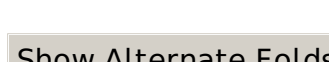


[illegible]

Sense Strand Reads

Anti-sense strand reads

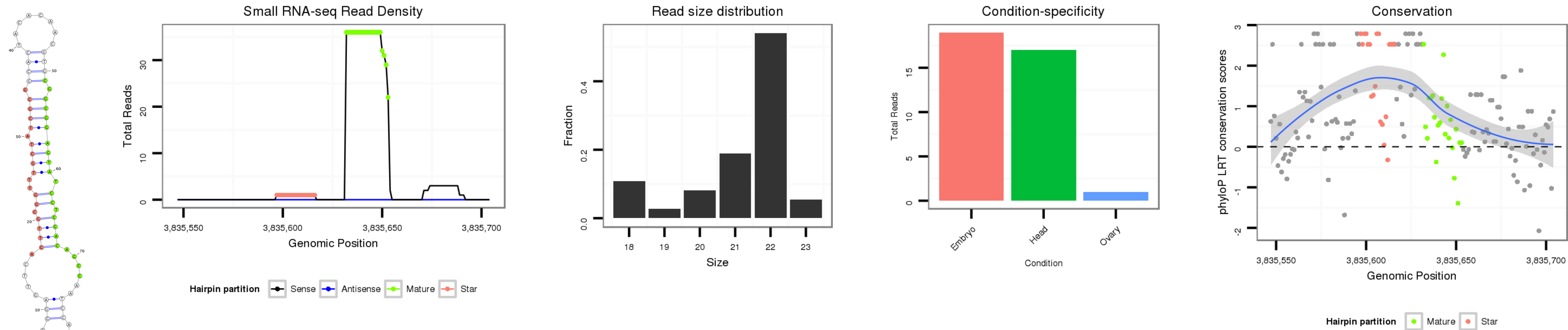
D. H. $\rightarrow$ C. H. $\rightarrow$ H. $\rightarrow$ H. $\rightarrow$ H.

Re-alignment of all predicted orthologs

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

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Show Alternate Folds

Flybase annnotation

intron [2r_3824372_3842698_+]; utr5 [utr5_plus_3251]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

[illegible]

Anti-sense strand reads

										SRR553486	SRR553487	SRR618934	
GGTCCTGCTACCTACACAGGACCGGTCTGTGGCGGACAGGTCCCGCTCAAGCTCAACGCCAAACGATAGCGCGGTGATGTGTGCACCGCGCTCATAGAGAGCTGTCTGTTAGTATAGGCGTAGGAAGAAAGCGTAGAGACTTAGCGCTGAGAAGCGCA										M023 Makindu 3 day-old head ovaries	M024 NRT_0-2 hours male eggs	SRR618934 dsim w501 ovaries	
*****(((((.....)))))).....*****										Read size	Hit Mismatch	Total Count	Norm Total

Show Alignment With Reads

[illegible]

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

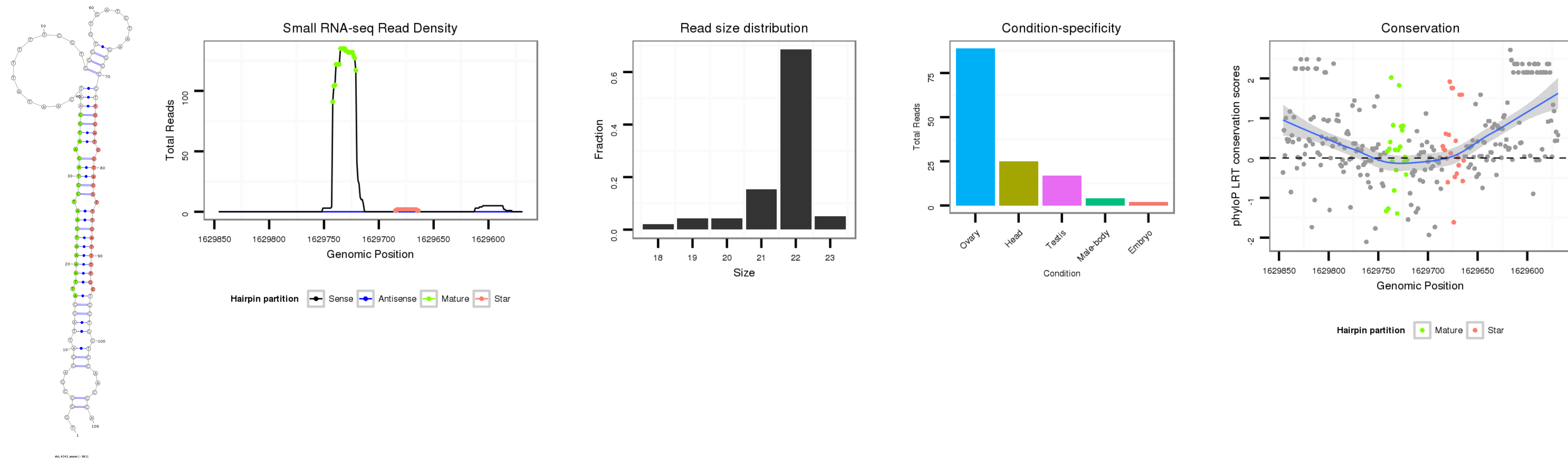
	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	1
rescue.candidate	2

	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	2
rescue.candidate	3

dsi_4243	31:1629619-1629796 -	candidate-rescued	Canonical miRNA	intron	[View on UCSC Genome Browser (Cornell Mirror)]
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Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Show Alternate Fields

Flybase annotation

intron [31_16296_19_1629796_-]; CDS [31_1628579_1629618_-]; CDS [31_1629797_1630043_-]

No Repeatable elements found

Sense Strand Reads

[illegible]

Anti-sense strand reads

Genomic coordinates		Gene		Transcript		Protein		Database		Accession		Description		Date		Version		Author		Contact		License	
chr	start	end	name	transcript	protein	db	acc	name	date	version	author	contact	license	date	version	author	contact	license	date	version	author	contact	license
chr1	1000000	1000000	Gene	transcript	protein	db	acc	name	date	version	author	contact	license	date	version	author	contact	license	date	version	author	contact	license

Show Alignment With Reads

Re-alignment of all predicted orthologs

[illegible]

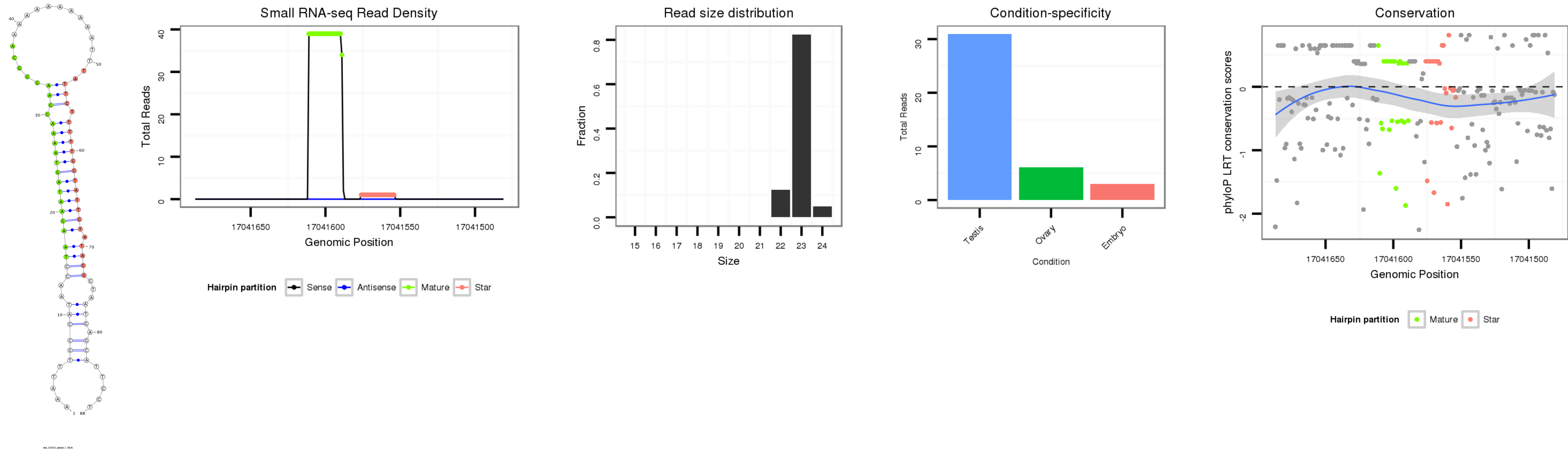
Generated: 09/08/2015 at 08:03 PM

	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	2
rescue.candidate	3

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dsi_32435	2r:17041531-17041637 -	Known Ortholog	Testes-restricted	3pUTR	[View on UCSC Genome Browser (Cornell Mirror)]

Legend: ■ **match** ■ **star** ■ **mismatch in alignment** ■ **mismatch in read**

Predicted structure



Show Alternate Folds

Flybase annotation

utr3 [utr3_minus_3798]

No Repeatable elements found

Sense Strand Reads

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

	Read # size	Mismatch	Hit Count	Total Norm	Total	SRR902009 testis	SRR553486 Makindu 3 day-old ovaries	M025 embryo	SRR553487 NRT_0-2 hours eggs	GSM343915 embryo	SRR553488 RT_0-2 hours eggs	SRR618934 dsim w501 ovaries	SRR902008 ovaries
GCAGAAAACTAACCAAAAGTGCACAGATTGAAAAAACAAGAAGTGTATATTTCATCAAATTTGCCATAACC	23	0	1	32.00	32	29	2	0	1	0	0	0	0
*****	22	0	1	5.00	5	1	1	2	0	1	0	0	0
*****	24	0	1	2.00	2	1	0	0	0	0	1	0	0
*****	24	1	1	1.00	1	1	0	0	0	0	0	0	0
*****	25	2	1	1.00	1	1	0	0	0	0	0	0	0
*****	24	1	1	1.00	1	1	0	0	0	0	0	0	0
*****	23	0	1	1.00	1	0	1	0	0	0	0	0	0
*****	23	0	17	0.06	1	0	1	0	0	0	0	0	0

Anti-sense strand reads

	Read # size	Mismatch	Hit Count	Total Norm	Total	SRR618934 dsim w501 ovaries	SRR553486 Makindu 3 day-old ovaries	SRR553488 RT_0-2 hours eggs	SRR902008 ovaries
CGTCTTTTGATTGGTGTTCACGTCTAACTTTTTTTGTGTCTTACACATAAAAGTAGTTAAACGGTATTGG	15	0	5	0.20	1	1	0	0	0
*****	15	0	5	0.20	1	1	0	0	0

Show Alignment With Reads

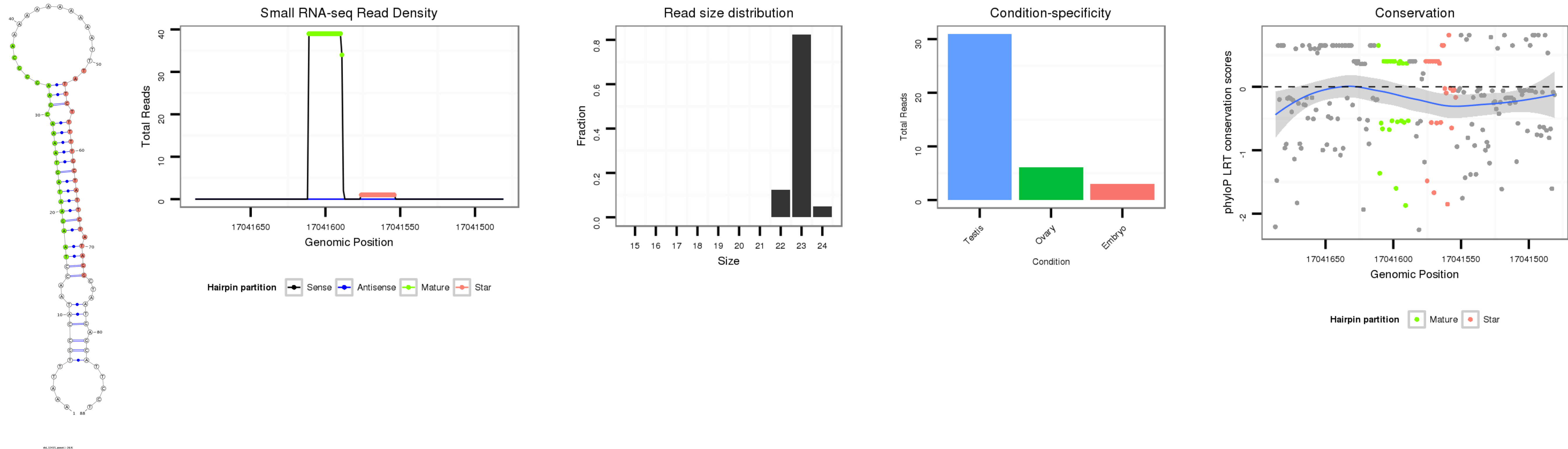
Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droSim2	2r:17041481-17041687 -	dsi_32435	GCAGAAAACTAACCAAAAG--TGCACA-----GATTG-AAAA--AAAAAC--A-CAAGAATGTGATATTTCATCAAATTTGCCATAACC
droSec2	scaffold_1:14026217-14026433 -	dse_339	GCAGAAAACTAACCAACCAAG--TGCACA-----GATTG-AAAAA-AAAAAC--A-CAAGAATGTGATATTTCATCAAATTTGCCATAACC
dm3	chr2R:16472011-16472235 -	dme-mir-2498	GCAGAAAACCTAACACAAAG--TGCACA-----GATTG-AAAAA-AAAAAC--A-CAAGAATGTGATATTTCATCAAATTTGCCATAACC
droBre2	scaffold_4845:10617179-10617473 -	der_95	TCAGAAAACCAACACCTTAGT-TGCACA-----GAATG-AAAACTAAATTT-GT-AAAAATGTGATATTTCATCAAATTTGCCATAACC
droYak3	2R:12723977-12724282 +	dya_34	TCAGAAAACCTAACACCTTTTG-TGCACA-----GAATG-AAAACTAAATTT-GT-AAAAATGTGATATTTCATCAAATTTGCCATAACC
droEug1	scf7180000409474:1489613-1489692 +		CT-----
droBia1	scf7180000302291:2815853-2815854 +		CG-----
droE11	scf7180000491201:736708-736920 -		AAATTAATTAACACATTCGAATTTTCAGCAAAATATATGTGTGCCAATAAGCTTAAATAATGAACGATTT-CAAGAAATTAATTTT-----ATAACCTG-----TGCTA-----TAAAGAAACAGCG-----AGATAACAAATTAAGAAATAATGTTTATATTCAAATCCGGACTTTTAAAGGTGAGTAATCCGCATCCTTATGCGGTTTTCATTTTCG-----

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dsi_32435	2r:17041531-17041637 -	Known Ortholog	Testes-restricted	3pUTR	[View on UCSC Genome Browser (Cornell Mirror)]

Legend: ■ **match** ■ **star** ■ **mismatch in alignment** ■ **mismatch in read**

Predicted structure



Show Alternate Folds

Flybase annotation

utr3 [utr3_minus_3798]

No Repeatable elements found

Sense Strand Reads

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

	Read # size	Mismatch	Hit Count	Total Norm	Total	SRR902009 testis	SRR553486 Makindu 3 day-old ovaries	M025 embryo	SRR553487 NRT_0-2 hours eggs	GSM343915 embryo	SRR553488 RT_0-2 hours eggs	SRR618934 dsim w501 ovaries	SRR902008 ovaries
GCAGAAAACTAACCAAAAGTGCACAGATTGAAAAAACAAGAAGTGTATATTTCATCAAATTTGCCATAACC	23	0	1	32.00	32	29	2	0	1	0	0	0	0
*****	22	0	1	5.00	5	1	1	2	0	1	0	0	0
*****	24	0	1	2.00	2	1	0	0	0	0	1	0	0
*****	24	1	1	1.00	1	1	0	0	0	0	0	0	0
*****	25	2	1	1.00	1	1	0	0	0	0	0	0	0
*****	24	1	1	1.00	1	1	0	0	0	0	0	0	0
*****	23	0	1	1.00	1	0	1	0	0	0	0	0	0
*****	23	0	17	0.06	1	0	1	0	0	0	0	0	0

Anti-sense strand reads

	Read # size	Mismatch	Hit Count	Total Norm	Total	SRR618934 dsim w501 ovaries	SRR553486 Makindu 3 day-old ovaries	SRR553488 RT_0-2 hours eggs	SRR902008 ovaries
CGTCTTTTGATTGGTGTTCACGTGTCTAACTTTTTTTGTGTCTTACACATAAAAGTAGTTTAAACGGTATTGG	15	0	5	0.20	1	1	0	0	0
*****	15	0	5	0.20	1	1	0	0	0

Show Alignment With Reads

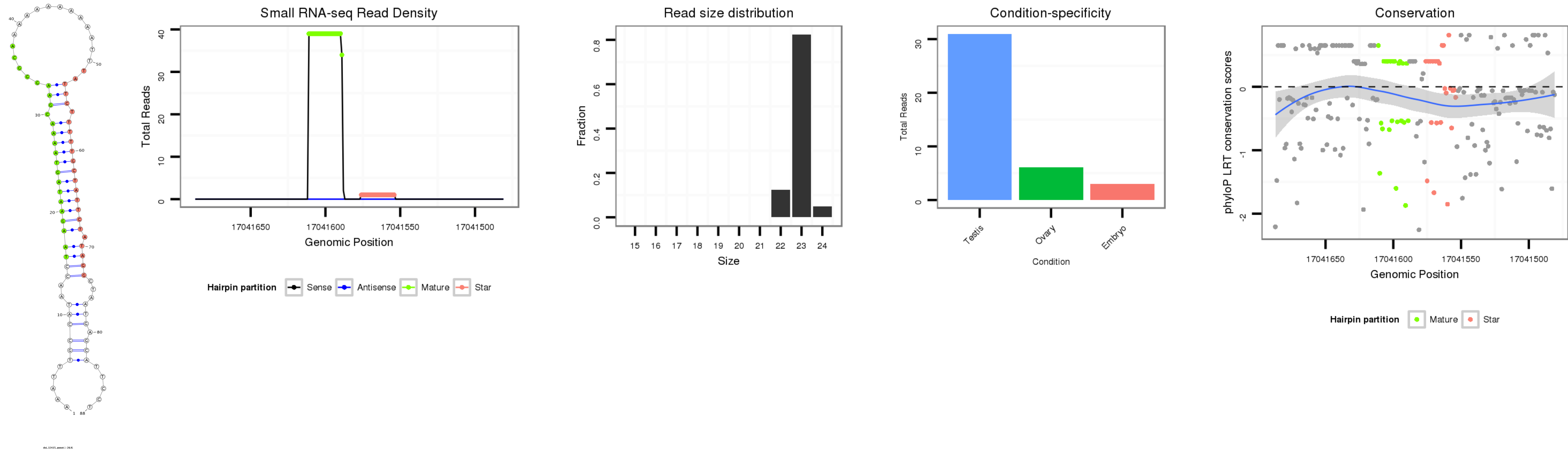
Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droSim2	2r:17041481-17041687 -	dsi_32435	GCAGAAAACTAACCAAAAG--TGCACA-----GATTG-AAAA--AAAAC--A-CAAGAATGTGATATTTCATCAAATTTGCCATAACC
droSec2	scaffold_1:14026217-14026433 -	dse_339	GCAGAAAACTAACCAACCAAG--TGCACA-----GATTG-AAAAA-AAAAC--A-CAAGAATGTGATATTTCATCAAATTTGCCATAACC
dm3	chr2R:16472011-16472235 -	dme-mir-2498	GCAGAAACTAACACAAAG--TGCACA-----GATTG-AAAAA-AAAAC--A-CAAGAATGTGATATTTCATCA
droBre2	scaffold_4845:10617179-10617473 -	der_95	TCAGAAAACCAACACCTTAGT--TGCAAA-----GAATG--AAACCTAAAT--GT--AAAGATGTGATATTTCATCAAAATGCCATAACC
droYak3	2R:12723977-12724282 +	dya_34	TCAGAAACCTACACCTTTTG--TGCAAA-----GA--A--AAACCTAAAT--GTAAATATATATATTTCATCAAAATGCCATAACC
droEug1	scf7180000409474:1489613-1489692 +		CT-----
droBia1	scf7180000302291:2815853-2815854 +		CG-----
droE11	scf7180000491201:736708-736920 -		AAATAAATTAAACACATTCGAATTTTCAGCAAAATATATGTGTGCCAATAACGTTAAATAAATGAACGATTT--CAAGAAATTAATTTT-----ATAACCTG-----TGCTA-----TAAAGAACACGCT--AGATAACAAATTATAGAAATAAT--GTTTATATTCAAATCCGGACTTTTAAAGGTGAGTAATCCGCATCCTTATGCGGTTTTCATTTTCG-----

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dsi_32435	2r:17041531-17041637 -	Known Ortholog	Testes-restricted	3pUTR	[View on UCSC Genome Browser (Cornell Mirror)]

Legend: ■ **match** ■ **star** ■ **mismatch in alignment** ■ **mismatch in read**

Predicted structure



Show Alternate Folds

Flybase annotation

utr3 [utr3_minus_3798]

No Repeatable elements found

Sense Strand Reads

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

	Read # size	Mismatch	Hit Count	Total Norm	Total	SRR902009 testis	SRR553486 Makindu 3 day-old ovaries	M025 embryo	SRR553487 NRT_0-2 hours eggs	GSM343915 embryo	SRR553488 RT_0-2 hours eggs	SRR618934 dsim w501 ovaries	SRR902008 ovaries
GCAGAAAACTAACCAAAAGTGCACAGATTGAAAAAACAAGAAGTGTATATTTCATCAAATTTGCCATAACC	23	0	1	32.00	32	29	2	0	1	0	0	0	0
*****	22	0	1	5.00	5	1	1	2	0	1	0	0	0
*****	24	0	1	2.00	2	1	0	0	0	0	1	0	0
*****	24	1	1	1.00	1	1	0	0	0	0	0	0	0
*****	25	2	1	1.00	1	1	0	0	0	0	0	0	0
*****	24	1	1	1.00	1	1	0	0	0	0	0	0	0
*****	23	0	1	1.00	1	0	1	0	0	0	0	0	0
*****	23	0	17	0.06	1	0	1	0	0	0	0	0	0

Anti-sense strand reads

	Read # size	Mismatch	Hit Count	Total Norm	Total	SRR618934 dsim w501 ovaries	SRR553486 Makindu 3 day-old ovaries	SRR553488 RT_0-2 hours eggs	SRR902008 ovaries
CGTCTTTTGATTGGTGTTCACGTCTAACTTTTTTTGTGTCTTACACATAAAAGTAGTTAAACGGTATTGG	15	0	5	0.20	1	1	0	0	0
*****	15	0	5	0.20	1	1	0	0	0

Show Alignment With Reads

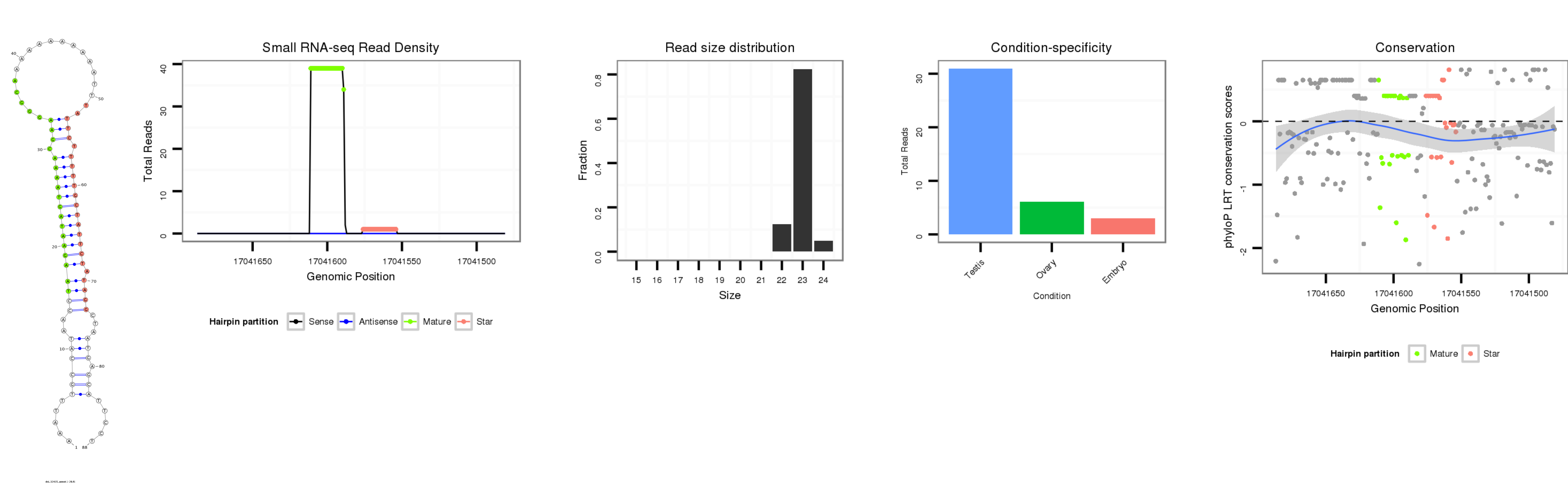
Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droSim2	2r:17041481-17041687 -	dsi_32435	GCAGAAAACTAACCAAAAG--TGCACA-----GATTG-AAAA--AAAAC--A-CAAGAATGTGATATTTCATCAAATTTGCCATAACC
droSec2	scaffold_1:14026217-14026433 -	dse_339	GCAGAAAACTAACCAACCAAG--TGCACA-----GATTG-AAAAA-AAAAC--A-CAAGAATGTGATATTTCATCAAATTTGCCATAACC
dm3	chr2R:16472011-16472235 -	dme-mir-2498	GCAGAAACTAACACAAAG--TGCACA-----GATTG-AAAAA-AAAAC--A-CAAGAATGTGATATTTCATCA
droBre2	scaffold_4845:10617179-10617473 -	der_95	TCAGAAAACCAACACCTTAGT--TGCAAA-----GAATG--AAACCTAAAT--GT--AAAGATGTGATATTTCATCAAAATTCGCATAACCC
droYak3	2R:12723977-12724282 +	dya_34	TCAGAAACCTACACCTTTTG--TGCAAA-----GA--A--AAACCTAAAT--GTAAAGATGTGATATTTCATCAAAATTCGCATAACCC
droEug1	scf7180000409474:1489613-1489692 +		CT-----
droBia1	scf7180000302291:2815853-2815854 +		CG-----
droE11	scf7180000491201:736708-736920 -		AAAGAAATTAACACATTCGAATTTTCAGCAAAATATATGTGTGCCAATAAGCTTAAAGAAATGAACGATTT--CAAGAAATTAATTTT-----ATAACCTG-----TGCTA-----TAAAGAAACAGCT--AATAACAAATTATAGAAATAAT--GTTTATATTCAAATCCGGACTTTTAAAGGTGAGTAATCCGCATCCTTATGCGGTATTTCATTTTCG-----

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dsi_32435	2r:17041531-17041637 -	Known Ortholog	Testes-restricted	3pUTR	[View on UCSC Genome Browser (Cornell Mirror)]

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Show Alternate Folds

Flybase annotation

utr3 [utr3_minus_3798]

No Repeatable elements found

Sense Strand Reads

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

	Read # size	Mismatch	Hit Count	Total Norm	Total	SRR902009 testis	SRR553486 Makindu 3 day-old ovaries	M025 embryo	SRR553487 NRT_0-2 hours eggs	GSM343915 embryo	SRR553488 RT_0-2 hours eggs	SRR618934 dsim w501 ovaries	SRR902008 ovaries
GCAGAAAACTAACCAAAAGTGCACAGATTGAAAAAACAAGAAGTGTATATTTCATCAAATTTGCCATAACC	23	0	1	32.00	32	29	2	0	1	0	0	0	0
*****	22	0	1	5.00	5	1	1	2	0	1	0	0	0
*****	24	0	1	2.00	2	1	0	0	0	0	1	0	0
*****	24	1	1	1.00	1	1	0	0	0	0	0	0	0
*****	25	2	1	1.00	1	1	0	0	0	0	0	0	0
*****	24	1	1	1.00	1	1	0	0	0	0	0	0	0
*****	23	0	1	1.00	1	0	1	0	0	0	0	0	0
*****	23	0	17	0.06	1	0	1	0	0	0	0	0	0

Anti-sense strand reads

	Read # size	Mismatch	Hit Count	Total Norm	Total	SRR618934 dsim w501 ovaries	SRR553486 Makindu 3 day-old ovaries	SRR553488 RT_0-2 hours eggs	SRR902008 ovaries
CGTCTTTTGATTGGTGTTCACGTCTAACTTTTTTTGTGTCTTACACATAAAAGTAGTTAAACGGTATTGG	15	0	5	0.20	1	1	0	0	0
*****	15	0	5	0.20	1	1	0	0	0

Show Alignment With Reads

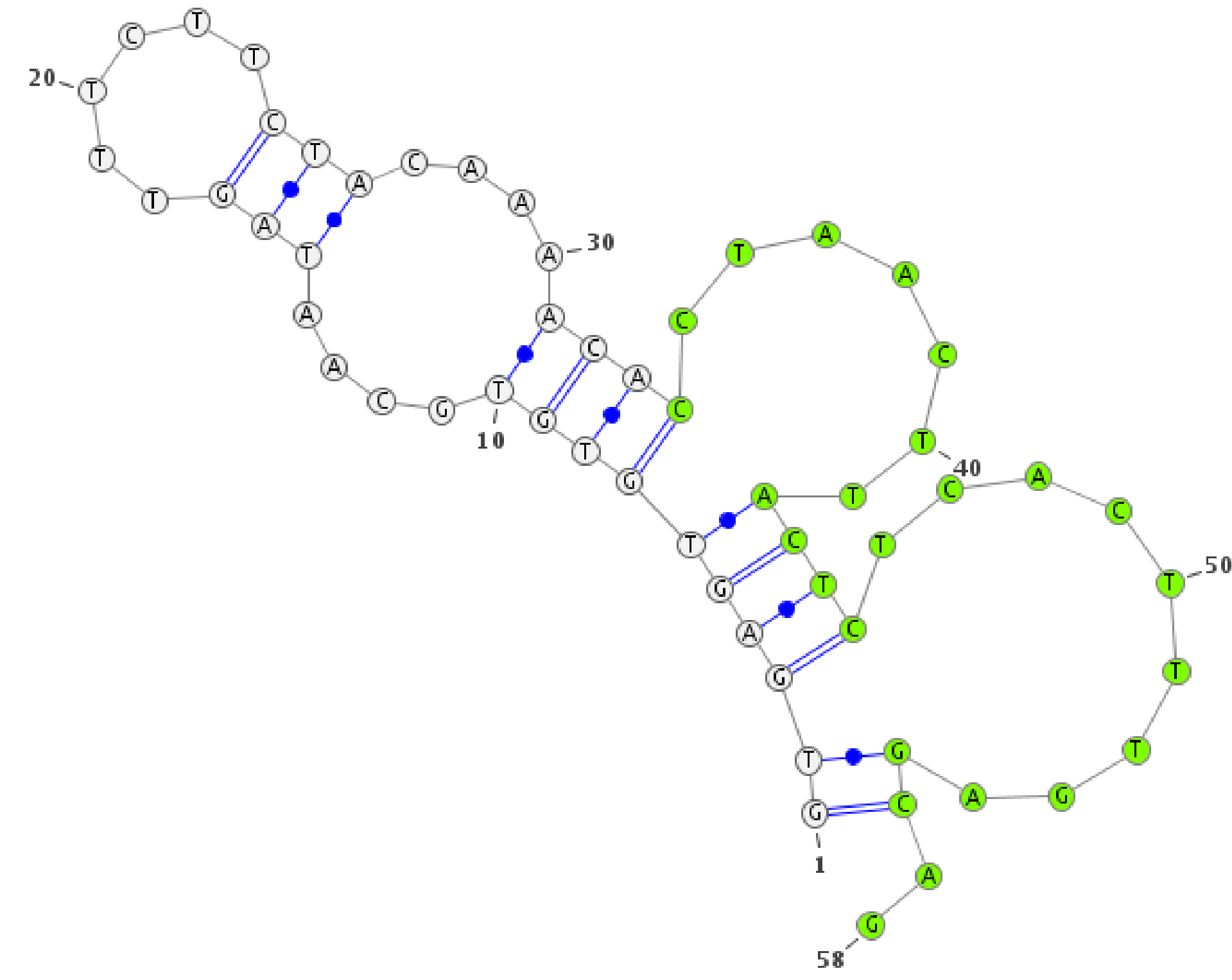
Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droSim2	2r:17041481-17041687 -	dsi_32435	GCAGAAAACTAACCAAAAG--TGCACA-----GATTG-AAAA--AAAAC--A-CAAGAATGTGATATTTCATCAAATTTGCCATAACC
droSec2	scaffold_1:14026217-14026433 -	dse_339	GCAGAAAACTAACCAACCAAG--TGCACA-----GATTG-AAAAA-AAAAC--A-CAAGAATGTGATATTTCATCAAATTTGCCATAACC
dm3	chr2R:16472011-16472235 -	dme-mir-2498	GCAGAAACTAACACAAAG--TGCACA-----GATTG-AAAAA-AAAAC--A-CAAGAATGTGATATTTCATCA
droBre2	scaffold_4845:10617179-10617473 -	der_95	TCAGAAAACCAACACCTTAGT--TGCAAA-----GAATG--AAACCTAAAT--GT--AAAGATGTGATATTTCATCAAAAT
droYak3	2R:12723977-12724282 +	dya_34	TCAGAAACCTACACCTTTTG--TGCAAA-----GA--A--AAACCTAAAT--GTAAATATATATATTTCATCAAAAT
droEug1	scf7180000409474:1489613-1489692 +		CT-----
droBia1	scf7180000302291:2815853-2815854 +		CG-----
droEla1	scf7180000491201:736708-736920 -		AAATTAATTAACACATGGAATTTGCAAGCAATATATGTGTGCCAATAAGCTTAAATAATGAACGATTT--CAAGAAATTAATTTT

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dsi_5234	2r:8934112-8934169 -	candidate-rescued	Mirtron	antisense_to_3pUTR	[View on UCSC Genome Browser (Cornell Mirror)]

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



dsi_5234_annot [- 3.3]

Show Alternate Folds

Flybase annotation

Antisense to utr3 [utr3_plus_2240]; intron [2r_8934112_8934169_-]; CDS [2r_8934170_8934352_-]; CDS [2r_8933892_8934111_-]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

	Read #	Hit	Total	M023	O002	SRR618934	M053	O001	M024	M025	GSM343915	SRR553486	SRR553488	SRR902009	
TTCTTTTGGAGTCGGCCACATCGTTGGCACGGAAATCCGCAACCCAGGAGGTGAGTGTGTCGAATAGTTTCTTCTCATAAAACA	size	Mismatch	Count	Norm	Total	head	Head	dsim w501	female body	Testis	male embryo	embryo	Makindu_3 day-old ovaries	RT_0-2 hours eggs	testis
.....CCTAACTTACTCTCAGTTTGAGCAG.....	25	0	1	14.00	14	10	0	2	1	0	0	1	0	0	0
.....CTAACTTACTCTCAGTTTGAGCAG.....	24	0	1	12.00	12	11	0	0	0	0	1	0	0	0	0
.....CCTAACTTACTCTCAGTTTGAGCAG.....	26	0	1	3.00	3	0	2	0	0	1	0	0	0	0	0
.....CCTAACTTACTCTCAGTTTGA.....	21	0	1	3.00	3	0	2	0	0	1	0	0	0	0	0
.....CCTAACTTACTCTCAGTTTGAGCAG.....	25	0	1	2.00	2	0	1	0	0	1	0	0	0	0	0
.....TAAGCAGTGTCCAGGTCTCTGGAGTC.....	25	0	1	2.00	2	0	0	2	0	0	0	0	0	0	0
.....CCTAACTTACTCTCAGTTT.....	19	0	1	2.00	2	0	2	0	0	0	0	0	0	0	0
.....CTAACTTACTCTCAGTTTGAGCA.....	23	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....GAGTCGGCCACATCGTTGGCAGCG.....	24	0	1	1.00	1	0	0	0	1	0	0	0	0	0	0
.....ACCTAACTTACTCTCAGTTTGAGCAG.....	26	0	1	1.00	1	0	1	0	0	0	0	0	0	0	0
.....GTCCAGGTCTGGAGTCTTTATCCGGCG.....	29	0	1	1.00	1	0	0	0	0	0	1	0	0	0	0
.....CCTAACTTACTCTCAGTTTGAGCA.....	24	0	1	1.00	1	0	1	0	0	0	0	0	0	0	0
.....TTGGAGTCGGCCACATCGTTG.....	21	0	1	1.00	1	0	0	0	0	0	1	0	0	0	0
.....CCTAACTTACTCTCAGTTTGAGCAG.....	23	0	1	1.00	1	0	0	1	0	0	0	0	0	0	0
.....ACTCTCAGTTTGAGCAG.....	17	0	1	1.00	1	0	0	1	0	0	0	0	0	0	0
.....GAGTCGGCCACATCGTTGGCACGAAA.....	28	0	1	1.00	1	0	0	0	1	0	0	0	0	0	0
.....ACCTAACTTACTCTCAGTTT.....	20	0	1	1.00	1	0	1	0	0	0	0	0	0	0	0
.....CTAACTTACTCTCAGTTTG.....	19	0	1	1.00	1	0	1	0	0	0	0	0	0	0	0
.....GTCCAGGTCTGGAGTCTTTATCCGGCG.....	26	0	1	1.00	1	0	0	0	0	0	0	1	0	0	0
.....GAGTCGGCCACATCGTTGGCA.....	22	0	1	1.00	1	0	0	0	1	0	0	0	0	0	0
.....ACCTAACTTACTCTCAGTTTG.....	21	0	1	1.00	1	0	0	0	0	1	0	0	0	0	0
.....TAACTTACTCTCAGTTTG.....	18	0	2	1.00	2	0	2	0	0	0	0	0	0	0	0

Anti-sense strand reads

AAGAAAACCTCAGCGGTGTGAACCGTGCCCTTTTAGCGGTTGGTCTCTCACTCACACAGGTTATCAAAGAGATGTTTTGT	Read #	Hit	Total	M023	M024	Chicharo_3 day-old ovaries	SRR618934	RT_0-2 hours eggs
***** ((((((((((.....)))).....)))).....)))).....*****	size	Mismatch	Count	Norm	Total	head	male body	dsim w501
.....TCGTCACAGGTCCAGGACCTCA.....	22	0	1	1.00	1	1	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droSim2	2r:8934062-8934219 -	dsi_5234	TTCTTTTGGAGTCGGCCACATCGTTGGCACGGAAATCCGCAACCCAGGAGGTGAGTGTGTGCAA-----TAG---TTTCT--TCTAC-----AAAA-CACTA-----AC-----TTACTCTCAC-----TTTGAGCAGCTAAGCAGTGTCCAGGTCTCTGGAGTCTTTTATCCGGCGCATCAAGGAGGT
droSec2	scaf101_145774676-5774833 -	dse_657	TTCTTTTGGAGTCGGCCACATCGTTGGCACGGAAATCCGCAACCCAGGAGGTGAGTGTGTGCAA-----TAG---TTTCT--TCTAC-----AAAA-CACTA-----AC-----TTACTCTCA-----TTTGAGCAGCTAAGCAGTGTCCAGGTCTCTGGAGTCTTTTATCCGCGCATCAAGGAGGT
dm3	chr2R:8228885-8228042 -	dme_375	TTCTGTTGGAGTCGCCACATCGTTGGCAGGAAATCCGCAACCCAGGAGGTGAGTGTGTGCAA-----TG---TTTCA--TCTAC-----AAAA-CACTA-----AC-----TTACTCTCA-----TTTGAGCAGCTAAGCAGCTCCAGGTCTCTGGAGTCTTTATCCGCGCATCAAGGAGGT
droEre2	scaf101_484517563219-17563380 +		TTCTGTTGGAGTCGCCACATCGTTGGCAGGAAATCCGCAACCCAGGAGGTGAGTGTGTGCAA-----TAG---TTTCT--TCTAC-----AAAA-CACTA-----AC-----TTACTCTCA-----TTTGAGCAGCTAAGCAGCTCCAGGTCTCTGGAGTCTTTATCCGCGCATCAAGGAGGT
droYak3	2R:8721073-8721230 +		TTCTGTTGGAGTCGCCACATCGTTGGCAGGAAATCCGCAACCCAGGAGGTGAGTGTGTGCAA-----TG---TTTCA--TCTAC-----AAAA-CACTA-----AC-----TTACTCTCA-----TTTGAGCAGCTAAGCAGCTCCAGGTCTCTGGAGTCTTTATCCGCGCATCAAGGAGGT
droEug1	scaf11800004094621:1887205-1887260 +		TTCTGTTGGAGTCGCCACATCGTTGGCAGGAAATCCGCAACCCAGGAGGTGAGTGTGTGCAA-----TAG---TTTCT--TCTAC-----AAAA-CACTA-----AC-----TTACTCTCA-----TTTGAGCAGCTAAGCAGCTCCAGGTCTCTGGAGTCTTTATCCGCGCATCAAGGAGGT
droBial	scaf1180000301754:1686756-1686912 +		TTCTGTTGGAGTCGCCACATCGTTGGCAGGAAATCCGCAACCCAGGAGGTGAGTGTGTGCAA-----TAG---TTTCT--TCTAC-----AAAA-CACTA-----AC-----TTACTCTCA-----TTTGAGCAGCTAAGCAGCTCCAGGTCTCTGGAGTCTTTATCCGCGCATCAAGGAGGT
droTak1	scaf1180000415398:78730-78886 -		TTCTGTTGGAGTCGCCACATCGTTGGCAGGAAATCCGCAACCCAGGAGGTGAGTGTGTGCAA-----TAG---TTTCT--TCTAC-----AAAA-CACTA-----AC-----TTACTCTCA-----TTTGAGCAGCTAAGCAGCTCCAGGTCTCTGGAGTCTTTATCCGCGCATCAAGGAGGT
droE1el	scaf11800004910271:123459-123614 -		TTCTGTTGGAGTCGCCACATCGTTGGCAGGAAATCCGCAACCCAGGAGGTGAGTGTGTGCAA-----TAG---TTTCT--TCTAC-----AAAA-CACTA-----AC-----TTACTCTCA-----TTTGAGCAGCTAAGCAGCTCCAGGTCTCTGGAGTCTTTATCCGCGCATCAAGGAGGT
droRho1	scaf1180000074969:13491-134646 -		TTCTGTTGGAGTCGCCACATCGTTGGCAGGAAATCCGCAACCCAGGAGGTGAGTGTGTGCAA-----TAG---TTTCT--TCTAC-----AAAA-CACTA-----AC-----TTACTCTCA-----TTTGAGCAGCTAAGCAGCTCCAGGTCTCTGGAGTCTTTATCCGCGCATCAAGGAGGT
droPic1	scaf1180000453778:303990-304146 +		TTCTGTTGGAGTCGCCACATCGTTGGCAGGAAATCCGCAACCCAGGAGGTGAGTGTGTGCAA-----TAG---TTTCT--TCTAC-----AAAA-CACTA-----AC-----TTACTCTCA-----TTTGAGCAGCTAAGCAGCTCCAGGTCTCTGGAGTCTTTATCCGCGCATCAAGGAGGT
droKik1	scaf1180000302682:2161706-1461863 +		TTCTGTTGGAGTCGCCACATCGTTGGCAGGAAATCCGCAACCCAGGAGGTGAGTGTGTGCAA-----TAG---TTTCT--TCTAC-----AAAA-CACTA-----AC-----TTACTCTCA-----TTTGAGCAGCTAAGCAGCTCCAGGTCTCTGGAGTCTTTATCCGCGCATCAAGGAGGT
droAna3	scaf101_13266:5520914-5521074 -		TTCTGTTGGAGTCGCCACATCGTTGGCAGGAAATCCGCAACCCAGGAGGTGAGTGTGTGCAA-----TAG---TTTCT--TCTAC-----AAAA-CACTA-----AC-----TTACTCTCA-----TTTGAGCAGCTAAGCAGCTCCAGGTCTCTGGAGTCTTTATCCGCGCATCAAGGAGGT
droBip1	scaf1180000395404:57206-57363 +		TTCTGTTGGAGTCGCCACATCGTTGGCAGGAAATCCGCAACCCAGGAGGTGAGTGTGTGCAA-----TAG---TTTCT--TCTAC-----AAAA-CACTA-----AC-----TTACTCTCA-----TTTGAGCAGCTAAGCAGCTCCAGGTCTCTGGAGTCTTTATCCGCGCATCAAGGAGGT
dp5	1:2793338-2793505 +		TTCTGTTGGAGTCGCCACATCGTTGGCAGGAAATCCGCAACCCAGGAGGTGAGTGTGTGCAA-----TAG---TTTCT--TCTAC-----AAAA-CACTA-----AC-----TTACTCTCA-----TTTGAGCAGCTAAGCAGCTCCAGGTCTCTGGAGTCTTTATCCGCGCATCAAGGAGGT
droPer2	scaf101_212983317-2983480 +		TTCTGTTGGAGTCGCCACATCGTTGGCAGGAAATCCGCAACCCAGGAGGTGAGTGTGTGCAA-----TAG---TTTCT--TCTAC-----AAAA-CACTA-----AC-----TTACTCTCA-----TTTGAGCAGCTAAGCAGCTCCAGGTCTCTGGAGTCTTTATCCGCGCATCAAGGAGGT
droW112	scaf2_1100000004558:467069-1467236 -		TTCTGTTGGAGTCGCCACATCGTTGGCAGGAAATCCGCAACCCAGGAGGTGAGTGTGTGCAA-----TAG---TTTCT--TCTAC-----AAAA-CACTA-----AC-----TTACTCTCA-----TTTGAGCAGCTAAGCAGCTCCAGGTCTCTGGAGTCTTTATCCGCGCATCAAGGAGGT
droVir3	scaf101_12875:6603637-6603795 +		TTCTGTTGGAGTCGCCACATCGTTGGCAGGAAATCCGCAACCCAGGAGGTGAGTGTGTGCAA-----TAG---TTTCT--TCTAC-----AAAA-CACTA-----AC-----TTACTCTCA-----TTTGAGCAGCTAAGCAGCTCCAGGTCTCTGGAGTCTTTATCCGCGCATCAAGGAGGT
droMo3	scaf101_6496:23406104-23406269 -		TTCTGTTGGAGTCGCCACATCGTTGGCAGGAAATCCGCAACCCAGGAGGTGAGTGTGTGCAA-----TAG---TTTCT--TCTAC-----AAAA-CACTA-----AC-----TTACTCTCA-----TTTGAGCAGCTAAGCAGCTCCAGGTCTCTGGAGTCTTTATCCGCGCATCAAGGAGGT
droGr12	scaf101_15112:1486644-1486803 +		TTCTGTTGGAGTCGCCACATCGTTGGCAGGAAATCCGCAACCCAGGAGGTGAGTGTGTGCAA-----TAG---TTTCT--TCTAC-----AAAA-CACTA-----AC-----TTACTCTCA-----TTTGAGCAGCTAAGCAGCTCCAGGTCTCTGGAGTCTTTATCCGCGCATCAAGGAGGT

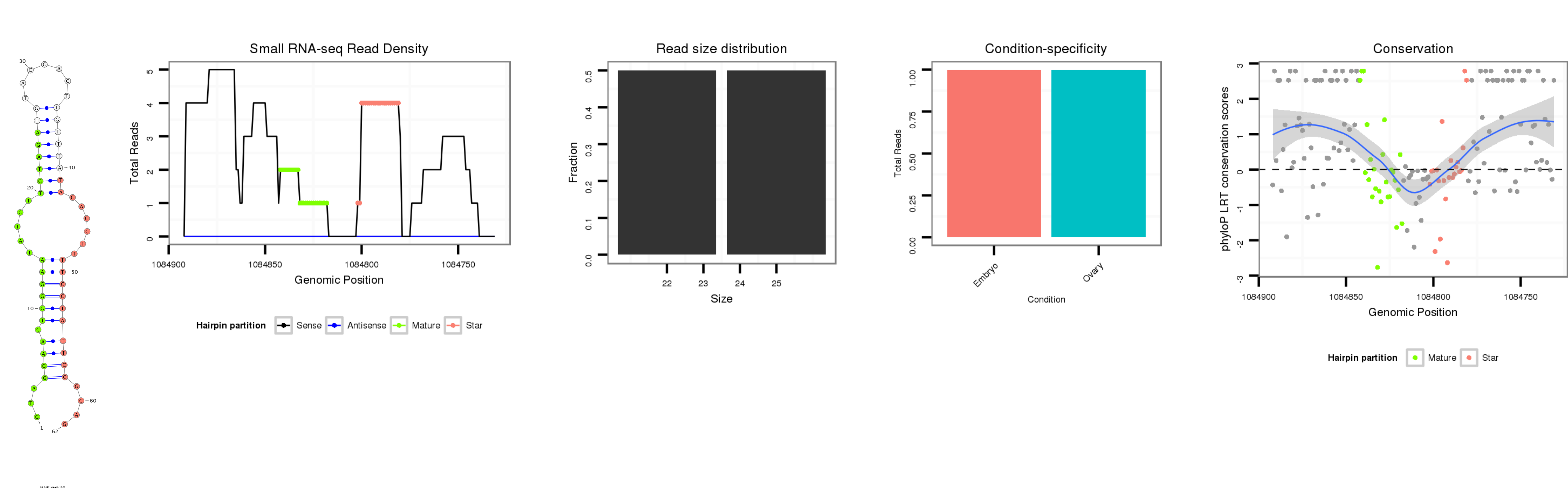
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crit.hair	0
crit.total	1
crit.pairing	0
crit.top3	1
crit.topn3	1
crit.lun	1
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	2

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dsi_2442	3r:1084781-1084842 -	candidate-rescued	Mirtron	intron	[View on UCSC Genome Browser (Cornell Mirror)]

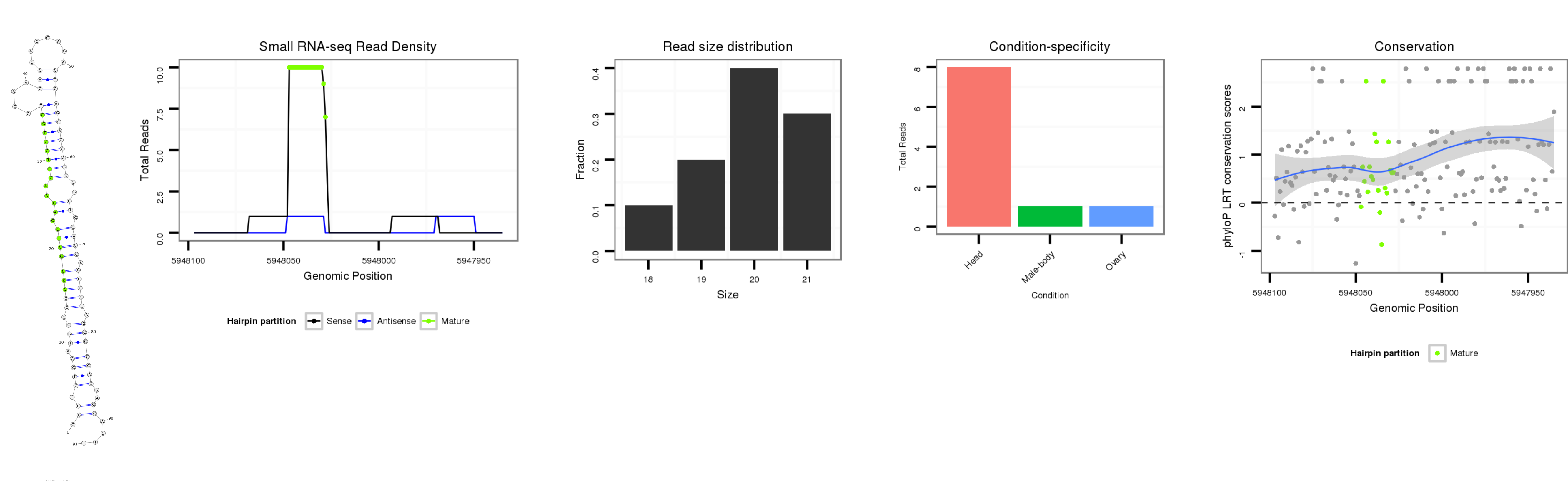
Legend: ■ mature ★ mismatch in alignment ■ mismatch in read

Predicted structure



Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Show Alternate Folds

Sense Strand Reads

hide 3p reads show mid mismatch reads

[illegible]

Anti-sense strand reads

[illegible]

Show Alignment With Reads

Re-alignment of all predicted orthologs

[illegible]

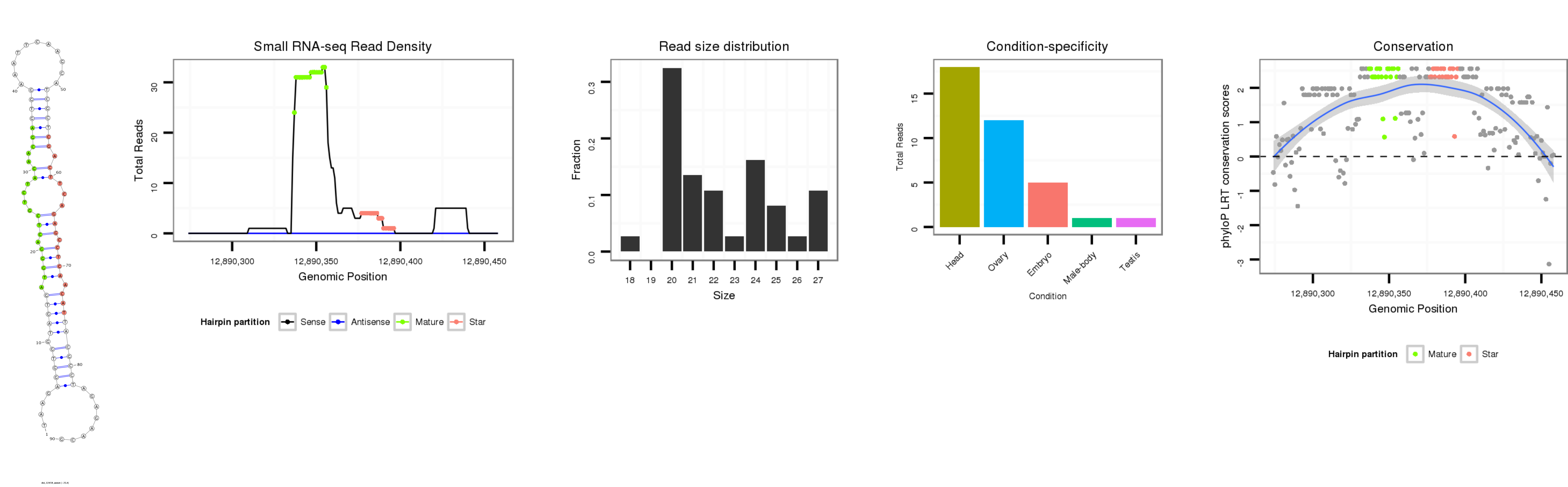
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	PASS/FAIL
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crit.tptop3	0
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	1
rescue.candidate	2

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:
dsi_32459	x:12890324-12890408 +	candidate-rescued	Canonical miRNA	intergenic

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

Predicted structure



Show Alternate Folds

Sense Strand Reads

hide 3p reads show mid mismatch reads

Read #	Hit	Total	M023	M025	SRR618934	SRR553485	SRR553488	M053	SRR553487	SRR902009	GSM343915	Makindu_3
size	Mismatch	Count	head	embryo	dsim w501	Chicharo_3	RT_0-2	M024	NRT_0-2	testis	embryo	ovaries
20	0	1	7.00	7	6	0	0	0	0	0	0	0
24	0	1	5.00	5	0	0	3	1	0	0	1	0
20	0	1	4.00	4	4	0	0	0	0	0	0	0
19	0	1	4.00	4	0	4	0	0	0	0	0	0
21	0	1	4.00	4	0	4	0	0	0	0	0	0
22	0	1	3.00	3	3	0	0	0	0	0	0	0
27	0	1	2.00	2	0	0	2	0	0	0	0	0
25	0	1	2.00	2	0	0	1	0	0	0	0	0
27	0	1	2.00	2	2	0	0	0	0	0	0	0
24	0	1	1.00	1	0	0	0	1	0	0	0	0
21	0	1	1.00	1	0	1	0	0	0	0	0	0
18	0	1	1.00	1	0	0	0	1	0	0	0	0
25	0	1	1.00	1	0	0	1	0	0	0	0	0
21	0	1	1.00	1	0	1	0	0	0	0	0	0
26	0	1	1.00	1	0	0	0	0	0	0	1	0
22	0	1	1.00	1	1	0	0	0	0	0	0	0
23	0	1	1.00	1	0	0	0	0	0	0	0	0
20	1	1	1.00	1	1	0	0	0	0	0	0	0
23	0	1	1.00	1	1	0	0	0	0	0	0	0
20	0	1	1.00	1	1	0	0	0	0	0	0	0
21	1	1	1.00	1	0	1	0	0	0	0	0	0

Anti-sense strand reads

Read #	Hit	Total	SRR553488	SRR553487	SRR553485	SRR618934	SRR902009
size	Mismatch	Count	RT_0-2	NRT_0-2	Chicharo_3	dsim w501	testis
20	0	1	7.00	7	6	0	0
24	0	1	5.00	5	0	0	3
20	0	1	4.00	4	4	0	0
19	0	1	4.00	4	0	4	0
21	0	1	4.00	4	0	4	0
22	0	1	3.00	3	3	0	0
27	0	1	2.00	2	0	0	2
25	0	1	2.00	2	0	0	1
27	0	1	2.00	2	2	0	0
24	0	1	1.00	1	0	0	0
21	0	1	1.00	1	0	1	0
18	0	1	1.00	1	0	0	0
25	0	1	1.00	1	0	0	1
21	0	1	1.00	1	0	1	0
26	0	1	1.00	1	0	0	0
22	0	1	1.00	1	1	0	0
23	0	1	1.00	1	0	0	0
20	1	1	1.00	1	1	0	0
23	0	1	1.00	1	1	0	0
20	0	1	1.00	1	1	0	0
21	1	1	1.00	1	0	1	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droSim2	x:12890274-12890458 +	dsi_32459	TAAC-AAATAAG--AAAC---CATA-AGC--GGGAAC TTGGTCTGAAAGACCCCA--A---ATAAG-AGGTGGTAGTCATGGGACTCGTCTAGAACGAGTGGAAATTC--AAGCATCGCTGG-ACCTTCAGAGCCTCAACATACGCC-TAGAGAAC-GAC-ATCAGGT--TTAGATCATTCGACCCCGCTTAGAA-----ACA---GA---AAAT-----T---GA
droSec2	scaffold_20:193496-193680 +	dse_1847	TAAC-AAATAAG--AAAC---CATA-AGC--GGGAAC TTGGTCTGAAAGACCCCA--A---ATAAG-AGGTGGTAGTCATGGGACTCGTCTAGAACGAGTGGAAATTC--AAGCATCGCTGG-ACCTTCAGAGCCTCAACATACGCC-TAGAGAAC-GAC-ATCAGGT--TTAGATCATTCGACCCCGCTTAGAA-----ACA---GA---AAAT-----T---GA
dm3	chrX:13553556-13553740 +	dme_424	TAAC-AATAAG--AAAC---CATA-AGC--GGGAAC TTGGTCTGAAAGACCCCA--A---ATAAG-AGGTGGTAGTCATGGGACTCGTCTAGAACGAGTGGAAATTC--AAGCATCGCTGG-ACCTTCAGAGCCTCAACATACGCC-TAGAGAAC-GAC-ATCAGGT--TTAGATCATTCGACCCCGCTTAGAA-----ACA---GA---AAAT-----T---GA
droEre2	scaffold_4690:13329650-13329839 -	dex_1524	TAAC-AATAAG--AAAC---CATA-AGC--GGGAAC TTGGTCTGAAAGACCCCA--A---ATAAG-AGGTGGTAGTCATGGGACTCGTCTAGAACGAGTGGAAATTC--AAGCATCGCTGG-ACCTTCAGAGCCTCAACATACGCC-TAGAGAAC-GAC-ATCAGGT--TTAGATCATTCGACCCCGCTTAGAA-----ACA---GA---AAAT-----T---GA
droYak3	X:7836395-7836583 +	dya_1799	TAAC-AATAAG--AAAC---CATA-AGC--GGGAAC TTGGTCTGAAAGACCCCA--A---ATAAG-AGGTGGTAGTCATGGGACTCGTCTAGAACGAGTGGAAATTC--AAGCATCGCTGG-ACCTTCAGAGCCTCAACATACGCC-TAGAGAAC-GAC-ATCAGGT--TTAGATCATTCGACCCCGCTTAGAA-----ACA---GA---AAAT-----T---GA
droEug1	scf7180000408958:35913-36111 -		TAAC-AATAAG--AAAC---CATA-AGC--GGGAAC TTGGTCTGAAAGACCCCA--A---ATAAG-AGGTGGTAGTCATGGGACTCGTCTAGAACGAGTGGAAATTC--AAGCATCGCTGG-ACCTTCAGAGCCTCAACATACGCC-TAGAGAAC-GAC-ATCAGGT--TTAGATCATTCGACCCCGCTTAGAA-----ACA---GA---AAAT-----T---GA
droBial	scf7180000302041:563671-563853 +		TAAC-AATAAG--AAAC---CATA-AGC--GGGAAC TTGGTCTGAAAGACCCCA--A---ATAAG-AGGTGGTAGTCATGGGACTCGTCTAGAACGAGTGGAAATTC--AAGCATCGCTGG-ACCTTCAGAGCCTCAACATACGCC-TAGAGAAC-GAC-ATCAGGT--TTAGATCATTCGACCCCGCTTAGAA-----ACA---GA---AAAT-----T---GA
droTak1	scf7180000414393:30808-31003 -		TAAC-AATAAG--AAAC---CATA-AGC--GGGAAC TTGGTCTGAAAGACCCCA--A---ATAAG-AGGTGGTAGTCATGGGACTCGTCTAGAACGAGTGGAAATTC--AAGCATCGCTGG-ACCTTCAGAGCCTCAACATACGCC-TAGAGAAC-GAC-ATCAGGT--TTAGATCATTCGACCCCGCTTAGAA-----ACA---GA---AAAT-----T---GA
droEl1	scf7180000491044:215067-215264 +		TAAC-AATAAG--AAAC---CATA-AGC--GGGAAC TTGGTCTGAAAGACCCCA--A---ATAAG-AGGTGGTAGTCATGGGACTCGTCTAGAACGAGTGGAAATTC--AAGCATCGCTGG-ACCTTCAGAGCCTCAACATACGCC-TAGAGAAC-GAC-ATCAGGT--TTAGATCATTCGACCCCGCTTAGAA-----ACA---GA---AAAT-----T---GA
droRho1	scf7180000779510:38391-38586 +		TAAC-AATAAG--AAAC---CATA-AGC--GGGAAC TTGGTCTGAAAGACCCCA--A---ATAAG-AGGTGGTAGTCATGGGACTCGTCTAGAACGAGTGGAAATTC--AAGCATCGCTGG-ACCTTCAGAGCCTCAACATACGCC-TAGAGAAC-GAC-ATCAGGT--TTAGATCATTCGACCCCGCTTAGAA-----ACA---GA---AAAT-----T---GA
droFic1	scf7180000454073:1442990-1443193 +		TAAC-AATAAG--AAAC---CATA-AGC--GGGAAC TTGGTCTGAAAGACCCCA--A---ATAAG-AGGTGGTAGTCATGGGACTCGTCTAGAACGAGTGGAAATTC--AAGCATCGCTGG-ACCTTCAGAGCCTCAACATACGCC-TAGAGAAC-GAC-ATCAGGT--TTAGATCATTCGACCCCGCTTAGAA-----ACA---GA---AAAT-----T---GA
droKik1	scf7180000302698:307798-307879 -		TAAC-AATAAG--AAAC---CATA-AGC--GGGAAC TTGGTCTGAAAGACCCCA--A---ATAAG-AGGTGGTAGTCATGGGACTCGTCTAGAACGAGTGGAAATTC--AAGCATCGCTGG-ACCTTCAGAGCCTCAACATACGCC-TAGAGAAC-GAC-ATCAGGT--TTAGATCATTCGACCCCGCTTAGAA-----ACA---GA---AAAT-----T---GA
droAna3	scaffold_13334:472144-472320 +	dan_4039	TAAC-AATAAG--AAAC---CATA-AGC--GGGAAC TTGGTCTGAAAGACCCCA--A---ATAAG-AGGTGGTAGTCATGGGACTCGTCTAGAACGAGTGGAAATTC--AAGCATCGCTGG-ACCTTCAGAGCCTCAACATACGCC-TAGAGAAC-GAC-ATCAGGT--TTAGATCATTCGACCCCGCTTAGAA-----ACA---GA---AAAT-----T---GA
droBip1	scf7180000396431:1081233-1081414 -		TAAC-AATAAG--AAAC---CATA-AGC--GGGAAC TTGGTCTGAAAGACCCCA--A---ATAAG-AGGTGGTAGTCATGGGACTCGTCTAGAACGAGTGGAAATTC--AAGCATCGCTGG-ACCTTCAGAGCCTCAACATACGCC-TAGAGAAC-GAC-ATCAGGT--TTAGATCATTCGACCCCGCTTAGAA-----ACA---GA---AAAT-----T---GA
dp5	XI_group3b:100225-100382 +	dps_110	TAAC-AATAAG--AAAC---CATA-AGC--GGGAAC TTGGTCTGAAAGACCCCA--A---ATAAG-AGGTGGTAGTCATGGGACTCGTCTAGAACGAGTGGAAATTC--AAGCATCGCTGG-ACCTTCAGAGCCTCAACATACGCC-TAGAGAAC-GAC-ATCAGGT--TTAGATCATTCGACCCCGCTTAGAA-----ACA---GA---AAAT-----T---GA
droPer2	scaffold_56:124031-124187 +	dpe_157	TAAC-AATAAG--AAAC---CATA-AGC--GGGAAC TTGGTCTGAAAGACCCCA--A---ATAAG-AGGTGGTAGTCATGGGACTCGTCTAGAACGAGTGGAAATTC--AAGCATCGCTGG-ACCTTCAGAGCCTCAACATACGCC-TAGAGAAC-GAC-ATCAGGT--TTAGATCATTCGACCCCGCTTAGAA-----ACA---GA---AAAT-----T---GA
droVir3	scaffold_12970:5369119-5369203 -	dvi_24642	TAAC-AATAAG--AAAC---CATA-AGC--GGGAAC TTGGTCTGAAAGACCCCA--A---ATAAG-AGGTGGTAGTCATGGGACTCGTCTAGAACGAGTGGAAATTC--AAGCATCGCTGG-ACCTTCAGAGCCTCAACATACGCC-TAGAGAAC-GAC-ATCAGGT--TTAGATCATTCGACCCCGCTTAGAA-----ACA---GA---AAAT-----T---GA
droMoJ3	scaffold_6473:4951753-4951833 -	dmo_3154	TAAC-AATAAG--AAAC---CATA-AGC--GGGAAC TTGGTCTGAAAGACCCCA--A---ATAAG-AGGTGGTAGTCATGGGACTCGTCTAGAACGAGTGGAAATTC--AAGCATCGCTGG-ACCTTCAGAGCCTCAACATACGCC-TAGAGAAC-GAC-ATCAGGT--TTAGATCATTCGACCCCGCTTAGAA-----ACA---GA---AAAT-----T---GA
droGri2	scaffold_15203:9467764-9467849 +	dgr_467	TAAC-AATAAG--AAAC---CATA-AGC--GGGAAC TTGGTCTGAAAGACCCCA--A---ATAAG-AGGTGGTAGTCATGGGACTCGTCTAGAACGAGTGGAAATTC--AAGCATCGCTGG-ACCTTCAGAGCCTCAACATACGCC-TAGAGAAC-GAC-ATCAGGT--TTAGATCATTCGACCCCGCTTAGAA-----ACA---GA---AAAT-----T---GA

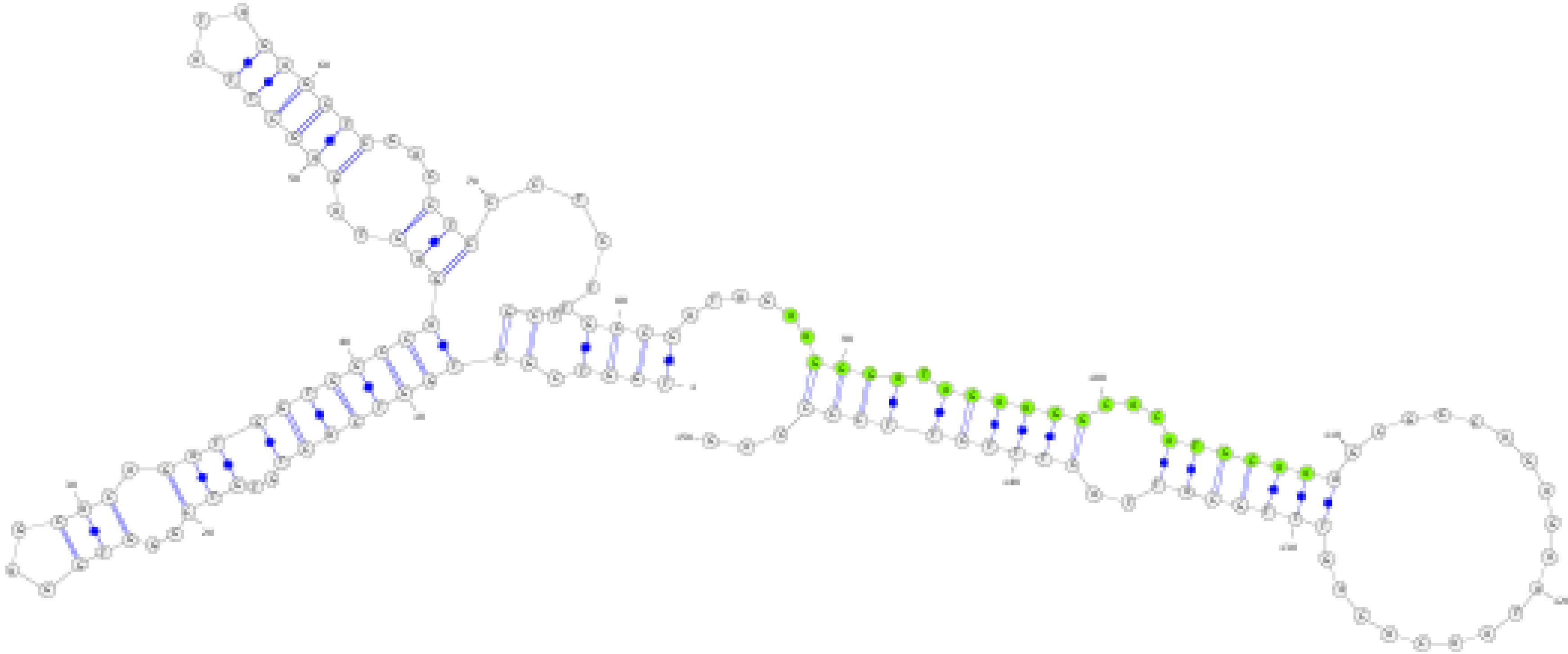
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PASS/FAIL	
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crit.total	1
crit.pairing	1
crit.top3	1
crit.tltop3	1
crit.un	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	2
rescue.candidate	9

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dsi_25795	x:1162559-1162708 +	candidate-rescued	5p_tailed_mirtron	5pUTR	[View on UCSC Genome Browser (Cornell Mirror)]

Legend: ■ **mirna** ■ **star** ■ **mismatch in alignment** ■ **mismatch in read**

Predicted structure



dsi_25795_annot [-44.2]

Show Alternate Folds

Flybase annotation

utr5 [utr5_plus_13574]; utr5 [utr5_plus_13575]

No Repeatable elements found

Sense Strand Reads

	Read #		Hit	Total						SRR902009	M023	SRR618934		M053	GSM343915	SRR553488	SRR553486	SRR553487
	size	Mismatch	Count	Norm	Total	testis	head	ovaries	dsim v501	head	ovaries	male	female	embryo	male	RT_0-2	Makindu_3	NRT_0-2
GGGATCGGATCGATTGCTAGGGGTGTGTGTGCAATCAGGAGTGGGGCGATGGTCGTGGTCACTGTGTCTGGGTGGAGCAGAGATGGTGGCCAGAGTAGAGCTTATAGAGCTCGACCTCCCTCTTGCTGCCGATACAGGGATAGAGGCACATGCAAGCGCCAGAGAATAACACAGTTTGCATTACTTTCTTCCCGACGTTTCAGAACGGCTGAAATGGAGAAGACTCCCCGGGTACA	22	0	1	7.00	7	5	0	2		0	2	0	0	0	0	0	0	0
.....AAGGGATAGAGGCACATGCAA.....TGCATTACTTTCTTCCCGA.....	21	1	1	2.00	2	0	0	0		0	0	0	1	1	0	0	0	0
.....AAGGGATAGAGGCACATGCAAA.....	23	0	1	2.00	2	1	0	0		0	0	1	0	0	0	0	0	0
.....AAGGGATAGAGGCACATGCA.....	21	0	1	1.00	1	1	0	0		0	0	0	0	0	0	0	0	0
.....TTGCATTACTTTCTTCCCGA.....	22	1	1	1.00	1	0	0	1		0	1	0	0	0	0	0	0	0

Anti-sense strand reads

	Read #		Hit	Total						SRR618934	M023	SRR553488	SRR553487		M053
	size	Mismatch	Count	Norm	Total	dsim v501	head	male	ovaries	head	male	body	RT_0-2	NRT_0-2	female
CCCTAGCTAGCTAAACGATCCCCACACACAGTTAGTCTCCACCCCGCTACCGACGACCAAGTGACACAGCCACCTCGTGTCTACCACCGGTCTCATCTCGAATATCTCGAGCTGGAGGGAAGCAGCGGCTATCTCCCTATCTTCCGTGTACGTTTCGGGGTCTCTTATTGTGTCAAACGTAATGAAGAAGGGGTCGAAGTGCTGCAGAACGTTTGCOCGACTTTTACCTCTTCTGAGGGGCCATGT	20	0	1	1.00	1	0	1	0	0	0	0	0	0	0	0
.....GGTCTCTTATTGTGTCAAAC.....	20	0	1	1.00	1										

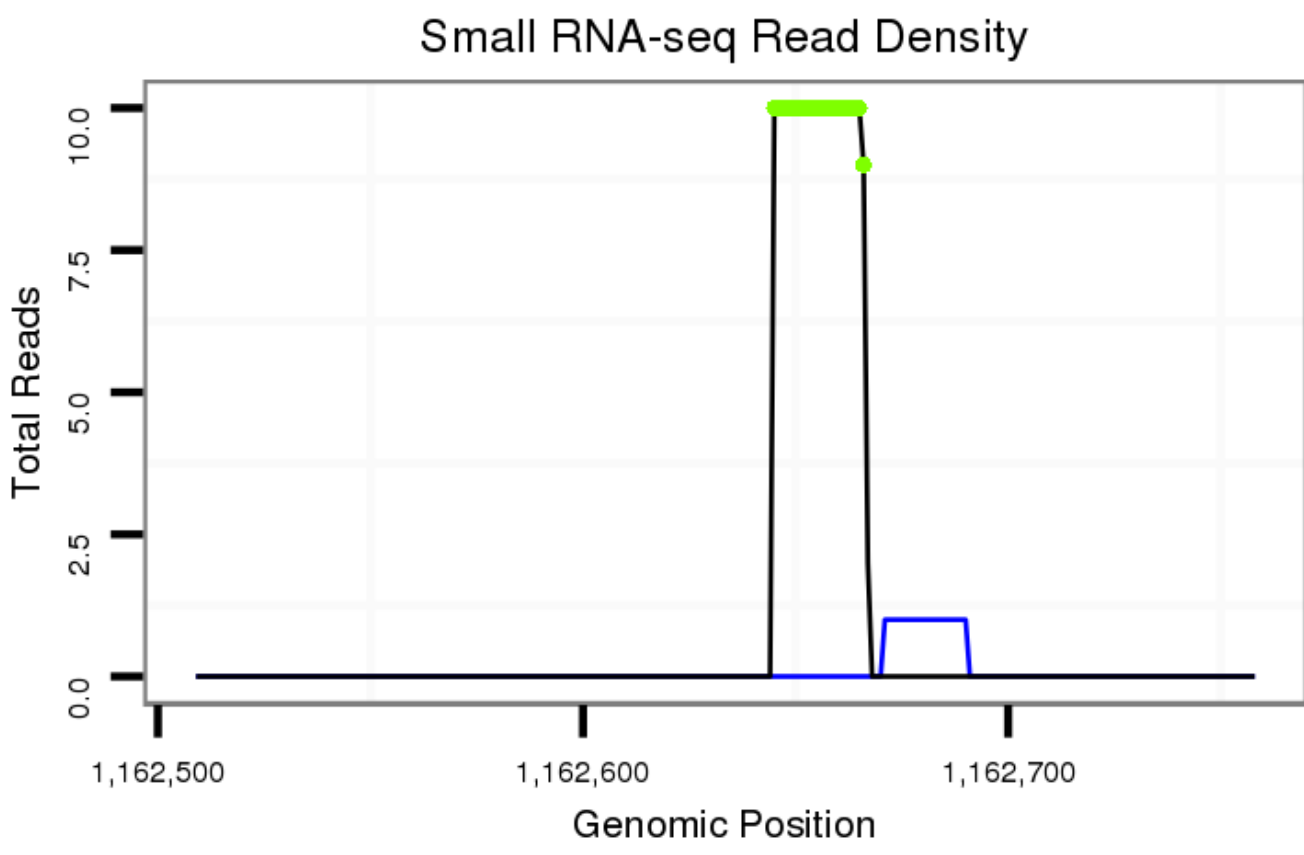
Show Alignment With Reads

Re-alignment of all predicted orthologs

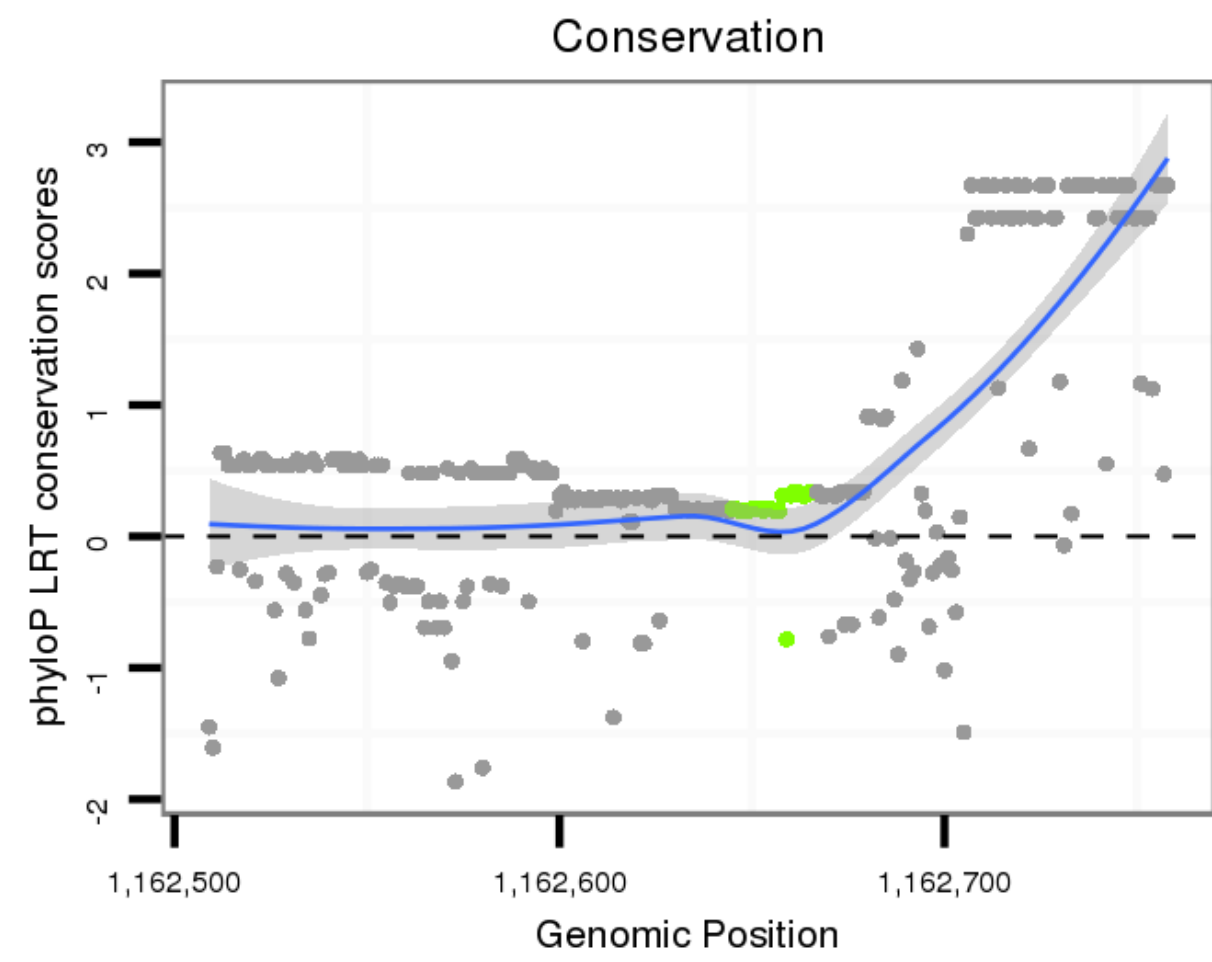
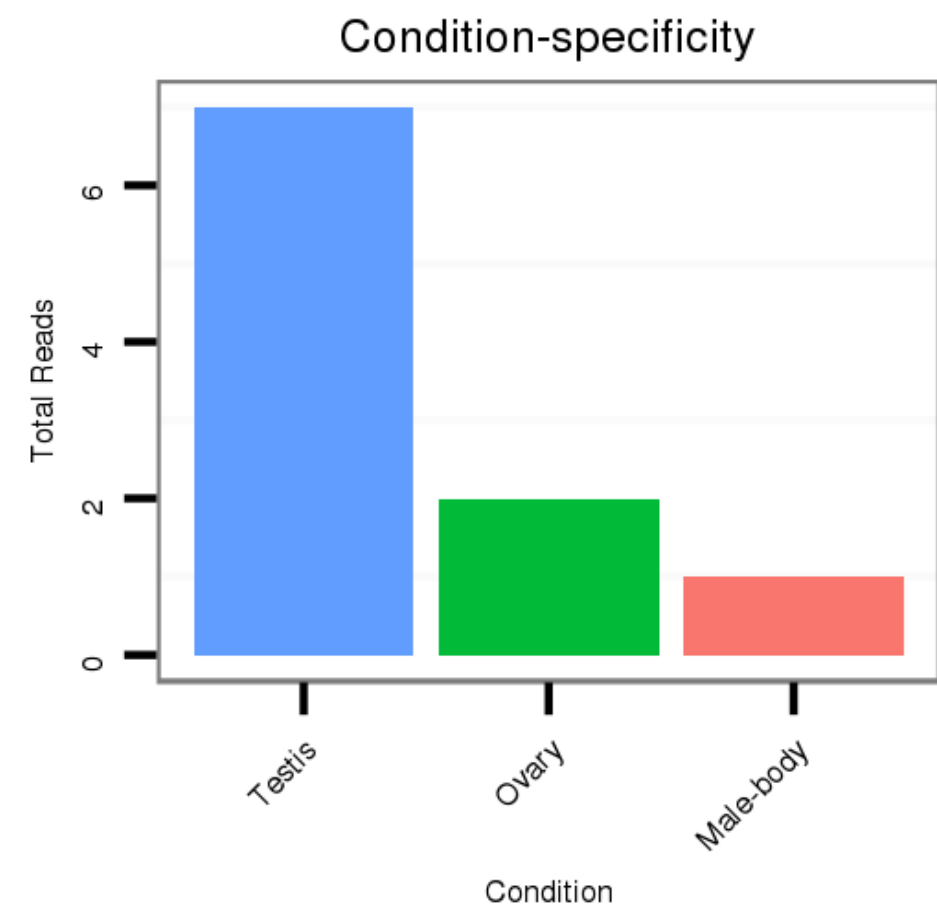
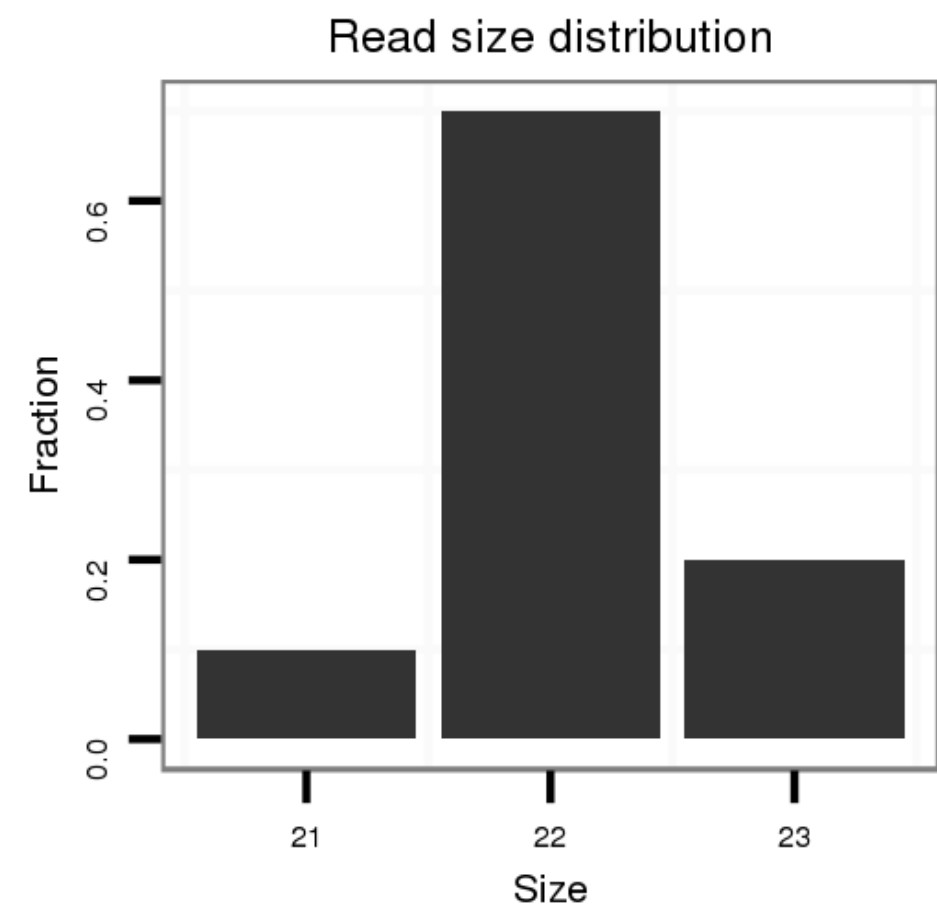
Species	Coordinate	ID	Alignment
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crit.lari	1
crit.back	1
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Hairpin partition ☐ Sense ☒ Antisense ☒ Mature

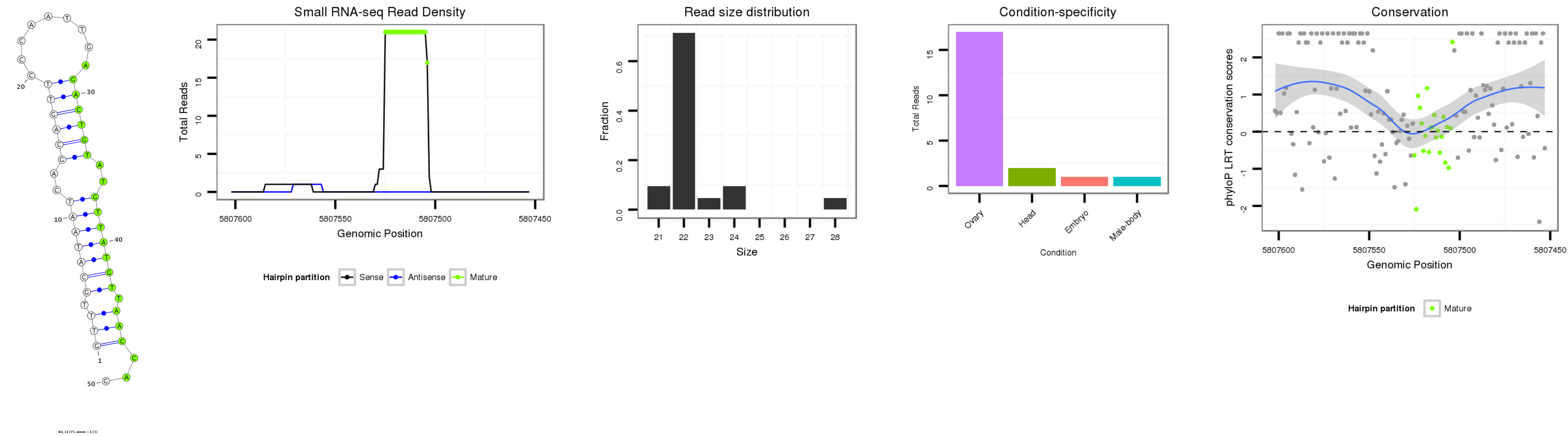


Hairpin partition ☒ Mature

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dsi_11275	21:5807503-5807552 -	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 [21_5807503_5807552_-]; CDS [21_5807553_5807678_-]; CDS [21_5807350_5807502_-]; utr5 [utr5_minus_715]; utr5 [utr5_minus_716]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

	Read size	# Mismatch	Hit Count	Total Norm	Total	SRR553486 Makindu_3 day-old ovaries	SRR553485 Chicharo_3 day-old ovaries	M023 head	M025 embryo	M024 male body	SRR902009 testis	SRR618934 dsim w501 ovaries	SRR553487 NRT_0-2 hours eggs	SRR553488 RT_0-2 hours eggs
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.....AGACTGTATGTTATGTTAAACCA.....	22	0	1	15.00	15	8	5	2	0	0	0	0	0	0
.....AGACTGTATGTTATGTTAAACC.....	21	0	1	2.00	2	1	0	0	0	1	0	0	0	0
.....TTGAGACTGTATGTTATGTTAAACC.....	24	0	1	2.00	2	1	1	0	0	0	0	0	0	0
.....GGCTGGACCTTCTGGAGCTGCAGC.....	24	0	1	1.00	1	0	0	0	0	0	1	0	0	0
.....TGAGACTGTATGTTATGTTAAACCA.....	26	1	1	1.00	1	0	0	0	1	0	0	0	0	0
.....AGACTGTATGTTATGTTAAACCA.....	23	0	1	1.00	1	0	1	0	0	0	0	0	0	0
.....AATTGAGACTGTATGTTATGTTAAACCA.....	28	0	1	1.00	1	0	0	0	1	0	0	0	0	0

Anti-sense strand reads

	Read #	# Mismatch	Hit Count	Total Norm	Total	SRR618934 dsim w501 ovaries	SRR553487 NRT_0-2 hours eggs	SRR553488 RT_0-2 hours eggs	SRR553485 Chicharo_3 day-old ovaries
CTACTCGTATTGCGTCACCGACCTGGAAGACCTCGACGTCGTCATGCTTCCAAACGTATTAGTCGTCGAAGGGTTAACTCTGACATACAACAATTTGGTCCTTTGGATGTCCTCAAGTCGTGGCACCTGCTGCACCAACCTGTAGTGCCTG	15	0	1	1.00	1	1	0	0	0
.....CTCGACGTCGTCATG.....	15	0	1	1.00	1	1	0	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

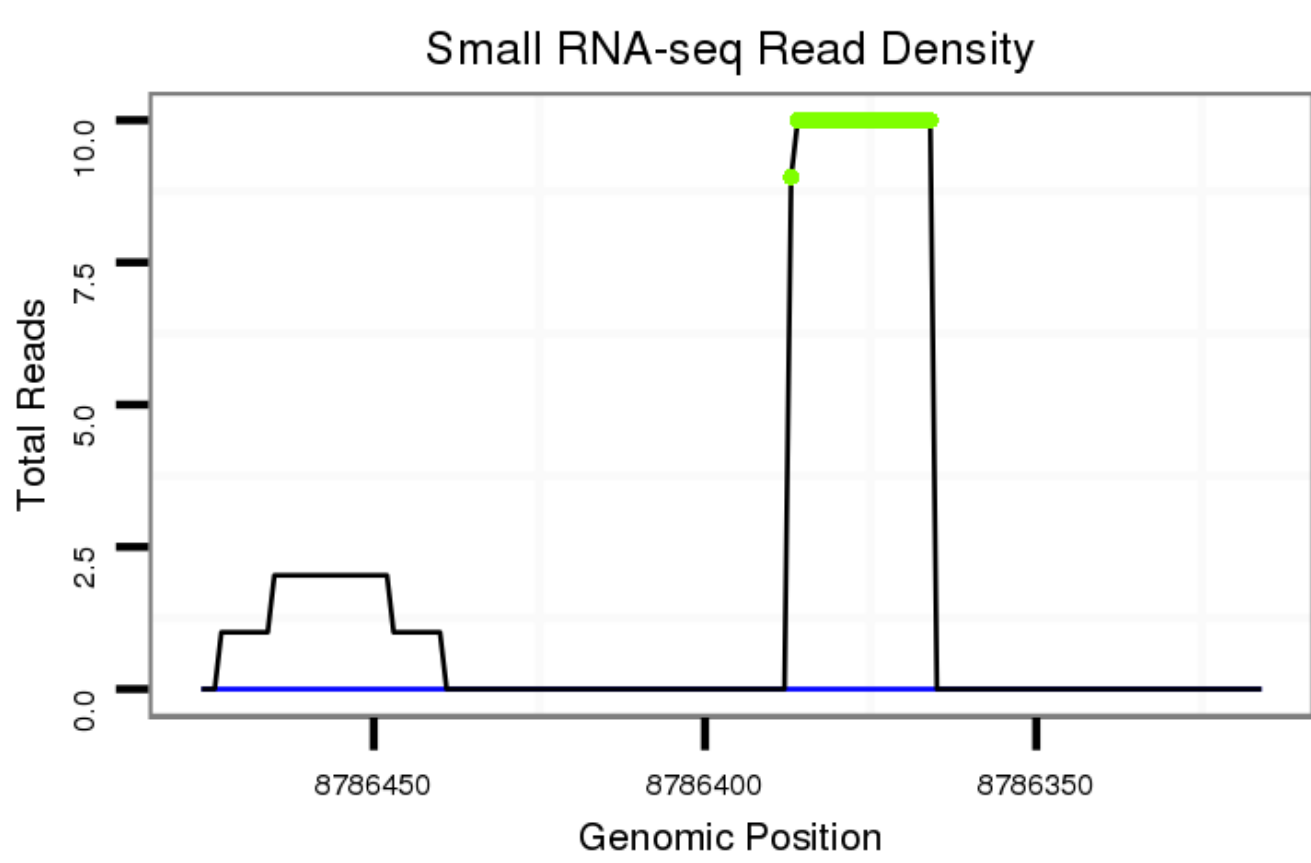
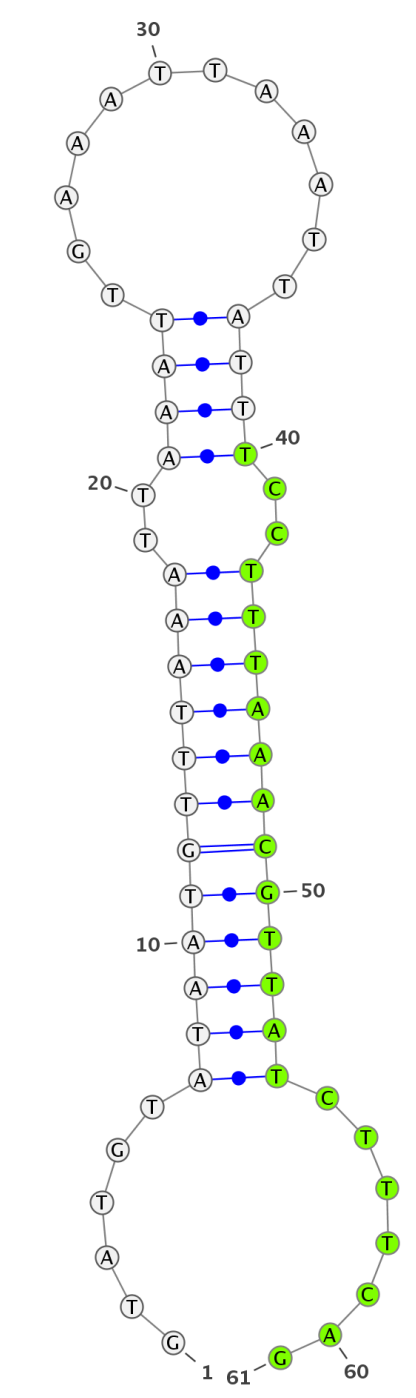
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droSec2	scaffold_5:4082859-4083008 -		GATGAGCATAAGCGAGTGGCTGGACCTTCTGGAGCTGCAGCAGTACGAAGTTTGCATGATCAGCA--GT-----TCCC-----A-----ATTGAGACTGT-----ATGT--T-----ATGTTAAATAAGAAACCTACAGGAGTTCAGCACCGTGGACGACGTGGTGGACATCACGGAC
dm3	chr2L:6011886-6012035 -	dme_428	GATGAGCATAAGCGAGTGGCTGGACCTTCTGGAGCTGCAGCAGTACGAAGTTTGCATGATCAGCA--GT-----TCCC-----A-----ATTGAGACTGT-----ATGT--T-----ATGTTAAACCGAAACCTACAGGAGTTCAGCACCGTGGACGACGTGGTGGACATCACGGAC
droPer2	scaffold_4929:6102345-6102494 -		GATGAGCATAAGCGAGTGGCTGGACCTTCTGGAGCTGCAGCAGTACGAAGTTTGCATGATCAGCA--GT-----TCCC-----A-----ATTGAGACTGT-----ATGT--T-----ATGCTTACCGAAACCTTCAGGAGTTCAGCACTGTGGACGACGTGGTGGACATCACGGAC
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droPer2	scaffold_1:257520-257675 +		GATGAGCATAAGCGAGTGGCTGGACCTTCTGGAGCTGCAGCAGTACGAAGTTTGGCGCTCTC-----T-----TG-----ACCTG-----C-----CCAA--CAC--CAT--TTTCATTGATCCTTGCCTTAAAGTAACCTTCAGGAGTTCAGCACTGTGACGAGTGGTGGACATCACGGAC
droW112	scf2_1100000004521:7945716-7945815 +		AGCTATGATTAAGCGAGTGGCTGGACCTTCTGGAGCTGCAGCAGTACGAAGTTTGAAGTCTAGCC--TACCCTAATGA--GCCCA-----GATCCCAACTAA-----AGAT--CCTTCA-----CAATTAACCGAAACCTTCAGGAGTTCAGCACTGTGACGAGTGGTGGATTAATACGGAC
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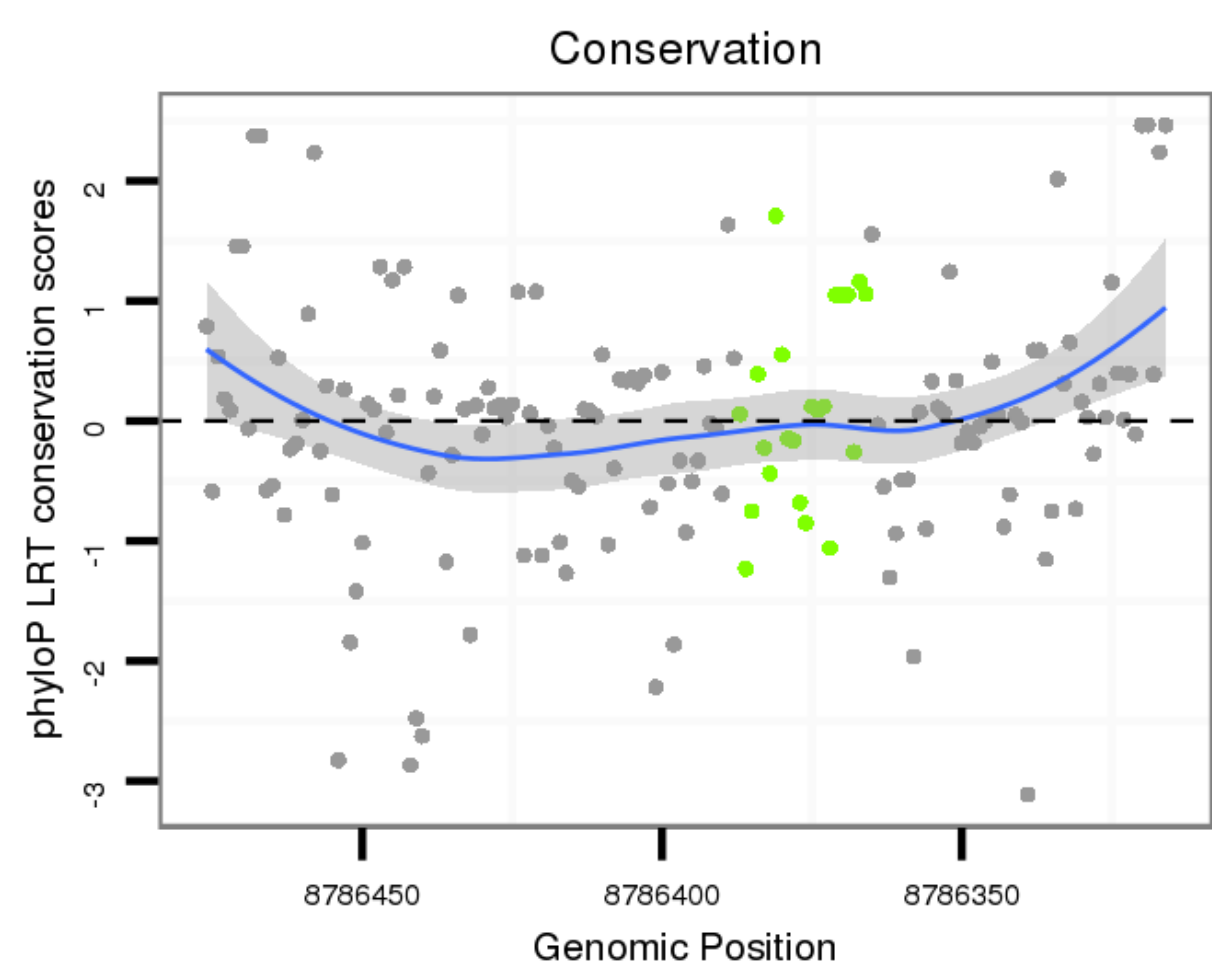
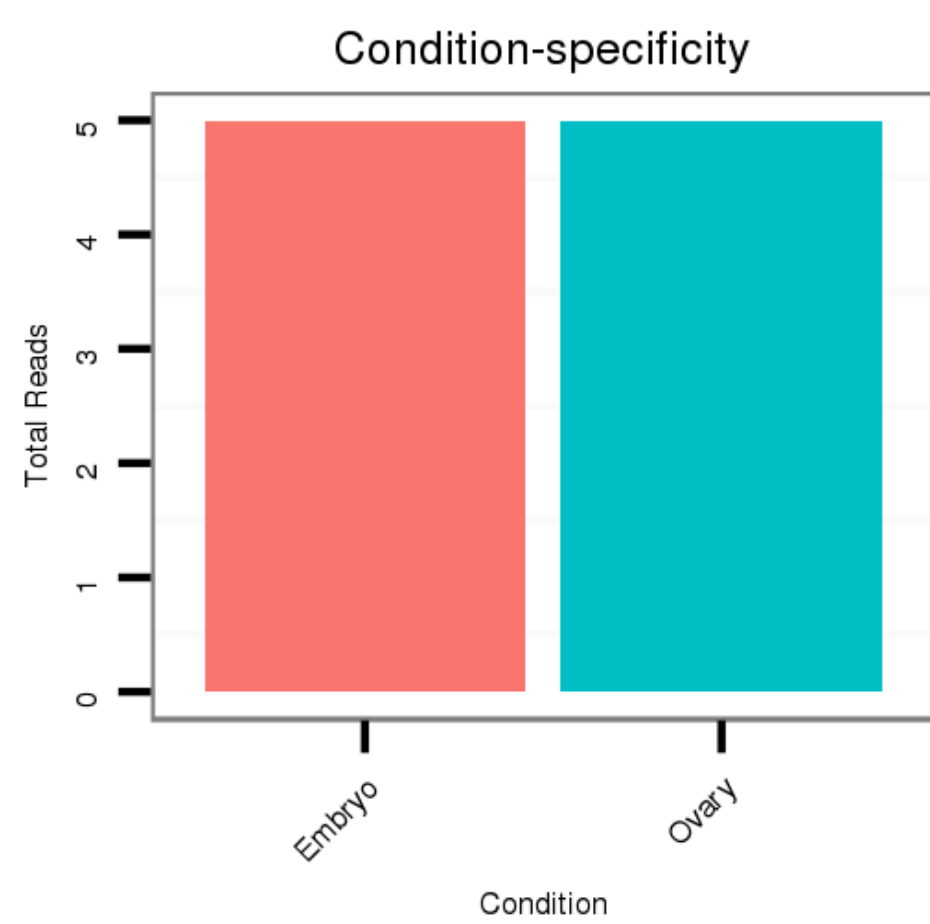
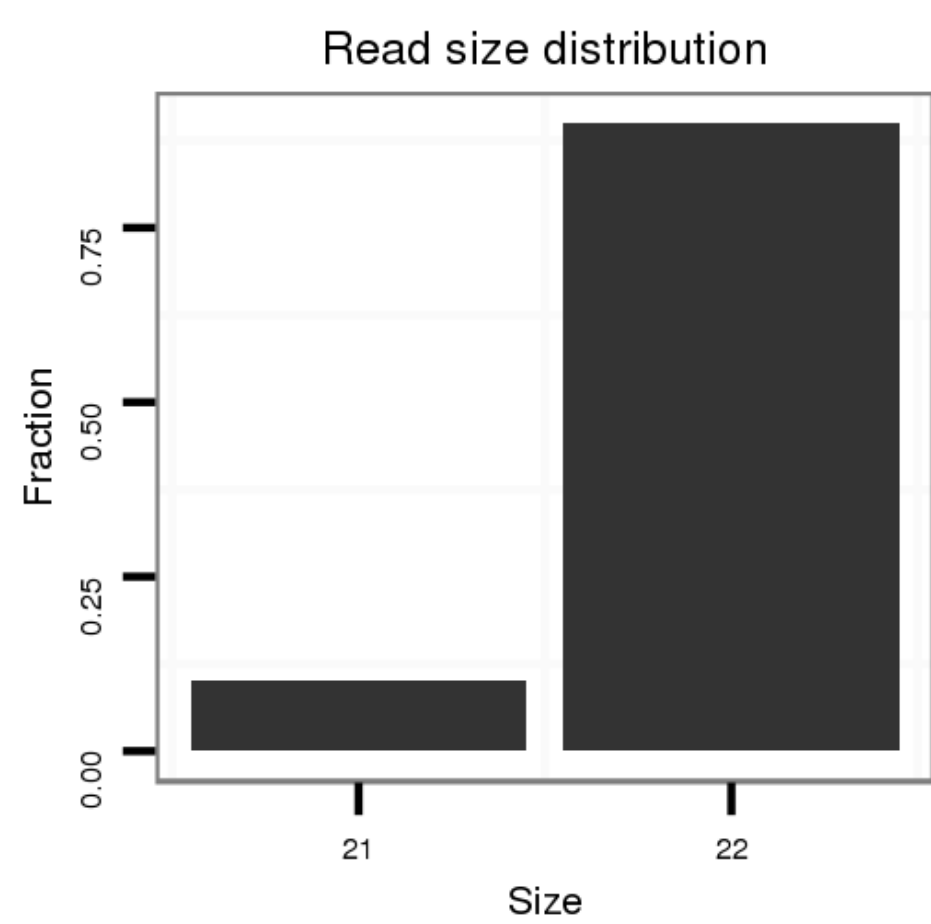
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crit.back	1
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rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	2

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Hairpin partition Sense Antisense Mature



Hairpin partition ☒ Mature

[Show Alternate Folds](#)

Flybase annotation

intron [3l_8786366_8786426_-]; CDS [3l_8786138_8786365_-]; CDS [3l_8786427_8786924_-]; utr3 [utr3_minus_5231]

Repeatable elements

Name	Class	Family	Strand
AT_rich	Low_complexity	Low_complexity	+

Sense Strand Reads

hide 3p reads show mid mismatch reads

[illegible]

Anti-sense strand reads

										SRR553488		SRR553485			
										SRR618934	M025	GSB343915	RT_0-2	Chicharo_3	SRR902009
										dsim w501	embryo	embryo	day-0	ovaries	testis
										ovaries	embryo	embryo	eggs	ovaries	testis
										Read #	Hit	Total	Normal	Total	
										size	Mismatch	Count	Size	Total	
										ovaries	embryo	embryo	eggs	ovaries	testis
										ovaries	embryo	embryo	eggs	ovaries	testis

Show Alignment With Reads

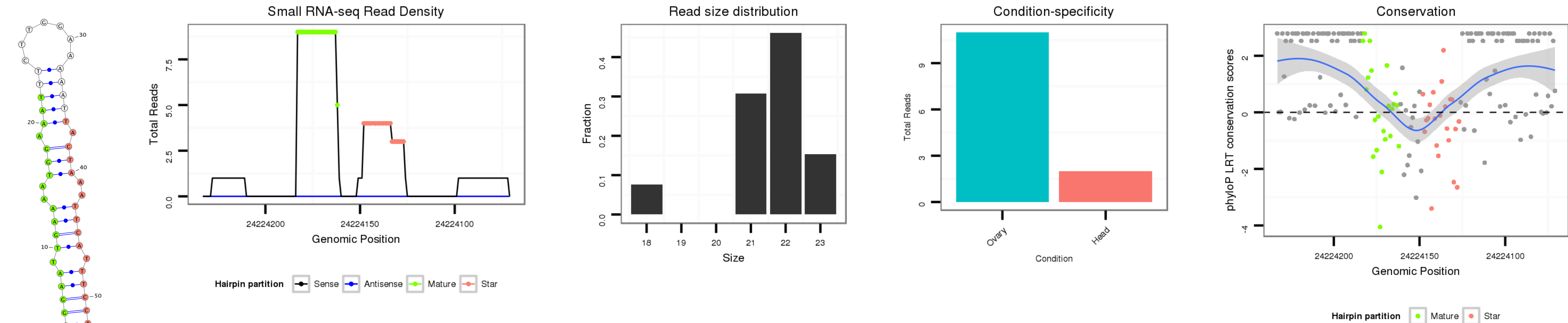
Re-alignment of all predicted orthologs

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droSe2	scaffold_0:1272767-1272927 +	AGGCCATATTTCGAAGGATTCG-----GACACGAAGGATCT--GGA-----GCCAGCGAAAGTATGTATAA-----TGTT-----TAAATTAAATTGAA-----TTAAATTATTTCCTTTAAAC-----G-----TTATCTTCAGACCATCAGCGCTCCTCGGAAAGTGAGAAATCCCGGGAGAA---GGGTATGTG
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droBu1	scf718000409467:2131161-213289 +	AGGCCATATTTCGAAGGATTCG-----GACACGAAGGATCT--GGA-----GCCAGCGAAAGTATGTATAA-----TGTT-----TAAATTAAATTGAA-----TTAAATTATTTCCTTTAAAC-----G-----TTATCTTCAGACCATCAGCGCTCCTCGGAAAGTGAGAAATCCCGGGAGAA---GGGTATGTG
droBl1	scf7180004300910:2201068-2201263 +	AGGCCATATTTCGAAGGATTCG-----GACACGAAGGATCT--GGA-----GCCAGCGAAAGTATGTATAA-----TGTT-----TAAATTAAATTGAA-----TTAAATTATTTCCTTTAAAC-----G-----TTATCTTCAGACCATCAGCGCTCCTCGGAAAGTGAGAAATCCCGGGAGAA---GGGTATGTG
droTaK1	scf718000415356:189680-189759 +	AGGCCATATTTCGAAGGATTCG-----GACACGAAGGATCT--GGA-----GCCAGCGAAAGTATGTATAA-----TGTT-----TAAATTAAATTGAA-----TTAAATTATTTCCTTTAAAC-----G-----TTATCTTCAGACCATCAGCGCTCCTCGGAAAGTGAGAAATCCCGGGAGAA---GGGTATGTG
droEl1	scf718000491193:3241621-3241707 +	AGGCCATATTTCGAAGGATTCG-----GACACGAAGGATCT--GGA-----GCCAGCGAAAGTATGTATAA-----TGTT-----TAAATTAAATTGAA-----TTAAATTATTTCCTTTAAAC-----G-----TTATCTTCAGACCATCAGCGCTCCTCGGAAAGTGAGAAATCCCGGGAGAA---GGGTATGTG
droRb1	scf718000779318:225364-225487 +	AGGCCATATTTCGAAGGATTCG-----GACACGAAGGATCT--GGA-----GCCAGCGAAAGTATGTATAA-----TGTT-----TAAATTAAATTGAA-----TTAAATTATTTCCTTTAAAC-----G-----TTATCTTCAGACCATCAGCGCTCCTCGGAAAGTGAGAAATCCCGGGAGAA---GGGTATGTG
droFl1	scf718000451564:97417-97470 +	AGGCCATATTTCGAAGGATTCG-----GACACGAAGGATCT--GGA-----GCCAGCGAAAGTATGTATAA-----TGTT-----TAAATTAAATTGAA-----TTAAATTATTTCCTTTAAAC-----G-----TTATCTTCAGACCATCAGCGCTCCTCGGAAAGTGAGAAATCCCGGGAGAA---GGGTATGTG
droKl1	scf718000302319:41894-42032 +	AGGCCATATTTCGAAGGATTCG-----GACACGAAGGATCT--GGA-----GCCAGCGAAAGTATGTATAA-----TGTT-----TAAATTAAATTGAA-----TTAAATTATTTCCTTTAAAC-----G-----TTATCTTCAGACCATCAGCGCTCCTCGGAAAGTGAGAAATCCCGGGAGAA---GGGTATGTG
droAn3	scaffold_13337:7649166-7649185 +	AGGCCATATTTCGAAGGATTCG-----GACACGAAGGATCT--GGA-----GCCAGCGAAAGTATGTATAA-----TGTT-----TAAATTAAATTGAA-----TTAAATTATTTCCTTTAAAC-----G-----TTATCTTCAGACCATCAGCGCTCCTCGGAAAGTGAGAAATCCCGGGAGAA---GGGTATGTG
droB1p1	scf718000395543:315242-315259 +	AGGCCATATTTCGAAGGATTCG-----GACACGAAGGATCT--GGA-----GCCAGCGAAAGTATGTATAA-----TGTT-----TAAATTAAATTGAA-----TTAAATTATTTCCTTTAAAC-----G-----TTATCTTCAGACCATCAGCGCTCCTCGGAAAGTGAGAAATCCCGGGAGAA---GGGTATGTG
dp5	2:3062794-3062816 +	AGGCCATATTTCGAAGGATTCG-----GACACGAAGGATCT--GGA-----GCCAGCGAAAGTATGTATAA-----TGTT-----TAAATTAAATTGAA-----TTAAATTATTTCCTTTAAAC-----G-----TTATCTTCAGACCATCAGCGCTCCTCGGAAAGTGAGAAATCCCGGGAGAA---GGGTATGTG
droPe2	scaffold_0:2875935-2875957 +	AGGCCATATTTCGAAGGATTCG-----GACACGAAGGATCT--GGA-----GCCAGCGAAAGTATGTATAA-----TGTT-----TAAATTAAATTGAA-----TTAAATTATTTCCTTTAAAC-----G-----TTATCTTCAGACCATCAGCGCTCCTCGGAAAGTGAGAAATCCCGGGAGAA---GGGTATGTG
droW12	scf2_110000004921:2673717-267385 +	AGGCCATATTTCGAAGGATTCG-----GACACGAAGGATCT--GGA-----GCCAGCGAAAGTATGTATAA-----TGTT-----TAAATTAAATTGAA-----TTAAATTATTTCCTTTAAAC-----G-----TTATCTTCAGACCATCAGCGCTCCTCGGAAAGTGAGAAATCCCGGGAGAA---GGGTATGTG
droV13	scaffold_13049:16511068-16511281 +	AGGCCATATTTCGAAGGATTCG-----GACACGAAGGATCT--GGA-----GCCAGCGAAAGTATGTATAA-----TGTT-----TAAATTAAATTGAA-----TTAAATTATTTCCTTTAAAC-----G-----TTATCTTCAGACCATCAGCGCTCCTCGGAAAGTGAGAAATCCCGGGAGAA---GGGTATGTG
droMo3	scaffold_6880:29219734-2921985 +	AGGCCATATTTCGAAGGATTCG-----GACACGAAGGATCT--GGA-----GCCAGCGAAAGTATGTATAA-----TGTT-----TAAATTAAATTGAA-----TTAAATTATTTCCTTTAAAC-----G-----TTATCTTCAGACCATCAGCGCTCCTCGGAAAGTGAGAAATCCCGGGAGAA---GGGTATGTG
droGr12	scaffold_15110:12199232-12199445 +	AGGCCATATTTCGAAGGATTCG-----GACACGAAGGATCT--GGA-----GCCAGCGAAAGTATGTATAA-----TGTT-----TAAATTAAATTGAA-----TTAAATTATTTCCTTTAAAC-----G-----TTATCTTCAGACCATCAGCGCTCCTCGGAAAGTGAGAAATCCCGGGAGAA---GGGTATGTG

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Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Show Alternate Folds

Flybase annotation

intron [3r_24224121_24224183_-]; CDS [3r_24223410_24224120_-]; CDS [3r_24224184_24224367_-]; utr5 [utr5_minus_10559]

Sense Strand Reads

hide 3p reads show mid mismatch reads

[illegible]

Anti-sense strand reads

TCGACGACGCTTCTCATGCTGCTCTTCTTCTTGTCAAATTCAGTTCACATTCTTAACCTTTAAGAACCTTTTAAATGATTAAAGTAAAGGAATAAAAGGCTGTTGGTTGTGTGTAACACCTCTTTATACCACCGCTTCGTAAGATGTCCA										Read #	0	Hit	3	Total	0.33	1	0	1	0	0
*****..(((((((.(((.(.(((.(((.(.....)))))).)))).))))).*****										Size Mismatch	15	0	3	0.33	1	0	1	0	0	
.....AAGTAAAGGAATAA.....																				
Show Alignment With Reads																				

Re-alignment of all predicted orthologs

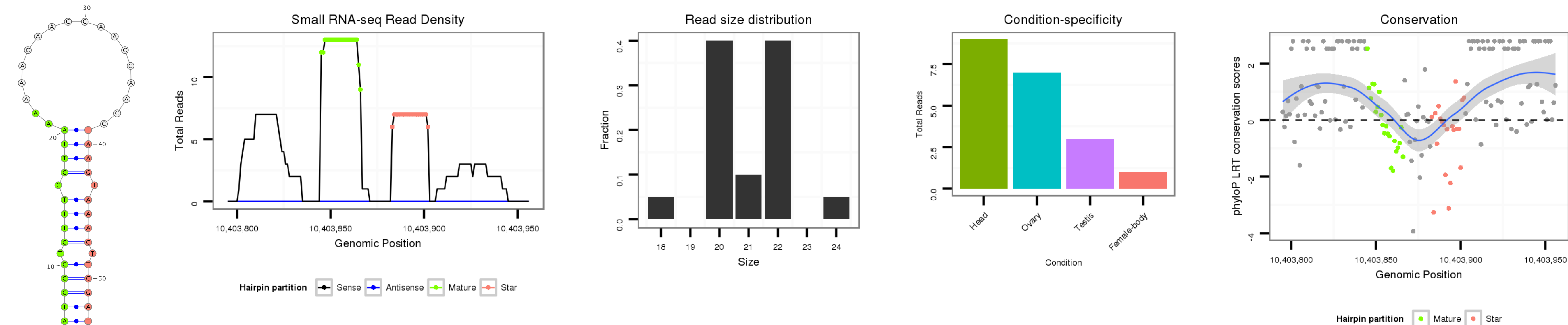
Species	Coordinate	ID	Alignment
droSim2	3r:24224071-24224233 -	dsi_14257	AGCTGCTGCAGAAAGGATACGACGAGAAGAAGAACAGTTTAAGTCAAGT TTAAGGA --ATTGAA--A-AT-----GGAAA--T-TCTTGGAA-A---AAT-----A-----CTAA--AT--T-CAT---TTCC--TTTATTTCCGACACCAAAACACACATTGTGGAGAAATATGTTGGCGAAGAGCATCTACAGGT
droSeo2	scaffold_4:3725175-3725338 -		AGCTGCTGCAGAAAGGATACGACGAGAAGAAGAACAGTTTAAGTCAAGT TTAAGGA --ATTGAA--A-AT-----GGAAA--T-TCTTGGAA-A---AAT-----A-----CTAC--AT--C-CAT---TTCC--TTTATTTCCGACACCAAAACACACATTGTGGAGAAATATGTTGGCGAAGAGCATCTACAGGT
dm3	Chr3R:24863466-24863629 -	dme_431	AGCTGCTGCAGAAAGGATACGACGAGAAGAAGAACAGTTTAAGTCAAGT TTAAGTA --ATTGAA--A-AT-----GGAAA--T-TCTTGGAA-A---CAT-----A-----CTAT--AT--C-CAT---TTCC--TTTATTTCCGACACCAAAACACACATTGTGGAGAAATATGTTGGCGAAGAGCATCTACAGGT
droEre2	scaffold_4820:3170147-3170312 -		AGCTGCTGCAGAAAGGATACGACGAGAAGAAGAACAGTTTAAGTCAAGT TTAAGTA --ATT TGT --A---GGGC-TGGC T --T-TTTT SARAC ---AAT T ----- T -----TTAT--AG--C-CAT---TT TT TTCCCT TTCCGACACCAAAAC GCAT ATTGTGGAGAAAT SGA GGCGAAG GCATCT CAGGT
droYak3	3R:21635293-21635459 +		AGCTGCTGCAGAAAGGATACGACGAGAAGAAGAACAGTTTAAGTCAAGT TTAAGTA --ATT T T --A---GGCC-T TAAAT --A-TTCTT AGCAA ---AA C -----A-----CTAC--AA--C-CAT---TT TC -TT CTT TTCCGACACCAAAAC CACAT TTGTGGAGAAAT SGA GGCGAAGAGCAT CT CAGGT
droEup1	scf7180000409787:711802-711966 +		AAAT GCTGCAGAAAGGATACGACGAGAAGAAGAACAGTTTAAGTCAAGT TTAAGTA --ATT CTC --T---TAA A --TAA TT --T---ACCTA AA --GCGAG AT CTCCT AA -- T ----- T ---AATA--T-A--- ATTGCCAT TTAGAC AA AAAC GCAT ATTGTGAGAGAAAT SGA GGCGAAGAGCAT CT CAGGT
droBi1	scf7180000302113:3356433-3356595 -		AGCTGCTGCAGAAAGGATACGACGAGAAGAAGAACAGTTTAAGTCAAGT TTAAGTA --TT CTT --T---GATCAGAT----- T ---GACAT C GCAT GT CTCCT AT -- T ----- ACAT -T---TA--TT TCGATT TCAGAC AA AAAC GCAT ATTGTGGAGAA GTAT GGCGAAGAGCAT CT CAGGT
droTak1	scf7180000410579:179595-179759 +		AGCTGCTGCAGAAAGGATACGACGAGAAGAAGAACAGTTTAAGTCAAGT TTAAGTA --T AAATT --A---GGCA-T AAAT -- T ---CTT AA --G---G AC ----- T -----CCTT--AA--ACAT-T---TT AAATGCCAT TTCCAGACCAAAACACACATTGT SAGA GA GTGA GGCGAAGAGCAT CT CAGGT
droEle1	scf7180000491261:1442505-1442669 -		AGCTGCTGCAGAAAGGATACGACGAGAAGAAGAACAGTTTAAGTCAAGT TTAAGTA --TT ACT --T-AT---GACT-T A --A---AT GCCAAAGC --- A AAATT --T-----C---A---A-C-T---TT CTTTTAAAT TCAGACCAAAAC CACAT TTGTGGAGAA GTGA GGCGAAGAGCAT CT CAGGT
droRho1	scf7180000780007:183725-183889 +		AGCTGCT CC GAAAGGATACGACGAGAAGAAGAACAGTTTAAGTCAAGT TTAAGTA --TT AAA --T-AT---GATC--A-A-A---AT GCACAAGT --- A AAAT --T-----C---A---A-T-T---TT TCTTATAC TCGACCAAAAC CACAT TTGTGGAGAAAT SGT GGCGAAGAGCAT CT CAGGT
droFi1	scf7180000454073:3480963-3481122 +		AGCTGCT CC A AA AGGATACGACGAGAAGAAGAACAGTTTAAGTCAAGT TTAAGTC --T AC --A-A-A---TT AAAT --T-TT AAAG -G---TT TT -----T---AA AA --A-A--A-GT---TT TC -TT GC CTCTAGACCAAAAC CACAT TTGTGGAA AGTGA GGCGAAGAGCAT CT CAGGT
droKik1	scf7180000302276:836508-836665 -		AACT GCTGCAGAAAGGATACGACGAG AA AGGA GC AGTTTAAGTCAAGT TTAAGTC --TT TCGT --T-T ATTTTGT ----- T ---GT TC CA AAAT ---GC----- T ---AT--AA A --A-A C ----- CCCTC TTTCAGACCAAAAC CACAT TTGTGGAGAAAT SGCGG GA GC AGAGCAT CT CAGGT
droAna3	scaffold_13340:19704237-19704396 +		AGCTGCTGCAGAAAGGATACGACGAGAAGAAGAACAGTTTAAGTCAAGT TTAAGTA --GCC--TT A -C---AA ATC --T-TT ATGCC TA---AA A -----AA C --ACCGAC--CAT--- TT TC TTT AGAC AAAAC CACAT TTGTGGAGAAAT SGCGG GA GC AGAGCAT CT CAGGT
droBip1	scf7180000396413:2684845-2684998 -		AGCTGCT CC A AA AGGATACGAC AA AGGA AG GCAGTTTAAGTCAAGT TTAAGTA -- AGC --A-G A -----T AAAT --C C AT TAAG AA AG ---AA A -----A-----AA C --AG---A-CAT---T TT -----TT TC TCAGACAAAACACACATTGTGGAGAAAT SGCGG GA GC AGAGCAT CT CAGGT
dp5	2:13168818-13168992 +		AGCT AT CT CC AAAGGA TAC GA CA GAAGAAGAACAGTTTAAGTCAAGT TTAAGTCCTCGCC --TT T -T-T---AT TGTC ----- TA --- T -----TTTAT TATCTTCATC -C-AGCAGAC--GG TTGC CCCTC TT TGCTT TCAGACAAAAC CAT ATTGTGGAGAAATATGTTGGCGAAGAGCAT CT CAGGT
droPer2	scaffold_0:7283036-7283202 -		AGCT AT CT CC AAAGGA TAC GA CA GAAGAAGAACAGTTTAAGTCAAGT TTAAGTCCTCGCC --TT T -T-T---AT TGTT ----- TA --- T -----TTTAT TATC -C-AGCAGAC--GG TTGC CCCTC TT TACTT TCAGACAAAAC CAT ATTGTGGAGAAATATGTTGGCGAAGAGCAT CT CAGGT
droWi12	scf2_1100000004921:464640-464802 +		AACT GCTGCAGAAAGGATAC GA GAAGAAGAACAGTTTAAGTCAAGT TTAAGTT --TGCC-T CT -T---AATG--TT A -- T ---CT TC SA A -T---TAT TAATTG --T--- C ---A---A-C-T---TT A TT TAAT TCAGACAAAAC CACAT TTGTAGAGAAATATGCG GG GAAGAGCAT CT CAGGT
droVir3	scaffold_13047:18310440-18310595 -		AGCTGCTGCAGAAAGGATACGA GA GAAGAAGAACAGTTTAAGTCAAGT TTAGCTT -- CA GT T --A---AACTTAT----- T ---T GTCT TA A -A---AGC-----A-----CTAA--AA--T-AG-----TT TTCT TCAGACCAAAAC CACAT TTGTGGAA ATGA GA GTGA GGCGAAGAGCAT CT CAGGT
droMo3	scaffold_6540:13430162-13430318 +		AGCTGCTGC AA AGGA TAC GA CA GAAGAAGAACAGTTTAAGTCAAGT TTAGCT -- AA GT A --A T -----C-CA AA ---CC T -CT TG AA TC --A A ----- T -----CTAA--CA--C-TG-----TT TT ---CCC TT TCAGACAAAAC GCAT TTGTGGAA ATGA GA GTGA GGCGAAGAGCAT CT CAGGT
droGr12	scaffold_15074:6398670-6398825 +		AACT G

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

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Show Alternate Folds

Flybase annotation

intron [31_10403845_10403906_+]; CDS [31_10403907_10404034_+]; CDS [31_10403767_10403844_+]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

[illegible]

Anti-sense strand reads

Re-alignment of all predicted orthologs

[illegible]

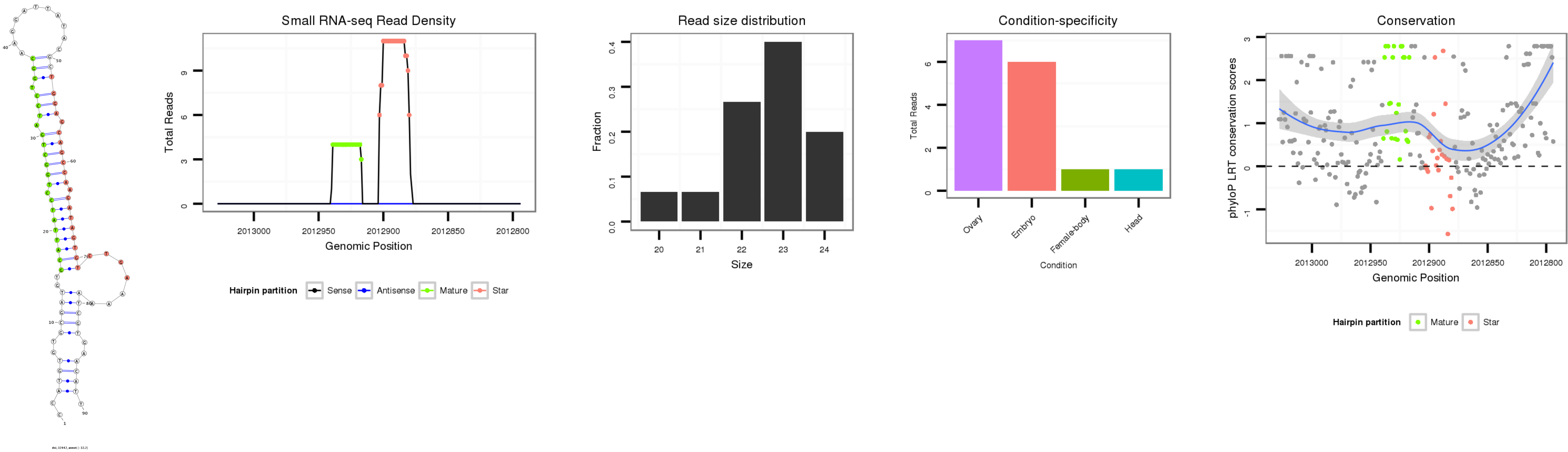
Generated: 09/08/2015 at 07:19 PM

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

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:
dsi_32442	31:2012844-2012978	candidate-rescued	Canonical miRNA	Intergenic
[View on UCSC Genome Browser (Conell Mirror)]				

Legend: **green** hit **red** mismatch in alignment **red** mismatch in row

Predicted structure



Show Alternate Folds

Sense Strand Reads

hide 3p reads show mid mismatch reads

	Read #	Hit	Total		M053	SRR618934	SRR553487	SRR553486	SRR553488	SRR553485	O002	SRR902008	GSM343915
	size	Mismatch	Count	Norm	Total	female dsim w501 ovaries	NRT_0-2 hours eggs	Makindu_3 day-old ovaries	M025 RT_0-2 hours embryo eggs	M024 Chicharo_3 day-old male ovaries body	Head ovaries	SRR902008	embryo
GCAAAAGATATCAAGCCATCTATATATATAGTCGAACCTGCACAAATCAAAGATCACGTATACGGCGTTCGCCATGTGTGCGATGTCATATCTCTGGCTGATCTGGC	23	0	1	3.00	3	0	0	0	0	3	0	0	0
.....GATTATCTCTGGCTGATCTGGC	24	0	1	3.00	3	0	1	0	2	0	0	0	0
.....GGAGCAGCCAGATAGTGTCTGA	22	0	1	2.00	2	0	0	0	0	2	0	0	0
.....TGGATATATCTGGCTGATCTGGC	23	0	1	1.00	1	0	0	0	0	0	0	0	1
.....AGCAGCCAAGATAGTGTCTGAAA	23	0	1	1.00	1	0	1	0	0	0	0	0	0
.....AGCAGCCAAGATAGTGTCTGAA	22	0	1	1.00	1	0	1	0	0	0	0	0	0
.....TGGAGCAGCCAAGATAGTGTCTG	23	0	1	1.00	1	0	1	0	0	0	0	0	0
.....TGGAGCAGCCAAGATAGTGTCTG	20	0	1	1.00	1	0	0	0	0	0	0	1	0
.....TGGAGCAGCCAAGATAGTGTCTG	22	0	1	1.00	1	1	0	0	0	0	0	0	0
.....AGCAGCCAAGATAGTGTCTGA	21	0	1	1.00	1	0	1	0	0	0	0	0	0

Anti-sense strand reads

										SRR553488		SRR553487		SRR553486		SRR618934							
										SRR50209		M024 RT_0-2 hours		NRT_0-2 hours		GSM343915		Makindu_3 day-old		dsim w501			
CGTTTGTCTATATCTCGTAGATATATATACGTTTGGACGTGTTTATGTTTCTAGTGCATATGCGCAAGACGTACACACGTACACAGTAAAGGATATCTCTTTCCTATAGGAGAACACAGAAAAGTTTATTAATAGC										Read #		Hit		Total		testis		male		eggs		embryo	
.....GATTATCTCTGGCTGATCTGGC										size		Mismatch		Count		Total							
.....GATTATCTCTGGCTGATCTGGC										size		Mismatch		Count		Total							
.....GATTATCTCTGGCTGATCTGGC										size		Mismatch		Count		Total							
.....GATTATCTCTGGCTGATCTGGC										size		Mismatch		Count		Total							
.....GATTATCTCTGGCTGATCTGGC										size		Mismatch		Count		Total							
.....GATTATCTCTGGCTGATCTGGC										size		Mismatch		Count		Total							
.....GATTATCTCTGGCTGATCTGGC										size		Mismatch		Count		Total							
.....GATTATCTCTGGCTGATCTGGC										size		Mismatch		Count		Total							
.....GATTATCTCTGGCTGATCTGGC										size		Mismatch		Count		Total							
.....GATTATCTCTGGCTGATCTGGC										size		Mismatch		Count		Total							
.....GATTATCTCTGGCTGATCTGGC										size		Mismatch		Count		Total							
.....GATTATCTCTGGCTGATCTGGC										size		Mismatch		Count		Total							
.....GATTATCTCTGGCTGATCTGGC										size		Mismatch		Count		Total							
.....GATTATCTCTGGCTGATCTGGC										size		Mismatch		Count		Total							
.....GATTATCTCTGGCTGATCTGGC										size		Mismatch		Count		Total							
.....GATTATCTCTGGCTGATCTGGC										size		Mismatch		Count		Total							
.....GATTATCTCTGGCTGATCTGGC										size		Mismatch		Count		Total							
.....GATTATCTCTGGCTGATCTGGC										size		Mismatch		Count		Total							
.....GATTATCTCTGGCTGATCTGGC										size		Mismatch		Count		Total							
.....GATTATCTCTGGCTGATCTGGC										size		Mismatch		Count		Total							
.....GATTATCTCTGGCTGATCTGGC										size		Mismatch		Count		Total							
.....GATTATCTCTGGCTGATCTGGC										size		Mismatch		Count		Total							
.....GATTATCTCTGGCTGATCTGGC										size		Mismatch		Count		Total							
.....GATTATCTCTGGCTGATCTGGC										size		Mismatch		Count		Total							
.....GATTATCTCTGGCTGATCTGGC										size		Mismatch		Count		Total							
.....GATTATCTCTGGCTGATCTGGC										size		Mismatch		Count		Total							
.....GATTATCTCTGGCTGATCTGGC										size		Mismatch		Count		Total							
.....GATTATCTCTGGCTGATCTGGC										size		Mismatch		Count		Total							
.....GATTATCTCTGGCTGATCTGGC										size		Mismatch		Count		Total							
.....GATTATCTCTGGCTGATCTGGC										size		Mismatch		Count		Total							
.....GATTATCTCTGGCTGATCTGGC										size		Mismatch		Count		Total							
.....GATTATCTCTGGCTGATCTGGC										size		Mismatch		Count		Total							
.....GATTATCTCTGGCTGATCTGGC										size		Mismatch		Count		Total							
.....GATTATCTCTGGCTGATCTGGC										size		Mismatch		Count		Total							
.....GATTATCTCTGGCTGATCTGGC										size		Mismatch		Count		Total							
.....GATTATCTCTGGCTGATCTGGC										size		Mismatch		Count		Total							
.....GATTATCTCTGGCTGATCTGGC										size		Mismatch		Count		Total							
.....GATTATCTCTGGCTGATCTGGC										size		Mismatch		Count		Total							
.....GATTATCTCTGGCTGATCTGGC										size		Mismatch		Count		Total							
.....GATTATCTCTGGCTGATCTGGC										size		Mismatch		Count		Total							
.....GATTATCTCTGGCTGATCTGGC										size		Mismatch		Count		Total							
.....GATTATCTCTGGCTGATCTGGC										size		Mismatch		Count		Total							
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.....GATTATCTCTGGCTGATCTGGC										size		Mismatch		Count		Total							
.....GATTATCTCTGGCTGATCTGGC										size		Mismatch		Count		Total							
.....GATTATCTCTGGCTGATCTGGC										size		Mismatch		Count		Total							
.....GATTATCTCTGGCTGATCTGGC										size		Mismatch		Count		Total							

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droSim2	11:2012794-2013028	dsi_32442	GCAAAAC-AGATATC-----AAGCCATCTAT-----A-----T-----ATAT-----AG--TCGAA--CCTGCACAAATCAAA-----AGATC-----ACGTATACG-----CGGTT-----CTG-CCATGTGTGGC-ATGTGCATATCTCTGGCTGATCTGGC
droSec2	scsFold_2:2140470-2140704	dsi_1837	GCAAAAC-AGATATC-----AAGCCATCTAT-----A-----T-----ATAT-----AG--TCGAA--CCTGCACAAATCAAA-----AGATC-----ACGTATACG-----CGGTT-----CTG-CCATGTGTGGC-ATGTGCATATCTCTGGCTGATCTGGC
dm3	chr31:2114883-2115119	dsi_114	GCAAAAC-AGATATC-----AAGCCATCTAT-----A-----TA-----ATAT-----AG--TCGAA--CCTGCACAAATCAAA-----AGATC-----ACGTATACG-----CGGTT-----CTG-CCATGTGTGGC-ATGTGCATATCTCTGGCTGATCTGGC
droEre2	scsFold_4:2842108748-2108982	dsi_94	GCAAAAC-AGATATC-----AAGCCATCTAT-----A-----TA-----ATAT-----AG--TCGAA--CCTGCACAAATCAAA-----AGATC-----ACGTATACG-----CGGTT-----CTG-CCATGTGTGGC-ATGTGCATATCTCTGGCTGATCTGGC
droTak3	11:2067724-2067957	dsi_1787	GCAAAAC-AGATATC-----AAGCCATCTAT-----A-----TA-----ATAT-----AG--TCGAA--CCTGCACAAATCAAA-----AGATC-----ACGTATACG-----CGGTT-----CTG-CCATGTGTGGC-ATGTGCATATCTCTGGCTGATCTGGC
droEug1	scsFold_6:4090911158083-4091158118	dsi_1837	GCAAAAC-AGATATC-----AAGCCATCTAT-----A-----TA-----ATAT-----AG--TCGAA--CCTGCACAAATCAAA-----AGATC-----ACGTATACG-----CGGTT-----CTG-CCATGTGTGGC-ATGTGCATATCTCTGGCTGATCTGGC
droBial	scsFold_10:202428:2837654-2837891		GCAAAAC-AGATATC-----AAGCCATCTAT-----A-----TA-----ATAT-----AG--TCGAA--CCTGCACAAATCAAA-----AGATC-----ACGTATACG-----CGGTT-----CTG-CCATGTGTGGC-ATGTGCATATCTCTGGCTGATCTGGC
droTak2	scsFold_10:414400:42851-428544		GCAAAAC-AGATATC-----AAGCCATCTAT-----A-----TA-----ATAT-----AG--TCGAA--CCTGCACAAATCAAA-----AGATC-----ACGTATACG-----CGGTT-----CTG-CCATGTGTGGC-ATGTGCATATCTCTGGCTGATCTGGC
droIel1	scsFold_10:2491249:3380268-3380509		GCAAAAC-AGATATC-----AAGCCATCTAT-----A-----ATATATCTCTATATAT-----A-----TA-----ATAT-----AG--TCGAA--CCTGCACAAATCAAA-----AGATC-----ACGTATACG-----CGGTT-----CTG-CCATGTGTGGC-ATGTGCATATCTCTGGCTGATCTGGC
droRho1	scsFold_10:7921143014-792144		GCAAAAC-AGATATC-----AAGCCATCTAT-----A-----TA-----ATAT-----AG--TCGAA--CCTGCACAAATCAAA-----AGATC-----ACGTATACG-----CGGTT-----CTG-CCATGTGTGGC-ATGTGCATATCTCTGGCTGATCTGGC
droFlo1	scsFold_10:453052:345687-345920		GCAAAAC-AGATATC-----AAGCCATCTAT-----A-----TA-----ATAT-----AG--TCGAA--CCTGCACAAATCAAA-----AGATC-----ACGTATACG-----CGGTT-----CTG-CCATGTGTGGC-ATGTGCATATCTCTGGCTGATCTGGC
droKil1	scsFold_10:202441:169231-169244		GCAAAAC-AGATATC-----AAGCCATCTAT-----A-----TA-----ATAT-----AG--TCGAA--CCTGCACAAATCAAA-----AGATC-----ACGTATACG-----CGGTT-----CTG-CCATGTGTGGC-ATGTGCATATCTCTGGCTGATCTGGC
droAna3	scsFold_13337:715292-715327	dsi_1842	GCAAAAC-AGATATC-----AAGCCATCTAT-----A-----TA-----ATAT-----AG--TCGAA--CCTGCACAAATCAAA-----AGATC-----ACGTATACG-----CGGTT-----CTG-CCATGTGTGGC-ATGTGCATATCTCTGGCTGATCTGGC
droBip1	scsFold_10:395155:42369-42370		GCAAAAC-AGATATC-----AAGCCATCTAT-----A-----TA-----ATAT-----AG--TCGAA--CCTGCACAAATCAAA-----AGATC-----ACGTATACG-----CGGTT-----CTG-CCATGTGTGGC-ATGTGCATATCTCTGGCTGATCTGGC
dp5	chr_group6:12020010-12020252		GCAAAAC-AGATATC-----AAGCCATCTAT-----A-----TA-----ATAT-----AG--TCGAA--CCTGCACAAATCAAA-----AGATC-----ACGTATACG-----CGGTT-----CTG-CCATGTGTGGC-ATGTGCATATCTCTGGCTGATCTGGC
droPer2	scsFold_34:30884:41155		GCAAAAC-AGATATC-----AAGCCATCTAT-----A-----TA-----ATAT-----AG--TCGAA--CCTGCACAAATCAAA-----AGATC-----ACGTATACG-----CGGTT-----CTG-CCATGTGTGGC-ATGTGCATATCTCTGGCTGATCTGGC
droW12	scsFold_11:0000004729:1284530-128454		GCAAAAC-AGATATC-----AAGCCATCTAT-----A-----TA-----ATAT-----AG--TCGAA--CCTGCACAAATCAAA-----AGATC-----ACGTATACG-----CGGTT-----CTG-CCATGTGTGGC-ATGTGCATATCTCTGGCTGATCTGGC
droVir3	scsFold_13049:11939061-11939316		GCAAAAC-AGATATC-----AAGCCATCTAT-----A-----TA-----ATAT-----AG--TCGAA--CCTGCACAAATCAAA-----AGATC-----ACGTATACG-----CGGTT-----CTG-CCATGTGTGGC-ATGTGCATATCTCTGGCTGATCTGGC
droMoj3	scsFold_6680:8821328-8821649		GCAAAAC-AGATATC-----AAGCCATCTAT-----A-----TA-----ATAT-----AG--TCGAA--CCTGCACAAATCAAA-----AGATC-----ACGTATACG-----CGGTT-----CTG-CCATGTGTGGC-ATGTGCATATCTCTGGCTGATCTGGC
droGrL1	scsFold_15110:11439147-11439414		GCAAAAC-AGATATC-----AAGCCATCTAT-----A-----TA-----ATAT-----AG--TCGAA--CCTGCACAAATCAAA-----AGATC-----ACGTATACG-----CGGTT-----CTG-CCATGTGTGGC-ATGTGCATATCTCTGGCTGATCTGGC

Generated: 09/08/2015 06:56 PM

chr.star 1
chr.top 0
chr.bottom 0
chr.pairing 1
chr.top 1
chr.bottom 1
chr.un 0
chr.back 1
rescue.dominant 1
rescue.known 0
rescue.confident 1
rescue.candidate 4

Predicted structure

Show Alternate Folds

Sense Strand Reads

hide 3p reads show mid mismatch reads

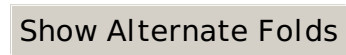
Anti-sense strand reads

Show Alignment With Reads

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

Predicted structure



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 07:19 PM

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

Predicted structure

Flybase annotation

No Repeatable elements found

Sense Strand Reads

[illegible]

Anti-sense strand reads

Show Alignment With Reads

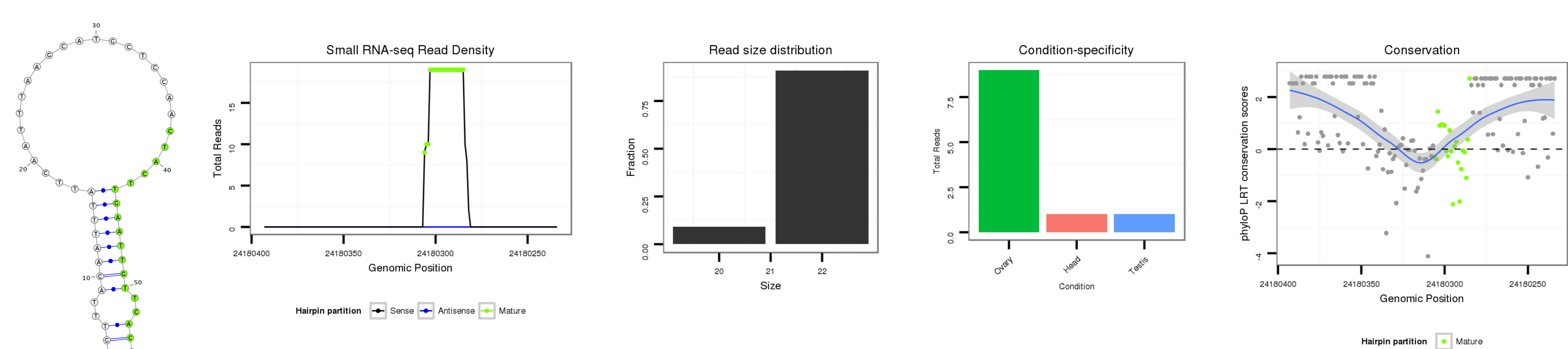
Re-alignment of all predicted orthologs

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

	PASS/FAIL
crit.star	1
crit.loop	0
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	1
rescue.dominant	1
rescue.known	0
rescue.confident	1
rescue.candidate	4

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Show Alternate Folds

Flybase annotation

intron [3r_24180284_24180343_-]; CDS [3r_24180344_24180583_-]; CDS [3r_24180026_24180283_-]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

					SRR553487	SRR553486	SRR553488						SRR618934	SRR553485			
					NRT_0-2 hours eggs	Makindu_3 day-old ovaries	RT_0-2 hours eggs	M024 male body	M023 head	M025 embryo		dsim w501 ovaries	Chicharo_3 day-old ovaries	O001 Testis	O002 Head	GSM343915 embryo	
Read #	Mismatch	Hit	Total	Total													
22	0	1	9.00	9	1	8	0	0	0	0	0	0	0	0	0	0	
21	0	1	6.00	6	0	6	0	0	0	0	0	0	0	0	0	0	
22	0	1	2.00	2	0	2	0	0	0	0	0	0	0	0	0	0	
20	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	1	0	
22	2	1	1.00	1	0	1	0	0	0	0	0	0	0	0	0	0	
18	1	1	1.00	1	0	0	1	0	0	0	0	0	0	0	0	0	
22	0	1	1.00	1	0	0	0	0	0	0	0	0	0	1	0	0	

Anti-sense strand reads

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

Show Alignment With Reads

Re-alignment of all predicted orthologs

[illegible]

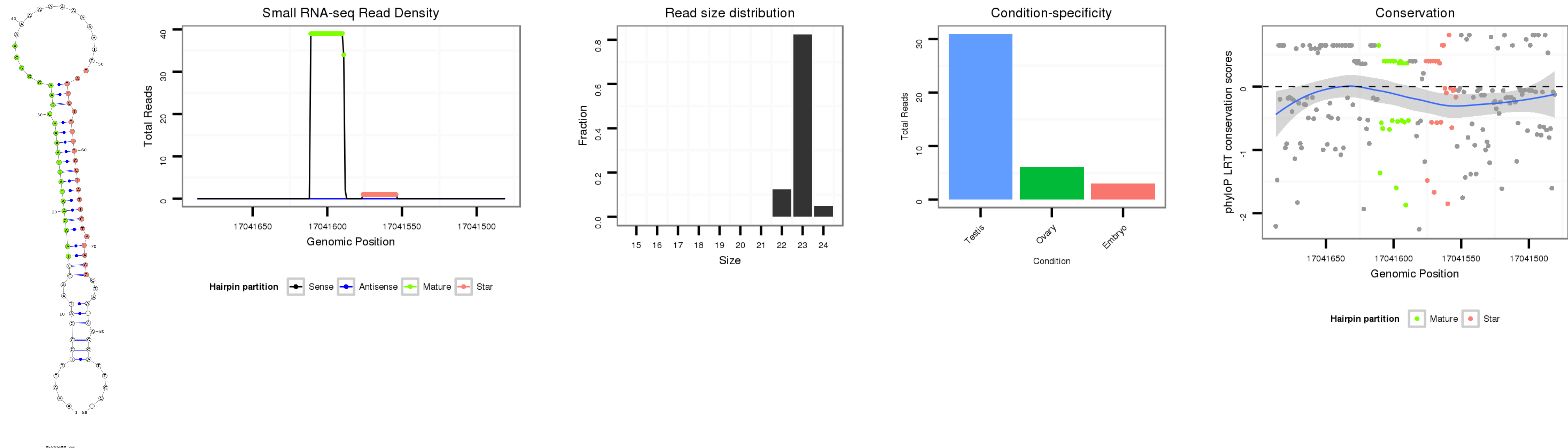
Generated: 09/08/2015 at 07:19 PM

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

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dsi_32435	2r:17041531-17041637 -	Known Ortholog	Testes-restricted	3pUTR	[View on UCSC Genome Browser (Cornell Mirror)]

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Show Alternate Folds

Flybase annotation

utr3 [utr3_minus_3798]

No Repeatable elements found

Sense Strand Reads

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

	Read # size	Mismatch	Hit Count	Total Norm	Total	SRR902009 testis	SRR553486 Makindu 3 day-old ovaries	M025 embryo	SRR553487 NRT_0-2 hours eggs	GSM343915 embryo	SRR553488 RT_0-2 hours eggs	SRR618934 dsim w501 ovaries	SRR902008 ovaries
GCAGAAAACTAACCAAAAGTGCACAGATTGAAAAAACAAGAAGTGTATATTTCATCAAATTTGCCATAACC	23	0	1	32.00	32	29	2	0	1	0	0	0	0
*****	22	0	1	5.00	5	1	1	2	0	1	0	0	0
*****	24	0	1	2.00	2	1	0	0	0	0	1	0	0
*****	24	0	1	2.00	2	1	0	0	0	0	1	0	0
*****	24	1	1	1.00	1	1	0	0	0	0	0	0	0
*****	25	2	1	1.00	1	1	0	0	0	0	0	0	0
*****	24	1	1	1.00	1	1	0	0	0	0	0	0	0
*****	23	0	1	1.00	1	0	1	0	0	0	0	0	0
*****	23	0	1	1.00	1	0	1	0	0	0	0	0	0
*****	15	0	17	0.06	1	0	1	0	0	0	0	0	0

Anti-sense strand reads

	Read # size	Mismatch	Hit Count	Total Norm	Total	SRR618934 dsim w501 ovaries	SRR553486 Makindu 3 day-old ovaries	SRR553488 RT_0-2 hours eggs	SRR902008 ovaries
CGTCTTTTGATTGGTGTTCACGTCTAACTTTTTTTGTGTCTTACACATAAAAGTAGTTAAACGGTATTGG	15	0	5	0.20	1	1	0	0	0
*****	15	0	5	0.20	1	1	0	0	0
*****	15	0	5	0.20	1	1	0	0	0

Show Alignment With Reads

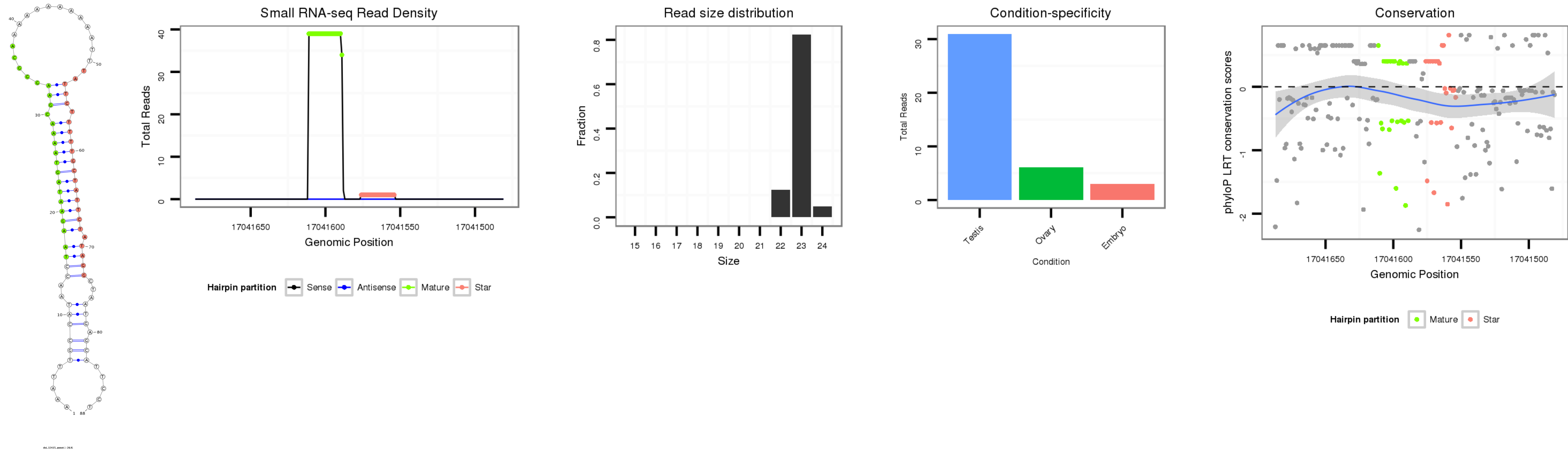
Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droSim2	2r:17041481-17041687 -	dsi_32435	GCAGAAAACTAACCAAAAG--TGCACA-----GATTG-AAAA--AAAAC--A-CAAGAATGTGATATTTCATCAAATTTGCCATAACC
droSec2	scaffold_1:14026217-14026433 -	dse_339	GCAGAAAACTAACCAACCAAG--TGCACA-----GATTG-AAAAA-AAAAC--A-CAAGAATGTGATATTTCATCAAATTTGCCATAACC
dm3	chr2R:16472011-16472235 -	dme-mir-2498	GCAGAAAACTAACCAAAAG--TGCACA-----GATTG-AAAAA-AAAAC--A-CAAGAATGTGATATTTCATCAAATTTGCCATAACC
droBre2	scaffold_4845:10617179-10617473 -	der_95	TCAGAAAACTAACCAACCAAG--TGCACA-----GATTG-AAAAA-AAAAC--A-CAAGAATGTGATATTTCATCAAATTTGCCATAACC
droYak3	2R:12723977-12724282 +	dya_34	TCAGAAAACTAACCAACCAAG--TGCACA-----GATTG-AAAAA-AAAAC--A-CAAGAATGTGATATTTCATCAAATTTGCCATAACC
droEug1	scf7180000409474:1489613-1489692 +		CT-----
droBia1	scf7180000302291:2815853-2815854 +		CG-----
droE11	scf7180000491201:736708-736920 -		AA-----

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dsi_32435	2r:17041531-17041637 -	Known Ortholog	Testes-restricted	3pUTR	[View on UCSC Genome Browser (Cornell Mirror)]

Legend: ■ **match** ■ **star** ■ **mismatch in alignment** ■ **mismatch in read**

Predicted structure



Show Alternate Folds

Flybase annotation

utr3 [utr3_minus_3798]

No Repeatable elements found

Sense Strand Reads

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

	Read # size	Hit Mismatch	Total Count	Norm	Total	SRR902009 testis	SRR553486 Makindu 3 day-old ovaries	M025 embryo	SRR553487 NRT_0-2 hours eggs	GSM343915 embryo	SRR553488 RT_0-2 hours eggs	SRR618934 dsim w501 ovaries	SRR902008 ovaries
GCAGAAAACTAACCAAAAGTGCACAGATTGAAAAAAAACACAAGAATGTGATATTTTCATCAAATTTGCCATAACC TAAGAATAGTAAACGAAGGGCA AAAAAAAAAATTTATTCTTTTTCGCTATTCTATAGGCTAATGAGCATTCCTTAAATACATATGTGTTTAAAAAAATGTATGCTCTCGCGAATTCCTCCGTTTTCGCGG	23	0	1	32.00	32	29	2	0	1	0	0	0	0
*****.....(((((((.....(((((((.....(((((((.....))))))))))))))))))))*****	22	0	1	5.00	5	1	1	2	0	1	0	0	0
.....TAAGAATAGTAAACGAAGGGCA.....	24	0	1	2.00	2	1	0	0	0	0	1	0	0
.....TAAGAATAGTAAACGAAGGGCAA.....	24	0	1	1.00	1	1	0	0	0	0	0	0	0
.....TAAGAATAGTAAACGAAGGGCA.....	25	2	1	1.00	1	1	0	0	0	0	0	0	0
.....TAAGAATAGTAAACGAAGGGCA.....	24	1	1	1.00	1	1	0	0	0	0	0	0	0
.....TAAGAATAGTAAACGAAGGGCA.....	23	0	1	1.00	1	0	1	0	0	0	0	0	0
.....TATTCTTTTTCGCTATTCTATAGG.....	24	1	1	1.00	1	1	0	0	0	0	0	0	0
.....AAGGGCAAAAAAAAA.....	15	0	17	0.06	1	0	1	0	0	0	0	0	0

Anti-sense strand reads

	Read # size	Hit Mismatch	Total Count	Norm	Total	SRR618934 dsim w501 ovaries	SRR553486 Makindu 3 day-old ovaries	SRR553488 RT_0-2 hours eggs	SRR902008 ovaries
CGTCTTTTGATTGGTGTTCACGTCTAACTTTTTTTGTGTCTTACACATAAAAGTAGTTTAAACGGTATTGGATTCTTATCATTTTGCTTCCCGTTTTTTTTTAAATAAGAAAAACGATAAGATATCCGATTACTCGTAAGGAATTTTATGTATACACAATTTTTTTCATACAGAGCGCTTAAGGAGGCAAAAGGCGC	15	0	5	0.20	1	1	0	0	0
*****.....(((((((.....(((((((.....(((((((.....))))))))))))))))*****									
.....TTTTTTAAATAAGA.....									

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droSim2	2r:17041481-17041687 -	dsi_32435	GCAGAAAACTAACCAAAAG--TGCACA-----GATTG-AAAA--AAAAC--A-CAAGAATGTGATATTTCATCAAATTTGCCATAACC TAAGAATAGTAAACGAAGGGCA AAAAAAAAAATTTATTCTTTTTCGCTATTCTATAGGCTAATGAGCATTCCTTAAATACATATGTGTTTAAAAAAATGTATGCTCTCGCGAATTCCTCCGTTTTCGCGG
droSec2	scaffold_1:14026217-14026433 -	dse_339	GCAGAAAACTAACCAACCAAG--TGCACA-----GATTG-AAAAA AAAA C--A-CAAGAATGTGATATTTCATCAAATTTGCCATAACC TAAGAATAGTAAACGAAGG CAAAAAAAAAATTCATTCTTTTTCGCTATTCTATAGGCTAATGAGCATTCCTTAAATACATATGTGTTTAAAAAAATGTATGCTCTCGCGAATTCCTCCGTTTTCGCGG
dm3	chr2R:16472011-16472235 -	dme-mir-2498	GCAGAAAACTAACCAAAAG--TGCACA-----GATTG-AAAAA AAAA C--A-CAAGAATGTGATATTTCATCAAATTTGCCATAACC TAAGAATAGTAAACGAAGGGCA AAAAAAAAAATTTATTCTTTTTCGCTATTCTATAGGCTAATGAGCATTCCTTAAATACATATGTGTTTAAAAAAATGTATGCTCTCGCGAATTCCTCCGTTTTCGCGG
droBre2	scaffold_4845:10617179-10617473 -	der_95	TCAGAAAACTAACCAACCAAG--TGCACA-----GATTG-AAAAA AAAA C--A-CAAGAATGTGATATTTCATCAAATTTGCCATAACC TAAGAATAGTAAACGAAGG CAAAAAAAAAATTTATTCTTTTTCGCTATTCTATAGGCTAATGAGCATTCCTTAAATACATATGTGTTTAAAAAAATGTATGCTCTCGCGAATTCCTCCGTTTTCGCGG
droYak3	2R:12723977-12724282 +	dya_34	TCAGAAAACTAACCAACCAAG--TGCACA-----GATTG-AAAAA AAAA C--A-CAAGAATGTGATATTTCATCAAATTTGCCATAACC TAAGAATAGTAAACGAAGG CAAAAAAAAAATTTATTCTTTTTCGCTATTCTATAGGCTAATGAGCATTCCTTAAATACATATGTGTTTAAAAAAATGTATGCTCTCGCGAATTCCTCCGTTTTCGCGG
droEug1	scf7180000409474:1489613-1489692 +		CT-----
droBia1	scf7180000302291:2815853-2815854 +		CG-----
droE11	scf7180000491201:736708-736920 -		AAAAAAATTAACACATTTTCAGCAATATATGTGTGCCAATAAGCTTAAAAAAATGAACGATTTC--CAAGAAATTAATTTT-----ATAACCTG-----TGCTA-----TAAAGAAACAGCG-----AGATAACAAATTAAGAAATAATGTTTATATTCAAATCCGGACTTTTAAACGGTGAGTAATCCGCATCCTTATGCGGTTTTCATTTTCGCG-----

