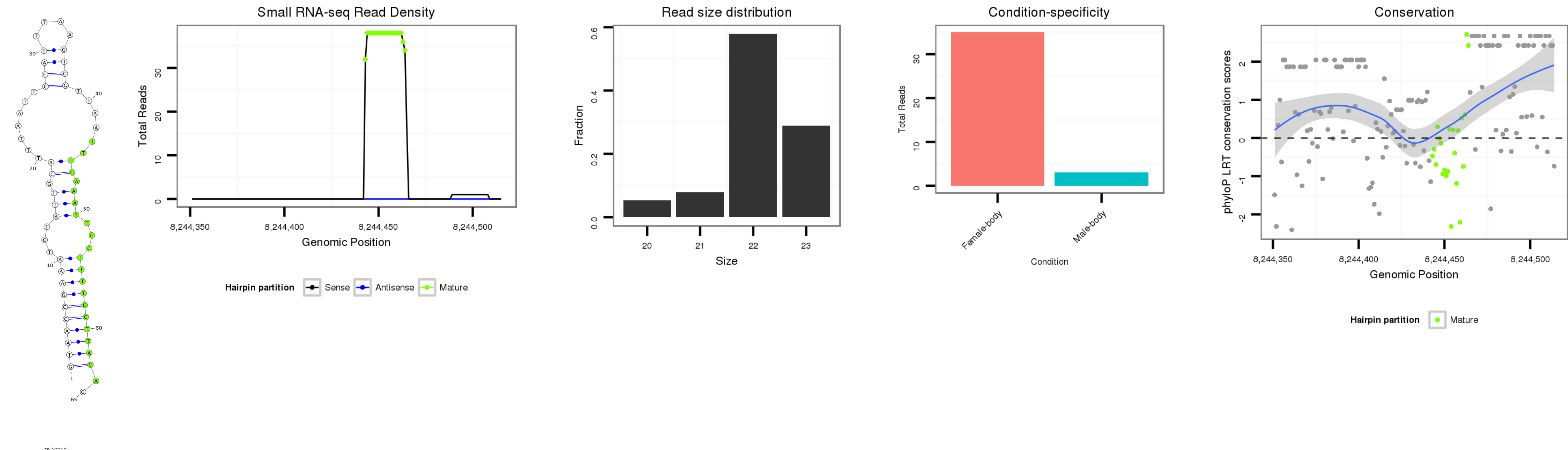


Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Show Alternate Folds

Flybase annotation

intron [Dgrn\GH21446-in]; CDS [Dgrn\GH21446-cds]; CDS [Dgrn\GH21446-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

										Read #	Hit	Total		M041	V109
										size	Mismatch	Count	Norm	female body	male body
GCCTCGAGCCTGAGACTGGCAAGGTGCTGTACGAATGGGTAAAAACATGTAAGCGAAATCTATTGCATTAAATCCATTAAAGTGGTTAAATTGAAATTCCTTTGCTTACAGCTTTTACATGCCCCACGGCTTGAGCATCGATCCCGAGGATAATGTGTGGG															
***** ((((((((((.....(((.....)))).....)).....)))).....)))).....															
.....TTTGAAATTCCTTTTGCTTACAG.....										22	0	1	17.00	17	0
.....TTTGAAATTCCTTTTGCTTACAG.....										23	0	1	11.00	11	9
.....TTTGAAATTCCTTTTGCTTACAG.....										22	0	1	5.00	5	0
.....TTTGAAATTCCTTTTGCTTAC.....										20	0	1	2.00	2	2
.....TTTGAAATTCCTTTTGCTTAC.....										21	0	1	2.00	2	1
.....TTTGAAATTCCTTTTGCTTAC.....										23	1	1	1.00	1	0
.....TTTGAAATTCCTTTTGCTTAC.....										21	0	1	1.00	1	0
.....GCATCGATCCCGAGGATAAT.....										20	0	1	1.00	1	0
.....TTTGAAATTCCTTTTGCTTAC.....										23	1	1	1.00	1	0

Anti-sense strand reads

CGGAGCTCGGAAGCTCTGACCGTTCCACGACATGCTTACCCCATTTTGTGACATTCGCTTTAGATAACGTAAATTAAAGGTAAATTCACCAATTAAACTTTAAGGAAAACGAATGTGAAAAATGTACGGGGTGCCGAACTCGTAGCTAGGGCTCCTATTACACACCC										Read #	Hit	Total		M041
***** ((((((((((.....(((.....))).....)).))).....)))))).....*****										size Mismatch	Count	Norm	Total	female body
Show Alignment With Reads														

Re-alignment of all predicted orthologs

[illegible]

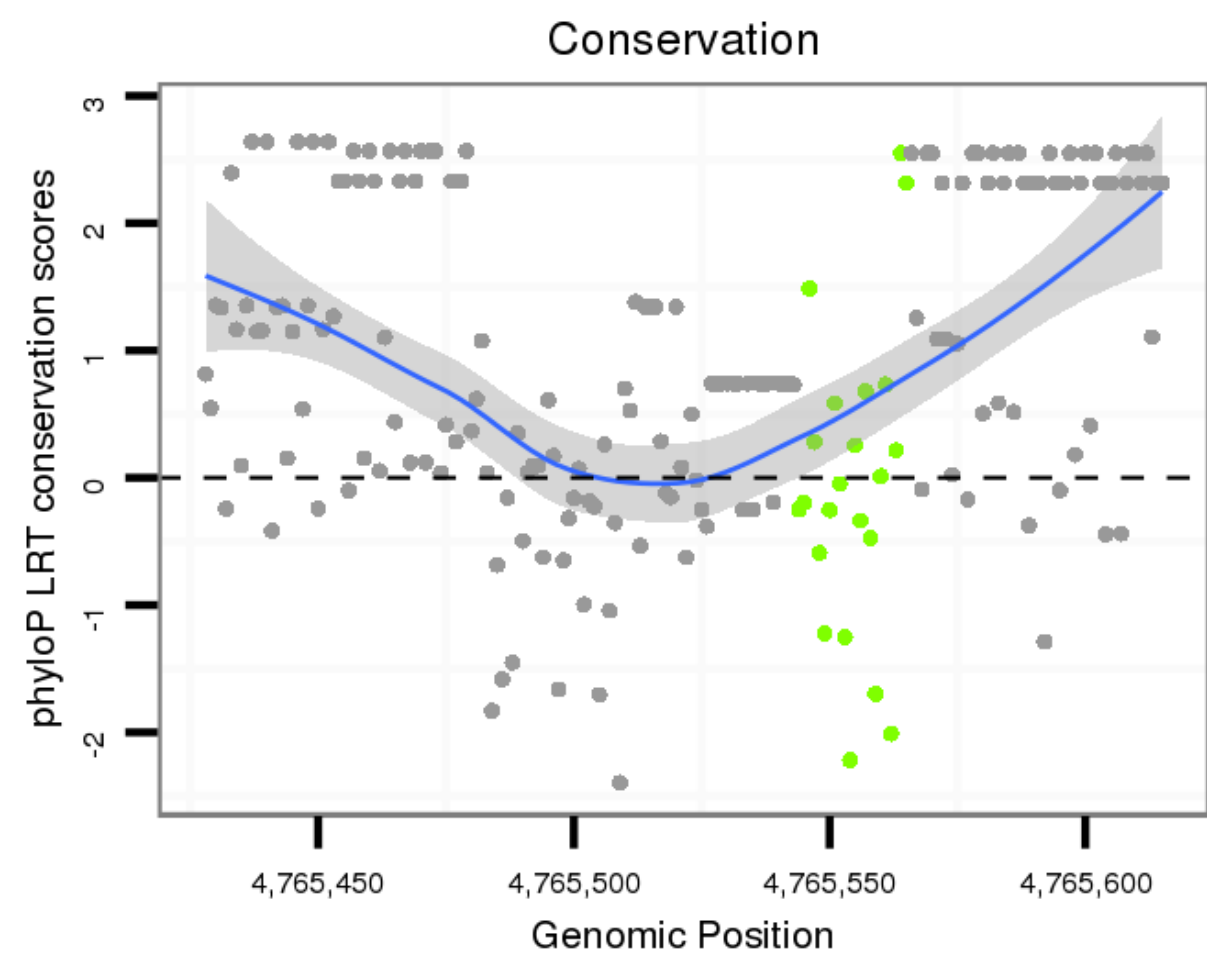
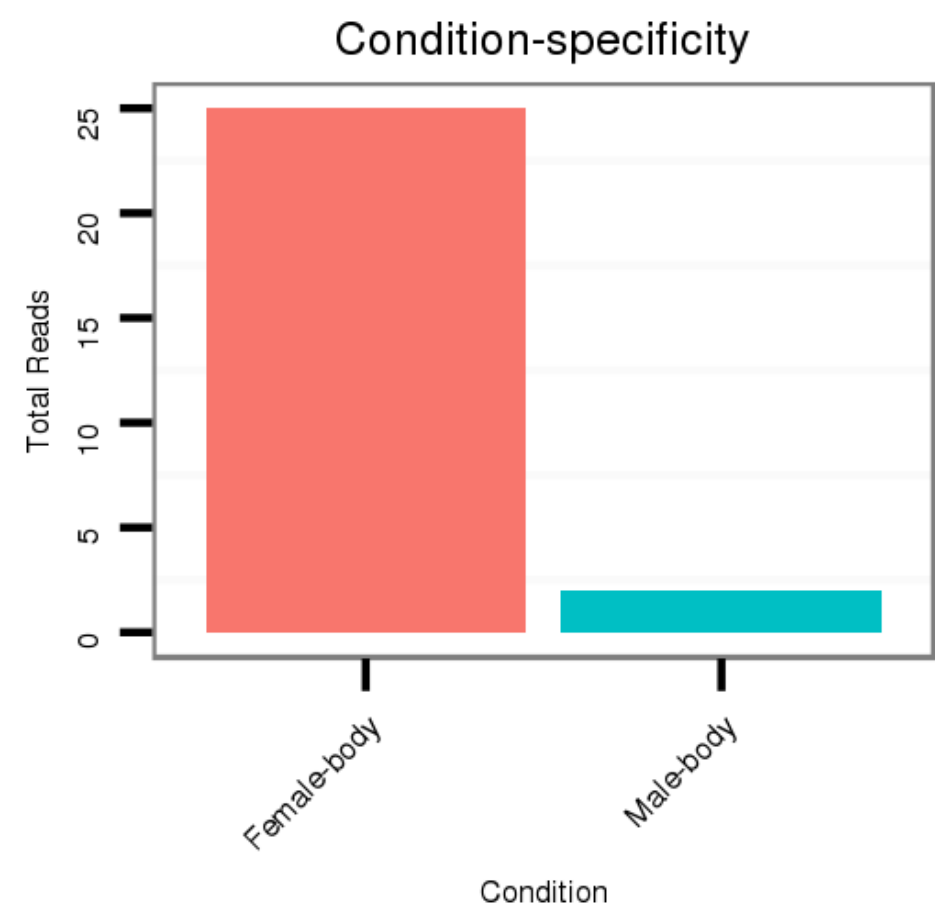
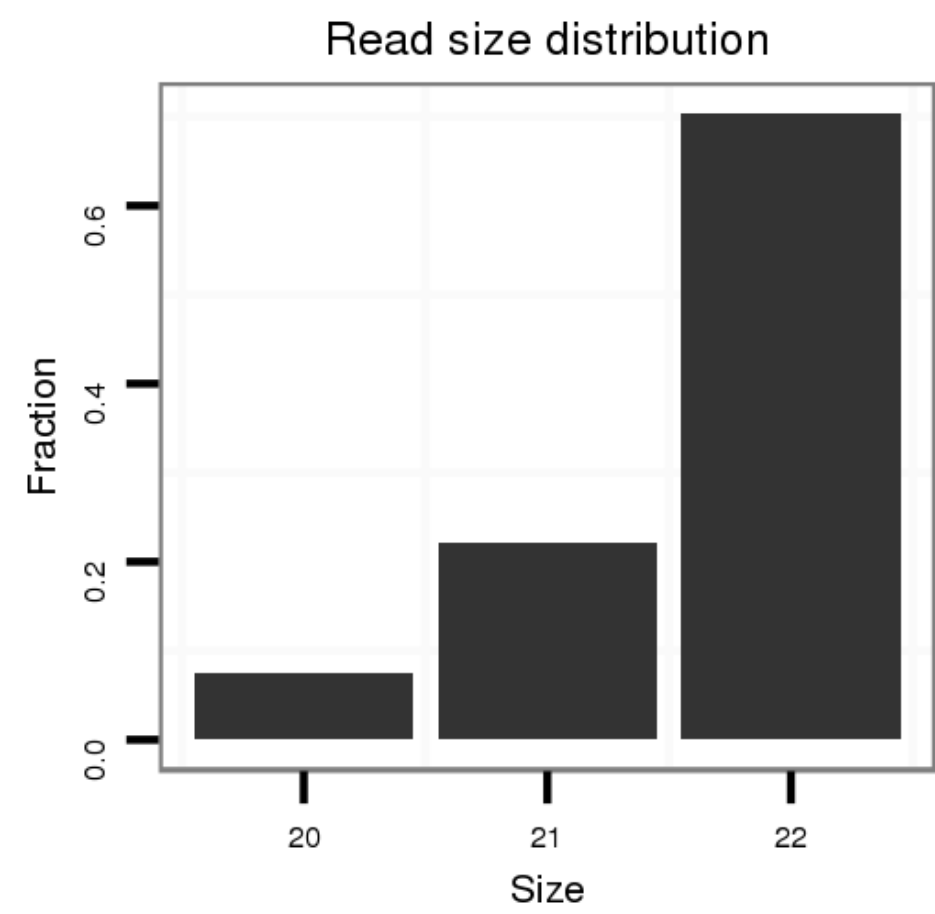
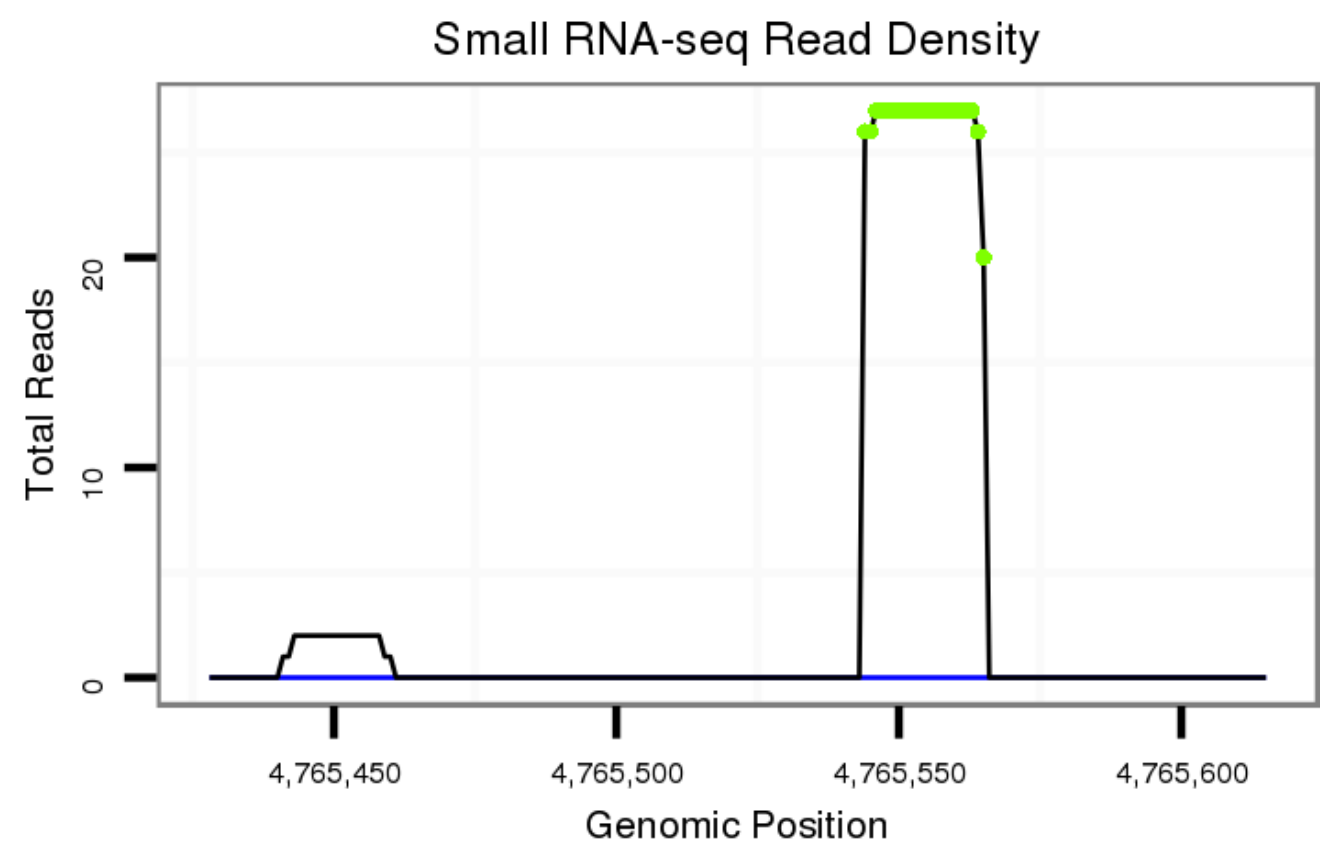
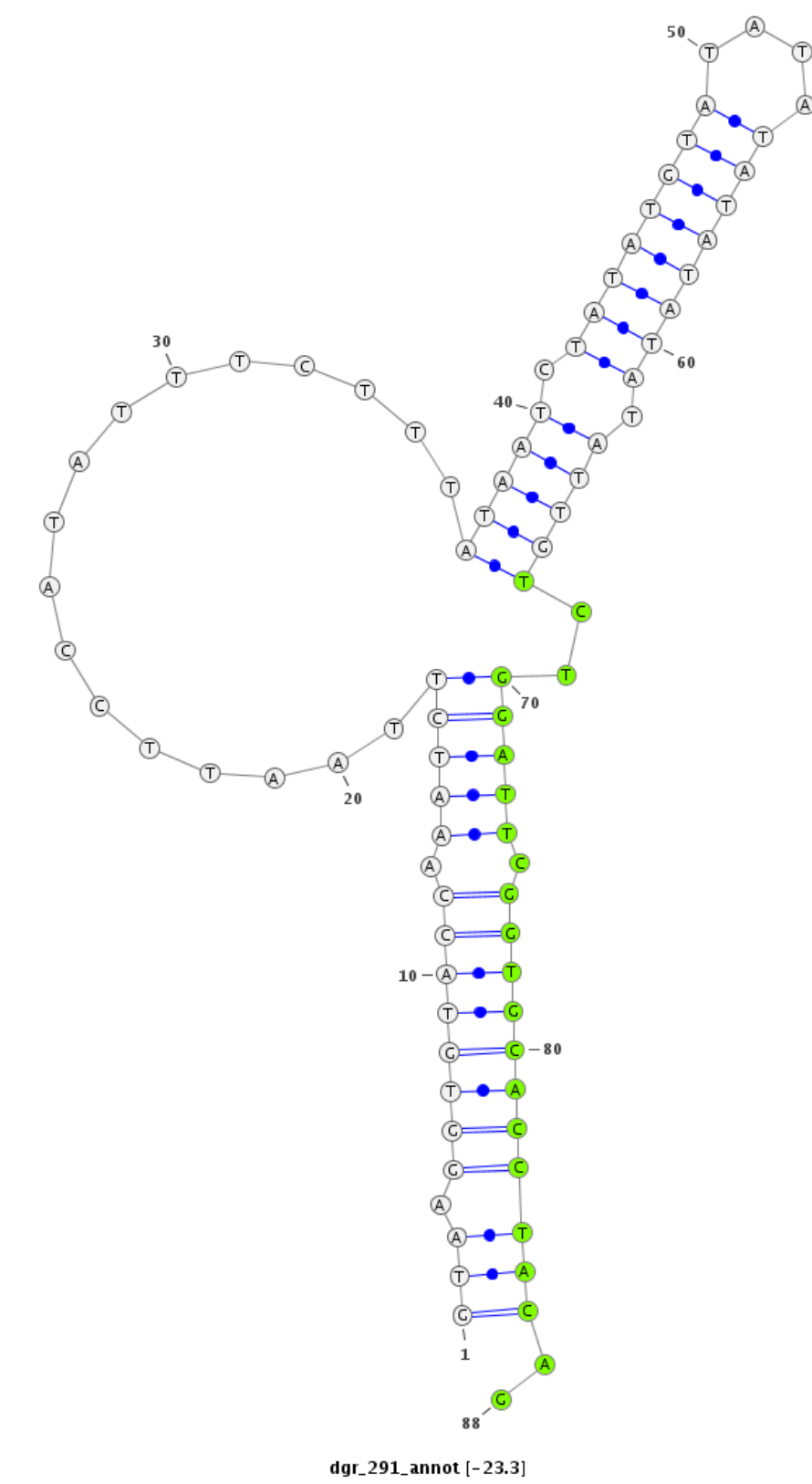
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	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	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

intron [DgrnGH16046-in]; CDS [DgrnGH16046-cds]; CDS [DgrnGH16046-cds]

Repeatable elements

Name	Class	Family	Strand
(TA)n	Simple_repeat	Simple_repeat	+

Sense Strand Reads

hide 3p reads show mid mismatch reads

						M041	V109
						female body	male body
Read #	Mismatch	Hit Count	Total Norm	Total			
AGAATGCGATTGTGTAGAGAATCATCGCTGTTTCGGTGAGACATATCGGGTAAGGTGTACCAAACTTAATCCATATTTCTTATAATCTATATGTATATATATATATATGCTGGATTTCGGTGCACCTACAGTAGTAAGGCCGCAACGATGAATCGGTTTCAGAGGATAGTGTGGATGAGCG							
*****(((.(((((((.(((.....(((((.(((((((.....))))))..))))..)))))))).*****							
.....TCTGGATTTCGGTGCACCTACAG.....	22	0	1	19.00	19	0	
.....TCTGGATTTCGGTGCACCTACAG.....	21	0	1	6.00	6	5	1
.....TCTGGATTTCGGTGCACCTACAG.....	18	0	1	1.00	1	1	0
.....TGGATTTCGGTGCACCTACAG.....	20	0	1	1.00	1	1	0
.....TGGATTTCGGTGCACCTACAG.....	18	0	1	1.00	1	1	0
.....TCTGGATTTCGGTGCACCTACAG.....	23	1	1	1.00	1	1	0
.....TCTGGATTTCGGTGCACCTACAG.....	20	0	1	1.00	1	0	1

Anti-sense strand reads

[illegible]

Show Alignment With Reads

Re-alignment of all predicted orthologs

[illegible]

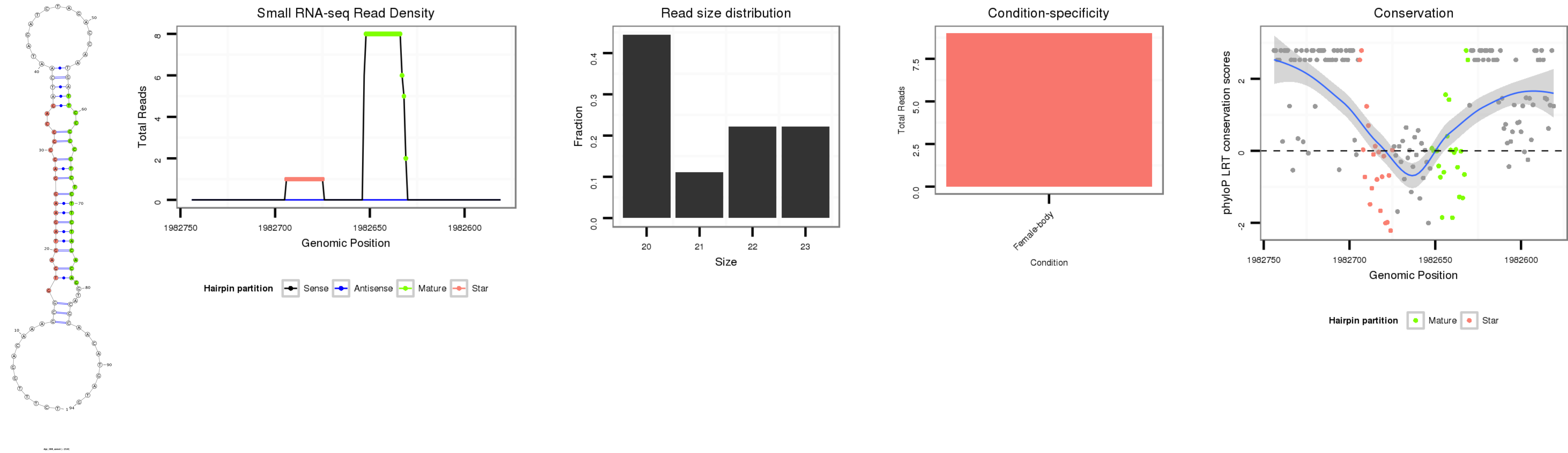
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	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dg_r_388	scaffold_15126:1982631-1982694 -	confident-exception	Canonical miRNA	intron	[View on UCSC Genome Browser (Cornell Mirror)]

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Show Alternate Folds

Flybase annotation

intron [DgriGH13340-in]; CDS [DgriGH13340-cds]; CDS [DgriGH13340-cds]

No Repeatable elements found

Sense Strand Reads

	Read size	# Mismatch	Hit Count	Total Norm	Total	M041 female body
TTGCAGAAATCGTGAGGAGCAGCATCGAATTGCGCGTCTTTGGACAAAGCGGTGAGT-AGAAGG-----A-----GCGGCAGATCAATAGAT-----CT-----AGACCA-ATG-----ATCCC--CCCTC-----TCTCTACACAGGTACGCAACATGATGCGCAAGTCTCAGCATTACACACGTACCACAAGCTG	23	1	1	3.00	3	3
*****.....(((.((.((((((((((.((.((((.....))))))..)).)).))))))..)))).....*****	20	0	1	2.00	2	2
.....ATCCCCCCTCTCTTCTACACAG.....	23	0	1	2.00	2	2
.....ATCCCCCCTCTCTTCTACACAG.....	22	0	1	2.00	2	2
.....ATCCCCCCTCTCTTCTACACAG.....	24	1	1	2.00	2	2
.....TTCCCCCCTCTCTTCTACACAG.....	21	0	1	1.00	1	1
.....TTCCCCCCTCTCTTCTACACAG.....	20	0	1	1.00	1	1
.....GTGAGTAGAAGGAGCGGCAG.....	20	0	1	1.00	1	1
.....TCCCCCCTCTCTTCTACACAG.....	22	1	1	1.00	1	1

Anti-sense strand reads

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

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droGr12	scaffold_15126:1982581-1982744 -	dg_r_388	TTGCAGAAATCGTGAGGAGCAGCATCGAATTGCGCGTCTTTGGACAAAGCGGTGAGT-AGAAGG-----A-----GCGGCAGATCAATAGAT-----CT-----AGACCA-ATG-----ATCCC--CCCTC-----TCTCTACACAGGTACGCAACATGATGCGCAAGTCTCAGCATTACACACGTACCACAA--G-----CTG-----
droVir3	scaffold_12963:15870340-15870497 +		TTGCAGAAATCGTGAGGAGCAGCATCGAATTGCGCGTCTTTGGACAAAGCGGTGAGT-GGAAC-----AGTT-AGAA-----AC--AT-----TT----TGAA--CCAACCTAA--TCTCGA-TC-----TTC-AGGTACGCAACATGATGCGCAAGTCTAGCATTACACGTACCACA-C--G-----CTG-----
droMoJ3	scaffold_6500:18874475-18874631 +		TTGCAGAAATCGTGAGGAGCAGCATCGAATTGCGCGTCTTTGGACAAAGCGGTGAGT-GGTATCGTAGATACATTAA-----TG-----AG-----CAAC--C--CTCAA--TTT-ATC-TC-----TTC-AGGTACGCAACATGATGCGCAAGTCTAGCATTACACGTACCACAA--G-----CTG-----
droW112	scf2_1100000004516:3647030-3647218 +		TTGCAGAAATCGTGAGGAGCAGCATCGAATTGCGCGTCTTTGGACAAAGCGGTGAGT-AGC-CCA-----TGAATATATATATGTATA-----CCTATAT--ATGA-TATACAATTTAA--A-----GT-----TTCT-----TGAAG-TTT-AGGTACGCAACATGATGCGCAAGTCTAGCATTACACGTACCACAA--G--AACATCTGCAACACCACAGCAA
dp5	4_group4:2969460-2969630 -		TTGCAGAAATCGTGAGGAGCAGCATCGAATTGCGCGTCTTTGGACAAAGCGGTGAGT-TC-----CTCCTGAATA-CGTTTAA-----GATTTC--ATTT-TTCACTATAATA--C-----GT-----TC-TGTTT-AGGTACGCAACATGATGCGCAAGTCTAGCATTACACGTACCACAA--ACCGAAAAATG-----
droPer2	scaffold_10:1984484-1984654 -		TTGCAGAAATCGTGAGGAGCAGCATCGAATTGCGCGTCTTTGGACAAAGCGGTGAGT-TC-----CTCCTGAATA-CGTTTAA-----GATTTC--ATTT-TTCACTATAATA--C-----GT-----TC-TGTTT-AGGTACGCAACATGATGCGCAAGTCTAGCATTACACGTACCACAA--ACCGAAAAATG-----
droAna3	scaffold_12916:14616914-14617087 -		TTGCAGAAATCGTGAGGAGCAGCATCGAATTGCGCGTCTTTGGACAAAGCGGTGAGT-ATC-----A-----A-----A-----AAC-TTTTCTTAATCACTTATCAGTGTTCATGCAATGTCTCT--CAAT-A-TC-AC-AGGTACGCAACATGATGCGCAAGTCTAGCATTACACGTACCACAA--ACCGAAAAATG-----
droBip1	scf7180000396572:2365045-2365215 +		TTGCAGAAATCGTGAGGAGCAGCATCGAATTGCGCGTCTTTGGACAAAGCGGTGAGT-TTATG-----A-TT-ATCATCA-AGATCCTTAT--A-----TTAA--TA--C-T-----T-----TTCTTT--GAAT-TA-T-AT-AGGTACGCAACATGATGCGCAAGTCTAGCATTACACGTACCACAA--ACCGAAAAATG-----
droKi1	scf7180000302472:2551454-2551629 +		TTGCAGAAATCGTGAGGAGCAGCATCGAATTGCGCGTCTTTGGACAAAGCGGTGAGT-CT-----ACT-AGATATAATAATTAACAGATGC-C-----AG--CA--TA--A-----A-----ATATGT--AAAA-TGC-TA-AGGTACGCAACATGATGCGCAAGTCTAGCATTACACGTACCACAA--TCTACCGAAAAATCT--
droFi1	scf7180000454111:191768-191931 -		TTGCAGAAATCGTGAGGAGCAGCATCGAATTGCGCGTCTTTGGACAAAGCGGTGAGT-GTC-----TATTACGCAACAAAGCA-----AATCTCT--AATT-AC-CCTTA-----A-----T-A-T-GTTT-AGGTACGCAACATGATGCGCAAGTCTAGCATTACACGTACCACAA--GCCGAAAAATG-----
droE1	scf7180000490971:100941-101110 +		TTGCAGAAATCGTGAGGAGCAGCATCGAATTGCGCGTCTTTGGACAAAGCGGTGAGT-AGCCAG-AGCC-----TCT--GAATATAT-G--T-----GCTGC--GATCTTT--AC-TA-ATCGTTAT-----A-----CTT-TA-----T-ACGTT-AGGTACGCAACATGATGCGCAAGTCTAGCATTACACGTACCACAA--ACCGAAAAATG-----
droRho1	scf7180000780122:14387-14558 +		TTGCAGAAATCGTGAGGAGCAGCATCGAATTGCGCGTCTTTGGACAAAGCGGTGAGT-CCC-----ACCA-AGTTAT-C--TAT-AGCA-----AATTGTT--AATA-AT--C--A-T-----TAA-----CTCTTA-----T-TT-AC-T-T-AGGTACGCAACATGATGCGCAAGTCTAGCATTACACGTACCACAA--ACCGAAAAATG-----
droBia1	scf7180000302422:2356985-2357155 +		TTGCAGAAATCGTGAGGAGCAGCATCGAATTGCGCGTCTTTGGACAAAGCGGTGAGT-CGC-----CACA-AATTAC-T--TAA--AGCTGC-C--GTTT-GTTA-ATGCTC-----A--T-----TCT-CA-----TCCCTGCT-AGGTACGCAACATGATGCGCAAGTCTAGCATTACACGTACCACAA--ACCGAAAAATG-----
droTak1	scf7180000415385:218637-218808 -		TTGCAGAAATCGTGAGGAGCAGCATCGAATTGCGCGTCTTTGGACAAAGCGGTGAGT-TGC-----CTCA-AAATAA-T--TTT--AGCCGC-C--AAAT-AATA-A--TA--C-G-G-----C-----ATCTTC--TAAT-TCCACG-C-AGGTACGCAACATGATGCGCAAGTCTAGCATTACACGTACCACAA--ACCGAAAAATG-----
droEug1	scf7180000409554:3785374-3785548 -		TTGCAGAAATCGTGAGGAGCAGCATCGAATTGCGCGTCTTTGGACAAAGCGGTGAGT-AAC-----CAA-AGTCTT--A--AA--AACA--AAAAG-----A-----CCATATAAATTATGCCCATCTT--CGAT-TACTC-TTT-AGGTACGCAACATGATGCGCAAGTCTAGCATTACACGTACCACAA--ACCGAAAAATG-----
dm3	chr21:10766074-10766240 -		TTGCAGAAATCGTGAGGAGCAGCATCGAATTGCGCGTCTTTGGACAAAGCGGTGAGT-TGA-----CGCT-GGAAAAAGGAGTAAACAAAC--A-T-----AG-----TAAT--C--A-G-----TGTC-A-----GACCTTT-AGGTACGCAACATGATGCGCAAGTCTAGCATTACACGTACCACAA--ACCGAAAAATG-----
droSim2	21:10442194-10442360 -		TTGCAGAAATCGTGAGGAGCAGCATCGAATTGCGCGTCTTTGGACAAAGCGGTGAGT-TAC-----TGCT-GGAAAAAGGAGTAAACAAAC--A-T-----AT-----TAAA--C--A-G-----TCTG-TC-----GT-TTT-AGGTACGCAACATGATGCGCAAGTCTAGCATTACACGTACCACAA--ACCGAAAAATG-----
droSec2	scaffold_3:6184588-6184754		TTGCAGAAATCGTGAGGAGCAGCATCGAATTGCGCGTCTTTGGACAAAGCGGTGAGT-TGC-----TGCT-AGAAAAAGGAGTAAACAAAC--A-T-----AT-----TAAT--C--A-G-----TCTG-TC-----GT-TTT-AGGTACGCAACATGATGCGCAAGTCTAGCATTACACGTACCACAA--ACCGAAAAATG-----
droYak3	Zk:7171321-7171487 -		TTGCAGAAATCGTGAGGAGCAGCATCGAATTGCGCGTCTTTGGACAAAGCGGTGAGT-TGC-----TCCT-AGAAAAAGGAGTAAACAAAC--A-T-----AG-----TAAT--C--C-G-----TGT-CCTC--GAGGTACGCAACATGATGCGCAAGTCTAGCATTACACGTACCACAA--ACCGAAAAATG-----
droEre2	scaffold_4929:14664786-14664957 +		TTGCAGAAATCGTGAGGAGCAGCATCGAATTGCGCGTCTTTGGACAAAGCGGTGAGT-TGC-----CACT-AGGAAAGAGGAGTAAACAAAC--A-T-----A--TC-TGTGCAAT--C--A-G-----TGTC-TC-----GT-TTTT-AGGTACGCAACATGATGCGCAAGTCTAGCATTACACGTACCACAA--ACCGAAAAATG-----

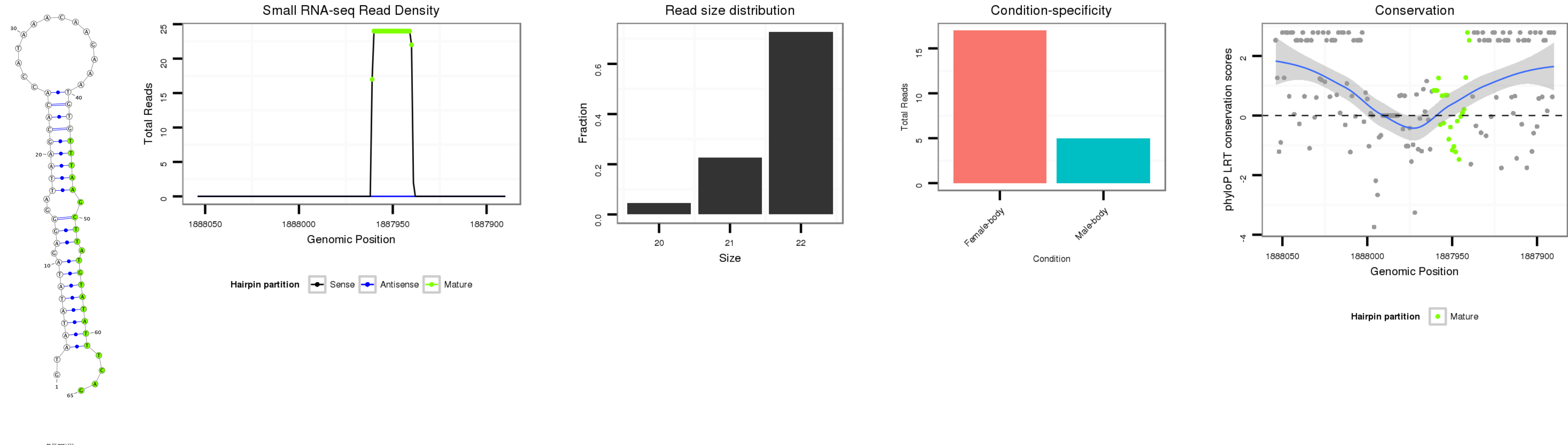
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	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.hair	1
crit.total	0
crit.pairing	1
crit.top3	1
crit.ttop3	1
crit.un	1
crit.back	1
rescue.total	0
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
 dgr_357 	 scaffold_15112:1887940-1888004 - 	 confident-exception 	 Mirtron 	 intron 	[View on UCSC Genome Browser (Cornell Mirror)]

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

Predicted structure



Show Alternate Folds

Flybase annotation

intron [Dgri|GH22773-in]; CDS [Dgri|GH22773-cds]; CDS [Dgri|GH22773-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

	Read # size	Mismatch	Hit Count	Norm	Total	M041 female body	V109 male body
GCCTGTACAATCGCCAAGGGCAGCTGGTGCAGCGCATCATCCTATCCGGGTAATATAGAGGGATTAAGCACACCATAAACAAGAAATGTGTTTAAGCTTATGTATATTTCAGTTTGTGTTCCGGGTTTTCGCTGGGATGCGGATGGGAACTCTTGGGCATCA							
*****.(((((((.(((.(((((((.....)))))))))).)))..))))))....*****							
.....TTAAGCTTATGTATATTTCAG.....	22	0	1	16.00	16	11	5
.....TTAAGCTTATGTATATTTCAG.....	21	0	1	4.00	4	4	0
.....TTAAGCTTATGTATATTTCAGT.....	22	0	1	2.00	2	0	2
.....TTAAGCTTATGTATATTTC.....	20	0	1	1.00	1	1	0
.....TTAAGCTTATGTATATTTC.....	21	0	1	1.00	1	1	0

Anti-sense strand reads

	Read # size	Mismatch	Hit Count	Norm	Total	M041 female body
CGGGACATGTTAGCGGTTCCTCGTGCACCAGTCGCGTAGTAGGATAGGCCCATATATATATCTCCCTAATTCGTGTGGTATTGTTCTTTACACAAATTCGAATACATATAAAGTCAAACACAAGCCCAAAACGGACCTACGCTACCCCTTGAGAACCCGTAGT						
*****.(((((((.(((.(((((((.....)))))))))).)))..))))))....*****						

Show Alignment With Reads

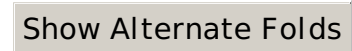
Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droGri2	scaffold_15112:1887890-1888054 -	dgr_357	GCCTGTACAATCGCCAAGGGCAGCTGGTGCAGCGCATCATCCTATCCGGGTAATATATA--GAGGATTAAGCACACCATAAA---CAA-----GAAAT-----G--T-----GTTAAGCTTATGTATATTTCAGTTTGTGTTCCGGGTTTTCGCTGGGATGCGGATGGGAACTCTTGGGCATCA
droVir3	scaffold_12875:4364455-4364609 +		GCCTGTACAATCGCOAAGGCAGCTGGTGCAGCGCATCATATCGCGGGTAATCTACAGAGTA-----CGCTTTAGGC-----G-----CATTT--TAAACAACC-----A-----ATCCATATTTCAGTTGTGCTCGGGTTTTCGCTGGGATTCGAGSGGAGCTTTGGGCATCA
droMoj3	scaffold_6496:13202285-13202436 +		GCCTGTACAATCGCCAAGGCAGCTGGTGCAGCGCATCATATCGCGGGTAATCTCA-----TAT-----ATCCTTATCAAT-----A-----TATTT--AT--TGTA--A-----A-----TCCCATTTTCAGTCTGCTCGGGTTTTCGCTGGGATTCGAGSGGAGCTTTGGGCATCA
droWil2	scf2_1100000004514:1352878-1353038 -		GCATGTATAAATCGTCAAGGTCAAATGGTGCAGCGCATCATATCTGCGGGTAAGCTAT-----TCC-----CACTATTC-----CAA-----TAATCCG-----A-----CAA--GTCACA-----TCTTTTAAATTTCAGCCCTGCTCGGGTTTTCGCTGGGATTCGAGSGGAGCTTTGGGCATCA
dp5	3:6564711-6564874 -		GCCTGTACAATCGCOAAGGCAGCTGGTGCAGCGCATCATCTCGCGGTAAAGCCAG-----CCC-----CCATTA--GTGTACT-----CAAA--ATATATTATCTGC--CTTAA-----A-----ATGTCCACAGCTGCTGAGGTTTGCATGGGCAATGAGSGGAGCTCTGGGCATCA
droPer2	scaffold_2:6785522-6785685 -		GCCTGTACAATCGCOAAGGCAGCTGGTGCAGCGCATCATCTCGCGGTAAAGCCAG-----CCC-----CCATTA--GTGTACT-----CAAA--ATATATTATCTGC--CTTAA-----A-----ATGTCCACAGCTGCTGTCAGGTTTGCATGGGCAATGAGSGGAGCTCTGGGCATCA
droAna3	scaffold_13266:9899819-9899973 +		GCCTGTACAAAGCCCAAGGGCAGCTGGTGCAGCGCATCATCTCGCGGTAAAGCTAT-----ACT-----ACGGC-----CAA-----GAATCT--A-----A-----TAA--AATAACA--TTTA-----A--CCGTCAGGCTGCTTCGGGTTTGCATGGGCAATGAGSGGAGCTCTGGGCATCA
droBip1	scf7180000396427:1042771-1042926 +		GCCTGTACAAAGCCCAAGGGCAGCTGGTGCAGCGCATCATCTCGCGGTAAAGCTAT-----ACT-----AGGC-----AAA-----GAATTTTAA--A--A-----AATCAAA--TTTA-----A--CCTTCAGTCTGCTTCGGGTTTTCGCTGGGATTCAGAGSGGAGCTCTGGGCATCA
droKik1	scf7180000302471:1643431-1643586 -		GCCTGTATAAAGCCCAAGGGCAGCTGGTGCAGCGCATCATCTCGCGGTAAAGCTAT-----ATC-----GATCTT-----CAT-----AGGA-----TGCCGTTAGG--TATAA-----A-----TCTGCTATCCAGGCTGCTTCGGGTTTGCATGGGATTCAGAGSGGAGCTCTGGGCATCA
droFic1	scf7180000454039:669937-670088 -		GCCTGTACAATCGCOAAGGGCAGCTGGTGCAGCGCATCATCTCTCGCGGTAAAGCTAT-----TCC-----GATTTCA--TAA-----ACAG-----A-----TTTCT--TATAA-----C-----TTTCCCTCCAGCCCTGCTTCGGGTTTTCGCTGGGATTCAGAGSGGAGCTCTGGGCATCA
droEle1	scf7180000491201:1828879-1829035 -		GCCTGTACAAAGCGTCAAGGGCAGCTGGTGCAGCGCATCATCTCTCGCGGTAAAGCTAT-----ACC-----ATCTTA-----A-----GAAATTA--TGATAATTAGT--AAAT-----A-----TCCCCCTCTCAGGCTGCTTCGGGTTTTCGCTGGGATTCAGAGSGGAGCTCTGGGCATCA
droRho1	scf7180000780066:262399-262551 +		GCCTGTACAATCGCOAAGGGCAGCTGGTGCAGCGCATCATCTCTCGCGGTAAAGCTAT-----ATCTAG-----GAA-----GTAA-----TGGC--CGA--AATAA-----A-----ACTGGTCCAGGCTGCTTCGGGTTTTCGCTGGGATTCAGAGSGGAGCTCTGGGCATCA
droBia1	scf7180000302143:2871480-2871631 -		GCCTGTACAAAGCCCAAGGGCAGCTGGTGCAGCGCATCATCTCTCGCGGTAAAGCTAT-----CCA-----CTTCCC-----AAA-----GTAG-----TATT--CAC--TTCAT-----A-----CTGTCTTCCAGAGCTGCTTCGGGTTTTCGCTGGGATTCAGAGSGGAGCTCTGGGCATCA
droTak1	scf7180000415910:126969-127123 +		GCCTGTACAATCGCAAGGTCAGCTGGTGCAGCGCATCATCTCTCGCGGTAAAGCTAT-----ACA-----GGTCCC--CAAA-----GCAA-----TGCCCTACT--AATTA-----A-----TCCCTCTACTAGCTGCTTCGGGTTTTCGCTGGGATTCAGAGSGGAGCTCTGGGCATCA
droEug1	scf7180000409474:2575308-2575460 +		GCCTGTACAATCGCAAGGTCAGCTGGTGCAGCGCATCATCTCTCGCGGTAAAGCTAT-----ATC-----ATTCCT--TAG-----A-----ATTATGAACAGT--AATAA-----A-----TCCCTCCAGGCTGCTTCGGGTTTTCGCTGGGATTCAGAGSGGAGCTCTGGGCATCA
dm3	chr2R:15378968-15379130 -		GCCTGTACAATCGCAAGGTCAGCTGGTGCAGCGCATCATCTCTCGCGGTAAAGCTAT-----CTC-----ATCTC--TACGTAAT-----AA--TGA--ATAATGACCACT--AATGG-----A-----ATCTCTCCAGGCTGCTTCGGGTTTTCGCTGGGATTCAGAGSGGAGCTCTGGGCATCA
droSim2	2r:16030244-16030406 -		GCCTGTACAATCGCAAGGTCAGCTGGTGCAGCGCATCATCTCTCGCGGTAAAGCTAT-----CTC-----ATATCC--ATGTAAAT-----AA--TGA--ATAATGACCACT--AATGG-----A-----ATCCCCTTCCAGGCTGCTTCGGGTTTTCGCTGGGATTCAGAGSGGAGCTCTGGGCATCA
droSec2	scaffold_1:12897515-12897672		GCCTGTACAATCGCAAGGTCAGCTGGTGCAGCGCATCATCTCTCGCGGTAAAGCTAT-----CTC-----ATCCCC--ATGTAAAT-----AA--TGA--ATAATGACCACT--AATGG-----A-----ATCTCTCCAGGCTGCTTCGGGTTTTCGCTGGGATTCAGAGSGGAGCTCTGGGCATCA
droYak3	ZR:13796718-13796873 +		GCCTGTACAATCGCAAGGTCAGCTGGTGCAGCGCATCATCTCTCGCGGTAAAGCTAT-----CCC-----GAATA--CAAT-----GTAA-----TAATGATCAGT--AATGC-----A-----ATCCTTCCAGGCTGCTTCGGGTTTTCGCTGGGATTCAGAGSGGAGCTCTGGGCATCA
droEre2	scaffold_4845:9577881-9578036 -		GCCTGTACAATCGCAAGGTCAGCTGGTGCAGCGCATCATCTCTCGCGGTAAAGCTAT-----TCC-----GATCCC--CAAT-----GCAA-----TAATGATCCGT--AATGC-----A-----AACCCTCCAGGCTGCTTCGGGTTTTCGCTGGGATTCAGAGSGGAGCTCTGGGCATCA

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

Predicted structure



Flybase annnotation

Antisense to utr3 [utr3_plus_5924]; intron [Dgri\GH19675-in]; CDS [Dgri\GH19675-cds]; CDS [Dgri\GH19675-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

[illegible]

Anti-sense strand reads

[illegible]

Re-alignment of all predicted orthologs

[illegible]

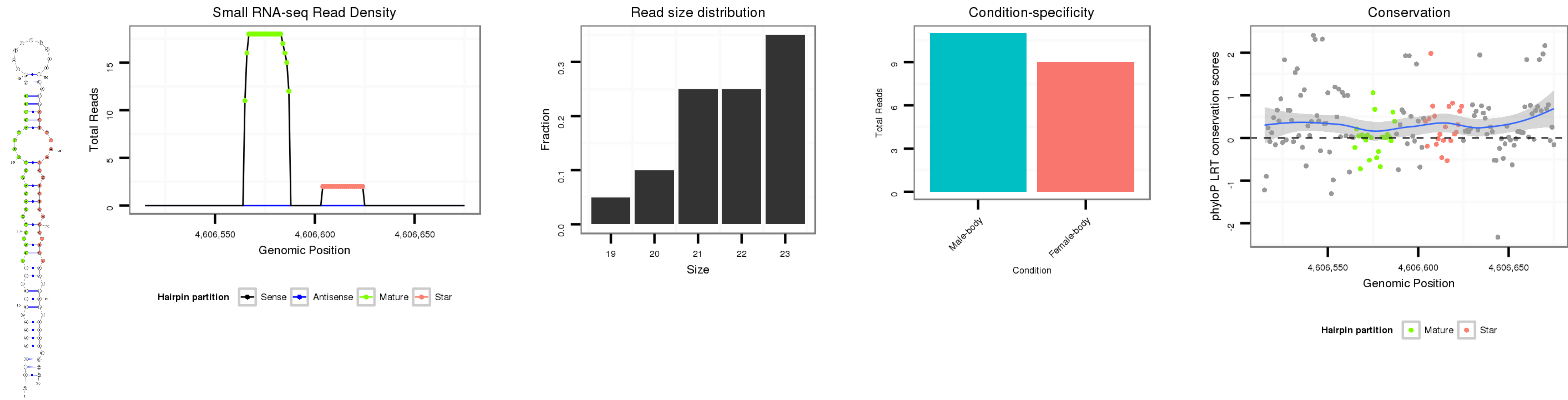
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	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dgr_61	scaffold_14906:4606565-4606625 +	candidate	Canonical miRNA	intron	[View on UCSC Genome Browser (Cornell Mirror)]

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Show Alternate Folds

Flybase annotation

intron [Dgri\GH19097-in]

No Repeatable elements found

Sense Strand Reads

[illegible]

Anti-sense strand reads

[illegible]

Show Alignment With Reads

Re-alignment of all predicted orthologs

[illegible]

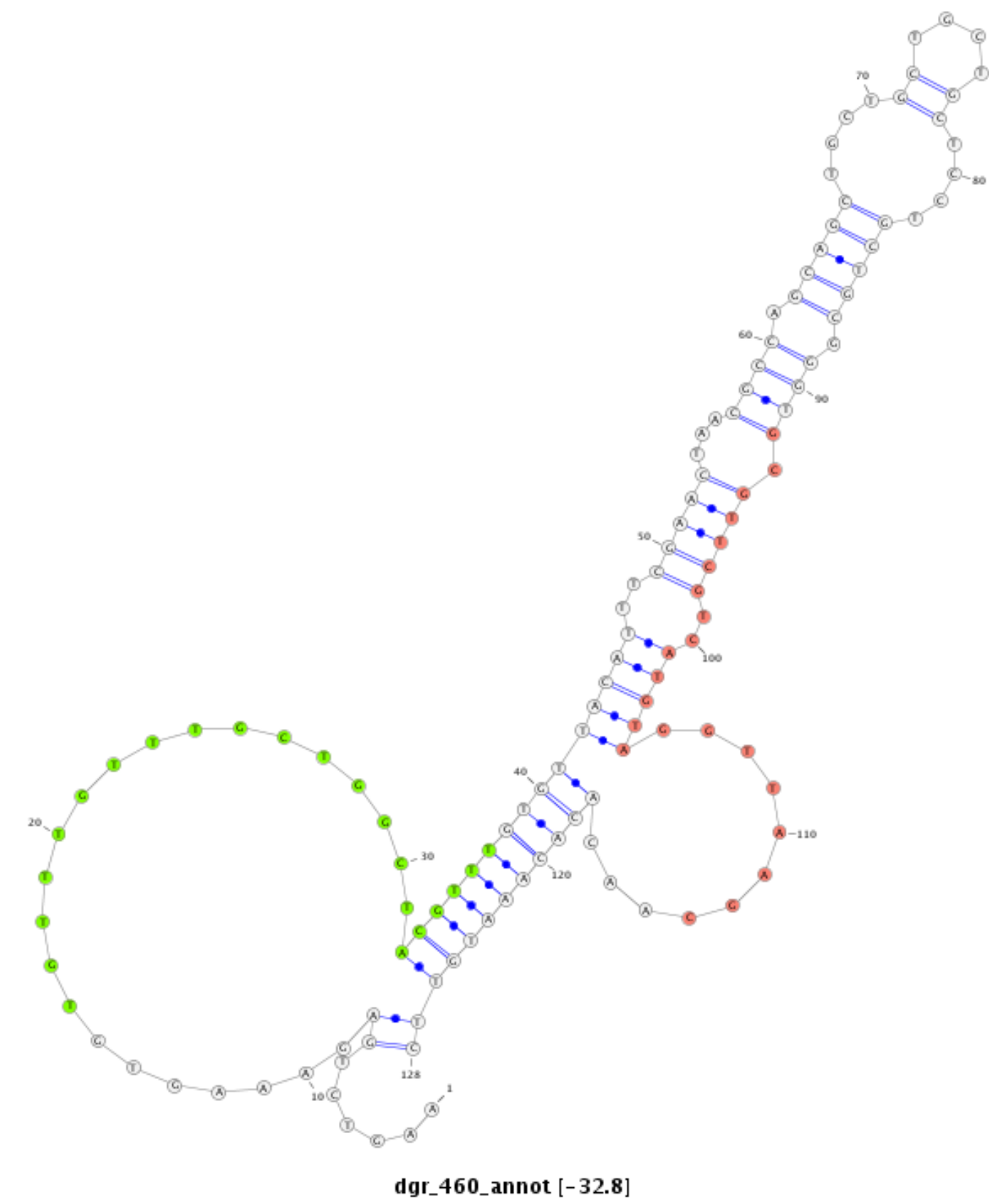
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	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

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

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Show Alternate Folds

Flybase annotation

intron [Dgr\GH19128-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

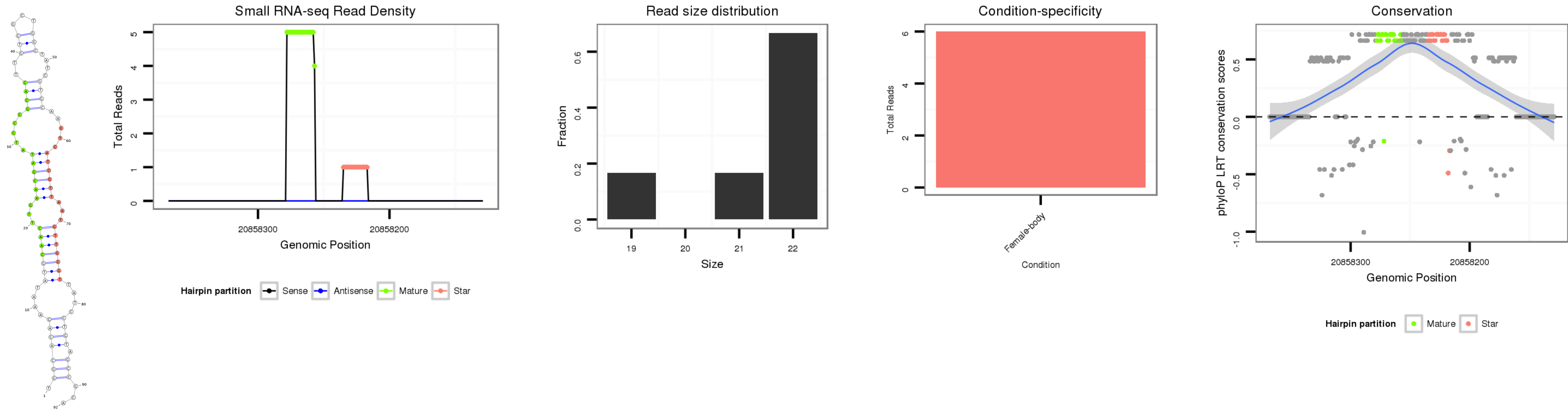
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	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	0
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	1
rescue.known	0
rescue.confident	7
rescue.candidate	5

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

ATAAATCAATAACTGCCTTAAATAGTGAAGAGAAGCTTGAATCGGTGAATCAATTCAACTTGAATGAAATCATGGCACAGAAATATGCAACTTGAACGATATCCCGCAC	TTGTCGCTGGCTATCGTGCAAGTCAATCGTTAATGTTGCGGTATCCTGTAGCCGCAAGCAACAATAATCTACCAAAATGGTAGTTAATAGTTACACATTGTTTCAACAAATAATACTTTAAGCATAAACT	Read size	# Mismatch	Hit Count	Total Norm	Total	M041 female body	V109 male body
*****.((((((...(((((((...((((((...(((...(((...)))...)))...)))...)))...)))...)))...))...*****		22	0	1	4.00	4	4	0
.....CAACTTGAACGATATCCCGCAC.....		21	0	1	1.00	1	1	0
.....CAACTTGAACGATATCCCGCA.....		19	0	1	1.00	1	1	0
.....GTCAATCGTTAATGTTGCGT.....								

Anti-sense strand reads

TATTAGTATTATGACGGAATTTATCACTTCTCTTCTCGAACTTAGCCACTTAGTTAAGTTGAACTTACTTTAGTACCGTGCTTTATACGTTGAACGTGCTATAGGCGCTGAACAGCAGCAGGATAGCACGTT CAGTAGCAATTAACAACGCA ATAGGACATCGGGCTTCGTTGTTATTAGATGGTTTACCACAAATTATCAATGTGTAAACAAGTGTGTTATTATGAAATTCGTATTTGA					Read #		Hit	Total	
*****.(((((((...(((((((...(((((((...(((...)))...)))...)))...)))...)))...)))...))...*****					size	Mismatch	Count	Norm	Total
No data available in table									

No data available in table

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droGr12	scaffold1_15110:20858129-20858368 -	dgr_464	ATAAATCAATAACTGCCTTAAATAGTGAAGAGAAGAAGCTTGAATC-GGTGAATCAATTCAACTTGAATGAAATCATGGCACAGAAATATGCAACTTGAACGATATCCCGCACTTGTCGCTGGCTATCGTGCAASTCATCGTTAATGTTGCGTTATCCTGTAGCC-----GCA---AGCAACAATAATCTACCAAAATGGTAGTTAATAG---TTACACATTGTTTCAACAAATAATACTTTAAGCATAAACT
droVir3	scaffold1_13049:22675495-22675660 +	dvi_17	-----GAAGCTTGAGCGTATGTAAACG-----CAATT-AAAAGAAATGCGTTACAGAAATTTGCAACTTAACGATATCCCGCACTTGTCGCTGGCTATCGTGCAASTCATCGTTAATGTTGCGCGATCTGTGAC-----TTAAAGACAAC-----AAGTGGACGTAAAGACATAATTACAC-----
droMoJ3	scaffold1_6680:17294272-1729443 PASSFAIL	dmo_221	-----TAAAGATGTTGGCCAGAGATTTGCAACTTAACGATATCCCGCACTTGTCGCTGGCTATCGTGCAASTCATCGTTAATGTTGCGCGATCTGTGACCTATAGTACAACCACAAATAGTATTTATAAAATTTGGTAGGCCAGACTAATATAAGAAGTGCA---AGGAC-----

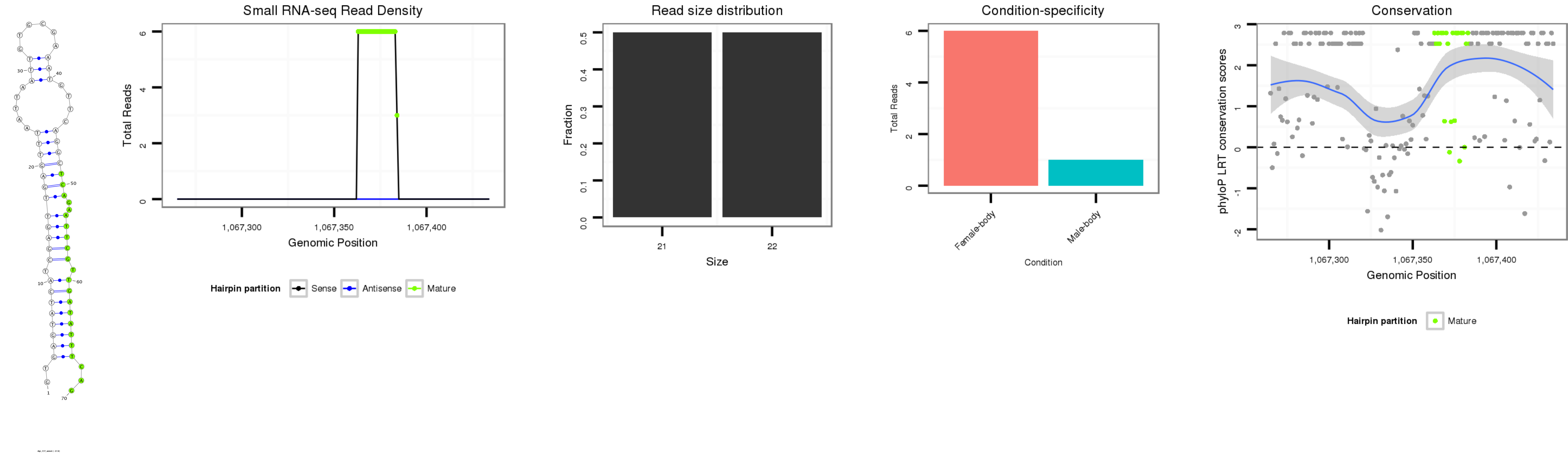
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crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	1
rescue.known	0
rescue.confident	3
rescue.candidate	2

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dgr_227	scaffold_14978:1067315-1067384 +	confident-exception	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 [DgriGH25212-in]; CDS [DgriGH25212-cds]; CDS [DgriGH25212-cds]

No Repeatable elements found

mature	star
1. dgr_227 scaffold_14978:1067363-1067384 +	
2. scaffold_15252:179220-179241 +	

Sense Strand Reads

CGGCGCGGAGCAAGCCGCGCAAGGTGATGTGCTATGTGGGACCGAAACAGGTGAGTATCATCGAGTTGAGTTTAAATTAATTGTGCGAAATGTTTCAGGC							M041	V109
TCAGAATTCGTTGATATTTTCAG	Read #	Mismatch	Hit	Total			female body	male body
*****.(((((((.((((((((((.....((.....))).....))))).))))).))))*****	size		Count	Norm	Total			
.....TCAGAATTCGTTGATATTTTCAG	23	1	2	5.00	10	4	6	
.....TCAGAATTCGTTGATATTTTCAG	22	0	2	3.50	7	6	1	
.....TCAGAATTCGTTGATATTTCA	21	0	2	3.00	6	5	1	
.....CAGAATTCGTTGATATTTTCAG	21	0	2	0.50	1	1	0	

Anti-sense strand reads

GCGCGCCTCGTTCGGCGGTTCCACTACAGCATACACCCCTGGCTTTGTCCACTCATAGTAGCTCAACTCAAATTAATTAAACACGCTTTACAAGTCCG	Read #	Hit	Total		V109	M041
*****.(((((((.((((((((((.....((.....))).....))))).))))).))))*****	size	Mismatch	Count	Norm	male body	female body
.....AGTCTTAAAGCAACTATAAAGTCATTGGTAGTTCCTTTACTATAACTTCAAGTATGGGTCGCATAACGCTG						

Show Alignment With Reads

Re-alignment of all predicted orthologs

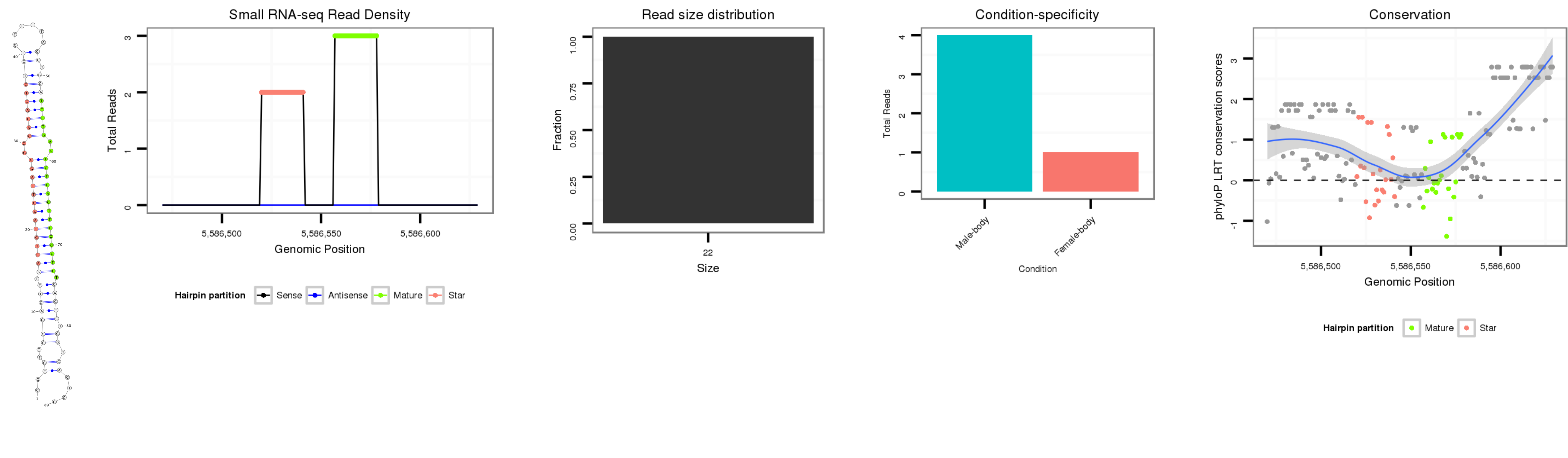
Species	Coordinate	ID	Alignment
droGri2	scaffold_14978:1067265-1067434 +	dgr_227	CGGCGCGGAGCAAGCCGCGCAAGGTGATGTGCTATGTGGGACCGAAACAGGTGAGTATC-AT--CGAGT-----TGA---GTTTAATT--AATTGTGCGAAATGTT--CAGGC
droVir3	scaffold_12963:12587183-12587352 -		CGAGCGGAGCAAGCCGCGCAAGGTGATGTGCTATGTGGGACCGAAACAGGTGAGTCTC-ATAGT-----TG--CAG--ATGAATTC--ATTGTGCGAAATGTT--CAGGC
droMoJ3	scaffold_6500:29345391-29345563 +		CGACAAAGCAGCAACCGCGCAAGGTGATGTGCTATGTGGGACCGCAACAGGTGAGTATCTG--GCACA-----TA--AG--CACCGTTA--TTTGTGCGAAATGTT--CAGGC
droW112	scf2_1100000004521:885307-885481 -		CGCCAAAGTAAACCGCGCAAGTCTCTGCTATGTGGGACCAACAGGTGAGTGGATC--GAAAGACTCCA--C-----TT--TTGACC-----CCCTAGCAAAATGTT--CAGGC
dp5	4_group3:8815770-8815944 +		CGCGAAAGCAGCAAGCCCGCAAGGTACCTGCTATGTGGGACCAACAGGTGAGTATCAG--G-----CCCCAGGGCTTCTGGCG--GG--G-----AACTAGAAATGTT--CAGGC
droPer2	scaffold_1:10267568-10267742 +		CGCGAAAGCAGCAAGCCCGCAAGGTACCTGCTATGTGGGACCAACAGGTGAGTATCAG--G-----CCCCAGGGCTTCTGGCG--GG--G-----AACTAGAAATGTT--CAGGC
droAna3	scaffold_12916:6435981-6436151 -		CGCGAAAGCAGCAAGCCCGCAAGGTCTCTGCTATGTGGGACCAACAGGTGAGTGGTCA--C-----CA--GCT--GCGCAATCTTATCCCATGAAAGCGC--AGGGC
droBip1	scf7180000396568:381400-381570 +		CGCGAAAGTAAAGCCCGCAAGGTCTCTGCTATGTGGGACCAACAGGTGAGTGGGCA--C-----CA--GG--GCGCAATCTTATCCCATGAAAGCGC--AGGGC
droKik1	scf7180000302408:261544-261719 +		CGCGCAAGCAAGCCCGCAAGGTCTCTGCTATGTGGGACCAACAGGTGAGTATCAG--C-----GCCGTA--GA--AACCGATTGGGATCGAGCAAAATGTT--CAGGC
droFic1	scf7180000453949:91940-92110 -		CGCGCAAGCAAGCCCGCAAGGTCTCTGCTATGTGGGACCAACAGGTGAGTGGCAG--C-----TG--GG--AGCCGATGATGTTGTGTGAAATGTC--AGGGC
droEle1	scf7180000491273:1270200-1270370 -		CGCGCAAGCAAGCCCGCAAGGTCTCTGCTATGTGGGACCAACAGGTGAGTGGCAG--C-----AC--TG--AGCAGGTGATGCTGCAATGAAATGTC--AGGGC
droRho1	scf7180000777965:66924-67094 -		CTCTCAAAACAAGCCCGCAAGGTCTCTGCTATGTGGGACCAACAGGTGAGTGGTCA--A-----GC--TG--AACCCGCTGATCTGCAATGAAATGTC--AGGGC
droBia1	scf7180000302408:243800-243972 +		TCCTCAAGCAAGCCCGCAAGGTCTCTGCTATGTGGGACCAACAGGTGAGTGGACAA--C-----TC--TGCAACACCATG--TGGTATTGCGAGAAATGTC--AGGGC
droTak1	scf7180000415779:511856-512025 +		CTCTCAAGCAAGCCCGCAAGGTCTCTGCTATGTGGGACCAACAGGTGAGTGGGAA--C-----TC--AAG--ATTACGATGATCTGCTGAAATGTC--AGGGC
droEug1	scf7180000407253:241343-241513 +		TATCTCAAAACAAGCCCGCAAGGTCTCTGCTATGTGGGACCAACAGGTGAGTGGTCAT--A-----AC--AAG--AATAGATGATATTGCGAAATGTC--AGGGC
dm3	chr21:2028200-2028370 +		CTCTCAAGCAAGCCCGCAAGGTCTCTGCTATGTGGGACCAACAGGTGAGTGGTAT--C-----TG--GG--AGCAGCTGACATCTGCTGAAATGTC--AGGGC
droSim2	21:1938179-1938349 +	dai_5264	CTCTCAAGCAAGCCCGCAAGGTCTCTGCTATGTGGGACCAACAGGTGAGTGGTAT--C-----TG--GG--AGCAGCTGACATCTGCTGAAATGTC--AGGGC
droSec2	scaffold_14:1974672-1974842		CTCTCAAGCAAGCCCGCAAGGTCTCTGCTATGTGGGACCAACAGGTGAGTGGTAT--C-----TG--GG--AGCAGCTGACATCTGCTGAAATGTC--AGGGC
droYak3	Z1:2013493-2013663 +		CTCTCAAGCAAGCCCGCAAGGTCTCTGCTATGTGGGACCAACAGGTGAGTGGTAG--C-----TC--GG--AACAGATTGATATCTGCTGAAATGTC--AGGGC
droEre2	scaffold_4929:2075550-2075720 +		CTCTCAAGCAAGCCCGCAAGGTCTCTGCTATGTGGGACCAACAGGTGAGTGGTAG--C-----TC--GG--AACAGCTGATATCTGCTGAAATGTC--AGGGC

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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	1

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Show Alternate Folds

Flybase annnotation

intron [Dgrn\GH13755-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

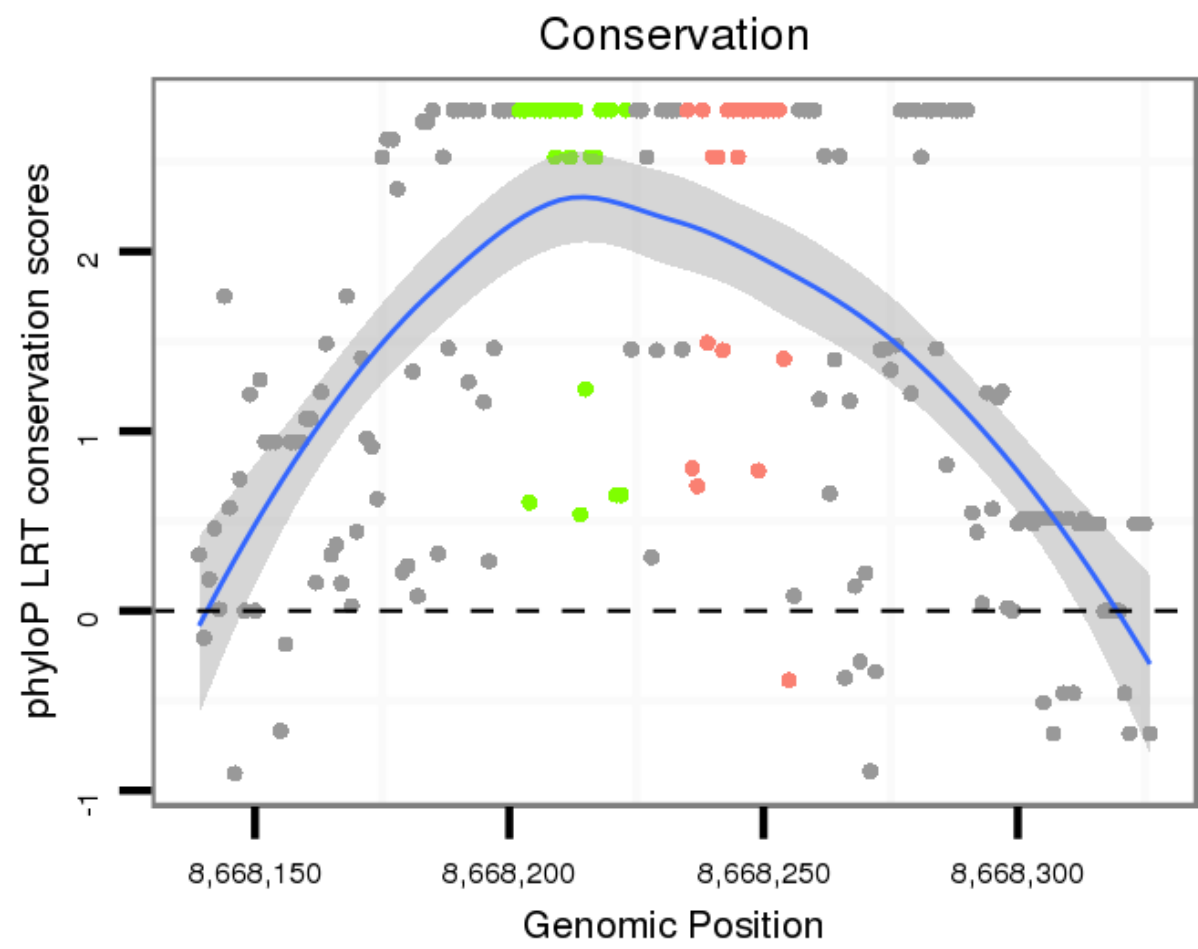
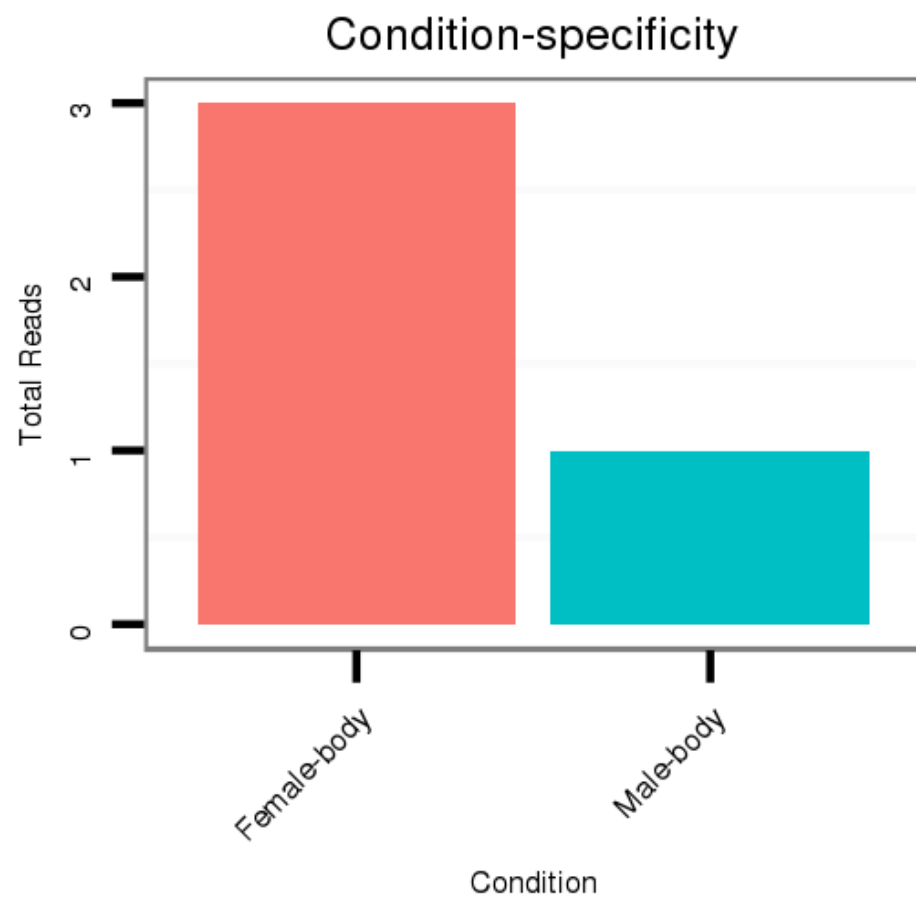
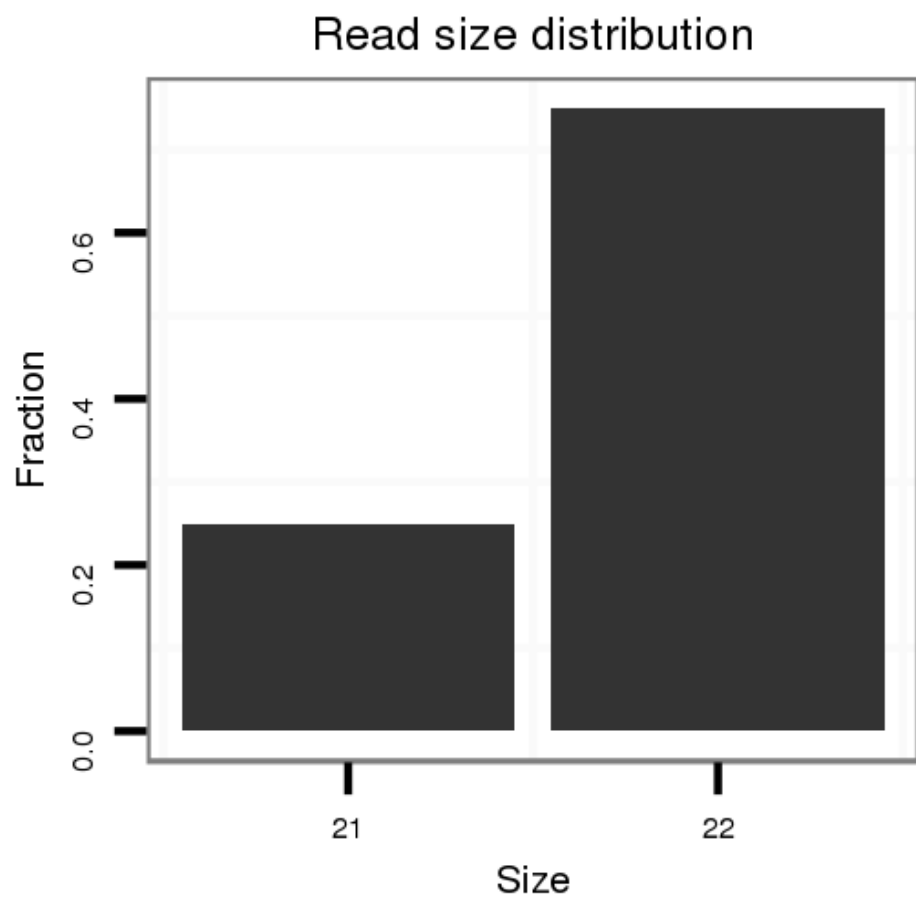
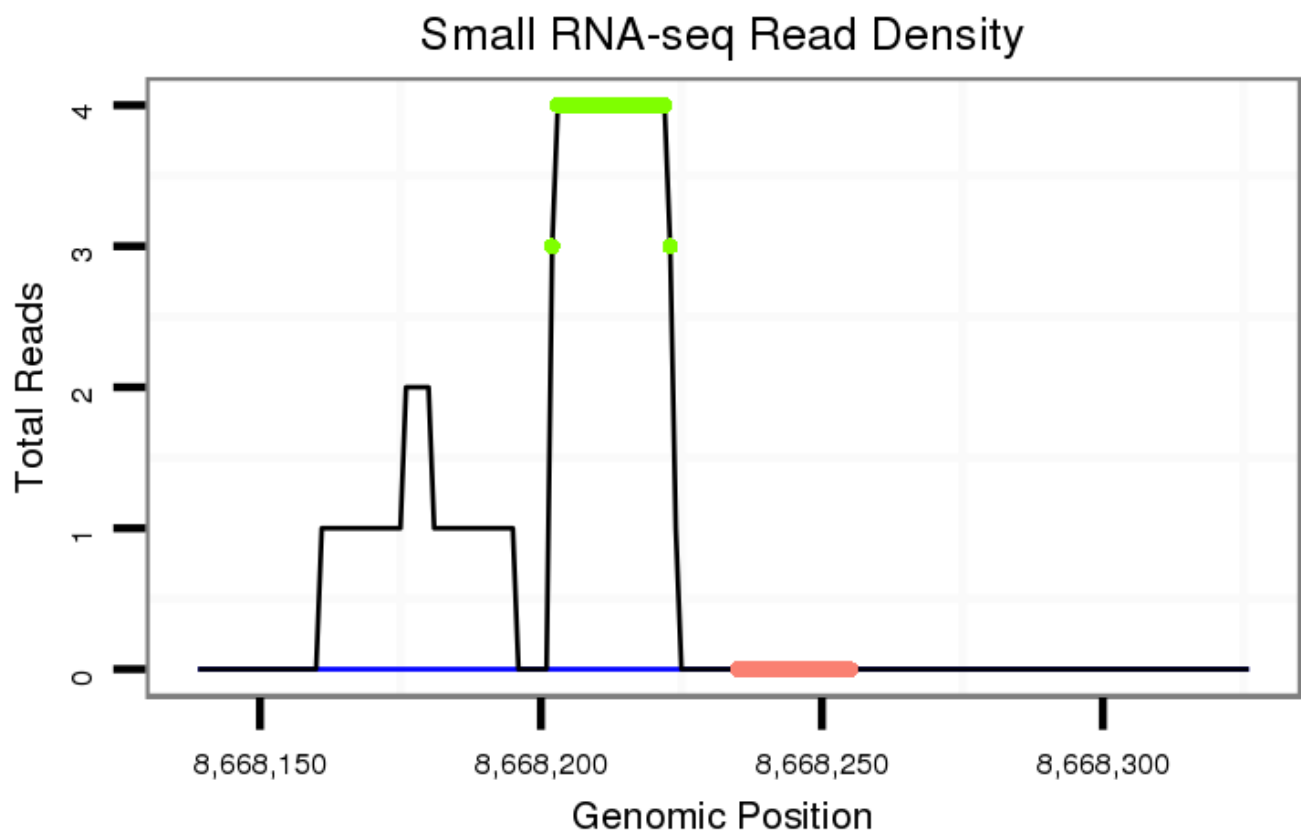
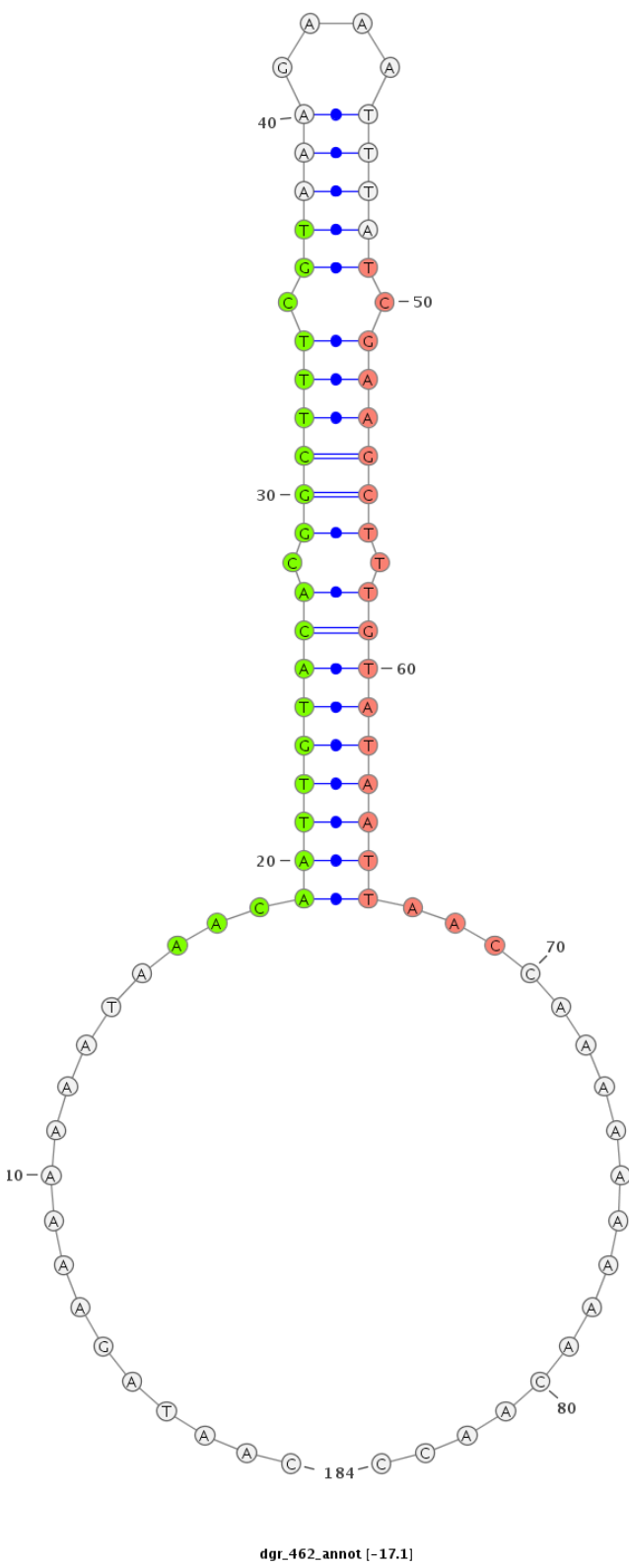
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	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Hairpin partition **Mature** **Star**

Show Alternate Folds

Flybase annotation

intergenic

Repeatable elements

Name	Class	Family	Strand
A-rich	Low_complexity	Low_complexity	+

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	scaffold14_14906:8668139-8668326 +	dgr_462	ATACGAAAACTAAAAA-----AA-----AAAGTGAACAAC-----CC-----AACC-----AACAAACAATAGAA-----A-----AAAATAAAC-AATTGTACACGGCTTTCCGTAAGAAATTTATCGAAGCTTTGTATAATTAAACCAAAAAAACAACTGATC-TTTGTGTTATTATTGCTTTATTCCAACATTCTTAGCACCCAACTGCCCC
droVir3	scaffold1_13047:1835004-1835189 +	dvi_24634	AAATGAGC-----AA-----AAAGAGAACAAC-----CC-----AACC--AACACAATAGAAAA-AAAAACAATAAAATAATAATTGTGTACACGGCTTTCCGTAAGAAATTTATCGAAGCTTTGTATAATTAAACAAAAAA-AAACCTTGAACTTTGTGTTATTATTATTACA-CAACAATTAACACCC-----CTCCCA
droMoJ3	scaffold6_6540:3761891-3762070 +	dmo_3126	AACGAAA--C-AAAATGAAAGAA-----GAAGAGTGA-----ACCGAAC-C-----AACACAAAATAAAACAATAGAAAATAAAATAAAC-AATTGTACAC-TGCTTTCCGTAAGAAATTTATCGAAGCTTTGTATAATTAAACAAAAAA--A--AATGAACTTTGTGTTATTATTGATTATT-----
droWi12	scf2_1100000004902:4649914-4650077 +	dwi_5415	AACGAAA--C-AAAAGAAAAGAAAGTTTA-----AAAAATGA-----AAAC-C-AACCAAC--C-----AACC-----AACAAAACAATAGAA-----A-----AAATAAAC-AATTGTACACGGCTTTCTATAAGAAATTATATAGAGCTTTGTATAATTACCAAAAAAAACCAAAAA-TTGTGTTATTATTGT-----A-----
dp5	2:127294869-27295026 -	dps_3827	ACC-----A-----A-----CTTACA-AACCAATCCATTCAAC-A-----GAAAAACAATAGAAAG-ACAAA-AAAAAAGAAATAA-A-AATTGTACACGGCTTTCTATAAGAAATTATATAGAGCTTTGTATGATTAAACAAAAAA--AACCCAAA-TTTGTGTTATTATTGCAATT-----
droPer2	scaffold1_6:2585071-2585227 -	dpe_2481	ACC-----A-----A-----CTTACA-AACCAATCCATTCAAC-A-----GAAAAACAATAGAAAG-ACAAA-AAAAAAGAAATAA-A-AATTGTACACGGCTTTCTATAAGAAATTATATAGAGCTTTGTATGATTAAACAAAAAAACACCCCAA-TTTGTGTTATTATTGCAATT-----
droAna3	scaffold1_13340:11049297-11049436 -	dan_90	AACCAATAA-----A-----TTGAAAGAAACAAACCCG-----TC-----AACC-AACCAACAATAGAA-----A-----AAATAAAC-AATTGTACACGGCTTTCCGTAAGAAATTATATAGAGCTTTGTATAATTAGAAAA-----AACAAA-TTTGTGTTATTATT-----
droBiP1	scf7180000396374:34256-34391 +		AAA--AAA--C-A-----A-----AAAGAAATG--CC-----TC-----AACC-AACCAACAATAGAA-----A-----AAATAAAC-AATTGTACACGGCTTTCCGTAAGAAATTATATAGAGCTTTGTATAATTAAACAAAA-----AACAAA-TTTGTGTTATTATTGCCATA-----
droKiK1	scf7180000302247:250351-250497 +		CCC-----A-----A-----C-A-CAAAAACCAAC--C-----AACC-ATCAACAAAACAATAGAAAG-A-----AAAAACAATAAAC-AATTGTACATGCTTTCCGTAAGAAATTATATAGAGCTTTGTATAATTAAACAAAAAG-AC-AAACAAA-TTTGTGTTATTATTGCCATT-----
droFiC1	scf7180000454106:2527577-2527718 +		CCC-----A-----A-----C-A-CAAAACCAAC--CAAC-AACC-AACCAACAAAACAATAGAA-----A-----AACCAATAAAC-AATTGTACACGGCTTTCCGTAAGAAATTATATAGAGCTTTGTATAATTAAACAAAAAA--A--ACCTCCAA-ATTGTGTTATTATTGCCATT-----
droE1e1	scf7180000491212:1154178-1154316 +		ACC-----A-----A-----C-A-CAAAAGATC--CAAC-AACC-AAC-----AACCAATAAA-----A-----AAAAACAATAAAC-AATTGTACACGGCTTTCCGTAAGAAATTATATAGAGCTTTGTATAATTAAACAAAAAG-A--ACCTCCAA-TTTGTGTTATTATTGCCATT-----
droRho1	scf7180000778307:14064-14204 +		ACC-----A-----A-----C-A-CAAAAACCAAC--C-----AACC-AACATCAAAACAATAGAA-----A-----AAAAACAATAAAC-AATTGTACACGGCTTTCCGTAAGAAATTATATCGAAGCTTTGTATAATTAAACAAAAAA--A--ACCTCCAA-TTTGTGTTATTATTGCCATT-----
droBia1	scf7180000302402:7353515-7353651 -		CCC-----A-----A-----C-A-CAAAAACCAAC-----C-C-AACAAACAATAGAA-----A-----AAA-CAATAAAC-AATTGTACACGGCTTTCCGTAAGAAATTATATAGAGCTTTGTATAATTAAACAAAAAA-AC-AAACAAA-TTTGTGTTATTATTGCCATT-----
droTak1	scf7180000414009:179083-179222 +		ACC-----A-----A-----CTA-TAAAAACCAAC--C-----AACC-AACAAACAACAATAGAA-----A-----AAACCAATAAAC-AATTGTACACGGCTTTCCGTAAGAAATTATATAGAGCTTTGTATAATTAAACAAAA-A--A--ACCTCAA-TTTGTGTTATTATTGCCATT-----
droEug1	scf7180000409490:80951-81102 +		AACGAAA-----A-----A-----ATG--CCCA-CAAAAACCAAC--C-----AACC-AACACAAAACAATAGAA-----A-----AAAAATCAATAAAC-AATTGTACATGCTTTCCGTAAGAAATTATATAGAGCTTTGTATAATTAAACAAAAAA--A--ACCTCAA-TTTGTGTTATTATTGCCATT-----
dm3	chr3R:4640252-4640392 -	dme_421	ACC-----A-----A-----CC-ACA-AACCAAA--C-----AA--C-AACACAAAACAATAGAA-----A-----AAAGAAATAAAC-AATTGTACATGCTTTCCGTAAGAAATTTATGAAGCTTTGTATGATTAAACAAAAAA--TCCAAA-TTTGTGTTATTATTGCCATT-----
droSim2	3r:16351736-16351881 +	dsi_75	ACC-----A-----A-----CC-ACA-AACCAAA--C-----AA--CAACAAACAACAATAGAA-----A-----AAAAACAATAAAC-AATTGTACATGCTTTCCGTAAGAAATTTATGAAGCTTTGTATGATTAAACAAAAAA--A--TCTGAA-TTTGTGTTATTATTGCCATT-----
droSec2	scaffold_0:17217384-17217525 +	dse_1834	ACC-----A-----A-----CC-ACA-AACCAAA--C-----AA--CAACACAAAACAATAGAA-----A-----AAAAACAATAAAC-AATTGTACATGCTTTCCGTAAGAAATTTATGAAGCTTTGTATGATTAAACAAAAAA--A--TTGTGAA-TTTGTGTTATTATTGCCATT-----
droYak3	3R:8702186-8702327 -	dya_1796	ACC-----A-----A-----CG-TCA-AACCAAA-----C-C-AACACAAAACAATAGAAAG-----A-----AAAAACAATAAAC-AATTGTACATGCTTTCCGTAAGAAATTATATAGAGCTTTGTATAATTAAACAAAAAA--TCTCAA-TTTGTGTTATTATTGCCATT-----
droPer2	scaffold1_4770:16945907-16946043 +	der_1521	ACC-----A-----A-----CC-ACA-AACCAAA-----C-C-AACACAAAACAATAGAA-----A-----AAAAACAATAAAC-AATTGTACATGCTTTCCGTAAGAAATTATATAGAGCTTTGTATAATTAAACAAAAAA--A--TCTCAA-TTTGTGTTATTATTGCCATT-----

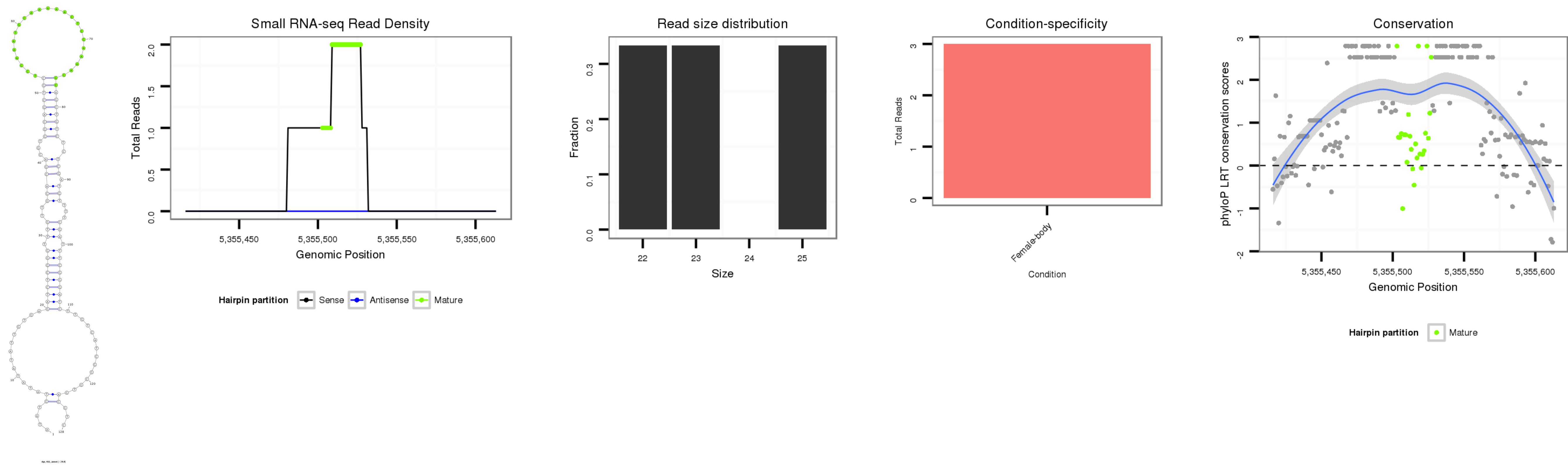
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	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	8
rescue.candidate	4

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dgr_461	scaffold_14906:5355466-5355563 +	candidate	Canonical miRNA	intron	[view on UCSC Genome Browser (Cornell Mirror)]

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Show Alternate Folds

Flybase annotation

intron [Dgr\GH19128-in]

No Repeatable elements found

Sense Strand Reads

[illegible]

Anti-sense strand reads

[illegible]

Show Alignment With Reads

Re-alignment of all predicted orthologs

[illegible]

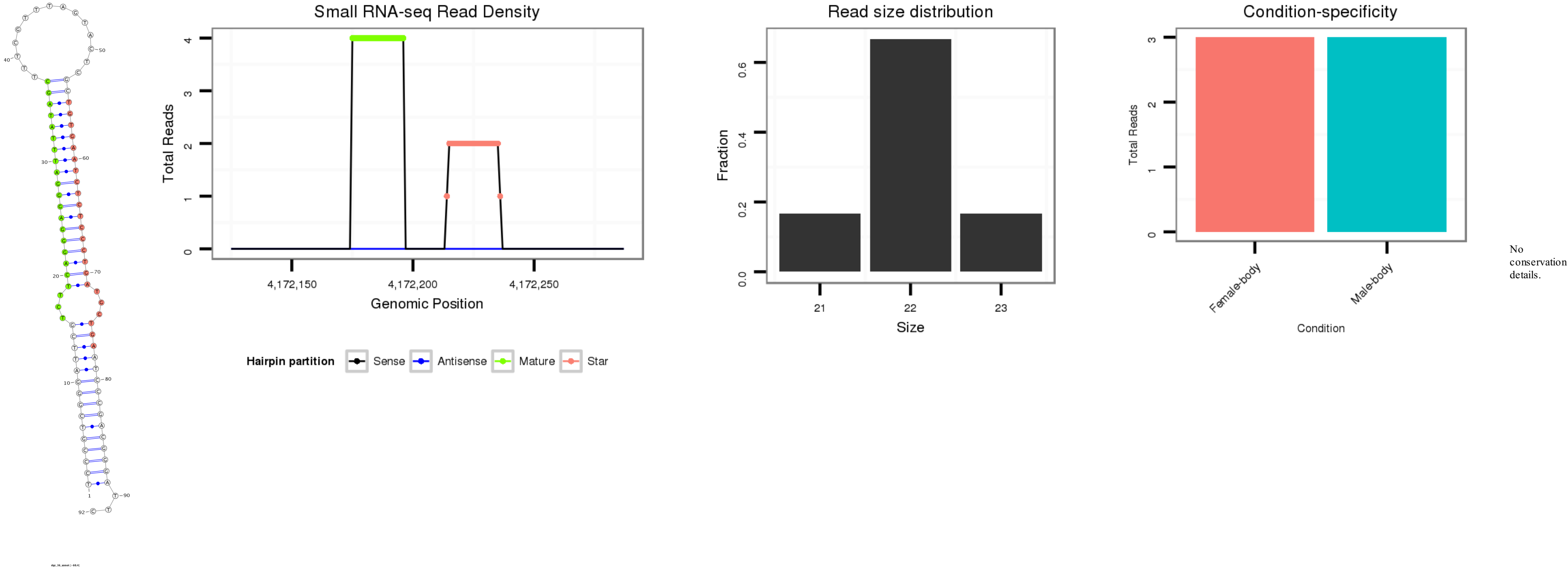
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crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	0
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	0
rescue.total	0
rescue.dominant	1
rescue.known	0
rescue.confident	3
rescue.candidate	9

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dgr_36	scaffold_14906:4172175-4172237 +	candidate	Canonical miRNA	intergenic	[View on UCSC Genome Browser {Cornell Mirror}]

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Show Alternate Folds

Flybase annotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

TCTTTGTAATATGTTTTTTTGTTAATTGCACAAACTCCCGTCGGGATTTCG TCTTCAGGGAGGGATTATAGC TTTCGTTTAGTACTCGC TGTGAATCTCTCCCTGATGCTGA ATCCCGACGGGATTCAAAATCTAGACAAATTTAACCTGGAGCCAGCAATAC	Read size	# Mismatch	Hit Count	Total Norm	Total	M041 female body	V109 male body
.....TCTTCAGGGAGGGATTATAGC.....	22	0	1	4.00	4	2	2
.....TGTGAATCTCTCCCTGATGCTGA.....	23	0	1	1.00	1	0	1
.....GTGAATCTCTCCCTGATGCTG.....	21	0	1	1.00	1	1	0

Anti-sense strand reads

AGAAACATTATACAAAAACAATTACGTGTTTGAGGGCAGCCCTAAGC AGAAGTCCCTCCCTAAATATCG AAAGCAAATCATGAGCG ACACTTAGAGAGGGACTACGACT TAGGGCTGCCCTAAGTTTTAGATCTGTTTAAATTGGACCTCGGTCGTTATG	Read size	# Mismatch	Hit Count	Total Norm	Total	M041 female body
*****((((((((((((((...((((((((((((((((((...))))))))))))))))...))))))))))))))))...*****						

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droGri2	scaffold_14906:4172125-4172287 +	dgr_36	TCTTTGTAATATGTTTTTTTGTTAATTGCACAAACTCCCGTCGGGATTTCG TCTTCAGGGAGGGATTATAGC TTTCGTTTAGTACTCGC TGTGAATCTCTCCCTGATGCTGA ATCCCGACGGGATTCAAAATCTAGACAAATTTAACCTGGAGCCAGCAATAC

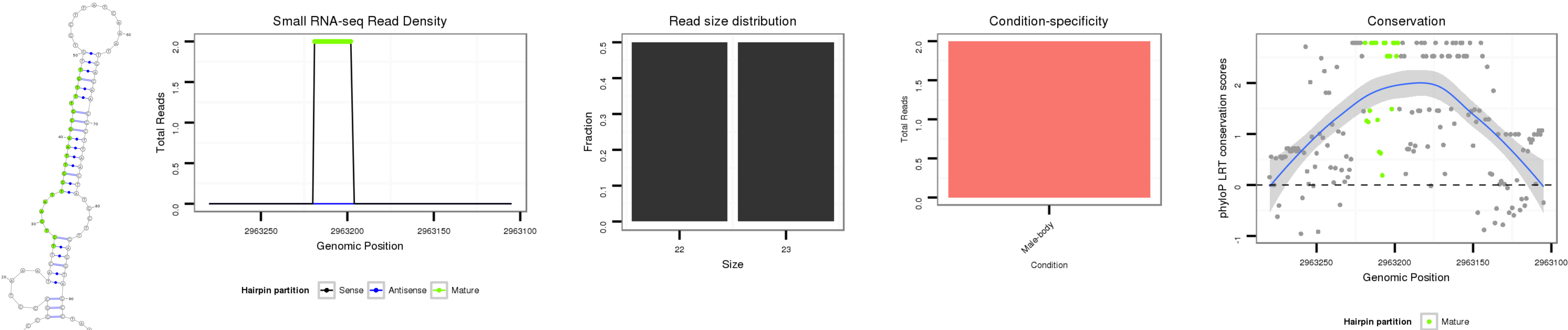
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PASS/FAIL	
crit.no	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dgr_468	scaffold_14906:2963155-2963230 -	candidate	Canonical miRNA	antisense_to_intron	[View on UCSC Genome Browser (Cornell Mirror)]

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

Predicted structure



Show Alternate Folds

Flybase annotation

Antisense to intron [Dgri/GH18982-in]

No Repeatable elements found

Sense Strand Reads

AATAGAATCAAAAGGATGTGATGTGTGTGAGTGTGTGTCGAGTACCGCGCTAAATACTTCTGAATTGGTTAAGCGTTTGTGTGCTTATCAAATTGACAACGCTTAACTATGCTTGAGGTAGCCTAATTGTTTCAACAAGCTTCCCGCCGGGCTGTGGTTTTCTGTGTGTGTT	Read size	# Mismatch	Hit Count	Total Norm	Total	male body	V109
*****((.....(((.....((((.....((((((((.....)))))))))))))).....))))*****	22	0	1	1.00	1	1	
.....TCTGAATTGGTTAAGCGTTTGT.....	23	0	1	1.00	1	1	
.....TCTGAATTGGTTAAGCGTTTGT.....	23	0	1	1.00	1	1	

Anti-sense strand reads

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

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droGri2	scaffold_14906:2963105-2963280 -	dgr_468	AATAGAATCAAAAGGATGTGA-----T--GT---GTG-----TGTGA--GTGT-----GTGTCGA-----GTACCGCGCTAAATACTTCTGAATTGGTTAAGCGTTTGTGTGCT---TATCA-AATTGACAACGCTTAACTATGCTTGAGGTAGCC--TAATTGTTTCAACAAGCTTCCCGCCGGGCTGTGG-----TTTTCTGTGTGTGT
droVir3	scaffold_12855:6808843-6808998 -	dvi_24643	A-----AAGGATGTG-----T--GT---CGG-----TGGG--GTGT-----G-----GT--GTGTCCCTTTCTAAATACTCTGAATTGGTTAAGCGTTTGTGTGCT---TATCA-AATTGACACGCTTAACGTGCTTGAGGTAGCC--TAATTCTTCAACAAGCCACCCACCGGGTCGTG-----TGTCCGTGT-
droMoj3	scaffold_6540:25792842-25793042 +	dmo_3123	AA--CCCTCAAAGGATGTGCGTAGGTGTCTACCTTATCTCTAATCTGTCTGTGTG--GTGTT-----G-----GT--GTSTACCGTTGCTAAATACTTCGAATTGGTTAAGCGTTTGTGTGCT---TATCA-AATTGACAACGCTTAACTGTGCTTGAGGTAGCC--TAATTGTTTCAACAAGCTTCCCGCCGASGTGTGCTATGTGCGACATGGA-----GTGTGTG
droWil2	scf2_1100000004943:14640097-14640209 +		T-----T-----G-----GT---GTG-----TGTG--GTGT-----GTG-----T-----SACTTAAATACTTCGAATTGCTAAGCGTTTGTGTGCTCCCTTCA-AATTGACATAGCTTAACCTAATCTATGCTTGAGGTAGCCCTTAATTCTTC-----G-----G-----
dp5	2:21156538-21156677 -	dps_3835	C-----G-----G-----GT---G-----G-----G-----G-----TAAATACTTCGAATTGGTTAAGCGTTTGTGTGCT---TATTA-AACTGACAAAGCTTCCCGTGTGAGGTAGCC--CTAATTGATTCCACAAAGCATCACTCAASAGGATGAGTGACACACATGATTGTGTGTGTG
droPer2	scaffold_3:3931037-3931174 -	dpe_2496	C-----G-----G-----GT---G-----G-----G-----G-----TAAATACTTCGAATTGGTTAAGCGTTTGTGTGCT---TATTA-AACTGACAAAGCTTCCCGTGTGAGGTAGCC--CTAATTGATTCCACAAAGCATCACTCAASAGGATGAGTGACACACATGACT--GTGTGTG
droAna3	scaffold_13340:3669042-3669160 -		G-----G-----G-----GT---GTG-----TGTG--GTGT-----GTG-----GTGA--TGA--GA---GCTGCTAAATACTTCGAATTGCTAAGCGTTTGTGTGAT---TATCA-AATTGACAAAGCTTAGCTGTGCTTGAGGTAGCC--AAGATTAATCTACAA-----G-----G-----
droBip1	scf7180000396712:683549-683665 +		A-----G-----G-----T-----CCGTGTGTCTGCT--GTGT--G-----GTGACCTCTGCTAAATACTTCGAATTGCTAAGCGTTTGTGTGAT---TATCG-AATTGACAAAGCTTAGCTGTGCTTGAGGTAGCC--AAGATGAATCTACA-----G-----G-----
droKik1	scf7180000302639:1624815-1624947 +		T-----G-----G-----GT---GTG-----TGC--GTG-----GCGGCTGTGCGCTCCTGTGTGT--GTTTGCTAAATACTTCGAATTGCTAAGCGTTTGTGTGCT---TATCA-AATTGACAACGCTTAGCTGTGCTTGAGGTAGCC--AAATTGTTTCAACAGAG-----G-----G-----
droPic1	scf7180000454055:1329879-1330008 -		T-----G-----G-----GT---GTG-----CGG-----GTG--GTG-----GTATG--GTG--G-----GTGCTTTGCTAAATACTTCGAATTGCTAAGCGTTTGTGTGCC--CATCA-AATTGACAACGCTTAGCTGTGCTTGAGGTAGCC--AAATTGATTCTACGAGC-----G-----G-----
droEle1	scf7180000491280:3121561-3121680 -		T-----G-----G-----GT---GTG-----CAGG--GTGT-----G-----GT--GTGTCTTTGCTAAATACTTCGAATTGCTAAGCGTTTGTGTGCTC--CATCA-AATTGACAAGCTTAGCTGTGCTTGAGGTAGCC--AAATTGATTCTACATGC-----G-----G-----
droRho1	scf7180000779501:512618-512746 +		T-----G-----G-----GT---GTG-----GTG--GTGTGTGTCTG--GTG--G-----CCT--GGGTCTTTGCTAAATACTTCGAATTGCTAAGCGTTTGTGTGCTC--CATCA-AATTGACAAAGCTTAGCTGTGCTTGAGGTAGCC--AAATTGTTTCAACA-----G-----G-----
droBial	scf7180000302136:2259480-2259591 -		T-----G-----G-----GT---G-----G-----G-----G-----TGT--G-----GT--ACT--TTTACTTTGCTAAATACTTCGAATTGAACCAAGCGTTTGTGTGCC--CATCA-AATTGACAACGCTTAGCTGTGCTTGAGGTAGCC--AAATCGTTTCAACATGC-----G-----G-----
droTak1	scf7180000415257:293365-293496 -		T-----G-----G-----GT---GTG-----TGTG--GTGTGTATCTCTGTGCTCTG-----T--GASTAGCTTTGCTAAATACTTCGAATTGCTAAGCGTTTGTGTGCC--CATCA-AATTGACAACGCTTAGCTGTGCTTGAGGTAGCC--AAATTGTTTCAACA-----G-----G-----
droEug1	scf7180000409798:1138208-1138315 +		T-----G-----G-----GT---G-----G-----G-----G-----GT--CCT--GTGTACTTTGCTAAATACTTCGAATTGGTTAAGCGTTTGTGTGCC--CATCA-AATTGACAACGCTTAGCTGTGCTTGAGGTAGCC--AAATTGTTTCAACA-----G-----G-----
dm3	chr3R:21413247-21413378 -	dme_166	T-----G-----G-----GT---G-----G-----G-----G-----G-----G-----GTATC--GTGTCTCTGTGC--CCT--GTGTCTTTGCTAAATACTTCGAATTGCTAAGCGTTTGTGTGCA--CATTA-AATTGACAACGCTTAGCTGTGCTTGAGGTAGCC--AACTGTTTCAACATGC-----G-----G-----
droSim2	3r:20925642-20925773 -	dsi_32434	T-----G-----G-----GT---G-----G-----G-----G-----G-----G-----GTATC--GTGTCTCTGTGC--CCT--GTGTCTTTGCTAAATACTTCGAATTGCTAAGCGTTTGTGTGCA--CATTA-AATTGACAACGCTTAGCTGTGCTTGAGGTAGCC--AACTGTTTCAACATGC-----G-----G-----
droSec2	scaffold_13:201192-201323 -	dse_150	T-----G-----G-----GT---G-----G-----G-----G-----G-----G-----GTATC--GTGTCTCTGTGC--CCT--GTGTCTTTGCTAAATACTTCGAATTGCTAAGCGTTTGTGTGCA--CATTA-AATTGACAACGCTTAGCTGTGCTTGAGGTAGCC--AACTGTTTCAACATGC-----G-----G-----
droYak3	3R:25065959-25066090 +	dya_69	T-----G-----G-----GT---G-----G-----G-----G-----G-----G-----GTATC--GTGTCTCTGTGC--CCT--GTGTCTTTGCTAAATACTTCGAATTGCTAAGCGTTTGTGTGCA--CATTA-AATTGACAACGCTTAGCTGTGCTTGAGGTAGCC--AACTGTTTCAACATGC-----G-----G-----
droEre2	scaffold_4820:6629168-6629304 ±		T-----G-----G-----GT---GTG-----GTG--GTGTGTGTATC--GTGTCTCTGTGC--CCT--GTGTCTTTGCTAAATACTTCGAATTGCTAAGCGTTTGTGTGCA--CATTA-AATTGACAACGCTTAGCTGTGCTTGAGGTAGCC--AACTGTTTCAACATGC-----G-----G-----

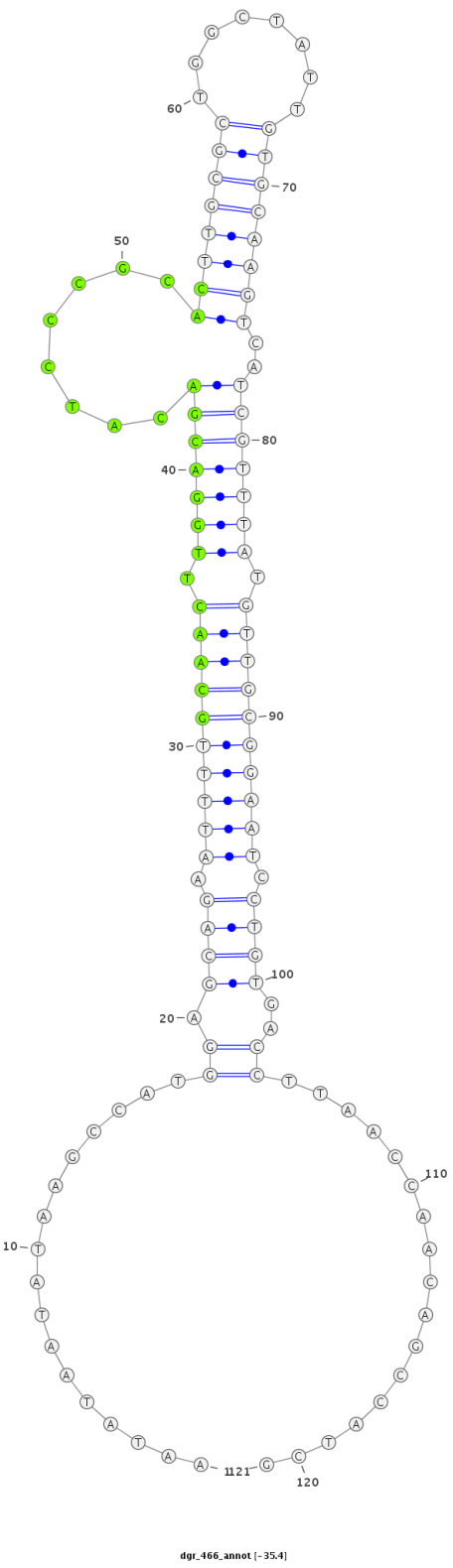
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	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	0
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	1
rescue.known	0
rescue.confident	1
rescue.candidate	8

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dgr_466	scaffold_15110:20857844-20857934 -	candidate	Canonical miRNA	intergenic	[View on UCSC Genome Browser (Cornell Mirror)]

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

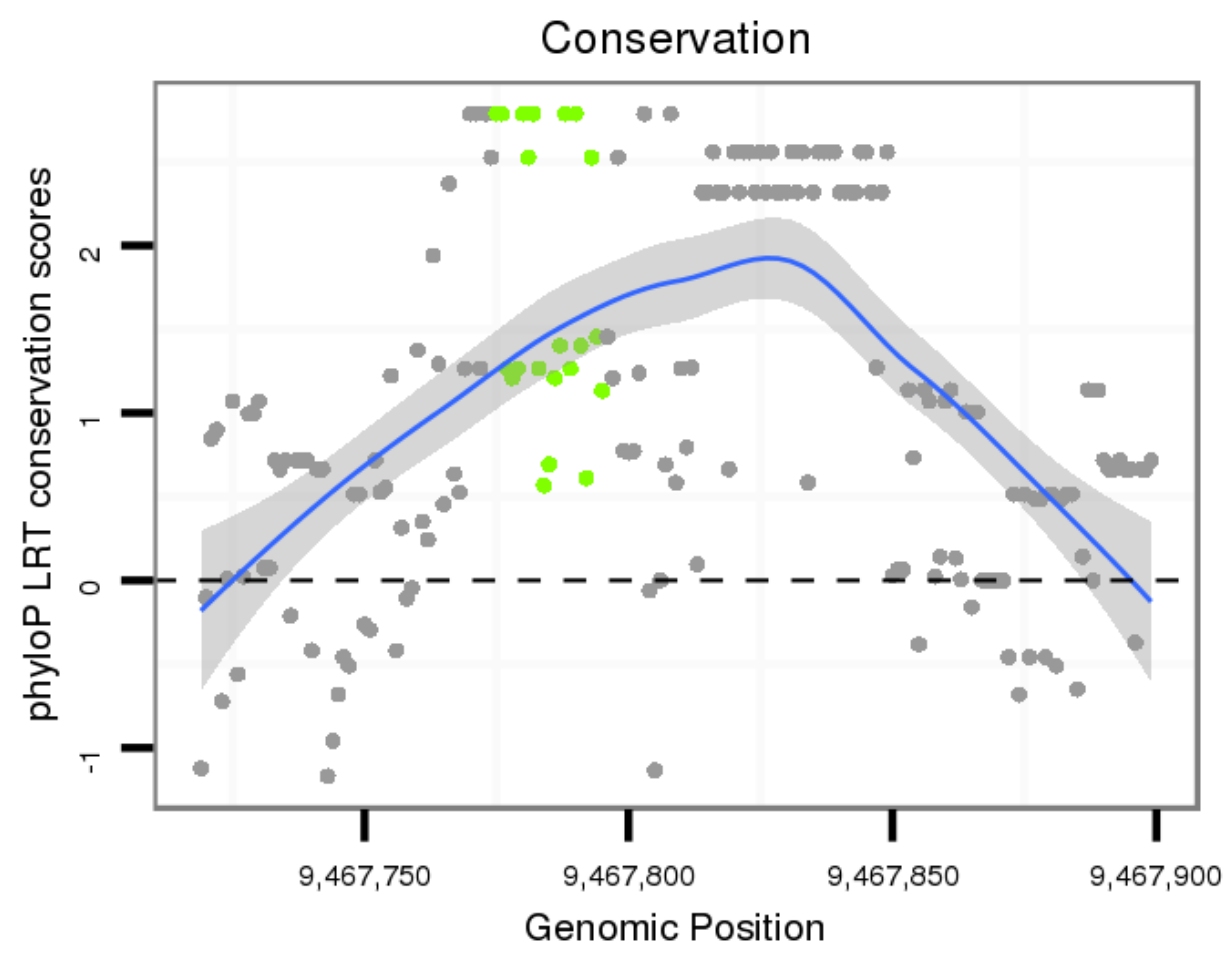
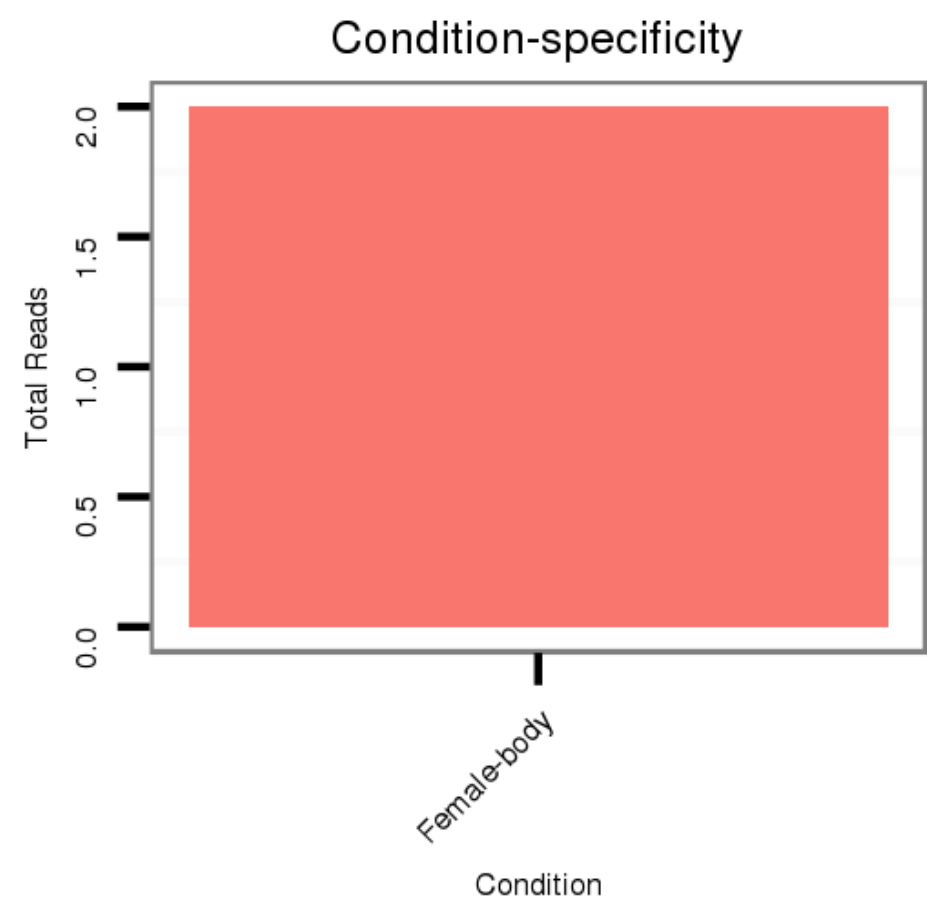
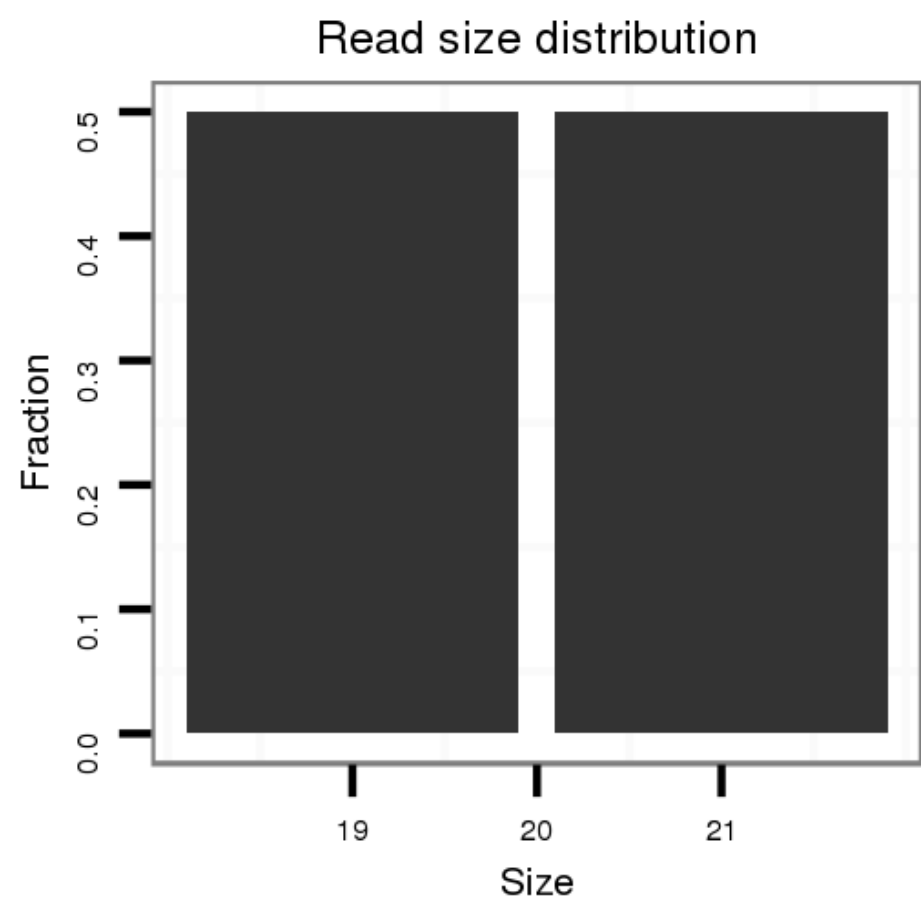
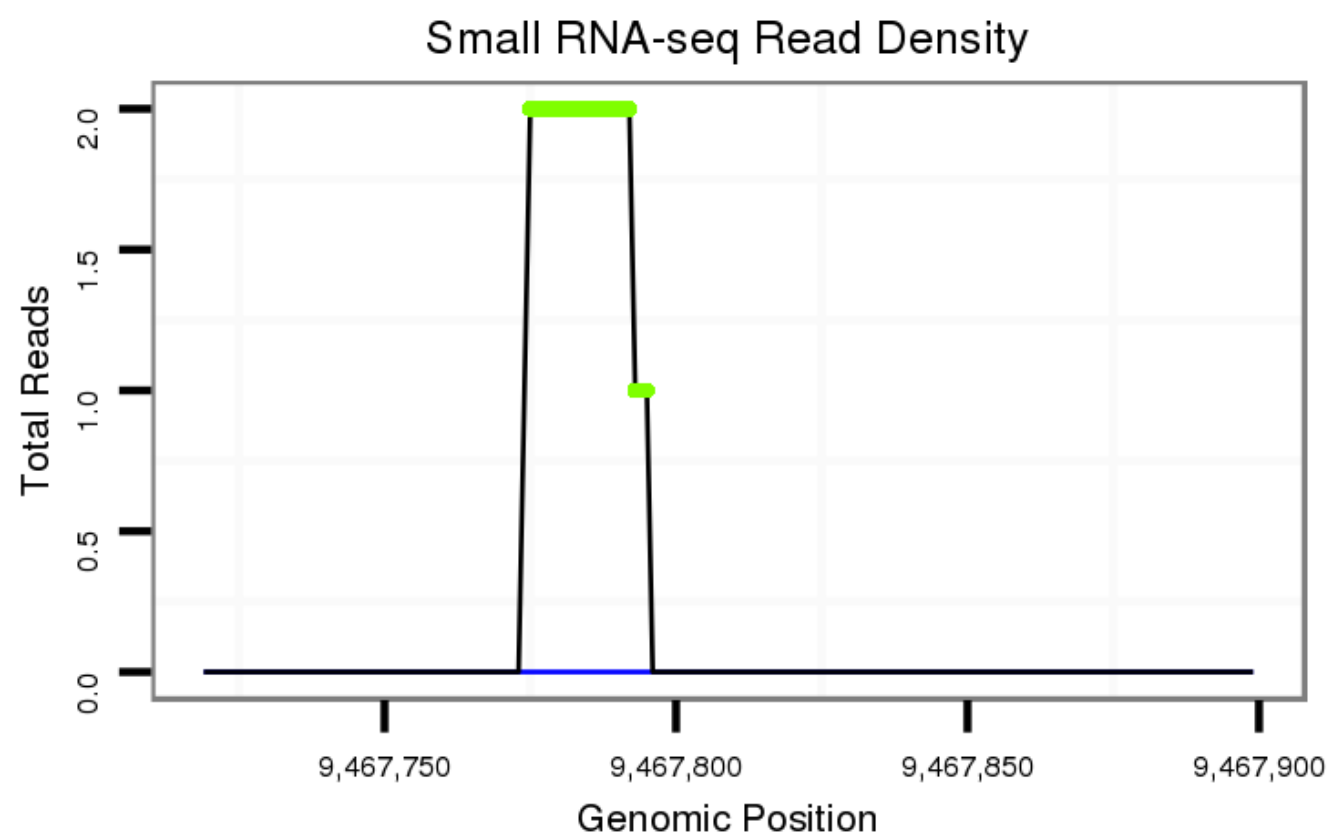
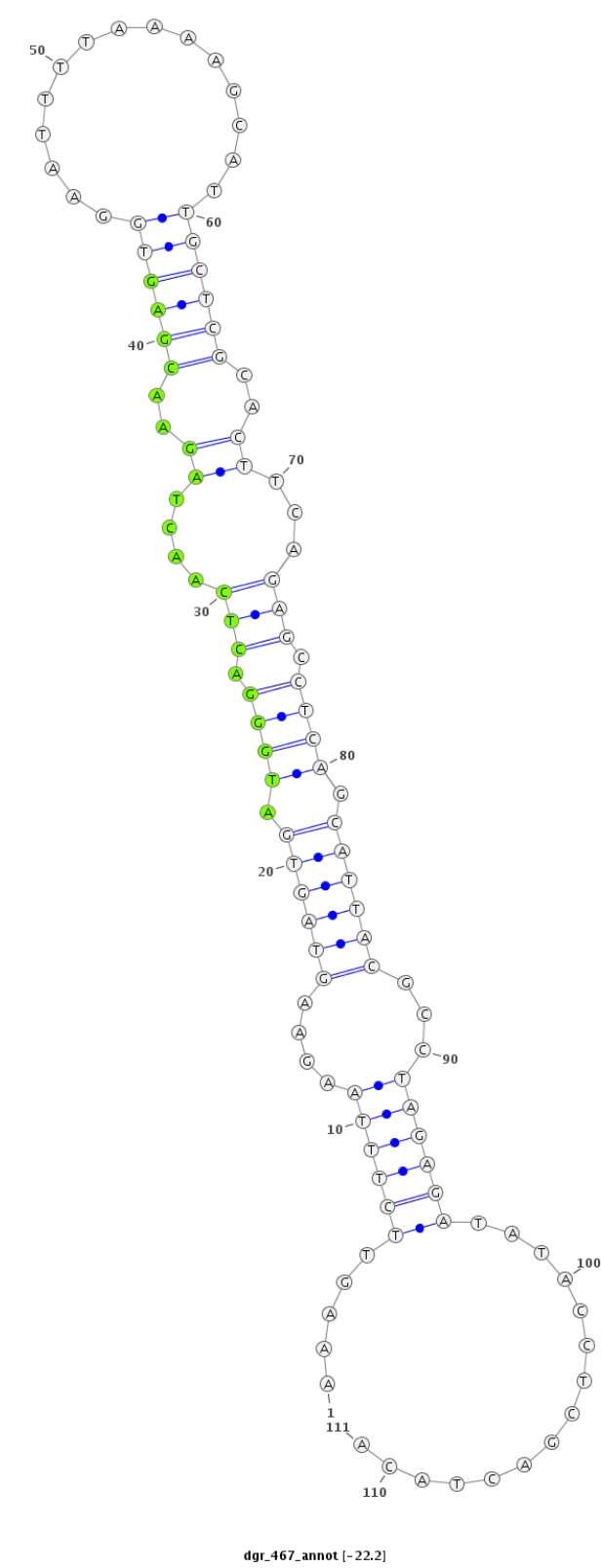
Predicted structure



ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dgr_467	scaffold_15203:9467769-9467849 +	candidate	Canonical miRNA	intron	[View on UCSC Genome Browser (Cornell Mirror)]

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Hairpin partition ● Sense ● Antisense ● Mature

Hairpin partition ● Mature

Show Alternate Folds

Flybase annnotation

intron [DgriGH12805-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

	Read #	Hit	Total		M041
	size	Mismatch	Count	Norm	body
GTCTAATCAGCTGCACAGTTTAGGCATTTATAAGAAAGTTCTTTAAGAAGTAGTCA ATGGGACTCAACTAGAACGAG TGGAATTTTAAAGCATTGCTCGCACTTCAGAGCCTCAGCATTACGCC-TAGAGATATACCTCGACTACAAACAAAATGTGCCCATGAT-----ATACAA-----GGTGGTG-----GT	21	0	1	1.00	1

.....ATGGGACTCAACTAGAACGAG.....	19	0	1	1.00	1
.....GATGGGACTCAACTAGAAC.....					

Anti-sense strand reads

	Read #	Hit	Total	
	size	Mismatch	Count	Norm
CAGATTAGTCGAGCTGTCAAATCCGTAAATATTCTTTCAAGAAATCTTCATCAC TACCCGTGAGTTGATCTTGCTC ACCTTAAATTTTCGTAACGAGCGTGAAGTCTCGGAGTCGTAATGCGGATCTCTATATGGAGCTGATGTTTGTTTTACAGGGTACTATATGTTCCACCACCA				

No data available in table				

Show Alignment With Reads

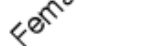
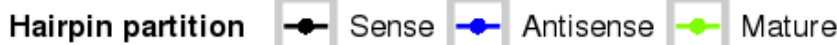
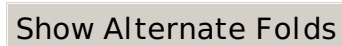
Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droGri2	scaffold_15203:9467719-9467899 +	dgr_467	GTCTAATCAGCTGCACAGTTTAGGCATTTAT-----AAGAA-----AGTTC---TTT---AAGAAGTAGTCA ATGGGACTCAACTAGAACGAG TGGAATTTTAAAGCATTGCTCGCACTTCAGAGCCTCAGCATTACGCC-TAGAGATATACCTCGACTACAAACAAAATGTGCCCATGAT-----ATACAA-----GGTGGTG-----GT
droVir3	scaffold_12970:5369069-5369255 -	dvi_24642	CACTGGTCAGCTGCACAA TTTGGTTCCAA TAT GGGTATACA --A-----AGC GTTC ---TTT---AAGAGTAGTGA ATGGGACTCA CTAGAACGAG TGGAAT TA TT--AAGCATTGCTCGCACTTCAGAGCCTCAGCATTACGCC-TAGAGAA ATA --TC AACTAC -----G TTTACCP AGAT CC TAG A TA AA -----GGTGG CCGTGCAG GT
droMoJ3	scaffold_6473:4951680-4951883 -	dmo_3154	TA---AT TC SCTGCACAA TTTAGGCA ----A-----CAGAA ACTGT TAAC CTTC ---TTT---AC AG CTAGTGA ATGGGACTCA CTAGAACGAG TGGAAT TA TT--TAGCATTGCTCGCACTTCAGAGCCTCAGCATTACGCC-TAGAGAA ATA --TC AACTAC -----G TTTACCP AGAT CC TAG A TA AA -----GGTGG CCGTGCAG GT
droWil2	scf2_1100000004511:3414745-3414817 -		CTCT TA TAGCTAT TC -----TGA-----T TA TAC---T TA ATAGCA TA T ATG AT ATAAGTCT AG ACA CT CTCT TT TC ---A ATT -----
dp5	XL_group3b:100284-100361 +	dps_110	-----
droPer2	scaffold_56:124089-124166 +	dpe_157	-----STAGTGA ATGGGACTC GT CTAGAACGAG CGGAATTT C ---AA CA ATTGCTCG- ACTTCAGAGCCTCA CATTACGCC -TAGAGA-----
droAna3	scaffold_13334:472175-472265 +	dan_4039	T-----STAGTGA ATGGGACTC GT CTAGAACGAG TGGAATTT T -GAGCAT C CTCG- ACTTCAGAGCCTCA CATTACGCC -TAGAGA-----
droBip1	scf7180000396431:1081275-1081358 -		-----AG CTG STAGTGA ATGGGACTC GT CTAGAACGAG TGGAATTT C -AAGCATTGCTCG- ACTTCAGAGCCTCA CATTACGCC -TAGAGA-----
droKik1	scf7180000302698:307852-307934 -		-----AG CTG STAGTGA ATGGGACTC GT CTAGAACGAG TGGAATTT A -AAGCAT C CTCG- ACTTCAGAGCCTCA CATTACGCC -TAGAGA-----
droFic1	scf7180000454073:1443039-1443126 +		T-----TAAGAG CTG STAGTGA ATGGGACTC GT CTAGAACGAG TGGAATTT C -AAGCAT C CTCG- ACTTCAGAGCCTCA CATTACGCC -TAGAGA-----
droEie1	scf7180000491044:215100-215199 +		CA-----A-----AG AC CTAAAT AGAG CTG STAGTGA ATGGGACTC GT CTAGAACGAG TGGAATTT C -AAGCATTGCTCG- ACTTCAGAGCCTCA CATTACGCC -TAG CGA -----
droRho1	scf7180000779510:38423-38522 +		CA-----A-----AG AC CTAAAT AGAG CTG STAGTGA ATGGGACTC GT CTAGAACGAG TGG CA TT TA -AAGCAT C CTCG- ACTTCAGAGCCTCA CATTACGCC -TAGAGA-----
droBia1	scf7180000302041:563722-563824 +		-----AG CTG STAGTGA ATGGGACTC GT CTAGAACGAG TGGAATTT C -AGC CGG CTCG- ACTTCAGAGCCTCAGCATTACGCC -TAGAGAA CCGACAT CG CT TTAG A -----T CA AA TA -----
droTak1	scf7180000414393:30874-30961 -		T-----TAAGAG CTG STAGTGA ATGGGACTC GT CTAGAACGAG TGGAATTT C -AAGC CTC CTCG- ACTTCAGAGCCTCA CATTACGCC -TAGAGA-----
droEug1	scf7180000408958:35983-36065 -		-----AG CTG STAGTGA ATGGGACTC GT CTAGAACGAG TGGAATTT C -AAGCAT C CTCG- ACTTCAGAGCCTCA CATTACGCC -TAGAGA-----
dm3	chrX:13553607-13553690 +		-----AG CTG STAGTGA ATGGGACTC GT CTAGAACTGAG TGGAATTT CA -AAGCAT C CTCG- ACTTCAGAGCCTCA CATTACGCC -TAGAGA-----
droSim1	X:12890326-12890408 -		-----AG CTG STAGTGA ATGGGACTC GT CTAGAACGAG TGGAATTT C -AAGCAT C CTCG- ACTTCAGAGCCTCA CATTACGCC -TAGAGA-----
droSec2	scaffold_20:193548-193630 +		-----AG CTG STAGTGA ATGGGACTC GT CTAGAACGAG TGGAATTT C -AAGCAT C CTCG- ACTTCAGAGCCTCA CATTACGCC -TAGAGA-----
droYak3	X:7836451-7836533 +		-----AG CTG STAGTGA ATGGGACTC GT CTAGAACGAG TGGAATTT C -AAGCAT C CTCG- ACTTCAGAGCCTCA CATTACGCC -TAGAGA-----
droEre2	scaffold_4690:13329706-13329788 -		-----AG CTG STAGTGA ATGGGACTC GT CTAGAACGAG TGGAATTT C -AAGCAT C CTCG- ACTTCAGAGCCTCA CATTACGCC -TAGAGA-----

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

Predicted structure



Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

[illegible]

Anti-sense strand reads

Re-alignment of all predicted orthologs

[illegible]

Generated: 09/08/2015 at 07:35 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	0
crit.uri	0
crit.back	0
rescue.total	0
rescue.dominant	1
rescue.known	0
rescue.confident	2
rescue.candidate	10