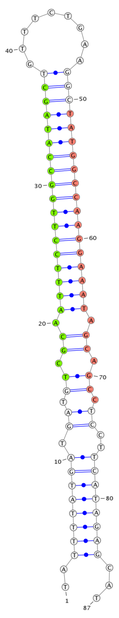
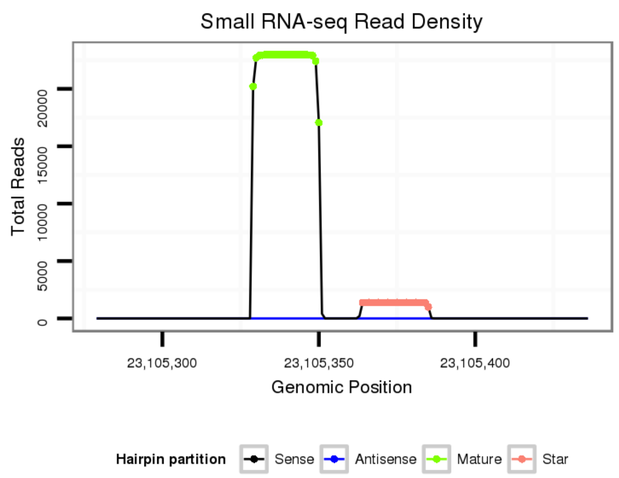
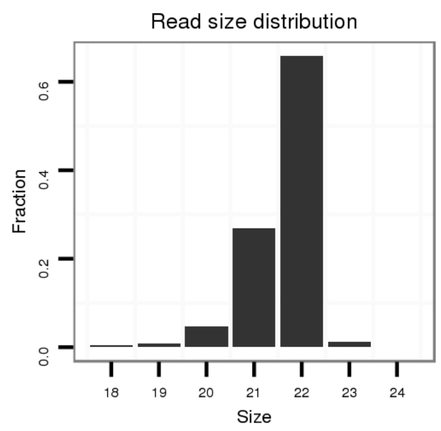
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dya_18	**3R:23105329-23105386 +**	**confident**	**Canonical miRNA**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

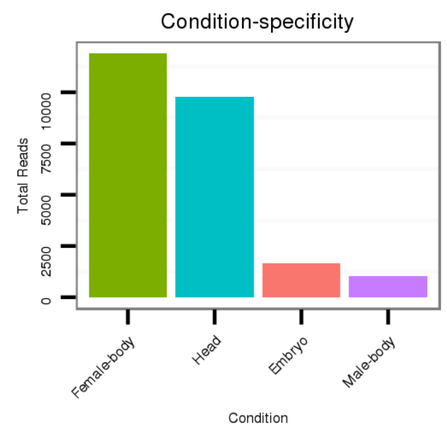
Legend: mature star mismatch in alignment mismatch in read

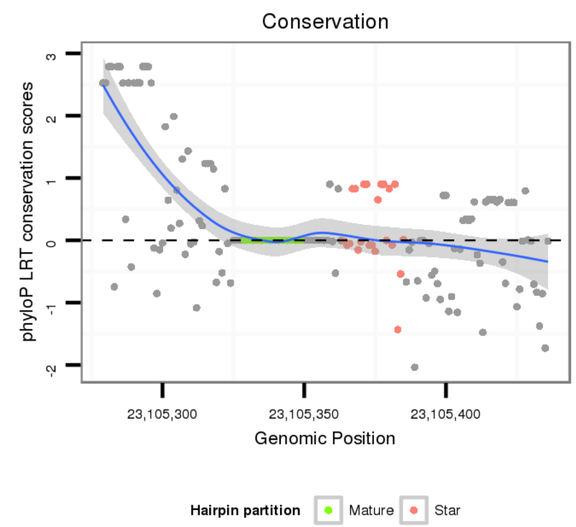
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dyak\GE10559-in]; CDS [Dyak\GE10559-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

CCTTTAACTCGCGGTAAGCAACGATATTCTACGCCTATTTTATGATGATGTCGCAATTTCCTTGGCCATAGCTGTTTCTGAAGGCTATGGCCAAGGAAATAGCAGCCTCCTTCATAGAGCATTCAAACAGACGGACAAAGTGTTTAATCCAACAAAGA	Read size	# Mismatch	Hit Count	Total Norm	Total	M043 female body	M026 head	V058 head	V052 head	M056 embryo	V120 male body	V046 embryo
********..(((((((((.((.((.((.((((((((((((((((((.....)))))))))))))))))).)).)).)).)).))))))))...**********												
.....TCGCAATTTCCTTGGCCATAGC.....	22	0	1	14767.00	14767	7959	3453	1254	770	1066	180	85
.....TCGCAATTTCCTTGGCCATAG.....	21	0	1	4701.00	4701	1867	1239	767	473	59	290	6
.....CGCAATTTCCTTGGCCATAGC.....	21	0	1	1643.00	1643	1249	240	74	38	25	16	1
.....TATGGCCAAGGAAATAGCAGCC.....	22	0	1	943.00	943	26	104	292	119	243	121	38
.....CGCAATTTCCTTGGCCATAG.....	20	0	1	600.00	600	323	136	62	46	3	28	2
.....TCGCAATTTCCTTGGCCATA.....	20	0	1	381.00	381	100	46	35	25	7	167	1
.....TCGCAATTTCCTTGGCCATAGCT.....	23	0	1	264.00	264	63	25	50	31	7	88	0
.....CTATGGCCAAGGAAATAGCAGC.....	22	0	1	186.00	186	10	3	86	27	9	48	3
.....TATGGCCAAGGAAATAGCAGC.....	21	0	1	176.00	176	4	4	64	26	30	26	22
.....GCAATTTCCTTGGCCATAGC.....	20	0	1	155.00	155	107	4	22	18	2	1	1
.....CGCAATTTCCTTGGCCATAGCT.....	22	0	1	143.00	143	37	11	27	13	2	52	1
.....CGCAATTTCCTTGGCCATA.....	19	0	1	104.00	104	30	35	20	12	1	6	0
.....TCGCAATTTCCTTGGCCATAGT.....	22	1	1	83.00	83	28	5	29	10	2	9	0
.....TCGCAATTTCCTTGGCCATAGCA.....	23	1	1	75.00	75	42	14	8	9	0	2	0
.....AATTTCCTTGGCCATAGC.....	18	0	1	52.00	52	47	0	0	0	5	0	0
.....TCGCAATTTCCTTGGCCA.....	18	0	1	40.00	40	1	28	4	6	1	0	0
.....TCGCAATTTCCTTGGCCAT.....	19	0	1	40.00	40	15	2	11	9	2	0	1
.....TATGGCCAAGGAAATAGCAGCCT.....	23	0	1	37.00	37	1	2	17	8	1	8	0
.....GCAATTTCCTTGGCCATAG.....	19	0	1	36.00	36	19	0	7	8	0	2	0
.....TCGCAATTTCCTTGGCCATAGG.....	22	1	1	27.00	27	22	4	0	1	0	0	0
.....TCGCAATTTCCTTGGCCATAGCTT.....	24	1	1	25.00	25	5	6	5	3	0	6	0
.....CAATTTCCTTGGCCATAGC.....	19	0	1	25.00	25	19	3	1	0	2	0	0
.....TCGCAATTTCCTTGGCCATAGA.....	22	1	1	22.00	22	13	3	2	2	1	1	0
.....CGCAATTTCCTTGGCCATAGCA.....	22	1	1	17.00	17	10	4	2	1	0	0	0
.....CGCAATTTCCTTGGCCATAGT.....	21	1	1	15.00	15	6	3	3	2	0	1	0
.....CTATGGCCAAGGAAATAGCAG.....	21	0	1	15.00	15	1	0	10	2	1	1	0
.....CGCAATTTCCTTGGCCATAGCTT.....	23	1	1	14.00	14	4	2	3	1	0	4	0
.....TCGCAATTTCCTTGGCCATAT.....	21	1	1	13.00	13	0	0	10	2	0	1	0
.....TCGCAATTTCCTTGGCCATAGCG.....	23	1	1	12.00	12	5	4	1	0	2	0	0
.....CTATGGCCAAGGAAATAGCAGCC.....	23	0	1	10.00	10	0	3	0	0	7	0	0
.....TCGCAATTTCCTTGGCCATAC.....	21	1	1	9.00	9	0	9	0	0	0	0	0
.....GTCGCAATTTCCTTGGCCATAGC.....	23	0	1	9.00	9	7	2	0	0	0	0	0
.....CGCAATTTCCTTGGCCAT.....	18	0	1	8.00	8	0	3	4	1	0	0	0
.....TATGGCCAAGGAAATAGCAGCCA.....	23	1	1	7.00	7	0	0	4	2	1	0	0
.....CGCAATTTCCTTGGCCATAGCC.....	22	1	1	6.00	6	0	5	0	0	1	0	0
.....CGCAATTTCCTTGGCCATAT.....	20	1	1	5.00	5	1	0	2	1	0	1	0
.....CAATTTCCTTGGCCATAG.....	18	0	1	5.00	5	5	0	0	0	0	0	0
.....TATGGCCAAGGAAATAGCAGCCC.....	23	1	1	5.00	5	0	1	1	2	1	0	0
.....TCGCAATTTCCTTGGCCATAA.....	21	1	1	5.00	5	1	1	1	1	0	1	0
.....TATGGCCAAGGAAATAGCAG.....	20	0	1	5.00	5	1	0	0	0	1	1	2
.....GCAATTTCCTTGGCCATAGCT.....	21	0	1	5.00	5	3	0	2	0	0	0	0
.....CGCAATTTCCTTGGCCATAGG.....	21	1	1	4.00	4	0	3	0	1	0	0	0
.....ATGGCCAAGGAAATAGCAGCC.....	21	0	1	4.00	4	1	0	2	0	1	0	0
.....AGGCTATGGCCAAGGAAATAGC.....	22	0	1	4.00	4	0	1	0	3	0	0	0
.....GCAATTTCCTTGGCCATA.....	18	0	1	4.00	4	2	0	0	0	0	2	0
.....GTCGCAATTTCCTTGGCCATAG.....	22	0	1	4.00	4	2	2	0	0	0	0	0
.....CGCAATTTCCTTGGCCATAGCTA.....	23	1	1	4.00	4	3	0	0	1	0	0	0
.....TCGCAATTTCCTTGGCCATAGCTA.....	24	1	1	3.00	3	0	0	2	1	0	0	0
.....TATGGCCAAGGAAATAGCA.....	19	0	1	3.00	3	0	0	1	0	0	0	2
.....CTATGGCCAAGGAAATAGCAGT.....	22	1	1	3.00	3	0	0	1	1	0	0	1
.....CGCAATTTCCTTGGCCATAGA.....	21	1	1	3.00	3	2	0	1	0	0	0	0
.....CGCAATTTCCTTGGCCATAGCTG.....	23	0	1	2.00	2	1	0	1	0	0	0	0
.....CTATGGCCAAGGAAATAGCA.....	20	0	1	2.00	2	0	0	2	0	0	0	0
.....TATGGCCAAGGAAATAGCAGCT.....	22	1	1	2.00	2	0	0	1	0	0	0	1
.....TCGCAATTTCCTTGGCCATAGCAAA.....	25	3	1	2.00	2	1	0	0	0	0	1	0
.....CGCAATTTCCTTGGCCATC.....	19	1	1	2.00	2	1	1	0	0	0	0	0
.....TCGCAATTTCCTTGGCCT.....	18	1	2	1.50	3	0	1	0	1	0	1	0
.....CGCAATTTCCTTGGCCATT.....	19	1	2	1.50	3	2	0	1	0	0	0	0
.....CGCAATTTCCTTGGCCAA.....	18	1	2	1.50	3	0	2	1	0	0	0	0
.....CGCAATTTCCTTGGCCATAC.....	20	1	1	1.00	1	0	1	0	0	0	0	0
.....CTATGGCCAAGGAAATAGCAGCCT.....	24	0	1	1.00	1	0	1	0	0	0	0	0
.....TATGGCCAAGGAAATAGC.....	18	0	1	1.00	1	0	0	1	0	0	0	0
.....ATGGCCAAGGAAATAGCAGCCT.....	22	0	1	1.00	1	0	0	1	0	0	0	0
.....GTCGCAATTTCCTTGGCCATA.....	21	0	1	1.00	1	1	0	0	0	0	0	0

Anti-sense strand reads

GGAAATTGAGCGCCATTCGTTGCTATAAGATGCGGATAAAATACTACTACAGCGTTAAAGGAACCGGTATCGACAAAGACTTCCGATACCGGTTCCTTTATCGTCGGAGGAAGTATCTCGTAAGTTTGTCTGCCTGTTTCACAAATTAGGTTGTTTCT	Read size	# Mismatch	Hit Count	Total Norm	Total	M056 embryo	M026 head	V058 head	M043 female body
********..(((((((((.((.((.((.((((((((((((((((((.....)))))))))))))))))).)).)).)).)).))))))))...**********									
.....AACGATACCGGTTCCTTTA.....	19	2	18	0.06	1	1	0	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droYak3	3R:23105279-23105436 +	dya_18	CCTTTAACTCGCGGTAAGCAACGATATTCTACGCCTATTTTATGATGATGTCGCAATTTCCTTGGCCATAGCTGTTTCTGAAGGCTATGG--CCAAGGAAATAGCAGCCTCCTTCATAGAGCATTCAAA--CAGA----------CGGACAAAGTGTTTAATCCAA----------CAAAGA
droEre2	scaffold_4820:4655149-4655291 +		CCTTTAACTCCCGGTAAGTCCAGATATCCTACGCCTATTTATAGAC----------ACAGCTATGG--CCAAGGAAATAGCAACATCGGA--CATAAG-------------TA----------GAGGCCAAAAGAGCAGGTTCGTCCAACTGACGGCCAAAGTGTTTACTTCAA----------CAAGGA
droSec2	scaffold_22:17725-17835 -		CCTTCAACTCCCGGTAAGCCAGATATCCTACGCCTATTTATAGAC----------ACAGCCATGG--TCAAGGAAATAGCAACACTGCA--AATAGAATCCACA--CAGAAA----------TTGGCTAGTCAAAC---**----------**----------**-----**
droSim2	3r:22808972-22809091 -		CCTTCAACTCCCGGTAAGCCAGATATCCTACGCCTATTTATAGAC----------ACAGTCATGG--TCAAGGAAATAGCAACACTGCA--AATAGAATCCACA--CAGAGA----------TTGGCTAGTCAAACT--**----------**GA----------CGCACA
dm3	chr3R:23383930-23384060 -		CCTTCAACTCCCGGTAAGCCAGATATCCTACGCCTATTTATAGAC----------ACAGCCATGG--TCAAGGAAATAGCAACACTGCA--AATAGAATCTACA--CAGAAA----------TAGGGTAGTCAAACTTA----------GCTTAGATCAA----------CAAAAA
droEug1	scf7180000409770:859077-859117 -		CCTTTAACTCCCGGTAAGCCAGATATTCTATAAGTATTTT----------**----------**----**----------**----------**----------**
droBia1	scf7180000302075:1546827-1546865 +		CCTTCAACTCCCGGTAAGTGCAGATATTCTATAAGGATT----------**----------**----**----------**----------**----------**
droTak1	scf7180000413872:243089-243128 -		CCTTCAACTCCCGGTAAGTCCAGATATTCTATAGGTATTT----------**----------**----**----------**----------**----------**
droEle1	scf7180000491261:1869285-1869398 -		CCTTCAACTCCCGGTAAGCCAGATACTCTATAAGTATTTATAGAT----------ACAGCTGCGG--TCAAAATAATAGCACAATTGTA--AATTAA-------**----**TAGTTTAATTG----------TA----------TCTTAAATCAA----------GGTTGA
droRho1	scf7180000779682:2375-2414 +		CCTTCAACTCCCGGTAAGCCAGATATTGATAAGTATTT----------**----------**----**----------**----------**----------**
droFic1	scf7180000453826:332068-332107 +		CCTTTAACTCCCGGTAAGCCAGATATTGCATAGGTATTT----------**----------**----**----------**----------**----------**
droKik1	scf7180000302697:652068-652233 -		CCTTCAACACTCGGTAAGGTCAGATATTCCACGGT-------GCCC----------ACGGCTACGGGATTAAGG--ATTGAAGTAATGGC--ACAGGAATGTGGTCG-----TAGATTCACTGGTTCAGACAAAAAAGGATAATAAAGCGGTT---TCCAAAACCATTCAAAGT-------TCATTATATATTTTTAGAAG
droAna3	scaffold_13340:19307042-19307059 +		CCTTCAACTCGCGGTAAG----------**----------**----**----------**----------**----------**
droBip1	scf7180000396413:3059143-3059160 -		CCTTTAACTCGCGGTAAG----------**----------**----**----------**----------**----------**
dp5	2:9030502-9030529 -		CCTTTAACACTCGGTAAGCGGCGGATT----------**----------**----**----------**----------**----------**
droPer2	scaffold_0:2843324-2843348 -		CCTTTAACACTCGGTAAGCGGCGGT----------**----------**----**----------**----------**----------**
droWil2	scf2_1100000004902:3622319-3622346 -		CCTTTAACACGCGGTAAGTTATGGAATT----------**----------**----**----------**----------**----------**
droVir3	scaffold_13047:17948248-17948265 -		CCTTTAACTCACGGTAAG----------**----------**----**----------**----------**----------**
droMoj3	scaffold_6540:13763597-13763614 +		CCTTCAACTCGCGGTAAG----------**----------**----**----------**----------**----------**
droGri2	scaffold_15074:6696032-6696049 +		CCTTTAACTCGCGGTAAG----------**----------**----**----------**----------**----------**

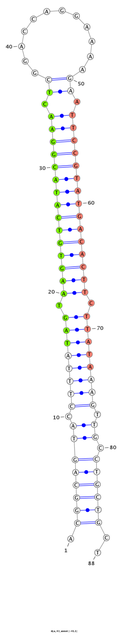
Generated: 09/08/2015 at 07:39 PM

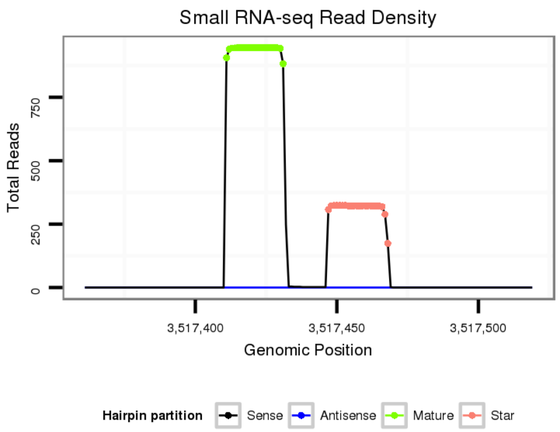
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

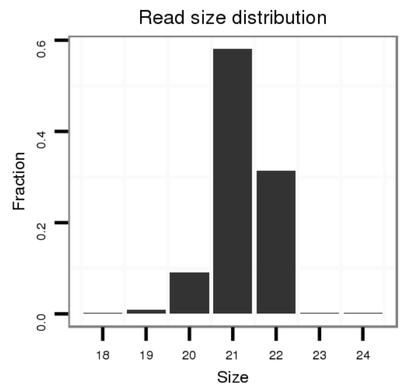
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dya_43	**2L:3517411-3517469 +**	**confident**	**Canonical miRNA**	**3pUTR**	[View on UCSC Genome Browser {Cornell Mirror}]

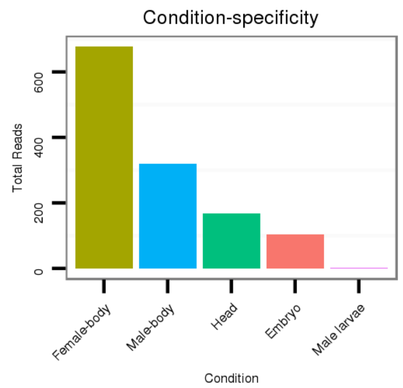
Legend: mature star mismatch in alignment mismatch in read

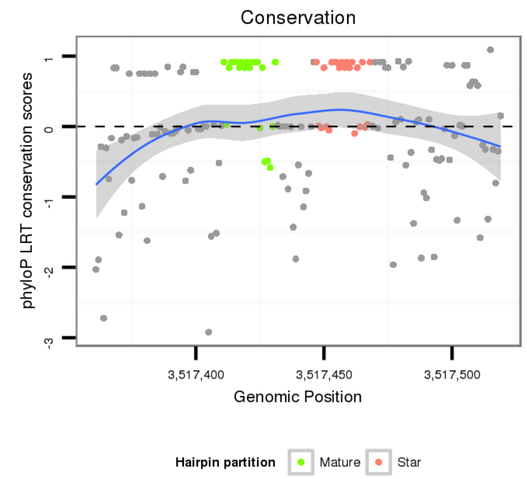
Predicted structure











Show Alternate Folds

Flybase annnotation

utr3 [utr3_plus_263]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

AATCTGGATATACTCTTATAGTTTAGGGTCGCACAACGGCAGTACCTTTATAGTAAGTGTCATACGGAACTCGGACCAGGAAAAGAATTCCGTATGACACTTCTTATAAAGTTGCCTGCTGCTTACATCTAATGTAGTTTATATAAGAAGCTCGACTGT ********************************.(((((((.(((((((.(((((((((((((((.((.....)).)))))))))))))))).)))))))).)).))))))..	Read size	# Mismatch	Hit Count	Total Norm	Total	M043 female body	V120 male body	M026 head	M056 embryo	V046 embryo	V058 head	V052 head	SRR1275488 Male larvae
.....TAGTAAGTGTCATACGGAACT.....	21	0	1	611.00	611	221	237	132	14	1	3	3	0
.....TAGTAAGTGTCATACGGAACTC.....	22	0	1	231.00	231	98	53	4	50	17	4	4	1
.....ATTCCGTATGACACTTCTTATA.....	22	0	1	165.00	165	157	2	3	2	1	0	0	0
.....ATTCCGTATGACACTTCTTAT.....	21	0	1	110.00	110	98	1	0	10	1	0	0	0
.....TAGTAAGTGTCATACGGAAC.....	20	0	1	60.00	60	23	24	9	1	0	3	0	0
.....ATTCCGTATGACACTTCTTA.....	20	0	1	25.00	25	21	0	1	3	0	0	0	0
.....AGTAAGTGTCATACGGAACT.....	20	0	1	22.00	22	22	0	0	0	0	0	0	0
.....TAGTAAGTGTCATACGGAACG.....	21	1	1	15.00	15	0	0	9	6	0	0	0	0
.....AGTAAGTGTCATACGGAACTC.....	21	0	1	11.00	11	11	0	0	0	0	0	0	0
.....TTCCGTATGACACTTCTTATA.....	21	0	1	6.00	6	6	0	0	0	0	0	0	0
.....TTCCGTATGACACTTCTTA.....	19	0	1	5.00	5	5	0	0	0	0	0	0	0
.....TTCCGTATGACACTTCTTAT.....	20	0	1	5.00	5	5	0	0	0	0	0	0	0
.....GTAAGTGTCATACGGAACTC.....	20	0	1	2.00	2	2	0	0	0	0	0	0	0
.....TAGTAAGTGTCATACGGAACG.....	21	1	1	2.00	2	1	0	1	0	0	0	0	0
.....TAGTAAGTGTCATACGGAACTCT.....	23	1	1	2.00	2	1	0	0	0	0	0	1	0
.....GTAAGTGTCATACGGAACT.....	19	0	1	2.00	2	1	0	1	0	0	0	0	0
.....TAGTAAGTGTCATACGGAA.....	19	0	1	2.00	2	0	1	0	0	0	1	0	0
.....ATTCCGTATGACACTTCTT.....	19	0	1	2.00	2	0	0	1	1	0	0	0	0
.....CGGACCAGGAAAAGAATTCCGT.....	22	0	1	2.00	2	0	2	0	0	0	0	0	0
.....ATTCCGTATGACACTTCTTATAA.....	23	0	1	2.00	2	2	0	0	0	0	0	0	0
.....ATTCCGTATGACACTTCT.....	18	0	1	1.00	1	0	0	0	1	0	0	0	0
.....ATTCCGTATGACACTTCTAT.....	20	2	1	1.00	1	1	0	0	0	0	0	0	0
.....AGTAAGTGTCATACGGAAC.....	19	0	1	1.00	1	1	0	0	0	0	0	0	0
.....AGTAAGTGTCATACGGAACTCT.....	22	1	1	1.00	1	1	0	0	0	0	0	0	0
.....AAGTGTCATACGGAACTC.....	18	0	1	1.00	1	0	0	0	1	0	0	0	0
.....TAGTAAGTGTCATACGGAACTCA.....	23	1	1	1.00	1	0	0	0	0	0	0	1	0
.....TAGTAAGTGTCATACGGAACTCGG.....	24	0	1	1.00	1	1	0	0	0	0	0	0	0
.....TCCGTATGACACTTCTTATA.....	20	0	1	1.00	1	1	0	0	0	0	0	0	0
.....TAGTAAGTGTCATACGGAAA.....	20	1	1	1.00	1	1	0	0	0	0	0	0	0
.....TAGTAAGTGTCATACGGA.....	18	0	1	1.00	1	1	0	0	0	0	0	0	0
.....TAAGTGTCATACGGAACTCGGACC.....	24	0	1	1.00	1	1	0	0	0	0	0	0	0
.....TAGTAAGTGTCATACGGAACTG.....	22	1	1	1.00	1	1	0	0	0	0	0	0	0
.....ATTCCGTATGACACTTCTTAG.....	21	1	1	1.00	1	0	0	0	1	0	0	0	0

Anti-sense strand reads

TTAGACCTATATGAGAATATCAAATCCCAGCGTGTTGCCGTCATGGAAATATCATTCACAGTATGCCTTGAGCCTGGTCCTTTTCTTAAGGCATACTGTGAAGAATATTTCAACGGACGACGAATGTAGATTACATCAAATATATTCTTCGAGCTGACA **********.(((((((.(((((((.(((((((((((((((.((.....)).)))))))))))))))).)))))))).)).))))))..	Read size	# Mismatch	Hit Count	Total Norm	Total	V058 head

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droYak3	2L:3517361-3517519 +	dya_43	AATCTGGATA-----TACTCTTATAGTTTAG----GGTCGCACAACGGCAGTACCTTTATAGTAAGTGTCATACGGAACTCGGAC-CAGGAAAAGAATTCCG-TATGACACTTCTTATAAAGTTGCCTGCTGCTTA--CATCTAA----------TGTAGTTTATATAA----------GAAGCTCGACTGT
droEre2	scaffold_4929:3565640-3565747 +		CGTAC-----------------------TTAAGTAGTAAGTGTCATAAGGAACTCG---------GAACTCCG-TATGACACTTCTTGTAAAGTTGCATGCGATTG--CACACAA----------TGTAGTTTATATAA----------GAAGCGCGACTGT
droSec2	scaffold_5:1629630-1629724 +		AATCTGGATGGATTATTGTTTTACAATTTAA----GGTCGCACAACAGCAGTATCTT----------TGCTGTTGTGTAGTTAG----------TGTAGTTTATATAAG----------TTCACACTGT
droSim2	2L:3386891-3386975 +		TGGATA-----TATTGTTTTACAGTTTAA----GGTCGCACAACAGCAGTATCTT----------ATGTGCTTA--CATCTAG----------TGTAGTTTATATAAG----------TTCACACTGT
dm3	chr2L:3527291-3527383 +		AATCTGGATGGATTATTCTTTACAGTTTAA----GGTCGCACAACAGCAAAGGTAC----------TGCTGCTTA--CAGCTAG----------GGTAGTTTAAGTAAG----------CTCACACTGT
droEug1	scf7180000409554:2558809-2558961 -		ATTCTTGATACATTTACCTTTGAAATATTATATTTTTCGCACATGAGCAGTAAATGTATAGTAAGTGTCATACGAGCATTGAATTGTAATATGAAATGCCCC-TATGACACTTCCTGTACAGTTGCTGGCTGATGA--CATCCAA----------AG----------AGAAAACTC
droBia1	scf7180000302408:1809516-1809655 +		AATGAAAATTA----------A----TTTCCAACATTGGCCGTACATTTATGGTAAGTGTCATACGAGTATTGAATGTTAGGCAGGAATGCTC-TATGACACTCCCTGAAAAGTTGCTTGCT---CC--CATTCAA----------GAGTTTTTGCATAAG----------ATTCATGGT
droTak1	scf7180000415399:501631-501805 +		ATTCTGAATGAAGTCAATTCGTATATTTTAA----GTTGGCTCACCGGCAGTAAATTTATAGTAAGTGTCATACGGGCATTGGAAATGTGACGAGAATGCCCC-TATGACACTCCCTGTAAAGTTGCTCGCTGATTA--CGTCTAA----------TAGATTATAATAAGGGCCACTACATGC----------TTCACACTT
droEle1	scf7180000490728:209168-209378 +		TT--------------------------CATAGTAAGTGTCATACGGACATTAAGAATACAAACAGAATGCCCATATGACACTTCCTGTAAATTTGCTGGCTGATTA--CATCTTTAAAATAAAAAACATTAAAAAAGAACAAAATTCTACTAGTGCAAAGCAATTGAAGTGC----------CTCTGAAAGCTACTAACTTACAAAAAAAAATATTACTAACTTGCTATACAAAGAAGTTCGACTGT
droRho1	scf7180000779523:214251-214280 +		CTAAT----------TTAATTATTATAAA----------GAAGTTCGACTGT

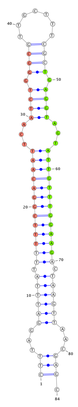
Generated: 09/08/2015 at 07:39 PM

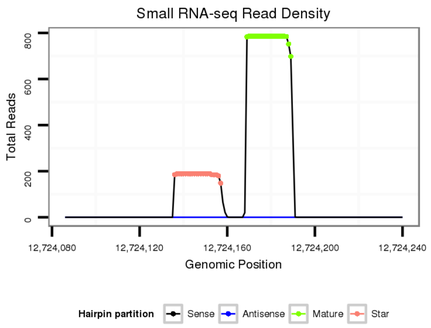
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

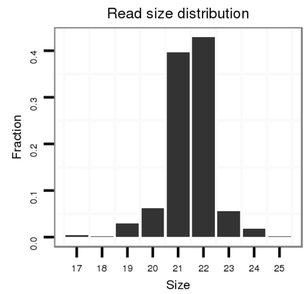
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dya_34	**2R:12724136-12724190 +**	**confident**	**Testes-restricted**	**intergenic**	[View on UCSC Genome Browser [Cornell Mirror]]

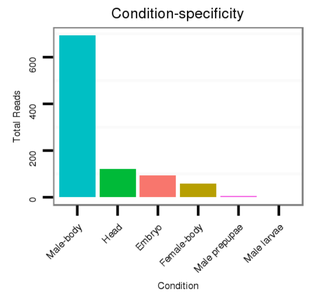
Legend: mature star mismatch in alignment mismatch in read

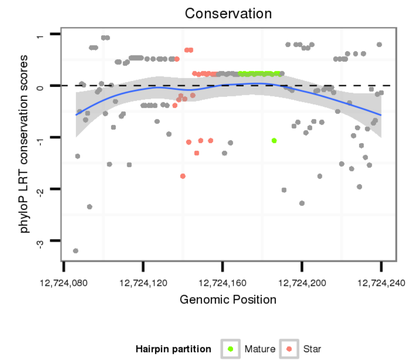
Predicted structure











Show Alternate Folds

Flybase annotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

```
ATTTTCTCTTTGTTATTCTGCAATGGATTTATTTGCTTTAGGATTTATTTTTTCGGACAATTCAATCTGGGCGTTGCTTTCGCTGAGGTAGTATTGTTTGGAAGACTAAGTTAACGAGCATTCATCTCATTTTTGAAATTTTGTGTTCATGAGTG
************************************(((...((((((.((((((((((((((...((((.((((.......)))).)))))...)))))))))))))).))))))...)))).************************************
```

Read size	# Mismatch	Hit Count	Total Norm	Total	V120 male body	M026 head	M056 embryo	M043 female body	V046 embryo	SRR1275484 Male prepupae	V058 head	SRR1275488 Male larvae	V052 head
21	0	1	348.00	348	300	16	12	14	2	2	2	0	0
22	0	1	333.00	333	263	23	25	13	8	1	0	0	0
22	0	1	81.00	81	16	29	19	8	8	0	0	0	1
23	1	1	53.00	53	42	8	1	2	0	0	0	0	0
20	0	1	51.00	51	49	1	1	0	0	0	0	0	0
23	0	1	43.00	43	8	16	9	9	1	0	0	0	0
21	0	1	32.00	32	8	15	2	6	1	0	0	0	0
21	1	1	32.00	32	30	1	0	1	0	0	0	0	0
19	0	1	29.00	29	26	2	1	0	0	0	0	0	0
23	1	1	24.00	24	24	0	0	0	0	0	0	0	0
22	1	1	23.00	23	8	14	1	0	0	0	0	0	0
24	0	1	18.00	18	4	12	1	1	0	0	0	0	0
21	1	1	17.00	17	15	2	0	0	0	0	0	0	0
23	1	1	15.00	15	2	13	0	0	0	0	0	0	0
20	1	1	12.00	12	9	3	0	0	0	0	0	0	0
23	0	1	10.00	10	9	0	1	0	0	0	0	0	0
22	1	1	10.00	10	7	0	1	0	0	0	2	0	0
23	2	1	9.00	9	2	7	0	0	0	0	0	0	0
24	2	1	8.00	8	6	0	0	0	0	2	0	0	0
19	1	1	7.00	7	7	0	0	0	0	0	0	0	0
22	1	1	5.00	5	5	0	0	0	0	0	0	0	0
23	2	1	5.00	5	3	2	0	0	0	0	0	0	0
20	0	1	4.00	4	1	2	0	1	0	0	0	0	0
17	0	1	4.00	4	0	0	0	0	0	3	0	1	0
20	0	1	4.00	4	4	0	0	0	0	0	0	0	0
24	1	1	3.00	3	0	3	0	0	0	0	0	0	0
24	1	1	3.00	3	0	1	2	0	0	0	0	0	0
26	1	1	3.00	3	1	0	0	1	0	1	0	0	0
23	1	1	3.00	3	0	3	0	0	0	0	0	0	0
23	2	1	3.00	3	3	0	0	0	0	0	0	0	0
21	0	1	3.00	3	3	0	0	0	0	0	0	0	0
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22	1	1	2.00	2	2	0	0	0	0	0	0	0	0
25	0	1	2.00	2	0	2	0	0	0	0	0	0	0
20	2	1	2.00	2	2	0	0	0	0	0	0	0	0
22	1	1	2.00	2	0	2	0	0	0	0	0	0	0
23	2	1	1.00	1	0	1	0	0	0	0	0	0	0
23	2	1	1.00	1	1	0	0	0	0	0	0	0	0
22	0	1	1.00	1	0	0	0	1	0	0	0	0	0
18	0	1	1.00	1	0	0	0	0	0	1	0	0	0
23	3	1	1.00	1	1	0	0	0	0	0	0	0	0
20	0	1	1.00	1	1	0	0	0	0	0	0	0	0
22	2	1	1.00	1	1	0	0	0	0	0	0	0	0
21	2	1	1.00	1	1	0	0	0	0	0	0	0	0
25	3	1	1.00	1	1	0	0	0	0	0	0	0	0
23	0	1	1.00	1	1	0	0	0	0	0	0	0	0
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24	1	1	1.00	1	1	0	0	0	0	0	0	0	0
18	1	1	1.00	1	1	0	0	0	0	0	0	0	0
18	1	1	1.00	1	1	0	0	0	0	0	0	0	0
24	2	1	1.00	1	1	0	0	0	0	0	0	0	0
22	1	1	1.00	1	1	0	0	0	0	0	0	0	0
22	2	1	1.00	1	1	0	0	0	0	0	0	0	0
18	1	1	1.00	1	1	0	0	0	0	0	0	0	0
21	0	1	1.00	1	0	0	0	1	0	0	0	0	0
23	3	1	1.00	1	1	0	0	0	0	0	0	0	0
18	0	1	1.00	1	1	0	0	0	0	0	0	0	0
22	3	2	0.50	1	1	0	0	0	0	0	0	0	0
21	3	5	0.40	2	2	0	0	0	0	0	0	0	0
19	2	3	0.33	1	1	0	0	0	0	0	0	0	0
21	3	4	0.25	1	1	0	0	0	0	0	0	0	0

Anti-sense strand reads

```
TAAAAGAGAAACAATAAGACGTTACCTAAATAAACGAAATCCTAAATAAAAAAGCCTGTTAAGTTAGACCCGCAACGAAAGCGACTCCATCATAACAAACCTTCTGATTCAATTGCTCGTAAGTAGAGTAAAAACTTTAAAACACAAGTACTCAC
************************************(((...((((((.((((((((((((((...((((.((((.......)))).)))))...)))))))))))))).))))))...)))).************************************
```

Read size	# Mismatch	Hit Count	Total Norm	Total

No data available in table

Show Alignment With Reads

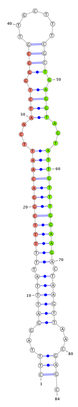
Re-alignment of all predicted orthologs

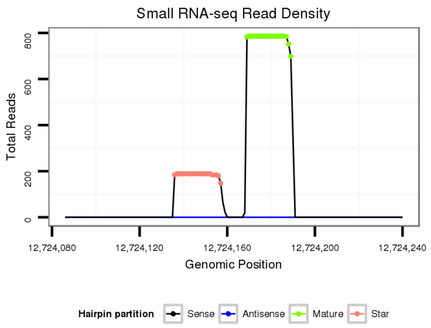
Species	Coordinate	ID	Alignment
droYak3	2R:12724086-12724240 +	dya_34	AT----TTTCTCTTTGTTATT------------CTGCAATGGATTTATTT-------GCTTTAGGATTTA------TTTTTTCGGACAATTCAATCTGGGCGTTGCTTTCGCTGAGGTAGTATTGTTTGGAAGACTAAGTTAACGAGC----------ATTCATCTCATTT-TTGAAAT----------TTTGTGTTCATGAGTG
droEre2	scaffold_4845:10618676-10618838 -	der_25	GT----TTTCT----GTTATTTTACTATATAA----------CTATTTATGAAGAAGCTTTAGGATTTA-------ATTTTTCGACAATCGCATCTAGGCGTTGTCTATCGCTGAGGTAGTATTGTTTGAAGATAAGTTAAGTTAAACGCG----------AATCATCAAAATT-TTAAAATGTG----------AATAATGTATCATTAGTG
droSec2	scaffold_1:14026259-14026320 -		GT----ATTCTTTTGTATT------------CTA--TATCTCTAACGAGC----------ATTCCTTAAAATT-----A----------CATATGTATCATTAGTG
droSim2	2r:17041524-17041580 -		AATTTTATTCTTTTGTATT------------CTA--TATCTCTAAATAATT------------------------------------ATTCCTTAAAATT----AT-TA----------AATATTGTG
dm3	chr2R:16472054-16472133 -		TATGGTATTCTTTTGTATT------------ATA--AAAGTTTACGAGC----------TAA----------GCTAACG----------ATTCATTAAAATT----AT-TA----------CATACATTTATAGTG
droEug1	scf7180000409474:1489443-1489565		TT----TTGGC------AATT------------AC--ATATTAAG----------GTAAAATAAATCGCTTTCTTAAAAATCAAGTGCTTAATATTGAAAGTATGATTATTAAAATAATATTTATTTACATTTAAAGCACTTTCGAATTTTTAAGATAACTCAATGGGTGTACATTTTTAAATAATTATTGTTCGAGCGTTGAGTTATTTTAAGAATTAATGTGTTAGTCGTAATAA-------------------------------GTGAAATG
droTak1	scaffold_100900:100735-100900 -		AC----CTTCT-TTTATTACT---CTTGATAATTCTTGTAAAAGTA-----------ATTAAAACATCTTTATTGATTTAAACAGAGAA----------ATAAGTTTATCTTA----------ATTCCCTAAAAATGGTTAAAGCTAAAAAAGTGCGTGTTTAAGTTCCTATCGGAATCAGTACTTTTATTTGCTTTCCTGGATT
droRho1	scf7180000780104:83008-83037 -		AT----TATTTATTTGTTATT------------ATAT-----TTTATTT---

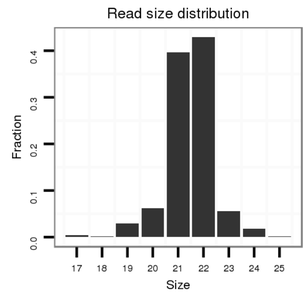
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dya_34	**2R:12724136-12724190 +**	**confident**	**Testes-restricted**	**intergenic**	[View on UCSC Genome Browser [Cornell Mirror]]

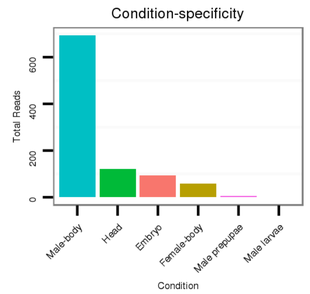
Legend: mature star mismatch in alignment mismatch in read

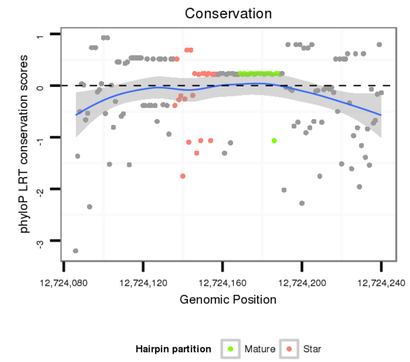
Predicted structure











Show Alternate Folds

Flybase annotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

```
ATTTTCTCTTTGTTATTCTGCAATGGATTTATTTGCTTTAGGATTTATTTTTTCGGACAATTCAATCTGGGCGTTGCTTTCGCTGAGGTAGTATTGTTTGGAAGACTAAGTTAACGAGCATTCATCTCATTTTTGAAATTTTGTGTTCATGAGTG
************************************(((...((((((.((((((((((((((...((((.((((.......)))).)))))...)))))))))))))).))))))...)))).************************************
```

Read size	# Mismatch	Hit Count	Total Norm	Total	V120 male body	M026 head	M056 embryo	M043 female body	V046 embryo	SRR1275484 Male prepupae	V058 head	SRR1275488 Male larvae	V052 head
21	0	1	348.00	348	300	16	12	14	2	2	2	0	0
22	0	1	333.00	333	263	23	25	13	8	1	0	0	0
22	0	1	81.00	81	16	29	19	8	8	0	0	0	1
23	1	1	53.00	53	42	8	1	2	0	0	0	0	0
20	0	1	51.00	51	49	1	1	0	0	0	0	0	0
23	0	1	43.00	43	8	16	9	9	1	0	0	0	0
21	0	1	32.00	32	8	15	2	6	1	0	0	0	0
21	1	1	32.00	32	30	1	0	1	0	0	0	0	0
19	0	1	29.00	29	26	2	1	0	0	0	0	0	0
23	1	1	24.00	24	24	0	0	0	0	0	0	0	0
22	1	1	23.00	23	8	14	1	0	0	0	0	0	0
24	0	1	18.00	18	4	12	1	1	0	0	0	0	0
21	1	1	17.00	17	15	2	0	0	0	0	0	0	0
23	1	1	15.00	15	2	13	0	0	0	0	0	0	0
20	1	1	12.00	12	9	3	0	0	0	0	0	0	0
23	0	1	10.00	10	9	0	1	0	0	0	0	0	0
22	1	1	10.00	10	7	0	1	0	0	0	2	0	0
23	2	1	9.00	9	2	7	0	0	0	0	0	0	0
24	2	1	8.00	8	6	0	0	0	0	2	0	0	0
19	1	1	7.00	7	7	0	0	0	0	0	0	0	0
22	1	1	5.00	5	5	0	0	0	0	0	0	0	0
23	2	1	5.00	5	3	2	0	0	0	0	0	0	0
20	0	1	4.00	4	1	2	0	1	0	0	0	0	0
17	0	1	4.00	4	0	0	0	0	0	3	0	1	0
20	0	1	4.00	4	4	0	0	0	0	0	0	0	0
24	1	1	3.00	3	0	3	0	0	0	0	0	0	0
24	1	1	3.00	3	0	1	2	0	0	0	0	0	0
26	1	1	3.00	3	1	0	0	1	0	1	0	0	0
23	1	1	3.00	3	0	3	0	0	0	0	0	0	0
23	2	1	3.00	3	3	0	0	0	0	0	0	0	0
21	0	1	3.00	3	3	0	0	0	0	0	0	0	0
22	0	1	3.00	3	1	0	1	1	0	0	0	0	0
21	2	1	2.00	2	2	0	0	0	0	0	0	0	0
21	0	1	2.00	2	0	0	0	2	0	0	0	0	0
22	1	1	2.00	2	2	0	0	0	0	0	0	0	0
25	0	1	2.00	2	0	2	0	0	0	0	0	0	0
20	2	1	2.00	2	2	0	0	0	0	0	0	0	0
22	1	1	2.00	2	0	2	0	0	0	0	0	0	0
23	2	1	1.00	1	0	1	0	0	0	0	0	0	0
23	2	1	1.00	1	1	0	0	0	0	0	0	0	0
22	0	1	1.00	1	0	0	0	1	0	0	0	0	0
18	0	1	1.00	1	0	0	0	0	0	1	0	0	0
23	3	1	1.00	1	1	0	0	0	0	0	0	0	0
20	0	1	1.00	1	1	0	0	0	0	0	0	0	0
22	2	1	1.00	1	1	0	0	0	0	0	0	0	0
21	2	1	1.00	1	1	0	0	0	0	0	0	0	0
25	3	1	1.00	1	1	0	0	0	0	0	0	0	0
23	0	1	1.00	1	1	0	0	0	0	0	0	0	0
23	0	1	1.00	1	0	0	0	1	0	0	0	0	0
24	1	1	1.00	1	0	1	0	0	0	0	0	0	0
20	0	1	1.00	1	0	0	1	0	0	0	0	0	0
24	1	1	1.00	1	1	0	0	0	0	0	0	0	0
18	1	1	1.00	1	1	0	0	0	0	0	0	0	0
18	1	1	1.00	1	1	0	0	0	0	0	0	0	0
24	2	1	1.00	1	1	0	0	0	0	0	0	0	0
22	1	1	1.00	1	1	0	0	0	0	0	0	0	0
22	2	1	1.00	1	1	0	0	0	0	0	0	0	0
18	1	1	1.00	1	1	0	0	0	0	0	0	0	0
21	0	1	1.00	1	0	0	0	1	0	0	0	0	0
23	3	1	1.00	1	1	0	0	0	0	0	0	0	0
18	0	1	1.00	1	1	0	0	0	0	0	0	0	0
22	3	2	0.50	1	1	0	0	0	0	0	0	0	0
21	3	5	0.40	2	2	0	0	0	0	0	0	0	0
19	2	3	0.33	1	1	0	0	0	0	0	0	0	0
21	3	4	0.25	1	1	0	0	0	0	0	0	0	0

Anti-sense strand reads

```
TAAAAGAGAAACAATAAGACGTTACCTAAATAAACGAAATCCTAAATAAAAAAGCCTGTTAAGTTAGACCCGCAACGAAAGCGACTCCATCATAACAAACCTTCTGATTCAATTGCTCGTAAGTAGAGTAAAAACTTTAAAACACAAGTACTCAC
************************************(((...((((((.((((((((((((((...((((.((((.......)))).)))))...)))))))))))))).))))))...)))).************************************
```

Read size	# Mismatch	Hit Count	Total Norm	Total

No data available in table

Show Alignment With Reads

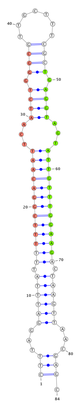
Re-alignment of all predicted orthologs

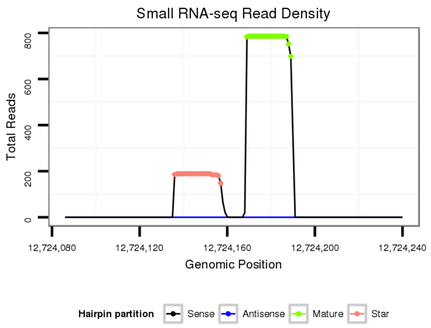
Species	Coordinate	ID	Alignment
droYak3	2R:12724086-12724240 +	dya_34	AT----TTTCTCTTTGTTATT------------CTGCAATGGATTTATTT-------GCTTTAGGATTTA------TTTTTTCGGACAATTCAATCTGGGCGTTGCTTTCGCTGAGGTAGTATTGTTTGGAAGACTAAGTTAACGAGC----------ATTCATCTCATTT-TTGAAAT----------TTTGTGTTCATGAGTG
droEre2	scaffold_4845:10618676-10618838 -	der_25	GT----TTTCT----GTTATTTTACTATATAA----------CTATTTATGAAGAAGCTTTAGGATTTA-------ATTTTTCGACAATCGCATCTAGGCGTTGTCTATCGCTGAGGTAGTATTGTTTGAAGATAAGTTAAGTTAAACGCG----------AATCATCAAAATT-TTAAAATGTG----------AATAATGTATCATTAGTG
droSec2	scaffold_1:14026259-14026320 -		GT----ATTCTTTTGTATT------------CTA--TATCTCTAACGAGC----------ATTCCTTAAAATT-----A----------CATATGTATCATTAGTG
droSim2	2r:17041524-17041580 -		AATTTTATTCTTTTGTATT------------CTA--TATCTCTAAATAATT------------------------------------ATTCCTTAAAATT----AT-TA----------AATATTGTG
dm3	chr2R:16472054-16472133 -		TATGGTATTCTTTTGTATT------------ATA--AAAGTTTACGAGC----------TAA----------GCTAACG----------ATTCATTAAAATT----AT-TA----------CATACATTTATAGTG
droEug1	scf7180000409474:1489443-1489565		TT----TTGGC------AATT------------AC--ATATTAAG----------GTAAAATAAATCGCTTTCTTAAAAATCAAGTGCTTAATATTGAAAGTATGATTATTAAAATAATATTTATTTACATTTAAAGCACTTTCGAATTTTTAAGATAACTCAATGGGTGTACATTTTTAAATAATTATTGTTCGAGCGTTGAGTTATTTTAAGAATTAATGTGTTAGTCGTAATAA-------------------------------GTGAAATG
droTak1	scaffold_100900:100735-100900 -		AC----CTTCT-TTTATTACT---CTTGATAATTCTTGTAAAAGTA-----------ATTAAAACATCTTTATTGATTTAAACAGAGAA----------ATAAGTTTATCTTA----------ATTCCCTAAAAATGGTTAAAGCTAAAAAAGTGCGTGTTTAAGTTCCTATCGGAATCAGTACTTTTATTTGCTTTCCTGGATT
droRho1	scf7180000780104:83008-83037 -		AT----TATTTATTTGTTATT------------ATAT-----TTTATTT---

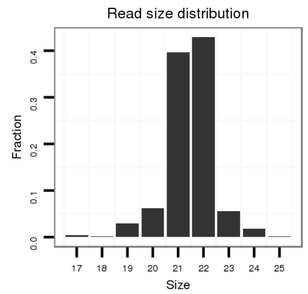
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dya_34	**2R:12724136-12724190 +**	**confident**	**Testes-restricted**	**intergenic**	[View on UCSC Genome Browser [Cornell Mirror]]

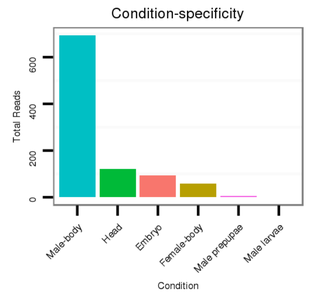
Legend: mature star mismatch in alignment mismatch in read

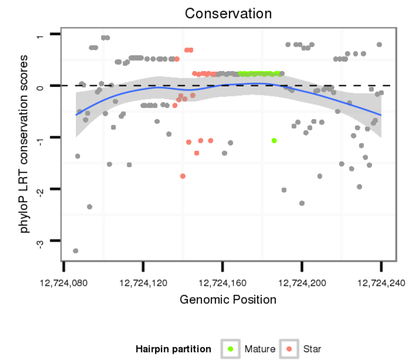
Predicted structure











Show Alternate Folds

Flybase annotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

```
ATTTTCTCTTTGTTATTCTGCAATGGATTTATTTGCTTTAGGATTTATTTTTTCGGACAATTCAATCTGGGCGTTGCTTTCGCTGAGGTAGTATTGTTTGGAAGACTAAGTTAACGAGCATTCATCTCATTTTTGAAATTTTGTGTTCATGAGTG
************************************(((...((((((.((((((((((((((...((((.((((.......)))).)))))...)))))))))))))).))))))...)))).************************************
```

Read size	# Mismatch	Hit Count	Total Norm	Total	V120 male body	M026 head	M056 embryo	M043 female body	V046 embryo	SRR1275484 Male prepupae	V058 head	SRR1275488 Male larvae	V052 head
21	0	1	348.00	348	300	16	12	14	2	2	2	0	0
22	0	1	333.00	333	263	23	25	13	8	1	0	0	0
22	0	1	81.00	81	16	29	19	8	8	0	0	0	1
23	1	1	53.00	53	42	8	1	2	0	0	0	0	0
20	0	1	51.00	51	49	1	1	0	0	0	0	0	0
23	0	1	43.00	43	8	16	9	9	1	0	0	0	0
21	0	1	32.00	32	8	15	2	6	1	0	0	0	0
21	1	1	32.00	32	30	1	0	1	0	0	0	0	0
19	0	1	29.00	29	26	2	1	0	0	0	0	0	0
23	1	1	24.00	24	24	0	0	0	0	0	0	0	0
22	1	1	23.00	23	8	14	1	0	0	0	0	0	0
24	0	1	18.00	18	4	12	1	1	0	0	0	0	0
21	1	1	17.00	17	15	2	0	0	0	0	0	0	0
23	1	1	15.00	15	2	13	0	0	0	0	0	0	0
20	1	1	12.00	12	9	3	0	0	0	0	0	0	0
23	0	1	10.00	10	9	0	1	0	0	0	0	0	0
22	1	1	10.00	10	7	0	1	0	0	0	2	0	0
23	2	1	9.00	9	2	7	0	0	0	0	0	0	0
24	2	1	8.00	8	6	0	0	0	0	2	0	0	0
19	1	1	7.00	7	7	0	0	0	0	0	0	0	0
22	1	1	5.00	5	5	0	0	0	0	0	0	0	0
23	2	1	5.00	5	3	2	0	0	0	0	0	0	0
20	0	1	4.00	4	1	2	0	1	0	0	0	0	0
17	0	1	4.00	4	0	0	0	0	0	3	0	1	0
20	0	1	4.00	4	4	0	0	0	0	0	0	0	0
24	1	1	3.00	3	0	3	0	0	0	0	0	0	0
24	1	1	3.00	3	0	1	2	0	0	0	0	0	0
26	1	1	3.00	3	1	0	0	1	0	1	0	0	0
23	1	1	3.00	3	0	3	0	0	0	0	0	0	0
23	2	1	3.00	3	3	0	0	0	0	0	0	0	0
21	0	1	3.00	3	3	0	0	0	0	0	0	0	0
22	0	1	3.00	3	1	0	1	1	0	0	0	0	0
21	2	1	2.00	2	2	0	0	0	0	0	0	0	0
21	0	1	2.00	2	0	0	0	2	0	0	0	0	0
22	1	1	2.00	2	2	0	0	0	0	0	0	0	0
25	0	1	2.00	2	0	2	0	0	0	0	0	0	0
20	2	1	2.00	2	2	0	0	0	0	0	0	0	0
22	1	1	2.00	2	0	2	0	0	0	0	0	0	0
23	2	1	1.00	1	0	1	0	0	0	0	0	0	0
23	2	1	1.00	1	1	0	0	0	0	0	0	0	0
22	0	1	1.00	1	0	0	0	1	0	0	0	0	0
18	0	1	1.00	1	0	0	0	0	0	1	0	0	0
23	3	1	1.00	1	1	0	0	0	0	0	0	0	0
20	0	1	1.00	1	1	0	0	0	0	0	0	0	0
22	2	1	1.00	1	1	0	0	0	0	0	0	0	0
21	2	1	1.00	1	1	0	0	0	0	0	0	0	0
25	3	1	1.00	1	1	0	0	0	0	0	0	0	0
23	0	1	1.00	1	1	0	0	0	0	0	0	0	0
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18	1	1	1.00	1	1	0	0	0	0	0	0	0	0
18	1	1	1.00	1	1	0	0	0	0	0	0	0	0
24	2	1	1.00	1	1	0	0	0	0	0	0	0	0
22	1	1	1.00	1	1	0	0	0	0	0	0	0	0
22	2	1	1.00	1	1	0	0	0	0	0	0	0	0
18	1	1	1.00	1	1	0	0	0	0	0	0	0	0
21	0	1	1.00	1	0	0	0	1	0	0	0	0	0
23	3	1	1.00	1	1	0	0	0	0	0	0	0	0
18	0	1	1.00	1	1	0	0	0	0	0	0	0	0
22	3	2	0.50	1	1	0	0	0	0	0	0	0	0
21	3	5	0.40	2	2	0	0	0	0	0	0	0	0
19	2	3	0.33	1	1	0	0	0	0	0	0	0	0
21	3	4	0.25	1	1	0	0	0	0	0	0	0	0

Anti-sense strand reads

```
TAAAAGAGAAACAATAAGACGTTACCTAAATAAACGAAATCCTAAATAAAAAAGCCTGTTAAGTTAGACCCGCAACGAAAGCGACTCCATCATAACAAACCTTCTGATTCAATTGCTCGTAAGTAGAGTAAAAACTTTAAAACACAAGTACTCAC
************************************(((...((((((.((((((((((((((...((((.((((.......)))).)))))...)))))))))))))).))))))...)))).************************************
```

Read size	# Mismatch	Hit Count	Total Norm	Total

No data available in table

Show Alignment With Reads

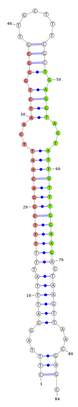
Re-alignment of all predicted orthologs

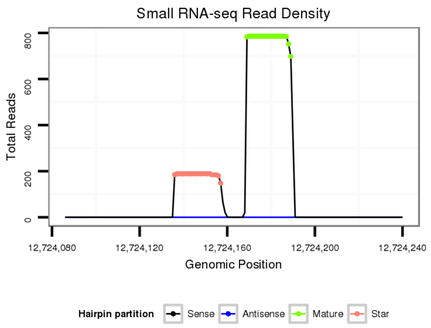
Species	Coordinate	ID	Alignment
droYak3	2R:12724086-12724240 +	dya_34	AT----TTTCTCTTTGTTATT------------CTGCAATGGATTTATTT-------GCTTTAGGATTTA------TTTTTTCGGACAATTCAATCTGGGCGTTGCTTTCGCTGAGGTAGTATTGTTTGGAAGACTAAGTTAACGAGC----------ATTCATCTCATTT-TTGAAAT----------TTTGTGTTCATGAGTG
droEre2	scaffold_4845:10618676-10618838 -	der_25	GT----TTTCT----GTTATTTTACTATATAA----------CTATTTATGAAGAAGCTTTAGGATTTA-------ATTTTTCGACAATCGCATCTAGGCGTTGTCTATCGCTGAGGTAGTATTGTTTGAAGATAAGTTAAGTTAAACGCG----------AATCATCAAAATT-TTAAAATGTG----------AATAATGTATCATTAGTG
droSec2	scaffold_1:14026259-14026320 -		GT----ATTCTTTTGTATT------------CTA--TATCTCTAACGAGC----------ATTCCTTAAAATT-----A----------CATATGTATCATTAGTG
droSim2	2r:17041524-17041580 -		AATTTTATTCTTTTGTATT------------CTA--TATCTCTAAATAATT------------------------------------ATTCCTTAAAATT----AT-TA----------AATATTGTG
dm3	chr2R:16472054-16472133 -		TATGGTATTCTTTTGTATT------------ATA--AAAGTTTACGAGC----------TAA----------GCTAACG----------ATTCATTAAAATT----AT-TA----------CATACATTTATAGTG
droEug1	scf7180000409474:1489443-1489565		TT----TTGGC------AATT------------AC--ATATTAAG----------GTAAAATAAATCGCTTTCTTAAAAATCAAGTGCTTAATATTGAAAGTATGATTATTAAAATAATATTTATTTACATTTAAAGCACTTTCGAATTTTTAAGATAACTCAATGGGTGTACATTTTTAAATAATTATTGTTCGAGCGTTGAGTTATTTTAAGAATTAATGTGTTAGTCGTAATAA-------------------------------GTGAAATG
droTak1	scaffold_100900:100735-100900 -		AC----CTTCT-TTTATTACT---CTTGATAATTCTTGTAAAAGTA-----------ATTAAAACATCTTTATTGATTTAAACAGAGAA----------ATAAGTTTATCTTA----------ATTCCCTAAAAATGGTTAAAGCTAAAAAAGTGCGTGTTTAAGTTCCTATCGGAATCAGTACTTTTATTTGCTTTCCTGGATT
droRho1	scf7180000780104:83008-83037 -		AT----TATTTATTTGTTATT------------ATAT-----TTTATTT---

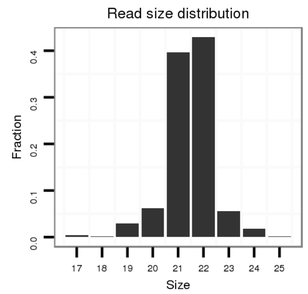
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dya_34	**2R:12724136-12724190 +**	**confident**	**Testes-restricted**	**intergenic**	[View on UCSC Genome Browser [Cornell Mirror]]

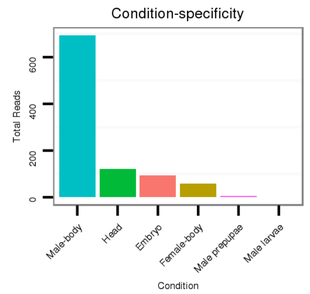
Legend: mature star mismatch in alignment mismatch in read

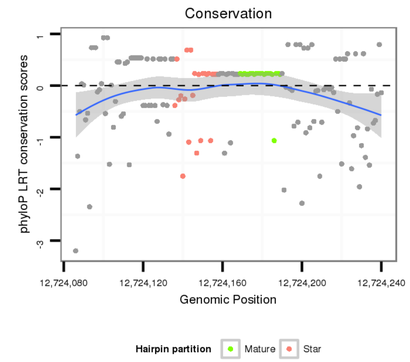
Predicted structure











Show Alternate Folds

Flybase annotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

```
ATTTTCTCTTTGTTATTCTGCAATGGATTTATTTGCTTTAGGATTTATTTTTTCGGACAATTCAATCTGGGCGTTGCTTTCGCTGAGGTAGTATTGTTTGGAAGACTAAGTTAACGAGCATTCATCTCATTTTTGAAATTTTGTGTTCATGAGTG
************************************(((...((((((.((((((((((((((...((((.((((.......)))).)))))...)))))))))))))).))))))...)))).************************************
```

Read size	# Mismatch	Hit Count	Total Norm	Total	V120 male body	M026 head	M056 embryo	M043 female body	V046 embryo	SRR1275484 Male prepupae	V058 head	SRR1275488 Male larvae	V052 head
21	0	1	348.00	348	300	16	12	14	2	2	2	0	0
22	0	1	333.00	333	263	23	25	13	8	1	0	0	0
22	0	1	81.00	81	16	29	19	8	8	0	0	0	1
23	1	1	53.00	53	42	8	1	2	0	0	0	0	0
20	0	1	51.00	51	49	1	1	0	0	0	0	0	0
23	0	1	43.00	43	8	16	9	9	1	0	0	0	0
21	0	1	32.00	32	8	15	2	6	1	0	0	0	0
21	1	1	32.00	32	30	1	0	1	0	0	0	0	0
19	0	1	29.00	29	26	2	1	0	0	0	0	0	0
23	1	1	24.00	24	24	0	0	0	0	0	0	0	0
22	1	1	23.00	23	8	14	1	0	0	0	0	0	0
24	0	1	18.00	18	4	12	1	1	0	0	0	0	0
21	1	1	17.00	17	15	2	0	0	0	0	0	0	0
23	1	1	15.00	15	2	13	0	0	0	0	0	0	0
20	1	1	12.00	12	9	3	0	0	0	0	0	0	0
23	0	1	10.00	10	9	0	1	0	0	0	0	0	0
22	1	1	10.00	10	7	0	1	0	0	0	2	0	0
23	2	1	9.00	9	2	7	0	0	0	0	0	0	0
24	2	1	8.00	8	6	0	0	0	0	2	0	0	0
19	1	1	7.00	7	7	0	0	0	0	0	0	0	0
22	1	1	5.00	5	5	0	0	0	0	0	0	0	0
23	2	1	5.00	5	3	2	0	0	0	0	0	0	0
20	0	1	4.00	4	1	2	0	1	0	0	0	0	0
17	0	1	4.00	4	0	0	0	0	0	3	0	1	0
20	0	1	4.00	4	4	0	0	0	0	0	0	0	0
24	1	1	3.00	3	0	3	0	0	0	0	0	0	0
24	1	1	3.00	3	0	1	2	0	0	0	0	0	0
26	1	1	3.00	3	1	0	0	1	0	1	0	0	0
23	1	1	3.00	3	0	3	0	0	0	0	0	0	0
23	2	1	3.00	3	3	0	0	0	0	0	0	0	0
21	0	1	3.00	3	3	0	0	0	0	0	0	0	0
22	0	1	3.00	3	1	0	1	1	0	0	0	0	0
21	2	1	2.00	2	2	0	0	0	0	0	0	0	0
21	0	1	2.00	2	0	0	0	2	0	0	0	0	0
22	1	1	2.00	2	2	0	0	0	0	0	0	0	0
25	0	1	2.00	2	0	2	0	0	0	0	0	0	0
20	2	1	2.00	2	2	0	0	0	0	0	0	0	0
22	1	1	2.00	2	0	2	0	0	0	0	0	0	0
23	2	1	1.00	1	0	1	0	0	0	0	0	0	0
23	2	1	1.00	1	1	0	0	0	0	0	0	0	0
22	0	1	1.00	1	0	0	0	1	0	0	0	0	0
18	0	1	1.00	1	0	0	0	0	0	1	0	0	0
23	3	1	1.00	1	1	0	0	0	0	0	0	0	0
20	0	1	1.00	1	1	0	0	0	0	0	0	0	0
22	2	1	1.00	1	1	0	0	0	0	0	0	0	0
21	2	1	1.00	1	1	0	0	0	0	0	0	0	0
25	3	1	1.00	1	1	0	0	0	0	0	0	0	0
23	0	1	1.00	1	1	0	0	0	0	0	0	0	0
23	0	1	1.00	1	0	0	0	1	0	0	0	0	0
24	1	1	1.00	1	0	1	0	0	0	0	0	0	0
20	0	1	1.00	1	0	0	1	0	0	0	0	0	0
24	1	1	1.00	1	1	0	0	0	0	0	0	0	0
18	1	1	1.00	1	1	0	0	0	0	0	0	0	0
18	1	1	1.00	1	1	0	0	0	0	0	0	0	0
24	2	1	1.00	1	1	0	0	0	0	0	0	0	0
22	1	1	1.00	1	1	0	0	0	0	0	0	0	0
22	2	1	1.00	1	1	0	0	0	0	0	0	0	0
18	1	1	1.00	1	1	0	0	0	0	0	0	0	0
21	0	1	1.00	1	0	0	0	1	0	0	0	0	0
23	3	1	1.00	1	1	0	0	0	0	0	0	0	0
18	0	1	1.00	1	1	0	0	0	0	0	0	0	0
22	3	2	0.50	1	1	0	0	0	0	0	0	0	0
21	3	5	0.40	2	2	0	0	0	0	0	0	0	0
19	2	3	0.33	1	1	0	0	0	0	0	0	0	0
21	3	4	0.25	1	1	0	0	0	0	0	0	0	0

Anti-sense strand reads

```
TAAAAGAGAAACAATAAGACGTTACCTAAATAAACGAAATCCTAAATAAAAAAGCCTGTTAAGTTAGACCCGCAACGAAAGCGACTCCATCATAACAAACCTTCTGATTCAATTGCTCGTAAGTAGAGTAAAAACTTTAAAACACAAGTACTCAC
************************************(((...((((((.((((((((((((((...((((.((((.......)))).)))))...)))))))))))))).))))))...)))).************************************
```

Read size	# Mismatch	Hit Count	Total Norm	Total

No data available in table

Show Alignment With Reads

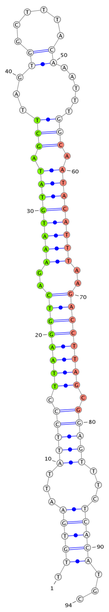
Re-alignment of all predicted orthologs

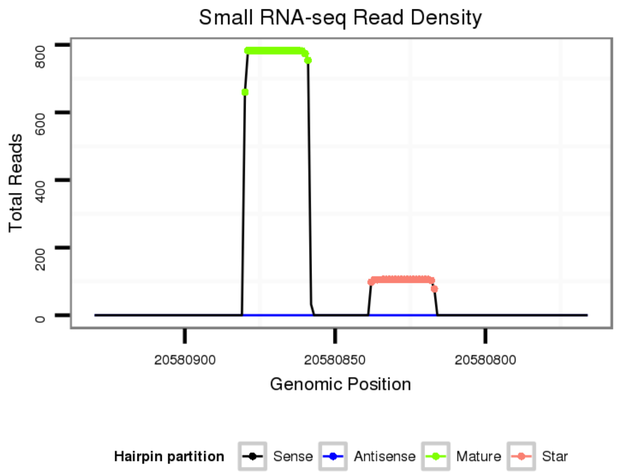
Species	Coordinate	ID	Alignment
droYak3	2R:12724086-12724240 +	dya_34	AT----TTTCTCTTTGTTATT------------CTGCAATGGATTTATTT-------GCTTTAGGATTTA------TTTTTTCGGACAATTCAATCTGGGCGTTGCTTTCGCTGAGGTAGTATTGTTTGGAAGACTAAGTTAACGAGC----------ATTCATCTCATTT-TTGAAAT----------TTTGTGTTCATGAGTG
droEre2	scaffold_4845:10618676-10618838 -	der_25	GT----TTTCT----GTTATTTTACTATATAA----------CTATTTATGAAGAAGCTTTAGGATTTA-------ATTTTTCGACAATCGCATCTAGGCGTTGTCTATCGCTGAGGTAGTATTGTTTGAAGATAAGTTAAGTTAAACGCG----------AATCATCAAAATT-TTAAAATGTG----------AATAATGTATCATTAGTG
droSec2	scaffold_1:14026259-14026320 -		GT----ATTCTTTTGTATT------------CTA--TATCTCTAACGAGC----------ATTCCTTAAAATT-----A----------CATATGTATCATTAGTG
droSim2	2r:17041524-17041580 -		AATTTTATTCTTTTGTATT------------CTA--TATCTCTAAATAATT------------------------------------ATTCCTTAAAATT----AT-TA----------AATATTGTG
dm3	chr2R:16472054-16472133 -		TATGGTATTCTTTTGTATT------------ATA--AAAGTTTACGAGC----------TAA----------GCTAACG----------ATTCATTAAAATT----AT-TA----------CATACATTTATAGTG
droEug1	scf7180000409474:1489443-1489565		TT----TTGGC------AATT------------AC--ATATTAAG----------GTAAAATAAATCGCTTTCTTAAAAATCAAGTGCTTAATATTGAAAGTATGATTATTAAAATAATATTTATTTACATTTAAAGCACTTTCGAATTTTTAAGATAACTCAATGGGTGTACATTTTTAAATAATTATTGTTCGAGCGTTGAGTTATTTTAAGAATTAATGTGTTAGTCGTAATAA-------------------------------GTGAAATG
droTak1	scaffold_100900:100735-100900 -		AC----CTTCT-TTTATTACT---CTTGATAATTCTTGTAAAAGTA-----------ATTAAAACATCTTTATTGATTTAAACAGAGAA----------ATAAGTTTATCTTA----------ATTCCCTAAAAATGGTTAAAGCTAAAAAAGTGCGTGTTTAAGTTCCTATCGGAATCAGTACTTTTATTTGCTTTCCTGGATT
droRho1	scf7180000780104:83008-83037 -		AT----TATTTATTTGTTATT------------ATAT-----TTTATTT---

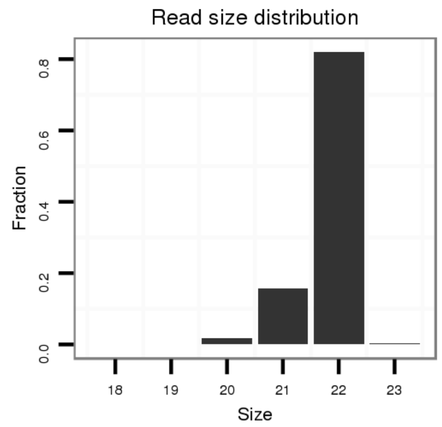
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dya_40	**X:20580816-20580880 -**	**confident**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

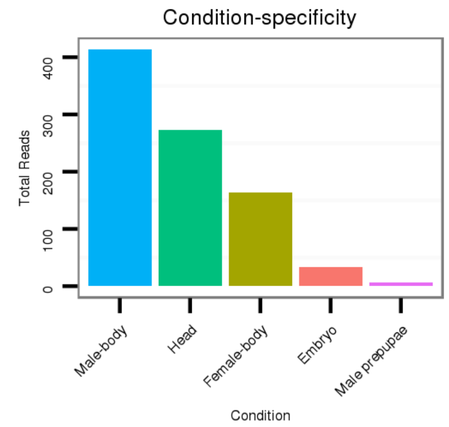
Legend: mature star mismatch in alignment mismatch in read

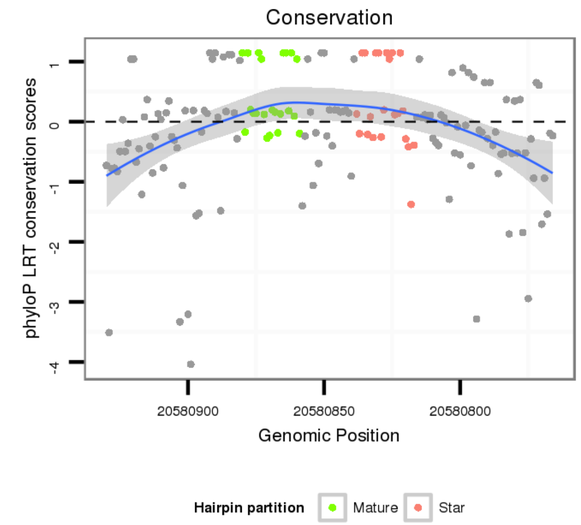
Predicted structure











Show Alternate Folds

Flybase annotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

```
GTGGTAGATTTCGGGGCTAAGAAACCAGGACGTCTTTGTGAATTATTCCCTTAAGGTCAGAAATGTATAGCTTAGTGGCTTTACAAATTTGGCAATACATTTAAGACCTTAGCGGAGTTTCTCACATGCCTTCCATAAAAGTGTCTAGTCTAGACAATTTAAAAA
**********************************.(((((...(((((.(((((((((..(((((((((.(((...((......)).....))).))))))))..)))))))))..)))))...)))))...**********************************
```

Read size	# Mismatch	Hit Count	Total Norm	Total	male body	head	female body	embryo	head	Male prepupae	embryo	Male prepupae
					V120	M026	M043	M056	V058	SRR1275484	V046	SRR1275486
22	0	1	627.00	627	311	214	78	17	5	0	1	1
21	0	1	95.00	95	34	43	16	1	0	0	1	0
22	0	1	74.00	74	25	0	43	5	1	0	0	0
22	1	1	34.00	34	0	29	0	5	0	0	0	0
22	0	1	28.00	28	21	4	1	1	1	0	0	0
21	0	1	21.00	21	2	0	12	7	0	0	0	0
21	0	1	20.00	20	13	5	1	0	0	1	0	0
23	1	1	17.00	17	15	0	2	0	0	0	0	0
20	0	1	8.00	8	5	0	0	0	0	3	0	0
21	1	1	8.00	8	0	6	0	2	0	0	0	0
20	0	1	4.00	4	0	0	4	0	0	0	0	0
23	0	1	4.00	4	3	0	1	0	0	0	0	0
21	0	1	3.00	3	0	0	3	0	0	0	0	0
20	0	1	3.00	3	0	0	3	0	0	0	0	0
22	1	1	2.00	2	0	2	0	0	0	0	0	0
22	1	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
18	0	1	1.00	1	0	0	1	0	0	0	0	0
19	0	1	1.00	1	0	0	0	0	0	1	0	0
24	2	1	1.00	1	1	0	0	0	0	0	0	0

Anti-sense strand reads

```
CACCATCTAAAGCCCCGATTCTTTGGTCCTGCAGAAACACTTAATAAGGGAATTCCAGTCTTTACATATCGAATCACCGAAATGTTTAAACCGTTATGTAAATTCTGGAATCGCCTCAAAGAGTGTACGGAAGGTATTTTCACAGATCAGATCTGTTAAATTTTT
**********************************.(((((...(((((.(((((((((..(((((((((.(((...((......)).....))).))))))))..)))))))))..)))))...)))))...**********************************
```

Read size	# Mismatch	Hit Count	Total Norm	Total	M043 female body

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droYak3	X:20580766-20580930 -	dya_40	GTGGTAGATTTCGGGGC-TAAGAA-ACC--------------------------------AGGACG---TCTTTGTGAATTATTCCCTTAAGGTCAGAAATGTATAGCTTAGTGGCTTTACAAATTTGGCAATACATTTAAGACCTTA-GCGGAGTTTCTCACATGCCTTCCATAAAAGTGTCTAGTCTAG--------------------------------ACAATTTAAAAA-------
droEre2	scaffold_4690:17924486-17924691 -	der_47	TCGCCAGATTTCGTGGC-TGAG-AA-TT-ATT---------------GCCT-GGAACCTCGAGA---TTGTTGTGAA--ATTCCCTTAAGGTCAGGAAGTATAGCTCAGTGATTT-GCGAATTTAGCAATACATTCTAGACCTTT-GCGGAGTTTTTCAAAGGTCTTCCGTGAAAGTGTTCTGCT-TGTTTTTGTGAATCTATCTTGGGTAACTCTAGTCTAGAGCACT--GCCA-------
droSec2	scaffold_8:3725796-3725971 -	dse_127	TGAGA----TTCAGAGC-TAAGTA-ATA-ATT---------------GAGT-TGGAGCTCGA-CTTTTTGTAGTGAAGTATTCCCTCAAGGTCTAGAAAGTAGAGCTCAGTAATTTTACAAATTTGGCAATGCATTCAAGACCTGT-GCGGAGTTATTTACACGTCGTCCATCAAAGTGTTTTGTTTTG--------------------------------CTGGTTTGAAAG-------
droSim2	x:20141507-20141683 -	dsi_6	TAAGA---TTTCAGAGC-TAAGTA-ATA-ATT---------------GAGT-TGGAGCTCGA-CTTTTTGTAGTGAAGTATTCCCTCAAGGTCTAGAAAGTAGAGCTCAGTAATTTTACAAATTTGGCAATGCATTCAAGACCTGT-GCGGAGTTATTTACACGTCGTCCATCAAAGTGTTTTGTTTTG--------------------------------CTGGTTTAAAAG-------
dm3	chrX:21443068-21443248 -	dme_444	GCCA---------AGGC-TAAGTG-ATA-ATTGAATCTGGAAATAATAGAAT-GGAAG-AAAAA---TGGAAATGA---------TAATAATGTGGAAAGTAGAGCTCAGTAATTTTACAAATTTGGCAATGCCTTCAAGACCTGT-GCGGAGTTTTTTACACGTCTTCCATTAAAGTGTTTTGTTTTG--------------------------------TTTGTTTGATAAGTATTTG
droEug1	scf7180000408193:45603-45752 +		TCGGAAGTATTCCTG-G-AAAGTAA-ATCATT-----T---------AACT-TACACTTTCA-TTTCAAATTGTGA-GTATTTTCTTAAGGTCTGAACAGTATAGCTCAGTAACTTAAGAAATTCTGCAATACATTCAAGACTTTTTGGAAAGCTTTGCACTTGTGTTCG----------**********--------
droTak1	scf7180000415769:353399-353509 -		TTGGTGACATTGGTG-GGTAAG-AA-TT-AAA---------------T---------**--AATT---TTCTTGTGAACTTTTTCCTTAAGGTCTGGGAAGTATAGCTAAGTGATTTTAAATATTCTGCAATGCATTCAAGACCTT-**********----------**********--------
droEle1	scf7180000491087:1002207-1002323 +		AATAA----------******---**********-AGCCA---TTTTTGTGAAATATTTTCTTAAGGTCTTGAAGATATATCTTAGTAATTTTAAAAAGTCAGTAATATTTTCAAGAACTTATATAAAGTGTTTTTGTCGTGTTTGTTAT----------**********--------
droRho1	scf7180000779411:16505-16674 +		TCGGAGGTATTTGTG-T-GAACAAA-TT-AAT---------------TTCTTTGGGCTTT-AAC---TTTTTGTGAAATATTTTCTTAAGGTCTGAAAGTATATCAATGTATATTAAAAAATTCTGCTATATTTTAAAGACCTTTTGCAAAGTGTTTTACTCGGGATTGTTGATATTCCC--------**********TTAAATTATAAA-------
droFic1	scf7180000453926:397652-397794 -		TCGGAAGTGTTTGTG-GGAGGG-AA-TT-CCT----CC-GAAGT----GACT-AAGCCGCAGAAG---TGTCTGTGATATATTTCTTAAGGTCTGGAAAGTATAGCAACGCATTTTA-AACTCCTGCCATACATTCAAGACCTTT-TGTAAATTTCCTAC**********----------**********--------

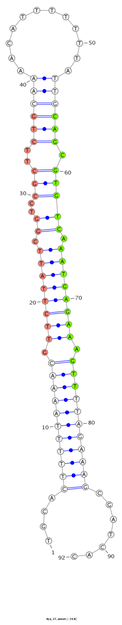
Generated: 09/08/2015 at 07:39 PM

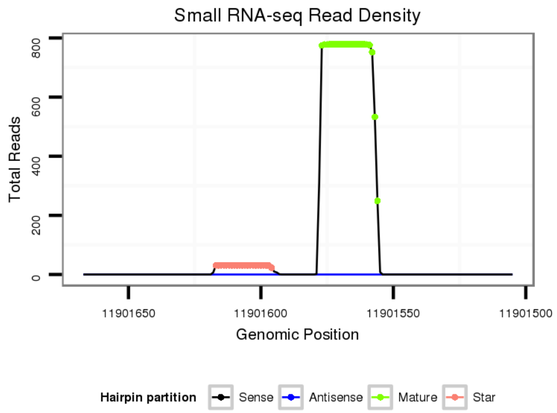
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	4
rescue.candidate	0

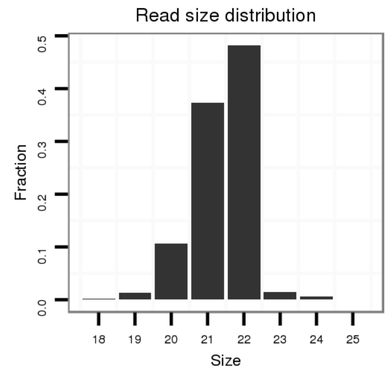
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dya_37	**X:11901555-11901617 -**	**confident**	**Testes-restricted**	**antisense_to_intron**	[View on UCSC Genome Browser {Cornell Mirror}]

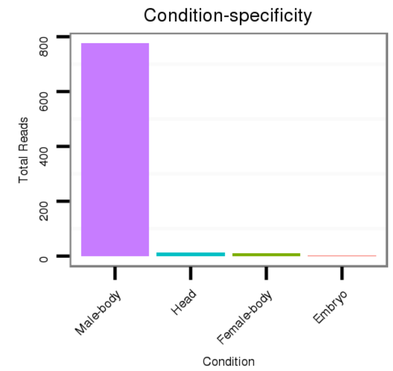
Legend: mature star mismatch in alignment mismatch in read

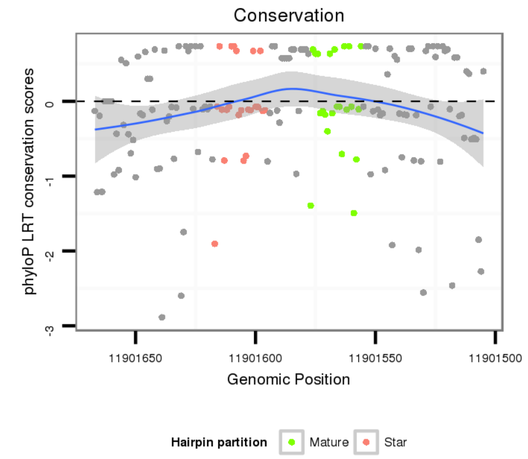
Predicted structure











Show Alternate Folds

Flybase annnotation

Antisense to intron [Dyak\GE17381-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

ATTAAAACACAAAGTGCATACATATTCAAACATAATGCACTTTTTAAAACGTTCTTATTCGGTCCGCTTCTGCAAAACATTTTTTATTGCAGCGTGTCAAATGAGAAAGTTTTAGAAAGCGATCACAATCAACAGCACAAAATATCTACATTTATGTTTAAA	Read size	# Mismatch	Hit Count	Total Norm	Total	V120 male body	M043 female body	M026 head	V052 head	M056 embryo	V058 head	V046 embryo
**********												
.....CAGCGTGTCAAATGAGAAAGTT.....	22	0	1	237.00	237	232	2	2	0	0	1	0
.....GCAGCGTGTCAAATGAGAAAG.....	21	0	1	149.00	149	147	1	0	0	0	1	0
.....CAGCGTGTCAAATGAGAAAGT.....	21	0	1	143.00	143	141	1	0	0	0	0	1
.....GCAGCGTGTCAAATGAGAAAGT.....	22	0	1	138.00	138	130	4	2	1	1	0	0
.....CAGCGTGTCAAATGAGAAAG.....	20	0	1	68.00	68	68	0	0	0	0	0	0
.....GCAGCGTGTCAAATGAGAAA.....	20	0	1	15.00	15	14	0	0	1	0	0	0
.....GTTCTTATTCGGTCCGCTTCTG.....	22	0	1	10.00	10	6	0	4	0	0	0	0
.....CAGCGTGTCAAATGAGAAA.....	19	0	1	9.00	9	9	0	0	0	0	0	0
.....CAGCGTGTCAAATGAGAAAGTTT.....	23	0	1	8.00	8	8	0	0	0	0	0	0
.....GTTCTTATTCGGTCCGCTTCT.....	21	0	1	7.00	7	7	0	0	0	0	0	0
.....GTTCTTATTCGGTCCGCTTCTGCA.....	24	0	1	5.00	5	3	1	1	0	0	0	0
.....GCAGCGTGTCAAATGAGAAAGTT.....	23	0	1	3.00	3	2	0	0	0	1	0	0
.....CGTTCTTATTCGGTCCGCTTCTG.....	23	0	1	3.00	3	3	0	0	0	0	0	0
.....CGTTCTTATTCGGTCCGCTTCTGCAG.....	26	1	1	2.00	2	1	1	0	0	0	0	0
.....TGCAGCGTGTCAAATGAGAAAG.....	22	0	1	2.00	2	2	0	0	0	0	0	0
.....GTTCTTATTCGGTCCGCTTCTGCAT.....	25	1	1	2.00	2	0	0	2	0	0	0	0
.....CGTTCTTATTCGGTCCGCTTCTGC.....	24	0	1	2.00	2	1	1	0	0	0	0	0
.....GCAGCGTGTCAAATGAGAA.....	19	0	1	2.00	2	2	0	0	0	0	0	0
.....AGCGTGTCAAATGAGAAAGT.....	20	0	1	2.00	2	2	0	0	0	0	0	0
.....GCAGCGTGTCAAATGAGAAAT.....	21	1	1	1.00	1	1	0	0	0	0	0	0
.....GCAGCGTGTCAAATGAGAAAGC.....	22	1	1	1.00	1	1	0	0	0	0	0	0
.....GCAGCGTGTCAAATGAGA.....	18	0	1	1.00	1	0	0	0	1	0	0	0
.....GTTCTTATTCGGTCCGCTTCTGCAA.....	25	0	1	1.00	1	1	0	0	0	0	0	0
.....CGTGTCAAATGAGAAAGT.....	18	0	1	1.00	1	1	0	0	0	0	0	0
.....CAGCGTGTCAAATGAGAAG.....	19	1	1	1.00	1	1	0	0	0	0	0	0
.....AGCGTGTCAAATGAGAAAGTT.....	21	0	1	1.00	1	0	1	0	0	0	0	0
.....CGTTCTTATTCGGTCCGCTTC.....	21	0	1	1.00	1	0	1	0	0	0	0	0
.....CGTTCTTATTCGGTCCGCTTCTGCA.....	25	0	1	1.00	1	1	0	0	0	0	0	0
.....GCAGCGTGTCAAATGAGAAGT.....	21	2	1	1.00	1	1	0	0	0	0	0	0
.....GTTCTTATTCGGTCCGCTTCTGC.....	23	0	1	1.00	1	1	0	0	0	0	0	0

Anti-sense strand reads

TAATTTTGTGTTTCACGTATGTATAAGTTTGTATTACGTGAAAAATTTTGCAAGAATAAGCCAGGCGAAGACGTTTTGTAAAAAAATAACGTCGCACAGTTTACTCTTTCAAAATCTTTCGCTAGTGTTAGTTGTCGTGTTTTATAGATGTAAATACAAATTT	Read size	# Mismatch	Hit Count	Total Norm	Total	M043 female body	V058 head
**********							

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droYak3	X:11901505-11901667 -	dya_37	ATTAAAACA--CAAAGTGCATACATATTCAA---A----------CATAATGCACTTTTTAAAACGTTCTTATTCGGTCCGCTTCTGCAAAACATTT----------TTTTATTGCAGCGTGTCAAATGAGAAAGTTTTAGAAAGCGAT---------CACAATCAACAGCACAAAATA-TCTACA---TTTATGTTTAAA
droEre2	scaffold_4690:9672324-9672463 +	der_34	ATAC----CA--------GTAG--------GT----------TATACTGT-----AT-TATACTTTTTAAAACATTCTTATTCGGTCCGCTTCTGCAAAGT----------TTTTATTGCAGCGTGTCAAATGAGAAAGTTTTAGAAAGCGAT---------TACAATCAACAACGCAAAATA-TC----A-TATGTTTAAA
droSec2	scaffold_8:1717184-1717318 +		AATC----AGACGAAGCTTATACATATTTGC---A----------GTAAATACACTATTTGAGACGTTCTTATTCGGTACGCTTCTGCAAA------ATGAGAAAGCTTTAAAAGCGAT---------CACAATCAACAAGCCAAA-TA-TCTTTA---TTTATGTTTCGA
droSim2	x:18324513-18324658 +		AATC----AGACAAAGCTTATACATATTTATT---T----------TTACTATATTTATTAATAATGCACTATTTGAGACGTTCTTATTCGGTACGCTTCTGCAAA------ATAGAAAGCTTTAAAAGGCAAT---------CACAATCAACAAGCCAAA-TA-TCTAAA---TTTATGTTTCAA
dm3	chrX:19435346-19435555 +		ATTT----ATG----------CTTGA---AAACAACGAAATTTTCAAAGTTCACGTATTATGTCTTCAGACTAATAGAGGTTTGTCTTAATTCTAT-----AT-ATTTACTTTTTATATATATTCTCTTCCTCTTTCAGCTTTAAAA-----GTTAACCAAG-------AATTTTCTTTCCATTGAGCAATCCAATCAAATGTTTATAGA-------TGTCACAGAATC-TCTATACAGTTCGTGCGGGCA
droBia1	scf7180000301495:532208-532361 +		TGT------T--T---------TTA--TTTGTCTAA----------ATAAATACACTTTCTAAAATGTTCACATTCTGCCGCTTCAGCCAAATATTTTAGGTTCTCGGATTAAAGAATTA----------TTTTATTGAAGCGTGCCGAATGAGAACATTTTATGAATG-T---------AAGTTTAAT---TACAAAATG-TCTA---T----------
droTak1	scf7180000412694:24241-24442 -		A--C----GAAAAATGCTTGTACA--TTCGACTAA----------ATAAATATACTTTATAAAATATTCTCATTCGGTCCGCTTCTGTAAAATATTTAAACATTTCGTATTTAAAGTTTAAATTAAAATTTTAAACGCATGTTCTATTGCAGCGTGCCGAATGAGAATATTTTATAAAGTA-TATTTTTTTATG--ACCCAACAGGTCAAA-TAGTCTAAA---TTT---------

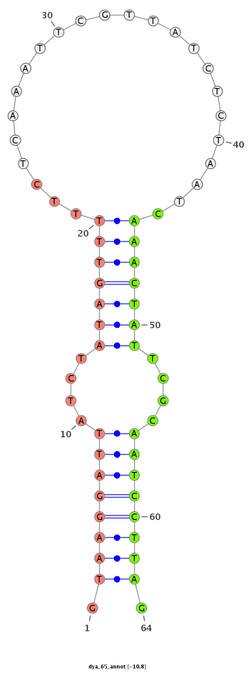
Generated: 09/08/2015 at 07:56 PM

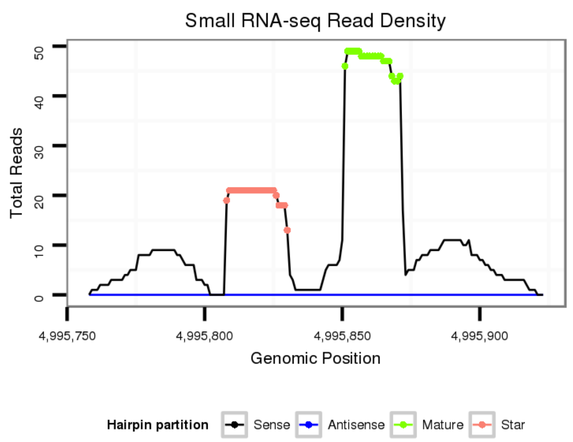
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	2
rescue.candidate	0

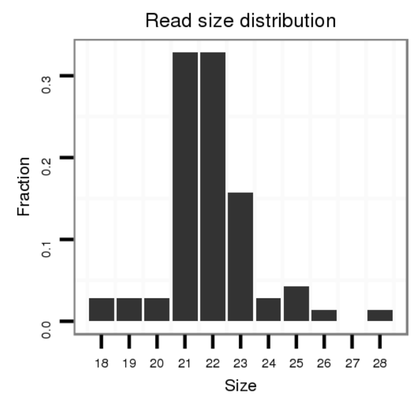
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dya_65	**3L:4995808-4995873 +**	**confident**	**Mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

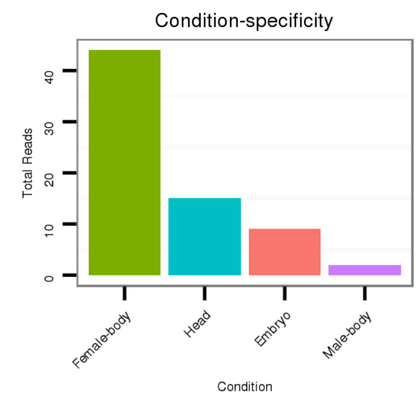
Legend: mature star mismatch in alignment mismatch in read

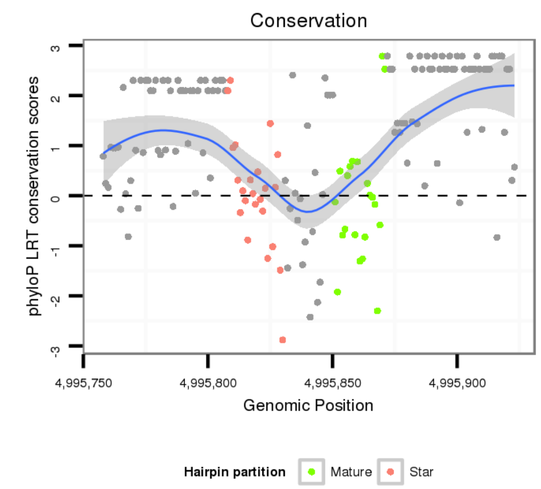
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dyak\GE21446-in]; CDS [Dyak\GE21446-cds]; CDS [Dyak\GE21446-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

ATGCGGCTGCCCAGCTGAAGCAGCAGACGCTGGCTCGTCAGAGCCAGAAGGTAAGGATTATCTATAGTTTTTCTCAAATTCGTTATCTCTAATCAAACTATTCGCAATCCTTAGAGCAACAACAAGAAGCAGCACCAGCAGCTATGCCGCAGTGCCATCAAGCGGG **********.(((((((((....(((((((.....)))))))....)))))))))..**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M056 embryo	M043 female body	V058 head	V120 male body	V052 head	V046 embryo	M026 head	GSM1528802 follicle cells
.....CAAACTATTCGCAATCCTTAGT.....	22	1	1	290.00	290	146	77	26	16	13	8	4	0
.....CAAACTATTCGCAATCCTTAGC.....	22	1	1	54.00	54	53	1	0	0	0	0	0	0
.....CAAACTATTCGCAATCCTTAG.....	21	0	1	21.00	21	2	15	2	1	1	0	0	0
.....CAAACTATTCGCAATCCTTAGA.....	22	0	1	13.00	13	2	9	0	0	1	1	0	0
.....AAACTATTCGCAATCCTTAGT.....	21	1	1	9.00	9	1	8	0	0	0	0	0	0
.....GTAAGGATTATCTATAGTTTTTC.....	23	0	1	8.00	8	1	2	0	0	0	1	4	0
.....TCAAACTATTCGCAATCCTTAGT.....	23	1	1	8.00	8	2	5	0	0	0	1	0	0
.....GTAAGGATTATCTATAGTTTTT.....	22	0	1	5.00	5	0	5	0	0	0	0	0	0
.....CAAACTATTCGCAATCCTTAGG.....	22	1	1	3.00	3	0	2	0	0	0	0	1	0
.....AGCAGCAGACGCTGGCTCGTC.....	21	0	1	3.00	3	0	0	0	0	0	0	0	3
.....CTATTCGCAATCCTTAGT.....	18	1	1	2.00	2	1	1	0	0	0	0	0	0
.....AAACTATTCGCAATCCTTAG.....	20	0	1	2.00	2	0	2	0	0	0	0	0	0
.....TCAAACTATTCGCAATCCTTAG.....	22	0	1	2.00	2	0	1	0	0	1	0	0	0
.....CAACAAGAAGCAGCACCAGC.....	20	0	1	2.00	2	0	0	0	1	0	1	0	0
.....TAAGGATTATCTATAGTTTTTC.....	22	0	1	2.00	2	0	0	0	0	0	0	2	0
.....GTAAGGATTATCTATAGTT.....	19	0	1	2.00	2	0	0	1	1	0	0	0	0
.....GTAAGGATTATCTATAGTTTTTCTC.....	25	0	1	2.00	2	0	1	0	0	0	0	1	0
.....GTAAGGATTATCTATAGT.....	18	0	1	1.00	1	0	0	1	0	0	0	0	0
.....CAAACTATTCGCAATCCTTAGTT.....	23	2	1	1.00	1	1	0	0	0	0	0	0	0
.....TCTCTAATCAAACTATTCGCAA.....	22	0	1	1.00	1	0	1	0	0	0	0	0	0
.....TCTAATCAAACTATTCGCAATCC.....	23	0	1	1.00	1	1	0	0	0	0	0	0	0
.....GCAACAACAAGAAGCAGCACCAGC.....	24	0	1	1.00	1	0	0	0	1	0	0	0	0
.....GTAAGGATTATCTATAGTTTTTCT.....	24	0	1	1.00	1	0	1	0	0	0	0	0	0
.....GCCCAGCTGAAGCAGCAGACGCTG.....	24	0	1	1.00	1	0	1	0	0	0	0	0	0
.....CAAACTATTCGCAATCCT.....	18	0	1	1.00	1	0	0	0	0	0	0	1	0
....GGCTGCCCAGCTGAAGCAGCA.....	21	0	1	1.00	1	0	1	0	0	0	0	0	0
.....TCAAACTATTCGCAATCCTTAGC.....	23	1	1	1.00	1	1	0	0	0	0	0	0	0
.....ATCAAACTATTCGCAATCCTTAG.....	23	0	1	1.00	1	0	1	0	0	0	0	0	0
.....ACTATTCGCAATCCTTAGT.....	19	1	1	1.00	1	0	1	0	0	0	0	0	0
.....AAACTATTCGCAATCCTTAGA.....	21	0	1	1.00	1	0	1	0	0	0	0	0	0
.....GACGCTGGCTCGTCAGAGC.....	19	0	1	1.00	1	0	1	0	0	0	0	0	0
.....GAGCAACAACAAGAAGCAGCACC.....	23	0	1	1.00	1	0	0	0	1	0	0	0	0
.....TCTCTAATCAAACTATTCGCAATCC.....	25	0	1	1.00	1	0	1	0	0	0	0	0	0
.....GCTGAAGCAGCAGACGCTGGC.....	21	0	1	1.00	1	1	0	0	0	0	0	0	0
.....CTCTAATCAAACTATTCGCAATCC.....	24	0	1	1.00	1	0	1	0	0	0	0	0	0
.....AGCAGACGCTGGCTCGTCAGA.....	21	0	1	1.00	1	0	0	0	1	0	0	0	0
.....TGAAGCAGCAGACGCTGGCT.....	20	0	1	1.00	1	0	1	0	0	0	0	0	0
.....TCAAACTATTCGCAATCCTTA.....	21	0	1	1.00	1	0	1	0	0	0	0	0	0
.....AGCAGCTATGCCGCAGTGCCATCA.....	24	0	1	1.00	1	0	1	0	0	0	0	0	0
.TGCGGCTGCCCAGCTGAAGC.....	20	0	1	1.00	1	0	1	0	0	0	0	0	0
.....GCAGCACCAGCAGCTATG.....	18	0	1	1.00	1	0	1	0	0	0	0	0	0
.....CAGCACCAGCAGCTATGCCGCA.....	22	0	1	1.00	1	0	1	0	0	0	0	0	0
.....CTCTAATCAAACTATTCGCAATCCTTAG.....	28	0	1	1.00	1	0	1	0	0	0	0	0	0
.....CAGCTATGCCGCAGTGCCATC.....	21	0	1	1.00	1	0	0	0	0	0	1	0	0
.....AGAAGCAGCACCAGCAGCTATGCC.....	24	0	1	1.00	1	0	1	0	0	0	0	0	0
.....CAAACTATTCGCAATCCTTATC.....	22	2	1	1.00	1	1	0	0	0	0	0	0	0
.....GCAACAACAAGAAGCAGCACCAGCAGC.....	27	0	1	1.00	1	0	1	0	0	0	0	0	0
.....CAGACGCTGGCTCGTCAGAGC.....	21	0	1	1.00	1	1	0	0	0	0	0	0	0
.....CAAACTATTCGCAATCCTTATT.....	22	2	1	1.00	1	1	0	0	0	0	0	0	0
.....TCAAATTCGTTATCTCTAATCAAACT.....	26	0	1	1.00	1	0	1	0	0	0	0	0	0
.....ACAAGAAGCAGCACCAGCAGCTA.....	23	0	1	1.00	1	0	0	0	1	0	0	0	0
.....GCTATGCCGCAGTGCCATCAAGC...	23	0	1	1.00	1	0	1	0	0	0	0	0	0
.....CAACAACAAGAAGCAGCACC.....	20	0	1	1.00	1	0	0	0	1	0	0	0	0
.....GAGCAACAACAAGAAGCAGCACCAGCA.....	27	0	1	1.00	1	0	0	0	1	0	0	0	0
.....TCAAACTATTCGCAATCCTTAGA.....	23	0	1	1.00	1	1	0	0	0	0	0	0	0
.....CAAGAAGCAGCACCAGCAGC.....	20	0	2	0.50	1	0	1	0	0	0	0	0	0
.....TCGTCAGAGCCAGAAGAG.....	18	2	8	0.13	1	1	0	0	0	0	0	0	0

Anti-sense strand reads

TACGCCGACGGGTCGACTTCGTCGTCTGCGACCGAGCAGTCTCGGTCTTCCATTCCTAATAGATATCAAAAAGAGTTTAAGCAATAGAGATTAGTTTGATAAGCGTTAGGAATCTCGTTGTTGTTCTTCGTCGTGGTCGTCGATACGGCGTCACGGTAGTTCGCCC **********.(((((((((....(((((((.....)))))))....)))))))))..**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M043 female body	M056 embryo

Show Alignment With Reads

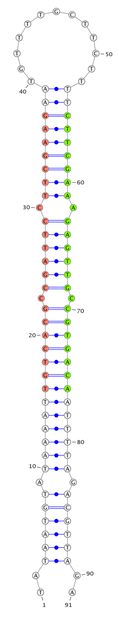
Re-alignment of all predicted orthologs

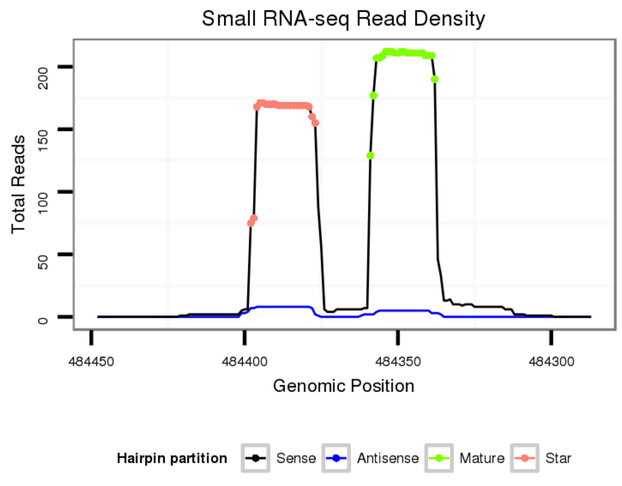
Species	Coordinate	ID	Alignment
droYak3	3L:4995758-4995923 +	dya_65	ATGCGGCTGCCCAGCTGAAGCAGCAGACGCTGGCTCGTCAGAGCCAGAAGGTAAGGA----------TT------ATCTA----------TAGTTT----------TTCTCAAATTCG---TT-ATCTCTAATCAAACTATT---C----------GCAATCCTTAGAGCAACAACAAGAAGCAGCACCAGCAGCTATGCCGCAGTGCCATCAAGCGGG
droEre2	scaffold_4784:7128261-7128423 +		ATGCGGCCGCCCAGTTGAAGCAGCAGACATGGCTCGTCAGAGCCAGAAGGTAAGGACTCTA----------TTTAGTGGC--------------------GAG--------TGTGCAAAGCGCT--G-A--TCTAATCAA-------------------ACCCAATCCTTAGAGCAACAACAAGAAGCAGCACCAGCAGCTCTGCCGCAGTGCCATCAAGCGGG
droSec2	scaffold_2:4408722-4408897 +		ATGCGGCCGTACAGTTGAAGCAGCAGACGCTGGCTCGTCAGAGCCAGAAGGTAAGGA----------TT------ACACG----------TA----------GTACAA---------TGGTAAAGTGT--ATG-ATCTCTAATAGATGTATC---CT--TTCT-ATCCAATCCATAGAGCAAGAACAAGAAGCAGCACCAGCAGCTCTGCCGCAGTGCCATGAAGCGGG
droSim2	3L:4371862-4372037 +		ATGCGGCCGTACAGTTGAAGCAGCAGACGCTGGCTCGTCAGAGCCAGAAGGTAAGGA----------TT------ACACG----------TA----------GTACAA---------TGGTAAAGTGT--ATG-ATCTCTAATAGATGTATC---CT--TTCT-ATCCAATCCATAGAGCAAGAACAAGAAGCAGCACCAGCAGCTCTGCCGCAGTGCCATCAAGCGGG
dm3	chr3L:4419614-4419791 +		ATGCGGCCGTACAGTTGAAGCAGCAGACGCTGGCTCGTCAGAGTCAGAAGGTAAGGA----------TT------ACACA----------TA----------TTACC--------ACAAAGGGTAAAAGTAT--ATG-ATCTCTAATAGATCTATC---CT--TTCT-ACCCAATCCATAGAGCAAGAACAAGAAGCAGCACCAGCAGCTCTGCCGCAGTGCCATCAAGCGGG
droEug1	scf7180000409466:2181695-2181864 +		ATGCGGCTGCCCAGCTGAAGCAGCAGACGCTGGCTCGTCAGAGCCAGAAGGTAAGGA----------A------G----------AG----------GAGCAA--------TGATGAGTTGA--CTT-GTTCCTAATCTA--TATT---CA--CTTT-ATTTAACCTTCAGAGCAACAACAAGAAGCAGCACCAGCAGCTCTGCCGCAGTGCCATTAAGCGGG
droBia1	scf7180000302428:10050211-10050402 -		ATGCGGCCGCCCAGCTGAAGCAGCAGACGCTGGCTCGTCAGAGCCAGAAGGTAAGGA----------TCGTGGGGACACG--TCTTTGTGGGGAAATGTTCCGG-GT-T--T----------TCG-TGAGTTGA--ATAATTTCCTAAT--------C---CT--CTCC-GCCTCACCCGCAGAGCAACAACAAGAAGCAGCACCAGCAGCTCTGCCGCAGTGCCATCAAGCGGG
droTak1	scf7180000415941:290531-290639 +		AGTTTTTTGT----------**--------**----------**----------**-----GAATTGA--CTT-GTTTCTAATCCATATATT---GC--TCTC-ATTTCACCCACAGAGCAACAACAAGAAGCAGCACCAGCAGCTCTGCCGCAGTGCCATCAAGCGGG
droEle1	scf7180000491249:5307459-5307548 +		T----------**--------**----------**----------**----------AATCCTAATCAATATATC---CA--CTTT-ATCCCATCCACAGAGCAACAATAAGAAGCAGCACCAGCAGCTCTGCCGCAGTGCCATCAAGCGGG
droRho1	scf7180000780120:38108-38229 -		AAA----------AA----------CA-----A----------TTTAAAATT-T--T----------TGGTAAAATTGA--CTT-ATGCCTAATCCAGATATC---CA--CTTT-ATGCCATCCACAGAGCAACAACAAGAAGCAGCACCAGCAGCTCTGCCGCAGTGCCATCAAGCGGG
droFic1	scf7180000454065:1168601-1168716 -		AAA----------AA----------TT-----A----------TTTAA-CTGT--T----------TGG-TAAATTGA--TTA-GCATTTAATCTATATAAT---T-------TTTGTATCTCCAGAGCAACAACAAGAAGCAGCACCAGCAGCTCTGCCGCAGTGCCATCAAGCGGG
droKik1	scf7180000302486:489692-489850 -		ATGCGGCCGCTCAGCTGAAGCAGCAGACGCTGGCTCGTCAGAGCCAGAAGGTAAGGA----------TT------A-ACAAGGCTA----------TATAA---------TAAATAGAGTTTAA--T---TAA--------ATT---T-------CGCCAATTTTTAGAGCAACAACAAGAAGCAGCACCAGCAGCTCTGCCGCAGCGCCATTAAGCGGG
droAna3	scaffold_13337:2500252-2500416 +		ATGCGGCCGCTCAGCTGAAGCAGCAAACTCTGGCTCGTCAGAGCCAGAAGGTAAGGACATT----------**--------**----------TTAA--TCC--TTCGAA---------TAAAAA---------TAAGAAAAATGT--ATA-ATCT-----T---------T-------GATGTATCCATAGAGCAACAATAAGAAGCAGCACCAGCAGCTGTGCCGCAGCGCCATCAAGCGGG
droBip1	scf7180000396741:253622-253779 -		ATGCGGCCGCTCAGCTCAAGCAGCAAACTCTGGCTCGACAGAGTCAGAAGGTAAGCCCACT----------**--------**----AAGGAT----------TAAAAA---------TAGGGAAAATTTT--G-ATTAAA----------T-------AATTTATCCACAGAGCAACAATAAGAAGCAGCACCAGCAGCTGTGCCGCAGCGCCATCAAGCGGG
dp5	XR_group8:2511666-2511836 +		ATGCGGCGGCCCAATTGAAGCAGCAGACTCTGGCACGCCAAAGCCAGAAGGTAATGCCACCAGAATTCTTCACCATTTCTGTGGC--------**--------**----------**----------**-------AGCACAT--T--T---GCTAATG---------T---CA--CTCTCTTTCCTCCTCTAGAGCAACAACAAGAAGCAGCATCAGCAGCTGTGCCGCAGCGCCATCAAGCGGT
droPer2	scaffold_24:538240-538410 -		ATGCGGCGGCCCAATTGAAGCAGCAGACTCTGGCACGCCAAAGCCAGAAGGTAATGCCACCAGATTTCCTTACCATTTCTGTGGC--------**--------**----------**----------**-------AGCACAT--T--T---GCTAATG---------T---CG--CTCTCTTTCCTCCTCCCAGAGCAACAACAAGAAGCAGCATCAGCAGCTGTGCCGCAGCGCCATCAAGCGGT
droWil2	scf2_1100000004511:10892276-10892445 -		ATGCGGCGGCTCAGCTGAAGCAACAGACTCTGGCTCGCCAAAGCCAGAAGGTAAATA----------CA------CACATATCCA----------TACTTCCTGCTCTTAAACTAATCCATCGCAA---------TTATTGA-----T---T----------**--------**----------TACCTTTTTAGAGCAACAACAAGAAGCAGCACCAGCAGCTATGTCGCAGCGCCATCAAACGTT
droVir3	scaffold_13049:32913-33089 -		ATGCGGCGAGAAGTTGAAGCAGCAGACGCTGGCTCGTCAAAGCCAGAAGGTGAGTA----------GC-----C-GCAAATCTG----------**----------**-TACT---------CGGAAGAAGCGCCT---=--ACCTAATCTCGAACTCTTTGT--CTCT-CTCTCCCATGCAGAGCCTCGGCAAGCAGCAGCATCAGCAGCTCTGCCGCAGCGCCATGAAGCGCG
droMoj3	scaffold_6680:1094850-1095027 +		ATGCGGCGGCAGAGCTGAAGCAGCAGACCTTGGCTCGTCAAAGCCAGAAGGTGGGTC----------GC-----CCATTGCT----------**----------**TTGACATATACA---CCAAAGA-----------TACTAATCTCTCTCTCTCTCCTCTCTCTCTCTCTGTGTTAGAGCCACAACAAGAAGCAGCATCAGCAGCTGTGCCGCAGCGCCATTAAGCCG
droGri2	scf7180000780120:38108-38229 -		T----------**--------**----------**----------**----

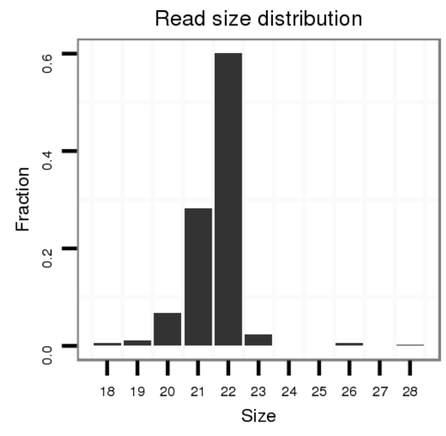
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dya_66	**v2_chr2h_random_005:484337-484398 -**	**confident**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

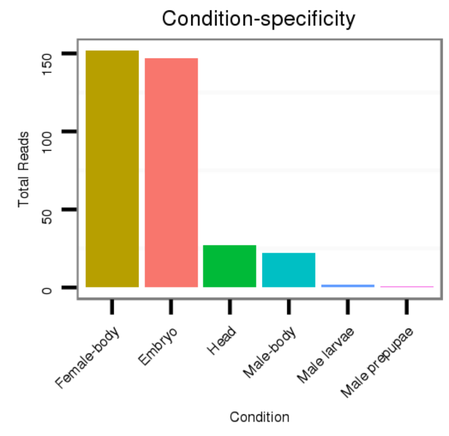
Legend: mature star **mismatch in alignment** mismatch in read

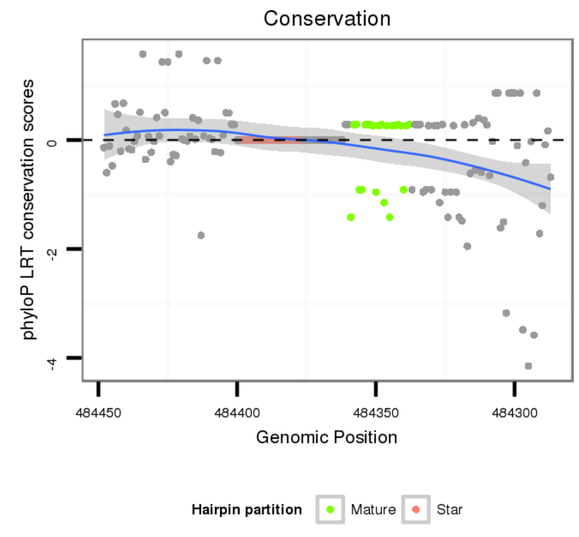
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

Repeatable elements

Name	Class	Family	Strand
DNAREP1_DM	RC	Helitron	+

Sense Strand Reads

hide 3p reads show mid mismatch reads

AGTATTTAGCGCAGTAAAGGAGACATTTTCTACTGTATAATGTATAAAATTGTCACGCCGATTCCTTCGAAGAATGTTTTGCTTCTTTTCTTCGAAAGAGTTGCCGTGACAATTTTAGACGTTAGAGACCAAGCGTTGCCAAAATATTTTTATGATAACGAT **********	Read size	# Mismatch	Hit Count	Total Norm	Total	M056 embryo	M043 female body	V120 male body	M026 head	V046 embryo	V058 head	SRR1275484 Male prepupae	SRR1275488 Male larvae	V052 head
.....CTTCGAAAGAGTTGCCGTGACA.....	22	0	1	101.00	101	21	56	13	1	2	6	1	1	0
.....TGTCACGCCGATTCCTTCGAAG.....	22	0	1	57.00	57	27	26	0	0	4	0	0	0	0
.....TCACGCCGATTCCTTCGAAGAA.....	22	0	1	47.00	47	32	10	0	0	4	1	0	0	0
.....TTCGAAAGAGTTGCCGTGACA.....	21	0	1	35.00	35	11	22	0	2	0	0	0	0	0
.....TCACGCCGATTCCTTCGAAGA.....	21	0	1	33.00	33	17	11	2	0	3	0	0	0	0
.....CTTCGAAAGAGTTGCCGTGAC.....	21	0	1	17.00	17	8	3	0	4	0	1	0	1	0
.....TCGAAAGAGTTGCCGTGACAAT.....	22	0	1	15.00	15	11	3	1	0	0	0	0	0	0
.....TCGAAAGAGTTGCCGTGACA.....	20	0	1	9.00	9	1	1	0	6	0	1	0	0	0
.....TCACGCCGATTCCTTCGAAG.....	20	0	1	7.00	7	3	3	0	0	1	0	0	0	0
.....TTCGAAAGAGTTGCCGTGACAAT.....	23	0	1	6.00	6	2	2	0	1	0	0	1	0	0
.....TGTCACGCCGATTCCTTCGAA.....	21	0	1	5.00	5	2	2	0	0	0	0	0	0	1
.....TGTCACGCCGATTCCTTCGA.....	20	0	1	5.00	5	3	1	0	0	1	0	0	0	0
.....TCGAAAGAGTTGCCGTGACAA.....	21	0	1	5.00	5	0	1	2	1	0	0	0	0	1
.....TTCGAAAGAGTTGCCGTGACAA.....	22	0	1	5.00	5	0	4	1	0	0	0	0	0	0
.....TCACGCCGATTCCTTCGAAGAAA.....	23	1	1	4.00	4	4	0	0	0	0	0	0	0	0
.....TCGAAAGAGTTGCCGTGACAAC.....	22	1	1	3.00	3	3	0	0	0	0	0	0	0	0
.....CTTCGAAAGAGTTGCCGTGACAA.....	23	0	1	3.00	3	0	2	1	0	0	0	0	0	0
.....AAAGAGTTGCCGTGACAATTTT.....	22	0	1	3.00	3	2	1	0	0	0	0	0	0	0
.....TGTCACGCCGATTCCTTCGAAGT.....	23	1	1	3.00	3	1	2	0	0	0	0	0	0	0
.....AATTGTCACGCCGATTCCTTCGA.....	23	0	1	2.00	2	1	0	0	0	1	0	0	0	0
.....TTCGAAAGAGTTGCCGTGAC.....	20	0	1	2.00	2	0	0	0	1	0	1	0	0	0
.....TCGAAAGAGTTGCCGTGACAATT.....	23	0	1	2.00	2	1	1	0	0	0	0	0	0	0
.....TTAGACGTTAGAGACCAAGCGT.....	22	0	1	2.00	2	1	0	1	0	0	0	0	0	0
.....GTCACGCCGATTCCTTCGAAG.....	21	0	1	2.00	2	0	2	0	0	0	0	0	0	0
.....CACGCCGATTCCTTCGAAGAAA.....	22	1	1	2.00	2	2	0	0	0	0	0	0	0	0
.....CACGCCGATTCCTTCGAAG.....	19	0	1	2.00	2	0	2	0	0	0	0	0	0	0
.....TCACGCCGATTCCTTCGAAGAC.....	22	1	1	2.00	2	2	0	0	0	0	0	0	0	0
.....TCACGCCGATTCCTTCGAAGAAT.....	23	0	1	2.00	2	1	1	0	0	0	0	0	0	0
.....TGTCACGCCGATTCCTTCGAAGA.....	23	0	1	2.00	2	1	1	0	0	0	0	0	0	0
.....GTTGCCGTGACAATTTTAGACGTT.....	24	0	1	2.00	2	1	1	0	0	0	0	0	0	0
.....ATGTTTTGCTTCTTTTCTTCGAAAGA.....	26	0	1	2.00	2	0	2	0	0	0	0	0	0	0
.....GTTGCCGTGACAATTTTAGA.....	20	0	1	1.00	1	0	0	0	0	1	0	0	0	0
.....TACTGTATAATGTATAAAATTGTCACGCC.....	29	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....GTTGCCGTGACAATTTTAGAC.....	21	0	1	1.00	1	0	0	0	1	0	0	0	0	0
.....ATTGTCACGCCGATTCCTTCGA.....	22	0	1	1.00	1	0	0	0	0	1	0	0	0	0
.....TCACGCCGATTCCTTCGAAGAAAA.....	24	2	1	1.00	1	1	0	0	0	0	0	0	0	0
.....CTTCGAAAGAGTTGCCGTGG.....	20	1	1	1.00	1	0	0	0	1	0	0	0	0	0
.....AATGTTTTGCTTCTTTTCT.....	19	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....GTTAGAGACCAAGCGTTGCCAAAATATTT.....	29	0	1	1.00	1	0	0	1	0	0	0	0	0	0
.....TTGCTTCTTTTCTTCGAAAGA.....	21	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....ATTTTAGACGTTAGAGACCAAGCGT.....	25	0	1	1.00	1	0	0	1	0	0	0	0	0	0
.....ATTTTAGACGTTAGAGACCAAG.....	22	0	1	1.00	1	0	0	1	0	0	0	0	0	0
.....TTCTACTGTATAATGTATAAAATTGTCA.....	28	0	1	1.00	1	0	1	0	0	0	0	0	0	0
.....CTTCGAAAGAGTTGCCGTGACT.....	22	1	1	1.00	1	0	1	0	0	0	0	0	0	0
.....GTCACGCCGATTCCTTCGAAGA.....	22	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....GTTAGAGACCAAGCGTTGCC.....	20	0	1	1.00	1	0	0	1	0	0	0	0	0	0
.....CTTCGAAAGAGTTGCCGTGAGC.....	22	2	1	1.00	1	1	0	0	0	0	0	0	0	0
.....TTCGAAAGAGTTGCCGTGT.....	19	1	1	1.00	1	0	1	0	0	0	0	0	0	0
.....GTCACGCCGATTCCTTCGAAGAA.....	23	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....TTCGAAAGAGTTGCCGTGACAATA.....	24	1	1	1.00	1	0	1	0	0	0	0	0	0	0
.....TGTCACGCCGATTCCTTCGAAA.....	22	1	1	1.00	1	1	0	0	0	0	0	0	0	0
.....AATTGTCACGCCGATTCCTTCG.....	22	0	1	1.00	1	0	1	0	0	0	0	0	0	0
.....ATGTTTTGCTTCTTTTCTTCGAAAGAGT.....	28	0	1	1.00	1	0	0	1	0	0	0	0	0	0
.....TGTCACGCCGATTCCTTCGAAGC.....	23	1	1	1.00	1	1	0	0	0	0	0	0	0	0
.....TTGCTTCTTTTCTTCGAAA.....	19	0	1	1.00	1	0	1	0	0	0	0	0	0	0
.....CACGCCGATTCCTTCGAAGAA.....	21	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....GAAAGAGTTGCCGTGACAATTTT.....	23	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....TTTAGACGTTAGAGACCAAGCGT.....	23	0	1	1.00	1	0	0	1	0	0	0	0	0	0
.....TGTCACGCCGATTCCTTCGAATT.....	23	2	1	1.00	1	0	1	0	0	0	0	0	0	0
.....TCGAAAGAGTTGCCGTGACT.....	20	1	1	1.00	1	0	0	1	0	0	0	0	0	0
.....TCACGCCGATTCCTTCGAAA.....	20	1	1	1.00	1	1	0	0	0	0	0	0	0	0
.....GAAAGAGTTGCCGTGACA.....	18	0	1	1.00	1	0	0	1	0	0	0	0	0	0
.....CTTCGAAAGAGTTGCCGT.....	18	0	1	1.00	1	0	1	0	0	0	0	0	0	0
.....TTCGAAAGAGTTGCCGTGG.....	19	1	1	1.00	1	0	0	0	1	0	0	0	0	0
.....TTCTTCGAAAGAGTTGCCGT.....	20	0	1	1.00	1	0	0	1	0	0	0	0	0	0
.....TAGACGTTAGAGACCAAG.....	18	0	1	1.00	1	0	0	0	1	0	0	0	0	0

Anti-sense strand reads

TCATAAATCGCGTCATTTCCTCTGTAAAAGATGACATATTACATATTTTAACAGTGCGGCTAAGGAAGCTTCTTACAAAACGAAGAAAAGAAGCTTTCTCAACGGCACTGTTAAAATCTGCAATCTCTGGTTCGCAACGGTTTTATAAAAATACTATTGCTA **********	Read size	# Mismatch	Hit Count	Total Norm	Total	M056 embryo	M043 female body	M026 head	V120 male body	V058 head
.....ACAGTGCGGCTAAGGAAGCTT.....	21	0	1	2.00	2	2	0	0	0	0
.....TTAACAGTGCGGCTAAGGAAGCTT.....	24	0	1	2.00	2	0	1	0	1	0
.....AGCTTTCTCAACGGCACTGTT.....	21	0	1	1.00	1	1	0	0	0	0
.....AACAGTGCGGCTAAGGAAGCTT.....	22	0	1	1.00	1	1	0	0	0	0
.....GCTTTCTCAACGGCACTGTTA.....	21	0	1	1.00	1	1	0	0	0	0
.....AGCTTTCTCAACGGCACTGTTA.....	22	0	1	1.00	1	1	0	0	0	0
.....TTAACAGTGCGGCTAAGGAAGCT.....	23	0	1	1.00	1	1	0	0	0	0
.....AAGAAGCTTTCTCAACGGCACT.....	22	0	1	1.00	1	0	1	0	0	0
.....AAAGAAGCTTTCTCAACGGCACT.....	23	0	1	1.00	1	0	1	0	0	0
.....AGTGCGGCTAAGGAAGCTTCT.....	21	0	1	1.00	1	1	0	0	0	0
.....GGAAGCTTTCTCAACGGCACT.....	21	1	1	1.00	1	0	0	1	0	0
.....ACAGTGCGGCTAAGGAAGCTTC.....	22	0	1	1.00	1	0	1	0	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droYak3	v2_chr2h_random_005:484287-484448 -	dya_66	AGTATTTAGCGCAGTAAAGGAGACATTTTCTACTGTATAATGTATAAAATTGTCACGCCGATTCCTTCGAAGAATGTTTTGCTTCTTTTCTTCGAAAGAGTTGCCGTGACAATTTTAGACGTTA-GAGACCAA----G------CGTTGCCAAAATATTTTTATGATAACGAT
droEre2	scaffold_4929:23708454-23708534 +		TTTTT-CAAAAGTGTGGGCATGACAGTTTCCGCCGTTTCTGGCA----------T--AAGTGTTT-GTGG-CAAAGTGTTTTTTCAAATCGAT
droSec2	scaffold_39:271435-271506 -		TTTTT-CAAAAGTGTGGGCGTGCAGTTCTGGTCGGTTCTGGG----------T----GCAAAAGTTTTTTAGCAAATCGAC
droSim2	21:20690807-20690881 +		TTATT-TAAAAGTGTGGCCGTGACCGTTTT-GTAGGTTTGAGAA----------GAG----A-----CGTGGCCAAAGGGTTTTTGGTATACCGAT
dm3	chr3LHet:1227193-1227288 +		AAA----------AATGTATTAA----------TTGTTTAAAGTGTGGCGTGGCAGTTTAGGGCGGTTTCTGTGG--GTAAGGGTGGGCTTGG-CAAAAAATTTCTTCGAGATTGAT
droBia1	scf7180000297215:8504-8548 -		AGTTTGCTACGCAGTGAAGGAGACGTTTCGGACCCATAAAGTATA----------T----T------
droTak1	scf7180000413074:3933-3983 -		AGTTTGCAACGCAGTGAAGGAGACGTTTCGGACCCATAAAGTATA----------T----T------TATTT
droEle1	scf7180000490566:209382-209427 -		AGTTTGCAACGCAGTGAAGGAGACATTTCGGACCTATAAAGTATA----------T----T------
droRho1	scf7180000775655:3054-3099 -		AGTGTGCAACGCAGTAAAGGAGACATCTCGGACCTATAAAGTATA----------T----T------
~~droFic1~~	~~scf7180000453555:9271-9315 +~~		~~AGTTTGCAACGCAGTGAAGGAGACGCCTCAGACCCCA-AATGTATA~~
droKik1	scf7180000300513:2385-2430 +		AGTTTGCAACGCAGTGAAGGAGCGTTTCGGACCCTATAAAGTATA----------T----T------
droAna3	scaffold_12933:45548-45593 +		AGTGTGCAACGCAGTAAAGGAGACATCTCGGACCCATAAAGTATA----------T----T------
droBip1	scf7180000395516:9149-9196 +		AGTGTGCAACGCAGTGAAGGAGACATCTCGGACCCTATAAAGTATA----------T----T------AA
droPer2	scaffold_3647:478-512 -		GGGGCGAGTT--T----------T----T------TGAAATATTTTTGTAGCAGTGAC

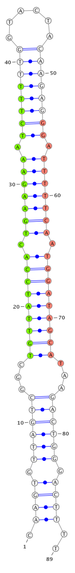
Generated: 09/08/2015 at 07:39 PM

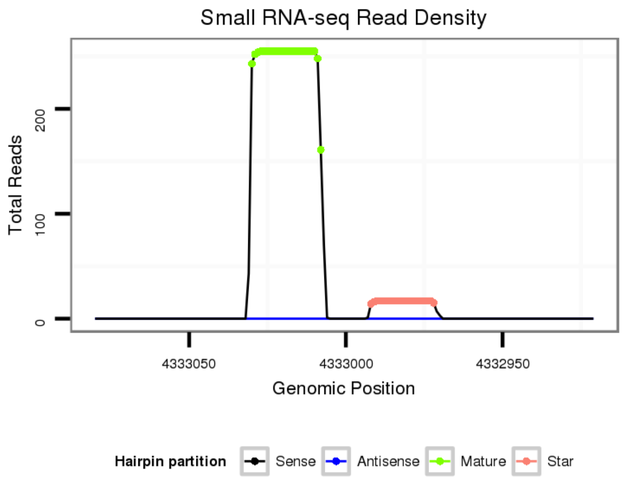
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

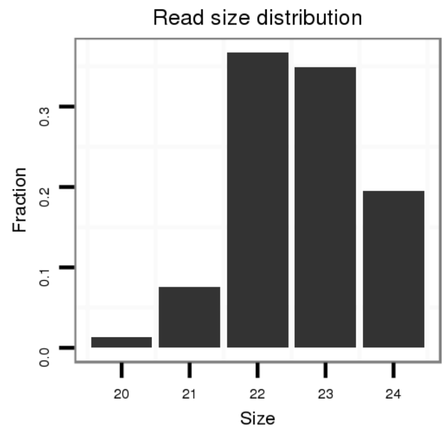
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dya_60	**2R:4332971-4333030 -**	**confident**	**Canonical miRNA**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

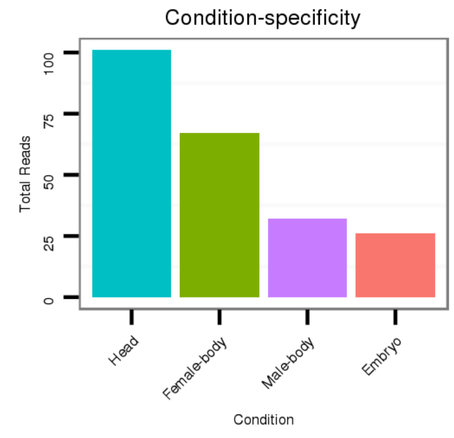
Legend: mature star **mismatch in alignment** mismatch in read

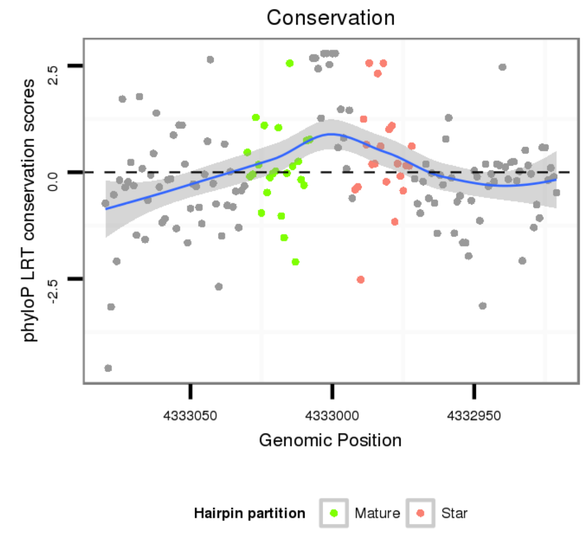
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dyak\Mhc-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

GCTTGTTATTGAAGTTTCTAGTTCAGAGTGAACCTCAAGTGTTAGTCGGCTGTTATCCACTGAAGAAATCTTTTTGGTACTACAAGAGGGATTTTTCAATGGATAGCATAAGACTGGGACTTTTGCATGACCACAAGCACTTCAATAGCTTGAAATGTAG **********.((((.(((((((...(((((((((.(((((((.(((((((.....)))))))).)))))))).)))))))))...)))))))..))))..**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M026 head	M043 female body	M056 embryo	V120 male body	V058 head	V046 embryo	V052 head	SRR1275486 Male prepupae
.....TGTTATCCACTGAAGAAATCTTT.....	23	0	1	77.00	77	22	28	5	19	1	2	0	0
.....TGTTATCCACTGAAGAAATCTT.....	22	0	1	72.00	72	43	9	11	6	1	2	0	0
.....TGTTATCCACTGAAGAAATCTTTT.....	24	0	1	44.00	44	27	10	3	1	1	1	1	0
.....CTGTTATCCACTGAAGAAATCTTTT.....	25	0	1	22.00	22	6	3	12	1	0	0	0	0
.....CTGTTATCCACTGAAGAAATCTT.....	23	0	1	12.00	12	2	5	4	0	1	0	0	0
.....CTGTTATCCACTGAAGAAATCTTT.....	24	0	1	9.00	9	0	4	2	1	1	1	0	0
.....TGTTATCCACTGAAGAAATCT.....	21	0	1	7.00	7	2	1	2	2	0	0	0	0
.....GGATTTTTCAATGGATAGCAT.....	21	0	1	7.00	7	0	6	0	1	0	0	0	0
.....GTTATCCACTGAAGAAATCTTT.....	22	0	1	5.00	5	0	5	0	0	0	0	0	0
.....GGATTTTTCAATGGATAGCATA.....	22	0	1	3.00	3	0	2	0	1	0	0	0	0
.....GTTATCCACTGAAGAAATCTT.....	21	0	1	3.00	3	0	3	0	0	0	0	0	0
.....TTATCCACTGAAGAAATCTTTT.....	22	0	1	2.00	2	2	0	0	0	0	0	0	0
.....GGATTTTTCAATGGATAGCA.....	20	0	1	2.00	2	1	0	0	1	0	0	0	0
.....CTGTTATCCACTGAAGAAATCTTTC.....	25	1	1	2.00	2	0	0	2	0	0	0	0	0
.....TGTTATCCACTGAAGAAATCTTA.....	23	1	1	1.00	1	1	0	0	0	0	0	0	0
.....GATTTTTCAATGGATAGCAT.....	20	0	1	1.00	1	0	0	0	1	0	0	0	0
.....GGATTTTTCAATGGATAGCATAA.....	23	0	1	1.00	1	0	0	1	0	0	0	0	0
.....TGTTATCCACTGAAGAAATCTTTTA.....	25	1	1	1.00	1	0	0	0	0	1	0	0	0
.....TATCCACTGAAGAAATCTTTTT.....	22	0	1	1.00	1	0	1	0	0	0	0	0	0
.....GTTATCCACTGAAGAAATCTTTT.....	23	0	1	1.00	1	0	1	0	0	0	0	0	0
.....GATTTTTCAATGGATAGCATAA.....	22	0	1	1.00	1	0	1	0	0	0	0	0	0
.....TTATCCACTGAAGAAATCTTTTTT.....	24	1	1	1.00	1	1	0	0	0	0	0	0	0
.....GGGATTTTTCAATGGATAGCATA.....	23	0	1	1.00	1	0	1	0	0	0	0	0	0
.....ATTTTTCAATGGATAGCATAA.....	21	0	1	1.00	1	0	1	0	0	0	0	0	0
.....TGTTATCCACTGAAGAAATCTTC.....	23	1	1	1.00	1	0	0	1	0	0	0	0	0

Anti-sense strand reads

CGAACAATAACTTCAAAGATCAAGTCTCACTTGGAGTTCACAATCAGCCGACAATAGGTGACTTCTTTAGAAAAACCATGATGTTCTCCCTAAAAAGTTACCTATCGTATTCTGACCCTGAAAACGTACTGGTGTTCGTGAAGTTATCGAACTTTACATC **********.((((.(((((((...(((((((((.(((((((.(((((((.....)))))))).)))))))).)))))))))...)))))))..))))..**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V046 embryo

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droYak3	2R:4332921-4333080 -	dya_60	GCTTGTTATTGAAGTTTCTAGTT-CAGA-GT-GAAC----------CTCAAGT-GTTAGT-CGGCTGTTATCCACTGAAGA----AATC-TTTTTG----------GTACTACAAGAGG---G-ATTTTTCAATGGA-TAGCATAAGACTGGGACTTTTGCATG------ACC-ACAAGCACTTCAA---TAG-CTTGAAATGTAG
droEre2	scaffold_4845:19839670-19839829 +	der_201	GTCTGTTATTGAAGTTTCTAACT-TAGG-GT-CGAC----------CTAAAGT-ATTAGT-CGGCTGTTACCCAATGAAGA----AATC-TTTTTG----------GTACTACAAAAAG---G-GTTTTTCAATGGA-TAGCATAAGACTGGACTTTTGCATG------ACC-CAAAACACTTCAA---TAA-CTTAGAATGTAG
droSec2	scaffold_7:415740-415894 +	dse_1849	GTCTTATGGTCGAG--T---ACT-TATG-GT-CGAC----------CTAAAGT-GTTAGT-CAACTGCTACCCAATGAAGA----AATC-TTCTTG----------GTACTACAAGAAG---G-GTTTTTCAATGGA-TAGCATAAGACTGGGACTTTGTCATG------ACC-CTATACATTTCAA---TAG-CTTATAATGTAG
droSim2	21:16335692-16335846 +		GTCTTATGGTCGAG--T---ACT-TATG-GT-CGAT----------CTAAAGT-GTTAGT-CAACTGCTACCCAATGAAGA----AATC-TTCTTG----------GTACTACAAGAAG---G-GTTTTTCAATGGA-TAGCATAAGCTGGGACTTTGTCCTG------ACC-CTATACACTTCAA---TAG-CTTATAATGTAG
dm3	chr2L:16768935-16769098 +	dme_456	GCTAT----TGAAGAGTC----T-TATG-GT-CGAC----------CTAAAGT-GTTAGT-CAATTGTTACCCAATGGGAA----AATC-TTCTTGGTACTACTACTACTACTACAAGAAG---G-GTTTTTCAATGGA-TAGCATAAGACTGGGACTTTGTCATG------ACC-TCATACACTTCAA---TAG-CTTATAATGTAG
droEug1	scf7180000408961:341899-342044 +		GGCTTA----------ATT-AAAG-GA-TTTT----------ATAAAGT-TCTCGC-TGCATGCTACCCTGGAAAA----ACTC-TTTTTG----------GTACTACGGAAAG---A-TTCTTTCGAAGGG-TACCAAGAGCCAGGAATTTT-TAATT------ACC-CAAGAAACTTCAA---TGCCTTACAACGTAG
droBia1	scf7180000301468:936842-936988 +		AAGCC----------T---GTA-AAGG-GT-CTTT----------CCAAAGA-GCTCGT-CCCTTGTTATCTCTGGACAA----ATTC-TTTTTG----------GTACTAAAAAAG---G-GTTTATCAATGGG-TAGCAATGAGCCGCAGCTTGAAAGTC------ACC-CCGAGAAACTTCAA---TAACCCCCCTATGTAG
droTak1	scf7180000415914:515714-515874 +		GTCGGTTATTGTAGTAACTATCTTAAGG-GT-GATT----------CTAAAAA-AACTGT-CACTTGTTATCCCGGGTTAA----ATTC-TTTTTG----------GTACTAAAAAAG---G-GTTTTTCAATGGC-TAACAAGGGCGCGGGATTTGGAAACC------GCC-CGAGAAACTTCAA---TAA-CCTTTTATGTAG
droEle1	scf7180000490579:573571-573710 -		GATCTTTC----------TTAAAG-GT-TGTT----------CAAAAGT-GTTTGC-AGCTTGTTACCCATGCGCAA----AGTC-TTTTTG----------GTACTACAAAAAG---G-TTATTTCAATGGC-TAGCAAGAGCCAGGGATTTTTAAACA------A-C-CAAGGAACTTTAT---TAG-G----AATGT--
droRho1	scf7180000780103:213379-213537 -		GGGTT--ATTCAAGGATCTTTCTGAAAG-GT-TGTT----------CCGAAGT-GCTTGC-AGCTTGTTGCCCATGGAAAA----AGTC-ATTTTG----------GTACTACAAAAAG---G-GTTTTTCAATGGC-TAGTAAGACGCAGGAATTTTGATACT------ACC-CAAAGAACTTTAA---TAA-CTTGTTATGTAG
droFic1	scf7180000454078:695815-695972 +		GGTTACTAAAGGAA---CTTTTATGAAG-AT-TGTT----------CTAAATC-AGTTGT-CATTTTCCACCCCTGGAAGA----AGTC-TTTTTG----------GTACTACAGAAAG---G-GTTTTTCAAGGGG-TGGCCAATGGCATAGATTTGAAGTCC------ACT-CTAAGAACTTTAG---TAA-CTCATTATGTTC
droKik1	scf7180000302472:34996-35145 +		CTTTGTTA----------G-GGG-GT-AGCT----------C---ATCAATG-GCTCAC-CCTTTGTTACCTCTGGCAA----GGTA-ATTTTG----------GTACTACAAAATCC---A-TTTTGTCAATGGG-TTACAAGGGAAAGAAGAAGGGGCCACCC----CTA-CCTAGAACTCCAAGAGCTC-TCCTTACTAGAG
droAna3	scaffold_12916:7328515-7328663 +		TCTTTA----------G--AG-GC-GTTT----------CATGGGAAAAT-AATTGTGTATTTGTTGGTGCTTGACAA----AATCGGTTTTG----------GTACTACAAGACT---TACTTTTTCAAGGGT-CAACAAGTAGCCATTATTTTAC-ATA--CGAAGCCCTAAAGACCTCCAA---TAT-CTT---ATGAAA
droBip1	scf7180000396566:498307-498470 +		TTATT----GAAGAT-CTTTTA-AGCG-GT-GAAT----------GGCAAAATATATAGCCTATTTATTGATCTTTGATAA----AATACGTTTTG----------GTACTAAATACT---TACTTTTTCAAAGGT-CAACAAGTAACTATTATTTTGCCTAT--TAAAGCCAAAAAGAACTTTAA---TAT-CTTTTGAAAATG
dp5	4_group3:3011891-3012051 -		ATTGGTTCTTAGAGCTCCTAATT-AGGGGT-TGTCT----------CGAAAGA-AATTGC-TGGAAGTTACCTCTTTCCAA----GACCTGTTTTG----------GTACTACAAAATAA---G-GTTTTGCAAATGTGTGCAA-CAGCAAGGTCTTCGAGAGT------TCC-CTGTAGAA--TGA---GCC-CTAAGAATGATG
droPer2	scaffold_1:4498589-4498749 -		ATTGGTTCTTAGAGCTCCTAATT-AGGGGT-TGTCT----------CGAAAGA-AATTGC-TGGAAGTTACCCCTTTCCAA----GACCTTTTTTG----------GTACTACAAAATAA---G-ATTTTGCAAATGTGTGCAA-CAGCAAGGTCTTCGAGAGT------TCC-CTGTAGAA--TGA---GCC-CTAAGAATGATG
droWil2	scf2_1100000004577:1126300-1126418 +		AATTTT----GTAAATCA-----------------TAATGAAGAAATTGAAAGTTTTT----GAACAAA-CATTTT-TTC----------TTA-TATTTG----------GTACTACAAATAT---G-----------AATGAAAA-------C-T--T-TGT-ACAAATGTTCAAA---CTC-ATTATGATATAT
droVir3	scaffold_12963:10115743-10115882 +		GCCTA----------G-GTG-GTTCGTC----------TAGAAGG-ACTCAA-TATTGCCTGCCCTTTGCTAA----GCCTTCAC---------TTTTGGTACTACAAAAGG---A-GCTTAACAAATGG-TGGTCGGTGCCGAGGCCTTTTTGCGA------GAA-TTGAGCACTTTGA---AAA-GCTAATG----C
droMoj3	scaffold_6500:2796056-2796182 +		GAGTTTTA----------T--TG-GT-TGGA----------CTGG-GT-G--CAA-CATGAACTGACATCGCCTAAAACAACA-TTTTTG----------GTACTACAAAATACTTGCTTTAGCCAATAT-CATCTAA-TCCGCACCCTTTTGGTT------------------------TAG---ATTGTCTCA
droGri2	scaffold_15252:13249793-13249926 +		CCTAA----------T--TG-GC-TCAA----------TTAAAGT-TAATTC-CATTAACTGACATTTGGTGA----ATGA-TTTTTG----------GTACTACAAATG---A-CTTTAACAAATGGCCAGTTAG-CGTGAAGACTTTGTG--A------ACC-GAAAGGTCTTTTG---AAA-CTTGTG----AG

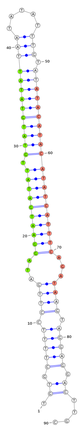
Generated: 09/08/2015 at 07:40 PM

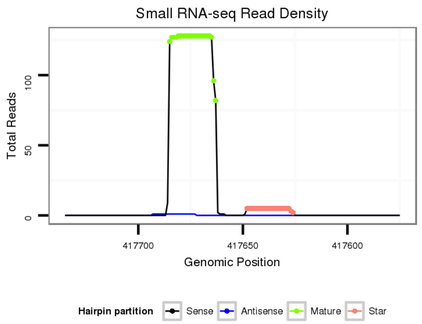
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	2

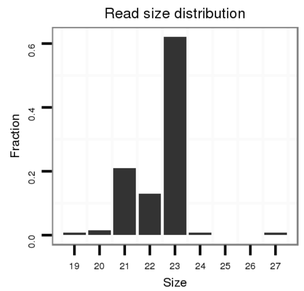
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dya_68	**3R:417625-417685 -**	**confident**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser [Cornell Mirror]]

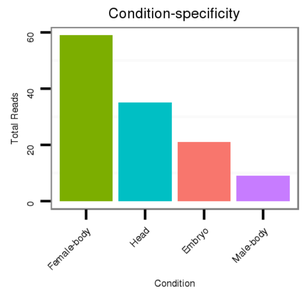
Legend: mature star **mismatch in alignment** mismatch in read

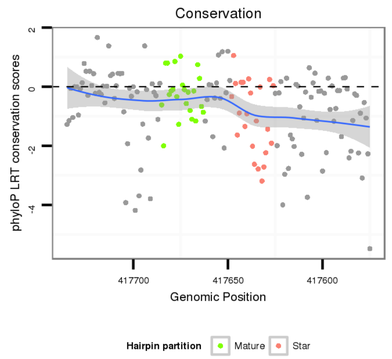
Predicted structure











Show Alternate Folds

Flybase annotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

GAACTCGTCTACAGCGTTCTCTCTTGTTTTTACCTTGTGCTTTTCCTTGATAGGAATGATATTGTATGTATATTAATATATTTGTATATACATACATATCATTTCAGATAAGTAGGAGGACTTGCGTCTTAACTAAACATATGAACAAAGTATTCAGCGGG **********.((.(((((.((((...((((((((((.((((((((((((.....))).))))))))))))))))))...)))))).))))))..))....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M043 female body	V058 head	V046 embryo	M026 head	M056 embryo	V120 male body	V052 head
.....TAGGAATGATATTGTATGTATAT.....	23	0	1	75.00	75	37	7	13	6	4	5	3
.....TAGGAATGATATTGTATGTAT.....	21	0	1	25.00	25	5	8	0	5	1	3	3
.....TAGGAATGATATTGTATGTATA.....	22	0	1	12.00	12	8	1	0	0	2	1	0
.....ATAGGAATGATATTGTATGTAT.....	22	0	1	5.00	5	0	1	0	0	2	0	2
.....TAGGAATGATATTGTATGTATATA.....	24	1	1	2.00	2	2	0	0	0	0	0	0
.....AGGAATGATATTGTATGTATAT.....	22	0	1	2.00	2	2	0	0	0	0	0	0
.....ATAGGAATGATATTGTATGTATAT.....	24	0	1	2.00	2	0	0	0	0	1	1	0
.....ATACATACATATCATTTCAGATA.....	23	0	1	2.00	2	1	0	1	0	0	0	0
.....ATAGGAATGATATTGTATGTATA.....	23	0	1	2.00	2	1	1	0	0	0	0	0
.....ATACATACATATCATTTCAGAT.....	22	0	1	1.00	1	1	0	0	0	0	0	0
.....TATACATACATATCATTTCAGA.....	22	0	1	1.00	1	1	0	0	0	0	0	0
.....AGGAATGATATTGTATGTATATA.....	23	1	1	1.00	1	1	0	0	0	0	0	0
.....AATGATATTGTATGTATAT.....	19	0	1	1.00	1	1	0	0	0	0	0	0
.....TAGGAATGATATTGTATGTATAA.....	23	1	1	1.00	1	1	0	0	0	0	0	0
.....TAGGAATGATATTGTATGTA.....	20	0	1	1.00	1	0	0	0	1	0	0	0
.....TAGGAATGATATTGTATGTATATTAAT.....	27	0	1	1.00	1	0	0	0	1	0	0	0
.....AGGAATGATATTGTATGTAT.....	20	0	1	1.00	1	1	0	0	0	0	0	0
.....TAGGAATGATATTGTATGTATATT.....	24	0	1	1.00	1	1	0	0	0	0	0	0
.....ATACATACATATCATTTCAGA.....	21	0	1	1.00	1	1	0	0	0	0	0	0

Anti-sense strand reads

CTTGAGCAGATGTCGCAAGAGAGAACAAAAATGGAACACGAAAAGGAACTATCCTTACTATAACATACATATAATTATATAAACATATATGTATGTATAGTAAAGTCTATTCATCCTCCTGAACGCAGAATTGATTTGTATACTTGTTTCATAAGTCGCCC **********.((.(((((.((((...((((((((((.((((((((((((.....))).))))))))))))))))))...)))))).))))))..))....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M043 female body	V120 male body
.....AAGGAACTATCCTTACTATAA.....	21	0	1	1.00	1	1	0

Show Alignment With Reads

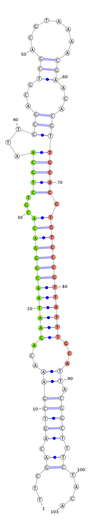
Re-alignment of all predicted orthologs

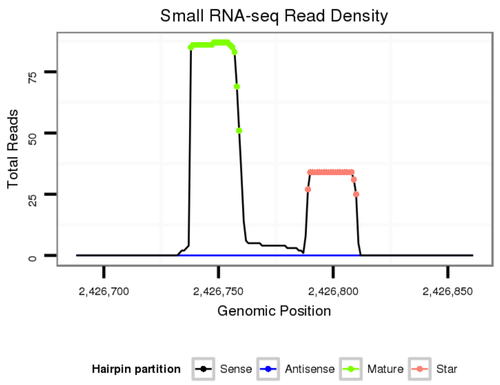
Species	Coordinate	ID	Alignment
droYak3	3R:417575-417735 -	dya_68	GAACTCGTCTACAGC-GTTCTCTCTTGTTTTTACCTTG---TGCTTTT----------C------C--TTGATAGGAATGATATTGTATGTAT----------ATT----------AATATATTTGTATATA-CATA----------CA----TATCA----------TTTCAGAT-------AAGTAGGAGGA----------CTTG----C--GTCTTAACTAAACATA--TGAA------CAAAGTA-TTCAGCGGG
droEre2	scaffold_4784:25382776-25382941 +		GAACTCACCTACAGC-ATCATCCTTGTTTTTTCTTTAAAT-CG---C----------CTTTTATTTAAACAAAATGTATAGTATATACAC----------T----------A-ATGTATATA-----TATGTATAGTATATACACATA----------TC----TATAT----------A-ATGTA-TAGTATATCACATAAG--T----------T--T-------TATATATA--TGTA------TCTAT-T-TATACATAT
droSec2	scaffold_82:50233-50373 +		GAGATCGATATAGC-CTTCTCTCTTGCTTTCGTTTTG---CCATTT----------TTGGAA----------T------T--------AATTGGTAAAAGGTAAT----------GAA----------AATGGCATTTCCTAATG-CTAT----------CT----ATGCT----------TTTCAGAC-------AAA--------T----------TTGCTTTTAA--GTA-----CAACAA--TGAA------AAAACA-TC-----C
droSim2	21:21820034-21820175 +		GAAATCGATATAGC-ATTCTCTCTTGATTTTTTTTATAAA-TA---T----------CTCCGCTACAAGCAAAATATAGG--AC---TA---ATC----------T----------T----CA---ATATATAATATA----------T----------AAT----------AAAGTTA-TAATGTGATAATAGATACAC----------CTTG----C--GTG----------C--CAAGTACGTGCAAAGTA--------T
dm3	chr2RHet:3169079-3169237 +		AAACTCGATATAGC-ATTCTCTCTTGATAGAAATTGACT--TATTT----------T----------CCC---GTT----------T----------AGCATGTATATTTATTACT---ATTGTT----------T----------T----------AA----------TGAAAACT----TACCT----------GTGGAGTTATTTCA---CGAA----------AAGTACGATG----------CAA----T--GTG----GAAAATATA--ACAG------CAAAGAG-TCACAAATT
droEug1	scf7180000408885:21655-21816 +		ACACTCGATATAGC-GTTCTCTCTTGTTTTATGTTTAAAA--TATAT---GCTCGAAATGTATATCTTTCATTTGA----------T----------T----------G--A-T----------A-TACATTTTAAT---T----------T----------TCCGTTTCC----TATTT----------CCCCAGAT-------AATAAGGAA----------TAAACTTG----C--AACTCA--TGGGTGTA--CGAA------GAAATTA-TGTGCCGAC
droBia1	scf7180000301300:14577-14738 -		GAACTCGATATAGC-GTTCTCTCTTGTTATTATATA---TATTATATGTA----------T----------T----------GAC----------ATTTATATAAATATCAATCTAT---A-T----------T----------ATAAACATAAATA----TACAT----------ATAAATATAT---A-ATATAT----------AAATATAAA--T----------TATAT--A----TGTAAA--TA--TAAATATA--TATA------CAAA-T-TTAAATACA
droTak1	scf7180000415447:21541-21708 -		CCACCCGATATAGC-GTTCTCTCTTGTTTTTTATTTAACT-TG---A----------TTT--TATA----------T----------T----------AGTTAATTTTTTAGT---TTAGTTTAAAAAAATGATCCATTTATATTATTTA----------A----TATTA----------TAACAGTA----------A-----CAG--T----------TATTAAGAA--A-TTG----A--GTGTTCACTACACAA--TA--T------CAAATATATTAGTCGGA
droEle1	scf7180000491238:130220-130377 +		AAACTCGATATAGC-GTTCTCTCTTGTTTTTATTTACG--TCTTTA----------CTTCGATAAATAGTAATTATTTA-----CA---AAC----------T----TACGAC----------T----------T----------T----TATATTATTAATAAAAATCAGACAACA----------T----------T----------T

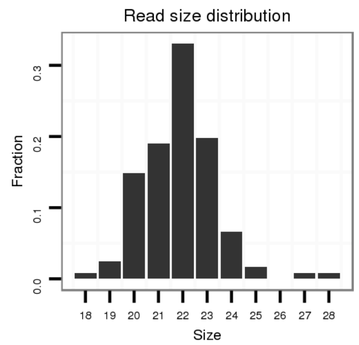
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dya_147	**3L:2426738-2426811 +**	**confident**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser [Cornell Mirror]]

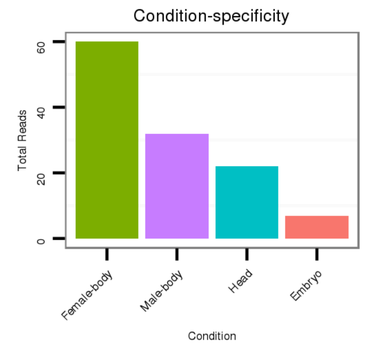
Legend: mature star **mismatch in alignment** mismatch in read

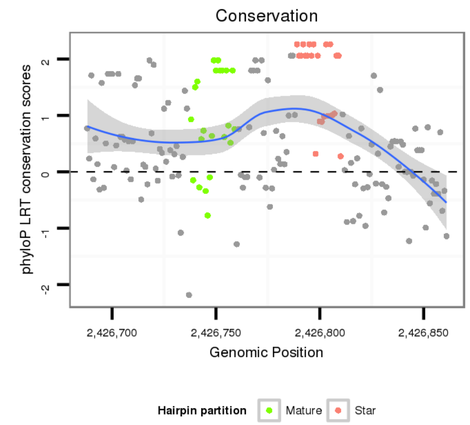
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

TTAAAAACCGAAACCTTTTCATAAAACTCGACAAATTCGACAGTCGAAACAGAATAACGGGACACGTGTGCAATTGCGACGTCGACGTAAAACGAACACGTTGCACCTGTCCCGTTATTTGCATTACGGCTTTCTACATTTTCTACCAATTAAATGTAGATACATACATATGTA **********...((.(((((((...((((((((((((...(((((...(((...(((...(((.....)))...)))))))))).))))))))))))))...)).)))))).))....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M043 female body	V120 male body	V058 head	M056 embryo	V052 head	M026 head
.....AGAATAACGGGACACGTGTGCA.....	22	0	1	21.00	21	14	2	4	1	0	0
.....AGAATAACGGGACACGTGTGCAA.....	23	0	1	18.00	18	6	9	1	0	2	0
.....AGAATAACGGGACACGTGTGC.....	21	0	1	17.00	17	1	10	2	4	0	0
.....TGCACCTGTCCCGTTATTTGCA.....	22	0	1	13.00	13	10	0	0	0	3	0
.....AGAATAACGGGACACGTGTG.....	20	0	1	13.00	13	5	5	2	0	1	0
.....AGAATAACGGGACACGTGTGCAAT.....	24	0	1	8.00	8	5	2	1	0	0	0
.....TTGCACCTGTCCCGTTATTTGCA.....	23	0	1	5.00	5	5	0	0	0	0	0
.....GCACCTGTCCCGTTATTTGCAT.....	22	0	1	4.00	4	2	2	0	0	0	0
.....TGCACCTGTCCCGTTATTTG.....	20	0	1	3.00	3	3	0	0	0	0	0
.....TGCACCTGTCCCGTTATTTGC.....	21	0	1	3.00	3	2	0	0	0	1	0
.....AGAATAACGGGACACGTGCAG.....	23	1	1	2.00	2	0	1	0	1	0	0
.....AGAATAACGGGACACGTGT.....	19	0	1	2.00	2	0	1	1	0	0	0
.....TTGCACCTGTCCCGTTATTTGC.....	22	0	1	2.00	2	1	0	0	1	0	0
.....GCACCTGTCCCGTTATTTGCA.....	21	0	1	2.00	2	1	0	0	0	1	0
.....AGAATAACGGGACACGTGTGT.....	21	1	1	2.00	2	1	0	0	1	0	0
.....ATTGCGACGTCGACGTAAAACGAAC.....	25	0	1	1.00	1	0	0	0	1	0	0
.....AAACAGAATAACGGGACACGT.....	21	0	1	1.00	1	0	1	0	0	0	0
.....TTGCGACGTCGACGTAAAACGAACACGT.....	28	0	1	1.00	1	0	0	0	0	0	1
.....AGAATAACGGGACACGTG.....	18	0	1	1.00	1	0	0	0	0	1	0
.....GAAACAGAATAACGGGACACGTGTGC.....	26	0	1	1.00	1	0	1	0	0	0	0
.....CAGAATAACGGGACACGTGTGCAA.....	24	0	1	1.00	1	1	0	0	0	0	0
.....ATTGCGACGTCGACGTAAAA.....	20	0	1	1.00	1	1	0	0	0	0	0
.....ACAGAATAACGGGACACGTGTGCAA.....	25	0	1	1.00	1	0	1	0	0	0	0
.....GACACGTGTGCAATTGCGACG.....	21	0	1	1.00	1	1	0	0	0	0	0
.....AGAATAACGGGACACGTGTGCAATT.....	25	0	1	1.00	1	0	1	0	0	0	0
.....GCACCTGTCCCGTTATTTGC.....	20	0	1	1.00	1	1	0	0	0	0	0
.....ATTGCGACGTCGACGTAAAACGAACAC.....	27	0	1	1.00	1	0	0	0	0	0	1
.....AGAATAACGGGACACGTGTGCAT.....	23	1	1	1.00	1	0	1	0	0	0	0
.....GAATAACGGGACACGTGTG.....	19	0	1	1.00	1	1	0	0	0	0	0
.....AGAATAACGGGACACGTGGC.....	20	2	1	1.00	1	0	0	1	0	0	0
.....TGCACCTGTCCCGTTATTTGCAT.....	23	0	1	1.00	1	1	0	0	0	0	0

Anti-sense strand reads

AATTTTTGGCTTTGGAAAAGTATTTTGAGCTGTTTAAGCTGTCAGCTTTGTCTTATTGCCCTGTGCACACGTTAACGCTGCAGCTGCATTTTGCTTGTGCAACGTGGACAGGGCAATAAACGTAATGCCGAAAGATGTAAAAGATGGTTAATTTACATCTATGTATGTATACAT **********...((.(((((((...((((((((((((...(((((...(((...(((...(((.....)))...)))))))))).))))))))))))))...)).)))))).))....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M043 female body	V058 head

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droYak3	3L:2426688-2426861 +	dya_147	TTAAAAACC-GAAACCTTTT---CATAAAA--C-TCG-ACAAA--TTCGACAGTC----GAAACAG----------AATA----------AC----------GGGACACGTGTGCAATTGCGACGTCGACGTA----------AAACGAACACGTTGCACCTGTCCC-GTTAT---TTGCATTACGGCTTTCT-----ACA-T------TTTCTACCAATTAAATGTAG----------ATA--C------ATACATATGTA----------
droEre2	scaffold_4784:9488868-9489036 -		TTA-AAACC-GAAACTTTT---CATAAAA--C-CCG-ACAAA--TTCGACAGTC----GAAACAG----------AAAA----------AC----------GAGACACGTGAGCATTGCGACGTCGATGTA----------AAATTAACACGTTGCACCTGTCCN-GTTAT---TTGCATTCGGATATTCT-----ACA-T------GTTCTACCAATGAAATGTAG----------ATATGT------AC----GTA----------
droSec2	scaffold_0:1738307-1738472 -		TTA-AAACC-GAAACCTTTG---CATAAAA--A-CCG-AAAAA--TTCGACAGTC----GAAAGAAAA----------AAGA----------AC----------GGGACACGCGTGCATTTTCGACGTCGACGTA----------GAACGAACACGTTGCACCTGTCCC-GTTAT---TTGCATTACGGCTTTCT-----ACA-T------TTTCGGCCAATTAAACGA--**----------**TGATATGT------**----------**----------
droSim2	3L:9266561-9266726 -		TTA-AAACC-GAAACCTTTT---CATAAAA--A-CCG-AAAAA--TTCGACAGTC----GAAAGAAAAA----------AAGA----------AC----------GGGACACGCGTGCATTTTCGACGTCGACGTA----------GAACGAACACGTTGCACCTGTCCC-GTTAT---TTGCATTACGGCTTTCT-----ACA-T------TTTTGGCCAATTAAATAAA-**----------**TG---**-**------**-------**ATA----------
dm3	chr3L:9497749-9497929 -		----AAACC-GAAACCTTTT---CATAAAA--A-CCG-AAAAA--TTCGACAGTC----AAAAAAAA----------AAAA----------AC----------GGGACACGCGTGCATTTTCGACGTCGAACGTA----------AAACGAACACGTTGCACCTGTCCC-GTTAT---TTGCATTACGGCTTTCT-----ACA-T------TTTTTT----------**--------TGGCTGATATGTGGATATTTGT----GGATATATTTGGATGATT**
droEug1	scf7180000409711:1360967-1361130 -		TTA-AAACT-GAAATCTTTT---TA-AAAA--T-CCG-ACAAT--TTGAACCATC----AAAAAAATA----------**--**AA----------A-----------GGGAAGACACGCGTGCATTTGGTACGTCGACATAAAATGATATACATATACGAAAAAATTACCACGTTGCACCTGTCCC-ATTAT---TTGCATT**---------**-----**---**-**-**-----**---**CTACCAATTAATTTTAG----------**---**-**-**-----**-------**GA----------
droBia1	scf7180000302428:8279111-8279224 +		TTA-NGG-G-GAAACCTCG---**-------**-**-**--A-AG----**---------**----**------**----------**---**A----------A-----------GAGACACGCGTGCACTGCGCGACGTCGAC**---**----------**-------**ACGTTGCACCTGTCCC-GTTAT---TGCGGGCGCTCTTTGC----GCAATCTCAATTTTGTACCAATTAA**------**----------**---**-**-**-----**----------**----------
droTak1	scf7180000415664:133030-133168 +		TTA-AAACC-GAAACCTTTT---CATAAAA--C-CCA-ACAA--TTCGAT----**----**------**----------**----**----------**--**----------**--GACACGCGTGCATTTGCGACGTCGACATTA----------**TAATGACCACGTTGCACCTGTCCC-GTTAT---TTGCATTCGGTTCTCTACAT**-ACA-T------TTTCAAGCAATTAATT**----**----------**---**-**-**-----**----------**----------
droEle1	scf7180000490564:270084-270257 -		TTA-AAGCG-GAAACCTTTT---CACAAAA--C-CCA-ACAGT--TTCGACAGTC----AAAA**---**----------**----------**-A--**----------**AAACGTTCTTATT-TTTTTGTTGGTTGGACACGCGTGCAATG-GAGACGTCAACGTCA----------**AGATGCCACGTTGCACCTGTGCC-GTTGT---TTGCATTCGGGCTATCA-----ACA-T------TTTCGACCAATTAAATT**---**----------**---**-**-**-----**-------**TTG----------
droRho1	scf7180000780168:18820-18988 +		TTA-NCGCG-GAAACCTTTT---GCACAAA--G-CCA-ACAAT--TTCGACAGTC----AAAA**---**----------**----------**----**-----**A-----**GAAACGT**CTTATTATTTTTTTGGTTGGACACGCGTGCAATG-GAGACGTCACGTCG----------**AGATGCCACGTTGCACCTGTCCC-GTTGTT-TTGCATTCGGGCTATCA-----ACA-T------TTTCGACCAATTA**-------**----------**---**-**-**-----**----------**----------
droFic1	scf7180000453807:642519-642682 -		TTA-AAACC-GAAACCTTTT---CAAAA-AA--T-CCG-ACAA--**--------**GG---G**------**----------**----------**-AAAACGAAA**-----**AAAA-GTTCTTTAT---ATTTTGGGTCGGACACGCGTGCAAT-TGAACGTCGACATTA----------**AAATGCCACGTTGCACCTGTCCC-GTTAT---TTGCATTTGGACTCTGA-----TCA-T------TTTCTACCAATTATAT**----**----------**---**-**-**-----**----------**----------
droKik1	scf7180000302486:2192219-2192429 +		TTA-AAGCC-GAAACCTTTT---CAAAAAA--C-CAG-ACAGATTTTCGACAGTT---ACAAAAA---GAACATAAAACG-GAGGAAAAGGACGAATAAATAATAAACGTTCTT-----TATTTTCGGTTGGACACGCGTGCAGT-GTGACGTCGACGTTAAC----------**GAATGCACACGTTGCACCTGTCCC-GTTATTATTTGCATTT--------**----**---**-**-**-----**---CTGGCAATTAAATTTCGGCCTCTTCGTG----**---**-**-**-----**-------**GCT----------
droAna3	scaffold_13337:3754449-3754637 -		TAATTAACCTAAAACCTTTTGTTCAAAAAA--C-CCAGACAA--TG---CAGTCCGCTTCA----**----------**AGGGAAGAGGAAAATATGAAA-----GAATTGATG-T-----TTTTTCCGGTGGTACACGCGTCCAGATTCGACGTGAAC**---**----------**--ATGCCAGCGATGCACCTGTCCCTGTTAT---TTGCATAAGAGGCCASA-----TGC-T------CTTCTCCCGAAAAAAAA**---**----------**---**-**-**-----**-------**TTG----------
droBip1	scf7180000395954:152212-152400 -		TAATTAACCTAAAACATTTTATACAAAAAAGCCCGAGACAAT--G---CTGTCTCTTACA----**----------**AAGGAAGAGGAAAATGTGAAA-----GAATGGTT-------TTTTTCCGGTGGTACACGCGTCCGATTCGACGTGAAC**---**----------**--ATGCCAGCGATGCACCTGTCCC-GCTAT---TTGCATAACAGCCTATA---T-AGC-T------AGTCAAAATTTTG---T**---**----------**---**-**-**-----**-------**TA----------
dp5	XR_group8:2390541-2390698 -		AC-------**----------**----------**-------**--CCACGGACA---**----------**----**-------**----**-------**---GAACCAAAAAGGAGACCAGAAACTGAAA-----GAATCGTT**----------**TTAATGGGACACGCGTGCAGTCTTAGGGTCGACGTCA----------**ATTTGCCACAGTTGCACCTGTTCC-GTTAT---TTGCATTACGTTTTTC----TGAAATTTTCGTT**----------**---TGT------CTGCCCCTGTC----------
droPer2	scaffold_24:664114-664271 +		AC-------**----------**----------**-------**--CCACGGACA---**----------**----**-------**----**-------**---GAACCAAAAAGGAGACCAGAAACTGAAA-----GAATCGTT**----------**TTAATGGGACACGCGTGCAGTCTTAGGGTCGACGTCA----------**ATTTGCCACAGTTGCACCTGTTCC-GTTAT---TTGCATTACGTTTTTC----TGAAATTTTCGTT**----------**---TGT------CTGCCCCTGTC----------
droWil2	scf2_1100000004762:2737644-2737681 -		**--------**-**---------**----**-------**--**---**-**-----**----------**----**-------**----**-----------**--**----------**----------**--------**ACGTTGCACCTGTCCC-GTTATTA-ATGCTTGACGATTT**--**----**---**-**-**-----**----------**---**-**-**-----**----------**----------

Generated: 09/08/2015 at 07:40 PM

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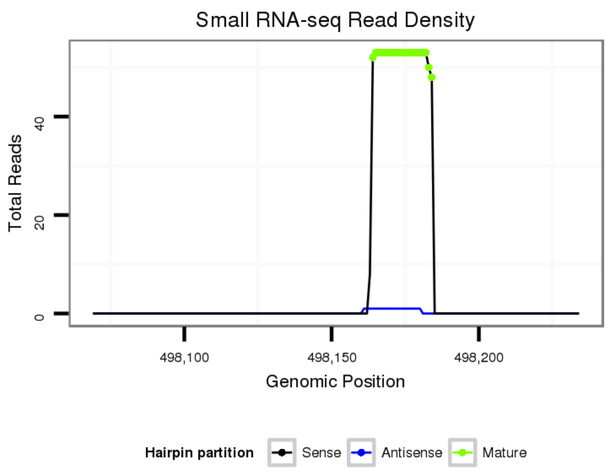
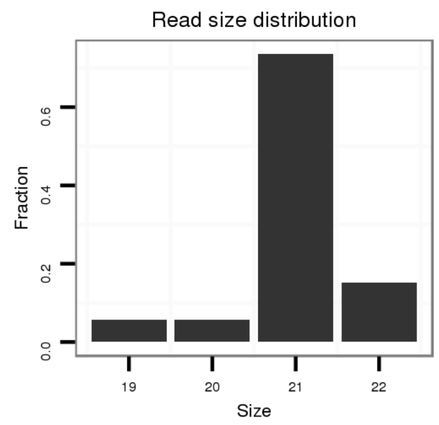
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

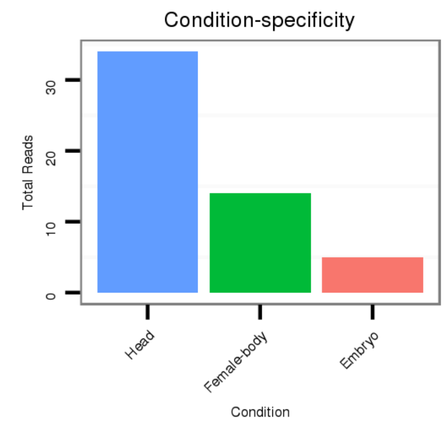
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dya_889	**3R:498119-498184 +**	**candidate**	**Mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

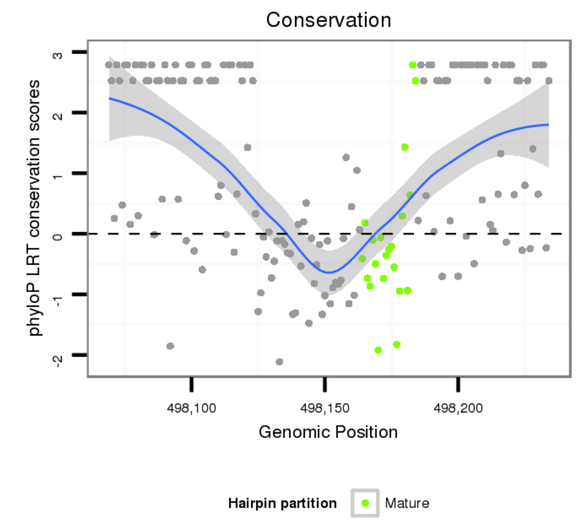
Legend: mature star mismatch in alignment mismatch in read

Predicted structure









Show Alternate Folds

Flybase annnotation

intron [Dyak\GE25405-in]; CDS [Dyak\GE25405-cds]; CDS [Dyak\GE25405-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

AGCTGCAAGGTAATGGTGGCGACCGACGCCATCGGTATGGGCTTAAACCTGTAAGTAAATTTTTAACATACATATGTGGCTGGTCCAAATATAATGCGTGCAAAATTTACTTGCAGGAGCATTCGTCGAATCATATTCTACTCACTAATTAAACCGTCGATAAATG **********(((((((((((..((.((.((((.(((.....)))).)))).)).)).)).)))))))))))..**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V058 head	M056 embryo	V052 head	M043 female body	V046 embryo	M026 head	V120 male body
.....GCGTGCAAAATTTACTTGCAGT.....	22	1	1	206.00	206	69	35	41	21	34	3	3
.....GCGTGCAAAATTTACTTGCAG.....	21	0	1	39.00	39	19	0	4	12	4	0	0
.....CGTGCAAAATTTACTTGCAGT.....	21	1	1	14.00	14	4	2	1	7	0	0	0
.....TGCGTGCAAAATTTACTTGCAG.....	22	0	1	8.00	8	5	0	2	0	1	0	0
.....GCGTGCAAAATTTACTTGCAGC.....	22	1	1	8.00	8	0	8	0	0	0	0	0
.....GCGTGCAAAATTTACTTGCAGA.....	22	1	1	7.00	7	1	0	0	5	1	0	0
.....GCGTGCAAAATTTACTTGC.....	19	0	1	3.00	3	1	0	0	1	0	1	0
.....GTGCAAAATTTACTTGCAGT.....	20	1	1	2.00	2	0	1	0	1	0	0	0
.....GCGTGCAAAATTTACTTGCA.....	20	0	1	2.00	2	2	0	0	0	0	0	0
.....GCGTGCAAAATTTACTTGCG.....	20	1	1	1.00	1	0	0	0	0	0	1	0
.....CGTGCAAAATTTACTTGCAG.....	20	0	1	1.00	1	0	0	0	1	0	0	0
.....GGCGACCGACGCCATCGGTATGGGCC.....	26	1	1	1.00	1	0	1	0	0	0	0	0

Anti-sense strand reads

TCGACGTTCCATTACCACCGCTGGCTGCGGTAGCCATACCCGAATTTGGACATTCATTTAAAAATTGTATGTATACACCGACCAGGTTTATATTACGCACGTTTTAAATGAACGTCCTCGTAAGCAGCTTAGTATAAGATGAGTGATTAATTTGGCAGCTATTTAC **********(((((((((((..((.((.((((.(((.....)))).)))).)).)).)).)))))))))))..**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M043 female body
.....TTACGCACGTTTTAAATGAA.....	20	0	1	1.00	1	1

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droYak3	3R:498069-498234 +	dya_889	AGCTGCAAGGTAATGGTGGCGACCGACGCCATCGGTATGGGCTTAAACCTGTAAGTAAATTTTTAAC---A--TACATATG--TGGCTGGTC------CAAATATA----ATGCGTGC----------AAAATTTACTTGCAGGAGCATTCGTCGAATCATATTCTACTCACTAATTAAACCGTCGATAAATG
droEre2	scaffold_4770:489407-489569 +		AGCTGCAAGGTAATGGTGGCGACTGACGCCATAGGTATGGGCTTGAACCTGTAAGTGAATTATT---C--CACATATG--TGGCTGTC------CAAATTTA----ATGCGTGC----------GAAATTTACTTGCAGGAGCATTCGTCGAATCATATTCTACTCACTGATTAAGCCGTCGATGAATG
droSec2	scaffold_6:257612-257772 +		AGCTGCAAGGTAATGGTGGCGACTGACGCCATCGGTATGGGCTTGAACCTGTAAGTAGAATATT---C--CACATATG--TGGCTT-CC------CAAATATA----ATTCCCAC----------GA-ATGTACTTGCAGGAGCATTCGTCGAATCATATTTTACTCACTGATCAAGCCGTCGATGAATG
droSim2	3r:122183-122343 +		AGCTGCAAGGTAATGGTGGCGACTGACGCCATCGGTATGGGCTTGAACCTGTAAGTAGAATATT---C--CACATATG--TGGCAT-CC------CAAATATA----ATGCCCGC----------GA-ATGTACTTGCAGAAGCATTCGTCGAATCATATTTTACTCACTGATCAAGCCGTCGATGAATG
dm3	chr3R:138768-138929 +		AGCTGCAAGGTAATGGTGGCGACTGACGCCATCGGTATGGGCTTGAACCTGTAAGTAAAATATT---C--TATATATG--TGGCTTGCC------AAAATATA----ATGCCCGC----------GA-ATGTACTTGCAGGAGCATTCGTCGAATCATATTTTACTCACTGATCAAGCCGTCGATGAATG
droEug1	scf7180000409759:73594-73756 +		AGCTGCAAGGTAATGGTTGCGACAGACGCAATCGGAATGGGCTTGAATTTGTAAGTACAATATT---C--TGTATACT--TTTTCCGGA------CAGATCTA----ATGTGCAT----------ATTATATACCTACAGGAGCATTCGTCGAATCATATTTATTCCTTGATCAAGCCGACGATGAACG
droBia1	scf7180000302098:344950-345113 -		AGCTGCAAAGTAATGGTAGCGACAGACGCCATAGGCATGGGCTTGAACCTGTAAGAGAGATGTTGC---A-GCA--TTTGGGTTCCAGC------CAGATCTT----AAGCGGAC----------GTATTTACTTACAGAAGCATTCGTCGAATAATATTCTATTCCTTGATCAAGCCGACGATGAATG
droTak1	scf7180000414401:16834-16993 +		AGCTGCAAAGTAATGGTGGCGACAGACGCCATCGGAATGGGCTAAACCTGTAAGTGAAATG-----G-ATAA--TTTGGGTTCCGGC------CATTATCTA----AAGCGCAT----------GATATTTCCTTGCAGAAGCATTCGTCGAATTATATTTTATTCCTTGATCAAGCGAACGATGAATG
droEle1	scf7180000491104:1877358-1877526 +		AGCTGCAAGGTAATGGTGGCGACGGACGCCATCGGCATGGGCTTGAATCTGTAAGTGAAACATTTC-----G---CGAATTG--TTGTTTGGATGATTAGATGTGAA----ATACCCC----------GATTCTGCCTTTCAGGAGCATTCGCGAATCATTTCTAATCCCTGATCAAGCCGACGATGAACG
droRho1	scf7180000761807:7664-7827 +		AGCTGCAAGGTAATGGTGGCGACGGACGCCATCGGGATGGGCTTGAATCTGTAAGTATAATATGTC-----G-AAGTTTG--TTTTTTGGC------CACATCTG----ATGCGCAC----------AACATTTATTTCAGGAGCATTCGTCGAATCATATTCTAATCCTTGATCAAGCCGTCTATGAATG
droFic1	scf7180000454096:1262908-1263075 +		AGTTGCAAGGTAATGGTGGCGACCGACGCCATCGGCATGGGCTTGAACCTGTAAGTAGAGTGCCTC-----G-GACA--ATTAGTTTTTGAGCAAC--TGAGCCTT----ATACGCAC----------GATATTCGTTTGCAGGAGTATACGCCGAATCATATTTATTCGTTGATCAAGCCGACGATGAATG
droKik1	scf7180000302778:533350-533509 -		AGCTGCAAGGTGATGGTAGCCACAGACGCCATTGGCATGGGCCTAAATCTGTAAGAGAAACAAT-----A-TTA------ATCCATAGC------TCAGTCTGCTTCAAC---TC----------CAATTTCTTTTGCAGGAGCATTCGCCGTATCATATTCTATTCCCTGGTCAAGCCCACGATGAATG
droAna3	scaffold_13340:11144596-11144755 +		AGTTGTAAAGTAATGGTAGCCACAGATGCGATTGGAATGGGCTTGAACTTGTGAGTAGGAGAGT-----CC-CTTACTTC--TAAA-----------------------TCGAGACA-ATTGATATGTTTATCTCTTTATAGGAGTATACGCCGAATAATATTTTACTCCTTGGTGAAGCCGACGATGAACG
droBip1	scf7180000396691:53118-53279 +		AGTTGCAAAGTTATGGTAGCAACAGATGCGATTGGAATGGGTTTGAACTTGTAAGTAGGAGAAT-----CC-CCTATTTA--TAA------------------AATCGAAATAAACTGAAACCCTTATCTCTCGATAGGAGCATACGCCGTATTATATTTTACTCCTTGGTGAAGCCGACGATGAACG
dp5	2:24789413-24789570 -		AGCTGCAAGGTAATGGTAGCCACGGACGCCATTGGCATGGGTTTGAATCTGTAAGTGAGCTATTTC-----G---T------GGGAATCAAT------TTTATCTTCGTTAAATC---------------AATCTTCACTGCAGGAGCATCCGCCGAATCATTTCTACTCCTTGGTCAAGCCCACAATGAACG
droPer2	scaffold_6:90294-90452 -		AGCTGCAAGGTAATGGTAGCCACGGACGCCATTGGCATGGGTTTGAATCTGTAAGTGAGCTATTGC-----G---T------GGGAATCAAT------TTTATCTTCGTTAAAT---C----------AATCTTCACTTGCAGGAGCATCCGCCGAATCATTTCTACTCCTTGGTCAAGCCCACAATGAACG
droWil2	scf2_1100000004902:9788006-9788164 -		AGCTGCAAAGTAATGGTAGCCACCGATGCTATCGGTATGGGCTTGAATCTGTAAGTGGACTCTGATTATTC--CTTGCATG--TGAAATAAT------GGAATT-----TATT---------------------AATCTTTGCAGGAGCATACGCCGAATTATCTTTACTCCTAGTCAAGCCGACACTAAATG
droVir3	scaffold_12855:2838295-2838451 +		AGTTGTAAAGTAATGGTGGCCACTGATGCTATTGGCATGGGCTTAAATCTGTAAGTTTGTTGGATT---TG--ATA-----------AACTTT------TTACTGTT----ATATTAAA----------GT-AAACACTTATAGGAGCATTCGTCGCATTATATTCTACTGTTGGTCAAACCCACGATGAATG
droMoj3	scaffold_6540:10375244-10375400 -		AGCTGTAAAGTAATGGTAGCCACCGATGCTATAGGCATGGGCTTAAATCTGTAAGGTTAACATT-----G--CTTAAATA--TTT-----A------AAAATATT----TTATTAAT----------GC-CCTTTATTGCAGAAGCATTCGTCGCATTATTTCTACTCGTTGGTTAAGCCCACAATGAATG
droGri2	scaffold_14906:3829510-3829667 -		AGCTGCAAAGTCATGGTAGCCACAGATGCCATTGGCATGGGCTTAAACCTGTAAGTCTGCTC-----G---CATTCATT--TATTCA-C------TCAATTCC----ATTAATAA----------ATCACTCAATTACAGGAGCATTCGTCGCATAATTTCTACTCGTTGGTGAAGCCGACGATGAACG

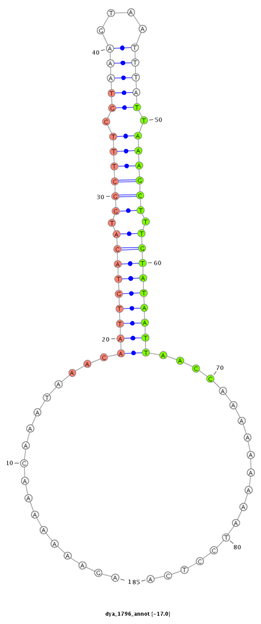
Generated: 09/08/2015 at 10:32 PM

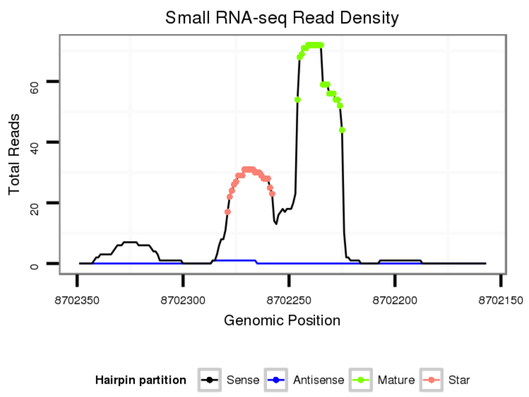
	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

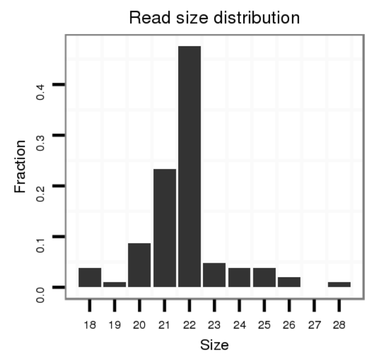
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dya_1796	**3R:8702207-8702299 -**	**confident**	**Canonical miRNA**	**3pUTR**	[View on UCSC Genome Browser (Cornell Mirror)]

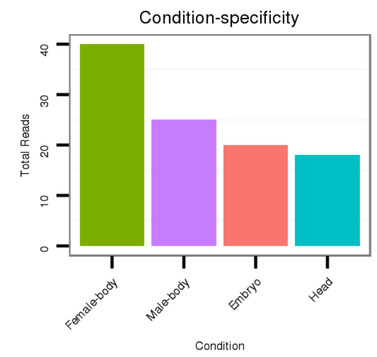
Legend: mature star mismatch in alignment mismatch in read

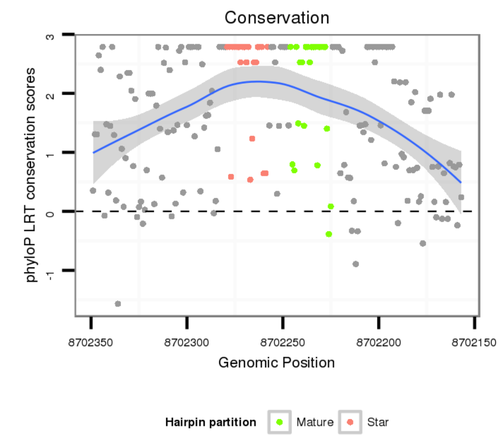
Predicted structure











Show Alternate Folds

Flybase annotation

utr3 [utr3_minus_7095]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TTTTGAGAAAAAAGAAAGAAAAAACCCGTCAAACCAAACAACAACAACAAAACAATAGAAGAAAAAAAACAAATAAACAATTGTACATGGCTTTCGTAAAGTAATTTATTAAAGCTTTGTATAATTAACCAAAAAAAATCCTCAAATTTGTGTTTTCATTTGCGTTATCACGTACAGTTTTTCGTTGGCAATTTTAA	Read size	# Mismatch	Hit Count	Total Norm	Total	M043 female body	V120 male body	M056 embryo	M026 head	V058 head	V052 head	V046 embryo
**********.....(((((((((.(((((((.((((....)))))).)))))).)))))))))).....**********												
.....TTAAAGCTTTGTATAATTAACC.....	22	0	1	27.00	27	6	2	9	8	0	1	1
.....AGTAATTTATTAAAGCTTTGT.....	21	0	1	7.00	7	1	6	0	0	0	0	0
.....TAAAGCTTTGTATAATTAACC.....	21	0	1	6.00	6	2	2	0	2	0	0	0
.....TAAAGCTTTGTATAATTAACCA.....	22	0	1	6.00	6	4	0	0	0	2	0	0
.....TTAAAGCTTTGTATAATTAAGT.....	22	1	1	6.00	6	2	1	0	3	0	0	0
.....AACAATTGTACATGGCTTTCGT.....	22	0	1	4.00	4	1	1	2	0	0	0	0
.....TTAAAGCTTTGTATAATTAAC.....	21	0	1	3.00	3	2	0	0	0	1	0	0
.....ATTAAAGCTTTGTATAATTAAC.....	22	0	1	3.00	3	1	0	1	0	1	0	0
.....TTGTACATGGCTTTCGTAAAGT.....	22	0	1	2.00	2	0	1	0	0	1	0	0
.....TATTAAAGCTTTGTATAATT.....	20	0	1	2.00	2	2	0	0	0	0	0	0
.....GTAAAGTAATTTATTAAAGCTTTGT.....	25	0	1	2.00	2	0	2	0	0	0	0	0
.....AATTGTACATGGCTTTCGTAA.....	21	0	1	2.00	2	1	1	0	0	0	0	0
.....TAAAGCTTTGTATAATTAAC.....	20	0	1	2.00	2	1	0	1	0	0	0	0
.....ACAATTGTACATGGCTTTCGTA.....	22	0	1	2.00	2	2	0	0	0	0	0	0
.....TACATGGCTTTCGTAAAGTAATTT.....	24	0	1	2.00	2	2	0	0	0	0	0	0
.....ACAATTGTACATGGCTTTCGT.....	21	0	1	2.00	2	2	0	0	0	0	0	0
.....AATAAACAATTGTACATGGCTTTCGT.....	26	0	1	2.00	2	1	1	0	0	0	0	0
.....CAATTGTACATGGCTTTCGTAA.....	22	0	1	2.00	2	1	1	0	0	0	0	0
.....GAAAAACCCGTCAAACCAAA.....	20	0	1	1.00	1	1	0	0	0	0	0	0
.....ATTGTACATGGCTTTCGT.....	18	0	1	1.00	1	0	0	0	0	0	1	0
.....ACAATTGTACATGGCTTTC.....	19	0	1	1.00	1	1	0	0	0	0	0	0
.....AGAAAAACCCGTCAAACCAAAC.....	22	0	1	1.00	1	1	0	0	0	0	0	0
.....AAGCTTTGTATAATTAACCAAA.....	22	0	1	1.00	1	1	0	0	0	0	0	0
.....ATTTATTAAAGCTTTGTATA.....	20	0	1	1.00	1	0	1	0	0	0	0	0
.....AAAGTAATTTATTAAAGCTTTGT.....	23	0	1	1.00	1	0	1	0	0	0	0	0
.....AACAATTGTACATGGCTTTCG.....	21	0	1	1.00	1	0	0	0	0	0	1	0
.....AAAGCTTTGTATAATTAACCA.....	21	0	1	1.00	1	0	1	0	0	0	0	0
.....AAATAAACAATTGTACATGGCTTTC.....	25	0	1	1.00	1	0	0	1	0	0	0	0
.....AATAAACAATTGTACATGGCTTTC.....	24	0	1	1.00	1	1	0	0	0	0	0	0
.....AACCCGTCAAACCAAACAACAACAAAAC.....	28	0	1	1.00	1	1	0	0	0	0	0	0
.....AAACAATTGTACATGGCTTTC.....	21	0	1	1.00	1	1	0	0	0	0	0	0
.....TTAAAGCTTTGTATAATTAACCT.....	23	1	1	1.00	1	1	0	0	0	0	0	0
.....AAACAATTGTACATGGCTTTCGT.....	23	0	1	1.00	1	0	1	0	0	0	0	0
.....AAAAAAGAAAGAAAAACCCGT.....	21	0	1	1.00	1	0	1	0	0	0	0	0
.....TTAAAGCTTTGTATAATTAA.....	20	0	1	1.00	1	1	0	0	0	0	0	0
.....GCTTTGTATAATTAACCAAAAAAAA.....	25	0	1	1.00	1	1	0	0	0	0	0	0
.....AAAAAGAAAGAAAAACCCGTCAAACCA.....	27	0	1	1.00	1	0	1	0	0	0	0	0
.....ACAAATAAACAATTGTACATGGC.....	23	0	1	1.00	1	1	0	0	0	0	0	0
.....AAAAACCCGTCAAACCAAAC.....	20	0	1	1.00	1	0	1	0	0	0	0	0
.....ATTAAAGCTTTGTATAATTAA.....	21	0	1	1.00	1	1	0	0	0	0	0	0
.....AATTGTACATGGCTTTCGTAT.....	21	1	1	1.00	1	1	0	0	0	0	0	0
.....TAATTTATTAAAGCTTTGTATA.....	22	0	1	1.00	1	0	1	0	0	0	0	0
.....AAAGAAAGAAAAAACCCGTCAAACC.....	24	0	1	1.00	1	0	1	0	0	0	0	0
.....GTAAAGTAATTTATTAAAGCTTTGTATA.....	28	0	1	1.00	1	1	0	0	0	0	0	0
.....ATTAAAGCTTTGTATAATG.....	19	1	1	1.00	1	0	0	1	0	0	0	0
.....GTAATTTATTAAAGCTTTGT.....	20	0	1	1.00	1	0	1	0	0	0	0	0
.....AAACAATTGTACATGGCT.....	18	0	1	1.00	1	0	0	1	0	0	0	0
.....CAATTGTACATGGCTTTCGTC.....	21	1	1	1.00	1	1	0	0	0	0	0	0
.....AAATAAACAATTGTACAT.....	18	0	1	1.00	1	1	0	0	0	0	0	0
.....ATTAAAGCTTTGTATAATTAACC.....	23	0	1	1.00	1	0	0	1	0	0	0	0
.....AACAATTGTACATGGCTTTC.....	20	0	1	1.00	1	0	0	1	0	0	0	0
.....TTTGTGTTTTCATTTGCGTT.....	20	0	1	1.00	1	0	1	0	0	0	0	0
.....AATTTATTAAAGCTTTGT.....	18	0	1	1.00	1	0	0	0	0	0	0	1
.....AAGCTTTGTATAATTAACCA.....	20	0	1	1.00	1	1	0	0	0	0	0	0
.....ATAAACAATTGTACATGGCTTTC.....	23	0	1	1.00	1	0	0	1	0	0	0	0
.....AAGTAATTTATTAAAGCTTTGT.....	22	0	1	1.00	1	0	1	0	0	0	0	0
.....ATAAACAATTGTACATGGCTTTCG.....	24	0	1	1.00	1	0	1	0	0	0	0	0

Anti-sense strand reads

AAAACTCTTTTTTCTTTCTTTTTGGGCAGTTTGGTTTGTTGTTGTTTTGTTATCTTCTTTTTTTGTTTATTTGTTTAACATGTACCGAAAGCATTTCATTAAATAATTTCGAAACATATTAATTGGTTTTTTTTTAGGAGTTTAAACACAAAAGTAAACGCAATAGTGCATGTCAAAAAGCAACCGTTAAAATT	Read size	# Mismatch	Hit Count	Total Norm	Total	M043 female body	V058 head	M026 head	GSM1528802 follicle cells
**********.....(((((((((.(((((((.(((((....)))))).)))))).)))))))))).....**********									
.....TGTTTATTTGTTAACATGTAC.....	21	0	1	1.00	1	1	0	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droYak3	3R:8702157-8702349 -	dya_1796	-TTTTGAGAAAAAAG----------AAAGAAA----------AACCC-GTCAAA-CC----------AAACAACA-ACA--------AAACAATAGAAGAA---------AAAAACAAATAAA-CAATTGTACATGGCTTTCGTAAAGTAATTTATTAAAGCTTTGTATAATTAACCAAAAAAAA--AT-CCTCAAA-TTTGTGTTTTCATTTGCGTTAT---CACGTACAGT-TTTTCGTT-----GGCAATTTTAA
droEre2	scaffold_4770:16945885-16946072 +	der_1521	-ATTTGAGAAAAAAG----------A-AGAAA----------AACCC-CACAAA-C----------CAAACAACA-ACA--------AAACAATAGAAAA---------AAACAAATAAA-CAATTGTACATGGCTTTCGTAAAGTAATTTATTAAAGCTTTGTATAATTAACCAAAAAAA--AT-CCTCAAA-TTTGTGTTTTCATTTGCGTTAT---CACGTACAGT-TTTTCGTT-----GGCAATTTCAA
droSec2	scaffold_0:17217363-17217554 +	dse_1844	-ATTTGAGAAAAAAG----------AAAGAAA----------A-CCC-CACAAA-CGAA--------ACAA-CAACA-ACA--------AAACAATAGAAAA---------AAAACAAATAAA-CAATTGTACATGGCTTTCGTAAAGAAATTTATTAAAGCTTTGTATCATTAACCAAAAAAA--AT-TCTCAAA-TTTGTGTTTTCATTTGCGTTAT---CACGTACAGT-TTTTCATT-----GGCAATTTTAA
droSim2	3r:16351715-16351910 +	dsi_75	-ATTTGAGAAAAAAG----------AAAGAAA----------A-CCC-CACAAA-CGAA--------ACAACC----A---ACAACAACAAACAATAGAAAA---------AAAAACAAATAAA-CAATTGTACATGGCTTTCGTAAAGAAATTTATTAAAGCTTTGTATCATTAACCAAAAAAA--AT-CCTCAAA-TTTGTGTTTTCATTTGCGTTAT---CACGTACAGT-TTTTCGTT-----GGCAATTTTAA
dm3	chr3R:4640223-4640413 -	dme_421	-ATTTGAGAAAAAAG----------AAAGAAA----------A-CCC-CACAAA-CCAA--------ACAAA-CAACA-ACA--------AAACAATAGAAAA---------AAGAAATAAA-CAATTGTACATGGCTTTCGTAAAGAAATTTATGAAGCGCTTTGTATCATTAACCAAAAAAAA--AT-CCACAAA-TTTGTGTTTTCATTTGCGTTAT---CACGTACAGT-TTTTCGTT-----GGCACTTTTAA
droEug1	scf7180000409490:80930-81131 +		-ATTTGATGAA--CAAG----------AGGAAAAAACGAAA----------T-CCC-CACAAACGAA--------CCAACCAACA-ACA--------AAACAATAGAAAA---------AAAATCAAATAAA-CAATTGTACATGGCTTTCGTAAAGTAATTTATTAAAGCTTTGTATAATTAACAAAAAAA---AA-CCTCAAA-TTTGTGTTTTCATTTGCGTTAT---CACGTACAGT-TTTTCGTT-----GGCAATTTTAT
droBia1	scf7180000302402:7353486-7353675 -		-ATTTGAAAAAAAT--------C----------G-AAAGAAA----------A-CCC-CACAAACC----------AACCAACA-ACA--------AATCCATAGAAAA---------AA-CCAATAAA-CAATTGTACACGGCTTTCGTAAAGTAATTTATTAAAGCTTTGTATAATTAACAAAAAAAA--CA-ACCAAAA-TTTGTGTTTTCATTTGCGTTAT---CACGTACGGT-TTTTCGTT-----GGCAATTTTAT
droTak1	scf7180000414009:179058-179251 +		CATTTGAGAAAAAA--------AC----------G-AAAGAAA----------A-CCC-TATAAACGAA--------CCAACCAACA-ACA--------AAACAATAGAAAA---------AACAAATAAA-CAATTGTACACGGCTTTCGTAAAGTAATTTATTAAAGCTTTGTATAATTAAAAAAAA-A--AA-CCTCAAA-TTTGTGTTTTCATTTGCGTTAT---CACGTACAAT-TTTTCGTT-----GGCCATTTTAT
droEle1	scf7180000491212:1154154-1154344 +		-ATTTGAGAAAAAT--------A----------G-AAAGAAA----------A-ACC-CACAAAAGCAT--------CCA-CCAACT-AGC--------AACAATAAAAA--------AAACAAATAAA-CAATTGTACACGGCTTTCGTAAAGTAATTTATTAAAGCTTTGTATAATTAACAAAAAAG--AA-CCCCAAA-TTTGTGTTTTCATTTGCGTTAT---CACGTAAAAT-TTTTCGTT-----GGCCATTTTAT
droRho1	scf7180000778307:14039-14232 +		-ATTTGAGAAAAAT--------A----------G-AAAGAAAA----------A-ACC-CACAAACGAA--------CCAACCAACA-TCA--------AAACAATAGAAAA---------AAACAAATAAA-CAATTGTACACGGCTTTCGTAAAGCAATTTATTCAAGCTTTGTATAATTAACAAAAAAA--AA-CCTCAAA-TTTGTGTTTTCATTTGCGTCAT---CACGTACAAT-TTTTTGTT-----GGCCATTTTAT
droFic1	scf7180000454106:2527554-2527747 +		-TTTTGAGAAAAAG--------C----------G-AATGAAA----------A-CCC-CACAAACGAA--CCA---CCAACCAACC-ACA--------AAACAATAGAAAA---------AAACAAATAAA-CAATTGTACACGGCTTTCGTAAAGTAATTTATTAAAGCTTTGTATAATTAACAAAAAAA--AA-CCTCCAA-ATTGTGTTTTCATTTGCCTTAT---CACGTACCAT-TTTTCGTT-----TGTAATTTTAT
droKik1	scf7180000302247:250327-250526 +		-ATTTGAGAAAAACA--------AC----------T-AAAGAAA----------A-CCC-CACAAACGAA--------CCAACCATCA-ACA--------AAACAATAGAAGAA-A------AAAAACAAAATAAA-CAATTGTACATGGCTTTCGTAAAGTAATTTATTAAAGCTTTGTATAATTAAAAAAAGAA--CA-ACCAAAA-TTTGTGTTTTCATTTGCCTTAT---CACGTACACT-TTTTCGTT-----GGGCATTTTAT
droAna3	scaffold_13340:11049275-11049454 -	dan_90	-ATTTGAAAGAA--GAAAAAAAAAC----------A-AAA-----------------TATTTGAAAAAGAA-AT----------CAACCCTCAACCAACC-ACA--------AAGCAATAGAAAA---------------AATAAA-CAATTGTACACGGCTTTCGTAAAGTCATTTATTAAAGCTTGTATAATTAAGAAAAA-----------C-AACAAA-TTTGTGTTTTCATTT-------------------TGCATTTAGAATGGCAATCTAAT
droBip1	scf7180000396374:34239-34401 +		-ATTTGAAAAAAAAAAAAAAAAC----------A-AAAGAAA----------T-CCC-------------TCAACCAACC-ACA--------AACCAATAGAAAA---------------AATAAA-CAATTGTACACGGCTTTCGTAAAGTCATTTATTAAAGCTTGTATAATTAACAAAAAA-A---------A-CAAA-TTTGTGTTTTCATTT-------------------TCCAT-----AAGAATCTGAA
dp5	2:27294837-27295048 -	dps_3827	-ATTTGAGAAAAACA----------AAAGAAA----------AACCCTTACAAA-CGAAAT------CCATTCAACACAAA--------AAACAATAGAAGAA-CAAAAA-AAAAAGAAAATAAA-AAATTGTACACGGCTTTTAATGAAGTAATTTGTTAAAGCTTTGTATCATTAACAAAAAAAA--AA-AACCAAA-TTTGTGTTTTCATTTGCATTTTATACCGTTTACTTTTTTAGTT-----GGCCATTTATT
droPer2	scaffold_6:2585036-2585249 -	dpe_2481	-ATTTGAGAAAAACA----------AAAGAAA----------AACCCTTACAAA-CGAAAT------CCATTCAACACAAA--------AAACAATAGAAGAA-CAAAAA-AAAAAGAAAATAAA-AAATTGTACACGGCTTTTAATGAAGTAATTTGTTAAAGCTTTGTATCATTAACAAAAAAAAAAAA-CGCCAAA-TTTGTGTTTTCATTTGCATTTTGTAACCGTTTACTTTTTTAGTT-----GGCCATTCATT
droWil2	scf2_1100000004902:4649890-4650075 +	dwi_5415	-ATTTGAGAAAAAAT--------ACAAAAAAAAAACCAAAACAAAAGA--------------------AAAGAAAAGTTT---AAAAA-ATCAAA-ACAA--------CCAACCAACCAACA--------AAACAATAGAAA---------------AATAAA-CAATTGTACACCCCAAAAAAAAAAACC-CCAAAAA-TTTTGTTTTTCATTTG--------------------------------------
droVir3	scaffold_13047:1834994-1835158 +	dvi_24634	-GAATGAAACCAAAT--------G----------ACCAAA----------AAGAG-AA----------CAAG--CCAACCAACA--AA--------AAACAATAGAAAAA-AAAACATAAAAAAAAATAAATAAATTGTACACGGCTTTCGTAAAGAAATTTATTCAAGCTTTGTATAATTAACAAAAAAAA--AAGCTTCAAC-TTTGTGTTTTCATTT--------------------------------
droMoj3	scaffold_6540:3761875-3762078 +	dmo_3126	-A----AAAAAAAA--------A----AAAAAAAAACGAAACAAAATG--------------------AAAGAAAG-------AAGAG-AT----------GAAG--CCAACCAACA-ACA--AAAAAAAACCAATAGAAAAACTAAAA-AAAAAAAAAATAAA-CAATTGTACACTGCTTTCGTAAAGAAATTTATTCAAGCTTTGTATAATTAAAAAAAAAA--AA-ACTCAACTTTTGTGTTTTCATTTGATTTATT--TACATACA---------------------
droGri2	scaffold_14906:8668115-8668297 +	dgr_462	-ATTTGAGAAAACAG--------C----------GAAAAGAAATACGAAAAACTAAAAAAAAAAAA---------AAGTG-AA----------CAAG--CCAACCA---ACA--------AAACAATAGAAAA---------------AAATAAA-CAATTGTACACGGCTTTCGTAAAGAAATTTATCCAAGCTTTGTATAATTAACCAAAAAAAACAA-CCTCATC-TTTGTGTTATTATTTGCTTTAT----------

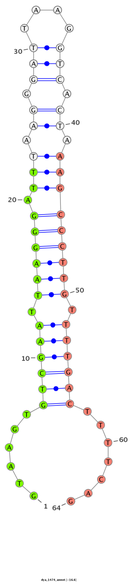
Generated: 09/08/2015 at 07:40 PM

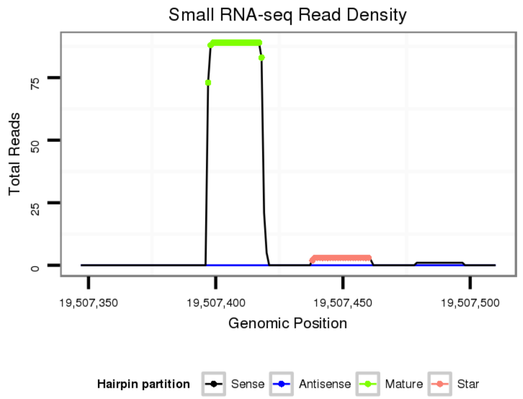
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	8
rescue.candidate	4

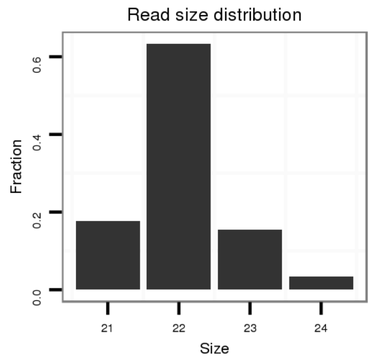
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dya_1474	**X:19507397-19507460 +**	**confident**	**Mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

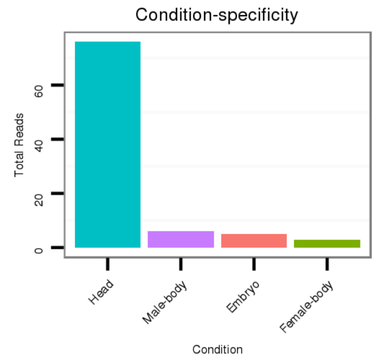
Legend: mature star **mismatch in alignment** mismatch in read

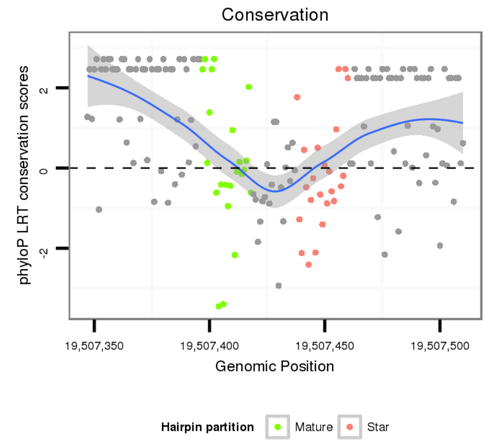
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dyak\GE17877-in]; CDS [Dyak\GE17877-cds]; CDS [Dyak\GE17877-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

```
GGCGTCCTCATGGGCATCGCCGTGCGCACTGGATCGCCCCTGAGCATCAAGTAAGTGTCGAATTAAGGGATTTAAGGGATTAAGGTCACTAAAGCCCTTGTTTTGACTTTTCAGTTTGGCGGAGCCTGTATGGCGTCAATTGACGGGCGAGATTCTACGGCCCA
**********************************************......(((((((.(((((((.(((.((.((.(((....))).)).).)))))))))..)))))).......**********************************************
```

Read size	# Mismatch	Hit Count	Total Norm	Total	M026 head	M056 embryo	V120 male body	V058 head	M043 female body	
22	0	1	53.00	53	45	1	5	2	0	....GTAAGTGTCGAATTAAGGGATT....
23	0	1	11.00	11	9	2	0	0	0	....GTAAGTGTCGAATTAAGGGATTT....
21	0	1	9.00	9	8	0	0	0	1	....TAAGTGTCGAATTAAGGGATT....
21	0	1	6.00	6	5	0	0	1	0	....GTAAGTGTCGAATTAAGGGAT....
22	0	1	4.00	4	1	1	1	0	1	....TAAGTGTCGAATTAAGGGATTT....
24	0	1	3.00	3	3	0	0	0	0	....GTAAGTGTCGAATTAAGGGATTTA....
23	0	1	2.00	2	2	0	0	0	0	....TAAGTGTCGAATTAAGGGATTT....
23	1	1	1.00	1	1	0	0	0	0	....GTAAGTGTCGAATTAAGGGATTG....
23	0	1	1.00	1	0	0	0	0	1	....AAGCCCTTGTTTTGACTTTTCAG....
19	0	1	1.00	1	0	0	0	0	1	....GCGTCAATTGACGGGCGAG....
24	0	1	1.00	1	0	1	0	0	0	....AAGCCCTTGTTTTGACTTTTCAGT....
20	1	1	1.00	1	1	0	0	0	0	....GTAAGTGTCGAATTAAGGGG....
21	0	1	1.00	1	0	1	0	0	0	....AAGTGTCGAATTAAGGGATTT....
23	0	1	1.00	1	0	1	0	0	0	....AGCCCTTGTTTTGACTTTTCAGT....
23	1	1	1.00	1	0	1	0	0	0	....AAGCCCTTGTTTTGACTTTTCAG....

Anti-sense strand reads

```
CCGCAGGAGTACCCGTAGCGGCACGCGTGACCTAGCGGGGACTCGTAGTTCATTCACAGCTTAATTCCCTAAATTCCCTAATTCCAGTGATTTCGGGAACAAAACTGAAAAGTCAAACCGCCTCGGACATACCGCAGTTAACTGCCCGCTCTAAGATGCCGGGT
**********************************************......(((((((.(((((((.(((.((.((.(((....))).)).).)))))))))..)))))).......**********************************************
```

Read size	# Mismatch	Hit Count	Total Norm	Total	V058 head

Show Alignment With Reads

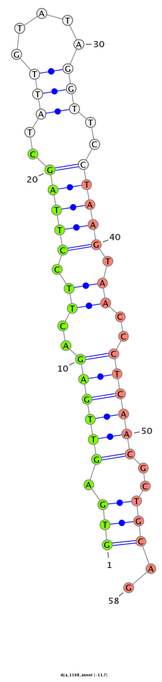
Re-alignment of all predicted orthologs

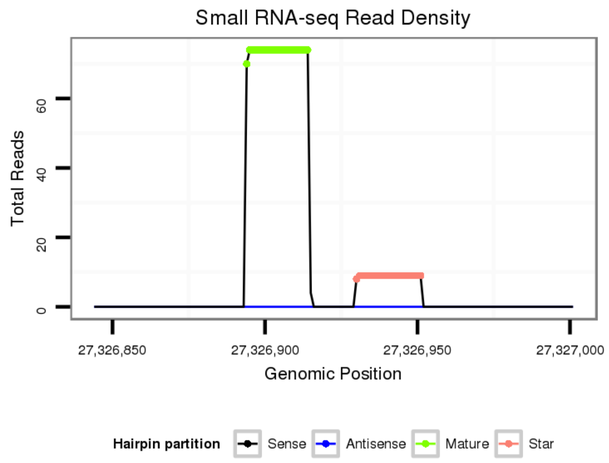
Species	Coordinate	ID	Alignment
droYak3	X:19507347-19507510 +	dya_1474	GGCGTCCTCATGGGCATCGCCGTGCGCACTGGATCGCCCCTGAGCATCAAGTAAGTGTCG--AATTA----------AG--GGATTT----------AAGGGATTAA----------GGTCACTAAAGCCCT------TGTT---TTG-ACTTTTCAGTTTGGCGGAGCCTGTATGGCGTCAATTGACGGGCGAGATTCTACGGCCCA
droEre2	scaffold_4690:10349332-10349491 +		GGCGTCCTCATGGGCATCGCCGTGCGCACAGGATCGCCGCTGAGCATCAAGTAAGTGTCC--*****----------**--******----------**********--------CGATCC----------TTGTCACC-GAG---CT-AGTCACTAACGCCCG-----CGTT---TTG-ACATTTCAGTTTGGCTGAGCCCGTGTGGCGCAATTGACGGGCGAGGTTCTACGGCCCA
droSec2	scaffold_8:2474901-2475080 +		GGCGTCCTCATGGGCATCGCCGTGCGTACAGGATCGCCGCTAAGCATCAAGTAAGTGTCG--AGTTC----------AG--GGATAC----------CTC-----AATAAC-----CGATCC----------TTG-----G-GCCACTA-TGTCACTATGACCT-----TGTT---TTG-ATATTTCAGTTTGGCGGAGCCTGTGTGGCGTCAATTGACGGGCGAGGTTCTACGGCCCA
droSim2	x:19038982-19039161 +	dsi_16471	GGCGTCCTCATGGGCATCGCCGTGCGTACAGGATCGCCGCTGAGCATCAAGTAAGTGTCG--AGTTC----------AG--GGATAC----------CTC-----AATAAC-----CGATCC----------TTG-----G-GGGACTA-TGTCACTATGACCT-----TGTT---TTG-ATATTTCAGTTTGGCGGAACCTGTGTGGCGTCAATTGACGGGCGAGGTTCTACGGCCCA
dm3	chrX:20281513-20281681 +		GGCGTCCTCATGGGCATCGCCGTGCGTACAGGATCGCCGCTGAGCATCAAGTAAGTGTCG--AGTTC----------AG--GGATAA----------CGATAGTAATAAC-----CGA----------**TCACTAATTCCCT------TGTT---CTA-ATATTTCAGTTTGGCGGAGCCTGTGTGGCGTCAATTGACGGGCGAGGTTCTACGGCCCA
droEugl	scf7180000409230:103659-103821 -		GGTGTGCTCATGGGCATCGCCGTACGCACGGATCGCCGCTGAGTATCAAGTGCAGTACGA--TTC----------AA--GCGTAAC----------********--------C----------TTG-----G-T---TA-TGACACCTAAACCATTG---TGTT---CTA-ACTTTCTAGTTTGGCGGAGCCTGTGTGGCGACGCTGACGGCGAGGTCTTGCGACCCA
droBia1	scf7180000302126:3037527-3037687 +		GGCGTCCTCATGGGCATCGCCGTGCGTACCGGATCCCCCTGAGCATCAAGTGCAGTAGAA--TA----------GG--******----------**********--AT----TGATCC----------TTG-----G-A----TG-GGCATTATTACGTT------CTCC---CTG-CGCTTTCAGTTTGGCGGAGCCGCGTGTGGCGCAGCTGACCGGCGAGATACGTGCGGCCCA
droTak1	scf7180000415248:36285-36358 -		A**********----------**********--------**********----------**********----------**********-----CTATTATGTGT------TACC---CT-TTTTTAGCTTGGCGGAGCCGCTTTGGCGTCAGCTGACCGGCGAGATCGTGCGGCCCA
droEle1	scf7180000491272:1366244-1366303 +		GGCGTGCTCATGGGCATCGCCGTGCGCACCGGATCGCCGCTGAGCATCAAGTCAGTAGCG--*****----------**********--------**********----------**********----------**********----

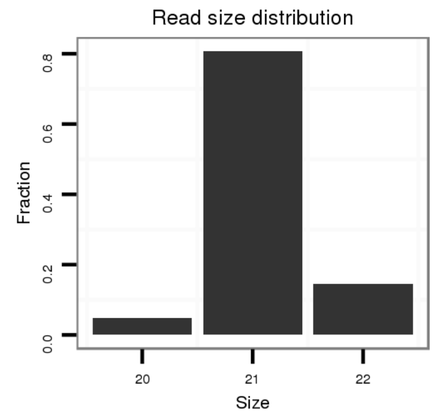
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dya_1168	**3R:27326894-27326951 +**	**confident**	**Mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

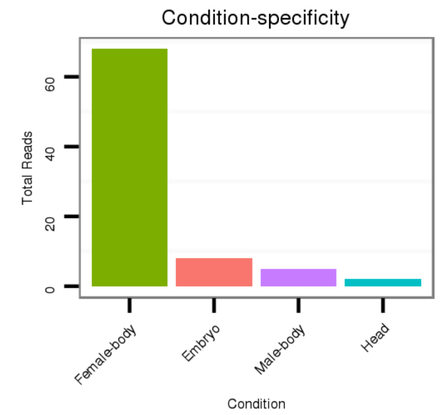
Legend: mature star mismatch in alignment mismatch in read

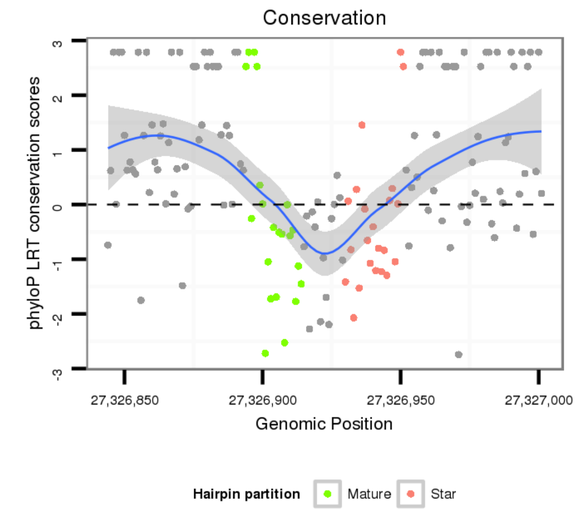
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dyak\GE10890-in]; CDS [Dyak\GE10890-cds]; CDS [Dyak\GE10890-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

```
GATCTTCCAGGTGCAGTACCAGGTCGTAACGCCCATGTGGCGCAGCAAACGTGAGTTGAGACTTCCTTAGCTATTGTATAGGTTCCTAAGTAACCCTCAACGCTGCAGGTTCCGATCTAGTGCCCGGAATCCTGGCCTTCGTCACCTGTTTGGTGCTG
```

Read size	# Mismatch	Hit Count	Total Norm	Total		M043 female body	M056 embryo	V120 male	V058 head	M026 body head	V052 head
21	0	1	66.00	66		57	6	1	0	1	1
22	0	1	8.00	8		2	2	4	0	0	0
20	0	1	4.00	4		4	0	0	0	0	0
22	0	1	4.00	4		4	0	0	0	0	0
23	1	1	3.00	3		0	3	0	0	0	0
23	1	1	3.00	3		1	2	0	0	0	0
21	0	1	1.00	1		1	0	0	0	0	0

Anti-sense strand reads

```
CTAGAAGGTCCACGTCATGGTCCAGCATTGCGGGTACACCGCGTCGTTTGCACTCAACTCTGAAGGAATCGATAACATATCCAAGGATTCATTGGGAGTTGCGACGTCCAAGGCTAGATCACGGGCCTTAGGACCGGAAGCAGTGGACAAACCACGAC
```

Read size	# Mismatch	Hit Count	Total Norm	Total		M056 embryo

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droYak3	3R:27326844-27327001 +	dya_1168	GATCTTCCAGGTGCAGTACCAGGTCGTAACGCCCATGTGGCGCAGCAAACGTGAGTT---GAGACTTCCTTAG-C----------TATT-------G-TATAGGTTC--CTAA--GTAA-------CC-CTC--AACGCTGCAGGTTCCGATCTAGTGCCCGGAATCCTGGCCTTCGTCACCTGTTTGGTGCTG
droEre2	scaffold_4820:1597775-1597929 -		GATCTTCCAGGTTCAGTACCAGGTCGTAACGCCCATGTGGCGCAGCAAACGTGAGTT---GCGACTTCCTTAG-C----------TGTT-------G-TATGCATTC--CCAA--GTAA-------CC-C---TCTTTGCAGGTTCCGATCTAGTGCCCGGAATCCTGGCCTTCGTCACCTGTTTGGTACTG
droSec2	scaffold_4:5233939-5234096 +	dse_121	GATCTTCCAGGTTCAGTACCAGGTCGTAACGCCCATGTGGCGCAGCAAACGTGAGTT---GAGACTTCCTTAG-T----------TAGT-------A-TTTATATTC--CTAA--GTAA-------CC-CTC--AACGTTGCAGGTTCCGATCTAGTGCCCGGCATCCTGGCCTTCATCACCTGTTTGGTAGTG
droSim2	3r:25726995-25727152 +		GATCTTCCAGGTTCAGTACCAGGTCGTAACGCCCATGTGGCGCAGCAAACGTGAGTT---AAGACTTCCTTAG-T----------TAGT-------A-TTTATATTC--CTAT--GTAA-------CC-CTC--AACGTTGCAGGTTCCGATCTAGTGCCCGGCATCCTGGCCTTCGTCACCTGTTTGGTAGTG
dm3	chr3R:26407102-26407259 +		GATCTTCCAGGTTCAGTACCAGGTCGTAACGCCCATGTGGCGCAGCAAACGTGAGTT---GAGACTTCCTTGA-T----------TAGT-------A-TTTATATTC--CTAA--GTTA-------CC-TTC--AACGTTGCAGGTTCCGATCTAGTGCCTGGCATCCTGGCCTTCGTCACCTGTTTGGTAGTG
droEug1	scf7180000409555:913014-913173 +		GATCTTCCAGGTCCAGTACCAGGTCGTAACGCCCATGTGGCGAAGCAAACGTGAGTT---AGGACTGGCTCAGTC----------TAAT-------T-GATATATTC--CTCA--GTAA-------TCTCTC--ATCCTTTCAGGTTCCGATCTAGTGCCGGGAATTCTGGCCTTTGTTACCTGTCTGGTGCTG
droBia1	scf7180000302113:954541-954695 -		GATCTTCCAGGTCCAGTACCAGGTCGTGACGCCCATGTGGCGCAGCAAACGTGAGCT---CCGAACTAGTTAG------------TT---T-------AGTATGTATTC--CAAA--GTAA-------TC-GCT--AATCTACCAGGCTCCGATCTAGTGCCCGGCATCCTGGCCTTCGTCACCTGCTTGGTGCTG
droTak1	scf7180000415367:388018-388196 +		GATCTTCATGGTCCAGTACCGAGTGATCAAGCCCATGTGGCATAGTAAAGTGAGTT---AAAAAAAGATGGCTTACATGAAAAAGCGAAGTTGGTTA-----CTA-----AT-A-TGTGT--GTCA---TTTTTCTCT--TTGCCCACAGAAACGCATCTCATACCCGGTTTGGGTGCCTTTTTCGCCTGTCTGGTTGTG
droEle1	scf7180000491280:2733647-2733796 +		GATCTTCCAGGTCCAATACCAGGTGATAACACCCATGTGGCGCAGTAAACGTAAGTG---TTACCCTCCTAG-C----------CA--------T-----ATCC--CCAT--CTCA-------CT-CTT-ATTTCCATAGGTTCCGATCTAGTTCCTGGAATCCTGGCCTTTGTCACCTGTTTGGTGCTG
droRho1	scf7180000778339:27033-27191 -		GATCTTCCAGGTCCAATACCAGGTCGTAACCCCCATGTGGCGCAGCAAACGTGAGCG---TAATCCTATTTAG------------TGGT-------G-TTCATAATC-TTCAC--CTCA-------CT-TTT-ATTTTTCAAAGGTTCCGATTTAGTCCCTGGAATCCTGGCCTTTGTAACCTGTTTGGTGTTG
droFic1	scf7180000454106:65018-65172 -		CATCTTCCAGGTGCAGTTCCAAGTCGTGACGCCCATGTGGCGCAGCAAACGTGAGTT---CACTGGTCCCTTT-C----------CAA-----CCA-----AT-C-TGCGA--CTCA-------CT-CCC-AATCCCCACAGGCTCCGATTTAGTGCCCGGCATCCTGGCCTTCGTCACCTGCTTGGTGCTG
droKik1	scf7180000302390:371877-372039 +		GATCTTCCAGGTTCAATACCAAGTCGTCACACCCATGTGGCGCAGCAAACGTGAGTA---GAGAACATCTTAT-T----------TATT----AAAA-ATAAATTTT--CCAA--ATAA-------GC-AGAAATATTTTACAGGCTCTGATTTAGTCCCTGGCATGTTGGCCTTTATCACCTGCTTGGTGCTG
droAna3	scaffold_12911:4575918-4576078 -		TATCTTCCAGGTCCAGTACCAGGTCGTCACGCCCATGTGGCGCAGCAAACGTAAGTC---CAGCGGTCCACCG-G----------GAGG-------G-TCTCTAATCATGAAA--CTCA-------CT-ATA-CATCCTATTAGGTTCCGATTTAGTACCTGGTATCCTGGCCTTTGTCACCTGTCTGGTTCTA
droBip1	scf7180000396640:1418467-1418627 -		CATCTTCCAGGTTCAGTACCAGGTCGTCACGCCCATGTGGCGCAGCAAACGTAAGTC---CAGACATCCATCG-G----------GAGA-------G-TATCTAACCATACAA--GTCA-------CT-ATA-CATCCTATTAGGTTCCGATTTAGTGCCTGGTATCCTGGCCTTTGTCACTTGTCTGGTTGTA
dp5	2:1123743-1123900 -		AATTTTCCAGGTCCAGTACCAGGTCGTCACGCCCATGTGGCGCAGCAACGTGAGTTTTGCGA-G-TCCTGCT-C----------CAT-------T-TCCCCTGTC--TAT--ATCA---TT--CCTCTC--AACCTACCAGGCTCCGATCTAGTGCCTGGCATCCTGGCCTTCGTCACCTGCCTGGTGCTG
droPer2	scaffold_7:730577-730737 +		GGTGTTCATGATCGAAGTCAAGGTGGTTAAGCCCATGTGGCGATCGAAGAGTAAGTA---CATGGGAAGATTA-A----------A-----GAAG-------A-TTAAACGTC--TAATT-GTAA-------CA-TGGAAATTTTTGCAGAAAGCGATCTGGTGCCCGGTGTGGGCAGTTTCGTTGCCTGTCTGGTGCTG
droWil2	scf2_1100000004943:9913601-9913761 +		CATTTTCCAAGTTCAGTATCAGATCGTCACGCCCATGTGGCGTAGTAAACGTAAGTT---CCGTACTCCAAAG-A----------AATG-------A-TTTTCAGTGATTTGA--CCTTTGA----CC-T--TTATTTATAGGATCCGATTTAGTGCCTGGCATATTTGGTTTCATGTGCTGTCTTGTAATG
droVir3	scaffold_13047:15955878-15956033 +		AGTGTTCCAGGTGCAGTACCAGATCGTGGTGCCCATGTGGCGCAGCAAACGTAAGTT---GATGGCTTCAGCG-C----------CGG-------T-CAAGCGTT---TATTTGGAA-------TA-TCC--GCATTTACAGGCCGTGATCTTGTGCCTGGACTGCTGGCGTTCATCACCTGCCTGGTGCTT
droMoj3	scaffold_6540:19481224-19481382 +		AGTGTTCCAGGTCCAGTACCAAATCGTAGGCCCGATGTGGCGCAGCAAACGTGAGCT---CGA-CTTCCTGAA-T----------TG-CTGTCTTAAATT-----GT-C-TTCAA--TTCA-------TT-CTC--A-AATTACAGGCTCTGATCTTGTGCCCGGTCTGCTGGCGTTCGTCACCTGCCTTGTGCTG
droGri2	scaffold_14830:4057715-4057874 -		AGTTTTTCAACTTCAGTATCAGATCGTGTTGCCCTTGTGGCGCAGCAACGCGTGAGTT---GAAGTCATCTTATT-C----------CAAT-------A-CTGCAGTTC--TTATTTACAA-------TT-CTT--CAATTTTCAGGCTCCGATCTTGTGCCTGGCGTGCTGGCCTTTTTCGCCTGTCTGGTTACTT

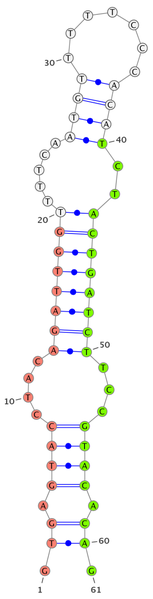
Generated: 09/08/2015 at 07:00 PM

	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

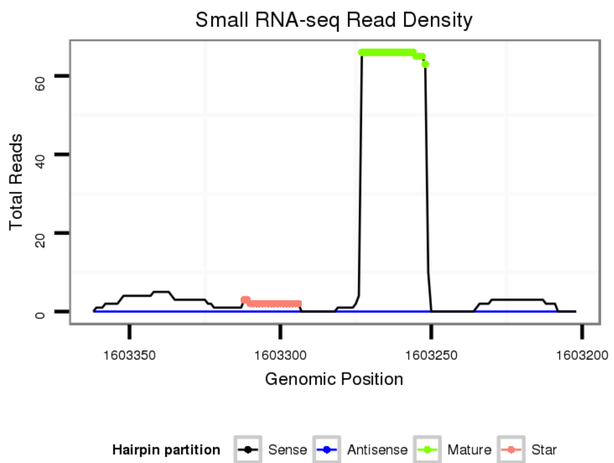
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dya_665	**3L:1603252-1603312 -**	**candidate-rescued**	**Mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

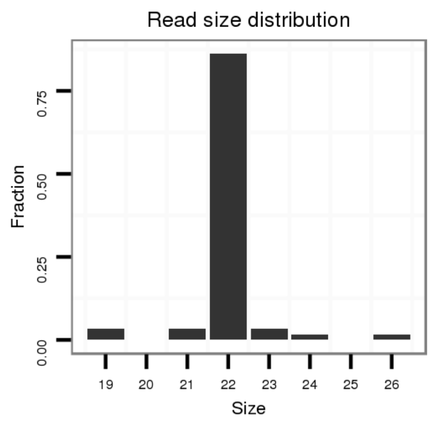
Legend: mature star **mismatch in alignment** mismatch in read

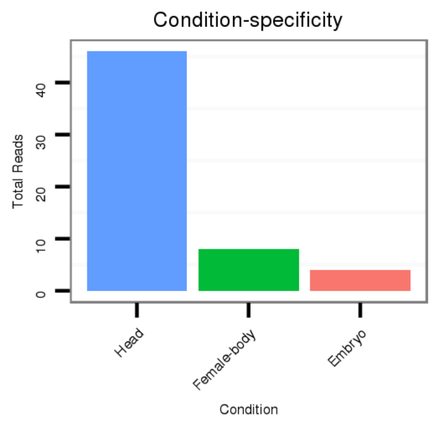
Predicted structure

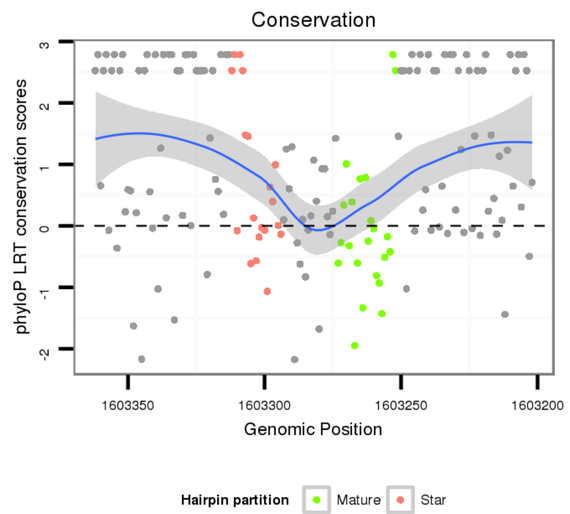


dya_665, score: (-9.9)









Show Alternate Folds

Flybase annnotation

intron [Dyak\GE20937-in]; CDS [Dyak\GE20937-cds]; CDS [Dyak\GE20937-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

CAGGAACATGATACCCGAGATGTGGTCATCGCCTACTGGGCGAGACTATAGTGAGTACCTACAGATTGGTTTTCAATGTTTTTCCCACATCTACTGATCTTCCGTACACAGTGCCCTCCAGGTGGGCCTTAAGGCCTCCACCCAAACGGGCGAGGAAACAA **********.((.((((....((((((((.....((((.....))))..))))))))...))))).)).**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M026 head	M043 female body	M056 embryo	V046 embryo	V120 male body	V058 head
.....TCTACTGATCTTCCGTACACAG.....	22	0	1	50.00	50	45	2	2	1	0	0
.....TCTACTGATCTTCCGTACACAGT.....	23	0	1	10.00	10	2	0	4	2	0	2
.....TCTACTGATCTTCCGTACACAGC.....	23	1	1	2.00	2	0	0	2	0	0	0
.....GTGAGTACCTACAGATTGG.....	19	0	1	2.00	2	0	2	0	0	0	0
.....TCTACTGATCTTCCGTACACAC.....	22	1	1	2.00	2	2	0	0	0	0	0
.....ATCTACTGATCTTCCGTACACAG.....	23	0	1	2.00	2	0	1	1	0	0	0
.....TCTACTGATCTTCCGTACACA.....	21	0	1	2.00	2	0	2	0	0	0	0
.....CATCTACTGATCTTCCGTACACAG.....	24	0	1	1.00	1	1	0	0	0	0	0
.....CTTAAGGCCTCCACCCAAACGGG.....	23	0	1	1.00	1	0	1	0	0	0	0
.....TTAAGGCCTCCACCCAAACGGGCGAG.....	26	0	1	1.00	1	0	1	0	0	0	0
.....TCTACTGATCTTCCGTACACAT.....	22	1	1	1.00	1	0	1	0	0	0	0
.....CTACTGGGCGAGACTATAGT.....	20	0	1	1.00	1	0	0	0	0	1	0
.....TTCCCACATCTACTGATCTTCCGTAC.....	26	0	1	1.00	1	0	1	0	0	0	0
.....TGTGGTCATCGCCTACTGGG.....	20	0	1	1.00	1	0	0	1	0	0	0
....AACATGATACCCGAGATGTGGTC.....	23	0	1	1.00	1	0	0	0	0	1	0
.....GGCCTCCACCCAAACGGGCGAG.....	22	0	1	1.00	1	0	1	0	0	0	0
.....GATACCCGAGATGTGGTCATCGC.....	23	0	1	1.00	1	0	1	0	0	0	0
.....ATACCCGAGATGTGGTCATCGCCTACTG.....	28	0	1	1.00	1	0	1	0	0	0	0
.AGGAACATGATACCCGAGATGTGGT.....	25	0	1	1.00	1	0	0	0	0	1	0

Anti-sense strand reads

GTCCTTGTACTATGGGCTCTACACCAGTAGCGGATGACCCGCTCTGATATCACTCATGGATGTCTAACCAAAAGTTACAAAAAGGGTGTAGATGACTAGAAGGCATGTGTCACGGGAGGTCCACCCGGAATTCCGGAGGTGGGTTTGCCCGCTCCTTTGTT **********.((.((((....((((((((.....((((.....))))..))))))))...))))).)).**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M043 female body	GSM1528802 follicle cells	V120 male body

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droYak3	3L:1603202-1603362 -	dya_665	CAGGAACATGATACCCGAGATGTGGTCATCGCCTACTGGGCGAGACTATAGTGAGTACCT-------ACAGATTGGTTTTCAATG--TTTTTCCC----------ACATCT-ACTGA----------T-----CTTCCG-----TACACAGTGCCCTCCAGGTGGGCCTTAAGGCCTCCACCCAAACGGGCGAGGAAACAA
droEre2	scaffold_4784:1632087-1632247 -		CAGGAGCATGATACCCGCATGTGGTCATCGCCTACTGGGCGAGACTATAGTGAGTACCT-------ACAGATTGGTTTTCCTTG--TTTTGCCC----------GTATTT-ACTGA----------T-----CTCCCG-----GATACAGTGCTCTGCAGGTGGGCCTCAAGGCCTCCACCCAAACGGGCGAGGAAACCA
droSec2	scaffold_2:1678753-1678913 -		CAGGAACATGATACCCGGATGTGGTCATCGCCTACTGGGCGAGACTCTAGTGAGTATCT-------ACAGATTGGTTTTTCTTG--TTTTGCCC----------GTATTT-ACTCA----------T-----CTTCCG-----TATCCAGTGCTCTCCAGGTGGGCCTCAAAGCCTCCAGTCAAACGGGTGAGGAAACCA
droSim2	3L:1562351-1562511 -		CAGGAACATGATACCCGGATGTGGTCATCGCCTACTGGGCGAGACTCTAGTGAGTATCT-------ACAGATTGGTTTTCTTG--TTTTGCCC----------GTATTT-ACTCA----------T-----CTTCCG-----TATCCAGTGCTCTCCAGGTGGGCCTCAAAGCCTCCACCCAAACGGGTGAGGAAACCA
dm3	chr3L:1652579-1652739 -	dme_387	CAGGAACATGATACCCGGATGTGGTCATCGCCTACTGGGCGAGACTCTAGTGAGTATCT-------ACAGATTAGTTTTCTTG--TTTTGCCC----------GTATTT-ACTCA----------T-----CTTCCG-----ATCCAGTGCTCTCCAGGTGGGCCTCAAAGCCTCCACCCAAACGGGTGAAGAAACCA
droEug1	scf7180000409007:470812-470975 -		CAGGAACAGACACACGGATGTATCATAGCCTATTGGGGTAGACTCTAGTAAGCACCT-------ACATATTGTTTTGCTTG--TT-----C----------GTATTT-AATAAT-TTTG----------TG-T----CTTTCTG-----AATCTAGTGCCCTCCAGGTGGGCCTCAAGGCCTCCACCCAAACGGGAGAGGAAACTA
droBia1	scf7180000300910:1773550-1773711 -		CAGGAGCAGACACCCGAGATGTGGTCATAGCCTACTGGGCGAGATTATAGTAAGTACCC-------ATAGATCGGTTTTT----T--------**********GTACTT-ACTTATGGTTC----------TT-TGTCCTCTCCCG-----GACCTAGTGCCCTCCAGATTGGCCTCAAGGCCTCCACCCAAACGGGTCAGGAAACCA
droTak1	scf7180000415095:120167-120338 +		CAGGAGCAGACACTCGAGATGTGGTCATCGCCTACTGGGCGAGATTATAGTAAGTACCT-------GGAGATTGTTTTTCCTTT--A-------**********TAAGC----CCCGTATTTGATGTCCTTTG----------TT-T----GATCCCT-----GAACTAGTGCCCTCCAGATTGGCCTCAAGGCCTCCACCCAAACGGGCGAGGAAACCA
droEle1	scf7180000491249:3923335-3923506 +		CAAGAGCATGACACAAGGGATGTATCATTGCCTACTGGGCGAGACTCTAGTAAGTACCT-------ACAATATTGTTTTACCCTG-T-------**********CCCGG----TGTGTATTT-AAATTTAATTC----------TT-T----GTTTCCG-----GATCTAGTGCCCTCCAGGTGGGTCTCAAGGCGTCCACCCAAACGGGTGAGGAAACCA
droRho1	scf7180000776850:295553-295723 +		CAGGAGCAGACACCCGAGATGTGGTCATTGCCTACTGGGCAAGACTCTAGTAAGTACCT-------ACAGATTGTGTTTTCCTT--********ACCCAG----TGTGTATTT-ACTGTTCTTTG----------TG-T----GCTCCCG-----GCTCTAGTGCGCTCCAGGTGGGTCTCAAGGCGTCCACCCAATCGCTGAGGAAACCA
droFic1	scf7180000454113:428982-429150 +		CAGGAACAGACACCCGGATGTGGTCATTGCTTACTGGGCAAGACTCTAGTAAGTACCC-------ACAGAATTCTTTCGTCTA--********----------AG-CG--TGTGTATTT-ACTATTTCTTG----------GT-T----GTCTCCA-----ATCCGAGTGCCCTCCAATGTGGGTCTCAAGGCCTCCACCCAAACGGGCGAGGAAACCA
droKik1	scf7180000302577:124501-124667 -		CAAGAGCAGACACAAGGGATTTGGTCATCGCCTACTGGGCCAGACTCTAGTGAGTATTG------**********TTA--TTTTCTTG--TTT-----**********AATAA-AG--GATGCATGTG-ACTGATATAGT----------GGT-----GTTTCC-----TCTCTAGTGCCCTTCAGGTGGGACTCAAAGCCTCCACCCAGACGGGGCGAGGAGACCA
droAna3	scaffold_13337:1184902-1185065 +		CAGGAGCATGATTCGAGAGATTTTGTGATAGCCTATTGGGCGAGACTCTAGTAAGTAACC-------ATTG----TTTATTGTTG--AA-----**********TGGCT--CTGGCT-AATCT----------CTG-T----CTCTTCTCAACC--TCCTTAGTGCTCTCCAGGTAGGCTTGAAGGCCTCTACCCAAACTGCAGAGGAAACCA
droBip1	scf7180000396371:1517466-1517632 +		CAGGAGCATGATTCGAGAGATTTCGTGATAGCCTATTGGGCGAGACTCTAGTAAGTAATC-------**********---CATTGTTTATGGTCG--A-------**********TTGGG----T--GTAATT-AATAA---TTG----------CT-------CTTCTTAAACTCTATTAAGTGCTCTCCAGGTAGGCTTAAAGGTGTGTACCCAAACGGGCAGAGGAAACCA
dp5	XR_group6:7798451-7798609 -		CAGGAGCAGACAATCGCGACATTGTGATCGCCTACTGGGCAAGAATTTAGTGAGTACCT-------**********TTGTTTTTTTTT--********ACAAAACG----AATATT-**********AATTG----------TT-T----CATCTAC-----TGTGCAGTGCTCTGCAAGTAGGCCTAAAGGCCTCTACGCAAACCGGCGAGGAGACAA
droPer2	scaffold_27:656936-657095 +		CAGGAGCAGACAATCGCGACATTGTGATCGCCTACTGGGCAAGAATTTAGTGAGTACCT-------**********TTGTTTTTTTTT--**T**********ACAAAACG----AATATT-**********AATTG----------TT-T----CATCTAC-----TGTGCAGTGCTCTGCAAGTAGGCCTAAAGGCCTCCAGCGAAACCGGCGAGGAGACAA
droWil2	scf2_1100000004837:1566396-1566559 -		CAGGAACATGACAATCGGGATGTGATCATTGCATATTGGGGAAGACTCTAGTGAGTGTAA-------A----------**********--********----------GG----AAAAAG-**********AAAAGTAATATCCATTTGGTTTAAATGTTTG-T----T-TATTAT-----ATTCCAGTGCCCTGCAGGTGGGTCTGAAGGCCTCCACCCAGAGTCCCGAGGAAACGA
droVir3	scaffold_13049:2269111-2269282 -		CAGGAGCAGATTCGCGTGACGTTGTCATAGCCTACTGGGCAAGACTCTAGTAAGTAAT-------CCCAG---TCCTTACGTTCCA------A--------AGAAAA----CTCGAAATA-ACAATTTTTTG----------TT-T----AATTAAT-----TACAAAGTGCGCTGCAAGTTGGCCTAAAGGCATGTACACAGAGCGCCGAAGAGACTA
droMoj3	scaffold_6654:1595690-1595865 +		CAGGAGCATGATTCGCGTGACATTGTCATAGCCTACTGGGCAAGGCTCTAGTAAGTAGAT-------GCGCGATGGGTTTGCCTG--**********CCAGTAAATTTCGCATAAGC----AAAATG-**********TTTTT----------GT-T----AAATTAAT-----TCTAAAGTGCGCTGCAAATTGGCTTAAAGGCGTCATGTCAGAGCGCAGAGGAGACTC
droGri2	scaffold_15110:3305448-3305630 -		CAGGAGCATGATACTCGCGACGTCGTTATTGCGTATTGGGGTCGGCTCTAGTGAGTAAAATTTATAATC-CA---TTTCTT----**********GGAAATGG----AAAAAAA-ACA--**********ATTTGGTTTATTTT-TTT-T----CTATATTCTATTTTTGTTAAACCGCGTCTACAAGTTGGCCTAAAAGCATCCAGACAAACCGCCGAGGAGACAC

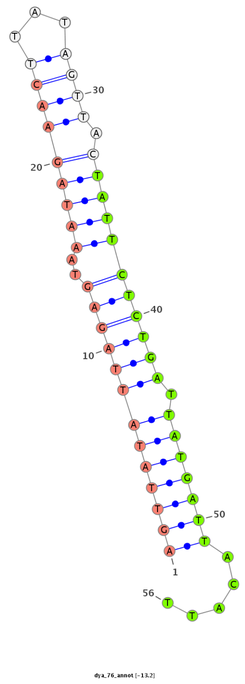
Generated: 09/08/2015 at 10:33 PM

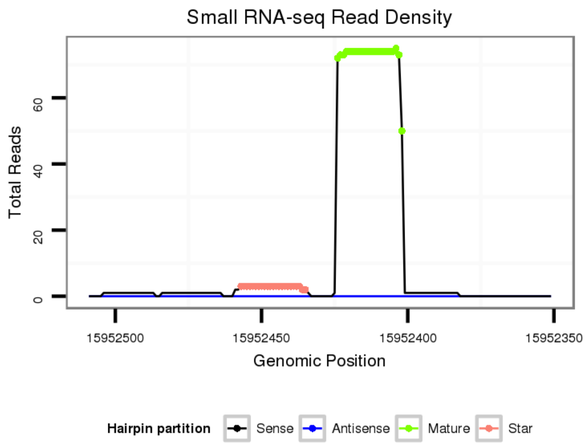
	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	1

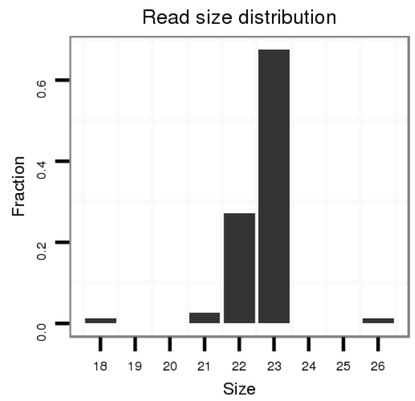
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dya_76	**2R:15952401-15952459 -**	**confident**	**3p_tailed_mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

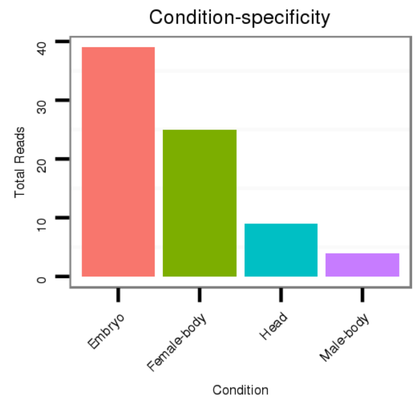
Legend: mature star mismatch in alignment mismatch in read

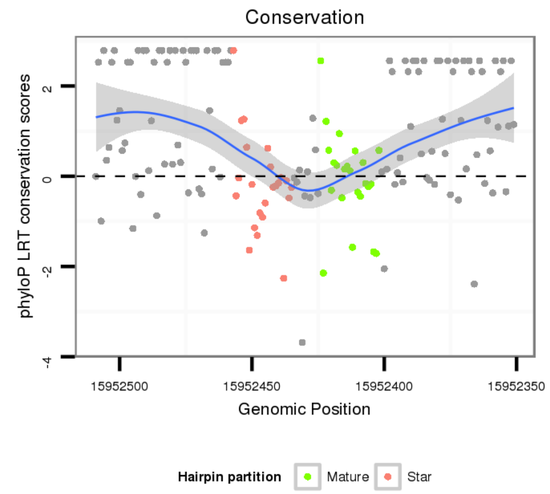
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dyak\GE11859-in]; CDS [Dyak\GE11859-cds]; CDS [Dyak\GE11859-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

```
TCCAAGGAGAGTCGTTTGAAGGCATTTGAAAATTCGTTTGTCAAGATTGGGTAGTTATATTAGAGTAAATAGAACTTATAGTTACTATTCTCTGATTATGATTACATTTTCAGGGGAAGCATGCTAGTCAATCTGGACAAATCGCTGCAAATGGTGGAA
**************************************************((((((((((((..(((((((((...)))))).))))))))))).)))))))).....**************************************************
```

	Read size	# Mismatch	Hit Count	Total Norm	Total	M056 embryo	M043 female body	V046 embryo	V120 male body	V052 head	V058 head	M026 head
.....TATTCTCTGATTATGATTACATT.....	23	0	1	49.00	49	17	11	16	1	1	2	1
.....TATTCTCTGATTATGATTACAT.....	22	0	1	21.00	21	2	9	3	2	2	1	2
.....TATTCTCTGATTATGATTACAC.....	22	1	1	3.00	3	3	0	0	0	0	0	0
.....AGTTATATTAGAGTAAATAGAAC.....	23	0	1	1.00	1	0	1	0	0	0	0	0
.....TATTCTCTGATTATGATTACA.....	21	0	1	1.00	1	0	1	0	0	0	0	0
.....GGAGAGTCGTTTGAAGGC.....	18	0	1	1.00	1	1	0	0	0	0	0	0
.....CTATTCTCTGATTATGATTACAT.....	23	0	1	1.00	1	0	1	0	0	0	0	0
.....TCTCTGATTATGATTACA.....	18	0	1	1.00	1	0	1	0	0	0	0	0
.....TTGAAAATTCGTTTGTCAAGA.....	21	0	1	1.00	1	0	0	0	1	0	0	0
.....TATTCTCTGATTATGATTACATA.....	23	1	1	1.00	1	0	0	1	0	0	0	0
.....TATTCTCTGATTATGATTACATC.....	23	1	1	1.00	1	1	0	0	0	0	0	0
.....ATTCTCTGATTATGATTACAT.....	21	0	1	1.00	1	0	1	0	0	0	0	0
.....ATTTTCAGGGGAAGCATGCTAG.....	22	0	1	1.00	1	0	0	0	1	0	0	0
.....GTAGTTATATTAGAGTAAATAGA.....	23	0	1	1.00	1	0	0	0	1	0	0	0
.....GTAGTTATATTAGAGTAAATAGAACT.....	26	0	1	1.00	1	1	0	0	0	0	0	0

Anti-sense strand reads

```
AGGTTCCTCTCAGCAAACTTCCGTAAACTTTTAAGCAAACAGTTCTAACCCATCAATATAATCTCATTTATCTTGAATATCAATGATAAGAGACTAATACTAATGTAAAAGTCCCCTTCGTACGATCAGTTAGACCTGTTTAGCGACGTTTACCACCTT
**************************************************((((((((((((..(((((((((...)))))).))))))))))).)))))))).....**************************************************
```

Read size	# Mismatch	Hit Count	Total Norm	Total	M056 embryo

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droYak3	2R:15952351-15952509 -	dya_76	TCCAAGGAGAGTCGTTTGAAGGCATTTGAAAATTCGTTTGTCAAGATTGGGTAGTTATATTAG--AGTAAA--TAGAAGT----------TATAGT--------TACTATTCTCTGATT---ATGA-TTAC-ATTTTCAGGGGAAGCATGCTAGTCAATCTGGACAAATCGCTGCAAATGGTGGAA
droEre2	scaffold_4845:7466785-7466939 +		TCCAAGGAGAGTCGCCTGAAGGCTTTGAGAATTCGTTTGTAAGATTGGGTAGATATT--TC--CGTAAA--TAGAGCT----------TATAGT--------TATTATTCTCTGATT---ATGA-TT--ATTTTCAGGGGAAGCATGCTAGCGAATCTAGACAAATCGCTGCAATTCGTGGAA
droSec2	scaffold_9:1788314-1788471 -		TCCAAGGAGAGTCGCTGAAGGCATTTGAGACTTCTTTTGTAAGATTGGGTATATATT--TG--AGTAAA--TAGGGCG----------TTCAGT--------TACTATTTTCTGATT---ATAA-TTAGTATTTTCAGGGGCAGCATGCTAGTCAATCTAGACAAATCGCTGCAAATGGTGAAA
droSim2	2r:19015954-19016111 -		TCCAAGGAGAGTCGCCTGAAGGCATTTGAGACTTGTTTTGTAAGATTGGGTATATATT--TG--AGTAAA--TAGGGCG----------TTCAGT--------TACTATTTTCTGATT---ATAA-TTAGTATTTTCAGGGGCAGCATGCTAGTCAATCTAGACAAATCACTGCAAATGGTGGAA
dm3	chr2R:18489686-18489843 -		TCCAAGGAGACTCGCCTGAAGGCATTTGAGAATTCTTTTGTAAGATTGGGTAGATATT--TG--AGTAAA--TAGGGCG----------TTCAGT--------TACTATTCTCTGATT---ATAA-TTAATGGTTTCAGGGGCAGCATGCTAATCAATCTAGACAAATCGCTGCAATTGGTGGAA
droEug1	scf7180000409672:6414715-6414871 -		TCCAAGGAGAGTCGCTTAAAAGCCTTTGAAAATTCGTTTAATAAATTGGGTAGATATACAGG--TGTAGG--TTCAGCT----------TAAAAT--------AACTCATCTCTGATT---CTCT-TC--CATTCCAGGGGCAGTATGCTAGTTAATCTGGATAAATCACTGCAAATGGTTGAA
droBia1	scf7180000302143:2177366-2177513 +		TCCAAGGAGAGTCGACTGAAGGCTTTGAGAATTCATTTATCAAGATTGGGTAGATATT--TG--TATAGG--CAGAGCT----------GCAAGA--------TACTA-------ATT---ACT-TC--AATTTCAGGGGAAGCATGCTGTTAATCTCGACAAATCGCTGCAAATGGTCGAA
droTak1	scf7180000415739:382360-382514 -		TCCAAGGAGAGTCGCTGAAGGCTTTGAGAATTCGTTTGTCAAGATTGGGTAGATATT--TT--TTTAGG--TACACCT----------TACTGA--------TACTCATCTCGCATT---TCT-TT--CATTCAGGGGAAGCATGCTAGTTAATCTGGACAAATCGCTGCAAATGGTCGAA
droEle1	scf7180000491022:67191-67341 -		TCCAAGGAGAGTCGACTGAAGGCTTTGAGAATTCTTTTGTCAAGATCGGGTATATATT--AG--TGTAGG--TATAGCT----------TAAAAT--------TACTCATGCTTGATT---ATGC-----TTTTCAGAGGAAGCATGCTCCTTAATCTTGACAAATCGCTGCAAATGGTCGAA
droRho1	scf7180000780232:21525-21683 -		TGTAAGGAGAGTCGACTGAAGGCTTTGAGAATTCGTTTGTCAAGATTGGGTAGATATATCTTTATCTAGG--TATAGCT----------TATAGT--------TAATAATCCTTATT---ATGC-TT--CATTGTAGGGGAAGCATGCTAGTTAATTTGGACAAATCACTGCAAATGGTCGAA
droFic1	scf7180000454066:2429070-2429224 -		TCGAAGGAGAGTCGACTGAAGGCTTTGAGAATTCGTTTGTCAAGATTGGGTAGATACA--TG--TGTGAA--CAAAGCG----------TATAGT--------TACTTATCTCTGCTT---TTTT-AT--TTTTACAGGGGAAGCATGCTAGTTAATCTCGAGAAATCATTGCAATTGGTCGAA
droKik1	scf7180000302476:1532426-1532605 +		CCCAGGGAGAGTCGCCTGAAGGCTTTGAGAAGTCCTTTGCCAAGATCGGGTAAGTAAC--G---GGAGGGAGCAATTAATTAAGCATCTATTCTTAACT---T-----ATTCTACTTAACGTGTGATTTTTGG-T-TCCTTTTGGCAGCTCCAGCATGATAACCAATCTGGACAAGTCTCTGCAAATGGTCGAG
droAna3	scaffold_13266:7268264-7268419 +		CCCAAGGAGAGCCGCCTAAAGGCATTCGAGAATTCGTTTAAGAAAATAGGGTATGCTT---TC--CGTAGG--TTCAGTT----------TAGGGC--------TAGTGATTCTTAAGC-TTTTAG-TT--TCGTACAGGGGCAGCATGATAACCAATCTGGACAAGTCACTGCAACTGGTGGAG
droBip1	scf7180000396384:85657-85808 +		TGAAAGGAAAGCCGCCTTAAGGCATTTGAGAATTCGTTTAAAAAATCGGGTATGTTT---CC--TGTAGA--TTCAGCT----------TATGGA--------TATTGATTCTAAAC---GTTT-TT--CGTGCAGGGCCAGCATGGTAACCAATCTGGAGCAGTCACTGCAGCTGGTGGAG
dp5	3:7098341-7098498 -		CCCAGGGAGTCCCGCTTGAAGTGCTTCGAAAACTCATTTGCCAGAATCGGGTAGATATACACG--CTTGCA--TAGCGCT----------CAGGGT--------TACTCATCTCTGATT---GTGTGTC--TGTTCCAGGGGAAGCATGATAGCAAATTTGGAAAGTCCATGCAACTGGTCGAG
droPer2	scaffold_2:7297910-7298067 -		CCCATGGAGTCCCGCCTGAAGTGCTTCGAAAACTCATTTGCCAGAATCGGGTAGATATACACG--CTTGCA--TAGCGCT----------CAGGGT--------TGCTCATCTCTGATT---GTGTGTC--TGTTCCAGGGGAAGCATGATAGCAAATTTGGAAAGTCCATGCAACTGGTCGAG
droWil2	scf2_1100000004558:424006-424058 -		GCGAAAGAGAGTCCCTTAAAGCCTTTGAGAATTCATTTAATAAAATTGGGTA---
droVir3	scaffold_12875:12614577-12614733 -		TGCAAGGAGAGTCGACTCAAAGCATTCGAGAGTTCATTTGTCAAAATCGGGTATTTATG--CA--TATACA--GACGGGA----------CACTGT---AAAAATTCTAAT-----ATT---CTGTGCC--TCATGACAGGGGCAGCATGATAGCGAATCTGGACAAGTCGCTGCATATGGTGGAG
droMoj3	scaffold_6496:19880896-19881054 -		TGCAAGGAGAGTCGACTCAAGGCATTCGAGAGGTCATTTCAAAAGATCGGGTATTTATGCTCA--TATAC---TGAAAT----------ACACAATGTCAAAGTACTTAA-----GTG---CTAAACT--AATTATAGAAGCAGCATGATTGCCAACCTGGATAAATCCCTGACTATGGTGGAG
droGri2	scaffold_15245:7747141-7747296 +		TCAAAGAGAGTCGACTGAAAGCATTCGAGAGTTCATTTCATAAAATCGGGTATTTATA--T--AGAAAA--TTGATGT----------ACGAATAGA--------TATTAATTGGTCCCA---TTGC-T---TTCATTAGTTGCAGCATGATTGCAAATCTGGACAAATCACTGCATATGGTCGAG

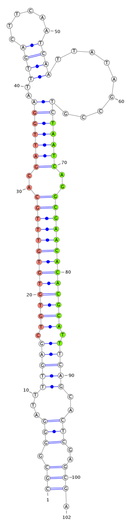
Generated: 09/08/2015 at 07:00 PM

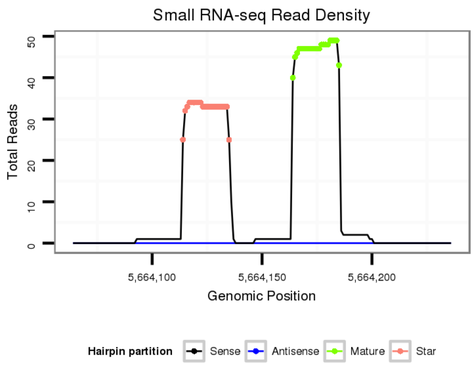
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

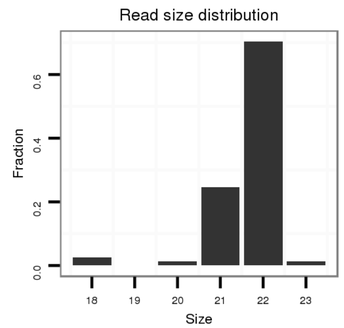
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dya_114	**X:5664114-5664186 +**	**confident**	**Canonical miRNA**	**intron**	[View on UCSC Genome Browser [Cornell Mirror]]

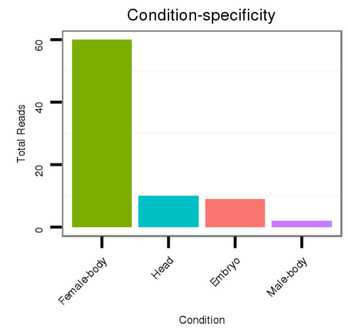
Legend: mature star mismatch in alignment mismatch in read

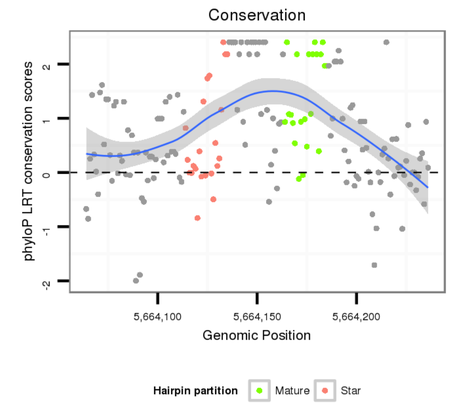
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dyak\GE16919-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

ATCGGGGCATTTTCCCACCCTCTTGTCGACGCTTTCGCGGGGATTTTGAGCTGTGTGTGTTTGCACGATTGGAATTTGACTTCAATCAATTATAGCCGTCTAATCAGGCGAACACACGCATTTCAGCACTCGAGCGAGCACTTGCGTTTGATAAGTGGGTAGAGCAGCAGGGA **********(((.(((...((((((.((((((((((((..(((((((..((((.....)))).....)))))))..))))))))))))).))))))..)))..))).**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M043 female body	V046 embryo	V058 head	V052 head	M056 embryo	V120 male body	M026 head
.....TAATCAGGCGAACACACGCATT.....	22	0	1	34.00	34	32	0	0	2	0	0	0
.....CTGTGTGTGTTTGCACGATTGG.....	22	0	1	15.00	15	11	1	1	0	2	0	0
.....CTGTGTGTGTTTGCACGATTG.....	21	0	1	8.00	8	1	4	0	2	0	0	1
.....TGTGTGTGTTTGCACGATTGGA.....	22	0	1	7.00	7	3	1	2	0	0	1	0
.....TAATCAGGCGAACACACGCAT.....	21	0	1	5.00	5	3	0	2	0	0	0	0
.....AATCAGGCGAACACACGCATT.....	21	0	1	4.00	4	4	0	0	0	0	0	0
.....TGTGTGTTTGCACGATTGGAA.....	21	0	1	1.00	1	1	0	0	0	0	0	0
.....ACACGCATTTCAGCACTCGAGC.....	22	0	1	1.00	1	0	0	0	1	0	0	0
.....ATCAGGCGAACACACGCATT.....	20	0	1	1.00	1	0	0	0	0	1	0	0
.....GCATTTCAGCACTCGAGCGA.....	20	0	1	1.00	1	1	0	0	0	0	0	0
.....CGCTTTCGCGGGGATTTTGAGCTGTGTGTG.....	30	0	1	1.00	1	0	0	0	0	0	1	0
.....CAGGCGAACACACGCATT.....	18	0	1	1.00	1	1	0	0	0	0	0	0
.....AATCAATTATAGCCGTCTAAT.....	21	0	1	1.00	1	0	0	0	0	0	1	0
.....GTGTGTGTTTGCACGATTGGA.....	21	0	1	1.00	1	1	0	0	0	0	0	0
.....CTGTGTGTGTTTGCACGATTGGA.....	23	0	1	1.00	1	1	0	0	0	0	0	0
.....AATCAGGCGAACACACGCATTT.....	22	0	1	1.00	1	1	0	0	0	0	0	0
.....TAATCAGGCGAACACACGCATTGG.....	24	2	1	1.00	1	1	0	0	0	0	0	0
.....TCAGGCGAACACACGCAT.....	18	0	1	1.00	1	1	0	0	0	0	0	0

Anti-sense strand reads

TAGCCCCGTAAAAGGGTGGGAGAACAGCTGCGAAAGCGCCCCTAAAACTCGACACACACAAACGTGCTAACCTTAAACTGAAGTTAGTTAATATCGGCAGATTAGTCCGCTTGTGTGCGTAAAGTCGTGAGCTCGCTCGTGAACGCAAACTATTCACCCATCTCGTCGTCCCT **********(((.(((...((((((.((((((((((((..(((((((..((((.....)))).....)))))))..))))))))))))).))))))..)))..))).**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V046 embryo

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droYak3	X:5664064-5664236 +	dya_114	ATCGG-GGCATTTTC-------C-CACCCTC---TTGTC-GA--CGCTTTCGC-GGGGATTTTGAGCTG------TGT----------G--TGTTTGCACGATTGGAATTTGACT-TCAATCAAT-TATAGCC---GTCTAATCAGGCG----------AACACACGCATTTC-AG-CACTCGAGC---------GAGCACTTGCGTTT----------GAT-AAGTG-GG----------TAG----------AGCAGCAGGGA----------
droEre2	scaffold_4690:115494-115669 -		A-CGGTGGCATTTTC-------C-CACCCCGGTTGCC-GA--CGTTTCGC-GGGG-TTTTGAGCTG------T-T----------A--TGTTTGCACGATTGGAATTTGACT-TCAATCAAT-TAAGTC---GTCTAATCAGGCG----------AACGCC----AACACACATTTC-AG-CACTCGAGC---------GAGCACTTGGTTT----------GAT-AAGTG-GG----------CAG----------AG---TAGGGA----------
droSec2	scaffold_10:2442110-2442283 -		A-CGGCGCGCATTTTC-------C-CACCCC--TTGGCCTT-CGCTTTCGC-GGGGATTTTGAGCTG------TGTGTTCT--------T--TGTTTGCACGATTGGAATTTGACT-TCAATCAAT-TAGATGC---GTCTAATCAGGCG----------AACACACGCATTTC-AG-CACTC----------GAGCACTTGCGTT----------GATTATGTG-GG----------CCG----------AG--GCAGGGA----------
droSim2	x:2482933-2483105 -		A-CGGCGGGCATTTTC-------C-CACCCC--TTGTCAA--CGCTTTCGC-GGGGATTTTGAGCTG------TGTGTTCT--------T--TGTTTGCACGATTGGAATTTGACT-TCAATCAAT-TAGAGCC---GTCTAATCAGGCG----------AACACACGCATTTC-AG-CACTC----------GAGCACTTGCGTT----------GATTATGCG-GG----------CCG----------AG--GCAGGGA----------
dm3	chrX:2682055-2682233 -		A-CGGCCGCATTTTC-------C-CACCCC--TTGGCCAACGCGCTTTTGC-GTGGATTTTGGCTA------TGTGTTCT--------T--TGTTTGCACGATTGGAATTTGACT-TCAATCAAT-TAGAGCC---GTCTAATCAGGCG----------AAC--G----AACACACGCATTTC-AG-CACTC----C---------GAGCACTTGCGTT----------GATTATGTG-GG----------CAG----------AG---CAGGGA----------
droEug1	scf7180000409061:215664-215829 -		-----GGCATTTTC-------C-CAACCCC--C-----T---A-ATTTCGCTGGGGATTTTGAGTT-------G-TTTG----T---G--CGTTTGCCGATTGGAATTTGACT-TCAATCAAT-TAGAGCC---GTCTAATCTGGCG----------AACACACGCATTTC-AG-CACTCGAGC---------AAGCACTTGCC-C----------GATACGCGAT-AAGTGCGG----------CAG----------AG---CAGCGA----------
droBia1	scf7180000302126:2642880-2643020 +		GC-GGA-G-------------C-CACCC---------T---C---TTTGCGC-GGGGATTTTGAG-G-------C-----T--------A--TGTTTGCCGATGGAATTTGACT-TCAATCAAT-TAGGGCC---GTCTAATCAGGCG----------AACACACGCATTTC-AG-CACTC----------GAGCACTTGCC-C----------GAT-AAG-G--GG----------CCG----------AG---CAGGGA----------
droTak1	scf7180000415769:1075842-1075994 -		ATCGGCGGCATTTTC-------C-CACCC---------T---C---TTTCGC-GGGGATTTTGAGTT-------GT----------A--TGTTTGCCGATTGGAATTTGACTTTCAATCAAT-TAGAGCC---GTCTAATCAGGCG----------AACACACGCATTTC-AG-CACTC----------AAGCACTTGCGTTC----------GAT-AAGTG-GA----------TGG----------AA---CAGGGA----------
droEle1	scf7180000490141:276813-276977 +		ATCGGCGGCATTTTC-------C-CCCC---------T---C---TTTCGC-GGGGATTTTGCGCTGGGCACTCTGTGCTCT--------G--TATTTGCCGATTGGAATTTGACT-TCAATCAATTTGGAGCC---GTCTAATCAGGCG----------AACACACGCATTTC-AG-CACTC----------GAGCACTCGAGC-T----------ACCCCGAT-AAGTG-GG----------CCC----------CCCCCGAGA----------
droRho1	scf7180000779467:308846-309010 +		GTCGGCGGCATTTTC-------C-CACCC---------T---C---TTTCGC-GGGGATTTTGCGCTGGGCGCTCTGTGTTCT--------G--TATTGTGCCGATTGGAATTTGACT-TCAATCAATTTGTAGAGCC---GTCTAATCAGGCG----------AACACACGCATTTC-AG-CACTC----------GAGCACTCGAGT-T----------CCCCCGAT-AAGTG-GG----------CCC----------CCCCCGAGA----------
droFic1	scf7180000454072:551734-551899 +		TT-GGCGGGCACTTCGAGGAGAGC-CACCCCCTCTT---C---C---------GGGACCTTTAGCTG------GCCGCTCTTCTGTGGGTTGTG-TTGTGTCGCTTGGAATTCGACT-TCAATCAAT-TATAGCA---GTCTAATCAGGCG----------AACACACGCATTTG-AG-CACTC----------GAGCACTTGCGG-C----------GAT-AAGTG-GG----------CCC----------CCCCCGAGA----------
droKik1	scf7180000302592:2027698-2027846 -		ATCGGCGGCATTTTT-------CCTTCC---C-----T---C---GAATCT---GAATTTTC-----C-----C-----T--------G--TATTGTGCCCTTTGGAATTTGACT-TCAATCAAT-TAGAGCA---GTCTAATCCCAA----------AACACACGCATTTC-AG-CACTC----------GAGCACTTGCTTT----------GAT-AAGCG-GG----------A-G-----G-----G-AG--A-CGGGC------TA----------
droAna3	scaffold_13248:371930-372091 +		-----C---------C-------C-C-------C-----T---C---C---------C-------C-----C-----C-----C--C----TGACCGATTGGAATTTGACT-TCAATCAAT-TAGAGCGCGGTCTAATCAAAA----------AACACACGCATTTCCAGCCACTT----------GAGCACC----C-C----------GGT-AGTA-CCGAGAGCCTCTTATCAGA-ATCAGGGCCTAGCCCGGA---GGTGGGGACTGGGGCATGGAGGAGGTGGAATAT
droBip1	scf7180000392940:37580-37737 -		-----C---------C-------C-C-------C-----T---C---C---------C-------C-----C-----C-----C--C----TGACCGATTGGAATTTGACT-TCAATCAAT-TAGAGCGCGGTCTAATCAGAAA----------AACACACGCATTTC-AGCCACTTGAGCC--CAACCCACACCCCTTTCCC-CTACCGCCTAGCCCCTAGCCGAT-CA---C---------TCTTATCAGA-ATCAGGGCCTAGCCTGGG---GGCGGGC----------
dp5	XL_group1e:2107809-2107938 -		TGTGTTACCAT---C-------C-C-------C-----T---C---C---------C-------C-----C-----C-----C--C-----GTTGAATTGGAATTTGACT-TCAATCAAT-TAGAGCCCGGTCTAATCACTTCGCGT----------AGCGCTGCTGTCGCACACGCATTTC-AGCCACTTC----------AGTCACCGGCGC-T----------TAT-----C---------CAGA-AGC----------AG---GGCAGC----------
droVir3	scaffold_12472:38888-39008 +		-----C---------C-------C-C-------C-----T---C---C---------C-------C-----C-----C-----C--C----------TTGGAATTTGATTCTCAATCAAT-TACCGTTT--G-GGAACCAGGTA----------TTCCAATTGGATTCGTGCC-----CACACACACA----CG-CAGACATGGATATACGCTCAGTTCTTGTGGC-T----------TAT-----C---------CAG-TAA----------AC---TGGGAA----------
droGri2	scaffold_15203:2164897-2165020 -		A-----C---------C-------C-C-------C-----T---C---C---------C-------C-----C-----C-----C--C----------TTGGAATTTGATACAGT-TATTGCT--GGG-AGCAACTTTCCTACCCATGCTTTCTTATCGGACT----------CGTCACACA----C--C----C----------ACACAACTTATTTT----------GTTTTCTTG-TG------GCTTATCAATCAG----------AA--CTGTAAA----------

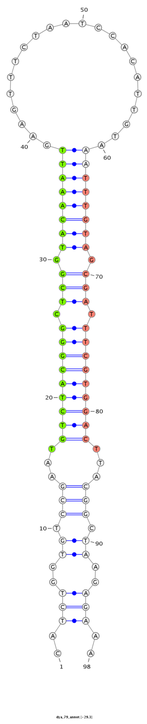
Generated: 09/08/2015 at 07:40 PM

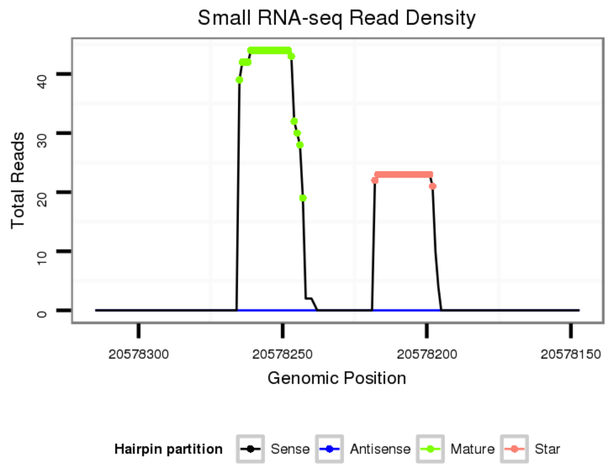
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

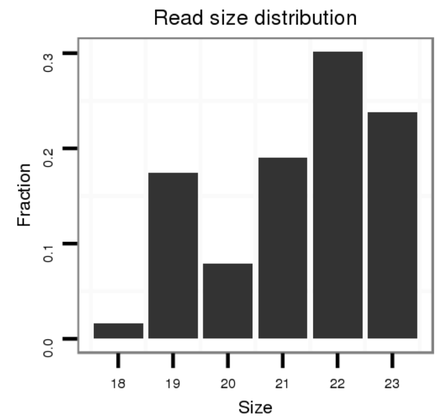
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dya_79	**X:20578197-20578265 -**	**confident**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

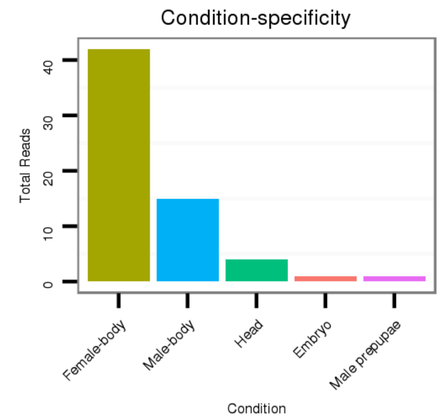
Legend: mature star mismatch in alignment mismatch in read

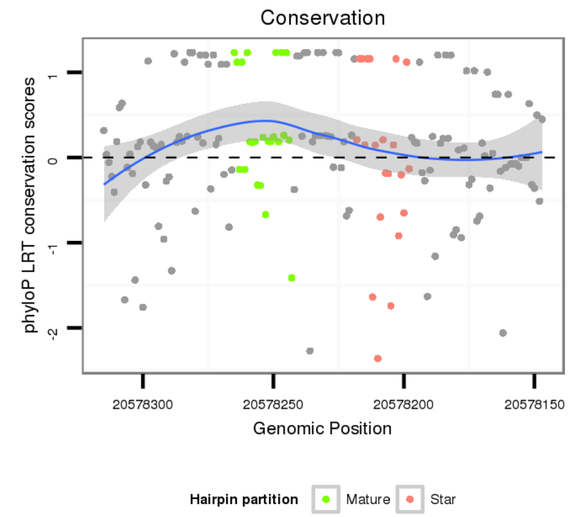
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

GACCGACTGAAAGCTACAAAGGATAAGTGTGCTTTCATCTGGTGTCCGAATGTCTACGGGCTCGGTACAAATTGAAGTTTCTAATCCACATTGTAAATTTGTAGCGATTTCGTGGACTTACGGCTAAGAGAAATGTGATCAACGGAGTAATAGCGAGTTATTAAACGAG **********..(((..((.(((...(((((((((.((((.(((((((.....)))))))).))).))))))))...))).)).)..)))..	Read size	# Mismatch	Hit Count	Total Norm	Total	M043 female body	V120 male body	head	head	embryo	Male prepupae
.....TGTCTACGGGCTCGGTACAAATT.....	23	0	1	14.00	14	12	2	0	0	0	0
.....TGTCTACGGGCTCGGTACA.....	19	0	1	11.00	11	9	1	1	0	0	0
.....TTTGTAGCGATTTCGTGGACT.....	21	0	1	10.00	10	6	1	3	0	0	0
.....TGTCTACGGGCTCGGTACAAAT.....	22	0	1	9.00	9	5	3	0	0	1	0
.....TTTGTAGCGATTTCGTGGACTT.....	22	0	1	6.00	6	3	3	0	0	0	0
.....TTTGTAGCGATTTCGTGGACTTA.....	23	0	1	4.00	4	2	0	2	0	0	0
.....GTCTACGGGCTCGGTACAAATT.....	22	0	1	3.00	3	3	0	0	0	0	0
.....TGTCTACGGGCTCGGTACAA.....	20	0	1	2.00	2	1	1	0	0	0	0
.....TTTGTAGCGATTTCGTGGAC.....	20	0	1	2.00	2	1	0	0	0	0	1
.....TGTCTACGGGCTCGGTACAAA.....	21	0	1	2.00	2	0	2	0	0	0	0
.....TACGGGCTCGGTACAAATTGAA.....	22	0	1	1.00	1	0	1	0	0	0	0
.....TTTGTAGCGATTTCGTGGACG.....	21	1	1	1.00	1	0	0	1	0	0	0
.....TACGGGCTCGGTACAAATTGAAG.....	23	0	1	1.00	1	0	1	0	0	0	0
.....TGTCTACGGGCTCGGTAC.....	18	0	1	1.00	1	1	0	0	0	0	0
.....TTGTAGCGATTTCGTGGACT.....	20	0	1	1.00	1	1	0	0	0	0	0

Anti-sense strand reads

CTGGCTGACTTTCGATGTTTCCTATTCACACGAAAGTAGACCACAGGCTTACAGATGCCCGAGCCATGTTTAACTTCAAAGATTAGGTGTAACATTTAAACATCGCTAAAGCACCTGAATGCCGATTCTCTTTACACTAGTTGCCTCATTATCGCTCAATAATTTGCTC **********..(((..((.(((...(((((((((.((((.(((((((.....)))))))).))).))))))))...))).)).)..)))..	Read size	# Mismatch	Hit Count	Total Norm	Total	M043 female body	V120 male body

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droYak3	X:20578147-20578315 -	dya_79	GACCGA----CTGAAAGCTACAAAGGA-TAAGTGTGCTTTCATCTGGTGTCCGAATGTCTACGGGCTCGGTACAAATT----GAAGTTTCTAATCCACATTGTA-AATT-TG--TAGCGATTTCGTGGACTTACGGCTAA-GAGAAATGTGATCAACGGAGTAA----TAGCGAGTTATTAAACGAG
droEre2	scaffold_4690:17921928-17922090 -	der_1514	GGCCGA----CTAATGCTGCAAAGGA-GAAATGCGCTTTCATCTGGTGTCCGAATGTCTACGGGCTAGGTACAAA--------TTTCCCAGTAAATATTGTA-AATT-TG--TAGCCATTTCGTGGACTTACGGCAA-GAGAAATGCGATCAGCAGAGTGATTGATAGTGAAAA---AACG--
droSec2	scaffold_8:3723259-3723424 -		GACCGA----CTAAAAGCCGAAAGCA-GAGCTGTGCTTTCCTTTGGTGTCCGCGTGCCCACAGGCCAAATACAAATT---GAAATTTTATAATTAATATTGCA-AATT-TG--TAGCGCTTGAGTAAGCCTACGGCAAATAAAAAATGCGATCAGCAATGTGATTAATAGTGAATTA---------
droSim2	x:20138911-20139055 -		GACCGACCG-----------------------ACTTTCCTTTGGTGTCCGCGTGCCCAGAGGCCAGATACAAATT---GAAATTTTATAATTAATATTGCA-AATT-TG--TAGCGCTTGAGTAAGCCTACGGCAAATAAGAAATGCGATCAGCAATGTGATTAATAGTGAATTA---------
dm3	chrX:21440485-21440624 -		GACCGGTCGATAAAAGCTGAAAAGCA-GAGCATGCTTTCC----------TGTCTACGGGCTAGATACATATT---GAAATTTTATAATTAATATTGTA-TAATATAATTAATATAATTATAGCCTACGGCTAA-----------------GTGATTTATAGCGAATTA---------
droEug1	scf7180000408193:48526-48673 +		GACCCA----------AAACTAAAAGGGACCAAATGTGCTTTCATCTGCTGTCCGGTTGTCTACGGGCTGGGTACAAATT---AGAATTTCCTAATTAACATAGAG-AATT-TG--TACCAATTTCGTTGACCTCCGGATCG-AAGAAATATGTCCGACGAAGTCA-----------------
droBia1	scf7180000302432:105545-105653 +		AAA---------------------------TGTGCATTCATCTGGTGTCTGGATGTCTATGG-TTTGGTATAAAGT----GAATTTGCTAATTAATATTACG-AATT-TG--TAGCGCTTTTGTGGCCTTTCACAATGA-GAGAAAT-----------------------------
droTak1	scf7180000415769:350539-350691 -		AAGTC-------GGAAGTTCAATGGAACCAGTTGTGCTTTTATCTGGTGTCCGATGTCTACGGATTCGGTACAAATA----GAATTTTCTAATTAATATTGAACAATT-TG--TAAGAATGCCGTCGACTTCCGGATAA-AAGAAATATGGCAGCTAAGTAATAAC-----------------
droEle1	scf7180000491087:1005162-1005312 +		GAATCA----------AACTCAAAGAGA-TTATTGTGCTTTCATCTGGTTTCCGGATGTCTACGGATTTGGAACAAATAATTTTAATTTACTAATTAGTATTGAA-A-------------TGCTTCCGGCAAA-GAGAAATGTGTCCGCAGAATGGTTAATATAAAATTG---AGTGG
droRho1	scf7180000769553:623-790 -		GGA-------CTGAAACCTCAAAGGGACCTATTGTGCTTTTATCTGGTGCCTGGATGCCCACGGAATTGGTACAAATCATTTTAATTTACTAATTAATATTGAA-AATT-TG--TAACGATTTTGTGGACTGCCGACAAA-GAGGATTGGTGCCGCAGAATGGTTGATATTAATTG---AA----
droFic1	scf7180000453926:392990-393127 -		GAA-------------GCCTACAAGGACCCATTGTGCTTTTATCTGCTGTCCGATGTCTACGATTTGGTACAAATC----TAAATTTCCTAATTAATATCGAC-AATT-TG--TAACAATTTTGTGGACTTCCGGCAA-AAGAAATCTTCCCACCAGA-----------------
dp5	XR_group1a:1240252-1240260 +		GAACGATTG--
droPer2	scaffold_263:12126-12134 -		GAACGATTG--

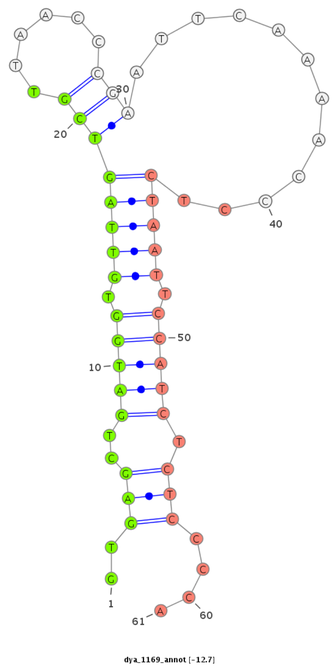
Generated: 09/08/2015 at 07:40 PM

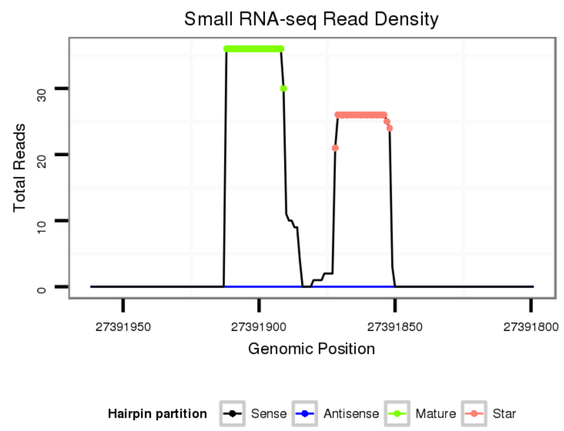
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	2
rescue.candidate	0

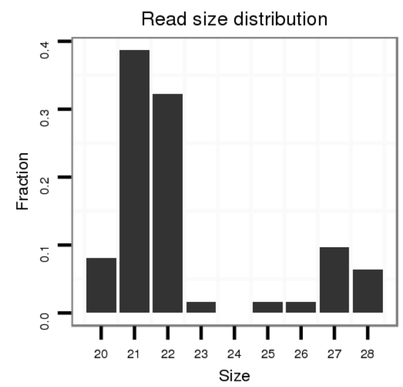
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dya_1169	**3R:27391849-27391912 -**	**confident**	**3p_tailed_mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

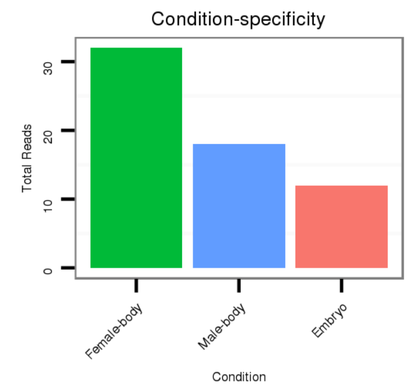
Legend: mature star mismatch in alignment mismatch in read

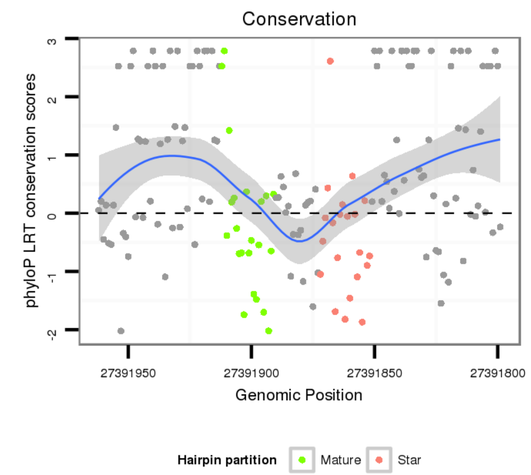
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dyak\GE23370-in]; CDS [Dyak\GE23370-cds]; CDS [Dyak\GE23370-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

```
TCCGCTCACAAGACACGCATCCTGTCCAGTGATTGTGGGCTCCAAATGGGGTGAGCTGATGGTGTTAGTCGTTAACCCGAATTCAAAACCCTCTAATTCCATCTCTCCCCACAGTGATGACCGAGTGGATACGCGAAAGCCGGCAGATCTTCATCAGACCATGC
**************************************************..(((..(((((.(((((((((.....)))).............)))))).)))))..))))....**************************************************
```

Read size	# Mismatch	Hit Count	Total Norm	Total	M043 female body	V120 male body	M056 embryo	V046 embryo
.....GTGAGCTGATGGTGTTAGTCGT..... 22	0	1	19.00	19	6	12	1	0
.....CTCTAATTCCATCTCTCCCCA..... 21	0	1	17.00	17	12	0	3	2
.....GTGAGCTGATGGTGTTAGTCG..... 21	0	1	6.00	6	2	3	0	1
.....GTGAGCTGATGGTGTTAGTCGTTAACC..... 27	0	1	5.00	5	2	2	0	1
.....GTGAGCTGATGGTGTTAGTCGTTAACCC..... 28	0	1	4.00	4	3	0	1	0
.....TCTAATTCCATCTCTCCCCA..... 20	0	1	4.00	4	3	0	1	0
.....CTCTAATTCCATCTCTCCCCAC..... 22	0	1	1.00	1	0	0	1	0
.....TCTAATTCCATCTCTCCCCAC..... 21	0	1	1.00	1	1	0	0	0
.....CTCTAATTCCATCTCTCCCC..... 20	0	1	1.00	1	1	0	0	0
.....AACCCTCTAATTCCATCTCTCCCCAC..... 26	0	1	1.00	1	1	0	0	0
.....CTCTAATTCCATCTCTCCCCAA..... 22	1	1	1.00	1	1	0	0	0
.....TCAAAACCCTCTAATTCCATCTCTCCC..... 27	0	1	1.00	1	1	0	0	0
.....GTGAGCTGATGGTGTTAGTCGTTAA..... 25	0	1	1.00	1	0	0	0	1
.....GTGAGCTGATGGTGTTAGTCT..... 21	1	1	1.00	1	0	1	0	0
.....GTGAGCTGATGGTGTTAGTCGTT..... 23	0	1	1.00	1	0	1	0	0

Anti-sense strand reads

```
AGGCGAGTGTTCTGTGCGTAGGACAGGTCACTAACACCCGAGGTTTACCCCACTCGACTACCACAATCAGCAATTGGGCTTAAGTTTTGGGAGATTAAGGTAGAGAGGGGTGTCACTACTGGCTCACCTATGCGCTTTCGGCCGTCTAGAAGTAGTCTGGTACG
**************************************************..(((..(((((.(((((((((.....)))).............)))))).)))))..))))....**************************************************
```

Read size	# Mismatch	Hit Count	Total Norm	Total	M043 female body	V058 head	V120 male body	M026 head	V052 head

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droYak3	3R:27391799-27391962 -	dya_1169	TCCGCTCACAAGACACGCATCCTGTCCAGTGATTGTGGGCTCCAAATGGGGTGAGCTGATGGTG----TTAG-TCGTTAACCCGA---ATTCAAA-------ACCCTC----TAATTCCATC----T--CTCCCCACAGTGATGACCGAGTGGATACGCGAAAGCCGGCAGATCTTCATCAGACCATGC
droEre2	scaffold_4820:1527411-1527574 +		TCGCCTCACAAGACACGCATCCTGTCCAGTGCTTGTGGGTTCCAAATGGGGTGAGCTGATGGTG----TTAG-TCGTTAACCCGA---ATTCAAA-------ACCCTC----TAACTCCAAC----T--CCCAGGACAGTGATGACCGAGTGGATACACGAAGCCCGGCAGATCTTCATCAGACCCTGC
droSec2	scaffold_4:5296323-5296480 -		TCCCCGCACAAAGCACGCCGCCTGTCCAGTGATTGTGGGTTCCAAATGGGGTGAGTTGATG---------A-TAGTTGACCCGA---CTTCAAA-------CCCCTC----TATATCCAAC----T--CCTCCGACAGTGATGACCGAGTGGATACGCGAAAAGCGGCAGATCTTCATCAGACCCTGC
droSim2	3r:25789652-25789809 -	dsi_15001	TCCCCGCACAAGCACGCCGCCTGTCCAGTGATTGTGGGTTCCAAATGGGGTGAGTTGATG---------A-TAGTTGACCCGA---CTTCAAA-------CCCCTC----TAAATCCAAC----T--CCTCCGACAGTGATGACCGAGTGGATACGCGAAAAGCGGCAGATCTTCATCAGACCCTGC
dm3	chr3R:26469639-26469806 -		TCCCCGCACAAGCACGCCGCCTGTCCAGTGATTGTGGGTTCCAAATGGGGTGAGTTGATGATAGTTGATAG-TCATTAATCCGT---CTTCAAA-------CCCCTC----TAAATTCAAT----T--CCTCCGACAGTGATGACCGAGTGGATACGCGAAAAGCGGCAGATCTTCATCAGACCCTGC
droEug1	scf7180000405064:1400-1562 -		TCCCTCAACTATGCATGCGCCTGTCCAGTGATTGTGGGCTCTAAATGGGGTAAGGATGA--AT----AGAA-TTCCCA------AT-CTAAACAACTCT--GAATTCC--ATATT--AA----CTTTATTTGCCAGTAATGACCGAGTGGATCCGCGAATATGCCCAGATTTTCAAAAGCGCCTGT
droBia1	scf7180000302113:884045-884202 +		TCCCCTCACCAGACATGCCGCCTGTCCCGTGATTGTGGGCTCCAAATGGGGTGAGTTTCC--TG----CCAG-TGATTAACCTTA---AATTAAA-------ACCCCT----CAATCCCAAA---CT--TT-----TAGTGATGACCGAGTGGATACGCGAACGCGGCAGATCTTATCAGACCCTGC
droTak1	scf7180000415367:311977-312132 +		CCCCCTCACATAGACATGCCGCCTGTCCCGTGATTGTGGGCTCCAAATGGGGTGAGTTTCG--TG----CCAG-TGATTAACCTTA---AATCAAA-------TCCCCT---TTAACCCCCA-----------ACTAGTGATGACCGAGTGGATACGCGAACGACGGCAGATCTTTATCAGACCCTGC
droEle1	scf7180000491280:2803996-2804158 -		TCCCCGCAGTCGACATGCCGCCTGCCCAGTGATTGTGGGATCCAAATGGGGTGAGTTCCG--TG----CCAA-TGATTAACCCGA---AATTAAA-------CCTAGC---TTAACCCCTAC----T--CTCGTGACAGTGATGACCGAGTGGATACGCGAATGCCGGCAATCTTTATCAGACCCTGT
droRho1	scf7180000758935:14009-14161 -		TCCCCGCACACAACATGCCGCCTGCCCAGTGATAGTGGGTTCCAAATGGGGTGAGTTTCG--TG----CCAG-TGATTAACCCGA---ATTTAAA-------------------ACCCAC----T--CTCTTGACAGTGATGACCGAGTGGATACGCGAATGGAAGCAGATCTTTATCAGACCCTGT
droFic1	scf7180000453782:821244-821404 +		GCCCCTCACAAGCACGCCGCCTGTCCGGTGATTGTGGGCTCCAAGTGGGGTAAGTTCCC--AT----CCCT-TGATTAACCTGC---AATTGAG-------TCCCTT----TAACCCCGA----T--CCGTTGACAGTGATGACCAAGTGGATACGCGAGCGGGCCAGATATTTACCAGACCCTGC
droKik1	scf7180000302390:444097-444258 -		TCTCCTTTCAAGACACATGCCGCCGGTGATTTCGGGCTCCAAGTGGGGTGAGTGCCG--AG----TCTG-TGATTAACCCCA---ACGGATG-------ACTATT----TAACCCCCAA----T--TTGGGGGCAGTGATGACCGAGTGGATAAGGAACAAGCCCAGATGTTTATAAGCGCCTGT
droAna3	scaffold_12911:4512125-4512282 +		GCCAACCACCCTGCATGTCCGCTGTCCGGTCATCGTAGGCTCCAAATGGGGTGACAATAC----------AAG-TGTATATCCTCA---A----TA-------TCTAGT---TTAAAACATAT----TTTTCCGTTTCAGTGATGACCCAGTGGATACGTAGGGTAGTCAAATCTTTGCCAGACCCTGT
droBip1	scf7180000396640:1350938-1351097 +		CAAAACCACCATGCATGCCGCATGTCCGCTCATCGTAGGCTCCAAATGGGGTGAGTATAC--AA----ACAT-TATATT---CCTAA---A----AA-------TCTAGT---TAAAAGCATATTTTATT--TCTGATTCAGTGATGACCCAGTGGATACGTGAACGTAGTCAAATCATTGTCAGACCCTGT
dp5	2:735690-735846 +		TTCGTCCACCACGCATGCCGCCTGCCCCATCATCGTGGGCTCCAAATGGGGTCCCTACTA--T-----------CCCTGGATGTGC---TTGCCAT-------CTGCTA----TATCCCTCCC----T--TTTATTGCAGTGTTGACCCAATGGATACGCGAACGTAACCAGATCTTCATCAGCCCATGC
droPer2	scaffold_7:3521732-3521888 +		TTCGTCCACCACGCATGCCGCCTGCCCCATCATCGTGGGCTCCAAATGGGGTCCCTACTA--T-----------CCCTGGATGTGC---TTGCCAT-------CTGCTA----TATCCCTCCC----T--TTTATTGCAGTGTTGACCCAATGGATACGCGAACGTAACCAGATCTTCATCAGCCCATGC
droWil2	scf2_1100000004943:9989228-9989389 -		CCGAGACACACTGCATGCAGCTTCCCAGTGATAGTTGGTTCTAAATGGGGTAAATTTCA--AA----TCAT-TTACAAATCTAT---ATATA--------ACAATT---TTAACAC-GATT----TTATGCTTAATAGTTTGCAACAAATGGATACGCGAACGTGACGCATCTTCAGACGACCTTGC
droVir3	scaffold_13047:11155196-11155349 -		TCCAAAAACGGTTCACGCCGCATGTCCGTCATTGTTGGCTCTAAGTATGGTGAGTGCTC--TGA---AATT-TGATTAGTTTCCCCAATTGAAA---A---TT-----------A-----------C-CATGTTTTAGTGATGACTAAATGGATTTATAACATGGATCAGATATTTAGAAGACCTTGC
droMoj3	scaffold_6540:30492297-30492455 +		TCCACAAACACTGCACGCCGCCTGCCCAGTGATAGTGGGCTCCAAGTGGGGTAAGTATAA--CC----TAAGTCCCTTCA-----------CAATACAAACAT--GGATGAC--A---T--GA----CTCTACTTCACAGTTTGTAACAAGTGGATACGCGAACGACAACAAGTATTCCGAAGACCCTGT
droGri2	scaffold_14624:1248152-1248313 -		TAGAAACACTATACATGCCGCCTGTCCCGTTATAGTTGGCTCCAAATGGGGTAATTATCA--TAT---ATAT-TTATTAAATGTCG---A---CAA-------TACTA----TACATATACA----TTATATTTCACAGTGTGCAACAAATGGATACGTGAAAATGAACAGATGTTTACAAGCCGCTGC

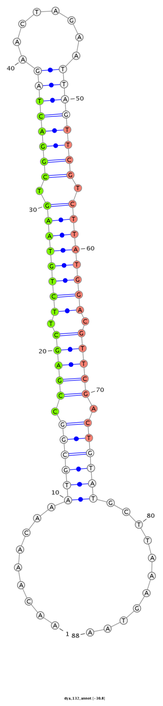
Generated: 09/08/2015 at 07:00 PM

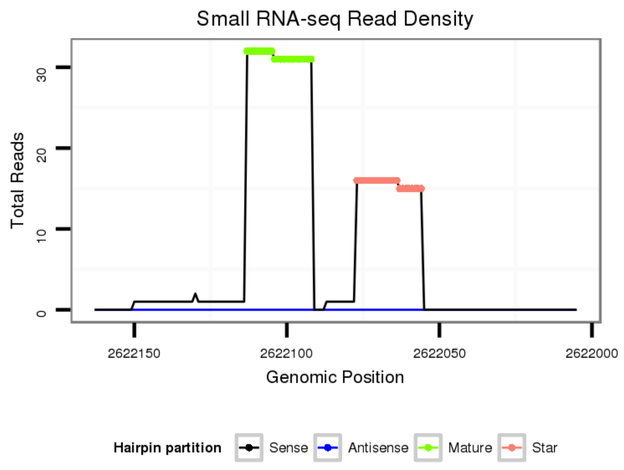
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

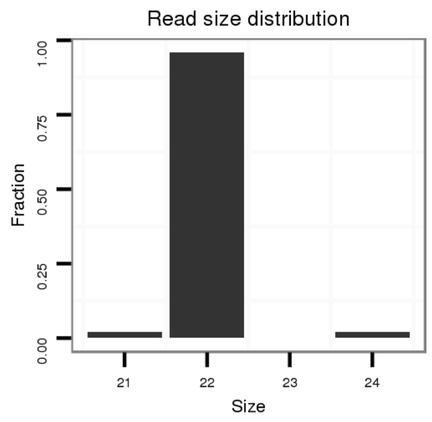
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dya_132	**3R:2622055-2622113 -**	**confident**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

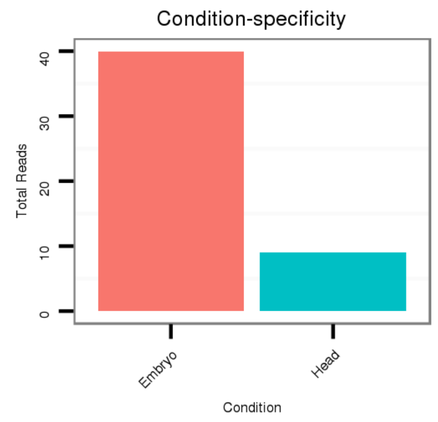
Legend: mature star **mismatch in alignment** mismatch in read

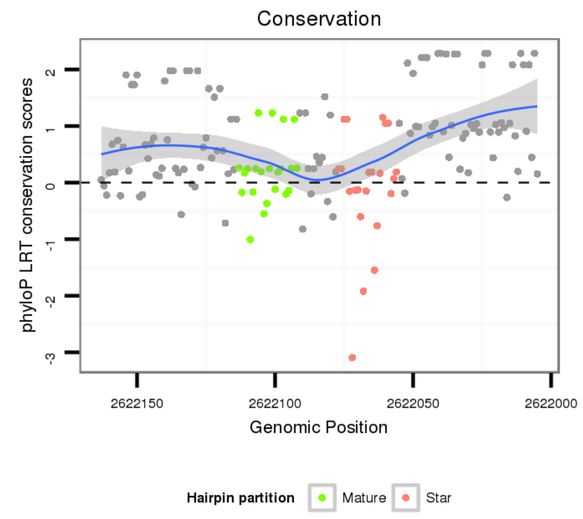
Predicted structure











dya_132_mmu1 (-38.8)

Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

mature	star
1. dya_132 3R:2622092-2622113 - 2. dya_133 v2_chr3R_random_227:2967-2988 -	1. dya_132 3R:2622056-2622077 - 2. dya_133 v2_chr3R_random_227:2931-2952 -

Sense Strand Reads

hide 3p reads | show mid mismatch reads

AACAAAACCAAGCAACAAAAACAGTAATCGTAATGAACAAACAAATGCGGCCGAGCTTCTGTAAGTCGGACTAGAACTAGAATTAGTTCGTCTTATGGACGTTCGACTGTATGCTTAAAGTAATGTTAAACATGTATGCAACAAGATTAGTGAGCCTTG **********.....(((((((.(((((.((((((((.((((((((.....)))))))).)))))))).)))))).)))))).....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M056 embryo	M026 head	M043 female body	V120 male body	GSM1528802 follicle cells	V052 head
.....CCGAGCTTCTGTAAGTCGGACT.....	22	0	2	31.50	63	52	11	0	0	0	0
.....TTCGTCTTATGGACGTTCGACT.....	22	0	2	15.50	31	26	4	0	0	0	1
.....CCGAGCTTCTGTAAGTCGGACC.....	22	1	2	4.00	8	4	4	0	0	0	0
.....TTCGTCTTATGGACGTTCGACC.....	22	1	2	2.50	5	5	0	0	0	0	0
.....TGAACAAACAAATGCGGCCGAGCTTC.....	26	0	1	1.00	1	0	0	1	0	0	0
.....AACAAAAACAGTAATCGTAAT.....	21	0	1	1.00	1	0	0	0	1	0	0
.....CTAGAATTAGTTCGTCTTATGGAC.....	24	0	2	1.00	2	0	2	0	0	0	0
.....TATGGACGTTCGACTGTATGCTTAAAGT.....	28	0	2	0.50	1	0	1	0	0	0	0
.....CCGAGCTTCTGTAAGTCGGACG.....	22	1	2	0.50	1	0	1	0	0	0	0
.....TCGTCTTATGGACGTTCGACC.....	21	1	2	0.50	1	1	0	0	0	0	0
.....TCGTCTTATGGACGTTCGACT.....	21	0	2	0.50	1	1	0	0	0	0	0
.....TTCGTCTTATGGACGTTCGAC.....	21	0	2	0.50	1	1	0	0	0	0	0
.....TTCGTCTTATGGACGTTCGACA.....	22	1	2	0.50	1	0	0	1	0	0	0
.....ACAAATGCGGCCGAGCTTCTGTAAGTC.....	27	0	2	0.50	1	1	0	0	0	0	0

Anti-sense strand reads

TTGTTTTGGTTCGTTGTTTTTGTCATTAGCATTACTTGTTTGTTTACGCCGGCTCGAAGACATTCAGCCTGATCTTGATCTTAATCAAGCAGAATACCTGCAAGCTGACATACGAATTTCATTACAATTTGTACATACGTTGTTCTAATCACTCGGAAC **********.....(((((((.(((((.((((((((.((((((((.....)))))))).)))))))).)))))).)))))).....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V058 head	M043 female body
.....CTGCAAGCTGACATACGAATT.....	21	0	2	0.50	1	0	1

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droYak3	3R:2622005-2622163 -	dya_132	AACA-AA----------ACCAAGCA-ACAAA----------AACAGT-AATCGTAATGAACAAACAAATGCGGCCGAGCTTCTGTAAGTCGGACTAGAACTAGAAT----------TAGTTCGTCTTATGGAC-GTTCGACTGTATGCTTAAA--GTAATGTTAAACATG----------TATGCAACAAGATTAGTGAGCCTTG
droEre2	scaffold_4770:7615285-7615443 +	der_1525	AACA-AA----------ACCAAGCA-ACAAA----------AACAGT-AAACGTAATGAACAAACAAATGCGGTCGAGCTTCGGTAAGTCGGACCACAACTAGAAAC----------AGTTCGCGGTATGGAC-GTTCGACTGTATGCTTAAA--GTAATGTTAAACATG----------TATGCAACAAGTTTAGTGAGCCTTG
droSec2	scaffold_12:131818-131969 +	dse_1848	AACA-AA----------ACCAAGCA-ACAAA----------AACAGT-AATCGTAATGAACAAACAAATGCGGTCGAACATCAGTAAGTCGAACTAGATCTACGAAT----------ATAGTTCGCCTTGCGGAG-GTTCGTCTGTGTGCTTAAA--GTAAT---------G----------TATGCAACAAGTTTAGTGAGCCTTG
droSim2	3r:7258350-7258510 +	dsi_32443	AACA-AA----------ACCAAGCA-ACAAA----------AACAGT-AATCGTAATGAACAAACAAATGCGGTCGAGCATCAGTAAGTCGAACTAGATCTACGAAT----------ATAGTTCGCCTTGCGGAG-GTTCGTCTGTGTGCTTAAA--GTAATGTTAAACATG----------TATGCAACAAGTTTAGTGAGCCTTG
dm3	chr3R:14020088-14020253 -	dme_386	AACA-AA----------ACCAAGCA-ACAAA----------AACTGT-AATCGTAATGAACAAACAAATGCGGTCGAATATTCGTAAGTCGGACTAGATCTA----------TGTAACGAATATAGTTCGCCTTGCGGAC-ATTCGACTGTTGCTTAAA--GTAATGTTAAACATG----------TATGCAACAAGTTTAGTGAGCCTTG
droEug1	scf7180000409246:369753-369951 -		AGGA-AA----------AGTAAGCA-AGAAA----------AGCAGT-AATCGTAATGAACAAACAAATGCAGTTGAACTTCTGTAAAACGAACTACAATTAGAAGTAAAAGTAAAATTTATAAATGAACTTGAAGTTCTGCTTGTGGTTCGAATTAGAGAC-GTTCGACTGTGTACTTAAA-TGTAATGTTAAACATG----------TATGCAACAAGTTCAGTGAGCCTTG
droBia1	scf7180000299102:1950387-1950582 +		AACA-AA----------ACCAAGCAGGCAAA----------AATAGT-AATTGTAATGAACAAACGAGCAGAGTCGAACTTCTGTATGTCAAACTAGAACTAGAATACGAGCAAAATCTGTAAAGAAACTTGAAGTTCTCTTTTGATTCGACTCACAGAT-ATTCGACTGCA---CTAAA--GTAATATAAAACATG----------TATGCAACAAGTTTAGTGAGCCTTG
droTak1	scf7180000414450:147939-148092 -		AACA---AACAGT-AATCGTAAAAACA--------GAGTTTAATTTCTTTACGTCCACTAGAACTAGAATATACAAGTAAAATCTTTGAAAGAACTTGGAGTTCTATTTGTAGTTCGATTTACAG--------------------AATGTTAAACATG----------TATGCAACAAGTTTAGTGAGCCTTG
droEle1	scf7180000491008:2241887-2241081 +		AAAA-AG----------AAAATCCAAGCACCAAA----------AACAGT-AATGTCAATAAACAAGCAAAAACAGTCGAACTTCTACAAGTCGAACTAGAACTAGAATCACAAGTTAAAT---------AACTTGAAGTTCTGTTTATGGACGGAAGATGTAACATTTCGACTGTATACTAAAA--TAAATGTAAAAATG----------TATGCAACAAGTTAGGTGAGCCTTG
droRho1	scf7180000778633:31152-31353 -		AACAAAA----------ACCAAGCAAGCAAA----------AA----AACAGT-AATCCCAATGAACAAGCAAACAGAGTCGGTCTTCTATAAGTCGAACTATAACTGGAAATACAAGTACAATTACAAAGCTAAATAGAAGTGATGTTTATGGTTCGAGTTATAGTA-GTTCGACAGTATACTTAAA--GTGATGTTAAACATG----------TATGCAACAAGTTAAGTAAGCCCTG
droFic1	scf7180000453800:497473-497669 -		AACA-AA----------ACCAAGCA-AACAA----------AGCAGT-AATCGTAAAGAACAAGCAAAAACAGTCGAACTTCTATAAGTCGAGCTAGAAAAAGAAAGCAAGTAATATCTCGAAAC-AACTTAAAGTTCTCATTTTAGTTCGAGTTGTAGAT-GGTCGTGTGTTTACTTAAA--GTAATGTTAAACATG----------TATGCAACAAGTTTAGTGAGCCTTG
droKik1	scf7180000302809:267120-267229 +		GACA-AA----------AACAAGCA-GCAAAGGCAACAGCAACAC----AGCAGT-AATCTAAATGAGCAAGCAAATA----------TATACTTAAA--GTAATGTTAAACATG----------TACGCAAGTAGTTAAGTGAGTCCT-
droAna3	scaffold_13340:15787955-15788050 -		TGAG-AA----------AGCATGCA-AC----------AGCAGT-AAGCTTAATGAACAAGCAAAT----------ATACTTAAA--GTAATGTTTAACATCT------ACATATGCAACAAGTTAAGTGAGTCTTT
droBip1	scf7180000396708:4245005-4245108 +		AA--AA----------ACCATGCA-ACAGC----------AGCTGCAAAGCTTAATGAACAAGCAAAT----------ATACTTAAA--GTAATGTTTAACATCTATGCAAACATATGCAACAAGTTAAGTGAGTCTTT
dp5	2:29111760-29111892 -		AGCC-CCCTCCCCACCCAGAAAGGGAACGAACAGGCACACAGA---------AACCCAGCCGGGAGT-AATCATAAAAGAG----------AGAAACAAAAGCAAA----------AATACTTAAA--GTAATGTTAAA---A----------TATGCAACAAGTCTAGCAAGTCTTC
droPer2	scaffold_6:4436054-4436186 -		AGCC-CCCTCCCCACCCAGAAAGGGAACGAACAGGCACAGAGA---------AACCCAGCCGGGAGT-AATCATAAAAGAG----------AGAAACAAAAGCAAA----------AATACTTAAA--GTAATGTTAAA---A----------TATGCAACAAGTCTAGCAAGTCTTC
droMoj3	scaffold_6540:2479607-2479661 +		T---------------------------------------AGAACTACAATGTATTTAGCAAGTCTTC

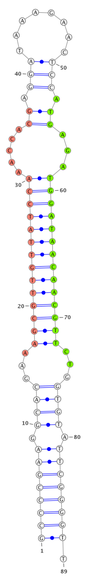
Generated: 09/08/2015 at 07:47 PM

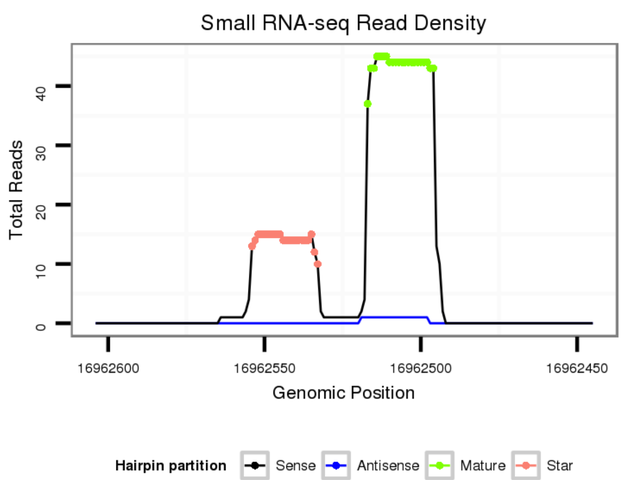
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	4

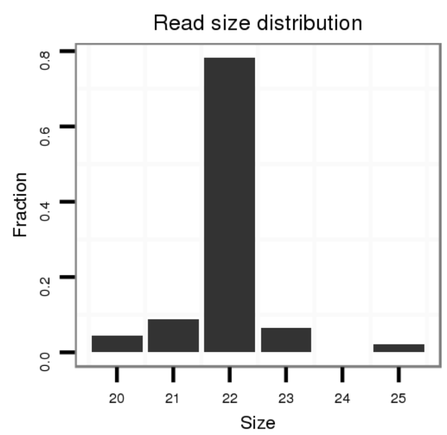
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dya_70	**2R:16962495-16962554 -**	**confident**	**Canonical miRNA**	**3pUTR**	[View on UCSC Genome Browser {Cornell Mirror}]

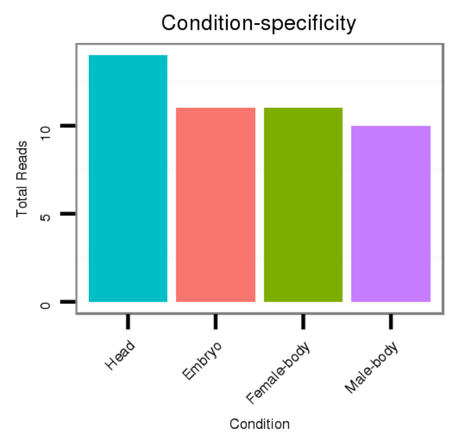
Legend: mature star mismatch in alignment mismatch in read

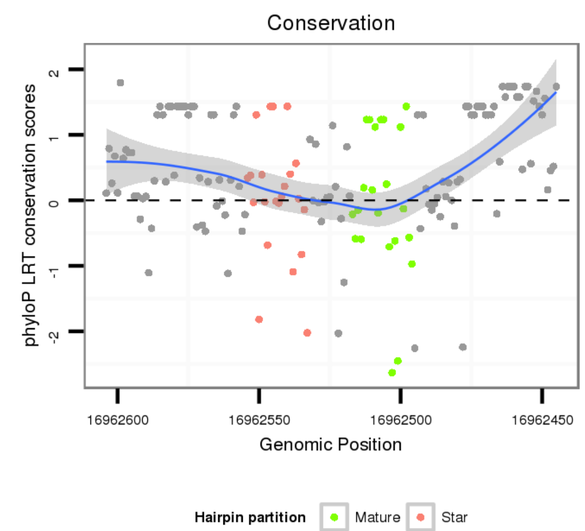
Predicted structure











Show Alternate Folds

Flybase annnotation

utr3 [utr3_plus_2556]; CDS [Dyak\GE11757-cds]; intron [Dyak\GE11757-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

CTTGCCCTAACCCAACCGCTCGTTTAATTGTTAATGCCCCGAAGGCACGAAAGCGTTGTTATCCAAACCACGAGGATAAAGAACTCCATGAGATGGATAACAACGTTCTGGTGTATTCGGGGTTCTCAAGCTTTGGCATAACTAACCGAATGTACCCCGA **********((((((((.((((...((((((((((((((.....((.(((.....))).)).))...)))))))))))))...)))).)))))))).**********	**Read size**	**# Mismatch**	**Hit Count**	**Total Norm**	**Total**	**V120 male body**	**M043 female body**	**V058 head**	**M056 embryo**	**V046 embryo**	**M026 head**	**V052 head**
.....ATGAGATGGATAACAACGTTCT.....	22	0	1	28.00	28	7	6	7	4	2	2	0
.....AAGCGTTGTTATCCAAACCACG.....	22	0	1	7.00	7	0	3	0	2	2	0	0
.....TGAGATGGATAACAACGTTCTGG.....	23	0	1	4.00	4	1	1	1	0	0	0	1
.....AAAGCGTTGTTATCCAAACCAC.....	22	0	1	2.00	2	2	0	0	0	0	0	0
.....AAGCGTTGTTATCCAAACCA.....	20	0	1	2.00	2	1	0	1	0	0	0	0
.....ATGAGATGGATAACAACGTTCTG.....	23	0	1	2.00	2	0	1	1	0	0	0	0
.....ATGAGATGGATAACAACGTTCTGGT.....	25	0	1	2.00	2	2	0	0	0	0	0	0
.....AGATGGATAACAACGTTCTGG.....	21	0	1	2.00	2	1	1	0	0	0	0	0
.....TGAGATGGATAACAACGTTCT.....	21	0	1	1.00	1	1	0	0	0	0	0	0
.....CATGAGATGGATAACAACGTTCT.....	23	0	1	1.00	1	0	0	0	0	0	1	0
.....GAAGGCACGAAAGCGTTGTT.....	20	0	1	1.00	1	1	0	0	0	0	0	0
.....ATGAGATGGATAACAACGTTCTGG.....	24	0	1	1.00	1	0	1	0	0	0	0	0
.....AAAGCGTTGTTATCCAAACCC.....	21	1	1	1.00	1	0	0	0	0	0	0	1
.....GCGTTGTTATCCAAACCACGA.....	21	0	1	1.00	1	0	0	0	1	0	0	0
.....GAAAGCGTTGTTATCCAAACCA.....	22	0	1	1.00	1	0	1	0	0	0	0	0
.....TGAGATGGATAACAACGTTCTG.....	22	0	1	1.00	1	1	0	0	0	0	0	0
.....AGCGTTGTTATCCAAACCACG.....	21	0	1	1.00	1	0	1	0	0	0	0	0
.....ACGAGGATAAAGAACTCCATGAGAT.....	25	0	1	1.00	1	0	0	0	0	0	1	0
.....TGAGATGGATAACAACGTTCTGT.....	23	1	1	1.00	1	1	0	0	0	0	0	0
.....ATGAGATGGATAACAACGTTCC.....	22	1	1	1.00	1	0	0	0	0	0	1	0
.....CATGAGATGGATAACAACGTT.....	21	0	1	1.00	1	0	0	1	0	0	0	0
.....TGAGATGGATAACAACGTTCTGGTT.....	25	1	1	1.00	1	0	0	0	0	0	0	1
.....CCATGAGATGGATAACAACGTTCTGG.....	26	0	1	1.00	1	1	0	0	0	0	0	0

Anti-sense strand reads

GAACGGGATTGGGTTGGCGAGCAAATTAACAATTACGGGGCTTCCGTGCTTTCGCAACAATAGGTTTGGTGCTCCTATTTCTTGAGGTACTCTACCTATTGTTGCAAGACCACATAAGCCCCAAGAGTTCGAAACCGTATTGATTGGCTTACATGGGGCT **********((((((((.((((...((((((((((((((.....((.(((.....))).)).))...)))))))))))))...)))).)))))))).**********	**Read size**	**# Mismatch**	**Hit Count**	**Total Norm**	**Total**	**M043 female body**	**V058 head**
.....GGTACTCTACCTATTGTTGCAA.....	22	0	1	1.00	1	1	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droYak3	2R:16962445-16962604 -	dya_70	CTT-GCCCTAACCCAA-C-CGCTCGTTTAAT--TGTT-AATGCCCCGAA-----GGCACG--AAAGCGTTGTTATCCAAA----------CC----------ACGAGGATAAAG-AACTCCATGAGATGGATAACAACGTTCT-GGTGTAT-TCG--GGGTTCTCAAGCT---TTGGCA-TAACTAACCGAATGT--ACCC----CGA
droEre2	scaffold_4845:13836848-13837009 -		CTT-GCCCTAACAGCCCT-CGCTCGTTTAAT--TGTT-AATGCCCCGAAC---ATGCACG--AAAGCGTTGTTATCCATT----------C----------ACGAGGATTAAG-AACTCCATGAGATGGATAACGATGTTCT-AGTGTATATG--GGGTTCTCAAGCT---TTGGCA-TAACTAACCGAATGT--ACCC----CAA
droSec2	scaffold_1:9516158-9516332 +		CTT-GCCCTAACCCCCCAACGCTCGTTTAAT--TGTT-AATGCCCAGAA-----TGCACG--AAAGCGTTGTTATCCATTTG-GAGCTAGTGTT-----C----------CCAATGATTACG-AGCTCCATGCGATGGATAAGAACGTTCT-TGTGTATGTCG--GGGCTCTTAAGCT---TTGGCA-TAACTAACCGAATGT--ACCC----CGA
droSim2	2r:12690778-12690952 +		CTT-GCCCTAACCCCCCAACGCTCGTTTAAT--TGTT-AATGCCCAGAA-----TGCACG--AAAGCGTTGTTATCCATTTG-GAGCTAGTGTT-----C----------CCAATGATTACG-AGCTCCATGCGATGGATAAGGACGTTCT-AGTGTATGTCG--GGGTTCTCAAGCT---TTGGCA-TAACTAACCGAATGT--ACCC----CGA
dm3	chr2R:12020731-12020905 +		CTT-GCCCTAACCACCCAATGCTCGTTTAAT--TGTT-AATGCCCAGAA-----TGCACG--AAAGCGTTGTTATCCATTTG-GAGCTAGTGTT-----C----------CCCATGATTAAG-ACGACCATGCAATGGATAAGAACGTTCT-TGTGTATGTCG--GGGTTCTTAAGCT---TTGGCA-TAACTAACCGAATGT--ACCC----CGA
droEug1	scf7180000409672:927790-927953 +		CTT-GCCCTAATGCCC--AGCTCGTTTAAT--TGTT-TATGCCCAGGATGAAATGCACG--AAAACTTATTTATCCATCTT----------------------------AGGACTAAGGA-TTCCTAAAGATTGATAGCTAGCCTTA-CGCGTATTCGTCGGGCTCTTAAGCT---TTGGCA-TAACTAACCGAATGT--ACCC----CGA
droBia1	scf7180000301506:2969721-2969869 +		CTA-GCCCTAACCCCC-A-AGCTCGTTTAAT--TGTT-TACGCCCAAAG-----TGCACCGTAAAACCCTGTTAACCATGTG-AAG----------------------------------ATATGATGGATAACTGGGTTTTTGGCGCAGGTGA--GGGTCCCTAAGCT---TTGGCA-TAACTAACCGAATGT--ACCC----CGA
droTak1	scf7180000415795:535773-535921 -		CTT-GCCCTAACCCCC-A-AGCTCGTTTAAT--TGTTTAATACCCAGAA-----GGCACT--GAAACTTAGTTATCCATCGGGAAG----------------------------------TTAGATGGGTAACTCTGTTTCAAGTGCAACG-A--GGGTTCCAAAGCTTC-TTGGCA-TAACTAACCGAATGT--ACCC----CGA
droEle1	scf7180000491107:1034478-1034633 +		CTT-GCCCTAACCCCCC-CGCTCGTTTAAT--TGTT-TATACCCAGAAC----AGCACG--AAAGCATATTTATCCATCAG-AGTCTA----------G-A-TCCTTAAAGATGGTTAAACACCCTCT-AGTGCCAGT-G--GGGTCCTTAAGCT---TTGGCA-TAACTAACCGAATGT--ACCC----CGA
droRho1	scf7180000779911:72894-73071 -		CTT-GCCCTAACCCCC--ATCTCGTTTAAT--TGTT-TACACCCAGAAT----GGCACG--AAAACTTATTTTTCCATAAG-GATCCAAGGTC-----CAACCTATATACTT----------CTGAGGA-TACCTGAAGATGGTTAAATTTGTTGC-AGTGCCAGTC--GGGTTCTTAAGCT---TTGGCA-AAACTAACCGAATGT--ACCC----CGA
droFic1	scf7180000453948:1268677-1268854 +		CTG-GCCCTAACCGCC-A-AGCTCTTTTAAT--TGTT-TATGACCAGAC-----TACACA--GAGACATAATTATTCATCAG-GATCTTTG---------C----ATTATATTACTTACCA------AAG-AT---CTTATGATGGATAATGATGTTGC-AGTGCCAGTCTGGTTGTTATTAAGCTTT-TTGGCA-AAACTAACCGAATGT--ACCT----CGA
droKik1	scf7180000302476:2722568-2722734 +		TTTCGCCCTAACCCCC-A-AGCTCGTTAAATTTTGTT-ACAACCCCGTCC----TGCACG--GCAACCTATTTGGTCATCTT-GATCGTATTATCTTAACA----------AGTAGCCT---G-CAG----------TGC-AGCGCAAGG-G--GTTTCCTAAGCTTTTTGGCATTGACTAACCGAATGTGTACCCCCTTCGA
droAna3	scaffold_13266:15389946-15389970 -		TTT-GCCAA--AAACTAACCGAAAGT--------GA
droBip1	scf7180000396547:1659547-1659572 +		TTT-GCCCAAA---AACTAACCAAAT------C----TGA
dp5	3:18641351-18641371 +		ACT-AACCTGTTTTATCC---CTCC------
droPer2	scaffold_34:588346-588366 +		ACT-AACCTGTTTTATCC---CTCC------

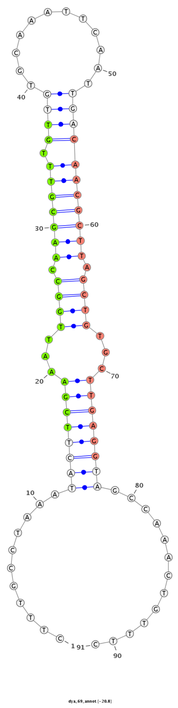
Generated: 09/08/2015 at 07:43 PM

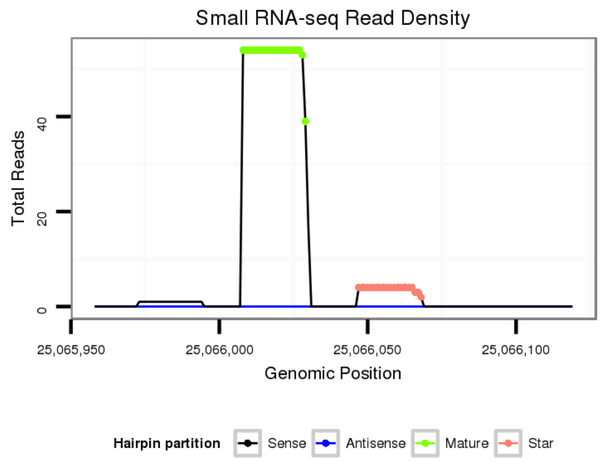
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

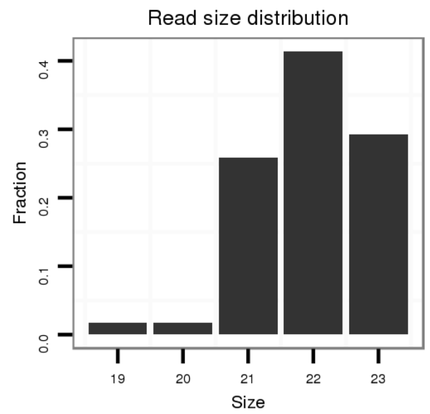
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dya_69	**3R:25066008-25066069 +**	**confident**	**Canonical miRNA**	**antisense_to_intron**	[View on UCSC Genome Browser {Cornell Mirror}]

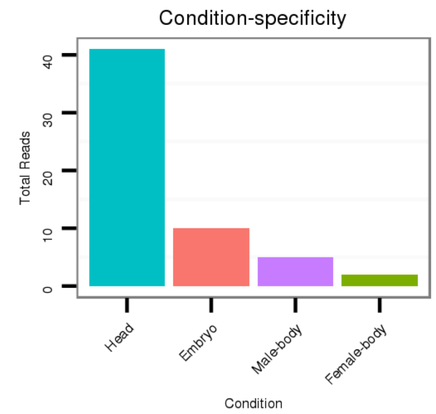
Legend: mature star mismatch in alignment mismatch in read

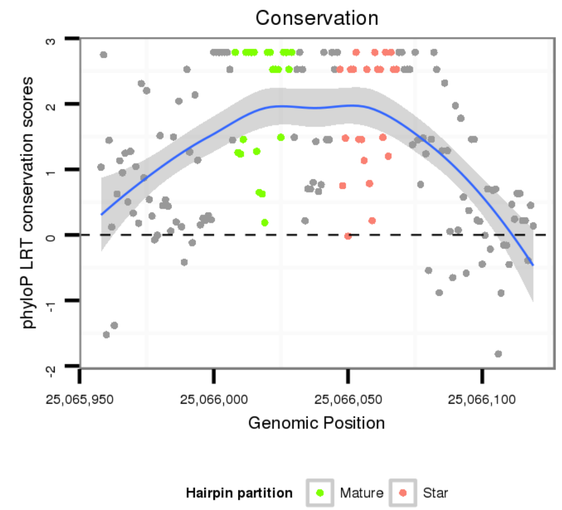
Predicted structure











Show Alternate Folds

Flybase annnotation

Antisense to intron [Dyak\GE23609-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

GTATGCGTGTGTATCTGTGTCCTGTGCCCTGTGTCCTTTGCCTAAATACTTCGAAATTGGCCAAGCGTTTGTTGTGCAAATTCAATTGACAACGCTTAGCTGTGCTTGAGGTAGCCAAACTGTTTCAACATGCGAAAAGGGTTCATCTGGCCATCATCCTGT **********.....(((((((...((((.(((((((.((((.....)))))))))).))))...)))))))).....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V058 head	M056 embryo	V052 head	M026 head	V120 male body	M043 female body	V046 embryo
.....TCGAAATTGGCCAAGCGTTTGT.....	22	0	1	22.00	22	12	1	3	3	2	1	0
.....TCGAAATTGGCCAAGCGTTTGTT.....	23	0	1	17.00	17	5	6	2	3	1	0	0
.....TCGAAATTGGCCAAGCGTTTG.....	21	0	1	14.00	14	9	0	3	0	1	1	0
.....CAACGCTTAGCTGTGCTTGAGG.....	22	0	1	2.00	2	0	1	0	0	0	0	1
.....CAACGCTTAGCTGTGCTTGAG.....	21	0	1	1.00	1	0	1	0	0	0	0	0
.....TCGAAATTGGCCAAGCGTTTGTG.....	23	1	1	1.00	1	0	1	0	0	0	0	0
.....TCGAAATTGGCCAAGCGTTT.....	20	0	1	1.00	1	0	0	0	0	1	0	0
.....CAACGCTTAGCTGTGCTTG.....	19	0	1	1.00	1	0	0	1	0	0	0	0
.....TGTGTCCTGTGCCCTGTGTCCT.....	22	0	1	1.00	1	0	1	0	0	0	0	0
.....TCGAAATTGGCCAAGCGTTTGTTT.....	24	1	1	1.00	1	1	0	0	0	0	0	0
.....TCGAAATTGGCCAAGCGTTTGG.....	22	1	1	1.00	1	0	0	0	1	0	0	0

Anti-sense strand reads

CATACGCACACATAGACACAGGACACGGGACACAGGAAACGGATTTATGAAGCTTTAACCGGTTCGCAAACAACACGTTTAAGTTAACTGTTGCGAATCGACACGAACTCCATCGGTTTGACAAAGTTGTACGCTTTTCCCAAGTAGACCGGTAGTAGGACA **********.....(((((((...((((.(((((((.((((.....)))))))))).))))...)))))))).....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V120 male body

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droYak3	3R:25065958-25066119 +	dya_69	GTATGCGTGTG----------TATCTGTGTCC---TGTG--CCCT---------GTGTCCTTTGCCTAAATACTTCGAAATTGGCCAAGCGTTTGTTGTGCA---AATTC-AATTGACAACGCTTAGCTGTGCTTGAGGTAGCC--AAACTGTTTCAACATGCG--AA--AAGGGTTC--ATCT----------GGCC-----ATC----------ATCCTGT---
droEre2	scaffold_4820:6629172-6629329 +	der_1511	GTGTGCGTGTG----------TATCTGTGTCC---TGTG--CCCT---------GTGTCCTTTGCCTAAATACTTCGAAATTGGCCAAGCGCTTGTCGTGCA---CATTA-AATTGACAACGCTTAGCTGTGCCTGAGGTAGCC--AAACTGTTTCAACATGCG--AA--AAGGGTTC------------TGCA-----GTC----------ATCCTGT---
droSec2	scaffold_13:201172-201315 -	dse_150	---------TG----------TATCTGTGTCC---TGTG--CCCT---------GTGTCCTTTGCCTAAATACTTCGAAATTGGCCAAGCGTTTGTTGTGCA---CATTA-AATTGACAACGCTTAGCTGTGCTTGAGGTAGCC--AAACTGTTTCTACATGCG--AA--AAGGGTTC------------GCAA-----ATC----------AT-------
droSim2	3r:20925622-20925774 -	dsi_32434	GTATGCATGTG----------TATCTGTGTCC---TGTG--CCCT---------GTGTCCTTTGCCTAAATACTTCGAAATTGGCCAAGCGTTTGTTGTGCA---CTTTA-AATTGACAACGCTTAGCTGTGCTTGAGGTAGCC--AAACTGTTTCTACATGCG--AA--AAGGGTTC------------TCAA-----ATC----------AT-------
dm3	chr3R:21413227-21413370 -	dme_166	---------TG----------TATCTGTGTCC---TGTG--CCCT---------GTGTCCTTTGCCTAAATACTTCGAAATTGGCCAAGCGTTTGTTGTGCA---CATTA-AATTGACAACGCTTAGCTGTGCTTGAGGTAGCC--AAACTGTTTCTACATGCG--AA--AAGGGTTC------------TCAA-----ATC----------AT-------
droEug1	scf7180000409798:1138188-1138333 +		GTATCTG--TG----------TAGCTGTGTCC---TGTG--TCCT---------GTGTACTTTGCCTAAATACTTCGAAATTGGTTAAGCGTTTGTTGTGGC---CATCA-AATTGACAACGCTTAGCTGTGCTTGAGGTAGCC--AAATTGTTTCATCATC--------------------------------AATATCTGCATCT----GCA---
droBia1	scf7180000302136:2259464-2259611 -		GTATCTG----------------------TGTCC---TACG--TCCTGTGTGTACTTTGTACTTTGCCTAAATACTTCGAAATTAACCAAGCGTTTGTTGTGCC---CATCA-AATTGACAACGCTTAGCTTTGCTTGAGGTAGCC--AAATCGTTTCCACATGCG--AA--GAGGGTGC--------------T---------------GGGTG--
droTak1	scf7180000415257:293340-293491 -		GTATGCGTGTG----------TATCTC-----TGTG--TCCTGT-------GAGTACTTTGCCTAAATACTTCGAAATTGGCCAAGCGTTTGTTGTGCC---CATCA-AATTGACAACGCTTAGCTTTGCTTGAGGTAGCC--AAATTGTTTCAACATTCG--AA--GAGGATT--------------GTGC-TGCA-----TTT----------AT-------
droEle1	scf7180000491280:3121552-3121695 -		GTGTGTGTGTG----------TATCTGTGTGCATGTGTG--T-GT---------GTGTGCTTTGCCTAAATACTTCGAAATTGGCCAAGCGTTTGTTGTGTC---CATCA-AATTGACATCGCTTAGCTGTGCTTGAGGTAGCC--AAATTGATTCTACATGCA--AA--AGGGGT---
droRho1	scf7180000779501:512625-512757 +		GTCAGTGTGTG----------TATCTGTG-------------GCCT---------GGGTGCTTTGCCTAAATACTTCGAAATTGGCTAAGCGTTTGTTGTGTC---CATCA-AATTGACAATGCTTAGCTGTGCTTGAGGTAGCC--AAATTGTTTCTACATTGA--AA--GGG--------------------------------GT---
droFic1	scf7180000454055:1329856-1330003 -		GTGTGCGTGTA----------TGTGTGT-------GTG---CG--------TGTGCTTTGCCTAAATACTTCGAAATTGGCCAAGCGTTTGTTGTGCC---CATCA-AATTGACAACGCTTAGCCGTGCTTGAGGTAGCC--AAATTGATTCTACGAGCA--AA--GGGGTG--------------ACAACGAGCATT----------GC---
droKik1	scf7180000302639:1624824-1624966 +		GTGTGCG----------------------GC---TGTGCGTCCTGT-------GTGTG-TTTGGATAAATACTTCGAAATTGGCCAAGCGTTTGTTGTGCT---TATCA-AATTGACAACGCTTAGCTGTGCTTGAGGTAGCC--AAATTGTTTCAACAGACGGGAAGAGAGGGTGC--------------G---------GGT---
droAna3	scaffold_13340:3669031-3669156 -		GTTTGTGTGTG----------TG------ATG-------------AGAG-TCTGCCTAAATACTTCGAAATTGGCTAAGCGTTTGTTGTGATT---TACCA-AATTGACAATGCTAAGCTGTGCTTGAGGTAGCC--AAGATAAATCTACAA-------------CAGG--------------AC-----CT----------CGT---
droBip1	scf7180000396712:683557-683680 +		GTGTGTGTGTG----------T----------------------GAGG-CTGCCTAAATACTTCGAAATTGGCTAAGCGTTTGTTGTGATT---TATCG-AATTGACAATGCTAAGCTGTGCTTGAGGTAGCC--AAGATGAATCTACAC--G--AA--CAGG--------------AC-----CT----------CGT---
dp5	2:21156532-21156728 -	dps_3835	GTATCTGCATGTGTCACCGTATCTGTATCTGTATCC---TGTA--TG-T---------CCGTGCTTCG-TTAAATACTTCGAAATTGGTTAAGCGTTTGTTGTGCT---TATTA-AACTGACAAAGCTTTGCCGTGCTTGAGGTAGCC-CTAATTGATTCCACAAACG--AC--A-------TCACCTGAAGAGGATGAGTGACACACATGACTGTGTGTGTGT-----GTGTT
droPer2	scaffold_3:3931031-3931215 -	dpe_2496	GTGTCACCGTA----------TCTGTATCTGTATCC---TGTA--TG-T---------CCGTGCTTCG-TTAAATACTTCGAAATTGGTTAAGCGTTTGTTGTGCT---TATTA-AACTGACAAAGCTTTGCCGTGCTTGAGGTAGCC-CTAATTGATTCCACAAACG--AC--A-------TCACCTGAAGAGGATGAGTGACACACATGACTGTGTGTGTGT-----GTG--
droWil2	scf2_1100000004943:14640098-14640209 +		GTTTGTGTGTG----------TGTGTGT-------------G-----GAGTTAAATACTTCGAAATTGATTAAGCGTTTGTTGTGTTCCATTTCA-ATTTGACTATGCTTAACTATGCTTGAGGTAGCCTCTAATTGCTTC---
droVir3	scaffold_12855:6808868-6808987 -	dvi_24643	-TGTGCGTGCG----------TGTGTG-----------T---------GTGTGCCTTTTCTAAATACCTTGAAATTGGTTAAGCGTTTGTTGTGCT---TATCA-AATTGACGACGCTTAACTGTGCTTCAGGTAGCC--TAATTGCTTCAACAAGG---
droMoj3	scaffold_6540:25792877-25793004 +	dmo_3123	ATGTGAGTGTG----------TGTGTGTGTT-------------TGT---------GTGTACCGTTCTAAATACTTCGAAATTGGTTAAGCGTTTGTTGTGCT---TATCAAAATTGACAACGCTTACTGTGCTTGAGGTAGCC--TAATTGTTTCAACAAGG---
droGri2	scaffold_14906:2963137-2963259 -	dgr_468	-TGTGTGTGTG----------AGTGTGTGTGC-------------AGTAGCGGCCCTAAATACTTCTGAATTGGTTAAGCGTTTGTTGTGCT---TATCA-AATTGACAACGCTTACTATGCTTGAGGTAGCC--TAATTGTTTCAACAAGG---

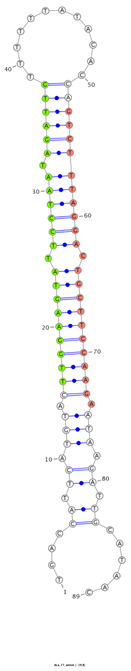
Generated: 09/08/2015 at 07:41 PM

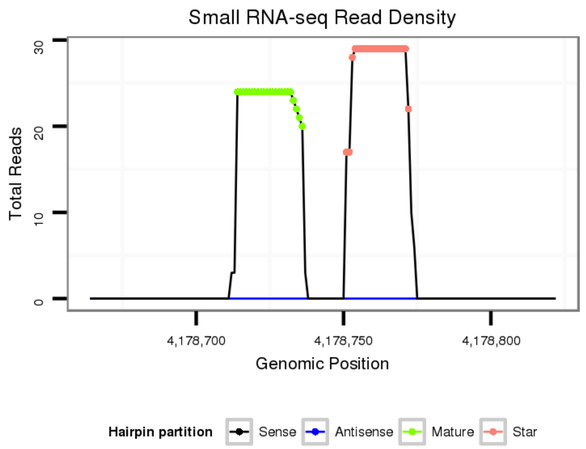
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	8

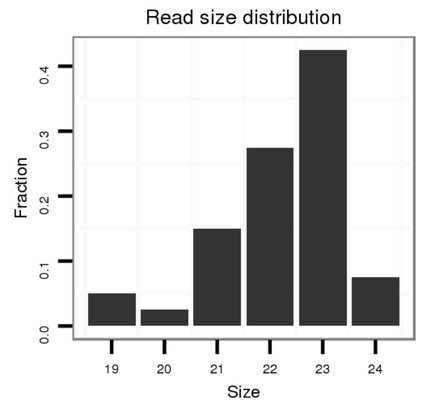
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dya_77	**X:4178714-4178772 +**	**confident**	**Testes-restricted**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

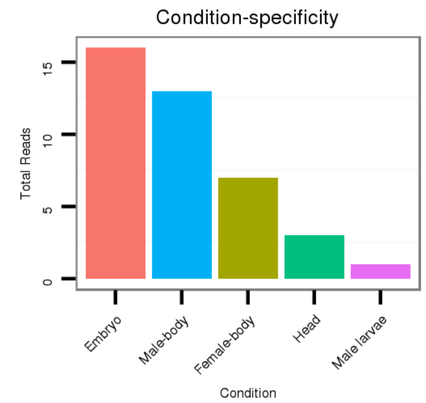
Legend: mature star mismatch in alignment mismatch in read

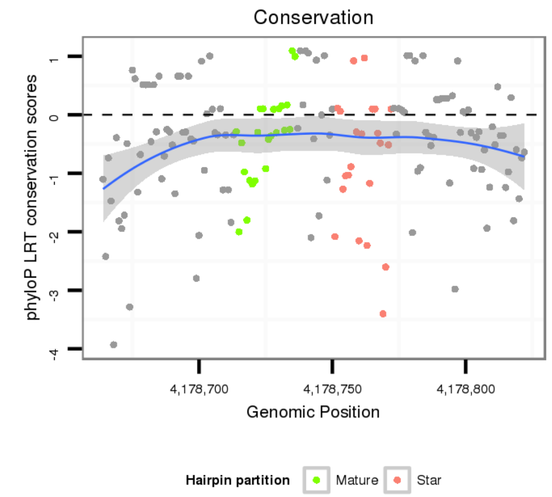
Predicted structure











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	M056 embryo	V120 male body	M043 female body	V046 embryo	M026 head	SRR1275488 Male larvae	V058 head
TGATGTTTCACATCCAAACACAGACGGAAATGATTTGACCATTCATGTACTTGGAAGTATTCCTAATAGATTGTTTTTTATACACCAGTCTTTAGGACTGCTTCCAAGAATAAGATTGCATAACTGCATAATCCTGCAAAAAAAATTCAAATATATATT												
**********....((.((.(((.((((((((((.((((((.((((((.....)))))))))))).)))))))))).))).)).)).....**********												
.....TTGGAAGTATTCCTAATAGATTG.....	23	0	1	17.00	17	2	11	1	2	0	0	1
.....GTCTTTAGGACTGCTTCCAAGA.....	22	0	1	10.00	10	7	0	2	0	0	1	0
.....GTCTTTAGGACTGCTTCCAAG.....	21	0	1	6.00	6	1	0	1	2	2	0	0
.....CTTTAGGACTGCTTCCAAGAAT.....	22	0	1	6.00	6	2	1	2	0	1	0	0
.....TTGGAAGTATTCCTAATAGATTGT.....	24	0	1	3.00	3	0	2	0	1	0	0	0
.....CTTTAGGACTGCTTCCAAGAA.....	21	0	1	3.00	3	2	1	0	0	0	0	0
.....TTGGAAGTATTCCTAATAGATTGA.....	24	1	1	1.00	1	0	0	0	1	0	0	0
.....ACTTGGAAGTATTCCTAATAG.....	21	0	1	1.00	1	0	1	0	0	0	0	0
.....ACTTGGAAGTATTCCTAATAGAC.....	23	1	1	1.00	1	1	0	0	0	0	0	0
.....TTTAGGACTGCTTCCAAGA.....	19	0	1	1.00	1	1	0	0	0	0	0	0
.....ACTTGGAAGTATTCCTAATAGA.....	22	0	1	1.00	1	1	0	0	0	0	0	0
.....CTTTAGGACTGCTTCCAAG.....	19	0	1	1.00	1	0	0	1	0	0	0	0
.....GTCTTTAGGACTGCTTCCAAGAAA.....	24	1	1	1.00	1	0	0	0	1	0	0	0
.....TTGGAAGTATTCCTAATAGATT.....	22	0	1	1.00	1	0	0	1	0	0	0	0
.....CTTTAGGACTGCTTCCAAGAAA.....	22	1	1	1.00	1	0	0	0	1	0	0	0
.....CTTTAGGACTGCTTCCAAGA.....	20	0	1	1.00	1	0	0	1	0	0	0	0
.....GTCTTTAGGACTGCTTCCAAGAA.....	23	0	1	1.00	1	0	1	0	0	0	0	0
.....ACTTGGAAGTATTCCTAATAGAT.....	23	0	1	1.00	1	1	0	0	0	0	0	0
.....GTCTTTAGGACTGCTTCCAAGAT.....	23	1	1	1.00	1	1	0	0	0	0	0	0

Anti-sense strand reads

	Read size	# Mismatch	Hit Count	Total Norm	Total	M043 female body
ACTACAAAGTGTAGGTTTGTGTCTGCCTTTACTAAACTGGTAAGTACATGAACCTTCATAAGGATTATCTAACAAAAAATATGTGGTCAGAAATCCTGACGAAGGTTCTTATTCTAACGTATTGACGTATTAGGACGTTTTTTTAAGTTTATATATAA						
**********....((.((.(((.((((((((((.((((((.((((((.....)))))))))))).)))))))))).))).)).)).....**********						

Show Alignment With Reads

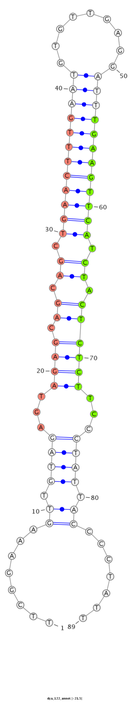
Re-alignment of all predicted orthologs

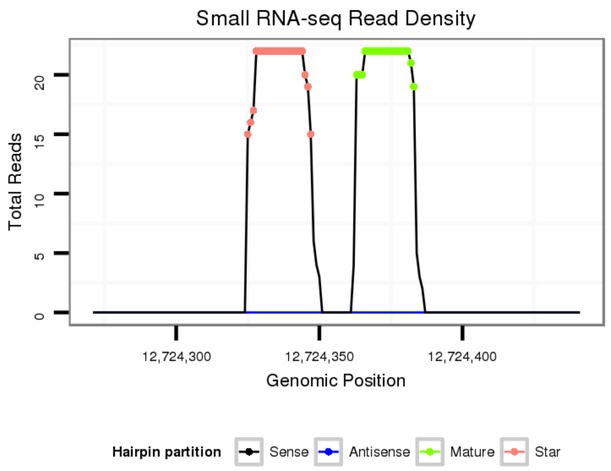
Species	Coordinate	ID	Alignment
droYak3	X:4178664-4178822 +	dya_77	TGATGTTTCAC-------ATC----------CAAACACAGACGGAAATGAT----------TTGACCATTCATGTACTTGGAAGTATTCCTAATAGATTGTTTT-TTATACACCAGTCTTTAG-GACTGCTTCCAAGAATAAGATTGCATA-ACTGCATAATCCTGCAAAAAAAA----------TTCAA--ATATATATT---------
droEre2	scaffold_4690:1630157-1630359 -	der_170	TAATTTTGTAGGAACGAAATAAAACGATCGAACGAAATAAAAATATCA-AGTTAAAAA---TATAT----------AAAATCATTCTAAATCATGGAAAAATATCAATAAATTGTTTT--ATTCATCAATTCATTCTAT--TTTTGTGAATGAAATGTTTT-AGT-------GCTGCAACAGTGTGTTA-------AAATAAATGAAAA----CT--TTTTTGTTGATTTCATAAC
droSec2	scaffold_4:2465130-2465257 +	dse_38	GAATATTACAA-------AT----------T----------ATTACCATTCATATCCTGCACAGTGTTCCTAATAGTCTGTTATT-TATTACAGAAACG-TTGG-GATATACTTTGGAGATAAGGATGGCATA-A-C-------GCTGCAAAAATAAGTAT-------A----------------------AACATA-T---------
droSim2	x:3953201-3953338 -		CACAACCATAT---ATGTAGCCCGTGTGAGTATTCCTAATATACTGTTTT-TGATACACCAGTCGTCAG-TGATACTTTCAGGAATAAGATGGCATA-ATCGCATACTCCGGCAAAAATAAATAT-------A----------AA----TT--TGTATATATGTAT---------
dm3	chrX:4259496-4259672 -		TTATCAATCATC----TAATCAATCCATCAATCTAAGAT-TGATTTCAGTGCTAAAAAGAGTGAAC----------ACAACCATTTACGCCATTGAAAGTAGTCCTAAAAAGACTGTTTT-TAATACACCAGTCGTCAG-TGATACTTTCAGGAATA--ATCGCATA-A-------TCCATCATTAATT--------------------------------------TGTTTGATTTTTATAAA
droBia1	scf7180000301703:499839-499925 +		T--AGATTGCTTT-TAGTGCATCAATCTGGTGTTATCTTTTTCGAACAAGATGGCTTT-CCC-------GCTGCAAATACAGATAT----------------------------T--AAATATGTC---------
droTak1	scf7180000415394:1165310-1165394 +		TTAACTTTCGA-------ATT--TATCCATCAAAAACACAAGATTCGTCTTTTCATCATTCATGTTTTACG-GATGTTTTCATTAGAATGTTTT-T--

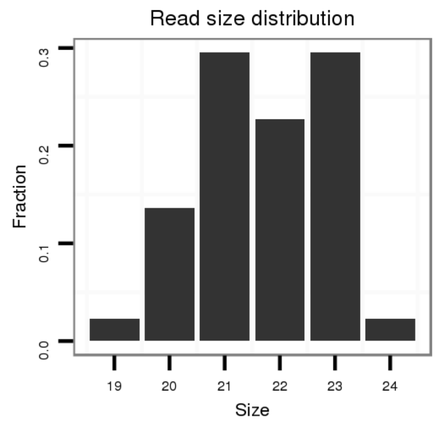
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dya_122	**2R:12724321-12724391 +**	**confident**	**Testes-restricted**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

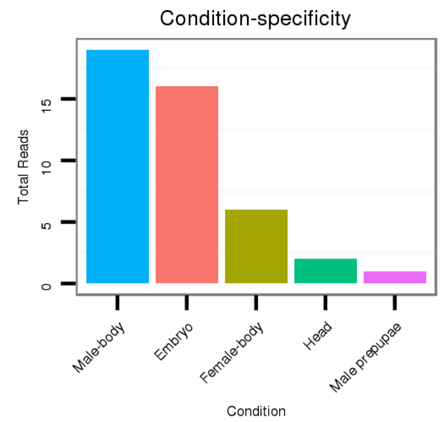
Legend: mature star mismatch in alignment mismatch in read

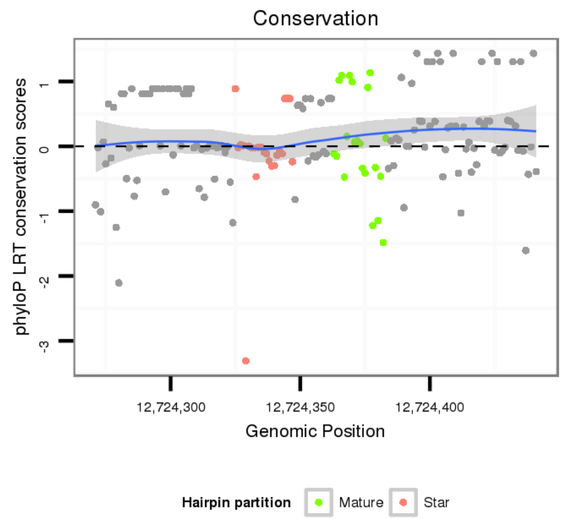
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TTTGATTCTCCGCGTGAACGCCATTTTAAATATTCTCTCTTCGGAAAGTTGTAGAGTAGAGCAGCAGCTGAACTTTGAATGTGTTGAGGATTTGAAGTTCATCTACTCTCTTCCCCTATTACCCCTATTGCCATCCTGCTCTAAACTTCTGCATTCCACTTTGTCCCGTTTT **********.....((.((((...((((.((.((.(((((((((((.....)))))))))))).)).)))))).....))))).))).....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V120 male body	M056 embryo	M043 female body	V046 embryo	M026 head	SRR1275484 Male prepupae	V058 head
.....TGAAGTTCATCTACTCTCTTC.....	21	0	1	11.00	11	1	5	3	2	0	0	0
.....AGTAGAGCAGCAGCTGAACTTTG.....	23	0	1	8.00	8	5	0	1	1	0	1	0
.....AGTAGAGCAGCAGCTGAACTTT.....	22	0	1	4.00	4	4	0	0	0	0	0	0
.....TTGAAGTTCATCTACTCTCTTC.....	22	0	1	3.00	3	1	2	0	0	0	0	0
.....AGAGCAGCAGCTGAACTTTGAAT.....	23	0	1	3.00	3	3	0	0	0	0	0	0
.....TGAAGTTCATCTACTCTCTTCT.....	22	1	1	2.00	2	0	0	2	0	0	0	0
.....AGTTCATCTACTCTCTTCCCT.....	21	0	1	2.00	2	0	2	0	0	0	0	0
.....TGAAGTTCATCTACTCTCTT.....	20	0	1	2.00	2	1	1	0	0	0	0	0
.....AGTAGAGCAGCAGCTGAACT.....	20	0	1	2.00	2	1	0	0	0	1	0	0
.....AGTAGAGCAGCAGCTGAACTTTT.....	23	1	1	1.00	1	1	0	0	0	0	0	0
.....TGAAGTTCATCTACTCTCT.....	19	0	1	1.00	1	1	0	0	0	0	0	0
.....TGAAGTTCATCTACTCTCTTCC.....	22	0	1	1.00	1	0	1	0	0	0	0	0
.....GTAGAGCAGCAGCTGAACTT.....	20	0	1	1.00	1	1	0	0	0	0	0	0
.....TAGAGCAGCAGCTGAACTTTGA.....	22	0	1	1.00	1	0	0	0	0	0	0	1
.....TGAAGTTCATCTACTCTCTTCCC.....	23	0	1	1.00	1	0	1	0	0	0	0	0
.....AGTAGAGCAGCAGCTGAACTTTGA.....	24	0	1	1.00	1	1	0	0	0	0	0	0
.....TGAAGTTCATCTACTCTCTTT.....	21	1	1	1.00	1	0	1	0	0	0	0	0
.....AGAGCAGCAGCTGAACTTTG.....	20	0	1	1.00	1	0	0	1	0	0	0	0
.....TGAAGTTCATCTACTCTCTTCCA.....	23	1	1	1.00	1	1	0	0	0	0	0	0
.....AGAGCAGCAGCTGAACTTTGAA.....	22	0	1	1.00	1	0	0	1	0	0	0	0
.....AGAGCAGCAGCTGAACTTTGAAA.....	23	1	1	1.00	1	1	0	0	0	0	0	0
.....TTGAAGTTCATCTACTCTCTTCC.....	23	0	1	1.00	1	0	1	0	0	0	0	0
.....AAGTTCATCTACTCTCTTCCCG.....	22	1	1	1.00	1	0	0	0	0	1	0	0

Anti-sense strand reads

AAACTAAGAGGCGCACTTGCGGTAAAATTTATAAGAGAGAAGCCTTTCAACATCTCATCTCGTCGTCGACTTGAAACTTACACAACTCCTAAACTTCAAGTAGATGAGAGAAGGGATAATGGGGATAACGGTAGGACGAGATTTGAAGACGTAAGGTGAAACAGGGCAAAA **********.....((.((((...((((.((.((.(((((((((((.....)))))))))))).)).)))))).....))))).))).....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V120 male body	V046 embryo	M056 embryo	M043 female body	V052 head

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droYak3	2R:12724271-12724441 +	dya_122	TTTGATT-CTCCGCGTGAACGCCATTTTAAATATTCTCTC--TT---C----------GGAAAG--TTGT----------AGAGTAGAGCAGCAGCTGAACTTTGAATGTGTTGAGGATTTGAAGTTCATCTACTCTCT-TCCCTATTACCCCTATTGCCATCCTGCTCTAAACTTCTGCATTCCACTTTGT----------CCCGTTTT----------
droEre2	scaffold_4845:10618479-10618645 -		TTCGATATCC-CGCGTGGACGCCATTTTCAATATTCTCTC--TT---\-----------CGAATG--TTGT----------AAAGCACAGCAGCAGCTGATTTTTGCATGTGTTGAGAATTTGAAGTTCATCTACTCTCT-CCCCTATTA--CCTATTGCCATCCCGCTCTAAACTTCTGCATTCCACTTTGT----------CCCGTTTT----------
droSec2	scaffold_1:14026086-14026229 -		TTCGATTTCGCGCGTTGCCGCCATTTTCAATATTCTCTC--TC---C----------CGAAAG--TTGT----------AAAGTAAAGCAAC-----AACTTTGCATGTTTTGAGAGTTCGAAGTTCA----------\-----------TACTGTCATCCCGCTCTAAACCTCTGCATTCCATATTGT----------CCCGTTTT----------
droSim2	2r:17041350-17041493 -		TCCGTTTTCGCGCGTTGCCGCCATTTTCAATATTCTCTC--TC---C----------CGAAAG--TTGT----------AGAGTAAAGCAAC-----AACTTTGCATGTTTTGAGAGTTCGAAGTTCA----------\-----------TACTGTCATCCCGCTCTAAACCTCTGCATTCCATATTGT----------CCCGTTTT----------
dm3	chr2R:16471880-16472023 -		TTCGATTTCCTCGCGTTGCCGCCATTTTCAATATTCTCTC--TC---C----------CGAAAG--TTGT----------AGAGTAGAGCAA-----AACTTTGCATGTTTTGAGAGTTCGAAGTTCA----------\-----------TACTGTCATCCCGCTCTAAACCTCTGCATTCCATTGTGT----------CCCGTTTT----------
droEug1	scf7180000409474:1489686-1489845 +		TTTGTTT-CGTCGTAT-AACGCCATTTTCAA-ATTCTCTCCTAT-TCTCCAC--------AAAAAG--TTCTCCACACTTTCAAAGTCAAGTGCAGC----------------------------------TGCACTGCTTTATTC--CCTGTAGCCATCCCGCTCTAAACTTTGCATTCGCGTTTTGTGACATTTGTTTTCCTATCTT----------
droBia1	scf7180000302291:2815850-2816014 +		CTC----\---CGGATAAACGCCATTATAAACATCCTCTC--TTCTCC----------CAAGAAGAGTGC----------CGAATAAAGCAGCCGTTGAACTTTG---TTTGTGAATTTAAATTCGACTGCTGCCTTACCCCATTA--CCTATTGCCATCTCGCTCCGAGCCTCTGCACTCCGTTTTGT----------CCCGTTTT----------
droTak1	scf7180000415401:100290-100462 -		-------\---CGTATAAACGCCATTTTAAATATTCTCTT--TC-TCCCTTTAATATGTACATATG--TAGT----------TGAGTAGCGGTTGCATTCAGACTTTCAATGTTTGTAGAATTTGAAATTCGATTCCTTCCTTATCCTATTA--CCTATTGCCATCCCGCTCTACACTTCTGCATTTCGTATTG-----------CCCAATTT----------
droEle1	scf7180000491201:736570-736643 -		ATTAA--\-----------------------------\---\-\-----------\-----\-\---\---------\-----------------------------------AAGTTCAACCTCTTCTCTGCT--------CTATTGCCATCTTGCTCTCAACTTCTGTCTTCCTCTTAGT----------CCCGTTTC----------
droRho1	scf7180000780104:82663-82736 -		TCTGA--\-----------------------------\---\-\-----------\-----\-\---\---------\-----------------------------------AACTCAACAGCT----\-CTCTGTTT--CTTATTGCCATCTCGCTTGGAACTTCTGCATTTCTTTTTGC----------TCCTATTT----------
droFic1	scf7180000454039:1776577-1776656 -		ATCGA--\-----------------------------\---\-\-----------\-----\-\---\---------\-----------------------------------AAGTTCAACTCCTTTGCCGCTCCAGTG--CCTATTGCCGTCCCTTTCCG-ATAATTGCATTCCTTTTTGT----------TCAATTTG----------
droKik1	scf7180000302471:942139-942211 -		C------\-----------------------------\---\-\-----------\-----\-\---\---------\-----------------------------------\-----------CTATAGCCATCTCGCTCTAACTTGTCGCATTCGTTTTGT----------CCCTGCTACGAATGCCGGTGCAAAGAAGAAAT
droAna3	scaffold_13266:4132431-4132433 +		TTT----\-----------------------------\---\-\-----------\-----\-\---\---------\-----------------------------------\---\----------\-------\----------

Generated: 09/08/2015 at 07:57 PM

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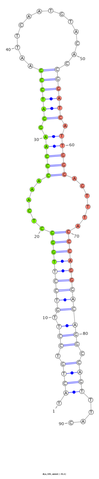
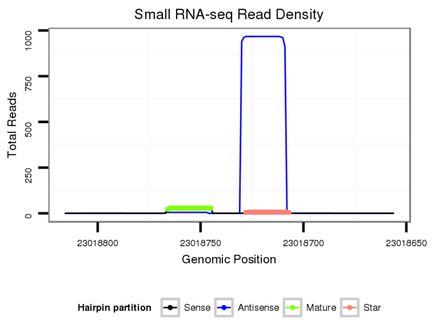
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

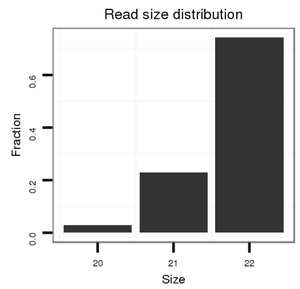
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dya_101	**3R:23018706-23018766 -**	**confident**	**Canonical miRNA**	**antisense_to_intron**	[View on UCSC Genome Browser [Cornell Mirror]]

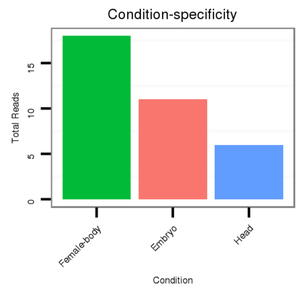
Legend: mature star mismatch in alignment mismatch in read

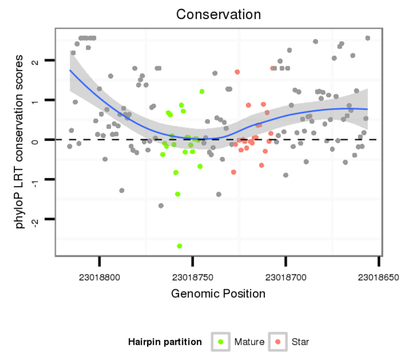
Predicted structure











Show Alternate Folds

Flybase annnotation

Antisense to intron [Dyak/GE10550-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

AAGGAGTTAACAAACATTGGGCCCTTCGCGGGCACTACTGTCCTTGTCCTTGGGCTCAAACCCAAGGATCCGGAATTCAATGTACACCGGATCATTGGGAGTTTACCCAGGGACAGGCCAGTTTACATCATCTATACACCTTGCGTATAGGTATATTGGTTA **********.((((.(((.(((((((((.....(((((.(((((((.....)))))))..)))))).....)))))))))))).))))....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M043 female body	M056 embryo	M026 head	V058 head	V052 head	V120 male body
.....TGGGCTCAAACCCAAGGATCCG.....	22	0	1	22.00	22	9	8	3	1	1	0
.....GGGCTCAAACCCAAGGATCCG.....	21	0	1	5.00	5	4	1	0	0	0	0
.....GATCATTGGGAGTTTACCCAGG.....	22	0	1	4.00	4	2	1	0	1	0	0
.....GATCATTGGGAGTTTACCCAG.....	21	0	1	1.00	1	1	0	0	0	0	0
.....GGCTCAAACCCAAGGATCCG.....	20	0	1	1.00	1	1	0	0	0	0	0
.....ATCATTGGGAGTTTACCCAGG.....	21	0	1	1.00	1	1	0	0	0	0	0
.....TGGGCTCAAACCCAAGGATCC.....	21	0	1	1.00	1	0	1	0	0	0	0

Anti-sense strand reads

TTCCTCAATTGTTTGTAACCCGGGAAGCGCCCGTGATGACAGGAACAGGAACCCGAGTTTGGGTTCCTAGGCTTAAGTTACATGTGGCCTAGTAACCCTCAAATGGGTCCCTGTCCGGTCAAATGTAGTAGATATGTGGAACGCATATCCATATAACCAAT **********.((((.(((.(((((((((.....(((((.(((((((.....)))))))..)))))).....)))))))))))).))))....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M043 female body	V058 head	M026 head	V052 head	V120 male body	M056 embryo	V046 embryo
.....GCCTAGTAACCCTCAAATGGGT.....	22	0	1	888.00	888	334	190	193	90	67	9	5
.....GCCTAGTAACCCTCAAATGGG.....	21	0	1	44.00	44	44	0	0	0	0	0	0
.....GCCTAGTAACCCTCAAATGGGT.....	23	1	1	33.00	33	7	5	1	1	19	0	0
.....CCTAGTAACCCTCAAATGGGT.....	21	0	1	17.00	17	13	1	1	0	0	2	0
.....CCTAGTAACCCTCAAATGGG.....	20	0	1	5.00	5	5	0	0	0	0	0	0
.....AACCCGAGTTTGGGTTCCTAG.....	21	0	1	5.00	5	4	1	0	0	0	0	0
.....GCCTAGTAACCCTCAAATGG.....	20	0	1	4.00	4	4	0	0	0	0	0	0
.....CTAGTAACCCTCAAATGGGT.....	20	0	1	4.00	4	0	0	0	0	0	4	0
.....GCCTAGTAACCCTCAAATG.....	19	0	1	2.00	2	2	0	0	0	0	0	0
.....GCCTAGTAACCCTCAAATGGGT.....	22	1	1	2.00	2	1	1	0	0	0	0	0
.....CTAGTAACCCTCAAATGG.....	18	0	1	1.00	1	1	0	0	0	0	0	0
.....GCCTAGTAACCCTCAAATGGG.....	22	1	1	1.00	1	1	0	0	0	0	0	0
.....GCCTAGTAACCCTCAAATGGG.....	22	1	1	1.00	1	1	0	0	0	0	0	0
.....CTGTCCGGTCAAATGTAGTAG.....	21	0	1	1.00	1	1	0	0	0	0	0	0
.....GCCTAGTAACCCTCAAATGGGT.....	22	1	1	1.00	1	0	0	0	0	1	0	0
.....GACCCGAGTTTGGGTTCCTAG.....	21	1	1	1.00	1	0	1	0	0	0	0	0
.....TTGTTTGTAACCCGGGAAGCGC.....	22	0	1	1.00	1	0	0	0	0	1	0	0
.....GCCTAGTAACCCTCAAATGGGTC.....	23	0	1	1.00	1	1	0	0	0	0	0	0
.....GGCCTAGTAACCCTCAAATGGGT.....	23	0	1	1.00	1	0	0	1	0	0	0	0

Show Alignment With Reads

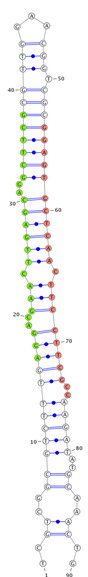
Re-alignment of all predicted orthologs

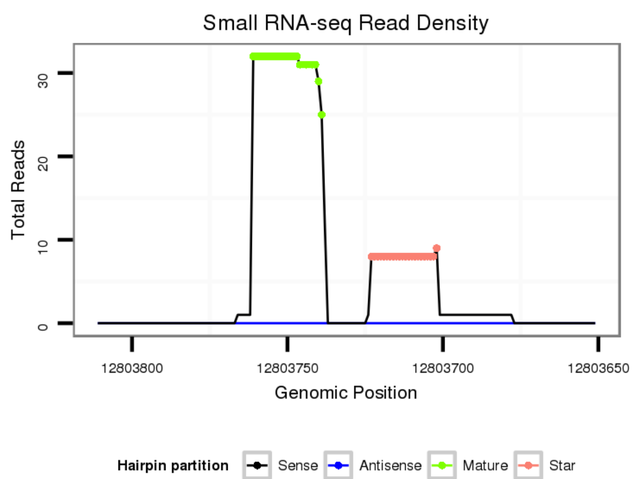
Species	Coordinate	ID	Alignment
droYak3	3R:23018656-23018816 -	dya_101	AAGGA-GTTAACAAACA-TTGGGC------C--------CTTCG--CGGGCACTACTGTCCTTGTCCTTGGGCTCAAACCCAAG----------GATCCG----A-----ATTCAAT-----GTACACCG----------ATCATT--GGGAGT--TTA-CCCAGGGACAG-GCCAGTTTACA------TCA----TCTATACACCTTGCG----------TATA----------GGTATA----TTGGTTA
droEre2	scaffold_4820:4569024-4569213 -	der_100	AAGGA-GTTAACAAACA-TTGGGC------C--------CTTCG--CGGGCACTACTGTCCTTGCCCTGGGGAGAATCCCAAG----------GATCG----G-----ATTCTAT-----GTACACCC----------ATCATT--GGGAGT--TTG-CCCAGGGACAG-GCCAGTTTACA------TCA----TCTATACACCTTAGGGG----------GCT-AGCCC----------TTGAAGAATGCATAAACATATA----------GGTATA----TTGGTTA
droSec2	scaffold_22:111544-111742 +	dse_1838	AAGGA-GTTAACAAACA-TTGGGC------C--------CTTCG--CGGGCACTACTGTCCTGACCTTGCCCGAAGGAGAATCCCAAG----------GATCG----G-----ATTCAAT-----GTACACCG----------ATCGTT--GGGAGT--TTA-CCCAGGGACAG-GCCAGTTTACA------TCA----TC----------CGGG----------GCT-AACCC----------TCGAAGAATGCATAAACATATGTG----------TGTATAT----GTAGGTATGTATGTATA----TTGGTTA
droSim2	3r:22893184-22893382 +	dsi_32470	AAGGA-GTTAACAAACA-TTGGGC------C--------CTTCG--CGGGCACTACTGTCCTGACCTTGCCCGAAGGAGAACCCAAG----------GATCG----G-----ATTCAAT-----GTACACCG----------ATCGTT--GGGAGT--TTA-CCCAGGGACAG-GCCAGTTTACA------TCA----TC----------CGGG----------GCT-AACCC----------TCGAAGAATGCATAAACATATGTA----------TGTATAT----GTAGGTATGTATGTATA----TTGGTTA
dm3	chr3R:23468154-23468356 +	dme_454	AAGGA-GTTAACAAACA-TTGGGC------C--------CTTCG--CGGGCACTACTGTCCTGACCTTGCCCGAAGGAACCCAAG----------GATCG----G-----ATTCAAT-----GTACACCG----------ATCGTT--GGGAGT--TTA-CCCAGGGACAG-GCCAGTTTACA------TCA----TC----------CGGG----------GCT-AACCC----------TCGAAGAATGCATAACATATGTA----------TGTATATGTATGTAGGTATGTATGTATA----TTGGTTA
droEug1	scf7180000409770:952512-952687 +		AAGGA-GTTAACAAACA-TTGGGC------C--------CTCTGGAGGGCACTACTGTCCTTGTCCTAAAGGAGAATCCCAAG----------------GCCCC----T-----CCCCC----------ATCATT-AGGGAG-TTTGTTAGGGACAG-GTCAGTTTACA------TTA----TCTATACACCTTG-AAGG----------GCT-AACCA----------TTGAAGAATGCATAAACATATATA----------TGTATGTATA----TTGGTTA
droBia1	scf7180000302075:1453638-1453810 -		GGGGA-GTTAACAAAAA-TTGGC------C--------CTGTG--CGGGGTCTACTGACCTTGCCCTGAGGAGATTTACCAAG----------------GCCCC----T-----CCCCC----------ATCATT--GGGATCCTGCATGTGGGCCAG-GCCAGTTTACA------CTA----TCTATCCACCTCTAAGG----------GCT-GGCCA----------TTGAAGAGTGCATAAACACATA----------GGTATGTA--TATTG----TTGGTTA
droTak1	scf7180000413872:362752-362869 +		AAGGA-GTTAACAAACC-TTGTC--C------T--------CCCCC----C-------GCTGACCCTGCCCTTGGGGAAGGTCCCAAG----------------G-----C----T-----CCCCC----------TCATT--GGGATACTGCTGTGAGGGGAG-GTCAGTTCTGTA------TTA----TCTATACA--TTAATGTA----------TTATTG----TTGATTA
droEle1	scf7180000491261:1964194-1964381 +		AAGGA-GTTAACAAACA-TCGGGC------C--------CTCTGGTTGGGCAGTACTGTCCTTGCCCAAAGGAGTGTCCTCG----------------CTCA----G-----ATTAAAT-----TTCATCCTT----------TCTG--GGCGAA--TTG-TCAGGGCCAG-GTCAGTTTACA------GTA----TCTATACACCTT-AAGG----------ACTAAACCA----------TTGAAGAATGCATAAACATAT----------ATA----TGGTTA
droRho1	scf7180000779391:18284-18480 -		AAGGA-GTTAACAAACA-TTGGGC------C--------CTTGG-CGGGGCATACTGTCCTTGCCCTGGAGGAGAAACCTCG----------------CTAAATGTGATTTTAATCCAAT-----TTCATCCTT----------TTTTT--GCCGAA--TTG-TCAGGGCCAG-GCAGAGTTACA------TCA----TCTATACACCTT-AAGG----------GCT-AACCA----------TTGAAGAATGCATAAACATAT----------ATA----TGGTTA
droFic1	scf7180000453826:246823-247008 -		GAGGA-GTTAACAAACA-TTGTGG------C--------CTCTG--GGGGCTTACTGTCTGTGCCCACAAGGATTTACCCAAG----------------ATCAC----T-----GCCTAT-----ATACACCTG----------ATCTTCAAGGATT--TTG-TCCTGCCAG-ATCAGCTTACA------TTA----TCTATACAATTT-AAGG----------GTT-GACCA----------TTGAAATTGCATAAACACATACA----------A-----TGGTTA
droKik1	scf7180000302697:740338-740508 +		GGGGA-GTTAACAAACA-TCGGGGTGCTGC------CT----T--------TCTGCCCTGGCAGAGTGACCTCAG----------------CTGGGCCTGTGGTTAAATTCAAT-----TTACACCTGGCCGGATCGCAAGAGCATCCCTCCTCTCC--GGGGAT--CTG-CCCAGGGCCAG-GCAGCGCATA------TCC----TCATCATAGTTT---------------------------------------GTTTAGCTA
droAna3	scaffold_13340:19221655-19221848 -		AAGGA-TTTAACAAACA-TTGAGC------C--------TCC--CG--TGGCCAATCCTGTCCTTGCCCAAGGGGCACCTTTG----------------TTCCA----T-----TTTAAATTTAATAGTAAC-----TTTT

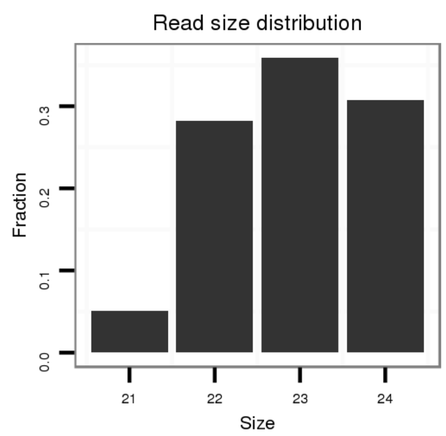
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dya_73	**3R:12803701-12803761 -**	**confident**	**Canonical miRNA**	**CDS**	[View on UCSC Genome Browser {Cornell Mirror}]

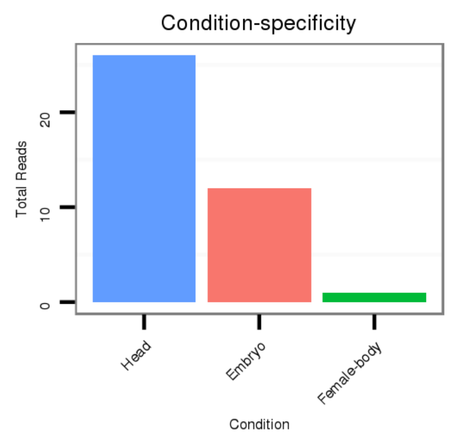
Legend: mature star **mismatch in alignment** mismatch in read

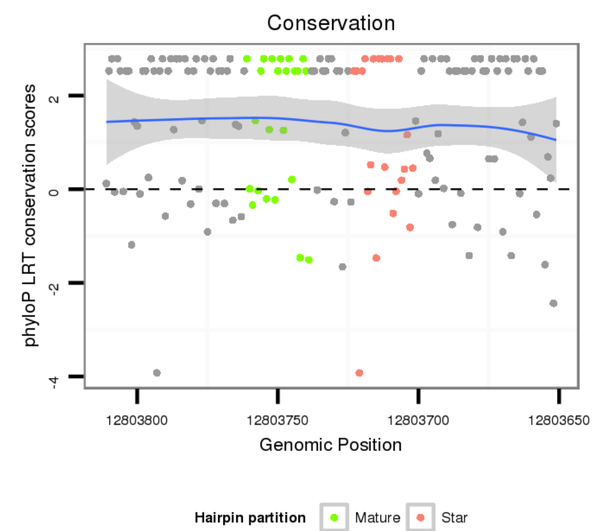
Predicted structure











Show Alternate Folds

Flybase annnotation

CDS [Dyak\GE24494-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

CGACACTCCTACGGGCACGGTGGACTTCTGCCAGATCGTCGGCGTCTTTGAGGACGAACTTGAGCAGGCTTCGCGTTGGAACGGTCGCGGAGTGCTCAACTTCCTTCGCCAAGATATGCAAACTGGCGGCGACTGGCTGGTGACAAACATGGATCGCCCGA **********	Read size	# Mismatch	Hit Count	Total Norm	Total	M026 head	M056 embryo	V046 embryo	V058 head	M043 female body	V052 head	V120 male body
.....AGGACGAACTTGAGCAGGCTTCG.....	23	0	1	13.00	13	9	1	1	1	1	0	0
.....AGGACGAACTTGAGCAGGCTTCGC.....	24	0	1	12.00	12	7	2	1	2	0	0	0
.....GGAGTGCTCAACTTCCTTCGCC.....	22	0	1	7.00	7	1	6	0	0	0	0	0
.....AGGACGAACTTGAGCAGGCTTC.....	22	0	1	4.00	4	4	0	0	0	0	0	0
.....AGGACGAACTTGAGCAGGCTT.....	21	0	1	2.00	2	2	0	0	0	0	0	0
.....AGGACGAACTTGAGCAGGCTTCGCT.....	25	1	1	2.00	2	2	0	0	0	0	0	0
.....AGGACGAACTTGAGCAGGCTTCGG.....	24	1	1	1.00	1	1	0	0	0	0	0	0
.....CTTTGAGGACGAACTTGAGC.....	20	0	1	1.00	1	0	0	0	0	0	0	1
.....AGGACGAACTTGAGCAGGCTTT.....	22	1	1	1.00	1	1	0	0	0	0	0	0
.....AGGACGAACTTGAGCAGGCTTCGCG.....	25	1	1	1.00	1	0	1	0	0	0	0	0
.....AGGACGAACTTGAGCAGGCTTCT.....	23	1	1	1.00	1	1	0	0	0	0	0	0
.....CAAGATATGCAAACTGGCGGCGACT.....	25	0	1	1.00	1	0	1	0	0	0	0	0
.....AGGACGAACTTGAGCAGGCTTA.....	22	1	1	1.00	1	0	1	0	0	0	0	0
.....CGGAGTGCTCAACTTCCTTCGCC.....	23	0	1	1.00	1	0	1	0	0	0	0	0

Anti-sense strand reads

GCTGTGAGGATGCCCGTGCCACCTGAAGACGGTCTAGCAGCCGCAGAAACTCCTGCTTGAACTCGTCCGAAGCGCAACCTTGCCAGCGCCTCACGAGTTGAAGGAAGCGGTTCTATACGTTTGACCGCCGCTGACCGACCACTGTTTGTACCTAGCGGGCT **********	Read size	# Mismatch	Hit Count	Total Norm	Total	M056 embryo

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droYak3	3R:12803651-12803811 -	dya_73	CGACACTCCTACGGGCACGGTGGACTTCTGCCAGATCGTCGGCGTCTTTGAGGACGAACTTGAGCAGGCTTCGCGTTGGAACGGTCGCGGAGTGCTCAACTTCCTTCGCCAAGATATGCAAACTGGCGGCGACTGGCTGGTGACAAACATGGATCGCCCGA
droEre2	scaffold_4770:13134647-13134807 +		CGACACTCCCACGGGCACTGTGGACTTCTGCCAAATCGTCGGCGTCTTTGAGGATGAACTTGAGCAGGCATCGCGTTGGAATGGTCGCGCGTGCTTAACTTCCTTCGCCAAGATATGCAAACTGGCGGAGACTGGCTCGTCACTAACATGGATCGCCCGA
droSec2	scaffold_0:13468396-13468556 +		CGACACTCCCACCGGCAGAGTAGACTTCTGCCAAATTGTCGGCGTCTTCGACGACGAGCTTGAGCAGGCATCGCGTTGGAACGGCCGCCGGTGTGCTTAACTTTCTTCGCCAGGATATGCAAACTGGCGGTGATTGGCTGGTGACTAACATGGATCGCCAAA
droSim2	3r:12641774-12641934 +		CGACACTCCCACCGGCACGGTGGACTTCTGCCAGATTGTCGGCGTCTTTGACGACGAGCTTGAGCAGGCATCGCGTTGGAACGGCCGCCGGTGTGCTTAACTTCCTTCGCCAGGATATGCAAACTGGCGGTGATTGGCTGGTGACTAACATGGATCGCCAAA
dm3	chr3R:8516449-8516609 -		CGACACTCCCACGGGCACGGTGGACTTCTGCCAGATCGTCGGCGTCTTTGACGACGAACTTGAGCAGGCATCGCGTTGGAACGGCCGCCGGTGTGCTCAACTTCCTTCGCCAAGATATGCAAACTGGCGGTGATTGGCTGGTGACTAACATGGATCGCCAGA
droEug1	scf7180000409804:709430-709590 -		CGAGACACCTACCGGCAGTGTAGACTTCTGCCAGATCGTCGGAGTTTTTGAAAACGAACTAGAGCAGGCTTCACGTTGGAACGGACGTGGAGTGCTCAACTTTTGCGTGAAGATGTACAGACGGGCGGCGACTGGTTGGTAACCAACATGGATCGCCAA
droBia1	scf7180000302402:204649-204809 -		CGAGACGCCCACCGGTACTGTGGACTTCTGTCAGCTTGTCGGCGTTTCGAAGACGAACTGGAGCAAGCCTCTCGTTGGAATGGACGCGGAGTGCTCAACTTCCTGCGGCAGGATGTGCAGACGGGCGGCGACTGGCTGGTGACCAACATGGACGGACCGA
droTak1	scf7180000415366:23850-24010 +		CGAGACGCCCACGGGCACGGTGGACTTTGTGTCAGATCGTCGGCGTGTTTGAGACCGAACTGGAGCAAGCCTCCCGTTGGAATGGACGTGGGTGCTCAACTTCCTGCGCCAGGATGTGCAGACGGGCGGCGACTGGCTGGTGACCAACATGGACCGGCCCA
droEle1	scf7180000490994:209036-209196 -		TGAGACGCCCACCGGCAGCGTGGACTTCTGCCAGATCGTCGGCGTCTTTGAGAATGAGCTGGAGCAGGCCTCCGCGTGGAACGGACGCGGCGTGCTCAACTTCTTGCGCCAGGATGTGCAGACGGGCGGCGACTGGCTGGTGACCAACATGGACGGACCA
droRho1	scf7180000779900:100466-100626 -		TGAGACGCCCACCGGCAGAGTGGACTTCTGCCAGATTGTCGGCGTCTTTGAGAACGAGCTGGAGCAGGCCTCGCGCTGGAATGGACGCGGAGTGCTCAACTTTCTGCGCCAGGATGTGCAGACGGGAGGCGACTGGCTGGTGACCAACATGGAGCGCCCGA
droFic1	scf7180000453812:584361-584521 +		CGAGACGCCGACCGGAACGGTAGACTTCTGTCAGATTGTGGGCGTCTTCGAGGACGAACTAGAGCAGGCTTCTCGTTGGAACGGACGCGGAGTGCTCAACTTCCTGCGAGAGATGTTCAAACTGGCGGAGATGGCTAGTGACAAACATGGACCGCCCGA
droKik1	scf7180000302256:543145-543305 +		CGAGACGCCCTTCGGTAGCGTAGACTTCTGCCAGATTGTGGGCGTCTTCGAGAACGAGCTGGAGCAGGCCTCTCGCTGGAATGGTCGCGGCGTCCTCAACTTCCTGCGCCAGGAGGTGCAGACGGGCGGTGACTGGCTGGTCACCAATATGGATCGGACGA
droAna3	scaffold_13340:6660150-6660310 +		AGAAACGCCGTTTGGCAGTGTGGATTTCTGCCAAATCGTTGGAGTGTTCGAAAACGAATTGGAGCAAGCGTCCCGATGGAACGGACGTGGAGTCCTAAACTTTCTTCGAGAGGATGTGCAAACTGGAGGCGATTGGCTGGTGACCAACATGGACGCGACAA
droBip1	scf7180000396708:2179994-2180154 -		AGAAACGCCTTTTGGCAGTGTGGATTTCTGTCAGATCGTTGGTGTGTTTGAAAACGAATTGGAGCAAGCTTCTCGATGGAACGGCCGTGGCGTTCTAAACTTTCTTCGGCAGGATGTGCAAACTGGAGGCGATTGGCTGGTGACAAATATGGACCGAAAAA
dp5	2:10662699-10662859 +		CGAGACACCGTTTGGCAGCGTTGACTTTTGTCAGATTGTTGGTGTCTTTGAGCACGAGCTAGAGCAAGCTTCGCGCTGGAACGGTCGCGGGGTTTTCAATTTCCTGCGCCAGGATATCCAGACTGGCGGCGAGTGGCTGGTTACAAACATGGAACGAACGA
droPer2	scaffold_0:9817176-9817336 -		CGAGACACCGTTTGGCAGCGTTGACTTTTGTCAGATTGTTGGCGTCTTTGAGCACGAGCTGGAGCAAGCTTCGCGCTGGAACGGCCGCCGGAGTTTTCAATTTCCTGCGCCAGGATATCCAGACAGGCGGCGAGTGGCTGGTTACAAACATGGAACGAACAA
droWil2	scf2_1100000004943:2436158-2436318 -		TGAAACACCCTTTGGCAGTGTGGACTTTGTGCCAGATTGTCGGAGTCTTTGAGGATGAGCTAGAGCAGGCCTCACGTTGGAACGGAAGGGCGTTTTAAACTTTTGCGCCGGGATGTGCAAACTGGGGGAGAGTGGTTGGTCACGAATATGCACGCGATCC
droVir3	scaffold_13047:8068028-8068188 +		TGACACACCCTTTGGCAGTGTGGACTTTTGTCAGATAGTTGGCGTAACCGAGGAGGAACTGGAACAGGCTTCACGCTGGAACGGCCGTGGCGTCTTGAATTTTTTGTCTAAAGACGTGCAGACAGGCGGCGATTGGCTGGTTACCAATATGCACGCGCAGAA
droMoj3	scaffold_6540:28122714-28122874 -		TGACACGCCTTTTGGCAGAGTTGACTTCTGCCAAATAGTTGGCGTTACCGAGGAGGAACTGGAGCAGGCCTCACGCTGGAACGGCCGTGGCGTCTTGAATTTCTTGGCTAAGGATGTGCAGACAGGCGGCGAATGGCTGGTTACCAACATGCAGCGGCACCA
droGri2	scaffold_15074:1554626-1554786 -		TGACACACCCTTTGGCAGTGTGGACTTTTGCCAGATAGTCGGCGTCACCGAGGAGGAACTGGAGCAGGCCTCACGGTGGAATGGTCGTGGTGTCCTCAACTTCCTCGCCAAAGATGTGCAGACTGGTGGGATTGGCTGGTGACGAATCTGCAGCGGCAGAA

Generated: 09/08/2015 at 07:41 PM

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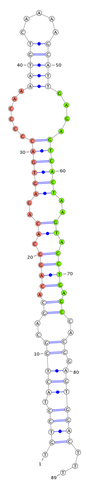
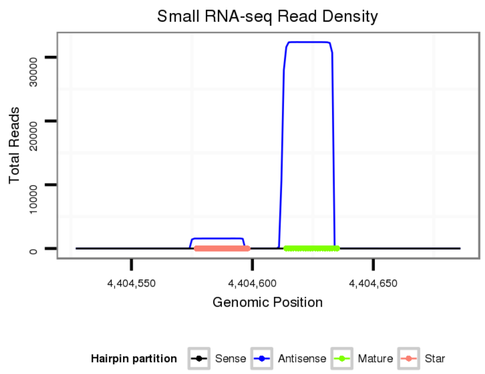
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

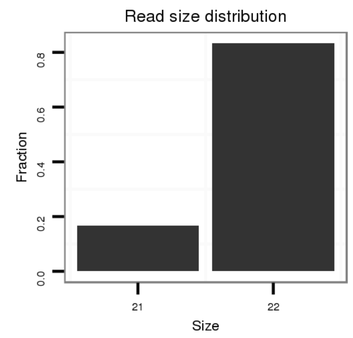
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dya_78	**2R:4404577-4404636 +**	**confident**	**Canonical miRNA**	**antisense_to_intron**	[View on UCSC Genome Browser [Cornell Mirror]]

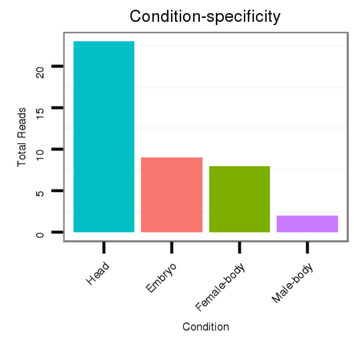
Legend: mature star mismatch in alignment mismatch in read

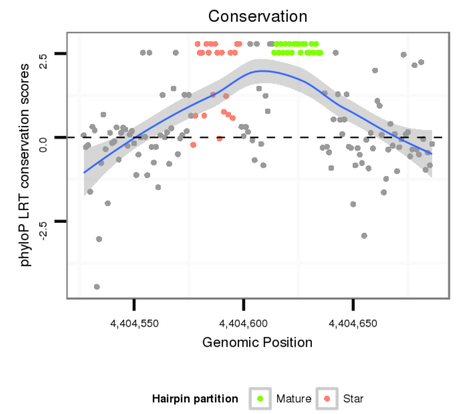
Predicted structure











Show Alternate Folds

Flybase annnotation

Antisense to intron [Dyak\GE12755-in]; Antisense to pre_miRNA [Dyak\mir-306-RM]; Antisense to utr5 [utr5_plus_2209]; Antisense to miRNA [Dyak\miR-306-RA]; Antisense to miRNA [Dyak\miR-306-star-RB]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

```
CTTATTCCAATGTAAATCACTTTATTTGTGGATTATGTCCTACTGGCAGCACAGGCACAGGAGTGACCCCCAAAATGTCAAAAGCATTGAGAGTCACTAAGTACCTGAGCCACCGAGTGGACTTTAAAACTTTTCACTGATTTATACACAGATTTAATCGA
**********************************.((((.(((((..((.((((.((..((((((.....(((((.....)))))....))))))..)).)))).)).)).)).)))))))...**********************************
```

Read size	# Mismatch	Hit Count	Total Norm	Total	M026 head	M056 embryo	M043 female body	V058 head	V052 head	V120 male body	
22	0	1	29.00	29	18	8	2	1	0	0	....GAGAGTCACTAAGTACCTGAGC....
22	0	1	5.00	5	0	1	2	1	0	1	....ACAGGCACAGAGTGACCCCCAA....
21	0	1	5.00	5	0	0	2	1	1	1	....ACAGGCACAGAGTGACCCCCA....
21	0	1	2.00	2	0	0	2	0	0	0	....GAGAGTCACTAAGTACCTGAG....
22	0	1	1.00	1	1	0	0	0	0	0	....AGAGTCACTAAGTACCTGAGCC....
22	1	1	1.00	1	1	0	0	0	0	0	....GAGAGTCACTAAGTACCTGAGT....

Anti-sense strand reads

```
GAATAAGGTTACATTTAGTGAAATAAACACCTAATACAGGATGACCGTCGTGTCCGTGTCTCACTGGGGGTTTTACAGTTTTCGTAACTCTCAGTGATTCATGGACTCGGTGGCTCACCTGAAATTTTGAAAAGTGACTAAATATGTGTCTAAATTAGCT
**********************************.(((((.(((((..((.((((.((..((((((.....(((((.....)))))....))))))..)).)))).)).)).)).)))))))...**********************************
```

Read size	# Mismatch	Hit Count	Total Norm	Total	M043 female body	M056 embryo	V046 embryo	M026 head	V058 head	V052 head	V120 male body	GSM1528802 follicle cells	SRR1275484 Male prepupae	SRR1275488 Male larvae	
21	0	1	16357.00	16357	8256	5064	1930	740	191	122	32	21	0	1	....ACTCTCAGTGATTCATGGACT....
22	0	1	9791.00	9791	5861	1922	963	653	235	127	26	0	4	0	....AACTCTCAGTGATTCATGGACT....
20	0	1	3549.00	3549	409	2152	78	682	134	90	3	0	1	0	....CTCTCAGTGATTCATGGACT....
22	0	1	1364.00	1364	187	1066	105	4	2	0	0	0	0	0	....CGTGTCCGTGTCTCACTGGGGG....
23	1	1	1292.00	1292	633	311	102	192	31	13	8	0	2	0	....AAACTCTCAGTGATTCATGGACT....
20	0	1	857.00	857	856	1	0	0	0	0	0	0	0	0	....ACTCTCAGTGATTCATGGAC....
19	0	1	742.00	742	119	60	5	507	31	19	0	0	1	0	....TCTCAGTGATTCATGGACT....
22	1	1	676.00	676	222	336	31	72	12	2	0	1	0	0	....CACTCTCAGTGATTCATGGACT....
21	0	1	614.00	614	612	1	0	0	0	1	0	0	0	0	....AACTCTCAGTGATTCATGGAC....
23	0	1	220.00	220	107	97	6	7	2	0	1	0	0	0	....TAACTCTCAGTGATTCATGGACT....
23	2	1	184.00	184	16	99	3	66	0	0	0	0	0	0	....CCACTCTCAGTGATTCATGGACT....
24	2	1	156.00	156	80	47	8	17	2	1	0	0	1	0	....AAAACTCTCAGTGATTCATGGACT....
23	1	1	144.00	144	32	104	3	5	0	0	0	0	0	0	....GAACTCTCAGTGATTCATGGACT....
21	0	1	139.00	139	82	43	11	0	0	2	1	0	0	0	....GTGTCCGTGTCTCACTGGGGG....
22	1	1	119.00	119	68	34	2	10	2	1	2	0	0	0	....TACTCTCAGTGATTCATGGACT....
19	1	1	92.00	92	0	20	0	72	0	0	0	0	0	0	....CCTCAGTGATTCATGGACT....
21	1	1	89.00	89	17	12	3	56	0	1	0	0	0	0	....TCTCTCAGTGATTCATGGACT....
22	1	1	67.00	67	67	0	0	0	0	0	0	0	0	0	....AAACTCTCAGTGATTCATGGAC....
20	0	1	61.00	61	43	1	13	0	4	0	0	0	0	0	....AACTCTCAGTGATTCATGGA....
23	2	1	52.00	52	12	27	3	9	1	0	0	0	0	0	....ACACTCTCAGTGATTCATGGACT....
21	1	1	50.00	50	0	8	13	23	6	0	0	0	0	0	....CCTCTCAGTGATTCATGGACT....
25	3	1	50.00	50	31	10	1	7	1	0	0	0	0	0	....AAAAACTCTCAGTGATTCATGGACT....
19	0	1	48.00	48	28	0	19	0	0	1	0	0	0	0	....ACTCTCAGTGATTCATGGA....
19	0	1	36.00	36	34	2	0	0	0	0	0	0	0	0	....CTCTCAGTGATTCATGGAC....
21	0	1	36.00	36	23	11	0	2	0	0	0	0	0	0	....CGTGTCCGTGTCTCACTGGGG....
23	1	1	35.00	35	22	11	0	2	0	0	0	0	0	0	....GAACTCTCAGTGATTCATGGACT....
18	0	1	27.00	27	5	9	0	11	2	0	0	0	0	0	....CTCAGTGATTCATGGACT....
21	1	1	23.00	23	22	1	0	0	0	0	0	0	0	0	....CACTCTCAGTGATTCATGGAC....
21	1	1	22.00	22	2	2	3	15	0	0	0	0	0	0	....GCTCTCAGTGATTCATGGACT....
24	2	1	21.00	21	4	14	2	1	0	0	0	0	0	0	....ACAACTCTCAGTGATTCATGGACT....
22	1	1	19.00	19	0	0	18	1	0	0	0	0	0	0	....GGTGTCCGTGTCTCACTGGGGG....
22	1	1	19.00	19	12	1	1	4	1	0	0	0	0	0	....GACTCTCAGTGATTCATGGACT....
23	0	1	17.00	17	1	11	3	2	0	0	0	0	0	0	....TCGTGTCCGTGTCTCACTGGGGG....
19	1	1	13.00	13	0	0	0	13	0	0	0	0	0	0	....GCTCAGTGATTCATGGACT....
24	1	1	13.00	13	3	8	1	1	0	0	0	0	0	0	....TTAACTCTCAGTGATTCATGGACT....
22	0	1	12.00	12	8	2	1	0	0	0	1	0	0	0	....ACTCTCAGTGATTCATGGACTC....
21	0	1	10.00	10	1	3	0	3	2	1	0	0	0	0	....CTCTCAGTGATTCATGGACTC....
23	1	1	9.00	9	0	7	2	0	0	0	0	0	0	0	....CCGTGTCCGTGTCTCACTGGGGG....
24	2	1	9.00	9	2	6	0	1	0	0	0	0	0	0	....TCAACTCTCAGTGATTCATGGACT....
24	2	1	9.00	9	2	6	0	0	1	0	0	0	0	0	....TAAACTCTCAGTGATTCATGGACT....
21	1	1	8.00	8	8	0	0	0	0	0	0	0	0	0	....TACTCTCAGTGATTCATGGAC....
24	3	1	8.00	8	1	6	0	1	0	0	0	0	0	0	....ACCACTCTCAGTGATTCATGGACT....
20	0	1	8.00	8	0	7	1	0	0	0	0	0	0	0	....CGGTGGCTCACCTGAAATTT....
20	1	1	8.00	8	0	5	0	1	2	0	0	0	0	0	....TTCTCAGTGATTCATGGACT....
21	1	1	7.00	7	5	0	1	1	0	0	0	0	0	0	....AAACTCTCAGTGATTCATGGA....
18	0	1	7.00	7	5	1	0	1	0	0	0	0	0	0	....ACTCTCAGTGATTCATGG....
24	2	1	7.00	7	1	4	0	2	0	0	0	0	0	0	....CAAACTCTCAGTGATTCATGGACT....
29	0	1	7.00	7	0	0	0	0	0	0	0	7	0	0	....TGGGGGTTTTACAGTTTTCGTAACTCTCA....
22	1	1	7.00	7	4	1	2	0	0	0	0	0	0	0	....TGTGTCCGTGTCTCACTGGGGG....
22	0	1	7.00	7	7	0	0	0	0	0	0	0	0	0	....TAACTCTCAGTGATTCATGGAC....
18	0	1	7.00	7	6	0	0	1	0	0	0	0	0	0	....TCTCAGTGATTCATGGAC....
22	1	1	6.00	6	6	0	0	0	0	0	0	0	0	0	....GAACTCTCAGTGATTCATGGAC....
18	0	1	6.00	6	4	0	1	1	0	0	0	0	0	0	....CTCTCAGTGATTCATGGA....
19	0	1	6.00	6	6	0	0	0	0	0	0	0	0	0	....AACTCTCAGTGATTCATGG....
23	2	1	5.00	5	5	0	0	0	0	0	0	0	0	0	....AAAACTCTCAGTGATTCATGGAC....
18	0	1	5.00	5	2	0	0	3	0	0	0	0	0	0	....TCCGTGTCTCACTGGGGG....
23	0	1	5.00	5	3	0	2	0	0	0	0	0	0	0	....AACTCTCAGTGATTCATGGACTC....
20	0	1	5.00	5	5	0	0	0	0	0	0	0	0	0	....GTGTCCGTGTCTCACTGGGG....
24	3	1	5.00	5	5	0	0	0	0	0	0	0	0	0	....AAAAACTCTCAGTGATTCATGGAC....
16	0	1	5.00	5	0	0	0	0	0	0	0	0	5	0	....CAGTGATTCATGGACT....
24	1	1	4.00	4	3	1	0	0	0	0	0	0	0	0	....ATAACTCTCAGTGATTCATGGACT....
24	3	1	4.00	4	4	0	0	0	0	0	0	0	0	0	....AACACTCTCAGTGATTCATGGACT....
24	2	1	4.00	4	2	2	0	0	0	0	0	0	0	0	....TGAACTCTCAGTGATTCATGGACT....
22	1	1	4.00	4	1	3	0	0	0	0	0	0	0	0	....AGTGTCCGTGTCTCACTGGGGG....
22	2	1	4.00	4	3	0	0	1	0	0	0	0	0	0	....TTCTCTCAGTGATTCATGGACT....
20	1	1	4.00	4	2	1	0	0	1	0	0	0	0	0	....ATCTCAGTGATTCATGGACT....
18	0	1	3.00	3	3	0	0	0	0	0	0	0	0	0	....AACTCTCAGTGATTCATG....
24	3	1	3.00	3	1	2	0	0	0	0	0	0	0	0	....TCGACTCTCAGTGATTCATGGACT....
23	1	1	3.00	3	3	0	0	0	0	0	0	0	0	0	....ACGTGTCCGTGTCTCACTGGGGG....
19	0	1	3.00	3	0	3	0	0	0	0	0	0	0	0	....GTCCGTGTCTCACTGGGGG....
19	0	1	3.00	3	0	3	0	0	0	0	0	0	0	0	....CGGTGGCTCACCTGAAATT....
22	0	1	3.00	3	0	2	1	0	0	0	0	0	0	0	....CGGTGGCTCACCTGAAATTTTG....
21	2	1	2.00	2	1	0	0	0	1	0	0	0	0	0	....GTTCTCAGTGATTCATGGACT....
19	0	1	2.00	2	2	0	0	0	0	0	0	0	0	0	....CGTGTCCGTGTCTCACTGG....
23	2	1	2.00	2	0	2	0	0	0	0	0	0	0	0	....CTACTCTCAGTGATTCATGGACT....
23	0	1	2.00	2	2	0	0	0	0	0	0	0	0	0	....ACTCTCAGTGATTCATGGACTCG....

Show Alignment With Reads

Re-alignment of all predicted orthologs

```
Species   Coordinate                          ID      Alignment
droYak3   2R:4404527-4404686 +                dya_78  CTTA-TTCCAATGTA-------A----------------------------A----------------------------TCACTTTA-------------TTTGTGGA-TTATGTCCTACTG-----GCAGCACAGGCACAGAGTGACCCCCAAAAT-GTCAAAA-GC--------ATTGAGAGTCACTAAGTACCTGAGCCA---CCGAGTGGACTTTAAAAC------------TTTTC------ACTGAT--TTAT---------ACACA------GAT-------------------------------TTAATC------GA
droEre2   scaffold_4845:19768016-19768189 -   CTTA-TTCCAATGCA------ATTCA-----CTTG------TA-CTTA----------------------------TCACTTTA-----------TTTGTTGA-TTGCGTCGCACTG-----GCAGCACAGGCACAGAGTGACCCCCAAAAT-GTCAAAA-GC--------ATTGAGAGTCACTAAGTACCTGAGCCA---CCGAGTGGAGACTTAAAC------------TATTC------ACTGAC--TTGT---------ACACA------GAT-------------------------------TTAAGC------GA
droSec2   scaffold_7:345388-345554 -          CTCA-TTTCAATGTA------ATTCA-----CTGC------TA-CTTA----------------------------TCCCTTTA-------------TTTGTAGA-TTATGTCCCACTG-----GCAGCACAGGCACAGAGTGACCCCCAAAAT-GTCAAAC-GC--------ATTGAGAGTCACTAAGTACCTGAGCCA---TCGAGTGGAATTTTAAAC------------GTTC------ACTGAT--TTAA---------ACAG------------------------------------------------------AACTA------AA
droSim2   21:16265198-16265364 -              CTCA-TTTCAATGTA------ATTCA-----CTGC------TA-CTTA----------------------------TCACTTTA-------------TTTGTAGA-TTATGTCCCACTG-----GCAGCACAGGCACAGAGTGACCCCCAAAAT-GTCAAAC-GC--------ATTGAGAGTCACTAAGTACCTGAGCCA---TCGAGTGGACTTTTAAAC------------TATTC------ACTGAT--TTAA---------ACAG------------------------------------------------------AACTA------AA
dm3       chr2L:16698371-16698543 +           CTCA-TTTCAATGTA------TTTCACTGATATCA-----CTGATTA----------------------------TCACTTTA-------------TTTGTAGA-TTATGTCCCACTG-----GCAGCACAGGCACAGAGTGACCCCCAAAAT-GTCAAAA-GC--------ATTGAGAGTCACTAAGTACCTGAGCCA---TCGAGTGGACTTTTAAAC------------TATTC------ACTGAT--TTAA---------ACAG------------------------------------------------------ACAA------GA
droEug1   scf7180000408961:272327-272479 -    CTTC-TTGATATGTA------AAT----------------------------------------------------TCACTTTA-------------TTTGTAGAGATTGCCTCACTA----GCAGCACAGGCACAGAGCGACTGCCCAAATGT-GTCAAAA-TC--------ATTGAGAGTCACTAAGTACCTGAGCCA---TTAAGTGGACTTCGAAAAA------------TAGTC------ACTTG---CCCCCA------CATT------GAT-------------------------------CCCCCC------CA
droBia1   scf7180000301468:857975-858143 -    CTTC-TTATATTATA------T-ATA-----CTA------------------------------------------TTTTTG------TATTTCTTTGTAGA-GAGGCGCTCACG----GCAGCGCAGGTACAGAGCGACTGCCAAACT-GTCGAAA-GC--------ATTGAGAGTCACTAAGTACCTGAGCCA---CCTAGTAAGCTTGAATTC------A----TTTTC------ACTGAT--AA-A---------ACACT------TAT-------------------------------CCACAA------GC
droTak1   scf7180000415914:422623-422783 -    CTTA-TTTATT----------------------------------------------------TA-TTTA----------------------ACACTTTAT---------TTCTGTGGA-GAATGCCTTACTG----GCGGCGCAGGCACAGAGCGACTGCCAAAAT-GTCGAAA-GC--------ATTGAGAGTCACTAAGTACCTGAGCCA---TCGAGTGGCCTTAAAAGA------G----ATATGC------ACTGAT--ATATAAT------ATAC------------------------------------------AACTC------AT
droEle1   scf7180000490579:645512-645691 +    CTTT-TTAACATGTTGGTTGTGATGAA-----ACTA------TA-TTTA----------------------------TCACTTTA-----------CCTGTAGA-CATTGCTTCACTG----GCAGCACAGGCACAGAGCGACTGCCAAAAT-GTCAAAA-GC--------ATTGAGAGTCACTAAGTACCTGAGGAA---T-AAGTGGCCTTAAAATC------A-----AATGC------ACGCTTATAAAT---------ATAGTGA----TAT-------------------------------CCCCCC------GA
droRho1   scf7180000768553:9354-9529 -        CATA-TTGGT--TTT------ATTGCA-----ATTA------TA-GTTA----------------------------ACACTTTT-----------AATGGGGA-GAATGCTTCACTG----GCAGCACAGGCACAGAGCGACTGCCAAAAT-GTCGAAA-GC--------ATTGAGAGTCACTAAGTACCTGAGCCA---TCGAGTGGCCTCAAAAAT------A-----ATGACT---ACTGAG--ATAT---------ACAGTGACACTGTT-------------------------------CCCCCC------CC
droFic1   scf7180000454078:624028-624202 -    CTGG-TTGTAACCTG--TTGTAATCAA-----CTTA------TT-TTTA----------------------------ACACTTTT-----------TTTTGTAGAGAATGTCTTACTT----GCAGCACAGGCACAGAGCGACTGCCAAAAT-GTGAAAA-GC--------ATTGAGAGTCACTAAGTACCTGAGCCA---TCGAGCAAGCACAGAAAA------------ATGC------ACTGCT--ATAG---------CCACT------GAT-------------------------------CCCCCC------GA
droKik1   scf7180000302382:529266-529477 -    TTTA-ATA--ATTTA------AT----------------------------------------------------TGATGT-A----------AGTATTGA-GTTTGCTCACCT-----ACAGCCTAGGCACAGAGAGACTCTCAAAACTTTTCAAGGCA--------TTTGAGAGTCACTAAGTACCTGAGCCATCATCAAGTGGGACTGGTAT------------TACAGC------ACTTG---CCCC-AAACACAAAACAGTTGCACTTTTT-TACACTGATAAAAAT--ACACTTAATTAATTA-CTAAATTTTGAAAAT
droAna3   scaffold_12916:15864829-15864973 +  TATA-TTTTAAAC--------------------------------------------------------------AA----------------------TTTTTTTA----------ATAGAAGA-TATAGTCGCACTG----ATGGCCCAGGCACATAGTGCGTCCCAAAAT-GTCAAAA-GC--------ATTGAGAGTCACTAAGTACCTGAGCTA---CCTAGTGGACTTCTGG---------------C------ACTT---CCCC---------TCAC------AT-------------------------------CCCAATCG------GA
droBip1   scf7180000396717:103548-103712 +  TATA-TTTCAAC---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------
dp5       4_group3:8443787-8443945 -          TTTA-TTAAAC---------------A----CTTA------TT-AGGA----------------------------ACACCCTT----------AATCGTTGCAGTTGCATCACG----CCAGTGCAGGCACAGAGAGACTCTCAAGATGTCGAAA-GC--------ATTGAGAGTCACTAAGTACCTGAGCCGG--GAAAGTGTGCTTGTAGAT------------AAATC------ACTCG---CCCC-ATA----AAG---------------------------------------------AACTC------GA
droPer2   scaffold_1:9894906-9895069 -        ACAC-TCTAAATATA------A--CA-----CTTA------TT-AGGA----------------------------ACACCCTT----------AATCGTTGCAGTTGCATCACG----CCAGTGCAGGCACAGAGAGACTCTCAAGATGTCGAAA-GC--------ATTGAGAGTCACTAAGTACCTGAGCCGG--GAAAGTGTGCTTGTAGAT------------AAATC------ACTCG---CCCC-ATA----AAG---------------------------------------------AACTC------GA
droWil2   scf2_1100000004945:873668-873873 +  CTATAAHA--ATATG------T--CA-----CTATATATCACACACAC----------------------------ACACA-CA----------CATGATGT-TGACATTCCGCAGACACAAGAGTCTAGGTACAGAGCGTCTCTCAAGTCTATATATATTC--------TTTGAGAGTCACTAAGTACCTGAGCTG---TTTAG---GCAGAGATTACTCGTATCA------CTTT---CCCT---CCCC---------CTATATGTCACTTTTTTGT-----------CACCTTATGGATAAGTATTTAATA------GG
droVir3   scaffold_12963:12863161-12863336 +  CTCC-CGGTCACGG------T-TCA-----GGG----------------------------TCACGTTA--TG---CATCTCGTCGTTGG-TTGTGCAGCACG----GCGGCACAGGCACAGAGCGACCCTCAAGGT-ATGCAAA-GCAATAGATGATTGAGAGTCACTAAGTACCTGAGCAG---CGGGTGTGCAGGGCGGG------AGGAGTTCAGC------ACGGAA--A--A---------GCAC------------------------------------AATT------GA
droMoj3   scaffold_6500:7201933-7202117 -    CGTT-T-ACATTACA------AGACA-----CTTC------CA-CTTGTATTCTCTAGTCCGGGGAGTTCGAACTCGATATTCACAA----------TTCTGTGGCTGTTGTGCAACACG----GCGGCACAGGCACAGAGCGACCCTCAAACGT-ATGCAAA-GCAATATGTGATTGAGAGTCACTAAGTACCTGAGCTG---CAGCGTGTGCTGGACATC------A-----------------------------------------------------------------------------------
droGri2   scaffold_14978:830841-831068 -    CGTA-TAG--ATGTA------AC--A-----CAAATCGACACTCAAAG----------------------GACACAAATCACTTGGG----------TATGGTGT-GAATGCAACACGT----GCAACACAGGCACAGAGCGACCCTCAAACGGCGTGCAATT-CAATGTTGATTGAGAGTCACTAAGTACCTGAGCAG---GAAGTGTGCAGCGGATT--------G---------GATTG-GTTTT---------CCAC------ATTTAACACTGATAATGATTAACACAAGAATAAGAA-CCAATGGACGAACGA
```

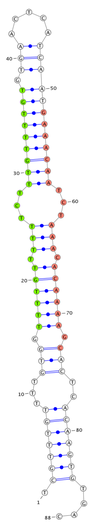
Generated: 09/08/2015 at 07:41 PM

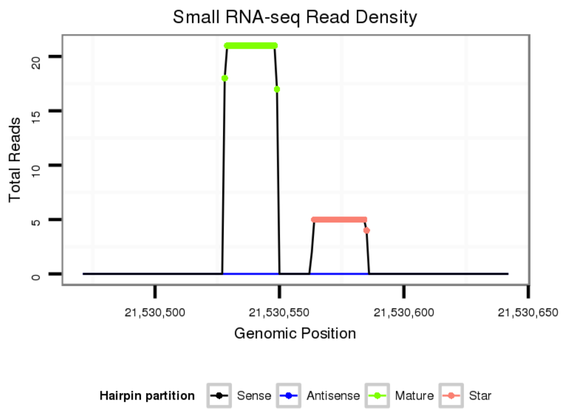
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.totop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

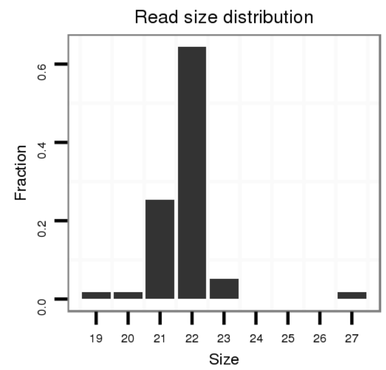
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dya_1781	**3L:21530521-21530592 +**	**confident**	**Canonical miRNA**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

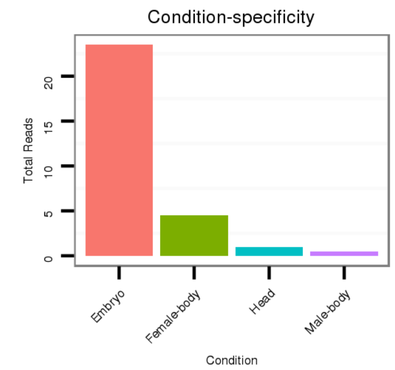
Legend: mature star **mismatch in alignment** mismatch in read

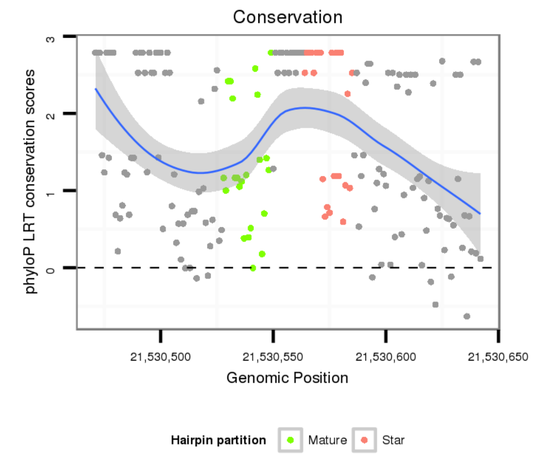
Predicted structure











Show Alternate Folds

Flybase annotation

intron [Dyak\GE22525-in]

No Repeatable elements found

mature	star
1. dya_1781 3L:21530528-21530549 + 2. v2_chr3L_random_149:54878-54899 -	1. dya_1781 3L:21530564-21530585 + 2. v2_chr3L_random_149:54842-54863 -

Sense Strand Reads

hide 3p reads | show mid mismatch reads

```
TTTACATTTTCAACGATTTGAAGGTCGTTTCCACTGTTATTCTCGTTTGTTTTGTGGTTTTGTTTTTTCTTTGTTTTTGTGAACTCATCAATGAAACAATCTAAACACAAAAGCACTCACAAGTGTGACACAGAACGTGACAAAAAAATATAAAAAACTATAAAAATACAG
****************************************.(((((((...(((.(((((((.(((...(((((((((.(((.....)))))))))))...)))).)))))).)))..)))))))....****************************************
```

Read size	# Mismatch	Hit Count	Total Norm	Total	M056 embryo	M043 female body	GSM1528802 follicle cells	V046 embryo	M026 head	V058 head	V120 male body
22	0	2	14.00	28	25	0	0	2	1	0	0
21	0	2	4.00	8	3	2	0	2	0	1	0
22	0	2	3.50	7	7	0	0	0	0	0	0
21	0	2	3.00	6	5	0	0	0	0	0	1
23	0	2	1.50	3	2	1	0	0	0	0	0
22	1	4	1.50	6	5	0	0	0	1	0	0
22	0	2	1.00	2	1	1	0	0	0	0	0
19	0	2	0.50	1	0	1	0	0	0	0	0
27	0	2	0.50	1	0	1	0	0	0	0	0
22	0	2	0.50	1	0	1	0	0	0	0	0
20	0	2	0.50	1	0	1	0	0	0	0	0
21	0	2	0.50	1	0	1	0	0	0	0	0
21	1	4	0.25	1	1	0	0	0	0	0	0

Anti-sense strand reads

```
AAATGTAAAAGTTGCTAAACTTCCAGCAAAGGTGACAATAAGAGCAAACAAAACACCAAAACAAAAAAGAAACAAAACACACTTGAGTAGTTACTTTGTTAGATTTGTGTTTTCGTGAGTGTTCACACTGTGTCTTGCACTGTTTTTTTATATTTTTTGATATTTTTATGTC
****************************************.(((((((...(((.(((((((.(((...(((((((((.(((.....)))))))))))...)))).)))))).)))..)))))))....****************************************
```

Read size	# Mismatch	Hit Count	Total Norm	Total	V058 head	M043 female body

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droYak3	3L:21530471-21530642 +	dya_1781	TTTACA----------TTTTCAA-CG-ATTTGAAGGTC---GTT-TCCACTGTTATTCTCGTTTGT-----TTTGTGGTT-TTGTTTTT---------TCTT---------TG-------TTTTGTGTGAACTCATCAATGAAACAATCT----------AA-------ACACAAAAGC-----ACTCACAAGTGTGACACAGA-------ACGT-------GACAAAAAAATATA----------AAAAACTATAAAAATACAG
droEre2	scaffold_4784:18883304-18883475 -	der_109	TTTACA----------TTTTCAG-CG-ATTTGAAGGTC---GTT-TCCACTGTTATTCACGTTTGT-----TTTGTGGTT-TTGTTTTT---------TCTT---------TG-------TTTTGTGTGAACTCATCAATGAAACAATCT----------GA-------ACACAAAAGC-----ACTCACAAGTGTGACACAGA-------ACGT-------GACAAAAAAATATA----------AAAAACTATAAAGTTACAG
droSec2	scaffold_19:1028753-1028929 -	dse_158	TTTACA----------TTTTCAG-CG-TTTTGAAGGTC---GTT-TCCACTGTTATTCACGTTTGT-----TTTGTGGTT-TTGTTTTT---------TCTT---------TG-------TTTTGTGTGAACTCATCAATGAAACAATCT----------AA-------ACACAAAAGC-----ACTCACAAGTGTGACACAGA-------ACGT-------GACAAAAAAAATA--T----------ATAAAAAAACTATAAAGATACAG
droSim2	3L:18687163-18687338 -	dsi_96	TTTACA----------TTTTCAG-CG-TTTTGAAGGTC---GTT-TCCACTGTTATTCACGTTTGT-----TTTGTGGTT-TTGTTTTT---------TCTT---------TG-------TTTTGTGTGAACTCATCAATGAAACAATCT----------AA-------ACACAAAAGC-----ACTCACAAGTGTGACACAGA-------ACGT-------GACAAATAAATATA--A----------AAAAAAAACTATAAAGATACAG
dm3	chr3L:19064529-19064707 -		TTTACA----------TTTTCAG-CG-TTTTGAAGGTC---GTT-TCCACTGTTATTCACGTTTGT-----TTTGTGGTT-TTGTTTTT-------TTTCTT---------TG-------TTTTGTATGAACTCATCAATGAAACAATCT----------AA-------ACACAAAAGC-----ACTCACAAGTGTGACACAGA-------ACGT-------GACAAAAAAATATA--A----------AAAAAAAACTATAAAGACACAG
droEug1	scf7180000409471:411249-411433 +		TTTACA----------TTTTCAA-CG-TTTTGAAGGTC---GTT-TCCACTGTTATTCGCGTTTGT----TTTTGTGATT-TTGCCTTTTCTTT---TGTCTT---------TG-------TTTTGTGTGAACTCATCAATGAAACAATCT----------AA-------ACACAAAAGC-----ACTCACAAGTGTGACACAGA-------ACGT-------GACAAAAAAATATA--AAA----------AACAAAAACTATAAAGATATAG
droBia1	scf7180000302529:420853-421025 +		TTTACA----------TTTCCAA-CG-TTTTGAAGGTC---GTT-TCCACTGTTATTCACGTTTGT----TTTCGTGGCT-TTGTTTTC---------TCTT---------TG-------TTTTGTGTGAACTCATCAATGAAACAATCT----------AA-------ACACAAAAGC-----ACTCACAAGTGTGACACAGA-------ACGT-------GACAAAACAATACA----------AAAAAATTATAAAGATATAG
droTak1	scf7180000414021:74757-74932 -		TTTACA----------TTTCCAA-CG-TTTTGAAGGTC---GTT-TCCACTGTTATTCACGTTTGT----TTTTGTGGTT-TTGTTTTT---------TCTT---------TG-------TTTTGTGTGAACTCATCAATGAAACAATCT----------AA-------ACACAAAAGC-----ACTCACAAGTGTGACACAGA-------ACGT-------GACAAAAAAATATA----------AAAAAGAACTATAAAGATATAG
droEle1	scf7180000491249:6350642-6350817 -		TTTACA----------TTTTCAA-CG-TTTTGAAGGTC---GTT-TCCACTGTTATTCACGATTGT----TTTTGTGGTT-TTGTTTTC---------TCTT---------TG-------TTTTGTGTGAACTCATCAATGAAACAATCT----------AA-------ACACAAAAGC-----ACTCACAAGTGTGACACAGA-------ACGT-------GACAAAAAAATAAA----------AAAAAAAACTATAAAGATATAG
droRho1	scf7180000776835:40-213 -		TTTACA----------TTTTCAA-CGTTTTGAAGGTC---GTT-TCCACTGTTATTCACGATTGT----TTTTGTGGTT-TTGTTTTT---------TCTT---------TG-------TTTTGTGTGAACTCATCAATGAAACAATCT----------AA-------ACACAAAAGC-----ACTCACAAGTGTGACACAGA-------ACGT-------GACAAAAAAACA------------AAAAAAACTATAAAGATATAG
droFic1	scf7180000453824:438422-438589 -		TTTACA----------TTTTCAA-CG-TTTTGAAGGTC---GTT-TCCACTGCTGTTGACGATTGT----TTTTGTGGTT-TTGTTTTT---------TCTT---------TG-------TTTTGTGTGAACTCATCAATGAAACAATCC----------AA-------ACACAAAAGC-----ACTCACAAGTGTGACACAGA-------ACGT-------GACAAAAAA-----------AAACAGTATAGCCATATAG
droKik1	scf7180000302251:117769-117967 -		TTTACA----------TTTTCAA-CG-TTTTGAAGGTC---GTT-TCCACTGTTATTCACGATTGC----TTTTGTGGTTTTTGTTTTTT-GTTTTTCGTCTT---------TG-------TTTTGTGTGAACTCATCAATGAAACAATCT----------AA-------ACACAAAAGC-----ACTCACAAGTGTGACACAGA-------ACGT-------GACAAAAAATATAAAAAAAAATAA--ACGAAAAAAAACTATAAAGATATAG
droAna3	scaffold_13337:18377655-18377833 +		TTTACA----------CTTTTCAAAG-CCTGAAGATC---GTT-TCCACCGA----------GC----TCTTGTGGTT-TTGTTTTT---------TCTT---------TG-------TTTTGTGTGAACTCATCAATGAAACAATCT----------AA-------ACACAAAAGC-----ACTCACAAATATGACACAGA-------ACGT-------GACAAATAAATAAA--AAGAAAAAAATGACAAAAAAAACTATAAAGATATAG
droBip1	scf7180000396741:1561610-1561776 +		TTTACA----------TTTTCAA-CG-CTTTGAAGGTC---GTC-TCCAGAGT----------GT----TATTGTGGTT-TTGTTTT-----------------------------GTGTGTGAACTCATCAATGAAACAATCT----------AA-------ACACAAAAGC-----ACTCACAAATATGACAGAGA-------ACGT-------GACAAATAAATAAA--AAAAAACA---GCAAAAAAAACTATAAAGATATAG
dp5	XR_group8:7140817-7141006 -		TTTACAAGTTTTGTTGTTGTTGTTTTTGTTGTTTTCAAACG-TTTTGAAGGTC---GTTTTGCACTGT---------GTGT----TTCTGTGGTT-TTGTTTTC-GCTCCTTTTTGCCCATTTGTGTG-------TGTGATGTGAACTCATCAATGAAACAATCC----------CAAAC----ACACAAAAGC----CACTCACAAGTGTCACACAA-------------------------AAAAAAAAC----AAACACAC
droPer2	scaffold_36:165526-165702 +		TTTACAAGTTTTGT----GTTGTTTTTGTTGTTTTCAAACG-TTTTGAAGGTC---GTTTTGCACTGT---------GTGT----TTCTGTGGTT-TTGTTTTC-GCTCCTTTTTGCCCATTTGTGTG-------TGTGATGTGAACTCATCAATGAAACAATCC----------CAAAC----ACACAAAAGC----CACTCACAAGTGTCACACAA-------------------------AAAAAAAAC----------
droWil2	scf2_1100000004762:3231740-3231887 +		TTTACA----------TTTGAAAACT-TTTTGAAGGTCATTGTT-TCCACTTA----------------A-------------------TGTG---------TG-------CTGTGTGTGAACTCATCAATGAAACAATAC----------AC-------ACACAC--GC--AC-ACACACAACA-GCACAGAGA-------ACGT-------GACAAAACAAAA--------------AAAAAAAACTCATAATACTATAT
droVir3	scaffold_13049:13362168-13362297 -		TTTACA----------TTTTTCA-CG-TTTTGAAGGTC---GTT-TCCACTGT---AGCGCGATTGTT---GTCAGTGTTA-TTGTTGTT---------GCGA---------T-------TATTGTGTGAACTCATCAATGAAACAATAC----------AGAGAACCCAACACA----C-----ACACACAAATGTG--
droMoj3	scaffold_6680:13991806-13992015 +		TTTACA----------TTTTTCA-CG-TTTTGAAGGTC---GTT-TCCACTGTGCGCGAATCTTTGT-CATTGTTGTCG---TTGTTGTT-GCTCTTGTGC---------TGCTGCGATTATTGTGTGAACTCATCAATGAAACAATACAGAAAGAATCGTGGACAA-------ACACACA--GACTT-ACACT---CTGTTGTAATATAAAGGCCGATGT-------GATAAGCACACGATA----------TAGAGCTATATATATATAT
droGri2	scaffold_15110:18794165-18794321 -		TTTTAA----------TTTTTCA-CG-TTTTGAAGGTC---GTT-TGCACTGT---GGACGTT-GT---TATTGTTGTT-------------------TGTT---------TG-------TTTTGTGTGAACTCATCAATGAAACAATAC----------AATGG-----AGAGAACACAC----AGGCGCACAAGCG--------AACTGCTTTTGGACAGA--GATACT----------ACAGAGGCAGACACACACAC

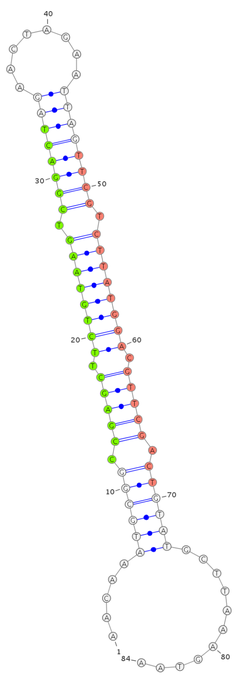
Generated: 09/08/2015 at 07:47 PM

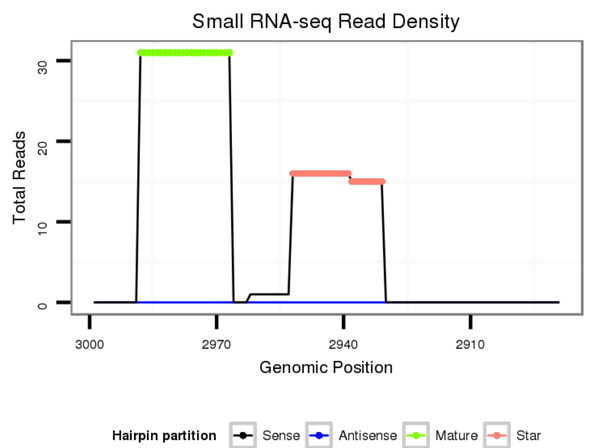
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	2
rescue.candidate	2

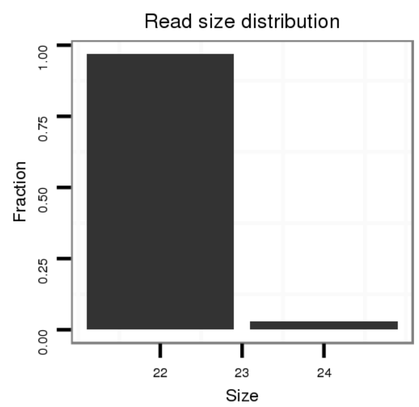
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dya_133	**v2_chr3R_random_227:2939-2997 -**	**confident**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

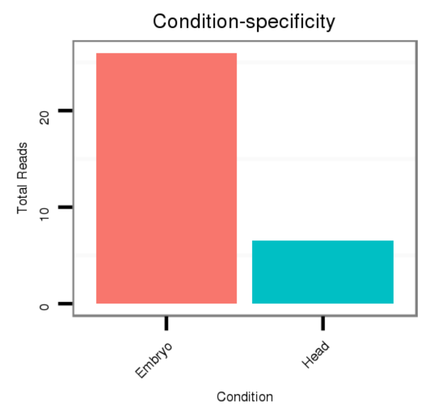
Legend: mature star mismatch in alignment mismatch in read

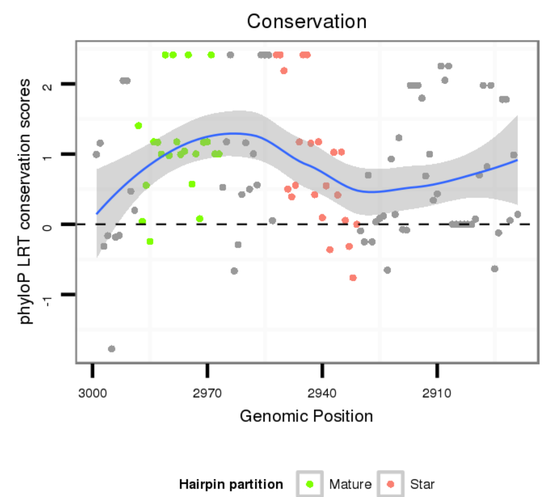
Predicted structure











dya_133_annot [-30.8]

Show Alternate Folds

Flybase annotation

intergenic

No Repeatable elements found

mature	star
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Sense Strand Reads

hide 3p reads show mid mismatch reads

AACAAATGCGGCCGAGCTTCTGTAAGTCGGACTAGAACTAGAATTAGTTCGTCTTATGGACGTTCGACTGTATGCTTAAAGTAATGTTAAACATGTATGCAACAAGATTAG .....((((((.(((((.(((((((((.((((((((.....)))))))).)))))))).)))))).)))))).....********** Read size	# Mismatch	Hit Count	Total Norm	Total	M056 embryo	M026 head	M043 female body	GSM1528802 follicle cells	V052 head
...........CCGAGCTTCTGTAAGTCGGACT..... 22	0	2	31.50	63	52	11	0	0	0
.....TTCGTCTTATGGACGTTCGACT..... 22	0	2	15.50	31	26	4	0	0	1
...........CCGAGCTTCTGTAAGTCGGACG..... 22	1	2	4.00	8	4	4	0	0	0
.....TTCGTCTTATGGACGTTCGACG..... 22	1	2	2.50	5	5	0	0	0	0
.....CTAGAATTAGTTCGTCTTATGGAC..... 24	0	2	1.00	2	0	2	0	0	0
.....TTCGTCTTATGGACGTTCGACA..... 22	1	2	0.50	1	0	0	1	0	0
...........CCGAGCTTCTGTAAGTCGGACG..... 22	1	2	0.50	1	0	1	0	0	0
.....TCGTCTTATGGACGTTCGACC..... 21	1	2	0.50	1	1	0	0	0	0
.ACAAATGCGGCCGAGCTTCTGTAAGTC..... 27	0	2	0.50	1	1	0	0	0	0
.....TATGGACGTTCGACTGTATGCTTAAAGT..... 28	0	2	0.50	1	0	1	0	0	0
.....TCGTCTTATGGACGTTCGACT..... 21	0	2	0.50	1	1	0	0	0	0
.....TTCGTCTTATGGACGTTCGAC..... 21	0	2	0.50	1	1	0	0	0	0

Anti-sense strand reads

TTGTTTACGCCGGCTCGAAGACATTCAGCCTGATCTTGATCTTAATCAAGCAGAATACCTGCAAGCTGACATACGAATTTCATTACAATTTGTACATACGTTGTTCTAATC **********.....((((((.(((((.(((((((((.((((((((.....)))))))).)))))))).)))))).))))))..... Read size	# Mismatch	Hit Count	Total Norm	Total	M043 female body	V058 head
.....CTGCAAGCTGACATACGAATT..... 21	0	2	0.50	1	1	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droYak3	v2_chr3R_random_227:2889-2999 -	dya_133	AAC-AAAT-GCGGCCG-AGCTTCTGTA-A-GTCGG---------A-CTA-GAA-C-TAGAATTAGTTCGT-CTTATGGA----CGTTC-GACTGTATG----CTTAAA---G-TAATGTTAAACATGTATGCA----------ACAAG--ATTAG
droEre2	scaffold_4770:7616328-7616437 +		CAGA----AGGAGCAA-CAATTGTAGA-A-ACATA---------A-CCT-AAT-GAAAAGTTTACTTCA--AATATCAC----ACTTA-ACT------ ------ ---T-GAATGCTGTACA-------- ---AACAAAAGTCG-TAAAGTGCATAATATATAAA
droSec2	scaffold_12:132866-132977 +		CGC-AGAT-GGAGCAACCAATTGTAGA-AAACATA---------A-CCT-AAT-GAAAAGTTTACTTCA--AATATCAC----ATTTA-ACT------ ------ ---T-GAATGCTGTACA-------- ---AACAAAAGTCT-TAAAGTGCATAAAATATA--
droSim2	3r:7259412-7259523 +		CGC-AGAT-GGAGCAACCAATTGTAGA-AAACATA---------A-CCT-AAT-GAAAAGTTTACTTCA--AATATCAC----ACTTA-ACT------ ------ ---T-GAATGCTGTACA-------- ---AACAAAAGTCT-TAAAGTGCATAATATATA--
dm3	chr3R:14019035-14019146 -		CGC-AGAT-GGAGCAAACAATTGTAGA-AATCATA---------A-TCT-AAT-GAAAAGTTTACTTCA--AATATCAC----ACTTA-ACT------ ------ ---T-GAATGCTGTACA-------- ---AACAAAAGTCT-TAAAGTGCATAAAACATA--
droEug1	scf7180000409246:368761-368866 -		CAAA----AGGAGCAAACAATTGTAGA-AAACATA---------A-CCT-AAA-GAAAAGTTTACTTCAA-AATATCAC----ACTTAAACA------ ------ ---T-AAATGCTGTACA-------- ---AACAAAAGTCT-TAAAGTGCATAAA-- -----
droBia1	scf7180000299102:1951426-1951541 +		CAGCGTGA-GGAGCAA-CAATTGTAGA-A-ACATA---------A-CCT-AAT-GCAAAGTTTACTTCAG-AATATCAAACACACTTA-ACA------ ------ ---C-GAATGCTGTACA-------- ---AACAAAAGTCT-TAAAGTGCATAAAATATA--
droTak1	scf7180000414450:146996-147108 -		CAG-GCAA-GGAGCAA-CAATTGTAGA-A-ACATA---------A-CCT-AAT-GAAAAGTTTACTTCAA-GATATCAC----ACTTA-ACA------ ------ ---C-GAATGCTGTACA-------- ---AACAAAAGTCT-TAAAGTGCATAAAATATGAA
droEle1	scf7180000491008:2242902-2243003 +		CA-----------A-CAATTGTAGA-A-ACATA---------A-CCT-AAA-GAATAGATTACTTCAA-AATATCAC----ACTTA-ACT------ ------ ---T-GAATGCTGTACA-------- ---AACAAAAGTCT-TAAAGTACATAAAATATAAA
droRho1	scf7180000778633:30211-30313 -		CA-----------A-CAATTGTAGA-A-ACATA---------A-CCT-AAA-GAAAAGTTTATTCAA-AATATCAC----ACCTA-ACA------ ------ ---T-GAATGCTGTACA------A--- AACAAAAGTCT-TAAAGTACATATAATATAAA
droFic1	scf7180000453800:496513-496621 -		CAAA----CGGAGCAA-CAATTGTAGA-A-ACATA---------A-CCT-AAA-GAAAAGTTTACTTCA--AATATCAT----ACTTA-ACA------ ------ ---T-GAATGCTGTACA-------- ---AACAAAAGTCT-TAAAGTACATACAATATA-A
droKik1	scf7180000302809:268101-268219 +		CAA----GGGAACGGCAAATTGTAGA-A-ACCTA---------A-CCT-AAA-GA-AAGTTTACTTCAA-AATACTAC----TCTTAAGCT-A---- ----ACAACA---C-GAATGCTGTACA-------- ---AACAAAAGTCTATAAGGTACATACAACATAAA
droAna3	scaffold_13340:15786876-15786988 -		CAAA----AGG---AAAAAATTGTAGA-A-ACATA---------A-CCT-AAT-TACAAGTTTACTTCAA-AATATCAC----AGTTA-TGA-----A---- ----AATGAT-AAATGCTGTACA-------- ---AACAAAAGTCTATAAAGTGCATAGAATAT---
droBip1	scf7180000396708:4249441-4249556 +		CAAA----AGG---AAAAAATTGTAGA-A-ACATA---------A-CCT-AATTAAAAAGTTTACTTCAA-AATATCAC----AGTTA-AAA-----AAAAAACC-AATGATAAAATGCTGTACA-------- ---AACAAAAGTCTATAAAGTGCATA-- --- -----
dp5	2:29110649-29110784 -		CAAA----GGGAACGA-CAAATGTAGA-A-ACCTAAAAAACCTAACCCC-AAT-GCAACGTTTAATTCAAAAATATCAC----ATTCA-ATT-AAAAA----ACAAAA---T-GAATGCTGTACA------AAACAAACAATATTTA-TAAAGTACATAGAATATA--
droPer2	scaffold_6:4434957-4435092 -		CAAA----GGGAACGA-CAAATGTAGA-A-ACCTAAAAAACCTAACCCC-AAT-GCAACGTTTAATTCAAAAATATCAC----ATTCA-ATT-AAAAA----ACAAAA---T-GAATGCTGTACA------AAACAAACAATATTTA-TAAAGTACATAGAATATA--
droVir3	scaffold_13047:6639926-6639979 +		CA-----GGG---AA-CAAATGTAGC-AAACCTA---------A-CCT-AA--- AAAGTTTACTTCGAAAATATCAC----A----- --------- ------ ---- ------------------ ---------- ----- -- -----
droGri2	scaffold_14830:1388950-1389032 +		CA-----GGG---AACAAAATGTAGCAAACCTA---------A-CCTAAA-TAAAAGTTTACTTCAAAAATATCAC----ACTAAAAC------ ------ ---- ------AAAACA------A--- AACAAAAAT---------- ----- -- -----

Generated: 09/08/2015 at 07:50 PM

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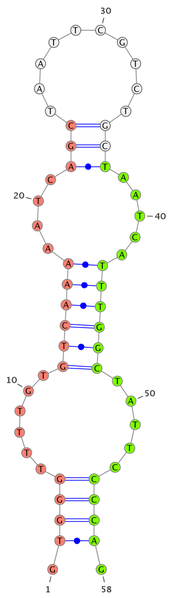
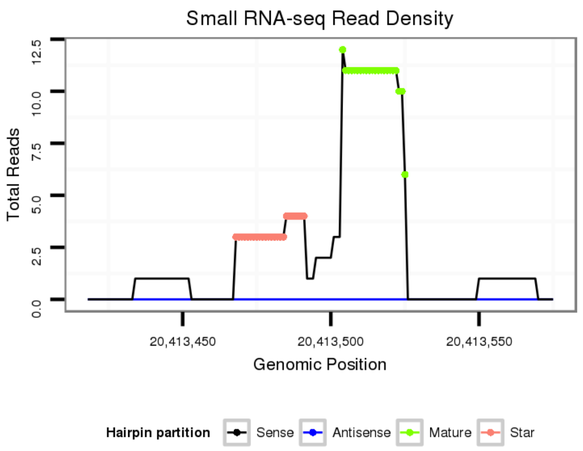
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

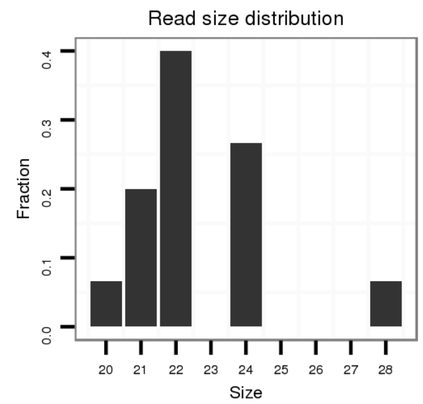
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dya_1486	**X:20413468-20413525 +**	**confident**	**Mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

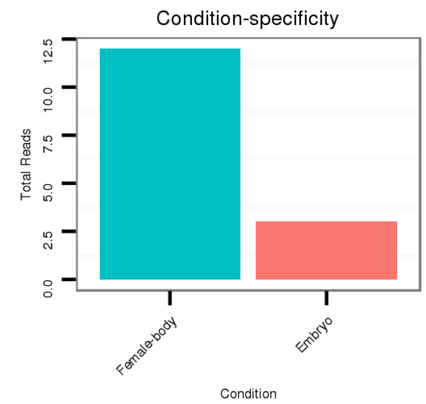
Legend: mature star mismatch in alignment mismatch in read

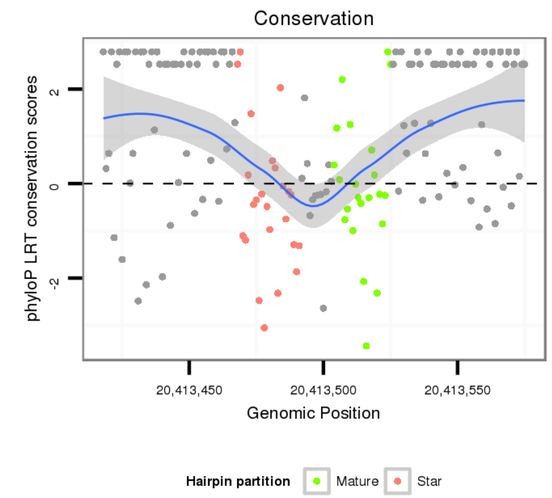
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dyak\GE17924-in]; CDS [Dyak\GE17924-cds]; CDS [Dyak\GE17924-cds]; utr5 [utr5_plus_15862]; utr5 [utr5_plus_15863]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

```
ATCTCCTCAATCTCATAGACACTCCTGGTCACGTAGATTTTTCCAATGAAGTGGGTTTTGTGTCAAAAATCAGCTAATTCGTCTGCTAATCATTTGGCTATTCCCCAGGTTTCCCGATCTCTGGCTGCCTGCGATGGTGTGGTACTCCTGGTGGACGC
**************************************************.((((.....((((((....(((.........)))).....)))))).....)))).**************************************************
```

Read size	# Mismatch	Hit Count	Total Norm	Total	GSM1528802 follicle cells	M043 female body	M056 embryo	V046 embryo	V052 head	V058 head	V120 male body	
23	1	1	14.00	14	0	4	5	2	1	1	1	.....TAATCATTTGGCTATTCCCCAGT.....
22	0	1	6.00	6	0	6	0	0	0	0	0	.....TAATCATTTGGCTATTCCCCAG.....
21	0	1	3.00	3	0	2	1	0	0	0	0	.....TAATCATTTGGCTATTCCCCA.....
24	0	1	3.00	3	0	1	1	1	0	0	0	.....GTGGGTTTTGTGTCAAAAATCAGC.....
23	1	1	2.00	2	0	0	2	0	0	0	0	.....TAATCATTTGGCTATTCCCCAGG.....
24	0	1	1.00	1	0	1	0	0	0	0	0	.....TGCTAATCATTTGGCTATTCCCCA.....
28	0	1	1.00	1	0	1	0	0	0	0	0	.....TTCGTCTGCTAATCATTTGGCTATTCCC.....
20	0	1	1.00	1	0	1	0	0	0	0	0	.....GATGGTGTGGTACTCCTGGT.....
20	0	1	1.00	1	0	1	0	0	0	0	0	.....AATCAGCTAATTCGTCTGCT.....
22	2	1	1.00	1	0	1	0	0	0	0	0	.....TAATCATTTGGCTATTCCCCTT.....
19	0	1	1.00	1	0	1	0	0	0	0	0	.....AGACACTCCTGGTCACGTA.....

Anti-sense strand reads

```
TAGAGGAGTTAGAGTATCTGTGAGGACCAGTGCATCTAAAAAGGTTACTTCACCCAAAACACAGTTTTTAGTCGATTAAGCAGACGATTAGTAAACCGATAAGGGGTCCAAAGGGCTAGAGACCGACGGACGCTACCACACCATGAGGACCACCTGCG
**************************************************.((((.....((((((....(((.........)))).....)))))).....)))).**************************************************
```

Read size	# Mismatch	Hit Count	Total Norm	Total	V052 head

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droYak3	X:20413418-20413575 +	dya_1486	ATCTCCTCAATCTCATAGACACTCCTGGTCACGTAGATTTTTCCAATGAAGTGGGTTTTGTGTCAA----------A-AA---TC----------AGCTAA------TTCGTC----------T----------GCTAATCATTT---GGCTAT----------TCCCCAGGTTTCCCGATCTCTGGCTGCCTGCGATGGT-GTGGTACTCCTGGTGGACGC
droEre2	scaffold_4690:17765035-17765191 +		ATCTGCTCAACCTTATTGACACTCCTGGTCACGTCGATTTCTCCAATGAAGTGGGTTTCAGGTCAA----------A-AG---TC----------AGCTAA------TTATTT----------T----------GCTAATCATT-----GCGCAT----------TACACAGGTTTCCCGATCTCTGGCTGCCTGCGATGGT-GTGGTACTCCTGGTGGACGC
droSec2	scaffold_8:3542420-3542577 +		ATCTGCTGAACCTCATTGACACTCCTGGTCACGTGGATTTTTCCAATGAAGTGTGTATCATGTCAA----------A-AG---TC----------AGCTAA------TTCTTC----------T----------GCTAATCATTT---GCCCAT----------TACCCAGGTTTCCCGATCTCTGGCTGCCTGCGACGGG-GTGGTGCTCCTGGTGGACGC
droSim2	x:19967765-19967922 +		ATCTGCTGAACCTCATTGACACTCCTGGTCACGTGGATTTTTCCAATGAAGTGTGTATCATGTCAA----------A-AG---TC----------AGCTAA------TTCTTC----------T----------GCTAATCATTT---GCCCAT----------TACCCAGGTTTCCCGATCTCTGGCTGCCTGCGACGGG-GTGGTACTCCTGGTGGACGC
dm3	chrX:21234579-21234736 +		ATCTGCTGAACCTCATTGACACTCCTGGTCACGTGGATTTTTCCAATGAAGTGTGTTTCATGTCAA----------A-AG---TC----------TGCTAA------TTCTTC----------T----------GCTAATCATTT---GCCCAT----------TACCCAGGTTTCCCGATCTCTGGCTGCCTGCGACGGG-GTGGTACTCCTGGTGGACGC
droEug1	scf7180000408193:240718-240874 -		ACCTACTCAACCTCATAGACACTCCAGGCCACGTTGATTTTTCTAATGACGTGGGTTTCAACCTAA----------A-AA---CT----------TCCTAA------AAC-TT----------T----------GCAAATAATCT---GTTGAT----------TCTTTAGGTCTCCCGCTCCTGGCAGCTTGCGATGGC-GTGGTCTCCTGGTTGACGC
droBia1	scf7180000302432:378011-378166 -		ATCTGCTTAACCTCATAGACACTCCCGGTCACGTGGACTTCTCCAATGAGGTATGTTTCATGCCAC----------A-AA---TC----------CAGAAC------C----T----------T----------GCTAATCCTTT-GTGTCCAT----------TCGCAAGGTCTCCCGCTCGCTAGCCGCCTGCGATGGA-GTGGTCTCCTGGTGGACGC
droTak1	scf7180000415769:198069-198230 -		ATCTGCTCAATCTCATCGACACGCCCGGTCACGTGGATTTCTCCAATGAGTGGGCTAATCCCG-TTACA----------T--T---TA----------TGT---------------ATCTACCATTCCATGCTAATCCTTG---GTTTTC----------ATGCCAGGTTTCCCGCTCGCTGGCGGCCTGCGATGGC-GTGGTCCTCCTGGTGGACGC
droEle1	scf7180000491087:1173072-1173239 -		ATCTCCTCAACCTCATCGACACGCCCGGTCACGTTGATTTCTCCAATGAGGTCGGGTCTTAAATCAC----------A-T---T---T---AGTCACCACAAAT------C-ACC-TTCACA----------C----------GCTAATCCTCTAAGATCCGAT----------TCTCAGGTCTCCCGCTCGCTGGCTGCTTGCGATGGC-GTTGTCCTTCTGGTCGACGC
droRho1	scf7180000779980:56334-56491 -		ATCTGCTCAACCTTATAGACACCCCGGTCACGTGGATTTCTCCAATGAGGTCGGTTTCAGACCAC----------A-AA---TC----------TGTC--------TTCTCG----------C----------GCTAATTCTAT-ATGCCAAT----------TCCTCAGGTCTCCCGCTCGCTGGCTGGTTGTGATGGC-GTGGTGCTCCTAGTCGACGC
droFic1	scf7180000453926:207190-207342 +		ATCTGCTAAACCTTATTGACACCCCGGTCACGTTGACTTCTCCAATGAGTGGGTTA-AGACCAG----------A-TA---GC----------CGAT--------TGCTCG----------T----------GCTAATACT-----GTAAAT----------TCTCCAGGTCTCCCGCTCTCTGGCTGCCTGCGACGGG-GTGGTCCTCTTAGTGGACGC
droKik1	scf7180000302586:292924-293078 +		ATCTGCTGAACCTAATTGACACTCCTGGTCACGTGGACTTCTCCAATGAGGTATCTTTAGT---A-T---T---T---ATTTTTCTCG---T----------CATTT---GCGCTTTACTCATTCATACGTATTTGCAGGTCTCCCGCTCGCTGGCCGCCTGCGATGGC-GTCGTTCTTCTGGTGGACGC
droAna3	scaffold_13117:3149338-3149502 -		ACCTCCTCAACCTCATTGACACGCCCGGTCACGTGGATTTCTCGAACGAGGTGAGTGCCATGGCATTGAA----------TCCAATTCC-A-GT---CC----------ATCTAA------CCACTC----------T----------TCTA-------CCTTCTG----------TTGAAGGTCTCCCGCTCCTGGCTGCCTGTGACGGG-GTAGTCCTCCTGGTGGACGC
droBip1	scf7180000395515:19375-19538 -		ACCTCCTCAACCTGATCGACACGCCCGGTCACGTGGATTTCTCAAATGAGGTTATTCTTATGCTACAGAA----------ACCAAATAC-A-GA---CC----------AAGTAA------CCACTC----------C----------TCTAC--CTT-------------------TGGACCCAGGTCTCCCGCTCCTGGCTGCCTGTGACGGG-GTAGTCCTCCTGGTGGATGC
dp5	XL_group1a:1473929-1474108 -		ACCTCTCTGAACCTGATCGACACCCCGGCCACGTGGACTTCTCCAATGAGTGGGTGGGAG--CAGCGGGTTCTTTTTCTGAATCAG--------T---T---T---ACTCATCCTGAATT------C-GTTT-C----------T----------------------TTGTCCCAATTCTCGATGTACTTAGGTTTTCCCGCTCGCTGGCAGCCTGTGATGGC-GTTATCCTCCTGGTGGATGC
droPer2	scaffold_499:10575-10754 -		ACCTTCTGAACCTGATCGACACCCCGGCCACGTGGACTTCTCCAATGAGTGGGTGGGAG--CAGCGGGTTCTTTGTCTGAATCAG--------T---T---T---ACTCATCCTGAATT------C-GTTT-C----------T----------------------TTGTCCCAATTCTCGATGTACTTAGGTTTCCCGCTCGCTGGCAGCCTGTGATGGC-GTTATCCTCCTGGTGGATGC
droWil2	scf2_11000000004909:8782015-8782188 -		ATTTACTCAACCTTATTGATACACCAGGTCATGTTGACTTCTCGAATGAGGTAAATGGAAT--CTA----------AGCTCCAATAAA----------TCTCTTAACTT--------ATTAACACA-------T----------AATTTTTGTCT-ATTTTTCT----------TTTTAGGTTTCCCGCTCTTTGGCCGCCTGTGATGGT-GTGATCTTTTGGTCGATGC
droVir3	scaffold_13042:4323552-4323707 +		ATCTGCTGAATTTAATGGATACGCCTGGCCACGTGGATTTCTCCAACGAGGTTTGTTGCGTGT---------------------------------------A-ATTCATT----------CAAT--------CTCTGT----------C----------GGGATTTAATGC---ATGATT----------CTTGCAGGTCTCCCGCTCGCTGGCGGCCTGCGATGGCCCGTCATCCTCGCTGGTGGATGC
droMoj3	scaffold_6359:2109515-2109671 -		ATTTGCTAAACCTAATGGATACACCTGGCCATGTGGACTTCTCCAATGAGGTACGTTGTGG--CCTTGGA----------A-T---T---T---TA----------TGTT--------GTATGA----------T----------GGGATTTATAT-GATTTCAT----------CTTGCAGGTCTCTCGCTCGTTGGCCGCATGCGATGGT-GTTATTCTCTCGTAGATGC
droGri2	scaffold_14853:7180638-7180810 +		ATCTGCTCAATTTGATTGATACGCCCGGACACGTGGATTTCTCAAATGAGTGCGTATTTCAGGTC----------A-AA---TT----------TTGAA-ATTG--------GAAAGTTTAAAGTTGTT----------GTACTTGATC-GTCCTAAT----------TGTGCAGGTTTCCCGCTCGCTGGCCGCCTGTGATGGC-GTCATTCTCTCGTAGACGC

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