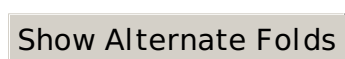


Predicted structure



Sense Strand Reads

hide 3p reads show mid mismatch reads

Anti-sense strand reads

Show Alignment With Reads

Re-alignment of all predicted orthologs

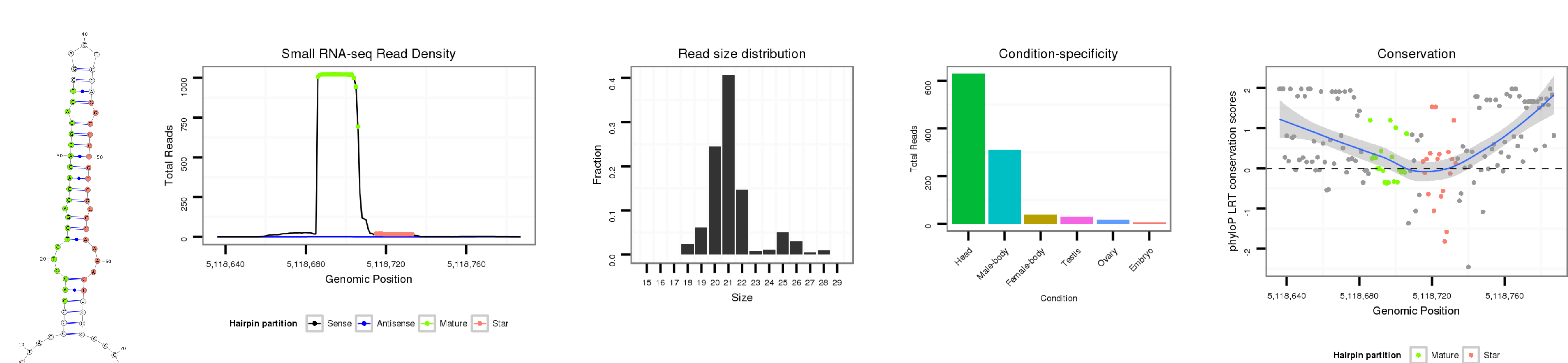
Generated: 09/08/2015 at 08:13 PM

	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	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	4
rescue.confident	4
rescue.candidate	1

ID:	Coordinate:	Confidence:	Class:	Genomic Location:	
dsi_21	21:5118686-5118737 +	confident	Canonical miRNA	3pUTR	[View on UCSC Genome Browser (Cornell Mirror)]

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Flybase annnotation

utr3 [utr3_plus_406]

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]

Generated: 09/08/2015 at 07:59 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	0
crit.back	0
rescue.total	1
rescue.dominant	1
rescue.known	1
rescue.confident	1
rescue.candidate	0

Predicted structure



Sense Strand Reads

hide 3p reads show mid mismatch reads

[illegible]

Anti-sense strand reads

[illegible]

Re-alignment of all predicted orthologs

[illegible]

Generated: 09/08/2015 at 08:00 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	0
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

three_prime_UTR [2r 5309532 5309869 +]; utr3 [utr3_plus 1921]

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 08:00 PM



doi:10.1002/1522-2675(200003)132:3<353::AID-HLCA353>3.0.CO;2-1

max_pink_CIR (SI_1050151)

No Repeatable elements found

hide 3p reads | show mid mismatch reads

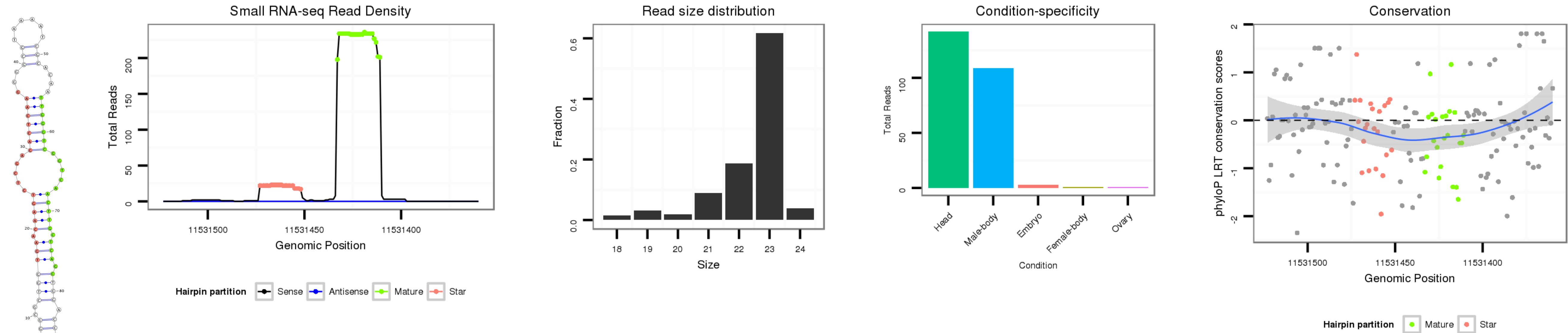
Anti-sense strand reads

Show Alignment With Reads

Generated: 09/08/2015 at 08:00 PM

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Show Alternate Folds

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

[illegible]

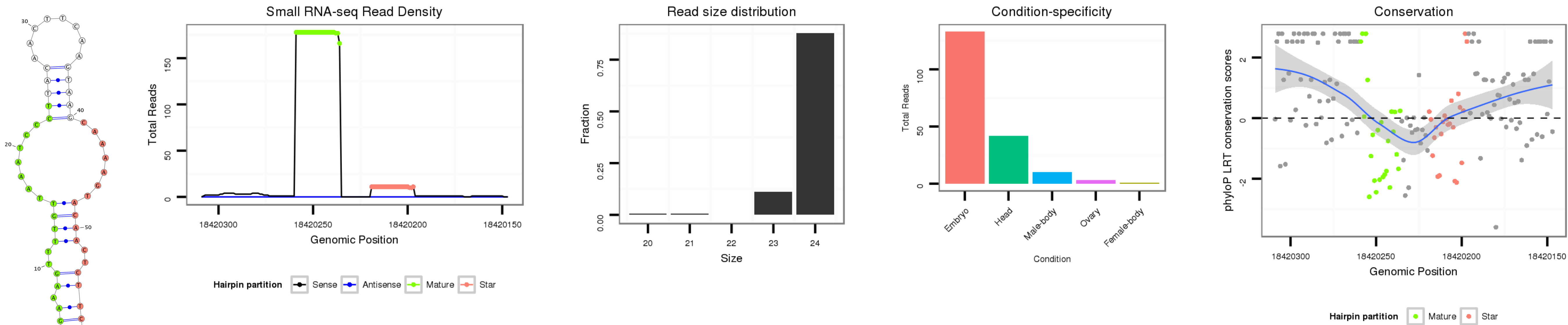
Generated: 09/08/2015 at 08:00 PM

	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	0
rescue.candidate	1


```
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



Show Alternate Folds

Flybase annotation

intron[x_18420197_18420259_-]; CDS[x_18420260_18421474_-]; CDS[x_18419916_18420196_-]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

[illegible]

Anti-sense strand reads

										SRR553488		SRR618934				
CTTGACAGTGCTGCTCCTGTGATGTGTGTCGCGCAGCTGTTGAGGCCCTCATCTTTCAAAACAATTAGGAGAAATGTTGAAGTTCATTCTGTTTCATGTTGAGAAGAAAGTCGTTTTCAGCGCAACGGCTACGAGAGGTATCACTGAGGGTGCGCCCTCTGCA										SRR902009		RT 0-2	M024			
										Read #	Hit	Total	testis	hours	male	dsim w501
										size	Mismatch	Count	Norm	eggs	body	ovaries
										Total	Total					
*****.(((.((..(((.....(((.....))))).))))).)).....*****																
Show Alignment With Reads																

Re-alignment of all predicted orthologs

[illegible]

Generated: 09/08/2015 at 10:37 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	2
rescue.candidate	0

Legend: green = **green** red = **red** blue = **blue** purple = **purple**

Sense Strand Reads

[illegible][illegible][illegible]

Precision	Coordinate	ID	Alignment
dros1m2	44270601-4270778	del_108	CGGTACTCTCGACAA-----GCAG--TT-CTC--CTCT--TCTGCCACGGCGGCAGCAGCAGCGCA-----ATAA-----CAACCAATAC-----AGTCAGTCCATCAGCAGCTGGATG--CCAGCAG-----TGTGTGT-----TGTT-----GTGTGTGACACGG--TGCAGTAGAGTCGCA--CAG-----GAGAAAGAGAA-----AG--AGCGGGGCGAAGACCGAG
drosE2	scaffold_4:2149664-2150135	del_197	CGGTACTCTCGACAA-----GCAG--TT-CTC--CTCT--TCTGCCACGGCGGCAGCAGCAGCGCA-----ATAA-----CAACCAATAC-----AGTCAGTCCATCAGCAGCTGGATG--CCAGCAG-----TGTGTGT-----TGTT-----GTGTGTGACACGG--TGCAGTAGAGTCGCA--CAG-----G-----AGAA-----AG--AGCGCG--SCAGAAACCGAG
dm3	chrX:4579780-4579933	del_464	CGGTACTCTCGACAA-----GCAG--TT-CTC--CTCT--TCTGCCACGGCGGCAGCAGCAGCGCA-----ATAA-----CAACCAATAC-----AGTCAGTCCATCAGCAGCTGGATG--CCAGCAG-----TGTGTGT-----TGTT-----GTGTGTGACACGG--TGCAGTAGAGTCGCA--CAG-----GAG--SAGAGAA-----AG--AGCGCG--SCAG--SCCAGAA
drosE2	scaffold_4690:1957109-	del_133	CGGTACTCTCGACAA-----GCAG--TT-CTC--CTCT--TCTGCCACGGCGGCAGCAGCAGCGCA-----ATAA-----CAACCAATAC-----AGTCAGTCCATCAGCAGCTGGATG--CCAGCAG-----TGTGTGT-----TGTT-----GTGTGTGACACGG--TGCAGTAGAGTCGCA--CAG-----G-----SAGAGAA-----AG--AGCGCG--SCAGAAACCGAG
drosYak3	X:3860422-3860596		CGGTACTCTCGACAA-----GCAG--TT-CTC--CTCT--TCTGCCACGGCGGCAGCAGCAGCGCA-----ATAA-----CAACCAATAC-----AGTCAGTCCATCAGCAGCTGGATG--CCAGCAG-----TGTGTGT-----TGTT-----GTGTGTGACACGG--TGCAGTAGAGTCGCA--CAG-----GAG--SAGAGAA-----AG--AGCGCG--SCAGAAACCGAG
drosYak3	scaffold_409548:355289-355458		CGGTACTCTCGACAA-----GCAG--TT-CTC--CTCT--TCTGCCACGGCGGCAGCAGCAGCGCA-----ATAA-----CAACCAATAC-----AGTCAGTCCATCAGCAGCTGGATG--CCAGCAG-----TGTGTGT-----TGTT-----GTGTGTGACACGG--TGCAGTAGAGTCGCA--CAG-----G-----SAGAGAA-----AG--AGCGCG--SCAGAAACCGAG
drosB1a1	scaffold_301703:117349-117538		CGGTACTCTCGACAA-----GCAG--TT-CTC--CTCT--TCTGCCACGGCGGCAGCAGCAGCGCA-----ATAA-----CAACCAATAC-----AGTCAGTCCATCAGCAGCTGGATG--CCAGCAG-----TGTGTGT-----TGTT-----GTGTGTGACACGG--TGCAGTAGAGTCGCA--CAG-----GAG--SAGAGAA-----AG--AGCGCG--SCAGAAACCGAG
drosTak1	scaffold_00414746:63453-63601		CGGTACTCTCGACAA-----GCAG--TT-CTC--CTCT--TCTGCCACGGCGGCAGCAGCAGCGCA-----ATAA-----CAACCAATAC-----AGTCAGTCCATCAGCAGCTGGATG--CCAGCAG-----TGTGTGT-----TGTT-----GTGTGTGACACGG--TGCAGTAGAGTCGCA--CAG-----G-----SAGAGAA-----AG--AGCGCG--SCAGAAACCGAG
drosE1a1	scaffold_0491011:1727310-1727462		CGGTACTCTCGACAA-----GCAG--TT-CTC--CTCT--TCTGCCACGGCGGCAGCAGCAGCGCA-----ATAA-----CAACCAATAC-----AGTCAGTCCATCAGCAGCTGGATG--CCAGCAG-----TGTGTGT-----TGTT-----GTGTGTGACACGG--TGCAGTAGAGTCGCA--CAG-----GAG--SAGAGAA-----AG--AGCGCG--SCAGAAACCGAG
drosRho1	scaffold_778083:144963-145121		CGGTACTCTCGACAA-----GCAG--TT-CTC--CTCT--TCTGCCACGGCGGCAGCAGCAGCGCA-----ATAA-----CAACCAATAC-----AGTCAGTCCATCAGCAGCTGGATG--CCAGCAG-----TGTGTGT-----TGTT-----GTGTGTGACACGG--TGCAGTAGAGTCGCA--CAG-----GAG--SAGAGAA-----AG--AGCGCG--SCAGAAACCGAG
drosF1c1	scaffold_00453775:107965-109123		CGGTACTCTCGACAA-----GCAG--TT-CTC--CTCT--TCTGCCACGGCGGCAGCAGCAGCGCA-----ATAA-----CAACCAATAC-----AGTCAGTCCATCAGCAGCTGGATG--CCAGCAG-----TGTGTGT-----TGTT-----GTGTGTGACACGG--TGCAGTAGAGTCGCA--CAG-----GAG--SAGAGAA-----AG--AGCGCG--SCAGAAACCGAG
drosK1k1	scaffold_00024069:89835-89979		CGGTACTCTCGACAA-----GCAG--TT-CTC--CTCT--TCTGCCACGGCGGCAGCAGCAGCGCA-----ATAA-----CAACCAATAC-----AGTCAGTCCATCAGCAGCTGGATG--CCAGCAG-----TGTGTGT-----TGTT-----GTGTGTGACACGG--TGCAGTAGAGTCGCA--CAG-----GAG--SAGAGAA-----AG--AGCGCG--SCAGAAACCGAG
drosAna3	scaffold_13117:432231-4322779	del_4061	CGGTACTCTCGACAA-----GCAG--TT-CTC--CTCT--TCTGCCACGGCGGCAGCAGCAGCGCA-----ATAA-----CAACCAATAC-----AGTCAGTCCATCAGCAGCTGGATG--CCAGCAG-----TGTGTGT-----TGTT-----GTGTGTGACACGG--TGCAGTAGAGTCGCA--CAG-----GAG--SAGAGAA-----AG--AGCGCG--SCAGAAACCGAG
drosB1p1	scaffold_00039638:89283-89431		CGGTACTCTCGACAA-----GCAG--TT-CTC--CTCT--TCTGCCACGGCGGCAGCAGCAGCGCA-----ATAA-----CAACCAATAC-----AGTCAGTCCATCAGCAGCTGGATG--CCAGCAG-----TGTGTGT-----TGTT-----GTGTGTGACACGG--TGCAGTAGAGTCGCA--CAG-----GAG--SAGAGAA-----AG--AGCGCG--SCAGAAACCGAG
dp5	XL group16:7670682-7670807	del_3841	CGGTACTCTCGACAA-----GCAG--TT-CTC--CTCT--TCTGCCACGGCGGCAGCAGCAGCGCA-----ATAA-----CAACCAATAC-----AGTCAGTCCATCAGCAGCTGGATG--CCAGCAG-----TGTGTGT-----TGTT-----GTGTGTGACACGG--TGCAGTAGAGTCGCA--CAG-----GAG--SAGAGAA-----AG--AGCGCG--SCAGAAACCGAG
drosPer2	scaffold_13:885449-885613	del_2526	CGGTACTCTCGACAA-----GCAG--TT-CTC--CTCT--TCTGCCACGGCGGCAGCAGCAGCGCA-----ATAA-----CAACCAATAC-----AGTCAGTCCATCAGCAGCTGGATG--CCAGCAG-----TGTGTGT-----TGTT-----GTGTGTGACACGG--TGCAGTAGAGTCGCA--CAG-----GAG--SAGAGAA-----AG--AGCGCG--SCAGAAACCGAG
drosM12	scaffold_1100000004903:7418273-7418466	del_5065	CGGTACTCTCGACAA-----GCAG--TT-CTC--CTCT--TCTGCCACGGCGGCAGCAGCAGCGCA-----ATAA-----CAACCAATAC-----AGTCAGTCCATCAGCAGCTGGATG--CCAGCAG-----TGTGTGT-----TGTT-----GTGTGTGACACGG--TGCAGTAGAGTCGCA--CAG-----GAG--SAGAGAA-----AG--AGCGCG--SCAGAAACCGAG
drosMoJ3	scaffold_6473:8732297-8732425		CGGTACTCTCGACAA-----GCAG--TT-CTC--CTCT--TCTGCCACGGCGGCAGCAGCAGCGCA-----ATAA-----CAACCAATAC-----AGTCAGTCCATCAGCAGCTGGATG--CCAGCAG-----TGTGTGT-----TGTT-----GTGTGTGACACGG--TGCAGTAGAGTCGCA--CAG-----GAG--SAGAGAA-----AG--AGCGCG--SCAGAAACCGAG
drosGr12	scaffold_15110:1566727-15667348		CGGTACTCTCGACAA-----GCAG--TT-CTC--CTCT--TCTGCCACGGCGGCAGCAGCAGCGCA-----ATAA-----CAACCAATAC-----AGTCAGTCCATCAGCAGCTGGATG--CCAGCAG-----TGTGTGT-----TGTT-----GTGTGTGACACGG--TGCAGTAGAGTCGCA--CAG-----GAG--SAGAGAA-----AG--AGCGCG--SCAGAAACCGAG

Legend: mature star mismatch in alignment mismatch in read

utr3 [utr3_plus_8729]

No Repeatable elements found

hide 3p reads | show mid mismatch reads

[illegible][illegible][illegible]

Generated: 09/08/2015 at 08:01 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	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

Predicted structure



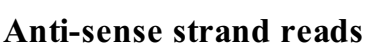
Flybase annotation

utr3 [utr3_minus_7095]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

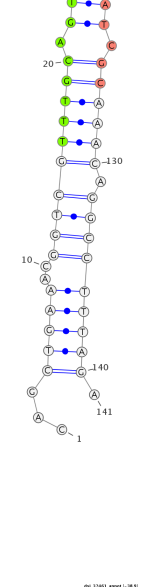
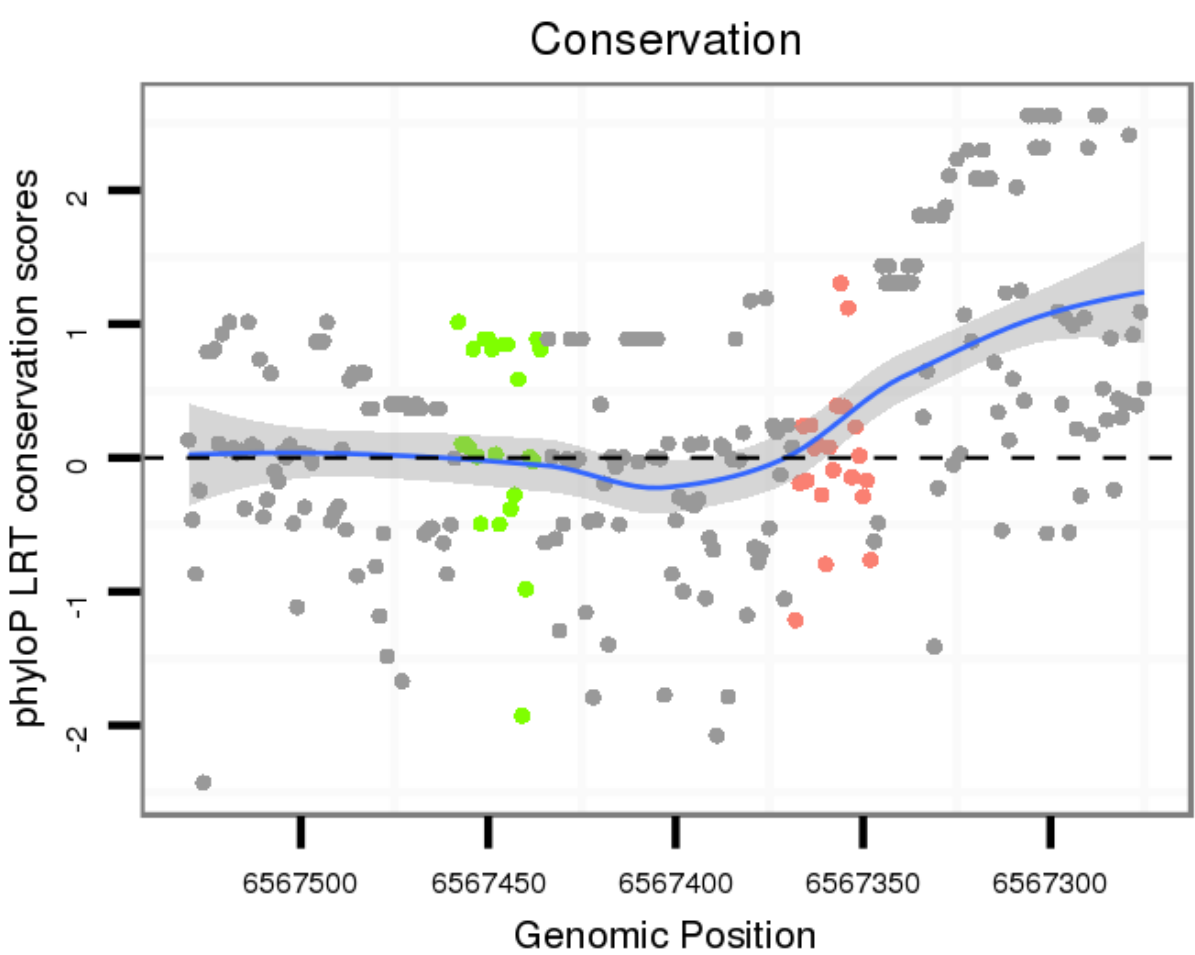
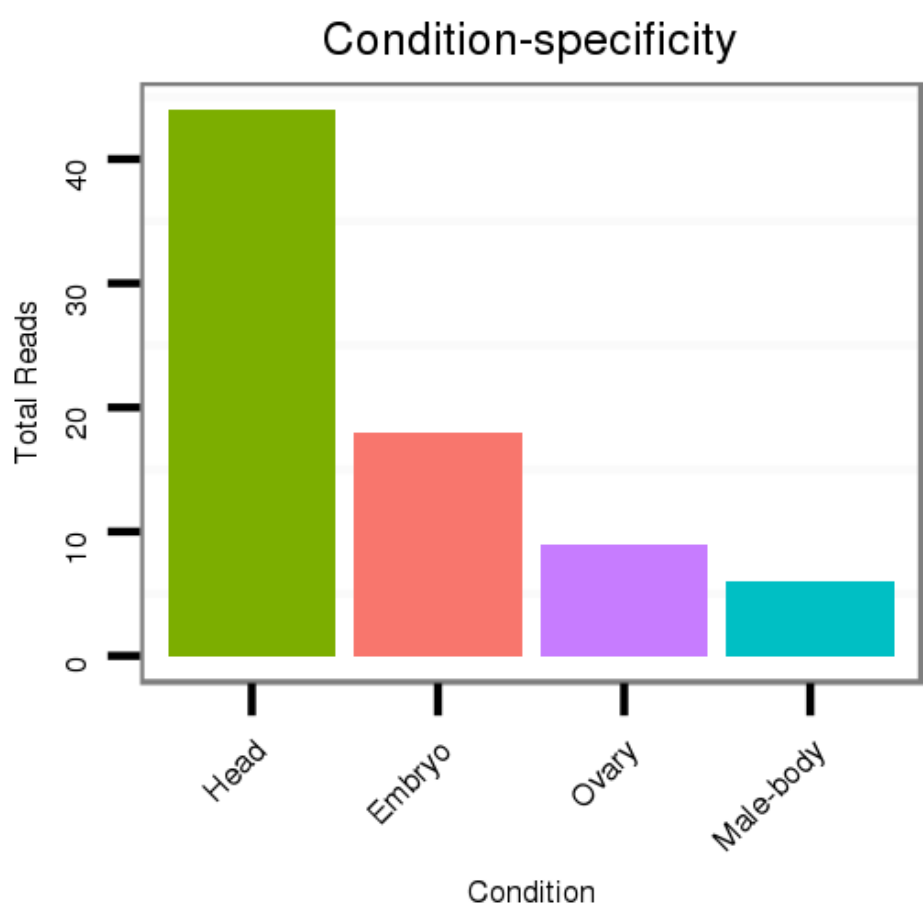
Show Alignment With Reads

Re-alignment of all predicted orthologs

Generated: 09/08/2015 at 08:01 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	8
rescue.candidate	4

Legend: mature star mismatch in alignment mismatch in read



Flybase annotation

intron [21_6565778_6570336_-]; utr5 [utr5_minus_830]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

[illegible]

Anti-sense strand reads

[illegible]

Re-alignment of all predicted orthologs

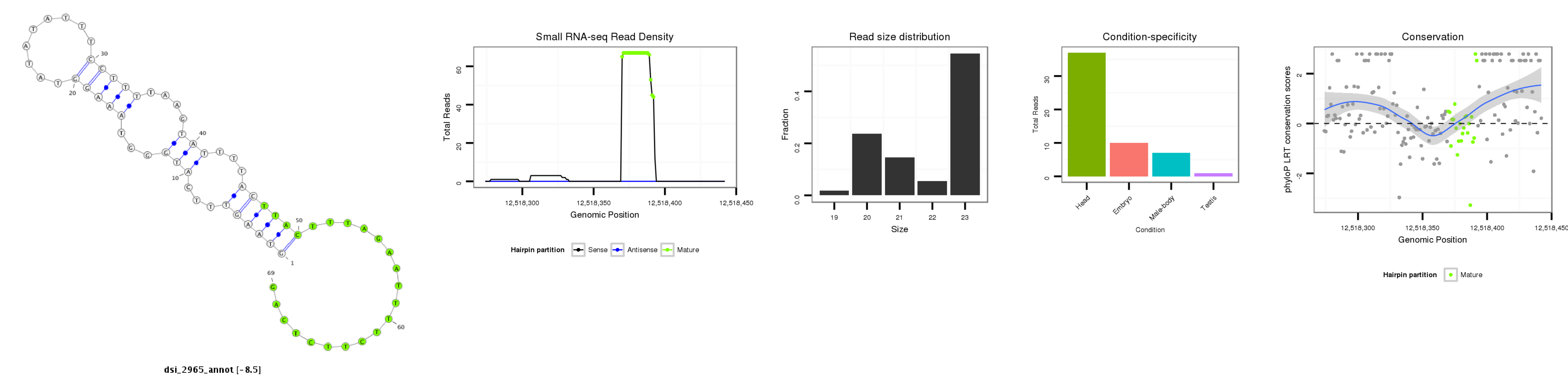
Species	Coordinate	ID	Alignment
droS1m2	21:6567275-6567530 - ds1_32461		TTCTTTAAGTCTTGA AAAA--GAAATTTTC AA-----TACAGAAAATAGACATTTCG-----CGGTAACTCAGCTGA AAC--GGTCG-----TTTGCAGTTCAATTGGTTGAGTGGCTTTCTTCGAAAATTTAAAC--TTTAAAAATACATA-----CTTTTAAAGCGTTAAATCG-----ATT--CCGAGTTAACTACT--AATCGAACTGAATCGGA-AACAGGCGCT-TTAGATCCAAAGA--AAAC--CCACCGATA-----GAAACATGTCCAAAGCGATACCAATGATCGTCGTCCTT
droSe2c	scaffold_3:2330957-2332312 - dae_1819		TTCTTAAGTCTTGA AAAA--GAAATTTTC AA-----TACAGAAAATAGACATTTCG-----CGGTAACTCAGCTGA AAC--GGTA-----TTTGCAGTTCAATTGGTTGAGTGGCTTTCTTCGGAATTTAAAC--TTTAAAAATACATA-----CTTTTAAAGCGTTAAATCG-----ATT--CCGAGTTAACTACT--AACCGAACTGAACCGGA-AACAGGCGCT-TTAGATCCAAAGA--AAAC--CCACCGATA-----GAAACATGTCCAAAGCGATACCAATGATCGTCGTCCTT
dm3	chr2L:6793338-6793581 - dme_435		TTCTTAAGTCTTGA AAAA--GAAATTTTC AA-----TACGAAAAATAGACATTTCG-----GATTTACAGCTGA AAC--GTCG-----TTTGAATCAATTCTGTCAGTGGCTTTATTCGGAATTTAAAC--TTTAAAAATACATA-----CTTTTAAAGCGTTAAATCG-----ATT--CCGAGTTAACTACT--AACCGAACTGAACCGGA-AACAGGCGCT-TTAGATCCAAAGA--AAAC--CCACCGATA-----GAAACATGTCCAAAGCGATACCAATGATCGTCGTCCTT
droE9e2	scaffold_14:929:15709671-15709934 - droE9e2		TTCTTAAGTCTTGA AAAA--GAAATTTTC AA-----TACAGAAAATAGACATTTCG-----GAATTTGAGACATTAGCTCGACACATTTCGGA-----TTTGCAGTTTCG-----GTCGAGTGGCTTTCTTCGGAATTTAAAC--TTTAAAAATACATA-----CTTTTAAAGCGTTAAATCG-----ATT--CCGAGTTAACTACT--AACCGAACTGAACCGGA-AACAGGCGCT-TTAGATCCAAAGA--AAAC--CCACCGATA-----GAAACATGTCCAAAGCGATACCAATGATCGTCGTCCTT
droYaK3	2L:6115189-6115466 - dya_1803		TTCTTAAGTCTTGA AAAA--GAAATTTTC AA-----TACAGAAAATAGACATTTCG-----GATTTACAGCTGA AAC--GTCG-----TTTGAATCAATTCTGTCAGTGGCTTTATTCGGAATTTAAAC--TTTAAAAATACATA-----CTTTTAAAGCGTTAAATCG-----ATT--CCGAGTTAACTACT--AACCGAACTGAACCGGA-AACAGGCGCT-TTAGATCCAAAGA--AAAC--CCACCGATA-----GAAACATGTCCAAAGCGATACCAATGATCGTCGTCCTT
droEup1	scf7180000409463:2325815-2326039 - droEup1		TGAGTAAGTCTTGA AAAA--GAAATTTTC AA-----TACAGAAAATAGACATTTCG-----GATTTACAGCTGA AAC--GTCG-----TTTGAATCAATTCTGTCAGTGGCTTTATTCGGAATTTAAAC--TTTAAAAATACATA-----CTTTTAAAGCGTTAAATCG-----ATT--CCGAGTTAACTACT--AACCGAACTGAACCGGA-AACAGGCGCT-TTAGATCCAAAGA--AAAC--CCACCGATA-----GAAACATGTCCAAAGCGATACCAATGATCGTCGTCCTT
droB1a1	scf718000040302422:2558328-2558554 - droB1a1		AA-----GTGCTTGA AAAA--GAAATTTTC AA-----TACAGAAAATAGACATTTCG-----GATTTACAGCTGA AAC--GTCG-----TTTGAATCAATTCTGTCAGTGGCTTTATTCGGAATTTAAAC--TTTAAAAATACATA-----CTTTTAAAGCGTTAAATCG-----ATT--CCGAGTTAACTACT--AACCGAACTGAACCGGA-AACAGGCGCT-TTAGATCCAAAGA--AAAC--CCACCGATA-----GAAACATGTCCAAAGCGATACCAATGATCGTCGTCCTT
droTaK1	scf7180000415361:102122-102337 - droTaK1		AA-----TAAGTCTTGA AAAA--GAAATTTTC AA-----TACAGAAAATAGACATTTCG-----GATTTACAGCTGA AAC--GTCG-----TTTGAATCAATTCTGTCAGTGGCTTTATTCGGAATTTAAAC--TTTAAAAATACATA-----CTTTTAAAGCGTTAAATCG-----ATT--CCGAGTTAACTACT--AACCGAACTGAACCGGA-AACAGGCGCT-TTAGATCCAAAGA--AAAC--CCACCGATA-----GAAACATGTCCAAAGCGATACCAATGATCGTCGTCCTT
droE1e1	scf7180000490640:430471-490666 - droE1e1		AA-----TACTTGA AAAA--GAAATTTTC AA-----TACAGAAAATAGACATTTCG-----GATTTACAGCTGA AAC--GTCG-----TTTGAATCAATTCTGTCAGTGGCTTTATTCGGAATTTAAAC--TTTAAAAATACATA-----CTTTTAAAGCGTTAAATCG-----ATT--CCGAGTTAACTACT--AACCGAACTGAACCGGA-AACAGGCGCT-TTAGATCCAAAGA--AAAC--CCACCGATA-----GAAACATGTCCAAAGCGATACCAATGATCGTCGTCCTT
droRho1	scf7180000778441:56107-56207 - droRho1		AA-----TACTTGA AAAA--GAAATTTTC AA-----TACAGAAAATAGACATTTCG-----GATTTACAGCTGA AAC--GTCG-----TTTGAATCAATTCTGTCAGTGGCTTTATTCGGAATTTAAAC--TTTAAAAATACATA-----CTTTTAAAGCGTTAAATCG-----ATT--CCGAGTTAACTACT--AACCGAACTGAACCGGA-AACAGGCGCT-TTAGATCCAAAGA--AAAC--CCACCGATA-----GAAACATGTCCAAAGCGATACCAATGATCGTCGTCCTT
droFlc1	scf71800004053815:1315573-131657 - droFlc1		AA-----TACTTGA AAAA--GAAATTTTC AA-----TACAGAAAATAGACATTTCG-----GATTTACAGCTGA AAC--GTCG-----TTTGAATCAATTCTGTCAGTGGCTTTATTCGGAATTTAAAC--TTTAAAAATACATA-----CTTTTAAAGCGTTAAATCG-----ATT--CCGAGTTAACTACT--AACCGAACTGAACCGGA-AACAGGCGCT-TTAGATCCAAAGA--AAAC--CCACCGATA-----GAAACATGTCCAAAGCGATACCAATGATCGTCGTCCTT
droK1k1	scf7180000302468:363257-363365 - droK1k1		AA-----TACTTGA AAAA--GAAATTTTC AA-----TACAGAAAATAGACATTTCG-----GATTTACAGCTGA AAC--GTCG-----TTTGAATCAATTCTGTCAGTGGCTTTATTCGGAATTTAAAC--TTTAAAAATACATA-----CTTTTAAAGCGTTAAATCG-----ATT--CCGAGTTAACTACT--AACCGAACTGAACCGGA-AACAGGCGCT-TTAGATCCAAAGA--AAAC--CCACCGATA-----GAAACATGTCCAAAGCGATACCAATGATCGTCGTCCTT
droAna3	scaffold_12916:8371491-8371525 - droAna3		AA-----TACTTGA AAAA--GAAATTTTC AA-----TACAGAAAATAGACATTTCG-----GATTTACAGCTGA AAC--GTCG-----TTTGAATCAATTCTGTCAGTGGCTTTATTCGGAATTTAAAC--TTTAAAAATACATA-----CTTTTAAAGCGTTAAATCG-----ATT--CCGAGTTAACTACT--AACCGAACTGAACCGGA-AACAGGCGCT-TTAGATCCAAAGA--AAAC--CCACCGATA-----GAAACATGTCCAAAGCGATACCAATGATCGTCGTCCTT
droB1p1	scf7180000396572:3021716-3021750 - droB1p1		AA-----TACTTGA AAAA--GAAATTTTC AA-----TACAGAAAATAGACATTTCG-----GATTTACAGCTGA AAC--GTCG-----TTTGAATCAATTCTGTCAGTGGCTTTATTCGGAATTTAAAC--TTTAAAAATACATA-----CTTTTAAAGCGTTAAATCG-----ATT--CCGAGTTAACTACT--AACCGAACTGAACCGGA-AACAGGCGCT-TTAGATCCAAAGA--AAAC--CCACCGATA-----GAAACATGTCCAAAGCGATACCAATGATCGTCGTCCTT
dp5	4_group1:3902207-3902255 - dp5		AA-----TACTTGA AAAA--GAAATTTTC AA-----TACAGAAAATAGACATTTCG-----GATTTACAGCTGA AAC--GTCG-----TTTGAATCAATTCTGTCAGTGGCTTTATTCGGAATTTAAAC--TTTAAAAATACATA-----CTTTTAAAGCGTTAAATCG-----ATT--CCGAGTTAACTACT--AACCGAACTGAACCGGA-AACAGGCGCT-TTAGATCCAAAGA--AAAC--CCACCGATA-----GAAACATGTCCAAAGCGATACCAATGATCGTCGTCCTT
droPer2	scaffold_5:1368113-1368161 - droPer2		AA-----TACTTGA AAAA--GAAATTTTC AA-----TACAGAAAATAGACATTTCG-----GATTTACAGCTGA AAC--GTCG-----TTTGAATCAATTCTGTCAGTGGCTTTATTCGGAATTTAAAC--TTTAAAAATACATA-----CTTTTAAAGCGTTAAATCG-----ATT--CCGAGTTAACTACT--AACCGAACTGAACCGGA-AACAGGCGCT-TTAGATCCAAAGA--AAAC--CCACCGATA-----GAAACATGTCCAAAGCGATACCAATGATCGTCGTCCTT
droVlr3	scaffold_12963:3844060-3844104 - droVlr3		AA-----TACTTGA AAAA--GAAATTTTC AA-----TACAGAAAATAGACATTTCG-----GATTTACAGCTGA AAC--GTCG-----TTTGAATCAATTCTGTCAGTGGCTTTATTCGGAATTTAAAC--TTTAAAAATACATA-----CTTTTAAAGCGTTAAATCG-----ATT--CCGAGTTAACTACT--AACCGAACTGAACCGGA-AACAGGCGCT-TTAGATCCAAAGA--AAAC--CCACCGATA-----GAAACATGTCCAAAGCGATACCAATGATCGTCGTCCTT
droMoJ3	scaffold_6500:7696803-7696856 - droMoJ3		AA-----TACTTGA AAAA--GAAATTTTC AA-----TACAGAAAATAGACATTTCG-----GATTTACAGCTGA AAC--GTCG-----TTTGAATCAATTCTGTCAGTGGCTTTATTCGGAATTTAAAC--TTTAAAAATACATA-----CTTTTAAAGCGTTAAATCG-----ATT--CCGAGTTAACTACT--AACCGAACTGAACCGGA-AACAGGCGCT-TTAGATCCAAAGA--AAAC--CCACCGATA-----GAAACATGTCCAAAGCGATACCAATGATCGTCGTCCTT
droG12	scaffold_15252:1552984-1553032 - droG12		AA-----TACTTGA AAAA--GAAATTTTC AA-----TACAGAAAATAGACATTTCG-----GATTTACAGCTGA AAC--GTCG-----TTTGAATCAATTCTGTCAGTGGCTTTATTCGGAATTTAAAC--TTTAAAAATACATA-----CTTTTAAAGCGTTAAATCG-----ATT--CCGAGTTAACTACT--AACCGAACTGAACCGGA-AACAGGCGCT-TTAGATCCAAAGA--AAAC--CCACCGATA-----GAAACATGTCCAAAGCGATACCAATGATCGTCGTCCTT

Generated: 09/08/2015 at 08:03 PM

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dsi_2965	3l:12518324-12518392 +	candidate	Mirtron	intron	[View on UCSC Genome Browser (Cornell Mirror)]

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



dsi_2965_annot [-8.5]

Show Alternate Folds

Flybase annotation

intron [3l_12518324_12518392_+]; CDS [3l_12518393_12518584_+]; CDS [3l_12518167_12518323_+]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

	Read #	Hit	Total		M025	M023	M024	M053	O002	SRR618934	O001	SRR553488
	size	Count	Norm	Total	embryo	head	male	body	Head	dsim w501	Testis	RT_0-2 hours eggs
TCATTTTGGCCTGTTAAATTCCTTTACATAGGTGAGCGGAATGTTCAATGTAAGTTTCATGGGTAAGGTATATATTTCCCTTTAAGTATTTTAC	24	1	51.00	51	36	13	2	0	0	0	0	0
*****(((((((.....)))))).....))))*****	23	0	30.00	30	6	17	6	0	0	0	1	0
.....TACTTTAGAAATTTCTTCTCAG.....	20	0	13.00	13	1	11	1	0	0	0	0	0
.....TACTTTAGAAATTTCTTCTCAG.....	24	0	12.00	12	2	6	3	1	0	0	0	0
.....TACTTTAGAAATTTCTTCTCAG.....	21	0	8.00	8	3	5	0	0	0	0	0	0
.....TACTTTAGAAATTTCTTCTCAG.....	24	1	8.00	8	6	2	0	0	0	0	0	0
.....TACTTTAGAAATTTCTTCTCAG.....	24	1	3.00	3	2	1	0	0	0	0	0	0
.....TACTTTAGAAATTTCTTCTCAG.....	25	1	2.00	2	2	0	0	0	0	0	0	0
.....TACTTTAGAAATTTCTTCTCAG.....	22	0	2.00	2	0	1	0	0	1	0	0	0
.....GTGAGCGGAATGTTCAATGTAA.....	22	0	1.00	1	0	0	0	0	1	0	0	0
.....TACTTTAGAAATTTCTTCTCAG.....	19	0	1.00	1	0	1	0	0	0	0	0	0
.....TACTTTAGAAATTTCTTCTCAG.....	23	1	1.00	1	1	0	0	0	0	0	0	0
.....TTAGAAATTTCTTCTCAG.....	19	1	1.00	1	0	0	0	1	0	0	0	0
.....GTGAGCGGAATGTTCAATGTAA.....	25	0	1.00	1	0	0	0	0	0	1	0	0
.....TTTGTGCCTGTTAAATTCCT.....	20	0	1.00	1	1	0	0	0	0	0	0	0
.....GTGAGCGGAATGTTCAATGTAA.....	22	0	1.00	1	0	1	0	0	0	0	0	0
.....GTGAGCGGAATGTTCAATGTAA.....	27	0	1.00	1	0	0	0	0	0	1	0	0
.....TACTTTAGAAATTTCTTCTCAG.....	23	1	1.00	1	1	0	0	0	0	0	0	0

Anti-sense strand reads

																SRR553488	
																SRR618934	GSM343915
																RT 0-2	
																dsim w501	
																ovaries	embryo
																eggs	

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droSim2	11:12518274-12518442 +	dsi_2965	TCATTTTGGCCTGTTAAATTCCTTTACATAGGTGAGCGGAATGTTCAATGTAAGTTTCATGGGTAAGG-----TATAATTTCC---TT-TT-----AAGTA-TTTTAC
droSec2	scaffold_0:5001053-5001221 +		TCATTTTGGCCTGTTAAATTCCTTTACATAGGAGCGGAATGTTCAATGTAAGTTTCATGGGTAAGG-----TATAATTTCC---TT-TT-----AAGTA-TTTTAC
dm3	chr3l:12816735-12816903 +		TCATTTTGGCCTGTTAAATTCCTTTACATAGGAGCGGAATGTTCAATGTAAGTTTCATGGGTAAGG-----TATAATTTCC---TT-TT-----AAGTA-TTTTAC
droBre2	scaffold_4784:12829234-12829398 +		TCATTTTGGCCTGTTAAATTCCTTTACATAGGAGCGGAATGTTCAATGTAAGTTTCATGGGTAAGG-----TATAATTTCC---TT-TT-----AAGTA-TTTTAC
droYak3	3l:12891459-12891622 +		TCATTTTGGCCTGTTAAATTCCTTTACATAGGAGCGGAATGTTCAATGTAAGTTTCATGGGTAAGG-----TATAATTTCC---TT-TT-----AAGTA-TTTTAC
droBug1	scaffold_491466:4913962-4914116 +		TCATTTTGGCCTGTTAAATTCCTTTACATAGGAGCGGAATGTTCAATGTAAGTTTCATGGGTAAGG-----TATAATTTCC---TT-TT-----AAGTA-TTTTAC
droBial	scaffold_302529:802518-802681 =		TCATTTTGGCCTGTTAAATTCCTTTACATAGGAGCGGAATGTTCAATGTAAGTTTCATGGGTAAGG-----TATAATTTCC---TT-TT-----AAGTA-TTTTAC
droTak1	scaffold_415185:7455-7618 =		TCATTTTGGCCTGTTAAATTCCTTTACATAGGAGCGGAATGTTCAATGTAAGTTTCATGGGTAAGG-----TATAATTTCC---TT-TT-----AAGTA-TTTTAC
droIel1	scaffold_491255:1210900-1211063 +		TCATTTTGGCCTGTTAAATTCCTTTACATAGGAGCGGAATGTTCAATGTAAGTTTCATGGGTAAGG-----TATAATTTCC---TT-TT-----AAGTA-TTTTAC
droRho1	scaffold_77230:29994-30157 =		TCATTTTGGCCTGTTAAATTCCTTTACATAGGAGCGGAATGTTCAATGTAAGTTTCATGGGTAAGG-----TATAATTTCC---TT-TT-----AAGTA-TTTTAC
droPic1	scaffold_453839:192207-192368 =		TCATTTTGGCCTGTTAAATTCCTTTACATAGGAGCGGAATGTTCAATGTAAGTTTCATGGGTAAGG-----TATAATTTCC---TT-TT-----AAGTA-TTTTAC
droKik1	scaffold_302272:461796-461961 +		TCATTTTGGCCTGTTAAATTCCTTTACATAGGAGCGGAATGTTCAATGTAAGTTTCATGGGTAAGG-----TATAATTTCC---TT-TT-----AAGTA-TTTTAC
droAna3	scaffold_13337:19772938-19773105 =		TCATTTTGGCCTGTTAAATTCCTTTACATAGGAGCGGAATGTTCAATGTAAGTTTCATGGGTAAGG-----TATAATTTCC---TT-TT-----AAGTA-TTTTAC
droBip1	scaffold_396360:962053-962210 =		TCATTTTGGCCTGTTAAATTCCTTTACATAGGAGCGGAATGTTCAATGTAAGTTTCATGGGTAAGG-----TATAATTTCC---TT-TT-----AAGTA-TTTTAC
dp5	XR_gdup6:11852007-11852160 =		TCATTTTGGCCTGTTAAATTCCTTTACATAGGAGCGGAATGTTCAATGTAAGTTTCATGGGTAAGG-----TATAATTTCC---TT-TT-----AAGTA-TTTTAC
droPer2	scaffold_20:1576751-1576912 =		TCATTTTGGCCTGTTAAATTCCTTTACATAGGAGCGGAATGTTCAATGTAAGTTTCATGGGTAAGG-----TATAATTTCC---TT-TT-----AAGTA-TTTTAC
droW12	scaffold_11000000451:5506563-5506716 +		TCATTTTGGCCTGTTAAATTCCTTTACATAGGAGCGGAATGTTCAATGTAAGTTTCATGGGTAAGG-----TATAATTTCC---TT-TT-----AAGTA-TTTTAC
droVir3	scaffold_13049:2270548-22705709 =	dsi_20982	TCATTTTGGCCTGTTAAATTCCTTTACATAGGAGCGGAATGTTCAATGTAAGTTTCATGGGTAAGG-----TATAATTTCC---TT-TT-----AAGTA-TTTTAC
droMo3	scaffold_6680:17323455-17323610 =		TCATTTTGGCCTGTTAAATTCCTTTACATAGGAGCGGAATGTTCAATGTAAGTTTCATGGGTAAGG-----TATAATTTCC---TT-TT-----AAGTA-TTTTAC
droGr12	scaffold_15110:20827274-20827433 +		TCATTTTGGCCTGTTAAATTCCTTTACATAGGAGCGGAATGTTCAATGTAAGTTTCATGGGTAAGG-----TATAATTTCC---TT-TT-----AAGTA-TTTTAC

Generated: 09/08/2015 at 07:16 PM

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

Legend: mature star mismatch in alignment mismatch in read

Predicted structure

Flybase annotation

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

Anti-sense strand reads

Show Alignment With Reads

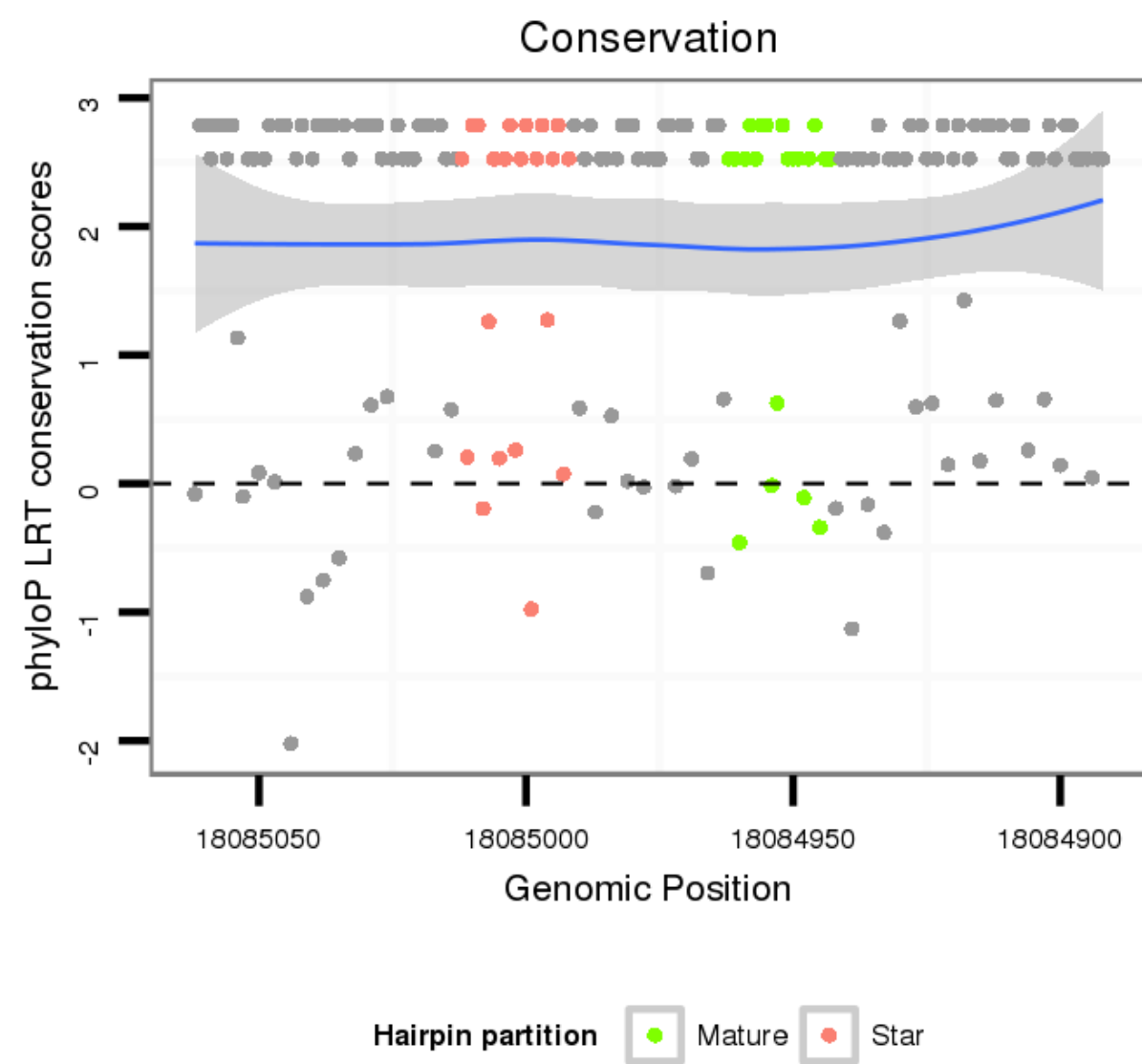
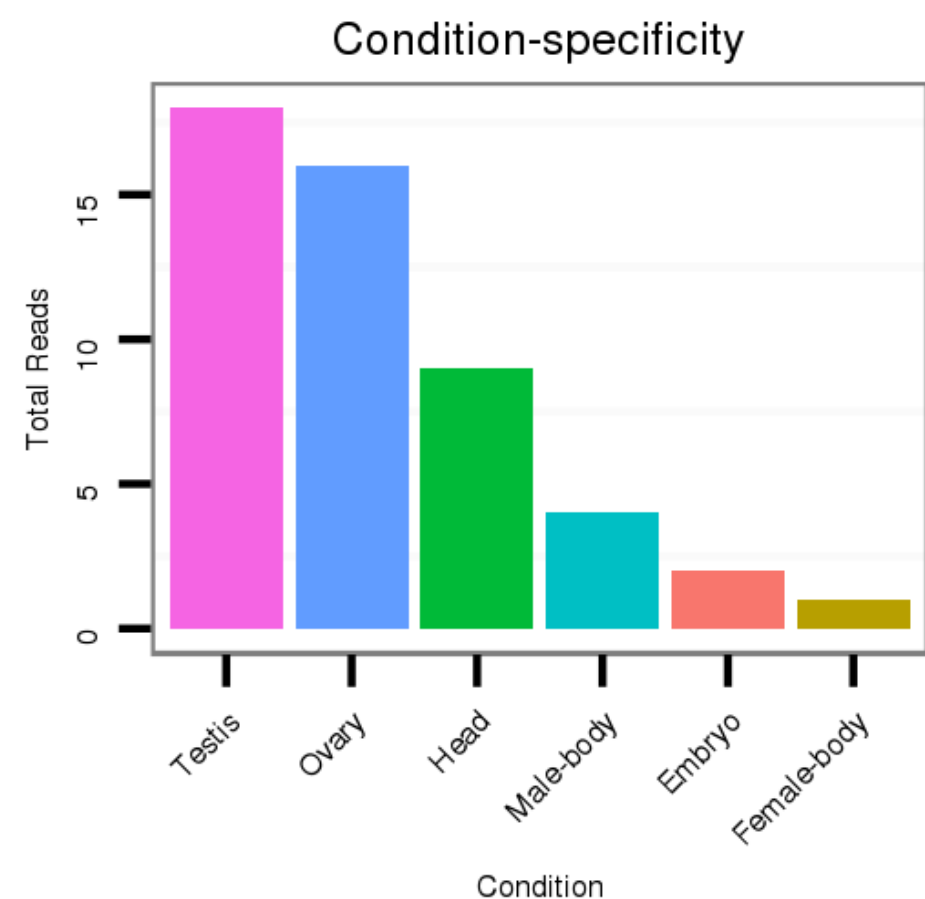
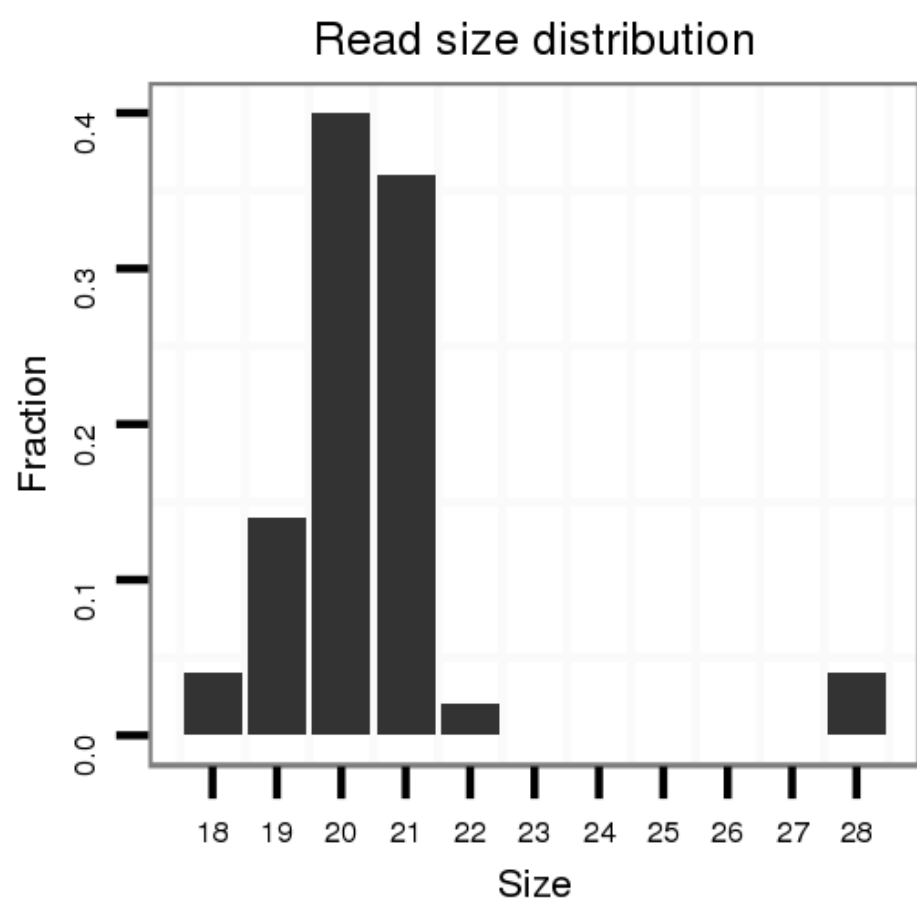
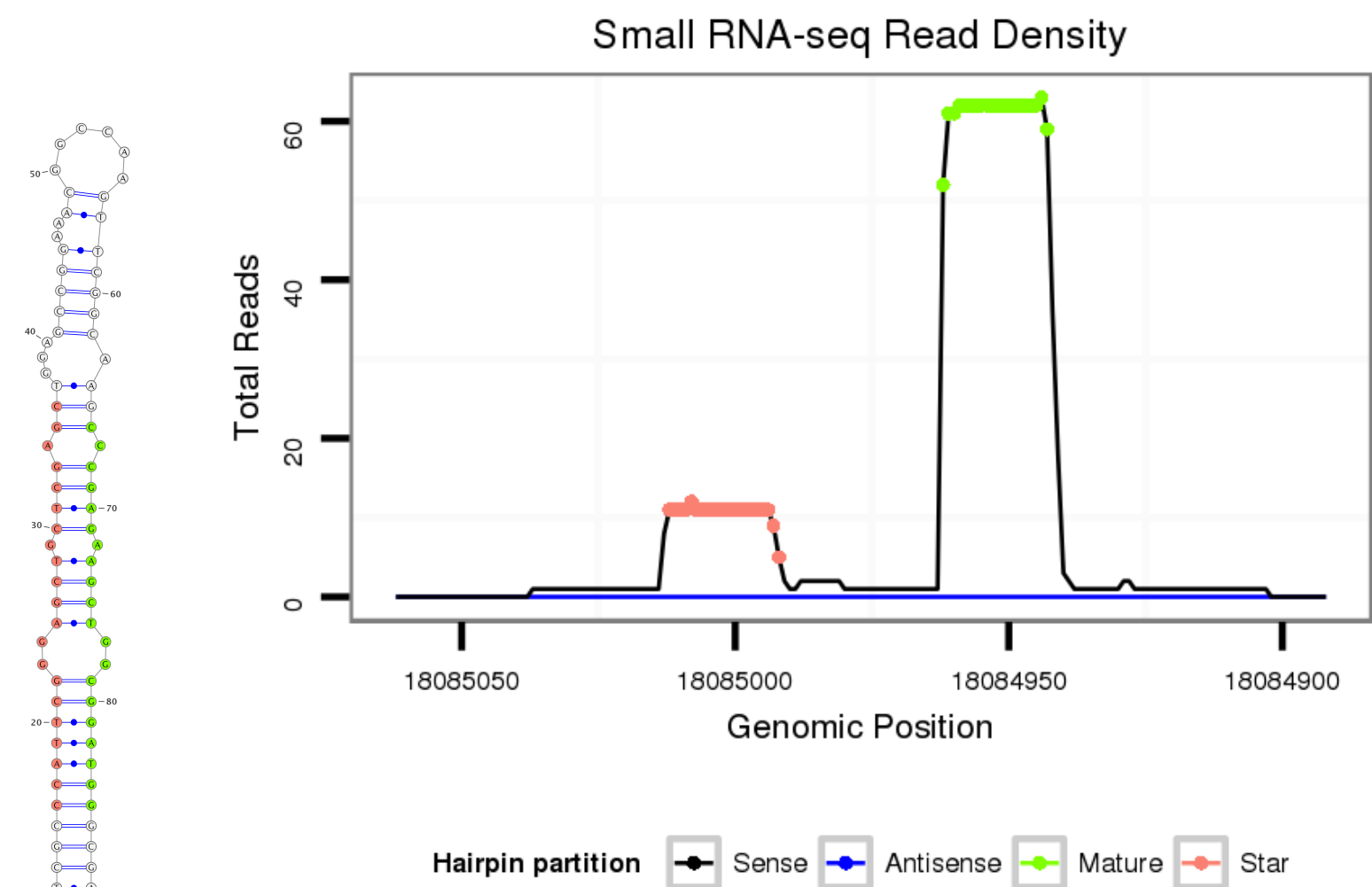
Re-alignment of all predicted orthologs

Generated: 09/08/2015 at 08:01 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	0
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

CDS [3r_18084798_18085208_-]

No Repeatable elements found

Sense Strand Reads

hide 3p reads

[illegible]

Anti-sense strand reads

[illegible]

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droSim2	chr1:18094892-18085062 =	ids_103	CATGATGAGCCCGGAGATCGACGAGTTCAGCAACTCAGTGCCTAAATCGCCATTCGGGAGCTGCTCGAGCTGGAGCCGGAAACGCCCAAGTTCGGCAAGCCGAGAGCTGGCGGATGCGCAGCGGTGCGCGTTACCGTGATGTTCTTCGAAAGGAACCTCCGTGG
droSeec	scaffold_0:181916384-181916554 =		CATGATGAGCCCGGAGATCGACGAGTTCAGCAACTCAGTGCCTAAATCGCCATTCGGGAGCTGCTCGAGCTGGAGCCGGAAACGCCCAAGTTCGGCAAGCCGAGAGAGCTGGCGGATGCGCAGCGGTGCGCGTTACCGTGATGTTCTTCGAAAGGAACCTCCGTGG
dm3	chr3R:18553925-18560095 =	ids_409	CATGATGAGCCCGGAGATCGACGAGTTCAGCAACTCAGTGCCTAAATCGCCATTCGGGAGCTGCTCGAGCTGGAGCCGGAAACGCCCAAGTTCGGCAAGCCGAGAGAGCTGGCGGATGCGCAGCGGTGCGCGTTACCGTGATGTTCTTCGAAAGGAACCTCCGTGG
droEre2	scaffold_4820:19313201-19313215 =		CATGATGAGCCCGGAGATCGACGAGTTCAGCAACTCAGTGCCTAAATCGCCATTCGGGAGCTGCTCGAGCTGGAGCCGGAAACGCCCAAGTTCGGCAAGCCGAGAGAGCTGGCGGATGCGCAGCGGTGCGCGTTACCGTGATGTTCTTCGAAAGGAACCTCCGTGG
droYak3	chr1:19409947-19410117 =		CATGATGAGCCCGGAGATCGACGAGTTCAGCAACTCAGTGCCTAAATCGCCATTCGGGAGCTGCTCGAGCTGGAGCCGGAAACGCCCAAGTTCGGCAAGCCGAGAGAGCTGGCGGATGCGCAGCGGTGCGCGTTACCGTGATGTTCTTCGAAAGGAACCTCCGTGG
droEug1	scaffold00409768:1704122-17041292 =		CATGATGAGCCCGGAGATCGACGAGTTCAGCAACTCAGTGCCTAAATCGCCATTCGGGAGCTGCTCGAGCTGGAGCCGGAAACGCCCAAGTTCGGCAAGCCGAGAGAGCTGGCGGATGCGCAGCGGTGCGCGTTACCGTGATGTTCTTCGAAAGGAACCTCCGTGG
droBla1	scaffold180000302402:15151775-15151945 =		CATGATGAGCCCGGAGATCGACGAGTTCAGCAACTCAGTGCCTAAATCGCCATTCGGGAGCTGCTCGAGCTGGAGCCGGAAACGCCCAAGTTCGGCAAGCCGAGAGAGCTGGCGGATGCGCAGCGGTGCGCGTTACCGTGATGTTCTTCGAAAGGAACCTCCGTGG
droTak1	scaffold180000415417:96871-97041 =		CATGATGAGCCCGGAGATCGACGAGTTCAGCAACTCAGTGCCTAAATCGCCATTCGGGAGCTGCTCGAGCTGGAGCCGGAAACGCCCAAGTTCGGCAAGCCGAGAGAGCTGGCGGATGCGCAGCGGTGCGCGTTACCGTGATGTTCTTCGAAAGGAACCTCCGTGG
droEle1	scaffold180000491017:254771-254941 =		CATGATGAGCCCGGAGATCGACGAGTTCAGCAACTCAGTGCCTAAATCGCCATTCGGGAGCTGCTCGAGCTGGAGCCGGAAACGCCCAAGTTCGGCAAGCCGAGAGAGCTGGCGGATGCGCAGCGGTGCGCGTTACCGTGATGTTCTTCGAAAGGAACCTCCGTGG
droRho1	scaffold18000077285:53295-53465 =		CATGATGAGCCCGGAGATCGACGAGTTCAGCAACTCAGTGCCTAAATCGCCATTCGGGAGCTGCTCGAGCTGGAGCCGGAAACGCCCAAGTTCGGCAAGCCGAGAGAGCTGGCGGATGCGCAGCGGTGCGCGTTACCGTGATGTTCTTCGAAAGGAACCTCCGTGG
droFic1	scaffold180000454055:259477-259647 =		CATGATGAGCCCGGAGATCGACGAGTTCAGCAACTCAGTGCCTAAATCGCCATTCGGGAGCTGCTCGAGCTGGAGCCGGAAACGCCCAAGTTCGGCAAGCCGAGAGAGCTGGCGGATGCGCAGCGGTGCGCGTTACCGTGATGTTCTTCGAAAGGAACCTCCGTGG
droKik1	scaffold180000302697:1118492-1118662 =		CATGATGAGCCCGGAGATCGACGAGTTCAGCAACTCAGTGCCTAAATCGCCATTCGGGAGCTGCTCGAGCTGGAGCCGGAAACGCCCAAGTTCGGCAAGCCGAGAGAGCTGGCGGATGCGCAGCGGTGCGCGTTACCGTGATGTTCTTCGAAAGGAACCTCCGTGG
droAma3	scaffold_13340:12755642-12755812 =		CATGATGAGCCCGGAGATCGACGAGTTCAGCAACTCAGTGCCTAAATCGCCATTCGGGAGCTGCTCGAGCTGGAGCCGGAAACGCCCAAGTTCGGCAAGCCGAGAGAGCTGGCGGATGCGCAGCGGTGCGCGTTACCGTGATGTTCTTCGAAAGGAACCTCCGTGG
droBip1	scaffold180000396691:1641758-1641928 =		CATGATGAGCCCGGAGATCGACGAGTTCAGCAACTCAGTGCCTAAATCGCCATTCGGGAGCTGCTCGAGCTGGAGCCGGAAACGCCCAAGTTCGGCAAGCCGAGAGAGCTGGCGGATGCGCAGCGGTGCGCGTTACCGTGATGTTCTTCGAAAGGAACCTCCGTGG
dp5	2:62733971-6274141 =		CATGATGAGCCCGGAGATCGACGAGTTCAGCAACTCAGTGCCTAAATCGCCATTCGGGAGCTGCTCGAGCTGGAGCCGGAAACGCCCAAGTTCGGCAAGCCGAGAGAGCTGGCGGATGCGCAGCGGTGCGCGTTACCGTGATGTTCTTCGAAAGGAACCTCCGTGG
droPer2	scaffold_0:98164-98334 =		CATGATGAGCCCGGAGATCGACGAGTTCAGCAACTCAGTGCCTAAATCGCCATTCGGGAGCTGCTCGAGCTGGAGCCGGAAACGCCCAAGTTCGGCAAGCCGAGAGAGCTGGCGGATGCGCAGCGGTGCGCGTTACCGTGATGTTCTTCGAAAGGAACCTCCGTGG
droW12	scaffold_1100000004902:1472426-1472596 =		CATGATGAGCCCGGAGATCGACGAGTTCAGCAACTCAGTGCCTAAATCGCCATTCGGGAGCTGCTCGAGCTGGAGCCGGAAACGCCCAAGTTCGGCAAGCCGAGAGAGCTGGCGGATGCGCAGCGGTGCGCGTTACCGTGATGTTCTTCGAAAGGAACCTCCGTGG
droVir3	scaffold_13047:13210686-13210866 =		CATGATGAGCCCGGAGATCGACGAGTTCAGCAACTCAGTGCCTAAATCGCCATTCGGGAGCTGCTCGAGCTGGAGCCGGAAACGCCCAAGTTCGGCAAGCCGAGAGAGCTGGCGGATGCGCAGCGGTGCGCGTTACCGTGATGTTCTTCGAAAGGAACCTCCGTGG
droMo3	scaffold_1069:6540:10445719-10445889 =		CATGATGAGCCCGGAGATCGACGAGTTCAGCAACTCAGTGCCTAAATCGCCATTCGGGAGCTGCTCGAGCTGGAGCCGGAAACGCCCAAGTTCGGCAAGCCGAGAGAGCTGGCGGATGCGCAGCGGTGCGCGTTACCGTGATGTTCTTCGAAAGGAACCTCCGTGG
droGr12	scaffold_14906:4481380-4481550 =		CATGATGAGCCCGGAGATCGACGAGTTCAGCAACTCAGTGCCTAAATCGCCATTCGGGAGCTGCTCGAGCTGGAGCCGGAAACGCCCAAGTTCGGCAAGCCGAGAGAGCTGGCGGATGCGCAGCGGTGCGCGTTACCGTGATGTTCTTCGAAAGGAACCTCCGTGG

Generated: 09/08/2015 at 08:01 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	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	1

	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

	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	2

Flybase annotation

Antisense to utr3 (utr3_minus_5980)

No Repeatable elements found

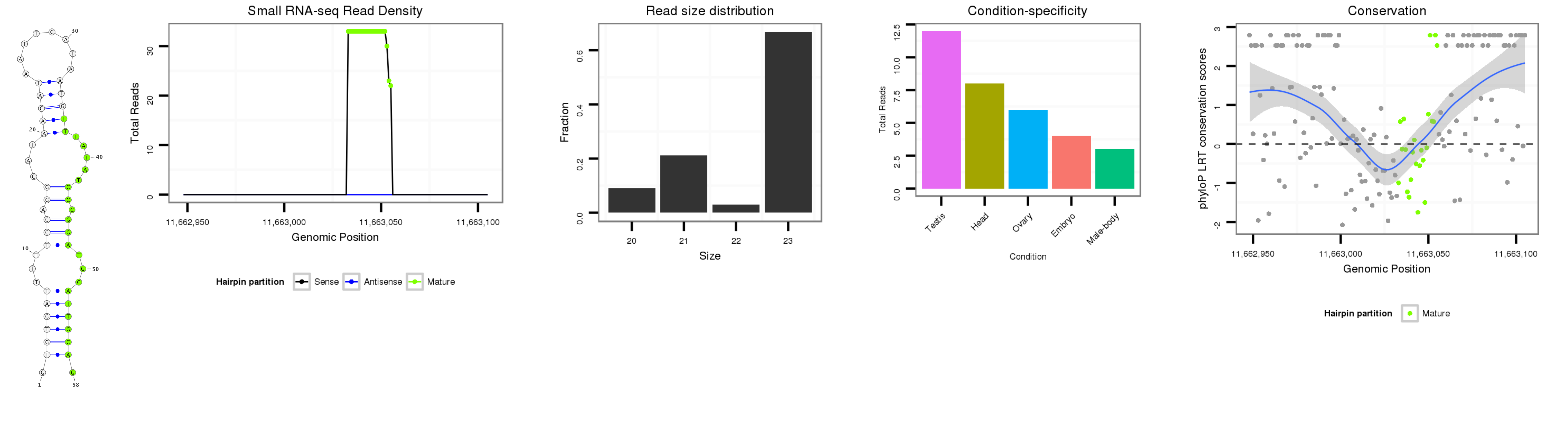
Sense Strand Reads

Show Alignment With Reads

Re-alignment of all predicted

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Show Alternate Folds

Flybase annnotation

intron [2l_11662998_11663055_+]; CDS [2l_11662699_11662997_+]; CDS [2l_11663056_11663245_+]; utr5 [utr5_plus_1704]; utr5 [utr5_plus_1705]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

										Read #	Hit	Total			SRR90209	SRR553486	SRR553488		SRR553487	SRR618934		
										size	Mismatch	Count	Norm	Total	testis	Makindu 3 day-old ovaries	M023 head eggs	M025 embryo	M024 male body	NRT 0-2 hours eggs	dsim w501 ovaries	
TGTCGGCGGGTTAAAGCACCCAAAATGGTTCAGCCCTGTACAAAATAGGTGTGATTTTCCAGGCATAACATAATTCATAATGTTTATATCCCGGATGCATTGCAGCTCCCATCTCCCGAAGACCACCAACCATCAGATCTTCGGAGTGCAGTTCA										23	0	1	22.00	22	10	1	1	1	4	3	1	1
*****. ((((((((((.....)))).....)))).)))).*****										23	0	1	22.00	22	10	1	1	1	4	3	1	1
.....TTTATATCCCGGATGCATTGCAG.....										23	0	1	22.00	22	10	1	1	1	4	3	1	1
.....TTTATATCCCGGATGCATTGCAGT.....										24	1	1	13.00	13	9	4	0	0	0	0	0	0
.....TTTATATCCCGGATGCATTGC.....										21	0	1	7.00	7	1	0	6	0	0	0	0	0
.....TTTATATCCCGGATGCATTGCAG.....										24	1	1	4.00	4	2	1	0	1	0	0	0	0
.....TTTATATCCCGGATGCATTGCAG.....										23	1	1	4.00	4	1	2	0	1	0	0	0	0
.....TTTATATCCCGGATGCATTG.....										20	0	1	3.00	3	1	0	1	1	0	0	0	0
.....TTTATATCCCGGATGCATTGCAGAA.....										26	3	1	2.00	2	1	1	0	0	0	0	0	0
.....TTTATATCCCGGATGCATTGCAGAA.....										24	2	1	2.00	2	2	0	0	0	0	0	0	0
.....TTTATATCCCGGATGCATTGCAGAA.....										25	2	1	2.00	2	2	0	0	0	0	0	0	0
.....TTTATATCCCGGATGCATTGCAG.....										23	1	1	1.00	1	0	0	0	0	1	0	0	0
.....TTTATATCCCGGATGCATTGCAGTA.....										25	2	1	1.00	1	1	0	0	0	0	0	0	0
.....TTTATATCCCGGATGCATTGCA.....										22	0	1	1.00	1	0	1	0	0	0	0	0	0

Anti-sense strand reads

[illegible]

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droSim2	21:11662948-11663105 +	ds1_11938	TGTCGGCGGGTTAAGGCACCCAAAATGGTTCAGCCCTTGTCACAAATATAGGTGTGATTTTCCAGGC-----ATAACATAATTC-----ATAA---TG-----TTTATATCCCGGAT---GCATTGCAGCTCCCATGTCCGCGAAGACCACAACCATCAGATCTTCGGAGTGCGAGTTCA
droSec2	scaffold_16:190669-190826 +		TGTCGGCGGGTTAAGGCACCCAAAATGGTTCAGCCCTTGTCACAAATATAGGTGTGATTTTCCAGGC-----ATAACATAATTC-----ATAA---AG-----TTTATATCCCGGAT---GCATTGCAGCTCCCATGTCCGCGAAGACCACAACCATCAGATCTTTGGAGTGCGAGTTCA
dm3	chr2L:111991222-11991379 +	dme_429	TGTCGGCGGGTTAAGGCACCCAAAATGGTTCAGCCCTTGTCACAAATATAGGTGTGATTTTCCAGGC-----AGACATAAGCTC-----ATAA---TG-----TTTATATCCCGGAT---GCATTGCAGCTCCCATGTCCGCGAGACCACACCATCAGATCTTCGGAGTGCGAGTTCA
droEr2	scaffold_4929:13418888-13419044 -		TGTCGGCGGGTTAAAGCGCCGCAAAAATGGTTCAGCCCTGTGTACAAATATAGGTGCTCTTTTACCTTATGSC-----ACCGCATAATGCT-----ACCTT---AG-----ATTATATCCCGGAT---GCATTGCAGCTCCCATGTCCGCGAGACCACAACCAACAGATCTTTGGCTGCGAGTTCA
droYak3	2h:8414072-8414271 -		TGTCGGCGGGTTAAGGCAGCAAAAATGGTTCAGCCCTGTGTACAAATATAGGTAGCTTTTACCTTATGSC-----TCCACATAAATGCT-----ACCTT---AG-----TTAATTATCCCAAG---GCATTGCAGCTCCCATGTTCGCGAAGACCACAACCAACAGATCTTTGGCTGCGAGTTCA
droEug1	scf7180000409122:383549-383706 -		TGTCGGCGGGTTAAAGCGCAAAAATGGTTCACCCGCTATACAAATAGGTGTGATTTCCAGGC-----GATTAACAGACTT-----GCTT---AG-----TTTATACCTCTGCG---GCATTGCAGCTCCCATGTCTCGAGAACACACCATCAGATCTTTGGCTGCGAGTTCA
droBia1	scf7180000302422:1027715-1027871 -		TGTCGCAAGGGTCAAGGCTCCCAAAAATGGTTCACCCGCTGTACAAATACAGGTGTAAGCTTCTTTGGG-----ATATGATACATTT-----GCTT---GC-----CTTAAGTCCCGTA---ACACGTCAGCTCCCATGTCTCGCGAGACCACAACCAACAGATCTTTGGCTGCGAGTTCA
droTak1	scf7180000415863:255471-255628 -		TGTCGCTAGGTTAAGGCTCCCAAAAATGGTTCAGCCGCTGTACAAATACAGGTGSAATTCCTTAAGG-----CTAACATCAGTT-----TCTA---AG-----CTTATCTTGAT---GACTTCGAGCTCCCATGTCCGCTAGAGACCAATACCAACAGATCTTCGGCTGCGAGTTCA
droEle1	scf7180000491028:3175553-3175709 -		TGTCGCAAGGGTTAAGGCTCCCAAAAATGGTTCCACCGCTGTACAAATACAGGTGCAATTCCTTAAGG-----CTGAGTTGATTT-----CTGT---AT-----ATTATATCTCAT---GCATTGCAGCTCCCATGTCCGCTAGAGACCAACCAACAGATCTTCGGCTGCGAGTTCA
droRho1	scf7180000779410:512327-512494 +		TGTCGGCGCTTAAGGCTCCCAAAAATGGTTCACCCGCTATACAAATACAGGTGSAATTTCTTTGGT-----GAAA-TT-----AAATAAG-----TAC-----TATATATATATGTAATTATAAACGAAT---TAATTGCAGTTCCCATGTCCGCGAGSATTACACAACCAACAGATCTTTGGCTGCGAGTTCA
droFic1	scf7180000453936:182019-182173 -		TGTCGGCGCTTAAGGCACCAAAAATGGTTCACCCGCTGTACAAATACAGGTGSAATTTCTTTGGT-----GATATGAGATTT-----AAAT---T-----TAATTCCCGTTTG---GAATTGCAGTTCCCACCTTCGCGAGACCACAACCAACAGATCTTCGGCTGCGAGTTTA
droKik1	scf7180000301476:566037-566191 -		TGTCGCAAGGGTCAAGGCTCCCAAAAATGGTTCACCCGCTGTACAAATACAGGTGTAAGAG-AC-----G-TT-----C-----GGATTTTAGTAACCAA-----TCTATCTCCGAAT---GCTTCGAGCTGTATGTCTGCTAGAGACCACAACCAACAGATCTTTGGCTGCGAGTTTA
droAna3	scaffold_12916:4417795-4417957 +		TGTCGCGGGGCTAGCGCACCAAGCTATGTCAGCCACTATACAAATATAGGTGTAAGGTAATAC-----G-----A-TT-----TAAAAAA-----TACAATTTTGTGA-----GT-----ATTT-----AGTC-----CTGCTTAT---TTCTTCGAGCTGCATGTATCGGAGATACCAATCATCAGATTTTGGCTGCGAGTTTA
droBip1	scf7180000396737:365848-366012 -		TGTCGCGGGGTCAAGGCTCCCAAGCTTGGTTCAGCCACTATACAAATACAGGTAAATTAATTT-----G-----AAA-----AAAGAAA-----AA-CAAAATTTATGGA-----GC-----ATA-----TAATC-----GCATCTTAT---GCTTGAGCTGTATGTATCGGAGSATTACACAATCATCAGATTTTGGCTGCGAGTTTA
dp5	4_group3:7280922-7281081 -		TGTCGCTAGGCTCAAGGCACCAAAAATGGTTCACCCGCTGTACAAATACAGGTGTAAGGCTG-----T-----T-----GCCCA-----GGTGTGACGCTTC-----T-----TGTCGTGG-----TGTGACTACCT-----GC-----CTTTTCGAGCTCCCACTGTAAGSATTACACAATCATCAGATTTTGGCTGCGAGTTTA
droPer2	scaffold_1:8726638-8726797 -		TGTCGCTAGGCTCAAGGCACCAAAAATGGTTCACCCGCTGTACAAATACAGGTGTAAGGCTG-----T-----T-----GCCCA-----GGTGTGACGCTTC-----T-----TGTCGTGG-----TGTGACTACCT-----GC-----CTTTTCGAGCTCCCACTGTAAGSATTACACAATCATCAGATTTTGGCTGCGAGTTTA
droWil2	scf2_11000000004521:2703913-2704077 +		TGTCGGCGGGCTAAAGSCACCAGAAATGTTCTCAACCCGCTGTACAAATACAGGTAGSAGAA-AC-----T-----AGCMA-----AAGGGT-CA---AGGATATCTGA-----TG-----GTG-----AATATCTCATCT---CGTTTAAGCTATCATGTTCGCGAGSATTACCAATCATCAGATTTTGGCTGCGAGTTTA
droVit3	scaffold_12963:13200218-13200379 +		TGTCGGCGCTTAAGGCTCCCAAAAATGGTTCACCTCTGTACAAATATAGGTGCTCAAT-----AAAAAATA-----CAAT-----GA-AATGAATTTATT-----TTCATG-----TTCCGTAAATTGTTTCAGCTATTCATCCGCGAGACCACAATCATCAATATCTTTGGCTGCGAGTTTA
droMoJ3	scaffold_6500:16745192-16745353 +		TGTCGAAGGGCTAAGGCTCCCAAAAATGGTTCAGCCCTCAATTAATATAGGTGATT---T-C---AGTGCCAG-----TGTGCG-----GC-ATTGAAGTTGT-----T-----TTTATCTA-----TTCAATATCCCTCTTCGAGCAGCTATGTTCGCGAGSATTACCAATCATCAATATTTGGCTGCGAGTTTA
droGr12	scaffold_15126:6659693-6659874 -		TGTCGGCGGGTCAAGGCTCCCAAAAATGGTTCAGCCGCTGTTCAAATACAGGTAGSAGTA-G-----T-AC-TT-----ATATATATATATATAT-----ATA-T-----ATATATATATATATA-----TATAATAATAATAATTGATTAAAT-----CT-----CTTGTCAGCTATCATGTATCGTASATTACCAATCATCAATATTTGGCTGCGAGTTTA

Generated: 09/08/2015 at 07:19 PM

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

	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	1

Predicted structure

Flybase annotation

intron[3r 14856841 14864299 -];utr5[utr5 plus 10181]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

hide 3p reads show mid mismatch reads

Anti-sense strand reads

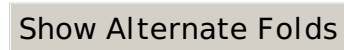
Show Alignment With Reads

Re-alignment of all predicted orthologs

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

crit.star
crit.loop
crit.mor
crit.half
crit.total
crit.pairing
crit.top3
crit.tpop3
crit.uri
crit.back
rescue.total
rescue.dominant
rescue.known
rescue.confident
rescue.candidate

Predicted structure



Sense Strand Reads

hide 3p reads show mid mismatch reads

Anti-sense strand reads

Show Alignment With Reads

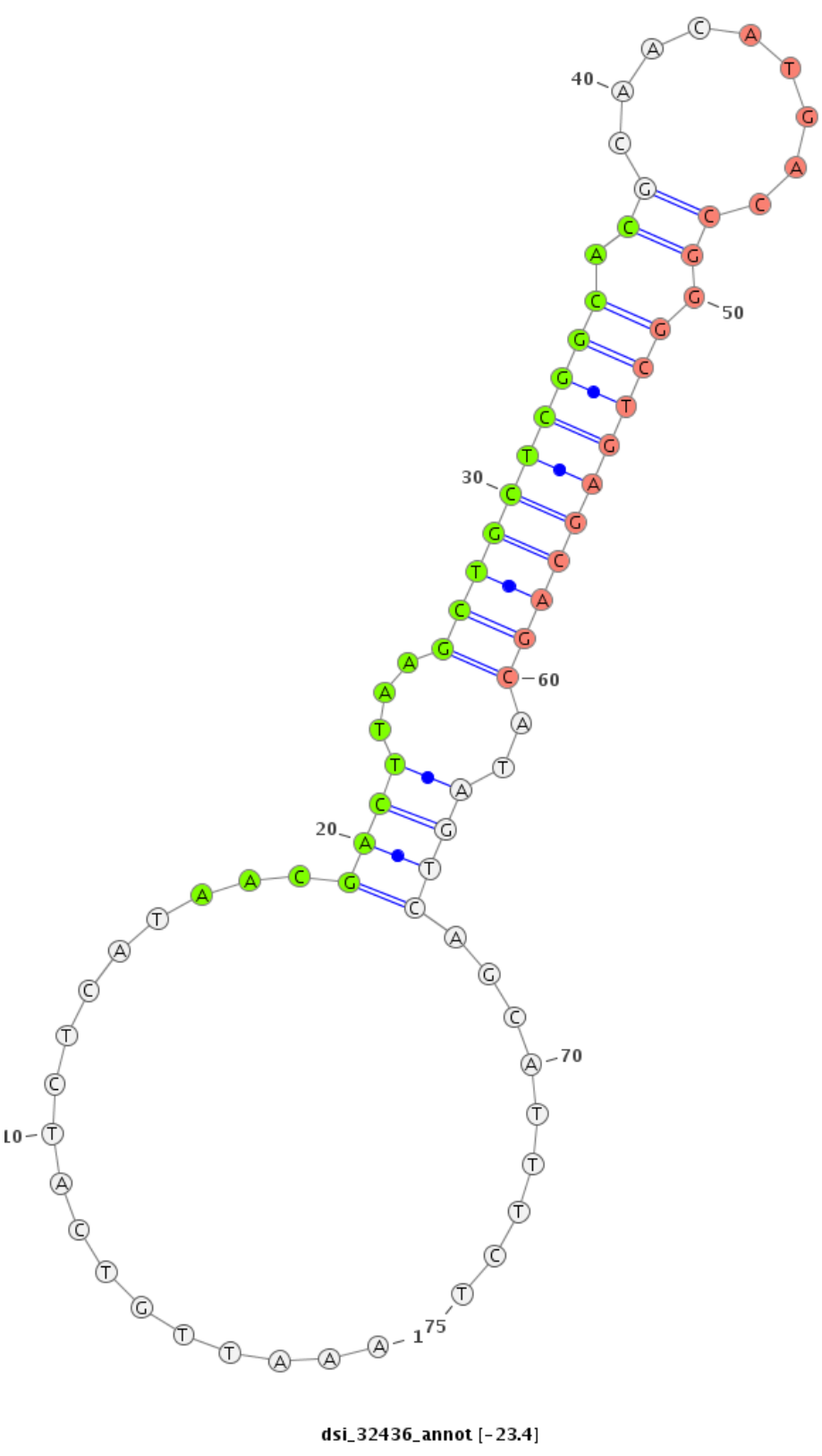
Re-alignment of all predicted orthologs

Generated: 09/08/2015 at 08:02 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	2
rescue.candidate	2

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Show Alternate Folds

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

[illegible]

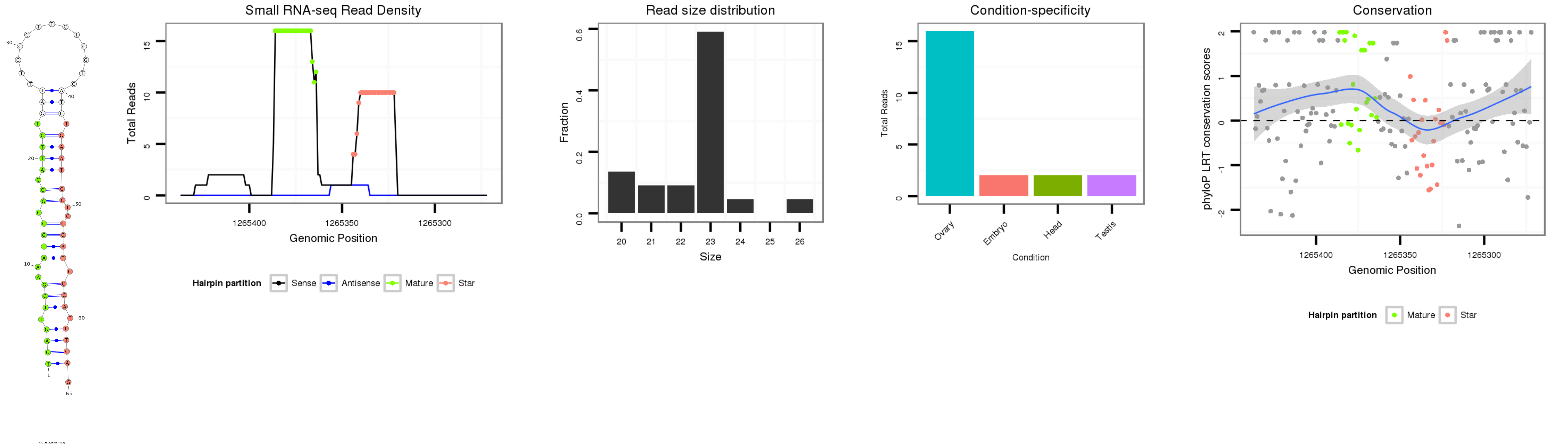
Generated: 09/08/2015 at 08:04 PM

	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	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	4

	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

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Show Alternate Folds

Flybase annotation

intron [31_1265322_1265387_-]; CDS [31_1263339_1265321_-]; CDS [31_1265388_1265529_-]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

[illegible]

Anti-sense strand reads

					SRR553487	SRR553488	SRR553485	SRR553486								
AGGACCCGTCTTTTATTGTCTGCATGACCTCTGGTAGTGGGTGCTTCGCGCTCAACCTTTACGCCGTAAGACTAAAGGAAGAGCAGTAGACTTAGGAGGGTAGGGTAAAGTC					Read #				SRR902009	M023	M024	NRT 0-2 hours eggs	SRR618934	RT 0-2 hours eggs	Chicharo_3 day-old ovaries	Makindu_3 day-old ovaries
*****(((.(.((.(.(.(((.(.(.....)))))))).)))..)))..))).*****					size	Mismatch	Total Count	Norm	Total	testis	head	male body	dsm w501 ovaries	w501 ovaries	day-old ovaries	day-old ovaries
.....GAAGAGCAGTAGACTTAGGAG.....					21	0	1	1.00	1	1	0	0	0	0	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

[illegible]

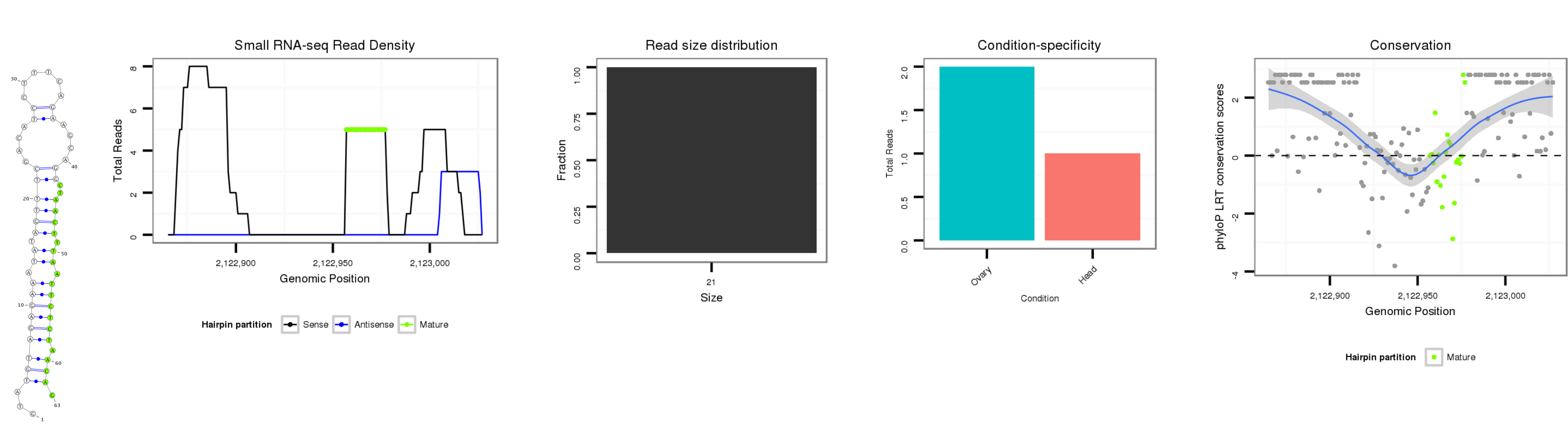
Generated: 09/08/2015 at 10:37 PM

	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

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dsi_10932	21:2122915-2122977 +	candidate	Mirtron	intron	[View on UCSC Genome Browser (Cornell Mirror)]

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

Predicted structure



Show Alternate Folds

Flybase annotation

intron [21_2122915_2122977_+]; CDS [21_2122978_2123096_+]; CDS [21_2122787_2122914_+]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

	Read size	# Mismatch	Hit Count	Total Norm	Total	M025 embryo	M023 head	Makindu_3 day-old ovaries	Chicharo_3 day-old ovaries	SRR902009 testis	SRR553486 RT_0-2 hours eggs	M024 male body	GSM343915 embryo	NRT_0-2 hours eggs	O001 Testis	SRR618934 dsim w501 ovaries
CGCGTGATGATCGAGAAATCTGGAATGCGGCGACGTGGTCTATGTACAAGGTATGTTTCGACATCCTTTCAGAAGCAGCGTAACCTTTAATTCTCTAACAGGAAATGATACTGAAATCGGATCAGCAGACGGGAGACGTTCTACTCGATG	22	1	1	35.00	35	17	11	4	0	0	1	1	0	1	0	0
.....CTAACCTTTAATTCTCTAACAG.....	21	0	1	3.00	3	0	1	0	0	0	2	0	0	0	0	0
.....CTAACCTTTAATTCTCTAACAG.....	22	0	1	2.00	2	1	1	0	0	0	0	0	0	0	0	0
.....CTAACCTTTAATTCTCTAACAG.....	26	0	1	2.00	2	0	0	1	1	0	0	0	0	0	0	0
.....GATGATCGAGAAATCTGGAATGCGGC.....	17	0	1	1.00	1	0	0	0	1	0	0	0	0	0	0	0
.....TGATGATCGAGAAATCT.....	18	0	1	1.00	1	0	0	0	0	0	0	1	0	0	0	0
.....ATGATCGAGAAATCTGGA.....	21	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	1
.....GATCAGCAGACGGGAGACGTT.....	21	0	1	1.00	1	0	0	0	0	1	0	0	0	0	0	0
.....CTGAAATCGGATCAGCAGACG.....	21	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0
.....CGAGAAATCTGGAATGCGGCG.....	21	0	1	1.00	1	0	0	0	0	1	0	0	0	0	0	0
.....CGAGAAATCTGGAATGCGGCG.....	18	0	1	1.00	1	0	1	0	0	0	0	0	0	0	0	0
.....TGAATCGGATCAGCAGACG.....	27	0	1	1.00	1	0	0	0	1	0	0	0	0	0	0	0
.....GATCGAGAAATCTGGAATGCGGCGAGCT.....	28	0	1	1.00	1	0	0	0	0	0	0	1	0	0	0	0
.....GATCGAGAAATCTGGAATGCGGC.....	23	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0
.....CTAACCTTTAATTCTCTAACAG.....	18	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0
.....GATCAGCAGACGGGAGAC.....	22	1	1	1.00	1	0	1	0	0	0	0	0	0	0	0	0
.....ATGCGCGACGTGGTCTA.....	18	0	1	1.00	1	0	0	0	0	0	0	0	0	0	1	0
.....CGGATCAGCAGACGGGAGACG.....	22	0	1	1.00	1	0	0	0	0	1	0	0	0	0	0	0

Anti-sense strand reads

	Read size	# Mismatch	Hit Count	Total Norm	Total	M023 head	Makindu_3 day-old ovaries	RT_0-2 hours eggs	NRT_0-2 hours eggs
GCGCACTACTAGCTCTTTTAGACCTTACGCGCTGCACCAGATACATGTTCCATACATCTCTTTATATCAAAGCTGTAGGAAAGTCTTCGTCGCGATTGAAATTAAGAGATTGCTCTTAACTATGACTTTAGCCTAGTCTGCGCCCTGCAAGATGAGCTAC	21	0	1	2.00	2	2	0	0	0
.....TGCCCTCTGCAAGATGAGCTA.....	21	1	1	2.00	2	2	0	0	0
.....GCGCCCTCTGCAAGATGAGCTA.....	21	0	1	1.00	1	0	1	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droSim2	21:2122865-2123027 +	dsi_10932	CGCGTGATGATCGAGAAATCTGGAATGCGGCGACGTGGTCTATGTACAAGGTATGT---AGA--GAAATAT--AGTTTCGA-----CATCC-----TTTC-AGAAGC----AGGCTA-A---C-T-TTAATTC-----TCTAACAGGAAATGATACTGAAATCGGATCAGCAGACGGGAGACGTTCTACTCGATG
droSec2	scaffold_4325:644-806 +		CGCGTGATGATCGAGAAATCTGGAATGCGGCGACGTGGTCTATGTACAAGGTATGT---AGA--GAAATAT--GTTTCGA-----CATCC-----TTTC-AGAAGC----AGGCTA-A---C-T-TTAATTC-----GACACAGGAAATGATACTGAAATCGGATCAGCAGACGGGAGACGTTCTACTCGATG
dm3	chr21:2229344-2229506 +		CGCGTGATGATCGAGAAATCTGGAATGCGGCGACGTGGTCTATGTACAAGGTATGT---ANA--GAAATCT--AGTTTCGA-----CATCC-----TTTC-AGAAGC----AGGCTA-A---C-T-TTAATTC-----GACACAGGAAATGATACTGAAATCGGATCAGCAGACGGGAGACGTTCTACTCGATG
droBre2	scaffold_4929:2264492-2264658 +		CGCGTGATGATCGAGAACTCTGGAATGCGGCGACGTGGCTATGTACAAGGTACAT---AAATCCAAACATAGAGTTTCCAA---AAATCGGATCAGCAGACG---CTCC-----TTTC-AGAAGC----ACAATA-A---T-C-G-GATT---GACACAGAAATGATACTGAAATCGGATCAGCAGACGGGAGACGTTCTACTCGATG
droYak3	21:2202443-2202598 +		CGCGTGATGATCGAGAAATCTGGAATGCGGCGACGTGGTCTATGTACAAGGTAT---ACA--GAAAT---CGA-----CATCC-----CTT-AGAAGC----TTTCTA-A---T-T-ACAAATT---ACTACAGAAATGATACTGAAATCGGATCAGCAGACGGGAGACGTTCTACTCGATG
droEug1	scf7180000409554:4006313-4006482 +		CGTGATGATCGAGAAATCGGAATGCGGCGACGTGGCTATGTACAAGGTAAAT---AACATAAATAA--AGAAAAA-----CATCT-----TTAA-AGAAAT---ATTAC-A---A-A-ACAATTG-G-TAA---T-TT-AGA---AAATTGATCTGAAATCGGATCAGCAGACGGGAGACGTTCTACTCGATG
droBial	scf7180000301500:37246-37416 -		CGCGTGATGATCGAGAAATCGGAATGCGGCGACGTGGCTATGTACAAGGTAT---ACA--AAATAA--A-----AA---TC-TGCTTATG---GAGATCTCT-A-AAAGC----AACTC-A---TTT-AATAATTG-----TTTACAGAAATTTGATCTGAAATCGGATCAGCAGACGGGAGACGTTCTACTCGATG
droTak1	scf7180000416008:509256-509428 -		CGCGTGATGATCGAGAAATCTGGAATGCGGCGACGTGGCTATGTACAAGGTAT---CAA--TAA---GCA---AATGCATTGCA-----ATCCAAATCTCT---GAAGT-----AAATA-A---T-T-A-TATTG-G-T-----TTTGACAAATTTATCTGAAATCGGATCAGCAGACGGGAGACGTTCTACTCGATG
droE1el	scf7180000791273:1043637-1043811 -		CGCGTGATGATCGAGAAATCTGGAATGCGGCGACGTGGCTATGTACAAGGTAT---ANA--AAACAAACAA--A-----AATGCAGATGCA-----CAATT-----CTGA-AGAAAT---GAAATA-A---T-T-ACAAATTTCG-T-TCTCTACAGAAATTTGATCTGAAATCGGATCAGCAGACGGGAGACGTTCTACTCGATG
droRho1	scf7180000779340:7383-7554 +		CGCGTGATGATCGAGAAATCTGGAATGCGGCGACGTGGCTATGTACAAGGTATAC---AAA--CAACAA--A-----AAGCAAATGCA-----CATCT-----CTGA-AGAAAT---TACCA-A---T-C-AAAT-TC---TATTCTCTCTGACAAATTTATCTGAAATCGGATCAGCAGACGGGAGACGTTCTACTCGATG
droFic1	scf7180000453924:106853-107017 +		CGCGTGATGATCGAGAAATCTGGAATGCGGCGACGTGGCTATGTACAAGGTATGT---AAA--CAACAA--A-----AATGCAGATGCG-----CATCT-----TTTG-AGAAAT---ATATATTTAACTTCTCT---TCACAGAAATTTGATACTGAAATCGGATCAGCAGACGGGAGACGTTCTACTCGATG
droKix1	scf7180000302408:484959-485130 +		CGTGATGATCGAGAAATCTGGAATGCGGCGACGTGGCTATGTACAAGGTATATTGTAA---CAATAAA--GC-----ATC-----TTTGATAA---ACAAA--AACTAA-TT---AAATC-A---G-G---TG---TTTTTTCTAACACAAATTTATCTGAAATCGGATCAGCAGACGGGAGACGTTCTACTCGATG
droAna3	scaffold_12916:6242055-6242211 -		CGTGATGATCGAGAAATCGGAATGCGGCGACGTGGCTATGTACAAGGTATAC---AAA--AAACTT---A-----TA-----TT---CA---TTAA--ACTTAA-TC---GAA-A---TA---TACATTT---CTTTAGAAATTTGATTTGAAATCGGATCAGCAGACGGGAGACGTTCTACTCGATG
droBip1	scf7180000396568:587240-587404 +		CGTGATGATCGAGAAATCGGAATGCGGCGACGTGGCTATGTACAAGGTATGT---AAA--AAATAA--ACAATAA-----ACCTC-----TTTA-AAAAAT---TCCTA-A---C-T-AATAATG---T-----GA-TGACAAATTTGATTTGAAATCGGATCAGCAGACGGGAGACGTTCTACTCGATG
dp5	4_group3:4204883-4205054 -		CGTGATGATCGAGAAATCTGGAATGCGGCGACGTGGCTATGTACAAGGTGGGTCGTAA--GAAATAC--AC-----ATA---TGATGTG---GACCC---CTTTAA-ATG---ATTCC-A---TA-CTTTG-----TCCTACAAATTTGATACTGAAATCGGATCAGCAGACGGGAGACGTTCTACTCGATG
droPer2	scaffold_1:5687763-5687930 -		CGTGATGATCGAGAAATCTGGAATGCGGCGACGTGGCTATGTACAAGGTGGGTCGTAA--GAAATAC--AC-----ATA---TG---TG---GACCC---CTTTAA-ATG---ATTCC-A---TA-CTTTG-----TCCTACAAATTTGATACTGAAATCGGATCAGCAGACGGGAGACGTTCTACTCGATG
droW12	scf2_1100000004521:2182398-2182560 +		CGTGATGATCGAGAAATCTGGAATGCGGCGACGTGGCTATGTACAAGGTATGT---TTTTCTCTCA---CTTTATG---ATTCA-----TGAC---TTTA-AG---AAATA-TG-AC---T-T---T---G-TGACAAATTTGATACTGAAATCGGATCAGCAGACGGGAGACGTTCTACTCGATG
droVir3	scaffold_12963:13657305-13657458 +		CGTGATGATCGAGAAATCGGAATGCGGCGACGTGGCTATGTACAAGGTCCCT---AAC-TAA---G---G-TA-----TT---CC-----ATCA-TAAGCA---CAAATA-A---TC-T-G---TCA---T-----G-TGACAAATTTGATTTGAAATCGGATCAGCAGACGGGAGACGTTCTACTCGATG
droMo3	scaffold_6500:24500436-24500602 -		CGTGATGATCGAGAAATCGGAATGCGGCGACGTGGCTATGTACAAGGTATA---ACA--AAATCT---GAA---CA-----CATCC-----ATCA-TAAGTC---ACAATA-A---TAT-G-GATTGTGATT---GTGTGTAAAGCAATACTGAAATCGGATCAGCAGACGGGAGACGTTCTACTCGATG
droGr12	scaffold_15126:6206669-6206832 -		CGTGATGATCGAGAAATCGGAATGCGGCGACGTGGCTATGTACAAGGTACAT---ATA--TC---AC--AGTTTGAC-----CATCT-----TCC-AGCTAAACCCGAAATA-A---ACT-T-T-G---T-----G-TGACAAATTTGATTTGAAATCGGATCAGCAGACGGGAGACGTTCTACTCGATG

Generated: 09/08/2015 at 07:18 PM

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