUGAGUAUCUCAAAAAUUGUUACAUUUCAG		
(.((((((.(.(	(.((((((.((().))).))))))))))))))))		
. UAAGUGUAAGACUU	JUCUUGAGU	1	1
	UCUCAAAAAUUGUUACAUUUCA.	3	1
	UCUCAAAAAUUGUUACAUUUCAG	10	1
D.melanogaster	GTAAGTGTAAGACTTTCTTGAGTTACCCGCGATGAG	TATCTCAAAAATTG	rTACATTTCAG
D.simulans	GTAAGTGTAAGACTTTCTTGAGTTACCCGCGATGAG	FATCTCAAAAATTG	rTACATTTCAG
D.yakuba	$\tt GTAAGTGTAAGACTTTCTTGAGTTACCCGCGA{\color{red}GGAG{\color{black} GGAG{\color{black} GGAG{\color{back} GGAG{\color{black} GGAG{b$	FATCTCAAAAATT <mark>A</mark>	rTacatttcag
D.ananassae	GTAAGTTTTGAATACTTCTACTCTATCTTGGA-ATG	r <mark>c</mark> tctca <mark>t</mark> aa <mark>t</mark> tgt	CCATCTTCTAG
D.pseudoobscura	GTAAGTTCGAGAATCCCAAACACATAAGTTCTTTTTTA	-ACATCCAAA	TATTTTGTAG
D.mojavensis	GTAAGGACCAATTGGTAAAGTGAGAAATTGGAAGAAA	I'TTATTGAAATTTA'	TACTCGTGTTTAG

## mir-1010

# **reads:** 193

Most abundant read: UUUCACCUAUCGUUCCAUUUGCAG

Host gene: CG31163-RA CG31163-RB CG31163-RC

**Intron coordinates:** chr3R:18118600-18118671(+)

	# reads	# loci
GUAAGUGGUGUAGAUGAAACAAAUUUACCAACAAUUUUGUUGGAUUGUUUCACCUAUCGUUCCAUUUGCAG		
(((((((((((((((((((((((((((((((((((((((		
GUAAGUGGUGUAGAUGA	1	1
GUAAGUGGUGUAGAUGAAA	2	1
GUAAGUGGUGUAGAUGAAAC	3	1
GUAAGUGGUGUAGAUGAAACA	30	1
GUAAGUGGUGUAGAUGAAACAA	1	1
	10	1
	39	1
	38	1
	64	1
	3	1
	1	1
UUCACCUAUCGUUCCAUUUGCAG	1	1

## mir-1011

# reads:

Most abundant read: UUAUUGGUUCAAAUCGCUCGCAG
Host gene: CG17274-RA CG17274-RB
Intron coordinates: chr3R:16679026-16679080(-)

		<u>#</u> _	reads	# loci			
GUGAGUUUUUGAGCC	GUGAGUUUUUGAGCCAGGAAUAUAGUUCUUAUUAUUGGUUCAAAUCGCUCGC						
(((((((((((	((.(((()))).)))))))))))						
			2	1			
_							
D.melanogaster	GTGAGTTTTTGAGCCAGGAATATAGTT	CTTAT	TAT-	TGGTTCAAATCGCTCGCAG			
D.simulans	GTGAGTTTTTGAGCCAGGAATATAGTT	CTTAT	TAT-	TGGTTCAAATCGCTCGCAG			
D.yakuba	GTGAGTTTTTGAGCCAGGAATATAATT	CTTAT	TAT-	TGGTTCAAATCGCTCGCAG			
D.ananassae	GTGAGTCTTTGAACCAGGAATATAATT	<b>TG</b> TAT	<mark>A</mark> TAT-	TGGTTCAAATCGCTCG <mark>T</mark> AG			
D.pseudoobscura	GTGAGATTTTGAATCTAATATATAATATAATC	CGTACGT	GTATATA	TGGTTCAAAT <mark>TA</mark> CTCG <b>T</b> AG			
D.virilis	GTGAGTCATTGAACCAGGAATATATGTATGTAA	TTCTTAT	ATAT-	TGGTTCAAATTTCTCGCAG			
D.mojavensis	GTGAGTCTTTGAGCCAGGAATATATGTTCAT	CTTAT	TAT-	TGGTTCAAATCTCTCGTAG			

## mir-1012

# reads: 101

Most abundant read: UUAGUCAAAGAUUUUCCCCAUAG
Host gene: CG31072-RA CG31072-RB
Intron coordinates: chr3R:22687070-22687129(-)

	# reads	<u># loci</u>
GUGGGUAGAACUUUGAUUAAUAUUGCUUGAAAAAUAUUAGUCAAAGAUUUUCCCCAUAG		
(((((.((((((((((((((((())))))))))		
GUGGGUAGAACUUUGAUUA	1	1
GUGGGUAGAACUUUGAUUAA	5	1
GUGGGUAGAACUUUGAUUAAU	20	1
GUGGGUAGAACUUUGAUUAAUA	16	1
GUGGGUAGAACUUUGAUUAAUAU	1	1
	2	1
	56	1

D.melanogaster	GTGGGTAGAACTTTGATTAAT	-ATTGCTTGAAAAAT	-ATTAGTCAA	-AGATTTT-C	CCCATAG
D.simulans	GTGGGTAGAACTTTGATTAAT	-ATTGCTTGAGAA-T	-ATTAGTCAA	-AGATTTT-C	CCCATAG
D.yakuba	GTGGGTAGAACTTTGATTAAT	-ATTGCTTG <mark>C</mark> AA <mark>G</mark> AT	-ATTAGTCAA	-AG <mark>G</mark> TTTT <mark>T</mark> C	CCCATAG
D.ananassae	GTAGGTTTCAACCAAA	-TTTCCTTTGAGAGT	TCAGTTAACTT	TATATATT-C	TTTTTAG
D.pseudoobscura	GTGGGTAGT-CTCTCATATAT	-AGTTATAAAAGAACGAACAC	CAGTGGTTAA-GC	AATGCATT-T	CTTGTAG
D.virilis	GTACGGATTGTTTATTTA	-AATGCTTTATATAT	TTA <mark>TCT</mark> AT	-AAGCTAT-CTTTTTG	TTTGCAG
D.mojavensis	GTGTGTAAA-TATGGATTATT-ATTTATAAATTATCGAAAACT	TAACTTCTAATGTTT	- <b>-</b> TTA <mark>TATTT</mark>	-ATATTTT-CAACATA	CTCTCAG

## mir-1013

# **reads:** 17

Most abundant read: AUAAAAGUAUGCCGAACUCG

Host gene: CG12072-RA

**Intron coordinates:** chr3R:26617357-26617418(-)

	# reads	<u># loci</u>
GUGAGUUUCGUACACUUAAUUAAUAGGAUCGGCCGUUAAUAAAAGUAUGCCGAACUCGCAG		
(((((((((((((((((((((((((((((((((((((((		
UAAUAGGAUCGGCCGUUAAU	2	1
AUAAAAGUAUGCCGAACUCG	4	1
AUAAAAGUAUGCCGAACUCGC	4	1
AUAAAAGUAUGCCGAACUCGCA.	2	1
AUAAAAGUAUGCCGAACUCGCAG	4	1
	1	1

D.melanogaster	GTGAGTTTCGTACACTTAATTAATAGGATCGGCCGTTAATAAAAGTATGCCGAACTCGCAG
D.simulans	$\tt GTGAGTTTCGTACACTTAATTAATAGGATCGGCCGTTAATAAAAGTATGCCGAACTCGCAG$
D.yakuba	$\tt GTGAGTTTCGTACACTTAATTAAT {\color{red} TGGGA} {\color{red} CGGCCGTTAATAAAAGTATGCCGAACTCGCAG}$
D.ananassae	$\texttt{GTAATCT}\texttt{TTGAATAA}\\ \texttt{TTATCTGTGAGTTGTGGCATCTAATGATTGT}\texttt{TATCTTCCAG}\\$
D	

 $D.\,pseudoobscura\,\, {\tt GTAAGTCCATGAATTGCATCCCCCTTTGAT----TATTCTTTAATCTGGAAATCCCTGTGATCCCATAG}$ 

## mir-1014

# **reads:** 3

Most abundant read: AAAAUUCAUUUUCAUUUGCAG

Host gene: CG2196-RA

**Intron coordinates:** chr3R:27579245-27579313(-)

# loci	# reads	
		GUAUAAUGGAAAUAGAUUUUAAUCGCAGGCGCGUCAGUGGUUGAAUUAAAAUUCAUUUUCAUUUGCAG
		(((.(((((((((((((((((((((((((((((((((((
1	1	
1	2	

D.melanogaster GTATAATGGAAATAGATTTTAATCGCAGGCGCGTCAGTGGTTGAATTAAAATTCATTTTCATTTGCAG
D.simulans GTATAATGGAAATAGATTTTAATCGCTGGCGCGTCAGTGGTTGAATTAAAATTCATTTTCATTTGCAG
D.yakuba GTATAATGGAAATAGATTTTAATCGCAGGCGCGTCAGTGGTTGAATTAAAATTCATTTTCATTTGCAG
D.pseudoobscura GTACAATGAAATAGATTTTAATCGCGTTTCGTTTGGCGGTGAAATTAAAATTCATTTTCATTTACAG

## mir-1015

# reads: 8

Most abundant read: UCCUGGGACAUCUCUCUUGCAG

Host gene: CG6432-RA

**Intron coordinates:** chr3R:20164953-20165017(+)

		# reads	# loci
GUGAGUGAUGCUC	CAGUUAGCUUGGCUGAGUGAGGAUUUAAGUCCUGGGACAUCUCUCUUGCAG		
(.(((.(((	(((((((((()))))))).)).)))))).)		
GUGAGUGAUGCUC	CAGUUAGCUU	1	1
	UCCUGGGACAUCUCUCUGCA.	1	1
		6	1
D.melanogaste	r GTGAGTGATGCTCCAGTTAGCTTGGC-TGAGTGAGGATTTAAGTCCT	GGGACAT	CTCTCTTGCAG
D.simulans	GTGAGTGATGCTCCAGTTAGCTTGGC-TGAGTGAGGATTTAAGTCCT	GGGACAT	CTCTCTTGCAG
D.yakuba	$\tt GTGAGTGATGCTCCAGATAGCTTGAC-TGGGTGAGGATTTAAGTCCTGGGTGAGGATTTAAGTCCTGGGTGAGGATTTA$	GGGACAT	CTCTCTTGCAG
D.virilis	GTAAGTATTTAC-TTGATAACTCGTTAAACCTAAAGTCTG	TTAACCACTCTTATA	AACTATGCATCTAAACAG
D.mojavensis	GTAAGTTCATGAATTCATGTTCATGAATTTTTATCCAAGTAATTTC	TTTACGTTGT	CTTCTTAACAG

### mir-1016

# reads: 2

Most abundant read:UUCACCUCUCUCCAUACUUAGHost gene:CG8479-RA CG8479-RBIntron coordinates:chr2R:9747992-9748050(-)

		# reads	# loci
GUAAGUAUAGAGAG	BAUGUGAUUGGUAAAUUCCAAAGUUCACCUCUCCCAUACUUAG		
.(((((((.((((	(((((((((())))))))).))))))))))		
		2	1
D.melanogaster	GTAAGTATAGAGAGGATGTGATTGGTAAATTCCAAA	GTTCACCTCTCTCCAT	ACTTAG
D.simulans	GTAAGTACAGAGATGATGTAATGCGTAAATTCCAAAG	GTTCACCTCTCTCCAT	ACTTAG
D.yakuba	GTAAGTATAGAGGGGATGTGATGGGTAAATTCCAAAG	FTTCACCTCTCTCCAT	ACTTAG
D.ananassae	GTGAGTACTTGTAATAT A - AATCCATAAAT CAAAA	ACTCACTTTT-TCCA-	ACTTAG
D.pseudoobscura	R GTGAGTACACAATTCAATTCCTCGGCAAGG-CTATCGTCTGAA	ACTAATTTCCCTTCA-	-CTTATCCCTGCCCTGCAG
D.virilis	GTAAGTAGCAGGTGCTGAGTGCATGATTGTCTCTATA	CTTGATTATCTTTG-	CAG
D.mojavensis	GTAAGTAGAGCACGCATTTCCAGTACCCAACTATTCGTTACTATA	CTGTACAATTTTTG-	TAG

#### mir-1017

# reads: 148

Most abundant read:GAAAGCUCUACCCAAACUCAUCCHost gene:CG6844-RACG6844-RBIntron coordinates:chr3R:20314333-20314502(+)

	# reads	# loci
$\label{thm:constraint} GUGAGUUUAAAGCUUCCCAUCGCCACACUUACGCGAAAGCUCUACCCCAAACUCAUCCCCCAAAAUGAUCCCUUUUCUCCCCUUUUCCCAACACAUUUGUAUCCCACCUUCCUGGGGGGGUUUGUGGAUUGGUAACUGCUUCAAUGGCUGGACGGUUUAGGGGGGUUUAGGGGGGGG$		
((((((((((((((((((((((((((((((((((((		
UCCCAUCGCCA	1	0
	1	1
GAAAGCUCUACCCAAACUC	1	1
GAAAGCUCUACCCAAACUCA	3	1
GAAAGCUCUACCCAAACUCAU	14	1
GAAAGCUCUACCCAAACUCAUC	37	1
GAAAGCUCUACCCAAACUCAUCC	67	1
GAAAGCUCUACCCAAACUCAUCCC	23	1
	1	1
D.melanogaster GTGAGTTTAGTGGAGTTTAAAGCTTCCCATCGCCAGCATTGGGGAAAGCTCATCCCCG-AAAATGATCCCTT	:TGCTTCAATGGCTGGAC	GGTT-TAG
D. simulans GTGGTTTAGTGGAGTTTTAAAGCTTCCCATCGCCAGCAA-TTACGGGAAAGCTCATCCCCTG-AAAA	TGCTTCAATGGCTGGAC	GGTT-TAG
D. yakuba GTGGGTTTAGTGGGGTTTTAAGCTTCCCATCGCCAGCAATTAGGGGAAGCTCATCCCCTGAAAAA	TGCTGCAATGGCCATGGAC	TGTT-TAG
D. anamassae GTGAGTTTAGTGGAGTTTAATGCTTCTCACCGGCCCTTTCGCGAAAGCTCTACCCAAACTCATCCCCTG-AAAA	TGGCCTGCTGGATGGCT	TCTT-CAG
D. pseudoobscura GTOAGTTTTGTGGGGTTTTAAGTTAACAATCGCCGACAAAATTACGCGAAAGCATCATCCCTCA-CAA	TGGTATTCGGCTTGGAC	TGTTCCAG
D.virilis GTGAGTTTGTAAAGCTCTTACTTOCTCGCCACGCCCACGCGAAAGCTCTACCCAAACCCCAAACCCCACCCCATACCCAAACCCCATCCCCTG	TGCTGCACTCGCTGGCTCT	TGTTGAATGTT-CAG
D. mojavensis GTGAGTTTGGTGGAGTTTAAAGCTCACACTTTGCTCGCCACAAGCCCCCCCCACAAGCCCCCCCAACTCACTATG-AAAATCTATACTCCAAACCCGAATCCACTATG-AAAATCTATACTCCAAACCCGAATCCATTCA	TGCTGCTCTCGCTGGCCTT	NGATCAAATGTT-CAG

## *mir-62*

# **reads:** 1071

Most abundant read: UGAUAUGUAAUCUAGCUUACAG

**Host gene:** T07C5.1b T07C5.1c

**Intron coordinates:** chrX:12692524-12692582(+)

# reads	
	GUGAGUUAGAUCUCAUAUCCUUCCGCAAAAUGGAAAUGAUAUGUAAUCUAGCUUACAG
	(((((((((((((((((((((((((((((((((((((((
2	
2	
58	UGAUAUGUAAUCUAGCUUACA.
1008	UGAUAUGUAAUCUAGCUUACAG
1	

 $\begin{array}{ll} \textit{C.elegans} & \texttt{GTGAGTTAGATCTCATATCCTTCCGCAAAATGGAAATGATATGTAATCTAGCTTACAG} \\ \textit{C.briggsae} & \texttt{GTGGGTTAGATCCCATATCCTTCCGCTTGATGGAAATGATATGTAATCTAGCTTACAG} \\ \end{array}$ 

## mir-1018

# reads: 2

Most abundant read: AGAGAGAUCAUUGGACUUACAG

Host gene: Y59E1B.1

**Intron coordinates:** chrX:1879451-1879507(+)

	# reads	# LOC1
GUAAGUUCAUGAUUUCUCCCAUAUAUUUUUCAUGAGAGAGA		
(((((((((((((((((((((((((((((((((((((((		
	2	1

## mir-1019

# reads: 2

Most abundant read: GUGAGCAUUGUUCGAGUUUCAUUU

Host gene: M04C9.5

**Intron coordinates:** chrI:9369650-9369719(+)

	# reads	# loci
GUGAGCAUUGUUCGAGUUUCAUUUUUAAUAAAAUUUAUUU	CCAG	
(((((((((((((((((((())))))))		
GUGAGCAUUGUUCGAGUUUCAUUU	1	1
	CCAG 1	1
C.elegans GTGAGCATTGTTCG-AGTTTCatttttaataaaatttatttaaaaaCTGTAATTC	CCACATTGCTTTCCAG	
C. briggsae GTTTGCATTCTTTGAAGTGTCACAGTTCTATAACG	TCGCAGTTCCAG	

## mir-1020

# reads: 2

Most abundant read: GUAAGUGUUACAGAAUAAUCU

Host gene: T16G12.1

**Intron coordinates:** chrIII:10047630-10047700(-)

	# reads	# loci
GUAAGUGUUACAGAAUAAUCUUAGACAAAACAACUAAAAUUAAUGAAAAAUUAUUCUGUGACACUUUCAG		
(.((((((((((((((((()		
GUAAGUGUUACAGAAUAAUCU	1	1
	1	1

C.elegans GTAAGTGTTACAGAATAATCTTAGACAAAACAACTAAAATTAATGAAAAATTATTCTGTGACACTTTCAG
C.briggsae GTGAGGAACACATACAAATGTTGGAT------TTTATTC---GAATTTTCAG

**Table S3.** Quantification of signals from RNA blots of Figure 2c and 2d. Signals were first normalized to that of the loading control (U6), then to that of the control dsRNA (GFP). When signal was below detection (b.d.), the upper bound of the value, based on the normalized detection limit, is shown for relevant lanes.

Fig. 2c Quantification

					dsRNA				
_	GFP	drosha	dicer-1	loquacious	dicer-2	r2d2	drosha + dicer-1	ldbr(1)	ldbr(2)
pre-let-7 miRNA	1.0	0.03	3.54	0.90	0.51	0.60	0.14	0.48	0.91
<i>let-7</i> miRNA	1.0	0.45	1.36	1.58	1.37	2.02	0.23	1.90	3.80
pre-miR-1003 probe1	1.0	0.12	0.57	0.65	0.32	0.29	0.35	0.06	0.08
pre-miR-1003 lariat	b.d.	b.d.	b.d.	b.d.	b.d.	b.d.	b.d.	0.36	0.57
pre-miR-1003 probe2	1.0	0.10	0.51	0.68	0.36	0.32	0.31	0.03	0.03
miR-1003	1.0	0.92	0.08	0.09	0.81	0.31	0.10	b.d. (<.04)	b.d. (<.04)

Fig. 2d Quantification

	dsRNA							
_	GFP	drosha	dicer-1	loquacious	dicer-2	r2d2	drosha + dicer-1	ldbr(1)
pre-let-7 miRNA	1.0	b.d. (<.05)	4.56	2.19	1.15	1.51	0.15	1.05
<i>let-7</i> miRNA	1.0	0.17	0.85	1.61	1.21	0.41	0.21	0.91
pre-miR-1006 probe1	1.0	0.36	1.37	1.33	0.92	0.73	1.15	0.46
pre-miR-1006 lariat	b.d.	b.d.	b.d.	b.d.	b.d.	b.d.	b.d.	0.18
pre-miR-1006 probe2	1.0	0.34	1.37	1.41	1.10	0.86	1.28	0.53
miR-1006	1.0	0.73	0.14	0.15	0.56	0.31	0.37	0.37

>pCJ19 (pMT-puro\_mir-1006)
actagtAACAACGAATACATCCAGTCGGTGGCCCGGTGCCTGCAGATGATGCTCCGTGTGGATGAGTATCGATTTGCCTTTGTGGGAGTCGACGGAATCAGCACTCTGATCCGTATCTTGTCGAC
CCGTGTCAACTTCCAGGTGAGTTTGAAATTGAAATTGCTAAATTTTTGGTACAATTTTAAATTCGATTTCTTATTCATAGGTGCAATACCAGTTGATCTTTTGCCTGTGGGTGCTGACCTTCAAT AATGCCCAGCGCCTAAACGAAAAGAACTACGAGTTGCTGCGCATCCTCGTCCACCTCCTGGAAACCTCAAAAGATGCCATCATCCTTTCCGTCGCCTGCTTCGACATCGGGGAGTATGTGCGCCA CTATCCCCGCGCCAAGCAgcggccgc

>pCJ20 (pMT-puro\_miR-1003)
actaqtATAAAGCCGATAAGCGTGCGGAAATCGAAAAGACCGAGCGTGAACGACTGCAACAGCAGGAACGCGAGGATGAGATGGCCCTCAAGCTGCCAGAAGGTGGGTATCTGGA  ${\tt TGTGGTTGGCTCTGGCGGTCCTCTCACATTTTACATATTCACAGGCGCCGTGAGCTGCGTCACAAATATGGAACGCCCTCGAGTGGAAAGCTCTCGGACAGCGATGCCGAATCTGTGGCATCCGAAATCTGGACAGCGCCCTCGAGTGGAAAGCTCTCGGACAGCGATGCCGAATCTGTGGCCATCCGAAATCTGGACAGCGCTCTCGAAATCTGGACAGCGCTCTCGAAATCTGGACAGCGCTCTCGAAATCTGGACAGCGCTCTCGAAATCTGGACAGCGCTCTCGAAATCTGGACAGCGCTCTCGAAATCTGGACAGCGCTCTCGAAATCTGGACAGCGCTCTCGAAATCTGGACAGCGCTCTCGAAATCTGGACAGCGCTCTCGAAATCTGGACAGCGCTCTCGAAATCTGGACAGCGCTCTCGAAATCTGGAACGCCCTTCGAGTGGAAATCTGGAAATCTGGAACGCCTTGAGAATCTGGAACGCCTTCTGAAGTGAAATCTGGAACGCCTTCTGAAGTGAAATCTGGAACGCCTTCTGAAGTGAAATCTGGAACGCCTGAATCTGGAACGCCTTCTGAAGTGAAATCTGGAACGCCTTCTGAAGTGAAATCTGGAAATCTGGAAATCTGGAAATCTGGAAATCTGGAAATCTGGAAATCTGGAAATCTGGAAATCTGGAAATCTGGAAATCTGGAAATCTGGAAATCTGGAAATCTGGAAATCTGAAATCTGAAATTGAAATCTGAAATCTGAAATCTGAAATTTGAAATCTGAAATTGAAATTGAAATTGAAATTGAAATTTGAAATTGAAATTGAAATTGAAATTTGAAATTAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTAAATTGAAATTAAATTAAATTGAAATTAAATTAAATTGAAATTAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAATTTAAATTTTAAATTGAAATTGAAATTGAAATTGAAATTTAAATTTAAATTTAAATTGAAATTA$ AAGGACGgcggccgc

ATATĞTAATATGAAAACCATCGATAATAAATCGTAAAACTAAATTAAACTAAATATCCAACGTCATATAAATACAACTCAAAACGTCATAATAAGAAACTGATATGGTATAACAAACTCAAGTT 

>pCJ30 (p2032 miR-1003)

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>pCJ31 (p2032 mir-1006)
ggtaccAACAACGAATACATCCAGTCGGTGGCCCGGTGCCTGCAGATGATGCTCCGTGTGGATGAGTATCGATTTGCCTTTGTGGGAGTCGACGGAATCAGCACTCTGATCCGTATCTTGTCGAC AATGCCCAGCGCCTAAACGAAAAGAACTACGAGTTGCTGCGCATCCTCGTCCACCTCCTGGAAACCTCAAAAGATGCCATCATCCTTTCCGTCGCCTGGCATCGTCGGCAAATGTGCGCCA CTATCCCCGCGGCAAGCAgcggccgc

TTTGCCATCATCGTTTCAACCAAAAACCGAACCAATGATATCCAGAAGATCCTTTAAATACCAAACCACCTAGCAAAAAGGACTACCACCAAGGACCTTTTTTCTCTCTGGCAAATTGAGGTAGTAGGTTATAAGTAGTAATTACAATACCAAATCATACCAATCCAATCCAATCCAATCCCAATCCAATCCAATCCCAATCCCAATCAATC TGGCATTGGTGACATGTGCAAATGTTTGTATGGCTGATTCCCTGAGACCCTAACTTGTGACTTTTAATACCAGTTTCACAAGTTTTGATCTCCGGTATTGGACGCAAACTTGCTGggggccgc

>Drosha dsRNA

GGTCACCAGGCCGGGTTATAAGCCGTGTTCGCTACGCGTTGACCAATTGGACAGGAATAACTCCGATTTGCCCGAGTGCGTAGATCGCGAGACTGGAATCTCACATCCAGCAATCGTGCACTTTGGCATTTTGCATCCTCAGCTAAGCTACGCTAAGCTACGCTAAGCTACGCTAAGCTACGCTAAGCTCAAGCACATGTCGAAGCCCTCTTTCAAGGATAAGCGCAAG AACACATTAGTGAGCATTATGT

CATGCTGGCCACCCTGGAGCAGAGTGTGCTTTGCCAGATCGAGACGGCCAGTGATATTGTCACCGTGTTGCGTTACTGTTCCCGACCGCACGAATACATCGTACAGTGCGCCCCCTTCGAGATGGACGAACTG

>Loguacious dsRNA

ATGGACCAGGAGAATTTCCACGGCTCCAGCTTGCCGCAGCAGCTACAGAACCTCCACATCCAGCCGCAGCAGCAGCCCCCAATCCTGTCCAGACGGGATTTGCTCCACGCGGGCACTATAATAA  ${\tt CCTTGTCGGCCTGGGCAATGGAAATGCCGTCAGTGGTAGTCCGGTGAAGGGTGCTCCGCTGGGGCAGCGCCATGTGAAGCTCAAGAAGGAGAAGATATCCGCCCAGGTTGCGCAGCTGTCTCAGC$ 

AAAGTTCAACGCGAAGACCAAGGCTAAGATGAAAGTTATTTTGATTCCGGAGCTATGCTTCAATTTTAACTTTCCTGGGGATTTATGATCTTAAGTTTGATCCTACCCAGCATTTTAAACCGCA  ${\tt CGGAATGTCGACCCCTTGGGCAATGTCATACCAACTGAGGATATCGAGGAGCCGAAATCCCTTTTAGAGCCAATGCCCACAAAGTCCATTGAGGCGTCCGTGGCCAATCTTGAAATAACAGAATT$ TGGATTTTGAAGATAAGGAATACTGGGCAAAAAATCAGT

>R2D2 dsRNA

AGGCATTGCGCAGAAAGAAATTTACCA

>CG7942[1] (Debranching enzyme) dsRNA

GTGGCGAGCTGGTAGCACCAGTGCTGACCATATTCATTGGCGGCAACCATGAGGCCTCCAATTACCTGCAGGAGCTCCCATACGGCGGTTGGGTGGCTCCAAATATTTACTACCTTGGTTATGCC CCGCACAATCACAGCCAGAAGCTAGGAGATGCTGAATC

>CG7942[2] (Debranching enzyme)

TGCTTAGTTTTGTTGGCGAATGGCCTAGATCTGCCTGC

>GFP dsRNA

GATCACATGGTCCTGCTGGAGTTCGTGACCGCCGGGGATCACTCTCGGCATGGACGAGCTGTACAAGTAAAGCGGCCGCGACTCTAGATCATAATCAGCCATACCACATTTGTAGAGGTTTTA

>UTR insert CG11094

>UTR insert CG11094-mutant

>UTR insert CG1849

>UTR insert CG1849-mutant

>UTR insert CG5166a

>UTR insert CG5166a-mutant

>UTR insert CG6551

actagtTGATATCCACCCGATTCAAACCACAGCATCAGCATCCGCATCTATATTCGCATCAGCAACAGGAAACCTCTTGCCATGCTACCACACATCTGAGGACACTGATTTGTTAGCTCAAGAC
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AGATTTAAAAAATATCAATTAGTTTTTATGGAAATATGTTTCAATCGTAATAGGCATTTAAAAAAACATTTTACCCTAATTGAGTTTTTAAATCTCCAGAGGATTTCAACGCACCAATATTTTG
TACACCAACACCACATTGTTAAAATTTAAATTTTCACTCGAATTTCAAGTATTTTTTGTCATAAAAAATTATTTTTGTGTAAATCTCGgcggccgc

>UTR insert CG6551-mutant

actagtTGATATCCACCCGATTCAAACCACAGCATCAGCATCCGCATCTATATTCGCATCAGCAACAGGAAACCTCTTGCCATGCTACCACACATCTGAGGACACTGATTTGTTAGCTCAAGAC
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