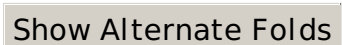


Predicted structure



Flybase annotation

intron [Dper¹GL17383-in]; CDS [Dper¹GL17383-cds]; CDS [Dper¹GL17383-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	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	2
rescue.candidate	0

Flybase annotation

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

Anti-sense strand reads

Show Alignment With Reads

Re-alignment of all predicted orthologs

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

Legend: mature star mismatch in alignment mismatch in read

Small RNA-seq read density

The left panel displays a schematic of the hairpin partition (left) and a line plot of total reads (y-axis, 0 to 1500) versus genomic position (x-axis, 375200 to 375050). The hairpin partition is a circular structure with 87 nucleotides, numbered 1 to 87. The line plot shows the total reads for four categories: Sense (black line), Antisense (blue line), Mature (green line), and Star (red line). The Mature reads show a sharp peak around 375150, while the Star reads show a smaller peak around 375100.

Read size distribution

The right panel displays a histogram of the read size distribution. The x-axis represents the size (18 to 25) and the y-axis represents the fraction (0.0 to 0.5). The distribution is unimodal, peaking at size 22 with a fraction of approximately 0.48.

No Repeatable elements found

hide 3p reads show mid mismatch reads

Anti-sense strand reads

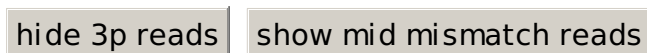
Show Alignment With Reads

Re-alignment of all predicted orthologs

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

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

Predicted structure



Re-alignment of all predicted orthologs

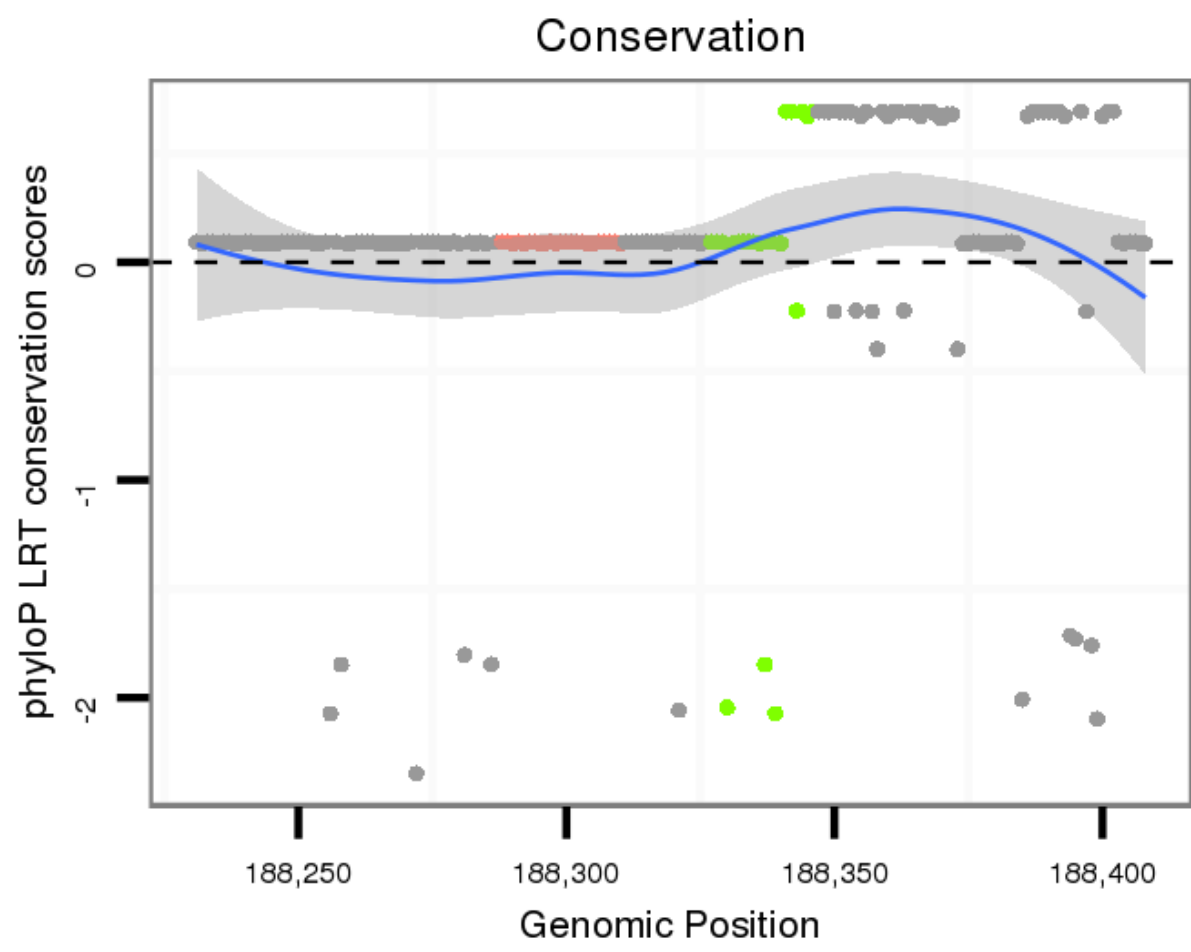
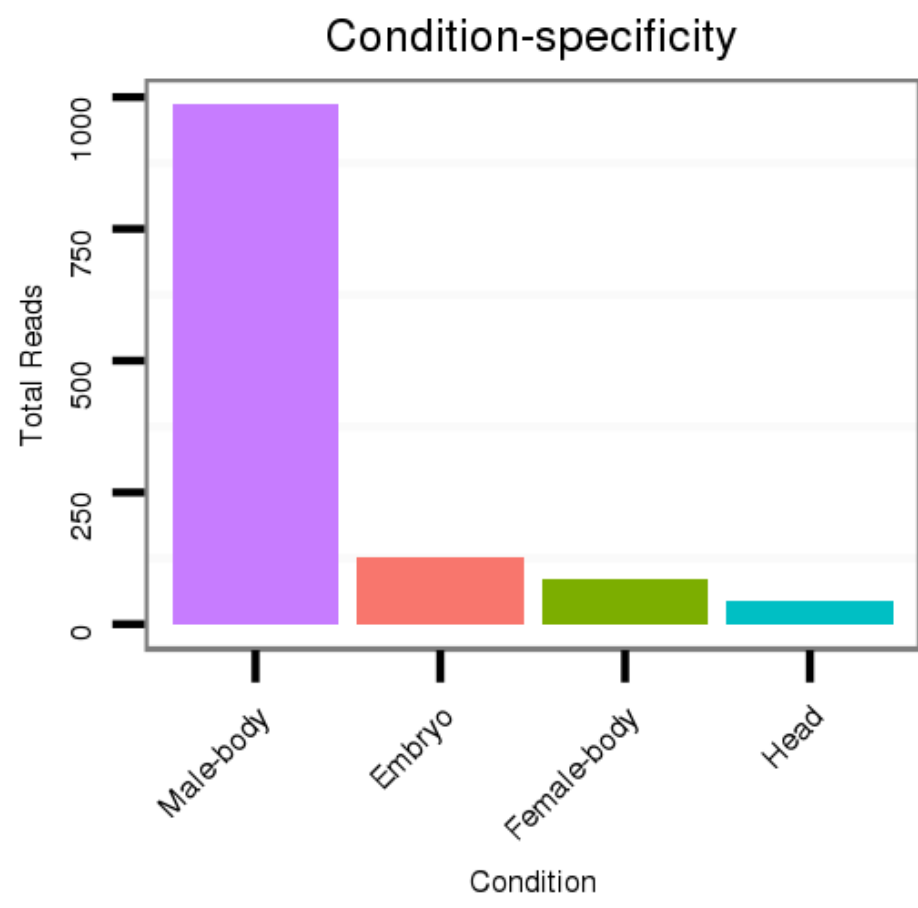
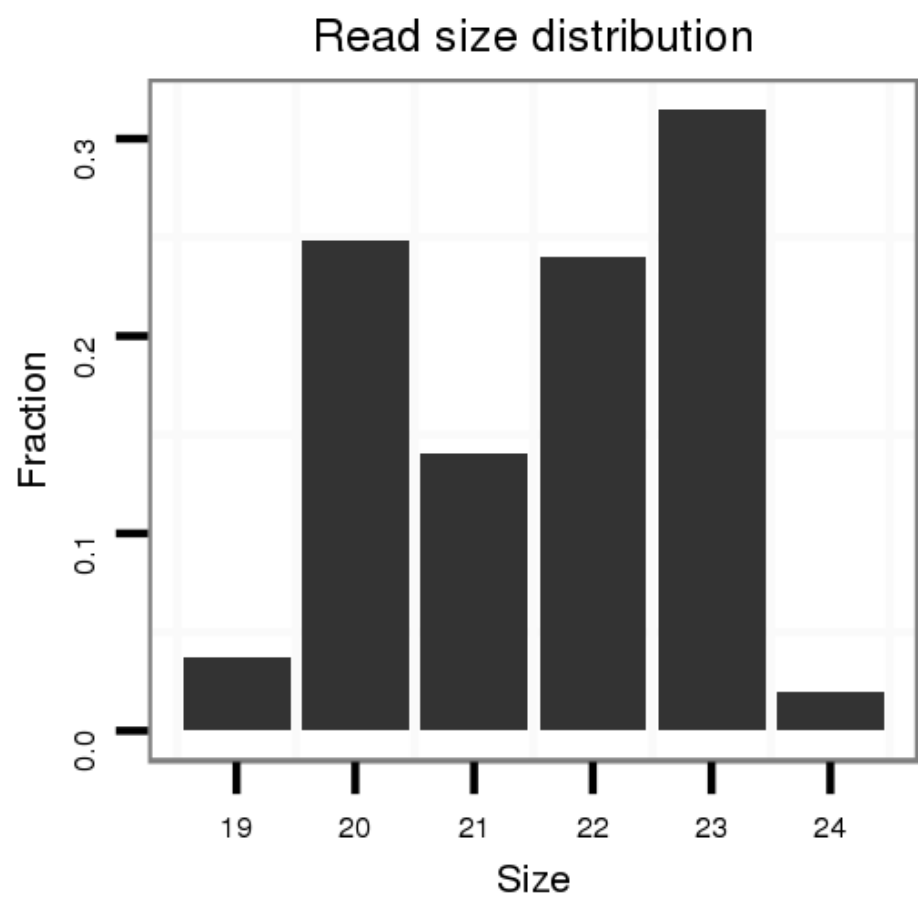
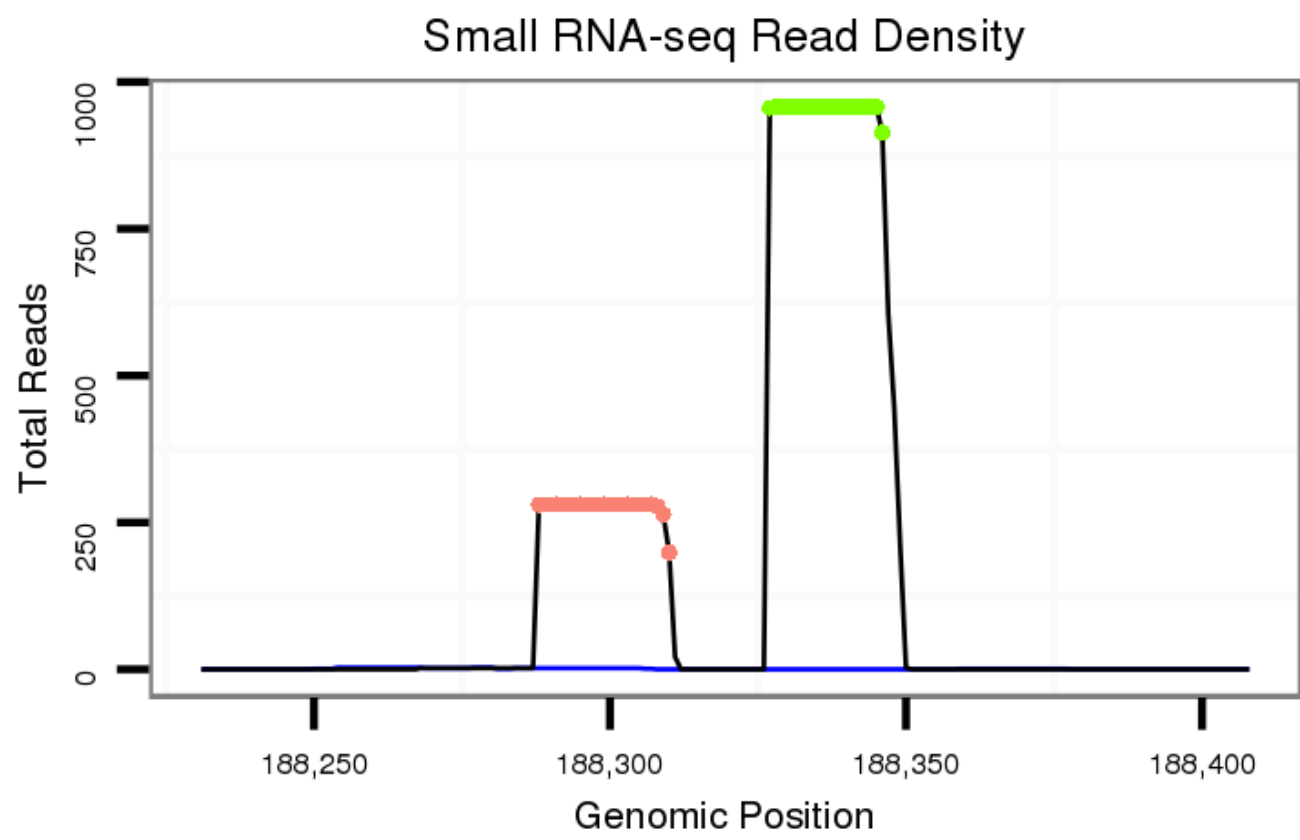
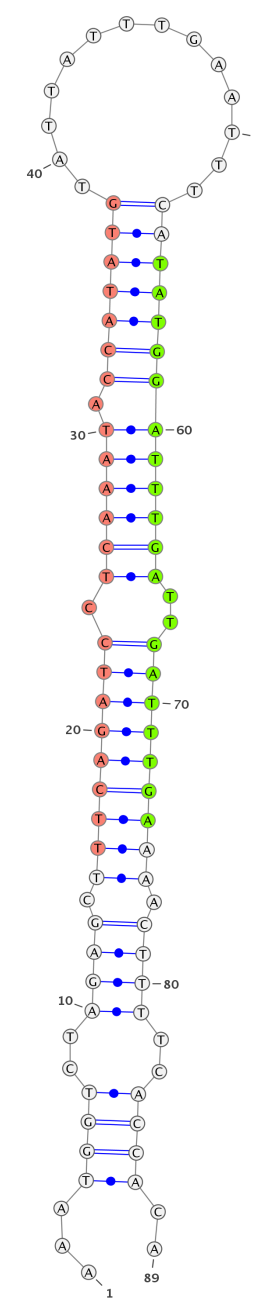
Generated: 09/08/2015 at 10:40 PM

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

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

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



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

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

						M042	M021	V057	V050	V042
						female body	embryo	head	head	embryo
AGATCAAGCAACCCGCTTATTGTCTAATGCTTTATCGGCCAGTTTACCAGATCTCGAAGTCTAGGAGTTTATGGTATAATAATAAACTAAAGTATACCTAAACTAACTAACTTTGAAAAGTG GTGTATATGTATGAGGGTTGGGGTCGGTATATACGCACAAGTAAC TCG	Read size	# Mismatch	Hit Count	Total Norm	Total					
.....(((((.....)))))).....	27	0	1	2.00	2	0	2	0	0	0
.....CTAATGCTTTATCGGCCAGTTTACGAG.....	19	0	1	1.00	1	0	1	0	0	0
.....TTTGCTAATGCTTTATCGGC.....	24	0	1	1.00	1	0	1	0	0	0
.....TCGAAGTCTAGGAGTTTATGGTA.....	19	0	1	1.00	1	0	1	0	0	0
.....TGATATATGTATGAGGGTT.....	29	0	1	1.00	1	0	1	0	0	0
.....CCAGATCTCGAAGTCTAGGAGTTTATGG.....										

Show Alignment With Reads

Re-alignment of all predicted orthologs

[illegible]

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

Show Alignment With Reads

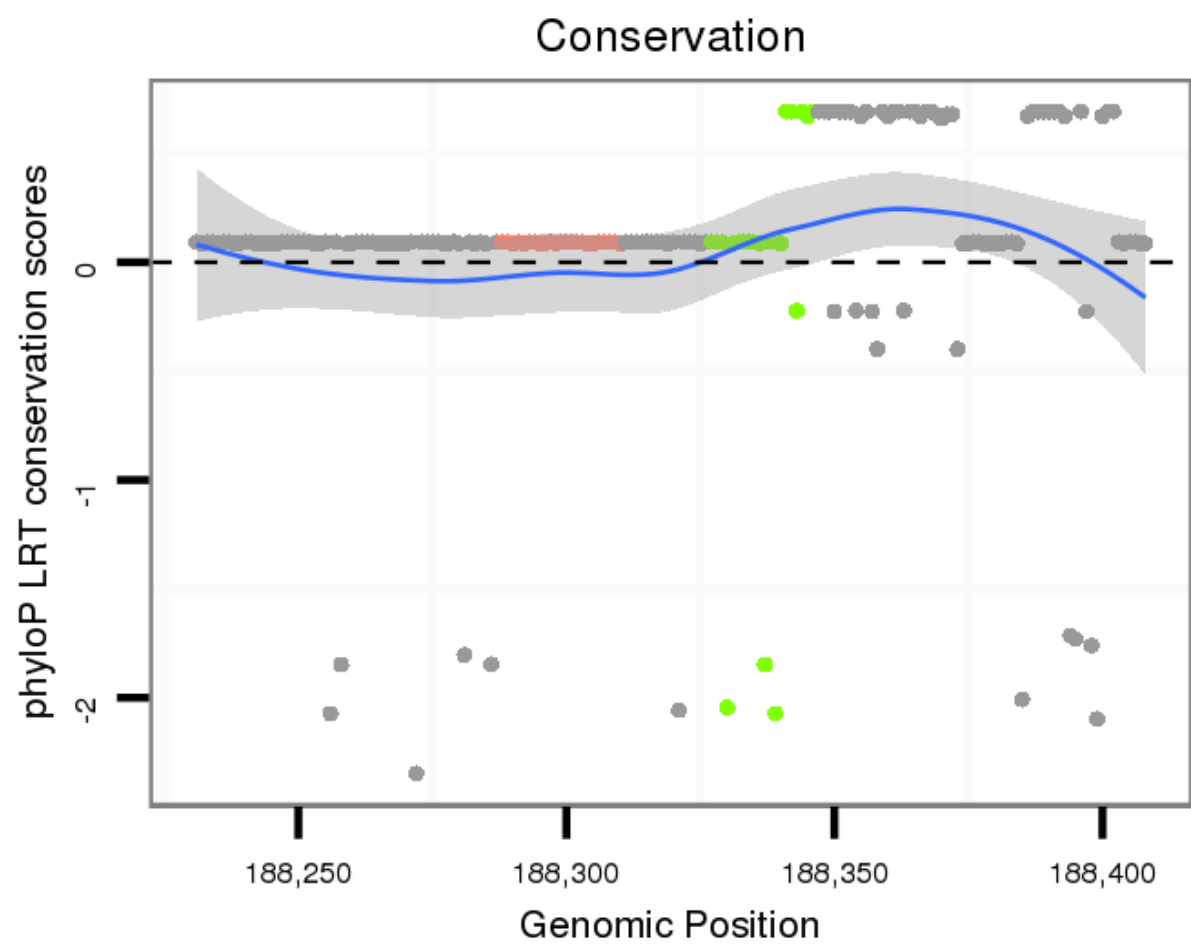
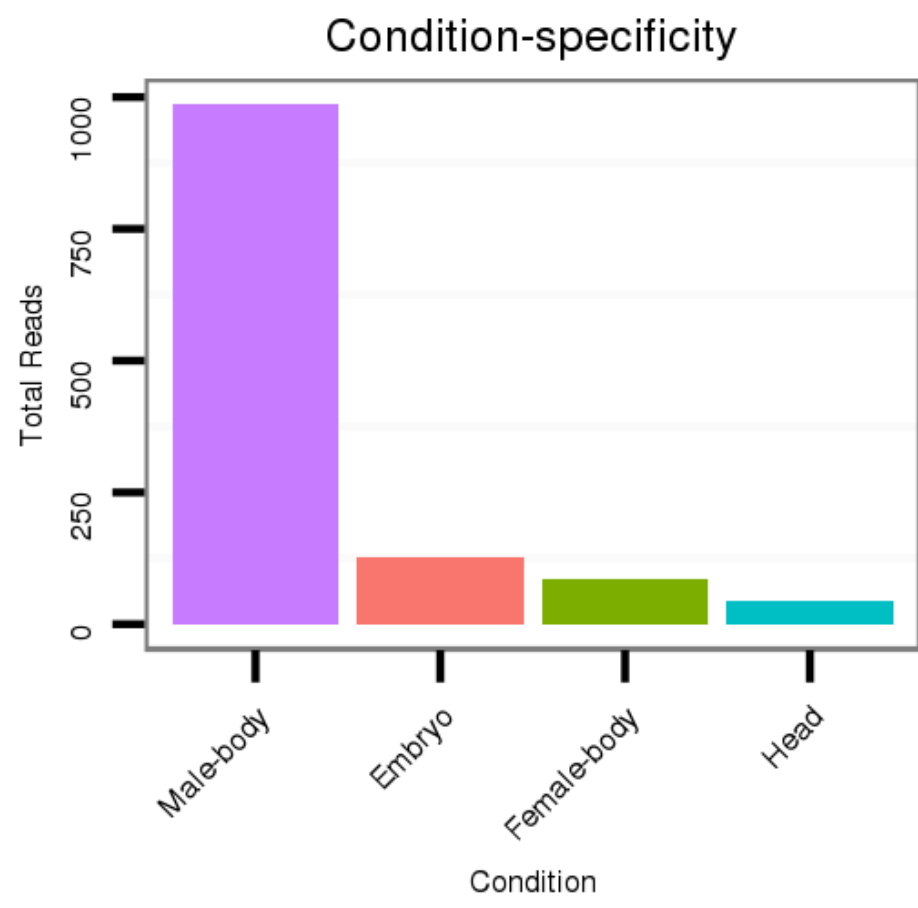
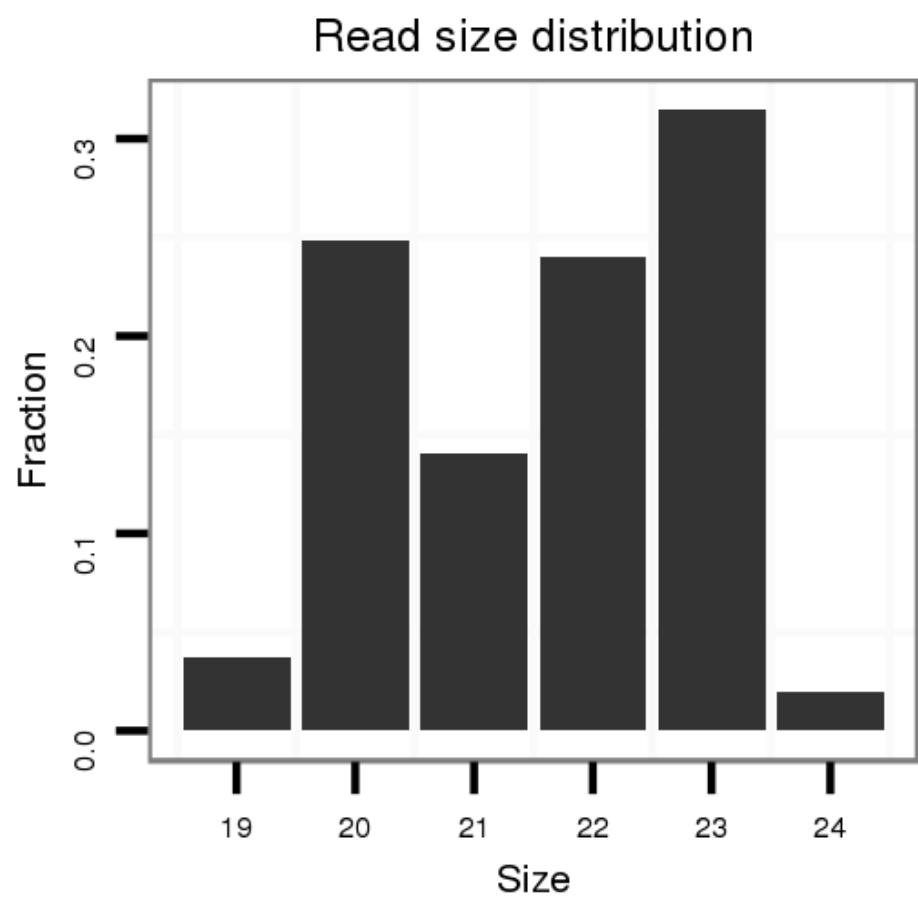
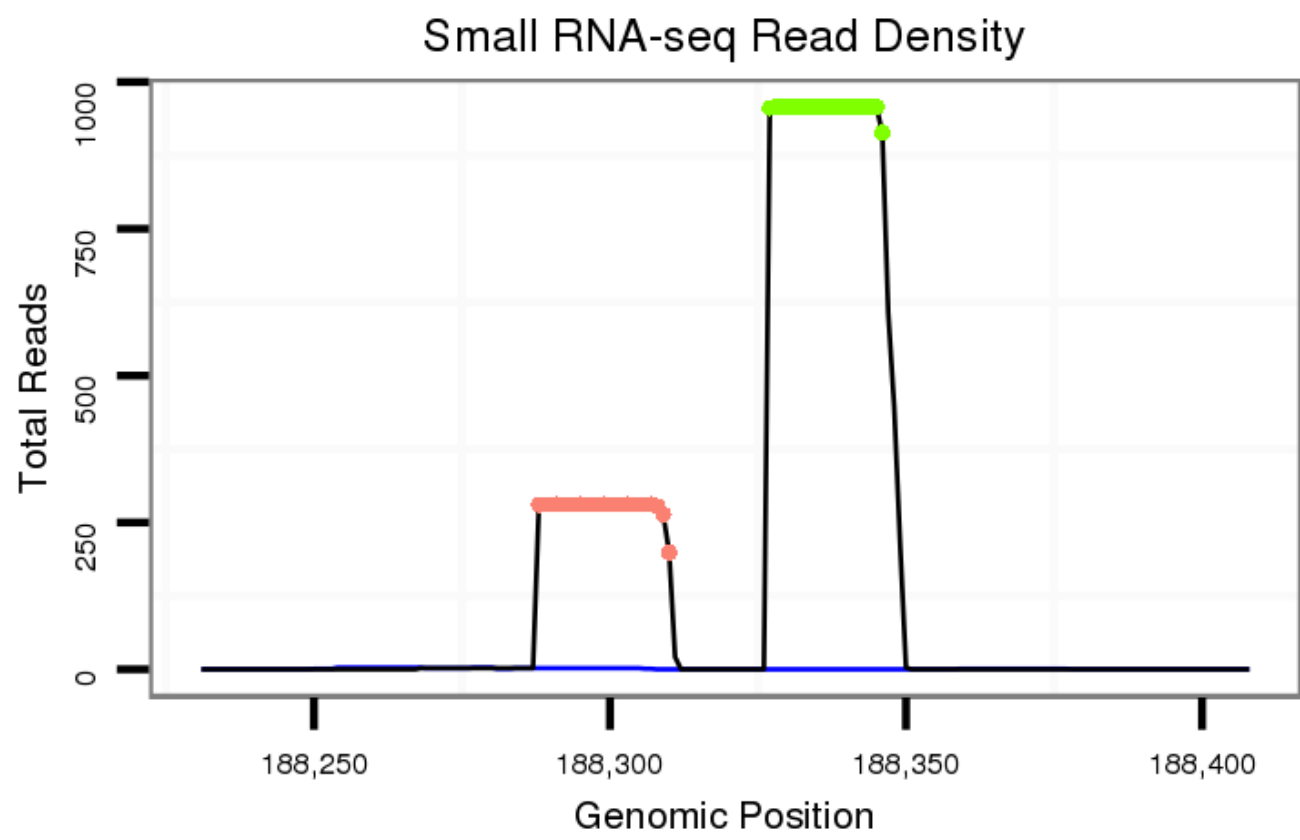
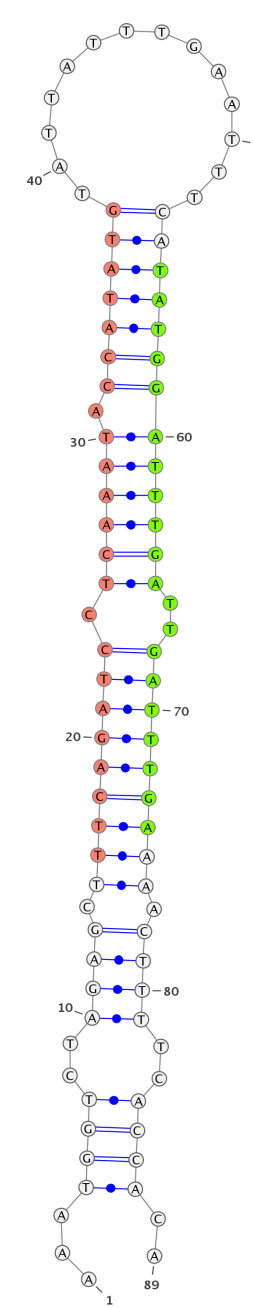
Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droPer2	scafold_13:188231-188408	dpe_333	TC TAGTTCGTTGGGCAATAAACGATTACGAATAGC---CGGGTCAAATGGTCTAGAGCTTT CAGATCCTCAAATACCATATG TATTATTGAATTTCAT TGGATTGTGATTGATTGA AAACTTTTCACCACATATACATACATCCAAACCCCAAGCCATATATG---CGTGTT---CATTTGAAGC
dp5	XL_groupie:8380388-8380572	dpe-mir-2517a-3	TC TAGTTCGTTGGGCAATAAACG GA CGAATAGC CCC GGGTCAAATGGT CCAGAG TT CAGATCCTCAAATACCATATG TATTATTGA CA TT CA T AT GATTTCG CG CAGATTGA AAACTTTTCACCACATATACAT --- CCCAACCCCAAG CA TATATG TATGATG CC TATTT CA T TG AGC
droW112	scafd2_1454014540:2020638-2020747		TC TAGTTCGTTGGGCAATAAACG GA CGAATAGC CCC GGGTCAAATGGT CCAGAG TT CAGATCCTCAAATACCATATG TATTATTGA CA TT CA T AT GATTTCG CG CAGATTGA AAACTTTTCACCACATATACAT --- CCCAACCCCAAG CA TATATG TATGATG CC TATTT CA T TG AGC

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

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



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

Show Alternate Folds

Flybase annotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

Anti-sense strand reads

						M042	M021	V057	V050	V042
						female body	embryo	head	head	embryo
AGATCAAGCAACCCGCTTATTGTCTAATGCTTTATCGGCCAGTTTACCAGATCTCGAAGTCTAGGAGTTTATGGTATAATAATAAACTAAAGTATACCTAAACTAACTAACTTTGAAAAGTG	Read									
*****(((((.....))))))))).....))))).....										

Show Alignment With Reads

Re-alignment of all predicted orthologs

[illegible]

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

Show Alignment With Reads

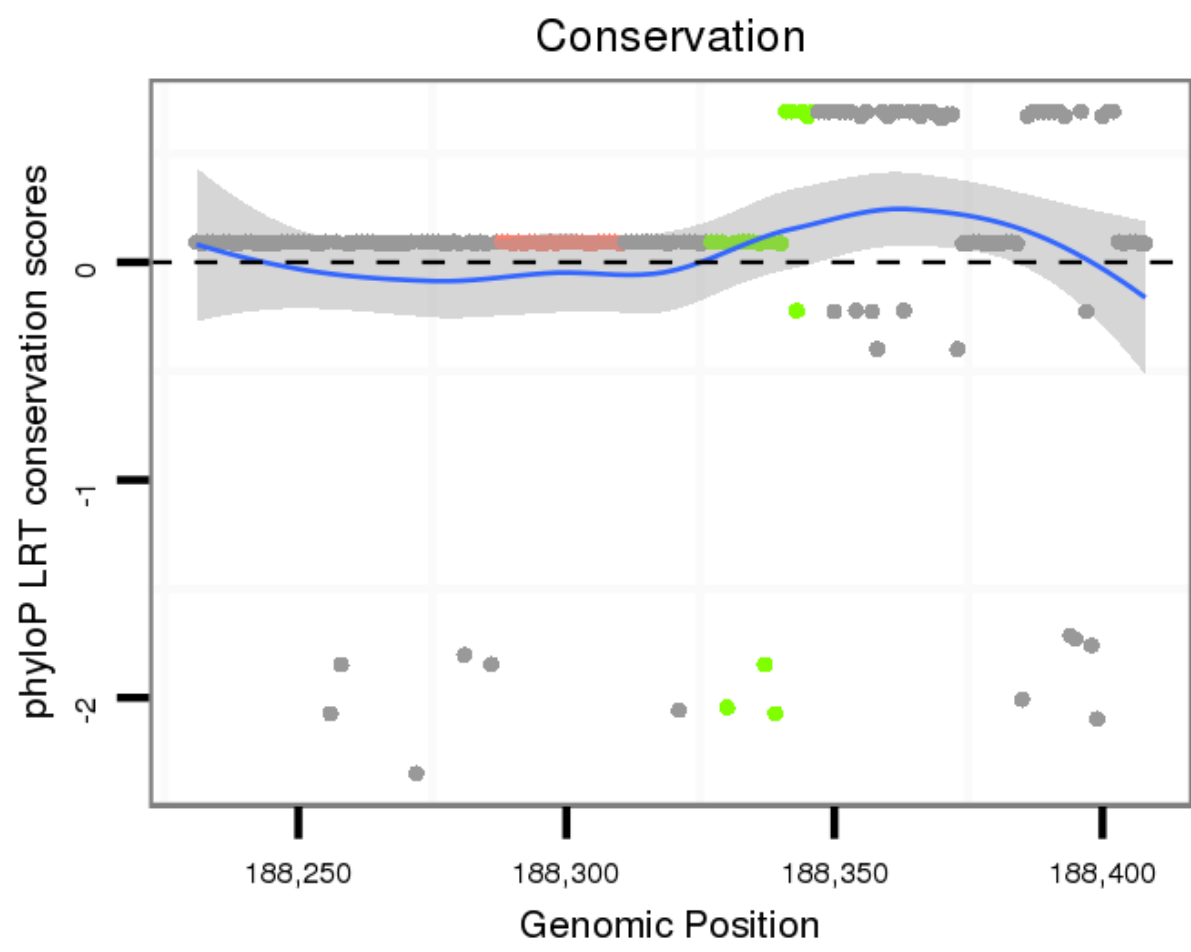
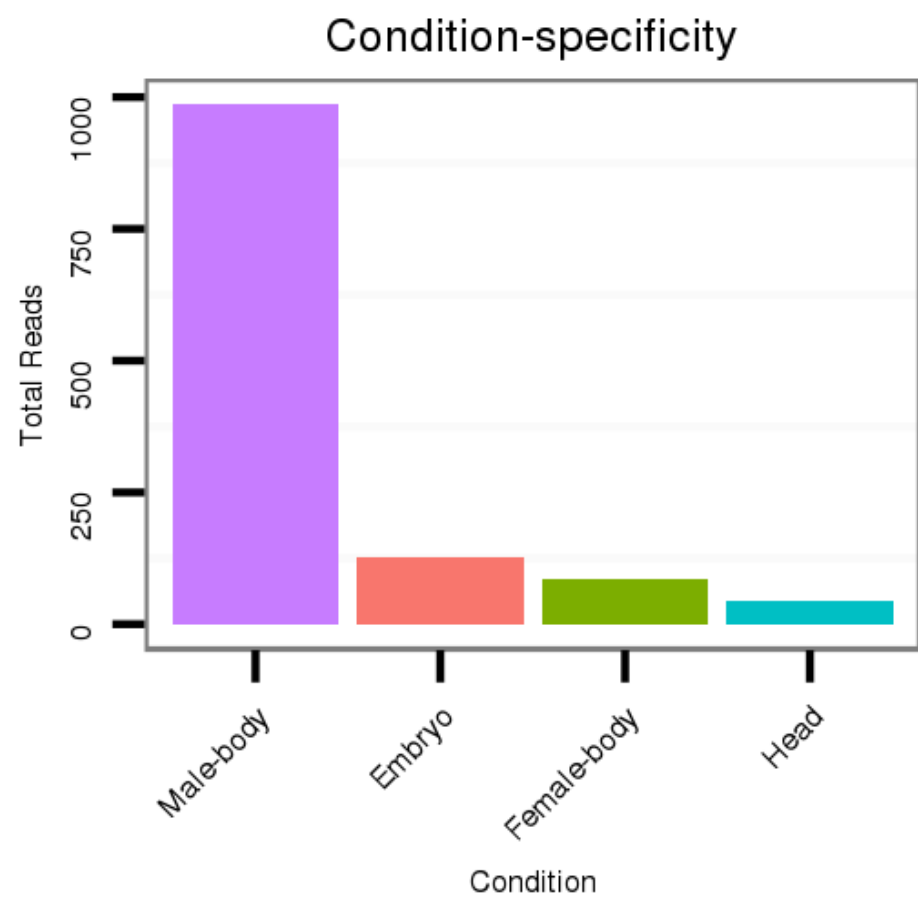
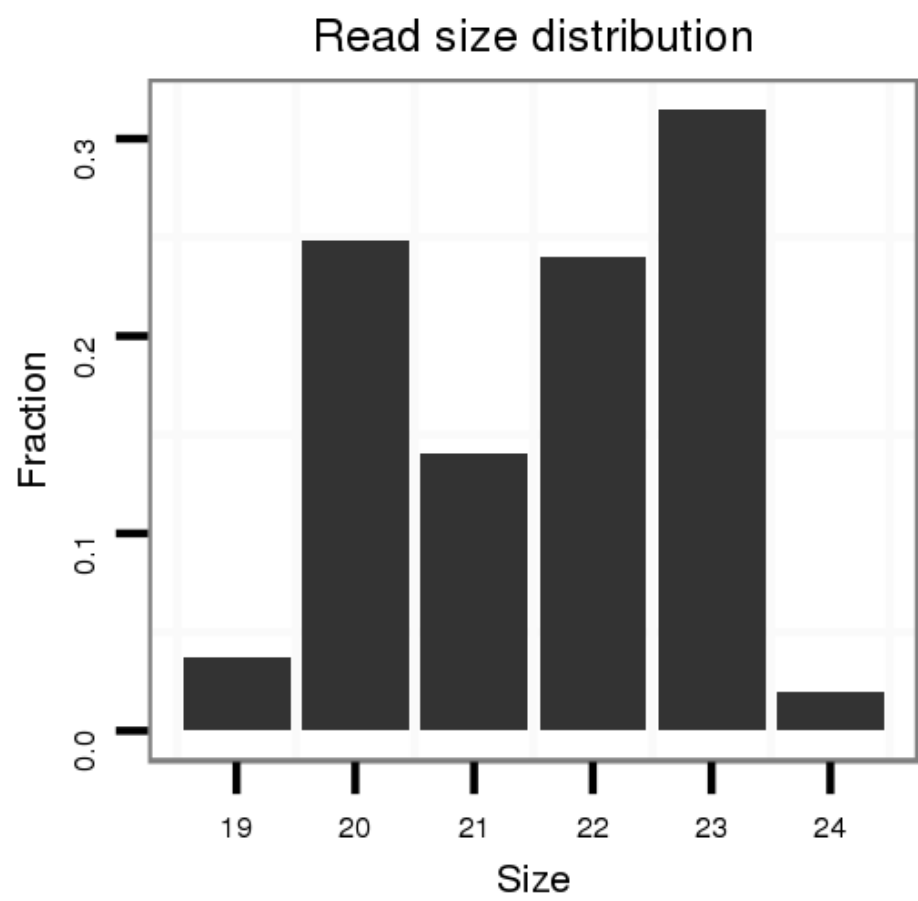
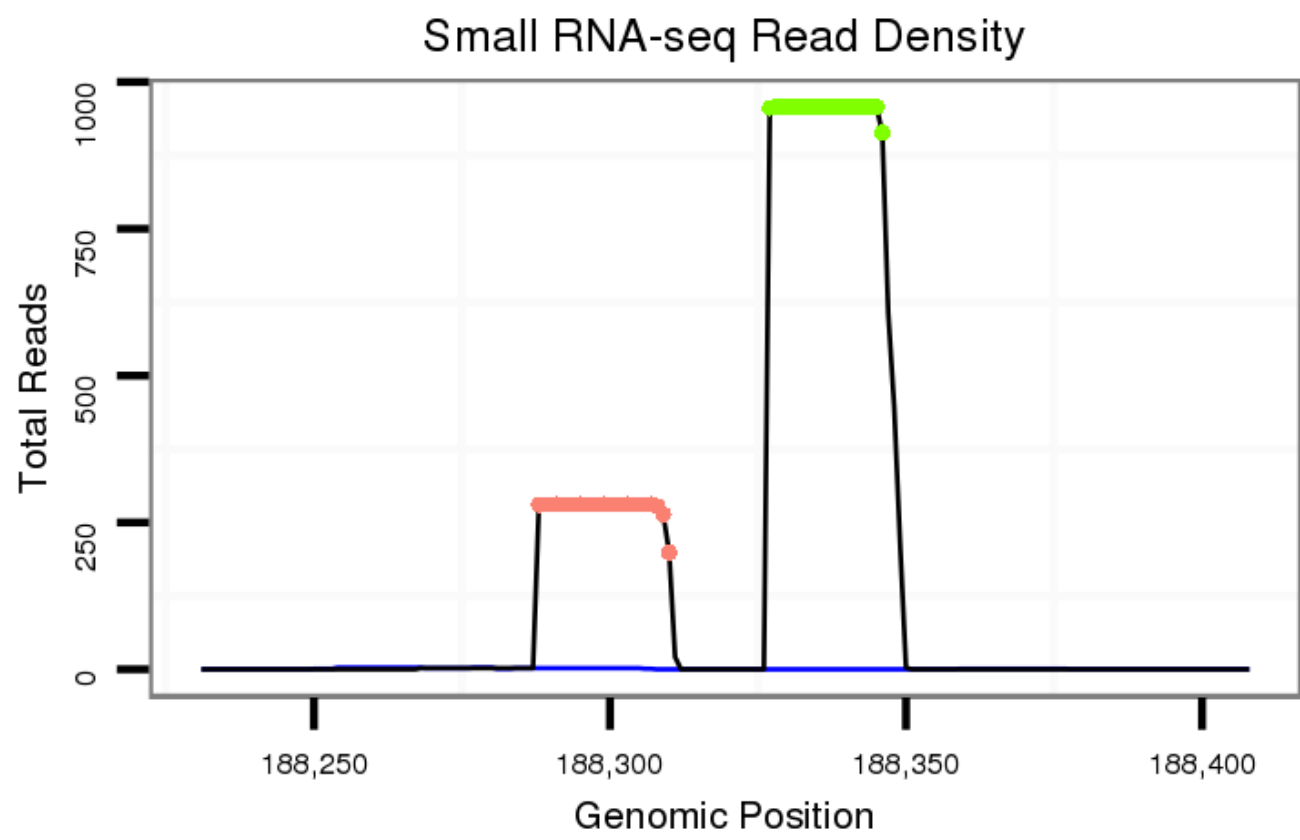
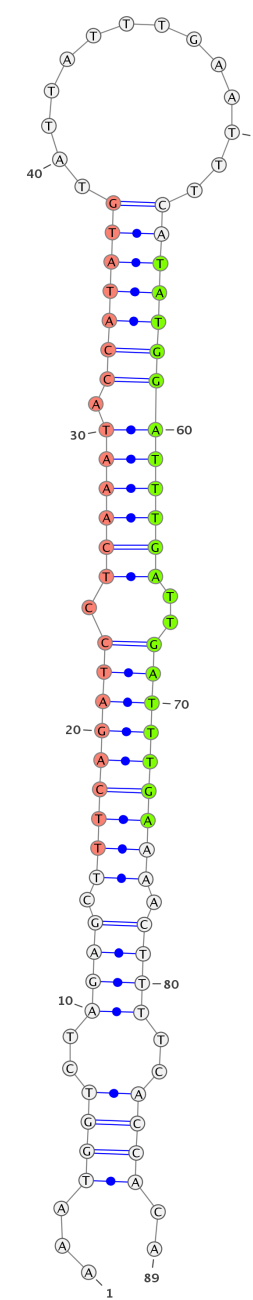
Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droPer2	scaafold_13:188231-188408	dpe_333	TC TAGTTCGTTGGGCGAATAAACGATTACGAATAGC---CGGGTCAAATGGTCTAGAGCTTT CAGATCCTCAAATACCATATGTATTATTGAAATTTCATG GATTGTTGATTGATTGGAACCTTTTCACCACATATACATACATCCAAACCCCAAGCCATATATG---CGTGTT---CATTTGAAGC
dp5	XL_groupie:8380388-8380572	dpe-mir-2517a-3	TC TAGTTCGTTGGGCGAATAAACGCGCGAATAGC CCC GGGTCAAATGGTCCAGAGCTTT CAGATCCTCAAATACCATATGTATTATTGGAATTTCATG TATTGTTGCGCGATTTGAACCTTTTCACCACATATACAT---CCCAACCCCAAGCATATATGATGATGACCTATTCATTGAAGC
droW112	scaf2_145014540:2020638-2020747		TC TAGTTCGTTGGGCGAATAAACGCGCGAATAGC CCC GGGTCAAATGGTCCAGAGCTTT CAGATCCTCAAATACCATATGTATTATTGGAATTTCATG TATTGTTGCGCGATTTGAACCTTTTCACCACATATACAT---CATATATG---TATGAGC---CAT

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

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Hairpin partition Mature Star

Show Alternate Folds

Flybase annotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

Anti-sense strand reads

[illegible]

Show Alignment With Reads

Re-alignment of all predicted orthologs

[illegible]

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

Show Alignment With Reads

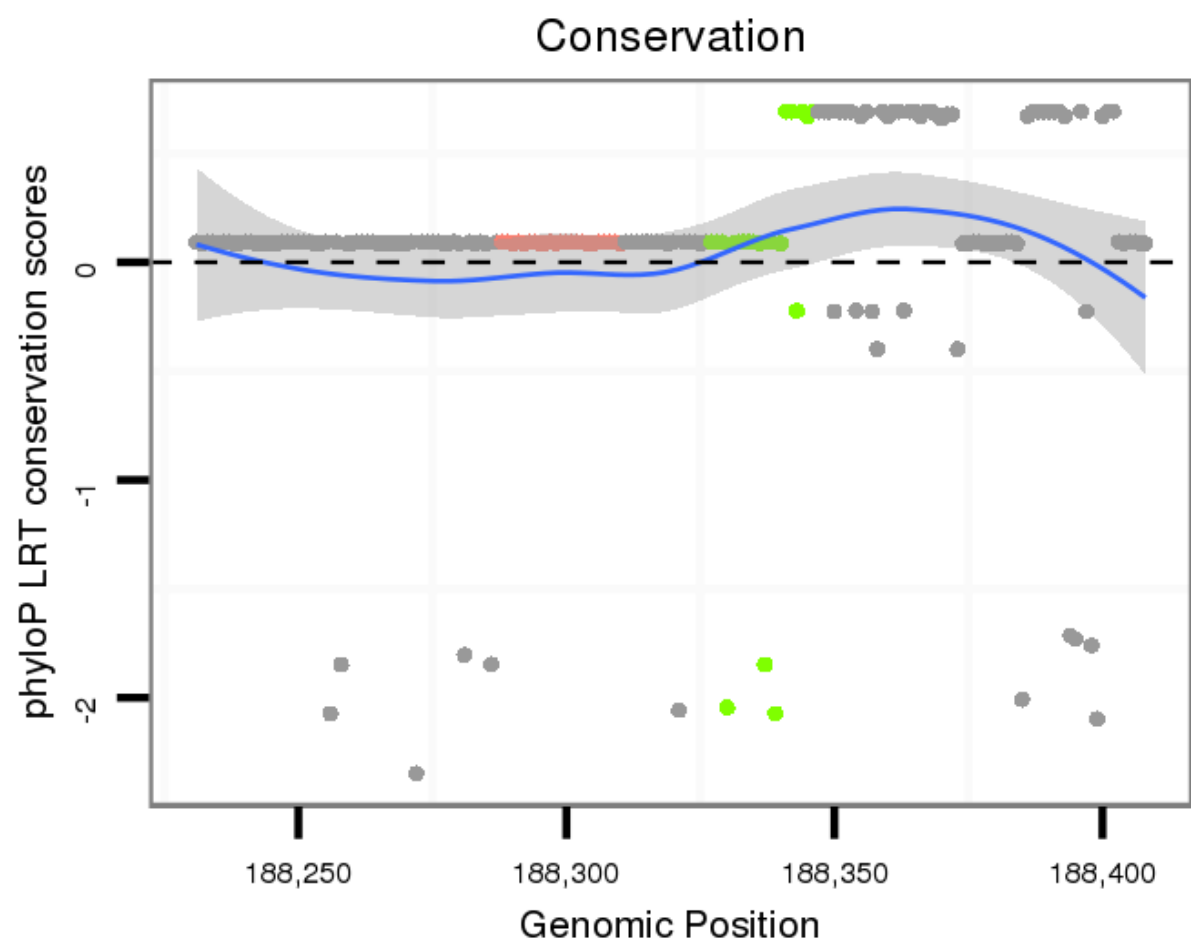
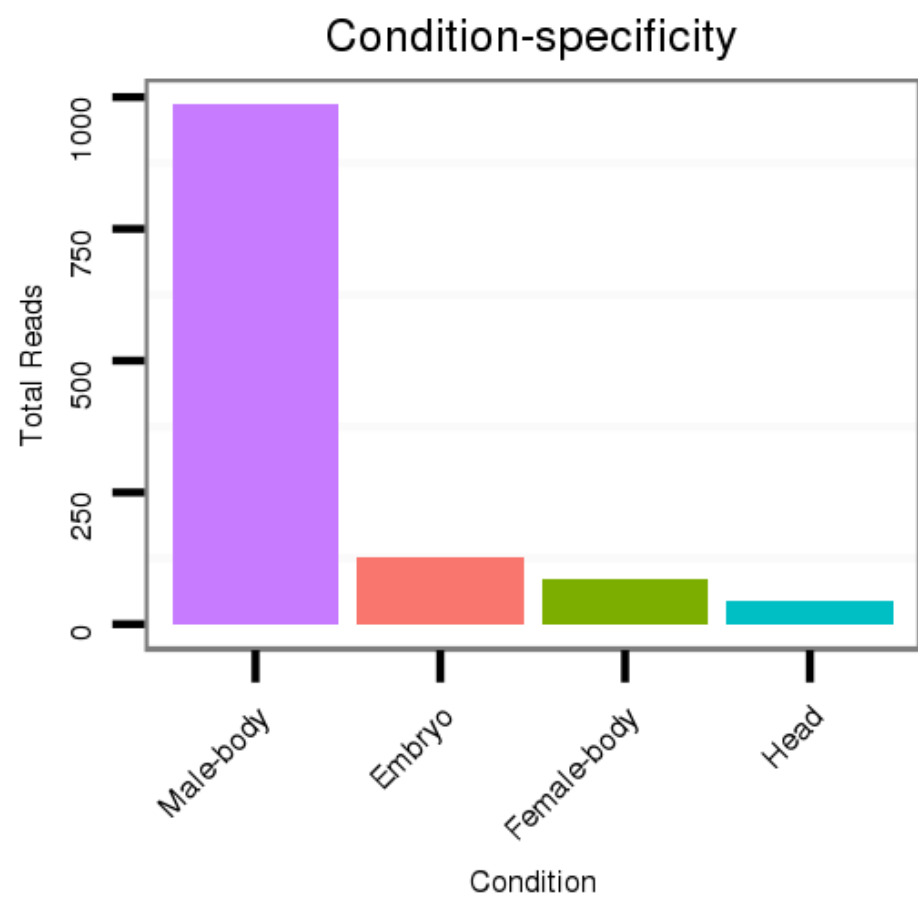
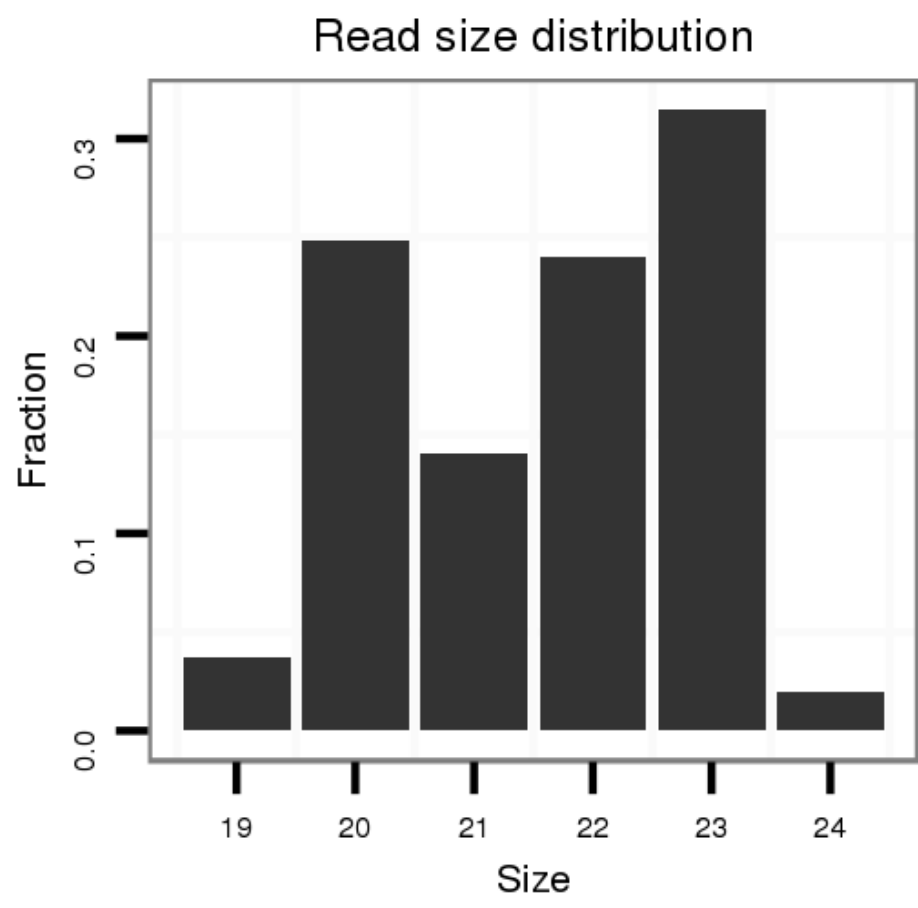
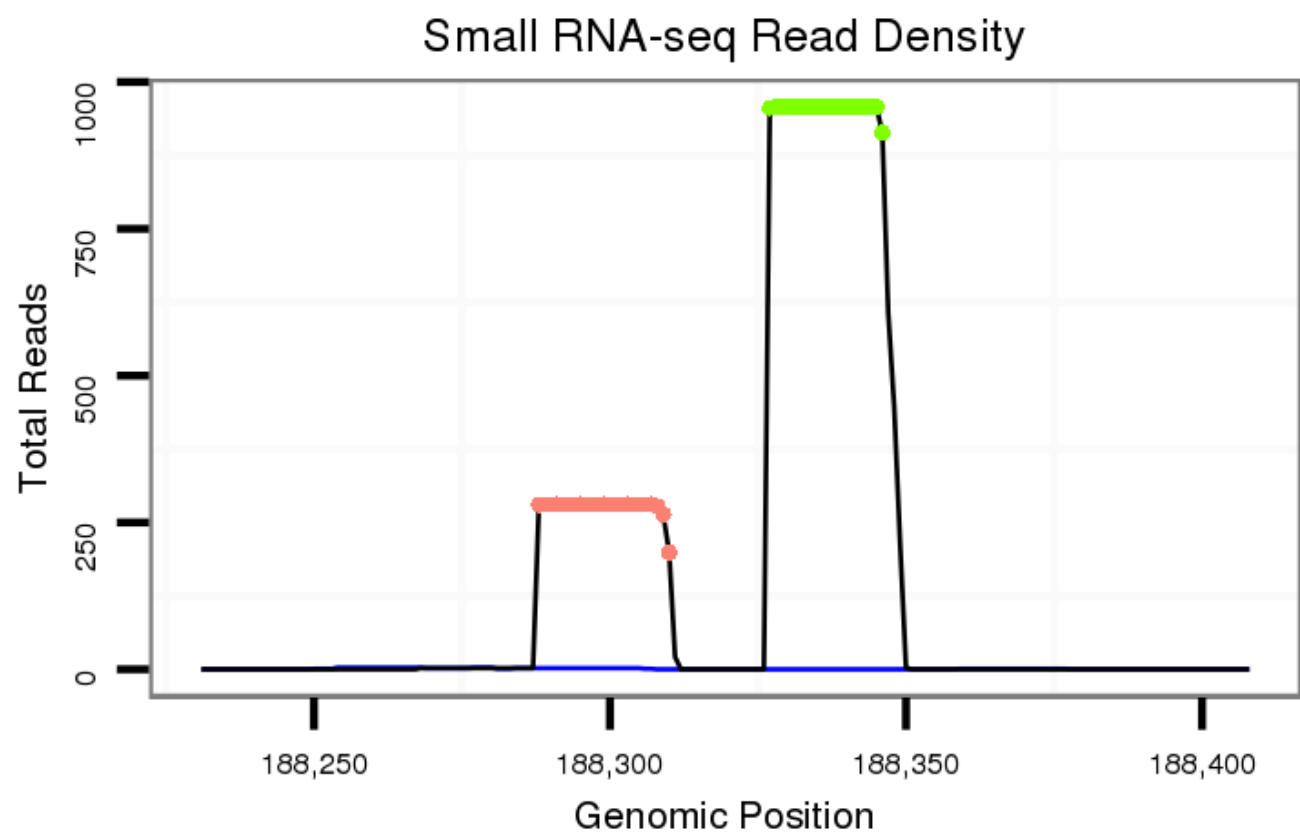
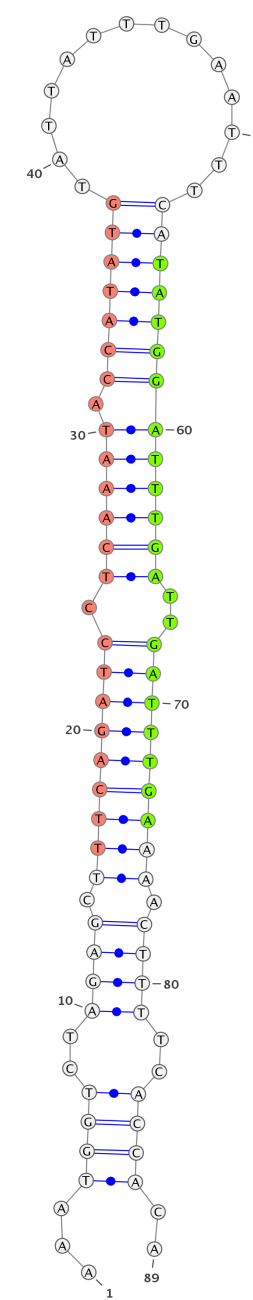
Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droPer2	scaafold_13:188231-188408	dpe_333	TC TAGTTCGTTGGGCGAATAAACGATTACGAATAGC---CGGGTCAAATGGTCTAGAGCTTT CAGATCCTCAAATACCATATGTATTATTGAAATTCAATGGAATTGGATTGATTGGAACCTTTTCACCACATATACATACATCCAAACCCCAAGCCATATATG---CGTGTT---CATTTGAAGC
dp5	XL_groupie:8380388-8380572	dpe-mir-2517a-3	TC TAGTTCGTTGGGCGAATAAACGCGAGTAATGAGC---CGGGTCAAATGGTCTAGAGCTTT CAGATCCTCAAATACCATATGTATTATTGAAATTCAATGGAATTGGATTGATTGGAACCTTTTCACCACATATACAT---CCCAACCCCAAGCATATATGATGATGACCTATTCATTGAAGC
droW112	scaf2_145014540:2020638-2020747		TC TAGTTCGTTGGGCGAATAAACGCGAGTAATGAGC---CGGGTCAAATGGTCTAGAGCTTT CAGATCCTCAAATACCATATGTATTATTGAAATTCAATGGAATTGGATTGATTGGAACCTTTTCACCACATATACAT---CATATATG---CATATATG---CAT

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

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Hairpin partition Mature Star

Show Alternate Folds

Flybase annotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

Anti-sense strand reads

	M042	V057	V050	V042						
	embryo	female body	head	head	embryo					
AGATCAAGCAACCCGCTTATTGTCTAATGCTTTATCGGCCAGTTTACCAGATCTCGAAAGTCTAGGAGTTTATGGTATAATAATAAACTAAAGTATACCTAAACTAACTAAACTTTGAAAAGTG GTGTATATGTATAGGGTTGGGGTCGGTATATACGCACAAGTAAC TCG	Read size	# Mismatch	Hit Count	Total Norm	Total	M021 embryo	M042 female body	V057 head	V050 head	V042 embryo
.....CTAATGCTTTATCGGCCAGTTTACGAG.....	27	0	1	2.00	2	2	0	0	0	0
.....TTTGCTAATGCTTTATCGGC.....	19	0	1	1.00	1	0	1	0	0	0
.....TCGAAGTCTAGGAGTTTATGGTA.....	24	0	1	1.00	1	0	0	0	0	0
.....TGATATATGTATAGAGTTT.....	19	0	1	1.00	1	0	1	0	0	0
.....CCAGATCTCGAAGTCTAGGAGTTTATGG.....	29	0	1	1.00	1	1	0	0	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

[illegible]

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

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droPer2	scaafold_13:188231-188408	dpe_333	TC TAGTTCGTTGGGCGAATAAACGATTACGAATAGC---CGGGTCAAATGGTCTAGAGCTTT CAGATCCTCAAATACCATATGTATTATTGAAATTCAATGGAATTGGATTGATTGGAACCTTTTCACCACATATACATACATCCAAACCCCAAGCCATATATG---CGTGTT---CATTTGAAGC
dp5	XL_groupie:8380388-8380572	dpe-mir-2517a-3	TC TAGTTCGTTGGGCGAATAAACGCGAGTAATGAGC---CGGGTCGAAATGGTCCAGAGCTTT CAGATCCTCAAATACCATATGTATTATTGGAATTCAATGATTGATTGCGCAGATTGGAACCTTTTCACCACATATACAT---CCCAACCCCAAGCATATATGATGATGACCTATTCATTGAAGC
droW112	scaf2_145014540:2020638-2020747		TC TAGTTCGTTGGGCGAATAAACGCGAGTAATGAGC---CGGGTCGAAATGGTCCAGAGCTTT CAGATCCTCAAATACCATATGTATTATTGGAATTCAATGATTGATTGCGCAGATTGGAACCTTTTCACCACATATACAT---CCCAACCCCAAGCATATATGATGATGACCTATTCATTGAAGC

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

Predicted structure

Show Alternate Folds

Flybase annotation

intron [Dper¹GL16980-in]; CDS [Dper¹GL16980-cds]; CDS [Dper¹GL16980-cds

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

[illegible]

Anti-sense strand reads

[illegible]

Re-alignment of all predicted orthologs

[illegible]

Generated: 09/08/2015 at 06:59 PM

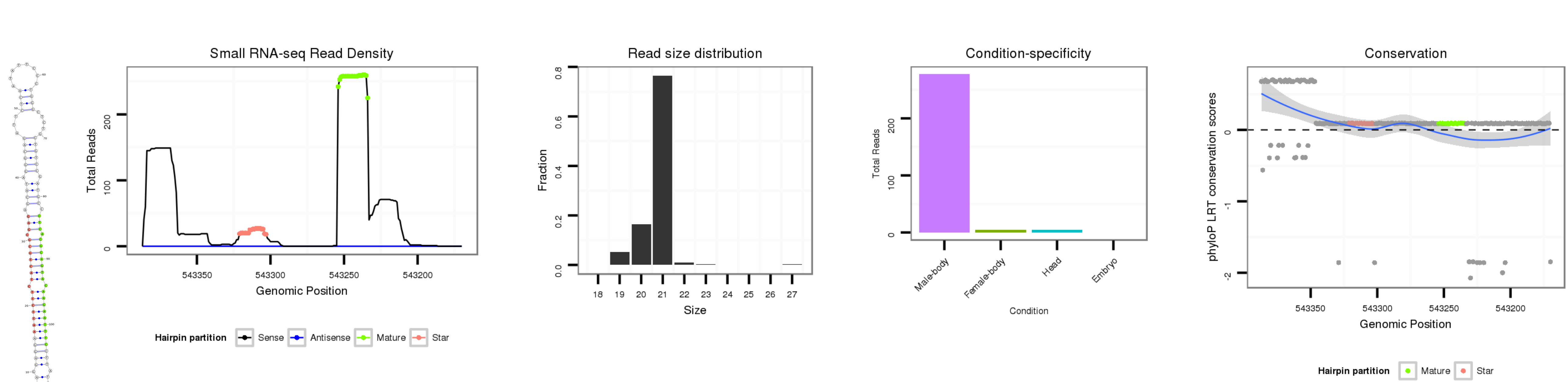
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	2
rescue.candidate	1

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

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dpe_2501	scaffold_18:543220-543337 -	Known Ortholog	Canonical miRNA	CDS	[View on UCSC Genome Browser (Cornell Mirror)]

Legend: mature star mismatch in alignment mismatch in read

Predicted structure

[Show Alternate Fol](#)

Flybase annnotation

CDS [Dper/GL19824-cds]; CDS [Dper/GL19825-cds]

No Repeatable elements found

mature	star
--------	------

1. [dpe_2502 scaffold_18:543031-543049](#) -
2. [dpe_2501 scaffold_18:543303-543321](#) -

Sense Strand Reads

hide 3p reads show mid mismatch reads

[illegible]

Anti-sense strand reads

[illegible]

Re-alignment of all predicted orthologs

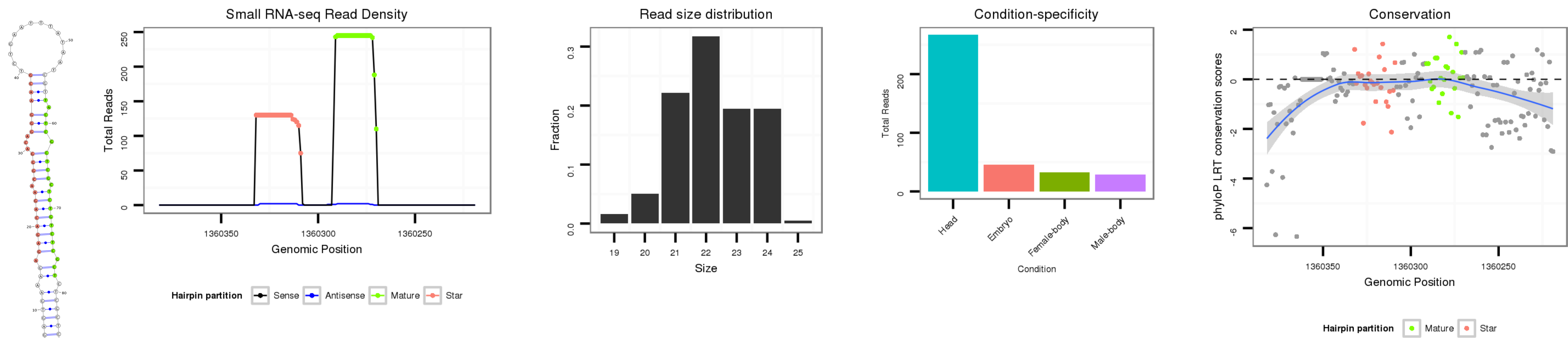
Species	Coordinate	ID	Alignment
dProBr2	scaffold_18:543170-543387_-	dps_2501	CCGTCGCTACGGTCAGTGCTGCCCTCAAAATGGCATGGTCGCTCTTCCTCTCGAGGAGGA AATTCCTCTACTGCGCGA AGCATAGGCGAGATTCTCAATATTCCTGGGCTCTGCTGCGATGCC CTACCGAGTACAAGAAATTC CTTATTGAAGGGGGAAGCTAGGACCGCAAAATGCAATGCCAGCATGATCCCATAGCCATAT
dp5	X1_group16:1655468-1655685_2545a-2	dps-mir-2545a-2	CCGTCGCTACGGTCAGTGCTGCCCTCAAAATGGCATGGTCGCTCTTCCTCTCGAGGAGGA AATTCCTCTACTGCGCGA AGCATAGGCGAGATTCTCAATATTCCTGGGCTCTGCTGCGATGCC CTACCGAGTACAAGAAATTC CTCGCGAGGAGG AGCTAGGACCACTGATGCAATGCCAGCATGATCCCATAGCCATAT
dProBr2	scaffold_4929:7008759-7008799_+		CGTGGCAATCG CTCG GTCTGG AGGCGCACTG CAATGG-----

Generated: 09/08/2015 at 07:48 PM

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dpe_81	scaffold_22:1360269-1360332 -	confident	Canonical miRNA	antisense_to_intron	[View on UCSC Genome Browser (Cornell Minor)]

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Show Alternate Folds

Flybase annotation

Antisense to intron [Dper/GL15936-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

[illegible]

Anti-sense strand reads

[illegible]

Show Alignment With Reads

Re-alignment of all predicted orthologs

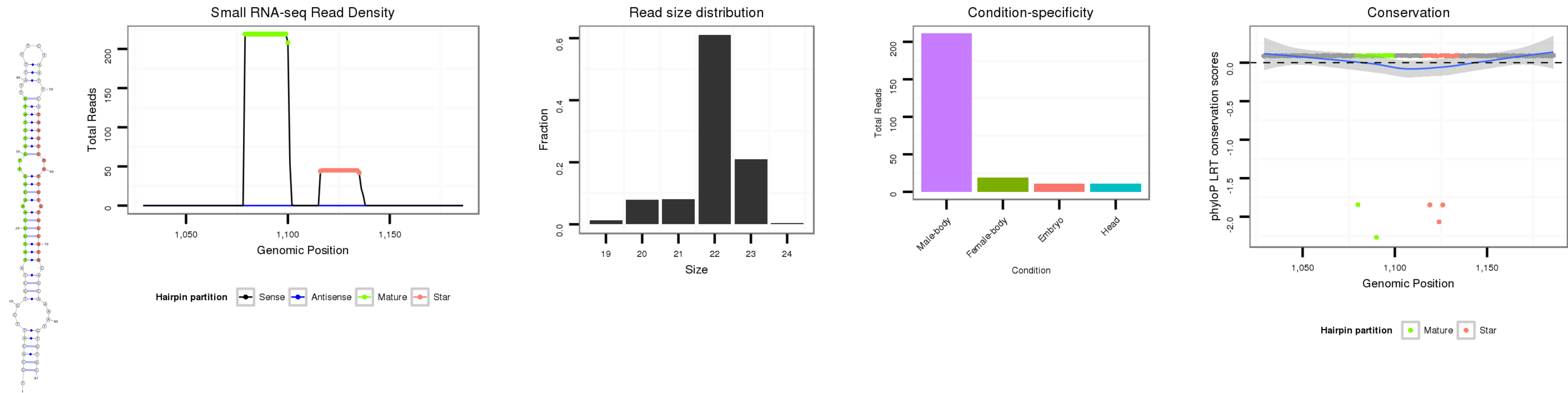
[illegible]

Generated: 09/08/2015 at 07:47 PM

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

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

Anti-sense strand reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droPer2	scaffold_7821:1029-1186 +	dpe_88	GTAACCGTGTGGAGGAAGTGTTCCTCCCAACCAATGCACATTCGTGCTATATGGCAACAGCTGATTATGTATTTCCTAATTCATAAGTCTCTGTCTGCCATACAGCAAAATGTGTCTCTATCCTGATGCATCCTATGCTGGCTTAGATCAGA
dp5	4_group4:3553239-3553396 +	dps_14	GTAACCGTGTGGAGGAAGTGTTCCTCCCAACCAATGCACATTCGTGCTATATGGCAACAGCTGATTATGTATTTCCTAATTCATAAATCTGCTATCTGCCATACAGCAAAATGTGTCTCTATCCTGATGCATCCTATGCTGGCTTAGATCAGA

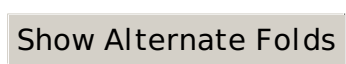
Generated: 09/08/2015 at 08:17 PM

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

Predicted structure

Predicted structure

Predicted structure



Flybase annotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

[illegible]

Re-alignment of all predicted orthologs

[illegible]

Generated: 09/08/2015 at 07:47 PM

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

Predicted structure

Predicted structure



Flybase annotation

No Repeatable elements found

1. dpe_77 scaffold_12:1984847-1984867+	1. dpe_77 scaffold_12:1984802-1984825+
2. dpe_76 scaffold_6388:231-251+	2. dpe_76 scaffold_6388:186-209+

hide 3p reads | show mid mismatch reads

(.....(((.....((.....))..)))..))))..),.....												size	Mismatch	Count	Norm	Total	head	body	tail	body	tail
..	ATCTCTCTCTTTGACACACAG	22	1	2	124.00	248	137	104	5	0	2	0									
..	ATCTCTCTCTTTGACACACAG	21	0	2	73.50	147	43	60	42	0	2	0									
..	ATCTCTCTCTTTGACACACA	20	0	2	9.00	18	6	9	3	0	0	0									
..	GTAATGTTGCAAGAGAGAATAGTGT	24	0	2	8.50	17	7	0	0	0	10	0									
..	GTAATGTTGCAAGAGAGAATAGT	22	0	2	7.00	14	0	2	0	0	12	0									
..	CATCTCTCTCTTTGACACACAG	22	0	2	6.50	13	5	6	2	0	0	0									
..	CATCTCTCTCTTTGACACACA	21	0	2	4.00	8	2	5	0	0	0	1									
..	GTAATGTTGCAAGAGAGAATAGTGT	25	0	2	3.50	7	4	1	0	2	0	0									
..	TCTCTCTCTTTGACACACAG	20	0	2	2.50	5	0	0	5	0	0	0									
..	TCTCTCTCTTTGACACACAG	21	1	2	2.50	5	4	1	0	0	0	0									
..	GTAATGTTGCAAGAGAGAATAG	21	0	2	2.00	4	2	0	0	2	0	0									
..	GTAATGTTGCAAGAGAGAAT	19	0	2	2.00	4	2	2	0	0	0	0									
..	GTAATGTTGCAAGAGAGAATAGTG	23	0	2	1.50	3	1	1	0	1	0	0									
..	CATCTCTCTCTTTGACACAC	20	0	2	1.50	3	2	0	1	0	0	0									
..	CATCTCTCTCTTTGACACACAG	23	1	2	1.00	2	0	1	1	0	0	0									
..	ATCTCTCTCTTTGACACAC	19	0	2	1.00	2	0	2	0	0	0	0									
..	TGGCTCGATCCACCGATAAC	21	0	2	1.00	2	1	1	0	0	0	0									
..	ATCTCTCTCTTTGACACACAG	23	2	2	1.00	2	2	0	0	0	0	0									
..	GTAATGTTGCAAGAGAGAATAG	22	1	2	1.00	2	1	0	0	1	0	0									
..	TCTCTCTTTGACACACAG	19	1	2	1.00	2	1	1	0	0	0	0									
..	TCTCTCTTTGACACACAG	18	0	2	1.00	2	1	1	0	0	0	0									
..	TCTCTCTCTTTGACACACAG	22	2	2	1.00	2	1	1	0	0	0	0									
..	ATCTCTCTCTTTGACACACAG	21	1	2	1.00	2	1	0	1	0	0	0									
..	TATCTTGCAGAGAGAATAGTGT	24	0	2	0.50	1	1	0	0	0	0	0									
..	GPAATGTTGCAAGAGAGAATA	21	1	2	0.50	1	1	0	0	0	0	0									
..	ATCTCTCTCTTTGACACACAG	22	1	2	0.50	1	0	1	0	0	0	0									
..	GCAGAACTACACCGAGGCC	18	0	2	0.50	1	0	0	0	0	0	1									
..	ATCTCTCTCTTTGACACACAG	21	1	2	0.50	1	0	0	1	0	0	0									
..	ATCTCTCTCTTTGACACACAG	22	1	2	0.50	1	0	0	1	0	0	0									
..	ATGTTGCAAGAGAGAATAGTGT	22	0	2	0.50	1	1	0	0	0	0	0									
..	ATCTCTCTCTTTGACACACAGG	22	0	2	0.50	1	1	0	0	0	0	0									
..	GTAATGTTGCAAGAGAGAATAGTG	24	1	2	0.50	1	0	1	0	0	0	0									
..	ATCTCTCTCTTTGACACACAG	22	2	6	0.17	1	1	0	0	0	0	0									

Show Alignment With Reads

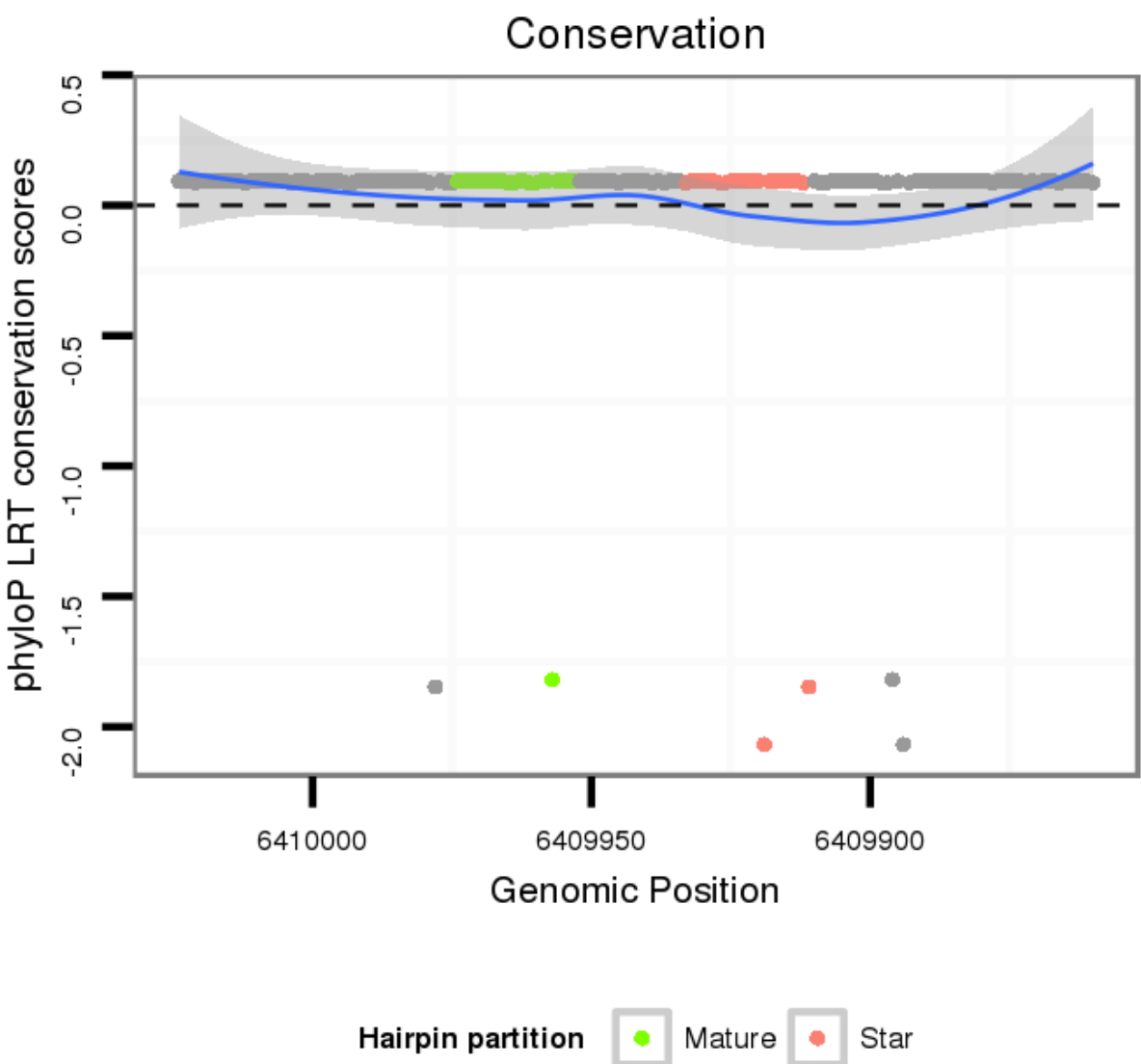
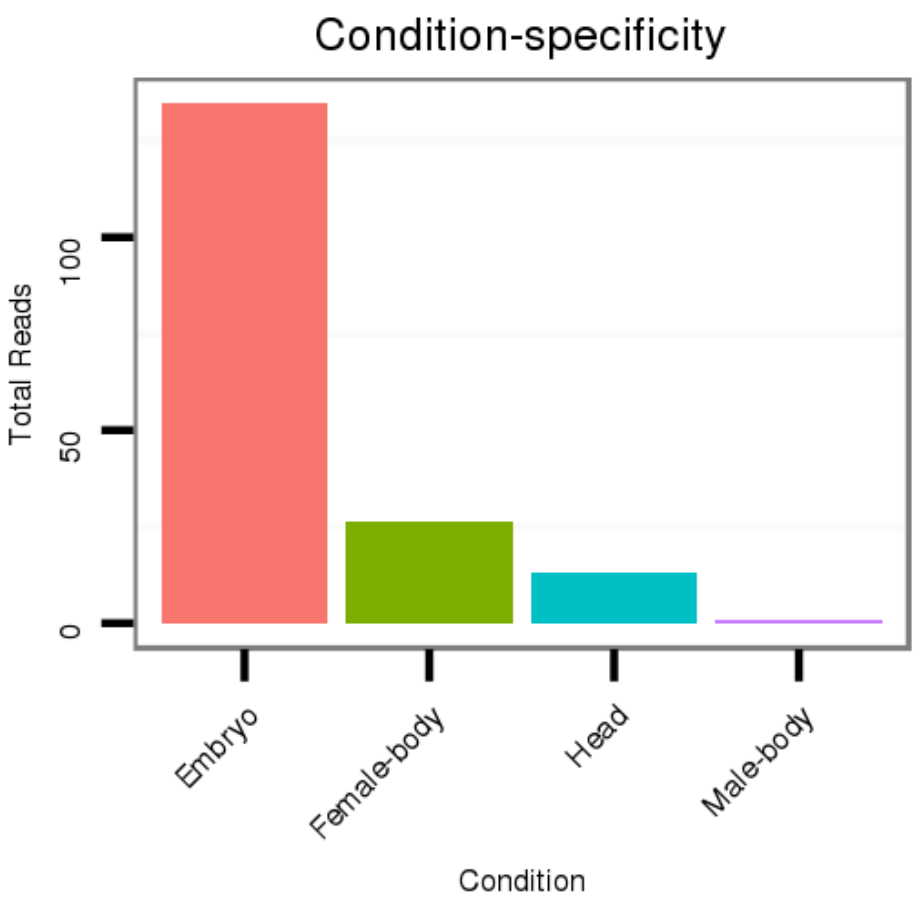
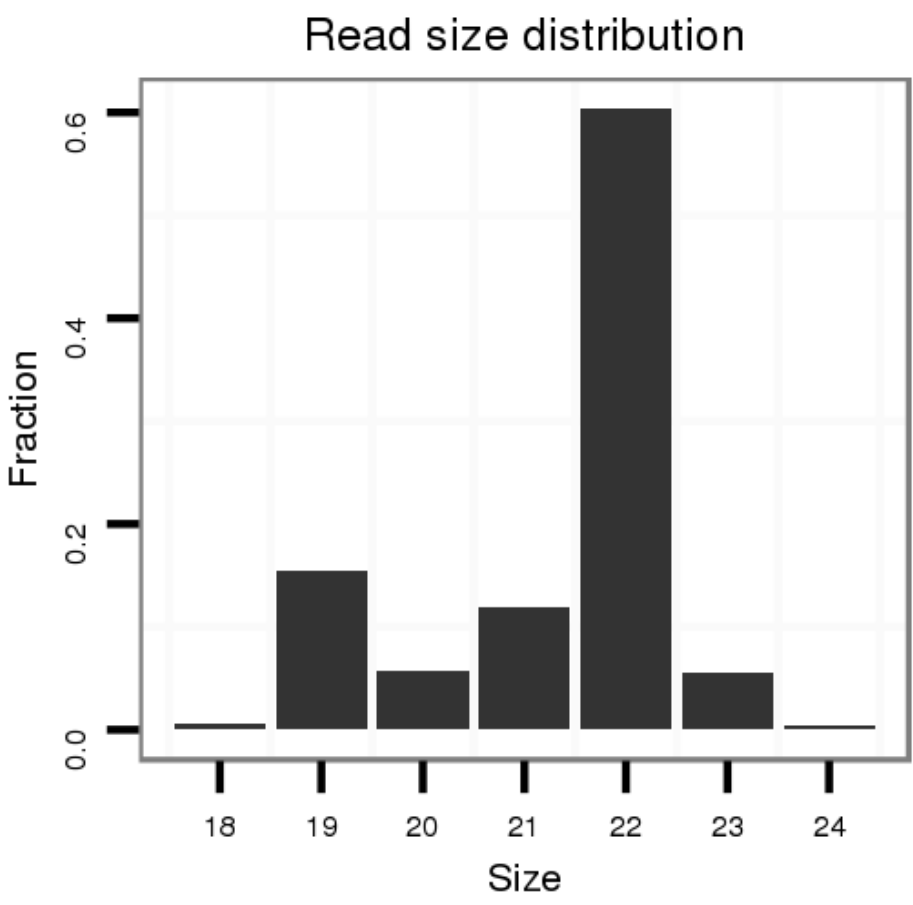
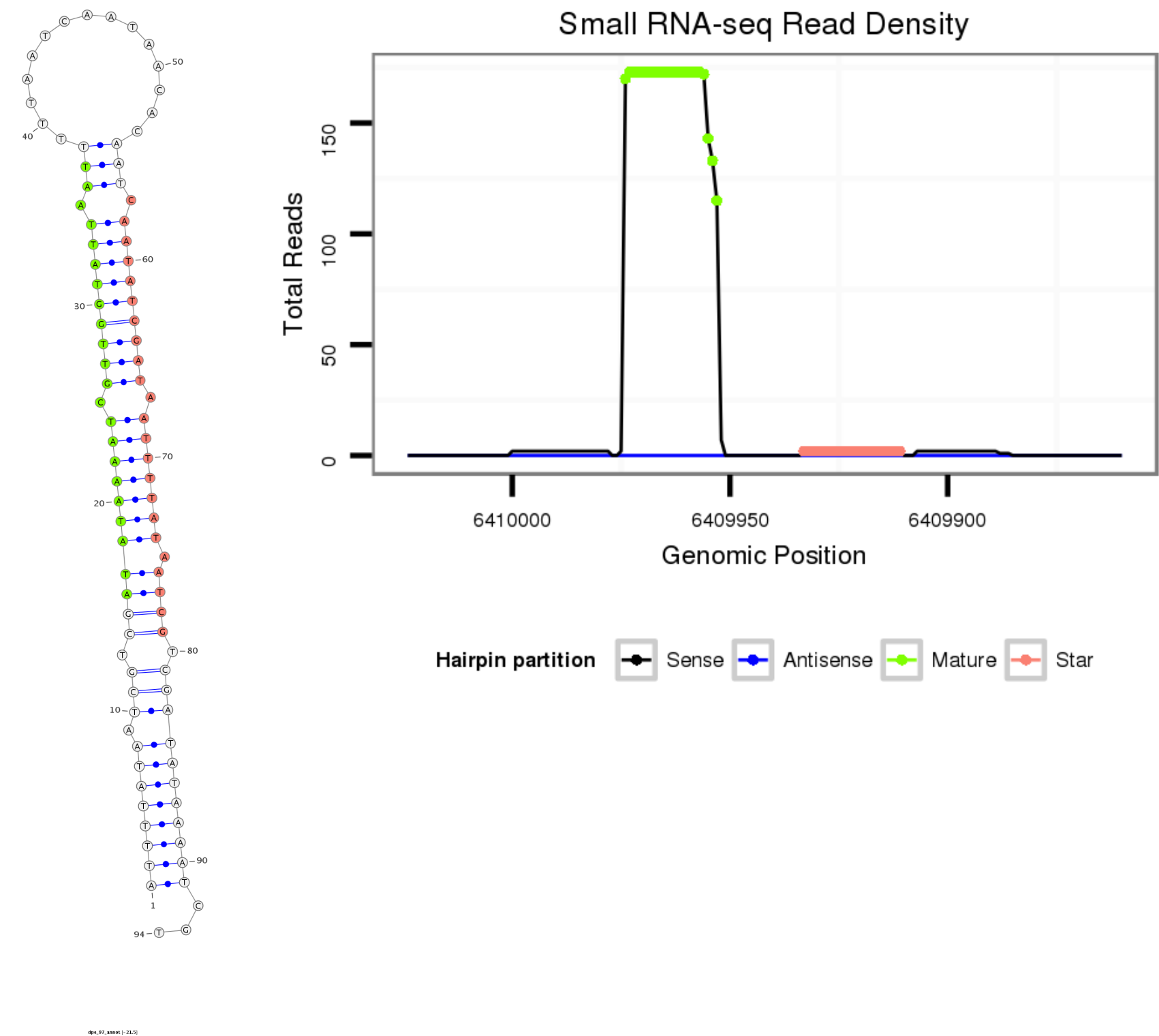
[illegible]

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

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dpe_97	scaffold_3:6409910-6409974 -	confident	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. scaffold_3:6409844-6409866 -	
2. dpe_97 scaffold_3:6409911-6409933 -	
3. scaffold_3:6409978-6410000 -	

Sense Strand Reads

hide 3p reads show mid mismatch reads

Read #	size	Mismatch	Hit Count	Total Norm	Total	M021 embryo	M042 female body	V050 head	V057 head	V042 embryo	V111 male body
22	0	1	105.00	105	84	17	0	3	1	0	0
19	0	1	27.00	27	18	1	6	0	1	1	1
21	0	1	18.00	18	18	0	0	0	0	0	0
22	1	1	10.00	10	10	0	0	0	0	0	0
20	0	1	10.00	10	5	3	2	0	0	0	0
23	2	1	8.00	8	5	3	0	0	0	0	0
23	0	1	7.00	7	7	0	0	0	0	0	0
25	3	1	5.00	5	5	0	0	0	0	0	0
24	2	1	4.00	4	4	0	0	0	0	0	0
21	0	1	3.00	3	0	3	0	0	0	0	0
23	1	1	3.00	3	3	0	0	0	0	0	0
23	0	3	2.67	8	0	5	1	1	1	0	0
23	0	3	2.67	8	0	5	1	1	1	0	0
20	0	1	2.00	2	2	0	0	0	0	0	0
25	2	1	1.00	1	1	0	0	0	0	0	0
18	0	1	1.00	1	0	0	0	0	1	0	0
22	0	1	1.00	1	1	0	0	0	0	0	0
19	0	1	1.00	1	0	0	0	0	1	0	0
24	0	3	0.67	2	0	1	0	0	0	1	0
24	0	3	0.67	2	0	1	0	0	0	1	0
22	0	3	0.33	1	0	0	1	0	0	0	0
22	0	3	0.33	1	0	1	0	0	0	0	0
22	0	3	0.33	1	0	0	1	0	0	0	0
22	0	3	0.33	1	0	1	0	0	0	0	0

Anti-sense strand reads

Read #	size	Mismatch	Hit Count	Total Norm	Total
22	0	1	105.00	105	84
19	0	1	27.00	27	18
21	0	1	18.00	18	18
22	1	1	10.00	10	10
20	0	1	10.00	10	5
23	2	1	8.00	8	5
23	0	1	7.00	7	7
25	3	1	5.00	5	5
24	2	1	4.00	4	4
21	0	1	3.00	3	0
23	1	1	3.00	3	3
23	0	3	2.67	8	0
23	0	3	2.67	8	0
20	0	1	2.00	2	2
25	2	1	1.00	1	1
18	0	1	1.00	1	0
22	0	1	1.00	1	1
19	0	1	1.00	1	0
24	0	3	0.67	2	0
24	0	3	0.67	2	0
22	0	3	0.33	1	0
22	0	3	0.33	1	0
22	0	3	0.33	1	0
22	0	3	0.33	1	0

Re-alignment of all predicted orthologs

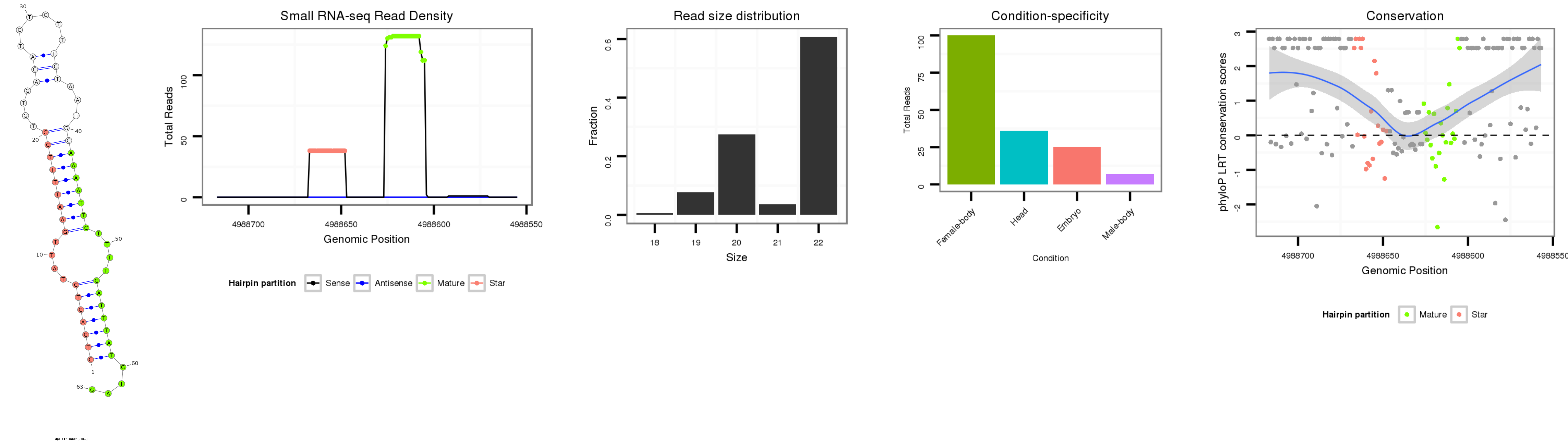
Species	Coordinate	ID	Alignment
droPer2	scaffold_3:6409860-6410024 -	dpe_97	TTACAAAATAATCAATAAAACAATCAATATCGATAATTTTATAATCGTCGATATAAAATCGTTTGTATTAAATTTTAAATCAATAACACAATCAATATCGATAATTTTATAATCG
dp5	2:23634820-23634984 =		TTACAAAATAATCAATAAAACAATCAATATCGATAATTTTATAATCGTCGATATAAAATCGTTTGTATTAAATTTTAAATCAATAACACAATCAATATCGATAATTTTATAATCG

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

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Show Alternate Folds

Flybase annotation

intron [Dper\GL25587-in]; CDS [Dper\GL25587-cds]; CDS [Dper\GL25587-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

TACGTTCCCCAACATCACTTGTAGTCGGTTTCATCATTAACCGCTTTC	Read #		Hit	Total		M042	V057	M021	V050	V111	V042
GTAGTCTATTGAATTTCC	size	Mismatch	Count	Norm	Total	female body	head	embryo	head	male body	embryo
*****(((((((.....((((((((.....((.....))).....))))))))......))))).*****	22	0	1	102.00	102	78	9	4	9	1	1
.....AAATTCCTTTGATTATGTAG.....	20	0	1	38.00	38	12	9	5	4	6	2
.....GTAGTCTATTGAATTTCC.....	19	0	1	13.00	13	0	1	12	0	0	0
.....AAATTCCTTTTGATTATATG.....	20	0	1	7.00	7	3	2	0	2	0	0
.....AAATTCCTTTTGATTATATGT.....	21	0	1	6.00	6	6	0	0	0	0	0
.....AAATTCCTTTTGATTATGTAG.....	23	1	1	2.00	2	0	1	0	1	0	0
.....AAATTCCTTTTGATTATGTAG.....	23	0	1	2.00	2	0	0	2	0	0	0
.....TTGGGACGGGCCGTGAATGTGT.....	22	0	1	1.00	1	0	0	0	0	1	0
.....AAATTCCTTTTGATTATGTAGA.....	24	1	1	1.00	1	1	0	0	0	0	0
.....TTCTTTTGATTATGTAG.....	18	0	1	1.00	1	0	0	0	0	0	1
.....AATTCCTTTTGATTATGTAG.....	20	0	1	1.00	1	1	0	0	0	0	0

Anti-sense strand reads

										M042
AGTGC AAGGGGTTTGTAGTGA AACTACGACCAAGTAGTAA TGGCGAAAC CACTCAGATAACTTAA AAGGACACTGTAGAGAAACATTACCTTTTAAGAA AACTAATACATCTAGACGCGCGGGAACCTGCCCGCACTTACACATAGGGAACAGACCAA										
*****(((((((.....((((((((.....((.....))).....)))))).....)))).....*****										Read # size Mismatch Count Norm Total
										female body

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droPer2	scaffold_5:4988557-4988717 - dpe_112		TCACGTTCCCAACATCACTTTGATGCTGGTTTCATCATTTACCGCTTTCTGTAGTCTA-TTGAA-----TT--TTCTGTGACATCTCTTTGTAATGG-AAAAAT-----TCTT--T-TGATTTATGAGATCTGCGGGCCCTTGGACGGCCGTGAATGTGTATCCCTTGTCCTGG
dp5	4_groups:488286-488446 - dps_109		TCACGTTCCCAACATCACTTTGATGCTGGTTTCATCATTTACCGCTTCTGTAGTCTA-TTGAA-----TT--TTCTGTGACATCTCTTTGTAATGG-AAAAAT-----TCTT--T-TGATTTATGAGATCTGCGGGCCCTTGGACGGCCGTGAATGTGTATCCCTTGTCCTGG
droW112	scf2_1100000004577:2571121-2571281 -		TACGTTCCCAACATCATTTTGATGCTGGTTTCATCATTAACGCTTTCTGTAGTCTA-TTGAA-----TTCAAACGA-----ATACTCTTAAT-G-TTAATT-TGT--TA--T-TCTTT-T-TAGATCTGCGCGCTTGGCGCAAGCTGTCAATGTTATCCCTTGTCCTGG
droVir3	scaffold_12963:14698075-14698235 -		TACGTTCCCAACATCATTTGATGCTGGTTTCATCATTAACCGCTTTCTGTAGTCTA-TTGAA-----TTCAAACGA-----ATACTCTTAAT-G-TTAATT-TGT--TA--T-TCTTT-T-TAGATCTGCGCGCTTGGCGCAAGCTGTCAATGTTATCCCTTGTCCTGG
droMo3	scaffold_6500:17627223-17627380 -		TCACGTTCCCAACATCATTTGATGCTGGTTTCATCATTAACGCTTTCTGTAGTCTA-TTGAA-----TTAA-----TGGTGAATAATATTTTTCAT-AAATAACT-TG---TA-TTC-TGATCTGCGCGCTTGGCGCAAGCTGTCAATGTTATCCCTTGTCCTGG
droGr12	scaffold_15126:1868129-1868299 +		TCACGTTCCCAACATCATTTGATGCTGGTTTCATCATTAACCGCTTTCTGTAGTCTA-TTGAA-----TTAA-----TAAATTTTGTATTATT-A---A-TTA-TAATAGATTTGGCGCTCTGGGACCTGCCGTGAATGTGTATCCCTTGTCCTGG
droAna3	scaffold_12916:8572270-8572425 -		TACGTTCCCAACATCATTTTGATGCTGGTTTCATCATTAACGCTTTCTGTAGTCTA-TTGAA-----TTAAATATTTTAACTAA-AAATA-----C-GA-C-TGAA-TTGTAGATCTGCGCGCTTGGCGCAAGCTGTCAATGTTATCCCTTGTCCTGG
droBip1	scf7180000396535:1089826-1089981 -		TACGTTCCCAACATCATTTTGATGCTGGTTTCATCATTAACGCTTTCTGTAGTCTA-TTGAA-----TTAAATATTTTAACTAA-AAATA-----C-GA-C-TGAA-TTGTAGATCTGCGCGCTTGGCGCAAGCTGTCAATGTTATCCCTTGTCCTGG
droK1k1	scf7180000302473:486009-486160 -		TACGTTCCCAACATCACTTTGATGCTGGTTTCATCATTAACCGCTTTCTGTAGTCTA-TTGAA-----TTAAATATTTTAACTAA-AAATA-----C-GA-C-TGAA-TTGTAGATCTGCGCGCTTGGCGCAAGCTGTCAATGTTATCCCTTGTCCTGG
droFic1	scf7180000453815:362261-362419 -		TACGTTCCCAACATCACTTTGATGCTGGTTTCATCATTAACCGCTTTCTGTAGTCTA-TTGAA-----TTAAATATTTTAACTAA-AAATA-----C-GA-C-TGAA-TTGTAGATCTGCGCGCTTGGCGCAAGCTGTCAATGTTATCCCTTGTCCTGG
droEle1	scf7180000490970:242361-242522 -		TACGTTCCCAACATCATTTTGATGCTGGTTTCATCATTAACGCTTTCTGTAGTCTA-TTGAA-----TTAAATATTTTAACTAA-AAATA-----C-GA-C-TGAA-TTGTAGATCTGCGCGCTTGGCGCAAGCTGTCAATGTTATCCCTTGTCCTGG
droRho1	scf7180000780014:189901-190060 -		TACGTTCCCAACATCATTTTGATGCTGGTTTCATCATTAACGCTTTCTGTAGTCTA-TTGAA-----TTAAATATTTTAACTAA-AAATA-----C-GA-C-TGAA-TTGTAGATCTGCGCGCTTGGCGCAAGCTGTCAATGTTATCCCTTGTCCTGG
droBia1	scf7180000302422:2777643-2777807 -		TACGTTCCCAACATCATTTTGATGCTGGTTTCATCATTAACGCTTTCTGTAGTCTA-TTGAA-----TTAAATATTTTAACTAA-AAATA-----C-GA-C-TGAA-TTGTAGATCTGCGCGCTTGGCGCAAGCTGTCAATGTTATCCCTTGTCCTGG
droTak1	scf7180000415104:133001-133157 -		TCACGTTCCCAACATCATTTTGATGCTGGTTTCATCATTAACGCTTTCTGTAGTCTA-TTGAA-----TTAAATATTTTAACTAA-AAATA-----C-GA-C-TGAA-TTGTAGATCTGCGCGCTTGGCGCAAGCTGTCAATGTTATCCCTTGTCCTGG
droEud1	scf7180000409463:2115716-2115875 +		TACGTTCCCAACATCATTTTGATGCTGGTTTCATCATTAACGCTTTCTGTAGTCTA-TTGAA-----TTAAATATTTTAACTAA-AAATA-----C-GA-C-TGAA-TTGTAGATCTGCGCGCTTGGCGCAAGCTGTCAATGTTATCCCTTGTCCTGG
dm3	chr2L:6681343-6681513 -		TCACGTTCCCAACATCATTTTGATGCTGGTTTCATCATTAACGCTTTCTGTAGTCTA-TTGAA-----TTAAATATTTTAACTAA-AAATA-----C-GA-C-TGAA-TTGTAGATCTGCGCGCTTGGCGCAAGCTGTCAATGTTATCCCTTGTCCTGG
droSim2	2L:6455060-6455229 -		TCACGTTCCCAACATCATTTTGATGCTGGTTTCATCATTAACGCTTTCTGTAGTCTA-TTGAA-----TTAAATATTTTAACTAA-AAATA-----C-GA-C-TGAA-TTGTAGATCTGCGCGCTTGGCGCAAGCTGTCAATGTTATCCCTTGTCCTGG
droSec2	scaffold_3:2220375-2220535 -		TCACGTTCCCAACATCATTTTGATGCTGGTTTCATCATTAACGCTTTCTGTAGTCTA-TTGAA-----TTAAATATTTTAACTAA-AAATA-----C-GA-C-TGAA-TTGTAGATCTGCGCGCTTGGCGCAAGCTGTCAATGTTATCCCTTGTCCTGG
droTak3	2L:6231850-6232015 +		TCACGTTCCCAACATCATTTTGATGCTGGTTTCATCATTAACGCTTTCTGTAGTCTA-TTGAA-----TTAAATATTTTAACTAA-AAATA-----C-GA-C-TGAA-TTGTAGATCTGCGCGCTTGGCGCAAGCTGTCAATGTTATCCCTTGTCCTGG
droEr2	scaffold_4929:15591484-15591645 -		TCACGTTCCCAACATCATTTTGATGCTGGTTTCATCATTAACGCTTTCTGTAGTCTA-TTGAA-----TTAAATATTTTAACTAA-AAATA-----C-GA-C-TGAA-TTGTAGATCTGCGCGCTTGGCGCAAGCTGTCAATGTTATCCCTTGTCCTGG

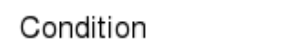
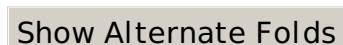
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	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	2
rescue.candidate	0

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

Predicted structure

Predicted structure



Flybase annotation

Flybase annotation

intron [Dper^ΔGL26753-in]; CDS [Dper^ΔGL26753-cds]; CDS [Dper^ΔGL26753-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads

show mid mismatch reads

GCGCCGTTGCGTGGCCTTGTTCGATCTGAGGAGCCAAAAGAGGATCTTCTGTGAGTGCCTATGTCAAACCCAAATGCTGGCGGAGCGCGCTTAATTGGGTTACACCTTTTCCACTCACACAGCCAAACAATGAGCATCCCGAGGTGATACAGTGGCGCAGTTGGCGCGAGGATT	Read #	size	Mismatch	Hit Count	Total Norm	Total	female body	V057 head	V050 head	M021 embryo	V042 embryo	V111 male body
*****(((((((.....(((((((.....)))))))))))).*****	22	0	1	39.00	39	23	7	8	0	1	0	
.....TTCACCTTTTCCACTCACACAG.....	22	0	1	12.00	12	6	5	1	0	0	0	
.....GTTACACCTTTTCCACTCACACA.....	21	0	1	7.00	7	4	1	2	0	0	0	
.....TTCACCTTTTCCACTCACACA.....	23	1	1	6.00	6	0	2	3	0	0	1	
.....GTTACACCTTTTCCACTCACACAG.....	23	0	1	5.00	5	4	0	0	0	1	0	
.....TTCACCTTTTCCACTCACAC.....	20	0	1	3.00	3	0	1	0	2	0	0	
.....CTGTTCGATCTGAGGAGC.....	19	0	1	3.00	3	0	0	0	3	0	0	
.....GTGAGTGCCTATGTCAAACCC.....	21	0	1	3.00	3	2	1	0	0	0	0	
.....GTTACACCTTTTCCACTCACACA.....	24	1	1	2.00	2	0	1	1	0	0	0	
.....GTGAGTGCCTATGTCAAACCC.....	20	0	1	2.00	2	1	0	1	0	0	0	
.....AATCTGGGCGAGCGCGCTTAATTGG.....	27	0	1	2.00	2	0	1	0	0	0	1	
.....ACCTTTTCCACTCACACAG.....	19	0	1	1.00	1	0	0	1	0	0	0	
.....GATACAGTCGGCCAGTTGGCGCG.....	23	0	1	1.00	1	1	0	0	0	0	0	
.....ATACAGTCGGCCAGTTGGCGCGA.....	23	0	1	1.00	1	0	0	0	1	0	0	
.....TGCTGGGCGAGCGCGCTTAATTGG.....	25	0	1	1.00	1	1	0	0	0	0	0	
.....GTTACACCTTTTCCACTCACAG.....	21	1	1	1.00	1	1	0	0	0	0	0	
.....CCTGTTCGATCTGAGGAGCCAAAAGGA.....	28	0	1	1.00	1	1	0	0	0	0	0	
.....GAGGCGCGCTTAATTGGGT.....	19	0	1	1.00	1	1	0	0	0	0	0	
.....TTCACCTTTTCCACTCACACAG.....	21	0	1	1.00	1	1	0	0	0	0	0	
.....GTGAGTGCCTATGTCAAACCC.....	20	0	1	1.00	1	1	0	0	0	0	0	
.....GTTACACCTTTTCCACTCACA.....	20	0	1	1.00	1	1	0	0	0	0	0	
.....GTTACACCTTTTCCACTCACAC.....	21	0	1	1.00	1	0	0	1	0	0	0	
.....CACCTTTTCCACTCACACA.....	19	0	1	1.00	1	1	0	0	0	0	0	

Anti-sense strand reads

[illegible]

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droPer2	scaffold_25:785638-785808	dpe_1260	GGCCGGTTGCGTGCCCTTGTTCGATCTGAGGACCAAAAGAGATCTTCTGTAGTGCC-TATG-----TCAAACCGAATGCTG-----GGC-----G-----AGC-----GCCGTCTAATTGGCTCA-CTTTT-----CC-A-CTCA-----CA--CAGCCAACATGAGCATCCCGAGGTGATACAGTCGGCCAGTTGGCGCGAGGAT
dp5	Xl_group1a:6527963-6528133	dps_2543	GGCCGGTTGCGTGCCCTTGTTCGATCTGAGGACCAAAAGAGATCTTCTGTAGTGCC-TATG-----TCAAACCGAATGCTG-----GGC-----G-----AGC-----GACGTCTAATTGGCTCA-CTTTT-----CC-A-CTCA-----CA--CAGCCAACATGAGCATCCCGAGGTGATACAGTCGGCCAGTTGGCGCGAGGAT
droWil2	scaffold_1100000004401:904031-904195		AGAGCTTCGTGGCGAGCTTCATCTGAGCGTGCAGGAGAGATATCTGTAGTTTACACATTTTATTCTC-A-----GGT-----TCCCGCTTGTGA-ATSCAT-G-TT-----A--A-TTTC-CAGCAACATGAGCATCCCGAGGTGATACAGTCGGCCAGTTGGCGCGAGGAT
droVir3	scaffold_12928:4070365-4070529		GGCTGCCTGTGGCGAGCTTCGATCTGCTGCGCAAAAGAGATCTTCTGTAGTAATG-----CGAGCGAATGCTGAG-----CGACTTACATTAACTGCCATTCAATAAATCTC-CAGCAACATGAGCATCCCGAGGTGATACAGTCGGCCAGTTGGCGCGAGGAT
droMoJ3	scaffold_6359:662123-662289		GGCTGCCTGTGGCGAGCTTCGATCTGCGSCCAAAAGGATATCTCTGTAGTAGACAAACATT-----GGCATTCGAAT-TGTA--ACTGTACFAAT-GA-CACG-G-CTT-----A--CTCT-C-CAGCAACATGAGCATCCCGAGGTGATACAGTCGGCCAGTTGGCGCGAGGAT
droGr12	scaffold_14853:596522-596685		AGCCGGTTCGTGGCGAGCTTCGATCTGCGSCCAAAAGGATATCTCTGTAGTAAATCAATTTCTAATTTTATGCTATA-A-----AAAT-----AAAT-----ATTC-----A-----TTT-----G-G-CCTC-TC-CAGCAACATGAGCATCCCGAGGTGATACAGTCGGCCAGTTGGCGCGAGGAT
droAna3	scaffold_13335:2206581-2206743		AGCCGGTTCGTGGCGAGCTTCGATCTGAGCGCAAAAGAGATATCTCTGTAGTTC-CTTG-----CGAGGTG-CTT-CGA-----GAA-A-ATAAATATAAG-AG-T-----CT-----T-G-C-A-TCCITTA-CAACATGAGCATCCCGAGGTGATACAGTCGGCCAGTTGGCGCGAGGAT
droBip1	scaffold_18000039371:738592-738753		AGCCGGTTCGTGGCGAGCTTCGATCTGAGTGCCAAAAGAGATATCTCTGTAGTCAAGSACCAGTCTT-A-----T-----TGAAGC-----GAT-----ACTCTATATAAGC-AG-A-----AT-----CC-TTC-C-TC-CAGCAACATGAGCATCCCGAGGTGATACAGTCGGCCAGTTGGCGCGAGGAT
droRik1	scaffold_17180000302610:412331-412496		AGCCGGCTGTGGCGAGCTTCGATCTGAGCAAAAGAGATCTTCTGTAGTTGTATATCTCTCGCGAGTACCCCCCACTCG-----TAA-GTCTAA-CAC-AA-A-----T-T-----T-C-TCTC-TC-CAGCAACATGAGCATCCCGAGGTGATACAGTCGGCCAGTTGGCGCGAGGAT
droFic1	scaffold_180000454072:707233-707396		AGCGGTTTCGTGGCGAGCTTCGATCTGAGCACTCAAAAGAGATCTTCTGTAGTAAACGCAATTTACATATGTCGAC-A-----AGC-----ATCTGTAA-C-TCGGGTTT-----T-A-T-GC-C-CAGCAACATGAGCATCCCGAGGTGATACAGTCGGCCAGTTGGCGCGAGGAT
droEle1	scaffold_1800004910061:1296775-1296956		AGCCGGCTGCTGGCGAGCTTCGATCTGAGCAAAAGAGATCTTCTGTAGTCAACGCTCTCTGCTG-A-----TCAT-T-----TAAACAACTCAAC-A-----AAC-----GCACTTAA-C-CCAATCT-----TT-TTC-CCGCGA-TAGCAACATGAGCATCCCGAGGTGATACAGTCGGCCAGTTGGCGCGAGGAT
droRho1	scaffold_176000763611:421203-421367		AGCCGGTTGCGTGCGAGCTTCGATCTGAGCAAAAGAGATCTTCTGTAGTCACAGCTCTCTCTCT-A-----AAAT-----TAA-----ATTCAATCGAA-G-T-----TTT-----TT-TGC-C-C-CAGCAACATGAGCATCCCGAGGTGATACAGTCGGCCAGTTGGCGCGAGGAT
droBia1	scaffold_180000301760:1902349-1902510		AGCCGGCTGCGTGCGAGCTTCGATCTGAGCAAAAGAGATCTTCTGTAGTCAACGCTCTCCCTTTTC-----CAAT-----SA-----ACTTCTAGTAAAGC-C-----CT-----TTGTTTC-C-C-CAGCAACATGAGCATCCCGAGGTGATACAGTCGGCCAGTTGGCGCGAGGAT
droTak1	scaffold_180000415873:314726-314887		AGCCGGCTGTGGCGAGCTTCGATCTGAGCAAAAGAGATCTTCTGTAGTCAC-TACTTTCTCTTTTC-----CAAG-----AGA-----ATCTGTAATAAAGT-C-----CT-----TCTTTC-A-CAGCAACAGCAGCAGSAGSGATGATACAGTCGGCCAGTTGGCGCGAGGAT
droEug1	scaffold_180000490955:129002-129162		AGCCGGTTGCGTGTGAGCTTCGATCTGAGCAAAAGAGATCTTCTGTAGTTAA-CCTCTCTCTTTT-A-----CTTA-----TGA-----ACATAAATAAG-GT-A-----ATT-----TG-GTTTC-C-C-CAGCAACATGAGCATCCCGAGGTGATACAGTCGGCCAGTTGGCGCGAGGAT
dm3	chrX:6700788-6700963		AGCCGGCTGCGTGCGAGCTTCGATCTGAGCACTCAAAAGAGATATCTGTAGTAAACCATTTTTPTTTTTTTTTTTTTTT-----AAAT-----AAAT-----ACCTTAACTAAAGT-G-----TTT-----AA-----ACCTTAACTAAAGT-G-----TTT-----TTGCTCTC-T-A-CAGCAACATGAGCATCCCGAGGTGATACAGTCGGCCAGTTGGCGCGAGGAT
droSim2	scaffold_4:35128-35290		AGCCGGCTGCGTGCGAGCTTCGATCTGAGCACTCAAAAGAGATATCTGTAGTAAACCATTTTCTCTCTA-----AAAT-----AAAT-----ACCTTAACTAAAGT-G-----TTT-----TTGCTCTC-T-A-CAGCAACATGAGCATCCCGAGGTGATACAGTCGGCCAGTTGGCGCGAGGAT
droSec2	scaffold_4:35128-35290		AGCCGGCTGCGTGCGAGCTTCGATCTGAGCACTCAAAAGAGATATCTGTAGTAAACCATTTTCTCTCTA-----AAAT-----AAAT-----ACCTTAACTAAAGT-G-----TTT-----TTGCTCTC-T-A-CAGCAACATGAGCATCCCGAGGTGATACAGTCGGCCAGTTGGCGCGAGGAT
droYak3	X1:2668188-2668347		AGCCGGCTGCGTGCGAGCTTCGATCTGAGCACTCAAAAGAGATATCTGTAGTAAACCATTTTCTCTCTA-----AAAT-----AAAT-----ACCTTAACTAAAGT-G-----TTT-----TTGCTCTC-T-A-CAGCAACATGAGCATCCCGAGGTGATACAGTCGGCCAGTTGGCGCGAGGAT
droEre2	scaffold_4690:15628870-15629029		AGCCGGCTGCGTGCGAGCTTCGATCTGAGCACTCAAAAGAGATATCTGTAGTAAACCATTTTCTCTCTA-----AAAT-----AAAT-----ACCTTAACTAAAGT-G-----TTT-----TTGCTCTC-T-A-CAGCAACATGAGCATCCCGAGGTGATACAGTCGGCCAGTTGGCGCGAGGAT

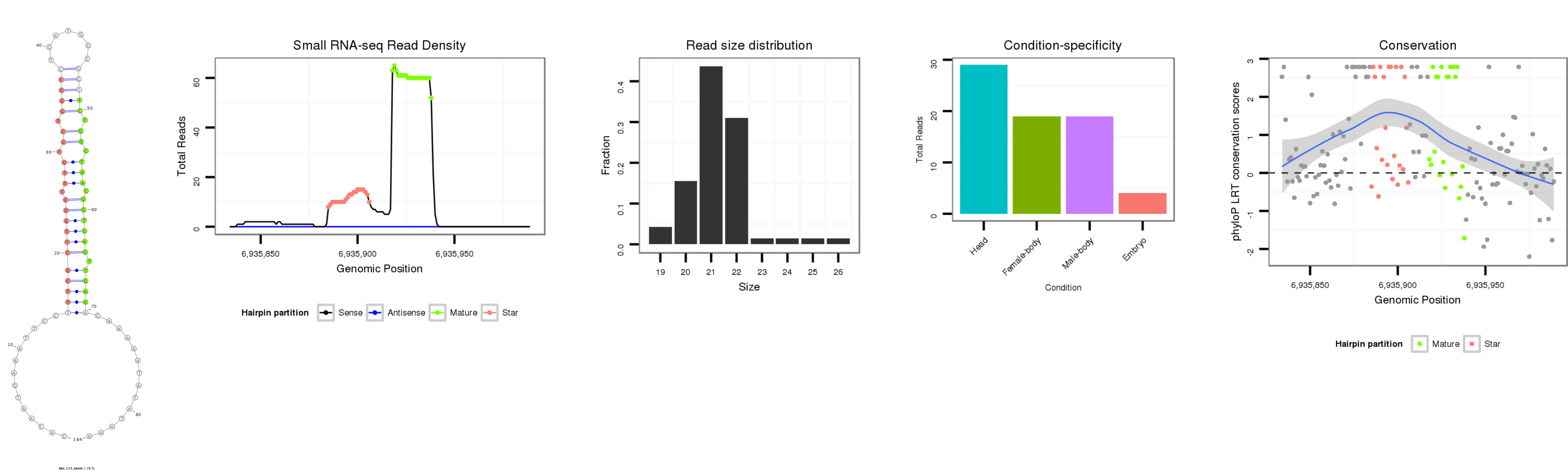
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	PASS/Fail
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crit.loop	0
crit.mor	0
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crit.total	1
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crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	2
rescue.candidate	0

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dpe_123	scaffold_4:6935884-6935939 +	confident	Canonical miRNA	intron	[View on UCSC Genome Browser (Cornell Mirror)]

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Show Alternate Folds

Flybase annotation

intron [Dper/GL17765-in]; CDS [Dper/GL17765-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

Read #	Hit	Total	V057	M042	V111	V050	V042	M021
size	Mismatch	Count	Norm	Total	female head	female body	male head	embryo
21	0	1	28.00	28	13	3	11	1
22	0	1	17.00	17	6	3	6	2
20	0	1	6.00	6	2	2	1	1
23	0	1	4.00	4	0	2	1	1
22	0	1	3.00	3	0	2	0	1
22	1	1	2.00	2	1	0	1	0
21	0	1	2.00	2	0	2	0	0
19	0	1	1.00	1	0	1	0	0
22	0	1	1.00	1	1	0	0	0
23	0	1	1.00	1	0	1	0	0
20	0	1	1.00	1	0	1	0	0
22	0	1	1.00	1	1	0	0	0
20	0	1	1.00	1	0	0	0	1
19	0	1	1.00	1	1	0	0	0
26	0	1	1.00	1	0	1	0	0
20	0	1	1.00	1	1	0	0	0
19	0	1	1.00	1	0	1	0	0
20	0	1	1.00	1	0	1	0	0
24	1	1	1.00	1	1	0	0	0
19	0	1	1.00	1	0	0	0	1
19	0	1	1.00	1	0	0	1	0
24	0	1	1.00	1	0	0	0	1
24	0	1	1.00	1	1	0	0	0
21	0	1	1.00	1	0	0	1	0
20	0	1	1.00	1	0	1	0	0
20	0	1	1.00	1	0	0	1	0
25	0	1	1.00	1	0	1	0	0

Anti-sense strand reads

CAACGGACGGACGGACGCCTGGTTTAGAAGTGATTAGGTGTTACTTTTAAGGAAGCGAAACGGAACAGGACCCGACTACCGCCGAGACCGGATGCCACTCAACTCTGTTTTATATATTTTCACATAAAATTTAAATTAATAATATAAATAAACACA															M042	V050	V057	V111
*****((																		

Show Alignment With Reads

Re-alignment of all predicted orthologs

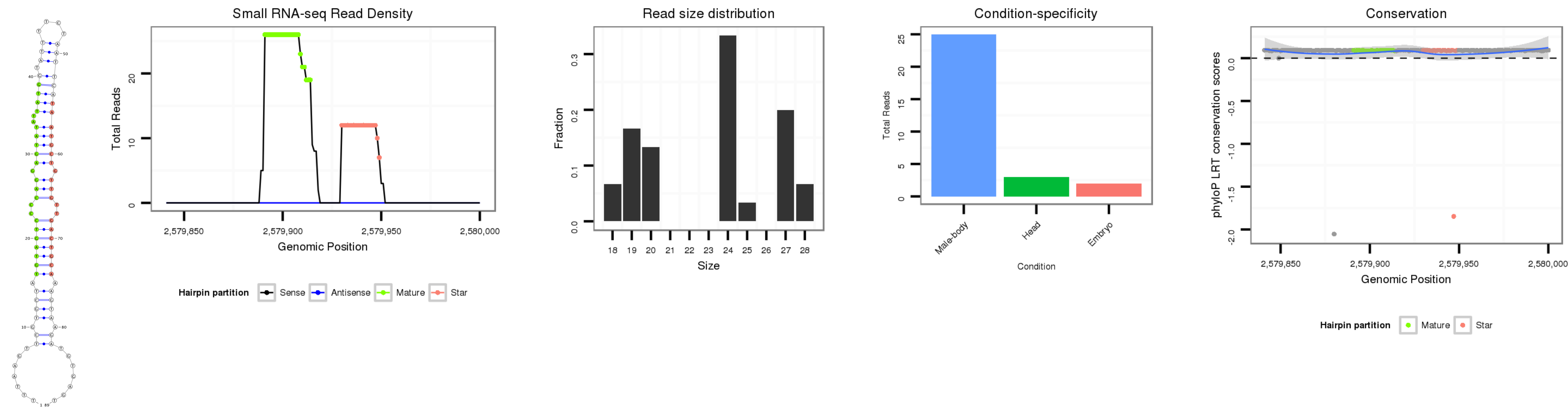
Species	Coordinate	ID	Alignment
droPer2	scaffold_4:6935834-6935989 -	dpe_123	GTTCCTGCCTGC-CGTGCACC---AAAT-----CTT--CACTAATCC-----ACAATGAAATTCCTTTCGCTTGCCCTTTGCTCGGGCTGATGGCGGCCTGGCTAACGGTGAGTTGAGACAAA--A-----ATATA-----TAAAAGTGAT-----TT--A--AATTTAATTATTATA-----TTTATTG---TGT
dp5	3:11535110-11535265 +	dpe_88	GTTCCTGCCTGC-CGTGCACC---AAAT-----CTT--CACTAATCC-----ACAATGAAATTCCTTTCGCTTGCCCTTTGCTCGGGCTGATGGCGGCCTGGCTAACGGTGAGTTGAGACAAA--A-----ATATA-----TAAAAGTGAT-----TT--A--AATTTAATTATTATA-----TTTATTG---TGT
droW112	scf2_1100000004954:3517015-3517155 -		GTTCCTGCCTGC-CGTGCACC---AAAT-----CTT--CACTAATCC-----ACAATGAAATTCCTTTCGCTTGCCCTTTGCTCGGGCTGATGGCGGCCTGGCTAACGGTGAGTTGAGACAAA--A-----ATATA-----TAAAAGTGAT-----TT--A--AATTTAATTATTATA-----TTTATTG---TGT
droV1r3	scaffold_12963:5776869-5777023 +		GTTCCTGCCTGC-CGTGCACC---AAAT-----CTT--CACTAATCC-----ACAATGAAATTCCTTTCGCTTGCCCTTTGCTCGGGCTGATGGCGGCCTGGCTAACGGTGAGTTGAGACAAA--A-----ATATA-----TAAAAGTGAT-----TT--A--AATTTAATTATTATA-----TTTATTG---TGT
droMoj3	scaffold_6496:6196795-6196970 +		GTTCCTGCCTGC-CGTGCACC---AAAT-----CTT--CACTAATCC-----ACAATGAAATTCCTTTCGCTTGCCCTTTGCTCGGGCTGATGGCGGCCTGGCTAACGGTGAGTTGAGACAAA--A-----ATATA-----TAAAAGTGAT-----TT--A--AATTTAATTATTATA-----TTTATTG---TGT
droGr12	scaffold_15252:7673893-7674052 -		GTTCCTGCCTGC-CGTGCACC---AAAT-----CTT--CACTAATCC-----ACAATGAAATTCCTTTCGCTTGCCCTTTGCTCGGGCTGATGGCGGCCTGGCTAACGGTGAGTTGAGACAAA--A-----ATATA-----TAAAAGTGAT-----TT--A--AATTTAATTATTATA-----TTTATTG---TGT
droAna3	scaffold_12916:10236226-10236369 -		GTTCCTGCCTGC-CGTGCACC---AAAT-----CTT--CACTAATCC-----ACAATGAAATTCCTTTCGCTTGCCCTTTGCTCGGGCTGATGGCGGCCTGGCTAACGGTGAGTTGAGACAAA--A-----ATATA-----TAAAAGTGAT-----TT--A--AATTTAATTATTATA-----TTTATTG---TGT
droBip1	scf7180000396769:1103296-1103437 -		GTTCCTGCCTGC-CGTGCACC---AAAT-----CTT--CACTAATCC-----ACAATGAAATTCCTTTCGCTTGCCCTTTGCTCGGGCTGATGGCGGCCTGGCTAACGGTGAGTTGAGACAAA--A-----ATATA-----TAAAAGTGAT-----TT--A--AATTTAATTATTATA-----TTTATTG---TGT
droKik1	scf7180000302471:64179-64358 -		GTTCCTGCCTGC-CGTGCACC---AAAT-----CTT--CACTAATCC-----ACAATGAAATTCCTTTCGCTTGCCCTTTGCTCGGGCTGATGGCGGCCTGGCTAACGGTGAGTTGAGACAAA--A-----ATATA-----TAAAAGTGAT-----TT--A--AATTTAATTATTATA-----TTTATTG---TGT
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droE1e1	scf7180000489694:114611-114786 +		GTTCCTGCCTGC-CGTGCACC---AAAT-----CTT--CACTAATCC-----ACAATGAAATTCCTTTCGCTTGCCCTTTGCTCGGGCTGATGGCGGCCTGGCTAACGGTGAGTTGAGACAAA--A-----ATATA-----TAAAAGTGAT-----TT--A--AATTTAATTATTATA-----TTTATTG---TGT
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droBia1	scf7180000302292:2305401-2305580 -		GTTCCTGCCTGC-CGTGCACC---AAAT-----CTT--CACTAATCC-----ACAATGAAATTCCTTTCGCTTGCCCTTTGCTCGGGCTGATGGCGGCCTGGCTAACGGTGAGTTGAGACAAA--A-----ATATA-----TAAAAGTGAT-----TT--A--AATTTAATTATTATA-----TTTATTG---TGT
droTak1	scf7180000416016:451699-451873 -		GTTCCTGCCTGC-CGTGCACC---AAAT-----CTT--CACTAATCC-----ACAATGAAATTCCTTTCGCTTGCCCTTTGCTCGGGCTGATGGCGGCCTGGCTAACGGTGAGTTGAGACAAA--A-----ATATA-----TAAAAGTGAT-----TT--A--AATTTAATTATTATA-----TTTATTG---TGT
droEug1	scf7180000409672:3286465-3286632 +		GTTCCTGCCTGC-CGTGCACC---AAAT-----CTT--CACTAATCC-----ACAATGAAATTCCTTTCGCTTGCCCTTTGCTCGGGCTGATGGCGGCCTGGCTAACGGTGAGTTGAGACAAA--A-----ATATA-----TAAAAGTGAT-----TT--A--AATTTAATTATTATA-----TTTATTG---TGT
dm3	chr2R:14275631-14275801 +		GTTCCTGCCTGC-CGTGCACC---AAAT-----CTT--CACTAATCC-----ACAATGAAATTCCTTTCGCTTGCCCTTTGCTCGGGCTGATGGCGGCCTGGCTAACGGTGAGTTGAGACAAA--A-----ATATA-----TAAAAGTGAT-----TT--A--AATTTAATTATTATA-----TTTATTG---TGT
droSim2	2r:14943075-14943245 +		GTTCCTGCCTGC-CGTGCACC---AAAT-----CTT--CACTAATCC-----ACAATGAAATTCCTTTCGCTTGCCCTTTGCTCGGGCTGATGGCGGCCTGGCTAACGGTGAGTTGAGACAAA--A-----ATATA-----TAAAAGTGAT-----TT--A--AATTTAATTATTATA-----TTTATTG---TGT
droSec2	scaffold_1:111750839-11751014 +		GTTCCTGCCTGC-CGTGCACC---AAAT-----CTT--CACTAATCC-----ACAATGAAATTCCTTTCGCTTGCCCTTTGCTCGGGCTGATGGCGGCCTGGCTAACGGTGAGTTGAGACAAA--A-----ATATA-----TAAAAGTGAT-----TT--A--AATTTAATTATTATA-----TTTATTG---TGT
droYak3	2R:14912646-14912815 -		GTTCCTGCCTGC-CGTGCACC---AAAT-----CTT--CACTAATCC-----ACAATGAAATTCCTTTCGCTTGCCCTTTGCTCGGGCTGATGGCGGCCTGGCTAACGGTGAGTTGAGACAAA--A-----ATATA-----TAAAAGTGAT-----TT--A--AATTTAATTATTATA-----TTTATTG---TGT
droEre2	scaffold_4845:8481608-8481755 +		GTTCCTGCCTGC-CGTGCACC---AAAT-----CTT--CACTAATCC-----ACAATGAAATTCCTTTCGCTTGCCCTTTGCTCGGGCTGATGGCGGCCTGGCTAACGGTGAGTTGAGACAAA--A-----ATATA-----TAAAAGTGAT-----TT--A--AATTTAATTATTATA-----TTTATTG---TGT

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

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



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

T										AGGTTAGGTTATTATTTTCAAAACGTAGATTA										AATTCAGCAGCAT										ACATCAGGGGTCCTCATATAATAC										CATAAAGATTAAGT										ATTACGACAACAAC										TGACGT										TTCATTCTACACTCATGAGGTGTTTCTTACTAATTACTTTTAATTCGTTT										Read #	Hit	Total		
*****																				(((										(((										(((										(((										(((										*****										size	Mismatch	Count	Norm	Total
No data available in table																																																																																				

No data available in table

Show Alignment With Reads

Re-alignment of all predicted orthologs

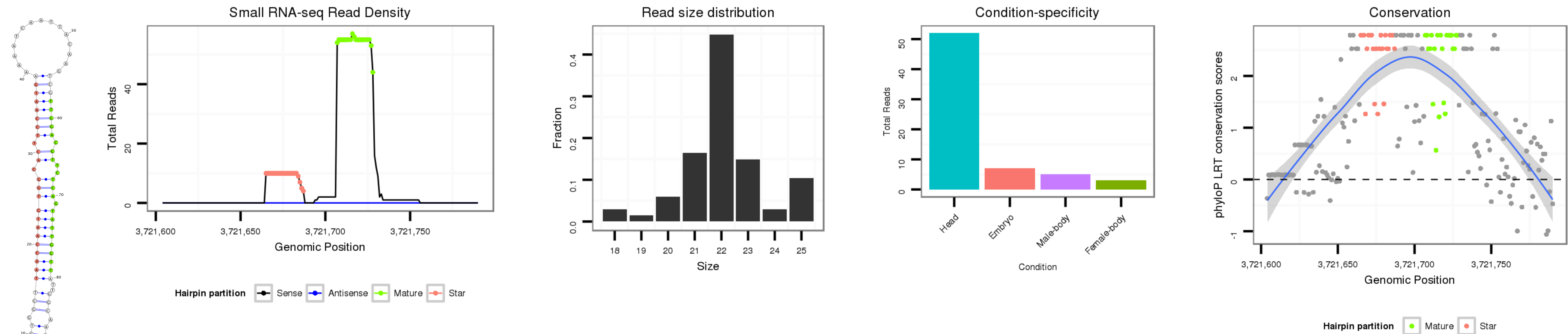
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dp5	4_group4:3551993-3552151_+	dps_18	AATCCAATCAATAATAAAAAAGTTTTGCATCTAATTTA G TTCTGTGCTA TGTAGTCCCAGGAGTATATTATG GTATTTTCTAATTC TAATGCTGTTGTGACTACA AAGTAAGATGTGAGTACTCCACAAAGATGATTAAATGAAAATTAAGCAAA

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

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Show Alternate Folds

Flybase annotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

[illegible]

Anti-sense strand reads

Show Alignment With Reads

Re-alignment of all predicted orthologs

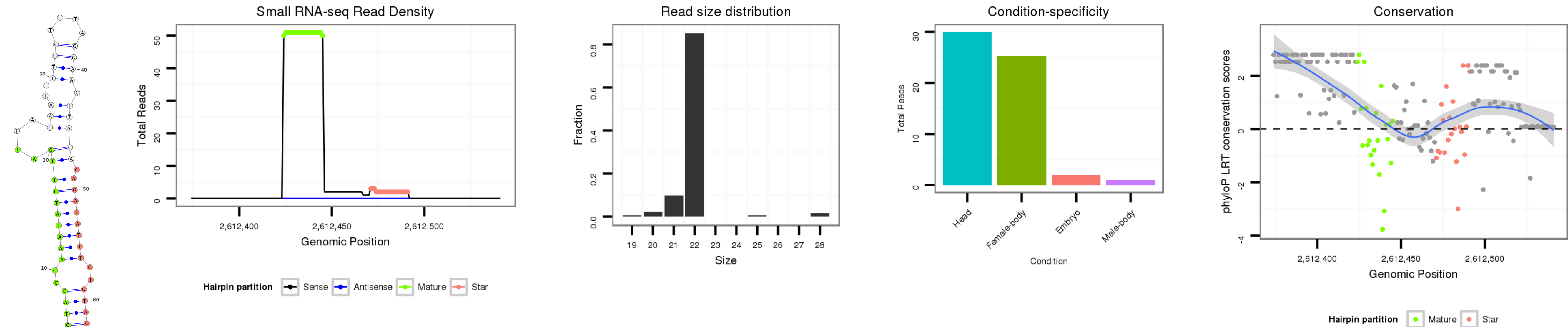
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dp5	2:16675560-16675746 -	dps_3828	CGGTTCTTTCCATGCTCCAATAAAGAAACGT-----GAAAGGTGACAAGTTG-----GGGGTCTTGGCTTAACCAATGTGGCACTTCCAATGAAAAATCAATTACAAGTCGTGGACGTCTCTCAGTATTGGTTATTGGCAAGAAGAGCCACAGGCAGCTATAAG--AG-----TT-----ACAATTGTAAGATAGATTAGCG-----CTT-----
droWi12	scf2_1100000004902:9400240:9400380 +	dvi_5416	CGGTTCTTTCCATGCTCCAATAAAGAAACGT-----GAAAGGTGACAAGTTG-----GGGGTCTTGGCTTAACCAATGTGGCACTTCCAATGAAAAATCAATTACAAGTCGTGGACGTCTCTCAGTATTGGTTATTGGCAAGAAGAGCCACAGGCAGCTATAAG--AG-----TT-----ACAATTGTAAGATAGATTAGCG-----CTT-----
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droMoJ3	scaffold_6540:7667621-7667797 -	dmo_270	CGGTTCTTTCCATGCTCCAATAAAGAAACGT-----GAAAGGTGACAAGTTG-----GGGGTCTTGGCTTAACCAATGTGGCACTTCCAATGAAAAATCAATTACAAGTCGTGGACGTCTCTCAGTATTGGTTATTGGCAAGAAGAGCCACAGGCAGCTATAAG--AG-----TT-----ACAATTGTAAGATAGATTAGCG-----CTT-----
droGr12	scaffold_14906:2448908-2449070 -	dgr_463	CGGTTCTTTCCATGCTCCAATAAAGAAACGT-----GAAAGGTGACAAGTTG-----GGGGTCTTGGCTTAACCAATGTGGCACTTCCAATGAAAAATCAATTACAAGTCGTGGACGTCTCTCAGTATTGGTTATTGGCAAGAAGAGCCACAGGCAGCTATAAG--AG-----TT-----ACAATTGTAAGATAGATTAGCG-----CTT-----
droAna3	scaffold_12911:3664247-3664417 -	dan_200	CGGTTCTTTCCATGCTCCAATAAAGAAACGT-----GAAAGGTGACAAGTTG-----GGGGTCTTGGCTTAACCAATGTGGCACTTCCAATGAAAAATCAATTACAAGTCGTGGACGTCTCTCAGTATTGGTTATTGGCAAGAAGAGCCACAGGCAGCTATAAG--AG-----TT-----ACAATTGTAAGATAGATTAGCG-----CTT-----
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droEle1	scf7180000491194:1479876-1480031 +		CGGTTCTTTCCATGCTCCAATAAAGAAACGT-----GAAAGGTGACAAGTTG-----GGGGTCTTGGCTTAACCAATGTGGCACTTCCAATGAAAAATCAATTACAAGTCGTGGACGTCTCTCAGTATTGGTTATTGGCAAGAAGAGCCACAGGCAGCTATAAG--AG-----TT-----ACAATTGTAAGATAGATTAGCG-----CTT-----
droRho1	scf7180000779322:264802-264948 -		CGGTTCTTTCCATGCTCCAATAAAGAAACGT-----GAAAGGTGACAAGTTG-----GGGGTCTTGGCTTAACCAATGTGGCACTTCCAATGAAAAATCAATTACAAGTCGTGGACGTCTCTCAGTATTGGTTATTGGCAAGAAGAGCCACAGGCAGCTATAAG--AG-----TT-----ACAATTGTAAGATAGATTAGCG-----CTT-----
droBia1	scf7180000302035:101939-102078 +		CGGTTCTTTCCATGCTCCAATAAAGAAACGT-----GAAAGGTGACAAGTTG-----GGGGTCTTGGCTTAACCAATGTGGCACTTCCAATGAAAAATCAATTACAAGTCGTGGACGTCTCTCAGTATTGGTTATTGGCAAGAAGAGCCACAGGCAGCTATAAG--AG-----TT-----ACAATTGTAAGATAGATTAGCG-----CTT-----
droTak1	scf7180000415712:510701-510827 +		CGGTTCTTTCCATGCTCCAATAAAGAAACGT-----GAAAGGTGACAAGTTG-----GGGGTCTTGGCTTAACCAATGTGGCACTTCCAATGAAAAATCAATTACAAGTCGTGGACGTCTCTCAGTATTGGTTATTGGCAAGAAGAGCCACAGGCAGCTATAAG--AG-----TT-----ACAATTGTAAGATAGATTAGCG-----CTT-----
droEug1	scf7180000409488:463410-463580 -		CGGTTCTTTCCATGCTCCAATAAAGAAACGT-----GAAAGGTGACAAGTTG-----GGGGTCTTGGCTTAACCAATGTGGCACTTCCAATGAAAAATCAATTACAAGTCGTGGACGTCTCTCAGTATTGGTTATTGGCAAGAAGAGCCACAGGCAGCTATAAG--AG-----TT-----ACAATTGTAAGATAGATTAGCG-----CTT-----
dm3	chr3R:27444091-27444224 +		CGGTTCTTTCCATGCTCCAATAAAGAAACGT-----GAAAGGTGACAAGTTG-----GGGGTCTTGGCTTAACCAATGTGGCACTTCCAATGAAAAATCAATTACAAGTCGTGGACGTCTCTCAGTATTGGTTATTGGCAAGAAGAGCCACAGGCAGCTATAAG--AG-----TT-----ACAATTGTAAGATAGATTAGCG-----CTT-----
droSim2	3:126724064-26724197 +	dsi_32457	CGGTTCTTTCCATGCTCCAATAAAGAAACGT-----GAAAGGTGACAAGTTG-----GGGGTCTTGGCTTAACCAATGTGGCACTTCCAATGAAAAATCAATTACAAGTCGTGGACGTCTCTCAGTATTGGTTATTGGCAAGAAGAGCCACAGGCAGCTATAAG--AG-----TT-----ACAATTGTAAGATAGATTAGCG-----CTT-----
droSec2	scaffold_2897:1133-1266 +	dss_1045	CGGTTCTTTCCATGCTCCAATAAAGAAACGT-----GAAAGGTGACAAGTTG-----GGGGTCTTGGCTTAACCAATGTGGCACTTCCAATGAAAAATCAATTACAAGTCGTGGACGTCTCTCAGTATTGGTTATTGGCAAGAAGAGCCACAGGCAGCTATAAG--AG-----TT-----ACAATTGTAAGATAGATTAGCG-----CTT-----
droYaK3	3R:28380205-28380344 +	dya_1797	CGGTTCTTTCCATGCTCCAATAAAGAAACGT-----GAAAGGTGACAAGTTG-----GGGGTCTTGGCTTAACCAATGTGGCACTTCCAATGAAAAATCAATTACAAGTCGTGGACGTCTCTCAGTATTGGTTATTGGCAAGAAGAGCCACAGGCAGCTATAAG--AG-----TT-----ACAATTGTAAGATAGATTAGCG-----CTT-----
droEre2	scaffold_4820:530483-530616 -	der_1522	CGGTTCTTTCCATGCTCCAATAAAGAAACGT-----GAAAGGTGACAAGTTG-----GGGGTCTTGGCTTAACCAATGTGGCACTTCCAATGAAAAATCAATTACAAGTCGTGGACGTCTCTCAGTATTGGTTATTGGCAAGAAGAGCCACAGGCAGCTATAAG--AG-----TT-----ACAATTGTAAGATAGATTAGCG-----CTT-----

Generated: 09/08/2015 at 07:48 PM

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

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_1761 scaffold_52608208-2608229+	1. dpe_1761 scaffold_52608255-2608275+
2. scaffold_52612174-2612195+	2. scaffold_52612221-2612241+
3. dpe_2503 scaffold_52612424-2612445+	3. dpe_2503 scaffold_52612471-2612491+

Sense Strand Reads

hide 3p reads | show mid mismatch reads

[illegible]

Anti-sense strand reads

[illegible]

Re-alignment of all predicted orthologs

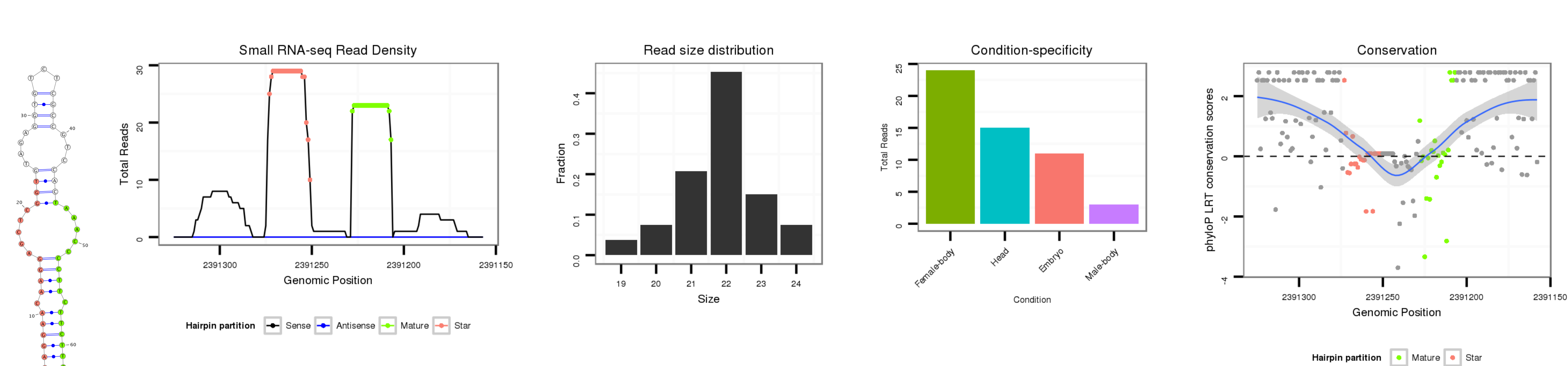
[illegible]

Generated: 09/08/2015 at 10:41 PM

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

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Show Alternate Folds

Flybase annotation

intron [Dper¹GL23610-in]; CDS [Dper¹GL23610-cds]; CDS [Dper¹GL23610-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads										show mid mismatch reads										
										Read #	Hit	Total	M042		M021	V057	V050	V111	V042	
										size	Mismatch	Count	Norm	Total	female body	embryo	head	male	embryo	
CAGAGCCGATCGATGCTCCCGATTGGTCAGCAGACTGCAGACAGATCAGGTACGAGGAAACAAGGAGCTCGGTCTAGAGGTGTCTCGCGCTCCACTAAACCCCTTCTTCTTCTACAGAACAGAGTGCTGTGATGACAGAATCTGATTATGGAGGAGCTGCTCGGCCGA																				
*****(((((((((((((((((((.....(((((.....)))))).....)))))).....))))))*****																				
.....TAAACCCCTTCTTCTTCTACAG.....										22	0	1	17.00	17	13	0	2	1	0	1
.....ACGAGAGGAAACAAGGAGCTCGGT.....										23	0	1	5.00	5	0	4	1	0	0	0
.....TACGAGAGGAAACAAGGAGCTCGGT.....										24	0	1	4.00	4	1	1	2	0	0	0
.....TAAACCCCTTCTTCTTCTACA.....										21	0	1	4.00	4	3	0	0	1	0	0
.....TACGAGAGGAAACAAGGAGCTC.....										21	0	1	4.00	4	1	3	0	0	0	0
.....CGAGAGGAAACAAGGAGCTCGG.....										21	0	1	3.00	3	1	0	2	0	0	0
.....TACGAGAGGAAACAAGGAGCTCG.....										22	0	1	3.00	3	1	0	2	0	0	0
.....TAAACCCCTTCTTCTTCTACAG.....										23	1	1	3.00	3	1	0	0	1	0	1
.....TACGAGAGGAAACAAGGAGCTCGG.....										23	0	1	3.00	3	1	0	2	0	0	0
.....ACGAGAGGAAACAAGGAGCTC.....										20	0	1	2.00	2	0	2	0	0	0	0
.....GTACGAGAGGAAACAAGGAGCTC.....										22	0	1	2.00	2	0	0	0	0	2	0
.....ACGAGAGGAAACAAGGAGCTCGG.....										23	1	1	1.00	1	0	1	0	0	0	0
.....GATTGGTCAGCACTGC.....										18	0	1	1.00	1	0	1	0	0	0	0
.....CGATGCTCCCGATTGGTCAGC.....										21	0	1	1.00	1	1	0	0	0	0	0
.....ATCACGAATCTGATTATGG.....										19	0	1	1.00	1	1	0	0	0	0	0
.....ACAAGGTGTGCTGATCAGCAATCT.....										25	0	1	1.00	1	0	1	0	0	0	0
.....ACGAGAGGAAACAAGGAGCTCGG.....										22	0	1	1.00	1	1	0	0	0	0	0
.....ATCACGAATCTGATTATGGA.....										20	0	1	1.00	1	1	0	0	0	0	0
.....CTCCCGATTGGTCAGCACTGC.....										23	0	1	1.00	1	1	0	0	0	0	0
.....TACGAGAGGAAACAAGGAGC.....										19	0	1	1.00	1	0	0	0	1	0	0
.....GATGCTCCCGATTGGTCAGCACTGC.....										27	0	1	1.00	1	1	0	0	0	0	0
.....TACGAGAGGAAACAAGGAGCTCG.....										23	1	1	1.00	1	0	0	0	1	0	0
.....TAAACCCCTTCTTCTTCTAC.....										20	0	1	1.00	1	1	0	0	0	0	0
.....GTAGAGGTGTCTCGCGTCTC.....										19	0	1	1.00	1	0	0	1	0	0	0
.....GCTCCCGATTGGTCAGCAGAC.....										21	0	1	1.00	1	0	1	0	0	0	0
.....AAACCCCTTCTTCTTCTACA.....										20	0	1	1.00	1	1	0	0	0	0	0
.....GAGAGGAAACAAGGAGCTCGGTG.....										22	0	1	1.00	1	0	0	0	0	1	0
.....TGCTCCCGATTGGTCAGCACTGCCGAC.....										28	0	1	1.00	1	0	1	0	0	0	0
.....GATGCTCCCGATTGGTCA.....										18	0	1	1.00	1	1	0	0	0	0	0
.....CTCCCGATTGGTCAGCACTGCCGAC.....										27	0	1	1.00	1	0	1	0	0	0	0
.....GATCACGAATCTGATTATGGAGAGCT.....										27	0	1	1.00	1	0	0	0	0	1	0
.....CAGACTGCCGACAGAATCAGGA.....										21	1	1	1.00	1	1	0	0	0	0	0

Anti-sense strand reads

[illegible]

Re-alignment of all predicted orthologs

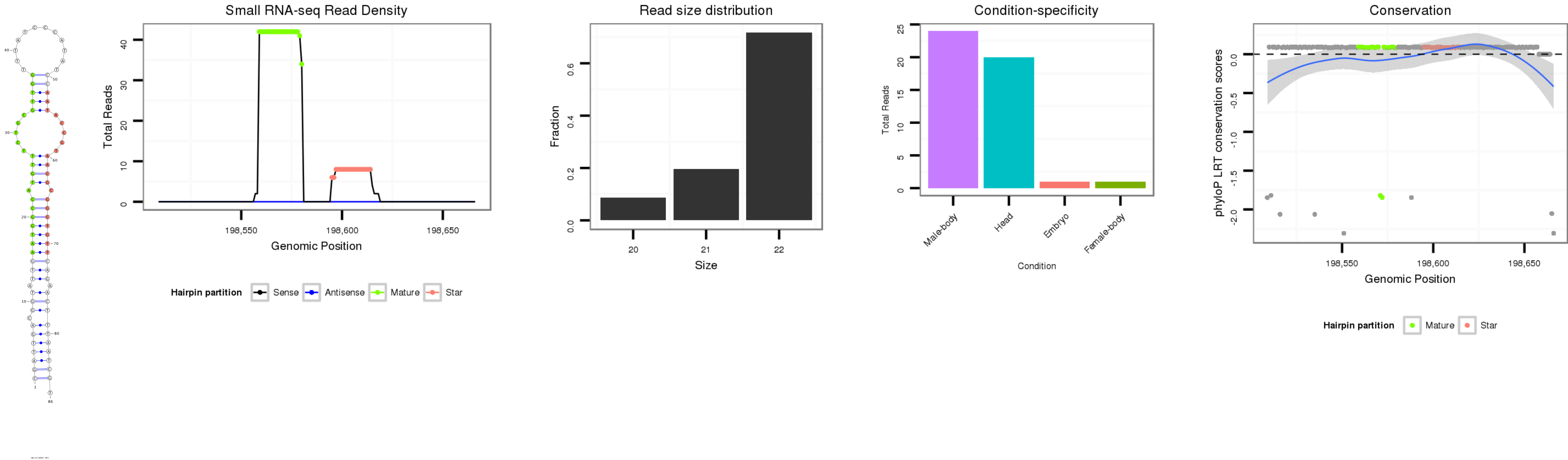
[illegible]

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

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

Legend: mature star mis match in alignment mismatch in read

Predicted structure



Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

														Read size	# Mismatch	Hit Count	Total Norm	Total	V111 male body	V057 head	V050 head	M042 female body	M021 embryo	V042 embryo	
GTTTTCGCAGTGAATGTGTACTCTGTTTGTAGCCGATTGACGGTATTGAAATGGCCATGTTTCTGCGTTGGTTTATCCCATATCCAAATACCGTAACGCGGCTGTTT																									
*****(((((((.(((.(((((((.(((. ((((.)))))))))))))))*****																									
.AATGGCCATGTTTCTGCGTTGG.														22	0	1	33.00	33	16	10	5	1	0	1	
.AATGGCCATGTTTCTGCGTTG.														21	0	1	7.00	7	3	3	1	0	0	0	
.AATACCGTAACGCGGCTGTT.														20	0	1	4.00	4	3	1	0	0	0	0	
.AATACCGTAACGCGGCTGTTT.														21	1	1	2.00	2	0	1	0	1	0	0	
.TACCGTAACGCGGCTGTTCAGA.														22	0	1	2.00	2	0	1	0	1	0	0	
.AATACCGTAACGCGGCTGTTT.														21	0	1	2.00	2	2	0	0	0	0	0	
.AATACCGTAACGCGGCTGTTT.														22	2	1	1.00	1	1	0	0	0	0	0	
.TGAATGGCCATGTTTCTGCGTTGG.														24	0	1	1.00	1	1	0	0	0	0	0	
.AATACCGTAACGCGGCTGTTT.														22	1	1	1.00	1	0	0	0	0	1	0	
.AATACCGTAACGCGGCTGTTT.														22	1	1	1.00	1	0	0	1	0	0	0	
.ATACCGTAACGCGGCTGTTT.														22	2	1	1.00	1	0	0	0	1	0	0	
.TGAATGGCCATGTTTCTGCGTT.														22	0	1	1.00	1	1	0	0	0	0	0	

Anti-sense strand reads

[illegible]

Show Alignment With Reads

Re-alignment of all predicted orthologs

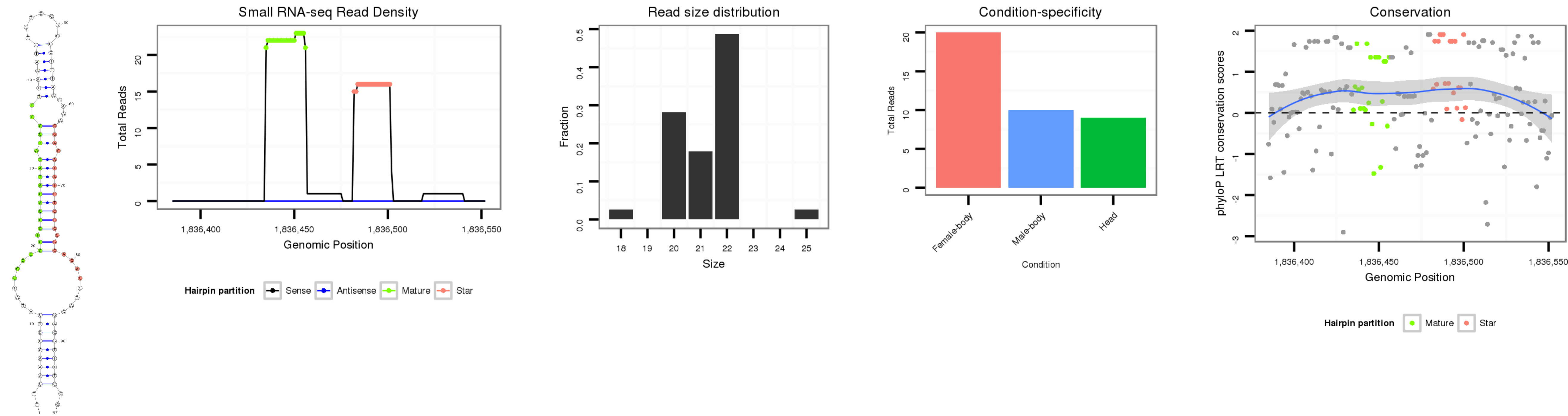
Species	Coordinate	ID	Alignment
droPer2	scaffold_13:198509-198666 +	dpe_122	GTTTTCTGCAGTGAAATGTGTACTCTGTTTGGACCGATTACGGTATTG AATGGCCATGTTTCTGCGTTGG TTTATCCCATATCC AATACCGTAACGCGGCTGTT CAGAACTTTAATCGTATTCTATCCCAATATCCTGTGAGT-----TGATGATACATAC
dp5	Xl_group1:8365729-8365890 -	dps_55	ATA TTCTCTCAGTGAAATGTGTACTCT TTTTGGACCGATTGAG GGTATTGAATGGCCATGTTATGCGTTGG TTTATCC ATATCCAAATACCGTAACGCGGCTGTT CAGAACTTTAATCGTATTCTATCCCAATATCCTGTGAGT GTCCAAAAAAATGAT-----CG

Generated: 09/08/2015 at 08:17 PM **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	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	2
rescue.candidate	0

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Show Alternate Folds

Flybase annotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

Anti-sense strand reads

GTACTTGACGGAGAAAGACCTCTGAAAAACAGCAAACTTCGCGAGTATAGGGCGAGCCTCTATATAGCGAAATTACAGAGCGGCAAAATGTTGCTGTATAGAGCGCGCTCTGATCCTGCAAAAGGCTGCTGTACAGCAGCCTCTATAACAGCAGCGGGGGT															V111
*****.((((((((((.....((.((((((((((.....)))))))).)))))))).)))))))).*****										Read #	Hit	Total		male	
.....TGTTCGCGTATAGAGGCG.....										Size	Mismatch	Count	Total	body	
.....TGTTCGCGTATAGAGGCG.....										19	0	12	0.08	1	

Show Alignment With Reads

Re-alignment of all predicted orthologs

[illegible]

Generated: 09/08/2015 at 09:52 PM

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

Legend: mature star mismatch in alignment mismatch in read



Flybase annotation

intron [Dper¹GL24434-in]; CDS [Dper¹GL24434-cds]; CDS [Dper¹GL24434-cds]

No Repeatable elements found

Sense Strand Reads

Anti-sense strand reads

Show Alignment With Reads

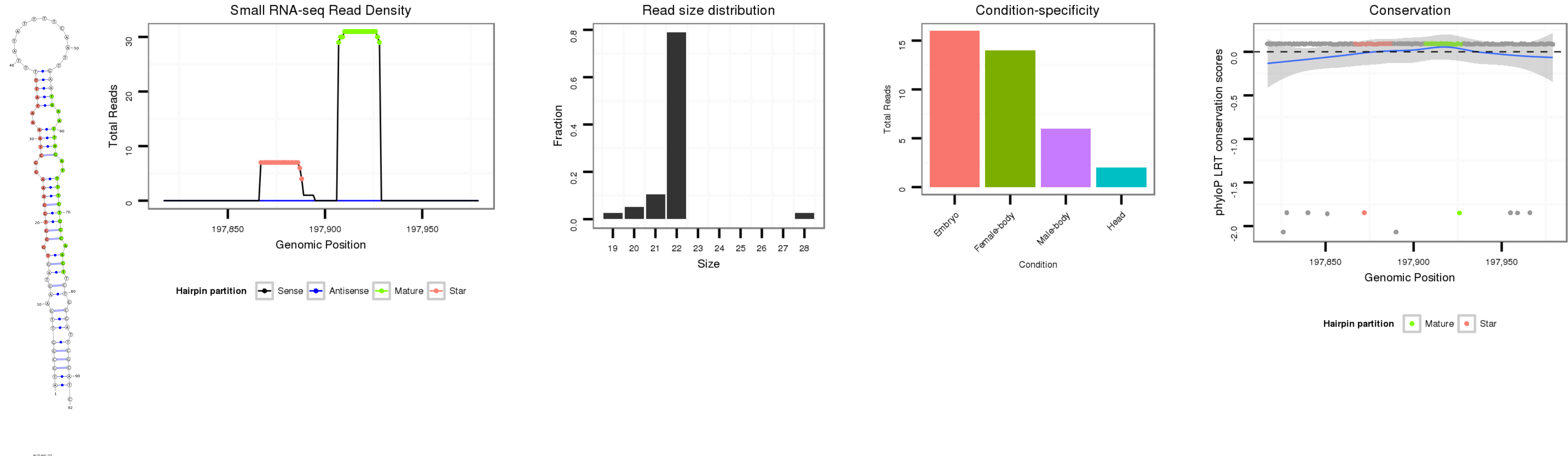
Re-alignment of all predicted orthologs

Generated: 09/08/2015 at 10:38 PM

	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.ttop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	2
rescue.candidate	0

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Show Alternate Folds

Flybase annotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

ATCATCATATTGTACTGTGAAGAGAACTGTTTATCGCGTTGAAGTAGTGGGTGGAAAGGCTAAAAATATTTTATATTTTCAATTGAATAAATTAGATTTTCTGCCAACTCTCGCATTCGCATCGACCCCTGTTTGTGCACCTCTCGGGAGCGATCGTTTC	Read #	size	Mismatch	Hit Count	Total Norm	Total	M021 embryo	M042 female body	V111 male body	V057 head	V050 head
*****(((((((.(.((.(.((((((.(.(((.(.((((((.....)))))).)))))).)))))).)))))).*****	22	0	1	27.00	27	14	12	1	0	0	
.....TGGGTGGAAAGGCTAAAAATATT.....TAAATTAGATTTTCTGCCAACT.....	22	0	1	3.00	3	0	1	1	0	1	
.....TAAATTAGATTTTCTGCCAACG.....	22	1	1	2.00	2	2	0	0	0	0	
.....TGGGTGGAAAGGCTAAAAATAT.....	21	0	1	2.00	2	0	0	2	0	0	
.....TAAATTAGATTTTCTGCCAACG.....	22	1	1	2.00	2	2	0	0	0	0	
.....TGGGTGGAAAGGCTAAAAATATTTC.....	25	2	1	1.00	1	0	1	0	0	0	
.....TGGGTGGAAAGGCTAAAAATA.....	20	0	1	1.00	1	0	0	1	0	0	
.....ATTAGATTTTCTGCCAACT.....	19	0	1	1.00	1	1	0	0	0	0	
.....TAAATTAGATTTTCTGCCAA.....	20	0	1	1.00	1	0	0	1	0	0	
.....AAATTAGATTTTCTGCCAACT.....	21	0	1	1.00	1	1	0	0	0	0	
.....TAAATTAGATTTTCTGCCAAC.....	21	0	1	1.00	1	0	1	0	0	0	
.....TGGGTGGAAAGGCTAAAAATATTTTATA.....	28	0	1	1.00	1	0	0	0	1	0	
.....GTTTTATCGCGTTGAAGTAG.....	20	0	2	0.50	1	0	0	1	0	0	

Anti-sense strand reads

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droPer2	scaffold_13:197817-197979_+	dpe_144	ATCATCATATTGTACTGTGAAGAGAACTGTTTATGCGGTTGAAGTAGTGGGTGGAAAGGCTAAAAATATTTTATATTTTCAATTGAAATAATTAGATTTTCTGCCAACTCTCGCATTCGCATCGACCCCTGTTTGTGCACTCTCGGAGCGATCGTTTC
dp5	Xl_group1:8366435-8366597_-	dps_73	ATCATCATATTTACTGTGAAGAACTGTTTCATGCGGTTGAAGTAGTGGGTAGAAAGGCTAAAAATATTTCATATTTTCAATTGAAATAATTAGATTTTCTGCCACTCTCGCATTCGCATCGACCCCTGTTTATGCTCTCTCGAGCGATCGTTTC

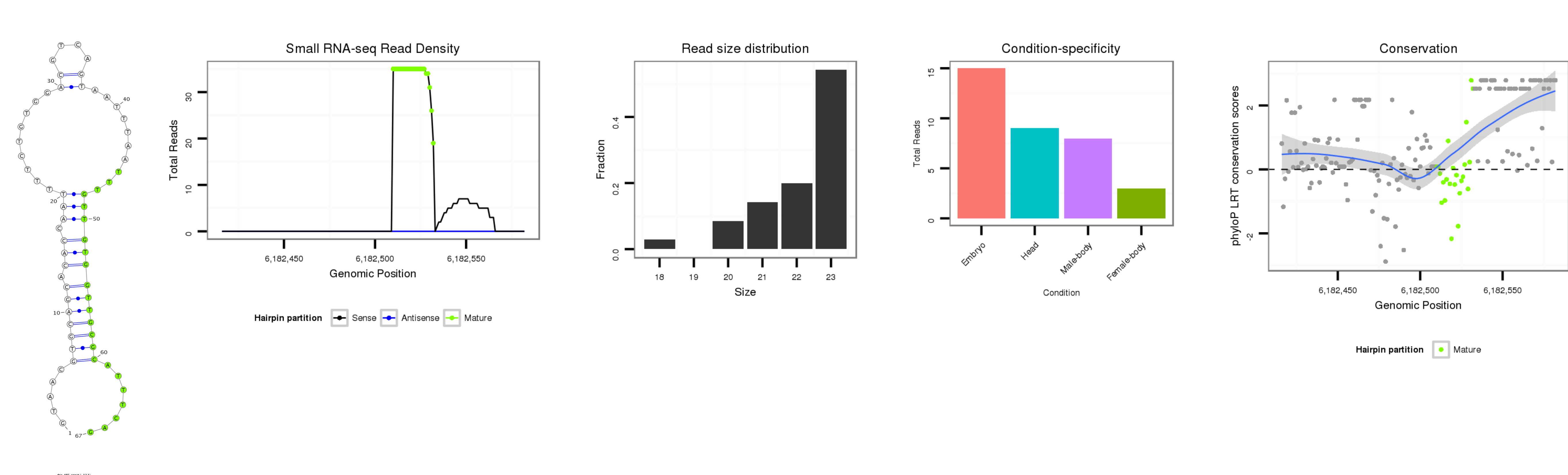
Generated: 09/08/2015 at 08:17 PM **PASS/FAIL**
crit.star

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

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dpe_405	scaffold_0:6182466-6182532 +	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\GL24166-in]; CDS [Dper\GL24166-cds]; CDS [Dper\GL24166-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 07:00 PM

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