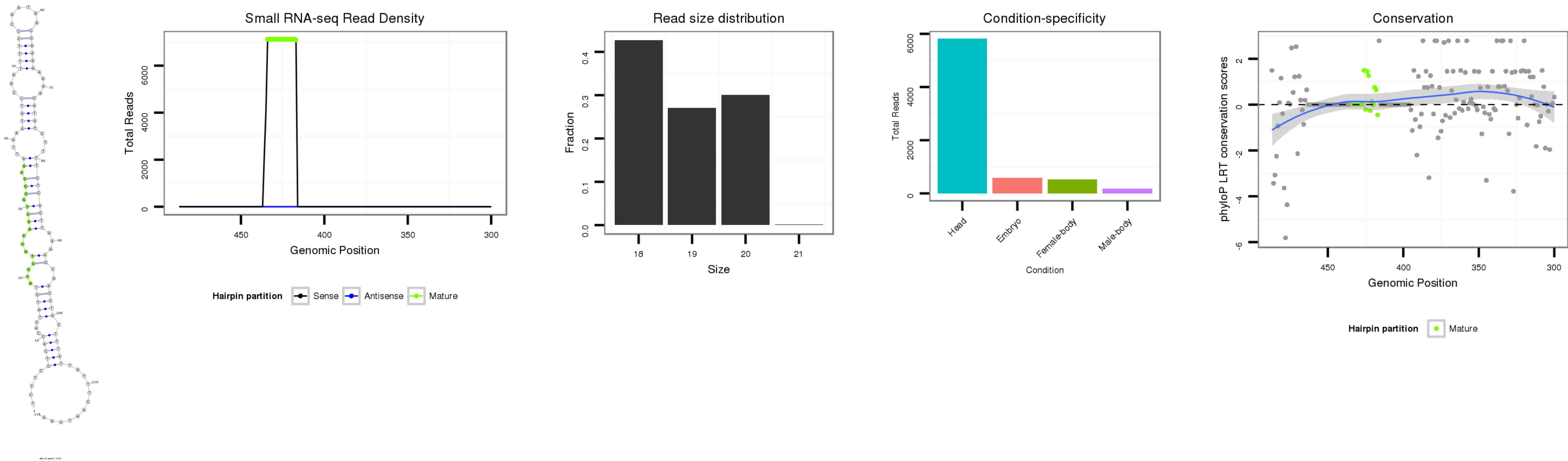


Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Show Alternate Folds

Flybase annotation

intergenic

Repeatable elements

Name	Class	Family	Strand
TVII	LTR	Gypsy	+

mature dwi_21_scf2_11000000008628417-434_- dwi_22_scf2_11000000004591180539-180556_-	star
---	-------------

Sense Strand Reads

hide 3p reads show mid mismatch reads

Read	#	Hit	Total	Total	V19	M045	V17	V18	M020
size	Mismatch	Count	Norm		head	female body	male body	embryo	head
18	0	2	3034.00	6068	4730	280	151	866	41
20	0	2	2140.50	4281	3654	377	44	202	4
19	0	2	1911.00	3822	3161	393	174	83	11
18	1	2	25.00	50	31	5	8	0	6
20	1	2	20.50	41	34	7	0	0	0
21	0	2	15.00	30	25	2	3	0	0
19	1	2	14.50	29	14	12	3	0	0
19	0	2	14.50	29	5	6	2	15	1
18	1	2	9.00	18	17	0	0	1	0
18	0	2	7.00	14	4	2	2	4	2
20	1	2	5.00	10	9	0	0	1	0

Anti-sense strand reads

[illegible]

Show Alignment With Reads

Re-alignment of all predicted orthologs

[illegible]

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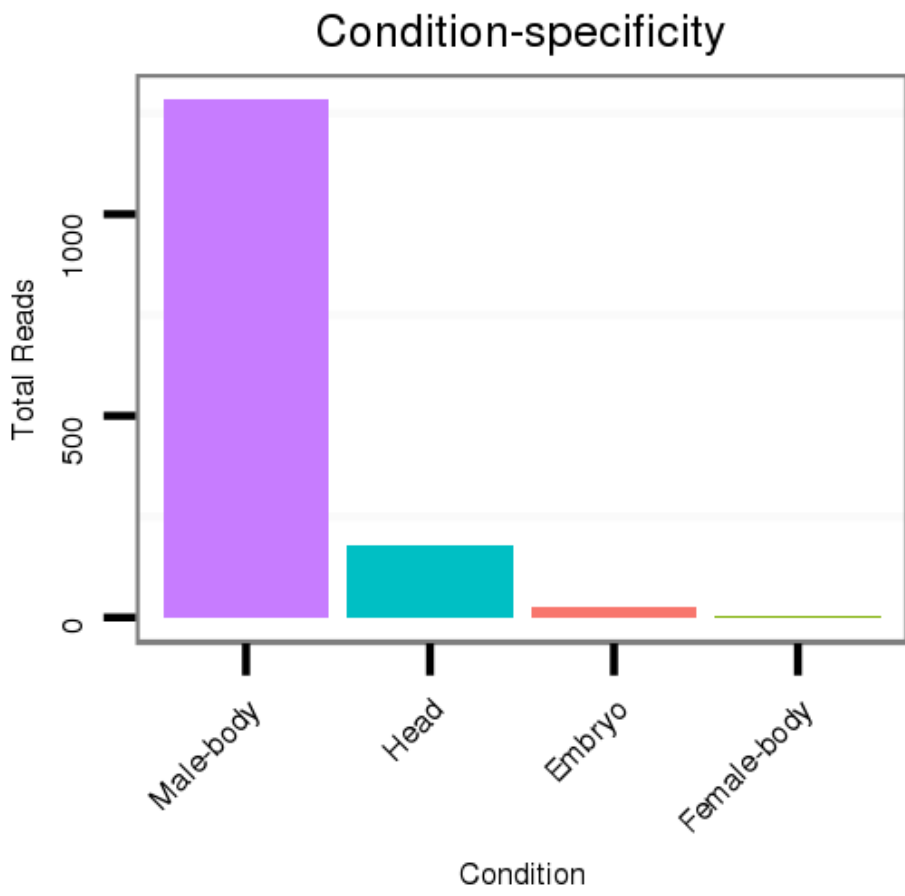
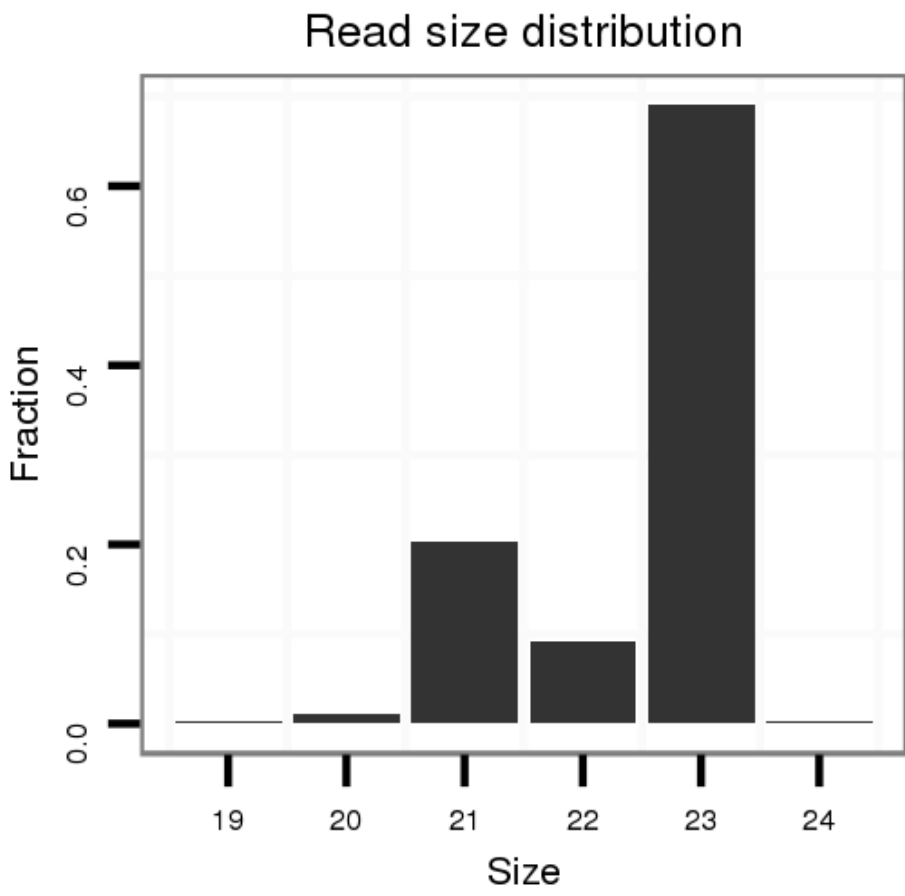
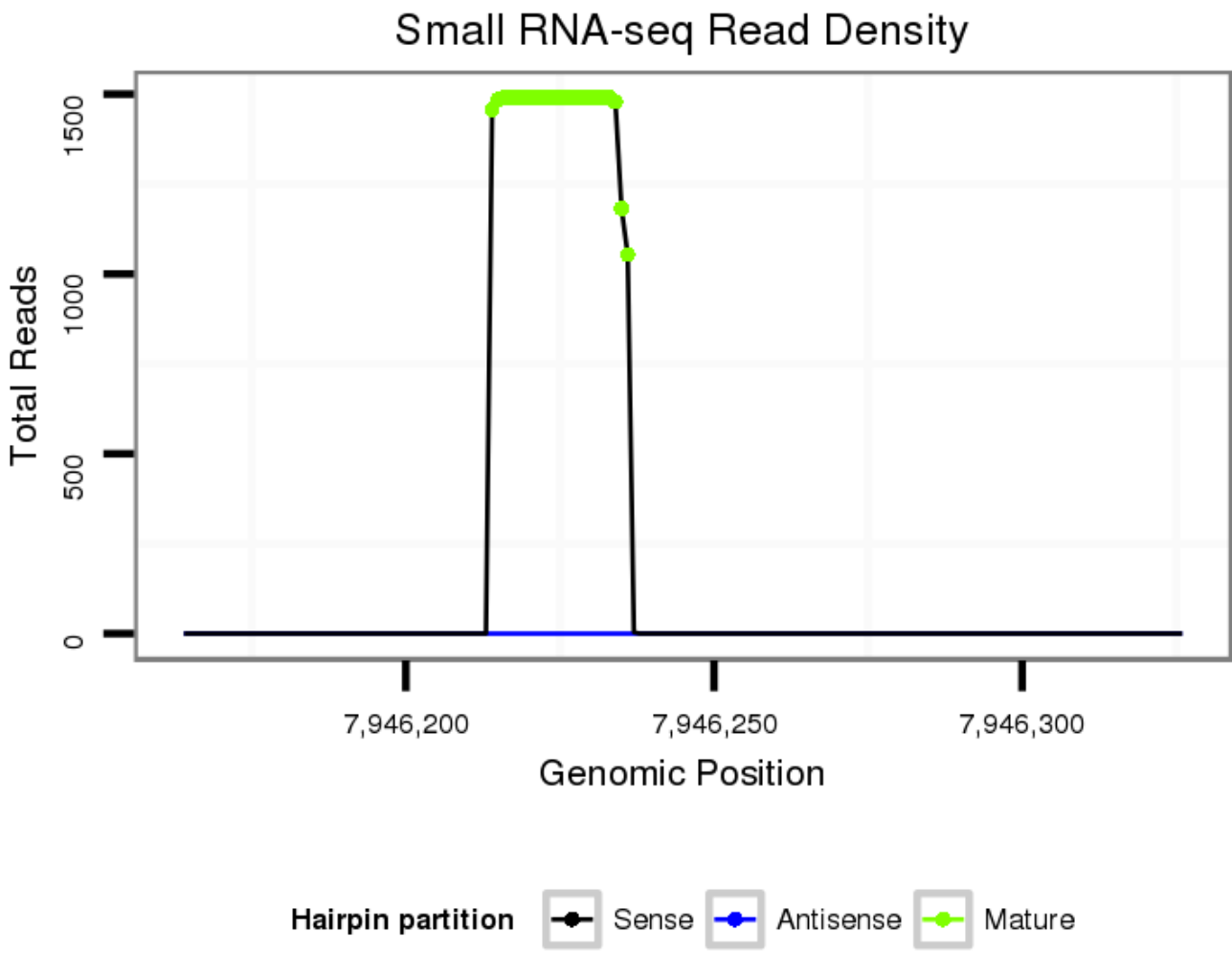
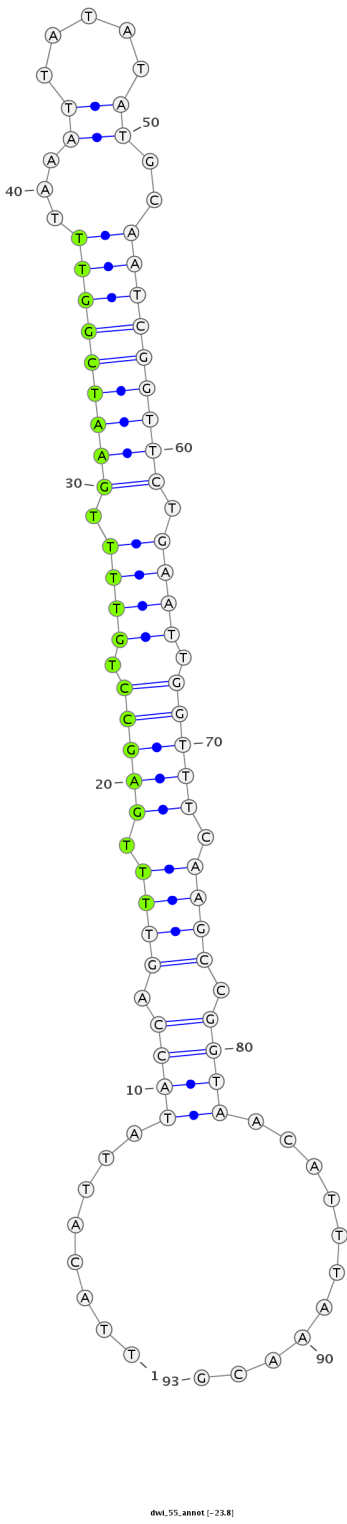
	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	0
crit.top3	1
crit.tptop3	0
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

Legend: nature star mismatch in alignment mismatch in read

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dwi_55	scf2_1100000004909:7946214-7946276 +	confident-exception	Testes-restricted	intergenic	[View on UCSC Genome Browser {Cornell Mirror}]

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



No conservation details.

Show Alternate Folds

Flybase annotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

AAAAAACGAATGAAAAGTTCAGGTTTTTAAGAATTTTACATTATACCAGT	TTTGAGCCTGTTTGAATCGGTT	TAAATTATATATGCAATCGGTTCTGAATTGGTTTCAAGCCGGTAACATTTAAACGTCGACGAATCGAAAGTTTCTATATTGTAATTAGAA	Read #		Hit	Total		V117	M020	V119	V118	M045
*****	size	Mismatch	Count	Norm	Total	male	head	head	embryo	body	body	body
TTTGAGCCTGTTTGAATCGGTT	23	0	1	1030.00	1030	898	77	33	20	2		
TTTGAGCCTGTTTGAATCGG	21	0	1	292.00	292	226	36	24	4	2		
TTTGAGCCTGTTTGAATCGGT	22	0	1	121.00	121	116	3	2	0	0		
TTGAGCCTGTTTGAATCGGTT	22	0	1	16.00	16	13	1	2	0	0		
TTTGAGCCTGTTTGAATCG	20	0	1	10.00	10	9	1	0	0	0		
TTGAGCCTGTTTGAATCGGT	21	0	1	6.00	6	6	0	0	0	0		
TTTGAGCCTGTTTGAATCGGT	23	1	1	5.00	5	4	0	1	0	0		
TGAGCCTGTTTGAATCGGTT	21	0	1	4.00	4	4	0	0	0	0		
TTTGAGCCTGTTTGAATCGGTTT	24	0	1	4.00	4	4	0	0	0	0		
TTGAGCCTGTTTGAATCGG	20	0	1	4.00	4	4	0	0	0	0		
TTGAGCCTGTTTGAATCG	19	0	1	2.00	2	2	0	0	0	0		
TTGAGCCTGTTTGAATCGGTTA	23	1	1	1.00	1	1	0	0	0	0		
TTTGAGCCTGTTTGAATCGGTTCC	25	2	1	1.00	1	1	0	0	0	0		
TGAGCCTGTTTGAATCGGT	20	0	1	1.00	1	1	0	0	0	0		
TTGAGCCTGTTTGAATCGGTA	22	1	1	1.00	1	1	0	0	0	0		
TGAGCCTGTTTGAATCGG	19	0	1	1.00	1	1	0	0	0	0		
TTTGAGCCTGTTTGAATCGC	21	1	1	1.00	1	1	0	0	0	0		

Anti-sense strand reads

TTTTTTGCTTACTTTTCAAGTCCAAAAATCTTAAAAATGTAATATGGTCAAACTCGGACAAAACCTAGCCAAATTTAATATATACGTTAGCCAAAGCTTAAACCAAGTTCGGCCATTGTAAATTTGCAGCTGCTTAGCTTTCAAAGATATAACATTAATCTT	Read #		Hit	Total		M045	M020	V118
*****	size	Mismatch	Count	Norm	Total	female	head	embryo
TTTTTTGCTTACTTTTCAAGTCCAAAAATCTTAAAAATGTAATATGGTCAAACTCGGACAAAACCTAGCCAAATTTAATATATACGTTAGCCAAAGCTTAAACCAAGTTCGGCCATTGTAAATTTGCAGCTGCTTAGCTTTCAAAGATATAACATTAATCTT						body	body	body

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
drowil2	scf2_1100000004909:7946164-7946326 +	dwi_55	AAAAAACGAATGAAAAGTTCAGGTTTTTAAGAATTTACATTATACCAGT TTTGAGCCTGTTTGAATCGGTT TAAATTATATATGCAATCGGTTCTGAATTGGTTTCAAGCCGGTAACATTTAAACGTCGACGAATCGAAAGTTTCTATATTGTAATTAGAA

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crit.star	0
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	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

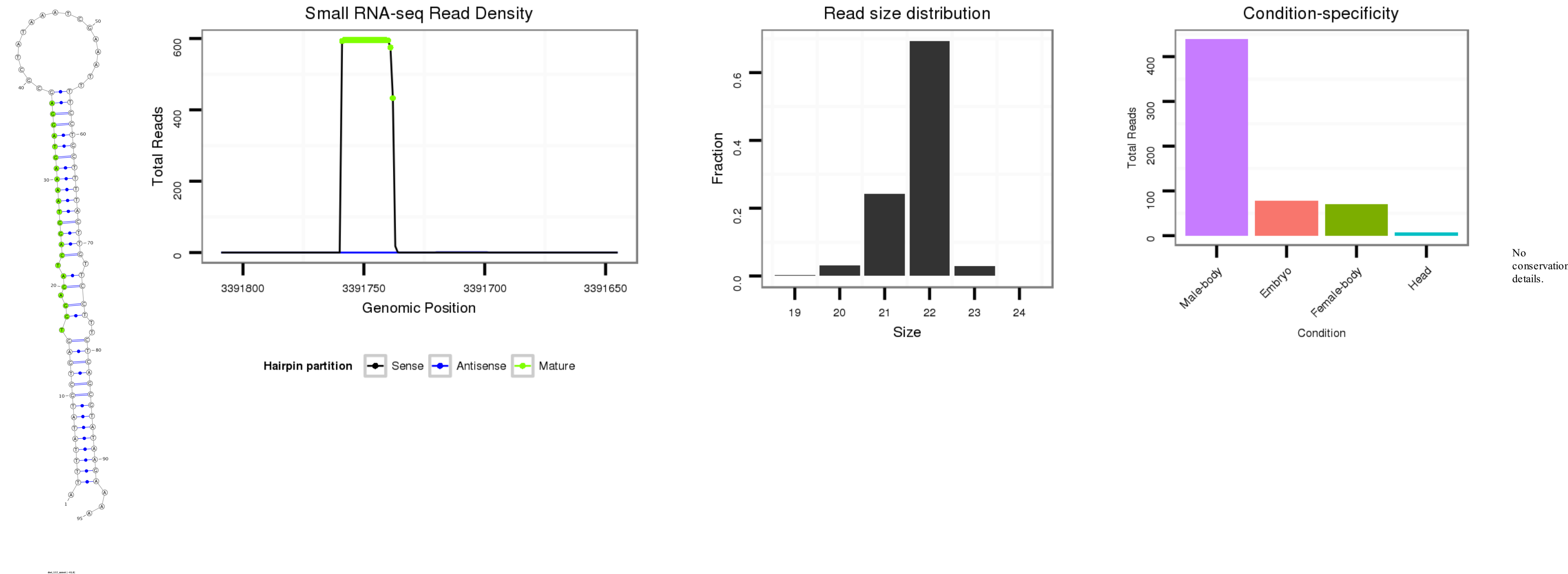


Anti-sense strand reads

Show Alignment With Reads

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Show Alternate Folds

Flybase annnotation

Antisense to intron [Dwil\GK17265-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

					V117	V118	M045	V119	M020
GACCTTTGACGCTAGGCATTTTTATTGATTCCTATTATATTTTATATGCTGAC	TGGAGATCAGGTAAAAGTAGGA	GCGCTATAAATCGAAATTTTCCTGCTTTTACTTGTTCCCTTCTCAGCGTATAAGAAAAACGAGATCAACCAATTCATATTTTAGGTAAGAGCT							
*****.(((((((((((.(.(.((((((((((((((.....)))))))))..)))))))))...*****	Read #	Mismatch	Hit Count	Total Norm	Total	male body	V117 embryo	female body	head head
.TGGAGATCAGGTAAAAGTAGGA	22	0	1	413.00	413	305	69	34	4
.TGGAGATCAGGTAAAAGTAGG.	21	0	1	142.00	142	100	6	33	3
.TGGAGATCAGGTAAAAGTAGGA	23	1	1	41.00	41	32	4	5	0
.TGGAGATCAGGTAAAAGTAG.	20	0	1	19.00	19	16	0	3	0
.TGGAGATCAGGTAAAAGTAGGAG.	23	0	1	17.00	17	14	3	0	0
.TGGAGATCAGGTAAAAGTAGGA	23	1	1	12.00	12	11	0	0	1
.TGGAGATCAGGTAAAAGTAGGAAA	24	2	1	7.00	7	6	0	1	0
.TGGAGATCAGGTAAAAGTAGGACT	24	1	1	3.00	3	2	1	0	0
.GGAGATCAGGTAAAAGTAGGA	21	0	1	2.00	2	1	0	1	0
.TGGAGATCAGGTAAAAGTAGGAC	23	1	1	2.00	2	1	0	0	1
.TGGAGATCAGGTAAAAGTAGGAAT	24	2	1	2.00	2	1	0	1	0
.TGGAGATCAGGTAAAAGTAGAC	21	1	1	1.00	1	1	0	0	0
.TGGAGATCAGGTAAAAGTAGGAGC	24	0	1	1.00	1	1	0	0	0
.GGAGATCAGGTAAAAGTAGGAAA	23	2	1	1.00	1	0	0	1	0
.TGGAGATCAGGTAAAAGTAGGT	22	1	1	1.00	1	1	0	0	0
.TGGAGATCAGGTAAAAGTA	19	0	1	1.00	1	1	0	0	0
.TGGAGATCAGGTAAAAGTAGGAGCGC	27	1	1	1.00	1	0	0	1	0
.TGGAGATCAGGTAAAAGTA	20	1	1	1.00	1	1	0	0	0
.TGGAGATCAGGTAAAAGTAGGC	22	1	1	1.00	1	1	0	0	0
.GGAGATCAGGTAAAAGTAG.	19	0	1	1.00	1	1	0	0	0
.TGGAGATCAGGTAAAAGTTC	20	2	1	1.00	1	1	0	0	0

Anti-sense strand reads

[illegible]

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droWil2	scf2_1100000004511:3391645-3391809 -	dwi_132	GACTTTGACGCTAGGCATTTTATTGATTCTATTATATTTATATGCTGAGTGGAGATCAGGTAAAGTAGGCGCCTATAAATCGAAATTTCTGCTTTTACTTGTTCCTTTCTCAGCGTATAAGAAAACGAGATCAACCAATTCATATTTAGGTAAGAGCT

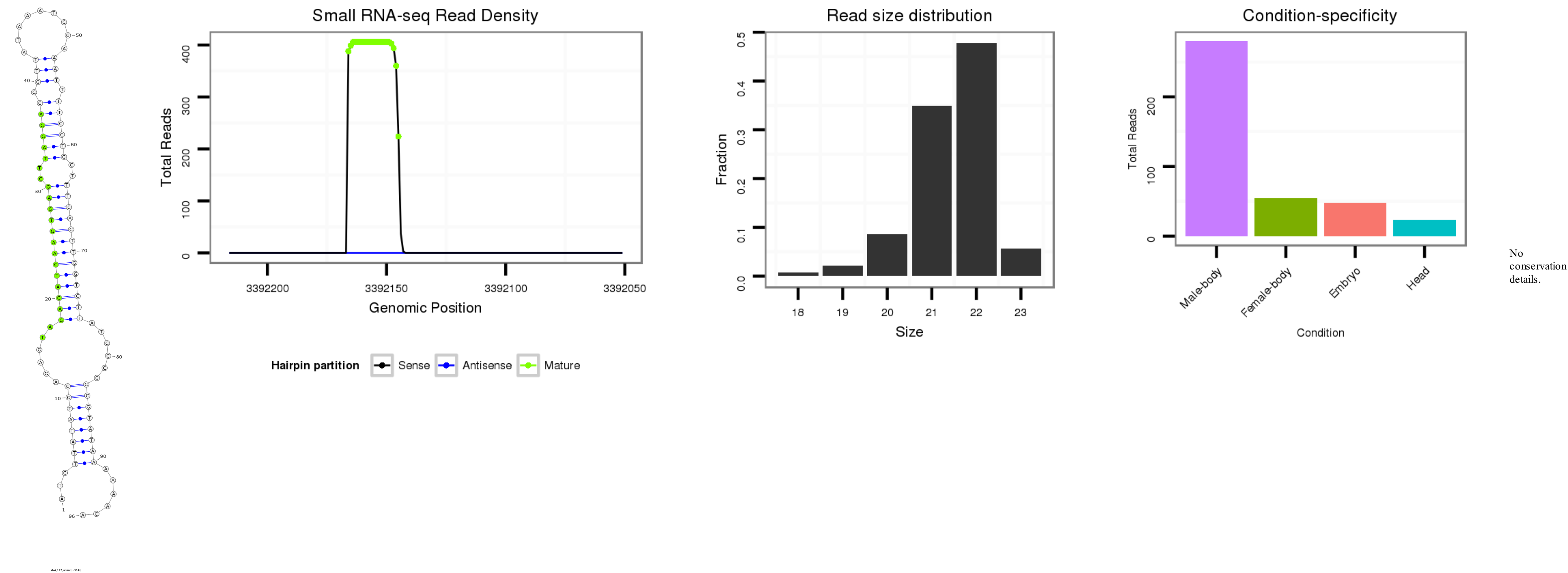
Generated: 09/08/2015 at 07:59 PM

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

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dwi_147	scf2_1100000004511:3392101-3392166 -	confident-exception	Testes-restricted	antisense_to_intron	[View on UCSC Genome Browser [Cornell Mirror]]

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Show Alternate Folds

Flybase annotation

Antisense to intron [Dwil\GK17265-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

AAACTTAGTGATCGTCGCGAGGATCATAAAAATCATATCTTATATGCAGAGTAGAGATCAAGTGAGCTTAGGAGCGTTATAAAATCGAAATTTTCCTGCCTTACACTTGGTCTTATCCCGCGGTATAAAAAACAAATCAAATCATTTTATTGTTTATTAAATAGACAG	Read size	# Mismatch	Hit Count	Total Norm	Total	V117 male body	M045 female body	V118 embryo	M020 head	V119 head
*****.(((((((.....(((((((((((.....)))))))).)))))))).*****	22	0	1	183.00	183	115	27	31	10	0
.....TAGAGATCAAGTGAGCTTAGGA.....	22	0	1	183.00	183	115	27	31	10	0
.....TAGAGATCAAGTGAGCTTAGG.....	21	0	1	136.00	136	106	20	9	0	1
.....TAGAGATCAAGTGAGCTTAGGAT.....	23	1	1	38.00	38	32	0	2	4	0
.....TAGAGATCAAGTGAGCTTAG.....	20	0	1	34.00	34	32	2	0	0	0
.....TAGAGATCAAGTGAGCTTAGGA.....	23	1	1	27.00	27	21	2	4	0	0
.....TAGAGATCAAGTGAGCTTAGGAG.....	23	0	1	23.00	23	16	2	5	0	0
.....TAGAGATCAAGTGAGCTTAGGT.....	22	1	1	17.00	17	17	0	0	0	0
.....TAGAGATCAAGTGAGCTTAGGTTT.....	24	3	1	10.00	10	10	0	0	0	0
.....TAGAGATCAAGTGAGCTTA.....	19	0	1	9.00	9	1	0	0	8	0
.....TAGAGATCAAGTGAGCTTAGGA.....	24	2	1	9.00	9	6	2	0	1	0
.....AGAGATCAAGTGAGCTTAGGAG.....	22	0	1	8.00	8	5	1	2	0	0
.....TAGAGATCAAGTGAGCTTAGGA.....	24	2	1	5.00	5	2	0	0	3	0
.....GAGATCAAGTGAGCTTAGGAG.....	21	0	1	3.00	3	2	1	0	0	0
.....AGAGATCAAGTGAGCTTAGGA.....	21	0	1	3.00	3	2	1	0	0	0
.....GAGATCAAGTGAGCTTAGGAGC.....	22	0	1	3.00	3	1	0	1	1	0
.....TAGAGATCAAGTGAGCTT.....	18	0	2	3.00	6	0	0	0	6	0
.....TAGAGATCAAGTGAGCTTAGGATTT.....	25	3	1	2.00	2	2	0	0	0	0
.....TAGAGATCAAGTGAGCTTAGT.....	21	1	1	2.00	2	2	0	0	0	0
.....TAGAGATCAAGTGAGCTTAGCA.....	21	1	1	2.00	2	2	0	0	0	0
.....TAGAGATCAAGTGAGCTTT.....	19	1	2	1.50	3	0	0	0	3	0
.....TAGAGATCAAGTGAGCTTAGGA.....	24	2	1	1.00	1	0	0	0	1	0
.....AGAGATCAAGTGAGCTTAGGAGTT.....	24	2	1	1.00	1	1	0	0	0	0
.....TAGAGATCAAGTGAGCTTAGGTTC.....	23	2	1	1.00	1	1	0	0	0	0
.....GAGATCAAGTGAGCTTAGGA.....	20	0	1	1.00	1	0	1	0	0	0
.....TAGAGATCAAGTGAGCTTAGGC.....	22	1	1	1.00	1	1	0	0	0	0
.....AGAGATCAAGTGAGCTTAGGA.....	22	1	1	1.00	1	0	1	0	0	0
.....TAGAGATCAAGTGAGCTTAGGC.....	22	1	1	1.00	1	0	0	0	1	0
.....TAGAGATCAAGTGAGCTTAGGA.....	25	3	1	1.00	1	1	0	0	0	0
.....TAGAGATCAAGTGAGCTTAGGTT.....	23	2	1	1.00	1	1	0	0	0	0
.....TAGAGATCAAGTGAGCTTAGC.....	21	1	1	1.00	1	1	0	0	0	0
.....TAGAGATCAAGTGAGCTTA.....	20	1	2	0.50	1	1	0	0	0	0

Anti-sense strand reads

[illegible]

Show Alignment With Reads

Re-alignment of all predicted orthologs

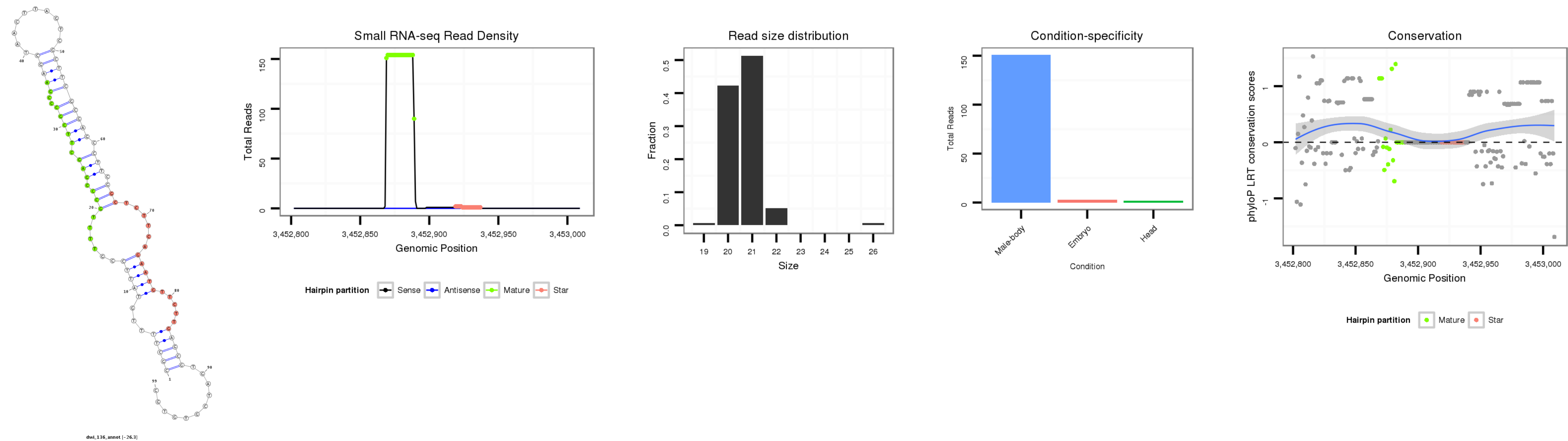
Species	Coordinate	ID	Alignment
droWil2	scf2_1100000004511:3392051-3392216 -	dwi_147	AAACTTAGTGATCGTCGCAGGATCATAAAAATCATATCTTATATGCAGAGTAGAGATCAAGTGAGCTTAGGAGCGTTATAAATCGAAATTTCTGCTTTCACTTGGTCTTATCCGCGGTATAAAAAACAATCAAATCATTATTATTGTTATTAAATAGACAG

Generated: 09/08/2015 at 08:00 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	0
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Show Alternate Folds

Flybase annotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

	Read #	Mismatch	Hit Count	Total Norm	Total	V117 male body	V118 embryo	V119 head	M045 female
AGAAAAACGAGCAACTCGCATCTTGCATATAGTCATCTCTTCATTGCGGTCGCTTTTGATATCCGTTTGGCCGAGCTTCGCCGGAAGCTAACTTAGTCGCTTCGCGAGCCTCGGCTCTTCAGAATGTTCTTGAGCGTGATCGTGTGCAGTCGTCGACGTGTGAAGTGAAGTAAAAAGTGAAGAAATTAATTATTGTCCAAA	21	0	1	79.00	79	77	1	1	0
*****(((.....(((.....(((.....(((.....(((.....)))))))))).)))).)).....)))).....))*****	20	0	1	63.00	63	62	1	0	0
.....TTTGGCCGAGCTTCGCCGGA.....	23	1	1	8.00	8	8	0	0	0
.....TTTGGCCGAGCTTCGCCGGA.....	22	0	1	7.00	7	5	1	1	0
.....TTTGGCCGAGCTTCGCCGGA.....	20	0	1	3.00	3	3	0	0	0
.....TTTGGCCGAGCTTCGCCGGA.....	19	1	1	2.00	2	2	0	0	0
.....TTTGGCCGAGCTTCGCCGGA.....	22	1	1	2.00	2	2	0	0	0
.....GTTTGGCCGAGCTTCGCCGGA.....	22	0	1	1.00	1	1	0	0	0
.....GCTCTTCAGAATGTTCTTG.....	19	0	1	1.00	1	1	0	0	0
.....TTTGGCCGAGCTTCGCCGGA.....	23	1	1	1.00	1	1	0	0	0
.....TTTGGCCGAGCTTCGCCGGAAG.....	24	1	1	1.00	1	1	0	0	0
.....GTTTGGCCGAGCTTCGCCG.....	21	0	1	1.00	1	1	0	0	0
.....TTTGGCCGAGCTTCGCCG.....	21	1	1	1.00	1	1	0	0	0
.....TAGTCGCTTCGCGAGCCTTCGCTCT.....	26	0	1	1.00	1	1	0	0	0

Anti-sense strand reads

TCTTTTTGCTCGTTGAGCGTAGAACGTATATCAGTAGAGAAGCTAAGCGCAGCGAAACATAAGGC AAACGGGCTCGAAGCGGCT TCGATTGAATCAGCGAAGCGCTCGGAAGC CGAGAAGCTCTTACAAGAAC TCGCCTAGCACACGTCAGCAGCATGCACACTTCACCTTCTTTATTTTCACCTTCTCTTTAATTAAATAACAGGTTT																					M045	V117	V119
***** ((((((... ((((((... (((... (((... ((((((... ((((((...)))))))))))...)))...)))...)))...)))...*****														Read #	Hit	Total					female	male	head
														size	Mismatch	Count	Norm	Total	body	body			

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droW112	scf2_1100000004513:3452802-3453009_+	dwi_136	AGAAAAACGAGCAA-----CTCG----CATCTTGCATATAGTCATCTCTTTTCATTCGCGTCGCTTTTGTATTCCGTTTGGCC---CGAGCTTCGCCCGAGCTAACTTAGTCGCTTCGGAGGCTTCG SCCTCTTCAGAAATGTTCTTG AGCGTGATCGTGTGCAGTCGTCGTACGTGTGAAGTAAAAATAAAGTGAAGAAATTAATTATTGTGCCAAA
droVir3	scaffold_12928:7455394-7455455_+		TAAGT-----GATGATCTGTACTTTTAGACACT AGAG AACTGAAAA CAAAAT TCC AAGAAAT GAAT-----
droMo3	scaffold_6328:2334507-2334583_+		AGAA CTATAACTTAA TAAATAGTCA AAACAACT AT-----TCAT CTCTTAATTCG ATTCGA-----TA TTAT TCTTATT TC -----G
droGr12	scaffold_15074:4785073-4785111_+		ATGTGT TAAGC -----GATGAT GTGTCCGTGC TCGT CG GTG-----
droPer2	scaffold_28:1009378-1009392_+		AAAAAAACGAGCAA-----AGAGT-----C
droAna3	scaffold_13248:2215639-2215677_+		AAAAAT AACAAGAA -----AA CAGAA T GA T GCAC -----AGAGT-----C
droBip1	scf7180000396733:566854-566864_+		AAAAAAACGA-----GAAAAA AGA -----
droKik1	scf7180000302808:48212-48222_+		CGAAAAA AGA -----GAAAAA AGA -----
droEle1	scf7180000491047:378926-378968_+		TAAG GT TA AA TAA-----G TA AA AA TAA TA TA AA T TA AGC-----
droTak1	scf7180000415846:426440-426447_+		AGCAAAA-----GAAAAA AGA -----
droEug1	scf7180000408993:2208-2260_+		GT TA CT-----CA TTGTT CG TC CA TTT GT TA CT TT ATT CC AG AT -----C
dm3	chrUextra:28928703-28928714_+		AGAA CAAA AGAG-----GAAAAA AGA -----
droEre2	scaffold_4770:4351398-4351407_+		AGAAAA CG -----GAAAAA AGA -----

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

Predicted structure



Flybase annnotation

intron [Dwil\GK13805-in]; CDS [Dwil\GK13805-cds]; CDS [Dwil\GK13805-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

Anti-sense strand reads

[illegible]

Show Alignment With Reads

Re-alignment of all predicted orthologs

[illegible]

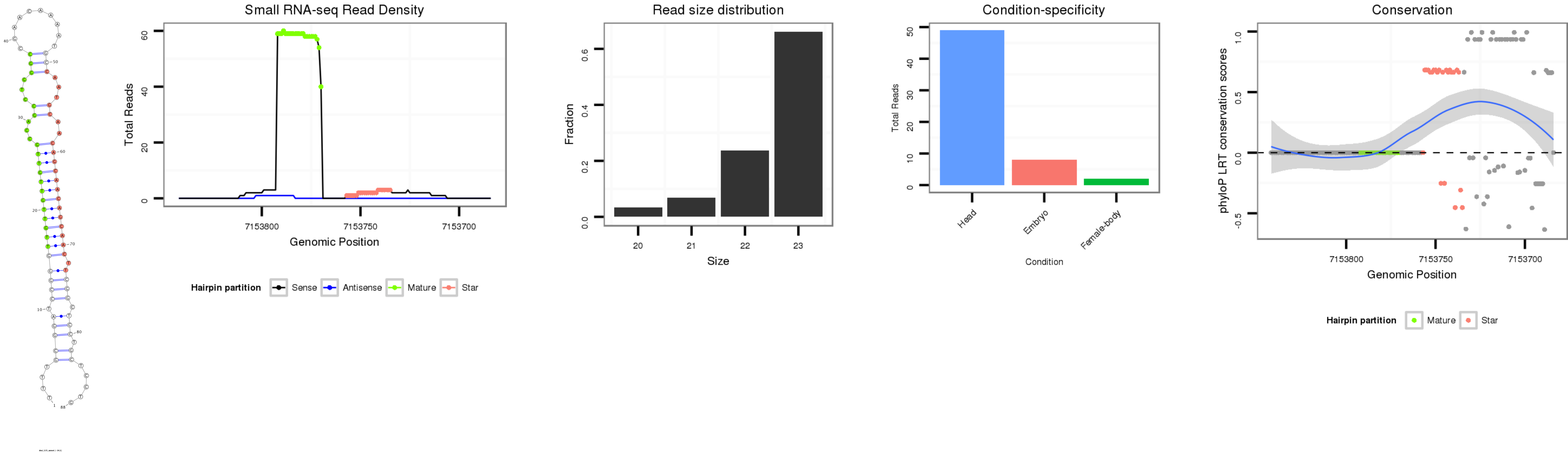
Generated: 08/18/2015 at 04:02 PM

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

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

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Show Alternate Folds

Flybase annotation

CDS [Dwil\GK25170-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

[illegible]

Anti-sense strand reads

Show Alignment With Reads

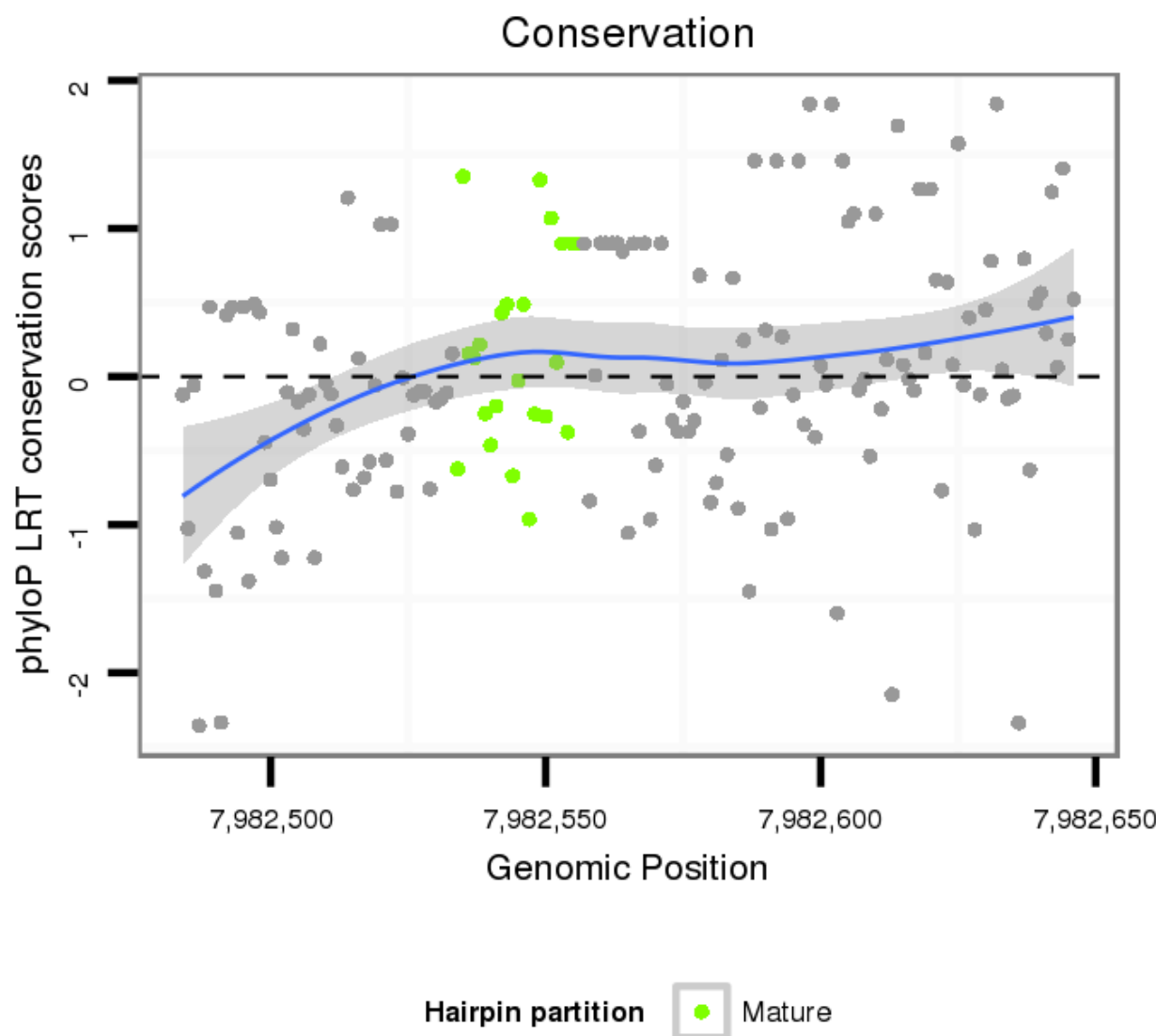
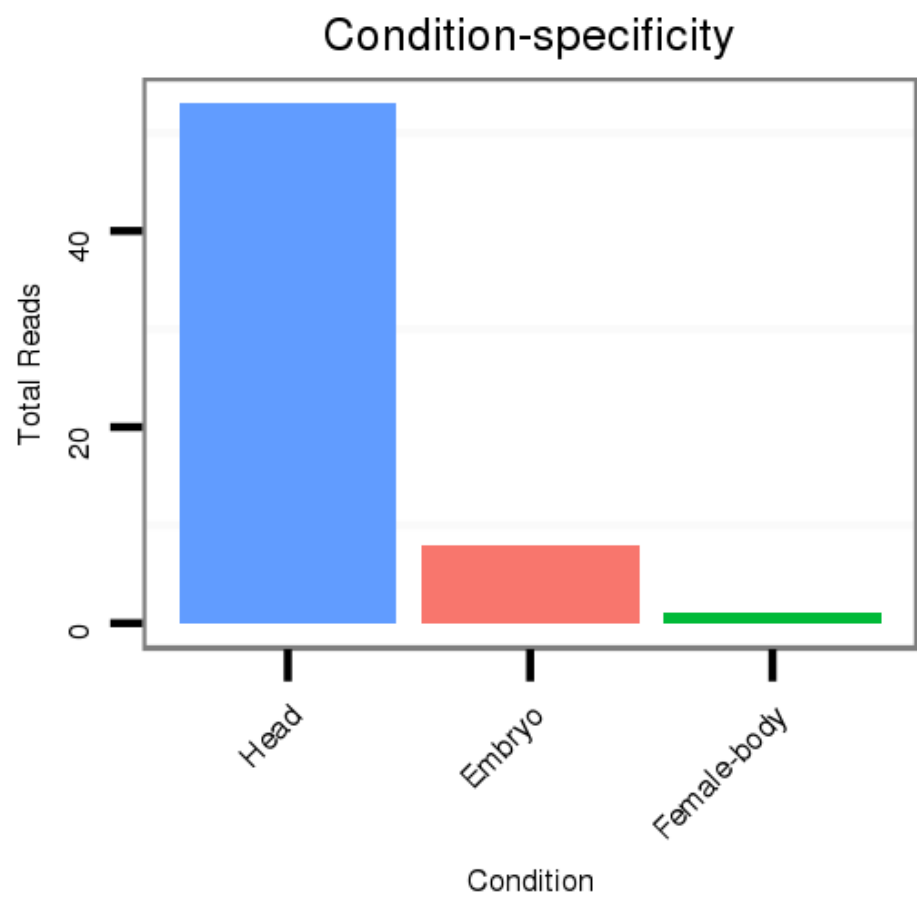
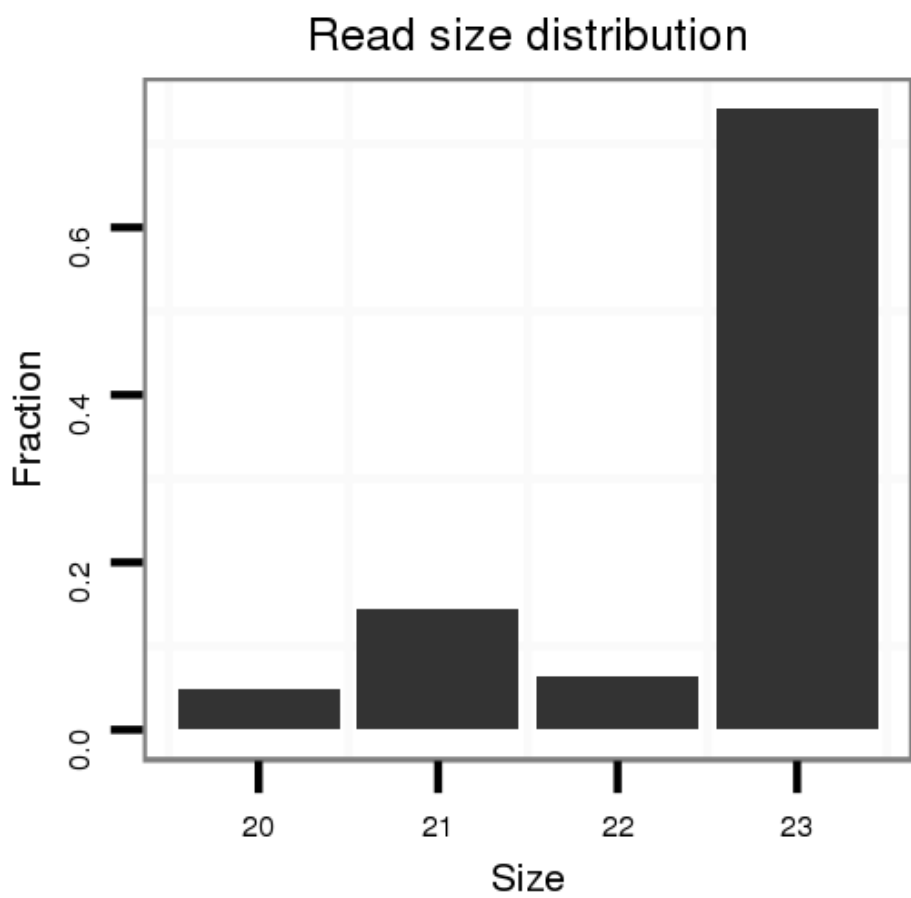
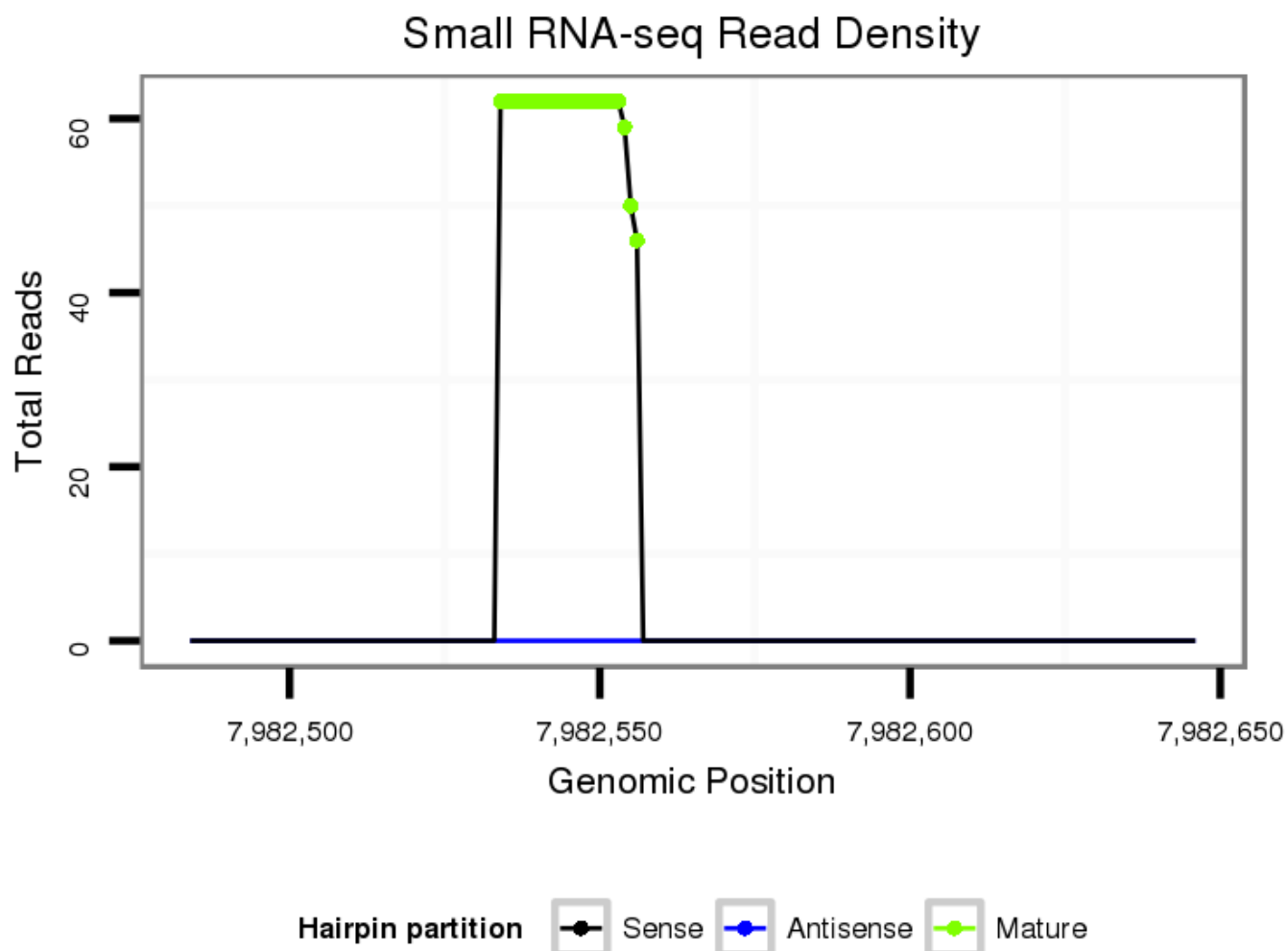
Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droW112	scf2_1100000004909:7153684-7153842_-	dwi_135	CAATTGACATGAAGACAATTTTACTTTTGCGGTATGTTTTGGCATCCGGCTTGTGTGTTGTCAGCCTGGGC GAACAAAATGC CAATGCAACAGCAAAGCAACTT CGGCTCTGCTCCTGCTTACAGTCGCGGCTGCCGCTCCAGCAATCTTGCCC
droGr12	scaffold_15203:3522820-3522879_+		-----AATGCAACAAGCAGCAGCAGAGCCTTnCGGCTCTGTCTGAGCAGCAAGCTGCAAGCTGCC-----
droPer2	scaffold_13:308965-309012_+		-----GCTCCTGCTCTGCTGnGCTGnGCTGnGCTCACGCnTTCnGGCTcTGCC-

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

Predicted structure



Flybase annnotation

intron [Dwil\GK25837-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]

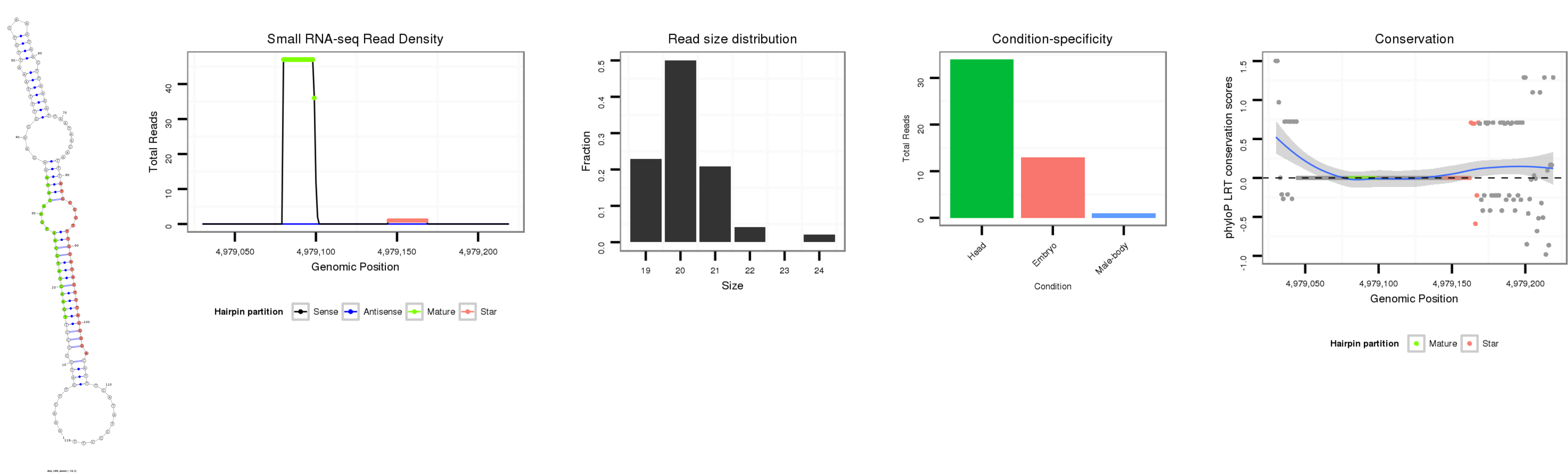
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crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
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crit.tptop3	0
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate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

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dwi_100	scf2_1100000004909:4979080-4979169 +	candidate	Canonical miRNA	intron	[View on UCSC Genome Browser (Cornell Mirror)]

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

Predicted structure



Show Alternate Folds

Flybase annnotation

intron [DwilGK25647-in]

No Repeatable elements found

Sense Strand Reads

Read #	Read size	Mismatch	Hit Count	Total Norm	Total	V119 head	M020 head	V118 embryo	V117 male body
1	20	0	1	24.00	24	16	7	1	0
2	19	0	1	11.00	11	3	8	0	0
3	21	0	1	10.00	10	0	0	9	1
4	22	0	1	2.00	2	0	0	2	0
5	24	0	1	1.00	1	0	0	1	0

Anti-sense strand reads

Read #	Read size	Mismatch	Hit Count	Total Norm	Total
1	20	0	1	24.00	24
2	19	0	1	11.00	11
3	21	0	1	10.00	10
4	22	0	1	2.00	2
5	24	0	1	1.00	1

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droWi12	scf2_1100000004909:4979030-4979219 +	dwi_100	TTTCTATACTTTTTAGTTAGGAATAATAAATGATAAACTTGATGCCCTTGAAGTATGCAATGAACATAAAGAACGTTTAAATTGTCAAATAACTTAAATTAATAACAATTTATGCCCTTTGCATACTTTAGGGGACATTTCATATCCCTTGACATCGTTTTTTATATGTATTGATGTTATGTGTTT-----
droMoJ3	scaffold_6328:147402-147471 +		TT-----AGGCAACTGCTCAGGTTTCTTACCTTGTAGCTTTATAGTTGACTTGTTCG-CCTGCACAGAGAAAC
droAna3	scaffold_13117:3765920-3765921 +		TT-----
droKik1	scf7180000302586:169398-169424 +		TTTCTTAATT-----ATCAT-----TTAATT-----
droRho1	scf7180000779914:607735-607759 -		TTT-----ATCTTATAGCACTTGTCCTTT-----

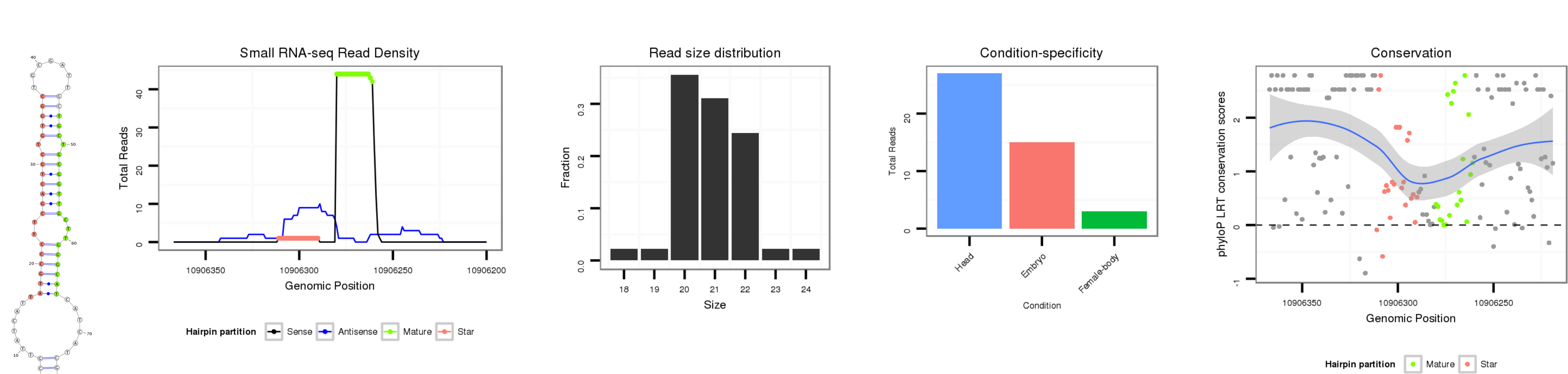
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PASS/FAIL	
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crit.mor	0
crit.hair	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.top3	1
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dwi_128	scf2_1100000004511:10906250-10906317 -	candidate	Canonical miRNA	antisense_to_CDS	[View on UCSC Genome Browser (Cornell Mirror)]

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Show Alternate Folds

Flybase annotation

Antisense to CDS [DwllfK617619-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

GTTATTCGGTGATGAGGTGGCGCTGGGCGGCATCATTTGACGGCGGCGCGGTTATCATATATGCCCTTCGACTGCTGTGGCTGCGATTGCTGCGGTTGCTTGGGCATCATCATCGCTCTCCATGCCGTTTCCACTCAACTCATTTGTTGCTGGCCGACGCCATTTTCTCC	Read #	Hit	Total		V119	V118	M045	M020	V117	
*****.(((.(((.....((((((.((((((.((((.....))))).)))))).....))))).).*****	size	Mismatch	Count	Norm	head	embryo	female body	head	male body	
.....TCTGCGGTTGCTTGGGCAT.....	20	0	1	16.00	16	10	3	3	0	0
.....TGCTGCGGTTGCTTGGGCATC.....	21	0	1	14.00	14	10	1	0	3	0
.....TGCTGCGGTTGCTTGGGCATCA.....	22	0	1	10.00	10	2	8	0	0	0
.....TGCTGCGGTTGCTTGGGCATC.....	22	1	1	1.00	1	1	0	0	0	0
.....TGCTGCGGTTGCTTGGGCA.....	19	0	1	1.00	1	0	0	0	1	0
.....TGCTGCGGTTGCTTGGGCATCAT.....	23	0	1	1.00	1	0	1	0	0	0
.....TATGCCCTTCGACTGCTGTGGC.....	22	0	1	1.00	1	0	1	0	0	0
.....TGCTGCGGTTGCTTGGGCATCATC.....	24	0	1	1.00	1	0	1	0	0	0
.....TGCTGCGGTTGCTTGGGC.....	18	0	1	1.00	1	1	0	0	0	0
.....TGCTGCGGTTGCTTGGGCATG.....	21	1	1	1.00	1	1	0	0	0	0

Anti-sense strand reads

CATAAGCCACTACTCCACCCGCACCCGCCGTAGTAACGTGCCGCCGCCGCAATAGTAATACGGGAAGCTGACGACACCGACGCTAAACACGAGCCCAAACGAAACCCGTTAGTAGCAGAGGTACGGCAAAGGTGAGTTGAGTAACAACGACCCGCGTCGGTAAAGAGG	Read #					V118	V117	M045	V119	M020
*****.(((.(((.....((((((.((((((.((((.....))))).)))))).....))))).).*****	size	Mismatch	Hit	Count	Norm	embryo	male	female	head	head
.....CGGGAAGCTGACGACACCGA.....	20	0	1	2.00	2	1	1	0	0	0
.....TGACGACACCGACGCTAACGA.....	21	0	1	2.00	2	1	1	0	0	0
.....CGGGAAGCTGACGACACCGACGCTAACG.....	28	0	1	1.00	1	0	0	0	0	1
.....CGGGAAGGTGAGTTGAGTA.....	20	0	1	1.00	1	0	1	0	0	0
.....AGCTGACGACACCGACGCTAACGA.....	24	0	1	1.00	1	1	0	0	0	0
.....ACGCTAACGACGACGCCAA.....	19	0	1	1.00	1	0	0	0	1	0
.....TAGTAGTAGCAGAGGTACGGCAAAGGT.....	27	0	1	1.00	1	0	1	0	0	0
.....TGACGACACCGACGCTAACG.....	20	0	1	1.00	1	0	0	1	0	0
.....GTAGTAGTAGCAGAGGTAC.....	19	0	1	1.00	1	1	0	0	0	0
.....CGGGAAGCTGACGACACCGACGCTAAC.....	27	0	1	1.00	1	1	0	0	0	0
.....CGGGAAGCTGACGACACCGACGC.....	23	0	1	1.00	1	1	0	0	0	0
.....CGGGAAGGTGAGTTGAGTTAGTAAC.....	22	0	1	1.00	1	0	1	0	0	0
.....CGCCGCGCAATAGTAATACGGGAAGC.....	27	0	1	1.00	1	1	0	0	0	0
.....CGCCGTAGTAACGTGCCGCCGCCG.....	24	0	1	1.00	1	0	1	0	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droH12	scf2_1100000004511:10906210-10906358 -	dwi_128	GATGAGGTGGGCGTGGGCGGCATATTGACGGCGCGCGGTTATCATATATGCCCTTCGACT-----GCTGTGGCTG-CGATTGCTGTCGG--TGCTTGGGCATCATCA--TCGCTCCAT-G---CCGTTCCACTC-----AACTCATTGTGCTGCCCGCAGC
droVi3	scaffold_13049:2654830-2655004 +		GAGSAGGTGGGCGTGGGCGGCATATGCTGGCGCGCGGTTATCATATATCCCTTCGACACTGGCAT-----TGTTGGGCATGGACATGGTGGG-----CA-GC-----TCTGTTCTGGTTCTGGTTCTTGT-----GCGAC--TGGG-----TGGCA--CTCTTTGG-----CCGTGCCACGCG-----TCATTGAGCATGGCCGCTC-
droMo3	scaffold_6654:1233460-1233632 -		GAGSAGGTGGGCGTGGGCGGCATATGCTGGCGCGGTTATCATATATGCCCTTCGACACGGGCAT-----CGTGGGCATAGACATTATAT-----GGGCA-GC-----TCTGATTCTGTTCTCGATCGCTATT-----GCGCG--TGGACTGG-----GA--CTCTTTGG-----CCGTGCCACGCG-----TCATTGAGCATGGC
droGri2	scaffold_15110:3651157-3651358 +		GAGSAGGTGGGCGTGGGCGGCATATGCTGGCGCGCGGTTATCATATATCCCTTCGACACGGGCAT-----TGTCGGGCATGGACATCATGTT-----CGGCA-GCAGCGCCACCTCTGACTCCTGTTGCAGTTGCTGTTGTT-----GCGCTTG--TATTAGTGGCATTGGCA--G--CTCTTTGG-----CCGTGCCACGCGTG-----GTTATTGAGCATGGCCGCG-T
dp5	XR_group6:9826449-9826591 +		GATGAGGTGGGCGTGGGCGGCATATGCTGGCGCGGTTATCATATATGCCCTTCGACGGCTGTGCT-----CATGGGCATGGGCATC-----GCGCACTTCA--CTCTCTCGGG-----CCGTGCCACGCGGA-----GGAGTCATGTTGTGGCCGCGCG
droPer2	scaffold_61:105396-105538 +		GATGAGGTGGGCGTGGGCGGCATATGCTGGCGCGGTTATCATATATGCCCTTCGACGGCTGTGCT-----CGTGGGCATGGGCATC-----GCGCACTTCA--CTCTCTCGGG-----CCGTGCCACGCGGA-----GGAGTCATGTTGTGGCCGCGCG
droAna3	scaffold_13337:3536420-3536616 -		GAGSAGGTGGGCGTGGGCGGCATATGCTGGCGCGGTTATCATATATCCCTTCGACGGC-CTTCCGTC-CGCTGGCATGGCATGGGCT-----GGACCTA-AAGGGCAT-----GGAATGG-----GGCTGGC-AATTTCA--CTCTCTCCCTGCAATCCACAATGCCACGCG-CTGGA--GGATCATGTTGTGGCCGCGCG
droBip1	scf7180000396387:68501-68697 -		GAGSAGGTGGGCGTGGGCGGCATATGCTGGCGCGGTTATCATATATCCCTTCGACGGC-CTTCCGTC-CGACGGCATCGGCATTGGGCT-----GGACCTA-AAGGGCAT-----GGAATGG-----TGCAGGC-AATTTCA--CTCTCTCCCTGCAATCCACAATGCCACGCG-CTGGA--GGATCATGTTGTGGCCGCGCG
droK1k1	scf7180000302486:2429352-2429527 -		GAGSAGGTGGGCGTGGGCGGCATATGCTGGCGCGGTTATCATATATCCCTTCGACGGC-----GGGCATGGGCATTGGCATGGAGCGCTGT-----AAGGGCATGCAACCGGT-----GAATTTCA--CTCTCTCCCTGCAATCCACAATGCCACGCG-CTGGA--GGATCATGTTGTGGCCGCGAGC
droFic1	scf7180000453807:995407-995609 -		GAGSAGGTGGGCGTGGGCGGCATATGCTGGCGCGGTTATCATATATCCCTTCGACGGC-GCTGC--T-TGTTGGGCATGGGCATTGGCGTCGACTTGCCCAAG-----AAGGGCATGCAACCGGTGCAAG-----CGCACTAATTTCA--CTCTCTCCCTGCAATCCACAATGCCACGCG-CTGGA--GGATCATGTTGTGGCCGCGCG
droE1e1	scf7180000490564:632564-632763 -		GAGSAGGTGGGCGTGGGCGGCATATGCTGGCGCGGTTATCATATATCCCTTCGACGGC-GCTC-----GTGGGCATGGGCATCGGCGTGGACCTGGCCAGG-----AAGGGCATGCAACCGGTGCAAG-----CGCACTAATTTCA--CTCTCTCCCTGCAATCCACAATGCCACGCG-CTGGA--GGATCATGTTGTGGCCGCGCG
droRho1	scf7180000776514:32650-32849		GAGSAGGTGGGCGTGGGCGGCATATGCTGGCGCGGTTATCATATATCCCTTCGACGGC-GCTC-----GTGGGCATGGGCATCGGCGTGGACCTGGCCAGG-----AAGGGCATGCAACCGGTGCAAG-----CGCACTAATTTCA--CTCTCTCCCTGCAATCCACAATGCCACGCG-CTGGA--GGATCATGTTGTGGCCGCGCG
droBia1	scf7180000302428:7914307-7914509 -		GAGSAGGTGGGCGTGGGCGGCATATGCTGGCGCGGTTATCATATATCCCTTCGACGGC-GCTGC-----GGCGGCATGGGCATGGCGTCGACCTGGCCAGG-----AAGGGCATGCAACCGGTGCAAG-----CATCGCACTAATTTCA--CTCTCTCCCTGCAATCCACAATGCCACGCG-CTGGA--GGATCATGTTGTGGCCGCGAGC
droTak1	scf7180000415269:179749-179939 -		GAGSAGGTGGGCGTGGGCGGCATATGCTGGCGCGGTTATCATATATCCCTTCGACGGC-----GTGGACGCTGGCGTGGGCATGGGCGTGCATTTGCCACAG-----ATC-----3G-----CGCACTAATTTCA--CTCTCTCCCTGCAATCCACAATGCCACGCG-CTGGA--GGATCATGTTGTGGCCGCGCG
droEug1	scf7180000409711:1709267-1709460 -		GAGSAGGTGGGCGTGGGCGGCATATGCTGGCGCGGTTATCATATATCCCTTCGACGGC-GCTC-----GTGGGCATGGGCATGGCGTCGACTTGCCACAG-----AAGGGCATGCAACCGGTGCAAG-----CGCACTAATTTCA--CTCTCTCCCTGCAATCCACAATGCCACGCG-CTGGA--GGATCATGTTGTGGCCGCGAGC
dm3	chr3L:9852393-9852586 +		GAGSAGGTGGGCGTGGGCGGCATATGCTGGCGCGGTTATCATATATCCCTTCGACGGC-GCTC-----GTGGGCATGGGCATCGGTGTCGATTGGCCAGT-----AAGGGCATGCAACCGGTGCAAG-----CGCACTAATTTCA--CTCTCTCCCTGCAATCCACAATGCCACGCG-CTGGA--GGATCATGTTGTGGCCGCGAGC
droSim2	31:9611848-9612041 +		GAGSAGGTGGGCGTGGGCGGCATATGCTGGCGCGGTTATCATATATCCCTTCGACGGC-GCTC-----GTGGGCATGGGCATCGGTGTCGACTTGCCACAGT-----AAGGGCATGCAACCGGTGCAAG-----CGCACTAATTTCA--CTCTCTCCCTGCAATCCACAATGCCACGCG-CTGGA--GGATCATGTTGTGGCCGCGAGC
droSec2	scaffold_0:2084737-2084930 +		GAGSAGGTGGGCGTGGGCGGCATATGCTGGCGCGGTTATCATATATCCCTTCGACGGC-GCTC-----GTGGGCATGGGCATCGGTGTCGATTGGCCAGT-----AAGGGCATGCAACCGGTGCAAG-----CGCACTAATTTCA--CTCTCTCCCTGCAATCCACAATGCCACGCG-CTGGA--GGATCATGTTGTGGCCGCGAGC
droYak3	31:9827573-9827766 +		GAGSAGGTGGGCGTGGGCGGCATATGCTGGCGCGGTTATCATATATCCCTTCGACGGC-GCTC-----GTGGGCATGGGCATCGGCGTCGATTGGCCAGT-----AAGGGCATGCAACCGGTGCAAG-----CGCACTAATTTCA--CTCTCTCCCTGCAATCCACAATGCCACGCG-CTGGA--GGATCATGTTGTGGCCGCGAGC
droEre2	scaffold_4784:9841880-9842073 +		GAGSAGGTGGGCGTGGGCGGCATATGCTGGCGCGGTTATCATATATCCCTTCGACGGC-GCTC-----GTGGGCATGGGCATCGGCGTCGATTGGCCAGT-----AAGGGCATGCAACCGGTGCAAG-----CGCACTAATTTCA--CTCTCTCCCTGCAATCCACAATGCCACGCG-CTGGA--GGATCATGTTGTGGCCGCGAGC

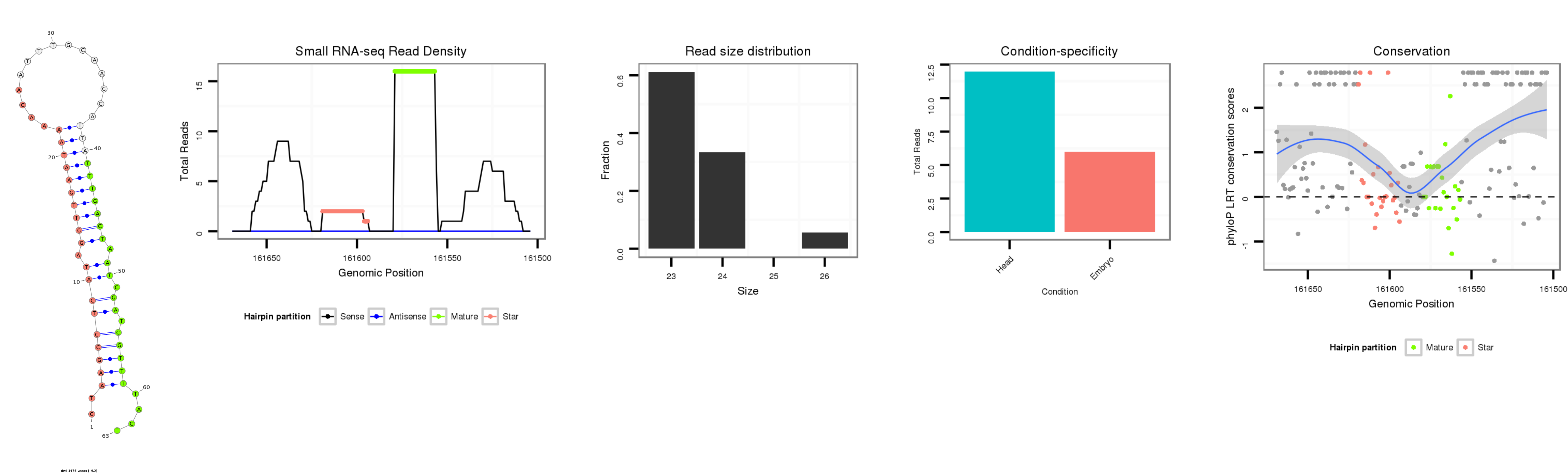
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crit.uni	0
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ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dwi_1476	scf2_1100000004558:161554-161619 -	candidate	3p_tailed_mirtron	5pUTR	[View on UCSC Genome Browser (Cornell Mirror)]

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Show Alternate Folds

Flybase annotation

utr5 [utr5_plus_3188]; intron [Dwil\GK22141-in]; CDS [Dwil\GK22141-cds]; CDS [Dwil\GK22141-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

[illegible]

Anti-sense strand reads

[illegible]

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
drow112	scaff2_1100000004558:161504-161669 -	dwi_1476	ACGACTCGA---ATGCCGCTAGTAATCAGCAGATTGAGGAGTTATCTAATCAG STAAGCGT CATA-GGTTGAATAAAACAATTTCGAAGCATTA TTGACT -AAT-CGAT-----CGT-TTTACTTAGGTCATGGACATGCGTTTAAATCTGGAGGGTTTGAAAAGGAGCGCGATT
drow1r3	scafffold_12875:15556464-15556640 -		A AG TCGG CTGG GC GCAATCC AA CAATCAGATTGAGGA A TT GC AG TCAG CTTC ---TC CACA GGTA-GAGGT GTCT ---GCAT CA ----- --- AT AGTATTC ATTTTGTGTTGTTGTT TCATATCG -C----- --- CT C AA AGGT AT GGTA AT GCCTTTAAATCTGGAGGG T GGAAAAGGAGCG GC CTT
drow1o3	scafffold_6496:8250708-8250887 -		ACGA TC CG STGACA SC GCAA CC AAATCA TC AGAT SA AG CG TC CAATCAG CTTC ---TC CG G - AAC -TAG AT -GT AT ---GCAAG TCGA ----- --- CAT ATATTTATATTTGTTTGTGTTGTT TCATAT CATC ----- --- CT C AA AG AA AT GGTA ATGCCT TA ATCTGGAGGG CT GG AA SA AGCGCGATT
drow1r2	scaffold_15245:12351860-12352024 +		ACGA TC CG CTGG GC GC ATCC AAATCA TC AGAT SA AG CG TC CAATCAG STAAC ---TC ACC - CAC -AGG GA AA CA TT AGCA CTGTT --- TA CT GTAT C CG ----- --- T C ----- --- G CCATC ----- --- TAT TAGGT AA ATGGACATGCC CT TAATCTGGAGGG T GG AA SA AGCGCGATT
dp5	3:912117-912280 +		TCGA TCGA CAAT GCC CT AGTA TC AG CA AA TC SA AG CG ATC AG CG AG TA GC - TACAG - CTA -CAG CA TTTTT --- CC AGC S ----- --- AT TGCATTCATCACAATTC ----- --- T T C CA AG GCATGG AA ATGCC CTA AA CT GTGA AG CGTTGG AA SA AGCGCG CTT
drow1er2	scaffold_211088649-1088812 +		TCGA TCGA CGAAT GCC CT AGTA TC AG CA AA TC SA AG CG ATC AG CG AG TA GC - TACAG - CTA -CAG CA TTTTT --- CC AGC S ----- --- AT TGCATTCATCACAATTC ----- --- T T C CA AG GCATGG AA ATGCC CTA AA CT GTGA AG CGTTGG AA SA AGCGCG CTT
drow1na3	scaffold_13266:18354314-18354470 -		ACGAG CG AGGCA CT CG CTC AG AA CAATCAGAT SA AG AG AT CT TAAC CAG GT GG ---TC AG G - ATC -AG AG GATTC ---SCAA AG TC ----- --- AA ----- --- A T ----- --- A A TAATA TCCGGAGC AGGT AA ATGGACATGCC CT TAATCTGAGGG T GA SA AAAGGAGCGCGATT
drow1p1	scaf71800000396735:1635887-1636043 -		ACGAG CG CGGCA CT CG CTC AG AA CAATCAGAT SA AG AG AT CT TAAC CAG GT GG ---TC AG G - ATC -AG AG ATG TG T ---CA AG AG TC ----- --- A ----- --- A A A CT TCCGG C AGGT AA ATGGACATGCC CT TAATCTGAGGG CT GA SA AAAGGAGCGCGATT
drow1k1	scaf71800000302273:72686-72845 -		ACGA TC AGGA AGCT CA CTC AC AAATCAGCAGATTGA SA AG AT CT TAAC CAG GT GG ---TC ATA - ATG -AG CA AA ACAA ---SCAA AG AT ----- --- T ----- --- T T ----- --- G CTAATAAT TGA TACC AGGT CA ATGGACATGCC CTA AA CT GTGA AG CGTTGG AA SA AGGAGCGCGATT
drow1c1	scaf71800000453955:653945-654101 -		ACGAG CG GCC CA CT CA CTC AC AAATCA TC AGATTGA SA AG AT CT TAAC CAG GT GG ---TC ATG - AAC -AG AG CAATTA ---SCAA AG AC ----- --- A ----- --- T T ----- --- A C TAA CT TAAGGA C AGGT CA ATGGACATGCC CTA AA CT GTGA AG CGTTGGAAAAGGAGCGCG CTT
drow1e1	scaf71800000491217:364693-364849 -		ACGAG CG GCC CA CT CA CTC AC AAATCAGCAGAT SA AG AG AT CT TAAC CAG GT GG ---TC ATC - AAC -TAG GC CT TA ---SCAA AG AC ----- --- A ----- --- A T ----- --- A A TAAT CT TAAGGA C AGGT CA ATGGACATGCC CTA AA CT GTGA AG CGTTGGAAAAGGAGCG GC CTT
drow1ho1	scaf71800000766551:111160-11316 -		ACGAG CG TGG CA CT CA CTC AC AAATCAGCAGAT SA AG AG AT CT TAAC CAG GT GG ---TC ATG - AAC -AG AG AATGA ---SCAA AG AC ----- --- A ----- --- C T ----- --- A A TAA CT TAAGGA C AGGT CA ATGGACATGCC CTA AA CT GTGA AG CGTTGA SA AGGA AG CG GC CTT
drow1a1	scaf71800000302292:3509148-3509304 -		ACGAG CG GCC CA CT CA CTC AC AAATCAGCAGAT SA AG AG AT CT TAAC CAG GT GG ---TC AG G - AAC -AG AG AAATGA ---SC CA AA AT TC ----- --- T T ----- --- A C TAAT CT TAAGGA C AGGT CA ATGGACATGCC CTA AA CT GTGA AG CGTTGA SA AGGAGCGCG CTT
drow1ak1	scaf71800000415420:450547-450703 -		ACGAG CG GCC CA CT CA CTC AC AAATCAGCA AT TA SA AG AG AT CT TAAC CAG GT GG ---TC AG G - AAC -AG AG AAATTA ---SCAA AA

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

Predicted structure

Flybase annotation

No Repeatable elements found

Sense Strand Reads

Anti-sense strand reads

Show Alignment With Reads

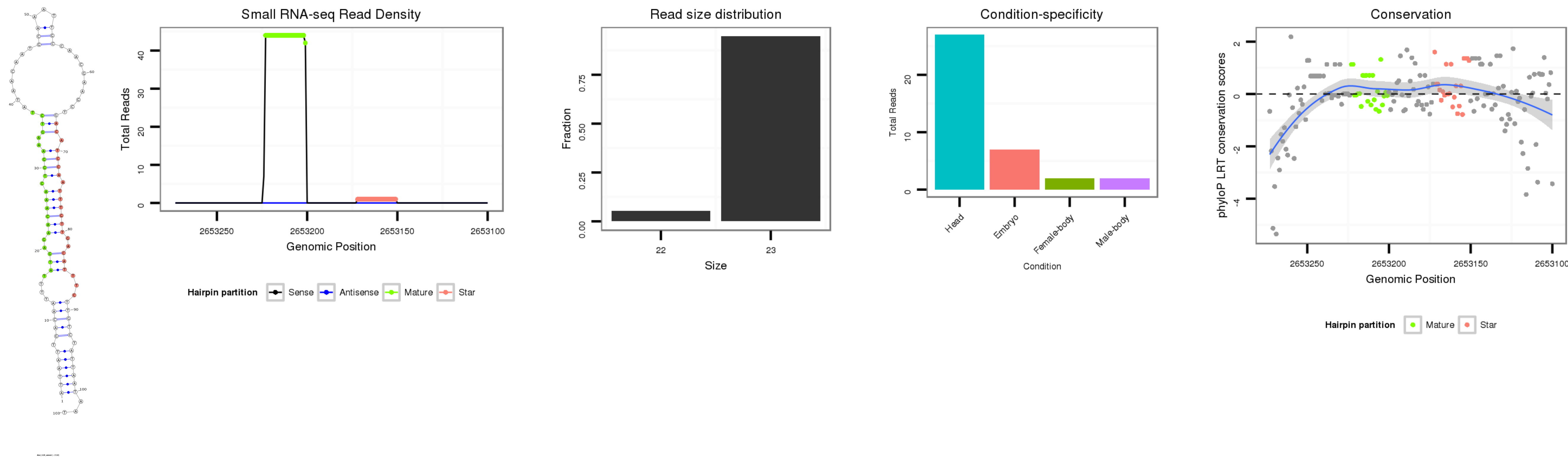
Re-alignment of all predicted orthologs

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crit.mor	0
crit.half	0
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crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	0
rescue.total	1
rescue.dominant	1
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

intergenic

No Repeatable elements found

Sense Strand Reads

Anti-sense strand reads

Show Alignment With Reads

Re-alignment of all predicted orthologs

[illegible]

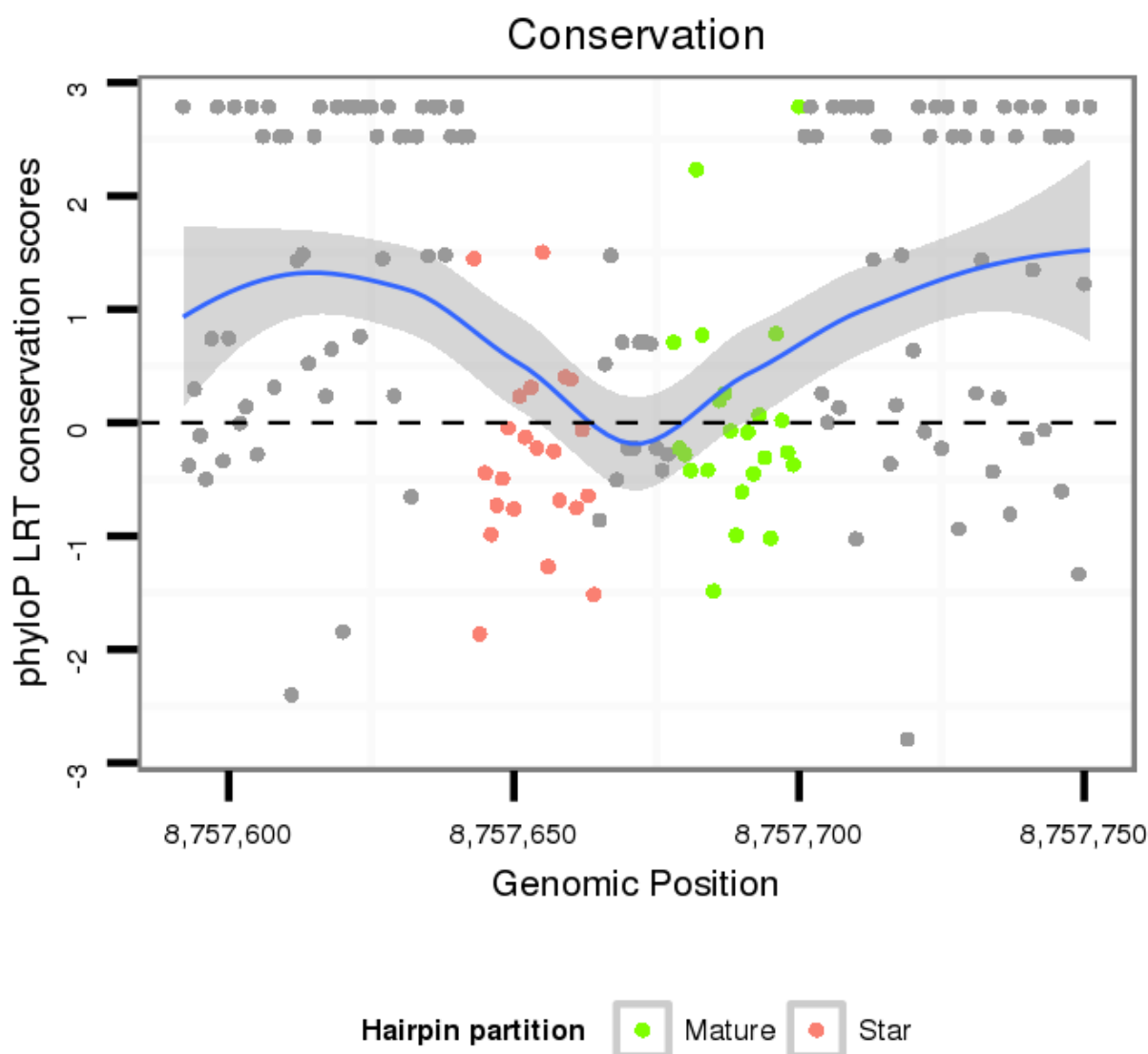
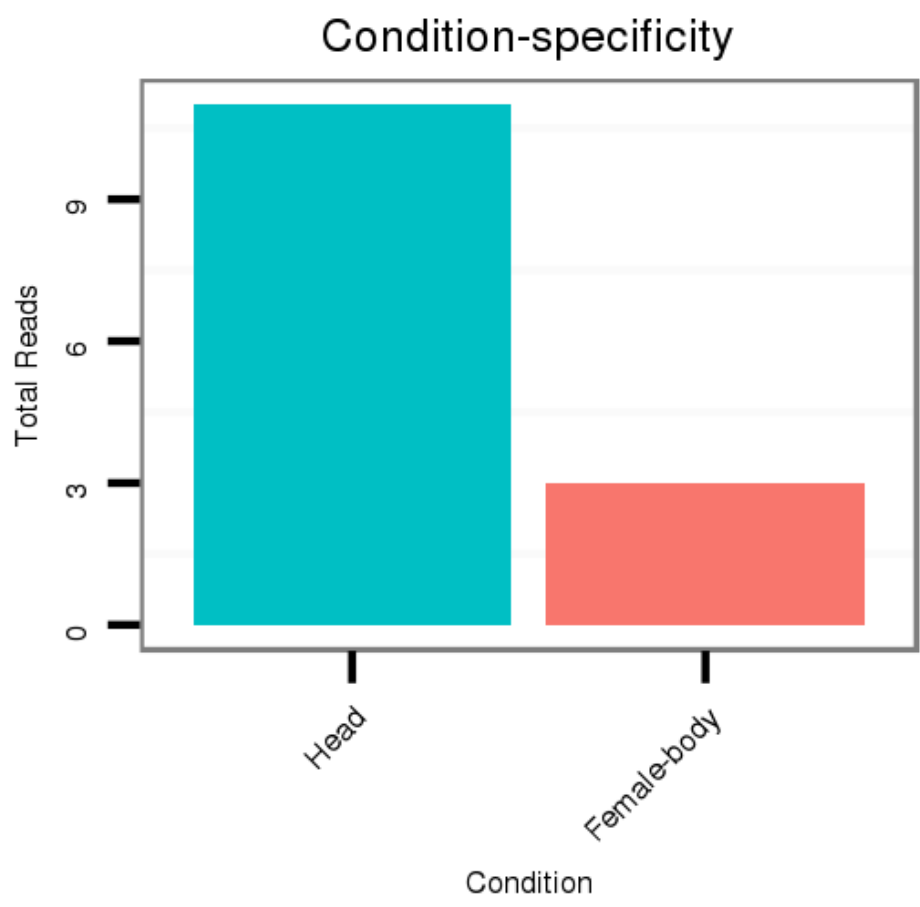
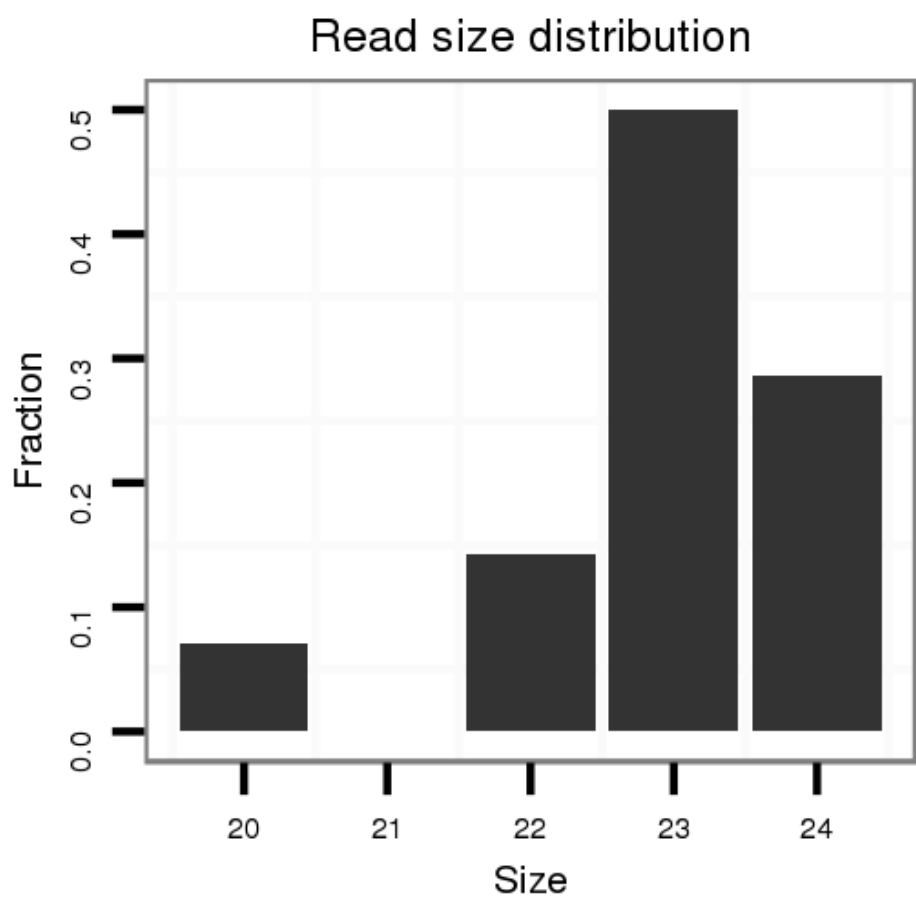
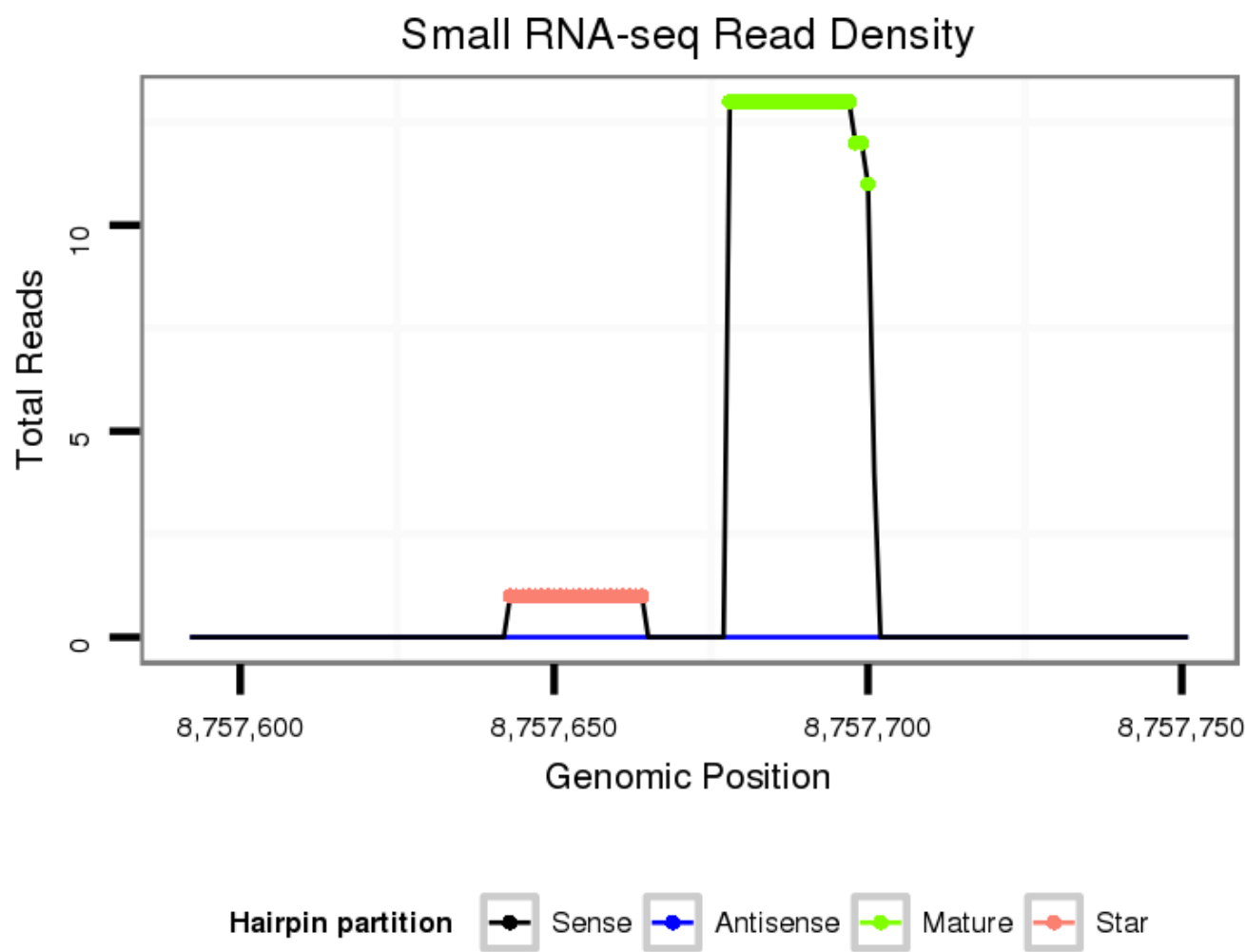
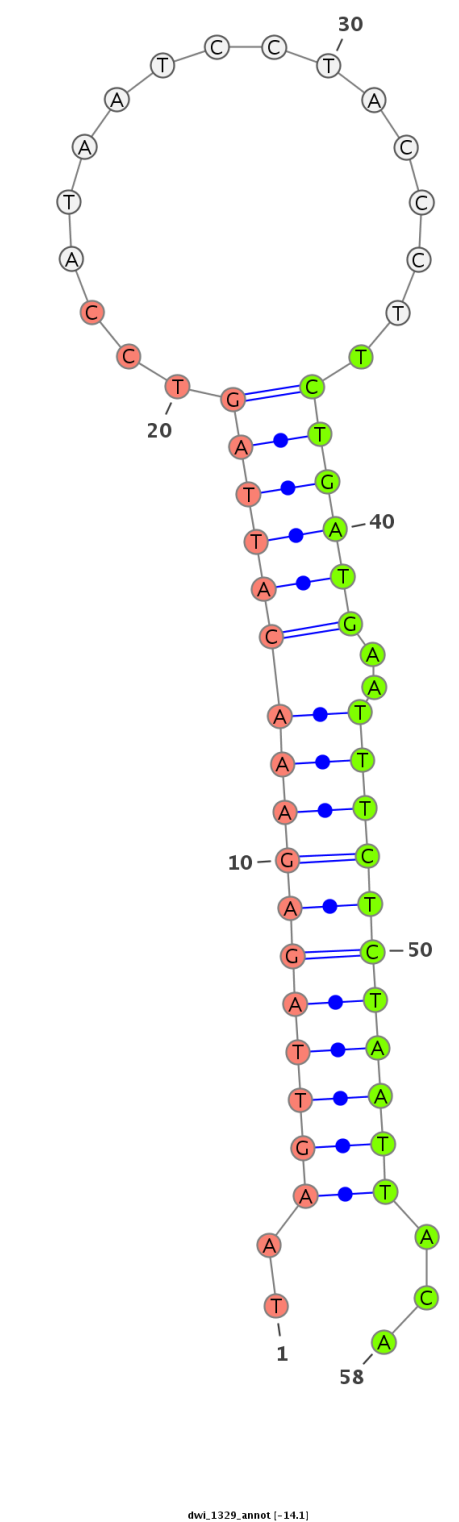
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	PASS/FAIL
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crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate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

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dwi_1329	scf2_1100000004521:8757642-8757701 +	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 [DwILGK15433-in]; CDS [DwILGK15433-cds]; CDS [DwILGK15433-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

	Read #	size	Mismatch	Hit	Count	Total	Norm	Total	V118	M020	M045	V119	V117
									embryo	head	female	head	male
TTAATATATTGCAACAAGCAAATGAATTGAAATGTTGGGTGAATATCAGGTAAGTTAGAGAAACATTAGTCCATAATCCTACCCTCTGATGAATTTCTCTAATTACAGAGCGTTTTTATACCCGTTTGGACACTCACACCATTGGAGTTGGTGAAC	23	0	1	7.00	7	0	7	0	7	0	0	0	0
.....TCTGATGAATTTCTCTAATTACA.....	24	0	1	4.00	4	0	3	1	0	0	0	0	0
.....TCTGATGAATTTCTCTAATTACAG.....	22	0	1	1.00	1	0	1	0	0	0	0	0	0
.....TCTGATGAATTTCTCTAATTAC.....	24	1	1	1.00	1	0	1	0	0	0	0	0	0
.....TCTGATGAATTTCTCTAATTAC.....	22	0	1	1.00	1	0	0	1	0	0	0	0	0
.....TAAGTTAGAGAAACATTAGTCC.....	22	0	1	1.00	1	0	0	1	0	0	0	0	0
.....TCTGATGAATTTCTCTAATT.....	20	0	1	1.00	1	0	0	1	0	0	0	0	0

Anti-sense strand reads

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

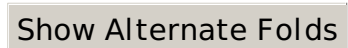
Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droWil2	scf2_1100000004521:8757592-8757751 +	dwi_1329	TTAATATATTGCAACAAGCAAATGAATTGAAATGTTGGGTGAATATCAGGTAAGTTA--G-A-----GAAACA-----T-----TAGTC-CATAA-----TCCTACCCTCTGATGAATTTCTCTAATTACAGAGCGTTTTTATACCCGTTTGGACACTCACACCATTGGAGTTGGTGAAC
droVir3	scaffold_12963:3483847-3484002 -		TCAGCAATTTTGCAAGCCAATGAGCCTTAAAAATGTTGGCGAATATCAGGTACAGGA-TTGT-C-T-----ATTGGTTTTTCATT-T-----AA-CAGGATTTTTTCTT-----TAT-----TTGTGAGAGCGTTTTTATACCCCTGGGGAACGCACACATTGGAGCTGGCGGACAT
droMoj3	scaffold_6500:13859016-13859197 -		TAAGATCTAGACAAGCCTACAGCCTTAAAAATGTTGGTGAATATCAGGTGAGAA-AGTCCAGA--GATAAGAGTCTGCAATATAATA--GAATTA-----T-----TATATTTTACTAAATATATGTCTCTATCATATAGAGGTTTTTATACCCCTCTTGGATACACACCTGGAGCTGGTGAACAT
droGri2	scaffold_15252:3041009-3041196 -		TGGGATCTTAGAGCAGCCCAATGAGCCTTAAAAATGTTGGGTGAATATCAGGTAAAGA-ATCT-TAA--AG--GA-CTGG-----AAAAGTGACTCTTTTTTTGTGTGTTTGTCTTTATTGCTAAT-AT-AAAAATTTT-----GA-----CTTTCAGAGAGTTTTTATACCCCTGGCAGATACACACACTGGAGCTTGGTGAACAT
dp5	4_group4:3291859-3292015 +		TCGGCCTTTGCAACAGSCAAACGAATGAAATGTTGGCGAATATCAGGTGCGAT-TA-G-ATA-----GAAGCTGTATTATA-G-----AA-CCTAGTAACGACTA-----TAT-----CTTCAGAGCTCTTATACCCCTTCGGACACACACATATGGACTTGGTGAAC
droPer2	scaffold_10:2313190-2313346 +		TSAGCCTTTGCAACAGSCAAACGAATGAAATGTTGGCGAATATCAGGTGGAG-TA-G-ATA-----GAAGCTGTATTATA-G-----AA-CCTASTAACGACTA-----TAT-----CTTCAGAGCTCTTATACCCCTTCGGACACACACATATGGACTTGGTGAAC
droAna3	scaffold_12916:10997600-10997749 -		TGGGAATCTGCAAGCCAATGAGCCTTAAAAATGTTGGGTGAATATCAGGTATGAG-ATTATTAT-TT--TGAAA-----CT-----TAAATCAT-----ANATGAAATATTAGAGCATCTTATACCCATGGGGAACCATACCATGAGCTTGGTGAAC
droBip1	scf7180000396572:655481-655632 -		TGGGAATTTTACAGCAAGCCAATGAGCCTTAAAAATGTTGGCAATATCAGGTATAAG-TTAA-TGG--G--CTTGA-----AAAACC-----T-----TAA--GCAATAACTTTTCAGAGCGTCTTATACCCCTTCGGGAACGCACACGATGAGCTTGGTGAAC
droKik1	scf7180000302389:545036-545191 +		TGCCCATATTGCAAGCCAATGAGCCTTAAAAATGTTGGCGAATATCAGGTCTCAA-ATCTT-TA--TA--TATTA-----CTAAAAA-A-----TATATAAT-----AATTAGAAATTATTAGAGCTTTTATCCCTACCTCAGACCATGAGTTTGGAGACT
droPic1	scf7180000453932:337906-338059 +		TAGCATTTTACAGCAAGCCAATGAGCCTTAAAAATGTTGGCGAATATCAGGTG-A-A-TTAA-TGA--GG--TGAACT-----ATTGACT-C-----ACGACTC-----AATTCATATTTCAGAGCATTTTATACCCCTTCGGACACGCACATCATGAGTTTGGAGACT
droEle1	scf7180000490076:25632-25786 +		TCAAATATTGCAACAAGCAAATGAGCCTTAAAAATGTTGGCGAATATCAGGTGCA-A-TTCA-AA--GA--TGTCC-----TTATAAT-T-----TAAATTA-----CATTTCAATCCTTCAGAGCGTATTATACCCTTCGGACACCATTCATGAGTTTGGAGACT
droRho1	scf7180000717891:37886-38040 -		TCAAATATTGCAACAAGCAAATGAGCCTTAAAAATGTTGGCGAATATCAGGTTCAA-A-TTCA-AA--GA--TGTGC-----AAATAGC-T-----TAAATGAT-----GATTCCTTTTTCAGAGCATATTATACCCTTCGGACACCATTCATGAGTTTGGAGAACT
droBia1	scf7180000302422:3721684-3721832 -		TCAAATATTGCAACAAGCAAATGAGCCTTAAAAATGTTGGCGAATATCAGGTACGC-TATA-AG--AA--AAAGG-----GAAATGG-A-----TAAATAAT-----A-----CATTTAGAGCGTTTTATACCCTTCGGACACCATTCATGAGTTTGGAGACT
droTak1	scf7180000415871:257335-257493 -		TCAAATATTGCAACAAGCAAATGAGCCTTAAAAATGTTGGCGAATATCAGGTCTACTTAA--CAAAATA--TAAGA-----AAACAA-T-----TAAATTT-----CAACGCTTATTTAGAGCGTTTTATACCCTTCAGGGAACCATCATGAGCTTGGTGAAC
droEug1	scf7180000409063:206259-206414 -		TAAATATTGCAACAAGCAAATGAGCCTTAAAAATGTTGGCGAATATCAGGTTCATC-TTCG-TAG--GC--CGTGA-----AAGAA-TACT-----TGT-T-----CAT--ATCCATTAATTTCAGAGCGTTTTATACCCTTCAGGATTCACCATCATGAGTTTGGAGACT
dm3	chr2L:21207640-21207797 +		TAATATATTGCAACAGSCAAATGAGCCTTAAAAATGTTGGCGAATATCAGGTTCGA-TTCT-TCA--AA--TGAGC-----AAAAGTG-T-----TAATA-CATAACGAGCTTT-----TAT-----ACCTAGAGCGTTTTATACCCTTCGGACACCATTCATGAGTTTGGTGAAC
droSim2	2L:20644728-20644885 +		TAATATATTGCAACAGSCAAATGAGCCTTAAAAATGTTGGCGAATATCAGGTTCGA-TTTT-TCA--AA--TAAGC-----AAAAGTG-T-----TAATA-CATAACGCCCTTT-----TAT-----CCCTAGAGCGTTTTATACCCTTCAGACACCATTCATGAGTTTGGTGAAC
droSec2	scaffold_18:1127835-1127992 +		TAATATATTGCAACAGSCCAATGAGCCTTAAAAATGTTGGCGAATATCAGGTTCGA-TTTT-TCA--AA--TGAGC-----AAAAGTG-T-----TAATA-CATAACGCCCTTT-----TAT-----CCCTAGAGCGTTTTATACCCTTCAGACACCATTCATGAGTTTGGTGAAC
droYak3	2R:1568453-1568611 -		TAATATATTGCAACAAGCAAATGAGCCTTAAAAATGTTGGCGAATATCAGGTTCGA-TTCA-TA--AA--TGAGC-----AAAAGTG-T-----A-C-A-ATTTCGAGCTTTA-----TAT-----CCCTAGAGCGTTTTATACCCTTCAGACACCATTCATGAGTTTGGTGAAC
droBre2	scaffold_4845:3293217-3293372 -		TCAAATATTGCAAGCAAGTGAAGCCTTAAAAATGTTGGCGAATATCAGGTTCGA-TTCA-TA--AG--TGATC-----AAAAGTG-T-----AA-CCTAAGGAGCTTT-----TAT-----ACCCCAAGAGCATTTTATACCCCTTCGGACACCATTCATGAGTTTGGTGAAC

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

Predicted structure



Flybase annotation

intron [Dwil/GK19799-in]; CDS [Dwil/GK19799-cds]; CDS [Dwil/GK19799-cds]

Repeatable elements

Sense Strand Reads

hide 3p reads

Anti-sense strand reads

Show Alignment With Reads

Re-alignment of all predicted orthologs

Generated: 09/08/2015 at 07:02 PM

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

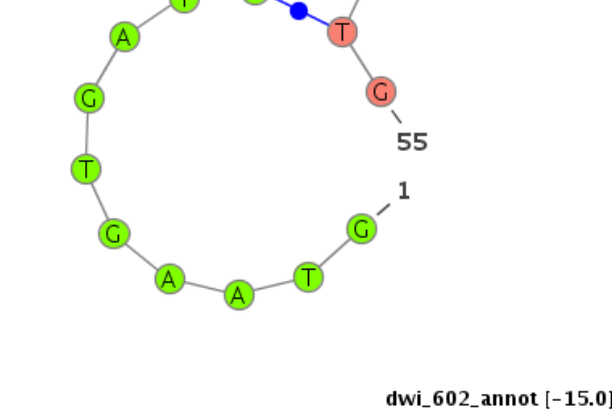
Predicted structure

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

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

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

Legend: mature star mismatch in alignment mismatch in read



Flybase annotation

intron [Dwil/GK17366-in]; CDS [Dwil/GK17366-cds]; CDS [Dwil/GK17366-cds]; utr3 [utr3_plus_3510]; utr3 [utr3_plus_3509]; utr5 [utr5_plus_6276]; utr5 [utr5_plus_6277]

No Repeatable elements found

hide 3p reads | show mid mismatch reads

[illegible]

Anti-sense strand reads

AGGTTCTCGACGTGGTTTAGCACACTCTCGACGGTTTCACTTCACAGGCTC CATTCACTACTAGTGTGCAGACCTT AGTTTTAGT TGGTAGGGCTACTACTACTA TACAACAAATGTCCATTTTCGACTGCATCACCGGTAAATTGTGATCTAAACCTATGACAGCTGTG									
*****.....(((((((((((.....))))))))))..))))).*****									
No data available in table									
Show Alignment With Reads									

Re-alignment of all predicted orthologs

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

Legend: mature star mismatch in alignment mismatch in read

Small RNA-seq Read Density

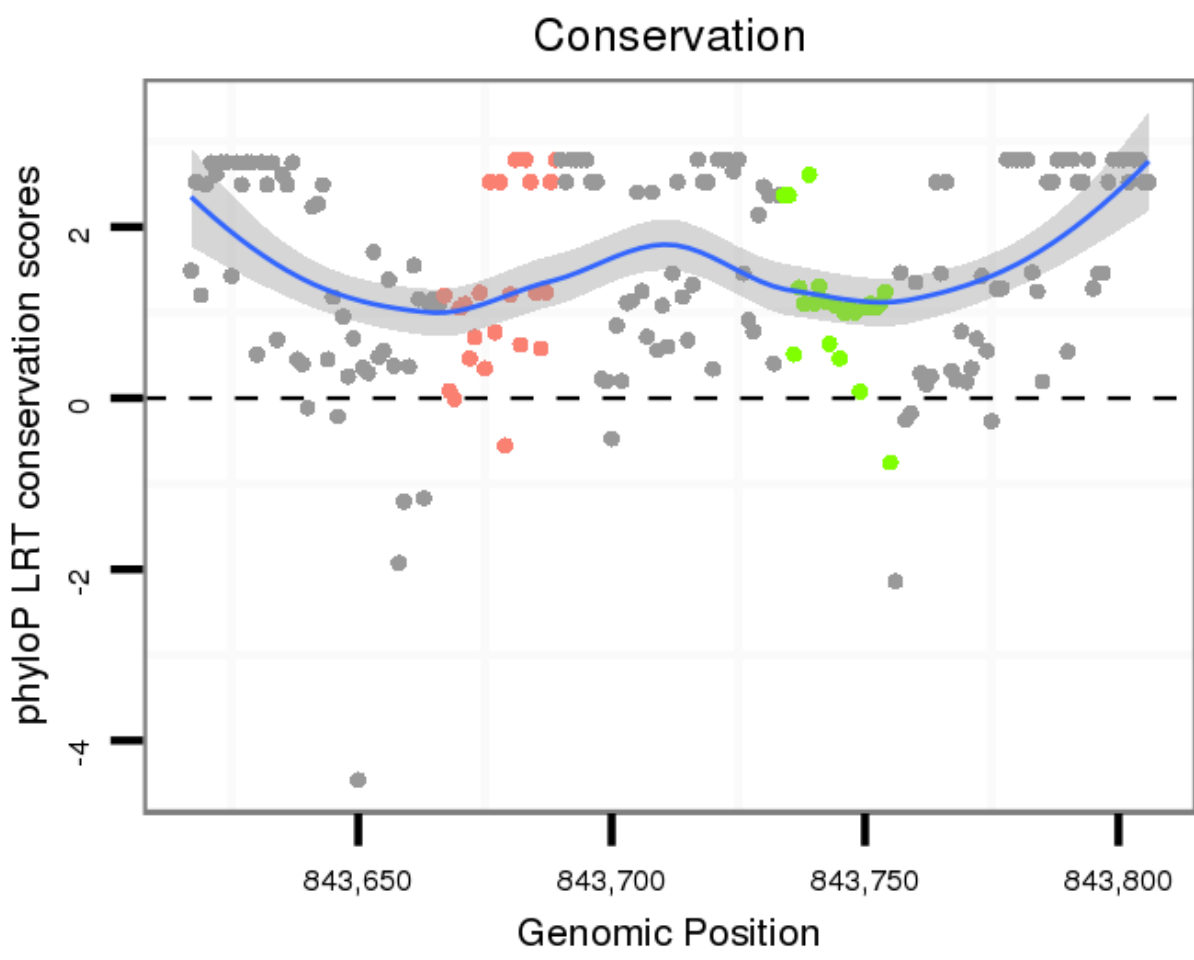
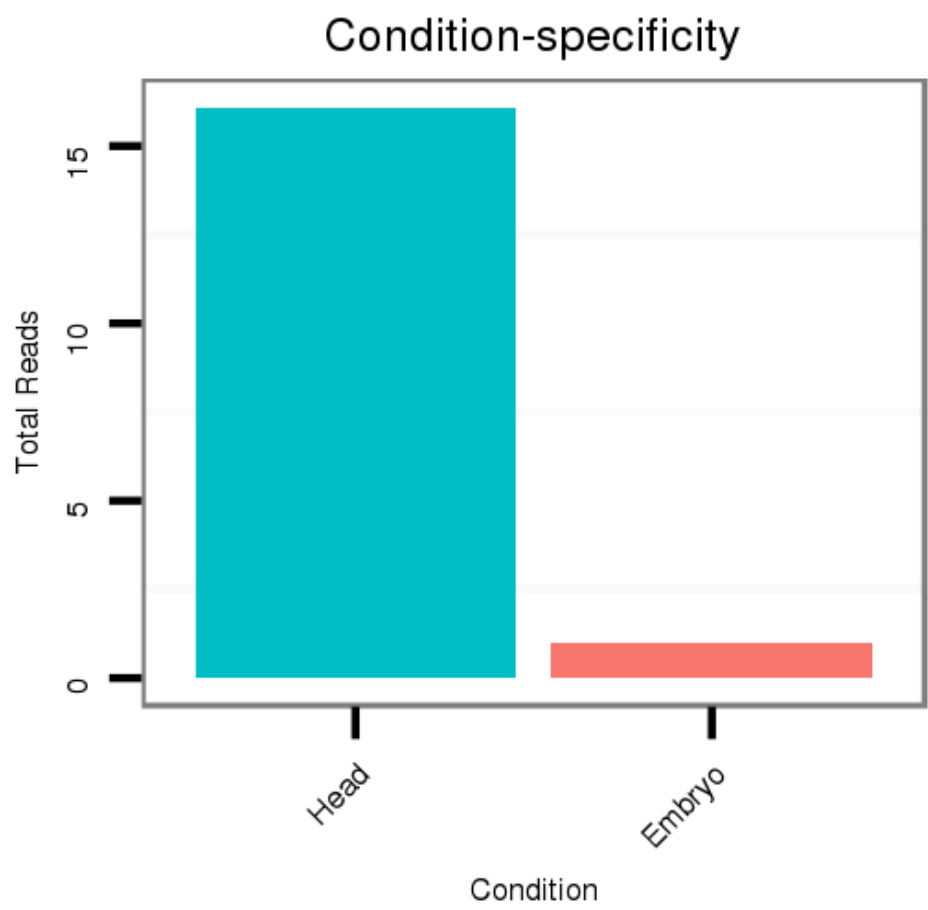
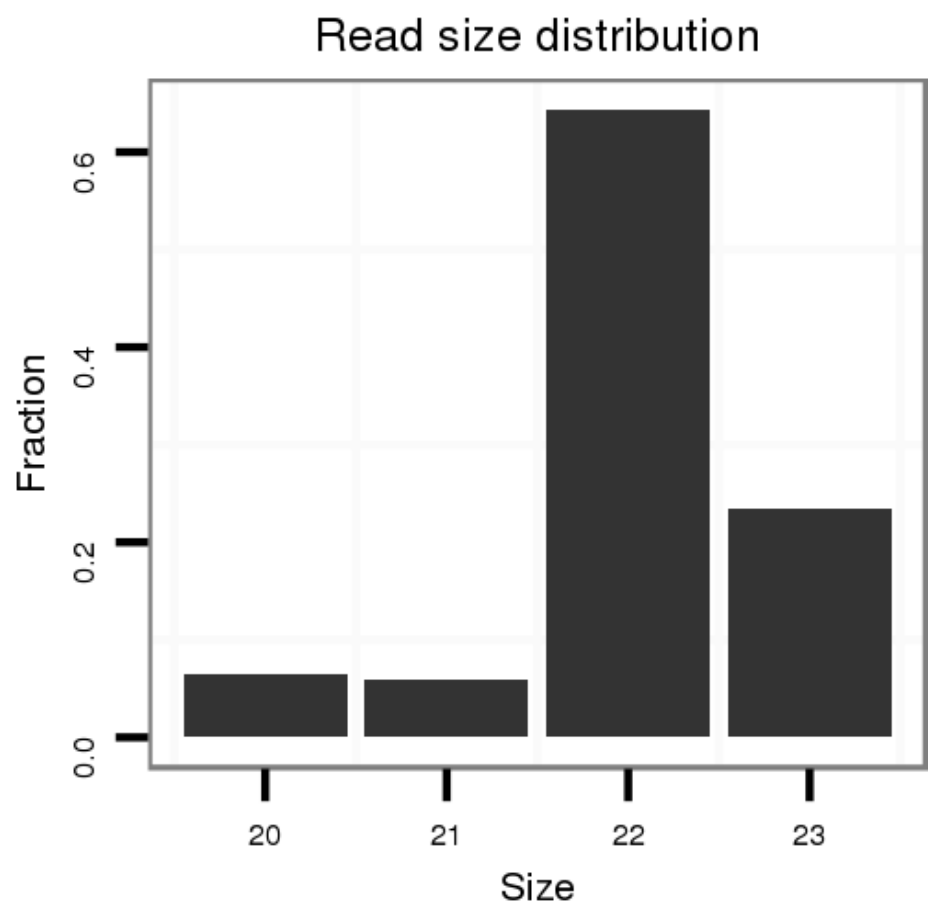
Total Reads

Genomic Position

843,650 843,700 843,750 843,800

Hairpin partition

- Sense
- Antisense
- Mature
- Star



matrice	star
	1. <u>dwi_161_scf2_11000000004510:843667-843689 +</u> 2. <u>scf2_11000000004516:887730-887752 +</u> 3. <u>scf2_11000000004762:3851680-3851702 +</u>

hide 3p reads | show mid mismatch reads

[illegible][illegible]

Re-alignment of all predicted orthologs

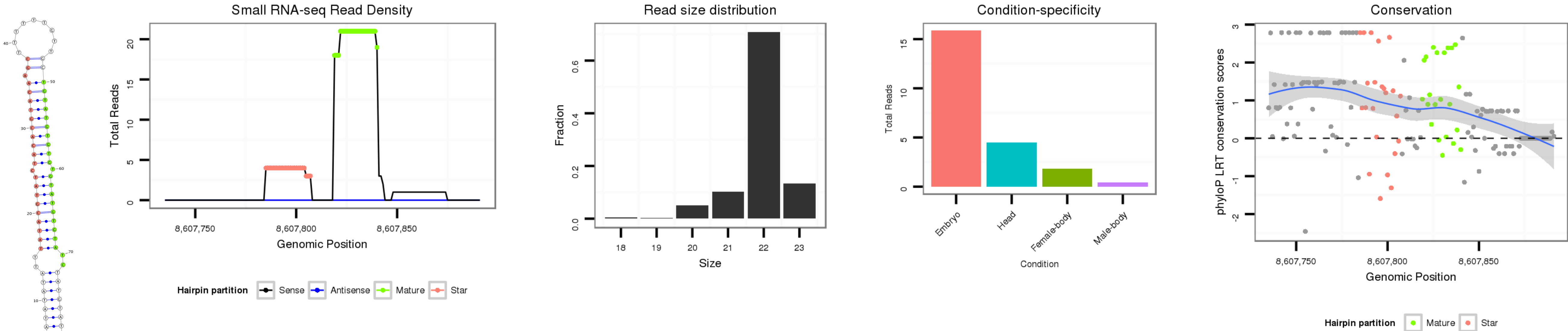
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crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	0
crit.uri	1
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Show Alternate Folds

Flybase annotation

intergenic

Repeatable elements

Name	Class	Family	Strand
(TATG) _n	Simple_repeat	Simple_repeat	+

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

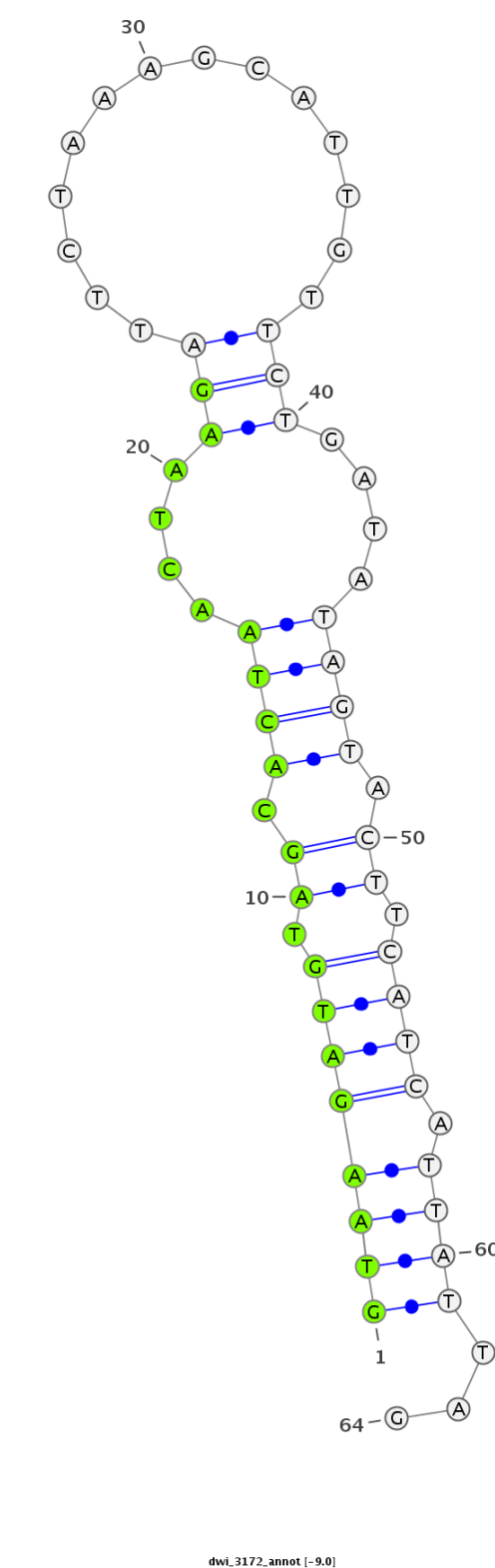
[illegible]

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crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
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 [Dwil\GK13665-in]; CDS [Dwil\GK13665-cds]; CDS [Dwil\GK13665-cds]; utr3 [utr3_minus_9352]

No Repeatable elements found

Sense Strand Reads

hide 3p reads

show mid mismatch reads

[illegible]

Anti-sense strand reads

[illegible]

Show Alignment With Reads

Re-alignment of all predicted orthologs

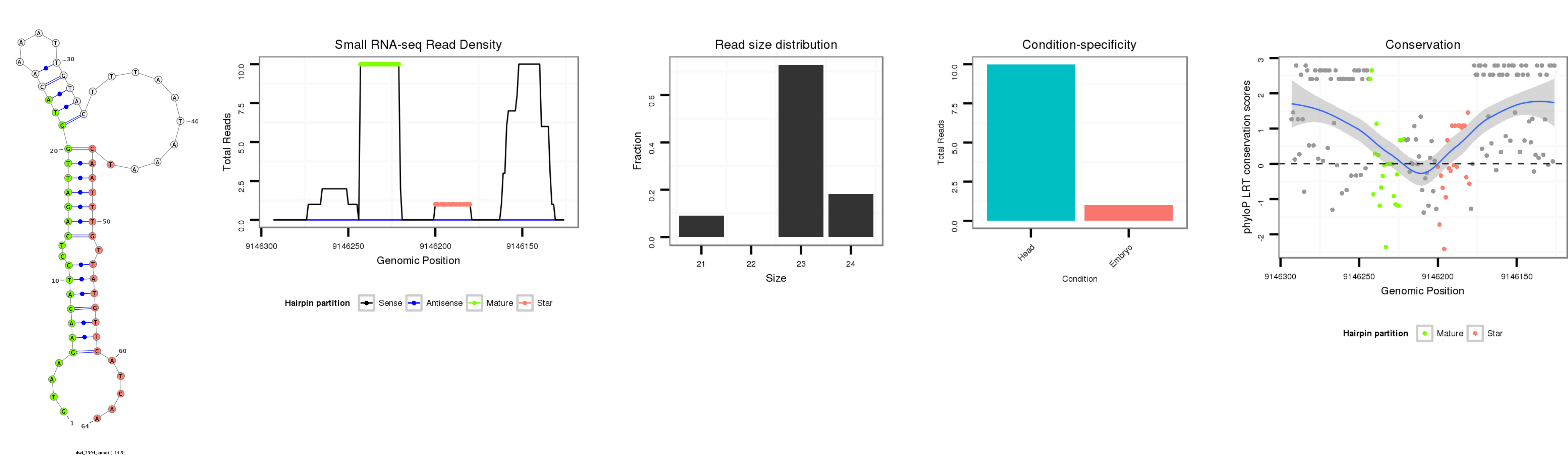
[illegible]

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

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Show Alternate Folds

Flybase annotation

intron [Dwil\GK13174-in]; CDS [Dwil\GK13174-cds]; CDS [Dwil\GK13174-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

Anti-sense strand reads

[illegible]

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
drow112	scaf2_1100000004943:9146126-9146293_	dwi_3394	CATAC TGGCTTCGCGACGAAAAATCATTCGCTGGTCTGTTATTGAATG GTAGAACATGCTCAGATTGG-----TA CAAAATTGTA-----CTTTAA--TAAATCAATT-TGT-----TATGTTTCAT-----C-----AAATAGGTATGATACGCTTTCACATCACATTGTTCTCTCGGCATTAGTCGCTAAAT
drow1r3	scaffoid_13047:11145473-11145627_		CATAC TGGCTTCGCGACGAAAAATCGCGCTGGTCCGCTATCGAATG GTANGTGGAG--ATAA-----AC GTAGAAAA GGTTA TTAAAT----- TATTTTGTGT T--TAGGTATGACCGCTTCACATCACATCGTTCTCT CTCGCT GTGCG AAAGT
drow1o3	scaffoid_6540:30613642-30613802_		CATAC TGGCTTCGCGACGAAATACGCGCTGGTCCGCTATCGAATG GTGCTGATGG--AGAA-----G-----GATAA-----CCAA TTATATATATATTCAT GAAA--TCTTCTC-----TTTC AGGTATGACCGCTTCACATCACATCGTTCTCTCGCATT GTGCG--AAAGT
drow1r12	scaffoid_14624:1042149-1042224_		ATTATTCAT ----- GTGCTGATGG--AGAA-----G-----GATAA-----CCAA TTATATATATATTCAT GAAA--TCTTCTC-----TTTC AGGTATGACCGCTTCACATCACATCGTTCTCTCGCATT GTGCG--AAAGT
dp5	2:14057601-14057766_		CACACCGGCTTCGCGACGAA GAAGTCGCACCGCGCC CTATTGAATG GTGCTGAATA--AGA GTGG GATTGGCTT ACGATTCA----- TGGCA--T-----GCACGC ----- GTTTTGTGGC ----- TGCA AGGTA CG GATACGCTTTCACATCACATCGTTCTCTCGG CGCG GTGCG CAAA
drow1er2	scaffoid_0.6384024-6384189_		CACACCGGCTTCGCGACGAA GAAGTCGCACCGCGCC CTATTGAATG GTGCTGAATG--AGA GTGG GTTTGGCTT ACGATTCA----- TGGCA--T-----GCACGC ----- GTTTTGTGGC ----- TGCA AGGTA CG GATACGCTTTCACATCACATCGTTCTCTCGG CGCG GTGCG CAAA
drow1na3	scaffoid_12911:3473180-3473339_		CATAC TGGCTTCGCGACGAA GAATCA TGCGCGGTCCGCTATTGAATG GTGCTGTTCT--TATA ----- CTGGCGCTTAC--CAAC CAAT CACA ----- GTGTACGTGT ----- CTTT TAGGTACGATACGCTTTC CG ATCA ATACG CTCTCGG CACTGTGCG--AAAGT
drow1bip1	scf7180000396640:336896-337054_		CATAC TGGCTTCGCGACGAA GAATCA TGCGCGGTCCGCTATTGAATG GTATGTTCTC--AA AT----- TTTATGATTTAA--CAAC CA ACACA ----- TTGCACTTGC ----- TTT TAGGTACGACCGCTTTCACATCA ATACG CTCTCGG CACTGTGCG--AAAGT
drow1k1k1	scf7180000301641:95600-95771_		CATAC TGGCTTCGCGACGAA GAAGTC CTGGTGGCTCTATTGAATG GTACTTTGT--AG GG----- AG--- ----- TTT ----- CGCTTCTCTTTATTTCA TTATTCAT TAATTA--A CTTGAA TTCTTGGC AGGTA CGAC CGCTTCACATCACATCGTTCTCTCGG CGCTGTGCG--AAAT
drow1f1c1	scf7180000454097:37587-37742_		CATAC TGGCTTCGCGACGAA GAAGTC CTGGTGGCTCTATTGAATG GTGTGTGTAG--A GAT----- GTCTTGCACAGC--TTTA ATTGATA AA-----G--TCTTAAT ----- TGTC AGGTA CGCG CTTCACATCACATCGTTCTCTCGG CACTGTGCG--AAAGT
drow1el1	scf7180000491194:1665822-1665978_		CATAC TGGCTTCGCGACGAA GAAGTC CTGGTGGCTCTATTGAATG GTGCTTAATG--A CA----- GTCTTAAGAAGC--TA TGAATT ACAA-----GACTCTGTAT ----- TGCA AGGTA CGCA CTTCACATCACATCGTTCTCTCGG CACTGTGCG--AAAGT
drow1rho1	scf7180000779322:76546-76702_		CATAC TGGCTTCGCGACGAA GAAGTC CTGGTGGCTCTATTGAATG GTGCTTCT--GCGAC-----GTTTGTGAGAGGA--TTCA AA TT--AAC ----- AGCTCTTTAT ----- TGCA AGGTA CGCA CTTCACATCACATCGG CACTGTGCG--AAAGT
drow1bi1	scf7180000302035:278214-278371_		CATAC TGGCTTCGCGACGAA GAAGTC CTGGTGGCTCTATTGAATG GTGCTGGAG--T GG----- CTCTGACAGGA--TCT CTTT CTAA ----- TGTTCTGTAT ----- TGCG AGGTA CGAC CTTCACATCACATCGTTCTCTCGG CACTGTGCG--AAAGT
drow1tak1	scf7180000415712:705480-705636_		CATAC TGGCTTCGCGACGAA GAAGTC CTGGTGGCTCTATTGAATG GTACGGGAT--ATA A----- CTTCTAGCAGGA--TCTGA AT ACAA-----AGTTCTTAAT ----- TTA AGGTA CGAC CTTCACATCACATCGTTCTCTCGG CACTGTGCG--AAAGT
drow1eug1	scf7180000409488:291202-291355_		CATAC TGGCTTCGCGACGAAAA GTAC TGCGCGCTGTTATCGAATG GTGCTGATA--G GAG----- GTTC CA----- TTAGAA--TCCGA -GTGCT -----AACTCTGTAT ----- TTTC AGGTATGACCGCTCT CT ATCA ATA CGTTCTCTCGG CACTAGTGTGCG--AAAGT
dm3	chr3R:27611971-27612129_		CATAC TGGCTTCGCGACGAAAA GTCT GGCGAGGCTCTTATCGAATG GTGCTGCCT--G GAG----- GTATTGACCGG--TATA ATT AGGAAC ----- ATCTTCTGTCT ----- TTA AGGTATGACCGCTCT CT ACAC ACAT CGTTCTCTCGG CACTAGTGTGCG--AAAGT
drow1sm2	3r:26887511-26887669_	dsi_14991	CATAC TGGCTTCGCGACGAAAA GTCT GGCGAGGCTCTTATCGAATG GTGCTGCCT--G GAG----- GTATTGACCGG--TATA ATT AGGAAC ----- ATCTTCTGTCT ----- TGCA AGGTATGACCGCTCT CT ACAC ACAT CGTTCTCTCGG CACTAGTGTGCG--AAAGT
drow1eoc1	chr2L:31266592-266680-3828546545-28546703_		CATAC TGGCTTCGCGACGAAAA GTCT GGCGAGGCTCTTATCGAATG GTGCTGCCT--G GAG----- GTATTGACCGG--TATA ATT AGGAAC ----- ATCTTCTGTCT ----- TGCA AGGTATGACCGCTCT CT ACAC ACAT CGTTCTCTCGG CACTAGTGTGCG--AAAGT
drow1ya3	3R:28546545-28546703_		CATAC TGGCTTCGCGACGAAAA GTCT GGCGAGGCTCTTATCGAATG GTGCTGCCT--G GAG----- GTATTGACCGG--TATA ATT AGGAAC ----- ATCTTCTGTCT ----- TGCA AGGTATGACCGCTCT CT ACAC ACAT CGTTCTCTCGG CACTAGTGTGCG--AAAGT
drow1er2	scaffoid_4820:358548-358706_		CATAC TGGCTTCGCGACGAAAA GTCT GGCGAGGCTCTTATCGAATG GTGCTGCCT--G GAG----- GTATTGACCGG--TATA ATT AGGAAC ----- ATCTTCTTAAC ----- TGCA AGGTATGACCGCTCT CT ACAC ACAT CGTTCTCTCG CACTAGTGTGCG--AAAGT

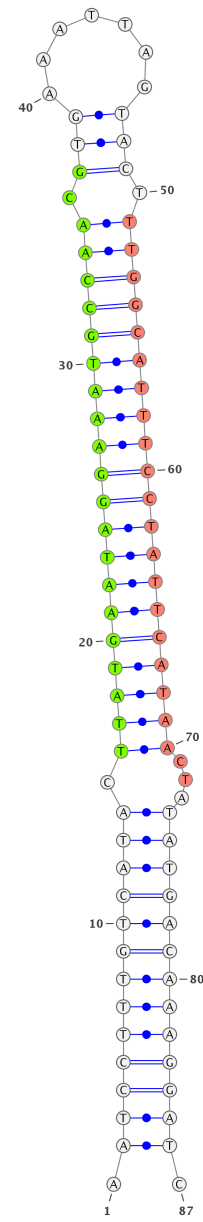
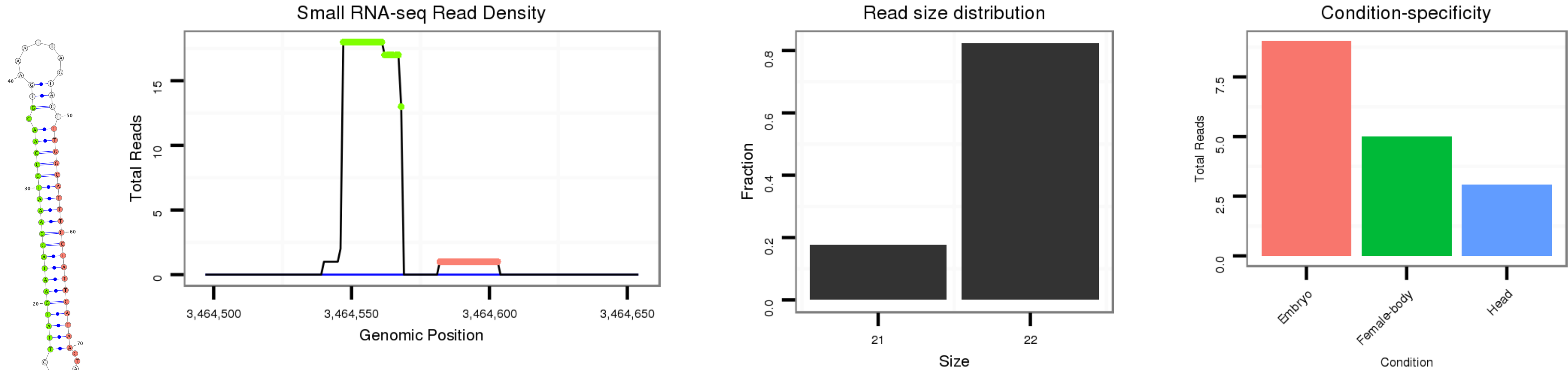
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crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	0
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dwi_127	scf2_1100000004513:3464547-3464604 +	candidate	Canonical miRNA	intron	[View on UCSC Genome Browser {Cornell Mirror}]

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Hairpin partition Sense Antisense Mature Star

No conservation details.

Show Alternate Folds

Flybase annotation

intron [DwilVGK21832-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

GAAATAGGTGAAATTAGTACTTAAATTAGTACTCAATCCTTTGTCATAC	TTATGAATAGGAAATGCCAACG	TGAAATTAGTACT	TTGGCATTTCCTATTCATAACT	TATATGACAAAGGATCAATAGAGGTATGTTTTATAGGTATTTCTGATTACTT															
*****.(((((((((((.(((((((((((((((((((((((.(((.....)))..))))))))))))))))))..))))))))))))).*****					Read #														
					size														
.....TTATGAATAGGAAATGCCAACG.....					22	0	1	13.00	13	8	3	2							
.....TTATGAATAGGAAATGCCAAC.....					21	0	1	3.00	3	1	1	1							
.....TTGGCATTTCCTATTCATAACT.....					22	0	1	1.00	1	0	1	0							
.....GTCATACTTATGAATAGGAAAT.....					22	0	1	1.00	1	1	0	0							
.....CTTATGAATAGGAAATGCCAAC.....					22	0	1	1.00	1	0	0	1							

Anti-sense strand reads

CTTTATCCACTTTAATCATGAATTTAATCATGAGTTAGGAAACAGTATG	AATACTTATCCTTTACGGTTGC	ACTTTAATCATGAAACCGTAAAGGATAAGTATTGA	TATACTGTTTCCTAGTTATCTCCATACAAAATATCCATAAAGACTAATGAA																
*****.(((((((((((.(((((((((((((((((((((((.(((.....)))..))))))))))))))))))..))))))))))))).*****					Read #														
					size														

No data available in table

Show Alignment With Reads

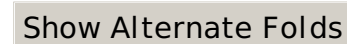
Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
drowil2	scf2_1100000004513:3464497-3464654 +	dwi_127	GAAATAGGTGAAATTAGTACTTAAATTAGTACTCAATCCTTTGTCATACTTATGAATAGGAAATGCCAACGTGAAATTAGTACTTTGGCATTTCCTATTCATAACTATATGACAAAGGATCAATAGAGGTATGTTTTATAGGTATTTCTGATTACTT

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

Predicted structure



Flybase annotation

intron [Dwil\GK12963-in]; CDS [Dwil\GK12963-cds]; CDS [Dwil\GK12963-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

[illegible]

Anti-sense strand reads

										M045
TGTGGCCGAAAAGTTAAAGTTCACAAACGTTAGCAAGGACTATTATAAGTTCAAACACTAAATCGACATCAGTTACCCCTTTAAGTCAACTTTACGAACAAGGCAGACGGACTTAAAGAGAACTTTGAAATTTATGAATAAGCTTTTTTGAAGCTCTCTCCTCACATACTTTGACACAGCTGTATGAGTTACTTTTCTAACTGTGCC										V118
										female
*****(((((.....)))))).....*****										embryo
Read #	size	Mismatch	Hit	Total	Count	Norm	Total	embryo	body	

Re-alignment of all predicted orthologs

[illegible]

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

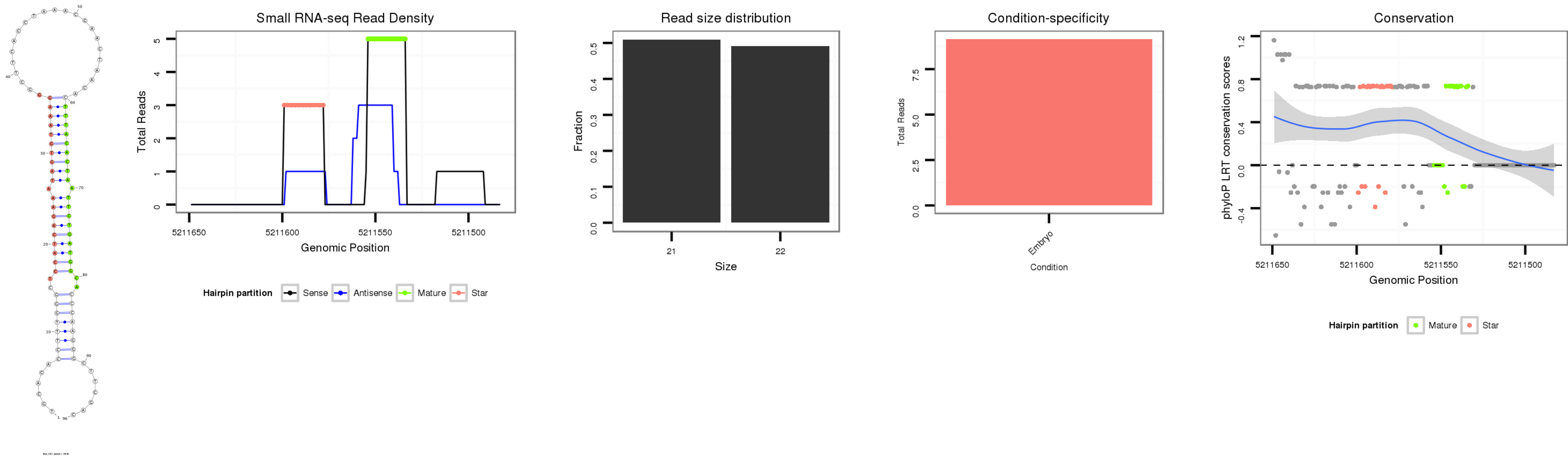
	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	0
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

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

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dwi_162	scf2_1100000004961:5211533-5211599 -	candidate	Canonical miRNA	intron	[View on UCSC Genome Browser (Cornell Mirror)]

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Show Alternate Folds

Flybase annotation

intron [Dwi]GK23358-in]

No Repeatable elements found

mature	star
1. scf2_1100000004516:3061040-3061060 - 2. scf2_1100000004762:6158513-6158533 - 3. dwi_162_scf2_1100000004961:5211534-5211554 -	

Sense Strand Reads

hide 3p reads show mid mismatch reads

	Read # size	Mismatch	Hit Count	Total Norm	Total	V118 embryo	M045 female body	M020 head
CCAGTCTTGAAGCTTCGATTCCACCTTTTTTATGTGCACACCTTTGGGC TCCATCAGAAATAGTGTAAGG GCTTCACCTAAACCAACTAACAC TTTACACTAATTCTGATGGCA CCCAAGGGCTTCGACTTTACCAACTAACTCGTTGATTTCGTGTGTGTGTT								
***** ((((((((((((((((((((((((((((((.....))))))))))))))))))))))))))))))))))) *****								
.....TTCACACTAATTCTGATGGCA.....	21	0	3	4.67	14	14	0	0
.....TCCATCAGAAATAGTGTAAGG.....	22	0	1	3.00	3	3	0	0
.....TTACCAACTAACTCGTTGATTTCGTG.....	26	0	1	1.00	1	0	1	0
.....CTTTACACTAATTCTGATGGCA.....	22	0	1	1.00	1	1	0	0
.....TTACACTAATTCTGATGGCACC.....	22	0	2	0.50	1	0	0	1
.....TTTACACTAATTCTGATGGCAC.....	22	0	2	0.50	1	1	0	0

Anti-sense strand reads

	Read # size	Mismatch	Hit Count	Total Norm	Total	V118 embryo	M045 female body	V119 head	V117 male body
GGTCAGAACTTCGAAGGCTAAGGTGAAAAAATACACGTGTGGAACCCG AGGTAGTCTTTATCACATTTC CGAAGTGGATTGGTTGATTGTG AAATGTGATTAAGACTACCGT GGGTCCCGAAGCTGAAATGGTTGATTGAGCAACTAAAGCACACACAACAA									
***** ((((((((((((((((((((((((((((((.....))))))))))))))))))))))))))))))))))) *****									
.....TGATTGTGAAATGTGATTAAGA.....	22	0	1	2.00	2	2	0	0	0
.....GGTAGTCTTTATCACATTTC	22	0	1	1.00	1	0	1	0	0
.....GTAGTCTTTATCACATTTC	22	1	1	1.00	1	1	0	0	0
.....TGAGGTAGTCTTTATCACATT	22	1	1	1.00	1	1	0	0	0
.....TTGTGAAATGTGATTAAGACTA.....	22	0	1	1.00	1	0	0	1	0
.....ATGATTGTGAAATGTGATTAAGA.....	23	1	1	1.00	1	0	1	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

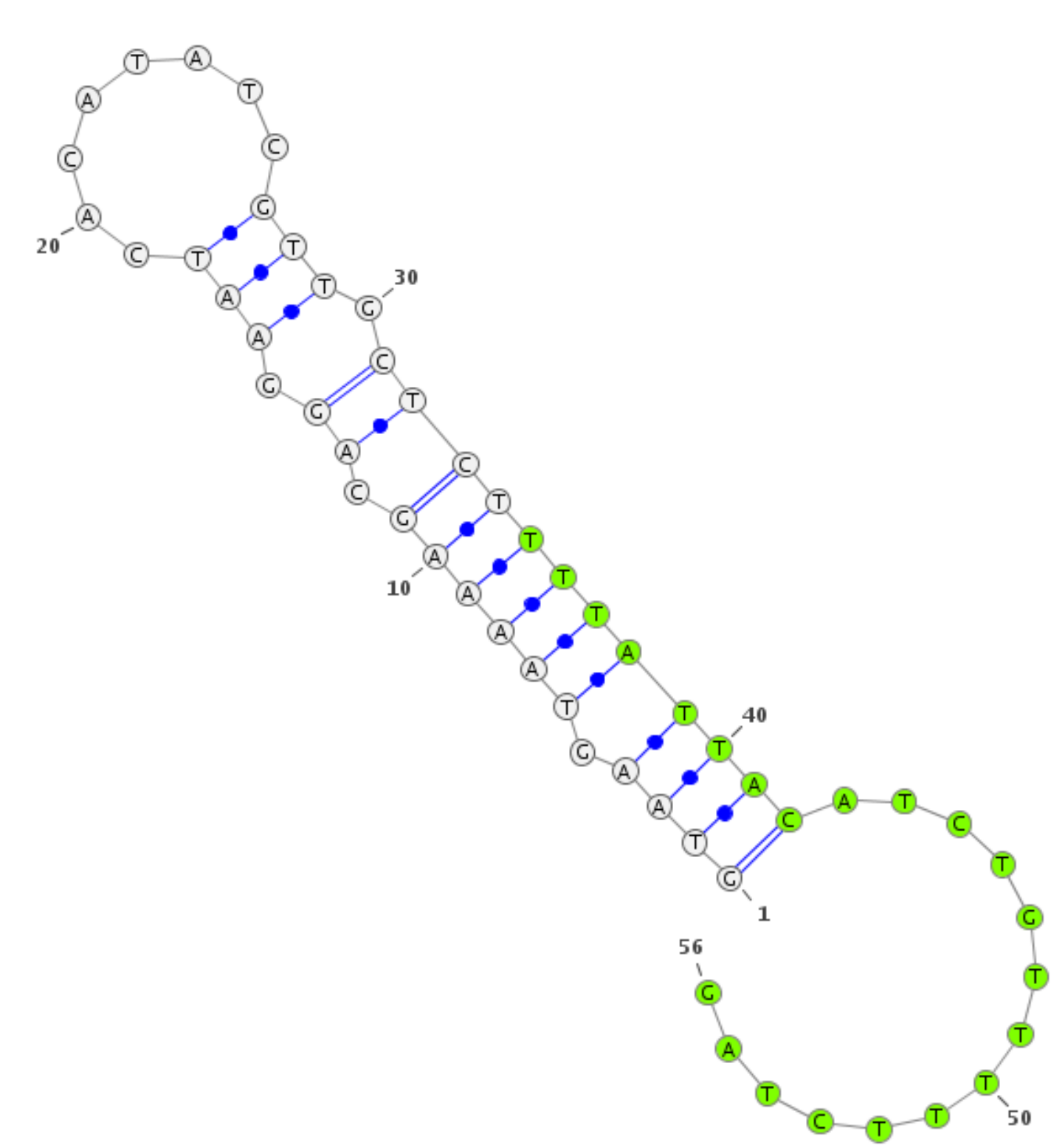
Species	Coordinate	ID	Alignment
droWil2	scf2_11000000004961:5211483-5211649 -	dwi_162	CCAGTCTTGAAGCTTCGATTCCACCTTTTTTATGTGCACACCTTTGGGC TCCATCAGAAATAGTGTA---- AAGG GCTTCACCTAAACCAACTAACAC TTTACACTAATTCTGATGGCA CCCAAGGGCTTCGACTTTACCAACTAACTCGTTGATTTCGTGTGTGTGTT
droPer2	scaffold_970:5861-5862 -		CC-----
droAna3	scaffold_13280:720802-720811 +		C AATCTTGA-----
droRho1	scf7180000772413:12338-12448 +		CCAGTCTT AATCTT AAGCGCTCCCTT CATTTCTCCTTTCTT CG-- AC TAC CAGAAC CG GTCAATCT AAGG GCTTC CG TAC GACCT TAA ----- T CAT TCTGAT AACATTC -----

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

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:
dwi_3966	scf2_1100000004963:1269369-1269424 -	candidate	Mirtron	intron
[View on UCSC Genome Browser (Cornell Mirror)]				

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

Predicted structure



dwi_3966_annot [-7.9]

Show Alternate Folds

Flybase annotation

intron [DwiflGK16082-in]; CDS [DwiflGK16082-cds]; CDS [DwiflGK16082-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

	Read #	Hit	Total		V118	V119	M020	M045	V117
	size	Mismatch	Count	Norm	embryo	head	head	female body	male body
AGTATCAGTTCGCCAAGCAGTTCACCGGATGTCATAATATCTTCTCCCAAGTAAGTAAAGCAGGAATACATATCGTTGCTCTTTTATTACATCTGTTTTCTAGGAATACATATGTGATACGTGAATATCTGCTGCTGGTTGGCTGATGTCGGT	22	0	1	9.00	9	4	3	2	0
*****(((.((((((.(.(((.....))..))))))))*****	21	0	1	4.00	4	2	1	1	0
.....TTTATTACATCTGTTTTCTAG.....	22	1	1	1.00	1	0	1	0	0
.....TTATTACATCTGTTTTCTAG.....	23	0	1	1.00	1	1	0	0	0
.....TCAGTTCGCCAAGCAGTTCACCG.....	23	0	1	1.00	1	1	0	0	0
.....TTTATTACATCTGTTTTCTAG.....	23	0	1	1.00	1	1	0	0	0

Anti-sense strand reads

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

Re-alignment of all predicted orthologs

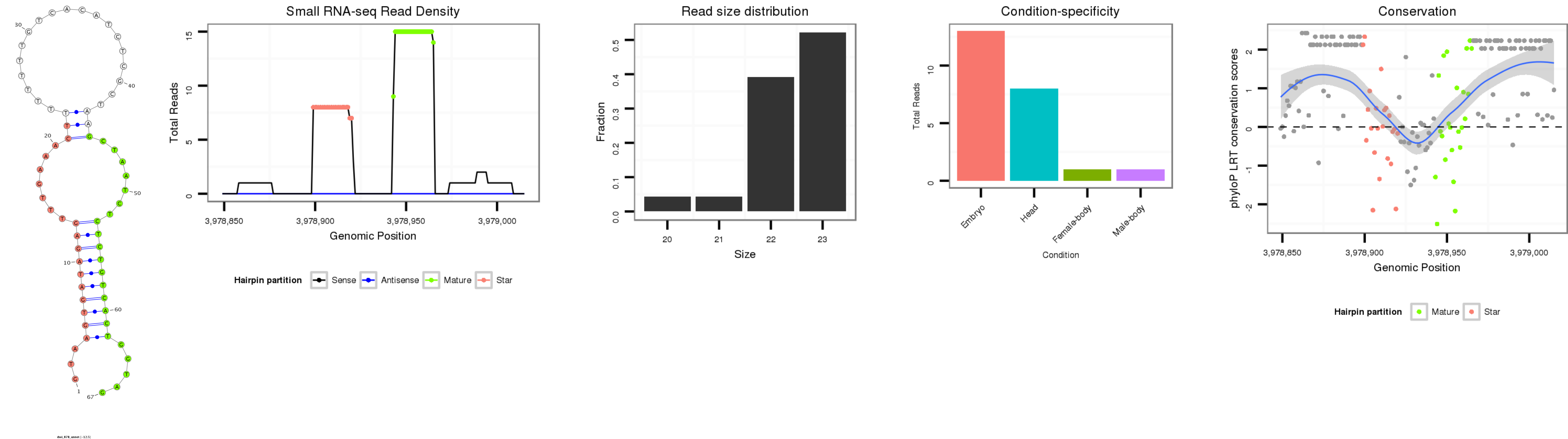
Species	Coordinate	ID	Alignment
droW112	scf2_1100000004963:1269319-1269474 -	dwi_3966	AGTATCAGTTCGCCAAGCAGTTCACCGGATGTCATAATATCTTCTCCCAAGTAAGTAAAGCAG---GAATCACA-----T-----A-----TCGTTGCT-----CT-----TT-TATTACATCT-----GTITTTCTAGGAATACATATGTGATACGTGAATATCTGCTGCTGGTTGGCTGATGTCGGT
droVir3	scaffold_13042:4765104-4765279 -		AATATCAGTTCGCCAAGCAATTCACGGCGTCACTTGATCTTTTCCCAAGTGAATATGAAGGC--TC-----C-----A-----TC-----GGTAAATTATATATATATATATATAAATACTA-----A-----AC-----GTITGCTCTAGGATTAATATGTATACGTGAATATCTGCTAAGCGGTGGCTGATGSCCGT
droMoJ3	scaffold_6328:4011121-4011183 -		TCG-----TCG-----GTITGCTCTAGGATTAATATGTATACGTGAATATCTGCTGCTGGTTGGCTGATGSCCGT
droGr12	scaffold_14853:320358-320523 +		AATACCAATTCGCCAAGCAATTCACCGGATGTCATAATATCTTCTCCCAAGTGAATATGAAGGC--TC-----C-----A-----TC-----GGTAAATTATATATATATATATAAATACTA-----A-----AC-----GTITGCTCTAGGATTAATATGTATACGTGAATATCTGCTGCTGGTTGGCTGATGSCCGT
dp5	Xl_group1a:4652560-4652722 -		AGTACCGGTTCCCAAGCAGTTCACGGATGTCACCAATCTTTTCCCAAGTGAATATGAAGGC--TC-----C-----A-----TC-----GGTAAATTATATATATATATATAAATACTA-----A-----AC-----GTITGCTCTAGGATTAATATGTATACGTGAATATCTGCTGCTGGTTGGCTGATGSCCGT
droPer2	scaffold_11:1241413-1241575 -		AGTACCGGTTCCCAAGCAGTTCACGGATGTCACCAATCTTTTCCCAAGTGAATATGAAGGC--TC-----C-----A-----TC-----GGTAAATTATATATATATATATAAATACTA-----A-----AC-----GTITGCTCTAGGATTAATATGTATACGTGAATATCTGCTGCTGGTTGGCTGATGSCCGT
droAna3	scaffold_13340:10981619-10981718 -		AGTACCAATTCGCCAAGCAATTCACCGGATGTCATAATATCTTCTCCCAAGTGAATATGAAGGC--TC-----C-----A-----TC-----GGTAAATTATATATATATATATAAATACTA-----A-----AC-----GTITGCTCTAGGATTAATATGTATACGTGAATATCTGCTGCTGGTTGGCTGATGSCCGT
droBiP1	scf7180000396374:99499-99598 +		AGTACCAATTCGCCAAGCAATTCACCGGATGTCATAATATCTTCTCCCAAGTGAATATGAAGGC--TC-----C-----A-----TC-----GGTAAATTATATATATATATATAAATACTA-----A-----AC-----GTITGCTCTAGGATTAATATGTATACGTGAATATCTGCTGCTGGTTGGCTGATGSCCGT
droKiK1	scf7180000302469:1011184-1011344 -		AGTACCAATTCGCCAAGCAATTCACCGGATGTCATAATATCTTCTCCCAAGTGAATATGAAGGC--TC-----C-----A-----TC-----GGTAAATTATATATATATATATAAATACTA-----A-----AC-----GTITGCTCTAGGATTAATATGTATACGTGAATATCTGCTGCTGGTTGGCTGATGSCCGT
droFiC1	scf7180000454072:1738908-1739067 -		AGTACCAATTCGCCAAGCAATTCACCGGATGTCATAATATCTTCTCCCAAGTGAATATGAAGGC--TC-----C-----A-----TC-----GGTAAATTATATATATATATATAAATACTA-----A-----AC-----GTITGCTCTAGGATTAATATGTATACGTGAATATCTGCTGCTGGTTGGCTGATGSCCGT
droElE1	scf7180000491043:173279-173452 -		AGTACCAATTCGCCAAGCAATTCACCGGATGTCATAATATCTTCTCCCAAGTGAATATGAAGGC--TC-----C-----A-----TC-----GGTAAATTATATATATATATATAAATACTA-----A-----AC-----GTITGCTCTAGGATTAATATGTATACGTGAATATCTGCTGCTGGTTGGCTGATGSCCGT
droRho1	scf7180000778083:103693-103853 -		AGTACCAATTCGCCAAGCAATTCACCGGATGTCATAATATCTTCTCCCAAGTGAATATGAAGGC--TC-----C-----A-----TC-----GGTAAATTATATATATATATATAAATACTA-----A-----AC-----GTITGCTCTAGGATTAATATGTATACGTGAATATCTGCTGCTGGTTGGCTGATGSCCGT
droBiA1	scf7180000301760:3953379-3953539 +		AGTACCAATTCGCCAAGCAATTCACCGGATGTCATAATATCTTCTCCCAAGTGAATATGAAGGC--TC-----C-----A-----TC-----GGTAAATTATATATATATATATAAATACTA-----A-----AC-----GTITGCTCTAGGATTAATATGTATACGTGAATATCTGCTGCTGGTTGGCTGATGSCCGT
droTak1	scf7180000415704:962330-962498 +		AGTACCAATTCGCCAAGCAATTCACCGGATGTCATAATATCTTCTCCCAAGTGAATATGAAGGC--TC-----C-----A-----TC-----GGTAAATTATATATATATATATAAATACTA-----A-----AC-----GTITGCTCTAGGATTAATATGTATACGTGAATATCTGCTGCTGGTTGGCTGATGSCCGT
droEuP1	scf7180000408994:74111-74277 +		AGTACCAATTCGCCAAGCAATTCACCGGATGTCATAATATCTTCTCCCAAGTGAATATGAAGGC--TC-----C-----A-----TC-----GGTAAATTATATATATATATATAAATACTA-----A-----AC-----GTITGCTCTAGGATTAATATGTATACGTGAATATCTGCTGCTGGTTGGCTGATGSCCGT
dm3	chrX:1365332-1365490 +		AGTACCGGTTTCGAAGCAGTTCACCGGATGTCACCAATCTTCTCCCAAGTGAATATGAAGGC--TC-----C-----A-----TC-----GGTAAATTATATATATATATATAAATACTA-----A-----AC-----GTITGCTCTAGGATTAATATGTATACGTGAATATCTGCTGCTGGTTGGCTGATGSCCGT
droSim2	x1245363-1245521 +		AGTACCGGTTTCGAAGCAGTTCACCGGATGTCACCAATCTTCTCCCAAGTGAATATGAAGGC--TC-----C-----A-----TC-----GGTAAATTATATATATATATATAAATACTA-----A-----AC-----GTITGCTCTAGGATTAATATGTATACGTGAATATCTGCTGCTGGTTGGCTGATGSCCGT
droSec2	scaffold_10:1192318-1192476		AGTACCGGTTTCGAAGCAGTTCACCGGATGTCACCAATCTTCTCCCAAGTGAATATGAAGGC--TC-----C-----A-----TC-----GGTAAATTATATATATATATATAAATACTA-----A-----AC-----GTITGCTCTAGGATTAATATGTATACGTGAATATCTGCTGCTGGTTGGCTGATGSCCGT
droYaK3	X:1270055-1270213 +		AGTACCGGTTTCGAAGCAGTTCACCGGATGTCACCAATCTTCTCCCAAGTGAATATGAAGGC--TC-----C-----A-----TC-----GGTAAATTATATATATATATATAAATACTA-----A-----AC-----GTITGCTCTAGGATTAATATGTATACGTGAATATCTGCTGCTGGTTGGCTGATGSCCGT
droEre2	scaffold_4644:1354832-1354991 +		AGTACCGGTTTCGAAGCAGTTCACCGGATGTCACCAATCTTCTCCCAAGTGAATATGAAGGC--TC-----C-----A-----TC-----GGTAAATTATATATATATATATAAATACTA-----A-----AC-----GTITGCTCTAGGATTAATATGTATACGTGAATATCTGCTGCTGGTTGGCTGATGSCCGT

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crit.star	PASS/FAIL
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.topo	0
crit.ptop3	1
crit.un	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Show Alternate Folds

Flybase annotation

intron [Dwil\GK21843-in]; CDS [Dwil\GK21843-cds]; CDS [Dwil\GK21843-cds]; utr5 [utr5_minus_4647]; utr5 [utr5_minus_4648]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

					V118	M020	V119	V117	M045
					embryo	head	head	male	female
								body	body
GCCAAAGGGCAGAATATACCCACACAAGTCCATCCACAAGGCAGTGCAAGGTAAGTGATAGAGTTTGAAACTTTTTTTGTGCATCTCGCTAAGCTAATCTCTCTGTCACTGGTAGATTCTCAGTGTGTTTGTGCCCACTGAGTCATGTGAGCATACCATCAATG	Read #	Hit	Total	Total					
*****((((((((((((..... ((.....)))))))))..... *****	size	Mismatch	Count	Norm					
.....GCTAATCTCTCTGTCACTGGTAG.....	23	0	1	9.00	5	3	0	0	1
.....CTAATCTCTCTGTCACTGGTAG.....	22	0	1	5.00	5	4	0	1	0
.....GTAAGTGATAGAGTTTGAAACT.....	22	0	1	4.00	4	1	0	2	1
.....GTAAGTGATAGAGTTTGAAACTT.....	23	0	1	3.00	3	2	0	1	0
.....GTAAGTGATAGAGTTTGAAA.....	20	0	1	1.00	1	1	0	0	0
.....GCTAATCTCTCTGTCACTGGC.....	21	1	1	1.00	1	0	1	0	0
.....CTGAGTCATGTGAGCATACC.....	20	0	1	1.00	1	1	0	0	0
.....CTAATCTCTCTGTCACTGGTA.....	21	0	1	1.00	1	0	1	0	0
.....CTAATCTCTCTGTCACTGGTAGA.....	25	2	1	1.00	1	1	0	0	0
.....TGTCGTTTGTGCCCACTGAGT.....	21	0	1	1.00	1	1	0	0	0
.....CAGAATATACCCACACAAG.....	19	0	1	1.00	1	0	1	0	0

Anti-sense strand reads

										M045	M020	V118
CGGTTCCCGCTTCTATATGGGTGTGTTCAAGTAGGTGTTCCGTCACGTTTCATTCACTATCTCAAACTTTGAAAAAAACAGTGTAGACGATTGATTAGAGAGACAGTGACCACTTAAGAGTCACAGCAACACGGTGACTCAGTACACTCGTATGGTAGTTAC										female body	head	embryo
*****...((((((((((.....((.....)))))))))).....*****										Read #	Hit	Total
										size	Count	Norm
										Mismatch		Total

Show Alignment With Reads

Re-alignment of all predicted orthologs

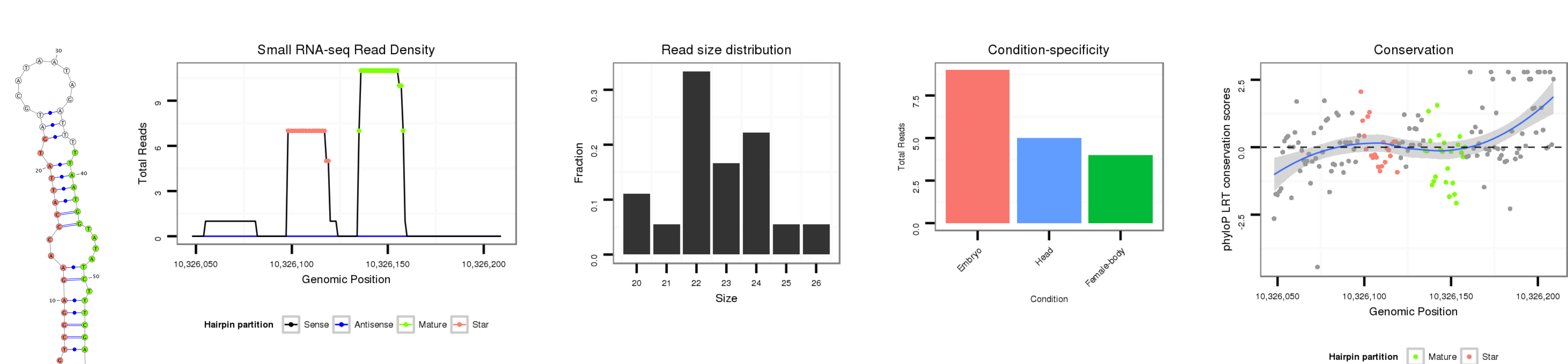
[illegible]

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

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Show Alternate Folds

Flybase annotation

intron [Dwil\GK10138-in]; CDS [Dwil\GK10138-cds]; CDS [Dwil\GK10138-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

[illegible]

Anti-sense strand reads

[illegible]

No data available in table

Show Alignment With Reads

Re-alignment of all predicted orthologs

Coordinate	ID	Alignment
droW112 scf2_110000004909:10326048-10326209 +	dwi_2870	ACCAC-----AA-----CAATTGCAATTGCACTGGACAG---GAGCGTAGTCATTCAAT-----AGAGTAAGTCGGAGAA-----CCCA-TTATG--ATGCATAATAG--ATT-----TTAATGG--TAT-----AT-CCT--TCG--GA-----TT-----ACGCGAGCAGCGAGAAATTGGAGTATTTCGTAATGAATGAAATATTTATTGCTG
droViR1 scaffoid_12970:8750329-8750490 +	dwi_13686	GGCAGAGGGCGTGC-----T-----GAGACAGCTCCGCAGATTAATAATTAAAGCAGCG---AAT-----GC-----CAATT--ACAQAAT--TTATTTTTAACTTAAATT--AT-----A-----A-----AGCGGCAATAGTTTCTAAAGCTAAAGCTGTGAGAGCTGCTGGGAATGGAATAATCTGCTGCTG
droMoJ scaffoid_6473:12765506-12765635 +		CTGTG--GATA-----AGCGAGTAATC--G-----AACGAACTT-----GAGC--GAA-----CTTGT--GGGACT-----A-AG--ATTTCGGTTTACCCCA--CC--CAG--CAGCTTGCAGAGCTTCCAGCAATTCAGCGCAATGGAATAATTCTGTTG
droGr12 scaffoid_15203:11484356-11484480 +		GTGTA---G-----AGTGACAGTGTGTGAGAAATTATAA-----A-TA--ATTA-TAATAATCCAA-----C-----C-----CACTCATT-----AGCATCATGACGAATACAAAGGSAACCTGCAG--CGACGTCGCGAATGCGATATGCTGTG
dp5 Xl_group1:9945422-9945577 -		CGCGC---G-----AGCTGAT-G---CA--GAGTC--CCG--GAA-----GASTAAGT-A-----CTCTCAACCCCTCA--GAATAGCTTATT-----G-----TTTAT--GGGAAT-----C--A--TTTTCG-----AGCGGCACAGCAG--CAGCAGCAGCACTGCGCGATTCCCGGGAATGGAATGATCGCTG
droPer2 scaffoid_22:288892-289044 -		TGCGC---G-----AGCTGAT-G---TA--GAGTC--CCG--GAA-----GASTAAGT-A-----CTCTCAACCCCTCA--GAATAGCTTATT-----G-----TTTAT--GGGAAT-----C--AA--TTTTGC-----AGCAGCAAC--AG--CAGCAGCAGCACTGCGCGATTCCCGGGAATGGAATGATCGCTG
droAna3 scaffoid_13137:550524-550704 +		GTCTC---GG--CATTTGCACTTCAACGATGG-----GAG--AAACAG-----AG--GCTGGGAGAGAGTGGGTGAGTACCCCAACAGAAC--GTGTGA--TAT--CA--CTAAAGTCTCTCT-----G--G--T--ACA-----CAGCGCAAAATGCCACCGATTTCAGCCGAATGGAATGATCGCTG
droBip1 scf7180000396540:3392-3549 +		ACCAGC--AAG--CGGTGCAACCGACGTATAGAG-----GAGGA--GCTGTGAT-----TGCGAAAGAA-----CGA--CATACATGTCGTATGTTATTATCA--GCAA--A--AAATTC--T--T--T-----TAGCGAAGACGGTCA--CGCTTTTACCCGATGGAATGGAATGATCGCTG
droKiK1 scf7180000302441:185181-185326 +		CAGCG--G-----AGTGTCC--GAGGAGCGAGGTCCAGAA-----AGATAAGT-----TCAAAGCTGT-----GA--TTGTATGCTCTATATAAATA-TAT--ATGTT-----A--G--CC-----CAGGACGATGGATGCGACCAATTCCTGTGAATGGAATGATCGCTG
droFic1 scf7180000454073:71207-71358 +		CTCG--GATAATCAATAGCTTCGATTTAA--C-----GAGGAGTATCGCG--GATGCTTTACATTCGGAAC-----ATT--AT--A-----G--AATGGTGAGTA--AAC--CA--T--T-----GTTACAG--AGCGGATGTGAGCTTCGCAATGAATGGAATGATCGCTG
droEle1 scf7180000491242:133172-133324 +		CCTCA--G-----CAGGTACGATTAACCTGTGCA-----GGAGCCATCGCA--GATGCT-----G-----TAGTAGCAACAAC--AC--A-----TGCACCTTTGTAGCGGTAAATCGTCC--GA--A--C--A--CT-----CAGACGCA--CGGATGCGAGAGCTCCGATGGAATGATCGCTG
droRho1 scf7180000768664:889-1020 +		ACCGC--G-----GACTTGCACTGTGCA-----GGAGCAGCCGCGATGCTG-----TTACAATCCAA-----ACAT--TTTGA--TCCAC--C--TAA-----A--GCA--TC--CG-----CAGCAGCGCCGGATGTGGAAGAGCGCGCCGAATGGAATGATCGCTG
droBial scf7180000302126:680756-680897 +		CTTCN--G-----GCTGCTTATGCTGCCA-----GAGGTACCCGCGATAAGCTATG--CA-----GCTGTAAT--AT--A--CATA--GTAT--TAGACAGGGATGTGGAAGAGCGGCTGATGGAATGGAATGATCGCTG
droTak1 scf7180000414222:5813-5929 +		CA---G-----GGAATCATCGCGATTAGT-----GCTCCCTTGAGT--TC--G--CCAAAMAT--A-----CCACTATCA--ATA--A--TC--AC-----CAGACGCA--GGATGTGGAAGACTTCGATCAGATGAATGGAATATGCTGCTG
droEug1 scf7180000409008:1298145-1298299 +		TCCAC--GAGGTAGCACTGCAATGCTGTGCA-----GGAGCAGCCGCGATAAGT-----CTATATTATTAANA--AT--A--TCC-----TAT-----AAATATCA--TATTAAAAGCA--A--C--CT--TT-----CAGACGCA--GATGTGGAAGCGGATTCGATGAATGGAATGATCGCTG
dm3 ChrX:11903568-11903711 +		C---G-----AATGCGATTGCACTGGCGAG-----GAGGAGCGCTGCGTAAGT-----TCGAATCGCATTAT--A-----CTTAACAT--A-----TCGCATTGAGAATA--T--C--TC--AT--T--C-----TAGAATCGAAGCTGTGCGACGCTCCGATCAGATGAATGGAATGATCGCTG
droSim2 x11279285-11279427 +		C---G-----AAGCGGATCGAGCTGCGAG-----GAGGAGCGCTGCGTAAGT-----TCCAACTGCAGT--AT--G--CTTAACAT--A-----TGCATGAGGAATA--T--C--AA--CT-----TAGAATCGAAGCTGTGCGACGCTCCGATCAGATGAATGGAATGATCGCTG
droEne scaffoid_58:119499-119792 +		GATCC--GAGCTGCACTGCACTGCACTGCA-----GAGGAGCGCTGCGTAAGT-----TCCAACTGCAGT--AT--G--CTTAACAT--A-----TCATGAGGAATA--T--C--AA--CT-----TAGAATCGAAGCTGTGCGACGCTCCGATCAGATGAATGGAATGATCGCTG
droYak1 X1194987-11949932 -		GATCC--GAGCTGCACTGCACTGCACTGCA-----GAGGAGCGCTGCGTAAGT-----TCCAACTGCAGT--AT--G--CTTAACAT--A-----TCATGAGGAATA--T--C--AA--CT-----TAGAATCGAAGCTGTGCGACGCTCCGATCAGATGAATGGAATGATCGCTG
droEre2 scaffoid_4690:14920007-14920161 -		TCCCG--GAGCCGCAAGCGCAATGATGTGCGAG-----GAGGATCCTTCGCGTAAGT-----CACAACTGCAGT--AA--A-----CCCAACAT--A-----CGGTAAGGAGAATA--T--A--C--CT-----TAGAATCGAAGCTGTGCGACGCTCCGATCAGATGAATGGAATGATCGCTG

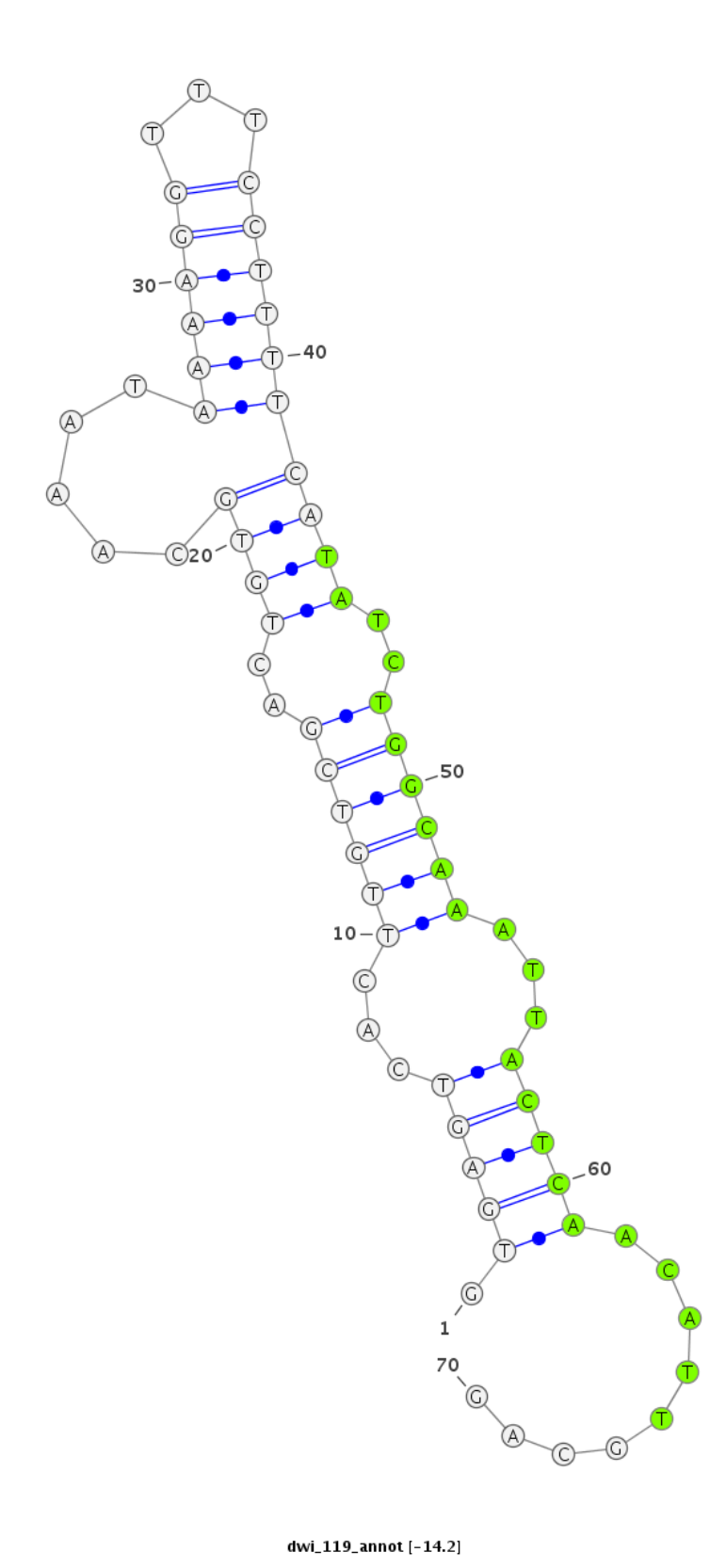
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	PASS/FAIL
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crit.uri	1
crit.back	1
rescue.total	1
rescue.dominant	1
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rescue.confident	0
rescue.candidate	1

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dwi_119	scf2_1100000004585:3269208-3269277 -	candidate	3p_tailed_mirtron	intron	[View on UCSC Genome Browser (Cornell Mirror)]

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

Predicted structure



Show Alternate Folds

Flybase annnotation

intron [DwilGK24377-in]; CDS [DwilGK24377-cds]; CDS [DwilGK24377-cds]; utr5 [utr5_plus_2979]; utr5 [utr5_plus_2978]

No Repeatable elements found

Sense Strand Reads

☐ hide 3p reads ☒ show mid mismatch reads

	Read # size	Mismatch Count	Hit Count	Total Norm	Total	M020 female head	M045 female body	V118 embryo	V119 head
ATGTGGACCCAAAGGGCGAATACGTTGCTACATGCTCCGATGATGGCAAAGTGAGTCACTTGTGCACTGTGCAAAATAAAAGGTTCTCCTTTTCAATCTGGCAAATTACTCAACATTGCAGGTTAACATCACAGGCCTCTTCAGTTGCGAGAACAATCAGAGCTTAAGCTT	23	0	1	13.00	13	9	1	2	1
.....TATCTGGCAAATTACTCAACATT.....	22	0	1	3.00	3	1	1	1	0
.....CTACATGCTCCGATGATGG.....	19	0	1	2.00	2	0	2	0	0
.....GTGAGTCACTTGTGCACTGTG.....	22	1	1	1.00	1	0	0	0	1
.....TATCTGGCAAATTACTCAACA.....	21	0	1	1.00	1	1	0	0	0

Anti-sense strand reads

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

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droW112	scf2_1100000004585:3269161-3269327 -	dwi_119	ATGTGGACCCAAAGGGCGAATACGTTGCTACATGCTCCGATGATGGCAAAGTGAGTCAC-----TTGTCGACTG---TGCA-----AATA-----AAAGG-TT-----TCCTTTTCAATCTGGCAAATTACTCAACATTGCAGGTTAACATCACAGGCCTCTTCAGTTGCGAGAACAATCAG-----AGCTTAAG
droVir3	scaffold_12963:2443012-2443177 -	dwi_10179	ATGTGGACCCAAAGGGCGAATACGTTGCTACATGCTCCGATGATGGCAAAGTGAGTCAC-----TGA---AAGG-GTG-TTACTAATTAATAGGGGCT-----TCATAC-----TA-TTTT-----ATTGCGATATTTTCAGGTCAATATACGGCTTTTCAGTGTGAGAAATATCAG-----AATCTTAG
droMoj3	scaffold_6500:12601219-12601377 -		ATGTGACCCAAAGGGCGAATACGTTGCTACATGCTCCGATGATGGCAAAGTGAGTCAC-----TAA---AA-GAATG-TTGATAATTGAGAGTCA-----CACAA------G-T-GAT-A-----ACA-----TTTCAGGTCAATATACGGCTTTTCAGTGTGCGAGAACAATCA-----AATCTCAG
droGri2	scaffold_15126:2570528-2570701 +		ATGTGGACCCAAAGGGCGAATACGTTGCTACATGCTCCGATGATGGCAAAGTGAGTCAC-----TCA---ATTCAA-CSCAA-----ATAAAG-----S-GG-AGAATCTTAAATATATATT-----G-TACCA-A-----CAT-----TTTCAGGTCAATATACGGCTTTTCAGTGTGAACAAACAA-----AATCTGA
dp5	4_group4:6460334-6460491 +		ACCTGACCCAAAGGGCGAATACGTTGCTACATGCTCCGATGATGGCAAAGTGAGTCAC-----TTT---GTGATGCTGG-----GTGGATGCGGCAATCACACA-CA-----GG-CAT-T-----TT-----TTTCAGGTCAACATACAGGCTCTTCAGTGTGCGAGAACAATCAG-----AATCTTAG
droPer2	scaffold_16:401426-401583 -		ACCTGACCCAAAGGGCGAATACGTTGCTACATGCTCCGATGATGGCAAAGTGAGTCAC-----TTT---GTGATGCTGG-----GTGGATGCGGCAATCACACA-CA-----GG-CAT-T-----TT-----TTTCAGGTCAACATACAGGCTCTTCAGTGTGCGAGAACAATCAG-----AATCTTAG
droAna3	scaffold_13258:822535-822687	dan_1648	ATGTGACCCAAAGGGCGAATACGTTGCTACATGCTCCGATGATGGCAAAGTGAGTCAATGTTTATTTAA---GCTT-----PATTGT-----A-AA-----CACAGGTCAACATACGGCTTTTCAGTGTGAACAAACAA-----AATCTGA
droBip1	scf7180000395375:11611-11759		ATGTGACCCAAAGGGCGAATACGTTGCTACATGCTCCGATGATGGCAAAGTGAGTCAATGTTTATTTAA---GGA-----CT-GTTCC-----S-AAT-----TA-ATTTC-----CTG-----TTTCAGGTCAACATACGGCTTTTCAGTGTGAACAAACAA-----AATCTGA
droK1k1	scf7180000301949:23398-23567		ATGTGGACCCAAAGGGCGAATACGTTGCTACATGCTCCGATGATGGCAAAGTGAGTCAATGTTTATTTAA---AATTA-ATG-----TTCATCAGCAGATTCATTAA-TA-----C-CATATATACATATATGA-TA-----CATAGGTCAATATACGGCTTTTCAGTGTGAACAAACAA-----AGCTAAG
droFic1	scf7180000449515:11136-11285		ATGTGGACCCAAAGGGCGAATACGTTGCTACATGCTCCGATGATGGCAAAGTGAGTCAATGTTTATTTAA---ACTGAAGGSCCT-----ATGATCA-----S-GA-T-----A-ATTG-----T-TA-----TTTCAGGTCAACATACGGCTTTTCAGTGTGAACAAACAA-----AATTAAG
droE1e1	scf7180000490719:11382-11530		ATGTGGACCCAAAGGGCGAATACGTTGCTACATGCTCCGATGATGGCAAAGTGAGTCAATGTTTATTTAA---CCTTAG-TGTC-----CTGAGTCG-----S-GC-T-----A-CTTCT-----T-TA-----CCACAGGTCAACATACGGCTTTTCAGTGTGAACAAACAA-----AATCTAAG
droRho1	scf7180000761822:3670-3818 -		ATGTGGACCCAAAGGGCGAATACGTTGCTACATGCTCCGATGATGGCAAAGTGAGTCAATGTTTATTTAA---TCTTAA-GTCA-----CTGAGTCA-----S-GC-T-----A-CTTCT-----T-TA-----CCACAGGTCAACATACGGCTTTTCAGTGTGAACAAACAA-----AATCTAAG
droB1a1	scf7180000302173:13689-13833		ATGTGACCCAAAGGGCGAATACGTTGCTACATGCTCCGATGATGGCAAAGTGAGTCAATGTTTATTTAA---CTTGAATGATG-----CTAATTAA-----A-AA-T-----A-CATC-----T-T-----TCAGGTCAACATACGGCTTTTCAGTGTGAACAAACAA-----AATTAAG
droTak1	scf7180000412928:28185-28329		ATGTGACCCAAAGGGCGAATACGTTGCTACATGCTCCGATGATGGCAAAGTGAGTCAATGTTTATTTAA---GCTTAA-GAT-----GATTAA-----S-CT-T-----A-CTT-T-----T-T-----TTTCAGGTCAACATACGGCTTTTCAGTGTGAACAAACAA-----AATCTAAG
droEug1	scf7180000408916:24800-24947		ATGTGGACCCAAAGGGCGAATACGTTGCTACATGCTCCGATGATGGCAAAGTGAGTCAATGTTTATTTAA---TTTAC-TGTGG-----CTTATTAG-----A-GA-T-----A-CTT-T-----A-CT-----CTAGGTCAATATACGGCTTTTCAGTGTGAACAAACAA-----AATCTAAG
dm3	chr2L:22818013-22818159 +		ATGTGACCCAAAGGGCGAATACGTTGCTACATGCTCCGATGATGGCAAAGTGAGTCAATGTTTATTTAA---GCTT-----GATAGCAATA-----TAAAA-CT-----TA-ATTCT-----CTTT-----GCCAGGTCAACATACGGCTTTTCAGTGTGAACAAACAA-----AGCTCAG
droSim2	21:22919271-22919417 +		ATGTGACCCAAAGGGCGAATACGTTGCTACATGCTCCGATGATGGCAAAGTGAGTCAATGTTTATTTAA---GCTT-----GATAGCAATA-----TAAAA-CT-----TA-ATTCT-----CTTT-----GCCAGGTCAACATACGGCTTTTCAGTGTGAACAAACAA-----AGCTCAG
droSec2	scaffold_72:89883-90029 +		ATGTGACCCAAAGGGCGAATACGTTGCTACATGCTCCGATGATGGCAAAGTGAGTCAATGTTTATTTAA---GCTT-----GATAGCAATA-----TAAAA-CT-----TA-ATTCT-----CTTT-----GCCAGGTCAACATACGGCTTTTCAGTGTGAACAAACAA-----AGCTCAG
droYak3	y2_chr2h_random_003:28027-28173 -		ATGTGACCCAAAGGGCGAATACGTTGCTACATGCTCCGATGATGGCAAAGTGAGTCAATGTTTATTTAA---GCTT-----GATAGCAATA-----TAAAA-CT-----TA-ATTCT-----CTTT-----GCCAGGTCAACATACGGCTTTTCAGTGTGAACAAACAA-----AGCTCAG
droBre2	scaffold_4845:556605-556751		ATGTGACCCAAAGGGCGAATACGTTGCTACATGCTCCGATGATGGCAAAGTGAGTCAATGTTTATTTAA---GCTT-----GATAGCAATA-----TAAAA-CT-----TA-ATTCT-----CTTT-----GCCAGGTCAACATACGGCTTTTCAGTGTGAACAAACAA-----AGCTCAG

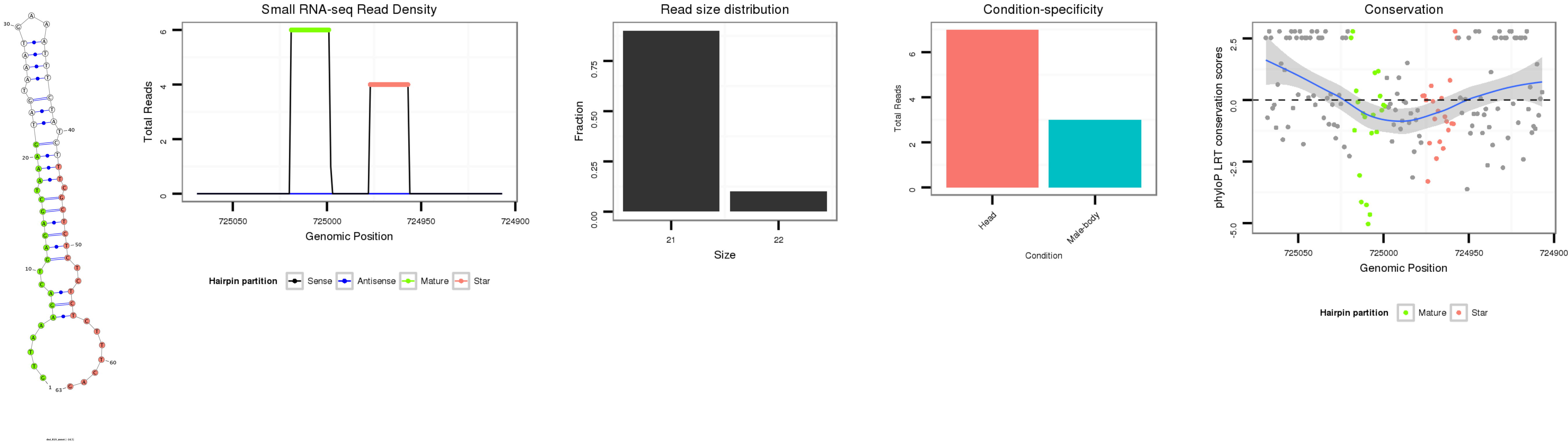
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rescue.dominant	1
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rescue.confident	0
rescue.candidate	1

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dwi_819	scf2_1100000004513:724957-725019 -	candidate	Mirtron	antisense_to_intron	[View on UCSC Genome Browser {Cornell Mirror}]

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

Predicted structure



Show Alternate Folds

Flybase annotation

Antisense to intron [DwilGK21697-in]; intron [DwilGK21603-in]; CDS [DwilGK21603-cds]; CDS [DwilGK21603-cds]; utr3 [utr3_minus_3304]; utr3 [utr3_minus_3303]

No Repeatable elements found

Sense Strand Reads

CCACGAACAAGGCAGAATGTACAGCTGAACAGGCCCTATCAATATACTGAGGTTAAAGACTGAGAGCTAAAGTAGTAAATGAAATTCTATCTTTTCGCTCTCTCTCTTTTCAGGGTCGGGCCATCTTTTCGCGCGGTTACCACTTCCACCCGTAACATATAA	Read #	size	Mismatch	Hit	Count	Total	Norm	Total	M020	V117	V119	M045
*****.....(((.....(((.....(((.....(((.....))))))..))))..))))..*****	21	0	1	5.00	5	4	1	0	0			
.....GTTAAAGACTGAGAGCTAAAG.....	21	0	1	4.00	4	2	1	1	0			
.....TTTCGCTCTCTCTCTCTTTTCAG.....	22	0	1	1.00	1	0	1	0	0			
.....GTTAAAGACTGAGAGCTAAAGT.....												

Anti-sense strand reads

GGTGCCTTGTTCCGCTCTTACATGTGCACTTGTCCGGATAGTTATATGACTCTAATTTCGACTCTCGATTTATCATTTTACTTTTAAAGATAGAAAGCGAGAGAGAGAGAAAGTCCAGCCCGGTAGAAAACGCCCCAAGTGGTAAAGGTGGCATTGTATATT	Read #	size	Mismatch	Hit	Count	Total	Norm	Total	M045	V117
*****.....(((.....(((.....(((.....(((.....))))))..))))..))))..*****									female body	male body

Re-alignment of all predicted orthologs

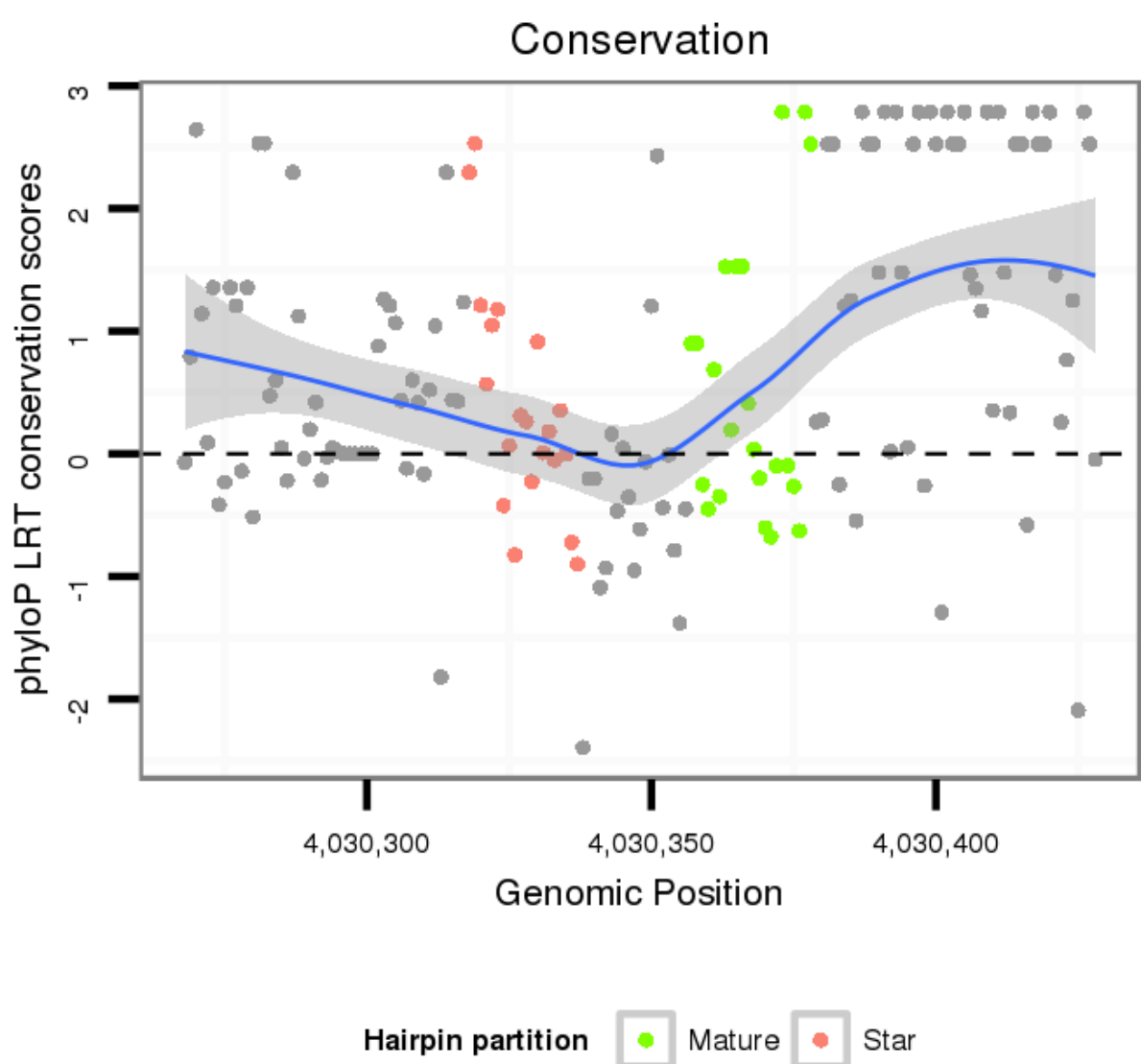
Species	Coordinate	ID	Alignment
droWil2	scf2_1100000004513:724907-725069 -	dwi_819	CCACGAACAAGGCAGAATGTACAGCTGAACAGGCCCTATCAATATACTGAGGTTAAAGACTGAG-----AGCTAAA---GTAGT-----A-----AA-----T-----GAAATTTCTATCT--TTGC--C-----TCTCTCTCTCTTTTCAGGGTCGGGCCATCTTTTCGCGCGGTTACCACTTCCACCCGTAACATATAA
droVir3	scaffold_12875:18819235-18819400 -		CACACAACAAACGAGAATGCACGCGCAGCAGGCTTACAAATTACASAGGTAAACAGACACATAC-TACT---ACT---CTAAC-----A-----AA-----T-----ACTATATGCGCGC-CATA--A-----CTACTTTCACCTTCAGGGTCGCGCATTCGTTGCTCGCTCGGCTCACCCCTTCCGCCCTGGTTATCAA
droMoJ3	scaffold_6540:10921876-10922032 -		CCACACCAAGGCASAATGCACAGCTGACGAGGCCCTATCARTACGSAATGCGCTTTCTCTT-TAA-----T-TAT--C-----TC--#-----TTTATGAT-CTG-AC-A--TATCGCTTTTATAGGCACGCTATCTTTCTATCCGCTCCTCGCTCCACCGCTACATGGC
droGri2	scaffold_14830:6258375-6258534 +		CACACCAAGGCASAATGCACAGCTGACGAGGCCCTACAAATACGSAATGCGTTGTGCTTCA-T-TATTGTGATGCG--A-----AA-----T-----AAC-----A---TGTC-----TCTCTTATTTTAGGCAAGTATCTTTCTATCCGCTCCTCGCTCCACCGCTACATGGC
dp5	2:8589086-8589244 +		CCACCAAGGCASAATGCACGCGCAGCAGGCTACATACACGSAATGANGATACAAAG-TCCT-----TGC---CTATCGGTTTTATTT-----A--T--A-AATCG---TTCGTATATAGGCACGCTGATCTTTCTGTCGCGCTCGCTCCACCGCTCAAAATGGC
droPer2	scaffold_0:2416453-2416611 +		CCACCAAGGCASAATGCACGCGCAGCAGGCTACATACACGSAATGANGATTACAAAG-TCCT-----TGC---CTATCGGTTTTATTT-----A--T--A-AATCG---TTCGTATATAGGCACGCTGATCTTTCTGTCGCGCTCGCTCCACCGCTCAAAATGGC
droAna3	scaffold_13266:15680518-15680673 -		CCACCAACAAGGCAGGTGCACAGCGCAACAGGCCCTATAGCTTACASAGSTACCTTCCTA-AAATTAGT-----CAT--A-----TA--AAG-----CAA--TT--AATT-----TAAATTTTATTATAGGCGAGCCATCTATTCTCAGATCACCGCTTTCCGCCATGGATTCAA
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droKik1	scf7180000302470:669296-669446 -		CCACCAACAAGTCGSAATGCACGCGCAACAGGCCCTACAAATCTCGSAGSTATTTACA-----TTAT-----GGT--T-----AAAA--TAA-----TTAA--TTATT-----TCTATAAATATAGGGTCGCGCCATTTATTCAACGCGTTCCAGCTTTCCGCCCTGGATTCAA
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droEle1	scf7180000491027:396377-396529 +		CCACCTCCAAAGTCGSAGTGTACGCGCAACAGGCCCTACAAATTTTASAGSTAGCTTCGA-A-TTGT-----GCTAANA-----TA--T-AG-----A-TTA--TC-C-----TTCTTTTTTTTCAGGGAGAGCATCTTTTCTCTGGTTCCGCTTTCCGCCATGGATTCAA
droRho1	scf7180000779468:100997-101149 +		CCACCTCCAAATTCGSAGTGTACGCGCAACAGGCCCTATATTTASAGSTAGGCCCTCTAG-T-TGG-----GGTAATA-----AA-----T-AG-----G-TTT--TC-A-----TTGGAACCTTTTCAGGGAAAGCATATTTCTGCAAGATCTCTTTCCGCCCTGGATTCAA
droBia1	scf7180000301506:2630913-2631068 +		CCACCAACCAATTCGSAATGCACGCGCAACAGGCCCTATCTCAGACTGAGTGGGTTTCCCTGT-TAAT-----GGT--A-----TATATT-TG-----A-TTG--CT-A-----TAACTCTCCACAGGGTCGGGTGCTCTTCTGCTCGGATCCGCTTTCCGCCCTGGATCGA
droTak1	scf7180000415346:21722-21879 -		CCACCTCCAAATTCGSAATGCACGCGCAACAGGCCCTATACACGACTGAGTTTGTCTGCGCTGT-TTT-----A--#-----TATATCTATATATATA-TATA-T-----TCAATATATCTTAGGGTCGCGCTTCCTTTCTGCTCGGATCACCATTTCCGCCCTGGATCAA
droBug1	scf7180000409672:2870343-2870493 -		CACCTCCAAATTCGSAATGCACGCGCAAGGCCCTACACGCACTGAGGTTAGTTTTCTG-A-TTTT-----T---TAACTTATTTTT-----A-TA-T-----ATAATTTACTATATAGGGTCGCGCTTCCTTTCTGCTCGGTTCCAGCTTTCCGCCCTGGATCAA
dm3	chr2R:12305160-12305319 -		CCACCAACCAATTCGSAATGCACGCGCAACAGGCCCTACAAATCTCAGAGSTAGTCTTAGAA-TACT-----TGC--C-----GAATA--T-TTACCATTT-TATT-T-----TCTCAAATTCCTAGGGAAAGCATATATTTCTGCAAGATCTCTTTCCGCCCTGGATTCAA
droSim2	2r:12981415-12981571 -		CCACCAATCAAAATTCGSAATGCACGCGCAACAGGCCCTACAAATCTCAGAGSTAGTCTTCCAA-A-TACT-----TGC--C-----GAGTATCT-T-A--TT-----TCGGATATTCCTAGGGAAGGCATATTTCTGCGCGGATCTCTTTCCGCCCTGGATTCAA
droSec2	scaffold_1:9800727-9800893 -		CACCTCCAAATTCGSAATGCACGCGCAACAGGCCCTACACGCACTGAGGTTAG-TTGA-TATCT-GGGT-AGGTGTC-----C-----T-TTAATATGAGAGC-TATG-T-TCTGATCTACACAGGGTCGCGCTGCTCTTCTGCTCGGATCCGCTTTCCACCAATGGATCAA
droYak3	2R:16681348-16681502 +		CACACCAAAATTCGSAATGCACGCGCAACAGGCCCTACAAATCTCAGAGSTAGTCTTCCAA-T-TAC-----TGT--A-----GAAAA-----CCATTA-T-TT-A-----TTTAAATCTTTTCAGGGAAAGCATATTTCTGCAAGATCTCTTTCCGCCCTGGATTCAA
droEre2	scaffold_4845:13556895-13557061 +		CACCTCCAAATTCGSAATGCACGCGCAACAGGCCCTACACGCACTGAGGTTAG-TTGA-TATCT-GAGG-GTATGTC-----C-----T---TCTACTATGAGAGC-TATG-T-----TCTGATATACAGGGTCGCTGCTCTTCTGCTCGGATCCGCTTTCCGCCATGGATCAA

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

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

Predicted structure



No Repeatable elements found

hide 3p reads show mid mismatch reads

Anti-sense strand reads

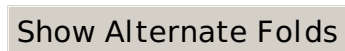
Show Alignment With Reads

Re-alignment of all predicted orthologs

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

Predicted structure



Flybase annotation

intron [Dwil\GK14881-in]; CDS [Dwil\GK14881-cds]; CDS [Dwil\GK14881-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

Anti-sense strand reads

[illegible]

No data available in table

Show Alignment With Reads

Re-alignment of all predicted orthologs

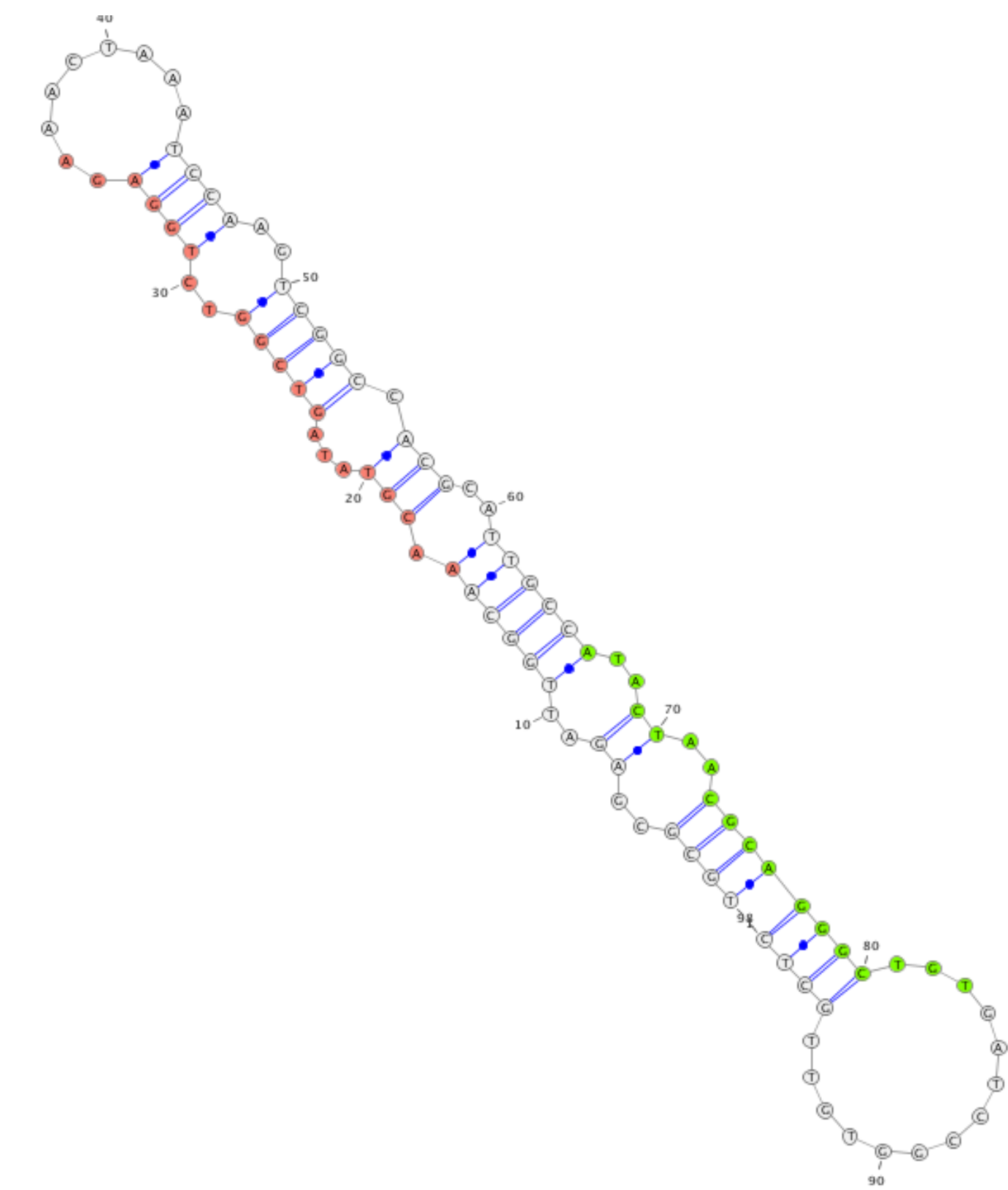
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crit_mor	0
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crit_top2	1
crit_top3	1
crit_urn	1
crit_back	1
rescue_total	1
rescue_dominant	0
rescue_known	0
rescue_confident	0
rescue_candidate	1

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dwi_5417	scf2_1100000004511:5276800-5276888 +	candidate	Canonical miRNA	CDS	[View on UCSC Genome Browser [Cornell Mirror]]

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



dwi_5417_annot [-28.4]

Show Alternate Folds

Flybase annotation

CDS [Dwif\GK17347-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

[illegible]

Anti-sense strand reads

TTCATCCGGCTCCGAGTACGGAAACGGTGACCGGTCCCGACCGGTTGCCTACTAGACGCGCTTAACCGT															M045
TTCGCATATCAGCCAGACCTCTTTGATTTAGGTTCAGCCGGTCGGTAACGC															
TAGTATTCGCTCCGACACTAGGCCACAACGAGTAAGTTTTTCTAAGCCAAC															
TCTCAAAGGCCAATGT															
(((((((.....)))))))))										Read #					female
(((((((.....)))))))))										size					body
(((((((.....)))))))))										Mismatch					
(((((((.....)))))))))										Count					
(((((((.....)))))))))										Norm					
(((((((.....)))))))))										Total					

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
drow12	ac7f1100000004511:5276750-5276938	dwi_5417	AATGAGCGGAGGCTCATGCTTTGCCATGCCCAGGGCTGGCCAAACGG---ATGATCTGCGCGAGATTGGCA AACGTAATAGTCGGTCTGGAGA AACTAAATCCAAGTCGCCACGCAATTGCC ATACTAACGAGGGCTG SATCCGGTGTGCTCATTTCAAAGA---TTCGGTTGAAGAGTTTCCGGTTACA
drow1r3	ac9aff01413049:22492152-22492343	dvi_158	AAGSAGCGGAGGGCCAGSCTTTGCCATCG CGCA SGCTGGGCC CGCG CACATGATGTCGG CG SAGATTGGCA CGGCGCGTGCTCCGCTCA TAATTAAC TAAT A CGCG CCACGCAATTGCC ATACG CACGAGGGCTG CG CGCCTGCTGCTAT CGCG CGA---TTCGGT CGA SAGTTTCC CG CTACA
drow1j3	ac9aff0146680:17099712-17099903	dmo_114	AAGSAGCGGAGGGCCAGSCTTTGCCAT CGCA SGCTGGGCC CGCG ATGCG CG SATCTCGG CG SAGATTGGCA AACGTTGCGTGCGCA TGGCCAA TAAT A CGCG CCACGCAATTGCC ATACG CACGAGGGCTG CG CGCCTGCTGCTAT CGCG CGA--- CAG GGT CGA SAGTT CG CGGTACA
drow1r2	ac9aff01415121:2023613-2023807	dgr_465	AATGAGCGGAGGGCCAGSCTTTGCCAT CGCA SGCTGGG CGCG ATGAG CG SATCTCGG CG SAGATTGGCA GGGCGTGCGTGCA TGGGCA TAAT A CGCG CCACGCAATTGCC ATACG CACGAGGGCTG CG GATCCCTGCTGCTAT CGCG CGA CGCG CGGT CGA SAGTT CG CGATTACA
dp5	XR_group6:27266746-27267454	dps_3829	AATGAGCGGAGGGCCAGTGCCTTTGCC CGCG CGAGGGCTGGCC CGCG ---AASATCTGCGCGAGATTGGCA CGGCGTGCGTGCGCTGGCA TAAC TAAT CC GGGCG AGCC CG CAGATTGCC ATACTAACGAGGGCTG GATCCCTGCTGCTAT CGCGCG CG---CTCGGTTGAAGAGTTTCCGGTACA
drow1er2	ac7f1266474:2666747-2666635	dpc_2483	AATGAGCGGAGGGCCAGTGCCTTTGCC CGCG CGAGGGCTGGCC CGCG ---AASATCTGCGCGAGATTGGCA CGGCGTGCGTGCGCTGGCA TAAC TAAT CC GGGCG AGCC CG CAGATTGCC ATACTAACGAGGGCTG GATCCCTGCTGCTAT CGCGCG CG---CTCGGTTGAAGAGTTTCCGGTACA
drow1a3	ac9aff0143337:4137395-4137583	dan_4038	AAGSAGCGGAGGGCCAGSCTTTGCC CGCG CGACAGCTGGCC CGCG ---GGATCTGCG CG SAGATTGGCA CGGCGTGCGTGCGCTG CGCA TAAT CG CT CGCGCGCC CG CGATTGCC AT CG CGCGAGGGCTG CG GATCCCTGCTGCTAT CGCG CGA---CTCGGTC CGA SAGTT CG CGGTACA
drow1p1	ac7f180000395450:265900-266088		AAGSAGCGGAGGGCCAGSCTTTGCC CGCG CGACAGCTGGCC CGCG ---GGATCTGCG CG SAGATTGGCA CGGCGTGCGTGCGCTG CGCA TAAT CG CT CGCGCGCC CG CGATTGCC AT CG CGCGAG CTC GATCCCTGCTGCTAT CGCG CGA---CTCGGTC CGA SAGTT CG CGGT CGCG
drow1k1	ac7f180000302272:666717-666905		AATGAGCGGAGGGCCAGSCTTTGCC CGCG CGA AAAA GGGCC CGCG ---AASATCTGCG CG SAGATTGGCA AACGCTGCGTGCGCA TGGCA TAAC TAATCC CTCG GGCCGCGCC CG CGATTGCC AT CG CGCGAG CTG GATCCCTGCTGCTAT CGCG CGA---TTCGGT CGA SAGTT CG CGGTACA
drow1c1	ac7f180000454048:724233-724422		AATGAGG CG AGGGCCAGSCTTTGCC CGCG GAGAA ACAG AAT GGGCC CGCG ---GGATCTGCGCGAGATTGGCA CGGCGTGCGTGCGCA TGGCA TAAC TAATCC GGGCG GGCC CG CGATTGCC ATACG CACGAGGGCTG CG GATCCCTGCTGCTAT CGCG CGA---TTCGGT CGA SAGTT CG CGGTACA
drow1e1	ac7f180000491255:1412089-1412277		AAGSAGCGGAGGGCCAGSCTTTGCC CGCG CGACAGCTGGCC CGCG ---GGATCTGCGCGAGATTGGCA CGGCGTGCGTGCGCA TGGCA TAAC TAATCC GGGCG GGCC CG CGATTGCC ATACG CACGAGGGCTG CG GATCCCTGCTGCTAT CGCG CGA---TTCGGT CGA SAGTT CG CGGT CGCG
drow1ho1	ac7f180000769477:9671151+		AAGSAGCGGAGGGCCAGSCTTTGCC CGCG CGACAGCTGGCC CGCG ---GGATCTGCGCGAGATTGGCA CGGCGTGCGTGCGCTGGCA TAAC TAAT CC GGGCG GGCC CG CGATTGCC ATACG CACGAGGGCTG CG GATCCCTGCTGCTAT CGCG CGA---TTCGGT CGA SAGTT CG CGGT CGCG
drow1b1	ac7f180000302193:2253856-2254044		AAGSAGCGGAGGGCCAGSCTTTGCC CGCG CGACAGCTGGCC CGCG ---GGATCTGCGCGAGATTGGCA CGGCGTGCGTGCGCTG CGCA TAAC TAATCC GGGCG GGCC CG CGATTGCC AT CG CG CGAGGGCTG CG GATCCCTGCTGCTAT CGCG CGA---TTCGGT CGA SAGTT CG CGGT CGCG
drow1ak1	ac7f180000415706:66147-66335		AAGSAGCGGAGGGCTCATGCTTTGCC CGCG CGACAGCTGGCC CGCG ---GGATCTGCGCGAGATTGGCA CGGCGTGCGTGCGCTGGCA TGGCA TAAT CC GGGCG GGCC CG CGATTGCC AT CG CG CGAGGGCTG CG SATCCCTGCTGCTAT CGCG CGA---CTCGGTC CGA SAGTT CG CGGT CGCG
drow1ug1	ac7f1800004039711:6101265-6101453		AAGSAGGCGGAGGCTCATGCTTTGCC CGCG CGACAG AAT GGGCC CGCG ---GGATCTGCG CG SAGATTGGCA CGGCTACGCGTGCGA TGGCA TAAT AA TAAT CG CG GGCC CG CGATTGCC AT CG CG CGAGGGCTG CG SATCCCTGCTGCTAT CGCG CGA---CTCGGTC CGA SAGTT CG CGGT CGCG
dm3	chr3k14:1301376-13013764	dme_245	AAGSAGGCGGAGGCTCATGCTTTGCC CGCG CGACAG AAT GGGCC CGCG ---GGATCTGCGCGAGATTGGCA CGGCTACGCGTGCGA TGGCA TAAT AA TAAT CG CG GGCC CG CGATTGCC AT CG CG CGAGGGCTG CG SATCCCTGCTGCTAT CGCG CGA---TTCGGT CGA SAGTT CG CGGT CGCG
drow1m2	ac112704025-12704213	dgl_32458	AAGSAGGCGGAGGCTCATGCTTTGCC CGCG CGACAG AAT GGGCC CGCG ---GGATCTGCGCGAGATTGGCA CGGCTACGCGTGCGA TGGAGAA AA AA CC GGGCG GGCC CG CGATTGCC AT CG CG CGAGGGCTG CG SATCCCTGCTGCTAT CGCG CGA---TTCGGT CGA SAGTT CG CGGT CGCG
drow1ec2	ac9aff0140158161:5185349	dye_1846	AATGAGCGGAGGGCTCATGCTTTGCC CGCG CGACAGCTGGCC CGCG ---GGATCTGCGCGAGATTGGCA CGGCTACGCGTGCGA TGGAGAA AA AA CC GGGCG GGCC CG CGATTGCC AT CG CG CGAGGGCTG CG SATCCCTGCTGCTAT CGCG CGA---TTCGGT CGA SAGTT CG CGGT CGCG
drow1ak3	ac11302479:13029667	dya_1798	AAG

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

Legend: mature star mismatch in alignment mismatch in read

Predicted structure

Ellyhaze annotation

iron [DWIGK1546-in]

hide 3p reads show mid mismatch reads

[illegible]

Re-alignment of all predicted orthologs

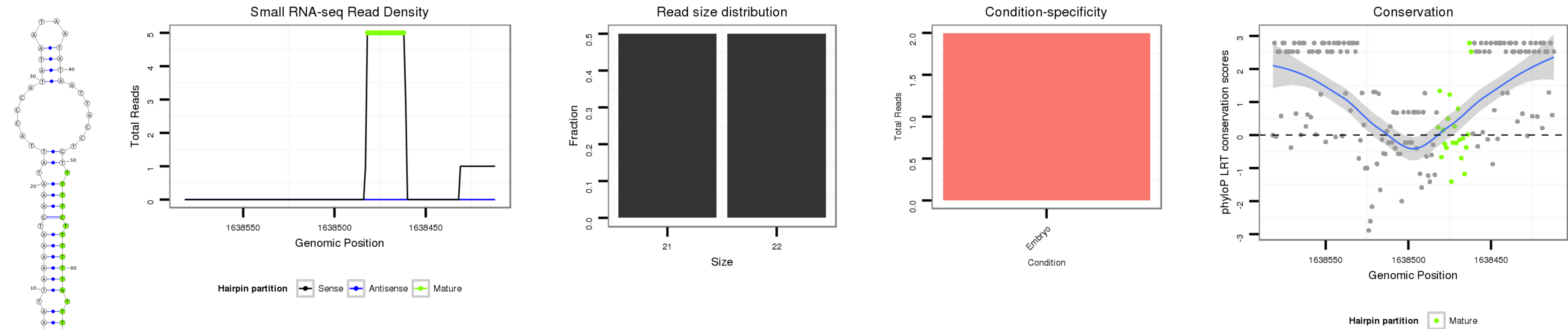
Species	Coordinate	ID	Alignment
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PASS/FAIL

rescue.candidate 9

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Show Alternate Folds

Flybase annotation

intron [Dwil\GK23609-in]; CDS [Dwil\GK23609-cds]; CDS [Dwil\GK23609-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

[illegible]

Anti-sense strand reads

GAACCTTACCGGGTACTCATGGCTGTCCGATAGTCGTATACTACGTTTTCATTTCATTAATTTTTACTTTTATAATGGGTATATTATTATATTAATGGACA AAAAGAAAAAATAACGAATC TAGACTCCAGGATTAGTTTACGTACGTCCTGTGTTCACCAAAACCGACG															M045
*****.(((((((.(((((((.(((.((.....(((.....))).....)).)))..)))))).)))))).*****										Read #	Hit	Total			female
										size	Mismatch	Count	Norm	Total	body

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droWi12	scf2_1100000004837:1638412-1638582_-	dwi_2287	CTTGGAAATGGCCCATGAGTACCGACACGGCTATCAGCATATGATGCAAAAGTAAGT-----AATTA-AA---AATGAAAT-----ATTACCATATAATAATA-----TAAT-----T-----ACCTGTGTTTCTT-----T---TTTATTGGCTTAGATCTGAGGTCTCAATCAAATGCATGCAAGGCACACAAGTGGTTGGCTGC
droVir3	scaffold_13049:18569080-18569245_+		CTGGCATGGCCAGAGATACCGACATGGCTACGAGCATATGATGCAAAAGTAGT-----GGTCAA---TAAAA---T-----A-----TTCAA---TGCAG-AGTGATTGATCAAATATCAA---TCAA---GAC-CCAACAGATCTGAGGTCTCGTAAGTGCATGCAAGGCACACAAGTGGTTGGCTGC
droMoj3	scaffold_6680:12677985-12678140_-		TTGGCATGGCCAGAGATATCGACATGGCTATCAGCATATGATGCAAAAGTAGT---GAAAT---ATAA---T-----AATATAT---AAAT---ATAATATATTATC---AT---GCACCCCAACAGGCTGAGGTCTCATTAAGTGCATGCAAGGCACACAAGTGGTTGGCTGC
droGr12	scaffold_15110:19045534-19045702_+		CTGGCATGGCCAGAGATACAGCATGGATCAGCATATGCTCAAGTAGT-----AATTC-AATCAATATATCA-----A-----CTCCA---A-AGCAATTTAAACTTACAAATTATA---GAC-ATAACAGATCGAGGTCTTATCAAAGTGCATGCAAGGCACACAAGTGGTTGGCTGC
dp5	XR_group8:8197302-8197471_-		CTGGCATGGCCCAAGTACAGCATGGCTACGAGCATATGTGCAAGTAAGC-----ATA-CA---CAGCAGCT---CCCGGGCGAGCAAGAA---CTAT---T---CTTAATTACAA---T---CTTTTCTTACAGATCGAAGTCTTATCAAAGTGCATGCAAGGCACCAAGTGGTGGCTGC
droPer2	scaffold_40:388400-388569_-		CTGGCATGGCCCAAGTACAGCATGGCTACGAGCATATGTGCAAGTAAGC---ATA-CA---CAGCAGCT---CCCGGGATGGCAAGAA---CTAT---T---CTTAATTACAA---T---CTTTTCTTACAGATCGAAGTCTTATCAAAGTGCATGCAAGGCACCAAGTGGTGGCTGC
droAna3	scaffold_13337:11129462-11129617_-		CTGGAAATGGCCAGAGATACAGCAGCGCTACAGCATATGATGCAAAAGTATATGTGATTATCTTACAGCCAT---T-----T-----C-----ATAA-AGATGATCAAA---T---ACAGCCTTGACAGTCCAGCTCTGGTAAGTGCATGCAAGGCACCAAGTGGTGGCTGC
droBip1	scf7180000396569:260451-260606_+		CTGGAAATGGCCAGAGATACAGCAGCGCTACAGCATATGATGCAAAAGTATATGTGATTATCTTAAAGCCATC---T-----T-----C-----ATAA-ACAAGATCAAA---T---GCAGCTTGACAGTCCAGCTCTCTGGTAAGTGCATGCAAGGCACCAAGTGGTGGCTGC
droK1k1	scf7180000302441:3506425-3506590_-		CTGGCATGGCCAGAGATACAGCATGGCTACAGCATATGATGCAAAAGTAAGT-----CCCGT-AAATATAGCCACACCCCTGGTA-----T-----CTTTA---TACCG-AAA-----T-----TTCATCTTTTGAGATCCAGTCTCATCAAAGTGCATGCAAGGCACCAAGTGGTGGCTGC
droFic1	scf7180000454065:1276455-1276610_-		TAAGCATGGCCCAAGTACAGCAGCGCTATCAGCATATGTGCAAAAGTAGT-----TAGA---AAAA---T-----CTTTTC---AAGA-CCGCTTATCACCACC-----T---TATCTGGCAGTCCAGTCTCATCAAAGTGCATGCAAGGCACCAAGTGGTGGCTGC
droEl1e	scf7180000491193:5155285-5155438_-		TTGGCATGGCCCAAGTACAGCAGCGCTACAGCATATGTGCAAAAGTAAGA---TATAGA---AAAG---T-----TTCCCC---AAGA-ATACTAATCA---T---TTCAATTATCGAGATCCAGTCTCATCAAAGTGCATGCAAGGCACCAAGTGGTGGCTGC
droRho1	scf7180000768856:49340-49494_+		CTGGCATGGCCCATGAGTACAGCAGCGCTACAGCATATGTGCAAAAGTAGA---CACAAA---AAGG---T-----TTTCCC---ATGA-ATACATACTCA---T---TTAAATTCTGCAGATCCAGTCTAATCAAAGTGCATGCAAGGCACCAAGTGGTGGCTGC
droBia1	scf7180000302193:5275099-5275257_+		CTAGCATGGCCCAAGATATAGCAGCGCTACAGCATATGTGCAAAAGTAGT---TTCGC---TATG---T-----TTCTTCC---AAGT-AGTTAAATTACAA---TTGAATTCTCTGAGATCCAGTCTCATCAAAGTGCATGCAAGGCACCAAGTGGTGGCTGC
droTak1	scf7180000415420:137652-137812_-		TTGGCATGGCCCAAGTACAGCATGGCTACGAGCATATGTGCAAAAGTAGT-----CGTGT---TATG---T-----CTTTTCC---A-AGGAATCCCTTTTACAC---T---CTGAATTCTTGAGATCCAGTCTCATCAAAGTGCATGCAAGGCACCAAGTGGTGGCTGC
droEug1	scf7180000409711:5218590-5218748_-		TTGGCATGGCCCAAGTATAGCAGCGCTATCAGCATATGTGCAAAAGTAGT---CTA-GT---TACTA---T-----ATTCTGT---AAAA-GAAGTTACTTATGC---T---ATGATTAATCTGCAGATCCAGTCTCATCAAAGTGCATGCAAGGCACCAAGTGGTGGCTGC
dm3	chr3L:20775381-20775540_-		TTGGCATGGCCCAAGTACAGCAGCGCTATCAGCATATGTGCAAAAGTAAGT---TAGT-AAACTTATGC---T-----TTTTCCC---ATC-ATACTTATTAACTCC---GTAAAT---TCCAGTCTGATCTCATCAAAGTGCATGCAAGGCACCAAGTGGTGGCTGC
droSim2	31:20336827-20336987_-		TTGGCATGGCCCAAGTACAGCAGCGCTATCAGCATATGTGCAAAAGTAGGT---TAA-A---CTCA---T-----CTTTCCCTTCA---AGTC-ATACTTATTAACTC---GCTAAATA-CCCCAGGCTGATCTCATCAAAGTGCATGCAAGGCACCAAGTGGTGGCTGC
droSec2	scaffold_11:674476-674637_-		TTGGCATGGCCCAAGTACAGCAGCGCTATCAGCATATGTGCAAAAGTAGGT---TAA-A---CTCA---T-----CTTTCCCTTCA---ATTC-ATACTTATTAACTC---GCTAAATCCCAGGCTGATCTCATCAAAGTGCATGCAAGGCACCAAGTGGTGGCTGC
droYak3	3L:19774545-19774703_+		TTGGCATGGCCAGAGTACAGCAGCGCTATCAGCATATGTGCAAAAGTAGGT---TAGGT---TATC---T-----CTTCCC---ATC-ATACTTATCAAC---CTTCAATG-CCGAGGCTGATCTCATCAAAGTGCATGCAAGGCACCAAGTGGTGGCTGC
droEr2e	scaffold_4784:20466176-20466334_-		TTGGCATGGCCCAAGTACAGCAGCGCTATCAGCATATGTGCAAAAGTAGT---TAGGT---TATC---T-----CTTCCC---ATC-ATACTTATTACAC---GTAAATTCCCAGGCTGATCTCATCAAAGTGCATGCAAGGCACCAAGTGGTGGCTGC

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

Predicted structure



Flybase annotation

intron [Dwil\GK21972-in]; CDS [Dwil\GK21972-cds]; CDS [Dwil\GK21972-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 10:37 PM

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