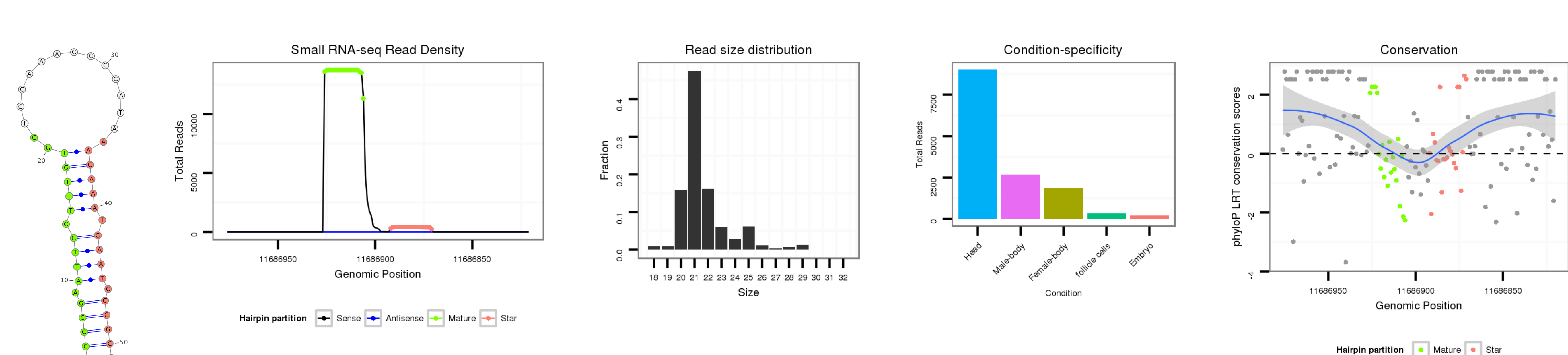


ID:	Coordinate:	Confidence:	Class:	Genomic Locale:
der_21	scaffold_4784:11686871-11686926 -	confident	Mirtron	intron
[View on UCSC Genome Browser [Cornell Mirror]]				

Legend: mature star mismatch in alignment mismatch in reac

Predicted structure



Flybase annotation

intron [Dere\GG13894-in]; CDS [Dere\GG13894-cds]; CDS [Dere\GG13894-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

[illegible]

Anti-sense strand reads

										M55	M57							
										female	embryo							
										body								
										body	embryo							
GACGGCCCTTGGCGCTGTAAACGAGTTCGACTGTCGCTGCGCGCCGCATTGCCTTAAGGAACACGAGGTTGGGGTATTGTTTACTTAAGGGCAAGTGGTCCCTTTGGTAGTGAGCACTGACGGAATCGCGGATTCGAAGCGCTTT										Read #	Hit	Total	Count	Norm	Total	1	0	
*****(((((((((((((((((((.....))))))))))))))*****										size	Mismatch					20	1	0
.....CTGTAAACGAGTTCGACTG.....																		

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droEw2	scaffold_4784:11686820-11686976	ser_21	CTGCCCGGAACCGACGACATTTCGCTCAAGCTGACAGACGACGGCGGCTAAAGCGAAAT-----T-----CCCTTT--GT--GCTCCAAACCCCATAT--ACAAAT-----GAA-----T--C--CGCCTTTGACGAGGGAACCATCACTCGTGACTGCTTAGCGCGCTAAGCTTCGCGAAG
droyaK3	311173885-11737011		CTGCCCGGAACCGACGACATTCGCTCAAGCTGACAGAGGACGCGGGCGTTAAGCGAA-----T-----T-----GT--GT--GCTCCAAACCCCATAT--ACAAAT-----GAA-----A--C--T--GCTTACGACGAGGGAACCATCACTCGTGACTGCTTAGCGCGCGAGCTTCGCGAAG
drosMe2	scaffold_6:3890154-3890310		CTGCCCGGAACCGACGACATTTCGCTCAAGCTGACAGAGGACGCGGGCGTTAAGCGAA-----A-----C-----GT--GT--GCTCCAAACCCCATAT--ACAAAT-----T-----A--C--T--GCTTACGAGGGAACCATCACTCGTGACTGCTTAGCGCGCGAGCTTCGCGAAG
drosMe2	3111411885-11412041		CTGCCCGGAACCGACGACATTTCGCTCAAGCTGACAGAGGACGCGGGCGTTAAGCGAA-----A-----C-----GT--GT--GCTCCAAACCCCATAT--ACAAAT-----T-----A--A--C--T--GCTTACGAGGGAACCATCACTCGTGACTGCTTAGCGCGCGAGCTTCGCGAAG
dm3	chr3b:11749001-11749157		CTGCCCGGAACCGACGACATTTCGCTCAAGCTGACAGAGGACGCGGGCGTTAAGCGAA-----T-----C-----GT--GT--GCTCCAAACCCCATAT--ACAAAT-----GAA-----A--C--T--GCTTACGAGGGAACCATCACTCGTGACTGCTTAGCGCGCGAGCTTCGCGAAG
droyu1	ncf178000040971:3579861-3580015		CTGCCCGGAACCGACGATTCGCTCAAGCTGACAGAGGACGCGGGCGTTAAGCGAA-----T-----C-----GT--GT--GCTCCAAACCCCATAT--ACAAAT-----GAA-----A--A--T--GCTTACGAGGGAACCATCACTCGTGACTGCTTAGCGCGCGAGCTTCGCGAAG
droyu1	ncf1780000402334:1478751-148029		CTGCCCGGAACCGACGACATTCGCTCAAGCTGACAGAGGACGCGGGCGTTAAGCGAA-----T-----T-----A--A--C--T--GCTTACGAGGGAACCATCACTCGTGACTGCTTAGCGCGCGAGCTTCGCGAAG
droyu1	ncf1780000414445:499052-49926		CTGCCCGGAACCGACGACATTCGCTCAAGCTGACAGAGGACGCGGGCGTTAAGCGAA-----GA-----T-----T-----A--T--A--T--GCTTACGAGGGAACCATCACTCGTGACTGCTTAGCGCGCGAGCTTCGCGAAG
droyu1	ncf1780000490993:2090492-2090655		CTGCCCGGAACCGACGACATTTCGCTCAAGCTGACAGAGGACGCGGGCGTTAAGCGAA-----T-----T-----G-----GT--GT--GCTCCAAACCCCATAT--ACAAAT-----T-----A--A--T--GCTTACGAGGGAACCATCACTCGTGACTGCTTAGCGCGCGAGCTTCGCGAAG
droyu1	ncf1780000767448:108021-108184		CTGCCCGGAACCGACGACATTTCGCTCAAGCTGACAGAGGACGCGGGCGTTAAGCGAA-----T-----T-----GT--GT--GCTCCAAACCCCATAT--ACAAAT-----T-----C--A--A--T--GCTTACGAGGGAACCATCACTCGTGACTGCTTAGCGCGCGAGCTTCGCGAAG
droyu1	ncf1780000454113:296197-296352		CTGCCCGGAACCGACGACATTCGCTCAAGCTGACAGAGGACGCGGGCGTTAAGCGAA-----T-----T-----G-----GT--GT--GCTCCAAACCCCATAT--ACAAAT-----T-----A--T--GCTTACGAGGGAACCATCACTCGTGACTGCTTAGCGCGCGAGCTTCGCGAAG
droyu1	ncf1780000302391:134212-134372		CTGCCCGGAACCGACGACATTCGCTCAAGCTGACAGAGGACGCGGGCGTTAAGCGAA-----T-----T-----G-----GT--GT--GCTCCAAACCCCATAT--ACAAAT-----T-----A--T--GCTTACGAGGGAACCATCACTCGTGACTGCTTAGCGCGCGAGCTTCGCGAAG
droyu1	ncf1780000413337:5968163-5968330		CTGCCCGGAACCGACGACATTCGCTCAAGCTGACAGAGGACGCGGGCGTTAAGCGAA-----T-----T-----G-----GT--GT--GCTCCAAACCCCATAT--ACAAAT-----T-----A--T--GCTTACGAGGGAACCATCACTCGTGACTGCTTAGCGCGCGAGCTTCGCGAAG
droyu1	ncf178000039518:31029-31196		CTGCCCGGAACCGACGACATTCGCTCAAGCTGACAGAGGACGCGGGCGTTAAGCGAA-----T-----T-----G-----GT--GT--GCTCCAAACCCCATAT--ACAAAT-----T-----A--T--GCTTACGAGGGAACCATCACTCGTGACTGCTTAGCGCGCGAGCTTCGCGAAG
dp5	XB_group6:9988715-9988875		CTGCCCGGAACCGACGACATTCGCTCAAGCTGACAGAGGACGCGGGCGTTAAGCGAA-----T-----T-----G-----GT--GT--GCTCCAAACCCCATAT--ACAAAT-----T-----A--T--GCTTACGAGGGAACCATCACTCGTGACTGCTTAGCGCGCGAGCTTCGCGAAG
droyu2	scaffold_61:269142-269302		CTGCCCGGAACCGACGACATTCGCTCAAGCTGACAGAGGACGCGGGCGTTAAGCGAA-----T-----T-----G-----GT--GT--GCTCCAAACCCCATAT--ACAAAT-----T-----A--T--GCTTACGAGGGAACCATCACTCGTGACTGCTTAGCGCGCGAGCTTCGCGAAG
droyu2	scf2_1100000004762:2640734-2640894		CTGCCCGGAACCGACGACATTCGCTCAAGCTGACAGAGGACGCGGGCGTTAAGCGAA-----T-----T-----G-----GT--GT--GCTCCAAACCCCATAT--ACAAAT-----T-----A--T--GCTTACGAGGGAACCATCACTCGTGACTGCTTAGCGCGCGAGCTTCGCGAAG
droyu2	scaffold_13049:23921073-23921173		CTGCCCGGAACCGACGACATTCGCTCAAGCTGACAGAGGACGCGGGCGTTAAGCGAA-----T-----T-----G-----GT--GT--GCTCCAAACCCCATAT--ACAAAT-----T-----A--T--GCTTACGAGGGAACCATCACTCGTGACTGCTTAGCGCGCGAGCTTCGCGAAG
droyu2	scaffold_6680:18548545-18548645		CTGCCCGGAACCGACGACATTCGCTCAAGCTGACAGAGGACGCGGGCGTTAAGCGAA-----T-----T-----G-----GT--GT--GCTCCAAACCCCATAT--ACAAAT-----T-----A--T--GCTTACGAGGGAACCATCACTCGTGACTGCTTAGCGCGCGAGCTTCGCGAAG
droyu2	scaffold_15110:9761190-9761290		CTGCCCGGAACCGACGACATTCGCTCAAGCTGACAGAGGACGCGGGCGTTAAGCGAA-----T-----T-----G-----GT--GT--GCTCCAAACCCCATAT--ACAAAT-----T-----A--T--GCTTACGAGGGAACCATCACTCGTGACTGCTTAGCGCGCGAGCTTCGCGAAG

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

Legend: mature star mismatch in alignment mismatch in read

Flybase annotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

Anti-sense strand reShow Alignment With Reads

Re-alignment of all predicted orthologs

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

Legend: mature star mismatch in alignment mismatch in read

Predicted structure

hide 3p reads | show mid mismatch reads

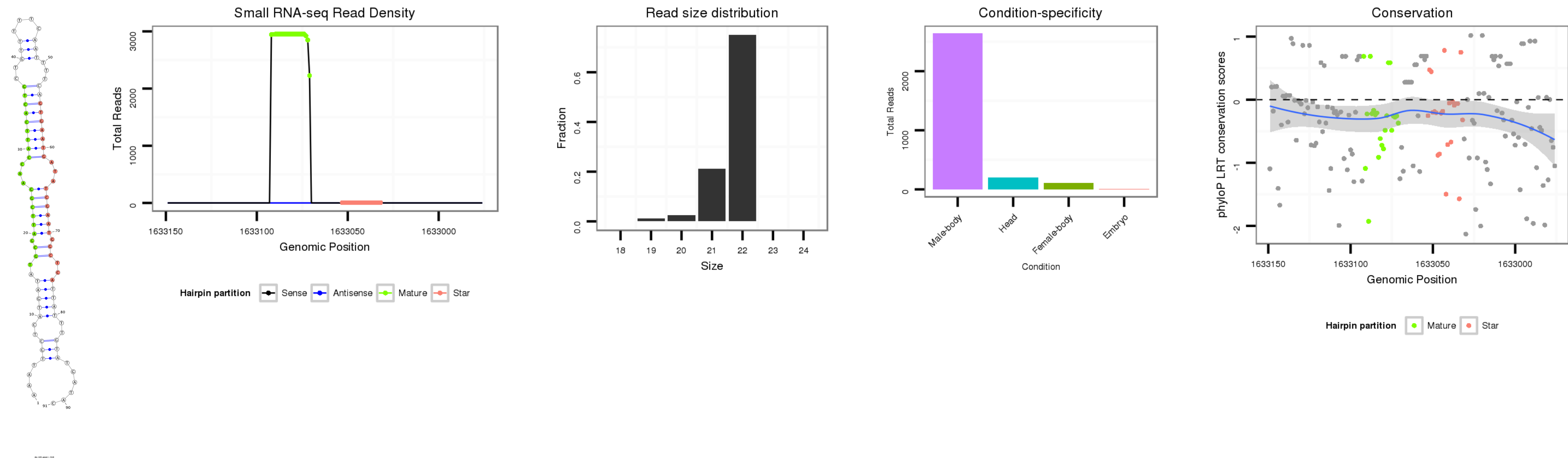
Anti-sense strand reads

Species	Coordinate	ID	Alignment
droEr2	scaffold_4690:9672310-9672467 +	der_34	ATC-----CGGCAAGTGAATACCAGT-ACTATACTGTAT-----CTATACTTTTTAAAC ATCTTATTTCGGTCGGCTTCTGCA AAG-----TTTTTATT GCAGCGTGTCAAATGAGAAAG TTTGAAGAGCGATTACAATCAACACCCAAAATATCA-----TATGTTTAAACTTT-
droYec2	k:11901500-11901684 -	dya_37	AT SCATAGCCAAAATGAATAAACAC CAAGTC CATACATATACAA ----- AACATAAA GC ACTTTTAAAC CTTCTTATTTCGGTCGGCTTCTGCAAAACAT -----TTTTTATT GCAGCGTGTCAAATGAGAAAG TTTGAAGAGCGATT CACAATCAACACCA GA AAAAATATC----- ACAT TTATGTTTAAACTTT C
droSec2	scaffold_817171185-1717322 +		ATC----- AGA CAAGCTT ATACATTTTG CACATAA GC ACTTTTAAAC CTTCTTATTTCGGTACGCTTCTGCAAA ----- ATGAGAAAGCG ATTGAAGAGGAT CACAATCAACACCCAA ATATGC ----- TTATT TATGTTT CGACT GA -
droSim2	k:18324514-18324662 +		ATC----- AGA CAAGCTT ATACATTTT ACTATAT TTACTAA GC ACTTT CTTCTTATTTCGGTACGCTTCTGCAAA ----- ATGAGAAAGCG TTTAAAG GC AT CACAATCAACAA GCCAA ATATGC ----- AAAT TATGTTT CACT GA -
dm3	chrX:19435279-19435297 +		TAC ----- ATA CAAA TT TAAT GC ----- CACTTT CTA AT TT CTC ATTTC GGCCGC CCTAGCAAA CTATTCCAGCCTTTTCCCTTCACAGC ATTT TATT GCACGTCG CA TATGAGAA AT TTTGAAGAG TCTAAGGCC CAAC AG CT AAAA T ATC GAAATGTC CA TTT TC ACTTT-
droTak1	scf7180000415526:14268-14426 +		T ----- CACTTT CTA AT TT CTC ATTTC GGCCGC CCTAGCAAA CTATTCCAGCCTTTTCCCTTCACAGC ATTT TATT GCACGTCG CA TATGAGAA AT TTTGAAGAG TCTAAGGCC CAAC AG CT AAAA T ATC GAAATGTC CA TTT TC ACTTT-

	PASS/FAIL
crit.star	1
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	0
rescue.dominant	0
rescue.known	0
rescue.confident	2
rescue.candidate	0

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Show Alternate Folds

Flybase annotation

Antisense to intron [Dere\GG18704-in]; utr3 [utr3_minus_9916]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

[illegible]

Anti-sense strand reads

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

Predicted structure

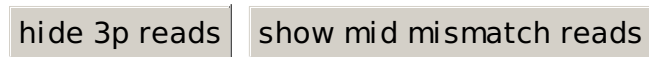
Show Alternate Folds

Flybase annotation

Antisense to intron [Dere\GG24636-in]

Repeatable elements

Sense Strand Reads



Anti-sense strand reads

[illegible]

Show Alignment With Reads

Re-alignment of all predicted orthologs

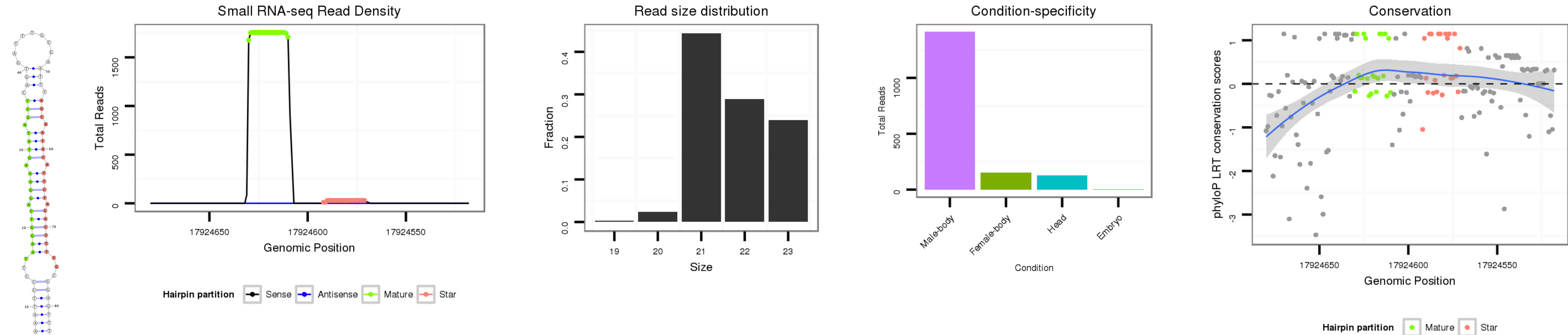
Species	Coordinate	ID	Alignment
droEre2	scf4allid_4929:644212-644367 +	der_50	AAA-AAAATA-----ATTAAAGGGAGAGAAGCACCCCG--CTTGCGTGCATGTATGTATGTATGTATGTGCGACGTGGCAATTTGCATGGACGTCGTACATACAACATACATAACTG-----CATGTGGAGC---ACCATTTT--TTGTAC---ACTTCTT-----GTGTTTTTTTTT
droYak3	ZL576928-577083 +		AACAAAAATC-----GTTCAAGGGGAAAGGACCCG--CTTGCA-----STATGTATGTATGTATGCGGACGTGGCAATTTGCGTGGACGTCGTACATACAACATACATACATATT-----GATGTCAGCG---GCCATTTTGCTTCTGCG--AG--CTTATT-----GTGT-----TTTTT
droSec2	chr12_14:571074-571218 +		AT-----ATG-----ATTAAAGGAAANAAGGACCCG--CTTGCA-----STATGTATGTATGTATGCGGACGTGGCAATTTGCATGGACGTCGTACATACAACATACATACAT-----GCGATGTCAGCG---GCCATTTTGCTTCTGCGTAC-----CTCTCTATTGGAAT-----GTGTTTATTTTTT
droSim2	ZL562354-562525 +		GAG-ATAATACTACTGTATAAAGGGAANAAGGACCCG--CGATT-----STATGTATGTATGTATGCGGACGTGGCAATTTGCATGGACGTCGTACATACAACATACATATAACAT-----AAATATAAATG---GCCATTGATCTCTGCG--CCTTCTATTGGAAT-----GTGTTT-----TTTTT
dm3	chr2L:588475-588629 +		AT-----ATG-----ATTAAAGGAAANAAGGACCCG--CTTGCA-----STATGTATGTATGTATGCGGACGTGGCAATTTGCATGGACGTCGTACATACAACATACATATAATGTATGTGAAGTGATATAAGCG---GAG-----GCTCTATTGGAAT-----GTGTTTATTTTTT
droTak1	scf7180000415856:190547-190552 -		AGT-AAAATG-----GTT-----TGATGTGTCGCGCGTGGCACTTTGCATGCT-----TAAATGATACATACATACATAC-----ATAT-----GTCAACCGCT-----TTTGTACG--GTCTCTATTGCAAAATGTCAATAAACTGTGTTATTTTA
droEle1	scf1800000491026:218418-218562 -		AA-ATGCGCTTTTTCAA-CAAGAGAAANAAGGACGAGAA--TGTCAT-----ATATGTATGCTGTGCGTGTGACCTTTCGCGCTCAAGGATGAGATGATACATACATACATACATCCCT-----GC-----AGCG---GACATTTT-----TTTATT-----TGTATT-----TGTGCTTTT
droRho1	scf7180000779917:483399-48543 -		ACA-ATATATC-----CCCTTAACTGGAAANAAGGACAAAATGDTCAACA-ATAATGTCACATATCACTGTAACCTCTGTGCTCCCTTTGACG-ATATGACACATGCAACATAC-----ATG-----ATATATCCGCG---GCCATGTT--TTGTGCTTGA-----ATTCTTAT

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

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Show Alternate Folds

Flybase annotation

Antisense to intron [Dere\GG19734-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

Anti-sense strand reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droErE2	scaffold_4690:17924518-17924680	der_47	CGTGGCTGAG-AATTA-TTGCCCTGGAACCTC-----GAG--AT--TGGTTGTGAA--ATTCCCTTAAGGTCAGGAAGTATAGCTCAGTGATT-TGCGAATTTAGCAATACATTCTAGACCTTTGCGAGTTTTTCAAAGGTCTTCCGTGAAAGTGTTCTG-----CTTGTTTTTGTGA-----ATCT
droYak3	X120580787-20580919	dya_40	CGCGGCTAAGAAACCA-----G-----GAG-GT-CTTTGTGAAATTATCCCTTAAGGTCAGAAATTATATAGCTTAGTGTCGCTTTACAAATTTGCAATACATTTAAGACCTTA-GCGGAGTTTTCACATGCTCTCCCAAAAGTGTT
droSeo2	scaffold_8:3725289-3725964	dse_127	CAGACTACAGTAATPAA-TTGAGTTGAGCTCTC-----GAG-TTTTTGTGTGAACTATTCCCTCAGGCTGTAAAGAGTAGAGCTCAGTAATTTACAAATTTGCAATGCATTCTAGACCTGTGCGGAGTTTATTACAGCTCTCCCAAAAGTGTTTGTGTTTTGTGCTTT-----GAAAGCATTAGT
droSim2	X120141512-20141675	dsi_6	CGAGCTACTAGTAATPAA-TTGAGTTGAGCTC-----GAG-TTTTTGTGTGAACTATTCCCTCAGGCTGTAAAGAGTAGAGCTCAGTAATTTACAAATTTGCAATGCATTCTAGACCTGTGCGGAGTTTATTACAGCTCTCCCAAAAGTGTTTGTGTTTTGTGCTTT-----GAAAGCATTAGT
dm3	chrX:21443073-21443238	dme_444	ATGCTAATATGAATCT-----GGAAATAATAGAAAGGAAAGAAAT--GAAATGA--T-----TAAATAAGGAAAGTAGAGCTCAGTAATTTACAAATTTGCAATGCATTCTAGACCTGTGCGGAGTTTATTACAGCTCTCCCAAAAGTGTTTGTGTTTTGTGTTT-----GA-----TAAGT
droRu1	scaf7180000408193:45614-45752		CCATCAAGTAATCTATTAACTTACAGTTT-----CAT-TTCAATTTGTGA-GATATTTCTAAGGCTGTAAAGTAGATAGCTCAGTAATTTAAGAAATTTCTGCAATACATTCTAGACCTTTTGAAGAGCTTTCACATTGTGTCTCC
droTak1	scaf7180000415763:353398-353498		GTCGCTAAGAAATPAA-AATA-----T-TT-TCTTTGTGAACTTTTCTTAAGGCTGTGGAAGTAGATAGCTAAGTGATTTAATAATTTCTGCAATGCATTCTAGACCTTT-----GAAAGCATTAGT
droEle1	scaf7180000491087:1001992-1002115		TTTSAAGAGAACTTTTAAATTTGTGTAA-----AAG-AT-TTTGTGAAATTTTCTTAAGGCTGTGAAGTATACCTTAGTGATTTAATAAGCTCGCAATATTCTAGACCTTT-----AAAGTGTTT-----
droRho1	scaf7180000774347:138-264		TGTCGAAGCAATPAA-TTTCTTTGGGCTTT-----AAG-T-TTTGTGAAATTTTCTTAAGGCTGTGAAGTAGATATCAATATATTAAATAATTTGCTATMTTTTAAGACCTTTTCAAAAGCTTTTA
droFic1	scaf7180000453926:397666-397783		TGTGGGAGCAATCTCC-TCGAAGTAGATTA-----AGCCGCAAG--GT-GTCGTGTATATTTTCTTAAGGCTGTGAAGTAGATAGCAACGCATTTAAACGCTCTGCAATACATTCTAGACCTTT-----GAAAGCATTAGT

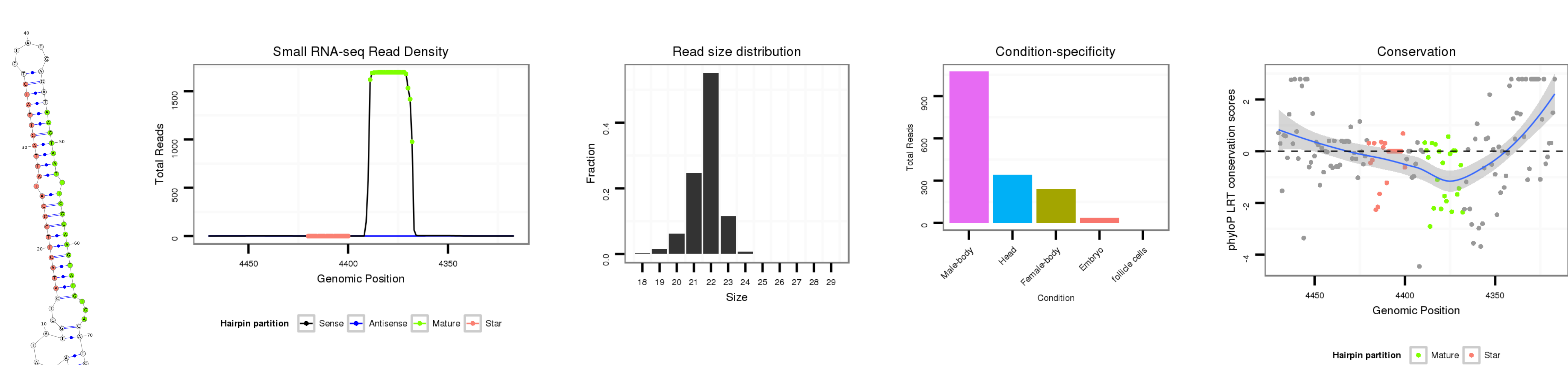
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	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	4
rescue.candidate	0

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
der_210	scaffold_1361:4367-4420 -	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

Repeatable elements

Name	Class	Family	Strand
IDEFIX I-int	LTR	Gypsy	

mature	star
1. der_210_scaffold_13614400-4420	
2. scaffold_2704-9047-9067+	
3. scaffold_3067-5076-5096	
4. scaffold_3146-3529-3549+	
5. scaffold_3264-3989-4009	
6. scaffold_4709-16154-16174+	
7. scaffold_4794-2407328-24402348	
8. scaffold_4794-2407329-25307289	
9. scaffold_4845-3796-379646+	
10. scaffold_4913-3741-3761+	

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

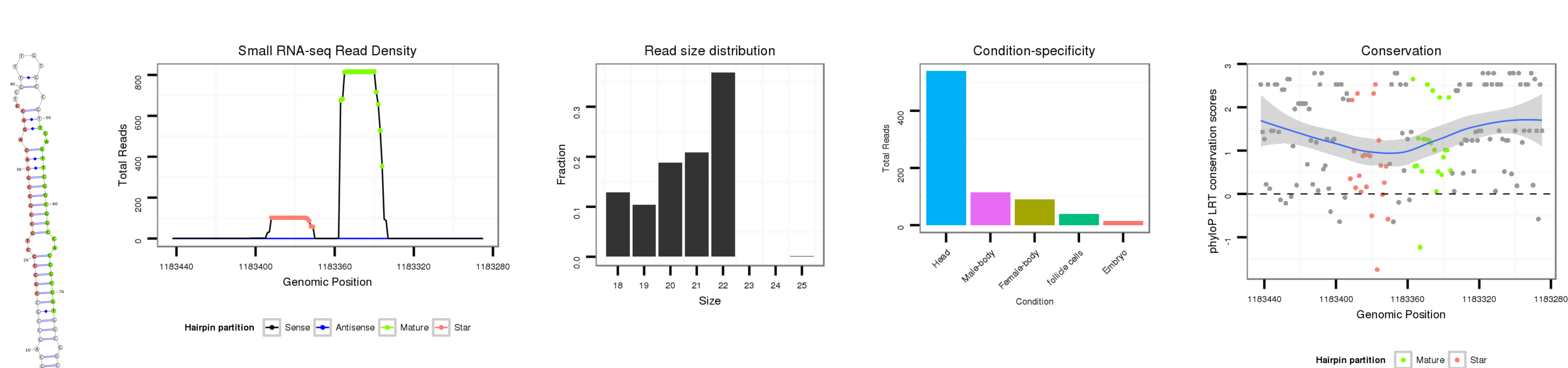
Species	Coordinate	ID	Alignment
droEre2	scafold1361:4317-4470	der_210	GTAGGTTTACTTCAAAATTTACTTCATTGCACATGGTG-----ACATATGGCTGACTTC--CCATATAACTATTGTAT--GA-GAT--AAGTAA-TTTG--GGAAGATGTCATCGCTT-A--ACTCTCTGGCTGGTC--TGG-----AATT--ATTGTATTACTTTTAAT--
droYak3	v2_chbtrn_5527:8492-8623		A-TGGTTTACTTCTATG-GGT-GA-TTAACTGGTG-----AAGGGGTAGTCGA-A-TA-----G-C-G-A--G-A-TG-C-ACCT--CGCT-ACCT-GTGGTC--TGG-----AATT--ATTGTATTACTTTTAAT--
droSec2	scafold1084:9787-9918		A-TGGTTTACTTCTATG-GGTGCA-TA-TGCTGGTG-----AATATGATGTCGA-A-TA-----G-C-G-ACCT--CGCT-ACCT-GTGGTC--TGG-----AATT--ATTGTATTACTTTTAAT--
droSim2	node_15741:508-639		A-TGGTTTACTTCAAAAT--GGTGGCA-TA-TA-TGGTG-----AATATGATGTCGA-A-TA-----G-C-G-ACCT--CGCT-ACCT-GTGGTC--TGG-----AATT--ATTGTATTACTTTTAAT--
dm3	chr01:1506065-1506193		A-TGGTTTACTTCTATG-GGTGCA-TA-TA-TGGTG-----AAGGGGTAGTCGA-A-TA-----G-C-G-ACCT--CGCT-ACCT-GTGGTC--TGG-----AATT--ATTGTATTACTTTTAAT--
droEug1	acf7180000407429:5128-5256		A-GCGGTTTATGCTACG-TCG-C-----GTGATG--ATTGCTGC-----TA-CT--GGATTA--CAAG--TG-T-AC--T-GTATG-TGGCTCTTTT--TTCTCT-CAGA-GCTG--TCG-----GATT--ATTGTATTACTTTTAAT--
droBla1	acf7180000302222:2691-2825		A-TAGGTTTATGCTAATG-TCG-C-----GATGTC--ATTGCTAC--TTGGCTA-----TAACAATAGAGACCT--TGGT-C-----ATTGGC-CGGT-GTGTGCGTGGC--TCG-----GATTAT-ATTGTATTACTTTTAAT--
droTak1	acf7180000415049:9611-9761	AA	A-GCGGTTTATGCTAATG-TCGCGC-----GATGTC--ATTGCTAC--GATTATAGAGTAC--TG-T-G-T--CATTAAGTTGTGTTGGG-CGGT--TGTCTCGGTC--TCG-----AATTATG-ATTGTATTACTTTTAAT--
droEle1	acf7180000489511:1311-1449		A-TAGGTTTATGCTAATG-TCG-C-----GATGTC--ATTGCTAC--TCAATA-----TAATTATC-A-G-SAG-TA-TA--AAO-ATTGTGCTCTT--GTGTCG-CCG-GTGTCGCGTCC--TCG-----AATT--ATTGTATTACTTTTAAT--
droRho1	acf7180000773232:398-539		A-TGGTTTATGCTAATG-TCG-C-----GATGTC--ATTGCTAC--TGTGATA-----TATGAAAAAAG--AC-G-TG-TCA-ATTGTGTTGTC--TCTGTGCTTTT--GTGTCG-CCG-GTGTCGCGTCC--TCG-----AATT--ATTGTATTACTTTTAAT--
droFic1	acf7180000430686:3975-4118		A-TGGTTTATGCTAATG-TCGCTC-----TTTGCGC--ATTGGAATGAAG--TTGGCTA-----TATTGAATCAATAG--ACG-CAA-T-A--TAG-GTTC-TTCACT-CAG-CGCTCTCGGTGTGTC--TCG-----AATT--ATTGTATTACTTTTAAT--
droKkl1	acf718000288521:1632-1760		A-GCGGTTTATGCTACG-TCGCGC-----TTTGACG--ATTGGAATCAAG--TTGACCA-----CATATGATCATGG--TCAATGACAC--TATTC--GGAAGTA-TA-C--GGT-TA--CATCTCTCGGTGTGTC--TCG-----ACG--ATT--ATTGTATTACTTTTAAT--
droAna3	scafold691:831-963		A-TGGTTTATGCTACG-TCGCGC-----TTCAGCG--CATATATATAGAC--ATAATA-----TAGTTATTATAT--AA-G-TA-TA--TTATCT--GGG-TA--TCTCGTGGAGTA--TCG-----AATT--ATTGTATTACTTTTAAT--
droBpl1	acf7180000385855:8913-9053		A-TGGTTTATGCTACG-TCGCGC-----TTCAGCG--CATATATATAGAC--ATAATA-----TAGTTATTATAT--AA-G-TA-TA--TTATCT--GGG-TA--TCTCGTGGAGTA--TCG-----AATT--ATTGTATTACTTTTAAT--
dp5	Unknown_singleton_1458:11146-11285		CA-TAGTTTATGCTACG-TGGGCG-----CTGTGCG--ATTGGAATGTAAG-----TTATGA--GGAAGTAGAGGAT--CAA-TA-T-G-T--TTG-ACG-CGCCGCTC-TA--ACT-CG-CGCTGTC--TCG-----AATT--ATTGTATTACTTTTAAT--
droPer2	scafold9123:271-411		AA-TAGATTATGCTACG-TGGGCG-----CTGTGCG--ATTGGAATGTAAG-----TTATGA--GGAAGTAGAGGAT--CAA-TA-T-G-T--TTG-ACG-CGCCGCTC-TA--ACT-CG-CGCTGTC--TCG-----AATT--ATTGTATTACTTTTAAT--
droW12	acg2_1100000004932:56224-56351		CGCTCTTTTC-GGTTTATGCTACG-TGGGCG-----CTGTGCG--ATTGGAATGTAAG-----TTATGA--GGAAGTAGAGGAT--CAA-TA-T-G-T--TTG-ACG-CGCCGCTC-TA--ACT-CG-CGCTGTC--TCG-----AATT--ATTGTATTACTTTTAAT--
droVir3	scafold4701:719-859		A-TAGATTATGCTACG-TGGGCG-----CTGTGCG--ATTGGAATGTAAG-----TTATGA--GGAAGTAGAGGAT--CAA-TA-T-G-T--TTG-ACG-CGCCGCTC-TA--ACT-CG-CGCTGTC--TCG-----AATT--ATTGTATTACTTTTAAT--
droMo3	scafold1774:724-829		A-TGGTTTATGCTACG-TGGGCG-----CTGTGCG--ATTGGAATGTAAG-----TTATGA--GGAAGTAGAGGAT--CAA-TA-T-G-T--TTG-ACG-CGCCGCTC-TA--ACT-CG-CGCTGTC--TCG-----AATT--ATTGTATTACTTTTAAT--
droGe12	scafold15124:75070-75201		A-TGGTTTATGCTACG-TGGGCG-----CTGTGCG--ATTGGAATGTAAG-----TTATGA--GGAAGTAGAGGAT--CAA-TA-T-G-T--TTG-ACG-CGCCGCTC-TA--ACT-CG-CGCTGTC--TCG-----AATT--ATTGTATTACTTTTAAT--

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ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
der_59	scaffold_4770:1183335-1183392 -	confident	Canonical miRNA	CDS	[View on UCSC Genome Browser (Cornell Mirror)]

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Show Alternate Folds

Flybase annnotation
CDS [Dere\GG11222-cds]

Repeatable elements

Name	Class	Family	Strand
Gypsy8-I_Dpse-int	LTR	Gypsy	-

Sense Strand Reads

hide 3p reads | show mid mismatch reads

[illegible]

Anti-sense strand reads

[illegible]

Re-alignment of all predicted orthologs

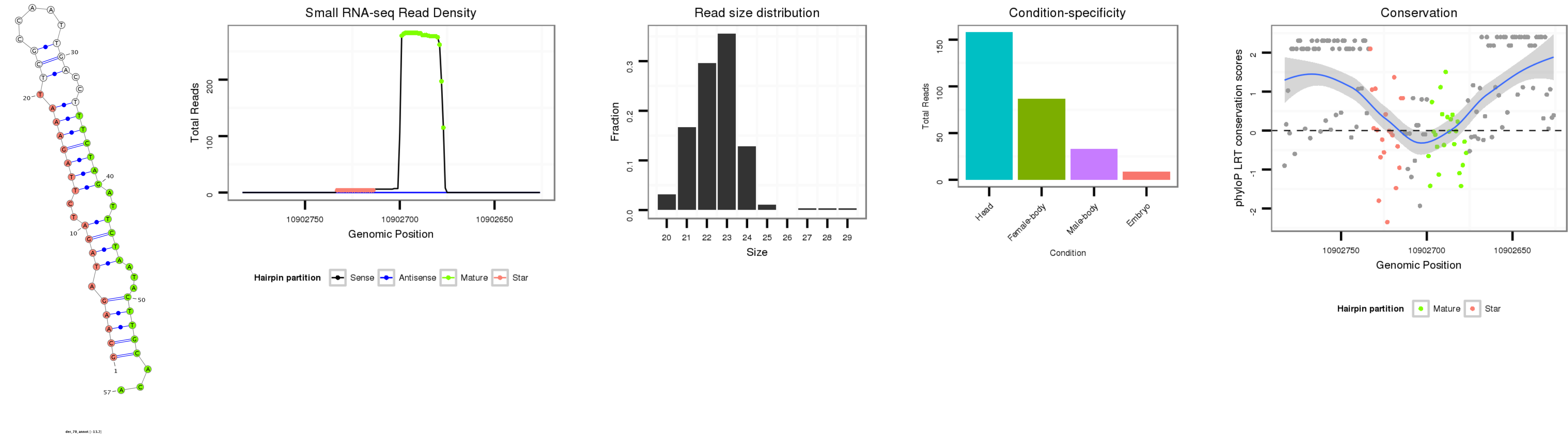
Accession	Coordinate	ID	Alignment
dRoEre2	scaf102_4770:1183285-1183442	der_59	CAGC--GGATGACCCCTACGCG-----GGGGCGCGCTGCTCAACTTGGACGCCGC GGCGCGTGCCGCGC -----GAC-----AGAGC--TCGTTTGTGCCCT TCAGTTCGCGGGCACACGC -----GG GG GGCG-----CCAGGCCACATTCCAGCAC--TGCC-----GCAGATCTCTGCTACACGT
dRoYak3	3R:1255641-1255798	dya_1786	CAGC--GGATGACCCCTACGCG-----GGGGCGCGCTGCTCAACTTGGACGCCGC GGCGCGTGCCGCGC -----GAC-----AGAGC--TCGTTTGTGCCCT TCACACGCGGGCACACGC -----GG GG GGCG-----CCAGGCCACATTCCAGCAC--TGCC-----GCAGATCTCTGCTACAC GT
dRoSeo2	scaf102_6:103361-1033768	dse_1834	CAGC--GGATGACCCCTACGCG-----GGGGCGCGCTGCTCAACTTGGACGCCGC GGCGCGTGCCGCGC -----CG-----AGAGC--TCGTTTGTGCCCT TCAGTTCGCGGGCACACGC -----GG GG GGCG-----CCAGGCCACATTCCAGCAC--TGCC-----GCAGATCTCTGCTACACGT
dRoSm12	3R:17596-817753	dsl_32437	CAGC--GGATGACCCCTACGCG-----GGGGCGCGCTGCTCAACTTGGACGCCGC GGCGCGTGTCGCGC -----CG-----AGAGC--TCGTTTGTGCCCT TCAGTTCGCGGGCACACGC -----GG GG GGCG-----CCAGGCCACATTCCAGCAC--TGCC-----GCAGATCTCTGCTACACGT
dm3	chr3R:31009-910256	dms_377	CAGC--GGATGACCCCTACGCG-----GGGGCGCGCTGCTCAACTTGGACGCCGC GGCGCGTGCCGCGC -----CG-----AGAGC--TCGTTTGTGCCCT TCAGTTCGCGGGCACACGC -----GG GG GGCG-----CCAGGCCACATTCCAGCAC--TGCC-----GCAGATCTCTGCTACACGT
dRoEuh1	scaf718000040975:861185-861342		CAGC--GGATGACCCCTAC GC -----GGGGCGCGCTGCTCAAC TGG ACGCC CG GGCGTGCCGCGC -----CG-----AGAGC--TCGTTTGTGCCCT TCAGTTCGCGGGCACACGC -----GG GG GGCG-----CCAGGCCACATTCCAGCAC--TGCC-----GCAGATCTCTGCTACACGT
dRoBial	scaf718000030241:644881-645035		CAGC--GGATGAC CGCTAC GC -----GGGGCGCGCTGCTCAAC TGG ACGCC CG GGCGTGCCGCGC -----GAC-----AGAGC--TCGTTTGTGCCCT TCAGTTCGCGGGCACACGC -----GG GG GGCG-----CCAGGCCACATTCCAGCAC--TGCC-----GCAGATCTCTGCTACACGT
dRoTak1	scaf7180000415789:614409-614563		CAGC--GGATGAC CGCTAC GC -----GGGGCGCGCTGCTCAAC TGG ACGCC CG GGCGTGCCGCGC -----GAC-----AGAGC--TCGTTTGTGCCCT TCAGTTCGCGGGCACACGC -----GG GG GGCG-----CCAGGCCACATTCCAGCAC--TGCC-----GCAGATCTCTGCTACACGT
dRoE1el	scaf7180000491104:2702015-2702157		CAGC--GGATGACCCCTAC GC -----GGGGCGCGCTGCTCAACTTGG CGCCGCGG CGACACGCGC -----GAC-----AGAGC--TCGTTTGTGCCCT TCAGTTCGCGGGCACACGC -----GG GG GGCG-----CCAGGCCACATTCCAGCAC--TGCC-----GCAGATCTCTGCTAC AGGT
dRoRho1	scaf7180000779558:37768-37910		CAGC--GGATGAC CGCTAC CGCG-----GGGGCGCGCTGCTCAACTTGGACGCCGC GGCGCGTGCCGCGC -----GAC-----AGAGC--TCGTTTGTGCCCT TCACCTCGCG -----GG GG GGCG-----CCAGGCCACATTCCAGCAC--TGCC-----GCAGATCTCTGCTACACGT
dRoFic1	scaf7180000453850:254234-254491		CAG A --GGATGACCCCTACGCG-----GGGGCGCGCTGCTCAACTTGG CGCCGCGG CGACACGCGC -----GAC-----AGAGC--TCGTTTGTGCCCT TCAGCTCGCGGGCACACGC -----GG GG GGCG-----CCAGGCCACATTCCAGCAC--TGCC-----GCAGATCTCTGCTACACGT
dRoKik1	scaf7180000302634:592889-59306		CAG A --GATGAC CGCTAC GC -----GGGGCGCGCTGCTCAAC TGG ACGCC CG GGCGTGCCGCGC -----AGAGC--TCGTTTGTGCCCT TCAGCTCGCGGGCACACGC -----GG GG GGCG-----CCAGGCCACATTCCAGCAC--TGCC-----GCAGATCTCTGCTACACGT
dRoAna3	scaf102_13340:23109635-23109792	dan_4055	CAGC--GGATGAC CGCTAC GC -----GGGGCGCGCTGCTCAAC TGG ACGCC CG GGCGTGCCGCGC -----GAG GG GGCG-----CCAGGCCACATTCCAGCAC--TGCC-----GCAGATCTCTGCTACAC GT
dRoBip1	scaf7180000356395:119273-117430		CAGC--GGATGAC CGCTAC GC -----GGGGCGCGCTGCTCAAC TGG ACGCC CG GGCGTGCCGCGC -----AGAGC--TCGTTTGTGCCCT TCAGTTCGCGGGCACACGC -----GG GG GGCG-----CCAGGCCACATTCCAGCAC--TGCC-----GCAGATCTCTGCTACACGT
dp5	4:21205641-21905801	dps_3837	CAGC--GGATGACCC CTAC GC -----GGGGCGCGCTCTCAAC TGG ACGCC CG GGCGTGCCGCGC -----AGAGC--TCGTTTGTGCCCT TCGTGGCG -----GG GG GGCG-----CCAGGCCACATTCCAGCAC--TGC AGCA SCAGAT CTCTGCTACAC GT
dRoPer2	scaf102_3:4687071-4687231		CAGC--GGATGACCC CTAC GC -----GGGGCGCGCTCTCAAC TGG ACGCC CG GGCGTGCCGCGC -----AGAGC--TCGTTTGTGCCCT TCGTGGCG -----GG GG GGCG-----CCAGGCCACATTCCAGCAC--TGC AGCA SCAGAT CTCTGCTACAC GT
dRoW12	scaf2_11000000049431:3032103-3032269	dwi_5421	CAGC--GGATGACCC CTAC GC -----GGGGCGCGCTCTCAAC TGG ACGCC CG GGCGTGCCGCGC -----GCAATTTGG CGATACGGCACACACACTGGAG -----AGAGC--TCGTTTGTGCCCT TCGTGGCG -----GG GG GGCG-----CCAGGCCACATTCCAGCAC--TGC AGCA SCAGAT CTCTGCTACAC GT
dRoV13	scaf102_12855:7979120-7979293	dvi_24653	CAGC ATC CGATGAC CGCTAC CGAG CGACGGCA CGCCCTGCT GTG CAGCGCGAC CGCGCGCGCAATTTCG -----G-----CAG AT --TCGTTTGTGCCCT TCGACACGGCGCGAGT -----GG CG CGAG-----GACGGCACATTCCAGCAC--TGC AGCA SCAGAT CTCTGCTACAC GT
dRoMo3	scaf102_6:540:23216860-23217038	dms_3161	CAGC ATC CGATGAC CGCTAC CGAG CGACGGCA CGCCCGCGCCCGCT GTG CGAGACCGAC CGCGCGCGCAATTTCG -----CG-----CAG AT --TCGTTTGTGCCCT TCGACACGGCGCGAGT -----GG CG CGAG-----GAGGGCACATTCCAGCAC--TGC AGCA SCAGAT CTCTGCTACAC GT
dRoGr12	scaf102_15245:7396537-7396680		CAAT -----GG CG CGCG-----G-----GGGG CG CGCT CAAC TGG CG -----TGC CG CT CGCTG CGT -----G CA -----TG TTG -----CGTTTGTGCC CGAC -----T AG -----T AG TGG CGCG -----GG GG GGCGCG ACG ----- AG CGACACCGTCCAGCAC AGAG CG -----G AG CGACCG CGAG CG

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	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	2
rescue.candidate	3

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Show Alternate Folds

Flybase annotation

Antisense to utr5 [utr5_plus_1467]; intron [Dere\GG23954-in]; CDS [Dere\GG23954-cds]; CDS [Dere\GG23954-cds]

No Repeatable elements found

Sense Strand Reads

[illegible]

Anti-sense strand reads

[illegible]

Re-alignment of all predicted orthologs

Accession	Coordinate	ID	Alignment
droEre2	scaffold_4929:10902626-10902783_-	der_20	DGGACCTGATGCTCCATGGTGTTCCTTCGATTCGAATGCTGATAGAAAGCAAGATA-----G-ATCTTA-----G---AAATTCGCCAATTG-----ACCTTCTAGATTCTAAT-ACITGCAG----AATAATTTTCAGCGGAACAAATGGATACAATATACCTGAAATTACGTT
droyaK3	21:12970329-12970486_-		DGGACCTGATGCTCCATGGTGTTCCTTCGATTCGAATGCTGATAGAAAGCAAGCTA-----A-ACTTTA-----G---AAATTCGCAATTG-----ACCTTCTAGATTCTAAT-ACITGCAG----AATAATTTTCAGCGGAACAAATGGATACAATATACCTGAAATTACGTT
drosEc2	scaffold_3:5721173-5721321=		DGGACCTGATGCTCCATGGTGTTCCTTCGATTCGAATGCTGATAGAAAGCAAGCTA-----A-AATTA-----G-TT-----TTG-----ACCTGTAATCTCTGAT-ACITGCAG----AATAATTTTCAGCGGAACAAATGGATACAATATACCTGAAATTACGTT
drosSm2	21:9974192-9974341_-		DGGACCTGATGCTCCATGGTGTTCCTTCGATTCGAATGCTGATAGAAAGCAAGCTA-----A-AATTA-----G-TT-----TTG-----ACCTTCTAGATTCTAAT-ACITGCAG----AATAATTTTCAGCGGAACAAATGGATACAATATACCTGAAATTACGTT
dm3	chr21:10236073-10236221_-		DGGACCTGATGCTCCATGGTGTTCCTTCGATTCGAATGCTGATAGAAAGCAAGCTA-----A-ATCTTA-----G-TT-----TTA-----ACCTAAAGATCTCTGAT-ACITGCAG----AATAATTTTCAGCGGAACAAATGGATACAATATACCTGAAATTACGTT
droyu1	scaf7180000409554:4624381-4624595_+		DGGACCTGATGCTCCATGGTGTTCCTTCGATTCGAATGCTGATAGAAAGCAAGCTA-----AATATTATTATTA-----G-----CCTTTC-----TCTCCTTTTCTCAGAAA-----TGTGATTTTGTATCGTACTATGGCTTCATGACCTAAATATTCTCTGATTCCTTCGCGCCACTTTTGA-ATTGTATTG-----TTG-TT-A-CAC-AT-TT-CA-AG-AA----AATAATTTTCAGCGGAACAAATGGATACAATATACCTGAAATTACGTT
droyB1a1	scaf7180000301468:426776-427045_-		DGGACCTGATGCTCCATGGTGTTCCTTCGATTCGAATGCTGATAGAAAGCAAGCTA-----A-AATTA-----G-TT-----TTA-----ACCTAAAGATCTCTGAT-ACITGCAG----AATAATTTTCAGCGGAACAAATGGATACAATATACCTGAAATTACGTT
droyTaki	scaf7180000415438:503268-503335_-		DGGACCTGATGCTCCATGGTGTTCCTTCGATTCGAATGCTGATAGAAAGCAAGCTA-----A-AATTA-----G-TT-----TTA-----ACCTAAAGATCTCTGAT-ACITGCAG----AATAATTTTCAGCGGAACAAATGGATACAATATACCTGAAATTACGTT
droyE1e1	scaf7180000491186:3384236-3384381_-		DGGACCTGATGCTCCATGGTGTTCCTTCGATTCGAATGCTGATAGAAAGCAAGCTA-----A-AATTA-----G-TT-----TTA-----ACCTAAAGATCTCTGAT-ACITGCAG----AATAATTTTCAGCGGAACAAATGGATACAATATACCTGAAATTACGTT
droyF1c1	scaf7180000453838:526776-526902_-		DGGACCTGATGCTCCATGGTGTTCCTTCGATTCGAATGCTGATAGAAAGCAAGCTA-----A-AATTA-----G-TT-----TTA-----ACCTAAAGATCTCTGAT-ACITGCAG----AATAATTTTCAGCGGAACAAATGGATACAATATACCTGAAATTACGTT
droyK1K1	scaf7180000302472:3040753-3040904_+		DGGACCTGATGCTCCATGGTGTTCCTTCGATTCGAATGCTGATAGAAAGCAAGCTA-----A-AATTA-----G-TT-----TTA-----ACCTAAAGATCTCTGAT-ACITGCAG----AATAATTTTCAGCGGAACAAATGGATACAATATACCTGAAATTACGTT
droyAna3	scaffold_12916:14124774-14124928_-		DGGACCTGATGCTCCATGGTGTTCCTTCGATTCGAATGCTGATAGAAAGCAAGCTA-----A-AATTA-----G-TT-----TTA-----ACCTAAAGATCTCTGAT-ACITGCAG----AATAATTTTCAGCGGAACAAATGGATACAATATACCTGAAATTACGTT
droyB1P1	scaf7180000396572:2831038-2831188_+		DGGACCTGATGCTCCATGGTGTTCCTTCGATTCGAATGCTGATAGAAAGCAAGCTA-----A-AATTA-----G-TT-----TTA-----ACCTAAAGATCTCTGAT-ACITGCAG----AATAATTTTCAGCGGAACAAATGGATACAATATACCTGAAATTACGTT
dp5	d_group2:1222173-1222237_-		DGGACCTGATGCTCCATGGTGTTCCTTCGATTCGAATGCTGATAGAAAGCAAGCTA-----A-AATTA-----G-TT-----TTA-----ACCTAAAGATCTCTGAT-ACITGCAG----AATAATTTTCAGCGGAACAAATGGATACAATATACCTGAAATTACGTT
droyPer2	scaffold_1:1239344-1239408=		DGGACCTGATGCTCCATGGTGTTCCTTCGATTCGAATGCTGATAGAAAGCAAGCTA-----A-AATTA-----G-TT-----TTA-----ACCTAAAGATCTCTGAT-ACITGCAG----AATAATTTTCAGCGGAACAAATGGATACAATATACCTGAAATTACGTT
droyW112	scaf2_1100000004852:711674-711753_+		DGGACCTGATGCTCCATGGTGTTCCTTCGATTCGAATGCTGATAGAAAGCAAGCTA-----A-AATTA-----G-TT-----TTA-----ACCTAAAGATCTCTGAT-ACITGCAG----AATAATTTTCAGCGGAACAAATGGATACAATATACCTGAAATTACGTT
droyV1r3	scaffold_12963:14163196-14163258_+		DGGACCTGATGCTCCATGGTGTTCCTTCGATTCGAATGCTGATAGAAAGCAAGCTA-----A-AATTA-----G-TT-----TTA-----ACCTAAAGATCTCTGAT-ACITGCAG----AATAATTTTCAGCGGAACAAATGGATACAATATACCTGAAATTACGTT
droyMoJ3	scaffold_6500:29815595-29815652_+		DGGACCTGATGCTCCATGGTGTTCCTTCGATTCGAATGCTGATAGAAAGCAAGCTA-----A-AATTA-----G-TT-----TTA-----ACCTAAAGATCTCTGAT-ACITGCAG----AATAATTTTCAGCGGAACAAATGGATACAATATACCTGAAATTACGTT
droyGr12	scaffold_15126:1713886-1714033_-		DGGACCTGATGCTCCATGGTGTTCCTTCGATTCGAATGCTGATAGAAAGCAAGCTA-----A-AATTA-----G-TT-----TTA-----ACCTAAAGATCTCTGAT-ACITGCAG----AATAATTTTCAGCGGAACAAATGGATACAATATACCTGAAATTACGTT

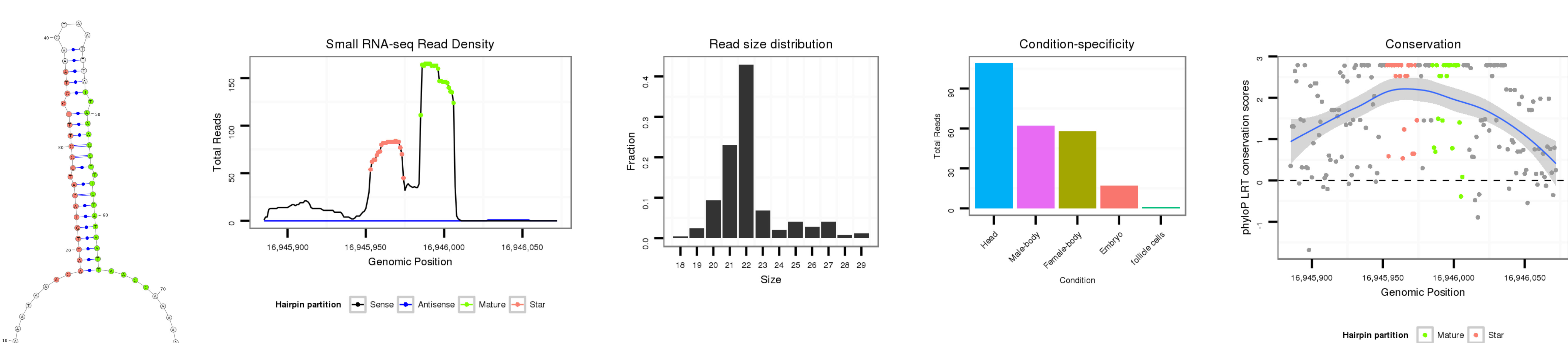
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	PASS/FAIL
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crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate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

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
der_1521	scaffold_4770:16945935-16946022 +	confident	Canonical miRNA	3pUTR	View on UCSC Genome Browser [Concill Mimir]

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



[Show Alternate Forms](#)

utr3 (utr3_minus_7095)

No Repeatable elements found

Sense Strand Reads

[illegible]

Anti-sense strand reads

										M55		V040		
										female		embryo		
										body				
TAAACACTTTTCTCTTTTGGGGGTGTTGGTTGTGTTGTTGTTATCTTTTGTGTTATTTGTTATCATGATGACCGAAGCACTTCATTAATGATTCGAACATATATGTTTTAGGAGTTTAAACACAAAAATAACGCAATGTCATGTCAAAAGACACCGTTAAAGTT										Read #	Hit	Total		
.....(((((((.(((((((.(((((((.)))))).)))))).)))))).....										size	Mismatch	Count	Norm	Total
.....AAAATAACGCAATAGTCATGTCAA.....										27	0	1	1.00	1
														0

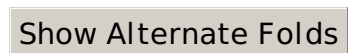
Show Alignment With Reads

Species	Coordinate	ID	Alignment
droE02	Acceffold_4776:1494585-1494602 +	Seq_1521	ATTGTGAAAAAG-----A-AGAAA-----ACCC-CACAA-CCA-----A-ACACA-ACA-----AACAAATGAAA-----AACAAATTA-CAATGTACATGGCTTGGTAAGTAATTTAAAGCTTTGTAAATTAAGAAAA---ATCT-CAAA-TTGTGTTTATTTCGGTAT---CACGTACAG-TTTGTGGCAATTGAA
droE03	Seq_1796	Seq_1796	ATTGTGAAAAAG-----A-AGAAA-----ACCC-CACAA-CCA-----A-ACACA-ACA-----AACAAATGAAA-----AACAAATTA-CAATGTACATGGCTTGGTAAGTAATTTAAAGCTTTGTAAATTAAGAAAA---ATCT-CAAA-TTGTGTTTATTTCGGTAT---CACGTACAG-TTTGTGGCAATTGAA
droE04	Acceffold_0:1721736-1721754 +	Seq_1844	ATTGTGAAAAAG-----A-AGAAA-----ACCC-CACAA-CCA-----A-ACACA-ACA-----AACAAATGAAA-----AACAAATTA-CAATGTACATGGCTTGGTAAGTAATTTAAAGCTTTGTAAATTAAGAAAA---ATCT-CAAA-TTGTGTTTATTTCGGTAT---CACGTACAG-TTTGTGGCAATTGAA
droE05	Acceffold_6:4351910 +	Seq_35	ATTGTGAAAAAG-----A-AGAAA-----ACCC-CACAA-CCA-----A-ACACA-ACA-----AACAAATGAAA-----AACAAATTA-CAATGTACATGGCTTGGTAAGTAATTTAAAGCTTTGTAAATTAAGAAAA---ATCT-CAAA-TTGTGTTTATTTCGGTAT---CACGTACAG-TTTGTGGCAATTGAA
dm3	Seq_421	Seq_421	ATTGTGAAAAAG-----A-AGAAA-----ACCC-CACAA-CCA-----A-ACACA-ACA-----AACAAATGAAA-----AACAAATTA-CAATGTACATGGCTTGGTAAGTAATTTAAAGCTTTGTAAATTAAGAAAA---ATCT-CAAA-TTGTGTTTATTTCGGTAT---CACGTACAG-TTTGTGGCAATTGAA
droE01	Acceffold_409490:8030-81131 +	Seq_1521	ATTGTGAAAAAG-----A-AGAAA-----ACCC-CACAA-CCA-----A-ACACA-ACA-----AACAAATGAAA-----AACAAATTA-CAATGTACATGGCTTGGTAAGTAATTTAAAGCTTTGTAAATTAAGAAAA---ATCT-CAAA-TTGTGTTTATTTCGGTAT---CACGTACAG-TTTGTGGCAATTGAA
droB11	Acceffold_7351486	Seq_1521	ATTGTGAAAAAG-----A-AGAAA-----ACCC-CACAA-CCA-----A-ACACA-ACA-----AACAAATGAAA-----AACAAATTA-CAATGTACATGGCTTGGTAAGTAATTTAAAGCTTTGTAAATTAAGAAAA---ATCT-CAAA-TTGTGTTTATTTCGGTAT---CACGTACAG-TTTGTGGCAATTGAA
droTa1	Acceffold_179059	Seq_1521	ATTGTGAAAAAG-----A-AGAAA-----ACCC-CACAA-CCA-----A-ACACA-ACA-----AACAAATGAAA-----AACAAATTA-CAATGTACATGGCTTGGTAAGTAATTTAAAGCTTTGTAAATTAAGAAAA---ATCT-CAAA-TTGTGTTTATTTCGGTAT---CACGTACAG-TTTGTGGCAATTGAA
droE11	Acceffold_1154154	Seq_1521	ATTGTGAAAAAG-----A-AGAAA-----ACCC-CACAA-CCA-----A-ACACA-ACA-----AACAAATGAAA-----AACAAATTA-CAATGTACATGGCTTGGTAAGTAATTTAAAGCTTTGTAAATTAAGAAAA---ATCT-CAAA-TTGTGTTTATTTCGGTAT---CACGTACAG-TTTGTGGCAATTGAA
droR01	Acceffold_14039	Seq_1521	ATTGTGAAAAAG-----A-AGAAA-----ACCC-CACAA-CCA-----A-ACACA-ACA-----AACAAATGAAA-----AACAAATTA-CAATGTACATGGCTTGGTAAGTAATTTAAAGCTTTGTAAATTAAGAAAA---ATCT-CAAA-TTGTGTTTATTTCGGTAT---CACGTACAG-TTTGTGGCAATTGAA
droF11	Acceffold_2527554	Seq_1521	ATTGTGAAAAAG-----A-AGAAA-----ACCC-CACAA-CCA-----A-ACACA-ACA-----AACAAATGAAA-----AACAAATTA-CAATGTACATGGCTTGGTAAGTAATTTAAAGCTTTGTAAATTAAGAAAA---ATCT-CAAA-TTGTGTTTATTTCGGTAT---CACGTACAG-TTTGTGGCAATTGAA
droK11	Acceffold_250327	Seq_1521	ATTGTGAAAAAG-----A-AGAAA-----ACCC-CACAA-CCA-----A-ACACA-ACA-----AACAAATGAAA-----AACAAATTA-CAATGTACATGGCTTGGTAAGTAATTTAAAGCTTTGTAAATTAAGAAAA---ATCT-CAAA-TTGTGTTTATTTCGGTAT---CACGTACAG-TTTGTGGCAATTGAA
droAn3	Seq_11049281	Seq_1521	ATTGTGAAAAAG-----A-AGAAA-----ACCC-CACAA-CCA-----A-ACACA-ACA-----AACAAATGAAA-----AACAAATTA-CAATGTACATGGCTTGGTAAGTAATTTAAAGCTTTGTAAATTAAGAAAA---ATCT-CAAA-TTGTGTTTATTTCGGTAT---CACGTACAG-TTTGTGGCAATTGAA
droB11	Acceffold_34239	Seq_1521	ATTGTGAAAAAG-----A-AGAAA-----ACCC-CACAA-CCA-----A-ACACA-ACA-----AACAAATGAAA-----AACAAATTA-CAATGTACATGGCTTGGTAAGTAATTTAAAGCTTTGTAAATTAAGAAAA---ATCT-CAAA-TTGTGTTTATTTCGGTAT---CACGTACAG-TTTGTGGCAATTGAA
dp5	Seq_2827	Seq_1521	ATTGTGAAAAAG-----A-AGAAA-----ACCC-CACAA-CCA-----A-ACACA-ACA-----AACAAATGAAA-----AACAAATTA-CAATGTACATGGCTTGGTAAGTAATTTAAAGCTTTGTAAATTAAGAAAA---ATCT-CAAA-TTGTGTTTATTTCGGTAT---CACGTACAG-TTTGTGGCAATTGAA
droE2	Acceffold_6:2585929	Seq_1521	ATTGTGAAAAAG-----A-AGAAA-----ACCC-CACAA-CCA-----A-ACACA-ACA-----AACAAATGAAA-----AACAAATTA-CAATGTACATGGCTTGGTAAGTAATTTAAAGCTTTGTAAATTAAGAAAA---ATCT-CAAA-TTGTGTTTATTTCGGTAT---CACGTACAG-TTTGTGGCAATTGAA
droK12	Acceffold_4648:3761875-3761911 +	Seq_1521	ATTGTGAAAAAG-----A-AGAAA-----ACCC-CACAA-CCA-----A-ACACA-ACA-----AACAAATGAAA-----AACAAATTA-CAATGTACATGGCTTGGTAAGTAATTTAAAGCTTTGTAAATTAAGAAAA---ATCT-CAAA-TTGTGTTTATTTCGGTAT---CACGTACAG-TTTGTGGCAATTGAA
droV13	Acceffold_13047:1834994-1835158 +	Seq_1521	ATTGTGAAAAAG-----A-AGAAA-----ACCC-CACAA-CCA-----A-ACACA-ACA-----AACAAATGAAA-----AACAAATTA-CAATGTACATGGCTTGGTAAGTAATTTAAAGCTTTGTAAATTAAGAAAA---ATCT-CAAA-TTGTGTTTATTTCGGTAT---CACGTACAG-TTTGTGGCAATTGAA
droE03	Acceffold_6540:3761875-3761911 +	Seq_1521	ATTGTGAAAAAG-----A-AGAAA-----ACCC-CACAA-CCA-----A-ACACA-ACA-----AACAAATGAAA-----AACAAATTA-CAATGTACATGGCTTGGTAAGTAATTTAAAGCTTTGTAAATTAAGAAAA---ATCT-CAAA-TTGTGTTTATTTCGGTAT---CACGTACAG-TTTGTGGCAATTGAA
droE12	Acceffold_14906:1868118-1868297 +	Seq_1521	ATTGTGAAAAAG-----A-AGAAA-----ACCC-CACAA-CCA-----A-ACACA-ACA-----AACAAATGAAA-----AACAAATTA-CAATGTACATGGCTTGGTAAGTAATTTAAAGCTTTGTAAATTAAGAAAA---ATCT-CAAA-TTGTGTTTATTTCGGTAT---CACGTACAG-TTTGTGGCAATTGAA

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	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.top30	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	8
rescue.candidate	4

Predicted structure



Flybase annotation

intron [Dere\GG17548-in]; CDS [Dere\GG17548-cds]; CDS [Dere\GG17548-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

Anti-sense strand reads

Show Alignment With Reads

Re-alignment of all predicted orthologs

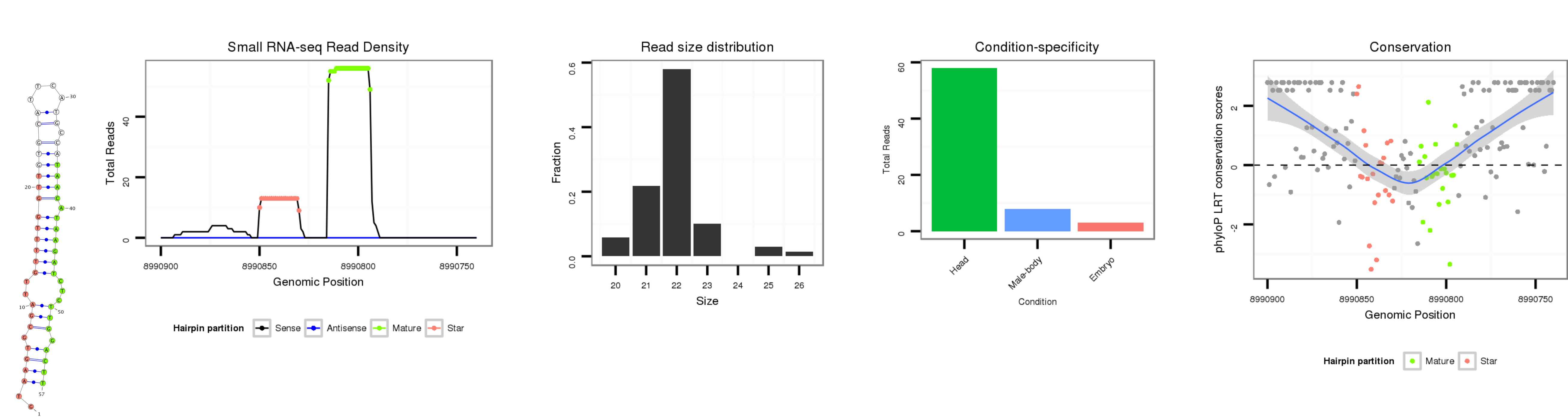
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	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	1
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

[illegible]

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Show Alternate Folds

Flybase annotation

intron [Dere\GG24076-in]; CDS [Dere\GG24076-cds]; CDS [Dere\GG24076-cds]

No Repeatable elements found

Sense Strand Reads

[illegible]

Anti-sense strand reads

Re-alignment of all predicted orthologs

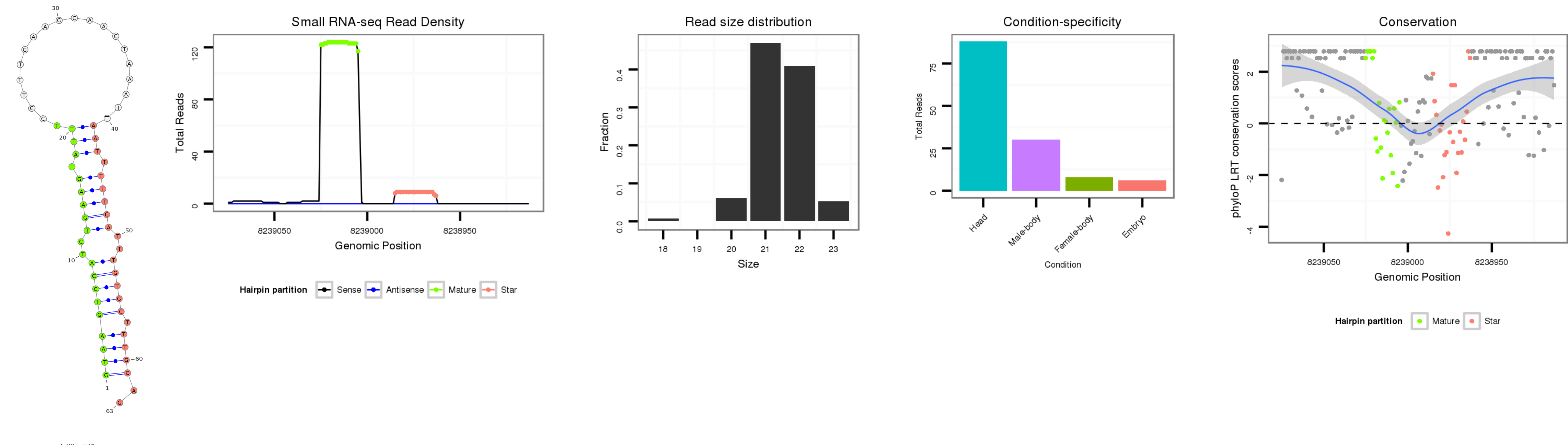
Species	Coordinate	ID	Alignment
droEre2	scaffold_4929:8990740-8990900 -	der_1282	TGTCACCAATTGACGAGAACTGCAGGTGAAGAC-----GGAGCAGAGCTCAGCGTAAGTG---CGATTG---TT-----TTGGTTGTGC-----A-----TTCATGCCATACATAA-----GATCTCTTG-----GACTTCACAGCGACAACACTGCGCTCTGCTGGAGCCAAACTTCGAAGAGAGCTGTGT
droYak3	21:18018273-18018439 +		TGTCACCAATTGACGAGAACTGCAGGTGAAGAC-----GGAGCAGAGCTCAGCGTAAGTG---CTTACG---TT-----TTGGTTGTGC-----A-----TTCATGCCATACATAA-----GATCTCTTG-----GACTTCACAGCGACAACACTGCGCTCTGCTGGAGCCAAACTTCGAAGAGAGCTGTGT
droSec2	scaffold_1:2986776-2986936		TGTCACCACTGACGAGAACTGCAGGTGAAGAC-----GGAGCAGAGCTCAGCGTAAGTG---TAAATG---TT-----TTGGTGTGC-----A-----TTCATGCCATACATAA-----GATCTCTTG-----GACTTCACAGCGACAACACTGCGCTCTGCTGGAGCCAAACTTCGAAGAGAGCTGTGT
droSim2	2r:6156991-6157149 +		TGTCACCACTGACGAGAACTGCAGGTGAAGAC-----GGAGCAGAGCTCAGCGTAAGTG---ATTG---TT-----TTGGTGTGC-----A-----TTCATGCCATACATAA-----GATCTCTTG-----GACTTCACAGCGACAACACTGCGCTCTGCTGGAGCCAAACTTCGAAGAGAGCTGTGT
dm3	chr28:5361656-5361816 +		TGTCACCACTGACGAGAACTGCAGGTGAAGAC-----GGAGCAGAGCTCAGCGTAAGTG---GATTG---TT-----TTGGTGTGC-----A-----TTCATGCCATACATAA-----GATCTCTTG-----GACTTCACAGCGACAACACTGCGCTCTGCTGGAGCCAAACTTCGAAGAGAGCTGTGT
droBug1	scf7180000409183:991667-991826 +		TGTCACCACTGACGAGAACTGCAGGTGAAGAC-----GGAGCAGAGCTCAGCGTAAGTG---GATTG---TT-----TTGGTGTGC-----A-----TTCATGCCATACATAA-----GATCTCTTG-----GACTTCACAGCGACAACACTGCGCTCTGCTGGAGCCAAACTTCGAAGAGAGCTGTGT
droBial	scf7180000301506:1353867-1354024 -		TGTCACCACTGACGAGAACTGCAGGTGAAGAC-----GGAGCAGAGCTCAGCGTAAGTG---ATTACG---TC-----TT-----TTGGTGTGC-----A-----TTCATGCCATACATAA-----GATCTCTTG-----GACTTCACAGCGACAACACTGCGCTCTGCTGGAGCCAAACTTCGAAGAGAGCTGTGT
droTak1	scf7180000415401:411947-412103 +		TGTCACCACTGACGAGAACTGCAGGTGAAGAC-----GGAGCAGAGCTCAGCGTAAGTG---TTAAAGTTATATTT-----AAAT-----A-----TTCATGCCATACATAA-----GATCTCTTG-----GACTTCACAGCGACAACACTGCGCTCTGCTGGAGCCAAACTTCGAAGAGAGCTGTGT
droEle1	scf7180000491107:1747228-1747428 -		TGTCACCACTGACGAGAACTGCAGGTGAAGAC-----GGAGCAGAGCTCAGCGTAAGTG---TTTAAAT-----AATTA-----A-----TTCATGCCATACATAA-----GATCTCTTG-----GACTTCACAGCGACAACACTGCGCTCTGCTGGAGCCAAACTTCGAAGAGAGCTGTGT
droRhol	scf7180000777217:252291-252449 -		TGTCACCACTGACGAGAACTGCAGGTGAAGAC-----GGAGCAGAGCTCAGCGTAAGTG---TTTAAAT-----AATTA-----A-----TTCATGCCATACATAA-----GATCTCTTG-----GACTTCACAGCGACAACACTGCGCTCTGCTGGAGCCAAACTTCGAAGAGAGCTGTGT
droPic1	scf7180000453858:1334592-1334765 -		TGTCACCACTGACGAGAACTGCAGGTGAAGACGGAGCAAGAGCTCAGCGTAAGTG---AACA-----ATGTC-----TT-----TT-----TTGGTGTGC-----A-----TTCATGCCATACATAA-----GATCTCTTG-----GACTTCACAGCGACAACACTGCGCTCTGCTGGAGCCAAACTTCGAAGAGAGCTGTGT
droKik1	scf7180000302476:745854-45950 -		TGTCACCACTGACGAGAACTGCAGGTGAAGAC-----GGAGCAGAGCTCAGCGTAAGTG---TTTAAAT-----AATTA-----A-----TTCATGCCATACATAA-----GATCTCTTG-----GACTTCACAGCGACAACACTGCGCTCTGCTGGAGCCAAACTTCGAAGAGAGCTGTGT
droAna2	scaffold_13266:257215-257369 -		TGTCACCACTGACGAGAACTGCAGGTGAAGAC-----GGAGCAGAGCTCAGCGTAAGTG---TTTAAAT-----AATTA-----A-----TTCATGCCATACATAA-----GATCTCTTG-----GACTTCACAGCGACAACACTGCGCTCTGCTGGAGCCAAACTTCGAAGAGAGCTGTGT
droBip1	scf7180000396730:1276875-1277036 -		TGTCACCACTGACGAGAACTGCAGGTGAAGAC-----GGAGCAGAGCTCAGCGTAAGTG---TTTAAAT-----AATTA-----A-----TTCATGCCATACATAA-----GATCTCTTG-----GACTTCACAGCGACAACACTGCGCTCTGCTGGAGCCAAACTTCGAAGAGAGCTGTGT
dp5	3:13956490-13956652 -		TGTCACCACTGACGAGAACTGCAGGTGAAGAC-----GGAGCAGAGCTCAGCGTAAGTG---TTTAAAT-----AATTA-----A-----TTCATGCCATACATAA-----GATCTCTTG-----GACTTCACAGCGACAACACTGCGCTCTGCTGGAGCCAAACTTCGAAGAGAGCTGTGT
droPer2	scaffold_4:1363364-1363526		TGTCACCACTGACGAGAACTGCAGGTGAAGAC-----GGAGCAGAGCTCAGCGTAAGTG---TTTAAAT-----AATTA-----A-----TTCATGCCATACATAA-----GATCTCTTG-----GACTTCACAGCGACAACACTGCGCTCTGCTGGAGCCAAACTTCGAAGAGAGCTGTGT
droWil2	scf2_1100000004514:748223-748388 -		TGTCACCACTGACGAGAACTGCAGGTGAAGAC-----GGAGCAGAGCTCAGCGTAAGTG---TTTAAAT-----AATTA-----A-----TTCATGCCATACATAA-----GATCTCTTG-----GACTTCACAGCGACAACACTGCGCTCTGCTGGAGCCAAACTTCGAAGAGAGCTGTGT
droVir3	scaffold_10324:134571-134742 +		TGTCACCACTGACGAGAACTGCAGGTGAAGAC-----GGAGCAGAGCTCAGCGTAAGTG---TTTAAAT-----AATTA-----A-----TTCATGCCATACATAA-----GATCTCTTG-----GACTTCACAGCGACAACACTGCGCTCTGCTGGAGCCAAACTTCGAAGAGAGCTGTGT
droMo3	scaffold_6496:1950374-1950543 +		TGTCACCACTGACGAGAACTGCAGGTGAAGAC-----GGAGCAGAGCTCAGCGTAAGTG---TTTAAAT-----AATTA-----A-----TTCATGCCATACATAA-----GATCTCTTG-----GACTTCACAGCGACAACACTGCGCTCTGCTGGAGCCAAACTTCGAAGAGAGCTGTGT
droGr12	scaffold_15245:15491552-15491786 -		TGTCACCACTGACGAGAACTGCAGGTGAAGAC-----GGAGCAGAGCTCAGCGTAAGTG---TTTAAAT-----AATTA-----A-----TTCATGCCATACATAA-----GATCTCTTG-----GACTTCACAGCGACAACACTGCGCTCTGCTGGAGCCAAACTTCGAAGAGAGCTGTGT

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

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Show Alternate Folds

Flybase annotation

intron [Dere\GG20992-in]; CDS [Dere\GG20992-cds]; CDS [Dere\GG20992-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

					V108	V107	M055	V040	V060	M057
GAACTACAAGCACAATAACATGGCCAGTTTCATAAGGCAATTGAATATGTGTAAGTGCATCTGAAGTATTTCCTTTGAAGCACTAAATTAAATTTTCATTGTGCTTTGCAGATGGATTTCATAAGATTACCTCTATTGACAATGGCGATTACGTTTTGAT	Read #	Mismatch	Hit Count	Total Norm	head	male body	female body	embryo	head	embryo
*****(((((((.....)))))))).*****	21	0	1	61.00	61	46	10	3	2	0
.....GTAAGTGCATCTGAAGTATTTC.....	22	0	1	53.00	53	30	18	0	3	1
.....GTAAGTGCATCTGAAGTATTTC.....AATTTTCATTGTGCTTTGCAG.....	23	0	1	6.00	6	3	0	3	0	0
.....GTAAGTGCATCTGAAGTATTTC.....	20	0	1	6.00	6	5	1	0	0	0
.....CTACAGAACAATAACATGGCCAGT.....	25	0	1	1.00	1	0	1	0	0	0
.....TAAGGCAATTGAATATGT.....	18	0	1	1.00	1	1	0	0	0	0
.....GTAAGTGCATCTGAAGTATTTC.....	23	1	1	1.00	1	1	0	0	0	0
.....TTGAATATGTGTAAGTGCATCTGAA.....	25	0	1	1.00	1	0	1	0	0	0
GAACTACAAGCACAATAAAC.....	19	0	1	1.00	1	0	1	0	0	0
.....GTGCATCTGAAGTATTTC.....	18	0	1	1.00	1	1	0	0	0	0
.....AATTTTCATTGTGCTTTGC.....	21	0	1	1.00	1	1	0	0	0	0
.....AATTTTCATTGTGCTTTGC.....	20	0	1	1.00	1	0	1	0	0	0
.....GTAAGTGCATCTGAAGTATTTC.....	23	0	1	1.00	1	0	1	0	0	0
.....AATTTTCATTGTGCTTTGCA.....	22	0	1	1.00	1	0	1	0	0	0
.....AAGTGCATCTGAAGTATTTC.....	20	0	1	1.00	1	1	0	0	0	0

Anti-sense strand reads

[illegible]

Show Alignment With Reads

Re-alignment of all predicted orthologs

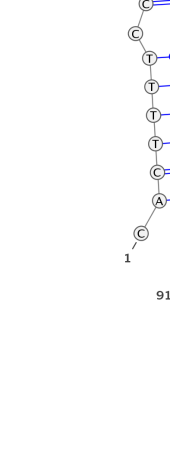
Species	Coordinate	ID	Alignment
droBre2	scaffold_4845:8238913-8239075 _	der_1069	GAACTACAAGCACAATAACATGGCCAGTTTCATAAGGCAATTGAATATGTSTAAGTGCAT-CTGA-----AGTATTCTTTGAAGC-----A-----ACTA--A-----ATTATTTT-TCAT---T-TGT---GCTTTCAGATGGGATTCATAAGATTACCTCTATTGACAATGGCGGATTACGTTTGTGAT
droYak3	2R:15166225-15166391 +		GAACTACAAGCACAATAACATGGCCAGTTTCATAAGGCAATTGAATATGTSTAAGTGCATCTGA-----CCCTGCGCTTGAAATCACTAACTAA-----FA-AA-----ATTC-TCAT---T-TGT---GCTTTCAGATGGATTCAAGAATCACCTCTATTGACAAGGCGGATTACGTTTGTGAT
droSec2	scaffold_1:11510184-11510354 _		GAACTACAAGCACAATAACATGGCCAGTTTCATAAGGCAATTGAATATGTSTAAGTAACTGA-----AGGGGCTCTTGAAATCACTAACTGAAA-----AA-CHC-TCAT---T-TGT---GCTTTCAGATGGATTCAAGAATCACCTCTATTGACAATGGCGGATTCACGTTTGTGAT
droSim2	2r:14700890-14701059 _	dsi_22134	GAACTACAAGCACAATAACATGGCCAGTTTCATAAGGCAATTGAATATGTSTAAGTAACTGA-----AGCGGCTCTTGAAATCACTAACTGAAA-----ACTA-AAATG-----AA-CHC-TC-A---T-TGT---GCTTTCAGATGGATTCAAGAATCACCTCTATTGACAATGGCGGATTCACGTTTGTGAT
dm3	chr2R:14020397-14020558 _		AAGTACAAGCACAATAACATGGCCAGTTTCATAAGGCAATTGAATATGTSTAAGTAACTGA-----AGCTGCTCTTGAAATCACTAACTGAAA-----ACTA-AAATG-----AAAT---T-TGT---GCTTTCAGATGGATTCAAGAATCACCTCTATTGACAATGGCGGATTCACGTTTGTGAT
droBuq1	scaffold_400409672:1074696-1074859 +		AAGTACAAGCACAATAACATGGCCAGTTTCATAAGGCAATTGAATATGTSTAAGTAACTG-----ATATCTCAGT-----TTAAACTCTT-----CTA-AA-----ATGCT-----TTT-----TATGAAAGATGGATTCAAGAATCACCTCATTGACAAGGAGGCTACGTTTGTGAT
droBial	scaffold_180000301754:2517732-2517890 +		GAACTACAAGCACAATAACATGGCCAGTTTCATCGGCAATTGAATATGTSTAAGTAGTG-----CATACA-----A-----TTTTAATTTGAAG-CT-----TAT-ATTCCTTTAA-----CACAAAAGATGGCTTCAGAAGATCACCTCATTGACAAGGAGGCTCGCTTGTGAT
droTak1	scaffold_1800000415795:378873-379031 _		GAACTACAAGCACAATAACATGGCCAGTTTCATAGGCAATTGAATATGTSTAAGTAGTG-----CATAAAAAAT-----GGAATATTAAAT-----TTAATTTGAAT-ATA-----CT-----AACTCAGATGGCTTCAGAAGATCACCTCATTGACAAGGAGGCTCGCTTGTGAT
droEl1	scaffold_1800000491214:181702-181862 +		AAGTACAAGCACAATAACATGGCCAGTTTCATAGGCAATTGAATATGTSTAAGTAGTG-----AATTAA-----ATTACAATTGGAGCAAG-----CTA-AAG-N-N-----A-----A-TT-----CTCAAAGATGGCTTCAGAAGATCACCTCATTGACAAGGCGGCTCGCTTGTGAT
droRho1	scaffold_1800000779949:86296-86457 +		GAACTACAAGCACAATAACATGGCCAGTTTCATCAGCAATTGAATATGTSTAAGTAGT-----AATT-----AAT-----AGAACATAAC-----TT-----AA-----GAC-----T-TTGTGAAATCTAAGATGGATTCAAGAATCACCTCATTGACAAGGCGGATCGCTTGTGAT
droFic1	scaffold_1800000453948:1417321-1417478 _		AAGTACAAGCACAATAACATGGCCAGTTTCATAGGCAATTGAATATGTSTAAGTAGT-----GA-----TAA-AAAGATCTAAATCATCTGATA-----A-----AA-----B-----G-----T-TT-----AATTAAGATGGCTTCAGAAGATCACCTCATTGACAAGGAGGCTCGCTTGTGAT
droKik1	scaffold_1800000302682:1202276-1202441 _		AAGTACAATAACACAATAACATGGCCAGTTTCATAGGCAATTGAATATGTSTAAGTAGT-----CTA-----GAAA-----AG-CAT-----AC-----TTAAACAATAGTAGTAA-CCA-----TGCTG-C-T-----T-TT-----GAACCCAGATGGCTTCAGAAATCACATCATSACAAAGGAGGCTCGCTTGTGAT
droAna3	scaffold_13266:2764528-2764688 _		AAGTACAAGCACAATAACATGGCCAGTTTCATCGGCAATTGAATATGTSTAAGTAGT-----CT-----ATACTC-----TTCTGT-----AAGTACTC-----CTT-----A-----CTAACCT-ATC-----C-TT-----GCCTTCAGATGGATTCAAGAATCACCTCATTGACAAGGCGGCTCGCTTGTGAT
droBip1	scaffold_1800000396427:1246607-1246768 _		AAGTACAAGCACAATAACATGGCCAGTTTCATCGGCAATTGAATATGTSTAAGTAGT-----ATC-----CAGAGCCTTAAGGA-AA-----GA-TTCCCT-----CTAACAGAT-AGCT-----T-TGT-----GATTTCAGATGGCTTCAGAAGATCACCTCATTGACAAGGCGGCTCGCTTGTGAT
dp5	3:6620854-6621023 _		AAGTACAAGCACAATAACATGGCCAGTTTCATAGGCAATTGAATATGTSTAAGTAGT-----AGGAC-----GCTCAAGTGACAAGATGGGAT-CTAAAG-AGTT-----TTTC-CTTTGTTT-----CCGTCAGATGGATTCAAGAATCACATCATTGAGATGAGGCTCGCTTGTGAT
droPer2	scaffold_2:6841670-6841839 _		AAGTACAAGCACAATAACATGGCCAGTTTCATAGGCAATTGAATATGTSTAAGTAGT-----AGGAC-----GCTCAAGTGACAAGATGGGAT-CTAAAG-AGTT-----TTTC-CTTTGTTT-----CCGTCAGATGGATTCAAGAATCACATCATTGAGATGAGGCTCGCTTGTGAT
droW12	scaffold_1100000004512:1800162-1800321 _		GAACTACAAGCACAATAACATGGCCAGTTTCATCGGCAATTGAATATGTSTAAGTAGT-----ATC-----GCAC-----GGA-A-----GTCCTTCAT-----A-----ATTATTTT-ATAT---T-TGT-----GCTCTAGATGGCTTCAGAAGATTACATGAGATGAGGCTCGCTTGTGAT
droVit3	scaffold_12875:8652844-8653008 _	dvi_5764	GAACTACAAGCACAATAACATGGCCAGTTTCATCGGCAATTGAATATGTSTAAGTAGT-----CAT-----ATG-----G-----TTTATTTTATTAAGTAAGA-----CTA-----A-----ACTACGAC-CTCG-----CTT-----GAATTCAGATGGCTTCATAAGATCACCTCATTGAGATGAGGCTCGCTTGTGAT
droMo3	scaffold_16436:1854908-18549176 _		GAACTACAAGCACAATAACATGGCCAGTTTCATCGGCAATTGAATATGTSTAAGTAGT-----CAT-----ATC-----G-----GC-----TCAATTAAGTAGTCT-----A-----TTAGATAGTAACTAATTA-----T-TA-----ATAATCAGATGGCTTCATAAGATCACCTCATTGAGATGAGGCTCGCTTGTGAT
droGr12	scaffold_15245:2054465-2054628 _		AAGTACAAGCACAATAACATGGCCAGTTTCATCGGCAATTGAATATGTSTAAGTAGT-----TA-----TTG-----GAT-----TTAACTCAGTTTGTCTACTTGAATTTT-ATCG-----C-TGT-----TCAATTCAGATGGCTTCATAAGATCACCTCATTGAGATGAGGCTCGCTTGTGAT

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

Predicted structure

Predicted structure



Flybase annotation

CDS [Dere\GG17404-cds]; intron [Dere\GG17404-in]

No Repeatable elements found

Sense Strand Reads

Anti-sense strand reads

Show Alignment With Reads

Re-alignment of all predicted orthologs

Generated: 09/08/2015 at 07:41 PM

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

Predicted structure



Flybase annotation

Antisense to utr5 [utr5 plus 5969]; utr5 [utr5 minus 4915]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

Anti-sense strand reads

Show Alignment With Reads

Re-alignment of all predicted orthologs

[illegible]

Generated: 09/08/2015 at 07:41 PM

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

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

Predicted structure

Flybase annnotation

Antisense to CDS [Dere\GG19578-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

Anti-sense strand reads

Show Alignment With Reads

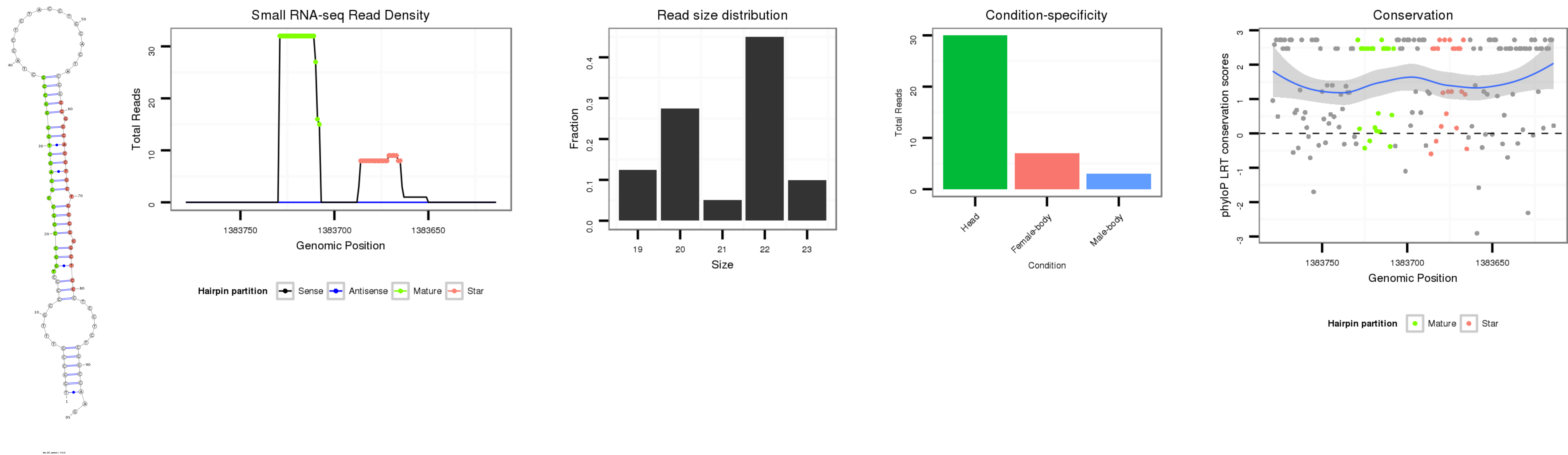
Re-alignment of all predicted orthologs

Generated: 09/08/2015 at 07:41 PM

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

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Show Alternate Folds

Flybase annotation

CDS [Dere\GG11082-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

CAACATGTGGTTCGCAATTCTGTGTCGCCAATTTGGCCGTTTGCGGGC	TGGCGGCGCGAGGTGGGGCCG	CTACCTCTACCTGCACTACGG	CCGCGACCTGCTGCCGGCTCC	TCTCCTCTCGGGCCAAAGAACCGCGCGCCCACTCCCCACTCTCGCCCAACAAG	Read size	# Mismatch	Hit Count	Total Norm	Total	V108 head	M055 female body	V060 head	V107 male	V040 embryo
*****(((((((.....))))))))).....))))).*****					22	0	1	15.00	15	7	3	5	0	0
.....TGGCCGCGCGCAGGTGGGGCG.....					20	0	1	11.00	11	6	3	0	2	0
.....TGGCCGCGCGCAGGTGGGGC.....					20	0	1	11.00	11	6	3	0	2	0
.....TGGCCGCGCGCAGGTGGGGCC					23	1	1	10.00	10	6	0	1	3	0
.....TGGCCGCGCGCAGGTGGGG.....					19	0	1	5.00	5	5	0	0	0	0
.....CCGCCACCTGCTGCGCGGCTCC.....					22	0	1	3.00	3	2	0	1	0	0
.....TGGCGGCGCGCAGGTGGCG					19	1	1	2.00	2	2	0	0	0	0
.....TGGCGGCGCGCAGGTGGGG					21	1	1	2.00	2	0	2	0	0	0
.....TGGCGGCGCGCAGGTGGGGCC					23	1	1	2.00	2	2	0	0	0	0
.....CCGCCACCTGCTGCGCGGCTCC.....					23	0	1	2.00	2	1	0	0	1	0
.....GCCGCCACCTGCTGCGCGGCTCC.....					23	0	1	2.00	2	2	0	0	0	0
.....TGGCGGCGCGCAGGTGGGG					20	1	1	1.00	1	1	0	0	0	0
.....TGGCGGCGCGCAGGTGGGG					20	1	1	1.00	1	1	0	0	0	0
.....GCGCTCCTCTCCTCTCGGCCAA.....					21	0	1	1.00	1	0	0	0	0	1
.....TGGCGGCGCGCAGGTGGGGCC					22	1	1	1.00	1	0	0	1	0	0
.....GCCGCCACCTGCTGCGCGGCT.....					21	0	1	1.00	1	1	0	0	0	0
.....TGGCGGCGCGCAGGTGGGGCC.....					21	0	1	1.00	1	0	1	0	0	0
.....TGGCGGCGCGCAGGTGGGGCCCA					24	2	1	1.00	1	0	0	1	0	0
.....TGGCGGCGCGCAGGTGGGGCC					22	2	1	1.00	1	0	0	0	1	0
.....TACGGCCGCGCACCTGCTGCG					20	1	2	0.50	1	0	1	0	0	0

Anti-sense strand reads

[illegible]

Show Alignment With Reads

Re-alignment of all predicted orthologs

[illegible]

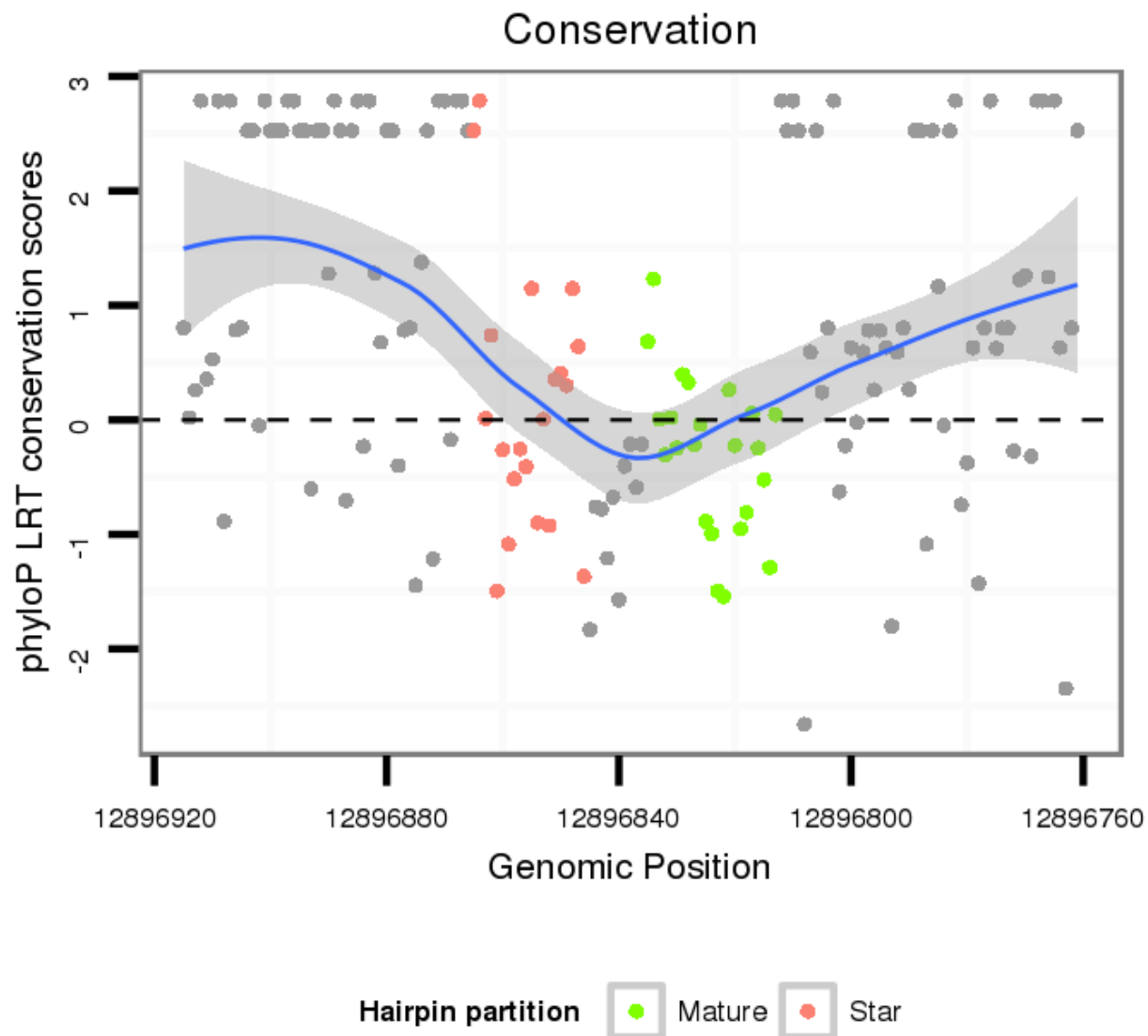
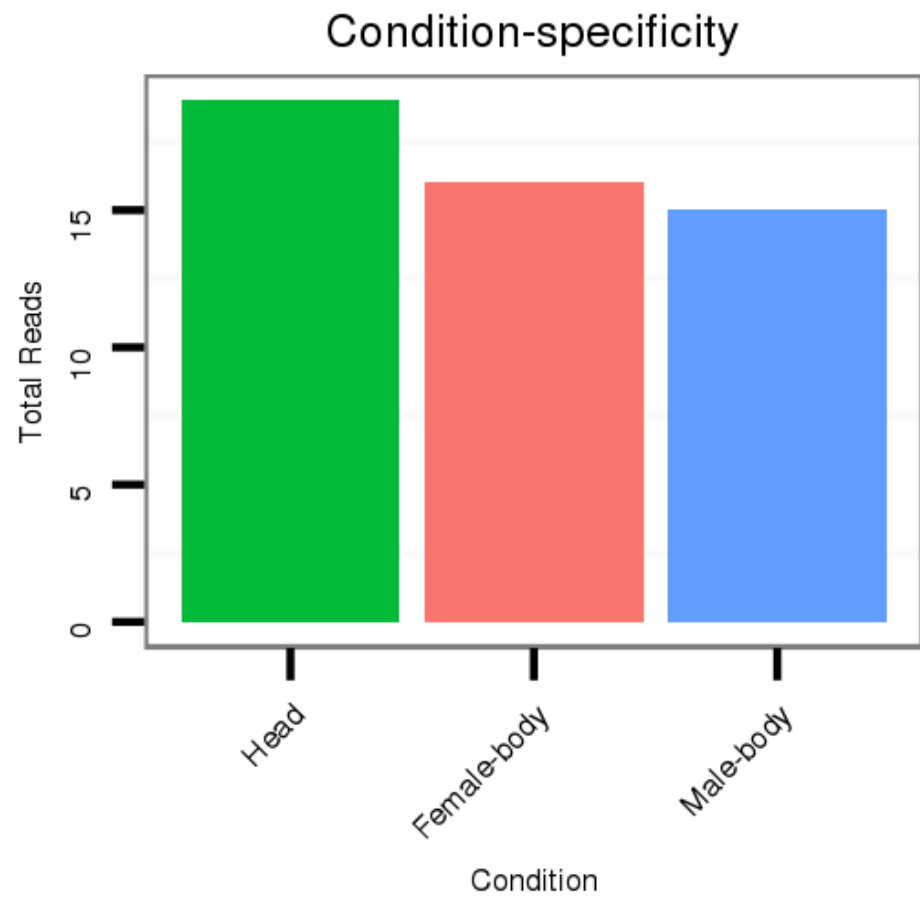
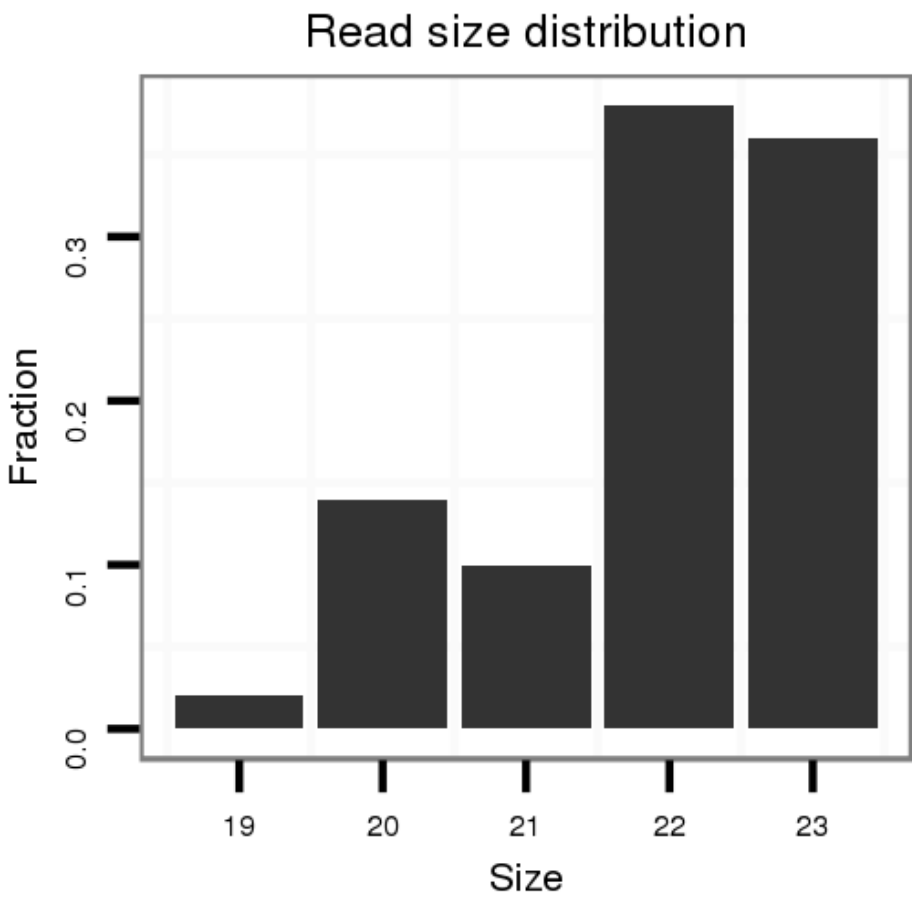
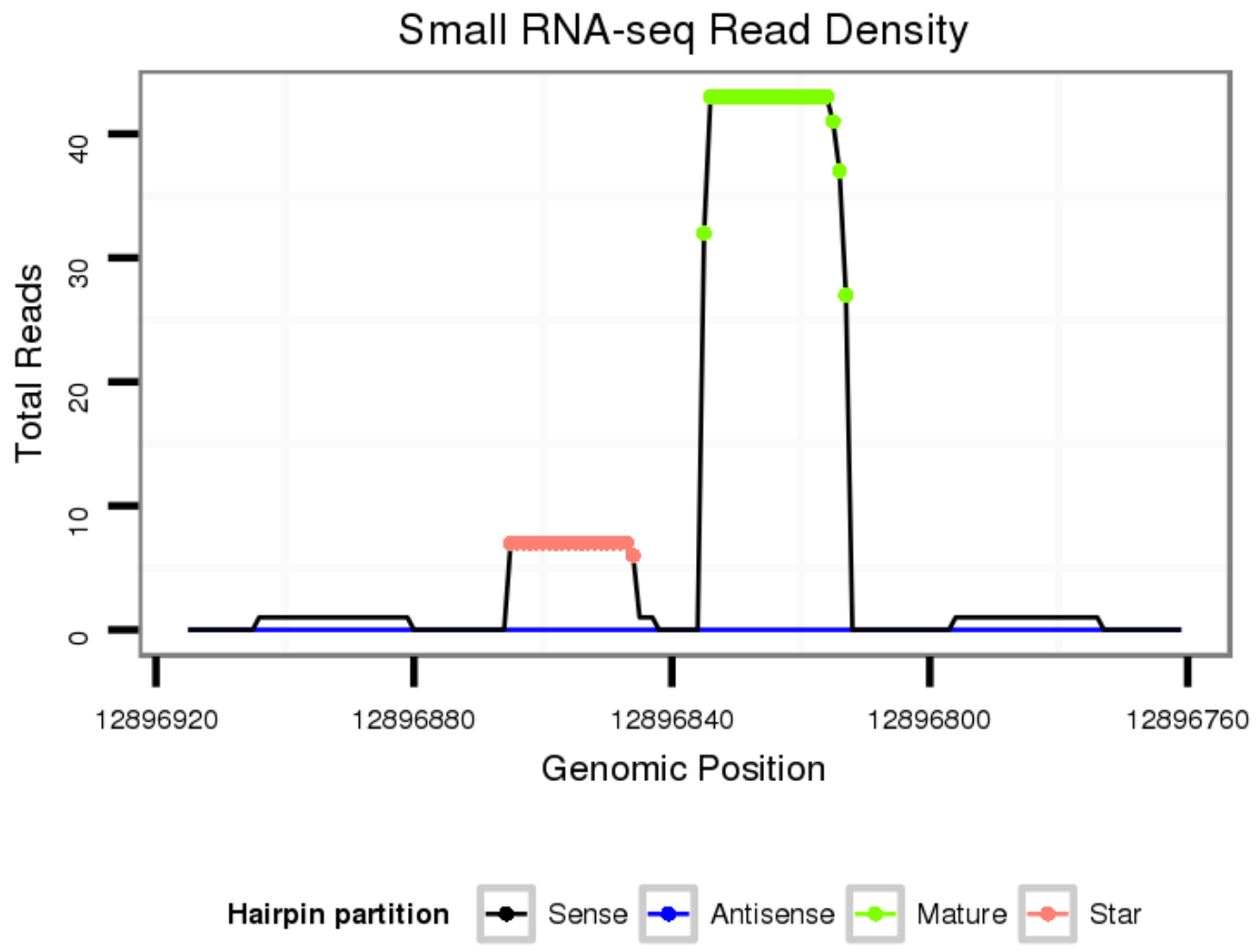
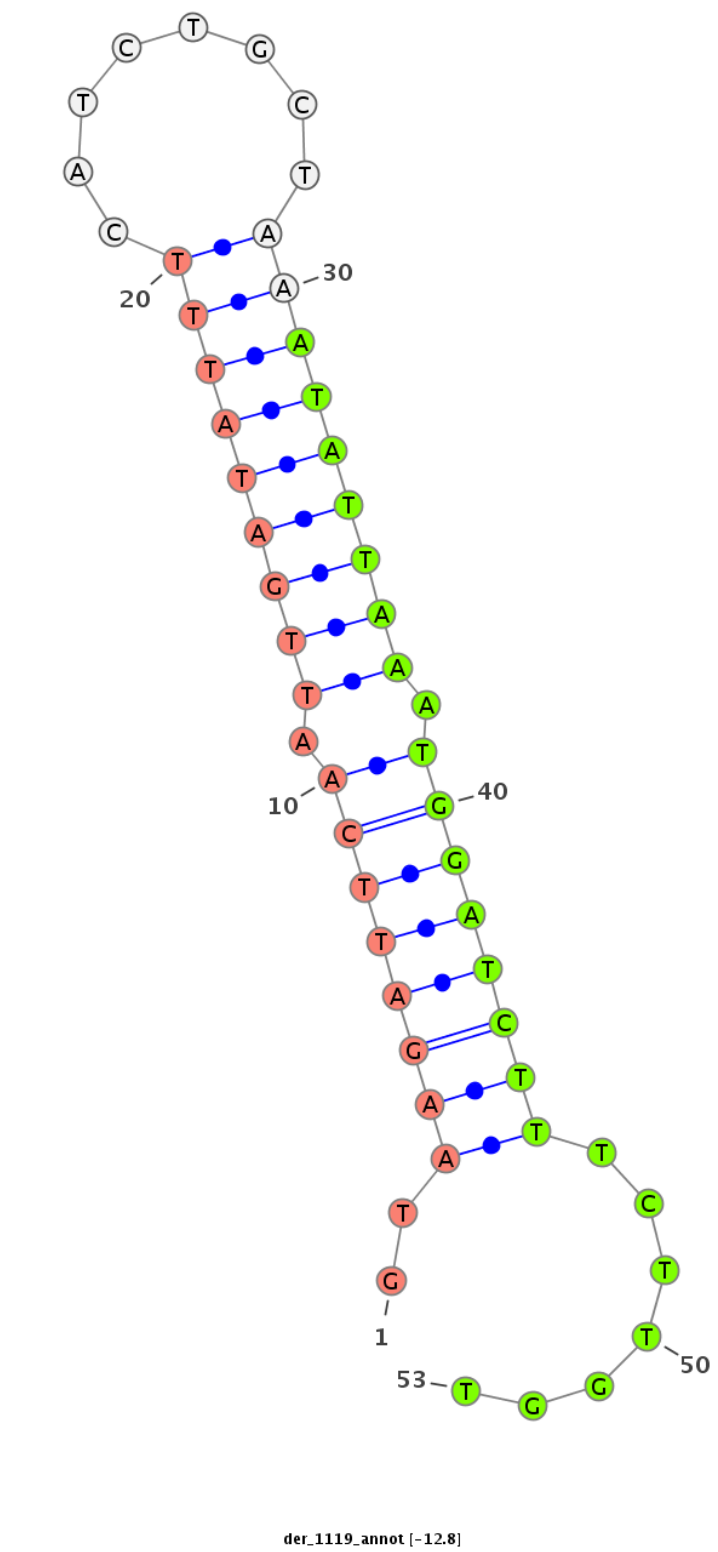
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	PASS/FAIL
crit.star	1
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crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate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

	PASS/FAIL
crit.star	1
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	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	2

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Show Alternate Folds

Flybase annotation

intron [Dere\GG20657-in]; CDS [Dere\GG20657-cds]; CDS [Dere\GG20657-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

TTGATTGTTTCCATGGGATCGGGCACTGATAACGCATCTCTTATATG STAAGATTCAATTGATATT CATCTGCTAA TATTAATGGATCTTCTTGGT AGTCACCCAACTCAGACGCAACCTCGGAAAGGATGTATCGATCACCAC	Read #	size	Mismatch	Hit	Count	Total Norm	Total	V108 head	V107 male	M055 female body	M057 embryo	V060 head
*****.(((((((.(((((((.....)))))))))).))))*****	23	0	1	17.00	17	8	7	1	0	1	0	1
.....ATATTAAGTGGATCTTCTTGGT.....	22	0	1	10.00	10	4	5	1	0	0	0	0
.....TATTAAGTGGATCTTCTTGGT.....	22	0	1	9.00	9	2	1	6	0	0	0	0
.....ATATTAAGTGGATCTTCTTGG.....	20	0	1	5.00	5	1	1	3	0	0	0	0
.....GTAAGATTCAATTGATATT.....	21	0	1	4.00	4	2	0	2	0	0	0	0
.....ATATTAAGTGGATCTTCTTGG.....	20	0	1	2.00	2	0	0	2	0	0	0	0
.....ATATTAAGTGGATCTTCTTGG G	23	1	1	1.00	1	1	0	0	0	0	0	0
.....TATTAAGTGGATCTTCTTGG A	22	1	1	1.00	1	1	0	0	0	0	0	0
.....TATTAAGTGGATCTTCTTGG.....	21	0	1	1.00	1	0	0	1	0	0	0	0
.....GTAAGATTCAATTGATATT.....	19	0	1	1.00	1	1	0	0	0	0	0	0
.....CCATGGGATCGGGCACTGATAAC.....	24	0	1	1.00	1	0	0	0	1	0	0	0
.....ATATTAAGTGGATCTTCTTGG G	22	1	1	1.00	1	0	1	0	0	0	0	0
.....GACGCAACCTCGGAAAGGATGT.....	23	0	1	1.00	1	0	1	0	0	0	0	0
.....GTAAGATTCAATTGATATTTCAT.....	23	0	1	1.00	1	0	1	0	0	0	0	0

Anti-sense strand reads

[illegible]

No data available in table

Show Alignment With Reads

Species	Coordinate	ID	Alignment
droBr2	scaffold_4845:12896761-12896915_-	der_1119	TTGATTGTTTCCATGGGATCGGGGCACTGATAACGGCATCTCTTATATG TAAGAT -----TCA--ATTGATATT CA -----T--CTGCTA-- AT --A-----T----T-AAATGGATCTTTCTTGG AG TCACCCAAC T CAGAGCGCAACCTCCGGAAGGATGTATCGCATCACCAC
droYa3	2R:18521992-18522146_-		TTGATTGTTTCCATGGGATCGGGGCACTGATA CGGCATCTCTTATATGTAATAT -----TCA--AT GATATTTCA -----T--CT GCTA --AAT--A-----T----T- AA TGGATCTTTCTTGG AG TCACCCAAC T CAGAGCGCA CT CCGGAAGGATGTATCGCATCACCAC
droSec2	scaffold_1:10453829-10453988_+		TTGATTGTTTCCATGGGATCGGGGCACTGATA CGGCATCTCTTAATGTAATATAC -----TCA-- ACTGATATTCTCGG -----A-- AACCTA --AAT--A-----T----T-AAATGGATCTTTCTTGG AG TC CCCAAC T C SAGAGCGCA CT CCGGAAGGATGTATCGCATCACCAC
droSim2	2r:13615978-13616137_+	dsi_8688	TTGATTGTTTCCATGGGATCGGGGCACTGATA CGGCATCTCTTAATGTAATATAC -----TCA-- ACTGATATTCTAGGA -----T-- AACCTA --AAT--A-----T----T-AAATGGATCTTTCTTGG AG TC CCCAAC T C SAGAGCGCA CT CCGGAAGGATGTATCGCATCACCAC
dm3	chr2R:12945306-12945467_+		TTGATTGTTTCCATGGGATCGGGGCACTGATA CGGCATCTCTTATATGTAATATATAT -----TCA-- ACTGATATTCTAGG -----T-- AACCTA --AAT--A-----T----T-AAATGG AGCTTC AGTCACCCAAC T CAGAG CA CT CT CCGGAAGGATGTATCGCATCACCAC
droEug1	scaf7180000409672:12173216-2173369_-		TTGATTGTT ACCG CTGGGATCGGGG ACCC CA AG CT GGCATCT CA AT ATG TAA CA ATTATTC ----- ACTGAG -----A----- C - ATCTC --AAT--A-----T----T- TTATG CA AT CA AGC AGTCACCCA AT CTC CA AG CA CT CCCG AG CA AG ATGATAT CT CA CC AC
droBia1	scaf7180000301754:5193485-5193643_+		TTGAT CT TA TCC CTGGGATCGGGGCACT GAT AG CG AT CGCATCT CA AT ATG TAA CA CTG -----T TA -- ATGA AT AGTTTGH -- A -- C -- AA ATC --AAT--A-----T----T- TA ATGGAT CT TA GA AC AGC AGTC CCCA AT CTC CA AG CA CT CCG GA CA AG ATG TA CT CA CC AC
droTak1	scaf7180000451598:45398-46144_+		ACAA CC GT AT TCC CTGGGATCGGGGCACT CA AG CT GG CA CT CTTATAT GT GAGAT GATTTC -----T TT -- ---- ATT CTTAAATG ----- A -- CT AT T --AAT--A----- C -----T TC ---- CA AT CTT CT AGTC TC TC AG CAC CC CA AT CTC CA AG CA CT CC CA AG CA AG AT CT CA CC AC
droEl1	scaf7180000491027:91703-91859_+		ACAA CC CT AT TCC CTGGGATCGGGGCACT CA AG CT GG CA CT CTTATAT G TAAGA G GT TTCC ----- TCG -----ATT CA -----T--CT TTA -- SAT --AG-----T----T- C - CTTT AC TT T TC AGTC TC TC AG CAC CC CA AT CTC CA AG CA CT CC CA AG CA AG AT CT CA CC AC
droRho1	scaf7180000780084:376378-376535_-		TTGAT CT TA TCC CTGGGATCGGGGCACT GAT AG CG AT CT CA AT ATG TAA A AG -----T TT -- AGA GAT GAG TA AGG ----- G -- CTTC --AAT--A----- C -----T- AA CGGA GT CT CTTGG AGC AGTC CCCA AT CTC CA AG CA CT CCG GA CA AG ATG TA CT CA CC AC
droFic1	scaf7180000453948:2484365-2484520_-		TTGA CC GT AT CC CTGGGATCGGGGCACT CA AG CT GG AT CT CA AT ATG TAA AG AT ----- ---- AGAA TT AT TT AG ----- CAG CA TC -- SAT --A-----T----T- T - CTGG TA -- CC CT GG AT AGTCACCCAAC T CAGAG CA CT CT CC CA AG CA AG ATG TA CT CA CC AC
droKik1	scaf7180000302470:1382810-1382966_+		TTGAT CT TA TCC CTGGGATCGGGGCACT CA AG CT GG AT CT CA AT ATG TAA AG CT ----- ---- AGAA TT AT TT AG ----- A -- GA AT AT CT TA -----T--T TT TT TA -- GGT --AT-- A -----T- TA CG TCAG CT TT AT AGTCACCCAAC TA CC SAGAG CA CT CT CC GA CA AG ATG TA CT CA CC AC
droAna3	scaffold_13266:13654913-13655061_-		TC GAT CT TA TCC ATGGGATG CA AG GCAT GTA AG GCAT AT CT ATATG TAAGTA AAAA ----- ---- TT CA TT CT TA -----T-- C AT TA -- TAT --A----- A -- ---- CC CT TA TTT CA TC AGTC CCCA AT CTC CA AG CA CT CCG GA CA AG ATG TA CT CA CC AC
droBip1	scaf7180000396759:2481828-2481987_+		TTGAT CT TA TCC ATGGGATG CA AG GCAT GTA AG GCAT AT CT ATATG TAAGTACAC TT ----- ---- TT TA TT GTT -----T-- CT CA TT --AAT--A----- ACC CA AA ATA CT CC AT CT TA

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

Predicted structure



Flybase annotation

intron [Dere\GG11189-in]

No Repeatable elements found

Sense Strand Reads

Anti-sense strand reads

Show Alignment With Reads

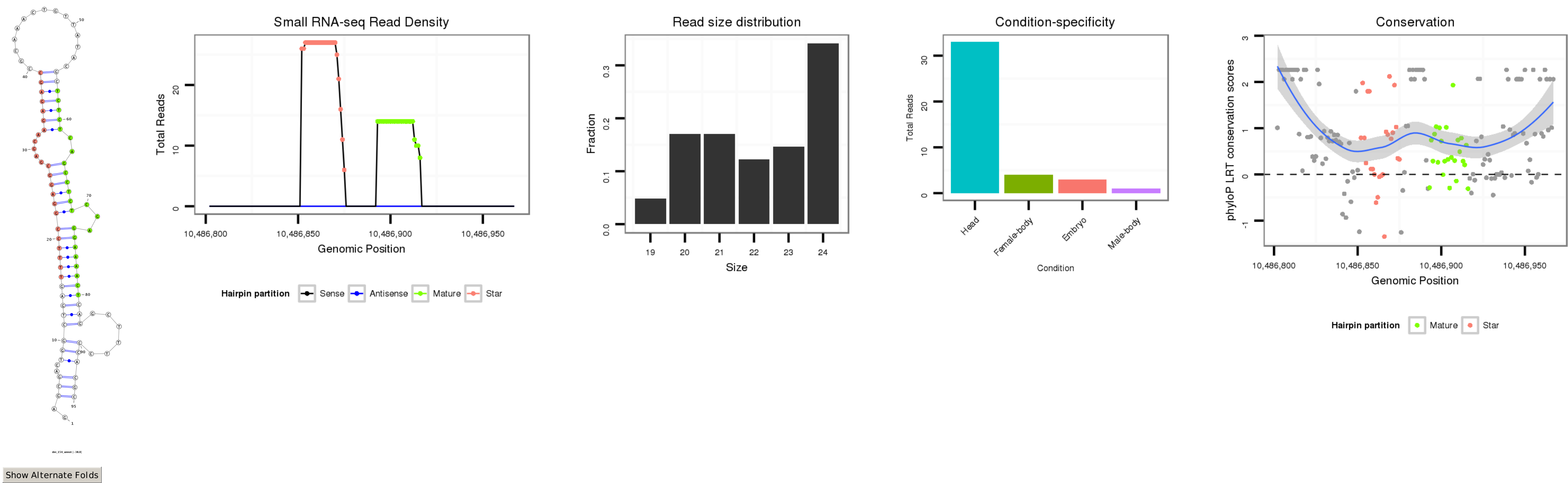
Re-alignment of all predicted orthologs

Generated: 09/08/2015 at 07:42 PM

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

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Flybase annotation

intergenic

No Repeatable elements found

Sense Strand Reads

[illegible]

Anti-sense strand reads

Show Alignment With Reads

Re-alignment of all predicted orthologs

[illegible]

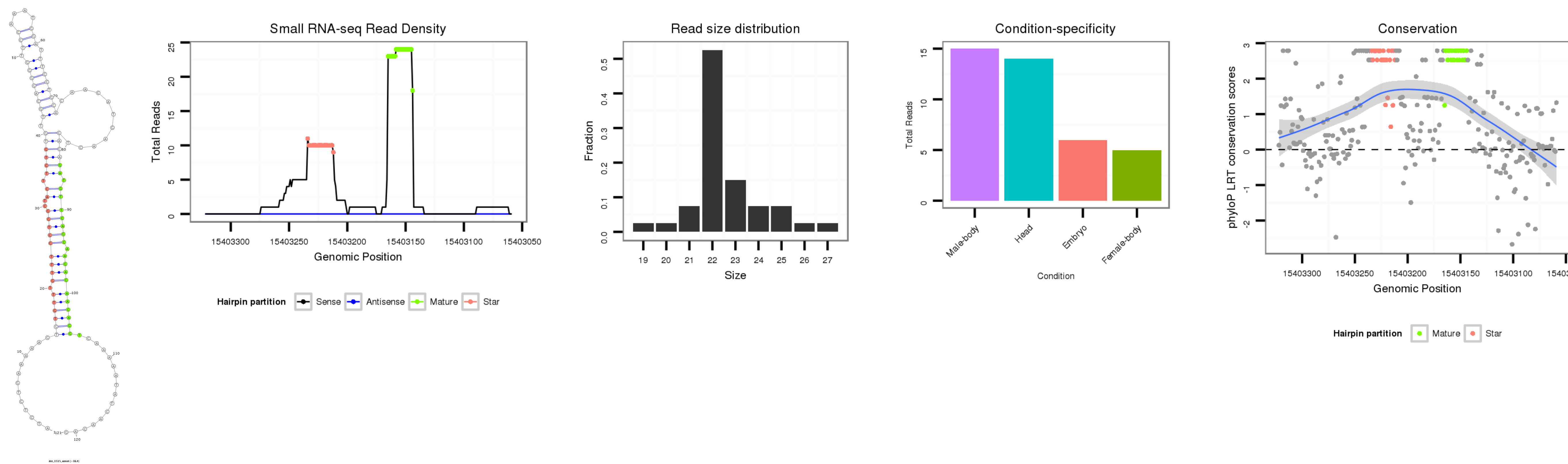
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	PASS/FAIL
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crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	0
crit.uri	0
crit.back	0
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	0
rescue.candidate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

der_1515	scaffold_4770:15403109-15403272 -	confident	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 [Dere\GG17540.in]; utr5 [utr5_plus_10181]

No Repeatable elements:

Sense strand Reads																								
hide 3p reads		show mid mismatch reads																						

Anti-sense strand reads

TGGGTCATCTATCATATATGTGTAAAGGGGTAAAGTGTAGGGTAACCTCGGGTACCTAGACCTCGGGCGTCTCTAGAGACATTTTCA-**TCACAAACAACACCGCATGACGAC**CAACGCTCCCAAGGATTCCTAAAGACGCTGTGTACTTCAGGTCT**TTACAGAGCTGTTCTGTTGTGCG**CTTTTATATGTCTCTTAAGTCTCAACCTCGAAGATTCGTAAATATTAGATTGGTCTTGCTAGCTTTCACATCTTTATTA

Read #	Hit	Total	size	Mismatch	Count	Norm	Total
1	1	1	100	0	0	0	100

female body

Show Alignment With Reads

Re-alignment of all predicted orthologs

[illegible]

Generated: 09/08/2015 at 07:42 PM

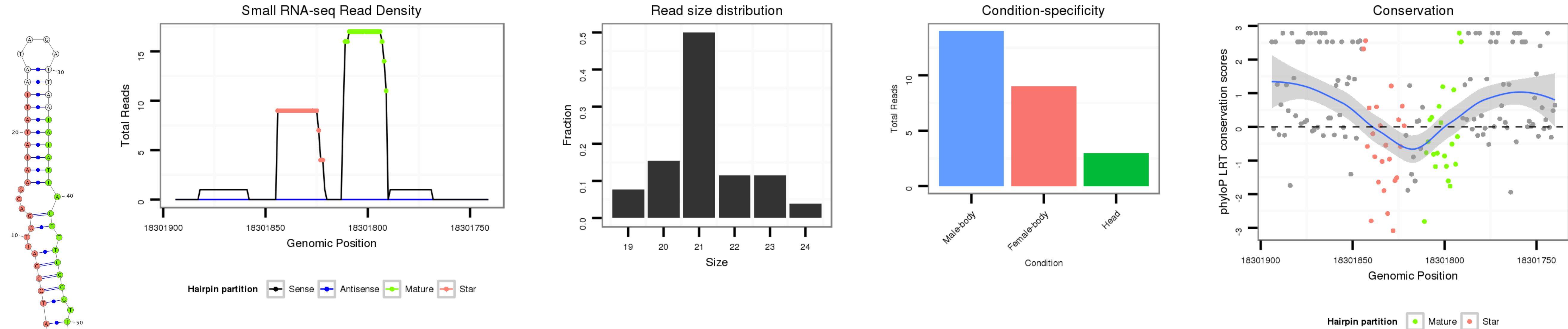
	PASS/FAIL
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crit.loop	0
crit.mor	0
crit.hall	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.ptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	7
rescue.candidate	8

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

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
der_130	scaffold_4929:18301791-18301844 -	confident	Mirtron	intron	[View on UCSC Genome Browser (Cornell Mirror)]

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

Predicted structure



Show Alternate Folds

Flybase annnotation

intron [Dere/GG23358-in]; CDS [Dere/GG23358-cds]; CDS [Dere/GG23358-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

CTGGCATTGGCTTTGCAGTCTACTTACTTTCCCGTCATCAAGATGAACAGGTATCCGATTGGACGAATATATTAAATAGATTAAATATATTACTTTTCGGGTTGCAGAAAAAATTATTTGACGAGCAGTGCGAAGTAATGGGCGCTTCTGGACTTGG	Read #		Hit	Total		V107	M055	V108	V060
*****(((((((((((((.....))))))))))..))))..))..*****	size	Mismatch	Count	Norm	Total	male	female	body	head
.....TATATTACTTTTCGGGTTGCAG.....	21	0	1	7.00	7	4	1	2	0
.....GTATCCGATTGGACGAATATATT.....	23	0	1	3.00	3	1	2	0	0
.....ATATATTACTTTTCGGGTTGCAG.....	23	1	1	3.00	3	0	1	2	0
.....ATATATTACTTTTCGGGTTGCAG.....	21	0	1	3.00	3	1	1	1	0
.....ATATATTACTTTTCGGGTTGCAG.....	22	0	1	3.00	3	2	1	0	0
.....GTATCCGATTGGACGAATATA.....	21	0	1	3.00	3	3	0	0	0
.....ATATATTACTTTTCGGGTTGC.....	20	0	1	2.00	2	0	2	0	0
.....GTATCCGATTGGACGAATAT.....	20	0	1	2.00	2	1	1	0	0
.....TATATTACTTTTCGGGTTGCAG.....	22	1	1	2.00	2	0	1	1	0
.....AAAAATTATTTGACGAGCAGT.....	21	0	1	1.00	1	1	0	0	0
.....TATTACTTTTCGGGTTGCAG.....	19	0	1	1.00	1	1	0	0	0
.....GTATCCGATTGGACGAATATATTA.....	24	0	1	1.00	1	0	1	0	0
.....TTGCAGTCTACTTACTTTCCCGTC.....	24	0	1	1.00	1	1	0	0	0
.....ATATATTACTTTTCGGGTTG.....	19	0	1	1.00	1	1	0	0	0

Anti-sense strand reads

GACCGTAACCGAAACGTCAGATGAATGAAAGGGCAGTAGTTCTACTTGTGCATAGGCTAAACCTGCCTATATATAATATATCTAATTATATAATGAAAGCCCAACGCTTTTTTAAATAAAGTCTCGTCAAGCTTCATTACCCGCGAAGACCTGAACC	Read #		Hit	Total	
*****(((((((((((((.....))))))))))..))))..))..*****	size	Mismatch	Count	Norm	Total
No data available in table					
Show Alignment With Reads					

Re-alignment of all predicted orthologs

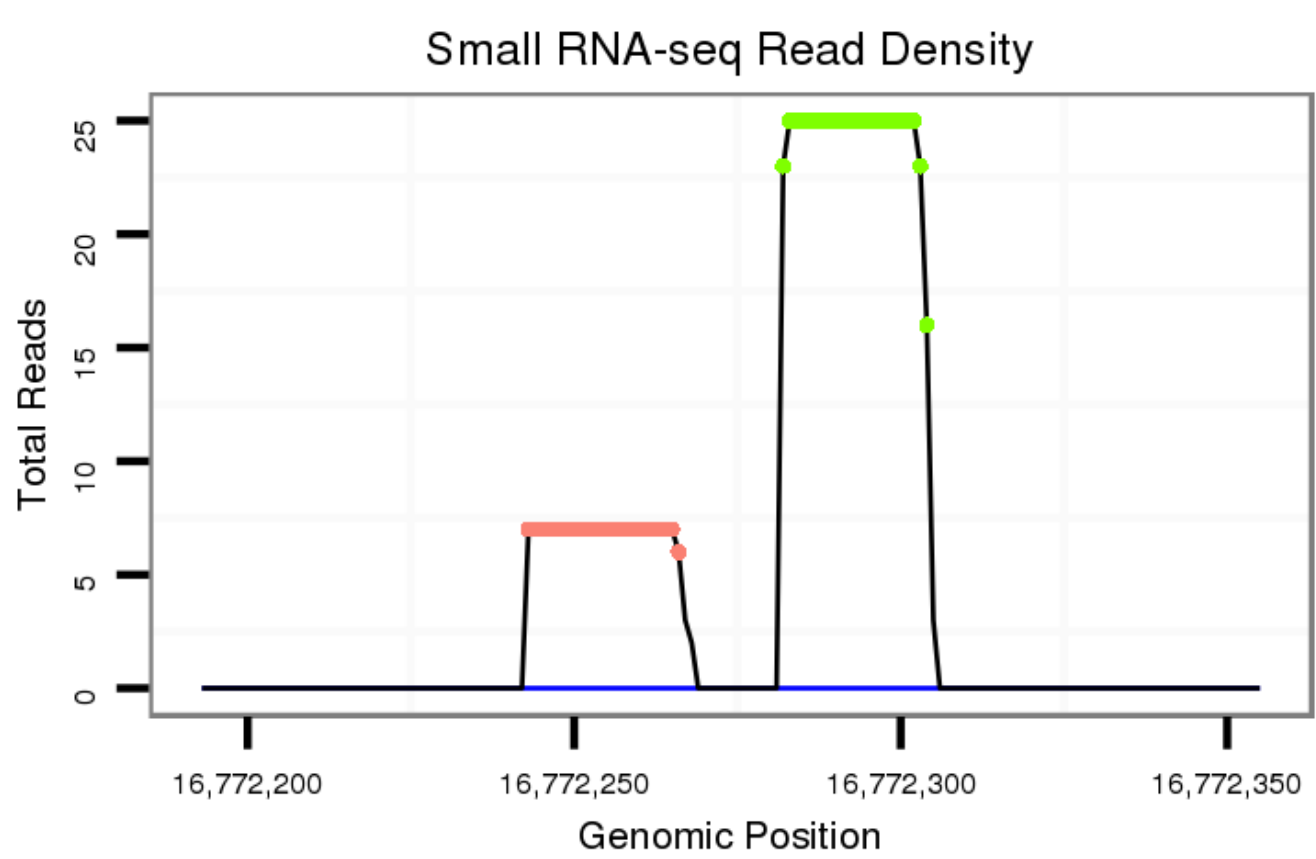
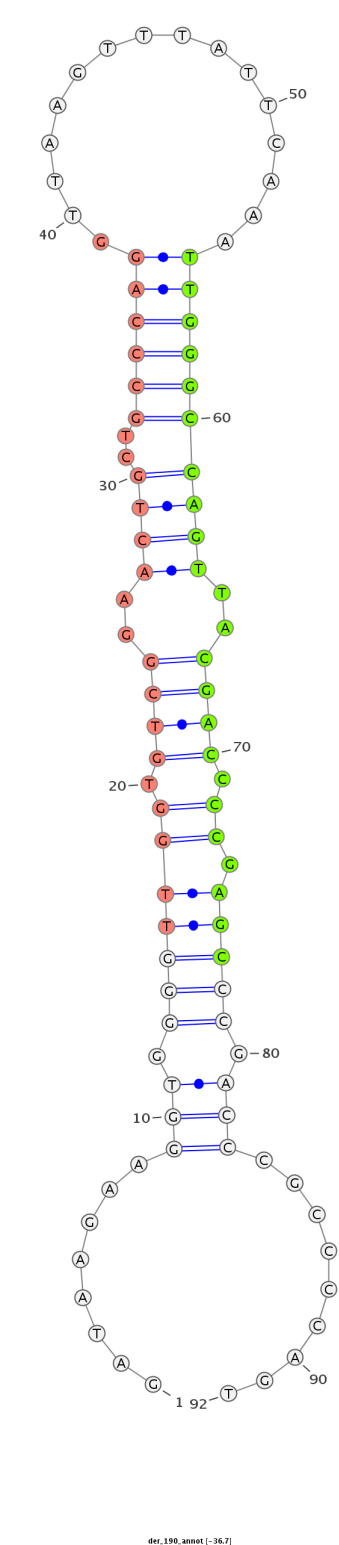
Species	Coordinate	ID	Alignment
droEre2	scaffold_4929:18301740-18301894 -	der_130	CTGGCATTGGCTTTGCAGTCTACTTACTTTCCCGTCATCAAGATGAACAGSTATCC-----GATTGGA--CGAA-----TATATT-----AATAGATTAAAT--TATT-----ACTTT-CGGGTTGCAGAAAAAATTATTTGACGAGCAGTGCGAAGTAATGGGCGCTTCTGGACTTGGT
droYak3	2L:16992502-16992664 +		CTGCCTTTGGCTTTGCAGTCTACTTACTTTCCCGTCATCAGATGAACAGGTATAC--AAATTAA--TC-C-----TAG--TCACGAATTAGATGATTAAAT--TATT-----ACTTT-CGGGTTGCAGAAAAAATTATTTAACCAGCAGTGCGAAGTAATGGGCGCTTCTGGACTTGGT
droSec2	scaffold_1:1978025-1978190 +		CTGGCTAGGCTTTGCAGTCTACTTACTTTTCGACATCCAGATGAACAGGTATCC-----GATTGGA--AGAA-----AACATTTCACAAAGCAATCTATATAAA--TATT-----GTTT-CGAA--TTCGACGAAAAAATTATTTAAGAGCAGTGCAGTCTCATGGGCGCTTCTGGACTTGGT
droSim2	2r:5151113-5151278 +		CTGGCTAGGCTTTGCAGTCTACTTACTTTTCGACATCCAGATGAACAGGTATACC-----GATTGGA--AGAA-----CAAAATTTCACATAGAAATCTATATAAA--CTT-----ACTTT-CGAA--TTCGACGAAAAAATTATTTAAGAGCAGTGCAGTCTCATGGGCGCTCTCTGACTTGGT
dm3	chr2R:4336352-4336517 +		CTGGCTAGGCTTTGCAGTCTACTTACTTTTCGACATCCAGATGAACAGGTATACC-----GATTGGA--AGAA-----CTAGTTTGACGAAGCCAAATTTATATAAA--TATT-----ACTTT-CG--TTCGACGAAAAAATTATTTAACCAGCAGTGCAGTCTCATGGGCGCTTCTGGACTTGGT
droEug1	scf7180000407691:196648-196810 +		CTGGAGTTGGCTTTGCAGTCTACCTGCTTCCAGGCACCAAGATGACAGGTAGC-----TAAATAC--CAC-----AAAACGAGTTTGAGA----TCACATTTCGA--TATTA-----CTTTTACCTACAGAAAAATTTATTCAGCAACAGTGCAGCTCATGGGCTGAATCGAGACTTGG
droBial	scf7180000302291:2222453-2222618 +		CTGGAGTTGGCTTCGAGTCTACCTGCTTCCAGGCATCAATGAACAGGTAGCC-----CATTTGC--AGC-----CAGTTTAAACGGTCTAATTAATTATAGC--TTC-----CTTTTTCCTTAAAGAAAAATCTATTGTATGACAGTGCGAAGTAATGGGCTGATTCGGACTTGGT
droTak1	scf7180000415627:219738-219903 +		CTGGAGTTGGCTTTGCAGTCTACCTGCTTCCAGGCATCCAGGAACAGGTATACC-----CCTTCC--AAAA-----CAGCTTTTCGACCAATGCCCTTTAAA--CATTA-----ACTTT-CAACTTCGACGAAAAATCTATTGTATGACAGTGCAGCTCATGGGCTATTCGGACTTGGT
droEle1	scf7180000491240:1162683-1162848 +		CCGCATCGGCTTTGCAGTCTACCTGCTTCCAGGCACCAAGATGACAGGTATGATC-----GATTGGA--GAAT-----TAGTTTCAGGCTTAAATCATCTTACTGATT-----GTTTTCTCTCACAGAAAAAATTATTTACCGAACAATGCGAGCTCATGGGCGCTTCTGGCTCGGT
droRho1	scf7180000770177:461531-461694 +		CTGGAGTTGGCTTTGCAGTCTATCTGCTTCCAGGCATCAATGAACAGGTATACC-----TATTTTC--GACC-----TAGTTTAA--CTCCAGCTCATCTTAATGATT-----GTTTTTCCTTACAGAAAAAATTATTTACCGAACAATGCGAAGTCTATGGGCTATTCGGACTGAT
droFic1	scf7180000453851:2002640-2002802 -		CTGGAGTTGGCTTTGCAGTCTATCTGCTTCCAGGCATCCAGGAACAGGTATACC-----TCCACA--AAAG-----AATCT--GGATCAACCTCATCTTAATCATT-----CTTTT-CGCCGTCAGAAAAATTTATTCAGCAACAGTGCAGCTCATGGGCTATCTGGACTCTGT
droKik1	scf7180000302277:189740-189898 +		CTGGAGCGGGCTTTGCCTCTATCTGCTTCCAGGCATCCAGGAACAGGTATGAA-----TAAATAT--CTAACTAATTAA-----TAAATACCATTA--TATATT-----CAAA--TTTAA--TTCAGCAGAAAAAATTATTTAGAGCAATGCGAAGTCTATGGGCGCTTCTGGCTTGGT
droAna3	scaffold_13266:1668872-1669031 -		CAGCAGTTTCCTTTGCAGTCTACTTCTTTCCAGGCATCCAGGAACAGGTATGATTATGATATATATAT-----TATAAATAA--AAC-----TTCCTTACCTA--ATCT-----CAATTCTCCCTTAAGAAAAAATTCTTGTAGCAATGCGAAGTCTATGGGCTCTGCACTTAAT
droBip1	scf7180000396730:2662584-2662739 -		CTGGCTTTTCCTTTGCAGTCTACTTCTTTCCAGGCATCCAGGAACAGGTATATA-----TTATGAT--ACTT-----TATAAATCTTT-----GCATTAAAC--TATT-----GATC--CCCCGTAAAGAAAAAATTCTTGTAGCAATGCGAAGTCTATGGGCTCTGCACTTAAT
dp5	4_group3:419174-419336 +		CCGCAGCTGCTTTGCTCTATCTCTCTCCAGGCAGAGCCAGCTATTT-----GACGCG--CAAC-----TCCTCCAGATTCGTGCGCGCTCCCTAA--GCG-----TTTTT-CGAACCGACCAAGAGCTGCAGTCTATGGGCTAGC---GACTGCAC
droPer2	scaffold_1:1895039-1895201 +		CCGCAGCTGCTTTGCTCTATCTCTCTCCAGGCAGAGCCAGCTATTT-----GACGCG--CAAC-----TCCTCCAGATTCGTGCGCGCTCCCTAA--GCG-----TTTTT-CGAACCGACCAAGAGCTGCAGTCTATGGGCTAGC---GACTGCAC
droW12	scf2_1100000004513:3159820-3159917 -		CCGCAGCTGCTTTGCTCTATCTCTCTCCAGGCAGAGCCAGCTATTT-----GACGCG--CAAC-----TCCTCCAGATTCGTGCGCGCTCCCTAA--GCG-----TTTTT-CGAACCGACCAAGAGCTGCAGTCTATGGGCTAGC---GACTGCAC
droVir3	scaffold_12875:9400159-9400323 +		CCGGCTGCTCATATGCTCTACTTACTATCCAGGTTTCGAGGAACAGGTATACA-----CACAATTATATGAGCTGCCTTA-----TACCTACCTA--TATTTT-----CTTTTCCTTCACTTACCACCGCTAACTTTTTCGAGAGCAGCTGCTATGGGCAAT---GAGATGCAT
droMoj3	scaffold_6496:17704766-17704922 -		CCGGCTGCTCTTTGCTCTATCTATCTATCCCGTTTCGAGGAACAGGTATATG-----CGCATTACCGCGCTGCCTAA-----TACCTAGACGA--GATTCTC-----TCTCTGTCTCCGACCAAACTCTATGAGAGAGCAAGCTCTATGGGCAAT---GAGCTCAT
droGr12	scaffold_15245:2672740-2672898 +		CCGGCTGCTGCTCTTTGCTCTATCTATCTATCCAGGTTTCGAGGAACAGGTATGAGT-----AATTTTAACTGATCAGCCTAA-----TACCTTGCCTAA--TCTTT-----CACT--TCAACCCACCGCAAACTATAGAGGAACAGCTCTATGGGCAATC---AATGCAT

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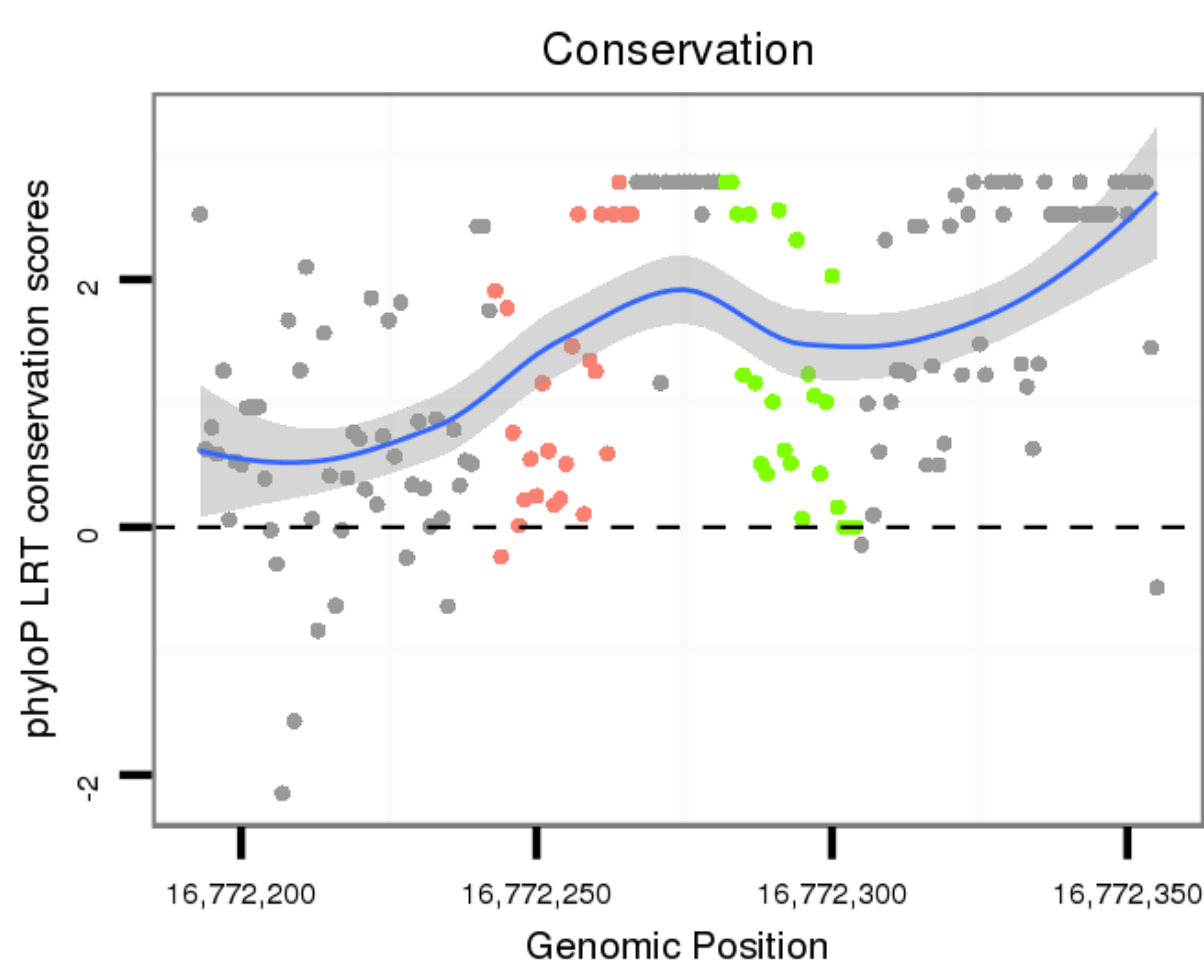
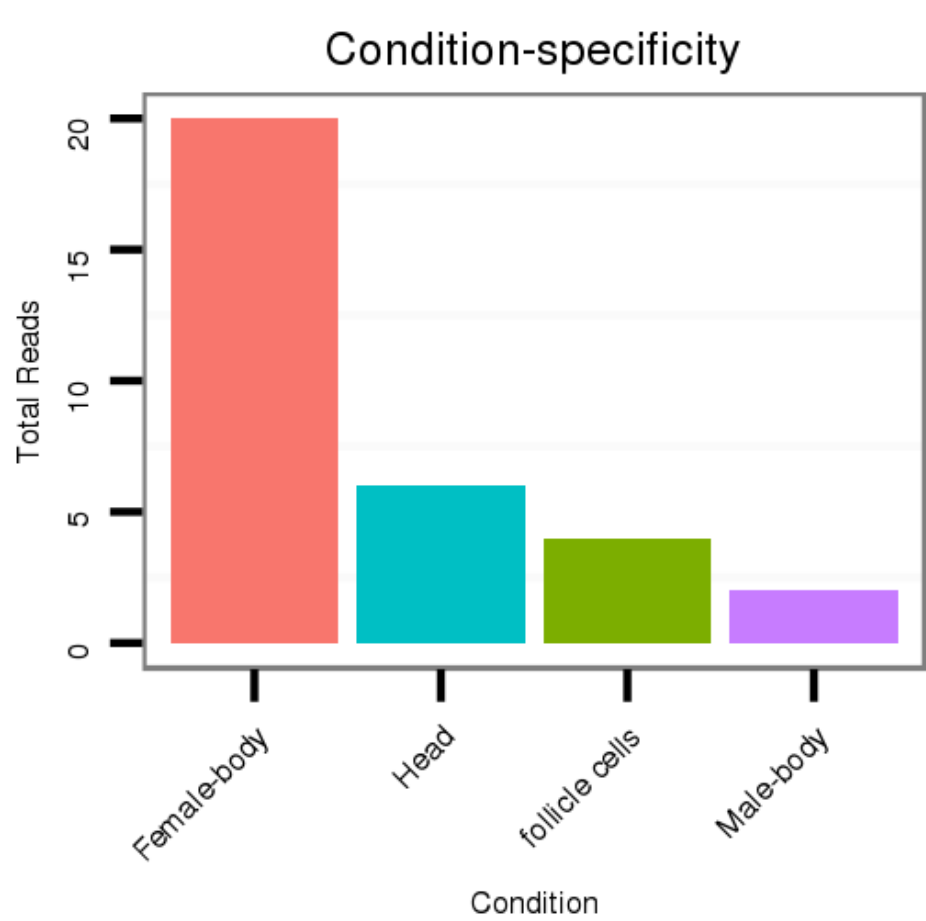
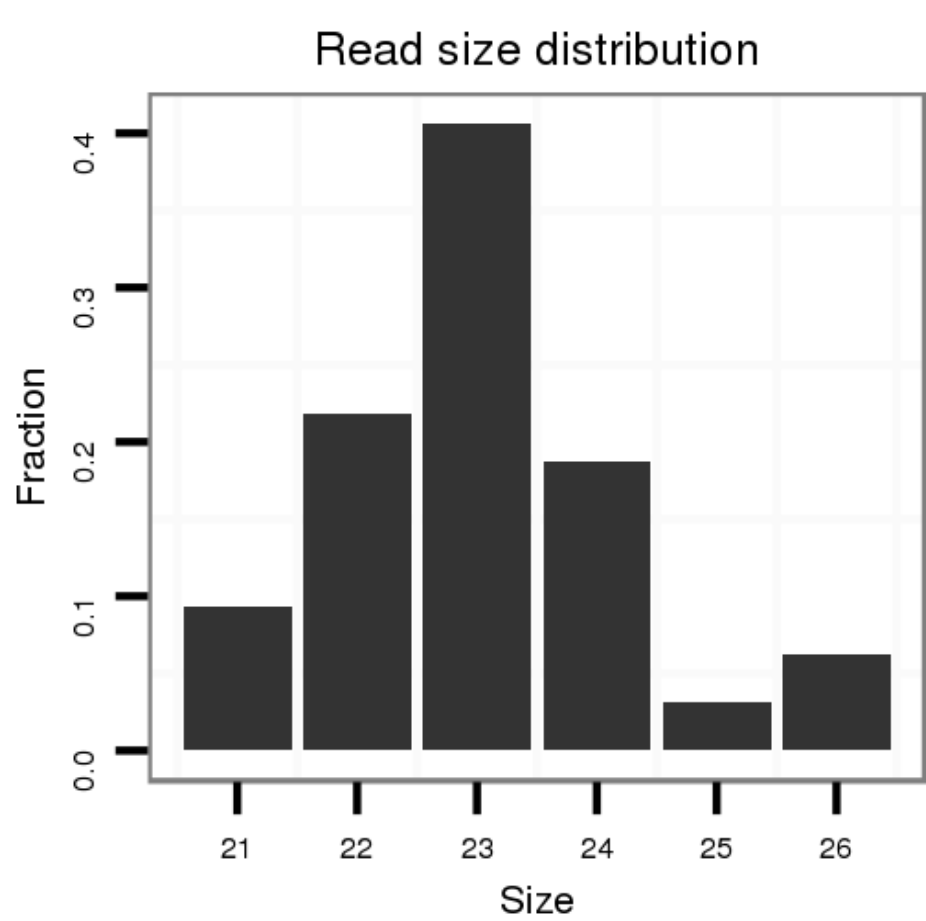
PASS/FAIL	
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.gtop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Hairpin partition Sense Antisense Mature Star



Hairpin partition Mature Star

Show Alternate Folds

Flybase annotation

Antisense to intron [Dere\GG23500-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

[illegible]

Anti-sense strand reads

Show Alignment With Reads

Re-alignment of all predicted orthologs

[illegible]

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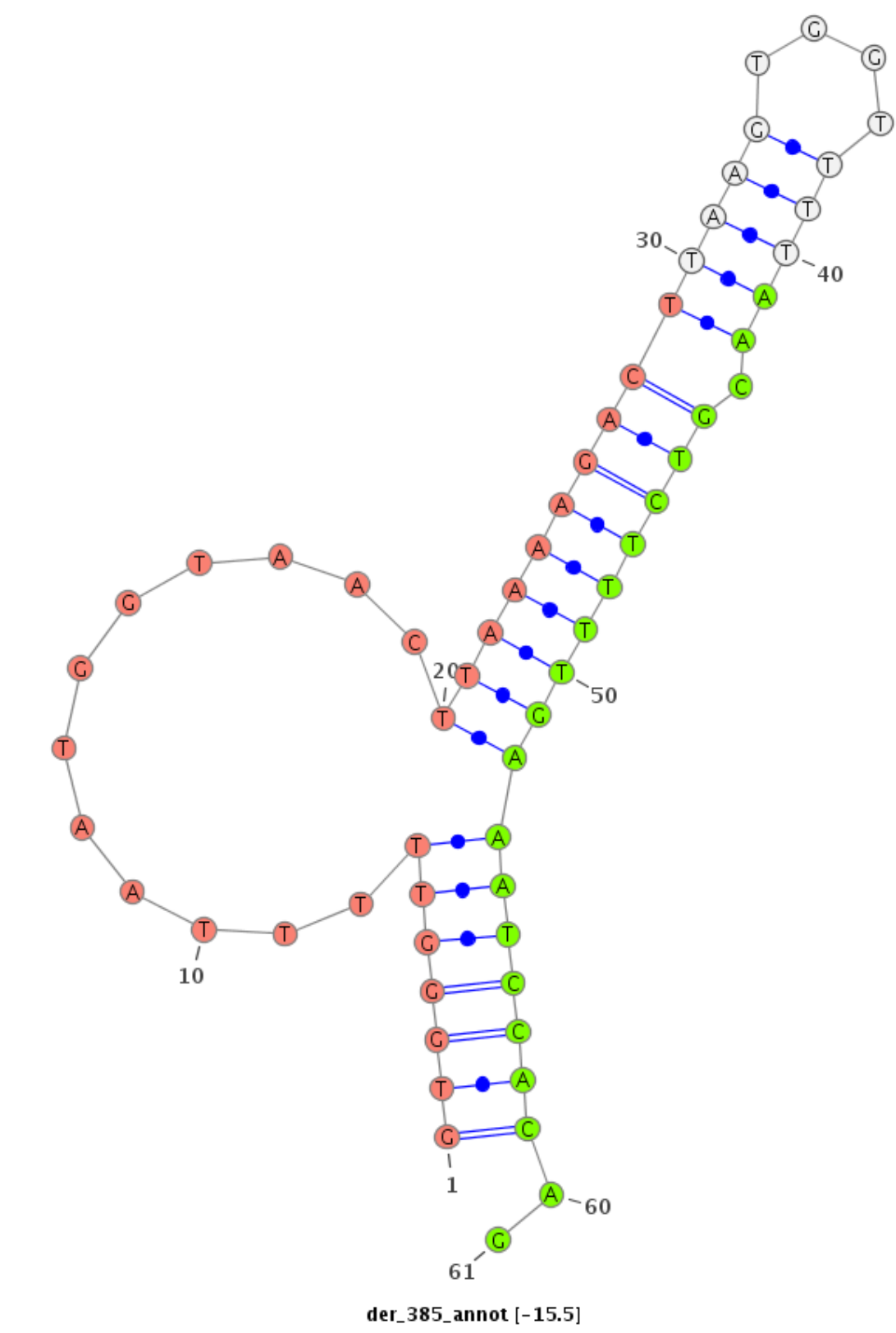
PASS/FAIL	
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.top3	1
crit.top3	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	2
rescue.candidate	2

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

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
der_385	scaffold_4690:6168018-6168078	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 [Dere\GG18281-in]; CDS [Dere\GG18281-cds]; CDS [Dere\GG18281-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

AGCTGGACCAAGCCCGACCACTACCCACTGCCGCACACATTAGCTGGGTTTTTAATGGTACTTAAAGACTTAAAGTGTTTAAAGCTTTTGAATCCACAGATCACCGTGACCGCACTGGATTCAGCAGAGCATCTGAAGTCCCCAA	Read #	Hit	Total		V108	M055	V107	V060	M057	V040
*****(((((((.....((((((((((((.....))))))))))))))))*****	size	Count	Norm	Total	head	female	male	head	embryo	embryo
.....AAGCTCTTTTGAATCCACAG	22	1	64.00	64	22	14	22	4	1	1
.....AAGCTCTTTTGAATCCACAG	21	0	15.00	15	4	5	1	0	0	0
.....AAGCTCTTTTGAATCCACAG	22	0	3.00	3	1	2	0	0	0	0
.....AAGCTCTTTTGAATCCACAG	21	1	2.00	2	0	2	0	0	0	0
.....AAGCTCTTTTGAATCCACAG	19	0	1.00	1	0	0	1	0	0	0
.....TAAGCTCTTTTGAATCCACAG	22	0	1.00	1	0	1	0	0	0	0
.....GATTGCAGCAGAGCATCTCT	25	0	1.00	1	0	0	1	0	0	0
.....CCGCACTGGATTCAGCAGAGCATCTGAAGT	22	0	1.00	1	0	1	0	0	0	0
.....ACCGTGACCGCACTGGATTGCAGC	25	0	1.00	1	0	1	0	0	0	0
.....GGAATTGCAGCAGCATCTCTGAAG	25	0	1.00	1	0	0	0	1	0	0
.....GTGGGTTTTTAATGGTACTTAAAGACT	29	0	1.00	1	0	1	0	0	0	0
.....AAGCTCTTTTGAATCCACAG	23	1	1.00	1	1	0	0	0	0	0
.....GTGGGTTTTTAATGGTAAC	19	0	1.00	1	1	0	0	0	0	0
.....CACTGGATTGCAGCAGAGC	19	0	1.00	1	1	0	0	0	0	0

Anti-sense strand reads

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