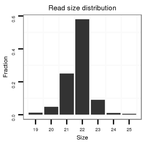
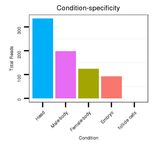
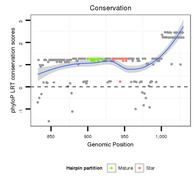
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:
der_1518	**scaffold_944:882-980 +**	**candidate-rescued**	**Canonical miRNA**	**intergenic**
				[View on UCSC Genome Browser (Cornell Mirror)]

Legend: [redacted] [redacted] [redacted] [redacted] [redacted]

Predicted structure







Show Alternate Folds

Flybase annotation

dRNA:Dsor1:RNRNA:G42941-RA]

No Repeatible elements found

mature	star
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Sense Strand Reads

Hide 3p reads Show mid mismatch reads

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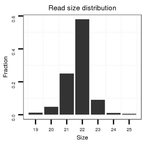
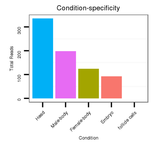
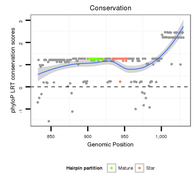
Legend: [redacted] [redacted] [redacted] [redacted] [redacted]

Predicted structure







Show Alternate Folds

Flybase annotation

dRNA:Dsor1:RNRNA:G42941-RA]

No Repeatible elements found

mature	star
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Sense Strand Reads

Hide 3p reads Show mid mismatch reads

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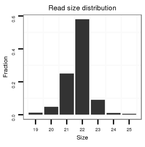
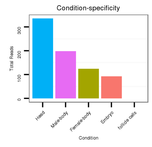
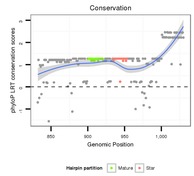
				[View on UCSC Genome Browser (Cornell Mirror)]

Legend: [redacted] [redacted] [redacted] [redacted] [redacted]

Predicted structure







Show Alternate Folds

Flybase annotation

dRNA:Dsor1:RNRNA:G42941-RA]

No Repeatible elements found

mature	star
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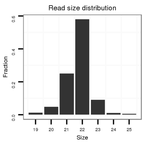
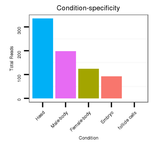
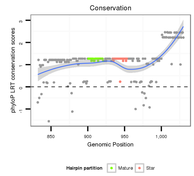
				[View on UCSC Genome Browser (Cornell Mirror)]

Legend: [redacted] [redacted] [redacted] [redacted] [redacted]

Predicted structure







Show Alternate Folds

Flybase annotation

dRNA:Dsor1:RNRNA:G42941-RA]

No Repeatible elements found

mature	star
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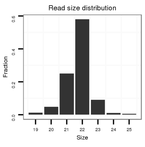
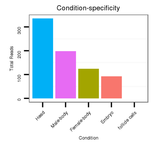
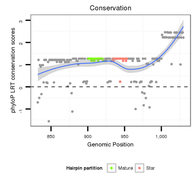
Predicted structure







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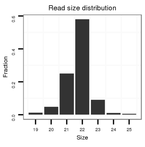

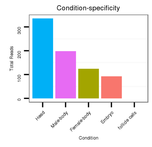

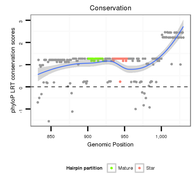

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No Repeatible elements found

mature	star
1. scaffold_667393:4-44 ; 2. der_1518 scaffold_944:901-922 ; 3. scaffold_946:788-830 ; 4. scaffold_944:882-980 ; 5. scaffold_994:251-314 ; 6. scaffold_1034:431-452 ; 7. scaffold_1181:545-561 ; 8. scaffold_1184:601-718 ; 9. scaffold_1187:1-1000 ; 10. scaffold_1352:872-2882 ; 11. scaffold_2038:332-353 ; 12. scaffold_2042:1-1000 ; 13. scaffold_3663:2256-2303 ; 14. scaffold_3613:357-378 ; 15. scaffold_3844:898-919 ; 16. scaffold_4652:589-608 ; 17. scaffold_4700:1-1000 ; 18. scaffold_4723:6004-6023 ; 19. scaffold_4835:67-638 ; 20. scaffold_4878:1-1000 ; 21. scaffold_4894:1-1000 ; 22. scaffold_5009:601-1012 ; 23. scaffold_4939:17901-17922 ; 24. scaffold_7118:921-1015 ; 25. scaffold_7120:1-1000 ; 26. scaffold_963:223-246 ; 27. scaffold_963:323-344 ; 28. scaffold_967:663-686 ; 29. scaffold_1024:644-665 ; 30. scaffold_1107:1-1000 ; 31. scaffold_1109:889-1112 ; 32. scaffold_1183:638-658 ; 33. scaffold_1184:1-1000 ; 34. scaffold_1185:621-651 ; 35. scaffold_1184:600-622 ; 36. scaffold_1126:570-591 ; 37. scaffold_3305:447-468 ; 38. scaffold_3304:1-1000 ; 39. scaffold_4288:791-812 ; 40. scaffold_4723:8035-8074 ; 41. scaffold_4702:8076-8097 ; 42. scaffold_4703:6639-6660 ;	1. der_1518 scaffold_944:934-955 ; 2. scaffold_946:831-852 ; 3. scaffold_946:788-830 ; 4. scaffold_944:901-922 ; 5. scaffold_994:314-334 ; 6. scaffold_1034:375-396 ; 7. scaffold_1181:528-547 ; 8. scaffold_1185:963-1000 ; 9. scaffold_1187:1-118 ; 10. scaffold_2044:86-107 ; 11. scaffold_2990:524-1543 ; 12. scaffold_2990:1-523 ; 13. scaffold_4005:64-87 ; 14. scaffold_4013:522-563 ; 15. scaffold_4723:6053-6078 ; 16. der_16 scaffold_4738:5963-5984? ; 17. scaffold_4835:638-659 ; 18. scaffold_4939:12285-12308 ; 19. scaffold_4939:17924-17943 ; 20. scaffold_4925:1093-1114 ; 21. scaffold_16:3190-413 ;

Sense Strand Reads

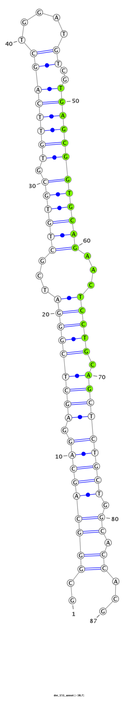
Hide 3p reads Show mid mismatch reads

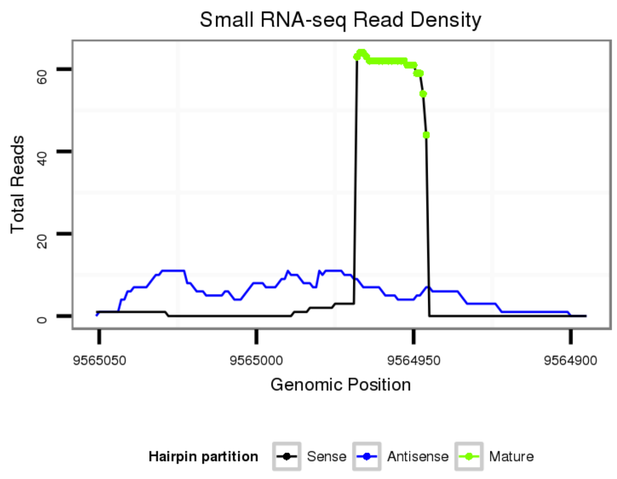
```
ATATGATACATATGTCTTATGTAAACTAAGACATTTCGACATTTATTTTAGTATAAAATACATTTATTGAAGGAATTGATATGTGCATAAAATACATTTGAAAAAAAAAAATTGACATTATATAAAAATGATATTATAAAACTCTAACGCGTGGATCACTCGGCTCATGGGTCGATG
****************************************((((((
```

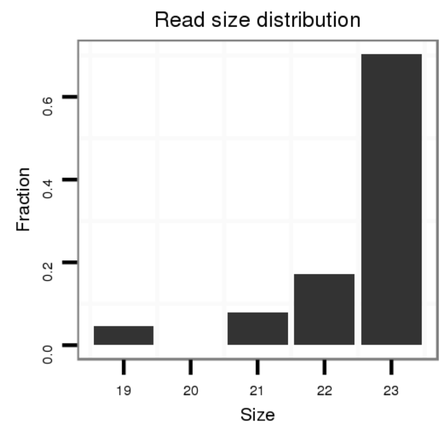
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
der_151	**scaffold_4820:9564945-9565001 -**	**candidate-rescued**	**Canonical miRNA**	**antisense_to_CDS**	[View on UCSC Genome Browser {Cornell Mirror}]

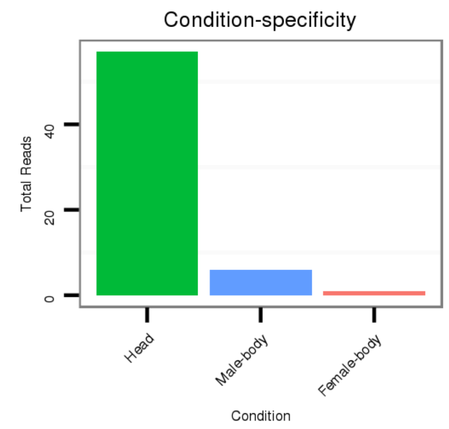
Legend: mature star mismatch in alignment mismatch in read

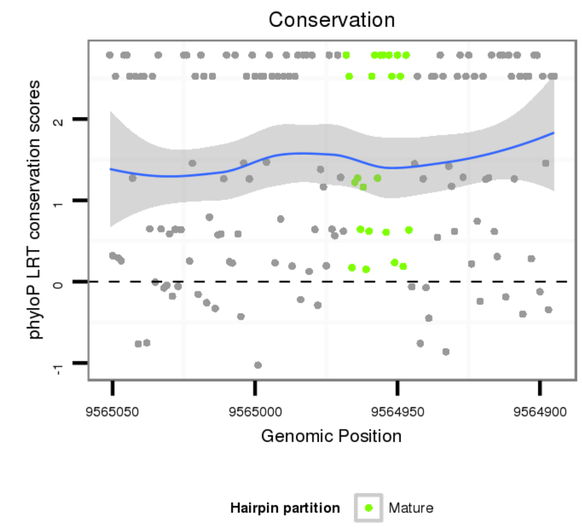
Predicted structure











Show Alternate Folds

Flybase annnotation

Antisense to CDS [Dere\GG12498-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TTGTGTAGCCAGGGGCCAGTCCGTCGAACTGCTCCGCGGGCAGCAGGAGCTCGGGATCGCTGTGCGTGTTCAGCTGGATGTCGTGAGCGGTGCAGAACTCCTGCAGCTCTGCTGGCACCACGCAGCACGTGGACAGGTTGACCTGGGCAATTGTGGG **********..(((((((((.(((((((((...((((((.(((((((.....)).)).))))))))))))...)))))).)))))))))).)).))...**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V108 head	V060 head	V107 male body	M055 female body	V040 embryo
...TGAGCGGTGCAGAACTCCTGCAG...	23	0	1	43.00	43	32	7	4	0	0
...TGAGCGGTGCAGAACTCCTGCA...	22	0	1	10.00	10	8	1	1	0	0
...TGAGCGGTGCAGAACTCCTGC...	21	0	1	5.00	5	5	0	0	0	0
...TGAGCGGTGCAGAACTCCTT...	20	1	1	2.00	2	2	0	0	0	0
...TGAGCGGTGCAGAACTCCT...	19	0	1	2.00	2	2	0	0	0	0
...TGAGCGGTGCAGAACTCCTGCAGT...	24	1	1	2.00	2	2	0	0	0	0
...GTGTTCAGCTGGATGTCGTT...	20	1	1	1.00	1	0	0	0	1	0
...GAGCGGTGCAGAACTCCTGCAG...	22	0	1	1.00	1	0	1	0	0	0
TTGTGTAGCCAGGGGCCAGTCCG...	23	0	1	1.00	1	0	1	0	0	0
...GCAGCAGGAGCTCGGGATT...	19	1	1	1.00	1	1	0	0	0	0
...TGAGCGGTGCAGAACTCCTGCAT...	23	1	1	1.00	1	1	0	0	0	0
...TTCAGCTGGATGTCGTGAG...	19	0	1	1.00	1	1	0	0	0	0
...TGAGCGGTGCAGAACTCCTGCCT...	23	2	1	1.00	1	1	0	0	0	0
...GATGTCGTGAGCGGTGCAGAACT...	23	0	1	1.00	1	0	0	1	0	0
...GCGTGTTCAGCTGGATGTCGTGA...	23	0	1	1.00	1	0	0	0	1	0
...GTGAGCGGTGCAGAACTCCTT...	21	1	1	1.00	1	1	0	0	0	0

Anti-sense strand reads

AACACATCGGTCCCCGGTCAGGCAGCTTGACGAGGCGCCCGTCGTCCTCGAGCCCTAGCGACACGCACAAGTCGACCTACAGCACTCGCCACGTCTTGAGGACGTCGAGACGACCGTGGTGCGTCGTGCACCTGTCCAACTGGACCCGTTAACACCC **********..(((((((((.(((((((((...((((((.(((((((.....)).)).))))))))))))...)))))).)))))))))).)).))...**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M055 female body	M057 embryo	V107 male body	V108 head	V040 embryo
...GGTCCCCGGTCAGGCAGCTTG...	21	0	1	3.00	3	0	1	1	0	1
...TCGACCTACAGCACTCGCCACG...	22	0	1	2.00	2	1	0	1	0	0
...TCCCCGGTCAGGCAGCTTGAC...	21	0	1	1.00	1	1	0	0	0	0
...TCGAGCCCTAGCGACACGC...	19	0	1	1.00	1	0	0	0	1	0
...ACGAGGCGCCCGTCGTCCTCGAGCC...	25	0	1	1.00	1	1	0	0	0	0
...GCAGCTTGACGAGGCGCCCGT...	21	0	1	1.00	1	1	0	0	0	0
...CTTGAGGACGTCGAGACGACCGT...	23	0	1	1.00	1	1	0	0	0	0
...CGTCGAGACGACCGTGGTGCGTCGTGC...	27	0	1	1.00	1	0	0	0	0	1
...CAGGCAGCTTGACGAGGCGCCCGTC...	25	0	1	1.00	1	0	0	1	0	0
...AGCCCTAGCGACACGCACA...	19	0	1	1.00	1	0	0	0	0	1
...TCGACCTACAGCACTCGCCAC...	21	0	1	1.00	1	0	0	1	0	0
...TCGACCTACAGCACTCGCCACGTCT...	25	0	1	1.00	1	0	0	1	0	0
...CCCGGTCAGGCAGCTTGACG...	20	0	1	1.00	1	1	0	0	0	0
...TCCCCGGTCAGGCAGCTTG...	19	0	1	1.00	1	0	0	1	0	0
...GACCTACAGCACTCGCCACGT...	21	0	1	1.00	1	0	0	0	1	0
...CACGCACAAGTCGACCTA...	18	0	1	1.00	1	0	0	0	1	0
...TCTTGAGGACGTCGAGACGACCGTG...	25	0	1	1.00	1	1	0	0	0	0
...TCGTCCTCGAGCCCTAGCGACACG...	24	0	1	1.00	1	1	0	0	0	0
...TCAGGCAGCTTGACGAGG...	18	0	1	1.00	1	0	0	1	0	0
...ACGAGGCGCCCGTCGTCCTCGAGCCCTAG...	29	0	1	1.00	1	1	0	0	0	0
...TCGCCACGTCTTGAGGACGTCG...	22	0	1	1.00	1	0	1	0	0	0
...TCTTGAGGACGTCGAGACGACCG...	23	0	1	1.00	1	0	0	0	1	0
...CGACACGCACAAGTCGACCTACAG...	24	0	1	1.00	1	0	1	0	0	0
...TCGACCTACAGCACTCGCCA...	20	0	1	1.00	1	0	0	1	0	0
...CGACACGCACAAGTCGACCTACAGCAC...	27	0	1	1.00	1	0	1	0	0	0
...CCTGTCCAACTGGACCCGTTA...	21	0	1	1.00	1	1	0	0	0	0
...GACACGCACAAGTCGACCTACAGCAC...	26	0	1	1.00	1	1	0	0	0	0
...GAGCCCTAGCGACACGCACAAG...	22	0	1	1.00	1	0	0	0	0	1
...CGAGACGACCGTGGTGCGTCGTGCA...	25	0	1	1.00	1	0	1	0	0	0
...CGTCCTCGAGCCCTAGCGAC...	20	0	1	1.00	1	0	1	0	0	0
...TCGAGACGACCGTGGTGCGTCGTG...	24	0	1	1.00	1	0	0	0	1	0
...CACGCACAAGTCGACCTACAGCA...	23	0	1	1.00	1	0	0	1	0	0
.ACACATCGGTCCCCGGTCAGGCAGCTTG...	28	0	1	1.00	1	0	0	1	0	0
...CGAGCCCTAGCGACACGCACAAGT...	24	0	1	1.00	1	0	0	0	1	0
...AGGCAGCTTGACGAGGCGCCCGTCG...	25	0	1	1.00	1	0	1	0	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droEre2	scaffold_4820:9564895-9565051 -	der_151	TTGTGTAGCCAGGGGCCAGTCCGTCGAACTGCTCCGCGGGCAGCAGGAGCTCGGGATCGCTGTGCGTGTTCAGCTGGATGTCGTGAGCGGTGCAGAACTCCTGCAGCTCTGCTGGCACCACGCAGCACGTGGACAGGTTGACCTGGGCAATTGTGGG
droYak3	3R:19361802-19361958 +		TTGTGTAGCCTGGGGCCAGTCCGTCGAACTGCTCTGCCGGCAGCAGGAGCTCGGGATCGCTGTGCGTGTTCAGCTGGATGTCATGAGCGGTGCAGAACTCCTGCACTTCCCGTGGCACCACGCAGCAAGTGGACAGGTTGACCTGGGCAATCGTGGG
droSec2	scaffold_0:18869132-18869288 +		TTGTGTAGCCAGGGACCAGTCCGTCGAACTGCTCCACGGGCAGCAGGAGCTCGGGATCGCTGTGCGTATTCAGCTGGATGTAGTGAGCGGTGCAGAATTCCTGCAGTTCTGGTGGCACCACGCAACACGTAGACAGGTTGACCTGGGCAATTGTGGG
droSim2	3r:18036605-18036761 +	dsi_32439	TTGTGTAGCCAGGGACCAGTCCGTCGAACTGCTCCACGGGCAGCAGGAGCTCGGGATCGCTGTGCGTATTCAGCTGGATGTCGTGAGCGGTGCAGAATTCCTGCAGTTCTGGTGGCACCACGCAGCACGTTGACAGGTTGACCTGGGCAATTGTGGG
dm3	chr3R:18511310-18511466 +	dme_378	TTGTGTAGCCAGGGACCAGTCCGTCGAACTGCTCCACGGGCAGCAGGAGCTCGGGATCGCTGTGCGTGTTCAGTTGGATGTCGTGAGCGGTGCAGAACTCCTGCAGTTCTGGTGGCACCACGCAGCACGTAGACAGGTTGACCTGGGCAATTGTGGG
droEug1	scf7180000409768:648693-648849 +		TTGTATAGCCCGGCGCCAGTCCGGCGAATTGCTCCTCGGACAGCAGAAGCTGAGGATCGCTGTGCGTGTTCAGTTGAATATCGTGCGCGGTGCAGAACTCCTGCAGTTCCGGTGGCACCACGCAGCAGGTTGATAGATTGACCTGTGCAATTGTCGG
droBia1	scf7180000302402:5202361-5202517 -		TTGTGTAGCCGGGCGCCAGCGCGGAGAACTGCTCTTCGGGCAGCAGGAGCTCGGGATCGCTGTGCGTGTTCAGCTGGATGTCGTGCGCGGTGCAGAACTCTTGCAGTTCCGGTGGCACAACGCAGCAGGTGGACAGGTTGACCTGGGCAATCGTGGG
droTak1	scf7180000415711:493750-493906 -		TTGTGTAGCCCGGCGCCAAACCGGCGAACTGCTCCTCGGGCAGCAGGAGCTCCGGATCGCTGTGCGTGTTCAGCTGGATGTCGTGCGCGGTGCAGAACTCCTGCAGTTCCGGCGCACCACGCAGCAGGTGGACAGGTTGACCTGGGCAATCGTGGG
droEle1	scf7180000491017:201737-201893 +		TGGAGTAGTCCGGCGCCAGTGCGGCGAACTGCTCCTCGGGCAGCAGGAGCTCGGGATCGCTGTGTGTGTTCAGCTGGATGTCGTGCGCGGTACAGAACTCCTGCAGATCCGCGGGCACCACGCAGCAGGTGGACAGATTGACCTGGGCAATCGTGGG
droRho1	scf7180000777285:111046-111202 -		TTGAGTAGCCCGGCGCAAGTGCTTCGAACTGCTCCTCGGGCAGCAGAAGCTCGGGATCGCTGTGCGTATTCAGTTGGATGTCGTGCGTGGTGCAGAACTCCTGCAGTTCAGCTGGCACAACGCAGCAGGTAGACAGATTGACCTGGGCAATCGTGGG
droFic1	scf7180000454055:315112-315268 -		TTGTGTAGCCCGGTGCTAGTTCGCGAACTGTTCTTCGGGCAGCAGCAGCTCGGGATCGCTGTGCGTGTTCAGCTGGATGTCGTGCGCGGCGCAGAACTCCTGCAGTTCCGGTGGCACCACGCAGCAGGTGGACAGGTTGACCTGGGCGATTGTGGG
droKik1	scf7180000302697:1062039-1062195 +		TTGTGTAGCCGGCGCCAGTCCGGCGAACTGTTCCTCGGGCAGCAGCAGCTCCGGGCTCGCTGTGCGTATTCAGCTGGATGTCGTGCGCGGCGCAAAACTCCTGCAGCTCCGCGGGCACCACGCAGCAGGTGGACAGATTCACCTGGGCAATCGTTGG
droAna3	scaffold_13340:8113587-8113743 -		TAGTGTAGCCAGGTGCCAGTCCAGAGAACTGCTCCTCCTGCAATAGCTGCTCCGGATCGCTGTGCGTGTTCAACTGGATGTCGTGCGCAGCGCAGAACTCCTGAAGCTCCGCCGGCACCACGCAGCAGGTGGACAAATTGACCTGTGCAATCGTAGG
droBip1	scf7180000396708:734184-734340 +		TAGAGTAGCCGGGTGCCAGTCCAGAGAACTGCTCCTCCTGCAATAGCTGCTCCGGATCGCTGTGCGTGTTCAACTGGATGTCGTGCGCAGCGCAGAACTCCTGAAGCTCCGCGCGGCACCACACACAGCAGGTGGACAGATTGACCTGGGCAATCGTAGG
dp5	2:12583687-12583843 +		TTGTGTAGCCGGCCGCCAGCCCAGAAAACTGTTCCTCCGGCAGCAGCAGCTCGGGATCGCCGTGTGTGTTCAGCTGGATGTCGTGCGCGGCACAGAACTCTTGCAGCTCCGTGGGCACACGCGCAGCAGGTGGACAGATTAACCTGCGCAATCGTGGG
droPer2	scaffold_0:7883586-7883742 -		TTGTGTAGCCAGGCGCGAGCCCAGAAAACTGTTCCTCCGGCAGCAGCAGCTCGGGATCGCCGTGTGTGTTTAGCTGGATGTCGTGCGCGCACAGAACTCTTGCAGCTCCGTGGGCACACGCGCAGCAGGTAGACAGATTAACCTGCGCAATCGTGGG
droWil2	scf2_1100000004902:6180367-6180523 -		TTGTGTAGCCGGGAACCAGCCCAGCGAATTGCTCCTCCTGCAATATGAGCTCCGGATCTCCGTGAGTATTCAACTGTATGTCGTGCGCGGTACAGAACTCCTGTAATTCGGCGGGCACCACGCAGCAGGTGGCCAAATTGACCTGTGCAATCGTAGG
droVir3	scaffold_12855:2361457-2361613 -		TCGAGTAGCCGGGTGCTAGCCAGCGAACTGTTCCTCGGGCAGCAGCAGCTCGGGATCACTGTGTGTGTTCAGCACCAGCTCATGCTCGCGACAGAATTCCTGCACTACAGCGGGCACCACGCAGCAAGCGGCCAGATTCACCTGTGCTATCGTGGG
droMoj3	scaffold_6540:34091892-34092048 +		TTGTATAGCCGGGGGCCAAGCATGCAAATTGCTCTTCAGCTAAAAGAAGCTCCGGATCGCTGTGTGTATTAAGTACCAACTCATGATCGCGACAGAATTCATGCAGTTCGGCTGGTACTACGCAGCAGGTGGCCAGATTTACCTGCGCTATCGTGGG
droGri2	scaffold_15074:2369168-2369324 -		TTGTATAGCCGGCGCCAGGAAGGAGAACCGTTCCTCGGGCAGCAACAGTTCGGGATCACTGTGTGTGTTCAGGACCAGCTCATGATCACGACAGAATTCCTGCAATTCCACGGGGACCACACAGCAGGCGGCCAGATTCACTTGTGCGATGGATGG

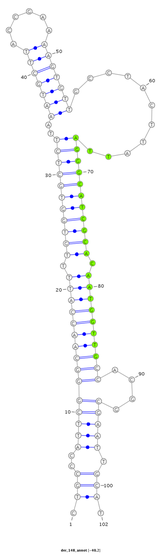
Generated: 09/08/2015 at 07:43 PM

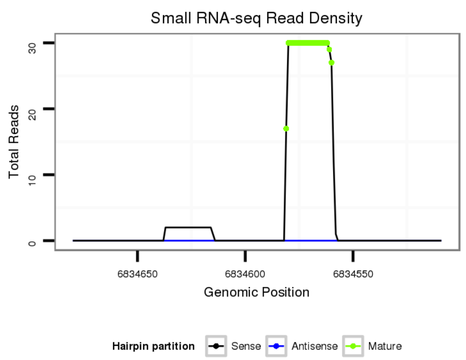
	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	1
rescue.candidate	2

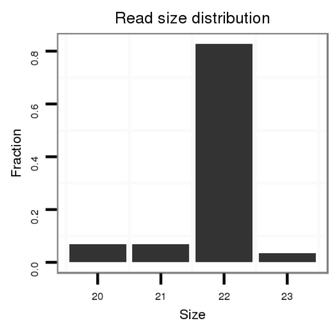
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
der_148	**scaffold_4770:6834559-6834630 -**	**candidate-rescued**	**Canonical miRNA**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

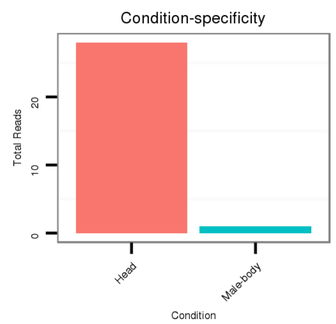
Legend: mature star mismatch in alignment mismatch in read

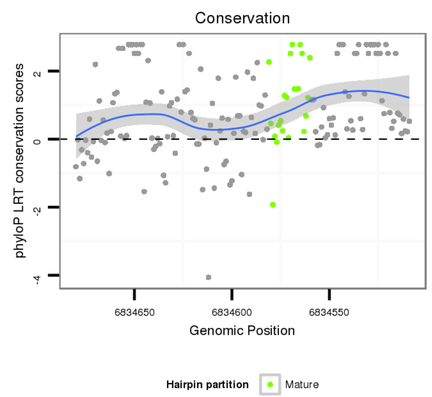
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dere\GG23097-in]; utr5 [utr5_plus_11278]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

TCTATAATGTACACACCATGTTTGTTGTTTCAGTTCTGCCCATTCGGGCAACCATTTTGTGGTGCTCTTAAATGCTTACCGAAAAGTGTTGCCTACTTATTAGGGCATCGCACAATGGTTGCCACGGCGAATTGCATTCGTCAGCTAATTGTATGTGCTTGAACCAACCTAT **********.(((..((((((((((((((.((((((((((..((((((.....)))))).....))))))))))).))))))))))....)))))..))).**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V108 head	V060 head	V107 male body
.....TTAGGGCATCGCACAATGGTTG.....	22	0	1	14.00	14	13	0	1
.....TAGGGCATCGCACAATGGTTGC.....	22	0	1	10.00	10	9	1	0
.....TTAGGGCATCGCACAATGGTTGC.....	23	0	1	1.00	1	1	0	0
.....TTAGGGCATCGCACAATGGTTG.....	20	0	1	1.00	1	1	0	0
.....TCGGGCAACCATTTTGTGGTGC.....	22	0	1	1.00	1	1	0	0
.....TTAGGGCATCGCACAATGGTTGT.....	23	1	1	1.00	1	1	0	0
.....TCGGGCAACCATTTTGTGGTGCT.....	23	0	1	1.00	1	1	0	0
.....TAGGGCATCGCACAATGGTT.....	20	0	1	1.00	1	1	0	0
.....TAGGGCATCGCACAATGGTTGCT.....	23	1	1	1.00	1	1	0	0
.....TTAGGGCATCGCACAATGGTT.....	21	0	1	1.00	1	1	0	0
.....TAGGGCATCGCACAATGGTTGCC.....	23	0	1	1.00	1	1	0	0
.....TAGGGCATCGCACAATGGTTG.....	21	0	1	1.00	1	1	0	0

Anti-sense strand reads

AGATATTACATGTGTGGTACAAACAACAAAGTCAAGACGGGTAAGCCCGTTGGTAAAACACCACGAGAATTTACGAATGGCTTTTCACAACGGATGAATAATCCCGTAGCGTGTTACCAACGGTGCCGCTTAACGTAAGCAGTCGATTAACATACACGAACTTGGTTGGATA **********.(((..((((((((((((((.((((((((((..((((((.....)))))).....))))))))))).))))))))))....)))))..))).**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V040 embryo	M057 embryo	M055 female body	V107 male body	GSM1528801 follicle cells	V108 head

Show Alignment With Reads

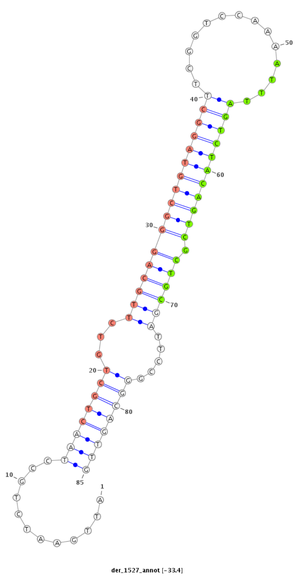
Re-alignment of all predicted orthologs

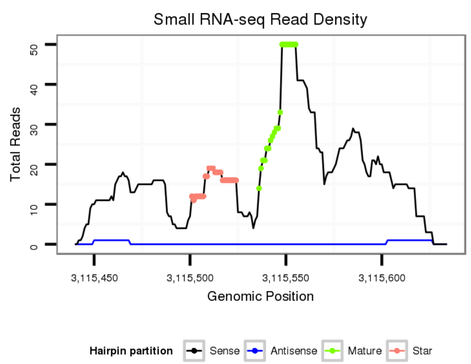
Species	Coordinate	ID	Alignment
droEre2	scaffold_4770:6834509-6834680 -	der_148	TCTATAA-----TG-----T-ACACACCATGTTT----GTTGTTTCAGTTCT-GCC-----CAT---TC----------GGGCAACCATTTTGT---------GGTGCTC---TTAAA----------TGCTTACCG-AAAAGTGTTGCCTACTTA--TTAGGGCATC--GC-ACAATGGTTGCC----------ACGG-CGAATTGCATTCGTCAGCTAATTGTATGTGCTTGAA-CCAA---CCTAT
droYak3	3R:3477220-3477391 +		TCTATAA-----TG-----T-AACACATATGTTT----GTTGTTTCAGTTCT-GCC-----CAT---TC----------CGGCAACCATTTTGT---------GGTGCTC---CAAAA----------TGCTTACTG-AAAAGTGTTGCCTACTTA--TTCGGGCATC--AC-AAAGTGGTTGCA----------ACGG-CGAATAGCATTCGTCAGCTAATTGTATGTGCTTGAA-CCAA---CCTAT
droSec2	scaffold_166:24903-25075 -	dse_137	TCTATAA-----TG-----TACACAACATATGTTT----GTTGTTTCAGTTCT-GCC-----CAG---CC----------CGGCAGCCATTTTGT---------GATGCTC---CAAAA----------TGCTCACCA-AAAAGTGTAGCATACATA--TTCGGGCATC--AC-AAAATGCTGCC----------ACGG-CGAATAGCATTTGTCAGCTAATTGTATGTGCTTGAA-CCCA---CCTAT
droSim2	3r:6460768-6460997 -		TCTATAA-----TG-----TACACAACATATGTTT----GTTGTTTCAGTTCT-GCC-----CAG---CC----------CGGCAGCCATTTTGT---------GATGGCC---TCAAATCCACGTCTTACTAACATCAGCTGTGAATCATAGCACCGCCGATGGTAGT-CGT-ATGCGCTCGATG-AAAAGTGTAGCCTACTTA--TTCGGGCATC--AC-AAAATGCTGCC----------ACGG-CGAATAGCATTTGTCAGCTAATTGTATGTGCTTGAA-CCCA---CCTAT
dm3	chr3R:14796588-14796767 +		TCTATAA-----TG-----TACACAACATATGTTT----AT-GTTTCAGTTCT-GCC-----CAG---CC----------TGGCAGCCATTTTGT---------GATGCTC---TTCGGA----------GCATCA--TGCTCACCG-AAAAGTGTAGCCTACTTA--TTAGGGCATC--AC-AAAATGCTGCC----------ACGG-CAAATAGCATTTGTCAGCTAATTGTATGTGCTTGAA-CCCA---CCTAT
droEug1	scf7180000409804:1035962-1036141 +		ACTTAA------TA-----T-ACACAAATGTTT----GTGGTTTCAGTTTTGCCTTTTTC----CC----------CCA---ACATGCACTCATTTTGC---------GGTGCCC---CAAAA----------GTTTCAC-T-AAAAGTGTTGCCTACTTA--TTAGGGCGCC--GC-AATATCTTTGCC----------ATAT-CGAATAACATTTATCAGCTAATTGTATGTGCTTGTA-CCAA---ACTAT
droBia1	scf7180000302402:546610-546791 +		CCTTAG------TA-----G-ACACAATCCGTTT----GTGGTTTCAGTTCT-GCC-----TAT---CC-CA--------TAA---GCGGGCAAACAGTTTGT---------GGCGCCC---CAAGG----------GGGTTTCTCCA-AAAGGCGTCGCCTACTTA--TTCGGGCGCC--AC-AAAATGGTTGCC----------CTGG-CGAATAGCATTTATCGCTAATTGTATGTGCTTGAA-CCAA---CCTAT
droTak1	scf7180000415256:289346-289524 +		TCCATAG------TA-----T-ACACAATCTGTTT----GTGGTTTCAGTTATGCCTTTGTCTATT---CC----------CGGCAAACATTTTGT---------GGTGCTT---CAAAG----------GCCTTAGAA-AAAAATGTGGCCTACTTA--TAAGGGCGCC--AC-AAAATGGTTGCC----------ATAG-CGAATAGCATTTATCAGCTAATTGTATGTGCTTGAT-CCAA---CCTAT
droEle1	scf7180000490994:547708-547881 +		TTCTCAG------TA-----T-ACACAATATGTTT----GTGGTTTCAGTTCT-GCC-----TTTTACT----------CGGCAAACATTTTGT---------GGTGCTC---TAAAT----------GTTTCAC-A-AAAAGTGTGGCCTACTTA--TTAGGGCGCC--CC-AAAATGGTTGCC----------ATAG-CGAATAGCATTTATCAGCTAATTGTATGTGCTTGAA-CCAA---CCTAT
droRho1	scf7180000779900:443440-443610 +		TCCTTAG------TA-----T-ACACAATATGTTT----GTGGTTTCAGTTCT-GCC-----TAT---CC----------CGGCAAACATTTTGT---------GGTGCTC---TAAAG----------GGTACAC-A-AAAATGTGGCCTACTTA--TTAGGGCGCC--CC-AAAATGGTTGCC----------ATAG-CGAATAGCATTTATCAGCTAATTGTATGTGCTTGAA-CCAA---CCTAT
droFic1	scf7180000453812:245395-245569 -		ACTTTAT------TG-----T-AACACATTTGTATT----GTGGTTTCAGTTATGCC-----AATCCCC----------CCGCAAACATTTTGT---------GGTGCCC---TAAAA----------GGTTCTTTTAAAAATGTTGCCTACTTA--TTCTGGCGCC--AC-AAAATCTTTGCC----------AAAG-CGAATAGCATTTATCAGCTAATTGTATGTGCTTGAA-CCAA---CCTTT
droKik1	scf7180000302256:208647-208785 -		TCCATAA------CC-----A-ACACAATGTTT----GTGGTTTCAGTTCT-GCC-----CC---CC----------CC-------AATTTGTTGAGTTTTGCGGTTACCC---GAAAA----------GGTTC----T----TTATGTCCTACTTA---TTGGGGCCC--CC-AAAATGGT----------CC----C----ACGATTTATTGCTAATTGTATGTGCTTGAA-CCCA---CCTAT
droAna3	scaffold_12911:3159704-3159893 +		ATTGTTC------TCT---AGCAAATATTCGTTT----GTGGTTTCAGTTGTTGACTATGT----CC---TA--------CATTTGCAAAACGAACATTTTGT---------GGCACCT---CCAAG----------CGTGAAGAGTTTGCCG-AAAAATATTGCCTACTA---TTTGAGCGCC--AC-AAAATGGTTGTC----------CTTG-CGAATAGCATTTAAAAGCTAATTGTATGTGCTTGAA-CCAA---CCCCAT
droBip1	scf7180000396640:34486-34666 +		TCTAAAA------CC-----A-CAATGTTCGTTT----GTGGTTTCAGTTGTTGAAATTGT----CC---TA--------CAAACGCATCAACAACCATTTTGT---------GGCCCCATCCATTCAAA----------A-----AATGTTGGCCG-AAAAGCATTGCCTACTA---TTTGAGCGCC--AC-AAAATGGTTGTC----------CTTG-CGAATAGCATTTCGAAAGCTAATTGTATGTGCTTGAA-CCAA---CCCCAT
dp5	2:14915948-14916138 +		TCCACCA------CTAACTGCAATCCCTGTTTTATCAATCATTTCAGTTGTGGCCCCTGCTCCTGTGACCCCCGTCCCCCTCCCCAGGGCAACCATTTTGC---------GCGCTCCCC----CC----------CGTCCCCCGCAAAGTGTAGCATACGTTCTTGGGGCGCACACTAAAATGGTTGCC----------ACAG-CGTAAAGCATTTAAACAGCTAATTTGTATGTGCTTGCGTACAA---CCTTT
droWil2	scaf2_1100000004921:3063650-3063829 +		CCAAACAGCATAATCCCCCATCCCCC

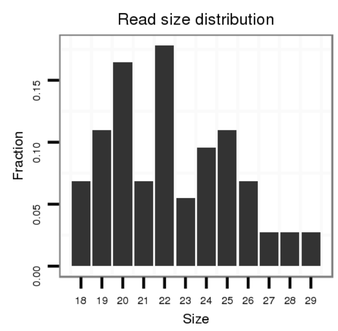
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
der_1527	**scaffold_4929:3115490-3115584 +**	**candidate-rescued**	**Canonical miRNA**	**3pUTR**	[View on UCSC Genome Browser (Cornell Mirror)]

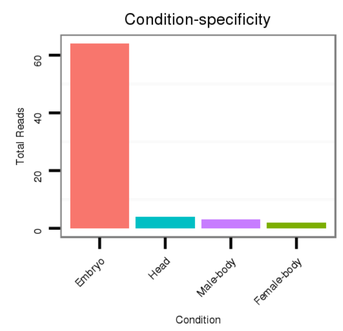
Legend: mature star mismatch in alignment mismatch in read

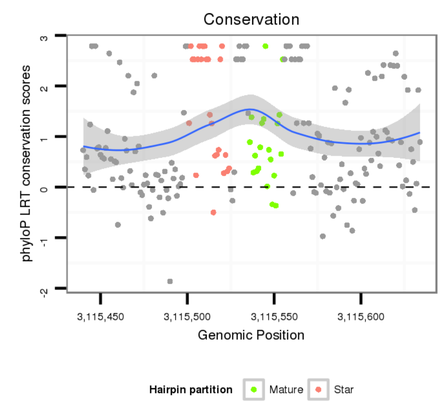
Predicted structure











Show Alternate Folds

Flybase annnotation

utr3 [utr3_plus_232]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

ATCCCAGTTACGCACAGCTAGAAGAGATCGGATTGGCGTCAATCGGATTGAATCTGCCTAACTGCTGTCTTGCAGGGCTGTAGGCTTCGGTCCAAAATTTAGTCTACAGTCGCTGCGATTCCGGGCAGTTGAAAGGATGCAAGATGAGAGGCCCAGTCCATGACACTTAACGCTTTGTGCACCGTACATTTTCAG	Read size	# Mismatch	Hit Count	Total Norm	Total	M057 embryo	V040 embryo	V107 male body	M055 female body	V108 head	V060 head
**********.....((((((((...((((((((((((((((.....))))))))))).))))))).....))))))))************											
.....ATTTAGTCTACAGTCGCTGC.....	20	0	1	7.00	7	2	5	0	0	0	0
.....GTCGCTGCGATTCCGGGCAGTT.....	22	0	1	6.00	6	1	5	0	0	0	0
.....GTCCATGACACTTAACGCTTTGT.....	23	0	1	6.00	6	5	1	0	0	0	0
.....CTGCTGTCTTGCAGGGCTGTAGGC.....	24	0	1	5.00	5	3	2	0	0	0	0
.....GTCGCTGCGATTCCGGGCA.....	19	0	1	5.00	5	2	3	0	0	0	0
.....GTCGCTGCGATTCCGGGC.....	18	0	1	4.00	4	4	0	0	0	0	0
.....AAATTTAGTCTACAGTCGCTGC.....	22	0	1	3.00	3	1	2	0	0	0	0
.....GTCGCTGCGATTCCGGGCAGT.....	21	0	1	3.00	3	3	0	0	0	0	0
.....CTTGCAGGGCTGTAGGCTTCGGTCC.....	25	0	1	3.00	3	2	1	0	0	0	0
.....GTCCATGACACTTAACGCTTTGTGCACC.....	28	0	1	3.00	3	3	0	0	0	0	0
.....AAGAGATCGGATTGGCGTCAATCGGAT.....	27	0	1	3.00	3	2	0	1	0	0	0
.....GTTGAAAGGATGCAAGATGAGAG.....	23	0	1	3.00	3	1	2	0	0	0	0
.....TAACGCTTTGTGCACCGTAC.....	20	0	1	3.00	3	2	1	0	0	0	0
.....TTTAGTCTACAGTCGCTGCGATTCC.....	25	0	1	2.00	2	2	0	0	0	0	0
.....AGTCGCTGCGATTCCGGGCAGTT.....	23	0	1	2.00	2	1	1	0	0	0	0
.....GTCCATGACACTTAACGCTTTGC.....	23	1	1	2.00	2	2	0	0	0	0	0
.....TTTAGTCTACAGTCGCTGCGATTCCGGGC.....	29	0	1	2.00	2	2	0	0	0	0	0
.....TCTACAGTCGCTGCGATTCC.....	20	0	1	2.00	2	0	2	0	0	0	0
.....GCAAGATGAGAGGCCCAGTCCAT.....	23	0	1	2.00	2	0	2	0	0	0	0
.....AAAGGATGCAAGATGAGAGGC.....	21	0	1	2.00	2	2	0	0	0	0	0
.....TACGCACAGCTAGAAGAGATC.....	21	0	1	2.00	2	2	0	0	0	0	0
.....AGAAGAGATCGGATTGGCGTCAATCGGA.....	28	0	1	1.00	1	0	0	0	1	0	0
.....GATTGGCGTCAATCGGATTGA.....	21	0	1	1.00	1	0	1	0	0	0	0
.....GGATTGGCGTCAATCGGATTGAATC.....	25	0	1	1.00	1	1	0	0	0	0	0
.....CATGACACTTAACGCTTTGT.....	20	0	1	1.00	1	0	1	0	0	0	0
.....AGTTACGCACAGCTAGAAGAGAT.....	23	0	1	1.00	1	0	0	1	0	0	0
.....AGTCTACAGTCGCTGCGATTCCGGGCA.....	27	0	1	1.00	1	1	0	0	0	0	0
.....GATTCCGGGCAGTTGAAAGGAT.....	22	0	1	1.00	1	0	1	0	0	0	0
.....TTGGCGTCAATCGGATTGA.....	19	0	1	1.00	1	1	0	0	0	0	0
.....TGGCGTCAATCGGATTGAATCTGC.....	24	0	1	1.00	1	0	1	0	0	0	0
.....ACTGCTGTCTTGCAGGGCTGTA.....	22	0	1	1.00	1	0	0	1	0	0	0
.....GTCGCTGCGATTCCGGGCG.....	19	1	1	1.00	1	0	1	0	0	0	0
.....AGATGAGAGGCCCAGTCCATGACACT.....	26	0	1	1.00	1	0	1	0	0	0	0
.....GTTGAAAGGATGCAAGATG.....	19	0	1	1.00	1	0	1	0	0	0	0
.....CTTGCAGGGCTGTAGGCTTCGGTC.....	24	0	1	1.00	1	0	1	0	0	0	0
.....TGAGAGGCCCAGTCCATGACACT.....	23	0	1	1.00	1	0	1	0	0	0	0
..CCCAGTTACGCACAGCTA.....	18	0	1	1.00	1	0	1	0	0	0	0
.....GATGCAAGATGAGAGGCCCAGT.....	22	0	1	1.00	1	1	0	0	0	0	0
.....GATGCAAGATGAGAGGCCCA.....	20	0	1	1.00	1	0	1	0	0	0	0
.....AATTTAGTCTACAGTCGCTGCGATTCC.....	27	0	1	1.00	1	0	0	0	0	1	0
.....ACGCACAGCTAGAAGAGATC.....	20	0	1	1.00	1	0	0	1	0	0	0
.....TTTAGTCTACAGTCGCTGC.....	19	0	1	1.00	1	0	1	0	0	0	0
.....TACGCACAGCTAGAAGAGATCGG.....	23	0	1	1.00	1	0	0	0	0	1	0
.....AAGAGATCGGATTGGCGTCAATCGGATT.....	28	0	1	1.00	1	0	0	1	0	0	0
.....GTCCATGACACTTAACGCT.....	19	0	1	1.00	1	1	0	0	0	0	0
.....ATGCAAGATGAGAGGCCCA.....	19	0	1	1.00	1	0	1	0	0	0	0
.....GATTCCGGGCAGTTGAAAG.....	19	0	1	1.00	1	0	0	0	0	0	1
.....TGCAAGATGAGAGGCCCAGTCC.....	22	0	1	1.00	1	0	1	0	0	0	0
.....AACTGCTGTCTTGCAGGG.....	18	0	1	1.00	1	0	1	0	0	0	0
.....TACAGTCGCTGCGATTCCGGGCAGTT.....	26	0	1	1.00	1	0	1	0	0	0	0
.....AGTCGCTGCGATTCCGGGCAG.....	21	0	1	1.00	1	1	0	0	0	0	0
.....GAGATCGGATTGGCGTCAATCGGAT.....	25	0	1	1.00	1	1	0	0	0	0	0
.....GATGAGAGGCCCAGTCCATGACAC.....	24	0	1	1.00	1	1	0	0	0	0	0
.....GGCTTCGGTCCAAAATTTAGTCTACA.....	26	0	1	1.00	1	1	0	0	0	0	0
.....TGAAAGGATGCAAGATGAGA.....	20	0	1	1.00	1	0	1	0	0	0	0
.....GATTCCGGGCAGTTGAAAGG.....	20	0	1	1.00	1	0	1	0	0	0	0
.....AGTTGAAAGGATGCAAGATGAGAG.....	24	0	1	1.00	1	0	1	0	0	0	0
.....TGCAGGGCTGTAGGCTTCGGTCCA.....	24	0	1	1.00	1	0	0	0	0	1	0
.....AGAGATCGGATTGGCGTCAATCGGAT.....	26	0	1	1.00	1	1	0	0	0	0	0
.....ACAGTCGCTGCGATTCCGGGC.....	21	0	1	1.00	1	1	0	0	0	0	0
.....TGCAAGATGAGAGGCCCA.....	18	0	1	1.00	1	0	0	0	1	0	0
.....AGTCTACAGTCGCTGCGATTCCGGGC.....	26	0	1	1.00	1	1	0	0	0	0	0
.....CTACAGTCGCTGCGATTCCGGGC.....	23	0	1	1.00	1	0	1	0	0	0	0
.....ATCGGATTGAATCTGCCTAAC.....	21	0	1	1.00	1	0	0	0	1	0	0
.....TGAAAGGATGCAAGATGAGAGGCCCA.....	26	0	1	1.00	1	1	0	0	0	0	0
.....AATTTAGTCTACAGTCGCTGCGATTC.....	26	0	1	1.00	1	0	0	1	0	0	0
.....AGTCTACAGTCGCTGCGATT.....	20	0	1	1.00	1	0	0	1	0	0	0
.....GGATTGGCGTCAATCGGAT.....	19	0	1	1.00	1	0	0	0	1	0	0
.....AACTGCTGTCTTGCAGGGCTGTAGGC.....	26	0	1	1.00	1	0	1	0	0	0	0
.....AGTTGAAAGGATGCAAGATGAGA.....	23	0	1	1.00	1	0	1	0	0	0	0
.....AGTTACGCACAGCTAGAAGAGATC.....	24	0	1	1.00	1	0	0	0	1	0	0
.....GCACAGCTAGAAGAGATC.....	18	0	1	1.00	1	0	0	0	0	1	0
.....GTCCATGACACTTAACGCTTTGTT.....	24	1	1	1.00	1	0	1	0	0	0	0
.....CTTGCAGGGCTGTAGGCTTC.....	20	0	1	1.00	1	0	0	0	1	0	0
.....ATGCAAGATGAGAGGCCCAGTCC.....	23	0	1	1.00	1	1	0	0	0	0	0
.....CCAAAATTTAGTCTACAGTCGCTGC.....	25	0	1	1.00	1	1	0	0	0	0	0
.....CTAACTGCTGTCTTGCAGGGCTGTAGGC.....	28	0	1	1.00	1	1	0	0	0	0	0
.....TTAGTCTACAGTCGCTGCGATTCCG.....	25	0	1	1.00	1	1	0	0	0	0	0
.....CAGTTACGCACAGCTAGAAGAG.....	22	0	1	1.00	1	0	0	1	0	0	0
.....GAAAGGATGCAAGATGAGAGGCCCA.....	25	0	1	1.00	1	1	0	0	0	0	0
.....TGCCTAACTGCTGTCTTGCAGGG.....	23	0	1	1.00	1	0	0	0	0	1	0
.....GTTGAAAGGATGCAAGATGAGAGGCCCA.....	28	0	1	1.00	1	1	0	0	0	0	0
.....ATTGGCGTCAATCGGATTGA.....	20	0	1	1.00	1	0	1	0	0	0	0
.....GCTGTCTTGCAGGGCTGTAGGC.....	22	0	1	1.00	1	0	1	0	0	0	0
.....GGATTGGCGTCAATCGGATTGAAT.....	24	0	1	1.00	1	1	0	0	0	0	0
.....TTAGTCTACAGTCGCTGCGATTCCGGGC.....	28	0	1	1.00	1	1	0	0	0	0	0
.....GTTGAAAGGATGCAAGATGAGAGGCC.....	26	0	1	1.00	1	1	0	0	0	0	0
.....AAGGATGCAAGATGAGAGG.....	19	0	1	1.00	1	0	1	0	0	0	0
.....CATGACACTTAACGCTTTGTGCACC.....	25	0	1	1.00	1	1	0	0	0	0	0
.....AGTCGCTGCGATTCCGGGC.....	19	0	1	1.00	1	1	0	0	0	0	0
.....ATCTGCCTAACTGCTGTCTTGC.....	22	0	1	1.00	1	1	0	0	0	0	0
.....GAGAGGCCCAGTCCATGACAC.....	21	0	1	1.00	1	0	0	1	0	0	0
.....GATCGGATTGGCGTCAATCGGAT.....	23	0	1	1.00	1	0	0	0	1	0	0
.....GTTACGCACAGCTAGAAGAGATC.....	23	0	1	1.00	1	0	0	1	0	0	0
.....TGCAGGGCTGTAGGCTTCGGTCCAA.....	25	0	1	1.00	1	0	0	0	1	0	0
.....GAGAGGCCCAGTCCATGACA.....	20	0	1	1.00	1	0	0	1	0	0	0
.....GCAAGATGAGAGGCCCAGTCCATGACA.....	27	0	1	1.00	1	0	0	1	0	0	0
.....TGAAAGGATGCAAGATGAGAG.....	21	0	1	1.00	1	0	1	0	0	0	0
.....TACGCACAGCTAGAAGAGATCG.....	22	0	1	1.00	1	1	0	0	0	0	0

Anti-sense strand reads

TAGGGTCAATGCGTGTCGATCTTCTCTAGCCTAACCGCAGTTAGCCTAACTTAGACGGATTGACGACAGAACGTCCCGACATCCGAAGCCAGGTTTTAAATCAGATGTCAGCGACGCTAAGGCCCGTCAACTTTCCTACGTTCTACTCTCCGGGTCAGGTACTGTGAATTGCGAAACACGTGGCATGTAAAAGTC	Read size	# Mismatch	Hit Count	Total Norm	Total	V107 male body	V108 head
**********.....((((((((...((((((((((((((((.....)))))))))).))))))).....))))))))**********							
.....GTGAATTGCGAAACACGTGGCATG.....	24	0	1	1.00	1	0	1
.....GCGTGTCGATCTTCTCTAG.....	19	0	1	1.00	1	1	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droEre2	scaffold_4929:3115440-3115634 +	der_1527	ATCCC----------AGTTA--CGCACAGCTAGAA--GAGA----------T----------CGGATT------GGCGT----CAATCGGA-TTGAATCTG--CC--TAACTGCTGTCTTGCAGGGC-T--GTAGGC---TTCGGTCCAAAAT----TT-AGTCTACAGTCGCTGCGATTCCG-GGCAGTTGAAA-GGATGCAA-GATGAGAG---GCCCA---GTCCATGACACTTAACGCTT--TGTGCACC-GT----------ACATTTTCAG----------
droYak3	2L:3063696-3063892 +	dya_1801	ATCCC----------AGTTA--CGCACAGCTAGAA--GAGA----------T----------CGGATC------GGCGT----CGATCGGA-TTAAGTCTG--CC--TAACTGCTGTCTTGCAGGGC-T--GTAGGC---TTTGGTCCAAAAT----TT-AGTCTACAGTCGCTGCGATTCCG-GGCAGTTGAAA-TGATGCAA-GATGAAGAGAGCCCG---GTCCATAACACTTAACGCTT--TGTGCACC-GT----------ACAATTT-CAG----------
droSec2	scaffold_5:1224940-1225145 +	dse_1854	ATCCC----------AGTTA--CGCACAGCTAGAA--GAGATAAGTCAA--CAGAT----------T----------TGGATT------TGCGT----CGATCGG-TTGAATCTG--CC--TAACTGCTGTCTTGCAGGGC-T--GTAGGC---TTCGGTCCAAAAT----TT-AGTCTACAGTGACTGCGATTCCG-GGCAGTTGAAA-TGATGCAA-GATGAGAG---GCCCA---GTCCATAACACTTAACGCTT--TGTGCACC-GT----------ACAATTT-CAG----------
droSim2	2L:2946882-2947087 +	dsi_32463	ATCCC----------AGTTA--CGCACAGCTAGAA--GAGATAAGTCAA--CAGAT----------T----------TGGATT------TGCGG----CGATCGG-TTGAATCTG--CC--TAACTGCTGTCTTGCAGGGC-T--GTAGGC---TTCGGTCCAAAAT----TT-AGTCTACAGTCGCTGCGATTCCG-GGCAGTTGAAA-TGATGCAA-GATGAGAG---GCCCA---GTCCATAACACTTAACGCTT--TGTGCACC-GT----------ACAATTT-CAG----------
dm3	chr2L:3067697-3067902 +	dme_436	ATCCC----------AGTTA--CGCACAGCTAGAA--GAGATAAGTTAA--CAGAT----------T----------TGGATT------TGCGT----CGATCGGA-TTGAATCTG--CC--TAACTGCTGTCTTGCAGGGC-T--GTAGGC---TTCGGTCCAAAAT----A-AGTCTACAGTCTCTGCGATTCCG-GGCAGTTGAAA-TGATGCAA-GATGAGAG---GGTCA---GTCCATAACACTTAACGCTT--TGTGCACC-GT----------ACAATTT-TAG----------
droEugl	scf7180000409554:3024268-3024474 -		ATCCC----------AGTTA--CGCACAGCTAAAA--GAGATAACTCAA--CAGGT----------CGGATT------GGAGG----GGATCGGA-TTGAATCTG--AT--TAACTGCTGTCTTGCAGCGGC-T--GTAGAG---TGTGGTCCAAAAT----TT-AGTCTATAGTCGCTGCGATCTG-GGCAGTTGTAA-GGATAAAAAGATGAGAG---GCCCA---AACCATGACACTTAACGCTT--TGTGCACC-AT----------ACAGATT-TAG----------
droBia1	scf7180000302188:2121990-2122201 +		AACCC----------AGTTA--CGCACAGCTAGAG--GAGATAAGTAAA--CAGAT----------CGGATTG--GACTGGAGT----GGATCGGA-TTGCATCGG--CC--TAACTGCTGTCTTGCAGGGC-C--GTAGAG---TTTGGTCCAAAAT----TT-AGTCTAGCGTCGCTGCGATTCCG-GGCAGTTGAAA-GGATGCAA-GACGAGAG---AGTCA---GTCCACTAGACTTAACGCTT--TGTGCACC-GT----------ACAGTTCCAG----------
droTak1	scf7180000415438:753080-753236 -		ATCCC----------AGTTG--CGCACAG------T----------T----------CGGATT------GAGTT----GGATCGGA-TGGCATCTG--CC--TAACTGCTGTCTTGCAGGGC-C--GTGGAG---TTTGGTCCAAAAT----TT-AGTCTATGGTCGCTGCGATTCCG-GGCAGTTGAAA-GGATGCGA-AATGAGAG---AGCCA---T---------ACCTAACGCTT--TGTGCACC-G----------T---------T----------
droEle1	scf7180000491046:1758532-1758739 +		ATCCC----------AGTTA--CGCACAGTTAGAA--GAGATAAGTCAA--CGGAT----------CGGATT------GGAGT----GGATCGGA-TTCCGTCTG--CC--TAACTGCGTCTTGCAGCAGC-T--GTAGTG---TTTGGTCCAAAAT----TT-AGTCTACAGCCGCTGCGATTCG-GGCAGTTGAAA-GGATGCAAGATGAGAG---GCCCA---GACCATGACACTTAACGCTT--TGTGCACC-GT----------ACAGTTCAGT----------
droRho1	scf7180000780028:158211-158416 +		ATCCC----------AGTTA--CGCACAGCTAGAG--GAGATAAGTCAA--CGGAT----------CGGATT------GGAAT----GGATTGGA-TTGCATCTG--CC--TAACTGCGTCTTGCAGCGGC-T--GTATTG---TTTGGTCCAAAAT----TT-AGTCTATAGTCGCTAGATGTG-GGCAGTTGAAA-TGATGCAA-GACGAGAG---GCCCA---ATCCATGACACTTAACGCTT--TGTGCACC-GT----------ACAGTTCAG----------
droFic1	scf7180000453924:1051713-1051930 +		ACCCC----------AGTTA--CGCACAGCTAGAA--GAGATAGG--A-------T----------CGGATT------GGAGTGGATGCATCGCC-TGGCATCTG--CC--TAACTGCGTCTTGCAGCGGC-C--GTAGAG---TTTGGTCCAAAAT----TT-AGCCTAGCGCCGCTAGGATCCG-GGCAGTTGAAA-GGATGCAG-GATGCGAGTTGGCCA---ACCCTTGACACTTAACGCTT--TGTGCACC-GT----------ACAGTTCAGTAGTTCAGTACAG
droKik1	scf7180000302246:274508-274656 +		ATCCC----------AGTTA--CGGGCAGG-----T----------T----------CGGATT------GGAGT----GGATCGGA-TTGCATCTG--CC--TAACTGCGTCTTGCAGCGGC-T--GTGGAG---TGTGGTCCAAA-T----A-AGTCTACAGTCGCTGCGATTCCG-GGCAGTTGATGT-GGCC--GA-TGC-----T------T-GGATGGCGACTTAACGCTTGCGTGTGCACC-G----AGAGA--AGAGTTCAG----------
droAna3	scaffold_12916:9588076-9588247 -	dan_4042	ATCCC----------AGTTAAGCGCACAGCTTTAA--G---T----------T----------CGAAGCGT-TT--ATCTG--CCATTAACTGCTGTCTTGCAGAGTC-T--GTGGAG---G-TGGTCCAAA-T----T-TGTCTACAGCGACTGCGATTCCG-GGCAGTTGAAATGTGAT--AA-TAGGGACT---GCCCAAAAACACATGACACT-GCGCTT--TGTGCACC-G----------AG----------
droBip1	scf7180000396580:1442837-1443009 +		ATCCC----------AGTTAAGCGCACAGCTTTAA--G---T----------T----------CGATGAGCATT---TCTG--CCATTAACTGCGTCTTGCAGCGTC-T--GTGGAG---G-TGGTCCAAA-T----T-TGTCTACAGCGCTGCGATTCCGGGCAGTTGCAAGTGAAGCGA-TAGGGATT---GCTCA--ATACATGACACTGCGCTT--TGTGCACC-G----------AG----------
dp5	Unknown_singleton_3046:18-209 +	dps_31	---CC----------AGTTA--CGCACAGCAGAA--AAGATAAAACTAATC---T----------CGGATCGGATG------TT-----------C-TTAAC----G--TAACTGCGTCTTGCAGCGGC-T--GTGGAG--ATATGGTCCAAAAT----TTCAGTCTACAGCGCTGCGATTCCG-GGCAGTTGATGT-GGAT----T---GGGAT---GCACCT--TTAAATGACACTTAACGCTA-TGTGCACA-GA---------GTACATT--AG----------
droPer2	scaffold_1:8612773-8612992 -	dpe_229	GTCCCAATATCAGTAATCCAAGAATTAACCATTA--CGCACAGCAGAA--AAGATAAAACTAATC---T----------CGGATCGGATG------TT-----------C-TTAAC----G--TAACTGCGTCTTGCAGCGGC-T--GTGGAG--ATATGGTCCAAAAT----TTCAGTCTACAGCGCTGCGATTCCG-GGCAGTTGATGT-GGAT----T---GGGAT---GCACCT--TTAAATGACACTTAACGCTA-TGTGCACA-GA---------GTACATT--AG----------
droWil2	scf2_1100000004945:407265-407435 +	dwi_5419	ATCAC----------AGTTA--CGCACAGTAAATACATATATCCT--CCAAAT----------G----TGAATT------AGATATAAGTTATATCCAGTGATGA-TT--TAATGCCGTCTTGCAGGGCTCTTGTAAGAATCCAGTCCAAA-TTAAA-A-TCTTTATTAGATCCTGCGATTCG-GGCAATTGAATT-GA-CA---T--------T-----T---------------------T----CACT--T----------G----------
droVir3	scaffold_12963:14467451-14467620 -	dvi_24646	ATTCA----------AATTA--TTTTAA------T----T----------CATGT-----CCAACAGTTTAGCAAGTC----------T------T-----T-------T-ATGT--AA--TG--TAACTGCGTCTTGCAGCGCT--GTGGATA-CAAACGTCCAAAAT----TT-AATGCACACGAGTGCGATTCG-GGCAGTTGA--T--------T--------T-----T-----TTTACTAAATCTTT--TATGCACATGTAAACATGGG--AGAGTGTCAG----------
droMoj3	scaffold_6500:15423873-15424047 -	dmo_3155	ATTTC----------AGTTT--CGAA--TCCAGAA--TAATT----------T----------CCCACAACCAACGATTT-----TGGAGGGTAGACAACAG---ACAGAGCCGCGATCGTCTT--TAACTGCGCTTGCAGCTGCT-GTGGATG-CCCACGTCCAATTA----G-AATGCACACGTGCTGCGATTCG-GGCAGTTGAGG-GGA-GCAA-GAGGAT---T-----T-----------------T--------T--T----------T----------
droGri2	scaffold_15252:2029209-2029384 +	dgr_469	GAATC----------AGTAA--TTTACAATTGGAA--TAGAGGAATCAT--CATAATTTGTATATCAATCTATATAATC----------T------T-----T-------T--TAC-AATG--AT--TAATGCGCTTTGCGGGGCT--GTGGGA-CCCACGTCCAAACA-AAAGTTTCCCACATGGTGCGGCGATTCG-AGCAGTTAAC-T--------T--------T---T--CA---GT---------TTA--ACTT--CATTCAGA--T----------T--------A----------

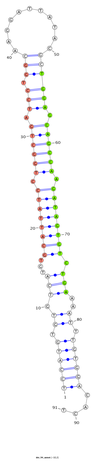
Generated: 09/08/2015 at 07:56 PM

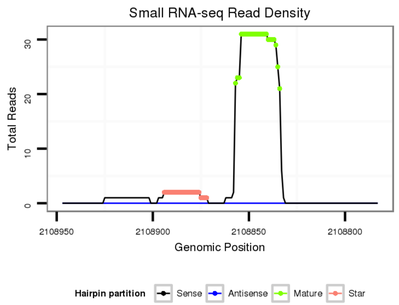
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	0
crit.ptop3	0
crit.uri	0
crit.back	0
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	2
rescue.candidate	10

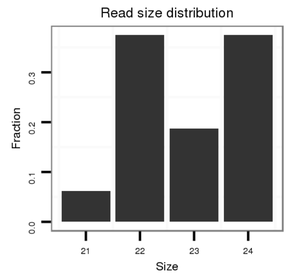
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
der_94	**scaffold_4784:2108833-2108897 -**	**candidate-rescued**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser [Cornell Mirror]]

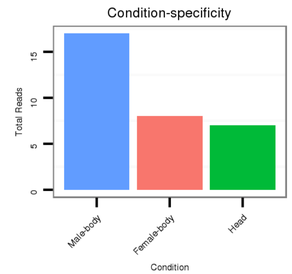
Legend: mature star mismatch in alignment mismatch in read

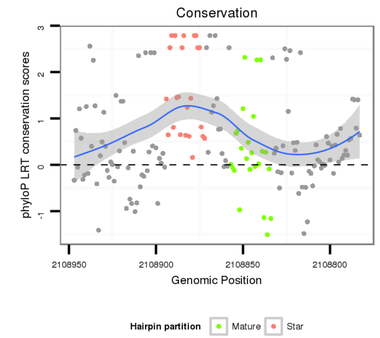
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

```
AACCTGCACAAATCAAAAGATCAAGTATACGCGGTCCTTCCATGTGTGTCATGTGCATTATCCTGGCTGATCCTGGCAAGGATTATACGCTGGAGCAGCCAAGATAGTGTCTGAAAATTTGTGGACACTCTCAAACGGAGATCATTGGGCCAATGCAAGGTTTTC
**********************************((((((.(.(.(((...(((((((((.(((((((.(((.(((.(((.........)))))).))))))).))))))))).)))..)).)))))))....**********************************
```

Read size	# Mismatch	Hit Count	Total Norm	Total	V107 male body	V108 head	M055 female body	V040 embryo	GSM1528801 follicle cells
24	0	1	12.00	12	7	4	1	0	0
22	0	1	5.00	5	5	0	0	0	0
22	0	1	4.00	4	1	1	2	0	0
23	0	1	4.00	4	3	1	0	0	0
21	0	1	2.00	2	1	0	1	0	0
22	0	1	1.00	1	0	0	1	0	0
23	0	1	1.00	1	0	0	1	0	0
23	0	1	1.00	1	0	0	1	0	0
22	0	1	1.00	1	0	0	1	0	0
24	0	1	1.00	1	0	0	1	0	0
23	0	1	1.00	1	1	0	0	0	0
22	0	1	1.00	1	0	1	0	0	0

Anti-sense strand reads

```
TTGGACGTGTTTAGTTTTCTAGTTCATATGCGCCAGGAAGGTACACACAGTACACGTAATAGGACCGACTAGGACCGTTCCTAATATGCGACCTCGTCGGTTCTATCACAGACTTTTAAACACCTGTGAGAGTTTGCCTCTAGTAACCCGGTTACGTTCCAAAAG
**********************************((((((.(.(.(((...(((((((((.(((((((.(((.(((.(((.........)))))).))))))).))))))))).)))..)).)))))))....**********************************
```

Read size	# Mismatch	Hit Count	Total Norm	Total	V107 male body	V060 head

Show Alignment With Reads

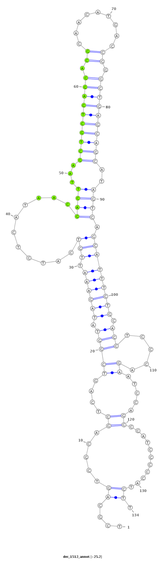
Re-alignment of all predicted orthologs

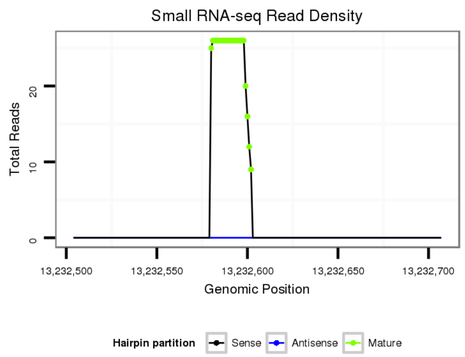
Species	Coordinate	ID	Alignment
droEre2	scaffold_4784:2108783-2109947 +	der_94	AACCTGC----------ACAAATCAA----------A--AGAT----------CAAGTATACGCGGTC-------CTTCCATGTGTGTC-ATGTGCATTATCCTGGC-----T--GATCCTGGCAAGGATTATACGCTGGAGCAG==========CCAAGAT----------AGTG-TCTGAAAATTTGTGGA----------C--ACTCTC-AAACGGAG-----ATCATTGGG--CCAATGC--A---AGGTTT---TC
droYak3	3L:2067759-2067922 -	dya_1787	AACCTGC----------ACAAATCAA----------A--AGAT----------CAGGTATACGCAGTC-------CTTCCATGTGTGC-ATATGCATTATCCTGGC-----T--GATCCTGGCAAGGATTTTACGCTGGAGCAG----------TAAGAT----------AGTG-TCTAAAAATATGTGG----------C--ATCTC-AAACGGAG-----ATTATTGGG--CCAATGC--A---AGGTTT---TC
droSec2	scaffold_2:2140505-2140669 -	dse_1837	AACCTGC----------ACAAATCAA----------A--AGAT----------CAGGTATACGCGGTG-------CTTCCATGTGTGC-ATGTGCATTATCCTGGC-----T--GATCCTGGCAAGGATTATACGCTGGAGCAG----------CCAAGAT----------AGTG-TCTGAAAATATGTGA----------C--ATCTC-AACCGGAG-----ATCACTGGG--CCAATGC--A---AGGTTT---TC
droSim2	3L:2012829-2012993 -	dsi_32442	AACCTGC----------ACAAATCAA----------A--AGAT----------CAGGTATACGCGGTG-------CTTCCATGTGTGC-ATGTGCATTATCCTGGC-----T--GATCCTGGCAAGGATTATACGCTGGAGCAG----------CCAAGAT----------AGTG-TCTGAAAATATGTGA----------C--ATCTC-AAACGGAG-----ATCACTGGG--CCAATGC--A---AGGTTT---TC
dm3	chr3L:2114918-2115082 -	dme_114	AACCTGC----------ACAAATCAA----------A--AGAT----------CAGGTATACGCGGTG-------CTTCCATGTGTGC-ATATGCATTATCCTGGC-----T--GATCCTGGCAAGGATTATACGCTGGAGCAG----------CCAAGAT----------AGTG-TCTGAAAATTTGTGA----------C--ATCTT-AAACGGAG-----ATCACTGGG--CCAATGC--A---AGGTTT---TC
droEug1	scf7180000409091:158118-158283 +		AACCTGC----------AGAATCAA----------A--AGAT----------CAGGTATATCCTGGC-----T--GATCCTGGCAAGGATTACGCTGGAGCAG----------CCAAGAT----------AATGCTGTATAAAATGTGGA----------A--ATCTT-TGAGAAAG-----ATCATTGGG--CCAATGC--A---AGGTTT---TC
droBia1	scf7180000302428:8837688-8837856 -		AACCTGC----------AGAATCAA----------A--AGAT----------CAGGTATATCGCGCTCCT-----TTCCATGTGTGTGAGTGTGCATTATCCTGGC-----T--GATCCTGGCAAGGATTACGCGCTGGAAGCG----------CCAAGAT----------AGTG-CGAGCAAAAGTGTGGA----------A--ATCTT-CGG-AAAG-----ATCATTGGG--CCAATGC--A---AGGTTT---TC
droTak1	scf7180000414400:42688-42864 -		AACCTGC----------AGAATCGA----------AAAAGATCTCAT--ATA--------GTGTA--TAGCCA-------GTGCCATGTGTGTGAATGTGCATTATCCTGGC-----T--GATCCTGGCAAGGATTAACGCGCTGGAAAAG==========CCAAGA----------AAAGCGAGAAATTTGTGA----------AAGA--A--------A--ATATT-CAAGAAAG-----ATCATTGGG--CCAATGC--A---AGGTTT---TC
droEle1	scf7180000491249:3380317-3380473 +		AACCTGC----------AGAGATGA----------AAGAGAT----------CAGGT---------------CCATGTGTGCGAATGTGCATTATCCTGGC-----T--GATCCGCGCAAGGATTACGCGCTGGAAGCG==========CCAAAATA--G--------AGTGCGCAAGAATTTGTGA----------A--ATCTT-AAGAAAAG-----TCATTGGG--CCAATGC--A---AGGTTT---TC
droRho1	scf7180000779211:43049-43201 -		AACCTGC----------AGAGATCGC----------T--AGAT----------GAG----------GGTCCATGTGTGCGAATGTGCATTAGCCTGGC-----T--GATCCTGGCAAGGATTACGCGCTGGAAGCAG==========CCAAAAT----------AGTGCGCGAGAAAGTGTGA----------A--CTTCT-GAGCGAAG-----ATCATTGGG--CCAATGC--A---AGGTTT---TC
droFic1	scf7180000453052:945722-945886 +		AACCTGC----------ACAGATTAA----------A--AGAT----------CAGGTATAGCGCTCCT-----TTCCATGTGTGTGAATGTGCATTATGTGGC-----T--GATCCTGGCAAGGATTACGCGAGGAAGCAG==========CCAAAAT----------AGTGACTCGAAAATGTGA----------A--ATCTC-GAAGAGAG-----ATCATTGGG--CCAAGGC--A---AGGTTT---TC
droKik1	scf7180000302441:1692352-1692503 +		TAGCGAG----------AGAGAT--A---TGCGA---A--AGCG---CTGC--ATATA----------TCTA---------GTGAATGTGCATTATCCTGGCTGCCGC--GATCCTGGCAAGGATTACGCTGAAAAG==========TCAGC----------AGTGACCCGAAAGCGTGA----------T--AT----------GCGTTGGGTTTGGCTGC--AGAGGGTTT---TC
droAna3	scaffold_13337:715323-715493 +	dan_4047	AAAAAAA----------CAAATCGA----------A--AGTAC--CTACCACTATC----------TCA-----GTGATTATAATGTGT--GCCCTGCATTGTCCTGCAC-----T--GATCCTGGCAAGGATTACGCGCTGGAAGCAG----------CCGTGCGCAGTGCCGTGG----------A--ATAGTGCGCGGTG-----GCCATCGA--CAATCTCAT---ACGCTT---TC
droBip1	scf7180000395155:42404-42570 -		AGAAAGAA----------GCAGATGA----------A--AGCA--CCTAC--ATATA----------T--CTTACAAGTGAGTAATGATGTGT--GCACCTGCATTGTCCTGGA-----ATATATCCTGCAAGGACGGAGCGCCAATAG----------CCGTGCGCGGTG----------AGTG-GCCTGTGCGTGGA----------A--ATAATTGCGCGGTG-----GCCATGCA--CAATCTCAT---ACGCTT---TC
dp5	XR_group6:12020040-12020220 -		C---TAT----------AAATATAGG----------AAGAAACATAT--ACATATA----------TCA----GGGATGTGTTGCATGTGCATGCGATTATCCTGGC-----T--GATCCTGGCAAGGATTATACGCCACTCGAG==========TGGGATAATGGCTCTCCC----TCCCTCTCTCTGTGGGAAAAAGGAGTTCAAACCAAT----TC--CTTTCTTTTTATTC----TCTTTTT----TTTTTTTTTTTC
droPer2	scaffold_33:40922-41110 -		TTTATGGTAT----------AAATATAGG----------AAGAAACATAT--ACATATA----------TCA----GGGATGTGTTGCATGTGCATGCGATTATCCTGGC-----T--GATCCTGGCAAGGATTATACGCCTCCGAG==========TGGGATAATGGCTCTCCC----TCCCTCTCTGTGGGAAAAAGGAGTTCAAACCAAT----TC--CTTTCTTTTTATTC----TTTTTT----TTTTTTTTTTTC
droWil2	scf2_1100000004729:1284523-1284717 +		TGTAA----------GTTTTTTTTTT

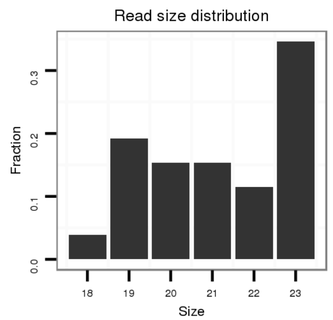
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
der_1512	**scaffold_4770:13232554-13232657 +**	**candidate-rescued**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser [Cornell Mirror]]

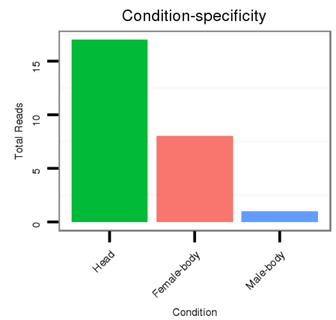
Legend: mature star mismatch in alignment mismatch in read

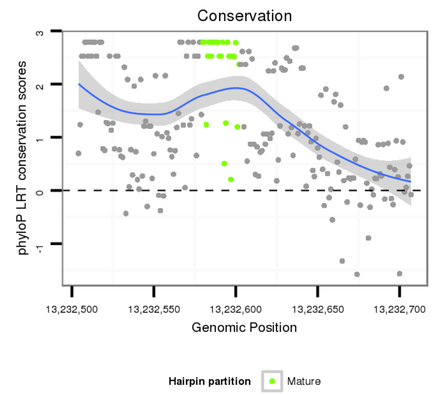
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

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ACGGAAGTGTTGATATGGCCGCAGCTCAGTCGCAGTCGCAGTCGCAGCTCAGTCGGTATAGAAATTGTCATCTCATAACGACTTAAGCTGCTCAGCACGCAACATGACCGGGCTGAGCAGCATAGTCAGCATTTCTGCACCTCCCAGAATCCAGCCCATCCCCCATCTTCCACCACTATTGCCACCCACTTTTCCAGCCCACTG
**********************************....((.....((.....(((((.(((((((.((((...........((((...(((((((((((.((.........)).))))))))))..)))).)))))))))).)))).....)).....)).....)).....)).**********************************
```

Read size	# Mismatch	Hit Count	Total Norm	Total	V108 head	M055 female body	V107 male body	V040 embryo
23	0	1	9.00	9	7	2	0	0
19	0	1	5.00	5	4	0	1	0
20	0	1	4.00	4	3	1	0	0
21	0	1	4.00	4	3	1	0	0
22	0	1	3.00	3	0	3	0	0
22	1	1	2.00	2	1	0	1	0
23	1	1	1.00	1	1	0	0	0
20	1	1	1.00	1	0	0	1	0
20	1	1	1.00	1	0	1	0	0
21	1	1	1.00	1	1	0	0	0
18	0	1	1.00	1	0	1	0	0

Anti-sense strand reads

```
TGCCTTCACAACTATACCGGCGTCGAGTCAGCGTCAGCGTCAGCGTCGAGTCAGCCATATCTTTAACAGTAGAGTATTGCTGAATTCGACGAGTCGTGCGTTGTACTGGCCCGACTCGTCGTATCAGTCGTAAAGACGTGGAGGGTCTTAGGTCGGGTAGGGGGTAGAAGGTGGTGATAACGGTGGGTGAAAAGGTCGGGTGAC
**********************************....((.....((.....(((((.(((((((.((((...........((((...(((((((((((.((.........)).))))))))))..)))).)))))))))).)))).....)).....)).....)).....)).**********************************
```

Read size	# Mismatch	Hit Count	Total Norm	Total	V107 male body	V040 embryo	V060 head	M055 female body

Show Alignment With Reads

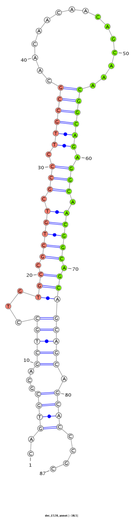
Re-alignment of all predicted orthologs

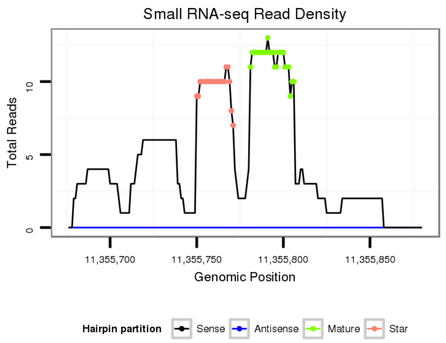
Species	Coordinate	ID	Alignment
droEre2	scaffold_4770:13232504-13232707 +	der_1512	ACGGAAGTGTTGATATGGC--CGCAGCT-CAGTCGCAGTCGCA-----GTCGCAG----------CTC----------AGTCGGTATAGAAATT-----GTCATCTCATAACGACTTAAGCTGCTCAGCACGCAACATGACCGGG-----CTGAGCAGCATAGTCAGCATTTCTGC-----ACCTCCCAGAATCCA-------G---------CCCATCCCCC---A----TCTTCCAC--CACTATTG----------CCACCCAC-TTTTCC-------AGCCCAC-TG
droYak3	3R:12705448-12705649 -	dya_1782	ACGGAAGTGTTGATATGGC--CGCAGCT-CAGTCGCAGTCGCA-----------G----------CTC----------AGTCGGTATAGAAATT-----GTCATCTCATAACGACTTAAGCTGCTCGCACGCAACATGACCGGG-----CTGAGCAGCATAGTCAGCATTTCTGC-----ACCTCCCAGAATCCA-------G---------CCCATCCGCG--AGTCGGCTCTTCCAC--CACGTGTTG----------CCACCCAC-TTTTCC-------AACCCAC-TG
droSec2	scaffold_0:13567281-13567479 +	dse_131	ACGGAAGTGTTGATATGGC--CGCAGCT-CAGTCGCAGTCGCA-----------G----------CTC----------AGTCGGTATAGAAATT-----GTCATCTCATAACGACTTAAGCTGCTCGCACGCAACATGACCGGG-----CTGAGCAGCATAGTCAGCATTTCTGC-----ACCTCCCAGAATCCA-------G---------CCCATCCGCGCTAG-----CAACACACTATTG----------CCACCCAC-TTTTCC-------AGCCCAC-TG
droSim2	3r:12738962-12739160 +	dsi_32436	ACGGAAGTGTTGATATGGC--CGCAGCT-CAGTCGCAGTCGCA-----------G----------CTC----------AGTCGGTATAGAAATT-----GTCATCTCATAACGACTTAAGCTGCTCGCACGCAACATGACCGGG-----CTGAGCAGCATAGTCAGCATTTCTGC-----ACCTCCCAGAATCCA-------G---------CCCATCCGCGCTAG-----CAACACACTATTG----------CCACCCAC-TTTTCC-------AGCCCGC-TG
dm3	chr3R:8419591-8419787 -	dme_234	ACGGAAGTGTTGATATGGC--CGCAGCT-CAGTCACAGTCGCA-----------G----------CTC----------AGTCGGTATAGAAATT-----GTCATCTCATAACGACTTAAGCTGCTCGCACGCAACATGACCGGG-----CTGAGCAGCATAGTCAGCATTTCTGC-----ACCTCCCAGAATCCA-------G---------CCCATCCGCGCTCAG-----CAAA--CACTATTG----------CCACCCAC-TTTTCC-------AACCCAC-TG
droEug1	acf7180000409615:635431-635621 -		ACGGAAGTGTTGATATGGC--CGCAGCT-CAGTCGCAGTCGCA-----------G----------CTC----------AGTCGGTATAGAAATT-----GTCATCTCATAACGACTTAAGCTGCTCGCACGCAACATGACGGGG-----CTGAGCAGCATAGTCAGCATTTCTGC-----ACCTCCCAGAATCCG-------T---------TTCAGCGCCGTT-T----------T---TAAA----------CACCCAC-TTGTCC----CACCAC-CCCAC-AG
droBia1	acf7180000302402:97555-97755 -		CCGGAAGTGTTGATATGGC--CGCAGCT-CAGTCGCAGTCGCC-----GTCGCAG----------CTCA-GTCG---CAATT----------SAGCGGTATAGAAATT-----GTCATCTCATAACGACTTAAGCTGCTCGCACGCAACATGACCGGG-----CTGAGCAGCATAGTCAGCATTTCTGC-----ACCTCCCAGCATCCA-------G---------CCACGCCGCGGGC----CCC---T-------CCACCCAC-TTT-CC-------AGCCCAC-TG
droTak1	acf7180000415366:130681-130875 +		ACGGAAGTGTTGATATGGC--CGCAGCT-CAGTCGCAGTCGCA-----------G----------CTCA-GTCG---CAATT----------SAGTCGGTATAGAAATT-----GTCATCTCATAACGACTTAAGCTGCTCGCACGCAACATGACCGGG-----CTGAGCAGCATAGTCAGCATTTCTGC-----ACCTCCCAGAATCCA-------G---------CCACGCGCGCG--C----------CCCCC-TT----------CCACCCAC-TTTTCC-------AACCCAC-TG
droEle1	acf7180000490994:97226-97421 -		ACGGAAGTGTTGATATGGC--CGCAGCT-CAGTCGCAG-CTCA-----GTCGCAG----------CTCA-GCCG---CAAGT----------SAGTCGGTATAGAAATT-----GTCATCTCATAACGACTTAAGCTGCTCGCACGCAACATGACCGGG-----CTGAGCAGCATAGTCAGCATTTCAGC-----ACCTCCCAGAATCCGGGCATATA----------CCCACGCC---C----------CCC-CCTTT-TC-------AACCCAC-TG
droRho1	acf7180000777772:6573-6767 -		AGGGAAGTGTTGATATGGC--CGCAGCT-CAGCGCGAGTCGCA-----------G----------CTCA-GTCG---CAAGT----------SAGTCGGTATAGAAATG-----GTCATCTCATAACGACTTAAGCTGCTCGCACGCAACATGACCGGG-----CTGAGCAGCATAGTCAGCATTTCTGC-----ACCTCCCAGAATCCA-------GAAACCAGCACCCA------C----------CCACCCG-C-TTTTCC-------AACCCAC-TG
droFic1	acf7180000453812:694069-694269 +		ACGGAAGTGTTGATCTAC--CGCAGCT-CAGTCGCAGTCGCA-----------G----------CTCA-GTCG---CACAT----------SAGTCGGTATAGAAATG-----GTCATCTCATAACGACTTAAGCTGCTCGCACGCAACATGACCGA-----CTGAGCAGCATAGTCAGCATTTCTGC-----ACCTCCCAGAATCCA-------G---------CC---------C----------A-CCACCCACTTACACACCCAC-TTCACC----CACCAC-CCCAC-TG
droKik1	acf7180000302256:649525-649726 +		ACGGAAGTGTTGCTATGGC--CGCAGCT-CAGCGCGTGTCGCA-----------G----------CTCA-GTCACTGAGAC---GCCGAGGCGCTGAGTC--GCTCTGTCGGTACAGAAATT-----GTCATCTCATAACGACTTAAGCTGCTCGCACGCAACATGACCGGG-----CTGAGCAGCATAGTCAGCATTTCTGC-----AGTCCCCAGAAGGCA-------G---------C----------C----------C----------C----------CCACCCAC-TTTTCC-------AACCCAC-TG
droAna3	scaffold_12911:3351170-3351290 -		ACGGAAGTGTTGATATGGC--CGCAGGC-TGC----------C-----------G----------CTG----------GGCGGGTGTAGGAATT-----GTCATCTCATAACGACTTAAGCTGCTCGCACGCAACATGAC---C----TGAGCAGCGTAGTCAGCATTTCTGC-----ACCTCC----------C----------C----------C

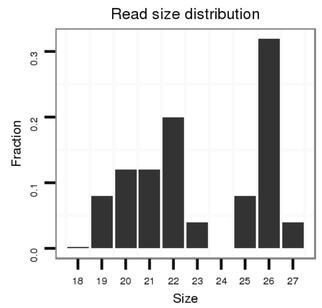
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
der_1520	**scaffold_4845:11355726-11355830 +**	**candidate-rescued**	**Canonical miRNA**	**CDS**	[View on UCSC Genome Browser [Cornell Mirror]]

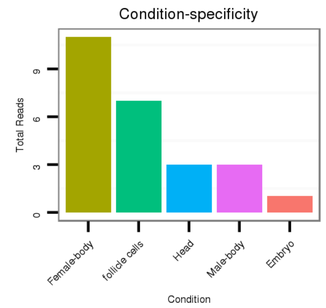
Legend: mature star **mismatch in alignment** mismatch in read

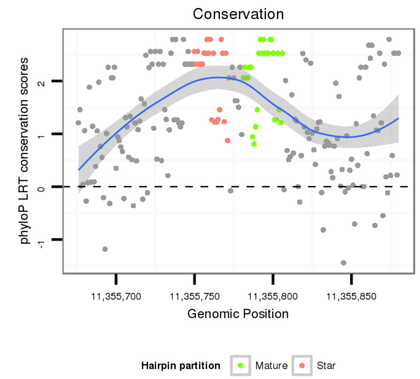
Predicted structure











Show Alternate Folds

Flybase annotation

CDS [Dere\GG22110-cds]

Repeatable elements

Name	Class	Family	Strand
(CAG)n	Simple_repeat	Simple_repeat	+

Sense Strand Reads

hide 3p reads show mid mismatch reads

```
CATATAGCGACCCAAGTCAAGGGAATCGCCAGCAGTAGCAAGCAACAGAAGCAACTGGCCAGTGCGCAGCTGCCTGTGCCGCTGTCGCCCTTGCCGCAACAACAACAGCAAACGGCAGAGGCAACGGCAGCAGCAGCAGCACCCGCCCACTCCAACGTATCCACCTCCGGTTCCCTTAGCACAATAGAAGGCTCTGCTTCGCCGC
*****************************************************..((((...(((((...(((.(((((.(((.((((((.................)))))).))).)))))).)))))))).)))).....*****************************************************
```

Read size	# Mismatch	Hit Count	Total Norm	Total	M055 female body	M057 embryo	V108 head	GSM1528801 follicle cells	V040 embryo	V107 male body	V060 head
26	0	1	7.00	7	0	0	0	7	0	0	0
22	0	1	3.00	3	3	0	0	0	0	0	0
19	0	1	2.00	2	1	0	1	0	0	0	0
27	0	1	2.00	2	1	0	1	0	0	0	0
20	0	1	2.00	2	1	0	0	0	0	1	0
24	0	1	2.00	2	0	2	0	0	0	0	0
19	0	1	1.00	1	1	0	0	0	0	0	0
26	0	1	1.00	1	0	1	0	0	0	0	0
25	0	1	1.00	1	1	0	0	0	0	0	0
26	0	1	1.00	1	0	0	1	0	0	0	0
23	0	1	1.00	1	0	0	1	0	0	0	0
19	0	1	1.00	1	0	1	0	0	0	0	0
27	0	1	1.00	1	1	0	0	0	0	0	0
27	0	1	1.00	1	1	0	0	0	0	0	0
19	1	1	1.00	1	0	0	1	0	0	0	0
22	0	1	1.00	1	0	0	1	0	0	0	0
24	0	1	1.00	1	0	1	0	0	0	0	0
21	0	1	1.00	1	0	0	1	0	0	0	0
22	1	1	1.00	1	0	0	1	0	0	0	0
21	0	1	1.00	1	0	1	0	0	0	0	0
24	0	1	1.00	1	1	0	0	0	0	0	0
18	0	20	0.05	1	0	1	0	0	0	0	0

Anti-sense strand reads

```
GTATATCGCTGGGTTCAGTTCCCTTAGCGGTCGTCATCGTTCGTTGTCTTCGTTGACCGGTCACGCGTCGACGGACACGGCGACAGCGGGAACGGCGTTGTTGTTGTCGTTTGCCGTCTCCGTTGCCGTCGTCGTCGTGGGCGGGTGAGGTTGCATAGGTGGAGGCCAAGGGAATCGTGTTATCTTCCGAGACGAAGCGGCG
*****************************************************..((((...(((((...(((.(((((.(((.((((((.................)))))).))).)))))).)))))))).)))).....*****************************************************
```

Read size	# Mismatch	Hit Count	Total Norm	Total	GSM1528801 follicle cells	V060 head	V040 embryo	V107 male body

Show Alignment With Reads

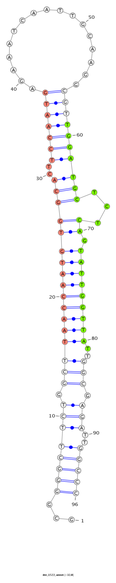
Re-alignment of all predicted orthologs

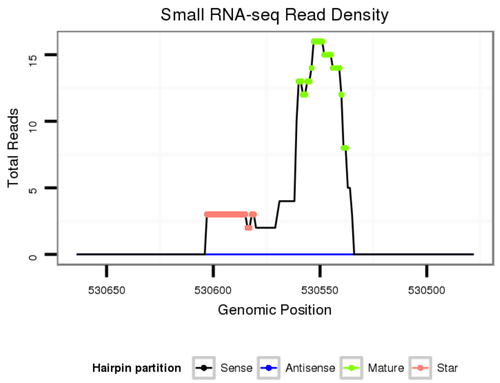
Species	Coordinate	ID	Alignment
droEre2	scaffold_4845:11355676-11355880 +	der_1520	CAT---ATAGCGACCCAAGTCAAGGGAATCGCCAGC------A--------GTAGCA-------------AG---CA------ACAGAAG---CAACTGGCCAGTGCGCAGCTGCCTGTGCCGCTGTCGCCCTTGCCGCAACA---ACAACAGCAAACGGCAGAGGCAACGGCAGCAGCAGCA-------------------GC---ACC----------CGCCCAC----------T--------CCAACGTA----------TCCACCT---------CCGGTTCCCTTAGCACAATAGAAGGCTCTGCTT----------CGCCGC
droYak3	2R:11976229-11976433 -	dya_1795	CAT---ATAGCGACCCAAGTCAAAGGAATCGCCAGC------A--------GAACA-------------AA---CA------ACAGAAG---CAACTGGCCAGTGCGCAGCTGCCTGTGCCGCTGTCGCCCTTGCCGCAACA---ACAACAGCAAACGGCAGAGGCAACGGCAGCAGCAGCA-------------------GC---ACC----------CGCCCAC----------T--------CCAACGTA----------TCAACCT---------CCGTTCCTCCAGCACAATAGAAGCCTCTGTT----------CGCCGC
droSec2	scaffold_9:543248-543455 +	dse_1843	CAT---ATAGCGACCCAAGTCAAGGGAATCGCCAGC------A------GCATAGCA-------------AA---CA------ACAGAAG---CAACTGGCCAGTGCGCAGCTGCCTGTGCCGCTGTCGCCCTTGCCGCAACA---ACAACAGCAAACGGCAGAGGCAACGGCAGCAGCAGCA-------------------GC---ACC----------CGCCCAC----------T--------CCAACGTA----------TCCACCT---------CCGTTCCTCCAGCACAATAGAAGCCTCTGTT----------TGCCGC
droSim2	2r:17766310-17766517 +	dsi_32456	CAT---ATAGCGACCCAAGTCAAGGGAATCGCCAGC------A------GCATAGCA-------------AA---CA------ACAGAAG---CAACTGGCCAGTGCGCAGCTGCCTGTGCCGCTGTCGCCCTTGCCGCAACA---ACAACAGCAAACGGCAGAGGCAACGGCAGCAGCAGCA-------------------GC---ACC----------CGCCCAC----------T--------CCAACGTA----------TCCACCT---------CCGTTCCTCCAGCACAATAGAAGCCTCTGTT----------TGCCGC
dm3	chr2R:17211888-17212089 +	dme_419	CAT---ATAGCGACCCAAGTCAAGGGAATCGCCAGC------A------GCAGCAGCA-------------AA---CA------ACAGAAG---CAACTGGCCAGTGCGCAGCTGCCTGTGCCGCTGTCGCCCTTGCCGCAACA---ACAACAGCAAACGGCAGAGGCAACGGCAGCAGCAGCA-------------------GC---ACC----------CGCCCAC----------T--------CCAACGTA----------TC----------CCGTTCCTCCAGCACAATAGAAGCCTCTGTT----------TGCCGC
droEug1	scf7180000409474:730362-730572 -		CAG---CATGCGACCCAAGTCAAGGGAATCGCCAGC------A---GCAGCAGTAGCA-------------A----A------ACAGAAG---CAACTGCCAGTGCGCAGCTGCCTGTGCCGCTGTCGCCCTTGCCGCAACA---ACAACAGCAAACGCACAGAGGCAACGGCAGCAGCAGCA-------------------A---AAG----------CGCCCAC----------T--------GTAATCCA----------TCCACCG------GACCTAGTACGACGAGCAGCACATAGAAGCCTCTGTT----------CGCCGC
droBia1	scf7180000302143:1194589-1194823 -		CAT---ATATGCGACCCAAGCCAAGGGAATCGCCAGC------AGCAGCAGCATAGCA-------------A----A------CCAGAAG---CAACTGGCCAGTGCGCAGCTGCCTGTGCCGCTGTCGCCCTTGCCGCAACA---ACAACAGCAAACGCACAGAGGCAACGGCAGCAGCAGCA-----GTAGCACTAGCAGTAGC---ACC----------CGCCCAC----------T--------CCAACCCA----------TCCCCCTCCGCCGGCTTACCACGATCAGCACATAGAAGCCTCTGTT----------TACCGC
droTak1	scf7180000415722:103138-103312 +		CAT---ATATGCGACCCAAGCCAAGGGAATCGCCAGC------A--------GTAGCA-------------A----A------A----AAGAAA---CAACTGGCCAGTGCGCAGCTGCCTGTGCCGCTGTCGCCCTTGCCGCAACA---ACAACAGCAAACGCACAGAGGCAACGGCAGCAGCAGCA------G--------CAGTAGC---ACC----------CGC----------A--------CCAACCCA----------TCCCCCT------CCTCCACACGCAGCAGCACATAGAAGCCTCTGTT----------CACGGC
droEle1	scf7180000491232:161869-162076 -		CATCAGCATGCGACCCAAGCCAAAGGAATCGCAAGC------A--------GCAGCA-------------A----A------ACAGAAG---CAACTGCCAGTGCGCAGCTGCCTGTGCCGCTGTCGCCCTTGCCGCAACA---ACAACAGCAAACGCACAGAGGCAACGGCAGCAGCAGCA-------------------GC---AAC----------CGCCCAC----------A--------CCAACCCA----------TCCCCCT------CCTCCACACGCAGCAGCACATAGAAGCCTCTGTT----------CGCCGC
droRho1	scf7180000780265:156473-156683 -		CAT---CTAGCGACCCAAGCCAAAGGAATCGCTAGC------A--------GTAGCA-------------A----A------ACAGAAG---CACTTACCCAGTGCGCAGCTGCCTGTGCCGCTGTCGCCCTTGCCGCAACA---ACAACAGCAAACGCACAGAGGCAACGGCAGCAGCAGCA------G--------CAGCAGC---AAC----------CGCCCAC----------A--------CCAACCCA----------TCCCCCT------CCACACACGCAGCAGCACATAGAATACCTCCTGTT----------CGCCCC
droFic1	scf7180000453811:56703-56922 -		CATCACCATGCGACCCAAGCCAAAGGAATCGCCAGC------A--------GTAGCA-------------A----A------ACAGAAG---CACTTGCCAGTGCGCAGCTGCCTGTGCCGCTGTCGCCCTTGCCGCAACAACAACAAGCAAACGCACAGAGGCAACGGCAGCAGCAGCA-------------------GC---ACC----------CGCCCAC----------TCAGCT---TACT----------CCAATCCA----------TCCCCCT------CATCTAATACCACCGCCACCATAGAAGCCTCTGTT----------CGCCGC
droKik1	scf7180000302411:441422-441668 +		CAG---CATGCGCCCCAAGCCAAGGGAGCTCGCCAGC------A--------GTAGCAAGCATCAGCACG---AGC---ACCAGCAGCAGAAG---CACTTGCCAGTGCGCAGCTGCCTGTGCCGCTGTCGCCCTTGCCGCAGC---C---AAGCAGCAAACGCACAGAGGCAACGGCAGC---C---ACGCCAG--------CAGCAGCACTGCC----------CGCCCAC----------T---CCACTCCATTCTACAA--GTTT-AAATTCTGCCT--------CCACCACCGCACCACATCTATAGAATCCTCCTAA----------CGCCGC
droAna3	scaffold_13266:5014085-5014313 +	dan_91	CAG---CAGGCGACCCAAGCCAAAGGAATCGCCGGC------A--------A-----ACAGCAGGCCA---AG---CAACAGCAGCAGAAGCCCCACTTGCCAGTGCGCAGCTGCCTGTGCCGCTGTTGCCGCAAC---C---AAGCAGCAAACGCACAGAGGCAACGGCAGC---C---ACGCCAG--------CGGCACGAGACCC----------CGCCCAAGC--------A--------TCAACC-------------TCCACCT------CCACCAGTAGCAACGAGCAGCATCATAGAATCCTCCTAGTT----------CGCCGC
droBip1	scf7180000395751:823775-824000 +		CAG---CATGCGACCCAAGCCAGCAAAGGAATCGCCAGCAAAG---A--------AGAGCA------GGCCAACGCA---CA------CAGAAGCCCCACTTGCCAGTGCGCAGCTGCCTGTGCCGCTGTCGCCCTTGCCGCAGC---C---ATGCAAACGCACAGAGGCAACGGCAGC---C---ACGCCAG--------CGGCACGAGACTCC----------CGCCCAAAC--------A--------CGCA----------CCACCT------CCTCCAGTAGCAACGAGCAGCATATAGAATCCTCCTGTT----------CGCCGC
dp5	3:9802137-9802349 -	dps_3826	CAG---------AGACAACCCAAAGGACTCGCCAGC------A------TCATGAGC-------------AACAGCA-----ACAGCAG---CACTTGCCAGTGCGCAGCTGCCTGTGCCGCTGTCGCCCTTGCCGCAGC---C---AAGCAGCAAACGCACAGAGGCAACGGCAGC---C---ACGCCAG--------TAGCACGC---ACGACCTACAACCACAAG----------------------C---------C----CAGCA----------CTCTCTCCCATCCCCACGCAGCATCATAGAAGCCTCCCGCCT----------CGCCGC
droPer2	scaffold_4:5118111-5118332 +	dpe_2480	CAG---------CACAACCCAAAGGACTCGCTAGC------A------TCATGTAGAC-------------AACAGCA-----ACAGCAG---CACTTGCCAGTGCGCAGCTGCCTGTGCCGCTGTCGCCCTTGCCGCAGC---C---AAGCAGCAAACGCACAGAGGCAACGGCAGC---C---ACGCCAG--------TAGCACGC---ACCACCTACAACCACAAACACACTCGTCTCATCCGCCCAC----------T--------CCCCCC

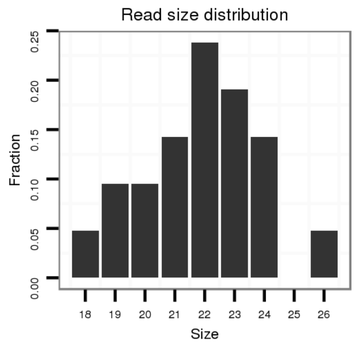
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
der_1522	**scaffold_4820:530528-530614 -**	**candidate-rescued**	**Canonical miRNA**	**5pUTR**	[View on UCSC Genome Browser [Cornell Mirror]]

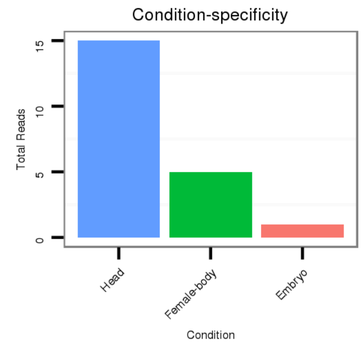
Legend: mature star mismatch in alignment mismatch in read

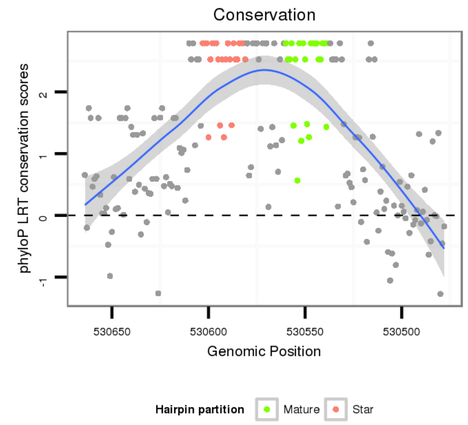
Predicted structure











Show Alternate Folds

Flybase annotation

utr5 [utr5_plus_12954]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

GTAGCAACGTCTACAATCCGCGAAAGTGCAGTCGCAGAATTTTCCGGCGGGGCTTCTGGCTTAACCAATGTGGCACTTCCAATGAGAAATCAATTGCAAGGCGTTGGATGCTCTCAGTATTGGTTATTGGCGAGATTGGCCCCGGGGCAGCATAACTAGACAGTTCCGATCAGTCCGCACTAAACCC	Read size	# Mismatch	Hit Count	Total Norm	Total	V108 head	M055 female body	GSM1528801 follicle cells	M057 embryo	V040 embryo	V107 male body
**********											
.....TTGGATGCTCTCAGTATTGGTT.....	22	0	1	4.00	4	4	0	0	0	0	0
.....TGGATGCTCTCAGTATTGGTTAT.....	23	0	1	3.00	3	3	0	0	0	0	0
.....TTGGATGCTCTCAGTATTGGT.....	21	0	1	2.00	2	2	0	0	0	0	0
.....TTGGATGCTCTCAGTATTGGTTATTGGT.....	28	1	1	2.00	2	0	0	2	0	0	0
.....TAACCAATGTGGCACTTCCA.....	20	0	1	1.00	1	0	0	0	1	0	0
.....TAACCAATGTGGCACTTCCAATG.....	23	0	1	1.00	1	0	0	0	0	0	0
.....GCAAGGCGTTGGATGCTCTCA.....	21	0	1	1.00	1	0	1	0	0	0	0
.....TCTCAGTATTGGTTATTG.....	18	0	1	1.00	1	1	0	0	0	0	0
.....ATGAGAAATCAATTGCAAGGCGTT.....	24	0	1	1.00	1	1	0	0	0	0	0
.....CTCTCAGTATTGGTTATTGG.....	20	0	1	1.00	1	0	1	0	0	0	0
.....GGATGCTCTCAGTATTGGTTATTG.....	24	0	1	1.00	1	0	1	0	0	0	0
.....TGAGAAATCAATTGCAAGGCGTTG.....	24	0	1	1.00	1	0	1	0	0	0	0
.....TGCAAGGCGTTGGATGCTCTCAGTAT.....	26	0	1	1.00	1	0	1	0	0	0	0
.....TTGGATGCTCTCAGTATTGGTTT.....	23	1	1	1.00	1	1	0	0	0	0	0
.....TGCTCTCAGTATTGGTTATTGG.....	22	0	1	1.00	1	1	0	0	0	0	0
.....TCTCAGTATTGGTTATTGG.....	19	0	1	1.00	1	1	0	0	0	0	0
.....TAACCAATGTGGCACTTCC.....	19	0	1	1.00	1	1	0	0	0	0	0

Anti-sense strand reads

CATCGTTGCAGATGTTAGGCGCTTTCACGTCAGCGTCTTAAAAGGCCGCCCCGAAGACCGAATTGGTTACACCGTGAAGGTTACTCTTTAGTTAACGTTCCGCAACCTACGAGAGTCATAACCATAACCGCTCTAACCGGGGCCCCGTCGTATTGATCTGTCAAGGCTAGTCAGGCGTGATTTGGG	Read size	# Mismatch	Hit Count	Total Norm	Total	GSM1528801 follicle cells	V107 male body	V040 embryo
**********								

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droEre2	scaffold_4820:530478-530664_-	der_1522	G-TAGCAACG----------TC-TACAATCC-----GCGAAAGTGC----------AG-----TCGCAGAA---TTT------TCCGGCG--GGGCTTCTGGCTTAACCAATGTGGCACTTCCAATGAGAAATCAATTGCAAGGCGTTGGATGCTCTCAGTATTGGTTATTGGCGAGATTGGCCCCGGGGCAGCATAACTAG----------AC----------AGTTCCGATCAGTCCGCACTAAACCC
droYak3	3R:28380157-28380343_+	dya_1797	G-TAGCAACG----------T-TGTAATCC-----GCGAAAGTGC----------AG-----TCGCAGAA---TTT------TCCGGCG--GGGCTTCTGGCTTAACCAATGTGGCACTTCCAATGAGAAATCAATTGCAAGGCGTTGGATGCTCTCAGTATTGGTTATTGGCGAGATTGGCCCCGGGACAGCATTACCAG----------AC----------GGTTCCGATTAGTCCGCAATTAAACCC
droSec2	scaffold_2807:1085-1271_+	dse_1845	G-TAGCAACG----------T-TACAATCC-----GCGAAAGTGC----------CG-----TCGCAGAA---TTT------TCCGGCG--GGGCTTCTGGCTTAACCAATGTGGCACTTCCAATGAGAAATCAATTGCAAGGCGTTGGATGCTCTCAGTATTGGTTATTGGCGAGATTGGCCCCGGGACAGCATTACTAG----------AC----------AGTTCCGATCAGTCCGCACTAAACCC
droSim2	3r:26724016-26724202_+	dsi_32457	G-TAGCAACG----------T-TACAATCC-----GCGAAAGTGC----------AG-----TCGCAGAA---TTT------TCCGGCG--GGGCTTCTGGCTTAACCAATGTGGCACTTCCAATGAGAAATCAATTGCAAGGCGTTGGATGCTCTCAGTATTGGTTATTGGCGAGATTGGCCCCGGGACAGCATTACTAG----------AC----------AGTTCCGATCAGTCCGCACTAAACCC
dm3	chr3R:27444043-27444229_+	dme_422	G-TAGCATCG----------T-TACAATCC-----GCGAAAGTGC----------AG-----TCGCAGAA---TTT------TCCGGCG--GGGCTTCTGGCTTAACCAATGTGGCACTTCCAATGAGAAATCAATTGCAAGGCGTTGGATGCTCTCAGTATTGGTTATTGGCGAGATTGGCCCCGGGACAGCATTACTAG----------AC----------AGTTCCGATCAGTCCGCACTAAACCC
droEug1	scf7180000409488:463421-463601_-		G-TAGCAACG----------T-TACAAATC-----GCGAAAGTGC----------**--------**AGAA---TTT------TCCGGCG-GGGCTTCTGGCTTAACCAATGTGGCACTTCCAATGAGAAATCAATTGCAAGGCGTTGGATGCTCTCAGTATTGGTTATTGGCGAGATTGGCCCCGAGACAGCATTTCTAA----------GC----------AGTTTCGTCAGTCCGAGTTAAAACT
droBia1	scf7180000302035:101882-102083_+		G-AAGCAACG----------TT-T-TGAATC-----GCGAAAGTGC----------AGTCGGCGTAGCAGAG---TTTC-CTCCTCCCGGCG--GGGCTTCTGGCTTAACCAATGTGGCACTTCCAATGAGAAATCAATTGCAAGGCGTTGGATGCTCTCTGTATTGGTTATTGGCGAGATTGGCCCCGAGGCAGCTGACTAGGTCTA----------GGC----------AGTTCCGATCAGTCCGAGTTAAACCC
droTak1	scf7180000415712:510640-510848_+		G-CAGCAACGTTT-TCCACTTCCATTTCCGCAGC-----GCGAAAGTGC----------**--------**AGAA---TTTCCCTTTTCCCGCGG--GGGCTTCTGGCTTAACCAATGTGGCACTTCCAATGAGAAATCAATTGCAAGGCGTTGGATGCTCTCAGTATTGGTTATTGGCGAGTTTGGCCCCGAGGCAGCATAACTATATCTA----------GAT----------CCG--CGTTCCGATCAGTCCGAGTTAAACCC
droEle1	scf7180000491194:1479823-1480036_+		ATTAGCAACG----------TT-TGTAAATC-----GCGAAAGTGC----------T--CGGAGTCTCAGAG---TTT------TTTGGCG-GGGCTTCTGGCTTAACCAATGTGGCACTTCCAATGAGAAATCAATTGCAAGACGTTGGATGCTCTCAGTATTGGTTATTGGCAAGATTGGCCCCGAGACAGCAGTATTCT----A----------GGCACTTGGATACCAATCCAATAGTTCCGATCAGTCCGCACTTAATAC
droRho1	scf7180000779322:264797-265012_-		G-TAGCAACG----------TT-TGTAAATC-----GAGAAAGTGGTTGGGGACGCGGTCGGCAG-----TCGCAGAG---TTT------TCCGGCG-GGGCTTCTGGCTTAACCAATGTGGCACTTCCAATGAGAAATCAATTGCAAGGCGTTGGATGCTCTCAGTATTGGTTATTGGCGAGATAGGCCCCTAGGCAGCATATTTAG----------GCACTGG-------TACCCATAGTTCCGATCAGTCCGAATTAAACCC
droFic1	scf7180000454114:125762-125960_+		G-TAGCAACA----------GT-AAAAAATC-----GCGAAAGTGC----------AG-----TCGAAGAG---TTT------ACCGGCG--GGGCTTCTGGCTTAACCAATGTGGCACTTCCAATGAGAAATCAATTGCAAGGCGTTGGATGCTCTCAGTATTGGTTATTGGCGAGATTGGCCCCGAGGCAGCGGTATTCG----------GCACTAG-------ACCCTATAGTTCCGATCAGTCCGAATTGAACC
droKik1	scf7180000302810:681809-682011_+		A-CAGAGACAAAA-AACACAACCGT-A-AGAATGGCGAGTCGGAAAGAGT---G----------G-----AGGCGTG---TTA-----TCCGGCGCGGGCTTCTGGCTTAACCAATGTGGCACTTCCAATGAGCAATCAATTGCAAGTCGTTGGATGCTCTCAGTATTGGTTATTGGCGAGATTGGCCCCGAGGCAGGTATAGTG----------T-T----------TGTTCCGTTAGTCCGAGT--AATTT
droAna3	scaffold_12911:3664262-3664461_-	dan_200	G-AAGCAACAAACCATCCGTACCGG-TAAGAATC-----GCGATT----C----------AG-----TCGCAGAAAAGTTA-----ACGGCG-GCCGATCTCGGCCTAACCAATGTGGCACTTCCAATGAGAAATCAATTGCAAGTCGTTGGATGCTCTCAGTATTGGTTATTGGCGAGATTGGCCCCGAGACAAATGTTGTCC----A----------CC----------CAGTGTAGTCCGTTCTAGTTTGAGCG
droBip1	scf7180000396640:523306-523505_-		G-AAGCAACAATTCATCGAAACCGG-TAAGATTC-----GCGATT----C----------AG-----TCGCAGAAAAGTTA-----ACGGCG-GCCGACTCTGGCCTAACCAATGTGGCACTTCCAATGAGAAATCAATTGCAAGTCGTTGGATGCTCTCAGTATTGGTTTTGGCGAGATTGGCCCCGCGGCAATGTTGTCT----A----------CCC----------AGTCTATTCCATTCT-AGGTTGCCC
dp5	2:16675555-16675698_-	dps_3828	G-**-------**----------**--**-**-------**-----**---------**----------**--**-----**-------**---**-------**--GGGTCTCTGGCTTAACCAATGTGGCACTTCCAATGAAAAATCAATTACAAGTCGTTGGACCTTCTCAGTATTGGTTATTGGCAAGAAGACCCACAGGCAGCTATAAGAGTTACA----------**--**----------ATTTTAAAGATAGATTAGGCTTAAGCA
droPer2	scaffold_0:3721652-3721795_+	dpe_2482	G-**-------**----------**--**-**-------**-----**---------**----------**--**-----**-------**---**-------**--GGGTCTCTGGCTTAACCAATGTGGCACTTCCAATGAAAAATCAATTACAAGTCGTTGGACCTTCTCAGTATTGGTTATTGGCAAGAAGACCCACAGGCAGCTATAAGAGTTACA----------**--**----------ATTTTAAAGATAGATTAGGCTTAAGCA
droWil2	scf2_1100000004902:9400240-9400376_+	dwi_5416	G-**-------**----------**--**-**-------**-----**---------**----------**--**-----**-------**---CTTCTAGCTTAAGCAATGCGACACTTCCAATGAGCAATCCATTCGAAATCGTTGGATGATATCAGTATTGGTTATTGGCGAGAAGCATCTAAAAGCAGCTTTAAGTT-AACAA----------AC----------AATT-AGATTGTAAGCATTATA---
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droMoj3	scaffold_6540:7667646-7667784_-	dmo_270	G-**-------**----------**--**-**-------**-----**---------**----------**--**-----**-------**--ATTTTTCTAGCTTAACCAATGTGGCAGCTCCAATGAAAAATCAATTCGAAATCGTTGGATGTCTCATATTGGTTATTGGCGAGAAGAGCTCAAACACAGCTATAAGAA----------AC----------GAAACCATCAAATATATGATATAAC
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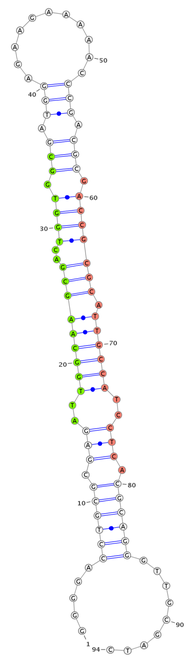
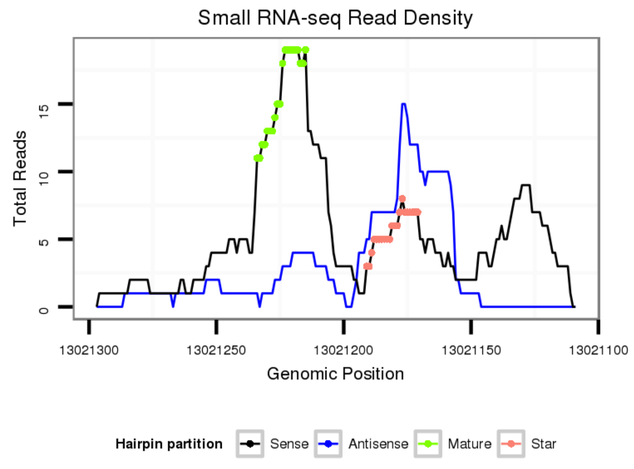
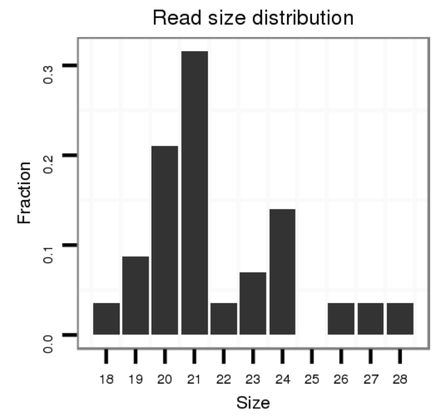
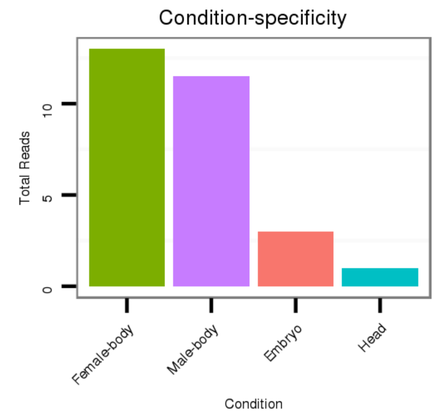
Legend: mature star **mismatch in alignment** mismatch in read

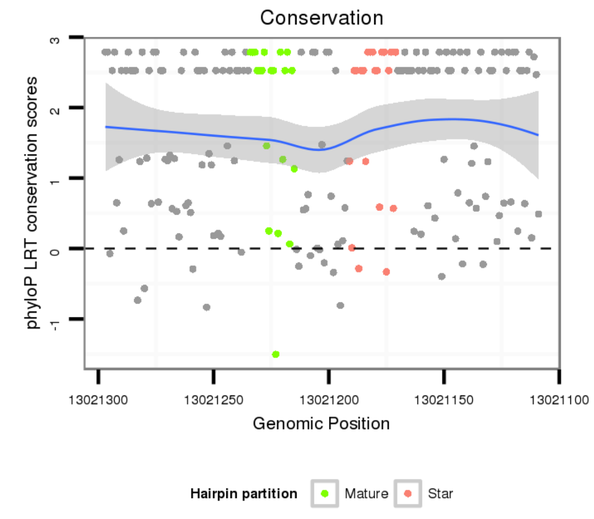
Predicted structure











der_1523_miR40 | +43.3

Show Alternate Folds

Flybase annotation

CDS [Dere\GG13787-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

AACGAGGCGGAGGCTCAGGCCTTCGCCGAGGCCCAGCAGTGGCCCAGCGGGGACCTGCGCGAGATTGGCAAGCGACTGGTGGCGATGGAGAAGAAAAACCCGACGCGACCGCGCATTGCCATCCTCACGCAGGGTTGCGATCCTGTGCTGCTCATCCAGCAGGATTCGGTGCAGGAGTTCCCGGTCACG **********.....((((((.(((..(((((((((..((((.(((.(((.....)))).))).)))))))).)))))).))).))))).....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M055 female body	V107 male body	V108 head	M057 embryo	V040 embryo
ATTGGCAAGCGACTGGTGGC	20	0	1	4.00	4	0	2	0	1	1
GACCGCGCATTGCCATCCTCA	21	0	1	2.00	2	2	0	0	0	0
CTCATCCAGCAGGATTCGGTG	21	0	1	2.00	2	2	0	0	0	0
GATTGGCAAGCGACTGGTGGC	21	0	1	2.00	2	1	1	0	0	0
GATTGGCAAGCGACTGGTGGCGA	23	0	1	1.00	1	1	0	0	0	0
ATTCGGTGCAGGAGTTCCCGGTC	23	0	1	1.00	1	0	1	0	0	0
AGGGTTGCGATCCTGTGCTGCTCA	24	0	1	1.00	1	0	0	0	0	0
ATCCTCACGCAGGGTTGCGAT	21	0	1	1.00	1	0	1	0	0	0
GATTCGGTGCAGGAGTTCC	19	0	1	1.00	1	0	0	1	0	0
CGACGCGACCGCGCATTGCCA	21	0	1	1.00	1	1	0	0	0	0
ACCTGCGCGAGATTGGCAAGCGACTGGT	28	0	1	1.00	1	1	0	0	0	0
GCAAGCGACTGGTGGCGATGGAGA	24	0	1	1.00	1	0	1	0	0	0
GACTGGTGGCGATGGAGAA	19	0	1	1.00	1	0	1	0	0	0
GCGACTGGTGGCGATGGAGAAGA	23	0	1	1.00	1	1	0	0	0	0
TTCGGTGCAGGAGTTCCCGTA	21	2	1	1.00	1	1	0	0	0	0
CAGCAGGATTCGGTGCAGG	19	0	1	1.00	1	1	0	0	0	0
CGATGGAGAAGAAAAACCCGA	21	0	1	1.00	1	0	1	0	0	0
CATCCTCACGCAGGGTTGCG	20	0	1	1.00	1	0	1	0	0	0
GCGCGAGATTGGCAAGCGACTGGT	24	0	1	1.00	1	0	1	0	0	0
TTCGGTGCAGGAGTTCCCGT	20	1	1	1.00	1	1	0	0	0	0
AAGCGACTGGTGGCGATGGAGAAG	24	0	1	1.00	1	1	0	0	0	0
AGCAGGATTCGGTGCAGGAGT	21	0	1	1.00	1	0	0	1	0	0
CAGCAGTGGCCCAGCGGGGACC	22	0	1	1.00	1	0	0	1	0	0
GGCGATGGAGAAGAAAAACCC	21	0	1	1.00	1	0	1	0	0	0
TGCCATCCTCACGCAGGGTT	20	0	1	1.00	1	1	0	0	0	0
CTCAGGCCTTCGCCGAGGCCCA	22	0	1	1.00	1	1	0	0	0	0
ACTGGTGGCGATGGAGAAG	19	0	1	1.00	1	0	1	0	0	0
GTGGCCCAGCGGGGACCTGCGC	22	0	1	1.00	1	0	0	1	0	0
TGCGATCCTGTGCTGCTCATCT	22	1	1	1.00	1	1	0	0	0	0
CCGCGCATTGCCATCCTCACG	21	0	1	1.00	1	1	0	0	0	0
GGTGCAGGAGTTCCCGGTCA	20	0	1	1.00	1	1	0	0	0	0
GACTGGTGGCGATGGAGAAGAAAAACC	27	0	1	1.00	1	0	0	1	0	0
GGCAAGCGACTGGTGGCGATGG	22	0	1	1.00	1	1	0	0	0	0
ACGAGGCGGAGGCTCAGGCC	20	0	1	1.00	1	0	1	0	0	0
TGGCAAGCGACTGGTGGCGATGGAGA	26	0	1	1.00	1	1	0	0	0	0
CGCGCATTGCCATCCTCACGCAGG	24	0	1	1.00	1	0	0	0	0	1
AGCGGGGACCTGCGCGAGATT	21	0	1	1.00	1	1	0	0	0	0
CAGGATTCGGTGCAGGAGTT	20	0	1	1.00	1	1	0	0	0	0
AGCGACTGGTGGCGATGGAGA	21	0	1	1.00	1	0	1	0	0	0
TTCGGTGCAGGAGTTCCCGGTC	22	0	1	1.00	1	1	0	0	0	0
GATCCTGTGCTGCTCATCCAGC	22	0	1	1.00	1	1	0	0	0	0
GACTGGTGGCGATGGAGA	18	0	1	1.00	1	1	0	0	0	0
CCAGCGGGGACCTGCGCGAGATTGGC	26	0	1	1.00	1	0	0	1	0	0
ATTGGCAAGCGACTGGTGG	19	0	2	0.50	1	0	1	0	0	0
GAGATTGGCAAGCGACTGGTTTT	23	3	2	0.50	1	1	0	0	0	0

Anti-sense strand reads

TTGCTCCGCCTCCGAGTCCGGAAGCGGCTCCGGGTCGTCACCGGGTCGCCCCTGGACGCGCTCTAACCGTTCGCTGACCACCGCTACCTCTTCTTTTTGGGCTGCGCTGGCGCGTAACGGTAGGAGTGCGTCCCAACGCTAGGACACGACGAGTAGGTCGTCCTAAGCCACGTCCTCAAGGGCCAGTGC **********.....((((((.(((..(((((((((..((((.(((.(((.....)))).))).)))))))).)))))).))).))))).....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M055 female body	V107 male body	V108 head	V040 embryo
TAGGAGTGCGTCCCAACGCTA	21	0	1	3.00	3	3	0	0	0
GTAGGAGTGCGTCCCAACGCTA	22	0	1	2.00	2	2	0	0	0
GTAGGAGTGCGTCCCAACGCT	21	0	1	2.00	2	2	0	0	0
GCGCTGGCGCGTAACGGTAG	20	0	1	1.00	1	0	1	0	0
TCCCAACGCTAGGACACGACG	21	0	1	1.00	1	1	0	0	0
TTGCGCTGGCGCGTAACGGTAG	22	1	1	1.00	1	0	0	1	0
GGAGTGCGTCCCAACGCTAGG	21	0	1	1.00	1	1	0	0	0
CCACCGCTACCTCTTCTTTTT	21	0	1	1.00	1	1	0	0	0
TTGCTAGGACACGACGAGTA	20	2	1	1.00	1	1	0	0	0
CCGAGTCCGGAAGCGGCTC	19	0	1	1.00	1	1	0	0	0
GGTAGGAGTGCGTCCCAACGC	21	0	1	1.00	1	1	0	0	0
CTGACCACCGCTACCTCTTCT	21	0	1	1.00	1	1	0	0	0
ACCGTTCGCTGACCACCGCTA	21	0	1	1.00	1	1	0	0	0
GGGTCGTCACCGGGTCGC	18	0	1	1.00	1	1	0	0	0
TGCGCTGGCGCGTAACGGTAG	21	0	1	1.00	1	0	0	1	0
CTGCGCTGGCGCGTAACGGTA	21	0	1	1.00	1	1	0	0	0
GGTCGCCCCTGGACGCGCTCT	21	0	1	1.00	1	1	0	0	0
TTCACCGGGTCGCCCCTGGACGC	23	1	1	1.00	1	1	0	0	0
TCGCTGACCACCGCTACCTCT	21	0	1	1.00	1	1	0	0	0
GGCGCGTAACGGTAGGAGT	19	0	1	1.00	1	0	1	0	0
CTGGCGCGTAACGGTAGGAGT	21	0	1	1.00	1	0	1	0	0
GCGCTGGCGCGTAACGGTA	19	0	1	1.00	1	1	0	0	0
GGCGCGTAACGGTAGGAGTGC	21	0	1	1.00	1	0	0	1	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droEre2	scaffold_4784:13021109-13021297 -	der_1523	AACGAGGCGGAGGCTCAGGCCTTCGCCGAGGCCCAGCAGTGGCCCAGCG---GGGACCTGCGCGAGATTGGCAAGCGACTGGTGGCGATGGAGAAGAAAAACCCGACGCGACCGCGCATTGCCATCCTCACGCAGGGTTGCGATCCTGTGCTGCTCATCCAGCAGGA---TTCGGTGCAGGAGTTCCCGGTCACG
droSim2	31:12704025-12704213 -	dsi_32458	AACGAGGCGGAGGCTCAGGCGTTCGCCGAGGCCCAGCAGTGGCCCAGCG---GGGACCTGCGCGAGATTGGCAAGCGATTGGTGGCGATGGAGAAGAAAAACCCGGCGCGGCGCGCATTGCCATTCTCACGCAGGGCTGCGATCCTGTACTGCTTATTCAGCAGGA---TTCGGTGCAGGAGTTCCCGGTCACG
droSec2	scaffold_0:5185161-5185349 -	dse_1846	AACGAGGCGGAGGCTCAGTCGTTCGCCGAGGCCCAGCAGTGGCCCAGCG---GGGACCTGCGCGAGATTGGCAAGCGATTGGTGGCGATGGAGAAGAAAAACCCGGCGCGGCGCGCATTGCCATTCTCACGCAGGGCTGCGATCCTGTACTGCTTATTCAGCAGGA---TTCGGTGCAGGAGTTCCCGGTCACG
droYak3	3L:13092479-13092667 -	dya_1798	AACGAGGCAGAGGCTCAGGCCTTCGCCGAGGCCCAGCAGTGGCCCAGCG---GGGACCTGCGCGAGATTGGCAAGCGACTGGTGGCGATGGAGAAGAAAAACCCGACGCGCGCGCGCATTGCCATCCTCACGCAGGGCTGCGATCCTGTGCTGCTTATTCAGCAGGA---TTCGGTGCAGGAGTTCCCGGTCACG
droEug1	scf7180000409711:6101265-6101453 -		AACGAGGCGGAGGCACAGCCTTCGCCGAGGCCCAGAATTGGCCAAGTG---GGGATCTTCGTGAGATTGGCAAGCGTCTGGTGGCGATGGGCAAATTAAATACGACGCGCCGCGCATTGCTATCCTCACGCAGGGCTGTGATCCTGTCCTGCTTATCCAACAGGA---CTCGGTACAGGAGTTCCCGGTCACG
droBia1	scf7180000302193:2253856-2254044 -		AACGAGGCGGAGGCACAGGCCTTCGCCGAGGCCCAGAGTTGGCCCAGCG---GGGATCTGCGCGAGATTGGCAAGCGCTGGTGGCGTCGACAAACTGAATCCGGCGCGGCGCGCATTGCCATTCTCACGCAGGGCTGCGACCCGTGCTGCTGTCCAGCAGGA---TTCGGTGCAGGAGTTCCCGGTCACG
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droKik1	scf7180000302272:666717-666905 -		AATGAGGCGGAGGGCAGGCCTTGCCGAGGCCCAAAAATGGCCGAGCG---AGGATCTGCGTGAGATTGGCAAACGTCTGGTGGCAATGGACAAACTAAATCCGTCGCCGCCACGCATTGCCATCCTCACGCAGGGTTGTGATCCCGTCCTGCTCATCCAGCAGGA---TTCGGTGCAGGAATTCCCGGTCACA
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droVir3	scaffold_13049:22492152-22492343 +	dvi_158	AACGAGGCGGAGGGCACGCCTTTGCCACTGCGCAAGGTTGGCCCGCCGACAATGATCTGCGTGAGATTGGCAAGCGCTGGTCGCGCGTGAATAAACTCAATACCGGGCGACCACGCATTGCCATACTCACGCAGGGCTGTGACCCCGTGCTGCTTATACAGCACGA---TTCGGTCCAGGAGTTTCCAGTGACA
droMoj3	scaffold_6680:17099712-17099903 +	dmo_114	AACGAAGCAGAGGCCATGCCTTTGCCACGGCGCAAGGCTGGCCGCCCGATGCGGATCTGCGTGAGATTGGCAAACGTTTGGTGGCACTGCCCAAAATCAATTCAGAGCGACCACGCATTGCCATACTCACGCAGGGCTGTGACCCCGTGCTGCTCATCCAGCACGA---CAAGGTCCAGGAGTTCCCGGTCACA
droGri2	scaffold_15121:203613-203807 +	dgr_465	AATGAGGCGGAGGCGAAGGCTTTTGCCACGGCACAAGGCTGGCGCCCGATGAGGATCTGCGTGAGATTGGCAGCGCTCTGGTTGCACTGGACAAATTGAATTCAGCGCCGACCACGCATTGCGATACTCACGCAGGGCTGTGATCCCGTGCTGCTCATCCAGCACGACGCCTCCGGTCCAGGAGTTCCCAGTTACA

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crit.total	0
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crit.uri	0
crit.back	0
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rescue.candidate	10

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
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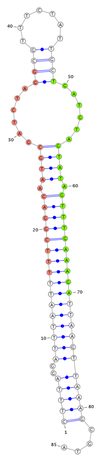
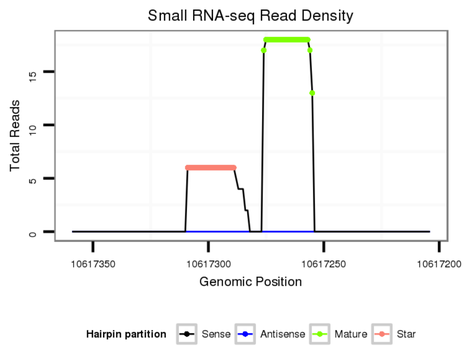
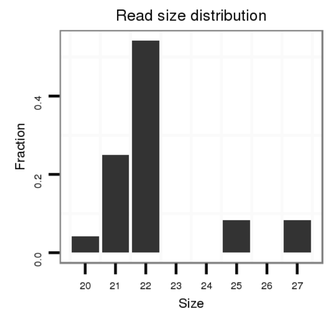
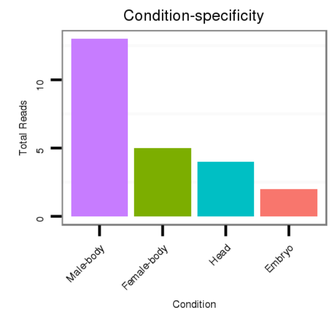
Legend: mature star mismatch in alignment mismatch in read

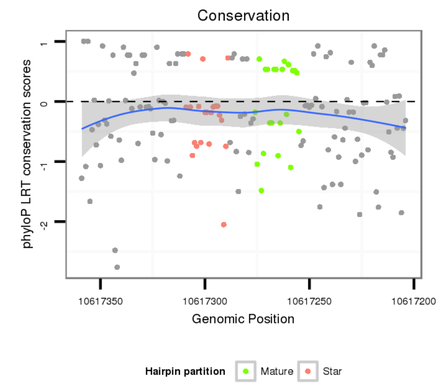
Predicted structure











Show Alternate Folds

Flybase annotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

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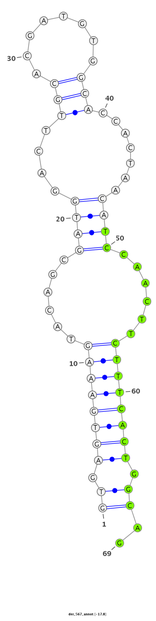
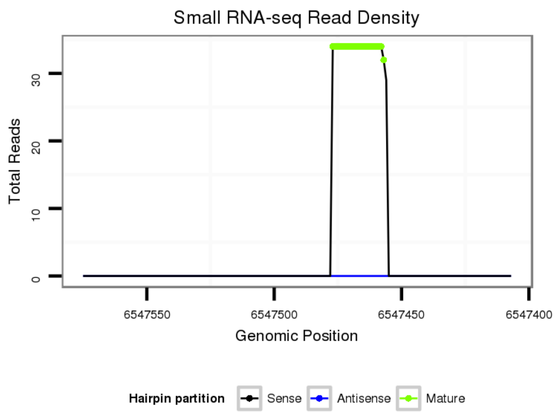
```

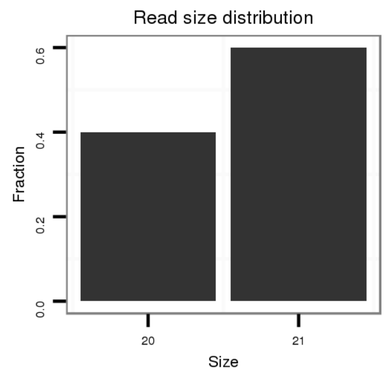
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
der_567	**scaffold_4770:6547457-6547525 -**	**candidate**	**Mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

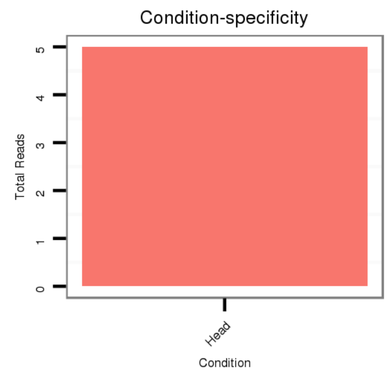
Legend: mature star mismatch in alignment mismatch in read

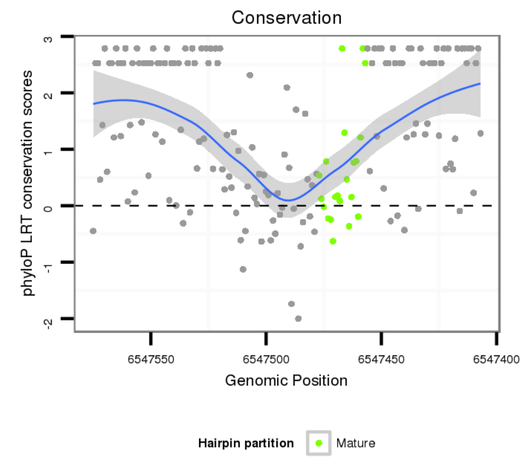
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dere\GG23206-in]; CDS [Dere\GG23206-cds]; CDS [Dere\GG23206-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

```
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                
GGGGATTCCCACCGAGAGCTGTGCCGAGGGCGTGGGCGTCTGCTGTGTGTGTGTGAGTGAAAGTACAGCGATGGACTTGCACGATGTGGCACCACTAACATCCAACTTCTTTCACTGGCAGTCGTCAATGGATGCGGCGATGTCACCAGCCAGCAGATCCTCTACTTCGAG V108 V107 V060 V040
**********((.(((((((.....((((....(((.........)))).....))))......)))))))).))..********** Read size | # Mismatch | Hit Count | Total Norm | Total | head | male body | head | embryo
.....TCCAACTTCTTTCACTGGCAGT..... 22 | 0 | 1 | 29.00 | 29 | 23 | 4 | 2 | 0
.....TCCAACTTCTTTCACTGGCAG..... 21 | 0 | 1 | 3.00 | 3 | 3 | 0 | 0 | 0
.....TCCAACTTCTTTCACTGGCA..... 20 | 0 | 1 | 2.00 | 2 | 2 | 0 | 0 | 0
.....TCCAACTTCTTTCACTGGCAGTT..... 23 | 1 | 1 | 1.00 | 1 | 1 | 0 | 0 | 0
```

Anti-sense strand reads

```
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                
CCCCTAAGGGTGGCTCTCGACACGGCTCCCGCACCCGCAGACGACACACACACTCACTTTCATGTCGCTACCTGAACGTGCTACACCGTGGTGATTGTAGGTTGAAGAAAGTGACCGTCAGCAGTTACCTACGCCGCTACAGTGGTCGGTCGTCTAGGAGATGAAGCTC V060 V108 V107
**********((.(((((((.....((((....(((.........)))).....))))......)))))))).))..********** Read size | # Mismatch | Hit Count | Total Norm | Total | head | head | male body
```

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droEre2	scaffold_4770:6547407-6547575 -	der_567	GGGGATTCCCACCGAGAGCTGTGCCGAGGGCGTGGGCGTCTGCTGTGTGTGTGTGAGTGAAA----------GTA--CAG-------CG----------AT---------G----------GACTTGCACG-A----TGTGGCACCACT----------AACATCCAAC---------TTCTTTCACTG--GCAGTCGTCAATGGATGCGGCGATGTCACCAGCCAGCAGATCCTCTACTTCGAG
droYak3	3R:3793871-3794047 +		CGGGATTCCCACCGAGAGCTGTGCCGAGGGCGTGGGCGTCTGCTGTGTGTGTGAAGTGAAA----------GTA--CAG-------CG----------AT---------C----------GATTTGCGCG-A----TATCAAAAG----ATCTCAC-----TAC--TCACATCTAAC---------TTGATTCACTT--GCAGTCGTCAATGGATGTGGCGATGTCACCAGCCAGCAGATCCTCTACTTCGAG
droSec2	scaffold_25:682357-682529 -		TGGGATTCCCACCGAGAGCTGTGCCGAGGGCGTGGGCGTCTGCTGTGTGTGTGAGTGAAA----------GTA--CAG-------CG----------AT---------C----------GATTTGCATG-A----TATCGAACCACTCACATCT----------ATCTAAC---------TTCTTTCACTT--GCAGTCGTCAATGGATGTGGCGATGTCACCAGCCAGCAGATCCTCTACTTCGAG
droSim2	3r:6178110-6178282 -	dsi_20785	TGGGATTCCCACCGAGAGCTGTGCCGAGGGCGTGGGCGTCTGCTGTGTGTGTGAGTGAAA----------GTA--CAG-------CG----------AT---------C----------GATTTGCATG-A----TATCGAACCACTAACATCT----------ATCTAAC---------TTCTTTCACTT--GCAGTCGTCAATGGATGTGGCGATGTCACCAGCCAGCAGATCCTCTACTTCGAG
dm3	chr3R:15084397-15084569 +		TGGGATTCCCACCGAGAGCTGTGCCGAGGGCGTGGGCGTCTGCTGTGTGTGTGAGTGAAA----------GTA--CAG-------CG----------AT---------C----------GATTTGCATG-A----TATCGAAACACTCACATCT----------ATCTAAC---------TTCATTCACTT--GCAGTCGTCAATGGATGTGGCGATGTCACCAGCCAGCAGATCCTCTACTTCGAA
droEug1	scf7180000409804:1349242-1349403 +		GGGGATTCCCACCGAGAGCTGCGCCGAGGGCGTGGGCGTCTGTGTGTGTGTGAGTGAAA----------GTC--CAA-------CG----------AT---------C----------GATTTGAAAG-A----TATCGA-----------AAATCTAAA---------ATCTTTCACTT--GCAGTCGTCAATGGATGTGGTGATGTCACCAGCCAGCAGATCCTCTACTTCGAG
droBia1	scf7180000302402:846250-846418 +		GGGGATTCCCACCGAGAGCTGTGCCGAGGGCGTGGGCGTCTGCTGTGTGTGTGAGTGAAA----------GTC--CAC-------CG----------AT---------C----------GATTTGCGCG-T----TATCCGAGATCT----------AAGATCTAAC---------ATCTTTCACTT--GCAGTCGTCAATGGATGTGGCGATGTCACCAGCCAGCAGATCCTCTACTTCGAG
droTak1	scf7180000410451:111104-111272 +		GGGGATTCCCACCGAGAGCTGTGCCGAGGGCGTGGGCGTATGCTGTGTGTGTGAGTGAAA----------GTC--CGC-------CG----------AT---------C----------GATTTGCACG-A----TATCGAAGATCC----------AACATGTAAA---------CTCTTTCACTT--GCAGTCGTCAATGGCTGTGGCGATGTCACCAGCCAGCAGATCCTCTACTTCGAG
droEle1	scf7180000490994:858866-859041 +		GGGGATTCCCACCGAGAGCTGTGCCGAGGGCGTGGGCGTTGCTGTGTGTGTGTGAGTGAAA----------GTC--CGC-------CG----------AT---------C----------GACTTGGCCA-A----GATCTAAGCTCTAACGTCA----------AACATCTAAC---------ATCTTTCATTT--GCAGTCGTCAATGGATGTGGCGATGTCACCAGCCAGCAGATCCTCTACTTCGAG
droRho1	scf7180000779522:16958-17112 +		GGGGATTCCCACCGAGAGCTGTGCCGAGGGCGTGGGCGTTGCTGTGTGTGTGTGAGTGAAA----------GTC--CGC-------CG----------AT---------C----------GATTTGCACG-A----G----------AT----------ATCTAAC---------ATCTTTCACTT--GCAGTCGTCAATGGATGTGGCGATGTAACCAGCCAGCAAATCCTCTACTTCGAG
droFic1	scf7180000454126:64938-65105 +		GGGGATTCCCACCGAGAGTTGTGCCGAGGGCGTGGGTGTATGTTGTGTGTGTGAGTGAAA----------GTC--CAC------TGATCCAC-------------T----------GATTTACAAG-C----GAT-------CT----------AACACCGATC---------TTCTTTCAGCTCAACAGTCGTCAATGGATGTGGCGATGTCACCAGCCAGCAGATCCTTTACTTCGAG
droKik1	scf7180000302707:304273-304438 +		GGGGATTCCCACCGAGAGCTGTGCCGAGGGCGTGGGCGTATGCTGTGTGTGTGAGTGAAA----------GTC--CAG-------G--------ATCAGAT---------C----------GATTCGGATT-A----GATCTA------ ----------ACATCCGGC---------ATCTTTCACTT--GCAGTCGTCAAGGGTGCGGAGATGTGACCAGCCAGCAGATTCTCTACTTCGAG
droAna3	scaffold_13340:15302669-15302824 -		GGGGATTCCCACAGAAAGCTGTGCCGAGGGCGTGGGTGTCTGCTGTGTGTGTGAGTGAAA----------GTT--GTC-------CG----------AT---------C----------TAAC------T----------TCCTAGAG------CTTGACC---------ATCCTTCTCTT--CCAGTCGTCAATGGATGCGGCGATGTCACCAGCCAGCAAATCCTTTACTTTGAG
droBip1	scf7180000396708:4731422-4731587 +		AGGGCTCCCACCGAAAGCTGTGCCGAGGGCGTGGGTGTCTGCTGTGTGTGTGAGTGAAA----------GTT--GTG-------G----------T----------T----------A----AATCCTACCAG-----CTCTTACATAAAT--AT-----TATAGTAA-----TATTTCCCT--CCAGTTGTCAATGGCTGCGGTGATGTCACCAGCCAACAAATCCTTTACTTCGAG
dp5	2:29533035-29533206 +		TGGCATTCCCACCGAAAGCTGTGCCGAGGGCGTGGGCGTCTGCTGTGTCTGTGAGTGAAA----------GTTGC-CAC------AAGTCCGAGG----AT---------C----------T----------T----CCACAAATGCAT--TTGCATCTAAA--TGCTATCCACTT----TC--GCAGTTGTCAAGGGATGTGGCGATGTCACCCGCCAGCAGATCGTTTACTTCGAG
droPer2	scaffold_6:4903732-4903903 +		TGGCATTCCCACCGAAAGCTGTGCCGAGGGCGTGGGCGTCTGCTGTGTCTGTGAGTGAAA----------GTTGC-CAC------AAGTCCGAGG----AT---------C----------T----CACAAATGCAT--TTGCATCTAAA--TTCTATCCACTT----TC--GCAGTTGTCAAGGGATGTGGCGATGTCACCCGCCAGCAGATCGTTTACTTCGAG
droWil2	scf2_1100000004943:3829843-3830004 +		TGGAATACCAACCGAAAGTTGTGCCGAAGGTGTTGGTGTTGTTGCATCTGTAAGTGG--------------------TC--GCC-------AA----------AC----------T----------GAAG------T----TTC--GAC--CCTGTTAATCTAGCGTGCT----AATCATTTT--CAAGTTGTCAATGGTTGTGGTTATACAACTAGCCAGCAGATTGTCTACTTTGAG
droVir3	scaffold_13047:16559345-16559545 -		TGGCATACCCACCGAGAGCTGTGCGAGGGTGTTGGCGCTGCTGCATCTGTGAGTGTAA----------GTA--GCC-------G--------CCCAGATGAACATAAAGTGATCAAGTGATCATGTACTCGGTTG-TGGTTTATC-AAGTGCT----------CAGACCTAAC---------GATTTCTTT--TCAGTTGTTAAGGGCTGCGGTGATGTTACCAGCCAGCAGACGGTTTACTTCGAG
droMoj3	scaffold_6540:12876035-12876190 -		CGGCATACCCACCGAAGCATGTGCCGAGGGTGTCGGCGCTGTTGCATCTGTGAGTACAT----------G--- ---------- ----------AAGTG---AAGTGATATTGCGTTTGCTTG-A---- ---------- ------GGC---------ACTTTCCTT--TCAGTTGTTAAGGGCTGTGGCGATGTTACCAGCCAGCAGATCGTTTACTTTGAG
droGri2	scaffold_15116:1514235-1514471 -		TGGCATACCCACCGAGAGCTGTGGTGAGGGTGTTGGTGCCTGTTGTATCTGTGAGTATGCGTTACATGTGTGCTCATGTGCACCATCAATAAAGAGTGATCA--AGTGCTCAAATGATC----------AACTGATCAAGTGATCATGTGCTTCATTG-TGGTTTATC-AAGTGCT----------CAGGCTTAAC---------GGCTTTCCTT--TCAGTTGTTAAGGGCTGCGGTGATGTTACCAGCCAGCAGACGGTATACTTCGAG

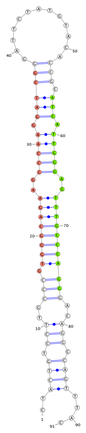
Generated: 09/08/2015 at 10:32 PM

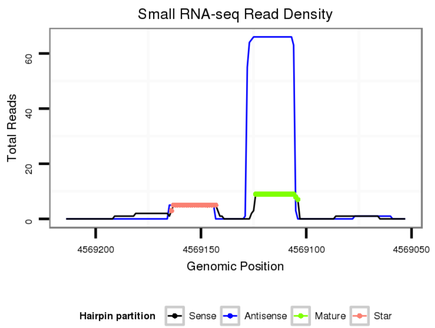
	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	2

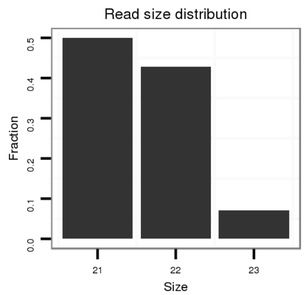
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
der_100	**scaffold_4820:4569103-4569164 -**	**candidate-rescued**	**Canonical miRNA**	**antisense_to_intron**	[View on UCSC Genome Browser [Cornell Mirror]]

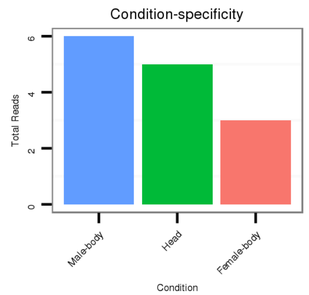
Legend: mature star **mismatch in alignment** mismatch in read

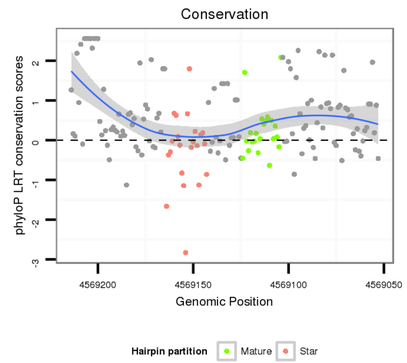
Predicted structure











Show Alternate Folds

Flybase annnotation

Antisense to intron [Dere\GG12102-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

```
AAAGGAGTTAACAAACATTGGGCCCTTCGCGGGCACTACTGTCCTTGCCCGTGGGCAGAAGCCCAAGGATCGGGATTCTATGTACACCGCATCATTGGGAGTTTGCCCAGGGACAGGCCAGTTTACATCATCTATACACCTTACGCGGGCTAGCCCTTGAAG
**********************************..((((.(((..(((.(((((((((..((((((.(((((((.............)))).)))).)))))).))))))))))))..)))).)))))....**********************************
```

Read size	# Mismatch	Hit Count	Total Norm	Total	V108 head	V107 male body	M055 female body	V060 head	M057 embryo
21	0	1	6.00	6	3	1	1	1	0
22	0	1	2.00	2	1	1	0	0	0
22	0	1	2.00	2	0	2	0	0	0
21	0	1	1.00	1	1	0	0	0	0
22	1	1	1.00	1	1	0	0	0	0
26	0	1	1.00	1	0	0	0	0	1
22	0	1	1.00	1	0	1	0	0	0
21	0	1	1.00	1	0	1	0	0	0
21	1	1	1.00	1	0	1	0	0	0
19	0	1	1.00	1	0	0	1	0	0
23	0	1	1.00	1	0	0	1	0	0
22	1	1	1.00	1	0	0	1	0	0
22	0	1	1.00	1	0	0	1	0	0
22	1	1	1.00	1	0	0	0	1	0

Anti-sense strand reads

```
TTTCCTCAATTGTTTGTAACCCGGGAAGCGCCCGTGATGACAGGAACGGGCACCCGTCTTCGGGTTCCTAGCCTAAGATACATGTGGCGTAGTAACCCTCAAACGGGTCCCTGTCCGGTCAAATGTAGTAGATATGTGGAATGCGCCCGATCGGGAACTTC
**********************************..((((.(((..(((.(((((((((..((((((.(((((((.............)))).)))).)))))).))))))))))))..)))).)))))....**********************************
```

Read size	# Mismatch	Hit Count	Total Norm	Total	V108 head	M055 female body	V040 embryo	V107 male body	V060 head
23	0	1	52.00	52	33	16	1	2	0
22	0	1	7.00	7	5	2	0	0	0
22	0	1	5.00	5	2	1	2	0	0
23	0	1	2.00	2	2	0	0	0	0
22	0	1	2.00	2	0	2	0	0	0
18	0	1	1.00	1	1	0	0	0	0
23	1	1	1.00	1	1	0	0	0	0
23	0	1	1.00	1	1	0	0	0	0
23	1	1	1.00	1	0	0	0	1	0
21	0	1	1.00	1	0	1	0	0	0
18	1	1	1.00	1	0	1	0	0	0
21	0	1	1.00	1	0	1	0	0	0

Show Alignment With Reads

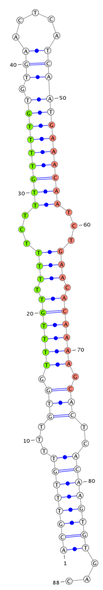
Re-alignment of all predicted orthologs

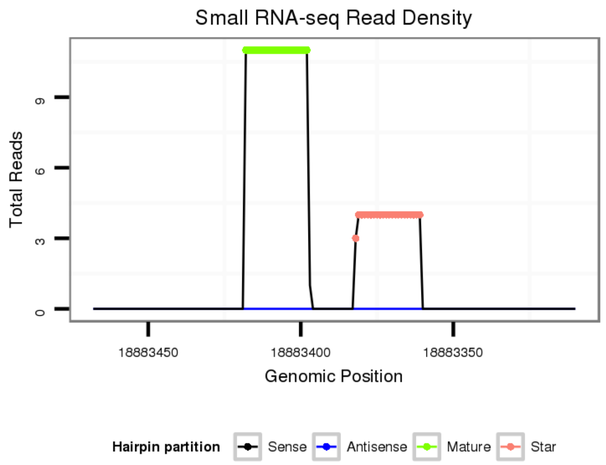
Species	Coordinate	ID	Alignment
droEre2	scaffold_4820:4569053-4569214 -	der_100	AAA--------GGA-GTTAACAAACATTG-GGCC-------CTTCG--CGGGCACTACTGTCC-TTGCCCGTGGGCAGAAGCCCAAGGATCGGG----------AT-----TCTATG-----TACACCGC----------ATCATT----------G-----GGAGT--TTGCCCAGGGACC--AGGCCAGTTTACATCATCTATACACCTTACGCGGGCT----------AGCCCTTG----------AAG
droYak3	3R:23018673-23018817 -	dya_101	AAA--------GGA-GTTAACAAACATTG-GGCC-------CTTCG--CGGGCACTACTGTCC-TTGCCGTGGGCTCAACCCAAGGATCGGA----------AT-----TCAATG-----TACACCGG----------ATCATT----------G-----GGAGT--TTACCCAGGGACC--AGGCCAGTTTACATCATCTATACACCTTGCG-------------------------------
droSec2	scaffold_22:111543-111693 +		AAA--------GGA-GTTAACAAACGCTGGGCC-------CTTCG--CGGGCACTGCTGACC-TTGCCGGAGCAGAATCCCAAGGATCGG----------AT-----TCAATG-----TGCACCGG----------ATCCTT----------G-----GGAGT--TTACCCAGGGACC--AGGCCAGCTTACATCATC----------GCGGGCT----------ACCCTCG----------
droSim2	3r:22893183-22893333 +		AAA--------GGA-GTTAACAAACGCTGGGCC-------CTTCG--CGGGCACTGCTGACC-TTGCCGGAGCAGAAACCCAAGGATCGG----------AT-----TCAATG-----TGCACCGG----------ATCCTT----------G-----GGAGT--TTACCCAGGGACC--AGGCCAGCTTACATCATC----------GCGGGCT----------ACCCTCG----------AAG
dm3	chr3R:23468153-23468303 +		AAA--------GGA-GTTAACAAACGCTGGGCC-------CTTCG--CGGGCACTACTGACC-TTGCCGGAGCAGAAACCCAAGGATCGG----------AT-----TCAATG-----TGCACCGG----------ATCCTT----------G-----GGAGT--TTACCCAGGGACC--AGGCCAGCTTACATCATC----------GCGGGCT----------ACCCTCG----------AAG
droEug1	scf7180000409770:952511-952652 +		AAA--------GGA-GTTAACAAACATTG-GGCC-------CTCTGTGAGGGCACTACTGTCC-TTGTGCAAAGCAGAATCCCAAGA-----------------------------------**-----**-----------------------TCATT----------A-----GGGAG-TTTTTAGGGACC--AGGCAGCAGTTTACATTATCTATACACCTTGCAAGGGCT----------AACGATTG----------AAG
droBia1	scf7180000302075:1453673-1453811 -		AGG--------GGA-GTTAACAAAATTG-GCC-------CTCTG--CGGGCTCTACTGACC-TTGCCGCTGAGCAGTTTACCAAGA-----------------------------------**-----**-----------------------TCATT----------G-----GGAGT-CCTTGATTGGGCC--AGGCCAGCTTACATCTATCTATGCACCTCTCAAGGGCT----------GGCGATTG----------AAG
droTak1	scf7180000413872:362751-362852 +		AAA--------GGA-GTTAACAAACGTTG-T---------**-----**-------GCTGACC-CTGCCCTGGGGCAGTCCCAAGG-----------------------------------**-----**-----------------------TCATT----------G-----GGAGATACTTGCTCAGGGGA--AGGCCAGCTTTATTATCTATACAATT----------**-------**----------AAG
droEle1	scf7180000491261:1964193-1964356 +		AAA--------GGA-GTTAACAAACATG-GGCC-------CTCTGTTGGGCAGTACTGTCC-TTGCCGAAAAGCAGTGTCCTAGGGTCAA-G----------------------------AT-----TAAATT-----TCATCCTT----------TTTCTC----------G-----GCGAA--TTGGTCAGGGGC--AGGCCAGCTTACATCATCTATACACCTTGCAAGGCT----------A----AACGATTG----------AAG
droRho1	scf7180000779391:18309-18481 -		AAA--------GGA-GTTAACAAACATTG-GGCC-------CTCTGCGGGGCAGTACTGTCC-TTGCCGATGAGCAGAAACCCAGGGTTAA-G----------------------TGTGATTTTAT-----GCAATT-----TCATCCTT----------TTTTTT----------G-----GCGAA--TTGGTCAGGGGC--AGGCCAGCTTACATCATCTATACACCTTGCAAGGGCT----------AACGATTG----------AAG
droFic1	scf7180000453826:246849-247009 -		AGA--------GGA-GTTAACAAACATTG-TGCC-------CTCTG--CGGGCTCTACTGTCT-TGTGCCGACAAAGCATTTACCCAAGATTCAGG----------G-----GCTATA-----TACACCTG----------ATCTTT----------CA----------A-----GGGAT--TTGGTCCTTGCGC--AGATCAGCTTACATTATCTATACAACTTGCAAGGGTT----------GACGATTG----------AAA
droKik1	scf7180000302697:740329-740498 +		AGGGACTAGGGGGA-GTTAACAAACATCGG-GGC-------**-----**-------GCTGCCTTGTGCCCGGGACAGTGATCTGAGC--TGGG---GC----------TGTG-----GTTAAATTCAATG-----TACACCTGGCCGGATCGCAAGAGCATCCCTCCTCTCC----------G-----GGATG-CTGCCCAGGGCC--AGGACAGCGGCATATCCTCAGATTAGTTT----------**-------**----------AAG
droAna3	scaffold_13340:19221691-19221849 -		AAA--------GGA-ATTAACAAACATTG-AGCC-------TCCCG--TGCCGATATCTGTCC-TTGCCCGAGGGAGAACCTTTGTTCCA---------------------------AT-----TGAATTTAATAGTA------**-----**-----------------**----**CA----------G-----GTGAT--CCTCCCAGGGACC--AGGACAGCTGACATCATCTATACACACTGCAAGGATA--------ATAGTATCTTATTG----------GAG
droBip1	scf7180000396413:3143036-3143179 +		AAA--------GGA-ATTAACAAACATTG-AGCC-------T----**-----**-----A-TGCCCCTGGGCGAGGCCTGTCTTCG---------------------------AT-----TGAATTTAATAGTA------**-----**-----------------**----**CA----------G-----GTGAT--CCTCCCAGGGACC--AGGACAGCTGACATCATCTATACACACTGCAAGGATA--------ATCGTATCTTATTG----------GAG
dp5	2:3822359-3822573 +		AAA--------GGA-ATTAACAAACATTG-TCTCTCTCAGCCTCTCG--AG**----------**-A-ACCGAGGGGCGCACCCAAT-------GCAGGTGGTTTTCTTTTGGTTAA---------**---**AATTC----AATT**-------**ATCGGATCGGTAAAGCCACCATCGCCGTGTGTCCGCCACTGGGAGAGAATCAGCTTATATGTATCATCATCTAA----------**-----**-GTATACACG-TTC----CTGCGGATAGTGG-TATAGTGCGC----------**-----**TC----------AACGATG----------GAG
droRer2	scaffold_7:528117-528331 -		AAA--------GGA-ATTAACAAACATTG-TCTCTCTCAGCCTCTCG--AG**----------**-A-ACCGAGGGGCGCACCCAAA-------GCAGGTGGTTTTCTTTTGGTTAA---------**---**AATTC----AATT**-------**ATCGGATCGGTAAAGCCACCATCGCCGTGTATCCGCCCCTGGGAGAGAATCAGCTTATATGTATCATCATCTAA----------**-----**-GTATACACG-TTC----CTGCGGATAGTGG-TATAGTGCGC----------**-----**TC----------AACGATG----------GAG
droVir3	scaffold_12855:2154417-2154529 +		AAA--------GGA-ATTAACAAAAGTTT-GGCG-------AA----**---------**CATCT-**----------**----------**----------**CTTGTTACG---------**---**A-**-----**-----**-----------**-----**-----**-----

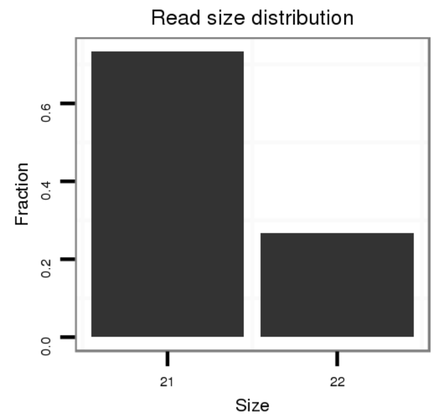
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
der_109	**scaffold_4784:18883360-18883418 -**	**candidate-rescued**	**Canonical miRNA**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

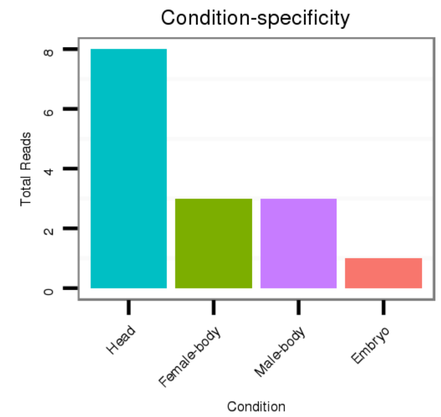
Legend: mature star **mismatch in alignment** mismatch in read

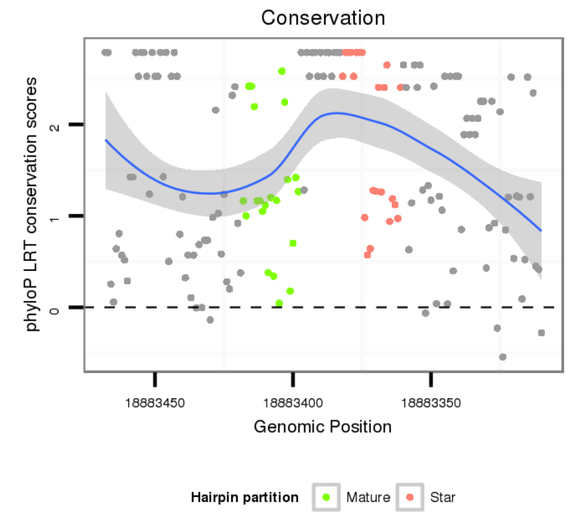
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dere\GG13428-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

```
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                
TTTCAGCGATTTGAAGGTCGTTTCCACTGTTATTCACGTTTGTTTTGTGGTTTTGTTTTTTCTTTGTTTTGTGTGAACTCATCAATGAAACAATCTGAACACAAAAGCACTCACAAGTGTGACACAGAACGTGACAAAAAAATATAAAAAACTATAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                
**********************************(((((((...(((.(((((((.(((...(((((((((.(((.....)))))))))))...)))).)))))))..)))).))))))))...**********************************
.....TTTTGTTTTTTTCTTTGTTTTG.....
.....GAAACAATCTGAACACAAAAGC.....
.....TTTTGTTTTTTTCTTTGTTTTGT.....
.....AAACAATCTGAACACAAAAGC.....
```

Read size	# Mismatch	Hit Count	Total Norm	Total	head	M055 female body	male body	embryo	head
21	0	1	10.00	10	5	2	3	0	0
22	0	1	3.00	3	2	0	0	1	0
22	0	1	1.00	1	1	0	0	0	0
21	0	1	1.00	1	0	1	0	0	0

Anti-sense strand reads

```
AAAGTCGCTAAACTTCCAGCAAAGGTGACAATAAGTGCAAACAAAACACCAAAACAAAAAAGAAACAAAACACACTTGAGTAGTTACTTTGTTAGACTTGTGTTTTCGTGAGTGTTCACACTGTGTCTTGCACTGTTTTTTTATATTTTTTGATATTTC
**********************************(((((((...(((.((((((.(((...(((((((((.(((.....)))))))))))...)))).))))))..)))).))))))))...**********************************
```

Read size	# Mismatch	Hit Count	Total Norm	Total	M057 embryo

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droEre2	scaffold_4784:18883310-18883468 -	der_109	TTTCAGCGA-TTTGAAGGTC---GTT-TCCACTGTTATTCACGTTTG-------TT-TTGTGGTTT-TGTTTTT----------TCTTTG-------TTTTGTGTGAACTCATCAATGAAACAATCT----------GAA--CACA-AAAG-CACTCACAA-GTGTGACACAGAACGTGACAAAAAAATAT----------A------AAAAACTATAAAG
droYak3	3L:21530478-21530636 +	dya_1781	TTTCAACGA-TTTGAAGGTC---GTT-TCCACTGTTATTGTCGTTTG-------TT-TTGTGGTTT-TGTTTTT----------TCTTTG-------TTTTGTGTGAACTCATCAATGAAACAATCT----------AAA--CACA-AAAG-CACTCACAA-GTGTGACACAGAACGTGACAAAAAAATAT----------A------AAAAACTATAAAA
droSec2	scaffold_19:1028759-1028922 -	dse_158	TTTCAGCGT-TTTGAAGGTC---GTT-TCCACTGTTATTCACGTTTG-------TT-TTGTGGTTT-TGTTTTT----------TCTTTG-------TTTTGTGTGAACTCATCAATGAAACAATCT----------AAA--CACA-AAAG-CACTCACAA-GTGTGACACAGAACGTGACAAAAAAAAAT--AT----------AT--A-AAAAAACTATAAAG
droSim2	3L:18687169-18687331 -	dsi_96	TTTCAGCGT-TTTGAAGGTC---GTT-TCCACTGTTATTCACGTTTG-------TT-TTGTGGTTT-TGTTTTT----------TCTTTG-------TTTTGTGTGAACTCATCAATGAAACAATCT----------AAA--CACA-AAAG-CACTCACAA-GTGTGACACAGAACGTGACAAATAAATAT----------AAA-A-AAAAAACTATAAAG
dm3	chr3L:19064535-19064700 -		TTTCAGCGT-TTTGAAGGTC---GTT-TCCACTGTTATTCACGTTTG-------TT-TTGTGGTTT-TGTTTTT---------TT------TCTTTG-------TTTTGTATGAACTCATCAATGAAACAATCT----------AAA--CACA-AAAG-CACTCACAA-GTGTGACACAGAACGTGACAAAAAAATAT--AA----------AA--A-AAAAAACTATAAAG
droEug1	scf7180000409471:411256-411427 +		TTTCAACGT-TTTGAAGGTC---GTT-TCCACTGTTATTGCGCGTTTG-------TTTTTGTGATTT-TGCCTTTTC-----TTTG------TCTTTG-------TTTTGTGTGAACTCATCAATGAAACAATCT----------AAA--CACA-AAAG-CACTCACAA-GTGTGACACAGAACGTGACAAAAAAATAT----------AAAAAAGAAAAACTATAAAG
droBia1	scf7180000302529:420860-421019 +		TTTCCAACGT-TTTGAAGGTC---GTT-TCCACTGTTATTCACGTTTG-------TTTTCGTGGCTT-TGTTTTC----------TCTTTG-------TTTTGTGTGAACTCATCAATGAAACAATCT----------AAA--CACA-AAAG-CACTCACAA-GTGTGACACAGAACGTGACAAAA-AATAC----------A-----AAAAATTATAAAG
droTak1	scf7180000414021:74763-74925 -		TTTCCAACGT-TTTGAAGGTC---GTT-TCCACTGTTATTCACGTTTG-------TTTTTGTGGTTT-TGTTTTT----------TCTTTG-------TTTTGTGTGAACTCATCAATGAAACAATCT----------AAA--CACA-AAAG-CACTCACAA-GTGTGACACAGAACGTGACAAAAAAATAT----------AA--A-AAACAACTATAAAG
droEle1	scf7180000491249:6350648-6350810 -		TTTCAACGT-TTTGAAGGTC---GTT-TCCACTGTTATTCACGATTG-------TTTTTGTGGTTT-TGTTTTC----------TCTTTG-------TTTTGTGTGAACTCATCAATGAAACAATCT----------AAA--CACA-AAAG-CACTCACAA-GTGTGACACAGAACGTGACAAAAAAATAA----------AA--A-AAAAAACTATAAAG
droRho1	scf7180000776835:46-206 -		TTTCAACGTTTTTGAAGGTC---GTT-TCCACTGTTATTCACGATTG-------TTTTTGTGGTTT-TGTTTTT----------TCTTTG-------TTTTGTGTGAACTCATCAATGAAACAATCT----------AAA--CACA-AAAG-CACTCACAA-GTGTGACACAGAACGTGACAAAAAAACA--A--A-AAAAAACTATAAAG
droFic1	scf7180000453824:438428-438582 -		TTTCAACGT-TTTGAAGGTC---GTT-TCCACTGCTGTTCACGATTG-------TTTTTGTGGTTT-TGTTTTT----------TCTTTG-------TTTTGTGTGAACTCATCAATGAAACAATCC----------AAA--CACA-AAAG-CACTCACAA-GTGTGACACAGAACGTGACAAAAAA--A-----AAACAGTATAGCC
droKik1	scf7180000302251:117775-117960 -		TTTCAACGT-TTTGAAGGTC---GTT-TCCACTGTTATTCACGATTG-------CTTTTTGTGGTTTTTGTTTTT-GTT--TTTCC------TCTTTG-------TTTTGTGTGAACTCATCAATGAAACAATCT----------AAA--CACA-AAAG-CACTCACAA-GTGTGACACAGAACGTGACAAAAAAGTATAAAAAAAAATAA--A----------CGA-----AAAAAACTATAAAG
droAna3	scaffold_13337:18377662-18377827 +		TTTTCAAAG-CCTGAAGATC---GTT-TCCACCGA----------G-------CTGTTGTGGTTT-TGTTTTT----------TCTTTG-------TTTTGTGTGAACTCATCAATGAAACAATCT----------AAA--CACA-AAAG-CACTCACAA-ATATGACACAGAACGTGACAAATAAATAA--AAAGAAAAAAATGA----------CA--A-AAAAAACTATAAAG
droBip1	scf7180000396741:1561617-1561770 +		TTTCAACGC-TTTGAAGGTC---GTC-TCCAGAGT----------G-------TTATTGTGGTTT-TGTTTT----------------------------GTGTGTGAACTCATCAATGAAACAATCT----------AAA--CACA-AAAG-CACTCACAA-ATATGACAGAGAACGTGACAAATAAATAA--AAAAAAACA---G----------CAA-----AAAAAACTATAAAG
dp5	XR_group8:7140822-7140973 -		TTTCAAACGT-TTTGAAGGTC---GTTTTGCACTGT---------GTG-------TTTCTGTGGTTT-TGTTTC-GCTCTTTTTGCCCATTTGTGTG-------TGTGATGTGAACTCATCAATGAAACAATCC----------CAAACACACA-AAAGCCACTCACAA-GTGTCACACAAAA----------------------------------A-----AAAAAACAAC---A
droPer2	scaffold_36:165555-165705 +		TTTCAAACGT-TTTGAAGGTC---GTTTTGCACTGT---------GTG-------TTTCTGTGGTTT-TGTTTC-GCTCTTTTTGCCCATTTGTGTG-------TGTGATGTGAACTCATCAATGAAACAATCC----------CAAACACACA-AAAGCCACTCACAA-GTGTCACACAAAA-------AAAAAACAC----------------------------A----------------
droWil2	scf2_1100000004762:3231747-3231881 +		TTTGAAAACTTTTTGAAGGTCATTGTT-TCCACTTA----------------------A--------------------------------TGTGTG-------CTGTGTGTGAACTCATCAATGAAACAATAC----------ACA--CACA-CGCA-CACACACAA-CAG-CACAGAGAACGTGACAAAACAAAAA----------------------------AA--A-AAAAATCATAATA
droVir3	scaffold_13049:13362168-13362290 -		TTTTTCACGT-TTTGAAGGTC---GTT-TCCACTGT---AGGCGATTCT------TGTCAGTGTTAT-TGTTGTT----------GGGAT-------TATTGTGTGAACTCATCAATGAAACAATAC----------AGAGAAGCCAACACA-CACACACAA-ATGTG---
droMoj3	scaffold_6680:13991813-13992009 +		TTTTCACGT-TTTGAAGGTC---GTT-TCCACTGTGCGCCAATCTTG-TCATTGTTGTCG-----T-TGTTGTT-GCTCTT---G------TCGCTGCTGCGATTATTGTGTGAACTCATCAATGAAACAATACAGAAAGAATCGTGGACAAA--CACA---CA-CACTTACACTCTGTTGTATATAAA----------GGCCGATGTGATAAGCACAGAT---A------TACAACTATATAT
droGri2	scaffold_15110:18794239-18794314 -		TTTTCACGT-TTTGAAGGTC---GTT-TGCACTGT---GCACGTT-G-------TTATTGTTGT---------------------------------TGTTGTGTGAACTCATCAATGAAACAAT---

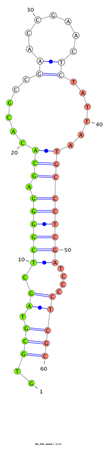
Generated: 09/08/2015 at 07:58 PM

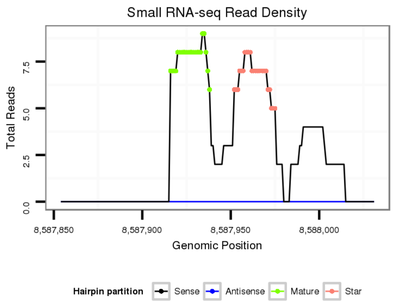
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	2
rescue.candidate	2

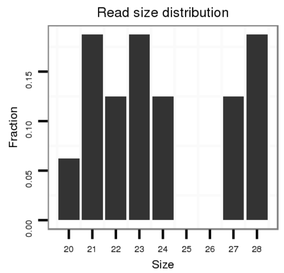
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
der_401	**scaffold_4690:8587904-8587981 +**	**candidate-rescued**	**Mirtron**	**intron**	[View on UCSC Genome Browser [Cornell Mirror]]

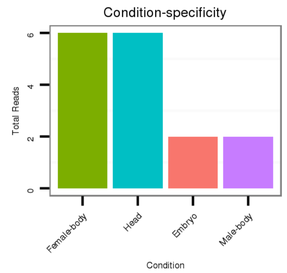
Legend: mature star mismatch in alignment mismatch in read

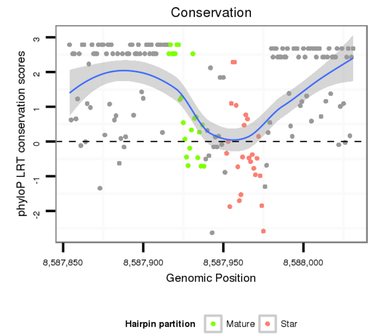
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dere\GG19161-in]; CDS [Dere\GG19161-cds]; CDS [Dere\GG19161-cds]; utr3 [utr3_plus_8558]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

```
AGCCGCCAAACTCGACGGTGATCCACACGACACCTGGCAATGCAGTGCAAGTGCGTAACAAAGTGCGTAGCTCGGGGAGCACACGCCCGAACCGAACTCTATTAATGCCCTCGATCCCCTCGCACACAGATCCCTCCAACCTTTCCGTGTAAGATCAAACCCGAACCGAACCGAACACGCAGCA
*************************************************************..(((.((.(((((((.(((.......((.......)).......)))))))))....)))))*************************************************
```

Read size	# Mismatch	Hit Count	Total Norm	Total	M055 female body	V108 head	M057 embryo	V107 male body	V060 head	V040 embryo
23	0	1	3.00	3	0	2	0	1	0	0
24	0	1	2.00	2	1	1	0	0	0	0
21	0	1	1.00	1	0	0	1	0	0	0
26	0	1	1.00	1	0	0	1	0	0	0
24	0	1	1.00	1	1	0	0	0	0	0
20	0	1	1.00	1	0	0	0	0	1	0
19	0	1	1.00	1	0	1	0	0	0	0
28	0	1	1.00	1	0	0	0	0	0	0
21	0	1	1.00	1	0	0	0	0	1	0
28	0	1	1.00	1	0	0	0	0	0	0
21	0	1	1.00	1	0	0	0	0	0	1
27	0	1	1.00	1	1	0	0	0	0	0
27	0	1	1.00	1	0	0	0	0	0	0
22	0	1	1.00	1	1	0	0	0	0	0
19	2	1	1.00	1	0	0	0	1	0	0
28	0	1	1.00	1	0	1	0	0	0	0

Anti-sense strand reads

```
TCGGCGGTTTGAGCTGCCACTAGGTGTGCTGTGGACCGTTACGTCACGTTCACGCATTGTTTCACGCATCGAGCCCCTCGTGTGCGGCTTGGCTTGAGATAATTACGGGAGCTAGGGGAGCGTGTGTCTAGGGAGGTTGGAAAGGCACATTCTAGTTTGGGCTTGGCTTGTGCGTCGT
*************************************************************..(((.((.(((((((.(((.......((.......)).......)))))))))....)))))*************************************************
```

Read size	# Mismatch	Hit Count	Total Norm	Total	V107 male body	V108 head

Show Alignment With Reads

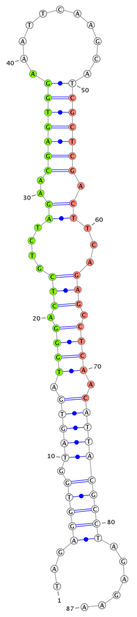
Re-alignment of all predicted orthologs

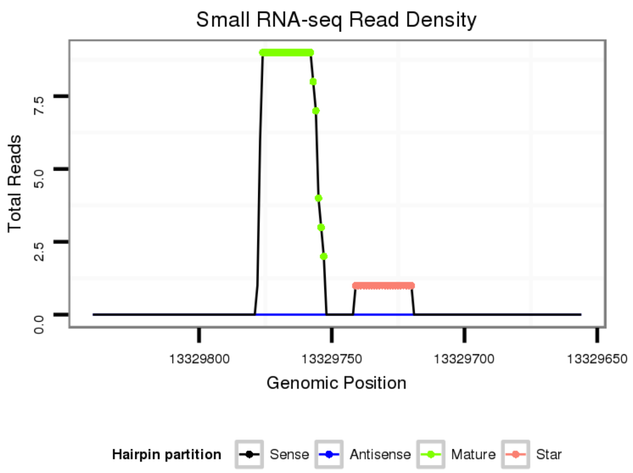
Species	Coordinate	ID	Alignment
droEre2	scaffold_4690:8587854-8588031 +	der_401	AGCCGCCAAACTCGACGGTGATCCACACGACACCTGGCAATGCAGTGCAAGTGCGTAACA---AAGTGCGTAGCTC----------G-GGGAGCACA----------CGC--CGA--------ACCGAACTC----------TATTAATGC--C----------A---TC--CCC----------TCG----------CA--CACAGATCCCTCCAACCTTTCC---GTGTAAGATCAAACCCGAACCGAACCGAACACGCAGCA
droYak3	X:16895111-16895288 +	dya_1456	AGCCGCCAAACTCGACGGTGATCCACACGACACCTGGCAATGCAGTGCAAGTGCGTAACA---AAGTGCGTAGCTC----------G-AGGAGCAGC----------CGC--CGA--------ACCGAACTC----------TATTAATGC--C----------A---TC--G----------A---TC--ACC----------TCG----------CA--CACAGATCCCTCCAACCTTTCC---GTGTAAGATCAAACCCGAACCGAACCGAACACGCAGCA
droSec2	scaffold_8:576711-576895 +		AGCCGCCCCAAGTCGACGGTGATCCACACGACACCTGGCAATGCAGTGCAAGTGCGTAACA---AAGTGCGTAGAA----------G-GGGAGCA--------TGGAGCACC--CGC--CGA--------ACCGAACTC----------TACTAATGA--A----------C----------TC--G----------A---TC--ACC----------TCG----------CA--CACAGATCCCTCCAACCTTTCC---GTGTAAGATCAAACCCGAACCGAACCGAACACGCAGCA
droSim2	X:17364855-17365039 +	dsi_32460	AGCCGCCCAAGTCGACGGTGATCCACACGACACCTGGCAATGCAGTGCAAGTGCGTAACA---AAGTGCGTAGAA----------G-GGGAGCA--------TGGAGCACC--CGC--CGA--------ACCGAACTC----------TACTAATGA--A----------C----------TC--G----------A---TC--ACC----------TCG----------CA--CACAGATCCCTCCAACCTTTCC---GTGTAAGATCAAACCCGAACCGAACCGAACACGCAGCA
dm3	chrX:18267185-18267369 +	dme_425	AGCCGCCCAACTCGACGGTGATCCACACGACACCTGGCAATGCAGTGCAAGTGCGTAACA---AAGTGCGTAGAA----------G-GGGAGCA--------CGGAGCACC--CGC--CGA--------ACCGAACTC----------TACTAATGA--A----------C----------TC--G----------A---TC--ACC----------TCG----------CA--CACAGATCCCTCCAACCTTTCC---GTGTAAGATCAAACCCGAACCGAACCGAACACGCAGCA
droEug1	scf1800000409528:449294-449472 +		AGCCGCCAAACTCGACGGTGATCCACACGACACCTGCAATGCAGTGCAAGTGCGTAACA---AAGTGCGTAGCTC----------A-GGGAGCAC----------CAG--CGA--------TTAAAACTG----------TATTAATAT--C----------A---TG--ACC----------A---TCA----------AA--TACAGATCCCTCCAACCTTTCC---GTGTAAGATCAAACCCGAACCGA-CACGCA-CA
droBia1	scf1800000302432:991025-991196 -		AGCCGCCCAAC---ACGGTGATCCACACGACACCTGGCAATGCAGTGCAAGTGCGTAACA---AAGTGCGTAGCTC----------A-GGGAGCAC----------CGC--CGA--------CCAAAACTC----------CACTAATGC--C----------C----------TC--G----------A---TG--ACC----------CCG----------A---TACAGATCCCTCCAACCTTTCC---GTGCAAGATCAAGCCCGAACCGAACACGCAGCA
droTak1	scf1800000415395:271880-272072 +		AGCCGCCCAACTCGACGGTGATCCACACGACACCTGGCAATGCAGTGCAAGTGCGTAACA---AAGTGCGTAGCTC----------A-GGGAGCAC----------CAC--CGA--------CCAAAACTC----------GATAATGT--C----------C----------TC--G----------T---AC-T-TA----------C---AT-TGCCTCCAACTTACCA---GTGCAAGATCAAACCCGAACCGA-CACGCAGCA
droEle1	scf1800000491006:507673-507853 +		AGCCGCCCAACTCGACGGTGATCCACACGACACCTGGCAATGCAGTGCAAGTGCGTAACA---AAGTGCGTAGCTC----------G-AGGAGCAGC----------CAT--CGA--------CCAAAACTG----------TATTAATGA--T----------TGTC----------TC--G----------A---TG--ACC----------TCC----------A---TACAGATCCCTCCAACCTTTCC---GTGTAAGATCAAACCCGAACCGA-CACGCAGCA
droRho1	scf1800000779985:1003450-1003621 +		AGCCGCCCAACTCGACGGTGATCCACACGACACCTGGCAATGCAGTGCAAGTGCGTAACA---AAGTGCGTAGCTC----------A-AGGAGCAGC----------CAC--CGA--------CCAGAACTG----------TACTAATT---C----------C----------C--C----------A---TG--ACC----------TCG----------C--CACAGATCCCTCCAACCTTTCC---GTGTAAGATCAAACCCGAACCGA-CACGCAGCA
droFic1	scf1800000453829:1364555-1364749 -		AGCCGCCCAACTCGACGGTGATCCACACGACACCTGGCAATGCAGTGCAAGTGCGTAAGA---AAGTGCGTAGCTC----------G-CGAGGCAGC----------TAT--CGA---GTTGACCAGAATA----------CTACTAATGC--C----------C----------TC--G----------T---TG--CTT----------C---TAACCTCCGAT---CCGT---ACAGATCCCTCCAACCTTTCC---GTGTAAGATCAAACCCGAACCGA-CACGCAGCA
droKik1	scf1800000302696:1335662-1335841 +		AGCCGCCCAAAACGACGGTGATCCACACGACCTCCGGCAATGCAGTGCAAGTGCGTAACA---AAGTGCGTAGCTC----------A-CGAGGCAGC----------CC--CCC--------CCCCCCCCC----------AAGTTGGAGCCGAACGACTAACGCA----------T----------T--C----------C----------TCCAATT----------TC--GAAGATCCCTCCAACCTTTCCGAGTGTGAATCAAACCAGACGACCGAACACGCAGCA
droAna3	scf1800000413248:931379-931586 -		AGCCGCCCAAAC---ACGGTGATCCACACGACCTCCGGCAATGCAGTGCAAGTGCGTAACA---AAGTGCGTAGCTC----------A-AAGAGCTC----------TCT--CGA--------CATTTTTT----------CATTAATTA--A----------TTATAATTATAATTATAATTTTAATAATTATT---TG--G----------A---AA--CCC----------TGC----------TTTATATA--TATAGATCCCTCCAACCTTTCC---GTGTAAGATCAAACCCGAACCGAACACGCAGCA
droBip1	scf1800000395920:35111-35313 +		ACCGCCCAAT---ACGGTGATCCACACGACCTCCGGCAATGCAGTCCAAGTGCGTAACA---AAGTGCGTAGCTCCCCTTAG----A-CAAAGTTTCAAATAAAAACATTATATATC--TAT--AAA--------TATAATTTA----------TAATAATTA--T----------T----------T--C----CTC--ATT----------TCA----------AT--TTAGATCCCTCCAAATTTTCC---GTGTAAATATCAAACCCGAACCGAACACGCAGCA
dp5	XL_group3a:228604-228785 +		AGCCAGCCAACTCGACGGTGATCCACACGACACCAACGCAATGCAGTGCAAGTGCGTAACA---AAGTGCGTAGCTG----------G-AAA---TTTG----------CCC--C----------
droPer2	scaffold_39:508452-508633 -		AGCCAGCCAACTCGACGGTGATCCACACGACACCAACGCAATGCAGTGCAAGTGCGTAACA---AAGTGCGTAGCTG----------G-AAA---TTTG----------CCC--C----------
droWil2	scf2_1100000004515:1509862-1510103 +		ACCGCCCCAATCGACGGTGATCCACACGACCTCCGGCAATGCAGTGCAAGTGCGTAACATCAATGCGTAGCTA----------G-ATGTGTA----------TCGTCCCCCATCCGCGAATCCTGAATCACAAACTGTTCCTCCCTACACAAAAGTTGTATCCCA-TTCCATGCTAAATCTTGTTTTCCATTTCTTGCTATTCCCCCGCCACGATCCCTCCAACCTTTCA---ATGTAAGATCAAACCCGAACCGAAGACCAGCA
droVir3	scaffold_12970:3051811-3051881 +		AGCCGCCCAAATCGACGGTGATCCACACGACACCAACGCAATGCAGTGCAAGTGCGTAACA---AAGTGCGTAGCT----------G-------------------------------CCC--C----------
droMoj3	scaffold_6473:3887612-3887865 +	dmo_665	AGCCGCCCAACACGACGGTGATCCACACGACACCAACGCAGCAGTGCAAGTGCGTAACA---AAGTGCGTAGCAGTTGCTAAAGTAAAGCATACCCAACGCAATTTTAAAACACACACACACACACACACACAGAGTCAGCCCCTCCACACACACACACACACACAGAGTCAGCCCCTCCACACACACACACACACACAGAGTCAGCCCCTCC

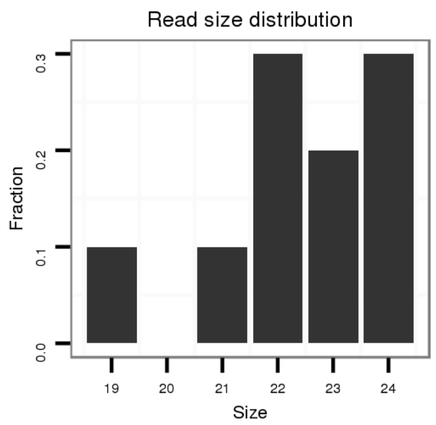
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
der_1524	**scaffold_4690:13329706-13329790 -**	**candidate-rescued**	**Canonical miRNA**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

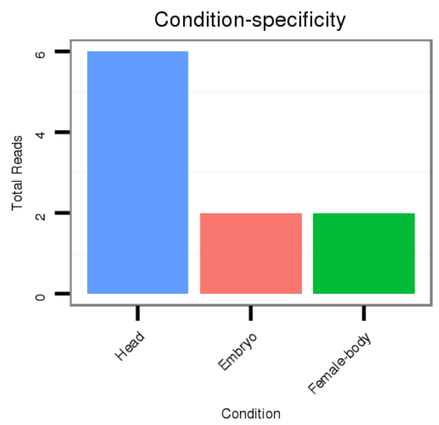
Legend: mature star **mismatch in alignment** mismatch in read

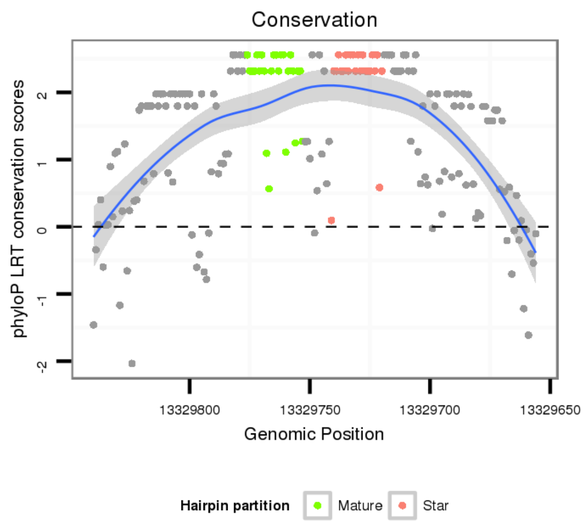
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dere\GG17798-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

TTAAACTTTAGGAACTATGAGCGGGAACTTGTTCTGAAAGACCCAAACTTAGAGGTGGTAGTGATGGGACTCGTCTAGAACGAGTGGAAATTCAAGCATCGCTCGACTTCAGAGCCTCAACATTACGCCTAGAGAACGACAACAGCTTTAGATCAATGCGACCCCGCTTAGGAATCGGGAAATAG	Read size	# Mismatch	Hit Count	Total Norm	Total	V108 head	M057 embryo	M055 female body	V060 head	GSM1528801 follicle cells
**********...(((((.(((((.((((.(((....((..(((((((.....)))))))..))...))).))))..))))))))))).....**********										
.....TGGGACTCGTCTAGAACGAGTGGA.....	24	0	1	2.00	2	1	0	1	0	0
.....ATGGGACTCGTCTAGAACGAGT.....	22	0	1	2.00	2	2	0	0	0	0
.....CGCTCGACTTCAGAGCCTCAAC.....	22	0	1	1.00	1	0	1	0	0	0
.....GATGGGACTCGTCTAGAACGAGT.....	23	0	1	1.00	1	0	1	0	0	0
.....TGGGACTCGTCTAGAACGAGTGGT.....	24	1	1	1.00	1	0	0	1	0	0
.....ATGGGACTCGTCTAGAACGAGTG.....	23	0	1	1.00	1	0	0	0	1	0
.....ATGGGACTCGTCTAGAACGAGA.....	22	1	1	1.00	1	1	0	0	0	0
.....TGGGACTCGTCTAGAACGA.....	19	0	1	1.00	1	1	0	0	0	0
.....ATGGGACTCGTCTAGAACGAG.....	21	0	1	1.00	1	1	0	0	0	0
.....ATGGGACTCGTCTAGAACGAGTGG.....	24	0	1	1.00	1	0	0	1	0	0

Anti-sense strand reads

AATTTGAAATCCTTGATACTCGCCCTTGAACAAGACTTTCTGGGTTTGAATCTCCACCATCACTACCCTGAGCAGATCTTGCTCACCTTTAAGTTCGTAGCGAGCTGAAGTCTCGGAGTTGTAATGCGGATCTCTTGCTGTTGTCGAAATCTAGTTACGCTGGGGCGAATCCTTAGCCCTTTATC	Read size	# Mismatch	Hit Count	Total Norm	Total	V040 embryo
**********...(((((.(((((.((((.(((....((..(((((((.....)))))))..))...))).))))..))))))))))).....**********						

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droEre2	scaffold_4690:13329656-13329840 -	der_1524	TTAAA-CTTTAGGAA-----CTATGAGCGGGAACTTGTTCTGAAAGACCCA-----AA---CTTAG-AGGTGGTAGTGATGGGACTCGTCTAGAACGAGTGGAAATTC--AAGCATCGCTCG-ACTTCAGAGCCTCAACATTACGCC-TAGAGAAC-GACAAC-AGCTT--TAGATCAATGCGACCCCGCTTAGG-A----ATCG----GGAAA---------TA-G
droYak3	X:7836394-7836583 +	dya_1799	TTAAG-AATTAGAAATAACAATGTAAGCGGGAACTTGTTCTGAAAGACCCA-----AA---ATAAG-AGGTGGTAGTGATGGGACTCGTCTAGAACGAGTGGAAATTC--AAGCATCGCTCG-ACTTCAGAGCCTCAACATTACGCC-TAGAGAAC-GACAAC-AGCTT--TAGATCAATGCGACCCCGCTTAGG-A----ATCG----AGAAT---------TG-G
droSec2	scaffold_20:193495-193674 +	dse_1847	ATAACAAATAAGAAA-----CCATAAGCGGGAACTTGGTCTGAAAGACCCC-----AA---ATAAG-AGGTGGTAGTGATGGGACTCGTCTAGAACGAGTGGAAATTC--AAGCATCGCTCG-ACTTCAGAGCCTCAACATTACGCC-TAGAGAAC-GACATC-AGGGT--TAGATCATTGCGACCCCGCTTAGG-A----AACG----AG---------**---**
droSim2	x:12890273-12890452 +	dsi_32459	ATAACAAATAAGAAA-----CCATAAGCGGGAACTTGGTCTGAAAGACCCC-----AA---ATAAG-AGGTGGTAGTGATGGGACTCGTCTAGAACGAGTGGAAATTC--AAGCATCGCTCG-ACTTCAGAGCCTCAACATTACGCC-TAGAGAAC-GACATC-AGGTT--TAGATCATTGCGACCCCGCTTAGA-A----ACAG----AA---------**---**
dm3	chrX:13553555-13553734 +	dme_424	ATAAG-AATTAGAAA-----CCATAAGCGGGAACTTGGTCTGAAAGACCCC-----AA---ATAAG-AGGTGGTAGTGATGGGACTCGTCTAGAATGAGTGGAAATTCA-AAGCATCGCTCG-ACTTCAGAGCCTCAACATTACGCC-TAGAGAAC-GACATC-AGGTT--TAGATCATTGCGATCCCGCTTAGG-A----AACG----AG---------**---**
droEug1	scf7180000408958:35928-36112 -		G-----GGAA-----TTTTAAGCGGGAACTTGTTCTGAAAGACCGA-----AAAATAAAAGAAGGTGGTAGTGATGGGACTCGTCTAGAACGAGTGGAAATTC--AAGCATCGCTCG-ACTTCAGAGCCTCAACATTACGCC-TAGAGAAC-GACAAC-AGCTT--TAGATCAATGCGACCCCGCTTAGGAGAATAATCG----AGTTA---------AG-G
droBia1	scf7180000302041:563677-563853 +		T-----TAGGCA-----CTGTAAGCGGGAACTTGTTCTGAAAGACCCC-----AG---ATAAG-AGGTGGTAGTGATGGGACTCGTCTAGAACGAGTGGAAATTC--AGCCGCGCTCG-ACTTCAGAGCCTCAGCATTACGCC-TAGAGAAC-GACATC-AGCTT--TAGATCAATGCGACCCCGCTTAGG-C----ATCA----GGCAC---------CG-A
droTak1	scf7180000414393:30814-31003 -		CTA---TAGGAA-----CTGTAAGCGGGAACTTGTTCTGAAAGACCAA-----AG---TTAAG-AGGTGGTAGTGATGGGACTCGTCTAGAACGAGTGGAAATTC--AAGCGTCGCTCG-ACTTCAGAGCCTCAACATTACGCC-TAGAGAAC-GACAAC-AGCTT--TAGATCAATGCGACCCCGCTTAGG-A----ATCG----AATATATTGCCCACTGGG
droEle1	scf7180000491044:215068-215250 +		AA---AATTAGAAA-----ATATAAGCGGGAACTTGTTCTGAAAGACCCT-----AA---ATAAG-AGGTGGTAGTGATGGGACTCGTCTAGAACGAGTGGAATTTC--AAGCATTGCTCG-ACTTCAGAGCCTCAACATTACGCC-TAGGGAAC-GACAACTAGCTT--TAGATCAATGCGACCCCGCTTAGG-A----ATCG----AGAAT---------TG-C
droRho1	scf7180000779510:38390-38573 +		TTG--AATTAGGAA-----CTGTAAGCGGGAACTTGTTCTGAAAGACCCT-----AA---ATAAG-AGGTGGTAGTGATGGGACTCGTCTAGAACGAGTGGCATTTA--AAGCATCGCTCG-ACTTCAGAGCCTCAACATTACGCC-TAGAGAAC-GACAAC-AGCTT--TAGATCAATGCGACCCCGCTTAGG-A----ACCG----AGTAT---------TGCG
droFic1	scf7180000454073:1442993-1443178 +		TCA--AATTAGAAA-----CTTCAAGCGGGAACTTGTTCTGAAAGAACCA-----AAA--TTAAG-AGGTGGTAGTGATGGGACTCGTCTAGAACGAGTGGAATTTC--AAGCATCGCTCG-ACTTCAGAGCCTCAACATTACGCC-TAGAGAACGGACAAC-AGCTT--TAGATCAATGCGACCCCGCTTAGG-A----ATCG----AGTAC---------TACG
droKik1	scf7180000302698:307804-307975 -		A-----------------TAAGCGGGAACTTGTTCTGAAAGACCCAATACAAA---ATAAG-AGGTGGTAGTGATGGGACTCGTCTAGAACGAGTGGAATTTA--AAGCATCGCTCG-ACTTCAGAGCCTCAACATTACGCC-TAGAGAAC-GACAAC-AATTT--TAGATCAATGCGACCCCGCTTAGG-A----GTTGTAGGAG---------**---**
droAna3	scaffold_13334:472145-472316 +	dan_4039	-----AGCGGGAACTTGTTCTGAAAGATCAAA--CAAT---TTAAG-AGGTGGTAGTGATGGGACTCGTCTAGAACGAGTGGAATTTTT-GAGCATCGCTCG-ACTTCAGAGCCTCAACATTACGCCTTAGAGAAAAGACAAC-AGCTT--TAGATCAATGCAACCCGCTTAGG-A----AGTG----CGAGC---------CT-G
droBip1	scf7180000396431:1081229-1081393 -		-----AGCGGGAACTTGTTCTGAAAGATCCAA--C-AG---TGAAG-AGGTGGTAGTGATGGGACTCGTCTAGAACGAGTGGAATTTTG-AAGCATTGCTCG-ACTTCAGAGCCTCAACATTACGCC-TAGAGACCAGACAAC-AGCTTTTTAGATCAATGACCACCCGCTTGGG-G----A----AGTA---------**---**
dp5	XL_group3b:100247-100389 +	dps_110	-----GTGGGTACTTGTTTTGAAAGAACAT-----AT---CGAAG-GGTTGGTAGTGATGGGACTCGTCTAGAACGAGCGGAATTTC--AAACATTGCTCG-ACTTCAGAGCCTCAACATTACGCC-TAGAGAAC-GCAACC-AGCTT--TCGACCA-TGCATCCG--------**-**----**----**----**-----**---------**---**
droPer2	scaffold_56:124053-124186 +	dpe_157	-----GTGGGTACTTGTTTGAAAGAACAT-----AT---CGAAG-GGTTGGTAGTGATGGGACTCGTCTAGAACGAGCGGAATTTC--AAACATTGCTCG-ACTTCAGAGCCTCAACATTACGCC-TAGAGAAC-GCAACC-AGCTT--TCGACCA----------**-**----**----**----**-----**---------**---**
droVir3	scaffold_12970:5369119-5369203 -	dvi_24642	A-----------------**----------**-----**--**---**-----**-AGAGGTAGTGATGGGACTCACCTAGAACGAGTGGAATATTT--AAGCATTGCTCGCACTTCAGAGCCTCAGCATTACGCC-TAGAGAA**-**------**-**-----**--**----------**-**----**----**----**-----**---------**---**
droMoj3	scaffold_6473:4951753-4951833 -	dmo_3154	-----**----------**-----**----------**-----**--**---**-----**----**----**GGTAGTGATGGGACTCACCTAGAACGAGTGGATTATTT--TAGCATTGCTCGCACTTCAGAGCCTCAGCATTACGCC-TAGAGAA**-**------**-**-----**--**----------**-**----**----**----**-----**---------**---**
droGri2	scaffold_15203:9467764-9467849 +	dgr_467	A-----**----------**-----**----------**-----**--**---**-----**-AGAAGTAGTGATGGGACTCAACTAGAACGAGTGGAATTTTAAAAGCATTGCTCGCACTTCAGAGCCTCAGCATTACGCC-TAGAGA**-**------**-**-----**--**----------**-**----**----**----**-----**---------**---**

Generated: 09/08/2015 at 07:58 PM

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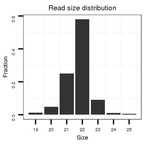
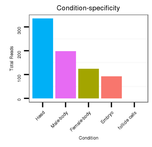
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	2
rescue.candidate	9

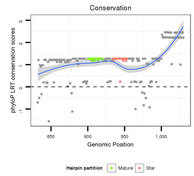
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:
der_1518	**scaffold_944:882-980 +**	**candidate-rescued**	**Canonical miRNA**	**intergenic**
				[View on UCSC Genome Browser (Cornell Mirror)]

Legend: [redacted] [redacted] [redacted] [redacted] [redacted]

Predicted structure







Show Alternate Folds

Flybase annotation

dRNA:Dsor1:RNRNA:G42941-RA]

No Repeatible elements found

mature	star
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Sense Strand Reads

Hide 3p reads Show mid mismatch reads

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ATATGATACATATGTCTTATGTAAACTAAGACATTTCGACATTTATTTTAGTATAAAATACATTTATTGAAGGAATTGATATGTGCATAAAATACATTTGAAAAAAAAAAATTGACATTATATAAAAATGATATTATAAAACTCTAACGCGTGGATCACTCGGCTCATGGGTCGATG
****************************************((((((
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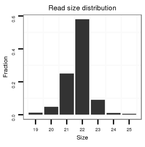
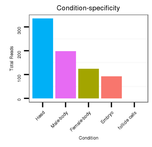
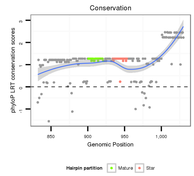
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:
der_1518	**scaffold_944:882-980 +**	**candidate-rescued**	**Canonical miRNA**	**intergenic**
				[View on UCSC Genome Browser (Cornell Mirror)]

Legend: [redacted] [redacted] [redacted] [redacted] [redacted]

Predicted structure







Show Alternate Folds

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dRNA:Dsor1:RNRNA:G42941-RA]

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mature	star
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Sense Strand Reads

Hide 3p reads Show mid mismatch reads

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****************************************((((((
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ID:	Coordinate:	Confidence:	Class:	Genomic Locale:
der_1518	**scaffold_944:882-980 +**	**candidate-rescued**	**Canonical miRNA**	**intergenic**
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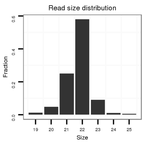
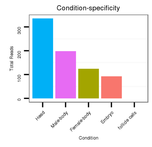
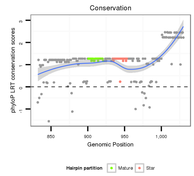
Legend: [redacted] [redacted] [redacted] [redacted] [redacted]

Predicted structure







Show Alternate Folds

Flybase annotation

dRNA:Dsor1:RNRNA:G42941-RA]

No Repeatible elements found

mature	star
1. scaffold_667393:4-44 ; 2. der_1518 scaffold_944:901-922 ; 3. scaffold_946:788-830 ; 4. scaffold_944:882-980 ; 5. scaffold_994:251-314 ; 6. scaffold_1034:431-452 ; 7. scaffold_1181:545-561 ; 8. scaffold_1184:601-718 ; 9. scaffold_1187:1-1000 ; 10. scaffold_1352:872-2882 ; 11. scaffold_2038:332-353 ; 12. scaffold_2042:1-1000 ; 13. scaffold_3663:2256-2303 ; 14. scaffold_3613:357-378 ; 15. scaffold_3844:898-919 ; 16. scaffold_4652:589-608 ; 17. scaffold_4700:1-1000 ; 18. scaffold_4723:6004-6023 ; 19. scaffold_4835:67-638 ; 20. scaffold_4878:1-1000 ; 21. scaffold_4894:1-1000 ; 22. scaffold_5009:601-1012 ; 23. scaffold_4939:17901-17922 ; 24. scaffold_7118:921-1015 ; 25. scaffold_7120:1-1000 ; 26. scaffold_963:223-246 ; 27. scaffold_963:323-344 ; 28. scaffold_967:663-686 ; 29. scaffold_1024:644-665 ; 30. scaffold_1107:1-1000 ; 31. scaffold_1109:889-1112 ; 32. scaffold_1183:638-658 ; 33. scaffold_1184:1-1000 ; 34. scaffold_1185:621-651 ; 35. scaffold_1184:600-622 ; 36. scaffold_1126:570-591 ; 37. scaffold_3305:447-468 ; 38. scaffold_3304:1-1000 ; 39. scaffold_4288:791-812 ; 40. scaffold_4723:8035-8074 ; 41. scaffold_4702:8076-8097 ; 42. scaffold_4703:6639-6660 ;	1. der_1518 scaffold_944:934-955 ; 2. scaffold_946:831-852 ; 3. scaffold_946:788-830 ; 4. scaffold_944:901-922 ; 5. scaffold_994:314-334 ; 6. scaffold_1034:375-396 ; 7. scaffold_1181:528-547 ; 8. scaffold_1185:963-1000 ; 9. scaffold_1187:1-118 ; 10. scaffold_2044:86-107 ; 11. scaffold_2990:524-1543 ; 12. scaffold_2990:1-523 ; 13. scaffold_4005:64-87 ; 14. scaffold_4013:522-563 ; 15. scaffold_4723:6053-6078 ; 16. der_16 scaffold_4738:5963-5984? ; 17. scaffold_4835:638-659 ; 18. scaffold_4939:12285-12308 ; 19. scaffold_4939:17924-17943 ; 20. scaffold_4925:1093-1114 ; 21. scaffold_16:3190-413 ;

Sense Strand Reads

Hide 3p reads Show mid mismatch reads

```
ATATGATACATATGTCTTATGTAAACTAAGACATTTCGACATTTATTTTAGTATAAAATACATTTATTGAAGGAATTGATATGTGCATAAAATACATTTGAAAAAAAAAAATTGACATTATATAAAAATGATATTATAAAACTCTAACGCGTGGATCACTCGGCTCATGGGTCGATG
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