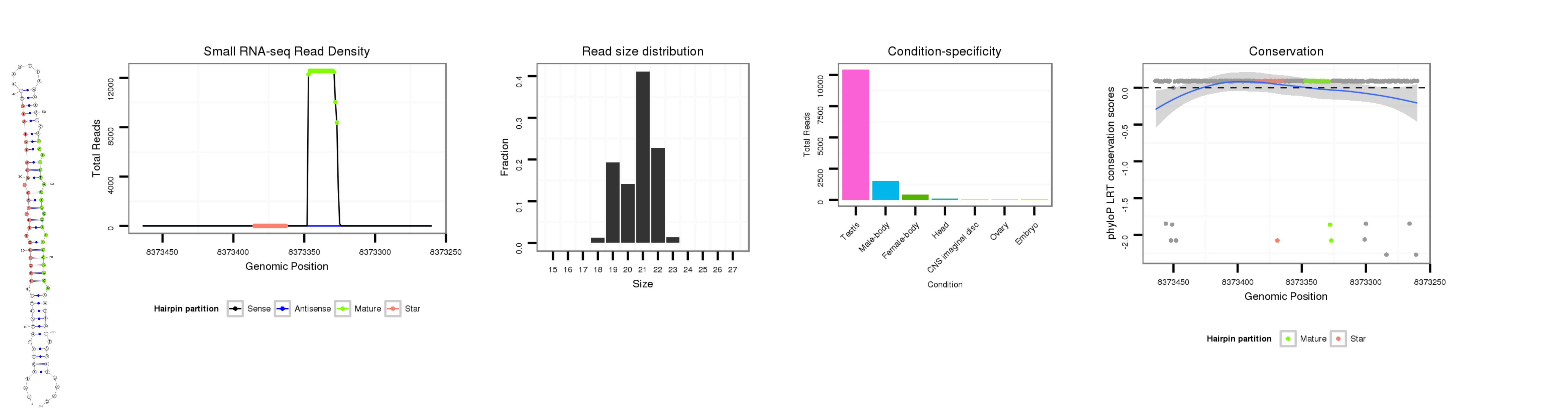


ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dps_3414	XL_group1e:8373310-8373414 -	candidate	Testes-restricted	intergenic	[View on UCSC Genome Browser (Cornell Mirror)]

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Flybase annotation

intergenic

No Repeatable elements found

matrnr	star
	1. dps_3414_XL_groupie:8373363-8373385- 2. dps-mir-2524-1_XL_groupie:8376708-8376730- 3. dps-mir-2524-2_XL_groupie:8377556-8377578- 4. dps_3416_XL_groupie:8381471-8381493-

Sense Strand Reads

hide 3p reads | show mid mismatch reads

[illegible]

Anti-sense strand reads

[illegible]

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
dp5	Xl_group18:83732460-8373464_-	Dpe_314	TATGCGCTAGTACCCATCATCGTGACATTAAGTCCAATCCGACAGGGAATCAAT--AGAGTTATATAGTTTATAGTTG CGCCGGTCCGACGACATGATG TTGAATTAATATCA ATTGTACTCGCAGTCGGCG CAATTATTAGTCAAGACGAGCGGTGTACGAAAGAGACCCGGACGACAAATCATTGGAAGTCTGGTACT
droPer2	scaffold_13:190901-111108_1	Dpe_313	TATGCGCTG CGTGTG TCATCATCGTGACATTAAGTCCAATCCGACAGGGAATCAAT CGAGAG TTATATAGTTTATAGTTG CGCCGGTCCGACGACGATGATG TTGAATTAATATCA ATTGTACTCGCAGTCGGCG CAATTATTAGTCAAGACGAGCGGTGTACGAAAGAGACCCGGAGCAATCATTGGAAGTCTGGTACT

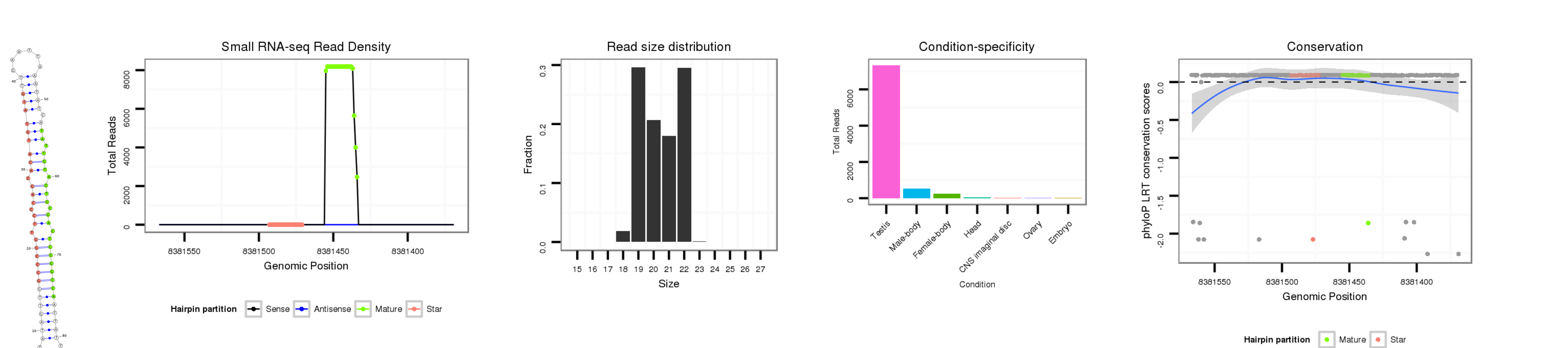
Generated: 09/08/2015 at 08:41 PM

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

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dps_3416	XL_group1e:8381419-8381517 -	candidate	Testes-restricted	intergenic	[View on UCSC Genome Browser (Cornell Mirror)]

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Flybase annotation

intergenic

No Repeatable elements found

mutare	star
1. dps-min-2524-1_XI_group18376671-8376692	1. dps_3414_XI_group18373363-8373385
2. dps-min-2524-2_XI_group18377519-8377540	2. dps-min-2524-1_XI_group18376708-8376730
3. dps_3416_XI_group18381434-8381455	3. dps-min-2524-2_XI_group18377556-8377578
	4. dps_3416_XI_group18381471-8381493

Sense Strand Reads

hide 3p reads | show mid mismatch reads

[illegible]

Anti-sense strand reads

[illegible]

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
dp5	Xl_group:8381392:8381567	dps_3146	TTATGACCCATACAGTCGACATTAAGTCCAATCGAACAGGGAATCAATAGAGAGTTATATAGTTTATAGTTG SCCCGGTTC CCGACACATGATG T GGAATTAATATCA ATTGTGAC TGGACTCGGGC GA ATTATTAGTCGAAGACAGCGGTGTACGAAAGGACCCGGAGCAATCATTTGSAAGTCGGGTAC
dpoPer2	scaffold_13:190910:scaff1107	dps_313	TCAGT CT CTCATCATGTCGACATTAAGTCCAATCGAACAGGGAATCAAT GA GAGTTATATAGTTTATAGTTG SCCCGGTTC CCGACAC CTGATG TGGAATTAATATCA ATTGTGAC TGGACTCGGG GA ATTATTAGTCGAAGACAGCGGTGTACGAAAGACCCGGAGCAATCATTTGSAAGTCGGGT G

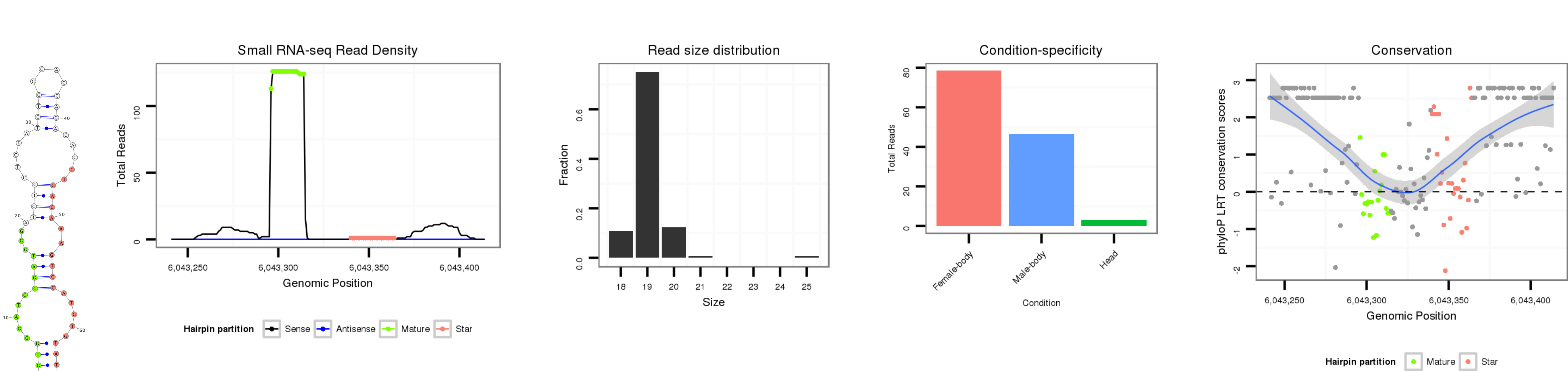
Generated: 09/08/2015 at 08:44 PM

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

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dps_3340	XR_group8:6043291-6043364 +	candidate	5p_tailed_mirtron	intron	[View on UCSC Genome Browser (Cornell Mirror)]

Legend: mature star mis match in alignment mismatch in read

Predicted structure



Show Alternate Folds

Flybase annotation

intron [Dpse/GA20377-in]; CDS [Dpse/GA20377-cds]; CDS [Dpse/GA20377-cds]

No Repeatable elements found

Sense Strand Reads

	Read # size	Mismatch	Hit Count	Total Norm	Total	M040 female body	V112 male head	GSM444067 head embryo	M062 embryo	GSM343916 embryo	M059 embryo	CNS imaginal disc	SRR902012
CGCCGCGGATGTTACATCGTGACGATGAGCCTGCGGGAGGAGCGAGGCGGGTGAGTGGGTTGGGATGGGATGTCCTCTATCTGCCACCAGACAGCTGACAAAGTCCATGTGTATCGTAGGGAATCCCATTAAGGACAACGATAGCTTGTCTGGCCATGCTGGCCGCGGA	19	0	1	96.00	96	54	39	2	1	0	0	0	
.....TGGGTTGGGATGGGATGGG.....	20	0	1	14.00	14	8	6	0	0	0	0	0	
.....TGGGTTGGGATGGGATGGGA.....	18	0	1	13.00	13	13	0	0	0	0	0	0	
.....GGGTTGGGATGGGATGGG.....	19	0	1	2.00	2	2	0	0	0	0	0	0	
.....GTGACAAAGTCCATGTGTATCTAG.....	25	0	1	1.00	1	1	0	0	0	0	0	0	
.....CGTGACGATGAGCCTGCGGGAGGAGC.....	26	0	1	1.00	1	0	0	0	0	0	0	1	
.....GAATTCCTTAAGGACAACGATAGCT.....	27	0	1	1.00	1	1	0	0	0	0	0	0	
.....CCCATTAAGGACAACGATAGCTTGTCT.....	26	0	1	1.00	1	1	0	0	0	0	0	0	
.....TGAGTGGGTTGGGATGGGAT.....	20	0	1	1.00	1	1	0	0	0	0	0	0	
.....GTGAGTGGGTTGGGATGGGA.....	20	0	1	1.00	1	0	1	0	0	0	0	0	
.....GCCTGCGGGAGGAGCGGAGGC.....	20	0	1	1.00	1	1	0	0	0	0	0	0	
.....GACAACGATAGCTTGTCTGGCC.....	21	0	1	1.00	1	0	0	0	0	0	1	0	
.....ATTAAGGACAACGATAGCTTGTCTGGCC.....	27	0	1	1.00	1	1	0	0	0	0	0	0	
.....TTAAGGACAACGATAGCTTGTCTGGCC.....	25	0	1	1.00	1	1	0	0	0	0	0	0	
.....GATAGCTTGTCTGGCCATGCT.....	20	0	1	1.00	1	1	0	0	0	0	0	0	
.....GATAGCTTGTCTGGCCATGCT.....	23	0	1	1.00	1	1	0	0	0	0	0	0	
.....GCCTGCGGGAGGAGCGGAGGC.....	23	0	1	1.00	1	1	0	0	0	0	0	0	
.....TGGGTTGGGATGGGATGGGAT.....	21	0	1	1.00	1	1	0	0	0	0	0	0	
.....AGCCTGCGGGAGGAGCGGAGGC.....	21	0	1	1.00	1	0	0	0	0	1	0	0	
.....GCTTGTCTGGCCATGCTGGC.....	19	0	1	1.00	1	1	0	0	0	0	0	0	
.....ATTAAGGACAACGATAGCTTGTCTGGCC.....	26	0	1	1.00	1	1	0	0	0	0	0	0	
.....ATTAAGGACAACGATAGCTT.....	20	0	1	1.00	1	1	0	0	0	0	0	0	
.....AACGATAGCTTGTCTGGCCATGCT.....	22	0	1	1.00	1	1	0	0	0	0	0	0	
.....AACGATAGCTTGTCTGGCCATGCT.....	22	0	1	1.00	1	0	0	0	1	0	0	0	
.....GAGCCTGCGGGAGGAGCGGAGGC.....	20	0	1	1.00	1	1	0	0	0	0	0	0	
.....GAGCCTGCGGGAGGAGCGGAG.....	20	0	1	1.00	1	1	0	0	0	0	0	0	
.....CATACGTGACGATGAGCCTGCT.....	21	0	1	1.00	1	1	0	0	0	0	0	0	
.....GGTGGGATGGGATGGGA.....	18	0	2	0.50	1	1	0	0	0	0	0	0	
.....TGGGTTGGGATGGGATGG.....	18	0	2	0.50	1	0	1	0	0	0	0	0	
.....GGGAGGAGCGGAGCGGCGA.....	19	2	18	0.06	1	1	0	0	0	0	0	0	

Anti-sense strand reads

	Read # size	Mismatch	Hit Count	Total Norm	Total	M040 female body	SRR902010 ovaries
CGCCGCGGTACAGATGACATGCTACTGCTGAGGAGCCCTCCTCTGCTCGGCCCACTACCCAGCCTTACCCCTACCTTACCTTACAGAGAGATAGCGTGGTCTGTGCTGCTGCTTACGGTATTCAGGTTACAGATAGCATCCCTTAAGGGTAATTCCTTGTGCTATGAACAGCGGTACGACCCGCGCGCT	18	0	12	0.08	1	0	1

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
dp5	XR_group8:6043241-6043414 +	dps_3340	CGCCGCGGATGTTACATCGTGACGATGAGCCTGCGGGAGGAGCGAGGCGGGTGAGTGGG-GT-----G--GGATGGGATGGGATGTCCTCT--ATC-----TGCCAC--CAG-----ACACGTGACAA-----AGTC-CATGTGATGCTAGGGAATTCCCATTAAGGACAACGATAGCTTGTCTGGCCATGCTGGCCGCCGA
droPer2	scaffold_45:440742-440915 +	dpe_1699	CGCCGCGGATGTTACATCGTGACGATGAGCCTGCGGGAGGAGCGAGGCGGGTGAGTGGG-GT-----G--GGATGGGATGGGATGTCCTCT--ATC-----TGCCAC--CAG-----ACACGTGACAA-----AGTC-CATGTGATGCTAGGGAATTCCCATTAAGGACAACGATAGCTTGTCTGGCCATGCTGGCCGCCGA
droW112	scf2_110000004762:1847012-1847220 -		CGCCGCGGATGTTACATCGTGACGATGAGCCTGCGGGAGGAGCGAGGCGGGTGAGTGGG-GT-----G--GGATGGGATGGGATGTCCTCT--ATC-----TGCCAC--CAG-----ACACGTGACAA-----AGTC-CATGTGATGCTAGGGAATTCCCATTAAGGACAACGATAGCTTGTCTGGCCATGCTGGCCGCCGA
droVir3	scaffold_13049:20936813-20936985 +		CGCCGCGGATGTTACATCGTGACGATGAGCCTGCGGGAGGAGCGAGGCGGGTGAGTGGG-GT-----G--GGATGGGATGGGATGTCCTCT--ATC-----TGCCAC--CAG-----ACACGTGACAA-----AGTC-CATGTGATGCTAGGGAATTCCCATTAAGGACAACGATAGCTTGTCTGGCCATGCTGGCCGCCGA
droMo3	scaffold_6680:15289925-15290122 +		CGCCGCGGATGTTACATCGTGACGATGAGCCTGCGGGAGGAGCGAGGCGGGTGAGTGGG-GT-----G--GGATGGGATGGGATGTCCTCT--ATC-----TGCCAC--CAG-----ACACGTGACAA-----AGTC-CATGTGATGCTAGGGAATTCCCATTAAGGACAACGATAGCTTGTCTGGCCATGCTGGCCGCCGA
droGr12	scaffold_15110:22762701-22762898 -		CGCCGCGGATGTTACATCGTGACGATGAGCCTGCGGGAGGAGCGAGGCGGGTGAGTGGG-GT-----G--GGATGGGATGGGATGTCCTCT--ATC-----TGCCAC--CAG-----ACACGTGACAA-----AGTC-CATGTGATGCTAGGGAATTCCCATTAAGGACAACGATAGCTTGTCTGGCCATGCTGGCCGCCGA
droAna3	scaffold_13337:21103697-21103859 +		CGCCGCGGATGTTACATCGTGACGATGAGCCTGCGGGAGGAGCGAGGCGGGTGAGTGGG-GT-----G--GGATGGGATGGGATGTCCTCT--ATC-----TGCCAC--CAG-----ACACGTGACAA-----AGTC-CATGTGATGCTAGGGAATTCCCATTAAGGACAACGATAGCTTGTCTGGCCATGCTGGCCGCCGA
droIip1	scf7180000396707:326502-326665 -		CGCCGCGGATGTTACATCGTGACGATGAGCCTGCGGGAGGAGCGAGGCGGGTGAGTGGG-GT-----G--GGATGGGATGGGATGTCCTCT--ATC-----TGCCAC--CAG-----ACACGTGACAA-----AGTC-CATGTGATGCTAGGGAATTCCCATTAAGGACAACGATAGCTTGTCTGGCCATGCTGGCCGCCGA
droIki1	scf7180000302441:2093041-2093212 -		CGCCGCGGATGTTACATCGTGACGATGAGCCTGCGGGAGGAGCGAGGCGGGTGAGTGGG-GT-----G--GGATGGGATGGGATGTCCTCT--ATC-----TGCCAC--CAG-----ACACGTGACAA-----AGTC-CATGTGATGCTAGGGAATTCCCATTAAGGACAACGATAGCTTGTCTGGCCATGCTGGCCGCCGA
droFic1	scf7180000453945:126432-126598 +		CGCCGCGGATGTTACATCGTGACGATGAGCCTGCGGGAGGAGCGAGGCGGGTGAGTGGG-GT-----G--GGATGGGATGGGATGTCCTCT--ATC-----TGCCAC--CAG-----ACACGTGACAA-----AGTC-CATGTGATGCTAGGGAATTCCCATTAAGGACAACGATAGCTTGTCTGGCCATGCTGGCCGCCGA
droEie1	scf7180000491199:864715-864874 -		CGCCGCGGATGTTACATCGTGACGATGAGCCTGCGGGAGGAGCGAGGCGGGTGAGTGGG-GT-----G--GGATGGGATGGGATGTCCTCT--ATC-----TGCCAC--CAG-----ACACGTGACAA-----AGTC-CATGTGATGCTAGGGAATTCCCATTAAGGACAACGATAGCTTGTCTGGCCATGCTGGCCGCCGA
droRho1	scf7180000759602:19100-19266 +		CGCCGCGGATGTTACATCGTGACGATGAGCCTGCGGGAGGAGCGAGGCGGGTGAGTGGG-GT-----G--GGATGGGATGGGATGTCCTCT--ATC-----TGCCAC--CAG-----ACACGTGACAA-----AGTC-CATGTGATGCTAGGGAATTCCCATTAAGGACAACGATAGCTTGTCTGGCCATGCTGGCCGCCGA
droBial	scf7180000302377:1314000-1314156 -		CGCCGCGGATGTTACATCGTGACGATGAGCCTGCGGGAGGAGCGAGGCGGGTGAGTGGG-GT-----G--GGATGGGATGGGATGTCCTCT--ATC-----TGCCAC--CAG-----ACACGTGACAA-----AGTC-CATGTGATGCTAGGGAATTCCCATTAAGGACAACGATAGCTTGTCTGGCCATGCTGGCCGCCGA
droTak1	scf7180000414002:118225-118385 +		CGCCGCGGATGTTACATCGTGACGATGAGCCTGCGGGAGGAGCGAGGCGGGTGAGTGGG-GT-----G--GGATGGGATGGGATGTCCTCT--ATC-----TGCCAC--CAG-----ACACGTGACAA-----AGTC-CATGTGATGCTAGGGAATTCCCATTAAGGACAACGATAGCTTGTCTGGCCATGCTGGCCGCCGA
droBugi	scf7180000409472:805669-805830 +		CGCCGCGGATGTTACATCGTGACGATGAGCCTGCGGGAGGAGCGAGGCGGGTGAGTGGG-GT-----G--GGATGGGATGGGATGTCCTCT--ATC-----TGCCAC--CAG-----ACACGTGACAA-----AGTC-CATGTGATGCTAGGGAATTCCCATTAAGGACAACGATAGCTTGTCTGGCCATGCTGGCCGCCGA
dm3	chr31:21970186-21970342 +		CGCCGCGGATGTTACATCGTGACGATGAGCCTGCGGGAGGAGCGAGGCGGGTGAGTGGG-GT-----G--GGATGGGATGGGATGTCCTCT--ATC-----TGCCAC--CAG-----ACACGTGACAA-----AGTC-CATGTGATGCTAGGGAATTCCCATTAAGGACAACGATAGCTTGTCTGGCCATGCTGGCCGCCGA
droIm2	31:21485379-21485535 +		CGCCGCGGATGTTACATCGTGACGATGAGCCTGCGGGAGGAGCGAGGCGGGTGAGTGGG-GT-----G--GGATGGGATGGGATGTCCTCT--ATC-----TGCCAC--CAG-----ACACGTGACAA-----AGTC-CATGTGATGCTAGGGAATTCCCATTAAGGACAACGATAGCTTGTCTGGCCATGCTGGCCGCCGA
droSec2	scaffold_11:1895774-1895930 +		CGCCGCGGATGTTACATCGTGACGATGAGCCTGCGGGAGGAGCGAGGCGGGTGAGTGGG-GT-----G--GGATGGGATGGGATGTCCTCT--ATC-----TGCCAC--CAG-----ACACGTGACAA-----AGTC-CATGTGATGCTAGGGAATTCCCATTAAGGACAACGATAGCTTGTCTGGCCATGCTGGCCGCCGA
droYak3	v2_chr31_random_30216321-6477 +		CGCCGCGGATGTTACATCGTGACGATGAGCCTGCGGGAGGAGCGAGGCGGGTGAGTGGG-GT-----G--GGATGGGATGGGATGTCCTCT--ATC-----TGCCAC--CAG-----ACACGTGACAA-----AGTC-CATGTGATGCTAGGGAATTCCCATTAAGGACAACGATAGCTTGTCTGGCCATGCTGGCCGCCGA
droEre2	scaffold_4784:21645046-21645210 +		CGCCGCGGATGTTACATCGTGACGATGAGCCTGCGGGAGGAGCGAGGCGGGTGAGTGGG-GT-----G--GGATGGGATGGGATGTCCTCT--ATC-----TGCCAC--CAG-----ACACGTGACAA-----AGTC-CATGTGATGCTAGGGAATTCCCATTAAGGACAACGATAGCTTGTCTGGCCATGCTGGCCGCCGA

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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.prior3	1
crit.kuri	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

mature	star
1. 2:12450392-12450412 - 2. dps_42_XL_group1a:4093864-4093884 +	

hide 3p reads show mid mismatch reads

Anti-sense strand reads

Show Alignment With Reads

Re-alignment of all predicted orthologs

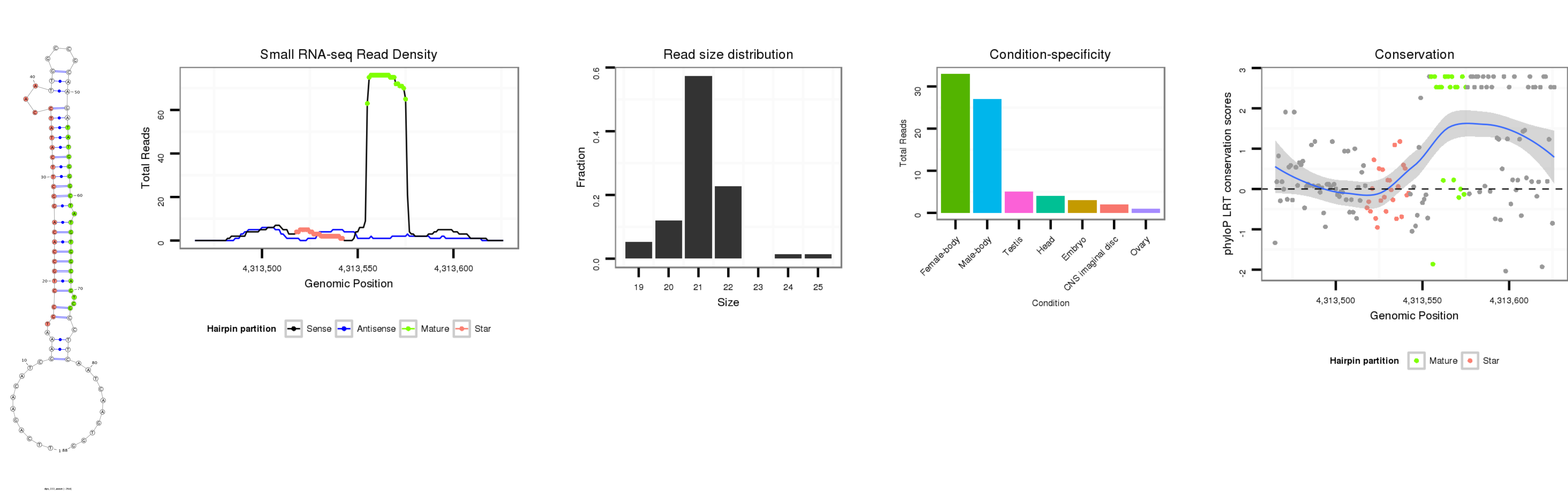
Generated: 09/08/2015 at 08:18 PM

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

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dps_222	3:4313515-4313576 +	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 [Dpse/GA24708-cds]

No Repeatable elements found

Sense Strand Reads

☐ hide 3p reads ☐ show mid mismatch reads

	Read #	Hit	Total		M040		SRR902011	GSM444067	M062	M059	SRR902012		GSM343916	SRR902010
	size	Mismatch	Count	Norm	Total	female body	male body	testis	head	head	embryo	CNS imaginal disc	embryo	ovaries
ACTGGATTCCTAAAACGTTAACAAAAGTGGTACTACAGTTCAGAACATCGAAATGCGCTGCCACAGGCTTCATATCCAAATTGGCCGCAAGAATATGGGGCTATGTGGCAGTCGCCTTCAATCAAGTGGATGCCGAACGCTCTCGCCAAGGTGGGTCCAAATAGGC	21	0	1	35.00	35	15	14	2	1	0	2	1	0	0
.....TATGGGGCTATGTGGCAGTCG.....	22	0	1	14.00	14	3	6	0	1	2	0	1	1	0
.....TATGGGGCTATGTGGCAGTCGC.....	20	0	1	6.00	6	6	0	0	0	0	0	0	0	0
.....TATGGGGCTATGTGGCAGTCG.....	22	1	1	4.00	4	1	3	0	0	0	0	0	0	0
.....TATGGGGCTATGTGGCAGTCG.....	20	0	1	3.00	3	1	2	0	0	0	0	0	0	0
.....TATGGGGCTATGTGGCAGTCGC.....	21	0	1	3.00	3	1	2	0	0	0	0	0	0	0
.....ATATGGGGCTATGTGGCAGTCG.....	22	0	1	3.00	3	3	0	0	0	0	0	0	0	0
.....GCAAGATATGGGGCTATGTGG.....	21	0	1	3.00	3	0	0	3	0	0	0	0	0	0
.....TGGTACTACAGTTCAGAACATC.....	22	0	1	2.00	2	0	0	2	0	0	0	0	0	0
.....ATGGGGCTATGTGGCAGTC.....	19	0	1	2.00	2	2	0	0	0	0	0	0	0	0
.....CGAAGATATGGGGCTATG.....	19	0	1	1.00	1	0	1	0	0	0	0	0	0	0
.....ACGTCTCGCCAAGGTGGTCC.....	22	1	1	1.00	1	0	1	0	0	0	0	0	0	0
.....TTAACAAAAGTGGTACTACAGTTCAGAA.....	28	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....TGCCTGCCACAGGCTTCATATCCAA.....	26	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....GAACATCGAAATGCTGCCACAGG.....	25	0	1	1.00	1	0	0	0	0	0	0	0	0	1
.....TCAATCAAGTGGATGCCGAACGTC.....	24	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....GTGGATGCCGAACGCTCTGCC.....	21	0	1	1.00	1	0	0	0	1	0	0	0	0	0
.....TATGGGGCTATGTGGCAGT.....	19	0	1	1.00	1	0	1	0	0	0	0	0	0	0
.....AAGATATGGGGCTATGTGGCA.....	21	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....AACAAAAGTGGTACTACAGTTCAGAAC.....	27	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....GCCTTCAATCAAGTGGATGCCGAAC.....	25	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....TTCAGAACATCGAAATGCTGCCA.....	24	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....ATATGGGGCTATGTGGCAGTC.....	23	2	1	1.00	1	1	0	0	0	0	0	0	0	0
.....TGGGGCTATGTGGCAGTCGCTT.....	23	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....ACAGTTCAGAACATCGAAATGCTGC.....	26	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....CCTTCAATCAAGTGGATGCC.....	20	1	1	1.00	1	0	1	0	0	0	0	0	0	0
.....AAGATATGGGGCTATGTGGCAGTC.....	24	0	1	1.00	1	0	1	0	0	0	0	0	0	0
.....TATGGGGCTATGTGGCAGTCGC.....	24	2	1	1.00	1	0	0	0	1	0	0	0	0	0
.....ATGGGGCTATGTGGCAGTCGCC.....	22	0	1	1.00	1	0	1	0	0	0	0	0	0	0
.....TATGGGGCTATGTGGCAGTCGCT.....	24	0	1	1.00	1	0	0	0	0	0	0	0	1	0
.....CCTGCCACAGGCTTCATATCC.....	21	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....TATGGGGCTATGTGGCAGTC.....	22	1	1	1.00	1	1	0	0	0	0	0	0	0	0
.....ATGGGGCTATGTGGCAGTC.....	21	1	1	1.00	1	1	0	0	0	0	0	0	0	0
.....TATGGGGCTATGTGGCAGTCGC.....	23	1	1	1.00	1	1	0	0	0	0	0	0	0	0
.....GATGCCGAACGCTCTGCCA.....	19	0	1	1.00	1	1	0	0	0	0	0	0	0	0

Anti-sense strand reads

	Read #	size	Mismatch	Hit	Count	Total	Norm	Total	SRR902011	testis	female body	M040	V112
TGACCTAAGGATTTTGAATGTGTTTCACCATGATGTCAAGTCTTGTAGCTTTACGGACGGTGTCCGAAGTATAGGTTAACCGGGCTTCTATACCCCGATACACCGTCAGCGGAAGTAGTTACCTACCGCTTGCAGACGGTTCCACCCAGGTTTATCCG	21	0	1	2.00	2	2	0	0					
*****(((.....((													

Show Alignment With Reads

Re-alignment of all predicted orthologs

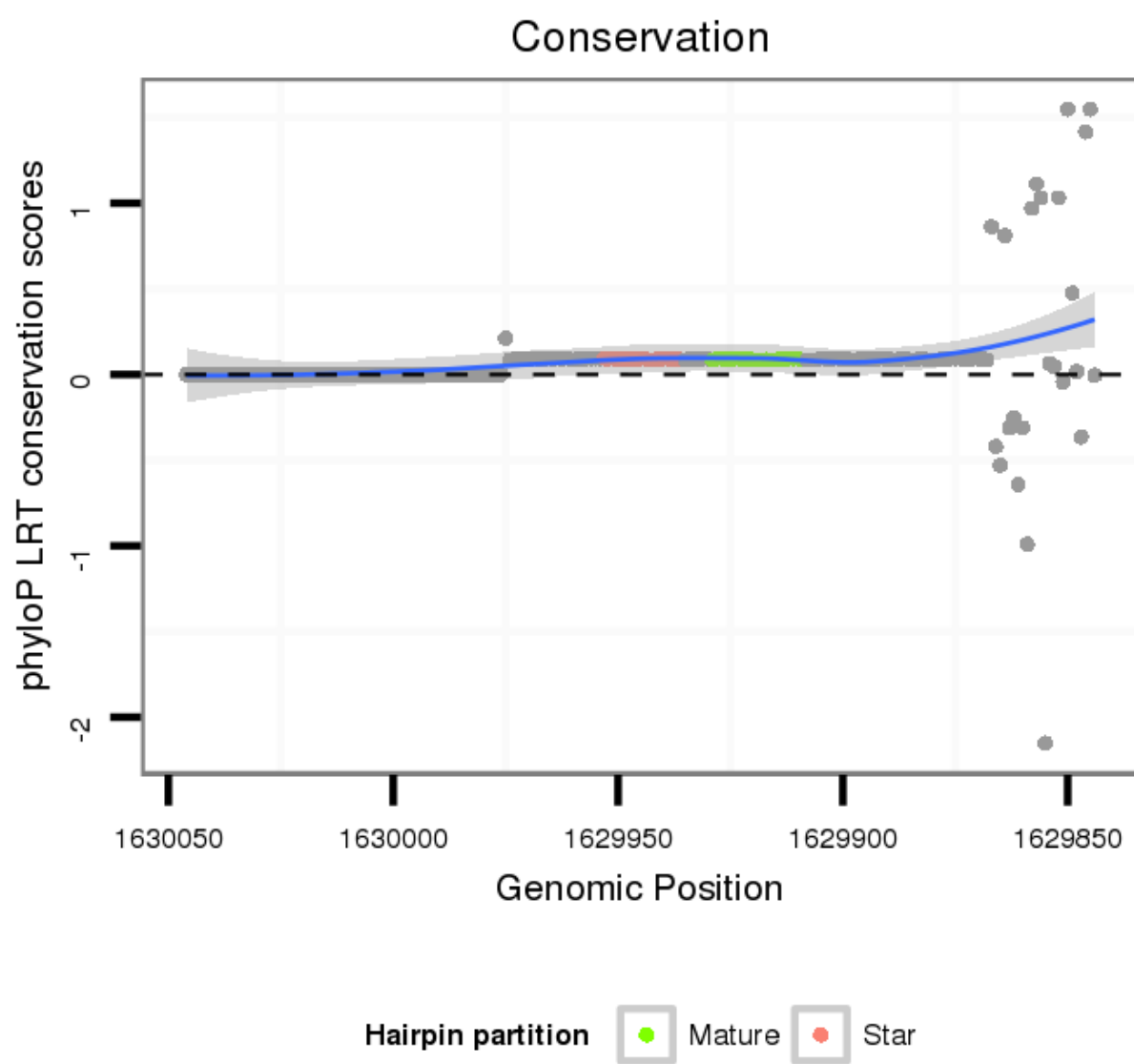
Species	Coordinate	ID	Alignment
dp5	1:4313465-4313626 +	dps_222	A-----CTG---GATTCCTAAAACGTTAACAAAAGTGGTACT-----ACAGTTCAGAACATCGAA--ATGCGCTGCCACAGGCTT---CATAT-----CCAAATTG-----GCCGCAAGAATATGGGGCTATGTGGCAGTCGCCTTCAATCAAGTGGATGCCGAACGCTCTCGCCAAGGTGGGTCCAAATAGGC
droPer2	scaffold_2:4502066-4502227 -		A-----CTG---GATTCCTAAAACGTTAACAAAAGTGGTACT-----ACAGTTCAGAACATCGAA--ATGCGCTGCCACAGGCTT---CATAT-----CCAAATTG-----GCCGCAAGAATATGGGGCTATGTGGCAGTCGCCTTCAAGTGGATGCGAAGTCTCGCCAAGGTGGGTCCAAATAGGC
droW112	scaf2_1100000004514:360186-160264 -		---GATTCCTAAAACGTTAACAAAAGTGGTACT-----ACAGTTCAGAACATCGAA--ATGCGCTGCCACAGGCTT---CATAT-----CCAAATTG-----GCCGCAAGAATATGGGGCTATGTGGCAGTCGCCTTCAATCAAGTGGATGCCGAACGCTCTCGCCAAGGTGGGTCCAAATAGGC
droVir3	scaffold_12875:4369897-4370097 -		---GATTCCTAAAACGTTAACAAAAGTGGTACT-----ACAGTTCAGAACATCGAA--ATGCGCTGCCACAGGCTT---CATAT-----CCAAATTG-----GCCGCAAGAATATGGGGCTATGTGGCAGTCGCCTTCAATCAAGTGGATGCCGAACGCTCTCGCCAAGGTGGGTCCAAATAGGC
droMoJ3	scaffold_6496:13207781-13207868 -		---GATTCCTAAAACGTTAACAAAAGTGGTACT-----ACAGTTCAGAACATCGAA--ATGCGCTGCCACAGGCTT---CATAT-----CCAAATTG-----GCCGCAAGAATATGGGGCTATGTGGCAGTCGCCTTCAATCAAGTGGATGCCGAACGCTCTCGCCAAGGTGGGTCCAAATAGGC
droGr12	scaffold_15112:1882204-1882365 +		A---GATTCCTAAAACGTTAACAAAAGTGGTACT-----ACAGTTCAGAACATCGAA--ATGCGCTGCCACAGGCTT---CATAT-----CCAAATTG-----GCCGCAAGAATATGGGGCTATGTGGCAGTCGCCTTCAATCAAGTGGATGCCGAACGCTCTCGCCAAGGTGGGTCCAAATAGGC
droAna3	scaffold_13266:7882243-7882321 +		---GATTCCTAAAACGTTAACAAAAGTGGTACT-----ACAGTTCAGAACATCGAA--ATGCGCTGCCACAGGCTT---CATAT-----CCAAATTG-----GCCGCAAGAATATGGGGCTATGTGGCAGTCGCCTTCAATCAAGTGGATGCCGAACGCTCTCGCCAAGGTGGGTCCAAATAGGC
droBip1	scaf7180000396759:943378-943450 -		---GATTCCTAAAACGTTAACAAAAGTGGTACT-----ACAGTTCAGAACATCGAA--ATGCGCTGCCACAGGCTT---CATAT-----CCAAATTG-----GCCGCAAGAATATGGGGCTATGTGGCAGTCGCCTTCAATCAAGTGGATGCCGAACGCTCTCGCCAAGGTGGGTCCAAATAGGC
droRik1	scaf7180000302682:1337408-1337575 +		---GATTCCTAAAACGTTAACAAAAGTGGTACT-----ACAGTTCAGAACATCGAA--ATGCGCTGCCACAGGCTT---CATAT-----CCAAATTG-----GCCGCAAGAATATGGGGCTATGTGGCAGTCGCCTTCAATCAAGTGGATGCCGAACGCTCTCGCCAAGGTGGGTCCAAATAGGC
droFic1	scaf7180000453948:1284873-1285001 -		A---GATTCCTAAAACGTTAACAAAAGTGGTACT-----ACAGTTCAGAACATCGAA--ATGCGCTGCCACAGGCTT---CATAT-----CCAAATTG-----GCCGCAAGAATATGGGGCTATGTGGCAGTCGCCTTCAATCAAGTGGATGCCGAACGCTCTCGCCAAGGTGGGTCCAAATAGGC
droLe1	scaf7180000491107:1051864-1051982 -		---GATTCCTAAAACGTTAACAAAAGTGGTACT-----ACAGTTCAGAACATCGAA--ATGCGCTGCCACAGGCTT---CATAT-----CCAAATTG-----GCCGCAAGAATATGGGGCTATGTGGCAGTCGCCTTCAATCAAGTGGATGCCGAACGCTCTCGCCAAGGTGGGTCCAAATAGGC
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droBia1	scaf7180000301506:2986358-2986486 -		A---GATTCCTAAAACGTTAACAAAAGTGGTACT-----ACAGTTCAGAACATCGAA--ATGCGCTGCCACAGGCTT---CATAT-----CCAAATTG-----GCCGCAAGAATATGGGGCTATGTGGCAGTCGCCTTCAATCAAGTGGATGCCGAACGCTCTCGCCAAGGTGGGTCCAAATAGGC
droTak1	scaf7180000415795:519193-519324 +		A---GATTCCTAAAACGTTAACAAAAGTGGTACT-----ACAGTTCAGAACATCGAA--ATGCGCTGCCACAGGCTT---CATAT-----CCAAATTG-----GCCGCAAGAATATGGGGCTATGTGGCAGTCGCCTTCAATCAAGTGGATGCCGAACGCTCTCGCCAAGGTGGGTCCAAATAGGC
droBui1	scaf7180000409672:946450-946522 -		---GATTCCTAAAACGTTAACAAAAGTGGTACT-----ACAGTTCAGAACATCGAA--ATGCGCTGCCACAGGCTT---CATAT-----CCAAATTG-----GCCGCAAGAATATGGGGCTATGTGGCAGTCGCCTTCAATCAAGTGGATGCCGAACGCTCTCGCCAAGGTGGGTCCAAATAGGC
dm3	chr2R:12036978-12037050 -		---GATTCCTAAAACGTTAACAAAAGTGGTACT-----ACAGTTCAGAACATCGAA--ATGCGCTGCCACAGGCTT---CATAT-----CCAAATTG-----GCCGCAAGAATATGGGGCTATGTGGCAGTCGCCTTCAATCAAGTGGATGCCGAACGCTCTCGCCAAGGTGGGTCCAAATAGGC
droSim2	chr12106865-12707011 -		TCGCCAAAGTGTATTAAATAA---GATTCCTAAAACGTTAACAAAAGTGGTACT-----ACAGTTCAGAACATCGAA--ATGCGCTGCCACAGGCTT---CATAT-----CCAAATTG-----GCCGCAAGAATATGGGGCTATGTGGCAGTCGCCTTCAATCAAGTGGATGCCGAACGCTCTCGCCAAGGTGGGTCCAAATAGGC
droSec2	scaffold_1:9532370-9532515 -		TCGCCAAAGTGTATTAAATAA---GATTCCTAAAACGTTAACAAAAGTGGTACT-----ACAGTTCAGAACATCGAA--ATGCGCTGCCACAGGCTT---CATAT-----CCAAATTG-----GCCGCAAGAATATGGGGCTATGTGGCAGTCGCCTTCAATCAAGTGGATGCCGAACGCTCTCGCCAAGGTGGGTCCAAATAGGC
droTak3	chr16346224-16346296 +		---GATTCCTAAAACGTTAACAAAAGTGGTACT-----ACAGTTCAGAACATCGAA--ATGCGCTGCCACAGGCTT---CATAT-----CCAAATTG-----GCCGCAAGAATATGGGGCTATGTGGCAGTCGCCTTCAATCAAGTGGATGCCGAACGCTCTCGCCAAGGTGGGTCCAAATAGGC
droFre2	scaffold_4845:13821045-13821117 +		---GATTCCTAAAACGTTAACAAAAGTGGTACT-----ACAGTTCAGAACATCGAA--ATGCGCTGCCACAGGCTT---CATAT-----CCAAATTG-----GCCGCAAGAATATGGGGCTATGTGGCAGTCGCCTTCAATCAAGTGGATGCCGAACGCTCTCGCCAAGGTGGGTCCAAATAGGC

Generated: 09/08/2015 at 08:16 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.top3	1
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

	PASS/FAIL
crit.star	0
crit.top3	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

Predicted structure



hide 3p reads show mid mismatch reads

Anti-sense strand reads

Show Alignment With Reads

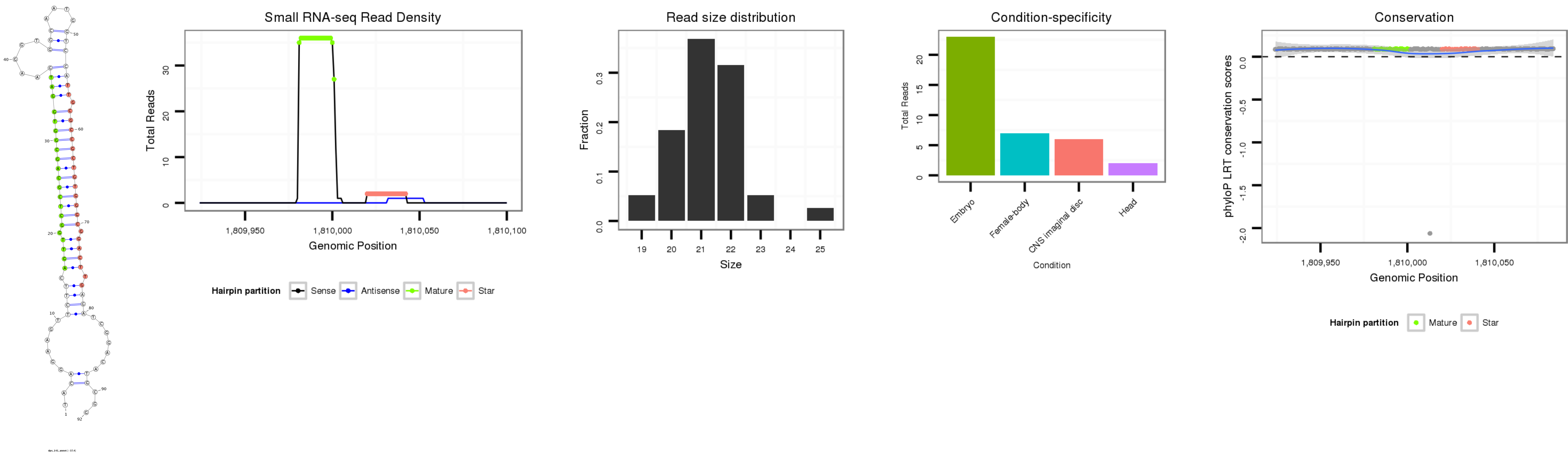
Re-alignment of all predicted orthologs

Generated: 08/16/2015 at 02:01 PM

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

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

Species	Coordinate	ID	Alignment
dp5	Xl_group3a:1809931-1810091_+	dps_141	CGATTGACCCCTCGTTCTCGTTGTGTAGCACACATACAGGAAGTCTTCAGTTGGCTCGCAGCGGTGGATGAAGGTGCAATGGTCCATTGCGCCGCTGTGGCGGACTTGAGATCGGACATGCGGTAAGGTGGAAGCACTATACAACCAATTTCCATA
droPer2	scaffold_76:243594-243754_-	dpe_2488	CGATTGACCCCTCGTTCTCGTTGTGTAGCACACATACAGGAAGTCTTCAGTTGGCTCGCAGCGGTGGATGAAGGTGCAATGGTCCAATGCGCCGCTGTGGCGGACTTGAGATCGGACATGCGGTAAGGTGGAAGCACTATACAACCAATTTCCATA

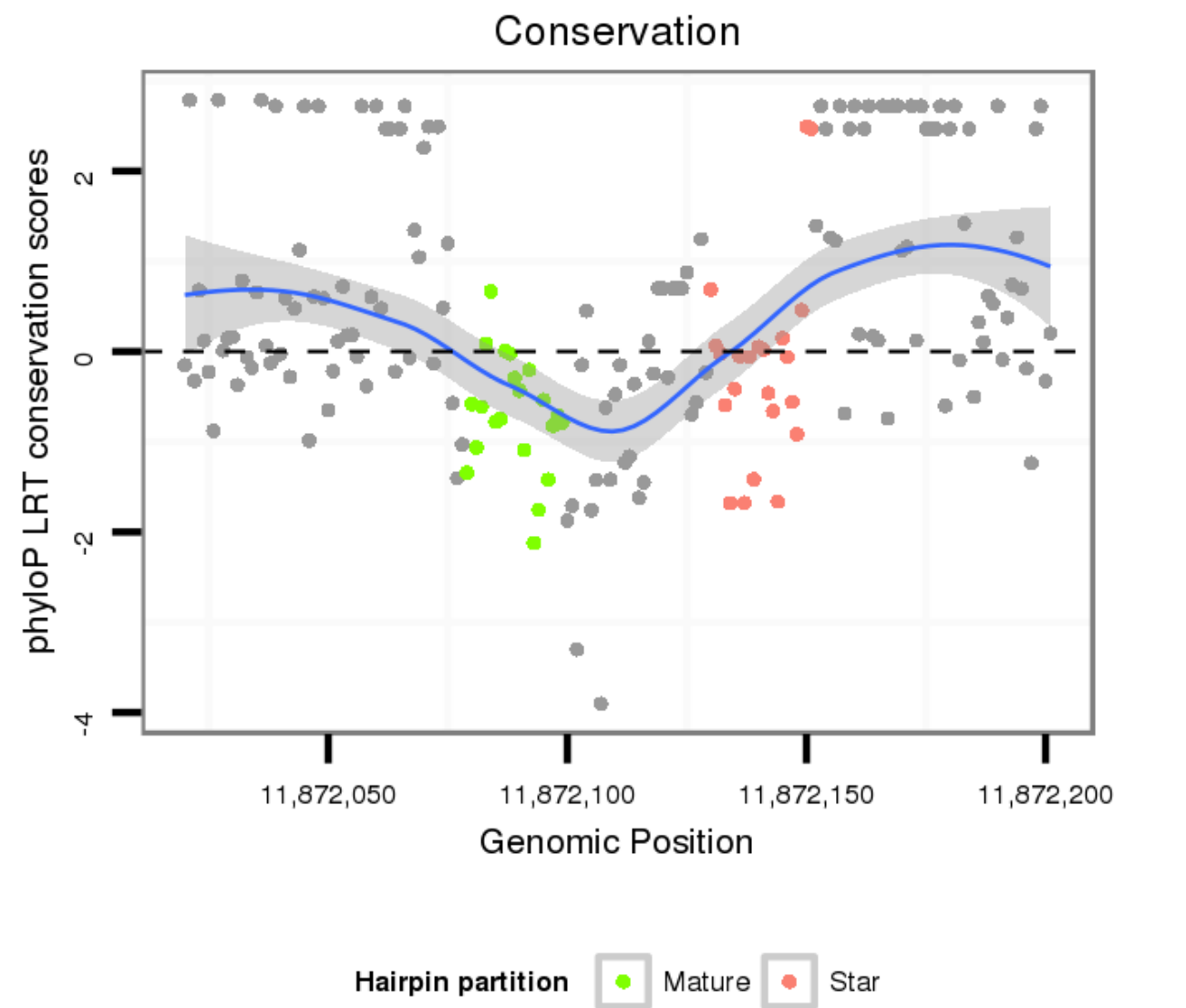
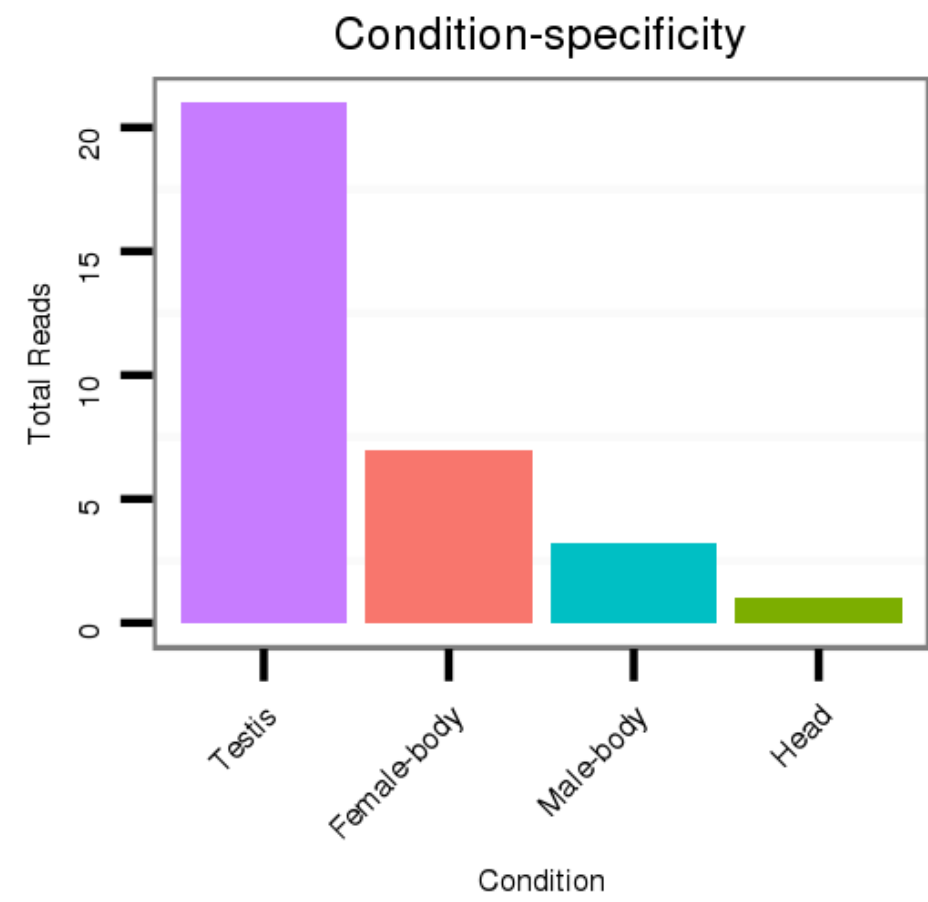
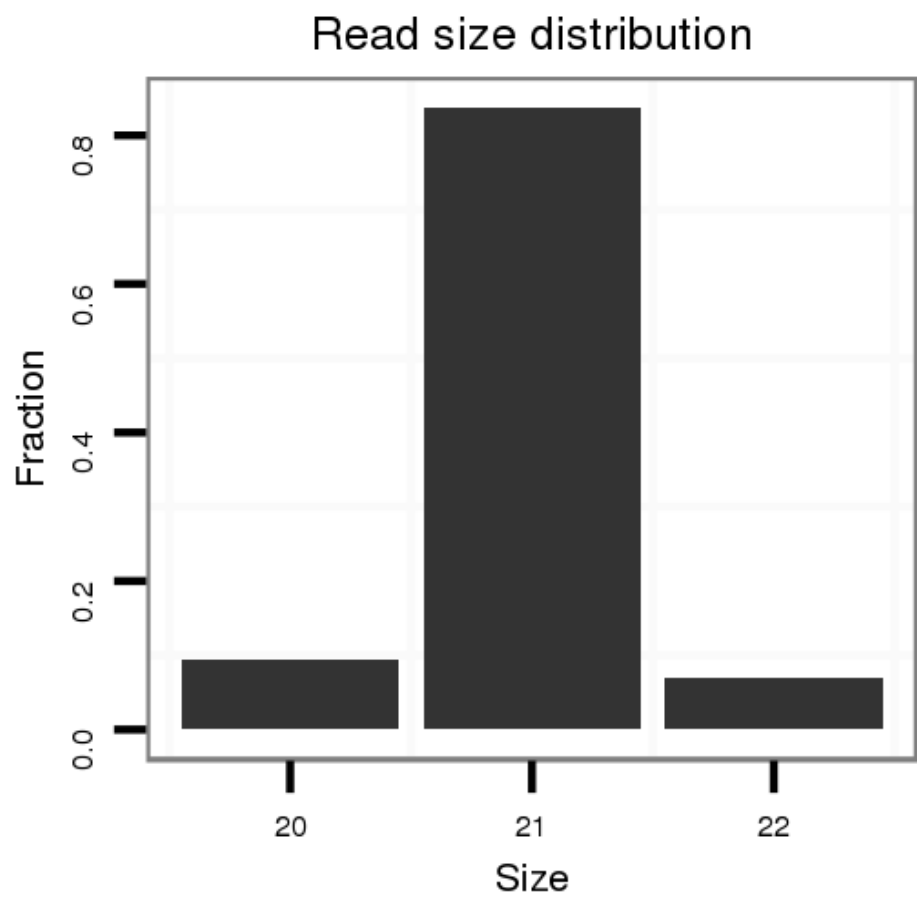
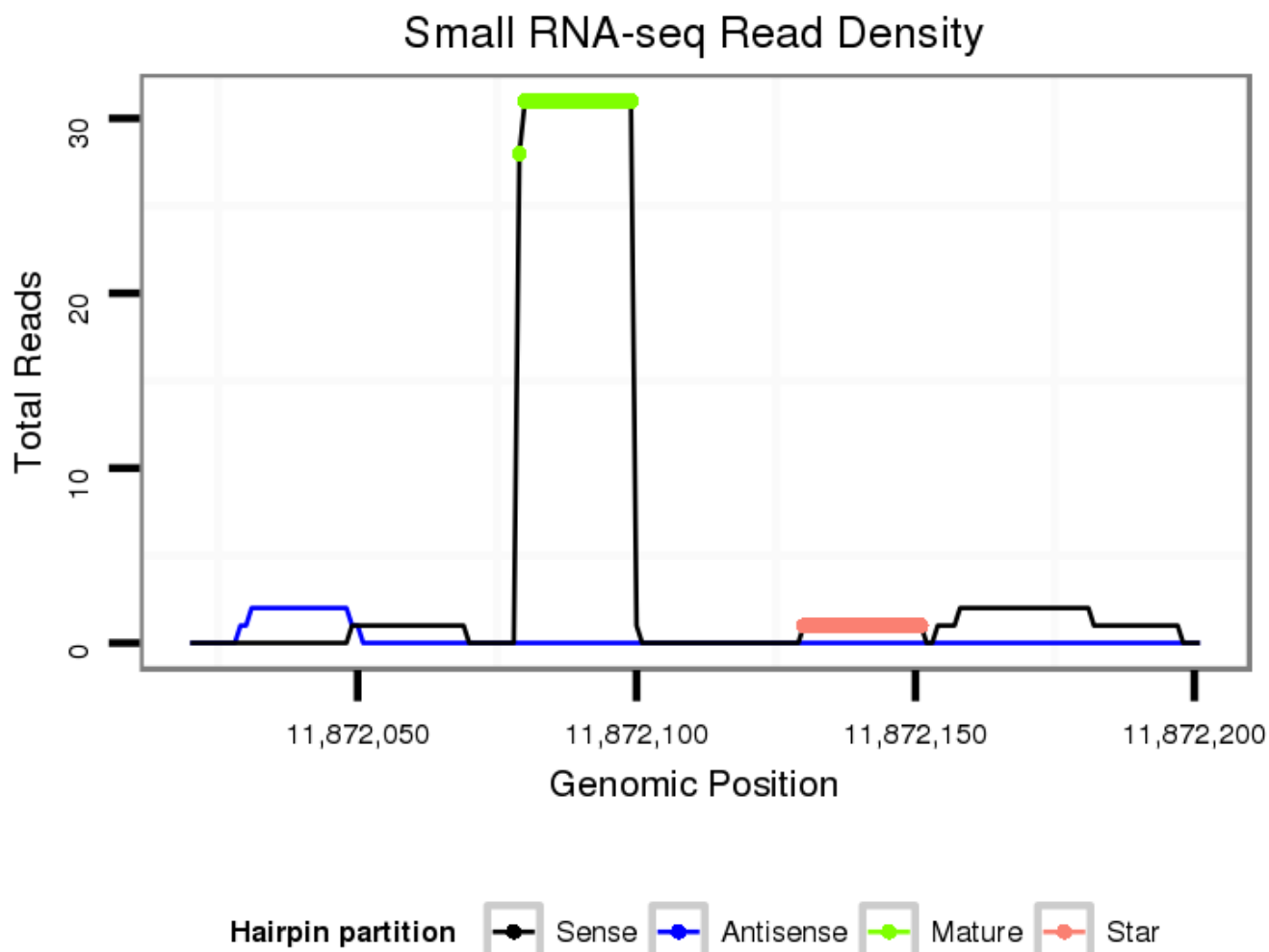
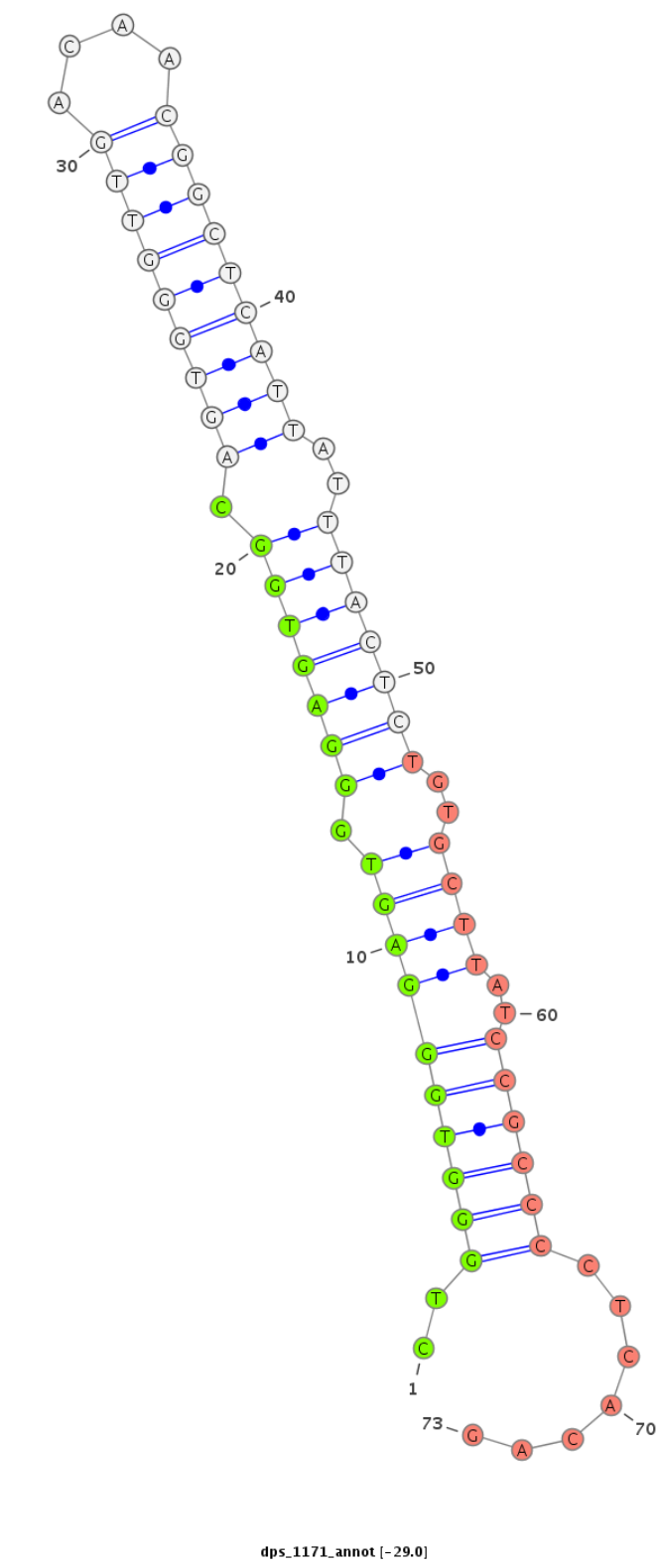
Generated: 09/08/2015 at 08:16 AM **PASS/FAIL**

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

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dps_1171	3:11872070-11872151 +	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 [Dpse\GA24914-in]; CDS [Dpse\GA24914-cds]; CDS [Dpse\GA24914-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

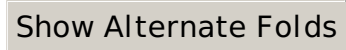
Re-alignment of all predicted orthologs

[illegible]

Generated: 09/08/2015 at 07:03 PM

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

Predicted structure



Flybase annotation

intron [Dpse\GA20377-in]; CDS [Dpse\GA20377-cds]; CDS [Dpse\GA20377-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

Anti-sense strand reads

Show Alignment With Reads

Re-alignment of all predicted orthologs

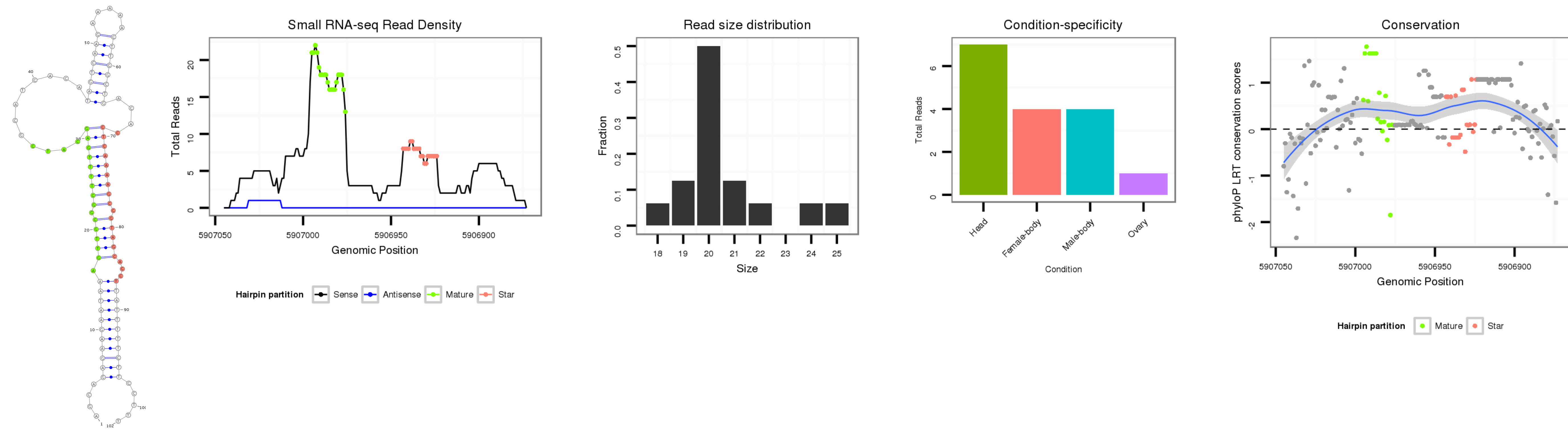
Generated: 09/08/2015 at 07:03 PM

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

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dps_76	XR_group6:5906923-5906995 -	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

intergeni

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

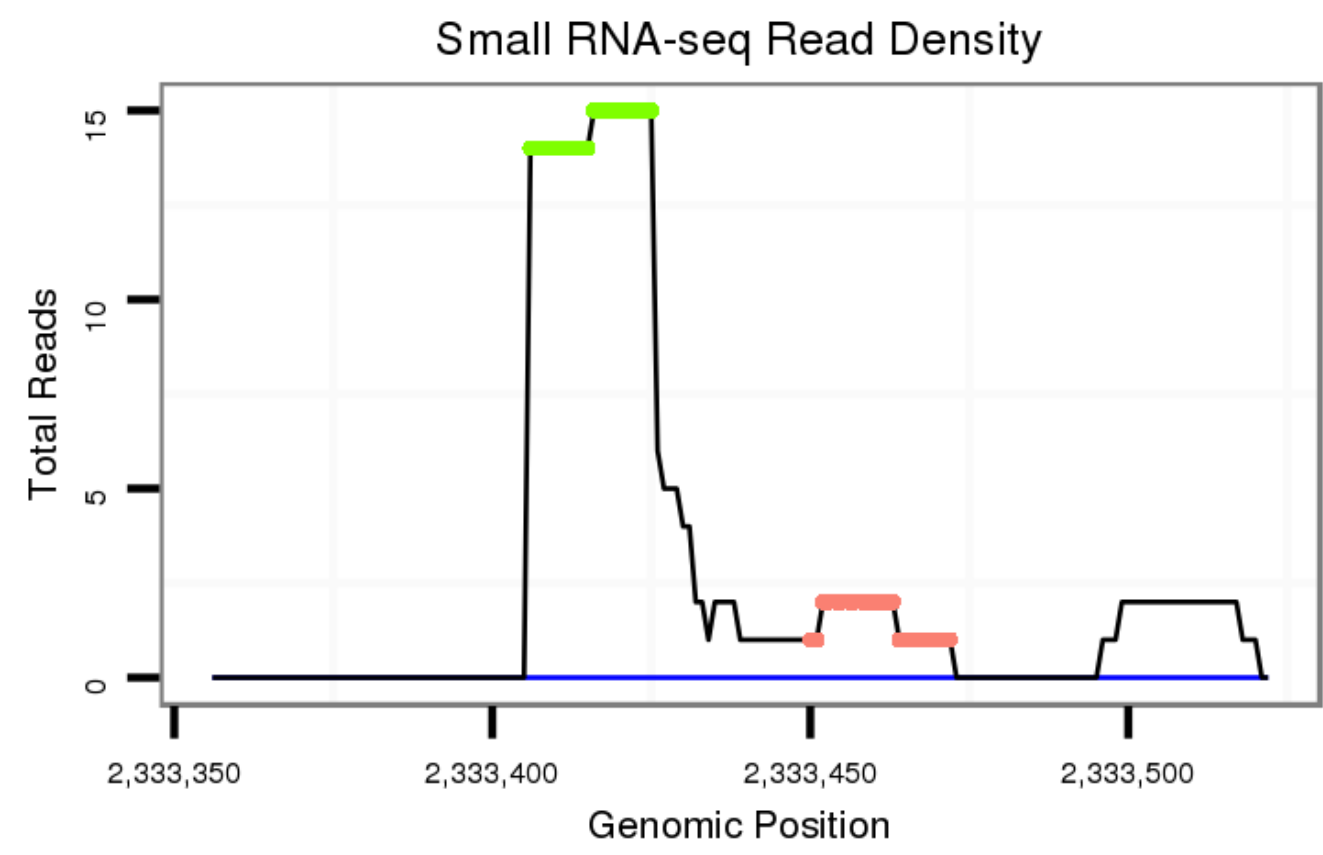
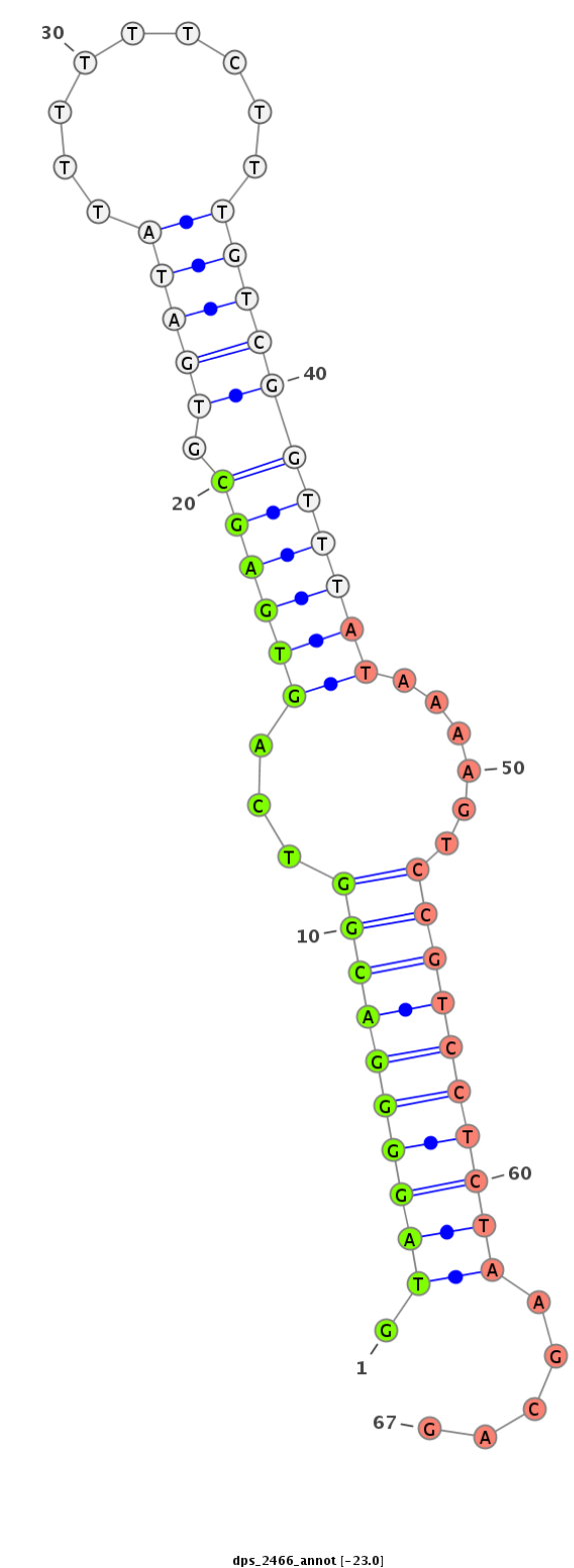
[illegible]

Generated: 09/08/2015 at 08:17 PM

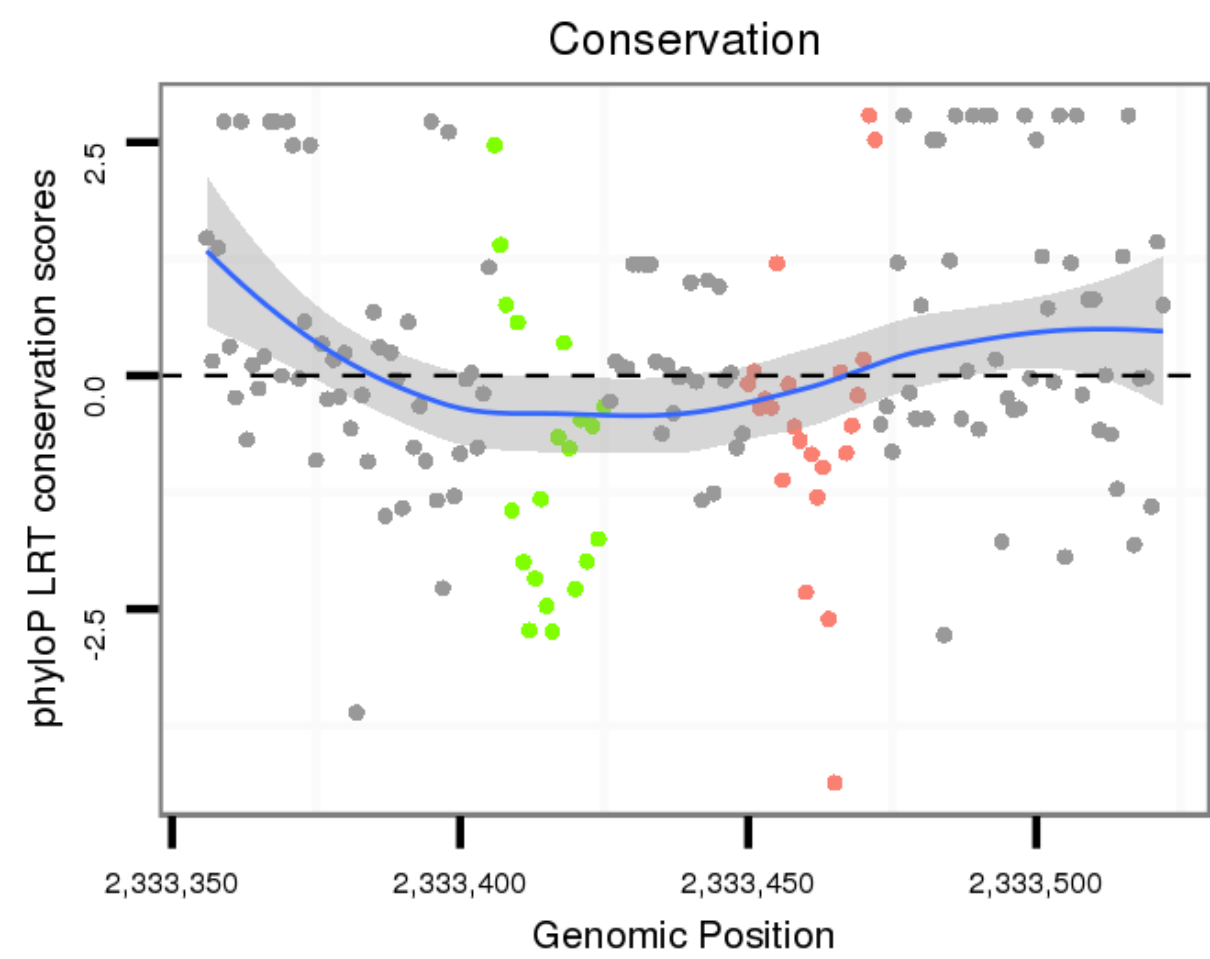
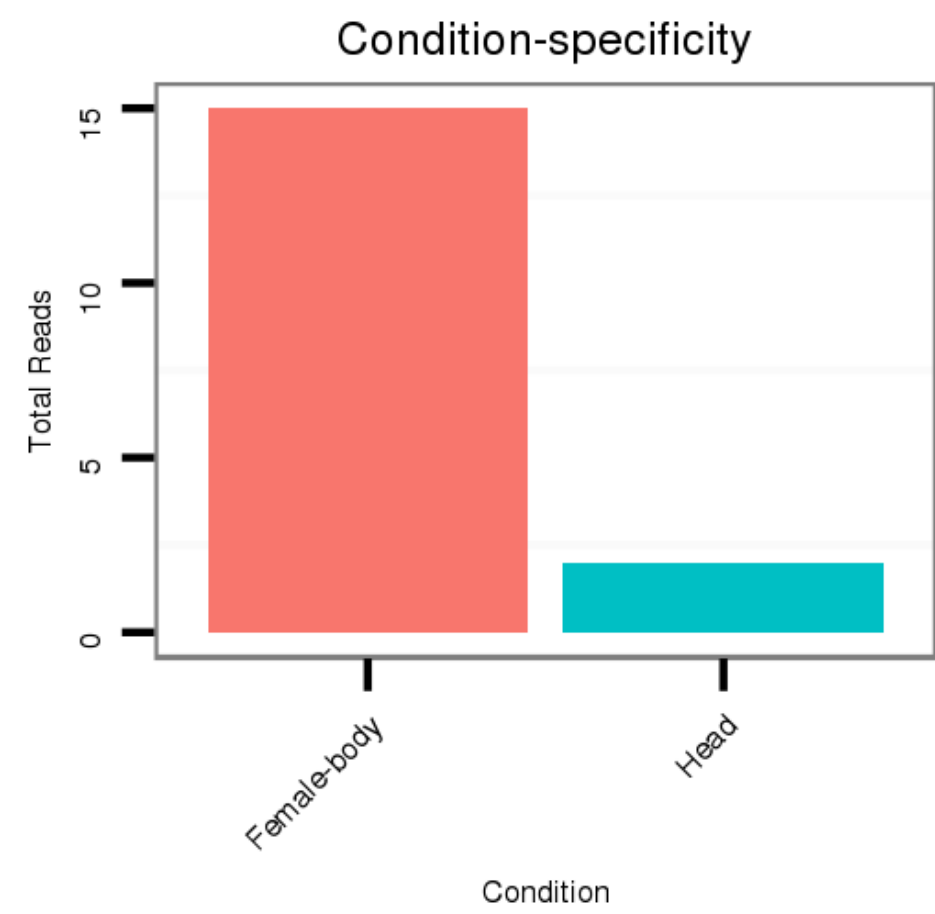
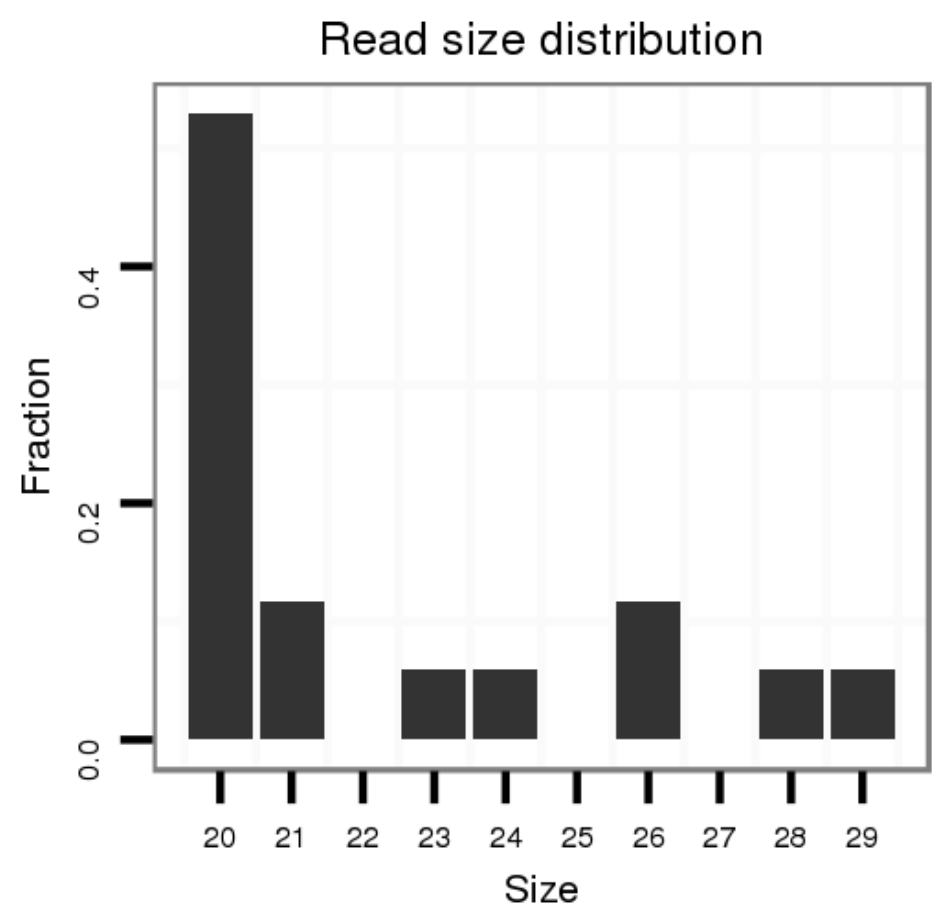
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	0
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Hairpin partition  **Sense**  **Antisense**  **Mature**  **Star**



Hairpin partition  **Mature**  **Star**

Show Alternate Folds

Flybase annotation

intron [Dpse\GA15315-in]; CDS [Dpse\GA15315-cds]; CDS [Dpse\GA15315-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

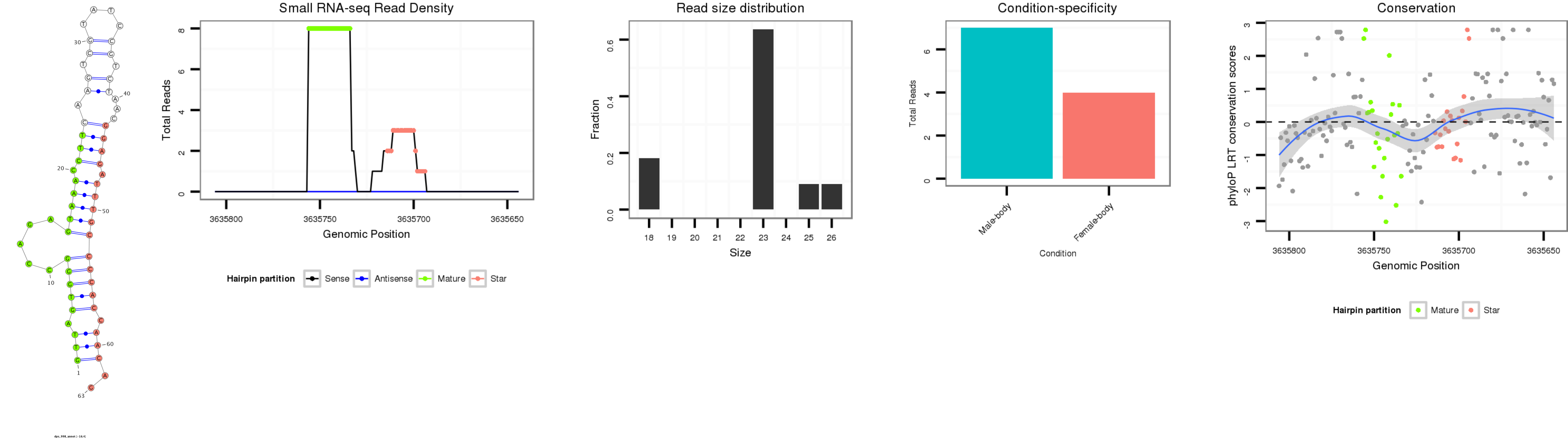
Re-alignment of all predicted orthologs

[illegible]

Generated: 09/08/2015 at 06:09 PM

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Show Alternate Folds

Flybase annotation

intron [Dpse\GA24472-in]; CDS [Dpse\GA24472-cds]; CDS [Dpse\GA24472-cds]

Sense Strand Reads

hide 3p reads show mid mismatch reads

[illegible]

Anti-sense strand reads

[illegible]

Re-alignment of all predicted orthologs

[illegible]

Generated: 08/18/2015 at 04:05 PM

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

Legend: mature star mismatch in alignment mismatch in read



hide 3p reads show mid mismatch reads

Anti-sense strand reads

Show Alignment With Reads[illegible]

```
Generated: 00:08:2015 at 08:17 PM
crit.crit
crit.loop
crit.mor
crit.half
crit.total
crit.pairing
crit.top3
crit.tptop3
crit.turi
crit.back
rescue.total
rescue.dominant
rescue.known
rescue.confident
rescue.candidate
```

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



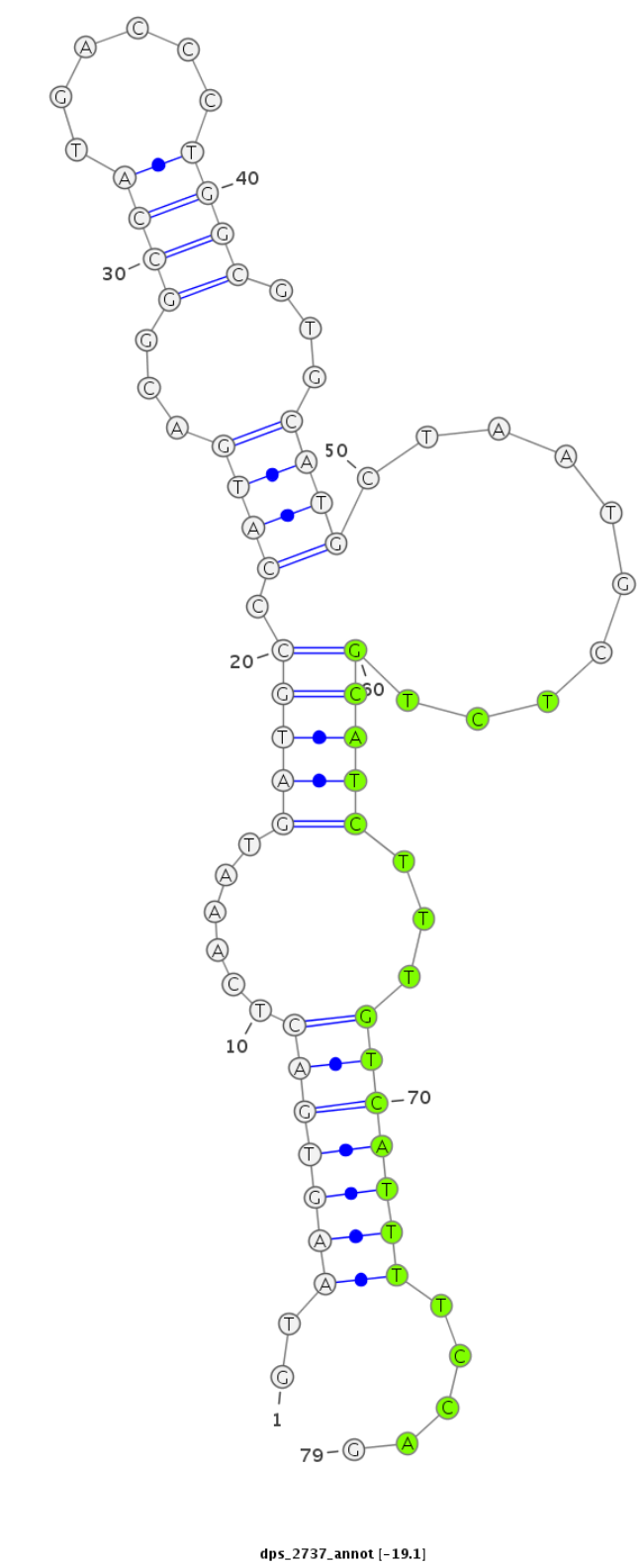
Generated: 09/08/2015 at 08:17 PM

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

intron [Dpse\GA11765-in]; CDS [Dpse\GA11765-cds]; CDS [Dpse\GA11765-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

[illegible]

Anti-sense strand reads

										Read #	Hit	Total		M040	SRR902012
										size	Count	Norm		female	V112
										Mismatch				body	CNS
														male	imaginal
														body	disc
GTTCCGGGTACAGTTAAGTCATAAGAAGTTTGTGCGAGCCTTCGACGAGGCATTCACTGAGTTTACTACGGGTACTGCGGTACTGGGACGCGACGTACGATTACGAGCGTGA AA ACGTA AA AGGTCGSTATGATGAAGGACCTAAGACCTCGCACCTCTGCCCTGACGACAAGGAC										23	1	1.00	1	1	0
*****.(((((((.....(((((((.....((((.....)))).....)))).....)))).....)))).....*****															
..CCGGGTACAGTTAAGTCATAAG.....															

Show Alignment With Reads

Re-alignment of all predicted orthologs

Accession	Coordinate	ID	Alignment
dp5	Xl_groupie:7529509-7529687	dps_2731	CAAGGCCCATGTCAATTCAGTATTCTTCAAACAGCTGCGAAAGCTGCTCCGTAAGTGACT--C-AAA-----TG-AT-----G-----CCCATAGC-----GGCCATGACCTTGG-----CGTGCATGC-----TAATGCCTGGC-----ATCTTTGT-----CAATTTTCCA--GCCATACTCATTCCTGGATTCTGGAGCGTGGAGACGGGACTGCTGTTCTCTG
droPer2	scaffold_13:1018701-1018879_-		CAAGGCCCATGTCAATTCAGTATTCTTCAAACAGCTGCGAAAGCTGCTCCGTAAGTGACT--C-AAA-----TG-AT-----G-----CCCATAGC-----GGCCATGACCTTGG-----CGTGCATGC-----TAATGCCTGGC-----ATCTTTGT-----CAATTTTCCA--GCCATACTCATTCCTGGATTCTGGAGCGTGGAGACGGGACTGCTGTTCTCTG
droW112	scf2_11000000004962:119667-119831_+		CAAGGCCCATGTCAATTCAGTATTCTTCAAACAGCTGCGAAAGCTGCTCCGTAAGTGACT--C-AAA-----TG-AT-----G-----CCCATAGC-----GGCCATGACCTTGG-----CGTGCATGC-----TAATGCCTGGC-----ATCTTTGT-----CAATTTTCCA--GCCATACTCATTCCTGGATTCTGGAGCGTGGAGACGGGACTGCTGTTCTCTG
droVir3	scaffold_12932:502732-502925_-		CAAGGCCCATGTCAATTCAGTATTCTTCAAACAGCTGCGAAAGCTGCTCCGTAAGTGACT--C-AAA-----TG-AT-----G-----CCCATAGC-----GGCCATGACCTTGG-----CGTGCATGC-----TAATGCCTGGC-----ATCTTTGT-----CAATTTTCCA--GCCATACTCATTCCTGGATTCTGGAGCGTGGAGACGGGACTGCTGTTCTCTG
droMoj3	scaffold_6473:1038672-1038840_+		CAAGGCCCATGTCAATTCAGTATTCTTCAAACAGCTGCGAAAGCTGCTCCGTAAGTGACT--C-AAA-----TG-AT-----G-----CCCATAGC-----GGCCATGACCTTGG-----CGTGCATGC-----TAATGCCTGGC-----ATCTTTGT-----CAATTTTCCA--GCCATACTCATTCCTGGATTCTGGAGCGTGGAGACGGGACTGCTGTTCTCTG
droGr12	scaffold_14853:251416-251584_-		CAAGGCCCATGTCAATTCAGTATTCTTCAAACAGCTGCGAAAGCTGCTCCGTAAGTGACT--C-AAA-----TG-AT-----G-----CCCATAGC-----GGCCATGACCTTGG-----CGTGCATGC-----TAATGCCTGGC-----ATCTTTGT-----CAATTTTCCA--GCCATACTCATTCCTGGATTCTGGAGCGTGGAGACGGGACTGCTGTTCTCTG
droAna3	scaffold_13417:2187804-2187980_-		CAAGGCCCATGTCAATTCAGTATTCTTCAAACAGCTGCGAAAGCTGCTCCGTAAGTGACT--C-AAA-----TG-AT-----G-----CCCATAGC-----GGCCATGACCTTGG-----CGTGCATGC-----TAATGCCTGGC-----ATCTTTGT-----CAATTTTCCA--GCCATACTCATTCCTGGATTCTGGAGCGTGGAGACGGGACTGCTGTTCTCTG
droBip1	scf17180000395334:3911-4091_+		CAAGGCCCATGTCAATTCAGTATTCTTCAAACAGCTGCGAAAGCTGCTCCGTAAGTGACT--C-AAA-----TG-AT-----G-----CCCATAGC-----GGCCATGACCTTGG-----CGTGCATGC-----TAATGCCTGGC-----ATCTTTGT-----CAATTTTCCA--GCCATACTCATTCCTGGATTCTGGAGCGTGGAGACGGGACTGCTGTTCTCTG
droKik1	scf17180000302696:505127-505288_+		CAAGGCCCATGTCAATTCAGTATTCTTCAAACAGCTGCGAAAGCTGCTCCGTAAGTGACT--C-AAA-----TG-AT-----G-----CCCATAGC-----GGCCATGACCTTGG-----CGTGCATGC-----TAATGCCTGGC-----ATCTTTGT-----CAATTTTCCA--GCCATACTCATTCCTGGATTCTGGAGCGTGGAGACGGGACTGCTGTTCTCTG
droFic1	scf17180000454073:1934324-1934500_+		CAAGGCCCATGTCAATTCAGTATTCTTCAAACAGCTGCGAAAGCTGCTCCGTAAGTGACT--C-AAA-----TG-AT-----G-----CCCATAGC-----GGCCATGACCTTGG-----CGTGCATGC-----TAATGCCTGGC-----ATCTTTGT-----CAATTTTCCA--GCCATACTCATTCCTGGATTCTGGAGCGTGGAGACGGGACTGCTGTTCTCTG
droLe1	scf17180000491023:691465-691640_+		CAAGGCCCATGTCAATTCAGTATTCTTCAAACAGCTGCGAAAGCTGCTCCGTAAGTGACT--C-AAA-----TG-AT-----G-----CCCATAGC-----GGCCATGACCTTGG-----CGTGCATGC-----TAATGCCTGGC-----ATCTTTGT-----CAATTTTCCA--GCCATACTCATTCCTGGATTCTGGAGCGTGGAGACGGGACTGCTGTTCTCTG
droRho1	scf17180000779944:26189-26368_+		CAAGGCCCATGTCAATTCAGTATTCTTCAAACAGCTGCGAAAGCTGCTCCGTAAGTGACT--C-AAA-----TG-AT-----G-----CCCATAGC-----GGCCATGACCTTGG-----CGTGCATGC-----TAATGCCTGGC-----ATCTTTGT-----CAATTTTCCA--GCCATACTCATTCCTGGATTCTGGAGCGTGGAGACGGGACTGCTGTTCTCTG
droBia1	scf17180000302041:438278-438436_-		CAAGGCCCATGTCAATTCAGTATTCTTCAAACAGCTGCGAAAGCTGCTCCGTAAGTGACT--C-AAA-----TG-AT-----G-----CCCATAGC-----GGCCATGACCTTGG-----CGTGCATGC-----TAATGCCTGGC-----ATCTTTGT-----CAATTTTCCA--GCCATACTCATTCCTGGATTCTGGAGCGTGGAGACGGGACTGCTGTTCTCTG
droTak1	scf17180000414393:145378-145546_+		CAAGGCCCATGTCAATTCAGTATTCTTCAAACAGCTGCGAAAGCTGCTCCGTAAGTGACT--C-AAA-----TG-AT-----G-----CCCATAGC-----GGCCATGACCTTGG-----CGTGCATGC-----TAATGCCTGGC-----ATCTTTGT-----CAATTTTCCA--GCCATACTCATTCCTGGATTCTGGAGCGTGGAGACGGGACTGCTGTTCTCTG
droBug1	scf17180000409230:692229-692388_-		CAAGGCCCATGTCAATTCAGTATTCTTCAAACAGCTGCGAAAGCTGCTCCGTAAGTGACT--C-AAA-----TG-AT-----G-----CCCATAGC-----GGCCATGACCTTGG-----CGTGCATGC-----TAATGCCTGGC-----ATCTTTGT-----CAATTTTCCA--GCCATACTCATTCCTGGATTCTGGAGCGTGGAGACGGGACTGCTGTTCTCTG
dm3	chrX:19650526-19650694_+		CAAGGCCCATGTCAATTCAGTATTCTTCAAACAGCTGCGAAAGCTGCTCCGTAAGTGACT--C-AAA-----TG-AT-----G-----CCCATAGC-----GGCCATGACCTTGG-----CGTGCATGC-----TAATGCCTGGC-----ATCTTTGT-----CAATTTTCCA--GCCATACTCATTCCTGGATTCTGGAGCGTGGAGACGGGACTGCTGTTCTCTG
droSim2	s1:8539691-18539855_+		CAAGGCCCATGTCAATTCAGTATTCTTCAAACAGCTGCGAAAGCTGCTCCGTAAGTGACT--C-AAA-----TG-AT-----G-----CCCATAGC-----GGCCATGACCTTGG-----CGTGCATGC-----TAATGCCTGGC-----ATCTTTGT-----CAATTTTCCA--GCCATACTCATTCCTGGATTCTGGAGCGTGGAGACGGGACTGCTGTTCTCTG
droSec2	scaffold_8:1925534-1925518		CAAGGCCCATGTCAATTCAGTATTCTTCAAACAGCTGCGAAAGCTGCTCCGTAAGTGACT--C-AAA-----TG-AT-----G-----CCCATAGC-----GGCCATGACCTTGG-----CGTGCATGC-----TAATGCCTGGC-----ATCTTTGT-----CAATTTTCCA--GCCATACTCATTCCTGGATTCTGGAGCGTGGAGACGGGACTGCTGTTCTCTG
droYak3	X:11698575-11698732_-		CAAGGCCCATGTCAATTCAGTATTCTTCAAACAGCTGCGAAAGCTGCTCCGTAAGTGACT--C-AAA-----TG-AT-----G-----CCCATAGC-----GGCCATGACCTTGG-----CGTGCATGC-----TAATGCCTGGC-----ATCTTTGT-----CAATTTTCCA--GCCATACTCATTCCTGGATTCTGGAGCGTGGAGACGGGACTGCTGTTCTCTG
droEre2	scaffold_4690:9872298-9872467_+		CAAGGCCCATGTCAATTCAGTATTCTTCAAACAGCTGCGAAAGCTGCTCCGTAAGTGACT--C-AAA-----TG-AT-----G-----CCCATAGC-----GGCCATGACCTTGG-----CGTGCATGC-----TAATGCCTGGC-----ATCTTTGT-----CAATTTTCCA--GCCATACTCATTCCTGGATTCTGGAGCGTGGAGACGGGACTGCTGTTCTCTG

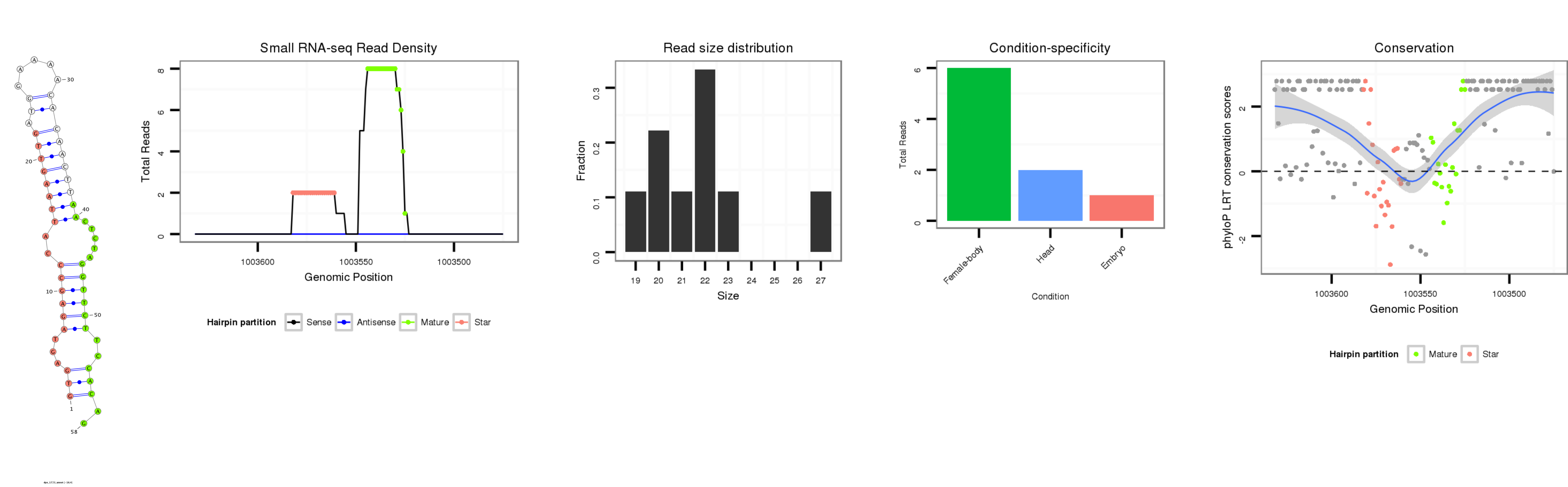
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crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:
dps_1723	4_group5:1003525-1003582 -	confident-exception	Mirtron	intron

Legend: nxtarc star mismatch in alignment mismatch in read

Predicted structure



Show Alternate Folds

Flybase annotation

intron [Dpse/Sema-1a-in]; CDS [Dpse/Sema-1a-cds]; CDS [Dpse/Sema-1a-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

CAAAAGCGAACCGATACGGAATCTGGAAATAGTCCGGACCATGCAATACG	GTGAGTAGAGCCCATTAAGTTGATGGAAAACAACTTAACTCTAGGTTCTTCCACAGATCAACCCAAGGATGGCAGCTACGACGATGGCAAAATTAATCATTGTGTGACA	Read #	Hit	Total		M059	M040	M062	GSM444067	GSM343916	
*****(((...(((...(((...(((...)))))))))...))))))...)).....		size	Mismatch	Count	Norm	Total	embryo	female body	head	head	embryo
.....AACTCTAGGTTCTTCCACAG		21	1	1	13.00	13	4	3	0	4	2
.....ACTTAAGTCTAGGTTCTTCCACAG		25	1	1	4.00	4	3	0	1	0	0
.....TAAGTCTAGGTTCTTCCACAG		20	0	1	2.00	2	0	2	0	0	0
.....ACTTAAGTCTAGGTTCTTCCAC		22	0	1	2.00	2	0	2	0	0	0
.....GTGAGTAGAGCCCATTAAGTTGATGGA		27	0	1	1.00	1	0	0	0	0	1
.....TAAGTCTAGGTTCTTCCACAG		22	1	1	1.00	1	0	0	1	0	0
.....GTGAGTAGAGCCCATTAAGTTG		22	0	1	1.00	1	0	0	0	1	0
.....ACTTAAGTCTAGGTTCTTCCACAG		25	2	1	1.00	1	1	0	0	0	0
.....AACTCTAGGTTCTTCCACAG		21	0	1	1.00	1	1	0	0	0	0
.....TAAGTCTAGGTTCTTCCACAG		22	1	1	1.00	1	1	0	0	0	0
.....ACTTAAGTCTAGGTTCTTCCA		21	0	1	1.00	1	0	1	0	0	0
.....AACTCTAGGTTCTTCCACAG		21	1	1	1.00	1	1	0	0	0	0
.....ACTTAAGTCTAGGTTCTTCCAC		23	0	1	1.00	1	0	1	0	0	0
.....ACTTAAGTCTAGGTTCTTC		19	0	1	1.00	1	0	1	0	0	0
.....CAAGGATGGCAGCTACCG		18	2	8	0.25	2	0	2	0	0	0

Anti-sense strand reads

GTTTTCGCTGGCTATGCCTTAGACCTTTATCAGGCTGGTACGTTATGCCACTCATCTCGGGTAATCAACTACCTTTTGTTGTAATGAGATCCAAAGGTTGTGTAGTTGGGTTCTACCGTCGATGCTGCTACCGTTTAATTAGTAACACTGT															M040	GSM343916	V112
Read #										Hit	Total			female	embryo	male	
size Mismatch Count										Norm	Total			body	body	body	
*****(((.....(((.....(((.....)))))))).....))))..)).*****																	

Show Alignment With Reads

Re-alignment of all predicted orthologs

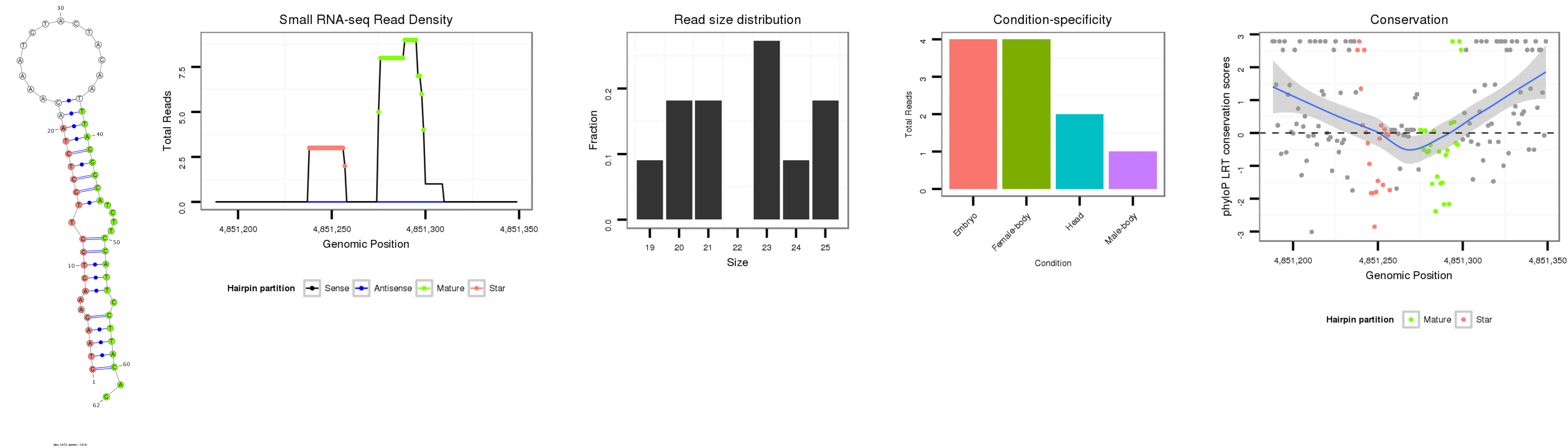
Species	Coordinate	ID	Alignment
dp5	4_group5:1003475-1003632 -	dps_1723	CAAAAGCGAACCGATACGGAATCTGGAAATAGTCCGGACCATGCAATACGCTGAGTAGAGCCCATTAAGTTGATGGAAAACAACTTAACTCTAGGTTCTTCCACAGATCAACCCAAGGATGGCAGCTACGACGATGGCAAAATTAATCATTGTGTGACA
droPer2	scaffold_5:5408890-5409047 -		CAAAAGCGAACCGATACGGAATCTGGAAATAGTCCGGACCATGCAATACGCTGAGTAGAGCCCATTAAGTTGATGGAAAACAACTTAACTCTAGGTTCTTCCACAGATCAACCCAAGGATGGCAGCTACGACGATGGCAAAATTAATCATTGTGTGACA
droW112	scaffold_1100000004884:1093124-1093284 +		CAAAAGCGAACCGATACGGAATCTGGAAATAGTCCGGACCATGCAATACGCTGAGTAGAGCCCATTAAGTTGATGGAAAACAACTTAACTCTAGGTTCTTCCACAGATCAACCCAAGGATGGCAGCTACGACGATGGCAAAATTAATCATTGTGTGACA
droVir3	scaffold_12963:5674688-5674885 -	dvl_10596	CAAAAGCGAACCGATACGGAATCTGGAAATAGTCCGGACCATGCAATACGCTGAGTAGAGCCCATTAAGTTGATGGAAAACAACTTAACTCTAGGTTCTTCCACAGATCAACCCAAGGATGGCAGCTACGACGATGGCAAAATTAATCATTGTGTGACA
droMo3	scaffold_6500:24797732-24797923 -		CAAAAGCGAACCGATACGGAATCTGGAAATAGTCCGGACCATGCAATACGCTGAGTAGAGCCCATTAAGTTGATGGAAAACAACTTAACTCTAGGTTCTTCCACAGATCAACCCAAGGATGGCAGCTACGACGATGGCAAAATTAATCATTGTGTGACA
droG12	scaffold_15252:7777068-7777285 +		CAAAAGCGAACCGATACGGAATCTGGAAATAGTCCGGACCATGCAATACGCTGAGTAGAGCCCATTAAGTTGATGGAAAACAACTTAACTCTAGGTTCTTCCACAGATCAACCCAAGGATGGCAGCTACGACGATGGCAAAATTAATCATTGTGTGACA
droAn3	scaffold_12916:10302953-10303116 +		CAAAAGCGAACCGATACGGAATCTGGAAATAGTCCGGACCATGCAATACGCTGAGTAGAGCCCATTAAGTTGATGGAAAACAACTTAACTCTAGGTTCTTCCACAGATCAACCCAAGGATGGCAGCTACGACGATGGCAAAATTAATCATTGTGTGACA
droB1p1	scaffold_3036769:1170441-1170602 +		CAAAAGCGAACCGATACGGAATCTGGAAATAGTCCGGACCATGCAATACGCTGAGTAGAGCCCATTAAGTTGATGGAAAACAACTTAACTCTAGGTTCTTCCACAGATCAACCCAAGGATGGCAGCTACGACGATGGCAAAATTAATCATTGTGTGACA
droK1k1	scaffold_302412:803457-803632 +		CAAAAGCGAACCGATACGGAATCTGGAAATAGTCCGGACCATGCAATACGCTGAGTAGAGCCCATTAAGTTGATGGAAAACAACTTAACTCTAGGTTCTTCCACAGATCAACCCAAGGATGGCAGCTACGACGATGGCAAAATTAATCATTGTGTGACA
droF1c1	scaffold_00454117:325062-325222 +		CAAAAGCGAACCGATACGGAATCTGGAAATAGTCCGGACCATGCAATACGCTGAGTAGAGCCCATTAAGTTGATGGAAAACAACTTAACTCTAGGTTCTTCCACAGATCAACCCAAGGATGGCAGCTACGACGATGGCAAAATTAATCATTGTGTGACA
droE1e1	scaffold_00491186:1482302-1482467 +		CAAAAGCGAACCGATACGGAATCTGGAAATAGTCCGGACCATGCAATACGCTGAGTAGAGCCCATTAAGTTGATGGAAAACAACTTAACTCTAGGTTCTTCCACAGATCAACCCAAGGATGGCAGCTACGACGATGGCAAAATTAATCATTGTGTGACA
droRh1	scaffold_00779312:198214-198376 -		CAAAAGCGAACCGATACGGAATCTGGAAATAGTCCGGACCATGCAATACGCTGAGTAGAGCCCATTAAGTTGATGGAAAACAACTTAACTCTAGGTTCTTCCACAGATCAACCCAAGGATGGCAGCTACGACGATGGCAAAATTAATCATTGTGTGACA
droB1a1	scaffold_00301518:1130260-1130423 -		CAAAAGCGAACCGATACGGAATCTGGAAATAGTCCGGACCATGCAATACGCTGAGTAGAGCCCATTAAGTTGATGGAAAACAACTTAACTCTAGGTTCTTCCACAGATCAACCCAAGGATGGCAGCTACGACGATGGCAAAATTAATCATTGTGTGACA
droFak1	scaffold_00410803:26754-26912 +		CAAAAGCGAACCGATACGGAATCTGGAAATAGTCCGGACCATGCAATACGCTGAGTAGAGCCCATTAAGTTGATGGAAAACAACTTAACTCTAGGTTCTTCCACAGATCAACCCAAGGATGGCAGCTACGACGATGGCAAAATTAATCATTGTGTGACA
droEug1	scaffold_00409554:857147-857302 -		CAAAAGCGAACCGATACGGAATCTGGAAATAGTCCGGACCATGCAATACGCTGAGTAGAGCCCATTAAGTTGATGGAAAACAACTTAACTCTAGGTTCTTCCACAGATCAACCCAAGGATGGCAGCTACGACGATGGCAAAATTAATCATTGTGTGACA
dm3	chr21:8660525-8660697 +		CAAAAGCGAACCGATACGGAATCTGGAAATAGTCCGGACCATGCAATACGCTGAGTAGAGCCCATTAAGTTGATGGAAAACAACTTAACTCTAGGTTCTTCCACAGATCAACCCAAGGATGGCAGCTACGACGATGGCAAAATTAATCATTGTGTGACA
droS1m2	chr21:8373678-8373846 +		CAAAAGCGAACCGATACGGAATCTGGAAATAGTCCGGACCATGCAATACGCTGAGTAGAGCCCATTAAGTTGATGGAAAACAACTTAACTCTAGGTTCTTCCACAGATCAACCCAAGGATGGCAGCTACGACGATGGCAAAATTAATCATTGTGTGACA
droSec2	scaffold_3:4139995-4140165 +		CAAAAGCGAACCGATACGGAATCTGGAAATAGTCCGGACCATGCAATACGCTGAGTAGAGCCCATTAAGTTGATGGAAAACAACTTAACTCTAGGTTCTTCCACAGATCAACCCAAGGATGGCAGCTACGACGATGGCAAAATTAATCATTGTGTGACA
droYak3	chr21:11304365-11304536 +		CAAAAGCGAACCGATACGGAATCTGGAAATAGTCCGGACCATGCAATACGCTGAGTAGAGCCCATTAAGTTGATGGAAAACAACTTAACTCTAGGTTCTTCCACAGATCAACCCAAGGATGGCAGCTACGACGATGGCAAAATTAATCATTGTGTGACA
droEr2e2	scaffold_4929:9252155-9252316 +		CAAAAGCGAACCGATACGGAATCTGGAAATAGTCCGGACCATGCAATACGCTGAGTAGAGCCCATTAAGTTGATGGAAAACAACTTAACTCTAGGTTCTTCCACAGATCAACCCAAGGATGGCAGCTACGACGATGGCAAAATTAATCATTGTGTGACA

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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.tptop3	1
crit.un	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 annnotation

intron [Dpse\GA16597-in]; CDS [Dpse\GA16597-cds]; CDS [Dpse\GA16597-cds]

Sense Strand Reads

hide 3p reads show mid mismatch reads

[illegible]

Anti-sense strand reads

ATAGACGCTCCTCGCTAAACGATACGAAACCTCTCCCTCTGATAGCAGTGCATTCTTTACCAACGAGATTCTTTTACATGATCTTAAATCCCGTAGAAGGTAAGGAATGTGTGATTTCGACCATTTATATTAGTATAGCGTAAATAGGTGTAGTTGCCTGT	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
dp5	4_group1:4851188-4851349 +	dps_1425	TATCTCGAGGAGCGCAATTGCTATGCTTTGGAGAGGGAGACTATCGTCACGTAAGAAAGT--GGTTGCTCTAAGAAA-ATGTACTAGAATTTAGGGC-----A-TC-TT-CCA-T-TCC--TTACAGAACTAAGCTGGTAATATAATCATATCGCATTATTCCACATCAACGGACA
droPer2	scaffold_5:365746-365907 -		TATCTCGAGGAGCGCAATTGCTATGCTTTGGAGAGGGAGACTATCGTCACGTAAGAAAGT--GGCGCTCTAAGAAA-ATGTACTAGAATTTAGGC-----A-TC-TT-CCA-T-TCC--TTACAGAACTAAGCTGGTAATATAATCATATCGCATTATTCCACATCAACGGACA
droW112	scf2_1100000004521:4472393-4472552 +		TATCTCGAGGAGCGTTTGCATGCTCTGGAGAAAAGACCAATATCAGCTAAGCTCAC---TTGTAGG--CA-TAT-----AACTGAATTCCTATTGATTTCCAATT-TAAT--TTACAGCCCAACTGATTCATTAATCATCTCCATTATTCCACTCAACGGCA
droVir3	scaffold_12963:19703766-19703926 -		TATTGCGACAAAGCCCACTCTTCTGCTAGAGAACGAGAAAGCTGTGACGTGATGACCCACATTGAACTG--AAACATA-AATAAAACCACT-----A--G-CC-A-T-T-GT--TTACAGTCCCGGCTATTAATAACCATATATCGCACTTCAACACACAATGGCA
droMoJ3	scaffold_6500:23499167-23499325 +		TATTACAGCTCGATTCATTCGTCTGCTAGAGATGAGAACTGCTGACGACGCA--TCAG--TTTA--AA-TATA-AATAAACCTCTCTCT-----A--ATTC-A-TTT-A-TT--TTTAGACCAACATTCGGTAATACAAATATCTGACACTTCAATAGCCCATGGCA
droGr12	scaffold_15252:11169008-11169165 -		TATTGCGACAAAGCCGAGCCGCTGCTGCTAGAACCCAGAAATTAATAAGTCACTTTT--TTTGTG-----CA-ATTTC-AATAA-----AA-ACAACCTAAATTTT--TATCTA-T-TT--CCTAGTTACGTTCTGGTAAATACCATATATCGCACTTCTGCACACAATGGCA
droAna3	scaffold_12916:4466234-4466391 +		TATCTCGAGGAAAGATTTCCTCTCTCTAGGAACCGAGCTCATATGTACGTAACTTAC--GAATCATATA--ACCTTA-----AAGCAGCTCTTATT-T--CAAGTA-T-TTCCGTAGCGCCAACTCTCTAATCTATAATCTGACATTGTCCACATCAAGGGTA
droBiP1	scf7180000396737:318841-318997 -		TATCTGCAAGACGATTCTCTATCTAAAGGAATATGAATCATATGTACGTAAAGTAA--GAACCTATCT--CCATTATA-----AATATAT--ATT--TTTAA-ATT-A-TTCCGTAGCGCCAACTCTGTAATCTATAATCTGACATTGTCCACATCAAGGGTA
droKik1	scf7180000320643:268258-268432 -		TACTGTCAGGAAGATTGCGCATCTCTGGAGAGGGAGAGCACTGTACGTAAGCATTG--CACCTGTATA--A--GAG--ACCTAAAGCTGTCTTTTTTTGAGATTTTGGACT-TCTAA--T-C-A-ATT-TCTAGACCCAACTGCTGTAATCTGCGCATCTCCACTCCAGGGCA
droFic1	scf7180000453842:700985-701144 -		TATTGCAAGAAAGATTTCGCGCTCTCTGGAACAGAAATCTATGTACGTAGCTAAAG--ATGAATTTT--AA-ATT-----AACAGATATTAAATAC--TTATT--AAT-C-TT--TTACAGCCCAACTCTCTAATCTATAATCTGACATTATCCACATCTAGGGCA
droEle1	scf7180000491338:394205-394353 +		TATTGCAAGAAAGATTTCGCGCTCTCTGGAACAGGAACATATGTACGTATGCGCA--CA-TTG--CA-TTT-----AGCAGATTTTAAAT--ATTG----AGT-TTTAGACCCCACTGCTGTAATCTATAATCTGCGATTATCCACATCTAGGGCA
droRho1	scf7180000780102:23129-23289 +		TATCTGCAAGAAAGATTTCGCTCTCTCTGGAAGGGAACCATGTAACTGAGCTTGCA--CATTTCTATA--AA-ATT-----AACAGAAATTAATAG--TCCCTT--ATT-TGTA-T-TTAGACCCCACTGCTGTAACCTATAATATCGCATTATCCACATCTAGGGCA
droBia1	scf7180000320242:6879459-6879620 +		TATCTCGAGGAAAGATTTCGCTCTCTCTGGAACGGGAGCTCATGTAACTGAGCTTATA--CTTTTATCTC--CA-ATT-----AATAATATTTAAACC--AGCC--AACAAATG-A-TT-TAGACCCCGCTGCTGTAACCTATAATATCGCATTATCCACATCTAGGGCA
droTak1	scf7180000415708:206495-206656 +		TATCTCGAGGAGGCAATTGCTGTGCTGCGGAAGGGAACGACGCTGACGTATGTTTCTCTATA--CAATTA-----AACATACTTTAATCT-AGTC-A-ATT-T-TA-T-GTTAGTCCCACTGCTGTAACCTATAATATCGCATTATCCACATCTAGGGCA
droEug1	scf7180000409767:85548-85708 +		TATCTCGAGGAAAGATTGCTGCTCTCTCTAGAGAAAGATCATCTGTAACGTAGCTTTC--ACTTCTCTG--TC-ACC-T-----AACAGATTTAAAT--TCTTAA-ATA-T-TAT-TTAGACCCCACTGTAACCTATAATATCGCATTATCCACATCTAGGGCA
dm3	chr21:5533693-5533852 +		TATCTCGAGGAGGATTGCTGCTCTCTCTAGGAACGGGAACCATGTAACTGAGCTTATA--TCAATGCTTA--GA-ATCT-----CAAGGATTATAAGAG--TCTCC--TTG-A-GT-TTTCAGACCCCACTGCTGTAACCTATAATATCGCATTATCCACATCTAGGGCA
droSim2	21:5338805-5338963 +		TATCTCGAGGAGGATTGCTGCTCTCTCTAGGAACGGGAGCTCATGTAACTGAGCTTATA--CAATGCTAG--G-ATCT-----CAAGGATTATAAGC--ACCC-ATC-A-TT-TTTCAGACCACTGCTGTAACCTATAATATCGCATTATCCACATCTAGGGCA
droFas3	chr16:10304875-10305232 +		TATCTCGAGGAGGATTGCTGCTCTCTCTAGGAACGGGAGCTCATGTAACTGAGCTTATA--CAATGCTAG--G-ATCT-----CAAGGATTATAAGC--TCTCC--TAT-A-CAT-TTTCAGACCACTGCTGTAACCTATAATATCGCATTATCCACATCTAGGGCA
droEre2	scaffold_4929:5619966-5620125 +		TATCTCGAGGAGGATTGCTGCTCTCTCTAGGAACGGGAGCTCATGTAACTGAGCTTATA--CAATGCTAG--G-ATCT-----AAAAGATTATAAAG--CTTCC--TAT-A-CAT-TTTCAGACCCCACTGTAACCTATAATATCGCATTATCCACATCTAGGGCA

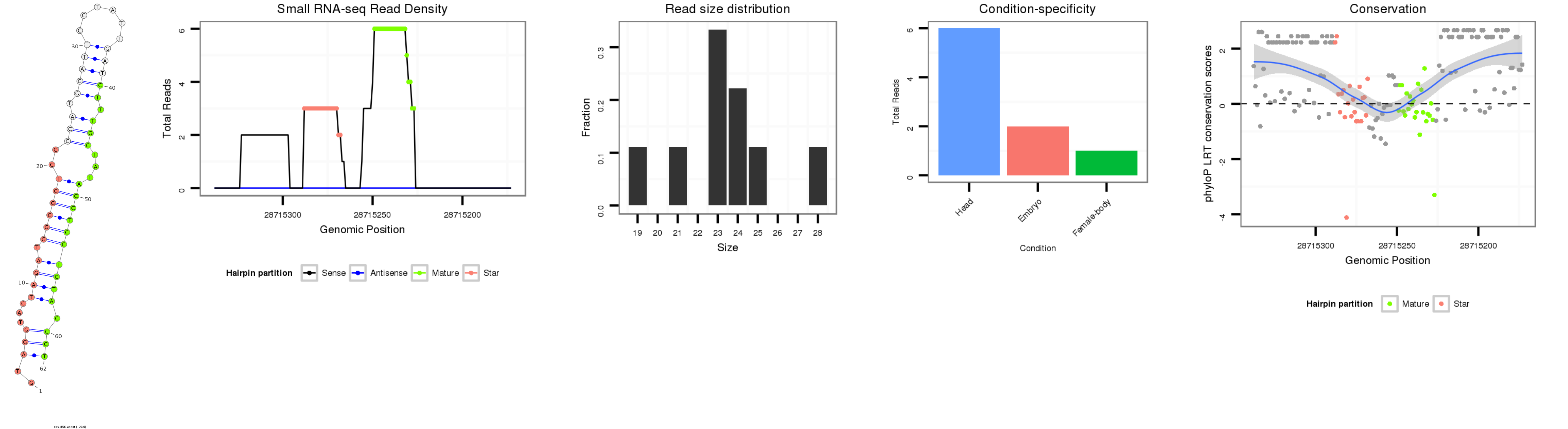
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crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dps_856	2:28715223-28715288	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 [Dpse/GA20257-in]; CDS [Dpse/GA20257-cds]; CDS [Dpse/GA20257-cds]; utr3 [utr3_minus_8032]; utr3 [utr3_minus_8031]; utr5 [utr5_minus_9370]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

	Read #	Read size	Mismatch	Hit	Count	Total	Norm	Total	M062	M040	GSM444067	M059	SRR902012	M022	V112
									head	female body	head	embryo	CNS imaginal disc	male body	male body
TTCTCTATTTCGGGCTCGGACGCTGTGATCTTAATGGACGGCTGCTTGAGGTAGGTACTAGATGGGGTCCCATGGATTTCGATTGATCTTTGGTATACCTCCTCTACCCCTAAAGGTGACGCTGTGGGACTATGTGCGCTATGGGGCCAACGATTTCATCGGGCA	23	0	1	2.00	2	1	0	0	1	0	0	1	0	0	0
*****..(((...(((.(.((((((.(.(((((.))))))..)))..))))))..)))*****	27	0	1	2.00	2	0	0	0	0	0	0	0	2	0	0
.....TGCACGCTGTGATCTTAATGGACGCGC.....CTTGGTATACCTCCTCTACCCCT.....	24	0	1	1.00	1	0	0	0	1	0	0	1	0	0	0
.....GTAGGTACTAGATGGGGGTCC.....TCTTTGGTATACCTCCTCTACCCCT.....	21	0	1	1.00	1	0	0	1	0	0	1	0	0	0	0
.....GTAGGTACTAGATGGGGGTCC.....ATTGATCTTTGGTATACCTCCTCT.....	24	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....GTAGGTACTAGATGGGGGTCC.....TATTGATCTTTGGTATACCTCCTCTACCCCT.....	23	0	1	1.00	1	0	1	0	0	0	0	0	0	0	0
.....GTAGGTACTAGATGGGGGTCC.....TATTGATCTTTGGTATACCTCCTCTACCCCT.....	28	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....GTAGGTACTAGATGGGGGTCC.....TATTGATCTTTGGTATACCTCCTCTACCCCT.....	19	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....GTAGGTACTAGATGGGGGTCC.....TATTGATCTTTGGTATACCTCCTCTACCCCT.....	25	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....GTAGGTACTAGATGGGGGTCC.....TATTGATCTTTGGTATACCTCCTCTACCCCT.....	19	2	2	0.50	1	0	1	0	0	1	0	0	0	0	0

Anti-sense strand reads

	Read #	Read size	Mismatch	Hit	Count	Total	Norm	Total	M040
									female body
AAGAGATAAGCCAGACGCTGCGACACTAGAAATTACCTGCCGACGAACCTCATTCCATGATCTACCCCCAGGGGTACCTAAGCATAACTAGAAACCATATGGAGGAGATGGGATTTCCACTGCGACACCCGTGATACACGCGATACCCCGGTTGCTAAAGTAGCCGCT									
*****..(((...(((.(.((((((.(.(((((.))))))..)))..))))))..)))*****									

Show Alignment With Reads

Re-alignment of all predicted orthologs

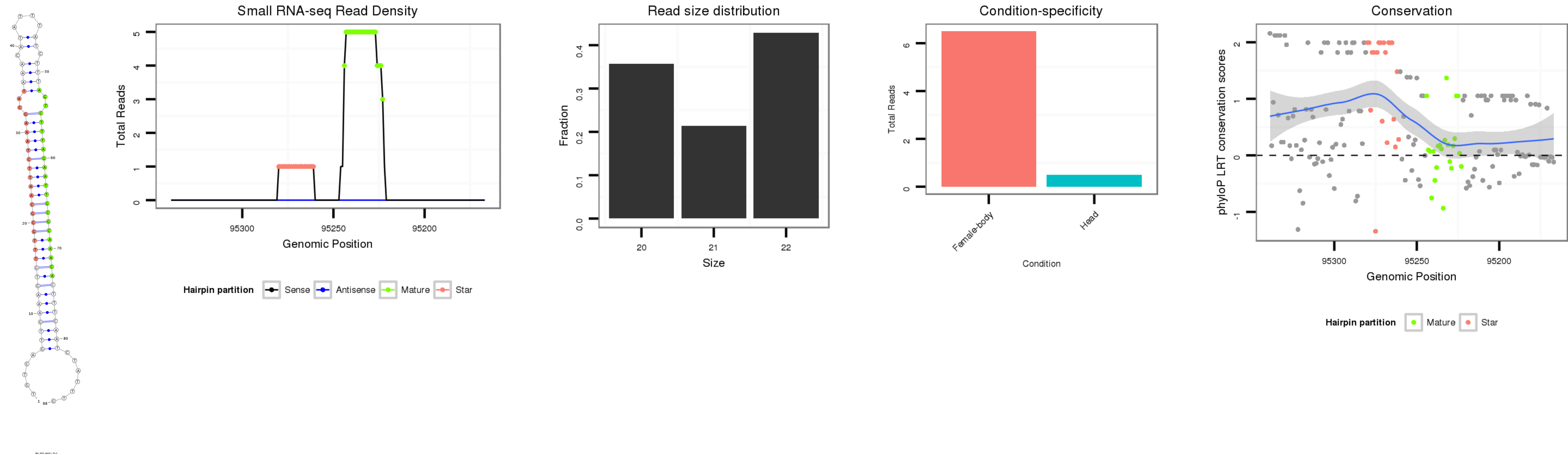
Species	Coordinate	ID	Alignment
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droPer2	scaffold_6:4047186-4047351 -	dpe_2489	TTCTCTATTTCGGGCTCGGACGCTGTGATCTTAATGGACGGCTGCTTGAGGTAGGTACT--AG-----ATGGGG-----TATTGATCTTTGGTA--TACC--TCCTCT-----ACCCAAAGGTGACGCTGTGGGACTATGTGCGCTATGGGGCCAACGATTTCATCGGGCA
droW112	scf2_1100000004902:4958392-4958551 +		TTCTCTATTTCGGGCTCGGACGCTGTGATCTTAATGGACGGCTGCTTGAGGTAGGTACT--AG-----ATGGGG-----TATTGATCTTTGGTA--TACC--TCCTCT-----ACCCAAAGGTGACGCTGTGGGACTATGTGCGCTATGGGGCCAACGATTTCATCGGGCA
droV1r3	scaffold_13047:6995746-6995825 +		TTCTCTATTTCGGGCTCGGACGCTGTGATCTTAATGGACGGCTGCTTGAGGTAGGTACT--AG-----ATGGGG-----TATTGATCTTTGGTA--TACC--TCCTCT-----ACCCAAAGGTGACGCTGTGGGACTATGTGCGCTATGGGGCCAACGATTTCATCGGGCA
droMoJ3	scaffold_6540:2882016-2882083 +		TTCTCTATTTCGGGCTCGGACGCTGTGATCTTAATGGACGGCTGCTTGAGGTAGGTACT--AG-----ATGGGG-----TATTGATCTTTGGTA--TACC--TCCTCT-----ACCCAAAGGTGACGCTGTGGGACTATGTGCGCTATGGGGCCAACGATTTCATCGGGCA
droGr12	scaffold_14830:2870480-2870531 +		TTCTCTATTTCGGGCTCGGACGCTGTGATCTTAATGGACGGCTGCTTGAGGTAGGTACT--AG-----ATGGGG-----TATTGATCTTTGGTA--TACC--TCCTCT-----ACCCAAAGGTGACGCTGTGGGACTATGTGCGCTATGGGGCCAACGATTTCATCGGGCA
droAna3	scaffold_13340:11996458-11996616 +		TTCTCTATTTCGGGCTCGGACGCTGTGATCTTAATGGACGGCTGCTTGAGGTAGGTACT--AG-----ATGGGG-----TATTGATCTTTGGTA--TACC--TCCTCT-----ACCCAAAGGTGACGCTGTGGGACTATGTGCGCTATGGGGCCAACGATTTCATCGGGCA
droBip1	scf718000039691:884694-884852 +		TTCTCTATTTCGGGCTCGGACGCTGTGATCTTAATGGACGGCTGCTTGAGGTAGGTACT--AG-----ATGGGG-----TATTGATCTTTGGTA--TACC--TCCTCT-----ACCCAAAGGTGACGCTGTGGGACTATGTGCGCTATGGGGCCAACGATTTCATCGGGCA
droK1k1	scf7180000302809:586254-586419 +		TTCTCTATTTCGGGCTCGGACGCTGTGATCTTAATGGACGGCTGCTTGAGGTAGGTACT--AG-----ATGGGG-----TATTGATCTTTGGTA--TACC--TCCTCT-----ACCCAAAGGTGACGCTGTGGGACTATGTGCGCTATGGGGCCAACGATTTCATCGGGCA
droF1c1	scf7180000453800:197185-197351 -		TTCTCTATTTCGGGCTCGGACGCTGTGATCTTAATGGACGGCTGCTTGAGGTAGGTACT--AG-----ATGGGG-----TATTGATCTTTGGTA--TACC--TCCTCT-----ACCCAAAGGTGACGCTGTGGGACTATGTGCGCTATGGGGCCAACGATTTCATCGGGCA
droE1e1	scf7180000491008:2552501-2552670 +		TTCTCTATTTCGGGCTCGGACGCTGTGATCTTAATGGACGGCTGCTTGAGGTAGGTACT--AG-----ATGGGG-----TATTGATCTTTGGTA--TACC--TCCTCT-----ACCCAAAGGTGACGCTGTGGGACTATGTGCGCTATGGGGCCAACGATTTCATCGGGCA
droRho1	scf7180000777406:3803-3956 -		TTCTCTATTTCGGGCTCGGACGCTGTGATCTTAATGGACGGCTGCTTGAGGTAGGTACT--AG-----ATGGGG-----TATTGATCTTTGGTA--TACC--TCCTCT-----ACCCAAAGGTGACGCTGTGGGACTATGTGCGCTATGGGGCCAACGATTTCATCGGGCA
droB1a1	scf7180000302113:3690220-3690378 +		TTCTCTATTTCGGGCTCGGACGCTGTGATCTTAATGGACGGCTGCTTGAGGTAGGTACT--AG-----ATGGGG-----TATTGATCTTTGGTA--TACC--TCCTCT-----ACCCAAAGGTGACGCTGTGGGACTATGTGCGCTATGGGGCCAACGATTTCATCGGGCA
droTak1	scf7180000415417:666167-666324 -		TTCTCTATTTCGGGCTCGGACGCTGTGATCTTAATGGACGGCTGCTTGAGGTAGGTACT--AG-----ATGGGG-----TATTGATCTTTGGTA--TACC--TCCTCT-----ACCCAAAGGTGACGCTGTGGGACTATGTGCGCTATGGGGCCAACGATTTCATCGGGCA
droEug1	scf7180000409246:62340-62502 -		TTCTCTATTTCGGGCTCGGACGCTGTGATCTTAATGGACGGCTGCTTGAGGTAGGTACT--AG-----ATGGGG-----TATTGATCTTTGGTA--TACC--TCCTCT-----ACCCAAAGGTGACGCTGTGGGACTATGTGCGCTATGGGGCCAACGATTTCATCGGGCA
dm3	chr3R:13716268-13716432 -		TTCTCTATTTCGGGCTCGGACGCTGTGATCTTAATGGACGGCTGCTTGAGGTAGGTACT--AG-----ATGGGG-----TATTGATCTTTGGTA--TACC--TCCTCT-----ACCCAAAGGTGACGCTGTGGGACTATGTGCGCTATGGGGCCAACGATTTCATCGGGCA
droSim2	3r:7551026-7551189 +		TTCTCTATTTCGGGCTCGGACGCTGTGATCTTAATGGACGGCTGCTTGAGGTAGGTACT--AG-----ATGGGG-----TATTGATCTTTGGTA--TACC--TCCTCT-----ACCCAAAGGTGACGCTGTGGGACTATGTGCGCTATGGGGCCAACGATTTCATCGGGCA
droYak3	v2 chr3R_random_203:1002-1058 -		TTCTCTATTTCGGGCTCGGACGCTGTGATCTTAATGGACGGCTGCTTGAGGTAGGTACT--AG-----ATGGGG-----TATTGATCTTTGGTA--TACC--TCCTCT-----ACCCAAAGGTGACGCTGTGGGACTATGTGCGCTATGGGGCCAACGATTTCATCGGGCA
droBre2	scaffold_4770:7908850-7909019 +		TTCTCTATTTCGGGCTCGGACGCTGTGATCTTAATGGACGGCTGCTTGAGGTAGGTACT--AG-----ATGGGG-----TATTGATCTTTGGTA--TACC--TCCTCT-----ACCCAAAGGTGACGCTGTGGGACTATGTGCGCTATGGGGCCAACGATTTCATCGGGCA

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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.top3	1
crit.uri	0
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

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
dp5	XR_group6:95167-95339 -	dps_3611	TAATTCATTTTG-AAGTGGG-----AATAAAAGAAAAGCAACACCGC--ACTGTCA--GTTGA--AAGTGTTCGGCGA-ATTCTAAAGCATAAACATA--TTTA-----TCTTTAGTCTTTAGAATTGCG--CAAAACACTTC-----AATCTATTTGGATTCCA-GGAGAATCTTGG-----GCTTGACATTTCAAATGCCTC-
droPer2	scaffold12_12:771663-771835 -		TAATTCATTTTG-AAGTGGG-----AATAAAAGAAAAGCAACACCGC--ACTGTCA--GTTGA--AAGTGTTCGGCGA-ATTCTAAAGCATAAACATA--TTTA-----TCTTTAGTCTTTAGAATTGCG--CAAAACACTTC-----AATCTATTTGGATTCCG-GGAGAATCTTGGGCTTGACATTTAAANAACCTC-----
droVir3	scaffold_13049:22356252-22356391 -		TCATTCAACCTTTGTCTCATAAAAACGAGTAGAACGTTAATAAAAGCCATCTAAATACAC--AGCSTCCGTGTTTC-CGAATAATGTTTGTCAC-ACCTCAAAGCTAACGATA--AATAATTTCAAACCTC-----AATATTTAAG--CA-----
droMo3	scaffold6_6540:19196384-19196393 +		TAATTAATTT-----
droKik1	scf7180000302686:1069487-1069569 -		TCATTCAACCTTTGAGTTGA-----AATAAAAGCCGGTAAATTAACGAGAAAGCSTCA--GTTAGCGATGATGTTTGCCCAACTCTAAAG-----
droFic1	scf7180000454065:1622372-1622449 -		TCATTCAACCTTTGCGTCTC-----GGTAAATCCCAAGCTAAATTAACGC--AGCSTCA--GTTGA--AAATGTTTGTCGAACCTCTAAAG-----
droEle1	scf7180000491000:1112871-1113095 +		TCATTCAACCTTTGAAACA-----GTAACTGTCACAGCAATTAATTAAC--AGCATCA--GTTGC--AAGTGTTCGCCAAAGCTCTAAAGCAATGATA--ATAATATCGCGAGCA--AAATTCACGCGTGCTAATT--AAATACTCCACAACTAACACTGGAGTAAACAAATTTGAGGCA--GTTGTGCGCTTTAAAGAATCTCGG--CAAAAGCATAAATTAACATTTTATGGAATCTC
droRho1	scf7180000779347:39882-39958 -		TCATTCAACCTTTGAGTTAA-----GGCAAAATCCCAAGCTAAATTAACCT--AGCATCA--GTTGC--AAATGTTGCGTCAACTCTAAAG-----
droBial	scf7180000302334:693997-694073 -		TCATTCAACCTTTGAGTTAA-----GGTAAATCCCAAGCTAAATTAACGC--AGCSTCA--GTTGC--AAATGTTTGTCGAACCTCTAAAG-----
droTak1	scf7180000415268:93449-93530 +		TCATTCAACCTTTGAGTTAA-----GGTAAATCCCAAGCTAAATTAACGC--AGCSTCA--GTTCA--AAATGTTTGTCGAACCTCTAAAGCAATA-----
droEug1	scf7180000408844:422472-422688 +		TCATTCAACCTTTCCCTTGA-----GCTGAGATCCCAAGCTAAACAGCC--AGCSTCA--GTTGC--AAATGTTTGCCCAACTCTAAAGCAATA--GATA--AAATACTTAGCGGGTTGCGGGTTTACTCAGGCCTTATACGAGTAGGTGATCAGCTGACACGTGGGGCAAAACAATTCGGAGGCAACATGATGCCCTTTATATAAGAATCTTGA-TAAAACATAAATAAC
dm3	chr3L:15687575-15687800 +		TCATTCAACCTTTGAGTTAG-----GGCAATTAATAAGCAAAATTAACGC--AGCTTCA--GTTGC--AAATGTTTGTCGAACCTCTAAAGCAATA--AAATAAACAATCCGCGGTTG--AATTTAACGCAAGCTATATA--AAAGAGTCCACAGCTGACACGGGTGGTAACAAATTTGGTGGCA--CTGATGCCCTTATATAAGAATCTCGG--CAAAGCATAAATAACATTTCAATGGAATCTC
droSim2	3L:15318299-15318522 +		TCATTCAACCTTTGAGTTAG-----GGCAATCCCAAGCAAAACACGC--AGCTTCA--GTTGC--AAATGTTTGTCGAACCTCTAAAGCAATA--AACAATCCGCGGTTG--AATTTAACGCAAGCTATATA--AAAGAGTCCACAGCTGACACGGGTGATAACAAATTTGAGGCA--CTGATGCCCTTATATAAGAATCTCGG--CAAAGCATAAATAACATTTCAATGGAATCTC
droSec2	scaffold_0:7798994-7799079 +		TCATTCAACCTTTGAGTTAG-----GGCAATCCCAAGCAAAACACGC--AGCTTCA--GTTGC--AAATGTTTGTCGAACCTCTAAAGCAATA--GATA-----
droYak3	v2_chr3L_random_094:73825-73900 +		TCATTCAACCTTTAAGTTGG-----GGTAATCAACAAGCAAAATGGCGC--AGCTTCA--GTTCA--AAATGTTTGCCCAACTCTAAAG-----
droEre2	scaffold4_4784:17944769-17944833 +		TCATTCAACCTTTGAGTTGA-----GTAAATTCGAAGCAAAATTAACGC--AGCTTCA--GTTCA--AAATGTTTGCCCAACTCTAAAG-----

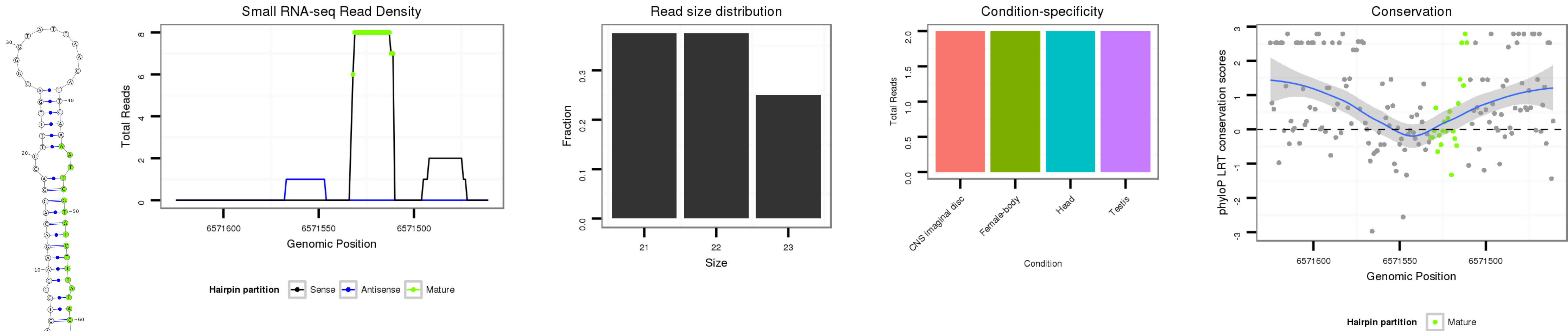
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	PASS/FAIL
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crit.mor	0
crit.half	0
crit.total	0
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crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	1
rescue.known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

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dps_1056	3:6571511-6571575 -	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 [Dpse'GA20985-in]; CDS [Dpse'GA20985-cds]; CDS [Dpse'GA20985-cds]

No Repeatable elements found

Sense Strand Reads

[hide 3p reads](#) [show mid mismatch reads](#)

Read #	size	Mismatch	Hit Count	Norm	Total	M040 female body	SRR902011 testis	SRR902012 CNS imaginal disc	GSM343916 embryo	GSM444067 head	M062 head
22	0	1	3.00	3	0	2	0	0	0	1	0
23	0	1	2.00	2	0	0	2	0	0	0	0
21	0	1	2.00	2	2	0	0	0	0	0	0
23	0	1	1.00	1	0	0	0	1	0	0	0
21	0	1	1.00	1	0	0	0	0	1	0	0
18	0	1	1.00	1	1	0	0	0	0	0	0
22	1	1	1.00	1	1	0	0	0	0	0	0

Anti-sense strand reads

Read #	size	Mismatch	Hit Count	Norm	Total	M040 female body	V112 male body
21	0	1	1.00	1	1	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
dp5	3:6571461-6571625 -	dps_1056	GTGCCAGGTGTGACGCCACCCTCGCCCTTTTCGCCCGTTCGAAACAGCGGTAAGTG-----GGA-----AGACACGACCTTTGAGGGGTAT--TAACATTGAA AATTC ---GTGT-C-TTTATACTGCAG GTTC CG-TG--AGCAGAAGAGTGCCTCGCTTCACCTTGGGCTATCTGTGCGCTC
droPer2	scaffold_2:6792316-6792480 -		GTGCCAGGTGTGACGCCACCCTCGCCCTTTTCGCCCGTTCGAAACAGCGGTAAGTG-----GG-----GAGACACGACCTTTGAGGGGTAT--TAACATTGAA AATTC ---GTGT-C-TTTATA TGCACT TTCCG-TG--AGCAGAAGAGTGCCTCGCTTCACCTTGGGCTATCTGTGCGCTC
droWil2	scf2_1100000004513:5763932-5764089 -		GAGCCGGCATTAACTCCGATCGCCCTTC CGAAGGAAACAAAGGTAA -----GTAGAGGC-TTA-----AAGAACTAATTATTCTTACTCATCAT-----T-----T---TC-T-C-TGACATT TGCACT ATCT CAACGGCA AA AAAGGCATT TCATGCACCTTAAAT CACTG SG GGCT
droVir3	scaffold_12875:8582749-8582904 -		GTGCCAGCGCT TCGAT CCACG AC GGCCCTTTTCGCC TCGCT TAAG CAG CGGTAAGT T -----AA T -----A-AATAT ACT AGCAC TTT SGT TCCT TTTAA T -----GA-G-C-T TCGCT TGCAG ATCT CG-TG--TAAGGAGCT---SAG GTCT CA GGTG AACTATTTGTGCGCGC
droMoJ3	scaffold_6496:18624360-18624520 +		CGCCAGCGCT TT CGCCAC GAA CA CCAT TC CA CGCGCG CAAC CAACGGTAAGT T -----CA A -----ATG-----CGCAATTAAG AAAT ---CAATATT TCCTT -HGCTACAA-G-GCG TCCT TGCAG CT CTCG-TG--AAA CA AA T ---CTCA AT CA GGTCA AACTATTTCTGTGCTC
droGri2	scaffold_15245:1991981-1992149 -		GT TC CGCACT TCAT CC TCAG CA CCAT TC CG CC CA GGTTCC AAG CAGCGGTAAGT TTGC --CTTAAGCCT TAA AGATT AACT AA TTATT TCG AAAT --TATTAT-----G-G- TTTTC TTA GCAC CTATCG-TG--AGAAG CTCA SG TT ---TC CA CG TAA CTATTT AA TTGG CT
droAna3	scaffold_13266:2702231-2702391 -		GT TC CGCA GTGA ATCCACCTCGCCCTTC CACT CA AG CTC CAAG ACGGGT CAGAC -----AA T -----ATTAAATTA TTCCGA - TTGG CA T ---CAATATTA A ---BAT---ACTT-C-T TTG T TGCAG GC CA CA GG --ATGAGAAG ACT CT CT ACT CACTTCA SGCTATTTGTGT GGCC
droBip1	scf7180000396427:1194437-1194597 -		GTGCC CG ATGA AT CCACCTCGCCCTTC CAG CT CC TC CAAC CAACGGGT CAGT C -----AC C -----GGTATTAT CTCCAA - CAGG CA T ---C AC ATTAA A ---PAT---ACTT-C-T TTGCT TGCAG ACA CA CG --ATGAGAAG ACT CT CT ACT CACTTCA SGCTATTTGTGT GGCC
droKik1	scf7180000302682:1147938-1148106 -		GTGCC CG GTGA AT CC CC CTCGCCCTTT CG CC CA GGTTCC CAAG ACGGGT CAG SACCGACCCCA -----AAGACACT SACCTTAT CG CA TT CGT TA T TAAC TA -----AT---TT-G-CT TTCA ATT TGCAG TTTCCG-TG--ATGAGAAG TCA SGCTCGCT CACTTGGGCTA CTTGTGCG CC
droFic1	scf7180000453809:314040-314202 +		GTGCC CG CT CAAT CC CC CTCGCCCTTC CG CC CG GGTTCC CAAG ACGGGT TAAC CA -----CA A -----G CA ACT SACCTTT CA TT GG CCCTAT TAACATTGA---T TC ---TT-C-TTT ATA T GA CTTTCCG-CG--AGCAGAAG GCTGC CTCGCT CA TTTGGGCT CT TGTGT GGCC
droEle1	scf7180000491214:3446546-3446708 +		GTGCC CG CT CAAT CC CC CTCGCCCTTC CG CC CG GGTTCC CAAG ACGGGT TAAC CA -----CC C -----GG CTCT SACCTTTT ATTAT TA ATAC CTATATTG-----C---TT-T-C-CT CA ATT TGCAG TTTCCG-TG--AGCAGAAG ACC CGCTCGCT CACTTGGGCTAT TTGTGT GGCC
droRho1	scf7180000779932:351721-351883 +		GTGCC CG CT CAAT CC CC CTCGCCCTTC CA CGCC CG GGTTCC CAAG ACGGGT TAAC CA -----CA A -----GAGCA TT CGCTTT CATTAT CTAT TAT CT CA TATTAT-----C---TT-T-T-CT CA ATT TGCAG TTTCCG-CG--AGCAGAAG ACC CGCTCGCT CACTTGGGCTAT TTGTGT GGCTC
droBia1	scf7180000302292:729235-729400 +		GTGCC CG CT CAAC CC CC CGCCCTTC CA CGCC CG GGTTCC CAAG ACGGGT TAAC CA -----CT C -----GAGAA TT ACCTTT CATT GG CCAT CACCCACATTGT---TTT---TC-CGT-T CA ATT TGCAG TTTCCG-CG--AGCAGAAG ACC CGCTCGCT CACTTGGGCTA CTTGTGCG CC
droTak1	scf7180000415820:330499-330657 +		GTGCC CG CT CAAT CC CC CTCGCCCTTC CG CC CG GGTTCC CAAG ACGGGT TAAC CA -----CT C -----GAGAA TT ACCTT CCATAT TC CA CC CTCA CT CA CT-----G---A-TAT TC CA TTGCAG TTTCCG-CG--ATGAGAAG ACC CGCTCGCT CACTTGGGCTA CTTGTGCG CC
droEug1	scf7180000409462:550094-550256 -		GTGCC CG CT CAAT CC CC CTCGCCCTTC CG CC CG GGTTCC CAAG ACGGGT TAAC CA -----CT T -----CAGAA TT SACCTTTT ATT GT CTAT GTGTATTGTT-----T---TT-T-C-CT CA ATT TGCAG TTTCCG-CG--ATGAGAAG ACC CGCTCGCT CACTTGGGCTA CTTGTGT GGCTC
dm3	chr2R:7923166-7923330 +		GTGCC CG CT CAAT CC CC CTCGCCCTTT AC CGCC CG GGTTCC CAAG ACGGGT TAAC CA -----CT G -----GG CA AT TC ACCTTT AA TTAT TCAT TAACAT CA ---G C ---TT TA CT CA ATT TGCAG TTTCCG-CG--AGCAGAAG CTGC CTCG CTCA CTTGGGCT CT TGTGCG CC
droSim2	2r:8626763-8626927 +		GTGCC CG CT CAAT CC CC CTCGCCCTTT AC CGCC CG GGTTCC CAAG ACGGGT TAAC CA -----CT G -----GG CA AT TC ACCTTT AA TTAT TCAT TAACAT CA ---G C ---TT TA CT CA ATT TGCAG TTTCCG-CG--AGCAGAAG CTGC CTCG CTCA CTTGGGCT CT TGTGCG CC
gflyBak3	2L:919194-919246-919272 +		GTGCC CG CT CAAC CC CC CTCGCCCTTT AC CGCC CG GGTTCC CAAG ACGGGT TAAC CA -----CT G -----GG CA AT TC ACCTTT AA TTAT TCAT TAACAT CA ---G C ---TT TA CT CA ATT TGCAG TTTCCG-CG--AGCAGAAG CTGC CTCG CTCA CTTGGGCT CT TGTGCG CC
droEre2	scaffold_4845:17872909-17873074 -		GTGCC CG CT ATAT CC CC CTCGCCCTTT AC CGCC CG GGTTCC CAAG ACGGGT TAAC CA -----TA A -----TGAA AT CCCTTT AA GT CTCA TATTAACAT GAA ---G C ---TT TA CT CA ATT TGCAG TTTCCG-CG--ATGAGAAG ACC CGCTCGCT CACTTGGGCTA CTTATGCG CTG

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

	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	8