

Legend: mature star mismatch in alignment mismatch in read

Predicted structure

Flybase annotation

CDS [Dsec\GM18990-cds]; utr3 [utr3_minus_9681]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

Anti-sense strand reads

No data available in table

Show Alignment With Reads

Re-alignment of all predicted orthologs

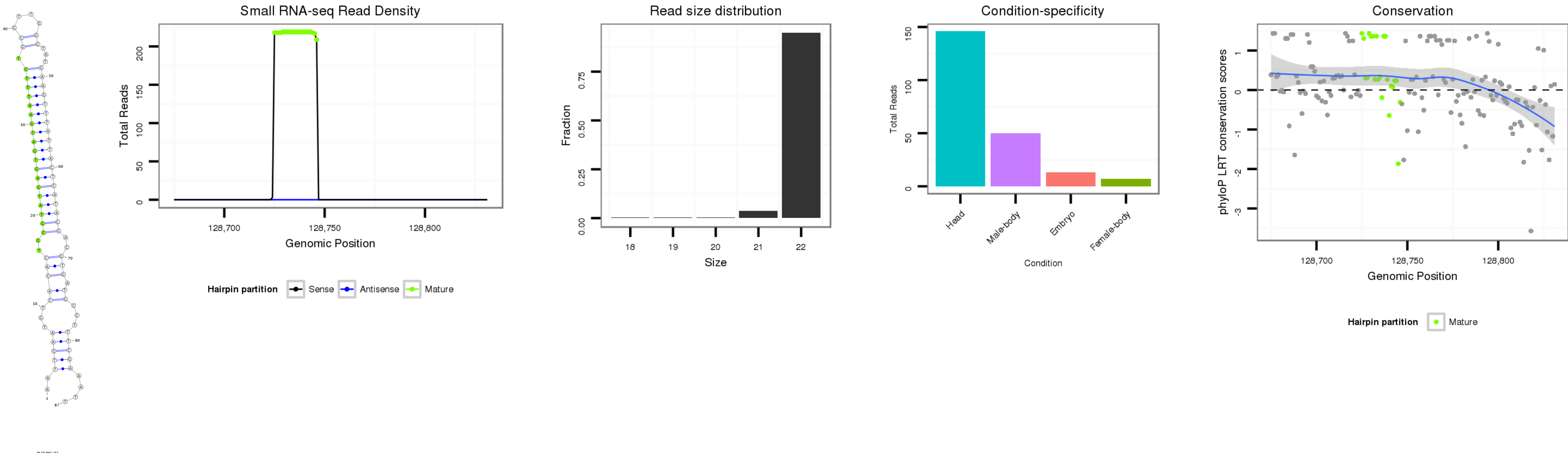
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	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	0
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	2

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dse_334	scaffold_31:128725-128781 +	candidate	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 annotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

[illegible]

Anti-sense strand reads

[illegible]

Re-alignment of all predicted orthologs

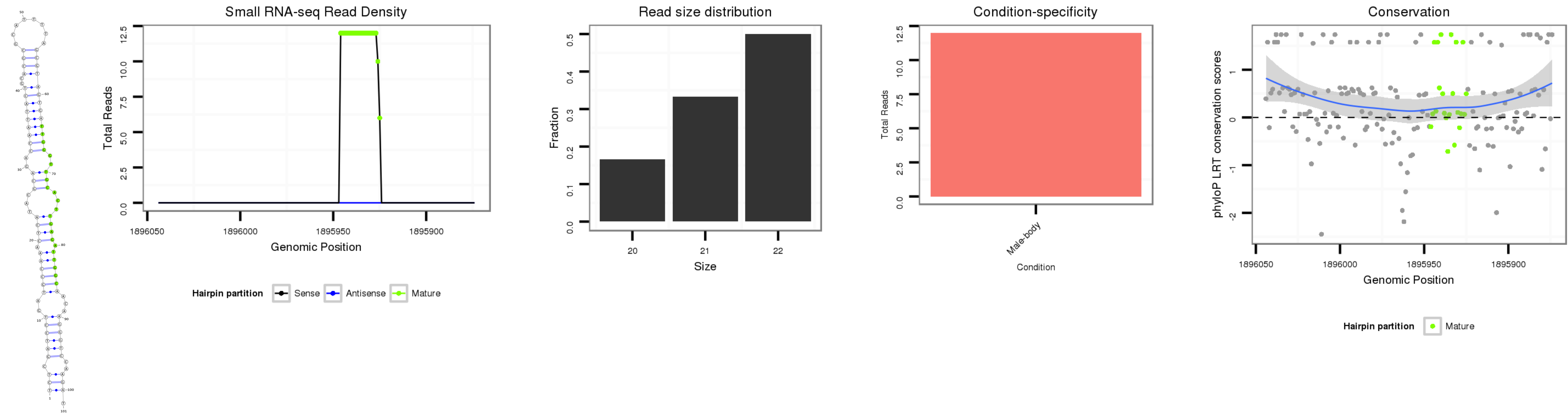
Species	Coordinate	ID	Alignment
droSec2	scaffold_31:128675-128831 +	dse_334	AAAAATAACGTTTCGCTGTGAAAA-----ACAGTGAAGCAATTGAATGTCA-----CAC TGCGTATGAGTGATGAATTTC GC G -----TTGGCTATG-A-----AGTTTATTACTCATACAGC-----TGATGCCTTTCGAATTTATTCCATGGGCCAACAA-----TGGATAAAGTGCA-----TAT
droSim2	3r:26748367-26748523 +		AAAAATAACGTTTCGCTGTGAAAA-----ACAGTGAAGCAATTGAATGTCA-----CAC TGCGTATGAGTGATGCATTTC GC G -----TTGGCTATG-A-----AGTTTATTACTCATACAGC-----TGATGCCTTTCGAATTTATTCCATGGGCCAAC GAA -----TGGATAAAGTGCA-----TAT
dm3	chr3R:27468407-27468550 +		AAAAATAACGTTTCGCTGTGAAAA-----ACAGTGAAGCAATTGAATGTCA-----CAC TGCGTATGAGTGATGCATTTC GC G -----TTGGCTATG CA -----AGTTTATTACTCATACAGC-----TGATGCCTTTCGAATTTATTCCATGGGCCAAC GAACTCTTCGC C AC -----TTGATAAAGTGCA-----TAT
droEre2	scaffold_4820:506067-506239 -		AAAAATAACG CTT CGCT TGA ----- A ACAGT G AGCAATTGAATGTCA-----CAC TGCGTATGAGTGATGCATTTC GC G ----- AT GGCT GTG -A-----AGTTTATTACTCATACAGC-----TGATGCCTTTCGAAT GATTTCAT GGGCC CSGAACT ----- -----CGTGC GTATCTGTAATGCTTTATCAAGAA ----- CA T
droYak3	3R:28405696-28405862 +		AAAAATAACGTTTCGCTGTGA A ----- A ACAGTGAAGCAATTGAATGTCA-----CAC TGCGTATGAGTGATGCATTTC GC G -----TTGGCT GTG -A-----AGTTTATTACTCATACAGC----- TG TG CC CTTC GAAATTTATT TCAT GGGCC AACTGA ACCTCAAG A AC ----- ATGC ATAAAGTGCA-----TAT
droEug1	scf7180000409488:438479-438646 -		AAAA AGCT CGTT TAA C GT TAA ----- CCCA CA CGCGATT TAATG CA -----CG TGCGTATGAGTGATGCATTTC GC ATG ----- AG GGCT TTG - C -----AGTTTAT C ACTCATAC GC TC TC ----- GGTCTCT TCAGTAAT ATTTC CA GTCTCTCACTGC AAGGAACAAGTGAA AACTG TA ----- T TAT
droBial	scf7180000302035:128356-128519 +		AAAAAT TG CGTT TAA TTGTGAAA-----ACAGT G AGCGATT TAATG CA -----CAC TGCGTATGAGTGATGCGTTTC GC G ----- AT GGCT TTG -A-----AGTTTATTACTCAT CC TC CGCTTGCC CC CC TC CG CAAT CACTTC CGG CS CAAC GCACT ----- AC -----AAAT TGTT ----- TTTAA ----- C T
droTak1	scf7180000415712:538796-538970 +		AAAAAT TG CGTT TAA CGTGA AA A CACGAGGAGTGA CA CAGTGAAGCGATT TAATG CA -----CAC TGCGTATGAGTGATGCATTTC GC G ----- AT GGCT TTG -A-----AGTTTATTACTCAT TC TC CGGACTGG CG GCCTTT CG CAATTATT TC CC AGGGA ACTGT ----- TTTTTAA ----- C
droE1el	scf7180000491194:1505895-1506062 +		AAA AT TG CG CTTAA CA TGA A -----ACAGT TG AGCG CTTAATG CA -----CAC TGCGTATTA ACCATGAAGAA AG CA ACCCTTGCTTTTCA AGCGTAGAGATTGTTGAATTGATGACATTTTAA AGTT CA ----- AT TC -----ATT TAG -- AA CA CTTAA TTG ----- GC GAT TAAGTTAG ----- T T
droRho1	scf7180000779322:236100-236242 -		AAA CA T TG CGTT TAA CA TGA ----- GT AT GAAGCGATT TTA ----- G CAATGA TGA A ----- -----AT CTTA ----- AG CGCTTT GGTAAATGGCTTA ATA CCGACGAG ----- CTTTCA ATATA ----- ATATTCCCATCTTAGTGGCATATAATTTGTACTCC
droFic1	scf7180000454114:150493-150608 +		AAAA CTG CG CTTAA C G AA ----- AT AGT CAAC CG GATT TAATG CA -----CAC TGCGTATGAGTGATG ----- AG ----- AA GGCT GTG - C ----- GT TTATTACT TA TCC CG----- AG TG CGCTTT GAAATTTATTTC ----- -----
droKik1	scf7180000302810:712617-712723 +		CAAA CT CG CTTAA C AAA ----- TTTGT CTAATG CA AAA AGTGC GTATGAGT TA AT TC ----- G ----- CTAATA ATT T ----- GT TTAT C ACTCATAC CA G ----- TG TC GT TTTGGGA ----- -----

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crit star

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

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Show Alternate Folds

Flybase annotation

utr3 [utr3_minus_2458]; CDS [Dsec\GM20698-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

Anti-sense strand reads

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droSe2	scaffold_1:1895874-1896044_-	dse_210	CGGGACTGCTATTAAACA-AAAAAAAATTGGATAGTTCTCGAT--CCTGATGCCAAACTCATACGCAGCAAACTACTGCACGC-GCATTTTAGCG-----TAGTGAATGGGTTCGACTTGAGATTGGCAACAAGGGTCCAAGATTCTCC-ACAATTC---GACGTATTAAAGA-TGT-----AATGTGT
droSim2	2r:5068557-5068728_-	dsi_32467	CGGGACTGCTATTAAACA-AAAAAAAATTGGATAGTTCTCGAT--CCTGATGCCAAACTCATACGCAGCA-CAATTACTGCACGC-GCATTTTAGCG-----TAGTGAATGGGTTCGACTTGAGATTGGCAACAAGGGTCCAAGATTCTCC-ACAATTC---GACGTATTAAAGA-TGT-----AATGTGT
dm3	chr2R:4249864-4250032_-	dme_465	CGGACTGCTATTAAAC-A-CAAAAAAA-TT-GAAGTTCTCGAT--CCTGATGCCAAACTCATACGCAGCAAACTACTGCACGC-TCATTTTAGCG-----TAGTGAATGGGTTCGACTTCGATTGGGCAACAAGGGTCCAAGATTCTCC-ACAATTA---CGGTATTAAAGA-TGT-----AATGTGT
droEre2	scaffold_4929:18383228-18383393_+		CGGGACTGCTATTAAACG-GAAC-----TGGATAGTCTTCGAT--CCTGATGCCAAACTCATACGCACCTCAATTACTTGCACGTCGATTTTAGCG-----TGTGAATGGGTTCGACTTCGATTGGGCAACAAGGGTCCAAGATTCTCC-ACAATTC---GACGTATTAAAGA-TGT-----AATGTGT
droYa3	2L:16905839-1690600_-		CGGACTGCTATTAAACG-GAACAA-AG-TGGAAGTCTTCGAT--CCTGATGCCAAACTCATATGCACCTCAATTACTTCAC-----TTTAGCG-----TGTGAATGGGTTCGACTTCGATTGGGCAACAAGGGTCCAAGATTCTCC-ACAATTC---GACGTATTAAAGA-TGT-----A-TGTGT
droEug1	scf7180000407691:116860-117021_-		CGGCTGCTATTAAACG-GAACACAA-TGGATAATTCTTGAT--CCTGATGTCATCTATCTCTGCTCAATCTTAAACA-----ATGCTG-----TGTGACGTGAATTGGAACAGAGATGTCTACGACATATGAGATTCTCC-ACAATTC---TAGATTAAAGA-TGT-----CTCSTGT
droBial	scf7180000302291:2118620-2118790_-		CGGGACTGCTATTAAACG-GAACACAA-GGATGCTCTTCGAT--CTCATTCCAATCTCGTCTCGTACCTCAAGCCATAATTTACATTATAGT-----TGTGAATGCAATTGGCTGACGCTGGCAACGATCTCTCAAGATTCTCC-CACATC---GACGTATTAAAGA-TGT-----CTCSTGT
droTak1	scf7180000415627:124495-124667_-		CGGGACTGCTATTAAACG-GAACACACA-GGATGCTCTTCGATCTCTGATCGCCAACTCATCGCACCTCATCCAGAACATTTGATCTTCACT-----TCTGACGTGAATTGGACGTGAGCTGGCAACAAGTGTCCAAGCTGGCC-CCTATC---GACGTATTAAAGA-TGT-----CTCSTGT
droEle1	scf7180000491240:1075257-1075437_-		CGGACTGCTATTAAAGCCGTACACAA-CGGATGCTCTTCGAT--CTGTGTGCCAAACTCATCGCACCTCAACAA-AAACACTT-TGCCATATAGT-----TGTGAATGCAATTGGACATGATTGGCAACAAGTGTCCAAGATTATCC-ACAAACT---GATGTATCAAGA-TGTACTAAACTGTATASTGT
droRho1	scf7180000770177:371011-371180_-		CGGGACTGCTATTAAACG-GTACACAA-AAGATGCTCTTCGCTGCTGTGCCAAACTCATCGCACCTCAACATAGAACACTT-GATTTCACATG-----TGTCTTCTGCAATTGGACGTGCATTGA-CAACAAGTGTCCAAGCTCTCC-ACAATTA---GCGTATTAAAGA-TGT-----ATCSTGT
droFic1	scf7180000453851:2085654-2085834_+		CGGGACTGCTTTCGACG-GAACCGAG--SAGTACTCTTGAT--CTGTGTGCCAAACTCATCGCACCCCAACCAACATTAACTGTCTCGCAATTTGTGGCTTAGTGTGATTTGTCTCTGGCTGCGATTGGGCAACAAGTATCCATGATTATTC-ACAAATC---GACCATTAAAGA-CTGT-----TTTGTGT
droKik1	scf7180000302277:102548-102718_-		AGGGACTGCTATTAAAGCG-GGTTACACT-CGGSCAGTCTCTCGAT--CCTGTGTGCCAAAGGCG-GGCCGCGACCTGACCCACASCACA-CACCATGTCTG-----TAG-AGCCCAATTGGACGTAGATTGGCAACAAGCATCG-GGCTTGGCC-TGGACCTGTACACACATAAACCG-TGT-----TTCSTCT
droAna3	scaffold_13266:1744899-1745052_+		AGGGACTGCTAACAAC-GGACACTAG-TGGATCACTCTGCTGCTGTGTGCCAGGCTCAAGTSCACTCAAGCCCAAA-ACGC-GAAACGCTTT-----TGTGACGTGAATTGGAATGAGAAGGGCAACATATCCGGGAA-----CGGCAACATTA-TA-----ATGTAT
droBip1	scf7180000396730:2737824-2737992_+		AGGGACTGCTAACAAC-GGACACTAG-TGGGCTCCCTCTGAT--ACTCTGCCAAACTCAAGGTSCACTCAAGTCAAAATCTTTC-CATGTGAT-----TGTGSCAATTGGAATGATGGGGCAACGATATCCGAGTGGGACAGTTATC---ATGTATTAAATA-TGT-----TTCSTGT

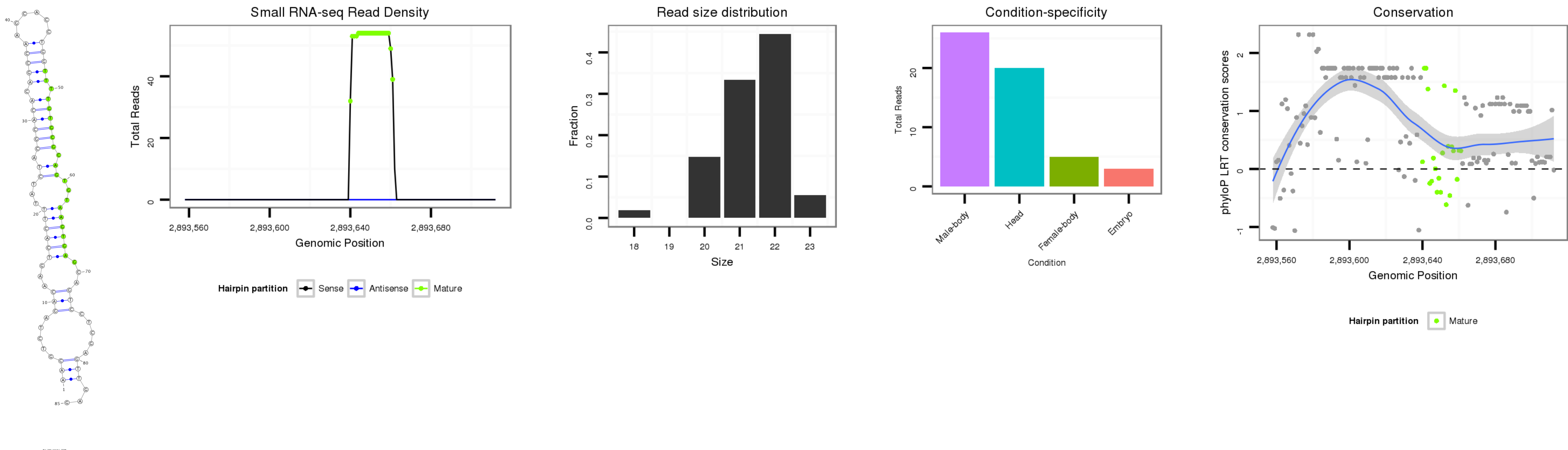
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	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dse_344	scaffold_9:2893608-2893662 +	candidate	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 annotation

intron [Dsec\GM16042-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

						V113	V115	M054	V114
TGTGTGTGTCAAGCACTACAGAAAAATAGTTTATAACGCTAGACAAGTCACTTTATCTACGCACACAGCCAAGCACCTGG	Read size	# Mismatch	Hit Count	Total Norm	Total body	male head	female body	embryo	
*****(((((.....(((((((.....)))))))))..))))).*****	22	0	1	17.00	17	7	8	2	0
.....TTTGTGCCGCGAGTGAAGTGAG.....	21	0	1	11.00	11	6	4	1	0
.....TTTGTGCCGCGAGTGAAGTGAG.....	22	0	1	7.00	7	2	3	0	2
.....TTTGTGCCGCGAGTGAAGTGAG.....	21	0	1	7.00	7	5	1	1	0
.....TTTGTGCCGCGAGTGAAGTG.....	20	0	1	5.00	5	3	2	0	0
.....TTTGTGCCGCGAGTGAAGTGAGC.....	23	0	1	3.00	3	2	0	0	1
.....TTTGTGCCGCGAGTGAAGTGAG.....	20	0	1	3.00	3	1	2	0	0
.....TTTGTGCCGCGAGTGAAGTGAG.....	22	1	1	1.00	1	1	0	0	0
.....TTTGTGCCGCGAGTGAAGTGAGCA.....	24	1	1	1.00	1	1	0	0	0
.....GTGCCGCGAGTGAAGTGAG.....	18	0	1	1.00	1	0	0	1	0
.....TTTGTGCCGCGAGTGAAGT.....	20	1	1	1.00	1	0	1	0	0
.....TTTGTGCCGCGAGTGAAGTCA.....	21	1	1	1.00	1	1	0	0	0
.....TTTGTGCCGCGAGTGAAGTGAGCA.....	23	1	1	1.00	1	0	1	0	0
.....TTTGTGCCGCGAGTGAAGTGAG.....	22	1	1	1.00	1	0	1	0	0

Anti-sense strand reads

[illegible]

Show Alignment With Reads

Re-alignment of all predicted orthologs

[illegible]

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

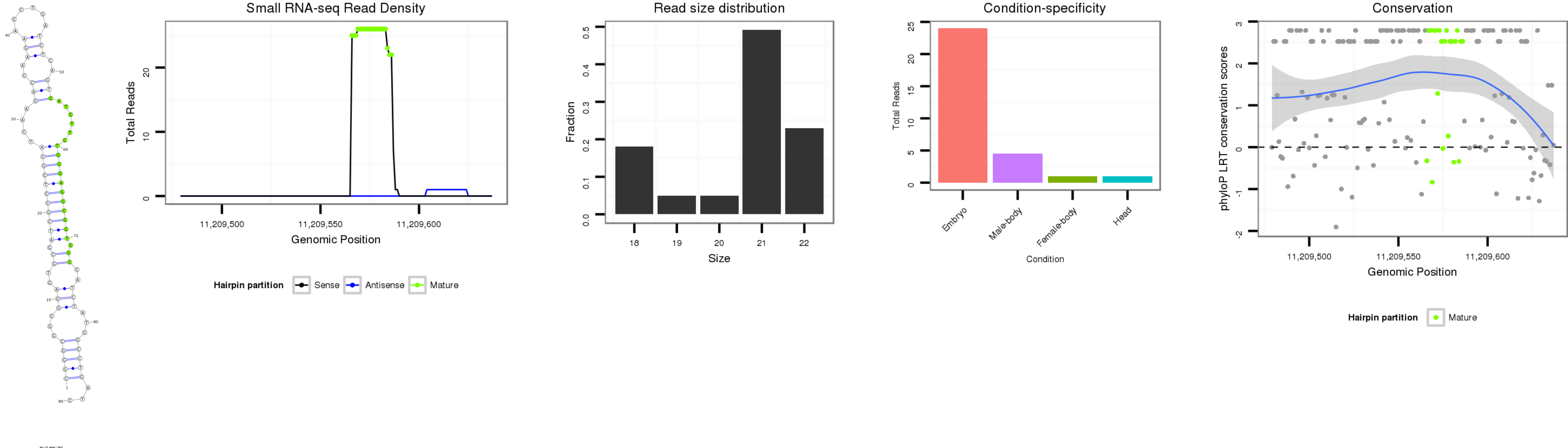
	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	2

	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	0
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dse_221	scaffold_0:11209529-11209587 +	candidate	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 [Dsec\GM25816-cds]; utr3 [utr3_minus_7729]

No Repeatable elements found

mature	star
1. scaffold_0:11206039-11206059 + 2. dse_221_scaffold_0:11209566-11209586 +	

Sense Strand Reads

hide 3p reads | show mid mismatch reads

CCCGAGTGGGATCTACATGATTGGAAGCAGTGTGGCGGGCGGGAGTGCAGATCGCCTCGCATCAAGACCAAGAACCTGATCTCAGT CATCTTCTCGCAGGCGGTGGC CATCTATGGCCTGATCACGGCCATCTGCTTCCGGCAACGTCAACAAGTT	Read #	Size	Mismatch	Hit Count	Total Norm	Total	V114	V113	M054		V115
							embryo	male	female	body	
*****(((((((.....(((.....)))..))).....)))))).....)))))).....)))).....*****	21	0	2	14.50	29	21	6	1	1		1
.....CATCTTCTCGCAGGCGGTGGC.....	22	0	2	6.50	13	9	2	1	1		1
.....CATCTTCTCGCAGGCGGTGGCC.....	22	0	2	3.00	6	6	0	0	0	0	0
.....CATCTTCTCGCAGGCGGT.....	18	0	2								
.....CTTCTCGCAGGCGGTGGC.....	18	0	2	1.50	3	3	0	0	0	0	0
.....CATCTTCTCGCAGGCGGTG.....	19	0	2	1.50	3	3	0	0	0	0	0
.....CATCTTCTCGCAGGCGGTGGCCAT.....	24	0	2	1.00	2	2	0	0	0	0	0
.....ATCTTCTCGCAGGCGGTG.....	21	0	2	0.50	1	1	0	0	0	0	0
.....ATCTTCTCGCAGGCGGTGGCC.....	21	0	2	0.50	1	1	0	0	0	0	0
.....CATCTTCTCGCAGGCGGTGG.....	20	0	2	0.50	1	0	1	0	0	0	0
.....ATCTTCTCGCAGGCGGTGGC.....	20	0	2	0.50	1	1	0	0	0	0	0
.....GTCATCTTCTCGCAGGCGGT.....	20	0	2	0.50	1	1	0	0	0	0	0
.....CATCTTCTCGCAGGCGGTGGCCA.....	23	0	2	0.50	1	0	1	0	0	0	0
.....TTCTCGCAGGCGGTGGCC.....	18	0	2	0.50	1	1	0	0	0	0	0
.....TCATCTTCTCGCAGGCGGTGGC.....	22	0	2	0.50	1	1	0	0	0	0	0
.....ATCTTCTCGCAGGCGGTGGCCAT.....	23	0	2	0.50	1	1	0	0	0	0	0
.....CTTCTCGCAGGCGGTGGCCA.....	20	0	2	0.50	1	1	0	0	0	0	0
.....ATCTTCTCGCAGGCGGTGGCCA.....	22	0	2	0.50	1	1	0	0	0	0	0

Anti-sense strand reads

Show Alignment With Reads

Species	Coordinate	ID	Alignment
droSec2	scaffold_0:11209479-11209637 +	dse_221	CGCCAGTGGGATCTACATGATTGGAAGCAGTGTGGCGGGCGGGAGTGCATCGCTCGCATCAAGACCAAGAACCTGATCTCAGTCACTCTTCTGCGAGCGGTGGCCATCTATGGCGTGATCAGGCCATCTGCTTTCCGGCAACGTCAACAA-GTT
droSim2	3r:10484072-10484230 +		CGCCAGTGGGATCTACATGATTGGAAGCAGTGTGGCGGGCGGGAGTGCATCGCTCGCATCAAGACCAAGAACCTGATCTCAGTCACTCTTCTGCGAGCGGGAGCCATCTATGGCGTGATCAGGCCATCTGCTTTCCGGCAACGTCAACAA-GTT
dm3	chr3R:10725635-10725793 -	dme_393	CGCCAGTGGATCTACATGATTGGAGCAGTGTGGCGGGCGGGAGTGCATCGCTCGCATCAAGACCAAGAACCTGATCTCAGTCACTCTTCTGCGAGCGGTGGCCATCTATGGCGTGATCAGGCCATCTGCTTTCCGGCAACGTCAACAA-GTT
droEre2	scaffold_4770:10261697-10261855 +		CGCCAGTGGATCTACATGATTGGAGCAGTGTGGCGGGAGTGCATCGCTCGCATCAAGACCAAGAACCTGATCTCAGTCACTCTTCTGCGAGCGGTGGCCATCTATGGCGTGATCAGGCCATCTGCTTTCCGGCAACGTCAACAA-GTT
droYak3	3R:15702076-15702234 +	dya_1815	CGCCAGTGGGATCTACATGATTGGAGCAGTGTGGCGGGCGGGAGTGCAGTACTCGCATCAAGACCAAGAACCTGATCTCAGTCACTCTTCTGCGAGCGGGTGGCCATCTATGGCGTGATCAGGCCATCTGCTTTCCGGCAACGTCAACAA-GTT
droEug1	scaf71800004093794:2983392-298550 +		TGCCATCGGGATCTACATGATTGGAGCAGTGTGGCGAGCGGGTGCATCGCCCGCATCAAGACCAAGAACCTGATCTCAGTCAATTCTCTGCGAGCGGGAGCCATATAGGGTTTGATCACAGCCATCTGCTATCCGGCACTTCTTCAGCAAG-GTT
droBial	scaf7180000302402:3691436-3691594 +		TGCCATCGGGATCTACATGATCGGCGCAGTGTGGCGGGCGGGTGCATCGCCCGCATCAAGACCAAGAACCTGATCTCAGTCACTCTTCTGCGAGCGGGTGGCCATCTATAGGGCTGATCAGGCCATCTGCTTTCCGGCAAGTCTGCGCA-GTT
droTak1	scaf71800004015397:180061-180219 +		TGCCATCCGGATCTACATGATTGGCGCAGTGTGGCGGGCGGGTGCATCGCTCGCATCAAGACCAAGAACCTGATCTCAGTCACTCTTCTGCGAGCGGGTGGCCATCTATAGGGCTGATCAGGCCATCTGCTTTCCGGCAAGTGGTGA-GCA
droE1el	scaf7180000486474:1271634-1271792 +		TGCCATGGGATCTACATGATTGGCGCAGTGTGGCGGGCGGGAGTGCATCGCCCGCATCAAGACCAAGAACCTGATCTCAGTCAATTCTCTGCGAGCGGGTGGCCATCTATAGGGCTGATCAAGCCATCTGCTTTCCGGCAAGTCTGCGCA-GTA
droRho1	scaf7180000777941:33450-33608 -		TGCCATCGGATCTACATGATTGGCGCAGTGTGGCGGGAGTGCATCGCCCGCATCAAGACCAAGAACCTGATCTCAGTCACTCTTCTGCGAGCGGGTGGCCATCTATAGGGCTGATCAGGCCATCTGCTTTCCGGCAAGTCTGCGCG-GTT
droFic1	scaf7180000454104:642402-642560 +		TGCCAGTGGATCTACATGATTGGAGCAGTGTGGCGGGCGGGTGCATCGCTCGCATCAAGACCAAGAACCTGATCTCAGTCACTCTTCTGCGAGCGGGTGGCCATCTATAGGGCTGATCAAGCCATCTGCTTTCCGGCAAGTCTGCGCA-GTT
droKik1	scaf7180000302461:997473-997631 +		CGCCCTGGATATATATGATTGGCAAGAGTGTGGCGGGCGGGAGTGCATCGCCGATCAAGACCAAGAACCTGATCTCAGTCAATTCTCTGCGAGCGGGAGCCATATATGTTTGATCACAGGCCATCTGCTTTCCGGCAAGTCTGCGCA-GTT
droAna3	scaffold_13340:5804540-5804698 -		CGCCGCCGATCTACATGACCGAGAGCGAGTGTGGCGGGAGTGCATCGCCCGCATCAAGACCAAGAACCTATTCATCACTCTTCTGCGAGCGGGTGGCCATCTATGGCGTGATCAGGCCATCTGCTTTCCGGAGATGTTGTGAGAA-TTT
droBip1	scaf7180000336708:3009702-3009860 +		CGCTGGCGATCTACATGACCGGAGCGAGTGTGGCGGGAGTGCATCGCCCGCATCAAGACCAAGAACCTATTCATCACTCTTCTGCGAGCGGGTGGCCATCTATGGCGTGATCAGGCCATCTGCTTTCCGGAGATGTTGTGAGAA-TTT
dp5	2:20661131-20661289 -		CGCCCTTGGATATCAATATCCGCGGACAGCATCTCGGGCGCGGGTCTCGCTCGCCCGCATCAAGACCAAGAACCTGATCTCGATCAATTCTCTGCGAGCGGATGGCCATCTATAGGGCTGATCAGGCCATAGTGTGTGAGAA-CGA
droPer2	scaffold_3:33416247-3416405 -	dpe_2524	CGCCCTTGGATATCAATATCCGCGGACAGCATCTCGGGCGGGTCTAAGCGTCCCGCATCAAGACCAAGAATTGATTCCTCATCTCTTCTGCGAGCGGCCTCGCCATCTATAGGGCTGATCAGGCCATCTGCTTTCCGGCAAGTGGTGA-GTT
droWil2	scaf2_1100000004902:8619615-8619774 +	dwi_5434	CGCCCTGCGATCTCAATAGCGGACAGCATCTCGGGCGGGTCTAAGCGTCCCGCATCAAGACCAAGAATTGATCTCTCGTCAATTCTCTGCGAGCGGTGGCCATCTATAGGGTTTGATCACAGCCATCTGATTTCCGGCAAGCGGAGGTC-GTT
droVir3	scaffold_13047:19131285-19131443 +	dvi_24653	CGCCCTTGGATATCAATATCCGCGGACAGCATCTCGGGCGGGTCTAAGCGTCCCGCATCAAGACCAAGAATTGATTCCTCATCTCTTCTGCGAGCGGCCTCGCCATCTATAGGGCTGATCAGGCCATCTGCTTTCCGGCAAGCGGAGCA-GTT
droMoJ3	scaffold_6540:14560044-14560202 -	dmo_3158	CGCCCTTGGATATCAATATCCGCGGACAGCATCTCGGGCGGGTCTAAGCGTCCCGCATCAAGACCAAGAATTGATTCCTCATCTCTTCTGCGAGCGGCCTCGCCATCTATAGGGCTGATCAGGCCATCTGCTTTCCGGTCAAGCGGAGGAG-GTT
droGr12	scaffold_14906:12137647-12137805 +	dgr_470	TGCCCTTGGATATCAATATCCGCGGACAGCATCTCGGGCGGGTCTAAGCGTCCCGCATCAAGACCAAGAATTGATTCCTCATCTCTTCTGCGAGCGGCCTCGCCATCTATGGCGTGATCAGGCCATCTGCTTTCCGGCAAGCGGAGGAG-GTT

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	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

Predicted structure



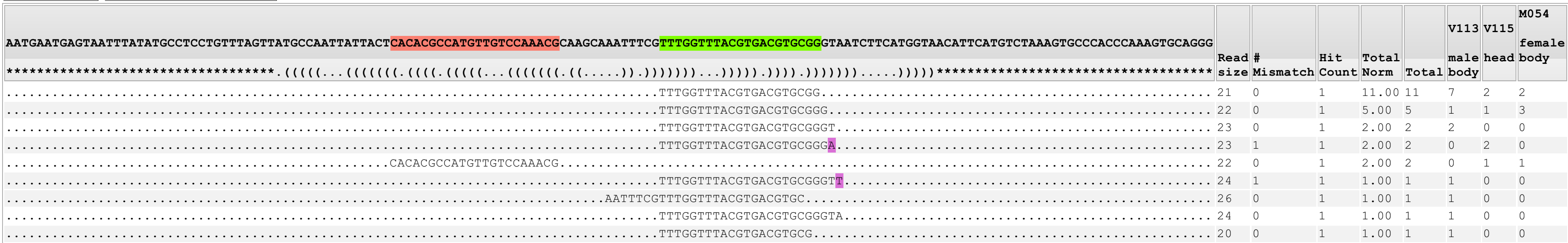
Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads



Anti-sense strand reads

										Read #	Mismatch	Hit	Total		M054	V113	V115	V114
										size		Count	Norm	Total	female body	male body	head	embryo
TTACTTACTCATTAATATACGGAGGACAAATCAATACGGTTAATAATGAGTGTGGGTACAAACAGGTTTGGCGTTCGTTTAAAGCAACCAAATGCACTGCACGCCATTAGAAGTACCATTGTAAGTACAGATTTACCGGGTGGGTTTCACGTCCC *****.(((((...((((((...((((((...((((((...(((...))))))...))))))...))))))...))))))*****										18	0	1	1.00	1	1	0	0	0
.....GATTTACCGGGTGGGTTT.....GAGATTTACCGGGTGGGT.....										18	1	2	0.50	1	1	0	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

[illegible]

Generated: 09/08/2015 at 07:44 PM

	PASS/FAIL
crit.star	0
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	0
rescue.candidate	3

Predicted structure

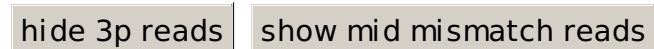


Flybase annotation

CDS [Dsec\GM19198-cds]

Repeatable elements

Sense Strand Reads



Anti-sense strand reads

Show Alignment With Reads

Re-alignment of all predicted orthologs

Generated: 09/08/2015 at 07:44 PM

	PASS/FAIL
crit.star	0
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	0
rescue.candidate	2

	PASS/FAIL
crit.star	(
crit.loop	(
crit.mor	(
crit.half	(
crit.total	(
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	(
crit.back	1
rescue.total	1
rescue.dominant	(
rescue.known	(
rescue.confident	(
rescue.candidate	3

	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	1
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

Legend: mature star mismatch in alignment mismatch in read

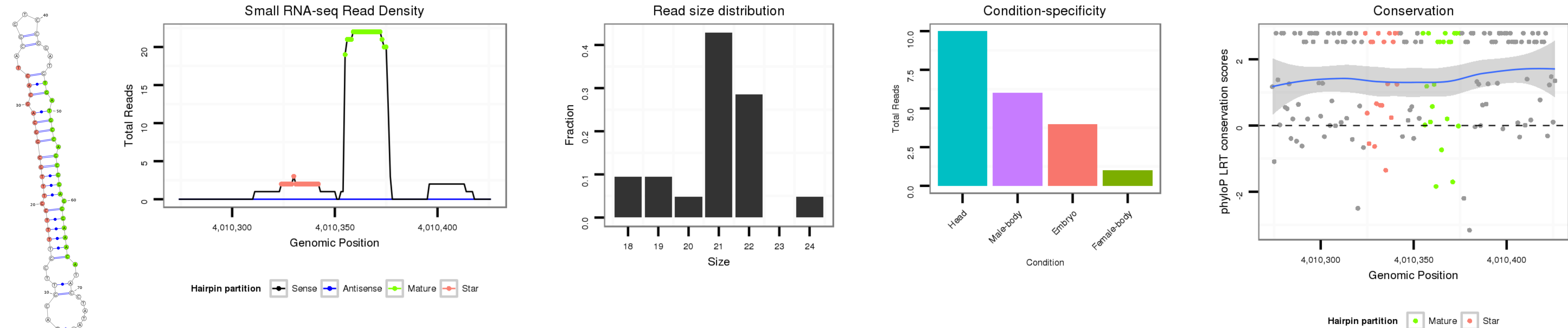
Flybase annotation

No Repeatable elements found

Show Alignment With Reads

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Show Alternate Folds

Flybase annotation

CDS [Dsec\GM17055-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

CATTTAAGCAGCTGCTGCCCTTCTACCGACAGCTCCACGGCTACGTTTCGTTTCGTTTGGCGCAGCACAACGGTCCGGATGTGATGCCAGCGGAGGGGAAACAACACCTATAAGCCTGCTGGGCAACATGTGGGGTCAGTCGTGGAACAGCAGTGC	Read #	Mismatch	Hit	Total	V113			V115			V114			M054
					male	head	embryo	male	head	embryo	male	head	embryo	
*****(((((.(((.(((((((.(((((((.(((.((...)))...)))...)))...)))...)))...)))...))*****	21	0	1	7.00	7	4	2	0	1	0	0	0	0	0
.....TGATGCCAGCGGAGGGGAAACA.....	22	0	1	6.00	6	2	4	0	0	0	0	0	0	0
.....TGATGCCAGCGGAGGGGAAACAT.....	23	0	1	3.00	3	3	0	0	0	0	0	0	0	0
.....TGATGCCAGCGGAGGGGAAACATA.....	19	1	1	2.00	2	2	0	0	0	0	0	0	0	0
.....TGATGCCAGCGGAGGGGAAAT.....	19	0	1	1.00	1	0	1	0	0	0	0	0	0	0
.....TGATGCCAGCGGAGGGGAAA.....	19	0	1	1.00	1	0	1	0	0	0	0	0	0	0
.....GATGCCAGCGGAGGGGAAACAT.....	21	0	1	1.00	1	0	1	0	0	0	0	0	0	0
.....TGTGATGCCAGCGGAGGGGAAACAT.....	24	0	1	1.00	1	0	0	1	0	0	0	0	0	0
.....TGATGCCAGCGGAGGGGAAA.....	18	0	1	1.00	1	0	1	0	0	0	0	0	0	0
.....CGGCTACGTTTCGTTTTTCGTT.....	20	0	1	1.00	1	0	1	0	0	0	0	0	0	0
.....CGCTACGTTTCGTTTTCGTT.....	19	0	1	1.00	1	0	0	1	0	0	0	0	0	0
.....TGATGCCAGCGGAGGGGAAACA.....	20	0	1	1.00	1	0	0	1	0	0	0	0	0	0
.....AACATGTGGGTCAGTCG.....	18	0	1	1.00	1	0	0	1	0	0	0	0	0	0
.....TTGCGGCAGCACTACGGTCCG.....	21	0	1	1.00	1	0	1	0	0	0	0	0	0	0
.....AACATGTGGGTCAGTCGTGGA.....	22	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....GCCAGCGGAGGGGAAACAT.....	18	0	1	1.00	1	0	0	1	0	0	0	0	0	0

Anti-sense strand reads

[illegible]

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droSec2	scaffold_3:4010274-4010426	dsd_309	CATTTAAGCAGCTGCTGCCCTTCTACCGACAGCTCCACGGCTACGTTCTGTTTCGTTTTCGGCGAGCAGCTACGGTCCGGATGTGATGCCACGGAGGGAACAATACCTATAAGCCTGCTGGGCAACATGTGGGTCAGTCGTGGAACGAGCTGC
droSim2	chr12:8421065-8421217 chr21:8523515-8523667	dsi_3473 dme_4242	CATTTAAGCAGCTGCTGCCCTTCTACGACAGCTCCACGGCTACGTTCTTCGTTTTCGGCGAGCAGCTACGGTCCGGATGTGATGCCGCGGAGGGAACAATACCTATAAGCCTGCTGGGCAACATGTGGGTCAGTCGTGGAACGAGCTGC
droEr2	scaffold1_4929:9117025-9117177		CATTTAAGCAGCTGCTGCCCTTCTACCGACAGCTCCACGGCTACGTTCTTCGTTTTCGGCGAGCAGCTACGGTCCGGATGTGATGCCGCGGAGGGAACAATACCTATAAGCCTGCTGGGCAACATGTGGGTCAGTCGTGGAACGAGCTGC
droYak3	2L:11169016-11169168		CATTTAAGCAGCTGCTGCCCTTCTACCGACAGCTCCACGGCTACGTTCTTCGTTTTCGGCGAGCAGCTACGGTCCGGATGTGATGCCGCGGAGGGAACAATACCTATAAGCCTGCTGGGCAACATGTGGGTCAGTCGTGGAACGAGCTGC
droEug1	scf1140000490554:1010373-1010525		CATTAAAGCAGCTGCTGCCCTTCTACCGACAGCTCCACGGCTACGTTCTTCGTTTTCGGCGAGCAGCTACGGTCCGGATGTGATGCCGCGGAGGGAACAATACCTATAAGCCTGCTGGGCAACATGTGGGTCAGTCGTGGAACGAGCTGC
droBial	scf7180000301518:1320694-1320846		CATTAAAGCAGCTGCTGCCCTTCTACCGACAGCTCCACGGCTACGTTCTTCGTTTTCGGCGAGCAGCTACGGTCCGGATGTGATGCCGCGGAGGGAACAATACCTATAAGCCTGCTGGGCAACATGTGGGTCAGTCGTGGAACGAGCTGC
droTak1	scf7180000413920:148687-148839		CATTAAAGCAGCTGCTGCCCTTCTACCGACAGCTCCACGGCTACGTTCTTCGTTTTCGGCGAGCAGCTACGGTCCGGATGTGATGCCGCGGAGGGAACAATACCTATAAGCCTGCTGGGCAACATGTGGGTCAGTCGTGGAACGAGCTGC
droE1e1	scf7180000491186:1325025-1325177		CATTTAAGCAGCTGCTGCCCTTCTACCGACAGCTCCACGGCTACGTTCTTCGTTTTCGGCGAGCAGCTACGGTCCGGATGTGATGCCGCGGAGGGAACAATACCTATAAGCCTGCTGGGCAACATGTGGGTCAGTCGTGGAACGAGCTGC
droRho1	scf7180000779312:349679-349831		CCTTAAAGCAGCTGCTGCCCTTCTACCGACAGCTCCACGGCTACGTTCTTCGTTTTCGGCGAGCAGCTACGGTCCGGATGTGATGCCGCGGAGGGAACAATACCTATAAGCCTGCTGGGCAACATGTGGGTCAGTCGTGGAACGAGCTGC
droFi1c1	scf7180000454117:185414-185566		CATTTAAGCAGCTGCTGCCCTTCTACCGACAGCTCCACGGCTACGTTCTTCGTTTTCGGCGAGCAGCTACGGTCCGGATGTGATGCCGCGGAGGGAACAATACCTATAAGCCTGCTGGGCAACATGTGGGTCAGTCGTGGAACGAGCTGC
droK1k1	scf7180000302412:653674-653826		CATTAAAGCAGCTGCTGCCCTTCTACCGACAGCTCCACGGCTACGTTCTTCGTTTTCGGCGAGCAGCTACGGTCCGGATGTGATGCCGCGGAGGGAACAATACCTATAAGCCTGCTGGGCAACATGTGGGTCAGTCGTGGAACGAGCTGC
droAna3	scaffold_12916:10167591-10167743	dan_4062	CCTTAAAGCAGCTGCTGCCCTTCTACCGACAGCTCCACGGCTACGTTCTTCGTTTTCGGCGAGCAGCTACGGTCCGGATGTGATGCCGCGGAGGGAACAATACCTATAAGCCTGCTGGGCAACATGTGGGTCAGTCGTGGAACGAGCTGC
droBip1	scf7180000396580:867242-867394		CCTTAAAGCAGCTGCTGCCCTTCTACCGACAGCTCCACGGCTACGTTCTTCGTTTTCGGCGAGCAGCTACGGTCCGGATGTGATGCCGCGGAGGGAACAATACCTATAAGCCTGCTGGGCAACATGTGGGTCAGTCGTGGAACGAGCTGC
dp5	Unknown_group_503:3367-3519		CTTAAAGCAGCTGCTGCCCTTCTACCGACAGCTCCACGGCTACGTTCTTCGTTTTCGGCGAGCAGCTACGGTCCGGATGTGATGCCGCGGAGGGAACAATACCTATAAGCCTGCTGGGCAACATGTGGGTCAGTCGTGGAACGAGCTGC
droPer2	scaffold_5:4192089-4192241		CTTAAAGCAGCTGCTGCCCTTCTACCGACAGCTCCACGGCTACGTTCTTCGTTTTCGGCGAGCAGCTACGGTCCGGATGTGATGCCGCGGAGGGAACAATACCTATAAGCCTGCTGGGCAACATGTGGGTCAGTCGTGGAACGAGCTGC
droW112	scf2_1100000004884:913288-913440		CATTTAAGCAGCTGCTGCCCTTCTACCGACAGCTCCACGGCTACGTTCTTCGTTTTCGGCGAGCAGCTACGGTCCGGATGTGATGCCGCGGAGGGAACAATACCTATAAGCCTGCTGGGCAACATGTGGGTCAGTCGTGGAACGAGCTGC
droVir3	scaffold_12963:14523065-14523217		CTTAAAGCAGCTGCTGCCCTTCTACCGACAGCTCCACGGCTACGTTCTTCGTTTTCGGCGAGCAGCTACGGTCCGGATGTGATGCCGCGGAGGGAACAATACCTATAAGCCTGCTGGGCAACATGTGGGTCAGTCGTGGAACGAGCTGC
droMo3	scaffold_6500:15479058-15479210		CTTAAAGCAGCTGCTGCCCTTCTACCGACAGCTCCACGGCTACGTTCTTCGTTTTCGGCGAGCAGCTACGGTCCGGATGTGATGCCGCGGAGGGAACAATACCTATAAGCCTGCTGGGCAACATGTGGGTCAGTCGTGGAACGAGCTGC
droGr12	scaffold_15252:1980990-1981142	dgr_474	CTTAAAGCAGCTGCTGCCCTTCTACCGACAGCTCCACGGCTACGTTCTTCGTTTTCGGCGAGCAGCTACGGTCCGGATGTGATGCCGCGGAGGGAACAATACCTATAAGCCTGCTGGGCAACATGTGGGTCAGTCGTGGAACGAGCTGC

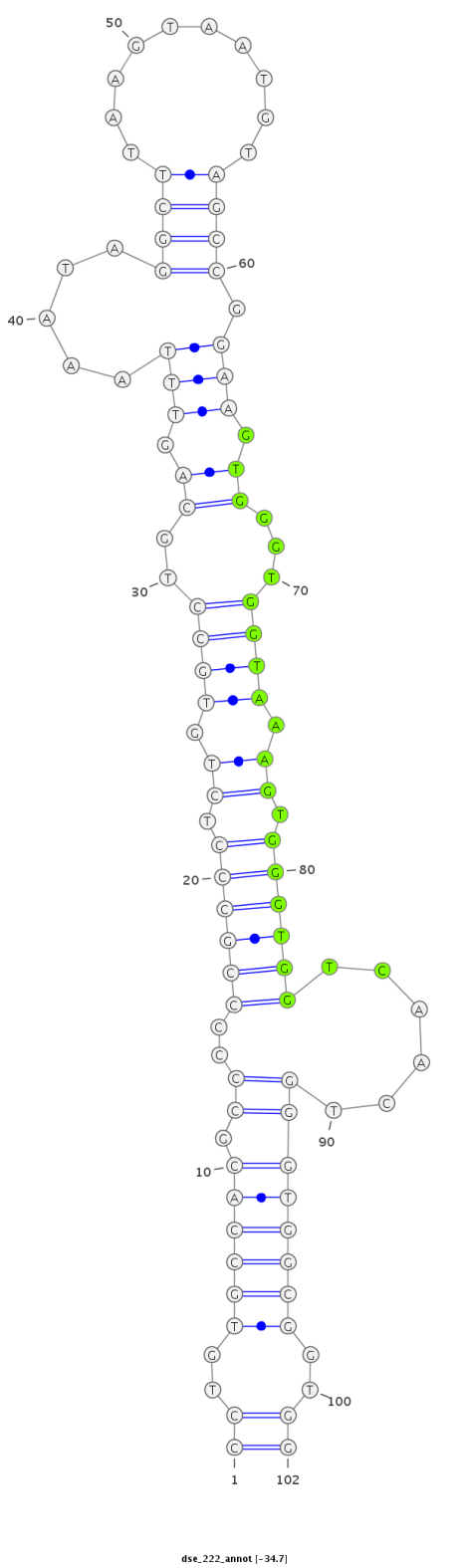
Generated: 09/08/2015 at 07:44 PM

	PASS/FAIL
crit.star	0
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	0
rescue.candidate	1

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dse_222	scaffold_10:2877273-2877344 +	candidate	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 annotation

intron [Dsec\GM19267-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

Anti-sense strand reads

Show Alignment With Reads

Co-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droSec2	acaffold_10:2877223-2877394	dse_222	GGCCTTCG---TTTGTGCTTTGATTGTGC---TACTGG---CCTGTGCCAGGCC---CCCC--GGCCTTCG-----GCCG---TCTG-----TGCTCGCAGTTTAAATAGGCTTAAG--TAATGTAG-----CCGG-AACTGGGTGGTAAAGTGGGTGGTAA--CTGGGT-----GGCGGT-----GG-----GGAAATGGAAATGCTTAAAGCTTCTAACA-TTTC-
droSim2	x:2923896-2924067 +	ds1_32464	GGCCTTCG---TTTGTGCTTTGATTGTGC---TAGGG---CCTGTGCCAGGCC---CCCC--GGCCTTCG-----GCCG---TCTG-----TGCTCGCAGTTTAAATAGGCTTAAG--TAATGTAG-----CCGG-AACTGGGTGGTAAAGTGGGTGGTAA--CTGGGT-----GGCGGT-----GG-----GGAAATGGAAATGCTTAAAGCTTCTAACA-TTTC-
dm3	chrX:3169718-3169879 +	dme_445	GGGCGCTG---TTTGTGCTTTGATTGTGC---TACTCG---CCTGTGCCAGGCC---CCCCTCGCGCTG-----GCCG---TCTG-----TGCTCGCAGTTTAAATAGGCTTAAGTAATGTAG-----CCGG-AACTGGGTGGTAAAGTGGGTGGTAA--CTGGGT-----GGCGGT-----GG-----GGAAATGGAAATGCTTAAAGCTTCTAACA-TTTC-
droEre2	acaffold_4690:579040-579219		GGCCTTCG---TTTGTGCTTTGATTGTGC---GCTCG---CCTGTGCCAGGCC---CCCCCGCTGCGCTG-----GCCG---TCTG-----TGCTCGCAGTTTAAATAGGCTTAAGTAATGTAG-----CCGG-AACTGGGTGGTAAAGTGGGTGGTAA--CTGGGTGGTAGAGTGGTTGG---GCTTGGT-----GGCGGT-----GG-----GGAAATGGAAATGCTTAAAGCTTCTAACA-TTTC-
droYaK3	x:5213414-5213589 -		GGCCTTCG---TTTGTGCTTTGATTGTGCCTGACTCG---CCTGTGCCAGGCC---CCCCCGCTGCGCTG-----GCCG---TCTG-----TGCTCGCAGTTTAAATAGGCTTAAG--TAATGTAG-----CCGG-AACTGGGTGGTAAAGTGGGTGGTAA--CTGGGT-----GGCGGT-----GG-----GGAAATGGAAATGCTTAAAGCTTCTAACA-TTTC-
droBug1	acf7180000408825:182122-82309 -		GGCCTTCG---TTTGTGCTTTGATTGTGC---GCTAC---GCTAGCCACGTC---CCCCCGCTGCGCTG-----GCCG---TCTG-----TGCTCGCAGTTTAAATAGGCTTAAG--TAATGTAG-----CCGG-AACTGGGTGGTAAAGTGGGTGGTAA--CTGGGT-----GGCGGT-----GG-----GGAAATGGAAATGCTTAAAGCTTCTAACA-TTTC-
droBia1	acf7180000302126:2047546-2047696 -		GGCCTTCG---TTTGTGCTTTGATTGTGC---GCTG---GCTAGCCACAG---CCCCCGCTGCGCTG-----GCCG---TCTG-----TGCTCGCAGTTTAAATAGGCTTAAG--TAATGTAG-----CCGG-AACTGGGTGGTAAAGTGGGTGGTAA--CTGGGT-----GGCGGT-----GG-----GGAAATGGAAATGCTTAAAGCTTCTAACA-TTTC-
droTak1	acf7180000415360:106950-107105 +		GGCCTTCG---TTTGTGCTTTGATTGTGC---GCTTCG---CCTAGGCCAGGCC---CCCCCGCTGCGCTG-----GCCG---TCTG-----TGCTCGCAGTTTAAATAGGCTTAAG--TAATGTAG-----CCGG-AACTGGGTGGTAAAGTGGGTGGTAA--CTGGGT-----GGCGGT-----GG-----GGAAATGGAAATGCTTAAAGCTTCTAACA-TTTC-
droBie1	acf7180000490996:342375-342524 +		GGCTTCAG---CTTGTGCTTTGATTGTGC---GCTAC---CCTAGGCCAGGCC---CCCCCGCTGCGCTG-----GCCG---TCTG-----TGCTCGCAGTTTAAATAGGCTTAAG--TAATGTAG-----CCGG-AACTGGGTGGTAAAGTGGGTGGTAA--CTGGGT-----GGCGGT-----GG-----GGAAATGGAAATGCTTAAAGCTTCTAACA-TTTC-
droRho1	acf7180000779397:361773-361938 +		GGCTTCG---TTTGTGCTTTGATTGTGC---GTAAC---CCTAGGCCAGGCC---CCCCCGCTGCGCTG-----GCCG---TCTG-----TGCTCGCAGTTTAAATAGGCTTAAG--TAATGTAG-----CCGG-AACTGGGTGGTAAAGTGGGTGGTAA--CTGGGT-----GGCGGT-----GG-----GGAAATGGAAATGCTTAAAGCTTCTAACA-TTTC-
droFic1	acf7180000454072:131038-131145 -		GGCCTTCGA---CTTGTGCTTTGATTGTGCCTC---GCTG-----GCTGCGCTG-----GCCG---TCTG-----TGCTCGCAGTTTAAATAGGCTTAAG--TAATGTAG-----CCGG-AACTGGGTGGTAAAGTGGGTGGTAA--CTGGGT-----GGCGGT-----GG-----GGAAATGGAAATGCTTAAAGCTTCTAACA-TTTC-
droKik1	acf7180000302344:1189307-1189500 -		GGCCTTCG---TTTGTGCTTTGATTGTGC---GCTACCTTAAGCTTGCAGGCC---CCCCCGCTGCGCTG-----GCCG---TCTG-----TGCTCGCAGTTTAAATAGGCTTAAG--TAATGTAG-----CCGG-AACTGGGTGGTAAAGTGGGTGGTAA--CTGGGT-----GGCGGT-----GG-----GGAAATGGAAATGCTTAAAGCTTCTAACA-TTTC-
droAna3	acaffold_12613:236226-236427 -	dan_4058	GAGCAG---TTTGTGCTTTGATTGTGC---GCTAC---CTAAAGCCATAGC---CCCGCATGACC---GCTGCTCTAGCCCCCTG---GCTAC---GCTGCTTAAATAGGCTTAAG--TAATGTAG-----CCGG-AACTGGGTGGTAAAGTGGGTGGTAA--CTGGGT-----GGCGGT-----GG-----GGAAATGGAAATGCTTAAAGCTTCTAACA-TTTC-
droBip1	acf7180000395930:13274-13501 -		GAGCAG---TTTGTGCTTTGATTGTGC---GCTAC---CTAAAGCCATAGCCTGGGCTGACCCAGACCAGCCAGCCCTCCG---GCTAC---GCTGCTTAAATAGGCTTAAG--TAATGTAG-----CCGG-AACTGGGTGGTAAAGTGGGTGGTAA--CTGGGT-----GGCGGT-----GG-----GGAAATGGAAATGCTTAAAGCTTCTAACA-TTTC-
dp5	Xt_group16:2694226-2694451 +		GGCCGCTG---TTTGTGCTTTGATTGTGCCTGCTAC---CTAAAGCCCTTC---GACCTCCCATC---GCTGCTCTAGCCCCCTG---GCTAC---GCTGCTTAAATAGGCTTAAG--TAATGTAG-----CCGG-AACTGGGTGGTAAAGTGGGTGGTAA--CTGGGT-----GGCGGT-----GG-----GGAAATGGAAATGCTTAAAGCTTCTAACA-TTTC-
droPer2	acaffold_18:1595248-1595470 +		GGCCGCTG---TTTGTGCTTTGATTGTGCCTGCTAC---CTAAAGCCCTTC---GACCTCCCATC---GCTGCTCTAGCCCCCTG---GCTAC---GCTGCTTAAATAGGCTTAAG--TAATGTAG-----CCGG-AACTGGGTGGTAAAGTGGGTGGTAA--CTGGGT-----GGCGGT-----GG-----GGAAATGGAAATGCTTAAAGCTTCTAACA-TTTC-
droW12	acf2_1100000004401:1012275-1012411 +		G-----TTTGTGCTTTGATTGTGC-----GCTGCTCTAGCCCCCTG---GCTAC---GCTGCTTAAATAGGCTTAAG--TAATGTAG-----CCGG-AACTGGGTGGTAAAGTGGGTGGTAA--CTGGGT-----GGCGGT-----GG-----GGAAATGGAAATGCTTAAAGCTTCTAACA-TTTC-

Generated: 09/08/2015 08:55:11 PM

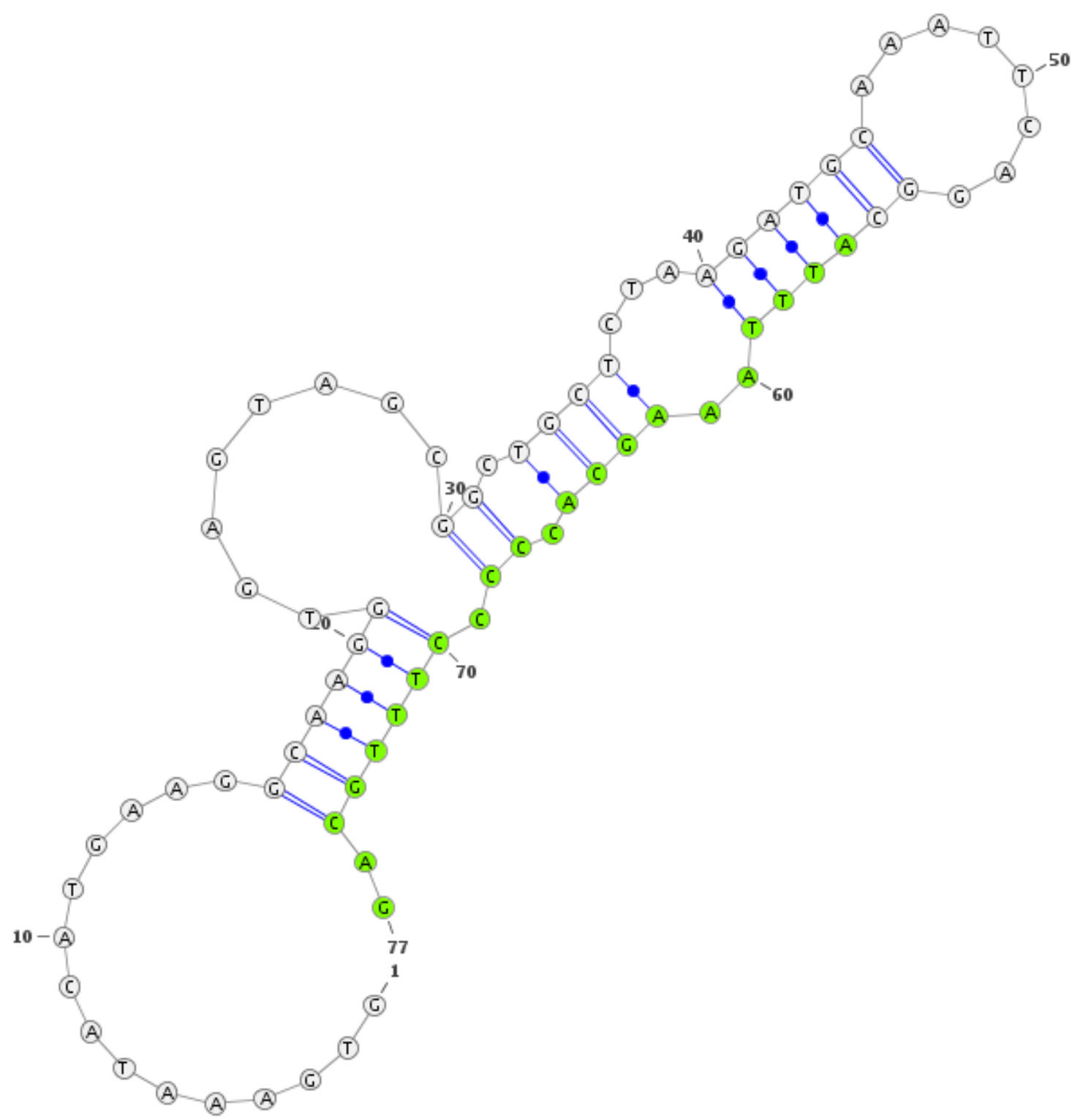
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

	PASS/FAIL
crit.star	0
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	0
rescue.candidate	1

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dse_1530	scaffold_7:3140859-3140935 -	candidate	Mirtron	CDS	[View on UCSC Genome Browser (Cornell Mirror)]

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



dse_1530_annot [-15.4]

Show Alternate Folds

Flybase annotation

CDS [Dsec\GM17002-cds]; intron [Dsec\GM17002-in]; CDS [Dsec\GM17002-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

Anti-sense strand reads

[illegible]

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
drosEc2	scaffold_7:3140809-3140985 - see 1530		TGCCCACTACAATGAAAGGATAATTTACCCATTATAATATGGCTAATTGTGAAATACATGAAGGCAGGTGAGTATGCGCT-----GCTCT-----AA-GAT--G-CAAAATTCAGGCATTTA-AAGCAC-----CCCTTTTGACCGGCTTGGAAACAGAGGTGATTGTGATTGATGATGGTAGTCGGATGGAA
drosIm2	21:19060115-19060291 -		TGCCCACTACAATGAAAGGATAATTTACCCATTATAATATGGCTAATTGTGAAATACATGAAGCAAGTGAGTATGCGCT-----GCTCT-----AA-GCT--G-CAAAATTCAGGCATTTA-AAGCT-----CCCTTTTGACCGGCTTGGAAACAGAGGTGATTGTGATTGATGATGGTAGTCGGATGGAA
dm3	chr2L:19526114-19526290 -		TGCCCACTACAATGAAAGGATAATTTACCCATTATAATATGGCTAATTGTGAAATACATGAAGGCAGGTGAGTATGCGCT-----GCTCT-----AA-GCT--G-CAAAATTCAGGCATTTA-AAGCT-----CCCTTTTGACCGGCTTGGAAACAGAGGTGATTGTGATTGATGATGGTAGTCGGATGGAA
drosEc2	scaffold_4845:4772697-4772873 +		TGCCCACTACAATGAAAGGATAATTTACCCATTATAATATGGCTAATTGTGAAATACATGAAGGCAGGTGAGTATGCGCT-----GCTCT-----GA-GCT--G-CAAAATTCAGGCATTTA-AAGCT-----CCCTTTTGACCGGCTTGGAAACAGAGGTGATTGTGATTGATGATGGTAGTCGGATGGAA
drosYak3	2R:6022269-6023145 -		TGCCCACTACAATGAAAGGATAATTTACCCATTATAATATGGCTAATTGTGAAATACATGAAGGCAGGTGAGTATGCGCT-----GCTCT-----GA-GCT--G-CAAAATTCAGGCATTTA-AAGCT-----CCTATTGACCGGCTTGGAAACAGAGGTGATTGTGATTGATGATGGTAGTCGGATGGAA
drosEug1	scf7180000409463:1838690-1838867 -		TGCCCACTACAATGAAAGGATAATTTACCCATTATAATATGGCTAATTGTGAAATACATGAAGGCAGGTGAGTATGCGCT-----GCTCT-----AA-GCT--G-CAAAATTCAGGCATTTA-AAGCT-----CCTATTGACCGGCTTGGAAACAGAGGTGATTGTGATTGATGATGGTAGTCGGATGGAA
drosBial	scf7180000302408:441313-441490 -		TGCCCACTACAAGCAAAAGGATAATTTACCCATTATAATATGGCTAATTGTGAAATACATGAAGGCAGGTGAGTATGCGCT-----GCTCT-----AA-GCT--G-CAAAATTCAGGCATTTA-AAGCT-----CCTATTGACCGGCTTGGAAACAGAGGTGATTGTGATTGATGATGGTAGTCGGATGGAA
drosTak1	scf7180000451515:993384-993561 +		TGCCCACTACAAGCAAAAGGATAATTTACCCATTATAATATGGCTAATTGTGAAATACATGAAGGCAGGTGAGTATGCGCT-----GCTCT-----AA-GCT--G-CAAAATTCAGGCATTTA-AAGCT-----CCTATTGACCGGCTTGGAAACAGAGGTGATTGTGATTGATGATGGTAGTCGGATGGAA
drosE1e1	scf7180000491046:3439283-3439460 +		TGCCCACTACAAGCAAAAGGATAATTTACCCATTATAATATGGCTAATTGTGAAATACATGAAGGCAGGTGAGTATGCGCT-----GCTCT-----AA-GCT--G-CAAAATTCAGGCATTTA-AAGCT-----CCTATTGACCGGCTTGGAAACAGAGGTGATTGTGATTGATGATGGTAGTCGGATGGAA
drosRho1	scf718000077913:128025-128201 -		TGCCCACTACAATGAAAGGATAATTTACCCATTATAATATGGCTAATTGTGAAATACATGAAGGCAGGTGAGTATGCGCT-----GCTCT-----AA-GCT--G-CAAAATTCAGGCATTTA-AAGCT-----CCTATTGACCGGCTTGGAAACAGAGGTGATTGTGATTGATGATGGTAGTCGGATGGAA
drosFic1	scf7180000454003:59002-59176 +		TGCCCACTACAAGCAAAAGGATAATTTACCCATTATAATATGGCTAATTGTGAAATACATGAAGGCAGGTGAGTATGCGCT-----GCTCT-----AA-GCT--G-CAAAATTCAGGCATTTA-AAGCT-----CCTATTGACCGGCTTGGAAACAGAGGTGATTGTGATTGATGATGGTAGTCGGATGGAA
drosKik1	scf7180000302382:796331-796507 +		TGCCCACTACAAGCAAAAGGATAATTTACCCATTATAATATGGCTAATTGTGAAATACATGAAGGCAGGTGAGTATGCGCT-----GCTCT-----AA-GCT--G-CAAAATTCAGGCATTTA-AAGCT-----CCTATTGACCGGCTTGGAAACAGAGGTGATTGTGATTGATGATGGTAGTCGGATGGAA
drosAna3	scaffold_12916:12052033-12052206 +		TGCCCACTACAATGAAAGGATAATTTACCCATTATAATATGGCTAATTGTGAAATACATGAAGGCAGGTGAGTATGCGCT-----GCTCT-----AA-GCT--G-CAAAATTCAGGCATTTA-AAGCT-----CCTATTGACCGGCTTGGAAACAGAGGTGATTGTGATTGATGATGGTAGTCGGATGGAA
drosBip1	scf7180000396769:401089-401262 +		TGCCCACTACAAGCAAAAGGATAATTTACCCATTATAATATGGCTAATTGTGAAATACATGAAGGCAGGTGAGTATGCGCT-----GCTCT-----AA-GCT--G-CAAAATTCAGGCATTTA-AAGCT-----CCTATTGACCGGCTTGGAAACAGAGGTGATTGTGATTGATGATGGTAGTCGGATGGAA
dp5	4_group1:1675787-1675967 +		TGCCCACTACAATGAAAGGATAATTTACCCATTATAATATGGCTAATTGTGAAATACATGAAGGCAGGTGAGTATGCGCT-----GCTCT-----AA-GCT--G-CAAAATTCAGGCATTTA-AAGCT-----CCTATTGACCGGCTTGGAAACAGAGGTGATTGTGATTGATGATGGTAGTCGGATGGAA
drosPer2	scaffold_5:3530495-3530675 -		TGCCCACTACAATGAAAGGATAATTTACCCATTATAATATGGCTAATTGTGAAATACATGAAGGCAGGTGAGTATGCGCT-----GCTCT-----AA-GCT--G-CAAAATTCAGGCATTTA-AAGCT-----CCTATTGACCGGCTTGGAAACAGAGGTGATTGTGATTGATGATGGTAGTCGGATGGAA
drosW12	scf2_1100000004521:6723034-6723224 -		TGCCCACTACAATGAAAGGATAATTTACCCATTATAATATGGCTAATTGTGAAATACATGAAGGCAGGTGAGTATGCGCT-----GCTCT-----AA-GCT--G-CAAAATTCAGGCATTTA-AAGCT-----CCTATTGACCGGCTTGGAAACAGAGGTGATTGTGATTGATGATGGTAGTCGGATGGAA
drosVir3	scaffold_12723:2914356-2914532 -		TGCCCACTACAATGAAAGGATAATTTACCCATTATAATATGGCTAATTGTGAAATACATGAAGGCAGGTGAGTATGCGCT-----GCTCT-----AA-GCT--G-CAAAATTCAGGCATTTA-AAGCT-----CCTATTGACCGGCTTGGAAACAGAGGTGATTGTGATTGATGATGGTAGTCGGATGGAA
drosMoj3	scaffold_6500:16185339-16185709 -		TGCCCACTACAATGAAAGGATAATTTACCCATTATAATATGGCTAATTGTGAAATACATGAAGGCAGGTGAGTATGCGCT-----GCTCT-----AA-GCT--G-CAAAATTCAGGCATTTA-AAGCT-----CCTATTGACCGGCTTGGAAACAGAGGTGATTGTGATTGATGATGGTAGTCGGATGGAA
drosGr12	scaffold_15126:565259-565441 +		TGCCCACTACAATGAAAGGATAATTTACCCATTATAATATGGCTAATTGTGAAATACATGAAGGCAGGTGAGTATGCGCT-----GCTCT-----AA-GCT--G-CAAAATTCAGGCATTTA-AAGCT-----CCTATTGACCGGCTTGGAAACAGAGGTGATTGTGATTGATGATGGTAGTCGGATGGAA

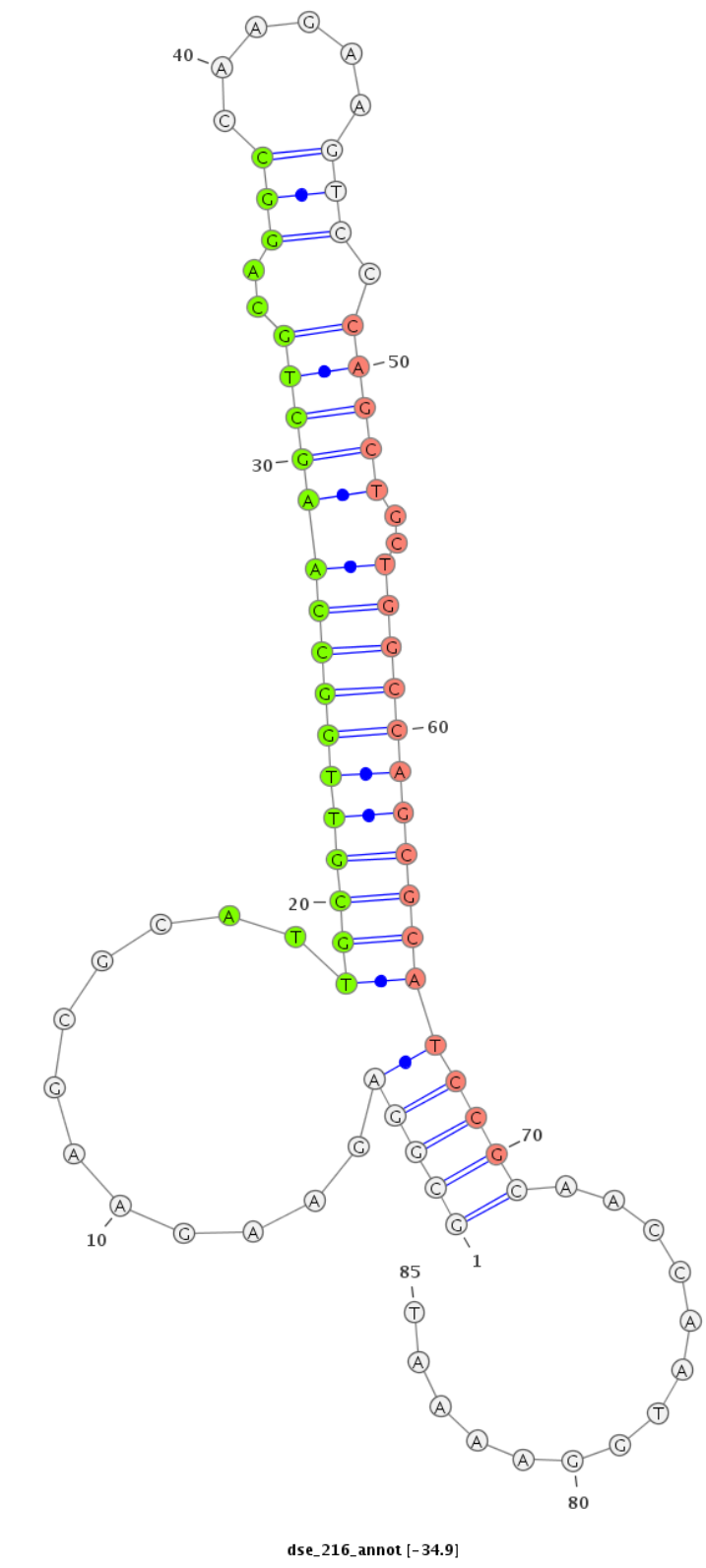
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```
crit.star
crit.loop
crit.mor
crit.half
crit.total
crit.pairing
crit.top3
crit.tptop3
crit.uri
crit.back
rescue.total
rescue.dominant
rescue.known
rescue.confident
rescue.candidate
```

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dse_216	scaffold_5:3042362-3042417 +	candidate	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 annnotation

CDS [Dsec GM18506-cds]; utr5 [utr5_plus_690]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

Read #	Read size	Mismatch	Hit Count	Hit Norm	Total Norm	Total	V115 head	V114 embryo	V113 male body
23	0	1	4.00	4	2	2	0		
21	0	1	4.00	4	2	0	2		
21	0	1	2.00	2	0	2	0		
22	0	1	2.00	2	1	0	1		
22	0	1	1.00	1	0	1	0		
18	0	1	1.00	1	1	0	0		
23	0	1	1.00	1	0	1	0		
19	1	1	1.00	1	1	0	0		

Anti-sense strand reads

Read #	Read size	Mismatch	Hit Count	Hit Norm	Total Norm	Total
23	0	1	4.00	4	2	2
21	0	1	4.00	4	2	0
21	0	1	2.00	2	0	2
22	0	1	2.00	2	1	0
22	0	1	1.00	1	0	1
18	0	1	1.00	1	1	0
23	0	1	1.00	1	0	1
19	1	1	1.00	1	1	0

No data available in table

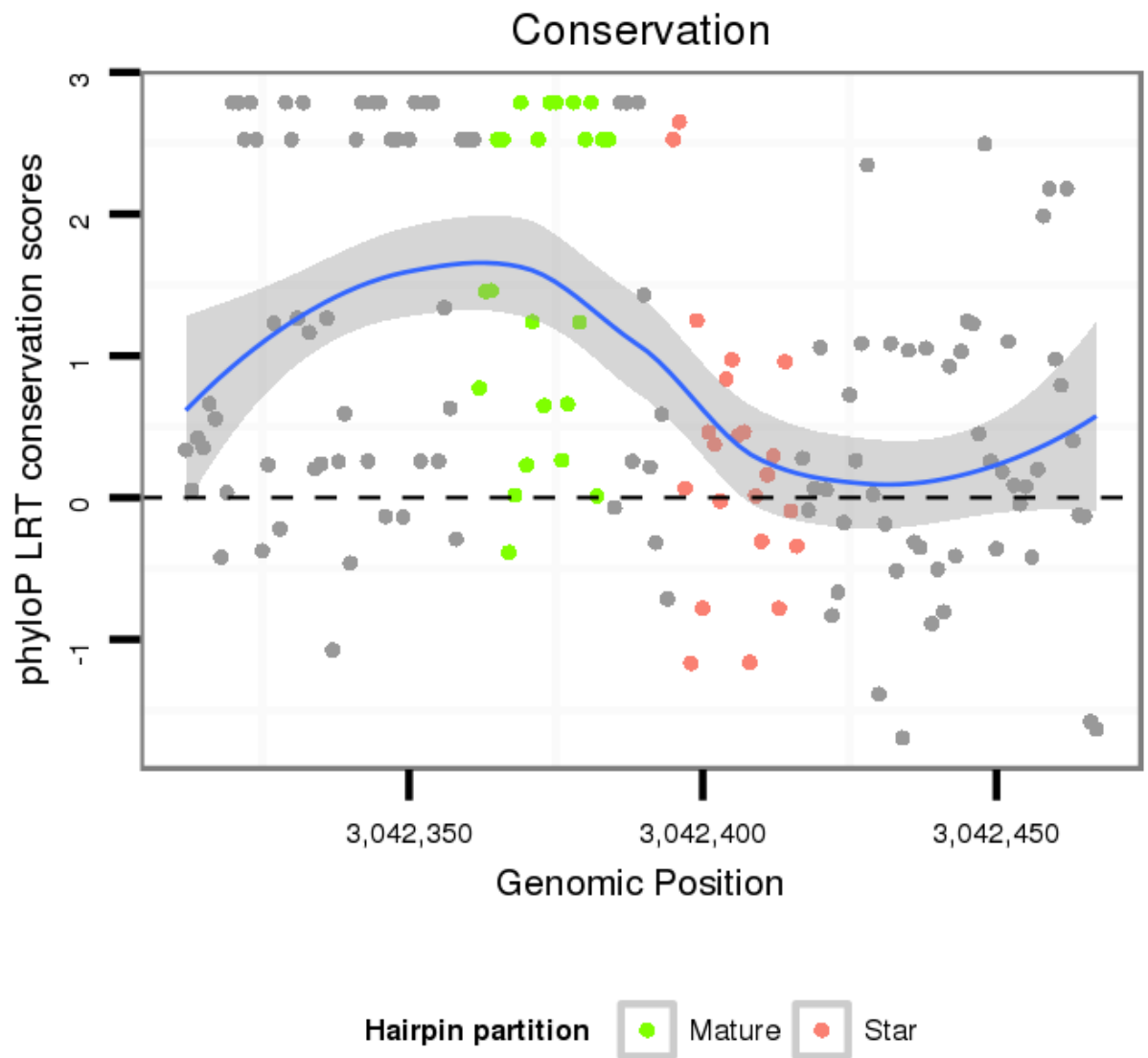
Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droSec2	scaffold_5:3042312-3042467 +	dse_216	GTC--GCAGCATGTCCACTTGCAGTTTCATCCGAGATAGCGGAGAAGAAGCGCATTGCGTTGGCCAAAGCTGCAGGC
droSim2	21:4769010-4769165 +	dse_32450	GTC--GCAGCATGTCCACTTGCAGTTTCATCCGAGATAGCGGAGAAGAAGCGCATTGCGCTGGCCAAAGCTGCAGGC
dm3	chr2L:4955575-4955730 +	dme_401	GTC--GCAGCATGTCCACTTGCAGTTTCATCCGAGATAGCGGAGAAGAAGCGCATTGCGCTGGCCAAAGCTGCAGGC
droEre2	scaffold_4929:5032026-5032178 +		GTC--GCAGCATGTCCACTTGCAGTTTCATCCGAAATAGCGGAGAAGAAGCGCATTGCGCTGGCCAAAGCTGCAGGC
droYak3	2L:10571233-10571388 -	dya_1788	GTC--GCAGCATGTCCACTTGCAGTTTCATCCGAAATAGCGGAGAAGAAGCGCATTGCGCTGGCCAAAGCTGCAGGC
droEug1	scf7180000409005:837269-837427 +		GTC--GCAGCATGTCCACTTGCAGTTTCATCCGAAATAGCGGAGAAGAAGCGCATTGCGCTGGCCAAAGCTGCAGGC
droBial	scf7180000302188:1539593-1539742 +		GTC--GCAGCATGTCCACTTGCAGTTTCATCCGAAATAGCGGAGAAGAAGCGCATTGCGCTGGCCAAAGCTGCAGGC
droTak1	scf7180000415705:273693-273827 +		GTC--GCAGCATGTCCACTTGCAGTTTCATCCGAAATAGCGGAGAAGAAGCGCATTGCGCTGGCCAAAGCTGCAGGC
droEle1	scf7180000491046:2622831-2622983 +		GTC--GCAGCATGTCCACTTGCAGTTTCATCCGAAATAGCGGAGAAGAAGCGCATTGCGCTGGCCAAAGCTGCAGGC
droRho1	scf7180000779695:7662-7814 +		ATC--GCAGCATGTCCACTTGCAGTTTCATCCGAAATAGCGGAGAAGAAGCGCATTGCGCTGGCCAAAGCTGCAGGC
droFic1	scf7180000453842:1297093-1297241 -		ATC--GCAGCATGTCCACTTGCAGTTTCATCCGAAATAGCGGAGAAGAAGCGCATTGCGCTGGCCAAAGCTGCAGGC
droK1k1	scf7180000302271:69334-69485 +		GTC--GCAGCATGTCCACTTGCAGTTTCATCCGAAATAGCGGAGAAGAAGCGCATTGCGCTGGCCAAAGCTGCAGGC
droAna3	scaffold_12943:2696429-2696577 +		TCATGCAATATGCTGCGCTGCAGTTCATCCGAAATAGCGGAGAAGAAGCGCATTGCGCTGGCCAAAGCTGCAGGC
droBip1	scf7180000396535:2094263-2094401 +		TCATGCAATATGCTGCGCTGCAGTTCATCCGAAATAGCGGAGAAGAAGCGCATTGCGCTGGCCAAAGCTGCAGGC
dp5	4_group4:1471207-1471338 +		TCATGCAATATGCTGCGCTGCAGTTCATCCGAAATAGCGGAGAAGAAGCGCATTGCGCTGGCCAAAGCTGCAGGC
droPer2	scaffold_10:473217-473343 +		TCATGCAATATGCTGCGCTGCAGTTCATCCGAAATAGCGGAGAAGAAGCGCATTGCGCTGGCCAAAGCTGCAGGC
droW112	scf2_1100000004585:1582250-1582382 -		GTC--GCAGCATGTCCACTTGCAGTTTCATCCGAAATAGCGGAGAAGAAGCGCATTGCGCTGGCCAAAGCTGCAGGC
droVir3	scaffold_13246:1175609-1175728 -		GA--ATGCAATATGCTGCGCTGCAGTTCATCCGAAATAGCGGAGAAGAAGCGCATTGCGCTGGCCAAAGCTGCAGGC
droMoj3	scaffold_6500:4738876-4738990 +		TCATGCAATATGCTGCGCTGCAGTTCATCCGAAATAGCGGAGAAGAAGCGCATTGCGCTGGCCAAAGCTGCAGGC
droGr12	scaffold_15252:16053753-16053849 +		TCATGCAATATGCTGCGCTGCAGTTCATCCGAAATAGCGGAGAAGAAGCGCATTGCGCTGGCCAAAGCTGCAGGC

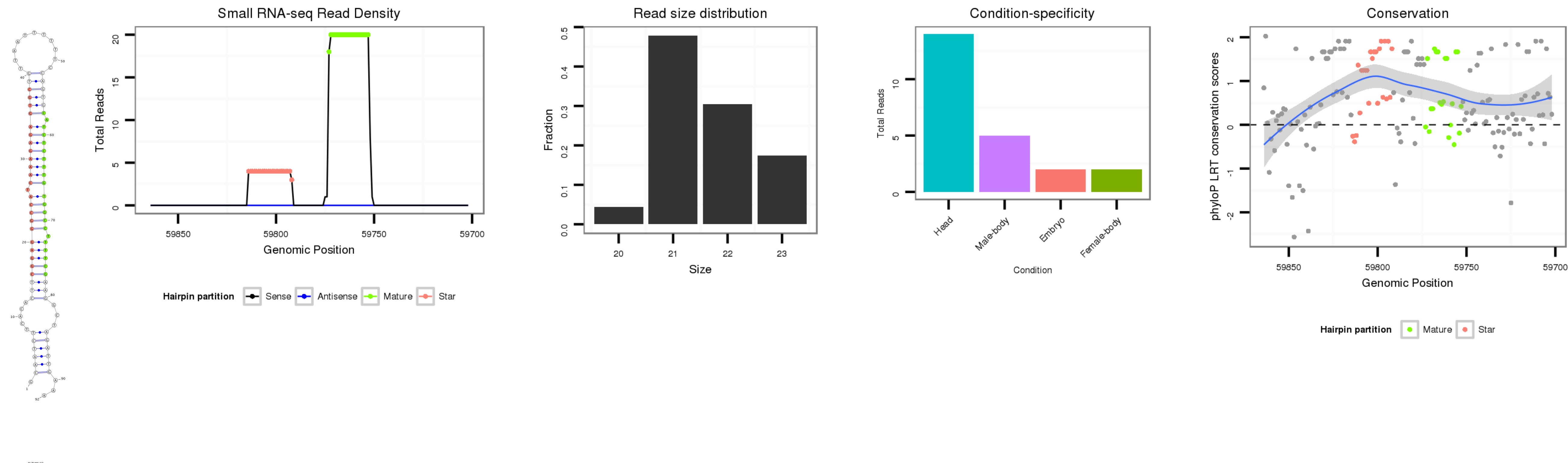
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	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tpop3	1
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	4



Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Show Alternate Folds

Flybase annotation

intron [Dsec\GM22246-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads

show mid mismatch reads

[illegible]

Anti-sense strand reads

CCACGCTCTTAGGTTAAAGTGCCTCGAGGCTCTACGTTAGAAAGTGTGAAGCCTCCCGTAGTTTCTCTCAGCAATTA AAAAAGGTCACGTAGAGAAACACCGGAAAGCCTTCGATCTAACTTTCAGGAAGAAACCCAAAGCAAGGCACCTTAATTGTGC																M054	V115	
*****.(((((((.....(((((((((((((((.....)))))).)))))))))).))))))....*****										Read #	Hit	Total				female	body	head
										size	Mismatch	Count	Norm	Total				

Show Alignment With Reads

Re-alignment of all predicted orthologs

[illegible]

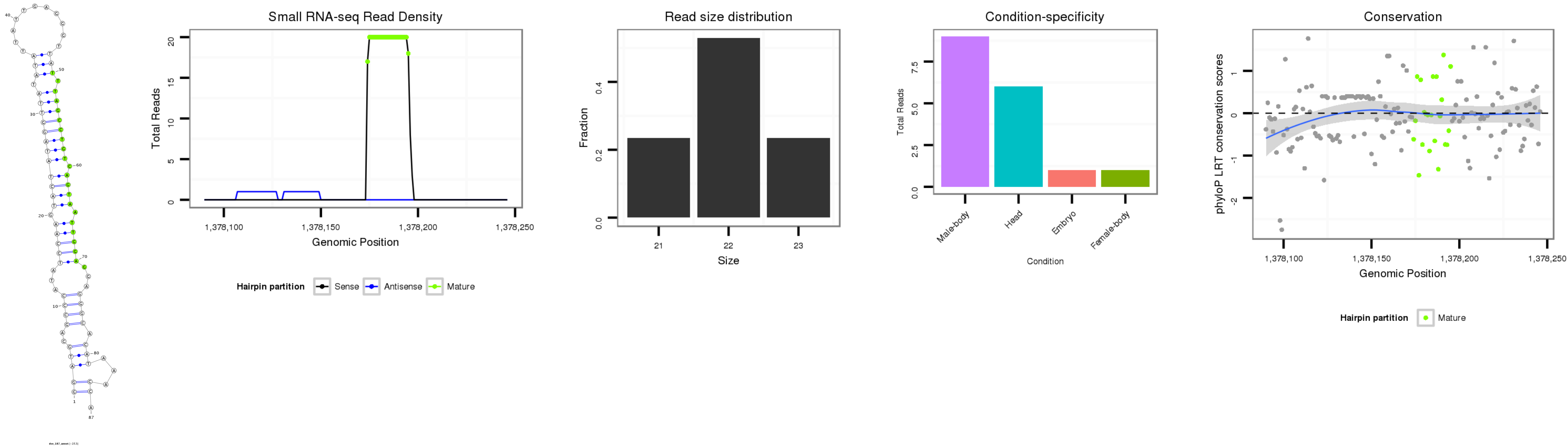
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crit.star
crit.loop
crit.mor
crit.half
crit.total
crit.pairing
crit.top3
crit.tptop3
crit.uri
crit.back
rescue.total
rescue.dominant
rescue.known
rescue.confident
rescue.candidate

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:
dse_187	scaffold_9:1378140-1378196 +	candidate	Canonical miRNA	intergenic

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

TAACACTCAGCTTTTTTCGGCCCATATATGTCGGATGCAGGCCATATCCAAGTACTATAGGTTATATATATTATTGGGGTTAATTAGCCTGTCAGTAATTGGAGGAGGGGCACATAAAACCCTGCTAGCTACCCATAAAATTGCACATTAGATAA	Read #	Hit	Total	V113	V115	V114	M054		
size Mismatch	Count	Norm	Total	male	head	embryo	female		
22 0 1 8.00 8 6 2 0 0	22	0	1	8.00	8	6	2	0	0
23 0 1 4.00 4 1 2 1 0	23	0	1	4.00	4	1	2	1	0
24 0 1 3.00 3 1 1 1 0	24	0	1	3.00	3	1	1	1	0
21 0 1 2.00 2 0 1 0 1	21	0	1	2.00	2	0	1	0	1
21 0 1 2.00 2 2 0 0 0	21	0	1	2.00	2	2	0	0	0
22 0 1 1.00 1 0 1 0 0	22	0	1	1.00	1	0	1	0	0
25 1 1 1.00 1 1 0 0 0	25	1	1	1.00	1	1	0	0	0

Anti-sense strand reads

ATTGTAGTGCAGAAAAAGCCGGGTGTATAACAGACCTACGTCGGGTATAGGTTTCATGATATCCAATATAATAAAGTCCCAATTAATCGGACAGTCATTAAAGCTGCTCCCGGTATTGGTGGCAGATCGATGGGTATTAAAGCTGTAATCTATT	Read #	Hit	Total	M054	V113	V114		
size Mismatch	Count	Norm	Total	female	male	embryo		
21 0 1 1.00 1 1 0 0 0	21	0	1	1.00	1	1	0	0
19 0 1 1.00 1 0 0 0 1	19	0	1	1.00	1	0	0	1

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droSec2	scaffold_9:1378090-1378246 +	dse_187	TAACACTCA-G-----CTTTTT-TCGGCC-----CACATATTGT-----CTGGATGCAGCCCATATCCAAGTACTATAG-----GT-----TATATA-TTATTGAGGGTTAATTAGCCTGTCAGT-----AATTGGAGGAGGGC-----ACA--TAAACCACCGTG-----CTAG--CTACCCATAAAT--TGCACATTAGATAA
droSim2	2r:18605608-18605764 +		TAACACTCA-G-----CTTAATT-TCGGC-----CACATCTTGT-----CTGGATGCAGCCCATATCCAAGTACTATAG-----GT-----TATATA-TTATTGAGGGTTATTAGCTGTCACT-----AATTGGAGGAGGGC-----ACA--TAAACCACCGTG-----CTAG--CTACCCATAAAT--TGCACATTAGATAA
dm3	chr2R:18067743-18067909 +	dme_459	TACACTCA-G-----CTTAATT-TCGGC-----CACATATTGT-----TGAAGSCAGCCCATATCCAAGTCTACAT-----GT-----TATATA-TTATTGAGGTTATTGTGTCACTTAGCAGTAATTGGAGGAGGGC-----ACA--TAAACCACCGTG-----CTAG--CTACCCATAAAT--TACACATTAGATAA
droEre2	scaffold_4845:12207191-12207370 +		AACACGA-G-----CTCACTT-TCGAA-----CACACAGT-----CTGGAAACACCCATATCCAAGTACT-----GT-----ATGGATAGGTCGATA-TTATTGCGGTATTGGCTTCGAGTAGCAGTAATTGTGC-----GGCAACC-----CTG--CTGCATATAAATACACACATTAGATAA
droYak3	2R:17813837-17814026 +		TACACTCA-A-----CTAAT-TCGGC-----CAGTATTCTTATTTHGGCAACCCCATATCCAAGTACTACA-----GT-----ATATAGAGG-----CATATATAGATAGTATATA-TTATTGCGGTATTGGCTTCGAGTAGCAGTAATTGTGC-----GGCAACC-----ACC--CAAACCACCGTG-----CTAG--CTGCCATAAAT--TACAGCTTAGATAA
droEug1	scf7180000409663:76779-76875 +		TGGGAAG-A-----TTGC-G-GAC-TAAGACGAACCCGCTATTACAT-----GT-----ATGTTCTACGAATACCCCTTAACAACTGCACAGAGCCTATCAATTGG-----GT-----TATATA-TTATTGAGGTTATTGTGTCACTTAGCAGTAATTGTGC-----GGCAACC-----CTG--CTGCCATAAAT--TACAGCTTAGATAA
droBia1	scf7180000301506:2419721-2419894 +		GACACGA-G-----ATC-----TCGACGAGCCCGCTGTTTACAA-----GT-----ATGTTCTATAGGTACCCGTATACGAACCTTTGTAAGCTTATCGAAGTG-----GT-----TATATA-TTATTGAGGTTATTGTGTCACTTAGCAGTAATTGTGC-----GGCAACC-----CTG--CTGCCATAAAT--TACAGCTTAGATAA
droTak1	scf7180000415346:244802-244891 +		TACACTCG-A-----TTA-----ATCGACGAGCCCGCCGTTTACAA-----GT-----ATGTTCTATAAGTACCCATAACTAGTATATAGAGCCTATATAA-----GT-----TATATA-TTATTGAGGTTATTGTGTCACTTAGCAGTAATTGTGC-----GGCAACC-----CTG--CTGCCATAAAT--TACAGCTTAGATAA
droElc1	scf7180000486721:875-1062 +		TACACTCG-A-----TCA-----ACTTCTGACGAGCCCGCTGTTTACAA-----GT-----ATGTTCTATAGGGTACCCGTGTTTCTGCTAGATAGAGCTTATTAGTTGG-----GT-----TATATA-TTATTGAGGTTATTGTGTCACTTAGCAGTAATTGTGC-----GGCAACC-----CTG--CTGCCATAAAT--TACAGCTTAGATAA
droRho1	scf7180000777716:31565-31732 +		TACACTCG-G-----ACAA-----AGCTTAAAGCCGAGCCCGCTGTTTACAA-----GT-----ATGTTCTATAGGTACCCGTATATTAAGATAGAGCTTATTGTGCGA-----GT-----TATATA-TTATTGAGGTTATTGTGTCACTTAGCAGTAATTGTGC-----GGCAACC-----CTG--CTGCCATAAAT--TACAGCTTAGATAA
droFic1	scf7180000453858:513679-513847 +		TACACTCG-A-----TCAG-ATCTTC-TCGCGCCGAGCCCGCTGTTTACAA-----GT-----ATGTTCTATAGGTACCCGTATATTAAGATAGAGCTTATTGTGCGA-----GT-----TATATA-TTATTGAGGTTATTGTGTCACTTAGCAGTAATTGTGC-----GGCAACC-----CTG--CTGCCATAAAT--TACAGCTTAGATAA
droKix1	scf7180000302232:54777-5581 +		TGCGAGAG-G-----TGCATGGGATGTTA-----GT-----TGGATACTATTACCTAGCAGCCACCTTAGCCATAA-----GT-----TATATA-TTATTGAGGTTATTGTGTCACTTAGCAGTAATTGTGC-----GGCAACC-----CTG--CTGCCATAAAT--TACAGCTTAGATAA
droAna3	scaffold_13266:10729230-10729247 +		GAAATATG-A-----ATTGTTT-T-----GT-----TGGATACTATTACCTAGCAGCCACCTTAGCCATAA-----GT-----TATATA-TTATTGAGGTTATTGTGTCACTTAGCAGTAATTGTGC-----GGCAACC-----CTG--CTGCCATAAAT--TACAGCTTAGATAA
droBip1	scf7180000396428:1158034-1158222 +		TACACTCA-GAATCGA-AGA-----TCAAG-----GTCTCGCGAGCCCGCTGTTTAA-----GT-----ATATTTTAGGAATGGCTACTTTTGGTTGTATAAGCTTATACGACAGATTCATATTGGGGGT-----GT-----TATATA-TTATTGAGGTTATTGTGTCACTTAGCAGTAATTGTGC-----GGCAACC-----CTG--CTGCCATAAAT--TACAGCTTAGATAA
dp5	11382330-19280510 +		AAATGCTCAAAATCGATGCGATGATCAG-CTTCGCGAGAGCGAGCCCGCAATTTACAT-----GT-----ACATACATATGTATGTGTCTATGTACGCGCTACAACCTTGGACAGAGTCCATCAGCTCAGTTGTA-----GT-----TATATA-TTATTGAGGTTATTGTGTCACTTAGCAGTAATTGTGC-----GGCAACC-----CTG--CTGCCATAAAT--TACAGCTTAGATAA
droPer2	scaffold_37:282677-282875 +		AAATGCTCAAAATCGATGCGATGATCAG-CTTCGCGAGAGCGAGCCCGCAATTTACAT-----GT-----TGGGTTCTATGTACGCGCTACAACCTTGGACAGAGTCCATCAGCTCAGTTGTA-----GT-----TATATA-TTATTGAGGTTATTGTGTCACTTAGCAGTAATTGTGC-----GGCAACC-----CTG--CTGCCATAAAT--TACAGCTTAGATAA

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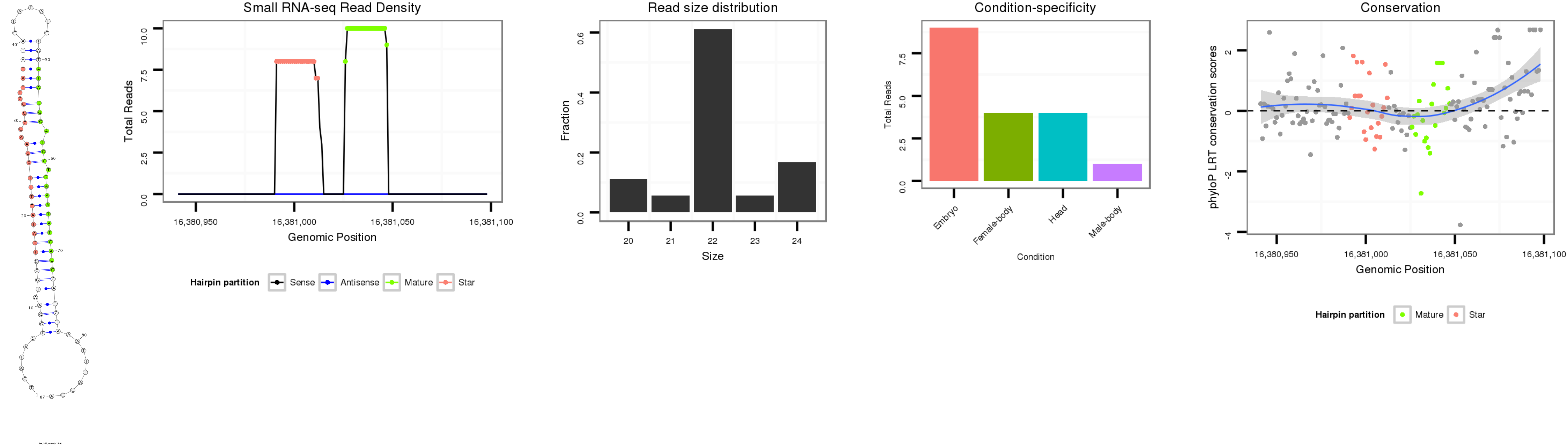
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.top33	1
crit.un	0
crit.back	0
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

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

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dse_162	scaffold_0:16380991-16381048 +	candidate	Canonical miRNA	intron	[View on UCSC Genome Browser (Cornell Mirror)]

Legend: ■ **match** ■ **mismatch in alignment** ■ **mismatch in read**

Predicted structure



Show Alternate Folds

Flybase annotation

intron [Dsec:GM26228-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

	Read # size	Mismatch	Hit Count	Total Total		V114 embryo body	M054 female body	V115 head	V113 male body
AATTACGAATGGCACACGCATTAAAGAAGAAATTCATACGTGGAATGGCGGATATTTGGGAACGCCCTTATATACTATATCTATATAGGCATCCTGAAATATCACGC	22	0	1	8.00	8	5	1	2	0
.....(((.(((((((((((((((((((.(((((((((((((((((((.))	22	0	1	3.00	3	0	1	1	1
.....TGATATTTTGGGAAGCCCTTAT.....	22	0	1	3.00	3	0	1	1	1
.....TGATATTTTGGGAAGCCCTTAT.....	24	0	1	3.00	3	3	0	0	0
.....TGATATTTTGGGAAGCCCTTATAT.....	20	0	1	1.00	1	1	0	0	0
.....TAGGCATCCTGAAATATCAC.....	23	0	1	1.00	1	0	1	0	0
.....TGATATTTTGGGAAGCCCTTATA.....	20	0	1	1.00	1	0	0	1	0
.....TGATATTTTGGGAAGCCCTT.....	21	0	1	1.00	1	0	1	0	0
.....TAGGCATCCTGAAATATCACCC.....									

Anti-sense strand reads

	Read # size	Mismatch	Hit Count	Total Total		V113 female body	M054 male body
TTAAGTCGTTACCGTGGCTAAATTTTCCTTTAAAGTATGACCTTACCCGCTATAAACCCTTGGCGGAATATATGATATAGATATATCCGTAGGACTTTATAGTGGCTAGATTTTAAATGGTTGGGGAAAACGTGAATGTGTGTCGTGAATACTAAAA							
.....(((.(((((((((((((((((((.(((((((((((((((((((.))							

Show Alignment With Reads

Re-alignment of all predicted orthologs

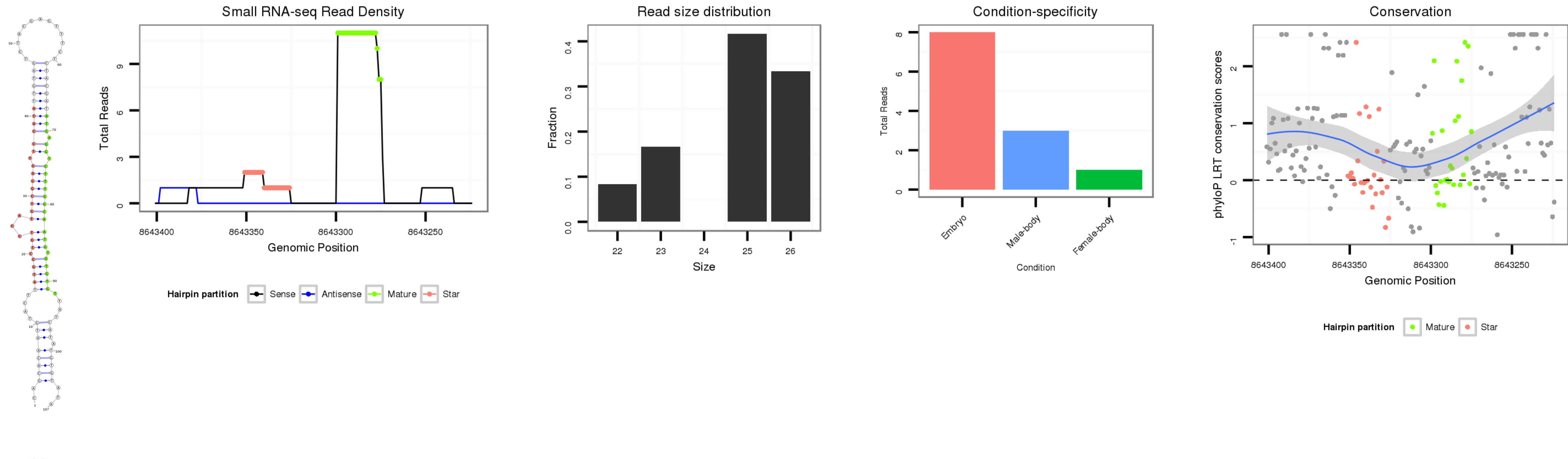
Species	Coordinate	ID	Alignment
droSec2	scf7180000491047:120367-120393 +	dse_162	AA-----TTCACGA-----ATGGCAC-----ACG-----CATTTAAAA-----GCAA-----ATTTC-----TACTGGAATGGGCGATATTT--GGAACG--C-----CC-----TTATATACTA-----TATCTA-----GTA-----GGC--ATCTGTG-AAATAT---C-A-----CATCTAAA-TTTACCA-----ACCC--TTTGCACCTTAC--AC---AC-----A-----GCACCTATG-----ATTTT--
droS1e2	3p15510348-15510505 +		AA-----TTCACGA-----AGCAC-----ACG-----CATTTAAA-----GCAA-----ATTTC-----TACTGGAATGGGCGATATTT--GGAACG--C-----CC-----TTATATACTA-----TATCTA-----GTA-----GGC--ATCTGTG-AAATAT---C-A-----CATCTAAA-TTTACCA-----ACCC--TTTGCACCTTAC--AC---AC-----A-----GCACCTATG-----ATTTT--
dm3	chr38:5515867-5516034 -		AA-----TTCACGA-----AGCAC-----ACG-----CATTTAAAA-----GCAA-----ATTTC-----TACTGGAATGGGCGATATTT--GGAACG--C-----CC-----TTATATACTA-----TATCTA-----GTA-----GGC--ATCTGTG-AAATAT---C-A-----CATCTAAA-TTTACCA-----ACCC--TTTGCACCTTAC--AC---AC-----A-----GCACCTATG-----ATTTT--
droEre2	scf71800004770:16081366-16081514 +		AA-----TTCACGA-----AGCAC-----ACG-----CATTTAAAA-----GCAA-----ATTTC-----TACTGGAATGGGCGATATTT--GGAACG--C-----CC-----TTATATACTA-----TATCTA-----GTA-----GGC--ATCTGTG-AAATAT---C-A-----CATCTAAA-TTTACCA-----ACCC--TTTGCACCTTAC--AC---AC-----A-----GCACCTATG-----ATTTT--
droYak3	3R:9570118-9570273 -		AA-----TTCACGA-----AGCAC-----ACG-----CATTTAAAA-----GCAA-----ATTTC-----TACTGGAATGGGCGATATTT--GGAACG--C-----CC-----TTATATACTA-----TATCTA-----GTA-----GGC--ATCTGTG-AAATAT---C-A-----CATCTAAA-TTTACCA-----ACCC--TTTGCACCTTAC--AC---AC-----A-----GCACCTATG-----ATTTT--
droBup1	scf7180000407136:1701135-170298 +		AA-----TTCACGA-----AGCAC-----ACG-----CATTTAAAA-----GCAA-----ATTTC-----TACTGGAATGGGCGATATTT--GGAACG--C-----CC-----TTATATACTA-----TATCTA-----GTA-----GGC--ATCTGTG-AAATAT---C-A-----CATCTAAA-TTTACCA-----ACCC--TTTGCACCTTAC--AC---AC-----A-----GCACCTATG-----ATTTT--
droB1a1	scf7180000202402:3002193-3002268 -		AA-----TTCACGA-----AGCAC-----ACG-----CATTTAAAA-----GCAA-----ATTTC-----TACTGGAATGGGCGATATTT--GGAACG--C-----CC-----TTATATACTA-----TATCTA-----GTA-----GGC--ATCTGTG-AAATAT---C-A-----CATCTAAA-TTTACCA-----ACCC--TTTGCACCTTAC--AC---AC-----A-----GCACCTATG-----ATTTT--
droTaK1	scf7180000415653:564048-564142 -		AA-----TTCACGA-----AGCAC-----ACG-----CATTTAAAA-----GCAA-----ATTTC-----TACTGGAATGGGCGATATTT--GGAACG--C-----CC-----TTATATACTA-----TATCTA-----GTA-----GGC--ATCTGTG-AAATAT---C-A-----CATCTAAA-TTTACCA-----ACCC--TTTGCACCTTAC--AC---AC-----A-----GCACCTATG-----ATTTT--
droE1e1	scf7180000491047:120367-120393 +		AA-----TTCACGA-----AGCAC-----ACG-----CATTTAAAA-----GCAA-----ATTTC-----TACTGGAATGGGCGATATTT--GGAACG--C-----CC-----TTATATACTA-----TATCTA-----GTA-----GGC--ATCTGTG-AAATAT---C-A-----CATCTAAA-TTTACCA-----ACCC--TTTGCACCTTAC--AC---AC-----A-----GCACCTATG-----ATTTT--
droRho1	scf7180000777865:298676-298922 -		AA-----TTCACGA-----AGCAC-----ACG-----CATTTAAAA-----GCAA-----ATTTC-----TACTGGAATGGGCGATATTT--GGAACG--C-----CC-----TTATATACTA-----TATCTA-----GTA-----GGC--ATCTGTG-AAATAT---C-A-----CATCTAAA-TTTACCA-----ACCC--TTTGCACCTTAC--AC---AC-----A-----GCACCTATG-----ATTTT--
droF1c1	scf7180000454104:1325303-1325481 +		AA-----TTCACGA-----AGCAC-----ACG-----CATTTAAAA-----GCAA-----ATTTC-----TACTGGAATGGGCGATATTT--GGAACG--C-----CC-----TTATATACTA-----TATCTA-----GTA-----GGC--ATCTGTG-AAATAT---C-A-----CATCTAAA-TTTACCA-----ACCC--TTTGCACCTTAC--AC---AC-----A-----GCACCTATG-----ATTTT--
droK1k1	scf7180000302461:163642-163903 +		AA-----TTCACGA-----AGCAC-----ACG-----CATTTAAAA-----GCAA-----ATTTC-----TACTGGAATGGGCGATATTT--GGAACG--C-----CC-----TTATATACTA-----TATCTA-----GTA-----GGC--ATCTGTG-AAATAT---C-A-----CATCTAAA-TTTACCA-----ACCC--TTTGCACCTTAC--AC---AC-----A-----GCACCTATG-----ATTTT--
droAna3	scf7180000454104:1325303-1325481 +		AA-----TTCACGA-----AGCAC-----ACG-----CATTTAAAA-----GCAA-----ATTTC-----TACTGGAATGGGCGATATTT--GGAACG--C-----CC-----TTATATACTA-----TATCTA-----GTA-----GGC--ATCTGTG-AAATAT---C-A-----CATCTAAA-TTTACCA-----ACCC--TTTGCACCTTAC--AC---AC-----A-----GCACCTATG-----ATTTT--
droB1p1	scf7180000396413:609347-609422 -		AA-----TTCACGA-----AGCAC-----ACG-----CATTTAAAA-----GCAA-----ATTTC-----TACTGGAATGGGCGATATTT--GGAACG--C-----CC-----TTATATACTA-----TATCTA-----GTA-----GGC--ATCTGTG-AAATAT---C-A-----CATCTAAA-TTTACCA-----ACCC--TTTGCACCTTAC--AC---AC-----A-----GCACCTATG-----ATTTT--
dp5	2:5542442-5542565 +		AA-----TTCACGA-----AGCAC-----ACG-----CATTTAAAA-----GCAA-----ATTTC-----TACTGGAATGGGCGATATTT--GGAACG--C-----CC-----TTATATACTA-----TATCTA-----GTA-----GGC--ATCTGTG-AAATAT---C-A-----CATCTAAA-TTTACCA-----ACCC--TTTGCACCTTAC--AC---AC-----A-----GCACCTATG-----ATTTT--
droPer2	scf7180000454104:1325303-1325481 +		AA-----TTCACGA-----AGCAC-----ACG-----CATTTAAAA-----GCAA-----ATTTC-----TACTGGAATGGGCGATATTT--GGAACG--C-----CC-----TTATATACTA-----TATCTA-----GTA-----GGC--ATCTGTG-AAATAT---C-A-----CATCTAAA-TTTACCA-----ACCC--TTTGCACCTTAC--AC---AC-----A-----GCACCTATG-----ATTTT--
droW12	scf2_1100000004502:107624-10776483 -		AA-----TTCACGA-----AGCAC-----ACG-----CATTTAAAA-----GCAA-----ATTTC-----TACTGGAATGGGCGATATTT--GGAACG--C-----CC-----TTATATACTA-----TATCTA-----GTA-----GGC--ATCTGTG-AAATAT---C-A-----CATCTAAA-TTTACCA-----ACCC--TTTGCACCTTAC--AC---AC-----A-----GCACCTATG-----ATTTT--
droMo3	scf7180000454104:1325303-1325481 +		AA-----TTCACGA-----AGCAC-----ACG-----CATTTAAAA-----GCAA-----ATTTC-----TACTGGAATGGGCGATATTT--GGAACG--C-----CC-----TTATATACTA-----TATCTA-----GTA-----GGC--ATCTGTG-AAATAT---C-A-----CATCTAAA-TTTACCA-----ACCC--TTTGCACCTTAC--AC---AC-----A-----GCACCTATG-----ATTTT--
droGr12	scf7180000454104:1325303-1325481 +		AA-----TTCACGA-----AGCAC-----ACG-----CATTTAAAA-----GCAA-----ATTTC-----TACTGGAATGGGCGATATTT--GGAACG--C-----CC-----TTATATACTA-----TATCTA-----GTA-----GGC--ATCTGTG-AAATAT---C-A-----CATCTAAA-TTTACCA-----ACCC--TTTGCACCTTAC--AC---AC-----A-----GCACCTATG-----ATTTT--

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crit.new	1
crit.loop	0
crit.mor	0
crit.half	0
crit.new	0
crit.pairing	1
crit.p3	1
crit.p3p3	1
crit.tot	1
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Show Alternate Folds

Flybase annotation

utr3 [utr3_minus_3161]

No Repeatable elements found

Sense Strand Reads

[illegible]

Anti-sense strand reads

[illegible]

Show Alignment With Reads

Re-alignment of all predicted orthologs

Coordinate	ID	Alignment
droSec2 scaff60d_18643224-8643401_-	dse_176	TGAG--CACTTAC--C-----TCAGCTCAA--AAGAAACCTA--TCGC-----A--GCACAAATGTACTT--ATGCC--TGTCATGTC--GGAGT--TC-----CATATTGTAGTCTACGAGTTTCTTACGATATAG--GTCITT--GSC-----AAT-----GTGTGTGTATCATAT--G----TGT-----ATAACGTCCTCTTAGTA---GTACA-TTTTACTT-GCTTATA--
droSec2 chr1:1820472-1182050_-	dsl_32468	TGAG--CACTTAC--C-----TCAGCTCAA--AAGAAACCTA--TCGC-----A--GCACAAATGTACTT--ATGCC--TGTCCTGTCT--GGAGT--TC-----CATATTGTAGTCTACGAGTTCTACGATATAG--CCTITT--GSC-----AAT-----GTGTGTGTATCATAT--G----TGT-----ATAACGTCCTCTTAGTA---GTACA-TTTTACTT-GCTTATA--
dm3 chr28:11150576-11150754_-	dme_442	TGAG--CACTTAC--C-----TCAGCTCAA--AAGAAACCTA--TCGC-----A--GCACAAATGTACTT--ATGCC--TGTCCTGTCT--GGAGT--TC-----CATATTGTAGTCTACGAGTTCTACGATATAG--GTCITT--GSC-----AAT-----GTGTGTATCATAT--G----TGT-----ATAACGTCCTCTTAGTA---GTACA-TTTTACTT-GCTTATA--
droEre2 scaff10d_4845:14713662-14713833_+	der_1536	TGAG--CACTTAC--C-----TCAGCTCAA--AAGAACCTA--TCGC-----A--GCACAAATGTACTT--ATGCC--TGTCCTGTCT--GGAGT--TC-----CATATTGTAGTCTACGAGTTCTACGATATAG--CCTITT--GSC-----AAT-----GTGTGTATCATAT--G----TGT-----ATAACGTCCTCTTAGTA---GTACA-TTTTACTT-GCTTATA--
droYak3 chr1:11072237-11072418_-		TGAG--CACTTAC--C-----TCAGCTCAA--AAGAAACCTA--TCGC-----A--GCAT--ATGTACTT--ATAACC--TGTCCTGTCT--GAAGT--TA-----CATATTGTAGTCTACGAGTTCTACGATATAG--CCTITT--GSC-----AAT-----GTGTGTATCATAT--GCTACGAT--ATAACGTCCTCTTAGTA---GTACA-TTTTACTT-GCTTATCT--
droEug1 scaff180000403672:8154-8343_-		TGAG--CACTTAC--C-----TCAGCTCAA--AAGAAACCTA--TCGC-----A--GCAT--ATGTACTT--ATAACC--TGTAACCTC--GAGT--TA-----CATATTGTAGTCTACGAGTTCTACGATATAG--GCTCTC--TCT--AATGTGTG--GT--GTGTCTGTATGTGTGTG--GTGTGTATCATAT--GCTGT--ATAACGTCCTCTTAGTA---GTACA-TTTTACTT-GCTTATCT--
droBla1 scaff180000302143:261904-262077_+		TGAG--CACTTAC--C-----TCAGCTCAA--AAGAAACCTA--TCGC-----A--GCAT--ATGTACTT--ATAACC--TGCAACCC--GAGT--C-----CATATTGTAGTCTACGAGTTCTACGATATAG--CCTCTC--CCT--AATGTGTG--GT--GTGTGTATCATAT--GCTGT--ATAACGTCCTCTTAGTA---GTACA-TTTTACTT-GCTTATCT--
droTak1 scaff180000415878:859119-859297_+		TGAG--CACTTAC--C-----TCAGCTCAA--AAGAAACCTA--TCGC-----A--GCAT--ATGTACTT--ATAACC--TGTAACCTC--GAGT--C-----CATATTGTAGTCTACGAGTTCTACGATATAG--CCTCTC--CCT--AATGTGTG--GT--GTGTGTATCATAT--GCTGT--ATAACGTCCTCTTAGTA---GTACA-TTTTACTT-GCTTATCT--
droEbl1 scaff180000491214:4007756-4007916_-		TGAG--CACTTAC--C-----TCAGCTCAA--AAGAAACCTA--TCGC-----A--GCAT--ATGTACTT--ATAACC--TGTAACCTC--GAGT--C-----CATATTGTAGTCTACGAGTTCTACGATATAG--CCTCTC--CCT--AATGTGTG--GT--GTGTGTATCATAT--GCTGT--ATAACGTCCTCTTAGTA---GTACA-TTTTACTT-GCTTATCT--
droRho1 scaff180000776849:680827-681000_+		TGAG--CACTTAC--C-----TCAGCTCAA--AAGAAACCTA--TCGC-----A--GCAT--ATGTACTT--ATAACC--TGTAACCTC--GAGT--C-----CATATTGTAGTCTACGAGTTCTACGATATAG--CCTCTC--CCT--AATGTGTG--GT--GTGTGTATCATAT--GCTGT--ATAACGTCCTCTTAGTA---GTACA-TTTTACTT-GCTTATCT--
droFic1 scaff180000453342:771787-771944_-		TGAG--CACTTAC--C-----TCAGCTCAA--AAGAAACCTA--TCGC-----A--GCAT--ATGTACTT--ATAACC--TGTAACCTCCGCTGCC--GAGT--C-----CATATTGTAGTCTACGAGTTCTACGATATAG--CCTCTC--CCT--AATGTGTG--GT--GTGTGTATCATAT--GCTGT--ATAACGTCCTCTTAGTA---GTACA-TTTTACTT-GCTTATCT--
droKik1 scaff180000302476:157888-157983_-		TGAG--CACTTAC--C-----TCAGCTCAA--AAGAAACCTA--TCGC-----A--GCAT--ATGTACTT--ATAACC--TGTAACCTC--GAGT--C-----CATATTGTAGTCTACGAGTTCTACGATATAG--CCTCTC--CCT--AATGTGTG--GT--GTGTGTATCATAT--GCTGT--ATAACGTCCTCTTAGTA---GTACA-TTTTACTT-GCTTATCT--
droAna3 scaff60d_13266:7588321-7588512_-		TGAG--CACTTAC--C-----TCAGCTCAA--AAGAAACCTA--TCGC-----A--GCAT--ATGTACTT--ATAACC--TGTAACCTC--GAGT--C-----CATATTGTAGTCTACGAGTTCTACGATATAG--CCTCTC--CCT--AATGTGTG--GT--GTGTGTATCATAT--GCTGT--ATAACGTCCTCTTAGTA---GTACA-TTTTACTT-GCTTATCT--
droBip1 scaff180000396759:1248387-1248569_+		TGAG--CACTTAC--C-----TCAGCTCAA--AAGAAACCTA--TCGC-----A--GCAT--ATGTACTT--ATAACC--TGTAACCTC--GAGT--C-----CATATTGTAGTCTACGAGTTCTACGATATAG--CCTCTC--CCT--AATGTGTG--GT--GTGTGTATCATAT--GCTGT--ATAACGTCCTCTTAGTA---GTACA-TTTTACTT-GCTTATCT--
dp5 chr54:1712-54138_-	dps_3845	TGTA--CACTTAC--C-----TGTAACCTC--ATTCT--A--GCAT--ATGTACTT--ATAACC--TGTAACCTC--GAGT--C-----CATATTGTAGTCTACGAGTTCTACGATATAG--CCTCTC--CCT--AATGTGTG--GT--GTGTGTATCATAT--GCTGT--ATAACGTCCTCTTAGTA---GTACA-TTTTACTT-GCTTATCT--
droPer2 scaff60d_21706732-706958_-	dpe_2516	TGTA--CACTTAC--C-----TGTAACCTC--ATTCT--A--GCAT--ATGTACTT--ATAACC--TGTAACCTC--GAGT--C-----CATATTGTAGTCTACGAGTTCTACGATATAG--CCTCTC--CCT--AATGTGTG--GT--GTGTGTATCATAT--GCTGT--ATAACGTCCTCTTAGTA---GTACA-TTTTACTT-GCTTATCT--
droVir1 scaff60d_10324:900494-900696_+	dvi_24651	TAATAAGCAAAAC--TAAACTCAAAATCTATATCT--A--TAATAACCTA--TAATC--A--GCAT--ATGTACTT--ATAACC--TGTAACCTC--GAGT--C-----CATATTGTAGTCTACGAGTTCTACGATATAG--CCTCTC--CCT--AATGTGTG--GT--GTGTGTATCATAT--GCTGT--ATAACGTCCTCTTAGTA---GTACA-TTTTACTT-GCTTATCT--
droMoJ3 scaff60d_6496:2771576-2771757_+		TAATAAGCAAAAC--TAAACTCAAAATCTATATCT--A--TAATAACCTA--TAATC--A--GCAT--ATGTACTT--ATAACC--TGTAACCTC--GAGT--C-----CATATTGTAGTCTACGAGTTCTACGATATAG--CCTCTC--CCT--AATGTGTG--GT--GTGTGTATCATAT--GCTGT--ATAACGTCCTCTTAGTA---GTACA-TTTTACTT-GCTTATCT--
droGr12 scaff60d_15245:8588359-8588544_+		TAATAAGCAAAAC--TAAACTCAAAATCTATATCT--A--TAATAACCTA--TAATC--A--GCAT--ATGTACTT--ATAACC--TGTAACCTC--GAGT--C-----CATATTGTAGTCTACGAGTTCTACGATATAG--CCTCTC--CCT--AATGTGTG--GT--GTGTGTATCATAT--GCTGT--ATAACGTCCTCTTAGTA---GTACA-TTTTACTT-GCTTATCT--

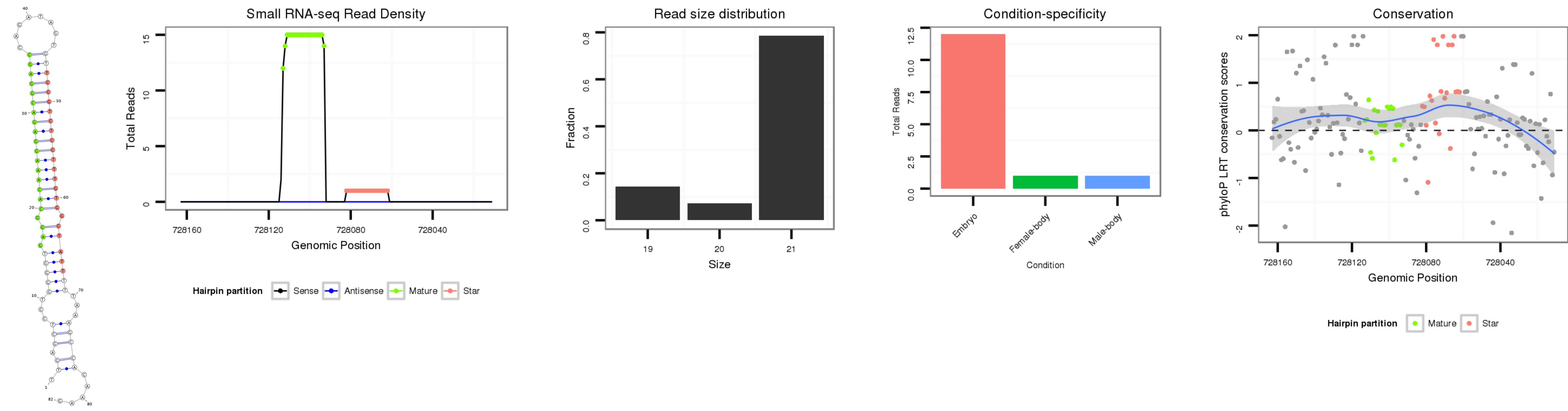
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	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

	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	0
crit.uri	1
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

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

[illegible]

Anti-sense strand reads

										M054	V113	V114
CGACGGCCGAGAGGTTGTAGACTCAACACGGATAAACTCGAGGACCCCACTCGGTGTTTCCTCTGCCTCGGCTCATCACAAGGCAGAGGAAACACCGATAAAATTCGGTGTTTCGGCGCAGAAACGAAGGGTCGATAAACTACACCTTA										female body	male body	embryo
*****.(.(((...(((.(.(((((((((((((((.....)))))))))))))))))))))).....*****										Read #	Hit	Total
										size	Mismatch	Count
										Norm	Total	

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droSec2	scaffold_6:728011-728163 -	dse_156	GCTGCCGCTCTC-----TCCACATCTGAGTTGTGCCTATTTGAGCTCCTGG-GGTGAGG----CACAAAGAGACGGAGGCAG--ATAGTGTTC-----GTCTCCTTTGGGTATTTTTAAAGCCACAAA--GCCCGCTCTCT--G--CTTCCCAGCTATT-----TGATGATGAAT
droSim2	3r:562739-562924 -	dsi_32452	GCTGCCGCTCTC-----TCCACATCTGAGTTGTGCCTATTGAGCTCCTGG-GGTGAGG----CACAAAGAGACGGAGGCAG--ATAGTGTTC-----ATCTCCTTTGGGTATTTTTAAAGCCACAAA--GCCCGCTCTCT--G--ATTCCCAGCTATTTCG-C-GCTAGTTGTCAGTCAGATCGATCCAA-----GTATGATGGAAT
dm3	chr3R:627985-628062 -		GCSCCGGC-TC-----TGACCTCTG--GGTGAGG----CACAT-----GTCTCCTTTGGGTATTTTTAAAGC-C-----ATCTGCTTCC-----GTCTCCTTTGGGTATTTTTAAAGC-C-----GTCTCCTTTGGGTATTTTTAAAGC-C-----GTATGATGGAAT
droEre2	scaffold_4770:935900-936033 -		C-----ACCCTCTGG-GGTGAGG----CACAT-----ATCTGCTTCC-----GTCTCCTTTGGGTATTTTTAAAGCCACAAA--GCCGCTCTCT--G--CTTCCCAGCTATTTCG-C-GCTAGTTGTCAGTCAGATCGATGTAC-----GTATGATGGAAT
droYak3	3R:946964-947099 -		CTAACAA-CA-----GTCTGG-GATAGG----CAT-----ACCTGCTTCCG--GTCTCCTTTGGGTCCTTTAAAA-----GCCAGCTCTCT--G--ATTCCCAGCTATTTCG-C-CTTATTAGTCAGTCAGATCGGTCTAA-----AGTAATGGAAT
droEug1	scf7180000409759:562257-562429 -		GCTGCG-----TCGCGTATCGAGCTCCTGG-GGTGAGG----CACAT-----TACCAGATCC-----GTCTCCTTTGTAATATTAACTG-C-GATTT-----GCCTACA--G--ATTCTAGACTCTTG-C-ATCAGCATCGAAGTAGTGTGTTTGACAGTAGGAATTTTGC-----CAGACTAATTC-TT-----ATTGATCGACAT
droBial	scf7180000302411:362044-362159 -		GCTGCGTCC-TC-----TCATTTCGAGTTTCGCCATTAACATTCCTGG-GGTGAGG----TTAT-----ATCTAACA-----GTCTCCTATTGTCACTATTTTAACTG-C-GATGCT-----GTCTCTA--G--ATTTTTAAA-----A
droTak1	scf7180000415261:499561-499757 +		GCTGCCCTC-TC-----TCATTCTCGACCCGCTATTCTAGCTCCTGG-GGTGAGG----CTT-----ATCCGCTTCC-----TCTCTATTGCGGTATTTTAACTG-C-GCTTA-----GAACTACTCTA-GTTTCC-----TCG-CAACTATAGCCAAACAAAATTAACTAATTGTATAAATTTATTGACACCTCCGAATTTGTAGAAGAAATAT-TC-----T-----TTGGAAT
droEle1	scf7180000491104:2403922-2404018 -		GCTGCCCTC-TC-----TCATTCTGAGTTTCGCAATTCTGAGCTCCTGG-GGTGAGG----AT-----AGACT-----CTTCTATCTGCTTCC-----GTCTCCTTTGTCACTATTTTA-----A-----A
droRho1	scf7180000778917:8474-8566 +		GCTGCCCTC-TC-----TCATTCTGAGTTTCGCAATTCTGAGCTCCTGG-GGTGAGG----GTCT-----TCTCTATCTGCTTCC-----GTCTCCTTTGGGTATTTTA-----A-----A
droFic1	scf7180000453903:234663-234820 -		GCTGCCCTC-T-----TCATCTCTGT-TTCGCAATTCTGAGCTCCTGG-GGTGAGG----CT-----CT--ATCTGCTTCTTCTGTCTGTTTGTCACTATTTTAAGTG-C-CAATTC-----CTT-T--G--TTTCCGCGATTTC-TTGTTGA-----GT-----TCTTAATTCCCTATCTGTAT-----CCT
droKik1	scf7180000302634:320675-320767 -		TTGCTCTG-T-----TCCATTCTGATTTTCGACTTTTGAGCTCCTGG-GGTGAGCAAAAGT-----CTAT-TTATTCTCA-----ATTCCCTTTGGGTATTTTA-----A-----A
droAna3	scaffold_13340:22849098-22849198 -		CTGTCGCATTC-----TCACCCG-G-----CGATCCCTGG-TATTCTC-----G-----T-----TCCTCCTTTGGGTATTTTTAACTA-GCACTTA-----CTTTCA--A--ATTCCAGATTA-----CAATG-----A
droBip1	scf7180000396424:1121644-1121749 -		GCTGCTGGC-TGCGTTG-----TCGCAATTCTGCTCTCTGG-GGTGAGG-----G-----GCTTTGGGTATTTTTAACTG-C-CACTTA-----CTTTGA--G--ATTCCAGATCTTGGT-ACTAGCT-----A
dp5	2:22164678-22164802 +		GCTGCCCTA-TGCGCTGTTGCCTATTTCCTATCTGCTGATGTCCTGGCT-GCTCT-----CATTTCTATCTCTG-C-CAATCTA-----CT--C-CCCCCCCCTT-TGTCTCCTTTGGGTATTTTAAGAG-GGT-----A-----A
droPer2	scaffold_3:4945718-4945842 +		GCTGCCCTA-TGCGCTGTTGCCTATTTCCTATCTGCTGATGTCCTGGCT-GCTCT-----CAATTCTATCTCTG-C-CAATCTA-----CT--C-CCCCCCCCTT-TGTCTCCTTTGGGTATTTTAAGAG-GGT-----A-----A

Generated: 09/08/2015 at 07:46 P.M. **PASS/FAIL**

crit.star	0
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	0
rescue.known	1
rescue.confident	0
rescue.candidate	2

Legend: mature star mismatch in alignment mismatch in read



intergenic

No Repeatable elements found

hide 3p reads | show mid mismatch reads

Anti-sense strand reads

Show Alignment With Reads

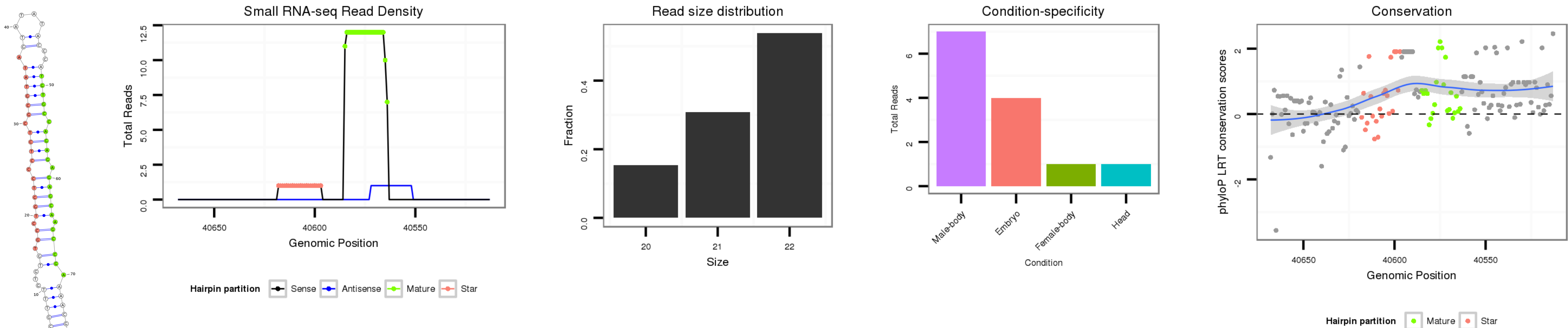
Species	Coordinate	ID	Alignment
droSec2	scaf11734609:1734832 -	dse_235	GTATCTCT TCGC ATACATACATATATAATGTACAATATAATGGTAGCAAGATGCTCGTGTC TCCCGTTTCGATGTT CATTTTTCGGTACTTGAG TCGTAATATGTTTACATG ATGAACATGTATGAAC ATGTGCAATATAT TTAGTAC CTAGTGC C GTCAACACAGCTCGATGCTCTGAAACTTGTGCCATAATACCAAGCGTCTTC
droSim2	K18341739:18341952 -	dse_32477	GTATCTCT TCGC ATAACAATACATATAAATGTG ATAATAATGGGTAGCA GATGCTCGTGTC TCCCGTTTCGATGTT CATTTTTCGGTACTTGAG TCGTAATATATG TACATGTATGAACATGTGCAATATAT TTAGTAC CTAGTGC C GTCAACACAGCTCGATGCTCTGAAACTTGTGCCATAATACCAAGAGGTCTTC
dm3	chrX:19452361:19452625 -	dse_462	ATG TCCTG GAACCTTT GCATATATACCAGACCTTCTCCTATCTCAGATATATCTAAAAAACA ATAAG TATA ATG GTGTA ATAATAATGGG AGCA GATG CTGTGTA ATT TCCTTTCG CTGTT CATTTTTCGGTACTTGAG TCGTAATATGTTG TACATGTATGAACATGTGCAATATAT TTAGTAC CTAGTGC GCACAGGTTTGTA C GTCAACACAGCTCGATGCTCTGAAACTTGTGCCATAATACCAAGAGTCTTC
droEre2	scaf1469019688622:9688737 -		GT TCGC ATG GTGTA ATAATAATGGG AGCA GATG CTGTGTA ATT TCCTTTCG CTGTT CATTTTTCGGTACTTGAG TCGTAATATGTTG TACATGTATGAACATGTGCAATATAT TTAGTAC CTAGTGC GCACAGGTTTGTA C GTCAACACAGCTCGATGCTCTGAAACTTGTGCCATAATACCAAGAGTCTTC
droYak3	K11886114:11886258 +		GT TCGC ATG GTGTA ATAATAATGGG AGCA GATG CTGTGTA ATT TCCTTTCG CTGTT CATTTTTCGGTACTTGAG TCGTAATATGTTG TACATGTATGAACATGTGCAATATAT TTAGTAC CTAGTGC GCACAGGTTTGTA C GTCAACACAGCTCGATGCTCTGAAACTTGTGCCATAATACCAAGAGTCTTC
droBug1	scaf1180000409230:880046:880107 +		GT TCGC ATG GTGTA ATAATAATGGG AGCA GATG CTGTGTA ATT TCCTTTCG CTGTT CATTTTTCGGTACTTGAG TCGTAATATGTTG TACATGTATGAACATGTGCAATATAT TTAGTAC CTAGTGC GCACAGGTTTGTA C GTCAACACAGCTCGATGCTCTGAAACTTGTGCCATAATACCAAGAGTCTTC
droBla1	scaf1180000302069:1151383:1151480 +		GA TCGC ATG GTGTA ATAATAATGGG AGCA GATG CTGTGTA ATT TCCTTTCG CTGTT CATTTTTCGGTACTTGAG TCGTAATATGTTG TACATGTATGAACATGTGCAATATAT TTAGTAC CTAGTGC GCACAGGTTTGTA C GTCAACACAGCTCGATGCTCTGAAACTTGTGCCATAATACCAAGAGTCTTC
droTak1	scaf1180000415169:845110:845122 +		GT TCGC ATG GTGTA ATAATAATGGG AGCA GATG CTGTGTA ATT TCCTTTCG CTGTT CATTTTTCGGTACTTGAG TCGTAATATGTTG TACATGTATGAACATGTGCAATATAT TTAGTAC CTAGTGC GCACAGGTTTGTA C GTCAACACAGCTCGATGCTCTGAAACTTGTGCCATAATACCAAGAGTCTTC
droEle3	scaf1180000490751:1118492:1118557 -		C TCGC ATG GTGTA ATAATAATGGG AGCA GATG CTGTGTA ATT TCCTTTCG CTGTT CATTTTTCGGTACTTGAG TCGTAATATGTTG TACATGTATGAACATGTGCAATATAT TTAGTAC CTAGTGC GCACAGGTTTGTA C GTCAACACAGCTCGATGCTCTGAAACTTGTGCCATAATACCAAGAGTCTTC
droRho1	scaf11800000761121:190453:190563 -		C TCGC ATG GTGTA ATAATAATGGG AGCA GATG CTGTGTA ATT TCCTTTCG CTGTT CATTTTTCGGTACTTGAG TCGTAATATGTTG TACATGTATGAACATGTGCAATATAT TTAGTAC CTAGTGC GCACAGGTTTGTA C GTCAACACAGCTCGATGCTCTGAAACTTGTGCCATAATACCAAGAGTCTTC
droPic1	scaf1180000454073:1733572:1733677 -		GT TCGC ATG GTGTA ATAATAATGGG AGCA GATG CTGTGTA ATT TCCTTTCG CTGTT CATTTTTCGGTACTTGAG TCGTAATATGTTG TACATGTATGAACATGTGCAATATAT TTAGTAC CTAGTGC GCACAGGTTTGTA C GTCAACACAGCTCGATGCTCTGAAACTTGTGCCATAATACCAAGAGTCTTC
droAna3	scaf113417:2468150:2468193 +		TCGC ATG GTGTA ATAATAATGGG AGCA GATG CTGTGTA ATT TCCTTTCG CTGTT CATTTTTCGGTACTTGAG TCGTAATATGTTG TACATGTATGAACATGTGCAATATAT TTAGTAC CTAGTGC GCACAGGTTTGTA C GTCAACACAGCTCGATGCTCTGAAACTTGTGCCATAATACCAAGAGTCTTC
droBip1	scaf1180000395874:40469:40472 -		TCGC ATG GTGTA ATAATAATGGG AGCA GATG CTGTGTA ATT TCCTTTCG CTGTT

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	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	0
rescue.candidate	1

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Show Alternate Folds

Flybase annnotation

utr5 [utr5_minus_10449]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

Read #	Match	Hit Count	Total Norm	male body	embryo	female body	V15 head
22	0	1	6.00	6	4	2	0
21	0	1	3.00	3	1	0	1
20	1	2	2.00	2	0	0	0
22	0	1	1.00	1	0	1	0
21	0	1	1.00	1	0	1	0

Anti-sense strand reads

[illegible]

Show Alignment With Reads

Re-alignment of all predicted orthologs

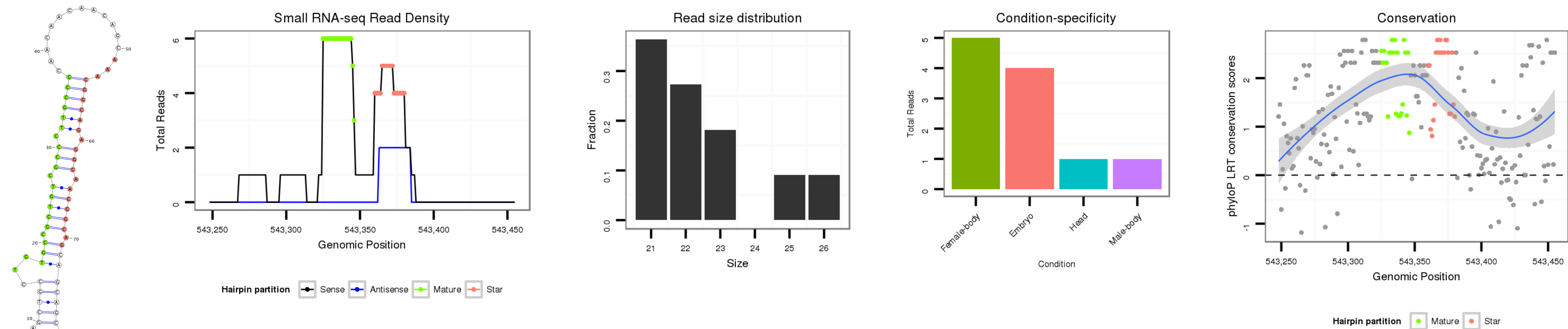
Species	Coordinate	ID	Alignment
droSec2	scaffold_22:40513-40668 -	dsr_167	TT--CGAAG-----TTACTAATACTAAGCAATAG--GCAGCAGGCTTTTC-----GTTTG-T-GTC TGCCTG -----CTCCCTC---T-----CGCGT--ATA GTATATACCC ---A TGTGCC--A--GAGAGA -----GCAAGCCGA AAACGAAAG -----A--GAGCGAGAGTC-----G-GGC---GAA--GGAAAAA--ATATCGCCACAGTT----
droSim2	3r:22831763-22831918 -	dsi_32249	TT--CGAAG-----TTACTAATACTA CAATAG --GCAGCAGGCTTTTC-----GTTTG-T-GTC TGCCTG -----CTCCCTC---T-----CGCGT--ATA GTATATACCC ---A TGTGCC--A--GAGAGA -----GCAAGCCGA AAACGAAAG -----A--GAGCGAGAGTC-----G-GGC---GAA--GGAAAAA--ATATCGCCACAGTT----
dm3	cbh3r:23406994-23407150 -	dme_400	TT--CGAAG-----T ACTAATACTACAATAG --GAGCAGGCTTTTC-----GTTTG-T-GTC TGCCTG -----CTCCCTC---T-----CGCGT--ATA GTATATACCC ---A TGTGCC--A--GAGAGA -----GCAAGCCGA AAACGAAAGAG -----A--GAGCGAGAGTC-----G-GGC---GAA--GGAAAAA--ATATCGCCACAGTT----
droEre2	scaffold_4820:4630735-4630883 +	der_1529	TT--CGAAG-----T ACCAATACTACAATAG --AAAGCAGGCTTTTC-----ATTTG-T- CCTGCCTG -----CTCCCTC---T-----CGCGT--ATA GTATATAC C---A TGTGA--A--GAGAGA -----GCAAGCCGA AAACGAAAG -----AAG-----A--GAGCGAGAGTC-----G-GGC---GAA--GGAAAAA--ATATCGCCACAGTT----
droYaK3	3R:23081054-23081202 +		TT--CGAAG-----T ACCAATACTACAATAG --AAAGCAGGCTTTTC-----ATTTG-T-GTC TGCCTG -----CTCCCTC---T-----CGCGT--ATA GTATATAC C---A TGTGA--A--GAGAGA -----GCAAGCCGA AAACGAAAG -----AAG-----A--GAGCGAGAGTC-----G-GGC---GAA--GGAAAAA--ATATCGCCACAGTT----
droBuq1	scf7180000409770:888896-889037 -	scf7180000409770:888896-889037 -	TT--CGAAG-----T ACTACAATAG --G CAATATC --ATT-- GGCAATTT -----ATTTG-T-GTC CAATA -----CT CTCTATC CTCTGCATGC -----A TGTGA--A--GAGAGA -----AAG-----A--GAGCGAGAGTC-----G-GGC---GAA--GGAAAAA--ATATCGCCACAGTT----
droBial	scf7180000302075:1520953-1521054 +		G -- TCAG -----T ACTACAATAG -- CT ----- GGCAATTT -----ATTTG-T-GTC CAATA -----CT CTCTATC CTCTGCATGC -----A TGTGA--A--GAGAGA -----G-----GA-----GAG-----A--GAG-----C-----G-GGC---GAA--GAAAAA ATATCTC GCACAGC -----
droTak1	scf7180000413872:284297-284432 -		TT--CGAAG-----T ACCAA -----CT CAATC CTC -- GT -- ATT -----G ATATG TG --G TGTC -- TGGG -- AGAGAT -----CGCGT--ATA GTATATAC C---A TGTGA--A--GAGAGA -----GAAAGAC CACGCCGA -----AAG-----A--GAG-----C-----G-GGC---GAA--GAAAAA--ATATCGCCACAGTT----
droEl1	scf7180000491261:189685-1896822 -		CT -- GAAG ----- C -- TCTA -----CT CAATTC -- CTC -- GG -- C -- CTC -----ATTTG-T-GTC TG -- TG -----CG CTTTC -----T-----G ACGT --ATA GTATATAC C---A TGTGGAAA --GAGAGA-----GCAAGCCGA AAACGAAAG -----AAG-----A--GAGCGAGAGTC-----G-GGC---GAA--GGAAAAA--ATATCGCCACAGTT----
droRho1	scf7180000767320:9615-9757 -		AACTCTCTAAG -----T ATAG --CT CTCTC -- CTC -- GG -- TTT -----GTTTG-T- ATCTC -- CTC -----CG CTC -----T-----G ACGT --ATA GTATATAC C---A TGTGAAACG SAGAGA -----GCA ACCGGA -----AAG-----A--GAGCGAGAGTC-----G-GGC---GAA--GAAAAA--ATATCGCCACAGTT----
droFic1	scf7180000453826:309218-309365 +		TT--TT TAAG -----T ACTA ----- CCCAATTC -- ATG -- GG -- T TACGA TTTG-T-GTC CTTTTCCAGT --CT CTCG -----T-----CGCGT--ATA GTATATAC C---A TGTGAAAT --GAGAGA-----GCAAGCCGA AAACGAAAG -----AAG-----A--GAGCGAGAGTC-----G-GGC---GAA--GGAAAAA--ATATCGCCACAGTT----
droKik1	scf7180000302697:675425-675570 -		AATTTT CGAAG-----T ACTG -----CT CAATTC -- CA -- GC --TTTTC-----T TCGC -- C --GTC TG -----T-----CGCGT ACT ATA GTATATAC C---A TGTGGG--G--GAGAGA -----AAGAGAGA GCCAAGAA -----AAG-----A--GAGCGAGAGTC-----G-GGC---GAA--GGAAAAA--ATATCGCCACAGTT----
droAna3	scaffold_13340:19285509-19285749 +	dan_4052	CAAAATATTTCCAATAT TTT-----CT CAATTC -- TTT -- CT -- A ----- CCA -- AACCCCTC -----T GTGTTC -----T-----G ACCT --ATA GTATATATAG -- CACCCACT -- CGA -----TG CAATTTTATCAAGAGAGA -----GAGGTAGT CGGGCACTTCCGCTCTCGAGTCTAGAGAAA GA--GAG AGAGAGCTCTCCCAACGGTAAAGCATGTCCGAACCGGGTATGGATAAAAT 3GC TAGCSAACTCSACAAAAA--SCGAACTSAAGAT-----
dp5	2:9056150-9056281 -		TT-- TC ----- TC ----- TC ----- GC ----- TGC -- TG -- TGCGGTCGTCTCTC ----- C ----- CAT --ATA GTATATAC CACACA AGA --A--GAGAGAG CCCCAGCCGAAAGAGA -----GTGGGAG AGCASCAGAGT -----AAT AGC -- AGA --GGAAAAA ATATATCTCCTCTCAGTT -----
droPer2	scaffold_0:2869233-2869364 -		TT-- TC ----- TC ----- TC -- TGC -- TG -- TGCGGTCGTCTCTC ----- C ----- CAT --ATA GTATATAC CACACA AGA --A--GAGAGAG CCCCAGCCGAAAGAGA -----GTGGGAG AGCASCAGAGT -----AAT AGC -- AGA --GGAAAAA ATATATCTCCTCTCAGTT -----
droW12	scf2_1100000004902:3644410-3644413 -		AG ----- TC ----- TC ----- GC ----- TGC -- TG -- TGCGGTCGTCTCTC ----- C ----- CAT --ATA GTATATAC CACACA AGA --A--GAGAGAG CCCCAGCCGAAAGAGA -----GTGGGAG AGCASCAGAGT -----AAT AGC -- AGA --GGAAAAA ATATATCTCCTCTCAGTT -----
droMoJ3	scaffold_6540:32543020-32543112 +		C ----- TC ----- TC ----- GC ----- TGC -- TG -- TGCGGTCGTCTCTC ----- C ----- CAT --ATA GTATATAC CACACA AGA --A--GAGAGAG CCCCAGCCGAAAGAGA -----GTGGGAG AGCASCAGAG

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crit.star	0
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	0
rescue.candidate	3

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Show Alternate Folds

Flybase annotation

CDS [Dsec\GM15831-cds]

Repeatable elements

Name	Class	Family	Strand
(CAG) _n	Simple_repeat	Simple_repeat	+

Sense Strand Reads

[illegible]

Anti-sense strand reads

Re-alignment of all predicted orthologs

Coordinate	ID	Alignment
droSec1 scaffold_9:543248-543455 +	dse_1843	CATA--TAGCGACCCAAGTGAAGGGAATGCCAGCAGC-----AGTAGCA-----AA--CAA-CAGAAG--CAACTGGCCAGTGGCAGCTGCCGTGGCGCGTGTGGCCCTTGGCGCAACA--ACAACAGCAAAACGGCAGAGGCAACGGCAGCAGCAGC-----AGC--ACC--CGCCAC--T--CCAACGTATCCACCTCGCTTTCT-----CCAGCAACAATAGAA--CTCTGTTT-----TGCCGC
droSim2 2:17176610-17176651 +	dsl_32456	CATA--TAGCGACCCAAGTGAAGGGAATGCCAGCAGC-----AGTAGCA-----AA--CAA-CAGAAG--CAACTGGCCAGTGGCAGCTGCCGTGGCGCGTGTGGCCCTTGGCGCAACA--ACAACAGCAAAACGGCAGAGGCAACGGCAGCAGCAGC-----AGC--ACC--CGCCAC--T--CCAACGTATCCACCTCGCTTTCT-----CCAGCAACAATAGAA--CTCTGTTT-----TGCCGC
dm3 chr2R:17211888-17212089 -	dme_419	CATA--TAGCGACCCAAGTGAAGGGAATGCCAGCAGC-----AGTAGCA-----AA--CAA-CAGAAG--CAACTGGCCAGTGGCAGCTGCCGTGGCGCGTGTGGCCCTTGGCGCAACA--ACAACAGCAAAACGGCAGAGGCAACGGCAGCAGCAGC-----AGC--ACC--CGCCAC--T--CCAACGTATCCACCTCGCTTTCT-----CCAGCAACAATAGAA--CTCTGTTT-----TGCCGC
droEre2 scaffold_4845:11355676-11355880 +	der_1520	CATA--TAGCGACCCAAGTGAAGGGAATGCCAGCAGC-----AGTAGCA-----AA--CAA-CAGAAG--CAACTGGCCAGTGGCAGCTGCCGTGGCGCGTGTGGCCCTTGGCGCAACA--ACAACAGCAAAACGGCAGAGGCAACGGCAGCAGCAGC-----AGC--ACC--CGCCAC--T--CCAACGTATCCACCTCGCTTTCT-----CCAGCAACAATAGAA--CTCTGTTT-----TGCCGC
droYak3 2R:11976229-11976433 +	dya_1795	CATA--TAGCGACCCAAGTGAAGGGAATGCCAGCAGC-----AGTAGCA-----AA--CAA-CAGAAG--CAACTGGCCAGTGGCAGCTGCCGTGGCGCGTGTGGCCCTTGGCGCAACA--ACAACAGCAAAACGGCAGAGGCAACGGCAGCAGCAGC-----AGC--ACC--CGCCAC--T--CCAACGTATCCACCTCGCTTTCT-----CCAGCAACAATAGAA--CTCTGTTT-----TGCCGC
droEug1 scf718000040974:730362-730372 -		CATCG--TGGCAGCCAAGCTGAAGGGAATGCCAGCAGC-----AGTAGCA-----AA--CAA-CAGAAG--CAACTGGCCAGTGGCAGCTGCCGTGGCGCGTGTGGCCCTTGGCGCAACA--ACAACAGCAAAACGGCAGAGGCAACGGCAGCAGCAGC-----AGC--ACC--CGCCAC--T--CCAACGTATCCACCTCGCTTTCT-----CCAGCAACAATAGAA--CTCTGTTT-----TGCCGC
droBial scf718000030214:1194589-1194623 -		CATA--TGGCAGCCAAGCTGAAGGGAATGCCAGCAGC-----AGTAGCA-----AA--CAA-CAGAAG--CAACTGGCCAGTGGCAGCTGCCGTGGCGCGTGTGGCCCTTGGCGCAACA--ACAACAGCAAAACGGCAGAGGCAACGGCAGCAGCAGC-----AGC--ACC--CGCCAC--T--CCAACGTATCCACCTCGCTTTCT-----CCAGCAACAATAGAA--CTCTGTTT-----TGCCGC
droTak1 scf718000041572:103138-103147 -		CATA--TGGCAGCCAAGCTGAAGGGAATGCCAGCAGC-----AGTAGCA-----AA--CAA-CAGAAG--CAACTGGCCAGTGGCAGCTGCCGTGGCGCGTGTGGCCCTTGGCGCAACA--ACAACAGCAAAACGGCAGAGGCAACGGCAGCAGCAGC-----AGC--ACC--CGCCAC--T--CCAACGTATCCACCTCGCTTTCT-----CCAGCAACAATAGAA--CTCTGTTT-----TGCCGC
droEle1 scf7180000491232:161869-162076 -		CATCAGC--TGGCAGCCAAGCTGAAGGGAATGCCAGCAGC-----AGTAGCA-----AA--CAA-CAGAAG--CAACTGGCCAGTGGCAGCTGCCGTGGCGCGTGTGGCCCTTGGCGCAACA--ACAACAGCAAAACGGCAGAGGCAACGGCAGCAGCAGC-----AGC--ACC--CGCCAC--T--CCAACGTATCCACCTCGCTTTCT-----CCAGCAACAATAGAA--CTCTGTTT-----TGCCGC
droRho1 scf7180000780265:156473-156683 -		CATCG--TGGCAGCCAAGCTGAAGGGAATGCCAGCAGC-----AGTAGCA-----AA--CAA-CAGAAG--CAACTGGCCAGTGGCAGCTGCCGTGGCGCGTGTGGCCCTTGGCGCAACA--ACAACAGCAAAACGGCAGAGGCAACGGCAGCAGCAGC-----AGC--ACC--CGCCAC--T--CCAACGTATCCACCTCGCTTTCT-----CCAGCAACAATAGAA--CTCTGTTT-----TGCCGC
droFiel scf7180000453811:56703-56922 -		CATCAGC--TGGCAGCCAAGCTGAAGGGAATGCCAGCAGC-----AGTAGCA-----AA--CAA-CAGAAG--CAACTGGCCAGTGGCAGCTGCCGTGGCGCGTGTGGCCCTTGGCGCAACA--ACAACAGCAAAACGGCAGAGGCAACGGCAGCAGCAGC-----AGC--ACC--CGCCAC--T--CCAACGTATCCACCTCGCTTTCT-----CCAGCAACAATAGAA--CTCTGTTT-----TGCCGC
droKik1 scf7180000302411:441422-441668 -		CATCG--ATGCGCAGCCAAGCTGAAGGGAATGCCAGCAGC-----AGTAGCA-----AA--CAA-CAGAAG--CAACTGGCCAGTGGCAGCTGCCGTGGCGCGTGTGGCCCTTGGCGCAACA--ACAACAGCAAAACGGCAGAGGCAACGGCAGCAGCAGC-----AGC--ACC--CGCCAC--T--CCAACGTATCCACCTCGCTTTCT-----CCAGCAACAATAGAA--CTCTGTTT-----TGCCGC
droAna3 scaffold_13266:5014085-5014313 +	dan_91	CATCG--AGGCGACCTAGCGCTGAAGGGAATGCCAGCAGC-----AGTAGCA-----AA--CAA-CAGAAG--CAACTGGCCAGTGGCAGCTGCCGTGGCGCGTGTGGCCCTTGGCGCAACA--ACAACAGCAAAACGGCAGAGGCAACGGCAGCAGCAGC-----AGC--ACC--CGCCAC--T--CCAACGTATCCACCTCGCTTTCT-----CCAGCAACAATAGAA--CTCTGTTT-----TGCCGC
droBip1 scf7180000395751:823775-824000 +		CATCG--ATGCGCAGCCAAGCTGAAGGGAATGCCAGCAGC-----AGTAGCA-----AA--CAA-CAGAAG--CAACTGGCCAGTGGCAGCTGCCGTGGCGCGTGTGGCCCTTGGCGCAACA--ACAACAGCAAAACGGCAGAGGCAACGGCAGCAGCAGC-----AGC--ACC--CGCCAC--T--CCAACGTATCCACCTCGCTTTCT-----CCAGCAACAATAGAA--CTCTGTTT-----TGCCGC
dp5 1:9802137-9802349 -	dps_3826	CATCG--ATGCGCAGCCAAGCTGAAGGGAATGCCAGCAGC-----AGTAGCA-----AA--CAA-CAGAAG--CAACTGGCCAGTGGCAGCTGCCGTGGCGCGTGTGGCCCTTGGCGCAACA--ACAACAGCAAAACGGCAGAGGCAACGGCAGCAGCAGC-----AGC--ACC--CGCCAC--T--CCAACGTATCCACCTCGCTTTCT-----CCAGCAACAATAGAA--CTCTGTTT-----TGCCGC
droPer1 scaffold_4:5118111-5118332 -	dpe_2480	CATCG--ATGCGCAGCCAAGCTGAAGGGAATGCCAGCAGC-----AGTAGCA-----AA--CAA-CAGAAG--CAACTGGCCAGTGGCAGCTGCCGTGGCGCGTGTGGCCCTTGGCGCAACA--ACAACAGCAAAACGGCAGAGGCAACGGCAGCAGCAGC-----AGC--ACC--CGCCAC--T--CCAACGTATCCACCTCGCTTTCT-----CCAGCAACAATAGAA--CTCTGTTT-----TGCCGC
droW112 scf2_1100000004510:1465966-1466124 +	dwl_5424	AG--TGGCAGCCAAGCTGAAGGGAATGCCAGCAGC-----AGTAGCA-----AA--CAA-CAGAAG--CAACTGGCCAGTGGCAGCTGCCGTGGCGCGTGTGGCCCTTGGCGCAACA--ACAACAGCAAAACGGCAGAGGCAACGGCAGCAGCAGC-----AGC--ACC--CGCCAC--T--CCAACGTATCCACCTCGCTTTCT-----CCAGCAACAATAGAA--CTCTGTTT-----TGCCGC
droVir1 scaffold_12875:18068715-18068893 -	dvl_24643	CATCG--AAC--TGGCAGCCAAGCTGAAGGGAATGCCAGCAGC-----AGTAGCA-----AA--CAA-CAGAAG--CAACTGGCCAGTGGCAGCTGCCGTGGCGCGTGTGGCCCTTGGCGCAACA--ACAACAGCAAAACGGCAGAGGCAACGGCAGCAGCAGC-----AGC--ACC--CGCCAC--T--CCAACGTATCCACCTCGCTTTCT-----CCAGCAACAATAGAA--CTCTGTTT-----TGCCGC
droMo3 scaffold_6:6496:11689326-11689523 -	dmo_3164	CATCG--AAC--TGGCAGCCAAGCTGAAGGGAATGCCAGCAGC-----AGTAGCA-----AA--CAA-CAGAAG--CAACTGGCCAGTGGCAGCTGCCGTGGCGCGTGTGGCCCTTGGCGCAACA--ACAACAGCAAAACGGCAGAGGCAACGGCAGCAGCAGC-----AGC--ACC--CGCCAC--T--CCAACGTATCCACCTCGCTTTCT-----CCAGCAACAATAGAA--CTCTGTTT-----TGCCGC
droEri2 scaffold_15245:4197227-4197430 -	dgr_473	CATCG--AAC--TGGCAGCCAAGCTGAAGGGAATGCCAGCAGC-----AGTAGCA-----AA--CAA-CAGAAG--CAACTGGCCAGTGGCAGCTGCCGTGGCGCGTGTGGCCCTTGGCGCAACA--ACAACAGCAAAACGGCAGAGGCAACGGCAGCAGCAGC-----AGC--ACC--CGCCAC--T--CCAACGTATCCACCTCGCTTTCT-----CCAGCAACAATAGAA--CTCTGTTT-----TGCCGC

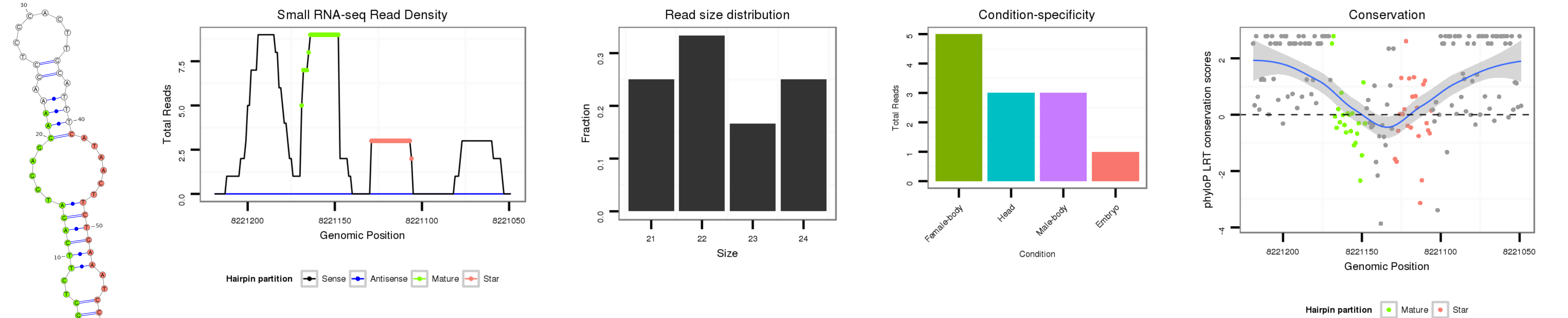
Generated: 09/08/2015 at 07:46 PM

	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	1
rescue.known	0
rescue.confident	1
rescue.candidate	7

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:
dse_466	scaffold_0:8221099-8221169 -	candidate	3p_tailed_mirtron	intron

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

Predicted structure



Show Alternate Folds

Flybase annotation

intron [Dsec/GM24444-in]; CDS [Dsec/GM24444-cds]; CDS [Dsec/GM24444-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

						M054		V115	V114
					V113	female			
					male	body	head	embryo	
CAAAGCCCTACGAGGTCAGAAGCCAGGAACCACTGGATTGCGCAAAAAG	Read #	Hit	Total						
CTAAGGTCTTCAGATGGAGGAA	size	Mismatch	Count	Norm	Total	body			
.....(((.....(((.....)))).....)))).....	22	0	1	4.00	4	2	1	0	1
.....GTAAGTCTTCAGATGGAGGAA.....	21	0	1	3.00	3	1	1	1	0
.....TAAGTCTTCAGATGGAGGAA.....	24	0	1	2.00	2	0	2	0	0
.....CATAACTTCTGAAATCCTTTCCGA.....	23	0	1	1.00	1	1	0	0	0
.....AACTACACGGAGAACTTTGTCCA.....	18	0	1	1.00	1	0	0	0	1
.....AGCCAGGAACCACTGGAT.....	21	0	1	1.00	1	0	0	1	0
.....AGCCAGGAACCACTGGATTGC.....	26	0	1	1.00	1	1	0	0	0
.....AGGAACCACTGGATTGCGCAAAAAG.....	22	0	1	1.00	1	0	0	0	1
.....GTCAGAAGCCAGGAACCACTGG.....	18	0	1	1.00	1	0	1	0	0
.....GAAAGCCAGGAACCACTGG.....	23	0	1	1.00	1	0	1	0	0
.....CATAACTTCTGAAATCCTTTCCG.....	20	0	1	1.00	1	1	0	0	0
.....AGGAACCACTGGATTGCGCA.....	24	0	1	1.00	1	0	0	1	0
.....GTCCTTCAGATGGAGGAAAAGCTCG.....	28	0	1	1.00	1	0	1	0	0
.....GCCCAACTACACGGAGAACTTTGTCCAG.....	24	0	1	1.00	1	1	0	0	0
.....GAAAGCCAGGAACCACTGGATTGCG.....	22	0	1	1.00	1	0	0	1	0
.....AGAGCCAGGAACCACTGGATT.....	23	0	1	1.00	1	0	0	1	0
.....GGTCTTCAGATGGAGGAAAAGCT.....	19	0	1	1.00	1	0	0	0	1
.....CAACTACACGGAGAACTTT.....	28	0	1	1.00	1	0	0	0	1
.....CTACAGGGTCAGAAGCCAGGAACCACT.....	18	1	2	0.50	1	0	0	1	0
.....GTAAGTCTTCAGATGG.....									

Anti-sense strand reads

	Read #	Hit	Total		V113
	size	Mismatch	Count	Norm	Total
GTTCCTGGAGTCTCCCACTCTTCGGTCTTGGTCACCTAAACGGTTTTTTCATCCAGAAAGTCTACCTCCTTTTCGAGCGTGAACGTAAAGTATTGAAGACTTTAGGAAAGGCTTTGAGTCCAAATTCCAAAGTGGGTGGGTTGATGTGCCTCTTGAACACAGGTCCGGTA					
*****.(((...(((((((.....(((.(.....)).)))).....))))).))....*****					

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droSec2	scafFold_0:8221049-8221219 -	dse_466	CAAAGCCCTACGAGGGTCAGAAGCCAGGAACCACTGGATTGCGCAAAAAGGTAAAGTCTTCAG--AT-GGAGG-----AAAGCTC-----GCACTT-----GCATTTCAT-----AACTT-CT---GAAATCCTTTCCGA-----A--ACTCAGGTTAAGGTTTTCACCCAGCCCACTACACGGAGAAGCTTTGTCCAGGCCAT
droSim2	31:15739944-15740112 -		CAAAGCCCTACGAGGGTCAGAAGCCAGGAACCACTGGATTGCGCAAAAAGGTAAAGTTC--AG--AT-AGAGA-----AAAGCTC-----GCACTT-----GCATTTCAT-----AACTT-T---GAAATCCTTTCCGA-----A--ACTCAGGTTAAGGTTTTCACCCAGCCCACTACACGGAGAAGCTTTGTCCAGGCCAT
dm3	chr3L:16121392-16121562 -	dme_463	CAAAGCCCTACGAGGGTCAGAAGCCAGGAACCACTGGATTGCGCAAAAAGGTAAAGTCTTCAG--G--GGCGG-----AAAGCTC-----GCACTT-----GCATTTTAT-----AACTT-CT---GAAATCGTTTCCGA-----A--CTCAGGTTAAGGTTTTCACCCAGCCCACTACACGGAGAAGCTTTGTCCAGGCCAT
droFre2	scafFold_4784:18369135-18369305 +		CAAAGCCCTACGAGGGTCAGAAGCCAGGAACCACTGGATTGCGCAAAAAGGTGAGGTCCTCAG--AT-GGCGG-----AAATCTC-----GCAGTT-----ACATTTTAT-----AACTT-CT---GAAATCGTTTCCGA-----A--CTCAGGTTAAGGTTTTCACCCAGCCCACTACACGGAGAAGCTTTGTCCAGGCCAT
droYak3	31:22056019-22056189 +		CAAAGCCCTACGAGGGTCAGAAGCCAGGAACCACTGGATTGCGCAAAAAGGTGAGTCTTCAG--AT-GGCGG-----GAAATCT-----GCAGTT-----GCATTTTAT-----AACTT-CT---GAAATCAATTTCCGA-----A--CTCAGGTTAAGGTTTTCACCCAGCCCACTACACGGAGAAGCTTTGTCCAGGCCAT
droEug1	scaf7180000409711:1219795-1219964 +		CAAAGCCCTACGAGGGTCAGAAGCCAGGAACCACTGGATTGCGCAAAAAGGTGAGGTCCTCAG--AT-ATATAT-----AAAGCTC-----GCAGTT-----ACATTTTAT-----AACTT-G---GAAATCAATTTCCGA-----A--ACGAGGTTAAAGTTTTCACCCCACTACACGGAGAAGCTTTGTCCAGGCCAT
droBial	scaf7180000302428:3998382-3998551 +		CAAAGCCCTACGAGGGTCAGAAGCCAGGAACCACTGGATTGCGCAAAAAGGTGGGTCCTCAG--AT-CATAC-----AAAGCTC-----TGTAAT-----GCATTCAT-----AACTT-G---GAAATCCAAATCCGA-----A--ACGAGGTTAAAGTTTTCACCCCACTACACGGAGAAGCTTTGTCCAGGCCAT
droTak1	scaf7180000414337:197349-197521 +		CAAAGCCCTACGAGGGTCAGAAGCCAGGAACCACTGGATTGCGCAAAAAGGTGGGTCCTCAG--A-GGTC-----AAATCTC-----ACGAT-----GCATTCCT-----AACTT-TG---GAAATCCATCCCA-----A--CTCAGGTTAAAGTTTTCACCCCACTACACGGAGAAGCTTTGTCCAGGCCAT
droEle1	scaf7180000491249:7320613-7320783 +		CAAAGCCCTACGAGGGTCAGAAGCCAGGAACCACTGGATTGCGCAAAAAGGTGGGTCCTCAG--A-AAATTC-----AAATCTC-----CAAT-----GCATTCCT-----AACTT-G---GAAATCTCTTT-----TCC--AA--CTCAGGTTAAAGTTTTCACCCAGCCCACTACACGGAGAAGCTTTGTCCAGGCCAT
droRho1	scaf7180000776525:9806-9977 +		CAAAGCCCTACGAGGGTCAGAAGCCAGGAACCACTGGATTGCGCAAAAAGGTGGGTCCTCAG--A-AAATTC-----AAATCTC-----CAAT-----GCATTCCT-----AACTT-G---GAAATCTCTTT-----TCC--GA--CTCAGGTTAAAGTTTTCACCCCACTACACGGAGAAGCTTTGTCCAGGCCAT
droFic1	scaf7180000453839:1504111-1504283 -		CAAAGCCCTACGAGGGTCAGAAGCCAGGAACCACTGGATTGCGCAAAAAGGTGGGTCCTCAG--A-AAATTC-----AAATCTC-----CAAT-----GCATTCCT-----AACTT-G---GAAATCTCTTT-----TCC--GA--CTCAGGTTAAAGTTTTCACCCCACTACACGGAGAAGCTTTGTCCAGGCCAT
droKik1	scaf7180000302486:2825651-2825829 -		CAAAGCCCTACGAGGGTCAGAAGCCAGGAACCACTGGATTGCGCAAAAAGGTGGGTCCTCAG--A-AAATTC-----AAATCTC-----CAAT-----GCATTCCT-----AACTT-G---GAAATCTCTTT-----TCC--GA--CTCAGGTTAAAGTTTTCACCCCACTACACGGAGAAGCTTTGTCCAGGCCAT
droAna3	scafFold_13337:10495681-10495853 +		CAAAGCCCTACGAGGGTCAGAAGCCAGGAACCACTGGATTGCGCAAAAAGGTGGGTCCTCAG--A-AAATTC-----AAATCTC-----CAAT-----GCATTCCT-----AACTT-G---GAAATCTCTTT-----TCC--GA--CTCAGGTTAAAGTTTTCACCCCACTACACGGAGAAGCTTTGTCCAGGCCAT
droBip1	scaf7180000396569:873531-873703 -		CAAAGCCCTACGAGGGTCAGAAGCCAGGAACCACTGGATTGCGCAAAAAGGTGGGTCCTCAG--A-AAATTC-----AAATCTC-----CAAT-----GCATTCCT-----AACTT-G---GAAATCTCTTT-----TCC--GA--CTCAGGTTAAAGTTTTCACCCCACTACACGGAGAAGCTTTGTCCAGGCCAT
dp5	XR_group8:1795952-1796121 -		CAAAGCCCTACGAGGGTCAGAAGCCAGGAACCACTGGATTGCGCAAAAAGGTGGGTCCTCAG--A-AAATTC-----AAATCTC-----CAAT-----GCATTCCT-----AACTT-G---GAAATCTCTTT-----TCC--GA--CTCAGGTTAAAGTTTTCACCCCACTACACGGAGAAGCTTTGTCCAGGCCAT
droPer2	scafFold_24:1254169-1254338 +		CAAAGCCCTACGAGGGTCAGAAGCCAGGAACCACTGGATTGCGCAAAAAGGTGGGTCCTCAG--A-AAATTC-----AAATCTC-----CAAT-----GCATTCCT-----AACTT-G---GAAATCTCTTT-----TCC--GA--CTCAGGTTAAAGTTTTCACCCCACTACACGGAGAAGCTTTGTCCAGGCCAT
droW12	scaf2_1100000004511:4929928-4930133 +		CAAAGCCCTACGAGGGTCAGAAGCCAGGAACCACTGGATTGCGCAAAAAGGTGGGTCCTCAG--A-AAATTC-----AAATCTC-----CAAT-----GCATTCCT-----AACTT-G---GAAATCTCTTT-----TCC--GA--CTCAGGTTAAAGTTTTCACCCCACTACACGGAGAAGCTTTGTCCAGGCCAT
droVir3	scafFold_13049:3971653-3971813 +		CAAAGCCCTACGAGGGTCAGAAGCCAGGAACCACTGGATTGCGCAAAAAGGTGGGTCCTCAG--A-AAATTC-----AAATCTC-----CAAT-----GCATTCCT-----AACTT-G---GAAATCTCTTT-----TCC--GA--CTCAGGTTAAAGTTTTCACCCCACTACACGGAGAAGCTTTGTCCAGGCCAT
droMo3	scafFold_6654:147204-147357 -		CAAAGCCCTACGAGGGTCAGAAGCCAGGAACCACTGGATTGCGCAAAAAGGTGGGTCCTCAG--A-AAATTC-----AAATCTC-----CAAT-----GCATTCCT-----AACTT-G---GAAATCTCTTT-----TCC--GA--CTCAGGTTAAAGTTTTCACCCCACTACACGGAGAAGCTTTGTCCAGGCCAT
droGr12	scafFold_15110:10772216-10772387 -		CAAAGCCCTACGAGGGTCAGAAGCCAGGAACCACTGGATTGCGCAAAAAGGTGGGTCCTCAG--A-AAATTC-----AAATCTC-----CAAT-----GCATTCCT-----AACTT-G---GAAATCTCTTT-----TCC--GA--CTCAGGTTAAAGTTTTCACCCCACTACACGGAGAAGCTTTGTCCAGGCCAT

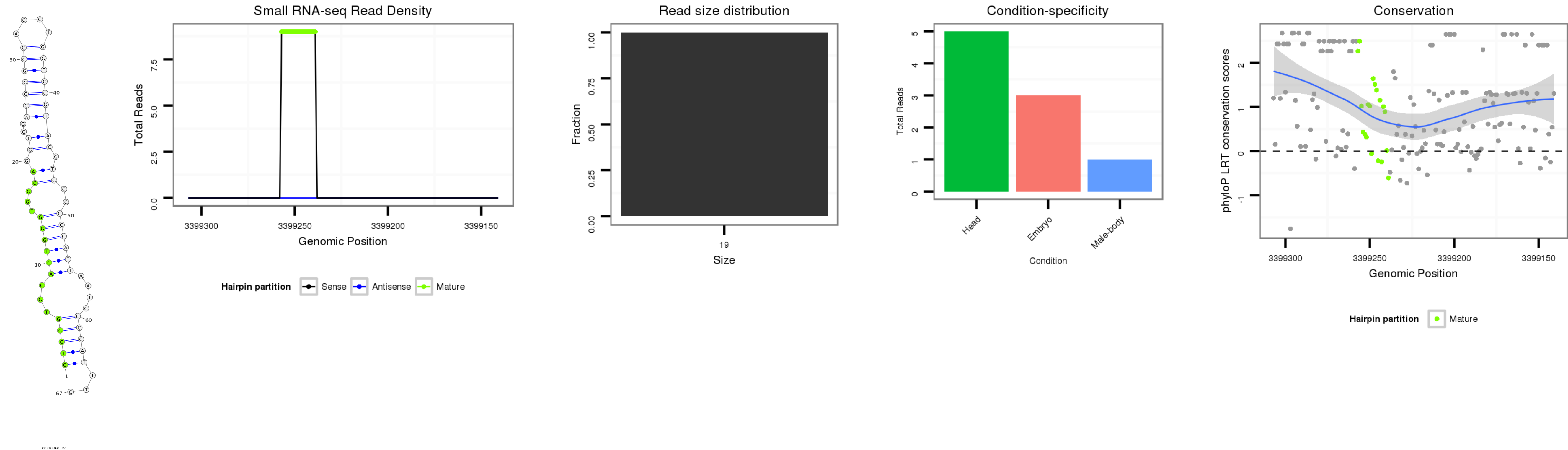
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	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tpot3	0
crit.un	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dse_349	scaffold_1:3399191-3399257 -	candidate	Mirtron	intron	[View on UCSC Genome Browser (Cornell Mirror)]

Legend: nature star mismatch in alignment mismatch in read

Predicted structure



Show Alternate Folds

Flybase annotation

intron [Dsec/GM20568-in]; CDS [Dsec/GM20568-cds]; CDS [Dsec/GM20568-cds]

No Repeatable elements found

Sense Strand Reads

GAGGCAC TGGGTTCTCTGGCAAGGTCCTGGTCGAGAAGTGTGTCGCGTAAGTGGGTGGAGTGGGTGGCAAGGTGGA CGGGCCAGCTGGTCCGTACGTGGCCCCATTAA TCCCCCATTTCCGCGATGGCTTATGCAATTATTATTAATTCGTGCAGGTCGTGCGGTGGCCT										Read #	Hit	Total		V115	V114	M054	V113
*****(((.....(((.....((.....(((.....)))))))).)).....																	

Anti-sense strand reads

					M054
CTCCGTGACCAAGGACCCGTTCCAGGACCAAGCTCTTCAACGACGCCATTCAACCACTCACCCACCGTCCACCTGCCGGTCGACAGGCATGCACCGGGTAATTAGGGGTAAAGGCCTACCGAATACGTTATAATAATTAAAGCAGTCCAGCACGCCACCGGA					female
*****((((((...(((...(((...(((...)))))))))...))))))...*****					body
Read #	Hit	Total			
size	Mismatch	Count	Norm	Total	

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droSec2	scaffold_1:3399141-3399307	dse_349	GAGGCAC
droSim2	2r:6565735-6565901	dsi_6537	GAGGCAC
dm3	chr2R:5788360-5788526	dme_407	GAGGCAC
droEre2	scaffold_4929:8580048-8580206		GAGGCAC
droYak3	2L:18413945-18414102		GAGGCAC
droEug1	scf7180000409209:387565-387723		GAGGCAC
droBial1	scf7180000301506:919171-919338		GAGGCAC
droTak1	scf7180000415870:481016-481179		GAGGCAC
droEle1	scf7180000491107:1307841-1308001		GAGGCAC
droRho1	scf7180000768901:309311-31088		GAGGCAC
droFic1	scf7180000453858:952956-953134		GAGGCAC
droKik1	scf7180000302476:2755028-2755196		GAGGCAC
droAna3	scaffold_13266:15297917-15298095		GAGGCAC
droBip1	scf7180000396547:1749894-1750072		GAGGCAC
dp5	3:10987194-10987368		GAGGCAC
droPer2	scaffold_4:6308596-6308770		GAGGCAC
droWil2	scf2_1100000004514:932358-932509		GAGGCAC
droVir3	scaffold_12875:20454606-20454683		C-----
droMoj3	scaffold_6540:13477686-13477812		GAGGCAC
droGri2	scaffold_15245:11091844-11091902		GAGGCAC

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

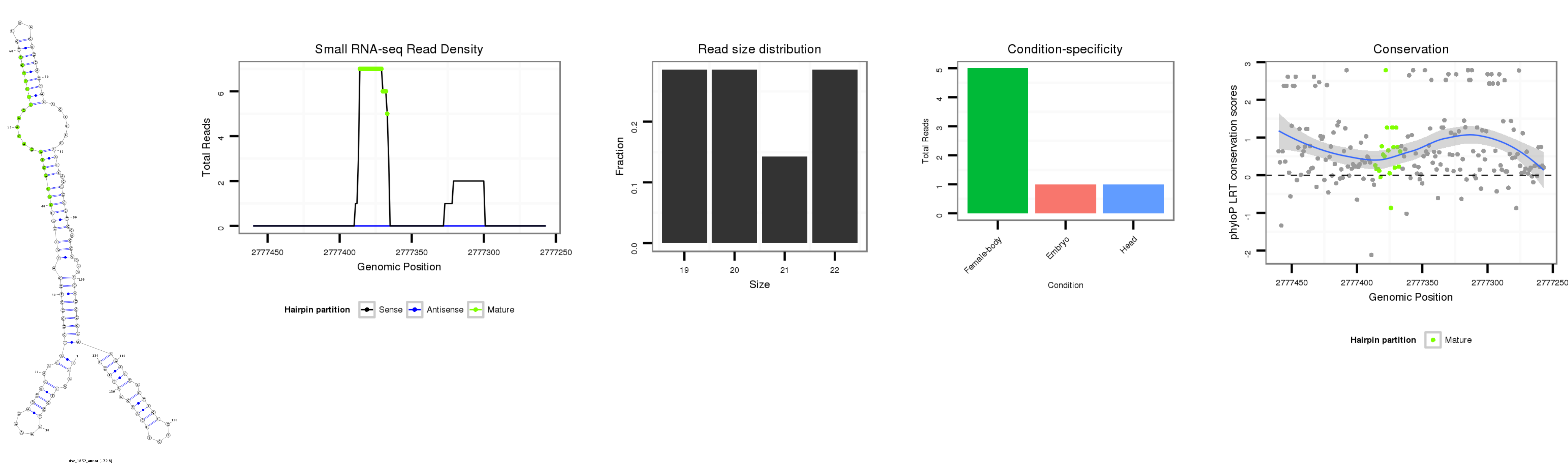
[illegible]

	PASS/FAIL
crit.star	0
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	0
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dse_1852	scaffold_1:2777307-2777410 -	candidate	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 annnotation

CDS [Dsec\GM20615-cds]

Repeatable elements

Name	Class	Family	Strand
(CTG)n	Simple_repeat	Simple_repeat	+

Sense Strand Reads

hide 3p reads

Read #	Hit	Total	Female	embryo	head
size	Mismatch	Count	body		
20	1	2.00	2	1	0
22	0	1	2.00	2	0
19	0	1	1.00	1	0
19	0	1	1.00	1	0
28	0	1	1.00	1	0
20	1	1	1.00	1	0
21	0	1	1.00	1	0
22	0	1	1.00	1	0
21	1	2	0.50	1	1

Anti-sense strand reads

ACACAGCTGGACCTGAGTGCAGGGTGTCGACGACGAGCTGACGACTTCTCGTCTTACACGCGACCTACGCGCC	CGCGGACACTCTGGAGACAGC	AGCTTGTGCTGCTGCTACTGCTGTGTCGCGGACGTCGTCGCGGTCTCTGCTCAACGACAGACGTGCTCAAGGTCTCTCGCGTGC	CGCGGTCCGCTCCGCTGAGCAGCTGGACACG	Read #	Hit	Total
*****(((((.....)))..))((((((.....(((.....(((.....(((.....)))))).....)))..)))..))).....))))(((((.....)))..)))*****				size Mismatch	Count	Norm Total
No data available in table						

Re-alignment of all predicted orthologs

[illegible]

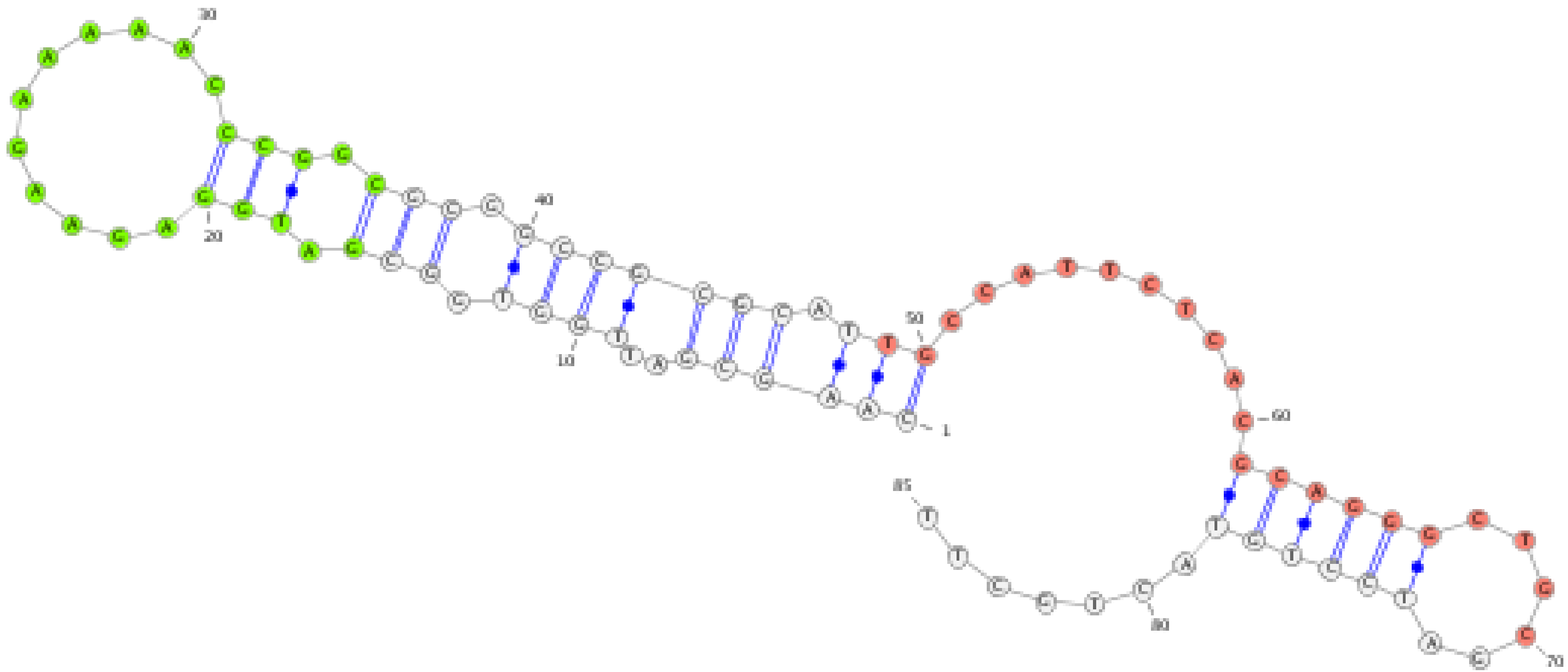
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	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	0
crit.top3	1
crit.tptop3	0
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	1
rescue.known	0
rescue.confident	1
rescue.candidate	2

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dse_1846	scaffold_0:5185211-5185299 -	candidate	Canonical miRNA	CDS	[View on UCSC Genome Browser (Cornell Mirror)]

Legend: ■ **miRNA** ■ **star** ■ **mismatch in alignment** ■ **mismatch in read**

Predicted structure



dse_1846_annot [-23.4]

Show Alternate Folds

Flybase annotation

CDS [Dsec:GM24613-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

	Read #		Hit	Total		V114	M054	V113	V115
	size	Mismatch	Count	Norm	Total	embryo	female body	male body	head
AACGAGGCGGAGGCTCAGTCTGTTCCGCCGAGGCCAGCAGTGGCCCGGGACCTGCGCGAGATTGGCAAGCGATTGGTGGCGGATGGAGAGAAAACCCGGGCGGGCCGCGCATTGGCATTCTCACGAGGGCTCGATCCTGTACTGCTTATTACGACGAGATTGGTGCGAGGAGTTCCTCCGGTCAAG	21	0	1	2.00	2	2	0	0	0
.....GATGAGAGAAAACCCGGC.....	22	0	1	1.00	1	0	1	0	0
.....CGGCCGCGCATTGGCATTCTCA.....	25	0	1	1.00	1	1	0	0	0
.....CAGCGGGGACCTGGCGAGATTGGC.....	21	0	1	1.00	1	0	0	1	0
.....ATTACGACGAGTTCGGTGCAG.....	26	0	1	1.00	1	0	0	1	0
.....GAGATTGGCAAGCGATTGGTGGCGAT.....	28	0	1	1.00	1	0	0	1	0
.....GCGAGATTGGCAAGCGATTGGTGGCGAT.....	21	0	1	1.00	1	1	0	0	0
.....AAGCGATTGGTGGCGATTGGA.....	22	0	1	1.00	1	1	0	0	0
.....GGCTCACTGCTTCCCGAG.....	20	0	1	1.00	1	1	0	0	0
.....CTGCTATTACGACGAGTTCGGTGCAGGA.....	19	0	1	1.00	1	1	0	0	0
.....GATTGGCAAGCGATTGGTGGCG.....	22	0	1	1.00	1	0	1	0	0
.....TTATTACGACGAGTTCGGT.....	19	0	1	1.00	1	1	0	0	0
.....GATTGGTGGCGATTGGAGA.....	18	0	1	1.00	1	0	1	0	0

Anti-sense strand reads

	Read #	Hit	Total		V114	V113
	size	Mismatch	Count	Norm	embryo	male body
TTGCTTCGCGCTCCGAGTCAGCAAGCGGGCTCCGGGTCGTACCGGGTCGCCCTTCAGCGCGCTCTAACCCTTGCCTTAACCAACCGCTACTCTCTCTTTTGGGCCGCGCCGCGCGCTAACGGTAAGAGTCGCTCCCGACGCTAGGACATGACGAATAAGTCGTCTTAAGCCACGCTCCTCAAGGCCACGTGC						
.....(((((((.....)))))))))).....						

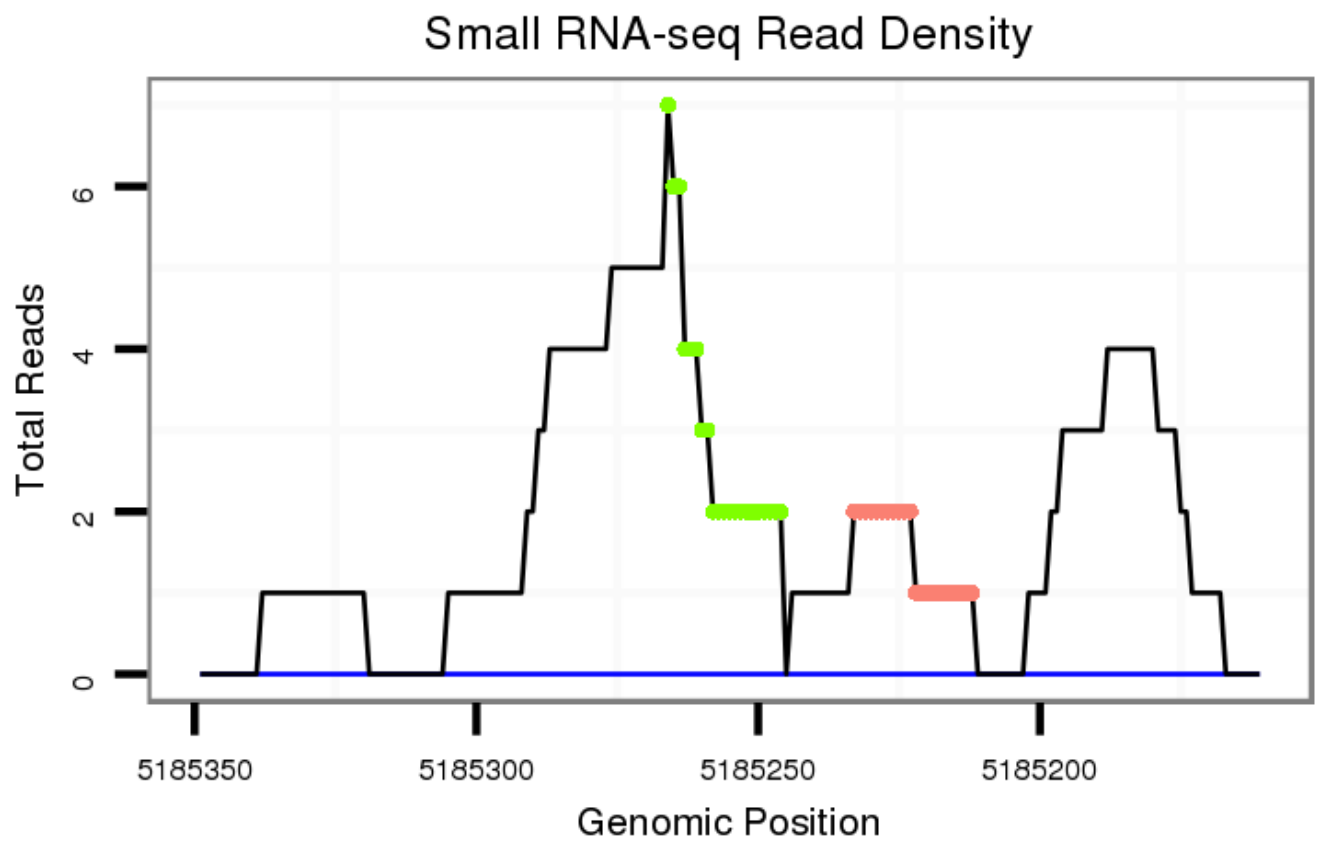
Show Alignment With Reads

Re-alignment of all predicted orthologs

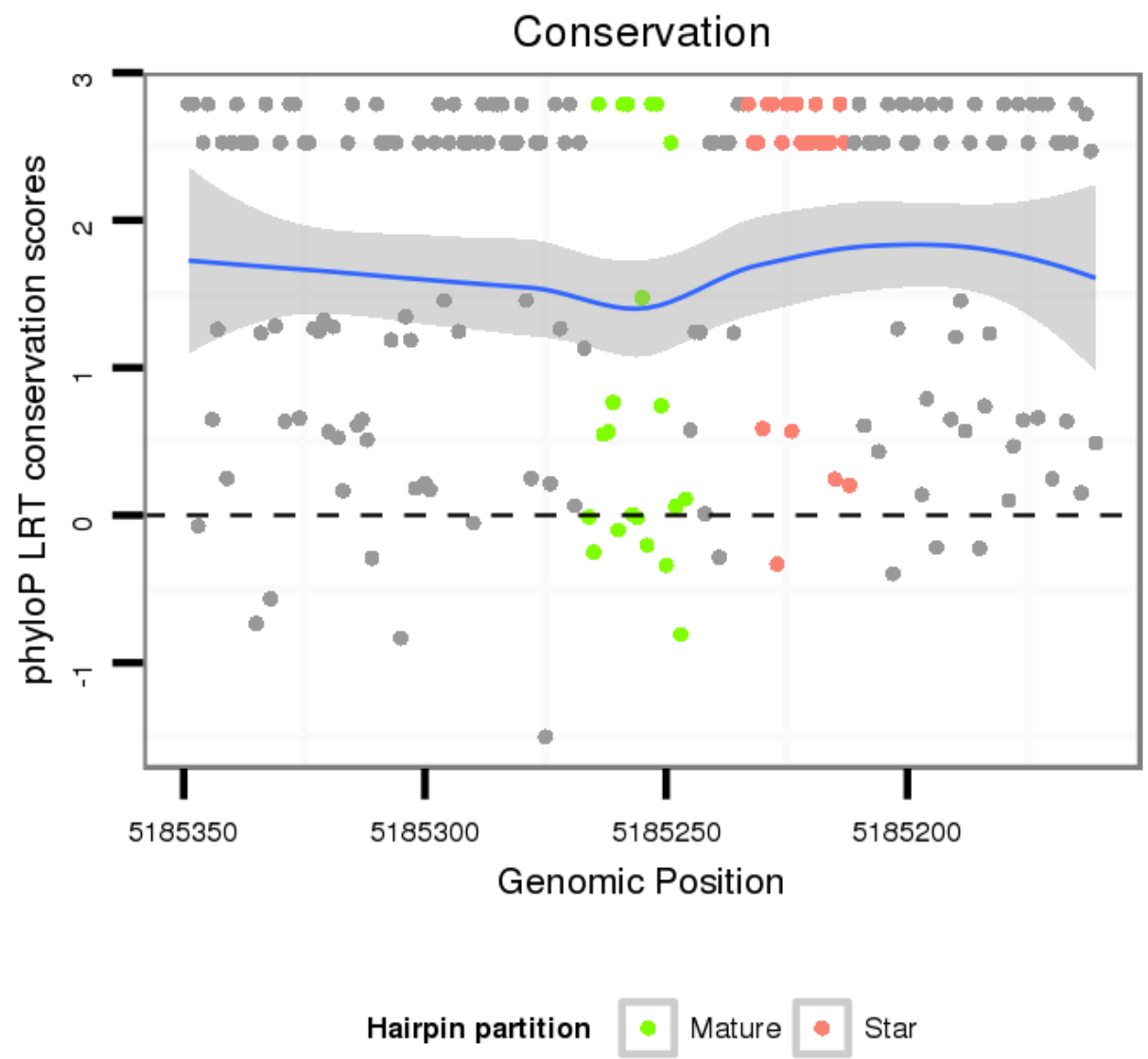
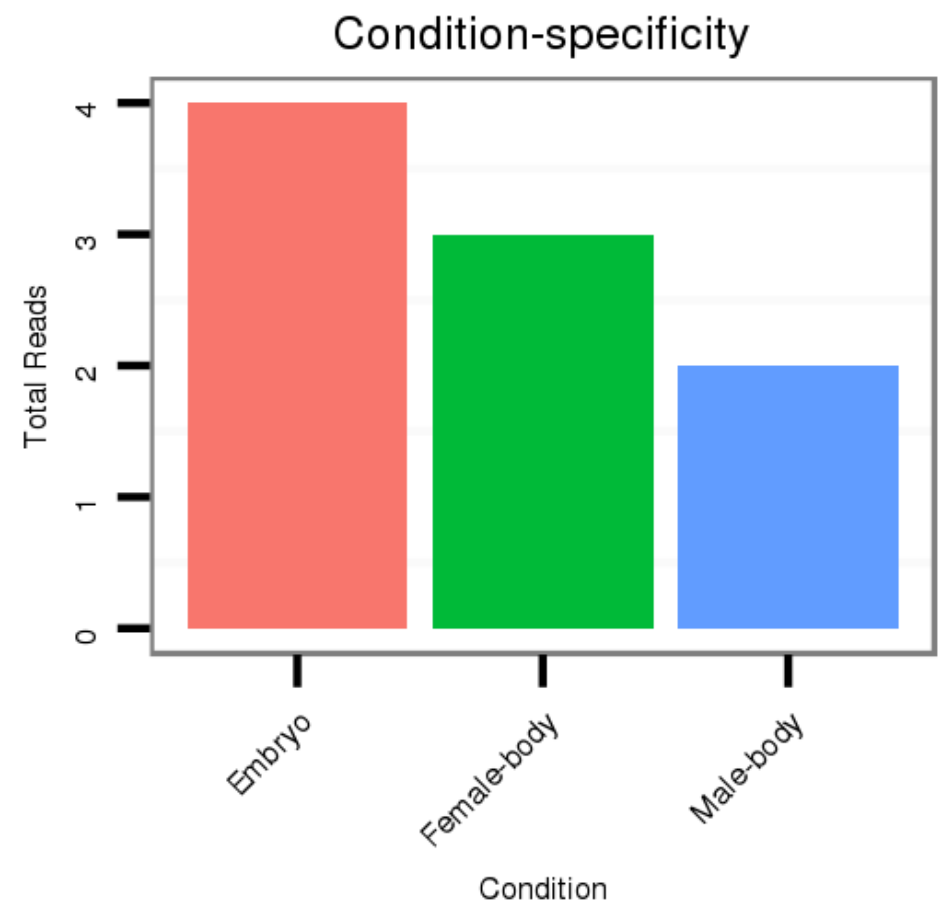
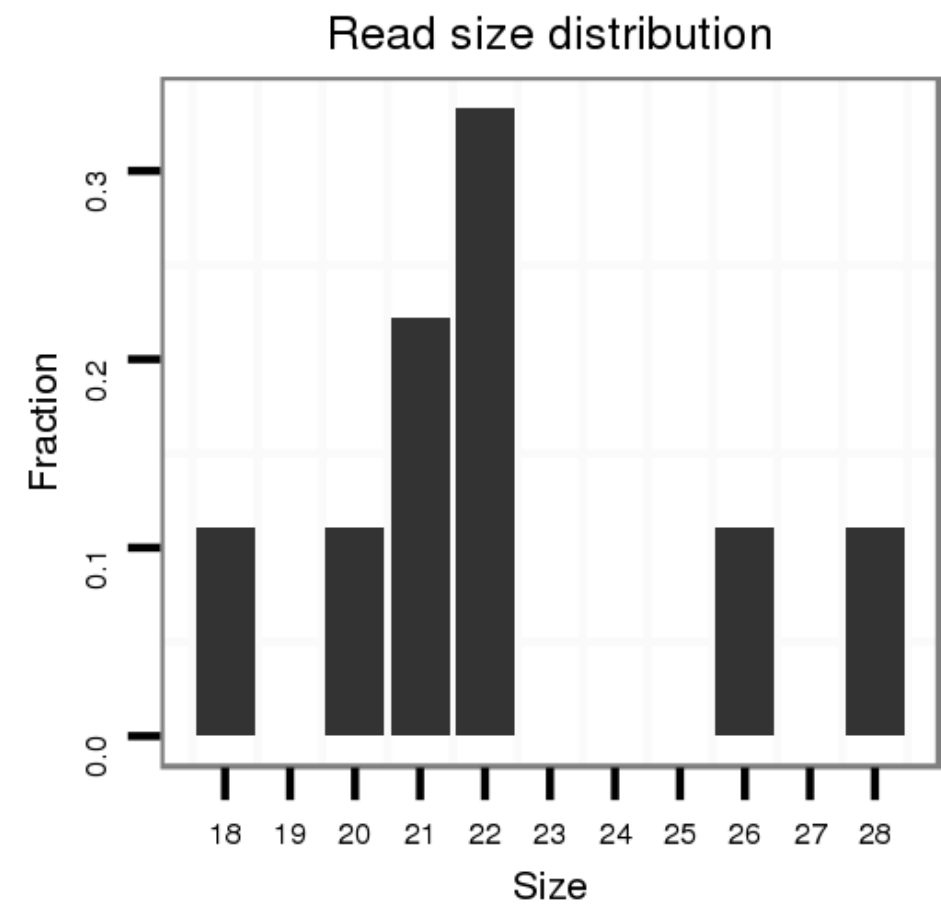
Species	Coordinate	ID	Alignment
drosSec2	scaffold_0:5185161-5185349 -	dse_1846	AACGAGGCGGAGGCTCAGTCTGTTCCGCCGAGGCCAGCAGTGGCCACAGC---GGGACCTGCGCGAGATTGGCAAGCGATTGGTGGCGATGGAGAGAAAACCCGGGCGGGCCGCGCATTGGCATTCTCACGAGGGCTCGATCCTGTACTGCTTATTACGACGAGATTGGTGCGAGGAGTTCCTCCGGTCAAG
drosIm2	31:12701025-1270213 -	dse_132458	AACGAGGCGGAGGCTCAGCTGTTCCGCCGAGGCCAGCAGTGGCCACAGC---GGGACCTGCGCGAGATTGGCAAGCGATTGGTGGCGATGGAGAGAAAACCCGGGCGGGCCGCGCATTGGCATTCTCACGAGGGCTCGATCCTGTACTGCTTATTACGACGAG---TTCGGTGCAGGAGTTCCTCCGGTCAAG
dm3	Chr3L:13013576-13013764 -	dme_245	AACGAGGCGGAGGCTCAGCTGTTCCGCCGAGGCCAGCAGTGGCCACAGC---GGGACCTGCGCGAGATTGGCAAGCGCTGGTGGCGATGGAGAGAAAACCCGAGCGGGCCGCGCATTGGCATTCTCACGAGGGCTCGATCCTGTACTGCTTATTACGACGAG---TTCGGTGCAGGAGTTCCTCCGGTCAAG
drosEre2	scaffold_4784:13021109-13021297 -	der_1523	AACGAGGCGGAGGCTCAGCTGTTCCGCCGAGGCCAGCAGTGGCCACAGC---GGGACCTGCGCGAGATTGGCAAGCGCTGGTGGCGATGGAGAGAAAACCCGAGCGGGCCGCGCATTGGCATTCTCACGAGGGCTCGATCCTGTACTGCTTATTACGACGAG---TTCGGTGCAGGAGTTCCTCCGGTCAAG
drosYak3	31:13052479-13052667 -	dya_1798	AACGAGGCTCAGGCTCAGCTGTTCCGCCGAGGCCAGCAGTGGCCACAGC---GGGACCTGCGCGAGATTGGCAAGCGCTGGTGGCGATGGAGAGAAAACCCGAGCGGGCCGCGCATTGGCATTCTCACGAGGGCTCGATCCTGTACTGCTTATTACGACGAG---TTCGGTGCAGGAGTTCCTCCGGTCAAG
drosEug1	hsaf180000409711:6101265-6101453 -		AACGAGGCGGAGGCTCAGCTGTTCCGCCGAGGCCACAGCTGGCCACAGC---GGGACCTGCGCGAGATTGGCAAGCGCTGGTGGCGATGGAGAGAAAACCCGAGCGGGCCGCGCATTGGCATTCTCACGAGGGCTCGATCCTGTACTGCTTATTACGACGAG---TTCGGTGCAGGAGTTCCTCCGGTCAAG
drosBla1	hsaf180000302193:2253856-2254044 -		AACGAGGCGGAGGCTCAGCTGTTCCGCCGAGGCCACAGCTGGCCACAGC---GGGACCTGCGCGAGATTGGCAAGCGCTGGTGGCGATGGAGAGAAAACCCGAGCGGGCCGCGCATTGGCATTCTCACGAGGGCTCGATCCTGTACTGCTTATTACGACGAG---TTCGGTGCAGGAGTTCCTCCGGTCAAG
drosTak1	hsaf180000415706:66147-66335 -		AACGAGCTCGAGGGCTCAGCTGTTCCGCCGAGGCCACAGCTGGCCACAGC---GGGACCTGCGCGAGATTGGCAAGCGCTGGTGGCGATGGAGAGAAAACCCGAGCGGGCCGCGCATTGGCATTCTCACGAGGGCTCGATCCTGTACTGCTTATTACGACGAG---TTCGGTGCAGGAGTTCCTCCGGTCAAG
drosEle1	hsaf180000491255:1412089-1412277 -		AACGAGGCGGAGGCTCAGCTGTTCCGCCGAGGCCACAGCTGGCCACAGC---GGGACCTGCGCGAGATTGGCAAGCGCTGGTGGCGATGGAGAGAAAACCCGAGCGGGCCGCGCATTGGCATTCTCACGAGGGCTCGATCCTGTACTGCTTATTACGACGAG---TTCGGTGCAGGAGTTCCTCCGGTCAAG
drosHbl1	hsaf180000769477:967-1151 +		AACGAGGCGGAGGCTCAGCTGTTCCGCCGAGGCCACAGCTGGCCACAGC---GGGACCTGCGCGAGATTGGCAAGCGCTGGTGGCGATGGAGAGAAAACCCGAGCGGGCCGCGCATTGGCATTCTCACGAGGGCTCGATCCTGTACTGCTTATTACGACGAG---TTCGGTGCAGGAGTTCCTCCGGTCAAG
drosFic1	hsaf180000454048:724234-724422 +		AACGAGGCTCAGGCTCAGCTGTTCCGCCGAGGCCACAGCTGGCCACAGC---GGGACCTGCGCGAGATTGGCAAGCGCTGGTGGCGATGGAGAGAAAACCCGAGCGGGCCGCGCATTGGCATTCTCACGAGGGCTCGATCCTGTACTGCTTATTACGACGAG---TTCGGTGCAGGAGTTCCTCCGGTCAAG
drosKik1	hsaf180000302212:666717-666905 -		AACGAGGCGGAGGCTCAGCTGTTCCGCCGAGGCCACAGCTGGCCACAGC---GGGACCTGCGCGAGATTGGCAAGCGCTGGTGGCGATGGAGAGAAAACCCGAGCGGGCCGCGCATTGGCATTCTCACGAGGGCTCGATCCTGTACTGCTTATTACGACGAG---TTCGGTGCAGGAGTTCCTCCGGTCAAG
drosAna3	scaffold_13337:1437395-1437583 +	dan_4038	AACGAGGCGGAGGCTCAGCTGTTCCGCCGAGGCCACAGCTGGCCACAGC---GGGACCTGCGCGAGATTGGCAAGCGCTGGTGGCGATGGAGAGAAAACCCGAGCGGGCCGCGCATTGGCATTCTCACGAGGGCTCGATCCTGTACTGCTTATTACGACGAG---TTCGGTGCAGGAGTTCCTCCGGTCAAG
drosBip1	hsaf180000395450:265900-266088 +		AACGAGGCGGAGGCTCAGCTGTTCCGCCGAGGCCACAGCTGGCCACAGC---GGGACCTGCGCGAGATTGGCAAGCGCTGGTGGCGATGGAGAGAAAACCCGAGCGGGCCGCGCATTGGCATTCTCACGAGGGCTCGATCCTGTACTGCTTATTACGACGAG---TTCGGTGCAGGAGTTCCTCCGGTCAAG
dp5	Xb_group6:14377266-14377454 -	dpe_3829	AACGAGGCGGAGGCTCAGCTGTTCCGCCGAGGCCACAGCTGGCCACAGC---GGGACCTGCGCGAGATTGGCAAGCGCTGGTGGCGATGGAGAGAAAACCCGAGCGGGCCGCGCATTGGCATTCTCACGAGGGCTCGATCCTGTACTGCTTATTACGACGAG---TTCGGTGCAGGAGTTCCTCCGGTCAAG
drosPer2	scaffold_9:2666447-2666635 -	dpe_2483	AACGAGGCGGAGGCTCAGCTGTTCCGCCGAGGCCACAGCTGGCCACAGC---GGGACCTGCGCGAGATTGGCAAGCGCTGGTGGCGATGGAGAGAAAACCCGAGCGGGCCGCGCATTGGCATTCTCACGAGGGCTCGATCCTGTACTGCTTATTACGACGAG---TTCGGTGCAGGAGTTCCTCCGGTCAAG
drosW112	acc2_1100000004511:5276750-5276938 +	dwl_5417	AACGAGGCGGAGGCTCAGCTGTTCCGCCGAGGCCACAGCTGGCCACAGC---GGGACCTGCGCGAGATTGGCAAGCGCTGGTGGCGATGGAGAGAAAACCCGAGCGGGCCGCGCATTGGCATTCTCACGAGGGCTCGATCCTGTACTGCTTATTACGACGAG---TTCGGTGCAGGAGTTCCTCCGGTCAAG
drosV1r3	scaffold_13049:22492152-22492344 +	dvi_158	AACGAGGCGGAGGCTCAGCTGTTCCGCCGAGGCCACAGCTGGCCACAGC---GGGACCTGCGCGAGATTGGCAAGCGCTGGTGGCGATGGAGAGAAAACCCGAGCGGGCCGCGCATTGGCATTCTCACGAGGGCTCGATCCTGTACTGCTTATTACGACGAG---TTCGGTGCAGGAGTTCCTCCGGTCAAG
drosMo3	scaffold_6680:17099712-17099903 +	dmo_114	AACGAGCTCAGGCTCAGCTGTTCCGCCGAGGCCACAGCTGGCCACAGC---GGGACCTGCGCGAGATTGGCAAGCGCTGGTGGCGATGGAGAGAAAACCCGAGCGGGCCGCGCATTGGCATTCTCACGAGGGCTCGATCCTGTACTGCTTATTACGACGAG---TTCGGTGCAGGAGTTCCTCCGGTCAAG
drosGr12	scaffold_15121:203613-203801 +	dgr_465	AACGAGGCGGAGGCTCAGCTGTTCCGCCGAGGCCACAGCTGGCCACAGC---GGGACCTGCGCGAGATTGGCAAGCGCTGGTGGCGATGGAGAGAAAACCCGAGCGGGCCGCGCATTGGCATTCTCACGAGGGCTCGATCCTGTACTGCTTATTACGACGAG---TTCGGTGCAGGAGTTCCTCCGGTCAAG

Generated: 09/08/2015 at 07:47 PM

	PASS/FAIL
crit.star	0
crit.hoop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	0
crit.top3	1
crit.top3p	1
crit.lari	0
crit.back	0
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	2
rescue.candidate	10

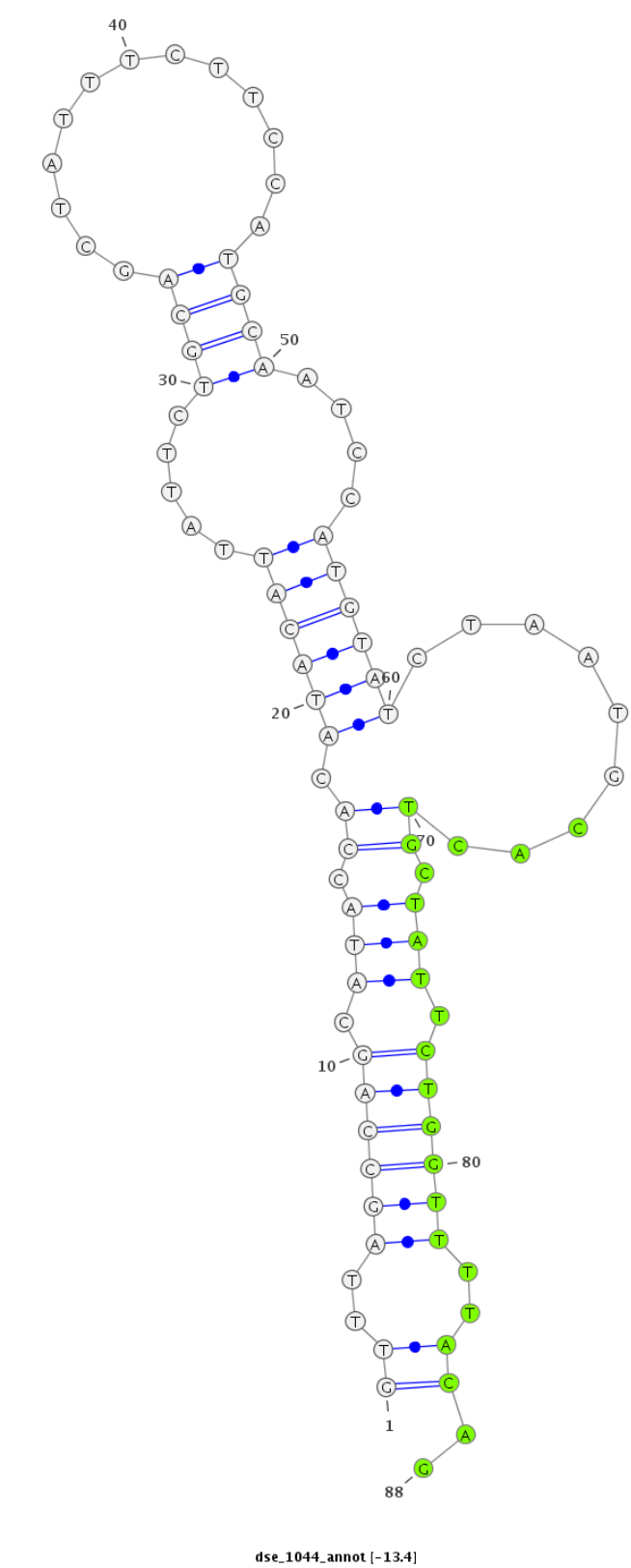


Hairpin partition Sense Antisense Mature Star



Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Show Alternate Folds

Flybase annotation

intron [Dsec\GM17595-in]; CDS [Dsec\GM17595-cds]; CDS [Dsec\GM17595-cds]; utr5 [utr5_minus_12408]; utr5 [utr5_minus_12409]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

										Read #						M054	V114	V115	V113
										size	Mismatch	Hit	Total			female body	embryo	head	male
												Count	Norm	Total					body
GAGACCTGCATTTCCCAAACTCAAAGAGAAACTGGAGGATCCTGATCCAGGTTTAGCCAGCATACCACATACATTATTCTGCAGCTATTTCCTCCATGCAATCCATGTATCTAATGCACTGCTATTCTGGTTTACAGGCTGTTCAATCAGCTGCCGTGAATGTAATATGTGAACTAGCAGCTAAGAAC																			
*****((((((((((((((.....(((.....)))))).....)))))).....)))))).....))))*****																			
.....ACTGCTATTCTGGTTTACAG.....										22	1	1	8.00	8	0	5	1	2	
.....CACTGCTATTCTGGTTTACAG.....										22	0	1	5.00	5	4	1	0	0	
.....CACTGCTATTCTGGTTTACA.....										21	0	1	2.00	2	1	0	1	0	
.....ACTGCTATTCTGGTTTACAG.....										21	0	1	1.00	1	1	0	0	0	

Anti-sense strand reads

[illegible]

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droSec2	scaffold_20:265627-265814	dsr_1048	GAGACCTGCATTTCCTCCAACTCAAGAGAAACTGGAGGATCCTGATCCAGGTTTAGCC-----AGCATACCA--CATAC-----GATCTTAATGCAGCTGC-----TATTC-----GGTTTTACAGGTGTTCAATCAGCTGCCGTGAATGTAATATGTGAATAGCAGCTAAGAAC
droSeIn2	X:12963147-1296331		GAGACCTGCATTTCCTCCAACTCAAGAGAAACTGGAGGATCCTGATCCAGGTTAAAC-----ACATACCA--CATAC-----GATCTTAATGCAGCTGC-----TATTC-----GGTTTTACAGGTGTTCAATCAGCTGCCGTGAATGTAATATGTGAATAGCAGCTAAGAAC
dm3	chrX:13627208-13627394		GAGACCTGCATTTCCTCCAACTCAAGAGAAACTGGAGATCTCGATCCAGGTTAAAC-----ACATCA--CATAC-----GATCTTAATGCAGCTGC-----TATTC-----GGTTTTACAGGTGTTCAATCAGCTGCCGTGAATGTAATATGTGAATAGCAGCTAAGAAC
droErE2	scaffold_4690:13256339-13256515		GAGACCTGCATTTCCTCCAACTCAAGAGAAACTGGAGATCCATCCAGGTTTAACCC-----AATAA--CAACAA--CATAC-----GATCTTAATGCAGCTGC-----TATTC-----GGTTTTACAGGTGTTCAATCAGCTGCCGTGAATGTAATATGTGAATAGCAGCTAAGAAC
droYak3	X:7921258-7921440		GAGACCTGCATTTCCTCCAACTCAAGAGAAACTGGAGATCTCGATCCAGGTTTAACCC-----AATAA--CAACAA--CATAC-----GATCTTAATGCAGCTGC-----TATTC-----GGTTTTACAGGTGTTCAATCAGCTGCCGTGAATGTAATATGTGAATAGCAGCTAAGAAC
droEug1	scf7180000409008:47604-47786		GAGACCTGCATTTCCTCCAACTCAAGAGAAACTGGAGATCCATCCAGGTTTAACCC-----AATAA--CAACAA--CATAC-----GATCTTAATGCAGCTGC-----TATTC-----GGTTTTACAGGTGTTCAATCAGCTGCCGTGAATGTAATATGTGAATAGCAGCTAAGAAC
droBia1	scf7180000302041:647633-647821		GAGCCTGCATTTCCTCCAACTCAAGAGAAACTGGAGATCCATCCAGGTTTAACCC-----CTAGAT--TA--CATAC-----TATTC-----GGTTTTACAGGTGTTCAATCAGCTGCCGTGAATGTAATATGTGAATAGCAGCTAAGAAC
droTak1	scf7180000414562:534968-535146		GAGACCTGCATTTCCTCCAACTCAAGAGAAACTGGAGATCCATCCAGGTTTAACCC-----GATTA--CAATAC-----TATTC-----GGTTTTACAGGTGTTCAATCAGCTGCCGTGAATGTAATATGTGAATAGCAGCTAAGAAC
droE1e1	scf7180000491044:95588-95769		GAGACCTGCATTTCCTCCAACTCAAGAGAAACTGGAGATCCATCCAGGTTTAACCC-----GATTA--CAATAC-----TATTC-----GGTTTTACAGGTGTTCAATCAGCTGCCGTGAATGTAATATGTGAATAGCAGCTAAGAAC
droRho1	scf7180000779342:7597-7776		GAGACCTGCATTTCCTCCAACTCAAGAGAAACTGGAGATCCATCCAGGTTTAACCC-----GATTA--CAATAC-----TATTC-----GGTTTTACAGGTGTTCAATCAGCTGCCGTGAATGTAATATGTGAATAGCAGCTAAGAAC
droFiC1	scf7180000454073:1342285-1342462		GAGACCTGCATTTCCTCCAACTCAAGAGAAACTGGAGATCCATCCAGGTTTAACCC-----GATTA--CAATAC-----TATTC-----GGTTTTACAGGTGTTCAATCAGCTGCCGTGAATGTAATATGTGAATAGCAGCTAAGAAC
droRiX1	scf7180000302592:1586093-1586261		GAGCCTGCATTTCCTCCAACTCAAGAGAAACTGGAGATCCATCCAGGTTTAACCC-----GATTA--CAATAC-----TATTC-----GGTTTTACAGGTGTTCAATCAGCTGCCGTGAATGTAATATGTGAATAGCAGCTAAGAAC
droAna3	scaffold_13248:2849217-2849374		GAGCCTGCATTTCCTCCAACTCAAGAGAAACTGGAGATCCATCCAGGTTTAACCC-----GATTA--CAATAC-----TATTC-----GGTTTTACAGGTGTTCAATCAGCTGCCGTGAATGTAATATGTGAATAGCAGCTAAGAAC
droBip1	scf7180000396429:158638-158795		AAGACCTGCATTTCCTCCAACTCAAGAGAAACTGGAGATCCATCCAGGTTTAACCC-----GATTA--CAATAC-----TATTC-----GGTTTTACAGGTGTTCAATCAGCTGCCGTGAATGTAATATGTGAATAGCAGCTAAGAAC
dp5	XL_group1:1271537-1271708		GAGACCTGCATTTCCTCCAACTCAAGAGAAACTGGAGATCCATCCAGGTTTAACCC-----GATTA--CAATAC-----TATTC-----GGTTTTACAGGTGTTCAATCAGCTGCCGTGAATGTAATATGTGAATAGCAGCTAAGAAC
droPer2	scaffold_18:117685-117856		GAGACCTGCATTTCCTCCAACTCAAGAGAAACTGGAGATCCATCCAGGTTTAACCC-----GATTA--CAATAC-----TATTC-----GGTTTTACAGGTGTTCAATCAGCTGCCGTGAATGTAATATGTGAATAGCAGCTAAGAAC
droW112	scf2_1100000004909:7682629-7682783		AAGACCTGCATTTCCTCCAACTCAAGAGAAACTGGAGATCCATCCAGGTTTAACCC-----GATTA--CAATAC-----TATTC-----GGTTTTACAGGTGTTCAATCAGCTGCCGTGAATGTAATATGTGAATAGCAGCTAAGAAC
droViF3	scaffold_12970:8004017-8004266		GAGCCTGCATTTCCTCCAACTCAAGAGAAACTGGAGATCCATCCAGGTTTAACCC-----GATTA--CAATAC-----TATTC-----GGTTTTACAGGTGTTCAATCAGCTGCCGTGAATGTAATATGTGAATAGCAGCTAAGAAC
droMoJ3	scaffold_6482:1526740-1526905		GAGCCTGCATTTCCTCCAACTCAAGAGAAACTGGAGATCCATCCAGGTTTAACCC-----GATTA--CAATAC-----TATTC-----GGTTTTACAGGTGTTCAATCAGCTGCCGTGAATGTAATATGTGAATAGCAGCTAAGAAC
droGr12	scaffold_15203:11067117-11067276		GAGCCTGCATTTCCTCCAACTCAAGAGAAACTGGAGATCCATCCAGGTTTAACCC-----GATTA--CAATAC-----TATTC-----GGTTTTACAGGTGTTCAATCAGCTGCCGTGAATGTAATATGTGAATAGCAGCTAAGAAC

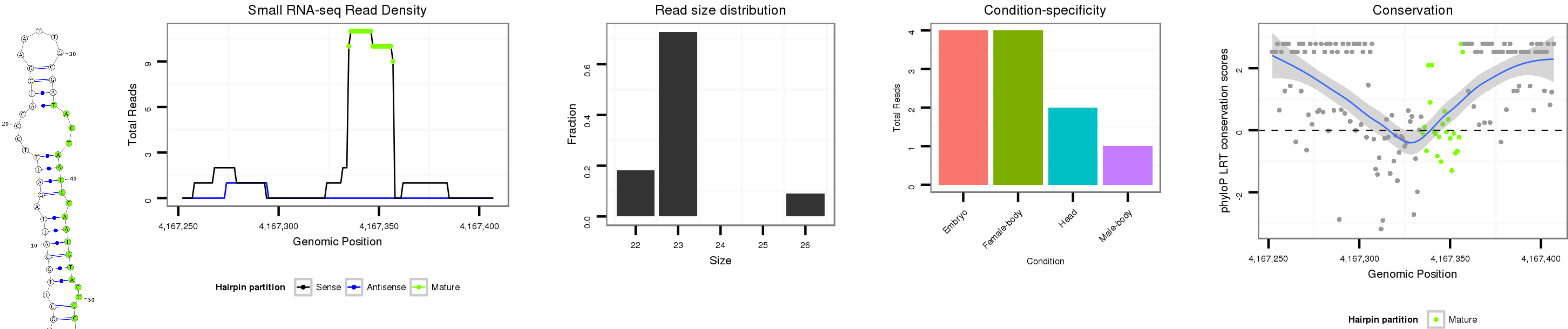
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	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dse_1294	scaffold_4:4167302-4167357 +	candidate	Mirtron	intron	[View on UCSC Genome Browser (Cornell Mirror)]

Legend: ■ mature ■ star ■ mis match in alignment ■ mismatch in read

Predicted structure



Show Alternate Folds

Flybase annotation

intron [Dsec/GM12786-int]; CDS [Dsec/GM12786-cds]; CDS [Dsec/GM12786-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

										M054		V115		V113			
										V114		female		head		male	
										embryo		body					
										Total		Total					
										Hit		Total					
										Mismatch		Count		Norm			
										Read #		size					
GGGACCACAATGCGCAGACCGTCTGCTCTCATCGCTGGATGATATAGTAGGTTGCAT--TAGA--TTT--C--CCATC-----G-----AATTGCGA-----TAC-TAATC-C-----A-----ATGT-----ACTC-CACAGAACTTTCACAGTTTGGCCAGATGAGGCCACGCCATCGAGAGCGATCA																	
*****(((.(((.(((.(.(((.....(((.....))).....))).....))).....*****																	
.....TACTAATCCAATGTACTCCACAG.....										23		0		1		7.00	
.....ACTAATCCAATGTACTCCACAG.....										22		0		1		1.00	
.....CGATACTAATCCAATGTACTCCACAG.....										26		0		1		1.00	
.....TCGAATTGGATACATAATCCAAT.....										23		0		1		1.00	
.....GACCGTCTGCTGCTCTCATCGCTGG.....										26		0		1		1.00	
.....ACAATGCCAGACCGTCTGTC.....										21		0		1		1.00	
.....TACTAATCCAATGTACTCCACA.....										22		0		1		1.00	
.....TTGCACAGTTTGGCCAGATGAG.....										23		0		1		1.00	

Anti-sense strand reads

										M054
CCCTGGTGTTACGGCTCTGGCAGCACGACGAGATAGCGACCTACTATATATCCAACGTAATCTAAAGGGTAGCTTAAAGCTATGATTAGGTTACATAGAGTGTCTTGAACGGTGTCAAACGGGTCTACTCCGGTGGGTAGCTCTCGTCTAGT										
										Read #
*****(((.(((.(((.(.(((.....(((.....))).....))).....*****										size
.....GCACGACGAGATAGCGACCT.....										Mismatch
										Hit
										Count
										Norm
										Total
										female body
										1

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droSec2	scaffold_4:4167252-4167407 +	dse_1294	GGGACCACAATGCGCAGACCGCTGCTGCTCTCATCGCTGGATGATATAGTAGGTTGCAT--TAGA--TTT--C--CCATC-----G-----AATTGCGA-----TAC-TAATC-C-----A-----ATGT-----ACTC-CACAGAACTTTCACAGTTTGGCCAGATGAGGCCACGCCATCGAGAGCGATCA
droSim2	3r:24668867-24669023 +		GGGACCACAATGCGCAGACCGCTGCTGCTCTCATCGCTGGATGATATAGTAGGTTGCAT--TAGA--TTT--C--CCATC-----G-----AATTGCGA-----TAC-TAATC-C-----A-----ATGT-----ACTC-CACAGAACTTTCACAGTTTGGCCAGATGAGGCCACGCCATCGAGAGCGATCA
dm3	chr3R:25308745-25308901 +		GGGACCACAATGCGCAGACCGCTGCTGCTCTCATCGCTGGATGATATAGTAGGTTGCAT--TAGA--TTT--C--CCATC-----G-----AATTGCGA-----TAC-TAATC-C-----A-----ATGT-----ACTC-CACAGAACTTTCACAGTTTGGCCAGATGAGGCCACGCCATCGAGAGCGATCA
droBre2	scaffold_4820:2696936-2697092 -		GGGACCACAATGCGCAGACCGCTGCTGCTCTCATCGCTGGATGATATAGTAGGTTGCAT--TAGA--TTT--C--CCATC-----G-----AATTGCGA-----TAC-TAATC-C-----A-----ATGT-----ACTC-CACAGAACTTTCACAGTTTGGCCAGATGAGGCCACGCCATCGAGAGCGATCA
droYak3	3R:21175252-21175408 -		GGGACCACAATGCGCAGACCGCTGCTGCTCTCATCGCTGGATGATATAGTAGGTTGCAT--TAGA--TTT--C--CCATC-----G-----AATTGCGA-----TAC-TAATC-C-----A-----ATGT-----ACTC-CACAGAACTTTCACAGTTTGGCCAGATGAGGCCACGCCATCGAGAGCGATCA
droEug1	scaffold_7:2337354-2337512 -		GGGACCACAATGCGCAGACCGCTGCTGCTCTCATCGCTGGATGATATAGTAGGTTGCAT--TAGA--TTT--C--CCATC-----G-----AATTGCGA-----TAC-TAATC-C-----A-----ATGT-----ACTC-CACAGAACTTTCACAGTTTGGCCAGATGAGGCCACGCCATCGAGAGCGATCA
droBial	scaffold_302136:2798729-2798887 -		GGGACCACAATGCGCAGACCGCTGCTGCTCTCATCGCTGGATGATATAGTAGGTTGCAT--TAGA--TTT--C--CCATC-----G-----AATTGCGA-----TAC-TAATC-C-----A-----ATGT-----ACTC-CACAGAACTTTCACAGTTTGGCCAGATGAGGCCACGCCATCGAGAGCGATCA
droTak1	scaffold_415765:871794-871951 -		GGGACCACAATGCGCAGACCGCTGCTGCTCTCATCGCTGGATGATATAGTAGGTTGCAT--TAGA--TTT--C--CCATC-----G-----AATTGCGA-----TAC-TAATC-C-----A-----ATGT-----ACTC-CACAGAACTTTCACAGTTTGGCCAGATGAGGCCACGCCATCGAGAGCGATCA
droEle1	scaffold_491280:1523119-1523362 +		GGGACCACAATGCGCAGACCGCTGCTGCTCTCATCGCTGGATGATATAGTAGGTTGCAT--TAGA--TTT--C--CCATC-----G-----AATTGCGA-----TAC-TAATC-C-----A-----ATGT-----ACTC-CACAGAACTTTCACAGTTTGGCCAGATGAGGCCACGCCATCGAGAGCGATCA
droRho1	scaffold_777929:9699-9959 +		GGGACCACAATGCGCAGACCGCTGCTGCTCTCATCGCTGGATGATATAGTAGGTTGCAT--TAGA--TTT--C--CCATC-----G-----AATTGCGA-----TAC-TAATC-C-----A-----ATGT-----ACTC-CACAGAACTTTCACAGTTTGGCCAGATGAGGCCACGCCATCGAGAGCGATCA
droFic1	scaffold_453776:609483-609645 +		GGGACCACAATGCGCAGACCGCTGCTGCTCTCATCGCTGGATGATATAGTAGGTTGCAT--TAGA--TTT--C--CCATC-----G-----AATTGCGA-----TAC-TAATC-C-----A-----ATGT-----ACTC-CACAGAACTTTCACAGTTTGGCCAGATGAGGCCACGCCATCGAGAGCGATCA
droKik1	scaffold_302166:120832-120994 -		GGGACCACAATGCGCAGACCGCTGCTGCTCTCATCGCTGGATGATATAGTAGGTTGCAT--TAGA--TTT--C--CCATC-----G-----AATTGCGA-----TAC-TAATC-C-----A-----ATGT-----ACTC-CACAGAACTTTCACAGTTTGGCCAGATGAGGCCACGCCATCGAGAGCGATCA
droAna3	scaffold_12911:4996480-4996639 +		GGGACCACAATGCGCAGACCGCTGCTGCTCTCATCGCTGGATGATATAGTAGGTTGCAT--TAGA--TTT--C--CCATC-----G-----AATTGCGA-----TAC-TAATC-C-----A-----ATGT-----ACTC-CACAGAACTTTCACAGTTTGGCCAGATGAGGCCACGCCATCGAGAGCGATCA
droBip1	scaffold_396640:1833120-1833277 +		GGGACCACAATGCGCAGACCGCTGCTGCTCTCATCGCTGGATGATATAGTAGGTTGCAT--TAGA--TTT--C--CCATC-----G-----AATTGCGA-----TAC-TAATC-C-----A-----ATGT-----ACTC-CACAGAACTTTCACAGTTTGGCCAGATGAGGCCACGCCATCGAGAGCGATCA
dp5	2:2169756-2169914 +		GGGACCACAATGCGCAGACCGCTGCTGCTCTCATCGCTGGATGATATAGTAGGTTGCAT--TAGA--TTT--C--CCATC-----G-----AATTGCGA-----TAC-TAATC-C-----A-----ATGT-----ACTC-CACAGAACTTTCACAGTTTGGCCAGATGAGGCCACGCCATCGAGAGCGATCA
droPer2	scaffold_7:2337354-2337512 -		GGGACCACAATGCGCAGACCGCTGCTGCTCTCATCGCTGGATGATATAGTAGGTTGCAT--TAGA--TTT--C--CCATC-----G-----AATTGCGA-----TAC-TAATC-C-----A-----ATGT-----ACTC-CACAGAACTTTCACAGTTTGGCCAGATGAGGCCACGCCATCGAGAGCGATCA
droW112	chr2_110000000:4902:8090071-8090234 +		GGGACCACAATGCGCAGACCGCTGCTGCTCTCATCGCTGGATGATATAGTAGGTTGCAT--TAGA--TTT--C--CCATC-----G-----AATTGCGA-----TAC-TAATC-C-----A-----ATGT-----ACTC-CACAGAACTTTCACAGTTTGGCCAGATGAGGCCACGCCATCGAGAGCGATCA
droV11r3	scaffold_12822:2851404-2851570 -		GGGACCACAATGCGCAGACCGCTGCTGCTCTCATCGCTGGATGATATAGTAGGTTGCAT--TAGA--TTT--C--CCATC-----G-----AATTGCGA-----TAC-TAATC-C-----A-----ATGT-----ACTC-CACAGAACTTTCACAGTTTGGCCAGATGAGGCCACGCCATCGAGAGCGATCA
droMo3	scaffold_6540:26782539-26782692 +		GGGACCACAATGCGCAGACCGCTGCTGCTCTCATCGCTGGATGATATAGTAGGTTGCAT--TAGA--TTT--C--CCATC-----G-----AATTGCGA-----TAC-TAATC-C-----A-----ATGT-----ACTC-CACAGAACTTTCACAGTTTGGCCAGATGAGGCCACGCCATCGAGAGCGATCA
droGr12	scaffold_14624:3598954-3599116 +		GGGACCACAATGCGCAGACCGCTGCTGCTCTCATCGCTGGATGATATAGTAGGTTGCAT--TAGA--TTT--C--CCATC-----G-----AATTGCGA-----TAC-TAATC-C-----A-----ATGT-----ACTC-CACAGAACTTTCACAGTTTGGCCAGATGAGGCCACGCCATCGAGAGCGATCA

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	PASS/FAIL
crit.sbar	0
crit.loop	0
crit.mor	0
crit.hair	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.top3	1
crit.uri	0
crit.back	1
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

Predicted structure

Flybase annotation

Antisense to intron [Dsec'GM16331-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

Anti-sense strand reads

Show Alignment With Reads

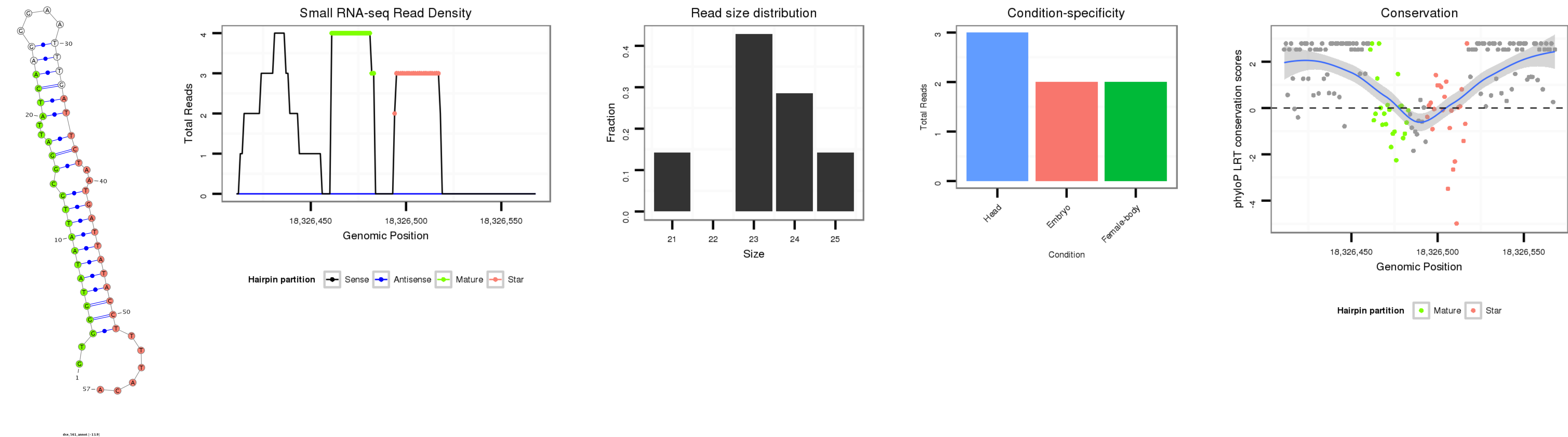
Re-alignment of all predicted orthologs

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	PASS/FAIL
crit.star	0
crit.loop	0
crit.mrnr	0
crit.half	0
crit.total	0
crit.pairing	0
crit.tsp3	1
crit.tsp3p3	1
crit.xm	0
crit.back	1
rescue.total	0
rescue.dominant	1
rescue.known	0
rescue.confidence	1
rescue.confidlow	2

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Show Alternate Folds

Flybase annotation

Antisense to intron [Dsec\GM23668-in]; intron [Dsec\GM26405-in]; CDS [Dsec\GM26405-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

					V115	V114	M054	V113
	Read #	Hit	Total	Total	head	embryo	female body	male body
	size	Mismatch	Count	Norm				
CTCGAGACCCAGCATCGAGGCGGTGCACAAGATCAAGTATCAGTGTGATAA GTGGGTATAATTGCGGATTATCA AGGGAATTG ATTCTTAATGATTATACCTTTTACAGT GCCATCTATGATAGGAGGCCAAATGATCTACAAAAATCGATGAGGTGC	23	0	1	3.00	3	2	1	0
*****.(((((((((((.(((.((((((.....))))))))..))))))))*****	25	0	1	1.00	1	0	1	0
.....GTGGGTATAATTGCGGATTATCA.....	23	0	1	1.00	1	0	1	0
.....G GTGCACAAGATCAAGTATCAGTGT	25	0	1	1.00	1	0	1	0
.....CGAGACCCAGCATCGAGGCGGTGCACA.....	26	0	1	1.00	1	0	0	1
.....AGACCCAGCATCGAGGCGGTGC.....	22	0	1	1.00	1	1	0	0
.....ATTCTAATGATTATACCTTTTACA.....	24	0	1	1.00	1	0	0	1
.....TTCTAATGATTATACCTTTTACAG.....	24	0	1	1.00	1	0	0	1
.....GTGGGTATAATTGCGGATTAT.....	21	0	1	1.00	1	1	0	0
.....ATTCTAATGATTATACCTTTTACAG.....	25	0	1	1.00	1	0	1	0
.....TCGAGGCGGTGCACAAGATC.....	20	0	1	1.00	1	0	0	1

Anti-sense strand reads

										M054
GAGCTCTGGGCTAGCTCCGCCAGTGTTCTAGTTCATAGTCACACTATT CACCCATATTAA CGCCTAATAGTTCCTTAAAC TA GATTACTAATATGGAAAT GT CACGGTAGATACATATTCCTCGCGGTTTACTAGATGTTTTAGTACTCCAGC										
*****.(((((((((((.(((.((((((.....)))))))))).))))))))).*****										
										Read #
										Hit
										Total
										size Mismatch Count Norm
										Total
										female body

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droSec2	scaffold_0_18326411-18326568 chr3R:17956119-17956277	dse_561	C-TCGAGACCCAGATCGAGCGGTGCACAAGATCAAGTATCAGTGTGTAAAGTGGG-TATAATTGC-----GGAT-TATCAAGGGAA--TTTGA-TT-----CTAATGA-----TT--AT-----A---CCTTTTACGTGCCATCTATGATAAGGAGCGCCAAATGATCTACAAAATCGATGAGGTGC
droSim2	3r:17494819-17494977		CCTCGAGACCCAGATCGAGCGGTGCACAAGATCAAGTATCAGTGTGTAAAGTGGG-TATAATTGC-----GAT-TATCAAGGGAA--TTTGA-TT-----CTAATCT-----TT--AT-----A---CCTTTTACGTGCCATCTATGATAAGGAGCGCCAAATGATCTACAAAATCGATGAGGTGC
dm3	chr3R:17956119-17956277		CCTCGAGACCCAGATCGAGCGGTGCACAAGATCAAGTATCAGTGTGTAAATGTC-TATAATTG-----GAT-TATCAAGGGAA--TTTGA-TT-----CTAATGA-----TT--AT-----A---TTTTTACGTGCCATCTATGATAAGGAAGCCAAATGATCTACAAAATCGATGAGGTGC
droFrE2	scaffold_4820:10121874-10122030		CCTCGAGACCCAGATCGAGCGGTGCACAAGATCAAGTATCAGTGTGTAAAGTGGG-TATCGTCG-----CGAC-TAAAGGGCA--CTCAA-TT-----CTAATGA-----TT--AT-----A---CTCGCAGTGCCATCTATCGAAGAGGCGCCAAATGATCTACAAAATCGAGGTGC
droYak3	3R:18804196-18804353		C-TCGAGACCCAGATCGAGCGGTGCACAAGATCAAGTATCAGTGTGTAAAGTGGG-TCAAACG-----TGAT-TATCAAGTCA--TCAATGA-----CTAATGA-----TT--AT-----C---GACCTTACGTGCCATCTATGAAGAGGCGCCAAATGATCTACAAAATCGATGAGGTGC
droEu1	scf7180000409768:72694-72857		CCTGGAACCCAGATCGAGCGGTGCACAAGATCAAGTATCAGTGTGTAAAGAA-TGCTCTA--AA-TATA-----CTTAAATGG--TCA--TGTTA-----ATATTAG-----ATT--TA-----TGA-TATATTTTGTGCCATCTATGAAGAGGCGCCAAATGATCTACAAAATCGATGAGGTGC
droBial	scf7180000302402:5784821-5784986		CCTCGAGACCCAGATCGAGCGGTGCACAAGATCAAGTATCAGTGTGTAAAGTGGG-TATCTCTG--GA-TACA-----CTTAAACAA--TAAATTA--ATAATG--T-----AT--CC--A--A-TTCTCCAGTGCCATCTCGAAGAGGCGCCAAATGATCTACAAAATCGATGAGGTGC
droTak1	scf7180000415711:1095404-1095566		CCTCGAGACCCAGATCGAGCGGTGCACAAGATCAAGTATCAGTGTGTAAAGTGGG-TATCTCTG--GA-AATA-----CTTAAACAA--TAAATTA--ATAATG--T-----AT--CC--A--A-TTCCCTTATGTGCCATCTATGAAGAGGCGCCAAATGATCTACAAAATCGATGAGGTGC
droEl1	scf7180000491212:2443820-2443979		C-TCGAGACCCAGATCGAGCGGTGCACAAGATCAAGTATCAGTGTGTAAAGTGGG-TATCTCTG--GT-----ATTAACGATAA--TT--T--CTCA-----ATTT--ATA--AACA--T--CATTTTTATGTGCCATCTATGAAGAGGCGCCAAATGATCTACAAAATCGATGAGGTGC
droRho1	scf7180000780293:60348-60506		C-TCGAGACCCAGATCGAGCGGTGCACAAGATCAAGTATCAGTGTGTAAAGAA-TATGCC--AA-T-----CAAAACAC--TT--TCTCA-----ATATTAA--ACG--CC-----A-TTTAATTATGTGCCATCTATGAAGAGGCGCCAAATGATCTACAAAATCGATGAGGTGC
droFic1	scf7180000454106:1113528-1113686		C-TCGAGACCCAGATCGAGCGGTGCACAAGATCAAGTATCAGTGTGACCAACAAAG--TG--TC--TA--AG-----AGAA-TATCAAGGA--TT--TCTTA-----CTAG-----TTAACA--TGCTTATGTGCCATCTCGAAGAGGCGCCAAATGATCTACAAAATCGATGAGGTGC
droKik1	scf7180000302461:2118275-2118430		C-TCGAGACCCAGATCGAGGTGTCACAAGATCAAGTATCAGTGTGTAAAGTGGG-TATAAGAG--GA-T-----GTT--A--TAT--TCTATTT--T-----ATATTAT--A--TT--AT-----A-TTTTCCAGTGCCATCTATGAAGAGGCGCCAAATGATCTACAAAATCGAGGTGC
droAna3	scaffold_13340:8957795-8957952		CCTCGAGACCCAGATCGAGGTGTCACAAGATCAAGTATCAGTGTGTAAAGAAAGCTCAG-----CAATGCT--T--TGA--TGTAATTTAT--TATTA--ACT--T--TGACTTTCAAGTGCCATCTCGAAGAGGCGCCAAATGATCTACAAAATCGATGAGGTGC
droBip1	scf7180000396712:110087-110251		CCTCGAGACCCAGATCGAGGTGTCACAAGATCAAGTATCAGTGTGTAAAGAGTGAATCCATCT-----ACCTATCCG--G-----GGTG-TATGATCT--ATGA-----TT--ATGT--G--ACCCTCATTTCAAGTGCCATCTCGAAGAGGCGCCAAATGATCTACAAAATCGATGAGGTGC
dp5	2:12123657-12123814		C-TCGAGACCCAGATCGAGGTGTCACAAGATCAAGTATCAGTGTGTAAAGTGA--TAACTCT-----ATTAAGGATGG--TTCCAT--CC--A--TAGATC--T--GCCCTTTTCAAGTGCCATCTATGAAGAGGCGCCAAATGATCTACAAAATCGATGAGGTGC
droPer2	scaffold_0:8372961-8373116		C-TCGAGACCCAGATCGAGGTGTCACAAGATCAAGTATCAGTGTGTAAAGTGA--TAACTCT-----ATTAAGGATGG--TTCCAT--A--TAGATC--T--GCCCTTTTCAAGTGCCATCTATGAAGGAAGCCAAATGATCTACAAAATCGATGAGGTGC
droWil2	scf2_1100000004943:12096631-12096792		C-TAGAGGTCTAATTAAGACGGTGAATAAATTAAGTATCAGTGTGTAAAGTGA--TAACTCT-----ATTAAGGATGG--TTCCAT--A--TAGATC--T--GCCCTTTTCAAGTGCCATCTATGAAGAGGCGCCAAATGATCTACAAAATCGATGAGGTGC
droVit3	scaffold_13047:8528825-8528983		C-TGAGAGACCCAGATCGAAGCTGTCGCAAAATTAAGTATCAGTGTGTAAAGAGTAACTCT-----GTCA--ATTT--GCAAGATGAACATCAATTA--GAA--TCCAAATGAGCCATCTATGATAAGGAGCGCCAAATGATCTACGATCGATGAGGTGC
droMoJ3	scaffold_6540:27630766-27630934		C-TGAGAGACCCAGATCGAAGCTGTCGCAAGATTAAGTATCAGTGTGTAAAGTGA--TGAATCTCTTTTGAATACTTCTCAA--G--AAG--CA--TAATGA--TA--ATCT--G--G--ACTTTACCTCAAGCCCATCTATGATAAGGAGCGCCAAATGATCTACGATCGATGAGGTGC
droGr12	scaffold_15074:1089041-1089210		C-TGAGAGACCCAGATCGAGGTGTCGCAAGATTAAGTATCAGTGTGTAAAGAGTGA--TGAATCTCTTTTGAATACTTCTCAA--G--AAG--CA--TAATGA--TA--ATCT--G--G--AAACGGTCTCAAAATG--CCAATCAAGCCCATCTATGATAAGGAGCGCCAAATGATCTACGATCGATGAGGTGC

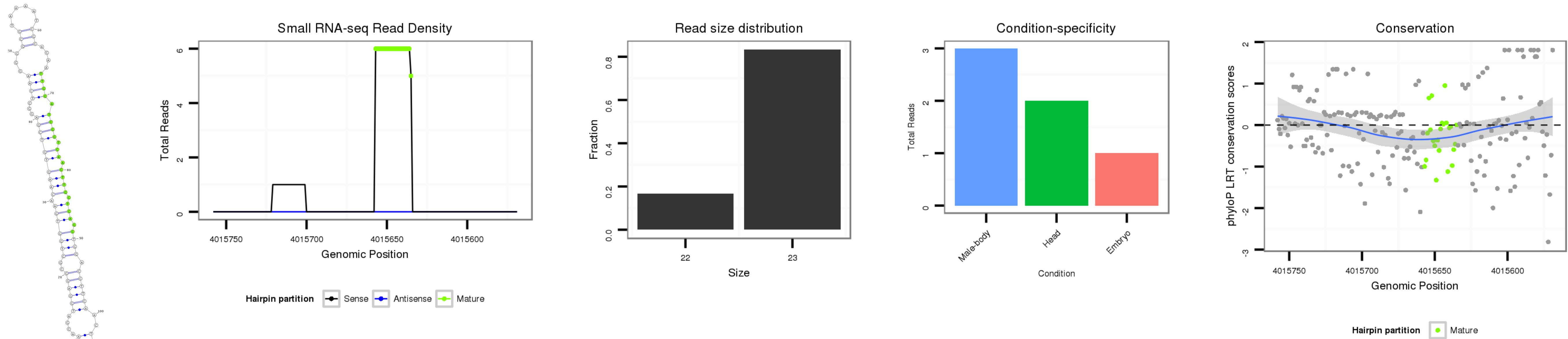
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	PASS/FAIL
crit.star	1
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crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate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

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dse_1851	scaffold_0:4015619-4015708	- candidate	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 annnotation

CDS [Dsec\GM24702-cds]; intron [Dsec\GM24702-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

AAGCTTCTGCAATAGCTAATGCTACCGCAGGCACCTAAGAGAAGTAACGATGGAGGCGCTGGTGAACAAGTGTCTGAGGCTCAAGGGCGCTAAATCGCACAAATGGATCGGTCAACTTGCTCAGCTGGACCTTCAACTACTCATCCACCACCAACAATCTTTGCACATAAACACCTTATTGCTGGGATAAAGAT																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																												
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Anti-sense strand reads

	Read #	Hit	Total		V114	V113	V115	M054
	size	Mismatch	Count	Norm	Total	embryo	male head body	female body
TTGGAAGACGTTATCGATTACGATGGCGTCCGTTGATTCTCTTCATTGCTACTCCGCGACCACCTTGTTCACAGCTCCGAGTTCGCCGCATTTTAGCGTGTAACTAGCCAGTTGAACGAGTTCGACCTGGAAGTTGATGAGTAGTGGTGGTGTGTAGAAACGTCGATTGTTGGATAACGACCCCTATTCTA								

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droSec2	scaffold_0:4015569-4015758 -	dse_1851	AAGCTTCTGCA-----ATAGCTAATGCTACC-----GCAGGCACCTAAGAGAAGTAACGATGGAGGCGCTGGTGAACAAGTGTCTGAGCTCAAGGGGCGT-----AA-----AATCGCACAAATGGATCG-----GTCA-----ACTTG-----CTCAGCTGGACCTTCAACTACTCATCCA-----CCACCACAAATCTTTGCACTAAACACCTATTGCTGGGATAAGAT
droSim2	31:11531345-11531534 -	dsl_36	AAGCTTCTGCA-----ATAGCTAATGCTACC-----GCAGGCACCTAAGAGAAGTAACGATGGAGGCGCTGGTGAACAAGTGTCTGAGCTCAAGGGGCGT-----AA-----AATCGCACAAATGGATCG-----GTCA-----ACTTG-----CTCAGCTGGACCTTCAACTACTCATCCA-----CCACCACAAATCTTTGCACTAAACACCTATTGCTGGGATAAGAT
dm3	chr3L:11829563-11829773 -	dme_458	AAGCTTCTGCA-----ATAGCTAATGCTACC-----GCAGGCACCTAAGAGAAGTAACGATGGAGGCGCTGGTGAACAAGTGTCTGAGCTCAAGGGGCGT-----AA-----AATCGCACAAATGGATCG-----GTCA-----ACTTG-----CTCAGCTGGACCTTCAACTACTCATCCA-----CCACCACAAATCTTTGCACTAAACACCTATTGCTGGGATAAGAT
droYak3	3L:11839375-11839410 +		AAGCTTCTGCA-----ATAGCTAATGCTACC-----GCAGGCACCTAAGAGAAGTAACGATGGAGGCGCTGGTGAACAAGTGTCTGAGCTCAAGGGGCGT-----AA-----AATCGCACAAATGGATCG-----GTCA-----ACTTG-----CTCAGCTGGACCTTCAACTACTCATCCA-----CCACCACAAATCTTTGCACTAAACACCTATTGCTGGGATAAGAT
droEug1	scf7180000409554:3289914-3290082 +		AAGCTTCTGCA-----ATAGCTAATGCTACC-----GCAGGCACCTAAGAGAAGTAACGATGGAGGCGCTGGTGAACAAGTGTCTGAGCTCAAGGGGCGT-----AA-----AATCGCACAAATGGATCG-----GTCA-----ACTTG-----CTCAGCTGGACCTTCAACTACTCATCCA-----CCACCACAAATCTTTGCACTAAACACCTATTGCTGGGATAAGAT
droBial	scf7180000302188:1829832-1830072 -		AAGCTTCTGCA-----ATAGCTAATGCTACC-----GCAGGCACCTAAGAGAAGTAACGATGGAGGCGCTGGTGAACAAGTGTCTGAGCTCAAGGGGCGT-----AA-----AATCGCACAAATGGATCG-----GTCA-----ACTTG-----CTCAGCTGGACCTTCAACTACTCATCCA-----CCACCACAAATCTTTGCACTAAACACCTATTGCTGGGATAAGAT
droTak1	scf7180000415705:584828-585092 -		AAGCTTCTGCA-----ATAGCTAATGCTACC-----GCAGGCACCTAAGAGAAGTAACGATGGAGGCGCTGGTGAACAAGTGTCTGAGCTCAAGGGGCGT-----AA-----AATCGCACAAATGGATCG-----GTCA-----ACTTG-----CTCAGCTGGACCTTCAACTACTCATCCA-----CCACCACAAATCTTTGCACTAAACACCTATTGCTGGGATAAGAT
droEle1	scf7180000419273:348108-348297 +		AAGCTTCTGCA-----ATAGCTAATGCTACC-----GCAGGCACCTAAGAGAAGTAACGATGGAGGCGCTGGTGAACAAGTGTCTGAGCTCAAGGGGCGT-----AA-----AATCGCACAAATGGATCG-----GTCA-----ACTTG-----CTCAGCTGGACCTTCAACTACTCATCCA-----CCACCACAAATCTTTGCACTAAACACCTATTGCTGGGATAAGAT
droFic1	scf7180000453924:782249-782483 -		AAGCTTCTGCA-----ATAGCTAATGCTACC-----GCAGGCACCTAAGAGAAGTAACGATGGAGGCGCTGGTGAACAAGTGTCTGAGCTCAAGGGGCGT-----AA-----AATCGCACAAATGGATCG-----GTCA-----ACTTG-----CTCAGCTGGACCTTCAACTACTCATCCA-----CCACCACAAATCTTTGCACTAAACACCTATTGCTGGGATAAGAT
droKik1	scf7180000302468:1176203-1176254 -		AAGCTTCTGCA-----ATAGCTAATGCTACC-----GCAGGCACCTAAGAGAAGTAACGATGGAGGCGCTGGTGAACAAGTGTCTGAGCTCAAGGGGCGT-----AA-----AATCGCACAAATGGATCG-----GTCA-----ACTTG-----CTCAGCTGGACCTTCAACTACTCATCCA-----CCACCACAAATCTTTGCACTAAACACCTATTGCTGGGATAAGAT
droBip1	scf7180000396554:1430939-1431063 -		AAGCTTCTGCA-----ATAGCTAATGCTACC-----GCAGGCACCTAAGAGAAGTAACGATGGAGGCGCTGGTGAACAAGTGTCTGAGCTCAAGGGGCGT-----AA-----AATCGCACAAATGGATCG-----GTCA-----ACTTG-----CTCAGCTGGACCTTCAACTACTCATCCA-----CCACCACAAATCTTTGCACTAAACACCTATTGCTGGGATAAGAT
dp5	4_group4:4495769-4495810 +		AAGCTTCTGCA-----ATAGCTAATGCTACC-----GCAGGCACCTAAGAGAAGTAACGATGGAGGCGCTGGTGAACAAGTGTCTGAGCTCAAGGGGCGT-----AA-----AATCGCACAAATGGATCG-----GTCA-----ACTTG-----CTCAGCTGGACCTTCAACTACTCATCCA-----CCACCACAAATCTTTGCACTAAACACCTATTGCTGGGATAAGAT
droPer2	scaffold_10:3406855-3406888 +		AAGCTTCTGCA-----ATAGCTAATGCTACC-----GCAGGCACCTAAGAGAAGTAACGATGGAGGCGCTGGTGAACAAGTGTCTGAGCTCAAGGGGCGT-----AA-----AATCGCACAAATGGATCG-----GTCA-----ACTTG-----CTCAGCTGGACCTTCAACTACTCATCCA-----CCACCACAAATCTTTGCACTAAACACCTATTGCTGGGATAAGAT

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crit.loop 0
crit.mor 0
crit.half 0
crit.total 0
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crit.uri 0
crit.back 1
rescue.total 0
rescue.dominant 1
rescue.known 0
rescue.confident 1
rescue.candidate 1

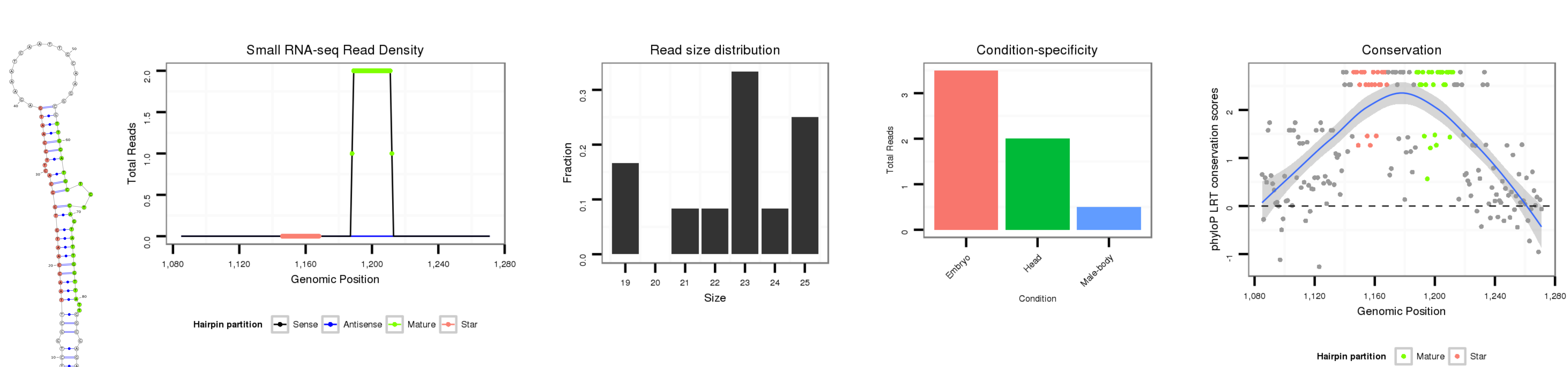
Coordinate	ID	Alignment
droSee2	scf1655253:655433+ chr28:2986001-2986188+ dme_430	Alignment droSee2 droSim1 dme3 droEre2 droTak3 droBug1 droBial droTak1 droEle1 droRho1 droFic1 droLiki droAna3 droBip1 dp5 droPer2 droW12 droVir1 droMo3 droGr1

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

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dse_1845	scaffold_2807:1135-1221 +	candidate	Canonical miRNA	intergenic	[View on UCSC Genome Browser (Cornell Mirror)]

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

Predicted structure



Show Alternate Folds

Flybase annotation

intergenic

No Repeatable elements found

nature	star
1. dse_1845 scaffold_2807:1188-1212+	1. dse_1845 scaffold_2807:1146-1168+
2. scaffold_31:104466-104490+	2. scaffold_31:104424-104446+

Sense Strand Reads

☐ hide 3p reads ☐ show mid mismatch reads

Read #	size	Mismatch	Hit	Count	Norm	Total	V114	V115	V113	M054
							embryo	head	male	female body
25	0	2	1.00	2	1	1	0	0	0	0
23	0	2	1.00	2	0	2	0	0	0	0
21	1	2	0.50	1	0	0	0	1	0	0
19	0	2	0.50	1	1	0	0	0	0	0
19	0	2	0.50	1	0	0	1	0	0	0
22	0	2	0.50	1	1	0	0	0	0	0
21	0	2	0.50	1	0	1	0	0	0	0
26	0	2	0.50	1	0	0	1	0	0	0
20	0	2	0.50	1	0	0	0	1	0	0
23	0	2	0.50	1	1	0	0	0	0	0
25	0	2	0.50	1	1	0	0	0	0	0
23	1	2	0.50	1	0	1	0	0	0	0
23	0	2	0.50	1	1	0	0	0	0	0
24	0	2	0.50	1	1	0	0	0	0	0

Anti-sense strand reads

Read #	size	Mismatch	Hit	Count	Norm	Total	M054	V113
							female body	male body
22	0	2	0.50	1	0	1	0	0
21	0	2	0.50	1	1	0	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droSec2	scaffold_2807:1085-1271 +	dse_1845	G--TAGCAACGTTTA-----CAATCC-----GCGAAAGTGC-----CG-----TCGCAGAA--TTT-----TCCGGCG--GGGCTTCTGGCTTAACCAATGTGGCACTTCCAATGAGAAATCAATTGCAAGGCCTTGGATGCTCTCAGTATTGGTTATTGGCGAGATTGGCCCCGGGACAGCATTACTAGACAGTTCCGATCAGTCCGCACATAAACCC
droSim2	3r:26724016-26724202 +	dse_1845	G--TAGCAACGTTTA-----CAATCC-----GCGAAAGTGC-----A-----TCGCAGAA--TTT-----TCCGGCG--GGGCTTCTGGCTTAACCAATGTGGCACTTCCAATGAGAAATCAATTGCAAGGCCTTGGATGCTCTCAGTATTGGTTATTGGCGAGATTGGCCCCGGGACAGCATTACT-A-----GAC-----AGTTCGGATCAGTCCG-----CACT-AAACCC-----
dm3	chr3R:27444043-27444229 +	dme_422	G--TAGCAACGTTTA-----CAATCC-----GCGAAAGTGC-----A-----TCGCAGAA--TTT-----TCCGGCG--GGGCTTCTGGCTTAACCAATGTGGCACTTCCAATGAGAAATCAATTGCAAGGCCTTGGATGCTCTCAGTATTGGTTATTGGCGAGATTGGCCCCGGGACAGCATTACT-A-----GAC-----AGTTCGGATCAGTCCG-----CACT-AAACCC-----
droPer2	scaffold_4820:530477-530664 +	der_1522	G--TAGCAACGTTTA-----CAATCC-----GCGAAAGTGC-----A-----TCGCAGAA--TTT-----TCCGGCG--GGGCTTCTGGCTTAACCAATGTGGCACTTCCAATGAGAAATCAATTGCAAGGCCTTGGATGCTCTCAGTATTGGTTATTGGCGAGATTGGCCCCGGGACAGCATTACT-A-----GAC-----AGTTCGGATCAGTCCG-----CACT-AAACCC-----
droYak3	3R:28380157-28380343 +	dya_1797	G--TAGCAACGTTTA-----CAATCC-----GCGAAAGTGC-----A-----TCGCAGAA--TTT-----TCCGGCG--GGGCTTCTGGCTTAACCAATGTGGCACTTCCAATGAGAAATCAATTGCAAGGCCTTGGATGCTCTCAGTATTGGTTATTGGCGAGATTGGCCCCGGGACAGCATTACT-A-----GAC-----AGTTCGGATCAGTCCG-----CACT-AAACCC-----
droEug1	scf7180000409488:463420-463601 -		G--TAGCAACGTTTA-----CAATCC-----GCGAAAGTGC-----A-----TCGCAGAA--TTT-----TCCGGCG--GGGCTTCTGGCTTAACCAATGTGGCACTTCCAATGAGAAATCAATTGCAAGGCCTTGGATGCTCTCAGTATTGGTTATTGGCGAGATTGGCCCCGGGACAGCATTACT-A-----GAC-----AGTTCGGATCAGTCCG-----CACT-AAACCC-----
droBia1	scf7180000302035:101881-102083 +		G--TAGCAACGTTTA-----CAATCC-----GCGAAAGTGC-----A-----TCGCAGAA--TTT-----TCCGGCG--GGGCTTCTGGCTTAACCAATGTGGCACTTCCAATGAGAAATCAATTGCAAGGCCTTGGATGCTCTCAGTATTGGTTATTGGCGAGATTGGCCCCGGGACAGCATTACT-A-----GAC-----AGTTCGGATCAGTCCG-----CACT-AAACCC-----
droTak1	scf7180000415712:510640-510848 +		G--TAGCAACGTTTA-----CAATCC-----GCGAAAGTGC-----A-----TCGCAGAA--TTT-----TCCGGCG--GGGCTTCTGGCTTAACCAATGTGGCACTTCCAATGAGAAATCAATTGCAAGGCCTTGGATGCTCTCAGTATTGGTTATTGGCGAGATTGGCCCCGGGACAGCATTACT-A-----GAC-----AGTTCGGATCAGTCCG-----CACT-AAACCC-----
droE1e1	scf7180000491194:1479822-1480037 +		G--TAGCAACGTTTA-----CAATCC-----GCGAAAGTGC-----A-----TCGCAGAA--TTT-----TCCGGCG--GGGCTTCTGGCTTAACCAATGTGGCACTTCCAATGAGAAATCAATTGCAAGGCCTTGGATGCTCTCAGTATTGGTTATTGGCGAGATTGGCCCCGGGACAGCATTACT-A-----GAC-----AGTTCGGATCAGTCCG-----CACT-AAACCC-----
droRho1	scf7180000779322:264797-265012 -		G--TAGCAACGTTTA-----CAATCC-----GCGAAAGTGC-----A-----TCGCAGAA--TTT-----TCCGGCG--GGGCTTCTGGCTTAACCAATGTGGCACTTCCAATGAGAAATCAATTGCAAGGCCTTGGATGCTCTCAGTATTGGTTATTGGCGAGATTGGCCCCGGGACAGCATTACT-A-----GAC-----AGTTCGGATCAGTCCG-----CACT-AAACCC-----
droFic1	scf7180000454114:125762-125965 +		G--TAGCAACGTTTA-----CAATCC-----GCGAAAGTGC-----A-----TCGCAGAA--TTT-----TCCGGCG--GGGCTTCTGGCTTAACCAATGTGGCACTTCCAATGAGAAATCAATTGCAAGGCCTTGGATGCTCTCAGTATTGGTTATTGGCGAGATTGGCCCCGGGACAGCATTACT-A-----GAC-----AGTTCGGATCAGTCCG-----CACT-AAACCC-----
droKik1	scf7180000302810:681812-682012 +		G--TAGCAACGTTTA-----CAATCC-----GCGAAAGTGC-----A-----TCGCAGAA--TTT-----TCCGGCG--GGGCTTCTGGCTTAACCAATGTGGCACTTCCAATGAGAAATCAATTGCAAGGCCTTGGATGCTCTCAGTATTGGTTATTGGCGAGATTGGCCCCGGGACAGCATTACT-A-----GAC-----AGTTCGGATCAGTCCG-----CACT-AAACCC-----
droAna3	scaffold_12911:3664259-3664461 -	dan_200	G--TAGCAACGTTTA-----CAATCC-----GCGAAAGTGC-----A-----TCGCAGAA--TTT-----TCCGGCG--GGGCTTCTGGCTTAACCAATGTGGCACTTCCAATGAGAAATCAATTGCAAGGCCTTGGATGCTCTCAGTATTGGTTATTGGCGAGATTGGCCCCGGGACAGCATTACT-A-----GAC-----AGTTCGGATCAGTCCG-----CACT-AAACCC-----
droBip1	scf7180000396640:523303-523505 -		G--TAGCAACGTTTA-----CAATCC-----GCGAAAGTGC-----A-----TCGCAGAA--TTT-----TCCGGCG--GGGCTTCTGGCTTAACCAATGTGGCACTTCCAATGAGAAATCAATTGCAAGGCCTTGGATGCTCTCAGTATTGGTTATTGGCGAGATTGGCCCCGGGACAGCATTACT-A-----GAC-----AGTTCGGATCAGTCCG-----CACT-AAACCC-----
dp5	2:16675955-1667598 -	dps_3828	G--TAGCAACGTTTA-----CAATCC-----GCGAAAGTGC-----A-----TCGCAGAA--TTT-----TCCGGCG--GGGCTTCTGGCTTAACCAATGTGGCACTTCCAATGAGAAATCAATTGCAAGGCCTTGGATGCTCTCAGTATTGGTTATTGGCGAGATTGGCCCCGGGACAGCATTACT-A-----GAC-----AGTTCGGATCAGTCCG-----CACT-AAACCC-----
droPer2	scaffold_0:3721652-3721795 +	dpe_2482	G--TAGCAACGTTTA-----CAATCC-----GCGAAAGTGC-----A-----TCGCAGAA--TTT-----TCCGGCG--GGGCTTCTGGCTTAACCAATGTGGCACTTCCAATGAGAAATCAATTGCAAGGCCTTGGATGCTCTCAGTATTGGTTATTGGCGAGATTGGCCCCGGGACAGCATTACT-A-----GAC-----AGTTCGGATCAGTCCG-----CACT-AAACCC-----
droN12	scf2_1100000004902:9400240-9400376 +	dwi_5416	G--TAGCAACGTTTA-----CAATCC-----GCGAAAGTGC-----A-----TCGCAGAA--TTT-----TCCGGCG--GGGCTTCTGGCTTAACCAATGTGGCACTTCCAATGAGAAATCAATTGCAAGGCCTTGGATGCTCTCAGTATTGGTTATTGGCGAGATTGGCCCCGGGACAGCATTACT-A-----GAC-----AGTTCGGATCAGTCCG-----CACT-AAACCC-----
droVir3	scaffold_13047:9559455-9559595 -	dvi_24635	G--TAGCAACGTTTA-----CAATCC-----GCGAAAGTGC-----A-----TCGCAGAA--TTT-----TCCGGCG--GGGCTTCTGGCTTAACCAATGTGGCACTTCCAATGAGAAATCAATTGCAAGGCCTTGGATGCTCTCAGTATTGGTTATTGGCGAGATTGGCCCCGGGACAGCATTACT-A-----GAC-----AGTTCGGATCAGTCCG-----CACT-AAACCC-----
droMo3	scaffold_6540:7667646-7667784 -	dmo_270	G--TAGCAACGTTTA-----CAATCC-----GCGAAAGTGC-----A-----TCGCAGAA--TTT-----TCCGGCG--GGGCTTCTGGCTTAACCAATGTGGCACTTCCAATGAGAAATCAATTGCAAGGCCTTGGATGCTCTCAGTATTGGTTATTGGCGAGATTGGCCCCGGGACAGCATTACT-A-----GAC-----AGTTCGGATCAGTCCG-----CACT-AAACCC-----
droGr12	scaffold_14906:2448932-2449065 -	dgr_463	G--TAGCAACGTTTA-----CAATCC-----GCGAAAGTGC-----A-----TCGCAGAA--TTT-----TCCGGCG--GGGCTTCTGGCTTAACCAATGTGGCACTTCCAATGAGAAATCAATTGCAAGGCCTTGGATGCTCTCAGTATTGGTTATTGGCGAGATTGGCCCCGGGACAGCATTACT-A-----GAC-----AGTTCGGATCAGTCCG-----CACT-AAACCC-----

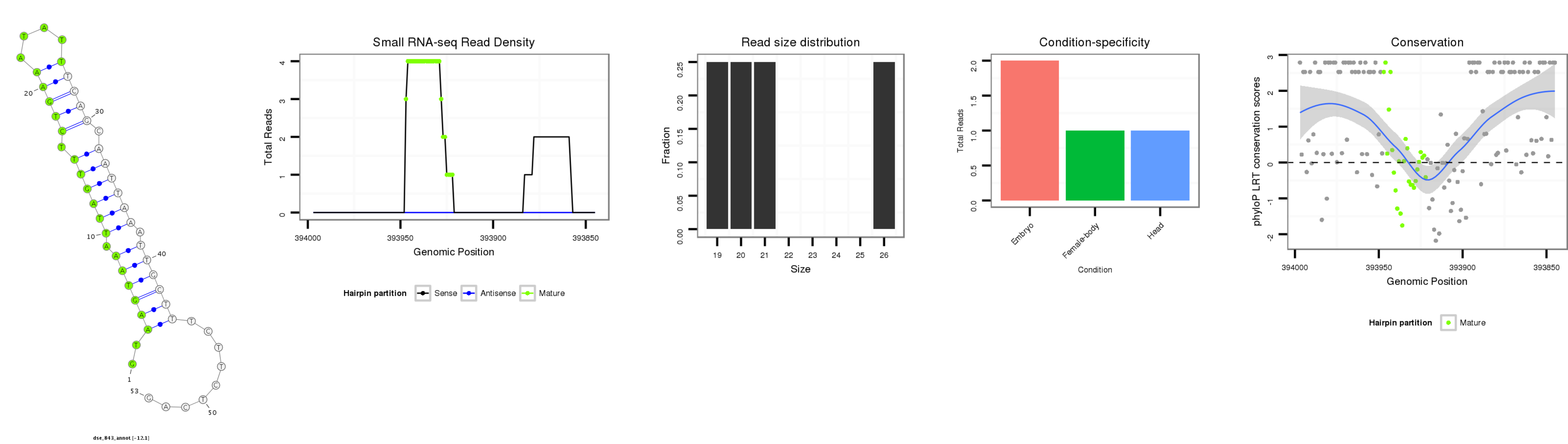
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PASS/FAIL	
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crit.mor	0
crit.hair	0
crit.total	0
crit.pairing	1
crit.tps3	1
crit.tps3	1
crit.tps3	1
crit.back	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	7
rescue.candidate	5

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dse_843	scaffold_14:393895-393947 -	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 annotation

intron [Dsec/GM16671-in]; CDS [Dsec/GM16671-cds]; CDS [Dsec/GM16671-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

Read #	Read size	Mismatch	Hit Count	Total Norm	Total	V114 embryo	M054 female body	V115 head
26	0	1	1.00	1	1	1	0	0
26	0	1	1.00	1	0	0	1	1
21	0	1	1.00	1	0	0	1	1
19	0	1	1.00	1	1	0	0	0
20	0	1	1.00	1	0	1	0	0
20	0	1	1.00	1	0	1	0	0
22	1	1	1.00	1	1	0	0	0

Anti-sense strand reads

Read #	Read size	Mismatch	Hit Count	Total Norm	Total	M054 female body
26	0	1	1.00	1	1	0
21	0	1	1.00	1	0	1
19	0	1	1.00	1	1	0
20	0	1	1.00	1	0	1
20	0	1	1.00	1	0	1
22	1	1	1.00	1	1	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

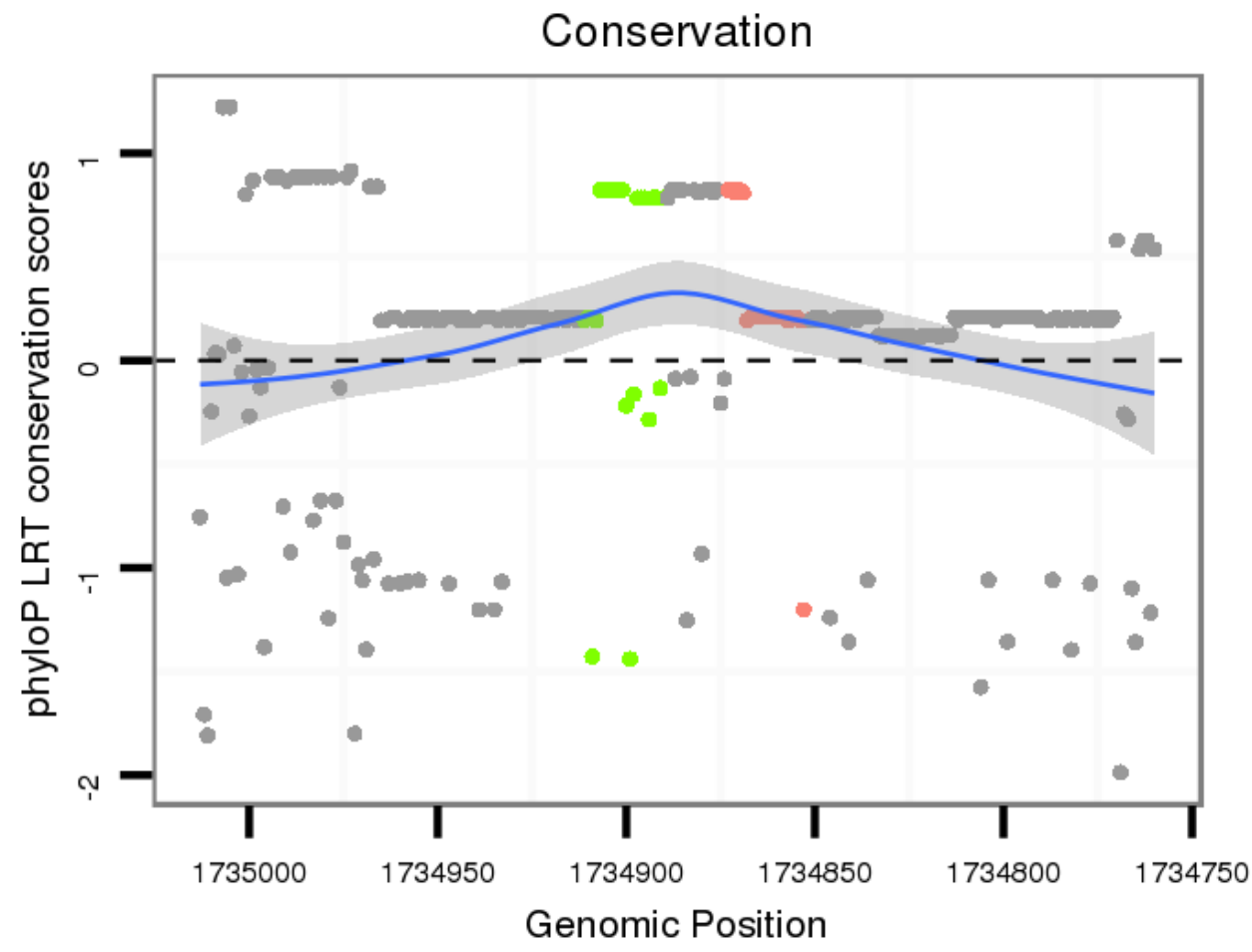
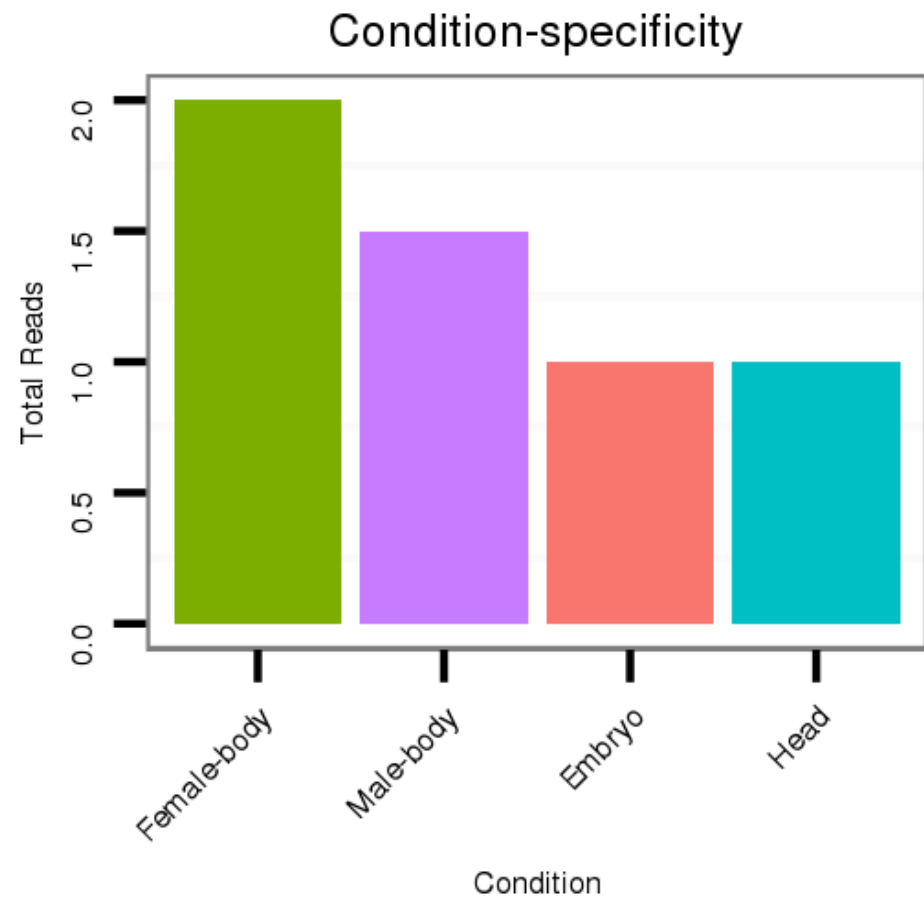
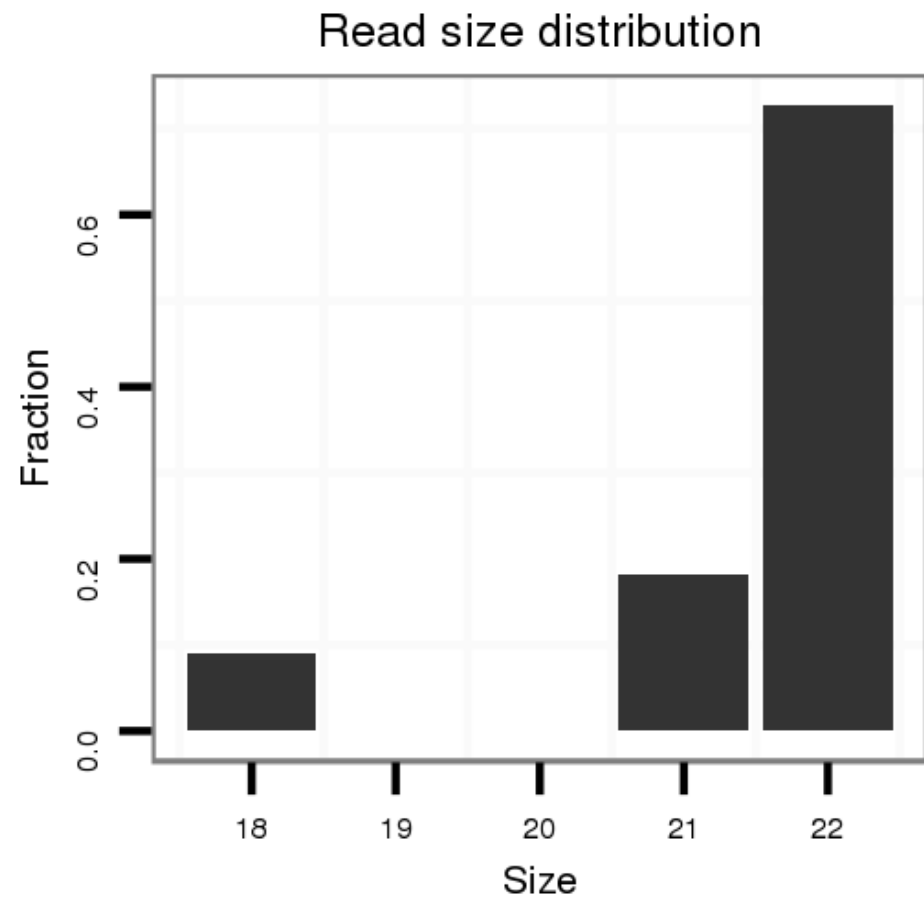
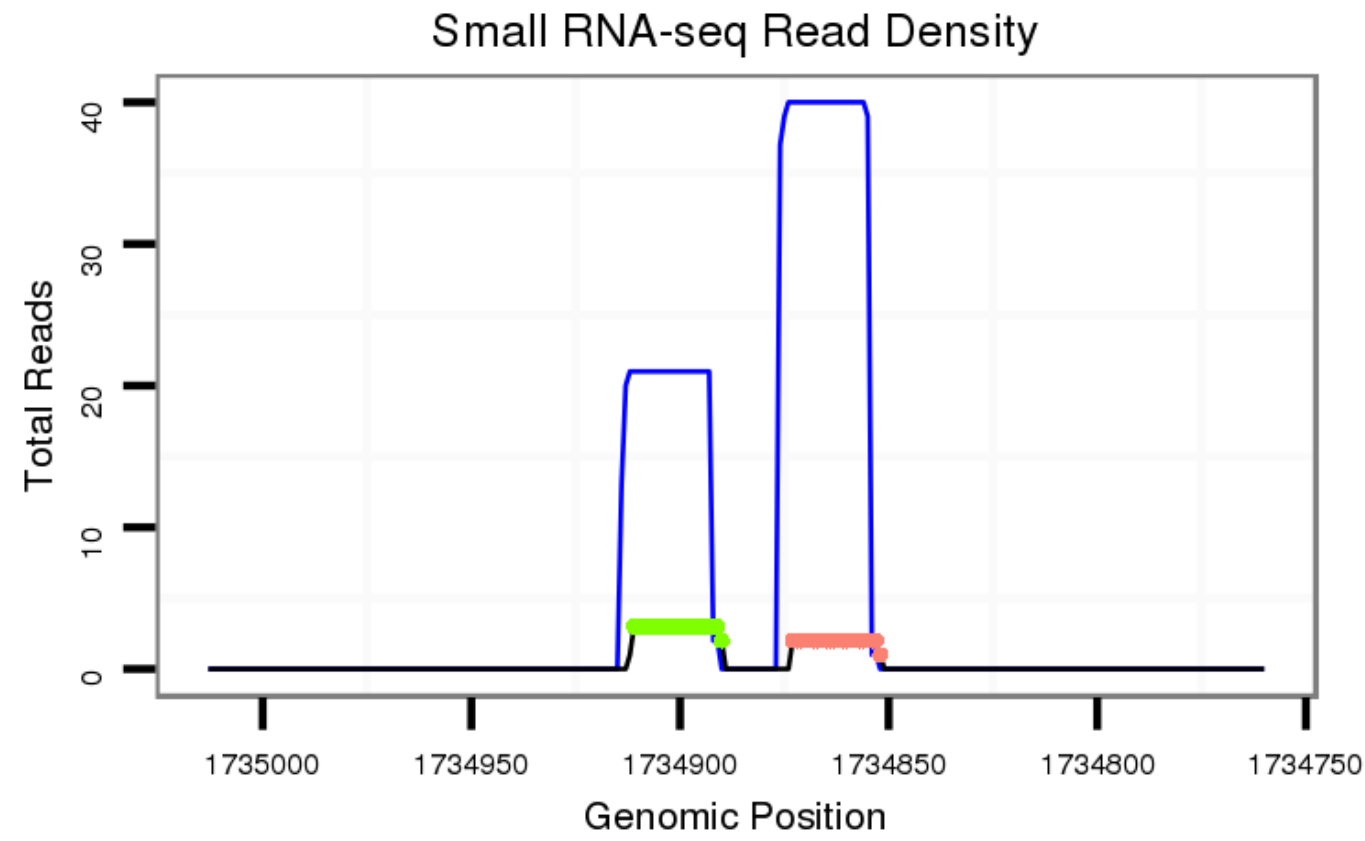
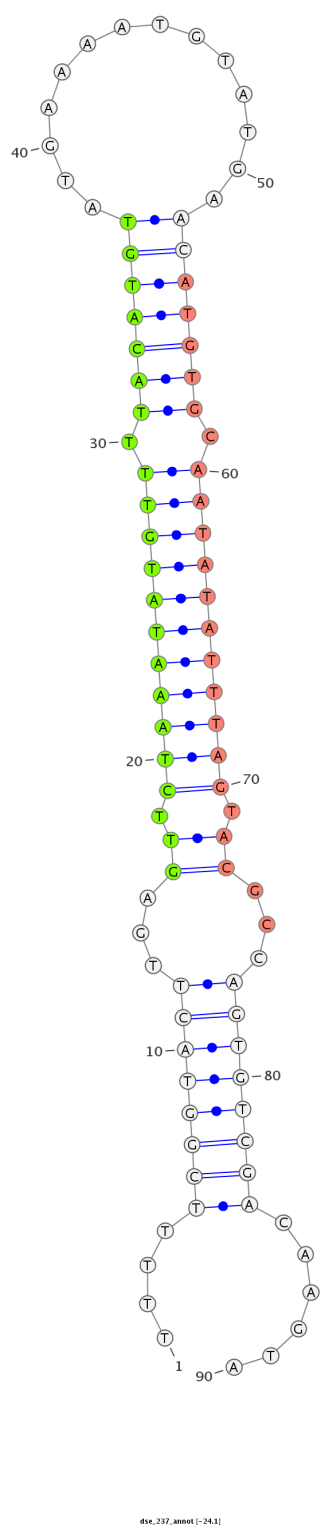
Species	Coordinate	ID	Alignment
droSec2	scaffold_14:393845-393997 -	dse_843	TTGGACGATTAGGCCCTTTTCTACGGCAACAAGACACAGGTTC
droSim2	21:382778-382930 -	ds1_15240	TTGGACGATTAGGCCCTTTTCTACGGCAACAAGACACAGGTTC
dm3	chr2L:410024-410176 -	dme_468	TTGGACGATTAGGCCCTTTTCTACGGCAACAAGACACAGGTTC
droBre2	scaffold_4929:461459-461615 -		TTGGACGATTAGGCCCTTTTCTACGGCAACAAGACACAGGTTC
droYak3	2L:393777-393933 -	dya_1818	TTGGACGATTAGGCCCTTTTCTACGGCAACAAGACACAGGTTC
droEug1	scf7180000409554:1138894-1139053 +		TTGGACGATTAGGCCCTTTTCTACGGCAACAAGACACAGGTTC
droBial	scf7180000403261:3431374-3431532 +		TTGGACGATTAGGCCCTTTTCTACGGCAACAAGACACAGGTTC
droTak1	scf7180000413017:107409-107573 +		TTGGACGATTAGGCCCTTTTCTACGGCAACAAGACACAGGTTC
droEl1	scf7180000491026:426398-427165 +		TTGGACGATTAGGCCCTTTTCTACGGCAACAAGACACAGGTTC
droRhol	scf7180000779917:25448-254606 +		TTGGACGATTAGGCCCTTTTCTACGGCAACAAGACACAGGTTC
droFic1	scf7180000453904:679991-680153 -		TTGGACGATTAGGCCCTTTTCTACGGCAACAAGACACAGGTTC
droKik1	scf7180000302270:751691-751854 +		TTGGACGATTAGGCCCTTTTCTACGGCAACAAGACACAGGTTC
droAna3	scaffold_12943:4843899-4844062 +		TTGGACGATTAGGCCCTTTTCTACGGCAACAAGACACAGGTTC
droBip1	scf7180000395654:190695-190859 -		TTGGACGATTAGGCCCTTTTCTACGGCAACAAGACACAGGTTC
dp5	4_group3:1223673-1223835 +		TTGGACGATTAGGCCCTTTTCTACGGCAACAAGACACAGGTTC
droPer2	scaffold_1:2694498-2694660 +		TTGGACGATTAGGCCCTTTTCTACGGCAACAAGACACAGGTTC
droWil2	scf2_1100000004585:2794455-2794616 +		TTGGACGATTAGGCCCTTTTCTACGGCAACAAGACACAGGTTC
droVir3	scaffold_12963:18812043-18812203 -		TTGGACGATTAGGCCCTTTTCTACGGCAACAAGACACAGGTTC
droMoj3	scaffold_6500:24357048-24357209 +		TTGGACGATTAGGCCCTTTTCTACGGCAACAAGACACAGGTTC
droGr12	scaffold_15252:6728532-6728696 -		TTGGACGATTAGGCCCTTTTCTACGGCAACAAGACACAGGTTC

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

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Hairpin partition Sense Antisense Mature Star

Hairpin partition Mature Star

Show Alternate Folds

Flybase annotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

[illegible]

Anti-sense strand reads

										V13	V15	M054	V14
										male	head	female	embryo
TTCATATATCATAGGAACATATCGTATCTTACATATTACATATTACCATCGTACTACAAGCACAAGGGGCAAGGCTACAAGTAAAAAGCCATGAAC	Read #	Hit	Total										
CAAGATTATACAAATGTAC	size	Count	Norm	Total	body								
.....(((((((.....))))))))).....*****	Mismatch												
.....(((.....)))))).....	22	0	2	36.00	72	48	14	4					
.....TGTACAGGTTATATAAATCAT.....	22	0	1	13.00	13	11	0	2					
.....ACTCAAGATTATACAAATGT.....	22	0	1	6.00	6	6	0	0					
.....CTCAAGATTATACAAATGT.....	21	0	2	2.00	4	4	0	0					
.....TGTACAGGTTATATAAATCAT.....	21	0	2	1.50	3	2	1	0					
.....TTGTACAGTTATATAAATCA.....	22	0	1	1.00	1	1	0	0					
.....TCAAGATTATACAAATGTAC.....	22	0	1	1.00	1	0	0	0					
.....GTACAGGTTATATAAATCATGCG.....	22	0	1	1.00	1	0	0	0					
.....CTCAAGATTATACAAATGTAC.....	22	0	1	1.00	1	0	0	0					
.....TGTACAGGTTATATAAATCA.....	20	0	2	0.50	1	1	0	0					
.....GTACAGGTTATATAAATCAT.....	20	0	2	0.50	1	1	0	0					
.....TGTACAGGTTATATAAATC.....	20	0	2	0.50	1	1	0	0					
.....TTGTACAGGTTATATAAATC.....	20	0	2	0.50	1	0	0	1					
.....TTGTACAGGTTATATAAATCAT.....	23	1	2	0.50	1	0	0	1					

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droSec2	scaffold_8:1734760-1735013_	dae_237_	AAGTATATAGTATCCCTTCGTATGACATATAGAAATGTATAATGTATAATGGGTAGCATGATG-----TTCGTGTTCTCC-CGTTTCGATGTTCAATTTTCGGTACTTGA GTCTCAAAATATGTTTACATGT ATGAAATGTATGAAC ATGTGCAATATATTAGTAGCG CAGTGTGCAAGATATATAGTATCCTTCGCATAACAATACATATATA-----ATGTACAATATAATGGGTAGCAAGATGCTCGTGT--TCTCCCGTTTC
droSim2	x:18341880-18342131_		AAGTATATAGTATCCCTTCGTATGACATATAGAAATGTATAATGTATAATGGGTAGCATGATG-----TTCGTGTTCTCC-CGTTTCGATGTTCAATTTTCGGTACTTGA GCTCAAAATATGATTACATGT ATGAAATGTATGAAC ATGTGCAATATATTAGTAGCG CAGTGTGCAAGATATATAGTATCCTTCGCATAACAATACATATATA SA -----ATGTACAATATAATGGGTAGCAAGATGCTCGTGT--TCTCCCGTTTC
dm3	chrX:19452505-19452786_	dme_470_	AAATATATAGTATCCCTTCGTATGACATATAGAAATGTATAATGTATAATGGGTAGCATGATG-----TTCGTGTTCTCC-CGTTTCGATGTTCAATTTTCGGTACTTGA GCTCAAAATATGATTACATGT ATGAAATGTATGAAC ATGTGCAATATATTAGTAGCG CAGTGTGCAAGATATATAGTATCCTTCGCATAACAATACATATATA SA -----ATGTACAATATAATGGGTAGCAAGATGCTCGTGT--TCTCCCGTTTC
droEr2	scaffold_4690:9688725-9688737_		GT ----- TCGCAATATATTAGTAGCG CAGTGTGCAAGATATATAGTATCCTTCGCATAACAATACATATATA SA -----ATGTACAATATAATGGGTAGCAAGATGCTCGTGT--TCTCCCGTTTC
droYak3	X:11886165-11886205_		AAATATAGTATCCCTTCGTATGACATATAGAAATGTATAATGTATAATGGGTAGCATGATG-----TTCGTGTTCTCC-CGTTTCGATGTTCAATTTTCGGTACTTGA GCTCAAAATATGATTACATGT ATGAAATGTATGAAC ATGTGCAATATATTAGTAGCG CAGTGTGCAAGATATATAGTATCCTTCGCATAACAATACATATATA SA -----ATGTACAATATAATGGGTAGCAAGATGCTCGTGT--TCTCCCGTTTC
droTak1	scf71800000415169:845110-845122_		GT ----- TCGCAATATATTAGTAGCG CAGTGTGCAAGATATATAGTATCCTTCGCATAACAATACATATATA SA -----ATGTACAATATAATGGGTAGCAAGATGCTCGTGT--TCTCCCGTTTC
droWil2	scf2_11000000004511:567451-567501_		GT ----- TCGCAATATATTAGTAGCG CAGTGTGCAAGATATATAGTATCCTTCGCATAACAATACATATATA SA -----ATGTACAATATAATGGGTAGCAAGATGCTCGTGT--TCTCCCGTTTC
droMo3	scaffold_6540:29855275-29855321_		AG ATATAGTATCCCTTCGTATGACATATAGAAATGTATAATGTATAATGGGTAGCATGATG-----TTCGTGTTCTCC-CGTTTCGATGTTCAATTTTCGGTACTTGA GCTCAAAATATGATTACATGT ATGAAATGTATGAAC ATGTGCAATATATTAGTAGCG CAGTGTGCAAGATATATAGTATCCTTCGCATAACAATACATATATA SA -----ATGTACAATATAATGGGTAGCAAGATGCTCGTGT--TCTCCCGTTTC

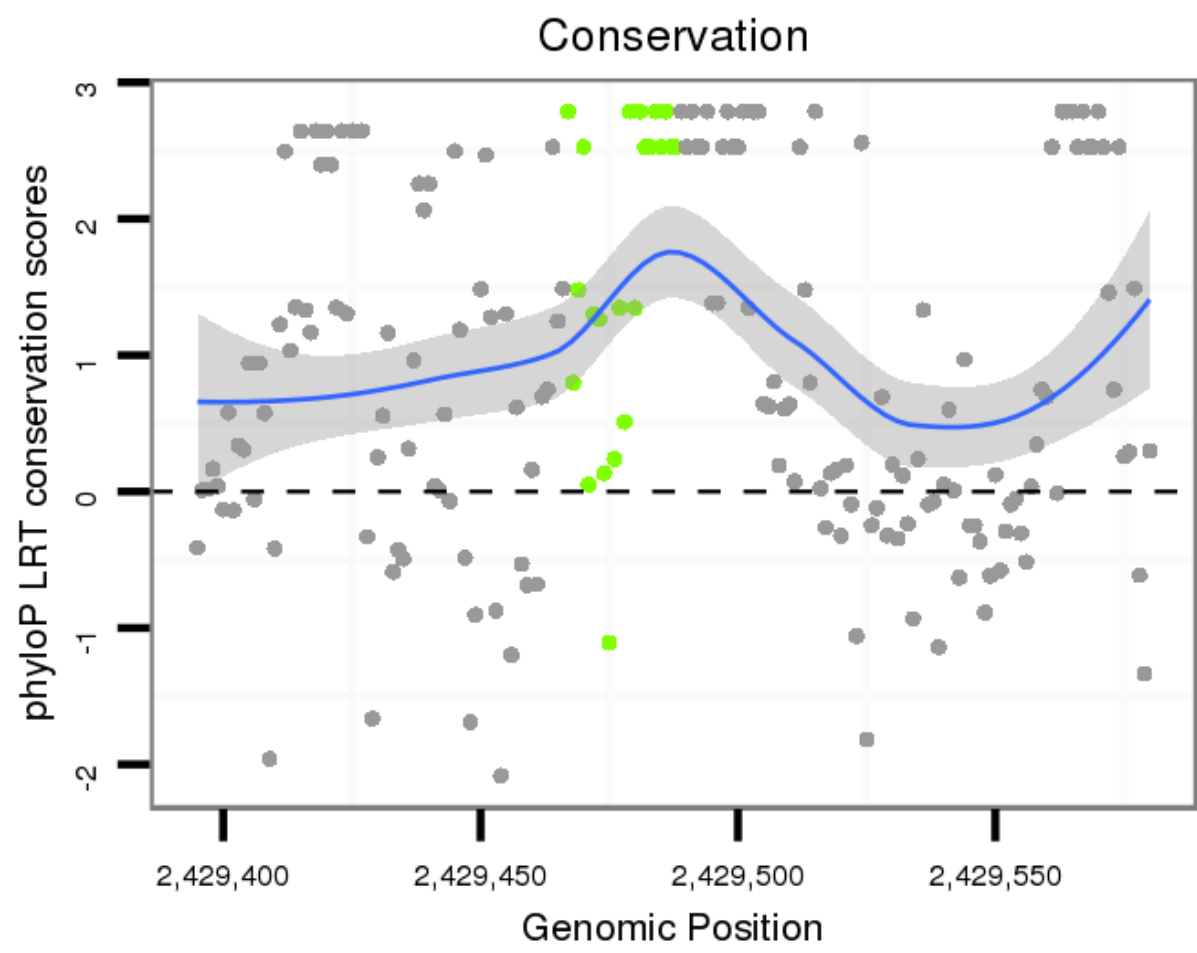
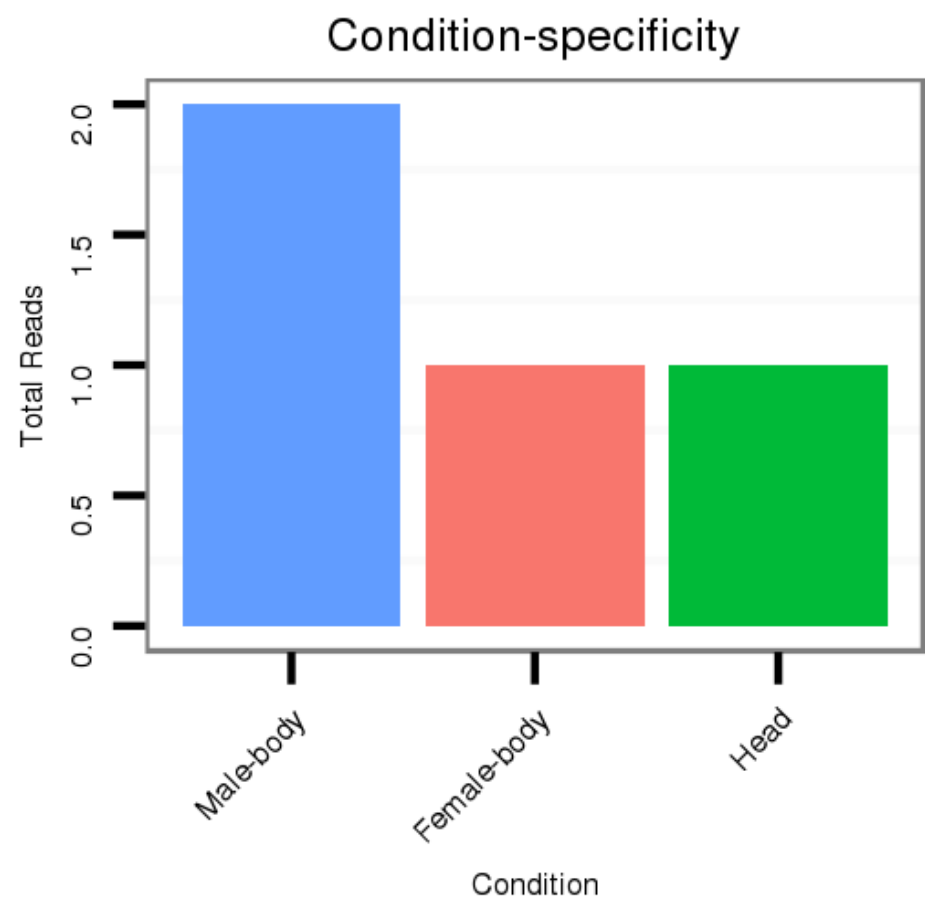
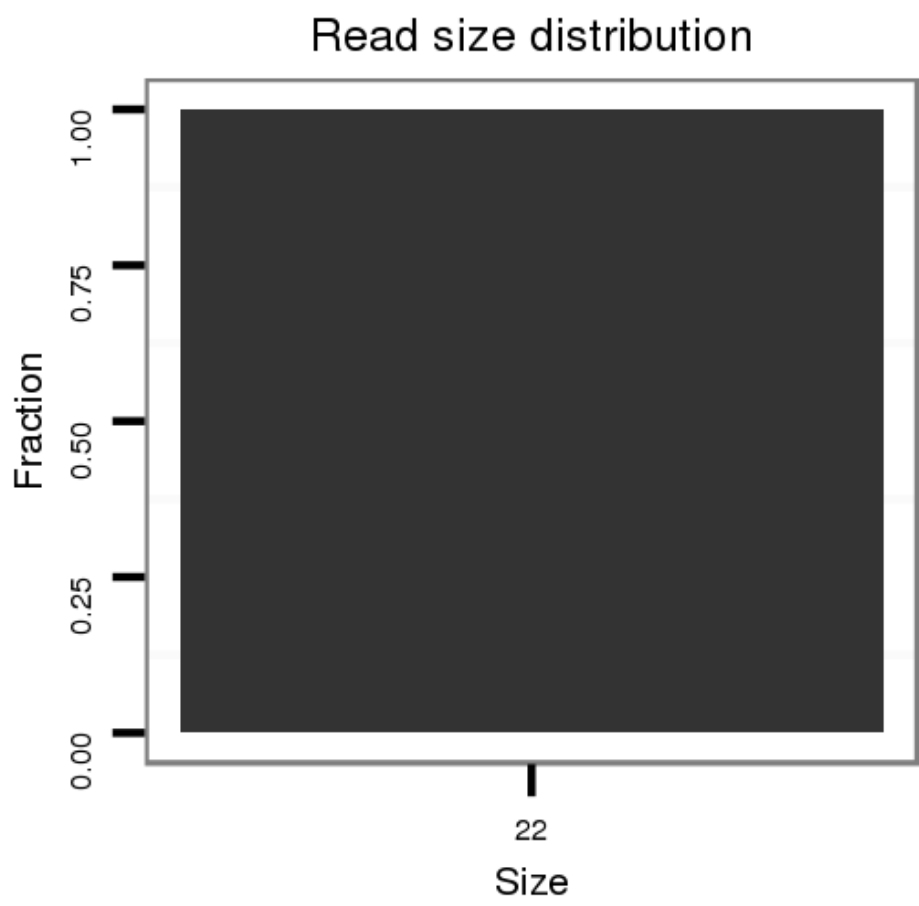
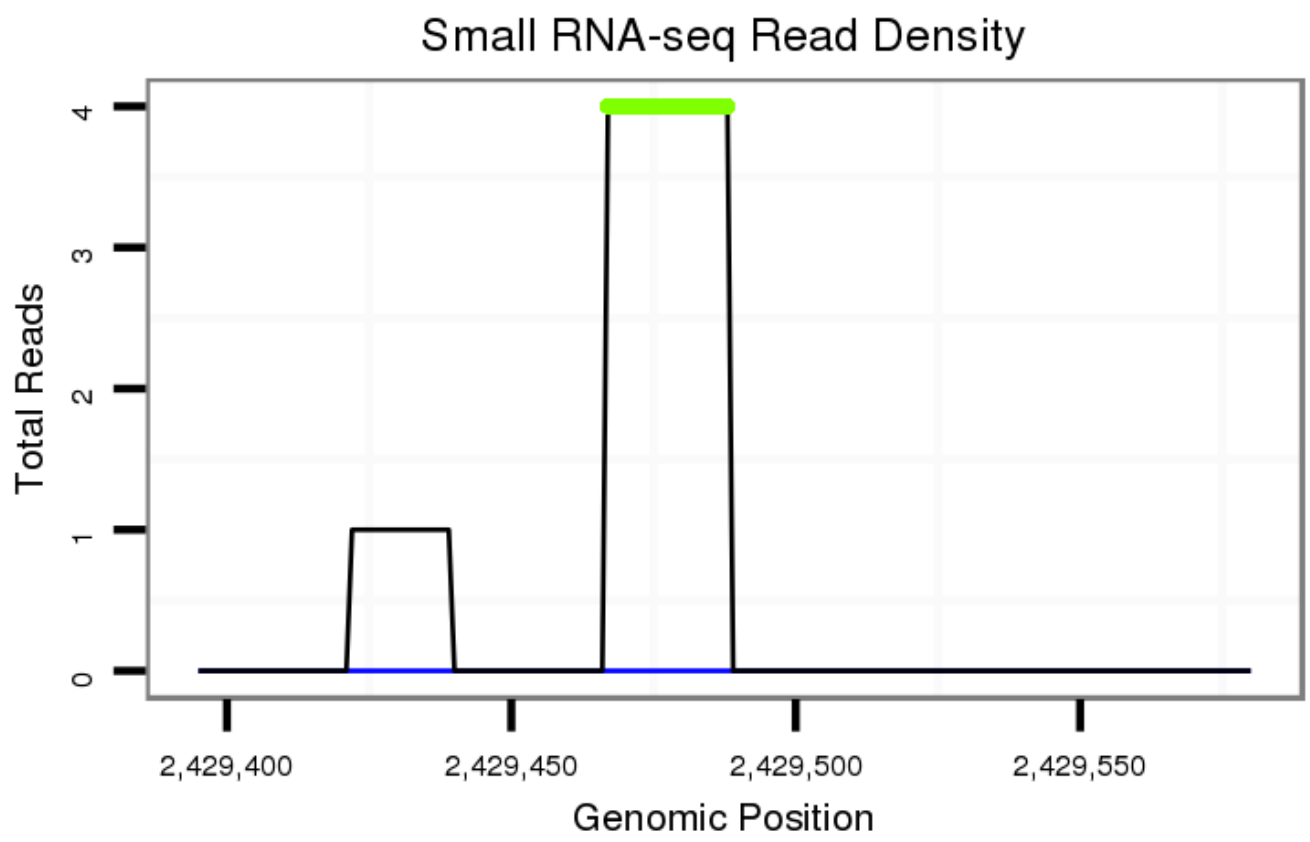
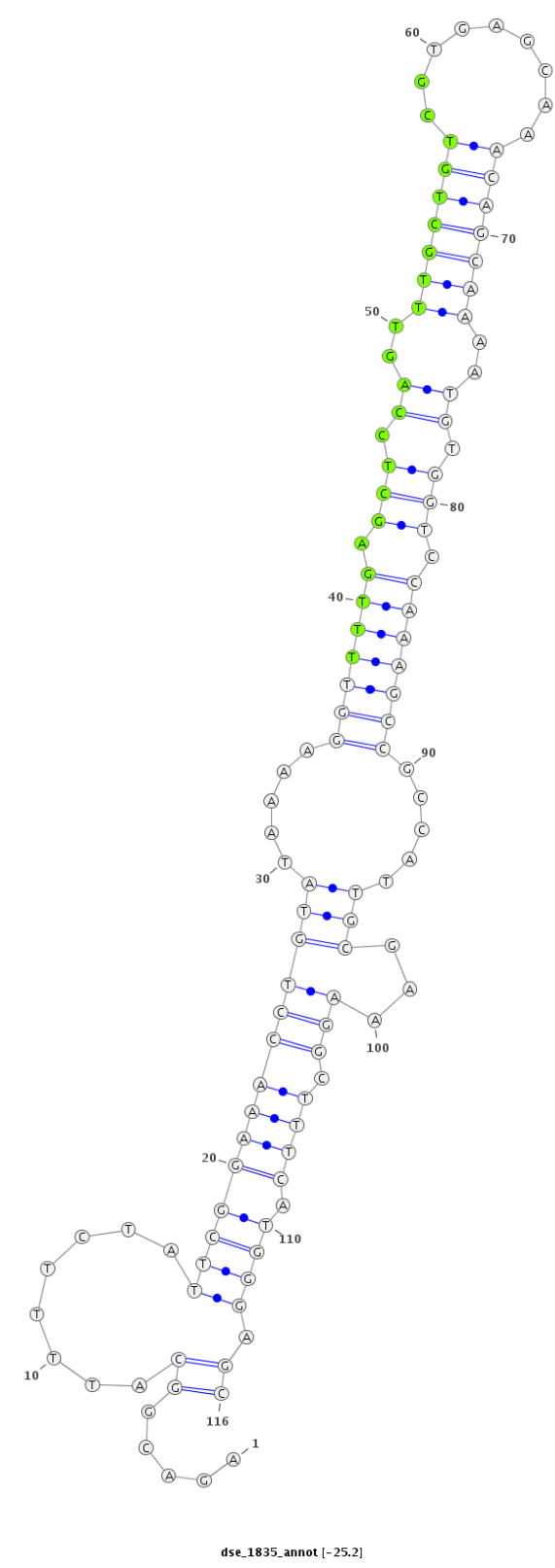
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crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dse_1835	scaffold_1:2429445-2429530 +	candidate	Canonical miRNA	3pUTR	[View on UCSC Genome Browser (Cornell Mirror)]

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Hairpin partition ■ Sense ■ Antisense ■ Mature

Hairpin partition ■ Mature

Show Alternate Folds

Flybase annotation

utr3 [utr3_plus_1952]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

					V113	M054	V114	V115
					male	female	embryo	head
Read #	Hit	Total			body	body		
size	Mismatch	Count	Norm	Total	body	body		
ACGTTTACTTAGTAGCAAGAATCACACGTTTTTCGACAGGGCATTTTCTATTTCGGAACCTGTATAAAAGGTTTGAGCTCCAGTTTGCTGTCTGTAGACAAACAGCAAAATGTGGTCCAAAGCCGCCATTCGAAAGGCTTTCATGGGAGCGCGGCCCATCAATCGAAACTGCAGTCGGTTTAGC								
*****(((((.....(((((((((((.....(((((((.(.(((.....)))))))).)).))))).))*****								
.....TTTGAGCTCCAGTTTGCTGTCTG.....								
.....GTTTTTCGACAGCGGCATT.....								
.....								

Anti-sense strand reads

TCGCAAAATGAATCATCGTCTCTAGTGTGCAAAAACGCTCGCGTAAAGATAAAGCCTTTGGACATATTTTCCA	AAACTCTGAGGTCAAACGACAGC	ACTCGTTTGTGCGTTTACACCAAGGTTTCGGCGGTAACGCTTTCCGAAAGTACCTTCGGCGCGGGGTAGTTAGCTTTGACGTCAGCCAATGC	Read #	Hit	Total	
*****(((((.....(((((((((((.....(((((((.(.(((.....)))))))).)).))))).))*****	size	Mismatch	Count	Norm	Total	Total
No data available in table						

Show Alignment With Reads

Re-alignment of all predicted orthologs

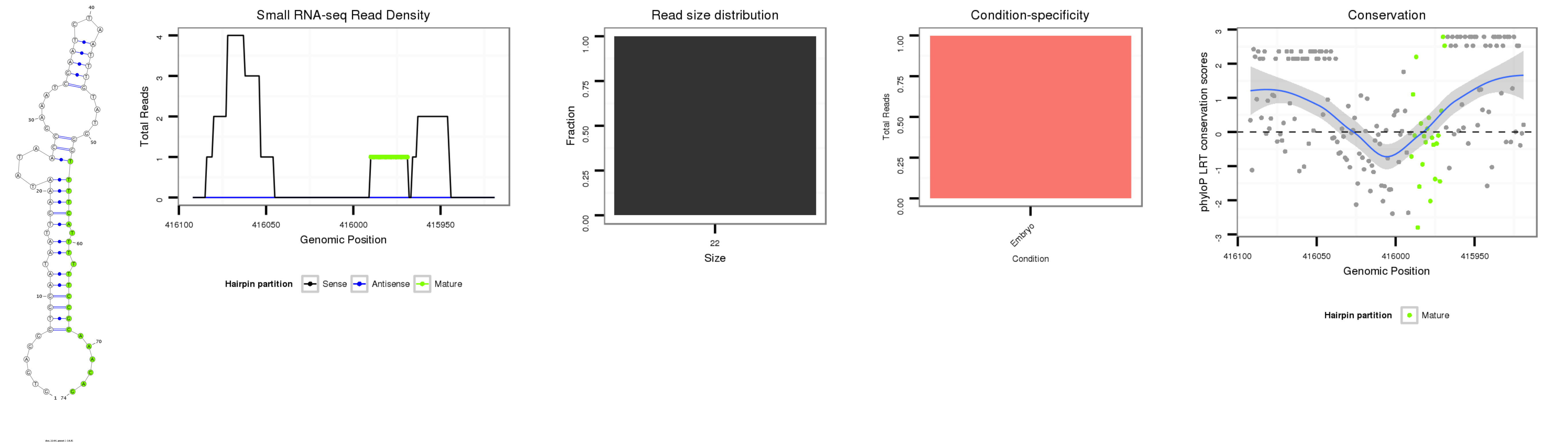
Species	Coordinate	ID	Alignment
droSec2	scaffold1_1:2429395-2429580 +	dse_1835	ACG-TT---TACTTAGTAG-CAAGAATCACACGTTTTTGC--A-----GACGGCAT--TTT-----CTATTTCGG---AAA-CCTGTATA-A-----AAGGT TTTGAGCTCCAGTTTGCTGTCTG TGAGCAAAACAGCAAAATGTGGTCCAAAGCCGCCA-----TTGCG-----AAAG-----GC-----T--TTCATGGGAGCCCGCGC-----CCCAT-CAATCGAAACTGCAGT-CGGTTACG---
droSim2	2x:5600449-5600634 +	dsi_32438	ACG-TT---TACTTAGTAG-CAAGAATCACACGTTTTTGC--A-----GACGGCAT--TTT-----CTATTTCGG---AAA-CCTGTATA-A-----AAGGT TTTGAGCTCCAGTTTGCTGTCTG TGAGCAAAACAGCAAAATGTGGTCCAAAGCCGCCA-----TTGCG-----AAAG-----GC-----T--TTCATGGGAGCCCGCGC-----CCCAT-CAATCGAAACTGCAGT-CGGTTACG---
dm3	chr2R:4791612-4791794 +	dme_379	ACG-TT---TACTTAGTAG-CAAGAATCACACGTTTTTGC--A-----GACGGCAT--TTT-----CTATTTCGG---AAA-CCTGTATA-A-----AAGGT TTTGAGCTCCAGTTTGCTGTCTG TGAGCAAAACAGCAAAATGTGGTCCAAAGCCGCCA-----TTGCG-----AAAG-----GC-----T--TTCATGGGAGCCCGCGC-----CCCAT-CAATCGAAACTGCAGT-CGGTTACG---
droEre2	scaffold4_4929:17858137-17858312 -	der_75	GCG-TT---TACTTAGTAG-CAAGAATCACACATTTTTCG--A-----GACGGCAT--TTT-----CTATTTCGG---AAA-CCTGTATA-A-----AAGGT TTTGAGCTCCAGTTTGCTGTCTG TGAGCAAAACAGCAAAATGTGGTCCAAAGCCGCCA-----TTGCG-----AAAG-----GC-----T--TTCATGGGAGCCCGCGC-----CCCAT-CAATCGAAACTGCAGT-CGGTTACG---
droYak3	2L:17449448-17449623 +	dya_1784	GCG-TT---TACTTAGTAG-CAAGAATCACACATTTTTCG--A-----GACGGCAT--TTT-----CTATTTCGG---AAA-CCTGTATA-A-----AAGGT TTTGAGCTCCAGTTTGCTGTCTG TGAGCAAAACAGCAAAATGTGGTCCAAAGCCGCCA-----TTGCG-----AAAG-----GC-----T--TTCATGGGAGCCCGCGC-----CCCAT-CAATCGAAACTGCAGT-CGGTTACG---
droEug1	scf7180000409183:445681-445854 +		GAG-TG---C-----AG-CAAGAATCACACATTTTTCG--A-----GACGGCAT--TTT-----CTATTTCGG---AAA-CCTGTATA-A-----AAGGT TTTGAGCTCCAGTTTGCTGTCTG TGAGCAAAACAGCAAAATGTGGTCCAAAGCCGCCA-----TTGCG-----AAAG-----GC-----T--TTCATGGGAGCCCGCGC-----CCCAT-CAATCGAAACTGCAGT-CGGTTACG---
droBial	scf7180000302291:2735848-2736014 +		GAG-TG---C-----AA-CAAGAATCACACATTTTTCG--A-----GACGGCAT--TTT-----CTATTTCGG---AAA-CCTGTATA-A-----AAGGT TTTGAGCTCCAGTTTGCTGTCTG TGAGCAAAACAGCAAAATGTGGTCCAAAGCCGCCA-----TTGCG-----AAAG-----GC-----T--TTCATGGGAGCCCGCGC-----CCCAT-CAATCGAAACTGCAGT-CGGTTACG---
droTak1	scf7180000415386:451363-451535 -		AGAGTG---C-----AA-CAAGAATCACACATTTTTCG--A-----GACGGCAT--TTT-----CTATTTCGG---AAA-CCTGTATA-A-----AAGGT TTTGAGCTCCAGTTTGCTGTCTG TGAGCAAAACAGCAAAATGTGGTCCAAAGCCGCCA-----TTGCG-----AAAG-----GC-----T--TTCATGGGAGCCCGCGC-----CCCAT-CAATCGAAACTGCAGT-CGGTTACG---
droEle1	scf7180000490483:67747-67915 -		GAG-TG---C-----AA-CAAGAATCACACATTTTTCG--A-----GACGGCAT--TTT-----CTATTTCGG---AAA-CCTGTATA-A-----AAGGT TTTGAGCTCCAGTTTGCTGTCTG TGAGCAAAACAGCAAAATGTGGTCCAAAGCCGCCA-----TTGCG-----AAAG-----GC-----T--TTCATGGGAGCCCGCGC-----CCCAT-CAATCGAAACTGCAGT-CGGTTACG---
droRho1	scf7180000780108:150187-150354 +		GAG-AA---C-----AC-CAAGAATCACACATTTTTCG--A-----GACGGCAT--TTT-----CTATTTCGG---AAA-CCTGTATA-A-----AAGGT TTTGAGCTCCAGTTTGCTGTCTG TGAGCAAAACAGCAAAATGTGGTCCAAAGCCGCCA-----TTGCG-----AAAG-----GC-----T--TTCATGGGAGCCCGCGC-----CCCAT-CAATCGAAACTGCAGT-CGGTTACG---
droFic1	scf7180000453851:1506165-1506336 -		TAG-TG---C-----AC-CAAGAATCACACATTTTTCG--A-----GACGGCAT--TTT-----CTATTTCGG---AAA-CCTGTATA-A-----AAGGT TTTGAGCTCCAGTTTGCTGTCTG TGAGCAAAACAGCAAAATGTGGTCCAAAGCCGCCA-----TTGCG-----AAAG-----GC-----T--TTCATGGGAGCCCGCGC-----CCCAT-CAATCGAAACTGCAGT-CGGTTACG---
droKik1	scf7180000302682:1354886-1355065 +		GAG-TGAGAAC-----TC-CAAGAATCACACATTTTTCG--A-----GACGGCAT--TTT-----CTATTTCGG---AAA-CCTGTATA-A-----AAGGT TTTGAGCTCCAGTTTGCTGTCTG TGAGCAAAACAGCAAAATGTGGTCCAAAGCCGCCA-----TTGCG-----AAAG-----GC-----T--TTCATGGGAGCCCGCGC-----CCCAT-CAATCGAAACTGCAGT-CGGTTACG---
droAna3	scaffold4_13266:1225288-1225478 -	dan_4056	GAG-TT---TACTTA-----CAAGAATCACACATTTTTCG--A-----GACGGCAT--TTT-----CTATTTCGG---AAA-CCTGTATA-A-----AAGGT TTTGAGCTCCAGTTTGCTGTCTG TGAGCAAAACAGCAAAATGTGGTCCAAAGCCGCCA-----TTGCG-----AAAG-----GC-----T--TTCATGGGAGCCCGCGC-----CCCAT-CAATCGAAACTGCAGT-CGGTTACG---
droBip1	scf7180000396730:2224846-2225050 -		GAG-TT---TACTTA-----CAAGAATCACACATTTTTCG--A-----GACGGCAT--TTT-----CTATTTCGG---AAA-CCTGTATA-A-----AAGGT TTTGAGCTCCAGTTTGCTGTCTG TGAGCAAAACAGCAAAATGTGGTCCAAAGCCGCCA-----TTGCG-----AAAG-----GC-----T--TTCATGGGAGCCCGCGC-----CCCAT-CAATCGAAACTGCAGT-CGGTTACG---
dp5	3:113606079-13606257 -	dps_3844	AAA-TT---AATTA-----CAAGAATCACACATTTTTCG--A-----GACGGCAT--TTT-----CTATTTCGG---AAA-CCTGTATA-A-----AAGGT TTTGAGCTCCAGTTTGCTGTCTG TGAGCAAAACAGCAAAATGTGGTCCAAAGCCGCCA-----TTGCG-----AAAG-----GC-----T--TTCATGGGAGCCCGCGC-----CCCAT-CAATCGAAACTGCAGT-CGGTTACG---
droPer2	scaffold4_2:8013574-8013752 +		AAA-TT---AATTA-----CAAGAATCACACATTTTTCG--A-----GACGGCAT--TTT-----CTATTTCGG---AAA-CCTGTATA-A-----AAGGT TTTGAGCTCCAGTTTGCTGTCTG TGAGCAAAACAGCAAAATGTGGTCCAAAGCCGCCA-----TTGCG-----AAAG-----GC-----T--TTCATGGGAGCCCGCGC-----CCCAT-CAATCGAAACTGCAGT-CGGTTACG---
droW112	scf2_1100000004510:2696663-2696874 -	dwi_5429	ATT-AT---TGCCTAGTAGAGAA-CAACACACATTTTTCG--A-----GACGGCAT--TTT-----CTATTTCGG---AAA-CCTGTATA-A-----AAGGT TTTGAGCTCCAGTTTGCTGTCTG TGAGCAAAACAGCAAAATGTGGTCCAAAGCCGCCA-----TTGCG-----AAAG-----GC-----T--TTCATGGGAGCCCGCGC-----CCCAT-CAATCGAAACTGCAGT-CGGTTACG---
droVir3	scaffold1_12875:1774792-1774976 +	dvi_24661	G-- -- -- -- --AATCACACATTTTTCG--A-----GACGGCAT--TTT-----CTATTTCGG---AAA-CCTGTATA-A-----AAGGT TTTGAGCTCCAGTTTGCTGTCTG TGAGCAAAACAGCAAAATGTGGTCCAAAGCCGCCA-----TTGCG-----AAAG-----GC-----T--TTCATGGGAGCCCGCGC-----CCCAT-CAATCGAAACTGCAGT-CGGTTACG---
droMor3	scaffold4_6496:13717199-13717331 -	dmo_3156	AA-- -- -- -- --AATCACACATTTTTCG--A-----GACGGCAT--TTT-----CTATTTCGG---AAA-CCTGTATA-A-----AAGGT TTTGAGCTCCAGTTTGCTGTCTG TGAGCAAAACAGCAAAATGTGGTCCAAAGCCGCCA-----TTGCG-----AAAG-----GC-----T--TTCATGGGAGCCCGCGC-----CCCAT-CAATCGAAACTGCAGT-CGGTTACG---
droGr12	scaffold1_15112:3869016-3869173 +		AAA-GT---TATTA-----CAAGAATCACACATTTTTCG--A-----GACGGCAT--TTT-----CTATTTCGG---AAA-CCTGTATA-A-----AAGGT TTTGAGCTCCAGTTTGCTGTCTG TGAGCAAAACAGCAAAATGTGGTCCAAAGCCGCCA-----TTGCG-----AAAG-----GC-----T--TTCATGGGAGCCCGCGC-----CCCAT-CAATCGAAACTGCAGT-CGGTTACG---

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PASS/FAIL	
crit.star	0
crit.loop	0
crit.mor	0
crit.hair	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tpot3	0
crit.un	0
crit.back	1
rescue.total	0
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	5

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Show Alternate Folds

Flybase annotation

intron [Dsec\GM16468-in]; CDS [Dsec\GM16468-cds]; CDS [Dsec\GM16468-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

						V113	V115	M054	V114
AGTGCTGTGACGAGATGCTGGATTGCTGTCGTCTCTGGGTATTGGTACCAGGTGAGGGTGAATAATTGAAATATAACGAAATCGAATCTAATTGTATGGCTTTTCATTTTTTCCGCCAAACAGCTGGTGCAAACACGATGAATCGCACAGAATCTACGTATTTCTGGGGC	Read #		Hit	Total		male	V115	female	V114
***** (((((((((((((... (((... ((((((...)))))))))...)))))))).)))))))). *****	size	Mismatch	Count	Norm	Total	body	head	body	embryo
.....TTTTTCATTTTTTCCGCCAAACAGT.....	23	1	1	6.00	6	0	1	2	3
.....GATTGCTGTGCTTCGTTCTGGGT.....	19	0	1	2.00	2	2	0	0	0
.....TTTTTCATTTTTTCCGCCAAACAGT.....	22	1	1	1.00	1	0	1	0	0
.....GCAAAACACGATGAATCG.....	18	0	1	1.00	1	0	0	0	1
.....TTTTTCATTTTTTCCGCCAAACAGT.....	23	1	1	1.00	1	0	0	0	1
.....GGTGCAAACACGATGAATCGC.....	22	0	1	1.00	1	0	0	0	1
.....TTTTTCATTTTTTCCGCCAAACAG.....	22	0	1	1.00	1	0	0	0	1
.....GTGCTTCTGGGTATTGGTAC.....	20	0	1	1.00	1	0	0	0	1
.....GAGCAGATGCTGGATTGCT.....	19	0	1	1.00	1	0	0	0	1
.....AGATGCTGGATTGCTGTCT.....	18	0	1	1.00	1	0	0	0	1

Anti-sense strand reads

TACGACACTCTGCTACGACCTAACGACAGCAAGACCCATAACCATGGTCCACTCCCACCTTATTAACCTTTATATGGCTTTAGCTTAGATTAAACATACCC AAAGTAAAAAGCGCTTTGTCG GACCACGTTTGTGCTACTTAGCTGTGCTTAGATGCATAAAGACCCCG	Read #	Hit	Total
*****.(((((((.(.(((((.(((.....(((.....(((.....)))))).....)))))).)).)))).*****	size	Mismatch	Count
No data available in table	Norm	Total	Total

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droSec2	scaffold 29:415919-416092	dse_1144	AGTGCCTGTGAGCAGATGCTGGATTGCTGCTGTTCTGGGTATTGGTACCAGGTGAGGGTGGAAATAATTGA-----AAATAACCGAAAT---CGAATCTAA-----T-TTGTAATGGGTTTTCAT-----TTTTTCGCAAAACAGCTGGTGCAAAACACGATGAATCGCACAGGAATCTACGTATTCTCTGGGGGC
droSim2	31:19363380-19363543	dsi_6715	AGTGCCTGTGAGCAGATGCTGGAGTGCCTGCTTCTGGGTATTGGTACCAGGTGAGGGTGGAGCTATTGA-----AAATAACCGAAAT---CGAATCTAA-----T-TTGA-----AT-----TTTTTCGCAAAACAGCTGGTGCAAAACACAGATGAATCGCACAGGAATCTACGTATTCTCTGGGGGC
dm3	chr31:19718257-19718430	-	AGTGCCTGTGAGCAGATGCTGGAGTGCCTGCTTCTGGGTATTGGTACCAGGTGAGGGAGGAATCATTGA-----AATTAACCCAAAT---CGAATCTAA-----T-TTGTAATGCTTTTTCAT-----TTTTTCGCAAAACAGCTGGTGCAAAACACGATGAATCGCACAGGAATCTACGTATTCTCTGGGGGC
droEre2	scaffold 4784:19510860-19511027	-	AGTGCCTGTGAGCAGATGCTGGAGTGCCTGCTTCTGGGTATTGGTACCAGGTGAGGAAT---GATTGA-----AATGAACCGAAAT---CGAATCTCA-----T-TTACATGGGT---ACAT-----GTTTTTGCAAAACAGCTGGTGCAAAACACATATGAACGCACACGAATCTACGTATTCTCTGGGGGC
droYak3	31:20808935-20809102	+	AGTGCCTGTGAGCAATATGCTGGAGTGCCTGCTTCTGGGTATTGGTACAGGTGAGAACT---GATTGA-----AATGAACCGAAAT---GTAAATATAA-----T-TTACATGAGT---ATAT-----GTTTTAGCAACAGCTGGTGCAAAACACATGAACGCACACGAATCTACGTATTCTCTGGGGGC
droEup1	scf718000040472:268344-268506	-	AGTGCCTGTGAGCAGATGATGAGTGCCTGCTCTGCTGCTATTGGTACAGGTGAGCTAT---GATTAA-----GATATAA---GT-----CGCTTTCCC---CAGGTGAGCTAT---GTAAATCTGT---TGAT-----GATATCCCCTACAGTGAATGTGCAAAACACGATGAACGCACCTCATCTACGTATTCTCTGGGGGC
droBia1	scf7180000302377:1885224-1885391	+	AATGCTCGCAGCAGATGCTGGAGTGCCTGCTGCTGCTAGTGGTACAGGTGAGGTAT---TACTTCG-----AAGTTGGCGGAGC---GCCACTATA-----T-TGATATCTAC---TGGT-----GATATCTCTTCTCAGCTTGTATCAAAACACAGATGAACGCACACCGATCTACGTATTCTCTGGGGGC
droTak1	scf7180000415304:7119-7281	+	AGTGCCTCGCAGCAGATGATGGATTGCTGCTGCTATCCGGTATTGGTACAGGTATGGAT---TTAT---AAGTAAATCTGGAAT---CGTATTTATA-----T-AAATACCTAT---ACAT-----GAA---TTCGTACAGCTAGTATCAAAACACGATGAACCGCTACACGATCTACGTGTTTCTGGGGGC
droEle1	scf7180000491255:2840147-2840217	-	TTTGTGTTGAGCTATGCTGGAGTGCCTGCTGCTACGGTACAGGTAACTTA---TATTAA-----TAATTA-----TTGGCCCTATGAATTACAACATAAATA-----A-----A---TTTAATTAT---ATTTAACGATCTTCCTTCTACAGCTATGTGCAACAGATGAACGCACACCGATCTACGTATTCTCTGGGGC
droRho1	scf718000077731:9987-10167	=	AATGTTGTGAGCTATGCTGGAGTGCCTGCTGCTACGGTACAGGTAACTTA---TATTAA-----TAATTA-----TTGGCCCTATGAATTACAACATAAATA-----A-----A---TTTAATTAT---ATTTAACGATCTTCCTTCTACAGCTATGTGCAACAGATGAACGCACACCGATCTACGTATTCTCTGGGGC
droFio1	scf7180000453831:275252-275321	-	TTGTTGTGAGCTATGCTGGAGTGCCTGCTGCTACGGTACAGGTAACTTA---TATTAA-----TAATTA-----TTGGCCCTATGAATTACAACATAAATA-----A-----A---TTTAATTAT---ATTTAACGATCTTCCTTCTACAGCTATGTGCAACAGATGAACGCACACCGATCTACGTATTCTCTGGGGC
droKik1	scf7180000302694:289866-289919	-	TTGTTGTGAGCTATGCTGGAGTGCCTGCTGCTACGGTACAGGTAACTTA---TATTAA-----TAATTA-----TTGGCCCTATGAATTACAACATAAATA-----A-----A---TTTAATTAT---ATTTAACGATCTTCCTTCTACAGCTATGTGCAACAGATGAACGCACACCGATCTACGTATTCTCTGGGGC
droAna3	scaffold 13337:17178679-17178848	+	AATGCTGTGAGCAGATGCTGAGCTGCTGCTGCTACGGTACAGGTAACTTA---TATTAA-----TAATTA-----TTGGCCCTATGAATTACAACATAAATA-----A-----A---TTTAATTAT---ATTTAACGATCTTCCTTCTACAGCTATGTGCAACAGATGAACGCACACCGATCTACGTATTCTCTGGGGC
droBip1	scf7180000396741:474651-474808	-	AGTGCCTGTGAGCAGATGCTGAGCTGCTGCTGCTACGGTACAGGTAACTTA---TATTAA-----TAATTA-----TTGGCCCTATGAATTACAACATAAATA-----A-----A---TTTAATTAT---ATTTAACGATCTTCCTTCTACAGCTATGTGCAACAGATGAACGCACACCGATCTACGTATTCTCTGGGGC
dp5	XR_group8:7793002-7793171	+	AATGCTCGCAACCTGGGCTCGATTGCTGCTGCTGCTGCTATTGGTACAGGTAGCTTCGAAATATACAC-----AAGCAGCTCGAAACACTCA-----A-----GGCTCAAGCT-----CTCTG-----TTGATCTTTGAGCTGGTCTAGAAACAGATGAACGCACAGCATCTACGTATTCTCTGGGGC
droPer2	scaffold 48:573843-574012	+	AATGCTCGCAACCTGGGCTCGATTGCTGCTGCTGCTGCTATTGGTACAGGTAGCTTCGAAATATACAC-----AAGCAGCTCGAAACACTCA-----A-----GGCTTTAAGCT-----CTCTG-----TTGATCTTTTACAGCTGGTGCAAGATACAGATGAACGCACAGCATCTACGTATTCTCTGGGGC
droW12	scf2_1100000004762:4860087-4860262	-	AATGCTGTGAGCAATATGCTTACCCTGCTGCTGCTGCTGCTATTGGTACAGGTAGCTTCGAAATATACAC-----AAGCAGCTCGAAACACTCA-----A-----GGCTTTAAGCT-----CTCTG-----TTGATCTTTTACAGCTGGTGCAAGATACAGATGAACGCACAGCATCTACGTATTCTCTGGGGC
droVir3	scaffold 13049:18967595-18967676	+	TAATGCTGTGAGCAGATGCTGAGCTGCTGCTGCTGCTGCTATTGGTACAGGTAGCTTCGAAATATACAC-----AAGCAGCTCGAAACACTCA-----A-----GGCTTTAAGCT-----CTCTG-----TTGATCTTTTACAGCTGGTGCAAGATACAGATGAACGCACAGCATCTACGTATTCTCTGGGGC
droMo3	scaffold 6680:12264702-12264869	-	AGTGCCTGTGAGCAGATGATTTCTCTGCTGCTGCTGCTGCTATTGGTACAGGTAGCTTCGAAATATACAC-----AAGCAGCTCGAAACACTCA-----A-----GGCTTTAAGCT-----CTCTG-----TTGATCTTTTACAGCTGGTGCAAGATACAGATGAACGCACAGCATCTACGTATTCTCTGGGGC
droGr12	scaffold 15110:16664416-16664608	+	AGTGCCTGTGAGCAGATGATACCTCTGCTGCTGCTGCTGCTATTGGTACAGGTAGCTTCGAAATATACAC-----AAGCAGCTCGAAACACTCA-----A-----GGCTTTAAGCT-----CTCTG-----TTGATCTTTTACAGCTGGTGCAAGATACAGATGAACGCACAGCATCTACGTATTCTCTGGGGC

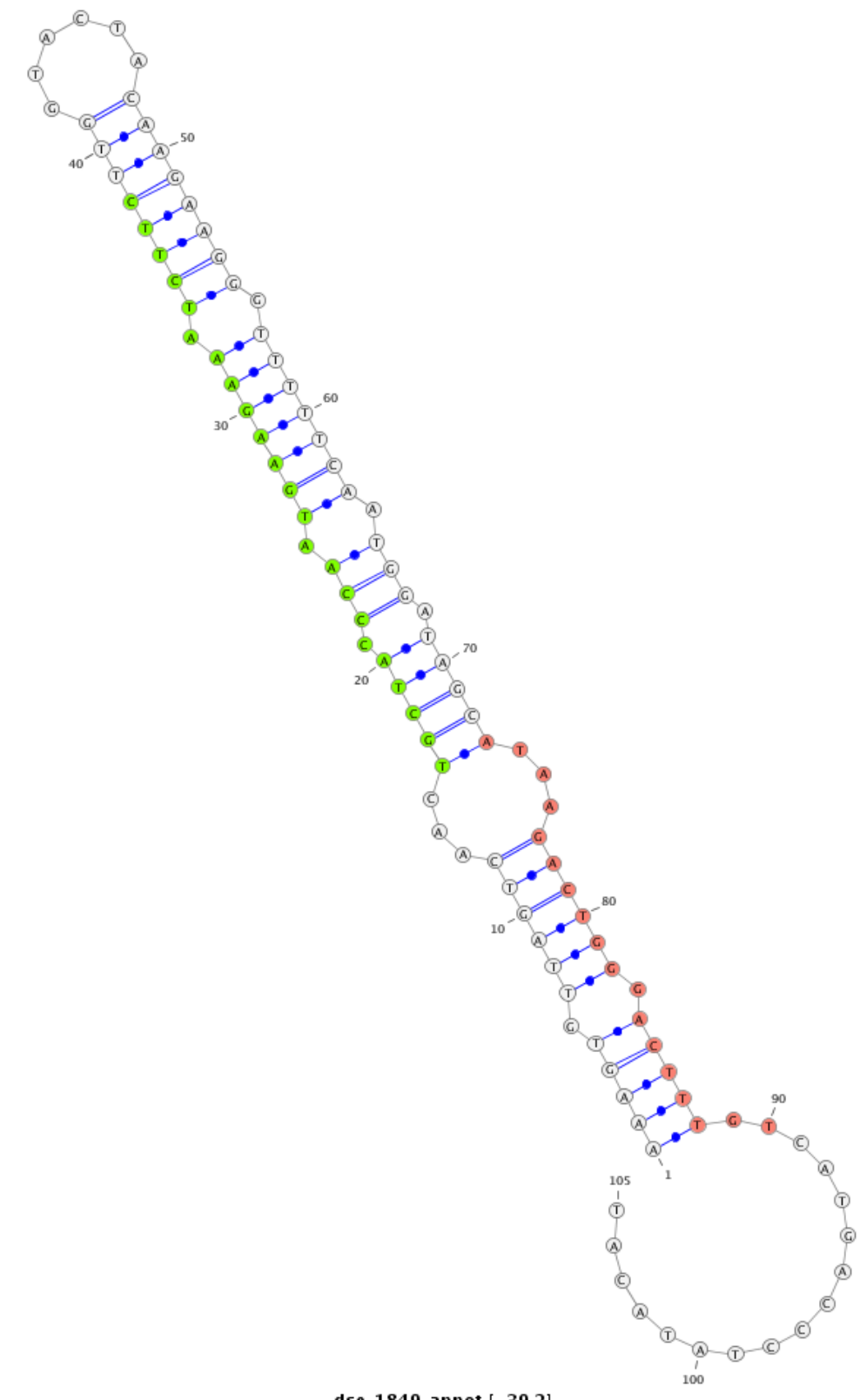
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	PASS/FAIL
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crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate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

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dse_1849	scaffold_7:415779-415868 +	candidate	Canonical miRNA	intron	[View on UCSC Genome Browser (Compl Mirror)]

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

Predicted structure



Show Alternate Folds

Flybase annotation

intron [Dsec/GM17204-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

	Read #	Read size	Hit Count	Mismatch	Total Norm	Total	V114 embryo	M054 female body	V113 male body	V115 head
GCTATTGAAGAGTCTTATGGTCGAGTACTTATGGTCGACCTAAAGTGTAGTCAAC	23	0	1	2.00	2	1	0	0	1	
*****	22	0	1	1.00	1	0	0	1	0	
*****	18	0	1	1.00	1	1	0	0	0	

Anti-sense strand reads

	Read #	Read size	Hit Count	Mismatch	Total Norm	Total	V113 male body	V115 head	M054 female body
CGATAACTTCTCAGAAATACCAGCTCATGAATACCAGCTGGATTTCACAATCAGTTG									

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droSec2	scaffold_7:415729-415918 +	dse_1849	GCTATT-GA-----AGAGTCTT-ATGGTCGAGTACTTATGG-TCGA-CCT-AAAG-TGTTAGT-CAAC
droSim2	21:16335681-16335870 +		GCTATT-GA-----AGAGTCTT-ATGGTCGAGTACTTATGG-TCGA-CT-AAAG-TGTTAGT-CAAC
dm3	chr2L:16768935-16769122 +	dme_456	GCTATT-GA-----AGAGTCTT-A-----TGG-TCGA-CCT-AAAG-TGTTAGT-CAAT
droEre2	scaffold_4845:19839662-19839853 +	der_201	GAT--G-AAAAGTCGTATTGAGATTTCAT-----ACTTASG-TCGA-CCT-AAAG-TATTAGT-CGG
droYaK3	2R:4332896-4333091 -	dya_60	GCTATTGAAATGCTTGTATTGAGATTTCAT-----GTCAGAS-TCGA-CCT-CAAG-TGTTAGT-CGG
droEug1	scf7180000408961:341888-342065 +		GCTATT-GA-----AGTGGCTTAAT-----AAAAG-ATTTTAT-AAAG-TTCTGGC-TGCA
droBial	scf7180000301468:936831-937014 +		GCTATT-GC-----AGTAAGCCTCT-----AAGSG-TCTTTTC-AAAG-AGTGT-CCT
droTak1	scf7180000415914:515704-515901 +		AACCTC-AAAAGTCGGTATTGTAATTAATCTCT-----AAGSG-TSAT-TCT-AAA
droEle1	scf7180000490579:573563-573720 -		GCTATT-CA-----AGATCTTTCT-----AAGSG-TCTTTTC-AAAG-TGTTAGT
droRho1	scf7180000780103:213355-213535 -		GCTATT-CA-----AGATCTTTCT-----AAGSG-TCTTTTC-AAAG-TGTTAGT
droFic1	scf7180000454078:695816-695997 +		GCTATT-CA-----AGATCTTTCT-----AAGSG-TCTTTTC-AAAG-TGTTAGT
droKik1	scf7180000302472:34983-35169 +		GCTATT-GC-----GATCTTTTGT-----AAGSG-TATCTTA-TGATGCTAC
droAna3	scaffold_12916:7328504-7328685 +		ATCTTT-CA-----AGATCTTTAA-----GGCGT-TCTTTTC-AAAG-TGTTAGT
droBipl	scf7180000396566:498306-498489 +		ATCTTT-GA-----AGATCTTTAA-----AGCSTGTAAT-SCGAATAA-TAT
dp5	4_group3:3011862-3012061 -		AACATC-GAAGATTGGTCTTAGAGCTCTCTA-----ATAGGSGGTCTCTCTC
droPer2	scaffold_1:4498560-4498759 -		AACATC-GAAGATTGGTCTTAGAGCTCTCTA-----ATAGGSGGTCTCTCTC
droW12	scf2_1100000004577:1126289-1126443 +		GCATTC-CA-----ACAACTTTTGT-----AAGSG-TATCTTA-TGATGCTAC
droVir3	scaffold_12963:10115732-10115898 +		CTCTTC-CA-----AGAGCTTAAT-----SGTTCCT-CTA-CAAG-SAGTCAA
droMoJ3	scaffold_6500:2796054-2796204 +		ATCACT-------TTT-AT-----SG-TTCG-ACT-GGG-TG-CAN
droGr12	scaffold_15252:13249781-13249952 +		AGCTTT-CA-----ATACCCTA-AT-----SG-CTCA-AT-AAAG-TAATTC

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crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	1
rescue.known	0
rescue.confident	1
rescue.candidate	2