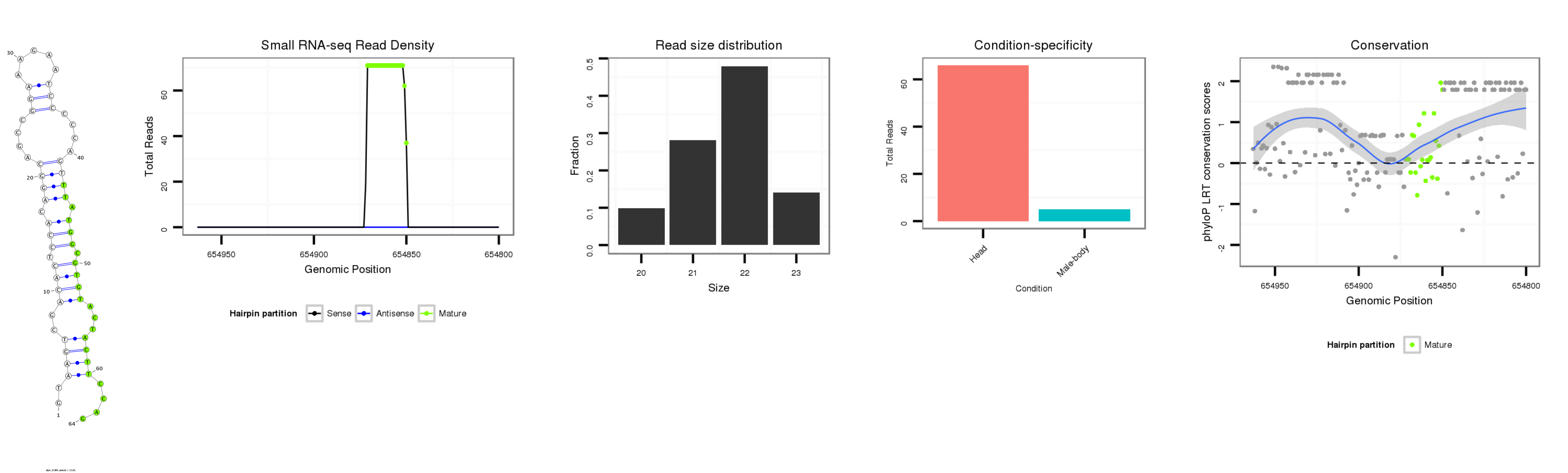


ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dpe_1180	scaffold_22:654850-654913 -	candidate	Mirtron	intron	[View on UCSC Genome Browser (Cornell Mirror)]

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Show Alternate Folds

Flybase annnotation

intron [Dper/GL15815-in]; CDS [Dper/GL15815-cds]; CDS [Dper/GL15815-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

TCACCGAGGCGGTGCTCAACTGTCGCGTAGGCATGCTCAAGGACAAGACGGTAAGTCGACATCCACAGGACGCCGGAAGAATCCCCAGT	TTATGGCGTGCTACTACTCCAG	TTATGTGGGTCAGACGCACCCAGCAAAAGGTGTCGCTGCTAACGGTGGG							V057	V050	V111	M021
*****	..(((..(((.(.(((.....((.....)))....))))..))))..*****	Read #	Hit	Total	Total	head	head	male	embryo			
.....TTATGGCGTGCTACTACTCCAG.....	22	0	1	27.00	27	14	12	1	0			
.....TTATGGCGTGCTACTACTCCA.....	21	0	1	18.00	18	11	7	0	0			
.....TTATGGCGTGCTACTACTCCAG.....	23	0	1	10.00	10	3	6	1	0			
.....TTATGGCGTGCTACTACTCCAG.....	23	1	1	7.00	7	1	6	0	0			
.....TTATGGCGTGCTACTACTCCA.....	22	0	1	7.00	7	1	6	0	0			
.....TTATGGCGTGCTACTACTCC.....	20	0	1	7.00	7	2	2	3	0			
.....TTATGGCGTGCTACTACTCC.....	21	0	1	2.00	2	2	0	0	0			
.....TTATGGCGTGCTACTACTCCAG.....	23	1	1	1.00	1	0	0	0	1			
.....TTATGGCGTGCTACTACTCCA.....	22	1	1	1.00	1	1	0	0	0			

Anti-sense strand reads

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

Show Alignment With Reads

Re-alignment of all predicted orthologs

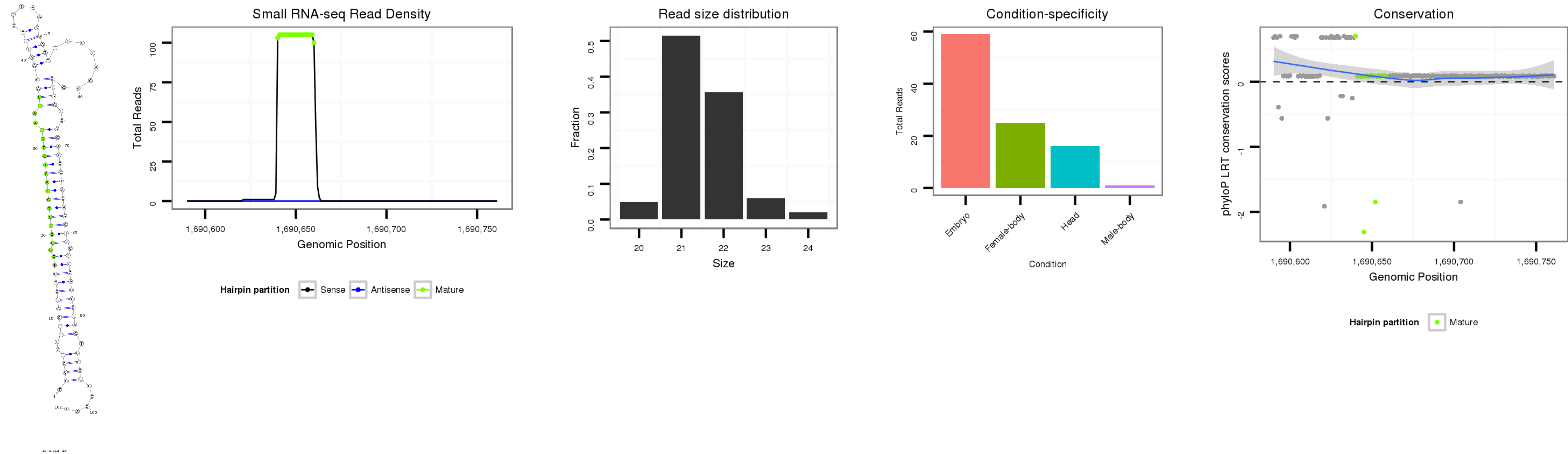
Species	Coordinate	ID	Alignment
droPer2	scaffold_22:654800-654963 -	dpe_1180	TCACCGAGGCGGTGCTCAACTGTCGCGTAGGCATGCTCAAGGACAAGACGGTAAGTCGACACT-----CCACAGGCAGCCGGAAGAATCCCCAGT
dp5	XI_group1e:9554233-9554396 +		TCACCGAGGCGGTGCTCAACTGTCGCGTAGGCATGCTCAAGGACAAGACGGTAAGTCGACACT-----CCACAGGCAGCCGGAAGAATC
droW112	scaf2_1100000004909:6258571-6258628 -		TCACCGAAGCGTCTCAATGTGCGTGGCATGCTCAAGGACAAGACGGTAAGT
droVir3	scaffold_12472:541612-541671 -		TCACGGAAGCGTGTGCTCAACTGTCGCGTGGCATGCTCAAGGAAGACGGTAAGCG
droMoJ3	scaffold_6308:2925135-2925200 +		CAT-----GTCC
droGri2	scaffold_15203:11018615-11018810 +		TCACGGAAGCGGTGCTCAATGTGCGCGTGGCATGCTCAAGGAAGACGGTAAGTTCATTACAATAAATTACAAAATATCTATGACATATCGGAAATATTCAAAATAGCTC
droAna3	scaffold_13417:3225673-3225728 +		TTT-----AGGTATGTGGTAAGACGCACAGCCGAAAAGGTATCCTCTTACTGTGG
droBlp1	scaf7180000396798:27115-27170 +		TTT-----AGGTATGTGGTAAGACGCACAGCCGAAAAGGTATCCTCTTACTGTGG
droKk1	scaf7180000302517:832064-832237 -		TCACGGAAGCGGTGCTCAACTGCGCGTGGCATGCTCAAGGACAAGACGGTGGTCTTGA-----GATATTATTATTAATCCTGATAGATAATACATGAATACATATATCCA
droFic1	scaf7180000453872:676940-676994 -		TCACGGAAGCGGTGCTCAATGTGCGTGGCATGCTCAAGGACAAGACGGTAAG-----TCCAGGTATGTGGGTCAGACCAAGCAAGAAAGGTATCCTCTTACTGTGG
droEle1	scaf7180000490777:7830-7892 +		GTCC-----TACT-----TCCAGGTATGTGGGTCAGACCAAGCAAGAAAGGTATCCTCTTACTGTGG
droRho1	scaf7180000779586:52912-52975 -		TCACGGAAGCGTGTCAACTGCCAATGGCATGCTCAAGGACAAGAGTAAGT
droBlal	scaf7180000302126:1078619-1078674 -		TCACGGAAGCGGTGCTCAACTGCCAATGGCATGCTCAAGGACAAGAGTAAGT
droTak1	scaf7180000415289:14542-14601 +		TCACGAGGCGGTGCTCAACTGCCAATGGCATGCTCAAGGACAAGAGTAAGT
droEug1	scaf7180000409092:175824-175896 -		AG--TATTTCTGTTTATTT-----TCAGGTATGTGGGTAAGCCAGAGCGAAGGTATCCTCTTACTGTGG
dm3	chrX:15961783-15961844 +		TCACGGAAGCGGTGCTCAATGCCAATGGCATGCTCAAGGAAGAGTAAGT
droS1m2	xi:15089396-15089457 +		TCACGGAAGCGTGTCAATGCCAATGGCATGCTCAAGGACAAGAGTAAGT
droSec2	scaffold_47:14235-14296 +		TCACGGAAGCGTGTCAATGCCAATGGCATGCTCAAGGACAAGAGTAAGT
droYak3	xi:10110079-10110138 +		TCACGGAAGCGGTGCTCAATGCCAATGGCATGCTCAAGGACAAGAGTAAGT
droEre2	scaffold_4690:11114908-11114977 -		TGGTATTAC-----CACT-----TCCAGGTATGTGGGTCAGCCAGAGCGCGAAGGTATCCTCTTACTGTGG

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PASS/FAIL	
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.top3	1
crit.uri	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 [Dper\GL16589-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

[illegible]

Anti-sense strand reads

Show Alignment With Reads

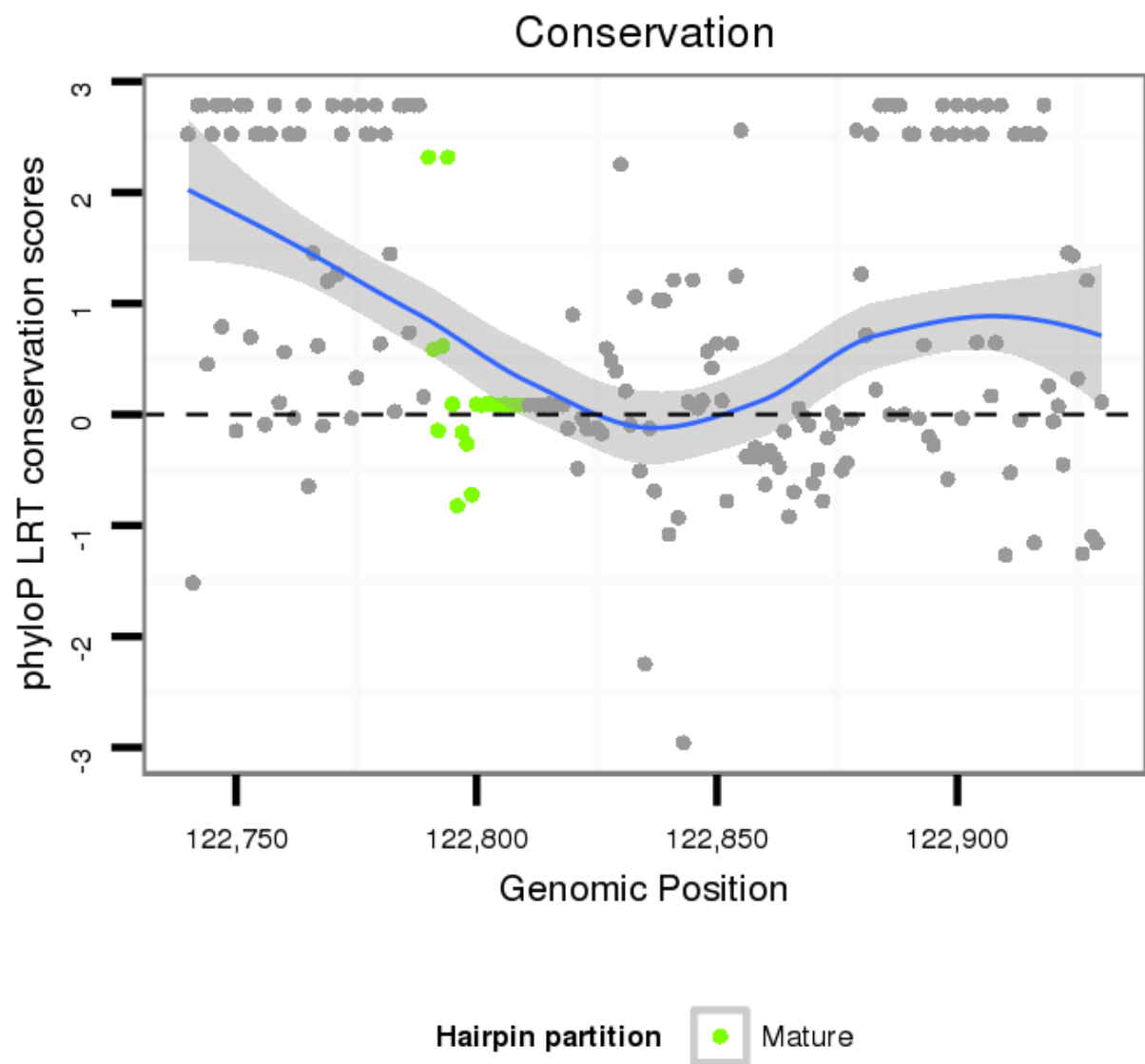
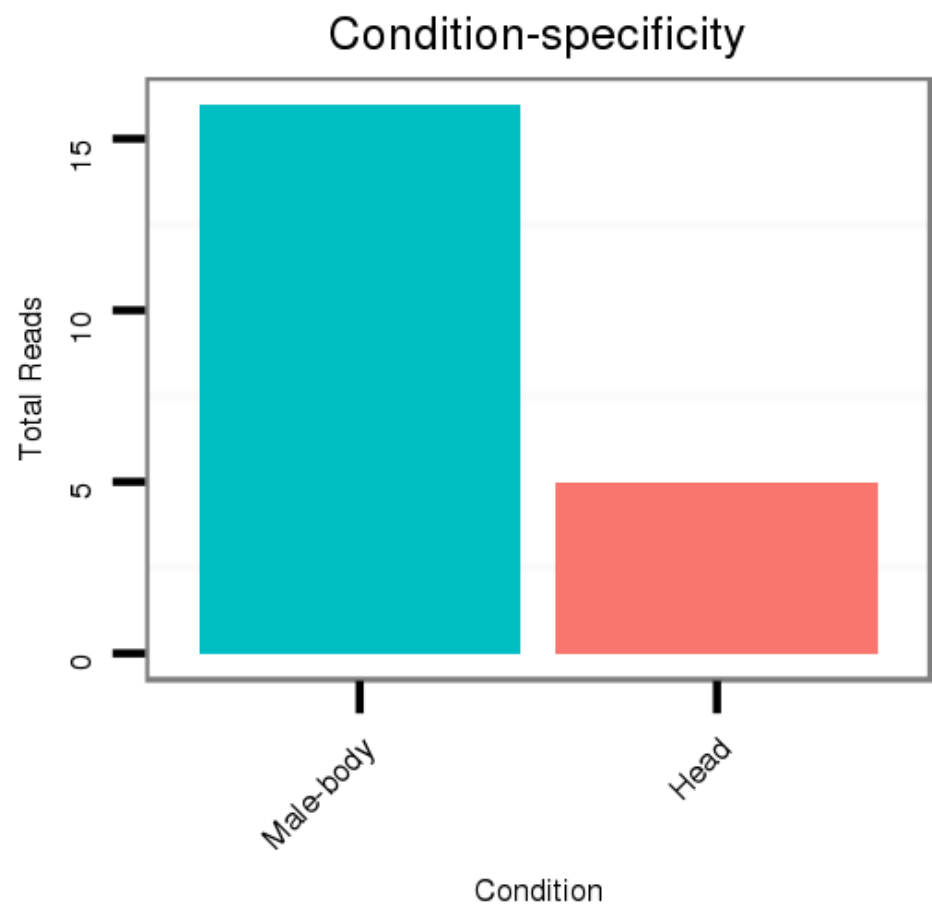
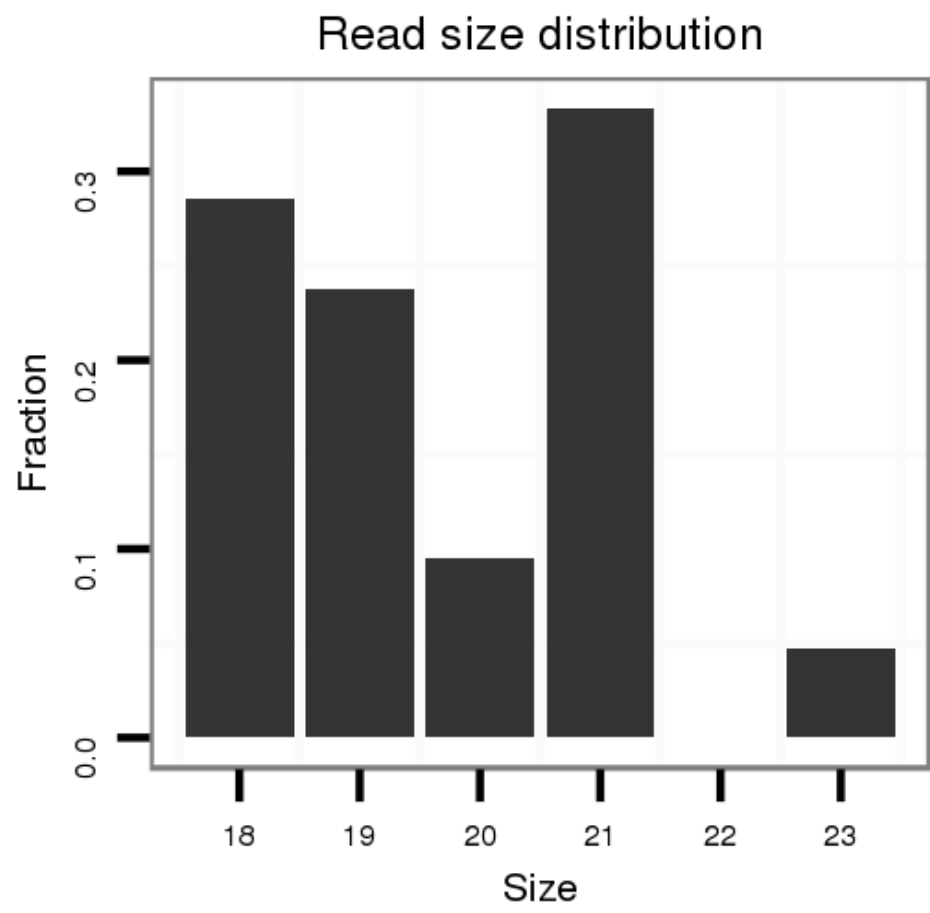
Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droPer2	scaffold_15:1690590-1690761_+	dpe_176	CTCGTCCTGCAAACTGAGACGGGGCGGAGGCCCGTGGGTCCTGGCCTG TGCCGCTGTAGTCTGTGAAC ACAATCTGTTAAGGATTTTCACACGTGGCGGCAGGCTACAGGTGCTGCAGGCCAGTGCCCCGATGCTCTCGCCACCGCCACCGTCGACGCTCAATCTAG
dp5	XL_group3a:1196731-1196902_-	dps_3582	CTCGTCCTGCAAACTGAGACGGGGCGGAGG CC GTGGGTCCTGGCCTG TGCCGCTGTAGCCTGTGAAC ACAATCTGTTAAGGATTTTCACACGTGGCGGCAGGCTACAGG G CTGCAGGCCAGTGCCCCGATGCTCTCGCCACCGCCACCGTCGACGCTCAATCTAG
droSec2	scaffold_15:683877-683908_-		CTC T TGG --- AACT ----- GGCC GTGGGTCT TGGCC AG---

Generated: 09/08/2015 at 07:49 PM **PASS/FAIL**

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



dpe_937_annot [-23.1]

No Repeatable elements found

hide 3p reads show mid mismatch reads

Anti-sense strand read:

Show Alignment With Reads

Re-alignment of all predicted orthologs

Accession	Coordinate	ID	Alignment
chrEpo2	hcaffold_131:122740-122930	Hpe_937	CGAAGGAATCTTTTCGCGACAGGACACAGACGAGGTGAGAGTCAATAAAGCTGGTGGCGGTGGGAAGCTG-----TTGCGC-----AT-----TTGCGCAA-----TGACGAATAAC-TGCGAGTTTTCATT-----TGACGCCATCTTTGGAGCAGACGTAGAGAGTTTCGCGCCACAGACGCAATCCCAA
dp5	2:4420268-4424048	dha_350	CGAAGGAATCTTTTCGCGACAGGACACAGACGAGGTGAGAGTCAATAAAGCTGGTGGCGGTGGGAAGCTG-----TTGCGC-----AT-----TTGCGCAA-----TGACGAATAAC-TGCGAGTTTTCATT-----TGACGCCATCTTTGGAGCAGACGTAGAGAGTTTCGCGCCACAGACGCAATCCCAA
chrH12	11:100000004921:3263050-3263149		CGAAGGAATCTTTTCGCGACAGGACACAGGAGTGGAGGTGATAAAGCTGGTGGCGGTGGGAAGCTG-----TTGCGC-----AT-----TTGCGCAA-----TGACGAATAAC-TGCGAGTTTTCATT-----TGACGCCATCTTTGGAGCAGACGTAGAGAGTTTCGCGCCACAGACGCAATCCCAA
chrV1r3	hcaffold_13047:12623658-12623822		CGAAGGAATCTTTTCGCGACAGGACACAGGAGTGGAGGTGATAAAGCTGGTGGCGGTGGGAAGCTG-----TTGCGC-----AT-----TTGCGCAA-----TGACGAATAAC-TGCGAGTTTTCATT-----TGACGCCATCTTTGGAGCAGACGTAGAGAGTTTCGCGCCACAGACGCAATCCCAA
chrMoJ3	hcaffold_6540:29212356-29213510		CGAAGGAATCTTTTCGCGACAGGACACAGGAGTGGAGGTGATAAAGCTGGTGGCGGTGGGAAGCTG-----TTGCGC-----AT-----TTGCGCAA-----TGACGAATAAC-TGCGAGTTTTCATT-----TGACGCCATCTTTGGAGCAGACGTAGAGAGTTTCGCGCCACAGACGCAATCCCAA
chrG12	hcaffold_15074:2109832-2109935		CGAAGGAATCTTTTCGCGACAGGACACAGGAGTGGAGGTGATAAAGCTGGTGGCGGTGGGAAGCTG-----TTGCGC-----AT-----TTGCGCAA-----TGACGAATAAC-TGCGAGTTTTCATT-----TGACGCCATCTTTGGAGCAGACGTAGAGAGTTTCGCGCCACAGACGCAATCCCAA
chrAna3	hcaffold_13340:5104990-5105160		CGAAGGAATCTTTTCGCGACAGGACACAGGAGTGGAGGTGATAAAGCTGGTGGCGGTGGGAAGCTG-----TTGCGC-----AT-----TTGCGCAA-----TGACGAATAAC-TGCGAGTTTTCATT-----TGACGCCATCTTTGGAGCAGACGTAGAGAGTTTCGCGCCACAGACGCAATCCCAA
chrB1p1	hcr7180000336359:30513-30683		CGAAGGAATCTTTTCGCGACAGGACACAGGAGTGGAGGTGATAAAGCTGGTGGCGGTGGGAAGCTG-----TTGCGC-----AT-----TTGCGCAA-----TGACGAATAAC-TGCGAGTTTTCATT-----TGACGCCATCTTTGGAGCAGACGTAGAGAGTTTCGCGCCACAGACGCAATCCCAA
chrK1k1	hcr7180000302468:105199-105209		CGAAGGAATCTTTTCGCGACAGGACACAGGAGTGGAGGTGATAAAGCTGGTGGCGGTGGGAAGCTG-----TTGCGC-----AT-----TTGCGCAA-----TGACGAATAAC-TGCGAGTTTTCATT-----TGACGCCATCTTTGGAGCAGACGTAGAGAGTTTCGCGCCACAGACGCAATCCCAA
chrF1c1	hcr7180000453782:32158-32314		CGAAGGAATCTTTTCGCGACAGGACACAGGAGTGGAGGTGATAAAGCTGGTGGCGGTGGGAAGCTG-----TTGCGC-----AT-----TTGCGCAA-----TGACGAATAAC-TGCGAGTTTTCATT-----TGACGCCATCTTTGGAGCAGACGTAGAGAGTTTCGCGCCACAGACGCAATCCCAA
chrE1e1	hcr7180000491194:1241263-1241422		CGAAGGAATCTTTTCGCGACAGGACACAGGAGTGGAGGTGATAAAGCTGGTGGCGGTGGGAAGCTG-----TTGCGC-----AT-----TTGCGCAA-----TGACGAATAAC-TGCGAGTTTTCATT-----TGACGCCATCTTTGGAGCAGACGTAGAGAGTTTCGCGCCACAGACGCAATCCCAA
chrRho1	hcr7180000077206:38103-38260		CGAAGGAATCTTTTCGCGACAGGACACAGGAGTGGAGGTGATAAAGCTGGTGGCGGTGGGAAGCTG-----TTGCGC-----AT-----TTGCGCAA-----TGACGAATAAC-TGCGAGTTTTCATT-----TGACGCCATCTTTGGAGCAGACGTAGAGAGTTTCGCGCCACAGACGCAATCCCAA
chrB1a1	hcr7180000302113:32558-32756		CGAAGGAATCTTTTCGCGACAGGACACAGGAGTGGAGGTGATAAAGCTGGTGGCGGTGGGAAGCTG-----TTGCGC-----AT-----TTGCGCAA-----TGACGAATAAC-TGCGAGTTTTCATT-----TGACGCCATCTTTGGAGCAGACGTAGAGAGTTTCGCGCCACAGACGCAATCCCAA
chrTak1	hcr7180000413286:361451-361610		CGAAGGAATCTTTTCGCGACAGGACACAGGAGTGGAGGTGATAAAGCTGGTGGCGGTGGGAAGCTG-----TTGCGC-----AT-----TTGCGCAA-----TGACGAATAAC-TGCGAGTTTTCATT-----TGACGCCATCTTTGGAGCAGACGTAGAGAGTTTCGCGCCACAGACGCAATCCCAA
chrBup1	hcr7180000409243:21474-21631		CGAAGGAATCTTTTCGCGACAGGACACAGGAGTGGAGGTGATAAAGCTGGTGGCGGTGGGAAGCTG-----TTGCGC-----AT-----TTGCGCAA-----TGACGAATAAC-TGCGAGTTTTCATT-----TGACGCCATCTTTGGAGCAGACGTAGAGAGTTTCGCGCCACAGACGCAATCCCAA
dm3	chr3R:2721729-27221894		CGAAGGAATCTTTTCGCGACAGGACACAGGAGTGGAGGTGATAAAGCTGGTGGCGGTGGGAAGCTG-----TTGCGC-----AT-----TTGCGCAA-----TGACGAATAAC-TGCGAGTTTTCATT-----TGACGCCATCTTTGGAGCAGACGTAGAGAGTTTCGCGCCACAGACGCAATCCCAA
chrS1m2	chr1:26513472-26513634		CGAAGGAATCTTTTCGCGACAGGACACAGGAGTGGAGGTGATAAAGCTGGTGGCGGTGGGAAGCTG-----TTGCGC-----AT-----TTGCGCAA-----TGACGAATAAC-TGCGAGTTTTCATT-----TGACGCCATCTTTGGAGCAGACGTAGAGAGTTTCGCGCCACAGACGCAATCCCAA
chrOY8Y3	chr7:444448464813874-44444847033		CGAAGGAATCTTTTCGCGACAGGACACAGGAGTGGAGGTGATAAAGCTGGTGGCGGTGGGAAGCTG-----TTGCGC-----AT-----TTGCGCAA-----TGACGAATAAC-TGCGAGTTTTCATT-----TGACGCCATCTTTGGAGCAGACGTAGAGAGTTTCGCGCCACAGACGCAATCCCAA
chrEre2	hcaffold_4_4820:760014-760176		CGAAGGAATCTTTTCGCGACAGGACACAGGAGTGGAGGTGATAAAGCTGGTGGCGGTGGGAAGCTG-----TTGCGC-----AT-----TTGCGCAA-----TGACGAATAAC-TGCGAGTTTTCATT-----TGACGCCATCTTTGGAGCAGACGTAGAGAGTTTCGCGCCACAGACGCAATCCCAA

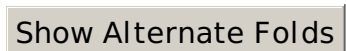
Generated: 09/08/2015 10:38 PM
PAGE 11

crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	0
crit.top3	1
crit.tptop3	0
crit.uri	0
crit.back	0
rescue.total	0
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	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: mature star mismatch in alignment mismatch in read

Predicted structure



Flybase annotation

CDS [Dper\GL13392-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

	Read size	# Mismatch	Hit Count	Total Norm	Total	M021 embryo	V042 embryo	M042 female body	V111 male body	V057 head
TCACGCTCGGAGAAATTCGAGCGCTGTGCTGTGCTCTACGAGAAGTCCCTGAATTCGGACCCGAAAACTGCGTAACTGGATGAAATTCGCCGAGCTGGAGAACTCTTGGGCGACACGGGAACGGGCAAGGGCCATATTGAGCTGGCCGT	18	0	2	25.00	50	47	2	1	0	0
*****.((((((.....(((.....(((.....(((.....)))..))))))))..)))..))))..*****	18	0	2	25.00	50	47	2	1	0	0
.....GTGCTGTGCTCTACGAGAA.....	19	0	1	2.00	2	2	0	0	0	0
.....GAAATTCGCCGAGCTGGA.....	18	1	2	2.00	4	4	0	0	0	0
.....GAAATTCGCCGAGCTGGG.....	19	0	2	1.50	3	3	0	0	0	0
.....GAAATTCGCCGAGCTGGAGA.....	20	0	2	1.50	3	0	2	0	1	0
.....GAAATTCGGACCCGAAAACTGCGT.....	23	0	1	1.00	1	1	0	0	0	0
.....CCGAAAACTGCTAACTGGATGA.....	25	0	1	1.00	1	1	0	0	0	0
.....GAAGTTCCTTGAATTCGGACCC.....	22	0	1	1.00	1	1	0	0	0	0
.....GCTGTGCTCTACGAGAAGTCCCTGAATT.....	28	0	1	1.00	1	0	1	0	0	0
.....CTGGGCGACACGGAAACGG.....	19	0	1	1.00	1	0	0	1	0	0
.....ATTCGGACCCGAAAACTGTC.....	19	0	1	1.00	1	1	0	0	0	0
.....AAATTCGCCGAGCTGGAGAA.....	20	0	2	1.00	2	2	0	0	0	0
.....GAAATTCGCCGAGCTGGAGAA.....	21	0	2	1.00	2	0	0	0	2	0
.....AAATTCGCCGAGCTGGAGA.....	19	0	3	1.00	3	2	1	0	0	0
.....AAATTCGCCGAGCTGGAG.....	18	0	4	0.50	2	2	0	0	0	0
.....AATTCGCCGAGCTGGAGA.....	18	0	3	0.33	1	1	0	0	0	0

Anti-sense strand reads

Show Alignment With Reads

Re-alignment of all predicted orthologs

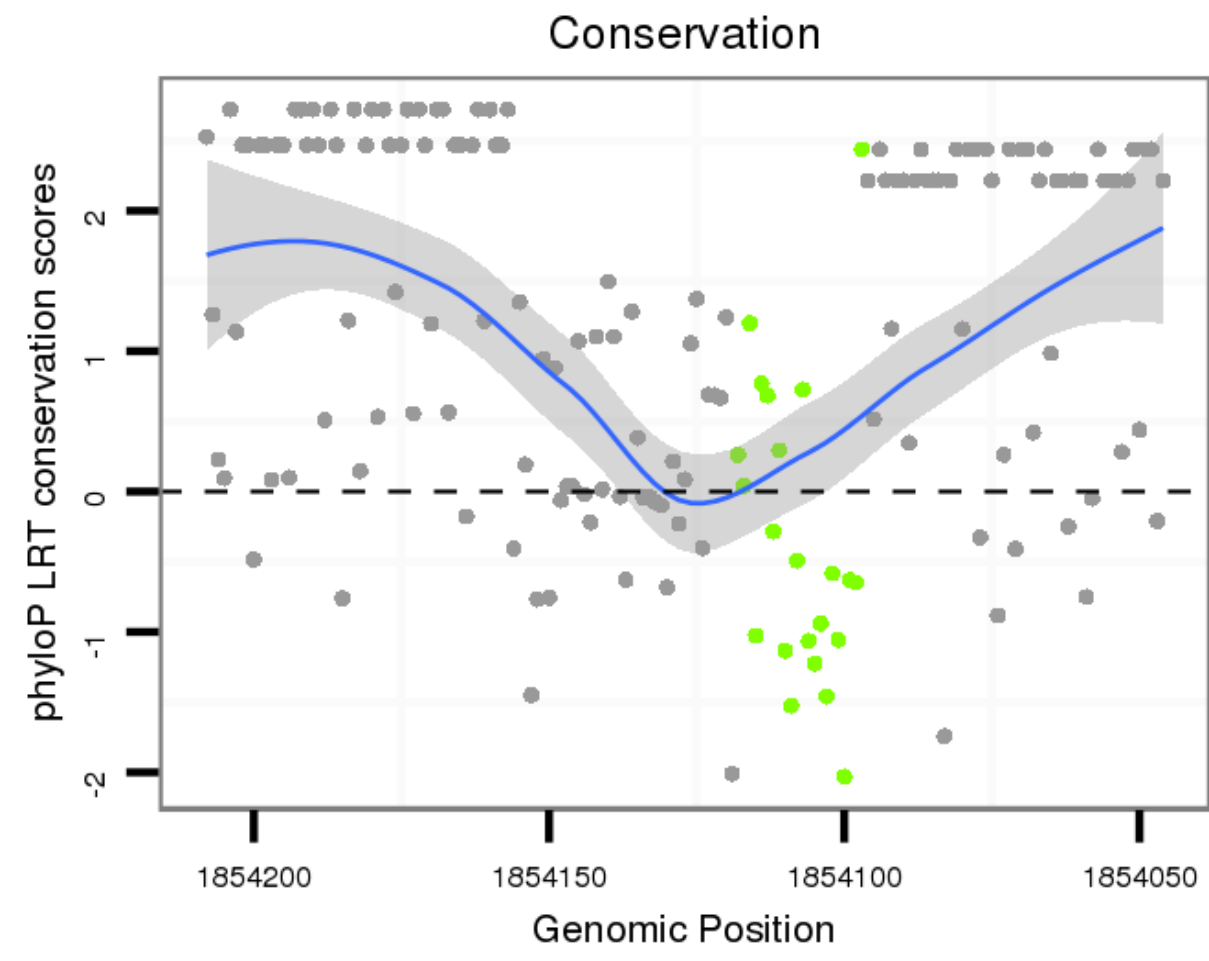
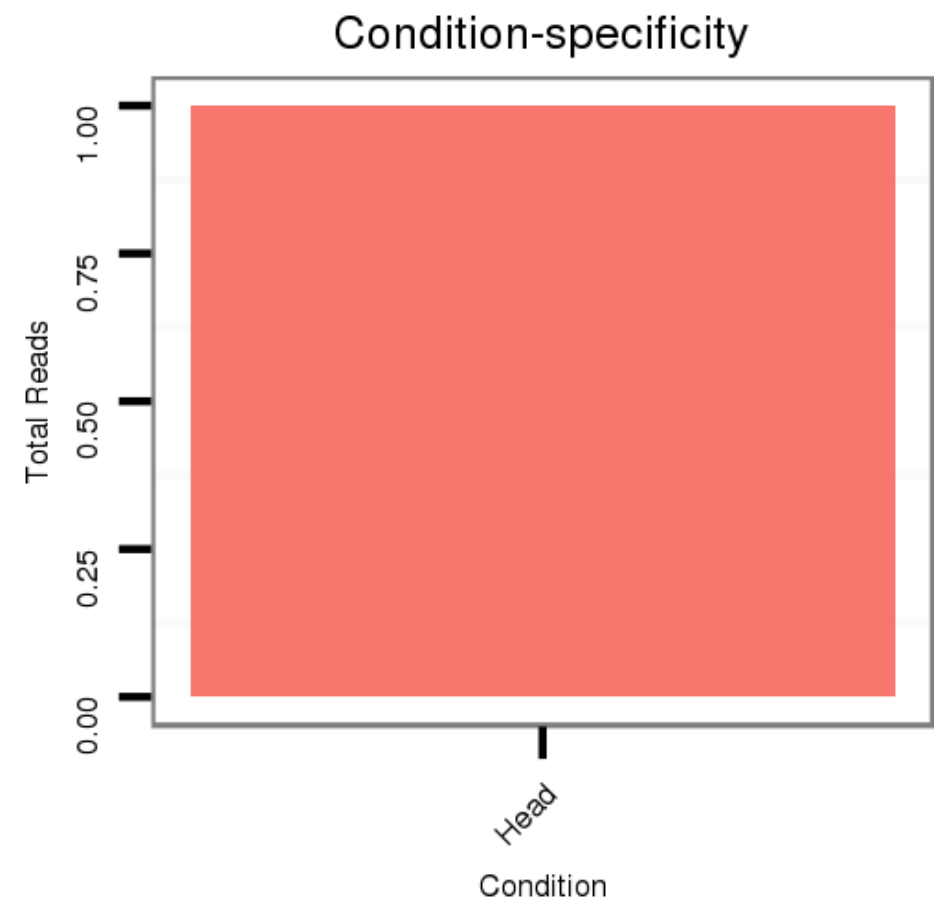
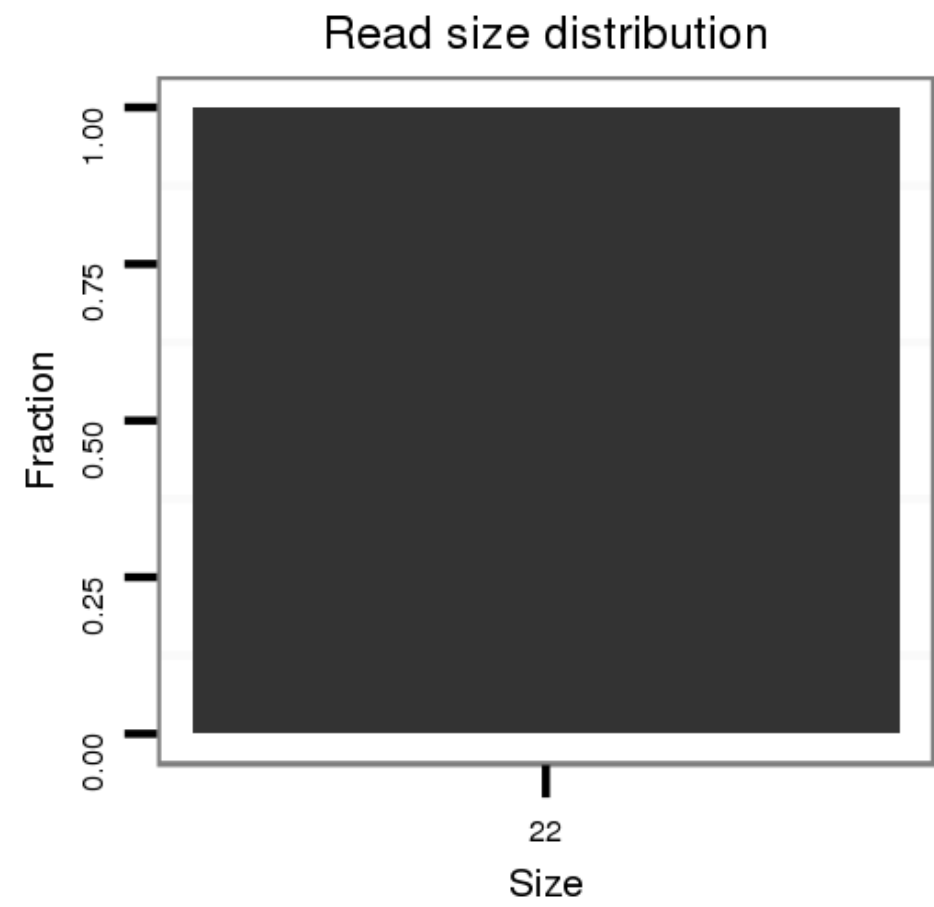
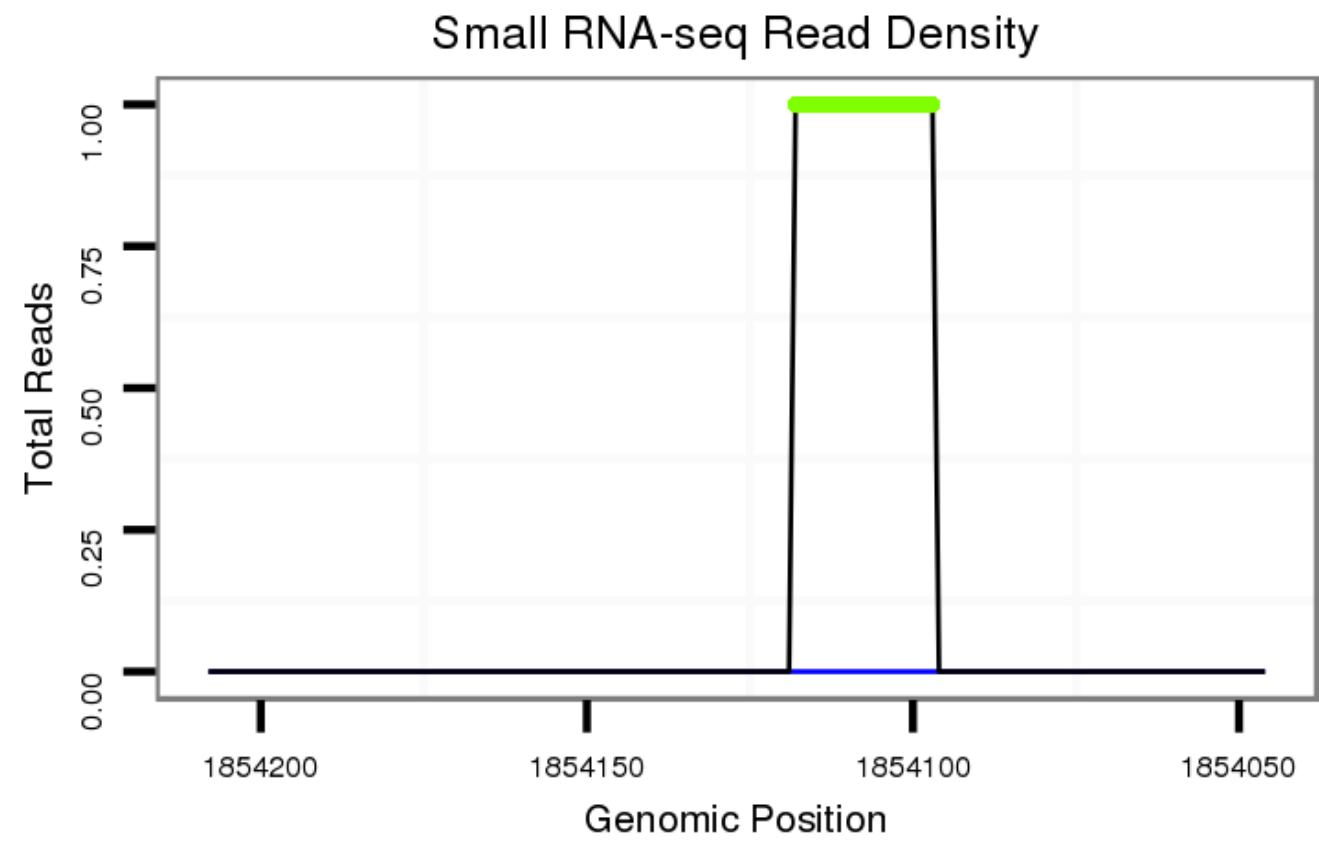
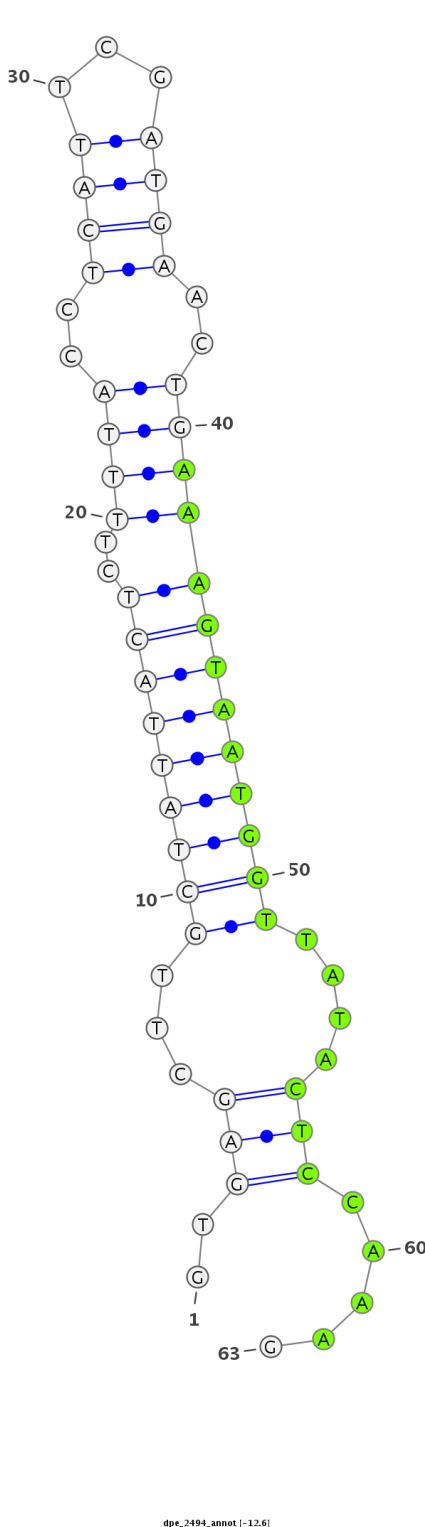
Species	Coordinate	ID	Alignment
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dp5	XL_group1a:157500-157650 -		TCCAGCTGCGAGAAATTCGAGCGCTGTCGTGCTCTACGAGAAGTTCCTTGAATTGCGACCGGAAATCGCTAACCTGGATGAATTTGCGCGAGCTGGAGAACCTCTTGGGCGACACGGAACGGGCAAGGCCATATTGAGCTGGCCGT
droW112	scaffold_110:0000004590:587622-587772 -		TCCAGCTGCGAGAAATTCGAGCGCTGTCGTGCTCTACGAGAAGTTCCTTGAATTGCGACCGGAAATCGCTAACCTGGATGAATTTGCGCGAGCTGGAGAACCTCTTGGGCGACACGGAACGGGCAAGGCCATATTGAGCTGGCCGT
droVir3	scaffold_12928:5641517-5641667 -		TTCAGCTGCGCGAATTTCGAGCGCTGTCGTGCTCTACGAGAAGTTCCTTGAATTGCGCGCGCGAATTCGCTACACTGGATGAATTTGCCGAAATGGAGAACCTCTGTTGGGCGACACGGAACGGGCAAGGCCATATTGAGCTGGCCGT
droMo3	scaffold_6359:4165941-4166091 -		TTCAGCTGCGCGAATTTCGAGCGCTGTCGTGCTCTACGAGAAGTTCCTTGAATTGCGCGCGCGAATTCGCTACACTGGATGAATTTGCCGAGCTGGAGAACCTCTGTTGGGCGACACGGAACGGGCAAGGCCATATTGAGCTGGCCGT
droGr12	scaffold_15203:1524378-1524528 -		TTCAGCTGCGCGAATTTCGAGCGCTGTCGTGCTCTACGAGAAGTTCCTTGAATTGCGCGCGCGAATTCGCTACACTGGATGAATTTGCCGAGCTGGAGAACCTCTGTTGGGCGACACGGAACGGGCAAGGCCATATTGAGCTGGCCGT
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droBip1	scf7180000396434:33627-33777 +		TCCAGCTGCGCGAATTTCGAGCGCTGTCGTGCTCTACGAGAAGTTCCTTGAATTGCGCGCGCGAATTCGCTACACTGGATGAATTTGCCGCGAGCTGGAGAACCTCTGTTGGGCGACACGGAACGGGCAAGGCCATATTGAGCTGGCCGT
droKik1	scf7180000302696:1647443-1647593 +		TCCAGCTGCGCGAATTTCGAGCGCTGTCGTGCTCTACGAGAAGTTCCTTGAATTGCGCGCGCGAATTCGCTACACTGGATGAATTTGCCGCGAGCTGGAGAACCTCTGTTGGGCGACACGGAACGGGCAAGGCCATATTGAGCTGGCCGT
droFic1	scf7180000453901:894986-895136 -		TTCAGCTGCGAGAAATTCGAGCGCTGTCGTGCTCTACGAGAAGTTCCTTGAATTGCGCGCGAGAAATTCGCTACACTGGATGAATTTGCCGAGCTGGAGAACCTCTGTTGGGCGACACGGAACGGGCAAGGCCATATTGAGCTGGCCGT
droE1e1	scf7180000491001:1702917-1703067 -		TCCAGCTGCGCGAATTTCGAGCGCTGTCGTGCTCTACGAGAAGTTCCTTGAATTGCGCGCGCGAATTCGCTACACTGGATGAATTTGCCGCGAGCTGGAGAACCTCTGTTGGGCGACACGGAACGGGCAAGGCCATATTGAGCTGGCCGT
droRho1	scf7180000779506:219092-219242 -		TCCAGCTGCGCGAATTTCGAGCGCTGTCGTGCTCTACGAGAAGTTCCTTGAATTGCGCGCGCGAATTCGCTACACTGGATGAATTTGCCGCGAGCTGGAGAACCTCTGTTGGGCGACACGGAACGGGCAAGGCCATATTGAGCTGGCCGT
droBia1	scf7180000301760:2126267-2126417 -		TTCAGCTGCGCGAATTTCGAGCGCTGTCGTGCTCTACGAGAAGTTCCTTGAATTGCGCGCGCGAATTCGCTACACTGGATGAATTTGCCGCGAGCTGGAGAACCTCTGTTGGGCGACACGGAACGGGCAAGGCCATATTGAGCTGGCCGT
droTak1	scf7180000415195:26227-26377 -		TCCAGCTGCGCGAATTTCGAGCGCTGTCGTGCTCTACGAGAAGTTCCTTGAATTGCGCGCGCGAATTCGCTACACTGGATGAATTTGCCGCGAGCTGGAGAACCTCTGTTGGGCGACACGGAACGGGCAAGGCCATATTGAGCTGGCCGT
droEug1	scf7180000409048:33477-33627 -		TTCAGCTGCGCGAATTTCGAGCGCTGTCGTGCTCTACGAGAAGTTCCTTGAATTGCGCGCGCGAATTCGCTACACTGGATGAATTTGCCGCGAGCTGGAGAACCTCTGTTGGGCGACACGGAACGGGCAAGGCCATATTGAGCTGGCCGT
dm3	chrX:2142337-2142487 -		TTCAGCTGCGCGAATTTCGAGCGCTGTCGTGCTCTACGAGAAGTTCCTTGAATTGCGACCGGAAATTCGCTAACCTGGATGAATTTGCGCGAGCTGGAGAACCTCTTGGGCGACACGGAACGGGCAAGGCCATATTGAGCTGGCCGT
droSim2	ix:1979913-1980063 -		TTCAGCTGCGCGAATTTCGAGCGCTGTCGTGCTCTACGAGAAGTTCCTTGAATTGCGACCGGAAATTCGCTAACCTGGATGAATTTGCGCGAGCTGGAGAACCTCTTGGGCGACACGGAACGGGCAAGGCCATATTGAGCTGGCCGT
droSec2	scaffold_110:1928265-1928415 -		TTCAGCTGCGCGAATTTCGAGCGCTGTCGTGCTCTACGAGAAGTTCCTTGAATTGCGACCGGAAATTCGCTAACCTGGATGAATTTGCGCGAGCTGGAGAACCTCTTGGGCGACACGGAACGGGCAAGGCCATATTGAGCTGGCCGT
droYak3	X:6186795-6186945 -		TTCAGCTGCGCGAATTTCGAGCGCTGTCGTGCTCTACGAGAAGTTCCTTGAATTGCGACCGGAAATTCGCTAACCTGGATGAATTTGCGCGAGCTGGAGAACCTCTTGGGCGACACGGAACGGGCAAGGCCATATTGAGCTGGCCGT
droEr2	scaffold_4644:2107421-2107571 -		TTCAGCTGCGCGAATTTCGAGCGCTGTCGTGCTCTACGAGAAGTTCCTTGAATTGCGACCGGAAATTCGCTAACCTGGATGAATTTGCGCGAGCTGGAGAACCTCTTGGGCGACACGGAACGGGCAAGGCCATATTGAGCTGGCCGT

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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	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 [Dper\GL13618-in]; CDS [Dper\GL13618-cds]; CDS [Dper\GL13618-cds]; utr3 [utr3_plus_6715]; utr3 [utr3_plus_6716]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

[illegible]

Anti-sense strand reads

CCGGACGCGCCACCGATGTCGTGGCACCCTCAGACTCATTAGCTCTGTCCACTCGAACGATAATGAGAAATGGAGTAAGCTACTTGAC TTTCATTACCAATATGAGGTTT CTACAGCTACCCGGTCTATAGGGATATGCTACCGGGCGACCGCGTCAAGC																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																									
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Show Alignment With Reads

Re-alignment of all predicted orthologs

[illegible]

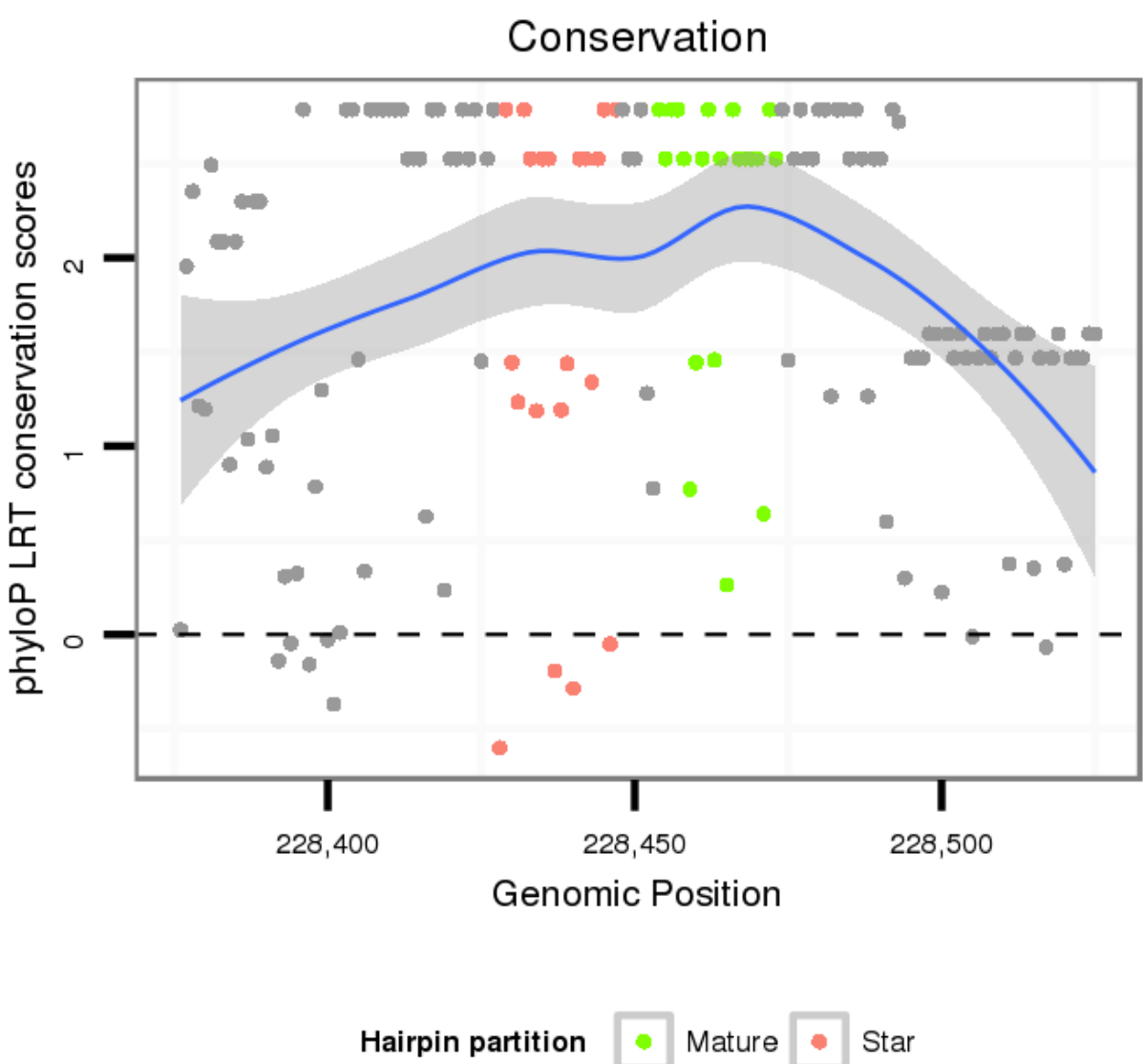
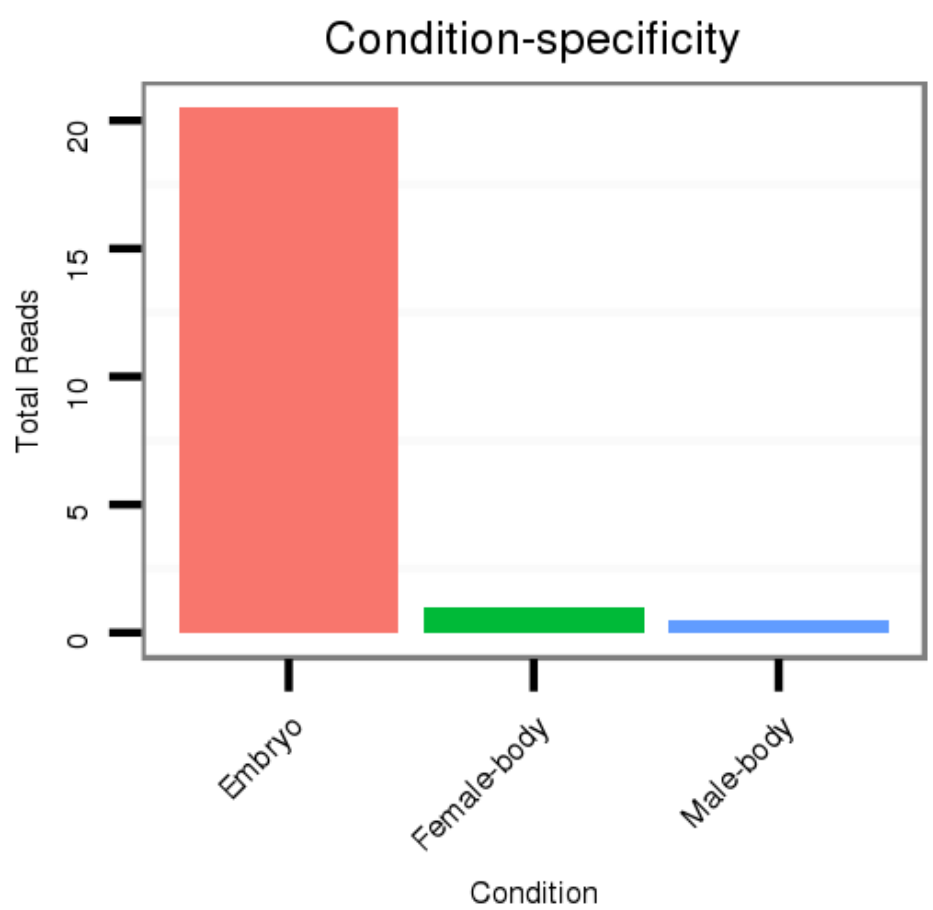
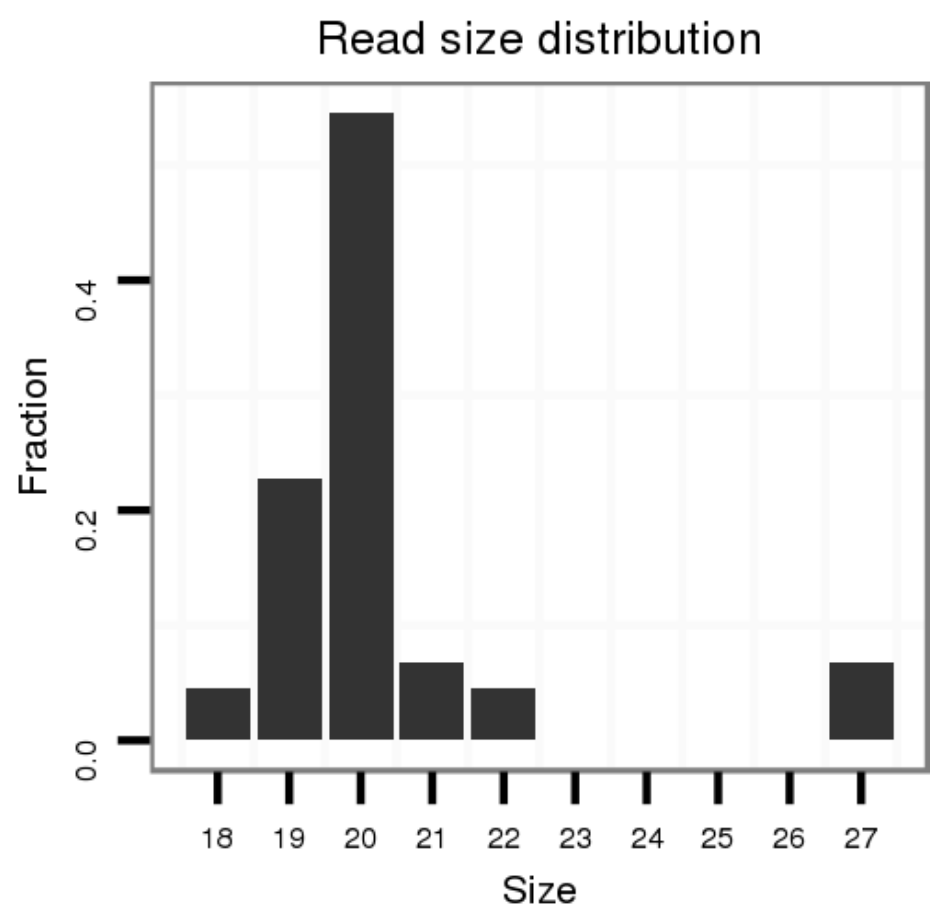
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crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	2

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

Legend: mature star mismatch in alignment mismatch in read

The diagram illustrates a DNA molecule with two circular plasmids and a linear segment. The left plasmid is red and labeled 10, 20, 1. The right plasmid is green and labeled 30, 40. A linear segment connects them, labeled 46. The linear segment contains a T-T mismatch and a C-C mismatch, both marked with blue dots.



Show Alternate Folds

intron [Dper¹GL16653-in]; CDS [Dper¹GL16653-cds]; CDS [Dper¹GL16653-cds]

No Repeatable elements found

mature	star
1. scaffold_26924566-6924585+	1. scaffold_26924540-6924559+
2. dpe_1979_scaffold_66228454-228473+	2. dpe_1979_scaffold_66228428-228447+

Sense Strand Reads

[illegible]

Anti-sense strand reads

AAAAAATTCGGCTTAAGCTAGTCTTCTATTGATTTTACCGAAACCACCTACAACTTCGGGGTGCCCTGATTTCCTCAACTGGTTGAAGGACCGGTTCGCTGATGTAGTCGCTATGGGCTAAACAGACACAAGCTAAGGGACCCGTT
 *****.....((((.....)))*****
 Show Alignment With Reads

Read #	Hit	Total	head	embryo	embryo
size Mismatch	Count	Norm	Total		

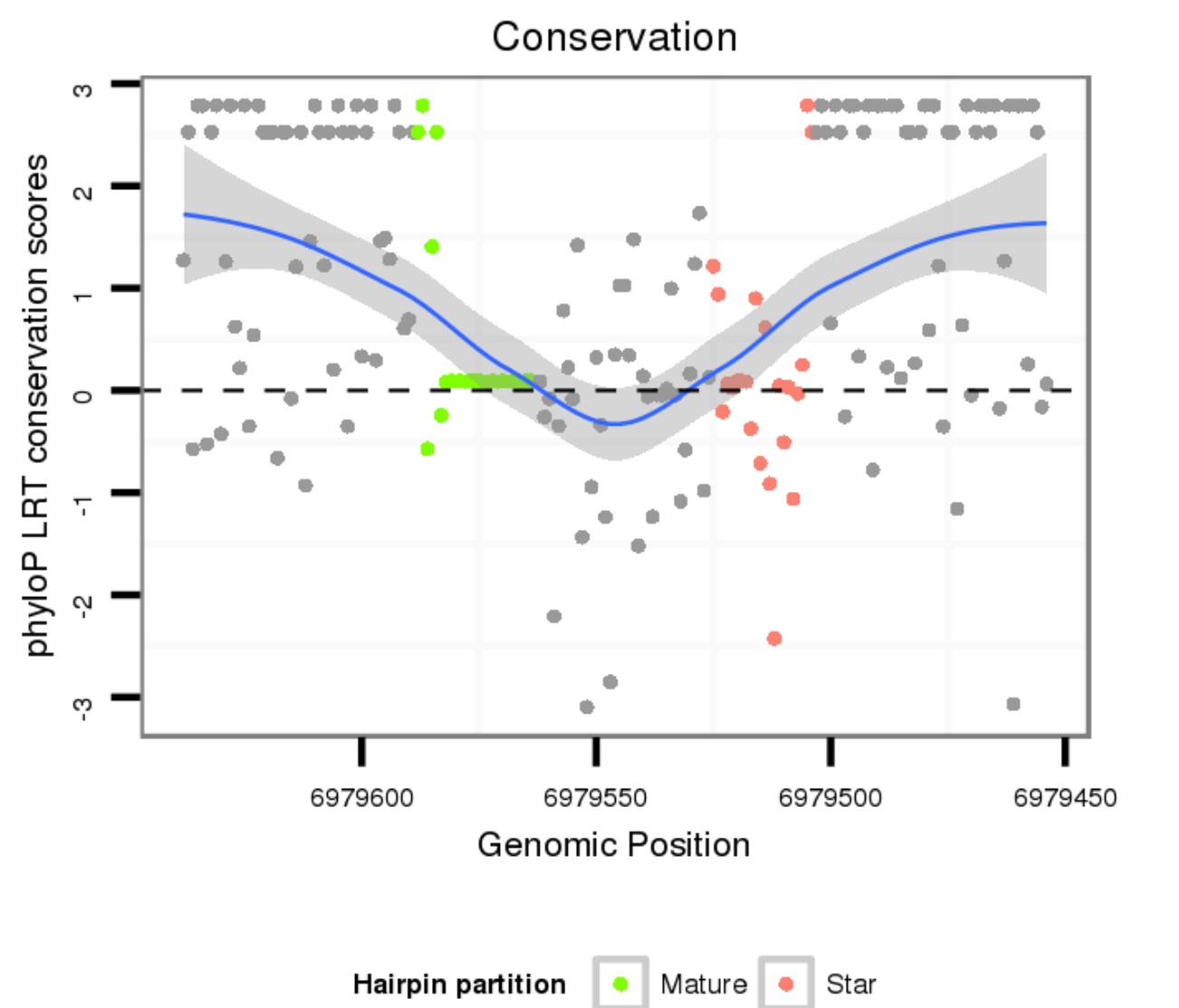
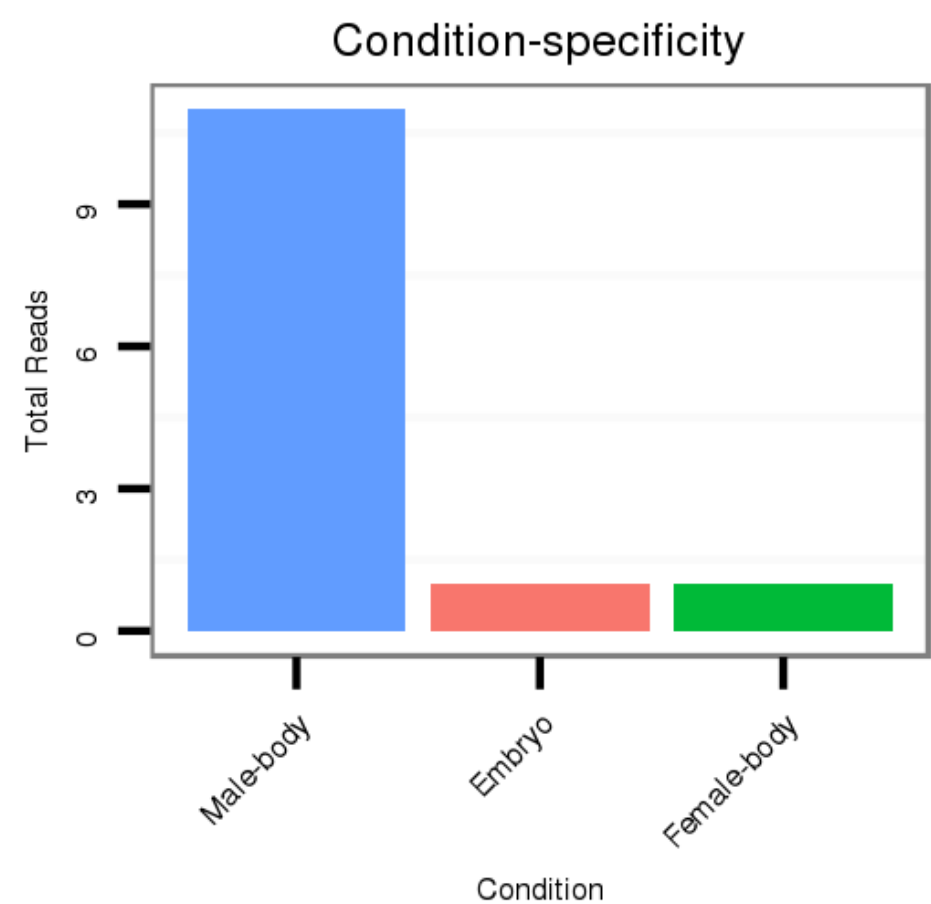
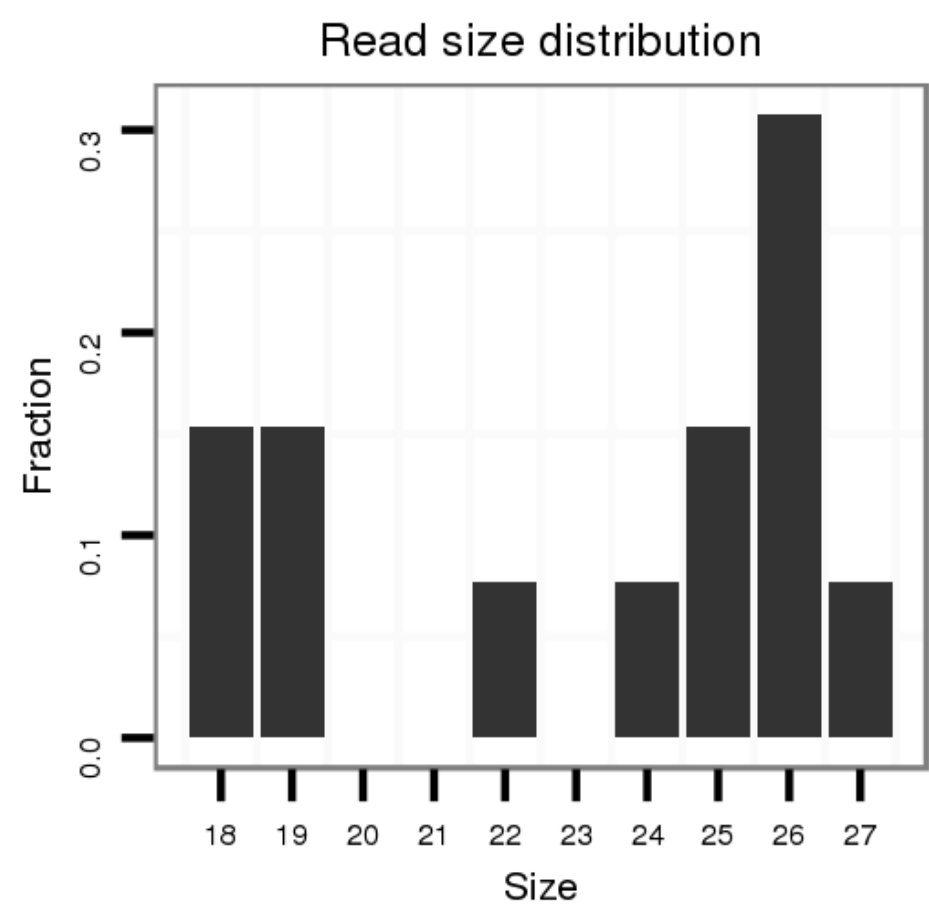
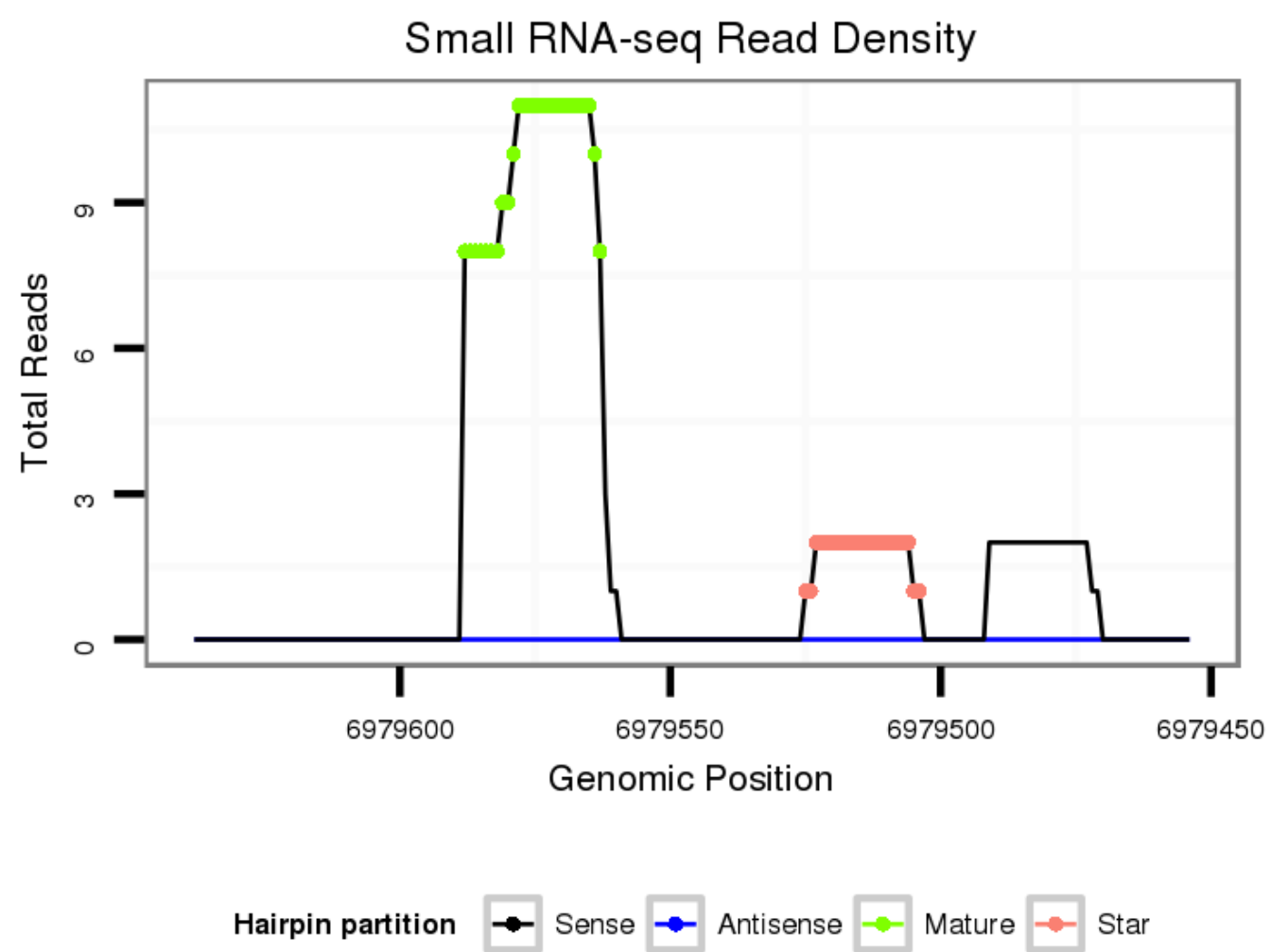
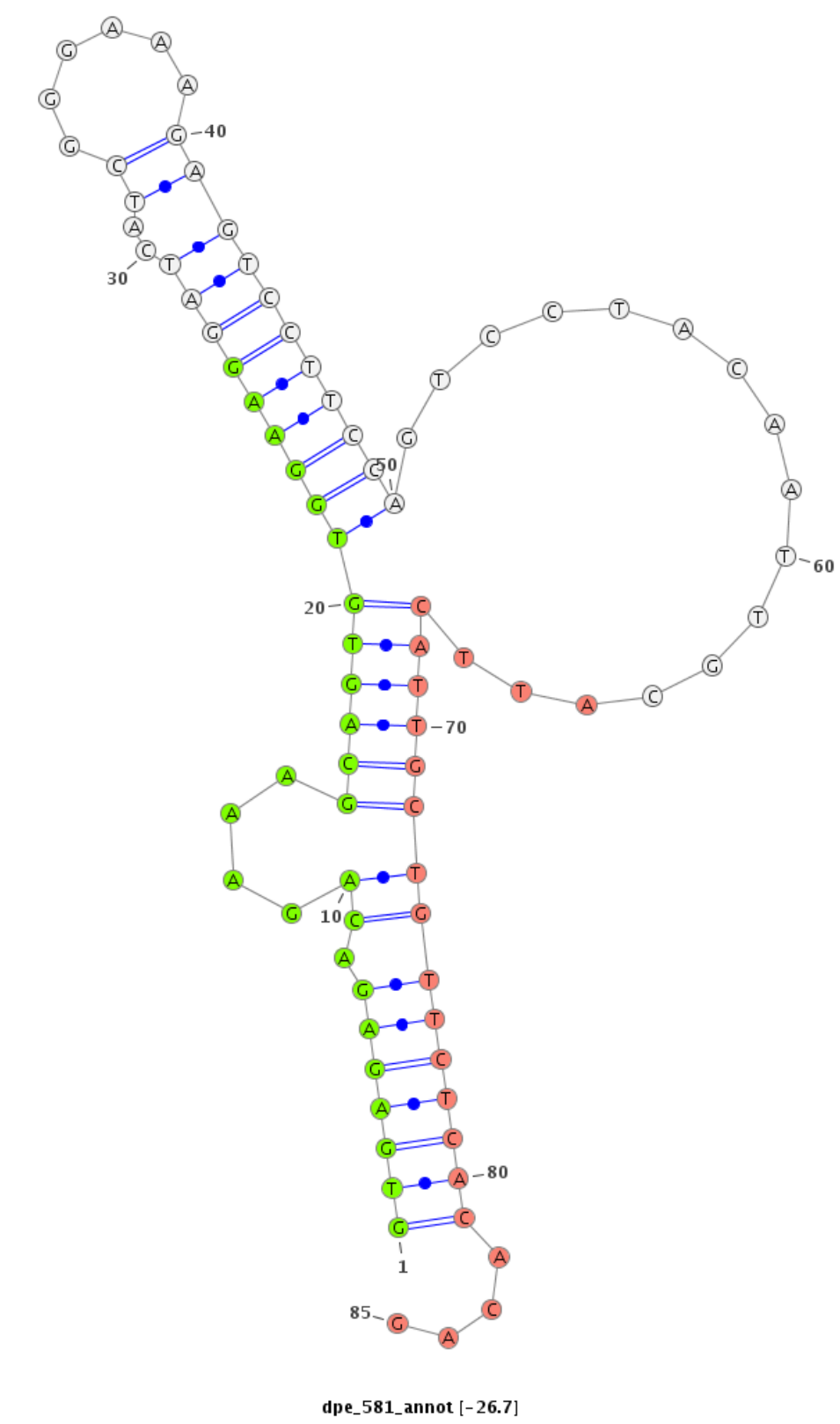
Re-alignment of all predicted orthologs

[illegible]

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	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	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

Predicted structure



Show Alternate Folds

Flybase annotation

intron [Dper\GL18644-in]; CDS [Dper\GL18644-cds]; CDS [Dper\GL18644-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

[illegible]

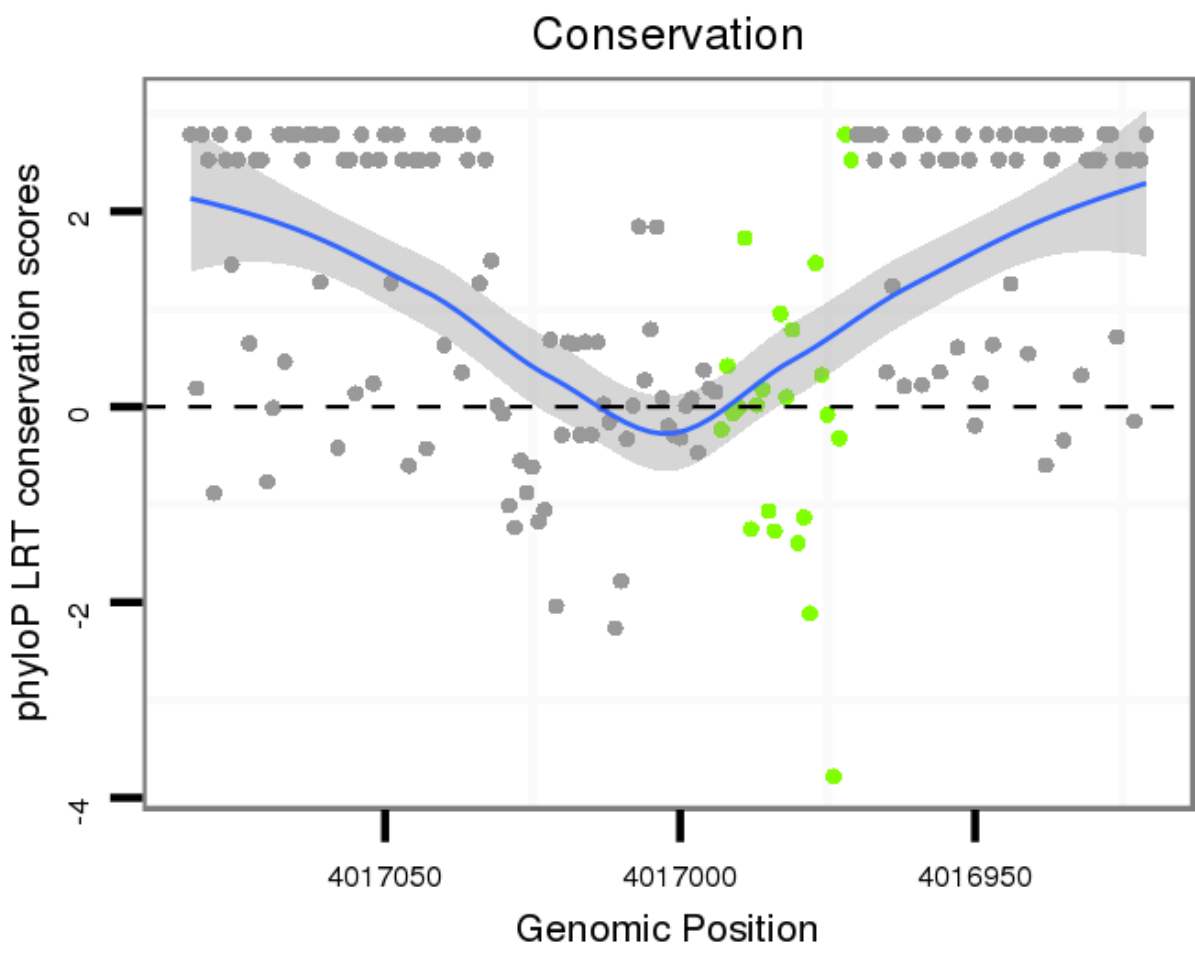
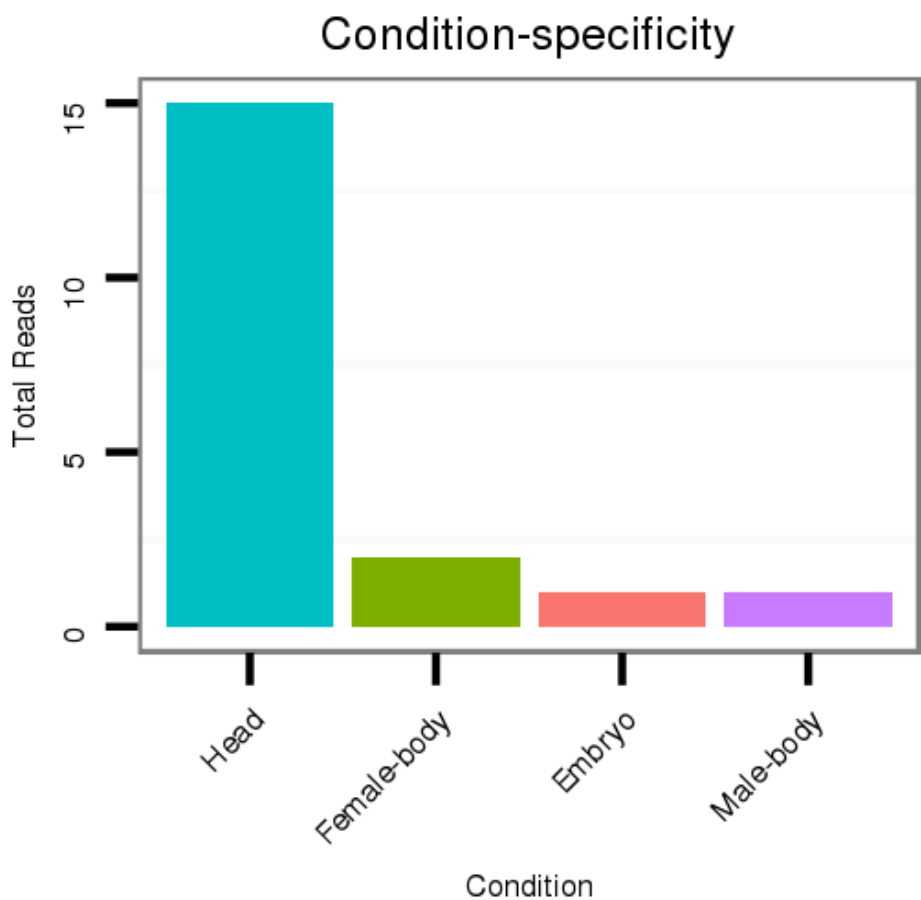
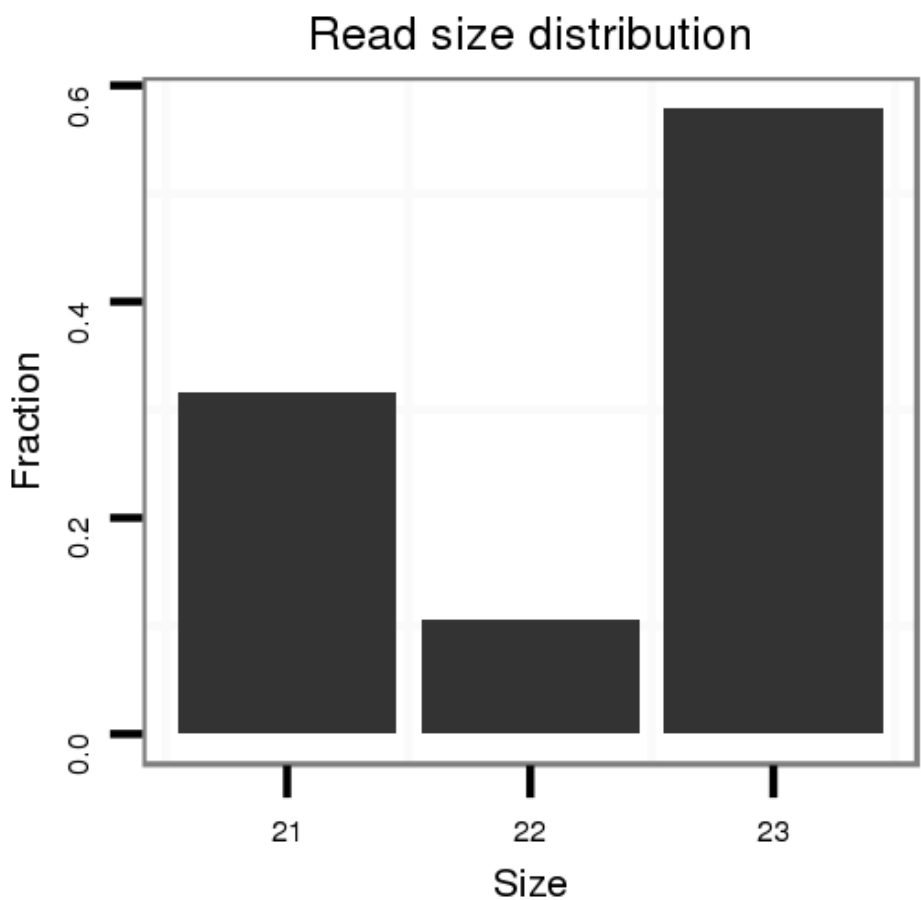
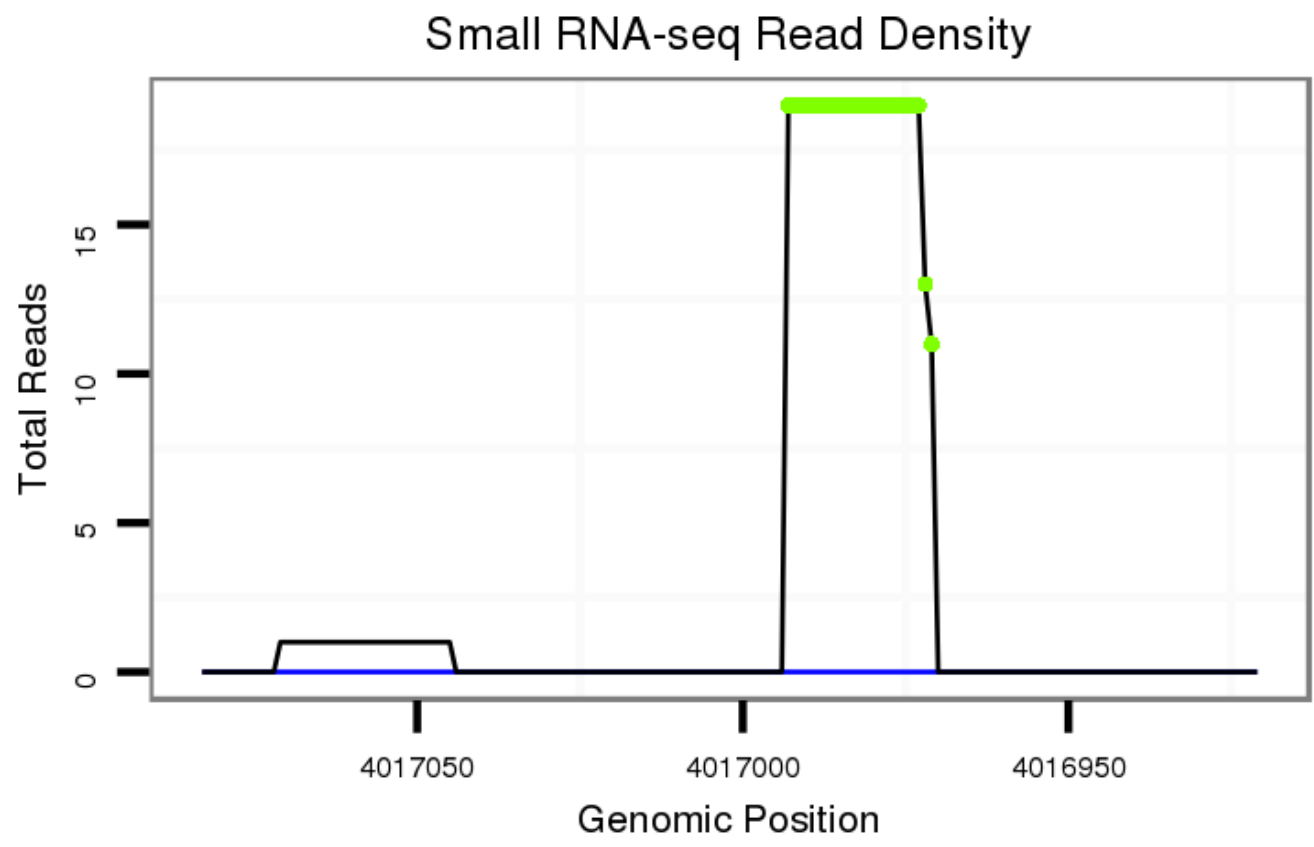
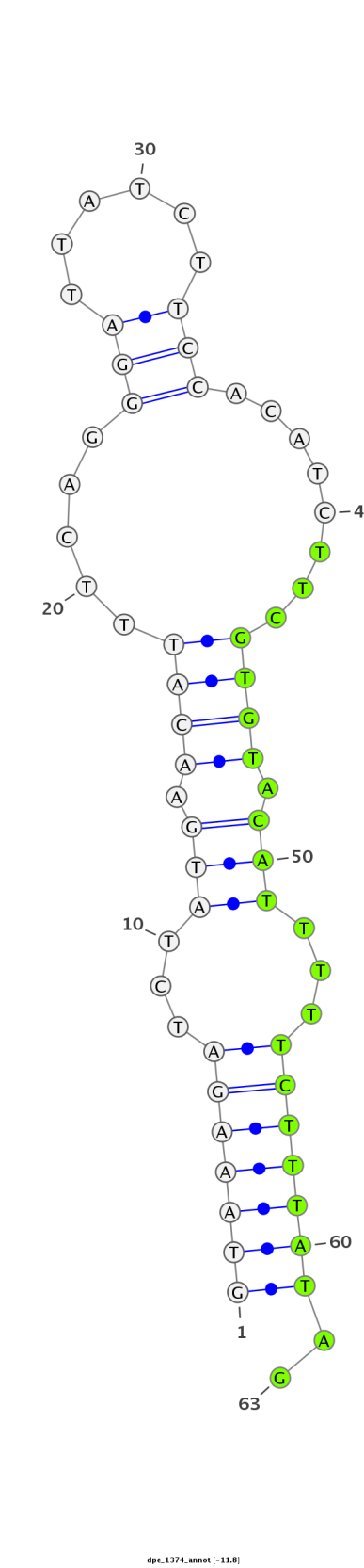
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	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	0
crit.uri	1
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dpe_1374	scaffold_3:4016971-4017033 -	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 [Dper.GL21668-in]; CDS [Dper.GL21668-cds]; CDS [Dper.GL21668-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

				V057	V050	M021	M042	V042	V111					
				head	head	embryo	female body	embryo	male body					
Read #	Hit	Total	Total											
size	Mismatch	Count	Norm											
AGACCAGCCAGGCCCTCATGTACTATGCTACGCACACGGCGCAAATTGAGGTAAAGATCTATGAACATTTTCAGGAGATTATCTCCACATCTTCGGTGACATTTTCTTTTATAGATTGTACGCAATGATCGTACGCTGGAGCAGATTGTCTTTCCCATACCCGA														
*****(((((((.....(((.....(((.....)))).....)))).....)))).....*****														
.....TTCGGTGACATTTTCTTTTATAG.....				23	0	1	11.00	11	4	4	1	1	0	1
.....TTCGGTGACATTTTCTTTTAT.....				21	0	1	6.00	6	3	3	0	0	0	0
.....TTCGGTGACATTTTCTTTTATA.....				22	0	1	2.00	2	0	1	0	1	0	0
.....CCCTCATGTACTATGCTACGCACACGG.....				27	0	1	1.00	1	0	0	1	0	0	0

Anti-sense strand reads

	Read #	Hit	Total		V057
	size	Count	Norm	Total	head
TCTGGTCCGTCCGGGAGTGACATGATACGATGCGTGTGCCCGCTTTAACTCCATTTCATAGATCTTGTAAAGTCCCTAATAGAAGGTGTAGAGCACATGTAAAAAGAAATATCTAACATGCGTTACTAGCATGCGACCTCGTCTAACAGAAAGGGTATGGGCT					
*****(((((((.....(((.....(((.....)))).....)))).....)))).....*****					

Show Alignment With Reads

Re-alignment of all predicted orthologs

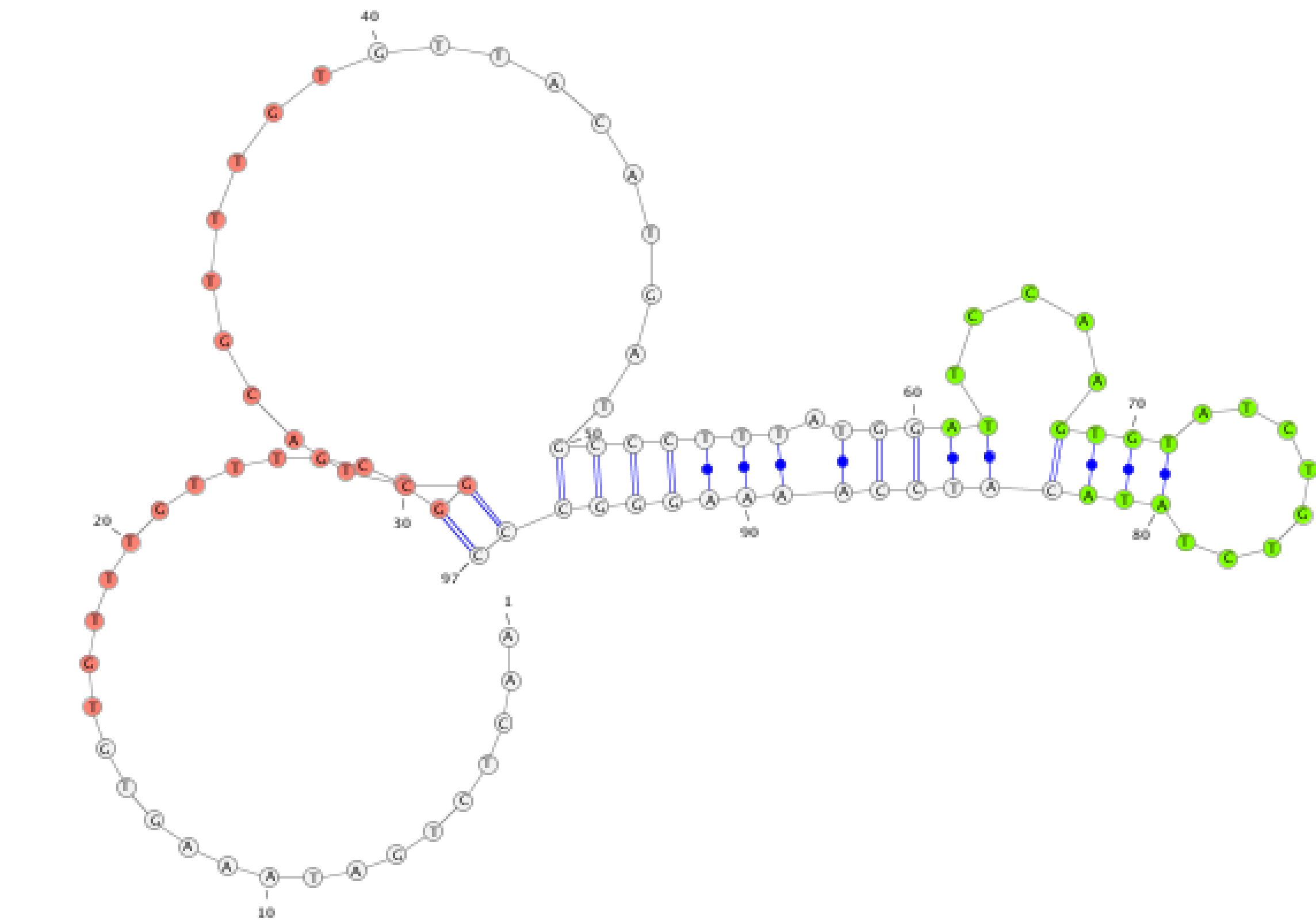
Species	Coordinate	ID	Alignment
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dp5	2:21235105-21235267 -		AGACCAGCCAGGCCCTCATGTACTATGCTACGCACACGGCGCAAATTGAGGTAAAGA-----TC-----TATGAACATTT-CA-GGGA-----TTATCTTCCAC-----ATC-TTCGTGTACATT-----TT--TCT-TTATAGATTGTACGCAATGATCGTACGCTGGAGCAGATTGTCTTTCCCATACCCGA
droW112	scaf2_1100000004521:6611707-6611863 +		AACACAGCCAGGCCCTCATGTACTATGCTACGCACACGGCGCAAATTGAGGTAAAGTGC-----TTAATATAACCGGACAAGAT-----TGAA-T-----TTAATAC-----AA-----ATA-TTTCTCATTGTTCGCAATGATCCAGCTTGAGCAGATTGTCTTCCCATACCCGA
droV1r3	scaf10ld_13047:16674212-16674464 -		AACACAGCCAGGCCCTCATGTACTATGCTACGCACACGGCGCAAATTGAGGTAAAGTGC-----TTAATATAACCGGACAAGAT-----TGAA-T-----TTAATAC-----AA-----ATA-TTTCTCATTGTTCGCAATGATCCAGCTTGAGCAGATTGTCTTCCCATACCCGA
droMo3j	scaf10ld_6540:12980062-12980229 -		AACACAGCCAGGCCCTCATGTACTATGCTACGCACACGGCGCAAATTGAGGTAAAGTGC-----TTAATATAACCGGACAAGAT-----TGAA-T-----TTAATAC-----AA-----ATA-TTTCTCATTGTTCGCAATGATCCAGCTTGAGCAGATTGTCTTCCCATACCCGA
droGr12	scaf10ld_14906:3092154-3092316 -		AGACCAGCCAGGCCCTCATGTACTATGCTACGCACACGGCGCAAATTGAGGTAAAGTGC-----TTAATATAACCGGACAAGAT-----TGAA-T-----TTAATAC-----AA-----ATA-TTTCTCATTGTTCGCAATGATCCAGCTTGAGCAGATTGTCTTCCCATACCCGA
droAna3	scaf10ld_13340:3831920-3832078 -		AGACCAGCCAGGCCCTCATGTACTATGCTACGCACACGGCGCAAATTGAGGTAAAGTGC-----TTAATATAACCGGACAAGAT-----TGAA-T-----TTAATAC-----AA-----ATA-TTTCTCATTGTTCGCAATGATCCAGCTTGAGCAGATTGTCTTCCCATACCCGA
droBip1	scaf7180000396570:676482-676639 +		AGACCAGCCAGGCCCTCATGTACTATGCTACGCACACGGCGCAAATTGAGGTAAAGTGC-----TTAATATAACCGGACAAGAT-----TGAA-T-----TTAATAC-----AA-----ATA-TTTCTCATTGTTCGCAATGATCCAGCTTGAGCAGATTGTCTTCCCATACCCGA
droR1k1	scaf7180000302461:787497-787655 +		AGACCAGCCAGGCCCTCATGTACTATGCTACGCACACGGCGCAAATTGAGGTAAAGTGC-----TTAATATAACCGGACAAGAT-----TGAA-T-----TTAATAC-----AA-----ATA-TTTCTCATTGTTCGCAATGATCCAGCTTGAGCAGATTGTCTTCCCATACCCGA
droF1c1	scaf7180000453850:761618-761778 +		AGACCAGCCAGGCCCTCATGTACTATGCTACGCACACGGCGCAAATTGAGGTAAAGTGC-----TTAATATAACCGGACAAGAT-----TGAA-T-----TTAATAC-----AA-----ATA-TTTCTCATTGTTCGCAATGATCCAGCTTGAGCAGATTGTCTTCCCATACCCGA
droE1e1	scaf7180000491021:87665-87825 -		AGACCAGCCAGGCCCTCATGTACTATGCTACGCACACGGCGCAAATTGAGGTAAAGTGC-----TTAATATAACCGGACAAGAT-----TGAA-T-----TTAATAC-----AA-----ATA-TTTCTCATTGTTCGCAATGATCCAGCTTGAGCAGATTGTCTTCCCATACCCGA
droRho1	scaf7180000776528:12432-12600		AGACCAGCCAGGCCCTCATGTACTATGCTACGCACACGGCGCAAATTGAGGTAAAGTGC-----TTAATATAACCGGACAAGAT-----TGAA-T-----TTAATAC-----AA-----ATA-TTTCTCATTGTTCGCAATGATCCAGCTTGAGCAGATTGTCTTCCCATACCCGA
droB1a1	scaf7180000296948:19651-19815		AGACCAGCCAGGCCCTCATGTACTATGCTACGCACACGGCGCAAATTGAGGTAAAGTGC-----TTAATATAACCGGACAAGAT-----TGAA-T-----TTAATAC-----AA-----ATA-TTTCTCATTGTTCGCAATGATCCAGCTTGAGCAGATTGTCTTCCCATACCCGA
droTak1	scaf7180000415754:446457-446619 -		AGACCAGCCAGGCCCTCATGTACTATGCTACGCACACGGCGCAAATTGAGGTAAAGTGC-----TTAATATAACCGGACAAGAT-----TGAA-T-----TTAATAC-----AA-----ATA-TTTCTCATTGTTCGCAATGATCCAGCTTGAGCAGATTGTCTTCCCATACCCGA
droEug1	scaf7180000409766:306396-306653 +		AGACCAGCCAGGCCCTCATGTACTATGCTACGCACACGGCGCAAATTGAGGTAAAGTGC-----TTAATATAACCGGACAAGAT-----TGAA-T-----TTAATAC-----AA-----ATA-TTTCTCATTGTTCGCAATGATCCAGCTTGAGCAGATTGTCTTCCCATACCCGA
dm3	chr3R:1362325-1362485 +		AGACCAGCCAGGCCCTCATGTACTATGCTACGCACACGGCGCAAATTGAGGTAAAGTGC-----TTAATATAACCGGACAAGAT-----TGAA-T-----TTAATAC-----AA-----ATA-TTTCTCATTGTTCGCAATGATCCAGCTTGAGCAGATTGTCTTCCCATACCCGA
droSim2	3r:1257078-1257237 +		AGACCAGCCAGGCCCTCATGTACTATGCTACGCACACGGCGCAAATTGAGGTAAAGTGC-----TTAATATAACCGGACAAGAT-----TGAA-T-----TTAATAC-----AA-----ATA-TTTCTCATTGTTCGCAATGATCCAGCTTGAGCAGATTGTCTTCCCATACCCGA
droY8k9	chr11Y:41529779379 +		AGACCAGCCAGGCCCTCATGTACTATGCTACGCACACGGCGCAAATTGAGGTAAAGTGC-----TTAATATAACCGGACAAGAT-----TGAA-T-----TTAATAC-----AA-----ATA-TTTCTCATTGTTCGCAATGATCCAGCTTGAGCAGATTGTCTTCCCATACCCGA
droEr2e	scaf10ld_4770:1630303-1630460 +		AGACCAGCCAGGCCCTCATGTACTATGCTACGCACACGGCGCAAATTGAGGTAAAGTGC-----TTAATATAACCGGACAAGAT-----TGAA-T-----TTAATAC-----AA-----ATA-TTTCTCATTGTTCGCAATGATCCAGCTTGAGCAGATTGTCTTCCCATACCCGA

Generated: 09/08/2015 at 10:39 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.ptp3	1
crit.uni	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



dpe_2478_annot [-12.5]

Show Alternate Folds

Flybase annotation

intron [Dper^{GL23696}-in]; utr5 [utr5_plus_10181]

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]

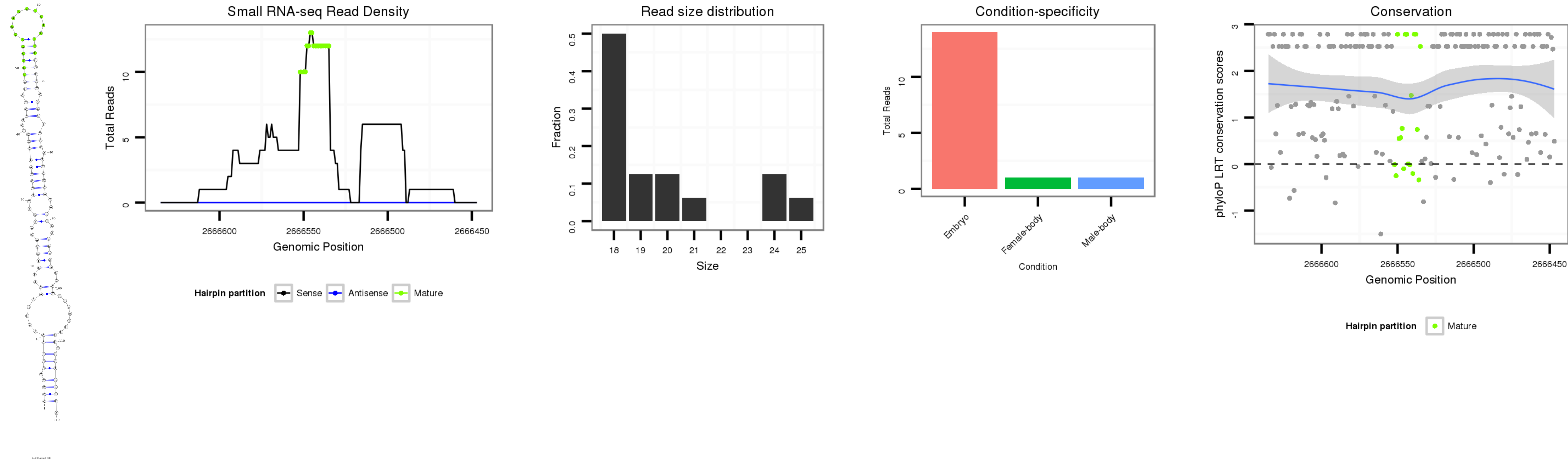
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	PASS/FAIL
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crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	0
crit.top3	1
crit.top3p3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	1
rescue.known	0
rescue.confident	7
rescue.candidate	5

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dpe_2483	scaffold_9:2666497-2666585 -	candidate	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 [Dper\GL24870-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

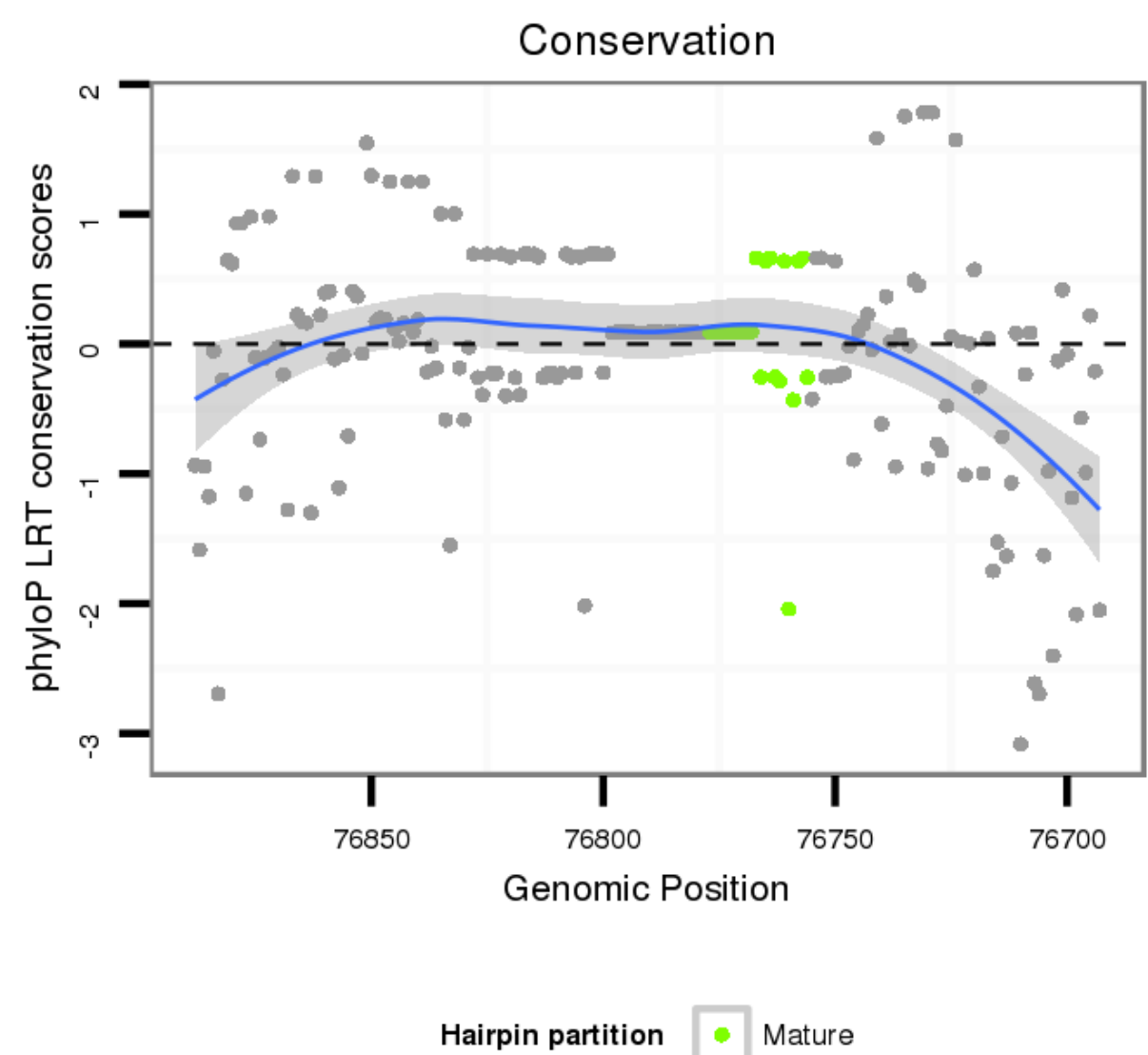
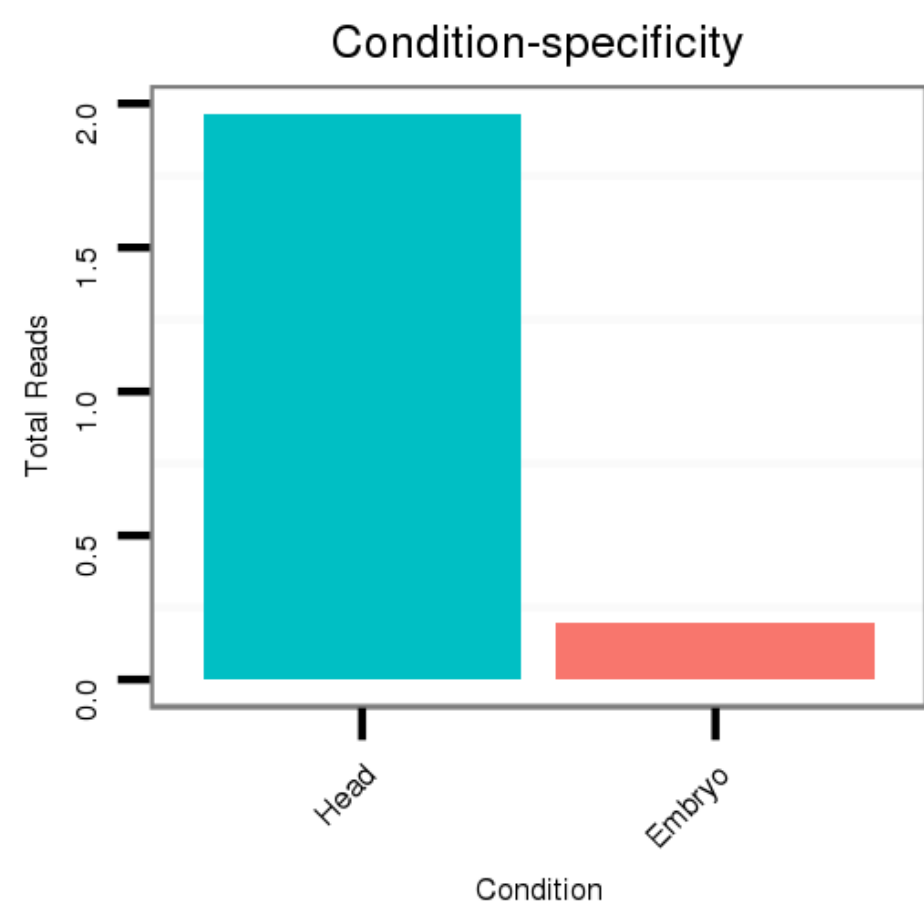
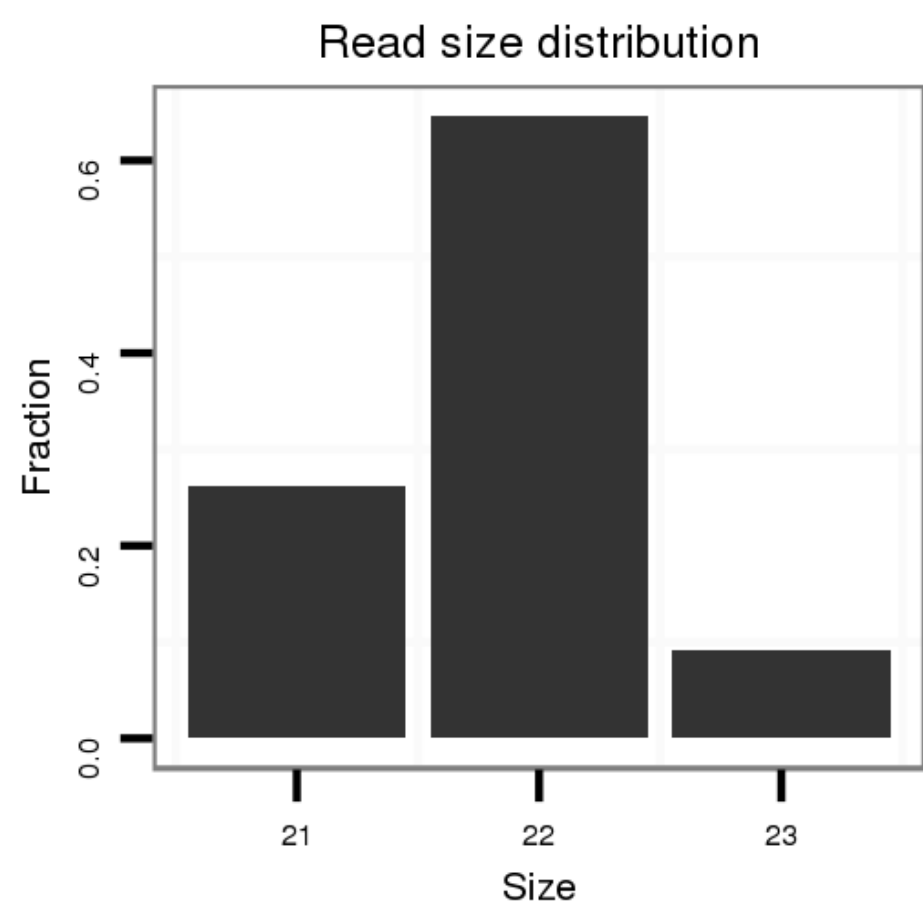
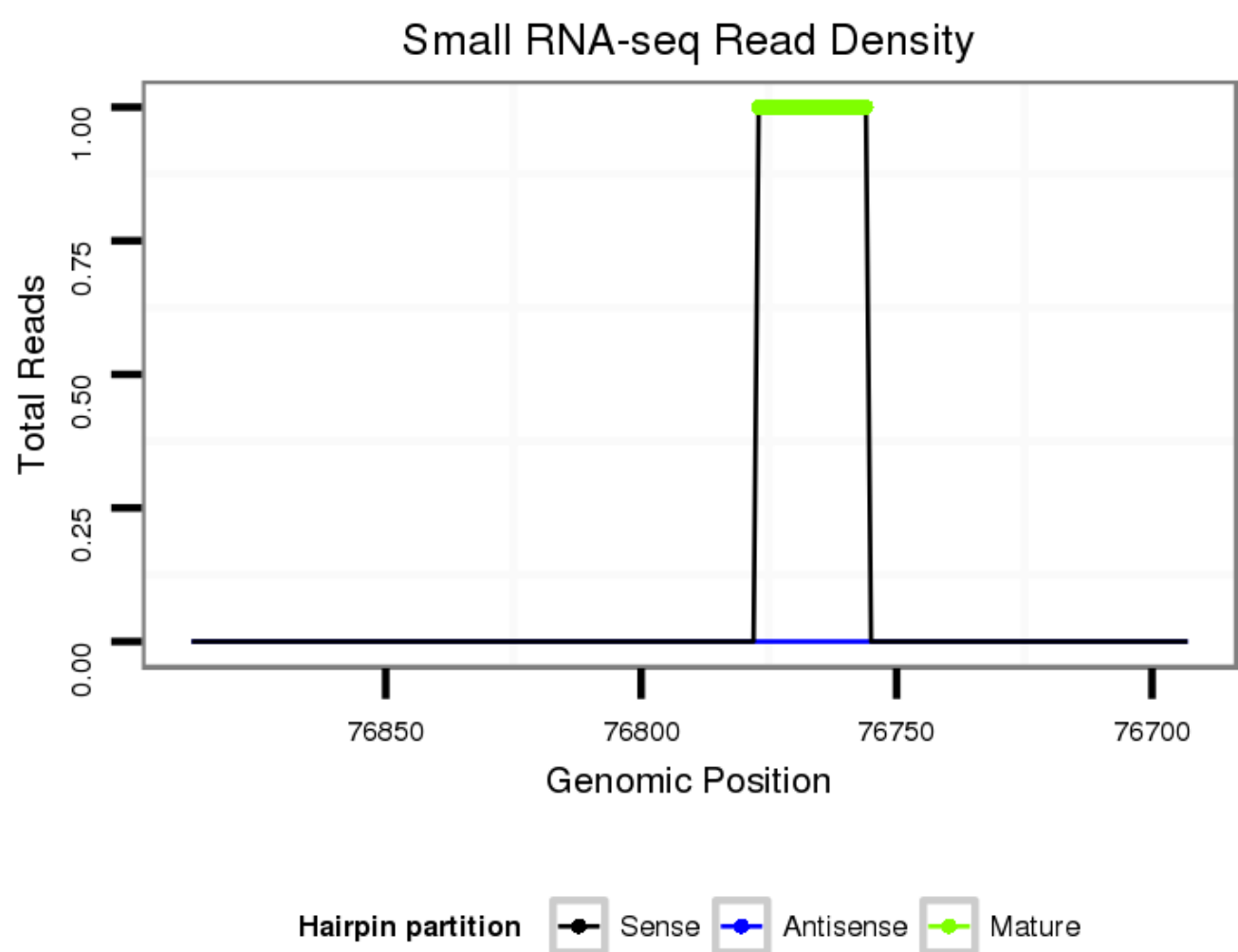
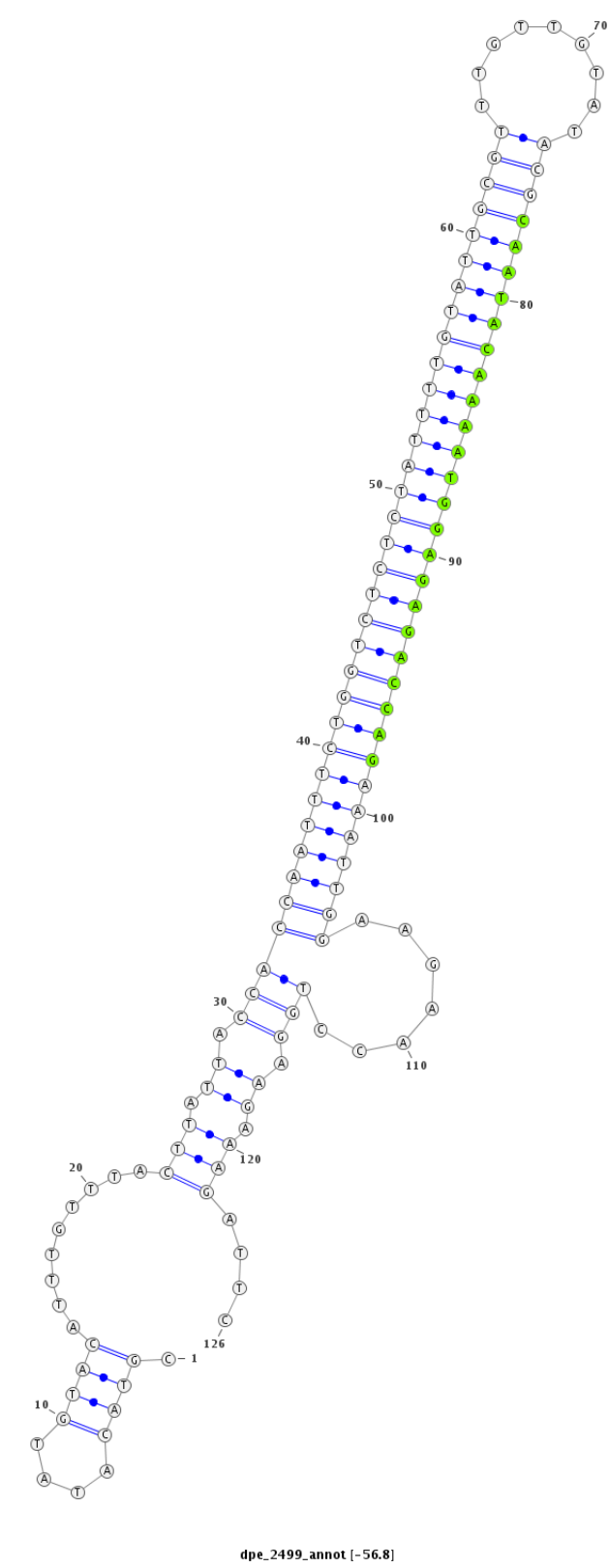
Species	Coordinate	ID	Alignment
droPer2	scaffold_9:2666447-2666635	dps_2483	AATGAGCGGAGGCGCATGCTTTTGTACGCCCCAGGGCTGGCCAGCCG---AAGATCTGCGCGAGATTGGCAAGCGCTCTGGTGGC CTGGGCAAACTGAATCG GGCGCGACCTCGCATATGCCATACTAACCGAGGGCTGTGATCCCCTGCTGCTCATCCAGCGGA---CTCGGTTGAAGAGTTTCCGGTCACA
dp5	XR_group6:4377266-4377454	dps_3829	AATGAGCGGAGGCGCATGCTTTTGTACGCCCCAGGGCTGGCCAGCCG---AAGATCTGCGCGAGATTGGCAAGCGCTCTGGTGGC CTGGGCAAACTGAATCG GGCGCGACCTCGCATATGCCATACTAACCGAGGGCTGTGATCCCCTGCTGCTCATCCAGCGGA---CTCGGTTGAAGAGTTTCCGGTCACA
droWi12	scf2_1100000004511:5276750-5276938	dwi_5417	AATGAGCGGAGGCGCATGCTTTTGC AC TCGCCAGGGCTGGCC AC GG--- GA TATCTGCGCGAGATTGGCA AA CT TA T GA CT GG CTGGCAAACTAATCC AAGT CG CGCCCGCATATGCCATACTAACCGAGGGCTGTGATCC GG GT GT GTCTAT CAAAA GA--- AT CGGTTGAAGAGTTTCCGGT AA CA
droVi3	scaffold_13049:22492152-22492343	dvi_158	AA S AGGCGGAGGCG CA GCCTTTTGC AC TGC S AA GGT GGCC CG CG CA TA T ATCTGCT GA TAGATTGGCAAGCG CT GGT GG CT CG CA T AA CT CA TA GA GGCGCGAC CT CGCATATGCCATACT CA CGCAGGGCTGTG AC CCGTGCTGTCT ATA TCAG CA CA GA --- AT CGGT CC AGAGTTTCC GT TC CA
droMo3	scaffold_6680:17099712-17099903	dmo_114	AA S AA SC HA S AGGCG CA TGCTTTTGC AC GGCG AA GGCTGGCC CG CG CA TCCG CA TCT GC TA SAGATTGGCA AA CT TA TGGTGG CA CT CG CA AA TA CA TA GA GGCGAC CT CGCATATGCCATACT CA CGCAGGGCTGTG AC CCGTGCTGCTCATCCAG CA CA GA --- CA AGGT CC AGAGTT CG CGGT CA CA
droGr12	scaffold_15121:203613-203807	dgr_465	AATGAGCGGAGGCG CA GCCTTTTGC AC GGCG AA GGCTGGCG CG CG CA TGA CA TCT GC TA SAGATTGGCA AA CT TA TGGTGG CA CT CG CA AA TA CA TA GA GGCGAC CT CGCATATGCCATACT CA CGCAGGGCTGTGATCCCCTGCTGCTCATCCAG CA CA CG CT CG CGGT CC AGAGTT CG CA CT TA CA
droAna3	scaffold_13337:4137395-4137583	dan_4038	AA S AGGCGGAGGCG CA GCCTT CG CGAGGCCAG AG CTGGCCGA CT GG--- GG SATCTGCG CA SAGATTGGCAAGCG CT GGTGGC CT TC S AC AC CT GA CT GG CA CT CG CA CT CG CGCATATGCCAT CT CA CGCAGGGCTGTGATCCCCTGCTGCT CT CCAG CA GA GA --- CT CGGT CC AGAGTT CG CGGT CA CA
droBiP1	scf7180000395450:265900-266088		AA S AGGCGGAGGCG CA GCCTT CG CGAGGCCAG AG CTGGCCGA CT GG--- GG SATCTGCG CA SAGATTGGCAAGCG CT GGTGGC CT TC S AC AC CT GA CT GG CA CT CG CA CT CG AA AG CT CG CAATTGCCAT CT CA CGCAGG TT CG GATCCCCTGCTGCT CT CCAG CA GA GA --- CT CGGT CC AGAGTT CG CGGT CA CA
droKi1k	scf7180000302272:666717-666905		AATGAGCGGAGGCG CA GCCTTTTGC CGA SGCCCA AAAA GGCCGA CG --- AG SATCTGCG CA SAGATTGGCA AA CT TA TGGTGG CA CT CG CA AA CT GA CT GG CA CT CG CGCATATGCCAT CT CA CGCAGG TT GT GATCCCCT GT CTCATCCAG CA GA GA --- AT CGGT CC AGAGTT CG CGGT CA CA
droFi1c	scf7180000454048:724234-724422		AATGAGCG S AGGCG CA GCCTT CG CGA AAA AGAA T GGCC AG CG--- GG SATCTGCGCGAGATTGGCAAGCG CT GGTGGC CT TC GA CA AA CT GA CT GG CA CT CG CGCATATGCCATACT CA CGCAGGGCT CG ATCCCCT GT GCTCATCCAG CA GA GA --- AT CGGT CC AGAGTT CG CGGT CA CA
droEl1	scf7180000491255:1412089-1412277		AA S AGGCGGAGG CA GCCTT CG CGA S GCCCA GA AT T GGCC AG CG--- GG SATCTGCGCGAGATTGGCAAGCG CT GGTGGC CT TC GA CA AA CT GA CT GG CA CT CG CGAC CT CGCATATGCCATACT CA CGCAGGGCT CG ATCCCCT GT GCTCATCCAG CA GA GA --- AT CGGT CC AGAGTT CG CGGT CA CA
droRh1	scf7180000769477:967-1151		AA S AGGCGGAGGCG CA GCCTT CG CGA S GCCCA GA AT T GGCC AG CG--- GG SATCTGCGCGAGATTGGCAAGCG CT GGTGGC CT TC GA CA AA CT GA CT GG CA CT CG CGCG CT CGCATATGCCATACT CA CGCAGGGCT CG ATCCCCT GT GCTCATCCAG CA GA GA --- AT CGGT CC AGAGTT CG CGGT CA CA
droBial	scf7180000302193:2253856-2254044		AA S AGGCGGAGGCG CA GCCTT CG CGA S GCCCA GA AT T GGCC AG CG--- GG SATCTGCGCGAGATTGGCAAGCG CT GGTGGC CT TC GA CA AA CT GA CT GG CA CT CG CGCG CT CGCATATGCCAT CT CA CGCAGGGCT CG ATCCCCT GT GCTCATCCAG CA GA GA --- AT CGGT CC AGAGTT CG CGGT CA CA
droTa1k	scf7180000415706:66147-66335		AA S AA T CGGAGG CT CA GCCTT CG CGA S GCCCA GA AT T GGCC AG CG--- GG SATCTGCGCGAGATTGGCAAGCG CT GGTGGC CT TC GA CA AA CT GA CT GG CA CT CG CGCG CT CGCATATGCCAT CT CA CGCAGGGCT CG ATCCCCT GT GCTCATCCAG CA GA GA --- CT CGGT CC AGAGTT CG CGGT CA CA
droEu1j	scf7180000409711:6101265-6101453		AA S AGGCGGAGGCG CA GCCTT CG CGA S GCCCA GA AT T GGCC AG CT GG --- GG SATCT TC CA SAGATTGGCAAGCGCTCTGGTGGC CT TC GA CA AA CT TA AT TA GA CGCGCG CT CGCATATGCCAT CT CA CGCAGGGCTGTGATCC GT GT GTCT AT CCAA CA GA GA --- CT CGGT AC AGAGTT CG CGGT CA CA
dm3	chr3L:13013576-13013764	dme_245	AA S AGGCGGAGGCG CA GCCTT CG CGA S GCCCA GC AG GG CT AG CG--- GG SAC T GGCGCGAGATTGGCAAGCG CT GGTGGC CT TC GA CA AA CT GA CT GG CA CT CG CGCG CT CGCATATGCCAT CT CA CGCAGGGCT CG ATCC GT AT CTGTCT ATA TCAG CA GA GA --- AT CGGT CC AGAGTT CG CGGT CA CA
droSim2	31:12704025-12704213	hsi_32458	AA S AGGCGGAGGCG CA GCCTT CG CGA S GCCCA GC AG GG CT AG CG--- GG SAC T GGCGCGAGATTGGCAAGCG CT GGTGGC CT TC GA CA AA CT GA CT GG CA CT CG CGCG CT CGCATATGCCAT CT CA CGCAGGGCT CG ATCC GT AT CTGTCT ATA TCAG CA GA GA --- AT CGGT CC AGAGTT CG CGGT CA CA
droSec3	scaffold_4:5105161-5105340	dys_1846	AA S AGGCGGAGGCG CA GCCTT CG CGA S GCCCA GC AG GG CT AG CG--- GG SAC T GGCGCGAGATTGGCAAGCG CT GGTGGC CT TC GA CA AA CT GA CT GG CA CT CG CGCG CT CGCATATGCCAT CT CA CGCAGGGCT CG ATCC GT AT CTGTCT ATA TCAG CA GA GA --- AT CGGT CC AGAGTT CG CGGT CA CA
droTak2	31:13092479-13092667	dya_1738	AA S AGGCG S AGGCG CA GCCTT CG CGA S GCCCA GC AG GG CT AG CG--- GG SAC T GGCGCGAGATTGGCAAGCG CT GGTGGC CT TC GA CA AA CT GA CT GG CA CT CG CGCG CT CGCATATGCCAT CT CA CGCAGGGCT CG ATCC GT AT CTGTCT ATA TCAG CA GA GA --- AT CGGT CC AGAGTT CG CGGT CA CA
droEr2	scaffold_4784:13021109-13021297	der_1523	AA S AGGCGGAGGCG CA GCCTT CG CGA S GCCCA GC AG GG CT AG CG--- GG SAC T GGCGCGAGATTGGCAAGCG CT GGTGGC CT TC GA CA AA CT GA CT GG CA CT CG CGCG CT CGCATATGCCAT CT CA CGCAGG TT CG ATCC GT AT GCTGCTCATCCAG CA GA GA --- AT CGGT CC AGAGTT CG CGGT CA CA

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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	0
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



Show Alternate Folds

Flybase annotation

intergenic

No Repeatable elements found

mature	star
1. dpe_2500 scaffold_168:19097-19118 -	
2. dpe_2282 scaffold_71:43517-43538 +	
3. dpe_2497 scaffold_71:55879-55900 +	
4. dpe_2498 scaffold_71:59528-59549 +	
5. dpe_2499 scaffold_71:76756-76777 -	

Sense Strand Reads

hide 3p reads | show mid mismatch reads

														V057	V050	V111	V042					
														Read #	Hit	Total		head	head	embryo		
														size	Mismatch	Count	Norm	Total	body	male		
*****.(((.....))).....((.(.((.....))))))))))))))))))))))))))))))))))))*****																						
.....CAATACAAAATGGAGAGACCAG.....														22	0	5	1.40	7	2	5	0	0
.....CAATACAAAATGGAGAGACCAGA.....														23	0	5	0.20	1	1	0	0	0
.....CAATACAAAATGGAGAGACCAG.....														23	1	5	0.20	1	1	0	0	0
.....ATACAAAATGGAGAGACCAGA.....														21	0	5	0.20	1	0	0	0	1
.....AATACAAAATGGAGAGACCAG.....														21	0	5	0.20	1	1	0	0	0
.....CAATACAAAATGGAGAGACCA.....														21	0	6	0.17	1	1	0	0	0
.....CAATACAAAATGGAGAGACCA.....														22	1	6	0.17	1	1	0	0	0

Anti-sense strand reads

[illegible]

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droPer2	scaffold_71:76693-76888 -	dpe_2499	ATCAAGGAGAAAAATAAGAGAAAGCAAAATACATACGTACATATGTACATTGTTTACTTATTACCACCAATTTCTGGTCTCTCTATTTTGTATTGCGTTTGTGTATACGCAATACAAATGGAGAGACCAGAAATTGGAAGAACCTGGAAGAAAGATTACACCATTCTGGACGACAT-CTAGTT-----GAAGAGCAAT
dp5	Unknown_group_61:9866-10061 -		ATCAAGGAGAAAAATAAGAGAAAGCAAAATACATACGTACATATGTACATTGTTTACTTATTACCACCAATTTCTGGTCTCTCAATTTTGTATTGCGTTTGTGTATACGCAATACAAATGGAGAGTCCAGAAATTGGAAGAACCTGGAAGAAAGATTACACATTCTGGACGACAT-CTAGTT-----GAAGAGCAAT
droW112	scf2_1100000009464:785-857 +		AAGGAG-----ATATCTATGTACATATGTATCTACATATATAAAGATTAACTCTTTCAAAATCCCAATTCT-----GATTT
droVir3	scaffold_13049:24530307-24530386 +		AAAGGA-----CAGCAGCAAGCCCTCGT-----CAGCAGTCTGGAGAGCAATCAGCCCGCTCGAGACCGSAT-CACA-A-----GAGAGGCTAC
droMoJ3	scaffold_6541:837165-837218 +		GGACAG-----CTTAACTTTGAAAGATTTAAGCCATTTAATCTTTACTT-CTGAC-----AGAACAG
droAna3	scaffold_13417:2735035-2735094 +		TTCCGA-----CAGCTTAAGAGCAGATTTAAGCCATTTAACCTGACTCT-CGATTC-----GAAACCAAT
droKik1	scf718000030170:307070-307131 +		AGCAATAAGAAAGAGCAAGCAACAAAGCAAAATAAACATACATATATATATATATCTCT-----AT
droEle1	scf7180000490899:17114-17193 +		ATAAAC-----TAATATGACACAAACCGGCAGACCTGACAAAGAGCTGAA-----CCTGACCT-TAGATG-----AAAAAAC-AAAATATAA
droRho1	scf7180000763762:2133-2184 +		CTCGA-----GGAAAGATTTCAGCCACTCGAGACAGCGT-CGCTCA-----GGA-----GATTACAC
droTak1	scf7180000041427:24235-24275 -		TGG-----AAGAAAGATTTAAGCCTTTGATTGTCTCA-CA-----GATGAT
dm3	chrU:5769325-5769363 +		AGATAG-----AGT-----GATATGTGGACTAAGN-NTAAT-----AA-CGAAC
droV185	scaffold_4690:12104483-12104521 -		GAAAG-----AAACAAAGAAAGAGAAATACATATTAAT-----GT

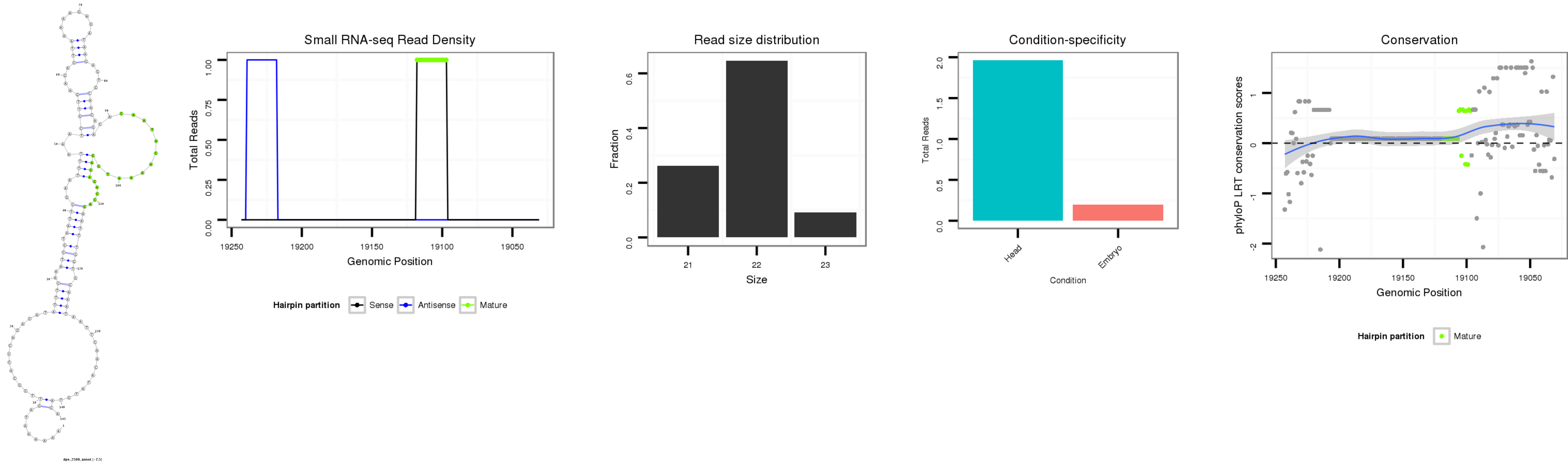
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crit.tp3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	1
rescue.known	3
rescue.confident	0
rescue.candidate	4

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dpe_2500	scaffold_168:19081-19193 -	candidate	Canonical miRNA	intergenic	[View on UCSC Genome Browser (Cornell Mirror)]

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Show Alternate Folds

Flybase annotation

intergenic

No Repeatable elements found

mature	star
1. dpe_2500 scaffold_168:19097-19118 - 2. dpe_2282 scaffold_7143317-43338 + 3. dpe_2497 scaffold_7155879-55900 - 4. dpe_2498 scaffold_7159528-59549 + 5. dpe_2499 scaffold_7176756-76777 -	

Sense Strand Reads

hide 3p reads show mid mismatch reads

AAATGCAACCCAGAAAAACAATGAATTACAATAAAAAAATAGTTCGCACCCAGACATATTTCAAATCGTAATTCGAATTTAAATCGTTGAAGACTTAAAAAGAGATAAGAGTGCAACAGACA	CAATACAAAATGGAGAGACCAG	AAATTGGTGGAATAATTCACATATGTACATATGTATGTGTATTGTCTCTCTTTTATGATT	Read #	size	Mismatch	Hit	Count	Norm	Total	Total	V057	V050	V042	V111
*****	*****	*****	22	0	5	1.40	7	2	5	0	0	0	0	0
*****	*****	*****	23	1	5	0.20	1	1	0	0	0	0	0	0
*****	*****	*****	21	0	5	0.20	1	0	0	1	0	0	0	0
*****	*****	*****	23	0	5	0.20	1	1	0	0	0	0	0	0
*****	*****	*****	21	0	5	0.20	1	1	0	0	0	0	0	0
*****	*****	*****	22	1	6	0.17	1	1	0	0	0	0	0	0
*****	*****	*****	21	0	6	0.17	1	1	0	0	0	0	0	0

Anti-sense strand reads

TTTACGTTGGGTTCTTTTGTACTTAATGTTATTTTTTTTTATCAAGCGTGGGTCTGTATAAAGTTTAGCATTAAAGCTTAAATTTAGCAACTTCTGAATTTTCTCTATTCTCACGTTGCTCTGT	GTTATGTTTTACCTCTCTGCTG	TTAAACCACTTTTATTAAAGTTGTATACATGTATACATACACACATAAACGAGAGAAAAATACTAA	Read #	size	Mismatch	Hit	Count	Norm	Total	Total	M021	V057
*****	*****	*****	22	0	1	1.00	1	1	0	0	0	0
*****	*****	*****	21	0	6	0.17	1	0	1	0	1	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droPer2	scaffold_168:19031-19243 -	dpe_2500	AAATGCAACCCAGAAAAACAATGAATTACAATAAAAAAATAGTTCGCACCCAGACATATTTCAAATCGTAATTCGAATTTAAATCGTTGAAGACTTAAAAAGAGATAAGAGTGCAACAGACA
dp5	Unknown_group_93:18126-18337 -		AAATGCAACCCAGAAAAACAATGAATTACAATAAA
droW112	scf2_1100000004822:2783788-2783821 -		AT
droGr12	scaffold_8775:922-986 +		ATT
droAna3	scaffold_13339:1263564-1263595 +		CAATATG
droB1p1	scf7180000393672:4785-4839 +		TTT
droK1k1	scf7180000299706:32792-32801 -		AAATCAAC
droE1e1	scf7180000491242:121686-		C
droRho1	scf7180000762342:6638-6688 +		AAAAATTA
droTak1	scf7180000413465:992-1133 +		GTCCATAC

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crit.star	0
crit.loop	0
crit.mor	0
crit.hair	0
crit.total	0
crit.paring	0
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	1
rescue.known	3
rescue.confident	0
rescue.candidate	4

Predicted structure



Flybase annnotation

intron [Dper\GL12021-in]; CDS [Dper\GL12021-cds]; CDS [Dper\GL12021-cds]; utr3 [utr3_minus_8031]; utr3 [utr3_minus_8032]; utr5 [utr5_minus_9370]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

Anti-sense strand reads

AAGAGATAAGCCAGACGCTGCACACTAGAATTAC	TGCCGACGAATC	CATCCATGATCATCCCCA	GGGGTACCTTAAGCATAACTAGAAACCATATGGAGGAGATGGGATTTC	CACTGCACACCCTGATACCGGATACCCCGTTGCTAAAGTAGCCGCT					V042
					Read #		Hit	Total	embryo
*****(((...(((...(((...(((...))))))..)))..))))).).....)					size Mismatch	Count	Norm	Total	

Show Alignment With Reads

Re-alignment of all predicted orthologs

[illegible]

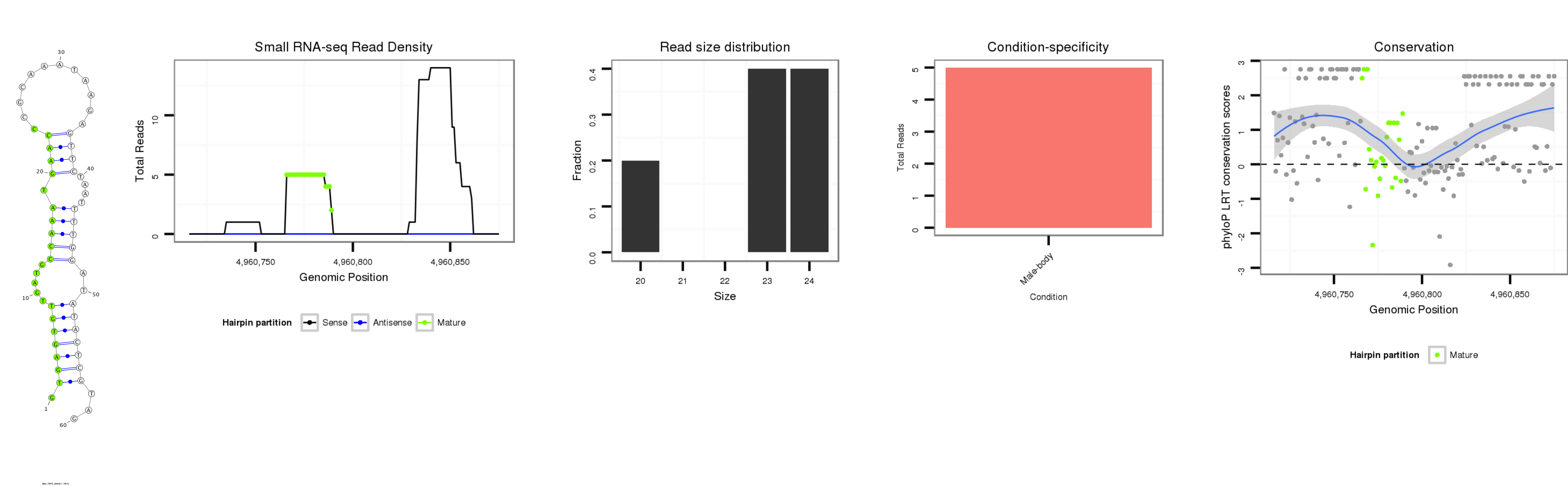
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	PASS/FAIL
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crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	0
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate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

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dpe_2493	scaffold_3:4960766-4960825 +	candidate	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 [Dper¹GL22220-in]; CDS [Dper¹GL22220-cds]; CDS [Dper¹GL22220-cds]

No Repeatable elements found

Sense Strand Reads

[illegible]

Anti-sense strand reads

[illegible]

Show Alignment With Reads

Re-alignment of all predicted orthologs

[illegible]

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

Legend: mature star mismatch in alignment mismatch in read



Flybase annotation

intron [Dper¹GL23696-in]; utr5 [utr5_plus_10181]**Repeatable element**

Sense Strand Reads

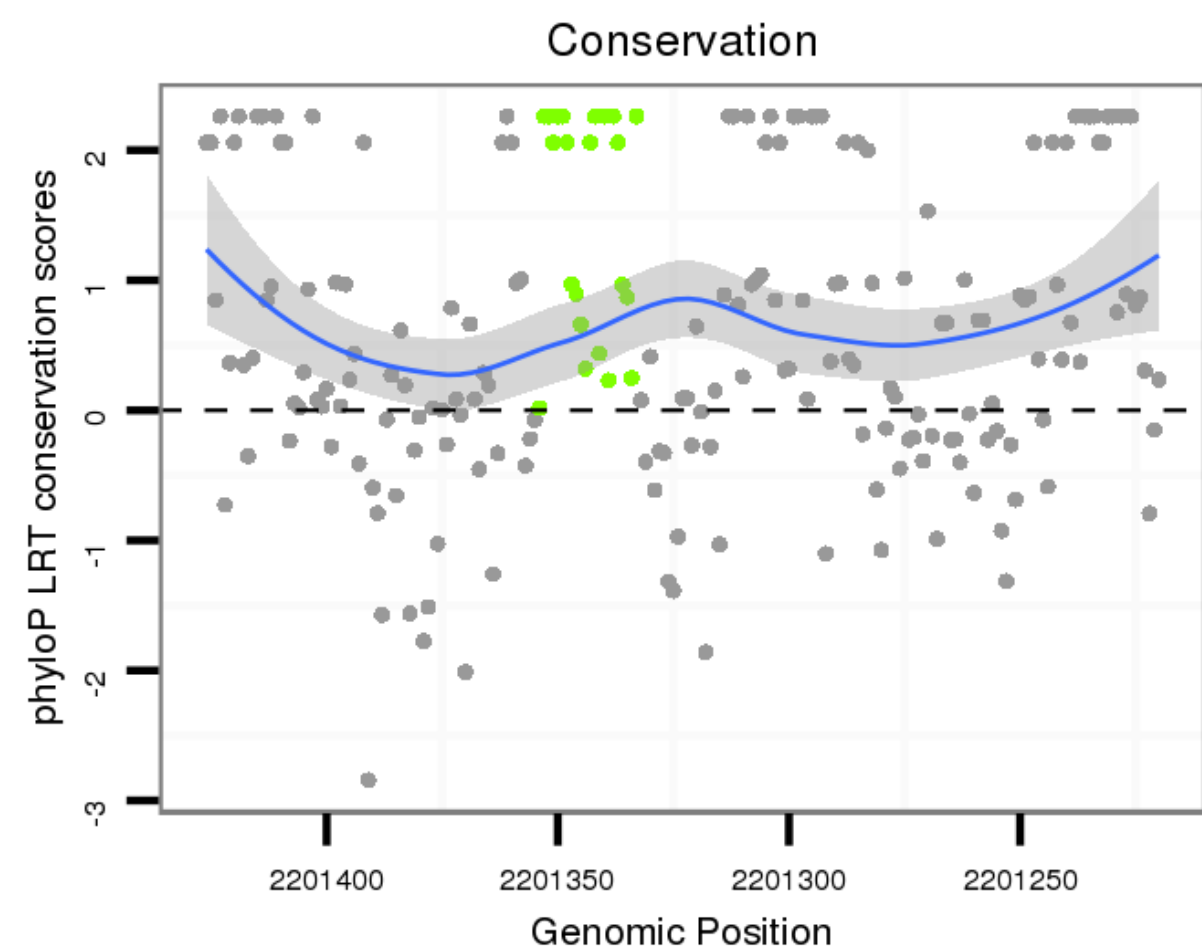
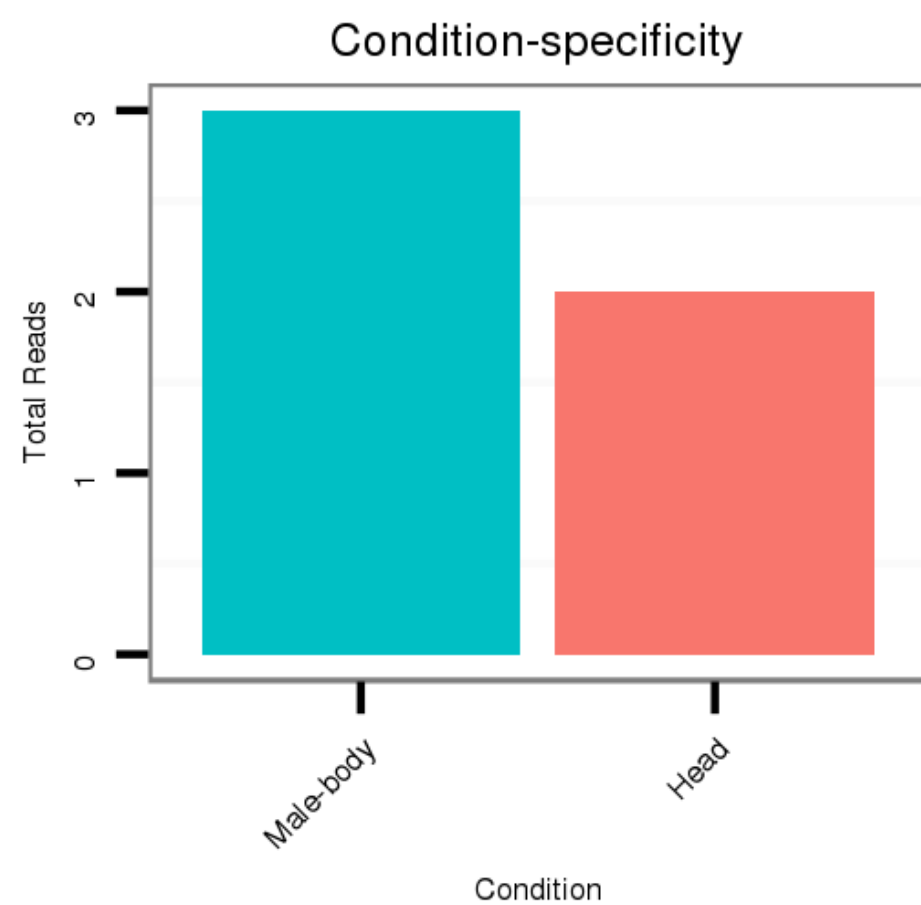
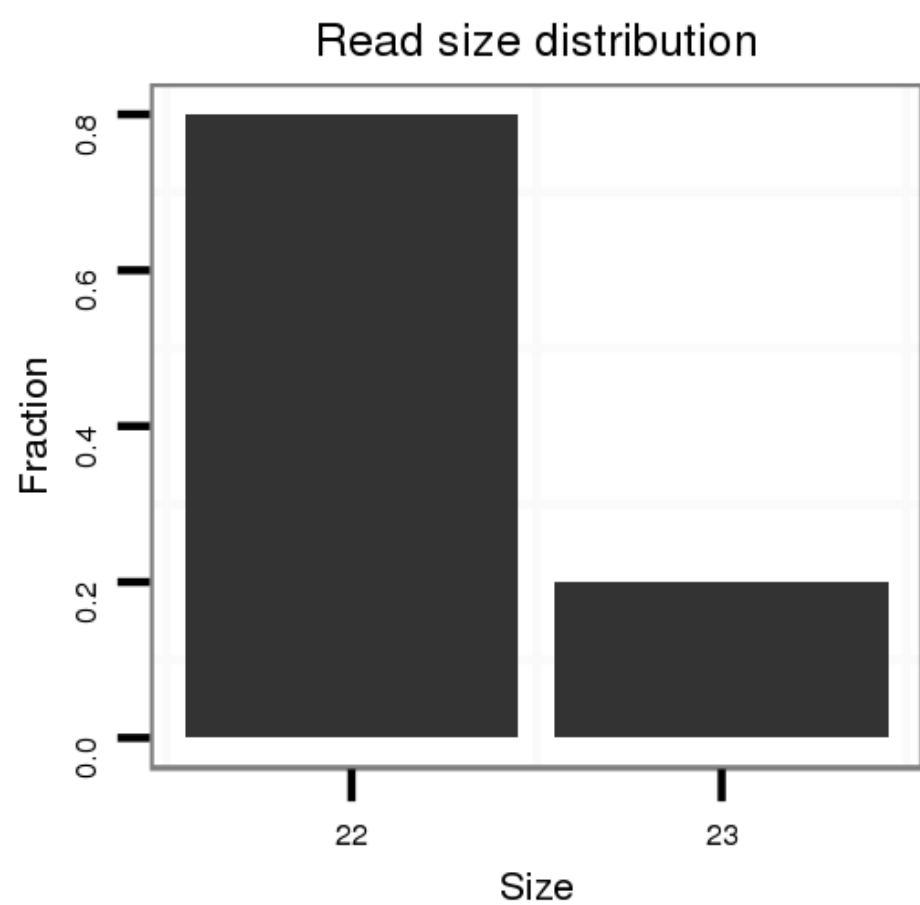
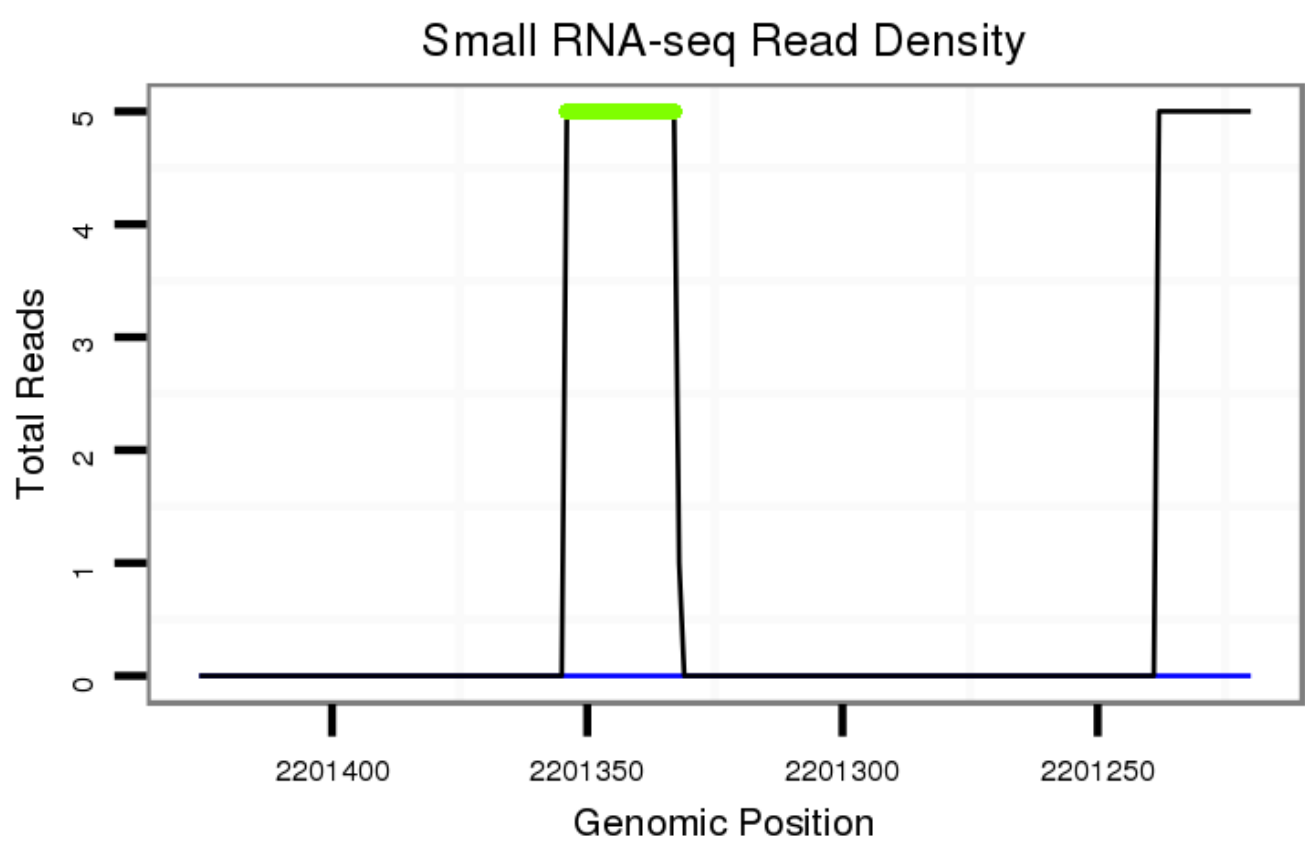
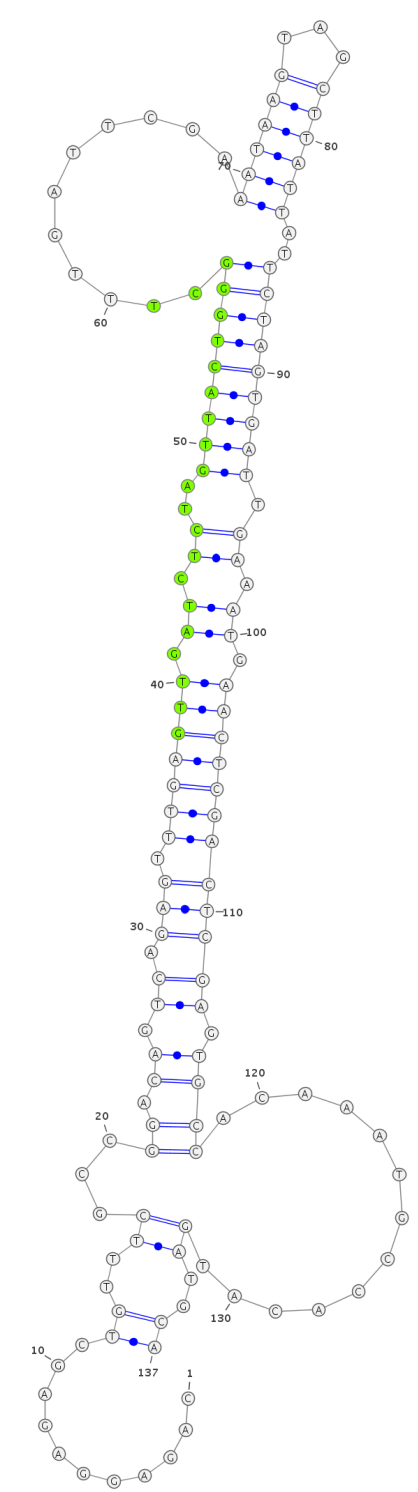
hide 3p reads | show mid mismatch reads

Show Alignment With Reads

Generated: 09/08/2015 at 07:51 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	0
crit.back	0
rescue.total	0
ue.dominant	1
rescue.known	0
ue.confident	3
ue.candidate	9

Legend: mature star mismatch in alignment mismatch in read



Flybase annotation

Antisense to intron [Dper\GL26641-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

[illegible]

Anti-sense strand reads

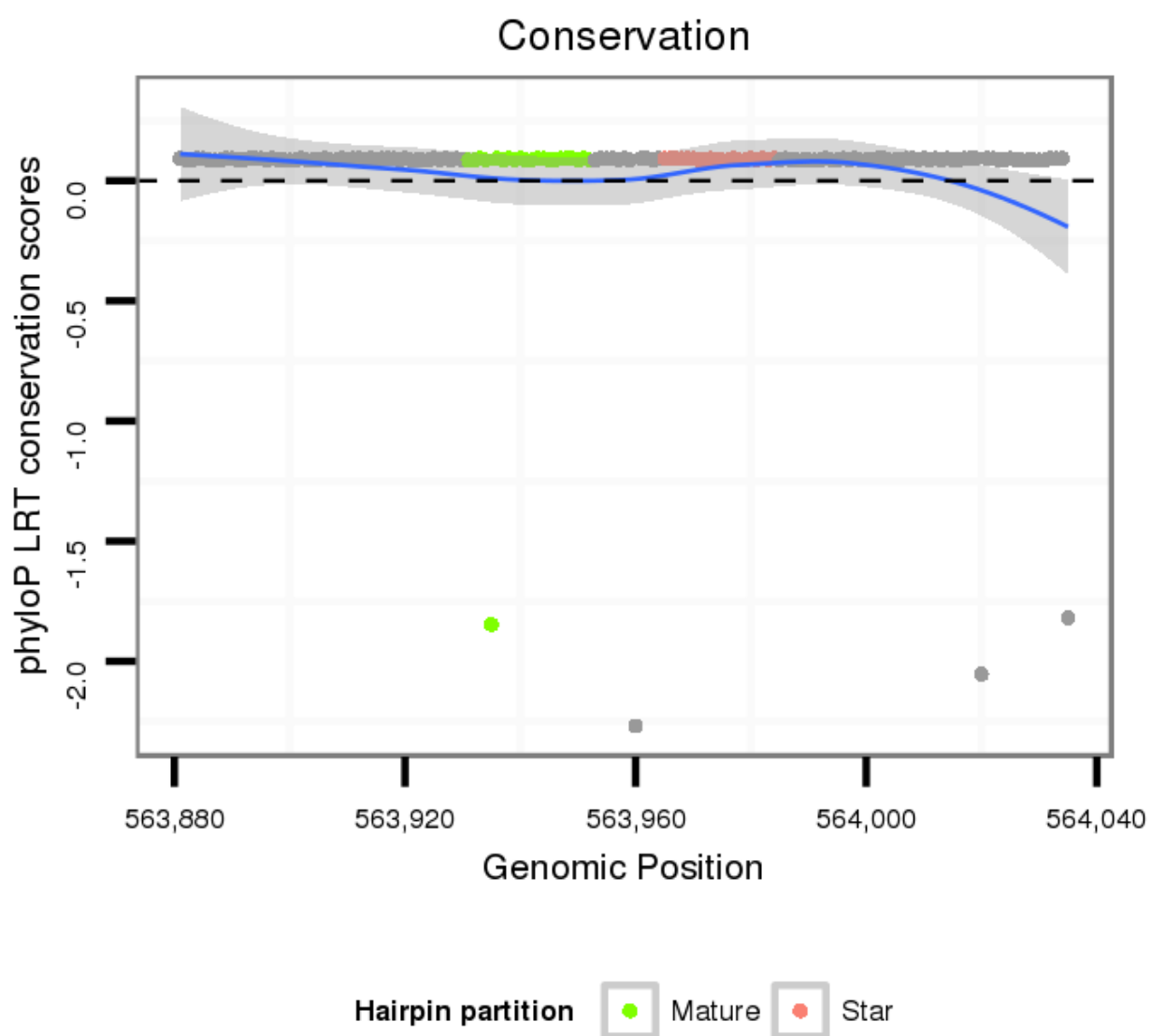
Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droPer2	scaffold_10:2201220-2201426	dpe_2504	GGAAATCCCTCAAATATGGCAGCCACTAA-AGACAACCAGAGGA-----GA--GCTGTT--TC-----GCC-G---GACAGTCAGAGTTTGA GTGATCTCTAGTTACTGGGG TTG--AT-TCGAAATAAGTAGCTTATTATTCTAGTGATTGAAATGAATCTG-ACTCG--AGTGCCACAAATGCCACATG---ATG-----CAAAT-GGAGCAGTCGTGTTTTAAGGTACAGA-----CTTTGA
dp5	4_group4:3182289-3182495	dps-mirc_2502	GGAAATCCCTCAAATATGGCAGCCACTAA-AGACAACCAGAGGA-----GA--GCTGTT--TC-----GCC-G---GACAGTCAGAGTTTGA GTGATCTCTAGTTACTGGGG TTG--AT-TCGAAATAAGTAGCTTATTATTCTAGTGATTGAAATGAATCTG-ACTCG--AGTGCCACAAATGCCACATG---ATG-----CAAAT-GGAGCAGTCGTGTTTTAAGGTACAGA-----CTTTGA
droW12	scf21100000004521:8625943-8626196	dwi_125	GG SACA CT TCT TA AA CTGGC CCAAATGTATAATGA - AGTG-ACA ----- ATGAAAAAGAAAAACCAAAACA GA----- ---- ---- ---- AATTG ----- TGT--GAAACTT S --- AGTTT SAGTT TACA TTGATC ACTG TTT ATGCA A T CAAA G - CASA --- CCCA ATT CG TATCT CC GAT C - AAAT AAAC CTG - GT TACAAA AA SCT ATAAT TGC TGAAA - TGC ATACACG TTTTCTATT ATA A AG A CC CTCA TTT TAAG TA SAGA AATGT TTGT CTTT AT
droAna3	scaffold_12916:11084929-11085147	dan_50	GG SACA CT TCT TA AA CTGGCA TCAAATCTGTG CAAC GGCA - SCAG ----- GA CTC -CA ----- ---- ---- ---- AAAGGACT ----- ACAGGAAA ----- GCGACTTA --- AGTC SAG CACT AT TTGATC ACTG TTACTCA A G T GT A T T CTC --- ATA AGCTT CG T TCT CC GAT C - AAAT ACG CTCG ACT TT GG ----- GC ----- ---- ---- ---- CAAC CACCT GGCGGA SG CA CT CAAG CTA TAAG TA SAGA AATA ATGT CTT CG
droBip1	scf7180000396572:742678-742896		GG SACA CT TCT TA AA CTGGCA TCAAATAAAG CAAT GGCA - CTG ----- GA CTT -CA ----- ---- ---- ---- T --- CAAGTACT ----- ATTTTGA A ----- GCTACATA --- AGT TC SAG TAT AT TTGATC ACTG TTACTCA A G T GT A T T CTC --- ATA AGCTT CG T TCT CC GAT C - AAAT ACAC CTCG ACT TT GG ----- GC ----- ---- ---- ---- CAAC CACCT GTGTCG GG SCA CT CAAG CTA TAAG TA SAGA AGTA ATGT CTT CG
droKiK1	scf7180000302389:430892-431107		GG SACA CT CT AA CT GGCAG CAAG GCCA AGT CCAG GGTG GAAA ----- GTGC ----- AA CACT GA ----- ---- ---- ---- AGGGC ----- ---- ---- ---- T --- CCGAG SAG T GGT TTGATC AC GT AACTCA A G CGT CA CG CA CG CA CTG CA CTT TCT CC GAT C - AAA CA AACTCG A ----- CTGCG ----- TCCAA C ----- AT CTTG ----- GA CT CCCT GGCCC AAG SCA CT CAAG CTA TAAG TA SAGA AAT GGCT GTCT GA
droFic1	scf7180000453932:197508-197706		GG SACA CT TCT TA AA CTGGCA TCAAATCTGTAT CAAT CCGC GAA ----- C ----- TG ----- PGA A ----- ---- ---- ---- CAAC GAAC -G ----- PG - TC S ----- GG STC SAG TT CTGT TTGATC AC GT TTACTCA A G CC A TT CTC --- CA C --- TCCGA CTT CG T TCT CC GAT C - AAA CA AACTCG A ----- CTGCG ----- AG ----- ---- ---- ---- CATCC -CC CG C T GG SCAG TC CAAG CTA TAAG TA SAGA AACT CTTT -----
droE1e1	scf7180000490753:30322-30522		GG SACA CT TCT TA AA CTGG CA TCAAATCTAT CAAT CAAC AAAT SAR AGCC CACTCT ----- CATAGT GA ----- ---- ---- ---- T --- CATCCT T ----- CG C AGAG TT CTCT TTGATC AC GT TTACTCA A G CT GT A T T CTC --- TC CTCG --- TTGCG CTT CG T TCT CC GAT C - AAAT CA AACTCG A ----- ---- ---- ---- AC ----- ---- ---- CAATT ACCTC --- GG SCA CT CAAG CTA TAAG TA SAGA AA GT TTGT CT CC
droRho1	scf7180000778253:33793-33992		GG SACA CT TCT TA AA CTGG CA TCAAATCTAT CAAT CAAC TGA AG AC ----- CT GA -CA ----- ---- ---- ---- T C ----- PG - CT TA GAC SAG TT CTCT TTGATC AC GT TTACTCA A G CT GT A T T CTC --- TC CTCG --- TCCGA CTT CG T TCT CC GAT C - AAAT CA AACTCG A ----- GT TT GA ----- ---- ---- ---- GH ----- ---- ---- T --- CAACT ACCTCG AC - GG SCA CT CAAG CTA TAAG TA SAGA AACT GT TTGT CT CA
droBia1	scf7180000302422:3830676-3830890		GG SACA CT TCT TA

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crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	0
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	1
rescue.known	3
rescue.confident	3
rescue.candidate	4

Predicted structure

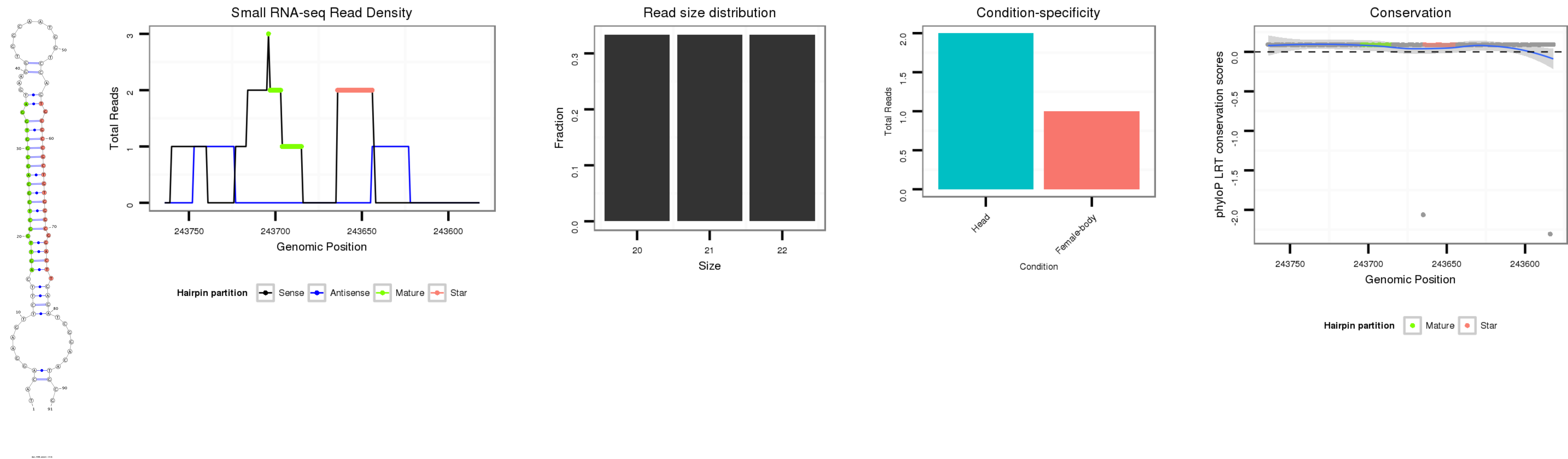


crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dpe_2488	scaffold_76:243632-243714 -	candidate	Canonical miRNA	intergenic	[View on UCSC Genome Browser (Cornell Mirror)]

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

Predicted structure



Show Alternate Folds

Flybase annotation

intergenic
No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

Read	#	Hit	Total		V042	V057	M042
size	Mismatch	Count	Norm	Total	embryo	head	female body
20	0	1	1.00	1	0	0	1
21	0	1	1.00	1	0	1	0
22	1	1	1.00	1	1	0	0
20	1	1	1.00	1	1	0	0
22	0	1	1.00	1	0	1	0
20	0	1	1.00	1	1	0	0
20	0	1	1.00	1	0	0	1
21	0	1	1.00	1	1	0	0

Anti-sense strand reads

Read	#	Hit	Total		M042	V057	V050
size	Mismatch	Count	Norm	Total	female body	head	head
24	0	1	1.00	1	1	0	0
22	0	1	1.00	1	1	0	0

Show Alignment With Reads

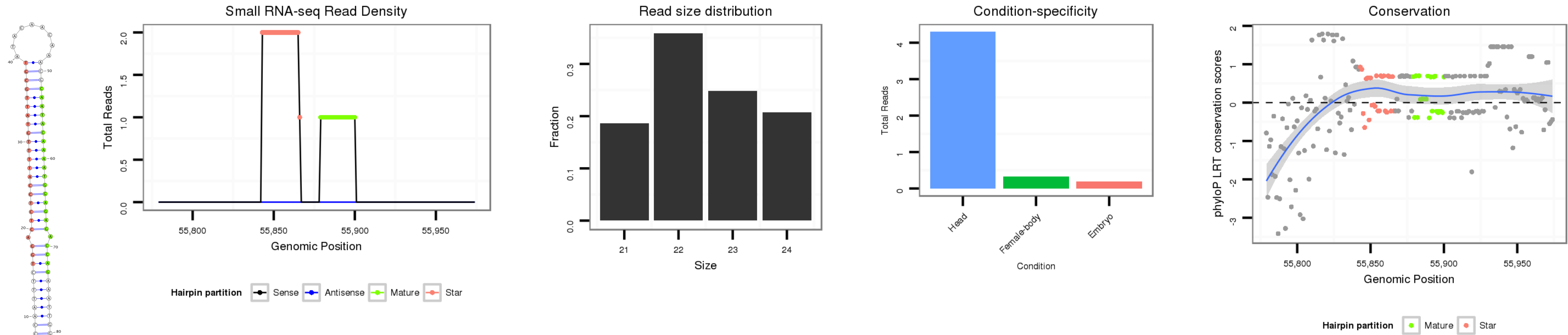
Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droPer2	scaffold_76:243582-243764 -	dpe_2488	TAGCCACTCTCGATTGACCCCTTCGTTCTCGCTTGTTAGCACACATACAGGAAGTTCTTCAGTTGGCTCGCAGCGGTGGAAGAAGTGGCAATGGTCCAGTGCGCCGCTGTGGGCGGACTTGAGATCGGACATGCGGTAAAGTGGAAGCACTATACAACCATTCCATAATCAATTAACAA
dp5	XL_group3a:1809921-1810103 +	dps_141	TAGCCACTCTCGATTGACCCCTTCGTTCTCGCTTGTTAGCACACATACAGGAAGTTCTTCAGTTGGCTCGCAGCGGTGGAAGAAGTGGCAATGGTCCAGTGCGCCGCTGTGGGCGGACTTGAGATCGGACATGCGGTAAAGTGGAAGCACTATACAACCATTCCATAATCAATTAACAA

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PASS/FAIL
crit.loop 0
crit.mor 0
crit.half 0
crit.total 0
crit.pairing 1
crit.top3 1
crit.tpop3 1
crit.uri 0
crit.back 1
rescue.total 1
rescue.dominant 0
rescue.known 0
rescue.confident 0
rescue.candidate 2

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Show Alternate Folds

Flybase annotation

intergenic

No Repeatable elements found

mature	star
1. dpe_2500 scaffold_168:19097-19118 -	1. dpe_2282 scaffold_174:3481-43504 +
2. dpe_2282 scaffold_174:43517-43538 +	2. dpe_2497 scaffold_175:55843-55866 +
3. dpe_2497 scaffold_175:55879-55900 +	3. dpe_2498 scaffold_175:59492-59515 +
4. dpe_2498 scaffold_175:59528-59549 +	
5. dpe_2499 scaffold_171:76756-76777 -	

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
droPer2	scaffold_71:55779-55974 +	ape_2497	ATTGCTCTTCAACT---AGATGTGTCGCAGAAATGSGTGAATCTTTCTCCAGGTCTTCCAA---TTTC TGGACTCTCCATT TGTATT GCCT ATACAACAAC CGAATACAAATGGAGAGACCA AAATTGGTGGTAATAGTAACAAATGTACATATGTACGTATGTATTGCTTTCTCTTTATTTTCTCCTTGAT
dp5	Unknown group_61:9886-10061	dps-mir-2574a-1	ATTGCTCTTCAACT---AGATGTGTCGCAGAAATGSGTGAATCTTTCTCCAGGTCTTCCAA---TTTC TGGACTCTCCATT TGTATT GCCT ATACAACAAC CGAATACAAATGGAGAGACCA AAATTGGTGGTAATAGT T AACAAATGTACATATGTACGTATGTATTGCTTTCTCTTTATTTTCTCCTTGAT
droWt12	scaffold_1100000009464:785-857 -		AAATACAGAA ----- TTCTGCAATTTT AAAG AGCTAAAGCTTTATATATGTAACA ACATACATATGTAC TA CA TATCTCTT -----
droVir3	scaffold_129121:149129-149174 -		AAATTACA ----- TATGTAC TA TGCTGCTTTTACAC CTTTATTT CTGC ----- C
droMo3	scaffold_1686:4262-4311 -		ATATATA ----- TAT TATATATA CTTTT TTT TATTTATTTAT ATATAT CTAT
droAna3	scaffold_13280:966419-966474 -		TCTCTTCCAA TC ----- SGASTCAGGTTAAATGCCTTAATCTCTCTTCAAGCCTGCTCC -----
droBip1	scaffold_180000396728:1940258-1940308 +		TCCGCTTTTCA GT ----- SGASTAGATCCAGCSCCTTAATCTATTTCCAGATT -----
droKik1	scaffold_180000301508:18980-19056 -		CTTGTCTT AG-AC ----- TTTCAATGTCGSAATGCAATCTTAATCTTTTCCAGCGTATCGCAAAAC TTCGCCATCTCA -----
droPic1	scaffold_180000453926:435168-435223 -		TGTA CTCTGTTCCG ----- GATCCTGCTTAAAGSCATGCAATCTCTCTTAATTT -----
droEle1	scaffold_180000490740:25725-25778 -		CAAGGCA ----- CATAT TAC TATATGGAAGAG CTCTTTA CGTTCA TATTC
droRho1	scaffold_180000779271:1863-1914 -		ATGCTCTCTG ----- GCSCAAAGTCATGTCGCTTAATCTCTGCTCTTAATTTCTC -----
droTak1	scaffold_180000414127:24235-24275 +		ATCACTCG ----- TGAC AAATCAAA SCCTTAATCTTTCTTCCA -----
droEug1	scaffold_180000409205:5001-5058		TGATTT CAG-TC ----- SCASTAGGTTTAAAGSTTGAATCTCTCTCTAGATTCTTCAA -----
dm3	chrU:5769325-5769363 -		CTTCTCTTAATTA ----- TTCTTCTCCAGTTATTA ----- CTCTATC -----
droSim2	21:21894425-21894483 -		TGACTCTGCA TGTA CTT GATCCTCTTAA CGATCAATCTTT CTCTAGGTTTC -----
droSec2	scaffold_5:33210-33268 +		TGACTCTGCA TGTA CTT GATCCTCTTAA CGATCAATCTTT CTCTAGGTTTC -----
droBre2	scaffold_4512:969297-969397 -		ACTGATCCGCA TC ----- GSCAAATGAGTGCCTTAATCTTTCTCCAAATGCTGCAACAC TTCCT ----- TTGCTCTGATCTCCGCAACAACTCTCGA ----- C

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Show Alignment With Reads

Re-alignment of all predicted orthologs

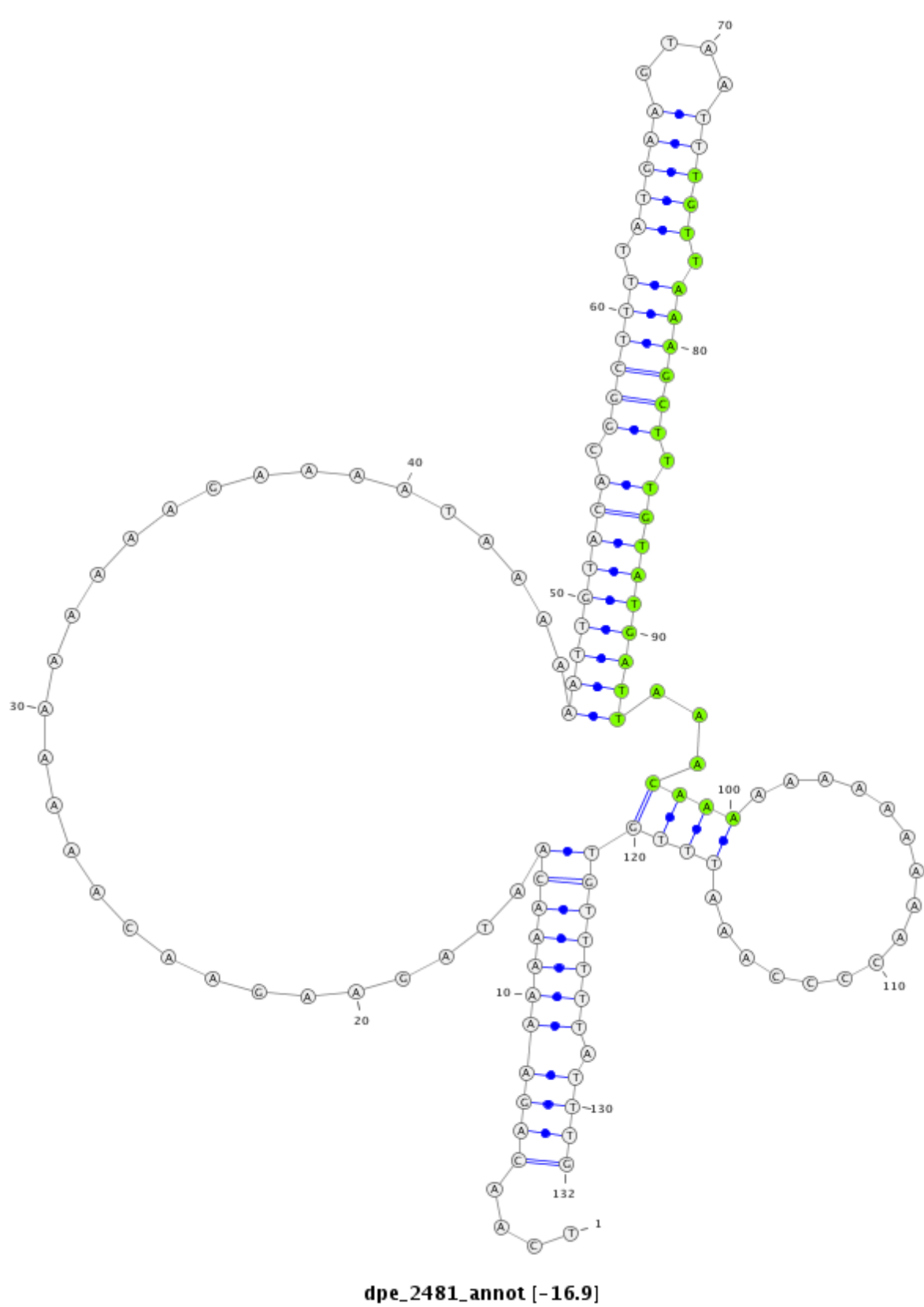
[illegible]

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	PASS/FAIL
crit.star	(0)
crit.loop	(0)
crit.mor	(0)
crit.half	(0)
crit.total	(0)
crit.pairing	(1)
crit.top3	(1)
crit.tptop3	(1)
crit.uri	(0)
crit.back	(1)
rescue.total	(1)
rescue.dominant	(1)
rescue.known	(3)
rescue.confident	(0)
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
T-rich	Low_complexity	Low_complexity	+

Sense Strand Reads

hide 3p reads | show mid mismatch reads

[illegible]

Anti-sense strand reads

[illegible]

Show Alignment With Reads

Re-alignment of all predicted orthologs

[illegible]

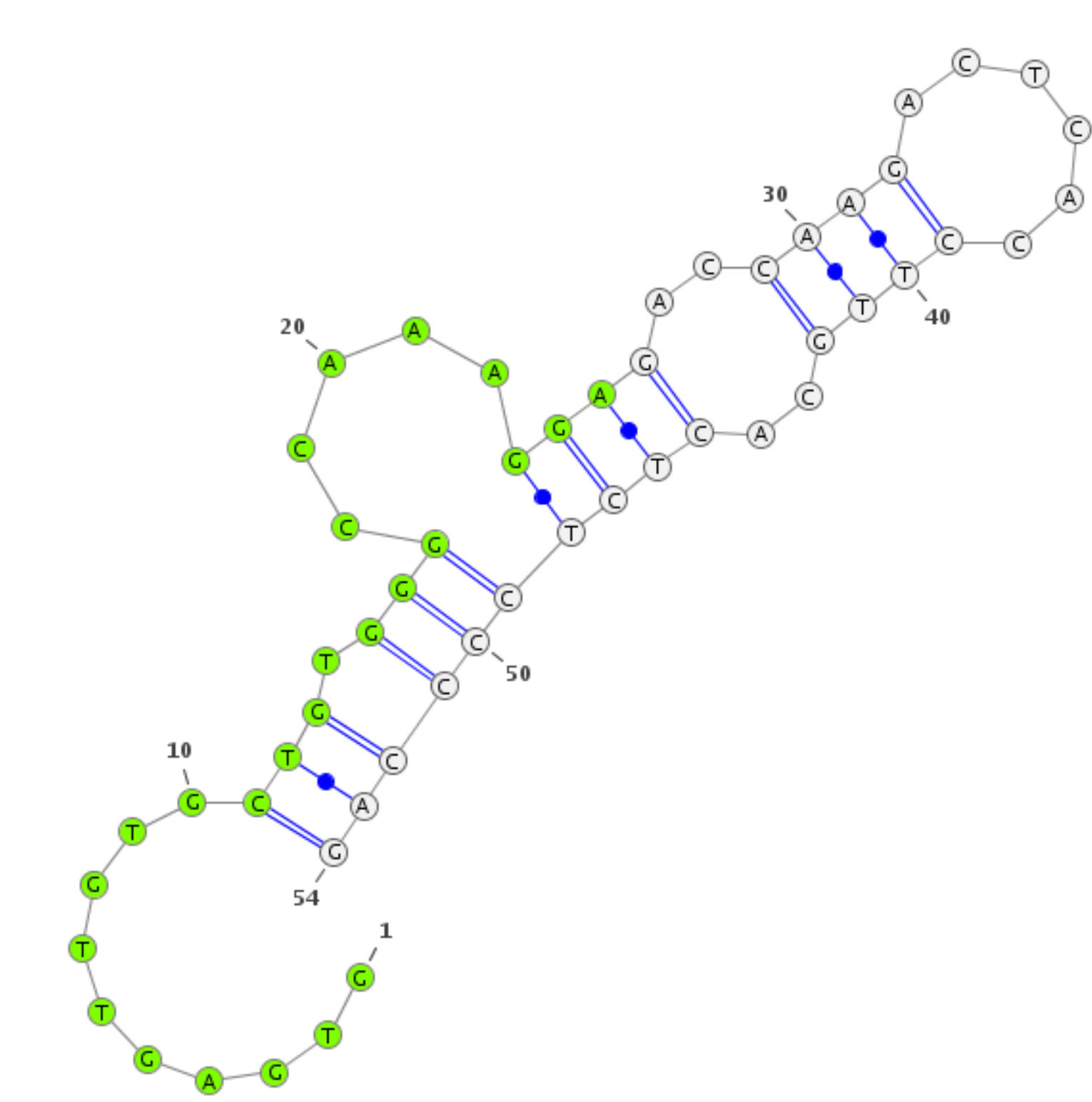
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	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	0
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	8
rescue.confident	8
rescue.candidate	4

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dpe_2485	scaffold_2:1608164-1608217 +	candidate	MiRNA	intron	[View on UCSC Genome Browser [Cornell Mirror]]

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

Predicted structure



dpe_2485_annot [-12..4]

Show Alternate Folds

Flybase annotation

intron [Dper.GLI1159-in]; CDS [Dper.GLI1159-cds]; CDS [Dper.GLI1159-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

CGCTCCCAAAACGGCTGACCGCTCTGACTGAGAACACAGATGATTCCCAAGGTGAGTTGTGCTGTGGGCCAAAGGAGACCAACAGACTCACCTTGCACCTCTCCCAAGATGCCCCGACGTCACGGCAGAGTCTCTGGGCGGCCAAAGTGCGCGGTTG	Read #	size	Mismatch	Hit	Count	Norm	Total	Total	M042 female body	V111 male body	V057 head	V050 head	M021 embryo	V042 embryo
*****(((.(((.....(((.....)))))))))*****														
.....GTGAGTTGTGCTGTGGCCAAAGGA.....	25	0	1	3.00	3	1	1	1	1	0	0	1	0	
.....GTGAGTTGTGCTGTGGCCAA.....	21	0	1	1.00	1	0	1	0	1	0	0	0	0	
.....GTGAGTTGTGCTGTGGCCAAA.....	22	0	1	1.00	1	0	1	0	1	0	0	0	0	
.....GTGAGTTGTGCTGTGGGCC.....	19	0	1	1.00	1	0	1	0	1	0	0	0	0	
.....AGAACACAGATGATTCCCAAG.....	21	0	2	0.50	1	1	0	0	0	0	0	0	0	

Anti-sense strand reads

CGCAGGGTTTGCCGACTGGCGAGACTGACTCTTGTGCTACTAAGGGTTCCACTCAACACGACCCGGTTTCCTCTGGTTCTGAGTGGAAACGTGAGAGGGGTCTACGGGGGCTGCAGTGCCGTCCTCAGGAGCCCGCGGTTTTCACGCGCCAAC	Read #	size	Mismatch	Hit	Count	Norm	Total	Total	M042 female body	V111 male body	V050 head	V057 head	M021 embryo	
*****(((.(((.....(((.....)))))))))*****														

Show Alignment With Reads

Re-alignment of all predicted orthologs

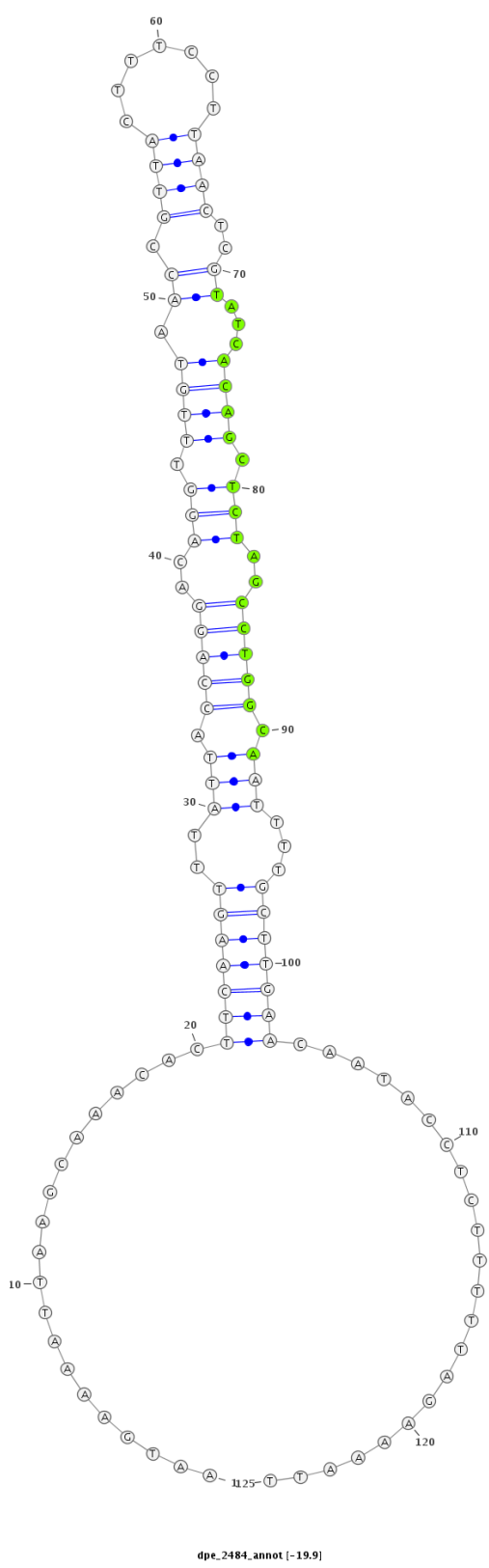
Species	Coordinate	ID	Alignment
droPer2	scaffold_2:1608114-1608267 +	dpe_2485	GCCTCCCAAAACGGCTGACCGCTCTGACTGAGAACACAGATGATTCCCAAGGTGAGTTGTGCTGTGGGCC-----GACCAA--GA-CTCACC-----TTG-----CACTCTCCCCAGATGCCCCGACGTCACGGCA-----GAG---TCCTCGGGCCGCCAAAGTGC
dp5	3:1434708-1434861 +	dpe_934	GCCTCCCAAAACGGCTGACCGCTCTGACTGAGAACACAGATGATTCCCAAGGTGAGTTGTGCTGTGGGCC-----GACCAA--GA-CTCACC-----TTG-----CACTCTCCCCAGATGCCCCGACGTCACGGCA-----GAG---TCCTCGGGCCGCCAAAGTGC
droW112	scf2_1100000004513:2801067-2801223 +		GCCTCCCAAGCGCTGACCTGACTGAGAACAGATGATTCCCAAGGTGAGTTGTGCTGTGGGCC-----GACCAA--GA-CTCACC-----TTG-----CACTCTCCCCAGATGCCCCGACGTCACGGCA-----GAG---TCCTCGGGCCGCCAAAGTGC
droVir3	scaffold_12875:1386889-1587036 --		GCCTCCCAAGCGCTGACCTGACTGAGAACAGATGATTCCCAAGGTGAGTTGTGCTGTGGGCC-----GACCAA--GA-CTCACC-----TTG-----CACTCTCCCCAGATGCCCCGACGTCACGGCA-----GAG---TCCTCGGGCCGCCAAAGTGC
droMo3	scaffold_6496:4638604-4698759 --		GCCTCCCAAGCGCTGACCTGACTGAGAACAGATGATTCCCAAGGTGAGTTGTGCTGTGGGCC-----GACCAA--GA-CTCACC-----TTG-----CACTCTCCCCAGATGCCCCGACGTCACGGCA-----GAG---TCCTCGGGCCGCCAAAGTGC
droGr12	scaffold_15245:9414646-9414813 +		GCCTCCCAAGCGCTGACCTGACTGAGAACAGATGATTCCCAAGGTGAGTTGTGCTGTGGGCC-----GACCAA--GA-CTCACC-----TTG-----CACTCTCCCCAGATGCCCCGACGTCACGGCA-----GAG---TCCTCGGGCCGCCAAAGTGC
droAna3	scaffold_13266:3379784-3379934 +		GCCTCCCAAGCGCTGACCTGACTGAGAACAGATGATTCCCAAGGTGAGTTGTGCTGTGGGCC-----GACCAA--GA-CTCACC-----TTG-----CACTCTCCCCAGATGCCCCGACGTCACGGCA-----GAG---TCCTCGGGCCGCCAAAGTGC
droBip1	scf7180000396427:1846735-1846889 +		GCCTCCCAAGCGCTGACCTGACTGAGAACAGATGATTCCCAAGGTGAGTTGTGCTGTGGGCC-----GACCAA--GA-CTCACC-----TTG-----CACTCTCCCCAGATGCCCCGACGTCACGGCA-----GAG---TCCTCGGGCCGCCAAAGTGC
droKi1	scf7180000302640:268567-268711 +		GCCTCCCAAGCGCTGACCTGACTGAGAACAGATGATTCCCAAGGTGAGTTGTGCTGTGGGCC-----GACCAA--GA-CTCACC-----TTG-----CACTCTCCCCAGATGCCCCGACGTCACGGCA-----GAG---TCCTCGGGCCGCCAAAGTGC
droPic1	scf7180000453955:106246-106407 --		GCCTCCCAAGCGCTGACCTGACTGAGAACAGATGATTCCCAAGGTGAGTTGTGCTGTGGGCC-----GACCAA--GA-CTCACC-----TTG-----CACTCTCCCCAGATGCCCCGACGTCACGGCA-----GAG---TCCTCGGGCCGCCAAAGTGC
droE1e1	scf7180000491265:302934-303083 +		GCCTCCCAAGCGCTGACCTGACTGAGAACAGATGATTCCCAAGGTGAGTTGTGCTGTGGGCC-----GACCAA--GA-CTCACC-----TTG-----CACTCTCCCCAGATGCCCCGACGTCACGGCA-----GAG---TCCTCGGGCCGCCAAAGTGC
droRho1	scf7180000779390:20784-20936 +		GCCTCCCAAGCGCTGACCTGACTGAGAACAGATGATTCCCAAGGTGAGTTGTGCTGTGGGCC-----GACCAA--GA-CTCACC-----TTG-----CACTCTCCCCAGATGCCCCGACGTCACGGCA-----GAG---TCCTCGGGCCGCCAAAGTGC
droBia1	scf7180000302292:2983537-2983702 --		GCCTCCCAAGCGCTGACCTGACTGAGAACAGATGATTCCCAAGGTGAGTTGTGCTGTGGGCC-----GACCAA--GA-CTCACC-----TTG-----CACTCTCCCCAGATGCCCCGACGTCACGGCA-----GAG---TCCTCGGGCCGCCAAAGTGC
droTak1	scf7180000411052:20260-20423 --		GCCTCCCAAGCGCTGACCTGACTGAGAACAGATGATTCCCAAGGTGAGTTGTGCTGTGGGCC-----GACCAA--GA-CTCACC-----TTG-----CACTCTCCCCAGATGCCCCGACGTCACGGCA-----GAG---TCCTCGGGCCGCCAAAGTGC
droEug1	scf7180000409672:5175967-5176134 +		GCCTCCCAAGCGCTGACCTGACTGAGAACAGATGATTCCCAAGGTGAGTTGTGCTGTGGGCC-----GACCAA--GA-CTCACC-----TTG-----CACTCTCCCCAGATGCCCCGACGTCACGGCA-----GAG---TCCTCGGGCCGCCAAAGTGC
dm3	chr2R:3166497-3166661 +		GCCTCCCAAGCGCTGACCTGACTGAGAACAGATGATTCCCAAGGTGAGTTGTGCTGTGGGCC-----GACCAA--GA-CTCACC-----TTG-----CACTCTCCCCAGATGCCCCGACGTCACGGCA-----GAG---TCCTCGGGCCGCCAAAGTGC
droSim2	2::3991942-3992106 +		GCCTCCCAAGCGCTGACCTGACTGAGAACAGATGATTCCCAAGGTGAGTTGTGCTGTGGGCC-----GACCAA--GA-CTCACC-----TTG-----CACTCTCCCCAGATGCCCCGACGTCACGGCA-----GAG---TCCTCGGGCCGCCAAAGTGC
droSe2	scaffold_1818000-818023 +		GCCTCCCAAGCGCTGACCTGACTGAGAACAGATGATTCCCAAGGTGAGTTGTGCTGTGGGCC-----GACCAA--GA-CTCACC-----TTG-----CACTCTCCCCAGATGCCCCGACGTCACGGCA-----GAG---TCCTCGGGCCGCCAAAGTGC
droYak3	2::1885144-1885194 +		GCCTCCCAAGCGCTGACCTGACTGAGAACAGATGATTCCCAAGGTGAGTTGTGCTGTGGGCC-----GACCAA--GA-CTCACC-----TTG-----CACTCTCCCCAGATGCCCCGACGTCACGGCA-----GAG---TCCTCGGGCCGCCAAAGTGC
droEre2	scaffold_4929:19427227-19427388 --		GCCTCCCAAGCGCTGACCTGACTGAGAACAGATGATTCCCAAGGTGAGTTGTGCTGTGGGCC-----GACCAA--GA-CTCACC-----TTG-----CACTCTCCCCAGATGCCCCGACGTCACGGCA-----GAG---TCCTCGGGCCGCCAAAGTGC

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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	0
crit.uni	1
crit.back	1
rescue.total	0
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	2

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Show Alternate Folds

Flybase annotation

intergenic

No Repeatable elements found

nature	star
1. dpe_2484_scaffold_10:2580054-2580074 +	
2. dpe_280_scaffold_10:2581065-2581085 +	
3. dpe_2507_scaffold_8585:293-313 +	
4. scaffold_7193:80-100 +	

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
droPer2	scaffold_10:2579949-2580143 +	dpe_2484	AAAGTAAGATGTGAGTACTCCACAAGAAATGATTAATGAAAAATAGCAACACTTCAAGTTTATTACCAGGACAGGTTGTAA-CCGTACTTTCCTTAACTCGTATCACAGCTCTAGCCTGGCAATTTGCTTGAACAATACCTCTTTTAGAAAATTCGAGAAAAGCGCACAAAGTTCAAAATGATCGAAGA
dp5	5_group4:3552100-3552295 +	dps_41	AAAGTAAGATGTGAGTACTCCACAAGAAATGATTAATGAAAAATAGCAACACTTCAAGTTTATTACCAGGCAGAGTTTGTAAACGTACTTTCCTTAACTCGTATCACAGCTCTAGCCTGGCAATTTCTTGAACAATACCTCTTTTAGAAAATTCGAGTAAGCGCACAAAGTTCAAAATGATCGAAGA

Generated: 09/08/2015 at 08:19 PM **PASS/FAIL**

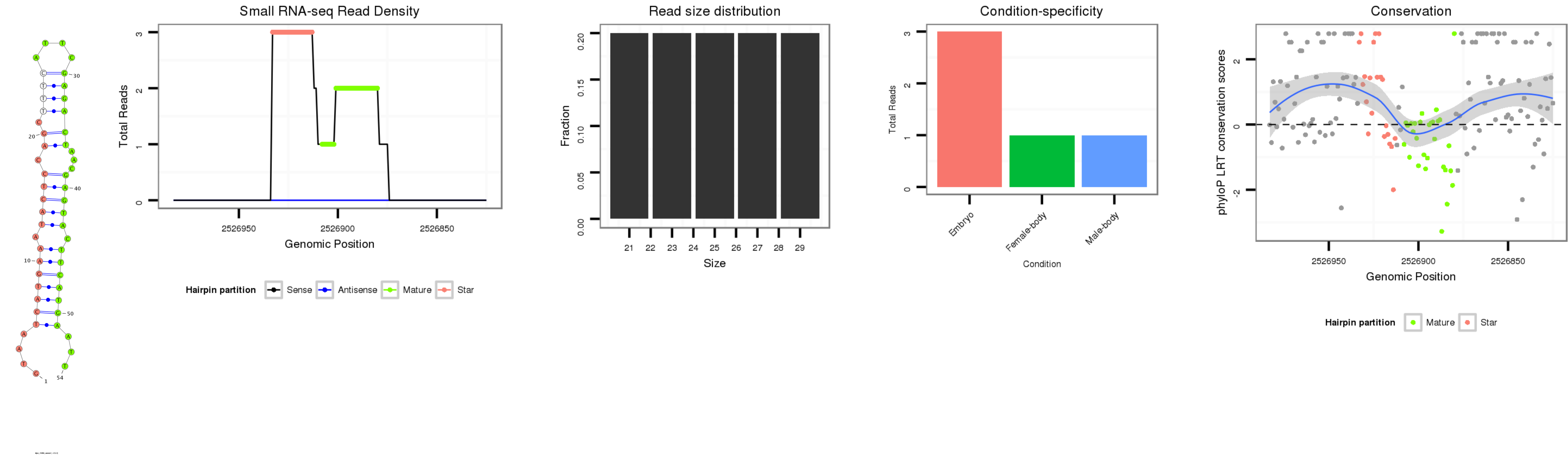
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	1
rescue.known	0
rescue.confident	1
rescue.candidate	1

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

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dpe_2486	scaffold_4:2526875-2526933 -	candidate	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 [Dper^{GL17035}-in]; CDS [Dper^{GL17035}-cds]; CDS [Dper^{GL17035}-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

Read #	size	Mismatch	Hit Count	Total Norm	Total	V042 embryo	M042 female body	M021 embryo	V111 male head body	V057
CAAACCAATTGCCCAAATACGGGGGAGCCAAACCTGCAAAAGTTTCAA	29	0	1	1.00	1	0	0	1	0	0
GTAAATCATGAAATACTCCAGCTTTC	25	1	1	1.00	1	0	1	0	0	0
ATTTCGAGACTAACGAGTACTTCATGAATT	25	0	1	1.00	1	1	0	0	0	0
ATTCGAGACTAACGAGTACTTCATGAATT	27	0	1	1.00	1	0	1	0	0	0
GTAAATCATGAAATACTCCAGCTTTC	21	0	1	1.00	1	1	0	0	0	0
GTAATCATGAAATACTCCAGCTTTC	23	0	1	1.00	1	0	0	0	1	0

Anti-sense strand reads

Read #	size	Mismatch	Hit Count	Total Norm	Total	M042 female body
GTTTGGTTAAACGGGTTTTATGCCCCCTCGGTTTGGACGTTTTCAAAGTT	29	0	1	1.00	1	0
CATTAGTACTTTATGAGGTCGAAAGTAAGCTCTGATTGCTCATGAAGTACTTAA	29	0	1	1.00	1	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

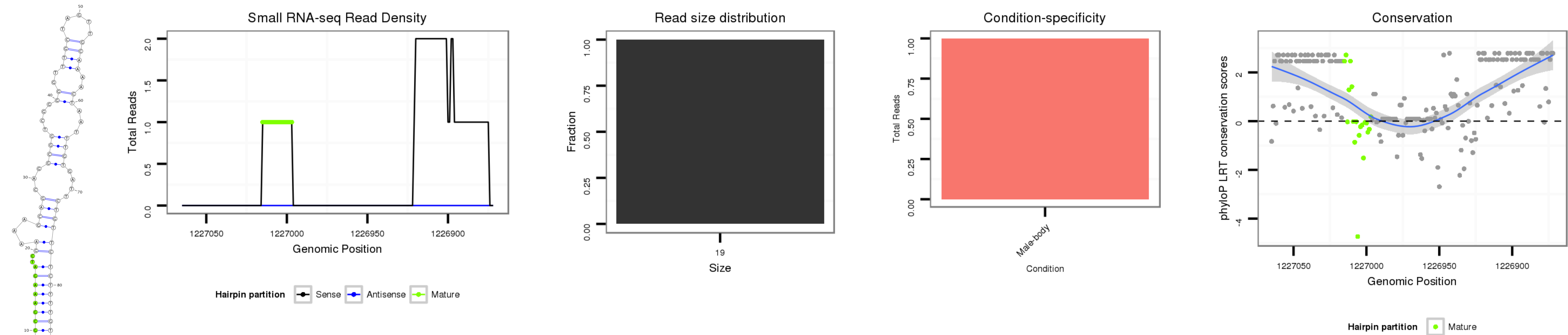
Species	Coordinate	ID	Alignment
droPer2	scaffold_4:2526825-2526983 -	dpe_2486	CAAACCAATTGCCCAAATACGGGGGAGCCAAACCTGCAAAAGTTTCAA
dp5	3:8642390-8642548 -	dps_1105	CAAACCAATTGCCCAAATACGGGGGAGCCAAACCTGCAAAAGTTTCAA
droW112	scf2_1100000004513:3399988-3400168 -		CAAATTAATTCAGCTATTA
droVir3	scaffold_12823:2274668-2274825 -		CGAAGATTCAGCTATTA
droMoJ3	scaffold_6496:1629722-1629879 -		CAAATTAATTCAGCTATTA
droGri2	scaffold_15245:15801041-15801202 +		CAAAGATTCAGCTATTA
droAna3	scaffold_13266:4095861-4096027 -		CAAATTAATTCAGCTATTA
droBip1	scf7180000396427:2540760-2540930 -		CAAAGATTCAGCTATTA
droKik1	scf7180000302471:978930-979095 +		CGAAGATTCAGCTATTA
droFic1	scf7180000454039:1812692-1812852 +		CGAAGATTCAGCTATTA
droEle1	scf7180000491201:775950-776116 +		CGAAGATTCAGCTATTA
droRho1	scf7180000780104:120099-120255 +		CGAAGATTCAGCTATTA
droBia1	scf7180000302292:1066895-1067061 -		CGAAGATTCAGCTATTA
droTak1	scf718000015401:138550-138720 +		CGAAGATTCAGCTATTA
droEug1	scf7180000409474:1454647-1454812 -		CGAAGATTCAGCTATTA
dm3	chr28:16506344-16506510 +		CGAAGATTCAGCTATTA
droSim2	2r:17075894-17076060 +		CGAAGATTCAGCTATTA
droSec2	scaffold_1:14060361-14060527 +		CGAAGATTCAGCTATTA
droYak3	2R:12690102-12690270 -		CGAAGATTCAGCTATTA
droEre2	scaffold_4845:10652743-10652911 +		CGAAGATTCAGCTATTA

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

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Show Alternate Folds

Flybase annotation

intron [Dper\GL12242-in]; CDS [Dper\GL12242-cds]; CDS [Dper\GL12242-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

Read #	Mismatch	Hit Count	Total Norm	Total	M021 embryo	M042 female body	V042 embryo	V111 male body	V057 head
18	1	1	2.00	2	2	0	0	0	0
24	0	1	1.00	1	1	0	0	0	0
19	0	1	1.00	1	0	0	0	1	0
25	0	1	1.00	1	0	1	0	0	0
20	0	1	1.00	1	1	0	0	0	0
22	1	1	1.00	1	0	1	0	0	0
27	1	1	1.00	1	1	0	0	0	0
22	2	6	0.17	1	0	1	0	0	0

Anti-sense strand reads

CGGGTACCTACTTCAGTCAGTTGTCGTGTCGAGAGCTTACGTAGTCGCCCACTCACCCGCCTTCTTAGCCTTTTCGTCGTCCGACGCCCAAACGATCAACGTTTTGATTAAACAATAAGACAAGAGAAAACAGGTGGGTCGTAGGCCGCTTCTAGGGGTACGTGGTGTTTCAGCGCCTTCTTACTA										V057	V050
						Read #	Hit	Total		head	head
*****((...((((((((((((...(((...(((...(((...)))...))...))))))))))))))...)).*****						size Mismatch	Count Norm	Total			

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droPer2	scaffold_6:1226872-1227065	dpe_2490	GCCCCATGGATGAAGTCAGTCAACAGAGCAGCGCTCTCGAATGCATCAGCGG GTGAGTGGGGC ----GAAAGAT-----GAAAGAGCAGCAGCGCGTCGGGGT--TTGCTAGTTGCA----AACTAATTGT--GAT-----TCT--GTTCTCTTTT--GTTCCA-----CCCAGCATCCGGCGAAGATCCCCAATGCACCACACCAAGTCGCGCAAGAATGAT
dp5	2:25893285-25893478 -	dps_794	GCCCCATGGATGAAGTCAGTCAACAGAGCAGCGCTCTCGAATGCATCAGCGG GTGAGTGGGGC ----GAAAGAT-----GAAAGAGCAGCAGCGCGTCGGGGT--TTGCTAGTTGCA----AACTAATTGT--GAT-----TCT--GTTCT CTTT --GTTCCA-----CCCAGCATCCGGCGAAGATCCCCAATGCACCACACCAAGTCGCGCAAGAATGAT
droW112	scf2_1100000011615:456-618 -		GCCCCATGGATGAAGT AGT CAACAGAG AGT CGCTCT CA ATGCATCAGCGG GTAGTAA CAATTGA --CGC A -----GAA TC CA A -----G AA CTGAACCT CT -- TCGTTT -----TG CAG CATCGG TGA AGATCC CA ATGCACCACACCAAGTCGCGCA AA TGAT
droVi13	scaffold_12855:10044836-10044991 -		ACC A ATGGATGAAGT AGT CAACAGAGC AGT CT TC CAATGC CT CAGC GTG GTG ACCTTTAA -- T AATC T ----- T ----- A ----- AG ----- AG AA A -- ACTGAGAC TT -- G ----- TCATCT ----- TA CAGCAT C GGCGAAGAT CC CAATG C ACCACACCAAGTCGCGCA AA CTGAT
droMo13	scaffold_6540:4000775-4000930 -		ACC A ATGGATGAAGTCAGTCAACAGAG TA CGCTCT CA ATGC CTC GC GTG GTG AAITCGAATG GT TT ----- AT ----- GTTCT CT -- ACTGAGGC CT -- G ----- TCGTCT ----- TG CAGCAT C GG TGA AGAT CC CA CTG C ACCAC CA CAAGTCGCGCA AA CTGAT
droGr12	scaffold_14830:1233927-1234091 -		CCC A ATGGAT CA CT AGT CAACAGAGCAGCTCT CA ATGCAT CGC CTG CTG ATAITAA -- C ATATAGACAT ----- T ----- GC GC CT ----- G CT CT -- ACTGAGAC TCT --G TC ----- TCGT ----- TG CAGCAT C GGCGAAGAT CC CAATG CA CT C ACCAC CA CAAGTCGCGCA AA CTGAT
droAn13	scaffold_12911:2122398-2122559 +		CCC A ATGG AG SA AGTC AGC CAACAGAGCAGCT TC GAATGCATCAGCGG GTAGTGG AT TGTT -- GTG -- AAAT TA ----- T ----- C AGTAG G ----- TA CTAATAACG AT -- TC -- C -- ATT TGG ----- CA CAGCAT C GGCGAAGAT CC CAATG C ACCACACCAAGTCGCGCAAG AA C AT
droBi11	scf17180000396714:956857-957017 -		ACC A ATGG AG SA AGTCAGTCAACAGAGCAGCT TC GAATGCATCAGCGG GTAGT AAAAGTC T -- T A ----- AAAT AGT ----- G ----- ACAGTAG C ----- AA CTAATAG CT --G TC -- TC -- ATT TTG ----- TA CAGCAT C GGCGAAGAT CC CA CTG C ACCACACCAAGTCGCGCA AA C AT
droKi11	scf17180000302247:509925-510084 +		GCCCCATGA CA SA AGTCAGT CA C SAGAGCAGCT TA CGAATGC CT CAGCGG GTGAGTC CAC C ----- ACGAC ----- CTT ----- CGA ----- AC -- CA CTACT CT AT TA CC -- TC T -- ATG C -- AT CTC -- CA CAGCAT C GGCGAAGAT CC CAATG C ACCACACCAAGTCGCGCA AA TGAT
droFi11	scf17180000453912:1952661-1952829 +		GCCCCATGA CA SA AGTCAGT CA C SAGAGCAG CT CT CA ATGCATCAGCGG GTGAGT A AAG AGC AAA TAT AT ACCAT ----- AA ----- GA -- AATT CC T -- GA CTTAAG -- ATC -- AT -- ATT TGCTAA C CAGCAT C GGCGAAGAT CC CA CTG C ACCACACCAAGTCGCGCAAGAATGAT
droEl11	scf17180000491080:2754692-2754857 +		GCCCCATGA CA CA CT CAGT CA C SAGAGCAGCTCTCGAATGCATCAGCGG GTAGTA AGA AAG -- CCGG CTGCTGCCCT ----- TA ----- GA -- CATT TC -- GA CTGACT -- TA A -- TT TAG -- ATT TA ----- CA CAGCAT C GGCGAAGAT CC CAATG C ACCACACCAAGTCGCGCAAGAATGAT
droRh11	scf17180000778039:38186-38353 +		GCCCCATGA CA CA CT CAGT CA C SAGAGCAGCTCTCGAATGCATCAGCGG GTAGTA AA AG -- C GG TT TAGCCCT ----- TTA ----- AA -- CATT TC -- GA CTAATT -- ATA -- TT TAT -- TTT ACT -- CA CAGCAT C GGCGAAGAT CC CAATG C ACCACACCAAGTCGCGCAAGAATGAT
droBi11	scf17180000302113:3895332-3895497 +		GCCCCATGG AG SA AGTCAGT CA C SAGAGCAGCTCTCGAATGCATCAGCGG GTGAGT ACA GC -- C CA TGAAGCCT ----- GA ----- GA -- CATT GC -- ACTGATT -- TTA -- TT CCC -- ATT TA ----- TC CAGCAT C GGCG GA CA CC CAATG C ACCACACCAAGTCGCGCAAGAATGAT
droTa11	scf17180000413103:19756-19829 +		----- GA ----- GA -- CATT GC -- ACTGATT -- TTA -- TT CCC -- ATT TA ----- TC CAGCAT C GGCGAAG CA CC CAATG C ACCACACCAAGTCGCGCAAGAATGAT
droEu11	scf17180000409562:44183-44347 -		ACC A ATGG AG SA AGTCAGT CA C SAGAGCAGCTCTCGAATGCATCAGCGG GTGAGT A AAA -- T GGTTC ACGCCTT ----- CGA ----- AA -- CATT ATC -- GA CTGATT -- TA A -- TT TTT -- ATT TA ----- TAT AG CAT C GGCGAAGAT CC CAATG C ACCACACCAAGTCGCGCAAGAATGAT
dm3	chr3R:13523835-13524001 -		CC CA ATGG AG SA AGTCAGT

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