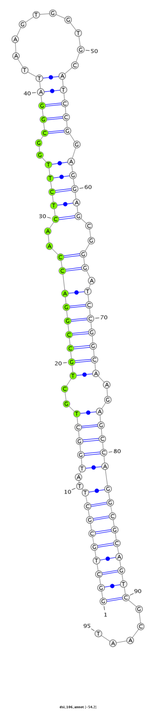
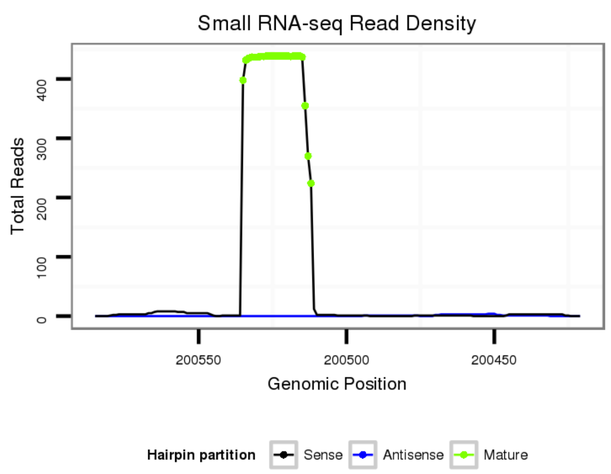
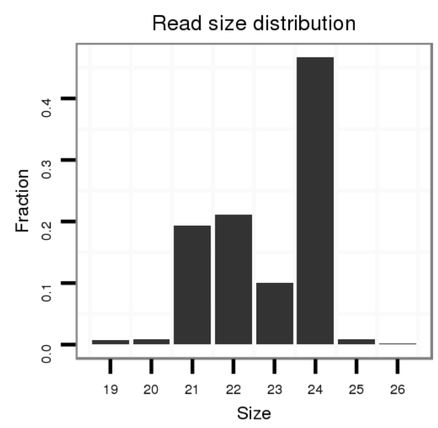
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dsi_106	**21:200471-200535 -**	**candidate**	**Canonical miRNA**	**3pUTR**	[View on UCSC Genome Browser {Cornell Mirror}]

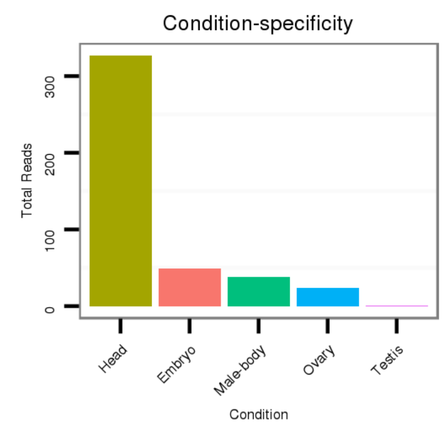
Legend: mature star mismatch in alignment mismatch in read

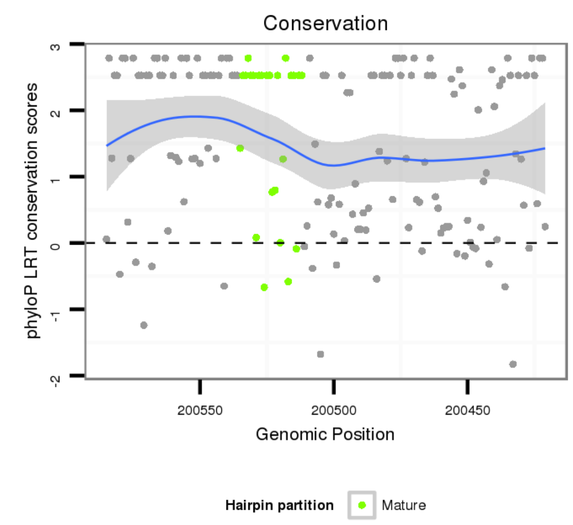
Predicted structure











Show Alternate Folds

Flybase annnotation

utr3 [utr3_minus_32]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

TTGGGTAATCTTGCAGGGATGGACACTCAGTCGCTGGCTGCGCTTATGGCTGCTGCCGGACCAACTCTTGGCGGATTAAGTGGTGCATCCGGAGGAGCGGGATCCGGCAAGAGCCAGGCGCAGTCGCAATCATCCGCCACTTCGTCATCGTCTTCGGCTAGTAAA ********(((((((((..(((((..(((((((((..(((((..(((((.....)))))).)))))..)).).)))))))..)))))))))))))).....	Read size	# Mismatch	Hit Count	Total Norm	Total	M023 head	M025 embryo	M024 male body	SRR553486 Makindu_3 day-old ovaries	SRR553485 Chicharo_3 day-old ovaries	SRR553487 NRT_0-2 hours eggs	SRR902009 testis	SRR902008 ovaries	SRR618934 dsim w501 ovaries	M053 female body	O002 Head	GSM343915 embryo
.....TGCTGCCGGACCAACTCTTGGCGG.....	24	0	1	200.00	200	146	32	16	3	3	0	0	0	0	0	0	0
.....TGCTGCCGGACCAACTCTTGGC.....	22	0	1	79.00	79	70	1	6	0	0	2	0	0	0	0	0	0
.....TGCTGCCGGACCAACTCTTGG.....	21	0	1	79.00	79	67	1	10	1	0	0	0	0	0	0	0	0
.....TGCTGCCGGACCAACTCTTGGCG.....	23	0	1	33.00	33	20	1	5	2	3	2	0	0	0	0	0	0
.....GCTGCCGGACCAACTCTTGGCG.....	22	0	1	13.00	13	4	5	0	1	2	1	0	0	0	0	0	0
.....GCTGCCGGACCAACTCTTGGCGG.....	23	0	1	10.00	10	4	6	0	0	0	0	0	0	0	0	0	0
.....GCTGCCGGACCAACTCTTGGC.....	21	0	1	5.00	5	5	0	0	0	0	0	0	0	0	0	0	0
.....TGCTGCCGGACCAACTCTTGGCGGA.....	25	0	1	4.00	4	3	1	0	0	0	0	0	0	0	0	0	0
.....GCTGCCGGACCAACTCTTGGCGGA.....	24	0	1	4.00	4	0	1	0	1	2	0	0	0	0	0	0	0
.....GCTGCCGGACCAACTCTTGG.....	20	0	1	2.00	2	1	0	1	0	0	0	0	0	0	0	0	0
.....TGCTGCCGGACCAACTCTTG.....	20	0	1	2.00	2	1	0	0	0	0	0	0	0	0	0	1	0
.....TTGCAGGGATGGACACTCAGTTT.....	23	2	1	2.00	2	0	0	0	0	0	0	2	0	0	0	0	0
.....ATGGACACTCAGTCGCTGGCT.....	21	0	1	2.00	2	0	0	0	0	0	0	1	0	1	0	0	0
.....GACACTCAGTCGCTGGCTG.....	19	0	1	1.00	1	0	0	1	0	0	0	0	0	0	0	0	0
.....TAATCTTGCAGGGATGGACACTCAGT.....	26	0	1	1.00	1	0	0	0	0	0	1	0	0	0	0	0	0
.....TGCTGCCGGACCAACTCTTGGCGT.....	24	1	1	1.00	1	0	0	1	0	0	0	0	0	0	0	0	0
.....AATCTTGCAGGGATGGACACTC.....	22	0	1	1.00	1	0	0	1	0	0	0	0	0	0	0	0	0
.....TTGGCGGATTAAGTGGTGCATCCGGA.....	26	0	1	1.00	1	0	0	0	1	0	0	0	0	0	0	0	0
.....TCCGGCAAGAGCCAGGCGCAGTCGCAAA.....	28	1	1	1.00	1	0	0	0	1	0	0	0	0	0	0	0	0
.....CTGCCGGACCAACTCTTGGCGG.....	22	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0	0
.....TCTTGCAGGGATGGACACTCAGT.....	23	0	1	1.00	1	0	0	0	0	0	0	0	1	0	0	0	0
.....TGCTGCCGGACCAACTCTTGGCGGG.....	25	1	1	1.00	1	0	1	0	0	0	0	0	0	0	0	0	0
.....CTGCCGGACCAACTCTTGG.....	19	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0	0
.....CTGCCGGACCAACTCTTGGCGGA.....	23	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0	0
.....CGGACCAACTCTTGGCGT.....	18	1	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0	0
.....TGCCGGACCAACTCTTGGCT.....	20	1	1	1.00	1	0	0	1	0	0	0	0	0	0	0	0	0
.....TGCCGGACCAACTCTTGGC.....	19	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0	0
.....TGCCGGACCAACTCTTGGCGG.....	21	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0	0
.....TTATGGCTGCTGCCGGACCAACT.....	23	0	1	1.00	1	0	0	0	0	0	0	0	0	0	1	0	0
.....AAGAGCCAGGCGCAGTCGCA.....	20	0	1	1.00	1	0	0	0	0	0	0	0	0	1	0	0	0
.....GACCAACTCTTGGCGGATTAAGTG.....	24	0	1	1.00	1	0	0	0	0	0	0	1	0	0	0	0	0
.....TTCGTCATCGTCTTCGGCT.....	19	0	1	1.00	1	0	1	0	0	0	0	0	0	0	0	0	0
.....GGACACTCAGTCGCTGGCTG.....	20	0	1	1.00	1	0	0	1	0	0	0	0	0	0	0	0	0
.....GGACACTCAGTCGCTGGCTGC.....	21	0	1	1.00	1	0	1	0	0	0	0	0	0	0	0	0	0
.....TGCTGCCGGACCAACTCTTGGCGGAA.....	26	1	1	1.00	1	0	0	0	0	0	0	0	1	0	0	0	0
.....TTCGTCATCGTCTTCGGCTAG....	21	0	1	1.00	1	0	0	0	0	0	0	0	1	0	0	0	0
.....CTTCGTCATCGTCTTCGGCT.....	20	0	1	1.00	1	0	1	0	0	0	0	0	0	0	0	0	0
.....TGCTGCCGGACCAACTCTTGGA.....	22	1	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0	0
.....TGCTGCCGGACCAACTCTTGGTT.....	23	2	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0	0
.....CGGACCAACTCTTGGCGGA.....	19	0	1	1.00	1	0	1	0	0	0	0	0	0	0	0	0	0
.....TCGTCATCGTCTTCGGCT.....	18	0	2	0.50	1	0	0	1	0	0	0	0	0	0	0	0	0
.....TTCGTCATCGTCTTCGGCG.....	19	1	2	0.50	1	0	1	0	0	0	0	0	0	0	0	0	0

Anti-sense strand reads

AACCCATTAGAACGTCCCTACCTGTGAGTCAGCGACCGACGCGAATACCGACGACGGCCTGGTTGAGAACCGCCTAATTCACCACGTAGGCCTCCTCGCCCTAGGCCGTTCTCGGTCCGCGTCAGCGTTAGTAGGCGGTGAAGCAGTAGCAGAAGCCGATCATTT ********(((((((((..(((((..(((((((((..(((((..(((((.....)))))).)))))..)).).)))))))..)))))))))))))).....	Read size	# Mismatch	Hit Count	Total Norm	Total	M023 head	SRR902008 ovaries	M024 male body	M053 female body	SRR618934 dsim w501 ovaries	SRR553488 RT_0-2 hours eggs
.....TCCGCGTCAGCGTTAGTAGGC.....	21	0	1	2.00	2	2	0	0	0	0	0
.....CTCCTCGCCCTAGGCCGTT.....	19	0	1	1.00	1	0	0	1	0	0	0
.....GGCGGTGAAGCAGTAGCAGAA.....	21	0	1	1.00	1	0	1	0	0	0	0
.....CGCGTCAGCGTTAGTAGGCGG.....	21	0	1	1.00	1	0	1	0	0	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droSim2	21:200421-200585 -	dsi_106	TTGGGTAATCTTGCAGGGATGGACACTCAGTCGCTGGCTGCGCTTATGGCTGCTGCCGGACCAACTCTTGGCGGATTAAGTGGTGCATCCGGAGGAGCGGGATCCGGCAAGAGCCAGGCGCAGTCGCAA----------TCATCCGCCACTTCGTCATCGTCTTCGGCTAGTAAA---
droSec2	scaffold_14:212346-212510 -	dse_1839	TTGGGTAATCTTGCAGGGATGGACACTCAGTCGCTGGCTGCGCTTATGGCTGCTGCCGGACCAACTCTTGGCGGATTAAGTGGTGCATCCGGAGGAGCGGGATCCGGCAAGAGCCAGGCGCAGTCGCAA----------TCATCCGCCACTTCGTCATCGTCTTCGGCTAGTAAA---
dm3	chr2L:214273-214437 -	dme_410	TTGGGTAATCTTGCAGGGATGGACACTCAGTCGCTGGCTGCGCTCATGGCTGCTGCCGGCGCCAACTCTTGGCGGATTAACTGGTGCATCCGGAGGAGCGGGCTCCGGCAAGAGCCAGGCGCAGTCGCAA----------TCATCCGCCACTTCGTCATCCTCTTCGGCTAGTAAA---
droEre2	scaffold_4929:259840-260004 -	der_1534	TTGGGTAATCTGGCGGGGATGGACACTCAGTCGCTGGCTGCGCTCATGGCTGCTGCCGGACCATCTCTTGGCGGATTAAGTGGTGCATCCGGAGGAGCGGGCTCCGGCAAGAGCCAGGCGCAGTCGCAA----------TCATCCGCCACTTCGTCATCCTCTTCGGCCAGTAAA---
droYak3	2L:206707-206871 -	dya_1802	TTGGGTAATCTGGCGGGTATGGATACTCAGTCGCTGGCTGCGCTCATGGCTGCTGCCGGCGCCAACTCTTGGCGGATTAGTGGTGCATCCGGAGGAGCGGGCTCCGGCAAGAGCCAGGCGCAGTCGCAA----------TCATCCGCCACTTCGTCCTCCTCTTCGGCTAGTAAA---
droEug1	scf7180000409461:602652-602822 +		CTAGGAAATCTGGCGGGGATGGATACCAATCGCTCGCTGCGCTCATGGCTGCTGCCGGACCTACTCTTGGAGGCTTGACAGGCGCGTCAGGAGGAGTGGGTTCCGGCAAGAGCCAGGCGCAGTC-----G------GGTGGTG-----------GCTCTTCCGCCGCTTCGTCATCCTGCTCGGCCAGTAAG---
droBia1	scf7180000301547:44590-44766 +		TTGGGAAATCTGGCGGGGATGGACACCCAGTCGCTGGCTGCGCTTATGGCTGCTGCCGGACCAACTCTTGGCGGATTGACTGGTGCGTCCGGAGGAGCGGGTTCCGGTAAGAGCCAGTCGCAGTCACAGTCG------GGTGGTG-----------GCTCATCCGCTGCTTCCTCATCCTCCTCGGCCAGTAAG---
droTak1	scf7180000413017:324221-324391 +		TTGGGCAATCTGGCCGGGATGGACACCCAGTCGCTGGCTGCGCTCATGGCTGCTGCCGGACCAACTCTTGGCGGATTGACTGGTGCATCCGGAGGAGCGGGTTCCGGCAAGAGCCAGGGGCAGTCACAGTCG------GG---TG-----------GCTCATCCGCCGCCTCCTCA---TCCTCGGCCAGCAAG---
droEle1	scf7180000490454:160021-160200 +		CTGGGAAATCTGGCGGGGATGGACACCCAGTCGTTGGCTGCGCTTATGGCTGCTGCCGGACCAACTCTAGGCGGATTGACGGGTGCTTCCGGAGGAGCGGGCTCCGGCAAGAGCCAGGTGCAGTCGCAGTCG------GGTGGCA-----------GCTCATCTGCGGCTTCCTCATCCTCTTCGGCCAGCAAGAAA
droRho1	scf7180000779252:239979-240155 -		TTGGGAAATCTAGCGGGGATGGACACCCAGTCGCTGGCTGCACTTATGGCTGCTGCCGGACCAACTCTAGGCGGATTGACTGGTGCTTCCGGAGGAGCGGGTTCCGGTAAGAGCCAGGTGCAGTCGCAGTCG------GGCGGTG-----------GCTCATCCGGTGCTTCCTCATCCTCTTCGGCCAGCAAG---
droFic1	scf7180000453904:479799-479975 -		CTGGGCAACCTGGCGGGCATGGACACCCAGTCGCTGGCTGCGCTAATGGCTGCTGCCGGACCAACTCTTGGCGGACTGACCGGTGCTTCCGGAGGAGCGGGTTCCGGCAAGAGCCAGGCGCAGTCGCAGTCG------GGCGGAG-----------GTTCCTCCGCCGCTTCCTCCTCCTCGGCCAGCAAG---
droKik1	scf7180000302401:520623-520781 -		TTGGGCAACTTAGGTGGGGATGGACACCCAGTCGCTGGCTGCGCTCATGGCTGCTGCCGGCCAACTCTTGGCGGTTTGACGGGTTCAGCCGGCGGGAGCGGGTTCCGGCAAGAGTCAAGGGCAGTCGTCG----------TGGGCCG---CCTCATCCTCCTCGGCCAGCAAG---
droAna3	scaffold_12943:4179562-4179729 +	dan_4050	TTGGGCAATCTGGCCGGTATGGACACCCAGTCGCTGGCAGCGCTGATGGCTGCTGCCGGACCATCGCTTGGAGGACTGACAGGCAGTTCCGGAGCGGCGGGATCCAGCAAGAACCAAGGCCAGTC-----T------GGCGGCG-----------GCTCCTCCAACT---CGTCCTCATCGTCGGCGAGCAAA---
droBip1	scf7180000395973:401628-401795 +		TTGGGCAACCTGGCGGGTATGGACACCCAGTCGCTGGCTGCGCTTATGGCGCTGCCGGCGCCTTCTCTCGGAGGGTTGACGGGCAGTTCCGGAGCGACGGGATCCGGCAAGAATCAAGGGCAGTC-----T------GGTGGCG-----------GCTCCTCGAACT---CGTCCTCATCATCGGCGAGCAAG---
dp5	4_group1:4397274-4397435 +	dps_3851	TTGGGAAATCTGGCGGGCATGGAGCCAATTCGCTGGCTGCGCTCATGGCTGCTGCATGGCCAACCCTGGCGGCCTCACAGGCAGCTGCGGCGG---GGGGTTCCGGCAAGAGTCAGTCGCAGGT-----C------GGCGGTGGCGGAGGCGGCAA----------GTCCTCCTCGTCCAGCAAG---
droPer2	scaffold_5:812682-812843 -	dpe_2515	TTGGGAAATCTGGCGGGCATGGACGCCAATTCGCTGGCTGCGCTCATGGCTGCTGCATGGCCAACCCTGGCGGCCTCACAGGCACCTCGGCCG---GGGGTTCCGGCAAGAGTCAGTCGCAGGT-----C------GGCGGTGGCGGAGGCGGCAA----------GTCCTCCTCGTCCAGCAAG---
droWil2	scf2_1100000004577:93984-94151 -	dwi_5426	TTGGGTAATCTGGCTGGTATGGATGCCCAGTCGCTGGCTGCGCTCATGGCTGCTGCCGGCGCCAACATTGGGTGGCCTAACGGGCAACTGTGG---TGCTGGATCCGGCAAGAGCCAGTCGCAGGG-----C------GGCGGCGGTG---------CATCTTCATCCACTTCGT---CGTCTTCATCGAGCAAA---
droVir3	scaffold_12963:8889400-8889570 +	dvi_24647	CTGGGTAATCTGGCCGGCATGGATGCCCAGTCGCTGGCTGCGCTCATGGCTGCTGCGGACCAACGCTCGGCGGCCTTACAGGCAGCAGCG--A-GCGCGGGCACCGGCAAGAGCCAGTCGCAGTC-----CAGCGCTGGCGGCA----------ACTCCTCCAGCGCCTCCT---CATGGCGGGCCAGCAAG---
droMoj3	scaffold_6500:2441430-2441603 -	dmo_3157	TTGGGTAATCTGGCGGGCATGGATGCCCAGTCACTGGCTGCGCTCATGGCTGCTGCTGGACCAACGCTTGGCGGCCTCACAGGCAGCAG---AAACGCGGGCACCGGCAAGAGCCAGTCGCAGTC-----C------AGTGGTGGCGGCA------ACTCCTCCAGCACCTCCTCCTCGTCGGCGGGCCAGCAAG---
droGri2	scaffold_15252:12898765-12898938 -	dgr_471	TTGGGTAATCTGGTGGCATGGATGCCCAGTCGCTGGCTGCGCTCATGGCTGCTGCGGTCCAACGCTCGGCGGCCTAACCGGCAGCTGCGG---CCTCGGCACCGGCAAGAGCCAGTCGCAGTC-----C------GGCGGCGGTGGCA------GCTCCTCCAGTGCCGGTTCCTGTTCAGCGGCCAGCAAG---

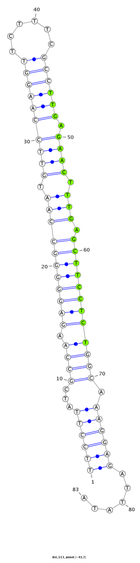
Generated: 09/08/2015 at 08:02 PM

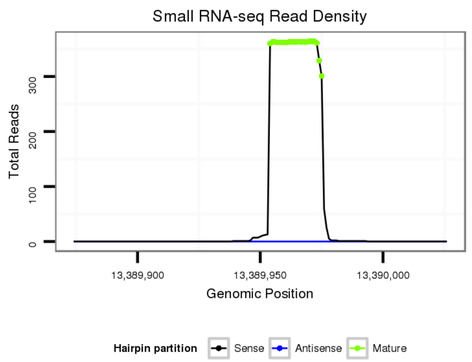
	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	0
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	0
rescue.known	0
rescue.confident	0
rescue.candidate	3

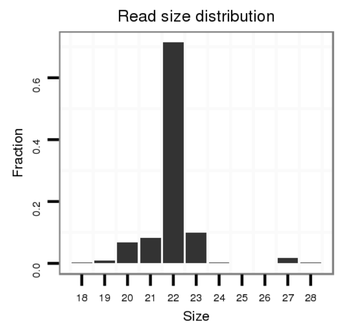
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dsi_113	**2r:13389924-13389976 +**	**candidate**	**Canonical miRNA**	**5pUTR**	[View on UCSC Genome Browser [Cornell Mirror]]

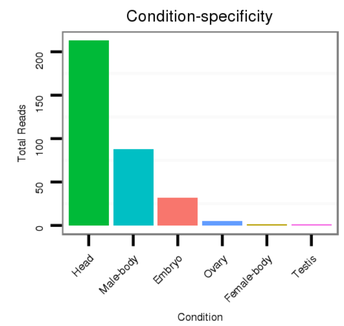
Legend: mature star mismatch in alignment mismatch in read

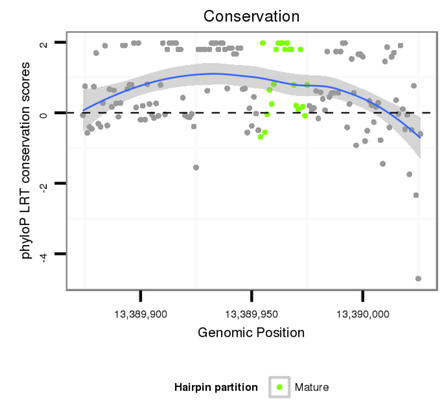
Predicted structure











Show Alternate Folds

Flybase annnotation

utr5 [utr5_plus_4718]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

AAAAGAAAGCAACACTCAAATAAACTCACAAAGAATTCCTTATCGCCAAGAGGGGGCCAATGTTCCAAGGTTCTTTCGCCTTGAGAACTTTGAGCTTCCTCTGGCAAAGGAGATTATAATGTACAAATAATGTTGCAATAACCAGTTGAATGC **********(((((...((((.((((((((((.((((((((((.....))))))).))))).))).))).))))))))))).))))))).....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M023 head	M024 male body	M025 embryo	SRR553485 Chicharo_3 day-old ovaries	SRR553486 Makindu_3 day-old ovaries	O002 Head	SRR553487 NRT_0-2 hours eggs	GSM343915 embryo	M053 female body	O001 Testis	SRR553488 RT_0-2 hours eggs	SRR618934 dsim w501 ovaries
.....TTGAGAACTTTGAGCTTCCTCT.....	22	0	1	241.00	241	158	67	12	0	1	2	0	0	1	0	0	0
.....TTGAGAACTTTGAGCTTCCTCTG.....	23	0	1	33.00	33	14	9	8	2	0	0	0	0	0	0	0	0
.....TTGAGAACTTTGAGCTTCCTCG.....	22	1	1	31.00	31	22	8	1	0	0	0	0	0	0	0	0	0
.....TTGAGAACTTTGAGCTTCCTC.....	21	0	1	28.00	28	21	4	2	0	0	0	1	0	0	0	0	0
.....TTGAGAACTTTGAGCTTCCT.....	20	0	1	23.00	23	16	6	0	0	1	0	0	0	0	0	0	0
.....TTGAGAACTTTGAGCTTCCTCTGG.....	24	0	1	18.00	18	5	4	4	2	1	0	0	1	0	0	1	0
.....TTGAGAACTTTGAGCTTCCTCTT.....	23	1	1	11.00	11	7	4	0	0	0	0	0	0	0	0	0	0
.....TTGAGAACTTTGAGCTTCCTCTGGT.....	25	1	1	7.00	7	2	0	3	1	0	0	1	0	0	0	0	0
.....TTGAGAACTTTGAGCTTCCTCG.....	22	1	1	6.00	6	4	2	0	0	0	0	0	0	0	0	0	0
.....TTTCGCCTTGAGAACTTTGAGCTTCCT.....	27	0	1	5.00	5	0	0	5	0	0	0	0	0	0	0	0	0
.....TTGAGAACTTTGAGCTTCCTGGC.....	25	0	1	3.00	3	2	0	1	0	0	0	0	0	0	0	0	0
.....TTGAGAACTTTGAGCTTCCTCTGGG.....	25	1	1	3.00	3	0	1	2	0	0	0	0	0	0	0	0	0
.....TTGAGAACTTTGAGCTTCCTCTGGA.....	25	1	1	3.00	3	0	2	1	0	0	0	0	0	0	0	0	0
.....TTGAGAACTTTGAGCTTCCTCTGCT.....	25	2	1	2.00	2	2	0	0	0	0	0	0	0	0	0	0	0
.....TTGAGAACTTTGAGCTTCCTCA.....	22	1	1	2.00	2	1	1	0	0	0	0	0	0	0	0	0	0
.....GCCTTGAGAACTTTGAGCTTCC.....	22	0	1	2.00	2	0	0	2	0	0	0	0	0	0	0	0	0
.....TTGAGAACTTTGAGCTTCCG.....	20	1	1	2.00	2	2	0	0	0	0	0	0	0	0	0	0	0
.....TTGAGAACTTTGAGCTTCCTCTGA.....	24	1	1	2.00	2	0	2	0	0	0	0	0	0	0	0	0	0
.....TGAGAACTTTGAGCTTCCT.....	19	0	1	2.00	2	1	0	0	0	0	0	1	0	0	0	0	0
.....CTTGAGAACTTTGAGCTTCCTCT.....	23	0	1	1.00	1	0	0	1	0	0	0	0	0	0	0	0	0
.....TTGAGAACTTTGAGCTTCCTCTGCTT.....	26	2	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0	0
.....TGAGAACTTTGAGCTTCCTCTGG.....	23	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0	0
.....CTTTCGCCTTGAGAACTTTGAGCTTCCT.....	28	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0	0
.....CGCCTTGAGAACTTTGAGCTTCCTCTG.....	27	0	1	1.00	1	0	1	0	0	0	0	0	0	0	0	0	0
.....TTGAGAACTTTGAGCTTCCTCTGGATTT.....	27	3	1	1.00	1	0	1	0	0	0	0	0	0	0	0	0	0
.....TGAGAACTTTGAGCTTCCG.....	19	1	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0	0
.....TTGAGAACTTTGAGCTTCCTCTGAT.....	25	2	1	1.00	1	0	1	0	0	0	0	0	0	0	0	0	0
.....CGCCTTGAGAACTTTGAGCTTCCT.....	24	0	1	1.00	1	0	1	0	0	0	0	0	0	0	0	0	0
.....TTGAGAACTTTGAGCTTCC.....	19	0	1	1.00	1	0	0	1	0	0	0	0	0	0	0	0	0
.....TTTGAGCTTCCTCTGGCAAA.....	20	0	1	1.00	1	0	0	1	0	0	0	0	0	0	0	0	0
.....CAAGGTTCTTTCGCCTTG.....	18	0	1	1.00	1	0	0	0	0	0	0	0	0	1	0	0	0
.....CCTTGAGAACTTTGAGCTTCCTCTGG.....	26	0	1	1.00	1	0	1	0	0	0	0	0	0	0	0	0	0
.....TCCTCTGGCAAAGGAGATTATAAT.....	24	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0	0

Anti-sense strand reads

TTTTCTTTCGTTGTGAGTTTATTTGAGTGTTTCTTAAGGAATAGCGGTTCTCCCCCGGTTACAAGGTTCCAAGAAAGCGGAACTCTTGAAACTCGAAGGAGACCGTTTCCTCTAATATTACATGTTTATTACAACGTTATTGGTCAACTTACG **********(((((...((((.((((((((((.(((((((((.....))))))).))))).))).))).))))))))))).))))))).....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	SRR553487 NRT_0-2 hours eggs

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droSim2	2r:13389874-13390026 +	dsi_113	AAAAGA----------AA----------GCAAC-ACT--------CAAATAAACTCA-----CAAAG--AATTCCTTATCGCCAA---------GAGGGGGCCAATGTTC--CAAGGTTCTTTCG----------CCTTGAGAACTTTGAGCTTCCTCT----------GGC----------AAAGGAGATTATAA----------T--GTACAAATAATGTT--GCAATAACC---------AG---------TT---G------AATGC
droSec2	scaffold_1:10223628-10223779 +		AAAAGA----------AA----------GAAAC-ACT--------CAAATAAACTCA-----CAAAG--AATTCCTTATCGCCAA---------GAGGGGGCCAATGTTC--CAAGGTTCTTTCG----------CCTTGAGAACTTTGAGCTTCCTCT----------GGC----------AAAGGAGATTATAA----------T--GTACAAATAATGTT--GCAATAACC---------AG---------TT---G------GATGC
dm3	chr2R:12718758-12718908 +	dme_411	AAGAAA----------AA----------AAAAC-ACT--------CAAATAAACTCA-----CAAAG--AATTCCTTATCGCCAA---------G--GGGGCCAATGTTC--TAAGGTTCTTTCG----------CCTTGAGAACTTTGAGCTTCCTCT----------GGC----------AAAGGAGATTATAA----------T--GTACAAATAATGTT--GCAATAACC---------AG---------TT---G------AAAGC
droEre2	scaffold_4845:13131250-13131399 -		AAAAGA----------AA----------GAAAC-ACT--------CAAATAAACTGC-----CAAGA--AATTGCTTATCGCCAA---------G--GGGGCCAATGTTC--CAAGGTTCTTTCG----------C-CTGAGACCTTTGAGCTTCCTCT----------GGA----------AAAGGAGATTATAA----------T--GTACAAATAATGTT--GCAATAACC---------AG---------TT---A------AACGC
droYak3	2R:16257353-16257515 -		AAAAGA----------AA----------GAAAC-ACT--------CAAATAAACTGC-----CAAAG--AATTCCTTATCGCCAA---------G--GGGGCCAATGTTCGCCAAGGTTCTTGTCG----------C-CTGAGAACTTTGAGCTTCCTCT----------GGAAA-T----------AAAGGAGATTATAA----------T--GTACAAATAATGTT--GCAATAACC---------AG---------TTAA-GCAGAATAACCC
droEug1	scf7180000409672:2416375-2416548 -		AAAAGA----------AC----------AAAAC-ACA--------AAAATAAACTGC-----CAAAG--ACTTGCTTATCGCCAA---------G--GGGGCCAATGTTC--CAAGGTTTTGTGCTA---TGCTGCGGCGTTGAGAACTTTGAGCTTCCTCT----------GGAAAG----------AAAGGAGATTATAAAAA----------T--T--TAAAATATATA--ACAAAAAAAAACCAAACCAG---------TT---A------AATTT
droBia1	scf7180000301506:2134358-2134513 +		GAAAAA----------AAAACG----------ACAAACGTT--------TAAATAAACTGC-----GAAAG--AATTGCTTATCGCCGG---------G--GGGGCCAATGTTC--CAAGGTTTTGTG----------G-GCGAGAACTTTGAGCTTCCTCT----------GGA----------AAAGGAGATTATAA----------ACCAT--GTGTAAAGCAT----------GAACC---------AG---------TT---G------GAGAA
droTak1	scf7180000415389:230381-230521 +		AAAAAA----------AA----------AC-GA-ATT--------TAAATAAACTGC-----CAAAG--AATTGCTTATCGCCAA---------GGGGGCCAATGTTC--CAAGGTTTTTT-G----------C-CTGAGAACTTTGAGCTTCCTCT----------GGA----------AAAGGAGATTATAA----------A--T--T-------TATATA--AAAATAACC---------AG---------TT---A------AACAA
droEle1	scf7180000491214:1653010-1653146 -		AAAA--------------------AAAAC-ACG--------TAAATGAACTGC-----CAAG--AATTGCTTATCGCCAA---------GGGGGCCAATGTTC--CAAGGTTTTGT--------------TTTGGAACTTTGAGCTTCCTCT----------GCA----------AGTGGAGATTATAA----------AC--T--GTAAAAATAAGA--------AACC---------T--T---A------AACAA
droRho1	scf7180000780084:626337-626473 -		AAAGAA----------AAAAC-ATT--------TAAATAAAATGC-----CAAAG--AATTGCTTATCGCCAA---------GGGGGCCAATGTTC--CAAGGTTTTGT--------------TTGAGCACTTTGAGCTTCCTCT----------GGA----------AATGGAGATTATAA----------ACT--T--GTAAAA--------AACGAACC---------AA---------CG---A------AACCA
droFic1	scf7180000453851:951342-951487 +		CAAGAA----------AAAC-ATT--------TAAATAAACTGC-----GAAG--AATTGCTTATCGCCAA---------GGGGGCCAATGTTC--CAAGGTTACTTG----------C-CTGAGAACTTTGAGCTTCCTCT----------GGA----------GGAGGAGATTATAA----------ACT--C--TTACAAACTA----T-CA---ACC---------AA---------CCAACG------TAAG-
droKik1	scf7180000302470:1132051-1132200 +		AAGAAG----------AGCGTA----------AAAAGC-ATT--------AAAATAAACTGAATAAATAGAG--TCTTGCTTATCGCCAG---------A-AGGGGCCAATGTTC--C----------TTTAGGAACTTTGAGCTTTCATT----------A--T----------AGAAGAGATTATAA----------AG--A--TTAAAAATTATGTAAATTAATAA--T---------AA---------AT---G------ACTGC
droAna3	scaffold_13266:13876762-13876965 -		AATAAA----------AG----------AAAAGAAATAAAAAGC-TTTAAAAAAACTAAATAAACTGC-----GAAGA--AATTCCTTATCGGCCTTTGGGCCACG-GGGGGCCAATGTTC--CAAGGTTTTCTCGAAAAAAATAAAAG-A-TTTGGTACTTTGAGCTCCCATT----------AAAA--AAAAAATTATAAAAAAAAGATTATAA----------TAAAACGATTAAAAGT-----T---A----A---------AA---------TT---A------AATTT
droBip1	scf7180000396759:2259353-2259528 +		AAAAAA----------AAATCAAAATAAAATAAAAGAAATAAAAAGC-TT--------TA---AAACTGC-----GAAGA--AATTCCTTATCGGA--T---------G--GGGGCCAATGTTC--CAAGGTTTTCTCGAAAAA---------A-TTTGATACTTTGAGCTCCCATT----------AAA----------AAAATACGATTTAAA----------CGG-T--TTAAAAATT-----T---A----A---------AATAAAATACACT---G------GA-GA
dp5	Unknown_singleton_1898:47672-47887 -		AACCCAGCCAAAAACTTAAACCGATTCTAAAAAA----------AAAAC-ATT--------CGAAGAGAATGA-----AATACATTATGTCTTATCGGGA---------ACTGGGGACAATGTTC--CAAGGTTTTCGAA----------AACTGAGAACTTTGAGCGGCGGACACTCGATAATAATTAACAAGAATTCTGGGCAATAAATATGTACATT----------AAAAGAAGAAAATACT----T--T----------A--AAAATAAG-----AAAAGAG---------GG---A------AACAA
droPer2	scaffold_4:6545542-6545731 +		TTAAAA----------AA----------TAAAC-GTT--------CGAAGAGAATGA-----AATACATTTGTCTTATCGGGA---------GTGGGGACAATGTTC--CAAGGTTTTCGAA----------AACTGAGAACTTTGAGCGGCGGACACTCGATAATAATTAACTAGAATTCTGGGCAATAAATATGTACATT----------AAAAGAAGAAAATACT----T--T----------A--AAAATAAG-----AAAAGAG---------GG---A------AACAA

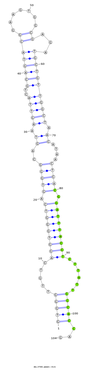
Generated: 09/08/2015 at 08:02 PM

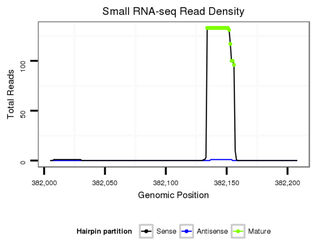
	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	2

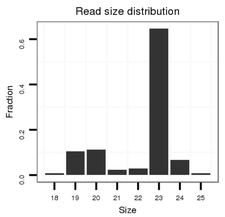
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dsi_27502	**x:382055-382158 +**	**candidate**	**Mirtron**	**intergenic**	[View on UCSC Genome Browser [Cornell Mirror]]

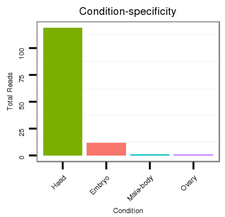
Legend: mature star 5mismatch in alignment mismatch in read

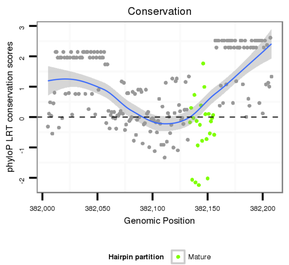
Predicted structure











Show Alternate Folds

Sense Strand Reads

hide 3p reads show mid mismatch reads

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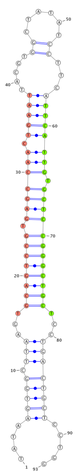
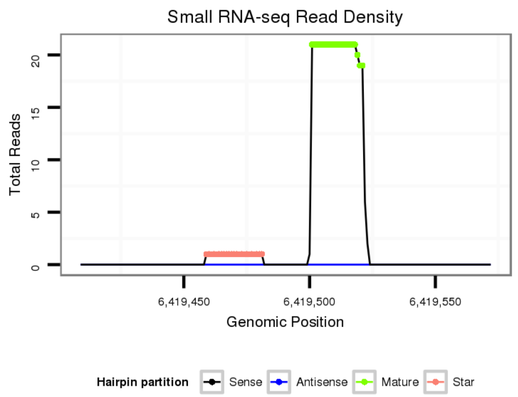
```

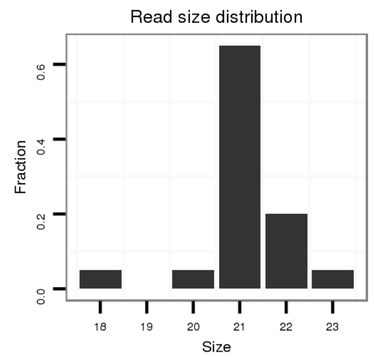
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dsi_135	**2r:6419459-6419522 +**	**candidate**	**Canonical miRNA**	**5pUTR**	[View on UCSC Genome Browser [Cornell Mirror]]

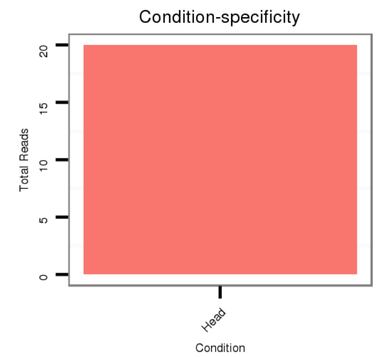
Legend: mature star mismatch in alignment mismatch in read

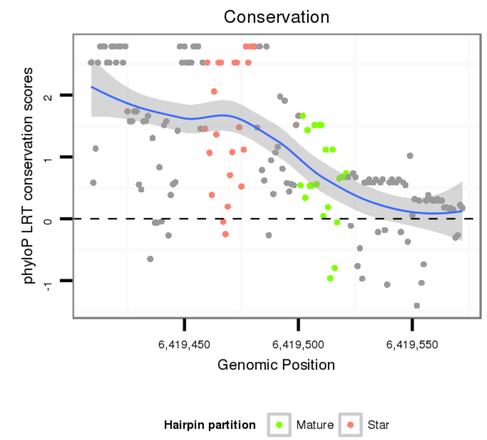
Predicted structure











Show Alternate Folds

Flybase annnotation

utr5 [utr5_plus_3653]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

CCGGAATGCAAGAAGTACGTATCCGTACGCTTGGTTATAAGTGGCTTAAGTGCAGTCCGTGAGCCAACTGAATTACGTGGCTATATCCTTCATTCATTGTGCTCCGGGCTGCTCCTGACTGCTCCTGGTTGCTCCTGGCAGCTCCTGGTTGCTCCTACCTTCTC **********....(((((.(((...(((((((((.(((((((.(((((.....((.....))...)))))))).)))))))))))...)))))))).....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M023 head	SRR618934 dsim w501 ovaries	GSM343915 embryo	SRR553487 NRT_0-2 hours eggs	SRR553488 RT_0-2 hours eggs	SRR902009 testis
.....TTCATTGTGCTCCGGGCTGCT.....	21	0	1	13.00	13	13	0	0	0	0	0
.....TTCATTGTGCTCCGGGCTGCTC.....	22	0	1	4.00	4	4	0	0	0	0	0
.....TTCATTGTGCTCCGGGCTGCTCC.....	23	0	1	2.00	2	2	0	0	0	0	0
.....TTCATTGTGCTCCGGGCTGCG.....	21	1	1	2.00	2	2	0	0	0	0	0
.....TGCAGTCCGTGAGCCAACTGAAT.....	23	0	1	1.00	1	1	0	0	0	0	0
.....GTGCTCCGGGCTGCTCCTGG.....	20	1	1	1.00	1	1	0	0	0	0	0
.....TTCATTGTGCTCCGGGCTGCTT.....	22	1	1	1.00	1	1	0	0	0	0	0
.....TTCATTGTGCTCCGGGCT.....	18	0	1	1.00	1	1	0	0	0	0	0
.....ATTCATTGTGCTCCGGGCTG.....	20	0	1	1.00	1	1	0	0	0	0	0

Anti-sense strand reads

GGCCTTACGTTCTTCATGCATAGGCATGCGAACCAATATTCACCGAATTCACGTCAGGCACTCGGTTGACTTAATGCACCGATATAGGAAGTAAGTAACACGAGGCCCGACGAGGACTGACGAGGACCAACGAGGACCGTCGAGGACCAACGAGGATGGAAGAG **********....(((((.(((...(((((((((.(((((((.(((((.....((.....))...)))))))).)))))))))))...)))))))).....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	SRR902009 testis

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droSim2	2r:6419409-6419572 +	dsi_135	CCGGAATGCAAGAAGTACGTATCC----------GTA------CGCTTGGTTATAAGTGGCTTAAGTGCAGT---CCGTG-AGCC-AACTGAATTACGTGGCTATA---------TCCT---TCATTCA----TTGTGCTCCGGGC--T----------GCTCCTGA--CTGCTCCTGGTT--GCTCCTGG---CA----------GCTCCTGGTTGCTCCTACC----------TTCTC
droSec2	scaffold_1:3250639-3250791 +		CCGGAATGCAAGAAGTACGTATCC----------GTA------CGCTTGGTTATAAGTGGCTTAAGTGCAGT---CCGTG-AGCC-AACTGAATTACGTGGCTATA---------TCCT---TCATTCA----TTGTGCTCCGGGC--T----------GCTCCTGA--CTGCTCCTGGTT--GCTCCTGG---CA-------GGAGC----------TCC----------TTCTC
dm3	chr2R:5641469-5641632 +		CCGGAATGCAAGAAGTACGTATCC----------GTA------CGCTTGGTTATAAGTGGCTTAAGTGCAGT---CCGTG-AGCC-AACTGAATTACGTGGCTATA---------TCCT---TCATTCA----TTGTGCTCCTGGT--T----------GCTCCTGA--CTGCTCCTGGTT--GCTCCTGG---CA----------GCTCC-AGGTTGCTCCTACC----------TCTCC
droEre2	scaffold_4929:8722719-8722873 -		CCGGAATGCAAGAAGTACGTATCC----------GTG------CGCTTGGCTATAAGTGGCTTAAGTGCAGT---CCGTG-GCCC-AACTGAATTACGTGGCTATA---------TCCT---TCATTCA----TTGTGCTCCTGGT--T----------GCTCCTGT--AGGCTCCTGGTT--GCTCCTGG---CA----------GCTCCTAGTTGCTCC-----------
droYak3	2L:18267486-18267633 +		CCGGAATGCAAGAAGTACGTATCC----------GTC--CGTAGCGCTTGGTTATAAGTGGCTTAAGTGCAGT---CCGTG-AGCC-AACTGAATTACGTGGCTATA---------TCCT---TCATTCA----TTGTGCTCCTGGT--T----------GCTCTGTGC--ATGCTCCTAGTT--CCTCCTAG---------T----------TGCTC
droEugl	scf7180000409209:526483-526642 -		CCGGAATGCAAGAAGTACGTATCC----------GTA------C----GGTTATAAGTGGCTTAAGTGCAGT---CCGTG-AGCC-AACTGAATTAAGTAGTTATA---------TCCT---TCATTCA----TTGTGCTCCTGATTCTGCCCCGGATCCTGTGCCTGCTCCTGTTCCAGCTCCTCTT---------CCAGC----------TCC----------TGCTC
droBia1	scf7180000301506:1071727-1071904 -		CCGGAATGCAAGAAGTACGTATCC----------GTA------C----GGTTATAAGTGGCTTAAGTGCAGT---CCGTG-AGCC-AACTGAATTAAGTAGTTATA---------TCCT---TCATTCA----TTGTGCTCCTGTT--T----------CCTGCTCCTGCTCCTGCTCCTGATCCCGCTCCTGGTCCCACTCCTGGTCCCACTCCTGTGCCAGC----------TCC----------TGCTC
droTak1	scf7180000415870:656721-656850 -		CCGGAATGCAAGAAGTACGTATCC----------GTA------C----GGTTATAAGTGGCTTAAGTGCAGT---CCGTG-AGCC-AACTGAATTAAGTAGTTATA---------TCCT---TCATTCA----TTGTGCTCCTGT--T----------TCCTGCTCCAACTCCTGCTCCTGA--TC
droEle1	scf7180000491107:1463910-1464033 -		CCGGAATGCAAGAAGTACGTATCC----------GTA------C----GGTTATAAGTGGCTTAAGTGCAGT---CCGTG-AGCC-AGCTGAATTAAGTAGTTATA---------TCCT---TCATTCA----TTGTGCTCCGGC--T----------TCCAGCTC--------------------------------GAGG----------TCC----------AGCTG
droRho1	scf7180000777217:538816-538921 +		CCGGAATGCAAGAAGTACGTATCC----------GTA------C----GGTTATAAGTGGCTTAAGTGCAGT---CCGTG-AGCC-AGCTGAATTAAGTAGTTATA---------TCCT---TCATTCA----TTGTGCTCACC--T----------TC--TC
droFic1	scf7180000453858:1085865-1086011 -		CCGGAATGCAAGAAGTACGTATCCGAGTATCCGATTCTCCGGGTATCCGAGTATCCGTGTATCCGTG------C----GGCTTTAAGTGGCTTAAGTGCAGT---CCGAG-AGCC-GGCTGAATTACGTAGTTGTG---------TCC---TCATTCA----GGTAGCCTGCC--T----------TCC----------TC---------------------------------------
droKik1	scf7180000302476:1052160-1052290 +		CCGGAATGCAAGAAGTACGTATCC----------GTG------C----GGGGATAAGTGGCTTAAGTGCAGT---CCGGG-AGCC-AGCTGAATTAAGTAGTTATAGGACGAGTATGTT---TCATTCA----TTGTGCG------T----------AGC----------TCTGTGGCCTCTGTGTGTGC
droAna3	scaffold_13266:12913976-12914062 +		CCGGAATGCAAGAAGTACGTACCC----------GTATCCGT-ATTCGG--AAGAGTGGCTTAAGTGCTGA---CCATA-AGCC-AACTGAATTAATAGGTTATA---------TC--TC
droBip1	scf7180000396730:1007747-1007846 -		CCGGAATGCAAGAAGTACGTATTC----------G--------GT--AAAGTGGCTTAAGTGCAGA---CCATA-AGCC-AACTGAATTAAGTGGTTATA---------TACGGGTCGAATG-GTCCATTGTGCT------T----------TC---------------------------------------
dp5	3:14265158-14265223 +		CTGGAATGCAAGAAGT-------------------------AAGTGGCTTAAGAGCAGT---CCGAGAAGCC-AACTGAATTAAGTGGCTATA---------TG--
droPer2	scaffold_4:1050697-1050762 -		CTGGAATGCAAGAAGT-------------------------AAGTGGCTTAAGAGCAGT---CCGAGAAGCC-AACTGAATTAAGTGGCTATA---------TG--
droWil2	scf2_1100000004514:3610134-3610194 +		CAAGAATGCAAGAAGT-------------------------AAGTGGCTTATGTGCTGTTTCCCATAAAGCCAAAGTGAATTATATT--
droVir3	scaffold_12875:5954337-5954395 +		CGAGAATGCAAGAAGT-------------------------AAGTGGCTTAAGTGT---CCCAGCGACC-AAGTGAATTAAGTAGCGA--
droMoj3	scaffold_6496:24094987-24095041 -		CGAGAATGCAAGAAGT-------------------------AAGTGGCTTAAGTG---T---CCGAGCGACC-AAGTGAATTAAGTG---
droGri2	scaffold_15112:875136-875194 +		CGAGAATGCAAGAAGT-------------------------AAGTGGCTTAAGTGT--T---CCACC-GCCC-AAGTGAATTAAGTTACGA--

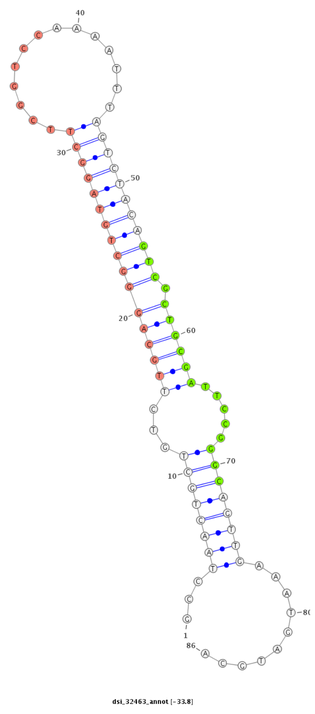
Generated: 09/08/2015 at 08:02 PM

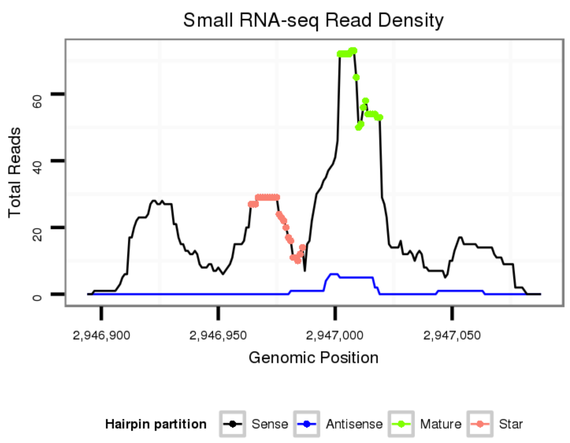
	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.ptop3	1
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

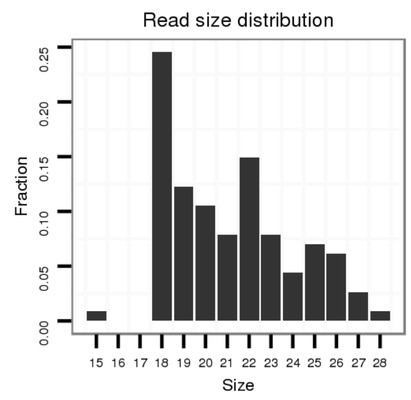
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dsi_32463	**2l:2946944-2947038 +**	**candidate**	**Canonical miRNA**	**3pUTR**	[View on UCSC Genome Browser {Cornell Mirror}]

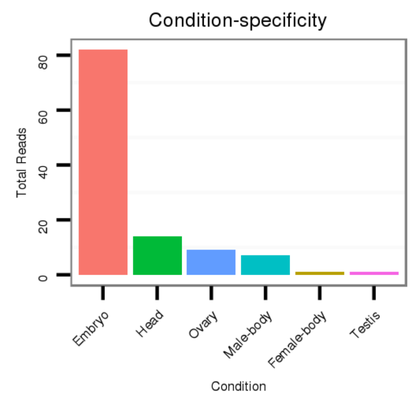
Legend: mature star mismatch in alignment mismatch in read

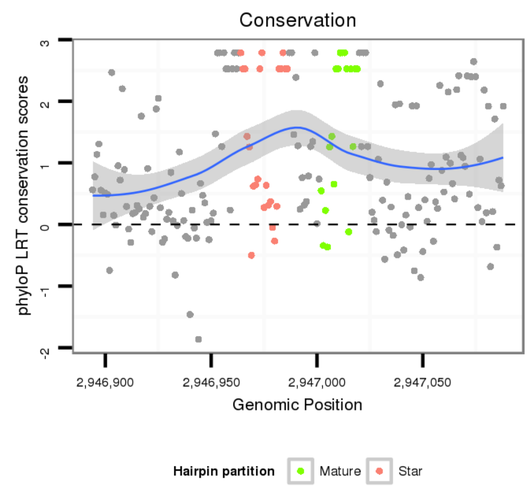
Predicted structure











Show Alternate Folds

Flybase annnotation

three_prime_UTR [2l_2946687_2947368_+]; utr3 [utr3_plus_232]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

CACAGCTAGAAGAGATAAGTCAACAGATTGGATTTGCGCCGATCGGCTTGAATCTGCCTAACTGCTGTCTTGCAGGGCTGTAGGCTTCGGTCCAAAATTTAGTCTACAGTCGCTGCGATTCCGGGCAGTTGAAATGATGCAAGATGAGAGGCCCAGTCCATAACACTTAACGCTTTGTGCACCGTACAATTCAGT **********...((((((((...(((((((((((((((((.....)))))))))))).))))))).....)))))))).....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M025 embryo	M023 head	GSM343915 embryo	M024 male body	SRR618934 dsim w501 ovaries	M053 female body	SRR553486 Makindu_3 day-old ovaries	SRR553485 Chicharo_3 day-old ovaries	SRR902009 testis	O002 Head	SRR553487 NRT_0-2 hours eggs
.....GTCGCTGCGATTCCGGGC.....	18	0	1	18.00	18	15	0	0	3	0	0	0	0	0	0	0
.....AAATTTAGTCTACAGTCGCTGC.....	22	0	1	7.00	7	5	0	0	1	0	1	0	0	0	0	0
.....TGCAGGGCTGTAGGCTTCGGTCC.....	23	0	1	5.00	5	2	1	1	1	0	0	0	0	0	0	0
.....GTCAACAGATTGGATTTGC.....	19	0	1	5.00	5	5	0	0	0	0	0	0	0	0	0	0
.....GTCGCTGCGATTCCGGGCAGT.....	21	0	1	4.00	4	3	0	0	0	1	0	0	0	0	0	0
.....ATTTAGTCTACAGTCGCTGC.....	20	0	1	4.00	4	3	0	1	0	0	0	0	0	0	0	0
.....CTTGCAGGGCTGTAGGCTTCGGTCC.....	25	0	1	3.00	3	3	0	0	0	0	0	0	0	0	0	0
.....GATTCCGGGCAGTTGAAAT.....	19	0	1	3.00	3	1	2	0	0	0	0	0	0	0	0	0
.....GCTGTCTTGCAGGGCTGTA.....	19	0	1	3.00	3	3	0	0	0	0	0	0	0	0	0	0
.....TGCAGGGCTGTAGGCTTC.....	18	0	1	3.00	3	1	2	0	0	0	0	0	0	0	0	0
.....TTAGTCTACAGTCGCTGCGATT.....	22	0	1	3.00	3	0	3	0	0	0	0	0	0	0	0	0
.....CCATAACACTTAACGCTTTGTGCACC.....	26	0	1	3.00	3	3	0	0	0	0	0	0	0	0	0	0
.....TTCCGGGCAGTTGAAATGATGCAAGA.....	26	0	1	3.00	3	0	0	0	0	0	0	0	3	0	0	0
.....GTCGCTGCGATTCCGGGCAG.....	20	0	1	2.00	2	2	0	0	0	0	0	0	0	0	0	0
.....TGATGCAAGATGAGAGGCC.....	19	0	1	2.00	2	2	0	0	0	0	0	0	0	0	0	0
.....CCAAAATTTAGTCTACAGTCGCTGC.....	25	0	1	2.00	2	1	0	0	1	0	0	0	0	0	0	0
.....GTCGCTGCGATTCCGGGCA.....	19	0	1	2.00	2	2	0	0	0	0	0	0	0	0	0	0
.....CGGCTTGAATCTGCCTAACTGCTGTCT.....	27	0	1	2.00	2	0	0	0	2	0	0	0	0	0	0	0
.....CATAACACTTAACGCTTTGTGCACC.....	25	0	1	2.00	2	2	0	0	0	0	0	0	0	0	0	0
.....AGTCGCTGCGATTCCGGGC.....	19	0	1	2.00	2	2	0	0	0	0	0	0	0	0	0	0
.....TAAGTCAACAGATTGGATTTGCGCCGA.....	27	0	1	2.00	2	0	0	0	0	1	0	0	1	0	0	0
.....GTCAACAGATTGGATTTGCGCCGAT.....	25	0	1	2.00	2	2	0	0	0	0	0	0	0	0	0	0
.....TTTAGTCTACAGTCGCTGC.....	19	0	1	2.00	2	1	0	1	0	0	0	0	0	0	0	0
.....AAAATTTAGTCTACAGTCGCTG.....	22	0	1	2.00	2	2	0	0	0	0	0	0	0	0	0	0
.....CAACAGATTGGATTTGCGCCGATCGGCT.....	28	0	1	2.00	2	1	0	0	0	0	1	0	0	0	0	0
.....GTCGCTGCGATTCCGGGCAGG.....	21	1	1	2.00	2	2	0	0	0	0	0	0	0	0	0	0
.....GTCAACAGATTGGATTTGCGCC.....	22	0	1	2.00	2	2	0	0	0	0	0	0	0	0	0	0
.....TTTAGTCTACAGTCGCTG.....	18	0	1	2.00	2	2	0	0	0	0	0	0	0	0	0	0
.....AACAGATTGGATTTGCGC.....	18	0	1	2.00	2	1	1	0	0	0	0	0	0	0	0	0
.....AAATTTAGTCTACAGTCGCTG.....	21	0	1	2.00	2	2	0	0	0	0	0	0	0	0	0	0
.....GATAAGTCAACAGATTGGAT.....	20	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0
.....ATTTAGTCTACAGTCGCTGCGATT.....	24	0	1	1.00	1	0	0	1	0	0	0	0	0	0	0	0
.....ACTGCTGTCTTGCAGGGCTGTA.....	22	0	1	1.00	1	0	0	0	0	0	0	0	0	1	0	0
.....GCTGTCTTGCAGGGCTGTAGGCT.....	23	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0
.....GTCGCTGCGATTCCGGGCAGC.....	21	1	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0
.....CTACAGTCGCTGCGATTCCGGGCAGT.....	26	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0
.....TACAGTCGCTGCGATTCCGGGCAGT.....	25	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0
.....TGCAGGGCTGTAGGCTTCGGTCCA.....	24	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0
.....CTGCTGTCTTGCAGGGCTGTAGGC.....	24	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0
.....TCCGGGCAGTTGAAATGATGCAAGA.....	25	0	1	1.00	1	0	0	0	0	0	0	0	1	0	0	0
.....CAGTCGCTGCGATTCCGG.....	18	0	1	1.00	1	0	0	0	0	0	0	0	0	0	1	0
.....AACTGCTGTCTTGCAGGGCTGTAGGCTT.....	28	0	1	1.00	1	0	1	0	0	0	0	0	0	0	0	0
.....CGGCTTGAATCTGCCTAACT.....	20	0	1	1.00	1	0	1	0	0	0	0	0	0	0	0	0
.....ATAAGTCAACAGATTGGATTTGC.....	23	0	1	1.00	1	0	0	0	1	0	0	0	0	0	0	0
.....TGCTGTCTTGCAGGGCTGTAGG.....	22	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0
.....AGGGCTGTAGGCTTCGGTCC.....	20	0	1	1.00	1	0	1	0	0	0	0	0	0	0	0	0
.....AGTCTACAGTCGCTGCGATTCCGGGC.....	26	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0
.....GATGAGAGGCCCAGTCCATAACACT.....	25	0	1	1.00	1	0	0	1	0	0	0	0	0	0	0	0
.....AAATTTAGTCTACAGTCGCTGC.....	22	1	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0
.....GTCAACAGATTGGATTTGCGC.....	21	0	1	1.00	1	0	0	0	0	0	1	0	0	0	0	0
.....TGGATTTGCGCCGATCGGCTTGAATC.....	26	0	1	1.00	1	0	0	0	0	1	0	0	0	0	0	0
.....TTCCGGGCAGTTGAAATGATGCAAG.....	25	0	1	1.00	1	0	0	1	0	0	0	0	0	0	0	0
.....CAACAGATTGGATTTGCGC.....	19	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0
.....CAGTCCATAACACTTAACGCT.....	21	0	1	1.00	1	0	0	0	1	0	0	0	0	0	0	0
.....GTCCATAACACTTAACGCTTTGTGCACC.....	28	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0
.....TCTTGCAGGGCTGTAGGCT.....	19	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0
.....GTCTACAGTCGCTGCGATTCCGGGCAG.....	27	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0
.....TGCTGTCTTGCAGGGCTGTA.....	20	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0
.....CTACAGTCGCTGCGATTCCGGGC.....	23	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0
.....GTTGAAATGATGCAAGATGAGAGGCC.....	26	0	1	1.00	1	0	0	1	0	0	0	0	0	0	0	0
.....AGTCGCTGCGATTCCGGGCAGTT.....	23	0	1	1.00	1	0	0	1	0	0	0	0	0	0	0	0
.....CCTAACTGCTGTCTTGCAGGGCTGTAG.....	27	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0
.....GTCCATAACACTTAACGCTT.....	20	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0
.....TGCGATTCCGGGCAGTTGAAATGATG.....	26	0	1	1.00	1	0	0	0	0	0	0	1	0	0	0	0
.....TAGTCTACAGTCGCTGCGATTCCGGGC.....	27	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0
.....AGGGCTGTAGGCTTC.....	15	0	1	1.00	1	0	0	0	0	1	0	0	0	0	0	0
.....TTGGATTTGCGCCGATCGGC.....	20	0	1	1.00	1	0	0	1	0	0	0	0	0	0	0	0
.....TTCCGGGCAGTTGAAATGATGC.....	22	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0
.....ACAGTCGCTGCGATTCCGGGCAGT.....	24	0	1	1.00	1	0	0	0	0	1	0	0	0	0	0	0
.....GCAAGATGAGAGGCCCAGTCCAT.....	23	0	1	1.00	1	0	0	1	0	0	0	0	0	0	0	0
.....TGCAGGGCTGTAGGCTTCGG.....	20	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0
.....AGATGAGAGGCCCAGTCCA.....	19	0	1	1.00	1	0	0	1	0	0	0	0	0	0	0	0
.....AGTCGCTGCGATTCCGGGCAGT.....	22	0	1	1.00	1	0	0	0	0	0	0	1	0	0	0	0
.....ATTTAGTCTACAGTCGCTG.....	19	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0
.....AATTTAGTCTACAGTCGCTGC.....	21	0	1	1.00	1	0	0	1	0	0	0	0	0	0	0	0
.....AGTCGCTGCGATTCCGGGCA.....	20	0	1	1.00	1	0	0	1	0	0	0	0	0	0	0	0
.....CTTGAATCTGCCTAACTGC.....	19	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0
.....TCTGCCTAACTGCTGTCT.....	18	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0
.....TGTCTTGCAGGGCTGTAGGCT.....	21	0	1	1.00	1	0	1	0	0	0	0	0	0	0	0	0
.....TTGGATTTGCGCCGATCGGCTTGAATC.....	27	0	1	1.00	1	0	0	0	0	1	0	0	0	0	0	0
.....ATAACACTTAACGCTTTGTGCACCGTAC.....	28	0	1	1.00	1	0	0	1	0	0	0	0	0	0	0	0
.....CAGTCGCTGCGATTCCGGGC.....	20	0	1	1.00	1	0	0	0	1	0	0	0	0	0	0	0
.....TCCGGGCAGTTGAAATGATGC.....	21	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0
.....GCCGATCGGCTTGAATCTGC.....	20	0	1	1.00	1	0	0	0	0	0	1	0	0	0	0	0
.....AGATGAGAGGCCCAGTCCAT.....	20	0	1	1.00	1	0	0	1	0	0	0	0	0	0	0	0
.....CTTGCAGGGCTGTAGGCTTC.....	20	0	1	1.00	1	0	1	0	0	0	0	0	0	0	0	0
...AGCTAGAAGAGATAAGTCAACAGATTG.....	27	0	1	1.00	1	0	0	0	1	0	0	0	0	0	0	0
.....TTGGATTTGCGCCGATCGGCC.....	21	1	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0
.....TTGGATTTGCGCCGATCGGCTT.....	22	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0
.....GTCCATAACACTTAACGCTTTGT.....	23	0	1	1.00	1	0	0	0	0	0	1	0	0	0	0	0
.....ATTGGATTTGCGCCGATCGGCT.....	22	0	1	1.00	1	0	0	0	1	0	0	0	0	0	0	0
.....GTCAACAGATTGGATTTGCGCCGATC.....	26	0	1	1.00	1	0	0	1	0	0	0	0	0	0	0	0
.....GTCTACAGTCGCTGCGAT.....	18	0	1	1.00	1	0	0	0	0	0	0	0	0	0	1	0
.....TCTACAGTCGCTGCGATTCCGGGCAG.....	26	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0
.....ATTCCGGGCAGTTGAAAT.....	18	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0
.....AAGTCAACAGATTGGATTTGC.....	21	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0
.....GTCCATAACACTTAACGCT.....	19	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0
.....ACAGATTGGATTTGCGCCGAT.....	21	0	1	1.00	1	0	0	1	0	0	0	0	0	0	0	0
.....TTAGTCTACAGTCGCTGC.....	18	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0
.....TTTGCGCCGATCGGCTTGAATCTGCC.....	26	0	1	1.00	1	0	0	0	0	0	0	1	0	0	0	0
.....TCCGGGCAGTTGAAATGATGCAAGATG.....	27	0	1	1.00	1	0	0	0	0	0	0	0	0	1	0	0
.....CAAAATTTAGTCTACAGTCGCTG.....	23	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0
.....CAAAATTTAGTCTACAGTCGCTGC.....	24	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0
.....AGTCCATAACACTTAACGCTTTGTGCACC.....	29	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0
.....TAACACTTAACGCTTTGTGCACCGTACA.....	28	0	1	1.00	1	0	0	0	0	0	1	0	0	0	0	0
.....GCTGTCTTGCAGGGCTGTAGGC.....	22	0	1	1.00	1	0	0	1	0	0	0	0	0	0	0	0
.....ATAACACTTAACGCTTTGT.....	19	0	1	1.00	1	0	0	1	0	0	0	0	0	0	0	0

Anti-sense strand reads

GTGTCGATCTTCTCTATTCAGTTGTCTAACCTAAACGCGGCTAGCCGAACTTAGACGGATTGACGACAGAACGTCCCGACATCCGAAGCCAGGTTTTAAATCAGATGTCAGCGACGCTAAGGCCCGTCAACTTTACTACGTTCTACTCTCCGGGTCAGGTATTGTGAATTGCGAAACACGTGGCATGTTAAGTCA **********...((((((((...(((((((((((((((((.....)))))))))))).))))))).....)))))))).....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M023 head	M024 male body	SRR553486 Makindu_3 day-old ovaries	SRR618934 dsim w501 ovaries	SRR553488 RT_0-2 hours eggs
.....AGATGTCAGCGACGCTAAGGC.....	21	0	1	3.00	3	3	0	0	0	0
.....GATGTCAGCGACGCTAAGGCCC.....	22	0	1	1.00	1	1	0	0	0	0
.....ATGTCAGCGACGCTAAGGCCC.....	21	0	1	1.00	1	1	0	0	0	0
.....TCCGACATCCGAAGCCAGGTTT.....	22	1	1	1.00	1	1	0	0	0	0
.....CGGGTCAGGTATTGTGAATT.....	20	0	1	1.00	1	0	0	1	0	0
.....GCCAGGTTTTAAATCAGATGT.....	21	0	1	1.00	1	0	1	0	0	0

Show Alignment With Reads

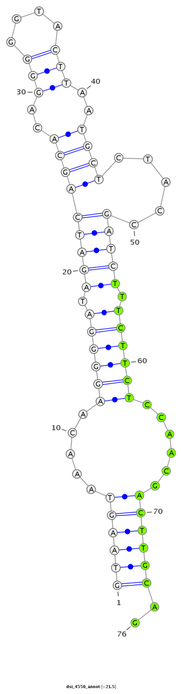
Re-alignment of all predicted orthologs

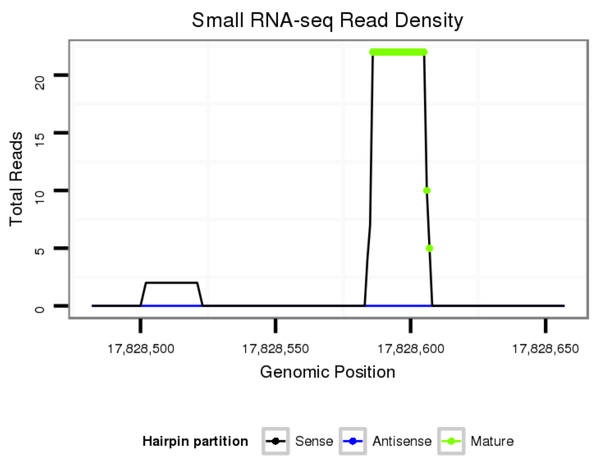
Species	Coordinate	ID	Alignment
droSim2	2l:2946894-2947088 +	dsi_32463	CACAGCTAGA--AGAGATAAGT-----CAACA------GAT--TGGATTTGCGC----CGATCGG----CT---TGAATCT--GCC--TAACTGCTGTCTTGCAGGGC-T--GTAGGC---TTCGGTCCAAA---ATTT-AGTCTACAGTCGCTGCGATTCCG-GGCAGTTGAAA-TG---ATGCAA-GATGAGAG---GCCCA---GTCCATAACACTTAACGCTT--TGTGCACC-GT-----ACAATT-CA----------GT
droSec2	scaffold_5:1224952-1225146 +	dse_1854	CACAGCTAGA--AGAGATAAGT-----CAACA------GAT--TGGATTTGCGT----CGATCGG----CT---TGAATCT--GCC--TAACTGCTGTCTTGCAGGGC-T--GTAGGC---TTCGGTCCAAA---ATTT-AGTCTACAGTCACTGCGATTCCG-GGCAGTTGAAA-TG---ATGCAA-GATGAGAG---GCCCA---GTCCATAACACTTAACGCTT--TGTGCACC-GT-----ACAATT-CA----------GT
dm3	Chr2L:3067709-3067903 +	dme_436	CACAGCTAGA--AGAGATAAGT-----TAACA------GAT--TGGATTTGCGT----CGATCGG----AT---TGAATCT--GCC--TAACTGCTGTCTTGCAGGGC-T--GTAGGC---TTCGGTCCAAA---ATTA-AGTCTACAGTCTCTGCGATTCCG-GGCAGTTGAAA-TG---ATGCAA-GATGAGAG---GCTCA---GTCCATAACACTTAACGCTT--TGTGCACC-GT-----ACAATT-TA----------GT
droEre2	scaffold_4929:3115452-3115635 +	der_1527	CACAGCTAGA--AGAGAT----------------GGGATTGCGT----CAATCGG----AT---TGAATCT--GCC--TAACTGCTGTCTTGCAGGGC-T--GTAGGC---TTCGGTCCAAA---ATTT-AGTCTACAGTCGCTGCGATTCCG-GGCAGTTGAAA-GG---ATGCAA-GATGAGAG---GCCCA---GTCCATGACACTTAACGCTT--TGTGCACC-GT-----ACATTTCA----------GT
droYak3	2L:3063708-3063893 +	dya_1801	CACAGCTAGA--AGAGAT----------------GGGATCGGCGT----CGATCGG----AT---TAAGTCT--GCC--TAACTGCTGTCTTGCAGGGC-T--GTAGGC---TTTGGTCCAAA---ATTT-AGTCTACAGTCGCTGCGATTCCG-GGCAGTTGAAA-TG---ATGCAA-GATGAAAGAGACGCCGG---GTCCATAACACTTAACGCTT--TGTGCACC-GT-----ACAATT-CA----------GT
droEug1	scf7180000409554:3024267-3024462 -		CACAGCTAAA--AGAGATAAGT-----CAACA------GGT--GGGATTGGAGC----GGATCGG----AT---TGAATCT--GAT--TAACTGCTGTCTTGCAGCGC-T--GTAGAC---TGTGGTCCAAA---ATTT-AGTCTATAGTCGCTGCGATTCTG-GGCAGTTGTAA-GG---ATAAAAAGATGAGAG---GCCCA---AACCATCACACTTAACGCTT--TGTGCACC-AT-----ACAGAT-TA----------GT
droBia1	scf7180000302188:2122002-2122202 +		CACAGCTAGA--GGAGATAAGT-----AAACAGAT--GGGAT--TGGACTGGAGT----GGATCGG----AT---TGCATGG--GCC--TAACTGCTGTCTTGCAGGGC-C--GTAGAC---TTTGGTCCAAA---ATTT-AGTCTACGTCGCTGCGATTCCG-GGCAGTTGAAA-GG---ATGCAA-GACGAGAG---AGTCA---GTCCACTAGACTTAACGCTT--TGTGCACC-GT-----ACAGTTCCA----------GT
droTak1	scf7180000415438:753079-753224 -		CACAG-----------------GAGT----GGATCGG----AT---GGCATCT--GCC--TAACTGCTGTCTTGCAGGGC-C--GTGGAC---TTTGGTCCAAA---ATTT-AGTCTATGTCGCTGCGATTCCG-GGCAGTTGAAA-GG---ATGGCA-AATGAGAG---ACCCA---------ACCTAACGCTT--TGTGCACC-GT------------------------
droEle1	scf7180000491046:1758544-1758740 +		CACAGTTAGA--AGAGATAAGT-----CAACG------GAT--GGGATTGGAGT----GGATCGG----AT---TGCGTCT--GCC--TAACTGCGTCTTGCAGCAC-T--GTAGTC---TTTGGTCCAAA---ATTT-AGTCTACAGCCGCTGCGATTCTG-GGCAGTTGAAA-GG---ATGCAATGATGACAG---GCCCA---GACCATCACACTTAACGCTT--TGTGCACC-GT-----ACACTT-CAG----------TT
droRho1	scf7180000780028:158223-158417 +		CACAGCTAGA--GGAGATAAGT-----CAACG------GAT--GGGATTGGAAT----GGATTGG----AT---TGGATCT--GCC--TAACTGCGTCTTGCAGCGC-T--GTATTC---TTTGGTCCAAA---ATTT-AGTCTATAGTCGCTACGATTCTG-GGCAGTTGAAA-TG---ATCCAA-GACGAGAG---GCCCA---ATCCATCACACTTAACGCTT--TGTGCACC-GT-----ACAGTT-CA----------GT
droFic1	scf7180000453924:1051725-1051931 +		CACAGCTAGA--AGAGATAG-----------GAT--GGGATTGGAGTGGATCGATCG----CT---GGGATCT--GCC--TAACTGCGTCTTGCAGCGC-C--GTAGAC---TTTGGTCCAAA---ATTT-AGCCTACGGCGCTACGATTCCG-GGCAGTTGAAA-GG---ATCCAG-GATGGGAGT-GGCCCA---ACCCTTCACACTTAACGCTT--TGTGCACC-GT-----ACAGTT-CAGTAGTTCAGTACAGT
droKik1	scf7180000302246:274520-274657 +		GCCAGG-----------------GAT--GGGATTGGAGTGGATCGATCG----CT---GGGATCT--GCC--TAACTGCGTCTTGCAGCGCCT--GTGGAC---TGTGGTCCAAA---TTA-AGTCTACAGTCGCTGCGATTCCG-GGCAGTTGAGT-GGCCGATGGTG---------------GATCGCACTTAACGCTTCGTGTGCACC-GCAGAGAAGAGTT-CA----------GT
droAna3	scaffold_12916:9588076-9588233 -	dan_4042	CACAGCTTTA--AGGT-----------GAT--GGGATTGGAGT----GGATCGG----TT---T--ATCT--CCCATTAACTGCTGTCTTGCAGAGTCT--GTGGAC---G-TGGTCCAAA---T-T-TGTCTACAGCCACTGCGATTCCG-GGCAGTTGAAAGTG---AT--AA-TACGGACT---CCCCAAAAACACATCACATCT-GCGCTT--TGTGCACC-GC-----AG-----------
droBip1	scf7180000396580:1442851-1443009 +		CACAGCTTTA--AGGT-----------GAT--GGGATTGGAGT----GGATCGG----CA-T-T---TCT--CCCATTAACTGCGTCTTGCAGCGTCT--GTGGAC---G-TGGTCCAAA---TTT-TGTCTACAGCCGCTGCGATTCCGGGGCAGTTGCAAGTG---AAACCA-TACGGATT---CCTCAA--ATACATCACATCT-GCGCTT--TGTGCACC-GC-----AG-----------
dp5	Unknown_singleton_3046:27-210 +	dps_31	CACAGCAACA--AAAGATAAAA-----CTA--ATCTCCGAT--GGGATG-----------------TTCCTTAAAC-----GT--TAACTGCGTCTTGCAGCGCCT--GTGGACG--ATAGGTCCAAA---ATTTCAGTCTACAGACGCTGCGATTCCG-GGCAGTTGAGT-GG---AT----------GGGAT---CCACCT--TTAAATCACACTTAAAGCTA--TGTGCACA-GA---GTACAGT--A----------
droPer2	scaffold_1:8612772-8612955 -	dpe_229	CACAGCAACA--AAAGATAAAA-----CTA--ATCTCCGAT--GGGATG-----------------TTCCTTAAAC-----GT--TAACTGCGTCTTGCAGCGCCT--GTGGACG--ATAGGTCCAAA---ATTTCAGTCTACAGACGCTGCGATTCCG-GGCAGTTGAGT-GG---AT----------GGGAT---CCACCT--TTAAATCACACTTAAAGCTA--TGTGCACA-GA---GTACAGT--A----------
droWil2	scf2_1100000004945:407277-407435 +	dwi_5419	CACAGTTAAATACATGATATAT----CCTCCA-AATGTGAAT--TAGATATAAGT----T-ATATC----CA---GTGATCG--ATT--TAATTGCCGTCTTGCAGGGTCTTTGTAAAGAATCCAGGTCCAAATTT-AAAT-TCTTTATAGATCCTGCGATTCTG-GGCAATTGAAT-GA---C----------A-----------------A-

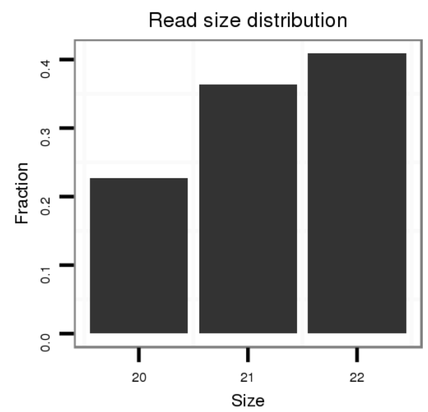
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dsi_4550	**3r:17828532-17828607 +**	**candidate**	**Mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

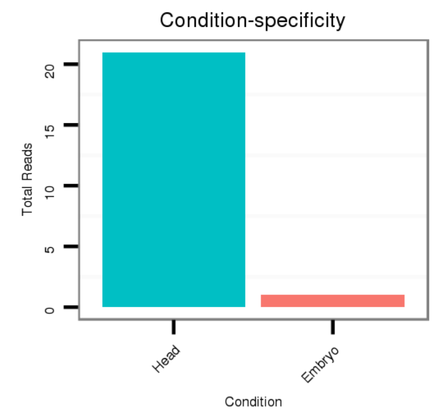
Legend: mature star mismatch in alignment mismatch in read

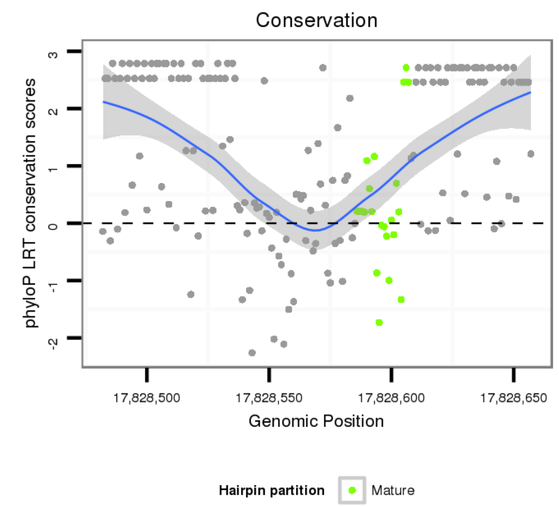
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [3r_17828532_17828607_+]; CDS [3r_17828608_17828843_+]; CDS [3r_17828181_17828531_+]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

TGCCACGCTCCAGCTGGACGACTATAATGTGCAGGCACTGACGCCACAGAGTAAGTAAACAAGGGGATAGATCAGCACAGGGGGTACTTAATGCTCTACCGATCTTTCTTCTCCAACGACTTGCAGGCCACCACTCCACCGTGTTCAATACCATGTCCAACGTTCAGGTCGGCGGC **********(((((.....(((((.(((((((((..(((....)))..))))).....)))))).)))))).....)))))..**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M023 head	M025 embryo	SRR618934 dsim w501 ovaries	M024 male body
.....TTTCTTCTCCAACGACTTGCAG.....	22	0	1	5.00	5	4	1	0	0
.....TTTCTTCTCCAACGACTTGCA.....	21	0	1	5.00	5	5	0	0	0
.....TTTCTTCTCCAACGACTTGC.....	20	0	1	5.00	5	5	0	0	0
.....TCTTTCTTCTCCAACGACTTGC.....	22	0	1	4.00	4	4	0	0	0
.....CTTTCTTCTCCAACGACTTGC.....	21	0	1	3.00	3	3	0	0	0
.....ACTATAATGTGCAGGCACTG.....	20	0	1	1.00	1	1	0	0	0
.....CTTTCTTCTCCAACGACTTGT.....	21	1	1	1.00	1	1	0	0	0
.....GACTATAATGTGCAGGCACTGA.....	22	0	1	1.00	1	0	1	0	0

Anti-sense strand reads

ACGGTGCGAGGTCGACCTGCTGATATTACACGTCCGTGACTGCGGTGTCTCATTCATTTGTTCCCCTATCTAGTCGTGTCCCCCATGAATTACGAGATGGCTAGAAAGAAGAGGTTGCTGAACGTCCGGTGGTGAGGTGGCACAAGTTATGGTACAGGTTGCAAGTCCAGCCGCCG **********(((((.....(((((.(((((((((..(((....)))..))))).....)))))).)))))).....)))))..**********	Read size	# Mismatch	Hit Count	Total Norm	Total	SRR553488 RT_0-2 hours eggs	SRR618934 dsim w501 ovaries	M024 male body	SRR553487 NRT_0-2 hours eggs	SRR553485 Chicharo_3 day-old ovaries	SRR553486 Makindu_3 day-old ovaries
.....AAATTACGAGATGGCT.....	16	1	2	0.50	1	1	0	0	0	0	0

Show Alignment With Reads

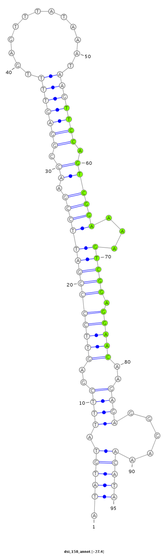
Re-alignment of all predicted orthologs

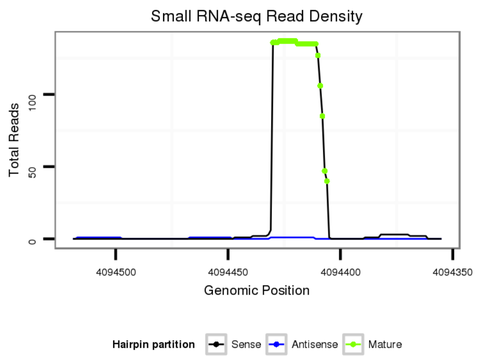
Species	Coordinate	ID	Alignment
droSim2	3r:17828482-17828657 +	dsi_4550	TGCCACGCTCCAGCTGGACGACTATAATGTGCAGGCACTGACGCCACAGAGTAAGTAAACAAG----------GGGATAGATCAGCA-CAGGGG----------GT-ACTTAATGC---------T-CTA----CCGATCTTTCTTCT---CC-----AA----------C--G----------AC--TTGCAGGCCACCACTCCACCGTGTTCAATACCATGTCCAACGTTCAGGTCGGCGGC
droSec2	scaffold_0:18659430-18659605 +		TGCCACGCTCCAGCTGGACGACTATAATGTGCAGGCACTGACGCCACAGAGTAAGTAAACAAG----------GGGATAGATCAGCA-CAGGGG----------GT-AGCTAATGC---------T-CTA----CCGATCTTTCTTCT---CC-----AA----------C--G----------GC--TTGCAGGCCACCACTCCACCGTGTTCAATACCATGTCCAACGTTCAGGTCGGCGGC
dm3	chr3R:18305126-18305301 +		TGCCACGCTCCAACTGGACGACTACAATGTGCAGGCACTGACGCCACAGAGTAAGTAAACAAG----------GGGATAGATCAGCA-CAGGGG----------GT-ATCTAATGC---------T-CTA----CCGAACTTTCTTCT---CC-----AA----------C--G----------AC--TTGCAGGCCACCACTCCACCGTGTTCAATACCATGTCCAACGTTCAGGTCGGCGGC
droEre2	scaffold_4820:9772219-9772390 -		TGCCACGCTCCAGCTGGACGACTACAATGTGCAGGCACTGACGCCGCAGAGTAAGTGAGCCG----------GGGATAGATCAGCG-CAGGGG----------GT-AGCTAATGC---------T-CTA----CCGATC----TTCT---CC-----AA----------T--G----------AC--TTTCAGGCCACCACTCCACCGTGTTCAATACCATGTCCAACGTTCAGGTCGGCGGC
droYak3	3R:19150546-19150721 +		TGCCACGCTCCAGCTGGACGACTACAATGTGCAGGCACTGACGCCACAGAGTAAGTAGACAAG----------GGGATAGTTCAGCG-CAGGGG----------GT-ACCTAATGC---------T-CTA----CCGATC----TTCTTCTCCA----AA----------C--G----------AC--TTTCAGGCCACCACTCCACCGTGTTCAATACCATGTCCAACGTTCAGGTCGGCGGC
droEug1	scf7180000409768:428647-428819 +		TGCAACGCTTCAACTGGACGACTACAATGTACAGGCACTGACGCCGCAGAGTAAGTGCATAAG----------GGGATAGCCTTTTA-ACGGGG----------GTAACCTAATAC---------T-CTT----TCGATC----TTCT---TG----AA----------C--G----------AC--TTGCAGGCCATCATTCGACCGTGTTCAATACCATGTCAAATGTTCAGGTCGGCGGC
droBia1	scf7180000302402:5425651-5425828 -		CGCAACGCTGCAGCTGGACGACTACAATGTGCAGGCGCTCACGCCGCAGAGTAAGTGGACG-GGGG---------TTAGACACAGCCTTGGT-GCGGGG----------GT-ACTTAACTC---------TGCTT----TCGATC----TTCT---TC-----CC----------C--A----------C--TGGCAGGCCATCACTCGACCGTGTTCAATACCATGTCCAACGTTCAGGTCGGCGGC
droTak1	scf7180000415711:718929-719106 -		CGCCACGCTCCAGCTGGACGACTACAATGTGCAGGCACTCACGCCGCAGAGTAAGTGGATAAG----------GGGATAGTTTCGT-TTAGGG-GTAGG---------GT-GCCTAATTATC--------T-CTT----CCAATG----TTTT---GT-----AA----------C--A----------AT--TTTCAGGCCACCACTCGACCGTGTTCAATACCATGTCCAACGTTCAGGTCGGCGGC
droEle1	scf7180000491280:4472480-4472653 -		TGCCACGCTCCAGCTGGACGACTACAATGTGCAGGCACTCACGCCGCAGAGTAAGTGGATGT----------GGGATGGGCTATCATTAGGGG----------GT-ATCTAATGG---------G-ATT----TCGATG----TTCT---TC-----AA----------C--G----------ACTCTTGCAGGCCACCATTCGACCGTGTTCAATACCATGTCCAACGTTCAGGTCGGCGGC
droRho1	scf7180000779677:159161-159237 +		TGCCACGCTCCAGCTGGACGACTACAATGTGCAGGCACTCACGCCGCAGAGTAAGTGGGTGGG----------ATGGGGGATGGGTC----------------------

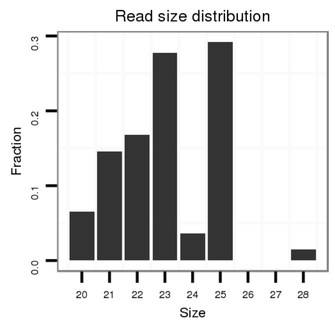
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dsi_150	**3l:4094405-4094469 -**	**candidate**	**Canonical miRNA**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

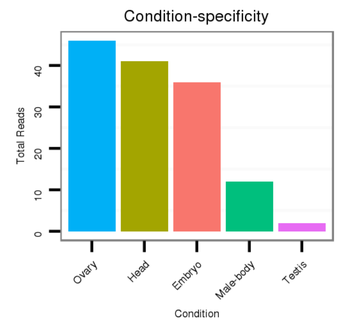
Legend: mature star mismatch in alignment mismatch in read

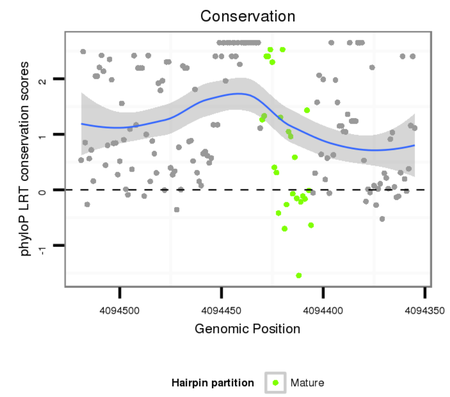
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [3l_4094133_4094770_-]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

AAGCCAAAAGTGTCTGCCCCCTAGAAATGGGGGATATATGTATTTCGAGTTCCCCGATTCCGAACCGGAGTTTTGAGTTTATAAATAAGTTCCAGTCGGAAAAGTCGGAGGAACAAGAGAGGGAAACATACATTATTTTCACGTACTTCTCTCTGCCTCTCTCGC	Read size	# Mismatch	Hit Count	Total Norm	Total	M023 head	M025 embryo	SRR553485 Chicharo_3 day-old ovaries	M024 male body	SRR553487 RT_0-2 hours eggs	SRR553488 RT_0-2 hours eggs	SRR553486 Makindu_3 day-old ovaries	GSM343915 embryo	O002 Head	SRR618934 dsim w501 ovaries	M053 female body	O001 Testis	SRR902009 testis
....TTCCAGTCGGAAAAGTCGGAGGAAC....	25	0	1	39.00	39	8	17	5	5	1	1	2	0	0	0	0	0	0
....TTCCAGTCGGAAAAGTCGGAGGA....	23	0	1	38.00	38	7	10	10	2	5	0	2	1	1	0	0	0	0
....TTCCAGTCGGAAAAGTCGGAGG....	22	0	1	21.00	21	5	3	4	1	1	4	0	0	1	0	0	1	1
....TTCCAGTCGGAAAAGTCGGAG....	21	0	1	19.00	19	8	1	1	2	0	4	1	1	1	0	0	0	0
....TTCCAGTCGGAAAAGTCGGAGGAACC....	26	1	1	10.00	10	3	5	1	1	0	0	0	0	0	0	0	0	0
....TTCCAGTCGGAAAAGTCGGA....	20	0	1	8.00	8	6	0	0	1	0	0	1	0	0	0	0	0	0
....TTCCAGTCGGAAAAGTCGGAGGAA....	24	0	1	5.00	5	1	1	0	0	1	0	0	0	0	2	0	0	0
....TTCCAGTCGGAAAAGTCGGAGGA....	24	1	1	4.00	4	0	1	0	3	0	0	0	0	0	0	0	0	0
....GTTCCAGTCGGAAAAGTCGGAG....	22	0	1	2.00	2	1	0	0	0	0	0	0	0	0	1	0	0	0
....TTCACGTACTTCTCTCTGCCT....	21	0	1	2.00	2	0	1	0	1	0	0	0	0	0	0	0	0	0
....GTTCCAGTCGGAAAAGTCGGAGGAA....	25	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0	0	0
....ATAAATAAGTTCCAGTCGGA....	20	0	1	1.00	1	0	0	0	0	0	0	0	1	0	0	0	0	0
....TTGAGTTTATAAATAAGTTCCAGTCGGA....	28	0	1	1.00	1	0	0	0	1	0	0	0	0	0	0	0	0	0
....TTCCAGTCGGAAAAGTCGGAGGAAA....	25	1	1	1.00	1	0	0	0	0	0	0	1	0	0	0	0	0	0
....CAGTCGGAAAAGTCGGAGGAA....	21	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0	0	0
....TTCCAGTCGGAAAAGTCGGAC....	21	1	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0	0	0
....CATTATTTTCACGTACTTCT....	20	0	1	1.00	1	0	0	0	1	0	0	0	0	0	0	0	0	0
....GTTCCAGTCGGAAAAGTCGGG....	21	1	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0	0	0
....AGTTCCAGTCGGAAAAGTCGGAGGAACA....	28	0	1	1.00	1	0	1	0	0	0	0	0	0	0	0	0	0	0

Anti-sense strand reads

TTCGGTTTTCACAGACGGGGGATCTTTACCCCCTATATACATAAAGCTCAAGGGGCTAAGGCTTGGCCTCAAAACTCAAATATTTATTCAAGGTCAGCCTTTTCAGCCTCCTTGTTCTCTCCCTTTGTATGTAATAAAAGTGCATGAAGAGAGACGGAGAGAGCG	Read size	# Mismatch	Hit Count	Total Norm	Total	M025 embryo	SRR618934 dsim w501 ovaries	SRR902009 testis	SRR553488 RT_0-2 hours eggs	M024 male body	GSM343915 embryo
..CGGTTTTCACAGACGGGGGA....	20	0	1	1.00	1	0	0	1	0	0	0
....CAAGGTCAGCCTTTTCAGCC....	20	0	1	1.00	1	1	0	0	0	0	0
....GGGCTAAGGCTTGGCCTCA....	19	0	1	1.00	1	0	1	0	0	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droSim2	3l:4094355-4094519 -	dsi_150	AAGCCAA---AAGTGTCTGCCCCC-TAG-AAATGGGGG-ATA-TAT----------GT---ATTTCGAGTT----------CC----------CCGATTCCG--AACCGGAGTTTTGAGTTTATAAATAAGTT----------CCAGTC-GG-AAAA------GTCGGAGGAAC-AA--GAGAGGG-AAACATACATTATTTTCAC----------GTACTTCTCTCTG-CCTC--TCT
droSec2	scaffold_2:4126552-4126718 -	dse_1840	AAGCCAA---AAGTGTCTGCCCCC-TAG-AAATGGGGG-ATA-TAT----------GT---ATTTCGAGTT----------CC----------CCGATTCCG--AACCGGAGTTTTGAGTTTATAAATAAGTT----------CCAGCC-GG-AAAA------GTCGGAGGAAC-AAGAGAGAGGG-AAACATACATTATTTTCAC----------GTACTTCTCTG-CCTC--TCT
dm3	chr3L:4134045-4134211 -	dme_412	AAGCCAA---AAGTGTCTGCCCCC-TAG-AAATGGGGG-ATA-TAT----------GT---ATTTCGAGTT----------CC----------CCGATTCCG--AACCGGAGTTTTGAGTTTATAAATAAGTT----------CCAGTC-GG-AAAA------GTCGTTGGAAC-AAGAGAGAGGG-AAACATACATTATTTTCC----------GTACTTCTCACTG-CTCC--TCT
droEre2	scaffold_4784:6843077-6843244 -	der_1517	AAGCCAA---AAGTGTCTGCCCCC-TAG-AAATGGGGGCATA-TAT----------GT---ATTTCGAGTT----------CC----------CCGATTCCG--AACAGGAGTTTTGAGTTTATAAATAAGTT----------CCAGTC-GG-AAAA------GTCGAGGAAC-AAGCGAGAGGA-AAACATACATTATTTTCC----------GTACTTCTCTCTG-TCTC--TCT
droYak3	3L:4705301-4705469 -	dya_1792	AAGCCAA---AAGTGTCTGCCCCC-TAG-AAATGGGTCATA-TAT----------GT---ATTTCGAGTT----------CC----------CCCGATTCCG--AACCGGAGTTTTGAGTTTATAAATAAGTT----------CCAGTC-GG-AAAA------GTCGGTGGAAC-AAGCGAGAGGG-AAACATACATTATTTTCC----------GTACTTCTCTCTG-TCTC--TCT
droEug1	scf7180000409466:1901004-1901181 -		AAGCCACG---AAGTGTCTGCCCCC-TCG-AAATGGGTCGAA-TTTCGCTGCCTGCCGTGT---GTTTCGCGTT----------CC----------CCCGATTCCG--ATCCGGAGTTTTGAGTTTATAAATAAGTT----------CCAGTC-TG-AAAA------C---AAGGAAG-AAGAGAGAAGG-AAACATACATTATTTTCC----------GTAATTTTCTCTG-T--C--TCT
droBia1	scf7180000302428:833729-833895 -		AAGCCACG---AAGTGTCTCCCCC-TCA-AAATGGGTCGAT-T---------------T---ATTTCGAGTT----------CC----------CCCGATTCCG--ATCCGGAGTTTTGAGTTTATAAATAAGTT----------CCAGTCCTG-AAGCCGAACGACCAGAC-GAGC-CAGCGAGAGGG-ACACATCCGTTATTTTCC----------GTAATTTCCTCTG-T--C--TCT
droTak1	scf7180000415778:22383-22529 +		AAGCCACG---AAGTGTCTCCCCC-TCG-AAATGGGTCGAT-T---------------T---ATTTCGAGTT----------CC----------CCCGATTCCG--ATCCGGAGTTTTGAGTTTATAAATAAGTT------C------TCCAGTC-CCCG--------CCCAGAAT--C--GA--CAA-AC----ACAT---TTTCC----------GTAATTTCTCTGTATTCTC--TCT
droEle1	scf7180000491249:4988011-4988143 -		-------T---CGTCTGCCCCC-TCG-AAATGGGTCGAT-T---------------T---GTTTCGTGTT----------CC----------CCCGAT-----T-TCGGAGTTTTGAGTTTATAAATAAGTT----------CCAGTC-TG-ACA-------TAAAA-AAGCGAGAAGG-AAACATACAT---TTTCC----------CTAATTTCTCTATG-T--C--TCT
droRho1	scf7180000779198:19085-19216 +		-------T---CGTCTGCCCCC-TCG-AAATGGGTCGAT-T---------------T---GTTTCGCGCT----------CC----------CCC------G--ATCCGGAGTTTTGAGTTTATAAATAAGTT----------CCAGTC-TG-AC-------CAAAA-AAGCGAGAAGG-AAACATACAT---TTTCC----------CTAATTTCTCTATG-C--C--TCT
droFic1	scf7180000454113:1363566-1363707 -		AAGCCACG---AAGTGTCTGCCCCC-TCGAAAACGGGTCGAAAT-AT----------T---T--------T----------CC----------CCG--TCCG--ATTCGGAGTTTTGAGTTTATAAATAAGTT----------CCAGTC-TG-AG-------CAAAC-CGAGAGAAGG-AAACATACAT---TTTCC----------CTAATTTCTCTCTT-T--C--TCT
droKik1	scf7180000302383:514852-515013 -		AAG----T---AAGTGTCTGCCCCCCTCG-AAATGGGCAAA-GA-TTCGC----TGCCGTGT---GTTTCGCGCT----------CC----------CCCCAA-TCCGTCGTCCGGAGTTTTGAGTTTATAAATAAGTT------G-GTGTCTCCAGTA-CCCGCGCA-------CC---ACCACGAGAGGGAGAAGG-AAACC-ACAT---TTTCC----------G-----------T--C--TCT
droAna3	scaffold_13337:14554333-14554483 -		AA-----T---GTGCCTCCCAGT-T-CCGGATGGGACAAAAT-TTTGA----TGCCGTGT---GTTTCGTGTCT----------CC----------CCC-------AACCGAAGTATGAGTTTATAAATAAGTCC------G-ATGTTTCCAC--T--A---------------T--T-GATAAGAA-AA----ACAT---TTTCCGTCCGACGTCGTCGTCGCCGTCCTGTCGTCC--TCT
droBip1	scf7180000396641:755046-755186 +		CAGTCGG---T-----------T---T--ATGGGACAAAAT-TTTGA----TGCCGTGT---GTTTCGTGTCT----------CC----------CCC-------AACCGAAGTATGAGTTTATAAATAAGTCC------G-ATGTTTCCAC--T--A---------------T--T-GATAAGAA-AA----ACAT---TTTCCGTCCGACGTCCCCGTCGACGTCCTGTCGTCC--GCT
dp5	XR_group8:8300080-8300287 -		AA-----T---GTGCCTGCCCCC-CTC-ATATGGGTCAAAAT-TTTTT----TCCCGTGT---GTTCTA----------TGTGCTTGTTGTGCCTTT----------CC----------CCCAAACCCGCTCAACCGGAGTTGAGTTTATAAATAAGTT------G-ATGTTTCCAC--T--A---------------T--T----GGA-AT----ACAT---TTTTCCT----------G-C--TCCCTGCCACCGCCGCCGCTGCTGCTGCTGCTGCTGATGTCGCTCTGCCTCTGCCATCGTAGTCGTCGC
droPer2	scaffold_40:490636-490843 -		AA-----T---GTGCCTGCCCCC-CTC-ATATGGGTCAAAAT-TTTTT----TCCCGTGT---GTTCTA----------TGTGCTTGTTGTGCCTTT----------CC----------CCCAAACCCGCTCAACCGGAGTTGAGTTTATAAATAAGTT------G-ATGTTTCCAC--T--A---------------T--T----GGA-AT----ACAT---TTTTCCT----------G-C--TCCCTGCCACCGCCGCCGCTGCTGCTGCTGCTGCTGATGTCGCTCTGCCTCTGCCATCGTAGTCGTCGC
droWil2	scf2_1100000004762:4227419-4227509 -		GAAGAA---AAGT---------T---T--------T---T---------T-----------T---------T---------T-----------T---------T-AACCGGAGTTTGAGTTTATAAATAAGTT------G-ATGTTTCCAC--T--A---------------T--T----GGA-AAA----CATTATTTTCCGC----------TTCCTCTCTCTCTCC--C--TGC
droVir3	scaffold_13049:1988826-1989022 -		AAGCCAGAAGAAGTGTTGG----TTC-ATATGGGTCAAAAT-TTT-GC----CCCCGTGTGTTTTTTCGAGTTCCT-GCTATGTGCTTGTTGT---TTTGCCCCCGCTAATTCCCCCACCAACCCTCTCTCAA-AACGTCAACCGGAGTTTTGAGTTTATAAATAAAATTCGTTCAAAGTTTCC----T--T----------T--T-AGAGGA-AAAC----AT---TTTTC----------T--------GCTG-CCCC--CGC
droMoj3	scaffold_6654:1847069-1847251 +		AAG----T---AAGTGTCTGGTT--T--G-ATATGGGTCAAAAT-TT-GC----CCCCGTGTGTTTTTTCAAGTTCCTTACAGTGTGGCTGTTGT---TTTGCCAGCGCTAAATCCC----------C------CCT--TACCGGAGTTTTGAGTTTATAAATAAAATTCGTTCAAAGTTTCCAC--T--A---------------T--T----GGAAAA----ACAT---TTTTCT----------CCGTCACCTCAGCCG-CAGC--CAG

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

	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.ptop3	1
crit.uri	0
crit.back	1
rescue.total	1
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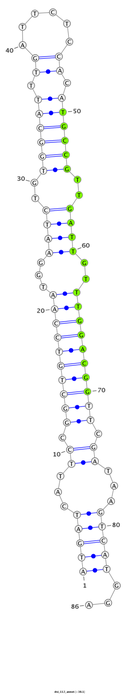
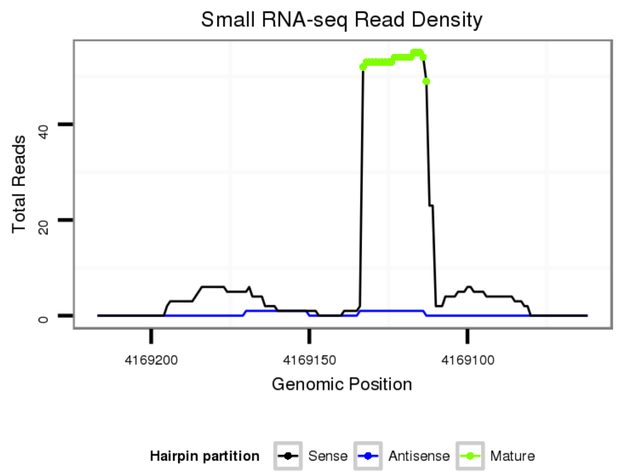
rescue.known	0
rescue.confident	0
rescue.candidate	5

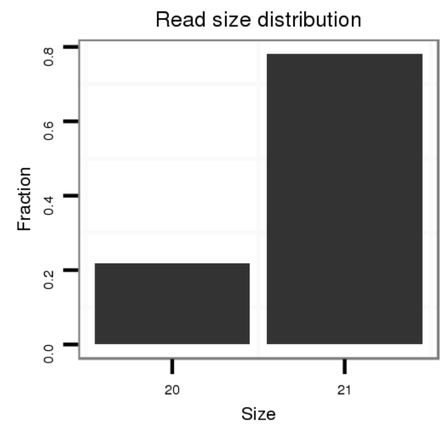
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dsi_112	**3r:4169112-4169167 -**	**candidate**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

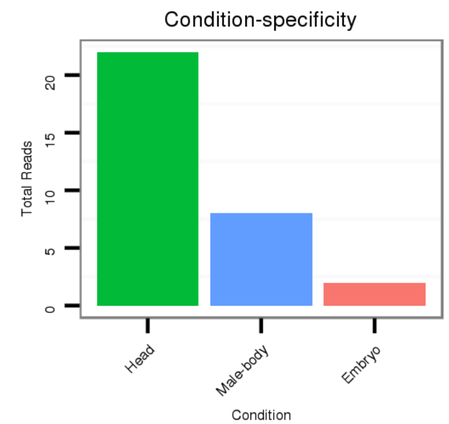
Legend: mature star mismatch in alignment mismatch in read

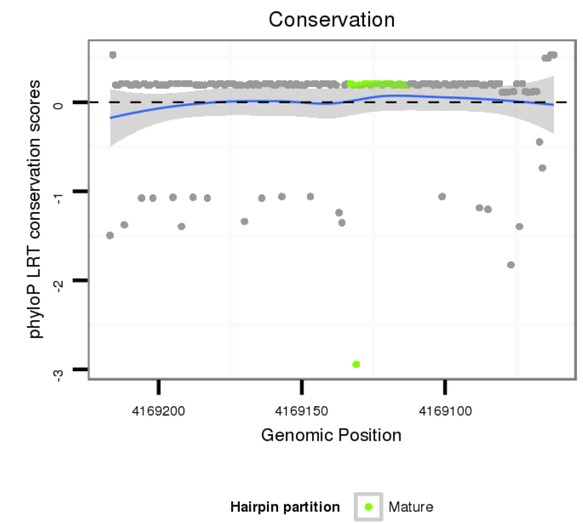
Predicted structure











Show Alternate Folds

Sense Strand Reads

hide 3p reads show mid mismatch reads

CAGCTTAGCTCCACGGACGCCATAAGTATTGGCCCATGATCATTCCGGCTGTCCAATGGAATCTGTGGCATTTGATTCTCCACATGCCGTTGATTGTTTGGACGGTTCGATAAGTCATGGAGATCTTTATCGCTGTAGGCGATAAACGTACGGCAT ********(((((...((.((((((((((...((((..((((((.((.....)).)))))).))))..)))).))))))))))).))...)))))...********	Read size	# Mismatch	Hit Count	Total Norm	Total	M023 head	M024 male body	M025 embryo	SRR553485 Chicharo_3 day-old ovaries	SRR553486 Makindu_3 day-old ovaries	SRR553487 NRT_0-2 hours eggs	O001 Testis	SRR618934 dsim w501 ovaries	M053 female body	SRR902008 ovaries
.....TGCCGTTGATTGTTTGGACGG.....	21	0	1	25.00	25	20	4	1	0	0	0	0	0	0	0
.....TGCCGTTGATTGTTTGGACGGTT.....	23	0	1	20.00	20	15	2	2	0	1	0	0	0	0	0
.....TGCCGTTGATTGTTTGGACG.....	20	0	1	5.00	5	1	4	0	0	0	0	0	0	0	0
.....TAAGTCATGGAGATCTTTATCGCTGTA.....	27	0	1	2.00	2	0	0	0	2	0	0	0	0	0	0
.....TAAGTATTGGCCCATGATCATTCCGGC.....	27	0	1	2.00	2	0	0	0	1	0	1	0	0	0	0
.....ATGCCGTTGATTGTTTGGAC.....	20	0	1	1.00	1	0	0	1	0	0	0	0	0	0	0
.....TGTTTGGACGGTTCGATAAGTCATGGAGA.....	29	0	1	1.00	1	0	0	0	1	0	0	0	0	0	0
.....TGGAGATCTTTATCG.....	15	0	1	1.00	1	0	0	0	0	0	1	0	0	0	0
.....TGCCGTTGATTGTTTGGACA.....	20	1	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....AAGTATTGGCCCATGATC.....	18	0	1	1.00	1	0	0	0	0	0	0	1	0	0	0
.....CCCATGATCATTCCGGCTGTC.....	21	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....TCCACATGCCGTTGATTGTTTGGACGGTT.....	29	0	1	1.00	1	0	0	1	0	0	0	0	0	0	0
.....CCATGATCATTCCGGCTGTCCAAT.....	24	0	1	1.00	1	0	0	0	0	0	0	1	0	0	0
.....GACGGTTCGATAAGTCATG.....	19	0	1	1.00	1	0	0	0	0	0	0	0	1	0	0
.....CTGTCCAATGGAATCTGTGGCA.....	22	0	1	1.00	1	0	0	0	0	1	0	0	0	0	0
.....GCCCATGATCATTCCGGCTGTC.....	22	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....TCATGGAGATCTTTATCGCTG.....	21	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....GCCGTTGATTGTTTGGACGG.....	20	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0

Anti-sense strand reads

GTCGAATCGAGGTGCCTGCGGTATTCATAACCGGGTACTAGTAAGGCCGACAGGTTACCTTAGACACCGTAAACTAAGAGGTGTACGGCAACTAACAAACCTGCCAAGCTATTCAGTACCTCTAGAAATAGCGACATCCGCTATTTGCATGCCGTA ********(((((...((.((((((((((...((((..((((((.((.....)).)))))).))))..)))).))))))))))).))...)))))...********	Read size	# Mismatch	Hit Count	Total Norm	Total	SRR553487 NRT_0-2 hours eggs	SRR553486 Makindu_3 day-ovaries	M023 head	O002 Head	SRR553488 RT_0-2 hours eggs	GSM343915 embryo
.....TACGGCAACTAACAAACCTGC.....	21	0	1	1.00	1	0	0	0	1	0	0
.....CGACAGGTTACCTTAGACAC.....	20	0	1	1.00	1	0	0	1	0	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droSim2	3r:4169062-4169217 -	dsi_112	CAGCTTAGCTCCACGGACGCCATAAGTATTGGCCCATGATCATTCCGGCTGTCCAATGGAATCTGTGGCATTTGATTCTCCACATGCCGTTGATTGTTTGGACGGTTCGATAAGTCATGGAGATCTTTATCGCTGTAGGCGATAA-------ACGTACGGCAT
droSec2	scaffold_6:4347946-4348108 -		CAGCTAAGCTCCACGGACGCCATAAGTATTGGCCCATGATCATTCCGACTGTCCAATGGAATCTGTGGCATTTGATTCTGTGCATGACGTTGATTGTTTGGACGGTTCGATAAGTCATGGAGATCTTTATCGCTGTAGGCTATTACAGAGTGACGTACGGCAT
dm3	chr3R:17143181-17143330 +		AAGCTAAGCTCTACGAACGCCAAAACTATAGGCCTATGATCATTCCGACTGTCTAATGGAGTCTGTGGCACTTGATTCTCCACATGGCGTTGATTGTTTGGACGGTTCGATAAGTCGTGGAGATCTTTAGCGATGTA-----TTACAAAG--------TGCAT
droEle1	scf7180000490996:52187-52194 +		TA----------TGGCAT

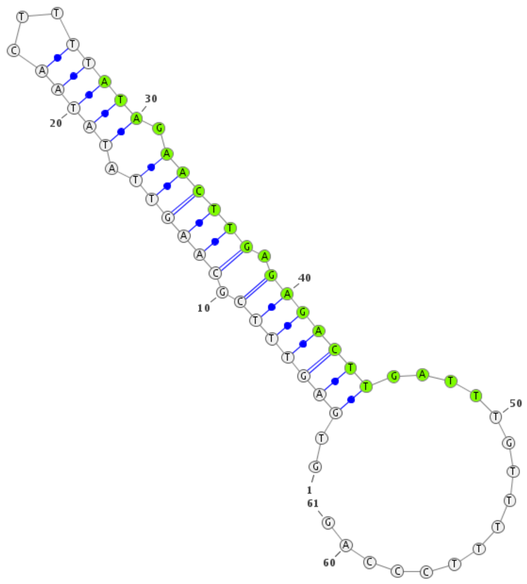
Generated: 06/08/2015 at 08:03 PM

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

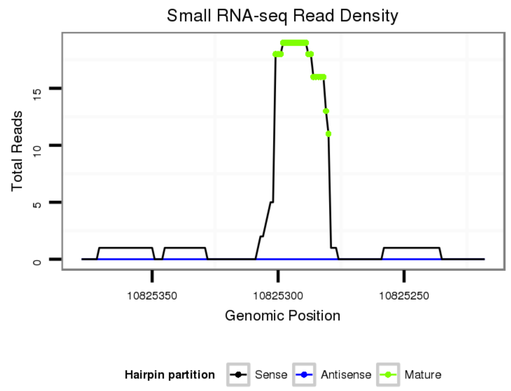
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dsi_20162	**2r:10825268-10825328 -**	**candidate**	**3p_tailed_mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

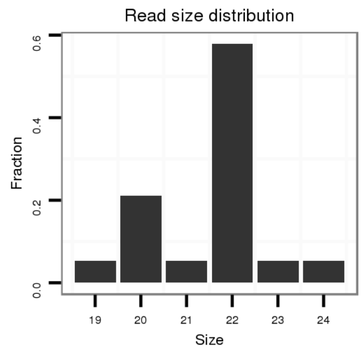
Legend: mature star mismatch in alignment mismatch in read

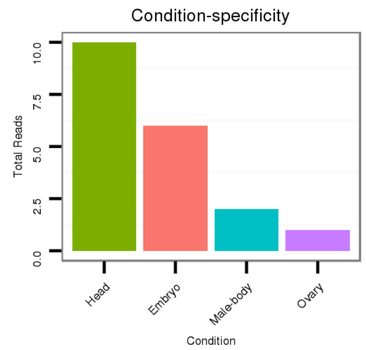
Predicted structure

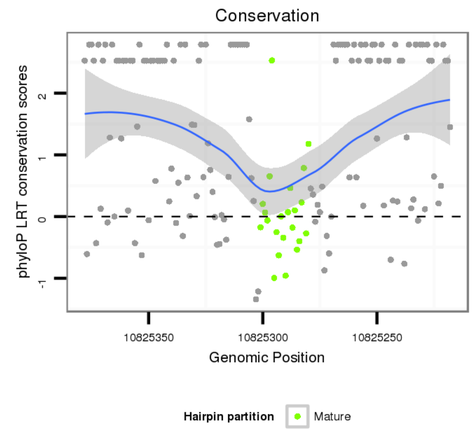


dsi_20162_annot [-15.1]









Show Alternate Folds

Flybase annnotation

intron [2r_10825268_10825328_-]; CDS [2r_10825329_10825626_-]; CDS [2r_10825132_10825267_-]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

GCTACATCGTCCTGGGCGGCGCCATCGGCGGGGGCGTGTCGCTGAGCAAAGTGAGTTTCGCAAGTTATATAACTTTTATAGAACTTGAGAGACTTGATTTGTTTTTCCCAGAAATACGAGGACTGGAAGGATGGACTGCCGGATTTTAAGTGGCTGGAGGA **********..(((((((.(((((((.(((((...))))).)))))))..))))))).....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M025 embryo	SRR553486 Makindu_3 day-old ovaries	M023 head	M024 male body	SRR618934 dsim w501 ovaries	SRR553488 RT_0-2 hours eggs	O001 Testis	SRR902009 testis	SRR553487 NRT_0-2 hours eggs
.....ATAGAACTTGAGAGACTTGATT.....	22	0	1	10.00	10	4	0	6	0	0	0	0	0	0
.....ATAGAACTTGAGAGACTTGA.....	20	0	1	3.00	3	0	0	2	0	1	0	0	0	0
.....ATAGAACTTGAGAGACTTGAAA.....	22	2	1	3.00	3	3	0	0	0	0	0	0	0	0
.....TTATAGAACTTGAGAGACTTGAA.....	23	1	1	2.00	2	2	0	0	0	0	0	0	0	0
.....TAGAACTTGAGAGACTTGATA.....	21	1	1	2.00	2	2	0	0	0	0	0	0	0	0
.....TATAGAACTTGAGAGACTTGATA.....	23	1	1	2.00	2	2	0	0	0	0	0	0	0	0
.....ATAGAACTTGAGAGACTTGAA.....	21	1	1	2.00	2	2	0	0	0	0	0	0	0	0
.....GAACTTGAGAGACTTGATTTGT.....	22	0	1	1.00	1	0	0	1	0	0	0	0	0	0
.....CGTCCTGGGCGGCGCCATCGGC.....	22	0	1	1.00	1	0	1	0	0	0	0	0	0	0
.....ACTTTTATAGAACTTGAGAGA.....	21	0	1	1.00	1	0	0	0	1	0	0	0	0	0
.....TTTTATAGAACTTGAGAGA.....	19	0	1	1.00	1	0	0	1	0	0	0	0	0	0
.....AACTTTTATAGAACTTGAGA.....	20	0	1	1.00	1	0	0	0	1	0	0	0	0	0
.....TTTATAGAACTTGAGAGACTTGAT.....	24	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....GCGTGTCGCTGAGCAAA.....	17	0	1	1.00	1	0	0	0	0	1	0	0	0	0
.....TTATAGAACTTGAGAGACTTGAT.....	23	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....GACTGGAAGGATGGACTGCCGGA.....	23	0	1	1.00	1	0	0	0	0	0	0	1	0	0
.....TTTATAGAACTTGAGAGACTTGAC.....	24	1	1	1.00	1	1	0	0	0	0	0	0	0	0
.....ATAGAACTTGAGAGACTTGAGA.....	22	2	2	0.50	1	1	0	0	0	0	0	0	0	0
.....GACTGGAAGGATGGAA.....	16	1	9	0.11	1	0	0	0	0	1	0	0	0	0

Anti-sense strand reads

CGATGTAGCAGGACCCGCCGCGGGTAGCCGCCCCCGCACAGCGACTCGTTTCACTCAAAGCGTTCAATATATTGAAAATATCTTGAACTCTCTGAACTAAACAAAAAGGGTCTTTATGCTCCTGACCTTCCTACCTGACGGCCTAAAATTCACCGACCTCCT **********..(((((((.(((((((.(((((...))))).)))))))..))))))).....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M024 male body	M023 head	SRR553488 RT_0-2 hours eggs	SRR553486 Makindu_3 day-old ovaries	M053 female body	SRR618934 dsim w501 ovaries

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droSim2	2r:10825218-10825378 -	dsi_20162	GCTACATCGTCCTGGGCGGCGCCATCGGCGGGGGCGTGTCGCTGAGCAAAGTGAGTT--------TCGC----------AAGTTATATAA--CTTTTA-TAG-AA----------CT--TGAGAGACTTGATTTGTTTTT----------C-CCAGAAATACGAGGACTGGAAGGATGGACTGCCGGATTTTAAGTGGCTGGAGGA
droSec2	scaffold_1:7629910-7630070 -		GCTACATCGTCCTGGGCGGCGCCATCGGCGGGGGCGTGTCGCTGAGCAAAGTGAGTT--------TCGC----------AAGTTATATAA--CTTGTA-TAG-AA----------CT--TGAGAGACTTGATTTGTTTTG----------C-CCAGAAATACGAGGACTGGAAGGATGGACTGCCGGATTTTAAGTGGCTGGAGGA
dm3	chr2R:10122284-10122444 -		GATACATCGTCCTGGGCGGCGCCATCGGCGGGGGCGTGTCGCTGAGCAAAGTGAGTT--------TCGC----------AAGTTATATAA--CTTGTA-TAG-AA----------CT--TAGAGAGATGATTTGTTTTG----------C-GCAGAAATACGAGGATGGAAGGATGGACTGCCGAATTTTAAGTGGCTGGAGGA
droEre2	scaffold_4845:15721323-15721483 +		GATAGCTCGTGTTGGGCGGCGCCATCGGCGGGGGCGTGAGGCTGAAATCAGTGAGTT--------TCGC----------AAGTTATATAA--GCTGTA-TTG-AA----------CT--TAGAGAGATGACTTGTTTTG----------C-CCAGAAATACGAGGACTGGAAGGATGGACTGCCTGATTTTAAGTGGCTGGAGGA
droYak3	2R:10059343-10059504 -		GATACATCGTAGTGGGCGGCGCCATTGGCGGGGGCGTGTCGCTGAGCAAAGTGAGTT--------TCGC----------AAGTTATATAA--CTTGCA-TAG-AA----------CT--TATGAGAGATGACTTGTTTTG----------CGCCAGAAATACGAGGACTGGAAGGATGGACTGCCGGATTTTAAGTGGCTGGAGGA
droEug1	scf7180000409462:2722316-2722475 +		GATACATAGTCCTAGGCGGCGCCATTGGTGGGGGCGTGTCGCTGAGCAAAGTGAGTT--------TCGC----------AAGTTATATAA--CTTGTA-GCA-AA----------CT--TAAGAGAGGTGATGTTTTT----------G-TCAGAAATACGAGGACTGGAAGGATGGATACCGGATTTTAAGTGGCTGGAGGA
droBia1	scf7180000301506:3142779-3142948 +		GCTACCTCGTCCTGGGCGGCGCCATTGGCGGGGGCGTGTCGCTGAGCAAAGTGAGTT--------TCGC----------AAGTTATATAA--CTACAATGCAG-TGT---TG---AGAA----------CC--CAGTCTGTATGATCTGCTTTG----------C-CCAGAAATACGAGGACTGGAAGGATGGCCTGCCGGATTCAAGTGGCTGGAGGA
droTak1	scf7180000414111:26552-26707 -		GCTACGTCGTCCTGGGCGGCGCCATCGGCGGGGGCGTGTCGCTGAGCAAGTGAGTT--------TTCC----------AGGTTATATAA--CTAGGTTGTAA-A----------TC--TAA------AGATTGTTTTG----------GTGTAGAAATACGAGGACTGGAAGGATGGCCTGCCGGATTCAAGTGGCTGGAGGA
droEle1	scf7180000491349:751299-751462 +		GCTACATCGTCCTGGGCGGCGCCATCGGCGGGGGCGTGTCGCTGAGCAAAGTGAGTT--------TCGC----------AGTTATATAACACTCGTTTGCAA-A----------TT--CAAAAGATACGCATTGTTTTT----------GCCCAGAAATACGAGGACTGGAAGGATGGCCTGCCCGATTCAAGTGGCTGGAGGA
droRho1	scf7180000777200:438467-438629 -		GCTACGTCGTCCTGGGCGGCGCAATCGGTGGGGGCGTGTCGCTGAGCAAAGTGAGTT--------TCGC----------AAGTTATATAATATCTGTTTGCAA-A----------TT--CAAGAGATACGATTTGTTTTT----------C-CCAGAAATACGAGGACTGGAAGGATGGCCTGCCGCGATTCAAGTGGCTGGAGGA
droFic1	scf7180000453948:310691-310854 +		GCTACGTCGTCCTAGGCGGCGCCATCGGCGGGGGCGTGTCGCTGAGTAAAGTGAGTT--------TCGC----------AAGTTATATAA--CTTGGTTCCCA-A----------G-CTAAACAAACA-GATTTGTTTTTT----------TTTTAGAAATACGAGGACTGGAAGGATGGCCTGCCGGATTTAAGTGGCTGGAGGA
droKik1	scf7180000302366:808962-809126 -		GCTACCTCGTCCTGGGCGGCGCCATTGGCGGGGGCGTGTCGCTGAGCAAAGTGAGTT--------GGCG----------GTGTTATATAA--CTTTTA-GCAA-A----------AAC--TGAGAG-TTTGTGTTCCTTTTTA-------TGG-ATAGAAATACGAGGACTGGAAGGAGGCTGCCGGACATCAAGTGGCTGGAGGA
droAna3	scaffold_13266:5802295-5802455 +		GGTACGTCGTCCTGGGCGGTGCGATAGGCGGGGGCGTGTCTGAGTAAAGTAAGTT--------TCGC----------AAATTATATAA--CTTCGA-T---T--TTGCGAAGGTACATTT----------T---TT-GTTTGA-----T---------TTTAGAAATACGAGGACTGGAAGGAGGCTGCCAGATATGAAGTGGCTGCAGGA
droBip1	scf7180000396372:416164-416330 +		GGTACCTCGTTCTAGGCGGTGCTATAGGTGGGGGCGTGACTCTCAATAAAGTAAGTT--------TGC----------AAATTATATAA--CTTCGA-T---T--TTGGCAGTGTACCATT----------T---TT-TTTTTGACT--TTATT----------T-TCAGAAATACGAGGACTGGAAGGATGGTCTGCCAGATATGAAGTGGCTGCAGGA
dp5	3:17371128-17371300 -		GATACCTCGTGCTGGGTGGTGCCATTGGCGGTGGCGTATCCCTAAGCAAAGTGAGCT--------C---------AC-GCTTCATTGGCGGTTATATAATA--T---GCAA-AGTG-------ATAATTATTTTATCAAAA--TG-------CGAT-------CT-TGCAGAAATACGAGGACTGGAAGGATGGCTTGCCTGACATGAAATGGCTACAGGA
droPer2	scaffold_31:421075-421247 +		GATACCTCGTGCTGGGTGGTGCCATTGGCGGTGGCGTATCCCTAAGCAAAGTGAGCT--------C---------AC-GCTTCATTGGCGGTTATATAATA--T---GCAA-AGTG-------ATAATTATTTTATCAAAA--TG-------CGAT-------CT-TGCAGAAATACGAGGACTGGAAGGATGGCTTGCCTGACATGAAGTGGCTACAGGA
droWil2	scf2_1100000004513:1838030-1838194 +		GCTACATTGTGCTAGGCGGAGCTATAGGCGGCGGCGTCTCCTTAAGCAAAGTGAGAG--------ACTG----------GA--GGCGATTATATAATG--T---GCCA-TTT----------T---T---------TCATTTGATTATTTGACAATTGCA-TGCAGAAATATGAAGACTGGAAAGATGGCTTACCGACTTAAATGGCTGGAGGA
droVir3	scaffold_12875:17584559-17584721 +		GTTACCTTGTGCTGGGCGGTGCCATTGGCGGTGGCGTTTCATTAAGCAAAGTAAGTA--------GTAAATCTAGC-AGCCCA----TTGTTATATAATG--T---GCAA-TTT----------T---G--------CAATTGTACA-----------CG-TGCAGAAATACGAGGATGGAAGGAGGCTACCGATATGAAGTGGCTAGAGGT
droMoj3	scaffold_6496:11206669-11206839 +		GTTACCTAGTGCTGGGCGGTGCTATTGGCGGTGGCGTTTCATTGAGCAAAGTGAGTACAAAGAAATCGC---TAG--TCTCCCATTACTGTTATATAATG--T---GCCA-A----------T---T------ATGCAATTGTGCACG-----------TGCAGAAATACGAGGATTGGAAGGAGGCTGCCAGATATGAAATGGCTAGAGGA
droGri2	scaffold_15245:14098712-14098883 -		GTTACATTGTGCTGGGCGGCGCTGTTGGCGGTGGCGTTTCCCTGAGCAAGGTGAGTGAAAATAAGTTATCTAATAAGTTA----ATTGTTATATAATT--G---GCAA-AAT----------T---T---------GCATTTGTGCA-----------CG-TGCAGAAATATGAAGATTGGAAGGATGGCCTGCCCGATTTCAAATGGCTCGAGGA

Generated: 09/08/2015 at 07:16 PM

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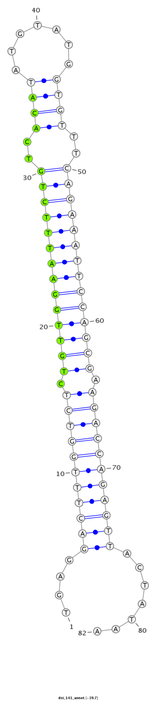
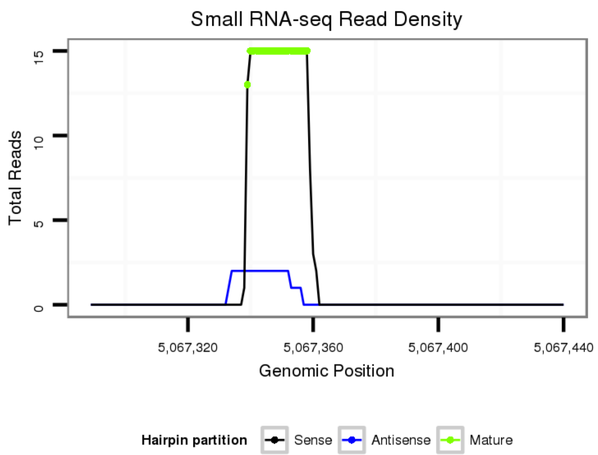
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	0
crit.tptop3	0
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

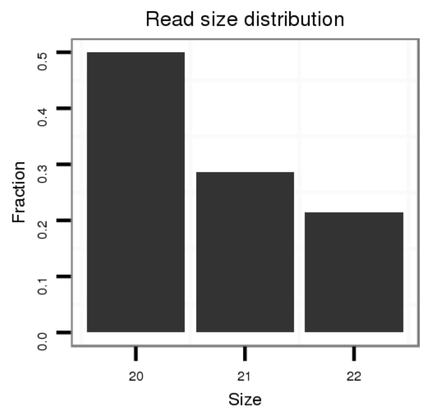
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dsi_141	**2r:5067339-5067390 +**	**candidate**	**Canonical miRNA**	**antisense_to_5pUTR**	[View on UCSC Genome Browser {Cornell Mirror}]

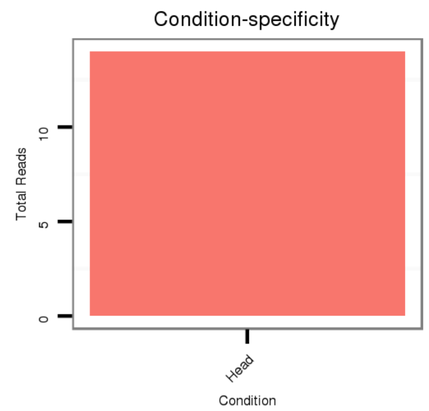
Legend: mature star mismatch in alignment mismatch in read

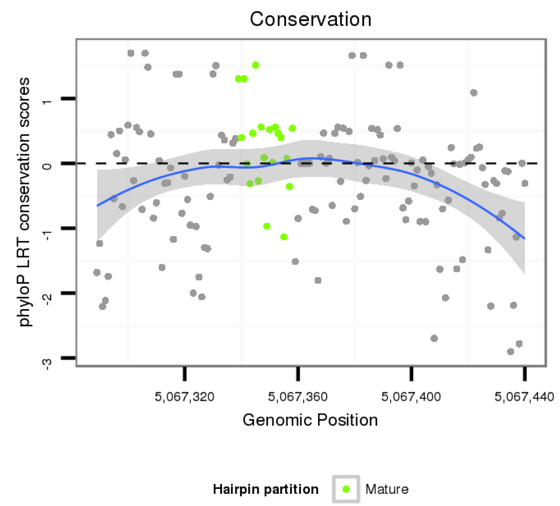
Predicted structure











Show Alternate Folds

Flybase annnotation

Antisense to utr5 [utr5_minus_2867]; Antisense to CDS [2r_5067422_5068297_-]; Antisense to utr3 [utr3_minus_2457]; Antisense to three_prime_UTR [2r_5067421_5067421_-]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

AAGCTTGTGATTTCTGGTGATTAAGGGCTTGCCGTTGAGGACTTTGGTCTCTGTTGGAATTTCTGTCACATATGTATGGTGTTTCAGAAATTCCAGCGAAGACCAGAGTTACTATAACCTTCGACTATGGACTTCATGTTCCCCTGGAAGTA **********....((((((((((.((((((((((((((..((((.....))))..))))))))))))))).))))))))))).....**********	**Read size**	**# Mismatch**	**Hit Count**	**Total Norm**	**Total**	**M023 head**	**O002 Head**	**SRR553486 Makindu_3 day-old ovaries**	**SRR618934 dsim w501 ovaries**
.....CTGTTGGAATTTCTGTCACA.....	20	0	1	7.00	7	7	0	0	0
.....CTGTTGGAATTTCTGTCACAT.....	21	0	1	4.00	4	2	2	0	0
.....TGTTGGAATTTCTGTCACATAT.....	22	0	1	2.00	2	0	2	0	0
.....TCTGTTGGAATTTCTGTCACAT.....	22	0	1	1.00	1	1	0	0	0
.....CTGTTGGAATTTCTGTCACATA.....	22	0	1	1.00	1	1	0	0	0

Anti-sense strand reads

TTCGAACACTAAAGACCACTAATTCCCGAACGGCAACTCCTGAAACCAGAGACAACCTTAAAGACAGTGTATACATACCACAAAGTCTTTAAGGTCGCTTCTGGTCTCAATGATATTGGAAGCTGATACCTGAAGTACAAGGGGACCTTCAT **********....((((((((((.((((((((((((((..((((.....))))..))))))))))))))).))))))))))).....**********	**Read size**	**# Mismatch**	**Hit Count**	**Total Norm**	**Total**	**SRR902009 testis**	**SRR618934 dsim w501 ovaries**	**SRR553488 RT_0-2 hours eggs**
.....CCAGAGACAACCTTAAAGACAGT.....	23	0	1	1.00	1	1	0	0
.....ACCAGAGACAACCTTAAAGA.....	20	0	1	1.00	1	1	0	0
.....GAACGGCAACTCCTGA.....	16	1	6	0.17	1	0	1	0

Show Alignment With Reads

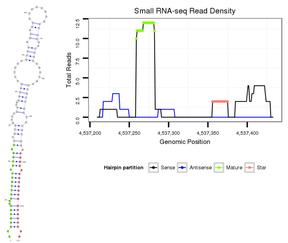
Re-alignment of all predicted orthologs

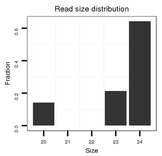
Species	Coordinate	ID	Alignment
droSim2	2r:5067289-5067440 +	dsi_141	AA----------GCTTGTGATTTCTGGTGATTAAGGGCTTGCC---GTTGAGGACTTTGGTCTCTGTTGGAATTTCTGTCACATATGTATGGTGTTTCAGAAATTCCAGCGAAGACCAGAGTTACT-ATAACCTTC------G-----ACTATGG-A----------CTTCATGTTCCCCTGGAAGTA
droSec2	scaffold_1:1894610-1894757 +		AA----------GTTTGTGATTTCTGGTGAAGAAGGGCTTGCC---GGTGAGGACTTTGGTCTCTGTTGGAATTTCTGTTACATA----TGGTGTTTCAGAAATTCCAGCGAAGACCAGAGTTACT-ATAACCTTC------G-----ACTATGG-A----------CTTCATGTTCCCCTGGAAGTA
dm3	chr2R:4248603-4248747 +		AC----------GTTTATGATTTCTGGTGAAG---GGCTTGCC---GTTCAGGACTTTGGTCTCTGTTGGAATTTTTGTTACATT----TTGTGTTACAAAAATTCCAGCGAAGACCCCAGTTACT-ATAACCTG------G-----GATACGG-T----------CTTCATCTTCCCCTGGAAGTA
droEre2	scaffold_4929:18384492-18384615 -		TA----------AGGTACCAC----------GTTTGGTCTCCGTAGGGATTTCTGTTACATG----AGGGTTTCAGAAATCCCAACCGGAGACCACAGTTACC-GGAACCATC------A-----GTTGTGG-TCT-----T----------CATCTTCACGATCCCCTGGAGGAA
droYak3	2L:16904578-16904728 +		AA----------GTTTATGATTTTTGGTGAGT---GGCTTGTT---GCTCGGACTTTGGTCTCTGCAGGGATCTCTGTAACATA----AGGTGTTTCAGAAATCCCAGCGGAGACCACAGTTACT-GTAGCCATC------G-----GTTGTGG-TCT-----T----------CATCTTCACGATCCCCTGCGAAAA
droEug1	scf7180000407691:115548-115701 +		TCT--------TAGCTGTTTGGTTTCTGATGAAGATAAGCTT-----CTGATACTGTGGTTTCTGTTGGAGTATCTGTAACATT----AGCTACCTCAGATATTCTAGCAGATATCACAGTCAAG-ATAAGCCCT------G-----TTTAGTCCTGT-----C----------AGTCTTCATCGCTTGGAGCGACAA
droBia1	scf7180000302291:2117395-2117549 +		AA----------GAATATGGTTTCTGCTGAAG---GGGTTGCC---C-AAAAGTGTGGCCTCTGCTGGGATTTCTGTTGAACA----AGATGTTTCAGAGATCTCAGCAGAGATCACAGCGGAG-ATGGGACTT------G-----ATCCTTA-TCGTAATCT----------CATTCTCATGAGCGCGGATAACAG
droTak1	scf7180000415627:123357-123494 +		AAACCATAGAGGTAGAAATATGATTTCTGGTGATG---GGATTTTCCCATTTTTTTACTGTAGCCTCTGTTGGGATATCTATTACATA----TGGCGTTTTAGAGATCCCAGCAGAGATCACAGGA---CTCATGGACTGCGTGCGGAG
droEle1	scf7180000491240:1073862-1074082 +		ATGCTTC--------GCCTATGGTTTTTGGT-------TCT-----CTCTTGCTGAGGGCTCTGTTGGGACATCCGTAACAGA----AACTGTTTCGGAGATTCTAGCAGAGACCACAGATGAG-AAAACCGCA------G-----CTTAAGA-TCATAATTTTCAGGGACTGTTGTGTGTTTGGACAAGTGGCGCATCGGTGTTCAGAGATCCTAGCAGAGATTACAGATCGCAATCTTCATGGACTCTGGGAAAA
droRho1	scf7180000770177:369660-369789 +		GG----------C--TATGTTCTCTAATG----------CTATGGGCTCTGTTGGGATATCTGTTACAAA----AACTGTTCCAGAGATCCTAGCAGAGATCACAGATGAG-AAAACCCTA------G-----CTTAAGA-TAC-----C----------AATCTTCATGGGTGCGGCGACAA
droFic1	scf7180000453851:2087353-2087488 -		GA----------AT--TCGTTTCTGGTGGAG---GGGTTAGT---TTAGAGGTGTGTGCTCTGTTACGATATCTGTTACAGA----GGATGTTTCATATATCCTAGTAGAGCTCACAGCTAAG-AAATCCATC------TTTTTA---AAGC-TCT----------AGTCC-T---TGGAG
droKik1	scf7180000302277:101349-101472 +		AA----------TATGGCTTCTGATGAATGGGGCT-----CTGCTGTGGGAATCCCTGCTGGAGC----AATTGCAGCAGAGCTTCAAAGAGGGATCACAGCAGGATGCAGTATCT------A-----TCTATGG-T----------TCCGCCTGTCGGCTCAGA
droAna3	scaffold_13266:1746138-1746270 -		GTG--------TGAAT-ATTGGCTTCCGGTGATTGAAAGTTTG---CGGGAACTATGCAAAGTC----CTTTGCTCCAAGCATCAAATGAAGGAGTTTGCATAG-GTGGGACTCTTAGAATTTTTG---AGGT-GCC----------TGAG----------GACAG-T---TGGGG
droBip1	scf7180000396730:2739160-2739201 -		TA----------ATA-TTGGCTTTCGGTGATTGCAAGTTTTC-----CGGGGACTGTG----------GCTTTTCTTTTTT

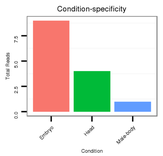
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dsi_6205	**2r:4537259-4537383 +**	**candidate**	**3p_tailed_mirtron**	**intron**	[View on UCSC Genome Browser] [Cornell Mirtor]

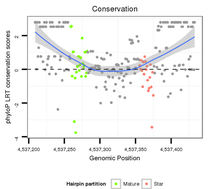
Legend: sense, 5p, 3p, mismatch in arly-one or, mismatch in seed

Predicted structure









Show Alternate Folds

Flybase annotation

intron [2r_4537259_4537383_+]; CDS [2r_4537384_4537794_+]; CDS [2r_4536600_4537258_+]

No Repeatable element found

Sense Strand Reads

hide 3p reads show mxd mismatch reads

	Read # size	Mismatch	Hit Count	Total Norm	Total	M025 embryo	M023 head	SRR902009 testis	M024 male body	0001 testis	SRR553486 Makindo_3 day-old ovaries	GSM634915 embryo	SRR553489 RT_0-2 hours eggs
TTCTTCAGTCGCGCAGCGAGGAGTCCTGGAAGCGGGAGACAGAGATCTACAGGTGAATACAGTTATTTGTGACTCTGAATTTGTTAAACAGTTTCCCATGAAGGAACGTGCCCTAGTCCAGTCACTCACTCTGTGCTCTATGAATAAATAATCGTACTTTATTTTCACAGCACATATTGCTACAGACATGAAAATATTCTCGATTCATCGGCTCCGACA												
**********													
.....	24	0	1	9.00	9	8	1	0	0	0	0	0	0
.....	18	0	1	2.00	2	0	0	0	0	2	0	0	0
.....	20	0	1	2.00	2	0	2	0	0	0	0	0	0
.....	24	1	1	2.00	2	0	0	0	0	0	0	0	0
.....	21	0	1	1.00	1	0	1	0	0	0	0	0	0
.....	21	1	1	1.00	1	1	0	0	0	0	0	0	0
.....	23	0	1	1.00	1	0	1	0	0	0	0	0	0
.....	23	1	1	1.00	1	0	0	0	0	0	0	0	0
.....	23	0	1	1.00	1	0	0	0	0	1	0	0	0
.....	23	0	1	1.00	1	0	0	0	0	0	0	0	0
.....	24	1	1	1.00	1	1	0	0	0	0	0	0	0
.....	22	0	1	1.00	1	0	0	0	0	0	1	0	0
.....	23	0	1	1.00	1	0	0	0	0	1	0	0	0

Anti-sense strand reads

	Read # size	Mismatch	Hit Count	Total Norm	Total	M24 male eggs	SRR553488 RT_0-2 hours male body	SRR818934 dsim w501 ovaries	SRR553487 RT_0-2 hours eggs	SRR553484 Makindo_3 day-old ovaries
AAGAAGTCAGCGCTGCTCCTCAGGACCTTCGCCCTCTGTCCTAGATGTCACTCATGGTCTAATAAACACTGGCACATTAAACAATTTGTCAAAGGGTACTTCCTGCACGGGATCAGTCAGTAGTGATGACAACGAGATACTTATTAATTATTAGCATGAAATAAAAAATCGTGGTATAACCATGCTGTACTTTTATAGAGCCTAAGTAGCCGAGCTGT										
**********										
.....	21	0	1	2.00	2	2	0	0	0	0
.....	21	0	1	1.00	1	1	0	0	0	0
.....	21	0	1	1.00	1	0	1	0	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
dsim6	scaffold_14933:431933..4	Dsi_dsi	TTCTTCAGTCGCGCAGCGAGGAGTCCTGGAACGCGGGAGACAGAGATCTACAGGTGAATACAGTTATTTGTGACTCTGAATTTGTTAAACAGTTTCCCATGAAGGAACGTGCCCTAGTCCAGTCACTCACTCTGTGCTCTATGAATAAATAATCGTACTTTATTTTCACAGCACATATTGCTACAGACATGAAAATATTCTCGATTCATCGGCTCCGACA----------
dsim6	scaffold_11332:23..132268		TTCTTCAGTCGCGCAGCGAGGAGTCCTGGAACGCGGGAGACAGAGATCTACAGGTGAATACAGTTATTTGTGACTCTGAATTTGTTAAACAGTTTCCCATGAAGGAACGTGCCCTAGTCCAGTCACTCACTCTGTGCTCTATGAATAAATAATCGTACTTTATTTTCACAGCACATATTGCTACAGACATGAAAATATTCTCGATTCATCGGCTCCGACA----------
dsh3	scaffold_1835822:4436664..4		TTCTTCAGTCGCGCAGCGAGGAGTCCTGGAACGCGGGAGACAGAGATCTACAGGTGAATACAGTTATTTGTGACTCTGAATTTGTTAAACAGTTTCCCATGAAGGAACGTGCCCTAGTCCAGTCACTCACTCTGTGCTCTATGAATAAATAATCGTACTTTATTTTCACAGCACATATTGCTACAGACATGAAAATATTCTCGATTCATCGGCTCCGACA----------
dsim6	scaffold_6323:1933233..1934966..		TTCTTCAGTCGCGCAGCGAGGAGTCCTGGAACGCGGGAGACAGAGATCTACAGGTGAATACAGTTATTTGTGACTCTGAATTTGTTAAACAGTTTCCCATGAAGGAACGTGCCCTAGTCCAGTCACTCACTCTGTGCTCTATGAATAAATAATCGTACTTTATTTTCACAGCACATATTGCTACAGACATGAAAATATTCTCGATTCATCGGCTCCGACA----------
dsim6	scaffold_14933:1..1466134..		TTCTTCAGTCGCGCAGCGAGGAGTCCTGGAACGCGGGAGACAGAGATCTACAGGTGAATACAGTTATTTGTGACTCTGAATTTGTTAAACAGTTTCCCATGAAGGAACGTGCCCTAGTCCAGTCACTCACTCTGTGCTCTATGAATAAATAATCGTACTTTATTTTCACAGCACATATTGCTACAGACATGAAAATATTCTCGATTCATCGGCTCCGACA----------
dsrdop1	scaffold_6000:6292..5174293..		TTCTTCAGTCGCGCAGCGAGGAGTCCTGGAACGCGGGAGACAGAGATCTACAGGTGAATACAGTTATTTGTGACTCTGAATTTGTTAAACAGTTTCCCATGAAGGAACGTGCCCTAGTCCAGTCACTCACTCTGTGCTCTATGAATAAATAATCGTACTTTATTTTCACAGCACATATTGCTACAGACATGAAAATATTCTCGATTCATCGGCTCCGACA----------
dsrdop1	scaffold_6000:3013061..5174..-		TTCTTCAGTCGCGCAGCGAGGAGTCCTGGAACGCGGGAGACAGAGATCTACAGGTGAATACAGTTATTTGTGACTCTGAATTTGTTAAACAGTTTCCCATGAAGGAACGTGCCCTAGTCCAGTCACTCACTCTGTGCTCTATGAATAAATAATCGTACTTTATTTTCACAGCACATATTGCTACAGACATGAAAATATTCTCGATTCATCGGCTCCGACA----------
dsrdtak1	scaffold_6000:6413981..5835015..		TTCTTCAGTCGCGCAGCGAGGAGTCCTGGAACGCGGGAGACAGAGATCTACAGGTGAATACAGTTATTTGTGACTCTGAATTTGTTAAACAGTTTCCCATGAAGGAACGTGCCCTAGTCCAGTCACTCACTCTGTGCTCTATGAATAAATAATCGTACTTTATTTTCACAGCACATATTGCTACAGACATGAAAATATTCTCGATTCATCGGCTCCGACA----------
dsrdtak1	scaffold_6000:6304831..4865..5059		TTCTTCAGTCGCGCAGCGAGGAGTCCTGGAACGCGGGAGACAGAGATCTACAGGTGAATACAGTTATTTGTGACTCTGAATTTGTTAAACAGTTTCCCATGAAGGAACGTGCCCTAGTCCAGTCACTCACTCTGTGCTCTATGAATAAATAATCGTACTTTATTTTCACAGCACATATTGCTACAGACATGAAAATATTCTCGATTCATCGGCTCCGACA----------
dsrdhu3	scaffold_6000:3801088..2174350..		TTCTTCAGTCGCGCAGCGAGGAGTCCTGGAACGCGGGAGACAGAGATCTACAGGTGAATACAGTTATTTGTGACTCTGAATTTGTTAAACAGTTTCCCATGAAGGAACGTGCCCTAGTCCAGTCACTCACTCTGTGCTCTATGAATAAATAATCGTACTTTATTTTCACAGCACATATTGCTACAGACATGAAAATATTCTCGATTCATCGGCTCCGACA----------
dsrdfu1	scaffold_6000:6352..5152282..		TTCTTCAGTCGCGCAGCGAGGAGTCCTGGAACGCGGGAGACAGAGATCTACAGGTGAATACAGTTATTTGTGACTCTGAATTTGTTAAACAGTTTCCCATGAAGGAACGTGCCCTAGTCCAGTCACTCACTCTGTGCTCTATGAATAAATAATCGTACTTTATTTTCACAGCACATATTGCTACAGACATGAAAATATTCTCGATTCATCGGCTCCGACA----------
dsrk1	scaffold_6000:3224711..3274271..		TTCTTCAGTCGCGCAGCGAGGAGTCCTGGAACGCGGGAGACAGAGATCTACAGGTGAATACAGTTATTTGTGACTCTGAATTTGTTAAACAGTTTCCCATGAAGGAACGTGCCCTAGTCCAGTCACTCACTCTGTGCTCTATGAATAAATAATCGTACTTTATTTTCACAGCACATATTGCTACAGACATGAAAATATTCTCGATTCATCGGCTCCGACA----------
dsrdkm1	scaffold_1329:1164..1814..		TTCTTCAGTCGCGCAGCGAGGAGTCCTGGAACGCGGGAGACAGAGATCTACAGGTGAATACAGTTATTTGTGACTCTGAATTTGTTAAACAGTTTCCCATGAAGGAACGTGCCCTAGTCCAGTCACTCACTCTGTGCTCTATGAATAAATAATCGTACTTTATTTTCACAGCACATATTGCTACAGACATGAAAATATTCTCGATTCATCGGCTCCGACA----------
dsrdop1	scaffold_6000:3365..5152819..		TTCTTCAGTCGCGCAGCGAGGAGTCCTGGAACGCGGGAGACAGAGATCTACAGGTGAATACAGTTATTTGTGACTCTGAATTTGTTAAACAGTTTCCCATGAAGGAACGTGCCCTAGTCCAGTCACTCACTCTGTGCTCTATGAATAAATAATCGTACTTTATTTTCACAGCACATATTGCTACAGACATGAAAATATTCTCGATTCATCGGCTCCGACA----------
dp3	scaffold_2:1234..1..-		TTCTTCAGTCGCGCAGCGAGGAGTCCTGGAACGCGGGAGACAGAGATCTACAGGTGAATACAGTTATTTGTGACTCTGAATTTGTTAAACAGTTTCCCATGAAGGAACGTGCCCTAGTCCAGTCACTCACTCTGTGCTCTATGAATAAATAATCGTACTTTATTTTCACAGCACATATTGCTACAGACATGAAAATATTCTCGATTCATCGGCTCCGACA----------
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dsrfl1	scaffold_1400000:4558..1813578..		TTCTTCAGTCGCGCAGCGAGGAGTCCTGGAACGCGGGAGACAGAGATCTACAGGTGAATACAGTTATTTGTGACTCTGAATTTGTTAAACAGTTTCCCATGAAGGAACGTGCCCTAGTCCAGTCACTCACTCTGTGCTCTATGAATAAATAATCGTACTTTATTTTCACAGCACATATTGCTACAGACATGAAAATATTCTCGATTCATCGGCTCCGACA----------
dsrfl2	scaffold_6000:2187..862507..		TTCTTCAGTCGCGCAGCGAGGAGTCCTGGAACGCGGGAGACAGAGATCTACAGGTGAATACAGTTATTTGTGACTCTGAATTTGTTAAACAGTTTCCCATGAAGGAACGTGCCCTAGTCCAGTCACTCACTCTGTGCTCTATGAATAAATAATCGTACTTTATTTTCACAGCACATATTGCTACAGACATGAAAATATTCTCGATTCATCGGCTCCGACA----------
dsrfm3	scaffold_6000:3..1382263..		TTCTTCAGTCGCGCAGCGAGGAGTCCTGGAACGCGGGAGACAGAGATCTACAGGTGAATACAGTTATTTGTGACTCTGAATTTGTTAAACAGTTTCCCATGAAGGAACGTGCCCTAGTCCAGTCACTCACTCTGTGCTCTATGAATAAATAATCGTACTTTATTTTCACAGCACATATTGCTACAGACATGAAAATATTCTCGATTCATCGGCTCCGACA----------
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Generated: 09/08/2015 at 07:16 PM

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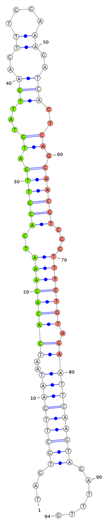
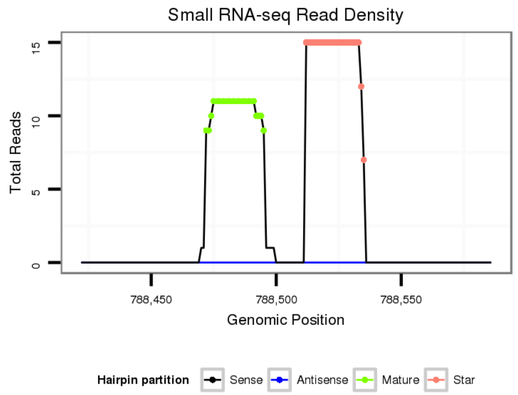
cds.ant	0
cds.ant	0
cds.sense	0
cds.sense	0
cds.sense

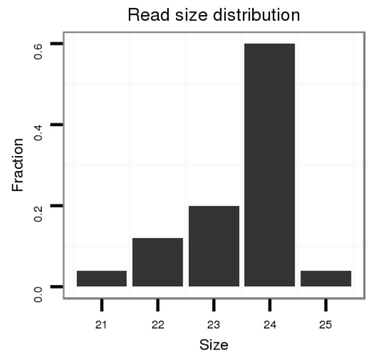
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dsi_90	**3l:788472-788536 +**	**candidate**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

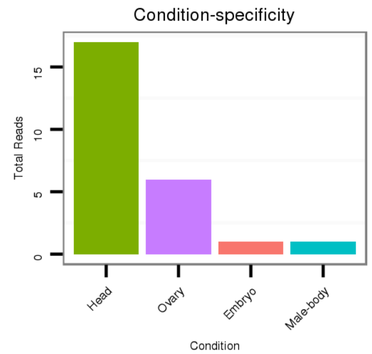
Legend: mature star mismatch in alignment mismatch in read

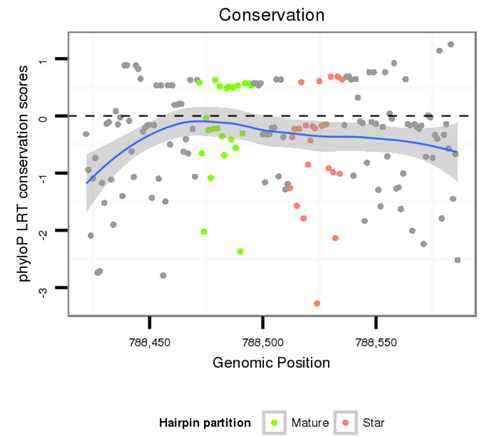
Predicted structure











Show Alternate Folds

Sense Strand Reads

hide 3p reads show mid mismatch reads

AAGGGGCTAAATGTTACATTCATTTTGACATTTAGTAGTGCTTGAATAATCACAGAAATCACGTTGATGTATTGAAGTTTGGAAAGATCACTCAGCAACGTCGCTTTCTGTAGAATTCAAGTAGATTTGACTTCATTACCTTTTCACAGATTCTAAAGAATTATA **********...(((((((((..(((((((((..((((((.((...(((..((....)).))).))..)).)))))).....))))))).))))))))))).....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M023 head	SRR618934 dsim w501 ovaries	M024 male body	M025 embryo	O002 Head	GSM343915 embryo
.....CACAGAAATCACGTTGATGTATTG.....	24	0	1	8.00	8	5	0	1	1	1	0
.....CTCAGCAACGTCGCTTTCTGTAGA.....	24	0	1	7.00	7	5	2	0	0	0	0
.....CTCAGCAACGTCGCTTTCTGTAG.....	23	0	1	5.00	5	3	2	0	0	0	0
.....CTCAGCAACGTCGCTTTCTGTA.....	22	0	1	3.00	3	3	0	0	0	0	0
.....AGAAATCACGTTGATGTATTGAAGT.....	25	0	1	1.00	1	0	1	0	0	0	0
.....ATCACAGAAATCACGTTGATGT.....	22	0	1	1.00	1	0	1	0	0	0	0
.....CAGAAATCACGTTGATGTATT.....	21	0	1	1.00	1	0	1	0	0	0	0

Anti-sense strand reads

TTCCCCGATTTACAATGTAAGTAAAACTGTAAATCATCACGAACTTATTAGTGTCTTTAGTGCAACTACATAACTTCAAACCTTTCTAGTGAGTCGTTGCAGCGAAAGACATCTTAAGTTCATCTAAACTGAAGTAATGGAAAAGTGTCTAAGATTTCTTAATAT **********...(((((((((..(((((((((..((((((.((...(((..((....)).))).))..)).)))))).....))))))).))))))))))).....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	SRR553486 Makindu_3 day-old ovaries	SRR553487 NRT_0-2 hours eggs	SRR553488 RT_0-2 hours eggs	SRR618934 dsim w501 ovaries	SRR553485 Chicharo_3 day-old ovaries

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droSim2	3l:788422-788586 +	dsi_90	AAGGGG---CTA----------AATGTT----------ACATTCATTTT----------GACATTTAGTAGTGCTTGAATAATCACAGAAATCACGTTGATGTATTGAA-GTTTGGAAAGATCACTCAGCAACGTCGCTTTCTGTAGAATTCA----------AGTAGATTTGAC----------TTCAT-TACC--------TTTTCACAGATTCTAAAGAATT--ATA
droSec2	scaffold_2:852355-852496 +		TAGGTG---CTA----------AATGTT----------ATATTCATTTT----------GAGCTTTATTAGTGCTT----------TGATCTATTGAA-GTTTGGAAAGATCCCTGGCAACGTCTCTTTCTGAAGAATTCA----------AGTAAATCTGAT----------TTGAT-TACC--------TTGTCACAGTCTCTAAAGAATT--CC
dm3	chr3L:824561-824716 +		TATGTT---GCTA----------CATTTT----------ACATTCATTTT----------GACATTCAACAGTGCTTAAATAATCATAGAAATCAG------TATTGAA-GTTCGGAAAGATCCCTCAGCAAC-----TGTGTGAAAAATTG----------GTTTA----------AGTAGATTTCAT----------TTGGT-TACA--------TTTTAGGAGTTTCCAAAGAAT--TTC
droEre2	scaffold_4784:840102-840255 +		TATATACCTTTT----------AACT--------**----------**----------**----------**---CGAAAATACGCACCGGCCGCGTCGCGTTCTGAAGAATTGCGTGCCATCTCTGCTTGACTATTCATTTGAAGCGCTCTCTC--TAAATTGTGACTTCTATGAAATCTCTGAT-TCGT--------TTCTACAGATTCTAAAGAACT--CGC
droYak3	3L:820097-820223 +		TGTGTT---CTA----------ATGTT----------ACATTATTT----------C-------AGTTATTTTAAGCAAT----------GATGTTCCTTTCTCTA--GTTCA----------AGTTGCTTTGCCACTACTATCAAATCTCTGAT-TGTTTCTATGCTGCTTTCACAGTTGCTAAATAATT--**---**
droEug1	scf7180000409184:858501-858574 +		TTTGAT---ATT----------ATTTC----------**---------**GGAAATAAGAAACACTAATTATTGTATAATCCACTCATTACTTTGGTGTATATT----------**----------**----------**----------**----------GCT--CTA
droTak1	scf7180000415111:303046-303070 -		TTCTAA---AAA----------**-----**----------**---------**----------**----------**----------**----------**----------**----------**----------**----------**----------**----------ACTCCTTAAAATT--ATC
droEle1	scf7180000491249:1022112-1022126 +		TTCTAA---**---**----------**-----**----------**---------**----------**----------**----------**----------**----------**----------**----------**----------**----------ATCAAT--ATG
droFic1	scf7180000453052:411482-411619 -		AAAGGA---CTT----------AAGTTA----------AAATACTTT--**----------**----------**----------**----------**----------**----------**----------**----------**----------A**----------**----------**--AAATAAA--GTGCTAATTTTAGCA-----AAAGTATTACACT
droKik1	scf7180000302383:193742-193859 +		TGGGGA---TGATCTTGAGGCTTTAGATATACAAAATATCAAATCTTATATATGTATTGTTTT----------GAAAT----------**----------**GC----------**----------**----------**----------**----------**----------**----------**--AAATTTTGATTTTTATAGAATTTCAATCTATA--------**----------**TTTTTGATACTT--AAA
droAna3	scaffold_13337:11791505-11791515 +		ACATGG---CCA----------AA**---**----------**----------**----------**----------**----------**----------**----------**----------**----------**----------**----------**----------**----------**----------**--**

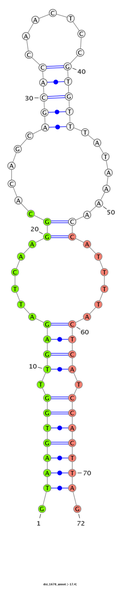
Generated: October 2015 at 08:04 PM

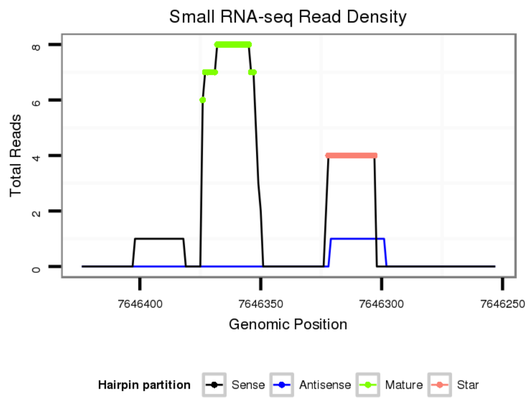
	PASS/FAIL
crit.star	1
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

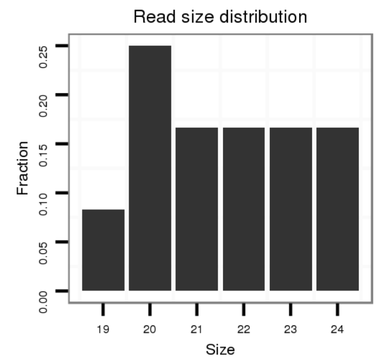
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dsi_1670	**3r:7646303-7646374 -**	**candidate**	**Mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

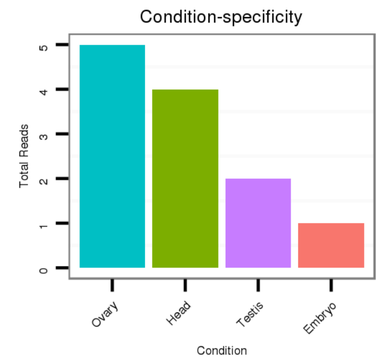
Legend: mature star **mismatch in alignment** mismatch in read

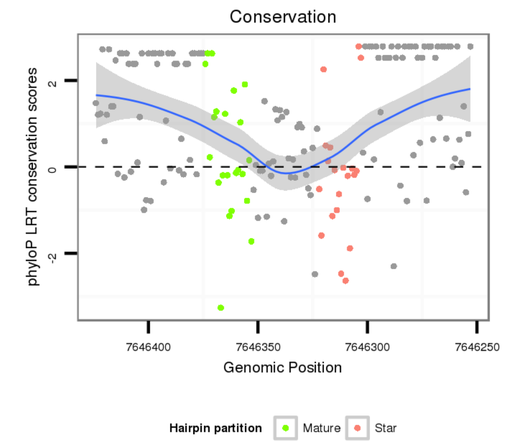
Predicted structure











Show Alternate Folds

Flybase annotation

intron [3r_7646303_7646374_-]; CDS [3r_7646219_7646302_-]; CDS [3r_7646375_7646425_-]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

```
TGGAGCAAACCTTCTCGGCCCTTTTGAACTTCGTTTGGGTAGCCTACAATGTAAGTGGTTGAGATTCAAGGCACAGCAGCACCAACTCCGTGTTTATAAAACCATTTTACTCATCCACTTAGATCTATTGCTGGCTGGTGGTCTTCTCGCAGTACCAGATATTCCTGGAGAT
**************************************************.(((((((.((((......((.....(((((.......)))))).....)).....)))).)))))))..**************************************************
```

Read size	# Mismatch	Hit Count	Total Norm	Total	SRR618934 dsim w501 ovaries	GSM343915 embryo	O002 Head	SRR902009 testis	SRR553486 Makindu_3 day-old ovaries	SRR553487 NRT_0-2 hours eggs	SRR553485 Chicharo_3 day-old ovaries	M024 male body	SRR553488 RT_0-2 hours eggs	M023 head
.....GTAAGTGGTTGAGATTCAAGGCAA..... 24	1	1	2.00	2	0	0	0	2	0	0	0	0	0	0
.....GTAAGTGGTTGAGATTCAAGGC..... 22	0	1	2.00	2	1	1	0	0	0	0	0	0	0	0
.....CATTTTACTCATCCACTTAG..... 20	0	1	2.00	2	0	0	2	0	0	0	0	0	0	0
.....GTAAGTGGTTGAGATTCAAGGCA..... 23	0	1	2.00	2	0	0	0	2	0	0	0	0	0	0
.....CCATTTTACTCATCCACTTAG..... 21	0	1	2.00	2	0	0	2	0	0	0	0	0	0	0
.....TAAGTGGTTGAGATTCAAGGCACA..... 24	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....GGTTGAGATTCAAGGCACA..... 19	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....GTAAGTGGTTGAGATTCAAG..... 20	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....TTTGAACTTCGTTTGGGTAGC..... 21	0	1	1.00	1	0	0	0	0	0	1	0	0	0	0
.....CATTTTACTCATCCACTTAGA..... 22	1	1	1.00	1	0	1	0	0	0	0	0	0	0	0
.....GTAAGTGGTTGAGATTCAAGGCAC..... 24	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....TGTAAGTGGTTGAGC..... 15	1	11	0.91	10	6	0	0	0	0	1	1	0	2	0
...AGCAAACCTTCTCGG..... 15	0	2	0.50	1	0	0	0	0	0	0	0	0	1	0

Anti-sense strand reads

```
ACCTCGTTTGGAAGAGCCGGGAAAACTTGAAGCAAACCCATCGGATGTTACATTCACCAACTCTAAGTTCCGTGTCGTCGTGGTTGAGGCACAAATATTTTGGTAAAATGAGTAGGTGAATCTAGATAACGACCGACCACCAGAAGAGCGTCATGGTCTATAAGGACCTCTA
**************************************************.(((((((.((((......((.....(((((.......)))))).....)).....)))).)))))))..**************************************************
```

Read size	# Mismatch	Hit Count	Total Norm	Total	M053 female body	SRR553485 Chicharo_3 day-old ovaries	SRR553486 Makindu_3 day-old ovaries	SRR553488 RT_0-2 hours eggs
.....TAAAATGAGTAGGTGAATCTAGA..... 23	0	1	1.00	1	1	0	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droSim2	3r:7646253-7646424 -	dsi_1670	TGGAGCAAACCTTCTCGGCCCTTTTGAACTTCGTTTGGGTAGCCTACAATGTAAGTG----------GTT-------GAGATTCA----AG----------GCACAGC----------AGCACCA---------A---CTCC----------GTGTTTATAAA------AC----------CA----T----TTTACTC--ATCCACTTAGATCTATTGCTGGCTGGTGGTCTTCTCGCAGTACCAGATATTCCTGGAGAT
droSec2	scaffold_12:532448-532628 -		TGGAGCAAACCTTCTCGGCCCTTTTGAACTTCGTTTGGGTAGCCTACAATGTAAGTG----------ATT-------GAGATTCA----AG----------GAACGGC----------AACACCA---------ATTT----CTGGATCATTATGTTTATAAA------CC----------CA----T----TTTACTC--ATTCACTTAGATCTATTGCTGGCTAGTGGTCTTCTCGCAGTACCAGATATTCCTGGAGAT
dm3	chr3R:13621586-13621766 +		TGGAGCAAACCTTCTCGGCCCTTTTGAACTTCGTTTGGGTAGCCTACAATGTAAGTG----------ATT-------GAATTCA----AG----------GCACAGC----------AACACCA---------ACTC----CTGTATCATTATGTTTATAAA------CC----------CA----T----TTTACTC--ATCCACTTAGATCTATTGCTGGCTGGTGGTCTTCTCGCAGTACCAGATATTCCTGGAGAT
droEre2	scaffold_4770:8009151-8009323 -	der_574	TGGAGCAAACCTTCTCGGCCCTTTTAAACTTGTTTGGGTAGCCTATAATGTAAGTG----------GTT-------GAGACTCA----AG----------GA---TC----CTGGCTTTTCATGTATATAAACTTTT--AC----------A-CG----T----TTTACAC--TTTCCTCAGATTATTGCTGGCTGGTGGTCTTCTCGCAGTACCAGATATTCCTGGAGAT
droYak3	3R:2201155-2201320 +	dya_913	TGGAGCAAACCTTCTCGGCCCTTTTAAACTTGTTTGGGTAGCCTATAATGTAAGTG----------GTT-------GAGATTCA----A---ATC----CTGGATCATCATGTTTATAAA------CC----------CA----T----TTTACTT--ATACCTCAGATCTATTGCTGGCTGGTGGTCTTTCGCAATACCAGATATTCCTGGAGAT
droEugl	scf7180000409562:148599-148760 +		TGGAGCAAAGTTTCTCGGCTCTTTTAAACTTCGTTTGGTGTGGATATAATGTAAGTT---GTAATTTTGT----------TC--CG----T----TTATTCC--CTGCCTTCAGATCTATTGCTGGCTTGTGGTCTTTCGCAGTACCAGATATTGTTGAAAAT
droBial	scf7180000302113:3790677-3790840 -		TGGAGCAAAGTTTATCAGCTCTACTGAACTTCGTTTGGGTCGCCTACAATGTAAGTT---CTTCACCTGA----------AC-----ATTCCAA---------A-A-ATTTATTAA------CC----------CA----T----TTTATTGCATATCCACAGATCTACTGCTGGCTGGTGGTCTTCTCGCAGTACCAGATATTCCTGAAGAT
droTakl	scf7180000414009:357512-357676 -		TGGAGCAAACCTTCTCAGCTCTTTTAAACTTGTTTGGTGTGCCTATAATGTAAGTT----------ATT-------GGAAAACC---AA----------GAG--C----A-TTTCTACA------CT----TAAATTACCCCT----T----TATTTG--TTTTCCCCAGATTTACTGCTGGCTGGTGGTCTTCTCGCAGTACCAGATATTGTTGAAGAT
droElel	scf7180000491080:2657503-2657580 -		TTAATAAAGT----------GTT-------GAA----T----TTT--TC--GTCCTTCAGGTTTACTGCTGGCTTGTAGTGTTCTCGCAATACCAGATATTTTTAAAAAT
droRhol	scf7180000777768:12754-12820 -		C----------GTT-------GAA----T----CGT----CA--ATGTCCTCAGATCTACTGCTGGCTTGTGGTCTTCTCGCAGTACCAGATCTTGTTGAAAAT
droFic1	scf7180000453912:1853031-1853266 -		TGGAGCAAACCTTCTCGGCTCTTTTAAACTTGTTTGGGTCGCCTACAATGTGAGTA---TT---AAA--AAAGTTTAAATTCTCTTACTCAAACATTATTTA----TCTGTACTTGTTTTAAAACAAC---ATACTGAAATGTTTGAGTAC-----GGTTTTAAATATT----A-GAGTGATC--GTTTATAA------AC----------GA----T----TTTTGCG---GTTCTCAGATATTGCTGGCTCGTGGTCTTCTCGCATACCAGATCTTCTTGAAAAT
droKikl	scf7180000302276:713380-713550 -		TGGAGCAAACCTTCTCGGCTCTCCTGAACTTCGTCTGGGTCGCCTACAATGTGAGTGCCAGC--ACTTGG----------TC--------TT--AA----ATATTTATTTA------CTCT--ATTTC----------A-ACGATATTCTTTATT----T--CCCCACTTAGATCTACTGCTGGCTGGTGGTCTTTCGCAGTACCAGATCTTGTTGAACAT
droAna3	scaffold_13340:10780517-10780681 -		TGGAGCAAAGTTTTCGGCGTACTGAACTTCGTCTGGGTCGCCTACAATGTAAAGT---AT--ACCTGG----------TT--------TC--AA---AGCA--TT----------C--------CTAA-A-TCTTATCCC----------A-AG----T----TTACTCT--TTTCCCCAGATATACTGCTGGCTGGTGGTCTTCTCGCAATACCAGATCTTTTTGGAAAT
droBipl	scf7180000396374:302830-302993 +		TGGAGCAAAGTTTTCGGCGTTGTGAACTTCGTTTGGGTCGCCTACAATGTAAAGT---AT--TCCTGG----------TT--------TT--TAA---AACA--TT----------A--------TTCAA-G-TCTTA--AC----------A-TA---AT----TTATTAT--TTTCTGGTAGATATACTGCTGGCTTGTCGTCTTCTCGCAGTACCAGATCTTTTTGGAAAT
dp5	2:25971927-25972084 +		TGGAACAAACCTTTCGGCTCTGCTCAACTTCGTTTGGATGCCTACAATGTGAGTA----------A--------------AATATACGAATAT--------GCG-AT--------CCC----------A----------TCTTA--AGC----------AA----T----TTTCTCT--GCTTCGATAGATATACTGTTGGCTGGTAGTCTTCTCTCAGTACCAGATCTTCTTGCAAAT
droPer2	scaffold_6:1305478-1305635 +		TGGAACAAACCTTTCGGCTCTGCTCAACTTCGTTTGGATGCCTACAATGTGAGTA----------A--------------ATATACGAATAT--------GCG-AT--------CCC----------A----------TCTTA--AGC----------AA----T----TTTCTCT--GCTTCGATAGATATACTGTTGGCTGGTAGTCTTCTCTCAGTACCAGATCTTCTTACAAAT
droWil2	scf2_1100000004921:1652724-1652885 +		TGGAGCAGAGATTTTCGGCGCTTTTGAACTTTGTTTGGGTCGCCTACAATGTAAGTA---TT---CCA--TGA----AAACTTTGTTA--------TTCA----AA----------AACTAAT----------AG-----CCC----T-----TTTGTGTCA------CTTTTTAAGATTTATTGCTGGCTAGTTGTATTCTCGCAATATCAAATCTTTTTGGCTTT
droVir3	scaffold_12963:10224199-10224348 -		TGGAGCAAAGATTCTCGGCGTGCTAAACTTCGTTTGGGTCGCTTATAATGTAAGTT---GA----------CATGCAGTTGT--------G-GT--------GACC----------A----------ATTTA--AC----------CA----T----TT--------CTGGTTTAGTTATACTGCTGGCTGGTCGTATTCTCCCAGTACCAATCTTCCTGGAGAT
droMoj3	scaffold_6500:18937486-18937649 -		TGGAGCAAAGATTCTCAGCGCTAATAAACTTCGTTTGGGTCGCCTATAATGTAAGTT----------AA--------CATAAAC----------AATTCCA----------A---GCA----------GTATTTA-A-TG----SAAATTTAA--------CTCTCATTTAGATATACTGCTGGCTCGTTGTTTTCTCGCATACCAATATCTTCTGTGGAAT
droGri2	scaffold_14830:1310046-1310205 +		TGGAGCAAAGATTCTCGGCGTGTTGAACTTCTTTGGATGGTACAATGTAAGTT----------GTT-------TAAAT--------AATTACA----------AACCT----TTGGCATTTTTGTTTA--A-------TACAA--ATCCTTCAGTTATACTGCTGGCTCGTTGTCTTCTCGCATATTCAAATCTTGTTGGAGTT

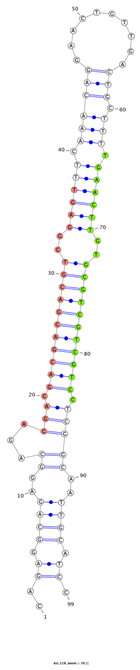
Generated: 09/08/2015 at 07:16 PM

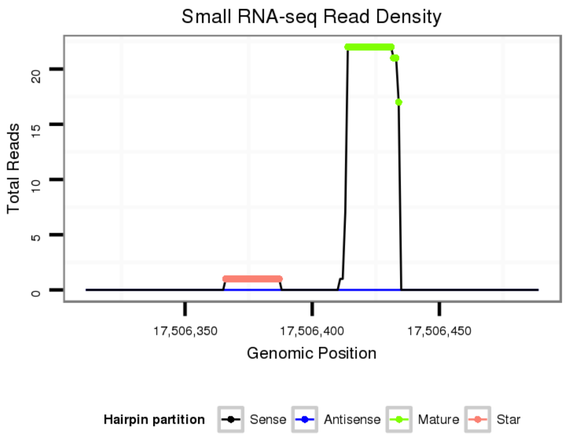
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

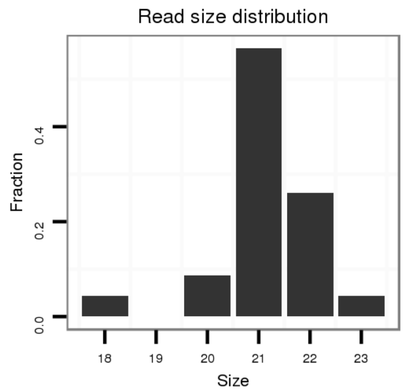
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dsi_118	**3r:17506361-17506439 +**	**candidate**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

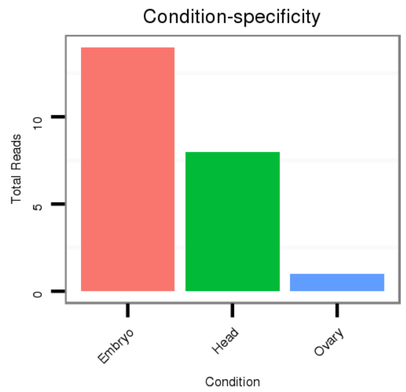
Legend: mature star mismatch in alignment mismatch in read

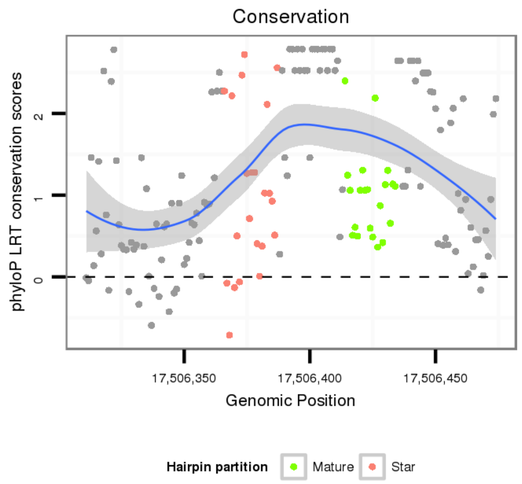
Predicted structure











Show Alternate Folds

Sense Strand Reads

hide 3p reads show mid mismatch reads

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CGATGATGATGTAATGATGACGATGTGGCAGTGGCAGTAACAGAGGCAGAGGCAGACGACGACGACGACGACGTCGGAGTTTCAAACAGGAACTGTTGACTGCTTTTGAACTTGTGCGTCGTCGTCCTCGGCAATTGCATCCTTAGACAATGACGCGTCCATAGAAGGCGGCAGCAGAATGA
****************************************..((.((((..((...(((.(((((((((((..((((((.((((((..........))).))).)))))).))))))))))).)))))..)))).)).****************************************
```

Read size	# Mismatch	Hit Count	Total Norm	Total	M025 embryo	M023 head	SRR618934 dsim w501 ovaries	GSM343915 embryo	SRR553487 NRT_0-2 hours eggs	O002 Head	M024 male body	SRR553485 Chicharo_3 day-old ovaries	SRR553488 RT_0-2 hours eggs
21	0	1	12.00	12	7	5	0	0	0	0	0	0	0
22	0	1	5.00	5	3	1	0	1	0	0	0	0	0
20	0	1	2.00	2	2	0	0	0	0	0	0	0	0
22	0	1	1.00	1	0	0	1	0	0	0	0	0	0
21	0	1	1.00	1	0	1	0	0	0	0	0	0	0
23	0	1	1.00	1	1	0	0	0	0	0	0	0	0
21	1	1	1.00	1	0	0	0	0	1	0	0	0	0

Anti-sense strand reads

```
GCTACTACTACATTACTACTGCTACACCGTCACCGTCATTGTCTCCGTCTCCGTCTGCTGCTGCTGCTGCAGCCTCAAAGTTTGTCCTTGACAACTGACGAAAACTTGAACACGCAGCAGCAGGAGCCGTTAACGTAGGAATCTGTTACTGCGCAGGTATCTTCCGCCGTCGTCTTACT
****************************************..((.((((..((...(((.(((((((((((..((((((.((((((..........))).))).)))))).))))))))))).)))))..)))).)).****************************************
```

Read size	# Mismatch	Hit Count	Total Norm	Total	SRR553485 Chicharo_3 day-old ovaries	SRR553486 Makindu_3 day-old ovaries	SRR618934 dsim w501 ovaries	M025 embryo	SRR902009 testis	GSM343915 embryo
18	1	3	0.33	1	0	0	0	1	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droSim2	3r:17506322-17506485 +	dsi_118	TA------A----------TGATGACGAT--GTGGCAGT-GGCAGTAACAGAGGCAG---------AGGC--AGACGACGACGAC---GAC---------GT-----C--GGAGT-TTCAAACAG----------GAACTGTTGACTGCTTTTGAACTT------GTGCG----------TCGTCGTCCT---CGGCAATTGCATCCTTAGACAATGACGCGTCCATAGAAGGCGGCAGCAGA----------
droSec2	scaffold_0:18337677-18337834 +		TA------A----------TGATGACGAT--GTGGCAGT-GGCAGTAACAGAGGCAG-------------AC--ACGACGACGAC---GAC---------GT-----C--GGAGT-TTCAAACAG----------GAACTGTTGACTGCTTTTGAACTT------GTGCG----------TCGTCGTCCT---CGGCAATTGCATCCTTAGACAATGACGCGTCCATAGAAGGCGGCAGCAGA----------
dm3	chr3R:17967485-17967658 +		TA------A----------TGATGACGAT--GTGGCAGT-GGCAGTAACAGAGGCAG---------AGGC---AGACGACGAC---GTC---------GT-----C--GGAGT-TTCAAACAGGCCC--TGCGAACAGGAACTGTTGACTGCTTTTGAACTT------GTGCG----------TCGTCGTCCT---CGGCAATTGCATCCTTAGACAATGACGCGTCCATAGAAGGCGGCAGTAGA----------
droEre2	scaffold_4820:10110048-10110196 -		TA------A----------TGATGACGAT--GTGGCAGT-GGCAGT----------------GGC---ACAGAACGAC---GAC---------GT-----C--GGAGT-TTCAAACAG----------GAACTGTTGACTGCTTTTGAACTT------GTGCG----------TCGTCGTCCT---CGGCAATTGCATCCTTAGACAATGACGCGTCCATAGAAGGCGGCAGCAGA----------
droYak3	3R:18816303-18816470 +		TA------A----------TGATGACGAT--GTGGCAGT-GGCAGC----------GGC---ATAGGACGAC---GAC---------GT-----C--GGAGT-TTCAAACAGGCCC--TGCGAACAGGAACTGTTGACTGCTTTTGAACTT------GTGCGTCGTCG--------TCATCGTCCT---CGGCAATTGCATCCTTAGACAATGACGCGTCCATAGAAGGCGGCAGCAGA----------
droEug1	scf7180000409768:88060-88215 +		TA------A----------TGATGACGAT--G-------G----------GGC---TGAGGATGAGGACGTGGACGACGATGT-----C--GGAGT-TTCAAACAG-------CGAGC-GGAACTGTTGACTGCTTTTGAACTT------GTGCG----------TCGTCGTCCT---CGGCAATTGCATCCTTAGACAATGACGCGTCCATGAAGGCGGCAGCAGA----------
droBia1	scf7180000302402:5771726-5771872 -		CA------A----------TGATGACGAT--G-------G----------GGC---AGAGGATGAGGACGTC---------GT-----C--GGAGT-TTCAAACAG-------CGAGC-GGAACTGTTGACTGCTTTTGAACTT------GTGCG----------TCGTCGTCCT---CGGCAATTGCATCCTTAGACAATGACGCGTCCACAGAAGGCGGCTGCAGA----------
droTak1	scf7180000415711:1081318-1081475 -		CA------ATGGTGA-----TGATGATGAT--G-------G----------GCC---AGAGGATGAC---GAT---------GTGGCAG-C--GGAGT-TTCAAACAG-------CGAGC-GGAACTGTTGACTGCTTTTGAACTT------GTGCGTCC----------TCGTCGTCCT---CGGCAATTGCATCCTTAGACAATGACGCGTCCATAGAAGGCGGCAGCAGA----------
droEle1	scf7180000491212:2458555-2458698 +		TA------A----------TGATGACGAT--G-------G----------GGC---AGAGGATGAC---GAC---------GC-----C--GGAGT-TTCGAACAG-------CGAGC-GGAACTGTTGACTGCTTTTGAACTT------GTGCG----------TCGTCGTCCT---CGGCAATTGCATCCTTAGACAATGACGCGTCCACAGAAGGCAGAGCAGA----------
droRho1	scf7180000780293:46119-46262 -		TA------A----------TGATGACGAT--G-------G----------GGC---AGAGGATGAC---GAC---------GT-----C--GGAGT-TTCAAACAG-------CGAGC-GGAACTGTTGACTGCTTTTGAACTT------GTGCG----------TCGTCGTCCT---CGGCAATTGCATCCTTAGACAATGACGCGTCCATAGAAGGCAGCAGCAGA----------
droFic1	scf7180000454106:1126013-1126156 +		TT------A----------TGATGACGAT--G-------G----------GGC---AGAGGATGAC---GAC---------GT-----C--GGAGT-TTCAAACAG-------CGAGC-GGAACTGTTGACTGCTTTTGAACTT------GTGCG----------TCGTCGTCCT---CGGCAATTGCATCCTTAGACAATGACGCGTCCATAGAAGTCGGCGCGCAGA----------
droKik1	scf7180000302461:2096831-2096999 -		TG------A----------TGATGATGAT--GTTGTTGT-TGTAATGAT-GACGATG---------GGC---AGAGGATGAC---GAA---------GC-----C--AGAGT-TTCAAACAGGAA-----CGAGC-GGAACTGTTGACTGCTTTTGAACTT------GTGCG----------TCGTCGTCCT---CGGCAATTGCATCCTTAGACAATGACGCACATAGAAGGCGACAGCAGA----------
droAna3	scaffold_13340:8968346-8968486 +		CA------A----------TGATGATGAT--G-------G----------GGCAC--AAGAGGATGAGGCCGTA---------GC-----C--GGAGT-TTCGAACCG-------CGAGC-TGAGCTGTTGACTGCTTTTGAACTT------GTGCG----------------TCCT---CGGCAATTGCATCCTTAGACAATGACACACATAGAGAT---CCCGGA----------
droBip1	scf7180000396712:120024-120159 +		TG------A----------TGATGATGAT--G-------G----------GGCACAGAGAGATGAC---GC---------------------GC-CCTAGCCAGG-------CTAGC-TGAGCTGTTGACTGCTTTTGAACTTGTACTTGTGCG----------TCGTCGTCCCGACAGGCAATTGCATCCTTAGACAATGAGACACATA----------
dp5	2:12134270-12134394 +		TG------A----------GC--------GGCAG-GGCAG----------GAGGCACGA-GGC---------------------AGGGAAAGTAG-----TCT-GCAAC-GGAACTGTTGACTGCTTTTGAACTT------GTGCGTCGTCGTCG--TCGTCGTCGTCCT---CGGCAATTGCATCCTTAGACAATGAGAC----------
droPer2	scaffold_0:8362600-8362747 -		TG------A----------GCCAGGGGAT--CGGGCAGGAGGCAGGA-----GGCAGGAGGCAAGT-GGC---------------------AGGGAAAGTAG-----TCT-GCAAC-GGAACTGTTGACTGCTTTTGAACTT------GTGCG----------TCGTCGTCCT---CGGCAATTGCATCCTTAGACAATGAGAC------AGAAAGAGGGA-AAGA----------
droWil2	scf2_1100000004943:12107811-12107953 +		TGCTTACAATGATGATGATGATGATGATGATGAT--G-------G----------GTGC---------TGAC---GAG-----AGAGT-----C--TGAGT-TTCAGACAGGAA------CTC---TTGTGTTGACTGCTTTTGAACTT------GTGCGTCGTCTTCAAAACCTCGTCGTCCT---C---CGTTGCATCCTTAGACAATGAG----------
droVir3	scaffold_13047:8512737-8512872 -		AA------A----------GGATGACGAT--G-------G----------GTCGT---------------------AGAGGAAGAGTTTTCCAACAG----------AAGGTTTGACTGCTTTTGAACTT------GTATG----------CCGCATACTT---ACACGCAAAATAAATAGAAATG-------CATAAAAC----TAGCAGATGCACGGCTGCACAGAGGG
droMoj3	scaffold_6540:27646985-27647076 +		CA------G----------CGAAGCG-AT--ATGAAAAT-CGC----------GTTAG---AAAGGATGAC---GAT---------GTCGCGGCAGAAGAGT-TT-------------TTCCAACGGGAGCGCGTTGACTGCTTTTGAACTT------G---
droGri2	scaffold_15074:1102666-1102794 +		TA------A----------CAACGACGAGCCATGAAAAT-CGC----------GTGAG---AATGGATGAC---GAC---------GC-GTCGTCGCTGAGT-TT-----CC-------CAAGCTGAAGCTGTTGACTGCTTTTGAACTT------GTCTG----------TAAATGTGTG---CGCGTGTCGGCATCCTTAGAC----------

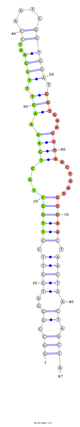
Generated: 09/08/2015 at 08:04 PM

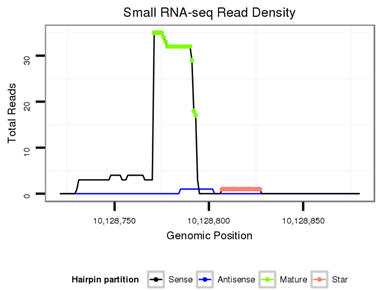
	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

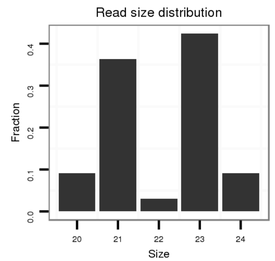
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dsi_165	**2r:10128771-10128830 +**	**candidate**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser [Cornell Mirror]]

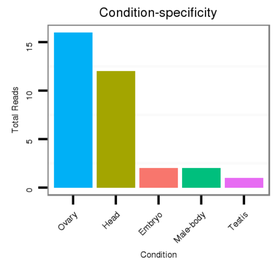
Legend: mature star mismatch in alignment mismatch in read

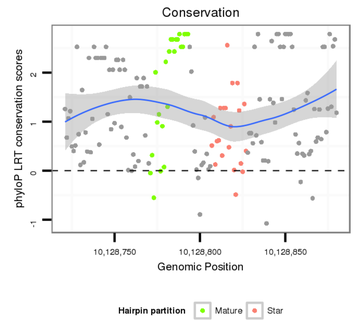
Predicted structure











Show Alternate Folds

Sense Strand Reads

hide 3p reads show mid mismatch reads

```
CAGTTCAATTCTGGGGGTCGTCGGGAAGCCTTACGTGGCCGGGATGGTTCGTTGGCTGCTGAGAACTTTCCAATCCAATCGGTGGATGGTGAACTTAACTAATGCCAACTAACTAACTACTAGCCAACAACTGTTAACGACCCACAAAAGCCTGGCCACAAAAG
********************************(((.(..(((((.(((((((...((((.(((.((((..((....)))))))..)))...))))......)))))))..)))))..)).)))..**********************************
```

Read size	# Mismatch	Hit Count	Total Norm	Total	M023 head	SRR553486 Makindu_3 day-old ovaries	SRR553485 Chicharo_3 day-old ovaries	M025 embryo	SRR618934 dsim w501 ovaries	M024 male body	SRR902009 testis	O002 Head	GSM343915 embryo	SRR553488 RT_0-2 hours eggs
23	0	1	14.00	14	2	2	6	1	0	1	1	0	1	0
21	0	1	11.00	11	6	3	2	0	0	0	0	0	0	0
24	0	1	3.00	3	0	2	1	0	0	0	0	0	0	0
20	0	1	3.00	3	2	0	0	0	0	1	0	0	0	0
22	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0
24	1	1	1.00	1	0	0	0	1	0	0	0	0	0	0
21	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0
25	0	1	1.00	1	0	0	0	0	1	0	0	0	0	0
21	0	1	1.00	1	0	0	0	0	0	1	0	0	0	0
23	0	1	1.00	1	0	1	0	0	0	0	0	0	0	0
18	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0

Anti-sense strand reads

```
GTCAAGTTAAGACCCCCAGCAGCCTTCGGAATGCACCGGCCCTACCAAGCAACCGACGACTCTTGAAAGGTTAGGTTAGCCACCTACCACTTGAATTGATTACGGTTGATTGATTGATCGGTTGTTGACAATTGCTGGGTGTTTTCGGACCGGTGTTTTC
*************************************(((.(((.(((((.(((((((...((((.(((.((((..((....)))))))..)))...))))......)))))))..)))))..)).)))..**********************************
```

Read size	# Mismatch	Hit Count	Total Norm	Total	M023 head	SRR553485 Chicharo_3 day-old ovaries	SRR553487 NRT_0-2 hours eggs
18	0	1	1.00	1	1	0	0

Show Alignment With Reads

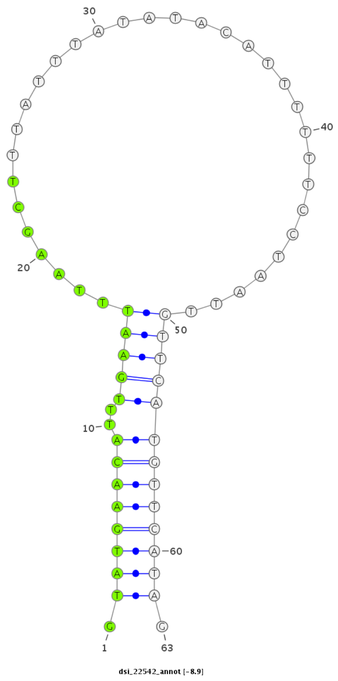
Re-alignment of all predicted orthologs

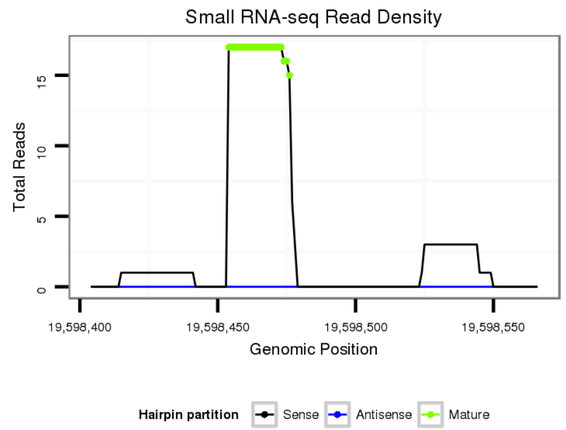
Species	Coordinate	ID	Alignment
droSim2	2r:10128721-10128880 +	dsi_165	CAGTTC--AATTCTG----------GGGGT--C-GTCGGAAGCCTTACGTGGCCG-G----------GATGGTTCG----TTGG--CTGCTG----------AGAACTTTCCAATC--CAA----------TCGGTG----------GATGGTGAAC----------TTAACTAATGCCAACTAACTAACTAGC----CAACAACTGTTAACGACC----------CACA----AAAGCCTG----GCCACAA-AAG
droSec2	scaffold_1:6983739-6983898 +		CAGTTC--AATTCTG----------GGGGT--C-GTCGGAAGCCTTACGTGGCCG-G----------GATGGTTCG----TTGG--CTGCTG----------AGAACTTTCCAATC--CAA----------TCGGTG----------GATGGCGAAC----------TTAACTAATGCCAACTAACTAGC----CAACAACTGTTAACGACC----------CACA----AAAGCCTG----GCCACAA-AAG
dm3	chr2R:9465540-9465702 +		CAGTTC--AATTCTG----------GGGGT--C-GTCGGAAGCCTTACGTGGCCG-G----------GATGGTTCG----CTGG--CTGCTG----------AGAACTTTCCAATC--CAA----------TCGGTG----------G-TGCGAAC----------TTAACTAATGCCAACTAACTAACTAC-CAAC-AACAACTGTTAACGAC----------CACA----AAAGCCTG----GCCACAA-AAG
droEre2	scaffold_4845:16348780-16348936 -		CAGTTC--AATTCTG----------GGGGT--C-GTCGGAAGCCTTACGTGG---G--CTGCAG--A---GAGCAG----------GCGGAGGCGAAGGAACTTTCCAATC--CAA----------TCGGTG----------GATGGCGAAC----------TTAACTAATGCCAACTACTCTAAC----------AACAACTGTTAACGAC----------CACA----AAACCTG----GCCACAA-AAG
droYak3	2R:7483168-7483339 -		CAGTTC--AATTCTG----------GGGGT--C-GTCGGAAGCCTTACGTGG---G--CTGCAG--A---CAGCT GAGAGAAGAGGAGGAG GAGGAGGCGAAGGAACTTTCCAATC--CAA----------TCGCTG----------GATGGCGAAC----------TTAACTAATGCCAACTACTCTAAC----------AACAACTGTTAACGAC----------CACA----AAACCTG----GCCACAA-AAG
droEug1	scf7180000409462:3398106-3398270 -		CAGTTC--AATTCTG----------GGGGT--C-GTCGGAAGCCTTACGTGGACG-G----------GATGGTTCA----CTGG--CTGCCGAA---AAGCAG----------AAAGAACTTTCCAATC--CAA----------TCGGTGG----------A-----TGTGGATATC----GATGGCAAAC----------TTAAG-----GG----ACTAAC----------AAACAACTGTTAACGAC----------AAC----AAACCTG----GCCACAA-AAG
droBia1	scf7180000302291:694711-694861 -		CAGTTC--AATTCTG----------GGGGT--C-GTCGGAAGCCTTACGTGGACG-G----------GAGGTTCA----CTGG--CTGCCGAA---AAGCAG----------GAAGAACTTTCCAATC--CAA----------G--CAGG----------A-----TGTG----------GAGGCAAAC----------TTAAG-----GTG----ACTAAC----------AACAACTGTTAACGAC----------AAA----AAACCTG----GCCACAA-AAG
droYak1	scf7180000415401:1189962-1190112 -		CAGTTC--AATTCTG----------GGGGT--C-GTCGGAAGCCTTACGTGGACG-G----------GATGGTTCA----CTGG--CTGCCGAA---CAGCAG----------AAAGAACTTTCCAATC--CAA----------G--CTGG----------A-----TGTG----------GATGGCAAAC----------TTAAG-----GG----ACTAAC----------AAACAACTGTTAACGAC----------AAA----AAACCTG----GCCACAA-AAG
droEle1	scf7180000491282:712037-712191 +		CAGTTC--AATTCTG----------GGGGT--C-GTCGGAAGCCTTACGTGGACG-G----------GATGGTTCA----CTGG--CTGCCGAA---AAGCAG----------AAAGAACTTTCCAATC--CAA----------G--CGTG----------A-----CGTG----------GATGGCAAAC----------TTAAG-----GG----ACTAAC----------AAACAACTGTTAACGAC----------AAA----AAACCTG CAAACCACAA-AAG
droRho1	scf7180000758477:993-1143 -		CAGTTC--AATTCTG----------GGGGT--C-GTCGGAAGCCTTACGTGGACG-G----------GATGGTTCA----CTGG--CTGCCGAA---AAGCAG----------AAAGAACTTTCCAATC--CAA----------G--GGTG----------A-----TGTG----------GATGGCAGAC----------TTAAG-----GG----ACTAAC----------AAACAACTGTTAACGAC----------AAA----AAACCTG----GCCACAA-AAG
droFic1	scf7180000454039:281957-282115 +		CAGTTC--AATTCTG----------GGGGT--C-GTCGGAAGCCTTACGTGGCCG-G----------GATGGTTCA----CTGAGTCGCCGAA---AGGCAG----------AAAGAACTTTCCAATC--CAA----------TCGGTGC----------A-----TGTG----------GATGGCAAAC----------TTAAG-----GG----ACTAAC----------AAACAACTGTTAACGAC----------AAA----AAACCTG----GCCGCAAAAG
droKik1	scf7180000302638:199112-199331 -		CAGTTC--AATGCTG----------GGGGT--C-GACGGAAGCCTTAGTGGGCATGGGCCTGGG----------CTGG--CATGGGTTCCGCCGCCG--CTGCCGAA---AAGCAG----------AAAGAACTTTCCAATC--CAA----------TCATGCGCAGACGCGAGCGGTGTGTGTGGT-CAGTGTGTA-TGTGTGTGTGTGTG--TATTGGCAAG----------GCAGCGCT----TAACTAAC----------AAACAACTGTTAACGAC----------AAA----AAACCTG----GCCACAA-AG
droAna3	scaffold_13266:16768145-16768389 +		CAGTTC--GA---TG----------GGGGT--C-GTCGGAAGCCTTAGTGGA-A-TGG---GGGCAGAAGCCACCAGCAGCAGCAACAGCAGCAAAAGCAGCAACTGGATGGCTGGCAGAGAGGTTCA----CCG---CG-CG-GAAAGAAAGCAG----------AGAAAGAACTTTCCAAT-AGCAA----------TGTGTG----------TGT---GT-TGTGTG-TGTGTGCGGAAAATGGCAAAC----------TTAACTGT---GA----ACTAAC----------AAACAACTGTTAACGAC----------AAA----AAACCTG----GCCACAA-AAG
droBip1	scf7180000396735:20710-20942 +		CAGTTC--G-A---TG----------GGGGT--C-GTCGGAAGCCTTAGTGGA-A-TGA---TGGCA--------GCAGCACCAACAGCAG----------CTGGATGGATGGCAGAGGTTCA----TCG---CT-CG-GAAGGAAAGCAG----------AGAAAGAACTTTCCAAT-AGCAA----------CGGTGC----------GTGTGTGT-CTAGCTGTGT---GT-TGTGTG-TGTGTGCGGAAAATGGCAAAC----------TTAACTA-T--GA----ACTAAC----------AAACAACTGTTAACGAC----------AAA----AAACCTG----GCCACAA-AAG
dp5	3:14617468-14617634 -		CAG-GATGG---G----------GGGGT--C-GTCGGAAGCCTAGTGGAA-G-TGA--G----------ATGGTCCG----CTGG--CTGCCGAGCGA-----GC--AAAAGAAAGACCGAATGA-----AAGAAGAACTTTCCAAT-A-CAG----------TGTGG----------CGTGGGTTGC----------GGGCGCG----------TTA-------G----ACTAAC----------AAACAACTGTTAACGCAG----------AAA----AGAAA-ACCACAA-AAG
droPer2	scaffold_4:2988808-2988974 +		CAG-GATGG---G----------GGGGT--C-GTCGGAAGCCTTAGTGGA-A-TGA--G----------ATGGTCCG----CTGG--CTGCCGAGCGA-----GC--AAAAGAAAGACCGAATGA-----AAGAAGAACTTTCCAAT-A-CAG----------TGTGG----------CGTGGGTTGC----------GGGCGCG----------TTA-------G----ACTAAC----------AAACAACTGTTAACGCAG----------AAA----AGAAA-ACCACAA-AAG
droWil2	scf2_1100000004514:3813723-3813878 +		CAGTTC--AATGCCAACTATAGGAAGAGGGAAAACGGTGAAGGGGGTGAGACGAA-TA-TTGTCGTCGAAGCCTTAGATGAA--G--AAAGAAGAACTTTCCAAT-AGC---A----------G-AAAC----AAAC-----AAAAACTGTTAACGAC----------CAAAACAC--AAAA----ACCACAC--AAA
droVir3	scaffold_12875:11132308-11132423 -		T---G----------G---G----------G---G----------G

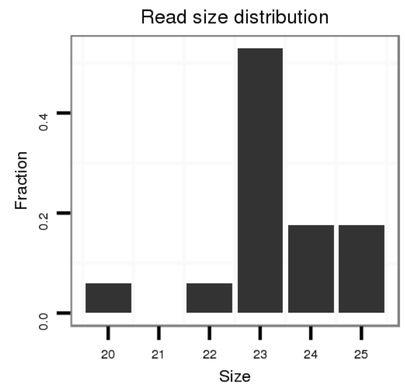
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dsi_22542	**3l:19598454-19598516 +**	**candidate**	**Mirtron**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

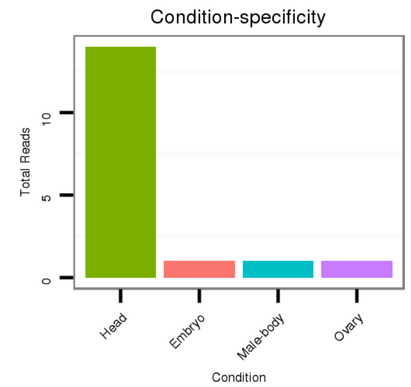
Legend: mature star mismatch in alignment mismatch in read

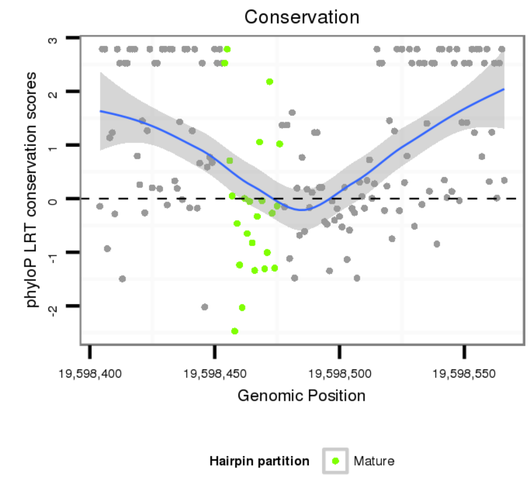
Predicted structure











Show Alternate Folds

Sense Strand Reads

hide 3p reads show mid mismatch reads

TATAGTTTCCGGAAATCTTGTCGGGTACTTTGAAATTGATTCAAAAACAGGTATGAACATTTGAATTTAAGCTTTATTTATATACATTTTTTCCTAATTGTTCATGTTCATAGGAGTGATTAAGACGACAGAACGCAAATTGGATAGAGAAAATCAAGCGGAA ********** .(((((((..(((((.....)))))))))))). **********	Read size	# Mismatch	Hit Count	Total Norm	Total	M023 head	M024 male body	SRR553488 RT_0-2 hours eggs	M053 female body	SRR553486 Makindu_3 day-old ovaries	M025 embryo	SRR553487 NRT_0-2 hours eggs	SRR618934 dsim w501 ovaries
.....GTATGAACATTTGAATTTAAGCT.....	23	0	1	9.00	9	7	1	0	0	0	1	0	0
.....GTATGAACATTTGAATTTAAGCTT.....	24	0	1	3.00	3	2	0	0	0	1	0	0	0
.....GTATGAACATTTGAATTTAAGCTTT.....	25	0	1	3.00	3	3	0	0	0	0	0	0	0
.....AAGACGACAGAACGCAAATT.....	20	0	1	2.00	2	0	2	0	0	0	0	0	0
.....GAAATCTTGTCGGGTACTTTGAAATTG.....	27	0	1	1.00	1	0	0	0	1	0	0	0	0
.....GTATGAACATTTGAATTTAAGC.....	22	0	1	1.00	1	1	0	0	0	0	0	0	0
.....GTATGAACATTTGAATTTAAGCG.....	23	1	1	1.00	1	1	0	0	0	0	0	0	0
.....GTATGAACATTTGAATTTAA.....	20	0	1	1.00	1	1	0	0	0	0	0	0	0
.....TAAGACGACAGAACGCAAATTGGATA.....	26	0	1	1.00	1	0	0	1	0	0	0	0	0

Anti-sense strand reads

ATATCAAAGGCCTTTAGAACAGCCCATGAAACTTTAACTAAGTTTTTGTCCATACTTGTAAACTTAAATTCGAAATAAATATATGTAAAAAAGGATTAACAAGTACAAGTATCCTCACTAATTCTGCTGTCTTGCGTTTAACCTATCTCTTTTAGTTCGCCTT ********** .(((((((..(((((.....)))))))))))). **********	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
droSim2	3l:19598404-19598566 +	dsi_22542	TATAGTTTCCGGAAATCTTGTCGGGTACTTTGAAATTGATTCAAAAACAGGTATGAACATTTG----------AA------TTTAAG--C----TT-------TATTTATAT----------ACA-----TTTTTTCCTA----------ATT--GTTCATGTTCATAGGAGTGATTAAGACGACAGAACGCAAATTGGATAGAGAAAATCAAGCGGAA
droSec2	scaffold_29:650612-650774 +		TATAGTTTCCGGAAATCTTGTCGGGTACTTTGAAATTGATTCGAAAACAGGTATGAATATTTG----------AA------TTTAAA--C----TT-------TATTTATAT----------GCA-----TTTTTTCCTA----------ATG--TTTCATGTTCTTAGGAGTGATTAAGACGACAGAACGCAAATTGGATAGAGAAAATCAAGCGGAA
dm3	chr3L:20005734-20005888 +		CATAGTTTCCGGAAATCTTGTCGGGTACTTTGAAATTGATTCGAAAACAGGTACGAATA----------A-------A-TAAG--C----TT-------TAGTTATAA----------ACA-----TTTTTTCCTA----------ATT--GTTCATGTTCTTAGGAGTGATTAAGACGACAGAACGCAAATTGGATAGAGAAAATCAAGCGGAA
droEre2	scaffold_4784:19746265-19746423 +		TATAGTTTCTGGAAATCTGGTCGGGTACTTTGAAATTGATTCGAAAACAGGTACCATTCCTTAA----------T-------AAGTT-GAGTT--------GATAT----------ATA-----TT--TAGTTA----------ATT--GTTCATGTTCTTAGGAGTGATTAAACGACAGAACGCAAATTGGATAGAGAAAATCAAGCGGAA
droYak3	v2_chr3L_random_219:702-862 +		TATTGTTTCTGGAAATCTGGTCGGGTACTTTGAAATTGATTCGAAAACAGGTACAAACATTTA----------AA------TATAATT-TAATT--------GAAAT----------ATA-----TT--TAATTC----------ACT--GTTCTTGTTCTTAGGGTTGATTAAACGACAGAACGCAAATTGGACAGAGAAAATCAAGCGGAG
droEug1	scf7180000409711:5935600-5935759 -		CATAGTTTCTGGAAATCTGGTCGGCTATTTCAAATTGACTCCAAAACAGGTAATA-ACCTTA-A----------AAA------ATT-AGATT--GAAACTTAATTA----------A--TA---------TA----------TT--ATT--TTGTGTAACCTTAGGAGTGATTAAACGACTGAACGTAAGCTGGATAGAGAAAATCAAGCAGAA
droBia1	scf7180000302193:2785846-2786007 +		TATTGTTTCTGGAAATCTAGTCGGCTATTTGAAATTGATTCAAAAACAGGTACCCTTTTCCCG----------GT------TCTAA--G---TT-TATT-----GTTTA----------ATA-----TT--AATGCA----------AATT--TATTATAATTTAAGGAGTTATAACAACCACTGAACGTAAACTGGACAGAGAAAATCAGGCAGAA
droTak1	scf7180000415392:121328-121485 -		TATCGTTTCCGGAAATCTGGTCGGCTACTTTGAAATTGATTCAAAAACAGGTATTAAA-TTTA-T----------AAA------TTCA----AAGT-TTCATT----------TTTTTA--AATAT----------A----------A----TTTATGCATTCTAAGGAGTAATTACAACCACTGAACGCAAACTGGATAGAGAAAATCAAGCAGAA
droEle1	scf7180000491193:4297731-4297891 +		TATCGTTTCCGGAAATCTGGTCGGCTACTTCGAGATCGATTCGAAAACAGGTAATTATATTCA-A----------AAA------ATT-ACATT--TAATTTGAATA----------A--CA-------TGA----------CTT--GCTTATGATTTTAGGAGTAATCAAAACAACTGAACGCAAATTGGACAGAGAAAATCAAGCGGAA
droRho1	scf7180000777710:16697-16857 -		TATCGTTTCCGGAAATCTGGTCGGCTACTTTGAAATTGATCAAAAACAGGTAAATTTATTTA-A----------ATA------GAT-AAATT--TTAGCTTAAATT----------A--CA-------ATCA----------ATT--GTTTATATTTTTAGGAGTGATCAAAACACTGAACGCAAACTGGACAGAGAAAACCAAGCGGAA
droFic1	scf7180000454113:2305538-2305695 -		CATCGTATCGGGAAACTTCGGTCGGCTACTTTGAAATCGATTCAAAAACAGGTAACATAA---G----------AAAACG----AAA--T-----TT-------TAGTTATAA----------AA-ATTCA----------A----------A---CGTTGATTGTATTTTTAGGAGTGATTAAAACGACTGAGCGAAAGTTGGACAGAGAAAATCAAGCGGAA
droKik1	scf7180000302686:453390-453551 +		CATTGTGTCTGGAAACTTCGTTGGCTACTTTGAAATTGATCCAAAAACAGGTAAAACAAATCG----------AA------GGCACATC-TAAGC--------GTA------AT----------ATT-----TT--CATTT----------A-TAT-TTGCATTATTTTAGGAGTAATTAAGAGCACTGAGCGCAAATTGGACAGAGAAAATCAGGCAGAG
droAna3	scaffold_13337:5128579-5128736 -		TATAGTTTCTGGAAATCTGTTGGCTACTTTGAAATTGATTCCAAAACAGGTAAGACAATAT----------TT----------TA------TTCA----C-CTTT--------TACAA----------C--------TT--TACTTT----------A-TTTTTATGATAATTGTAGGTGTTATTAGAACCACGGACGCAAACTGGACAGAGAAAATCAGGCAGAG
droBip1	scf7180000396371:462699-462858 -		TATTGTTTCTGGAAATCTGGTTGGCTACTTTGAAATTGATTCCAAAACAGGTAAGACAGTATG----------T-------TTATT--C-----TT-------T-GTTAAAA----------ATA-----TT--TCCTTTA----------A-TTTTTTTGATAATTTAAGGAGTTATAAGAACCACGGACGCAAACTGGACAGAGAAAATCAAGCAGAG
dp5	Unknown_singleton_2399:3327-3532 -		TATTGTGTCTGGAAATCTAGTGGGATACTTTAAAATAGATTCCATAACAGGTAAAGTTATTCA-TCGCCGTAAAAC--CACATCCTTCAAAACCCTATTAAATCCAATTATAATTGTCAC-------A---TTTATT----------ATGTAA--TATGT----------A----------T---TGCTCTTTGTACTTGTAGGTGCTATTAAAACTACTGACGCAAACTGGATCCGAAAACCAAGCAGAA
droPer2	scaffold_88:5705-5910 -		TATTGTGTCTGGAAATCTAGTGGGATACTTTAAAATAGATTCCATAACAGGTAAAGTTATTCA-TCGTCGTAAAAC--CACATCCTTCAAAACCTTATTAAATCCAATTATAATTGTCAC-------A---TTTATT----------ATGTAA--TATGT----------A----------T---TGCTCTTTGTACTTGTAGGTGCTATTAAAACTACTGAACGCAAACTGGATCGAGAAAACCAAGCAGAA
droWil2	scf2_1100000004540:962486-962647 +		CATCATATCCGGAAATCTGGTTGGATATTTCGAGATTAATTCATAACAGGTAAACTAGTCTA-A----------C-------A-GATT-AGTTT--C-------AAATCTT----TTTTAA--TA---------TG----------TT--TTT--TTTTGGATTTTAAGGCGTTCTTAAAACGACAGCACGAAACTCGACAGAGAAAATCAAGCTGAA
droVir3	scaffold_13049:17947548-17947715 +		TATTACTTCCGGAAATCATGTAGGATACTTTGATATTGAGCGGCATACAGGTGACTACGCCA-G----------GAA------TTTA----GAAT--A------A------ATATCATTTTTAATGTAT--AA---------AATA----------TTT--GTTTTTTTTATAGGATTGCTTAAAACGACGGAACGAAAGCTAGACAGAGACAATCAATCAGAA
droMoj3	scaffold_6680:23471858-23472023 +		TATTACATCTGGAAATCTGATTGGGTATTTTCCATTAGAACCACACACAGGTAACTAAATAG-GCAATGAAATACTTAATATAATTAT----------AAGTA----------AATTA----------AAT--TTAAAAATATTTAGGAATTGTAAGAAGTACAGAACGTAAACTTGACAGAGAGAATCAAGCAGAA
droGri2	scaffold_15110:23990609-23990774 +		TATTATTTCTGGAAATTTGGTTGGATATTTCGACATAGACCCTAATACAGGTTAGCACAAAT----------TCTTA----------AA------AAAAA---GTGTA--------TT--AA---------TTAATTGCTTATTT--AAAA--CCCAAATTTATTTAGGTGTTCTAAAACGACAGAACGAAACTTGACAGAGAAAATCAAGCAGAA

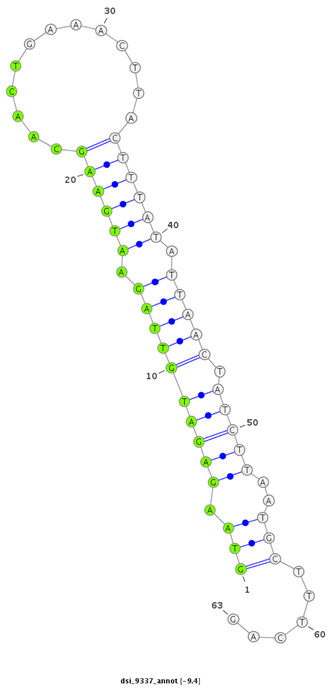
Generated: 09/08/2015 at 07:17 PM

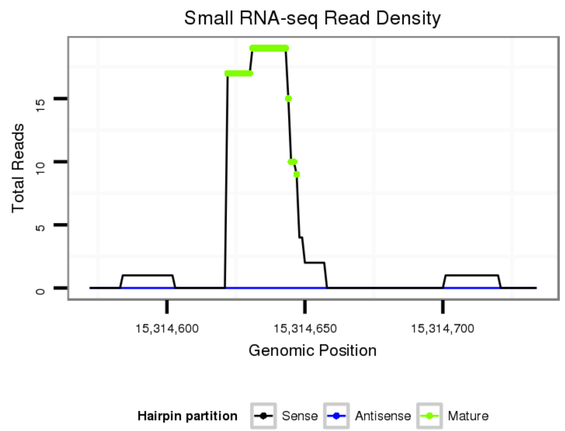
	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	0
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

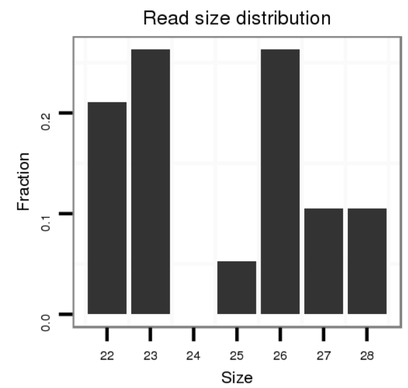
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dsi_9337	**x:15314622-15314684 +**	**candidate**	**Mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

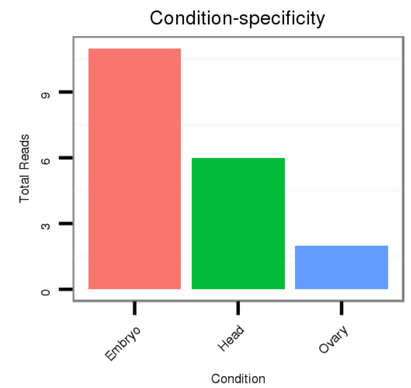
Legend: mature star mismatch in alignment mismatch in read

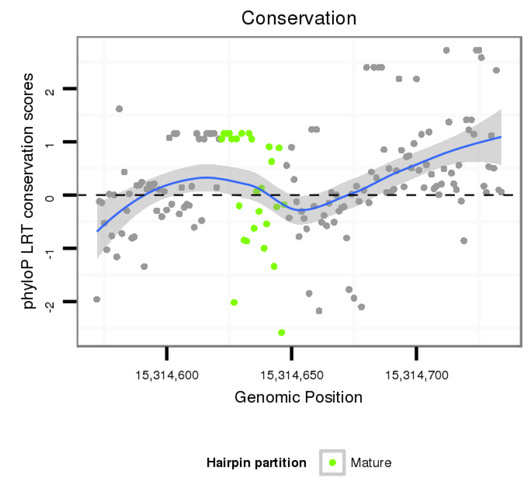
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [x_15314622_15314684_+]; CDS [x_15314685_15315276_+]; CDS [x_15314517_15314621_+]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

AAACCCCGAATCTGGGCGACCTTTCTTCATTTTTGGTTCATCCGAAAACGGTAAGAGATGTTAGAATGAAGCAACTGAAACTTACTTTATATTAACTATCTTAATGCTTTCAGATCAAAGTCCAGTTCCTTCAAAATCTGAAGACACAAGTGATATTTGTCGC **********(((.(((((((((.(((((((.....)))))))..)))))..)))))..)))).....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M025 embryo	M023 head	M024 male body	SRR553488 RT_0-2 hours eggs	M053 female body	O002 Head	SRR553486 Makindu_3 day-old ovaries	SRR553485 Chicharo_3 day-old ovaries
.....GTAAGAGATGTTAGAATGAAGCAACT.....	26	0	1	5.00	5	4	1	0	0	0	0	0	0
.....GTAAGAGATGTTAGAATGAAGCA.....	23	0	1	5.00	5	3	2	0	0	0	0	0	0
.....GTAAGAGATGTTAGAATGAAGC.....	22	0	1	4.00	4	1	2	0	0	0	1	0	0
.....GTTAGAATGAAGCAACTGAAACTTACT.....	27	0	1	2.00	2	2	0	0	0	0	0	0	0
.....GTAAGAGATGTTAGAATGAAGCAACTGA.....	28	0	1	2.00	2	0	0	0	1	0	0	1	0
.....TGGGCGACCTTTCTTCATT.....	19	0	1	1.00	1	0	0	0	0	1	0	0	0
.....GTAAGAGATGTTAGAATGAAGCAAC.....	25	0	1	1.00	1	1	0	0	0	0	0	0	0
.....TTCAAAATCTGAAGACACAA.....	20	0	1	1.00	1	0	0	1	0	0	0	0	0
.....GTAAGAGATGTTAGAATGAAGCAACG.....	26	1	1	1.00	1	1	0	0	0	0	0	0	0

Anti-sense strand reads

TTTGGGGCTTAGACCCGCTGGAAAGAAGTAAAAACCAAGTAGGCTTTTGCCATTCTCTACAATCTTACTTCGTTGACTTTGAATGAAATATAATTGATAGAATTACGAAAGTCTAGTTTCAGGTCAAGGAAGTTTTAGACTTCTGTGTTCACTATAAACAGCG **********(((.(((((((((.(((((((.....)))))))..)))))..)))))..)))).....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	SRR553486 Makindu_3 day-old ovaries	SRR553488 RT_0-2 hours eggs
.....TCAAGTAGGCTTTTG.....	15	1	9	0.11	1	1	0

Show Alignment With Reads

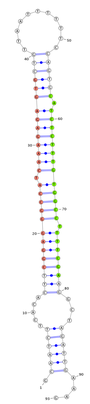
Re-alignment of all predicted orthologs

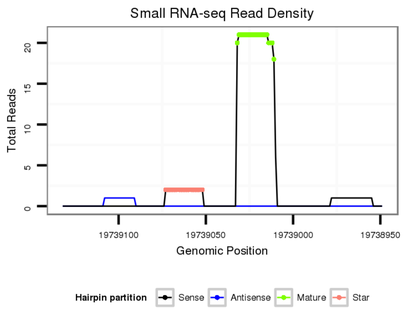
Species	Coordinate	ID	Alignment
droSim2	x:15314572-15314734 +	dsi_9337	A---AACCCCGAATCTGGGCGACCTTTCTTCATTTTTGGTT-CATCCGAAAACGGTAAGAGATGTTAG---AAT----------GAAGCA------ACTGAAACTTACTTTATATTAACTA-TCTTAATG----------CTTTCA--GATCAAAGTCCAGTTCCTTCA-----AAATCTG-AAGACACAAGTGATATTTGTCGC
droSec2	scaffold_17:21595-21757 +		A---AACCCCGAATCTGGGCGACCTTACTTCATTTTTGGTT-CATCCGAAAACGGTAAGAGATGTTAG---AAT----------GAAGCA------AATGAAACTTACGTTATATTAACTA-TCTGAATG----------ATTTCA--GATCAAAGTCCAGTTCCTTCA-----AAATCTG-AAGACACAAGTGATATTTGTCGC
dm3	chrX:16194859-16195021 +		G---AACTGTGAATCTGGGCGACCTTTTTTCATATTTGGTT-CATCCGAAAACGGTAAGAGATGTTAG---AAT----------GAAGAATAG----AATGA---ATACGTTACATTAACTA-TCTTAATG----------ATTTCA--GATCAAAGTCCAGTTCCTTTA-----AAATCTG-AAGACACAAGTGATATTTCTCGC
droEre2	scaffold_4690:10892967-10893124 -		G---ATCCCTGGATCCGGGCGACCTGTTTCGTTTTCGGCT-CATCCGAAAACGGTAAGAGATGTTAG---CAT----------GAAGCA------AGTGA-AG-----TTAACCTAATTATGCTTATTTG----------GTTTTA--GATCAAAATCCAGTTCCTTCA-----AAATCTG-AAGACACAAGTGATATTTGTCGC
droYak3	v2_chrX_random_001:37734-37887 +		G---ATACCTGGATCGGGGCGACCTGTCTTCATTTTCGGTT-CATCCGAAAACGGTAAGTGATATTAG---CAA----------GAA---------GA-GAAG-----TTAACTTAACTA-TCGTAATG----------GTTTCA--GATCCAAATCCAGTTCCTTCA-----AAATCTG-AAGACACAAGTGATATTTGTCGC
droEug1	scf7180000409008:1415139-1415307 -		G---ATGAGTGGATCGGAGCGATCTGTCCAGGTTTTGGATC-AATCCGAAAACGGTAAGAGATTCTATTGAAAT-TATCATCATTTAAAACAAA----------ATGAAAT----------TCAACTT-GTACAATG----------TTTCCA--GATCAAAATCCAGTTCCTTCA-----AAATCTG-AAGACACAAGTGATATTTGTCGC
droBia1	scf7180000302126:810796-810963 -		GCAGATCCCTGGATCCGGAGCGACCGTCCAGGTTTTGGATC-AGTCTGAAAATGGTAAGTGATAATATTGCAAT----------CCAGGCCAAGGCAA---GAAG-----TAACCTTGAAAC-TCTTTTTG----------TTTTCA--GATCAACATCCAGTTCCTTCA-----AAATCCG-AAGACACCAGTGATATTTGTCGC
droTak1	scf7180000415289:257138-257289 +		C---TC---CTCAAGCGGGCGAGCTGT------TTT-GGCTCACTCTGAAAACGGTAAGCGGTTCTAG---AGTCTAG----TTTTGAGATGGGAAGCA------AC----------TCAACTA-TGACTAAC----------TTTTCA--GATCAAAATCCAGTTCCTTTA-----AAATCTG-AAGACACAAGTGATATTTGTCGC
droEle1	scf7180000491182:81550-81636 -		T---TACTTTACAATCATGTATT--CTAA---TTATTG----------CTTTCA--GATCAAAATCCAGTACCTTCA-----AAATCTG-AAGACACAAGTGATATTTGTCGC
droRho1	scf7180000778073:54-115 -		G---ATGCCTGGACCTGGCCGATCTGTCCAGTCTTGGGTT-ACTCTGAAAACGGTAAGCGATTTT---
droFic1	scf7180000453495:467913-468076 +		G---ATCCCCGATCCGTTCGAAATGTCCAGCTTTTGATTT-ACTCTGAAAACGGTAAGCGGTCTAT---ATT----------AGA----------AAACTCCGTTTATACCAC---TTAGTGTTTGTTGTCTTTTCTTTA--GATCAAAATCCAGTTCCTTCA-----AAACCTG-AAGACACAAGTGATATTTGTCGC
droKik1	scf7180000301902:4747-4803 +		A---TT----------TTAC TG----------CTTACA--GATGGGCAGCCAGCTCCTCCA-----AAATCAG-AAGCGTGTGACCAT--------
droAna3	scaffold_13137:1161590-1161642 -		T---TACA--GATCAAAGCCC---CCCTTTA-----ATTGATA-ATCAAATCAGTGATACAAGTCCA
droBip1	scf7180000393699:66757-66828 +		T---TATA----------TTCTA-TGCAATCT----------TTTACA--GATCAAAGTCG---CCCTTCA-----AATGATA-AACAAAAGAGTGATACAGGTCCA
dp5	XL_grouple:10401280-10401303 +		G---TTTTTTT

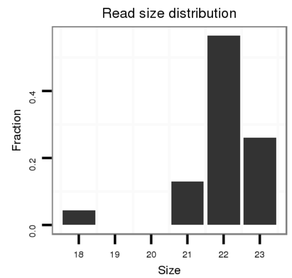
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dsi_26799	**3l:19738999-19739082 -**	**candidate**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser [Cornell Mirror]]

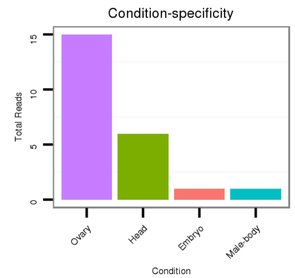
Legend: mature star mismatch in alignment mismatch in read

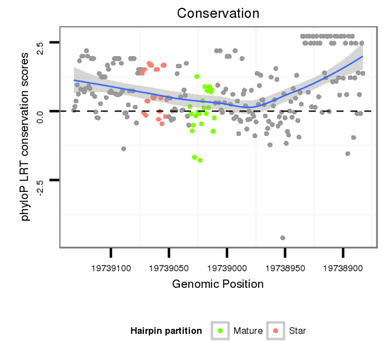
Predicted structure











Show Alternate Folds

Sense Strand Reads

hide 3p reads show mid mismatch reads

GGATGCAGAATCAACTACATCCCATTTCCACGCGACCTCCAGATGCAATCTTCACACTTCGGAGGGCCATCAAAGAGAGTGCTGTTAATTTTTTCCAGTGCATCTCTTTGTGGCCTTTTCGAAGGCTAGATTGAAAGGTCCTTCTGTTTGGGTTCGTTCCGCGAATTAACAGATTGGGTTCTGC	Read size	# Mismatch	Hit Count	Total Norm	Total	SRR553486 Makindu_3 day-old ovaries	SRR553485 Chicharo_3 day-old ovaries	SRR553487 NRT_0-2 hours eggs	M023 head	O002 Head	GSM343915 embryo	SRR553488 RT_0-2 hours eggs	M024 male body	SRR618934 dsim w501 ovaries	M025 embryo	SRR902009 testis
**********.((((((.....((((((((((((((.((((((((((((((.....)))))))).))))))))))))))..))))))))...)))))))....**********																
.....CATCTCTTTGTGGCCTTTTCGA.....	22	0	1	11.00	11	3	5	0	0	2	0	0	1	0	0	0
.....CATCTCTTTGTGGCCTTTTCGAA.....	23	0	1	6.00	6	1	1	2	0	0	1	1	0	0	0	0
.....CATCTCTTTGTGGCCTTTTCG.....	21	0	1	2.00	2	0	0	0	2	0	0	0	0	0	0	0
.....CATCTCTTTGTGGCCTTTTCGAAA.....	25	2	1	2.00	2	1	1	1	0	0	0	0	0	0	0	0
.....CGGAGGGCCATCAAAGAGAGTG.....	22	0	1	2.00	2	1	0	0	1	0	0	0	0	0	0	0
.....CATCTCTTTGTGGCCTTTTCGAAA.....	24	1	1	2.00	2	0	0	2	0	0	0	0	0	0	0	0
.....CGTTCCGCGAATTAACAGATTGGG.....	24	0	1	1.00	1	0	0	0	0	0	1	0	0	0	0	0
.....CATCTCTTTGTGGCCTTT.....	18	0	1	1.00	1	0	0	0	0	1	0	0	0	0	0	0
.....ATCTCTTTGTGGCCTTTTCGA.....	21	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0

Anti-sense strand reads

CCTACGTCTTAGTTGATGTAGGGTAAAGGTGCGCTGGAGGTCTACGTTAGAAGTGTGAAGCCTCCCGGTAGTTTCTCTCAGGACAATTAAAAAAGGTCACGTAGAGAAACACCGGAAAAGCTTCCGATCTAACTTTCCAGGAAGACAAACCCAAGCAAGGCGCTTAATTGTCTAACCCAAGACG	Read size	# Mismatch	Hit Count	Total Norm	Total	SRR553488 RT_0-2 hours eggs	0001 Testis	SRR553487 NRT_0-2 hours eggs	SRR553485 Chicharo_3 day-old ovaries	SRR553486 Makindu_3 day-old ovaries	SRR618934 dsim w501 ovaries
**********.((((((.....((((((((((((((.((((((((((((((.....)))))))).))))))))))))))..))))))))...)))))))....**********											
.....AAAGGTGCGCTGGAGGTC.....	18	0	1	1.00	1	0	1	0	0	0	0
.....GCAATTAAAAAAGGT.....	15	1	20	0.05	1	1	0	0	0	0	0

Show Alignment With Reads

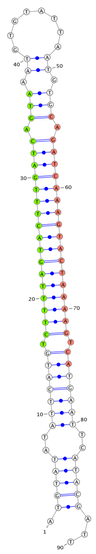
Re-alignment of all predicted orthologs

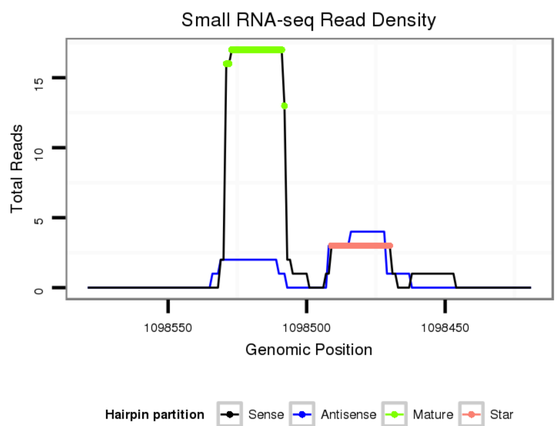
Species	Coordinate	ID	Alignment
droSim2	3l:19738843-19739092 -	dsi_26799	A--------G-ATGCAATCTTCACACTTCGGAG-GGCCATCAAAGAGAGTGCTGT----------TAATTTTTTCCAGT-GCATCTCTTTGTGGCCTTTTCGAAGGCTAGATTGAAAGGTCCTTC-----TG-TT------TGGGTTCGTTCGGCGAATTA------ACAGATTGGGT--TCT--GCGTCAAT----------AAGAT----------A----------GCTCTTATTCGCCCACTTAATGCTG-GACT------CATTCATTTGTTTAGGTCTCCAGTTCCGAGTTCTTCTCCGTGTCATTCTGCCTGGACTCGTCGCA
droSec2	scaffold_11:59590-59833 -	dse_206	A--------G-ATGCAATCTTCACACTTCGGAG-GGCCATCAAAGAGAGTGCTGT----------TAATTTTTTCCAGT-GCATCTCTTTGTGGCCTTTTCGAAGGCTAGATTGAAAGGTCCTTC-----T-TT------TGGGTTCGTTCGGCGAATTA------ACAG----GGGT--TCT--GCGTCAAT----------AAGAT----------A----------GCTCTTATTCGCCCACTTAATGCTA-GACT------CATTCATTTGTTTAGGTCTCCAGTTCCGAGTCTTCTCCGTGTCATTCTGCCTGGACTCGTCGCA
dm3	chr3L:20149049-20149314 +	dme_467	A--------G-ATGCAATCTTCACACTTCGGAGCGGCCATCAAAGAGAGTGCTACC----G-TGGCTT---CGTCGCTGG---------TAATTTTTGCCAGT-GCATCTCTTTGTGGCTTTTCGAAGGCTAGATTGAAGGGTCCTTC-----AT-TT------TGGGTTCGCGCATGAATTA------ACAGATTGGGT--TCT--GCGTCAAT----------AAGAT----------A----------GCTCTTATTCAACCACTTAAGCGTG-GAC------CATTCATTTGTTTAGGTCTCCAGTTCCGAGTCTTCTCCGTGTCATTCTGCGTGGACTCGTCGCA
droEre2	scaffold_4784:19876231-19876489 -		A--------G-ATGCAATCTTCACACTTCGGAG-GGCCATCAAAGAGAGTGCTG----G-GG--GGC---GGGCGCTAG---------TAATTTTTGTCAGT-GCATCTCTTTGTGGCTTTTGAAGGCTAGATTGAAAGGTCCTTC-----T-T-------AAGCTCGCGTCGCGTGAATTG------ACAGATTGGG--TCT--GTATCAG----------GGGCT----------G----------TCTTATTCGCCCACTTAATGCTGGAA-------TGTTCATTTGTTTAGGTCTCCAGTTCCGAGTTCTTCTCCGTGTCATTCTGCCTGGACTCGTCGCA
droYak3	v2_chr3L_random_040:5131-5405 -		A-ATCCTCCAAG-ATGCAATCTTCACACTTCGGAG-GGCCATCAAAGAGAGTGCTG----GAGGC---GGTAGGCGGTCGCTAG---------TAATTTTTTCAGT-GCATCTCTTTGTGGCCTTTTCGAATGCTAGATTGAAAGGTCCTAT-----T-T-------TGGCTCGCGTCGCGTGAATTG------ACAGATTGGGT--TCT--GTATCAG----------GGAAT----------G----------TCTTATTCGCCCACTTAATGCGA-TAC------CATTCATTTGTTTAGGTCTCCAGTTCCGAGTTCTTCTCCGTGTCATTCTGCTGGACTCGTCGCA
droEug1	scf7180000409711:5801074-5801365 +		A--------G-ATGCAATCTTCACACTTCGAG-GGCCATCAAAGAGAGTGCTG----G-GC--AGC---AGTAGGAAG---------TGATTTTTGTCAGT-GCATCTCTTTGTGGCCTTTTGAAGGCTAGATTAAAAGGTCGGTTCGTCGT-TT------TTTTTGCGCGTTGAATTG------ACAGATTAGGT--TCT--AGCTCAG----------CC--AGGAGTGGTAGACCAGAAGTACTTCAATGTCAATC---G----------G----------TCTTTCTTCGTTTAAT-TGC-GAGT------TATCATTCGTTTAGGTCTCCAGTTCCGAGTTCTTCTCCGTGTCATTCTGCCTGGATCGTCGCA
droBia1	scf7180000302193:2928013-2928302 -		A--------G-ATGCAATCTTCACACTTCGGAG-GGCCATCAAAGAGAGTGCTG----G-GC--TGT---AGTCGCCA---------AATCGAGTTTTTGCCAGT-GCATCTCTTTGTGGCCCTTTGAAGGCCAGATTAGCAGGCGTTGAAGG-TT------TTTTTGCGCTTGAATTG------ACAGATTAGGT--TCT--GCTCAGC----------AGGAGTGGTGACCAAAAGTTCCTAACGGTCAACGCAAG----------G-----TCGTTACTTATTTGCGTT------TATCAGTCGTTTAGGTCTCCAGCTCCGAGTTCTTCTCCGTGTCATTCTGCCTGGATCGTGGCA
droTak1	scf7180000415868:104912-105187 -		A--------G-ATGCAATCTTCACACTTCGGAG-GGCCATCAAAGAGAGTGCTG----G-GC--AGTCAGTAGTCGCAAGTCGCAAATCGCATTTTTGTCAGTGTGACCTCTTTGTGGCCCTTTGAAGACAGATTAAAAGGTGTT-----T-T-------TGTTTGCGCGTTGAATTGCAGATACAGATTAGCACTCT--GTATCAG----------AGGAGTGGTGACCAAAAGTCCTCAAATGCAACG---G----------G----------TATTCGTAACTTAATTTGCGACT------TTTGCATTCGTTTAGGTCTCCAGCTCCGAGTTCTTCTCCGTGTCATTCTGCCTGGATCGTCGCA
droEle1	scf7180000491193:4461858-4462148 -		A--------G-ATGCAATCTTCACACTTCAGAA-GGCCATCAAAGAGAGTGCTG----G-GC--GGC---AGTCCCAAG---------CGATTTTTGCCAGT-GCATCTCTTTGTGGCCCTTTGAAGGCTAGATTAAAAGGTGTTG-----T-T-------TGTTTGCGCGTTGAATTGCAGATACAGATTAGCACTCT--GTATCAG----------GGAAGTGGTGACCAAAAGTCCTCAAATGCAACG---G----------G----------TATTCGTAACTTAATTTGCGACT------TTTGCATTCGTTTAGGTCTCCAGCTCCGAGTTCTTCTCCGTGTCATTCTGCCTGGATCGTCGCA
droFic1	scf7180000454113:2159944-2160235 +		A--------G-ATGCAATCTTCACACTTCGGAG-GGCCATCAAAGAGAGTGCTGC----G-GCACGAA---AGTCGCCAG---------TGATTTTTGTCAGT-GCATCTCTTTGTGGCCCCTCGAGTTGTGATTAAAAGGTGGCCCCC-T-TT------TCGTTTGCGCGTTGAATTG------ACAGATTAGGT--TCT--GCGTCAAG----------GCGAAGCGGCAGACCAAAAGTTCCCAAATGTCAACA---G-----TATTCGCTTTGGTTAA-----G----------TTTGCTGTCGAGTA------TATCGTTTGTTTAGGTCTCCAGCTCCGAGTTCTTCTCCGTGTCATTCTGCTGGATCGTCGCA
droKik1	scf7180000302441:2884761-2885052 -		A--------G-ATGCAATCTTCACACTTCGAG-GGCCATCAAAGAGAGTGCTGCTCCTCTG---GC---------AGTCGCAAG---------TGATTTTTGCCAGT-GCATCTCTTTGTGGCCCTTTGAAGGCTAATTAAAAGGCTTTTG-----GTT------TTTTTGCGCGCGTGAATTC------ACAGATTAAGTCTCA--GCGTCAAG----------GCGAAGAAGTGTA----------G----------GAAAAGTGGGGAAAATTATTCAAAAAATAGATT-GATATATAGATCAATCTGTGTGAGTTATCCTTGATTCGTTTAGGTCTCCAGCTCCGAGTTCTTCTCCGTGTCATTCTGCCTGGACTCGTCGCA
droAna3	scaffold_13337:6271300-6271658 -		A--------GATGCAATCTTCACACTTAC----T----CTCAACGAGATTGCTGTT----G-CAC---------AGTTGAAAG---------TAATTTTTGTCAGT-GCATCTCTTTGCGGCTGTTTTTCGGAAAG------CAGCGATGTTGGG-CTGTT-CTGCGTGAATTG------T-TGATTGACAT--TGT--GCTTTAACCTTAAGGACATGCCCCAGTAAT----------A----------AGTCTTATT---------A-TTT-TGTATT------TATTCGTTCAGTTAGGTTCCAGTTCCGAGTTCTTCTCCGTGTCATTCTGTTTGGACTCGCGCA
droBip1	scf7180000396709:26816-27075 -		A--------A-ATGCAATCTTCACACTTAC----T----CTCAACGAGATTGCTGTT----G-CAC---------AGTTGAAAG---------TAATTTTTGTCAGT-GCATCTCTTTGCGGCTGATTTCGGCGCG------CAGCGATGTTGGG-CTGTT-CTGCGTGAATTG------T-TGATTGACAT--TGT--GCTTTAACCTTTAAGGACCAACCCTGGTAAT----------G----------AGTCTTAT------ATTT---TGTGTATT------CATTCGTTCAGTTAGGTTCCAGTTCCGAGTTCTTCTCCGTGTCATTCTGTTTGGACTCGCGCA
dp5	XR_group6:2022677-2022855 -		C--------G-CT-------TCGTATT-----T------CCAGAAGAGTAGATACATATAT---GC---------TTA-----GGATTTCTG-----T-----C----------TTAGCATGGATACC-----T-TT------CAAATTTAATCCAGAATTG------C-CAA----CAG-CTTTACTTGTCAGT----------AAGAAC----------G----------CTTG----------T-----CATCGTTCCGCTAGGTTCCAGTTCCGAGTTCTTCTCCGTGTCTTTGTGGCTGGACTCGTCGCA
droPer2	scaffold_9:315849-316027 -		C--------G-CT-------TCGTATT-----T------CCAGAAGAGTAGATACATATAT---GC---------TTA-----GGATTTCTG-----T-----C----------TTAGCATGGATACC-----T-TT------CAAATTTAATCCAGAATTG------C-CAA----CAG-CTTTACTTGTCAGT----------AAGAAC----------G----------CTTG----------T-----CATCGTTCCGCTAGGTTCCAGTTCCGAGTTCTTCTCCGTGTCTTTGTGGCTGGACTCGTCGCA
droWil2	scf2_1100000004511:3212923-3213073 +		A--------G-TCTTGATTTTCAT---------T--T-----T-------T-------CTTATATGGAATTA----AGCGATTTAAT--TAA--AA-------T----------TACGTTTA----------G----------TAAGACTATTCACAATTTTTCC----------TA---T-AAATTCTA-----TATATATATATTAGGTATCCAGCTCCGATTCTTCTCCGTGTCATTCTGCGCTAGACTCTGGCA
droVir3	scaffold_13049:18506703-18506757 -		G--------T---T-----T-------T-------T-----T-----T-----

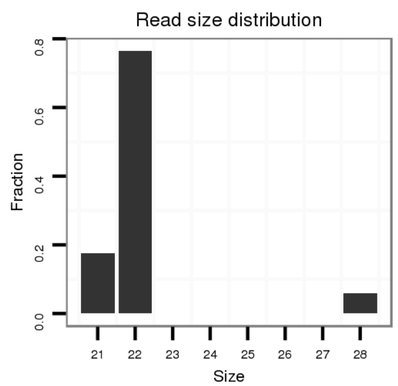
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dsi_124	**x:1098469-1098529 -**	**candidate**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

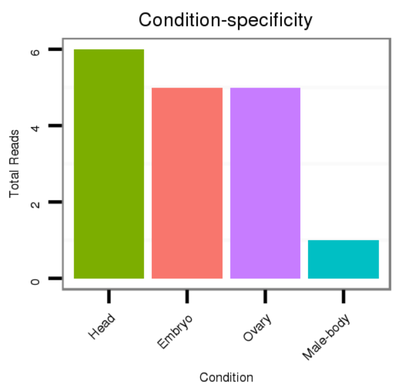
Legend: mature star mismatch in alignment mismatch in read

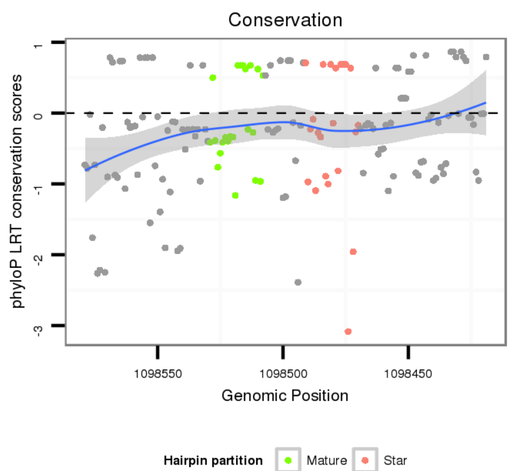
Predicted structure











Show Alternate Folds

Sense Strand Reads

hide 3p reads show mid mismatch reads

ATAATGAGCAACCTTTATACTCAAATGTTACATGTATGTATATATTCATGTCTTTTAGTACTTTGATCAGTAAATGTGTATTAATGTGCAGATCAAAGTACTAAAAGTCATGAATTCATACGATTTTTTTTTTAATATAAGTATGGAACATGCTTGCCATG ********** .(((((..(((((((.((((((((((((((((.(((.((.....)).))).)))))))))))))))).))))))..))))).. **********	Read size	# Mismatch	Hit Count	Total Norm	Total	M023 head	SRR553485 Chicharo_3 day-old ovaries	M025 embryo	SRR553486 Makindu_3 day-old ovaries	SRR553488 RT_0-2 hours eggs	SRR553487 NRT_0-2 hours eggs	SRR618934 dsim w501 ovaries	M024 male body	O002 Head
.....TCTTTTAGTACTTTGATCAGTA.....	22	0	1	11.00	11	3	0	5	0	0	1	2	0	0
.....TCTTTTAGTACTTTGATCAGT.....	21	0	1	3.00	3	2	0	0	0	0	0	0	1	0
.....CAGATCAAAGTACTAAAAGTCA.....	22	0	1	2.00	2	0	1	0	0	0	0	0	0	1
.....TGTCTTTTAGTACTTTGATCAGT.....	23	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....TGTCTTTTAGTACTTTGATCAGTAAA.....	26	0	1	1.00	1	0	1	0	0	0	0	0	0	0
.....TGCAGATCAAAGTACTAAAAGTCATG.....	26	0	1	1.00	1	0	1	0	0	0	0	0	0	0
.....TTTTAGTACTTTGATCAGTAAATGTGTA.....	28	0	1	1.00	1	0	1	0	0	0	0	0	0	0
.....ATACGATTTTTTTTTT.....	16	0	2	1.00	2	0	0	0	2	0	0	0	0	0
.....ATACGATTTTTTTTT.....	15	0	9	0.33	3	0	3	0	0	0	0	0	0	0

Anti-sense strand reads

TATTACTCGTTGGAAATATGAGTTTACAATGTACATACATATATAAGTACAGAAAATCATGAAACTAGTCATTTACACATAATTACACGTCTAGTTTCATGATTTTCAGTACTTAAGTATGCTAAAAAAAAAATTATATTCATACCTTGTACGAACGGTAC ********** .(((((..(((((((.((((((((((((((((.(((.((.....)).))).)))))))))))))))).))))))..))))).. **********	Read size	# Mismatch	Hit Count	Total Norm	Total	SRR553485 Chicharo_3 day-old ovaries	SRR553488 RT_0-2 hours eggs	M023 head	M024 male body	GSM343915 embryo	M053 female body	SRR902009 testis
.....CGTCTAGTTTCATGATTTTCA.....	21	0	1	3.00	3	3	0	0	0	0	0	0
.....ACAGAAAATCATGAAACTAGTCAT.....	24	0	1	1.00	1	1	0	0	0	0	0	0
.....TTCATGATTTTCAGTACTTAAG.....	22	0	1	1.00	1	0	0	1	0	0	0	0
.....AGTACAGAAAATCATGAAACTAGT.....	24	0	1	1.00	1	0	0	0	0	1	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droSim2	x:1098419-1098579 -	dsi_124	ATAATGAGCAACCTTT--ATACT------C----------AAATGTTACATGTATGT---ATA--TATTCAT------GTCT----------TTTAGTACTTTGATCAGTAAATGTGTATT------AATGTGCAGATCA----------AAGTACTAAAAGTCATGAATTCATACGATT-TTTTTTTTAATATAAGTATGGAACATGCTTGCCATG
droSec2	scaffold_10:1042292-1042455 -		ATAATGAGAAACCTTT--ATACT------C----------AAATGTTATATGTATGT---ATATATATTCAT------GTCT----------TTTAGTACTTTGATCAGTAAATGTGTATT------AATTTGCAGATCA----------AAGTACTAAAAGTCATGAATTCATACGTTTTTTTTTTAATATAAGTATGGAACATGCTTGCCATG
dm3	chrX:1209202-1209286 -		TTTGCAC---AAATACTAAACGACATAATTTCATACTTTT-TTTTTTTTAATATAAGTATGGAACATGCTTACCATG
droEre2	scaffold_4644:1200979-1201094 -		AAAATGTGTCACACTT-GTATT------C----------AAATATTGTGGAATCA---TGATATTTTGTTAGACC----------ACGTCCATGTACTAAATGCGATGAACTCCCTGTTGT-T-----TGGGAATGAA----------
droYak3	X:1126910-1127058 -		ATAGTATGCCACAT---------------A----------ACATGTCACAAATA--G---------------GTGGT------AATGTGCTGGCCAAGCCATT--TCAAA----------TACTCTTTTGCTAGACG----------ATGTCAATGTACCAAAGGAGCTGCATTCCCTGTTG-----TTTGGGAATACATTCGAACATG------ATG
droBia1	scf7180000301760:2190636-2190651 +		----------GAACATGCCTACGATG
droTak1	scf7180000415289:390061-390247 -		TAAAAAC-GTACACTTATATTTC------C----------AAATTTTATTCGGTTTTTCAAGACATATTTATGATATCA----TAT--------TTGGATTTGATTTGA--ATACATTTT------ATAGGGCATACTC----TTAGACAAATGATTTTTGAGCATACAATTTTTATTTTGTAAAACAGTGTTTTA----------TTTTTAAAAACTAATTGAACTTGCTAAACGAG
droFic1	scf7180000454072:1899190-1899390 +		ATATTCAAACACTTTT--TCTTTGGTCATAATATACGTTTTAAATATAATACGTACAA---TTT--TGGCAAC------GAACC----------TTAACGAGTTTGTTTCCCAATTACATAATGCAAGCAAACATGCATAA--CGATTTACTTTTAAACATAACTACTTGCCAAACGAGAGAATCCATATGTAT-T-----TGTGTATAAATTAAGAACATGCTTATTATG

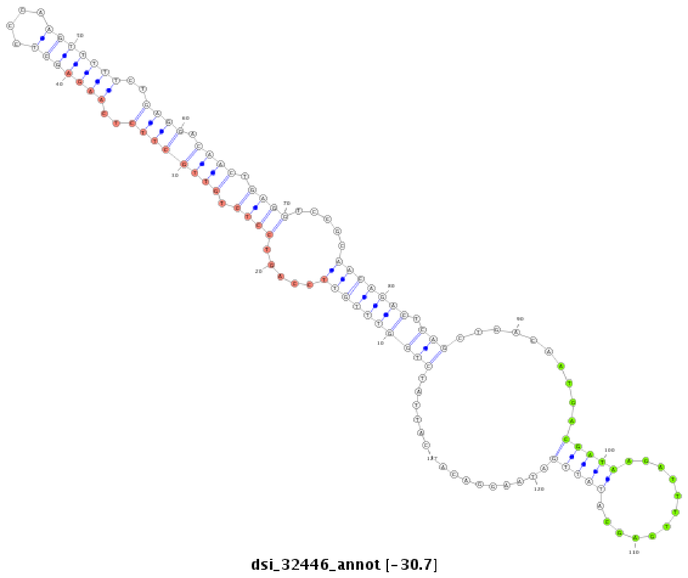
Generated: 02/15/2015 at 08:05 PM

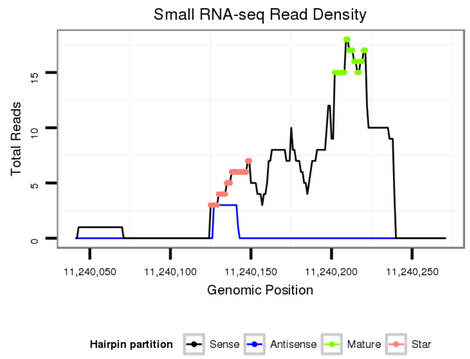
	PASS/FAIL
crit.size	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

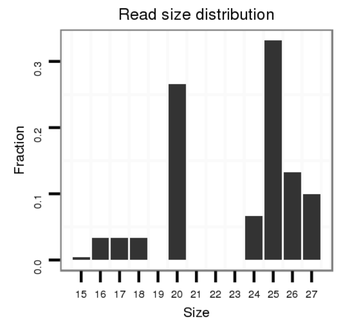
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dsi_32446	**3r:11240091-11240221 +**	**candidate**	**Canonical miRNA**	**3pUTR**	[View on UCSC Genome Browser {Cornell Mirror}]

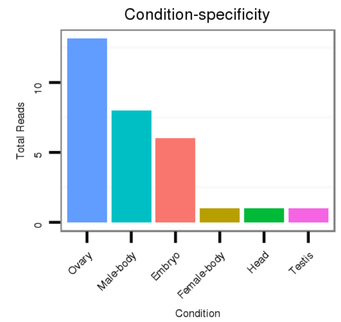
Legend: mature star mismatch in alignment mismatch in read

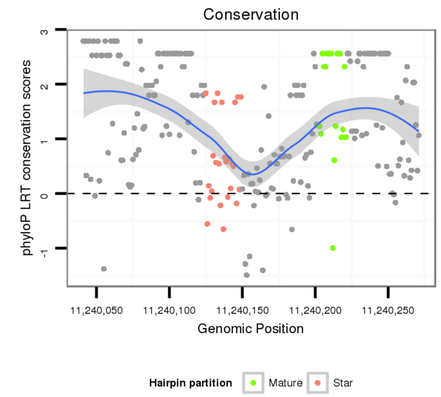
Predicted structure











Show Alternate Folds

Flybase annnotation

three_prime_UTR [3r_11240065_11240809_+]; CDS [3r_11239901_11240064_+]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

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AACTACGTAGAACCGTGTGTCTAAGCCTCGCATCGATATTCTAAACATGCCAACCATTACAATAATCTGCATTATCTGGTTTGTTCCAGTCCTCTGTTGCTTCTCAAGAGCTCCCAAGTTTTTCTGAGGACAACTGAGGTCCGCAACAGACTCAGCTGACAATGACGATAAGATTTTGAGCATATTGATAAGGACAATTATACAATTACACACATACACAAGCACAGCAGG
*************************************************************.....((((((((((.....((((.(((((((((.((((((((....)))))))..)))))..)))))..)))))).....)))))))..)))).....((((.............)))))).........*********************************
```

Read size	# Mismatch	Hit Count	Total Norm	Total	SRR553485 Chicharo_3 day-old ovaries	SRR618934 dsim w501 ovaries	SRR553486 Makindu_3 day-old ovaries	M024 male body	M025 embryo	SRR553487 NRT_0-2 hours eggs	SRR902008 ovaries	M053 female body	SRR1275483 Male prepupae	SRR553488 RT_0-2 hours eggs	SRR902009 testis	M023 head	0001 Testis
20	0	1	6.00	6	0	0	0	4	2	0	0	0	0	0	0	0	0
25	0	1	3.00	3	0	0	0	0	3	0	0	0	0	0	0	0	0
18	0	1	3.00	3	0	1	0	1	1	0	0	0	0	0	0	0	0
25	0	1	3.00	3	0	3	0	0	0	0	0	0	0	0	0	0	0
26	0	1	2.00	2	2	0	0	0	0	0	0	0	0	0	0	0	0
25	0	1	2.00	2	1	0	0	0	0	1	0	0	0	0	0	0	0
30	0	1	2.00	2	1	0	1	0	0	0	0	0	0	0	0	0	0
16	0	1	1.00	1	0	1	0	0	0	0	0	0	0	0	0	0	0
20	0	1	1.00	1	0	0	0	1	0	0	0	0	0	0	0	0	0
26	0	1	1.00	1	0	0	0	0	1	0	0	0	0	0	0	0	0
21	0	1	1.00	1	0	0	0	0	1	0	0	0	0	0	0	0	0
26	0	1	1.00	1	0	0	0	0	0	0	0	1	0	0	0	0	0
24	0	1	1.00	1	0	0	0	1	0	0	0	0	0	0	0	0	0
25	0	1	1.00	1	0	0	0	0	1	0	0	0	0	0	0	0	0
27	0	1	1.00	1	0	0	1	0	0	0	0	0	0	0	0	0	0
17	0	1	1.00	1	0	1	0	0	0	0	0	0	0	0	0	0	0
26	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	0	1
25	0	1	1.00	1	0	0	0	0	0	0	1	0	0	0	0	0	0
27	0	1	1.00	1	0	1	0	0	0	0	0	0	0	0	0	0	0
18	0	1	1.00	1	0	0	0	1	0	0	0	0	0	0	0	0	0
27	0	1	1.00	1	0	1	0	0	0	0	0	0	0	0	0	0	0
25	0	1	1.00	1	0	0	0	0	0	0	0	1	0	0	0	0	0
24	0	1	1.00	1	0	0	0	1	0	0	0	0	0	0	0	0	0
27	0	1	1.00	1	0	0	1	0	0	0	0	0	0	0	0	0	0
20	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	1	0
28	0	1	1.00	1	0	0	0	1	0	0	0	0	0	0	0	0	0
25	0	1	1.00	1	0	1	0	0	0	0	0	0	0	0	0	0	0
25	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0	0	0
20	0	1	1.00	1	0	0	0	1	0	0	0	0	0	0	0	0	0
15	0	7	0.14	1	0	1	0	0	0	0	0	0	0	0	0	0	0

Anti-sense strand reads

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TTGATGCATCTTGGCACACAGATTCGGAGCGTAGCTATAAGATTTGTACGGTTGGTAATGTTATTAGACGTAATAGACCAAACAAGGTCAGGAGACAACGAAGAGTTCTCGAGGGTTCAAAAAGACTCCTGTTGACTCCAGGCGTTGTCTGAGTCGACTGTTACTGCTATTCTAAAACTCGTATAACTATTCCTGTTAATATGTTAATGTGTGTATGTGTTCGTGTCGTCC
**********************************.....((((((((((.....((((.(((((((((.((((((((....)))))))..)))))..)))))..)))))).....)))))))..)))).....((((.............)))))).........*************************************************************************
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Read size	# Mismatch	Hit Count	Total Norm	Total	SRR553486 Makindu_3 day-old ovaries	SRR618934 dsim w501 ovaries	SRR553488 RT_0-2 hours eggs	SRR902008 ovaries	SRR902009 testis	SRR553487 NRT_0-2 hours eggs	M024 male body
15	0	7	2.29	16	0	16	0	0	0	0	0
16	0	7	1.14	8	0	8	0	0	0	0	0
15	0	7	0.43	3	0	2	1	0	0	0	0
17	1	7	0.14	1	0	1	0	0	0	0	0
15	1	20	0.10	2	1	1	0	0	0	0	0
16	1	12	0.08	1	0	0	1	0	0	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droSim2	3r:11240041-11240271 +	dsi_32446	AACTACGTAGAACCGTGTGTCTAA----------GCCTCGCA---TCG----------ATATTCTA--AACATGCCAACCATTACAATAATCTGCATTATCTGGTTT-GTTCCAGTCCTCTGTTGCTTCTCAAGAGC-TCC------C-AAGTTT----------T---TCTGAGGACAACTGAGGTCCGCAACAGACTCAGCTGACAATGACGATAAG-ATTTTGAGCATA--TTGATAAGGACAAT-TATACAATTACAC--------ACA--TACAC-------AAGCACAGCAGG
droSec2	scaffold_0:12070525-12070754 +	dse_108	AACTACGTAGAACCGTGTGTCTAA----------GCCTCGCA---TCG----------ATATTCTA--AACATGCCAACCATTACAATAATCTGCATTATCTGGTT-GTTCCAGTCCTCTGTTGCTTCTCAAGAGC-TTC------C-AAGAT-----------------T---TTGAGGACAACTGAGGACCGCAACAGACTCAGCTGACAATGACGATAAG-ATTTTGAGCATA--TTGATAAGGACAAT-TATACAATTACAC--------ACA--TACAC-------AAGCACAGCAGG
dm3	chr3R:9945566-9945810 -	dme_446	AACTACGTAGAGCGTGTGTCTAA----------GCCTCGCA---TCG----------ATATTCTA--AACATGCCAACCATTACAATAATCTGCATCATCTGGTC-GTTCCAGTCCTCTGCTGCTTCTCAAGAGC-TCC------AAAAAATTCAATTCAGTTATC--GGAGAG--T---T------AGACTGAGGACCGCAACAGACTCAGCTGACAATGACGATAAG-ATTTTGAGCATA--TTATAAGGACAAT-TATACAATTACAC--------ACG--TACAC-------AAGCACAGCAGG
droEre2	scaffold_4770:9494379-9494628 -	der_1532	AATTACGTGAGCGTGTGTCTAA----------GCCTCGCG---TCT----------ATATTCTA--AACATGCCAACCATTACAATAATCTGCATTATCTGGTCT-GTTCCAATCCTCGCCTGCTTCTCAAGAGC-TCC------C-AAGATTTCAATTGA-GTATC--GGGGAC--A---TCTGAGGTCAACTGAGGACCGCAACAGACTCAGCTGACAATGACGATAAC-ATTTTGAGCATA--TTGATAAGGACAAT-TATACAATTACAC--------ACG--TACAC-------AAGCACAGCAGG
droYak3	3R:16483018-16483268 +	dya_1812	AATTACGTAGAGCGTGTGTCTAA----------GCCTCGCA---ACG----------ATAATCTA--AACATGCCAACCATTACAATAATCTGCATTATCTGGTCT-GTTCCAGTCCTCCGTTGCTTCTCAAGAGC-TTC------A-AAGATTCGATAGAGTTTTT--GGGGAC--T---TCTGAGCTCAACTGCGGACCGCAACAGACTCAGCTGACAATGACGATAAT-ATTTTGAGCATA--TTGATAAGGACAAT-TATACAATTACAC--------ACG--TACAC-------AAGCACAGCAGG
droEug1	scf7180000409584:571066-571317 +		AATTATGTAGAGCGTGTGTCTAA----------GCCTCGCC---TCG----------ATATTCTA--AACATGCCAACCATTACAATAATCTGCATTATCTAGTCT-GTTACAGTCCTCCGCTGCTTCTCAAGAAC-TCC------C-GTCATTGAATTAAAGAATC--TAAGAT--T---TCTAGGGACAACTGAGGACCGCAACAGCGTAGTGACAATGACGATAAG-ATTTTGAGCATA--TTGATAAGGACAAT-TATAGAATTAAC--------ACG-TACAC-------AAGCACAGCAGG
droBia1	scf7180000302402:2747959-2748207 -		AATTACGTAGAGCGTGTGTCTAA----------GCCTCGCC---TCG----------ATATTCTA--AACATGCCAACCATTACAATAATCTGCATTATCTGGTCT-GTTCCAGTCCTCCGATGCTTCTCAAGAAC-GAC------CAGATTTCGTTTCTGTGATC--AGGGGCTG---TATGAGGGACAACTGAGGACCGCAACAGCGTCAGTGACAATGACGATAAC-ATTTTGAGCATA--TTGATAAGGACAAT-TATACAATTACAC--------ACG--****-------AAGCACAGCAGG
droTak1	scf7180000415380:857198-857450 -		AATTACGTAGAGCGTGTGTCTAA----------GCCCGCG---TCG----------ATATTCTA--AACATGCCAACCATTACAATAATCTGCATTATCTGGTCT-GTTCCAGTCCTCGCGTGCTTCTCAAGAAC-CTC------T-AAGATATCATTTCAATGATC--AGGGACGG---TGTGAGGACAACTGAGGACCGCAACAGCGTCAGTGACAATGACGATAAC-ATTTTGAGCATA--TTGATAAGGACAAT-TATACAATTACAC--------ACG--CAAAC-------AAGCACAGCAGG
droEle1	scf7180000491047:1202034-1202283 +		AATTACGTAGAGCGTGTGTCTAA----------GCCTCGCC---TCG----------ATATTCTT--AACATGCCAACCATTACAATAATCTGCATTATCTGGCCT-GTTGCAGCCTCTGCTACTTCTCAAGAAC-TCC------C-AATTTTCGCTTAG-ATATC--GAGGGC--T---TCTGAGGACAAGTGAGGTTCGCAACAGCGTCGTGTGACAATGACGATAAC-ATTTTGAGCATA--TTGATAAGGACAAT-TATACAATTACAC--------CCG--TACGC-------AAGCACAGCAGG
droRho1	scf7180000778033:13673-13922 -		AATTACGTAGAGCGTGTGTCTAA----------GCCTCGCC---TCG----------ATATTCTA--AACATGCCAACCATTACAATAATCTGCATTATCTGGCCT-GTTCTGGTCCTCTGCTGATCGCGCGAGAAC-CGC------C-AAGATATCCCTTGG-ACATC--GAGTTC--T---TTTGAGGACAACTGAGGAACCGAGACAGCGTCGTGTGACAATGACGATAAA-ATTTTGAGCATA--TTGATAAGGACAAT-TATACAATTACAC--------AAG--TACAC-------AAGCACAGCAGG
droFic1	scf7180000453912:451974-452225 -		AATTACGTAGAGCCGTGTGTTCTAA----------GCCTCGCC---TCG----------ATATTCTA--AACATGCCAACCATTACAATAATCTGCATTATCTGGTT-GTTCCAGTCCTCTGCTGTTCTCGAGAAC-CGC------C-AAGATTTCGTTTAG-GTTATC--GAGTTC--T---TCTCGGGACAACTGAGGATCGCAACAGCGTCGTGTGACAATGACGATAAC-ATTTTGAGCATA--TTGATAAGGACAAT-TATACAATTACAC--------ACCTACACAC-------AAGCACAGCAGG
droKik1	scf7180000297719:32317-32513 +		AACTATGTGAGCGTGTGTCTAA--A----------GCCTCGGCTACTCGCTACTCTATATATACACATATTCTA--AACATGCCAACCATTACAATAATCTGCATTATCGACTTGTT-AGA----------*------*----------GGC---TC--CTT---------GAGGTTTGAACAGCGTCGTTTGACAATGACGATAACCATTTTGAGCATT--*-----AAGGACAATTATACAATTACAC--------***--C----AAG
droAna3	scaffold_13340:20519464-20519697 +	dan_4045	AATTACGTGAGCGTGTGTCTAA----------GCCTCGCA---CGG----------ATATTCTA--AACATGCCAACCATTACAATAATCTGCATTATCCATGTCT-GTTTTGCTCCTCTGCTGTTCTTGT-GAGTGCC------AAAAA---*----------AAGAA--T---TCTATGGACAGCGGAGCCGCAACAGCGTCGCGCGACATGACGATAAGCATTTTGAGCATA--TTGATAAGGACAAT-TATACAATTAAC--------ATA--TACAC-------AAGCACAGCAGG
droBip1	scf7180000396413:1886055-1886286 -		AATTACGTGAGCGTGTGTCTAA----------GCCTCGCA---CGG----------ATATTCTA--AACATGCCAACCATTACAATAATCTGCATTATCCATGCCT-GTTTTGCTCCTCTGCTGTCCTTCAATT-GC-TCT------GAAAA----*----------AAGGA--G---TCTGAGGACAGCGGAGGACCGCAACAGCGTCGCGTGACAATGACGATAAC-ATTTTGAGCATA--TTGATAAGGACAAT-TATACAATTAAC--------ATA--TACAC-------AAGCACAGCAGG
dp5	2:13441286-13441567 +	dps_3842	AACTATGTGAGCGTGCGTCTAATTTAGAGCTGCTGCGGCTGCTT----**--CG----------*TATTCTAAAAACATGCCAACCATTACAATAATCTGCATTATCTGGTCT-GTTCCCGTCTCGAGGCTGCCGAAAAG-*---AAAACTC-GAGACTTTACTAAA-CTCTTTTTTCGAT--TTCTTTT---GGAGCTAAGACCGGCACAGACTCGTTTGACAATGACGATAACCGATTTTGAGCATATTTGATAAGGACAAT-TATACAATTACAGCCACATACACA--CACACAAACACTAGCACACA--AGG
droPer2	scaffold_0:7007805-7008084 -		AACTATGTGAGCGTGCGTCTAATTTAGAGCTGCTGCGGCTGCTT----**--CG----------*TATTCTAAAAACATGCCAACCATTACAATAATCTGCATTATCTGGTCT-GTTCCCGTCTCGAGCGTGCCGAAAAG-*---AAAACTC-GAGACTTTACTAAA-CTCTT--TGCGAT--TCTTTTT---GGAGCTAAGACCGGCACAGACTCGTTTGACAATGACGATAACCGATTTTGAGCATATTTGATAAGGACAAT-TATACAATTACAGCCACATACATA--CACACAAACACTAGCACAC--AGG
droWil2	scf2_1100000004902:10821088-10821134 -		AATTATGTGAGCGTGTGTCTAA--A----------GCACTGCGTTAG----------GTGTTCTA--**********----------**********----------*--------*-*------*-*------*----------*---**********----------*----------*----------*----------*----------*--*-----*-------**********
droVir3	scaffold_13047:17985286-17985419 -		AATTATGTGAGCGATGTGTCTAA----------GCACTGCA--ATG----------GAATT---*--------AACAATAATAATAATATGCATTAT-******----------*--------*-*------*-*------*----------*---**********----------GACAAAGACGATAACCGATTCCGCATA--TTGATAATGATAAT-TATCTAACTACAC--------CCA--*-----*-------CAGCCCAGCTCT
droMoj3	scaffold_6540:13726427-13726557 +		AATTATGTGAAACCGTGTGTCTAA----------GCACTGCA--ACG----------GAATT---*--------AACAATAACAATAATATGCATTAT-******----------*--------*-*------*-*------*----------*---**********----------AACGCAAACGATAAG-ATTTCGCATA--TTGATAATGATAAT-TATACAACTACAC--------***--*-----*-------CCGCAGCGCACG
droGri2	scaffold_14846:23906-24040 -		AATTATGTGAGCGATGCGTCTAA----------GCACTGCC---AAT----------GGAATCAA--*******CAACAATAACAATAATATGCATTAT-******----------*--------*-*------*-*------*----------*---**********----------GACAAAGACGATAACCGATTTCGCATACGAAGTAATGATAAT-TATACAACTACAC--------CCA--*-----*-------***CAGTGCACG

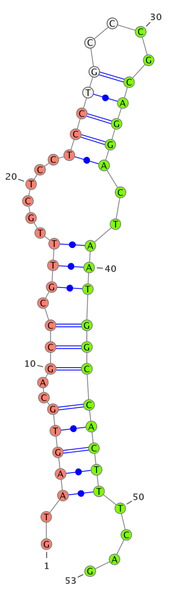
Generated: 09/08/2015 at 08:05 PM

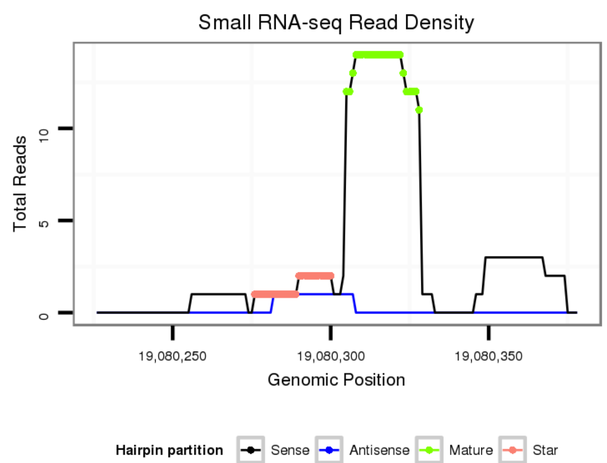
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.mid	0
crit.pairing	0
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	0
rescue.total	0
rescue.dominant	1
rescue.known	0
rescue.confident	1
rescue.candidate	1

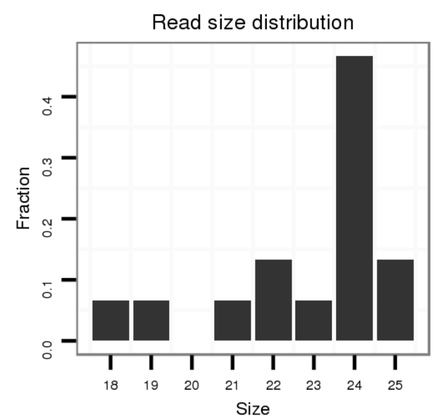
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dsi_16076	**2r:19080276-19080328 +**	**candidate**	**Mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

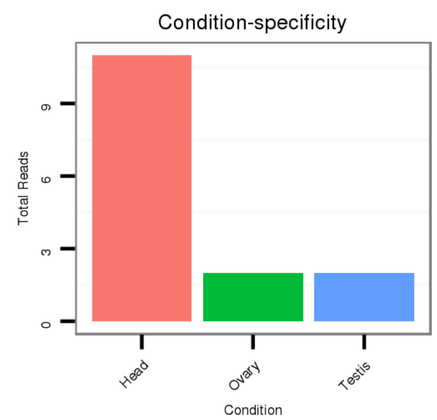
Legend: mature star **mismatch in alignment** mismatch in read

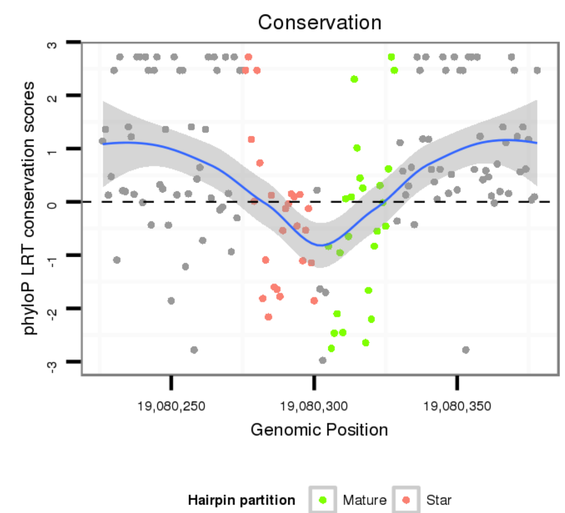
Predicted structure











dsi_16076_mmm [1-31,3]

Show Alternate Folds

Flybase annnotation

intron [2r_19080276_19080328_+]; CDS [2r_19080329_19080431_+]; CDS [2r_19080143_19080275_+]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

GAGCCCAACACCAAGACCCACCTGATGGCCCTCCTCATCTGCATGCTGGGGTAAGTGCAGCCCGTTTGCTCCTCCTGCCCGCAGGACTAATGGCCACTTTCAGGGGCATTTGCTGCTGCTGCATTCCGTACTGCACCGACTCCTGCCAGTCGG **********..(((((..(((.(((.....(((((....)))))..)))))))))))....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M023 head	M025 embryo	SRR553486 Makindu_3 day-old ovaries	O002 Head	M053 female body	O001 Testis	SRR902009 testis	SRR618934 dsim w501 ovaries	SRR553488 RT_0-2 hours eggs
.....CGCAGGACTAATGGCCACTTTCAG.....	24	0	1	7.00	7	5	0	2	0	0	0	0	0	0
.....TTCCGTACTGCACCGACTCCTGCCAG....	26	0	1	2.00	2	0	2	0	0	0	0	0	0	0
.....CTCCTCATCTGCATGCTG.....	18	0	1	1.00	1	0	1	0	0	0	0	0	0	0
.....CGCAGGACTAATGGCCACTTTCAGC.....	24	1	1	1.00	1	1	0	0	0	0	0	0	0	0
.....AGGACTAATGGCCACTTTCAG.....	21	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....CGCAGGACTAATGGCCAC.....	18	0	1	1.00	1	0	0	0	1	0	0	0	0	0
.....CAGGACTAATGGCCACTTTCAG.....	22	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....GTAAGTGCAGCCCGTTTGCTCCTCC.....	25	0	1	1.00	1	0	0	0	0	0	1	0	0	0
.....CGCAGGACTAATGGCCACTTTCAGT.....	25	1	1	1.00	1	0	0	1	0	0	0	0	0	0
.....CGCAGGACTAATGGCCACTTTCA.....	23	0	1	1.00	1	0	0	0	0	0	0	1	0	0
.....GCATTCCGTACTGCACCGACTC.....	22	0	1	1.00	1	0	1	0	0	0	0	0	0	0
.....CGCAGGACTAATGGCCACT.....	19	0	1	1.00	1	0	0	0	1	0	0	0	0	0
.....CCGCAGGACTAATGGCCACTTTCAG.....	25	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....TTTGCTCCTCCTGCCCGCAGGA.....	22	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....CTAATGGCCACTTTCAGGGGC.....	21	0	1	1.00	1	0	0	0	0	1	0	0	0	0

Anti-sense strand reads

CTCGGGTTGTGGTTCTGGGTGGACTACCGGGAGGAGTAGACGTACGACCCCATTCACGTCGGGCAAACGAGGAGGACGGGCGTCCTGATTACCGGTGAAAGTCCCCGTAAACGACGACGACGTAAGGCATGACGTGGCTGAGGACGGTCAGCC **********..(((((..(((.(((.....(((((....)))))..)))))))))))....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M024 male body	SRR553487 NRT_0-2 hours eggs	SRR902009 testis
.....CGTCGGGCAAACGAGGAGGACGGGCG.....	26	0	1	1.00	1	1	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droSim2	2r:19080226-19080378 +	dsi_16076	GAGCCCAACACCAAGACCCACCTGATGGCCCTCCTCATCTGCATGCTGGGGTAAGTGCAGC-------CCG----------TTTGCTCCTCCT------GCCC-GCAGGACTA---ATGGC----------CACTTTCAGGGGCATTTGCTGCTGCTGCATTCCGTACTGCACCGACTCCTGCCAGTCGG
droSec2	scaffold_9:1853605-1853757 +		GAGCCCAACACCAAGACCCACCTGATGGCCCTCCTCATCTGCATGCTGGGGTAAGTGCAGC-------CCG----------TTTGCTCCTCCT------GCCC-GCAGGACTA---ATGCC----------CATTTTCAGGGGCATTTGCTGCTGCTGCATTCCGTACTCCACCGACTCCTGCCAGTCGG
dm3	chr2R:18551577-18551729 +		GAGCCCAGCACCAAGACCCACCTGTGGCCCTAGTCATCTGCATGCTGGGGTAAGTGCAGC-------CCG----------TTTGCTCCACCT------GCCC-GCAGGACTA---ATGGC----------CATTTTCAGGGGCATTTGCTGCTGCTGCATTCCGTACTGCACCGACTCCTGCCAGTCGG
droEre2	scaffold_4845:7404914-7405066 -		GAGCCCAGCACCAAGACCCATCTGCTGGCCCTCCTCATCTGCATGCTGGGGTAAGTGCATC-------ACG----------TTTGCTCCTCCT------GCCA-ACGGAACTA---ATGCA----------CATTTCCAGGGGCATTTGCTGCTGCTGCATTCCCTACTGCACCGACTCCTGCCAGTCGG
droYak3	2R:16014639-16014803 +		GAGCCGAGCACCAAGACCCATCTGCTGGCGCTGCTCATCTGCATGCTGGGGTAAGTGCATGCAC----CTG----------TTTGCTGTTTGCTCCAATGGAC-TCCGGATTTA---ATGCC----------AC----TAATTTTCAGGGGCATTTGCTGCTGCTGCATTCCGTACTGCACCGACTCCTGCCAGTCGG
droEugl	scf7180000409672:6488523-6488684 +		GAGCCCAGTACCAAGACCCATTTGCTGGCTCTTCTAATCTGTATGCTTGGGTAAGTTGTTTTAA--TCACAT----------TAAAATTCTTTT------CTTAACTAATAAA---ATCCT----------G----TATCCTGTAGGGGCATTTGCTGCTGCTGCATTCCATATTGCACCGACTCCTGCCAGTCGG
droBia1	scf7180000302143:2092605-2092757 -		GAGGCTAGTACCAAGACTCACTTGCTGGCCCTCCTTATCTGCTTGCTGGGGTAAGTTATTG-------ATG----------TTTGATCCTTTT------GGCA-AGTACACTA---ATCCA----------GATTGTTAGGGACATCTGCTGCTGCTGCATTCCGTACTGCAGGAGCTCCTGCAAATCGG
droTak1	scf7180000415379:775412-775570 +		GAGCCAAGTACCAAAACCCATTTGCTGGCCCTCTTATCTGCATGTTGGGGTATGTATATG------GTG----------TCTGCTCCTTCA-----CAAA-TTG------------AAACTAAATCTG---AT--CC----TGTCTTTTAGGGGAATCTGCTGCTGCTGCATTCCCTACTGCACCGACTCTTGCCAGTCGG
droEle1	scf7180000486668:470-623 +		GAACCAAGTACCAAGACCCATTTGCTGGCCCTTCTTATTTGTATGCTGGGGTAAGTAATTA-------TAG----------TTTGATCCTTTT------GCCAACAAGGACTA---ATCCT----------TTTTTTTAGGGGCATTTGCTGTTGCTGCATTCCATACTGCACCGACTCCTGCCAATCGG
droRho1	scf7180000768400:21711-21862 +		GAGCCTAGTACCAAGACCCATTTGATTGCCCTCTTATCTGCATGTTGGGGTAAGTAACTA-------AAG----------GTTGATCCTCTT------GTCA-ATATTAACA---ATCC-----------------------TGTTTTTAGGGGCTTTGCTGCTGCTGCATTCCGTACTGCAGCGACTCCTGTCAGTCGG
droFic1	scf7180000454066:2504988-2505143 +		GAGCCAAGCACCAAAACCCAGTTGTTGGCTCTTGTCATCTGCATGCTTGGGTATGTTACTA-------ACT----------TTTAACAATTTT------**----**---------**---**-----AAGATAATTGTGTGAATTTTG-----TTTTTTTAGTGGCATTTGCTGCTGTTGCATTCCATACTGCACCGACTCCTGCCAGTCGG
droKik1	scf7180000302470:448039-448192 -		CAGCCCAGTACCAAGACCCATTTGCTGGCCTTGCTAATCTGCTTGATTGGGTACGTATTTG-------**---**----------ATTGGTAATCCT----A-GAAT-CCTGGACTA---ATCTT----------AC----TCTCCACAGAGGAATCTGCTGCTGCTGCATTCCCTACTGCACCGACTCCTGCCAGTCGG
droAna3	scaffold_13266:10903078-10903241 -		GCTCCCAGTGTGAAAACCCATTGCATGGCCGCCTCCTTTGCATCCTTGGGTAAGCGACTGCAAGATCTAAT-------TAT----------ATTGCTCTGCCT------TATC-TAATCTCTA---CCTTC----------CTGAAACAGTCTGTGGTGCTTCGCCTGTCTACCCTACTGGCCACCAGCTGCATGAACG
dp5	3:4032018-4032172 +		GAGCCCAACAGTAAAACACATCTTCTGGGTCTCGGCATTTGCCTGTTGGGGTAGGTTAAAC-------ACA----------ATCGAAACAGGG------ACAT-CGGGGACTA---ATCCT----------TT----TCTTGGCAGGGGCATATGCTGCGTCTGCATTCCCTACTGCACCAATTCCTGCCAGACGG
droPer2	scaffold_2:4218079-4218233 +		GAGCCCAAACAGTAAAACACATCTTCTGGGTCTCGGCATTTGCCTGTTGGGGTAGGTTAAAC-------ACA----------ATCGAAACAGGG------ACAT-CGGGGACTA---ATCCT----------TT----TCTTGGCAGGGGCATATGCTGCGTCTGCATTCCCTACTGCACCAATTCCTGCCAGACGG
droWil2	scf2_1100000004513:4070566-4070724 -		GACGCCAGCACCAAGACGCATTTGTTTGCTCTTGGATTTGTCTGGTTGGGTAAGTCCAAA-------ATT----------ATTCATTTTTT------TAAC-TTT------------TATTATATAATG---TT--GA----TGTTTTCAGTGGCTGTTGCTGTGCCTGTATTCGTATTGTGTCGATTCCTGCCAGAGTG
droVir3	scaffold_12875:13759950-13760109 +		GAGCCCAGCACCAAGACCCATCTCTTGGCGCTGCTCATTTGCCTGTGGGGGTGAGTAGTGA-----TCGCGT------T----------CGGGAACCATCT------GTTTACCATCGATA---ATCTG----------T----TGACTTGCAGCGGCATCTGTTGCTGCTGTGTGCCGTACTGTGTGGACTCTTGCCAGAGCG
droMoj3	scaffold_6496:9172451-9172632 +	dmo_1053	GAGCCGAGCACCAAGACGCATCTATTGGCCCTACTCATTTGTCTAGTGGGGTGAGCCAAGC-----TCTAATATATATATATATGTGTATATATGTATGTATGTATGT-----A-------TATA-TATTCTATA---AC-TA----------TA-----TCCTTGCAGCGGCATCTGTTGCTGCTGTGTGCCCTACTGGGTGTGGACTCCTGCCAGAGCG
droGri2	scaffold_15245:17488809-17488960 -		GAGCCCAACACTAAGACACATCTCTCGGATTGCTCATCTGTATAATGGGGTAAGTAGCGC-------AAA----------**----------**T------CACT-CAAGGATCAATAATCCT----------CTTATCTGACTTGCAGCGGCATCTGTTGCTGTTGCATACCCTACTGTGTGAAATCATGCCAGACCG

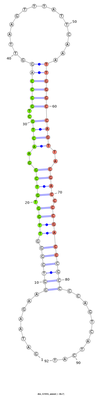
Generated: 09/08/2015 at 07:17 PM

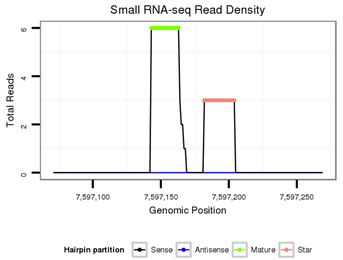
	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

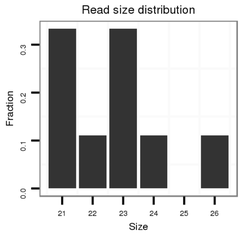
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dsi_32441	**2l:7597121-7597219 +**	**candidate**	**Canonical miRNA**	**antisense_to_intron**	[View on UCSC Genome Browser [Cornell Mirror]]

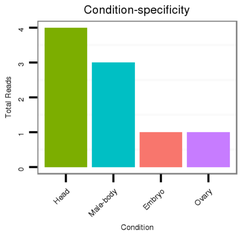
Legend: mature star mismatch in alignment mismatch in read

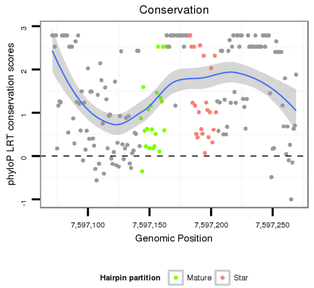
Predicted structure











Show Alternate Folds

Flybase annnotation

Antisense to intron [2l_7596986_7597842_-]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

ATGTGGGAATAAACGCCGTATTCTACGGGGATAAGGTGGGGGTGCTGTTCCGTTGATGATAAGAAGGTGGGGTTGGTGTCGGAACTGCTGCCCAGGTTAAGTTTATTCAAATTGGGCCAGTTACGACCCCGACCCGCCCCAGTCATCATCATCATTGTTTGGCCCAGGGGCAACATTATGCCACGCCCCCTGCAACCGC	Read size	# Mismatch	Hit Count	Total Norm	Total	head	M023 male body	M024 day-old ovaries	SRR553485 Chichero_3 day-old ovaries	SRR553486 Makindu_3 day-old ovaries	GSM343915 embryo	SRR902009 testis	SRR553488 RT_0-2 hours eggs	SRR618934 dsim w501 ovaries	SRR553487 NRT_0-2 hours eggs
**********.....(((((((.(((((.((((..(((((..(((((((.....))))))))))..))))).))))))))))).....**********															
.....TTGGTGTCGGAACTGCTGCCC.....	21	0	1	3.00	3	2	1	0	0	0	0	0	0	0	0
.....TTGGGCCAGTTACGACCCCGACC.....	23	0	1	3.00	3	1	1	0	1	0	0	0	0	0	0
.....TTGGTGTCGGAACTGCTGCCCAGG.....	24	0	1	1.00	1	0	1	0	0	0	0	0	0	0	0
.....TTGGTGTCGGAACTGCTGCCCA.....	22	0	1	1.00	1	0	0	0	0	1	0	0	0	0	0
.....TTGGTGTCGGAACTGCTGCCCAGGTT.....	26	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0

Anti-sense strand reads

TACACCCTTATTTGCGGCATAAGATGCCCCTATTCCACCCCCACGACAAGGCAACTACTATTCTTCCACCCCAACCACAGCCTTGACGACGGGTCCAATTCAAATAAGTTTAACCCGGTCAATGCTGGGGCTGGGCGGGGTCAGTAGTAGTAGTAACAAACCGGGTCCCCGTTGTAATACGGTGCGGGGACGTTGGCG	Read size	# Mismatch	Hit Count	Total Norm	Total	SRR618934 dsim w501 ovaries	SRR553486 Makindu_3 day-old ovaries
**********.....(((((((.(((((.((((..(((((..(((((((.....))))))))))..))))).))))))))))).....**********							

Show Alignment With Reads

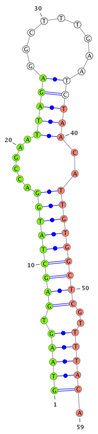
Re-alignment of all predicted orthologs

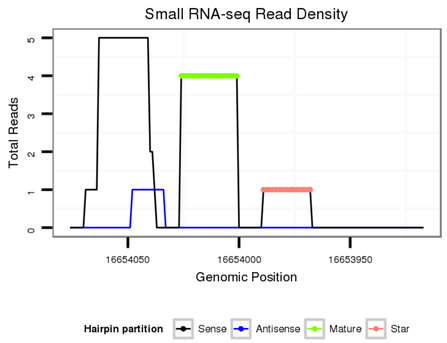
Species	Coordinate	ID	Alignment
droSim2	2l:7597071-7597269 +	dsi_32441	ATGTGGGAATAAACGCCGTATT--CTACGG----GG----------ATAA----------GG--TGGG-GGTGCTGTTCC----------GTTGATGATAA------GAAGGTGGGGC----------TGGTGTCGGAACT-----G---CTGCCCAGGTTAAGTTTATTCAAATTGGGCCAGTT--A-----CGACCCCG-----ACCC----------G-CCCCAGTCATCAT---CATCATTGTT----------TGGCCCAGGGGCAACATTATG----CCACGCCCCCTG----------CAA----------CCGC
droSec2	scaffold_3:3364996-3365194 +	dse_1836	ATGTGGGAATAAACGCCGTATT--CTACGG----GG----------ATAA----------GG--TGGG-GGTGCTGTTCC----------GTTGATGATAA------GAAGGTGGGGC----------TGGTGTCGGAACT-----G---CTGCCCAGGTTAAGTTTATTCAAATTGGGCCAGTT--A-----CGACCCCG-----ACCC----------G-CCCCAGTCATCAT---CATCATTGTT----------TGGCCCAGGGGCAACATTATG----CCACGCCCCCTG----------CAA----------CCGC
dm3	chr2L:7850626-7850824 +		ATGTGGGAATAAACGCCGTATT--CTACGG----GG----------ATAA----------GG--TGGG-GGTGCTGTTCC----------GTTGATGATAA------GAAGGTGGGGC----------TGGTGTCGGAACT-----G---CTGCCCAGGTTAAGTTTATTCAAATTGGGCCAGTT--A-----CGACCCCG-----ACCC----------G-CCCCAGTCATCAT---CATCATTGTT----------TGGCCCAGGGGCAACATTATG----CCACGCCCCCTG----------CAA----------CCGC
droEre2	scaffold_4929:16772171-16772375 +	der_190	ATGTGGGAATAAACGCCGTATT--CTACGG----GG----------ATAA----------GG--AGGG-GGTGCTGTTCC----------GTTGATGATAA------GAAGGTGGGGC----------TGGTGTCGGAACT-----G---CTGCCCAGGTTAAGTTTATTCAAATTGGGCCAGTT--A-----CGACCCCGAGCCCGACC----------G-CCCCAGTCATCAT---CATCATTGTT----------TGGCCCAGGGGCAACATTAG----CCACGCCCCCTG----------G-G----------CCGC
droYak3	2L:5246058-5246268 +		ATGTGGGAATAAACGCCGTATT--CTACGG----GG----------ATAA----------GG--TGGG-GGTGCTGTTCC----------GTTGATGATAA------GAAGGTGGGCA----------GGGGTGTT------TGGTGTCGGAACT-----G---CTGCCCAGGTTAAGTTTATTCAAATTGGGCCAGTT--A-----CGACCCCG-----ACCC----------G-CCCCAGTCATCAT---CATCATTGTT----------TGGCCCAGGGGCAACATTA-GCAAGCCACGCCCCCTG----------CA----------CCGC
droEug1	scf1800000404463:893461-893686 -		ATGTGGGAATAAACGCCGTATT--CTACGG----GGAAGTCTG----------GA---TA-A--AGAG----------AGAGAGAGTAA----GA-TGGG-GG-T------G----------T--T-A-TGATGATAA------GGG-GTGGGG----------AGTGTCGGAACT-----G---CTGCCCAGGTTAAGTTTATTCAAATTGGGCCAGTT--A-----CGACCCCG-----ACCC-GCGAAC----------TGGCCCAGGGGCAACATTATG----CCACGCCC-TG----------CA----------CCGC
droBia1	scf1800000301518:690148-690339 -		ATGTGGGAATAAACGCCGTATT--CTACGG----GG----------ATAA----------A-AGTGGG-GG--------T----------GTTGATGATA-------GAGGGTGGGGC----------AGGTGTCGGAACT-----G---CTGCCCAGGTTAAGTTTATTCAAATTGGGCCAGTT--A-----AAGCCCG-----ACCC----------G-CCCCAGTCATCA---CATCATTGTT----------TGGCCCAGGGGCAACATTA-G----GCACGCCCCCTG----------CA----------CCGC
droTak1	scf1800000415876:487759-487951 -		ATGTGGGAATAAACGCCGTATT--CTACGG----GG----------ATAA----------GG--G-G-GG-GG-C-----T----------T--T-GTTGATGATAA------GAAGGTTGGCA----------GGATTCGGAACT-----G---CTGCCCAGGTTAAGTTTATTCAAATTGGGCCAGTT--A-----CGACCCCG-----ACCC----------G-CCCCAGTCATCAT---CATCATTGTT----------TGGCCCAGGGGCAACATTATG----CCACGCCCCCTG----------CAA----------CCGC
droEle1	scf1800000491028:1167920-1168118 -		ATGTGGGAATAAACGCCGTATT--CTACGGGGGAAGTG----------T----------T---TGGG-GT--------T----------GTTGATGATAA------GAG-GTGGGC----------GTGTCGGAAGTGGCCA-GTTGGCCCAGGTTAAGTTTATTCAAATTGGGCCAGTTATA-----CGACCCCG-----ACCC----------G-CCCCAGTCATCAT---CATCATTGTT----------TGGCCCAGGGGCAACATTATG----CCACGCCCCCA----------CCAG----------CCGC
droRho1	scf1800000778576:3664-3856 +		ATGTGGGAATAAACGCCGTATT--CTACGG----GGAAGTG----------T----------T---TGGG-GT--G-----T----------GTTGATGATAA------GAG-GTGGGC----------GA-------GTGTCGGAACT-----G---TGCCCAGGTTAAGTTTATTCAAATTGGGCCAGTT--A-----CGACCCCG-----ACCC----------G-CCCCAGTCATCAT---CATCATTGTT----------TGGCCCAGGGGCAACATTA-G----CCACGCCCCCTG----------CAA----------CCGC
droPse1	scf1800000454115:654156-654402 +		ATGTGGGAATAAACGCCGTATT--CTACGG----GGAGTGCGGATGCCAATGCGGATGCCAATGCGGGATAGCGGGGGGTGCGGGGGGCGGATGTTGAT----------T---T----T----------T---AATGCGAA-------GA----GGGGGTGC----------AGTGTCGGAACT-----G---CTGCCCAGGTTAAGTTTATTCAAATTGGGCCAGTT--A-----CGACCCCG-----ACCC----------G-CCCCAGTCATCAT---CATCATTGTT----------TGGCCCAGGGGCAACATTA-GCCATGCCACGCCCCCTGTCCCTG----------T----------CC----------CCGC
droKik1	scf1800000302570:197659-197912 -		ATGTGGGAATAAACGCCGTATT--CTACGG----GG----------ATAA----------AGAG----------TGTGA----T---T--GG-GGGGT-----T----------TCAG-GTGATGATA-------GAGGGGCGGG----------GGGGGCGAACT-----GGGCTGCCCAGGTTAAGTTTATTCAAATTGGGCCAGTT--A-----CGACCCCG-----ACCC----------G-CCCCAGTCATCAT---CATCATTGTT----------TGGCCCAGGGGCAACATTA-G----CGACGCCCCCA-GTCCACGTTCCCAGGTTCCCCAGTTCCGCGTTAACCC-----ACACTTTCCCG---CACAACCCCAAT-G
droAna3	scaffold_12943:1454011-1454230 -		ATGTGGGAATAAACGCCGTATT--CTACGG----GGGAGTTTG----------T----------T---TGTTGATA-A---AGAG----------T----T----T----------T----------T-----GTGTGAATAGGGGGG

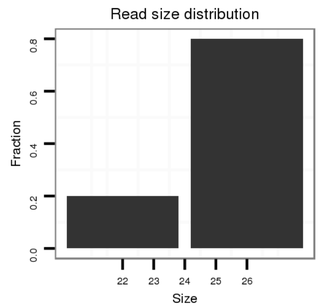
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dsi_6282	**x:16653967-16654026 -**	**candidate**	**Mirtron**	**intron**	[View on UCSC Genome Browser [Cornell Mirror]]

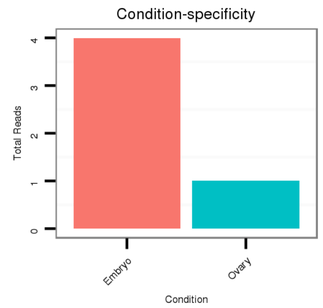
Legend: mature star mismatch in alignment mismatch in read

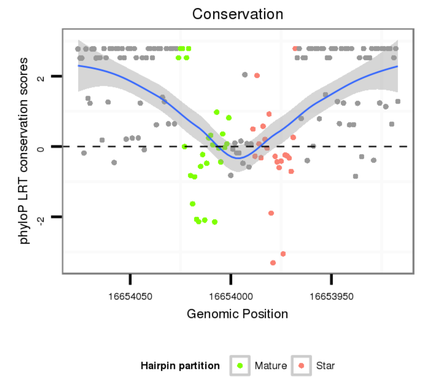
Predicted structure











Show Alternate Folds

Flybase annotation

intron [x_16653967_16654026_-]; CDS [x_16654027_16654205_-]; CDS [x_16653724_16653966_-]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

TCGCTTCAAGGGCAGCTTCATGACCTTCTCGGCGGATCAATATGTCAAGTGTAAGTGAGCTATGGACCGAATTAGAGGCTTTGAATCTAACATTGTGGCTCGTTTTACAGTTGCGTTCTATAATCCATTCCTGAAGACAGCCTGGGACAACAAGTACGAG **********(((((.(((((((((.....(((((.....)))))..)))))))))..)))))..**********	Read size	# Mismatch	Hit Count	Total Norm	Total	SRR553485 Chicharo_3 day-old ovaries	M025 embryo	M023 head	SRR553486 Makindu_3 day-old ovaries	GSM343915 embryo	M024 male body	SRR902009 testis	SRR618934 dsim w501 ovaries	SRR553487 NRT_0-2 hours eggs
.....GTAAGTGAGCTATGGACCGAATTAGA.....	26	0	1	4.00	4	0	4	0	0	0	0	0	0	0
.....AGCTTCATGACCTTCTCGGCGGA.....	23	0	1	2.00	2	0	0	1	0	1	0	0	0	0
.....AGCTTCATGACCTTCTCGGCGGAT.....	23	1	1	1.00	1	0	0	1	0	0	0	0	0	0
.....TAACATTGTGGCTCGTTTTACA.....	22	0	1	1.00	1	0	0	0	1	0	0	0	0	0
.....AGCTTCATGACCTTCTCGGCGGATCA.....	26	0	1	1.00	1	0	0	1	0	0	0	0	0	0
.....GTAAGTGAGCTATGGACCGAATTAG.....	25	1	1	1.00	1	0	0	0	1	0	0	0	0	0
.....AGCTTCATGACCTTCTCGGCGGATC.....	25	0	1	1.00	1	0	0	0	0	0	1	0	0	0
.....AAGGGCAGCTTCATGACCTTCTCGGCGGA.....	29	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....GTGGCTCGTTTTACAAA.....	17	2	20	0.05	1	0	0	0	0	0	0	0	1	0

Anti-sense strand reads

AGCGAAGTTCCCGTCGAAGTACTGGAAGAGCCGCCTAGTTATACAGTTCACATTCACTCGATACCTGGCTTAATCTCCGAAACTTAGATTGTAACACCGAGCAAAATGTCAACGCAAGATATTAGGTAAGGACTTCTGTCGGACCCTGTTGTTCATGCTC **********(((((.(((((((((.....((((.....)))))..))))))))..))))))..**********	Read size	# Mismatch	Hit Count	Total Norm	Total	SRR553488 RT_0-2 hours eggs	SRR553486 Makindu_3 day-old ovaries	SRR553487 NRT_0-2 hours eggs
.....AGCCGCCTAGTTATA.....	15	0	1	1.00	1	1	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droSim2	x:16653917-16654076 -	dsi_6282	TCGCTTCAAGGGCAGCTTCATGACCTTCTCGGCGGATCAATATGTCAAGTGTAAGTGAG---------C----T----------ATGGAC----------C----------GA----------ATTAGAGGCTTT----------GAATCTAA----------CATTGT-GGC--------T--CGTTTTACAGTTGCGTTCTATAATCCATTCCTGAAGACAGCCTGGGACAACAAGTACGAG
droSec2	scaffold_17:1383591-1383740 -		---------GGCAGCTTCATGACGTTCTCGGCGGATCAATATGTCAAGTGTAAGTGAG---------C----T----------ATGGAC----------C----------GA----------ATTAGAGGCTTT----------GAATCTAA----------CATTGT-GGC--------T--CGTTTTACAGTTGCGTTCTATAATCCATTCCTGAAGACAGCATGGGACAACAAGTACGAA
dm3	chrX:17540877-17541041 -		TCGCTTCAAGGGCAGCTTTATGACCTTCTCGGCGGATCAATATGTCAAGTGTAAGTGAATGGAA----C----T----------ATGGAA----------C----------GA----------ATTAGAGGCTTC----------GAATCTAA----------CATTGT-TTC--------T--CGTTTTACAGTTGCGTTCTATAATCCATTCCTGAAGACAGCCTGGGACAACAAGTACGAG
droEre2	scaffold_4690:7877360-7877522 -		TCGCTTCAAGGGCAGCTTCATGACCTTCTCGGCTGATCATATGTCAAGTGTAAGTGAA---------C----G----------ATGGAA----------T----------GA----------AC---------CAAGTTCAATTT----------GAATCTAA----------CATTGT-GGC--------C--CGCTTTACAGTCGCGTTCTATAATCCATTCCTGAAGACAGCCTGGGATAACAAGTACGAG
droYak3	X:16168169-16168328 -		TCGCTTCAAGGGCAGCTTCATGACCTTCTCGGCGGATCATATGTCAAGTGTAAGTGAA---------T----T----------ATGAAA----------C----------AA----------ATTCGAGGGATT----------GAATCTTA----------GTTGT-GAC--------T--CGTTCTACAGTTGCGTTCTATAATCCATTCCTGAAGACGGCATGGGACAACAAGTACGAG
droEug1	scf7180000409271:613608-613768 -		TCGCTTCAAGGGCAGCTTCATGACCTTTTCGGCGGATCATATGTCAAGTGTAAGTGAA---------C----A----------TGAAA----------C----------GA----------ATTAGAGAGCCT----------AAACCTAA----------CATTAT-TTAT--------A--TATTTTTAGTTGCGTTCTACAATCCATTCCTGAAGACGGCATGGGATAACAAGTACGAG
droBia1	scf7180000301760:3559442-3559611 -		TCGCTTCAAGGGCAGCTTTATGACCTTCTCGGCGGATCATACGTCAAGTGTAAGTCGG---------A----C----------T-----C----------GA----------AGTGGAGGTGGTGAGCCTGAGCCGG----------CCTAACACGA----GTTGT-GAC--------T--CTGTCCACAGTTGCGTTCTATAATCCATTCCTGAAGACGCCTGGGACAACAAGTACGAG
droTak1	scf7180000415210:484177-484343 +		TCGCTTCAAGGGCAGCTTTATGACCTTCTCGGCGGATCATACGTCAAGTGTAAGTGAA---------A----C----------T-----C----------TTGGTTT----------TA----------AATGG----------A--AGATATTTT----------AAACCTAA----------CTTAAT-TCT---CTC--T--C-CCCCACAGTTGCGTTCTATAATCCATTCCTGAAGACGCCTGGGACAACAAGTACGAG
droEle1	scf7180000491277:548642-548805 -		TCGCTTCAAGGGCAGCTTCATGACCTTTTCGGCGGATCATATGTCAAGTGTAAGTGAA---------A----C----------ATTGAA----------C----------AA----------ATAAC--ATGGGAAG----------CTTATTG--ccc----TGAA----------CTTAT-TGT--------C--C-GAAGACAGTTGCGTTCTATAATCCATTCCTGAAGACAGCCTGGGACAACAAGTACGAG
droRho1	scf7180000779980:83870-84027 -		TCGCTTCAAGGGCAGCTTCATGACCTTTTCGGCAGATCATATGTCAAGTGTAAGTGAA---------A----C----------TAAGAA----------C----------AA----------ATGCGTA-TTT----------GAACCTAA----------CTTAAT-TGT--------C--C-ATTTACAGTTGCGTTCTATAACCCATTCCTGAAGACAGCCTGGGACAACAAGTACGAG
droFic1	scf7180000453926:176106-176263 +		TCGCTTCAAGGGCAGCTTCATGACCTTCTCGGCGGATCATATATCAAGTGTAGTGCTA---------C----T----------TCGGAC----------C----------AA----------GTTAGATATTTC----------GAACCTAA----------CTTAT-GCT--------T--C-GTTCACAGTTGCGTTCTATAATCCATTTTTGAAGACGCCTGGGACAACAAGTACGAG
droKik1	scf7180000030258b:265814-265986 +		TCGCTTCAAGGGCAGCTTCATGACCTTTTCGGCGGATCATATGTCAAGTGTAAGTTGG---------A----T----------ATT---------TAAATTAATTTA----------C----------GATTAAAAAAACACA----------AA----------CTAATTGCCACGTTGC--------C-----GTC--------G--GTACGACAGTTGCGTTTTATAATCCATTCCTGAAGACGCCTGGGATAACAAGTACGAG
droAna3	scaffold_13335:2185782-2185946 -		TCGCTTCAAGGGCAGCTTCATGACCTTCTCGAGCGGATCATATGTCAAGTGTAGTGCCATC-------C-----T----------ATCC---------CACTCTATCTCA----------C----------TATAAAAAAAATATTAAGTTAAAAACTTT----------GAAT---------C-----T---C---------C--C-----TTTAGTTGCGTTTTATAATCCATTCCTAAAAAATGCCTGGGATAATAAGTACGAG
droBip1	scf7180000393717:17900-18076 -		TCGCTTCAAGGGCAGCTTCATGACCTTCTCGAGCGGATCATATGTCAAGTGTAGTTTTTC---C---C----A----------TAAAAA----------C----------CC----------AA--------CTGGATTAAT----------A----ATAATATGATATTT---AT-ATA-TATATTTTTTTGGTTTTAGTTGCGTTTTATAATCCATTCCTGAAGACATGCCTGGGATAACAAGTACGAG
dp5	XL_groupla:1518378-1518574 -		TCGCTTCAAGGGCAGCTTCATGACATTCTCAGCGGATCATATGTTAAATGTAAGTCCATC---CCCAATCCCCCAG-----TCCCTGCCAATCCATAAACGG-CGGATCAA----------C----------GA----------TCCTTGATCAAGTCGAATGG------TGATATGTTGC--------C--------C-ATC--------T--GTTTTGCAGTTGCGTTCTATAATCCATTCCTGAAGACGTGCCTGGGACAACAAGTACGAG
droPer2	scaffold_53:284067-284263 +		TCGCTTCAAGGGCAGCTTCATGACATTCTCAGCGGATCATATGTTAAATGTAAGTCCATC---CCCAATCCGCCAG-----TCCCTGCCAATCCATAAACGG-CGGATCAA----------C----------GA----------TCCTTGATCAAGTCGAATGG------TGATATGTTGC--------C--------C-ATC--------T--GTTTTGCAGTTGCGTTCTATAATCCATTCCTGAAGACGTGCCTGGGACAACAAGTACGAG
droWil2	scf2_1100000004590:2106445-2106614 -		TCGCTTCAAGGGCAGCTTTATGACCTTCTCGGCCGATCATATGTTAAATGTAAGTAG---------C----T----------C-----C----------TGAAAGAGTTATACTCGTGCATACTCGTTACAA----------TATACCTAT---C----------C--------C--------GTGTAT-ATT--------T--AAATTCCAGTTGCGTTCTATAATCCATTCCTGAAAACGCATGGGATAACAAATATAGAG
droVir3	scaffold_13042:4289093-4289261 +		TCGCTACAAGGGCAGCTTTATGACCTTCTCGGCGGATCAATATGTCAAGTGTAGTGTCCATACAA----C----CATTAAAATCCTTGCC----------C-----C----------GA----------C----------GA----------AGATTTTT----------AATTCGTTTG--------C--CTTTTGCGAGTTGCGTTTTATAATCCATTCCTGAAGACGCCTGGGATAACAAATACGAG
droMoj3	scaffold_6359:2135476-2135651 -		TCGCTACAAGGGCAGCTTCATGACCTTCTCAGCGGATCAATATGTCAAGTGTAGTGTGCC---------A----A----------TAGGA----------C----------GA----------AA--------TTAATCATTTTGACTGC------TG----TTAATTCAATCTCT----CT-ATC-TCTGTCAT--T---TATTTAGTGCGCTTCTACAATCCATTCTGTGAAGACGCATGGGATAACAAATACGAG
droGri2	scaffold_14853:7155598-7155798 +		TCGCTACAAGGGCAGCTTTATGACATTCTCAGCGATCAATATGTCAAGTGTAGTGTGCC---------C--AACAATTATAAC----CAAATACACTGATTATTTATTAGTGCTT----------GTTGGTTTGAAATGTTAATGAATGAATGAATGAATTT----------GAGTCGTTGCGTTCTATAATCCATTCCTGAAGACGCCTGGGACAACAAATATAGAG

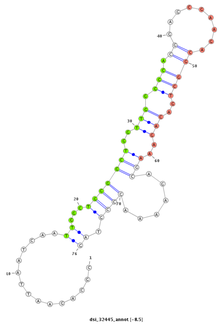
Generated: 09/08/2015 at 07:17 PM

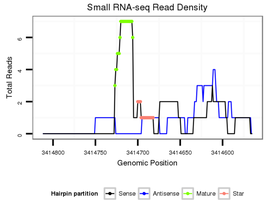
	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

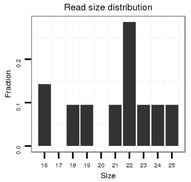
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dsi_32445	**2r:3414615-3414762 -**	**candidate**	**Canonical miRNA**	**antisense_to_intron**	[View on UCSC Genome Browser (Cornell Mirror)]

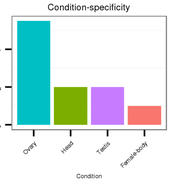
Legend: loops star mismatch in alignment mismatch in seed

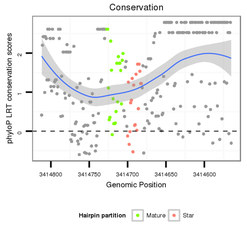
Predicted structure











Show Alternate Folds

Flybase annotation

Antisense to intron [2r_3414642_3436615_+]; Antisense to CDS [2r_3414453_3414641_+]; Antisense to utr5 [utr5_plus_3360]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

CGTTCACTTTTGCGTCGTTTTCTGTCGTCGTCGTGACTGACTTGCCCCGCCCCCTGCGACCCGCGCCGCGCAGAATAATCAATTTGGCTGGGCTGGTTGGGGCAGCGACGGAAGACGGCTGACAGAAAGCAGAAACCCGTAGCCAAAACCAGCCGAATTTCACTTACCAGGCACACCGAGGGTTCGGCGATTTTTTCAGGTCTGGGCCTTGCGCACAAAGTGCTTGTAATTGTAGTGCGAC	Read # size	Mismatch	Hit Count	Total Norm	Total	SRR92008 ovaries	SRR618934 dsim ovaries	SRR618934 w501 head	M023 head	O002 Testis	SRR92009 testis	SRR553488 RT_0-2 hours eggs	M053 female body	O001 Testis	SRR553486 Makindu_3 day-old ovaries	M024 male body	SRR553486 GSM343915 embryo
....TTGGCTGGGGCTGGTTGGGGCA....	22	0	1	3.00	3	1	0	0	0	2	0	0	0	0	0	0	0
....CGAAGACGGCTGACAGAAA....	19	0	1	1.00	1	0	0	0	1	0	0	0	0	0	0	0	0
....ACCGAACCGTTCCGCGATTTTT....	23	0	1	1.00	1	0	0	0	1	0	0	0	0	0	0	0	0
....GGGGCTGGTTGGGGCACGGA....	20	1	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	0
....ATTTTTTCCAGGTCTGGGCCT....	22	0	1	1.00	1	0	0	0	1	0	0	0	0	0	0	2	0
....GGGGCTGGTTGGGGCA....	16	0	1	1.00	1	0	1	0	0	0	0	0	0	0	0	0	0
....AACCCGTAGCCAAAACCAGCCGA....	23	0	1	1.00	1	0	0	0	0	0	0	1	0	0	0	0	0
....GCTGGGGCTGGTTGGGGC....	18	0	1	1.00	1	0	0	1	0	0	0	0	0	0	0	0	0
....TTGGCTGGGGCTGGTTGGGGCACGGA....	27	1	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0	0
....TTCCAGGTCTGGGCCTTG....	18	0	1	1.00	1	0	0	0	0	0	0	0	1	0	0	0	0
....ACCCGTAGCCAAAACCAGCCGAATT....	25	0	1	1.00	1	0	0	0	0	1	0	0	0	0	0	0	0
....TGCTTGTAATTGTAGTGC....	18	0	1	1.00	1	0	0	0	0	0	0	0	0	1	0	0	0
....GGGCTGGTTGGGGCACGGACGAA....	24	0	1	1.00	1	0	0	0	0	0	0	0	1	0	0	0	0
....TGGCTGGGGCTGGTTGGGGCA....	21	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0	0
....GCCAAAACCAGCCGAA....	16	0	2	0.50	1	0	1	0	0	0	0	0	0	0	0	0	0

Anti-sense strand reads

GCAAGTGAAACGCAGCAAAGACACGACGACGCAGCTGACTGAACGGGGCGGGGGACGCTGGGCGCGGGCGCGTTCTTAATTAGTTAACGACCCCGACCAACCCGTGCCTGCCTCTGCCGACTGTCTTT	Read # size	Mismatch	Hit Count	Total Norm	Total	M053 female body	SRR553485 M024 male body	SRR553485 Chicharo_3 day-old ovaries	SRR618934 dsim w501 ovaries	SRR92009 testis	SRR553486 M025 day-old ovaries	SRR553486 O002 embryo	SRR553488 RT_0-2 hours Head eggs
....TGCCGACTGTCTTTCGTCTTT....	21	0	1	1.00	1	1	0	0	0	0	0	0	0
....CTGTTTACCGAGCATTAACATCACGC....	27	0	1	1.00	1	1	0	0	0	0	0	0	0
....CCGCTAAACAAAGGTCCA....	18	0	1	1.00	1	0	0	0	0	0	0	1	0
....TCGCAAAGCCGCTAAACAAAGG....	22	0	1	1.00	1	0	0	0	0	0	0	0	0
....GTCCGTGTGGCTCGCAAA....	18	0	1	1.00	1	0	0	0	0	0	1	0	0
....GCGCGGGCGTCTTAATTAGTTA....	24	0	1	1.00	1	0	1	0	0	0	0	0	0
....GTTTTGGTCGCTTAAAGTGA....	21	0	1	1.00	1	0	0	0	1	0	0	0	0
....GGCTCGCAAAGCCGCTAAACAAAGGT....	26	0	1	1.00	1	0	0	1	0	0	0	0	0
....AGGTCCAGACCCGGACGCGTG....	22	0	1	1.00	1	0	0	1	0	0	0	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
StroSim	2r:3414615-3414832 -	dsi_32445	CGTTCACTTTTGCGTCGTTTTCTGT----------CGTCGTCGTCGACTG----------ACTTGCCCCGCCCC-CTG+----------C+---GA----------C++CCGCGCC-+C----------GCGCAGAAT-TAATCAA-GCTGGGGCTGGTTGGGGCAGGAC----------GGCTGACAGAAC----------AGA----------AAACCCGT-AG----------CCA-AAACCAGC----CGAATTTCACTTACCAGGCACACCGAGGGTTCGGCGATTTTTTCAGGTCTGGGCCTTGCGCACAAAGTGCTTGTAATTGTAGTGCGAC
StroSec	scaffold_4:216579-216819 -	dsi_145	CGTTCACTTTTGCGTCGTTTTCTGT----------CGTCGTCGTCGACTG----------ACTTGCCCCGCCCC-CTG+----------C+---GA----------C++CCGCGCC-+C----------GCGCAGAAT-TAATCAA-GCTGGGGCTGGTTGGGGCAGGAC----------GGCTGACAGAAC----------AGA----------AAACCCGT-AG----------CCA-AAACCAGC----CGAATTTCACTTACCAGGCACACCGAGGGTTCGGCGATTTTTTCAGGTCTGGGCCTTGCGCACAAAGTGCTTGTAATTGTAGTGCGAC
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StroEre	scaffold_4929:1393078-1395314 +	Ere_1535	CGTTCACTTTTGCGTCGTTTTCTGT----------CGTCGTCGTCGACTG----------ACTTGCCCCGCCCC-CTG+----------C+---GA----------C++CCGCGCC-+C----------GCGCAGAAT-TAATCAA-GCTGGGGCTGGTTGGGGCAGGAC----------GGCTGACAGAAC----------AGA----------AAACCCGT-AG----------CCA-AAACCAGC----CGAATTTCACTTACCAGGCACACCGAGGGTTCGGCGATTTTTTCAGGTCTGGGCCTTGCGCACAAAGTGCTTGTAATTGTAGTGCGAC
StroTak	Sta_1516	Sta_1516	CGTTCACTTTTGCGTCGTTTTCTGT----------CGTCGTCGTCGACTG----------ACTTGCCCCGCCCC-CTG+----------C+---GA----------C++CCGCGCC-+C----------GCGCAGAAT-TAATCAA-GCTGGGGCTGGTTGGGGCAGGAC----------GGCTGACAGAAC----------AGA----------AAACCCGT-AG----------CCA-AAACCAGC----CGAATTTCACTTACCAGGCACACCGAGGGTTCGGCGATTTTTTCAGGTCTGGGCCTTGCGCACAAAGTGCTTGTAATTGTAGTGCGAC
StroEsp	scf7180000428822:1423786- 1424046 -		CGTTCACTTTTGCGTCGTTTTCTGT----------CGTCGTCGTCGACTG----------ACTTGCCCCGCCCC-CTG+----------C+---GA----------C++CCGCGCC-+C----------GCGCAGAAT-TAATCAA-GCTGGGGCTGGTTGGGGCAGGAC----------GGCTGACAGAAC----------AGA----------AAACCCGT-AG----------CCA-AAACCAGC----CGAATTTCACTTACCAGGCACACCGAGGGTTCGGCGATTTTTTCAGGTCTGGGCCTTGCGCACAAAGTGCTTGTAATTGTAGTGCGAC
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StroWil	scf2_31000000049341:2045234- 2046083 +		CTTTGCTTTTTGCGTCGTTTTCTGT----------CGTCGTCGTCGACTG----------ACTTGCCCCGCCCC-CTG+----------C+---GA----------C++CCGCGCC-+C----------GCGCAGAAT-TAATCAA-GCTGGGGCTGGTTGGGGCAGGAC----------GGCTGACAGAAC----------AGA----------AAACCCGT-AG----------CCA-AAACCAGC----CGAATTTCACTTACCAGGCACACCGAGGGTTCGGCGATTTTTTCAGGTCTGGGCCTTGCGCACAAAGTGCTTGTAATTGTAGTGCGAC
StroVir	scaffold_12875:154323397- 154324185 +		----------CGTCGTCGTCGACTG----------ACTTGCCCCGCCCC-CTG+----------C+---GA----------C++CCGCGCC-+C----------GCGCAGAAT-TAATCAA-GCTGGGGCTGGTTGGGGCAGGAC----------GGCTGACAGAAC----------AGA----------AAACCCGT-AG----------CCA-AAACCAGC----CGAATTTCACTTACCAGGCACACCGAGGGTTCGGCGATTTTTTCAGGTCTGGGCCTTGCGCACAAAGTGCTTGTAATTGTAGTGCGAC
StroNoj	scaffold_4936:836632- 836509 +	Sno_3163	CGTTCACTTTTGCGTCGTTTTCTGTCACTTGACACTTGCTTTTGCTGCCCTCTGCCACCGCCACCTCCGCCACGGGCTCAGCTCTGGGCCATTCTGCCTCGTCGTCGACTG----------ACTTGCCCCGCCCC-CTG+----------C+---GA----------C++CCGCGCC-+C----------GCGCAGAAT-TAATCAA-GCTGGGGCTGGTTGGGGCAGGAC----------GGCTGACAGAAC----------AGA----------AAACCCGT-AG----------CCA-AAACCAGC----CGAATTTCACTTACCAGGCACACCGAGGGTTCGGCGATTTTTTCAGGTCTGGGCCTTGCGCACAAAGTGCTTGTAATTGTAGTGCGAC
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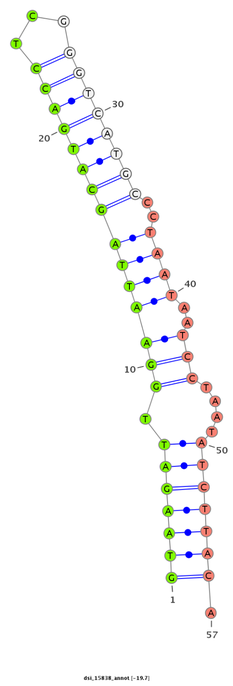
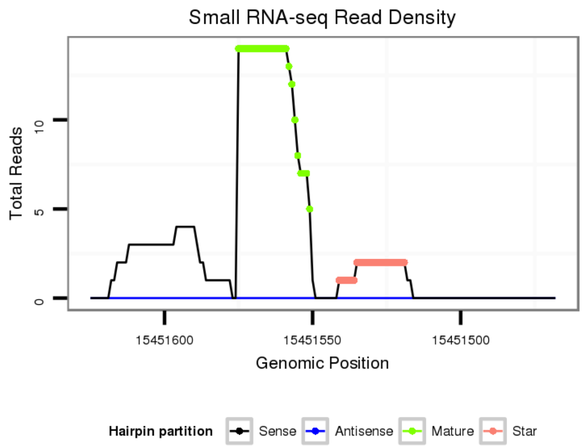
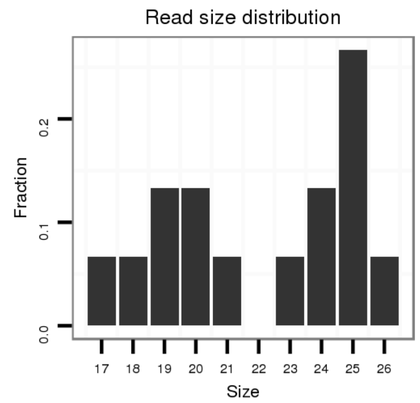
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dsi_15838	**x:15451518-15451575 -**	**candidate**	**Mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

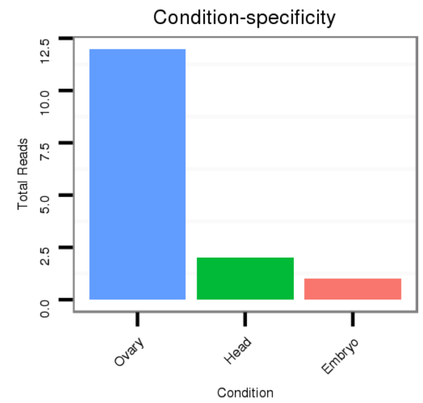
Legend: mature star **mismatch in alignment** mismatch in read

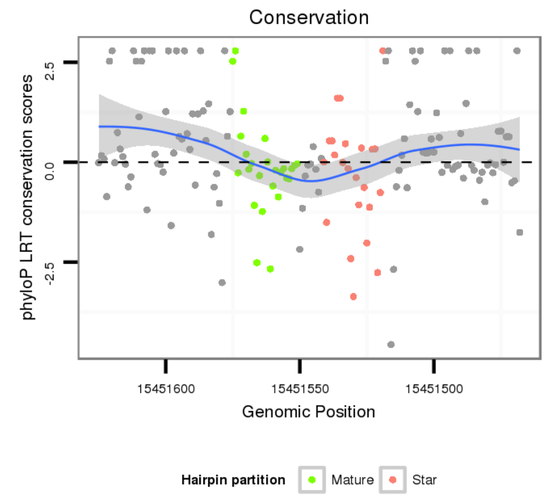
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [x_15451518_15451575_-]; CDS [x_15451576_15451765_-]; CDS [x_15451327_15451517_-]; utr3 [utr3_minus_10869]; utr3 [utr3_minus_10868]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

AAAGCACTACGCCAGCCTCAAGGATCTGAACAAATCGCACGATTCTCTGGGTAAGATTGGAATTAGCATGACCTCGGGTCATGCCCTAATAATCCTAATATCTTACAGTCTCGCGCATGGAGATCGCCCTGAAGGATCTCCTGGCGTCCAAGGGAGTT **********(((((((.((((((((((((((...)))))))).))))..)))....)))))))).**********	Read size	# Mismatch	Hit Count	Total Norm	Total	SRR618934 dsim w501 ovaries	SRR553488 RT_0-2 hours eggs	M023 head	SRR553486 Makindu_3 day-old ovaries	SRR553487 NRT_0-2 hours eggs	M025 embryo	M053 female body	SRR553485 Chicharo_3 day-old ovaries	SRR902008 ovaries	SRR902009 testis	GSM343915 embryo
.....GTAAGATTGGAATTAGCATGACCTC.....	25	0	1	4.00	4	2	0	0	1	1	0	0	0	0	0	0
.....GTAAGATTGGAATTAGCATGACCT.....	24	0	1	2.00	2	1	0	0	0	0	0	0	0	1	0	0
.....GTAAGATTGGAATTAGCAT.....	19	0	1	2.00	2	0	1	0	0	1	0	0	0	0	0	0
.....GTAAGATTGGAATTAGCATG.....	20	0	1	2.00	2	1	0	0	0	0	1	0	0	0	0	0
.....GTAAGATTGGAATTAGCA.....	18	0	1	1.00	1	0	0	1	0	0	0	0	0	0	0	0
.....AGCCTCAAGGATCTGAACAAATCGCA.....	26	0	1	1.00	1	0	1	0	0	0	0	0	0	0	0	0
.....TACGCCAGCCTCAAGGATCTGAACAAATC.....	29	0	1	1.00	1	0	0	0	0	0	0	0	1	0	0	0
.....AATCCTAATATCTTACAGT.....	19	0	1	1.00	1	0	0	0	1	0	0	0	0	0	0	0
.....GTAAGATTGGAATTAGCATGACCTCG.....	26	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0
.....GTAAGATTGGAATTAGCATGA.....	21	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0
.....CCTAATAATCCTAATATCTTACA.....	23	0	1	1.00	1	0	0	1	0	0	0	0	0	0	0	0
.....GTAAGATTGGAATTAGC.....	17	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0
.....ACAAATCGCACGATTCTCT.....	19	0	1	1.00	1	0	0	0	0	0	0	1	0	0	0	0
.....CGCCAGCCTCAAGGATCTGAACAAATCG.....	28	0	1	1.00	1	0	1	0	0	0	0	0	0	0	0	0

Anti-sense strand reads

TTTCGTGATGCGGTCGGAGTTCCTAGACTTGTTTAGCGTGCTAAGAGACCCATTCTAACCTTAATCGTACTGGAGCCCAGTACGGGATTATTAGGATTATAGAATGTCAGAGCGCGTACCTCTAGCGGGACTTCCTAGAGGACCGCAGGTTCCCTCAA **********(((((((.((((((((((((((...)))))))).))))..)))....)))))))).**********	Read size	# Mismatch	Hit Count	Total Norm	Total	SRR553488 RT_0-2 hours eggs	SRR553487 NRT_0-2 hours eggs	SRR553485 Chicharo_3 day-old ovaries	SRR553486 Makindu_3 day-old ovaries
.....TCTGCTAAGAGACCCAT.....	17	2	10	0.10	1	0	1	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droSim2	x:15451468-15451625 -	dsi_15838	AAAGCACTACGCCAGCCTCAAGGATCTGAACAAATCGCACGATTCTCTGGGTAAGATTGGAATTAGC-A--TGACC----------TCGG-G----TCATGCCCTAATAATC----------CTA-AT--ATCTTACAGTCTCGCGCATGGAGATCGCCCTGAAGGATCTCCTGGCGTCCAAGGGAGTT
droSec2	scaffold_17:161807-161964 -		AAGGCACTACGCCAGCCTCAAGGATCTGAACAAATCGCACGATTCTCTGGGTAAGATTGGAATTAGC-A--TGACC----------TCAA-A----TCATGCCCTAATAATC----------CTA-AT--ATCTTACAGTATCGCGCATGGAGATCGCCCTGAAGGATCTCCTGGCGTCCAAGGGAGTT
dm3	chrX:16341946-16342113 -		AAAGCACTACGCTAGCCTCAAGGATCTTAACAAATCGCACGATTCTTTGGGTAAGATTGGAATTGGC-G--TGACC----------TCGG-G----CCATGCCCTAATAATT--------C----------TGATATCCTTGG-AT--TCCTTACAGTGCAGCTCATGGAGAAGGCCCTGAAGGATCTTCTGGTGTCCAAGGGAGTT
droEre2	scaffold_4690:10755728-10755888 +		AAAACCACTACGATAGCCTTAAGGATCTAAACAAAACGCACGACTCTCTGGGTAAGATTGGAATTTCG-G--------CCAA-----CCGG-G----CCAAGG----A------TATGC--C----------TAATAT---CCTAAT--TCCTTGCAGTACAACGCATGGAGAGGGCCCTGAAGGAGTTCTTGGTTGGCAAGGGCGTT
droYak3	X:10461208-10461370 -		AAAACACTATGCCAGCCTCAAGGATCTAAACAAAACGCATGACCAACTGGGTAAGATTTGAATTGC-G--------CCAA-----TCAG-G----CCATGC----A------CATAC--C----------TAATATCCTTGG-AT--ACCTTGCAGTGCAGCGCATGGAGAGCGCCCTGAAGGAGTTCCTGGCGGCAAGGGGATT
droEug1	scf7180000409110:204146-204309 +		GGAACATTACAACAGCCTCAAGGACTGGACAAGTCTCACGACCCATTGGGTAAATTTGGAGT-----A--TTAT---GCTA-----ATAG-C----TCATTT----T------TATAT--C----------TCTCATGATTTCATT--TTATTTAGTTGCACGGATGGAGAGCAGCTTGAAGGAGTTCCTAGCGCCAAAGGAATA
droBia1	scf7180000302421:1934527-1934696 +		GAGGCACTACACCAGCCTCAAGGATCTGGACAAGACCCACGATGCCCTGGGTAAGAGCAGCT--GG-ACTGCGTCC----------TCAG-C----TTG----------GTCAGC--ACAACTAACCCGTGTTCTTCGATT--CGCCCCAAGTTGCGCGCATGGAGAGCGCCTGAAGGAGTTCCTGGCGGCAAGGGAATC
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droRho1	scf7180000780067:37810-37974 +		AAGACATTACAACAGCCTCAAGGTTCTAGACAAGTCCCACGATCCCATGGGTGAGAGTACTCT--T-AAAT--ATT----------T--------T--------TTAATTT----ATTTTGAAGACAAATAT----CC-CTTAA-AT--GCATTTTAGTCCCACGATGGAAAGCAGTTTAAGGAGTTCCTGACGAGCAAGGGGATT
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droKik1	scf7180000301710:77178-77340 -		ACAGCACGTCCCGAGCCTTAAGTTTCTCGACAAATCCCACCAGGACCTGGGTAAGTGTGCTT--AA-ACTC--CTTCATATACACATAC----------ATATCT----------TAAATTTTACTATT--ATTTTACAGTTACACGCTGGAAGAGGCCCTCAGGGACTTCTTGAAGGGACGGGGAGTG
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droVir3	scaffold_13049:21790283-21790450 -	dvi_20905	GCAGCATTATGACAGTCTAAAGGTCCTCAACCAATCGCACGAAAAATGGGTTTGTAGATTA--AA-----CAAACGTACTTA-----TATATATGCTCGTTTAT--ATAACTAA----AC--CTTT-AT--AATTTCTAGTGCTTCGCATGGAGCAGGCCCTCAAGAGCTTTTTACATCAAAAGGCATT
droMoj3	scaffold_6500:7441884-7442042 -		GCAACATTTTGACAGTCTGAAAGTGCTCAATGCAATCCACGTGGGCTTAGGTAAGTAAAGGT--GA-GGTA--ATT----------AA-CA----------TATTTTAAATATGTC----------TTGT--CTGT-TT--ACTATGCAGTTGAACGCATGAAGAATGGTATGATCCGTTTTCTTGAATGAAAAATGTG
droGri2	scaffold_15053:143152-143306 -		GCAACATTACGACAGTCTAAAGGTCTCAACGAATCGCACGAGAAAATGAGTTCGTAGATTA--CA-AATACAAT----------CTGT-A----TTATTTT---------CTAA----------CTTAT-GT--ATTTCACAGTCATAGCCATGGAGGAGGCCTGAAGAGCTTCTTTGTATCGAAAGGGATT

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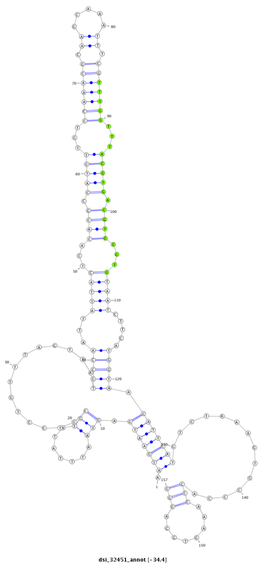
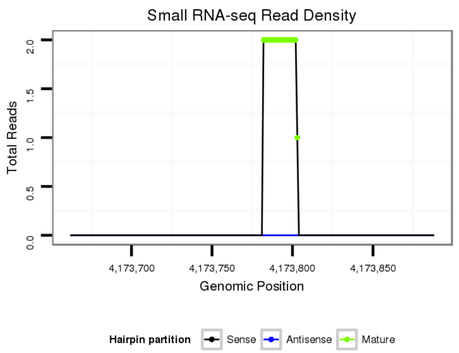
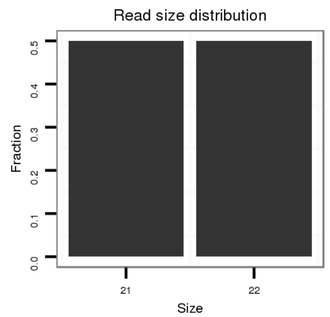
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dsi_32451	**3l:4173712-4173838 +**	**candidate**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser [Cornell Mirror]]

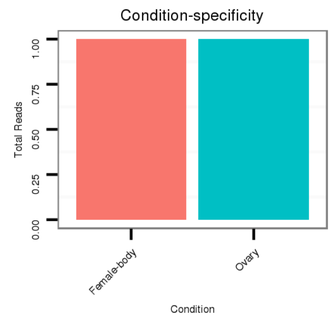
Legend: mature star mismatch in alignment mismatch in read

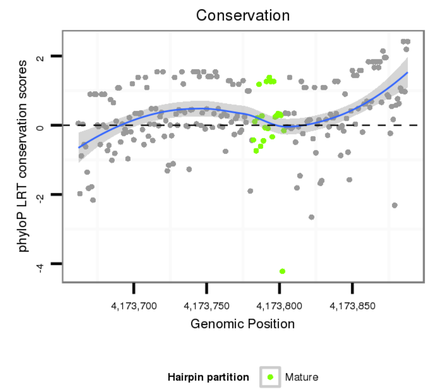
Predicted structure











Show Alternate Folds

Sense Strand Reads

hide 3p reads show mid mismatch reads

TGAAACCAAATTTACAATTGGATATGTAAACACTCAATGAATGAGTAATTTATATGCCTCCTGTTTAGTTATGCCAATTATTACTCACACGCCATGTTGTCCAAACGCAAGCAAATTTCGTTTGGTTTACGTGACGTGCGTGTAATCTTCATGGTAACATTCATGTCTAAAGTGCCCACCCAAAGTGCAGGGTATCAAAACAAGATCAATCGTTCGCTGCCACTCGT	Read size	# Mismatch	Hit Count	Total Norm	Total	SRR553485 Chicharo_3 day-old ovaries	SRR553486 Makindu_3 day-old ovaries	SRR553487 NRT_0-2 hours eggs	SRR618934 dsim w501 ovaries	M053 female body	SRR902009 testis	M025 embryo	SRR553488 RT_0-2 hours eggs
**********													
.....TTTGGTTTACGTGACGTGCGG.....	21	1	1	7.00	7	6	0	1	0	0	0	0	0
.....TTTGGTTTACGTGACGTGCGGA.....	22	2	1	1.00	1	1	0	0	0	0	0	0	0
.....TTTGGTTTACGTGACGTGCGTG.....	22	0	1	1.00	1	0	0	0	1	0	0	0	0
.....TTTGGTTTACGTGACGTGCGT.....	21	0	1	1.00	1	0	0	0	0	1	0	0	0

Anti-sense strand reads

ACTTTGGTTTAAATGTTAACCTATACATTTGTGAGTTACTTACTCATTAAATATACGGAGGACAAATCAATACGGTTAATAATGAGTGTGCGGTACAACAGGTTTGCGTTCGTTTAAAGCAAACCAAATGCACTGCACGCACATTAGAAGTACCATTGTAAGTACAGATTTCACGGGTGGGTTTCACGTCCCATAGTTTTGTTCTAGTTAGCAAGCGACGGTGAGCA	Read size	# Mismatch	Hit Count	Total Norm	Total	SRR553486 Makindu_3 day-old ovaries	SRR553485 Chicharo_3 day-old ovaries	SRR553487 NRT_0-2 hours eggs	SRR553488 RT_0-2 hours eggs	M053 female body	SRR618934 dsim w501 ovaries
**********											
.....AGGGTGGGTTTCACG.....	15	1	19	0.16	3	0	3	0	0	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droSim2	3l:4173662-4173888 +	dsi_32451	TGA----------AA---CCAAATTTACAATTGGATATGTAAAC---A----------C----------TCAATGAATGAGTAATTTATA------TGCCTCCTGTT----------TAGTTATGCCAATTATTACTCACACGCCATGTTGTCC------AAACGCAAGCAAATTTCGTTTGGTTTACGTGACGTGCGTGTAATCTT----CATGGTAA-CATTCATG---------TCTAAAG-----TGCCCACCCAAAGTGCAGGGTATCAAAACAAGATCAATC------GTT-CG----CTGCCACTCGT
droSec2	scaffold_2:4210382-4210609 +	dse_149	TGA----------AA---CCAAATTTACAATTGGATATGTAAAC---A----------C----------TCAATGAATGAGTAATTTATA------TGCCTCCTGTT----------TAGTTATGCCAATTATTACTCACACGCCATGTTGTCC------AAACGCAAGCAAATTTCGTTTGGTTTACGTGACGTGCGGGTAATCTT----CATGGTAA-CATTCATG---------TCTAAAG-----TGCCCACCCAAAGTGCAGGGTATCAAAACAAGATCAATC------GTT-CG----CTGCCACTCGT
dm3	chr3L:4213525-4213777 +	dme_404	TGA----------AA---CCAAGATTACAATTGGATATGTAAAC---A----------CTCATTTGGCGAACATACTTCAATCAAGATTTGAATATGTAATTTGAA------TGCCTGTGTT----------AAGTTATGCCGATTATTACTCACACGCCATGTTGTCC------AAACGCAAGCAAATTTCGCTTGGTTTGCGTGACGTGCGAGTAATCTT----CATGGTAA-CATTCATG---------TGCAATG-----TGCCCACCCAAAGTGCAGGGTATCAAAACAAGATCAATC------GTT-CG----CAGCCACTCGT
droEre2	scaffold_4784:6926001-6926191 +		TTT----------TA---TTTACATTACAATTGGATGTGTAAAC---A----------C----------ATAATTGAATTAGTAATTTGAA------TGCCTTGTGTT----------TAGTTATGCCGATTATTACTCACCGGCGATGCT----------TACGTGACTAACGCAATAATCT----CAATGTAA-CATTCATG---------TGCAAAG-----TGCCCAGT-----TGCAGGGTATCAAAACAAGATCAATC------GTT-TG----CTGCCACTCGT
droYak3	3L:4787835-4788036 +		TAA----------AAATATTTAATTTACAATTGGATGTA----GC---A----------C----------ATAAC----GCAATAATTTAAATAAGTAAGTTTATT------TGCCTATGTGT----------TAGTTATGCCGCTTATTACTCATACGCCATGTT----------TACGTGACTAACAGACAATCT----GTTGTAGTAA-CATGCATG---------TGCAAAG-----TGCCCAGT-----TGCAGGGTATCAAAACAAGATCAATC------GTT-TG----CTGCCACTCGT
droEugl	scf7180000409466:1979085-1979355 +		CAA----------AG---TCAAAGTTACCATTGAA---ATAAGGAACTTTCATAAATTTTATGAAAGAGT----TTTGCAAAAATGCC----ATAATAATTTGGGTAATCTAATTTGAA------TACCTTGCATT----------TAGTTATGCAGCTTATTAGCAACACGCCATGTGCGCA------AAACGCAAGCAACTTTGTTAGGTTACGATGCGGTATGTGTAATGTTT---CCAGCAAA-TTTAAATGTA---------CTTAAATATTATACCCAGTGATA-GATAAGATGTATTAAGACAAGATCAATC------GTT-TG----CTGCCACGTAGT
droBial	scf7180000302428:923562-923760 +		TG----------A---A----------A---A----------A----------A------AAATAACCAATTTGAA------TGCCTTGCATG----------TAGTTATGCAGCTGATTACTCACACGCCATGTTGCTTT------AAACGCTAGTGAATTTGTTGGCCTTACGTGCGGTATCGATAATCTTTT-TCTTAGGTAA-CTTAAACATATTAGAAATGCAAAG----TTACCCAGT-----CATAGATATCTGAACAAGATCAATC------GTTTTGCTT--CGCCTCTCGT
droTak1	scf7180000415707:7715-7908 -		TG----------A---A----------A---A----------A----------A------AAATAACAAATTTGAA------TGCCTTGCATT----------CAGTTATGCAGTTTATTACTCACACGCCATGTTGCCC------AAACGTTAGCAAGTTTGTTAGGTTTACATGCGGTATCGATAATCTCTT--TAAAGAAAGCTTAAATA---------TAAAAAGTAAAGTACCCACG-----GTTAGGGTATCTGAACAAGATCAATC------GTTTTGCTT--GGCCACTCGT
droEle1	scf7180000491249:5082968-5083213 +		TAT----------AA---AAGAGCTTAAAATAAACT--------A---A----------A----------ACC----ATAATCATTAAATAAGTAAGTTGTA------TGCCTTGATTTAAGTTATGCAGCTGAGTTATGCAGGCTTATTACTCACACGCCATGTTGCCTT------AAACGAAAGCAAATTTAGGCTGGTTCACGTGCGGTATCATAATTTGTTGTTAGGTAA-CTTCCATG---------TGTAAAAAGAAAACACCCAGT-----GTTAGATGTATCAAAACGAGATCAATC------GTTTTGCTGGCCAGCACTCGT
droRho1	scf7180000779786:5197-5471 +		AATTCTCTATTAGAACAAAGGAATTTATTCAATTTGTATTATGTTTATAA----A----------AAGCGC----TTAATAAAAATCCC----AGAAAATTTAAATAAGTAATTTGAA------TGCCTTGAATT----------TAGTTATGCAGCTTATTACTCACACGCCATGTTGCCTT------AAACGAAAGCAAATTTGAGCTGGCTTACGTGCGGTATCGTGTATGTTATGGCTAA-CTTCCATG---------TATAAAGTGAGGTACCCAGT-----TTTAGATGTATCAAAACAAGATCAATC------GTT-CGCTT--GGCCACTCGT
droFic1	scf7180000454113:1447877-1447918 +		---A----------A---A----------A---A----------A----------A------A----------A----------A------A----------A------A----------A---A-------A-------A-------A------A----------GTAGATGTATCAAAACAAGATCAATC------GTT-TGCTT--GGCCACTCGT
droKik1	scf7180000302383:601638-601691 +		AA----------A---A----------A---A----------A----------A------A----------TGTAAA----TGCTTGTGAA----------A-TGTGTGCAAATTATTACTCATACGCAGTGTTGCT------A----------A---A-------A-------A-------A------A----------A------A--A--A----A----------
droAna3	scaffold_13337:14637452-14637639 +		ATG----------A---A----------GAATT---A----------A----------ACTAATGAATAATTA-TATGACTTTTATATTT-CATC----------AAGCCATTTAGATATCAGCGATACGCCGTGTGTTGTTGGCTTGAAGCATGATAAA------CTATCCACACGTGTCGTATGATGTTTTT---TGAAG---A-------A-------A------AAAATTTTAGAA-GCTAGAGCATCAAAACAAGATCAATC------GTT-GG----TCGCCACTCGT
droBip1	scf7180000396641:673906-673944 -		---A----------A---A----------A---A----------A----------A------A----------A----------A------A----------A------A----------A---A-------A-------A-------A------A----------AGAGCATCAAAACAAGATCAATC------GTT-GA----TCGCCACTCGT
dp5	XR_group8:8380530-8380571 +		AT-----------A---A----------A---A----------A----------A------A----------A----------A------A----------A------A----------A---A-------A-------A-------A------A----------AAAAAAAAGATCATCACAGTGTGCGCGCA---GGCCACTCGT
droPer2	scaffold_40:572650-572688 +		AA----------A---A----------A---A----------A----------A------A----------A----------A------A----------A------A----------A---A-------A-------A-------A------A----------AAAAAGATCATCACAGTGTGCGCGCA---GGCCACTCGT
droVir3	scaffold_13049:2094210-2094215 +		A--A----------A---A----------A---A----------A----------A------A----------A----------A------A----------A---A-------A-------A-------A------A----------A------A--A--A----A------TTCGT
droMoj3	scaffold_6654:1759694-1759707 -		A--A----------A---A----------A---A----------A----------A------A----------A----------A------A----------A---A-------A-------A-------A------A----------TC------GTT--A------A---CGACTCGT
droGri2	scaffold_15110:3145440-3145445 +		---A----------A---A----------A---A----------A----------A------A----------A----------A------A----------A---A-------A-------A-------A------A----------A------A--A--A----A------ACTCGT

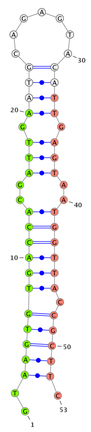
Generated: 09/08/2015 at 08:06 PM

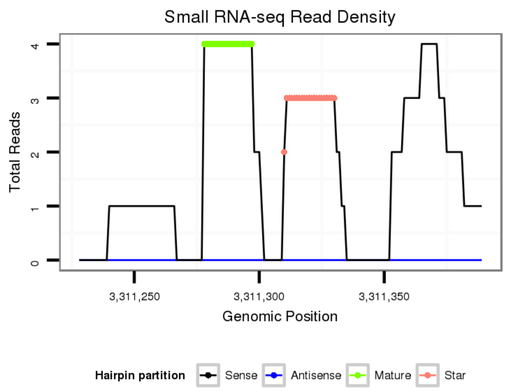
	Passed Filter
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	0
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	3

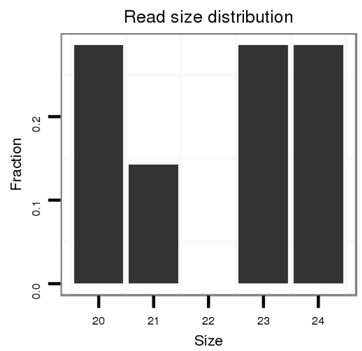
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dsi_8223	**x:3311278-3311339 +**	**candidate**	**3p_tailed_mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

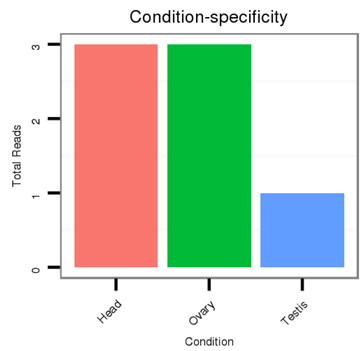
Legend: mature star mismatch in alignment mismatch in read

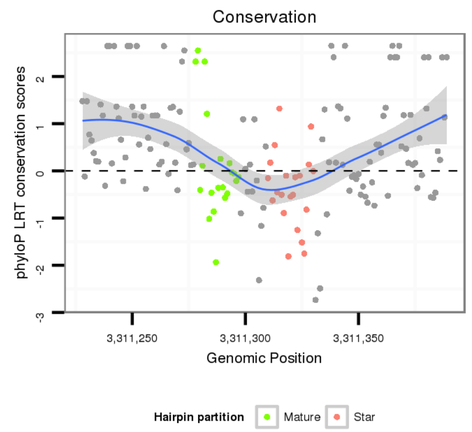
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [x_3311278_3311339_+]; CDS [x_3311340_3311487_+]; CDS [x_3311118_3311277_+]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

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AGAAAACATCCAACTTGACAATACTTGACACGGCCCACAAATATGTCAAGGTAAGTGTGACCACGATTGAATGCAGAGTACATTGAGTAATGGTTACCGCTTCTGGTTGCAGGACTTGATTCAGTATGGTTGCGAGCAGGAGGCGACGGTAGAGAAACTGGC  Read size  # Mismatch  Hit Count  Total Norm  Total  SRR618934 dsim w501 ovaries  SRR902009 testis  SRR553486 Makindu_3 day-old ovaries  M053 female body  O002 Head  M024 male body  M023 head  SRR902008 ovaries  SRR553488 RT_0-2 hours eggs
**********************************************..(((((((((((..(((.((((.......)))).)))..)))))))).)))))).**************************************************************
.......................................GTAAGTGTGACCACGATTGA.......................................................................................... 20  0  1  2.00  2  0  0  0  0  2  0  0  0  0
.......................................................................................ATGGTTGCGAGCAGGAGGCGAC............................ 22  0  1  1.00  1  1  0  0  0  0  0  0  0  0
.......................................................................................TGCGAGCAGGAGGCGACGGTAGAG......................... 19  0  1  1.00  1  0  0  0  0  0  0  0  0  0
.......................................GTAAGTGTGACCACGATTGAATG....................................................................................... 24  0  1  1.00  1  0  1  0  0  0  0  0  0  0
.......................................GTAAGTGTGACCACGATTGAATGC...................................................................................... 23  0  1  1.00  1  1  0  0  0  0  0  0  0  0
............ACTTGACAATACTTGACACGGCCCACA....................................................................................................... 24  0  1  1.00  1  0  0  0  0  0  1  0  0  0
.......................................................................TTGAGTAATGGTTACCGCTTC.......................................... 27  0  1  1.00  1  1  0  0  0  0  0  0  0  0
.......................................................................................AGGAGGCGACGGTAGAGAAACTGGC..................... 21  0  1  1.00  1  0  1  0  0  0  0  0  0  0
.......................................................................TTGAGTAATGGTTACCGCTTCTG........................................ 25  0  1  1.00  1  0  0  0  0  0  0  1  0  0
.......................................................................TGAGTAATGGTTACCGCTTCTGGT....................................... 23  0  1  1.00  1  1  0  0  0  0  0  0  0  0
```

Anti-sense strand reads

```
TCTTTTGTAGGTTGAACTGTTATGAACTGTGCCGGGTGTTTATACAGTTCCATTCACACTGGTGCTAACTTACGTCTCATGTAACTCATTACCAATGGCGAAGACCAACGTCCTGAACTAAGTCATACCAACGCTCGTCCTCCGCTGCCATCTCTTTGACCG  Read size  # Mismatch  Hit Count  Total Norm  Total  M023 head  M025 embryo  SRR553488 RT_0-2 hours eggs  M053 female body  SRR553486 Makindu_3 day-old ovaries
*******************************************************..(((((((((((..(((.((((.......)))).)))..)))))))).)))))).*********************************************
```

Show Alignment With Reads

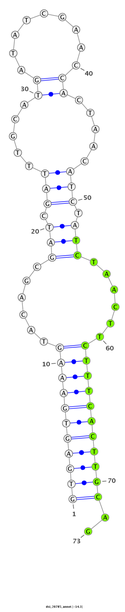
Re-alignment of all predicted orthologs

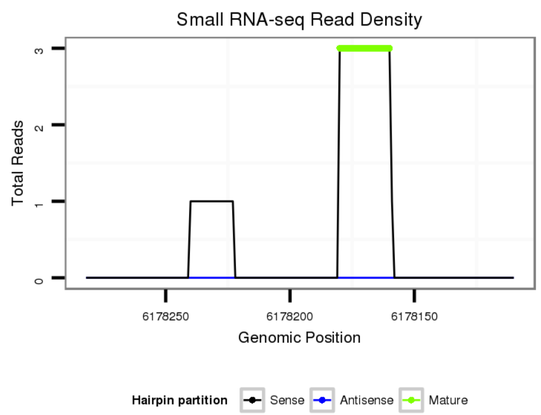
Species	Coordinate	ID	Alignment
droSim2	x:3311228-3311389 +	dsi_8223	AGAAAACATCCAACTTGACAATACTTGACACGGCCCACAAATATGTCAAGG-TAAGTG--TGA----------CCACGATTGAATGCAGA----------G----------TACATT---GAGTA----------A---TGGTTACCGCTTC----------T-----GGTTGCAGGAC-TTGATTCAGTATGGTTGCGAGCAGGAGGCGACGGTAGAGAAAC-----TGGC
droSec2	scaffold_4:3103865-3104026 -		AGAAAACATCCAACTTGACAATACTTGACACGGCCCACAAATATGTCAAGG-TAAGTG--TGA----------CCACGATTGAATGCAGA----------A----------TACATT---GAGTA----------A---TGGTTACCGCTTC----------T-----GGTTGCAGGAC-TTGATTCAGTATGGTTGCGAGCAGGAGGCGACGGTAGAGAAAC-----TGGC
dm3	ChrX:3593257-3593421 +		AGAAAACATCAAACTTGACAATACTTGACACGGCCCACAAATATGTCAATG-TAAGTG--TGA----------CCACGATTGTGTGTAGA----------A----------TACATT---GAGTA---------ATG--A---TGGTTACGCGTTC----------T-----GGTTGCAGTCC-TTGAGTCAGGAATTTGCGAGCAGGAGGCGAAGATAGAGAAAC-----TGGC
droEre2	scaffold_4690:989380-989548 +		AGAAAACATCCAACTTGACAATACTCGACACGGCCAACAAATATGTTAAGG-TAAGCCTGTCT----------TCACGATTGAATGCAGAA---CAG----------A----------CACATT---GACTA----------A---TGTTTACACTTT-------TCTG-----TGTTGCAGGAC-TTGATTAGTATGGTTCGAGCAGGAGACGAGTGTAGAGAAAC-----TGGC
droYak3	X:4812067-4812227 -		AGAAAACATCCAACTTGACAATACTCGACACGGCCCACAAATATGTAAGG-TAAGTG--TGT----------CCACGATTGAATGCAGA----------A----------CACATT---GACTA----------A---TGGTTACCTCT-----------C-----TGTTGCAGGAC-TTGATTCAGTATGATTGCGAGCAGGAGGCGAGGGTAGAGAAAC-----TGGC
droEug1	scf7180000408900:161501-161687 -		AGAACACCTCCAACTTGACAATACTCGAATACGGCCCACAAATATGTCAAGG-TTAGTC--TTTGAAATC----------A----ATAAATATGGCTTTACAATAATC-------GA---AGAAATCGAGTT-------AAATGTATTAATAATTTTTT--------TTC-----GATTTCAGCAA-TTGAGCACACTGATCGCGACAGGAGGCGAGGTGGAGAAGC-----TGGC
droBia1	scf7180000302126:1518243-1518357 -		AAATGTGCGCA--GACGATTGTATA----------A----------ATCATT---AATTA----------A---TGGCCGCCTTTGC---------TGTATTTTTATGCAGCAA-TTGAGCAGCGTGGCGCGAGCAGGAGGCGAGGTGGAGAGGC-----TGGC
droTak1	scf7180000415078:234266-234320 +		AGAACACCTCCAATTTGACAATACTCGAATACGGCCCACAAATTTGTCAAGG-TGAG--

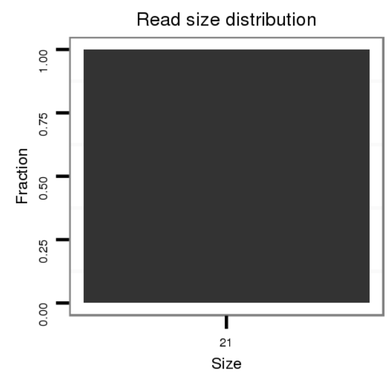
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dsi_20785	**3r:6178160-6178232 -**	**candidate**	**Mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

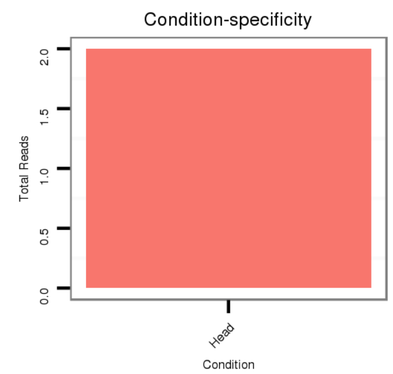
Legend: mature star mismatch in alignment mismatch in read

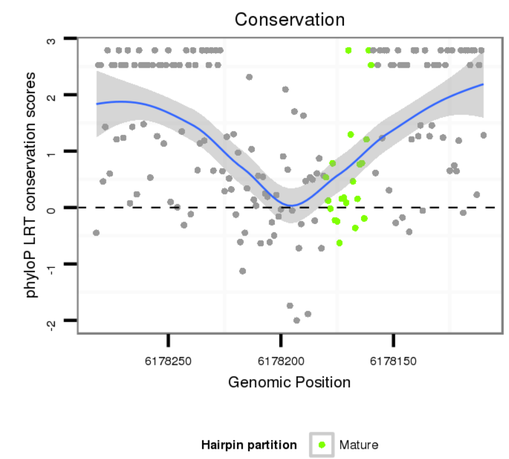
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [3r_6178160_6178232_-]; CDS [3r_6178233_6178647_-]; CDS [3r_6178005_6178159_-]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

```
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                
```

Read size	# Mismatch	Hit Count	Total Norm	Total	head	embryo	Head	SRR553488 hours eggs	SRR553486 day-old ovaries	SRR553487 hours eggs
21	0	1	2.00	2	2	0	0	0	0	0
22	0	1	1.00	1	0	1	0	0	0	0
18	0	1	1.00	1	0	0	1	0	0	0

Anti-sense strand reads

```
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                
```

Read size	# Mismatch	Hit Count	Total Norm	Total	SRR902009 testis	SRR553488 RT_0-2 hours eggs	SRR553486 Makindu_3 day-old ovaries	SRR618934 dsim w501 ovaries	SRR902008 ovaries

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droSim2	3r:6178110-6178282 -	dsi_20785	
droSec2	scaffold_25:682357-682529 -		
dm3	chr3R:15084397-15084569 +		
droEre2	scaffold_4770:6547407-6547575 -	der_567	
droYak3	3R:3793871-3794047 +		
droEug1	scf7180000409804:1349242-1349403 +		
droBia1	scf7180000302402:846250-846418 +		
droTak1	scf7180000410451:111104-111272 +		
droEle1	scf7180000490994:858866-859041 +		
droRho1	scf7180000779522:16958-17112 +		
droFic1	scf7180000454126:64938-65105 +		
droKik1	scf7180000302707:304273-304438 +		
droAna3	scaffold_13340:15302669-15302824 -		
droBip1	scf7180000396708:4731422-4731587 +		
dp5	2:29533035-29533206 +		
droPer2	scaffold_6:4903732-4903903 +		
droWil2	scf2_1100000004943:3829843-3830004 +		
droVir3	scaffold_13047:16559345-16559545 -		
droMoj3	scaffold_6540:12876035-12876190 -		
droGri2	scaffold_15116:1514235-1514471 -		

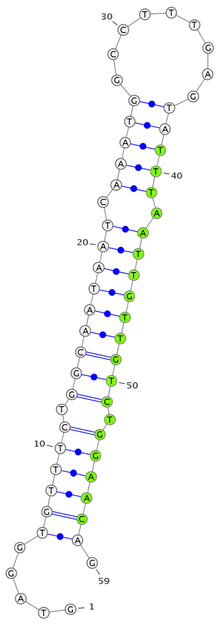
Generated: 09/08/2015 at 07:18 PM

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

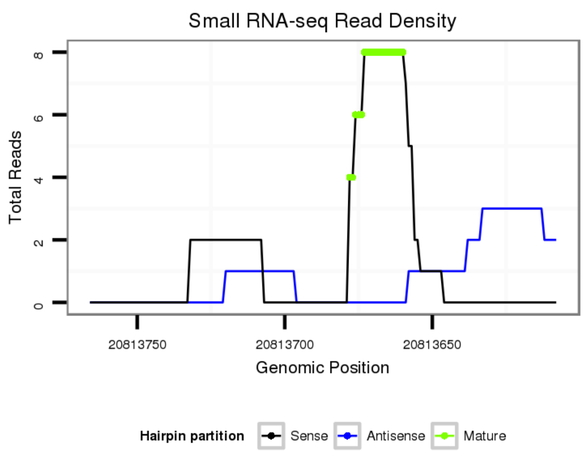
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dsi_28068	**x:20813658-20813716 -**	**candidate**	**Mirtron**	**3pUTR**	[View on UCSC Genome Browser {Cornell Mirror}]

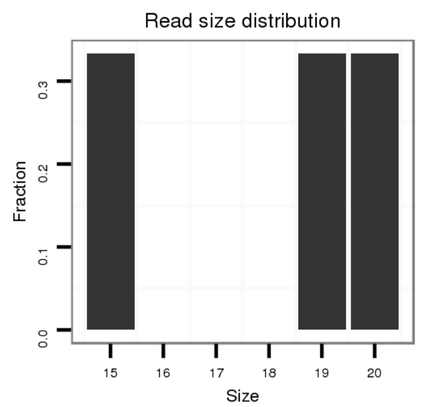
Legend: mature star mismatch in alignment mismatch in read

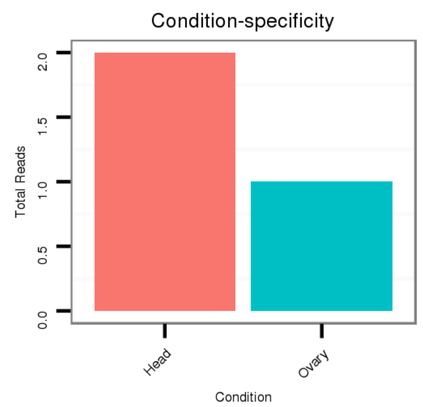
Predicted structure

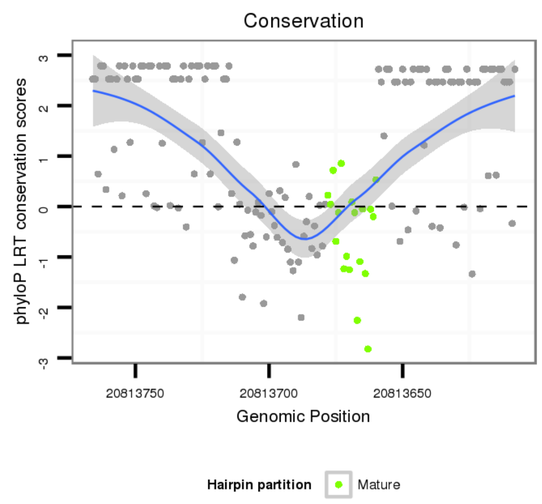


dsi_28068_annot [-16.4]









Show Alternate Folds

Flybase annnotation

utr3 [utr3_minus_11389]; utr3 [utr3_minus_11388]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

CCCATACCCGAATGCTGGATCTACCTGTTCCGTGTGGAGAAGCACTTCAGGTAGGTGTTTCTGGCAATAATCAAATGGCCTTTGAGTATTTAATTGTTGTCTGGAACAGATATGGTTCGGTTAAGTCAGCTCATCGGCGAACAGGCAAGATCAAGGGTA **********.....((((((.(((((((((.(((((.....)))))).)))))))))..))))))..**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M023 head	SRR553485 Chicharo_3 day-old ovaries	SRR553486 Makindu_3 day-old ovaries	SRR553487 NRT_0-2 hours eggs	M024 male body	M025 embryo	SRR553488 RT_0-2 hours eggs
.....TTTAATTGTTGTCTGGAACAGT.....	22	1	1	18.00	18	17	0	0	0	0	1	0
.....TTTAATTGTTGTCTGGAACAGC.....	22	1	1	5.00	5	4	0	0	0	1	0	0
.....TTTAATTGTTGTCTGGAACAGG.....	22	1	1	2.00	2	2	0	0	0	0	0	0
.....TTTAATTGTTGTCTGGAACAGA.....	22	0	1	2.00	2	1	1	0	0	0	0	0
.....TGGAGAAGCACTTCAGGTAGGTGTT.....	25	0	1	2.00	2	0	0	2	0	0	0	0
.....TAATTGTTGTCTGGAACAGTA.....	21	2	1	1.00	1	1	0	0	0	0	0	0
.....TTGTTGTCTGGAACAGATATGGTTCGG.....	27	0	1	1.00	1	0	1	0	0	0	0	0
.....TTTAATTGTTGTCTGGAAC.....	19	0	1	1.00	1	1	0	0	0	0	0	0
.....TAATTGTTGTCTGGAACAGATA.....	22	0	1	1.00	1	0	1	0	0	0	0	0
.....TTAATTGTTGTCTGGAACAGT.....	21	1	1	1.00	1	1	0	0	0	0	0	0
.....TAATTGTTGTCTGGAACAGA.....	20	0	1	1.00	1	1	0	0	0	0	0	0
.....TTTAATTGTTGTCTGGAACA.....	20	0	1	1.00	1	1	0	0	0	0	0	0
.....TTGTTGTCTGGAACA.....	15	0	1	1.00	1	0	0	0	0	0	0	1

Anti-sense strand reads

GGGTATGGGCTTACGACCTAGATGGACAAGGCACACCTCTTCGTGAAGTCCATCCACAAAGACCGTTATTAGTTTACCGGAAACTCATAAATTAACAACAGACCTTGTCTATACCAAGCCAATTCAGTCGAGTAGCCGCTTGTCCGTTCTAGTTCCCAT **********.....((((((.(((((((((.(((((.....)))))).)))))))))..))))))..**********	Read size	# Mismatch	Hit Count	Total Norm	Total	SRR553488 RT_0-2 hours eggs	SRR618934 dsim w501 ovaries	SRR553487 NRT_0-2 hours eggs	SRR553485 Chicharo_3 day-old ovaries
.....AGCCGCTTGTCCGTTCTAGTTCCCAT	26	0	1	2.00	2	0	0	1	1
.....AAGTAGCCGCTTGTC.....	15	1	13	1.23	16	16	0	0	0
.....AGTCCATCCACAAAGACCGTTATT.....	24	0	1	1.00	1	0	0	1	0
.....CGAGTAGCCGCTTGTCCGTTCTAGTT.....	26	0	1	1.00	1	0	1	0	0
.....CTATACCAAGCCAATTCAGTCGAGT.....	25	0	1	1.00	1	0	1	0	0
.....AGAGTAGCCGCTTGTC.....	16	1	4	0.25	1	1	0	0	0

Show Alignment With Reads

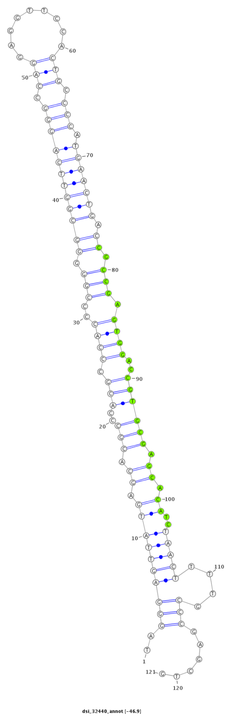
Re-alignment of all predicted orthologs

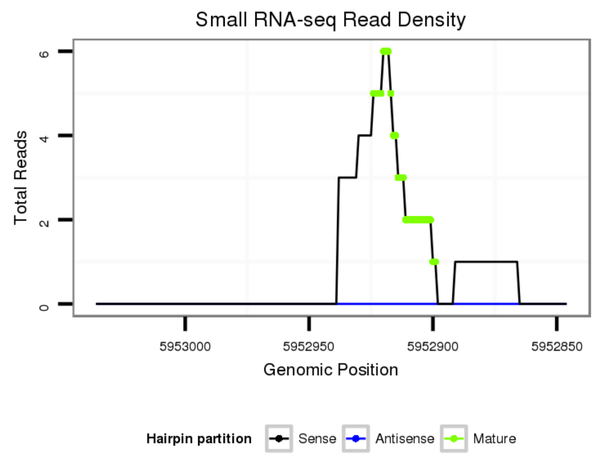
Species	Coordinate	ID	Alignment
droSim2	x:20813608-20813766 -	dsi_28068	CCCATACCCGAATGCTGGATCTACCTGTTCCGTGTGGAGAAGCACTTCAGGTAGGTGTTTCT--GGC---------AA-TA----------ATCAAATGGCCTTT----------GAGTATTTAAT----------TGTTG-----TCTGGAACAGATATGGTTCGGTTAAGTCAGCTCATCGGCGAACAGGCAAGATCAAGGGTA
droSec2	scaffold_39:311371-311529 -		CCCATACCCGAATGCTGGATCTACCTGTTCCGTGTGGAGAAGCACTTCAGGTAGGTGTTTCT--GGC---------AA-TA----------ATCAAATGGCCTTT----------GAGTATTTAAT----------TGTTG-----TCTGGAACAGATATGGTTCGGTTAAGTCAGCTCATCGGCGAACAGGCAAGATCAAGGGTA
dm3	chrX:22386564-22386722 -		CCCATACCCGAATGCTGGATCTACCTGTTTCGTGTGGAGAAGCACTTCAGGTAAGTGTTTCT--GGC---------AA-TA----------ATCATATGGCCTTT----------GAGTATTTTAT----------TGTTG-----CCTGAAACAGATATGGTTCGGTTAAGTCAGCTCATCGGCGAACAGGCAAGATCAAGGGTA
droEre2	scaffold_4690:18650571-18650729 -		CCCATACCCGAATGCTGGATCTACCTGTTTCGTGTGGAGAAGCACTTCAGGTGAGTATTTCC--GGC---------AC-TA----------ATCATCTGGGTTTT----------AAGTATTTAAT----------GGTGG-----TCCGGAACAGATATGGTTCGGTTAAGTCAGCTCATCGGCGAACAGGCAAGATCAAGGGTA
droYak3	X:21718783-21718941 -		CCGATACCCGAATGCTGGATCTACTTGTTCCGTGTCGAGAAGCACTTCAGGTGAGTATTTCC--GGC---------AA-TA----------GTCATCTGGGTTTT----------GAGTATTTAAT----------GGTAC-----CCTGAAACAGATATGGCTCGGTTAAGTCAGCTCATCGGCGAACAGGCAAGATTAAGGGTA
droEug1	scf7180000408987:119901-120066 +		CCTATTCCCGAATGCTGGATTTATCTGTTCCGCGTGGAGAAGCACTTTAGGTGGATATTTCT--GGT---------GA-TA----------ATCAACCGTGTTCC----------AGGAAATTAAT-----AGCAT----TTCTGT----CT-----------ATGATAACAGATACGGCTCGGTCAAGTCGGGCATCGACGAACAGGTAAAATCAAGGGAA
droBia1	scf7180000299500:31889-32064 -		CCCATTCCCGAATGCTGGATCTATTTGTTCCGCGTAGAGAAGCACTTTCGGTGGGTATTTCT--GGG---------AA-CG----------GTCAACGGGTTTTCTG---GTACT-TAATAATTTA-----CATTTGCT----------TCGGCATC--ATTAAAACAGATACGGTTCGGTCAAGTCCGGACATCGGCGAACTGGCAAGATCAAGGGAA
droTak1	scf7180000415769:11988-12147 -		CCCATTCCCGAGTGCTGGATTTACTGTTCCGCGTGGAGAAGCACTTCAGGTGGGAGTTTGT--GGA---------TA-TT----------TAATG-----TC-ATACA--TAC---ATACATTTACT----------TGTGG-----GCTACTACAGATATGGATCAGTCAAGTCGGCACATCGACGAACTGGCAAGATTAAGGGAA
droEle1	scf7180000491087:510853-510926 +		CCCATTCCCGAGTGCTGGATCTACCTGTTCCGCGTGGAGAAGCACTTCAGGTGAGCATCTCT--GGC---------GA-TG----------ACTAA---------CTT----------CT-----CT-----CTTCCT-----CTCTCT-----CTCTCT-----CTCT

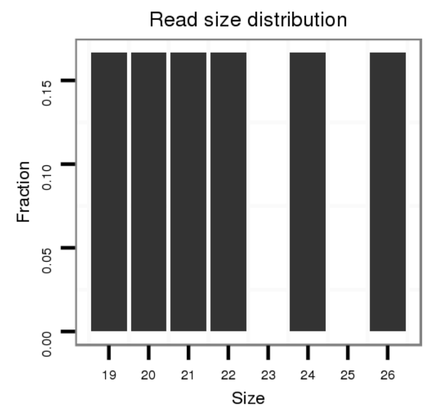
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dsi_32440	**2r:5952896-5952986 -**	**candidate**	**Canonical miRNA**	**CDS**	[View on UCSC Genome Browser {Cornell Mirror}]

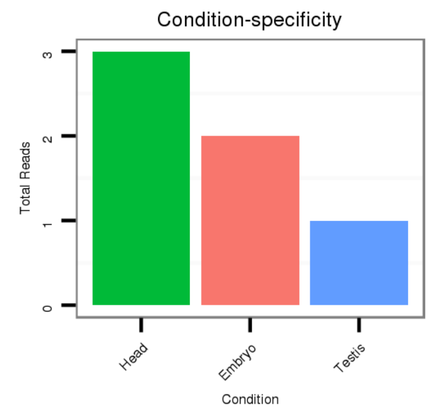
Legend: mature star mismatch in alignment mismatch in read

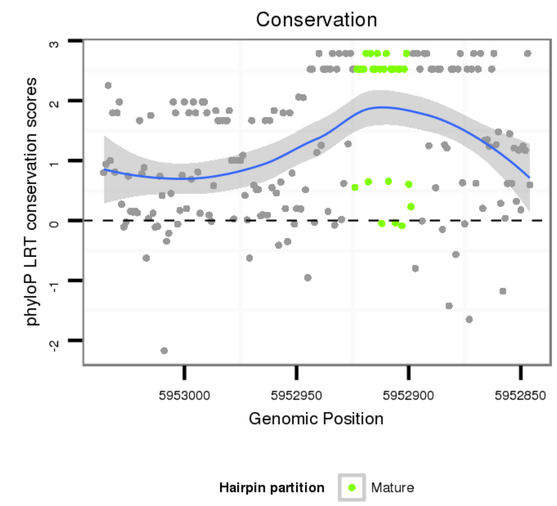
Predicted structure











Show Alternate Folds

Flybase annotation

CDS [2r_5952768_5952992_-]; five_prime_UTR [2r_5952993_5953423_-]; utr5 [utr5_minus_2991]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

AAATGTGTTCATGCCACGATCGCAAAACAAGTGTTTAGGGAGTTATGAGCACGCCCACGCCCACCCCGGGGGCGGTTCAGGGCCAGGAGGTTCCACTGCCCCATGAACTGACCGCCGAGTGGACCGTGCGAGCACATCTAACTTTTGCCCGAGCTGGTGAAACGGTGCAAAAGGAGTTCAGTGCTCCGGAG **********..((((((((((.((.(((..(((.((((..(((.((((((((((((.(((.....))).))).)))))))).)).)))).))))..)))))).)).)).)..)))))....)))).....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M023 head	SRR618934 dsim w501 ovaries	M025 embryo	SRR553485 Chicharo_3 day-old ovaries	SRR902009 testis	GSM343915 embryo	SRR553486 Makindu_3 day-old ovaries	SRR553488 RT_0-2 hours eggs
.....CCCCATGAACTGACCGCCGAGTT.....	23	1	1	1.00	1	1	0	0	0	0	0	0	0
.....CGCCGAGTGGACCGTGCGAGCACATC.....	26	0	1	1.00	1	0	0	0	0	0	1	0	0
.....CCCCATGAACTGACCGCCGAGT.....	22	0	1	1.00	1	1	0	0	0	0	0	0	0
.....CCCCATGAACTGACCGCCGAGTGG.....	24	0	1	1.00	1	1	0	0	0	0	0	0	0
.....CCCCATGAACTGACCGCCGAG.....	21	0	1	1.00	1	1	0	0	0	0	0	0	0
.....TGCCCGAGCTGGTGAAACGGTGCAAA.....	26	0	1	1.00	1	0	1	0	0	0	0	0	0
.....ACTGACCGCCGAGTGGACC.....	19	0	1	1.00	1	0	0	1	0	0	0	0	0
.....GAGTGGACCGTGCGAGCACA.....	20	0	1	1.00	1	0	0	0	0	1	0	0	0
.....AACTGACCGCCGAGTGGAA.....	19	1	1	1.00	1	0	0	0	1	0	0	0	0
.....CCGAGCTGGTGAAAC.....	15	0	2	0.50	1	0	0	0	0	0	0	1	0

Anti-sense strand reads

TTTACACAAGTACGGTGCTAGCGTTTTGTTCACAAATCCCTCAATACTCGTGCGGGTGCGGGTGGGGCCCCCGCCAAGTCCCGGTCCTCCAAGGTGACGGGGTACTTGACTGGCGGCTCACCTGGCACGCTCGTGTAGATTGAAAACGGGCTCGACCACTTTGCCACGTTTTCCTCAAGTCACGAGGCCTC **********..((((((((((.((.(((..(((.((((..(((.((((((((((((.(((.....))).))).)))))))).)).)))).))))..)))))).)).)).)..)))))....)))).....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	SRR618934 dsim w501 ovaries	M025 embryo

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droSim2	2r:5952846-5953036 -	dsi_32440	AAATGTGTTCATGCCACGATCGCAAAACAAGTGTTTAGGG------AGTTATGAGCACGCCCACGCCCA------------CC---------CCGGGGGCGGTTC-------A--GGGCCAGGAGGT---TCCACTGCCCCATGAACTGACCGCCGAGTGGACCGTGCGAGCACATCTAACTTTTGCCCGAGCT---GGTGAAACGGTGCAAAAGGAGTTCAGTGCTCC------GGAG
droSec2	scaffold_1:2782184-2782374 -		AAATGTGTTCATGCCACGACCGCAAAACAAGTGCTTAGGG------AGTCATGAGCACGCCCACGCCCA------------TT---------TCGGGGGCGGTTC-------A--GGGCCAGGAGGT---TCCACTGCGTCATGAACTGACCGCCGAGTGGACCGTGCGAGCACATCTAACTTTTGCCCGAGCT---GGTGAAACGGTGCAAAAGGAGTTCAGTGCTCC------GGAG
dm3	chr2R:5150240-5150430 -	dme_381	AAATGTGTTTATGCCACGACCGCAAAACAAGTGTTTAGGG------AGTCATGAGCACGCCCACGCCCA------------CT---------TCGGGGGCGGTTC-------A--GGGCCAGGAGGT---TCCACTGCCCCATGAACTGACCGCCGAGTGGACCGTGCGAGCACATCTAACTTTTGCCCGAGCT---GGCGAAACGGTGCAAAAGGAGTTCAGTGCTCC------GGAG
droEre2	scaffold_4929:17507595-17507785 +	der_84	AAATGTGTTTATGCCACGACCGCAAAACTAGTGCTTAGGA------AGTCATGAGCACGCCCACGCCCA------------CT---------CCGGGGTCGGTTC-------A--GGGCCAGCAAGT---TCCACTGCCCCATGAACTGACCGCCGAGTGGACCGTGCGAGCACATCTAACTTTTGCCCGAGCC---GGAGAGACAGTGCAAAAGGAGTTCAGTGCTCC------GGAC
droYak3	2L:17804669-17804859 -		AAATGTGTGTATGCCACGACCGCGAAACAAGTGCTTAGGG------AGTCATGAGCACGCCCACGCCCA------------CT---------TCAGGGGCGGTTC-------A--GGGCCAACAAGT---TCCGCTGCCCCATGAACTGACCGCCGAGTGGACCGTGCGAGCACATCTTACTTTTGCCCGAGCT---GGTGAGGCAGTGCAAAAGGAGTTCAGTGCTCC------GGAG
droEug1	scf7180000409183:792434-792627 -		AAATGTGTTCATGCTGCGACATACAATAAGTGCGTAGGG------AGTCATGAGTACGCCCACGCCCA------------CT------CCGCCGGGTGCGGTTC-------T--GGGCCAGCAGGT---TCCACTGCCCCACGAACTGACCGCCGAGTGGACGGTACGAGCACATCTTACTTTTGCCCGAGCT---GGTGAGCCCGTGCAAAAGGAGTTCAGTGCTCC------GGAG
droBia1	scf7180000301506:1574175-1574371 +		AAATGTGTTGTTGCTGCAATCGCACAAAAAGTGTGTAGGG------AGCCATGAGCACGCCCA------CGGCCACGACCAGT---------CCGGGGGCGGTTC-------C--GGGACAGCAGGT---ACCACTGCCCCACGAACTGACCGCCGAGTGGACGTGCGAGCACATCTCACTTTTGCCCGAGCC---GGTGAGCCTGTGCAAAAGGAGTTTAGTGCTCC------GGAG
droTak1	scf7180000415274:108701-108897 -		AAATGTGTTCATGCTGCGAGCGCAAAACAAGTGCGTAGGG------AGTCATGACCACGCCCA------CGCCCACGCCCAGT---------CCGGGGGCGGTTC-------T--GGGCCAGGAGGT---TCCACTGCCCCATGAACTGACCGCCGAGTGGACGTAGGCGCACATCTCACTTTTGCCCGAGCT---GGTGAGCCTGTGCAAAAGGAGTTTAGTGCTCC------GGAG
droEle1	scf7180000491201:975363-975559 -		AAATGTGTTCATGCTGCGATCGCAAAAACGGTGCGTAGGG------AGTCATGAGCACGCCCA------CGCCCACGCCCAGT---------CCGGGGGCTGTTC-------T--GGGCCAACAGGT---TCCACTGCCCCATGAATTGACCGCCGAGTGGACGTGCGAGCCCATCTCACTTTTGCCCGAGCT---GGTGAGCCGGTGCAAAAGGAGTTTGCTTCCCC------GGAG
droRho1	scf7180000777222:43363-43559 +		AAATGTGTCCATGCTGCGATCGCAAAATAAGTGCGTAGGG------AGTCATGAGCACGCCCA------CACCCACGCTTAGT---------CCGGGGGCGGTTC-------T--GGGCCAACAGGT---TCCACTGCCCCATGAATTGACCGCCGAGTGGACGTGCGAGCACATCTCACTTTTGCCCGAGCT---GGTGAGCCGGTGCAAAAGGAGTTTAGTGCTCC------GGAG
droFic1	scf7180000453851:1124231-1124433 +		AAATGAGTTCGTTTTGCGATCGCAAGAAGTGTGCGTAGGGAGTGGGAGTCATGAGCACGCCCA------CGCCCACGCCCAGT---------CCGGGGGCGGTTC-------T--GGGCCAGCAGGT---GCCACTGCCCCATGAGCTAACCGCCGAGTGGACGTGCGAGCACATCTCACTTTTGCCCGAGCA---GGTGAGCCCGTGCAAAAGGAGAGCAGTGCTCC------GGAG
droKik1	scf7180000302476:544606-544754 -		AAATGTGTTCATTG----------TGTCGTAAGGG---GTAGTCATGG----------**----------**----------A--GGAGCAGCAGGT---GCCCGTGCCCCACGAACTGACCGCCGATGGACAGTGCGGCACATCTCACCTTTGCCCGGCA---GGAGAGCCTGTGCAAAAGGAGTTAAGTGCACC------TGAG
droAna3	scaffold_13266:8418796-8419007 +		CAATGTGTTCATGCTGCGATCGTTAAGT---TGCTGAGGG------AGTCATGTCCACGCCCACACCCA------CACCCACGCCTACTGCCTCGGGAACAGCTGCTCCACTCGGGGGTCAGCAGGT---TCCACTGCCACACGAGCTGACCGCCGAGTGGACGTGCGAGCCCATCTAACCTTTGCCCGGCT---GGGGAGACCGTGCACAAGGAGTTTAGTGCTCC------GGAG
droBip1	scf7180000396759:393774-393976 -		CAATGTGTTCATGCTGCGATCGTAAAAC---TGCGTAGGG------AGTCATGTCCACGCCCACGCCCA------CT------GCCTCGGGGGCAGCTGCTCCTTCCGGTGGTCAGCAGGCTCCGCCACTGCCCCACGAACTGACCGCCGAGTGGACGTGCGAGCCCATTTGACTTTTGCCCGGGCT---GGGGAAACCGTACAGAAGGAGTTCTGTGCTCC------GGAG
dp5	3:9218191-9218375 -		CAATGTGTTCTGGCAACGA---------AAGTGCGTAAGGG---AGAGTCATGGCCACGCCCA------CTGCC-------**---------TCGTTGGCGGCTGC------T--GGAGT----GC---ACCCGTGCCCCACGAGCTGACGCCGAGTGGACAGTGCGCGCCCATCTCACCTTTGCCCGTGCC---GGAGAGGCGGTGCACAAGGAGTGCGTGCAGGGCCAGTGCAG
droPer2	scaffold_4:4541352-4541536 -		CAATGTGTTCTGGCAACGA---------AAGTGCGTAAGGG---AGAGTCATGGCCACGCCCA------CTGCC-------**---------TCGTTGGCGGCTGC------T--GGAGT----GC---ACCCGTTCCCCACGAGCTGACGCCGAGTGGACAGTGCGTGCCCATCTCACCTTTGCCCGTGCC---GGAGAGGCGGTGCACAAGGAGTGCGTACAGGGCCAGTGCAG
droWil2	scf2_1100000004822:1793460-1793560 +		----------**********----------**********----------**----------**********-------**----------T---TCCCTTGCCTCATGAATTGACTGCCGAATGGACAGTGCGTGCTCAGTTGACATTCGCCCGGAAT---GGTGAGCCAGTACAAAAGGAATATGTGAACA------GGAT
droVir3	scaffold_12875:14439701-14439802 -		----------**********----------**********----------**----------**********-------**----------GCGTTGCCTCATGAGCTGACCGCCGAGTGGACAGTGCGTGCACACGCTGAGATTCGGCCGGCGGGGGGTGAGCCAGTGCAGCGGGAGTTTAGCGCACA------GGAG
droMoj3	scaffold_6496:9905107-9905206 -		----------**********----------**********----------**----------**********-------**----------TCCCTTGCCTCATGAGCTGACCGCCGAGTGGACGTGCGTGCCCAATTGACATTCGGCCGTGCA---GGTGAGCCAGTGCAGCGGGAGTTCAATGCACA------GGAG
droGri2	scaffold_15245:14436423-14436541 -		CCAC----------GGAGGCGGA----------**********----------**----------**********-------**------ACAAGT---GCCGTTGCCTCATGAGCTGACCGCCGAGTGGACAGTGCGTGCCCAGCTGAGATTCGCACCGCGC---GGAGAGCCAGTGCAGCGTGAGTTTAGTGCAGG------GGAG

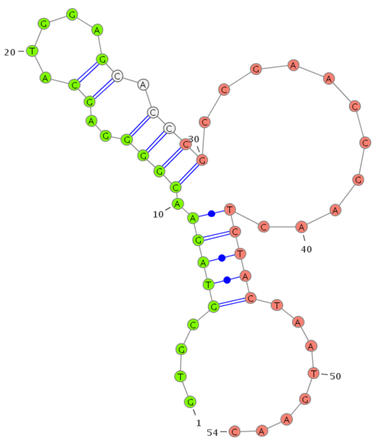
Generated: 09/08/2015 at 08:06 PM

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

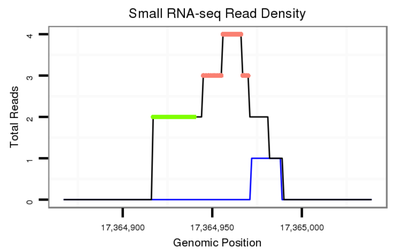
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dsi_32460	**x:17364917-17364989 +**	**candidate**	**MiRNA**	**3pUTR**	[View on UCSC Genome Browser [Cornell Mirror]]

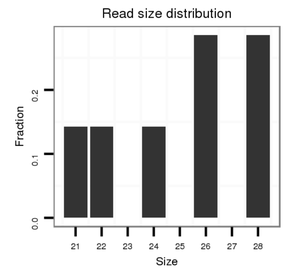
Legend: mature star mismatch in alignment mismatch in read

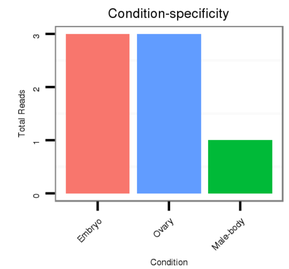
Predicted structure

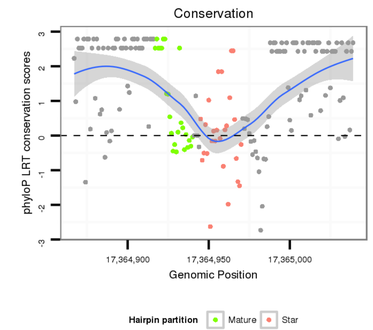


dsi_32460_annot [-9.5]









Show Alternate Folds

Flybase annnotation

utr3 [utr3_plus_8558]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

CGACGGTCATCCACACGACACCTGGCAATGCAGTGCAAGTGCGTAACAAAGTGCGTAGAACGGGGAGCATGGAGCACCCGCCGAACCGAACTCTACTAATGAACTCGATCACCTCGCACACAGATCCCTCCAACCTTTCCGTGTAAGATCAAGCCCGAACCGAACCACGCAGCA **********....(((((.((((..((.....)).)))).....)))))).....**********	Read # size	Mismatch	Hit Count	Total Norm	Total	SRR902009 testis	M025 embryo	SRR902008 ovaries	SRR618934 dsim w501 ovaries	SRR553486 Makindu_3 day-old ovaries	M024 male body	SRR553487 NRT_0-2 hours eggs	M023 head	GSM343915 embryo
.....GTGCGTAGAACGGGGAGCATGGAG.....	24	0	1	1.00	1	0	0	0	1	0	0	0	0	0
.....GTGCGTAGAACGGGGAGCATGGAGCACC.....	28	0	1	1.00	1	0	0	0	0	0	0	0	0	0
.....CGCCGAACCGAACTCTACTAATGAAC.....	26	0	1	1.00	1	0	0	0	0	1	0	0	0	0
.....CGCCGAACCGAACTCTACTAAT.....	22	0	1	1.00	1	0	0	1	0	0	0	0	0	0
.....GTGCGTAGAACGGGGAGCATGGAGCA.....	20	1	1	1.00	1	0	0	1	0	0	0	0	0	0
.....CTAATGAACTCGATCACCTCGCACACAG.....	28	0	1	1.00	1	0	0	1	0	0	0	0	0	0
.....ACTCTACTAATGAACTCGATCACCTC.....	26	0	1	1.00	1	0	0	0	1	0	0	0	0	0
.....CACCCGCCGAACCGAACTCTA.....	21	0	1	1.00	1	0	0	1	0	0	0	0	0	0

Anti-sense strand reads

GCTGCCAGTAGGTGTGCTGTGGACCGTTACGTCACGTTCACGCATTGTTTCACGCATCTTGCCCCTCGTACCTCGTGGGCGGGCTTGGCTTGAGATGATTACTTGAGCTAGTGGAGCGTGTGTCTAGGGAGGTTGGAAAGGCACATTCTAGTTCGGGCTTGGCTTGTGCGTCGT **********....(((((.((((..((.....)).)))).....)))))).....**********	Read # size	Mismatch	Hit Count	Total Norm	Total	SRR618934 dsim w501 ovaries	GSM343915 embryo	SRR553486 Makindu_3 day-old ovaries	SRR553488 RT_0-2 hours eggs
.....GCTAGTGGAGCGTGTGT.....	17	0	1	1.00	1	1	0	0	0
.....ACTTGAGCTAGTGGAG.....	16	0	2	0.50	1	0	0	1	0
.....AGCTAGTGGAGCGTG.....	15	0	4	0.25	1	1	0	0	0

Show Alignment With Reads

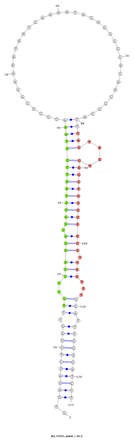
Re-alignment of all predicted orthologs

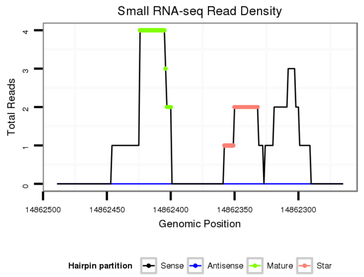
Species	Coordinate	ID	Alignment
droSim2	x:17364867-17365039 +	dsi_32460	CGACGGTCATCCACACGACACCTGGCAATGCAGTGCAAGTGCGTAACA---AAGTGCGTAGAAC------GGGGA---GCA--------------TGGAGCACCC--GCC-----GA----ACCGAACTCT----------ACTAATGAA----------TCGAT---CACC--------TCG----------C----ACACAGATCCCTCCAACCTTTCC---GTGTAAGATCAAGCCCGAACCGAACCACGCAGCA
droSec2	scaffold_8:576723-576895 +		CGACGGTCATCCACACGACACCTGGCAATGCAGTGCAAGTGCGTAACA---AAGTGCGTAGAAC------GGGGA---GCA--------------TGGAGCACCC--GCC-----GA----ACCGAACTCT----------ACTAATGAA----------TCGAT---CACC--------TCG----------C----ACACAGATCCCTCCAACCTTTCC---GTGTAAGATCAAGCCCGAACCGAACCACGCAGCA
dm3	chrX:18267197-18267369 +	dme_425	CGACGGTCATCCACACGACCCTGGCAATGCAGTGCAAGTGCGTAACA---CGGAGCACCC--GCC-----GA----ACCGAACTCT----------ACTAATGAA----------TCGAT---CACC--------TCG----------C----ACACAGATCCCTCCAACCTTTCC---GTGTAAGATCAAGCCCGAACCGAACCACGCAGCA
droEre2	scaffold_4690:8587866-8588031 +	der_401	CGACGGTACTCCACACGACACCTGGCAATGCAGTGCAAGTGCGTAACA---AAGTGCGTAGTC------GGGGA---GCACA--------------GCC-----GA----ACCGAACTCT----------ATAATGCC----------TCGAT---CGCC--------TCG----------C----ACACAGATCCCTCCAACCTTTCC---GTGTAAGATCAACCCGAACCGAACACGCAGCA
droYak3	X:16895123-16895288 +	dya_1456	CGACGGTCATCCACACGACACCTGGCAATGCAGTGCAAGTGCGTAACA---AAGTGCGTAGTC------AGGA---GCACC--------------GCC-----GA----ACCGAACTCT----------ATAATGCC----------TCGAT---CACC--------TCG----------C----ACACAGATCCCTCCAACCTTTCC---GTGTAAGATCAACCCGAACCGAACACGCAGCA
droEug1	scf7180000409528:449306-449472 +		CGACGGTCATCCACACGACACCCACGCAATGCAGTGCAAGTGCGTAACA---AAGTGCGTAGTC------AGGA---GCACC--------------GCC-----AG----T----TTAGAACTCT----------ATAATATC----------TCGAT---TACC--------ATTA----------C----ATACAGATCCCTCCAACCTTTCC---GTGTAAGATCAACCCGAACCGACACGCACGCA
droBia1	scf7180000302432:991025-991185 +		--ACGGTCATCCACACGACCCCTGGCAATGCAGTGCAAGTGCGTAACA---AAGTGCGTAGTC------AGGA---GCACC--------------GCC-----GA----GCAAAACTCG----------ACTAATGC----------CCGAT---TACC--------CG----------T----TACAGATCCCTCCATCCTTTCC---GTGCAAGATCAAGCCCGAACCGAACACGCAGCA
droTak1	scf7180000415395:271892-272072 +		CGACGGTCATCCACACGACACCCTGGCAATGCAGTGCAAGTGCGTAACA---AAGTGCGTAGTC------AGGA---GCACC--------------GCC-----AC----GA----GCAGAACTCT----------GATAATGC----------TCGCAA---CTTA--------CAT-GCCTCCAACTTAG----------CA----C----ACACAGATCCCTCCAACCTTTCC---GTGCAAGATCAACCCGAACCGACACGCAGCA
droEle1	scf7180000491006:507685-507853 +		CGACGGTCATCCACACGACACCCTGGCAATGCAGTGCAAGTGCGTAACA---AAGTGCGTAGTC------AGGA---GCACC--------------GCC-----AT----GA----GCAGAACTCT----------ATAATGAT----------TGTTCGAT---TACC--------TTC----------A----ATACAGATCCCTCCAACCTTTCC---GTGTAAGATCAACCCGAACCGACACGCAGCA
droRho1	scf7180000779985:1003462-1003621 +		CGACGGTCATCCACACGACCCCTGGCAATGCAGTGCAAGTGCGTAACA---AAGTGCGTAGTC------AAGGA---GCGCC--------------GCC-----AC----GA----GCAGAACTCT----------ACTAATTC----------TCGAT---TACC--------TCG----------C----CACAGATCCCTCCAACATTTCC---GTGTAAGATCAACCCGAACCGACACGCAGCA
droFic1	scf7180000453829:1364555-1364737 -		CGACGGTCATCCACACGACCCCTGGCAATGCAGTGCAAGTGCGTAAGA---AAGTGCGTAGTC------GGCGA---GCGCT--------------GCC-----AT----GAGTTGACGAGAATAT----------ACTAATGC----------TCGAT---TCTT--------TTTAAC----------CTCCGAT----------CG----T----TACAGATCCCTCCAACCTTTCC---GTGTAAGATCAACCCGAACCGACACGCAGCA
droKik1	scf7180000302696:1335674-1335841 +		CGACGGTCATCCACACGACCCCTGGCAATGCAGTGCAAGTGCGTAAGA---AAGTGCGTAGTC------AGCGA---GCGCC--------------GCC-----C----T----C----------AAGTTGGAGCCGAACGACTAACGCATC----------T----------TCG----------AATTTCCGAGTGTAAGATCAACCCGAACCGACACGCAGCA
droAna3	scaffold_13248:931379-931575 +		--ACGGTCATCCACACGACCCCTGGCAATGCAGTTCAAGTGCGTAACA---AAGTGCGTAGTC------AAAGA---GCTTC--------------T--CT----T----TA----ATTT-----C----------ATAAATAA----------TTATAATTATAATTATAATTTTA---TAATTTTTTGAAACCCTGC----------TTTA----------TA----T----ATACAGATCCCTCCAACTTTCC---GTGTAAGATCAACCCGAACCGAACACGCAGCA
droBip1	scf7180000395920:35122-35313 +		--ACGGTCATCCACACGACCCCTGGCAATGCAGTCAAAGTGCGTAACA---AAGTGCGTAGTC------CCCTTAGAAGA----GAGCTTTCAAATAAAAACA-TATATTTT-ATA----AA----TATATATAT----------TATAATTATT----------TTC--C----TATT--------TCA----------A----TTTACAGATCCCTCCAACATTTCC---GTGTAAGATCAACCCGAACCGAACACGCAGCA
dp5	XL_group3a:228616-228785 +		CACGGTCATCCACACGACCCCTGGCAATGCAGTGCAAGTGCGTAACA---AAGTGCGTAGCTGC------AAAA----CTTTG----------T--T----T----T----------AACGGGGCCAGCAGCCTC--------TC----TAAACTTT----------AT---T----T----------T----------ATTCCACT----------CG--AATA----T-CACAGATCCCTCCAACGTTTCC---ATGTAAGATCAACCCGAACCGAACACGCAGCA
droPer2	scaffold_39:508452-508621 -		CACGGTCATCCACACAACCCCTGGCAATGCAGTGCAAGTGCGTAACA---AAGTGCGTAGCTGC------AAAA----CTTTG----------T--T----T----T----------AACGGGGCCAGCAGCCTC--------TC----TAAACTTT----------AT---T----T----------T----------ATTCCACT----------CG--AAAA----T-CACAGATCCCTCCAACGTTTCC---ATGTAAGATCAACCCGAACCGAACACGCAGCA
droWil2	scf2_1100000004515:1509874-1510103 +		CGACGGTCATCCACACGACCCCTGGCAATGCAGTGCAAGTGCGTAAGATGCAAGTGCGTAGTC------ATCA----TCA----------CT-T-----C--AT----GC----T----------T--------TTGTAT---TAAC--------GT----------AATTCACGAAACTGTTCCTCCCTACACAAAAGTTGTATCCCATTCCATGCTAAATCTTGTTTTCCATTTCTTG-TATTGCACAGATCCCTCCAACGTTTCA---ATGTAAGATCAACCCGAACCGAACACGCAGCA
droVir3	scaffold_12970:3051823-3051880 +		CGACGGTCATCCACACGACCCCTGGCAATGCAGTGCAAGTGCGTAACA---AAGTGCGTAGCTGC------AAAA----CTTTG----------T--T----T----T----------T--------T----------T----------T----

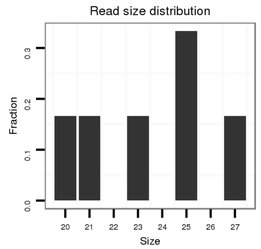
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dsi_32455	**3r:14862315-14862439 -**	**confident-exception**	**Canonical miRNA**	**intron**	[View on UCSC Genome Browser (Cornell Mirror)]

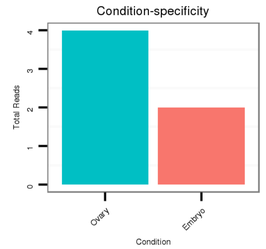
Legend: mature star mismatch in alignment mismatch in read

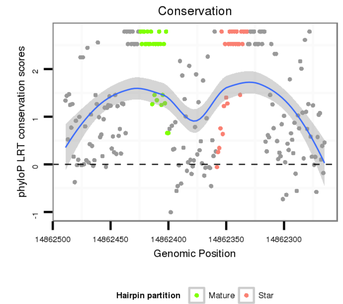
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [3r_14856841_14864299_+]; utr5 [utr5_plus_10181]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

ATGTGTATCTATATATGTATCTATAAAGTGTCCAGAGTTGTCAAGCGTCAGTGAGATCTCGGGTTTGTTGCACGACGAGACAGTTGCTAAACCCCCGCAAAATAATCAAAATACACCCCCACAACCCCATTTAGTACTCAGCTGTCTCTCGTTGTTTTCGATTTCGGGATCTTGACAACGACGCCATCGAATTGAAGACATTGACCCAGTGATTAGTTATATTAA	Read size	# Mismatch	Hit Count	Total Norm	Total	SRR902009 testis	SRR618934 dsim w501 ovaries	SRR553488 RT_0-2 hours eggs	M025 embryo	GSM343915 embryo	M024 male body	M053 female body	SRR553485 Chicharo_3 day-old ovaries	SRR902008 ovaries	SRR553486 Makindu_3 day-old ovaries
..TGTTGCACGACGAGACAGTTGCTAA	25	0	1	2.00	2	0	2	0	0	0	0	0	0	0	0
..TAGTACTCAGCTGTCTCTCGTTGTTTT	27	0	1	1.00	1	0	0	0	0	0	0	1	0	0	0
..TCGGGATCTTGACAACGACGCCAT	24	0	1	1.00	1	0	0	0	0	0	0	0	1	0	0
..CGCCATCGAATTGAAGAC	18	0	1	1.00	1	0	0	0	0	0	1	0	0	0	0
..AGCTGTCTCTCGTTGTTTTCGAT	23	0	1	1.00	1	0	0	0	0	1	0	0	0	0	0
..TGTTGCACGACGAGACAGTTG	21	0	1	1.00	1	0	0	0	0	0	1	0	0	0	0
..AGCGTCAGTGAGATCTCGGGTT	22	0	1	1.00	1	0	0	0	0	1	0	0	0	0	0
..TGTTGCACGACGAGACAGTT	20	0	1	1.00	1	0	0	1	0	0	0	0	0	0	0
..CTTGACAACGACGCCATCGA	20	0	1	1.00	1	0	0	0	0	0	0	0	1	0	0

Anti-sense strand reads

TACACATAGATATATACATAGATATTTCACAGGTCTCAACAGTTCGCAGTCACTCTAGAGCCCAAACAACGTGCTGCTCTGTCAACGATTTGGGGGCGTTTTATTAGTTTTATGTGGGGGTGTTGGGGTAATCATGAGTCGACAGAGAGCAACAAAAGCTAAAGCCCTAGAACTGTTGCTGCGGTAGCTTAACTTCTGTAACTGGGTCACTAATCAATATAATT	Read size	# Mismatch	Hit Count	Total Norm	Total	M053 female body	SRR553488 RT_0-2 hours eggs	SRR618934 dsim w501 ovaries	SRR553487 NRT_0-2 hours eggs	SRR553485 Chicharo_3 day-old ovaries	SRR553486 Makindu_3 day-old ovaries
..GCGCCCTAGAACTGTTGC	18	2	5	0.20	1	0	0	0	1	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droSim2	3r:14862265-14862489 +	dsi_32455	ATGTGTA--------TCTAT-ATA------TGTAT----------CTATA-----------AA----GTGTCCAG----------AGTT--GT----------CAAGCGTC-AGTGAGATCTCGGGTTTGTTGCACGACGAGACAGTTGCTAAAC--CCCC----------GCAAAA--TAATCAA----------AA--TACACCCCACAACCCCATTT--AGTACTCAGCTGTCTCTCGTTGTTTTCGATTTCGGGATCTTGACAACGACGC-----CATCGA-------ATTGAAGACATTG-----ACCCAG----------T--GATTA-----GTTAT----ATTAA
droSec2	scaffold_0:15728309-15728533 -	dse_1842	ATGTGTA--------TCTAT-ATA------TGTAT----------CTATA-----------AA----GTGTCCAG----------AGTT--GT----------CAAGCGTC-AGTGAGATCTCGGGTTTGTTGCACGACGAGACAGTTGCTAAACC--CCCC----------GCAAAA--TAATCAA----------AA--TACACCCCACAACCCCATTT--AGTACTCAGCTGTCTCTCGTTGTTTTCGATTTCGGGATCTTGACAACGACGC-----CATCGA-------ATTGAAGACATTG-----ACCCAG----------T--GATTA-----GTTAT----ATTAA
dm3	chr3R:6216925-6217149 +	dme_373	ATGTGTA--------TCTAT-ATA------TGTAT----------CTATA-----------AA----GTGTCCAG----------AGTT--GT----------CAAGCGTC-AGTTAGATCTCGGGTTTGTTGCACGACGAGACAGTTGCTAAAC--CCCC----------GCAAAA---TAATCAA----------AA--TACACCCCCACAA-T-CATTT--ATACTCAGCTGTCTCTCGTTGTTTTCGATTTCGGGATCTTGACAACGACGC-----CATCGA-------ATTGAAGACATTG-----ACCCAG----------T--GATTA-----GTAT----ATTAA
droEre2	scaffold_4770:15403301-15403535 -	dre_1519	ATGTGTA--------T-TAT-ATTCGTATCTGTAT----------CTATA-----------AA----GTGTCCAG----------AGTT--GT----------CAAGCGTC-AGTGAGATCTCGGGTTTGTTGCACGACGAGACAGTTGCTAAAC--T-CC-CC----------GCAAAA---TAATCAA----------AA--TACACCC-T-CAACCCCATTT--AGTACTCAGCTGTCTCTCGTTGTTTTCGATTTCGGGATCTTGACAACGACGC-----CATCGA-------ATTGAAGACATTG-----ACCCAG----------T--GATTA-----GTAT----ATTAA
droYak3	1R:10242680-10242915 +	dya_1794	ATGTGTACCCATGTACAAGTAT-ATA------TGTAT----------CTATA-----------AA----GTGTCCAG----------AGTT--GT----------CAAGCGTC-AGTGAGATCTCGGGTTTGTTGCACGACGAGACAGTTGCTAAAC--CCCC--A----------GCAAAA---TAATCAA----------AA--TACACCCCCACAACCCCATTT--AGTACTCAGCTGTCTCTCGTTGTTTTCGATTTCGGGATCTTGACAACGACGC-----CATCGA-------ATTGAAGACATTG-----ACCCAG----------T--GATTA-----GTAT----ATTAA
droEug1	scf7180000409692:687963-688195 +		ATGTGTA--------TCTAT-[redacted]-AT----------CTAT----------AA----GTGTCCAG----------AGTT--GT----------CAAGCGTC-AGTGAGATCTCGGGTTTGTTGCACGACGAGACAGTTGCTAAAC--CCCC-TTT--C----------TATA-------AAAAA--AGAAACAA----------TC--TACACC--CACAACCCCATTT--AATACTCAGCTGTCTCTCGTTGTTTTCGATTTCGGGATCTTGACAACGACGCA----ATCAAC-TTTGATCTGAAGACCGTG-----ACCCAG----------T--GATTA-----GTAT----ATTGA
droBia1	scf7180000302402:8304620-8304856 +		ATGTGT-[redacted]-T-AT-------TGTAT----------CTAT----------AA----GTGTCCAG----------AGTT--GT----------CAAGCGTC-AGTGAGATCTCGGGTTTGTTGCACGACGAGACAGTTGCTAAAC--CCCC-SCTCCGAG----------G--AGA---GAAAAAAAC----AA----------AA--GAC-AGCCCACAACCCCATTT--AATACTCAGCTGTCTCTCGTTGTTTTCGATTTCGGGATCTTGACAACGACGC-----CTCGA---TTCGATGCGAAGACCGTG-----ACCCAG----------T--GATTA-----GTAT----ATTGA
droTak1	scf7180000415380:1425635-1425858 -		ATGTGTA--------TCTAT-[redacted]-AT----------CTAT----------AA----GTGTCCAG----------AGTT--GT----------CAAGCGTC-AGTGAGATCTCGGGTTTGTTGCACGACGAGACAGTTGCTAAAC--CCCC--C----------CAAA-AAAAC----AA----------AAAGTACACC--CACAACCCCATTT--AATACTCAGCTGTCTCTCGTTGTTTTCGATTTCGGGATCTTGACAACGACGC-----CATCGA---TTTGATCTGAAGACCGTG-----ACCCAG----------T--GATTA-----GTAT----ATTGA
droEle1	scf7180000490995:524589-524803 +		ATGTGTA--------TC[redacted]-AT----------CTAT----------AA----GTGTCCAG----------AGTT--GT----------CAAGCGTC-AGTGAGATCTCGGGTTTGTTGCACGACGAGACAGTTGCTAAAC--CCCC----------A--A-A-AAAC----AA----------AA--TACACC--CACAACCCCATTT--AATACTCAGCTGTCTCTCGTTGTTTTCGATTTCGGGATCTTGACAACGACGC-----ACTCGA-------TCTGAAGACCATG-----ACCCAG----------T--GATTAATGGATGAT----ATTGA
droRho1	scf7180000777158:35501-35710 -		ATGTGTA--------TC[redacted]-AT----------CTAT----------AA----GTGTCCAG----------AGTT--GT----------CAAGCGTC-AGTGAGATCTCGGGTTTGTTGCACGACGAGACAGTTGCTAAAC--CCCC----------A--A-A-AAAC----AA----------AA--TACACC--CACAACCCCATTT--AATACTCAGCTGTCTCTCGTTGTTTTCGATTTCGGGATCTTGACAACGACGC-----CATCGA-------TCTGAAGACCGTG-----ACCCAG----------T--GATTA-----GTAT----ATTGA
droFic1	scf7180000453800:2293368-2293580 +		ATGTGTA--------TC[redacted]-AT----------CTAT----------AA----GTGTCCAG----------AGTT--GT----------CAAGCGTC-AGTGAGATCTCGGGTTTGTTGCACGACGAGACAGTTGCTAAAC--CC-C--CC----------CAA-A-AAAC----A----------AA--TACACCC-A-AACCCCATTT--AATACTCAGCTGTCTCTCGTTGTTTTCGATTTCGGGATCTTGACAACGACGC-----AATCGA-------TTTGAAGACCGTG-----ACCCAG----------T--GATTA-----GTAT----ATTGA
droKik1	scf7180000302475:1404666-1404904 +		ATGCG-CC-[redacted]-CATC-----TGTAT----------C-A-CC----------AA----GTGTCCAG----------AGTT--GT----------CAAGCGTC-AGTGAGATCTCGGGTTTGTTGCACGACGAGACAGTTGCTAAAC--CCCCA-CC-ACATC----------G----GAAAC----AAAATAATAAA-ATAT-AA--TAC-CCCC-CAACCCCATTT--AATACTCAGCTGTCTCTCGTTGTTTTCGATTTCGGGATCTTGACAACGACGC-----CTAGAGA----CGATG-AAAGACCGTG-----ACCCAG----------T--GATTA-----GTTT----ATTGA
droAna3	scaffold_13340:938685-938923 +	dan_4037	ATGTGTA--------T-TCAT-[redacted]-TGTAT----CCACAAGAT----------[redacted]-ACAGATA---A-----GTG-T--[redacted]-G--GT----------C-AGCGC-AGTGAGATCTCGGGTTTGTTGCACGACGAGACAGTTGCTAAAC--CCGC-GT----G----------GGGGAGCCC-----G-T-A-AAAC----AAAGACAAACAG----GC-CAG-CCCA-AAATA-CTA---A-TAGCGAGCTGTCTCTCGTTGTTTTCGATTTCGGGATCTTG-CAACGCGCAT---CATCGA-------TAT---------------A-AG----------T--GATTG----GTTG----ATTCG
droBip1	scf7180000394085:58809-59016 -		ATGTGTA--------TC-A-C-[redacted]-[redacted]-AAGAT----------[redacted]-GTGCCC-GTGTCCAG----------G-T-T--GT----------CAAGCGTC-AGTGAGATCTCGGGTTTGTTGCACGACGAGACAGTTGCTAACC--CC-CC--C----G----------GGGGAGG--G-AGAGA--A-AGAA-A--AGAAA-A----------CC--A-T--CCCA-AAAGAC-T-CATAGCGAGCTGTCTCTCGTTGTTTTCGATTTCGGGATCTTG-CAACGCGC-----ATC-A-G-------CATT-----A-T-AG----------T--GATTA----[redacted]
dp5	2:7251726-7252027 -	dps_3825	ATGTGTA--------T-CTAT-ATA------TGTAT-GTGTGTGCGAGAGAGTGTACGAGAGTATAT----------A----A-T-ATAG----------AGTT--GT-G----------CAGCGCTC-AGTGAGATCTCGGGTTTGTTGCACGACGAGACAGTTGCCCGCA-ACC-ACCCACCC-TCTTTCCCAGCAGAGCGCCATTGTGATGATGTTGTTGATGATGATGATGAGGAGGAGG--AGAGAA-----------GGAGGAGGAG----G-G--------CTT-T-CCAGTG-CAAGCGAGCTGTCTCTCGTTGTTTTCGATTTCGGGATCTTG-CAACGCGC-----CATCAA-G-------CATTGAACCA-----------C----TACGATATA----CAAT----ATATA
droPer2	scaffold_0:1112328-1112621 -	dpe_2479	ATGTGTA--------T-TCAT-ATA------TGTAT-GTG--GTGCGAGAGAGTGTACGAGAGTATAT----------A----A-T-ATAG----------AGTT--GT-G----------CAGCGCTC-AGTGAGATCTCGGGTTTGTTGCACGACGAGACAGTTGCCCGCA-ACC-ACCCACCC-TCTTTCCCAGCAGAGCGCCATTGTGAT-----GTTGATGATGATGATGAGGAGGAGG--AGAGAA-----------GGAGGAGGAG----G-G--------CTT-T-CCAGTG-CAAGCGAGCTGTCTCTCGTTGTTTTCGATTTCGGGATCTTG-CAACGCGC-----CATCAA-G-------CATTGAACCA-----------C----TACGATATA----CGAAT----ATATA
droWil2	scf2_1100000004902:91563-91759 -	dwi_5414	ATGTGTA--------T-GTA-TTA------TTCGT----------[redacted]-----------TT----G-----G----------GTTT--GT----------CAAGCGTC-GTATAGATCTCGGGTTTGTTGCACGACGCGCTAAACC--CCCC-CCTT--GCC----------ACACCCT-----CTT---TGC----A-ATGGTAAATAG----CT-CCCT-TT-TAAATTGT-TATTATTAGGCGCTGTCTCTCGTTGTTTTCGATTTCGGGATCTTATTACGA--------------------------CCCAG----------T--GATA-----------CA-T-----[redacted]
droVir3	scaffold_13047:936843-937029 -	dvi_125	ATGTGTA-C--------[redacted]-ATA------TGTAT----------CA-CG----------A----GTG-----------GTTT--AG----------AGCAAATGTGAGATCTCGGGTTTGTTGCACGACGAGCAGCTGCTGCAAT-----------A----------------------A-T-AAAA--TA-----------T--T----------------TCA--A-TAGCGAGCTGTCTCTCGTTGTTTTCGATTTCGGGATCTTGCCAACAGCGATCCA---CCA-----TGC-C-C-CCTG-----ACCCAG----------T--GATTA-----CAA-T-----[redacted]
droMoj3	scaffold_6540:4939653-4939854 +	dmo_129	ATGTGTA--------T-TCT-ATA------TGTAT----------A-TATATATTCCTGAACAAGGA----GTGT[redacted]-----GTTT--GT-G----------CAAAAATA-TGTGAGATCTCGGGTTTGTTGCACGACGAGCAGCTGCTGCAT-----------A----------------------A-T-S--------T--T----------AA-C-CA--A-TAGCGAGCTGTCTCTCGTTGTTTTCGATTTCGGGATCTTGAGCAGCAGCTGACCCCG---CCA-----TGC-------------C-CAGTGATAAGCAACAAG--GATTA-----GTGATAGTGATTAG
droGri2	scaffold_14906:5355374-5355618 +	dgr_461	ATGTGTA--------T-TAT-ATA------TGTAT-G-TAT----------A-TATATTGTT-----AGGA----GTGT---GATGTAATTGGCT-GGTTAGATATATATATATATATATATGTATTATATTGTGAGATCTCGGGTTTGTTGCACGACGTGCAGCTGGTCGCAATT-----------A----------------------A-T-S--------T--T----------AAAC-CG--AA-AGCGAGCTGTCTCTCGATGTTTTCGATTTCGGGATCTTG-TAGCGCGTGACCTGATCA-A----CCAAATATATCA----ACTAT-T-----------G--A-CCA-----A-G-A----ACCAA

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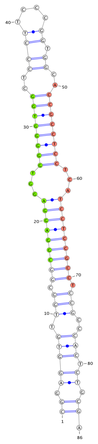
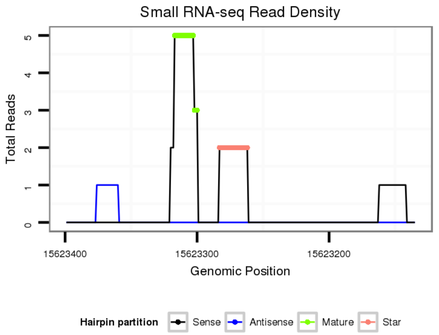
	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	1
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.ptop3	1
crit.uni	0
crit.back	0
rescue.star	0
rescue.dominant	0
rescue.known	0
rescue.confident	3
rescue.candidate	9

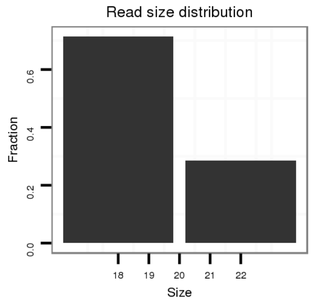
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dsi_32448	**3l:15623185-15623349 -**	**candidate**	**Canonical miRNA**	**CDS**	[View on UCSC Genome Browser [Cornell Mirror]]

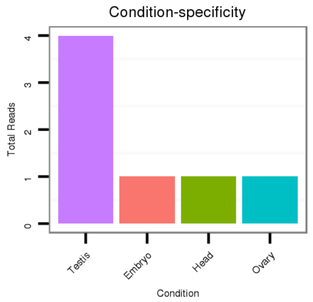
Legend: mature star **mismatch in alignment** mismatch in read

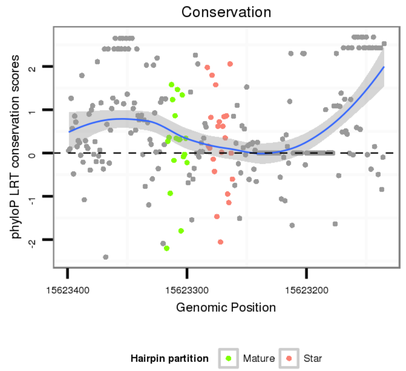
Predicted structure











Show Alternate Folds

Flybase annotation

CDS [3l_15623098_15623496_-]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

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size	Read # Mismatch	Hit Count	Total Norm	Total	SRR902009 testis	GSM343915 embryo	SRR902008 ovaries	SRR618934 dsim w501 ovaries	M023 head	O001 Testis	M053 female body	SRR553487 NRT_0-2 hours eggs	SRR1275483 Male prepupae	SRR1275487 Male larvae	M024 male body	SRR553488 RT_0-2 hours eggs
18	0	1	3.00	3	3	0	0	0	0	0	0	0	0	0	0	0
22	0	1	2.00	2	0	1	0	0	1	0	0	0	0	0	0	0
18	0	1	2.00	2	0	0	0	1	0	1	0	0	0	0	0	0
21	0	1	1.00	1	0	1	0	0	0	0	0	0	0	0	0	0

Anti-sense strand reads

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Read size	# Mismatch	Hit Count	Total Norm	Total	SRR553488 RT_0-2 hours eggs	SRR553487 NRT_0-2 hours eggs	SRR618934 dsim w501 ovaries	SRR902009 testis	SRR553486 Makindu_3 day-old ovaries	SRR553485 Chicharo_3 day-old ovaries	SRR902008 ovaries	GSM343915 embryo
17	0	1	1.00	1	0	0	1	0	0	0	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

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Species	Coordinate	ID	Alignment
droSim2	3l:15623135-15623399 -	dsi_32448	
droSec2	scaffold_0:8105349-8105580 -	dse_141	
dm3	chr3L:16004417-16004648 -	dme_398	
droEre2	scaffold_4784:18248785-18249019 -		
droYak3	v2_chr3L_random_063:45313-45550 +		
droEug1	scf1800000409824:59378-59582 -		
droBia1	scf1800000302334:363840-364038 +		
droTak1	scf1800000415815:285918-286113 -		
droEle1	scf1800000491193:5187656-5187872 +		
droRho1	scf1800000767651:14778-14976 +		
droPic1	scf1800000454065:1302305-1302523 +		
droKik1	scf1800000301706:18088-18319 +		
droAna3	scaffold_13337:11152549-11152741 +		
droBip1	scf1800000396569:234458-234644 -		
dp5	XR_group8:8226765-8226942 +		
droPer2	scaffold_40:417506-417683 +		
droWil2	scf2_1100000004837:1626531-1626581 -		
droVir3	scaffold_13049:18573167-18573254 +		
droMoj3	scaffold_6680:12673927-12674083 -		
droGri2	scaffold_15110:19050236-19050272 +		

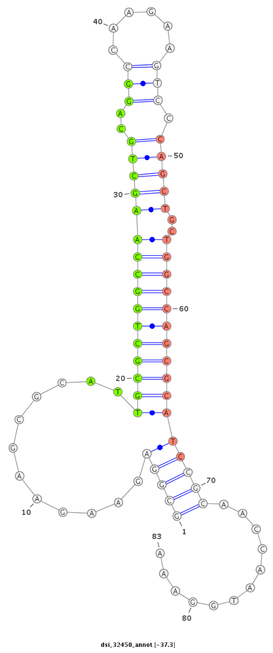
Generated: 09/08/2015 at 08:06 PM

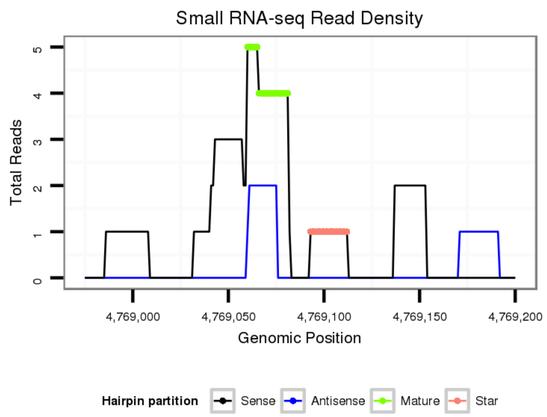
	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	2

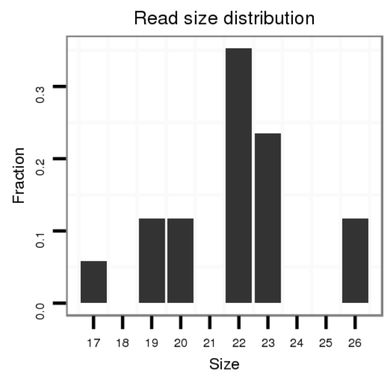
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dsi_32450	**2l:4769025-4769150 +**	**candidate**	**Canonical miRNA**	**CDS**	[View on UCSC Genome Browser {Cornell Mirror}]

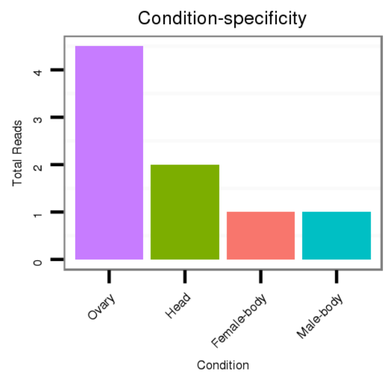
Legend: mature star mismatch in alignment mismatch in read

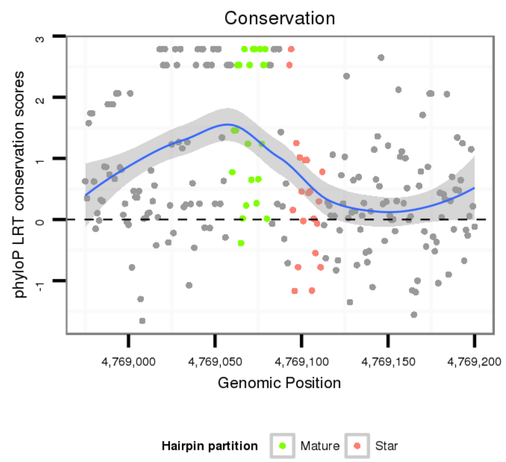
Predicted structure











Show Alternate Folds

Flybase annnotation

CDS [2l_4769018_4769784_+]; five_prime_UTR [2l_4768954_4769017_+]; utr5 [utr5_plus_690]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

TTGTTTATATATTCCGCCAAATTTCATCAATTGATGTCGCAGCATGTCCACTTGCAGTTCATCCGAGATAGCGGAGAAGAAGCGCATTGCGCTGGCCAAGCTGCAGGCCAAGAAGTCCCAGCTGCTGGCCAGCGCATCCGCAACCAATGGAAAATCAACAACGTCTGCAACAGGTGCGACGCAACATGCGAGTGATGCCAAATCGAGTCCAAATCAACCTCAGGCC **********(((((.....(((((((((((((((..(((.....))).)))))..)))))))))))))))).....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	SRR618934 dsim w501 ovaries	M024 male body	SRR553486 Makindu_3 day-old ovaries	SRR553488 RT_0-2 hours eggs	M023 head	M053 female body	O002 Head	SRR553485 Chicharo_3 day-old ovaries	GSM343915 embryo	SRR553487 NRT_0-2 hours eggs
.....ATTGCGCTGGCCAAGCTGCAGG.....	22	0	1	3.00	3	1	0	0	1	0	1	0	0	0	0
.....GTCTGCAACAGGTGCGA.....	17	0	4	2.25	9	9	0	0	0	0	0	0	0	0	0
.....CAGCTGCTGGCCAGCGCATC.....	20	0	1	1.00	1	0	0	0	0	1	0	0	0	0	0
.....TTCCGCCAAATTTCATCAATTGA.....	23	0	1	1.00	1	0	0	1	0	0	0	0	0	0	0
.....ATTGCGCTGGCCAAGCTGCAGGC.....	23	0	1	1.00	1	0	0	0	0	0	0	1	0	0	0
.....ATTGCGCTGGCCAAGCTGCAGGG.....	23	1	1	1.00	1	0	0	0	0	0	0	0	1	0	0
.....TAGCGGAGAAGAAGCGCATTGCG.....	23	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....TTCATCCGAGATAGCGGAGAAGAAGC.....	26	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....GATAGCGGAGAAGAAGCGC.....	19	0	1	1.00	1	0	1	0	0	0	0	0	0	0	0
.....AAGAAGCGCATTGCGCT.....	17	0	2	0.50	1	0	0	1	0	0	0	0	0	0	0
.....CGTCTGCAACAGGTGC.....	16	0	4	0.50	2	0	0	0	0	0	0	0	0	0	2
.....TCTGCAACAGGTGCGA.....	16	0	4	0.50	2	2	0	0	0	0	0	0	0	0	0
.....GTCTGCAACAGGTGC.....	15	0	4	0.25	1	1	0	0	0	0	0	0	0	0	0
.....TCTGCAACAGGTGCG.....	15	0	4	0.25	1	0	0	1	0	0	0	0	0	0	0
.....CGTCTGCAACAGGTGCG.....	17	0	4	0.25	1	1	0	0	0	0	0	0	0	0	0
.....CGTCTGCAACAGGTGCGA.....	18	1	5	0.20	1	1	0	0	0	0	0	0	0	0	0
.....CTGCAACAGGTGCGA.....	15	0	6	0.17	1	1	0	0	0	0	0	0	0	0	0

Anti-sense strand reads

AACAAATATATAAGGCGGTTTAAAGTAGTTAACTACAGCGTCGTACAGGTGAACGTCAAGTAGGCTCTATCGCCTCTTCTTCGCGTAACGCGACCGGTTCGACGTCCGGTTCTTCAGGGTCGACGACCGGTCGCGTAGGCGTTGGTTACCTTTTAGTTGTTGCAGACGTTGTCCACGCTGCGTTGTACGCTCACTACGGTTTAGCTCAGGTTTAGTTGGAGTCCGG **********(((((.....(((((((((((((((..(((.....))).)))))..)))))))))))))))).....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	SRR618934 dsim w501 ovaries	M024 male body	SRR902009 testis	SRR553487 NRT_0-2 hours eggs	GSM343915 embryo	SRR553486 Makindu_3 day-old ovaries
.....AACGCGACCGGTTCG.....	15	0	3	1.67	5	5	0	0	0	0	0
.....CGGTTTAGCTCAGGTTTAGTT.....	21	0	1	1.00	1	0	0	1	0	0	0
.....TAACGCGACCGGTTCG.....	16	0	1	1.00	1	1	0	0	0	0	0
.....GCAGACGTTGTCCACGC.....	17	0	4	0.50	2	2	0	0	0	0	0
.....CAGACGTTGTCCACGCT.....	17	0	4	0.50	2	2	0	0	0	0	0
.....GCAGACGTTGTCCACGCT.....	18	0	4	0.25	1	1	0	0	0	0	0
.....AGTGAACGTCAAGTA.....	15	1	20	0.05	1	0	0	0	0	0	1

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droSim2	2l:4768975-4769200 +	dsi_32450	TT---GTTTATATATTCCGCCAA--------ATTTCATCAATTGA--TGTCGCAGCATGTCCACTTGCAGTTCATCCGAGATAGCGGAGAAGAAGCGCATTGCGCTGGCCAAGCTGCAGGCCAAGAAGTCCCAGCTGCTGGCCAGCGCATCCGCAACCAATGGAAAA------TCAAC---AACGTC------TGCAACAGG---TGCGACGCAACATGCGA-----------GTGATGCCA---AATCGAGTCCAAATCAACCTCAGGCC
droSec2	scaffold_5:3042277-3042502 +	dse_216	TT---GTTTATATATTCCGCCAA--------ATTTCATCAATTGA--TGTCGCAGCATGTCCACTTGCAGTTCATCCGAGATAGCGGAGAAGAAGCGCATTGCGCTGGCCAAGCTGCAGGCCAAGAAGTCCCAGCTGCTGGCCAGCGCATCCGCAACCAATGGAAAA------TCAAC---AACGTC------TGCTAAAGG---TGCGACGCAACATGCGA-----------GTGATGCCA---AATCGAATCCAAATCAACCGCAGGCC
dm3	chr2L:4955540-4955765 +	dme_401	TT---GTTTATATATTCCGCCAA--------ATTTTATCAATTGA--TGTCGCAGCATGTCCACTTGCAGTTCATCCGAGATAGCGGAGAAGAAGCGCATTGCGCTGGCCAAATTGCAGGCCAAGAAATTCCCAGCTGCTGGCCAGCGCACGCGGCAACCAATGGAAAA------TCAAC---AACGTC------TGCAACAGG---TGCGACGCAACATGCGA-----------ATAATGGAA---AATCAAATCCCAATCAACCGCAGGCC
droEre2	scaffold_4929:5031991-5032213 +		TT---GTTTATAATTCCGCCAA--------ATTTCGTTAATTTA--TGTCGCAGCATGTCCACTTGCAGTTCATCCGAATAGCGGAGAAGAGCGCATTGCGCTGGCCAAATTGCAGGCCAAGAAGACCCAGCTGCTGGCCAGCGCATCCATATCCAACGGAAAA------TCAA----GGAC------TGCAACAGG---TGCTCCGCAGCATGCCC-----------ATAATGGAA---ATCGGATCCCAAACAACCGCAGGCC
droYak3	2L:10571198-10571423 -	dya_1788	TT---GTTTATATATTCCGCCAA--------ATTTCGTTAATTGT--TGTCGCAGCATGTCCACTTGCAGTTCATCCGAATAGCGGAGAAGAACGCATTGCGCTGGCCAAGCTGCAGGCCAAGAAGTCCCAGCTGCTGGCCAGCGCATCCACATCCAACGGAAAT------TCAAC---AACGAC------TGCAACAGG---TGCTCTACAACATTCCA-----------GTAATGGAA---ATCGAATCCCAACCAACCGCAGGCC
droEug1	scf7180000409005:837236-837462 +		--- GTTTATTATTCCGCCAA--------ATTTTGTTTATTGG--TGTCGCAGCATGTCCACTTGCAGTTCATCCGAATAGCGGAGAAGAAGCGCATTGCCTTGGCTAAGCTGCAACCCAAGAAGTCACAATTACTGCTACCACATCTACCTCAATGGAAAA------TCAAATCCAATGA------TCAACAAG---TGCGAACGCAACAATTC-----------GCAATGGAA---ATCCAAATCCAAACAACCCAGGCT
droBia1	scf7180000302188:1539555-1539777 +		TT-TCTGTTTGGTTATTCCGCCAA--------ATTTCGTCAATTTG--TGTCGCAGCATGTCCACTTGCAGTTCGTCCGAATAGCGGAGAAAAGCGCATTGCGCTGGCCAAGCTGCAGGCCAAGAAGTCCCAGCTGCTGGCCAGTGCATC------CGGCGGAAAG------TCAGC---GCGGAA------TCCAACAAG---TGCGCTGCAACAATCCA-----------CGAATGGAA---ATCGAAACCCAATAAACCGCAGGCC
droTak1	scf7180000415705:273650-273856 +		CT---GTTCTGTTTTTCCGCCAAATCTCAAAATCTCGTCAATTGT--TGTCGCAGCATGTCCACTTGCAGTTCGTCGCGAATAGCGGAGAAGAACGCATTGCGCTGGCCAAGCTGCAGGCCAAGAAGTCCCAGTTGCTGGCCAGTGCATC------CGGCGGAAAG------TCCAC---CGGGAC------TGCAACAAG---TC---------- ------GAA---ATGCGAATCCCAATCAACCGCAGGCC
droEle1	scf7180000491046:2622796-2623018 +		--- GTTTATTATTCCGCCAA--------ATTTCGTTAATTTTCCTGTTGCAGCATGTCCACCTGCAGTTCATCCGAATAGCGGAAAAGAAGCGCATTGCGCTGGCCAAGCTGCAGGCCAAGAAGTCCCAACTGCTGGCCACCACATC------CGCCGGAAAG------TCATC---CAGTGCTCC---GCCAACAAA---TGCGCAGCAACAAGTCC-----------GCAATCAAA---ATGCGAGTCCCAATCAACCGCTGGCC
droRho1	scf7180000779695:7627-7849 +		--- GTTTATTTAATCCGCCAA--------ATTTCGTTAATTGTCTTATCGCAGCATGTCCACTTGCAGTTCGTCCGAATAGCGGAGAAGAAGCGCCTTGCGCTGGCCAAGCTGCAAGCCAAGAAGTCCCAAGTACTGGCCAAGGCATC------CAGCGGAAAG------TCATC---CAGAGGTCC---TCCAGCAAA---TGCGCAGCAACAAGTCC-----------GCAATCAAA---ATGCGAGTCCCAATCAACCGCTGGCC
droFic1	scf7180000453842:1297058-1297272 -		--- GTTTACTAATTCCGCCAA--------ATTTCGTTAATC---TGTCGCAGCATGTCATCTTGCAGTTCGTCTGAAATTGCGGAGAAGAAGCGCATTGCGCTGGCCAAGCTGCAGGCCAAGAAGTCCCACTTGCTAGCCAGCTCAAG------CAGCGGAAAG------CTAAC---CAGCAA------TCCAACAAA---TGCGCAGCAACAAGTTG-----------CGAATAGAA---ACGGAATCCCAATCAACCACAAGCC
droKik1	scf7180000302271:69295-69527 +		TTGTTTGTTTTTATTTTCCGCCAA--------ATTTCGTCGCAAAT--TGTCGGGACATGTCCACATGCAGTGCGTCCGAGATTGCGGAGAAGAAGCGCATTGCTCTGTCCAAGCTGCAGGCCAAGAAGTCCCAGCTCCAGGCCAGTGGAA------TGGCGGGAGACCAGCCC---G---GAGGAT------TCCAACAGGCGCCGCCACGCAACAAGTCC-----------ACAGTGGAACCCATGGTAATCCCAATCAACCGCAGGCC
droAna3	scaffold_12943:2696398-2696609 +		--- GTTTATTATTCCGCCAA--------AAAAGCTTATTTGATTTCCATGCACAATGTCTGCCTGCAGTGCCATCGAAATCGCGGAGAAGAAACGCATTGCACTGGCCAAGCTGCAGGCGAAGAAGCGCAGATCCTAGCTGCC----------GGAAAAGCCACCCCGTC---GACAAG------TGCAACAAG---TGTGCAGCAAAAACCGC-----------AA-ACAA---ATGTGAACTCCAATGTCCCACAGGTC
droBip1	scf7180000396535:2094224-2094437 +		TT---GTTTATTATTCCGCCAA--------AAAACCTTATTTGATTAAATGCACAATGTCTGCCTGCAGTGCCACCGAATTGCCGAGAAGAAACGCATTGCACTAGCCAAGCTTCAGGCGAAGAAGACACAGCTCCTGGCTGCCGCGAGCAGCA--------ACC------TCGTC---CAGAAC------TCCAACAAG---TGCGCAGCAAAAACCCA-----------CAA--CAA---ATGGGAACTCCAATGTCCCACAGGTC
dp5	4_group4:1471206-1471364 +		TG----------------------------------GCTTAATATGTCCACTTGTAGCATTGCTGAATATAGCAGAAAAGAAGCGGGCTGCCTTGGCCAAGCTGCAACCCAAAAAGTGCAGCTC---GTCAACTC---------- ------ ------TAAGGGGCCGCCGACAAAAAA---CGCGCAGCAACAAGTAC----------- ---CAAATCCTCCCAGCTGGCCTCA
droPer2	scaffold_10:473217-473369 +		---------------------------------AGTATGTCCACTTGTAGCATTGCTGAATATAGCAGAAAAGAAGCGGGCTGCCTTGGCCAAGCTGCAACCCAAAAAGTCACAGCTC---GTCAACTC---------- ------ ------TAAGGGGCCGCCGACAAAAATT---CGCGCAGCAACAAGTAC----------- ---CAATCCTCCCAGCTGGCCTTA
droWil2	scf2_1100000004585:1582237-1582389 -		---------------------------------AATTCA--TGTTGTGAAATGTCCGCCTGCAGTGCTACGCGAATATAGCTGAAAAGAGGCGCATTGCCTTAGCCAAACTGCAACCCAAGAAGACCCAATTGTC----------CACATCTCCGAAAATT------CCATC---TGCGCC------TTCAACAGG---TTC---------- ------ ---------GGCTCACCTGACCGCC
droVir3	scaffold_13246:1175575-1175756 -		T----------ATATCCTGCAAA--------TTAGTATTAAGTAG--CGAG-AACGATGTCCGTCTGCACGGCTGCCGAGATAGCTGAGAAGCGACGGCATTGCACTGGCCAAGCTGCAGGCGAAAAAGCCCCAAGCGCCGGCCATAAAACCCCT---------- ------ ------ ------CCAACAAG---TGTCA-GCGAGCAGCTGGGCGCCAAGTCGC-------- ---------CAATCAACCTGT--AC
droMoj3	scaffold_6500:4738876-4739013 +		---------------------------------ATGTCAGTCTGCACAGCAGATGAGATTGCAGAGAAACCGCGCATCGCACTAGCCAAGCTGCAGGCTAAGAAAAACCAAACAGCACGCCGTAAATTC------AAACACAAA------ ------ ---CGC------CGCCACAAA---TGTCAA---------- ---------CCAACAATTGGGCCGA
droGri2	scaffold_15252:16053753-16053879 +		---------------------------------ATGTCAGTTTGCACATCCGCTGAGATAGCAGAGAAACGTCGCATTGCACTGGCTAAGCTGCAGGCAAAAACTAAACAA---------- ------ ------ ------ ---------GGCCCGCCAACAATTC----------AA-ATGCAA---AACCTGCTTCAAATT--ATTTTGAGCG

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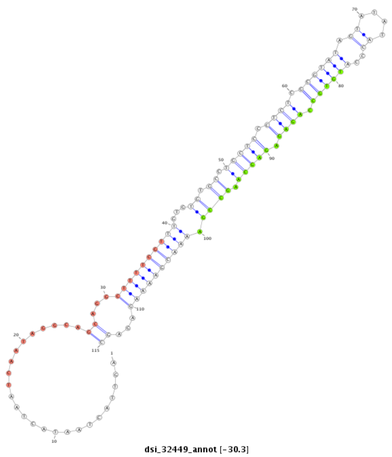
	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	0
rescue.total	0
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	4

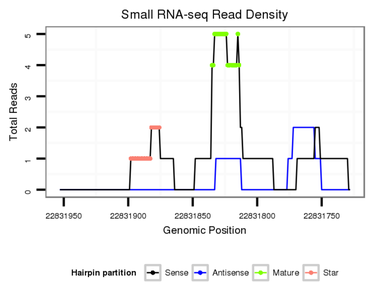
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dsi_32449	**3r:22831778-22831903 -**	**candidate**	**Canonical miRNA**	**5pUTR**	[View on UCSC Genome Browser (Cornell Mirror)]

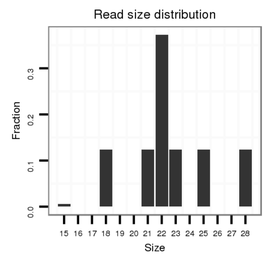
Legend: mature star mismatch in alignment mismatch in read

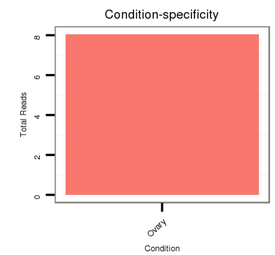
Predicted structure

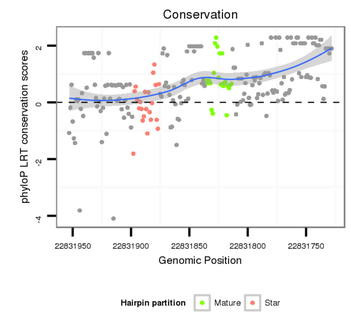


dsi_32449_annot [-30.3]









Show Alternate Folds

Flybase annnotation

utr5 [utr5_minus_10449]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

Read size	# Mismatch	Hit Count	Total Norm	Total	SRR618934 dsim w501 ovaries	SRR553486 Makindu_3 day-old ovaries	SRR553488 RT_0-2 hours eggs	M024 male body	SRR553485 Chicharo_3 day-old ovaries	SRR902008 ovaries	SRR902009 testis	SRR553487 NRT_0-2 hours eggs	M023 head
22	0	1	2.00	2	0	1	0	0	1	0	0	0	0
23	0	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	0	1	1.00	1	0	0	0	1	0	0	0	0	0
22	1	1	1.00	1	0	0	0	0	0	1	0	0	0
18	0	1	1.00	1	0	0	0	1	0	0	0	0	0
25	0	1	1.00	1	1	0	0	0	0	0	0	0	0
21	0	1	1.00	1	1	0	0	0	0	0	0	0	0
28	0	1	1.00	1	0	0	0	0	0	1	0	0	0
26	0	1	1.00	1	0	1	0	0	0	0	0	0	0
15	0	20	0.05	1	0	1	0	0	0	0	0	0	0

Anti-sense strand reads

Read size	# Mismatch	Hit Count	Total Norm	Total	SRR902009 testis	M023 head	SRR902008 ovaries	GSM343915 embryo	SRR553488 RT_0-2 hours eggs
21	0	1	1.00	1	1	0	0	0	0
22	0	1	1.00	1	1	0	0	0	0
20	0	1	1.00	1	0	1	0	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droSim2	3r:22831728-22831953 -	dsi_32449	
droSec2	scaffold_22:40478-40703 -	dse_167	
dm3	chr3R:23406959-23407185 -	dme_400	
droEre2	scaffold_4820:4630700-4630918 +	der_1529	
droYak3	3R:23081019-23081237 +		
droEug1	scf1800000409770:888857-889076 -		
droBia1	scf1800000302075:1520915-1521075 +		
droTak1	scf1800001413872:284259-284469 -		
droEle1	scf1800000491261:1896646-1896863 -		
droRho1	scf1800000767320:9576-9792 -		
droPic1	scf1800000453826:309181-309404 +		
droKik1	scf1800000302697:675387-675614 -		
droAna3	scaffold_13340:19285476-19285789 +	dan_4052	
droBip1	scf1800003966413:3081059-3081368 -		
dp5	2:9056108-9056281 -		
droPer2	scaffold_0:2869191-2869364 -		
droMoj3	scaffold_6540:32543020-32543139 +		

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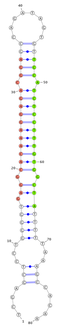
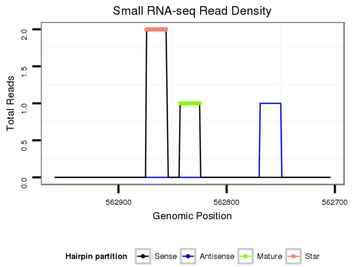
	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.log3	1
crit.unpaired	0
crit.ext	0
crit.back	0
rescue.total	0
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	3

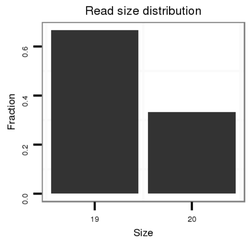
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dsi_32452	**3r:562754-562909 -**	**candidate**	**Canonical miRNA**	**intron**	[View on UCSC Genome Browser [Cornell Mirror]]

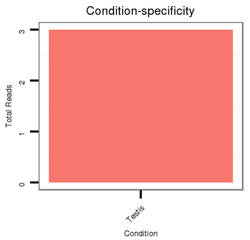
Legend: mature star mismatch in alignment mismatch in read

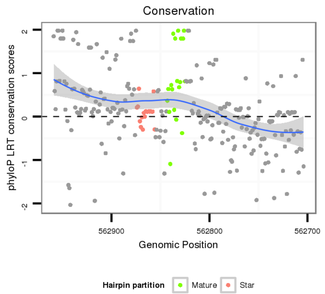
Predicted structure











Show Alternate Folds

Flybase annotation

intron [3r_562519_572532_-]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

AGCATTTCCTGTCTATGGCCCGATCACTCCGCATGGCTGCCGGCTCTCTCCACATCTGAGTTGTGCCTATTCGAGCTCCTGGGGTGAGGCACAAAGGAGACGGAGCCAGATAGTGTTCCATCTCCTTTGTGGCTATTTTTAAAGCCACAAAGCCCCGTCTTCTGTTTCCCAGCTATTTCGCGCTAGTTGTCAGTCCAGATCGATCCAACTTGTGATGGAATCATCTTATTAACCAGTTAATACTTTTCATGAGAAT	Read size	# Mismatch	Hit Count	Total Norm	Total	SRR902009 testis	SRR553488 RT_0-2 hours eggs	O001 Testis	SRR553487 NRT_0-2 hours eggs
....((((.(((((.((.((((((((((.(((((.....)))))).))))))))))).))))))).)))....									
.....TCCATCTCCTTTGTGGCTA.....	19	0	1	1.00	1	0	0	1	0
.....GAGGCACAAAGGAGACGGA.....	19	0	1	1.00	1	1	0	0	0
.....GAGGCACAAAGGAGACGGAG.....	20	0	1	1.00	1	1	0	0	0

Anti-sense strand reads

TCGTAAAGGACAGATACCGGGCTAGTGAGGCGTACCGACGGCCGAGAGAGGTGTAGACTCAACACGGATAAGCTCGAGGACCCCACTCCGTGTTTCCTCTGCCTCGGTCTATCACAAGGTAGAGGGAAACACCGATAAAAATTTCGGTGTTTCGGGGCAGAAGACAAAGGTCGATAAAGCGCGATCAACAGTCAGGTCTAGCTAGGTTGAACACTACCTTAGTAGAATAATTGGTCAATTATGAAAAGTACTCTTA	Read size	# Mismatch	Hit Count	Total Norm	Total	SRR902009 testis	SRR553485 Chicharo_3 day-old ovaries	SRR553488 RT_0-2 hours eggs	SRR618934 dsim w501 day-old ovaries	SRR553486 Makindu_3 day-old ovaries
....((((.(((((.((.((((((((((.(((((.....)))))).))))))))))).))))))).)))....										
.....GTCAGGTCTAGCTAGGTTGA.....	20	0	1	1.00	1	1	0	0	0	0

Show Alignment With Reads

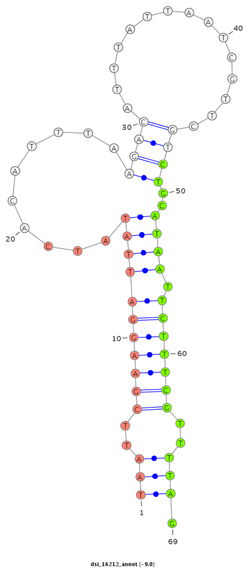
Re-alignment of all predicted orthologs

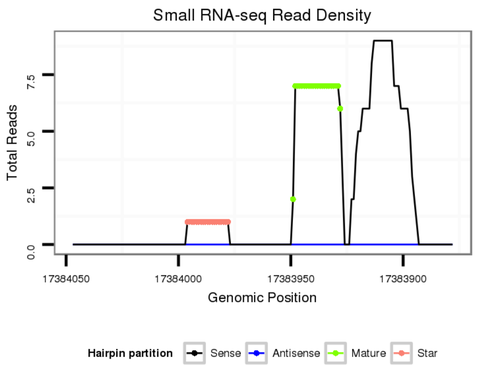
Species	Coordinate	ID	Alignment
droSim2	3r:562704-562959 -	dsi_32452	AGCATTTCCTGTCTATGGC------CCGATCACTCCGCATG---GCTGC------CGGCTCTCTC----------CACATCTGAGTTGTGCCTATTCGAGCTCCTGGG-GTGAGGCA-------CAAAGGAGACGGAGCCAGATAGTGTTCC----ATCTCCTTTGTGGCTATTTTTAAAGC----------CACAAAGCCCCGTCTTCTG-TTTCCCAGCTATTTCGCG-CTAGTTGTCAGTCCAGATCGATCC----------AACTTGTGATGGAATCATCTTATTAACCAGTTAA--------TACTTTTCATG----------AGAAT
droSec2	scaffold_61727976-728198 -	dse_136	AGCATTTCCTGTCTATGGC------CCGATCACTCCGCATG---GCTGC------CGGCTCTCTC----------CACATCTGAGTTGTGCCTATTCGAGCTCCTGGG-GTGAGGCA-------CAAAGGAGACGGAGCCAGATAGTGTTCC----CTCCCTTTGTGGCTATTTTTAAAGC----------CACAAAGCCCCGTCTTCTG-TTCCCAGCTATT-----T----------TGTGATGGAATCATCTTATTAACCAGTTAA--------TACTTTTCATG----------AGAAT
dm3	chr3R:627985-628097 -		AGCATTTCCTGTCTATGGC------CCGATCACTCCGCATG---GCTGC------CGGCTCTCTC----------CACTCTCC----------AGCTCCTGGG-GTGAGGCA-------CGA----------CTCGTTCC----CTCTCCTTGTGGCTATTTTTAAAGC----------C----------T----------T----------T

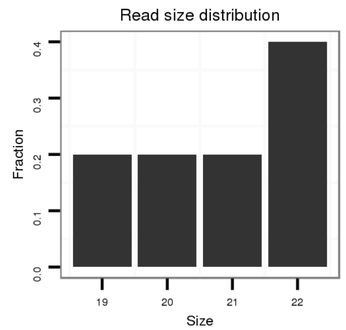
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dsi_16212	**3l:17383928-17383997 -**	**candidate**	**Mirtron**	**intron**	[View on UCSC Genome Browser [Cornell Mirror]]

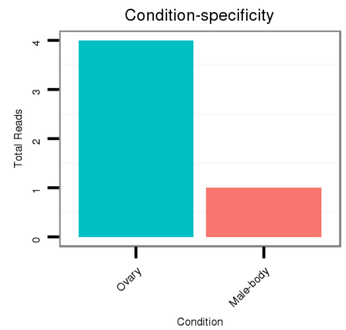
Legend: mature star mismatch in alignment mismatch in read

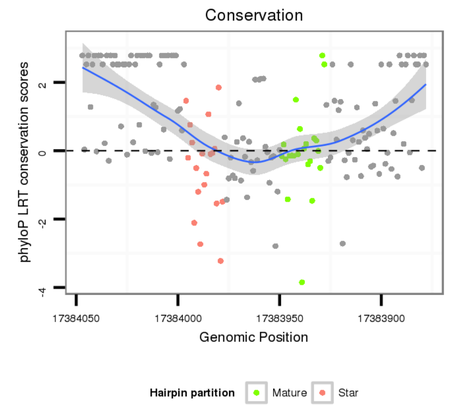
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [3l_17383928_17383997_-]; CDS [3l_17383998_17384201_-]; CDS [3l_17383797_17383927_-]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

ACGTGGTGATGCTGAGTGCTGCACACGATATTATCAAGCAGTTTAATCCGGTAATTCGAAGGATTATATCACATTTAAGACATTTATTAATCGTTCGTCTGCATAATTCTTTCGTTTTAGAGTGATGAATCGGAAGAAAGCTCGTCGGGAAGAAATTGTCACTTGGTTTC **********(((..(((((((((((.....((((.....))))..))))).))))))).))))).**********	Read size	# Mismatch	Hit Count	Total Norm	Total	SRR553487 NRT_0-2 hours eggs	SRR553488 RT_0-2 hours eggs	M024 male body	SRR553486 Makindu_3 day-old ovaries	SRR553485 Chicharo_3 day-old ovaries	M025 embryo	M053 female body	SRR618934 dsim w501 ovaries
.....TGCATAATTCTTTCGTTTTAGA.....	22	0	1	3.00	3	1	0	0	2	0	0	0	0
.....TGCATAATTCTTTCGTTTTAGT.....	22	1	1	3.00	3	0	1	0	2	0	0	0	0
.....ATGAATCGGAAGAAAGCTC.....	19	0	1	2.00	2	0	0	2	0	0	0	0	0
.....CTGCATAATTCTTTCGTTTTAG.....	22	0	1	2.00	2	0	0	0	0	2	0	0	0
.....TGCATAATTCTTTCGTTTTA.....	20	0	1	1.00	1	0	0	0	0	1	0	0	0
.....TAATTCGAAGGATTATATC.....	19	0	1	1.00	1	0	0	1	0	0	0	0	0
.....AAGAAAGCTCGTCGGGAAGA.....	20	0	1	1.00	1	0	0	1	0	0	0	0	0
.....TGCATAATTCTTTCGTTTTAG.....	21	0	1	1.00	1	0	0	0	1	0	0	0	0
.....AATCGGAAGAAAGCTCGTCGGGAA.....	24	0	1	1.00	1	0	0	1	0	0	0	0	0
.....TCGGAAGAAAGCTCGTCGGGA.....	21	0	1	1.00	1	0	0	1	0	0	0	0	0
.....GAATCGGAAGAAAGCTCGTCGGGAA.....	25	0	1	1.00	1	0	0	1	0	0	0	0	0
.....AGAAAGCTCGTCGGGAAG.....	18	0	1	1.00	1	0	0	1	0	0	0	0	0
.....TCGGAAGAAAGCTCGTCGGGAAGG.....	24	1	1	1.00	1	0	0	0	0	0	1	0	0
.....GAATCGGAAGAAAGCTCGTC.....	20	0	1	1.00	1	0	0	1	0	0	0	0	0
.....AAGAAAGCTCGTCGGGAAGAA.....	21	0	1	1.00	1	0	0	0	0	0	0	1	0

Anti-sense strand reads

TGCACCACTACGACTCACGACGTGTGCTATAATAGTTCGTCAAATTAGGCCATTAAGCTTCCTAATATAGTGTAAATTCTGTAAATAATTAGCAAGCAGACGTATTAAGAAAGCAAAATCTCACTACTTAGCCTTCTTTCGAGCAGCCCTTCTTTAACAGTGAACCAAAG **********(((..(((((((((((.....((((.....))))..))))).))))))).))))).**********	Read size	# Mismatch	Hit Count	Total Norm	Total	SRR618934 dsim w501 ovaries	M024 male body	SRR553488 RT_0-2 hours eggs	SRR553485 Chicharo_3 day-old ovaries

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droSim2	3l:17383878-17384047 -	dsi_16212	ACGTGGTGATGCTGAGTGCTGCACACGATATTATCAAGCAGTTTAATCC---GGTAATTCGA----------AGGA---TT----------ATATCACA---TTTAA----------GACA----------T-------TT------A---TTAATCGT----------TCGTCTGCATA----------ATT------CTT-TCGTTTTAGAGTG------ATGAATCGGAAGAAAGCTCGTCGGGAAGAAATTGTCACTTGGTTTC
droSec2	scaffold_0:9850468-9850639 -		ACGTGGTGATGCTGAGTGCTGCACACGATATTATCAAGCAGTTTAATCC---GGTAATTCGA----------ATAGGA---TT----------ATATCACA---TTTAA----------GACA----------T-------TT------A---TTAATCGT----------TCGTCTGCATA----------ATT------CTT-TCGTTTTAGAGTG------ATGAATCGGAAGAAAGCTCGTCGGGAAGAAATTGTCACTTGGTTTC
dm3	chr3L:17803764-17803935 -		ACGTGGTGATGCTGAGTGCTGCCACGATATTATCAAGCAGTTTAATCC---GGTAATTACA----------ATAGGA---TT----------ATAGCACT---TTTAA----------TACA----------T-------TT------A---TTAATTGT----------TCGCCTGCATA----------ATT------TTT-TCTTTTTAGAATG------ATGAATCGGAAGAAAGCTCGTCGGGAAGAAGTGTCACTTGGTTTC
droEre2	scaffold_4784:16058537-16058704 +		ACGTGGTGATGTGAGTGCTGCCCACGATATTATCAAGCAGTTTAATCC---GGTAGCATT--------TTAATTAA---TA----------ATAACAGT---TTTA----------TTTT----------T-------TT------A---TTAATTGC----------TGTCTGCATA----------ATT------CTTATTCTTTTAGAATG------ATGATTCTGAAGAAAGCTTGTCCGGAAGAAATTGTCACTTGGTATC
droYak3	3L:16252955-16253121 +		ACGTGGTGATGTGAGTGCTGCCCACGATATTATCAAGCAGTTTAATCC---GGTAGCATT--------TT----------AAATACCA---TAAAA----------GCCC----------T-------TC------A---TTAATTGT----------CAGTCTAATA----------ATT------ATTTATTTTTAGAGTG------ATGACTCTGAAGAAAGCTTGTCCGGAAGAAATTGTCACTTGGTATC
droEugl	scf7180000409471:1750192-1750373 +		ATGTGGTGATGCTGAGTGCTGCCCACGATATTATAAGCAGTTTAATCC---GGTGGGGTAT----ATTATA----ATTG-TT----------AC-TATTATT----------GCAT----------T---ATATCTAATAAA--T----------ATTCA----------A-AAATT--TT-ATTATACAGATG------ATGAATCTGAAGAAAGCTCGTCGGGTCTGAAGTGTCACTTGGTCTC
droBia1	scf7180000302193:1120695-1120884 -		ATGTGGTGATGCTGAGTGCTGCCCACGATATTATCAAGCAGTTTAATCC---GGTAGAAAAAAAAATTTTAA--T--TTA----------TTAAATTATATTATTT---AGTTT----------ATTAATTTA----------T-------TT------A---ATAACCGT----------TTACTGTT----------ATTA----TTCTTTTTCAGAACG------ATGAAAGTGAAGAAAGCTCGTCGGGTTGAAATTGTCACTTGGTGTC
droTak1	scf7180000415794:30970-31159 -		ATGTGGTGATGCTAGTGCTGCCCACGATATTATCAAGCAGTTTAATCC---GGTGGTGAATCAGATTTTT---TTGT--TAT----------TTAAAATCAATTGTA---GAAAT----------GGATGTATGC----------T-------CTATTT--A---TTAATTAT----TATTT----------ATTT----AAATATTTATAGAATG------ATGAAAGTGAAGACAGCTCCTCGGGTCTGAATTGTCACCTGGTATC
droEle1	scf7180000490993:726155-726336 -		ATGTGGTGATGTGAGTGCTGCCCACGATATCATCAAACAGTTTAATCC---GGTAGGACAAGAACATTTTA----------AAACATA----------TTTTCT---TAATTTTAAAA---TAA---T----------TAACCTGTGTGC----------CAATTATTA----ATT-TTGTTACAGAGTG------ATGACTCTGTAGAAAGCTCTTCTGATCGAAATTGTCATTTGGTCTC
droRho1	scf7180000779490:118108-118321 -		ATGTGGTGATGCTGAGTGCTGCCCACGATATCATCAAACAGTTTAATCC---GGTGGGAATA----------AAAACA----------CTTAG----------A----------GCAAATACCCAATATC--T-TA--------AGTCATATTTCAAAATTAAATTCGG-GTGCAAGACAATCTTATAACATAATCGAAAAA--TATTGTT-TCCATACAGAATG------ATGAATCTGAAGAGAGCTCTTCTGGAAGAAATTGCCATTTGGTATC
droFic1	scf7180000454107:1398481-1398694 -		ACGTAGTATGCTGAGTGCTGCCCACGATATTATAAGCAGTTTAATCC---GGTAGAGAA----------A---CCA-TTTCAAACATTACTTCTTAGAAAAAATATCACAAACATATTT-----**********---CCCTGCCTAATAGAGTCTTAATTTTT---TAATTACAAAA---T-----**********TA---------**********ATT--TTTTGTT-TTGTTACAGAATG------ATGATACCGAAGAGAGCTCGTCTGGTAGAAATTGTCACTTGGTATC
droKik1	scf7180000302626:224926-225090 -		ATGTGGTGATGCTGAGTGCTGCCCATGATATTATCAAACAGTTTAATCC---GGTGGGAAACAG-----TCT----**********------ATATC----**********TTTAATCCTTGATC----T----AACTCGAATTATATTTTA---------**********TT------TCT-TCCCCTTAGAATG------AGGAGCTCCTGAAAGCGATTCCGGTAGAAATTGCCATTTGGTGTC
droAna3	scaffold_13337:5371906-5372070 +		ATGTGGTGATGCTGAGTGCTGCCCACGATATCATCAAGCAGTTTAATCC---TGTAAATAAT----------A---TAATT----------AAATAA---A-----**********TATTTAATAAATTTT---A-TTA--------AATAATATTTCA---------**********---------AAT-CTTTTCTAGACCG------ATGATGCTGAGAGACAGCGATTCCGGCTAGAAATTGTCATTTGGTATC
droBip1	scf7180000396371:696689-696852 +		ATGTGGTGATGCTAGTGCTGCCCACGATATCATCAAACAATTTAATCC---TGTAAATAGC--------TA----ATAATA----------CCTAG----------A----------T---ATACCTAATACC--TATG--------AATAATAATCCA---------**********---------AAT-CGTTTCTAGACCG------ATGATGATGAAGAGACTTCTTCGGGCAGAAAGTGTCACTTGGTATC
dp5	XR_group6:10676213-10676380 -		ATGTGGTGATGTGAGTGCGGCCCACGACATATTATCAAGCAGTTCAATCC---GGTAGGCAA----------**********GATCAGGGATAACCTGA-----**********TCATCC---AAATCAG--A----CTAATCGT----------TTTCCTC----**********---------TGGT-CCCTGTCAGACCG------ATGACGATGAACCAGCGCCACGGGTAGCAACTGTCACTTGGTATC
droPer2	scaffold_20:588462-588629 -		ATGTGGTGATGTGAGTGCGGCCCACGACATATTATCAAGCAGTTCAATCC---GGTAGGCAA----------**********GATCAGACATAACCTGA-----**********TCATCC---AAATCAG--A----CTAATCGT----------TTTCCTC----**********---------TGGT-CCCTGTCAGACCG------ATGACGATGAACCAGCGCCACGGGTAGCAACTGTCACTTGGTATC
droWil2	scf2_1100000004762:2752685-2752850 -	dwi_2012	ATGTGGTATGCTAGTGCTGCCCATGATATCATCAAGCAATTCAATCC---GGTAGAGAGA----------GAGAGA----------GACA-----GAACCAGAGAGAGAA----------GACA----------C-------AA------A---CTAAT---------ACTA----------**********ACA-----ATCCCATTTCAGACAG------ACGAACGGACGAAGCCCCACAGGACGAGGCTCCATTTGGTCTC
droVir3	scaffold_13049:22202875-22203041 +		ACGTGGTGATGCTGAGTGCTGCCCACGATATCATGCGCAGTTTAATGATGAGGTGGATA----------AATATG----------GCTAT----------A----------TTGAGTGACTGATAGC--T-GA--------ACTGATATTTT----------**********---------**********---AATATACCTGAGGTGGATGATGGCCTGTTGCTGGCACAGGACCTGAGTGCATTTGGTATC
droMoj3	scaffold_6680:16811876-16812050 +		ATGTGGTATGCTGAGTGCGGCCCACGACATCATGCGCAGTTCAATGA--TGAAGTGG-G----------TTG----**********GATTCGAATTATATATGTA----------TATA----------T-------AT------A---TTAATTAA----------ATGC-------**********---AATA----TGCTCTTTCACCTGAGGTGGGGAGGTCGAGATCGGGCAAGGGCCCGGCATGCCATTTGGTATC
droGri2	scaffold_15110:21340234-21340399 -		ACGTGGTAATGCTGAGTGCTGCCCATGATATCATGATCAGTTTAATGAGAAGGTATGAATA----------TTCA-TC----------**********---ACAAA----**********----------TGTTCTTATAAATAA---AC---TAA----CTGATACT----------**********---------**********---CCATTTTACCATAGAAAGATCCCAATGATTTGCTGATAATCAACCCCATGCCATTTGGTATC

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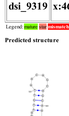
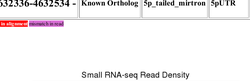
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

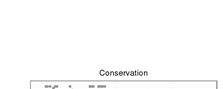
ID:	Coordinate:	Confidence:	Class:	Genome Locale:	
dsi_9319	**x:4632336-4632534 -**	**Known Ortholog**	**5p_tailed_mirtron**	**5pUTR**	[View on UCSC Genome Browser (Cornell Mirror)]

Legend: sense; star; mismatch in alignment; mismatch in seq

Predicted structure







Show Alternate Folds

Flybase annotation

utr5 [utr5_mma_13586]

No Repeatable elements found

Sense Strand Reads

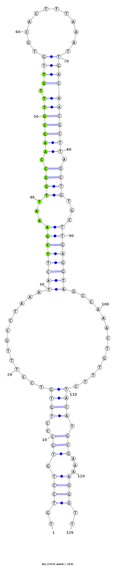
hide 3p reads | show mid mismatch reads

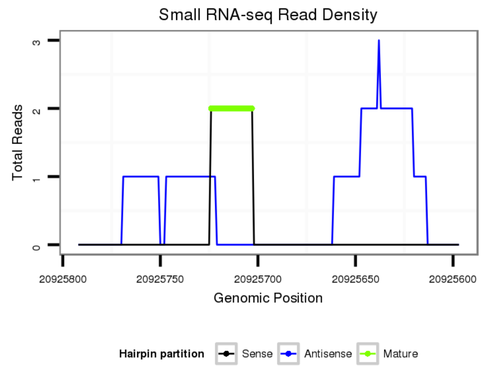
	Read # size	Mismatch	Hit Count	Total Norm	Total	dsim w501 ovaries	SRR618934 RT_0-2 hours eggs	GSM343915 embryo	SRR553485 Chicharo_3 day-old ovaries	SRR553486 Makindo_3 day-old head ovaries	SRR553487 M023 RNT_0-2 hours body	SRR553488 RT_0-2 hours eggs
CCCAAAAAAAAAAAAAAAAACCAAAACAAAAATGGACGAAAAGTGGACGAAAAGTGAGCAGAAAGTGGGGGGAAAAGCTAAAATTAATTTTTTTGTTTTTATTTCCAAGGCGCGCACTGGTGTGT

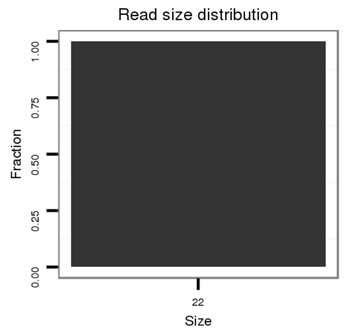
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dsi_32434	**3r:20925647-20925742 -**	**candidate**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser [Cornell Mirror]]

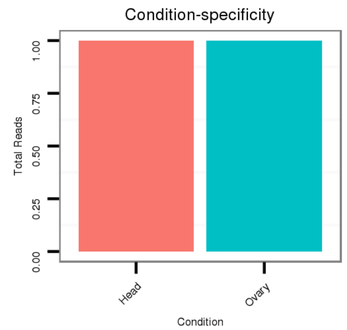
Legend: mature star mismatch in alignment mismatch in read

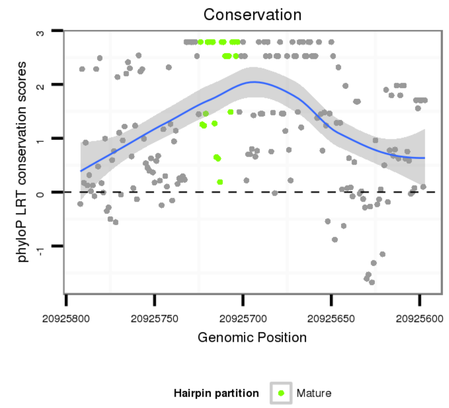
Predicted structure











Show Alternate Folds

Sense Strand Reads

hide 3p reads | show mid mismatch reads

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**********************************..((((.(((..((((.............(((((((...((((.(((((((.((((.............)))))))))))).))))...)))))))).............)))).)))...)))))..**********************************
.......................................................................TCGAAATTGGCCAAGCGTTTGT.......................................................................
```

Read size	# Mismatch	Hit Count	Total Norm	Total	SRR553487 NRT_0-2 hours eggs	M023 head	GSM343915 embryo	SRR553485 Chicharo_3 day-old ovaries	SRR553486 Makindu_3 day-old ovaries
22	0	1	2.00	2	1	1	0	0	0

Anti-sense strand reads

```
GAACCGTCGACACGCAGACATACGTACACATAGACACAGGACACGGGACACAGGAAACGGATTTATGAAGCTTTAACCGGTTCGCAAACAACACGTGAAATTTAACTGTTGCGAATCGACACGAACTCCATCGGTTTGACAAAGATGTACGCTTTTCCCAAGAGTTTAGTAGGACACGTAGGAACACGGTACTAAT
**********************************..((((.(((..((((.............(((((((...((((.(((((((.((((.............)))))))))))).))))...)))))))).............)))).)))...)))))..**********************************
.......................................................................TGTACGCTTTTCCCAAGAGTTTAGTAG.......................
.....................GGACACAGGAAACGGATTTATGAAGC.......................................................
.....................GTACACATAGACACAGGAC.............................................................
.......................................................................TTCCCAAGAGTTTAGTAGGACACGT.........................
.......................................................................CGGTTTGACAAAGATGTACGCTTT..........................
```

Read size	# Mismatch	Hit Count	Total Norm	Total	SRR553485 Chicharo_3 day-old ovaries	M025 embryo	O002 Head	SRR902008 ovaries	SRR553487 NRT_0-2 hours eggs
27	0	1	1.00	1	0	1	0	0	0
26	0	1	1.00	1	0	0	0	1	0
19	0	1	1.00	1	0	0	1	0	0
25	0	1	1.00	1	1	0	0	0	0
24	0	1	1.00	1	1	0	0	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droSim2	3r:20925597-20925792 -	dsi_32434	CTTGGCAGCTG----------TGCGTCTG---------TATGCATGTGT----------ATCTGTGTCC---T--GTGCCCTGT---------GTCCTTTGCCTAAATACTTCGAAATTGGCCAAGCGTTTGTTGTGCA---CTTTA-AATTGACAACGCTTAGCTGTGCTTGAGGTAGCC--AAACTGTTTCTACATGCGAA--------A--A--GGGTT---C--TC----------AAATCATC-----CT--GTGCATCCTTG---TGCCAT---GATTA
droSec2	scaffold_13:201147-201342 -	dse_150	CTCGGCAGCTG----------TGCGTCTG---------TATGCGTGTGT----------ATCTGTGTCC---T--GTGCCCTGT---------GTCCTTTGCCTAAATACTTCGAAATTGGCCAAGCGTTTGTTGTGCA---CATTA-AATTGACAACGCTTAGCTGTGCTTGAGGTAGCC--AAACTGTTTCTACATGCGAA--------A--A--GGGTT---C--GC----------AAATCATT-----CT--GTGCATCCTTG---TGCCAT---GATTA
dm3	chr3R:21413202-21413397 -	dme_166	CTCGGCAGCTG----------TGCGTCTG---------TATGCGTGTGT----------ATCTGTGTCC---T--GTGCCCTGT---------GTCCTTTGCCTAAATACTTCGAAATTGGCCAAGCGTTTGTTGTGCA---CATTA-AATTGACAACGCTTAGCTGTGCTTGAGGTAGCC--AAACTGTTTCTACATGCGAA--------A--A--GGGTT---C--TC----------AAATCATC-----CT--GTGCATCCTTG---TGCCAT---GATTA
droEre2	scaffold_4820:6629144-6629349 +	der_1511	CTCGGCAGCTG----------TGTGCGTGTATGCGTGTGTGTGTGCGTGTGT----------ATCTGTGTCC---T--GTGCCCTGT---------GTCCTTTGCCTAAATACTTCGAAATTGGCCAAGCGCTTGTCGTGCA---CATTA-AATTGACAACGCTTAGCTGTGCTTGAGGTAGCC--AAACTGTTTCTACATGCGAA--------A--A--GGGTT---C--TG----------CAGTCATC-----CT--GTGCATCCTTG---TGCCAT---GATTA
droYak3	3R:25065930-25066147 +	dya_69	CTCGGCAGCTG----------TGTGCGTGTATGCGTGCGTATGCGTGTGT----------ATCTGTGTCC---T--GTGCCCTGT---------GTCCTTTGCCTAAATACTTCGAAATTGGCCAAGCGTTTGTTGTGCA---AATTC-AATTGACAACGCTTAGCTGTGCTTGAGGTAGCC--AAACTGTTTCAACATGCGAA--------A--A--GGGTT---C--A-----------------TCTGGCCATCATCTGTTCT--GTGCATCCTTGCCGTGCCAT---GATTA
droEug1	scf7180000409798:1138164-1138368 +		CTCGGCAGCTG----------TATGT---------ATGAGTGTGTATCTG----------TGTAGCTGTGTCC---T--GTGTCCTGT---------GTACTTTGCCTAAATACTTCGAAATTGGTTAAGCGTTTGTTGTGCC---CATGA-AATTGACAACGCTTAGCTGTGCTTGAGGTAGCC--AAATTGTTTCATCAT-----------------------A--A--------CATTATCTGCATCTGCATCTG-CATCAGC-----CT--CGGCATCCTTG---TGCCAT---GATTA
droBia1	scf7180000302136:2259442-2259637 -		CTCGGCAGCTG----------TGCGTCTG---------TATGCGTGTGT----------ATCTGTGTCC---T--AGCTCCTGTGTGTACTTTGTACTTTGCCTAAATACTTCGAAATTAACCAAGCGTTTGTTGTGCC---CATGA-AATTGACAACGCTTAGCTGTGCTTGAGGTAGCC--AAATCGTTTCCACATGCGAA--------C--A--GGGTG---C--T----------GG---T-----CGCTGCATCCTTG---TGCCAT---GATTA
droTak1	scf7180000415257:293315-293519 -		CTCGGCAGCTGCGG----------CTG--TGTG--TGTGTGTG---------TATGCGTGTGT----------ATCT-----C---T--GTGTCCTGTGA------GTACTTTGCCTAAATACTTCGAAATTGGCCAAGCGTTTGTTGTGCC---CATGA-AATTGACAACGCTTAGCTGTGCTTGAGGTAGCC--AAATTGTTTCAACATCGAA--------C--A--GGATCTG-C--TC----------CATTTATC-----CT--CTGCATCCTTG---TGCCAT---GATTA
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droRho1	scf7180000779501:512609-512782 +		CTCGGCGCTGTA----------TGCGTCA----------TGTGTGTGT----------ATCTGTG---T--T----CCTGC---------GTGCTTTGCCTAAATACTTCGAAATTGGCTAAGCGTTTGTTGTGTC---CATGA-AATTGACAATGCTTAGCTGTGCTTGAGGTAGCC--AAATTGTTTCTACATGCAAA--------T--T--GGGG---T--T----------------------TC-----CT--CTGCATCCTTG---TGCCAT---GATTA
droFic1	scf7180000454055:1329831-1330036 -		CTCGGCAGATGTAGATG----------ATGTCGCATGTGTGCGTGTGCGT--GT----------ATGTGTG---T--T--TGT-GCCT---------GTGCTTTGCCTAAATACTTCGAAATTGGCCAAGCGTTTGTTGTGCC---CATGA-AATTGACAACGCTTAGCCGTGCTTGAGGTAGCC--AAATTGATTCTACGAGCAAA--------T--T--GGGGT--GACAACGAGG----------AATTGCA-----CT--CTGCATCCTTC---TGCCAT---GATTA
droKik1	scf7180000302639:1624806-1624992 +		CTCTGCAGCTG----------TGTGT---------TGCGCTGTGC----------CGCC---TGTCGTCCTGTGT------GTG-TTTGCATAAATACTTCGAAATTGGCCAAGCGTTTGTTGTGCT---TATGA-AATTGACAACGCTTAGCTGTGCTTGAGGTAGCC--AAATTGTTTCAACAGACGGG--------AAGAGAGGGTG---C--G----------GG---TC-----CT--CGTGCATCCTTG---TGCACT---GATAA
droAna3	scaffold_13340:3669019-3669178 -		CTCT----TG----------TGTGT--GGCC---------TATCCGTGTGT----------TTGTGTG---T--T-TGTGATGA--------GA-GTGTGCCTAAATACTTCGAAATTGGCTAAGCGTTTGTTGTGATT--TACCA-AATTGACAATGCTAAGCTGTGCTTGAGGTAGCC--AAGATGAAATCTACAACC----------A--A--GGA---T--T----------------------C-----CTCGTTGCATCCTTG---CC-----------
droBip1	scf7180000396712:683529-683692 +		ATCTCTGCCTT----------TGCGAGCC---------CATCCGTGTGT----------CTGTGTG---T--T-----TGT--------GAG-CTGCCTAAATACTTCGAAATTGGCTAAGCGTTTGTTGTGATT--TATCG-AATTGACAATGCTAAGCTGTGCTTGAGGTAGCC--AAGATGAATCTACAC--GAA--------C--A--GGA---T--T----------------------C-----CTCGTTGCATCCTTG---TC-----------
dp5	2:21156503-21156761 -	dps_3835	GTGTGCGCCTCTGCTCTCTGT------CTA--TG----TGT-----------T---G--AGTGTATCTGCATGTGTCACCGTATCTGTATCTGTATCC---T--GTAT-CTCC---------GTGCTTCG-TTAAATACTTCGAAATTGGTTAAGCGTTTGTTGTGG---TATTA-AAGTGACAAAGCTTTGCGTGCTTGAGGTAGCC-CTAATTGATTGCACAAACGATCATCACCTGAACA--GGATGAGTGACACACATGACTGTGTGTGTGTGTG-----T-----GT--GTGTGTATTG---TGGGTGGGATGATGA
droPer2	scaffold_3:3931002-3931258 -	dpe_2496	GTGTGCGCCTCGGCTCTCTGT------CTC--TC----TGT-----------T---G--AGTGTATCTGCATGTGTCACCGTATCTGTATCTGTATCC---T--GTAT-CTCC---------GTGCTTCG-TTAAATACTTCGAAATTGGTTAAGCGTTTGTTGTGG---TATTA-AAGTGACAAAGCTTTGCGTGCTTGAGGTAGCC-CTAATTGATTGCACAAACGATCATCACCTGAACA--GGATGAGTGACACACATGACTGTGTGTGTGTGTG-----T-----GT--GTGTGTATTG---TGGGTGGGATGATGA
droWil2	scf2_1100000004943:14640087-14640209 +		T---------GT----------C-------TGTAMGTG--------TTGTGTGTGT----------GTGTGTG---T--T--------GT--------GTGCTTTGCCTAAATACTTCGAAATTGATTAAGCGTTTGTTGTGTTCCATTTGA-ATTGACAATGCTTAGCTGTGCTTGAGGTAGCCTCTAATTGCTTG----------T--T--GGGG---T--T----------------------C-----CT--GTGCATCCTTG---TGCCAT---GATTA
droVir3	scaffold_12855:6808868-6808971 -	dvi_24643	----------T----------T-------T----------T----------T----------T--T------TGT--------GTGCCTTTTCTAAATACCTTGAAATTGGTTAAGCGTTTGTTGTGGT---TATGA-AATTGACCACGCTTACTGTGCTTCAGGTAGCC--TAATTGCTTCAACAAGC---------T--T--GGGG---T--T----------------------C-----CT--GTGCATCCTTG---TGCCAT---GATTA
droMoj3	scaffold_6540:25792865-25793004 +	dmo_3123	GTGTCTACGTG----------TATGTGAG---------TGTGTGTGTGT----------GTGTG-----T--T------TGT--------GTACGTTGCTAAATACTTCGAAATTGGTTAAGCGTTTGTTGTGT---TATGAAAATTGACAACGCTTACTGTGCTTGAGGTAGCC--TAATTGTTTCAACAAGC---------T--T--GGGG---T--T----------------------C-----CT--GTGCATCCTTG---TGCCAT---GATTA
droGri2	scaffold_14906:2963137-2963259 -	dgr_468	T---------GT----------C-------TGTGT---------T---G------A----------GTGTGTGTGC---A--T---------GTACGGGCGTAAATACTTCTGGAATTGGTTAAGCGTTTGTTGTGT---TATGA-AATTGACAACGCTTACGTATGCTTGAGGTAGCC--TAATTGTTTCAACAAGC---------T--T--GGGG---T--T----------------------C-----CT--GTGCATCCTTG---TGCCAT---GATTA

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crit.total	0
crit.pairing	1
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crit.uri	0
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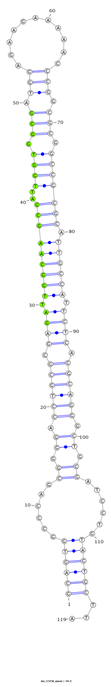
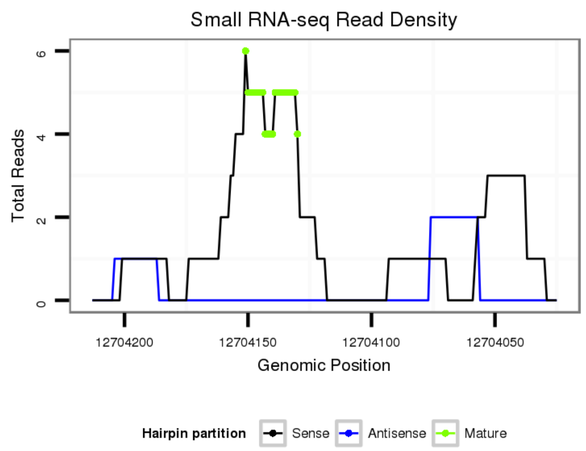
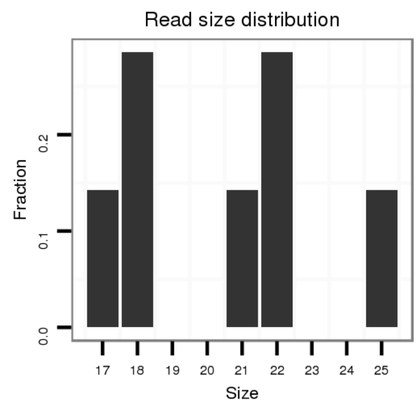
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dsi_32458	**3l:12704075-12704163 -**	**candidate**	**Canonical miRNA**	**CDS**	[View on UCSC Genome Browser [Cornell Mirror]]

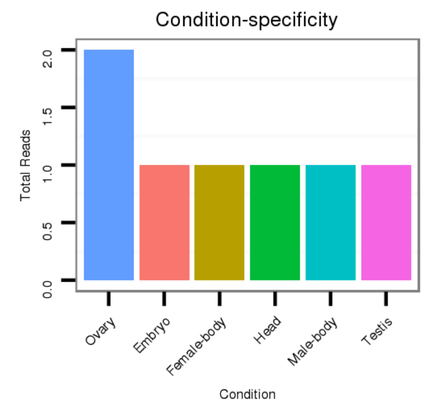
Legend: mature star mismatch in alignment mismatch in read

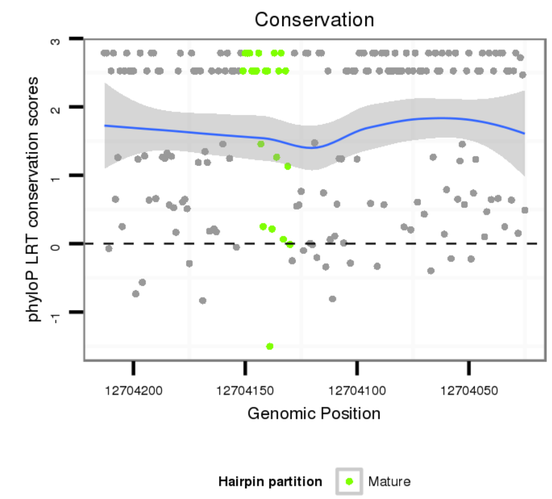
Predicted structure











Show Alternate Folds

Flybase annotation

CDS [3l_12703839_12704375_-]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

AACGAGGCGGAGGCTCAGGCGTTCGCCGAGGCCCAGCAGTGGCCCAGCGGGGACCTGCGCGAGATTGGCAAGCGATTGGTGGCGATGGAGAAGAAAAACCCGGCGCGGCCGCGCATTGCCATTCTCACGCAGGGCTGCGATCCTGTACTGCTTATTCAGCAGGATTCGGTGCAGGAGTTCCCGGTCACG **********(((((.....((.((.((((((.((((.((((((((((..((((.(((.(((.....)))).))).)))))))..)))))).)))).)))))).)).)).....)))))).....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M025 embryo	SRR618934 dsim w501 ovaries	SRR902009 testis	SRR553487 NRT_0-2 hours eggs	M024 male body	GSM343915 embryo	M023 head	M053 female body	SRR553485 Chicharo_3 day-old ovaries	SRR553488 RT_0-2 hours eggs	SRR553486 Makindu_3 day-old ovaries
.....GATTGGCAAGCGATTGGTGGCG.....	22	0	1	2.00	2	1	0	0	0	0	0	1	0	0	0	0
.....CAGCAGGATTCGGTGCAGGA.....	20	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0
.....GATTGGTGGCGATGGAGA.....	18	0	1	1.00	1	0	0	0	0	0	0	0	1	0	0	0
.....AGGATTCGGTGCAGGAGTTCCCGG.....	24	0	1	1.00	1	0	0	0	0	0	1	0	0	0	0	0
.....TGGCCCAGCGGGGACCTGCGCGAG.....	24	0	1	1.00	1	0	1	0	0	0	0	0	0	0	0	0
.....GCGCGAGATTGGCAAGC.....	17	0	1	1.00	1	0	1	0	0	0	0	0	0	0	0	0
.....ACCTGCGCGAGATTGGCA.....	18	0	1	1.00	1	0	0	0	0	0	0	0	0	1	0	0
.....GCTCAGGCGTTCGCCGAGG.....	19	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0
.....GCGAGATTGGCAAGCGATTGGTGGC.....	25	0	1	1.00	1	0	0	0	0	1	0	0	0	0	0	0
.....ATTGGTGGCGATGGAGAAGAA.....	21	0	1	1.00	1	0	0	1	0	0	0	0	0	0	0	0
.....ATTCTCACGCAGGGCTGCGATCCT.....	24	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0
.....TCAGCAGGATTCGGTGCAGGA.....	21	0	1	1.00	1	0	0	1	0	0	0	0	0	0	0	0
.....ACGCAGGGCTGCGATCCAC.....	19	2	2	0.50	1	0	1	0	0	0	0	0	0	0	0	0

Anti-sense strand reads

TTGCTCCGCCTCCGAGTCCGCAAGCGGCTCCGGGTCGTCACCGGGTCGCCCCTGGACGCGCTCTAACCGTTCGCTAACCACCGCTACCTCTTCTTTTTGGGCCGCGCCGGCGCGTAACGGTAAGAGTGCGTCCCGACGCTAGGACATGACGAATAAGTCGTCCTAAGCCACGTCCTCAAGGGCCAGTGC **********(((((.....((.((.((((((.((((.((((((((((..((((.(((.(((.....)))).))).)))))))..)))))).)))).)))))).)).)).....)))))).....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	SRR902009 testis	O002 Head	SRR553488 RT_0-2 hours eggs	SRR618934 dsim w501 ovaries	M025 embryo	M024 male body	SRR553486 Makindu_3 day-old ovaries
.....GCTAGGACATGACGAATAAG.....	20	0	1	2.00	2	2	0	0	0	0	0	0
.....CTCCGAGTCCGCAAGCGG.....	18	0	1	1.00	1	0	1	0	0	0	0	0
.....GTTTTTGGGCCGCGCC.....	16	1	4	0.25	1	0	0	1	0	0	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droSim2	3l:12704025-12704213 -	dsi_32458	AACGAGGCGGAGGCTCAGGCGTTCGCCGAGGCCCAGCAGTGGCCCAGCG---GGGACCTGCGCGAGATTGGCAAGCGATTGGTGGCGATGGAGAAGAAAAACCCGGCGCGGCCGCGCATTGCCATTCTCACGCAGGGCTGCGATCCTGTACTGCTTATTCAGCAGGA---TTCGGTGCAGGAGTTCCCGGTCACG
droSec2	scaffold_0:5185161-5185349 -	dse_1846	AACGAGGCGGAGGCTCAGTCGTTCGCCGAGGCCCAGCAGTGGCCCAGCG---GGGACCTGCGCGAGATTGGCAAGCGATTGGTGGCGATGGAGAAGAAAAACCCGGCGCGGCCGCGCATTGCCATTCTCACGCAGGGCTGCGATCCTGTACTGCTTATTCAGCAGGA---TTCGGTGCAGGAGTTCCCGGTCACG
dm3	chr3L:13013576-13013764 -	dme_245	AACGAGGCGGAGGCTCAGGCGTTCGCCGAGGCCCAGCAGTGGCCTAGCG---GGGACCTGCGCGAGATTGGCAAGCGACTGGTGGCGATGGAGAAGAAAAACCCGACGCGGCCGCGCATTGCCATTCTCACGCAGGGCTGCGATCCTGTACTGCTTATAGAGCAGGA---TTCGGTGCAGGAATTCCCGGTCACG
droEre2	scaffold_4784:13021109-13021297 -	der_1523	AACGAGGCGGAGGCTCAGGCCTTCGCCGAGGCCCAGCAGTGGCCCAGCG---GGGACCTGCGCGAGATTGGCAAGCGACTGGTGGCGATGGAGAAGAAAAACCCGACGCGACCGCGCATTGCCATCCTCACGCAGGGTTGCGATCCTGTCCTGCTCATCCAGCAGGA---TTCGGTGCAGGAGTTCCCGGTCACG
droYak3	3L:13092479-13092667 -	dya_1798	AACGAGGCAGAGGCTCAGGCCTTCGCCGAGGCCCAGCAGTGGCCCAGCG---GGGACCTGCGCGAGATTGGCAAGCGACTGGTGGCGATGGAGAAGAAAAACCCGACGCGGCCGCGCATTGCCATCCTCACGCAGGGCTGCGATCCTGTCCTGCTTATTCAGCAGGA---TTCGGTGCAGGAGTTCCCGGTCACG
droEug1	scf7180000409711:6101265-6101453 -		AACGAGGCGGAGGCACAAGCCTTCGCCGAGGCCCAGAATTGGCCAAGTG---GGGATCTTCGTGAGATTGGCAAGCCTCTGGTGGCGATGGCCAATTTAAATACCGACGCGGCCGCGCATTGCTATCCTCACGCAGGGCTGTGATCCTGTCCTGCTTATCCAACAGGA---CTCGGTACAGGAGTTCCCGGTCACG
droBia1	scf7180000302193:2253856-2254044 -		AACGAGGCGGAGGCACAGGCCTTCGCCGAGGCCCAGAGTTGGCCCAGCG---GGGATCTGCGCGAGATTGGCAAGCGGCTGGTGGCGTTCGACAAACTGAATCCGGCGCGGCCGCGCATTGCCATTCTCACGCAGGGCTGCGACCCCGCGCTGCTCTTCCAGCAGGA---TTCGGTGCAGGAGTTCCCGGTCACG
droTak1	scf7180000415706:66147-66335 -		AACGAATCGGAGGCTCAGGCCTTCGCCGAGGCCCAGAGTTGGCCCAGCG---GGGATCTGCGCGAGATTGGCAAGCGCCTGGTGGCGCTGGACAAGCTGAATCCGGCGCGGCCGCGCATTGCCATCCTCACGCAGGGCTGCGATCCCGTCCTGCTCATCCAGCAGGA---CTCGGTGCAGGAGTTCCCGGTCACG
droEle1	scf7180000491255:1412089-1412277 -		AACGAGGCGGAGGCACAGGCCTTCGCCGAGGCCCAGAACTGGCCCAGCG---GGGATCTGCGCGAGATTGGCAAGCGGCTGGTGGCGATGGACAAGCTGAATCCGACGCGACCCGCGCATTGCCATCTCACGCAGGGCTGCGATCCCGTCCTGCTCATCCAGCAGGA---TTCGGTGCAGGAGTTCCCGGTCACG
droRho1	scf7180000769477:967-1151 +		AACGAGGCGGAGGCACAGGCCTTCGCCGAGGCCCAGAACTGGCCAAGCG---GGGATCTGCGCGAGATTGGCAAGCGACTGGTGGCGCTGGACAAACTGAATCCGGCGCGGCCGCGCATTGCCATCTCACGCAGGGCTGCGATCCCGTCCTGCTCATCCAGCAGGA---TTCGGTGCAGGAGTTCCCGGT----
droFic1	scf7180000454048:724234-724422 +		AATGAGGCTGAGGCCCAGGCCTTCGCCGAGAAACAGAATTGGCCCAGCG---GGGATCTGCGCGAGATTGGCAAGCGACTGGTGGCGATGGACAAACTGAATCCGGCGCGGCCGCGCATTGCCATCTCACGCAGGGCTGCGATCCCGTCCTGCTCATCCAGCAGGA---TTCGGTGCAGGAGTTCCCGGTCACA
droKik1	scf7180000302272:666717-666905 -		AATGAGGCGGAGGCGCAGGCCTTTGCCGAGGCCCAAAATGGCCGAGCG---AGGATCTGCGTGAGATTGGCAAACGTCTGGTGGCAATGGACAAACTAAATCCGTCGCGGCCACGCATTGCCATCCTCACGCAGGGTTGTGATCCCGTCCTGCTCATCCAGCAGGA---TTCGGTGCAGGAATTCCCGGTCACA
droAna3	scaffold_13337:4137395-4137583 +	dan_4038	AACGAGGCGGAGGCGCAGGCCTTCGCCGAGGCCCAGAGCTGGCCGAGTG---GGGATCTGCGAGAGATTGGCAAGCGGCTGGTGGCGTTCGACAAGCTGAACACGTCGAGGCCGCGCATTGCCATTCTCACGCAGGGCTGTGATCCCGTCCTGCTCTTCCAGCAGGA---CTCGGTGCAGGAGTTCCCGGTCACA
droBip1	scf7180000395450:265900-266088 +		AACGAGGCGGAGGCGCAAGCCTTCGCCGAGGCCCAGAGCTGGCCGAGTG---GGGATCTGCGAGAGATTGGCAAGCGGCTGGTGGCGTTCGATAAGCTGAATACCTCAAAGCCCTCGAATTGCCATTCTCACGCAGGGTTGCGATCCCGTCCTGCTCTTCCAGCAGGA---CTCGGTGCAGGAGTTCCCGGTCACG
dp5	XR_group6:4377266-4377454 -	dps_3829	AATGAGGCGGAGGCGCATGCCTTTGCTACGGCCCAGGGCTGGCCGACCG---AAGATCTGCGCGAGATTGGCAAGCGTCTGGTGGCGCTGGACAAACTGAATCCGGCGCGACCTGGCATTGCCATATAACGCAGGGCTGTGATCCCGTCCTGCTCATCCAGCCGGA---CTCGGTTGAAGAGTTTCCGGTCACA
droPer2	scaffold_9:2666447-2666635 -	dpe_2483	AATGAGGCGGAGGCGCATGCCTTTGCTACGGCCCAGGGCTGGCCGACCG---AAGATCTGCGCGAGATTGGCAAGCGTCTGGTGGCGCTGGACAAACTGAATCCGGCGCGACCTGGCATTGCCATATAACGCAGGGCTGTGATCCCGTCCTGCTCATCCAGCCGGA---CTCGGTTGAAGAGTTTCCGGTCACA
droWil2	scf2_1100000004511:5276750-5276938 +	dwi_5417	AATGAGGCGGAGGCTCATGCCTTTGCGACTCGCCAGGGCTGGCCAACGG---ATGATCTGCGCGAGATTGGCAAGCGTATAGTCGGTCTGGAGAACTAAATCCAAGTCGGCCAGGCATTGCCATAGTAACGCAGGGCTGTGATCCCGTCTTGCTCATTCAAAAAGA---TTCGGTTGAAGAGTTTCCGGTTACA
droVir3	scaffold_13049:22492152-22492343 +	dvi_158	AACGAGGCGGAGGCGCAAGCCTTTGCCACTGCGCAAGGTTGGCCCGCCGACAATGATCTGCGTGAGATTGGCAAGCGCCTGGTCGCGCTGAATAAACTCAATACGGGCGCGACCACGCATTGCCATACTCACGCAGGGCTGTGACCCCGTCTGCTTATAGAGCACGA---TTCGGTCCAGGAGTTCCAGTGACA
droMoj3	scaffold_6680:17099712-17099903 +	dmo_114	AACGAAGCAGAGGCCCATGCCTTTGCCACGGGCGCAAGGCTGGCCCGCCGATGCGGATCTGCGTGAGATTGGCAACGTTTGGTGGCACTGCCCAAAATCAATTCAGAGCGACCACGCATTGCCATACTCACGCAGGGCTGTGACCCCGTCCTGCTCATCCAGCACGA---CAAGGTCCAGGAGTTCCCGGTCACA
droGri2	scaffold_15121:203613-203807 +	dgr_465	AATGAGGCGGAGGCGAAGGCTTTGCCACGGCACAGGCTGGCCGCCGATGAGGATCTGCGTGAGATTGGCAGGCCTCTGGTTGCACTGGACAAATTGAATTCAGCGCGACCACGCATTGCGATACTCACGCAGGGCTGTGATCCCGTCCTGCTCATCCAGCACGACGCTCCGGTCCAGGAGTTCCCAGTTACA

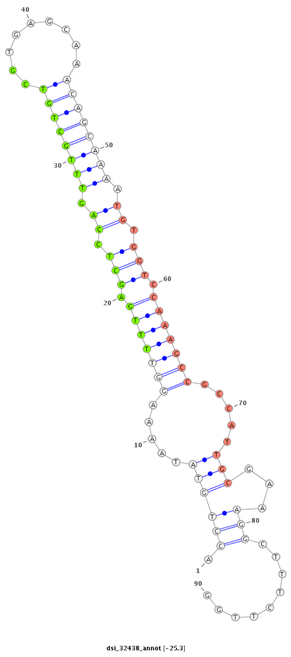
Generated: 09/08/2015 at 08:08 PM

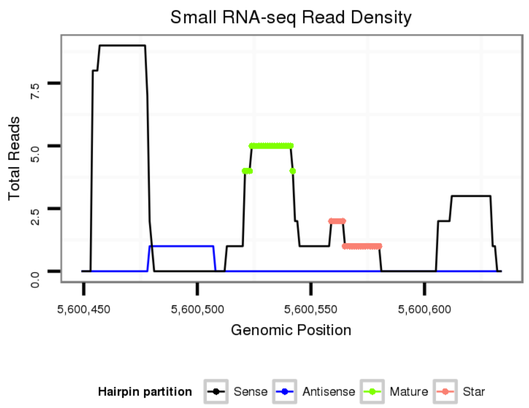
	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	0
crit.uri	0
crit.back	0
rescue.total	0
rescue.dominant	1
rescue.known	0
rescue.confident	2
rescue.candidate	10

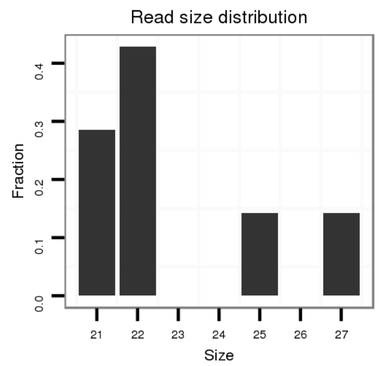
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dsi_32438	**2r:5600499-5600584 +**	**candidate**	**Canonical miRNA**	**3pUTR**	[View on UCSC Genome Browser {Cornell Mirror}]

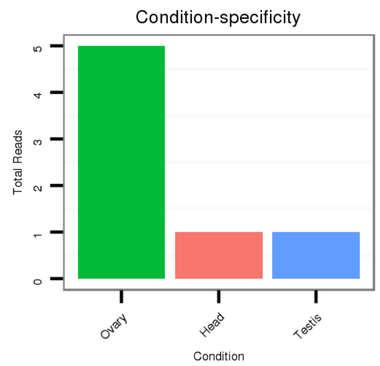
Legend: mature star mismatch in alignment mismatch in read

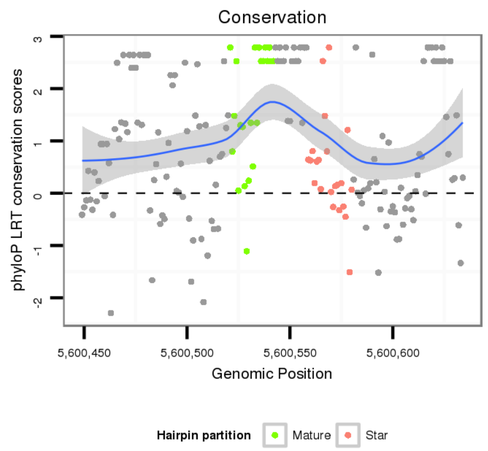
Predicted structure











Show Alternate Folds

Flybase annotation

three_prime_UTR [2r_5598918_5601140_+]; utr3 [utr3_plus_1952]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

ACGTTTACTTAGTAGCAAGAATCACACGTTTTTGCAGACGGCATTTTCTATTCGGAAACCTGTATAAAAGGTTTTGAGCTCCAGTTTGCTGTCGTGAGCAAACAGCAAAATGTGGTCCAAAGCCGCCATTGCGAAAGGCTTTCTTGGGAGCCGCCGCCCCATCAATCGAAACTGCAGTCGGTTACG **********.((((((.....(((((((.(((.((.((((((((.....)))))))).)).)))).)))))))).....)))...))).....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	SRR553485 Chicharo_3 day-old ovaries	SRR902009 testis	SRR553486 Makindu_3 day-old ovaries	M023 head	SRR553488 RT_0-2 hours eggs	O001 Testis	M025 embryo	GSM343915 embryo
.....TACTTAGTAGCAAGAATCACACGTT.....	25	0	1	5.00	5	3	0	2	0	0	0	0	0
.....TACTTAGTAGCAAGAATCACACGT.....	24	0	1	2.00	2	0	2	0	0	0	0	0	0
.....TTTGAGCTCCAGTTTGCTGTCG.....	22	0	1	2.00	2	2	0	0	0	0	0	0	0
.....CCCATCAATCGAAACTGCAGTCGG.....	24	0	1	2.00	2	0	2	0	0	0	0	0	0
.....TTAGTAGCAAGAATCACACGTTTT.....	24	0	1	1.00	1	1	0	0	0	0	0	0	0
.....TACTTAGTAGCAAGAATCACACGTTT.....	26	0	1	1.00	1	0	0	1	0	0	0	0	0
.....GAGCTCCAGTTTGCTGTCGTG.....	21	0	1	1.00	1	0	0	1	0	0	0	0	0
.....TGTGGTCCAAAGCCGCCATTGC.....	22	0	1	1.00	1	0	0	0	0	0	1	0	0
.....TGTCGTGAGCAAACAGCAAAATGTGGT.....	27	0	1	1.00	1	1	0	0	0	0	0	0	0
.....TTTGAGCTCCAGTTTGCTGTC.....	21	0	1	1.00	1	0	0	0	1	0	0	0	0
.....AATCGAAACTGCAGTCGGTT...	20	0	1	1.00	1	0	0	0	1	0	0	0	0
.....TAAAAGGTTTTGAGCTCCAGTTTGC.....	25	0	1	1.00	1	0	0	0	0	1	0	0	0

Anti-sense strand reads

TGCAAATGAATCATCGTTCTTAGTGTGCAAAAACGTCTGCCGTAAAAGATAAGCCTTTGGACATATTTTCCAAAACTCGAGGTCAAACGACAGCACTCGTTTGTCGTTTTACACCAGGTTTCGGCGGTAACGCTTTCCGAAAGAACCCTCGGCGGCGGGGTAGTTAGCTTTGACGTCAGCCAATGC **********.((((((.....(((((((.(((.((.((((((((.....)))))))).)).)))).)))))))).....)))...))).....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	SRR553485 Chicharo_3 day-old ovaries	SRR553486 Makindu_3 day-old ovaries	SRR553487 NRT_0-2 hours eggs
.....AAACGTCTGCCGTAAAAGATAAGCCTTTG.....	29	0	1	1.00	1	1	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droSim2	2r:5600449-5600634 +	dsi_32438	ACG-TT----TACTTAGTA-GCAAGAATCACACGTTTTTGC--A------GACGGCAT--TTT--------------CTATTCGG----AAA-CCTGTATA-A----------AAGGTTTTGAGCTCCAGTTTGCTGTCGTGAGCAAACAGCAAAATGTGGTCCAAAGCCGCCA----------TTGCG--------AAAG-GC----T----T--------TCTTGGGAGCCGCCGC--------CCCAT-CAATCGAAACTGCAGT-CGGTTACG----
droSec2	scaffold_1:2429395-2429580 +	dse_1835	ACG-TT----TACTTAGTA-GCAAGAATCACACGTTTTTGC--A------GACGGCAT--TTT--------------CTATTCGG----AAA-CCTGTATA-A----------AAGGTTTTGAGCTCCAGTTTGCTGTCGTGAGCAAACAGCAAAATGTGGTCCAAAGCCGCCA----------TTGCG--------AAAG-GC----T----T--------TCATGGGAGCCGCCGC--------CCCAT-CAATCGAAACTGCAGT-CGGTTACG----
dm3	chr2R:4791612-4791794 +	dme_379	ACG-TT----TACTTAGTA-CCAAGAATCACACGTTTTTGC--A------GACGGCAT--TTT--------------CTATTCGG----AAA-CCTATATA-A----------AAGGTTTTGAGCTCCAGTTTGCTGTCGTGAGCAAACAGCAAAATGTGGTCCAAAGCCGCCA----------TTGCG--------AAAG-GC----T----T--------TCATGGGAGCC---GC--------CCTAT-CAATCGAAACTGCAGT-CGGTTACG----
droEre2	scaffold_4929:17858137-17858312 -	der_75	GCG-TT----TACTTAGTA-CTAAGAATCACAGTTTTTGC--A------GAGGGCAT--TTT--------------CTTTT-GG----AA-CGTGTGTA-A----------AAGGCTTTGAGCTCCAGTTTGCTGTCGTGAGCAAACAGCAAAATGTGGTCCAAAGCCGCCA----------ATCGG--------ATAG-GT-G--A----C--------TTTGGGG-------GC--------CCCAA-TAATCGAAACTGCAGT-CGGTC-GG----
droYak3	2L:17449448-17449623 +	dya_1784	GTG-TT----TACTTATTA-CTAAGAATCACAGTTTTTGC--A------GACGACAT--TTT--------------CGTTT-GG----AA-CCTTTGTA-A----------AAGGTTTGAGCTCCAGTTTGCTGTCGTGAGCAAACAGCAAAATGTGAGTCCAAAGCCGACA----------ATTGG--------ACAG-GT-G--A----T--------TTTGGGG-------GC--------CCCAC-TTATCGAAACTGCAGT-CGGTT-AG----
droEug1	scf7180000409183:445681-445854 +		GAG-TG----C-------A-GTAAGAATCACAGTTTTTGA--A------GAGATCAT--TTTT--------------CTATTCTC----AAA-CTGTATA-C----------AAGGTTTTGAGCTTCAGTTTGCTGTCGTGAGCAAACAGCAAAATGCGGTCCAAAATGCGCT----------GTCGG--------AAAG-GT-G--A----T--------TTTTGGGCGT-----C--------ACCAT-AAATCTAAACTGCAGT-TGATTCGG----
droBia1	scf7180000302291:2735848-2736014 +		GAG-TG----C-------A-AAGAGAATCACAGTTTTTGC--A------GA--GCAT--TTT--------------CTATTGCA----AA-CATGTTTA-C----------AAGGTTTCGGACTACAGTTTGCTGTCGTGAGCAAACAGCAAAACGTTTTCCGAAGTCGCC----------TGCG--------AAAG-TT-A--A----C--------TTGAAGG-------GC--------ACCAC-AAATCGAAACTGCAGT-TGGTTTGG----
droTak1	scf7180000415386:451363-451535 -		AGAGTG----C-------A-ATAAGAATCACAGTTTTTGC--A------GAGAGCAT--TTT--------------CTTTTTAG----AA-CATGTTTA-C----------AAGGTTTTGACCACAGTTTGCTGTCGTGAGCAAACAGCAAAATGTTTCCAAATGGCCA----------ATTGG--------AAAG-TT-A--A----T--------TTTGAGG-----GGGC--------ACCAC-AAATCTAAACTGCAGT-TGGTT-TG----
droEle1	scf7180000490483:67747-67915 -		GAG-TG----T-------A-TTAAGAATCACAGTTTTTGC--A------GAGG-TATATTTT--------------CTTTTTCG----AAA-TATGTATA-C----------AAGGTTTTGACTACAGTTTGCTGTCGTGAGCAAACAGCAAAATGTGGCCCAAAACTGAA----------ATTCA--------AAAG-GT-T--A----T--------TATTGGG-------GC--------ACCAC-AAATCGAAACTGCAGT-TGGTT----
droRho1	scf7180000780108:150187-150354 +		GAG-AA----T-------A-CTAAGCATACACAGTTTTTC--A------GAGATTAT--TTATT--------------CTTTTTCA----AA-AATGTAGA-C----------AAGGTTCTGAACTATAGTTTGCTGTCGTGAGCAAACAGCAAAATGTGGCCCAGAATGGAA----------T-TTG--------AAAG-T-A--A----T--------TTTTGGG-------TC--------AAAAC-AAATCGAAACTGCAGT-TGGTT-TG----
droFic1	scf7180000453851:1506165-1506336 -		TAG-TG----T-------A-CTAAGAATCACAGTTTTTGC--A------GGGAGCAT--TTTT--------------CTTTTTTA----AAA-CGTGTAGA-A----------AAGGTTTTGAACTTCAGTTTGCTGTCGTGAGCAAACAGCAAAATGCGGCCCAAAACCGGCAA----------ATTCA--------AACA-GA-A--A----T--------TTTTGGG-------GC--------ACTAC-AAACCGAAACTGCAGT-TGGTT-TG----
droKik1	scf7180000302682:1354886-1355065 +		GAG-TGAGAAC-------T-CTAAGAATCACAGTTTTTAGACA------GAAGGTAT--TTC--------------CTTTTTCG----AA-CCTGTACA-C----------AAGGTTCTGGACTCCAGTTTGCTGTCGTGAGCAAACAGCAAAATGTGGCTCAGAGCCGACT----------TTCGG--------AAAACGT-A-TT----T--------TTTTGGG-------GG--------ACTAC-AAATCAAAACTGCAGT-TGGTTTGG----
droAna3	scf7180000396730:2224846-2225050 -	dan_4056	GAG-TT----TACT-----AAAAGAATCACAGTTTTTGC-CAAAAAAAAGAGCAT--TTTTTTTCTTG-TTTCGATTTTCGA----AAA-GTTCTGAA-A----------ATGGTTTTGACTTCAGTTTGCTGTCGTGAGCAAACAGCAAAATGTGGCCCAAAGCCGCCG----------A--TTCGG-----GCAAAC-GG-G--T----T--------T----------A--------ATTAC-AAATCAAAACTGCAGA-TGATT-TG----
droBip1	scf7180000396730:2224846-2225050 -		GAG-TT----TACT-----T-TAAGAATCACAGTTTTTGACAAA---AAAAACAT--TTTTTATGTTCGATTCGAAATTCGAAAAAAAA-GGTTCATA-C----------AAGGTTTTGAACTCCAATTTGCTGTCGTGAGCAAACAGCAAAATGTGGCCCAAAGCCGCCA----------TTCGG-----GCAAAG-GTTGACA----T--------TTTGGGT----GGGTA--------TTTCC-AAGTCAAAACTGCAGAACGAGT-TG----
dp5	3:13606079-13606257 -	dps_3844	AAA-TT----AAT------TTAAGAATCACAGTTTTTGA--A------GATG-GCT--TTT--------------GTTTTAAG----A-ACTTTGTCT----------GAGATTTTGAACACAGTTTGCTGTCGTGAGCAAACAGCAAAATGTGGCACAAAATGAACA----------TTCGG--------ATGG-AC----T----T-TAAGAATTTGAG---TTAGGGG--------CGTTC-AGATCAAAACTGCAGT-TGGTT-TA----
droPer2	scaffold_2:8013574-8013752 +		AAA-TT----AAT------TTAAGAATCACAGTTTTTGA--A------GATG-GCT--TTT--------------GTTTTAAG----A-ACTTTGTCT----------GAGATTTTGAACACAGTTTGCTGTCGTGAGCAAACAGCAAAATGTGGCACAAAATGAACA----------TTCGG--------ATGG-AC----T----T-TAAGAATTTGAG---TTAGGGG--------CGTTC-AGATCAAAACTGCAGT-TGGTT-TA----
droWil2	scf2_1100000004510:2696663-2696874 -	dwi_5429	ATTTAT----TGCTAGTAGAGAAAAACACACATTTTTTT-G------A-------T---TTTTTTTTTCAG----AAA-ATTCTCATAAAAATTGTTCTCTTTGTCAAATGTGGATTTGTATCAAATTTGCTGTCGTGAGCAAACAAAATTGTGACACAAAACCCTCG----------TTTTTTTTT