

Legend: mature star mismatch in alignment mismatch in read

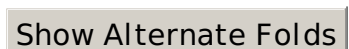
intergenic

No Repeatable elements found

hide 3p reads show mid mismatch reads

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Predicted structure



Flybase annotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

Anti-sense strand reads

No data available in table

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droSec2	scafFold_8:19169075-1916923	dse_57	T---TGCGT-TGTTTTATGGTAATCGG-----CGCATAACAA-----AAACC-ACA-CTACT-----A--CCA-----TCG-----CACC-----AC--CCAA ^{CC} CCACCGTGTGTCTT-----GGTGACGA-----GGGTGG-AG-----TG---GTGCGGTGG- ⁺ GTGTGGCATGGCATTTCGAATTAAC ⁺ TGGGCATAGTCCTTAA-AATTTTAA
droSim2	chr13345499-18345669+		T---TGCGT-TGTTTTATGGTAATCGG-----CGCATAACAA-----AAACC-ACA-CTAC ⁺ C-----A--CCGA-- ⁺ CCGCA ⁺ ACCAC ⁺ ACCCGC ⁺ -----ACC-----CCAA ^{CC} CCACCGTGTGTCTT-----GGTGCGCATGTCATTGSAATTAAC ⁺ TGGGCATAGTCCTTAA-AATTTTAA
dm3	chr36:18804948-18805102+		T---TGCGT-TGTTTTATGGTAATCGG-----CGCATAACAA-----AAACC-ACA- ⁺ CA ⁺ C-----A--CCGA ⁺ ACACGCA ⁺ CA ⁺ -----ACC-----CC ⁺ CA ^{CC} ACCCACCGTGTGTCTT-----GGTGCGCATGTCATTGSAATTAAC ⁺ TGGGCATAGTCCTTAA-AATTTTAA
droBre2	scafFold_4820:9263423-9263523		T---TGCGT-TGTTTTATGGTAATCGG-----CGCATAACAA-----A ⁺ ACC-ACA-CTAC ⁺ C-----A--CCG ⁺ CA ^{CC} CGCCGC ⁺ CA ⁺ CCGC ⁺ -----A ⁺ A-----C ⁺ CA ^{CC} CCACCGTGTGTCTT-----AG ⁺ GG ⁺ AG ⁺ GTGGGCATGGCATTGSAATTAAC ⁺ TGGGCATAGTCCTTAA-AATTTTAA
droYaK3	chr1364706-1364851+		T---TGCGT-TGTTTTATGGTAATCGG-----CGCATAACAA-----AAACC-ACA-CTAC ⁺ CA ⁺ -----C ⁺ CC ⁺ CGCA ⁺ C ⁺ -----AC ⁺ CC ⁺ CA ^{CC} CCACCGTGTGTCTT-----GGTGCGCATGTCATTGSAATTAAC ⁺ TGGGCATAGTCCTTAA-AATTTTAA
droEug1	scaf7180000403768:965430-965604		⁺ CGTGGCTCGTTTTATGGTAATCGG-----CGCATAACAA-----AAACC-ACA-TAC ⁺ CG ⁺ -----T ⁺ CG ⁺ CGCC ⁺ -----T ⁺ T ⁺ GC ⁺ -----CG ⁺ CG ^{CC} ATACCGTGTGTCTT-----AGAG ⁺ -----TTTGGCTCAA ⁺ AA ⁺ TA ⁺ AG ⁺ AGGG ⁺ GA ⁺ -----AA ⁺ CC ⁺ CG ⁺ CT ⁺ GTGGCATGGCATTGSAATTAAC ⁺ TGGGCATAGTCCTTAA-AATTTTAA
droBlal	scaf7180000302402:4896225-4896405		T---TGCGT-TGTTTTATGGTAATCGG-----CGCATAACAA-----AAACC- ⁺ CA ⁺ TAC ⁺ GCT ⁺ -----CAG ⁺ -CA ⁺ CAGCCC ⁺ -----CCGCCCC ⁺ TC ⁺ -----C ⁺ CG ⁺ T ⁺ GCC ⁺ CT ⁺ GCCCGGG ⁺ CC ⁺ CG ^{CC} CCACCGTGTGTCTT-----AG ⁺ GG ⁺ CT ⁺ -----C ⁺ AG ⁺ -----TG ⁺ GG ⁺ CG ⁺ GTGGCATGGCATTGSAATTAAC ⁺ TGGGCATAGTCCTTAA-AATTTTAA
droTak1	scaf7180000415400:68770-68942+		T---TGCGT-TGTTTTATGGTAATCGG-----CGCATAACAA-----AAACC-ACA-TAC ⁺ GG ⁺ -----T ⁺ CG ⁺ C ⁺ TGCC ⁺ C ⁺ C ⁺ A ⁺ -----A ⁺ TA ⁺ -----G ⁺ CC ⁺ CG ^{CC} CCACCGTGTGTCTT-----TAGAGAGCG ⁺ -----GCG ⁺ TAGAGGAG ⁺ -----TG ⁺ GG ⁺ CG ⁺ GTGGGCATGGCATTGSAATTAAC ⁺ TGGGCATAGTCCTTAA-AATTTTAA
droEle1	scaf7180000490453:54167-54337+		T---TGCGT-TGTTTTATGGTAATCGG-----CGCATAACAA-----AAACC-ACA-TAC ⁺ GG ⁺ -----T ⁺ CG ⁺ C ⁺ TGCC ⁺ C ⁺ C ⁺ G ⁺ -----AGCT ⁺ -----TTT ⁺ -----G ⁺ CC ⁺ CG ^{CC} CCACCGTGTGTCTTGTGTCTT-----GAA ⁺ -AGTT ⁺ -----ACG ⁺ -----TG ⁺ GG ⁺ CG ⁺ GTGGGCATGGCATTGSAATTAAC ⁺ TGGGCATAGTCCTTAA-AATTTTAA
droRho1	scaf7180000780164:127129-127295		T---TGCGT-TGTTTTATGGTAATCGG-----CGCATAACAA-----AAACC-ACA-TAC ⁺ GG ⁺ -----T ⁺ CG ⁺ C ⁺ TGCC ⁺ CG ⁺ G ⁺ -----AGCT ⁺ -----C ⁺ G ⁺ -----G ⁺ CC ⁺ CG ^{CC} CCACCGTGTGTCTTGTGTCTT-----TAGCGAGGT ⁺ -----GCC ⁺ -----T ⁺ G ⁺ GTG ⁺ CG ⁺ A ⁺ GTGGCATGGCATTGSAATTAAC ⁺ TGGGCATAGTCCTTAA-AATTTTAA
droFlc1	scaf7180000454055:12098-12281		T---TGCGT-TGTTTTATGGTAATCGG-----CGCATAACAA-----AAACC-ACA-TAC ⁺ GG ⁺ -----T ⁺ CG ⁺ C ⁺ TGCC ⁺ CTC ⁺ G ⁺ -----AGCT ⁺ -----CTT ⁺ -----G ⁺ CC ⁺ CG ^{CC} CCACCGTGTGTCTT-----TAGCGCGCAT ⁺ -----GCC ⁺ TGGGCGAGACGG ⁺ GTTTC ⁺ TCGG ⁺ CG ⁺ -----GTGTGGCATGGCATTGSAATTAAC ⁺ TGGGCATAGTCCTTAA-AATTTTAA
droKkl	scaf7180000302388:436606-436690		T---TAGCT-TGTTTTATGGTAATCGG-----CGCATAACAA-----AAACC-ACA-TAC ⁺ GCTTC ⁺ CGCCAG ⁺ -CA ⁺ GCCC ⁺ -T ⁺ -----CGAGTCTCGAGCT ⁺ G ⁺ -----TAGTCCAGTAGCCCGGGGAGTGC ⁺ CCACCGTGTGTCTT-----TAGG ⁺ -----C ⁺ G ⁺ -----TG ⁺ GG ⁺ AA ⁺ G ⁺ -----GTGTGGCATGGCATTGSAATTAAC ⁺ TGGGCATAGTCCTTAA-AATTTTAA
droAna3	scafFold_13340:12516216-12516419		T---TA ⁺ GS ⁺ -TGTTTTATGGTAATCGG-----CGCATAACAA-----AAACC-ACA-TAC ⁺ GCTCT ⁺ CGCCAG ⁺ -CG ⁺ GCCC ⁺ -T ⁺ -----TAGAGTCTCGAGCTTTGGGAGTCA ⁺ T ⁺ -----GCCAGCCCCA ⁺ CA ⁺ -TC ⁺ CG ^{CC} CCACCGTGTGTCTTCTGTGGCTTTGAGGGGGTGGGCTTT-----GGA ⁺ GTGGGCATGGCATTGSAATTAAC ⁺ TGGGCATAGTCCTTAA-AATTTTAA
droBip1	scaf7180000396691:1405174-1405368		T---TAGCT-TGTTTTATGGTAATCGG-----CGCATAACAA-----AAACC-ACA-TAC ⁺ GCTCCAGCCAG ⁺ -C ⁺ GGGCC ⁺ -T ⁺ -----TAGATTTTGAGCTCTGGGAGCTCA ⁺ T ⁺ -----GCCAGCTTACAC ⁺ CA ⁺ -TC ⁺ CG ^{CC} CCACCGTGTGTCTTCTGTGGCTTTGAGGGGGTGGGCTTT-----GGA ⁺ GTGGGCATGGCATTGSAATTAAC ⁺ TGGGCATAGTCCTTAA-AATTTTAA
dp5	2:6076985-6077158		T---TAGCT-TGTTTTATGGTAATCGG-----CGCATAACAA-----AAACC-ACA-TAC ⁺ CG ⁺ -CA ⁺ CGGCCCA ⁺ -----CAGC ⁺ A ⁺ -----CATACCTCGAGTGC ⁺ AT ⁺ AGCCAGGGTGA ⁺ -GG ⁺ CCACCGTGTGTCTTGTGTCTT-----GC ⁺ -----CA ⁺ GTGGCATGTCATTGSAATTAAC ⁺ TGGGCATAGTCCTTAA-AATTTTAA
droPer2	scafFold_19:1815855-1816023		T---TAGCT-CA ⁺ TTTTATGGTAATCGG-----CGCATTC ⁺ GA ⁺ -----AAGCC-ACA-TAC ⁺ CG ⁺ -G ⁺ CA ⁺ CGGCCA ⁺ -----CAGC ⁺ A ⁺ -----CATACCTCGAGAC ⁺ AT ⁺ AGCCAGGGTGA ⁺ -GG ⁺ CCACCGTGTGTCTTGTGTCTT-----GC ⁺ -----G ⁺ GTGGCATGGCATTGSAATTAAC ⁺ TGGGCATAGTCCTTAA-AATTTTAA
droW12	scaf2_110000004902:1227520-1227676		T---GA ⁺ CT-TGTTTTATCGTAATCGG-----CGCATAACAA-----AAAG ⁺ CA ⁺ -A ⁺ GA ⁺ AAAAA ⁺ AAACCGCC ⁺ -CA ⁺ CGCCC ⁺ -T ⁺ -----A ⁺ A ⁺ -CA ⁺ AA ^{CC} CCACCGTGTGTCTTGTGTCTT-----A ⁺ -----A ⁺ C ⁺

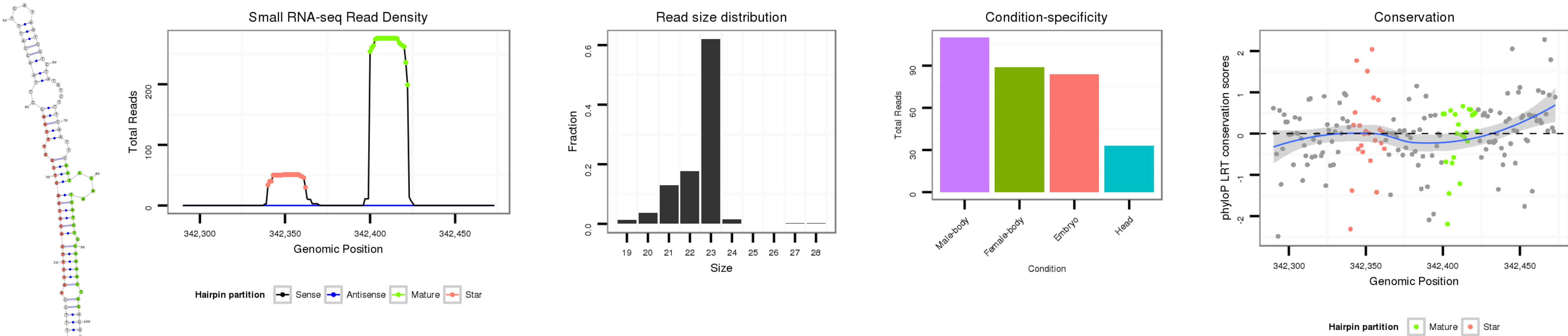
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	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	0
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

Legend: mature star mismatch in alignment mismatch in read

Predicted structure

Predicted structure



Show Alternate Folds

Flybase annotation

intron [Dsec\GM21724-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

[illegible]

Anti-sense strand reads

[illegible]

Show Alignment With Reads

Re-alignment of all predicted orthologs

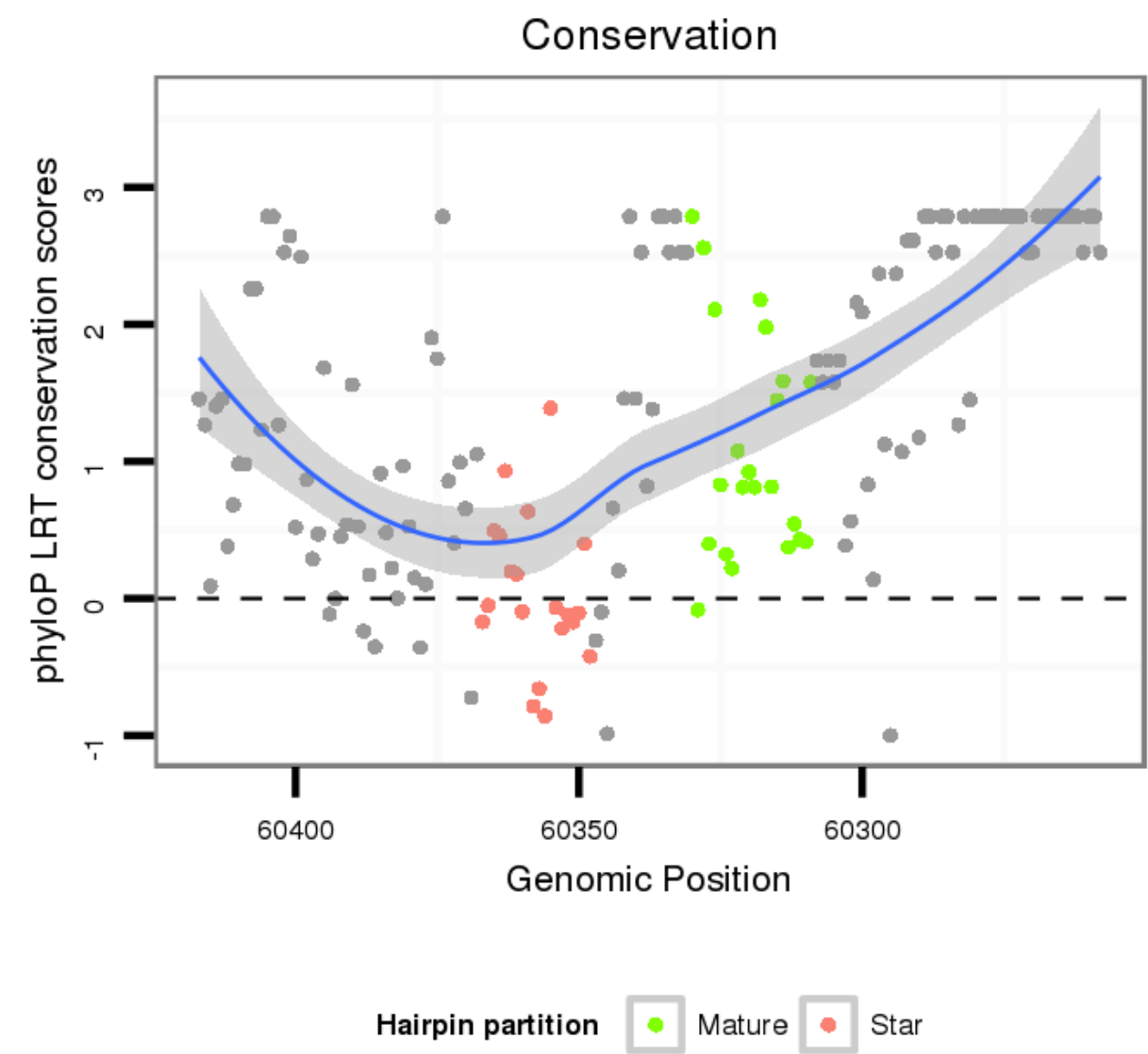
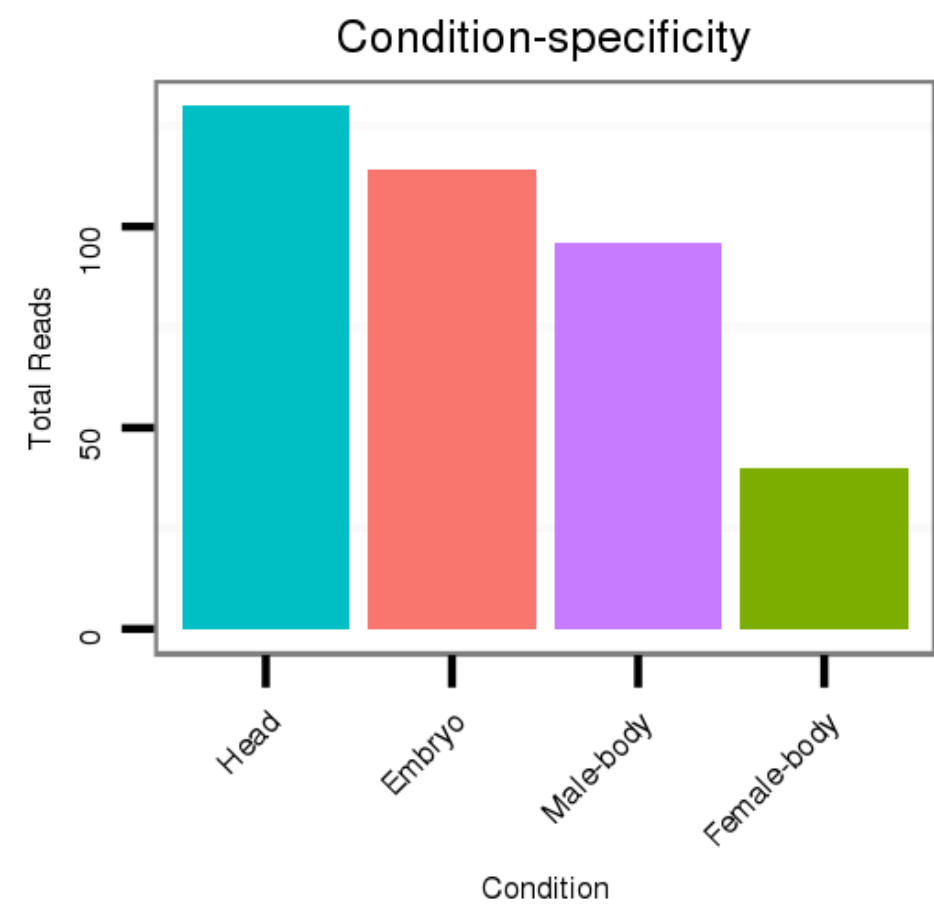
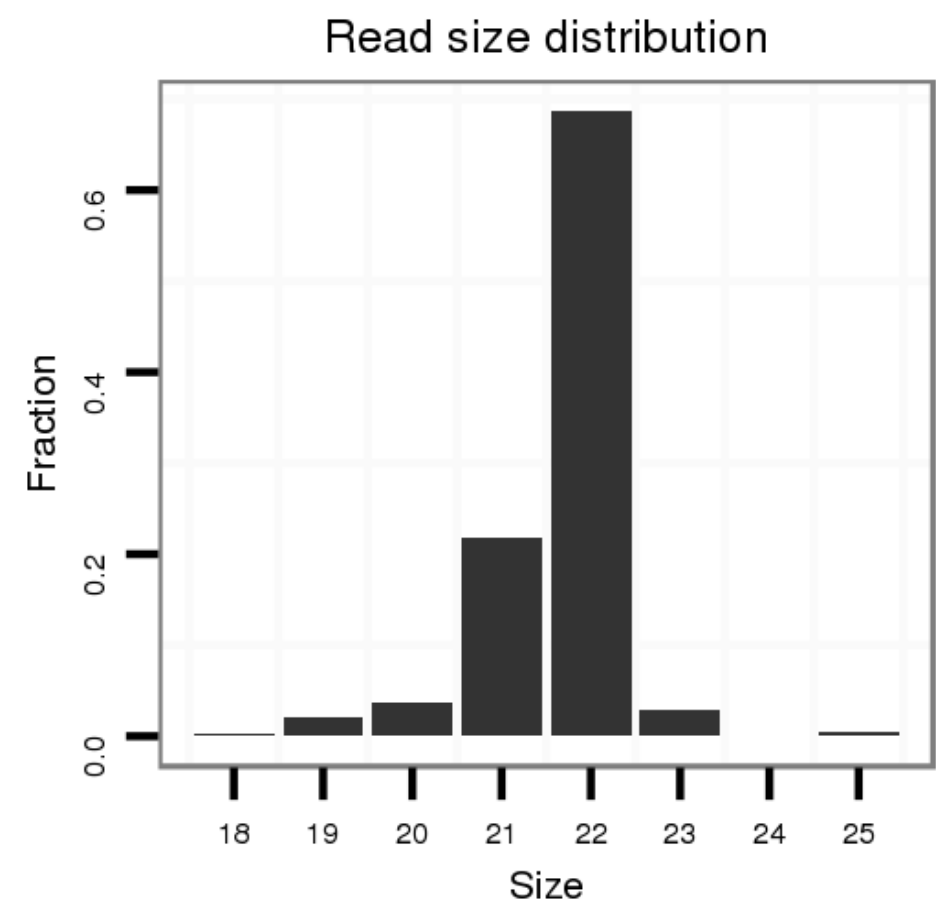
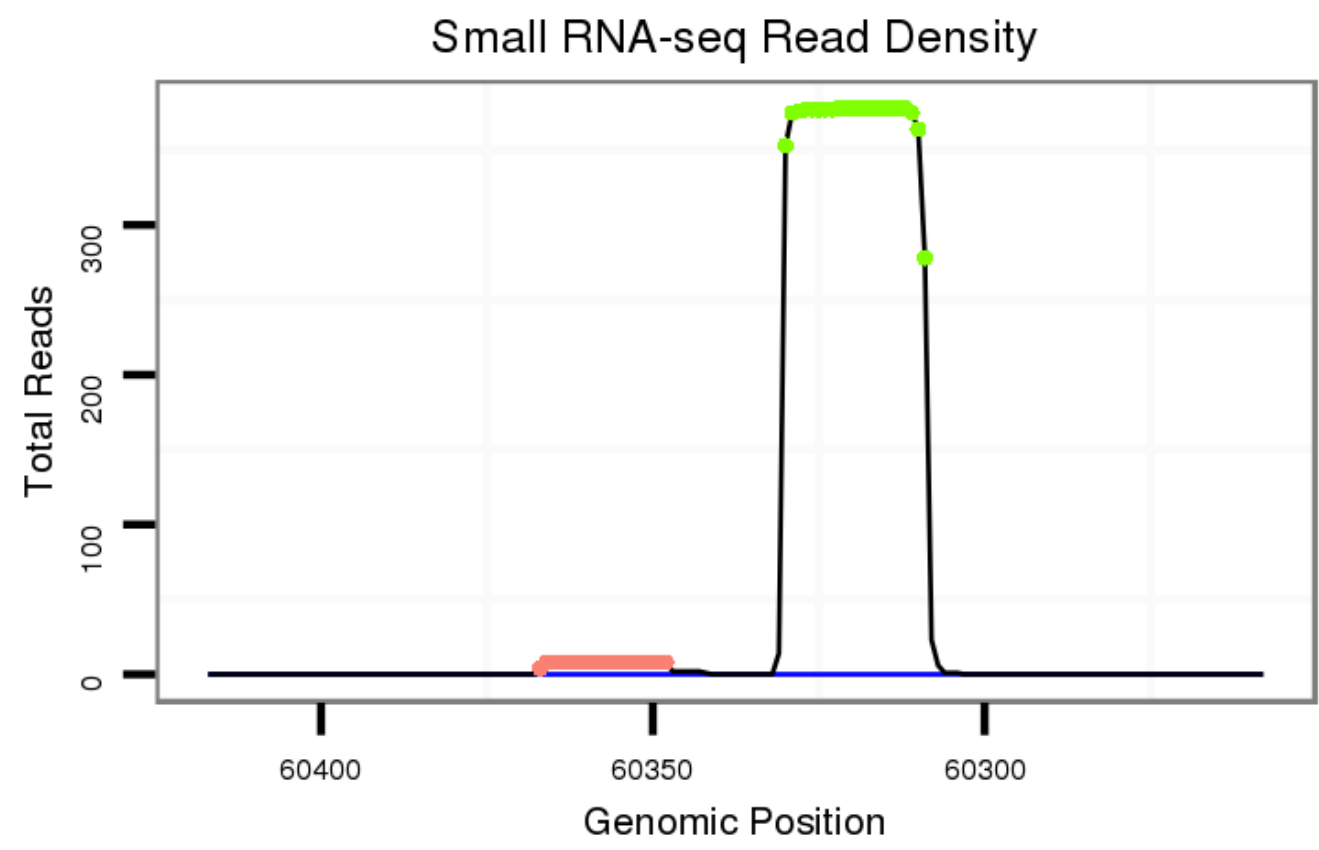
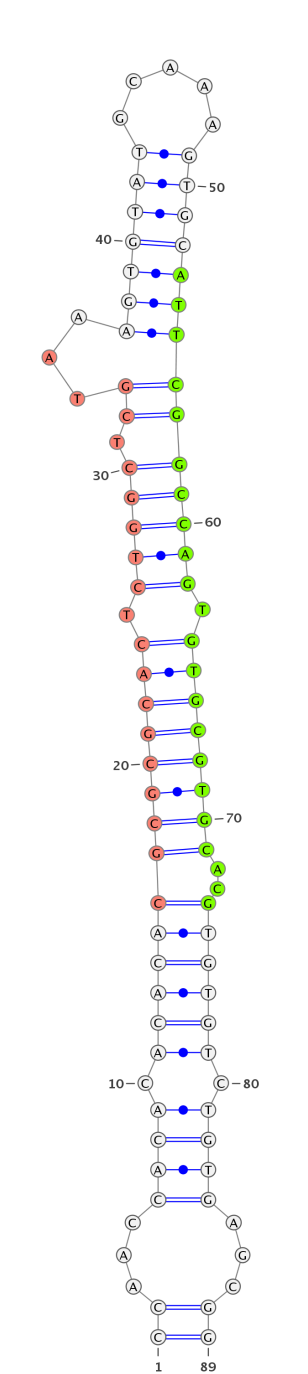
[illegible]

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

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Show Alternate Folds

Flybase annotation

utr5 [utr5_plus_11391]

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
drosSec2	scaf01d_25:60258-60417_-	dse_74	TCA-AA-----C-----TATATGTA--CG-TCATGC-----ACCATACACCCACCAA--CCAC-----A-----CAC-----A-----CA-----CGCGC-----GCACCTCG-----GTCGTA-AAGTGTATGCAAAGTGCATT-CGG-----CCAGTGTGCGTGCAAGTGTGTCTG-----GAGCGGCAACTACTTCGA-AATTTATTTTCGAATAATAGTAGTAA
drosSim1	1r:567258-556742_-		TCA-AA-----C-----TATATGTA--CG-TCATGC-----ACCATACACCCACCAA--CCAC-----A-----CAC-----A-----CA-----CA-A-A-CAAGCGACCTCTG-----GTCGTA-AAGTGTATGCAAAGTGCATT-G-----CCAGTGTGCGTGCAAGTGTGTCTG-----GAGCGGCAACTACTTCGA-AATTTATTTTCGAATAATAGTAGTAA
dm3	chr3R:15716366-15717134_+	dme_394	TCA-AA-----C-----TATATGTA--CG-TCATGC--ACGACCATACACCCACCAA-C-CCAC-----A-----CAC-----A-----TA-----CA-A-A-A-CAAGCGACCTCTG-----GTCGTA-AAGTGTATGCAAAGTGCATT-G-----CCAGTGTGCGTGCAAGTGTGTCTG-----GAGCGGCAACTACTTCGA-AATTTATTTTCGAATAATAGTAGTAA
drosE2	scaf01d_4770:5945777-5945936_-		TCA-AA-----C-----TATATGTA--CG-TCATGC-----ACCATACACCCGCGCAA--CCAC-----A-----CAC-----A-----CA-----CA-A-A-CAAGCGACCTCTG-----GTCGTA-AAGTGTATGCAAAGTGCATT-G-----GAGTGTGCGTGCAAGTGTGTCTG-----GAGCGGCAACTACTTCGA-AATTTATTTTCGAATAATAGTAGTAA
drosYak3	3R:4489431-4489592_+		TCA-AA-----C-----TATATGTA--CG-TCATGC-----ACCATACACCCACCAA--CCAC-----A-----CAC-----A-----CA-----CATAAGG-A-A-CAATG-----GTCGTA-AAGTGTATGCAAAGTGCATT-G-----GAGTGTGCGTGCAAGTGTGTCTG-----GAGCGGCAACTACTTCGA-AATTTATTTTCGAATAATAGTAGTAA
drosUg1	scaf1180000403804:2026281-2026440_+		TCA-AA-----C-----TATATGTA--CG-TCATAC-----ATTATACACCCACCAA--AAAC-----A-----CAC-----C-----AA-----CGG-A-A----GAG-A-----GGAATAA-AA-CATATGCAAAGTGCATTTCG-----GAGTGTGCGTGCAAGTGTGTCTG-----GAGCGCAACTACTTCGA-AATTTATTTTCGAATAATAGTAGTAA
drosBl1	scaf1180000302402:1493029-1493172_+		TCA-AA-----C-----TATATGTA--CG-TCA-CAC-----ATTGACACCCACCAA--AAAC-----A-----CAC-----C-----CA-----CA-A-ACG-----G-GG-----GGA-AAGG-G-CATATGCAAAGTGCATT-G-----GAGTGTGCGTGCAAGTGTGTCTG-----GCGCGCAACTACTTCGA-AATTTATTTTCGAATAATAGTAGTAA
drosTak1	scaf1180000415710:91436-91439_-		TCA-AA-----C-----TATATGTA--CG-TCATAC-----ATTATACACCCACCAA--AAAC-----A-----CAC-----A-----CG-----CA-A-A-A-C-----TGTGCG-----GGAATAA-AA-CATATGCAAAGTGCATT-G-----GAGTGTGCGTGCAAGTGTGTCTG-----GAGCGCAACTACTTCGA-AATTTATTTTCGAATAATAGTAGTAA
drosEle1	scaf1180000491008:1190017-1190148_-		TCA-AA-----C-----TATATGTA--CG-TCATAC-----ACCCACCA-CAC-----A-----A-----A-----A-----TA-A-A----SA-A-G-----GGAATAA-AA-CATATGCAAAGTGCATT-G-----GAGTGTGCGTGCAAGTGTGTCTG-----GAGCGCAACTACTTCGA-AATTTATTTTCGAATAATAGTAGTAA
drosRho1	scaf1180000780274:113407-113532_-		TCA-AA-----C-----TATATGTA--CG-TCATAC-----ACCCACCA-CAC-----A-----A-----A-----A-----TA-A-A----G-----GGAATAA-AA-CATATGCAAAGTGCATT-G-----GAGTGTGCGTGCAAGTGTGTCTG-----GAGCGCAACTACTTCGA-AATTTATTTTCGAATAATAGTAGTAA
drosFic1	scaf1180000454126:741120-741239_+		TCA-AA-----C-----TATATGTA--CG-TCATAC-----A-----C-----C-----C-----A-----A-----A-----A-----TA-CCATA-----CAATATGCAAAGTGCATT-G-----GAGTGTGCGTGCAAGTGTGTCTG-----GAGCGCAACTACTTCGA-AATTTATTTTCGAATAATAGTAGTAA
drosKik1	scaf1180000297926:99783-99925_-		TCA-AACTATACAT-----A-----CATATGTA--CG-TCATAC-----AGGACACCA-CAG-CAC-----A-----A-----A-----A-----GA-CA-A-A-A-C-----C-----G-----CGC-G-CATATGCAAAGTGCATT-G-----TGT-----TGTGTG-----GTCGCAACTACTTCGA-AATTTATTTTCGAATAATAGTAGTAA
drosAna3	scaf01d_13340:2298317-2298475_+		TTCGAA-----A-----TATATGTA--CG-TCATACGCACACATA-----A-----C-----ACAC-----GC-----ACACACT-----T-----GTAGAACATACA-CAGAGT-G-CATATGCAAAGTGCATT-A-----TG-ACA-GCGATCA-TGTGTG-----GCGCGCAACTACTTCGA-AATTTATTTTCGAATAATAGTAGTAA
drosBip1	scaf1180000396712:2043676-2043840_-		TTCGAAATATAC-----A-----TATATGTA--CG-TCATAC-----GACACACAC-----ACAGC-----CAC-----ACACACT-----T-----GTAGAACATACA-CAGAGT-G-CATATGCAAAGTGCATT-A-----TG-ACA-GCGATCA-TGTGTGA-----GCGCGCAACTACTTCGA-AATTTATTTTCGAATAATAGTAGTAA
dp5	2:26295161-26295316_-		TTC-AA-----A-----TATATGTA--C-----ATGCA-----CAGACACACACCGA-----GCACACACACT-----TAG-GGAGT-----GGGAGACAGAC-----ATGTCATATGCAAAGTGCATT-A-AAGCGGAATGAGAAAGTGTGCGTG-----G-----GTACTTCGA-AATTTATTTTCGAATAATAGTAGTAA
drosPer2	scaf01d_6:1625043-1625196_-		TTC-AA-----A-----TATATGTA--C-----ATGCA-----CAGACACACACCGA-----GCACACACACT-----TAG-GGAGT-----GGGAGACAGAC-----ATGTCATATGCAAAGTGCATT-A-AAGCGGAATGAGAAAGTGTGCGTG-----G-----GTACTTCGA-AATTTATTTTCGAATAATAGTAGTAA
drosW12	scaf2_1100000004921:4096662-4096809_-		TCA-ACGATATACACATCTAT-----TATATGTA--CGACATATAC-----ATAGCAATTCAT-----A-----TGCGCAT-----A-----CA-----A-----TA-A-A-TATAGTAAAT-----GCTGTA-AATGTATGCAAAGTGCATT-----GTCGCAACTACTTCGA-AATTTATTTTCGAATAATAGTAGTAA
drosVir3	scaf01d_12855:7419894-7420990_+		TCC-AAATATATAC-----AC-----G-----AAGCGCGACCTC-----A-----ATGCA-----CACACAC-----A-----CAC-----A-----CA-----CA-A-A-CAC-----TCAACA-G-----AT-----AASCAGATATGCAAAGTGCATT-A-----AAAGTGTG-----GCAAGCAGCAGCGAAGCAGCAGCAACAGCGCC-----GCAGCAGCAGCGCAGCGCGGCGCGGCAACTACTTCGA-AATTTATTTTCGAATAATAGTAGTAA
drosMoJ3	scaf01d_6340:25230849-25231091_+		TCC-AAATATATAC-----AC-----G-----AAGCGCGAC-----A-----TCCCATGCA-----A-----C-----CAGCTC-----A-----CA-----TA-----A-----G-CAGCA-TTAAAGTGCATT-A-----AAAGTGTG-----GCAAGCAGCAGCGAAGCAGCAGCAGCAGCGTCAAGCGCGCGCAGCGCGCTGAGGAGCGCAACTACTTCGA-AATTTATTTTCGAATAATAGTAGTAA
drosGr12	scaf01d_15074:5441151-5441334_-		TCA-CAATATATAC-----AC-----G-----AAGCGCGACCTC-----A-----TCCCATGCA-----A-----CACACAT-----A-----C-----CA-A-A-CAC-----ATGCACAT-----TATAT-TTCACTATGCAAAGTGCATT-A-----AGAGTGTG-----GCAAGCAGCAGCGAAGCAGCAACAGCAGCAGC-----A-----A-----GCGGCGCGGCAACTACTTCGA-AATTTATTTTCGAATAATAGTAGTAA

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

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

Predicted structure



Anti-sense strand reads

Show Alignment With Reads

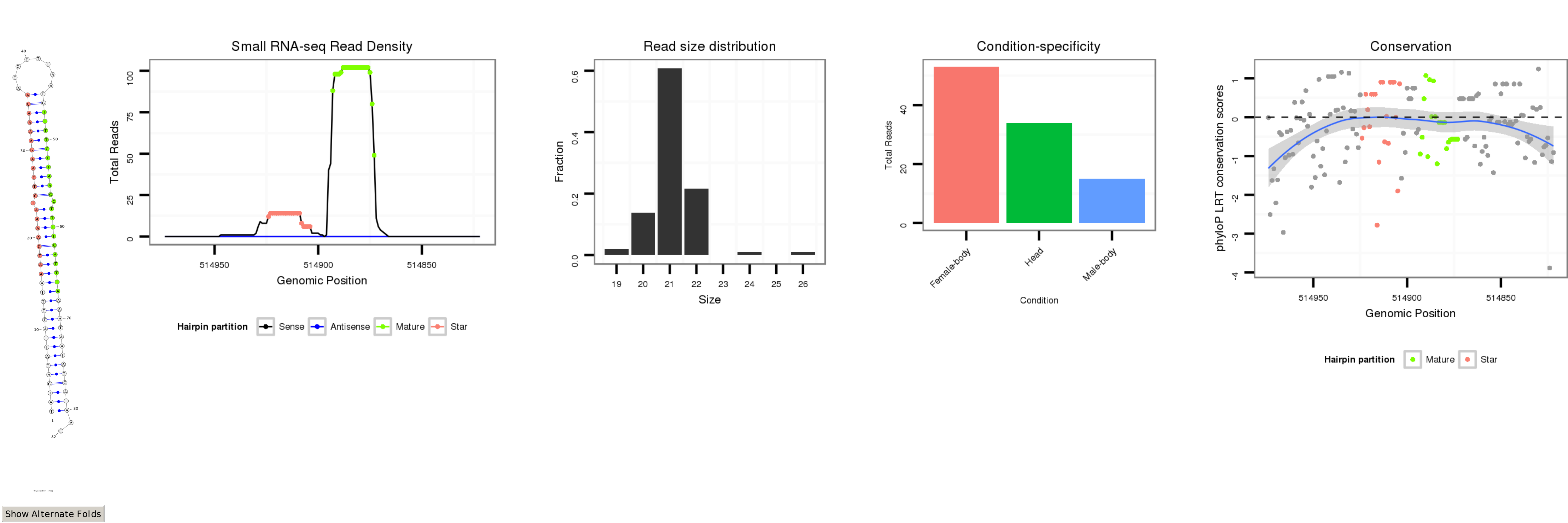
Re-alignment of all predicted orthologs

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

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Show Alternate Folds

Flybase annotation

intergenic

Repeatable elements

Name	Class	Family	Strand
AT_rich	Low_complexity	Low_complexity	+

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

[illegible]

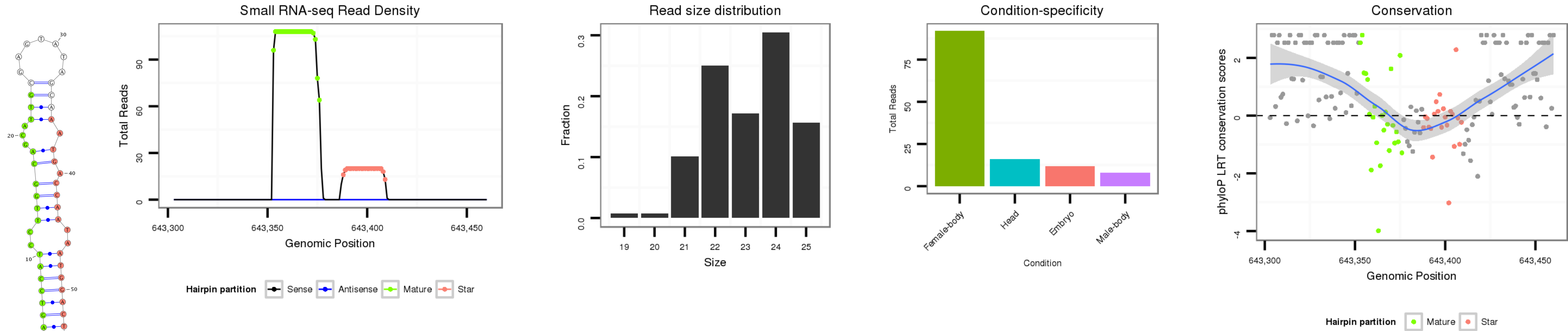
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	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	0
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dse_288	scaffold_12:643353-643410 +	confident	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 annotation

intron [Dsec/GM15347-in]; CDS [Dsec/GM15347-cds]; CDS [Dsec/GM15347-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

	Read size	# Mismatch	Hit Count	Total Norm	Total	M054 female body	V115 head	V114 embryo	V113 male body
CAAAGACTCAGAGCCCTATCCAGGCTACAATGCTAGGCCTCAAATTTATG GTAA GTCCATCCTTGGCAGCATT G CGAGTATAGCA AATGACCAATAATGGACTTTTTAT TTTTTAATCAGGTGCTTGGCAAAGCGGTACCCAGCAGTACCGGCCACAAT									
*****.(((((((.(((((.(((.....))))).)).))))).))*****									
.....GTAAGTCCATCCTTGGCAGCATTG.....	24	0	1	39.00	39	19	10	7	3
.....GTAAGTCCATCCTTGGCAGCAT.....	22	0	1	21.00	21	15	3	0	3
.....GTAAGTCCATCCTTGGCAGCATTG.....	25	0	1	19.00	19	16	1	2	0
.....GTAAGTCCATCCTTGGCAGCATT.....	23	0	1	13.00	13	9	1	2	1
.....AATGACCAATAATGGACTTTTT.....	22	0	1	5.00	5	5	0	0	0
.....TAAGTCCATCCTTGGCAGCATTG.....	23	0	1	5.00	5	4	0	0	1
.....GTAAGTCCATCCTTGGCAGCA.....	21	0	1	4.00	4	3	0	1	0
.....AAATGACCAATAATGGACTTTT.....	22	0	1	4.00	4	4	0	0	0
.....TAAGTCCATCCTTGGCAGCAT.....	21	0	1	4.00	4	3	1	0	0
.....AAATGACCAATAATGGACTTTT.....	23	0	1	4.00	4	4	0	0	0
.....AAATGACCAATAATGGACTTT.....	21	0	1	2.00	2	2	0	0	0
.....ATGACCAATAATGGACTTTT.....	21	0	1	2.00	2	2	0	0	0
.....GTAAGTCCATCCTTGGCAGCATTG.....	25	1	1	1.00	1	0	0	1	0
.....TAAGTCCATCCTTGGCAGCATTGCG.....	25	0	1	1.00	1	1	0	0	0
.....AAATGACCAATAATGGACTTTTT.....	24	1	1	1.00	1	1	0	0	0
.....TAAGTCCATCCTTGGCAGCATT.....	22	0	1	1.00	1	1	0	0	0
.....ATGACCAATAATGGACTTTTTA.....	22	0	1	1.00	1	1	0	0	0
.....TAAGTCCATCCTTGGCAGC.....	19	0	1	1.00	1	1	0	0	0
.....AATGACCAATAATGGACTTTT.....	21	0	1	1.00	1	1	0	0	0
.....AATGACCAATAATGGACTTTTT AAA	26	3	1	1.00	1	1	0	0	0
.....TGACCAATAATGGACTTTT.....	20	0	1	1.00	1	1	0	0	0
.....GTAAGTCCATCCTTGGCAGCATTG TT	27	2	1	1.00	1	1	0	0	0
.....GTAAGTCCATCCTTGGCAGCATTG A	25	1	1	1.00	1	1	0	0	0

Anti-sense strand reads

	Read # size	Mismatch	Hit Count	Total Norm	Total	M054 female body	V115 head
GTTTCGTGAGTGTGGGATAGGTCCGATGTTACGATCCGGAGTTTAAATAC CATT CAGGTAGGAACCGTC GTAA CGTCATATCGT TTACT GGTTATTACCTGAAAAATAAAATTAGTCCACGAAACCGTTTCGCCATGGGTGCTCATGGCCGGTGTTA							
*****.(((((((.(((((.(((.....))))).)).))))).))*****							

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droSec2	scaffold_12:643303-643460 +	dse_288	CAAAGACTC---ACAGCCCTATCCAGGCTACAATGCTAGGCCTCAAATTTATG GTAA GTCCATCCTTGGCAGCATT G CGAGTATAGCA AATGACCAATAATGGACTTTTTAT TTTTTAATCAGGTGCTTGGCAAAGCGGTACCCAGCAGTACCGGCCACAAT
droSim2	3r:7748803-7748956 +	dsi_8904	CAAAGACTC---ACAGCCCTATCCAGGCTACAATGCTAGGCCTCAAATTTATG GTAA GTCCATCCTTGGCAGCATT G CGAGTATAGCA AATGACCAATAATGGACTTTTTAT TTTTTAATCAGGTGCTTGGCAAAGCGGTACCCAGCAGTACCGGCCACAAT
dm3	chr3R:13519139-13519295 -		CAAAGACTC---ACAGCCCTATCCAGGCTACAATGCTAGGCCTCAAATTTATG GTAA GTCCATCCTTGGCAGCATT G CGAGTATAGCA AATGACCAATAATGGACTTTTTAT TTTTTAATCAGGTGCTTGGCAAAGCGGTACCCAGCAGTACCGGCCACAAT
droEre2	scaffold_4:4770:8111786-8111938 -		CAAAGACTC---ACAGCCCTATCCAGGCTACAATGCTAGGCCTCAAATTTATG GTAA GTCCATCCTTGGCAGCATT G CGAGTATAGCA AATGACCAATAATGGACTTTTTAT TTTTTAATCAGGTGCTTGGCAAAGCGGTACCCAGCAGTACCGGCCACAAT
droYak3	3R:2092034-2092182 -		CAAAGACTC---ACAGCCCTATCCAGGCTACAATGCTAGGCCTCAAATTTATG GTAA GTCCATCCTTGGCAGCATT G CGAGTATAGCA AATGACCAATAATGGACTTTTTAT TTTTTAATCAGGTGCTTGGCAAAGCGGTACCCAGCAGTACCGGCCACAAT
droEug1	scf7180000409562:39540-39685 -		CAAAGACTC---ACAGCCCTATCCAGGCTACAATGCTAGGCCTCAAATTTATG GTAA GTCCATCCTTGGCAGCATT G CGAGTATAGCA AATGACCAATAATGGACTTTTTAT TTTTTAATCAGGTGCTTGGCAAAGCGGTACCCAGCAGTACCGGCCACAAT
droBial	scf7180000302113:3899982-3900136 +		CAAAGACTC---ACAGCCCTATCCAGGCTACAATGCTAGGCCTCAAATTTATG GTAA GTCCATCCTTGGCAGCATT G CGAGTATAGCA AATGACCAATAATGGACTTTTTAT TTTTTAATCAGGTGCTTGGCAAAGCGGTACCCAGCAGTACCGGCCACAAT
droTak1	scf7180000413103:24997-25146 +		CAAAGACTC---ACAGCCCTATCCAGGCTACAATGCTAGGCCTCAAATTTATG GTAA GTCCATCCTTGGCAGCATT G CGAGTATAGCA AATGACCAATAATGGACTTTTTAT TTTTTAATCAGGTGCTTGGCAAAGCGGTACCCAGCAGTACCGGCCACAAT
droEle1	scf7180000491080:2759908-2760071 +		CAAAGACTC---ACAGCCCTATCCAGGCTACAATGCTAGGCCTCAAATTTATG GTAA GTCCATCCTTGGCAGCATT G CGAGTATAGCA AATGACCAATAATGGACTTTTTAT TTTTTAATCAGGTGCTTGGCAAAGCGGTACCCAGCAGTACCGGCCACAAT
droRho1	scf7180000778039:42905-43058 +		CAAAGACTC---ACAGCCCTATCCAGGCTACAATGCTAGGCCTCAAATTTATG GTAA GTCCATCCTTGGCAGCATT G CGAGTATAGCA AATGACCAATAATGGACTTTTTAT TTTTTAATCAGGTGCTTGGCAAAGCGGTACCCAGCAGTACCGGCCACAAT
droFlc1	scf7180000453912:1957498-1957655 +		CAAAGACTC---ACAGCCCTATCCAGGCTACAATGCTAGGCCTCAAATTTATG GTAA GTCCATCCTTGGCAGCATT G CGAGTATAGCA AATGACCAATAATGGACTTTTTAT TTTTTAATCAGGTGCTTGGCAAAGCGGTACCCAGCAGTACCGGCCACAAT
droK1k1	scf7180000302247:514912-515062 +		CAAAGACTC---ACAGCCCTATCCAGGCTACAATGCTAGGCCTCAAATTTATG GTAA GTCCATCCTTGGCAGCATT G CGAGTATAGCA AATGACCAATAATGGACTTTTTAT TTTTTAATCAGGTGCTTGGCAAAGCGGTACCCAGCAGTACCGGCCACAAT
droAna3	scaffold_12:911:2127051-2127205 +		CAAAGACTC---ACAGCCCTATCCAGGCTACAATGCTAGGCCTCAAATTTATG GTAA GTCCATCCTTGGCAGCATT G CGAGTATAGCA AATGACCAATAATGGACTTTTTAT TTTTTAATCAGGTGCTTGGCAAAGCGGTACCCAGCAGTACCGGCCACAAT
droBip1	scf7180000396714:952284-952438 -		CAAAGACTC---ACAGCCCTATCCAGGCTACAATGCTAGGCCTCAAATTTATG GTAA GTCCATCCTTGGCAGCATT G CGAGTATAGCA AATGACCAATAATGGACTTTTTAT TTTTTAATCAGGTGCTTGGCAAAGCGGTACCCAGCAGTACCGGCCACAAT
dp5	1:25888554-25888714 -		CAAAGACTC---ACAGCCCTATCCAGGCTACAATGCTAGGCCTCAAATTTATG GTAA GTCCATCCTTGGCAGCATT G CGAGTATAGCA AATGACCAATAATGGACTTTTTAT TTTTTAATCAGGTGCTTGGCAAAGCGGTACCCAGCAGTACCGGCCACAAT
droPer2	scaffold_6:1222908-1223068 -		CAAAGACTC---ACAGCCCTATCCAGGCTACAATGCTAGGCCTCAAATTTATG GTAA GTCCATCCTTGGCAGCATT G CGAGTATAGCA AATGACCAATAATGGACTTTTTAT TTTTTAATCAGGTGCTTGGCAAAGCGGTACCCAGCAGTACCGGCCACAAT
droW112	scf2_1100000013775:471-632 +		CAAAGACTC---ACAGCCCTATCCAGGCTACAATGCTAGGCCTCAAATTTATG GTAA GTCCATCCTTGGCAGCATT G CGAGTATAGCA AATGACCAATAATGGACTTTTTAT TTTTTAATCAGGTGCTTGGCAAAGCGGTACCCAGCAGTACCGGCCACAAT
droVir3	scaffold_12:855:10040886-10041037 -		CAAAGACTC---ACAGCCCTATCCAGGCTACAATGCTAGGCCTCAAATTTATG GTAA GTCCATCCTTGGCAGCATT G CGAGTATAGCA AATGACCAATAATGGACTTTTTAT TTTTTAATCAGGTGCTTGGCAAAGCGGTACCCAGCAGTACCGGCCACAAT
droMoJ3	scaffold_6:540:3996038-3996196 -		CAAAGACTC---ACAGCCCTATCCAGGCTACAATGCTAGGCCTCAAATTTATG GTAA GTCCATCCTTGGCAGCATT G CGAGTATAGCA AATGACCAATAATGGACTTTTTAT TTTTTAATCAGGTGCTTGGCAAAGCGGTACCCAGCAGTACCGGCCACAAT
droGr12	scaffold_14:830:1228748-1228904 -		CAAAGACTC---ACAGCCCTATCCAGGCTACAATGCTAGGCCTCAAATTTATG GTAA GTCCATCCTTGGCAGCATT G CGAGTATAGCA AATGACCAATAATGGACTTTTTAT TTTTTAATCAGGTGCTTGGCAAAGCGGTACCCAGCAGTACCGGCCACAAT

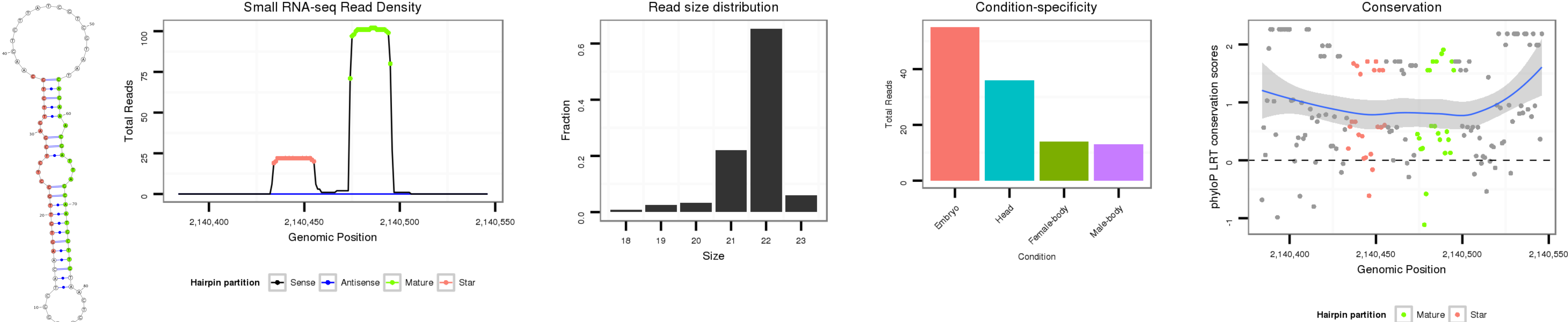
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PASS/FAIL	
crit.star	0
crit.loop	0
crit.mor	0
crit.hair	1
crit.total	1
crit.pairing	1
crit.top3	1
crit.tpot3	0
crit.un	1
crit.back	0
rescue.total	1
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dse_112	scaffold_1:2140434-2140496 +	confident	Canonical miRNA	3pUTR	[View on UCSC Genome Browser (Cornell Mirror)]

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

Predicted structure



Show Alternate Folds

Flybase annotation

utr3 [utr3_plus_1921]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

	Read #		Hit	Total		V114	V115	M054	V113
	size	Mismatch	Count	Norm	Total	embryo	head	female body	male body
GTAACTAATGTATTTATATGCTGTTTAAGAATGTCTGATAAATGGCTACAAGTGTTCGCTCGAGTTCGCAAGTCTTTATCGTCGTAATCAGAAACGATTAGCAATGCTTGTAACGTGGTTTATAAATTCGAATCCCAAAGTCATCGAAAGTGAAACCAAAAAAT	22	0	1	47.00	47	22	16	2	7
*****(((.....(((((((((((.....(((.....)))))))))).....))))*****	22	0	1	23.00	23	14	4	2	3
.....CAGAAACGATTAGCAATGCTTG.....	21	0	1	19.00	19	5	9	3	2
.....AGAAACGATTAGCAATGCTTGT.....	22	0	1	7.00	7	2	4	1	0
.....AGTGTTCGCTCTCGAGTTCTGC.....	23	0	1	6.00	6	3	2	0	1
.....AAGTGTTCGCTCTCGAGTTCTGC.....	21	0	1	4.00	4	2	0	1	1
.....AGTGTTCGCTCTCGAGTTCTGCA.....	23	0	1	3.00	3	2	0	1	0
.....TGTTGCCTCTCGAGTTCTGCAAG.....	23	0	1	2.00	2	2	0	0	0
.....GAAACGATTAGCAATGCTTG.....	20	0	1	1.00	1	1	0	0	0
.....AGTGTTCCTCTCGAGTTCTG.....	21	0	1	1.00	1	1	0	0	0
.....AAACGATTAGCAATGCTTG.....	19	0	1	1.00	1	0	0	1	0
.....CTGCAAGTCTTATCGTCGTAATC.....	23	0	1	1.00	1	1	0	0	0
.....AGTGTTCCTCTCGAGTT.....	18	0	1	1.00	1	0	0	1	0
.....AACGATTAGCAATGCTTGT.....	19	0	1	1.00	1	1	0	0	0
.....CAGAAACGATTAGCAATGCT.....	20	0	1	1.00	1	0	1	0	0
.....TCGTAATCAGAAACGATTAGC.....	21	0	1	1.00	1	1	0	0	0
.....AGTGTTCCTCTCGAGTTCT.....	20	0	1	1.00	1	0	1	0	0
.....AGCAATGCTTGTAACTGGTTT.....	21	0	1	1.00	1	1	0	0	0
.....CAGAAACGATTAGCAATGCTTGT.....	23	0	1	1.00	1	0	0	1	0
.....AAACGATTAGCAATGCTTG.....	21	2	1	1.00	1	0	0	1	0
.....AAACGATTAGCAATGCTTGT.....	20	0	1	1.00	1	0	1	0	0
.....GTGTTGCCTCTCGAGTTCTGC.....	21	0	1	1.00	1	0	0	1	0
.....CAGAAACGATTAGCAATGC.....	19	0	1	1.00	1	1	0	0	0
.....AGTGTTCCTCTCGAGTTCTG.....	22	1	1	1.00	1	0	1	0	0

Anti-sense strand reads

	Read #		Hit	Total		M054
	size	Mismatch	Count	Norm	Total	female body
CATTTCATTACATAAATATACGACAAATCTCTACAGACTATTTACCGATGTCACAAACGGAGAGCTCAAGACGTTTCAGAATAGCAGCATTAGTCTTTGCTAATCGTTACGAACATTGACCAAAATATTAAAGCTTAGGGTTTCAGTAGCTTTCACITTTGGTTTTTA						
*****(((.....(((((((((((.....(((.....)))))))))).....))))*****						

Show Alignment With Reads

Re-alignment of all predicted orthologs

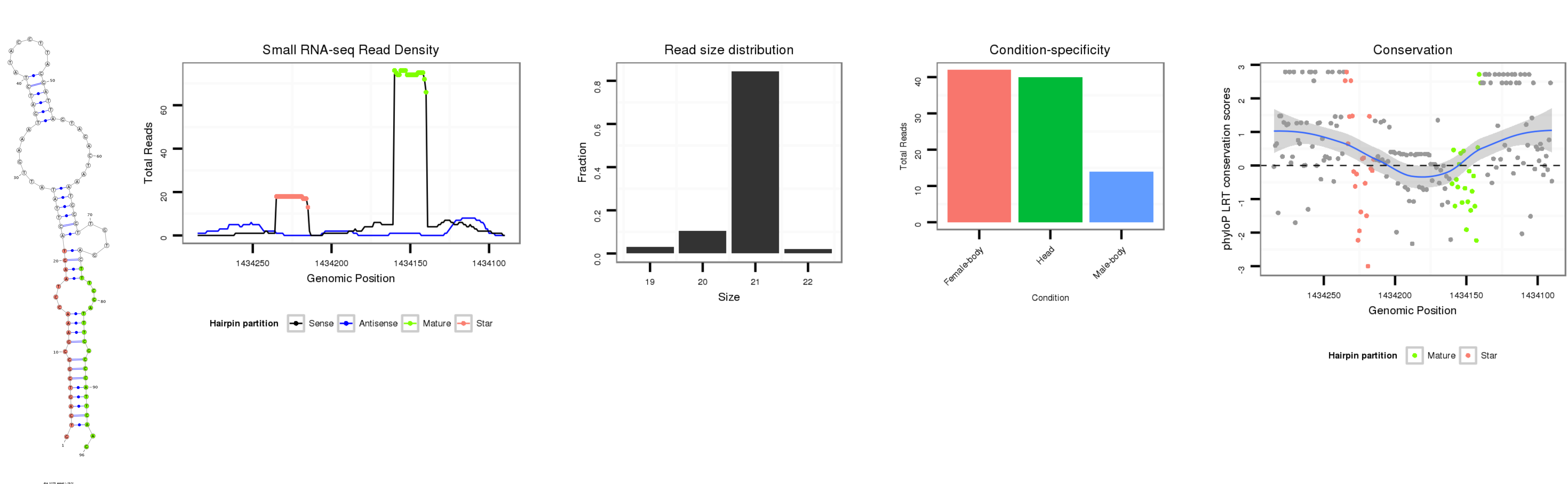
Species	Coordinate	ID	Alignment
droSec2	scaffold_1:2140384-2140546 +	dse_112	GTAAGTAATGTATTTATATGCTGTTTAAGAATGTCTGATAAATGGCTA-----CAAGT--GTT-GCCTCTCGAGT--TCTGCAAGT-----CTTATCGTCGTAATCAGAAACGATTAGC-----AATGCTTGTAAGTGGTTTATAATTCG--AATCCCAAAGTCATCGAAAGTGAAACCAAAAAAT
droSim2	chr:5309673-5309835 +	dsi_32	GTAAGTAATGTATTTATATGCTCTTTAAGAATGTCTGATAAATGGCTA-----CAAGT--GTT-GCCTCTCGAGT--TCTGCAAGT-----CTTATCGTCGTAATCAGAAACGATTAGC-----AATGCTTGTAAGTGGTTTATAATTCG--AATCCCAAAGTCATCGAAAGTGAAACCAAAAAAT
dm3	chr2R:4498534-4498709 +	dme_413	GTAAGTAATGTATTTATATGCTATTAAAGAATGTCTGATAAATGGCTA-----CAAGT--GTT-GCCTCTCGAGT--TCTGCAAGT-----CTTATCGTCGTAATCAGAAACGATTAGC-----AATGCTTGTAAGTGGTTTATAATTCG--AATCCCAAAGTCATCGAAAGTGAAACCAAAAAAT
droEre2	scaffold_4:4929:18141568-18141740 -	der_1528	TAAGTAATGTATTTATATGCTATTAAAGATGTCTGATAAATGGCTA-----CAAGT--GTT-GCCTCTCGAGT--TCTGCAAGT-----CTTATCGTCGTAATCAGAAACGATTAGC-----AATGCTTGTAAGTGGTTTATAATTCG--AATCCCAAAGTCATCGAAAGTGAAACCAAAAAAT
droYak3	2L:17155125-17155293 +		TAAGTAATGTATTTATATGCTATTAAAGATGTCTGATAAATGGCTA-----CAAGT--GTT-GCCTCTCGAGT--TCTGCAAGT-----CTTATCGTCGTAATCAGAAACGATTAGC-----AATGCTTGTAAGTGGTTTATAATTCG--AATCCCAAAGTCATCGAAAGTGAAACCAAAAAAT
droEug1	scf7180000409183:156737-156911 +		TAAGTAATGTATTTATATGCTATTAAAGATGTCTGATAAATGGCTA-----CAAGT--GTT-GCCTCTCGAGT--TCTGCAAGT-----CTTATCGTCGTAATCAGAAACGATTAGC-----AATGCTTGTAAGTGGTTTATAATTCG--AATCCCAAAGTCATCGAAAGTGAAACCAAAAAAT
droBial	scf7180000302291:2404238-2404417 +		TAAGTAATGTATTTATATGCTATTAAAGATGTCTGATAAATGGCTA-----CAAGT--GTT-GCCTCTCGAGT--TCTGCAAGT-----CTTATCGTCGTAATCAGAAACGATTAGC-----AATGCTTGTAAGTGGTTTATAATTCG--AATCCCAAAGTCATCGAAAGTGAAACCAAAAAAT
droTak1	scf7180000415401:1229823-1229983 -		TAAGTAATGTATTTATATGCTATTAAAGATGTCTGATAAATGGCTA-----CAAGT--GTT-GCCTCTCGAGT--TCTGCAAGT-----CTTATCGTCGTAATCAGAAACGATTAGC-----AATGCTTGTAAGTGGTTTATAATTCG--AATCCCAAAGTCATCGAAAGTGAAACCAAAAAAT
droEle1	scf7180000491240:1347757-1347912 +		TAAGTAATGTATTTATATGCTATTAAAGATGTCTGATAAATGGCTA-----CAAGT--GTT-GCCTCTCGAGT--TCTGCAAGT-----CTTATCGTCGTAATCAGAAACGATTAGC-----AATGCTTGTAAGTGGTTTATAATTCG--AATCCCAAAGTCATCGAAAGTGAAACCAAAAAAT
droRho1	scf7180000779971:31249-31241 +		TAAGTAATGTATTTATATGCTATTAAAGATGTCTGATAAATGGCTA-----CAAGT--GTT-GCCTCTCGAGT--TCTGCAAGT-----CTTATCGTCGTAATCAGAAACGATTAGC-----AATGCTTGTAAGTGGTTTATAATTCG--AATCCCAAAGTCATCGAAAGTGAAACCAAAAAAT
droFic1	scf7180000453851:1827091-1827258 -		TAAGTAATGTATTTATATGCTATTAAAGATGTCTGATAAATGGCTA-----CAAGT--GTT-GCCTCTCGAGT--TCTGCAAGT-----CTTATCGTCGTAATCAGAAACGATTAGC-----AATGCTTGTAAGTGGTTTATAATTCG--AATCCCAAAGTCATCGAAAGTGAAACCAAAAAAT
droK1k1	scf7180000302277:360641-360813 +		TAAGTAATGTATTTATATGCTATTAAAGATGTCTGATAAATGGCTA-----CAAGT--GTT-GCCTCTCGAGT--TCTGCAAGT-----CTTATCGTCGTAATCAGAAACGATTAGC-----AATGCTTGTAAGTGGTTTATAATTCG--AATCCCAAAGTCATCGAAAGTGAAACCAAAAAAT
droAna3	scaffold_1:13266:1507605-1507699 -		TAAGTAATGTATTTATATGCTATTAAAGATGTCTGATAAATGGCTA-----CAAGT--GTT-GCCTCTCGAGT--TCTGCAAGT-----CTTATCGTCGTAATCAGAAACGATTAGC-----AATGCTTGTAAGTGGTTTATAATTCG--AATCCCAAAGTCATCGAAAGTGAAACCAAAAAAT
droBip1	scf7180000396730:2502009-2502060 -		TAAGTAATGTATTTATATGCTATTAAAGATGTCTGATAAATGGCTA-----CAAGT--GTT-GCCTCTCGAGT--TCTGCAAGT-----CTTATCGTCGTAATCAGAAACGATTAGC-----AATGCTTGTAAGTGGTTTATAATTCG--AATCCCAAAGTCATCGAAAGTGAAACCAAAAAAT
dp5	3:5373284-5373458 -		TAAGTAATGTATTTATATGCTATTAAAGATGTCTGATAAATGGCTA-----CAAGT--GTT-GCCTCTCGAGT--TCTGCAAGT-----CTTATCGTCGTAATCAGAAACGATTAGC-----AATGCTTGTAAGTGGTTTATAATTCG--AATCCCAAAGTCATCGAAAGTGAAACCAAAAAAT
droPer2	scaffold_2:5578608-5578782 -		TAAGTAATGTATTTATATGCTATTAAAGATGTCTGATAAATGGCTA-----CAAGT--GTT-GCCTCTCGAGT--TCTGCAAGT-----CTTATCGTCGTAATCAGAAACGATTAGC-----AATGCTTGTAAGTGGTTTATAATTCG--AATCCCAAAGTCATCGAAAGTGAAACCAAAAAAT
droW12	scf2_1100000004512:2562412-2562439 +		TAAGTAATGTATTTATATGCTATTAAAGATGTCTGATAAATGGCTA-----CAAGT--GTT-GCCTCTCGAGT--TCTGCAAGT-----CTTATCGTCGTAATCAGAAACGATTAGC-----AATGCTTGTAAGTGGTTTATAATTCG--AATCCCAAAGTCATCGAAAGTGAAACCAAAAAAT
droGr12	scaffold_1:15126:4241352-4241382 -		TAAGTAATGTATTTATATGCTATTAAAGATGTCTGATAAATGGCTA-----CAAGT--GTT-GCCTCTCGAGT--TCTGCAAGT-----CTTATCGTCGTAATCAGAAACGATTAGC-----AATGCTTGTAAGTGGTTTATAATTCG--AATCCCAAAGTCATCGAAAGTGAAACCAAAAAAT

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

dse_1279	scaffold_4:1434140-1434235 -	confident	Mirtron	intron	[View on UCSC Genome Browser (Cornell Mirror)]
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Predicted structure



Show Alternate Folds

Flybase annotation

trntrn [Dsec\GM12412-in]; utr5 [utr5_plus_14039]; CDS [Dsec\GM12412-cds]; CDS [Dsec\GM12412-cds]; utr5 [utr5_plus_14038]

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]

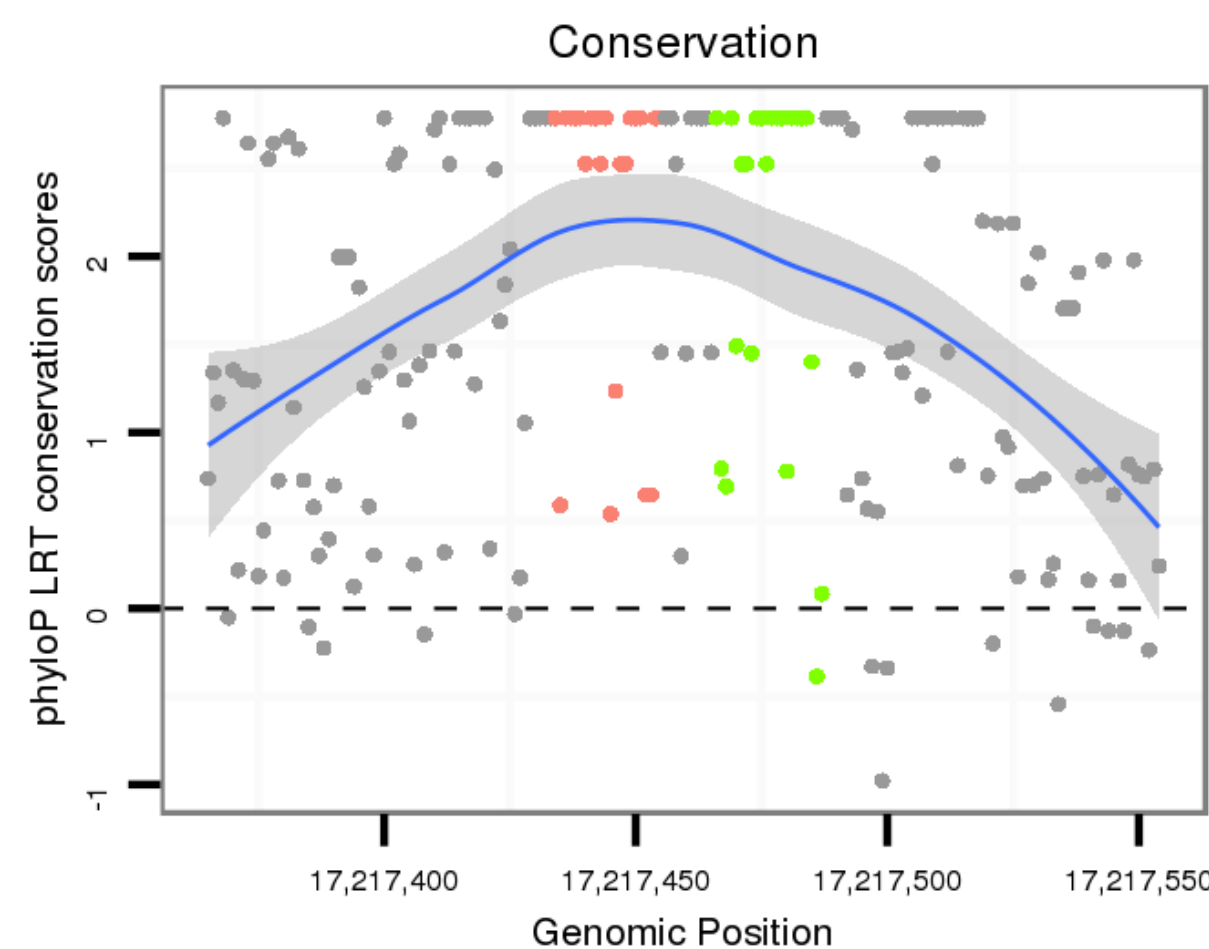
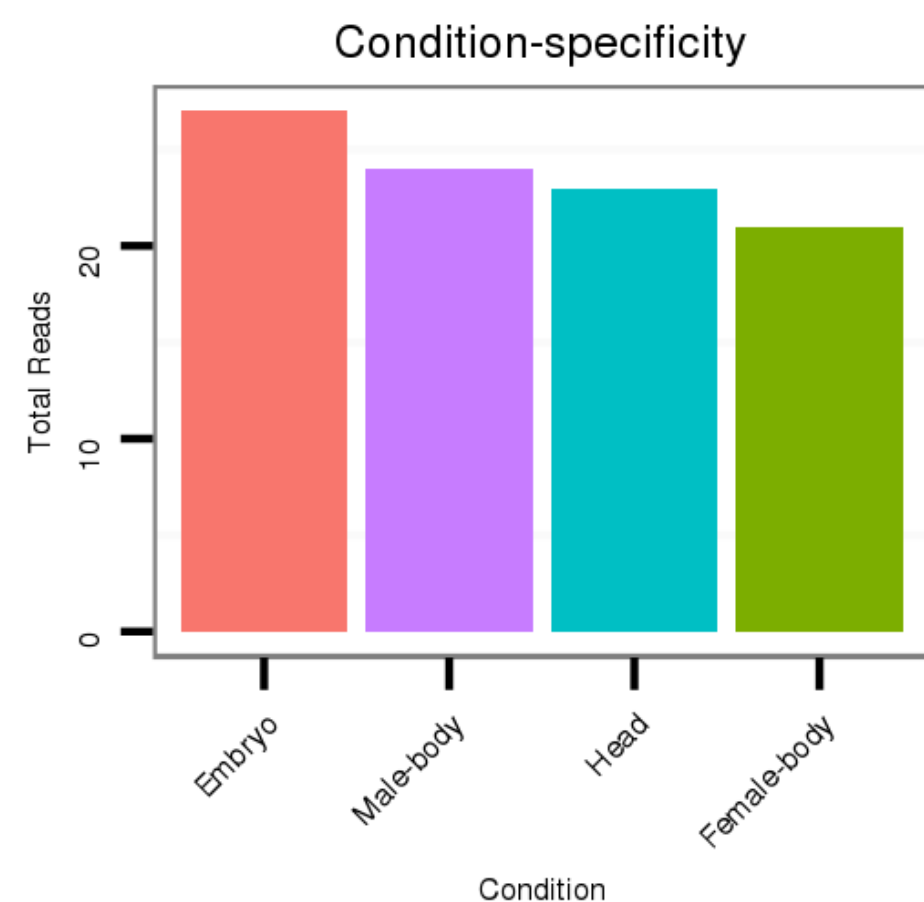
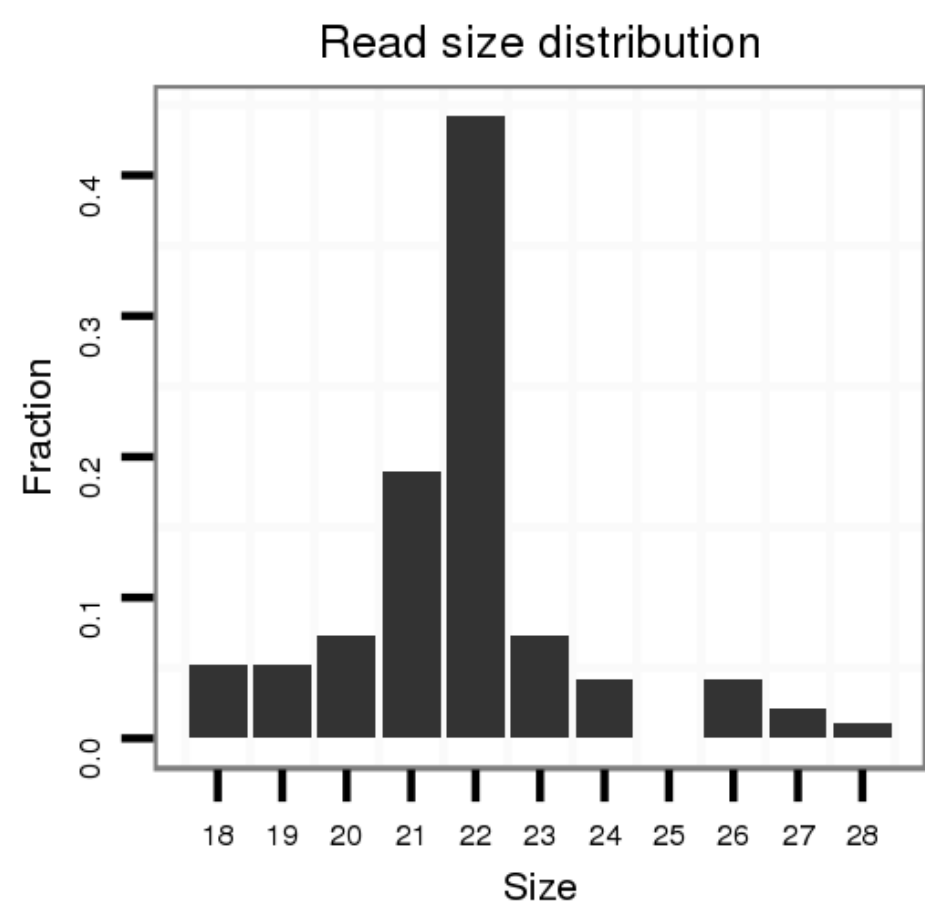
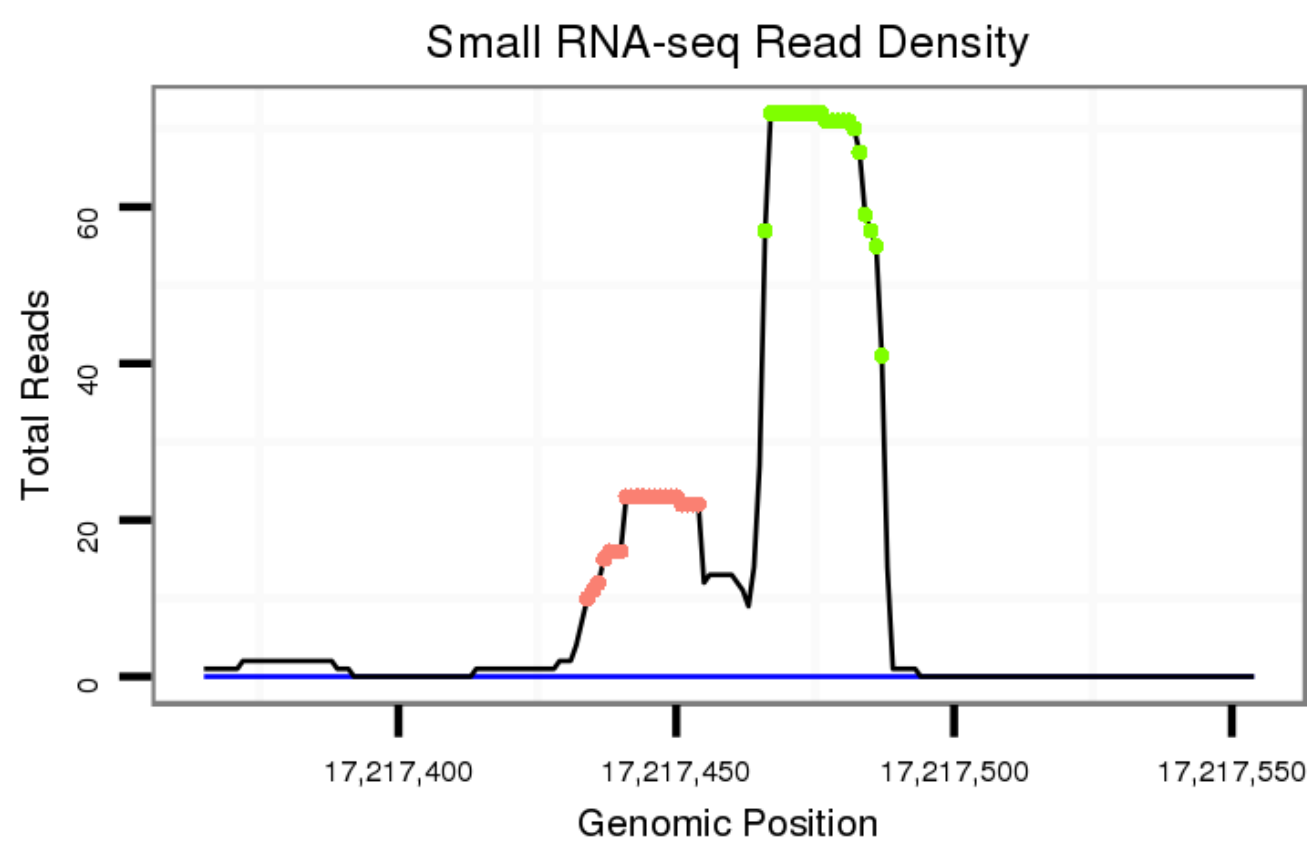
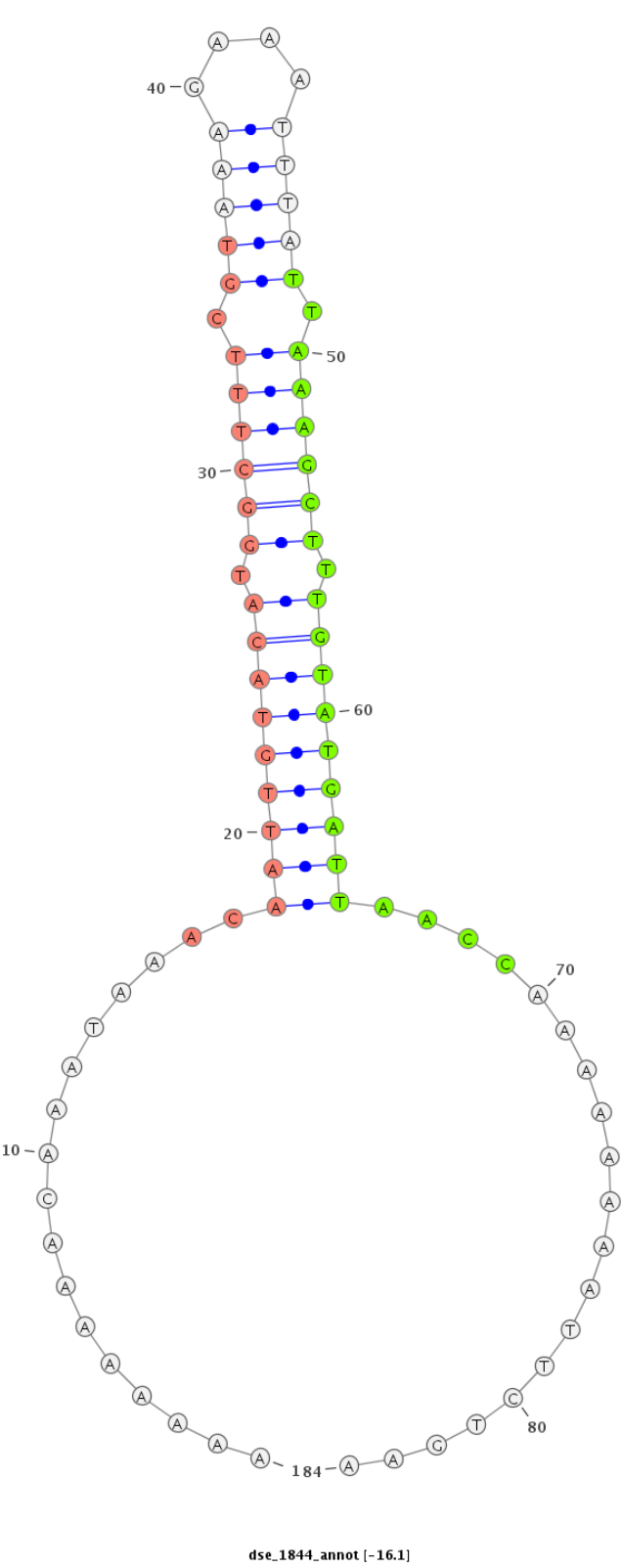
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	PASS/FAIL
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crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.top3p3	1
crit.xri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	2
rescue.candidate	0

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dse_1844	scaffold_0:17217415-17217504 +	confident	Canonical miRNA	3pUTR	[View on UCSC Genome Browser (Cornell Mirror)]

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Hairpin partition Sense Antisense Mature Star

Show Alternate Folds

Flybase annotation

utr3 [utr3_minus_7095]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

										V15 V14			M054	V13	
										head	embryo		female body	male body	
										Read #	Hit	Total	Total		
										Mismatch	Count	Normal	Total		
TTGAGAAAAAGAAAGAAACCCCAACAACCAACAACAACAACAATAGAAAAAAACAATAACAAATTGTCATGCGCTTCGTAAAGAAATTTAAAGCTGTTGATGATTAAACAAAAAAATTCGAAATTTGTGTTTATTTCGCGTTATCACGTCACAGTTTTCTCATTGCCAATTTAA	22	0	1	20,00	20	6	4	6	4						
..... ((((((((((((((((((((((.....	22	0	1	9,00	9	0	8	1	0						
.....TAAAGCTTTGTATGATTAAAC.....	22	0	1	20,00	20	6	4	6	4						
.....TAAAGCTTTGTATGATTAAAC.....	22	0	1	9,00	9	0	8	1	0						
.....ATTAAAGCTTTGTATGATTAAAC.....	22	0	1	7,00	7	1	4	0	2						
.....TAAAGCTTTGTATGATTAAAC.....	21	0	1	6,00	6	2	1	0	3						
.....TAAAGCTTTGTATGATTAAAC.....	21	0	1	6,00	6	2	0	2	2						
.....ACAATTGTACATGCGCTTCGT.....	21	0	1	3,00	3	1	0	1	1						
.....TAAAGCTTTGTATGATTAAACCA.....	23	0	1	3,00	3	0	3	0	0						
.....TATTAAAGCTTTGTATGATT.....	20	0	1	3,00	3	0	0	2	1						
.....ATTAAAGCTTTGTATGATT.....	19	0	1	3,00	3	0	1	1	1						
.....TACATGCGCTTCGTAAGAAAT.....	22	0	1	2,00	2	2	0	0	0						
.....TACATGCGCTTCGTAAGAAATTTAT.....	26	0	1	2,00	2	1	0	1	0						
.....TAAAGCTTTGTATGATTAAAC.....	22	1	1	2,00	2	1	0	1	0						
.....TAAAGCTTTGTATGATTAAAC.....	22	2	1	2,00	2	2	0	0	0						
.....AACAAATTGTACATGCGCTTCGT.....	22	0	1	2,00	2	1	0	0	1						
.....TAAAGCTTTGTATGATTAAAC.....	21	1	1	2,00	2	1	1	0	0						
.....ATTAAAGCTTTGTATGATT.....	18	0	1	2,00	2	0	2	0	0						
.....TAAAGCTTTGTATGATTAAAC.....	21	0	1	2,00	2	0	0	1	1						
.....ATTAAAGCTTTGTATGATTAAAC.....	20	0	1	1,00	1	0	0	0	1						
.....ATTAAAGCTTTGTATGATTAAACCA.....	24	0	1	1,00	1	0	0	1	0						
.....TAAAGCTTTGTATGATTAAAC.....	22	2	1	1,00	1	1	0	0	0						
.....TTGTACATGCGCTTCGTAAGAAAT.....	24	0	1	1,00	1	1	0	0	0						
.....AACAAATTGTACATGCGCTTCGT.....	19	0	1	1,00	1	0	0	1	0						
.....TAAAGCTTTGTATGATTAAAC.....	21	1	1	1,00	1	0	0	1	0						
.....TAAAGCTTTGTATGATTAAAC.....	20	0	1	1,00	1	1	0	0	0						
.....TATTAAAGCTTTGTATGATTAAAC.....	23	2	1	1,00	1	0	0	0	1						
.....TTATTAAAGCTTTGTATGATT.....	21	0	1	1,00	1	0	0	1	0						
.....AATAGAAAAAAACAATAACAATTT.....	26	0	1	1,00	1	1	0	0	0						
.....TACATGCGCTTCGTAAGAAATTT.....	23	0	1	1,00	1	1	0	0	0						
.....ATTAAAGCTTTGTATGATTAAAC.....	22	1	1	1,00	1	1	0	0	0						
.....ATTGTACATGCGCTTCGTAAGAAAT.....	24	0	1	1,00	1	0	0	0	1						
.....AAATTTATTAAAGCTTTGTATGATT.....	23	0	1	1,00	1	0	1	0	0						
.....AAGAAATTTATTAAAGCTTTGT.....	21	0	1	1,00	1	0	0	0	1						
.....TATTAAAGCTTTGTATGATTAAAC.....	21	0	1	1,00	1	0	0	0	1						
.....GTACATGCGCTTCGTAAGAAAT.....	20	0	1	1,00	1	0	0	1	0						
.....AAAGAAAGAAACCCCA.....	20	0	1	1,00	1	0	0	1	0						
.....CAATTGTACATGCGCTTCGT.....	20	0	1	1,00	1	0	0	0	1						
.....AATTATTAAAGCTTTGTATGATTAAAC.....	28	0	1	1,00	1	1	0	0	0						
.....AATTGTACATGCGCTTCGT.....	19	0	1	1,00	1	0	0	0	1						
.....TAAAGCTTTGTATGATTAAAC.....	21	1	1	1,00	1	0	0	0	1						
.....ATTGTACATGCGCTTCGT.....	18	0	1	1,00	1	0	1	0	0						
.....AATAACAATTGTACATGCGCTTCGT.....	26	0	1	1,00	1	0	0	0	1						
.....TAAAGCTTTGTATGATT.....	18	0	1	1,00	1	1	0	0	0						
.....AAAGCTTTGTATGATTAAAC.....	20	1	1	1,00	1	1	0	0	0						
.....AACAAATTGTACATGCGCTTCGT.....	23	0	1	1,00	1	0	1	0	0						
.....AACAAATTGTACATGCGCTTCGTA.....	23	0	1	1,00	1	0	0	0	1						
.....TATTAAAGCTTTGTATGATTAAAC.....	22	2	1	1,00	1	0	0	0	1						
.....ATTGTACATGCGCTTCGTAAGAAATTT.....	26	0	1	1,00	1	0	0	0	1						
.....TATTAAAGCTTTGTATGATTAAAC.....	23	1	1	1,00	1	0	0	0	1						
.....AAGAAATTTATTAAAGCTTTGTATGATT.....	27	0	1	1,00	1	0	0	1	0						
.....TACATGCGCTTCGTAAGAAAT.....	18	0	1	1,00	1	1	0	0	0						
.....TAAAGCTTTGTATGATTAAACAAAAAA.....	27	0	1	1,00	1	0	1	0	0						
TTGAGAAAAAGAAAGAAACCCCA.....	24	0	1	1,00	1	0	0	1	0						
.....TACATGCGCTTCGTAAGAAATTT.....	24	0	1	1,00	1	1	0	0	0						
.....TAAAGCTTTGTATGATTAAAC.....	22	3	2	0.50	1	1	0	0	0						
.....TATTAAAGCTTTGTATGATTAAAC.....	20	2	4	0.25	1	0	0	0	1						
.....TAAAGCTTTGTATGATTAAAC.....	22	3	6	0.17	1	1	0	0	0						

Anti-sense strand reads

[illegible]

No data available in table

Re-alignment of all predicted orthologs

[illegible]

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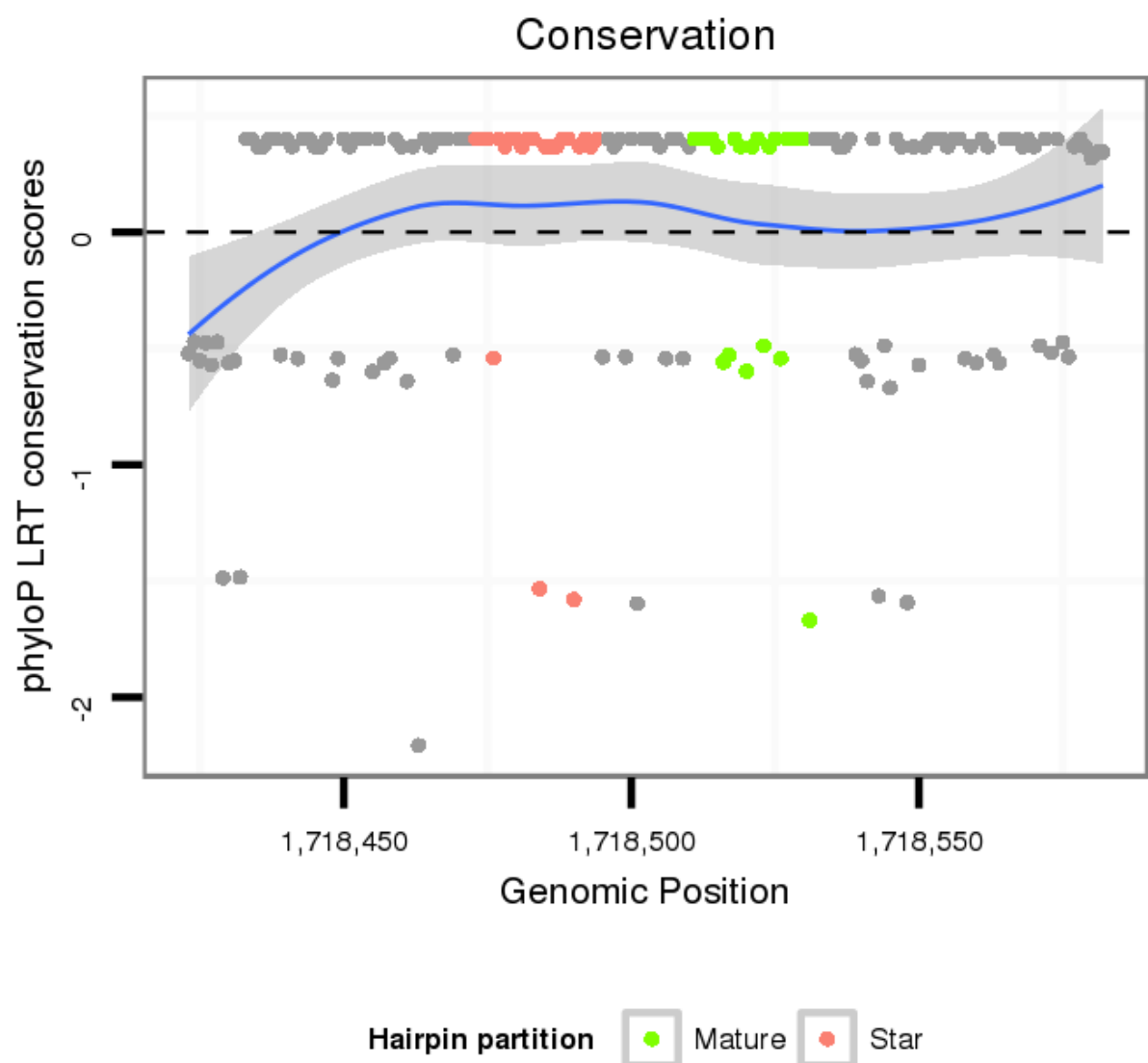
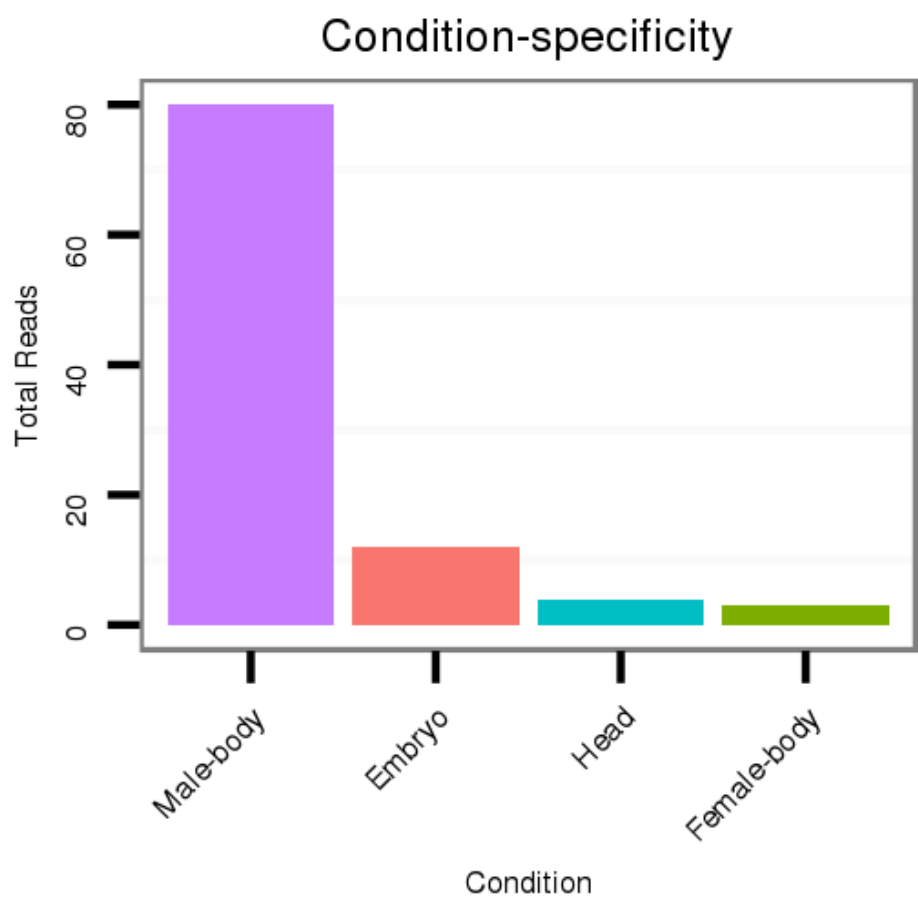
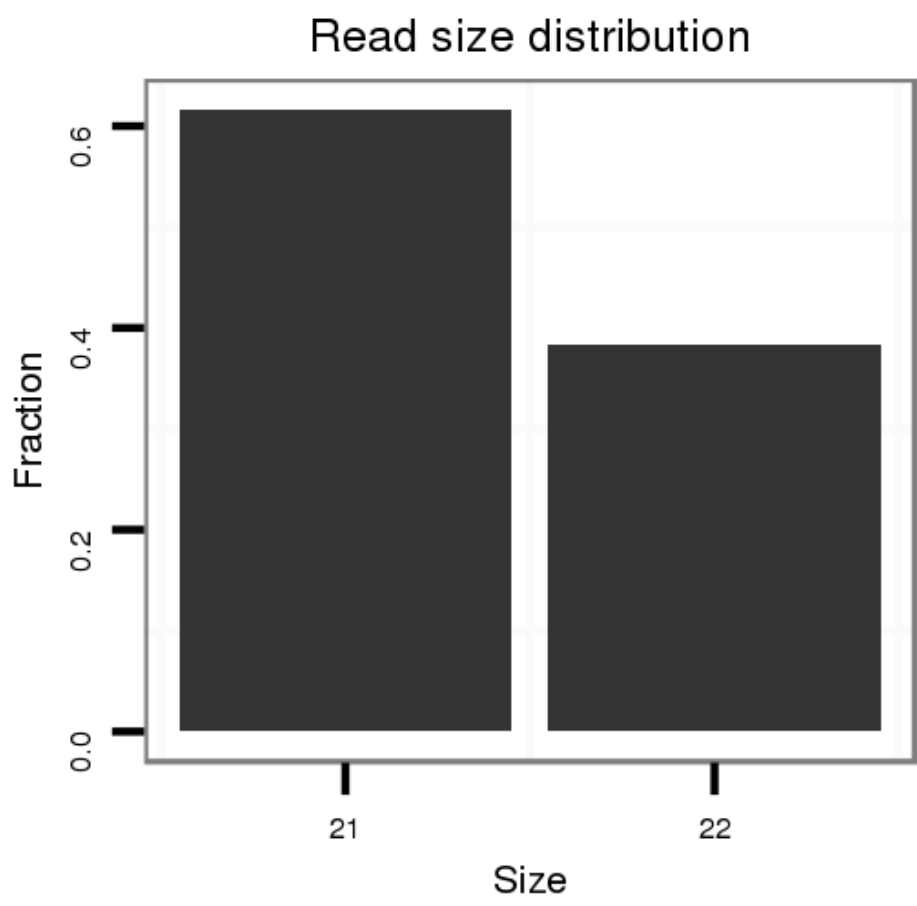
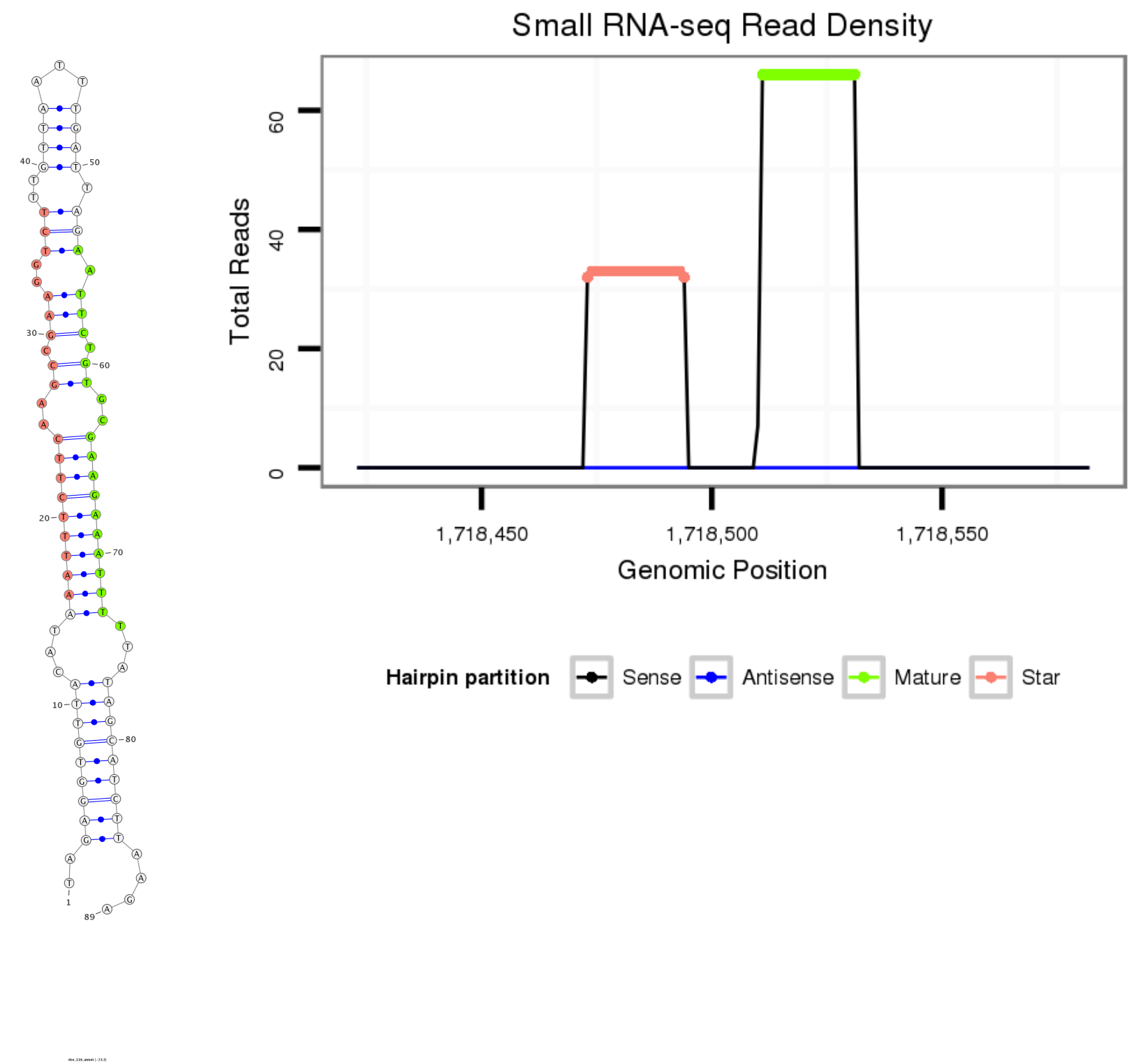
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	8
rescue.candidate	4

PASS/FAIL

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

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Show Alternate Folds

Flybase annnotation

Antisense to intron [Dsec\GM22737-in]

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

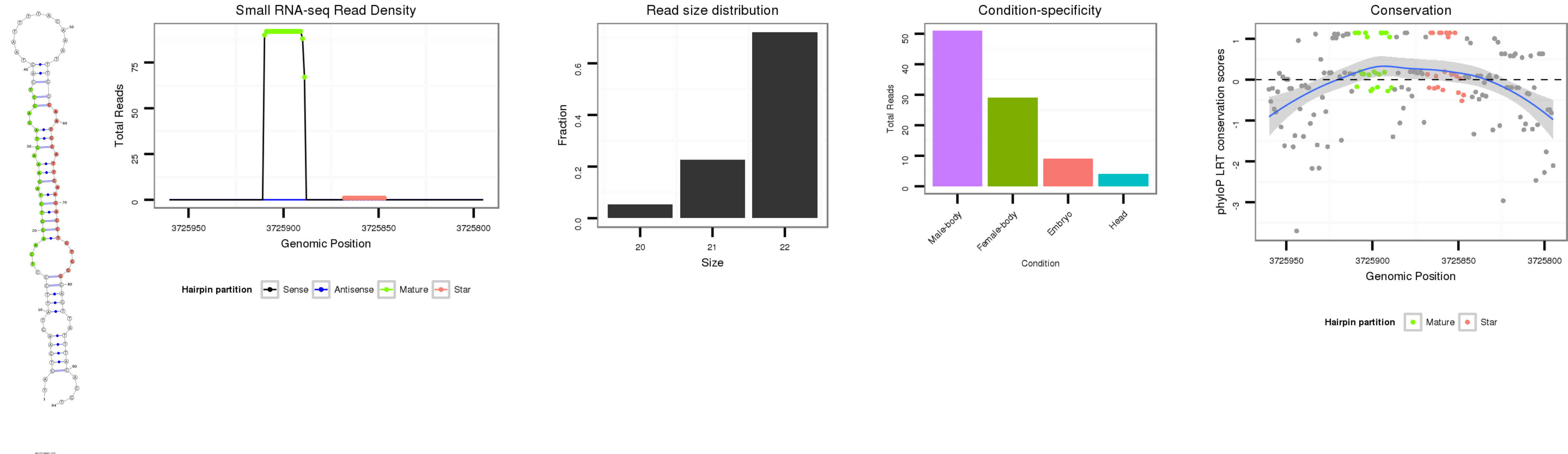
Species	Coordinate	ID	Alignment
droSec2	scaffold_8:1718423-1718582 +	dse_116	TACAAA---TGAATGGATGAGATTGGAAAAGATTGTG-----TAGAGGTGTTACATAAATTCTTCAAGCCGAAGGTCTTTGTTAATTGTATTAGAAATTCTGTGCGAAGAAATTTTATAGCATCTTA---AGAGCCTGAATCTTTCGAGCCAATCAGTT---GAGAGTCGAA
droSim2	x:18325710-18325871 +	dsi_203	TCCATCTTGAATGGATGAGATTGGAAAAGATTGTG-----TAGAGGTGTTACATAAATTCTTCAAAACCGAAGGTCTTTGTTAATTGTATTAGAAATTCTGTGCGAAGAAATTTTATAGCATCTTA---AGAGCCTGAATCTTTCGAGCCAATCAGTT---AAAGATCGAA
dm3	chrX:19436177-19436344 +		TACAAA---TGAATGGATGAAGATTGGAAGAAGATTGTGTAAGATACGGTGTGTTATATAAATTCTTCAAAACCGAAGTCTTTGTTAGCTTTGATTAGAAATTCTGTGCGAAGAAATTTTATAGCATCTTA---AGAGCCTGAATCTTTCGAGCCAATCAGTT---AAAGATCGAA
droEre2	scaffold_4690:9673148-9673307 +	der_57	TACACCA---GAGTATGGATGAGCTTGGATCGAGATTCTTA---CAGCGTGTTCATACATAATCTCTTCAAGCCGAAGGTCTATGTAAGTTTGCTGGAATTCTGTGGAAGAGATTTCATAGCATCTCGAATACAGTCTGGAATCTTCCAAAGCTAATCAGTT---GAATGTC---
droYak3	x:11900761-11900926 -	dya_55	AATTAAGACAAGATGGATGAGTGTGGAATGAGATTGTA-----CAGCGGTGTTACATAAATTCTTCAAGCCGAAGTCTATGTAATTGTTGGAATTCTGTGGAAGAGATTTCATAGCATCTCGAATAGAGCCTGAATCTCCAAAGCTAATCAGTT---GAATGTCGAA

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crit.star 0
crit.lo0p 0
crit.mor 0
crit.half 0
crit.total 1
crit.pairing 1
crit.top3 1
crit.tptop3 1
crit.uri 0
crit.back 1
rescue.total 0
rescue.dominant 0
rescue.known 0
rescue.confident 3
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

[illegible]

Anti-sense strand reads

Show Alignment With Reads

Re-alignment of all predicted orthologs

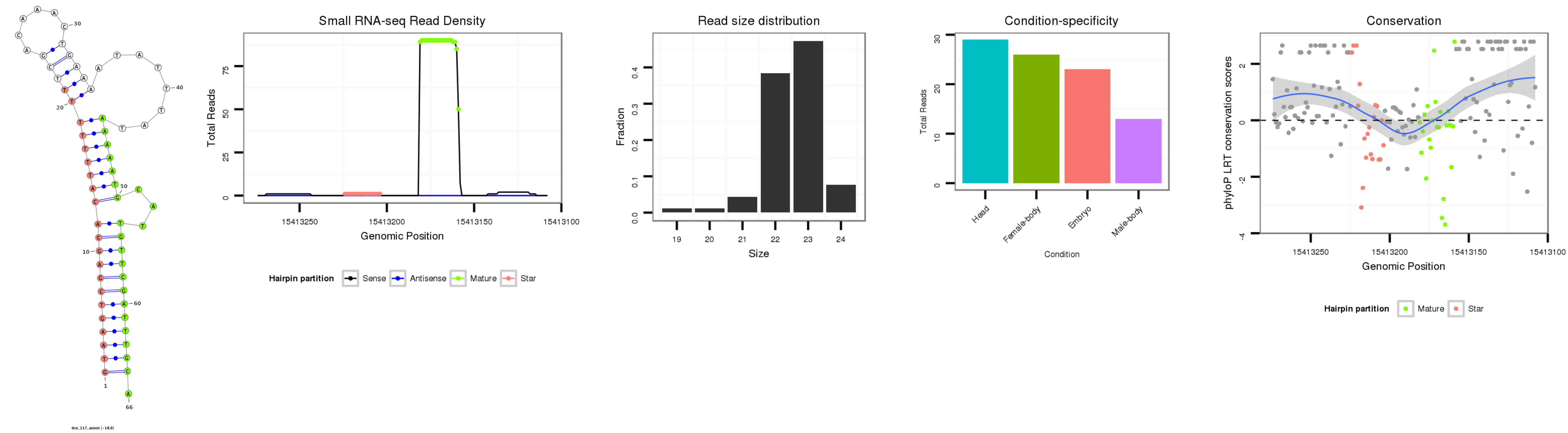
Species	Coordinate	ID	Alignment
droSec2	scaffold_8:3725795-3725960_	dse_127_	GCTAAGTAA--TAA-----TTGAGTTGGAGCTCGACITTTTGTAGTGAAGTATTCCCCTCAAGGCTAGAAAGTAGAGCTCAGTAATTTTACAAATTTGCAATGCATTCAAGACCTGT-GCGGAGTTATTACACGTCGTCATCAAAGT---GTTTT-GTTTTG-CITGTTT-GAAAGC-----
droSim2	x:20141506-20141671_	dsi_6	GCTAAGTAA--TAA-----TTGAGTTGGAGCTCGACITTTTGTAGTGAAGTATTCCCCTCAAGGCTAGAAAGTAGAGCTCAGTAATTTTACAAATTTGCAATGCATTCAAGACCTGT-GCGGAGTTATTACACGTCGTCATCAAAGT---GTTTT-GTTTTG-CITGTTT-AAAGC-----
dm3	chrX:21443073-21443242_	dme_444	GCTAAGTGA--TAA-----TTGAATCTGGAAATAAGAAATGGAAGAAAAATGGAATGCGAATTAARCTGGAAGTAGAGCTCAGTAATTTTACAAATTTGCAATGCCTCAAGACCTGT-GCGGAGTTTATTACACGTCGTCATCAAAGT---GTTTT-GTTTTG-PTTGTTTGATAGCT-----
droEre2	scaffold_4690:17924522-17924676_	der_47	GCTGGA--AA--TTA-----TTGCCGGAAGCTCGAGA--TTGTTGTGA--ATTCCCTCAAGGTAGAAAGTAGAGCTCAGTGATTTCGCAATTACCAATATTCGACACCTT-GCGGAGTTTTCGAAGTGTCCCGGAAGT---GTTCT----G-CTGTTTT-TGTSA-----
droYak3	X:20580765-20580915_	dya_40	GCTAAGAA--C-------CAGGAGS--TCTTTGTGAATATTCCCTCAAGGTAGAAATGTTTGTAGCTAGTGGCTTTACAAATTTGCAATACATTCAAGACCTTA-GCGGAGTTTCACACCTCTCCATTAAAGT---GTCAT-GTCTAG-ACAAATTT-AAATC-----
droEug1	scf718000408193:45617-45726_+		GCAAGTAA--A-------TCAT-----TTACTTACACTTTCATTTCAAATGTGA-STATTTCTCAAGGTCTGACAGTAGACTCAGTACCTTAACAAATTTTSCAATACATTCAAGACTT-----GTTCT-----G-----G-----G-----TGTTACTCCCTT
droTak1	scf7180000415769:353338-353498_		GCTGCSTAA--GAA-----TTAAAT-----AATTTCTCTGTGAATTTTCTTCAAGGTCTGCAAGTATAGCTAGTGAATTTTAAATATTCTSCAATGCATTCAAGACCTTTTSCAAG-GGTTCCACAGTCTTCTCTATTGSAATTGTTTTATSAAGTGTCTGTTT-GAAAGAA-----
droEle1	scf7180000491087:1001998-1002140_+		AAGCAAGTTT--T-------TAAT-----TTTGTT-----AAAACA--TTTCTGTGAATATTTCTCAAGGTCTTGAA-GATTACTTGTAGTAATTTTAAAAAGTGGTAAATATTATTCAGATCTCTGTAAAGTGTTTTTCAGTGTCTCT-----G-----G-----G-----TGTTACTCCCTT
droRho1	scf7180000774347:132-274_+		GGTATTGTGTCAACAAATTAA-----TTTCTTTGGCTTTACT--TTTCTGTGAATATTTCTCTCAAGGTCTGAAAGTATTCGAATSTATTTAAAAATTTCTCTTATTTCAAGACCTTTGCAAGTGTCTTACTCGTGATTC-----G-----G-----G-----TGTTACTCCCTT
droPic1	scf7180000453926:397642-397789_		AGTATTGTGGGAG--GGAAATTCCTCCGA-AGTGACTAAG-----CCG-----CAGAG--GTCTGTGAATATTTCTCAAGGTCTGAAAGTATAGCAACGCATTTTA-AACTCTCCATACATTCAAGACCTTTTGTAATTCCTACTGTGTCTCA-----G-----G-----G-----TGTTACTCCCTT

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

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Show Alternate Folds

Flybase annotation

intron [Dsec\GM23891-in]; CDS [Dsec\GM23891-cds]; CDS [Dsec\GM23891-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

TGGTGCCTCCGCCGGCTGAGGAAAAGGTCAAGCGCTGACGGATGCGGTAAGTCGAGCACATTTTTTCGACAAACTGAAATATTATATAAAATGCATTGTCGATTTCGAGGGCTTCGGCAATCTTCATATGCATGTCCAAGGTCTCGGGCTCTTTTAC	Read size	# Mismatch	Hit Count	Total Norm	Total	V114 embryo	V115 head	M054 female body	V113 male body
*****((((((((((((((((((((.....)))))).....)))))).....))))))*****	23	0	1	43.00	43	12	18	5	8
.....AAAATGCATTGTCGATTTCGA.....	22	0	1	35.00	35	7	8	16	4
.....AAAATGCATTGTCGATTTCG.....	22	0	1	35.00	35	7	8	16	4
.....AAAATGCATTGTCGATTTCGAGG.....	25	1	1	33.00	33	13	7	3	10
.....AAAATGCATTGTCGATTTCGAG.....	24	0	1	7.00	7	4	1	2	0
.....AAAATGCATTGTCGATTTCG.....	21	0	1	3.00	3	0	1	1	1
.....AAAATGCATTGTCGATTTCG.....	21	1	1	1.00	1	0	0	1	0
.....AAAATGCATTGTCGATTTCG.....	19	0	1	1.00	1	0	0	1	0
.....AAAATGCATTGTCGATTTCG.....	22	1	1	1.00	1	0	1	0	0
.....AAAATGCATTGTCGATTTCGAGG.....	26	2	1	1.00	1	0	0	0	1
.....TGCATGTCCAAGGTCTCGGGCT.....	22	0	1	1.00	1	0	1	0	0
.....CTCTCGCCGGCGCTGAGGAAAAGGT.....	26	0	1	1.00	1	1	0	0	0
.....TGCATTGTCGATTTCGAGG.....	20	1	1	1.00	1	0	1	0	0
.....GTAAGTCGAGCACATTTTTTT.....	21	0	1	1.00	1	0	1	0	0
.....AAAATGCATTGTCGATTTCG.....	21	0	1	1.00	1	0	0	1	0
.....CCTATCTGCATGTCCAAGGTCTCC.....	24	0	1	1.00	1	0	0	0	1

Anti-sense strand reads

					M054
ACCACGAGAGCGGCCCGCCTCCCTTTCCAGTTCGCGGACTGCCTACGC	CATTACAGCTCGTGAAAAAAA	AGCTGTTTGACTTTTATAAAT	TMTTACGTAAACAAGCTAAACGT	CCCGAAGCCGTTAGAAGGATAGACGTACAGGTTCCAGAGCCGAGAAAAATG	
*****	(((((((((((((((((((((((((((((.....))))))))))))) ..)))))))))				female body
Read #	size	Mismatch	Hit	Total	
			Count	Norm	Total

Show Alignment With Reads

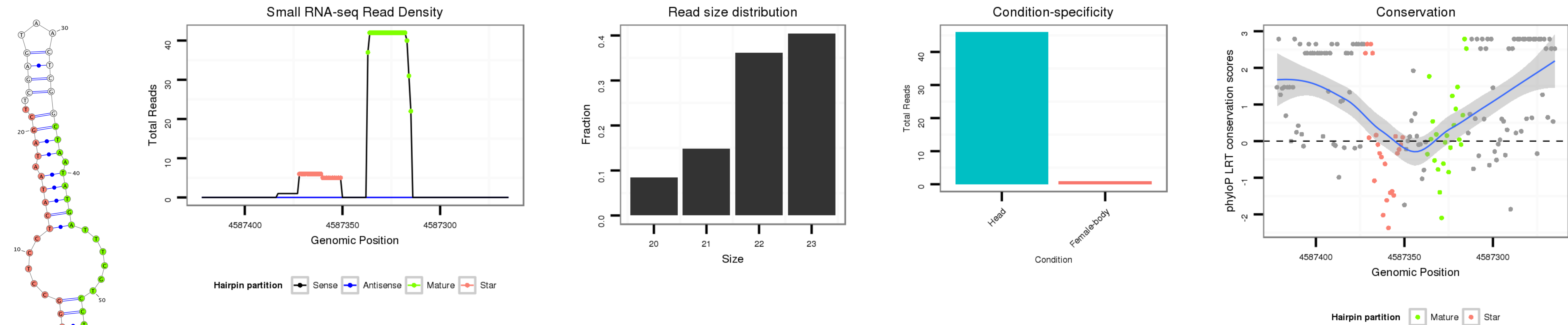
[illegible]

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

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Show Alternate Folds

Flybase annnotation

intron [Dsec\GM12206-in]; CDS [Dsec\GM12206-cds]; CDS [Dsec\GM12206-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

AAGAATTTTCATATTGTCCTCGAGCGGGGTGACTTGCACGGTGTCAAGAA GTGAGGCTCCTCATATAGCT TCGAGTAACTCGG GTAATATGATTTCGTCCTTGAAG GATCCTCGAGGAGTACCAGAGCACGGACAAATTCAACATTAACTGCACGG	Read #	Hit	Total		V15	M054	V113	
*****.(((.....(((.....(((.....)))))).....)))).....*****	size	Mismatch	Count	Norm	Total	head	female body	male body
.....CTAATATGATTTCGTCCTTGAAG.....	23	0	1	19.00	19	0	0	
.....CTAATATGATTTCGTCCTTGA.....	22	0	1	9.00	9	0	0	
.....CTAATATGATTTCGTCCTTGA.....	21	0	1	7.00	7	0	0	
.....GTGAGGCTCCTCATATAGCT.....	22	0	1	5.00	5	4	1	0
.....TAATATGATTTCGTCCTTGAAG.....	22	0	1	3.00	3	0	0	
.....CTAATATGATTTCGTCCTTG.....	20	0	1	2.00	2	2	0	0
.....TAATATGATTTCGTCCTTGA.....	20	0	1	2.00	2	2	0	0
.....TAATATGATTTCGTCCTTGAAG.....	23	1	1	1.00	1	1	0	0
.....GGTGTCAAGAGTGTGAGGCTCCT.....	23	0	1	1.00	1	1	0	0

Anti-sense strand reads

TCTCTAAAGTATAACAGGACGCTCGCCCCATGAACGGTCCACAGTTCTTCTCACTCCGAGGAGTATTATCGAAGCTCATTGAGGCCGATTATACTAAGCAGGAACCTCTCAGGAGCTCCTCATGTGCTCGTGCCTGTTTAAGTTGTAATTGACGTGCC																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																											
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Show Alignment With Reads

Re-alignment of all predicted orthologs

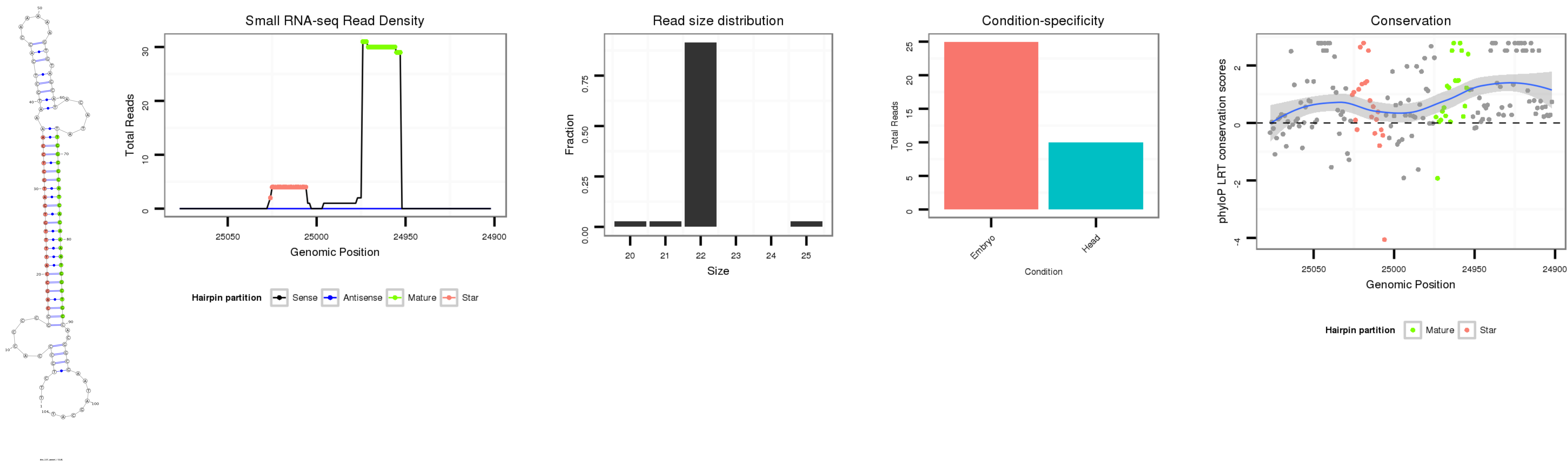
Species	Coordinate	ID	Alignment
droSec2	scaffold 4:4587265-4587422 -	Hse_1239	AAGAATTTTCATATTGTCCTGCGAGCGGGTGACTTGCCAGGTGTCAAGAAATGAGGCTCTCT-CATAAT-----A-----GC-----TTCGAGTAACTCG-----GCTAATA-----TGATTTTCGCTCTTGAAGATCTCTCGAGGAGTACCAGAGCA-----CGGACAAATTCAACATTAACCTGCACGG
droSim2	scf7180001648-25091805 -		AAGAATTTTCATATTGTCCTGCGAGCGGGTGACTTGCCAGGTGTCAAGAAATGAGGCTCTCT-CCAAAT-----G-----GC-----TTCGAGTAACTCG-----GCTAATA-----TGATTTTCGCTCTTGAAGATCTCTCGAGGAGTACCAGGCA-----CGGACAAATCAACATTAACCTGCACGG
dm3	chr3R:25745529-25745686 -		AAGAATTTTCATATTGTCCTGCGAGCGGGTGACTTGCCAGGTGTCAAGAAATGAGGCTCTCT-CCCTAT-----G-----GC-----TTCGAGTAACTCG-----GCTAATA-----TGATTTTCGCTCTTGAAGATCTCTCGAGGAGTACCAGGCA-----CGGACAAATCAACATTAACCTGCACGG
droEre2	scaffold 4820:2263154-2263315 +		AAGAATTTTCATATTGTCCTGCGAGCGGGTGACGCGCCAGGTGTCAAGAAATGAGGAGCGACCG-----GCCCGTTG-----GA-----TCCGCTTAACATG-----GCTAATA-----TCCTTTTCGCTCTTGAAGATCTCTCGAGGAGTACCAGGSA-----CGGACAAATCAACATTAACCTGCACGG
droYaK3	3R:20727498-20727655 +		AAGAATTTTCATATTGTCCTGCGAGCGGGTGACGCGCCAGGTGTCAAGAAATGAGGAGACCCCTTCTCC-----G-----A-----AATACGAGTAACCTG-----GCTAATA-----TCCTTTTCGCTCTTGAAGATCTCTCGAGGAGTACCAGGSA-----CGGACAAATCAACATTAACCTGCACCG
droEug1	scf7180000409555-216289-216448 -		AAGAATTTTCATATTGTCCTGCGAGCGGGTGACGCGGAGGTGTCAAGAAATGAGCGTGTTCGCGCTCCTCCTTT-----G-----GCGCTTCGCTTCAGTA-----TACCTTTTCGCTCTTGAAGATCTCTCGAGGAGTACCAGGSA-----CGGACAAATCAACATTAACCTGCACGG
droBial1	scf7180000302113:1662676-1662833 +		AAGAATTTTCATATTGCTCGGAGCGCGGTGATCGCCCGGTGTCAAGAAATGAGGCTTCTGCGTCTT-----G-----C-----T-----AATTCGCTCTCGA-----GCTATC-----ACGGAATACCTTTGAAGATCTCTCGAGGAGTACCAGGSA-----CGGACAAATCAACATTAACCTGCACGG
droTak1	scf7180000415765:122036-122200 -		AAGAATTTTCATATTGCTCTGCGAGCGCGGTGATCGCCCGGTGTCAAGAAATGAGCGTCAAT-TGGGAT-----G-----GTTCTTGG-----GATCTGAGTA-----CTAA-AGC-ATCCTCCCTAAACCSAAGATCTCTCGAGGAGTATTCGSA-----CGGACAAATCAACATTAACCTGCACGG
droEle1	scf7180000491280:2011236-2011399 -		AAGAATTTTCATATTGCTCTGCGAGCGCGGCSACCTACCGCGGTGTCAAGAAATGAGAGTGAA-G-----GTCCTTT-----CGA-TCTGATTCGAGTAATTC-----CGT-G-----ATTCCTGCTCCTTGAAGCTCTCTCGAGGAGATATGSA-----CGGACAAATCAACATTAACCTGCACGG
droRho1	scf7180000779336:242820-242976 +		AAGAAATTCATATTGCTCTGCGAGCGCGGTGACCTCCCGGTGTCAAGAAATGAGGCTGTGA-CAG---GTCCTTC-----GCG-TCTAACCCTGAGTA-----ATTCCTTTTCGCTCTTGAAGCTCTCTCGAGGAGATATGSA-----CGGACAAATCAACATTAACCTGCACGG
droFic1	scf7180000453826:857211-857371 +		AAGAATTTTCATATTGCTCTGCGAGCGCGGTGACCTCCCGGTGTCAAGAAATGAGCGGTAA-TGGTCTC-GTCCCTTT-----CGA-CTCGTTCTCGAGTA-----ATTCCTTTTCGCTCTTGAAGATCTCTGATGAGTATCGSA-----CGGACAAATCAACATTAACCTGCACGG
droKik1	scf7180000302475:1793114-1793199 -		TAGCTCTCCCTTT-----G-----G-----GCTAA-----GAGTTTCGCTCTTGAAGATCTCTGAGGATACCTCGSCT-----CGGATAGCTCAACATTAACCTGCACGG
droAna3	scaffold 13340:20741125-20741285 -		AAGAATTTTCATATTGCTCTGCGAGCGCGGTGATCTCCCGGTGTCAAGAAATGAGAGCTAAGCTTAA-TGCTCCTCCTGTTT-----TTC-TTTGTTGTSAGTA-----ATATATATCTCTTGAAGATATCGAGGAGTATTCGSA-----CGGAAAGCTTAACATTAACCTGCACGG
droBip1	scf7180000396413:1658033-1658191 +		AAGAATTTTCATTTGCTCTGCGAGCGCGGTGATATCCCGGTGTCAAGAAATGAGGCTGAG-TGCTCCA-GTTTAT-----CTTTTTTTGTCAGTA-----ATCCTTAATCTCTTGAAGATATCGAGGAGATATGSA-----CGGAAAGCTTAACATTAACCTGCACGG
dp5	2:844529-844695 -		AAGAATTTTCATCTGCTCTGCGAGCGCGGTGACCTCCCGGCTCAAGAAATGAGAGCTATTG-CA-CAG-----ACGTAAAGC-----GATCG-----TTGTTGGGTGGTTCG-----ATA-----ATTCCTTAACCTTGAAGATCTCTGAGGAGTTGAGGSA-----CGGAAAGCTCAACATTAACCTGCACGG
droPer2	scaffold 7:3626978-3627144 -		AAGAATTTTCATCTGCTCTGCGAGCGCGGTGACCTCCCGGCTCAAGAAATGAGAGCTATTG-CA-CAG-----ACGTAAAGC-----GATCG-----TTGTTGGGTGGTTCG-----ATA-----ATTCCTTAACCTTGAAGATCTCTGAGGAGTTGAGGSA-----CGGAAAGCTCAACATTAACCTGCACGG
droWil2	scf2_1100000004943:9034581-9034738 +		AAGAATTTTCATTTATCTCTGCGAGCGCGGTGATCTCAAGGTGTCAAGAAATGAGCTTAA-TGCTTTAA-A-----TCAGAAAGC-----TCGATTAATCTTA-----ATCG-----TGAA-----TCCAGGATCTTGAGGATAC-----GGAATGAGTGGGAATTCATTAATTAATGCACCG
droVir3	scaffold 12855:1685172-1685333 +	dvi_3434	AAGAAATTCATCTGCTCTGCGAGCGCGGTGATTTCCAGGTGTCAAAAGTTCAGTATTTCT-TGTG-----T-----G-----TCCCTGGCAG-----CTAATAGCAA-C-CAAGTG-TTC-TAGATTTCTTGAGGATATGCCCAACACCATCTGSAAGCTTAACATTAACCTGCACGG
droMoJ3	scaffold 6540:27405239-27405406 +		AAGAAATTCATCTGCTCTGCGAGCGCGGTGATTTGCCAGGTGTCAAAAGTTCAGTATTCATAGGAT-----GAGAA-----TCTGA-----CTAG-----GTAAT-CA-----ATGCTCGCTTACTAGAAATCTGAGGATACGCGCGACACCGCTGSAAGCTTAACATTAACCTGCACGG
droGr12	scaffold 14624:4220901-4221060 +		AAGAAATTCATTTAGCTCTGCGAGCGCGGTGATTTGGCGGTGTCAAGAAATCAGTATTTGATTGGAT-TTCCTTG-----G-----CAA-TC-----TAATG-A-CAGCCTAGGTTTCAGACTTCTGATGATATGCGGAGCACCATTCTGSAAGCTTAACATTAACCTGCACGG

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

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Show Alternate Folds

Flybase annotation

intron [Dsec\GM13643-in]; utr3 [utr3_plus_6270]; utr5 [utr5_plus_11278]

No Repeatable elements found

Sense Strand Reads

[illegible]

Anti-sense strand reads

[illegible]

Re-alignment of all predicted orthologs

[illegible]

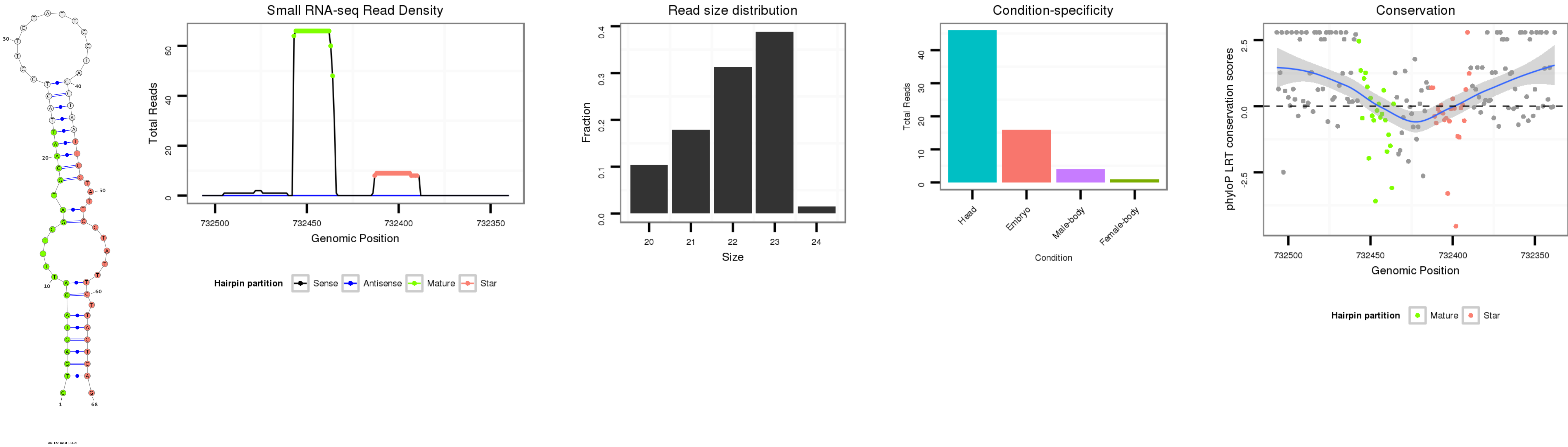
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	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	2

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dse_122	scaffold_20:732390-732457 -	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 [Dsec\GM17562-in]; CDS [Dsec\GM17562-cds]; CDS [Dsec\GM17562-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

AGCTCGAGTTGCTCGACCTGAGCTTCTGTGACAACATCATGGATCGGGATGTGAGTAGATTTTCGATGGAATTAGTCCTTCTATTCTAGCTAATTCCTATTCTTACTCAGTTCGATTGCTGGCGGAATGGTCGCGACAATTTAACGTGGACATCAAGAG	Read #	Mismatch	Hit Count	Total Norm	Total	V115 head	V114 embryo	M054 female body	V113 male body
*****.(((((((.....((((((((.....))))))))))..)).....))..))))).*****	23	0	1	26.00	26	15	9	0	2
.....GTGAGTAGATTTTCGATGGAATT.....	22	0	1	19.00	19	12	5	0	2
.....GTGAGTAGATTTTCGATGGAAT.....	21	0	1	12.00	12	11	1	0	0
.....GTGAGTAGATTTTCGATGGA.....	20	0	1	6.00	6	6	0	0	0
.....GTGAGTAGATTTTCGATGGA.....	20	0	1	6.00	6	1	4	1	0
.....TGAGTAGATTTTCGATGGAATT.....	22	0	1	2.00	2	0	1	1	0
.....GTGAGTAGATTTTCGATGGAAT.....	22	1	1	1.00	1	0	1	0	0
.....ATTCTATTCTCTATTCTTACTCAGT.....	26	0	1	1.00	1	0	0	1	0
.....GTGAGTAGATTTTCGATGGAATTA.....	24	0	1	1.00	1	1	0	0	0
.....TCCTATTCTCTATTCTTACTCAG.....	24	1	1	1.00	1	0	1	0	0
.....GACAACATCATGGATCGG.....	18	0	1	1.00	1	0	0	1	0
.....TCGACCTGAGCTTCTGTGACA.....	21	0	1	1.00	1	0	1	0	0
.....TCCTATTCTCTATTCTTACTCAGT.....	24	0	1	1.00	1	0	1	0	0
.....TTCTATTCTCTATTCTTACTCAGT.....	20	0	1	1.00	1	1	0	0	0

Anti-sense strand reads

TCGACGCTCAACGAGCTGGACTCGAAGACACTGTTGTAGTACCTAGCCCTA	CACTCATCTAAAGCTACCTTA	ATCAGGAAGATAAGGATCGATT	AAGGATAAGGATAAAGATGAGTCA	AGCTAAACGACCGCCTTACCACGCGTGTAAAT	TGCACCTGTAGTCTTC						V114	M054	V115	V113
*****.(((((((.....((.((((((((.....)))))))))).....)).....)).....).*****						Read #	Hit	Total			embryo	female	male	body
						size Mismatch	Count	Norm						
									Total					

Show Alignment With Reads

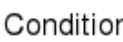
Re-alignment of all predicted orthologs

[illegible]

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

Predicted structure



Show Alternate Folds

Flybase annotation

Antisense to utr5 [utr5_minus_13073]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

Anti-sense strand reads

Show Alignment With Reads

Re-alignment of all predicted orthologs

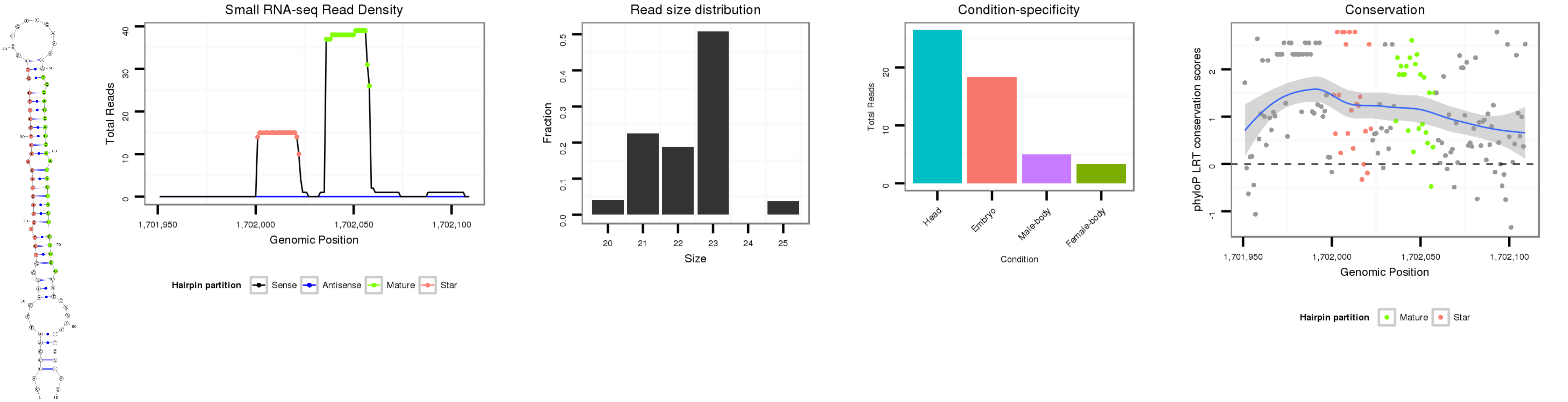
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	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	2
rescue.candidate	1

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dse_126	scaffold_1:1702001-1702059 +	confident	Canonical miRNA	CDS	[View on UCSC Genome Browser (Cornell Mirror)]

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

Predicted structure



Show Alternate Folds

Flybase annotation

CDS [Dsec/GM21015-cds]; utr5 [utr5_plus_3417]

Repeatable elements

Name	Class	Family	Strand
Gypsy8-1 Dpse-int	LTR	Gypsy	+

Sense Strand Reads

hide 3p reads show mid mismatch reads

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Anti-sense strand reads

	Read #	Hit	Total	Total	M054
	size	Mismatch	Count	Norm	female
ACGCTCCTCTCTCCGGTCGCCGTATTACGCGCCGCTGTCGCTTAAGTACCCAGAAACAACGACTACAAACAACGCGGCACCTTTCTACGTCGTCGTTGTCGTCGCCGCGTAGTTAAAGCGCTCGTCGTCGTCGATGTCCTTCCAGGTACACCGTCTCT					
*****.(((((((.(((.(((((((.((((((((((.....))))).)))))))).)))))))).))))).*****					

Show Alignment With Reads

Re-alignment of all predicted orthologs

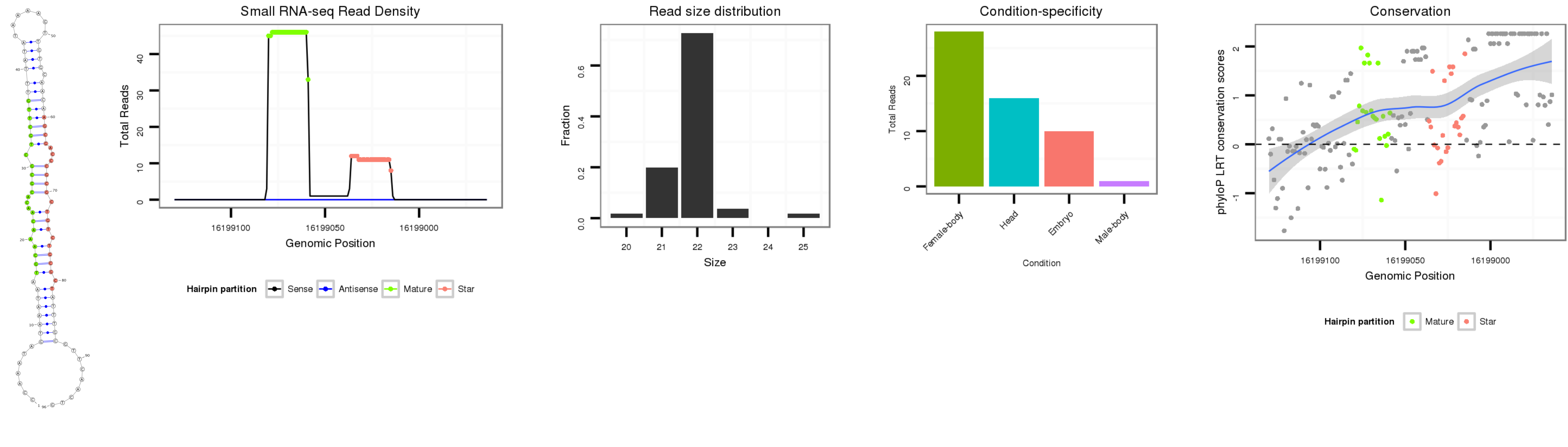
Species	Coordinate	ID	Alignment
droSec2	scaffold_1:1701951-1702109 +	dse_126	TGCGAGGAGAGAGGC--CAGCGGCATAATGCCGGCGACAGCGAATTCA-----TGGGCTCTTGTGCTGA-----TGTTGTG-----GTCGCCGT-----GGAAA--GATGCAGCAGC---AACAGCAGCGGGC--CATCAATTT--CGCA-----GCAGCAGCAGCAGCTACAGGAAGGTCCA-----GTGGCAGGA
droSim2	2r:4879074-4879232 +	dsi_14	TGCGAGGAGAGAGCGC--CAGCGGCATAATGCCGGCGACAGCGAATTCA-----TGGGCTCTTGTGCTG-----TGTTGTG-----GTCGCCGT-----GGAAA--GATGCAGCAGC---AACAGCAGCGGGC--CATCAATTT--CGCA-----GCAGCAGCAGCAGCTACAGGAAGGTCCA-----GTGGCAGGA
dm3	chr2R:4062137-4062295 +	dme_405	TGCGAGGAGAGAGCGC--CAGCGGCATAATGCCGGCGACAGCGAATTCA-----TGCCTCTTGTGCTG-----TGTTGTG-----GTCGCCGT-----GGAAA--GATGCAGCAGC---AACAGCAGCGGGC--CATCAATCT--CGCA-----GCAGCAGCAGCAGCTACAGGAAGGTCCA-----GTGGCAGGA
droEre2	scaffold_4929:18572407-18572565 -	der_1518	TGCGAGGAGAGAGCGC--CAGCGGCATAATGCCGGCGACAGCGAATTCA-----TGGGCTCTTGTGCTG-----TGTTGTG-----GTCGCCGT-----GGAAA--GATGCAGCAGC---AACAGCAGCGGGC--CATCAATCT--CGCA-----GCAGCAGCAGCAGCTACAGGAAGGTCCA-----GTGGCAGGA
droYak3	2L:16712475-16712633 +	dya_1790	TGCGAGGAGAGAGCGC--CAGCGGCATAATGCCGGCGACAGCGAATTCA-----TGGGCTCTTGTGCTG-----TGTTGTG-----GTCGCCGT-----GGAAA--GATGCAGCAGC---AACAGCAGCGGGC--CATCAATCT--CGCA-----GCAGCAGCAGCAGCTACAGGAAGGTCCA-----GTGGCAGGA
droEug1	scf7180000409474:2883197-2883367 +		TGCGAGGAGAGAGCGC--CAGCGGCATAATGCCGGCGACAGCGAATTCA-----TGGGCTCTTGTGCTG-----TGTTGTG-----GTCGCCGT-----GGAAA--GATGCAGCAGC---AACAGCAGCGGGC--CATCAATCT--CGCA-----GCAGCAGCAGCAGCTACAGGAAGGTCCA-----GTGGCAGGA
droBial	scf7180000302291:1913615-1913776 +		TGCGAGGAGAGAGCGC--CAGCGGCATAATGCCGGCGACAGCGAATTCA-----TGGGCTCTTGTGCTG-----TGTTGTG-----GTCGCCGT-----GGAAA--GATGCAGCAGC---AACAGCAGCGGGC--CATCAATCT--CGCA-----GCAGCAGCAGCAGCTACAGGAAGGTCCA-----GTGGCAGGA
droTak1	scf7180000415088:43555-43721 -		TGCGAGGAGAGAGCGC--CAGCGGCATAATGCCGGCGACAGCGAATTCA-----TGGGCTCTTGTGCTG-----TGTTGTG-----GTCGCCGT-----GGAAA--GATGCAGCAGC---AACAGCAGCGGGC--CATCAATCT--CGCA-----GCAGCAGCAGCAGCTACAGGAAGGTCCA-----GTGGCAGGA
droEle1	scf7180000491240:859170-859325 +		TGCGAGGAGAGAGCGC--CAGCGGCATAATGCCGGCGACAGCGAATTCA-----TGGGCTCTTGTGCTG-----TGTTGTG-----GTCGCCGT-----GGAAA--GATGCAGCAGC---AACAGCAGCGGGC--CATCAATCT--CGCA-----GCAGCAGCAGCAGCTACAGGAAGGTCCA-----GTGGCAGGA
droRho1	scf7180000770177:147425-147580 +		TGCGAGGAGAGAGCGC--CAGCGGCATAATGCCGGCGACAGCGAATTCA-----TGGGCTCTTGTGCTG-----TGTTGTG-----GTCGCCGT-----GGAAA--GATGCAGCAGC---AACAGCAGCGGGC--CATCAATCT--CGCA-----GCAGCAGCAGCAGCTACAGGAAGGTCCA-----GTGGCAGGA
droFic1	scf7180000453215:147147-147286 -		TGCGAGGAGAGAGCGC--CAGCGGCATAATGCCGGCGACAGCGAATTCA-----TGGGCTCTTGTGCTG-----TGTTGTG-----GTCGCCGT-----GGAAA--GATGCAGCAGC---AACAGCAGCGGGC--CATCAATCT--CGCA-----GCAGCAGCAGCAGCTACAGGAAGGTCCA-----GTGGCAGGA
droK1k1	scf7180000302411:115803-115943 -		TGCGAGGAGAGAGCGC--CAGCGGCATAATGCCGGCGACAGCGAATTCA-----TGGGCTCTTGTGCTG-----TGTTGTG-----GTCGCCGT-----GGAAA--GATGCAGCAGC---AACAGCAGCGGGC--CATCAATCT--CGCA-----GCAGCAGCAGCAGCTACAGGAAGGTCCA-----GTGGCAGGA
droAna3	scaffold_13266:1925319-1925461 -	dan_4048	TGCGAGGAGAGAGCGC--CAGCGGCATAATGCCGGCGACAGCGAATTCA-----TGGGCTCTTGTGCTG-----TGTTGTG-----GTCGCCGT-----GGAAA--GATGCAGCAGC---AACAGCAGCGGGC--CATCAATCT--CGCA-----GCAGCAGCAGCAGCTACAGGAAGGTCCA-----GTGGCAGGA
droBip1	scf7180000396730:2911821-2911954 -		TGCGAGGAGAGAGCGC--CAGCGGCATAATGCCGGCGACAGCGAATTCA-----TGGGCTCTTGTGCTG-----TGTTGTG-----GTCGCCGT-----GGAAA--GATGCAGCAGC---AACAGCAGCGGGC--CATCAATCT--CGCA-----GCAGCAGCAGCAGCTACAGGAAGGTCCA-----GTGGCAGGA
dp5	3:20444903-2045007 +		TGCGAGGAGAGAGCGC--CAGCGGCATAATGCCGGCGACAGCGAATTCA-----TGGGCTCTTGTGCTG-----TGTTGTG-----GTCGCCGT-----GGAAA--GATGCAGCAGC---AACAGCAGCGGGC--CATCAATCT--CGCA-----GCAGCAGCAGCAGCTACAGGAAGGTCCA-----GTGGCAGGA
droPer2	scaffold_2:2217508-2217612 +	dpe_2519	TGCGAGGAGAGAGCGC--CAGCGGCATAATGCCGGCGACAGCGAATTCA-----TGGGCTCTTGTGCTG-----TGTTGTG-----GTCGCCGT-----GGAAA--GATGCAGCAGC---AACAGCAGCGGGC--CATCAATCT--CGCA-----GCAGCAGCAGCAGCTACAGGAAGGTCCA-----GTGGCAGGA
droW12	scf2_1100000004729:2691966-2692109 -		TGCGAGGAGAGAGCGC--CAGCGGCATAATGCCGGCGACAGCGAATTCA-----TGGGCTCTTGTGCTG-----TGTTGTG-----GTCGCCGT-----GGAAA--GATGCAGCAGC---AACAGCAGCGGGC--CATCAATCT--CGCA-----GCAGCAGCAGCAGCTACAGGAAGGTCCA-----GTGGCAGGA
droVir3	scaffold_12875:9059120-9059250 +		TGCGAGGAGAGAGCGC--CAGCGGCATAATGCCGGCGACAGCGAATTCA-----TGGGCTCTTGTGCTG-----TGTTGTG-----GTCGCCGT-----GGAAA--GATGCAGCAGC---AACAGCAGCGGGC--CATCAATCT--CGCA-----GCAGCAGCAGCAGCTACAGGAAGGTCCA-----GTGGCAGGA
droMoJ3	scaffold_6496:18113608-18113745 -		TGCGAGGAGAGAGCGC--CAGCGGCATAATGCCGGCGACAGCGAATTCA-----TGGGCTCTTGTGCTG-----TGTTGTG-----GTCGCCGT-----GGAAA--GATGCAGCAGC---AACAGCAGCGGGC--CATCAATCT--CGCA-----GCAGCAGCAGCAGCTACAGGAAGGTCCA-----GTGGCAGGA
droGr12	scaffold_15245:2390645-2390785 +		TGCGAGGAGAGAGCGC--CAGCGGCATAATGCCGGCGACAGCGAATTCA-----TGGGCTCTTGTGCTG-----TGTTGTG-----GTCGCCGT-----GGAAA--GATGCAGCAGC---AACAGCAGCGGGC--CATCAATCT--CGCA-----GCAGCAGCAGCAGCTACAGGAAGGTCCA-----GTGGCAGGA

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

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Show Alternate Folds

Flybase annotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads

show mid mismatch reads

[illegible]

Anti-sense strand reads

[illegible]

Show Alignment With Reads

Re-alignment of all predicted orthologs

[illegible]

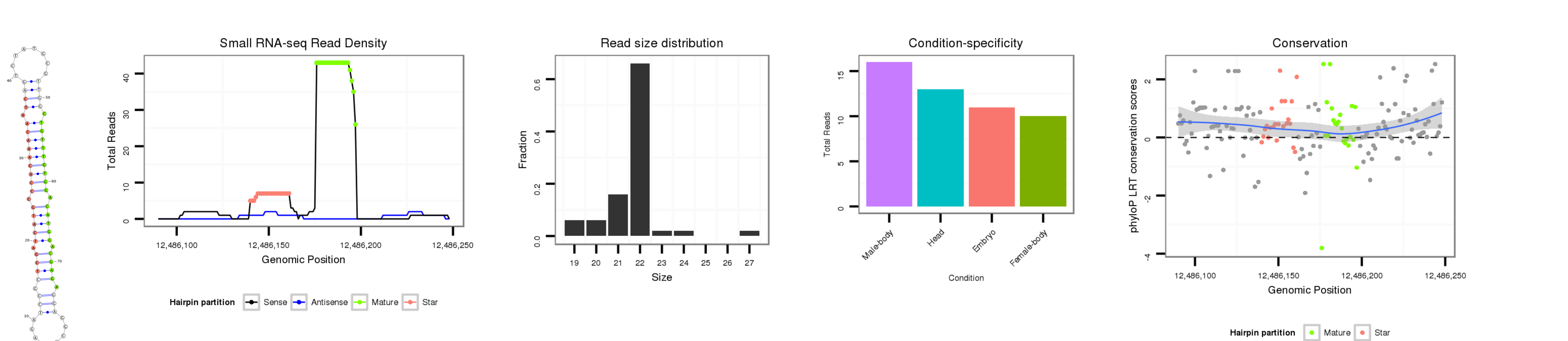
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	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dse_135	scaffold_0:12486140-12486198 +	confident	Canonical miRNA	antisense_to_3pUTR	[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 utr3 [utr3_plus_5889]; utr3 [utr3_minus_7616]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

	Read # size	Mismatch	Hit Count	Total Norm	Total	V113 male body	V115 head	M054 female body	V114 embryo
AGCAATATGTTTATTTTGGAGGAATAGCGTAATGGAATTTGATAGATCCGCTCGATCATGCCCAACAACAATCAGTCTATGCGTTGGCTGTTTGTGGACATGGACGAGAGGAGGCGGTTACAAAGTACAACATACGACACACACCGTGCATCAACCAACCGA	22	0	1	26.00	26	8	7	2	9
.....CTGTTTGTGGACATGGACGAGA.....	21	0	1	8.00	8	2	3	2	1
.....TCGATCATGCCCAACAACAATC.....	22	0	1	4.00	4	1	0	3	0
.....CTGTTTGTGGACATGGACG.....	19	0	1	3.00	3	3	0	0	0
.....CTGTTTGTGGACATGGACGA.....	20	0	1	3.00	3	0	0	2	1
.....CTGTTTGTGGACATGGACGAGA.....	23	1	1	3.00	3	2	0	1	0
.....TCGATCATGCCCAACAACAATCAG.....	24	0	1	1.00	1	0	1	0	0
.....TTTGTGGACATGGACGAGAGGAG.....	24	1	1	1.00	1	0	1	0	0
.....TTGGCTGTTTGTGGACATGGAC.....	22	0	1	1.00	1	1	0	0	0
.....CTGTTTGTGGACATGGACGAGA.....	23	1	1	1.00	1	0	0	1	0
.....TTTGAGGAATAGCGTAATGGAATTTG.....	26	0	1	1.00	1	0	0	0	1
.....ATCGCTTGGCTGTTTGTGGACATGGAC.....	27	0	1	1.00	1	1	0	0	0
.....ATCATGCCCAACAACAATCAGTC.....	23	0	1	1.00	1	0	0	1	0
.....ACACCGTGCATCAACCAACCG.....	21	0	1	1.00	1	0	1	0	0
.....ATTTTGAGGAATAGCGTAATG.....	21	0	1	1.00	1	0	0	1	0
.....CTGTTTGTGGACATGGACGAGAA.....	24	2	1	1.00	1	0	1	0	0
.....GCTGTTTGTGGACATGGACGAG.....	22	0	1	1.00	1	0	1	0	0
.....TTGGCTGTTTGTGGACATGG.....	21	1	1	1.00	1	1	0	0	0
.....TCATGCCCAACAACAATCAGTC.....	22	0	1	1.00	1	0	1	0	0

Anti-sense strand reads

	Read # size	Mismatch	Hit Count	Total Norm	Total	V113 male body	V115 head
TCGTTATACAAATAAACTCCTTATCGCATTTACCTTTAACTATCTAGGCCAGCTACTACGGGTGTTTGTGTACGAGATACGCCAACCSACAAACACCTGTACCTGCTCTCCTCCGCAAGTGTTCATGTTGTATGCTGTGTGTGGCAGTAGTTGGTTGGCT	21	0	1	1.00	1	1	0
.....TAGGCGAGCTAGTACGGGTGT.....	21	0	1	1.00	1	0	1
.....ATGTTGTATGCTGTGTGTGGCA.....	22	0	1	1.00	1	0	1
.....GTGTGGCAGCTAGTTGGTTG.....	20	0	1	1.00	1	1	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droSec2	scaffold_0:12486090-12486248 +	dse_135	AGCAAT-----ATGTTTAT--TTTGAGGAATAGCGTAATG-GAAATT-G--ATAGATCCGCTCGATCATGCCCAACAACAATCAGTCT-AT-G-----C-GTTGG-----CTGTTTGTGGACATGGAC-----GAGAGGAGGCG--TTAC---AA-----GT-----ACAACA-----TAC---GA--CACACACCGTGC-----ATCAACCAACCGA
droSim2	3r:11657846-11658004 +	dse_135	AGCAAT-----ATGTTTAT--TTTGAGGAATAGCGTAATG-GAAATT-G--ATAGATCCGCTCGATCATGCCCAACAACAATCAGTCT-AT-G-----C-GTTGG-----CTGTTTGTGGACATGGAC-----GAGAGGAGGCG--TTAC---AA-----GT-----ACAACA-----TAC---GA--CACACACCGTGC-----ATCAACCAACCGA
dm3	chr3R:9521062-9521220 -	dse_135	AGCAAT-----ATGTTTAT--TTTGAGGAATAGCGTAATG-GAAATT-G--ATAGATCCGCTCGATCATGCCCAACAACAATCAGTCT-AT-G-----C-GTTGG-----CTGTTTGTGGACATGGAC-----GAGAGGAGGCG--TTAC---AA-----GT-----ACAACA-----TAC---GA--CACACACCGTGC-----ATCAACCAACCGA
droEre2	scaffold_4770:12114097-12114258 +	der_1533	AGCAAT-----ATGTTTAT--TTTGAGGAATAGCGTAATG-GAAATT-A--ATAGATCCCTCGACATGCCCAACAACAATCAGTCT-AT-A-----C-GTTGG-----CTGTTTGTGGACATGGAC-----GAGAGGAGGCG--TTAC---AA-----GT-----ACAACA-----TAC---GA--CACACACCGTGC-----ATCAACCAACCGA
droYak3	3R:13829456-13829614 -		AGCAAT-----ATGTTTAT--TTTGAGGAATAGGAATAATG-GAAATT-A--ATAGATTCCTCGACATGCCCAACAACAATCAGTCT-AT-A-----C-GTTGG-----CTGTTTGTGGACATGGAC-----GAGAGGAGGCG--TTAC---AA-----GT-----ACAACA-----TAC---GA--CACACACCGTGC-----ATCAACCAACCGA
droEug1	scaf7180000409802:453288-453444 +		AGCAAT-----ATGTTTAT--TTTGAGGAATAGCGTAATG-GAAATT-A--ATAGATTCCTCGACATGCCCAACAACAATCAGTCT-AT-A-----C-GTTGG-----CTGTTTGTGGACATGGAC-----GAGAGGAGGCG--TTAC---AA-----GT-----ACAACA-----TAC---GA--CACACACCGTGC-----ATCAACCAACCGA
droBial	scaf7180000302402:2257639-2257797 -		AGCAAT-----ATGTTTAT--TTTGAGGAATAGCGTAATG-GAAATT-A--ATAGATTCCTCGACATGCCCAACAACAATCAGTCT-AT-A-----C-GTTGG-----CTGTTTGTGGACATGGAC-----GAGAGGAGGCG--TTAC---AA-----GT-----ACAACA-----TAC---GA--CACACACCGTGC-----ATCAACCAACCGA
droTak1	scaf7180000415380:348700-348870 -		AGCAAT-----ATGTTTAT--TTTGAGGAATAGCGTAATG-GAAATT-A--ATAGATTCCTCGACATGCCCAACAACAATCAGTCT-AT-A-----C-GTTGG-----CTGTTTGTGGACATGGAC-----GAGAGGAGGCG--TTAC---AA-----GT-----ACAACA-----TAC---GA--CACACACCGTGC-----ATCAACCAACCGA
droE1e1	scaf7180000491047:1670847-1671018 +		AGCAAT-----ATGTTTAT--TTTGAGGAATAGCGTAATG-GAAATT-A--ATAGATTCCTCGACATGCCCAACAACAATCAGTCT-AT-A-----C-GTTGG-----CTGTTTGTGGACATGGAC-----GAGAGGAGGCG--TTAC---AA-----GT-----ACAACA-----TAC---GA--CACACACCGTGC-----ATCAACCAACCGA
droRho1	scaf7180000679095:41483-41655 +		AGCAAT-----ATGTTTAT--TTTGAGGAATAGCGTAATG-GAAATT-A--ATAGATTCCTCGACATGCCCAACAACAATCAGTCT-AT-A-----C-GTTGG-----CTGTTTGTGGACATGGAC-----GAGAGGAGGCG--TTAC---AA-----GT-----ACAACA-----TAC---GA--CACACACCGTGC-----ATCAACCAACCGA
droFic1	scaf7180000453912:20388-20549 -		AGCAAT-----ATGTTTAT--TTTGAGGAATAGCGTAATG-GAAATT-A--ATAGATTCCTCGACATGCCCAACAACAATCAGTCT-AT-A-----C-GTTGG-----CTGTTTGTGGACATGGAC-----GAGAGGAGGCG--TTAC---AA-----GT-----ACAACA-----TAC---GA--CACACACCGTGC-----ATCAACCAACCGA
droK1k1	scaf7180000302706:531091-531275 -		AGCAAT-----ATGTTTAT--TTTGAGGAATAGCGTAATG-GAAATT-A--ATAGATTCCTCGACATGCCCAACAACAATCAGTCT-AT-A-----C-GTTGG-----CTGTTTGTGGACATGGAC-----GAGAGGAGGCG--TTAC---AA-----GT-----ACAACA-----TAC---GA--CACACACCGTGC-----ATCAACCAACCGA
droAna3	scaffold_13340:10521960-10522120 +	dan_4053	AGCAAT-----ATGTTTAT--TTTGAGGAATAGCGTAATG-GAAATT-A--ATAGATTCCTCGACATGCCCAACAACAATCAGTCT-AT-A-----C-GTTGG-----CTGTTTGTGGACATGGAC-----GAGAGGAGGCG--TTAC---AA-----GT-----ACAACA-----TAC---GA--CACACACCGTGC-----ATCAACCAACCGA
droBip1	scaf7180000396708:5537324-5537484 +		AGCAAT-----ATGTTTAT--TTTGAGGAATAGCGTAATG-GAAATT-A--ATAGATTCCTCGACATGCCCAACAACAATCAGTCT-AT-A-----C-GTTGG-----CTGTTTGTGGACATGGAC-----GAGAGGAGGCG--TTAC---AA-----GT-----ACAACA-----TAC---GA--CACACACCGTGC-----ATCAACCAACCGA
dp5	2:10072318-10072498 -	dps_3847	AGCAAT-----ATGTTTAT--TTTGAGGAATAGCGTAATG-GAAATT-A--ATAGATTCCTCGACATGCCCAACAACAATCAGTCT-AT-A-----C-GTTGG-----CTGTTTGTGGACATGGAC-----GAGAGGAGGCG--TTAC---AA-----GT-----ACAACA-----TAC---GA--CACACACCGTGC-----ATCAACCAACCGA
droPer2	scaffold_0:10409010-10409190	dps_2525	AGCAAT-----ATGTTTAT--TTTGAGGAATAGCGTAATG-GAAATT-A--ATAGATTCCTCGACATGCCCAACAACAATCAGTCT-AT-A-----C-GTTGG-----CTGTTTGTGGACATGGAC-----GAGAGGAGGCG--TTAC---AA-----GT-----ACAACA-----TAC---GA--CACACACCGTGC-----ATCAACCAACCGA
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droMo3	scaffold_6540:11623578-11623755 +		AGCAAT-----ATGTTTAT--TTTGAGGAATAGCGTAATG-GAAATT-A--ATAGATTCCTCGACATGCCCAACAACAATCAGTCT-AT-A-----C-GTTGG-----CTGTTTGTGGACATGGAC-----GAGAGGAGGCG--TTAC---AA-----GT-----ACAACA-----TAC---GA--CACACACCGTGC-----ATCAACCAACCGA

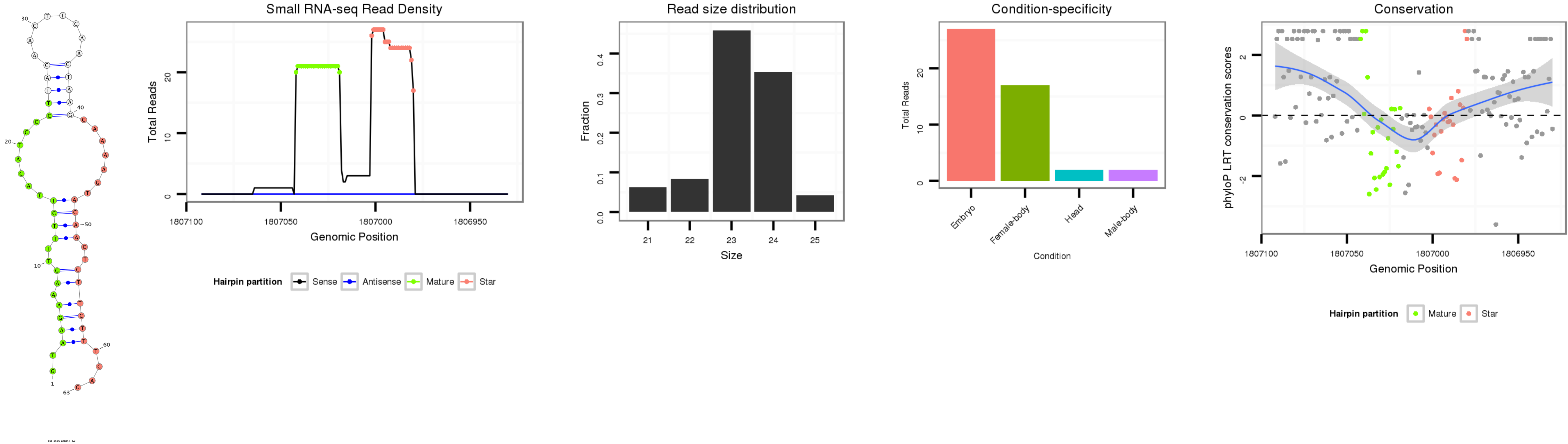
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PASS/FAIL	
crit.star	1
crit.loop	0
crit.mor	0
crit.hair	1
crit.total	1
crit.pairing	1
crit.top3	1
crit.ptop3	1
crit.uni	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	1
rescue.confident	0
rescue.candidate	2

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:
dse_1565	scaffold_8:1806980-1807042	confident	Mirtron	intron

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Show Alternate Folds

Flybase annotation

intron [Dsec/GM22724-in]; CDS [Dsec/GM22724-cds]; CDS [Dsec/GM22724-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

	Read #	size	Mismatch	Hit Count	Total Norm	Total	V114 embryo	M054 female body	V113	V115 male head body
GGACTGTCAACGACGAGGACAACTACACAGCGCGCTGGACAACCTCCGGAGGTAAGAAAGTTTGTTCATCCCTTACAACCTCAAGTAAGCAAAAGTACAACCTCTTCTTTTCAGACGAAGACTCGGTTGCCGATGCTCTCCATAGTGACTCCACGCGGGGACGT										
*****.(((.((.(((.....(((.....))))).))))).*****										
.....GTAAGAAAGTTTGTTCATCCCT.....	24	0	1	17.00	17	16	0	1	0	
.....CAAAAGTACAACCTCTTCTTTTCAG.....	23	0	1	17.00	17	6	11	0	0	
.....CAAAAGTACAACCTCTTCTTTTCAG	24	1	1	4.00	4	3	1	0	0	
.....CAAAAGTACAACCTCTTCTTTTCAG.....	22	0	1	4.00	4	1	3	0	0	
.....CAAAAGTACAACCTCTTCTTTTC.....	21	0	1	2.00	2	1	1	0	0	
.....TACAACCTCAAGTAAGCAAAAGT.....	23	0	1	2.00	2	1	0	1	0	
.....GTAAGAAAGTTTGTTCATCCCT.....	25	0	1	2.00	2	2	0	0	0	
.....AGCGCGCTGGACAACCTCCGGA.....	21	0	1	1.00	1	1	0	0	0	
.....AAAAGTACAACCTCTTCTTTTCAG.....	21	0	1	1.00	1	0	1	0	0	
.....AAAGTACAACCTCTTCTTTTCAG	22	1	1	1.00	1	1	0	0	0	
.....TAGAAAGTTTGTTCATCCCT.....	23	0	1	1.00	1	0	1	0	0	
.....AAAAGTACAACCTCTTCTTTTCAG.....	23	1	1	1.00	1	1	0	0	0	
.....GTAAGAAAGTTTGTTCATCCCT.....	23	0	1	1.00	1	0	0	0	1	
.....AACTTCAAGTAAGCAAAAGTACA.....	23	0	1	1.00	1	0	0	0	1	

Anti-sense strand reads

CCTGACAGTGTCTCTCTGTTGATGTGTGCGCGACCTGTTGAGGCGCTC	CATTCTTTCAAACAATGTAGGGA	ATGTTGAAGTTCATTCC	GTTTTTCATGTTGAGA	AAAGTCTGCTTTGACGCACGGCTACGAGAGGTATCACTGAGGGTGCGCCCTGCA																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																
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Show Alignment With Reads

Re-alignment of all predicted orthologs

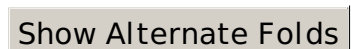
Species	Coordinate	ID	Alignment
droSec2	scaffold_8:1806930-1807092	dse_1565	GGACTGTCACGACGAGGACAACACTACACCAGCGCGCTGGACAACCTCCGGAGGTAAGAAAGTTT-----GTTA----CATCC--CGTACA-----ACCTT-----C-----AAGT-AAGCAAAAGTACAA-C-TC--T--T-TCTTTTCAGACGAAACTG-----CGTTGCCGAT-----GCTCTCCAT-A-----G---TGAC---TCCC---ACGCGGGGACGT
droSim2	chr1:18420147-18420309	dse_1565	GGACTGTCACGACGAGGACAACACTACACCAGCGCGCTGGACAACCTCCGGAGGTAAGAAAGTTT-----GTTA----ATCC--CGTACA-----ACCTT-----C-----AAGT-AAGCAAAAGTACAA-C-TC--T--T-TCTTTTCAGACGAAACTG-----CGTTGCCGAT-----GCTCTCCAT-A-----G---TGAC---TCCC---ACGCGGGGACGT
dm3	chrX:19526901-19527052	dse_448	GGACTGTCACGACGAGGACAACACTACACCAGCGCGCTGGACAACCTCCGGAGGTAAGAAAGTTT-----GTTA----ATCC--CGTACA-----ACCTT-----C-----AAGT-AAGCAAAAGTACAA-C-TC--T--T-TCTTTTCAGACGAAACTG-----CGTTGCCGAT-----GCTCTCCAT-A-----G---TGAC---TCCC---ACGCGGGGACGT
droRe2	scaffold_4630:9755114-9755271		GGACTGTCACGACGAGGACAACACTACACCAGCGCGCTGGACAACCTCCGGAGGTAAGGCAATTT-----GTA----ATCT--CGTACA-----ACCTT-----C-----AAGT-AAGCAAAAGTACAA-C-TC--T--T-TCTTTTCAGACGAAACTG-----CGTTGCCGAT-----GCTCTCCAT-A-----G---TGAC---TCCC---ACGCGGGGACGT
droYak3	chr1:1811126-1811286		ASANTCCACGAGGAGGACAACACTACACCAGCGCGCTGGACAACCTCCGGAGGTAAGGCAATTT-----CGTA----ATCC--CGTACA-----ACCTT-----C-----AAGT-AAGCAAAAGTACAA-C-TC--T--T-TCTTTTCAGACGAAACTG-----CGTTGCCGAT-----GCTCTCCAT-A-----G---TGAC---TCCC---ACGCGGGGACGT
droEug1	scaffold_18000040:9230-807144		ASANTCCACGAGGAGGACAACACTACACCAGCGCGCTGGACAACCTCCGGAGGTAAGGCAATTT-----AATA-CACCAATT--TGTA-----ACCTT-----C-----AAGT-AAGCAAAAGTACAA-C-TC--T--T-TCTTTTCAGACGAAACTG-----CGTTGCCGAT-----GCTCTCCAT-A-----G---TGAC---TCCC---ACGCGGGGACGT
droBlal	scaffold_18000030:2069-1076397-1076562		GGANTCCACGAGGAGGACAACACTACACCAGCGCGCTGGACAACCTCCGGAGGTAAGAAACAAATTT-----TCCT--GCT--CAGAA-----ACCTT-----C-----AAGT-AAGCAAAAGTACAA-C-TC--T--T-TCTTTTCAGACGAAACTG-----CGTTGCCGAT-----GCTCTCCAT-A-----G---TGAC---TCCC---ACGCGGGGACGT
droTak1	scaffold_18000041:5169-768891-769055		GGANTCCACGAGGAGGACAACACTACACCAGCGCGCTGGACAACCTCCGGAGGTAAGGCAATTT-----AGA----CAI-----ACCTT-----C-----AAGT-AAGCAAAAGTACAA-C-TC--T--T-TCTTTTCAGACGAAACTG-----CGTTGCCGAT-----GCTCTCCAT-A-----G---TGAC---TCCC---ACGCGGGGACGT
droElal	scaffold_18000040:51-1211514-1211685		ASANTCCACGAGGAGGACAACACTACACCAGCGCGCTGGACAACCTCCGGAGGTAAGAAACAAATTT-----ATA----ATT--GTTA-----ACCTT-----C-----AAGT-AAGCAAAAGTACAA-C-TC--T--T-TCTTTTCAGACGAAACTG-----CGTTGCCGAT-----GCTCTCCAT-A-----G---TGAC---TCCC---ACGCGGGGACGT
droRho1	scaffold_18000076:1121-105669-105833		ASANTCCACGAGGAGGACAACACTACACCAGCGCGCTGGACAACCTCCGGAGGTAAGAAACAAATTT-----GTA----CAT--GTTA-----ACCTT-----C-----AAGT-AAGCAAAAGTACAA-C-TC--T--T-TCTTTTCAGACGAAACTG-----CGTTGCCGAT-----GCTCTCCAT-A-----G---TGAC---TCCC---ACGCGGGGACGT
droPic1	scaffold_18000040:45073-1810552-1810719		GGANTCCACGAGGAGGACAACACTACACCAGCGCGCTGGACAACCTCCGGAGGTAAGAAACAAATTT-----GTA----CAT--GTTA-----ACCTT-----C-----AAGT-AAGCAAAAGTACAA-C-TC--T--T-TCTTTTCAGACGAAACTG-----CGTTGCCGAT-----GCTCTCCAT-A-----G---TGAC---TCCC---ACGCGGGGACGT
droRik1	scaffold_18000030:2696-470100-470268		GGACTCCACGACGAGGACAACACTACACCAGCGCGCTGGACAACCTCCGGAGGTAAGAAACAAATTT-----AGT-----ACCTT-----C-----AAGT-AAGCAAAAGTACAA-C-TC--T--T-TCTTTTCAGACGAAACTG-----CGTTGCCGAT-----GCTCTCCAT-A-----G---TGAC---TCCC---ACGCGGGGACGT
droAna3	scaffold_13417:1171717-1171884	dan_4051	GGACTCCACGACGAGGACAACACTACACCAGCGCGCTGGACAACCTCCGGAGGTAAGAAACAAATTT-----AGT-----ACCTT-----C-----AAGT-AAGCAAAAGTACAA-C-TC--T--T-TCTTTTCAGACGAAACTG-----CGTTGCCGAT-----GCTCTCCAT-A-----G---TGAC---TCCC---ACGCGGGGACGT
droBip1	scaffold_18000039:529-210200-210367		GGANTCCACGAGGAGGACAACACTACACCAGCGCGCTGGACAACCTCCGGAGGTAAGAAACAAATTT-----GTA----CAT--GTTA-----ACCTT-----C-----AAGT-AAGCAAAAGTACAA-C-TC--T--T-TCTTTTCAGACGAAACTG-----CGTTGCCGAT-----GCTCTCCAT-A-----G---TGAC---TCCC---ACGCGGGGACGT
dp5	XL group1a:567272-567296		GGACTCCACGACGAGGACAACACTACACCAGCGCGCTGGACAACCTCCGGAGGTAAGAAACAAATTT-----AGCG-----GAGAGCTGGAGAACATGTATCTTTCAAG-----ACCTT-----C-----AAGT-AAGCAAAAGTACAA-C-TC--T--T-TCTTTTCAGACGAAACTG-----CGTTGCCGAT-----GCTCTCCAT-A-----G---TGAC---TCCC---ACGCGGGGACGT
droPer2	scaffold_63:273829-274037		GGACTCCACGACGAGGACAACACTACACCAGCGCGCTGGACAACCTCCGGAGGTAAGAAACAAATTT-----AGCG-----GAGAGCTGGAGAACATGTATCTTTCAAG-----ACCTT-----C-----AAGT-AAGCAAAAGTACAA-C-TC--T--T-TCTTTTCAGACGAAACTG-----CGTTGCCGAT-----GCTCTCCAT-A-----G---TGAC---TCCC---ACGCGGGGACGT
droW12	scaffold_110000000:4909-6663958-6664149		GGANTCCACGAGGAGGACAACACTACACCAGCGCGCTGGACAACCTCCGGAGGTAAGAAACAAATTT-----AGT-----ACCTT-----C-----AAGT-AAGCAAAAGTACAA-C-TC--T--T-TCTTTTCAGACGAAACTG-----CGTTGCCGAT-----GCTCTCCAT-A-----G---TGAC---TCCC---ACGCGGGGACGT
droVir3	scaffold_13042:4250326-4250520		ASANTCCACGAGGAGGACAACACTACACCAGCGCGCTGGACAACCTCCGGAGGTAAGAAACAAATTT-----ATA-----ACCTT-----C-----AAGT-AAGCAAAAGTACAA-C-TC--T--T-TCTTTTCAGACGAAACTG-----CGTTGCCGAT-----GCTCTCCAT-A-----G---TGAC---TCCC---ACGCGGGGACGT
droMo3	scaffold_6359:2176513-2176727		ASANTCCACGAGGAGGACAACACTACACCAGCGCGCTGGACAACCTCCGGAGGTAAGAAACAAATTT-----ACCTT-----C-----AAGT-AAGCAAAAGTACAA-C-TC--T--T-TCTTTTCAGACGAAACTG-----CGTTGCCGAT-----GCTCTCCAT-A-----G---TGAC---TCCC---ACGCGGGGACGT
droGri2	scaffold_14853:7116446-7116669		ASANTCCACGAGGAGGACAACACTACACCAGCGCGCTGGACAACCTCCGGAGGTAAGAAACAAATTT-----ACCTT-----C-----AAGT-AAGCAAAAGTACAA-C-TC--T--T-TCTTTTCAGACGAAACTG-----CGTTGCCGAT-----GCTCTCCAT-A-----G---TGAC---TCCC---ACGCGGGGACGT

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

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Flybase annotation

intron [Dsec\GM23880-in]; utr5 [utr5_plus_10181]

No Repeatable elements found

Sense Strand Reads

[illegible]

Anti-sense strand reads

[illegible]

Show Alignment With Reads

Re-alignment of all predicted orthologs

[illegible]

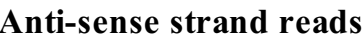
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	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	7
rescue.candidate	5

Show Alternate Folds

Sense Strand Reads

hide 3p reads show mid mismatch reads



Show Alignment With Reads

Re-alignment of all predicted orthologs

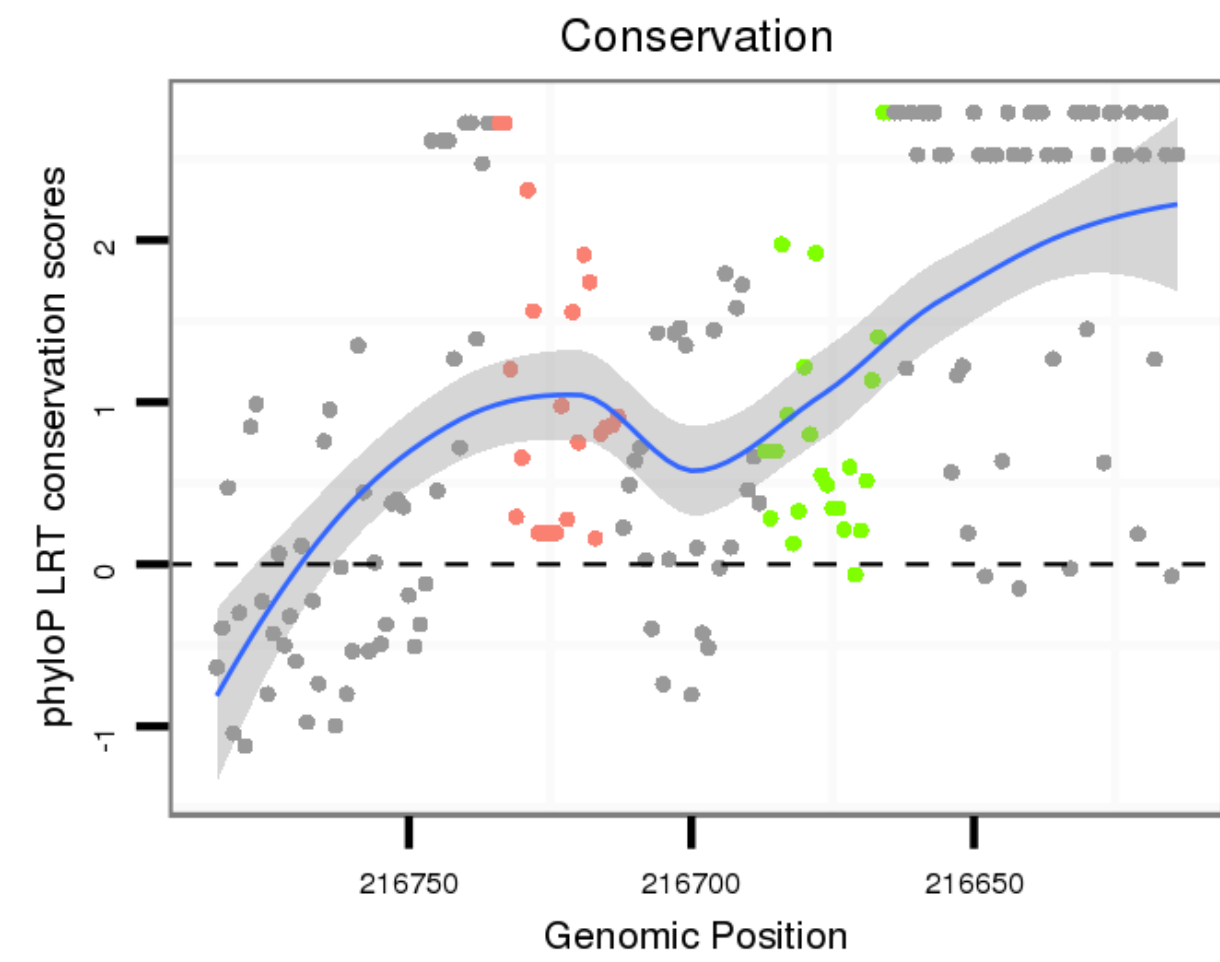
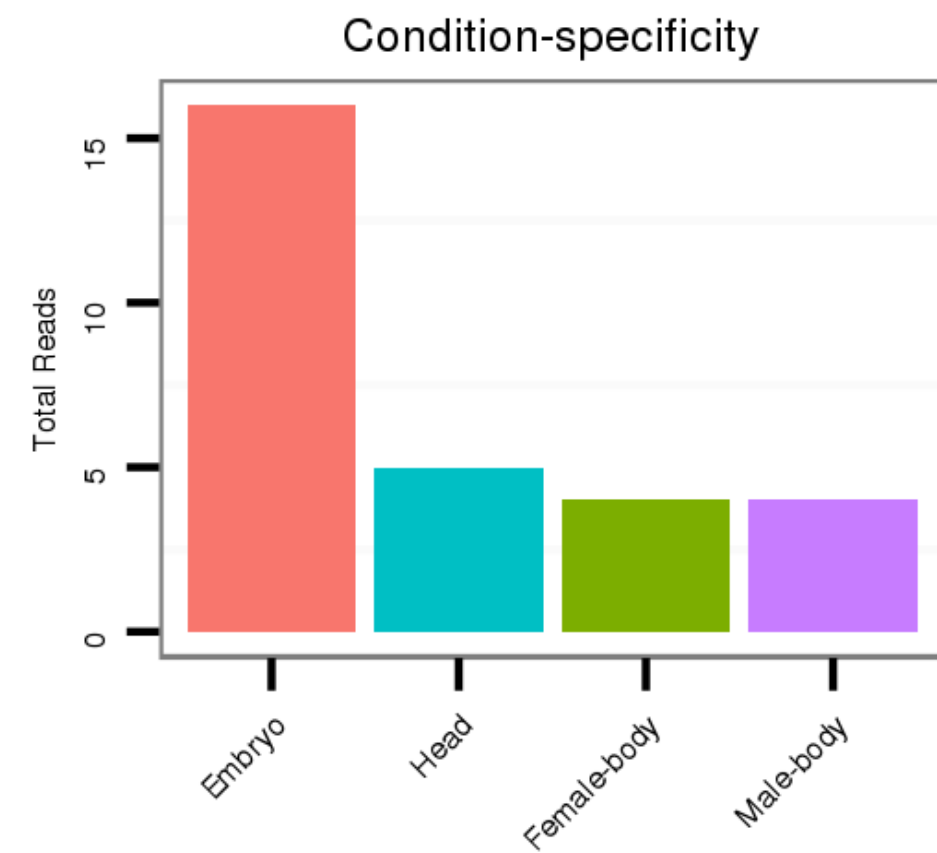
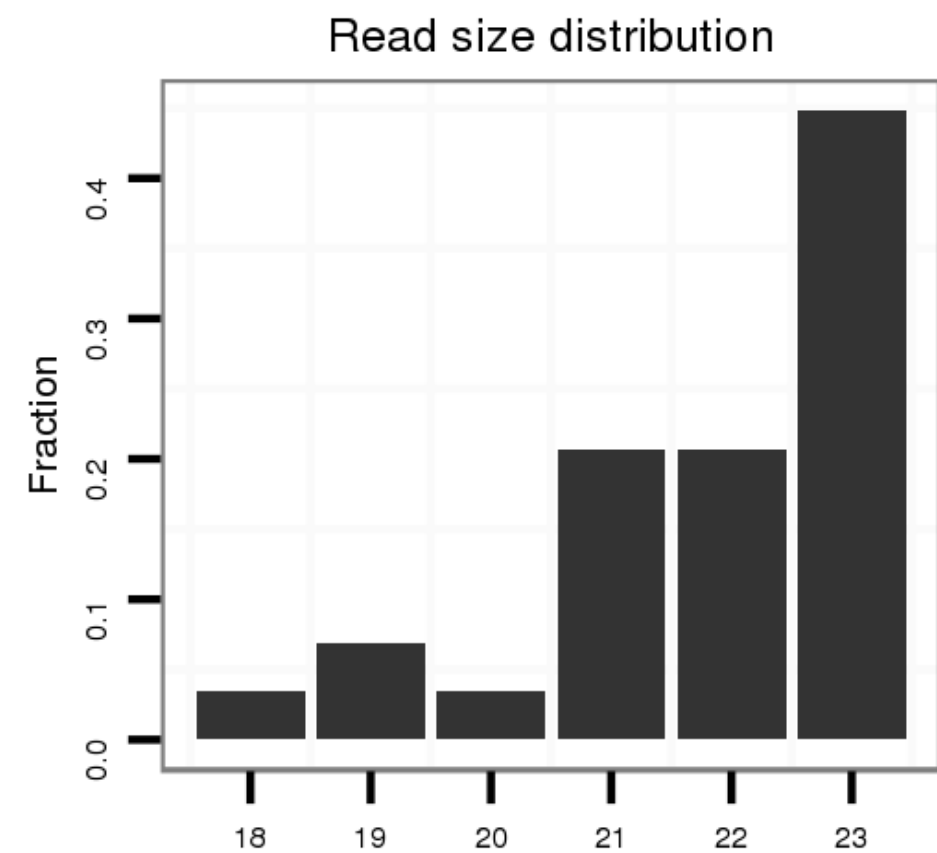
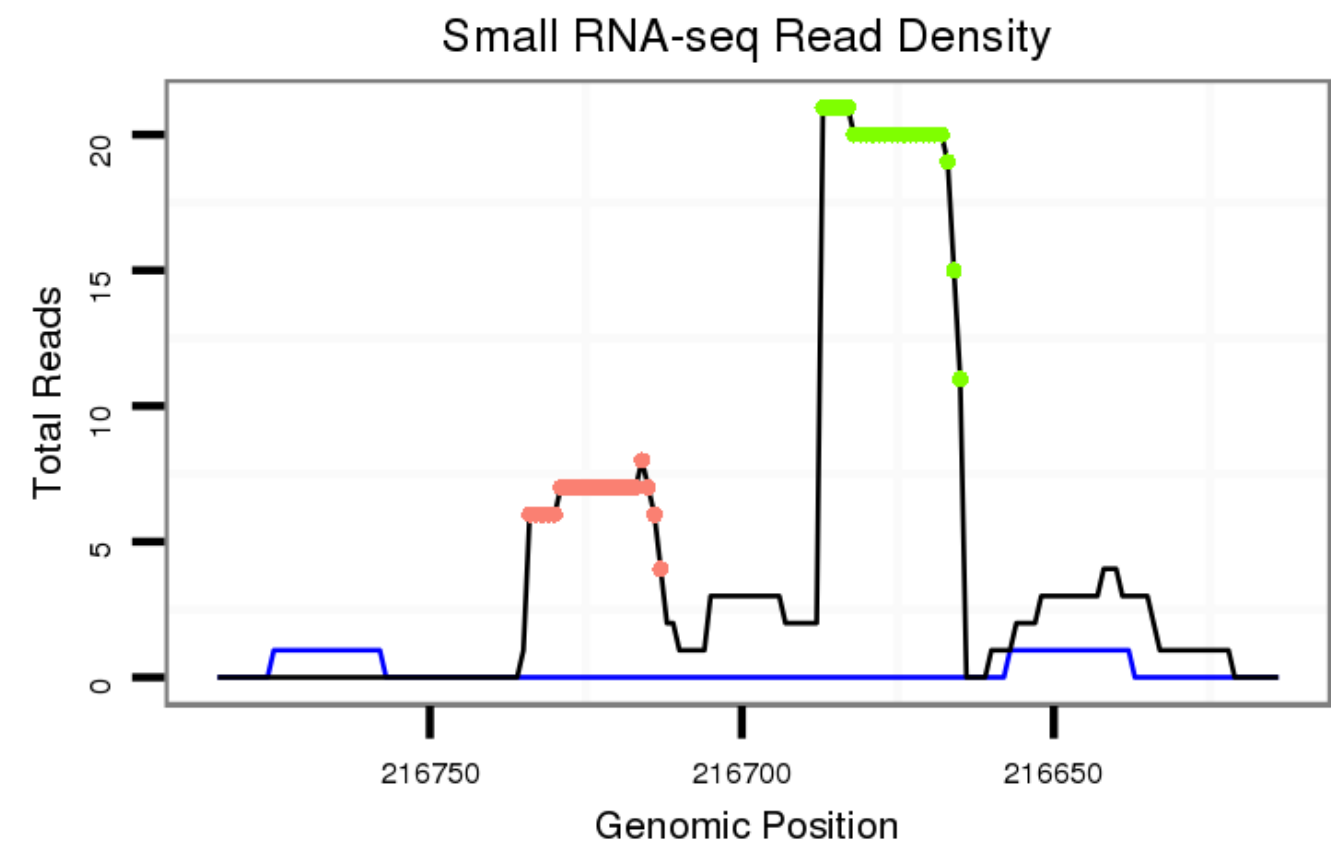
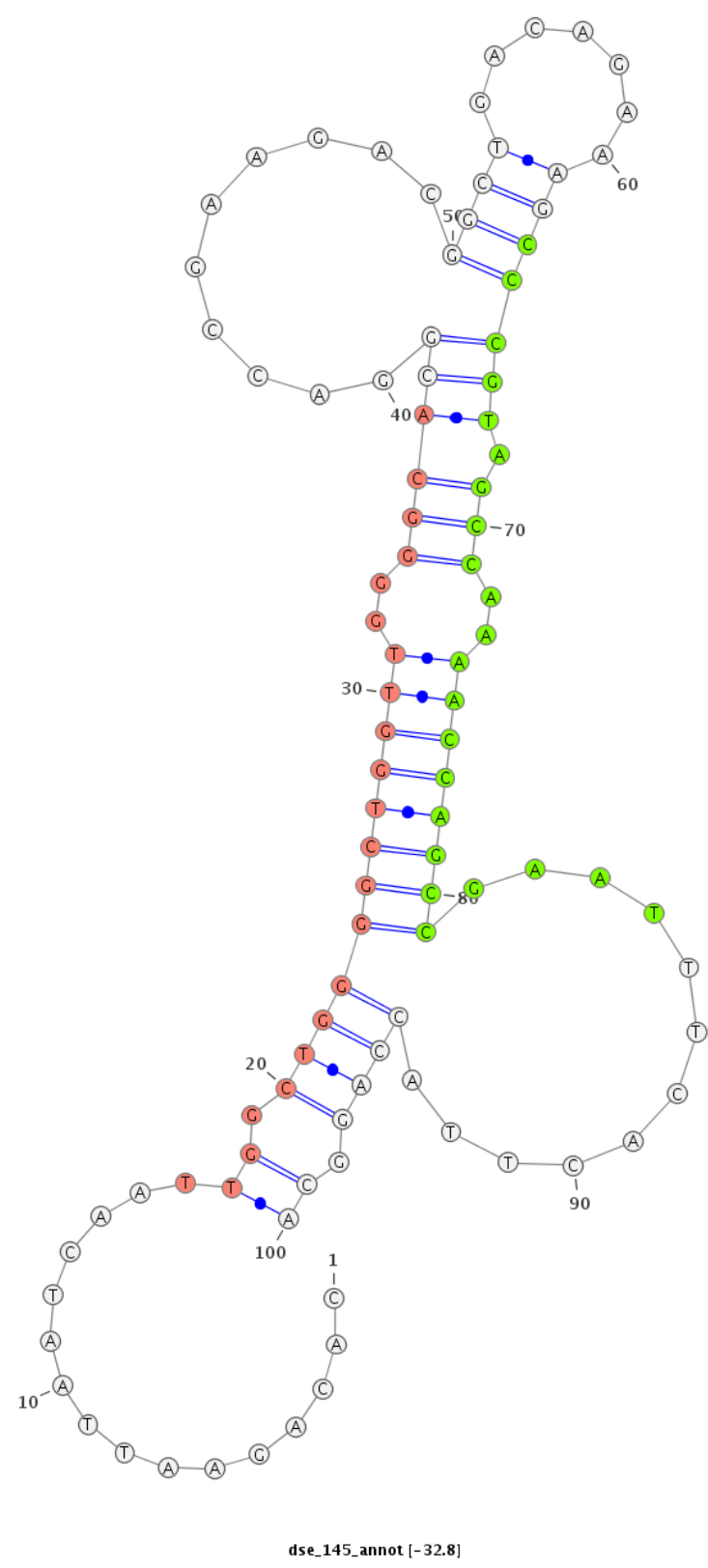
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	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	2
rescue.candidate	3

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dse_145	scaffold_1:216664-216734	confident	Canonical miRNA	antisense_to_intron	[View on UCSC Genome Browser [Cornell Minor]]

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Show Alternate Folds

Flybase annotation

Antisense to intron [Dsec\GM20885-in]; Antisense to CDS [Dsec\GM20885-cds]; Antisense to utr5 [utr5_plus_3160]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

										M054		V114		V113			
										female		male		V113			
										embryo body		head male		body			
										Hit		Total		Total			
										size		Mismatch		Count			
										Read #		Total		Total			
GACTGACTTGCCCGCCCTCGACACCGCGCCGCGACAAATTAATCAATGGCTGGGGCTGGTTGGGGACGGACGGAAGCGGTGCACAGAAACCCGTATGACCAAAACACGCCGAATTTACTTACACGACACACCGAGCGTTTCGGCGATTGTTTCCAGGCTCGGG										23	0	11.00	1	7	1	3	0
.....CTATACGACGACGCGG.....										22	0	4.00	4	3	0	1	0
.....CCCGTAGCCAAACACGCGCA.....										22	0	4.00	4	3	0	1	0
.....CCCGTAGCCAAACACGCGCA.....										22	0	2.00	2	0	1	0	1
.....TTGGCTGGGGCTGGTTGGGGCA.....										22	0	2.00	2	1	0	1	0
.....TTGGCTGGGGCTGGTTGGGGC.....										21	0	2.00	2	1	0	1	0
.....GTCACGGACGACGACGCGCTGAC.....										23	0	1.00	1	1	0	0	0
.....ATTGCTGGGGCTGGTTGGGG.....										23	0	1.00	1	1	0	0	0
.....AGACGCGCGGACGACGCGGAGG.....										18	0	1.00	1	0	1	0	0
.....CGTTGGGGGATTGTTTCCA.....										21	0	1.00	1	0	0	0	1
.....GCACACCGAGCGTTTCGGG.....										19	0	1.00	1	1	0	0	0
.....CCCGTAGCCAAACACGCGCA.....										22	1	1.00	1	1	0	0	0
.....CTTACGACGACACCGAGCGT.....										21	0	1.00	1	1	0	0	0
.....AGACGCGCGGACGACGCGT.....										20	0	1.00	1	1	0	0	0
.....TTGGCTGGGGCTGGTTGGGG.....										20	1	1.00	1	0	0	1	0
.....TGGGGCTGGTTGGGGACG.....										19	0	1.00	1	1	0	0	0
.....TTGGCTGGGGCTGGTTGGG.....										19	0	1.00	1	0	0	0	1
.....CCCGTAGCCAAACACGCGC.....										20	0	1.00	1	0	0	1	0
.....CGACGCGGACGCGTTCG.....										20	0	1.00	1	0	0	1	0
.....TTGGCTGGGGCTGGTTGGGGCA.....										24	1	1.00	1	0	1	0	0
.....GGGCTGGTTGGGGACGCGA.....										20	2	0.50	1	0	1	0	0

Anti-sense strand reads

Show Alignment With Reads

Re-alignment of all predicted orthologs

[illegible]

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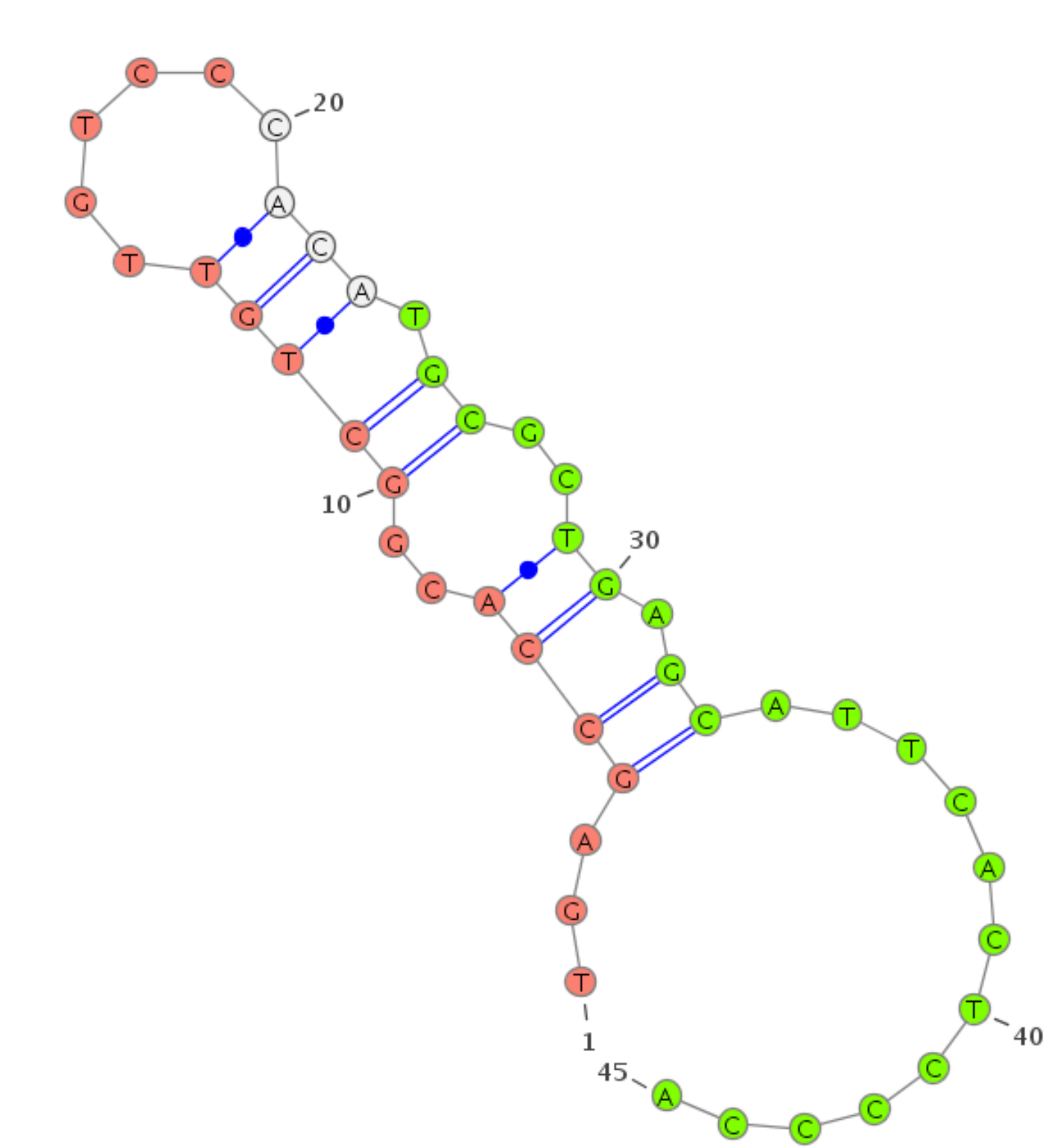
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mscr	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	2
rescue.candidate	1

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

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:
dse_1647	scaffold_9:2899892-2899945 +	confident	Mirtron	intron

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



dse_1647_annot [-6.5]

Show Alternate Folds

Flybase annotation

intron [Dsec/GM16042-in]; CDS [Dsec/GM16042-cds]; CDS [Dsec/GM16042-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

CGCATCCAGGACTACTCTGGGAGGATCACGGCTACTCGCTGGTGGACGGGTGAGTGA	Read #	Hit	Total		M054	V114	V115	V113
TGAGCCACGGCTGTTGTCC	size	Count	Norm	Total	female body	embryo	head	male body
.....((((((((.....))))).)).....	22	1	12.00	12	6	2	2	2
.....TGGCTGAGCATTCACTCCCA	23	1	7.00	7	2	4	1	0
.....TGGCTGAGCATTCACTCCCA	23	1	5.00	5	1	0	2	2
.....TGGCTGAGCATTCACTCCC	20	1	5.00	5	0	0	5	0
.....TGGCTGAGCATTCACTCCC	24	1	2.00	2	1	0	1	0
.....TGAGCCACGGCTGTTGTCC	19	1	1.00	1	0	1	0	0
CGCATCCAGGACTACTCTGGGAG	24	1	1.00	1	0	1	0	0
.....GTGAGTGATGAGCCACGGCTG	21	1	1.00	1	0	1	0	0
.....CGATGTGGGCATCTTCTTGA	21	1	1.00	1	0	1	0	0
.....GATGTGGGCATCTTCTTGA	21	1	1.00	1	0	1	0	0
.....GAGGATCACGGCTACTCGC	19	1	1.00	1	0	1	0	0
.....GTGAGTGATGAGCCACGGCT	20	1	1.00	1	0	1	0	0
.....TGAGCCACGGCTGTTGTCCC	20	1	1.00	1	0	0	1	0
.....GTGAGTGATGAGCCACGGC	19	1	1.00	1	0	1	0	0
.....CTCTGGGAGGATCACGGCT	20	1	1.00	1	1	0	0	0
.....ACGATGTGGGCATCTTCT	18	1	1.00	1	0	1	0	0
.....CCTGGGAGGATCACGGCTACTCGC	24	1	1.00	1	0	1	0	0
.....GACTACTCTCTGGGAGGAT	18	1	1.00	1	0	1	0	0
.....ATGAGCCACGGCTGTTGTCCC	21	1	1.00	1	0	1	0	0
.....ATGAGCCACGGCTGTTGTCCAC	23	1	1.00	1	0	1	0	0

Anti-sense strand reads

										M054	V115	V114			
GCGTAGTCTCTGATGAGGACCCCTCTAGTGCCGATGAGCGACCACTCGCCACTCACTACTCGGTGCCGACAACAGGGTGTACGCGACTCGTAAGTGAAGGGTCCGACATGTTGTCTACACCGCTAGAAGAACTCTGCGGTTCAAAGCCCGGCGGA										Read #	Hit	Total	female body	head	embryo
*****(((.....))).....*****										size Mismatch	Count	Norm	Total		

Show Alignment With Reads

Re-alignment of all predicted orthologs

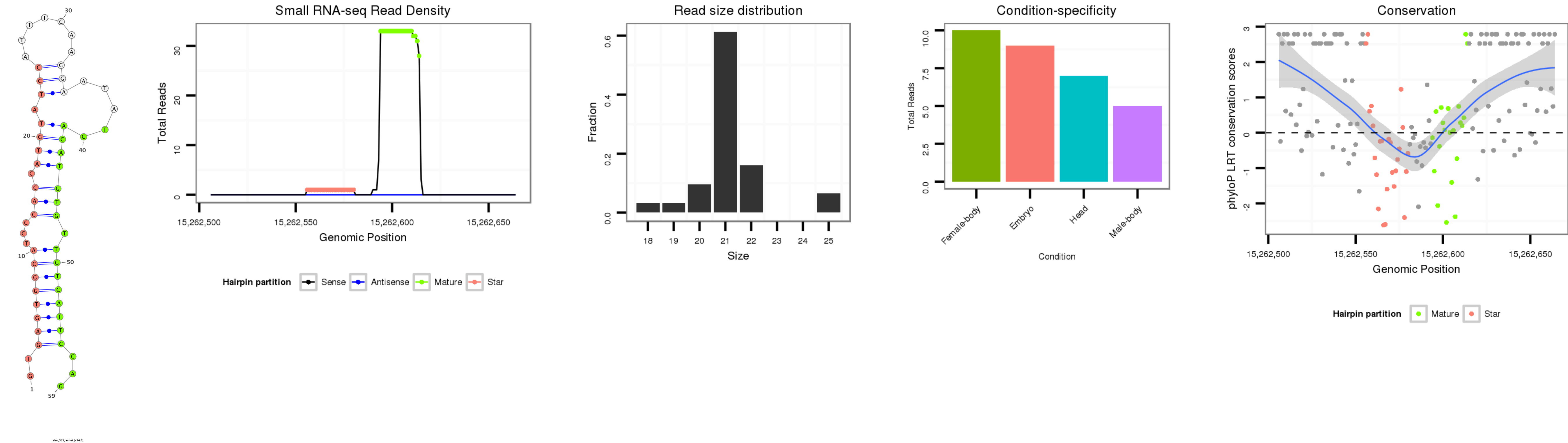
Species	Coordinate	ID	Alignment
droSec2	scaffold_9:2899842-2899995 +	dse_1647	CGCATCCAGGACTACTCTGGGAGGATCACGGCTACTCGCTGGTGGACGGGTGAGTGA
droSim2	chr:20128384-20128548 +		CGCATCCAGGACTACTCTGGGAGGATCACGGCTACTCGCTGGTGGACGGGTGAGTGA
dm3	chr2R13619445-13619609 +	dme_438	CGCATCCAGGACTACTCTGGGAGGATCACGGCTACTCGCTGGTGGACGGGTGAGTGA
droRe2	scaffold_4845:20982315-20982479 +		CGCATCCAGGACTACTCTGGGAGGATCACGGCTACTCGCTGGTGGACGGGTGAGTGA
droYak3	2R:19597538-19597708 +		CGCATCCAGGACTACTCTGGGAGGATCACGGCTACTCGCTGGTGGACGGGTGAGTGA
droBug1	scf7180000409474:23761-23924 -		CGCATCCAGGACTACTCTGGGAGGATCACGGCTACTCGCTGGTGGACGGGTGAGTGA
droBial	scf7180000302143:1776883-1771046 -		CGCATCCAGGACTACTCTGGGAGGATCACGGCTACTCGCTGGTGGACGGGTGAGTGA
droTak1	scf7180000415400:554549-554712 -		CGCATCCAGGACTACTCTGGGAGGATCACGGCTACTCGCTGGTGGACGGGTGAGTGA
droEle1	scf7180000491201:1150198-1150260 -		CGCATCCAGGACTACTCTGGGAGGATCACGGCTACTCGCTGGTGGACGGGTGAGTGA
droRho1	scf7180000778122:28604-28765 -		CGCATCCAGGACTACTCTGGGAGGATCACGGCTACTCGCTGGTGGACGGGTGAGTGA
droPic1	scf7180000453809:588918-58905 -		CGCATCCAGGACTACTCTGGGAGGATCACGGCTACTCGCTGGTGGACGGGTGAGTGA
droKik1	scf7180000302470:2105403-2105587 -		CGCATCCAGGACTACTCTGGGAGGATCACGGCTACTCGCTGGTGGACGGGTGAGTGA
droAna3	scaffold_13266:8258302-8258485 +		CGCATCCAGGACTACTCTGGGAGGATCACGGCTACTCGCTGGTGGACGGGTGAGTGA
droBip1	scf7180000396759:558695-558855 -		CGCATCCAGGACTACTCTGGGAGGATCACGGCTACTCGCTGGTGGACGGGTGAGTGA
dp5	3:9378856-9379015 -	dps_3840	CGCATCCAGGACTACTCTGGGAGGATCACGGCTACTCGCTGGTGGACGGGTGAGTGA
droPer2	scaffold_4:4702055-4702214 -		CGCATCCAGGACTACTCTGGGAGGATCACGGCTACTCGCTGGTGGACGGGTGAGTGA
droW12	scf2_1100000004954:2405570-2405731 -		CGCATCCAGGACTACTCTGGGAGGATCACGGCTACTCGCTGGTGGACGGGTGAGTGA
droVir3	scaffold_12823:521174-521349 -	dvi_2862	CGCATCCAGGACTACTCTGGGAGGATCACGGCTACTCGCTGGTGGACGGGTGAGTGA
droMo3	scaffold_6496:321427-321593 -		CGCATCCAGGACTACTCTGGGAGGATCACGGCTACTCGCTGGTGGACGGGTGAGTGA
droG12	scaffold_15245:6155642-6155814 +		CGCATCCAGGACTACTCTGGGAGGATCACGGCTACTCGCTGGTGGACGGGTGAGTGA

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

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Show Alternate Folds

Flybase annotation

intron [Dsec\GM26143-in]; CDS [Dsec\GM26143-cds]; CDS [Dsec\GM26143-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

ACGTCA	CGGAGT	TACCTG	CTGGTCC	TGGCGGA	ATATCA	CGGAGC	AGCAG	GTGAGTGGCATCC	ACCATGTATCC	ATTTC	AAGGA	ATACACATG	TGTGTCATTCC	AGCTAAC	GCACG	ATGATTT	ACCAGTGGG	CACCTATT	CTCTAC	TGTTGGTGCAGT	Read #	Mismatch	Hit Count	Total Norm	Total	M054 female body	V114 embryo	V115 head	V113 male body
*****. (((((((((...(((.(((.(.(((.....)))....))))))....))))))....))))*****																													
.....													TCACATG	TGTGTCATTCCAG							22	1	1	56.00	56	18	17	9	12
.....													TCACATG	TGTGTCATTCCAG							21	0	1	19.00	19	8	3	5	3
.....													TCACATG	TGTGTCATTCCAG							22	1	1	11.00	11	2	3	5	1
.....													ATCACATG	TGTGTCATTCCAG							22	0	1	5.00	5	0	5	0	0
.....													TCACATG	TGTGTCATTCCAGC							22	0	1	3.00	3	0	2	0	1
.....													TCACATG	TGTGTCATTCCA							20	0	1	3.00	3	0	0	1	2
.....													TCACATG	TGTGTCATTCCA	TTG						22	2	1	2.00	2	1	0	0	1
.....													AATAT	TCACATG	TGTGTCATTCCAG						25	0	1	1.00	1	1	0	0	0
.....								GTGAGTGGCATCC	ACCATGTATCC												25	0	1	1.00	1	1	0	0	0
.....													ATCACATG	TGTGTCATT							18	0	1	1.00	1	0	1	0	0
.....													TCACATG	TGTGTCATTCCAG							21	1	1	1.00	1	1	0	0	0
.....													TCACATG	TGTGTCATTCC							19	0	1	1.00	1	0	0	1	0

Anti-sense strand reads

Show Alignment With Reads

Re-alignment of all predicted orthologs

[illegible]

Generated: 09/08/2015 at 10:34 PM

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