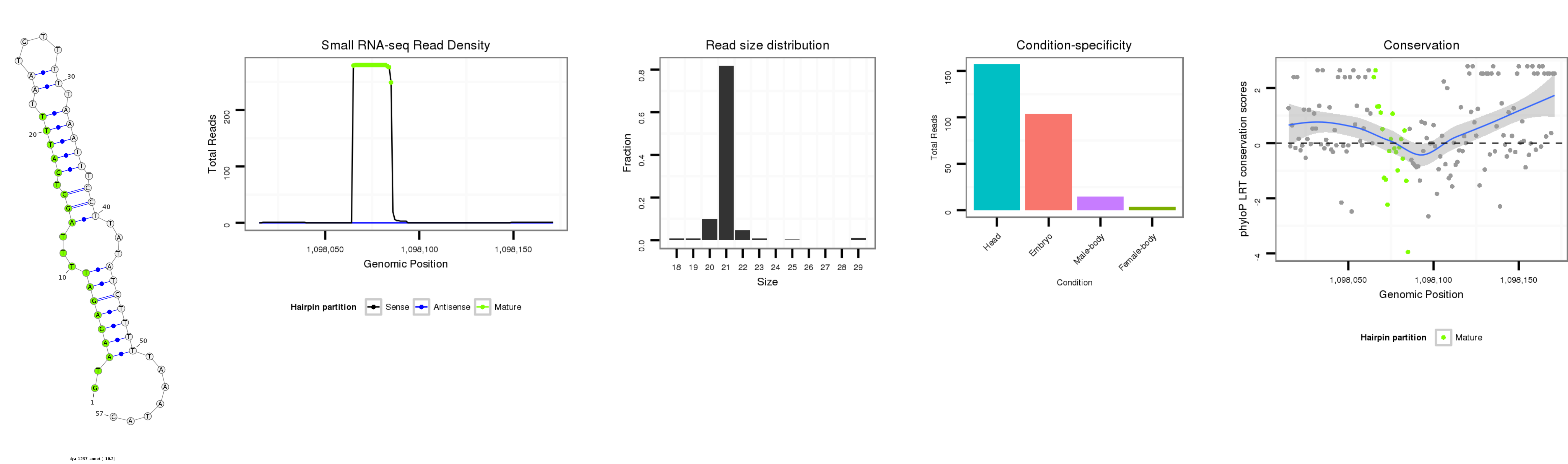


ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dya_1237	4:1098065-1098121 +	candidate	Mirtron	intron	[View on UCSC Genome Browser (Cornell Mirror)]

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Show Alternate Folds

Flybase annotation

intron [DyakGE14563-in]; CDS [DyakGE14563-cds]; CDS [DyakGE14563-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

CATCTGCATTAAATTAGTAATAGCCTACCCGAGGCTTCCAATGGACCAACTGTAAGAGATTTTAGGTGATTTTAATGTTTTTAAATTCCTTATATCTTTTTTAAATAGGTTTTTGGTGGTGAAGCTAATGCTACACATACCAGCTCTGAAAGCCCTCC	Read #	size	Mismatch	Hit	Total	Count	Norm	Total	M056	M026	V058	V120	V052	V046	M043
*****.(((((((...(((.(.((((.(.)))))))).))))).*****	21	0	1	229.00	229	89	88	23	13	8	5	3			
.....GTAAGAGATTTTAGGTGATTT.....	20	0	1	27.00	27	1	14	7	2	2	1	0			
.....GTAAGAGATTTTAGGTGATTT.....	22	0	1	13.00	13	7	3	2	0	1	0	0			
.....GTAAGAGATTTTAGGTGATT.....	21	1	1	6.00	6	5	0	1	0	0	0	0			
.....GTAAGAGATTTTAGGTGATTTAATGTTT.....	29	0	1	3.00	3	0	3	0	0	0	0	0			
.....GTAAGAGATTTTAGGTGA.....	18	0	1	2.00	2	0	1	0	0	0	1	0			
.....GTAAGAGATTTTAGGTGATTTTA.....	23	0	1	2.00	2	0	2	0	0	0	0	0			
.....GTAAGAGATTTTAGGTGAT.....	19	0	1	2.00	2	0	2	0	0	0	0	0			
.....GTAAGAGATTTTAGGTGATTTAAT.....	25	0	1	1.00	1	0	1	0	0	0	0	0			
..TCTGCATTAAATTAGTAATAGCCT.....	23	0	1	1.00	1	0	1	0	0	0	0	0			
.....TAAGAGATTTTAGGTGATTT.....	20	0	1	1.00	1	0	0	0	0	0	0	0			1
.....CATACCAGCTCTGAAAGCCCTCC	23	0	1	1.00	1	0	1	0	0	0	0	0			0
.....GTAAGAGATTTTAGGTGATT.....	20	1	1	1.00	1	1	0	0	0	0	0	0			0

Anti-sense strand reads

GTAGACGTAATTAATCATTATCGGATGGGCTCCGAAGGTTACTGGTTGACGATTCTCTAAATCCCAATAATTACAAAAATTTAAAGGAATATAGAAAAATTTTCCAAAACCCCAACTTCGATTACGATGTGTATGGTCGAGACTTTCGGGAGG	Read #	Hit	Total	
*****.(((((((...(((.(.((((.(.)))))))).))))).*****				
No data available in table				

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droYak3	4:1098015-1098171 +	dya_1237	CATCT---GCATTAATTAG-----T---AATAGCCTACCCGAGGCT---TCCAATGGACCAACTGTAAGAGATTT--TAGGTGA-----TTTAAATGTT-----TTTAAATTTCTTTATA-----TCTTTTT-----AAATAGGTTTTGGTGGTGAAGCTAAT--GCTACACATACCAGCTCTGAAAGCCCTCC
droEre2	scaffold4_4512:246624-246780 -		CATCT---GCATTAATTAG-----T---AATAGCCTACCCGAGGCT---TCCAATGGACCAACTGTAAGATATTT--CTTGA-----CGTAATATT-----TTATTTT-----AAATAGGTTCTGGTGGTGAAGCTAAT--GCTACACACACCAAGCTCTGAAAGCCCAAC
droSec2	scaffold4_66255-66411 +		CATCT---GCATTAATTAG-----T---AATAGCCTACCGAGGCT---TCCAATGGACCAACTGTAAGATATTT--TTTGA-----CATCATGTT-----TTTAAATTCCTTTATA-----CTTCTT-----AAATAGGTTTTGGTGGTGAAGCTAAT--CTACACACACCAAGCTCTGAAAGCCCAAC
droSim2	4:812847-813003 +		CATCT---GCATTAATTAG-----T---AATAGCCTACCGAGGCT---TCCAATGGACCAACTGTAAGAGATTT--TTTGA-----CATCATGTT-----TTTAAATTCCTTTATA-----CTTCTT-----AAATAGGTTTTGGTGGTGAAGCTAAT--CTACACACACCAAGCTCTGAAAGCCCAAC
dm3	chr4:1024989-1025145 +		CATCT---GCATTAATTAG-----T---AATAGCCTACCGAGGCT---TCCAATGGACCAACTGTAAGAGATTT--TTTGA-----CATCATGTT-----TTTAAATTCCTTTATA-----CTTCTT-----AAATAGGTTTTGGTGGTGAAGCTAAT--CTACACACACCAAGCTCTGAAAGCCCAAC
droEug1	scf7180000408984:211895-212044 -		CATCT---GCATTAATTAG-----C---AGTAGCTACCCGAGGCT---CCAATGGACCAACTGTAAGACGATCTCTT-----ACC-----TTGCATTTGTAATA-----TTAATTT-----AAATAGGTTCTGGGCGAGAGCTAAT--GCTCGCAATCAAACTCGAAAGTCCAC
droBia1	scf7180000301495:1014679-1014840 +		CATCT---GCATTAATTAG-----C---AATGCTACCCGAGGCT---CCAATGGACCAACTGTAAGATATTTTATTA-----AGATAGAT-----AT-----ATTAAGATTTCCTAATA-----ACATAGT-----TTATAGGTTCTGGGTGGAGAGCTAAT--GCACACACCACTCTGAAAGTCCAC
droTak1	scf7180000415212:103547-103704 +		CATCT---GCATTAATTAG-----C---AATGCTACCCGAGGCT---CCAATGGACCAACTGTAAGAGGTTT-----ATGA-----CCAATAG-----TTTACATTTGAAATA-----ACGATTT-----TAATAGGTTCTGGGTGGAGAGCTAGT--GCACACACCAAGCTCTGAAAGTCCAC
droEle1	scf7180000491238:116153-116310 -		CATCT---GCATTAATTAG-----C---AATGCTACCCGAGGCT---CCAATGGACCAACTGTAAGATGTTT-----TTT-----CCAATAG-----TTTACATTTGAAATA-----TTGCCA-----TAATAGGTTCTGGGTGGAGAGCTAAT--GCACACACCAAGCTCTGAAAGTCCAC
droRho1	scf7180000780283:15762-15920 +		CATCT---GCATTAATTAG-----C---AATGCTACCCGAGGCT---CCAATGGACCAACTGTAAGATATTTAATTTGA-----TTAATGAT-----TTTTCATTTGAAATA-----TTAGT-----TAAGAGGTTCTGGGTGGAGAGCTAAT--GCTCGCAACACAGCTCTGAAAGTCCAC
droFic1	scf7180000454040:600295-600456 +		CTCT---GCATTAATTAG-----C---AATGCTACCCGAGGCT---CCAATGGACCAACTGTAAGAGATTTCTTTGA-----CTGGCT-----AAATTAATTTTAAATA-----ATAGT-----TAATAGGTTCTGGGTGGAGAGCTAGT--GCACACACCAAGCTCTGAAAGTCCAC
droKik1	scf7180000302413:149023-149186 -		CTCT---GCATTAATTAG-----C---AATGCTACCCGAGGCT---CCAATGGACCAACTGTAAGATATTTAATTTGA-----CTGGCT-----AAATTAATTTTAAATA-----ATAGT-----TAATAGGTTCTGGGTGGAGAGCTAAT--GCACACACCAAGCTCTGAAAGTCCAC
droAna3	scaffold_13077:158748-158910 +		CATCT---GCATTAATTAG-----C---AATGCTACCCGAGGCT---CCAATGGACCAACTGTAAGATATTTAATTTGA-----CTGGCT-----AAATTAATTTTAAATA-----ATAGT-----TAATAGGTTCTGGGTGGAGAGCTAAT--GCACACACCAAGCTCTGAAAGTCCAC
droBip1	scf7180000396677:16540-16701 +		CATCT---GCATTAATTAG-----C---AATGCTACCCGAGGCT---CCAATGGACCAACTGTAAGATATTTAATTTGA-----CTGGCT-----AAATTAATTTTAAATA-----ATAGT-----TAATAGGTTCTGGGTGGAGAGCTAAT--GCACACACCAAGCTCTGAAAGTCCAC
dp5	Unknown_group_14:50442-50602 -		CTCT---GCATTAATTAG-----C---AATGCTACCCGAGGCT---CCAATGGACCAACTGTAAGATATTTAATTTGA-----CTGGCT-----AAATTAATTTTAAATA-----ATAGT-----TAATAGGTTCTGGGTGGAGAGCTAAT--GCACACACCAAGCTCTGAAAGTCCAC
droPer2	scaffold_106:70895-71055 +		CTCT---GCATTAATTAG-----C---AATGCTACCCGAGGCT---CCAATGGACCAACTGTAAGATATTTAATTTGA-----CTGGCT-----AAATTAATTTTAAATA-----ATAGT-----TAATAGGTTCTGGGTGGAGAGCTAAT--GCACACACCAAGCTCTGAAAGTCCAC
droW12	scf2_1100000004943:1337564-1337734 +		CTCT---GCATTAATTAG-----C---AATGCTACCCGAGGCT---CCAATGGACCAACTGTAAGATATTTAATTTGA-----CTGGCT-----AAATTAATTTTAAATA-----ATAGT-----TAATAGGTTCTGGGTGGAGAGCTAAT--GCACACACCAAGCTCTGAAAGTCCAC
droVir3	scaffold_13052:912765-912936 -		CTCT---GCATTAATTAG-----C---AATGCTACCCGAGGCT---CCAATGGACCAACTGTAAGATATTTAATTTGA-----CTGGCT-----AAATTAATTTTAAATA-----ATAGT-----TAATAGGTTCTGGGTGGAGAGCTAAT--GCACACACCAAGCTCTGAAAGTCCAC
droMor3	scaffold_6498:1310347-1310417 -		CTCT---GCATTAATTAG-----C---AATGCTACCCGAGGCT---CCAATGGACCAACTGTAAGATATTTAATTTGA-----CTGGCT-----AAATTAATTTTAAATA-----ATAGT-----TAATAGGTTCTGGGTGGAGAGCTAAT--GCACACACCAAGCTCTGAAAGTCCAC
droGr12	scaffold_14822:99092-99259 -		CTCT---GCATTAATTAG-----C---AATGCTACCCGAGGCT---CCAATGGACCAACTGTAAGATATTTAATTTGA-----CTGGCT-----AAATTAATTTTAAATA-----ATAGT-----TAATAGGTTCTGGGTGGAGAGCTAAT--GCACACACCAAGCTCTGAAAGTCCAC

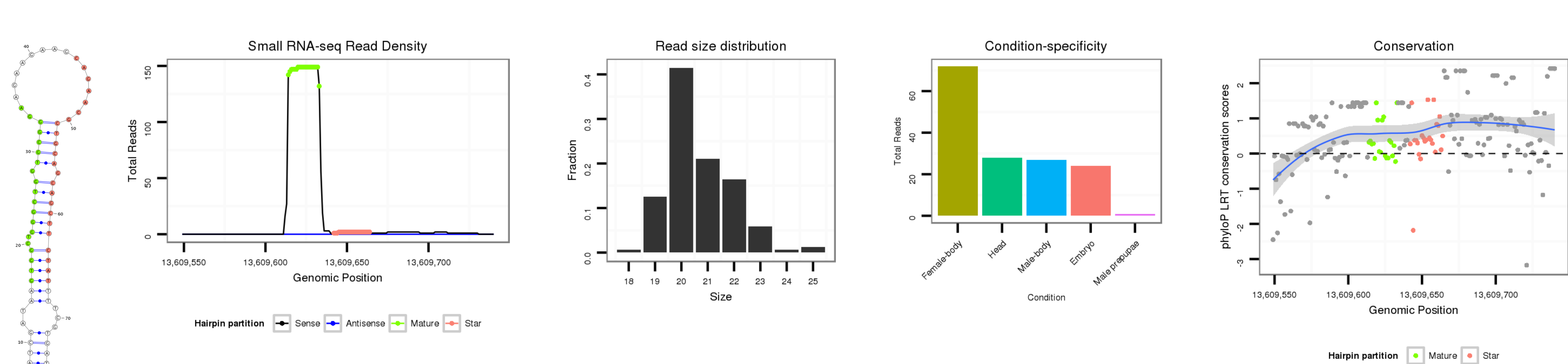
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PASS/FAIL	
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crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tplot3	0
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dya_1783	3L:13609599-13609690 +	candidate	Canonical miRNA	antisense_to_5pUTR	[View on UCSC Genome Browser (Cornell Mirror)]

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Show Alternate Folds

Flybase annotation

Antisense to utr5_minus_6595]; utr5_plus_7949]

No Repeatable elements found

Sense Strand Reads

[hide 3p reads](#) [show mid mismatch reads](#)

	Read #	size	Mismatch	Hit	Count	Norm	Total	M043	female	V058	V120	M056	V052	V046	M026	SRR1275486
								body	head	male	embryo	head	embryo	head	Male	prepupae
AACAACAACGAAAAAAGCTATCGGCGCTGTTGCTCCTACAATCGAACGGTGGCTGACTATCGATAA	20	0	1	61.00	61	22	12	16	6	3	1	0	1			
GTGGCTGGGCTGGTGC	21	0	1	24.00	24	16	4	1	1	2	0	0	0			
GTGGCTGGGCTGGTGC	19	0	1	16.00	16	7	5	2	1	1	0	0	0			
GTGGCTGGGCTGGTGC	22	0	1	14.00	14	4	1	3	5	0	1	0	0			
GTGGCTGGGCTGGTGC	23	0	1	8.00	8	4	0	3	1	0	0	0	0			
GTGGCTGGGCTGGTGC	22	0	1	6.00	6	1	0	1	4	0	0	0	0			
GTGGCTGGGCTGGTGC	21	0	1	6.00	6	2	0	1	3	0	0	0	0			
GTGGCTGGGCTGGTGC	22	0	1	5.00	5	5	0	0	0	0	0	0	0			
GTGGCTGGGCTGGTGC	20	1	1	3.00	3	1	1	0	0	1	0	0	0			
GTGGCTGGGCTGGTGC	22	1	1	3.00	3	0	0	0	0	0	3	0	0			
GTGGCTGGGCTGGTGC	20	0	1	2.00	2	2	0	0	0	0	0	0	0			
GTGGCTGGGCTGGTGC	20	1	1	2.00	2	0	2	0	0	0	0	0	0			
GTGGCTGGGCTGGTGC	21	1	1	2.00	2	0	0	0	0	2	0	0	0			
GTGGCTGGGCTGGTGC	19	0	1	2.00	2	2	0	0	0	0	0	0	0			
GTGGCTGGGCTGGTGC	18	0	1	1.00	1	1	0	0	0	0	0	0	0			
GTGGCTGGGCTGGTGC	21	1	1	1.00	1	1	0	0	0	0	0	0	0			
GTGGCTGGGCTGGTGC	22	1	1	1.00	1	0	0	0	1	0	0	0	0			
GTGGCTGGGCTGGTGC	23	0	1	1.00	1	0	0	1	0	0	0	0	0			
GTGGCTGGGCTGGTGC	21	1	1	1.00	1	0	0	0	0	0	0	0	1			
GTGGCTGGGCTGGTGC	21	0	1	1.00	1	1	0	0	0	0	0	0	0			
GTGGCTGGGCTGGTGC	20	0	1	1.00	1	1	0	0	0	0	0	0	0			
GTGGCTGGGCTGGTGC	23	0	1	1.00	1	1	0	0	0	0	0	0	0			
GTGGCTGGGCTGGTGC	19	0	1	1.00	1	1	0	0	0	0	0	0	0			
GTGGCTGGGCTGGTGC	27	0	1	1.00	1	1	0	0	0	0	0	0	0			
GTGGCTGGGCTGGTGC	24	0	1	1.00	1	1	0	0	0	0	0	0	0			
GTGGCTGGGCTGGTGC	20	1	1	1.00	1	1	0	0	0	0	0	0	0			
GTGGCTGGGCTGGTGC	21	0	1	1.00	1	0	0	0	1	0	0	0	0			
GTGGCTGGGCTGGTGC	20	1	1	1.00	1	1	0	0	0	0	0	0	0			
GTGGCTGGGCTGGTGC	19	1	1	1.00	1	1	0	0	0	0	0	0	0			
GTGGCTGGGCTGGTGC	25	0	1	1.00	1	1	0	0	0	0	0	0	0			
GTGGCTGGGCTGGTGC	25	0	1	1.00	1	1	0	0	0	0	0	0	0			
GTGGCTGGGCTGGTGC	19	1	1	1.00	1	0	0	1	0	0	0	0	0			

Anti-sense strand reads

	Read #	size	Mismatch	Count	Norm	Total	M056	M043
							embryo	female
TTGTTTGTGGTTTTTTTGATAGCGGCAACAGGAGTGTAGCTTGCCAGCGACTGATAGCTATT	20	0	1	61.00	61	22	12	16
GTGGCTGGGCTGGTGC	21	0	1	24.00	24	16	4	1
GTGGCTGGGCTGGTGC	19	0	1	16.00	16	7	5	2
GTGGCTGGGCTGGTGC	22	0	1	14.00	14	4	1	3
GTGGCTGGGCTGGTGC	23	0	1	8.00	8	4	0	3
GTGGCTGGGCTGGTGC	22	0	1	6.00	6	1	0	1
GTGGCTGGGCTGGTGC	21	0	1	6.00	6	2	0	1
GTGGCTGGGCTGGTGC	22	0	1	5.00	5	5	0	0
GTGGCTGGGCTGGTGC	20	1	1	3.00	3	1	1	0
GTGGCTGGGCTGGTGC	22	1	1	3.00	3	0	0	0
GTGGCTGGGCTGGTGC	20	0	1	2.00	2	2	0	0
GTGGCTGGGCTGGTGC	20	1	1	2.00	2	0	2	0
GTGGCTGGGCTGGTGC	21	1	1	2.00	2	0	0	0
GTGGCTGGGCTGGTGC	19	0	1	2.00	2	2	0	0
GTGGCTGGGCTGGTGC	18	0	1	1.00	1	1	0	0
GTGGCTGGGCTGGTGC	21	1	1	1.00	1	1	0	0
GTGGCTGGGCTGGTGC	22	1	1	1.00	1	0	0	1
GTGGCTGGGCTGGTGC	23	0	1	1.00	1	0	1	0
GTGGCTGGGCTGGTGC	21	1	1	1.00	1	0	0	0
GTGGCTGGGCTGGTGC	21	0	1	1.00	1	1	0	0
GTGGCTGGGCTGGTGC	20	0	1	1.00	1	1	0	0
GTGGCTGGGCTGGTGC	23	0	1	1.00	1	1	0	0
GTGGCTGGGCTGGTGC	19	0	1	1.00	1	1	0	0
GTGGCTGGGCTGGTGC	27	0	1	1.00	1	1	0	0
GTGGCTGGGCTGGTGC	24	0	1	1.00	1	1	0	0
GTGGCTGGGCTGGTGC	20	1	1	1.00	1	1	0	0
GTGGCTGGGCTGGTGC	21	0	1	1.00	1	0	0	1
GTGGCTGGGCTGGTGC	20	1	1	1.00	1	1	0	0
GTGGCTGGGCTGGTGC	19	1	1	1.00	1	1	0	0
GTGGCTGGGCTGGTGC	25	0	1	1.00	1	1	0	0
GTGGCTGGGCTGGTGC	25	0	1	1.00	1	1	0	0
GTGGCTGGGCTGGTGC	19	1	1	1.00	1	0	1	0

Re-alignment of all predicted orthologs

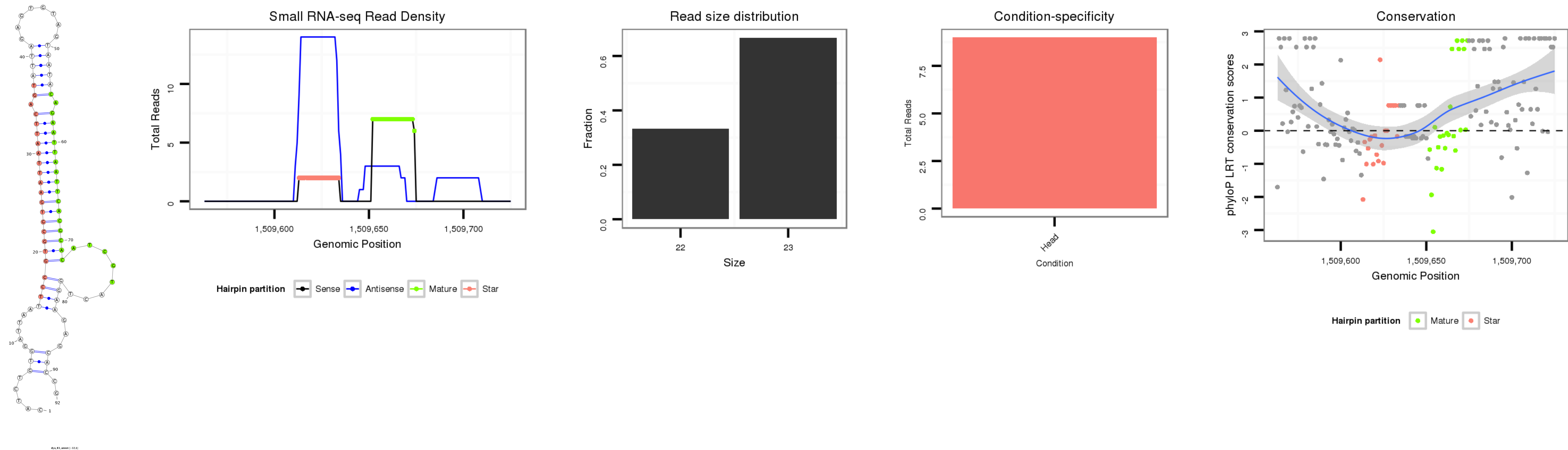
Species	Coordinate	ID	Alignment
droyak3	3L:13609549-13609740 +	dya_1783	AACA----AACAACCAAAAACTATCGGCGCTGTTGCTCCTACAATCGAACGGTGGCTGACTATCGATAA
droEr2	scaffold_4784:13519265-13519456 +	der_67	AACA----AACAACCAAAAACTATCGGCGCTGTTGCTCCTACAATCGAACGGTGGCTGACTATCGATAA
droSec2	scaffold_0:5681825-5682021 +		CTTC----AACAACCAAAAACTATCGGCGCTGTTGCTCCTACAATCGAACGGTGGCTGACTATCGATAA
droSim2	3L:13210124-13210324 +		AACCTCTGACCAACCAAAAACTATCGGCGCTGTTGCTCCTACAATCGAACGGTGGCTGACTATCGATAA
dm3	chr3L:13506389-13506589 +		GACTTTAGCAACCAAAAACTATCGGCGCTGTTGCTCCTACAATCGAACGGTGGCTGACTATCGATAA
droEug1	scf7180000409121:52039-52233 +		CAATTTGTTACATCAAACTATCGGCGCTGTTGCTCCTACAATCGAACGGTGGCTGACTATCGATAA
droBia1	scf7180000302428:6397236-6397314 +		C-----AACAACCAAAAACTATCGGCGCTGTTGCTCCTACAATCGAACGGTGGCTGACTATCGATAA
droTak1	scf7180000415429:216431-216505 +		C-----AACAACCAAAAACTATCGGCGCTGTTGCTCCTACAATCGAACGGTGGCTGACTATCGATAA
droEl1	scf7180000491255:1960976-1961156 +		C-----AACAACCAAAAACTATCGGCGCTGTTGCTCCTACAATCGAACGGTGGCTGACTATCGATAA
droRho1	scf7180000779509:106304-106479 +		C-----AACAACCAAAAACTATCGGCGCTGTTGCTCCTACAATCGAACGGTGGCTGACTATCGATAA
droFic1	scf7180000454048:191657-191856 +		CAACCA----CAACCAAAAACTATCGGCGCTGTTGCTCCTACAATCGAACGGTGGCTGACTATCGATAA
droKik1	scf7180000302808:501821-501910 +		C-----AACAACCAAAAACTATCGGCGCTGTTGCTCCTACAATCGAACGGTGGCTGACTATCGATAA
droAna3	scaffold_13337:21927615-21927629 +		A-----AACAACCAAAAACTATCGGCGCTGTTGCTCCTACAATCGAACGGTGGCTGACTATCGATAA
droBip1	scf7180000396730:397240-397308 +		CTT-----AACAACCAAAAACTATCGGCGCTGTTGCTCCTACAATCGAACGGTGGCTGACTATCGATAA
dp5	XB_group8:6926271-6926365 +		A-----AACAACCAAAAACTATCGGCGCTGTTGCTCCTACAATCGAACGGTGGCTGACTATCGATAA
droPer2	scaffold_36:381494-381588 +		A-----AACAACCAAAAACTATCGGCGCTGTTGCTCCTACAATCGAACGGTGGCTGACTATCGATAA
droVit3	scaffold_13049:17621318-17621513 +		CAACCA----AACAACCAAAAACTATCGGCGCTGTTGCTCCTACAATCGAACGGTGGCTGACTATCGATAA
droMo3	scaffold_6680:22666188-22666249 +		T-----AACAACCAAAAACTATCGGCGCTGTTGCTCCTACAATCGAACGGTGGCTGACTATCGATAA

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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.top3	1
crit.un	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	2

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Show Alternate Folds

Flybase annotation

Antisense to intron [Dyak\GE12909-in]; Antisense to CDS [Dyak\GE12909-cds]; Antisense to CDS [Dyak\GE12909-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

[illegible]

Anti-sense strand reads

						M026	M043	V120	M056	M058
						female	male	embryo		
Read #	size	Mismatch	Count	Norm	Total	head	body	body	head	
*****.((.(((.(((((((((((((((((((.(((((.)))))))).)))))))).)))))))).))))).)))).*****										
22	0	1	4.00	4	0	3	0	1	0	
21	0	1	3.00	3	1	1	0	1	0	
22	0	1	2.00	2	2	0	0	0	0	
22	0	1	2.00	2	2	0	0	0	0	
22	0	1	2.00	2	0	0	2	0	0	
22	0	1	1.00	1	0	1	0	0	0	
22	0	1	1.00	1	0	1	0	0	0	
23	0	1	1.00	1	1	0	0	0	0	
25	0	1	1.00	1	0	1	0	0	0	
23	1	1	1.00	1	0	1	0	0	0	
23	0	1	1.00	1	0	0	1	0	0	
22	0	1	1.00	1	1	0	0	0	0	

Show Alignment With Reads

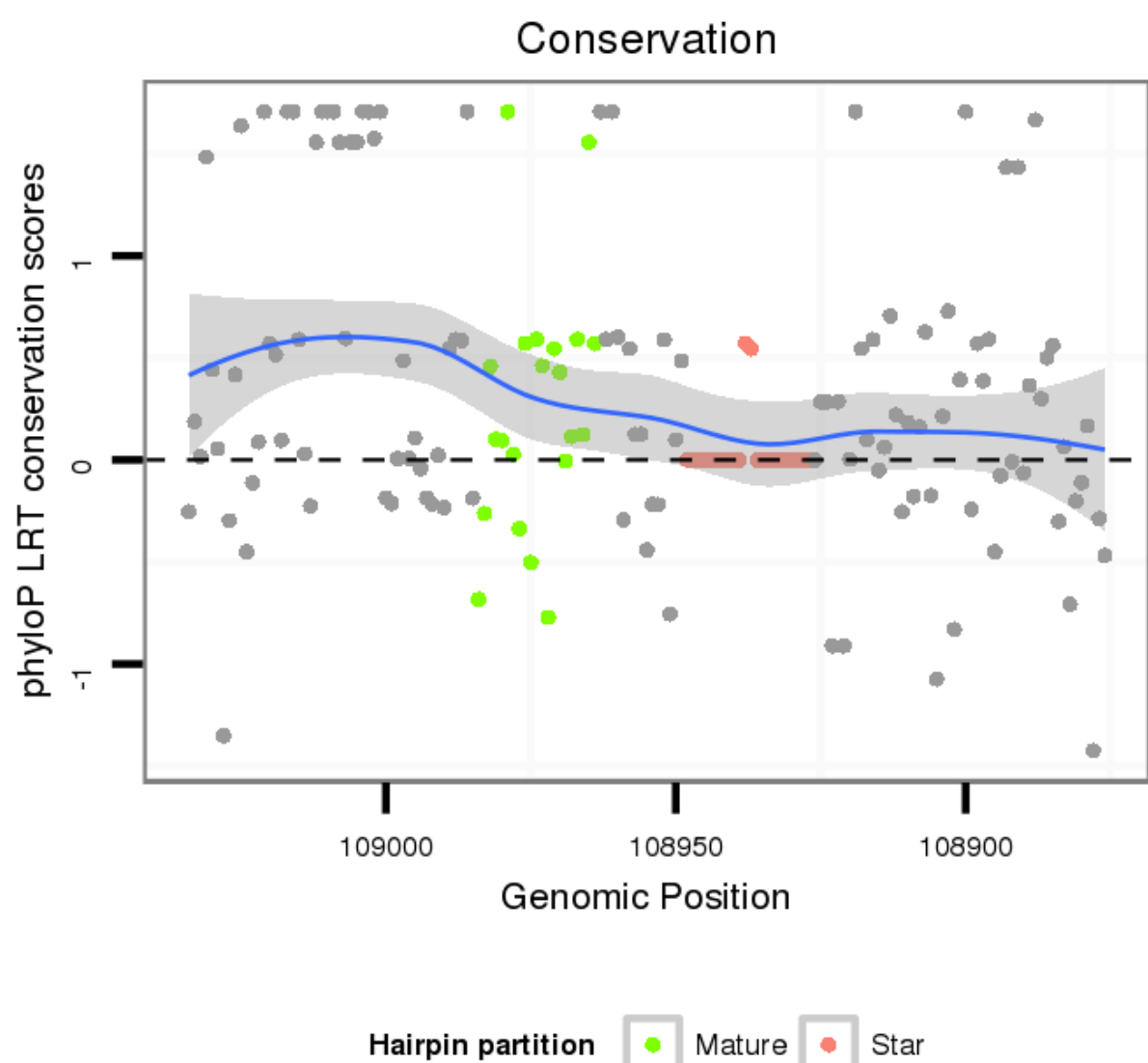
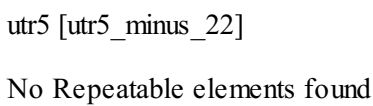
Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droYak2	ZR:1509563-1509725 +	dya_83	GTCTTCGAGGTCCCTTTTCGTCCTGC AAAAGA-----T-----ACACATCTGT-----GGATT A-ATTCGGTTCGGTGAATTAATT--CAGTATTAGAGTGTAGTAATAAGAAAT-----T-AA-TTCACGCACATCGTACTGGAAGACACCCTGTCTGTGCCATGAAGTTGAGCAGGTAGTTGACCA
droEr2	scaffold_4845:32355770-3235901 +		GTCTTCGCAAACTCCTTCGTCCTGC AAAATA-----T-----ACAATCTGT-----GGA---G-CG--ACTCTAATA-----G-----T-GA-TTCACGAAAGTCGTACTGGAAGACACCCTGTCTGTGCCATGAAGTTGAGCAGGTAGTTGACCA
droSe2	scaffold_18:1192723-1192856 -		GTCTTCGAGGTCCCTTTTCGTCCTGC AAAAGA-----T-----ATACATCTGT-----GGA---AT-ATGTCACTCCAAC-----T-----TCAT-----T-GA-TTCACGTACGTCGTACTGGAAGACACCCTGTCTGTGCCATGAAGTTGAGCAGGTAGTTGACCA
droSim2	21:20706279-20706412 -		GTCTTCGAGGTCCCTTTTCGTCCTGC AAAAGA-----T-----ATACATCTGT-----GGA---AT-ATGTCACTCCAAC-----T-----TCAT-----T-GA-TTCACGTACGTCGTACTGGAAGACACCCTGTCTGTGCCATGAAGTTGAGCAGGTAGTTGACCA
dm3	chr21:21261664-21261797 -		GTCTTCGAGGTCCCTTTTCGTCCTGC AAAAGA-----T-----ATATCTGT-----GGA---AT-ATGTCACTCCAAT-----T-----TCAT-----T-GA-TTCACGTACATCGTACTGGAAGACACCCTGTCTGTGCGATGAAGTTGAGCAGGTAGTTGACCA
droEu1	scf7180000409063:147362-147488 +		AACATGTAGGTCCTTCGTCCTGC AAAAGAGA-----T-----ACGAA-AGT-----GGA---G-----AGCCTATC-----T-----TCTGTA-----T-GA-GTCACTACGTCGTACTGGAAGACACCCTGTCTGTGCCATGAAGTTGAGCAGGTAGTTGACCA
droBial	scf7180000302422:3668069-3668203 +		ATCTGTGAGGTCCTTCGTCCTGC AAAAGATT-----T-----ACGTTTGA GTGTACAT-----TTAAATGAGTAAATG-----GGA---G-----GAGA-----A-GC-TTCACGCACATCGTACTGGTAAGACACGTGTCTGTGCCATGAAGTTGAGCAGGTAGTTGACCA
droTak1	scf7180000415871:197192-197330 +		AACCTGCAGGTCCCTTTTCCTCTGC AAAATA-----T-----TTTCACATAATAATG-----ACAAAACTAAATGAA-----GGA---G-----TAGTCG-----A-GC-TATACGCACATCGTACTGGTAAGACACCGTATCTGTGCCATGAAGTTGAGCAGGTAGTTGACCA
droEl1	scf7180000490640:37208-37360 -		AACCTGCAGGTCCCTTCGTCCTGC AAAACGSA-----T-----ACAAATCTGT-----AAAATCAGTGAATTTAGTGG-----AGCCCCAGACAGTG-----G-----CCTTAGTCGCACTCACGCACATCGTACTGGAAGACACCCTGTCTGTGCCATGAAGTTGAGCAGGTAGTTGACCA
droRho1	scf7180000758815:607-714 -		GTCTTCAGGTCCTTCGTCCTGC AAAACGSA-----T-----ACATCTGT-----GGA---GCGT--AGCCCTCA-----T-----TTTGA-----AGCG-----GACGCACGTGCGCAAGCACTGACAGGTAGTTGACCA
droFic1	scf7180000453932:419490-419622 -		AACCTGCAGGTCCCTTCGTCCTCA AAGCTA-----T-----ACATATCAAGG-----GGA---CCAT--AGTCCAATA-----T-----TATG-----AATACTACCTACGTCGTACTGAAGACACCCTGTCTGTGCCATGAAGTTGAGCAGGTAGTTGACCA
droK1k1	scf7180000302273:359792-359928 +		AACCTGCAATCTCTTCGTCCTGC AAAACGSA-----T-----AAGGATCTGT-----GGAAGGATGGC--ATTTGATAT-----T-----TTTGA-----T-GCTCTACTACATCGTACTGGAAGACACCCTGTCTGTGCCATGAAGTTGAGCAGGTAGTTGACCA
droAna3	scaffold_12916:10952792-10952922 +		ACCTGCAGAGCTTCGTCCTGC AAAACAGA-----A-----ACTATAAGAA-----AAGTA-----GGA---AGAG-----T-----TCTATA-----T-GTAACACTACATCGTACTGGAAGACACTGTCTGTGCCATGAAGTTGAGCAGGTAGTTGACCA
droBip1	scf7180000396572:612230-612359 -		ATCTGCAGAGCTTTTCGTCCTGC AAAACGSA-----T-----TACTTTGAGA-----CTAGAA-----GAA---AT-----AT-----TTTGA-----T-CAAACTTACATCGTACTGGAAGACACTGTCTGTGCCATGAAGTTGAGCAGGTAGTTGACCA
dp5	4_group4:3363632-3363762 +		ATCCCTAAGATCTCGCTCAACCTGAAAGCAGTCAAATGTTAG-----CCTAATCTCT-----GGA---ATCTCTGCCTGAA-----T-----TTCATCATCATATGCAAGACACCCTATCTGTGGCATGAAGTTGAGCAGGTAGTTGACCA
droPer2	scaffold_10:2383423-2383553 +		ATCCCTAAGATCTCGCTCAACCTGCAAGCAGTCAAATGTTAG-----CCTAATCTCT-----GGA---ATCTCTGCCTGAA-----T-----TTCATCATCATATGCAAGACACCCTATCTGTGGCATGAAGTTGAGCAGGTAGTTGACCA
droW12	scf2_1100000004884:728913-729067 -		AACCTGCAGATCTCTTCCTCAAAAATAGTAAATTTTAA-----TTA-----ATTGACATATTGAGAAAAAGCAAGGACATTAATTTGTCCA--CGACCAACATCATACTGGAATAGCACCCTATCTGTGCGATGAAGTTGAGCAGGTAGTTGACCA
droVit3	scaffold_12963:4299845-4299886 -		ACCTGCAGATCTCTTTCACTCAAAAAT-----T-----TTCTATGTCCATATGA-----AAGT-----GGG---ATAT--CATCTACATCGTACTGGAAGACACCCTATCTGTGCGCAAGTTGAGCAGGTAGTTGACCA
droMoJ3	scaffold_6500:8174880-8175016 -		ATCTGCAGAACTCTTTCACTCTGCGCGGSA-----A-----AATTT--AA-----GGAATTATA-----A---AAG--TATCGAT-----CGCGAAT-----T-GAATCGTTACATCGTACTGGAAGACACCCTGTCTGTGCGATGAAGTTGAGCAGGTAGTTGACCA
droGr12	scaffold_15252:1118730-1118869 -		ACCTGCAGATCTCTTCGTCCTCAATAATTA-----A-----AAT-----ATTGAATAG-----AAAACGTATCGATTACCT-----A-----ATTITGCT--GC-TTACTACATCGTACTGGAAGACACTGATCAAGCTGTGCAAAATGAGCAGGTAGTTGACCA

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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

Predicted structure



Anti-sense strand reads

Show Alignment With Reads

Re-alignment of all predicted orthologs

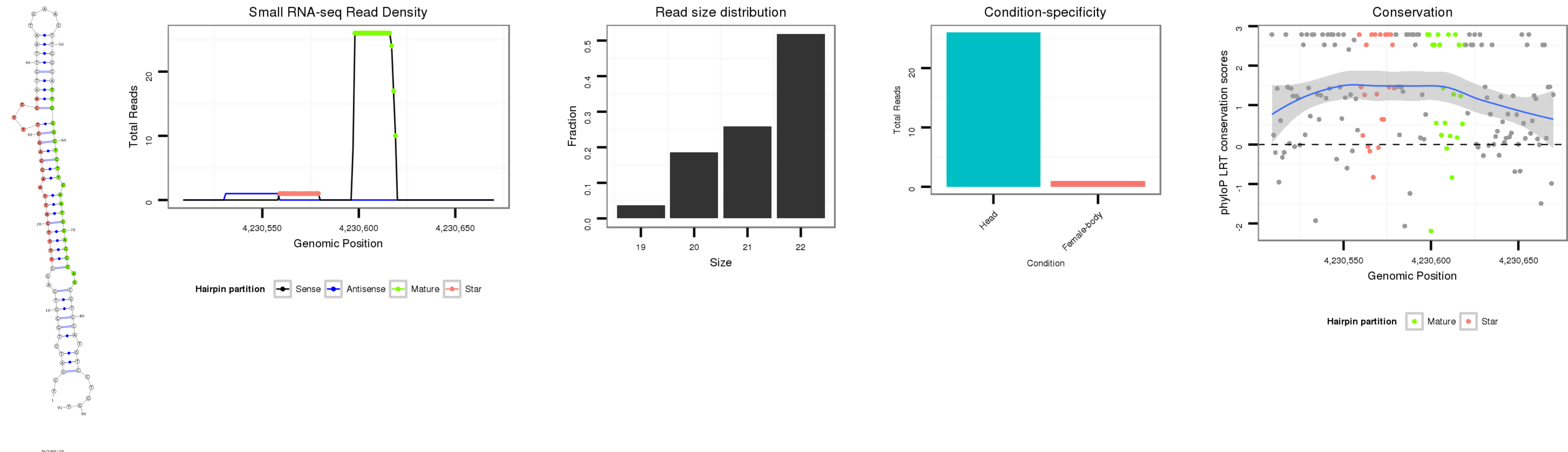
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	PASS/FAIL
crit.star	C
crit.loop	C
crit.mor	C
crit.half	C
crit.total	1
crit.pairing	C
crit.top3	1
crit.tptop3	C
crit.uri	C
crit.back	1
rescue.total	1
rescue.dominant	C
rescue.known	C
rescue.confident	C
rescue.candidate	1

dya_74	3R:4230559-4230620 +	candidate	Canonical miRNA	antisense_to_CDS	[View on UCSC Genome Browser (Cornell Mirror)]
--------	----------------------	-----------	-----------------	------------------	--

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Show Alternate Folds

Flybase annotation

Antisense to CDS [Dyak\GE25120-cds]

No Repeatable elements found

Sense Strand Reads

[illegible]

Anti-sense strand reads

Show Alignment With Reads

Re-alignment of all predicted orthologs

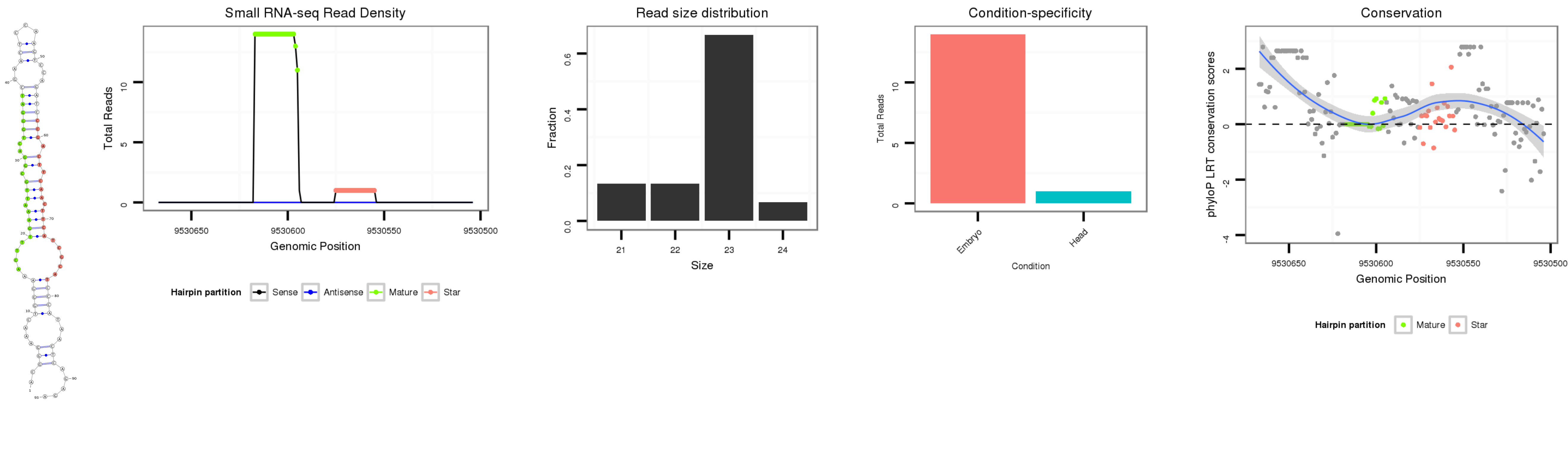
Species	Coordinate	ID	Alignment
droYak3	3R:4230509-4230670 +	dya_74	TTATTGCAATTTTCGCCGCTGATATAGCATCCATTTTCGATCTGGGTGAGGTTTTCATTAAAGGAGCTTTTCAATGTTTAATGAACCTGGCAATGGGCTCTTGAATGGAGGCAGCTCCAT---GTCTGGTCAACTGGCGCTGGAGCACCGAAGCTGCTGCCTTGG
droEre2	scaffold_4770:6181902-6182063 -		TGATTGCATTTTCGCCGCTGTATAGCATCCATTTTCGATCTGGGTGAGATTTCATTAAAGGAGCTTTTCAATGTTTAATGAACCTGGCAATGGCTCTTGAATGGAGGCAGCTCCAT---GTCTGGTCAACTGGCGCTGGAGCACCGAAGCTGCAAGCTTGG
droSec2	scaffold_25:318093-318254 -		TGATTGCATTTTCGCCGCTGTATATAGCATCCATTTTCGATCTGGGTGAGATTTCATTAAAGGAGCTTTTCAATGTTTAATGAACCTGGCAATGGGCTCTTGAATGGAGGCAGCTCCAT---GTCTGGTCAACTGGCGCTGGAGCACCGAAGCTGCTGCCTTGG
droSim2	3r:5806798-5806957 -		TGATTGCATTTTCGCCGCTGTATATAGCATCCATTTTCGATCTGGGTGAGATTTCATTAAAGGAGCTTTTCAATGTTTAATGAACCTGGCAATGGGCTCTTGAATGGAGGCAGCTCCAT---GTCTGGTCAACTGGCGCTGGAGCACCGAAGCTGCTGCCTTGG
dm3	chr3R:15459707-15459868 +		TGATTGCATTTTCGCCGCTGTATATAGCATCCATTTTCGATCTGGGTGAGATTTCATTAAAGGAGCTTTTCAATGTTTAATGAACCTGGCAATGGCTCTTGAATGGAGGCAGCTCCAT---GTCTGGTCAACTGGCGCTGGAGCACCGAAGCTGCTGCCTTGG
droBup1	scf7180000409804:1753048-1753209 +		TGGTCGATTTTCGCCGCTGTATATAGCATCCATTTTCGATCTGGGTGAGATTTCATTAAAGGAGCTTTTCAATGTTTAATGAACCTGGCAATGGCTCTTGAATGGAGGCAGCTCCAT---GTCTGGTCAACTGGCGCTGGAGCACCGAAGCTGCTGCCTTGG
droBial1	scf7180000302402:1239231-1239392 +		TGATTGCGTTTTTCGCCGCTGTATATAGCATCCATTTTCGATCTGGGTGAGATTTCATTAAAGGAGCTTTTCAATGTTTAATGAACCTGGCAATGGCTCTTGAATGGAGGCAGCTCCAT---GTCTGGTCAACTGGCGCTGGAGCACCGAAGCTGCTGCCTTGG
droTak1	scf7180000415710:360177-360338 +		TGATTGCGTTTTTCGCCGCTGTATATAGCATCCATTTTCGATCTGGGTGAGATTTCATTAAAGGAGCTTTTCAATGTTTAATGAACCTGGCAATGGCTCTTGAATGGAGGCAGCTCCAT---GTCTGGTCAACTGGCGCTGGAGCACCGAAGCTGCTGCCTTGG
droEl1	scf7180000486474:87807-87968 +		TGATCGATTTTCGCCGCTGTATATAGCATCCATTTTCGATCTGGGTGAGATTTCGGTGACAGCTTTTCAATGTTTAATGAACCTGGCAATGGCTCTTGAATGGAGGCAGCTCCAT---GTCTGGTCAACTGGCGCTGGAGCACCGAAGCTGCTGCCTTGG
droRho1	scf7180000778053:1720-1881 +		TGATCGATTTTCGCCGCTGTATATAGCATCCATTTTCGATCTGGGTGAGATTTCGGTGACAGCTTTTCAATGTTTAATGAACCTGGCAATGGCTCTTGAATGGAGGCAGCTCCAT---GTCTGGTCAACTGGCGCTGGAGCACCGAAGCTGCTGCCTTGG
droPie1	scf7180000454126:466403-466564 +		TGGTCGCTTTTCGCCGCTGTATATAGCATCCATTTTCGATCTGGGTGAGATTTCGGTGACAGCTTTTCAATGTTTAATGAACCTGGCAATGGCTCTTGAATGGAGGCAGCTCCAT---GTCTGGTCAACTGGCGCTGGAGCACCGAAGCTGCTGCCTTGG
droKik1	scf7180000302666:162338-162499 +		TTATTGCGTTTTTCGCCGCTGTATATAGCATCCATTTTCGATCTGGGTGAGATTTCGGTGACAGCTTTTCAATGTTTAATGAACCTGGCAATGGGCTCTTGAATGGAGGCAGCTCCAT---GTCTGGTCAACTGGCGCTGGAGCACCGAAGCTGCTGCCTTGG
droAna3	scaffold_13340:14941922-14942083 -		TGGTTTGTGTTTTTCGCCGCTGTATATAGCATCCATTTTCGATCTGGGTGAGATTTCGGTGACAGCTTTTCAATGTTTAATGAACCTGGCAATGGGCTCTTGAATGGAGGCAGCTCCAT---GTCTGGTCAACTGGCGCTGGAGCACCGAAGCTGCTGCCTTGG
droBip1	scf7180000395971:245035-245196 +		TGGTTTGTGTTTTTCGCCGCTGTATATAGCATCCATTTTCGATCTGGGTGAGATTTCGGTGACAGCTTTTCAATGTTTAATGAACCTGGCAATGGGCTCTTGAATGGAGGCAGCTCCAT---GTCTGGTCAACTGGCGCTGGAGCACCGAAGCTGCTGCCTTGG
dp5	2:29969064-29969225 +		TGAGAGATCCCGAGAGCTGATAGCATCGATTTTCGATCTGGGTGAGATTTCGGTGACAGCTTTTCAATGTTTAATGAACCTGGCAATGGGCTCTTGAATGGAGGCAGCTCCAT---GTCTGGTCAACTGGCGCTGGAGCACCGAAGCTGCTGCCTTGG
droPer2	scaffold_6:5338296-5338457 +		TGAGAGATCCCGAGAGCTGATAGCATCGATTTTCGATCTGGGTGAGATTTCGGTGACAGCTTTTCAATGTTTAATGAACCTGGCAATGGGCTCTTGAATGGAGGCAGCTCCAT---GTCTGGTCAACTGGCGCTGGAGCACCGAAGCTGCTGCCTTGG
droWil2	scf2_1100000004902:8342590-8342754 -		TATGCTATTTCGCCGCTGTATATAGCATCCATTTTCGATCTGGGTGAGATTTCGGTGACAGCTTTTCAATGTTTAATGAACCTGGCAATGGGCTCTTGAATGGAGGCAGCTCCAT---GTCTGGTCAACTGGCGCTGGAGCACCGAAGCTGCTGCCTTGG
droVir3	scaffold_13047:16119356-16119517 -		TGGTCGAGTTTTTCGCCGCTGTATATAGCATCCATTTTCGATCTGGGTGAGATTTCGGTGACAGCTTTTCAATGTTTAATGAACCTGGCAATGGGCTCTTGAATGGAGGCAGCTCCAT---GTCTGGTCAACTGGCGCTGGAGCACCGAAGCTGCTGCCTTGG
droMoJ3	scaffold_6540:14924277-14924438 -		TGGTCGATTTTCGCCGCTGTATATAGCATCCATTTTCGATCTGGGTGAGATTTCGGTGACAGCTTTTCAATGTTTAATGAACCTGGCAATGGGCTCTTGAATGGAGGCAGCTCCAT---GTCTGGTCAACTGGCGCTGGAGCACCGAAGCTGCTGCCTTGG
droGr12	scaffold_15116:968792-968944 -		TGGTCGATTTTCGCCGCTGTATATAGCATCCATTTTCGATCTGGGTGAGATTTCGGTGACAGCTTTTCAATGTTTAATGAACCTGGCAATGGGCTCTTGAATGGAGGCAGCTCCAT---GTCTGGTCAACTGGCGCTGGAGCACCGAAGCTGCTGCCTTGG

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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	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

AAACGCTGGTATAATATTATTACGTCCTCTCAAGACGGGAAACTGGGAACTTTGAAATTCGGGACTGGGATCGAACCTCAAGTCCAGATCCGACTTCAACTTCATCGCATCCCATAACTCAGAGATCGCGCTAGCGGGGGCGGTGGCGGTGGCGCGGT

*****(((.....(((

Anti-sense strand reads

[illegible]

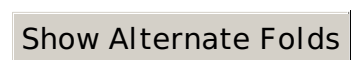
Re-alignment of all predicted orthologs

Coordinate	ID	Alignment
droYak3 Zr:19530504-9530667 -	dya_143	AAACGCTGGTTAAATTAATTTACGTGCTCTCAAGACG---GGAAAGTCTCGA AGTTTGAATTTCGGACTTGGATCGA-----ACTCC--AAGTC--CAGATCCGACITCA-A---CTTCA-TCGCA---CCCATAACTCAG-AGATGGCGTGA-----GGC--G--GGGGCGGTG-68CGGTGG-----CGG-T
droEre2 scaf01d_4845:18367456-18367584 -		AAACGCTGGTTAAATTAATTTACGTGCTCTCAGAGCG---CGGAGCTAC -----GGACTTGGATCGG-----ACTCC--AAGTCGGGAGCTCG-----CA-A---CTCA-TCGCA---CCCATAACTCAG-AGATGGGAGAG-----GC-----CGGG-----CGG-T
droSec2 scaf01d_14981493-4981607 -		AAACGCTGGTTAAATTAATTTACGTGCTCTCAAGACG---GGAAAGTCTAC -----GGACTTGGATCGG-----ACTCC--AAGTC-----TTGCG-A---CTCA-TCGCA---CCCATAACTCAAGAGATCGGGGTG-----GGCG--G-----GGG-----CGG-G
droSim2 Zr:8134719-8134852 +		AAACGCTGGTTAAATTAATTTACGTGCTCTCAAGACG---GGAAAGTCTAC -----GGACTTGGATCGG-----ACTCC--AAGTC--CAGATAGCACTTCG-A---CTCA-TCGCA---CCCATAACTCAAGAGATCGGGGTG-----GGCG--G-----GGG-----CGG-G
dm3 chr28:7430264-7430398 +		AAACGCTGGTTAAATTAATTTACGTGCTCTCAAGACG---GGAAAGTCTAC -----GGACTTGGATCGG-----ACTCC--AAGTC--CAGATCGAAGTTTCG-A---CTCA-TCGCA---CCCATAACTCAAGAGATCGGGGTG-----GGCG--G-----GGG-----CGG-G
droBug1 scf7180000409462:1072031-1072179 -		AAACGCTGGTTAAATTAATTTACGTGCTCTCAAGACG---GGAAAGTCTGAGACTTGGGACGCGGTACTCG---AAACTCCGGAGCTCCACATAC-----ATCC-----AAGCG-A---CTCA-TCGCA---CCCATAACTCAAGAGATCGGGGTG-----GGCG--G-----GGG-----CGG-G
droBia1 scf7180000302292:195749-195856 +		AAACGCTGGTTAAATTAATTTACGTGCTCTCAAGAGCG---AAGAGGCTCC AGACTCTCG-----DCA-----GCTCGGAGG-----CTCGCG---GTGCG-CGGC---A---CCCATAACTCAG-AGATGGCGGAG-----GG-----GGG-----CGG-G
droTak1 scf7180000415991:720611-720725 +		AAACGCTGGTTAAATTAATTTACGTGCTCTCAAGACG---GGAAAGTCTCG -----A-----CTGGAGCT-----GCGAG---CTCGCG---GTGCG-A---CCCATAACTCAAGAGATGGCGGAG-----AGG-----GGG-----CGG-G
droIel1 scf7180000491214:2887203-2887312 +		AAACGCTGGTTAAATTAATTTACGTGCTCTCAAGACG---GGAAAGTCTCA -----A-----G-----CTCGCG---GTGCG-A---CCCATAACTCAAGAGATGGCGGAG-----AGG-----GGG-----CGG-G
droRho1 scf7180000779263:118948-119053 -		AAACGCTGGTTAAATTAATTTACGTGCTCTCAAGACG---GGAAAGTCTCG -----A-----G-----CTCGCG---GTGCG-A---CCCATAACTCAG--SATCGGCGAAG-----GGGGAA--A-----AGGAG-----AGG-G
droIcl1 scf7180000453773:359782-359830 -		AAACGCTGGTTAAATTAATTTACGTGCTCTCAGACGCGAGGAGTCTCG---G-ATTC--AGACTCC -----A-----CTCGCG---GTGCG-A---CCCATAACTCAG--SATCGGCGGAG-----GAA--G--G-----GGG-----CGG-G
droKik1 scf7180000302386:462114-462172 -		CCAGCTCGTTAAATTAATTTACGTGCTCTCAGCGGAGGAGTCTCG---G-ATTC--AGACTCC -----A-----CTCGCG---GTGCG-A---CCCATAACTCAG--SATCGGCGGAG-----GAA--G--G-----GGG-----CGG-G
droAna2 scaf01d_13266:1141502-1141648 +		AAAGCTGGTTAAATTAATTTACGTGCTCTCAGCGGAGGAGTCTCG---G-ATTC--AGACTCC -----A-----CTCGCG---GTGCG-A---CCCATAACTCAG--SATCGGCGGAG-----GAA--G--G-----GGG-----CGG-G
droBip1 scf7180000396730:2134434-2134562 +		AAACGCTGGTTAAATTAATTTACGTGCTCTCAGCGGAGGAGTCTCG---G-ATTC--AGACTCC -----A-----CTCGCG---GTGCG-A---CCCATAACTCAG--SATCGGCGGAG-----GAA--G--G-----GGG-----CGG-G
dp5 144615015-14615132 +		AAACGCTGGTTAAATTAATTTACGTGCTCTCAGCGGAGGAGTCTCG---G-ATTC--AGACTCC -----A-----CTCGCG---GTGCG-A---CCCATAACTCAG--SATCGGCGGAG-----GAA--G--G-----GGG-----CGG-G
droPer1 scaf01d_24801835-4801952 -		AAACGCTGGTTAAATTAATTTACGTGCTCTCAGCGGAGGAGTCTCG---G-ATTC--AGACTCC -----A-----CTCGCG---GTGCG-A---CCCATAACTCAG--SATCGGCGGAG-----GAA--G--G-----GGG-----CGG-G
droWil2 scf2_1100000004558:1976450-1976612 -		AAAGCTGGTTAAATTAATTTACGTGCTCTCAGCGGAGGAGTCTCG---G-ATTC--AGACTCC -----A-----CTCGCG---GTGCG-A---CCCATAACTCAG--SATCGGCGGAG-----GAA--G--G-----GGG-----CGG-G
droVir1 scaf01d_12875:13033658-13033763 -		AAACGCTGGTTAAATTAATTTACGTGCTCTCAGCGGAGGAGTCTCG---G-ATTC--AGACTCC -----A-----CTCGCG---GTGCG-A---CCCATAACTCAG--SATCGGCGGAG-----GAA--G--G-----GGG-----CGG-G
droMoJ3 scaf01d_6496:20301287-20301369 -		AAACGCTGGTTAAATTAATTTACGTGCTCTCAGCGGAGGAGTCTCG---G-ATTC--AGACTCC -----A-----CTCGCG---GTGCG-A---CCCATAACTCAG--SATCGGCGGAG-----GAA--G--G-----GGG-----CGG-G
droGr12 scaf01d_15245:7336299-7336381 +		AAACGCTGGTTAAATTAATTTACGTGCTCTCAGCGGAGGAGTCTCG---G-ATTC--AGACTCC -----A-----CTCGCG---GTGCG-A---CCCATAACTCAG--SATCGGCGGAG-----GAA--G--G-----GGG-----CGG-G

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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

Predicted structure



Flybase annotation

intron [Dyak\GE21370-in]; utr5 [utr5_plus_6659]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

[illegible]

Anti-sense strand reads

[illegible]

No data available in table

Show Alignment With Reads

Re-alignment of all predicted orthologs

[illegible]

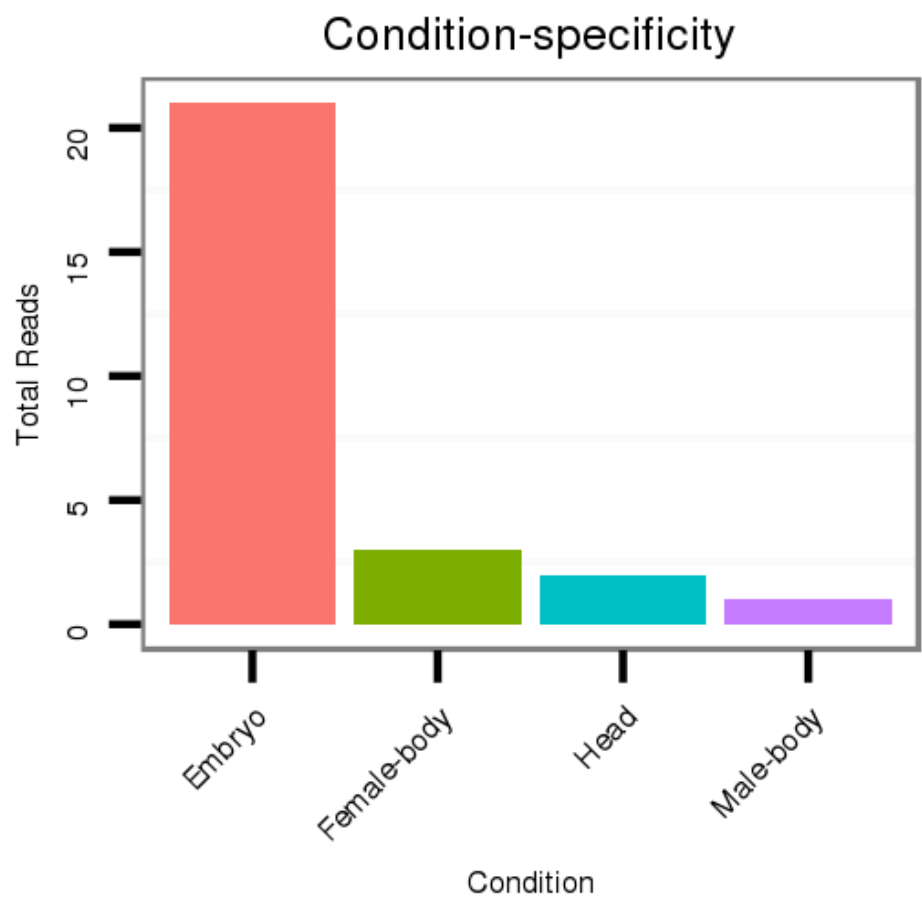
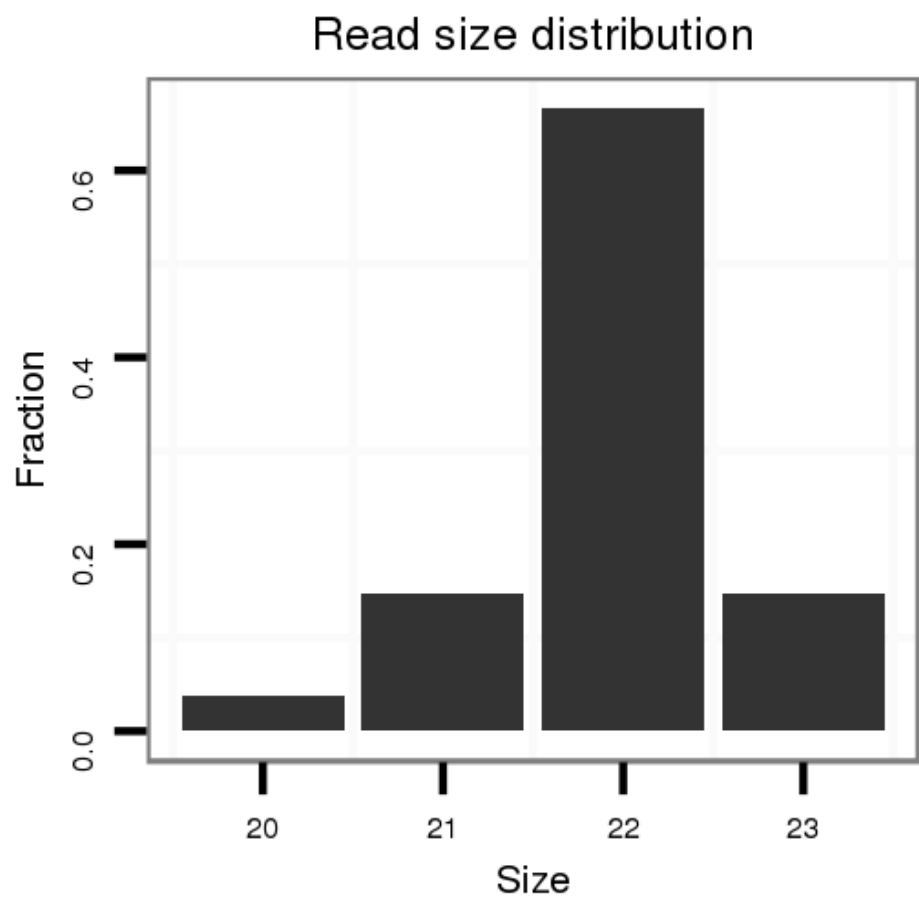
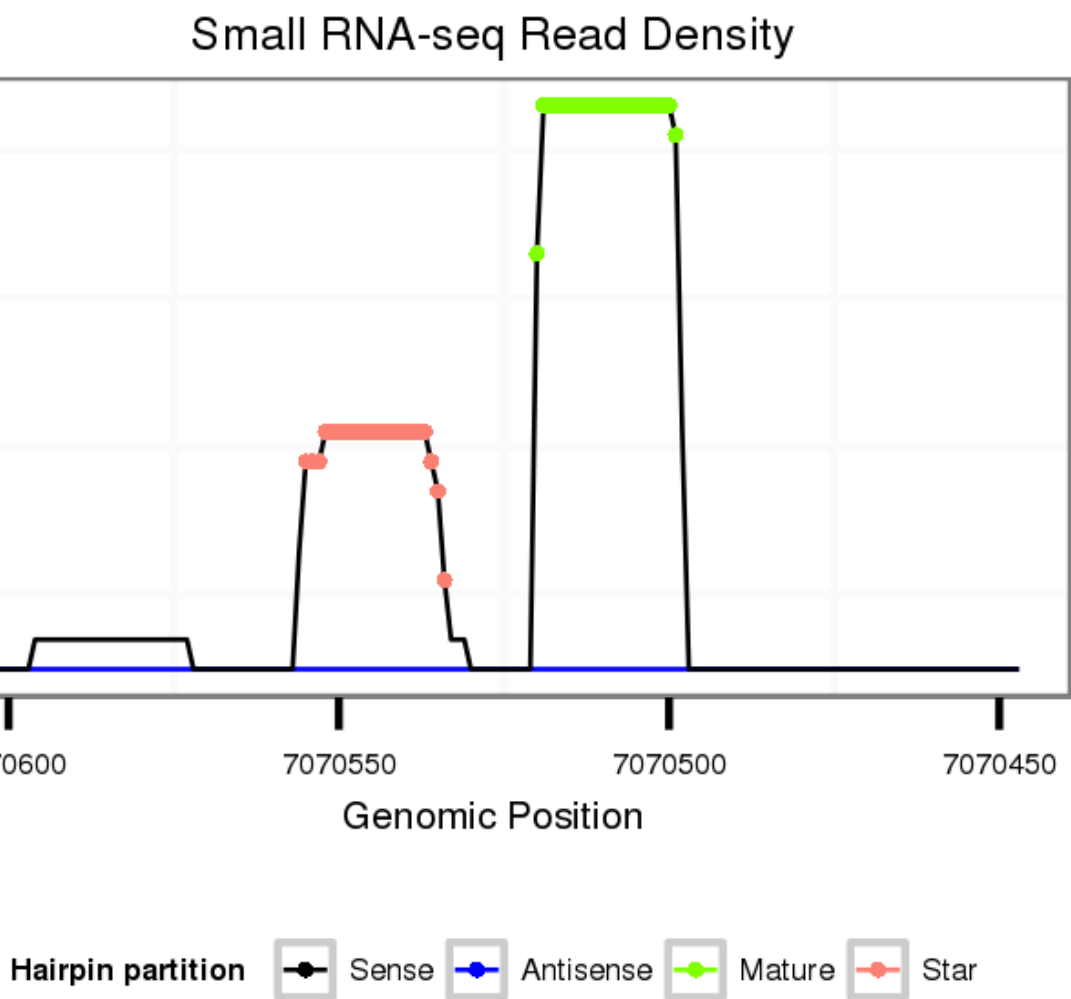
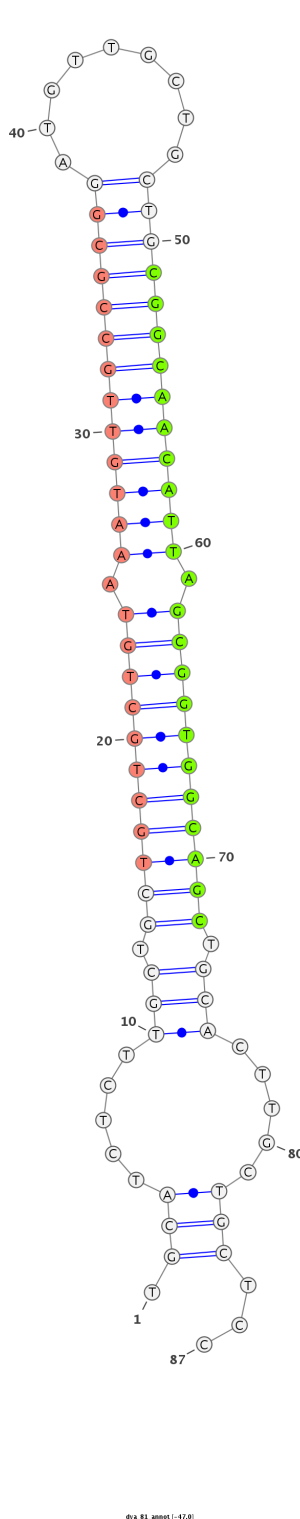
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	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	2

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dya_81	2R:7070497-7070556	candidate	Canonical miRNA	intergenic	[View on UCSC Genome Browser (Cornell Mirror)]

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

Predicted structure



Show Alternate Folds

Flybase annotation

intergenic

Repeatable elements

Name	Class	Family	Strand
(CAG)n	Simple_repeat	Simple_repeat	+
TART_DV	LINE	Jockey	+

Sense Strand Reads

hide 3p reads show mid mismatch reads

Read #	Read size	Hit	Total	M056	V046	V052	M043	V058	V120
size	Mismatch	Count	Norm	embryo	embryo	head	female	head	male
22	0	1	9.00	6	1	2	0	0	0
23	0	1	4.00	4	2	2	0	0	0
22	0	1	4.00	4	0	3	0	0	1
22	0	1	2.00	2	0	0	2	0	0
22	0	1	2.00	2	2	0	0	0	0
20	1	1	1.00	1	0	0	0	0	0
21	0	1	1.00	1	0	1	0	0	0
21	0	1	1.00	1	0	0	1	0	0
24	0	1	1.00	1	1	0	0	0	0
21	0	1	1.00	1	1	0	0	0	0
22	1	1	1.00	1	1	0	0	0	0
21	0	1	1.00	1	0	1	0	0	0
22	0	1	1.00	1	1	0	0	0	0
22	0	1	1.00	1	1	0	0	0	0
22	0	1	1.00	1	1	0	0	0	0

Anti-sense strand reads

Read #	Read size	Hit	Total	Total
22	0	1	9.00	9
23	0	1	4.00	4
22	0	1	4.00	4
22	0	1	2.00	2
22	0	1	2.00	2
20	1	1	1.00	1
21	0	1	1.00	1
21	0	1	1.00	1
24	0	1	1.00	1
21	0	1	1.00	1
22	1	1	1.00	1
21	0	1	1.00	1
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22	0	1	1.00	1

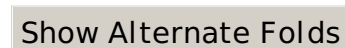
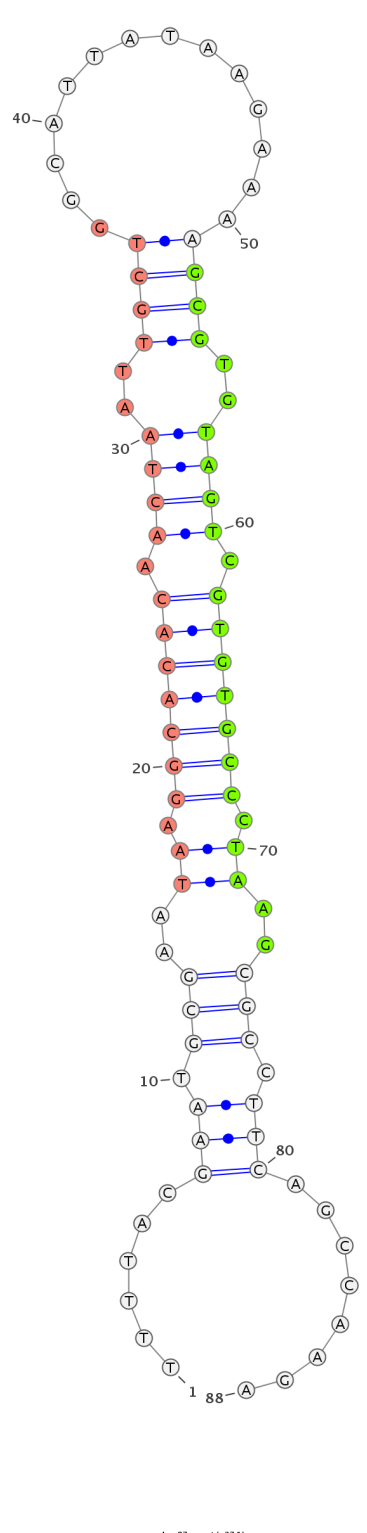
Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droYak3	2R:7070447-7070606 -	dya_1821	TGTTGCCGCTGTACATGTTGCCGCTG-----TTGCCG--CCACTGCATCTCTT---GCTGCT-----GCT-----GCTGTAATGTTGCCGCGA-----T---GTTGCTGCTGCGG---AACAT-T-AGCGGTGGC-----AGGTGCACTTGC-----TGCTCCGACCCCAAGATGCGGATATTAA--TTTGCTTAAC---ATTTC
droEre2	scaffold_4845:15938436-15938594 -		TGTTGCCGCTGTACATGTTGCCGCTG-----TTGCCG--CCACTGCATCTCTT---ACTGCT-----GCTGTAATGTTGCCGCGA-----T---GTTGCTGCTGCGG---AACAT-T-C-CCGTTGGC-----AGGTGCACTTGC-----TGCTCCGACCCCAAGATGCGGATATTAA--TTTGCTTAAC---ATTTC
droSec2	scaffold_1:7407990-7408149 +		TGTTGCCGCTGTACATGTTGCCGCTG-----TTGCCG--CCACTGCATCTCTT---GCTGCT-----GCTGTAATGTTGCCGCGA-----T---GTTGCTGCTGCGG---AACAT-T-T-CCGTTGGC-----AGGTGCACTTGC-----TGCTCCGACCCCAAGATGCGGATATTAA--TTTGCTTAAC---ATTTC
droSim2	2r:10570805-10570963 +		TGTTGCCGCTGTACATGTTGCCGCTG-----TTGCCG--CCACTGCATCTCTT---GCTGCT-----GCTGTAATGTTGCCGCGA-----T---GTTGCTGCTGCGG---AACAT-T-C-CCGTTGGC-----AGGTGCACTTGC-----TGCTCCGACCCCAAGATGCGGATATTAA--TTTGCTTAAC---ATTTC
dm3	chr2R:9882419-9882583 +		TGTTGCCGCTGTACATGTTGCCGCTG-----TTGCCG--CCACTGCATCTCTT---GCTGCT-----GCTGTAATGTTGCCGCGA-----T---GTTGCTGCTGCGG---AACAT-T-C-CCGTTGGC-----AGGTGCACTTGC-----TGCTCCGACCCCAAGATGCGGATATTAA--TTTGCTTAAC---ATTTC
droEu1	scf7180000409462:2961151-2961334 -		TGTTGCCGCTGTACATGTTGCCGCTG-----TTGCCG--CCACTGCATCTCTT---GCTGCT-----GCTGTAATGTTGCCGCGA-----T---GTTGCTGCTGCGG---AACAT-T-C-CCGTTGGC-----AGGTGCACTTGC-----TGCTCCGACCCCAAGATGCGGATATTAA--TTTGCTTAAC---ATTTC
droBial	scf7180000301592:35618-35790 +		TGTTGCCGCTGTACATGTTGCCGCTG-----TTGCCG--CCACTGCATCTCTT---GCTGCT-----GCTGTAATGTTGCCGCGA-----T---GTTGCTGCTGCGG---AACAT-T-C-CCGTTGGC-----AGGTGCACTTGC-----TGCTCCGACCCCAAGATGCGGATATTAA--TTTGCTTAAC---ATTTC
droTak1	scf7180000415376:102980-103117 +		TGTTGCCGCTGTACATGTTGCCGCTG-----TTGCCG--CCACTGCATCTCTT---GCTGCT-----GCTGTAATGTTGCCGCGA-----T---GTTGCTGCTGCGG---AACAT-T-C-CCGTTGGC-----AGGTGCACTTGC-----TGCTCCGACCCCAAGATGCGGATATTAA--TTTGCTTAAC---ATTTC
droEle1	scf7180000491214:67425-67595 -		TGTTGCCGCTGTACATGTTGCCGCTG-----TTGCCG--CCACTGCATCTCTT---GCTGCT-----GCTGTAATGTTGCCGCGA-----T---GTTGCTGCTGCGG---AACAT-T-C-CCGTTGGC-----AGGTGCACTTGC-----TGCTCCGACCCCAAGATGCGGATATTAA--TTTGCTTAAC---ATTTC
droRho1	scf7180000777200:203533-203703 +		TGTTGCCGCTGTACATGTTGCCGCTG-----TTGCCG--CCACTGCATCTCTT---GCTGCT-----GCTGTAATGTTGCCGCGA-----T---GTTGCTGCTGCGG---AACAT-T-C-CCGTTGGC-----AGGTGCACTTGC-----TGCTCCGACCCCAAGATGCGGATATTAA--TTTGCTTAAC---ATTTC
droFi1	scf7180000453948:530462-530640 -		TGTTGCCGCTGTACATGTTGCCGCTG-----TTGCCG--CCACTGCATCTCTT---GCTGCT-----GCTGTAATGTTGCCGCGA-----T---GTTGCTGCTGCGG---AACAT-T-C-CCGTTGGC-----AGGTGCACTTGC-----TGCTCCGACCCCAAGATGCGGATATTAA--TTTGCTTAAC---ATTTC
droK1k1	scf7180000302366:1305648-1305801 +		TGTTGCCGCTGTACATGTTGCCGCTG-----TTGCCG--CCACTGCATCTCTT---GCTGCT-----GCTGTAATGTTGCCGCGA-----T---GTTGCTGCTGCGG---AACAT-T-C-CCGTTGGC-----AGGTGCACTTGC-----TGCTCCGACCCCAAGATGCGGATATTAA--TTTGCTTAAC---ATTTC
droAna3	scaffold_13117:4608404-4608556 -		TGTTGCCGCTGTACATGTTGCCGCTG-----TTGCCG--CCACTGCATCTCTT---GCTGCT-----GCTGTAATGTTGCCGCGA-----T---GTTGCTGCTGCGG---AACAT-T-C-CCGTTGGC-----AGGTGCACTTGC-----TGCTCCGACCCCAAGATGCGGATATTAA--TTTGCTTAAC---ATTTC
droBip1	scf7180000396541:615627-615779 +		TGTTGCCGCTGTACATGTTGCCGCTG-----TTGCCG--CCACTGCATCTCTT---GCTGCT-----GCTGTAATGTTGCCGCGA-----T---GTTGCTGCTGCGG---AACAT-T-C-CCGTTGGC-----AGGTGCACTTGC-----TGCTCCGACCCCAAGATGCGGATATTAA--TTTGCTTAAC---ATTTC
dp5	Unknown_singleton_1849:5202-5366 -		TGTTGCCGCTGTACATGTTGCCGCTG-----TTGCCG--CCACTGCATCTCTT---GCTGCT-----GCTGTAATGTTGCCGCGA-----T---GTTGCTGCTGCGG---AACAT-T-C-CCGTTGGC-----AGGTGCACTTGC-----TGCTCCGACCCCAAGATGCGGATATTAA--TTTGCTTAAC---ATTTC
droPer2	scaffold_2:5826749-5826890 +		TGTTGCCGCTGTACATGTTGCCGCTG-----TTGCCG--CCACTGCATCTCTT---GCTGCT-----GCTGTAATGTTGCCGCGA-----T---GTTGCTGCTGCGG---AACAT-T-C-CCGTTGGC-----AGGTGCACTTGC-----TGCTCCGACCCCAAGATGCGGATATTAA--TTTGCTTAAC---ATTTC
droW12	scf2_1100000004967:3551565-3551717 +		TGTTGCCGCTGTACATGTTGCCGCTG-----TTGCCG--CCACTGCATCTCTT---GCTGCT-----GCTGTAATGTTGCCGCGA-----T---GTTGCTGCTGCGG---AACAT-T-C-CCGTTGGC-----AGGTGCACTTGC-----TGCTCCGACCCCAAGATGCGGATATTAA--TTTGCTTAAC---ATTTC
droVi3	scaffold_12928:511852-512012 -		TGTTGCCGCTGTACATGTTGCCGCTG-----TTGCCG--CCACTGCATCTCTT---GCTGCT-----GCTGTAATGTTGCCGCGA-----T---GTTGCTGCTGCGG---AACAT-T-C-CCGTTGGC-----AGGTGCACTTGC-----TGCTCCGACCCCAAGATGCGGATATTAA--TTTGCTTAAC---ATTTC
droMo3	scaffold_6500:16033594-16033752 +		TGTTGCCGCTGTACATGTTGCCGCTG-----TTGCCG--CCACTGCATCTCTT---GCTGCT-----GCTGTAATGTTGCCGCGA-----T---GTTGCTGCTGCGG---AACAT-T-C-CCGTTGGC-----AGGTGCACTTGC-----TGCTCCGACCCCAAGATGCGGATATTAA--TTTGCTTAAC---ATTTC
droGr12	scaffold_15245:11423090-11423247 +		TGTTGCCGCTGTACATGTTGCCGCTG-----TTGCCG--CCACTGCATCTCTT---GCTGCT-----GCTGTAATGTTGCCGCGA-----T---GTTGCTGCTGCGG---AACAT-T-C-CCGTTGGC-----AGGTGCACTTGC-----TGCTCCGACCCCAAGATGCGGATATTAA--TTTGCTTAAC---ATTTC

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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.top3	1
crit.un	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



intron [Dyak\GE25403-in]

No Repeatable elements found

No Repeatable elements found

hide 3p reads show mid mismatch reads

[illegible][illegible]

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droYaX3	3R:475254-47542 +	dya_87	CAAGGG-----TCCCTG--AGTGGATGG-----AAGAGCAA--ATGTTT-----TACGAATCGGAATAAAGGCACACAACCTAATTGCTGSCATTAT-----AAGAA-AA--CGCTGTAGTGTGTG--CGCTAAAGC-----GCC-----TTACGCCAAGATGGTCGGAACAGTCAAAATGCGCAT--GGCGGCGTAAT
droBr2e	scaffold_4770:464725-464929 +		CAAGGG-----ACCTG--AGTGGATGG-----AAGGCcAA--ATGCTTG-----CAGCAATGCGAATGAGGCACACAACCTAATTGCTGCAATTAT-----CAGAA-AA--CGCTGTAGTGTGTG--CAGGCGCGGAAATGCGAAATGCGAGA--TG-----CTGCGT--CCTGGCCAAGAGCCCTAAAGC-----GCC-----TTACGCCAAGATGGTCGGAACAGTCAAAATGCGCAT--GGCGGCGTAAT
droSe2d	scaffold_6:234702-234901 +		CAAGGG-----TCCCg--AGTGGATGG-----AAGAGCAA--ATGTTT-----CAGCAATGCGAATGAGGCCTACAACCTAATTGCTGCGATTAG-----CAGTTCGAA--CGCTGTAG--CCTGTG--CAGGCGCGGAAATGCG-----CTGCGG--CGTGGCCAAGAGCCCTAAAGC-----GCC--CTCAGCCC--TTACGCCAAGATGGTCGGAACAGTCAAAATGCGCAT--GGCGGCGTAAT
droSim2	3r:99799-99998 +		CAAGGG-----TCCCg--AGTGGATGG-----AAGAGCAA--ATGTTT-----CAGCAATGCGAATGAGGCCTACAACCTAATTGCTGCGATTAT-----CAGTTCGAA--CGCTGTAG--CCTGTG--CAGGCGCGGAAATGCG-----CTGCGG--CGTGGCCAAGAGCCCTAAAGC-----GCC--CTCAGCCC--TTACGCCAAGATGGTCGGAACAGTCAAAATGCGCAT--GGCGGCGTAAT
dm3	chr3R:115231-115429 +		CAAGGG-----TCCCg--AGTGGATGG-----AAGAGCAA--ATGTTT-----CAGCAATGCGAATGAGGCCTACAACCTAATTGCTGCGATTAT-----CAGTTCGAA--CGCTGTAG--CCTGTG--CAGGCGCGGAAATGCG-----CTGCGG--CGTGGCCAAGAGCTTTAAGC-----GCC--CTCAGCCCTG--TTTCCCAAGATGGTCGGAACAGTCAAAATGCGCAT--GGCGGCGTAAT
droEug1	scf7180000409759:49575-49728 -		GAAATSc-----TCGCTA--AGTAATGTGA-----AAGAACA--ATGTTT-----CAGCAATATAGAGGAGCACACACTAATTGCGGSCATTAT-----AAGAAC-AA-----AGTCTGTA-----CCGT--CCTAACCAAGAGCCCTGCGC-----GAT--TGC-----CCTT-----CAGTCAAAATGCGCAT--GGCGGCGTAAT
droB1a1	scf7180000302098:370641-370821 -		CAAGGG-----TCCCg--AGTGGCGCGGG-----AG--GAA--ATGTCT-----CAGCAATGCGAATGAGGCACACAACCTAATTGCTGCGCATAT-----AGTCRA--AG-----AG--CTGCACGCGTGAAATGCG-----CTCCGT--CCTAGCCAAGAGGCGCAGC-----GCC-----TTACGCCAAGATGTCGGAACAGTCAAAATGCGCAT--GGCGGCGTAAT
droTaX1	scf7180000414441:41794-41991 -		CAAGGG-----TCCCTG--AGTGGATGCAATGCGGATGTGG--AAGAGCAA--ATGTTT-----CAGCAATGCGAATGAGGCACACAACCTAATTGCTGCGATTAT-----AAGAA-AG-----CCTGTG--CAGCGCGTGAAATGCG-----CTCCGT--CCTAGCCAAGAGCCCTGAGC-----GCC-----TTACGCCAAGATGTCGGAACAGTCAAAATGCGCAT--GGCGGCGTAAT
droE1e1	scf7180000491104:1850737-1850899 +		CAAAATScg-----TCGCTg--CAATGGAATGTGAACGTGTACTGGGAGTgScAA--CTGScAGTGGCAGTGGATGCGGCAATG--GGCAGC-----AAGAA--CG-----AGTG-----AC-----GCC-----TTACGCCAAGATGGTGCAGACAGTCAAAATGCGCAT--GGCGGCGTAAT
droRho1	scf718000077910:20580-20773 -		AAAGGG-----TCGCTg--GTGGGAATGG-----AGSAGGAA--ATGCTTG-----CAGCAATGCGGGGGGSGCGACACTAATTGCTGSCATTAT-----AAGAA-AG-----GTCGTGTG--CAGGCGGTGAAATGCG-----CTCCGT--CC--CCCCAAGAGCCCTGAGC-----GCCGAAGAGTCCG--TCAGCCCAAGATGGTGCAGACAGTCAAAATGCGCAT--GGCGGCGTAAT
droF1c1	scf7180000454096:1238068-1238225 +		CAAAATCCAGCCCTTCCCTG--GCTG-----GAGAA--ATGCTCT-----CAGCAATGCGAGTGGCGCACTCAACTAATTGCTGCGCATG--GGG-----GGA--AG-----ATCTGT--TGGCGCGCGGAAATGCG-----CTTCTT-----TGC-----TTACGCCAAGATGTCGGAACAGTCAAAATGCGCAT--GGCGGCGTAAT
droK1k1	scf7180000302634:761129-761369 +		CCAAATAGG-----TCCCTg--G-----C-----AAGCGGG--TNGTTT-----TGCTGTGTGCACACGCTTAAACTAATTGCTGCGCCACACATTACATCTATGTACATACATACATACAGAA-AG-----AGTCTGTG--CAGGCGGTGAAATGICAA--CGGGATATCCTTGCGCTATCCTTGCTTCCGTTCTTTGTGAAGAGCGTAAGAGTCACTGCTC-----TTACGCCAAGATGTCGGAACAGTCAAAATGCGCAT--GGCGGCGTAAT
droAna3	scaffold_13340:11121479-11121552 +		A-----G-----GTGGAAATGGATGGGT--CAGTTCGAA--TTCGTAAT-----TA-----CGGGCAAAACTAATTGCTGCGCCAT-----AAGCAA-----GTCTGTG-----G-----G-----TTACGCCAAGATGTCGGAACAGTCAAAATGCGCAT--GGCGGCGTAAT
droB1p1	scf7180000396734:158009-158097 +		CGGGTg-----TTCCTT--ATCAAAATGAGT-----AAGAACAA--ATTCGTAAT-----TGTAGATACGAAAGAGAGAGTTTAACTAATTGCTTACAAATGA-----GTCGTAAGCA-----G-----G-----TTACGCCAAGATGTCGGAACAGTCAAAATGCGCAT--GGCGGCGTAAT
dp5	2:24817348-24817514 -		CAAAATScg-----TCGCTg--SCAAATAGG-----ACACGGTGTGG-----TCCCTGCGAGATGAGGCAATGCAACTAATTGCTGCGCCATC-----AAGAA--CG-----ACCGTGTGCAACCAGCGAGCTGTCAA--TGAGA-----TTTTCAGCTTGTCGG--AGACAGSAG--AGCCAGTGCATCT--GGTGCATTAAT
droPer2	scaffold_6117997-18163 -		CAAAATScg-----TCGCTg--SCAAATAGG-----ACACGGTGTGG-----TCCCTGCGAGATGAGGCAATGCAACTAATTGCTGCGCCATC-----AAGAA--CG-----ACCGTGTGCAACCAGCGAGCTGTCAA--TGAGA-----TTTTCAGCTTGTCGG--AGACAGSAG--AGCCAGTGCATCT--GGTGCATTAAT
droW12	scf2_1100000004902:9832863-9832912 -		CG-----G-----TACCACTAATTGCTGSCCTAA-----AAGAAATG-----AATGTGTGCAACCCAGCG-----G-----G-----TTACGCCAAGATGTCGGAACAGTCAAAATGCGCAT--GGCGGCGTAAT
droVi3	scaffold_12822:1409781-1409877 +		CAAGATSc-----TCGCTGCGCGTGGAGGCTG-----GGTGGTGGCAATGGC-----GNGGCTT-----GTAGCCCTGCGCAATCGGCTAACCACTAATTGCTGCGCCATTA-----AAGAA-AA-----G-----G-----TTACGCCAAGATGTCGGAACAGTCAAAATGCGCAT--GGCGGCGTAAT
droMo3	scaffold_6500:20224181-20224232 -		CTAGTA-----GTATG--AGTATGCTG-----TTAGCAA--ATGTATTC-----CAGCAATGCGAAT-----G-----G-----TTACGCCAAGATGTCGGAACAGTCAAAATGCGCAT--GGCGGCGTAAT

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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

Name	Class
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hide 3p reads show mid mismatch reads

Anti-sense strand reads

Show Alignment With Reads

Re-alignment of all predicted orthologs

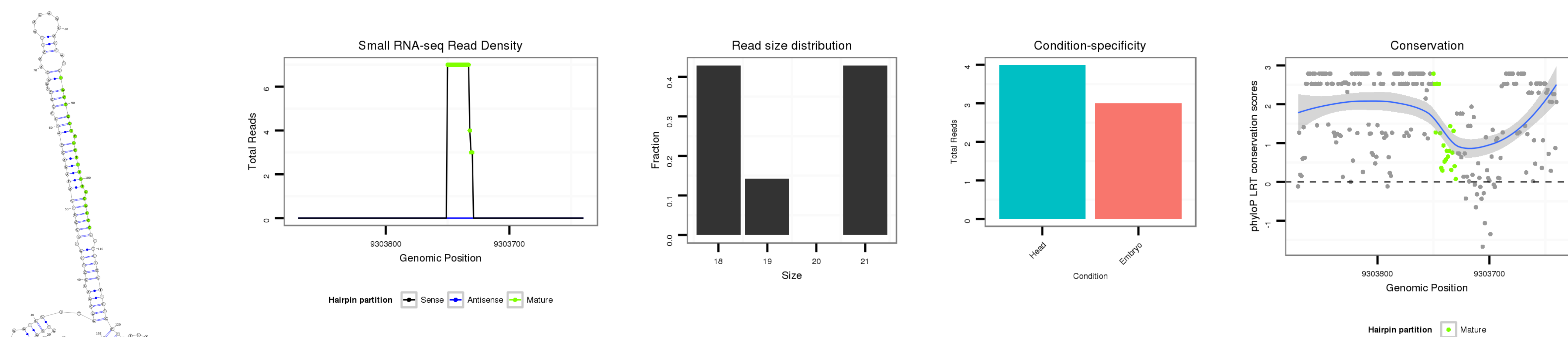
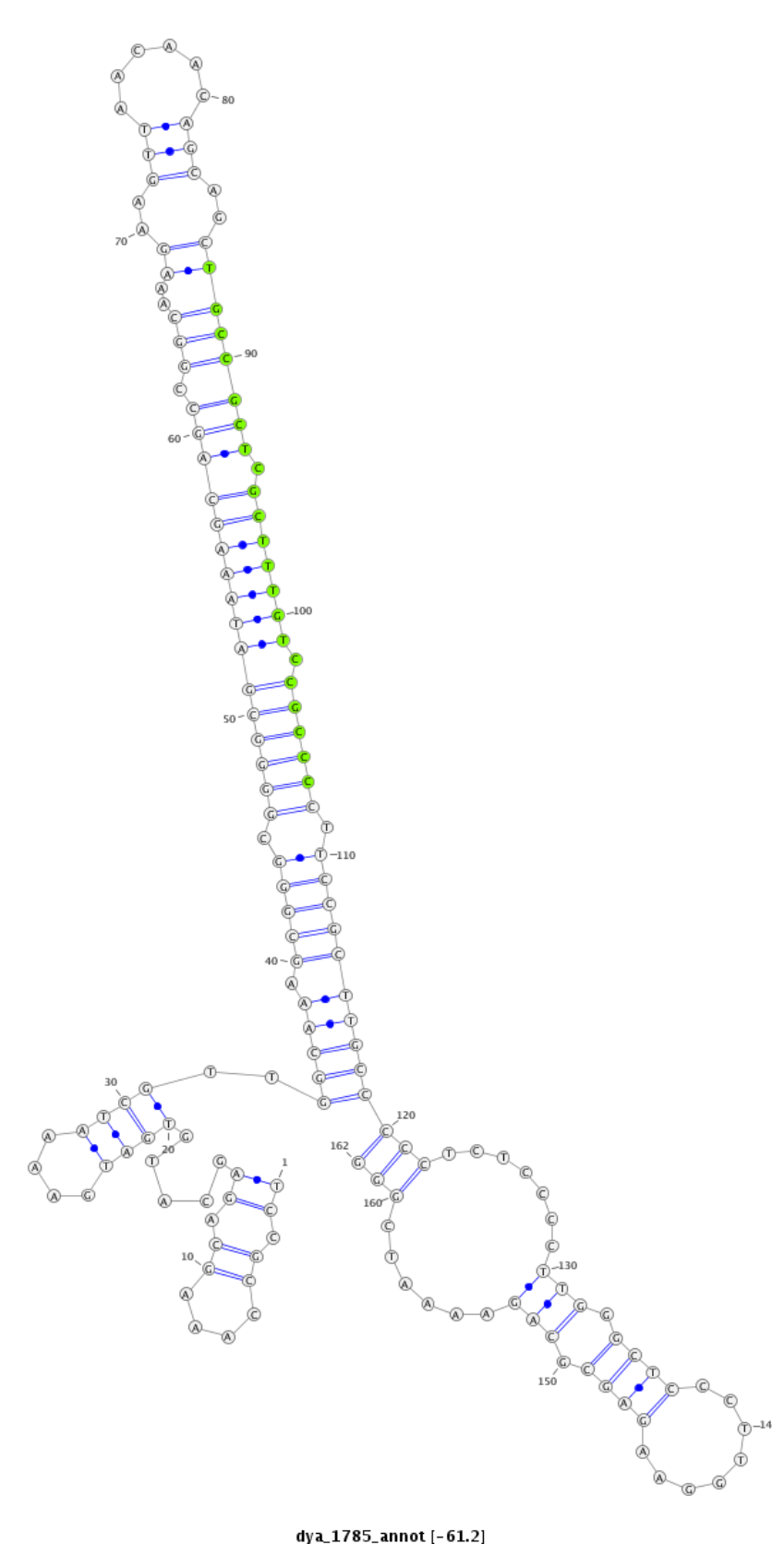
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	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	0
crit.uri	0
crit.back	0
rescue.total	0
rescue.dominant	1
rescue.known	0
rescue.confident	1
rescue.candidate	2

dya_1785	3L:9303690-9303821	-	candidate	Canonical miRNA	intron	[View on UCSC Genome Browser (Cornell Mirror)]
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Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Show Alternate Folds

Flybase annotation

intron (Dyak\GE20329-in)

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
dvoYa3	dvo_1785	CGACG---AGCATATA--CACATGACATTTTCATTGGG-G-----CTCCGCCAAAGCAGCATGTGATGAATTCGTTGGCAAGCGGGGGGGCGCATAAAGCAGCCGGC--AAAGAAGTTAAACA-----ACAGCAGC
dvoEre2	dvoTfoid_1784;2651795-14614910	CGACG---AGCATATA--CACATGACATTTTCATTGGG-G-----CTCCGCCAAAGCAGCATGTGATGAATTCGTTGGCAAGCGGGGGGGCGCATAAAGCAGCCGGC--AAAGAAGTTAAACA-----ACAGCAGC
dvoEre2	dvoTfoid_2;22656147-2456584	CGACG---AGCATATA--CACATGACATTTTCATTGGG-G-----CTCCGCCAAAGCAGCATGTGATGAATTCGTTGGCAAGCGGGGGGGCGCATAAAGCAGCCGGC--AAAGAAGTTAAACA-----ACAGCAGC
dvoEre2	dvoTfoid_31;2519489-2520186	CGACG---AGCATATA--CACATGACATTTTCATTGGG-G-----CTCCGCCAAAGCAGCATGTGATGAATTCGTTGGCAAGCGGGGGGGCGCATAAAGCAGCCGGC--AAAGAAGTTAAACA-----ACAGCAGC
dm3	dm31;2632622-2632859	CGACG---AGCATATA--CACATGACATTTTCATTGGG-G-----CTCCGCCAAAGCAGCATGTGATGAATTCGTTGGCAAGCGGGG-SCGATAAAGCAGCCGGC--AAAGAAGTTAAACA-----ACAGCAGC
dvoEru9	dvoTfoid000409466;359387-159261	CGACG---AGCATATA--CACATGACATTTTCATTGGG-G-----CTCCGCCAAAGCAGCATGTGATGAATTCGTTGGCAAGCGGGGGGGCGCATAAAGCAGCCGGC--AAAGAAGTTAAACA-----ACAGCAGC
dvoB1a1	dvoTfoid000302428;5411088-2411332	CGACG---AGCATATA--CACATGACATTTTCATTGGG-G-----CTCCGCCAAAGCAGCATGTGATGAATTCGTTGGCAAGCGGGGGG-GATAAAGCAGCCGGC--AAAGAAGTTAAACA-----ACAGCAGC
dvoTaK1	dvoTfoid0006415857;429796-130029	CGACG---AGCATATA--CACATGACATTTTCATTGGG-G-----CTCCGCCAAAGCAGCATGTGATGAATTCGTTGGCAAGCGGGGGCGCATAAAGCAGCCGGC--AAAGAAGTTAAACA-----ACAGCAGC
dvoE1a1	dvoTfoid000452149;2747802-2748037	CGACG---AGCATATA--CACATGACATTTTCATTGGG-G-----CTCCGCCAAAGCAGCATGTGATGAATTCGTTGGCAAGCGGGGGCGCATAAAGCAGCCGGC--AAAGAAGTTAAACA-----ACAGCAGC
dvoRho1	dvoTfoid000758401;130331-15569	CGACG---AGCATATA--CACATGACATTTTCATTGGG-G-----CTCCGCCAAAGCAGCATGTGATGAATTCGTTGGCAAGCGGGGGCGCATAAAGCAGCCGGC--AAAGAAGTTAAACA-----ACAGCAGC
dvoF1e1	dvoTfoid000454105;355648-355867	CGACG---AGCATATA--CACATGACATTTTCATTGGG-G-----CTCCGCCAAAGCAGCATGTGATGAATTCGTTGGCAAGCGGGGGG-GATAAAGCAGCCGGC--AAAGAAGTTAAACA-----ACAGCAGC
dvoK1K1	dvoTfoid000302441;1073418-1231722	CGG-T-AGCATATA--CACATGACATTTTCATTGGG-G-CTCCGCCAAAGCAGCATGTGATGAATTCGTTGGCAAGCGGGG-SCGATAAAGCAGCCGGC--AAAGAAGTTAAACA-----ACAGCAGC
dvoAn3	dvoTfoid_13337;9448842-2442093	CGG-T-AGCATATA--CACATGACATTTTCATTGGG-G-CTCCGCCAAAGCAGCATGTGATGAATTCGTTGGCAAGCGGGG-SCGATAAAGCAGCCGGC--AAAGAAGTTAAACA-----ACAGCAGC
dvoB1p1	dvoTfoid000396544;259759-260015	CGG-T-AGCATATA--CACATGACATTTTCATTGGG-G-CTCCGCCAAAGCAGCATGTGATGAATTCGTTGGCAAGCGGGG-SCGATAAAGCAGCCGGC--AAAGAAGTTAAACA-----ACAGCAGC
dp5	dp_group31;1305411-1305720	AG-T-AGCATATA--CACATGACATTTTCATTGGG-G-CTCCGCCAAAGCAGCATGTGATGAATTCGTTGGCAAGCGGGG-SCGATAAAGCAGCCGGC--AAAGAAGTTAAACA-----ACAGCAGC
dvoPe2	dvoTfoid_231;1336981-1337287	AG-T-AGCATATA--CACATGACATTTTCATTGGG-G-CTCCGCCAAAGCAGCATGTGATGAATTCGTTGGCAAGCGGGG-SCGATAAAGCAGCCGGC--AAAGAAGTTAAACA-----ACAGCAGC
dvoE12	dvoE_1100000004729;2260604-2260897	AG-T-AGCATATA--CACATGACATTTTCATTGGG-G-CTCCGCCAAAGCAGCATGTGATGAATTCGTTGGCAAGCGGGG-SCGATAAAGCAGCCGGC--AAAGAAGTTAAACA-----ACAGCAGC
dvoV13	dvoTfoid_13049;5111971-5112284	AG-T-AGCATATA--CACATGACATTTTCATTGGG-G-CTCCGCCAAAGCAGCATGTGATGAATTCGTTGGCAAGCGGGG-SCGATAAAGCAGCCGGC--AAAGAAGTTAAACA-----ACAGCAGC
dvoMe3	dvoTfoid_6680;1492681-1493028	AG-T-AGCATATA--CACATGACATTTTCATTGGG-G-CTCCGCCAAAGCAGCATGTGATGAATTCGTTGGCAAGCGGGG-SCGATAAAGCAGCCGGC--AAAGAAGTTAAACA-----ACAGCAGC
dvoE12	dvoTfoid_15110;9856191-9856493	AG-T-AGCATATA--CACATGACATTTTCATTGGG-G-CTCCGCCAAAGCAGCATGTGATGAATTCGTTGGCAAGCGGGG-SCGATAAAGCAGCCGGC--AAAGAAGTTAAACA-----ACAGCAGC

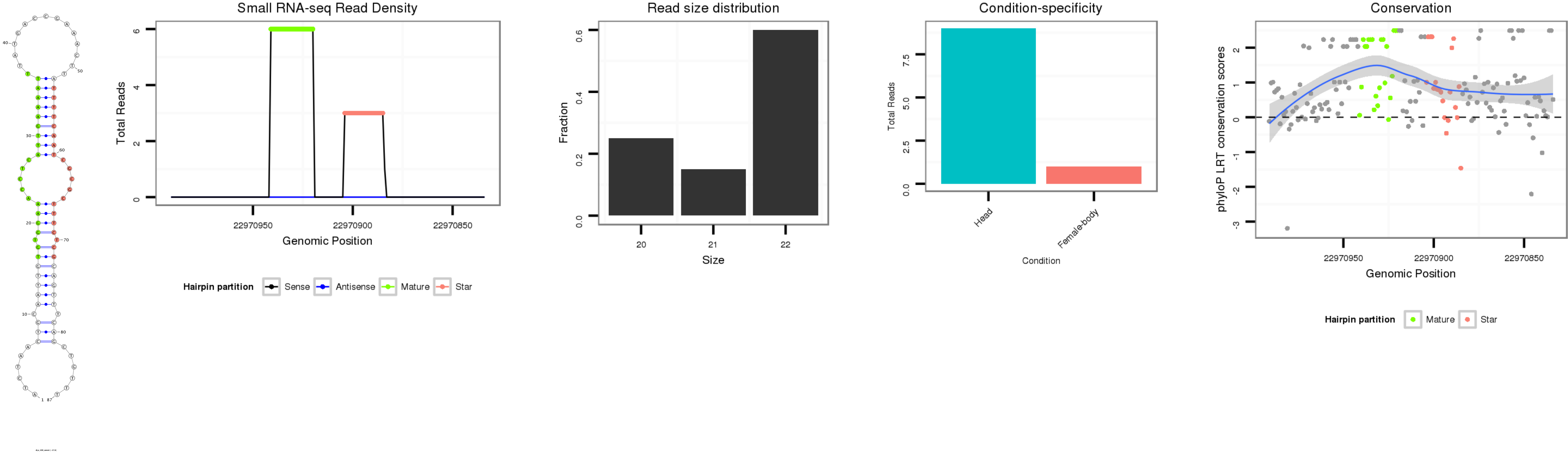
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crit.sum	0
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crit.mor	0
crit.half	0
crit.total	0
crit.pairing	0
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crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	2

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dya_100	3L:22970884-22970941 -	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

mature	star
1. dya_100 3L:22970920-22970941 -	1. dya_100 3L:22970885-22970904 -
2. dya_91 v2_chr3L_random_335:10537-10558 -	2. dya_91 v2_chr3L_random_335:10502-10521 -

Sense Strand Reads

hide 3p reads show mid mismatch reads

Read #	size	Mismatch	Hit Count	Total Norm	Total	M026 head	V058 head	M043 female body	V052 head
22	0	2	6.00	12	11	0	1	0	0
20	2	2.50	5	5	0	0	0	0	0
21	0	2	1.00	2	1	0	1	0	0
23	0	2	0.50	1	0	1	0	0	0
21	0	2	0.50	1	0	1	0	0	0
20	0	2	0.50	1	1	0	0	0	0

Anti-sense strand reads

Read #	size	Mismatch	Hit Count	Total Norm	Total	V052 head
22	0	2	6.00	12	11	0
20	2	2.50	5	5	0	0
21	0	2	1.00	2	1	0
23	0	2	0.50	1	0	1
21	0	2	0.50	1	0	1
20	0	2	0.50	1	1	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

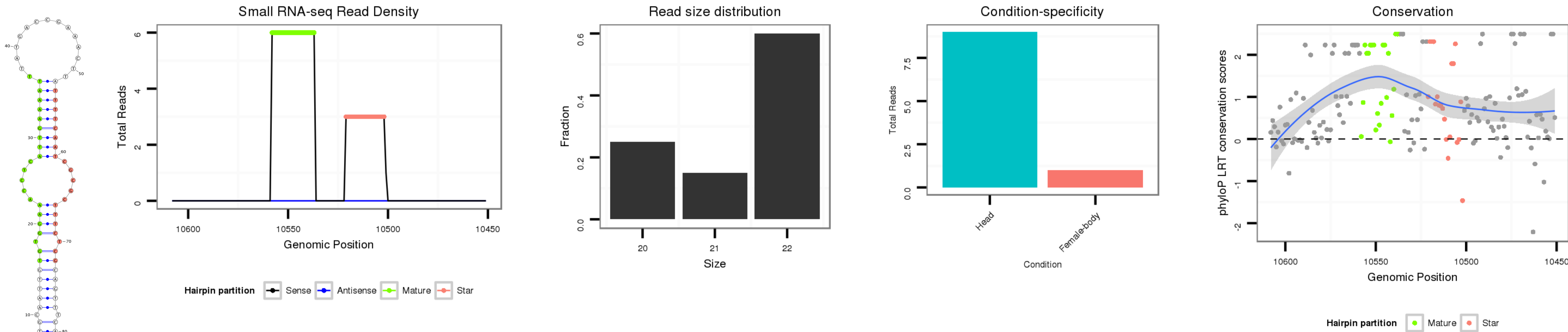
Species	Coordinate	ID	Alignment
droYak3	3L:22970834-22970991 -	dya_100	AATAAATAATATTGATGT-----T---A---TCATCGT-AAGTAAC-----GCA-TCTAATGCAATTGTGTGAAACCTC-----ATTGAAAATTATGACCGAA-ACTTAATTTCAATCGCGCTTTC---TCGCAGTTTC-----AGCTGTTTACCAGTTTT-----TC-ATGAGTCATGCCCAAGTCAAGGATT
droEre2	scafFold_4784:22179565-22179735 -		AATAAATAATAAATAATATTGATGATGATGA---TATCGGT-GAAAAA---GCA-TCCAACGCAATTGCTGTGAAACCTC-----ATTGAAAATTATGACCGAA-ACTTAATTTCAATCGCGCAATTC---CGGCAGTTTC-----AGCTGTTTACCAGTTTT-----TC-ATGAGTCATGCCAAGTCAAGGATT
droSec2	scafFold_11:2445762-2445925 -		AATAAATAATTAAATATC---ATGATGATGA---TATCGT-GAAAAA---GCA-TCCAACTGCAATTGTGTGAAACCTC-----ATTGAAAATTATGACCGAA-ACTTAATTTCAATCGCGCTTTC---TCGCAGTTTC-----AGCTGTTTACCAGTTTT-----TC-ATGAGTCATGCCAAGTCAAGGATT
droSim2	3L:22029765-22029925 -		AATAAATAATATTGATGAT---TATCGT-GAAAAA---GCA-TCCAACTGCAATTGTGTGAAACCTC-----ATTGAAAATTATGACCGAA-ACTTAATTTCAATCGCGCTTTC---TCGCAGTTTC-----AGCTGTTTACCAGTTTT-----TC-ATGAGTCATGCCAAGTCAAGGATT
dm3	chr3L:22510122-22510282 -		AATAAATAATATTGATGAT---TATCGT-GAAAAA---GCA-TCCAACTGCAATTGTGTGAAACCTC-----ATTGAAAATTATGACCGAA-ACTTAATTTCAATCGCGCTTTC---TCGCAGTTTC-----AGCTGTTTACCAGTTTT-----TC-ATGAGTCATGCCAAGTCAAGGATT
droEu1	scaf7180000403801:97669-97818 -		AATAAAC-----GATGA---TATCGT-GAAAAA---GCA-TCCAACTGCAATTGTGTGAAACCTC-----ATTGAAAATTATGACCGAA-ACTTAATTTCAATCGCGCTTTC---TCGCAGTTTC-----AGCTGTTTACCAGTTTT-----TC-ATGAGTCATGCCAAGTCAAGGATT
droBia1	scaf7180000302377:743192-743343 +		TAC-----TACGATGA---TATCGT-GAAAAA---GCA-TCCAACTGCAATTGTGTGAAACCTC-----ATTGAAAATTATGACCGAA-ACTTAATTTCAATCGCGCTTTC---TCGCAGTTTC-----AGCTGTTTACCAGTTTT-----TC-ATGAGTCATGCCAAGTCAAGGATT
droTak1	scaf7180000415491:453908-454058 -		AATAAAT-----GATGA---TATCGT-GAAAAA---GCA-TCCAACTGCAATTGTGTGAAACCTC-----ATTGAAAATTATGACCGAA-ACTTAATTTCAATCGCGCTTTC---TCGCAGTTTC-----AGCTGTTTACCAGTTTT-----TC-ATGAGTCATGCCAAGTCAAGGATT
droEle1	scaf7180000491199:235823-235978 +		AATAAATAATATTGATGA---TATCGT-GAAAAA---GCA-TCCAACTGCAATTGTGTGAAACCTC-----ATTGAAAATTATGACCGAA-ACTTAATTTCAATCGCGCTTTC---TCGCAGTTTC-----AGCTGTTTACCAGTTTT-----TC-ATGAGTCATGCCAAGTCAAGGATT
droRho1	scaf7180000779133:20660-20816 +		AATAAATAATATGACGA---TATCGT-GAAAAA---GCA-TCCAACTGCAATTGTGTGAAACCTC-----ATTGAAAATTATGACCGAA-ACTTAATTTCAATCGCGCTTTC---TCGCAGTTTC-----AGCTGTTTACCAGTTTT-----TC-ATGAGTCATGCCAAGTCAAGGATT
droFic1	scaf7180000453830:519731-519887 +		AATAAATAATACGATGA---TATCGT-GAAAAA---GCA-TCCAACTGCAATTGTGTGAAACCTC-----ATTGAAAATTATGACCGAA-ACTTAATTTCAATCGCGCTTTC---TCGCAGTTTC-----AGCTGTTTACCAGTTTT-----TC-ATGAGTCATGCCAAGTCAAGGATT
droK1k1	scaf7180000302808:847437-847580 -		CGP-----GATGA---TATCGT-GAAAAA---GCA-TCCAACTGCAATTGTGTGAAACCTC-----ATTGAAAATTATGACCGAA-ACTTAATTTCAATCGCGCTTTC---TCGCAGTTTC-----AGCTGTTTACCAGTTTT-----TC-ATGAGTCATGCCAAGTCAAGGATT
droAna3	scafFold_13337:22246817-22246904 -		G-----GATGA---TATCGT-GAAAAA---GCA-TCCAACTGCAATTGTGTGAAACCTC-----ATTGAAAATTATGACCGAA-ACTTAATTTCAATCGCGCTTTC---TCGCAGTTTC-----AGCTGTTTACCAGTTTT-----TC-ATGAGTCATGCCAAGTCAAGGATT
droBip1	scaf7180000396426:573747-573834 +		G-----GATGA---TATCGT-GAAAAA---GCA-TCCAACTGCAATTGTGTGAAACCTC-----ATTGAAAATTATGACCGAA-ACTTAATTTCAATCGCGCTTTC---TCGCAGTTTC-----AGCTGTTTACCAGTTTT-----TC-ATGAGTCATGCCAAGTCAAGGATT
dp5	KR_group8:185019-185207 -		AATAAATAGCTGCATGA---TATCGT-GAAAAA---GCA-TCCTGCTGAATTGCTGTGAAACCTC-----ATTGAAAATTATGACCGAA-ACTTAATTTCAATCGCGCTTTC---TCGCAGTTTC-----AGCTGTTTACCAGTTTT-----TC-ATGAGTCATGCCAAGTCAAGGATT
droPer2	scafFold_80:81812-81982 +		AATAAATAGCTGCATGA---TATCGT-GAAAAA---GCA-TCCTGCTGAATTGCTGTGAAACCTC-----ATTGAAAATTATGACCGAA-ACTTAATTTCAATCGCGCTTTC---TCGCAGTTTC-----AGCTGTTTACCAGTTTT-----TC-ATGAGTCATGCCAAGTCAAGGATT
droWil2	scaf2_1100000004511:7263987-7264208 +		AATGTAAAGT-----TATCGT-TAAGCACTTCGCTTTTTCCTCAATCACTGCAATTGCTGTGAAACCTC-----ATTGAAAATTATGACCGAA-ACTTAATTTCAATCGCGCTTTC---TCGCAGTTTC-----AGCTGTTTACCAGTTTT-----TC-ATGAGTCATGCCAAGTCAAGGATT
droGr12	scafFold_15110:14941120-14941261 -		TATATTTATTTTATTTTC---TAAATGTGCAAAA---GGAGAA---TCTCA-TCACTGCAATTGCTGTGAAACCTC-----ATTGAAAATTATGACCGAA-ACTTAATTTCAATCGCGCTTTC---TCGCAGTTTC-----AGCTGTTTACCAGTTTT-----TC-ATGAGTCATGCCAAGTCAAGGATT

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PASS/FAIL	1
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.panning	1
crit.top3	1
crit.tpop3	0
crit.un	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

intergenic

No Repeatable elements found

mature	star
1. dya_100_3L-22970920-22970941 -	1. dya_100_3L-22970885-22970904 -
2. dya_91_v2_chr3L_random_335:10537-10558 -	2. dya_91_v2_chr3L_random_335:10502-10521 -

Sense Strand Reads

hide 3p reads | show mid mismatch reads

[illegible]

Anti-sense strand reads

[illegible]

No data available in table

Show Alignment With Reads

Re-alignment of all predicted orthologs

[illegible]

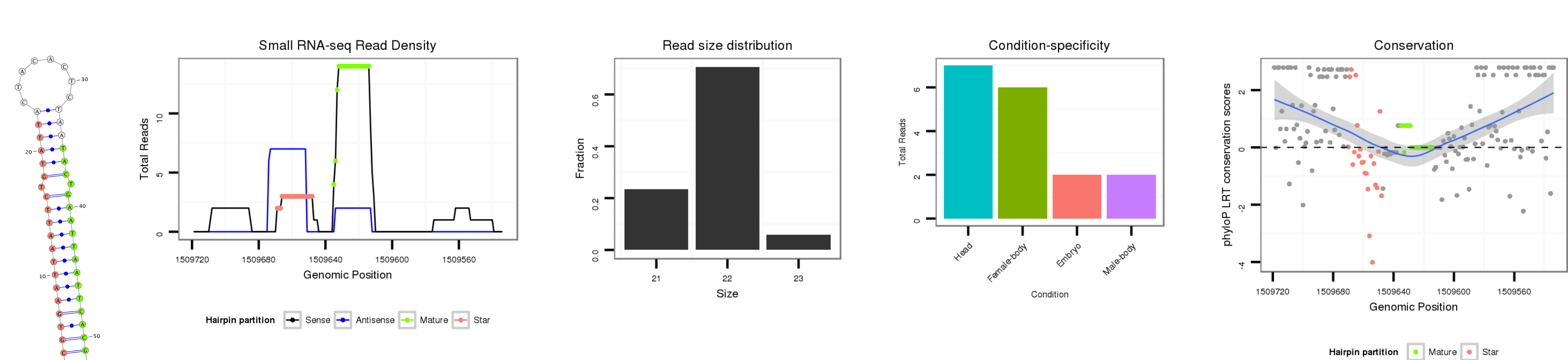
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	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dya_439	2R:1509584-1509669	confident-exception	3p_tailed_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 [DyakGE12909-in]; CDS [DyakGE12909-cds]; CDS [DyakGE12909-cds]

No Repeatable elements found

Sense Strand Reads

☐ hide 3p reads ☐ show mid mismatch reads

	Read # size	Mismatch	Hit Count	Total Norm	Total	M026 head	M043 female body	M056 embryo	V120 male	V058 head
ACTACCTGCTCAACTTCATCGGCACAGACACGGTGCTCTCCAGTACGATGTGGCGTAATTAATTCGTGTAATCTACTACACTTAACTACTGAATTAATTCACGCACGGGAATTAATCCACAGATGTGTATCTTTGCAGGACGAAAGGACCTGCAGGACCTTCAGATCAACGAATGGGACCCGGTGAT	22	0	1	4.00	4	0	3	1	0	0
.....TACTGAATTAATTCACGCACGG.....	21	0	1	3.00	3	1	1	1	0	0
.....CTGAATTAATTCACGCACGGA.....	22	0	1	2.00	2	2	0	0	0	0
.....GTGCGTGAATTAATTCGTGTAAT.....	22	0	1	2.00	2	2	0	0	0	0
.....TGAATTAATTCACGCACGGAAT.....	22	0	1	2.00	2	0	0	0	2	0
.....GGACCTGCAGGACCTTCAGATC.....	22	0	1	1.00	1	0	1	0	0	0
.....ACTGAATTAATTCACGCACGG.....	21	0	1	1.00	1	0	1	0	0	0
.....ACTGAATTAATTCACGCACGGA.....	22	0	1	1.00	1	0	1	0	0	0
.....CTGAATTAATTCACGCACGGAAT.....	23	0	1	1.00	1	1	0	0	0	0
.....CAACTTCATCGGCACAGACACGGTG.....	25	0	1	1.00	1	0	1	0	0	0
.....TACTGAATTAATTCACGCACGG.....	23	1	1	1.00	1	0	1	0	0	0
.....AAGCTTCATCGGCACAGACACGGT.....	23	0	1	1.00	1	0	0	0	1	0
.....CTTCAGATCAACGAATGGGACCC.....	23	0	1	1.00	1	1	0	0	0	0
.....GGACCTGCAGGACCTTCAGAT.....	21	1	1	1.00	1	0	0	1	0	0
.....CGTGAATTAATTCGTATTACT.....	22	0	1	1.00	1	1	0	0	0	0

Anti-sense strand reads

	Read # size	Mismatch	Hit Count	Total Norm	Total	M026 head	V058 head
TGATGGACGAGTTGAAGTAGCCGTGTCTGTGCCACGAGAAGGTATGCTCAACGCCACTTAATTAAGACATATGATGTGAGATTATGACTTAATTAAGTGCCTGCCCTTAATTAGTGTCTACACATAGAAAAGTCTCGCTTTCTCGAGCCTCCTGGAAGTCTAGTTGCTTACCTGGGCCACTA	23	0	1	6.00	6	6	0
.....TGCTACACGCACTTAATTAAGAC.....	22	0	1	2.00	2	0	2
.....GCTACACGCACTTAATTAAGAC.....	22	0	1	1.00	1	0	1
.....TGACTTAATTAAGTGGTGGCT.....	23	1	1	1.00	1	1	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

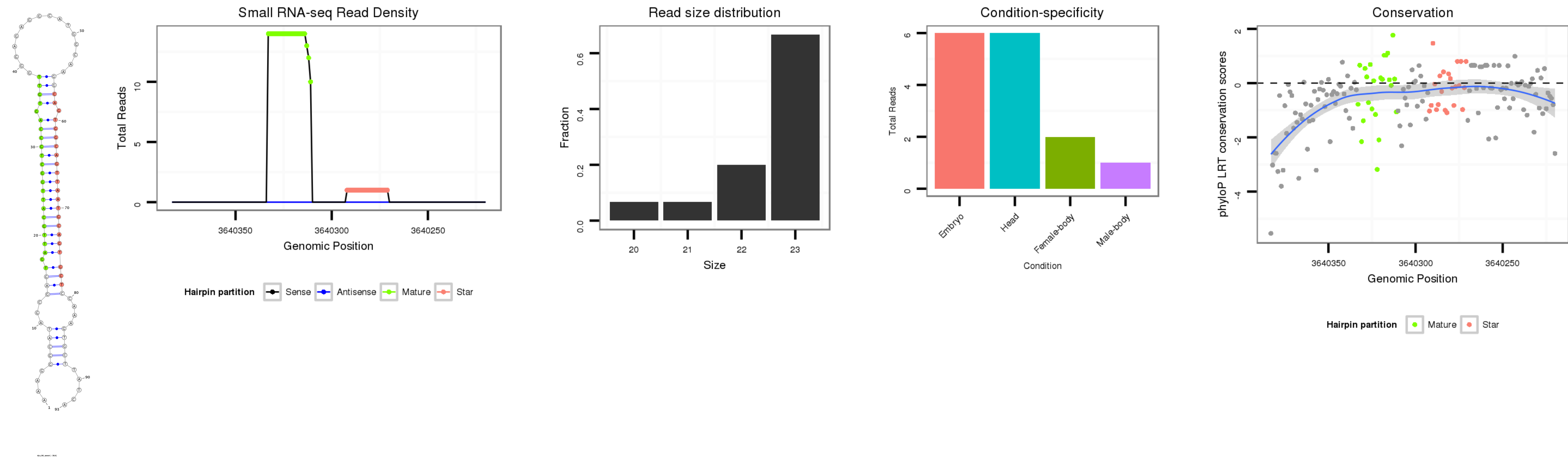
Species	Coordinate	ID	Alignment
droYak3	2R:1509534-1509719 -	dya_439	ACTACCTGCTCAACTTCATCGGCACAGACACGGTGCTCTCCAGTACGATGTGGCGTAAT-----TAATTCGTATTAC--T--A-----CACTCTAAACTG--AATTAATTCACGCACGGGAATTAATC-----CACAGATGT-----GT-ATCTTTTGCAGGACGAAAAGGACCTGCAGGACCTTCAGATCAACGAATGGGACCCGGTGAT
droEre2	scaffold_4845:3235741-3235895 -		ACTACCTGCTCAACTTCATCGGCACAGACACGGTGCTCTCCAGTACGATGTGGCGTAAT-----CAATTGATGATTAAGT--G-----GAG--GTC-----CACAGATGA-----GT-ATATTTTCAGGACGGAAGGATTTGCAGGACCTTCAGATCAACGAATGGGACCCGGTGAT
droSec2	scaffold_18:1192729-1192885 +		ACTACCTGCTCAACTTCATCGGCACAGACACGGTGCTCTCCAGTACGATGTGGCGTAAT-----CAAAAGAGAGGGAGTCCA-----CA--TTC-----CACAGATGT-----AT-ATCTTTTGCAGGACGAAAAGGACCTGCAGGACCTTCAGATCAACGAATGGGACCCGGTGAT
droSim2	2L:20706285-20706441 +	dai_29412	ACTACCTGCTCAACTTCATCGGCACAGACACGGTGCTCTCCAGTACGATGTGGCGTAAT-----CAAAAGAGAGGGAGTCCA-----CA--TTC-----CACAGATGT-----AT-ATCTTTTGCAGGACGAAAAGGACCTGCAGGACCTTCAGATCAACGAATGGGACCCGGTGAT
dm3	chr2L:21261670-21261826 +		ACTACCTGCTCAACTTCATCGGCACAGACACGGTGCTCTCCAGTACGATGTGGCGTAAT-----CAACTGAGAAATAGAGTCCA-----CA--TTC-----CACAGATGA-----AT-ATCTTTTGCAGGACGAAAAGGACCTGCAGGACCTTCAGATCAACGAATGGGACCCGGTGAT
droEug1	scf7180000409063:147333-147482 -		ATACCTGCTCAACTTCATCGGCACAGACACGGTGCTCTCCAGTACGATGTGGCGTAAT-----CATACAGAGATAGGGCT--T-----GTC--TAC-----GT-ATCTATTGCAGGACGGAAGGACCTTCAGATCAACGAATGGGACCCGGTGAT
droBial1	scf7180000302422:3668040-3668197 -		ATACCTGCTCAACTTCATCGGCACAGACACGGTGCTCTCCAGTACGATGTGGCGTAAT-----CTTCTC-----T--T-----CAATTACTCATTAAAT-----GTACATCTCAAC-----GT-AAAATTCAGGACGGAAGGCTGTCAACGAATGGGACCCGGTGAT
droTak1	scf7180000413871:197163-197324 -		ATACCTGCTCAACTTCATCGGCACAGACACGGTGCTCTCCAGTACGATGTGGCGTAAT-----CTGTCATTAAT--T--T-----CAATTAGTT-----TTGACATGATAGCTTAAGA--AA-ATTAATAAGGACCTGCAGGACCTTCAGATCAACGAATGGGACCCGGTGAT
droEle1	scf71800004090640:37214-37389 +		ACTACCTGCTCAACTTCATCGGCACAGACACGGTGCTCTCCAGTACGATGTGGCGTAAT-----CGAGCTAAGGCC--T--T-----ATGTCTGGGGCTCCACT-----AAATTCACCTGATTT-----TACGATG-----GT-ATCGTTGCAGGACGGAAGGACCTGCAGGACCTTCAGATCAACGAATGGGACCCGGTGAT
droRho1	scf7180000758815:613-743 +		ACTACCTGCTCAACTTCATCGGCACAGACACGGTGCTCTCCAGTACGATGTGGCGTAAT-----STGACCTC-----CTTCTAACTCAGGGCT--A-----CG--TTC-----CACGATCA-----GT-ATCGTTGCAGGACGGAAGGACCTGCAGGACCTTCAGATCAACGAATGGGACCCGGTGAT
droFic1	scf7180000453932:419496-419651 +		ACTACCTGCTCAACTTCATCGGCACAGACACGGTGCTCTCCAGTACGATGTGGCGTAAT-----TTCTCTTAATTTGGACT--A-----TG--GTC-----GT-ATACGTTGAGGACGGAAGGACCTGCAGGACCTTCAGATCAACGAATGGGACCCGGTGAT
droKil1	scf7180000302273:359763-359922 -		ACTACCTGCTCAACTTCATCGGCACAGACACGGTGCTCTCCAGTACGATGTGGCGTAAT-----CTCTAAATATCCAAT--GGCAT-----CC--TTC-----CACGATCC-----TT-ATCGTTGCAGGACGGAAGGACCTGCAGGACCTTCAGATCAACGAATGGGACCCGGTGAT
droAna3	scaffold_12916:10952763-10952916 -		ACTACCTGCTCAACTTCATCGGCACAGACACGGTGCTCTCCAGTACGATGTGGCGTAAT-----TCTTTTASAA--T--A-----TCTTCTCCTAGT-----TTCCTATAG-----TT-TCTCTTCAGGACGGAAGGACCTTCAGGACCTTCAGATCAACGAATGGGACCCGGTGAT
droBip1	scf7180000396572:612201-612353 -		ACTACCTGCTCAACTTCATCGGCACAGACACGGTGCTCTCCAGTACGATGTGGCGTAAT-----CTTTTAAATAT--T--T-----TTC-----TTC-----C--TTC--AGTCACAAAGTA-ATCGTTGCAGGACGGAAGGACCTTCAGGACCTTCAGATCAACGAATGGGACCCGGTGAT
dp5	4_group4:3363603-3363756 -		ACTACCTGCTCAACTTCATCGGCACAGACACGGTGCTCTCCAGTACGATGTGGCGTAAT-----TTCAGGCAGAG-----CA--TTC-----CAGAGATAT--AGCTAACATT--TCTGCTTCAGGACGGAAGGACCTTCAGGACCTTCAGATCAACGAATGGGACCCGGTGAT
droPer2	scaffold_10:2383394-2383547 -		ACTACCTGCTCAACTTCATCGGCACAGACACGGTGCTCTCCAGTACGATGTGGCGTAAT-----TTCAGGCAGAG-----CA--TTC-----CAGAGATAT--AGCTAACATT--TCTGCTTCAGGACGGAAGGACCTTCAGGACCTTCAGATCAACGAATGGGACCCGGTGAT
droW12	scf2_110000004484:728919-729096 +		ATACCTGCTCAACTTCATCGGCACAGACACGGTGCTCTCCAGTACGATGTGGCGTAAT-----GTGGAATAAT--T--T--ATGTCCTTTCTCTTTTCTCTCAATTTCTCA-----T-----T--AATTAAATTTACTGATTTTTCAGGACGGAAGGACCTTCAGGACCTTCAGATCAACGAATGGGACCCGGTGAT
droVir3	scaffold_12963:4299851-4300015 +		ACTACCTGCTCAACTTCATCGGCACAGACACGGTGCTCTCCAGTACGATGTGGCGTAAT-----TTCAGGCAGAG-----CA--TTC-----GATATCCCACT-----TTCATATGGAATCAAT--T--AATGTTTTCAGGACGGAAGGACCTTCAGGACCTTCAGATCAACGAATGGGACCCGGTGAT
droMo3	scaffold_6500:8174886-8175045 +		ATACCTGCTCAACTTCATCGGCACAGACACGGTGCTCTCCAGTACGATGTGGCGTAAT-----CAATTGGCGATCGATAA--T-----TTTT-----TATATTC--CAATAA--TT-TTCGGCGCAGACGGAAGGACCTTCAGGACCTTCAGATCAACGAATGGGACCCGGTGAT
droGr12	scaffold_15252:1118701-1118863 -		ACTACCTGCTCAACTTCATCGGCACAGACACGGTGCTCTCCAGTACGATGTGGCGTAAT-----CAAGCAAAAT--T--T--TCTAATCGATACGTTTTT-----CTATCAATA-----T-TTTAATTAAGGACGGAAGGACCTTCAGGACCTTCAGATCAACGAATGGGACCCGGTGAT

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	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.paring	1
crit.top3	1
crit.tpop3	0
crit.uni	1
crit.back	0
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

intron [Dyak\GE16375-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads

show mid mismatch reads

[illegible]

Anti-sense strand reads

[illegible]

Show Alignment With Reads

Re-alignment of all predicted orthologs

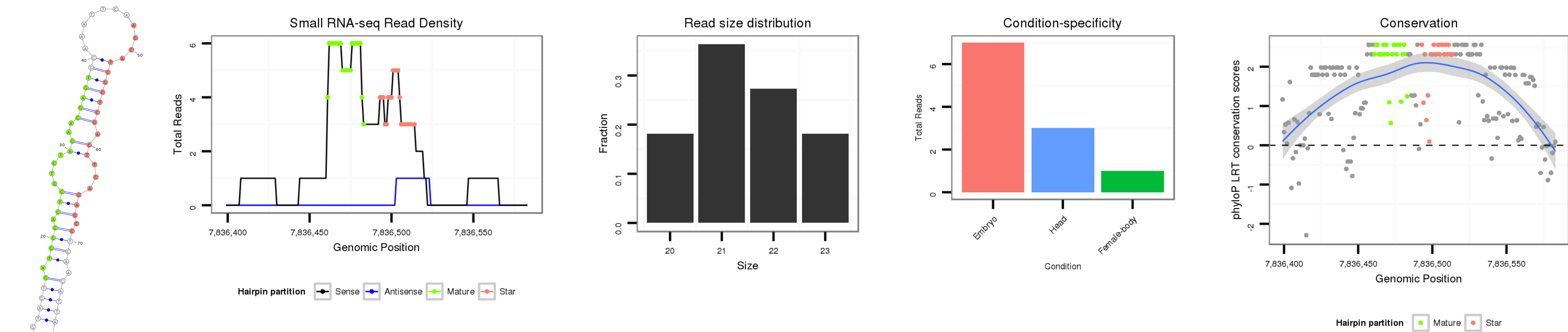
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	PASS/FAIL
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crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	0
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	0
rescue.known	1
rescue.confident	0
rescue.candidate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

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Show Alternate Folds

Flybase annotation

intron [Dyak\GE17094-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

AATTAGAAATAACATGTAAGCGGGAAC TTGTTCTGAAGACCCAAATAAGAGGTGGTAGT GATGGGACTCGTCTAGAACGAGT GGAAATTC CAAGCATCGCTCGACTTCAGAGCCTCAACATTACGCCTAGAGAACGACAACAGCTTTAGATCAATGGACCCCGCTTAGGAATCGAGAATTGG										Read #					M056	V058	M026	M043	V046	V052
*****((((((((((((((((((((((((((((((((((((((((((((((((*****										size	Mismatch	Hit	Total	Total	embryo	head	head	female	embryo	head
.....GATGGGACTCGTCTAGAACGAGT.....										23	0	1	2.00	2	0	0	0	0	0	0
.....GGAAATTCAGCATCGCTCGAC.....										22	0	1	1.00	1	0	0	0	0	0	0
.....TAGATCAATGGACCCCGC.....										19	0	1	1.00	1	0	0	0	0	0	0
.....AGCATCGCTCGACTTCAGAGCC.....										22	0	1	1.00	1	0	0	0	0	0	0
.....CGCTCGACTTCAGAGCCTCAAC.....										22	0	1	1.00	1	0	0	0	0	0	0
.....GAACGAGTGGAAATTCAGC.....										20	0	1	1.00	1	0	0	0	0	0	0
.....GGAAATTCAGCATCGCTCGA.....										21	0	1	1.00	1	0	0	0	0	0	0
.....TAACAATGTAAGCGGGAAC TTG.....										22	0	1	1.00	1	0	0	0	0	1	0
.....ATGGGACTCGTCTAGAACGA.....										20	0	1	1.00	1	0	0	1	0	0	0
.....GATGGGACTCGTCTAGAACGA.....										21	0	1	1.00	1	0	0	1	0	0	0
.....AAATAAGAGGTGGTAGTGATGGGACT.....										26	0	1	1.00	1	0	0	0	0	0	0
.....ATGGGACTCGTCTAGAACGAG.....										21	0	1	1.00	1	0	0	0	0	0	1
.....TCGACTTCAGAGCCTCAACAT.....										21	0	1	1.00	1	0	1	0	0	0	0

Anti-sense strand reads

[illegible]

Show Alignment With Reads

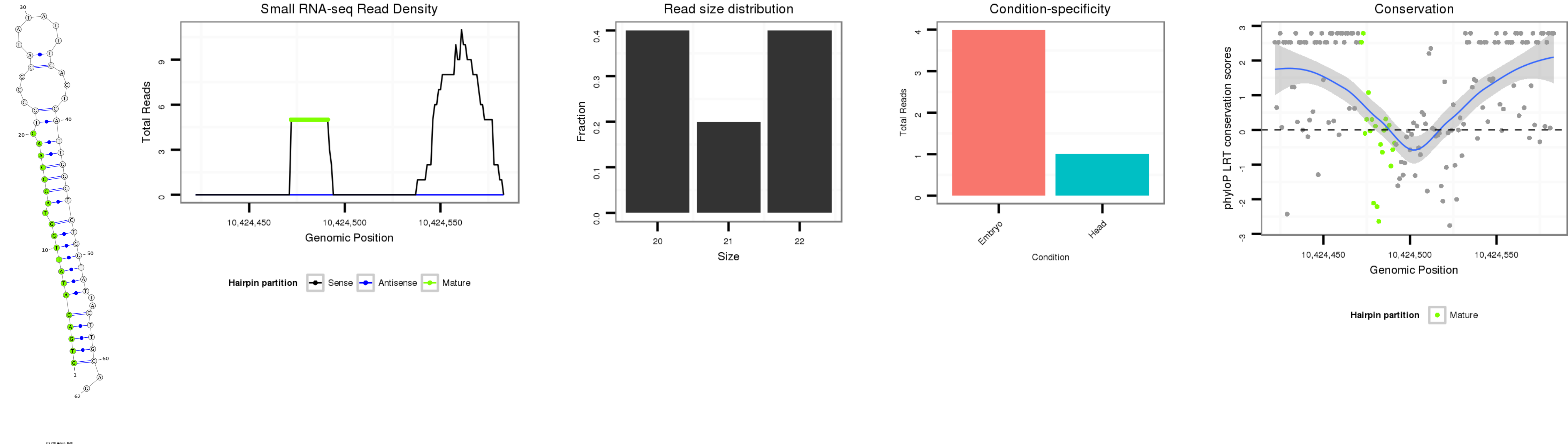
Species	Coordinate	ID	Alignment
droYak3	X:7836399-7836583 +	dya_1799	A-ATTAGAAA---TAACAATGTA-AGC--GGGAACCTGTTCTGAAAGACCCAA---A--ATAA--G-AGGTGGTAGT GATGGGACTCGTCTAGAACGAGT GGAAATTC--A- AGCATCGCTCG-ACCTTCAGAGCC TCAACATTACGCCT-AGAGAAC-GAC-AACAGCTT--TAGATCAATGCGACCCCGCTTAGGA-----ATCGAGA-----ATTGG
droEr2	scaffold14_4690:13329656-13329835 -	der_1524	C- TTTAGC --- AA --- TAAG -AGC--GGGAACCTGTTCTGAAAGACCCAA---A- CTTA --G-AGGTGGTAGT GATGGGACTCGTCTAGAACGAGT GGAAATTC--A- AGCATCGCTCG-ACCTTCAGAGCC TCAACATTACGCCT-AGAGAAC-GAC-AACAGCTT--TAGATCAATGCGACCCCGCTTAGGA-----ATCG GA -----A AGCA
droSe2	scaffold14_20:193500-193680 +	dse_1847	A- ATAAGA --- AA --- CA TA-AGC--GGGAACCT TC CTGAAAGACCC CA ---A--ATAA--G-AGGTGGTAGT GATGGGACTCGTCTAGAACGAGT GGAAATTC--A- AGCATCGCTCG-ACCTTCAGAGCC TCAACATTACGCCT-AGAGAAC-GAC-A ACAG GGT--TAGATCA AT TGGGACCCCGCTTAGGA-----A AC GAGA-----A CTGA
droSim2	X:12890278-12890458 +	dsi_32459	A- ATAAGA --- AA --- CA TA-AGC--GGGAACCT TC CTGAAAGACCC CA ---A--ATAA--G-AGGTGGTAGT GATGGGACTCGTCTAGAACGAGT GGAAATTC--A- AGCATCGCTCG-ACCTTCAGAGCC TCAACATTACGCCT-AGAGAAC-GAC-A ACAG GGT--TAGATCA AT TGGGACCCCGCTTAG GA -----A CA GA AA -----ATT GA
dm3	chrX1:3553560-3553740 +	dme_424	A- ATAAGA --- AA --- CA TA-AGC--GGGAACCT TC CTGAAAGACCC CA ---A--ATAA--G-AGGTGGTAGT GATGGGACTCGTCTAGAACGAGT GGAAATTC--A- AGCATCGCTCG-ACCTTCAGAGCC TCAACATTACGCCT-AGAGAAC-GAC-A ACAG GGT--TAGATCA AT TGGGACCCCGCTTAGGA-----A AC GAGA-----A CTGA
droEug1	scaffold100_048958:35922-36115 -		A- TTTGG --- AA --- TA TA-AGC--GGGAACCTGTTCTGAAAGACCC AA ---A--ATAA AA AGGTGGTAGT GATGGGACTCGTCTAGAACGAGT GGAAATTC--A- AGCATCGCTCG-ACCTTCAGAGCC TCAACATTACGCCT-AGAGAAC-GAC-AACAGCTT--TAGATCAATGCGACCCCGCTTAGGA GAATA ATCGAG TA ----- TAAGGACCTG
droBia1	scaffold180000302041:563675-563852 +		A-ATTAG CT --- CA --- TA TA-AGC--GGGAACCTGTTCTGAAAGACCC CA --- CT --ATAA--G-AGGTGGTAGT GATGGGACTCGTCTAGAACGAGT GGAAATTC--A- AGCCTGGCTCG-ACCTTCAGAGCC TCA CA CATTACGCCT-AGAGAAC-GAC-A ACAG CTT--TAGATCAATGCGACCCCGCTTAG CT -----ATC AGCT -----A CC -G
droTak1	scaffold180000414393:30815-30999 -		A- TTTGG --- AA --- TA TA-AGC--GGGAACCTGTTCTGAAAGACCC AA --- CT --ATAA--G-AGGTGGTAGT GATGGGACTCGTCTAGAACGAGT GGAAATTC--A- AGCCTGGCTCG-ACCTTCAGAGCC TCAACATTACGCCT-AGAGAAC-GAC-AACAGCTT--TAGATCAATGCGACCCCGCTTAGGA-----ATCGA ATATATT - GCCCA CTGG
droEl1	scaffold180000491044:215070-215257 +		A-ATTAGA CT --- AA --- TA TA-AGC--GGGAACCTGTTCTGAAAGACCC CA ---A--ATAA--G-AGGTGGTAGT GATGGGACTCGTCTAGAACGAGT GGAA TT TC--A- AGCATCTGCTCG-ACCTTCAGAGCC TCAACATTACGCCT-AG CT GAAC-GAC AA CTAGCTT--TAGATCAATGCGACCCCGCTTAGGA-----ATCGAGA-- ATT - SCAG CTGG
droRho1	scaffold180000779510:38394-38579 +		A- TTTAG --- AA --- TA TA-AGC--GGGAACCTGTTCTGAAAGACCC CA ---A--ATAA--G-AGGTGGTAGT GATGGGACTCGTCTAGAACGAGT GG CT AA TT TA--A- AGCATCGCTCG-ACCTTCAGAGCC TCAACATTACGCCT-AGAGAAC-GAC-AACAGCTT--TAGATCAATGCGACCCCGCTTAGGA-----A CT CGAG TA - ATT - SCGA CTGG
droFio1	scaffold180000454073:1442997-1443184 +		A- TTTAG --- AA --- TA TA-AGC--GGGAACCTGTTCTGAAAGACCC CA ---A--ATAA--G-AGGTGGTAGT GATGGGACTCGTCTAGAACGAGT GGAA TT TC--A- AGCATCGCTCG-ACCTTCAGAGCC TCAACATTACGCCT-AGAGAA CT GAC-AACAGCTT--TAGATCAATGCGACCCCGCTTAGGA-----ATCGAG TA - ACT - ACGA CTGG
droKik1	scaffold180000302698:307806-307975 -		A- TTTGG --- AA --- TA TA-AGC--GGGAACCTGTTCTGAAAGACCC AA TACAA TA--A--ATAA--G-AGGTGGTAGT GATGGGACTCGTCTAGAACGAGT GGAA TT TA--A- AGCATCGCTCG-ACCTTCAGAGCC TCAACATTACGCCT-AGAGAAC-GAC-A ACAA CTT--TAGATCAATGCGACCCCGCTTAGGA----- CTT CT CT ----- TA AG
droAna3	scaffold14_13334:472140-472316 +	dan_4039	A- TTTGG --- AA --- TA TA-AGC--GGGAACCTGTTCTGAAAGACCC AA CAAA TA--A--ATAA--G-AGGTGGTAGT GATGGGACTCGTCTAGAACGAGT GGAA TT TA--A- AGCATCGCTCG-ACCTTCAGAGCC TCAACATTACGCCT TA GAGAA AA SAC-AACAGCTT--TAGATCAATG CT CA AA CCCGCTTAGGA-----A CT CT GA----- GCCT CT
droBip1	scaffold180000396431:1081237-1081413 -		A- ACTAGAT TA TAGA AA--- AA TA AGC--GGGAACCTGTTCTGAAAGACCC AA --- CAGTGA AA--G-AGGTGGTAGT GATGGGACTCGTCTAGAACGAGT GGAA TT TA CT TC--A- AGCATCTGCTCG-ACCTTCAGAGCC TCAACATTACGCCT-AGAG CT GA CT SAC-AACAGCTT TT TAGATCAAT GA CC CA CCGCTT----- CT ----- CT -G
dp5	X: group3b:100229-100389 +	dps_110	A CTAG CTG--- TGA -- CAAA -AGC CT GG CT ACTTGT TT CTGAAAGAA CTA TA--- TA -- CG AA--G- CT TGGTAGT GATGGGACTCGTCTAGAACGAG CGAA TT TC--A- ACATCTGCTCG-ACCTTCAGAGCC TCAACATTACGCCT-AGAGAAC- CTA - ACAG CTT-- TC GA CA CT GC CT ----- CT ----- CT
droPer2	scaffold14_56:124035-124186 +	dpe_157	A CTAG CTG--- TGA -- CAAA -AGC CT GG CT ACTTGT TT CTGAAAGAA CTA TA--- TA -- CG AA--G- CT TGGTAGT GATGGGACTCGTCTAGAACGAG CGAA TT TC--A- ACATCTGCTCG-ACCTTCAGAGCC TCAACATTACGCCT-AGAGAAC- CTA - ACAG CTT-- TC GA CA CT GC CT ----- CT ----- CT
droVit3	scaffold14_12970:5369119-5369203 -	dvi_24642	A- TTTGG --- AA --- TA TA-AGC--GGGAACCTGTTCTGAAAGACCC AA --- CT TA TA TA--G-AGGTGGTAGT GATGGGACTCTAC TAGAACGAGTGGAA TA TA TA TA--A- AGCATCTGCTCGACTTC CAGAGCC CTCA CATTACGCCT-AGAGAA CT ----- CT ----- CT
droMoJ3	scaffold14_6473:4951753-4951833 -	dmo_3154	A- TTTGG --- AA --- TA TA-AGC--GGGAACCTGTTCTGAAAGACCC AA --- CT TA TA TA--G-AGGTGGTAGT GATGGGACTCTAC TAGAACGAGTGGAA TA TA TA TA--A- AGCATCTGCT

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	PASS/FAIL
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crit.loop	0
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crit.pairing	1
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crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	1
rescue.known	0
rescue.confident	2
rescue.candidate	9

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Show Alternate Folds

Flybase annnotation

intron [Dyak\GE18696-in]; CDS [Dyak\GE18696-cds]; CDS [Dyak\GE18696-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

[illegible]

Anti-sense strand reads

[illegible]

Show Alignment With Reads

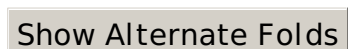
Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droYak3	Z1:10424422-10424583 +	dya_278	GCACGGCGGGCGGATGGTCCTCTGGGTCAATCCCAAGGTGTACATCAACCTG GTGAGATA --TTGG--T-AGCCA--AC TGCCGCATATATTT -----GACTCATT-----G-GCT-----CTGGTATTACT-TGCAGGACAAACCCGGAATACACATCTGCGGCTACTGCGGTCTGCGCTTCGTCAA
droEre2	scaffold_4929:5179964-5180125 -		GCACGGCGGGCGATGGTCC TGTGGG CATCCCAAGGTGTACATCAACCT GTGAGAGC --TTGA--T-AGC GT --AC TAAC GGCAT CAATT T-----GACTCATT-----G GAT ----- GGGTGTATT T-TGCAGGACAAACCCGGAATACACATCTGCGGCTACTGCGGTCTGCG TT TCGTCAA
droSec2	scaffold_9:3186281-3186442 -		GCACGGCGGGCGGATGGTCCTCTGGGTCAATCCCAAGGTGTACATCAACCTG GTGAGAT T--TGTA-T-AG CA --AC TAAC GGCAT CCATTA T-----GACTCATT-----G GAT ----- CATGATTT TT-TGCAGGACAAACCCGGAATACACATCTGCGGCTACTGCGG CT GCGCTTCGTCAA
droSm2	Z1:4913041-4913202 -	dsi_11251	GCACGGCGGGCGGATGGTCCTCTGGGTCAATCCCAAGGTGTACATCAACCTG GTGAGAT T--TGTA-T-AG CA --AC TAAC GGCAT CCATTT T-----GACTCATT-----G GAC ----- CATGTTT TTT-TGCAGGACAAACCCGGAATACACATCTGCGGCTACTGCGG CT GCGCTTCGTCAA
dm3	chr21:5099624-5099786 -		GCACGGCGGGCGGATGGTCCTCTGGGTCAATCCCA AGT GTACATCAACCTG GTGAGC T--TTAG-C-G GGT --TT TA SAGSCATA CACTT -----GACT CA TT-----G GAT ----- CATGTTT TTT-TGCAGGACAAACCCGGAATACACATCTGCGGCTACTGCGG CT GCGCTTCGTCAA
droEug1	scf7180000409005:987392-987553 -		GCACGGCGGGCGG ATGGTCC TCTGGGTCAATCCCAAGGTGTACATCAACCTG GTGAGAT T--TATT-T-AA TT --AC TGT GTGATATGA AC -----GACTCATT-----G GAT ----- CATGTTT TTT-TGCAGGACAAACCCGGAATACACATCTGCGGCTACTGCGGTCT AC GCTTCGTCAA
droBia1	scf7180000302261:538761-538920 -		GCACGGCGGGCGG ATGGTCC TCTGGGTCAATCCCAAGGTGTACATCAACCTG GTGAGAT C--TG--C-C TTG --AC TAG CTATCCATA T -----GACTCATT-----G GAT -----CT GGC CA CA T-TGCAGGACAA CCCGG AA CA CCACATCTGCGGCTACTGCGG CT GCGCTTCGTCAA
droTak1	scf7180000415204:29219-29381 +		GCACGG ATGGTCC TCTGGGTCAATCCCAAG GT GTACATCAACCTG GTGAGAT C--GA AA C-T-AG TT --TACAT TTT ATAG AAA -----ACAT ATA T----- TGGGTTC TC TC T-TGCAGGACAAACCCG GA ATCACATCTGCGGCTACTGCGGTCTGCGCTTCGTCAA
droEle1	scf7180000491273:118581-118739 +		GCACGGCGGGCGGATGGTCCTCTGGGTCAATCCCAAG GT GTACATCAATCTG GTGAGAT C--TA--T-AG CT --AC TAT CTATATAT A -----ACT CA TT-----G GAT ----- GCT CTTAC C -TGCAGGACAAACCCG GA ATCACATCTGCGGCTACTGCGG CT GCGCTTCGTCAA
droRho1	scf7180000779577:120412-120570 +		GCACGG ATGGTCC TCTGGGTCAATCCCAAG GT GTACATCAACCTG GTATAGAT C--TA--C-AG CT --AC TGT TTTGAT TA A-----A ACT CATT-----G GAA ----- TCCT T TT TAC C -GCAGGACAAACCCG GA ATCACATCTGCGGCTACTGCGG CT TGCGCTTCGTCAA
droFi1	scf7180000453842:1147231-1147388 +		GCAG ATGG ATGGCGGATGGTCCTCTGGGTCAATCCCAAG GT GTACATCAACCTG GTGAG TA--TC--T-AG CTT --G TA -TA CA TAT TAAC -----T AG CTATT-----G ATT ----- TATAA -TT CC CCAGGACAAACCCG GA ATCACATCTGCGG CT ACTGCGG CT GCGCTTCGTCAA
droKik1	scf7180000302643:772303-772464 +		GCACGG ATGGCGGATGGTCC TCTGGGTCAATCCCAAGGTGTACATCAACCTG GTGAG T T -----T-AG CT ACT TTCTG ----- CTGGG -----TT-----G CT ----- ATACTCTTTAATTAAAGTT -TG TAAT -T AT AGGACAA CCG SG AT CAATCACATCTGCGGCTACTGCGGT CT CGCTTCGTCAA
droAna3	scaffold_12916:10066885-10067045 +		G TA ATGGCGGCGGATGGTCC TCTGGG CATCCCAAGGTGTACATCAACCTG GTGAG T CAAAATC --T-----ATA-----ACA----- ATTTAGTT -T-AG CAC ----- CCTCTATTATAATATGGCTTT -T TC AGGACAA CCCGG AA TC AT CCG TCGCGGCTACT CTGG CTGCGCTTCGTCAA
droBip1	scf7180000396580:969042-969197 +		G TA ATGGCGGCGGATGGTCC TCTGGG CATCCCAAGGTGTACATCAACCTG GTGAG TA--A C --T-----TAA-----ACC----- ATTCAA T S -A-T CTAT ----- CCATTATTGATTAT SC -T TA T-T TA AGGACAA CCCGG AAAT CA CTGCGGCTACT CTGG CTGCGCTTCGTCAA
dp5	4_group3:2816471-2816623 +		GCAG ATGGCGGCGGATGGTCC TCTGGGTCAATCCCAAG GT GTACATCAATCTG GTAG CA C --TAT-T CT -----A-----T TGA ATAT CTG -----CG GA CT TTAA ----- CA - CA - ACAATC -TT GGT -TATAGGAC GC CCCG CTC TCACAT CT TGCGGCTACTGCGG CT GCGCTTCGTCAA
droPer2	scaffold_1:4302023-4302175 +		GCAG ATGGCGGCGGATGGTCC TCTGGGTCAATCCCAAG GT GTACATCAATCTG GTAG CA C --TAT-T CT -----A-----T TGA AAAT CTG -----CG GA CT TTAA ----- CA - CA - ACAATC -TT GGT -TATAGGAC GC CCCG CTC TCACAT CT TGCGGCTACTGCGG CT GCGCTTCGTCAA
droW12	scf2_1100000004585:1195817-1195983 +		G TA ATGGCGGCGG ATGGTCC ATGGGTCAATCCCAAGGTGTACATCAATCTG GTAG CA C --T TA AT T -----G-----T TCATG ----- ACA AAATGCAT TA TT A ----- TA T TA T TA T----- TGGTCC CT-T TA AGGACAAACCCG GA ATCACATCTGCGGCTACTGCGGT CT CGCTTCGTCAA
droVir3	scaffold_12963:11122933-11123089 +	dvi_11341	GCACGGCGGG ATGGTCC CTGG CA CCCA AG STGTACATCAATCTG GTATAT C-AAA-T-----ATA-----AGC----- ATT ----- GAGT S--AAC GT TTCTAGATAT TCCT ----- TATT T GT -TATAGG TAAC CCCG GA AT CA CTGCGGCTACT CTGG CTGCGCTTCGTCAA
droMoj3	scaffold_6500:19870950-19871111 +		GCACGG ATGG ATGGTCC CTGG CA TC CA AG STGTACATCAATCTG GTATAT C CA AT GC TA ATGC -AA-C-T-----A----- ATT GATGTGAAT TAAT S -T----- SCCATAA ----- TTATATG - CATC GC GTG -TATAGG TA AAACCCG GA AT CA CTGCGGCTACTGCGG CT GCGCTTCGTCAA
droGr12	scaffold_15252:5272913-5273078 +		GCACGG ATGA ATGGCGG ATGGTCC CTGG CA CCCA AG STGTACATCAATCTG GTAG CA C -TG-C--TT AT CGCGCTG CTTT -----GACT CA

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

Predicted structure



Flybase annotation

intron [Dyak\GE25609-in]

No Repeatable elements found

Sense Strand Reads

Anti-sense strand reads

Show Alignment With Reads

Re-alignment of all predicted orthologs

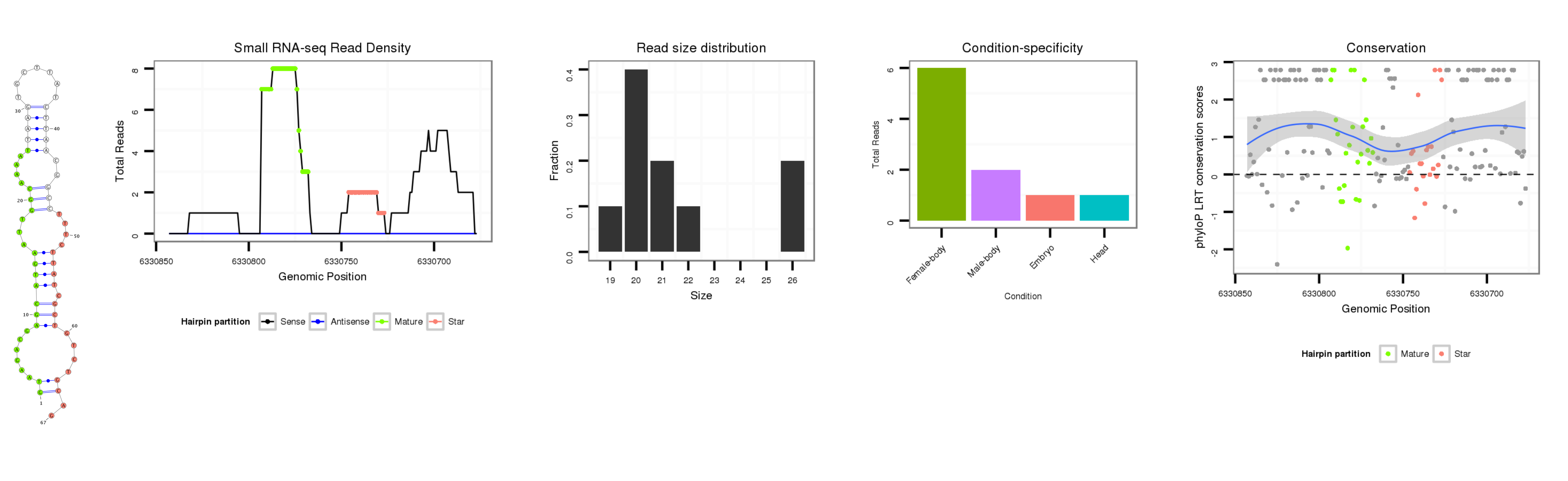
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	PASS/FAIL
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crit.loop	0
crit.mor	0
crit.hair	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate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

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dya_721	3L:6330727-6330793	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 [Dyak/GE20540-in]; CDS [Dyak/GE20540-cds]; CDS [Dyak/GE20540-cds]

No Repeatable elements found

Sense Strand Reads

	Read #	Hit	Total	Total	M043	V120	M026	M056	V058
	size	Mismatch	Count	Norm	female body	male body	head	embryo	head
*****((.....((((((.....(((.....((((.....)))))).....)))).....)).....)).....).....*****									
.....ATGACGAAGGTAAGA	18	2	1	2.00	2	0	0	0	0
.....GTAAGACGAGCATGAATTGGCAAAAT	26	0	1	2.00	2	1	0	1	0
.....GTAAGACGAGCATGAATTGG	20	0	1	2.00	2	1	1	0	0
.....GGACTTGATTTTGGCGGTGGA	21	0	1	1.00	1	1	0	0	0
.....GTAAGACGAGCATGAATTGGCA	22	0	1	1.00	1	1	0	0	0
.....TTGCCGGTGGAGGAGCGTATCGCCCC	25	0	1	1.00	1	1	0	0	0
.....GATTTTGGCGGTGGAGGAGC	20	0	1	1.00	1	0	1	0	0
.....CGAGCATGAATTGGCAAAAT	21	0	1	1.00	1	0	1	0	0
.....TTTCTTATCGCTGTCTGCAG	20	0	1	1.00	1	0	0	0	1
.....GGCCTTTCTTATCGCTGTCT	20	0	1	1.00	1	1	0	0	0
.....AAACGCTGCCGGACTIONGATT	21	0	1	1.00	1	1	0	0	0
.....GTAAGACGAGCATGAATTGG	19	0	1	1.00	1	1	0	0	0
.....GTAAGACGAGCATGAATTGGC	20	0	1	1.00	1	1	0	0	0
.....GTTTGGTTGTGGCGTGACCACTCCG	27	0	1	1.00	1	0	1	0	0
.....ACTTGATTTTGGCGGTGGAG	20	0	1	1.00	1	0	1	0	0

Anti-sense strand reads

	Read #	Hit	Total	Total	M026
	size	Mismatch	Count	Norm	head
*****((.....((((((.....(((.....((((.....)))))).....)))).....)).....)).....).....*****					
GTGGACGTTGCACAAACCAACCCGCACTGGTGAGGCGTACTGCTTCC					

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droYak3	3L:6330677-6330843 -	dya_721	CACCTGCAAGCGTTTGGTTGTGGGCGTGACCACCTCCGCCATGACGAAGGTAAGAGCGAGC-----ATGAATTGGCAAAA-TA--AG-----TGCTTATCTTAAACGGCC-----TTTCT-----TATCGC---TGTCTGCAGGAAAAACGCTGCCGGACTIONGATTTGCCGGTGGAGGAGCGTATCGCCCCG
droBre2	scaffold_4784:8451797-8451962 -		CACCTGAAGCGTTTGGTTGTGGGCGTAACACCTCCGCCATGACGAAGGTAAGAGCGAGC-----ATGAATTGGCAAAA-TA--AA-----TGCTTATCTTAAACGGCC-----TTTCT-----TATCGC---TGTCTGCAGGAAACACGCTGCCGGACTIONGATTTTGCCGTGGAGGAGCGTATCGCCCCG
droSec2	scaffold_2:5698039-5698205 -		CACCTGCAAGCGTTTGGTTGTGGGCGTAACACCTCCGCCATGACGAAGGTAAGAGCGAGC-----ATGAATTGGCAAAA-TA--AA-----ACTTATCTTAAACGGCC-----ATTCT-----TATCGC---TGTCTGCAGGAAACACGCTGCCGGACTIONGATTTTGCCGTGGAGGAGCGTATCGCCCCG
droSim2	3L:5674204-5674370 -	dsl_8966	CACCTGCAAGCGTTTGGTTGTGGGCGTAACACCTCCGCCATGACGAAGGTAAGAGCGAGC-----ATGAATTGGCAAAA-TA--AA-----ACTTATCTTAAACGGCC-----ATTCT-----TATCGC---TGTCTGCAGGAAACACGCTGCCGGACTIONGATTTTGCCGTGGAGGAGCGTATCGCCCCG
dm3	chr3L:5761184-5761350 -	dme_433	CACCTGCAAGCGTTTGGTTGTGGGCGTAACACCTCCGCCATGACGAAGGTAAGAGCGAGC-----ATGAATTGGCAAAA-TA--AA-----CTTATCTTAAACGGCC-----ATTCT-----TATCGC---TGTCTGCAGGAAACACGCTGCCGGACTIONGATTTTGCCGTGGAGGAGCGTATCGCCCCG
droEug1	scf7180000409466:3531118-3531284 -		AAGCAAGCGTTTGGTTGTGGGCGTAACACCTCCGCCATGACGAAGGTAAGAGCGAGC-----ATGAATTGGCAAAA-TA--GA-----TCTTATCTTAAACGGCC-----TTTGA-----TATCGC---TGTATGAGGAAACACGCTGCCGGACTIONGATTTTGCCGTGGAGGAGCGTATCGCCCCG
droBial1	scf7180000302193:3263790-3263955 -		CGCTGCAGAAAGCTTGGTTGTGGGCGTAACACCTCCGCCATGACGAAGGTAAGAGCGAGC-----ATGAATTGGCAAAA-TA--GA-----CTTATCTTAAACGGCC-----TTTGC-----TATCGC---TGTATGAGGAAACACCTGCCGGACTIONGATTTTGCCGTGGAGGAGCGTATCGCCCCG
droTak1	scf7180000415868:464165-464320 -		CACCTGCAGCGCTTGGTTGTGGGCGTGACCACTCCGCCATGACGAAGGTAAGAGCGAGC-----ATGAATTGGCAAAA-TA--GA-----CTTATCTTAAACGGCC-----TTT-----TATCGC---TGTATGAGGAAACACGCTGCCGGACTIONGATTTTGCCGTGGAGGAGCGTATCGCCCCG
droE1el	scf7180000491268:1253522-1253680 -		CACCTGCAGAAAGCTTGGTTGTGGGCGTGACCACTCCGCCATGACGAAGGTAAGAGCGAGC-----ATGAATTGGCAAAA-TA--GA-----TCTTATCTTAAACGGCC-----TTT-----TATCGC---TGTATGAGGAAACACGCTGCCGGACTIONGATTTTGCCGTGGAGGAGCGTATCGCCCCG
droRho1	scf7180000768851:39540-39698 -		TACATGCAAGCTTGGTTGTGGGCGTGACCACTCCGCCATGACGAAGGTAAGAGCGAGC-----ATGAATTGGCAAAA-TA--GA-----TCTTATCTTAAACGGCC-----TTT-----TATCGC---TGTATGAGGAAACACGCTGCCGGACTIONGATTTTGCCGTGGAGGAGCGTATCGCCCCG
droFic1	scf7180000453929:1855358-1855516 +		CACATGCAAGCTTGGTTGTGGGCGTAACACCTCCGCCATGACGAAGGTAAGAGCGAGC-----ATGAATTGGCAAAA-TA--GA-----TCTTATCTTAAACGGCC-----TTT-----TATCGC---TGTATGAGGAAACACGCTGCCGGACTIONGATTTTGCCGTGGAGGAGCGTATCGCCCCG
droKik1	scf7180000203686:58828-58997 -		CGCTGCAAGCGCTTGGTTGTGGGCGTGACCACTCCGCCATGACGAAGGTAAGAGCGAGC-----ATGAATTGGCAAAA-TA--GA-----TCTTATCTTAAACGGCC-----TTTGC-----TATCGCTGCTGTCTGCAGGAAACACGCTGCCGGACTIONGATTTTGCCGTGGAGGAGCGTATCGCCCCG
droAna3	scaffold_13337:12780135-12780299 +		TATGCAAGCTTGGTTGTGGGCGTGACCACTCCGCCATGACGAAGGTAAGAGCGAGC-----ATGAATTGGCAAAA-TA--GA-----TCTTATCTTAAACGGCC-----TTTAC-----TATCGC---TGTATGAGGAAACACGCTGCCGGACTIONGATTTTGCCGTGGAGGAGCGTATCGCCCCG
droBip1	scf7180000396589:1243096-1243259 -		TATGCAAGCTTGGTTGTGGGCGTGACCACTCCGCCATGACGAAGGTAAGAGCGAGC-----ATGAATTGGCAAAA-TA--GA-----TCTTATCTTAAACGGCC-----TTTAC-----TATCGC---TGTATGAGGAAACACGCTGCCGGACTIONGATTTTGCCGTGGAGGAGCGTATCGCCCCG
dp5	XR_group6:9792525-9792675 +		CACATGCAAGCGCTTGGTTGTGGGCGTAACACCTCCGCCATGACGAAGGTAAGAGCGAGC-----ATGAATTGGCAAAA-TA--GT-----TCTTATCTTAAACGGCC-----TTT-----TATCGC---TGTATGAGGAAACACGCTGCCGGACTIONGATTTTGCCGTGGAGGAGCGTATCGCCCCG
droPer2	scaffold_61:68100-68250 +		CACATGCAAGCGCTTGGTTGTGGGCGTAACACCTCCGCCATGACGAAGGTAAGAGCGAGC-----ATGAATTGGCAAAA-TA--GT-----TCTTATCTTAAACGGCC-----TTT-----TATCGC---TGTATGAGGAAACACGCTGCCGGACTIONGATTTTGCCGTGGAGGAGCGTATCGCCCCG
droM112	scf2_1100000004511:3789301-3789457 -		CGCTGCAGAAAGCTTGGTTGTGGGCGTGACCACTCCGCCATGACGAAGGTAAGAGCGAGC-----ATGAATTGGCAAAA-TA--GT-----TCTTATCTTAAACGGCC-----TTT-----TATCGC---TGTATGAGGAAACACGCTGCCGGACTIONGATTTTGCCGTGGAGGAGCGTATCGCCCCG
droV1r3	scaffold_13049:2212421-2212586 +		GGCTGCAGAAAGCTTGGTTGTGGGCGTAACACCTCCGCCATGACGAAGGTAAGAGCGAGC-----ATGAATTGGCAAAA-TA--GT-----TCTTATCTTAAACGGCC-----TTT-----TATCGC---TGTATGAGGAAACACGCTGCCGGACTIONGATTTTGCCGTGGAGGAGCGTATCGCCCCG
droMo3	scaffold_6654:1651110-1651283 -		CGCTGCAGAAAGCTTGGTTGTGGGCGTAACACCTCCGCCATGACGAAGGTAAGAGCGAGC-----ATGAATTGGCAAAA-TA--GT-----TCTTATCTTAAACGGCC-----TTT-----TATCGC---TGTATGAGGAAACACGCTGCCGGACTIONGATTTTGCCGTGGAGGAGCGTATCGCCCCG
droG1r2	scaffold_15110:3253137-3253342 +		CACCTGAAGCGTTTGGTTGTGGGCGTGACCACTCCGCCATGACGAAGGTAAGAGCGAGC-----ATGAATTGGCAAAA-TA--GT-----TCTTATCTTAAACGGCC-----TTT-----TATCGC---TGTATGAGGAAACACGCTGCCGGACTIONGATTTTGCCGTGGAGGAGCGTATCGCCCCG

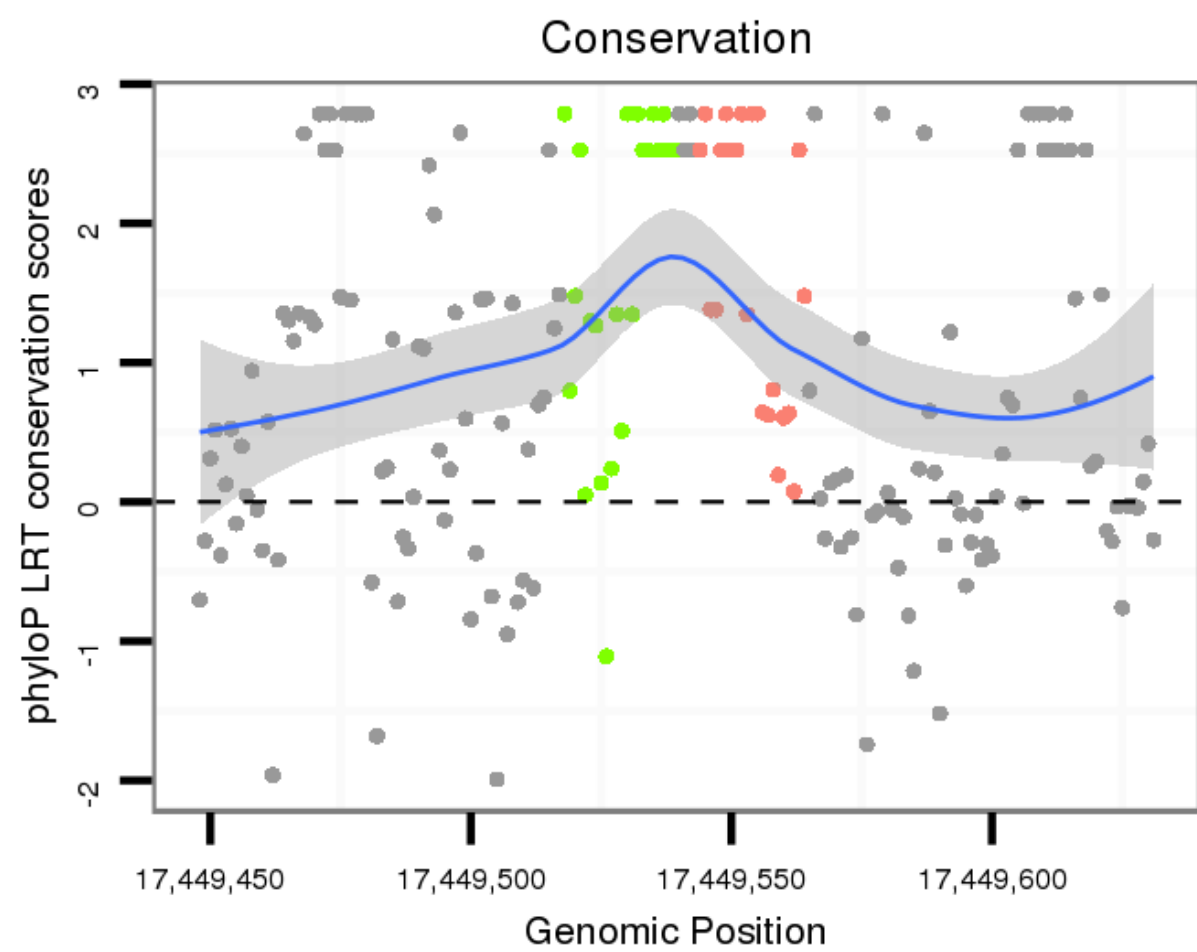
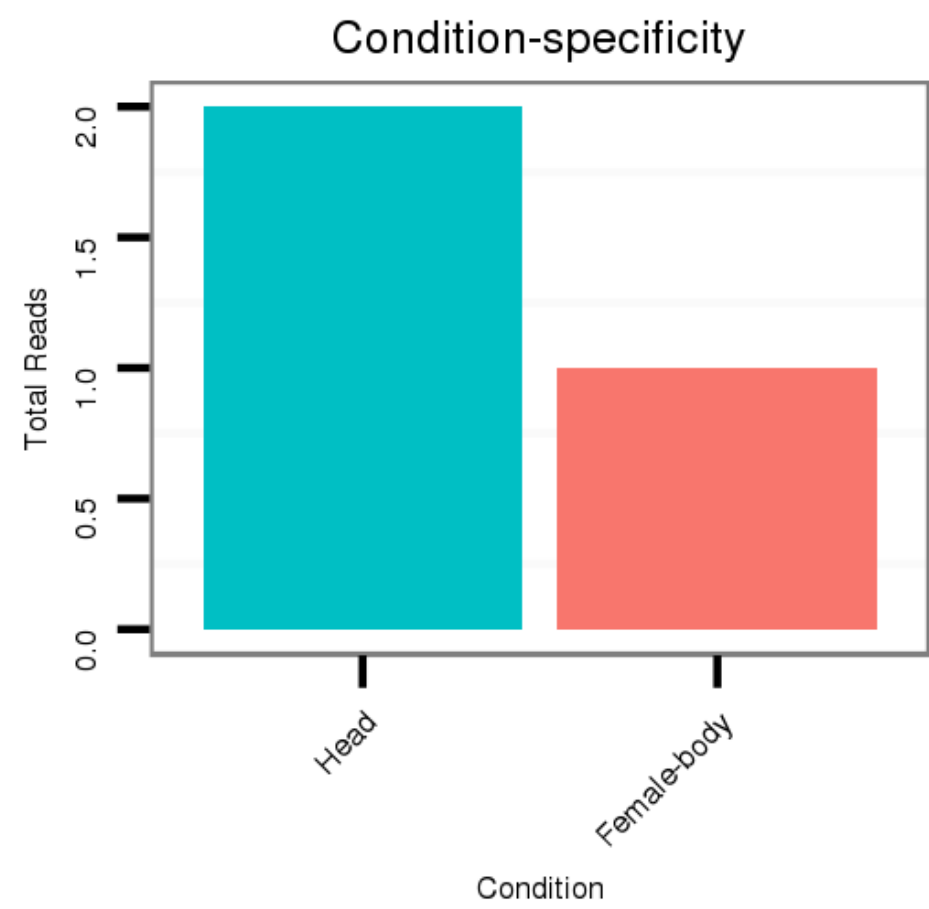
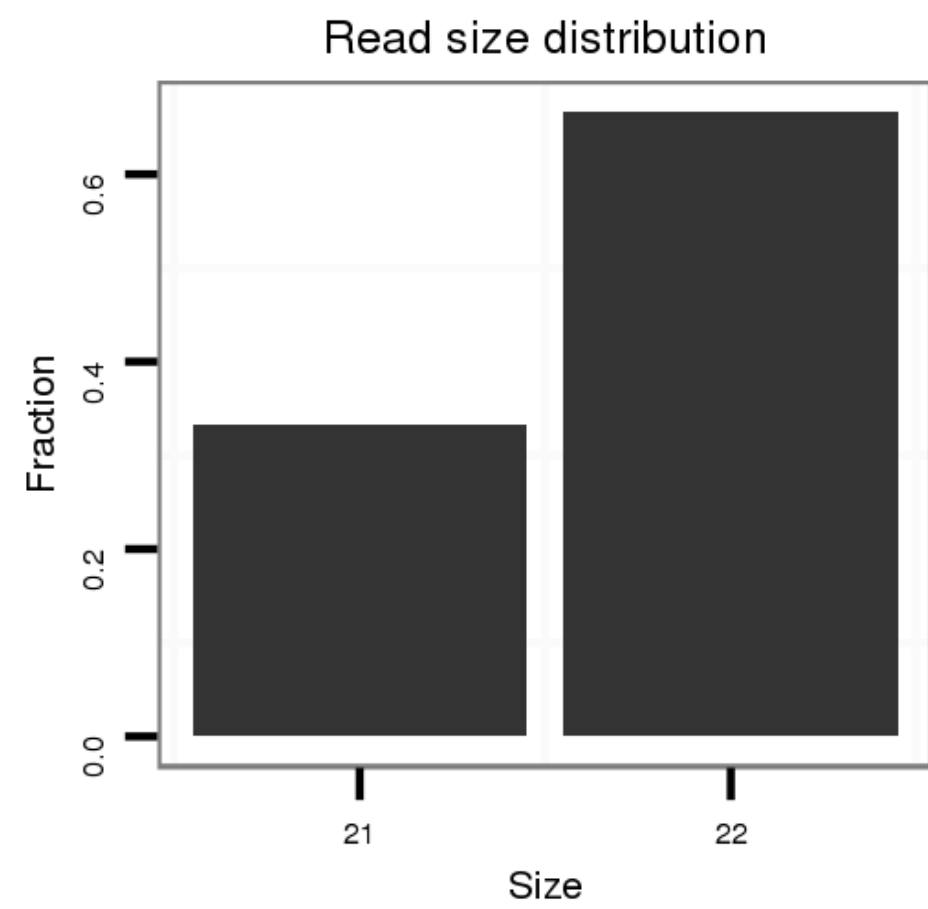
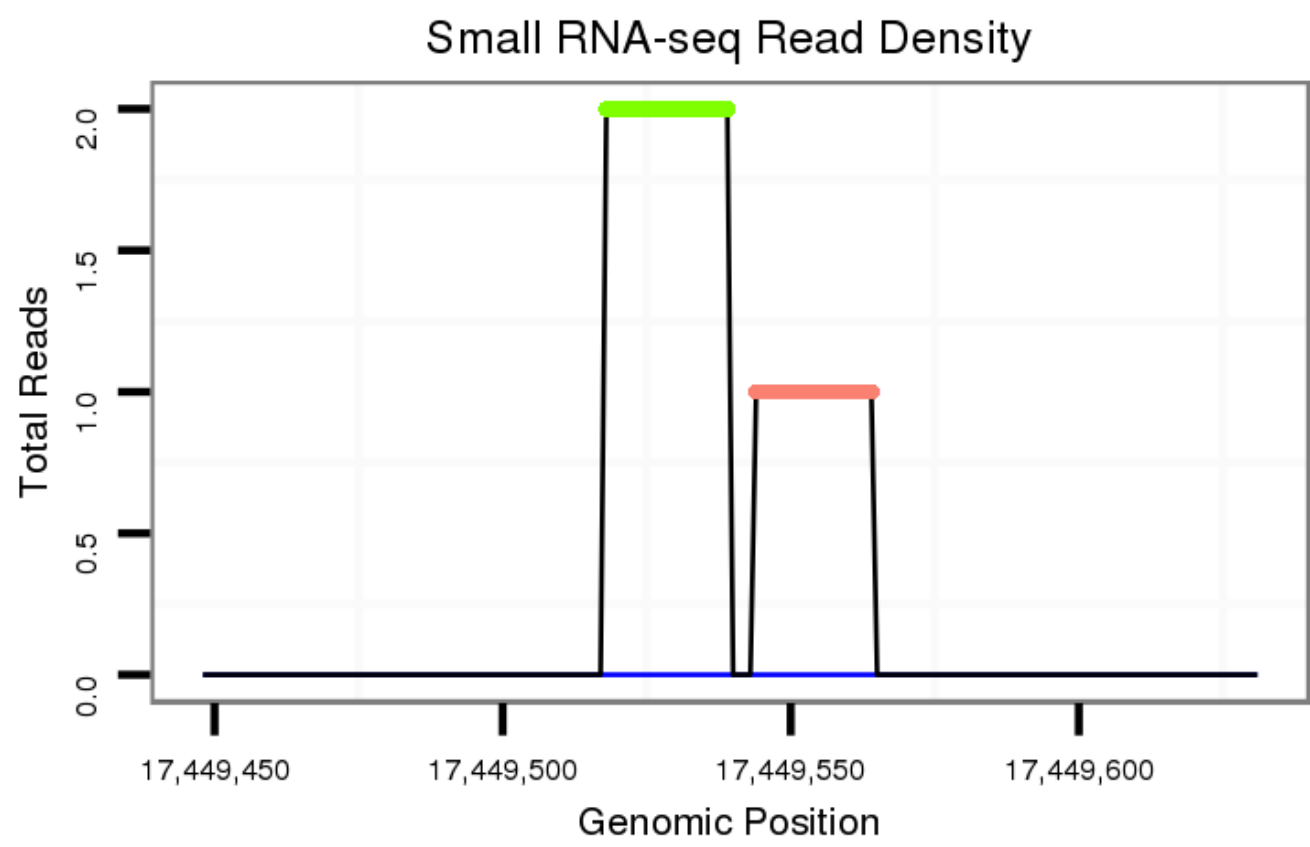
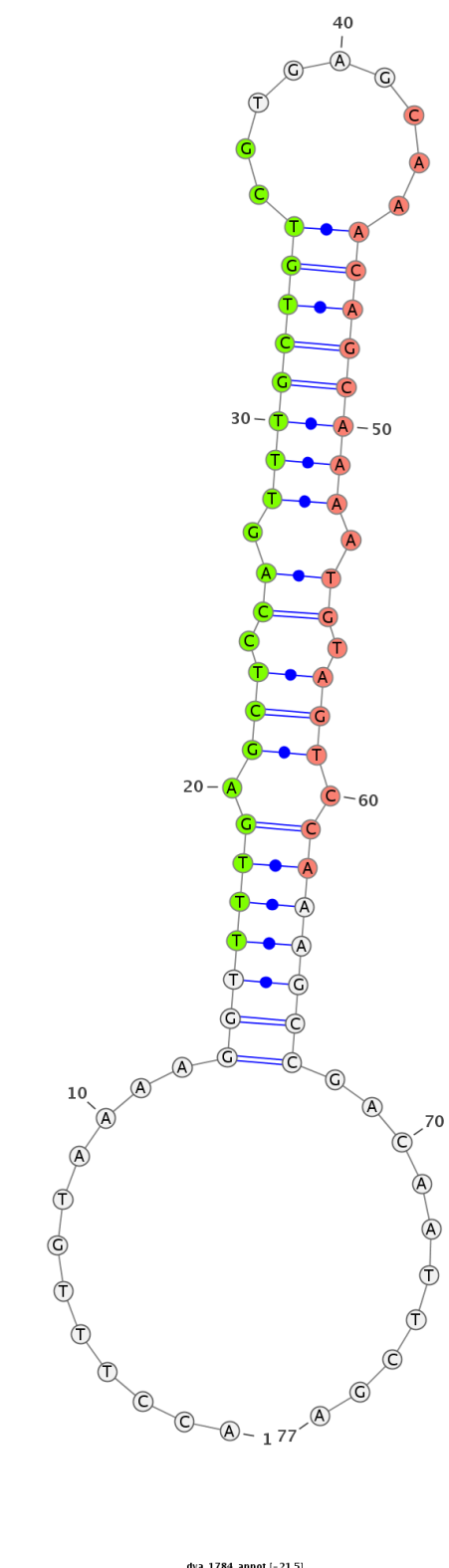
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	PASS/FAIL
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crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tpop3	1
crit.uri	0
crit.back	0
rescue.total	0
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	3

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dya_1800	X:12117938-12118004 +	Known Ortholog	MiRNA	intron	[View on UCSC Genome Browser (Cornell Mirror)]

	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	0
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crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	4

Legend: mature star mismatch in alignment mismatch in read



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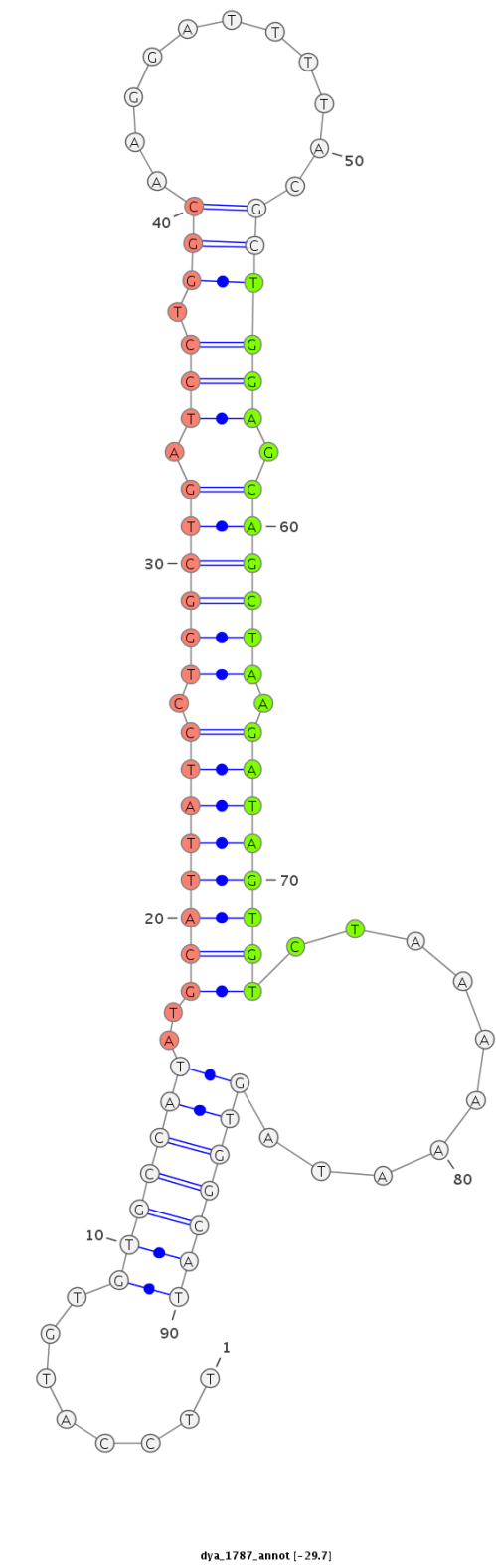
[illegible][illegible]

	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	1
crit.back	1
rescue.total	0
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	5

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dya_1787	3L:2067774-2067907	candidate	Canonical miRNA	intergenic	[View on UCSC Genome Browser (Cornell Mirror)]

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

Predicted structure



RNA2D (RNA2D-2012)

Show Alternate Folds

Flybase annotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

Read #	size	Mismatch	Hit	Total	Count	Norm	Total	M043 female body	V120 male body	M056 embryo	SRR1275484 Male prepupae	GSM1528802 follicle cells	V058 head
1	22	0	1	3.00	3	1	2	0	1	2	0	0	0
2	25	0	1	1.00	1	0	0	1	0	0	0	0	0
3	21	0	1	1.00	1	1	0	0	0	0	0	0	0
4	23	0	1	1.00	1	0	1	0	0	0	0	0	0
5	23	0	1	1.00	1	0	1	0	0	0	0	0	0

Anti-sense strand reads

Read #	size	Mismatch	Hit	Total	Count	Norm	Total	M043 female body
1	22	0	1	3.00	3	1	2	0
2	25	0	1	1.00	1	0	0	1
3	21	0	1	1.00	1	1	0	0
4	23	0	1	1.00	1	0	1	0
5	23	0	1	1.00	1	0	1	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droYak3	3L:2067774-2067957 -	dya_1787	GC AAA--CAGATATC---AAGCAATC-----TATA-----T-----ATAT-----AG---TCGA---ACCTGCACAAATCAAA---AGATC-----ACGTATACG---CAGTC---CTT--CCATGTGTGGC--ATGAGCATTATCCTTGGC-----T--GATCCTGGGAAGGATTTTACGC
droEre2	scarfoid_4784:2108748-2108982 -	dex_94	GC AAA--CAGATATC---AAGCAATC-----TATA-----T-----ATAT-----AG---TCGA---ACCTGCACAAATCAAA---AGATC-----ACGTATACG---CAGTC---CTT--CCATGTGTGGC--ATGAGCATTATCCTTGGC-----T--GATCCTGGGAAGGATTTTACGC
droSec2	scarfoid_2:2140470-2140704	dse_1837	GC AAA--CAGATATC---AAGCAATC-----TATA-----T-----ATAT-----AG---TCGA---ACCTGCACAAATCAAA---AGATC-----ACGTATACG---CAGTC---CTT--CCATGTGTGGC--ATGAGCATTATCCTTGGC-----T--GATCCTGGGAAGGATTTTACGC
groSino3	3L:2012794-2013028 -	dai_3244	GC AAA--CAGATATC---AAGCAATC-----TATA-----T-----ATAT-----AG---TCGA---ACCTGCACAAATCAAA---AGATC-----ACGTATACG---CAGTC---CTT--CCATGTGTGGC--ATGAGCATTATCCTTGGC-----T--GATCCTGGGAAGGATTTTACGC
dm3	chr3L:2114883-2115119 -	dme_114	GC AAA--CAGATATC---AAGCAATC-----TATA-----T-----ATAT-----AG---TCGA---ACCTGCACAAATCAAA---AGATC-----ACGTATACG---CAGTC---CTT--CCATGTGTGGC--ATGAGCATTATCCTTGGC-----T--GATCCTGGGAAGGATTTTACGC
groEup1	scf7180000409091:158083-158318 +		GC AAA--CAGATATC---AAGCAATC-----TATA-----T-----ATAT-----AG---TCGA---ACCTGCACAAATCAAA---AGATC-----ACGTATACG---CAGTC---CTT--CCATGTGTGGC--ATGAGCATTATCCTTGGC-----T--GATCCTGGGAAGGATTTTACGC
droB1a1	scf7180000302428:8837654-8847891 +		GC AAA--CAGATATC---AAGCAATC-----TATA-----T-----ATAT-----AG---TCGA---ACCTGCACAAATCAAA---AGATC-----ACGTATACG---CAGTC---CTT--CCATGTGTGGC--ATGAGCATTATCCTTGGC-----T--GATCCTGGGAAGGATTTTACGC
droTak1	scf1180000414400:42653-42859		GC AAA--CAGATATC---AAGCAATC-----TATA-----T-----ATAT-----AG---TCGA---ACCTGCACAAATCAAA---AGATC-----ACGTATACG---CAGTC---CTT--CCATGTGTGGC--ATGAGCATTATCCTTGGC-----T--GATCCTGGGAAGGATTTTACGC
droE1e1	scf7180000491249:3380268-3380509 +		GC AAA--CAGATATC---AAGCAATC-----TATA-----T-----ATAT-----AG---TCGA---ACCTGCACAAATCAAA---AGATC-----ACGTATACG---CAGTC---CTT--CCATGTGTGGC--ATGAGCATTATCCTTGGC-----T--GATCCTGGGAAGGATTTTACGC
droRho1	scf7180000779211:43014-43214		GC AAA--CAGATATC---AAGCAATC-----TATA-----T-----ATAT-----AG---TCGA---ACCTGCACAAATCAAA---AGATC-----ACGTATACG---CAGTC---CTT--CCATGTGTGGC--ATGAGCATTATCCTTGGC-----T--GATCCTGGGAAGGATTTTACGC
droFic1	scf1180000453052:1945687-245920 +		GC AAA--CAGATATC---AAGCAATC-----TATA-----T-----ATAT-----AG---TCGA---ACCTGCACAAATCAAA---AGATC-----ACGTATACG---CAGTC---CTT--CCATGTGTGGC--ATGAGCATTATCCTTGGC-----T--GATCCTGGGAAGGATTTTACGC
droK1k1	scf7180000302441:1692375-1692541 +		GC AAA--CAGATATC---AAGCAATC-----TATA-----T-----ATAT-----AG---TCGA---ACCTGCACAAATCAAA---AGATC-----ACGTATACG---CAGTC---CTT--CCATGTGTGGC--ATGAGCATTATCCTTGGC-----T--GATCCTGGGAAGGATTTTACGC
droAna3	scarfoid_13337:715292-715297 +	dan_4047	GC AAA--CAGATATC---AAGCAATC-----TATA-----T-----ATAT-----AG---TCGA---ACCTGCACAAATCAAA---AGATC-----ACGTATACG---CAGTC---CTT--CCATGTGTGGC--ATGAGCATTATCCTTGGC-----T--GATCCTGGGAAGGATTTTACGC
droBip1	scf7180000395155:42369-42600 -		GC AAA--CAGATATC---AAGCAATC-----TATA-----T-----ATAT-----AG---TCGA---ACCTGCACAAATCAAA---AGATC-----ACGTATACG---CAGTC---CTT--CCATGTGTGGC--ATGAGCATTATCCTTGGC-----T--GATCCTGGGAAGGATTTTACGC
dp5	RR_group61:2020010-12020252		GC AAA--CAGATATC---AAGCAATC-----TATA-----T-----ATAT-----AG---TCGA---ACCTGCACAAATCAAA---AGATC-----ACGTATACG---CAGTC---CTT--CCATGTGTGGC--ATGAGCATTATCCTTGGC-----T--GATCCTGGGAAGGATTTTACGC
droPe2	scarfoid_32:40894-41158 -		GC AAA--CAGATATC---AAGCAATC-----TATA-----T-----ATAT-----AG---TCGA---ACCTGCACAAATCAAA---AGATC-----ACGTATACG---CAGTC---CTT--CCATGTGTGGC--ATGAGCATTATCCTTGGC-----T--GATCCTGGGAAGGATTTTACGC
droW12	scf118000004729:1281520-1281532 +		GC AAA--CAGATATC---AAGCAATC-----TATA-----T-----ATAT-----AG---TCGA---ACCTGCACAAATCAAA---AGATC-----ACGTATACG---CAGTC---CTT--CCATGTGTGGC--ATGAGCATTATCCTTGGC-----T--GATCCTGGGAAGGATTTTACGC
droV13	scarfoid_130491:1990081-1993936 +		GC AAA--CAGATATC---AAGCAATC-----TATA-----T-----ATAT-----AG---TCGA---ACCTGCACAAATCAAA---AGATC-----ACGTATACG---CAGTC---CTT--CCATGTGTGGC--ATGAGCATTATCCTTGGC-----T--GATCCTGGGAAGGATTTTACGC
droMo3	scarfoid_6680:8821328-8821629 -		GC AAA--CAGATATC---AAGCAATC-----TATA-----T-----ATAT-----AG---TCGA---ACCTGCACAAATCAAA---AGATC-----ACGTATACG---CAGTC---CTT--CCATGTGTGGC--ATGAGCATTATCCTTGGC-----T--GATCCTGGGAAGGATTTTACGC
droGr12	scarfoid_15110:11439147-11439416 +		GC AAA--CAGATATC---AAGCAATC-----TATA-----T-----ATAT-----AG---TCGA---ACCTGCACAAATCAAA---AGATC-----ACGTATACG---CAGTC---CTT--CCATGTGTGGC--ATGAGCATTATCCTTGGC-----T--GATCCTGGGAAGGATTTTACGC

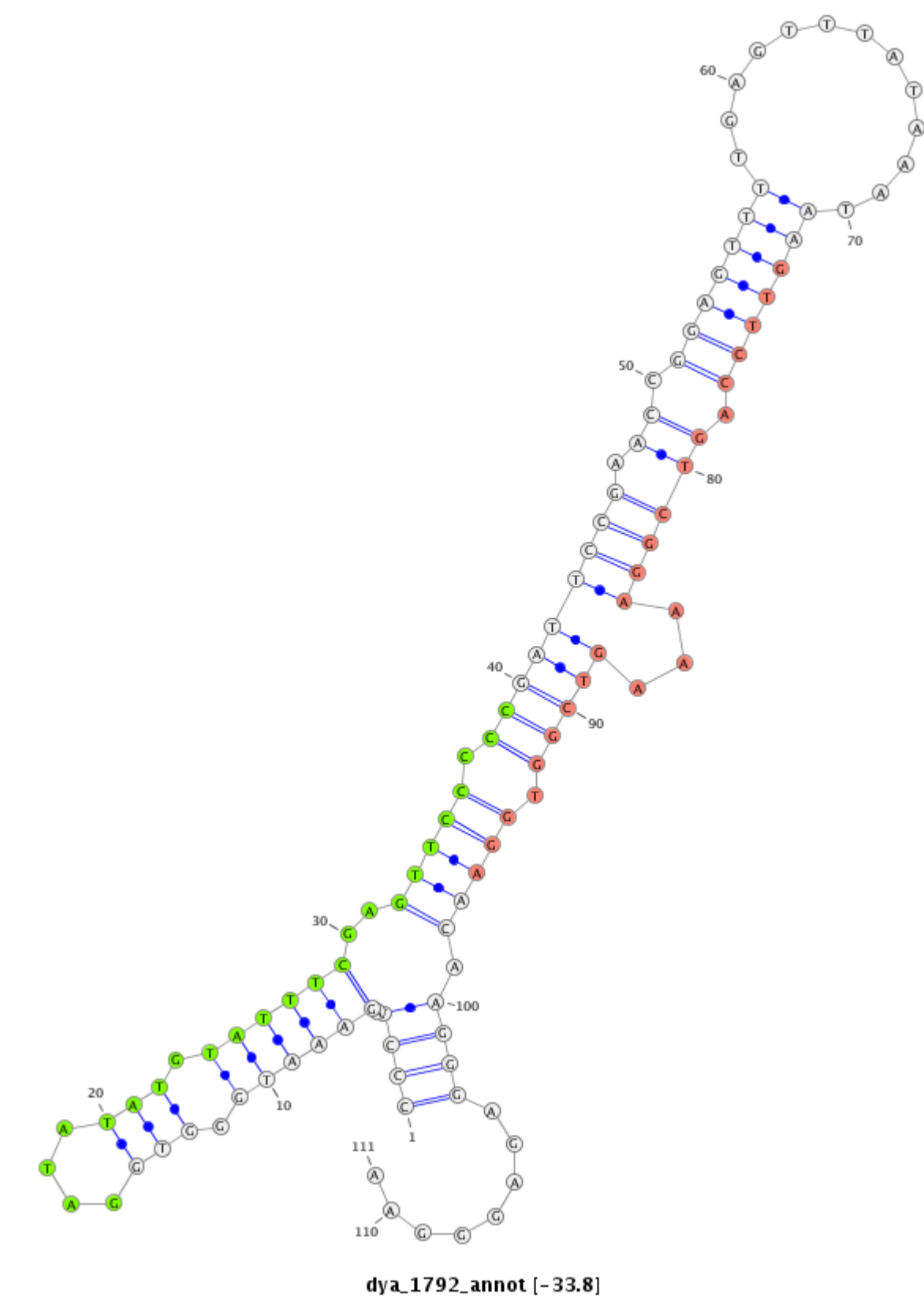
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rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	4

dya_1792	3L:4705316-4705454 -	candidate	Canonical miRNA	intron	[View on UCSC Genome Browser [Cornell Mirror]]
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Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Show Alternate Folds

Flybase annotation

intron [Dyak\GE20647-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

[illegible]

Anti-sense strand reads

[illegible]

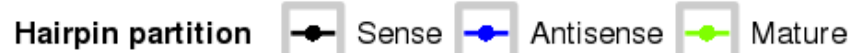
Show Alignment With Reads

Species		Coordinate	ID	Alignment
dfoYaK	31:4705266-4705304	+	dfoYa_1792	CA-GCGAGGCGAGAGACAGAG-----AAAAGAAAGCCGAGAGCCA--AAAGTGTCTGCCCCC-TAGAA-ATGGGTG--ATATA--TGATTTT--CGAG--T--TCCGCG--ATTCCG--AACCGGAGTTTGGAGTTTATAATAAA--TTC-----CAGTCGG-AA-AGTGGG-ACAAGGAGGAGGGAACATACATATTTTCC--GTACTTCTCTGT-CTCT--CTCGCTTGTGATCCGACGTGCTGCG--T--GC--GCT--G-GTGTGG
dfoPe2	31:4784188-47842	+	dfoPe2_151	CA-GCGAGGCGAGAGACAGAGAAAG-----AAAAGAAAGCCGAGAGCCA--AAAGTGTCTGCCCCC-TAGAA-ATGGGTG--ATATA--TGATTTT--CGAG--T--TCCGCG--ATTCCG--AACCGGAGTTTGGAGTTTATAATAAA--TTC-----CAGTCGG-AA-AGTGGG-ACAAGGAGGAGGGAACATACATATTTTCC--GTACTTCTCTGT-CTCT--CTCGCTTGTGATCCGACGTGCTGCG--T--GC--GCT--G-GTGTGG
dfoSe2	31:4126517-412673	+	dfoSe2_1840	CA-GCGAGGCGAGAGCGAGAGAAAGAAAG--AAAAGAAAGCCGAGAGCCA--AAAGTGTCTGCCCCC-TAGAA-ATGGGTG--ATATA--TGATTTT--CGAG--T--TCCGCG--ATTCCG--AACCGGAGTTTGGAGTTTATAATAAA--TTC-----CAGTCGG-AA-AGTGGG-ACAAGGAGGAGGGAACATACATATTTTCC--GTACTTCTCTGT-CTCT--CTCGCTTGTGATCCGACGTGCTGCG--T--GC--GCT--G-GTGTGG
dfoS1m2	31:4094320-4094564	+	dfoS1_150	CA-GCGAGGCGAGAGCGAGAGAAAGAAAG--AAAAGAAAGCCGAGAGCCA--AAAGTGTCTGCCCCC-TAGAA-ATGGGTG--ATATA--TGATTTT--CGAG--T--TCCGCG--ATTCCG--AACCGGAGTTTGGAGTTTATAATAAA--TTC-----CAGTCGG-AA-AGTGGG-ACAAGGAGGAGGGAACATACATATTTTCC--GTACTTCTCTGT-CTCT--CTCGCTTGTGATCCGACGTGCTGCG--T--GC--GCT--G-GTGTGG
dfoS1m3	31:4134010-4134256	+	dfoS1_412	CA-GCGAGGCGAGAGCGAGAGAAAGAAAG--AAAAGTGTCTGCCCCC-TAGAA-ATGGGTG--ATATA--TGATTTT--CGAG--T--TCCGCG--ATTCCG--AACCGGAGTTTGGAGTTTATAATAAA--TTC-----CAGTCGG-AA-AGTGGG-ACAAGGAGGAGGGAACATACATATTTTCC--GTACTTCTCTGT-CTCT--CTCGCTTGTGATCCGACGTGCTGCG--T--GC--GCT--G-GTGTGG
dfoBu1	31:7180020409466-1909794	+	dfoBu1_190136	CA-GCGAGGCGAGAGCGAGAGAAAGCC--AAAGTGTCTGCCCCC-TSAR-ATGGGTG--ATATA--TTTGGTGGCCCGCGCG--TTCG--T--TCCGCG--ATTCCG--AACCGGAGTTTGGAGTTTATAATAAA--TTC-----CAGTCGG-AA-AGTGGG-ACAAGGAGGAGGGAACATACATATTTTCC--GTACTTCTCTGT-CTCT--CTCGCTTGTGATCCGACGTGCTGCG--T--GC--GCT--G-GTGTGG
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dfoTaK1	31:7180004015778-22368	+	dfoTaK1_22566	CA-GCGAGGCGAGAGCGAGAGAAAGCC--AAAGTGTCTGCCCCC-TSAR-ATGGGTG--ATATA--TTTGGTGGCCCGCGCG--TTCG--T--TCCGCG--ATTCCG--AACCGGAGTTTGGAGTTTATAATAAA--TTC-----CAGTCGG-AA-AGTGGG-ACAAGGAGGAGGGAACATACATATTTTCC--GTACTTCTCTGT-CTCT--CTCGCTTGTGATCCGACGTGCTGCG--T--GC--GCT--G-GTGTGG
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dfoRho1	31:718000779198-19068	+	dfoRho1_19236	CA-GCGAGGCGAGAGCGAGAGAAAGCC--AAAGTGTCTGCCCCC-TSAR-ATGGGTG--ATATA--TTTGGTGGCCCGCGCG--TTCG--T--TCCGCG--ATTCCG--AACCGGAGTTTGGAGTTTATAATAAA--TTC-----CAGTCGG-AA-AGTGGG-ACAAGGAGGAGGGAACATACATATTTTCC--GTACTTCTCTGT-CTCT--CTCGCTTGTGATCCGACGTGCTGCG--T--GC--GCT--G-GTGTGG
dfoP1c1	31:7180004054113-136332	+	dfoP1c1_136332	CA-GCGAGGCGAGAGCGAGAGAAAGCC--AAAGTGTCTGCCCCC-TSAR-ATGGGTG--ATATA--TTTGGTGGCCCGCGCG--TTCG--T--TCCGCG--ATTCCG--AACCGGAGTTTGGAGTTTATAATAAA--TTC-----CAGTCGG-AA-AGTGGG-ACAAGGAGGAGGGAACATACATATTTTCC--GTACTTCTCTGT-CTCT--CTCGCTTGTGATCCGACGTGCTGCG--T--GC--GCT--G-GTGTGG
dfoK1K1	31:718000302383-514810	+	dfoK1K1_516076	CA-GCGAGGCGAGAGCGAGAGAAAGCC--AAAGTGTCTGCCCCC-TSAR-ATGGGTG--ATATA--TTTGGTGGCCCGCGCG--TTCG--T--TCCGCG--ATTCCG--AACCGGAGTTTGGAGTTTATAATAAA--TTC-----CAGTCGG-AA-AGTGGG-ACAAGGAGGAGGGAACATACATATTTTCC--GTACTTCTCTGT-CTCT--CTCGCTTGTGATCCGACGTGCTGCG--T--GC--GCT--G-GTGTGG
dfoAna3	31:718000413337-1455487	+	dfoAna3_1455491	CA-GCGAGGCGAGAGCGAGAGAAAGCC--AAAGTGTCTGCCCCC-TSAR-ATGGGTG--ATATA--TTTGGTGGCCCGCGCG--TTCG--T--TCCGCG--ATTCCG--AACCGGAGTTTGGAGTTTATAATAAA--TTC-----CAGTCGG-AA-AGTGGG-ACAAGGAGGAGGGAACATACATATTTTCC--GTACTTCTCTGT-CTCT--CTCGCTTGTGATCCGACGTGCTGCG--T--GC--GCT--G-GTGTGG
dfoB1p1	31:7180002396641-755024	+	dfoB1p1_75523	CA-GCGAGGCGAGAGCGAGAGAAAGCC--AAAGTGTCTGCCCCC-TSAR-ATGGGTG--ATATA--TTTGGTGGCCCGCGCG--TTCG--T--TCCGCG--ATTCCG--AACCGGAGTTTGGAGTTTATAATAAA--TTC-----CAGTCGG-AA-AGTGGG-ACAAGGAGGAGGGAACATACATATTTTCC--GTACTTCTCTGT-CTCT--CTCGCTTGTGATCCGACGTGCTGCG--T--GC--GCT--G-GTGTGG
dfoS1	31:7180002396641-755024	+	dfoS1_75523	CA-GCGAGGCGAGAGCGAGAGAAAGCC--AAAGTGTCTGCCCCC-TSAR-ATGGGTG--ATATA--TTTGGTGGCCCGCGCG--TTCG--T--TCCGCG--ATTCCG--AACCGGAGTTTGGAGTTTATAATAAA--TTC-----CAGTCGG-AA-AGTGGG-ACAAGGAGGAGGGAACATACATATTTTCC--GTACTTCTCTGT-CTCT--CTCGCTTGTGATCCGACGTGCTGCG--T--GC--GCT--G-GTGTGG
dfoPe2	31:7180002396641-755024	+	dfoPe2_75523	CA-GCGAGGCGAGAGCGAGAGAAAGCC--AAAGTGTCTGCCCCC-TSAR-ATGGGTG--ATATA--TTTGGTGGCCCGCGCG--TTCG--T--TCCGCG--ATTCCG--AACCGGAGTTTGGAGTTTATAATAAA--TTC-----CAGTCGG-AA-AGTGGG-ACAAGGAGGAGGGAACATACATATTTTCC--GTACTTCTCTGT-CTCT--CTCGCTTGTGATCCGACGTGCTGCG--T--GC--GCT--G-GTGTGG
dfoW112	31:7180002396641-755024	+	dfoW112_75523	CA-GCGAGGCGAGAGCGAGAGAAAGCC--AAAGTGTCTGCCCCC-TSAR-ATGGGTG--ATATA--TTTGGTGGCCCGCGCG--TTCG--T--TCCGCG--ATTCCG--AACCGGAGTTTGGAGTTTATAATAAA--TTC-----CAGTCGG-AA-AGTGGG-ACAAGGAGGAGGGAACATACATATTTTCC--GTACTTCTCTGT-CTCT--CTCGCTTGTGATCCGACGTGCTGCG--T--GC--GCT--G-GTGTGG
dfoV1r3	31:7180002396641-755024	+	dfoV1r3_75523	CA-GCGAGGCGAGAGCGAGAGAAAGCC--AAAGTGTCTGCCCCC-TSAR-ATGGGTG--ATATA--TTTGGTGGCCCGCGCG--TTCG--T--TCCGCG--ATTCCG--AACCGGAGTTTGGAGTTTATAATAAA--TTC-----CAGTCGG-AA-AGTGGG-ACAAGGAGGAGGGAACATACATATTTTCC--GTACTTCTCTGT-CTCT--CTCGCTTGTGATCCGACGTGCTGCG--T--GC--GCT--G-GTGTGG
dfoMoJ3	31:7180002396641-755024	+	dfoMoJ3_75523	CA-GCGAGGCGAGAGCGAGAGAAAGCC--AAAGTGTCTGCCCCC-TSAR-ATGGGTG--ATATA--TTTGGTGGCCCGCGCG--TTCG--T--TCCGCG--ATTCCG--AACCGGAGTTTGGAGTTTATAATAAA--TTC-----CAGTCGG-AA-AGTGGG-ACAAGGAGGAGGGAACATACATATTTTCC--GTACTTCTCTGT-CTCT--CTCGCTTGTGATCCGACGTGCTGCG--T--GC--GCT--G-GTGTGG
dfoS12	31:7180002396641-755024	+	dfoS12_75523	CA-GCGAGGCGAGAGCGAGAGAAAGCC--AAAGTGTCTGCCCCC-TSAR-ATGGGTG--ATATA--TTTGGTGGCCCGCGCG--TTCG--T--TCCGCG--ATTCCG--AACCGGAGTTTGGAGTTTATAATAAA--TTC-----C

Generated: 09/08/2015 at 07:49 PM

crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	0
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	0
rescue.total	0
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	5

Legend: mature star mismatch in alignment mismatch in read



No Repeatable elements found

hide 3p reads show mid mismatch reads

Show Alignment With Reads

[illegible]

	PASS/FAIL
crit.star	

crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	0
crit.uri	0
crit.back	0
rescue.total	0
rescue.dominant	1
rescue.known	3
rescue.confident	3
rescue.candidate	3