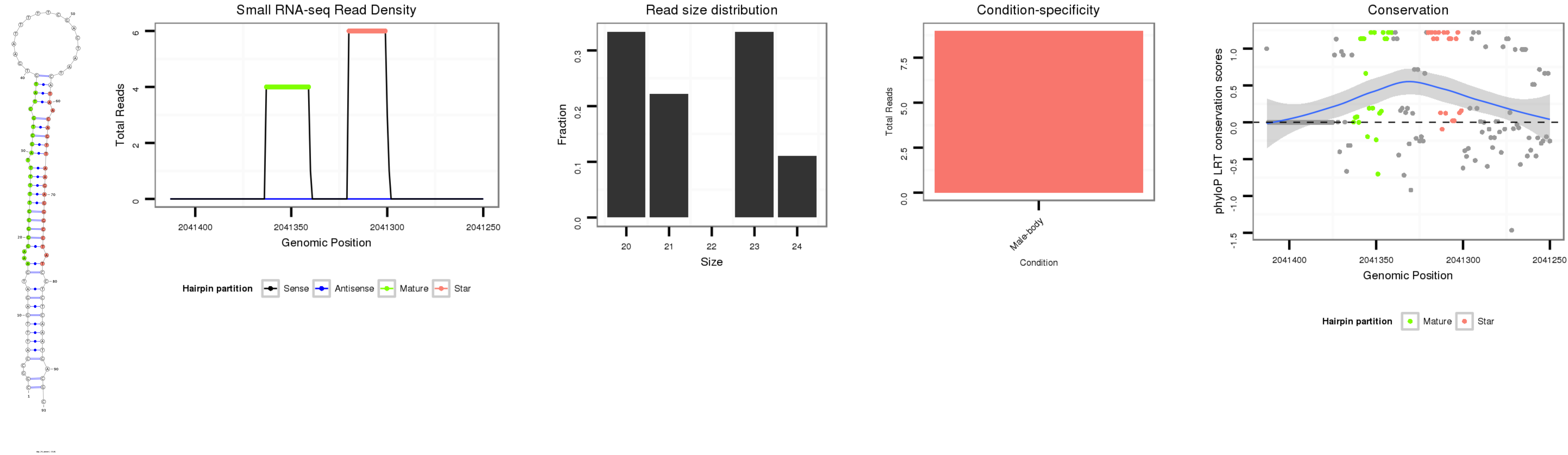


crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	1
rescue.confident	0
rescue.candidate	1

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	4
rescue.candidate	1

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

															V109	M041
ATAAGGCACCTTGTCCAAGTGTGTCATCGACCATCGGCCATTGAGATGAAAGGGCCTTTTACGCTGCTATGTGAATTTTCGACTAATCATTAACAGTTAAGAGGGCCTATCCTCTCAAATGACGCACGGGCAACAGCATTCGTGGCGGGGAATCTAGTGA										Read #		Hit	Total		male	female
*****((.((((((.(((.(((((((.(((.(((.(((.....)))))))))))))))))))).))))))))).))*****										size	Mismatch	Count	Norm	Total	body	body
.....AAAGGGCCTTTTACGCTGCTAT.....										23	0	1	3.00	3	3	0
.....TAACAGTTAAGAGGGCCTAT.....										20	0	1	3.00	3	3	0
.....TAACAGTTAAGAGGGCCTATC.....										21	0	1	2.00	2	2	0
.....TAACAGTTAAGAGGGCCTATCC.....										22	0	1	1.00	1	1	0
.....AAAGGGCCTTTTACGCTGCTATG.....										24	0	1	1.00	1	1	0

Anti-sense strand reads

[illegible]

Show Alignment With Reads

Re-alignment of all predicted orthologs

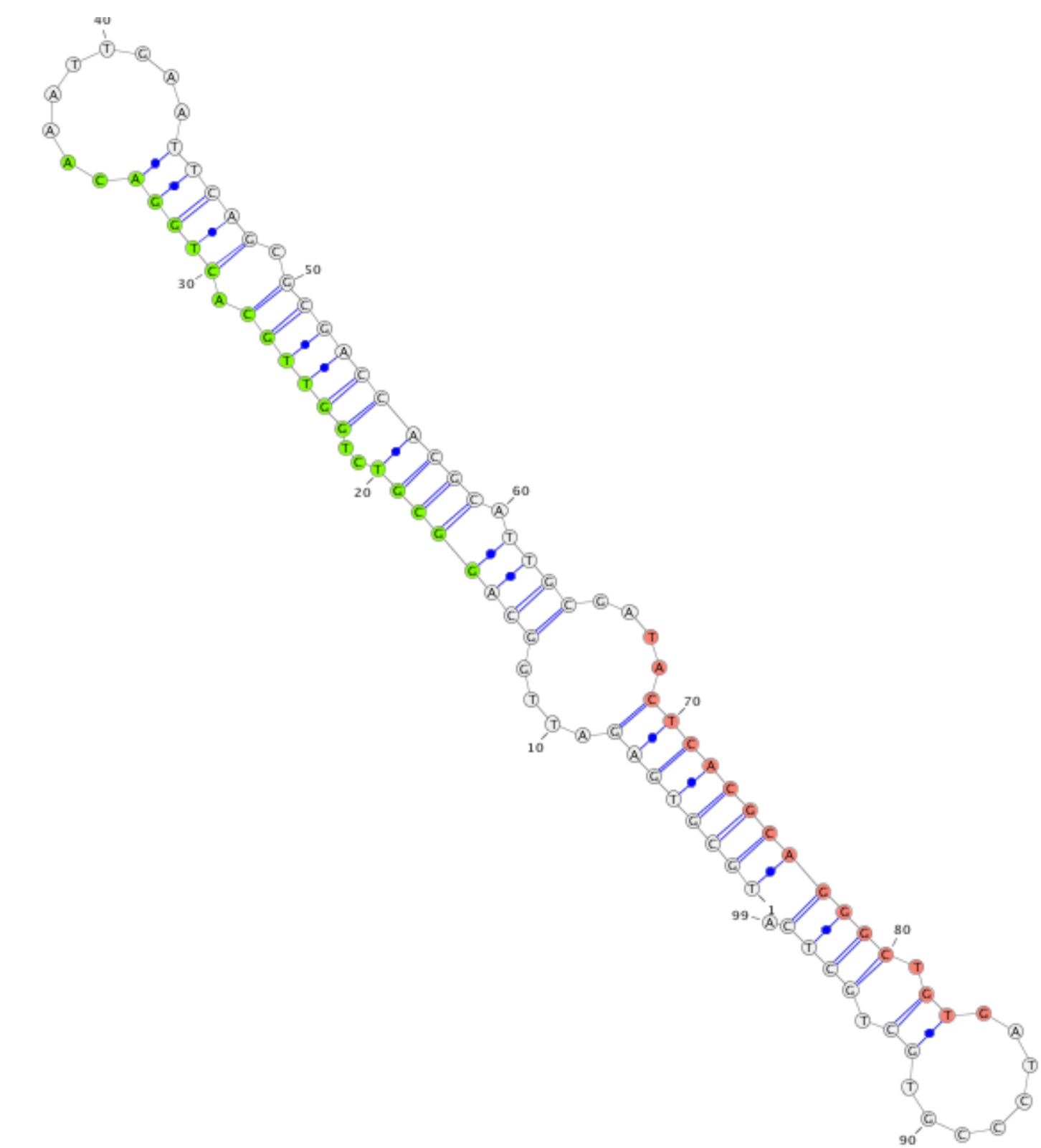
Species	Coordinate	ID	Alignment
droGri2	scaffold1_15081:2041250-2041413	dgr_24	ATAAGGCACCTTGCCAAGGTGTATCATCGACCATCGGCCATTGAGATCAAAAGGGCCTTTT ⁺ TAGCTGCTATGTGAATTTTTCGACTAATC-----ATAACAGTTA-AGAGGGCCTATCCTCTCAAATGACGCACGGGCAACAGCATTCTGGCG-----G-----GGAATCTGAGTA-----
droVir3	scaffold_13042:903134-903276		-----CATATGAAAGCCAAAGGCCCTTT ⁺ CGA ⁺ CTGCTATGTCTATTTTTGACTAGTATAGATAACAGTCTCAAGAGGGCCTTT ⁺ TGGCTCAAT-----GCAAAACA ⁺ SCCAATACGATAACGATAACGATAACAATAACGATAACTTAAAGCA-----
droMoJ3	scaffold_6328:2897735-2897868	dmo_91	A-----A-----GA- ⁺ GGCCCTTTT ⁺ GAT ⁺ TGCTATGTGATTCCTCGTATTTGGC ⁺ ATAGATAACAGTCTCAAGAGGGCCTTCGGGTTCATATACCTGTGCCATCTCTGCG-----CTCACAATC-----GGCAATATCGAT-----TTGSCG ⁺ STCATCGATA
droAna3	scaffold_13417:2460998-2461102		-----CAGTCTATGCAG- ⁺ GGC-CTA ⁺ CGA ⁺ CTGCTATGTCTACTTCAGG-----ATGAATAACAGTCAAGAGGCCCTTT ⁺ CACACCAAGTGAATCTCGGCCCTTGCAGACGTCTCG-----CTC-----
droBip1	scf7180000395874:33012-33104		A-----G- ⁺ GGG-CTA ⁺ CTA ⁺ TGCTATGTCTACCTCAGG-----ATGAATAACAGTCAAGAGGCCCTTT ⁺ CACACCAAGTGAATCTCGGCCCTTGCAGACGTCTCG-----CTC-----

Generated: 09/08/2015 at 07:35 PM **PASS/FAIL**

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	3
rescue.candidate	2

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



dgr_465_annot [-42.4]

Show Alternate Folds

Flybase annotation

CDS [Dgrn\GH23323-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

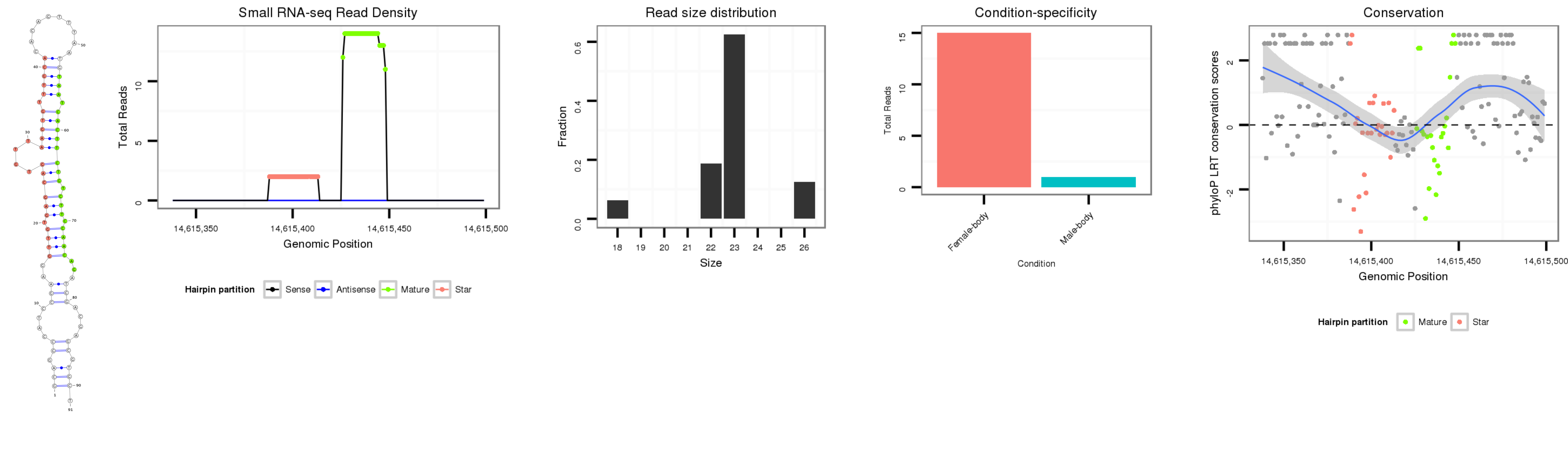
Species	Coordinate	ID	Alignment
droFrl2	scaffold15121:203616-203804	dgr_465	GAGGCGGAGGCGAAGCCTTTTGCCACGCGACAAGCGTGGCGCGCGATGAGGATCTGCGTGAGATTGGCAAGCGCTGGTGGCACTGGACAATTGAATTCAGCGCGACACGCATTGCGAAGCTCAGCGAGGGCTGTGATCCCGTGCTGCTCATCCAGCAGACGCTCCGGTCGAGGAGTTCCTCAAGTT
droVir1	scaffold13049:22492155-22493240	dvl_118	GAGGCGGAGGCGCAAGCGCTTTGCCACGCGCAAGGTGGCGCGCGCAAGATCTGCGTGAGATTGGCAAGCGCTGGTGGCACTGGACAATTGAATTCAGCGCGACACGCATTGCGAAGCTCAGCGAGGGCTGTGATCCCGTGCTGCTCATCCAGCAGACGCTCCGGTCGAGGAGTTCCTCAAGTT
droMo3	scaffold6680:17099715-17098900	dmo_114	GAGCGAGAGGCGCAAGCGCTTTGCCACGCGCGAGCTGGCGCGCGCGATCTGCGTGAGATTGGCAAGCGCTGGTGGCACTGGACAATTGAATTCAGCGCGACACGCATTGCGAAGCTCAGCGAGGGCTGTGATCCCGTGCTGCTCATCCAGCAGACGCTCCGGTCGAGGAGTTCCTCAAGTT
droH12	scf2110000000451:5276753-5276935	dwl_5417	GAGCGAGAGGCGCAAGCGCTTTGCCACGCGCGAGCTGGCGCGCGCGATCTGCGTGAGATTGGCAAGCGCTGGTGGCACTGGACAATTGAATTCAGCGCGACACGCATTGCGAAGCTCAGCGAGGGCTGTGATCCCGTGCTGCTCATCCAGCAGACGCTCCGGTCGAGGAGTTCCTCAAGTT
dp5	XR_group6:4377269-4377451	dps_3829	GAGGCGGAGGCGCAAGCGCTTTGCCACGCGCGAGCTGGCGCGCGCGATCTGCGTGAGATTGGCAAGCGCTGGTGGCACTGGACAATTGAATTCAGCGCGACACGCATTGCGAAGCTCAGCGAGGGCTGTGATCCCGTGCTGCTCATCCAGCAGACGCTCCGGTCGAGGAGTTCCTCAAGTT
droAna2	scaffold932666540:2666632	dne_2483	GAGGCGGAGGCGCAAGCGCTTTGCCACGCGCGAGCTGGCGCGCGCGATCTGCGTGAGATTGGCAAGCGCTGGTGGCACTGGACAATTGAATTCAGCGCGACACGCATTGCGAAGCTCAGCGAGGGCTGTGATCCCGTGCTGCTCATCCAGCAGACGCTCCGGTCGAGGAGTTCCTCAAGTT
droPns1	scaffold13337:4137398-4137580	dan_4043	GAGGCGGAGGCGCAAGCGCTTTGCCACGCGCGAGCTGGCGCGCGCGATCTGCGTGAGATTGGCAAGCGCTGGTGGCACTGGACAATTGAATTCAGCGCGACACGCATTGCGAAGCTCAGCGAGGGCTGTGATCCCGTGCTGCTCATCCAGCAGACGCTCCGGTCGAGGAGTTCCTCAAGTT
droBiPl	scf7180000395450:265900-266085		GAGGCGGAGGCGCAAGCGCTTTGCCACGCGCGAGCTGGCGCGCGCGATCTGCGTGAGATTGGCAAGCGCTGGTGGCACTGGACAATTGAATTCAGCGCGACACGCATTGCGAAGCTCAGCGAGGGCTGTGATCCCGTGCTGCTCATCCAGCAGACGCTCCGGTCGAGGAGTTCCTCAAGTT
droKiK1	scf7180000302272:666720-666902		GAGGCGGAGGCGCAAGCGCTTTGCCACGCGCGAGCTGGCGCGCGCGATCTGCGTGAGATTGGCAAGCGCTGGTGGCACTGGACAATTGAATTCAGCGCGACACGCATTGCGAAGCTCAGCGAGGGCTGTGATCCCGTGCTGCTCATCCAGCAGACGCTCCGGTCGAGGAGTTCCTCAAGTT
droFiCl	scf7180000454048:724237-724419		GAGGCGGAGGCGCAAGCGCTTTGCCACGCGCGAGCTGGCGCGCGCGATCTGCGTGAGATTGGCAAGCGCTGGTGGCACTGGACAATTGAATTCAGCGCGACACGCATTGCGAAGCTCAGCGAGGGCTGTGATCCCGTGCTGCTCATCCAGCAGACGCTCCGGTCGAGGAGTTCCTCAAGTT
droEiEl	scf7180000491255:1412092-1412274		GAGGCGGAGGCGCAAGCGCTTTGCCACGCGCGAGCTGGCGCGCGCGATCTGCGTGAGATTGGCAAGCGCTGGTGGCACTGGACAATTGAATTCAGCGCGACACGCATTGCGAAGCTCAGCGAGGGCTGTGATCCCGTGCTGCTCATCCAGCAGACGCTCCGGTCGAGGAGTTCCTCAAGTT
droRhoI	scf7180000679477:970-1151		GAGGCGGAGGCGCAAGCGCTTTGCCACGCGCGAGCTGGCGCGCGCGATCTGCGTGAGATTGGCAAGCGCTGGTGGCACTGGACAATTGAATTCAGCGCGACACGCATTGCGAAGCTCAGCGAGGGCTGTGATCCCGTGCTGCTCATCCAGCAGACGCTCCGGTCGAGGAGTTCCTCAAGTT
droBaI1	scf7180000302193:7233859-725404		GAGGCGGAGGCGCAAGCGCTTTGCCACGCGCGAGCTGGCGCGCGCGATCTGCGTGAGATTGGCAAGCGCTGGTGGCACTGGACAATTGAATTCAGCGCGACACGCATTGCGAAGCTCAGCGAGGGCTGTGATCCCGTGCTGCTCATCCAGCAGACGCTCCGGTCGAGGAGTTCCTCAAGTT
droTaK1	scf7180000415706:66150-66332		GAGCTCGAGGCGCAAGCGCTTTGCCACGCGCGAGCTGGCGCGCGCGATCTGCGTGAGATTGGCAAGCGCTGGTGGCACTGGACAATTGAATTCAGCGCGACACGCATTGCGAAGCTCAGCGAGGGCTGTGATCCCGTGCTGCTCATCCAGCAGACGCTCCGGTCGAGGAGTTCCTCAAGTT
droEugI	scf7180000409711:6102168-6101450		GAGGCGGAGGCGCAAGCGCTTTGCCACGCGCGAGCTGGCGCGCGCGATCTGCGTGAGATTGGCAAGCGCTGGTGGCACTGGACAATTGAATTCAGCGCGACACGCATTGCGAAGCTCAGCGAGGGCTGTGATCCCGTGCTGCTCATCCAGCAGACGCTCCGGTCGAGGAGTTCCTCAAGTT
dm3	chr31:13013579-13013761	dme_245	GAGGCGGAGGCGCAAGCGCTTTGCCACGCGCGAGCTGGCGCGCGCGATCTGCGTGAGATTGGCAAGCGCTGGTGGCACTGGACAATTGAATTCAGCGCGACACGCATTGCGAAGCTCAGCGAGGGCTGTGATCCCGTGCTGCTCATCCAGCAGACGCTCCGGTCGAGGAGTTCCTCAAGTT
droSim2	s1:12704028-12704210	dhl_32458	GAGGCGGAGGCGCAAGCGCTTTGCCACGCGCGAGCTGGCGCGCGCGATCTGCGTGAGATTGGCAAGCGCTGGTGGCACTGGACAATTGAATTCAGCGCGACACGCATTGCGAAGCTCAGCGAGGGCTGTGATCCCGTGCTGCTCATCCAGCAGACGCTCCGGTCGAGGAGTTCCTCAAGTT
droSec1	scaffold0_0:5185164-5185346	dse_1846	GAGGCGGAGGCGCAAGCGCTTTGCCACGCGCGAGCTGGCGCGCGCGATCTGCGTGAGATTGGCAAGCGCTGGTGGCACTGGACAATTGAATTCAGCGCGACACGCATTGCGAAGCTCAGCGAGGGCTGTGATCCCGTGCTGCTCATCCAGCAGACGCTCCGGTCGAGGAGTTCCTCAAGTT
droYaK3	s1:13092482-13092664	dya_1798	GAGGCGGAGGCGCAAGCGCTTTGCCACGCGCGAGCTGGCGCGCGCGATCTGCGTGAGATTGGCAAGCGCTGGTGGCACTGGACAATTGAATTCAGCGCGACACGCATTGCGAAGCTCAGCGAGGGCTGTGATCCCGTGCTGCTCATCCAGCAGACGCTCCGGTCGAGGAGTTCCTCAAGTT
droEre2	scaffold4784:13021112-13021294	der_1523	GAGGCGGAGGCGCAAGCGCTTTGCCACGCGCGAGCTGGCGCGCGCGATCTGCGTGAGATTGGCAAGCGCTGGTGGCACTGGACAATTGAATTCAGCGCGACACGCATTGCGAAGCTCAGCGAGGGCTGTGATCCCGTGCTGCTCATCCAGCAGACGCTCCGGTCGAGGAGTTCCTCAAGTT

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	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	0
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	0
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	2
rescue.candidate	10

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Show Alternate Folds

Flybase annotation

intron [Dgrn\GH16685-in]; CDS [Dgrn\GH16685-cds]; CDS [Dgrn\GH16685-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

	Read size	# Mismatch	Hit Count	Total Count	Norm	Total	M041 female body	V109 male body
TCCCGTGCAACGCGCTCCATCCAGTCGGCGCGGCAGGCCATCCGAAGGTGTGAGCAGTGTAAAGTTTGCACACAGTTTAATGTAATCACTTCTGCTTCCAACAGATCGACGAGCGTGCTCAAAGAACCAGATGAAGTGCCGACGGCTGCTCTCTC*****(((((... ((((((((((((... (((((((.....)))))))))....)))))).)....))..)).....)	23	0	1	10.00	10	1	0	
.....TAATCACTTCTGCTTCCAACAG.....	22	0	1	2.00	2	2	0	
.....TAATCACTTCTGCTTCCAACA.....	26	0	1	2.00	2	1	1	
.....GTGTGAGCAGTGTAAAGTTTGC.....	22	0	1	1.00	1	1	0	
.....AATCACTTCTGCTTCCAACAG.....	22	0	1	1.00	1	1	0	
.....AATCACTTCTGCTTCCA.....	18	0	1	1.00	1	1	0	

Anti-sense strand reads

No data available in table

Show Alignment With Reads

Re-alignment of all predicted orthologs

[illegible]

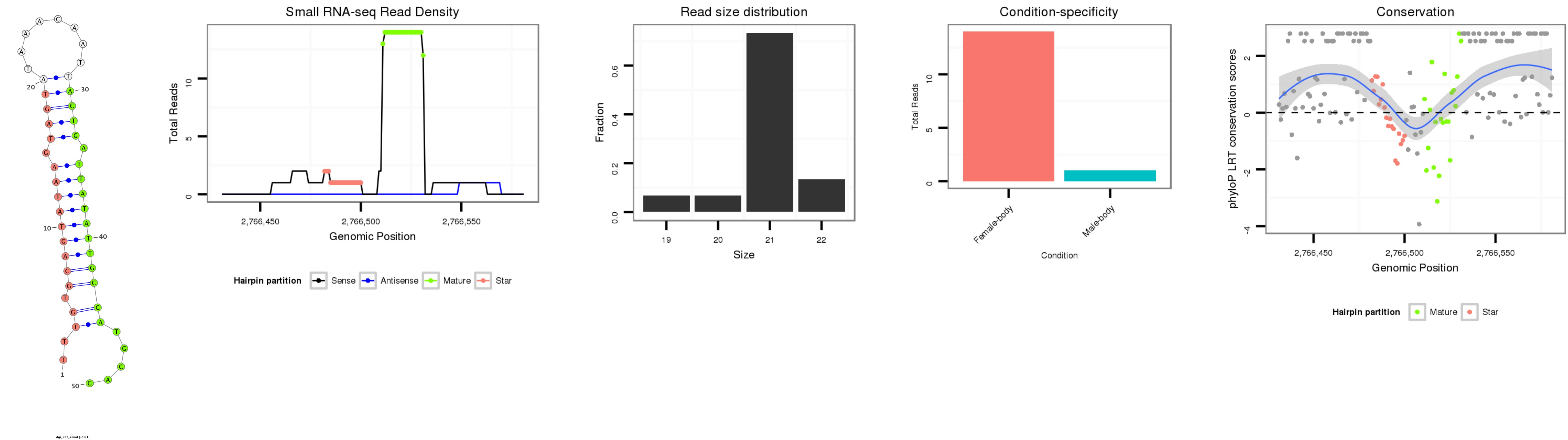
Generated: 09/08/2015 at 07:34 PM

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

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dgr_282	scaffold_15110:2766481-2766531 +	candidate-rescued	Mirtron	intron	[View on UCSC Genome Browser [Cornell Mirror]]

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

Predicted structure



Show Alternate Folds

Flybase annotation

intron [DgriGH15903-in]; CDS [DgriGH15903-cds]; CDS [DgriGH15903-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

	Read size	# Mismatch	Hit Count	Total Norm	Total	M041 female body	V109 male body
AGCAGCTGATTGAGCTGCGCAGCAACGCGGCTACAGCTACGAGGATGAGGTTTGTGCAGTATAAGTAGCTATAAACAAATTACTGATTATATTGCCATGCAGATCACCTGTTCCGAGCAGTGCCTGCCGGATTATCTCAACAAGCTAAAGTC	21	0	1	11.00	11	11	0
*****.((.(((((((.(((((.)))))))).))))))*****	22	0	1	2.00	2	2	0
.....ACTGATTATATTGCCATGCAG.....	19	0	1	1.00	1	0	1
.....TTACTGATTATATTGCCATGCA.....	19	0	1	1.00	1	1	0
.....TTTGTGCAGTATAAGTAGT.....	27	0	1	1.00	1	1	0
.....AGCTACGAGGATGAGGTTT.....	21	1	1	1.00	1	0	1
.....CTGATTATATTGCCATGCAG.....	20	0	1	1.00	1	1	0
.....ACGCGGCTACAGCTACGA.....	18	0	1	1.00	1	1	0

Anti-sense strand reads

	Read size	# Mismatch	Hit Count	Total Norm	Total	V109 male body
TCGTCGACTAACTCGACGCGTCGTTTTCGCCGATGTTCGATGCTCCTACTCCAAACAGCTCATATTCATCATATTTTGTTAAAGACTAAATAACGGTACGTCAGTGGACAAGCCTCGTCACGACGGCCTAATAGAGTTGTTTCGATTTTCAG	21	0	1	1.00	1	1
*****.((.(((((((.(((((.)))))))).))))))*****						

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droGri2	scaffold_15110:2766431-2766581 +	dgr_282	AGCAGCTGATTGAGCTGCGCAGCAACGCGGCTACAGCTACGAGGATGAGGTTTGTGCAGTA--TAAGTAGTATA--A---ACA-----TTTACTGA-----TTAT--ATTGCCATGC-AGATCACCTGTTCCGAGCAGTGCCTGCCGGATTATCTCAACAAGCTAAAGTC
droVir3	scaffold_13049:1678559-1678714 +		AGGCTGCTAANAAGCTGCGCAGCAACGCTACAGCTACGAGGATGAGGTTTGTGCAGTA--TAAGTAGTATA--A---ACA-----TTTACTGA-----TTAT--ATTGCCATGC-AGATCACCTGTTCCGAGCAGTGCCTGCCGGATTATCTCAACAAGCTAAAGTC
droMoj3	scaffold_6654:2140864-2141031 -		AGCTGCTAANAAGCTGCGCAGCAACGCTACAGCTACGAGGATGAGGTTTGTGCAGTA--TAAGTAGTATA--A---ACA-----TTTACTGA-----TTAT--ATTGCCATGC-AGATCACCTGTTCCGAGCAGTGCCTGCCGGATTATCTCAACAAGCTAAAGTC
droW12	scf2_1100000004511:6212236-6212411 +		CTCTGCTAANAAGCTGCGCAGCAACGCTACAGCTACGAGGATGAGGTTTGTGCAGTA--TAAGTAGTATA--A---ACA-----TTTACTGA-----TTAT--ATTGCCATGC-AGATCACCTGTTCCGAGCAGTGCCTGCCGGATTATCTCAACAAGCTAAAGTC
dp5	XR_group6:9098438-9098590 +		CGATTCTAGGGGAGCTGCGCGGCAACGCTACAGCTACGAGGATGAGGTTTGTGCAGTA--TAAGTAGTATA--A---ACA-----TTTACTGA-----TTAT--ATTGCCATGC-AGATCACCTGTTCCGAGCAGTGCCTGCCGGATTATCTCAACAAGCTAAAGTC
droPer2	scaffold_3345:4208-4360 -		CGATTCTAGGGGAGCTGCGCGGCAACGCTACAGCTACGAGGATGAGGTTTGTGCAGTA--TAAGTAGTATA--A---ACA-----TTTACTGA-----TTAT--ATTGCCATGC-AGATCACCTGTTCCGAGCAGTGCCTGCCGGATTATCTCAACAAGCTAAAGTC
droAna3	scaffold_13337:15564458-15564609 +		AGATTCTTTCGAGCTGCGCGGCAACGCTACAGCTACGAGGATGAGGTTTGTGCAGTA--TAAGTAGTATA--A---ACA-----TTTACTGA-----TTAT--ATTGCCATGC-AGATCACCTGTTCCGAGCAGTGCCTGCCGGATTATCTCAACAAGCTAAAGTC
droBip1	scf7180000395832:141660-141814 +		AGATTCTTTCGAGCTGCGCGGCAACGCTACAGCTACGAGGATGAGGTTTGTGCAGTA--TAAGTAGTATA--A---ACA-----TTTACTGA-----TTAT--ATTGCCATGC-AGATCACCTGTTCCGAGCAGTGCCTGCCGGATTATCTCAACAAGCTAAAGTC
droKik1	scf7180000302351:784267-784431 -		AGGTTCTAACACAACTGAGGGCAACGCTACAGCTACGAGGATGAGGTTTGTGCAGTA--TAAGTAGTATA--A---ACA-----TTTACTGA-----TTAT--ATTGCCATGC-AGATCACCTGTTCCGAGCAGTGCCTGCCGGATTATCTCAACAAGCTAAAGTC
droFic1	scf7180000453841:377811-377970 -		ATACTCTACCCAACTGAGGGCAACGCTACAGCTACGAGGATGAGGTTTGTGCAGTA--TAAGTAGTATA--A---ACA-----TTTACTGA-----TTAT--ATTGCCATGC-AGATCACCTGTTCCGAGCAGTGCCTGCCGGATTATCTCAACAAGCTAAAGTC
droEle1	scf7180000490564:1516903-1517062 +		ACACTCTTACCGAACTGAGGGCAACGCTACAGCTACGAGGATGAGGTTTGTGCAGTA--TAAGTAGTATA--A---ACA-----TTTACTGA-----TTAT--ATTGCCATGC-AGATCACCTGTTCCGAGCAGTGCCTGCCGGATTATCTCAACAAGCTAAAGTC
droRho1	scf7180000780091:312677-312838 +		ATACTCTTACCGAACTGAGGGCAACGCTACAGCTACGAGGATGAGGTTTGTGCAGTA--TAAGTAGTATA--A---ACA-----TTTACTGA-----TTAT--ATTGCCATGC-AGATCACCTGTTCCGAGCAGTGCCTGCCGGATTATCTCAACAAGCTAAAGTC
droBial	scf7180000302428:7070184-7070342 -		ATACCCTTACCCAACTGAGGGCAACGCTACAGCTACGAGGATGAGGTTTGTGCAGTA--TAAGTAGTATA--A---ACA-----TTTACTGA-----TTAT--ATTGCCATGC-AGATCACCTGTTCCGAGCAGTGCCTGCCGGATTATCTCAACAAGCTAAAGTC
droTak1	scf7180000416006:70980-71139 +		GTACTCTTACCGAACTGAGGGCAACGCTACAGCTACGAGGATGAGGTTTGTGCAGTA--TAAGTAGTATA--A---ACA-----TTTACTGA-----TTAT--ATTGCCATGC-AGATCACCTGTTCCGAGCAGTGCCTGCCGGATTATCTCAACAAGCTAAAGTC
droEug1	scf7180000409711:2528336-2528498 +		ATACTCTTACCGAACTGAGGGCAACGCTACAGCTACGAGGATGAGGTTTGTGCAGTA--TAAGTAGTATA--A---ACA-----TTTACTGA-----TTAT--ATTGCCATGC-AGATCACCTGTTCCGAGCAGTGCCTGCCGGATTATCTCAACAAGCTAAAGTC
dm3	chr3L:10656778-10656939 +		ATACCCTTACCCAACTGAGGGCAACGCTACAGCTACGAGGATGAGGTTTGTGCAGTA--TAAGTAGTATA--A---ACA-----TTTACTGA-----TTAT--ATTGCCATGC-AGATCACCTGTTCCGAGCAGTGCCTGCCGGATTATCTCAACAAGCTAAAGTC
droSim2	31:10403795-10403956 +	dai_30746	ATACCCTTACCCAACTGAGGGCAACGCTACAGCTACGAGGATGAGGTTTGTGCAGTA--TAAGTAGTATA--A---ACA-----TTTACTGA-----TTAT--ATTGCCATGC-AGATCACCTGTTCCGAGCAGTGCCTGCCGGATTATCTCAACAAGCTAAAGTC
droSec2	scaffold_0:2877921-2878082 +		ATACCCTTACCCAACTGAGGGCAACGCTACAGCTACGAGGATGAGGTTTGTGCAGTA--TAAGTAGTATA--A---ACA-----TTTACTGA-----TTAT--ATTGCCATGC-AGATCACCTGTTCCGAGCAGTGCCTGCCGGATTATCTCAACAAGCTAAAGTC
droYak3	3L:10655440-10655601 +		ATACCCTTACCCAACTGAGGGCAACGCTACAGCTACGAGGATGAGGTTTGTGCAGTA--TAAGTAGTATA--A---ACA-----TTTACTGA-----TTAT--ATTGCCATGC-AGATCACCTGTTCCGAGCAGTGCCTGCCGGATTATCTCAACAAGCTAAAGTC
droEre2	scaffold_4784:10655138-10655299 +		ATACCCTTACCCAACTGAGGGCAACGCTACAGCTACGAGGATGAGGTTTGTGCAGTA--TAAGTAGTATA--A---ACA-----TTTACTGA-----TTAT--ATTGCCATGC-AGATCACCTGTTCCGAGCAGTGCCTGCCGGATTATCTCAACAAGCTAAAGTC

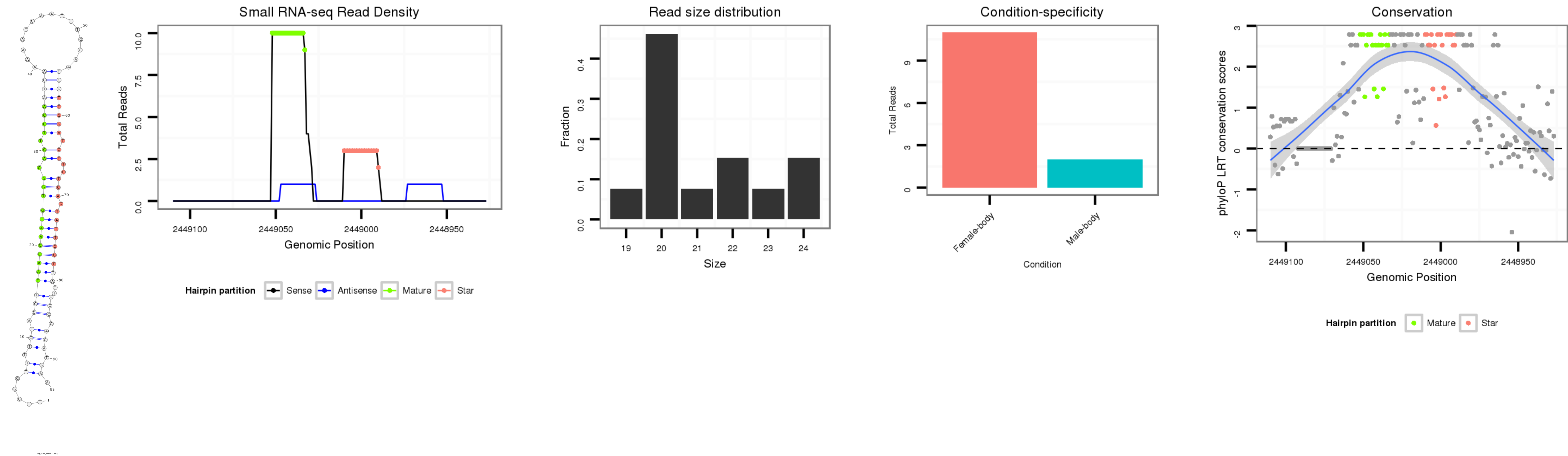
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	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.top3	1
crit.uri	1
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	2

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dgr_463	scaffold_14906:2448977-2449060 -	candidate-rescued	Canonical miRNA	intergenic	[View on UCSC Genome Browser (Cornell Mirror)]

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Show Alternate Folds

Flybase annotation

intergenic

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
droGr12	scaffold_14906:2448927-2449110 -	dgr_463	GAGATTAA-G-----CAAAGCAAAAAGGGCGGTCAGTTCGTAATAGATTGGGTTTCTAGCTTAACCAATGTGGCACTTCCTATGAAAAATCAATTTCGAATCGTTGGATGTTCTCAGTATTGGTTATTGGCCAGATGAATCCAACACAGCAATAATTAAA---ACCA-----AATAC-----AACACAAAAA---C-TGTA
droVit3	scaffold_13047:9559452-9559625 -	dvi_2463	CA-----TCCCTTTTCGACGACAAAGCGAG-----CGATTGGGTTTCTAGCTTAACCAATGTGGCACTTCCTATGAAAAATCAATTCAAAATCGTTGGATGTTCTCAGTATTGGTTATTGGCCAGAGAACCACCAACACAGCGATAAAGAAACCAAA---TAAAA---TAAACAACAAAAAG---CACTTA
droMo3	scaffold_6540:7667642-7667816 -	dmo_270	GAGCTGA-CCC--TCGACGACAAAGCGAA-----CGATTGCTTTTCTAGCTTAACCAATGTGGCACCACCTATGAAAAATCAATTCAAAATCGTTGGATGTTCTCAATATTGGTTATTGGCCAGAGAAGCCCAACACAGCGATAA-----GAAACGAAACCATCAAAATATTCGATTAA---A-----C-TGTA
droW12	scf2_1100000004902:9400242-9400366 +		-----TTCTAGCTTAATGAATGCGAACTTCCTATGCAAGATCGATTCAAAATCGTTGGATCACTCAGTATTGGTTATTGGCCAGAACATCAACAGAGTTAAAGTAAACAA---CAATTAGATTGTT-----CAATGAGTTGTT-----
dp5	2:16675577-16675703 -	dps_3828	ATGCGGGGCTCTCGCTTAACCAATGTGGCACTTCCTATGAAAAATCAATTACAAGTCGTGGAGTTCTCAGTATTGGTTATTGGCAGAGAAGCCCAACAGCGAGATAA---CAGTTACAA---AGTTACAA---TGTA
droPer2	scaffold_0:3721647-3721773 +	dpe_2482	ATGCGGGGCTCTCGCTTAACCAATGTGGCACTTCCTATGAAAAATCAATTACAAGTCGTGGAGTTCTCAGTATTGGTTATTGGCAGAGAAGCCCAACAGCGAGATAA---CAGTTACAA---AGTTACAA---TGTA
droAna3	scaffold_12911:3664275-3664396 -	dan_200	-----TTCTGSCCAACCAATGTGGCACTTCCTATGCAAAATCAATTCAAGTCGTGGATCTCTCAGTATTGGTTATTGGCAGATTGGGCCGCGACAACTGTGC-CACCCACTC---TAGTCCGT-----
droBip1	scf7180000396640:523322-523439 -		-----TCTGSCCAACCAATGTGGCACTTCCTATGCAAAATCAATTCAAGTCGTGGATCTCTCAGTATTGGTTATTGGCAGATTGGGCCCGCGCACTGTGC-TACCCAGTCT---TAGTC-----
droK1k1	scf7180000302810:681876-682022 +		GG-----GCCCTCTCGCTTAACCAATGTGGCACTTCCTATGCAAGATCAATTCAAGTCGTGGATCTCTCAGTATTGGTTATTGGCAGATTGGGCCAGCGAGCAGCAGTATAG---TTGT-TGTTCCGCTTAGTCGG-AGTAAATTTCCCCC-AAT---GT---
droFiO1	scf7180000454114:125810-125944 +		GG-----GCCCTCTCGCTTAACCAATGTGGCACTTCCTATGCAAGATCAATTCAAGCGCGTTGGATCTCTCAGTATTGGTTATTGGCAGATTGGGCCAGCGAGCGGTAT-TGG---CACTA---GCCCTAT-AGTTCGGATC---GT---
droEle1	scf7180000491194:1479877-1480024 +		GG-----GCCCTCTCGCTTAACCAATGTGGCACTTCCTATGCAAGATCAATTCAAGCGCGTTGGATCTCTCAGTATTGGTTATTGGCAGATTGGGCCAGCGAGCACTATTC-TAGC---CACTTGGATACCAATCGAAT-AGTTCGGATCAGTC---GT---
droRho1	scf7180000779322:264829-264947 -		GG-----GCCCTCTCGCTTAACCAATGTGGCACTTCCTATGCAAAATCAATTCAAGCGCGTTGGATCTCTCAGTATTGGTTATTGGCAGATAGGCCCTTAGCAGCAATATAGG---CACTG---GT-----GT---
droBia1	scf7180000302035:101939-102066 +		GG-----GCCCTCTCGCTTAACCAATGTGGCACTTCCTATGCAAAATCAATTCAAGCGCGTTGGATCTCTCTGATTGGTTATTGGCAGATTGGGCCAGCGAGCGTACCTTAGG---TAGCGAGTTCGGAT-----GT---
droTak1	scf7180000415712:510701-510838 +		GG-----GCCCTCTCGCTTAACCAATGTGGCACTTCCTATGCAAAATCAATTCAAGCGCGTTGGATCTCTCAGTATTGGTTATTGGCAGATTGGGCCAGCGAGCACTATA-TGA---GATCC-G-GGTTCCGATCAGTCCG-----GT---
droEup1	scf7180000409488:463456-463563 -		GG-----CCGGGCTCTCGCTTAACCAATGTGGCACTTCCTATGCAAAATCAATTCAAGCGCGTTGGATCTCTCAGTATTGGTTATTGGCAGATTGGGCCAGCGAGCA-----GT-----GT---
dm3	chr3R:27444091-27444228 +		GG-----GCCCTCTCGCTTAACCAATGTGGCACTTCCTATGCAAAATCAATTCAAGCGCGTTGGATCTCTCAGTATTGGTTATTGGCAGATTGGGCCCGGCAGACATAC---TAGACAGTTCGGATCAGTCCGCACTAAAC---GT---
droSim2	3r:26724064-26724207 +	dsi_3245f	GG-----GCCCTCTCGCTTAACCAATGTGGCACTTCCTATGCAAAATCAATTCAAGCGCGTTGGATCTCTCAGTATTGGTTATTGGCAGATTGGGCCCGGCAGACATAC---TAGACAGTTCGGATCAGTCCGCACTAAACCCCTCCG---GT---
droEaK3	38426800-38426801-38426802-38426803-38426804-38426805-38426806 +	dys_1747	GG-----GCCCTCTCGCTTAACCAATGTGGCACTTCCTATGCAAAATCAATTCAAGCGCGTTGGATCTCTCAGTATTGGTTATTGGCAGATTGGGCCCGGCAGACATAC---TAGACAGTTCGGATCAGTCCGCACTAAACCCCTCCG---GT---
droEre2	scaffold_4820:530473-530616 =	der_1522	GG-----GCCCTCTCGCTTAACCAATGTGGCACTTCCTATGCAAAATCAATTCAAGCGCGTTGGATCTCTCAGTATTGGTTATTGGCAGATTGGGCCCGGCAGACATAC---TAGACAGTTCGGATCAGTCCGCACTAAACCCCTCCG---GT---

Generated: 09/08/2015 at 07:36 PM

	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	7
rescue.candidate	5