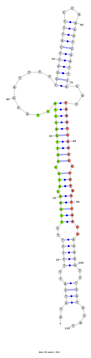
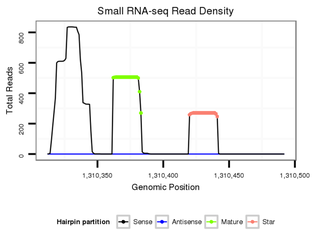
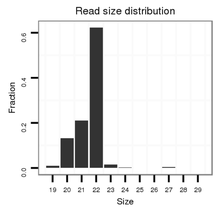
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_229	**scaffold_6308:1310362-1310442 +**	**confident-exception**	**Testes-restricted**	**3pUTR**	[View on UCSC Genome Browser [Cornell Mirror]]

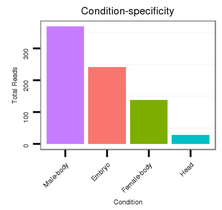
Legend: mature star mismatch in alignment mismatch in read

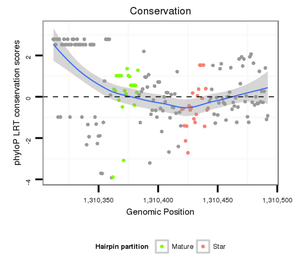
Predicted structure











Show Alternate Folds

Flybase annotation

tRNA [Dmo]tRNA:Gl25040-RA; utr3 [utr3_minus_6863]; utr5 [utr5_plus_8277]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

Read	# size	Mismatch	Hit Count	Total Norm	Total	V110 male body	M046 female body	M060 embryo	V056 head	V049 head	V041 embryo
ATCTTAAGGTCGTGAGTTCGAGCCTCACCCGGGGCATGTCATTTTTTTTCTTGAACATGCGGTTGATTTATTACGATTTTTGGATTCATTTCCAAAATGAATTCACATAAATCAACCCCATATTCAACCAAAAATTTGATGCATCATCAGACAAGAAAAATATAATAAAATGTGTCTACA											
********************************..((((..((((((..((((((.((((.((((((((((.....(((((((((((...)))))))))))...))))))))))..))))))..))))))....**********************************											
.....TCGAGCCTCACCCGGGGCADCA.....	22	3	6	355.50	2133	19	1185	887	19	19	4
.....TTGAACATGCGGTTGATTTATT.....	22	0	1	253.00	253	139	30	55	15	5	9
.....TAAATCAACCCCATATTCAACC.....	22	0	1	231.00	231	11	72	144	0	0	4
.....TTGAACATGCGGTTGATTTATT.....	23	1	1	168.00	168	161	5	0	1	1	0
.....TTGAACATGCGGTTGATTTAT.....	21	0	1	139.00	139	112	16	5	6	0	0
.....CGTGAGTTCGAGCCTCACCCGGGGCADCA.....	29	3	5	127.00	635	593	0	42	0	0	0
.....TTCGAGCCTCACCCGGGGCADCA.....	23	3	6	112.00	672	10	58	599	1	1	3
.....GTTCGAGCCTCACCCGGGG.....	19	0	5	101.80	509	258	178	8	34	27	4
.....GGTCGTGAGTTCGAGCCT.....	18	0	5	100.20	501	404	83	1	7	4	2
.....GTTCGAGCCTCACCCGGG.....	18	0	5	97.80	489	215	224	6	17	25	2
.....TTGAACATGCGGTTGATTTATT.....	22	1	1	92.00	92	90	1	1	0	0	0
.....TTGAACATGCGGTTGATTTA.....	20	0	1	90.00	90	88	0	0	0	2	0
.....GTTCGAGCCTCACCCGGGGCADCA.....	24	3	6	88.67	532	149	146	193	21	7	16
.....TGAGTTCGAGCCTCACCCGGGGCADCA.....	27	3	6	67.67	406	361	13	31	0	1	0
.....GGTCGTGAGTTCGAGCCTC.....	19	0	5	55.40	277	233	36	3	3	2	0
.....GGTCGTGAGTTCGAGCCTCA.....	20	0	5	51.00	255	209	33	2	5	4	2
...TTAAGGTCGTGAGTTCGAGCCTCA.....	24	0	5	49.80	249	223	19	0	5	2	0
.....GAGTTCGAGCCTCACCCGGGGCADCA.....	26	3	6	48.67	292	60	38	187	2	1	4
....TAAGGTCGTGAGTTCGAGCCTCA.....	23	0	5	46.20	231	199	26	0	3	3	0
.....CGAGCCTCACCCGGGGCADCA.....	21	3	7	41.57	291	0	158	128	2	3	0
.....GTGAGTTCGAGCCTCACCCGGGGCADCA.....	28	3	6	39.67	238	232	0	5	1	0	0
.....AAGGTCGTGAGTTCGAGCCTCACCCGGG.....	28	0	5	33.80	169	1	166	2	0	0	0
.....TCGTGAGTTCGAGCCTCACCCGGGGCADCA.....	30	3	5	29.80	149	149	0	0	0	0	0
.....GTGAGTTCGAGCCTCACCCGGGGCADCA.....	25	3	6	29.67	178	41	28	79	14	3	13
.....AAGGTCGTGAGTTCGAGCCTCA.....	22	0	5	26.80	134	102	20	1	7	3	1
.....AGGTCGTGAGTTCGAGCCTCACCCGGG.....	27	0	5	26.40	132	0	129	2	0	0	1
.....TTGAACATGCGGTTGATTTATCGC.....	23	2	1	24.00	24	22	0	0	0	2	0
.....AGGTCGTGAGTTCGAGCCTCA.....	21	0	5	21.80	109	84	15	3	2	4	1
.....TTGAACATGCGGTTGATTTATTCG.....	24	2	1	21.00	21	20	0	0	1	0	0
....TAAGGTCGTGAGTTCGAGCCT.....	21	0	5	18.00	90	60	28	0	2	0	0
.....AGGTCGTGAGTTCGAGCCT.....	19	0	5	17.40	87	49	34	0	0	2	2
.....TAAATCAACCCCATATTCAAC.....	21	0	1	16.00	16	2	4	9	0	0	1
.....GGTCGTGAGTTCGAGCCTCACCCGGGG.....	27	0	5	15.80	79	2	72	4	0	0	1
.....AAGGTCGTGAGTTCGAGCCT.....	20	0	5	15.80	79	46	29	0	2	2	0
.....TTGAACATGCGGTTGATTTA.....	21	1	1	15.00	15	15	0	0	0	0	0
....TAAGGTCGTGAGTTCGAGCCTC.....	22	0	5	13.40	67	50	15	1	1	0	0
...TTAAGGTCGTGAGTTCGAGC.....	20	0	5	11.80	59	50	7	1	1	0	0
...TTAAGGTCGTGAGTTCGAGCCT.....	22	0	5	11.40	57	36	18	0	1	2	0
....TAAGGTCGTGAGTTCGAGC.....	19	0	5	10.80	54	42	11	0	0	1	0
.....GAGCCTCACCCGGGGCADCA.....	20	3	9	10.11	91	0	40	50	1	0	0
.....GGTCGTGAGTTCGAGCCTCACCCGGG.....	26	0	5	8.80	44	0	43	1	0	0	0
.....TCGAGCCTCACCCGGGGCADC.....	21	2	5	8.60	43	0	9	34	0	0	0
.....AGGTCGTGAGTTCGAGCCTCACCCGGG.....	28	0	5	8.00	40	7	29	4	0	0	0
.....AGGTCGTGAGTTCGAGCC.....	18	0	5	7.80	39	32	6	0	1	0	0
.....AGGTCGTGAGTTCGAGCCTC.....	20	0	5	7.40	37	16	14	5	1	1	0
.....TTGAACATGCGGTTGATTTATA.....	22	1	1	7.00	7	6	1	0	0	0	0
.....TTGAACATGCGGTTGATTTATTA.....	23	0	1	7.00	7	5	0	0	0	0	2
.....TAAATCAACCCCATATTCAA.....	20	0	1	7.00	7	1	3	3	0	0	0
.....AGTTCGAGCCTCACCCGGG.....	19	0	5	6.20	31	4	21	0	2	3	1
.....TTGAACATGCGGTTGATTTATCG.....	24	2	1	6.00	6	5	1	0	0	0	0
.....TTGAACATGCGGTTGATTT.....	19	0	1	6.00	6	4	2	0	0	0	0
.....TAAATCAACCCCATATTCAACC.....	21	0	1	6.00	6	0	5	1	0	0	0
....TAAGGTCGTGAGTTCGAGCC.....	20	0	5	6.00	30	19	8	1	2	0	0
...TTAAGGTCGTGAGTTCGAGCCTC.....	18	0	5	5.80	29	25	4	0	0	0	0
.....GTTCGAGCCTCACCCGGGGC.....	23	0	5	5.60	28	17	8	0	3	0	0
.....AAGGTCGTGAGTTCGAGCCTC.....	20	0	5	5.40	27	1	16	2	2	5	1
.....AGTTCGAGCCTCACCCGGGCADC.....	21	0	5	5.40	27	13	11	1	2	0	0
.....TTGAACATGCGGTTGATT.....	24	2	5	5.40	27	0	0	25	1	0	1
.....TAAATCAACCCCATATTCAACCA.....	20	1	1	5.00	5	5	0	0	0	0	0
.....AGTTCGAGCCTCACCCGGG.....	23	0	1	5.00	5	0	1	3	0	0	1
.....AAGGTCGTGAGTTCGAGCC.....	20	0	5	5.00	25	6	15	0	1	2	1
...TTAAGGTCGTGAGTTCGAGCC.....	19	0	5	5.00	25	17	5	1	1	1	0
.....TAAATCAACCCCATATTCAACG.....	21	0	5	4.40	22	16	3	2	0	0	1
.....TTGAACATGCGGTTGATTTATTAG.....	22	1	1	4.00	4	2	2	0	0	0	0
.....TTGAACATGCGGTTGATTTATT.....	25	2	1	4.00	4	3	1	0	0	0	0
.....GTTCGAGCCTCACCCGGGGCADC.....	23	1	1	4.00	4	2	0	2	0	0	0
.....GAGCCTCACCCGGGGCADC.....	23	2	5	4.00	20	3	5	9	2	1	0
.....AGTTCGAGCCTCACCCGGG.....	19	2	6	3.67	22	0	0	22	0	0	0
.....TTCGAGCCTCACCCGGGGCADC.....	20	0	5	3.40	17	0	16	1	0	0	0
.....AGGTCGTGAGTTCGAGCCTCACCCGGGGC.....	22	2	5	3.40	17	0	4	13	0	0	0
.....TTGAACATGCGGTTGATTT.....	29	0	5	3.40	17	0	2	15	0	0	0
.....TTGAACATGCGGTTGATTTAATAGAT.....	20	1	1	3.00	3	3	0	0	0	0	0
.....TAAATCAACCCCATATTCAACC.....	20	0	1	3.00	3	0	1	2	0	0	0
.....TTGAACATGCGGTTGATTTATTAGGAT.....	27	0	1	3.00	3	3	0	0	0	0	0
.....TTGAACATGCGGTTGATTTATCGA.....	24	3	1	3.00	3	3	0	0	0	0	0
.....GTCGTGAGTTCGAGCCTC.....	18	0	5	3.00	15	4	10	0	0	0	1
.....GGTCGTGAGTTCGAGCCTCACCCGGGG.....	28	0	5	2.80	14	0	12	2	0	0	0
.....GAGTTCGAGCCTCACCCGGG.....	21	0	5	2.80	14	3	9	0	1	1	0
.....GTCGTGAGTTCGAGCCTCACCCGGGGCA.....	28	0	5	2.60	13	3	10	0	0	0	0
..CTTAAGGTCGTGAGTTCGAGCCT.....	23	0	5	2.40	12	4	6	0	1	1	0
.....TTCGAGCCTCACCCGGGG.....	18	0	5	2.20	11	0	11	0	0	0	0
.....ATCAACCCCATATTCAACC.....	19	0	1	2.00	2	0	0	2	0	0	0
.....TTGAACATGCGGTTGATTTATCGCG.....	25	3	1	2.00	2	2	0	0	0	0	0
.....TTGAACATGCGGTTGATTTATCG.....	24	2	1	2.00	2	2	0	0	0	0	0
.....TAAATCAACCCCATATTCAACG.....	22	1	1	2.00	2	1	0	1	0	0	0
.....TAAATCAACCCCATATTCAACCG.....	23	2	1	2.00	2	1	1	0	0	0	0
.....TGAACATGCGGTTGATTTATT.....	21	0	1	2.00	2	0	1	1	0	0	0
.....TTGAACATGCGGTTGATTTAG.....	24	1	1	2.00	2	1	0	1	0	0	0
.....TTGAACATGCGGTTGATTT.....	20	1	1	2.00	2	2	0	0	0	0	0
.....TAAATCAACCCCATATTCAACG.....	22	2	1	2.00	2	0	2	0	0	0	0
.....TTGAACATGCGGTTGATTTACG.....	23	2	1	2.00	2	2	0	0	0	0	0
.....TTGAACATGCGGTTGATTTATCG.....	23	2	1	2.00	2	1	1	0	0	0	0
.....TTGAACATGCGGTTGATTTATAC.....	24	0	1	2.00	2	2	0	0	0	0	0
.....GTCGTGAGTTCGAGCCTCACCCGGGG.....	26	0	5	2.00	10	1	9	0	0	0	0
.....AGGTCGTGAGTTCGAGCCTCACC.....	23	0	5	2.00	10	3	2	4	0	0	1
..CTTAAGGTCGTGAGTTCG.....	18	0	6	1.83	11	4	6	1	0	0	0
..CTTAAGGTCGTGAGTTCGAGCCTCA.....	25	0	5	1.80	9	5	4	0	0	0	0
.....AAGGTCGTGAGTTCGAGCCTCAC.....	23	0	5	1.80	9	1	8	0	0	0	0
.....GGTCGTGAGTTCGAGCCTCACC.....	22	0	5	1.80	9	0	3	5	0	0	1
.....AAGGTCGTGAGTTCGAGCCTCACC.....	24	0	5	1.80	9	1	3	3	0	0	2
.....GTCGTGAGTTCGAGCCTCA.....	19	0	5	1.80	9	6	3	0	0	0	0
.....TTCGAGCCTCACCCGGGGCADC.....	21	1	5	1.60	8	0	0	8	0	0	0
..CTTAAGGTCGTGAGTTCGAGC.....	21	0	5	1.60	8	6	2	0	0	0	0
.....CGAGCCTCACCCGGGGCADC.....	20	2	5	1.60	8	0	2	6	0	0	0
.....TAAATCAACCCCATATTCAACCG.....	22	2	2	1.50	3	0	2	1	0	0	0
.....GGTCGTGAGTTCGAGCCTCAC.....	21	0	5	1.40	7	0	4	4	0	1	2
.....AGTTCGAGCCTCACCCGG.....	18	0	5	1.40	7	0	4	0	0	3	0
.....TCGTGAGTTCGAGCCTCACCCGGGGCADC.....	28	1	5	1.20	6	2	1	3	0	0	0
.....TCGTGAGTTCGAGCCTCACCCGGGGCA.....	27	0	5	1.20	6	2	3	1	0	0	0
...TTAAGGTCGTGAGTTCGAGCCTCCAC.....	25	0	5	1.20	6	2	4	0	0	0	0
...TTAAGGTCGTGAGTTCGAGCCTCACCC.....	27	0	5	1.20	6	1	2	2	0	0	1
.....GTTCGAGCCTCACCCGGGCA.....	21	0	5	1.20	6	0	3	0	1	2	0
...TTAAGGTCGTGAGTTCGAGCCTCACC.....	26	0	5	1.20	6	4	2	0	0	0	0
...TTAAGGTCGTGAGTTCGA.....	18	0	6	1.17	7	5	1	0	1	0	0
.....TTAAATCAACCCCATATTCAAG.....	22	1	1	1.00	1	0	0	1	0	0	0
.....TTGAACATGCGGTTGATTTATTG.....	23	1	1	1.00	1	1	0	0	0	0	0
.....GAACATGCGGTTGATTTATTG.....	21	1	1	1.00	1	1	0	0	0	0	0
.....TTGAACATGCGGTTGATTTATTACGATT.....	28	0	1	1.00	1	1	0	0	0	0	0
.....GAACATGCGGTTGATTTATT.....	20	0	1	1.00	1	0	1	0	0	0	0
.....TTGAACATGCGGTTGATTTATCGATTT.....	29	0	1	1.00	1	1	0	0	0	0	0
.....TGAACATGCGGTTGATTTATG.....	22	1	1	1.00	1	0	1	0	0	0	0
.....TAAATCAACCCCATATTCAAC.....	20	0	1	1.00	1	0	1	0	0	0	0
.....TGAACATGCGGTTGATTTAT.....	20	0	1	1.00	1	0	1	0	0	0	0
.....TTGAACATGCGGTTGATTTATCG.....	24	2	1	1.00	1	1	0	0	0	0	0
.....TTGAACATGCGGTTGATTTACGA.....	23	2	1	1.00	1	1	0	0	0	0	0
.....TTCGAGCCTCACCCGGGCATGTCA.....	25	0	1	1.00	1	0	1	0	0	0	0
.....GTTCGAGCCTCACCCGGGG.....	21	0	5	1.00	5	1	3	1	0	0	0
.....TGAGTTCGAGCCTCACCCGGGG.....	22	0	5	1.00	5	3	2	0	0	0	0
.....TCGAGCCTCACCCGGGGCADC.....	20	1	5	1.00	5	0	0	5	0	0	0
.....AGGTCGTGAGTTCGAGCCTCAC.....	22	0	5	1.00	5	0	5	0	0	0	0
....TAAGGTCGTGAGTTCGAGCCTCCGGG.....	29	0	5	1.00	5	1	1	3	0	0	0
ATCTTAAGGTCGTGAGTTCGAGCCTCA.....	27	0	5	1.00	5	3	2	0	0	0	0
.....GTCGTGAGTTCGAGCCTCACCCGGGCA.....	29	1	5	1.00	5	0	0	5	0	0	0
.....TGAGTTCGAGCCTCACCCGGGGCADC.....	26	2	5	1.00	5	2	0	3	0	0	0
.....GTCGTGAGTTCGAGCCTCACCCGGG.....	25	0	5	1.00	5	0	5	0	0	0	0
.....GAGTTCGAGCCTCACCCGGGCA.....	23	0	5	0.80	4	2	1	1	0	0	0
.....GTCGTGAGTTCGAGCCTCACC.....	22	0	5	0.80	4	0	1	3	0	0	0
...TTAAGGTCGTGAGTTCGAG.....	19	0	5	0.80	4	3	1	0	0	0	0
.....AAGGTCGTGAGTTCGAGCCTCACCCGGG.....	29	0	5	0.80	4	0	0	4	0	0	0
.....GTGAGTTCGAGCCTCACCCGGGG.....	23	0	5	0.80	4	0	2	2	0	0	0
.....GTTCGAGCCTCACCCGGGGCADC.....	22	1	5	0.80	4	0	0	4	0	0	0
...TAAGGTCGTGAGTTCGAG.....	18	0	5	0.80	4	4	0	0	0	0	0
.....GAGTTCGAGCCTCACCCGG.....	19	0	5	0.80	4	0	4	0	0	0	0
.....CGTGAGTTCGAGCCTCACCCGGGGCADC.....	27	1	5	0.80	4	2	0	1	0	1	0
ATCTTAAGGTCGTGAGTTC.....	19	0	6	0.67	4	1	2	1	0	0	0
.....GTCGTGAGTTCGAGCCTCAC.....	20	0	5	0.60	3	1	2	0	0	0	0
.....GGTCGTGAGTTCGAGCCTCACCC.....	23	0	5	0.60	3	0	0	3	0	0	0
.....TTCGAGCCTCACCCGGGC.....	19	0	5	0.60	3	0	3	0	0	0	0
.....TTCGAGCCTCACCCGGGCA.....	20	0	5	0.60	3	0	2	1	0	0	0
.....CGTGAGTTCGAGCCTCACCCGGGGCA.....	26	0	5	0.60	3	3	0	0	0	0	0

Anti-sense strand reads

Read	# size	Mismatch	Hit Count	Total Norm	Total	V110 male body	M046 female body
TAGAATTCCAGCACTCAAGCTCGGAGTGGGCCCGTACAGTAAAAAAACAGACTTGTACGCCAACTAAATAATGCTAAAAACCTAAGTAAAGTTTTACTTAAGTGTAATTTAGTTGGGGTATAAGTTGGTTTTTAAACTACGTAGTAGTCTGTCTTTTTATATATTTTACACAGATGT							
********************************..((((..((((((..((((((.((((.((((((((((.....((((((((((...)))))))))))...))))))))))..))))))..))))))....**********************************							

Show Alignment With Reads

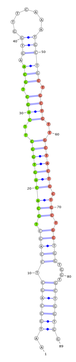
Re-alignment of all predicted orthologs

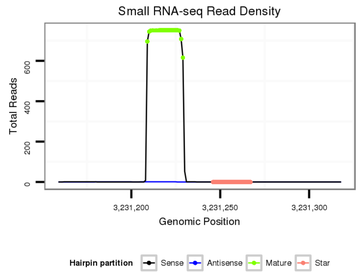
Species	Coordinate	ID	Alignment
			ATCTTAAGGTCGTGAGTTCGAGCCTCACCCGGGGCATG-TCA--TTT-TTT--TTC---TG----------AACATGCG----------G---TTGATTTATAC---------------------------GA-TTTTTGGAT--TCA--------TTT--CCAAAATGAATTCACATAAATC----------AC----------CCCATATTCAAC-----AAAAATTTG---ATGCATC-ATCAG--ACAA--GAAAAA----TATAATAA--AATGT---------------------------------------GTCTACA
droMoj3	scaffold_6308:1310312-1310492, +	dmo_229	
droVir3	scaffold_12875:4779185-4779364, -		ATCTG-GGGTCGTGTTCGAGCCTCACGTTGGGGCAAA-GTTGGGCAAAATTTTTTTT

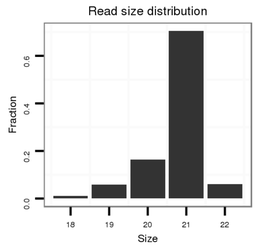
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_172	**scaffold_6680:3231209-3231268 +**	**confident-exception**	**Canonical miRNA**	**CDS**	[View on UCSC Genome Browser [Cornell Mirror]]

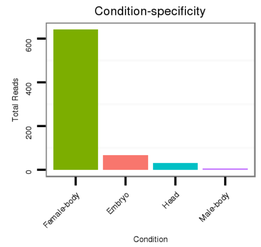
Legend: mature star mismatch in alignment mismatch in read

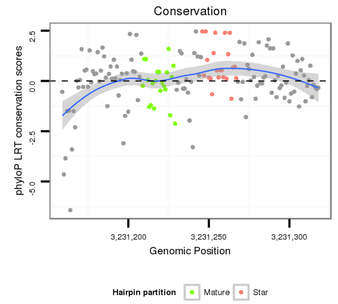
Predicted structure











Show Alternate Folds

Flybase annotation

CDS [Dmo]GH12833-cds]

Repeatable elements

Name	Class	Family	Strand
(CTG)n	Simple_repeat	Simple_repeat	+

mature **star**

1. scaffold_6473:4964872-4964893 +
2. scaffold_6473:6139966-6139987 -
3. scaffold_6496:6074006-6074027 +
4. scaffold_6496:18088249-18088270 +
5. scaffold_6500:23204575-23204596 +
6. scaffold_6500:26393251-26393272 +
7. scaffold_6540:10404872-10404893 -
8. scaffold_6540:31096861-31096882 -
9. scaffold_6540:32330780-32330801 +
10. scaffold_6680:1455058-1455079 -
11. dmo_172 scaffold_6680:3231246-3231267 +
12. scaffold_6680:9257922-9257943 +
13. scaffold_6680:19514561-19514582 -

Sense Strand Reads

hide 3p reads show mid mismatch reads

```
TTAGCTCCTATGCCATACTACAGAATCTACAGGATAATGCCAGCTCCAGCTGCACAGTGGCTTCAGCTGCAAGTGGTTCAAATGCTGCTGCTGTTGCTACTGCTGGTGGTGGTGCTGGTGGTGCTGCAGTGGCACCGCCCTTGCCGCCACGCAAATC
*********************************..(((((((.(((((.((((((((((..(((((.(((..(((.(((.......)))))))..)))))..))))))).))).))))))....)))))))..*********************************
```

Read size	# Mismatch	Hit Count	Total Norm	Total	M046 female body	M060 male body	V110 embryo	V056 male body	V049 head	V041 head	V041 embryo
21	0	1	520.00	520	457	41	2	8	6	6	
20	0	1	85.00	85	57	12	2	8	5	1	
22	0	1	45.00	45	39	2	1	2	0	1	
19	0	1	36.00	36	32	3	1	0	0	0	
20	0	1	35.00	35	35	0	0	0	0	0	
18	0	1	6.00	6	6	0	0	0	0	0	
21	1	1	5.00	5	0	1	0	0	3	1	
21	1	1	5.00	5	2	0	0	2	0	1	
21	0	1	4.00	4	4	0	0	0	0	0	
22	1	1	4.00	4	3	0	0	1	0	0	
19	0	1	4.00	4	4	0	0	0	0	0	
22	0	1	4.00	4	4	0	0	0	0	0	
19	0	1	3.00	3	2	1	0	0	0	0	
21	0	1	3.00	3	2	1	0	0	0	0	
22	1	1	3.00	3	1	0	0	0	2	0	
23	1	1	2.00	2	2	0	0	0	0	0	
20	1	1	2.00	2	0	0	0	2	0	0	
18	0	1	2.00	2	1	0	0	1	0	0	
20	0	1	2.00	2	1	1	0	0	0	0	
22	1	1	2.00	2	1	1	0	0	0	0	
19	0	1	1.00	1	0	1	0	0	0	0	
21	0	1	1.00	1	1	0	0	0	0	0	
23	1	1	1.00	1	1	0	0	0	0	0	
20	1	1	1.00	1	0	0	1	0	0	0	
18	0	1	1.00	1	1	0	0	0	0	0	
23	0	1	1.00	1	1	0	0	0	0	0	
24	2	1	1.00	1	0	0	0	1	0	0	
23	2	1	1.00	1	0	0	0	1	0	0	
23	2	1	1.00	1	0	0	0	0	0	0	
22	0	13	0.92	12	2	10	0	0	0	0	
20	2	3	0.33	1	1	0	0	0	0	0	
25	0	4	0.25	1	0	0	0	0	0	1	
21	0	18	0.17	3	3	0	0	0	0	0	
19	0	20	0.05	1	1	0	0	0	0	0	
20	0	20	0.05	1	1	0	0	0	0	0	

Anti-sense strand reads

```
AATCGAGGATACGGTATGATGTCTTAGATGTCCTATTACGGTCGAGGTCGACGTGTCACCGAAGTCGACGTTCACCAAGTTTACGACGACGACAACGATGACGACGACGACGACACCACGACCACCACGACGTCACCGTGGCGGGAACGGCGGTGCGTTTAG
*********************************..(((((((.(((((.((((((((((..((((.(((.(((.....)))))).))))..)))))))).))).))))))....)))))))..*********************************
```

Read size	# Mismatch	Hit Count	Total Norm	Total	M046 female body	V110 male body	M060 embryo	V049 head	V056 head	V041 embryo
21	0	1	1.00	1	1	0	0	0	0	0
21	0	1	1.00	1	1	0	0	0	0	0
22	0	20	0.55	11	1	0	8	1	0	1
20	0	2	0.50	1	0	1	0	0	0	0
21	0	20	0.15	3	1	0	0	2	0	0
23	0	19	0.11	2	1	1	0	0	0	0
19	0	20	0.05	1	0	0	0	0	1	0

Show Alignment With Reads

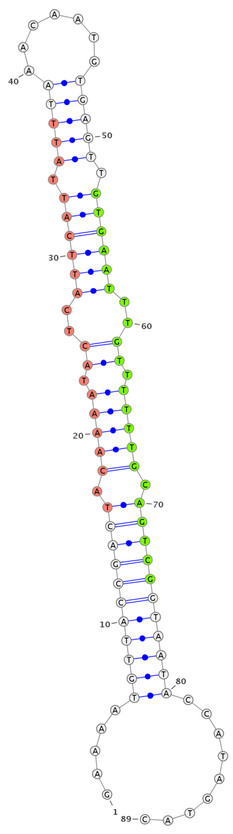
Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6680:3231159-3231318 +	dmo_172	TTAGCTCCTA-TG------CCATA----------CTACAGAATCTACAGGATAATGCCA----------GCTCCAGCTGCACAGTGGCTTC----------AGCTG---CA----------AGTGGT----------TCAAATGCTGCTGCTGT---TGCTACTGCTGCTGCTGGTGGTGCTGGT-----G----------GT--------GCTGCAGTGGCA---CCGC------CCT----------TGC----------CGCCACGCAAATC
droVir3	scaffold_13049:4839411-4839549 +		-AGCTCCTA-TG------CCATA----------CTACAGAATCTCAGGATCCGCCA----------GCTCCAGCTTTTTTTGAA---C----------AGGAA---C----------------------G-AGCAGAGAGAA---C---AGCAGTGCGAGAGAGCAGC------T----------AGC--------AGGA------GCT-GCTGCGTGGGCA---CCGC------CGC----------TGC----------CGCCCGCAAATC
droGri2	scaffold_15110:10089876-10090023 +		-AGCTCCTA-TG------CCATA----------CTACAGAATCTACAGGAT------GGCAGCATCGGGGCCAGC---A-CGACTCCTTTCCAATTTC-----------ATGC-----TCAG-CAGGTCACTGCTGTGGCTGGC-CGC---TGGCGCAGCGC----------T----------T-----TTGCAGTACGC---CCAC------CGC----------TGC----------CGCCACGCAAATC
droWil2	scaf2_11000000045111:9717916-9718055 -		-GCTGCTTT--TT-------CGT--G--------T-------GCAG-T----------A--ATGAT---T-----------GGC---TGCTGCTTTGCTACC----------GCTG---C-----------T-----T-----------GCTGCTAATGCTGCTGCTTT---TGCTAGCGCTGC----------CTT-CTGCTAATGCTTT-----AGC-----GC--TTGCTA----TTT-----AGC-----GGCCACCAA----------TGC----------CGCAATGGAATT
dp5	XR_group6:8997502-8997646 -		TTGTGTT--T--------CCT-------CGT--G--------T-------GCTG-T----------G--TTGCT---T-----------GGC---TTG---C----------GTTGCGCCGCTGCT-GCTGCTGCTGGTGC----------TTG-----CGCTGCTGTGTGGT---TGCT-CTGCTGTGGTGGTGGTGC-TGC-----T----------AGC-----GCT-GCTGCTTTGCGC---CGC-----TGG----------TGC----------CGCCACG-----CCCC
droPer2	scaffold_2:4852908-4853054 +		GCGGCTCCGA-TT-------CATT-T-------CCATGGAGTCCTCCGG---CAG--------T-------GCCA-T----------G--CAGCA---T-----------GC---TGCCGCCTGCTGCTGCTGTTGCT----------CTGCTG-----CT--GGTGATGCTGTGCTGG---TGCTGCTGCTGC----------TTGTGCTGGTGCTGC-----TGCT-----GC--TT---T-------CCC-----GTGCT----------CCC----------CCC----------CCCCCCCCCC
droAna3	scaffold_13266:7205495-7205667 +		CCGG-GGTTA-GA-------GC-TT-----------------------CTGAGATCGCTAGTCTCTAGTCTCT----------GC-----TGCAGTTGCTTGC---TCCGAGTGTTGTTGC----------CTT--T-TGCTGCTGATGTTGCTG-----TT--T-TGCTGCTGCTGC---CGC-CGCGAGTGGTGGTGCTGCTGC----------TTT-CTGCTAGT---TTTGA-----TGC-----GA-T----------CCC--CTGC-----TGC----------TGC----------CGCCACGC-CGCC
droBip1	scf7180000396589:2415596-2415737 +		CAG-A-AGTCA-TG------TT-L-----CTACTCCACACAATGCTTGTC---CAG--------T-------CACA----------ACAC-CATTATGC----------GC-----TAG-T--CAAGTGGAATGGCAAA---TCGTCGCTGCTGGTGCTG-A-T----------T--GGTT---CTGGA-----TCG-----TT-T----------CCC-----GC----------AGCTGGTGGAGTT----------CGCG-T-----G
droKik1	scf7180000302264:270642-270800 -		A-CCTCTTT--TT-------CCCT-------------------------T--TAG--------T-------GCAGAT----------T--ATGAT---T-GC----------TGC--TGATC----------CAGCCCCCCCC

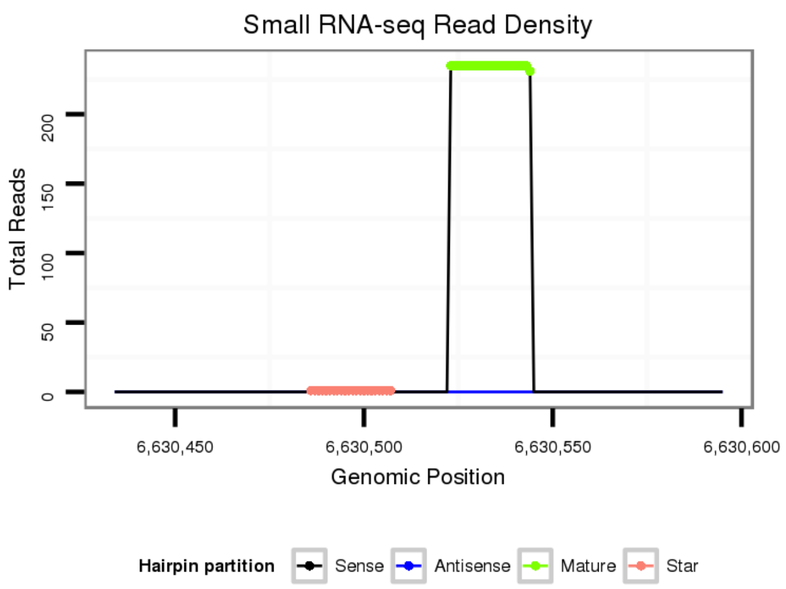
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_77	**scaffold_6540:6630484-6630545 +**	**candidate**	**Testes-restricted**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

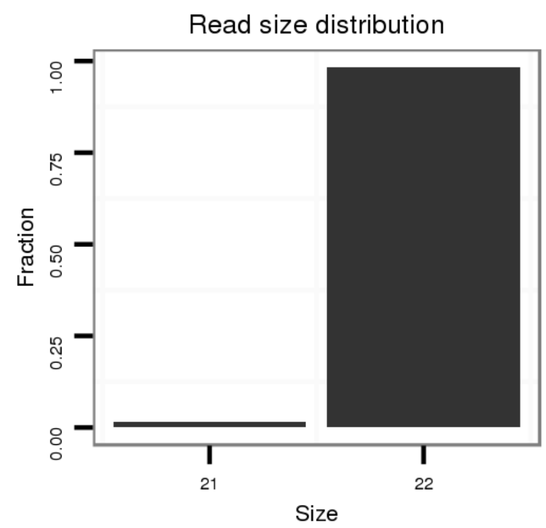
Legend: mature star **mismatch in alignment** mismatch in read

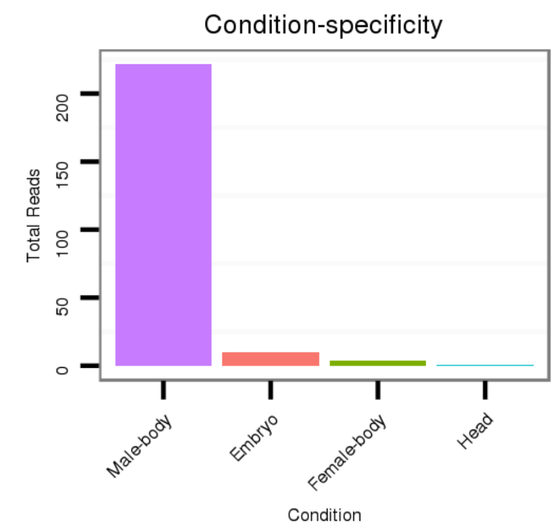
Predicted structure



dmo_77_annot [-77.7]







No conservation details.

Hairpin partition — Sense — Antisense — Mature — Star

Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TATACATATATGTATATATACACCATTTGGCTCATTGGAAAATGTTACCGACTACAAAATACTCATTCATTATTTAAACAATGTGAGTTGTGAATTTGTTTTTTGCAGTCGGTAATACCATAGTACAACGCTCTTAATTGTTTTTGTTTGGATTTTATGTAT **********.....(((((((((((.(((((.((..((((((.(((((.....)))))).)))))).))).)))))).))))))))))).....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V110 male body	M060 embryo	M046 female body	V041 embryo	V056 head
.....GTGAATTTGTTTTTTGCAGTCG.....	22	0	1	231.00	231	217	5	3	5	1
.....GTGAATTTGTTTTTTGCAGTC.....	21	0	1	4.00	4	4	0	0	0	0
.....GTGAATTTGTTTTTTGCAGTCT.....	22	1	1	2.00	2	2	0	0	0	0
.....GTGAATTTGTTTTTTGCAGTCGT.....	23	1	1	1.00	1	1	0	0	0	0
.....TACAAAATACTCATTCATTATT.....	22	0	1	1.00	1	0	0	1	0	0
.....ACTACAAAATACTCATTCATTA.....	22	0	2	0.50	1	1	0	0	0	0

Anti-sense strand reads

ATATGTATATACATATATATGTGGTAAACCGAGTAACCTTTTACAATGGCTGATGTTTTATGAGTAAGTAATAAATTTGTTACACTCAACACTTAAACAAAAAACGTCAGCCATTATGGTATCATGTTGCGAGAATTAACAAAAACAAACCTAAAATACATA **********.....(((((((((((.(((((.((..((((((.(((((.....)))))).)))))).))).)))))).))))))))))).....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V110 male body	M046 female body

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6540:6630434-6630595 +	dmo_77	TATACATATATGTATATATACACCATTTGGCTCATTGGAAAATGTTACCGACTACAAAATACTCATTCATTATTTAAACAATGTGAGTTGTGAATTTGTTTTTTGCAGTCGGTAATACCATAGTACAACGCTCTTAATTGTTTTTGTTTGGATTTTATGTAT

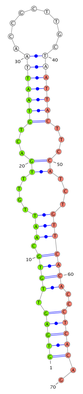
Generated: 06/03/2015 at 08:06 PM

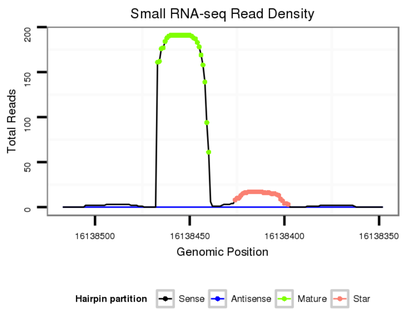
	PASS/FAIL
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

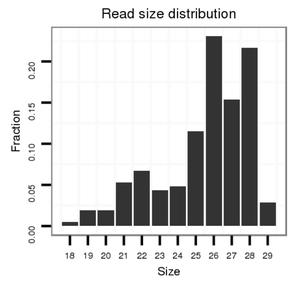
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_1572	**scaffold_6500:16138398-16138467 -**	**candidate**	**Mirtron**	**intron**	[View on UCSC Genome Browser [Cornell Mirror]]

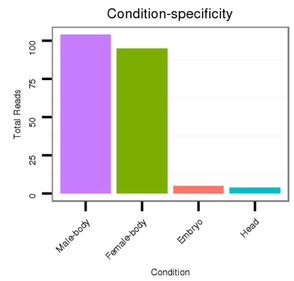
Legend: mature star mismatch in alignment mismatch in read

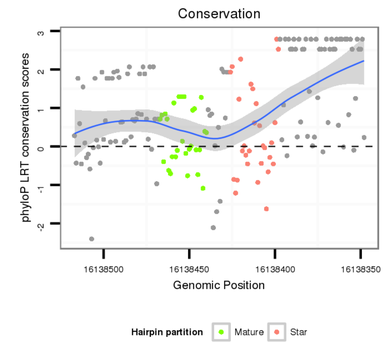
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [DmojGI10257-in]; CDS [DmojGI10257-cds]; CDS [DmojGI10257-cds]

No Repeatable elements found

Sense Strand Reads

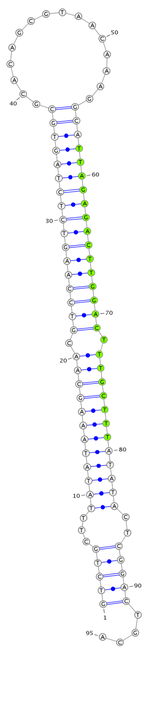
hide 3p reads show mid mismatch reads

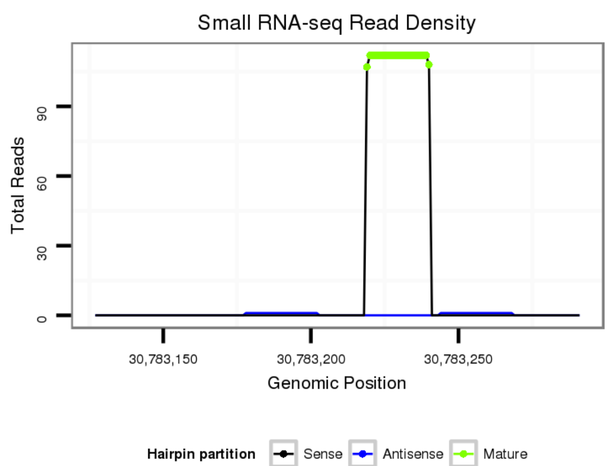
```
                                                
```

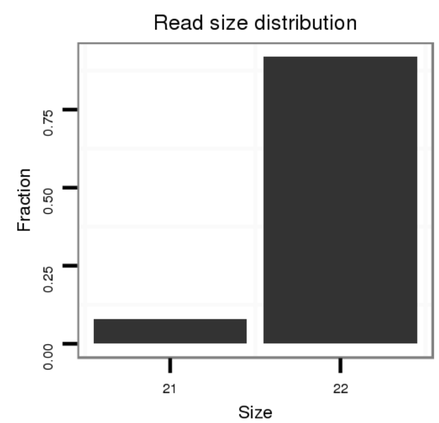
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_174	**scaffold_6500:30783177-30783241 +**	**candidate**	**Canonical miRNA**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

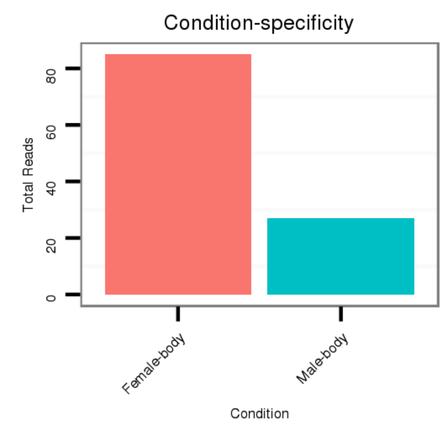
Legend: mature star mismatch in alignment mismatch in read

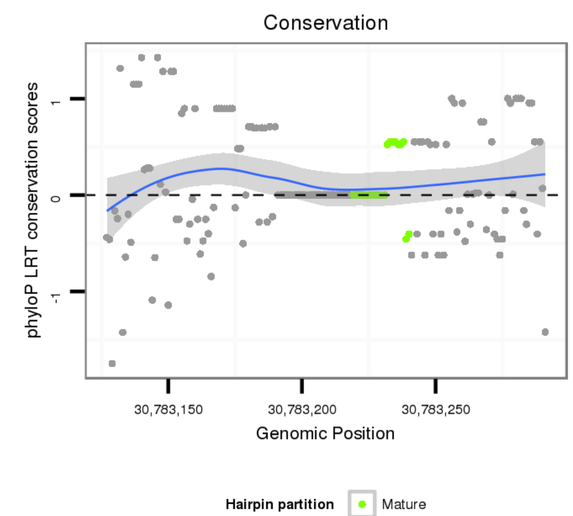
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [DmojGI18277-in]

Repeatable elements

Name	Class	Family	Strand
Helitron1_Dmoj	RC	Helitron	+

Sense Strand Reads

hide 3p reads show mid mismatch reads

AAAGATCCTGTTTTCCCAATTTTAATGGCATCATGGTCTGCTTTATATAAAGCAACGTCCAAGTCTCTAGTGCGCACAGCGTAACAAAGGCATTAGAGACTTGGACTTTGCTTTATATACTCGGACTGCACAGCGTTTGGGCTGTGAATGAGTATTCTGCAATCG **********(((((...((((((((((.((((((((((((((((.....))))))))))))))))).))))))))))..)))))....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M046 female body	V110 male body	M060 embryo
.....TTAGAGACTTGGACTTTGCTTT.....	22	0	1	103.00	103	80	23	0
.....TAGAGACTTGGACTTTGCTTT.....	21	0	1	5.00	5	5	0	0
.....TTAGAGACTTGGACTTTGCTT.....	21	0	1	4.00	4	0	4	0
.....TTAGAGACTTGGACTTTGCTTTT.....	23	1	1	2.00	2	1	1	0
.....TGGGCTGTGAATGAGTATTCTGCAAT..	26	0	20	0.05	1	0	0	1

Anti-sense strand reads

TTTCTAGGACAAAAGGGTTAAAATTACCGTAGTACCAGACGAAATATATTTCGTTGCAGGTTCAGAGATCACGCGTGTCGCATTGTTTCCGTAATCTCTGAACCTGAAACGAAATATATGAGCCTGACGTGTCGCAAACCCGACACTTACTCATAAGACGTTAGC **********(((((...((((((((((.((((((((((((((((.....))))))))))))))))).))))))))))..)))))....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M046 female body
.....CGTTGCAGGTTCAGAGATCACGCGT.....	25	0	1	1.00	1	1
.....ATGAGCCTGACGTGTCGCAAACCCG.....	25	0	1	1.00	1	1

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6500:30783127-30783291 +	dmo_174	AAAGATCCTGTTTTCCCAATTTTAATGGCATCATGGTCTGCTTTATATAAAGCAACGTCCAAGTCTCTAGTGCGCACAGCGTAACAAAGGCATTAGAGACTTGGACTTTGCTTTATATACTCGGACTGCACAGCGTTTGGGCTGTGAATGAGTATTCTGCAATCG
droVir3	scaffold_12970:4777915-4777968 +		AAAGATGTTGTTTTGTTTTTTTCCATAACAATATATATCTCTTTATATAAAA----------CA
droGri2	scaffold_15203:2989942-2990003 +		CCTGTT----------CTTTGCTACCTGTAATCAGCTGGTACTACTTATGG----TATCAAAGTATTTCGCAGTCG
droWil2	scf2_1100000004516:1391966-1392018 -		GTTT---------TTTTGATTTTGATGGCATTTTGTTCTAATTTATATC----AACGACGTAAT----------TT
droRho1	scf7180000773789:1394-1414 +		AATTATGTGCTTTTGTTAAT----------T
droTak1	scf7180000415845:203461-203493 +		GACTG----------CACAGCGAAAAAGCG------GAGAATTCTGG---TG
droSec2	scaffold_168:4674-4677 +		ATC----------A
droYak3	2R:1290141-1290167 -		AAGCATAGTTTTTTGTTTGTGTTTAT----------G

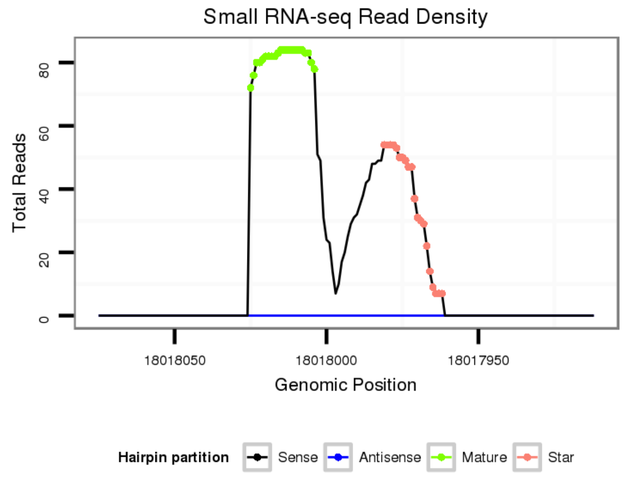
Generated: 09/08/2015 at 07:49 PM

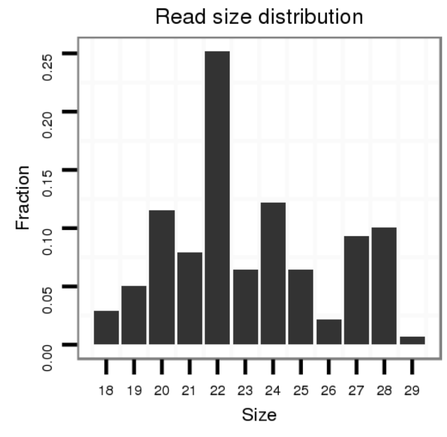
	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

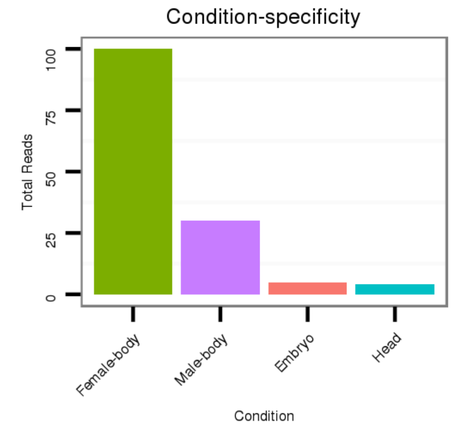
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_125	**scaffold_6540:18017962-18018025 -**	**confident-exception**	**Mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

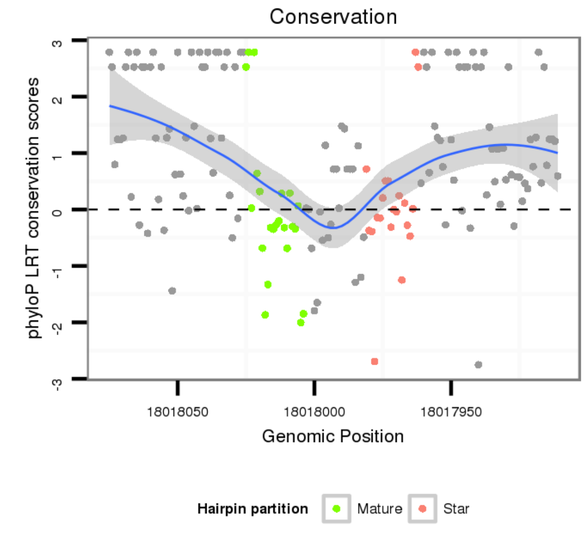
Legend: mature star mismatch in alignment mismatch in read

Predicted structure









Show Alternate Folds

Flybase annnotation

intron [Dmoj\GI22811-in]; CDS [Dmoj\GI22811-cds]; CDS [Dmoj\GI22811-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

AGTGCCGATGAGCCAGACTCGGAGCTGCCCAACTGCACCAAGCACACCAAGTAAGTTTGTCAGTTGCTTAGCATATTTAACTTTGTTAATGTACTTTGCATGGCATTCTTACAGAAGCAACAGCTCCACGCCCACGCACAGCGCCTCCTCATCCAGCAACAATG	Read size	# Mismatch	Hit Count	Total Norm	Total	M046 female body	V110 male body	M060 embryo	V041 embryo	V049 head	V056 head
**********(((((..(((((..(((..((.(((((.(((...)))))))).))..)))))))..)))))..**********											
.....GTAAGTTTGTCAGTTGCTTAGC.....	22	0	1	25.00	25	12	12	0	1	0	0
.....GTAAGTTTGTCAGTTGCTTAGCAT.....	24	0	1	14.00	14	4	9	1	0	0	0
.....GTAAGTTTGTCAGTTGCTTAGCATATTT.....	28	0	1	11.00	11	9	2	0	0	0	0
.....GTAAGTTTGTCAGTTGCTTAGCATATT.....	27	0	1	8.00	8	7	0	1	0	0	0
.....GTAAGTTTGTCAGTTGCTTAGCATA.....	25	0	1	6.00	6	4	2	0	0	0	0
.....TTTGCATGGCATTCTTACAG.....	20	0	1	5.00	5	2	1	0	0	2	0
.....CTTTGCATGGCATTCTTACAGT.....	22	1	1	3.00	3	2	0	1	0	0	0
.....CTTTGTTAATGTACTTTGCATGGCATTC.....	28	0	1	3.00	3	3	0	0	0	0	0
.....TTGTTAATGTACTTTGCATGGC.....	22	0	1	3.00	3	3	0	0	0	0	0
.....TTTGCATGGCATTCTTACAGT.....	21	1	1	2.00	2	0	0	0	1	0	1
.....TGTTAATGTACTTTGCATGGC.....	21	0	1	2.00	2	2	0	0	0	0	0
.....TAAGTTTGTCAGTTGCTTA.....	19	0	1	2.00	2	2	0	0	0	0	0
.....GTACTTTGCATGGCATTCTT.....	20	0	1	2.00	2	2	0	0	0	0	0
.....GTAAGTTTGTCAGTTGCTTAG.....	21	0	1	2.00	2	2	0	0	0	0	0
.....GTAAGTTTGTCAGTTGCTTA.....	20	0	1	2.00	2	0	1	0	1	0	0
.....TTTGTTAATGTACTTTGCATGGC.....	23	0	1	2.00	2	2	0	0	0	0	0
.....AAGTTTGTCAGTTGCTTAGCAT.....	22	0	1	2.00	2	0	2	0	0	0	0
.....GTAAGTTTGTCAGTTGCTTAGCA.....	23	0	1	2.00	2	0	0	0	0	1	1
.....AACTTTGTTAATGTACTTTGCATGGCA.....	27	0	1	2.00	2	2	0	0	0	0	0
.....ATGTACTTTGCATGGCATTCT.....	21	0	1	2.00	2	2	0	0	0	0	0
.....ATGTACTTTGCATGGCATTCTT.....	22	0	1	2.00	2	2	0	0	0	0	0
.....CTTTGTTAATGTACTTTGC.....	19	0	1	2.00	2	2	0	0	0	0	0
.....TAATGTACTTTGCATGGC.....	18	0	1	1.00	1	1	0	0	0	0	0
.....GTACTTTGCATGGCATTCTTACAGT.....	25	1	1	1.00	1	1	0	0	0	0	0
.....TTGTTAATGTACTTTGCATGGCATTCT.....	27	0	1	1.00	1	1	0	0	0	0	0
.....GTACTTTGCATGGCATTC.....	18	0	1	1.00	1	1	0	0	0	0	0
.....TCAGTTGCTTAGCATATTTA.....	20	0	1	1.00	1	1	0	0	0	0	0
.....CAGTTGCTTAGCATATTTAA.....	20	0	1	1.00	1	1	0	0	0	0	0
.....AAGTTTGTCAGTTGCTTAGC.....	20	0	1	1.00	1	1	0	0	0	0	0
.....GCATATTTAACTTTGTTAATGTA.....	23	0	1	1.00	1	0	0	1	0	0	0
.....TAATGTACTTTGCATGGCATT.....	21	0	1	1.00	1	1	0	0	0	0	0
.....AACTTTGTTAATGTACTTTGCATG.....	24	0	1	1.00	1	1	0	0	0	0	0
.....TTGCATGGCATTCTTACAGT.....	20	1	1	1.00	1	1	0	0	0	0	0
.....GTACTTTGCATGGCATTCT.....	19	0	1	1.00	1	1	0	0	0	0	0
.....CTTTGCATGGCATTCTTACAGTTT.....	24	3	1	1.00	1	0	0	1	0	0	0
.....AATGTACTTTGCATGGCATTC.....	21	0	1	1.00	1	1	0	0	0	0	0
.....TAATGTACTTTGCATGGCATTC.....	22	0	1	1.00	1	1	0	0	0	0	0
.....TAAGTTTGTCAGTTGCTTAGC.....	21	0	1	1.00	1	1	0	0	0	0	0
.....TGTTAATGTACTTTGCATGGCA.....	22	0	1	1.00	1	1	0	0	0	0	0
.....ACTTTGTTAATGTACTTTGCATGGCA.....	26	0	1	1.00	1	1	0	0	0	0	0
.....ACTTTGCATGGCATTCTTA.....	19	0	1	1.00	1	1	0	0	0	0	0
.....TTTGTCAGTTGCTTAGCATA.....	20	0	1	1.00	1	1	0	0	0	0	0
.....TTGTTAATGTACTTTGCATGGCA.....	23	0	1	1.00	1	1	0	0	0	0	0
.....GTTTGTCAGTTGCTTAGCAT.....	20	0	1	1.00	1	0	1	0	0	0	0
.....AAGTTTGTCAGTTGCTTAGCATATT.....	25	0	1	1.00	1	1	0	0	0	0	0
.....TTAATGTACTTTGCATGGCATTCT.....	24	0	1	1.00	1	1	0	0	0	0	0
.....ACTTTGTTAATGTACTTTG.....	19	0	1	1.00	1	1	0	0	0	0	0
.....TTTGTTAATGTACTTTGC.....	18	0	1	1.00	1	1	0	0	0	0	0
.....GTAAGTTTGTCAGTTGCTTAGCATAT.....	26	0	1	1.00	1	1	0	0	0	0	0
.....TGTACTTTGCATGGCATTCT.....	20	0	1	1.00	1	1	0	0	0	0	0
.....AATGTACTTTGCATGGCATTCT.....	22	0	1	1.00	1	1	0	0	0	0	0
.....ACTTTGTTAATGTACTTTGCATGGCAT.....	27	0	1	1.00	1	1	0	0	0	0	0
.....CTTTGTTAATGTACTTTGCATGGCA.....	25	0	1	1.00	1	1	0	0	0	0	0
.....ACTTTGTTAATGTACTTTGCATG.....	23	0	1	1.00	1	1	0	0	0	0	0
.....TAAGTTTGTCAGTTGCTTAGCAT.....	23	0	1	1.00	1	1	0	0	0	0	0
.....GTACTTTGCATGGCATTCTTACAG.....	24	0	1	1.00	1	1	0	0	0	0	0
.....CTTTGCATGGCATTCTTACAG.....	21	0	1	1.00	1	1	0	0	0	0	0
.....AACTTTGTTAATGTACTTTGCATGGC.....	26	0	1	1.00	1	1	0	0	0	0	0
.....CTTTGTTAATGTACTTTGCAT.....	21	0	1	1.00	1	1	0	0	0	0	0
.....GTTAATGTACTTTGCATGGC.....	20	0	1	1.00	1	1	0	0	0	0	0
.....AATGTACTTTGCATGGCATTCTT.....	23	0	1	1.00	1	1	0	0	0	0	0
.....TACTTTGCATGGCATTCTTACAGT.....	24	1	1	1.00	1	0	0	0	0	0	1
.....ACTTTGCATGGCATTCTTACAGT.....	23	1	1	1.00	1	0	0	1	0	0	0
.....GTAAGTTTGTCAGTTGCT.....	18	0	1	1.00	1	1	0	0	0	0	0
.....TGTTAATGTACTTTGCATGGCATTC.....	25	0	1	1.00	1	1	0	0	0	0	0
.....CTTTGTTAATGTACTTTGCATGGCATTCT.....	29	0	1	1.00	1	1	0	0	0	0	0
.....GTTAATGTACTTTGCATGGCATTCTTA.....	27	0	1	1.00	1	1	0	0	0	0	0

Anti-sense strand reads

TCACGGCTACTCGGTCTGAGCCTCGACGGGTTGACGTGGTTCGTGTGGTTCATTCAAACAGTCAACGAATCGTATAAATTGAAACAATTACATGAAACGTACCGTAAGAATGTCTTCGTTGTCGAGGTGCGGGTGCGTGTCGCGGAGGAGTAGGTCGTTGTTAC	Read size	# Mismatch	Hit Count	Total Norm	Total	V110 male body	M046 female body
**********(((((..(((((..(((..((.(((((.(((...)))))))).))..)))))))..)))))..**********							

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6540:18017911-18018075 -	dmo_125	AGTGCCGATGAGCCAGACTCGGAGCTGCCCAACTGCACCAAGCACACCAAGTAAGTTTGT-C------A--------GTT-GCTTAGCATA----TT---------TAA---CTTTGTTAATGTACTTT---------GCATGG-CATTCTTACAGAAGCAACAGCTCCACGCCCACGCACAGCGCCTCCTCA------TC---CAGCAACAATGC----------
droVir3	scaffold_13047:14577154-14577326 -		AGTGCCGATGAGCCGGACTGTGAGCTGTCTAACTGCACCAAGCACACAAAGTAAGTCTTACA------G--------ATT-TTAAGAAT-A----TT---------TCA---AATTATGAATCTGATCT---------ATGTGG-T-CTTTTACAGAAGCAACAACTCCACGCCTACGCATAGCGCCTCCTCAAGCAGCAACAAAAACAACAATGG----------
droGri2	scaffold_14830:5397995-5398170 +		AGTGCCGATGAGCCGGATAGTGATCTGCCCAACTGCACCAAACATACAAAGTAAGTTTCTT------G--------ACT-GCAGAATA-TCAATAC---------T--CAAATTATTAATATCCTTT---------AACCCC-CCCTCTCAGAAGTAACAGTTCCACGCCAACTCACAGCGCCTCCTCAAGAAACAATACCAACAGCAATGC----------
droWil2	scf2_1100000004921:3076626-3076785 +		AGTGCTGAAGATCCGAGGCAGAGCTATCCAATTGCAGTAAGCACACAAAGTAAGTAGCAGAATAGAAA--------GTA-ACTTAAGA-G-ATTCT---------A--TA----GTT---------ATG---TGTAC-ATTT------TATAGAAGCAACCAATGGACTCCTACACAATATGTCACCCC------TCGGC-CACAGCA--TC----------
dp5	2:9443626-9443778 +		AGTGCCGAGGAGCCAGAGAGTGACTTGCCCAACTGCACCAAGCATGCCAAGTAAGTGACATC------CCATCCACATTTAT---------CACAC-------AATA----TTT---------AATAATA-ACTAA---------TTGCAGAAGCAACCAGTCCACGCCCACTCACAGCAGCGCCTCC------------GCAGCGGCGC----------
droPer2	scaffold_0:3251516-3251665 +		AGTACCGAGGAGCCAGAGAGTGACTTGCCCAACTGCACCAAGCATGCCAAGTAAGTGACATC------CCATCCACATTTAT---------CACAC-------AATA----TTT---------AAT---A-ACTAA---------TTGCAGAAGCAACCAGTCCACGCCCACTCACAGCAGCGCCTCC------------GCAGCGGCGC----------
droAna3	scaffold_13340:17687896-17688054 +	dan_3147	AGTGCCGAGGAACCGACTGTAACTTGCCCAATTGCACCAAGCACTCAAAGTAAGTCGGC-C------A--------TTTAT---------TATTCAAAGCTATAAATA----TTT---------AAT---T-TCCCAATTTT-TCGCCTCAGGAGCAACCAGTCCACGCCCACCCACTCGTGCC------TCGAACAACAACAATGT----------
droBip1	scf7180000396721:240254-240412 -		AGTGCCGAGGAACCGACTGCAGCTTGCCCAATTGCACCAAGCAGTCAAAGTAAGCCAGC-C------A--------TTTAT---------TATTCAAAGCCTTCAATA----TTT---------AAT---T-TCCCATTTTT-CCGCCTCAGGAGCAACCAGTCCACGCCGACCCAGTGCGC------TCGAACAACAACAATGT----------
droKik1	scf7180000302706:851603-851767 -		AGCGGCCGAGGAGCCGGACAGCGAGTTGTCCAACTGCACCAAGCACACCAAGTAAGCCCAATC------G--------ATA-GCCCAATT-GTAGTCA---------CTAATA----ATT---------AAT---G-AACCACTTT---CCAAATCAGAAGCAATCAGTCAACGCCCACGCATAGCGCCTCCATC------GCAAACAACAACAATGC----------
droFic1	scf7180000454096:646700-646879 +		AGTGCCGAGGAGCCGGACAGCGAACTTCCAAATTGCAGTAAGCACACCAAGTGAGTCATACC------A--------ATT-ACCTGTGT-TTATTGC---------CTAATA----ATT---CT----TTT---T-TTATGTTT-T-CCAAATTAGAAGCAACCAATCCACGCCCACTCACAGCGTCTCCACC------TCAAACAACAACAATGCAAGCGTTCCCTC
droEle1	scf7180000491104:24736-24894 +		AGCGCCGAGGAACCGACACCGATTTGCCCAACTGCACCAAGCACTCCAAGTGATACAAGCC------A--------ATT---TACGT-GTACTTC---------TCAACG----ATT---------AAT---T-TGTTATTT-A-CCCATCTAGGAGCAACCAGTCCACGCCCACTCACAGTGTCTCCT--------CCAAAAACAACAATGC----------
droRho1	scf7180000772921:7590-7754 +		AGTGCCGAGGAACCAGAGAGCGATTTGGTGATCTGCACCAAGCACGCCAAGTAATTCGAGAG------A--------ATCAA--TACGT-GTATTCA---------TTAACG----ATT---------TAT---T-TTTTTTTT-T-CCAAACTAGGAGCAGCAGTCCACTCCCACCCACAGCGTCCTCC------TCGAACAACAACCATGC----------
droBia1	scf7180000302402:6114746-6114910 +		AGTGCCGAGGAACCGACACCGACTTGCCCAACTGCACCAAGCACACCAAGTGAGTTGAACT------A--------ACC-ACTATCAT-GTGTGCT---------TTAATG----ATT---------CAA---T-ATATATTT---CCCCTTTAGGAGCAACCAGTCCACTCCCACTCACAGCGTCTCGTCC------TCGAACAACAACAATGC----------
droTak1	scf7180000415711:346632-346794 -		AGTGCCGAGGAGCCGGACAGCGATTTGCCCAACTGCACCAAGCACTCAAAGTGAGTTTGACC------C--------TCA-ACTTTTGT-GTATTAT---------TATT----ACT---------CAT---A-ATATATTT---CCCCATTAGGAGCAACCAGTCCACGCCCAGTCACAGCGTTTCGAGC------TCGAACAACAACAATGC----------
droEug1	scf7180000409760:1053178-1053342 -		AGTGCCGAGGAGCCGGACACTGAATTGCCCAACTGCACCAAGCACTCCAAGTAAGTGACATA------A--------ATA-ACTTATTC-GAATTTT---------TTAATA----ATT---------AAT---T-TTCTTTTT---TCCAACAAGGAGCAACCAATCCACGCCTACCCACAGCGTCTCCACC------TCAAACAATAACAATGC----------
dm3	chr3R:17348705-17348863 +		AGTGCCGACGATCCGGACACCGATTTGCCCAATTGCACCAAGCACACCAAGTGAGTTTATAC------A--------ACA-GGTTA-----TGTTCC---------TTAGTA----ATT---------CAT---T-TAT-ATTT----TTAACCAGGAGCAACCAGTCCACGCCCACCCACAGCGTCTCCACC------TCCAACAACAACAATGC----------
droSim2	3r:3962205-3962365 -		AGTGCCGACGATCCGGACACCGATTTGCCCAATTGCACCAAGCACACCAAGTGATTTTATAC------A--------ACA-GCTTATTT-TTGGTCA---------TT--TA----ATT---------CAT---T-TAC-ATTT----TTAACCAGGAGCAACCAGTCCACGCCCACACACAGCGTCTCCACC------TCCAACAACAACAATGC----------
droSec2	scaffold_6:4140988-4141148 -		AGTGCCGACGATCCGGACACCGATTTGCCCAATTGCACCAAGCACACCAAGTGAGTTTATAC------A--------ACA-GCTTATGT-TTGGTCA---------T--TA----ATT---------CAT---T-TAT-ATTT----TTAACCAGGAGCAACCAGTCCACGCCCACACATAGCGTCTCCACC------TCCAACAACAACAATGC----------
droYak3	3R:6178740-6178902 +		AGTGCCGACGAGCCGGACACCGATTTGCCCAATTGCAGCAAGCATACCAAGTAAGTTTATAC------A--------ATA-GCTTACGT-GTGTTCC---------CTAGTA----ATT---------CAT---T-TAT-GTTT----CTAACTAGGAGCAACCAGTCCACACCCACGCACAGCGTCTCCACC------TCCAACAACAACAATGC----------
droEre2	scaffold_4770:4317302-4317464 -		AGTGCCGACGAGCCGGACACCGATTTGCCAAATTGCACCAAGCACACCAAGTGAGTTTATAC------A--------ATA-GCTTAGGT-TTGTTCC---------TTAGTA----ATT---------CAC---T-TAT-ATTT----CTAACTAGGAGTAACCAGTCCACGCCCACGCACAGCGTCTCCACT------TCCAACAACAACAATGC----------

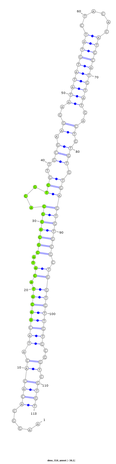
Generated: 09/08/2015 at 07:03 PM

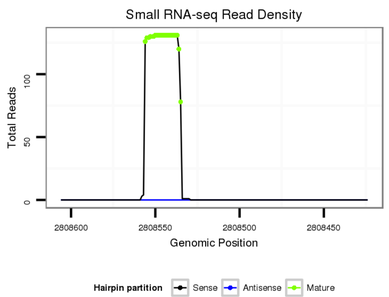
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	0
crit.uri	1
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

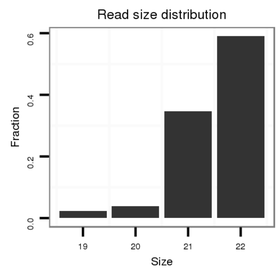
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_316	**scaffold_6328:2808474-2808556 -**	**candidate**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser [Cornell Mirror]]

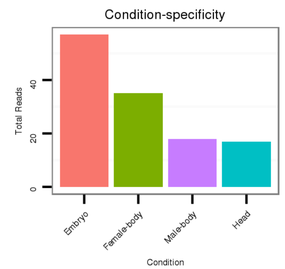
Legend: mature star mismatch in alignment mismatch in read

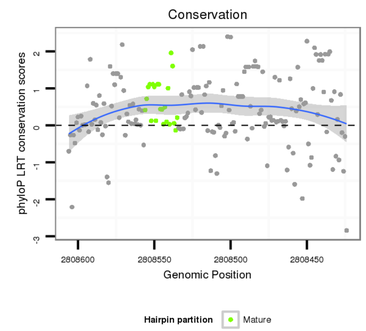
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

```
GAGACGTCGCGTTCATGCAAAGTAGTTGAAAAAAGAAGGCACACACATACAACATACATACGCACGCACGTCGTTGCGAAGGAATATATGTATCTACACATGCATGTATGACTGTGTGTGAGTGTGCGCTGGTGTTGTGCGGTCGTGTGTGCGTGTGTGTGTGTGCGTGCGTTAGCTAC
********************************.....((((((.(((((((.(((.(((((((...(((..(((..((..((((((((((.....)))))))))))..)).)))..)))))))))))..))))))))))..)).))))********************************
```

Read size	# Mismatch	Hit Count	Total Norm	Total	M060 embryo	M046 female body	V110 male body	V049 head	V041 embryo	V056 head
22	0	1	75.00	75	43	18	4	0	4	6
21	0	1	42.00	42	7	10	13	7	3	2
20	0	1	5.00	5	0	2	1	2	0	0
23	1	1	3.00	3	2	1	0	0	0	0
22	0	1	3.00	3	3	0	0	0	0	0
23	1	1	3.00	3	1	2	0	0	0	0
19	0	1	2.00	2	0	2	0	0	0	0
23	1	1	2.00	2	0	1	0	0	1	0
21	1	1	1.00	1	0	0	0	0	1	0
21	0	1	1.00	1	1	0	0	0	0	0
19	0	1	1.00	1	0	1	0	0	0	0
21	0	1	1.00	1	0	1	0	0	0	0
22	1	1	1.00	1	0	0	0	1	0	0
21	0	1	1.00	1	0	1	0	0	0	0
21	1	1	1.00	1	0	0	0	0	1	0
21	1	2	1.00	2	2	0	0	0	0	0

Anti-sense strand reads

```
CTCTGCAGCGCAAGTACGTTTCATCAACTTTTTTCTTCCGTGTGTGTATGTTGTATGTATGCGTGCGTGCAGCAACGCTTCCTTATATACATAGATGTGTACGTACATACTGACACACACTCACACGCGACCACAACACGCCAGCACACACGCACACACACACACACGCACGCAATCGATG
********************************.....((((((.(((((((.((..(((((((...(((..(((..((..((((((((((.....)))))))))))..)).)))..)))))))))))..))))))))))..)).))))********************************
```

Read size	# Mismatch	Hit Count	Total Norm	Total	M060 embryo
21	0	2	0.50	1	1

Show Alignment With Reads

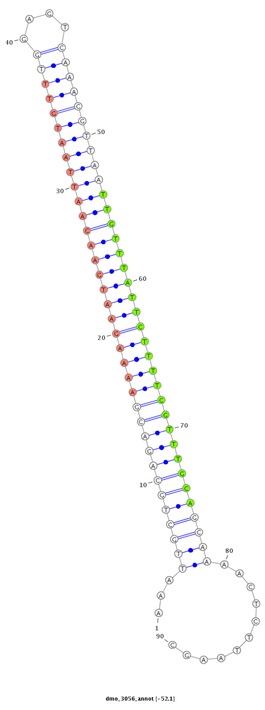
Re-alignment of all predicted orthologs

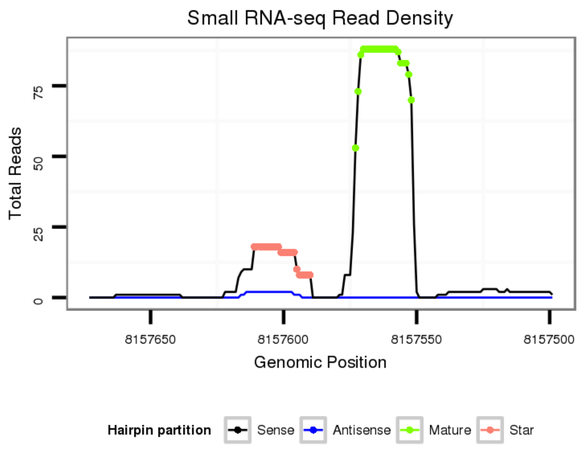
Species	Coordinate	ID	Alignment
droMoj3	scaffold_6328:2808424-2808616 -	dmo_316	GAG-------A---CGTCGCGTTCATGCAAAGTAGTTGAAAAAAG----------AAGGCACACACATACA----A-------CATACATACGCACGC---ACG----------TCGTT--GCGAAGGAATATATGTATCTACACATGCATGTATGACTGTGTGTGAGTGTGCGCT-GGT----------GTTGTGCGGT----------CGTGTGTGC-----G----------TG--TGTGTG--TGTGTGTGCGTGCGTTAG----------CTAC
droVir3	scaffold_13042:809853-810023 -		GAG-------A---CGTCGCGTTCATGCAAAGTAGTTGAAAAAAG----------AAGGCACACACATACA----A-------CATACATACGCACGC---ACG----------TCGTT--GCGAAGGAATATATGTATCTACACATGCATGTGAATGA--GTATGAGTGTGCGCT-G--G----------GTGTGTGCG----------GCC---G----------TG--TGTGTG--TGTGTGTGCGTGCGTTAG----------CTAC
droGri2	scaffold_15081:1201130-1201347 -		GAG-------A---CGTCGCGTCATGCAAAGTAGCAAAAAAG----------AAGGCACACACATAG-GACATCTTACATGCATACATACGCACGC---ACG----------TCGTT--GCGAAGGAATATATGTATCTACATATGCATATGCAT----GTATGAGTGTCGCT-ATGT----------GTTTGTGCGGTTGTATGTGCGTGTGTGTGTGTGCTT----------A---GT-T--G----------G--TGCTTG--TGTGTGTGCGTGCGTTAG----------CTAC
droWil2	scaffold_11000000004954:4849449-4849627 -		GAA-------A---AAAAAATTCACAAT----TTGAAAAAAG-CAAACACTCAAGGCAAAATGGCGGCAAGGCGAATGCATGCGC---TG----G-------G-------AGCT-TTTA----------ATGGCTTCTATATG--CGTGAGGATGATGTGTGTGTGTGTGTGTGTGT----------GT--G----------GTGTGTGTGT----------G-------T----------G----------TG--TGTGTG--TGTGTGTGTGTGTGTGTGT

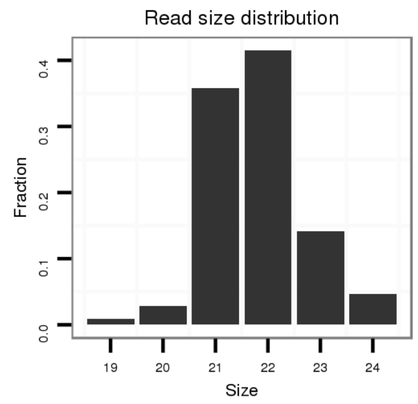
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_3056	**scaffold_6496:8157549-8157623 -**	**candidate**	**Canonical miRNA**	**CDS**	[View on UCSC Genome Browser {Cornell Mirror}]

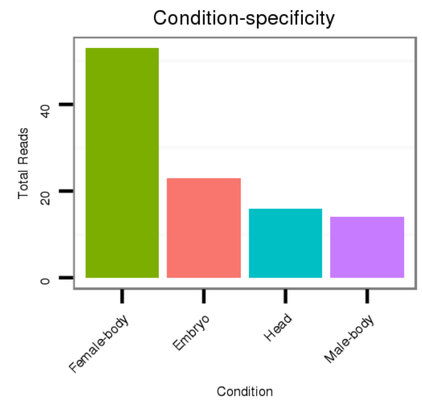
Legend: mature star mismatch in alignment mismatch in read

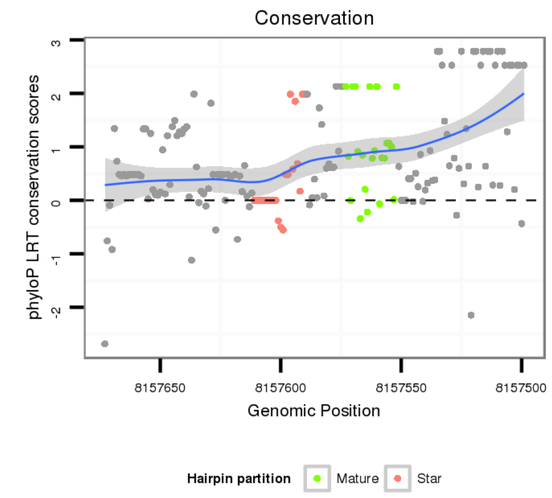
Predicted structure











Show Alternate Folds

Flybase annnotation

CDS [Dmoj\GI19305-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

GCACACACACATAAACAAACTATGCGCACACACACATAAACAAACAAAAATTGCTGCAGACGAAAAGAATGAACAATTAATGTTTGGAGTCAAACGTTAATTGTTTATTCTTTTCGTTTGCAGCAAAACTCTTAAGCTATGATTGGAGAACCCTATCAAATCGAGACGCGCCGGC	Read size	# Mismatch	Hit Count	Total Norm	Total	M046 female body	M060 embryo	V110 male body	V056 head	V049 head	V041 embryo
**********...((((((((((((((((((((((((((((((((((((....))))))))))))))))))))))))))))))))))))).....**********											
.....TTGTTTATTCTTTTCGTTTGCA.....	22	0	1	19.00	19	14	1	1	1	1	1
.....TGTTTATTCTTTTCGTTTGCA.....	21	0	1	16.00	16	11	0	2	1	2	0
.....GTTTATTCTTTTCGTTTGCAG.....	21	0	1	10.00	10	5	0	3	1	1	0
.....GTTTATTCTTTTCGTTTGCAGT.....	22	1	1	9.00	9	3	2	4	0	0	0
.....TTGTTTATTCTTTTCGTTTGCAG.....	23	0	1	9.00	9	4	1	1	2	0	1
.....AAAAGAATGAACAATTAATGTT.....	22	0	1	8.00	8	0	7	0	0	0	1
.....ATTGTTTATTCTTTTCGTTTGCA.....	23	0	1	6.00	6	3	1	0	2	0	0
.....ATTGTTTATTCTTTTCGTTTGC.....	22	0	1	6.00	6	3	0	2	1	0	0
.....CAGACGAAAAGAATGAACAATT.....	22	0	1	5.00	5	1	2	0	0	1	1
.....TTTATTCTTTTCGTTTGCAGT.....	21	1	2	4.50	9	2	0	6	1	0	0
.....TTAATTGTTTATTCTTTTCGT.....	21	0	1	4.00	4	0	1	3	0	0	0
.....TGTTTATTCTTTTCGTTTGCAG.....	22	0	1	3.00	3	1	1	1	0	0	0
.....TTAATTGTTTATTCTTTTCGTTTG.....	24	0	1	3.00	3	1	1	0	0	1	0
.....AAAAGAATGAACAATTAATGTG.....	22	1	1	2.00	2	0	2	0	0	0	0
.....TTGTTTATTCTTTTCGTTTGC.....	21	0	1	2.00	2	1	1	0	0	0	0
.....ATTGTTTATTCTTTTCGTTTGCAG.....	24	0	1	2.00	2	1	1	0	0	0	0
.....GTTTATTCTTTTCGTTTGCA.....	20	0	1	2.00	2	2	0	0	0	0	0
.....TGCTGCAGACGAAAAGAATGA.....	21	0	1	2.00	2	1	0	0	1	0	0
.....TTGTTTATTCTTTTCGTTTGCT.....	22	1	2	1.50	3	3	0	0	0	0	0
.....TTTATTCTTTTCGTTTGCAGC.....	21	0	1	1.00	1	0	1	0	0	0	0
.....ATAAACAAACTATGCGCACACACAC.....	25	0	1	1.00	1	1	0	0	0	0	0
.....TGTTTATTCTTTTCGTTTGC.....	20	0	1	1.00	1	1	0	0	0	0	0
.....GTTTATTCTTTTCGTTTGCAGC.....	22	0	1	1.00	1	1	0	0	0	0	0
.....TTGTTTATTCTTTTCGTTTGCAGT.....	24	1	1	1.00	1	0	1	0	0	0	0
.....CGTTAATTGTTTATTCTTTTCG.....	22	0	1	1.00	1	1	0	0	0	0	0
.....GACGAAAAGAATGAACAATTA.....	21	0	1	1.00	1	0	0	0	0	0	1
.....GCTATGATTGGAGAACCCT.....	19	0	1	1.00	1	0	1	0	0	0	0
.....ATTGTTTATTCTTTTCGTTTG.....	21	0	1	1.00	1	1	0	0	0	0	0
.....AACCCTATCAAATCGAGACGCGCCGG.	26	0	1	1.00	1	0	0	1	0	0	0
.....AAATCGAGACGCGCCGGC	18	0	1	1.00	1	1	0	0	0	0	0
.....TTGTTTATTCTTTTCGTTTGCAA.....	23	1	1	1.00	1	1	0	0	0	0	0
.....TTAAGCTATGATTGGAGAACCCTATCA.....	27	0	1	1.00	1	0	0	0	0	0	1
.....TTTATTCTTTTCGTTTGCA.....	19	0	1	1.00	1	1	0	0	0	0	0
.....AGACGAAAAGAATGAACAATTA.....	22	0	1	1.00	1	0	0	1	0	0	0
.....AGACGAAAAGAATGAACAATT.....	21	0	1	1.00	1	0	0	0	1	0	0
.....TTATTCTTTTCGTTTGCAGA.....	20	1	1	1.00	1	0	0	0	1	0	0

Anti-sense strand reads

CGTGTGTGTGTATTTGTTTGATACGCGTGTGTGTGTATTTGTTTGTTTTTAACGACGTCTGCTTTTCTTACTTGTTAATTACAAACCTCAGTTTGCAATTAACAAATAAGAAAAGCAAACGTCGTTTTGAGAATTCGATACTAACCTCTTGGGATAGTTTAGCTCTGCGCGGCCGG	Read size	# Mismatch	Hit Count	Total Norm	Total	M046 female body	V110 male body	V041 embryo
**********...((((((((((((((((((((((((((((((((((((....))))))))))))))))))))))))))))))))))))).....**********								
.....TGCTTTTCTTACTTGTTAATT.....	21	0	1	1.00	1	1	0	0
.....TCTGCTTTTCTTACTTGTTA.....	20	0	1	1.00	1	0	1	0

Show Alignment With Reads

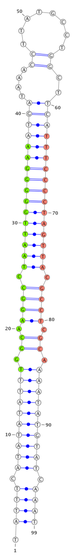
Re-alignment of all predicted orthologs

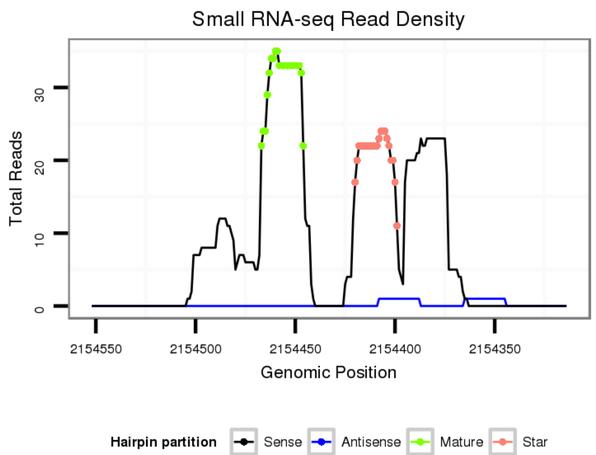
Species	Coordinate	ID	Alignment
droMoj3	scaffold_6496:8157499-8157673 -	dmo_3056	GCACACACACATAAACAAACTATG----------CGCACACACA--C------ATAAACAAACAAAAATTGCTGCAGACGAAAAGAATGAACAATTAATGTTTG----GAGT----------CAAACGTTAATTGTTTATTCTTT-----TCGTTTGCAGCAAAAC--T----------CTTAAGCTATGATTGGAGAACCCTATCAAATCGAGACGCGCCGGC
droVir3	scaffold_12875:15642436-15642606 +		CAGA-CACACATAAACAAACGTA----------GACACACACAC------ACACATAGACATAAA-TGCTTCAGGCA---------TTTATT--TATTTC--CCCCCT----AC-------AACCATTAATTGTTTATTCTTT-----TCGTTTGCAG------TTAAACTTTTTA------AGCAGGCCATGAGCGACCAACTATACCAGATAGAGACGCGCCGGC
droGri2	scaffold_15245:12444642-12444716 +		G----------TTTTTT

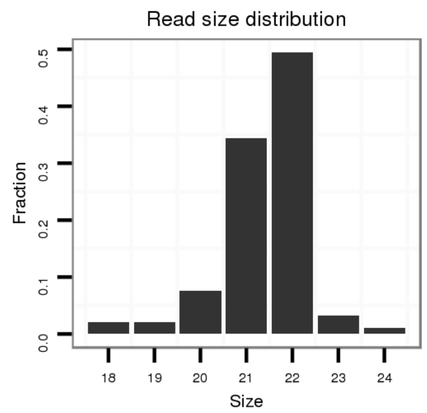
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_2709	**scaffold_6482:2154364-2154502 -**	**candidate**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

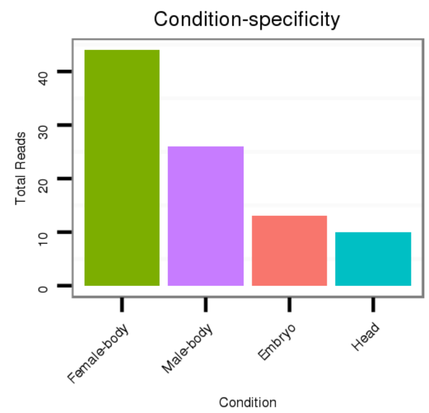
Legend: mature star mismatch in alignment mismatch in read

Predicted structure









No conservation details.

Show Alternate Folds

Flybase annotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

GAGACGATCGAGATATTTAGCATAAGTGCTATTAGAGATTAGTTGAAGTCAGTTGACTACTTTGTGTGCGTATTTCATATATATTTGGCAAGGCCTAATTGGGGGAAATGATAAACCTTATGCCTGGCTTCATTTCCCCTAGTTACGCCTCGCAAAATATGTATCAAATGCGCACAGGAAGTAGTTAACTCCTTCTAGGTCTAGGCTAGGAATAGTCAAAGGGCCAAGTAAAACGTGGC	Read size	# Mismatch	Hit Count	Total Norm	Total	M046 female body	V110 male body	M060 embryo	V056 head	V049 head	V041 embryo
**********.((((.((((((((((.((.((((.((((((((((((((((....((.....)).)))))))))))))))).)))).)).)))))))))).))))**********											
.....TATGTATCAAATGCGCACAGGA.....	22	0	1	11.00	11	2	5	0	2	0	2
.....TGGCAAGGCCTAATTGGGGGAA.....	22	0	1	9.00	9	6	1	1	1	0	0
.....TGGCAAGGCCTAATTGGGGGA.....	21	0	1	7.00	7	0	4	1	1	1	0
.....TTTCCCCTAGTTACGCCTCGCA.....	22	0	1	5.00	5	3	0	1	0	1	0
.....ATTTCCCCTAGTTACGCCTCGC.....	22	0	1	5.00	5	2	0	3	0	0	0
.....CAAGGCCTAATTGGGGGAAATG.....	22	0	1	4.00	4	4	0	0	0	0	0
.....TATGTATCAAATGCGCACAGG.....	21	0	1	4.00	4	3	1	0	0	0	0
.....GTTGACTACTTTGTGTGCGTA.....	21	0	1	4.00	4	2	2	0	0	0	0
.....ATTTCCCCTAGTTACGCCTCG.....	21	0	1	3.00	3	1	2	0	0	0	0
.....ATGTATCAAATGCGCACAGGA.....	21	0	1	2.00	2	2	0	0	0	0	0
.....AAGGCCTAATTGGGGGAAATG.....	21	0	1	2.00	2	0	1	0	1	0	0
.....GTGTGCGTATTTCATATATATT.....	22	0	1	2.00	2	2	0	0	0	0	0
.....TTGGCAAGGCCTAATTGGGGGA.....	22	0	1	2.00	2	0	2	0	0	0	0
.....AAATGCGCACAGGAAGTAGTT.....	21	0	1	2.00	2	0	1	0	1	0	0
.....TTCCCCTAGTTACGCCTCGC.....	20	0	1	1.00	1	1	0	0	0	0	0
.....GGCAAGGCCTAATTGGGGGA.....	20	0	1	1.00	1	1	0	0	0	0	0
.....CTTCATTTCCCCTAGTTACGCC.....	22	0	1	1.00	1	0	0	1	0	0	0
.....GCAAGGCCTAATTGGGGGT.....	19	1	1	1.00	1	1	0	0	0	0	0
.....AGGCCTAATTGGGGGAAATGAT.....	22	0	1	1.00	1	0	0	1	0	0	0
.....GCCTAATTGGGGGAAATG.....	18	0	1	1.00	1	0	0	1	0	0	0
.....TCAAATGCGCACAGGAAGTAGTC.....	23	1	1	1.00	1	0	1	0	0	0	0
.....ACGCCTCGCAAAATATGTATCA.....	22	0	1	1.00	1	1	0	0	0	0	0
.....AGGCCTAATTGGGGGAAATG.....	20	0	1	1.00	1	1	0	0	0	0	0
.....GTTGACTACTTTGTGTGCG.....	19	0	1	1.00	1	0	1	0	0	0	0
.....TGTGCGTATTTCATATATAT.....	20	0	1	1.00	1	1	0	0	0	0	0
.....AGTTGACTACTTTGTGTG.....	18	0	1	1.00	1	1	0	0	0	0	0
.....TTCATTTCCCCTAGTTACGCCT.....	22	0	1	1.00	1	1	0	0	0	0	0
.....TGCGCACAGGAAGTAGTTAAC.....	21	0	1	1.00	1	0	1	0	0	0	0
.....TCCCCTAGTTACGCCTCGCAAA.....	22	0	1	1.00	1	1	0	0	0	0	0
.....TCATATATATTTGGCAAGGC.....	20	0	1	1.00	1	1	0	0	0	0	0
.....GTGTGCGTATTTCATATAT.....	19	0	1	1.00	1	1	0	0	0	0	0
.....TTCCCCTAGTTACGCCTCGCAA.....	22	0	1	1.00	1	1	0	0	0	0	0
.....TCAAATGCGCACAGGAAGTAG.....	21	0	1	1.00	1	0	1	0	0	0	0
.....ATTTCCCCTAGTTACGCCTCGT.....	22	1	1	1.00	1	0	0	0	1	0	0
.....GGCAAGGCCTAATTGGGGGAA.....	21	0	1	1.00	1	1	0	0	0	0	0
.....CTTCATTTCCCCTAGTTACGCCT.....	23	0	1	1.00	1	1	0	0	0	0	0
.....ACTACTTTGTGTGCGTATTTCA.....	22	0	1	1.00	1	0	0	0	0	1	0
.....CTTCATTTCCCCTAGTTACGC.....	21	0	1	1.00	1	1	0	0	0	0	0
.....TCAGTTGACTACTTTGTGTGCGT.....	23	0	1	1.00	1	0	1	0	0	0	0
.....TTGGCAAGGCCTAATTGGGGGAAA.....	24	0	1	1.00	1	0	1	0	0	0	0
.....TTCATATATATTTGGCAAGGC.....	21	0	1	1.00	1	0	1	0	0	0	0
.....AAGGCCTAATTGGGGGAAATGA.....	22	0	1	1.00	1	0	1	0	0	0	0
.....CGCCTCGCAAAATATGTATCA.....	21	0	1	1.00	1	0	0	1	0	0	0
.....TTTCCCCTAGTTACGCCTCGCC.....	22	1	1	1.00	1	0	0	0	0	1	0
.....TCCCCTAGTTACGCCTCGCAAAA.....	23	0	1	1.00	1	0	0	0	1	0	0
.....CAAGGCCTAATTGGGGGAAATGA.....	23	0	1	1.00	1	0	0	1	0	0	0
.....TTCCCCTAGTTACGCCTCGCA.....	21	0	1	1.00	1	1	0	0	0	0	0
.....TGGCAAGGCCTAATTGGGGG.....	20	0	1	1.00	1	1	0	0	0	0	0
.....ATGTATCAAATGCGCACAGG.....	20	0	1	1.00	1	1	0	0	0	0	0
.....AATGCGCACAGGAAGTAGTTA.....	21	0	1	1.00	1	0	1	0	0	0	0
.....TATGTATCAAATGCGCACAGGAC.....	23	1	1	1.00	1	0	1	0	0	0	0

Anti-sense strand reads

CTCTGCTAGCTCTATAAATCGTATTCACGATAATCTCTAATCAACTTCAGTCAACTGATGAAACACACGCATAAAGTATATATAAACCGTTCCGGATTAACCCCCTTTACTATTTGGAATACGGACCGAAGTAAAGGGGATCAATGCGGAGCGTTTTATACATAGTTTACGCGTGTCCTTCATCAATTGAGGAAGATCCAGATCCGATCCTTATCAGTTTCCCGGTTCATTTTGCACCG	Read size	# Mismatch	Hit Count	Total Norm	Total	V110 male body	V049 head	M046 female body	V056 head
**********.((((.((((((((((.((.((((.((((((((((((((((....((.....)).)))))))))))))))).)))).)).)))))))))).))))**********									
.....TGCGGAGCGTTTTATACATAG.....	21	0	1	1.00	1	1	0	0	0
.....TGAGGAAGATCCAGATCCGAT.....	21	0	1	1.00	1	1	0	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6482:2154314-2154552 -	dmo_2709	GAGACGATCGAGATATTTAGCATAAGTGCTATTAGAGATTAGTTGAAGTCAGTTGACTACTTTGTGTGCGTATTTCATATATATTTGGCAAGGCCTAATTGGGGGAAATGATAAACCTTATGCCTGGCTTCATTTCCCCTAGTTACGCCTCGCAAAATATGTATCAAATGCGCACAGGAAGTAGTTAACTCCTTCTAGGTCTAGGCTAGGAATAGTCAAAGGGCCAAGTAAAACGTGGC

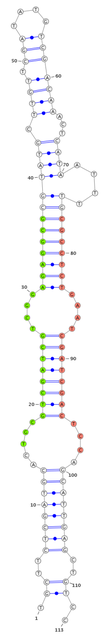
Generated: 09/08/2015 at 07:53 PM

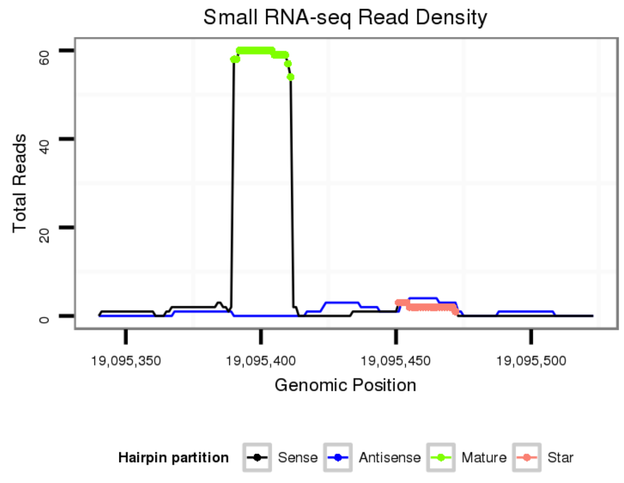
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	0
crit.tptop3	0
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

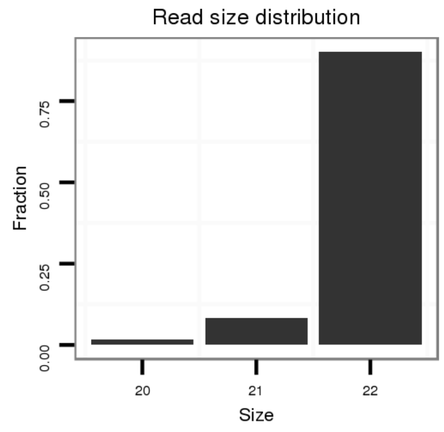
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_194	**scaffold_6680:19095390-19095473 +**	**candidate**	**Canonical miRNA**	**antisense_to_CDS**	[View on UCSC Genome Browser {Cornell Mirror}]

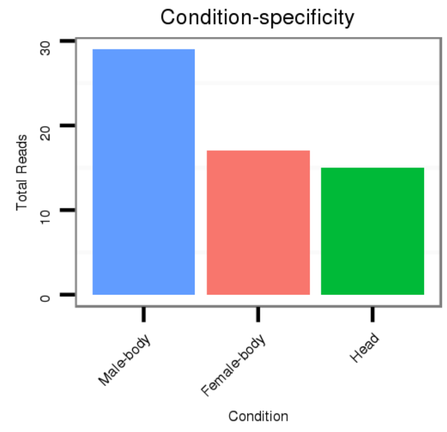
Legend: mature star mismatch in alignment mismatch in read

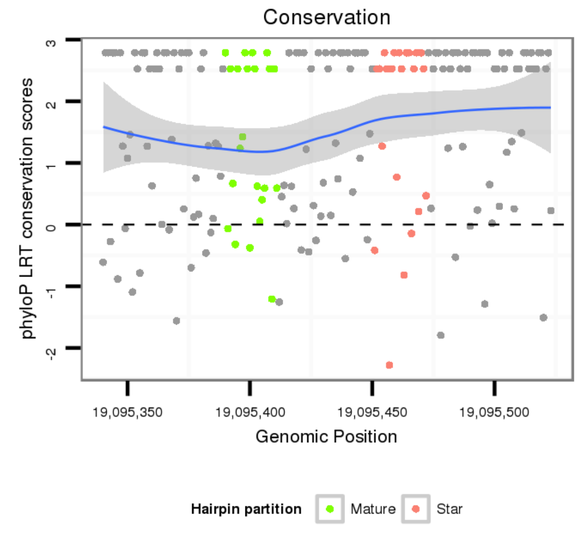
Predicted structure











Show Alternate Folds

Flybase annnotation

Antisense to CDS [DmojGI11543-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

TTTGTTGAGATACACGATGGCCTGGTTAAACGACTTGCTTCTCGATGCACTGCGTCGATCGTCGGAGAGGCGCGTATGCTTGTTCGATATGTCGACAAACTCATAATTTTGCGCCTCTGAATCGATCGACTCCAGCATTGAGCTGTCCTGCTTGTTCAGTGGATCCATGCCAAAGTCCATGGAG **********.((..(((((((.....(((((((....(((((((((((((.((((.(((....)))))))...))))....)))))))))....)))))))))....)))))))..))..**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V110 male body	M046 female body	V049 head	V056 head
.....TGCGTCGATCGTCGGAGAGGCG.....	22	0	1	52.00	52	26	13	7	6
.....TGCGTCGATCGTCGGAGAGGC.....	21	0	1	3.00	3	2	0	1	0
.....CGTCGATCGTCGGAGAGGCGCG.....	22	0	1	2.00	2	0	2	0	0
.....TGCGTCGATCGTCGGAGAGGCGA.....	23	1	1	1.00	1	0	1	0	0
.....CGCCTCTGAATCGATCGACTCC.....	22	0	1	1.00	1	0	0	0	1
.....TTAAACGACTTGCTTCTCGAT.....	21	0	1	1.00	1	0	1	0	0
.....ACAAACTCATAATTTTGCGCC.....	21	0	1	1.00	1	0	1	0	0
.....CTGCGTCGATCGTCGGAGAGG.....	21	0	1	1.00	1	0	1	0	0
.....ATGCACTGCGTCGATCGTCGG.....	21	0	1	1.00	1	0	1	0	0
.....TGCGTCGATCGTCGGAGAGG.....	20	0	1	1.00	1	1	0	0	0
.....AAACGACTTGCTTCTCGATGC.....	21	0	1	1.00	1	0	1	0	0
.....CGCCTCTGAATCGATCGACTC.....	21	0	1	1.00	1	0	1	0	0
.TTGTTGAGATACACGATGGC.....	20	0	1	1.00	1	0	1	0	0

Anti-sense strand reads

AAACAACTCTATGTGCTACCGGACCAATTTGCTGAACGAAGAGCTACGTGACGCAGCTAGCAGCCTCTCCGCGCATACGAACAAGCTATACAGCTGTTTGAGTATTAAAACGCGGAGACTTAGCTAGCTGAGGTCGTAACTCGACAGGACGAACAAGTCACCTAGGTACGGTTTCAGGTACCTC **********.((..(((((((.....(((((((....(((((((((((((.((((.(((....)))))))...))))....)))))))))....)))))))))....)))))))..))..**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M060 embryo	V110 male body	M046 female body	V049 head
.....CGGAGACTTAGCTAGCTGAGG.....	21	0	1	2.00	2	0	2	0	0
.....TAAAACGCGGAGACTTAGCTA.....	21	0	1	1.00	1	0	1	0	0
.....AGACTTAGCTAGCTGAGGTC.....	20	0	1	1.00	1	0	0	1	0
.....ACGAACAAGTCACCTAGGTAC.....	21	0	1	1.00	1	0	1	0	0
.....CGAACAAGCTATACAGCTGT.....	20	0	1	1.00	1	0	0	1	0
.....GCTATACAGCTGTTTGAGTAT.....	21	0	1	1.00	1	0	0	1	0
.....TTGCTGAACGAAGAGCTACGTG.....	22	0	1	1.00	1	0	0	1	0
.....AGCTATACAGCTGTTTGAGTA.....	21	0	1	1.00	1	0	1	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6680:19095340-19095523 +	dmo_194	TTTGTTGAGATACACGATGGCCTGGTTAAACGACTTGCTTCTCGATGCACTGCGTCGATCGTCGGAGAGGCGCGTATGCTTGTTCGATATGTCGACAAACTCATAATTTTGCGCCTCTGAATCGATCGACTCCAGCATTGAGCTGTCCTGCTTGTTCAGTGGATCCATGCCAAAGTCCATGGAG
droVir3	scaffold_13049:18311933-18312116 +	dvi_24641	TTTGTTGAGATAGACAATGGCCTGATTGAAGATTTGCTTCTGAGGCACTGCGTCGATCATCGGAGAGACGCACATGCTTATTGGATACGTCCACAAACTCATAATTCTGCGCCTCTGAATCTATGGACTCCAGCATTGAGCTGTCCTGCTTGTTCAGGGGATCCATGCCAAAGTCCATGGAG
droGri2	scaffold_15110:9332365-9332548 -		CTTGTTGAGCCTTACGATGGCCTGGTTGAAGGACTTGCTTCTTGCGGCACTGCGTCTATCGTCTCCGAGGCGTACATTCTTATTGGATATGTCGACGAATTCATAGTTTTGCGCCTCTGAATCGATCGATTCCAGCATTGAGCTGTCCTGCTTGTTCAGTGGATCCATGCCAAAGTCCATCGAA
droWil2	scf2_1100000004511:1514692-1514875 -		TTTATTAAGCCAGACAATGGCCTGATTGTAGGACTTGATTCTTGCGGCACTGCGTCGATCATCGGCGAGACGTATGTGTTTCTGTGTTATATCCACAAATTCATAGTTCTGGGCCTCCGAGTCAATTGATTCGAGCATTGAGCTATCTTGTTTATTCAAAGGATCCATGCCAAAGTCCATGGAA
dp5	XR_group6:4712935-4713118 +		CTTGTTCAGCCACACCATGGCCTGATTCTAAGACTTTGATCTCGCCGCACTGCGACGATCCTCGCTGAGACGCGCATTCTTCTGAGTTATGTCCACGAACTCGTAGTTCTGAGCCTCAGACTCGATCGACTCGAGCATCGAGCTGTCCTGTTTATTCAGCGGGTCGATGCCAAAGTCCATCGAG
droPer2	scaffold_9:3013732-3013915 +		CTTGTTCAGCCACACCATGGCCTGATTCTAAGACTTTGATCTCGCCGCACTGCGACGATCCTCGCTGAGACGCGCATTCTTCTGAGTTATGTCCACGAACTCGTAGTTCTGAGCCTCAGACTCGATCGACTCGAGCATCGAGCTGTCCTGCTTATTCAGCGGGTCGATGCCAAAGTCCATCGAG
droAna3	scaffold_13337:5003265-5003448 -		CTTATTCAGCCAGACGATGGACTGGTTCTAGGACTTCACCCTGCCCACACTTCTGCCGTCCTCGCTGAGTCTCCGGTTCTTTCTGCGAGATGTCCACAAACTCGTAGTTCTGAGCCTCCGAATCTATGGACTCCAGCATTGAGCTATCCTGTTTATTTAGTGGATCCATTCCAAAGTCCATGGAA
droBip1	scf7180000396371:334706-334889 -		CTTGTTCAGCCAGACGATGGACTGGTTCTAGGACTTGACCCTGCCCACACTCCTGCGATCCTCGCTGAGCCTCCGCGTTCTTCTGCGATATGTCCACAAACTCGTAGTTTTGAGCCTCTGAATCGATGGACTCCAGCATCGAGCTGTCCTGCTTGTTAAGTGGATCCATCCCAAAGTCCATCGAG
droKik1	scf7180000302686:595187-595370 +		CTTATTGAGCCAAACAATAGCCTGATTATACGACTTGATTCTGCTAATACTCCTTCGATCCTCGGTCAGTCGGCCATTCTTCTGTGCCACGTCCACAAACTCATAGTTTTGTGCTTCCGAATCAATGGACTCCAACATTGAGCTATCCTGCTTGTTCAGTGGATCCATGCCAAAGTCCATGGAG
droFic1	scf7180000453784:360556-360739 +		TTTATTCAGACACACGATGGCCTGGTTATACGATTTAATCCTAACCACACTCCTGCGATCCTCGCTGAGACGCGCGTTCTTCTGTGATACATCCAAAAACTCGTAGTTCTGTGCCTCCGAATCAATGGACTCCAACATCGAGCTATCCTGCTTGTTCAGTGGATCCACGCCAAAGTCCATAGAG
droEle1	scf7180000491255:2495777-2495960 +		CTTATTGAGCCACACAATGGCCTGGTTATAGGACTTAATCCTGGTCACACTCCGCCGATCCTCACTGAGCCGTGCGTTCTTCTGGAAACATCCAAAAACTCGTAGTTCTGCGCCTCCGAATCAATGGATTCCAGCATCGAACTGTCCTGCTTGTTCAGTGGATCCACGCCAAAGTCCATCGAG
droRho1	scf7180000760202:50706-50889 -		TTTATTCAAGCCACACGATGGCCTGGTTATACGATTTAATCCTGGTCAGCTCCTGCGATCCTCGCTGAGCCGTGCGTTTTTCTGTGAAACATCCAAAAATTCGTAGTTTTGTGCCTCAGAATCAATGGATTCCAACATCGAACTATCCTGCTTGTTCAGTGGATCCACGCCAAAGTCCATGGAG
droBia1	scf7180000302428:5871036-5871219 -		TTTGTTCAGCCAGACAATGGCCTGGTTGTAGGACTTGATCCTGGTCACACTCCTACGATCTTCGCTGAGCCGGGCGTTCTTTTGTGATACATCTAAAAATTCGTAGTTCTGTGCCTCCGAATCAATTGATTCCAGCATCGAGCTGTCCTGCTTGTTCAGTGGCTCCACTCCAAAGTCCATGGAG
droTak1	scf7180000415261:633258-633441 +		CTTATTAAGCCAGACAATGGCCTGGTTCTACGACTTTATCCTCGTCACACTTCTGCGATCTTCGCTGAGCCGCCGCGTTCTTCTGTGATACATCCAAAAATTCGTAGTTCTGCGCCTCCGAATCAATTGATTCCAGCATTGAGCTATCCTGCTTGTTTAGTGGCTCCACTCCAAAGTCCATGGAG
droEug1	scf7180000409456:224934-225117 +		TTTATTCAGACAGACGATGGCCTGGTTATAAGACTTAATTCTGCCACACTCCTGCGATCTTCGCTAAGCCGGGCATTTTTTTGTGATATATCCAAAAATTCGTAGTTCTGTGCCTCCGAATCAATTGATTCCAGCATCGAGCTATCCTGCTTGTTTAATGGCTCCACTCCAAAGTCCATGGAG
dm3	chr3L:14039176-14039359 +		CTTATTGAGACAGACGATGGACTGGTTATAGGACTTGATTCTGGTCAGCCTTCTGCGATCATCGCTGAGTCGTCCGTTCTTTTGTGAGACATCCAAAAACTCGTAGTTCAGTGCCTCCGAATCGATTGATTCCAGCATCGAGCTATCCTGCTTGTTCAGTGGATCCACTCCAAAGTCCATTGAG
droSim2	3L:13710311-13710494 +		CTTATTGAGCCAGACGATGGACTGGTTATAGGACTTGATTCTGGTCAGCCTTCTGCGATGATCGCTGAGCCGCCCCGTTCTTTTGTGAGACATCCAAAAATTCGTAGTTCAGTGCCTCCGAATCGATTGATTCCAGCATCGAGCTATCCTGCTTGTTCAGTGGATCCACTCCAAAGTCCATGGAG
droSec2	scaffold_0:6185479-6185662 +		CTTATTGAGCCAGACGATGGACTGGTTATAGGACTTGATTCTGGTCAGCCTTCTGCGATGATCGCTGAGCCGCCCCGTTCTTTTGTGAGACATCCAAAAACTCGTAGTTCAGTGCCTCCGAATCGATTGATTCCAGCATCGAGCTATCCTGCTTGTTCAGTGGATCCACTCCAAAGTCCATGGAG
droYak3	3L:14126249-14126432 +		CTTGTTGAGCCAGACGATGGCCTGGTTGTAGGACTTGATTCTGGCCAGCCTTCTGCGATGATCGCTGAGCCTCCGCGTTCTTTTGTGACACATCCAAAAATTCGTAGTTCAGTGCCTCCGAATCTATTGATTCCAGCATCGAGCTGTCCTGCTTGTTTAGCGGGTCCACTCCAAAGTCCATCGAG
droEre2	scaffold_4784:14029513-14029696 +		CTTGTTGAGCCAGACGATGGCCTGGTTATAGGACTTGATTCTGGTCAGCCTTCTGCGATGATCGCTGAGCCTCCGCGTTCTTTTGTGAGACATCCAAAAATTCGTAGTTCAGTGCCTCCGAATCTATTGATTCCAGCATCGAGCTATCCTGTTTGTTTAGTGGCTCCACTCCCAAGTCCATGGAG

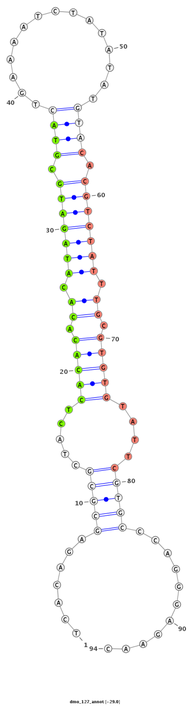
Generated: 09/08/2015 at 07:54 PM

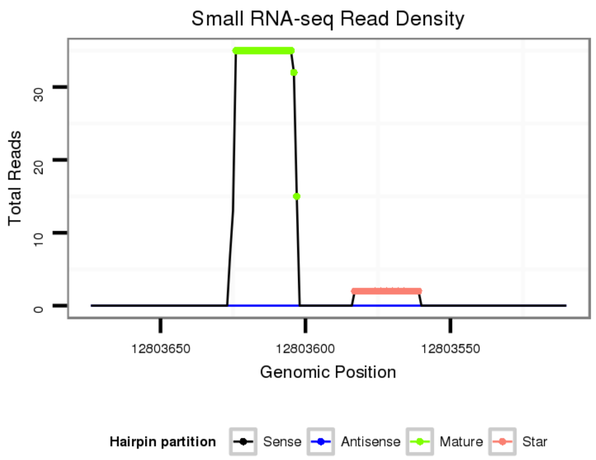
	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	2

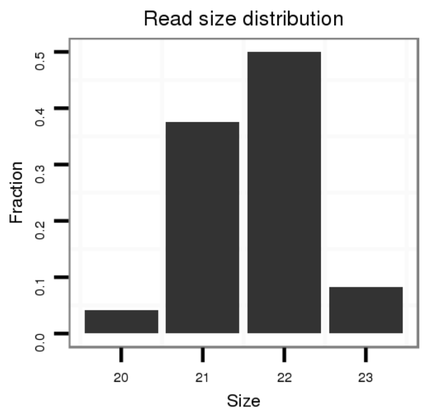
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_127	**scaffold_6496:12803560-12803624 -**	**candidate**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

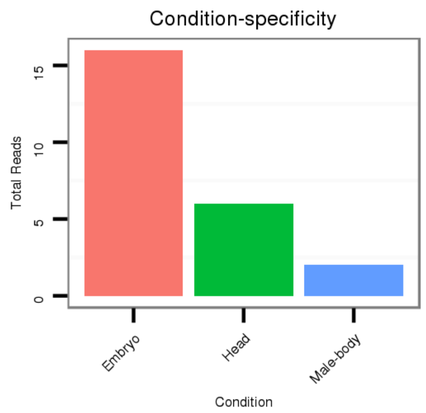
Legend: mature star mismatch in alignment mismatch in read

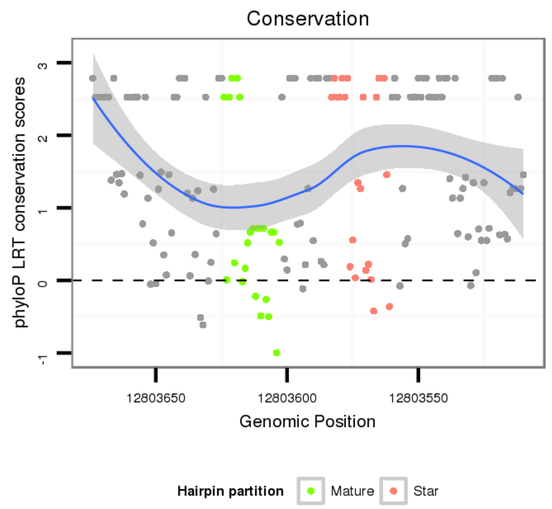
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

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TCGCCCGATACAGCCGCCATCGAGCAAACAGCCAATCACAGAGCGCGCTACTCACACACACATAGATGCGTACTGAAAATCTATATATGTACACGTCTATTTGCGTGTGTATTCGTGCCCAGGGAGAACGCGAGTTATTTGTTGCCACCCGTTTTATTGGCGGCA
************************************.......(((((.....(((((.((.(((((((.((((.............)))).)))))))).)).)))))....)))))...........************************************
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Read size	# Mismatch	Hit Count	Total Norm	Total	M060 embryo	V041 embryo	V056 head	V049 head	V110 male body
22	0	1	12.00	12	7	4	0	0	1
21	0	1	9.00	9	4	0	3	2	0
22	0	1	4.00	4	0	1	2	1	0
23	0	1	4.00	4	0	3	1	0	0
22	0	1	2.00	2	0	2	0	0	0
23	0	1	2.00	2	1	0	0	0	1
23	0	1	2.00	2	2	0	0	0	0
23	1	1	1.00	1	1	0	0	0	0
24	0	1	1.00	1	0	1	0	0	0
22	1	1	1.00	1	0	0	1	0	0
22	1	1	1.00	1	0	0	1	0	0
20	0	1	1.00	1	0	0	0	1	0

Anti-sense strand reads

```
AGCGGGCTATGTCGGCGGTAGCTCGTTTGTCGGTTAGTGTCTCGCGCGATGAGTGTGTGTGTATCTACGCATGACTTTTAGATATATACATGTGCAGATAAACGCACACATAAGCACGGGTCCCTCTTGCGCTCAATAAACAACGGTGGGCAAAATAACCGCCGT
************************************.......(((((.....(((((.((.(((((((.((((.............)))).)))))))).)).)))))....)))))...........************************************
```

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
droMoj3	scaffold_6496:12803510-12803674 -	dmo_127	TCGCCCGATACAGCCGCCATCGAGCAAACAGCCAATCACAGAGCGCGCTACTCACACACACATAGATGCGTACTGAAAATCTATATATGTACACGTCTATTTGCGTGTGTATTCGTGCCCAGGGAGAACGCGAGTTATTTG----TT-GC----------CACCCGTTTTA-TTGGCGGCA-
droVir3	scaffold_12875:19114274-19114438 -		TCGCCCGATTCAGCCGCCAGCGCGCAAATAGCCAATGACTGCTCGCACTACTCACACACACACAGAATCGGACTAAAAATCAGTATACGTACACGTCTGTTTGCGTGTGTATTAGTGCCCAGGGAGAACGCGAGTTATTTG----CT-GC----------CACCCGTTTTA-TTGGCGGCA-
droGri2	scaffold_15245:13145585-13145750 -		TCGCCCGATTCAGCCGCCATCGAGCAAATAGCCAATCGCATCACTCGCTACTCACACATACACACAATCGAACTGAAAATTCGTGTACATACACGTCTGTTTACATGTGTATATGTGCCCAGGGAGAACGCGAGTTATTTG----CTTG-----------CCACCCGTTTTA-TTGGCGGCA-
droWil2	scf2_1100000004510:684328-684494 +		TCGCCCGTTTTAGCCGCCATCGCCAATTGACCAATCAGAGCGCTTGTTACACACATAA----------ACGCAAATAGCGTATACATACACGTCTGTCTGCTTAAGTATTGGTGACAAGGGAGAACGCGAGTTCTTCCAAGCCT-TTGTAGGG---T------TTTTGTT-TTTGTTATTTAGTGC
dp5	3:17407322-17407484 -		TCGCCCGTTTTAGCCGCCATCGTGAAACAGCCAATCACAGCGCTTGTTACTCACACGCA----------ACAAAAATTGTGTGTACATACACGTCTATGTGCGCCTGTATTGGTGTTGCGGGAGAACGCGAGTTACTTG----CG-GCTT-------GGTTGATTTTGTT-TTTGTTGCGCGGCA-
droPer2	scaffold_31:384841-385003 +		TCGCCCGTTTTAGCCGCCATCGTGAAACAGCCAATCACAGCGCTTGTTACTCACACGCA----------ACAAAAATTGTGTGTACATACACGTCTATGTGCGCCTGTATTGGTGTTGCGGGAGAACGCGAGTTACTTG----CG-GCTT-------GGTTGATTTTGTT-TTTGTTGCGCGGCA-
droAna3	scaffold_13266:14507867-14508036 -		TCGCCCGTTTTAGCCGCCGTCGCAGCAACAGCCAATCACAGAGCGCGCTACTCACACACA----------GCAGAAAATCCGTGTACATACACGTCTCCCTGCGATAGTATTGGTGCCCGGGGAGAACGCGAGTTACTCG----CT-AAATGGAAATAT-GGTCATTTTATT-TTTGTTGCGCGGCA-
droBip1	scf7180000396428:317959-318128 +		TCGCCCGTTTTAGCCGCCGTCGCGGCAACAGCCAATCACAGCGCGCGCTACTCATAGCA----------GCAGAAAATCCGTGTACATACACGTCTCCCTGCGACAGTATTCGTGCCCGGGGAGAACGCGAGTTACTCG----CT-AAATGGAAATAT-GGTCATTTTATT-TTTGTTGCGCGGCA-
droKik1	scf7180000302411:338556-338722 +		TCGCCCGTTTTGCCGCCATCGCGCAAGAGCCAATCGCAGGCCGCGCTACGCATACAGG----------GCAGAAAATCCGTGTACATACACGTCTGCCTGCTGTCGTATTGGTGCCCGGGGAGAACGCGAGTTACTCG----CT-GTATGCGG---T-GTTCATTATTGTT-TTTGTTGCGCGGCA-
droFic1	scf7180000453215:708663-708830 -		TCGCCCGTTTTAGCCGCCATCGCGCGATCAGCCAATCACGCACGCGCTACACACAGCG----------GCAGAAAATCGTGTACATACACGTCTGAGCGCTGTTGTATTCGTGCCCGGGGAGAACGCGAGTTACTCG----CT-GCATAGAG---CGACCCATTATGTT-TTTGTTGCGCGGCA-
droEle1	scf7180000491349:713384-713550 +		TCGCCCGTTTTAGCCGCCATCGCGCGCAACAGCCAATCACAGGCCGCGCTACACACAGCA----------GCGGAAAATCCGTGTACATACACGTCTGAGCGCTGTGGTATTGGTGCCCGGGGAGAACGCGAGTTACTCG----CT-GCATAGTG---TGGACCATTATGT--TTTGTTGCGCGGCA-
droRho1	scf7180000777200:475398-475564 -		TCGCCCGTTTTAGCCGCCATCGCGACAACAGCCAATCACAGGCCGCGCTACACACAGCA----------GCGGAAAATCCGTGTACATACACGTCTGAGCGCTGTGGTATTGGTGCCCGGGGAGAACGCGAGTTACTCG----CT-GCATAGTG---TGGTCCATTATGT--TTTGTTGCGCGGCA-
droBia1	scf7180000301506:3105704-3105871 +		TCGCCCGTTTTAGCCGCCATCGCGCAACAGCCAATCGCAGGCGCGCGCTACACACAGCG----------GCAGAAAATCCGTGTATGTACACGTCTGAGCGCTGTGGTATTGGTGCCCGGGGAGAACGCGAGTTACTCG----CT-GCACAGAG---CGGTCCATTATGTT-TTTGTTGCGCGGCA-
droTak1	scf7180000414717:18785-18952 +		TCGCCCGTTTTAGCCGCCATCGCGCAACAGCCAATCACAGGCCGAGCTACGCATAGCG----------GCAGAAAATCCGTGTACATACACGTCTGAGCGCTGTGGTATTGGTGCCCGGGGAGAACGCGAGTTACTCG----CT-GTGCAGAA---TGGACCATTATGTT-TTTGTTGCGCGGCA-
droEug1	scf7180000409462:2685027-2685194 +		TCGCCCGTTTTAGCCGCCATCGCGCAACAGCCAATCGCAGGCGCTCGCTACACACAGCG----------GCAGAAAATCCGTGTATGTACACGTCTGAGCGCTGTGGTATTGGTGCCCGGGGAGAACGCGAGTTACTCG----CT-GCATAGAA---TGGGCCACTCTGTT-TTTGTTGCGCGGCA-
dm3	chr2R:10157744-10157911 -		TCGCCCGTTTTAGCCGCCATCGCGACTCGAGCCAATCACGGGCCGCGCTACACACAGCG----------GCAGAAAATCCGTGTACATACACGTCTGAGCGCTGTGGTATTGGTGCCCGGGGAGAACGCGAGTTACTCG----CT-GCATAGAG---TAGCCCACTATGTG-TTTATTGCGCGGCA-
droSim2	2r:10860796-10860963 -		TCGCCCGTTTTAGCCGCCAACGCGACAGCCAGCCAATCACAGGCCGCGCTACACACAGCG----------GCAGAAAATCCGTGTACATACACGTCTGAGCGCTGTGGTATTGGTGCCCGGGGAGAACGCGAGTTACTCG----CT-GCATAGAG---TAGCCCACTATGTG-TTTATTGCGCGGCA-
droSec2	scaffold_1:7665374-7665542 -		TCGCCCGTTTTAGCCGCCATCGCGACAGCAGCCAATCACAGACCGCGCTACACACAGCG----------GCAGAAAATCCGTGTACATACACGTCTGAGCGCTGTTGTATTGGTGCCCGGGGAGAACGCGAGTTACTCG----CT-GCATAGAGT--TAGCCCACTACGTG-TTTATTGCGCGGCA-
droYak3	2R:10094874-10095041 -		TCGCCCGTTTTAGCCGCCATCGCGACAACAACCAATCACAGGCCGCGCTACACACAGCG----------GCAGAAAATCCGTGTACATACACGTCTGAGCGCTGTGGTATTGGTGCCCGGGGAGAACGCGAGTTACTCG----CT-GCATAGAG---TAGCCCACTATGTG-TTTATTGCGCGGCA-
droEre2	scaffold_4845:15685313-15685480 +		TCGCCCGTTTTAGCCGCCATCGCGACAACAGCCAATCACAGGCCGCGCTACACACAGCG----------GCAGAAAATCCGTGTACATACACGTCTGAGCGCTGTGGTATTGGTGCCCGGGGAGAACGCGAGTTACTCG----CT-GCATAGAG---TAGCCCACTATGTG-TTTATTGCGCGGCA-

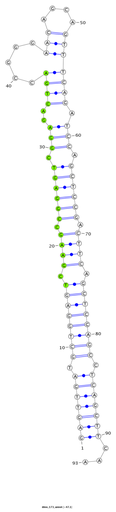
Generated: 09/08/2015 at 07:54 PM

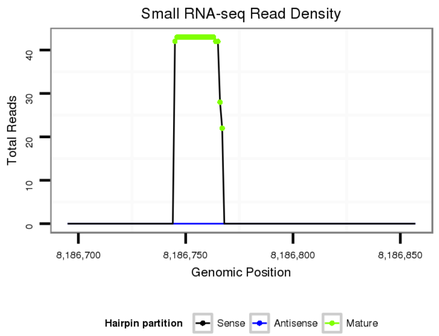
	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

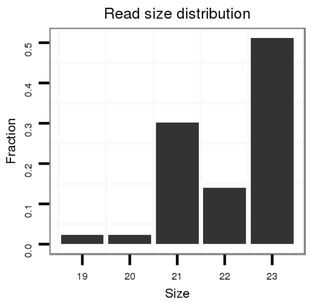
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_173	**scaffold_6473:8186745-8186807 +**	**candidate**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser [Cornell Mirror]]

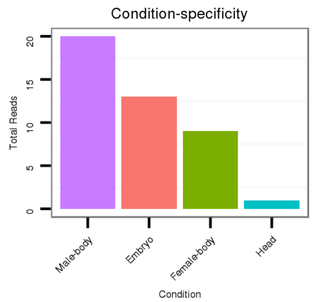
Legend: mature star mismatch in alignment mismatch in read

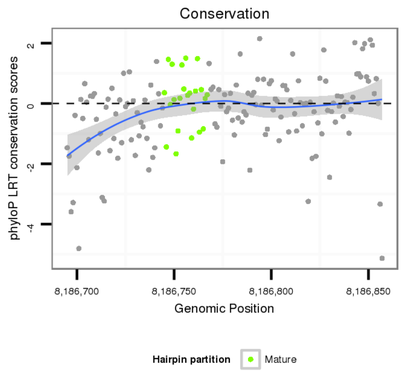
Predicted structure











Show Alternate Folds

Flybase annotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

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CAACGATGAATGCCCCACGGTCGGCGTCAGCGTCAGAGTTGATGCTGGAGTCGAAGCCGGAGTCGGAGACTGACCGGGAACAGCAGTTTCAGATCCAGCTCCGACTTCAGCTCCAGCCTCAGCTTCAAGCTTCAAGCTGCGGCCCCGAGTATCAAGTGTGTAA
**********(((((((.(((((((((.((((.(((((((.(((..((((.....(((....)))))))).))).)))))))).))))).)))))))).)))))))...**********
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Read size	# Mismatch	Hit Count	Total Norm	Total	V110 male body	M060 embryo	M046 female body	V041 embryo	V056 head	V049 head
23	0	1	22.00	22	12	6	3	1	0	0
21	0	1	13.00	13	5	4	2	1	0	1
22	0	1	6.00	6	3	0	2	1	0	0
21	1	1	1.00	1	0	0	0	0	1	0
22	1	1	1.00	1	1	0	0	0	0	0
24	1	1	1.00	1	1	0	0	0	0	0
19	0	1	1.00	1	0	0	1	0	0	0
22	1	1	1.00	1	1	0	0	0	0	0
22	1	1	1.00	1	1	0	0	0	0	0
20	0	1	1.00	1	0	0	1	0	0	0
23	1	1	1.00	1	1	0	0	0	0	0
25	2	1	1.00	1	1	0	0	0	0	0

Anti-sense strand reads

```
GTTGCTACTTACGGGGTGCCAGCCGCAGTCGCAGTCTCAACTACGACCTCAGCTTCGGCCTCAGCCTCTGACTGGCCCTTGTCGTCAAAGTCTAGGTCGAGGCTGAAGTCGAGGTCGGAGTCGAAGTTCGAAGTTCGACGCCGGGGCTCATAGTTCACACATT
**********(((((((.(((((((((.((((.(((((((.(((..((((.....(((....)))))))).))).)))))))).))))).)))))))).)))))))...**********
```

Read size	# Mismatch	Hit Count	Total Norm	Total	V049 head
23	0	1	22.00	22	

Show Alignment With Reads

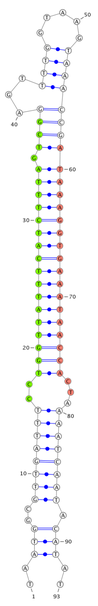
Re-alignment of all predicted orthologs

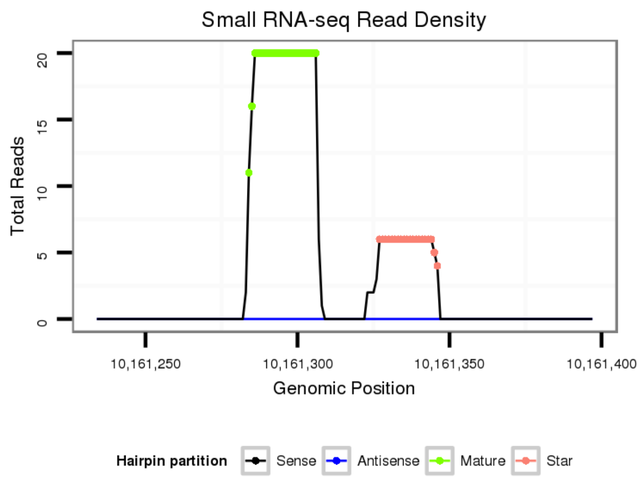
Species	Coordinate	ID	Alignment
droMoj3	scaffold_6473:8186695-8186857 +	dmo_173	CAA----------CG-ATGAATGCCCC----------A---------CGG--TCGG-------CGTCAGCGTCAGAGT---TGATGCTGGAGTCGAAGCC-----GGAGTCGGAGACT----------GACCGGGAACA----------G--CAGTTTCAGATCCAGCTCCGACTT-----CAGCTCCAGCCTC-----AGCTTCAAGCTTCAA-GCTGCG-----G----------CCCC------GAGTATCAAGTGTGTAA
droVir3	scaffold_12970:3682470-3682578 +		CAA----------CG-ACGAATGCCCC----------CAGCCAGAATGAGAG--TCAG-------A-CGA----GAGCC----------AGAG-----CT----------GGCGAGGAA--------------------

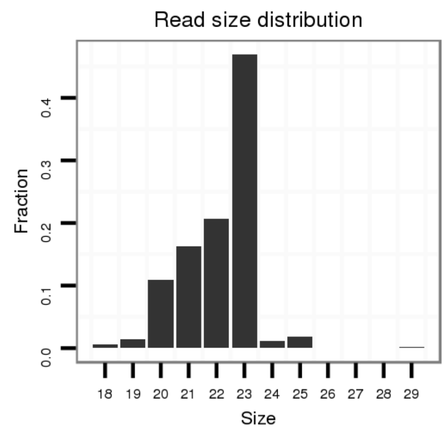
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_68	**scaffold_6473:10161284-10161347 +**	**confident-exception**	**Canonical miRNA**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

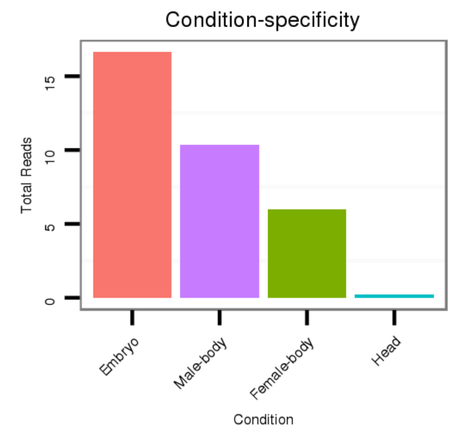
Legend: mature star mismatch in alignment mismatch in read

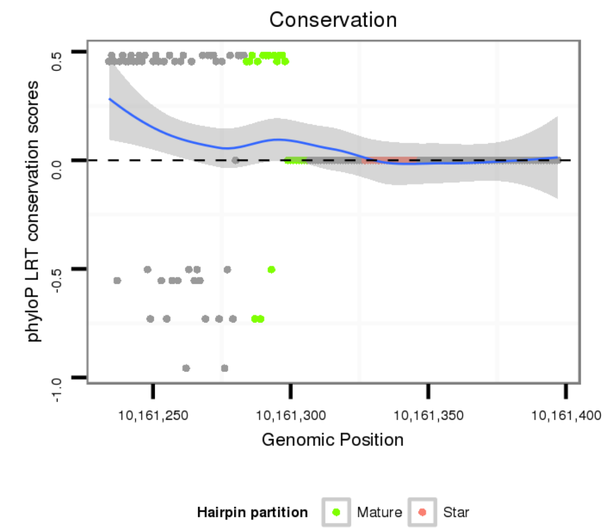
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dmoj\GI15760-in]

No Repeatable elements found

mature	star
1. dmo_69 scaffold_6473:8659200-8659222 - 2. dmo_68 scaffold_6473:10161284-10161306 +	1. dmo_3139 scaffold_6308:570088-570107 + 2. dmo_3140 scaffold_6308:570824-570843 - 3. dmo_3141 scaffold_6473:8642839-8642858 + 4. dmo_3142 scaffold_6473:8643580-8643599 - 5. dmo_69 scaffold_6473:8659160-8659179 - 6. dmo_3144 scaffold_6473:8660595-8660614 - 7. dmo_3145 scaffold_6473:9912692-9912711 - 8. dmo_3149 scaffold_6473:9914072-9914091 + 9. dmo_3150 scaffold_6473:9914850-9914869 - 10. dmo_3151 scaffold_6473:9918530-9918549 - 11. dmo_3152 scaffold_6473:9919882-9919901 + 12. dmo_3148 scaffold_6473:9927519-9927538 + 13. dmo_3147 scaffold_6473:9937997-9938016 + 14. dmo_3146 scaffold_6473:9971792-9971811 - 15. dmo_68 scaffold_6473:10161327-10161346 + 16. dmo_3133 scaffold_6473:10162125-10162144 - 17. dmo_3135 scaffold_6473:10167441-10167460 + 18. dmo_3137 scaffold_6473:10168232-10168251 - 19. dmo_3153 scaffold_6473:10193453-10193472 +

Sense Strand Reads

hide 3p reads show mid mismatch reads

CTGTGAGCTGCTGTGCCACTCATTCTCAGGCTGTTTAATGGCGTTGATTTCCTGGTTATTTCATCTTTAGTCGGAGTTTTGGTAAGTAAACCGATAAAGGTGAAATAACCACTAAAATCAATACATATTAAACTAGTGAGAGGAGCGAGTGCTCCAGGCTAGAC **********..(((..((((((((..((((((((((((((((((.((((...((((.....))))))))))))))))))))))))))...)))))))).)))..**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M060 embryo	V110 male body	M046 female body	V041 embryo	V056 head	V049 head
.....CCTGGTTATTTCATCTTTAGTCG.....	23	0	2	9.50	19	4	12	3	0	0	0
.....ATAAAGGTGAAATAACCACT.....	20	0	19	3.42	65	61	0	2	2	0	0
.....CTGGTTATTTCATCTTTAGTCGG.....	23	0	11	3.00	33	10	16	5	1	0	1
.....CTGGTTATTTCATCTTTAGTCG.....	22	0	11	2.82	31	4	7	19	1	0	0
.....TGGTTATTTCATCTTTAGTCG.....	21	0	20	2.70	54	2	21	24	6	1	0
.....TGGTTATTTCATCTTTAGTCGG.....	22	0	20	1.95	39	14	16	6	2	1	0
.....ACCGATAAAGGTGAAATAACCAC.....	23	0	15	1.67	25	25	0	0	0	0	0
.....TCCTGGTTATTTCATCTTTAGTCG.....	24	0	2	1.50	3	0	3	0	0	0	0
.....TGGTTATTTCATCTTTAGTCGGA.....	23	0	20	1.40	28	21	5	1	1	0	0
.....ACCGATAAAGGTGAAATAACCA.....	22	0	20	1.20	24	17	1	3	3	0	0
.....GATAAAGGTGAAATAACCACT.....	21	0	18	1.11	20	17	0	2	1	0	0
.....TCCTGGTTATTTCATCTTTAGTCGG.....	25	0	2	1.00	2	1	1	0	0	0	0
.....ATAAAGGTGAAATAACCACC.....	20	1	19	0.95	18	18	0	0	0	0	0
.....TCCTGGTTATTTCATCTTTAGT.....	22	0	2	0.50	1	1	0	0	0	0	0
.....TCCTGGTTATTTCATCTTTAGTC.....	23	0	2	0.50	1	1	0	0	0	0	0
.....CCTGGTTATTTCATCTTTAGT.....	21	0	2	0.50	1	1	0	0	0	0	0
.....CCTGGTTATTTCATCTTTAGTCGA.....	24	1	2	0.50	1	1	0	0	0	0	0
.....CCTGGTTATTTCATCTTTAGTCGC.....	24	1	2	0.50	1	0	1	0	0	0	0
.....CCTGGTTATTTCATCTTTAGTCGGA.....	25	0	2	0.50	1	1	0	0	0	0	0
.....ACCGATAAAGGTGAAATAACC.....	21	0	20	0.50	10	9	0	1	0	0	0
.....GTTATTTCATCTTTAGTCGGA.....	21	0	20	0.35	7	7	0	0	0	0	0
.....TTATTTCATCTTTAGTCGGAGTTT.....	24	0	18	0.33	6	4	0	2	0	0	0
.....GATAAAGGTGAAATAACCACTA.....	22	0	18	0.28	5	4	0	0	0	1	0
.....CGATAAAGGTGAAATAACCACT.....	22	0	18	0.28	5	5	0	0	0	0	0
.....ATAAAGGTGAAATAACCAC.....	19	0	19	0.26	5	5	0	0	0	0	0
.....GATAAAGGTGAAATAACCACC.....	21	1	18	0.22	4	4	0	0	0	0	0
.....ATAAAGGTGAAATAACCACTA.....	21	0	19	0.21	4	4	0	0	0	0	0
.....ACCGATAAAGGTGAAATAACCC.....	22	1	20	0.20	4	4	0	0	0	0	0
.....GTTATTTCATCTTTAGTCG.....	19	0	20	0.20	4	2	1	1	0	0	0
.....CTGGTTATTTCATCTTTAGTCGGT.....	24	1	11	0.18	2	1	0	1	0	0	0
.....CGATAAAGGTGAAATAACCACC.....	22	1	18	0.17	3	3	0	0	0	0	0
.....TTATTTCATCTTTAGTCG.....	18	0	20	0.15	3	1	0	2	0	0	0
.....CCGATAAAGGTGAAATAACCAC.....	22	0	18	0.11	2	2	0	0	0	0	0
.....ATAAAGGTGAAATAACCACTT.....	21	1	19	0.11	2	1	0	0	1	0	0
.....TATTTCATCTTTAGTCGGAGTT.....	22	0	20	0.10	2	2	0	0	0	0	0
.....AAACCGATAAAGGTGAAATAAC.....	22	0	20	0.10	2	2	0	0	0	0	0
.....CTGGTTATTTCATCTTTAGTCGGAG.....	25	0	11	0.09	1	0	1	0	0	0	0
.....CTGGTTATTTCATCTTTAGTCAA.....	23	2	11	0.09	1	0	0	1	0	0	0
.....CTGGTTATTTCATCTTTAGTCGGC.....	24	1	11	0.09	1	0	1	0	0	0	0
.....ACCGATAAAGGTGAAATAACCACA.....	24	1	15	0.07	1	0	0	1	0	0	0
.....ACCGATAAAGGTGAAATAACCACT.....	24	0	15	0.07	1	1	0	0	0	0	0
.....GATAAAGGTGAAATAACCAC.....	20	0	18	0.06	1	1	0	0	0	0	0
.....TTATTTCATCTTTAGTCGGAGTTTTGGTA.....	29	0	18	0.06	1	1	0	0	0	0	0
.....ATTTCATCTTTAGTCGGAGTTT.....	22	0	18	0.06	1	1	0	0	0	0	0
.....GATAAAGGTGAAATAACCACTAAC.....	24	1	18	0.06	1	1	0	0	0	0	0
.....GAGTTTTGGTAAGTAAACCG.....	20	0	18	0.06	1	1	0	0	0	0	0
.....CGATAAAGGTGAAATAACCACA.....	22	1	18	0.06	1	0	0	1	0	0	0
.....ATAAAGGTGAAATAACCACTGT.....	22	2	19	0.05	1	0	1	0	0	0	0
.....ATAAAGGTGAAATAACCACTTT.....	22	2	19	0.05	1	1	0	0	0	0	0
.....AAAGGTGAAATAACCACT.....	18	0	19	0.05	1	1	0	0	0	0	0
.....TTATTTCATCTTTAGTCGGAGTT.....	23	0	20	0.05	1	1	0	0	0	0	0
.....TGGTTATTTCATCTTTAGTCGGT.....	23	1	20	0.05	1	1	0	0	0	0	0
.....GTTATTTCATCTTTAGTCGGAA.....	22	1	20	0.05	1	1	0	0	0	0	0
.....GTTATTTCATCTTTAGTCGGC.....	21	1	20	0.05	1	1	0	0	0	0	0
.....CGATAAAGGTGAAATAACCC.....	20	1	20	0.05	1	1	0	0	0	0	0
.....TGGTTATTTCATCTTTAGTC.....	20	0	20	0.05	1	1	0	0	0	0	0
.....GGTTATTTCATCTTTAGTCG.....	20	0	20	0.05	1	0	0	1	0	0	0
.....CCGATAAAGGTGAAATAACCA.....	21	0	20	0.05	1	0	0	1	0	0	0
.....GGTTATTTCATCTTTAGTCGGC.....	22	1	20	0.05	1	1	0	0	0	0	0

Anti-sense strand reads

GACACTCGACGACACGGTGAGTAAGAGTCCGACAAATTACCGCAACTAAAGGACCAATAAAGTAGAAATCAGCCTCAAAACCATTCATTTGGCTATTTCCACTTTATTGGTGATTTTAGTTATGTATAATTTGATCACTCTCCTCGCTCACGAGGTCCGATCTG **********..(((..((((((((..((((((((((((((((((.((((...((((.....))))))))))))))))))))))))))...)))))))).)))..**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M046 female body	M060 embryo
.....AAGAAATCAGCCTCAAAACCAT.....	22	1	18	0.06	1	1	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6473:10161234-10161397 +	dmo_68	CTGTGAGCTGCTGTGCCACTCATTCTCAGGCTGT----------TTAATGGCGTTGATTTCCTGGTTATTTCATCTTTAGTCGGAGTTTTGGTAAGTAAACCGATAAAGGTGAAATAACCACTAAAATCAATACATATTAAACTAGTGAGAGGAGCGAGTGCTCCAGGCTAGAC
droVir3	scaffold_13047:13837530-13837603 +		CTGAGAGCTGCTGTAACACAGCTACAGACAGAAACTTTAAGATGTGAATGTGCCTT-TTTCCTTGGTATCTCATG----------

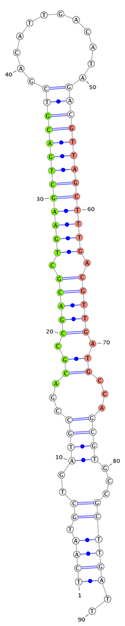
Generated: 09/08/2015 at 07:58 PM

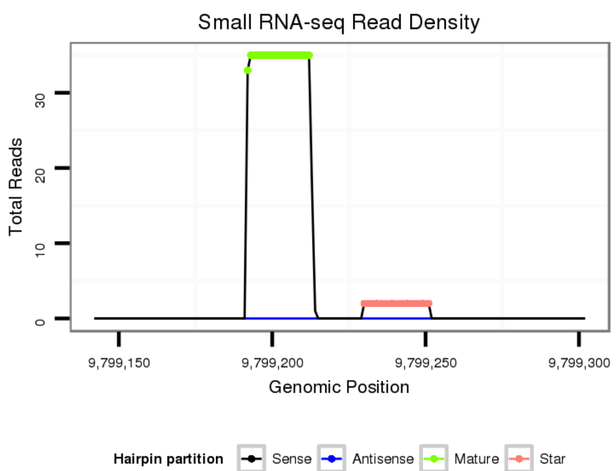
	PASS/FAIL
crit.star	1
crit.loop	1
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	0
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

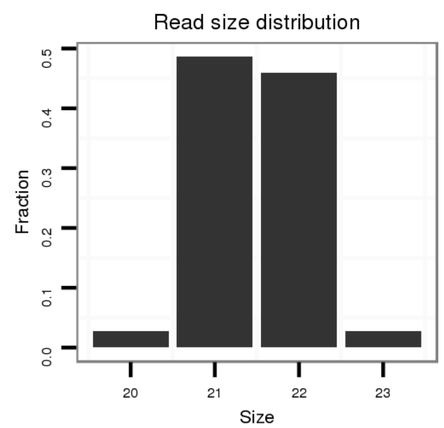
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_285	**scaffold_6473:9799192-9799252 +**	**candidate**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

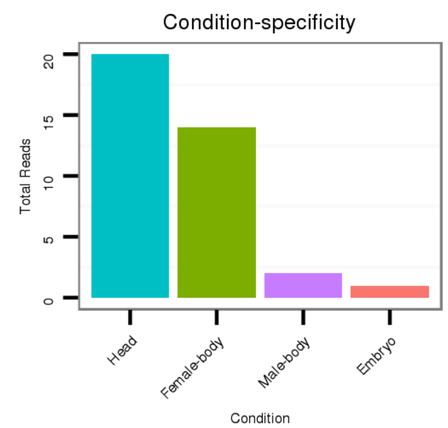
Legend: mature star mismatch in alignment mismatch in read

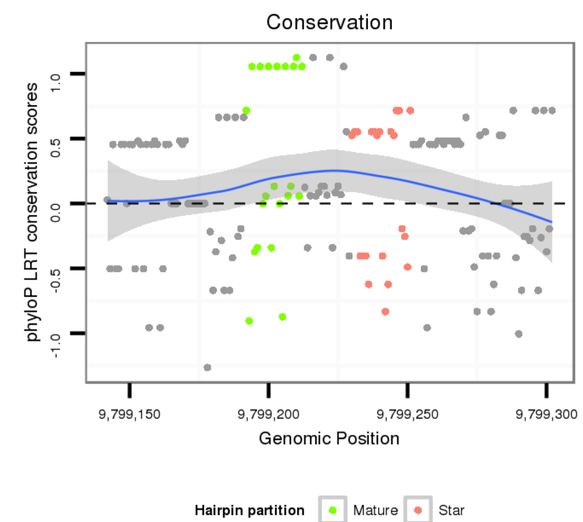
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

AAGTGCGTGGTACAGCCACCAGCTGAACATGGAATTCAATGCTGATGCCGACGCCGACGCTGAAGCTGACGTCGACATTGACATAGACGTTAGCTTTGACGTTGATGCCAGCGTGCCGCTTGATTGACACTCGGCGTACTACCAGGAAGAGCGGAAAAACA **********((((.((..((((...((.(((((.((((((((((.....))))))))))).)))))..))...))))...))))))..	Read size	# Mismatch	Hit Count	Total Norm	Total	M046 female body	V056 head	V049 head	V110 male body	M060 embryo
.....ACGCCGACGCTGAAGCTGACG.....	21	0	1	17.00	17	1	10	5	1	0
.....ACGCCGACGCTGAAGCTGACGT.....	22	0	1	15.00	15	8	3	2	1	1
.....GTTAGCTTTGACGTTGATGCCA.....	22	0	1	2.00	2	2	0	0	0	0
.....ACGCCGACGCTGAAGCTGACGTT.....	23	1	2	2.00	4	3	1	0	0	0
.....CGCCGACGCTGAAGCTGACGT.....	21	0	1	1.00	1	1	0	0	0	0
.....ACGCCGACGCTGAAGCTGACGTC.....	23	0	1	1.00	1	1	0	0	0	0
.....CGCCGACGCTGAAGCTGACG.....	20	0	2	1.00	2	2	0	0	0	0
.....ACGCCGACGCTGAAGCTGACGC.....	22	1	5	0.20	1	0	1	0	0	0

Anti-sense strand reads

TTCACGCACCATGTCGGTGGTCGACTTGTACCTTAAGTTACGACTACGGCTGCGGCTGCGACTTCGACTGCAGCTGTAACTGTATCTGCAATCGAAACTGCAACTACGGTCGCACGGCGAACTAACTGTGAGCCGCATGATGGTCCTTCTCGCCTTTTGT **********((((.((..((((...((.(((((.((((((((((.....))))))))))).)))))..))...))))...))))))..	Read size	# Mismatch	Hit Count	Total Norm	Total	V110 male body

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6473:9799142-9799302 +	dmo_285	AAGTGCGTGGTACAGCCACCAGCTGAACATGGAATTCAATGCTGATGCCGACGCCGACGCTGAAGCTGACGTCGACATTGACATAGACGTTAGCTTTGACGTTGATGCCAGCGTGCCGCTTGATTGACACTCG----------GCGTACTACCAGGAAGAGCGGAAAAACA
droVir3	scaffold_12970:11471999-11472125 -		AGGCACG-GGCACGGCACGGGC---ACA-------GGCCGTGGCAGTCGAAGTTGCCGTTGCCGTTGACGTTAACGTTAATGTTG-----------------ATGTCAGCGTAGCGCTTGATTGACACTCGCTCGTAGC---------------ATTCATAGACTAGCCA
droGri2	scaffold_15245:14940855-14940970 -		T----------TGATGCTGATGTTGATGCTGATGTTGATGCTGATGTTGATGTTAATGTTGATGTTGATGTTGATCGTGATATGA-----------------GCCTCATAATGACTCACCATGGGCGC---AAAAATGAAATAATA
droRho1	scf7180000777921:6011-6046 -		A----------TGTCGACGCCGACGCGCCGACGACGACGCCAACGCTG---

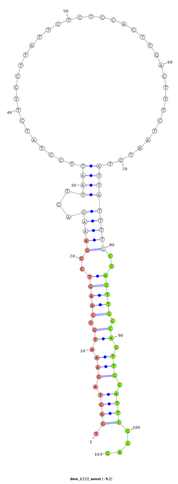
Generated: 08/18/2015 at 05:02 PM

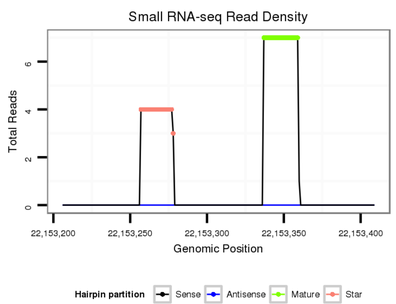
	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

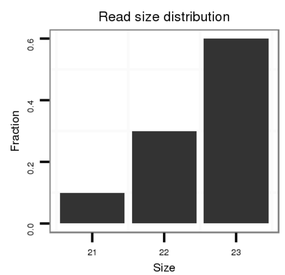
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_1222	**scaffold_6496:22153256-22153359 +**	**confident-exception**	**Mirtron**	**intron**	[View on UCSC Genome Browser [Cornell Mirror]]

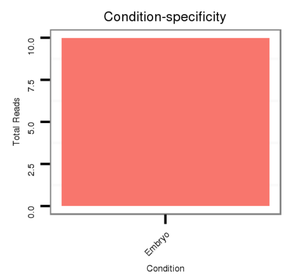
Legend: mature star mismatch in alignment mismatch in read

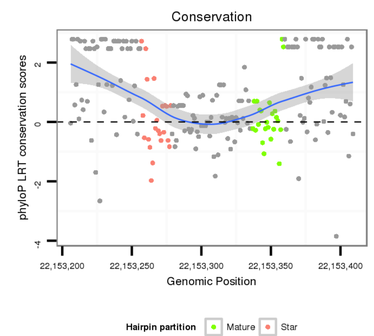
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [DmojGI21128-in]; CDS [DmojGI21128-cds]; CDS [DmojGI21128-cds]

No Repeatable elements found

Sense Strand Reads

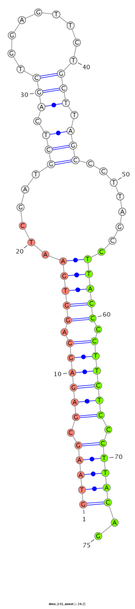
hide 3p reads show mid mismatch reads

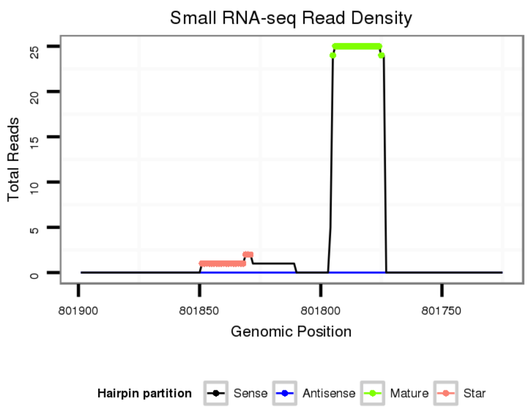
```
                                                
```

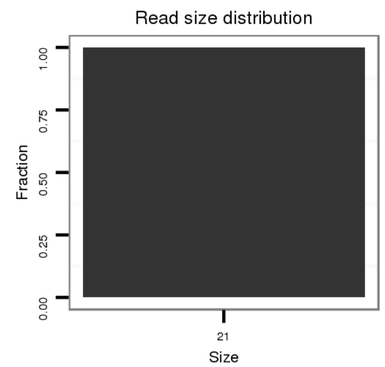
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_131	**scaffold_6308:801775-801849 -**	**confident-exception**	**Mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

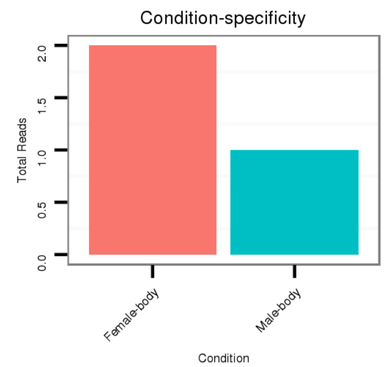
Legend: mature star mismatch in alignment mismatch in read

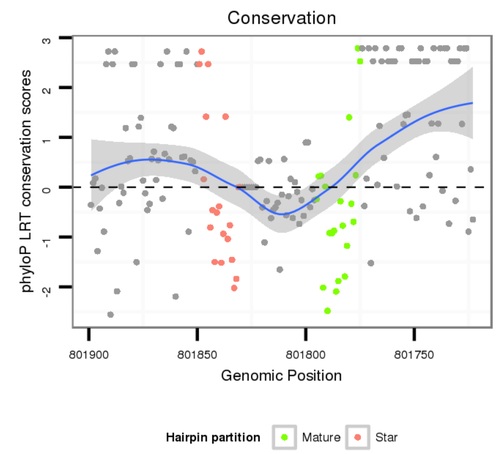
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dmoj\GI11012-in]; CDS [Dmoj\GI11012-cds]; CDS [Dmoj\GI11012-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

```
GGGCCTCCTGCTGCAGGCGGCCGAGCGGCGCGCTCTGCCAGCGTTGCAAGGTAAGCGAGAGGAGGTGAATCGATGCTCAGCTGGAGTTCTGCTTAGCCCTTAGCCTTACCCCTTCTCCCTTACAGTGCTCGATGCCTGGGGCAAGTTTCCGCACGGCCTGCTCTACGGCCATTTC
**************************************************(((((.(((((((.(((((.....(((.(((.........))).))).........)))))).)))))))..))))))..**************************************************
.......................................................................................CTTACCCCTTCTCCCTTACAGT.......................................................
.......................................................................................CCTTACCCCTTCTCCCTTACAGT.......................................................
.......................................................................................CCTTACCCCTTCTCCCTTACA........................................................
.......................................................................ATCGATGCTCAGCTGGAGTTC.........................................................................
.....................................................GTAAGCGAGAGGAGGTGAATC...........................................................................................
.......................................................................................TTACCCCTTCTCCCTTACAGA........................................................
.......................................................................................TTACCCCTTCTCCCTTACAGT.......................................................
```

Read size	# Mismatch	Hit Count	Total Norm	Total	V110 male body	M046 female body	V056 head	V049 head
22	0	1	19.00	19	14	4	0	1
23	0	1	4.00	4	2	1	1	0
21	0	1	1.00	1	0	1	0	0
21	0	1	1.00	1	0	1	0	0
21	0	1	1.00	1	1	0	0	0
21	1	1	1.00	1	0	1	0	0
21	0	1	1.00	1	0	1	0	0

Anti-sense strand reads

```
CCCGGAGGACGACGTCCGCCGGCTCGCCGCGCGCGAGACGGTCGCAACGTTCCATTCGCTCTCCTCCACTTAGCTACGAGTCGACCTCAAGACGAATCGGGAATCGGAATGGGGAAGAGGGAATGTCACGAGCTACGGACCCCGTTCAAAGGCGTGCCGGACGAGATGCCGGTAAAG
**************************************************(((((.(((((((.(((((.....(((.(((.........))).))).........)))))).)))))))..))))))..**************************************************
```

Read size	# Mismatch	Hit Count	Total Norm	Total	V056 head	V110 male body	M046 female body	V049 head

Show Alignment With Reads

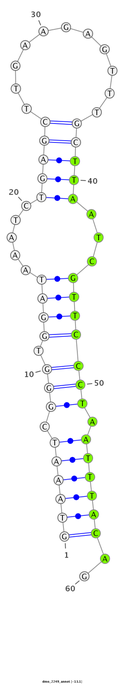
Re-alignment of all predicted orthologs

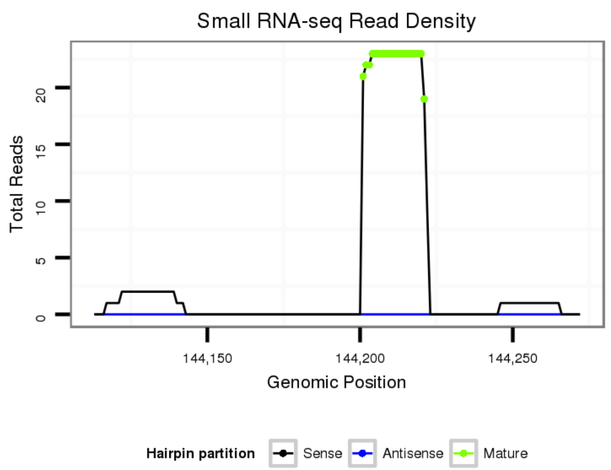
Species	Coordinate	ID	Alignment
droMoj3	scaffold_6308:801723-801899 -	dmo_131	GGGCCTCCTGCTGCAGGCGGCCGAGCGGCGCGCTCTGCCAGCGTTGCAAGGTAAGCGAGA--G----------G---AGG---------TGAATCGATGCTCAGCTGGAG----------TTCTGCT----------TAG--------CCCTTAGCCTTACCCCTTC----------T----CCCTTACAGTGCTCGATGCCTGGGGCAAGTTTCCGCACGGCCTGCTCTACGGCCATTTCAG
droVir3	scaffold_13042:3579065-3579236 -		GACCGGCTGCTTCAGGCGGCCGATGCGCACGCGCTGCCCGCGCTGCAAGGTAAGCAA----------GTCC--A--A--------GCT----------TA----------ACAGAGACTTTTTGCA---TTTAATCTAAGGCATTGGCCTTG---G--GC----TACTCTTAGTGCTGGATGGCTGGGGCAAGCTGCCGCATGGCCTGCTCTATGGTCACTTTAG
droGri2	scaffold_15203:2751383-2751554 -		GGGACTCCTGCTCCAGGCGGCCGATTTTCCAGCACTGCCCGCGCTGCGAGGTAAGCACTT--GACCCCAA--------A---G---ACA--------**----------**CAACTGTTATTCAATTGGCCAATTTATAAT**----------**---------**----------**GCT-----GCTTCTTCTAAACAGTTTTGGATGCCTGGGGCAAGTTTCCACATGGCCTGCTCTATGGCCACTTCAG
droWil2	scf2_1100000004902:975835-975985 -		CCAGAAACTCCTTCAAGAGGCTAACAATAAAGTTTATCGGCTCTTAAGGTAAGTTGAG--AGATTGA----------**----**---------**----------**---**TAT**----------**---**---------**GGCTTAAGATT----AT--CCTTTTTGGTATTAGTTGTAGATGCCTGGGGTAAATATCCACAAGGCCTGCTCTACGGCCACTTCTC
dp5	3:6084503-6084685 +		GCGTATCCTGCTTTTGGCGGCAGAGGCCAAAGCCGTTCCTGCTCTGCGTGGTGTAAGACTTC--TGCTACTAC--------CGCT----**----**---------**----------**-------**----------**---**---------**----------**-ACTGCCTGCTACTGCTACTGACCCACATTCTTCTGTCCTCAAAATCACC----GTTTGGCAGTCGTGGACTCTTGGGGAAAGTTTCCGCACGGCCTGCTCTATGGCCACTTTAT
droPer2	scaffold_2:6285431-6285613 +		GCGTCTCCTGCTTTTGGCGGCAGAGGCCAAAGCCGTTCCTGCTCTGCGTGGTGTAAGACTTC--TGCTACTAC--------CGCT----**----**---------**----------**-------**----------**---**---------**----------**-ACTGCCTGCTACTGCTACTGACCCACATTCTTCTGTCCTCAAAATCACC----GTTTGGCAGTCGTGGACTCTTGGGGAAAGTTTCCGCACGGCCTGCTCTATGGCCACTTTAT
droAna3	scaffold_13417:2399803-2399960 -		GCAAGCGTCCTGTCCTCGGCGGGGCCCAGGCTTGCAGGCTCTCGGAGGTAAGCCCCC--GATTTCA----------TGACGC--TTCCTC----**----------**---**---**CGA----------**GCCGTTA----**----------**AAACC----CA----TTCTGCAGTGCTCGACGCCTGGGGAAAGTTTCCGCAGGGACTCTCTACGGCCACTTTAC
droBip1	scf7180000394740:4720-4877 +		GCAAGTGCTCCTGACCGCGGCCGGGCGCAGCCTGCCCGCGCTCCGAGGTAAGCTCTC--AATTTTA----------CGACGA--TTCCTCTCAAGC----**----------**-------**----------**--CGTTA----**----------**AAACA----CA----TTCTTGCAGTGCTCGACGCCTGGGGAAAGTTCCGCTCAGGGCCTCTCTACGGCCACTTCAG
droKik1	scf7180000302696:404134-404295 +		GCGTCTGCTTCTGAAGGCCGCGGAGGCCAAGTCCTTGCCCGCTCTAAGAGGTGAGTTCTT--TGGGGGA----------GTGGGG--TCAGTC----**----------**---**TCT----------**GACAGTA----**----------**AACCA----CCCTCTTCCTTCCAGTGCTCGATGCCTGGGGCAAGTTCCCGCAGGGCCTGCTCTATGGCCACTTCAC
droFic1	scf7180000454155:442880-443047 +		TCGCCTCCTTCTCAAAGAGCCGAGAACAAATCCTTGCCAGGTCTTCGAGGTGAGTTTTTATGTT--------TAAAA---G---AAG---------TAA----------T----**----------**AAATATTTACTTAATAT----**----**--------TTTTTAAATT----GC----TTTTTGCAGTTTTTGATGCCTGGGGAAAGTTCCCACAGGTTTGCTTATGGCCACTTTGC
droEle1	scf7180000491273:2248599-2248654 -		A----------**----**---------**----**---------**----**---

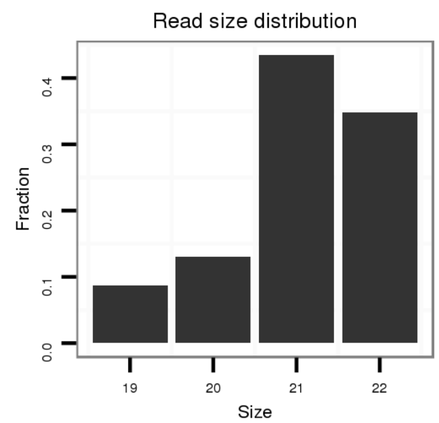
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_2249	**scaffold_6654:144163-144222 +**	**confident-exception**	**Mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

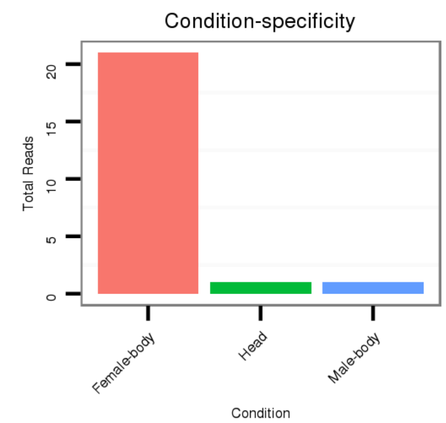
Legend: mature star mismatch in alignment mismatch in read

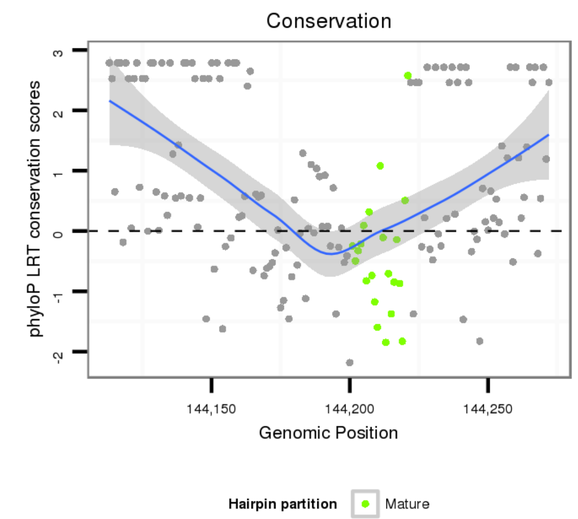
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [DmojGI16698-in]; CDS [DmojGI16698-cds]; CDS [DmojGI16698-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

AGCAAGTGTGATGCCAAGTTGCTGGAGAATACAACAGAAACACTGAATCGGTAAATCGGGTGGATAAATCTGAGCTTGAAGAGTTTGCTTAATCGTTCCCTAATTTACAGGGCCTTGTTGCTGGAACTGTCGTCTAATATGAAACTATACGATGAGCAGG **********(((((.(((.((((.....(((((.....)))))...)))))))).)))))..**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M046 female body	V110 male body	V049 head	V041 embryo	V056 head
.....TTAATCGTTCCCTAATTTACA.....	21	0	1	10.00	10	10	0	0	0	0
.....TTAATCGTTCCCTAATTTACAG.....	22	0	1	8.00	8	6	1	1	0	0
.....TTAATCGTTCCCTAATTTAC.....	20	0	1	3.00	3	3	0	0	0	0
.....TTAATCGTTCCCTAATTTACAGT.....	23	1	1	1.00	1	0	1	0	0	0
.....TTAATCGTTCCCTAATTTACT.....	21	1	1	1.00	1	0	1	0	0	0
.....TTAATCGTTCCCTAATTTACAGA.....	23	1	1	1.00	1	1	0	0	0	0
....AGTGTGATGCCAAGTTGCTGGAG.....	23	0	1	1.00	1	0	0	0	1	0
.....ATCGTTCCCTAATTTACAG.....	19	0	1	1.00	1	1	0	0	0	0
.....GATGCCAAGTTGCTGGAGAAT.....	21	0	1	1.00	1	0	0	1	0	0
.....CTAATATGAAACTATACGAT.....	20	0	1	1.00	1	1	0	0	0	0
.....TAATCGTTCCCTAATTTAC.....	19	0	1	1.00	1	1	0	0	0	0

Anti-sense strand reads

TCGTTCACACTACGGTTCAACGACCTCTTATGTTGTCTTTGTGACTTAGCCATTTAGCCCACCTATTTAGACTCGAACTTCTCAAACGAATTAGCAAGGGATTAAATGTCCCGGAACAACGACCTTGACAGCAGATTATACTTTGATATGCTACTCGTCC **********(((((.(((.((((.....(((((.....)))))...)))))))).)))))..**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V041 embryo	V049 head

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6654:144113-144272 +	dmo_2249	AGCAAGTGTGATGCCAAGTTGCTGGAGAATACAACAGAAACACTGAATCGGTAAATCGG-GTGGAT------AAA----------TCTGAGCT--------------------TG-AAGA--GT-TTG-CT----TAAT--------------------------------CGTTCC-CTAATTTACAGGGCCTTGTTGCTGGAACTGTCGTCTAATATGAAACTATACGATGAGCAGG
droVir3	scaffold_13049:3975766-3975921 -		AGCAAATGCGATGCCAAGCTGCTGGAGAATACAACGGATAGCTGAATCGGTAGGTGAC-ATGCCG------AAA----------ACTAAG--------------------CTTA-AAG-A-TTA---AT----------------------------CA-ATCCGT-CTAACTTACAGCGCCCTTTTGCTGGACCTCTCCTGCAATACGAAGCTGTGCGATGAACAGG
droGri2	scaffold_15110:10769150-10769309 +		AGCAAATGCGATGCCAAGCTGCTGGAGAACACGACCGAAACATTGAATCGGTATGAGCCATATATA------TTA----------T-------TAATATAT---------TTTA-TAT-A-TA---------T---A-T----------------------------A-ATCCTT-GATTATTACAGCGGTCTACTGCTGGAACTCTCGAGCAGCACGAAATTGTGTGATGAGCAGG
droWil2	scf2_1100000004511:4932791-4932956 -		AGTAAATGTGATGCCAATTATTGGAGAATACCACCGATACATTGAATAAGTGAGTGCA-TATAGAGAGTTTAGA----------GTTCAGTT--TG----------AT-----CA-AAT-A-TA---T----CATT--------------------------------GTTTCT-TCTATTTGCAGGGCCTTCCTTTTGGATCTTTCGATTGAGCGTAAACTATGCTGTGAACAGG
dp5	XR_group8:1793276-1793450 +		AGCAAATGCGAGGCCAAGCTGTTGCAGAACACGGCCGACAGCTTAATCGGTGAGTACT-------------------GCCTT--------------------AGACGA--GT-CCCA-G----TCGTAGTCCCCGTCCCAGAAGAGTAATACAATTCCA-----T-CTCCCTTACAGCGCCTTCCTGCTGGAACTCTCGCGCAGCAAGGACCTGTGCGATGAGCAGG
droPer2	scaffold_24:1256840-1257014 -		AGCAAATGCGAGGCCAAGCTGTTGCAGAACACGGCCGACAGCTTAATCGGTGAGTACT-------------------GCCTT--------------------AGACGA--GT-CCCA-G----TCGTAGTCCCCGTCCCAGAAGAGTAATACAATTCCA-----T-CTCCCTTACAGCGCCTTCCTGCTGGAACTCTCGCGCAGCAAGGACCTGTGCGATGAGCAGG
droAna3	scaffold_13337:10499121-10499279 -		AGCAAGTGTGAAGCCAAGCTGCTGGCCAACACGGCCGACACAATGAACCGGTAAGGATA-CATGTG-----CCTA----------------------ATTGGAATGAAGG-C-TTC---TCTA---AT--------------------------------AAATTT-TCTATTCGTAGCGCCCTTATGCTTGAACTGTCGCTTGGAAATCATCTCTGCAATGAAGAGG
droBip1	scf7180000396569:869924-870082 +		AGCAAGTGTGAAGCTAAGCTGCTGAACAACACGGCCGACAGCCTGAACCGGTAAGGATA-CATCTG-----CTTA----------ATCGTTATAGAGG-C-GTC---ATTA---AT--------------------------------ATAGTT-TCCATTTCCAGAGCCCTCATGCTTGAACTTTCGCAGGGCAAGCATCTCTGCAATGAAGAGG
droKik1	scf7180000302486:2822628-2822727 +		AGCAAGTGCGATGCCAAGCTGCTGGAGAACACGGCCGACACATTGAACG--GGGCCCTTGTTCTAGAGCTCTCGCTCAGCCAGAGTCTGTGCGATGAACAGG
droFic1	scf7180000453839:1501145-1501306 +		AGCAAATGTGATGCTAAGCTGTTAGAGAACACAGCCGATAGCCTAAACAAGTGAGTAAA-ATTAAA-----ATA----------T-------CA--CTTTTT---------TTTA-AAT-ACAACTCTATAT---A-AA----------------------------A-A-----TCCTCAACCAGGGGTCTTTTGTTGGAACTTTGCCTAAGCAAGGATCTCTGTGATGAGCAGG
droEle1	scf7180000491249:7323536-7323693 -		AGCAAGTGTGATGCCAAACTGCTGGAAAACACGGCTGATAGTCTAAACAAGTGAGTAAA-ATTGTA-----GTA----------A-------TTTA-------------ATTTAAAGT-T-TAC---CA-----T----------------------------TTATGTTGTTCACTGCAGGGGTCTTTTATTGGAACTCTCTTGAGCAAGGATCTCTGCGATGAGCAGG
droRho1	scf7180000776525:12679-12847 -		AGCAATTGTGATGCCAAGCTGCTGGAGAACACGGCTGATAGTTTAAACAAGTAAGTAAA-GTTTTA-----ATATTTTTTAAAA---------AGGTAA-------------------------------TTTATGTCTTTTCATGTATTT-TACCACCGCAGGGGTCTTTTGTTGGAACTCTGCCTCAACAAGGATCTCTGCGATGAGCAGG
droBia1	scf7180000302428:4001501-4001657 -		AGCAAATGTGATGCAAAGCTGCTGGAGAACACGGCAGATAGCCTGAACAAGTAAGTGAA-ATAAGA-----TGA----------T-------GTTAAGGA-------------AACTATAATCT---AT----------------------------A-A-TCGT-TTCACACACAGAGGTCTTCTGCTGGAACTGTGCCTCAGCAAGGACCTGTGTGATGAGCAGG
droTak1	scf7180000414337:202096-202151 -		AGCAAATGTGATGCCAAGTTGCTGGAGAACACGGCTGATAGTCTGAATAAGTGAGT--
droEug1	scf7180000409711:1222907-1223071 -		AGCAAATGTGATGCTAAGCTGCTGGAGAACACGGCTGATAGCCTAAATAAGTAAGTTTG-ATCAAA-----AGC----------C-TT----CG--CAAGTTTTCTAATATTTTT----------T-TTTACA-AA----------------------------TT---TCTTTCACAACGGGGTCTTCTGTTGGAACTATGTCTTAGCAAGGATCTCTGTGATGAACATG
dm3	chr3L:16118402-16118561 +		AGTAAATGTGATGCCAAGTTGCTGGAGAACACGGCCGACAGCCTGAACAAGTAAGTCAA-ACTATA-----ACA----------T-------CCTAAAAA-------------------TATTTATATATTTGCA-ATCTGT-TCCGCAAACAGAGCCCTTTTACTAGAACTGTGTCTCAGCAAGGATCTCTGTGATGAAAAGG
droSim2	3L:15736995-15737154 +		AGTAAATGTGATGCCAAGTTGCTGGAGAACACGGCCGACAGCCTGAACCACGTAAGTCAA-ACTATA-----ATA----------T-------CCTAACAA-------------------TATTTATATATTTCCA-ATCTGT-TCCGCACAATAGAGGACTTTTACTAGAACTGTCCTCAGCAAGGATCTCTGTGATGAAAAGG
droSec2	scaffold_0:8217981-8218140 +		AGTAAATGTGATGCCAAGTTGCTGGAGAACACGGCCGACAGCCTGAACAAGTAAGTCAA-ACTATA-----ATA----------T-------CCTAACAA-------------------TATTTATATATTTCCA-ATCTGT-TTCGCCCACAGAGGACTTTTATTAGAACTGTCCCTCAGCAAGGATCTCTGTGATGAAAAGG
droYak3	3L:22059218-22059375 -		AGCAAGTGTGATGCCAAGTTGCTGGAGAACACGACTGACAGCCTAAACAAGTAATATAT-ATTATA------TTA----------T-------ATTATATA-----------TATA----T-ATA---TTTA---AA----------------------------TTTCGT-TTCACACCCAGAGGGCTTTTACTAGAACTGTCCTTAGCAAGGATCTCTGTGATGAAAAGG
droEre2	scaffold_4784:18365982-18366136 +		AGCAAATGTGATGCCAAGTTGCTGGAGAACACGGCTGATAGCCTAAACAAGTGAGATAA-ACTATC------TTC----------T-------------------ATCAATATATA----T-TA---TTCA---AT----------------------------TTTCTT-TTCACACTCAGAGGACTTTTACTAGAACTGTGTCTTAGCAAGGATCTCTGTGATGAAAAGG

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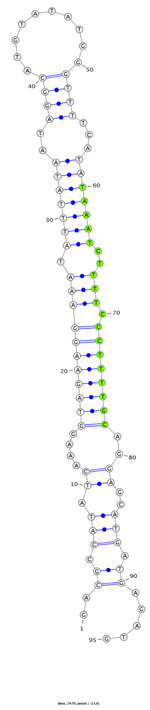
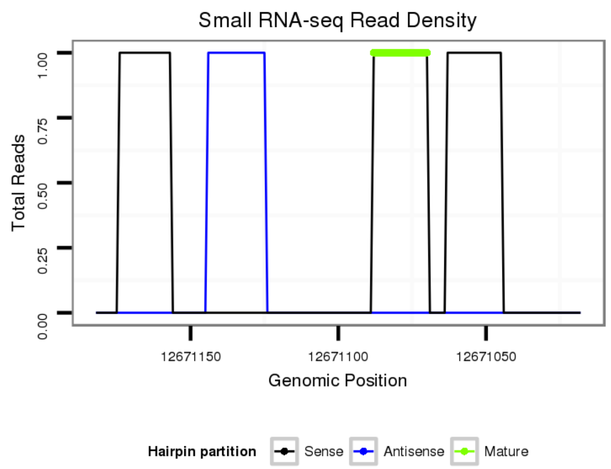
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

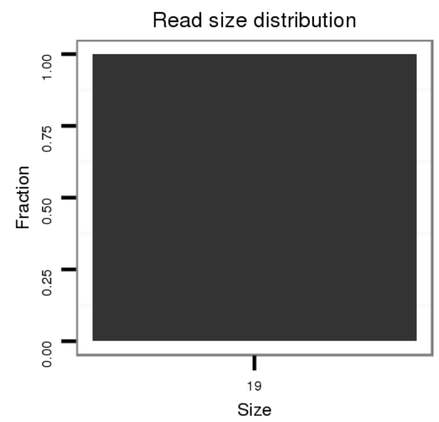
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_2470	**scaffold_6680:12671068-12671132 -**	**confident-exception**	**Canonical miRNA**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

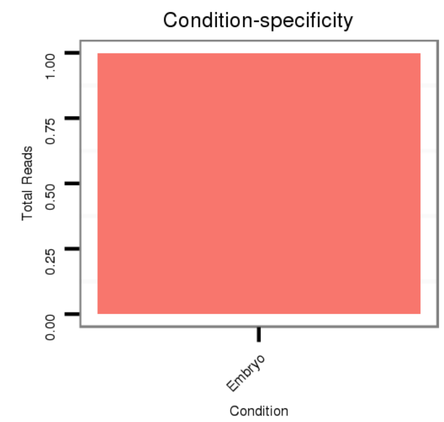
Legend: mature star mismatch in alignment mismatch in read

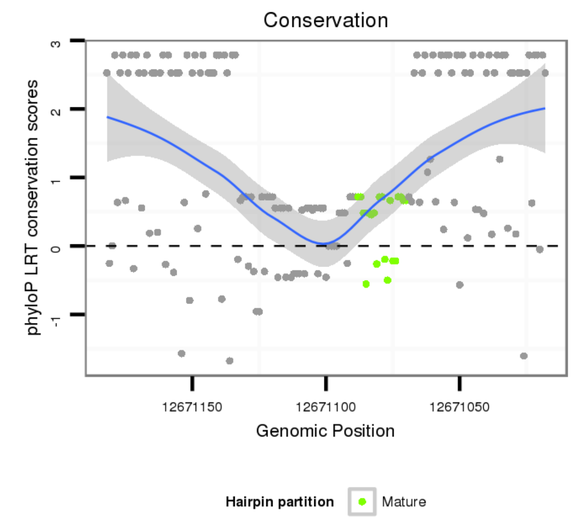
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [DmojGI11891-in]; CDS [DmojGI11891-cds]; CDS [DmojGI11891-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

GCTTGCAGGACTCCGAAGGCGATACGCCACTCCATGACGCCATATCAAAGGTAGAAGGAAATATTTATAATAGGCATGTATATGGGTTTTCATATAAATCTTTTCCCTTTTGCAGGAGCATGATGAGATGCTGTCGCTGTTGCTGGACTTTGGAGCTGACATCAC	Read size	# Mismatch	Hit Count	Total Norm	Total	M060 embryo	V041 embryo	M046 female body	V110 male body
..TAAATCTTTTCCCTTTTGCAGT..	22	1	1	7.00	7	6	1	0	0
..GACTCCGAAGGCGATACG..	18	0	1	1.00	1	0	0	1	0
..TAAATCTTTTCCCTTTTGCAGA..	22	1	1	1.00	1	1	0	0	0
..ATGATGAGATGCTGTCGCT..	19	0	1	1.00	1	0	1	0	0
..TAAATCTTTTCCCTTTTGC..	19	0	1	1.00	1	1	0	0	0
..ATGACGCCATATCAAAGGAGC..	21	3	7	0.14	1	0	0	0	1

Anti-sense strand reads

CGAACGTCCTGAGGCTTCCGCTATGCGGTGAGGTACTGCGGTATAGTTTCCATCTTCCTTTATAAATATTATCCGTACATATACCCAAAAGTATATTTAGAAAAGGGAAAACGTCCTCGTACTACTCTACGACAGCGACAACGACCTGAAACCTCGACTGTAGTG	Read size	# Mismatch	Hit Count	Total Norm	Total	M046 female body
..CGGTATAGTTTCCATCTTCC..	20	0	1	1.00	1	1

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6680:12671018-12671182 -	dmo_2470	GCTTGCAGGACTCCGAAGGCGATACGCCACTCCATGACGCCATATCAAAGGTAGAA----------GGAA-------ATATTTATAATAGGCATGTATATGGGTTTTCATATAAAT-CTTTTCCCTTTTGCAGGAGCATGATGAGATGCTGTCGCTGTTGCTGGACTTTGGAGCTGACATCAC
droVir3	scaffold_13049:18575910-18576092 +		GTTTGCAGGACTCCGAAGGTGACACGCCGCTCCACGATGCCATATCGAAGGTAGAGATTTAACAAAATGTTCTGATCTGCTGCGGATCTGTCTCTTAAAAG-------ATA----------TTTTATATAAATACTATTCACTTTTGCAGGAGCATGATGAGATGCTTTCGCTGCTGCTCGACTTTGGAGCTGATATCAC
droGri2	scaffold_15110:19053133-19053292 +		GTCTGCAGGACTCCGAGGGCGACACGCCGTTACACGATGCCATATCTAAAGTATAA----------TTAATGCTTGTATATATAAATCGAGTATGTGTAA-------TATATA---A---TTTACAATTGCAGGAACACGATGAGATGTTGTCGCTGCTGCTGGACTTTGGAGCCGACATAAC
droWil2	scf2_1100000004837:1624113-1624212 -		GTTTACAGGATTCGGAAGGCGACACTCCATTGCATGACGCCATCTGTAA---AGAACACAACGAAATGTTGTCTCTCCTCCTGATTTTGCCGCTGATATCAC
dp5	XR_group8:8229062-8229161 +		GTCTGCAGGATTCCGAGGGCGATACGCCGCTGCATGATGCCATCTCGAA---GGAGCACGATGAGATGCTGTCGCTGCTGCTGGACTTTGGGGCCGACATCAC
droPer2	scaffold_40:419803-419902 +		GTCTGCAGGATTCCGAGGGCGATACGCCGCTGCATGATGCCATCTCAAA---GGAGCACGATGAGATGCTATCGCTGCTGCTGGACTTTGGGGCCGACATCAC
droAna3	scaffold_13337:11155349-11155448 +		GCCTGCAGGATTCCGAGGGGGACACGCCCCTGCACGATGCCATATCCAA---GGAGCACGACGAGATGCTCTCCTGCTCCTGGACTTCGGGGCCGACATAAC
droBip1	scf7180000396569:231706-231805 -		GCTTGCAGGACTCCGAGGGGGACACGCCCCTGCACGATGCCATATCCAA---GGAGCACGACGAAATGCTCTCCTGCTCCTGGACTTCGGAGCAGACATCAC
droKik1	scf7180000301706:22129-22228 +		GTTTGCAGGACTCCGAGGGCGATACACGCCTGCACGATGCCATTTCAAA---GGAGCACGACGAGATGCTCTCCTGCTGCTGGACTTTGGGGCCAGACATAAC
droFic1	scf7180000454065:1305398-1305497 +		GCTTGCAGGATTCCGAGGGTGATACACGCCTGCACGATGCCATATCCAA---GGAGCACGACGAAATGCTGTCTGTGCTGCTGGACTTCGGGGCTGACATCAC
droEle1	scf7180000491193:5191220-5191319 +		GTTTGCAGGACTCCGAGGGCGACACCCACTCCACGATGCCATCTCCAA---GGAGCACGACGAGATGCTCTCCTGCTGCTGGACTTCGGGGCCGACATCAC
droRho1	scf7180000767651:18605-18704 +		GTTTGCAGGATTCCGAGGGCGATACACTCTCCACGATGCCATCTCCAA---GGAGCACGACGAGATGCTCTCCTGCTGCTTGACTTCGGGGCTGACATAAC
droBia1	scf7180000302334:366821-366920 +		GCTTGCAAGATTCCGAGGGCGATACACTCTTCACGATGCCATTTCCAA---AGAGCACGACGAGATGCTCTCCTGCTGCTGGACTTCGGGGCAGACATCAC
droTak1	scf7180000415815:282069-282168 -		GCCTTCAGGATTCCGAAGGCGACACACGCTGCACGATGCCATCTCCAA---GGAGCACGACGAGATGCTCTCCTTCTGCTGGACTTTGGGGCTGACATCAC
droEug1	scf7180000409824:56567-56666 -		GCTTGCAGGACTCCGAGGGCGATACACTCTTCACGATGCCATATCAAA---GGAGCACGACGAGATGCTCTCCTGTTGCTGGACTTCGGGGCTGACATCAC
dm3	chr3L:16001492-16001591 -		GTTTGCAAGATTCCGAGGGCGATACACCCTACACGATGCCATATCTAA---GGAGCACGACGAGATGCTGTCCCTGTTGCTGGACTTCGGGGCCGACATCAC
droSim2	3L:15620198-15620297 -		GTTTGCAAGATTCTGAGGGCGATACCCGCCTACACGATGCCATATCTAA---GGAGCACGACGAGATGCTGTCCCTGTTGCTGGACTTCGGGGCTGACATCAC
droSec2	scaffold_0:8102424-8102523 -		GTTTGCAAGATTCCGAGGGCGATACCCGCCTACACGATGCCATATCTAA---GGAGCACGACGAGATGCTGTCCCTGTTGCTGGACTTCGGGGCTGACATCAC
droYak3	v2_chr3L_random_063:48339-48438 +		GTTTGCAAGATTCCGAGGGCGATACCCGCCTACACGATGCCATATCTAA---GGAGCACGACGAGATGCTGTCCCTGTTGCTGGACTTCGGGGCTGACATCAC
droEre2	scaffold_4784:18245807-18245906 -		GTTTGCAAGATTCCGAGGGCGATACCCGCCTACACGATGCCATATCTAA---GGAGCACGACGAGATGCTGTCCCTGTTGCTGGACTTCGGGGCTGACATCAC

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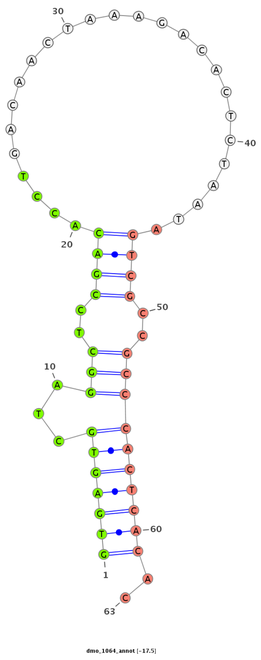
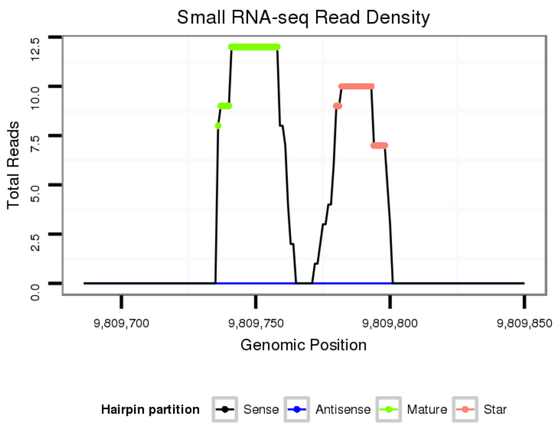
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

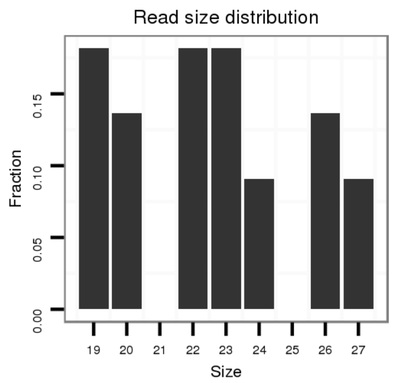
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_1064	**scaffold_6496:9809736-9809800 +**	**candidate**	**Mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

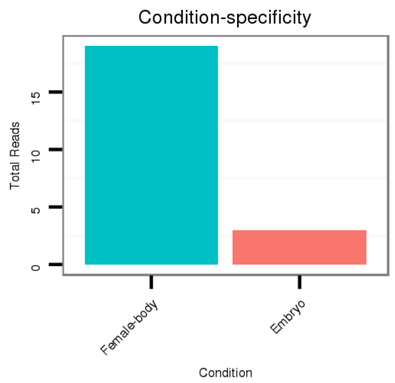
Legend: mature star mismatch in alignment mismatch in read

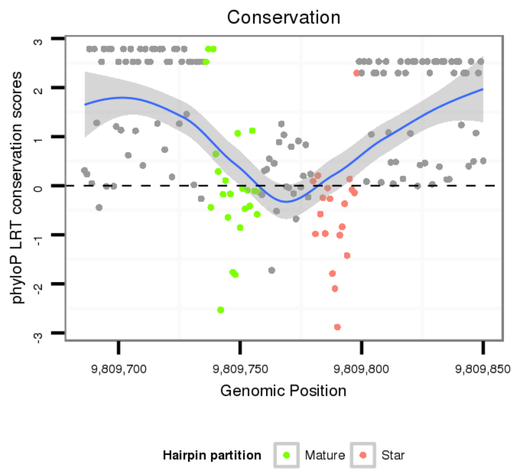
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [DmojGI20364-in]; CDS [DmojGI20364-cds]; CDS [DmojGI20364-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

```
CGTCTCACAGTTTCGCACCTCCGATTGCATTAATGCTTACGATGGCCCAGGTGAGTGCTAGGCTCCGACACCTGACAACTAAAGACACTCTAATAGTCGCCGCCCACTCACACAGAATGCGATGAGGACGAACAGAATATTTCAATTATTTTGAATGGCATCGAG
************************************************(((((((...((((.((((.........................)))))..)))))))))))..**************************************************
```

Read size	# Mismatch	Hit Count	Total Norm	Total	M046 female body	M060 embryo	V110 male body	V041 embryo
23	0	1	3.00	3	3	0	0	0
26	0	1	3.00	3	3	0	0	0
19	0	1	2.00	2	2	0	0	0
22	0	1	2.00	2	2	0	0	0
27	0	1	2.00	2	1	1	0	0
24	0	1	2.00	2	0	2	0	0
22	0	1	1.00	1	1	0	0	0
20	0	1	1.00	1	1	0	0	0
20	0	1	1.00	1	1	0	0	0
24	2	1	1.00	1	1	0	0	0
22	0	1	1.00	1	1	0	0	0
19	0	1	1.00	1	1	0	0	0
23	0	1	1.00	1	1	0	0	0
20	0	1	1.00	1	1	0	0	0
19	0	1	1.00	1	1	0	0	0

Anti-sense strand reads

```
GCAGAGTGTCAAAGCGTGGAGGCTAACGTAATTACGAATGCTACCGGGTCCACTCACGATCCGAGGCTGTGGACTGTTGATTTCTGTGAGATTATCAGCGGCGGGTGAGTGTGTCTTACGCTACTCCTGCTTGTCTTATAAAGTTAATAAAACTTACCGTAGCTC
************************************************(((((((...(((..((((.........................)))))..)))))))))))..**************************************************
```

Read size	# Mismatch	Hit Count	Total Norm	Total	V110 male body	M046 female body	M060 embryo	V041 embryo	V056 head

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6496:9809686-9809850 +	dmo_1064	CGTCTCACAGTTTCGCACCTCCGATTGCATTAATGCTTACGATGGCCCAGGTGAGTG-----C----------TAG-----G---------CTCCGAC----------ACCTGACAACTAA----------AGA----------CACTCTAATAGTCG----------CCG-----CCCACTCACACAGAATGCGATGAGGACGAACAGAATATTTCAATTATTTTGAATGGCATCGAG
droVir3	scaffold_12875:14348361-14348545 +		CGTTTCCGAATTTCGCACCTCCGACTGCATCAATGCCTACGATGGACCAGGTAAGTG-----CAGCA----------GCTGTCGGATGATAC---------ATTTACA----------AAAAAAAAAAAA----------AAACTAATACCCTGCCCTTGA-------T-------CTGGGTTTTGCAGAGTGCGATGAGGACGAGCAAACATTTCAATTATTCTGAATGGCAGCGAG
droGri2	scaffold_15245:14332324-14332508 +		AGTCTCACAGTTTCGCACCTCCGATTGCATCAATGCGTATGACGGCCAGGTAAGTG-----CTATCTCTCTTTCTCTCCGTCTCTCT-----CT---------CTCCGATATACTTAAATAGAGTAATGACCTGA----------CTCTTCATC----------CTGCAACAGAGTGCGACGAGGCTGACCAGAATCTTTCAATTATTTTGAACGGCAGCGAG
droWil2	scf2_1100000004514:18411-18578 -		AGTTTCCGAATTCAGGACCTCCGATTGCATCAATGCTTACGATGGCCAGGTAAAGC-----G----------GAAAA---G-----ACAC-A-----C----------ACACACACCTGAAATTTTTGGTGAATG----------AGTTTTC--AAATTGTTTGCAGATTGCGATGAGAACGAACAGAATATATCCATTATACTGAATGGAACTGAA
dp5	3:3630290-3630453 +		GGTCTCACAGTTCCGCACCTCGGACTGCATCAACGCCTACGATGGACCAGGTCAGTAGTCAG--TA----------G-----------G-----CG----------ATTACTCAATCGAAATCCAAGCTAAGTGAACGT----------TATCCCTTGCAGAGTGCGATGAGGCCGAACAGAACATCTCCATCATCTTGAATGGCAGCGAG
droPer2	scaffold_2:3820543-3820706 +		GGTCTCACAGTTCCGCACCTCGGACTGCATCAACGCCTACGATGGACCAGGTCAGTAGTCAG--TA----------G-----------G-----CG----------ATTACTCAATCGAAATCCAAGCTAAGTGAACGT----------TATCCCTTGCAGAGTGCGATGAGGCCGAACAGAACATCTCCATCATCTTGAATGGCAGCGAG
droAna3	scaffold_13266:4962462-4962517 +		GGTTTCACAATTCCGCACCTCGGACTGCATCAATGCCTACGATGGACCCGGTAAGT-----G----------GAAAA---G-----ACAC-A-----C----------ACACACACCTGAAATTTTTGGTGAATG----------AGTTTTC--AAATTGTTTGCAGATTGCGATGAGAACGAACAGAATATATCCATTATACTGAATGGAACTGAA
droBip1	scf7180000395751:771741-771796 +		GGTTTCACAGTTCCGCACCTCGGACTGCATCAACGCCTACGATGGACCCGGTAAGT-----G----------GAAAA---G-----ACAC-A-----C----------ACACACACCTGAAATTTTTGGTGAATG----------AGTTTTC--AAATTGTTTGCAGATTGCGATGAGAACGAACAGAATATATCCATTATACTGAATGGAACTGAA
droKik1	scf7180000302682:61447-61621 -		GGTTTCACAGTTCCGCACCTCGGACTGCATCAATGCCTACGATGGTCCAGGTTAGTATACCGG----------GGATTATGTAGTGA-----CTCT---------GTCAGA----------AAATTTC---GGTGTATATTTTTCG----------GG-----CTTTTTTCTTGCAGAATGCGACGAGGCTGAGCAGAACATCTCCATCATTTTGAATGGCAGCGAG
droFic1	scf7180000453811:106672-106845 -		GGTCTCACAGTTCCGCACCTCGGACTGCATCAATGCCTACGATGGACCTGGTTAGTTTTCAT--TG----------G-----CATAAAAA-------TATTTGCCC----------ATGATTGAGCTGT----------AATTTTA-------ATTTA---CTTTCT---CTCTGTGGCAGAATGCGACGAGTCCGAGCAGAACGTCTCAATCATCTTGAATGGCAGCGAG
droEle1	scf7180000491232:214552-214706 -		GATTTCGCAGTTCCGCACATCGGACTGCATCAATGCCTACGATGGACCAGGTAAGTT-----G----------A---GTGC----------CTTCCCC----------ATGATTGAGCTGA----------ATTTGTA-------ATT-----CAATTTTTGCAGAATCCGACGAGGCCGAGCAGAATCTCTCATCATCTTGAATGGCATCGAG
droRho1	scf7180000780265:209758-209922 -		GATTTCACAGTTTCGCACCTCGGACTGCATCAATGCCTACGATGGACCCGGTTAGTC-----G----------AATCG---T----------CTCCCC----------ATGATTGAGCTGA----------ATTTTTAACCCGCA----------CTCCC--CCTACATTTGCAGAATGCGACGAGGCCGAGCAGAACCTCTCAATCATCTTGAATGGCAGCGAG
droBia1	scf7180000302143:1245981-1246148 -		GGTTTCCGAGTTCCGCACCTCGGACTGCATCAATGCCTACGATGGACCTGGTAAGAG-----T----------GA-----T----------CTCCAGC----------CGATGATTGATCAGA----------AACTTTAGCCAGCA----------CTTCCTCCTGCCACCTCCAGAATGCGACGAGGCCGAGCAGAACGTCTCAATCATCCTGAATGGCAGCGAG
droTak1	scf7180000415722:40866-41033 +		GGTTTCGCAGTTTCGCACCTCGGACTGCATCAATGCCTACGATGGACCAGGTTAAT-----T----------GACT---CC----------CCACTCC----------CTGATTGATCAGA----------AATTTTAACCCGTA----------CTTCCTC--TGCTCCTCCCCAGAATGCGACGAGGCCGAGCAGAACGTCTCAATCATCCTGAATGGCAGCGAG
droEug1	scf7180000409474:779088-779248 -		GATTTCCCAGTTTCGCACATCGGACTGCATCAATGCCTACGATGGACCTGGTTAGAC-----T----------GC-----GC----------CTCCACT----------ATGATTGATCAGA----------AATTTTA-------AGCCAATAGG-----CGACTTTTTTCAGAATGCGATGAGGCCGAGCAGAACGTCTCAATCATCTTGAATGGCAGCGAG
dm3	chr2R:17163917-17164072 +		GCTTTCGAATTCCGCACCTCGGACTGCATCAATGCCTACGATGGACCTGGTTAGTG-----G----------GATGATGC----------GTTTCC----------ATAATTCAACTGA----------AATATTA-------AA-----CTTATTGCAGAATGCGACGATCCGAGCAGAACGTCTCAATCATCTTGAATGGCAGCGAA
droSim2	2r:17718407-17718562 +		GCTTTCGAATTCCGCACCTCGGACTGCATCAATGCCTACGATGGACCTGGTTAGTG-----G----------GATGATGC----------ATTTCC----------ATAATTCAACTGA----------AACATTA-------AA-----CCTTTTGCAGAATGCGACGATCCGAGCAGAACGTCTCAATCATCTTGAATGGCAGCGAA
droSec2	scaffold_9:493881-494036 +		GCTTTCGAATTCCGCACCTCGGACTGCATCAATGCCTACGATGGACCTGGTTAGTG-----G----------GATGATGC----------GTTTCC----------ATATTCAACTGA----------AACATTA-------AA-----CCTTTTGCAGAATGCGACGATCCGAGCAGAACGTCTCAATCATCTTGAATGGCAGCGAA
droYak3	2R:12024265-12024439 -		GGTTTCGAATTCCGCACCTCGGACTGCATCAATGCCTACGATGGACCTGGTTAGTG-----G----------GACGATGA----------GTTTCC----------ATATGTCAACTGA----------AACTGTAACCAGTGC-C-CCATTA-------AA-----CTTGTTTTTTGCAGAATGCGACGATCCGAGCAGAACGTCTCAATTATCTTGAATGGCAGCGAA
droEre2	scaffold_4845:11308014-11308192 +		GGTTTGCAGTTCCGCACCTCGGACTGCATCAATGCCTACGATGGACCTGGTTAGTA-----G----------GCATGATGA----------ATTTCC----------ATAATTCAGCTGA----------AACTGTAACCAGTGC-CACCATTCAACATTCA-------AA-----CTTTTTGCAGAATGCGACGATCCGAGCAGAACGTCTCAATCATCTTGAATGGCAGCGAA

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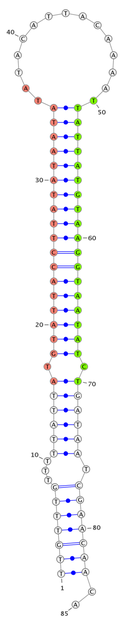
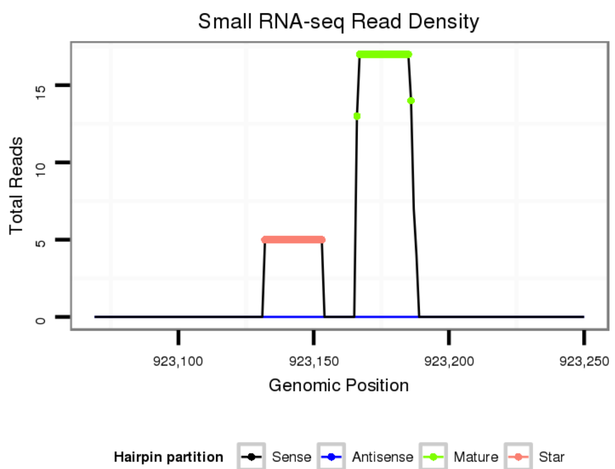
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	0
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

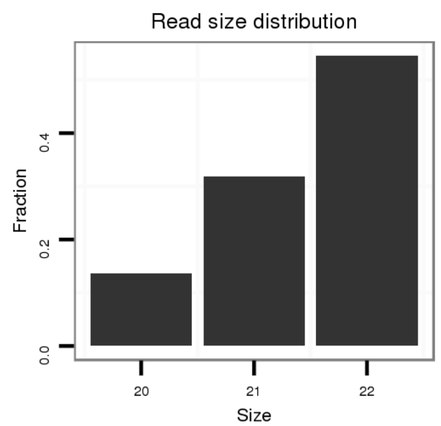
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_343	**scaffold_6359:923119-923200 +**	**candidate**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

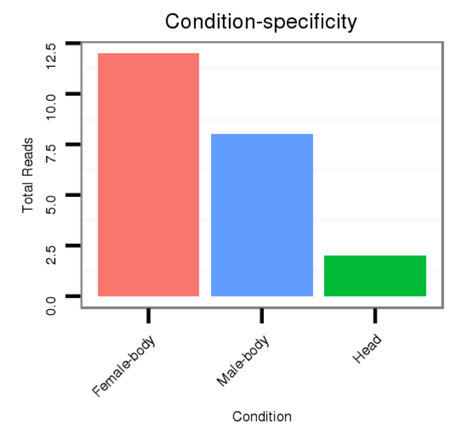
Legend: mature star mismatch in alignment mismatch in read

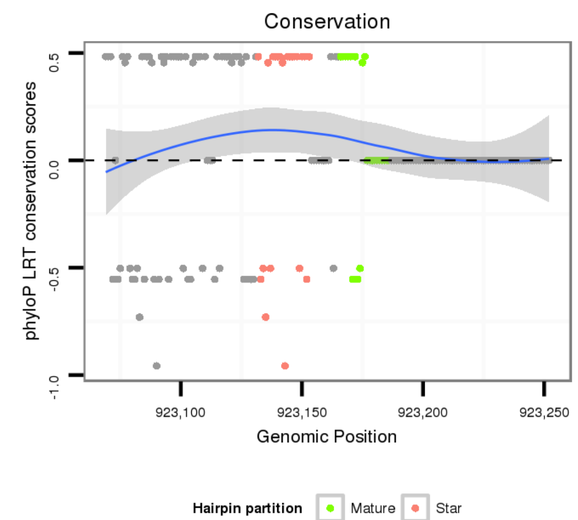
Predicted structure











dmo_343_secst | 2.0.1

Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TTGTGACAATTGCATTTGACAACAATATATCAATCTATGAGTATTGTTTTGTTTGTTTTTATTATGTATTACCTTATATAATATATACATTACAAAATTATTATGTAAGGTAATATCTGATAATCGAACAACATTTCATTCAATGCAATTAACTTTACTATATAGATAGCAGTTCTAGAAGA **********(((((((...(((((((.((((((((((((((((((.....)))))))))))))))))).)))))))..**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M046 female body	V110 male body	V049 head	V056 head
.....TTATTATGTAAGGTAATATCT.....	21	0	1	7.00	7	5	2	0	0
.....ATGTATTACCTTATATAATATA.....	22	0	1	5.00	5	3	2	0	0
.....TATTATGTAAGGTAATATCTGA.....	22	0	1	4.00	4	1	2	0	1
.....TTATTATGTAAGGTAATATCTG.....	22	0	1	3.00	3	2	0	1	0
.....TTATTATGTAAGGTAATATC.....	20	0	1	3.00	3	1	2	0	0

Anti-sense strand reads

AACACTGTTAACGTAAACTGTTGTTATATAGTTAGATACTCATAACAAAACAAACAAAAATAATACATAATGGAATATATTATATATGTAATGTTTTAATAATACATTCCATTATAGACTATTAGCTTGTTGTAAAGTAAGTTACGTTAATTGAAATGATATATCTATCGTCAAGATCTTCT **********(((((((...(((((((.((((((((((((((((((.....)))))))))))))))))).)))))))..**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M046 female body

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6359:923067-923250 +	dmo_343	TTTTGTGACAATTGCATTTGACAACAATATATCAA----------TCTATGAGTATTGTTTTGTTTGTTTTTATTATGTATTA----CCTTATATAATATATACATTACAAAATTATTATGTAAGGTAATATCTGATAATCGAACAACATTTCATTCAATGCAATTAACTTTACTATATAGATAGCAGTTCTAGAAGA
droVir3	scaffold_12822:3605195-3605306 -		TTTTA-AAACAGAAAAAATTGTGTACATATATTATTATCGTAAGAAAACTATAA---ATATTTTGTTTGATAAAATAGGGCATTATTTAGGTTATACAAAA--------ATAAAATTAATTCGT----------

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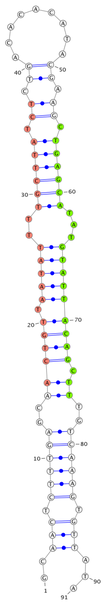
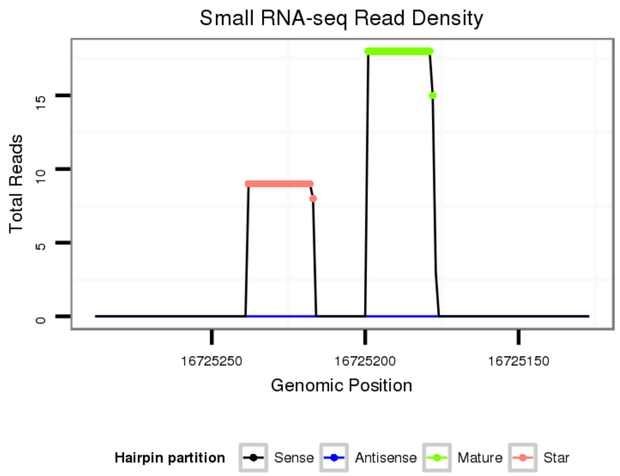
PASS/FAIL	
crit.star	1
crit.uri	1
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

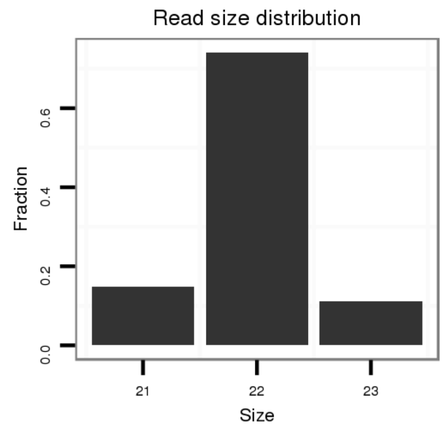
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_288	**scaffold_6680:16725177-16725238 -**	**candidate**	**Canonical miRNA**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

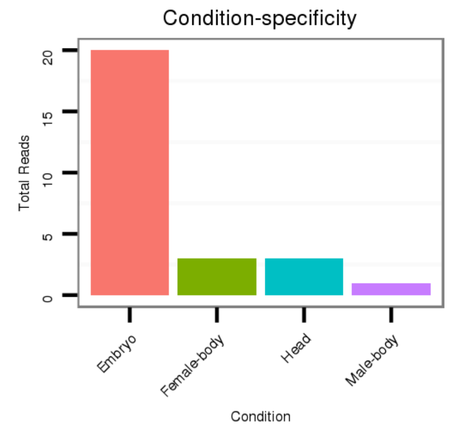
Legend: mature star mismatch in alignment mismatch in read

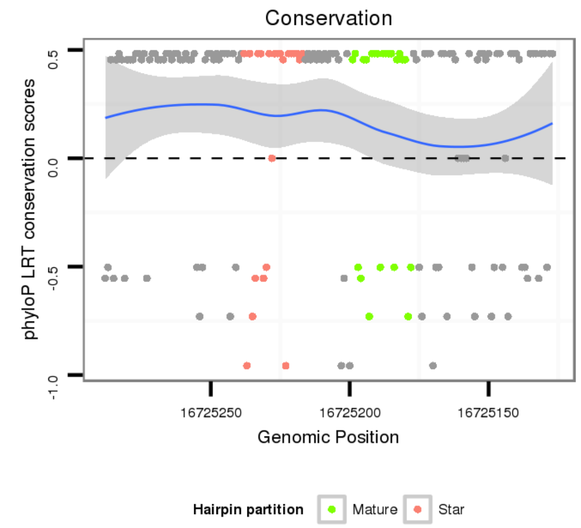
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [DmojGI11698-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

AGCACTCAGCGAACTTGTTCGCATGAACCAGCTACGCAACTCTTTGAGCAACTGTTAATATTTTGCTTATCTCTGACACACATACGAAGCTGAGCATATGTATTACAGCTTTGTCAAAGTGTTATACACACAGAGTAGAGGTTGGGTTAGTGTTATAATAAA **********..((((.((((((..((((((.(((((..((((((.((.((.....)).)).)))))))...)))))))))).))..)))))).)))...**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M060 embryo	M046 female body	V049 head	V041 embryo	V110 male body	V056 head
.....CTGAGCATATGTATTACAGCTT.....	22	0	1	12.00	12	7	1	3	0	1	0
.....ACTGTTAATATTTTGCTTATCT.....	22	0	1	8.00	8	8	0	0	0	0	0
.....CTGAGCATATGTATTACAGCTTT.....	23	0	1	3.00	3	2	1	0	0	0	0
.....CTGAGCATATGTATTACAGCT.....	21	0	1	3.00	3	2	0	0	1	0	0
.....ACTGTTAATATTTTGCTTATCC.....	22	1	1	2.00	2	2	0	0	0	0	0
.....ACTGTTAATATTTTGCTTATC.....	21	0	1	1.00	1	0	1	0	0	0	0

Anti-sense strand reads

TCGTGAGTCGCTTGAACAAGCGTACTTGGTCGATGCGTTGAGAAACTCGTTGACAATTATAAAACGAATAGAGACTGTGTGTATGCTTCGACTCGTATACATAATGTCGAACACAGTTTCACAATATGTGTGTCTCATCTCCAACCCAATCACAATATTATTT **********..(((.((((((..((((((.(((((..((((((.((.((.....)).)).)))))))...)))))))))).))..)))))).)))...**********	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
droMoj3	scaffold_6680:16725127-16725288 -	dmo_288	AGCACTC--AGCGAACTTGTTCGCAT----------GAACCAGCTACGCAACTCTTTGAGCAACTGTTAATATTTTGCTTATCT----------CTGACACACATACG----AAGCTGAGCATAT----GTATTACAGCTTTGTCAAAGTGTTATACACACAGAGTAGAGGTTGGGTTAGTGTTATAATAAA
droVir3	scaffold_13049:22129255-22129458 -		TACTCTCTATGCGAACTAGTTCGCATACACTTATCTGTAAATACGAAGAACCAGCTGAACAACTCTTTAACAAGTTATATCA-TTTGCTTATCTGCATATTTATGCACACACTGACACACATAGCCATATACCTATGCCTATATCTATTTGCAGCGCTGCAAAACCATTCTAC----AACGTAGATATTA-TTAGCAATATTATGAA

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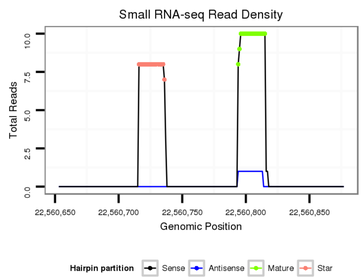
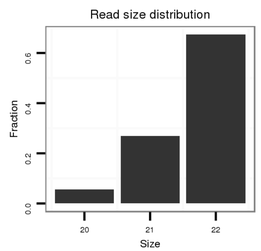
PASS/FAIL	
crit.star	1
crit.loop	1
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

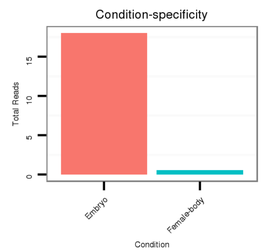
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_2740	**scaffold_6540:22560703-22560827 +**	**candidate**	**Canonical miRNA**	**intron**	[View on UCSC Genome Browser [Cornell Mirror]]

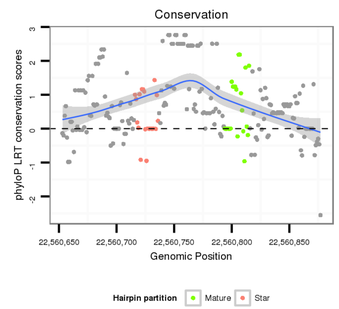
Legend: mature star mismatch in alignment mismatch in read

Predicted structure









Show Alternate Folds

Flybase annnotation

intron [DmoJGI10174-in]

Repeatable elements

Name	Class	Family	Strand
(TTGn	Simple_repeat	Simple_repeat	+
(CAAn	Simple_repeat	Simple_repeat	+

mature	star
	1. scaffold_6473:5796844-5796864 - 2. dmo_2740 scaffold_6540:22560716-22560736 +

Sense Strand Reads

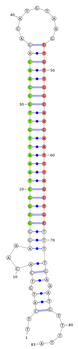
hide 3p reads show mid mismatch reads

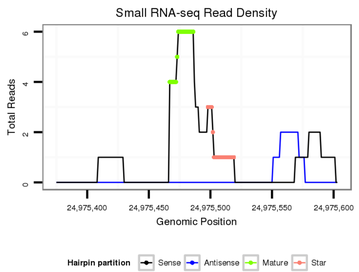
```
                                                
```

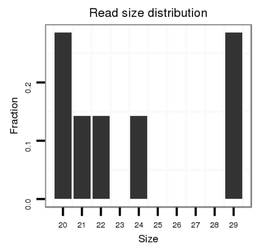
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_2782	**scaffold_6540:24975425-24975553 +**	**candidate**	**Canonical miRNA**	**CDS**	[View on UCSC Genome Browser [Cornell Mirror]]

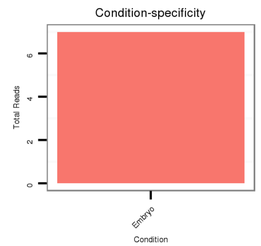
Legend: mature star mismatch in alignment mismatch in read

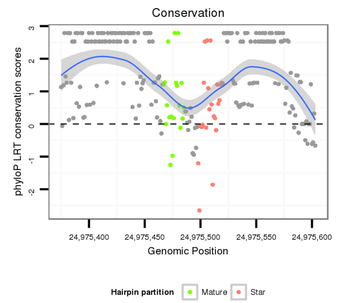
Predicted structure











Show Alternate Folds

Flybase annnotation

CDS [Dmo]GI10303-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

```
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                
GCCAACAATGCCCAAAATAATACGCTACACGGTTCCTGAGGTTCGTACAAGGACTTTTGGTAAATTCTTAAATACATTTCATGTCACAAAGGGCGGCTAAATTGTTGCCAACAGACATGTAAGCTGTTGGCAACAATTTAGCTGCTTTTGAAATGTTTTAAGAGTTTACCGGAAGTCCTGCTGAGCGTCACCCAAATCCAATAACCCTCTCAACAACAACAACAACAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                
**********..(((.(((...((((((((((((((((((((((((((.........)))))))))))))))))))))))))))..)))).....**********
.....GCGGCTAAATTGTTGCCAAC.....
.....GCGGCTAAATTGTTGCCAACAGAC.....
.....AATTGTTGCCAACAGACATGTAAGCTGT.....
.....CCTCTCAACAACAACAACAACA..
.....AATCCAATAACCCTCTCAACA.....
.....CTGTTGGCAACAATTTAGCTGC.....
.....GCGGCTAAATTGTTGCCAACA.....
.....CCTGAGGTTCGTACAAGGACT.....
.....GCGGCTAAATTGTTGCCAACAGC.....
```

Anti-sense strand reads

```
CGGTTGTTACGGGTTTTATTATGCGATGTGCCAAGGACTCCAAGCATGTTCCTGAAAACCATTTAAGAATTTATGTAAAGTACAGTGTTTCCCGCGATTTAACAACGGTTGTCTGTACATTCGACAACCGTTGTTAAATCGACGAAAACTTTACAAAATTCTCAAATGGCCTTCAGGACGACTCGCAGTGGGTTTAGGTTATTGGGAGAGTTGTTGTTGTTGTTGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                
**********..(((.(((...((((((((((((((((((((((((((.........)))))))))))))))))))))))))))..)))).....**********
.....CTCGCAGTGGGGTTTAGGTTA.....
.....GGACGACTCGCAGTGGGTTTA.....
```

Re-alignment of all predicted orthologs

```
Species  Coordinate                          ID          Alignment
droMoj3  scaffold_6540:24975375-             dmo_2782    GCC---AACAATGCCCAAAATAATACGCTACACGGTTCCTGAGGTTCGTACAAGGACTTTTGGTAAATTCTTAA-ATACATTTCATGTCA-CAAAG----------------------GCGGCTAA---ATTGTTGCCAAC-AG---AC-----AT----------------------GT------------------------------------------------------AA-----------G----CTGTTGGCAACAATTT----AGCTGCTTTT---GAAATGTTTTA-AGAGTTTACCGGAAGTCCTGCTGAGCGTCACCC-----------------AAATCCAATA----AC-----------------CCTCTCAACAACAACAA-----------------------CAACAAC
         24975603 +
droVir3  scaffold_12855:7690617-             ------C---AACAATGCCAGAATAATCCGCTACACGGTTCCTGAGGTTCGTACAAGGACTTTTGGTAAATTCAGAA-ATACATTTCAG-G-G--CAAAA----------------GCGGCTAA---CTTGTTGCAAA--G---G-----G-----------------G-----------------------------------ACAAATTGAAGCCGCAAATTGTGCATTTTTC-----------G-----G-TTGGCAAAGCGCG----AGCTGCTTTT---GAAATGTCTTA-CAGTTTACCGAGTTCACCGAGCGTCCTGCTGAGCGTCACCC-----------------AAATCCAATA----AC-----------------CCTCTCAA---------------------------------
         7690844 -
droGri2  scaffold_15074:5197840-             GCC---AGCAGTGCCAGAATAATCCGCTACACGGTTCCTGAGGTTCGTACAAGGACTTTTGGTAAACTCTGAAG-GCATTTCATG-CGCGAAA----------------GCGGCGT---CTGTTGCCAAC-T---G-----G-----------------G-----------------------------------GCAAATCGCTGCCATAA-----ATTGCC-----------A-----TGTTGGTAAACGCGC----AGCTGCTTTTTGCGAAATGTCTTA-AGAGTTTACCGCAGTCTGCTGAGCGTCACCC-----------------AAATCCAATA----AC-----------------CCTCTAACAA---AGT---------------------------AACCA
droWil2  scaf2_11000000004902:65880012-     ------A-G-G-C-CAAAATAAT-G-CTACACGGTTCCTGAGGTTCGTACAAGGACTTTTGGTAAATTCTGGAA-ATACATTTCAG-CA--GAAGAAAAAGAAAAGAAACAGAAAAGGAATT-ATCAA----A-G-A-TGCCGTATTGGA----AT----------------TCAAATTAAATTGC---------------------------------PGCCAAAAAGCT-----------------------T---T--TGATGTTT---TCCTTTCTCTCAGT----TGCCGCTGTTTCCTTT---GAAATGTCTTA-CAGTCCTGCTGAGCGTCACCCCACCACACCGCATACACAAAAACTTCCA----------T-AAAAAAAAAATAATAATG-ATACAATAA---AATAAAACAGACAAACAAATAGACAG--ACACA
         6588353 +
dp5      2:2576347l-2576379 +                Dpa_123     -G---AACAATGCCAGAATAGACTACACGGTTCCTGAGGTCGTACAAGGACTTTTGGTAAATTCTGAA-GATATTTCAG-CA-GAAGA----------------GCGGGCCG---GAGTTTCGACGT-ACCCTG-----G-----------------G-----------------------------------TG--AAGAAGCT-----------------------CGTCGTGAGGATCGTAG----GTCCGGGCAGCGCG----TGCGGCTTTT---GAAATGTCTTA-AGAGTTTACCGAGTCTACCGCTGAGCGTCACCC-----------------AATCCAATCCCCATAC----------AATAAC----------------G-----------------------TGTAAC
droPer2  scaffold_6111629958-1163206         Dpa_2243    -G---AACAATGCCAGAATAGACTACACGGTTCCTGAGGTCGTACAAGGACTTTTGGTAAATTCTGAA-GATATTTCAG-CA-GAAGA----------------GCGGGCCG---GAGTTTCGACGT-ACCCTG-----G-----------------G-----------------------------------TG--AAGAAGCT-----------------------CCTTCGTGAGGATCGTAG----GTCCGGGCAGCGCG----TGCGGCTTTT---GAAATGTCTTA-AGAGTTTACCGAGTCTACCGCTGAGCGTCACCC-----------------AATCCAATCCCCATAC----------AATAAC----------------G-----------------------TGTAAC
         -
droAna3  scaffold_13340:14074511-            GCCAAGAACATGCCAGAATACGCTACACGGTTCCTGAGGTCGTACAAGGACTTTGGTAAATCCGGAA-CCATTTCAG-A-T-AA----------------GCAT-CGG----CGTTTCAGGT-AGCCGG-----A-----------------T-----------------------------------A-----------T-----ATTGCCG-----------G----CAT-GGCGCAGCAGAGCG----GCAGGCTTTT---GAAATCGGCTT-T-T-T-TTACCGGCGGTCCTGCTGAGCGTCACCC-----------------AATCCAATT----AC-----------------AATAAC-CCTCTAA-----------------------
droBip1  scaf7180000395971:1084771-          GCCAAGAACATGCCAGAATACGCTACACGGTTCCTGAGGTCGTACAAGGACTTTGGTAAATCCGGAA-CCATTTCAG-A-TGGA----------------GCGCTCGG---GGCTGTTCAGGT-TCCGG-----A-----------------T-----------------------------------A-----------T-----ATTGCTG-----------G----CGTTGGTAGCGAGCG----GCAGGCTTTT---GAAATCGGCTT-T-T-T-TTACCGGCGGTCCTGCTGAGCGTCACCC-----------------AATCCAATT----AC-----------------AATAAC-CCTCTAAAAA-----------------------CCTCA
         1085007 +
droKik1  scaf7180000302706:1794288-          -G----AACAATGCCAGAATACCCGCTACACGGTCCTGAGGTCGTACAAGGACTTTGGTAAATCCGGAA-CCATTTCAG-A-TAAG----------------GCGGGCCG---CGCTCTCGCGGT-T-CCGGCTAT---AAAT-AGATCCACATCCGAATCGGAT-----------C-----GGATC-----------------T-----------------------------------A-----------T-----ATTGCCG-----------G----TGCCGCGCAGCGCGC----AGCTGCTTTT---GAAATCGGCTT-T-T-T-TTACCGGCGGTCCTGCTGAGCGTCACCC-----------------AATCCAATT----AC-----------------------------------------------
         1794530 +
droFic1  scaf7180000453488:226107-           GCC---AACAATGCCAGAATACCCGCTACACGGTCCTGAGGTCGTACAAGGACTTTGGTAAATCCGGAA-CCATTTCAG-A-TAAGA----------------GCGAGCGG-CGAACTCTCGCGGT-T-CCGGC-----TG-----------------G-GGATCCGGGGATAG-----GGATC-----------------T-----------------------------------TCGGAGTGGCG-----------G----CGGCGCAGCAGCGGCG----GGTGGCTTTT---GAAATCGGCTT-T-T-T-GTTTACGGCGGTCCTGCTGAGCGTCACGACGC-----------------AATCCAATT----AC-----------------AATAACCCTCG-----------------------
         226358 +
droEle1  scaf7180000491080:2089050-          -G----AACAATGCCAGAATACCCGCTACACGGTCCTGAGGTCGTACAAGGACTTTGGTAAATCCGGAA-CCATTTCAG-A-TAAGA----------------GCGGGCCG---CGCTCTCGCGGT-T-CCGGC-----TG-----------------G-----------------------------------A-----------T-----CCTACCT-----------G----CGGCCGCAGCGAGACG----AGCTGCTTTT---GAAATCGGCTT-T-T-T-GAACGTTACCGGCGGTCCTGCTGAGCGTCACCC-----------------AATCCAATT----AC-----------------AATAAC-CTCCAATTAC-----------------------
         2089291 +
droRho1  scaf7180000079338:48636-            -G----AACAATGCCAGAATACCCGCTACACGGTCCTGAGGTCGTACAAGGACTTTGGTAAATCCGGAA-CCATTTCAG-A-TAAG----------------GCGGGCCG---CGCTCTCGCGGT-T-CCGGC-----TG-----------------G-----------------------------------A-----------T-----ACTGCCT-----------G----TGCCGCGCAGCAGCGC----AGCTGCTTTT---GAAATCGGCTT-T-T-T-GAACGTTACCGGCGGTCCTGCTGAGCGTCACCC-----------------AATCCAATT----AC-----------------AATAAC-----------------------
         48871 +
droBia1  scaf7180000302113:3465600-          -G----AACAATGCCAGAATACCCGCTACACGGTCCTGAGGTCGTACAAGGACTTTGGTAAATCCGGAA-CCATTTCAG-A-TAAG----------------GCGGGCGG---GCGCTCGACGT-T-AGGCT-----A-----------------G-GGATCCGG-TGTATCACAGGGAGACT-----------C-----GGATC-----------------T-----------------------------------A-----------T-----ACTGACG-----------A----CATTGCGCGCGCGCGCGC----AGCTGCTTTT---GAAATCGGCTT-T-T-T-GTACCGGCGGTCCTGCTGAGCGTCACCC-----------------AATCCAATT----AC-----------------------------------------------
droTak1  scaf7180000410579:64911-            -G----AACAATGCCAGAATACCCGCTACACGGTCCTGAGGTCGTACAAGGACTTTGGTAAATCCGGAA-CCATTTCAG-A-TAAG----------------GCGGCCTG---GCGCTCGCGGT-T-CTT--TAAGAG-GTTGA----------------TG-AGATCCA-TATACCATATAAGGATCTAATCCAA----------AC-----------------A-----ATTGACT-----------G----CGTCGCGCAGCGCGCGC----AGCTGCTTTT---GAAATCGGCTT-T-T-T-GTACCGGCGGTCCTGCTGAGCGTCACCC-----------------AATCCAATT----AC-----------------AATAAC-----------------------
         49164 +
droEug1  scaf7180000409797:1238118-          -G----AACAATGCCAGAATACCCGCTACACGGTCCTGAGGTCGTACAAGGACTTTGGTAAATCCGGAA-CCATTTCAG-A-TAAG----------------GCAACGCG---ATTGCTCGCGGT-T-CCGGC-----T-----------------A-----------------------------------A-----------T-----ATA-----------A----CGTCGCGCAGCGAGCGC----AGCTGCTTTT---GAAATCGGCTT-T-T-T-GTACCGGCGGTCCTGCTGAGCGTCACCC-----------------AATCCAATT----AC-----------------AATAAC-----------------------
         1238341 +
dm3      chr3R:7594368-7594600 -              -G----AACAATGCCAGAATACCCGCTACACGGTCCTGAGGTCGTACAAGGACTTTGGTAAATCCGGAA-CCATTTCAG-A-TAAG----------------GCGGCCG-C---CCTCTCGCGGT-T-CCGGC-----A-----------------G-----------------------------------A-----------T-----ACTGACG-----------G----CGCCGCGCAGCGCGC----AGCTGCTTTT---GAAATCGGCTT-T-T-T-GTACCGGCGGTCCTGCTGAGCGTCACCC-----------------AATCCAATT----AC-----------------AATAAC-----------------------
droSim1  chr1:13505728-13505966 +            -G----AACAATGCCAGAATACCCGCTACACGGTCCTGAGGTCGTACAAGGACTTTGGTAAATCCGGAA-CCATTTCAG-A-TAAG----------------GCGGCTAC---CCCTCTCGCGG--T-CTCGC-----AT----------------GTGGTTTCCG-TATAG------CGATA-----------A-----------T-----ACTGACG-----------G----CTCGCGCAGCGAGCGC----AGCTGCTTTT---GAAATCGGCTT-T-T-T-GTACCGGCGGTCCTGCTGAGCGTCACCC-----------------AATCCAATT----AC-----------------AATAAC-----------------------
droSec1  scaffold_0114371239-                -G----AACAATGCCAGAATACCCGCTACACGGTCCTGAGGTCGTACAAGGACTTTGGTAAATCCGGAA-CCATTTCAG-A-TAAG----------------GCGGCTAC---CCCTCTCGCGG--T-CTCGC-----AT----------------GTGGTTTCCG-TATAG------CGATA-----------A-----------T-----ACTGACG-----------G----CTCGCGCAGCGAGCGC----AGCTGCTTTT---GAAATCGGCTT-T-T-T-GTACCGGCGGTCCTGCTGAGCGTCACCC-----------------AATCCAATT----AC-----------------AATAAC-----------------------
         14234460 +
droYak3  3R:18823626-16823864 +              -G----AACAATGCCAGAATACCCGCTACACGGTCCTGAGGTCGTACAAGGACTTTGGTAAATCCGGAA-CCATTTCAG-A-TAAG----------------GCGGCCG-C---CCCTCTCGCGG--T-CTCGC-----A-----------------G-----------------------------------A-----------T-----ACTGACG-----------G----AGCCGCGCAGCGAGCGC----AGCTGCTTTT---GAAATCGGCTT-T-T-T-GTACCGGCGGTCCTGCTGAGCGTCACCC-----------------AATCCAATT----AC-----------------AATAAC-----------------------
droEre2  scaffold_4770:14021914-             -G----AACAATGCCAGAATACCCGCTACACGGTCCTGAGGTCGTACAAGGACTTTGGTAAATCCGGAA-CCATTTCAG-A-TAAG----------------GCGGCCG-C---CCCTCTCGCGG--T-CTCGC-----A-----------------G-----------------------------------A-----------T-----ACTGACG-----------G----CGCCGCGCAGCGAGCGC----AGCTGCTTTT---GAAATCGGCTT-T-T-T-GTACCGGCGGTCCTGCTGAGCGTCACCC-----------------AATCCAATT----AC-----------------AATAAC-----------------------
         14022146 +
```

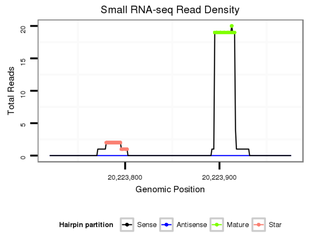
Generated: 09/08/2015 at 07:56 PM

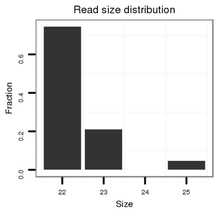
	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.miss	1
crit.pairing	1
crit.top3	1
crit.lproj3	1
crit.uri	0
crit.back	0
rescue.total	0
rescue.homo	1
rescue.linear	1
rescue.confident	1
rescue.candidate	1

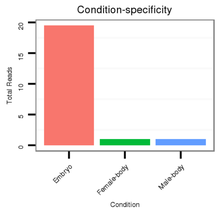
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_2634	**scaffold_6496:20223770-20223926 +**	**candidate**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser [Cornell Mirror]]

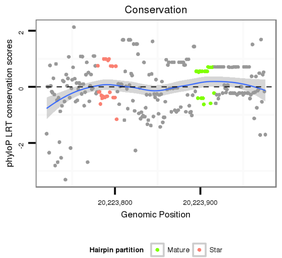
Legend: mature star mismatch in alignment mismatch in read

Predicted structure









Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

mature	star
	1. scaffold_6473:15703963-15703985 + 2. dmo_2634 scaffold_6496:20223780-20223802 +

Sense Strand Reads

hide 3p reads show mid mismatch reads

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            
CATGTATGTGCATAAAAAGTTCCTACATGTATATATAGAAACATGTATGTTTATGTACAGTGCATCAATAATGTCTTCGTACGTAACATACATATATACATATGTATGCATGGTGCCACAACTTAAGTGACACACTGTATATTTATTATACTCATTCATATTCTGTTGCTGTTGTACGTAGACATATTTGGCGCACTGTACATAAAAGCCTCACATCAATAATAACTTATTAATGGATTATAAATAAATGTTTTTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                
```

	Read size	# Mismatch	Hit Count	Total Norm	Total	M060 embryo	M046 female body	M046 male body	V110 embryo	V041 head	V049 head	V056 head
TACGTAGACATATTTGGCGCCAG	22	0	1	15.00	15	14	1	0	0	0	0	0
TACGTAGACATATTTGGCGCCAC	23	0	1	3.00	3	3	0	0	0	0	0	0
TACGTAGACATATTTGGCGCAC	22	1	1	2.00	2	1	1	0	0	0	0	0
TGCATCAATAATGTCTTCGTACA	23	0	2	1.50	3	3	0	0	0	0	0	0
TACGTAGACATATTTGGCGCCACT	24	1	1	1.00	1	1	0	0	0	0	0	0
TATGTACAGTGCATCAATAATGTCT	25	0	1	1.00	1	0	1	0	0	0	0	0
GCACTGTACATAAAAGCCT	19	0	1	1.00	1	1	0	0	0	0	0	0
TACGTAGACATATTTGGCGCCACC	23	1	1	1.00	1	1	0	0	0	0	0	0
TTGTACGTAGACATATTTGGCG	22	0	1	1.00	1	1	0	0	0	0	0	0

Anti-sense strand reads

```
GTACATACACGTATTTTTCAAGGATGTACATATATATCTTTGTACATACAAATACATGTCACGTAGTTATTACAGAAGCATGTCATTGTATGTATATATGTATACATACGTACCACGGTGTGAATTCACTGTGTGACATATAAATAATATGAGTAAGTATAAGACAACGACAACATGCATCTGTATAAACCGCGTGGACATGTATTTTCGGAGTGTAGTTATTATTGAATAATTACCTAATATTTATTTACAAAAGT
```

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
droMoj3	scaffold_4696:20223720-20223976 +	dmo_2634	
droVir3	scaffold_12970:1175595-1175767 -		
droGri2	scaffold_15203:5567813-5568018 +		
droWil2	scaffold_13000000043431:1664890-1665179 +		
dp5	XL_group1a:50297-50398 +		
droRer2	scaffold_14:2260658-2261176 +		
droAna3	scaffold_12923:1602853-1602926 -		
droBip1	ncf718000039643 4:443821-443871 -		
droKik1	ncf718000003022851:1638-1767 -		
droFic1	ncf718000004540721:2994618-2994668 -		
droEle1	ncf718000049127:1339697-1339749 -		
droRho1	ncf718000007799985:257517-257568 +		
droBia1	ncf718000003012327:32791-32920 -		
droYak1	ncf718000041481715040:5100 +		
droEug1	ncf718000040936 0:183-289 +		
dm3	chr3Dmatral:2819686-2819626 +		
droBen2	ncf718000041489356:57681 +		
droYak3	DR:16140441-16140618 -		
droEre2	scaffold_382:385-491 -		

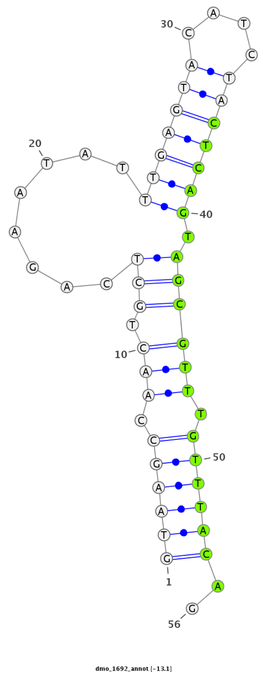
Generated: 09/08/2015 at 07:58 PM

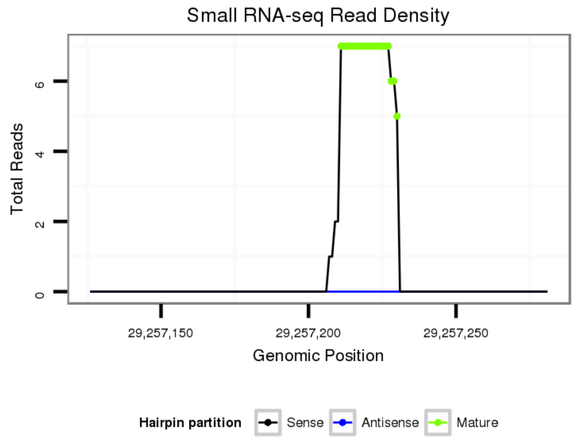
	Value
crit.star	0
crit.loop	0
crit.mor	0
crit.mat	0
crit.seed	0
crit.duplex	1
crit.loop3	1
crit.loop3	1
crit.loop5	1
crit.flank	1
rescue.total	1
rescue.mature	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

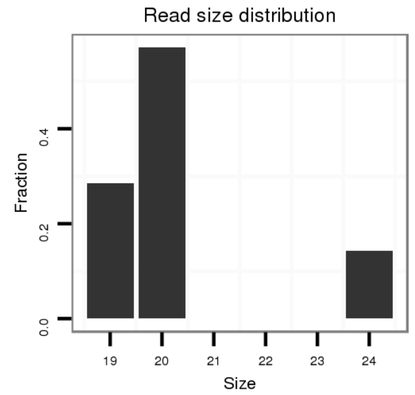
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_1692	**scaffold_6500:29257176-29257231 +**	**candidate**	**Mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

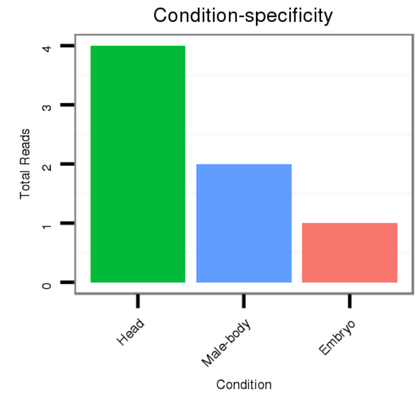
Legend: mature star mismatch in alignment mismatch in read

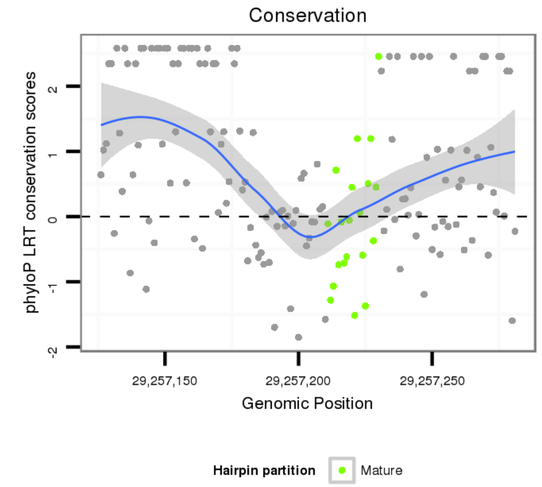
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dmoj\GI18235-in]; CDS [Dmoj\GI18235-cds]; CDS [Dmoj\GI18235-cds]

No Repeatable elements found

Sense Strand Reads

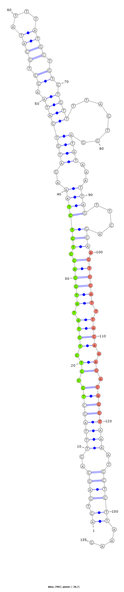
hide 3p reads show mid mismatch reads

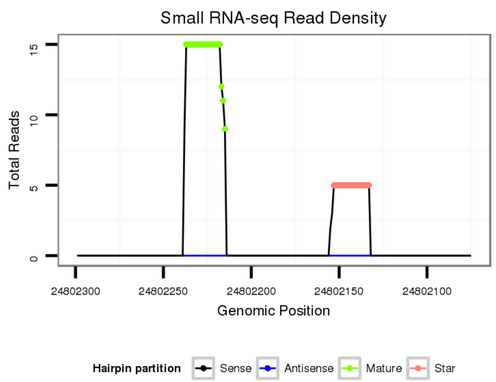
```
                                                
```

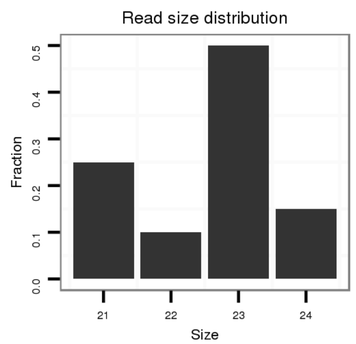
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_2962	**scaffold_6500:24802125-24802249 -**	**candidate**	**Canonical miRNA**	**intron**	[View on UCSC Genome Browser [Cornell Mirror]]

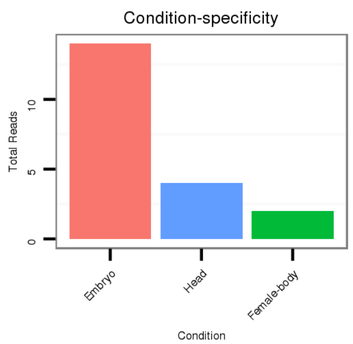
Legend: mature star mismatch in alignment mismatch in read

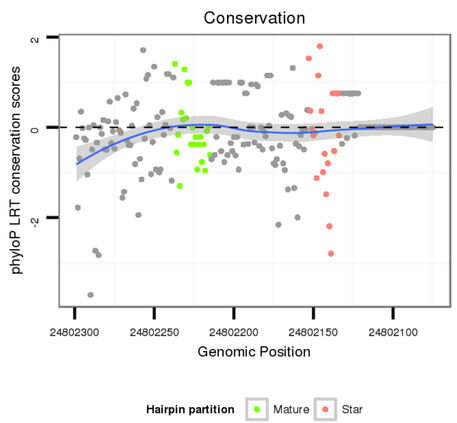
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dmo]GI21441-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

ATATTATATGCACTGATATATATTGTTAAAATTTAAATTAGAAACTCAGTGAGCAGTTTAGCTGCCTCTGTATATGGACCTGTCTAAAGATGTGATAAGCTGCATATTTATGCTGTCTGTTTTAGTGGATATAAATTAGTTCAGCAAGTCCATTTACAAAGACAGCTAAAATGCTCTTAAAGCATCAAAGCCCACACAAATTTGTTGATCAAATATAAAATATGA	Read size	# Mismatch	Hit Count	Total Norm	Total	M060 embryo	M046 female body	V041 embryo	V049 head	V056 head	V110 male body
((.((((..((((((((.((.((((.((((((.((((((..((((((((.((.((((....)))).)).)))).....)))).....)))...)))).....)))).))))))).))))).)).))))))..))))))....)											
.....TGCCTCTGTATATGGACCTGTCT.....	23	0	1	6.00	6	3	0	2	0	1	0
.....CTGCCTCTGTATATGGACCTG.....	21	0	1	3.00	3	0	1	0	2	0	0
.....CTGCCTCTGTATATGGACCTGTCT.....	24	0	1	3.00	3	2	0	1	0	0	0
.....AGTCCATTTACAAAGACAGCT.....	21	0	1	2.00	2	1	1	0	0	0	0
.....CAAGTCCATTTACAAAGACAGCT.....	23	0	1	2.00	2	2	0	0	0	0	0
.....CTGCCTCTGTATATGGACCTGTC.....	23	0	1	2.00	2	1	0	1	0	0	0
.....TGCCTCTGTATATGGACCTGTCTCCC.....	26	3	1	1.00	1	1	0	0	0	0	0
.....CTGCCTCTGTATATGGACCTGT.....	22	0	1	1.00	1	0	0	0	1	0	0
.....TGCCTCTGTATATGGACCTGTCG.....	23	1	1	1.00	1	1	0	0	0	0	0
.....AAGTCCATTTACAAAGACAGCT.....	22	0	1	1.00	1	1	0	0	0	0	0
.....TGCCTCTGTATATGGACCTGTCTC.....	24	1	1	1.00	1	0	0	1	0	0	0

Anti-sense strand reads

TATAATATACGTGACTATATATAACAATTTTAAATTTAATCTTTGAGTCACTCGTCAAATCGACGGAGACATATACCTGGACAGATTTCTACACTATTCGACGTATAAATACGACAGACAAAATCACCTATATTTAATCAAGTCGTTCAGGTAAATGTTTCTGTCGATTTTACGAGAATTTCGTAGTTTCGGGTGTGTTTAAACAACTAGTTTATATTTTATACT	Read size	# Mismatch	Hit Count	Total Norm	Total	M046 female body	V041 embryo	V110 male body	M060 embryo
((.((((..((((((((.((.((((.((((((.((((((..((((((((.((.((((....)))).)).)))).....)))).....)))...)))).....)))).))))))).))))).)).))))))..))))))....)									

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6500:24802075-24802299 -	dmo_2962	ATATTATATGCACTGATATATATTGTTAAAATTTAAATTAGAAACTCA--GTGAGCAGTTTAGC----------TGCCTCTGTATATGG-ACCTGTCTAAAGATGTGATAAGCTGCATATTTATGCTGTCTGTTTTAGTGGATATAAATTA--------GTTCAGCAAGTCCATTTACAAAG----------ACAGCTAAAATGCTCTTAAAGCATCAAAGCCCACACAAATTTGTTGATCAAATATAAAATATGA
droVir3	scaffold_13047:9328067-9328194 -		ATAT---ATGTATATATATATATTGTTGTTGTAAGTGG------GATTGTCAATTTGCCTATCGTATAAATGTGATATA---------A----------ATGTTGCCAGTTTTGAGAATACAAATTA--------AGCCTACAAATATTTTACAAA----------
droGri2	scaffold_15112:3285104-3285209 -		ATGTTATCTACATATA-----CAATTTCAATTGAAAATTGTAACTTC--GTTAAGAG------GTGAGATGCCTCTGTAAAAACTTTGACCCGCACATTTCACACTTCAGATT----------T---TTGC----------
droWil2	scf2_1100000004513:2965796-2965854 +		TA-TTATATTTATTGTATAATATCGTTTGAATTTAAATTAAGAG----A----------A----------A----------A--------TTTATAAAGGA--TAG-TATA----------
dp5	4_group1:285619-285662 -		GGGTTATATTTAAAATATATATATGATAATATTTAAATTAAA------A----------A----------A----------A--------A----------AA----------
droPer2	scaffold_1:280870-280913 -		GGGTTATATTTAAAATATATATATGATAATATTTAAATTAAA------A----------A----------A----------A--------A----------AA----------
droAna3	scaffold_13266:5999325-5999372 +		ATATTCTTTTTAAATACATATATTGTTAACATACTATTTTAAC----A----------A----------A----------A--------A----------TTCA----------
droBip1	scf7180000396691:1313821-1313859 -		GCATAAAAAATATTATTAGGAAC-------TTCAAGATAAGA-----A----------A----------A----------A--------A----------ATTC----------
droKik1	scf7180000302592:711788-711835 -		AAATTAAATTTCTATATGTATATTTTAATTTAATTAAATAG------AA----------A----------A----------A--------A----------TCTC----------
droFic1	scf7180000454113:1321285-1321353 +		ATATTTC---CACTGAAAGATG---ATAAGCTTT---TTGAAGCTTA--CTGAGAGGTTTAGC----------TACATATG------A----------A----------A--------A----------PATATAAA----------
droEle1	scf7180000491080:1634188-1634355 -		AATTATATGTACTGTATATATTTTTAAAATTT----------A----------A----------A----------A----------GAAAATTCATTATTTACATGAACATTTTGCCAAAACTTACTAAAGATCTGTTAGCAAATTATTAATTATTAAATAATTATTAATTAATTTAAAAGGTCTGGTGTCTGGCTAAAGAGCTTCAATGCTTT----------
droRho1	scf7180000780030:51739-51872 -		AGATAATTTCTGCTGTAAGTGATTTAAACCATATTTCCAAGCTTT----AAAT------ATCAGATGTCTCTGTATTTAT-ATCTACTTTAAAATTTGATACTTAAATATTGGTATTGTTTGTTTATAGCTAAACA----A----------A----------A--------A----------TTTA----------
droBia1	scf7180000302428:2208110-2208146 +		ATGGTATGCACATTAAAATGTATGTTTAAAATTA----------A----------A----------A----------A--------A----------A---GA----------
droTak1	scf7180000415229:218199-218282 -		ATTTGAAAAGAATTAAGTTATTTTGAATGTTTTAATTTGG------AAC----------A----------TATACTA------A----------A----------A----------GTT-TATTTTA--------AGCTTTGAAAAAA--TATTTTAA----------
droEug1	scf7180000409230:569630-569682 -		AGATTAAATATATAAA------AAACTTACTTAATAACTTAG------AACTTAGCAGCTTAC----------A----------A----------A----------A--------A----------T----------
dm3	chrU:9970108-9970143 +		ATATTTTTTTCACTTATAATATTTGCAAGAATTTA----------A----------A----------A----------A----------A--------A----------A----------
droSim2	x:13126925-13126932 +		TTATTTTA----------A----------A----------A----------A----------A----------A--------A----------A----------
droSec2	scaffold_10:972767-972822 +		TATATATTT-TGTTG----------A----------A----------A----------A----------A----------TTTGTGTATATATGATTA--------GTTTTGCAAAAAATTAACAAAG----------
droYak3	3R:8386162-8386203 -		TTGCGCTTGCTGCTTGAGTGCAT----------A----------A----------A----------A----------A----------TTAAATTT--------ACTCAGC----------CAGT----------

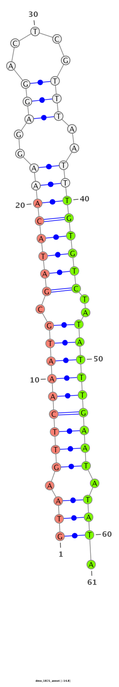
Generated: 09/08/2015 at 07:56 PM

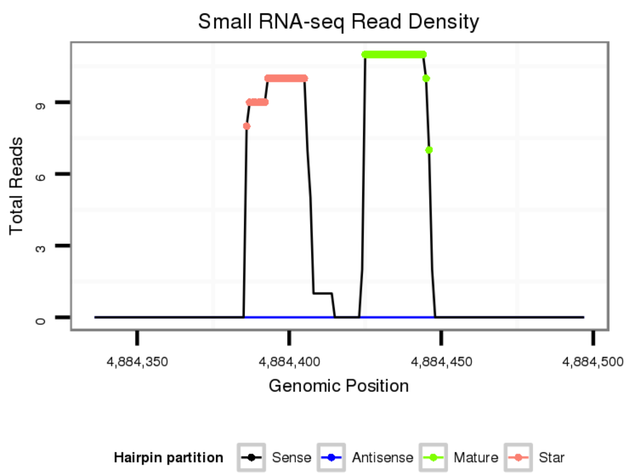
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

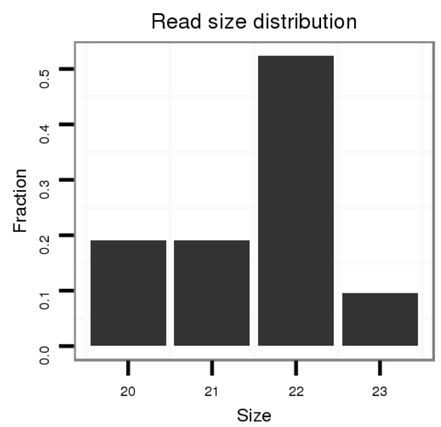
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_1821	**scaffold_6540:4884386-4884447 +**	**candidate**	**Mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

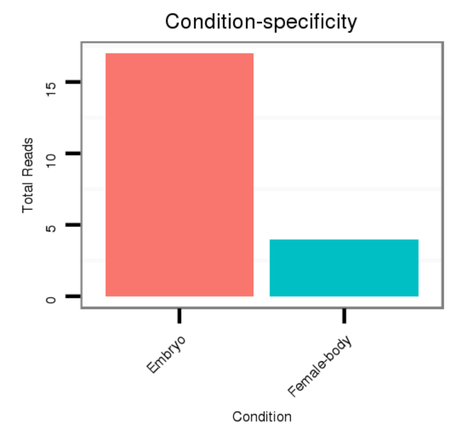
Legend: mature star mismatch in alignment mismatch in read

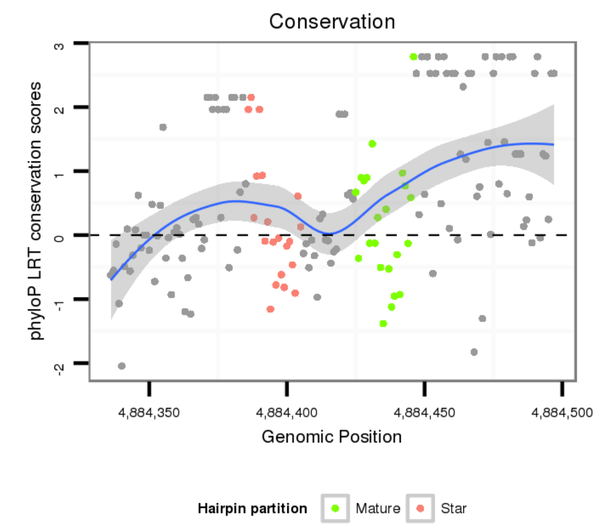
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dmoj\GI24024-in]; CDS [Dmoj\GI24024-cds]; CDS [Dmoj\GI24024-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

GTGAGTGTCGTCAAAAAGTTGTTTCTCATATCAGGATGAGTGCATTCGAAGTAAGTTCAAATGCGATACAAAGGAGGACTCGTTTAATTTGTGTCTATATTTGAATATATAGGTAACTGTGACCCCGACCCGTCTAAAACAAAAGAAATGCTCCGAGATTCG **********(((.(((((((((.(((((((..(((.....)))..)))))))).)))))))))..))))))))).))).**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M060 embryo	V041 embryo	M046 female body
.....TGTGTCTATATTTGAATATATA.....	22	0	1	5.00	5	2	2	1
.....GTAAGTTCAAATGCGATACA.....	20	0	1	3.00	3	1	1	1
.....GTAAGTTCAAATGCGATACAAA.....	22	0	1	3.00	3	1	1	1
.....TGTGTCTATATTTGAATATATAG.....	23	0	1	2.00	2	0	2	0
.....TTGTGTCTATATTTGAATATAT.....	22	0	1	2.00	2	1	1	0
.....GTAAGTTCAAATGCGATACAA.....	21	0	1	2.00	2	2	0	0
.....TGTGTCTATATTTGAATATAT.....	21	0	1	1.00	1	0	0	1
.....TAAGTTCAAATGCGATACAAA.....	21	0	1	1.00	1	1	0	0
.....TGTGTCTATATTTGAATATA.....	20	0	1	1.00	1	1	0	0
.....CAAATGCGATACAAAGGAGGAC.....	22	0	1	1.00	1	1	0	0

Anti-sense strand reads

CACTCACAGCAGTTTTTCAACAAAGAGTATAGTCCTACTCACGTAAGCTTCATTCAAGTTTACGCTATGTTTCCTCCTGAGCAAATTAAACACAGATATAAACTTATATATCCATTGACACTGGGGCTGGGCAGATTTTGTTTTCTTTACGAGGCTCTAAGC **********(((.(((((((((.(((((((..(((.....)))..)))))))).)))))))))..))))))))).))).**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V110 male body	V056 head	M046 female body	V049 head

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6540:4884336-4884497 +	dmo_1821	GTGAGTGTCGTCAAAAAGTTGTTT--------CTCATATCAGGATGAGTGCATTCGAAGTAAGTT----C--AAATGCGA----------TACAAAGGAGGA----------CTCGTTTAAT------T-TG--TGTCTATATTTGAATATATAGGTAACTGTGACCCCGACCCGTCTAAAACAAAAGAAATGCTCCGAGATTCG
droVir3	scaffold_13047:883254-883409 +		GCGCCGAGGAT----TGACTATAT--------CCAGTATCAACATGAGCGCGTTTGAGGTTAGTT----C--TCATATGA----------AACAAAGAAA-C----------CTTAATTAAT------T-TG--TGTCTGTCA-TTTAAATGTAGATAACTGTGACTCCGTGCGCGTCTTAGGCAAAAGAAGCGCATTGAGGTCG
droGri2	scaffold_14906:5409742-5409908 -		GCACAGGTGT----TAATTATACAAACG---CTAGCAACAAGATGAGCGCGTTTGAGGTGGGTT----C--ACGCAAAA----------AGCACAAAAAAGTA--------AAAATAAATGAATTTAAT------T-TGAA---------TGTATTTTTAGGTAACGGTGACGCCGTCGCGCCTCAAGCAAAAAAAGCGCATCGAGGACG
droWil2	scf2_1100000004943:8135366-8135536 +		TTGTTTGTCGT----TTGTTTGCCAA------AGAGAGAAGATGAGCGCGTTTCAGGTTAGTCG---C--TTGTTTAA----------AGTAGTGAACAAAATCCTTAATGAC------CTTGATTAAT------GATATATGTATATGC-TTGATTCTCAGATTACGTCACCCC---GGAACAAAACAAAGGAAGCGAATGGAGGCCG
dp5	2:1652654-1652816 -		GCAAGTGTTATT--TTCGTTGTGCCGG-----CATTTGGCGATGAGTGCGTTCGAGGTTAGTG----C--CTGTGCGA----------TTCGACAAAGAATTGTCTTTCT---------GGATTTAAG------GATTTA---------TGTACTTCGCAGGTCACAGTTACGCCGTCGCGCCTCAAACAAAAGAAGCACATCGAAGGTCG
droPer2	scaffold_7:1806578-1806740 -		GCCAGTGTTATT--TTCGTTGTGCCGG-----CATTTGGCGATGAGTGCGTTCGAGGTTAGTG----C--CTGTGCGA----------TTCGACAAAGAATTGTCTTTCT---------GGATTTAAG------GATTTA---------TGTACTTCGCAGGTCACAGTTACGCCGTCGCGCCTCAAACAAAAGAAGCACATCGAAGGTCG
droAna3	scaffold_12911:2608796-2608947 -		AAG--TGTTGT----TCGTTGA--------AATATTGCAATGAGCGCGTTTCGAGGTTAGTG----T--TTACAGCT----------ATGTCAGATTCAAAAATGAA----------TTCGTTTACT------G-TTCA---------TTTTCATTGCAGATCACAGTGACGCCGTCGCGTCTGAAGCAAAAGAAGCGGGTGGAAGGACG
droBip1	scf7180000396714:495921-496067 +		GT----------TGT--------GACTTGCAATGAGCGCGTTTCGAGGTTAGTG----T--TTACAGCT----------ATTTCACATACAAAAACTAA----------TTCGTTTACTTGCAATG-CGAA---------TTGTGCTTGTAGATCACGGTGACGCCGTCGCGTCAGAAGCAAAAGAAGCGGGTGGAAGGACG
droKik1	scf7180000302388:1603831-1603956 -		--
droFic1	scf7180000454106:1731679-1731845 -		TTGTTTAGTGC----------CAGTGCTTTTTGTTTCGCGATGAGCGCGTTTGAGGTTAGTG----G--CTTTTTGCTTCGCGGAGTTTAAAATGGTTTA-----CGCAGAAA----------AATTAAT------GGTTCC---------CGTTAATTGCAGATCACAGTGACGCCATCGCGCCTCAAACAAAAGAAGCGGGTCGAAGGACG
droEle1	scf7180000491194:640719-640860 +		TTGCCCAG----------CGGTCGCAATGAGCGCGTTTGAGGTTAGTTGAAGTTCTCATTTGG----------GAGTCCTTGGAAATA--------ACTGTGTA----------GCCC-TGAATTTGCAGATCACAGTGACGCCATCGCGTCTCAAGCAAAAGAAGCGCGCCGAAGGACG
droRho1	scf7180000779488:683908-683962 +		---
droBia1	scf7180000302402:4359992-4360049 +		A---
droTak1	scf7180000415310:559613-559670 -		A---
droEug1	scf7180000409881:306119-306173 +		---
dm3	chr3R:20579845-20579899 +		---
droSim2	3r:20094942-20094996 +		---
droSec2	scaffold_0:20915588-20915642 +		---
droYak3	3R:25918789-25918843 -		---
droEre2	scaffold_4820:7478591-7478651 -		---

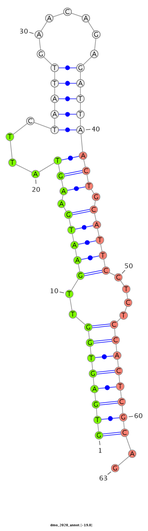
Generated: 09/08/2015 at 07:04 PM

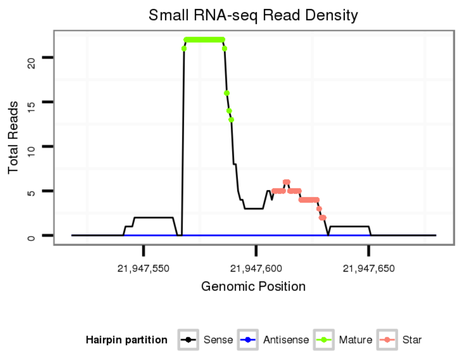
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

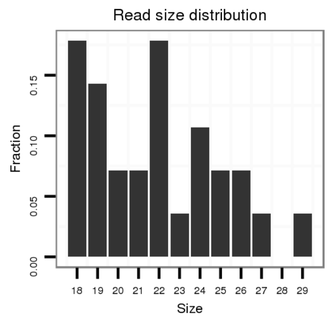
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_2020	**scaffold_6540:21947568-21947630 +**	**candidate**	**Mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

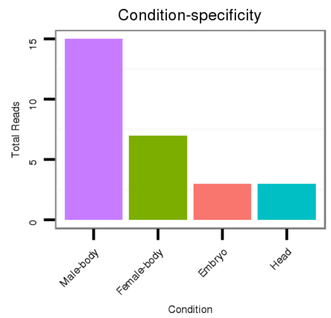
Legend: mature star mismatch in alignment mismatch in read

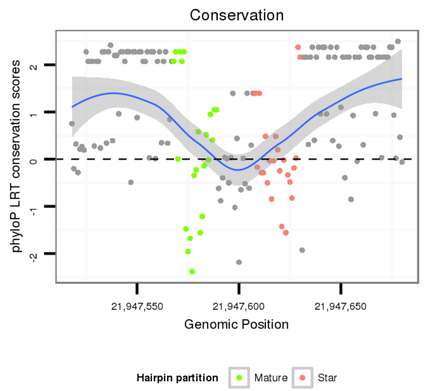
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [DmojGI10141-in]; CDS [DmojGI10141-cds]; CDS [DmojGI10141-cds]; utr5 [utr5_plus_11570]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

```
AACGGCAAGGCGGCCAAGAAGGCCTACAAGAAGATGGAGAAGGAGCAGCGGTGAGTGGTTGAATGAAGTATTCTAATTGAACAGAGATTAACTGCATTCCTCTCCACTCGCAGCCGCCAGGAGAAGGAGCAATCGCGTCGCGAGAAGGAGGCACGCAAACTGG
```

Read size	# Mismatch	Hit Count	Total Norm	Total	V110 male body	M060 embryo	M046 female body	V056 head	V041 embryo	V049 head
**********	(((((((..(((((.(((....(((((.....)))))))).)))))....))))))))..	**********								
.....GTGAGTGGTTGAATGAAGTATT.....	22	0	1	5.00	5	2	0	3	0	0	0
.....GTGAGTGGTTGAATGAAGT.....	19	0	1	4.00	4	3	0	1	0	0	0
.....GTGAGTGGTTGAATGAAG.....	18	0	1	3.00	3	1	0	0	0	1	1
.....GTGAGTGGTTGAATGAAGTATTCT.....	24	0	1	3.00	3	3	0	0	0	0	0
.....GTGAGTGGTTGAATGAAGTA.....	20	0	1	2.00	2	2	0	0	0	0	0
.....ACTGCATTCCTCTCCACTCGCAGC.....	24	0	1	1.00	1	0	1	0	0	0	0
.....ACTGCATTCCTCTCCACTCGCAGG.....	24	1	1	1.00	1	0	1	0	0	0	0
.....GTGAGTGGTTGAATGAAGTATTCTAA.....	27	0	1	1.00	1	1	0	0	0	0	0
.....TGAGTGGTTGAATGAAGT.....	18	0	1	1.00	1	0	1	0	0	0	0
.....TATTCTAATTGAACAGAGATTAACTGCAT.....	29	0	1	1.00	1	0	1	0	0	0	0
.....ATTAACTGCATTCCTCTCCACTCGC.....	25	0	1	1.00	1	0	0	1	0	0	0
.....ACTGCATTCCTCTCCACTCGCAGG.....	24	1	1	1.00	1	0	1	0	0	0	0
.....TACAAGAAGATGGAGAAGGAGC.....	22	0	1	1.00	1	1	0	0	0	0	0
.....GTGAGTGGTTGAATGAAGTATTCTA.....	25	0	1	1.00	1	0	0	0	1	0	0
.....ATTCCTCTCCACTCGCAG.....	18	0	1	1.00	1	0	0	1	0	0	0
.....TTGAACAGAGATTAACTGCATTCCTC.....	26	0	1	1.00	1	0	0	1	0	0	0
.....GCCAGGAGAAGGAGCAAT.....	18	0	1	1.00	1	0	0	0	1	0	0
.....TATTCTAATTGAACAGAGATT.....	21	0	1	1.00	1	0	0	0	1	0	0
.....TTAACTGCATTCCTCTCCACTCG.....	23	0	1	1.00	1	1	0	0	0	0	0
.....AGAAGATGGAGAAGGAGCA.....	19	0	1	1.00	1	1	0	0	0	0	0
.....GTGAGTGGTTGAATGAAGTAT.....	21	0	1	1.00	1	1	0	0	0	0	0
.....GTGAGTGGTTGAATGAAGTATTCTAA.....	26	0	1	1.00	1	1	0	0	0	0	0
.....TGCATTCCTCTCCACTCGCAGG.....	22	1	1	1.00	1	0	0	0	1	0	0

Anti-sense strand reads

```
TTGCCGTTCCGCCGGTTCTTCCGGATGTTCTTCTACCTCTTCCTCGTCGCCACTCACCAACTTACTTCATAAGATTAACTTGTCTCTAATTGACGTAAGGAGAGGTGAGCGTCGGCGGTCCTCTTCCTCGTTAGCGCAGCGCTCTTCCTCCGTGCGTTTGACC
```

Read size	# Mismatch	Hit Count	Total Norm	Total	V110 male body
**********	(((((((..(((((.(((....(((((.....)))))))).)))))....))))))))..	**********			

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6540:21947518-21947680 +	dmo_2020	AACGGCAAGGCGGCCAAGAAGGCCTACAAGAAGATGGAGAAGGAGCAGCGGTGAGTGGTTGAATGAAGTA----------TTCT------AATTGAACAGAG-------ATTAACTGCATTCCT---C--TCCACTCG----CAGCCGCCAGGAGAAGGAGCAATCGCGTCGCGAGAAGGAGGCACGCAAACTGG
droVir3	scaffold_13047:4427268-4427433 -		AAT-GCCAAGGCGGCCAAGAAGGCCTACAAGAAATGGAGAAAGAGCAGCGGTAAGTCCAAGAGACAGA----------CTC----------G---G------TAGCTATCAATG-------ATTAATATACTAACGCT---GCCCAG----CAGACGTCAGGAGAAGGAGCAATCACGCGCGAGAAGGAGGCCGCAAATTGG
droGri2	scaffold_14906:9904799-9904965 -		AAT-GCCAAGGCGCCCAAGAAGGCATACAAAAAGATGGAGAAGGAGCAGCGGTAAGTAACCG-----TA----------AGC----------GTA-------G---AAATTCGTTT-TAGCATTAACTAACTAATAATT--------TCGCAACCTTT----TAGACGCCAGGAGAAGGAACAACTCGCGTCGCGAGAAGGAGGCACGCAAACTGG
droWil2	scaf2_1100000004943:15967457-15967623 +		AAT-GCCAAGGCAGCCAAAAAGGCCTACAAAAAGATGGAGAAAGAACAAACGGTAAGTTCAGCT-----TA----------TT-----AAAACTA-----CGGCGGAAA----------CT----------G---------------QTATTAACTATCT----------CTT---T--CTCATATTCAATTAAGCGCCAGGAAAAGAACAAACACGTCGAGAAAGGAGGCTCGCAAATTGG
dp5	Unknown_group_713:4430-4592 +		AAT-GCCAAGGCGGCCAAAAAGGCCTACAAAAAGATGGAAAAGGAGCAGCGGTAAGTGGAGA-----TA----------CTC----------G---G--CCCCAGAT-TATCCTCAAACAAACACTAATT--------TCACTCATTTT----TAGCCGCCAGAGAAGGAGCAATCCCGCAGCGAGAAGGAGGCCGCAAATTGG
droPer2	scaffold_6:851311-851473 -		AAT-GCCAAGGCGGCCAAAAAGGCCTACAAAAAGATGGAAAAGGAGCAGCGGTAAGTGGAGA-----TA----------CTC----------G---G--CCCCAGAT-TATCATCAAACAAACACTAATT--------TCACTCATTTT----TAGCCGCCAGAGAAGGAGCAATCCCGCAGCGAGAAGGAGGCCGCAAATTGG
droAna3	scaffold_12911:2253884-2253954 +		AACGGCAAGGCGGCCAAGAAAGCCTACAAGAAGATGGAAAAAGAGCAAAGGTAAGTGTTGAATTTATA----------T
droBip1	scf7180000396714:821973-822038 -		TCTTGCC----------TT-----AA----CAGCGCCAGGAGAAGGAGCACTCGCACGCGAGAAGGAGGCCGCAACCTGG
droKik1	scf7180000302690:265324-265390 -		TTTATTT----------ATGCC----------A----CAGTCGCCAGGAGAAGGAGCACTCGCGACGCGAGAAGGAGGCCGCAACCTGG
droFic1	scf7180000454096:277915-277982 +		ATTATT----------T--CCCATCAT----CAGCCGCCAGGAGAAGGAGCACTCGCGCCGCGAGAAGGAGGCCGCAACCTGG
droEle1	scf7180000491080:877008-877077 +		AAT-GCCAAGGCGGCCAAGAAGGCCTACAAAAAGATGGAGAAGGAACAGCGGTGAGTTCCAGAAAAATA----------T
droRho1	scf7180000776572:6209-6276 +		ATTCCT----------TT--TGCCCA----CAGTCGCCAGGAGAAGGAGCACTCGCGACGCGAGAAGGAGGCCGCAACCTGG
droBia1	scf7180000302155:370489-370563 +		AACGGCAAGGCGGCCAAGAAGGCCTACAAGAAGATGGAGAAGGAGCAGCGGTGAGTATGAAAAAATTA----------TT----------TTA
droTak1	scf7180000415417:369590-369653 -		AAT-GCCAAGGCGGCCAAGAAGGCCTACAAGAAGATGGAGAAGGAGCAGCGGTGAGTGGTCAAAT------
droEug1	scf7180000409542:135048-135117 -		ATTTCT----------TTACGCCTCA----CAGACGCCAGAGAAGGAGCACTCGCGCCGCGAGAAGGAGGCCGCAACCTGG
dm3	chr3R:17004072-17004161 +		AAT-GCCAAGGCGGCCAAGAAGGCCTACAAAAAGATGGAAAAGGAGCAGCGGTAAGTCAAAAACGAAATTCAACTAGGCCTAGGGA
droSim2	3r:4306369-4306637 -	dsi_16444	AAT-GCCAAGGCGGCCAAGAAGGCCTACAAGAAGATGGAAAAGGAGCAGCGGTAAGTTCATAATCGAAATCTCAACTAGGCCTAGGGATTCATAAATTGCTAGAAAGTGTAGTATATTTTCAATTACTTAAAAAGAGCTA----------TACTATAGAGTATATAGCAACATGACTCGTGCCCAATTAAATGTCATTTGTACTAACAAAA------TTATTT-------TC---T-ACGCCA----CAGTCGCCAGGAGAAGGAGCACTCGCGACGCGAAAAGGAAGCCCGCAACCTGG
droSec2	scaffold_38:127957-128219 -		AAT-GCCAAGGCGGCCAAGAAGGCCTACAAGAAGATGGAAAAGGAGCAGCGGTAAGTCAATAACGAAATTCAACTAGGCCAAGGGATTATTCAATTGCTAGAAAGTGTAGTATATTTTCAATAACTTAAAAAGAGCTGGAACTAGGAAAAA----------TATT----------T-GTTCGTGCACAATTAAATGTCATTTGTACTAACAAAA------TTATTT-------TCT---T-ACGCCA----CAGTCGCCAGGAGAAGGAGCACTCGCCACGCGAAAAGGAAGCCCGCAACCTGG
droYak3	3R:5789587-5789696 +		AAT-GCCAAGGCGGCCAAGAAGGCCTACAAGAAGATGGAGAAGGAGCAGCGGTGAGTCCCAACCAAAATA----------GTAGAGAGTTATCCAAATTCGG---AATAGAA-------AACAACTCG-------TC---T-ACGCCA----CAGTCGCCAGGAGAAGGAGCACTCGCCACGCGAAAAGGAAGCCCGCAACCTGG
droEre2	scaffold_4770:4657170-4657239 -		AAT-GCCAAGGCGGCCAAGAAGGCCTACAAGAAGATGGAGAAGGAGCAGCGGTGAGTTCCAAACGACATA----------T

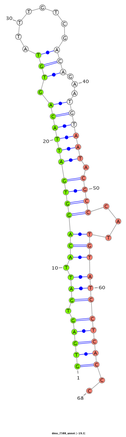
Generated: 09/08/2015 at 07:04 PM

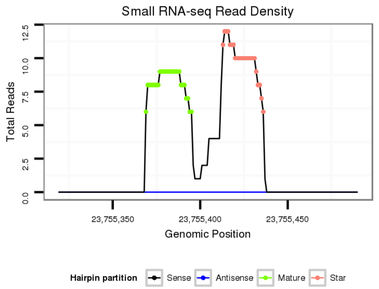
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.ptop3	0
crit.uri	1
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

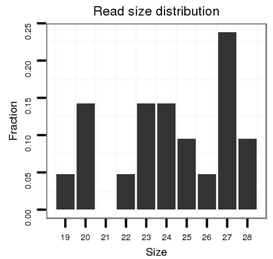
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_2588	**scaffold_6680:23755369-23755440 +**	**candidate**	**3p_tailed_mirtron**	**intron**	[View on UCSC Genome Browser [Cornell Mirror]]

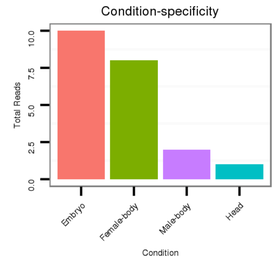
Legend: mature star mismatch in alignment mismatch in read

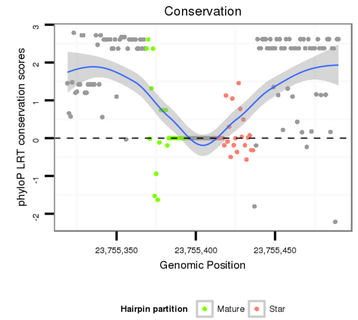
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [DmojGI13962-in]; CDS [DmojGI13962-cds]; CDS [DmojGI13962-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

```
AGCAAGCATATCCAAATATGAATATTAAGCAAGAAATACAAATACCTCAGGTGAGTGATTACAGGTGATTACAGTGTATTTGTCGACAGAATGTAATACGCCCATTGTATCCTCACCCCTAGGTATCCTCACTCACGCAATCGCCGGACTCATCACCCAGTCCCATAGCCAT
*************************************************((((.(((.(((((((((((((.(((.........)))...)))))))).))))...)))))))))))..*************************************************
```

Read size	# Mismatch	Hit Count	Total Norm	Total	M060 embryo	M046 female body	V110 male body	V056 head
27	0	1	4.00	4	0	2	1	1
24	0	1	2.00	2	2	0	0	0
25	0	1	2.00	2	1	1	0	0
23	0	1	1.00	1	1	0	0	0
19	0	1	1.00	1	0	0	1	0
23	0	1	1.00	1	0	1	0	0
20	0	1	1.00	1	0	1	0	0
24	1	1	1.00	1	0	1	0	0
22	1	1	1.00	1	0	1	0	0
28	0	1	1.00	1	1	0	0	0
20	0	1	1.00	1	1	0	0	0
20	0	1	1.00	1	1	0	0	0
24	0	1	1.00	1	0	1	0	0
28	0	1	1.00	1	0	1	0	0
22	0	1	1.00	1	0	1	0	0
23	0	1	1.00	1	1	0	0	0
26	0	1	1.00	1	1	0	0	0

Anti-sense strand reads

```
TCGTTCGTATAGGTTTATACTTATAATTCGTTCTTTATGTTTATGGAGTCACTCACTAATGTCCACTAATGTCACATAAACAGCTGTCTTACATTATGCGGGTAACATAGGAGTGGGGATCCATAGGAGTGAGTGCGTTAGCGGCCTGAGTAGTGGGTCAGGGTATCGGTA
*************************************************((((.(((.(((((((((((((.(((.........)))...)))))))).))))...)))))))))))..*************************************************
```

Read size	# Mismatch	Hit Count	Total Norm	Total	M046 female body	V110 male body

Show Alignment With Reads

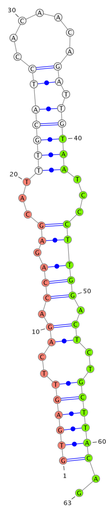
Re-alignment of all predicted orthologs

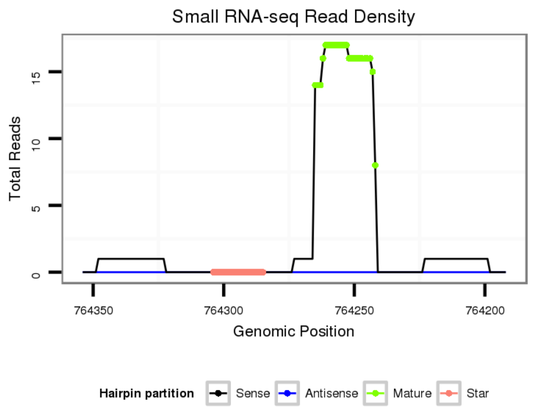
Species	Coordinate	ID	Alignment
droMoj3	scaffold_6680:23755319-23755490 +	dmo_2588	AGCAAGCATATCCAAATATGAATATTAAGCAAGAAATACAAATACCTCAGGTGAG---TGA---------T----------TACAGGTGATTACAGTGTATTTGTCGACAGAATGTAATACGCCCATTGTA----------TCC-----TCACCCCTAGGTATCCTCACTCACGCAATCGCCGGACTCATCACCCAGTCCCATAGCCAT
droVir3	scaffold_13049:18179845-18180007 +		AGCAAGCATATCCAAATATGAATATTAAGCAAGAAATGCAAATACCTCAGGTGAG---TCCAAATGTTCTAGACGATCGG----------CTG----------T-------A----------ACGAAACTAATGA--AATACCCTGTA----------TTTGCAGGTATCCTCACTCACGCAATCGCCGGACTCGTCGCCCAGCCCATGCGCAT
droGri2	scaffold_15110:24231623-24231787 +		AGCAAGCATATCCAAATATGAATATTAAGCAAGAAATGCAAATACCTCAGGTAAG---TGT---------T---------GGGATCGAACAAGCAA--CTGAAACAG----------AGT-----AC---TGATATGC-TTTTTTGT-----TTTATAGGTATCCTCACTCACGCAATCGCCGATCATCACCCAGCCCATGCGCAT
droWil2	scf2_1100000004762:1585901-1586091 +		AGCAAGCATATCCAAATATGAATATTAAGCAGAAATACAAATACCTCAGGTAAG---G--------TGCGCTTAGT----------C TGGATTCTCTTTACCCTACTCCCACTTGGAATCGTTTGTCACCTCTTCTTTTTCTCTTTTCGTCGT----------TGCAGGTATCCTCACTCACGCAATCGCCGGACTCATCGCCCAGCCCATGCGCAT
dp5	XR_group6:4215214-4215373 +		AGCAAGCATATCCAAATATGAATATTAAGCAGAAATGCAAATACCTCAGGTAAG---GC--------T---------TC----------GCCCGCGCA----------AGGATACTGAGGATAATATGCGGCATTTTCT----CACCA-CAGGTATCCTCACTCACGCAATCGCCGGACTCGTCGCCCAGCCCATGCGCAT
droPer2	scaffold_9:2505879-2506038 +		AGCAAGCATATCCAAATATGAATATTAAGCAGAAATGCAAATACCTCAGGTAAG---GC--------T---------TC----------GCCCGCGCA----------AGGATACTGAGGATAATATGCGGCATTTTCT----CACCA-CAGGTATCCTCACTCACGCAATCGCCGGACTCGTCGCCCAGCCCATGCGCAT
droAna3	scaffold_13337:18679669-18679834 +		AGCAAGCATATCCAAATATGAATATTAAGCAGAAATGCAAATACCTCAGGTGAG---AGA--------TGC--------TGGATGGGACTAAGTGG-CTGAAAC----------TAGG--ATTTCATTTCAAATATCCATTTT----------TTAGGTATCCTCACTCACGCAATCGCCGGACTCGTCGCCCAGCCCATGCGCAT
droBip1	scf718000039674l:1871946-1872112 +		AGCAAGCATATCCAAATATGAATATTAAGCAGAAATGCAAATACCTCAGGTGAG---CTG--------AAAGTCCTAAAG----------G CCTAACGTCCAGGGCATTTAATTTAATAATTCATTT----TTT-AAGGTATCCTCACTCACGCAATCGCCGGACTCGTCGCCCAGCCCATGCGCAT
droKik1	scf718000030224 8:222259-222451 +		AGCAAGCATATCCAAATATGAATATTAAGCAGAAATGCAAATACCTCAGGTGC---TA--------AAA----------ATTAAACAATAAA--TGAA--AATA----------TAAATATAAATTCTAAAATATAGGTATATTAAATATATAATTACAA----------A CCC-----TTCATTT-AGGTATCCTCACTCACGCAATCGCCGGACTCGTCACCCAGCCCATGCGCAT
droFic1	scf718000045382 4:111830-111913 -		CAGATTTATAAAGTCTGGA----------T----------T----------T

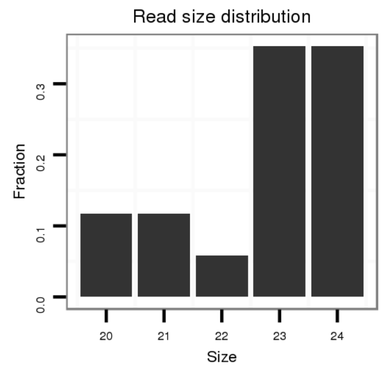
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_544	**scaffold_6359:764242-764304 -**	**confident-exception**	**Mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

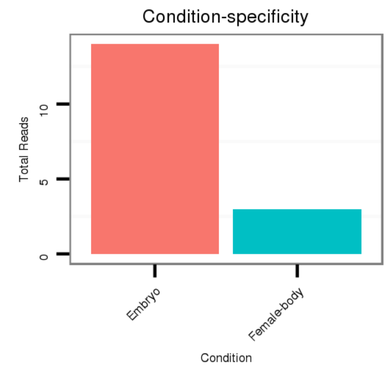
Legend: mature star mismatch in alignment mismatch in read

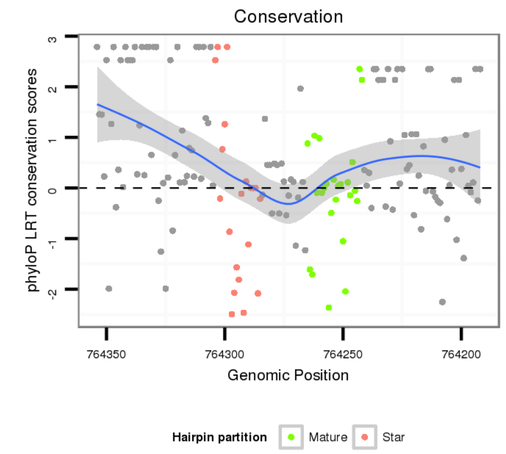
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [DmojGI21594-in]; CDS [DmojGI21594-cds]; CDS [DmojGI21594-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

TATGCCGTTAGCTGGGATCACTTCTTCTATGCGCTCAACAATTATTTCAAGTGAGTTCAGACCAGAGCATTTGCATCCACAACAGATTGTAATCCCTTGGACTCTGCTTACAGCAATATGCGCACAGACTATGATACCGTATCACCCGATAGTGGTTCGATTT ********** ((((((.. ((. (((.((... (((((((.....)).)))))...)))))).))..))))))) .. **********	Read size	# Mismatch	Hit Count	Total Norm	Total	M060 embryo	M046 female body	V041 embryo
.....TAATCCCTTGGACTCTGCTTACAG.....	24	0	1	6.00	6	6	0	0
.....TAATCCCTTGGACTCTGCTTACA.....	23	0	1	6.00	6	4	0	2
.....TCCCTTGGACTCTGCTTACAGT.....	22	1	1	3.00	3	2	1	0
.....TCCCTTGGACTCTGCTTACAG.....	21	0	1	1.00	1	0	1	0
.....GTTAGCTGGGATCACTTCTTCTATGC.....	26	0	1	1.00	1	0	1	0
.....ACAGATTGTAATCCCTTGGAC.....	21	0	1	1.00	1	1	0	0
.....TGATACCGTATCACCCGATAGTGGT.....	25	0	1	1.00	1	0	1	0
.....TAATCCCTTGGACTCTGCTTAC.....	22	0	1	1.00	1	1	0	0
.....GTGAGTTCAGACCAGAGCATC.....	21	1	1	1.00	1	1	0	0
.....TCCCTTGGACTCTGCTTACA.....	20	0	1	1.00	1	0	1	0
.....ATCCCTTGGACTCTGCTTACAGT.....	23	1	1	1.00	1	1	0	0
.....CCCTTGGACTCTGCTTACAG.....	20	0	1	1.00	1	0	1	0

Anti-sense strand reads

ATACGGCAATCGACCCTAGTGAAGAAGATACGCGAGTTGTTAATAAAGTTCACTCAAGTCTGGTCTCGTAAACGTAGGTGTTGTCTAACATTAGGGAACCTGAGACGAATGTCGTTATACGCGTGTCTGATACTATGGCATAGTGGGCTATCACCAAGCTAAA ********** ((((((.. ((. (((.((... (((((((.....)).)))))...)))))).))..))))))) .. **********	Read size	# Mismatch	Hit Count	Total Norm	Total	V110 male body	M046 female body	V056 head

Show Alignment With Reads

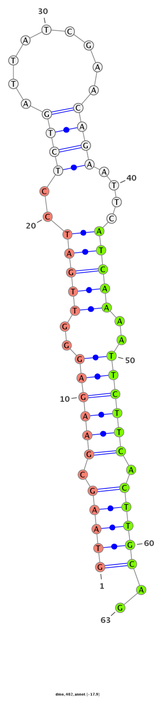
Re-alignment of all predicted orthologs

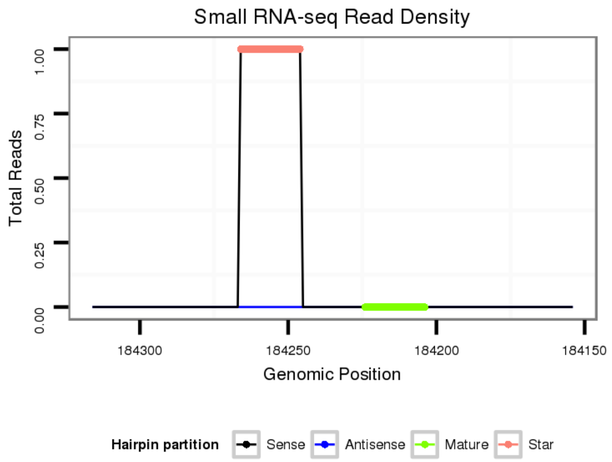
Species	Coordinate	ID	Alignment
droMoj3	scaffold_6359:764192-764354 -	dmo_544	TATGCCGTTAGCTGGGATCACTTCTTCTATGCGCTCAACAATTATTTCAAGTGAGTTCAGACCAGAGCA----------TTTGCATCCAC-AAC-AGATTG----------TAA-----TCCCTTGGACTC---------TGCTTACAGCAATATGCGCACAGA------CTATGATACCG-TATCA--CCCGATAGTGG----------TTCGATTT
droVir3	scaffold_12928:4169534-4169756 -	dvi_8843	TATGCCGTCAGCTGGGATCATTTCTTGAATGCGCTCAACAATTATTTCAAGTACGTGGTGTAGAA----------TAAATATCTCTCTAGGATAATTTAGTTTCC----AATAC----------GCGTCTAC-CAC-ACGTTA------TATAGA--A-AATCCATATACGCAAATTTTATTT----------AATATTTTGTTATATCCTTTACAGCAACATGCGAACGA------CTTCGACGC-AATGGCCAATGCCGGAGA----------TTCGATTT
droGri2	scaffold_14853:890711-890774 -		TATGCCGTCAGCTGGGACAATTTCTTTACGGCCTCAATTGTTATTTCACGTAAGTGCGCACCA-----------------------

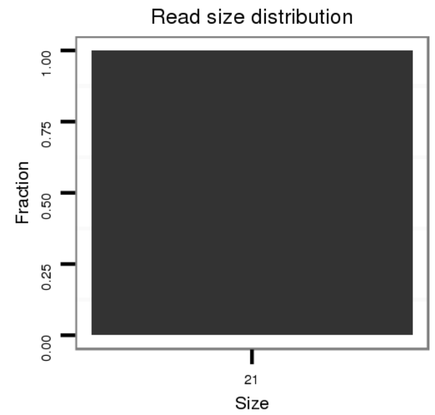
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_402	**scaffold_6308:184204-184266 -**	**confident-exception**	**Mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

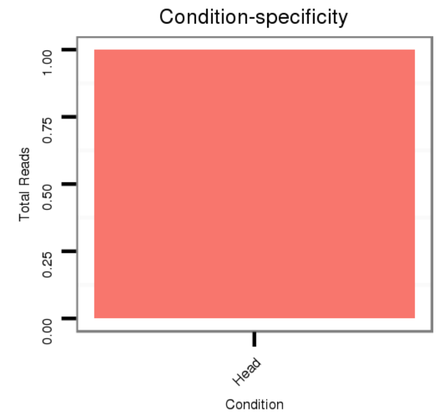
Legend: mature star **mismatch in alignment** mismatch in read

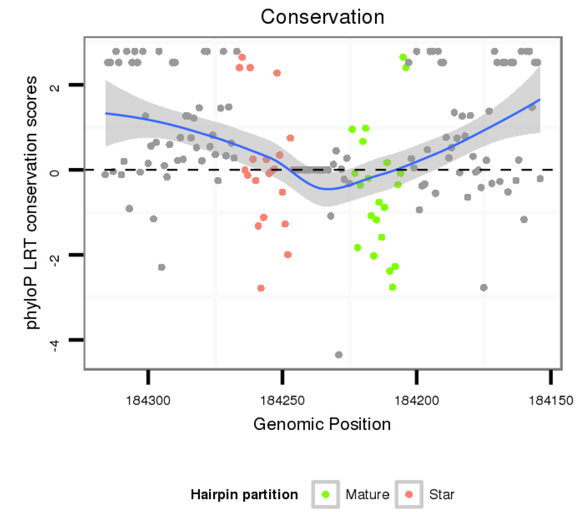
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dmoj\GI11054-in]; CDS [Dmoj\GI11054-cds]; CDS [Dmoj\GI11054-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

```
CCCCACAATGGAGCTGGCCGTGCAGCCCGATCTGCGATATAAGATAATCAGTAAGCGAAGAGGGTTGATCCTCTGATTATCGAACAGAATTCATCAAAATTCTTCACTTGCAGGTGTAAGGAAATGGTCGGAGGAGTTCACCTTCTGCGGCGGCCTGAATGCG
**************************************************(((((.(((((((..(((((..((((.........))))....)))))..)))))))..)))))..**************************************************
.......................................................................................ATCAAAATTCTTCACTTGCAGT.......................................................
.....................................................GTAAGCGAAGAGGGTTGATCC.............................................................................................
```

Read size	# Mismatch	Hit Count	Total Norm	Total	M060 embryo	V056 head	M046 female body
22	1	2	1.50	3	3	0	0
21	0	1	1.00	1	0	1	0

Anti-sense strand reads

```
GGGGTGTTACCTCGACCGGCACGTCGGGCTAGACGCTATATTCTATTAGTCATTCGCTTCTCCCAACTAGGAGACTAATAGCTTGTCTTAAGTAGTTTTAAGAAGTGAACGTCCACATTCCTTTACCAGCCTCCTCAAGTGGAAGACGCCGCCGGACTTACGC
**************************************************(((((.(((((((..(((((..((((.........))))....)))))..)))))))..)))))..**************************************************
```

Read size	# Mismatch	Hit Count	Total Norm	Total	V110 male body

Show Alignment With Reads

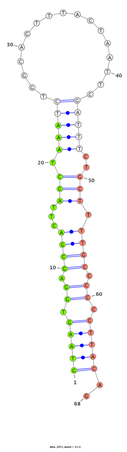
Re-alignment of all predicted orthologs

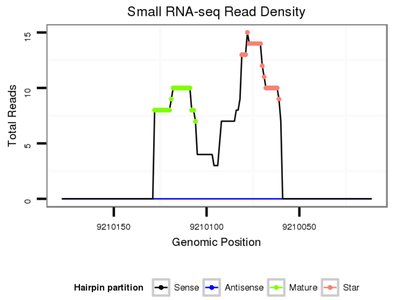
Species	Coordinate	ID	Alignment
droMoj3	scaffold_6308:184154-184316 -	dmo_402	CCCCACAATGGAGCTGGCCGTGCAGCCCGATCTGCGATATAA---GATAATCAGTAAGCGAAGAG----------GGTTGATCCTCTGATTATCGAAC-AGAATTCA----------TCA-AA---------ATTCTT-CACTTGCAGGTGTAAGGAAATGGTCGGAGGAGTTCACCTTCTGCGGCGGCCTGAATGCG
droVir3	scaffold_12932:374092-374285 +		TCCCACATTGGAGCTGCAAGTCCAGCCCAGCCGGGATATAA---TTTAATCAGTAAGTCAGAAC--GGAAGCCCAA---------GTTTAACGATATATAACATATATATATATATATAACTTTTCA-ACTGACTATTTGTCATTC-CATACGCAGGCATCACAAGTGGACGGGTGAGTACTCGTTTTGTGGTGGCCTCAATGCG
droGri2	scaffold_15116:465680-465779 +		TCCCACAATTGAGCTGGTCGTGCAGCCCAGCAAGGATACAA---TATAATCA----------GTTTT

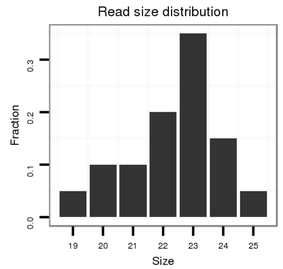
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_1052	**scaffold_6496:9210061-9210128 -**	**confident-exception**	**Mirtron**	**intron**	[View on UCSC Genome Browser [Cornell Mirror]]

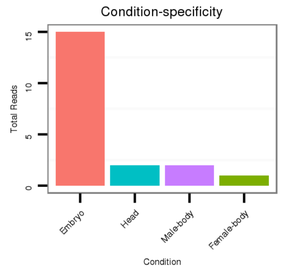
Legend: mature star mismatch in alignment mismatch in read

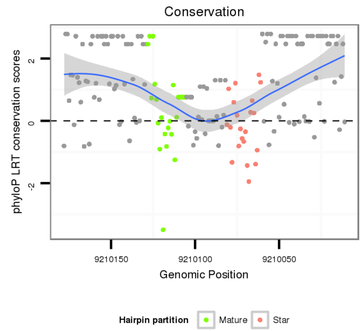
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [DmojGI19234-in]; CDS [DmojGI19234-cds]; CDS [DmojGI19234-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

```
TTACTTTAGGCGCCGCCATCAAATGACCAAAGAGCTGGGACACCTGAGCGGTAAGTGGAGCGACTTAGCTAAATCTGGCAGTTTACTAATTCGATTTCTGCTTTTGCCCCCCTTACAGTGGTCAGCGCCAATGAGATAACTGCTTTGAACATCAATAGCAAGGAGAGC
*********************************************((((.(.(.((((...(((.(((((.................)))))..))).))))..)).))))..**********************************************
```

Read size	# Mismatch	Hit Count	Total Norm	Total	M060 embryo	V110 male body	V049 head	V056 head	M046 female body	V041 embryo
22	0	1	4.00	4	3	0	0	1	0	0
23	0	1	4.00	4	2	1	1	0	0	0
20	0	1	2.00	2	2	0	0	0	0	0
19	0	1	2.00	2	1	0	0	1	0	0
22	0	1	2.00	2	2	0	0	0	0	0
23	0	1	1.00	1	1	0	0	0	0	0
24	0	1	1.00	1	0	1	0	0	0	0
23	1	1	1.00	1	1	0	0	0	0	0
24	0	1	1.00	1	0	1	0	0	0	0
22	0	1	1.00	1	0	0	0	0	0	1
23	0	1	1.00	1	1	0	0	0	0	0
25	0	1	1.00	1	1	0	0	0	0	0
19	0	1	1.00	1	0	0	0	1	0	0
21	0	1	1.00	1	1	0	0	0	0	0
24	1	1	1.00	1	1	0	0	0	0	0
22	0	1	1.00	1	1	0	0	0	0	0
23	0	1	1.00	1	1	0	0	0	0	0
23	0	1	1.00	1	1	0	0	0	0	0

Anti-sense strand reads

```
AATGAAATCCGCGGCGGTAGTTTACTGGTTTCTCGACCCTGTGGACTCGCCATTCACCTCGCTGAATCGATTTAGACCGTCAAATGATTAAGCTAAAGACGAAAACGGGGGGAATGTCACCAGTCGCGGTTACTCTATTGACGAAACTTGTAGTTATCGTTCCTCTCG
*********************************************((((.(.(.((((...(((.(((((.................)))))..))).))))..)).))))..**********************************************
```

Read size	# Mismatch	Hit Count	Total Norm	Total	V110 male body	V056 head

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6496:9210011-9210178 -	dmo_1052	TTACTTTAGGCGCCGCCATCAAATGACCAAAGAGCTGGGACACCTGAGCGGTAAGTGGA----------G------CGACTTAGCTAAA------TCTG---------GCA----------GTTTACTAATTCGATTTCTG----------CTTTT-GCCCCCCTTACAGTGGTCAGCGCCAATGAGATAACTGCTTTGAACATCAATAGCAAGGAGAGC
droVir3	scaffold_12875:13801405-13801564 -		TTACTTTAAGCGCGCATCAAATGACCAAAGAGCTGGGCAG-TGAGCGGTAAGCCAGCCATTAA-----T------ATG---------------G--T----------T--------TCTAT---ATATAACT--A-----ACGCTCGTCTTTTTGGCCAGTGGTAGCGCCAATGAGATAACGCGCAGTGAACATCAAGCAAGGAGAGC
droGri2	scaffold_15245:17448525-17448687 +		TTACTTGAAGCGCCGCATCAAATGACCAAGGAGCTGGGCATTTGAGTGGTAGTCATGGCCGCAA-----G------TTG---------AG-----------CTCT----------CACTTTTTATAACA---T-C---TTGTTTGCCTGCGTAGTTGTAGCGCAATGAGATAACGCGCAGTGAATCAAGCAAGGAGAGC
droWil2	scf2_1100000004513:4015492-4015652 +		TTATTTGAAGCGCAGCATCAAATGACCAAGGAGCTGGGACGTTAAGTGGTAAGTGGA----------A------**********----CGAG-----AC---------ACCCG--AACCCAAGACATTTT----------A--A---------A-----AAGCATTTCC--TGCTTTTTAGTGTGAGCGCAATGAGATGACGCTTGAATCATAATAGCAAGGAGAGC
dp5	3:4063532-4063695 -		TTACTTGAAGCGCAGCATCATCAATGACCAAGGAGCTGGGCACCTAAGTGGTAAGTGA----------A------**********----TGGA-----AC---------AGACTTTGATTGCAGCCTCCTG----------C--A---------T-------TCACATTTCC--TGCCAATTCTCAGTGTGAGCGCAAGGAATGACTGCCTGAATCATCAAGCAAGGAAGC
droPer2	scaffold_21425065-4250820 -		TTACTTGAAGCGCAGCATCATCAATGACCAAGGAGCTGGGCACCTAAGTGGTAAGTGA----------A------**********----TGGA-----AC---------AGACTTTGATTGCAGCCTCCTG----------C--A---------T-------TCACATTTCC--TGCCAATTCTGTAGTGTGAGCGCAAGGAATGACTGCCTGAATCATCAAGCAAGGAAGC
droAna3	scaffold_13266:14925622-14925775 -		TTACTTTAAAGAAACATCAGATGACCAAGGAGCTGGGCAGTTGAGTGGTAATAAGA-GTTTCCTTTCTCAAAGGATCAGATTTTAA-----**********----**********----**********----TCAAAG-TATTGAATTCCAGTGGTCAGCGAATGAGATGACGCGCAGTGAACATTAAGAGCAAGGAGAGC
droBip1	scf1800000396385:93374-93529 -		GTACTTTAAAGAAGCATCAAATGACAAAGGAGCTGGGCAGTTGAGTGGTAAGTAAGGATGTCTATTCTAAAAGGATCAGATTGCCA-----**********----**********----**********----TCAAAA-TTTGAATTCCAGTGGTCAGCGCAATGAGATGACGCGCAGTGAACATCAACAGCAAGGAGAGC
droKik1	scf1800000302470:407899-408058 +		TTACTTGAAAAAAGCATCAAATGACCAAGGAACTGGGCAATAGAGTGGTAAGTGTGAA----------G------**********----AC---------AC---------ATATTTAATAATAACAATCTTAT----------C--G---------G-------TTTAATT---TGCCATTTCCAGTGGTCAGCGCAAGGAGATGACTGCTTTAATCCAACAGCAAGGAGAGC
droFic1	scf1800000454066:2547017-2547271 -		TTACTTGAAAAAAAGCATCAAATGACCAAGGAACTGGGCAGTTAGTGGTAAGTGTTAGTTTGCG-----T------TAT---------**********----A-ACTATCCCG--**********----TCACAATTT--AAAAGATATCAATGTACATTAAACTAAAGCCAGGTTTAATTTAAACTAAAAAAATTGTTATAAGTCAAATCTGATTATATATAAC--TTATGT----AACG---T-T--T--T--AAA-ATATTTTCAGTGGTCAGCGCAAGGAGATAACGCGCAGTGAACATCAATAGCAAGGATGCG
droEle1	scf1800000491022:187109-187352 -		GTACTTTAAAGAAGCATCAAATGACCAAGGAGCTGGGCACCTAAGTGGTAAGTGTCAATTGAGGGGG-----T------TAT---------**********----C--------TTTGAGTGCATGCAAACTTTTGTAAACCAAACCTAGAAAGGTATTTTTATAAATGTATCATGTTCATTGTTAAGTAGACTTAATAATCATTTGT----------**********----TA-------AACA---T-T--T-TCT--AATATTCTTTTTTTTCAGTGGTCAGCGCAAGGAGATAACGCGCAGTGAACATCAATAGCAAGGAAGCC
droRho1	scf1800000779417:15257-15339 +		ATACTTTAAAGAAGCATCAAATGACCAAGGAGCTGGGCAGTTAAGTGGTAAGTGTTCATCTTCG-----AA------CC----------**********----**********----**********----**********----C-TCTGGTAAT----------
droBia1	scf1800000302143:2056796-2056979 +		GTACTTGAAAAAGAAGCATCAAATGACCAAGGAACTGGGACATTAAGTGGTAAGTCTTTGTTATCAA-----G------TAACTTATCTAAAAATATAGATTG--------GTT----------**********----G----------CCTGT---ATATAATATTTA----TTGTTTA--TTTGATGTTTAGTGGTCAGCGCAAGGAGATAACGCGCAGTGAACATCAATAGCAAGGAAGCC
droTak1	scf1800000415538:32339-32432 -		ATATAG----------**********----**********----**********----**********----**********----TT----------TTTTG----------**********----TAATCCAATACT----------T--T--ACT--ATATATCTCAGTGTCAGCGCAAGGAATAACGCGCAGTGAACATCAACAGCAAGGAGAGC
droEug1	scf1800000409672:6529601-6529809 -		GTACTTGAAAAAAGCATCAAATGACCAAGGAACTGGGCAGTTAAGTGGTAAGTGTTAGTTTTGTAA-----G------TAA---------GTGAA-----TCTTATGCAA----------CATGTATCAATATTATTATTTACTTAATCTATAATTTATATAG----------TA-------CATA---CTAT--T-CT--ACAATATGTGTGTCAGTGGTCAGCGCAAGGAGATAACGCGCAGTGAACATCAATAGCAAGGAAGCC
dm3	chr2R:18583465-18593626 -		GTACTTGAAGCGCAAGCATCAAATGACCAAGGAGCTGGGCAGTTAAGTGGTAAGTGCTGATTTTAA-----A------TAT---------**********----C--TTT--**********----TTTT----------TTTCAATACAATATAAACG--A--T--T--TGGAA-----TTTGTAGTGGTCAGCGCAAGGAGATAACGCGCTTGAACATCAATAGCAAGAGAGC
droSim2	2r:19112386-19112548 -		GTACTTGAAGCGCAAGCATCAAATGACCAAGGAGCTGGGCAGTTAAGTGGTAAGTGTGACTTTTAA-----C------TAT---------**********----C--TTT--**********----TTTT----------CAATACAATATAACA--A--A---A--A-ACA--TATTTTTCTAGTGGTCAGCGCAAGGAGATAACGCGCTTGAACATCAATAGCAAGAGAGC
droSec2	scaffold_9:1885557-1885717		GTACTTGAAGCGCAAGCATCAAATGACCAAGGAGCTGGGCAGTTAAGTGGTAAGTGTGATTTTAAA-----A------TAT---------**********----C--TTT--**********----T----------TTTCAATACAATATAACA--A--A---A--AC---TTTTTTTCTAGTGGTCAGCGCAAGGAGATAACGCGCTTGAACATCAATAGCAAGAGAGC
droYak3	2R:16048851-16049014 -		GTACTTGAAGCGCAAGCATCAAATGACCAAGGAGCTGGGCAGTTAAGTGGTAAGTGCTGACTTTGA-----G------TAT---------**********----C--TTT--**********----TTGTCA----------ATTGCATTGTAACA--A--A---T--ACA--TTTGTTTTCTAGTGGTCAGCGCAAGGAGATAACGCGCTTGAACATCAATAGCAAGAGAGC
droEre2	scaffold_4845:19943469-19943631 -		GTACTTTAAGCGCAAGCATCAAATGACCAAGGAGCTGGGCAGTTAAGTGGTAAGTACTGATTTCGA-----G------TAT---------**********----C--TTT--**********----TTTT----------CAACACAATATAACA--A--A---A--T--ACA--TTTGTTTTCTAGTGGTCAGCGCAAGGAGATAACGCGCTTGAACATCAATAGCAAGAGAGC

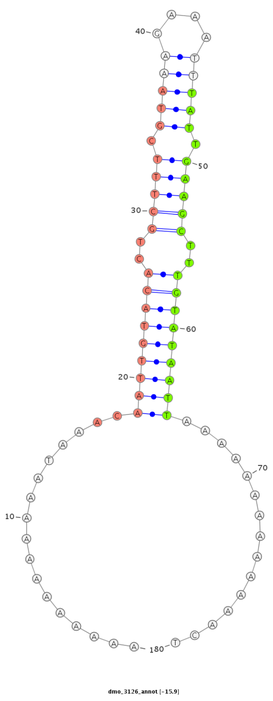
Generated: 09/08/2015 at 07:05 PM

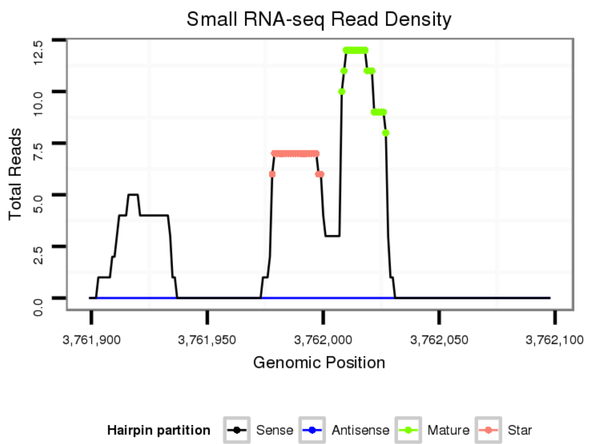
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.stop3	0
crit.uri	1
crit.back	1
rescue.total	1
rescue.mismatch	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

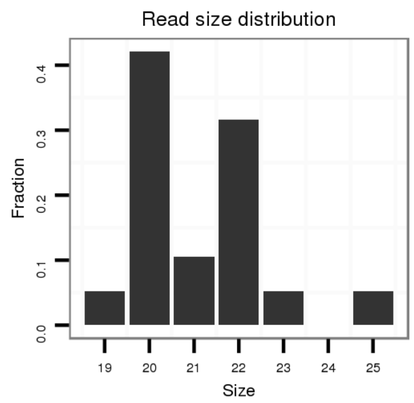
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_3126	**scaffold_6540:3761949-3762048 +**	**confident-exception**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

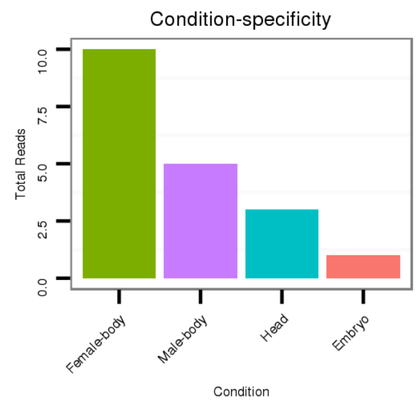
Legend: mature star mismatch in alignment mismatch in read

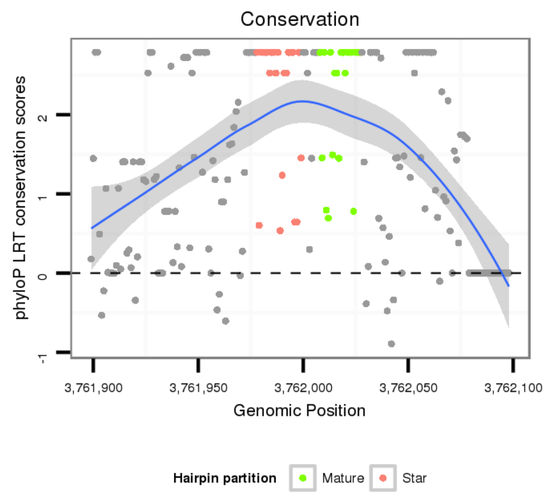
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

Repeatable elements

Name	Class	Family	Strand
A-rich	Low_complexity	Low_complexity	+

Sense Strand Reads

hide 3p reads show mid mismatch reads

```
CAAAATGAAAGAAAGAAGAGATGAACCCAACCAACAACAAAAAAAAACCAATAGAAAAAACTAAAAAAAAAAAAAAATAAACAATTGTACACTGCTTTCGTAAAGAAATTTATTGAAGCTTTGTATAATTAAAAAAAAAAAAACTGAACTTTTGTGTTTTTATTTGATTTATTTACATACATATATGTATGTGGTTATAAC
************************************************************.................(((((((((..(((((.(((((....)))))).)))))..)))))))))).............**************************************************
```

Read size	# Mismatch	Hit Count	Total Norm	Total	M046 female body	V110 male body	V049 head	M060 embryo	V056 head	V041 embryo
20	0	1	5.00	5	4	1	0	0	0	0
22	0	1	3.00	3	1	0	0	1	1	0
24	0	1	1.00	1	0	1	0	0	0	0
21	0	1	1.00	1	0	0	0	0	1	0
25	0	1	1.00	1	0	1	0	0	0	0
21	1	1	1.00	1	0	0	1	0	0	0
21	0	1	1.00	1	1	0	0	0	0	0
19	0	1	1.00	1	0	0	0	0	0	1
25	0	1	1.00	1	1	0	0	0	0	0
23	0	1	1.00	1	0	1	0	0	0	0
20	0	1	1.00	1	0	0	1	0	0	0
25	0	1	1.00	1	0	0	0	1	0	0
20	0	1	1.00	1	1	0	0	0	0	0
19	1	1	1.00	1	1	0	0	0	0	0
22	0	1	1.00	1	1	0	0	0	0	0
22	0	1	1.00	1	0	1	0	0	0	0
18	0	1	1.00	1	1	0	0	0	0	0
20	0	1	1.00	1	0	1	0	0	0	0
22	0	1	1.00	1	1	0	0	0	0	0
19	0	1	1.00	1	1	0	0	0	0	0
19	2	5	0.20	1	0	0	1	0	0	0

Anti-sense strand reads

```
GTTTTACTTTCTTTCTTCTCTACTTGGGTTGGTTGTTGTTTTTTTTTGGTTATCTTTTTTGATTTTTTTTTTTTTTATTTGTTAACATGTGACGAAAGCATTTCTTTAAATAACTTCGAAACATATTAATTTTTTTTTTTTTGACTTGAAAACACAAAAATAAACTAAATAAATGTATGTATATACATACACCAATATTG
*****************************************************.................(((((((((..(((((.(((((....)))))).)))))..)))))))))).............*****************************************************
```

Read size	# Mismatch	Hit Count	Total Norm	Total	V110 male body	M046 female body

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6540:3761899-3762098 +	dmo_3126	CA---AAATGAAAGAAAG----------AAGAGAT-----GAAC---------C----------CAACCAACAACAAAAAAAAACCAATAGAAAAAACTAAAA-AAAAAAAAAATAAAC-AATTGTACACTGCTTTCGTAAAGAAATTTATTGAAGCTTTGTATAATTAAAAAAAAAA----A-AACTGAACTTTTGTGTTTTTATTTGATTTATTTACATACATATATGTATGTGGTTATAAC
droVir3	scaffold_13047:1835002-1835164 +	dvi_24634	CG---AAATGAG--CAAA----------AAGAGAA-----CAA---------*--C------CCAACC------AAGA--AAAACAATAGAAA-AAAAAACATAAAAAAAAAATAAATAATAATTGTACACGGCTTTCGTAAAGAAATTTATTGAAGCTTTGTATAATTAACAAAAAAAA--AAACCTTGAAG-TTTGTGTTTTTATTTTATT----------GA----------
droGri2	scaffold_14906:8668147-8668298 +	dgr_462	AACTAAAAAAAA--AAAA----------AAGTGAA-----CAAC---------C----------CAACC------A---ACAAAACAATAGAAA---------------AAAATAAAC-AATTGTACACGGCTTTCGTAAAGAAATTTATCGAAGCTTTGTATAATTAACCAAAAAAAAACA-ACCTGATG-TTTGTGTTATTATTTGCTTTATT----------
droWil2	scf2_1100000004902:4649922-4650075 +	dwi_5415	CA---AAAGAAA--AGAAAAGTTT----AAAAAATCAAAACAA----------CCAA------CCAACC------A---ACAAAACAATAGAAA---------------AATAAAC-AATTGTACACGCGCTTTTATAAAGTAATTTATTAAAGCTTTGTATAATTACCCAAAAAAAAAA-CCCAAAAA-TTTTTGTTTTTATTTG----------
dp5	2:27294866-27295019 -	dps_3827	CA---AA----------------------------CCAAATCCATTCAACA-------G--AAAAACAATAGAAG-AACAAAAA-AAAAAGAAAATAAAA-AATTGTACACGCGCTTTTATGAAGTAATTTGTTAAAGCTTTGTATGATTAAACAAAAAAA--AA-AAACCAAA-TTTGTGTTTTTATTTGCATTTTT----TAG----------
droPer2	scaffold_6:2585075-2585220 -	dpe_2481	CA---AA----------------------------CCAAATCCATTCAACA-------G--AAAAACAATAGAAG-AACAAAAA-AAAAAGAAAATAAAA-AATTGTACACGCGCTTTTATGAAGTAATTTGTTAAAGCTTTGTATGATTAAACAAAAAAAAAA-ACCCCAAA-TTTGTGTTTTTATTTG----------
droAna3	scaffold_13340:11049297-11049433 -	dan_90	CA---AATA----------TTTGAAAAAGAAAAT-----CAAC---------C-C-------TCAACC------AACCACAAAGCAATAGAAA---------------AAATAAAC-AATTGTACACGCGCTTTCGTAAAGTGATTTATTAAAGCTTGTATAATTAACAAAAACA----*---ACAAA-TTTGTGTTTTTATTT----------
droBip1	scf7180000396374:34267-34385 +		CA---AAA----------------------------CCC------TCAACC------AACCACAAAGCAATAGAAA---------------AAATAAAC-AATTGTACACGCGCTTTCGTAAAGTGATTTATTAAAGCTTGTATAATTACAAAAACA----*---ACAAA-TTTGTGTTTTTATTT----------
droKik1	scf7180000302247:250356-250505 +		CA---AAA----------------------------CCAA------CCAACC------ATCAACAAAACAATAGAAG-AA-----A-AAAAACAAAATAAAC-AATTGTACATGGCTTTCGTAAAGTAATTTATTAAAGCTTTGTATAATTAAAAAAAAGA---AC-AACCAAAA-TTTGTGTTTTTATTTGCCTTATC-ACGTACA----------
droFic1	scf7180000454106:2527582-2527718 +		CA---AAG----------------------------CCAA--CCA-CCAACC------AACCACAAAACAATAGAAA---------------AAGAAATAAAC-AATTGTACACGCGCTTTCGTAAAGTAATTTATTAAAGCTTTGTATAATTAACAAAAAAA----A-ACCTCCAA-ATTGTGTTTTTATTTGCCTTAT----------
droEle1	scf7180000491212:1154183-1154316 +		CA---AAA----------------------------GCAT--CCA-CCAACC------AGCA-----ACAATAAA----------*--AAAACAAATAAAC-AATTGTACACGCGCTTTCGTAAAGTAATTTATTAAAGCTTTGTATAATTAACAAAAAAA---CA-ACCCCAAA-TTTGTGTTTTTATTTGCCTTAT----------
droRho1	scf7180000778307:14069-14212 +		CA---AAA----------------------------CCAA------CCAACC------AACATCAAAACAATAGAAA---------------*--AAAACAAATAAAC-AATTGTACACGCGCTTTCGTAAAGCAATTTATTGAAGCTTTGTATAATTAACAAAAAAA----A-ACCTCAAA-TTTGTGTTTTTATTTGCGTCATC-ACGTACA----------
droBia1	scf7180000302402:7353515-7353646 -		CA---AAA----------------------------C----------CAACC------AACAACAAACCCATAGAAA---------------***AAA-CAATAAAC-AATTGTACACGCGCTTTCGTAAAGTAATTTATTAAAGCTTTGTATAATTAACAAAAAAA--AC-AACCAAAA-TTTGTGTTTTTATTTGCCTTAT----------
droTak1	scf7180000414009:179079-179230 +		GA---AAA----------------------------CCCTATAAAACCAA------CCAACC------AACAACAAACAATAGAAA---------------***AAACAAATAAAC-AATTGTACACGCGCTTTCGTAAAGTAATTTATTAAAGCTTTGTATAATTAAAAAAAA--***AA-ACCTCAAA-TTTGTGTTTTTATTTGCGTTATC-ACGTACA----------
droEug1	scf7180000409490:80965-81110 +		CA---AAA----------------------------CCAA------CCAACC------AACAACAAACAATAGAAA---------AAAAATCAAATAAAC-AATTGTACATGGCTTTCGTAAAGTAATTTATTAAAGCTTTGTATAATTAACAAAAAAA----A-ACCTCAAA-TTTGTGTTTTCATTTGCGTTATC-ACGTACA----------
dm3	chr3R:4640244-4640386 -	dme_421	CA---AA----------------------------CCAA------ACAA-C------AACAACAAACAATAGAAA---------***AAACAAATAAAC-AATTGTACATGGCTTTCGTAAAGAAATTTATGAACGCTTTGTATGATTAACCAAAAAAA--AA-TCCACAAA-TTTGTGTTTTTATTTGCGTTATC-ACGTACA----------
droSim2	3r:16351742-16351889 +	dsi_75	CA---AA----------------------------CCAA------ACAAC----AACAACAAACAATAGAAA---------AAAAAACAAATAAAC-AATTGTACATGGCTTTCGTAAAGAAATTTATTAAAGCTTTGTATGATTAACCAAAAAA---AA-TCCTGAAA-TTTGTGTTTTTATTTGCGTTATC-ACGTACA----------
droSec2	scaffold_0:17217390-17217533 +	dse_1844	CA---AA----------------------------CCAA------ACAA-C------AACAACAAACAATAGAAA---------AAAAACAAATAAAC-AATTGTACATGGCTTTCGTAAAGAAATTTATTAAAGCTTTGTATGATTAACCAAAAAA---AA-TTCTGAAA-TTTGTGTTTTTATTTGCGTTATC-ACGTACA----------
droYak3	3R:8702178-8702321 -	dya_1796	CA---AA----------------------------C----------CAAACC------AACAACAAACAATAGAAG-A-------AAAAAACAAATAAAC-AATTGTACATGGCTTTCGTAAAGTAATTTATTAAAGCTTTGTATAATTAACCAAAAAAA--AA-TCCTCAAA-TTTGTGTTTTCATTTGCGTTATC-ACGTACA----------
droEre2	scaffold_4770:16945913-16946051 +	der_1521	CA---AA----------------------------C----------CAAACC------AACAACAAACAATAGAAA---------***AAAACAAATAAAC-AATTGTACATGGCTTTCGTAAAGTAATTTATTAAAGCTTTGTATAATTAACCAAAAAA----A-TCCTCAAA-TTTGTGTTTTTATTTGCGTTATC-ACGTACA----------

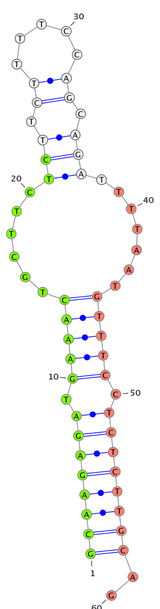
Generated: 09/08/2015 at 07:56 PM

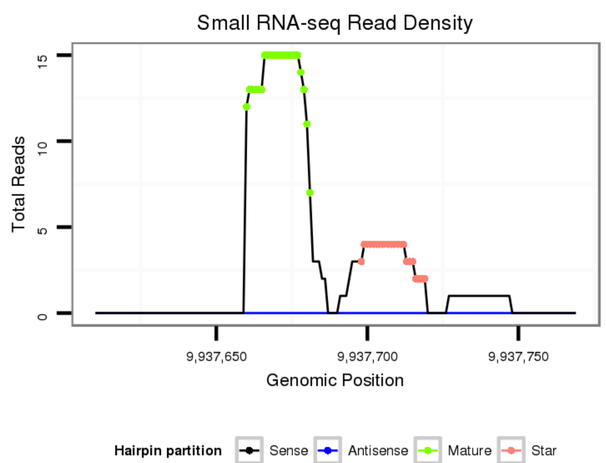
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	1
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	0
rescue.known	0
rescue.confident	8
rescue.candidate	4

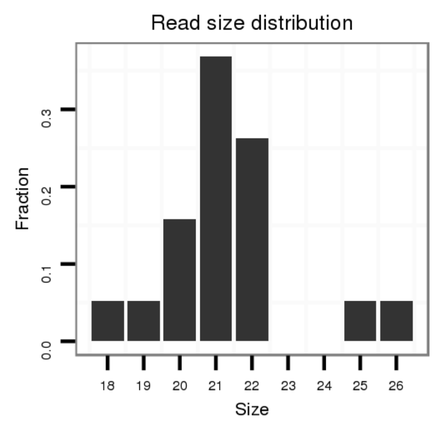
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_1066	**scaffold_6496:9937660-9937719 +**	**confident-exception**	**Mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

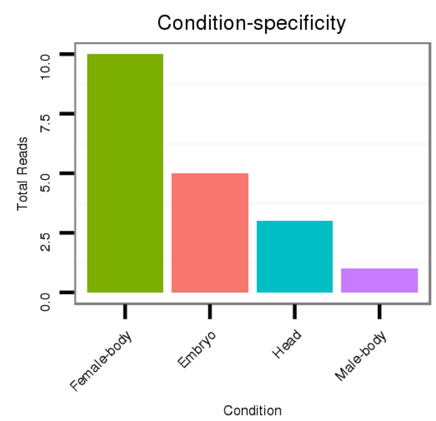
Legend: mature star **mismatch in alignment** mismatch in read

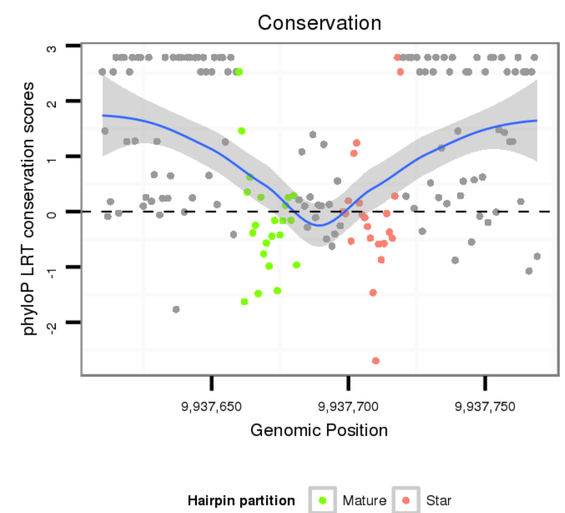
Predicted structure











dmo_1066, score1 = 18.83

Show Alternate Folds

Flybase annnotation

intron [DmojGI20374-in]; CDS [DmojGI20374-cds]; CDS [DmojGI20374-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

```
CAACGAGAAGGAGAACCTGATGCTGCTCTTCAAGAAGTGCGACAAGCATGGCAAGAGATGAAACTGCTTCTCTTCTTTTCCAGCAGATTTTAATGTTTCCTCTCTTGCAGATATTTCAGAGCAGATGCAGAAGGCTTTGAGCTACATCGCCGACGGCGTC
************************************************(((((((.(((((.....(((.((.....)).)))).....)))))).)))))))..**************************************************
```

Read size	# Mismatch	Hit Count	Total Norm	Total	M046 female body	M060 embryo	V056 head	V110 male body
22	0	1	4.00	4	0	3	1	0
21	0	1	3.00	3	2	0	1	0
21	0	1	2.00	2	2	0	0	0
20	0	1	2.00	2	0	1	0	1
20	0	1	1.00	1	1	0	0	0
18	0	1	1.00	1	0	0	1	0
19	0	1	1.00	1	1	0	0	0
22	0	1	1.00	1	1	0	0	0
21	0	1	1.00	1	0	1	0	0
26	0	1	1.00	1	1	0	0	0
25	0	1	1.00	1	1	0	0	0
21	0	1	1.00	1	1	0	0	0
21	1	1	1.00	1	0	1	0	0
23	1	1	1.00	1	0	0	0	1
21	0	1	1.00	1	0	1	0	0

Anti-sense strand reads

```
GTTGCTCTTCCTCTTGGACTACGACGAGAAGTTCTTCACGCTGTTCGTACCGTTCTCTACTTTGACGAAGAGAAGAAAAAGGTCGTCTAAAATTACAAAGGAGAGAACGTCTATAAAGTCTCGTCTACGTCTTCCGAAACTCGATGTAGCGGCTGCCGCAG
************************************************(((((((.(((((.....(((.((.....)).)))).....)))))).)))))))..**************************************************
```

Read size	# Mismatch	Hit Count	Total Norm	Total	M060 embryo	V056 head	M046 female body	V110 male body

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6496:9937610-9937769 +	dmo_1066	CAACGAGAAGGAGAACCTGATGCTGCTCTTCAAGAAGTGCGACAAGCATGGCAAGAGA----------TGAAACTGC--------TTCTCTT----------CTTTTC----------CAGCAGATTTTAATGTT-T---C--CT-----CT--CTTGCAGATATTTCAGAGCAGATGCAGAAGGCTTTGAGCTACATCGCCGACGGCGTC
droVir3	scaffold_12875:14471536-14471691 +	dvi_6870	CAACGAGAAGGAGAATCTGACGCTGCTCTTCAAGAAGTGCGATAAACATGGTGAGATC----------AGA------TCCT-CAA-----TTGC----------CTGTTGTAGCGCATAAAG----------------------A-------GC-T---GT-TT-----G--CTTTCAGATATTTCGGAGCAAATGCAAAAGGCGCTCAGCTACATAGCCGACGGAGTC
droGri2	scaffold_15245:14469966-14470122 +		CAACGAGAAGGAGAATCTGACGCTGCTCTTCAAGAAGTGCGATAAGCAGGGTAAGTAA----------A-----TGC--------TATCAGC----------GATTTC----------TAGTCAAT-----TGT-TATCCG-TAATCT--CC--TTCTCAGATATATCGGAGCAAATGCAAAAGGCGCTCAGCTATATAGCCGAATGGCGTC
droWil2	scf2_1100000004954:4220080-4220250 +		CAATGAGAAAGAGAATCTGGCTATGTTGTTTAAGAAGTGTGATAAGCATGCTGAGTAGATGT-CATCCA-------A--------ATCCTCTAT-GG----------------------TATAAGAAATTAT------TCCCACT-----TCT---TT-----T---ACTCATATTGTACACAGATATTTCGGAGCAGATGCAAAAGGCCTGTGCTATATAGTCGATGGTGTC
dp5	3:9242759-9242919 +		CTACGAAAAGGAGAACCTCACGCTTCTCTTCAAGAAGTGCGACAAGCAGGGTGAGCACGAGGAC--ACAAGAAACCATAACCATTTCCATT-----CTGATGT-AT---T---GGCT--TC--TCCTCAGACATTTCGGACCAGCTGCAGGCTGCGCCTGGGCTACATAGCTGATGGAGTT
droPer2	scaffold_4:4564941-4565101 +		CTACGAAAAGGAGAACCTCACGCTTCTCTTCAAGAAGTGCGACAAGCAGGGTGAGCACGAGGAC--ACAAGAAACCAGAACTATTCCCATT-----CTGATGT-AT---T---GGCT--TC--TCCTCAGACATTTCGGACCAGCTGCAGGCTGCCCTGGGCTACATAGCTGATGGAGTT
droAna3	scaffold_12430:38349-38509 -		CACGGAAAAGGAGAATCTTTCCTTGCTCTTTAAGAAGTGCGACAAGCAGGGTAAAGTT----------ATTGGATAATCCTTTTA-----T---AAACTCT---TTTATTGAT------TG-AATCCT--CC-----AC--CCTGCAGACATCTCGACCAGCTGCAGAGCGCCCTGGCTATATAGCCGACGGTGTT
droBip1	scf7180000396759:417529-417689 +		CACGGAAAAGGAGAACCTGTCGTTGCTTTCAAAAAGTGCGACAAGCAGGGTAACTTA----------AATGGTCCAACCTGTTA-----T---GAGCCTC----------A-TTA-----------TAATTG-ATTCCT--TA-----AC--CCTTCAGATATCTCGACCAGCTTCAAAGCGCCCTGGGCTACATAGCCGATGGTGTG
droKik1	scf7180000302470:1954524-1954682 +		CAGCGAGAAGGAGAACCTGTCGCTGCTGTTTAAGAAGTGCGACAAGCAAGGTTTGTAT----------ACCTT---CTTCT-AAA-----TTAA-GC----CTTATCCTTATACT------C----------CT-T---T---CCTTATAT--CCCACAGACATTTCGACCAGCTGCAGAGCGCCTTGGGTTACATAGCCGATGGCGTT
droFic1	scf7180000453851:1097893-1098053 -		CAGCGAGAAGGAGAACTTGTCGTTGCTCTTCAAAAAGTGCGATAAGCAGGGTTAGTTA----------AGTAAAAATCCG-TAA-----CTCTGTA----AGGTACATAATGCT------T----------TT-T---T---CCTT--TT--CCCATAGATATTTCGACCAACTGCATAACGCTTTAGTTACATAGCCGATGGTGTT
droEle1	scf7180000491201:1001748-1001902 +		CAGCGAGAAGGAGAACTTGTCGTTGCTATTCAAAAAGTGCGATAAGCAGGGTTCGTTT----------AGTTAGGATTCT-TGA-----TTCAGTC----ACTGACTTAC----G-----------------T---T---TTTT--CC--ACCACAGATATATCGGATGAGCTGCAAAACGCCTTGGGCTACATAGCCGACGGCGTT
droRho1	scf7180000777222:15222-15374 -		CAGCGAGAAGGAGAACTTGTCCTTATTGTTCAAAAAGTGCGATAAGCAGGGTAAGTTT----------AGTTTAGATCCT-TGA-----TTCAGTC----TCTGA-ATAT----------------T---T---TTTT--CT--TCCACAGATATTTCGACCAGCTGCAAAACGCCTTAGTTACATAGCCGATGGCGTA
droBia1	scf7180000301506:1546610-1546769 -		CACGGAGAAGGAGAACCTGTCGTTGCTGTTCAAAAAGTGCGATAAGCAGGGTAAGTTT----------GGTGAAAGCTTCT-TGG-----TTTCATC----------CTTTCT-----TAGTAAG----------------C-------TC-T---T---TCTT--CC--CAACCAGATATTTCGACCAGCTACAAAACGCCTTGGCTACCTAGCCGATGGTGTG
droTak1	scf7180000415401:198113-198272 +		CAGCGAAAAGGAGAACCTGTCGTTGCTATTCAAAAAGTGCGATAAGCAGGGTTAGTTA----------AGCTCAGACTATT-TTA-----TTCACCC----ACCCATCTAATGAT------C----------AT-T---T---CTA---CC--CACACAGATATTTCTGACCAGCTACAGAACGCCTTGGGCTACATAGCCGATGGCGTT
droEug1	scf7180000409183:817698-817859 +		CAGCGAAAAGGAAAACCTGTCGTTGCTTTTAAAAAGTGCGATAAGCAAGGTTTGCTA----------GAAAAAAATTTCT-TGA-----TTTAGTA----TCTTACAT------TAAAAGT----------C-------TC-T---T---TATT--CT--GTGACAGATATTTCGACCAGCTCCAGAACGCTTTGGTTATATAGCCGATGGCGTC
dm3	chr2R:5175359-5175517 +		CACCGAAAAGGAGAACCTATCTTTGCTGTTCAAAAAGTGCGATAAGCAGGGTAAGATA----------AGAAAATGC--------ATACATTATGGC----ACCAAAATAGTGCT------C----------TT-T---T---CGTT--TT--GCAATAGATATTTCGACCAGCTGCAGAACGCTTTGGCTACATAGCCGATGGAGTT
droSim2	2r:5978193-5978351 +		CACCGAAAAGGAGAACCTATCGTTGCTGTTCAAAAAGTGCGATAAGCAGGGTAAGATA----------AGAAAATGC--------ATCCATTAAGGC----ACTAAAATAATGCT------C----------TT-T---T---CGGT--TT--GCAATAGATATTTCGACCAGCTGCAGAACGCTTTGGCTACATAGCCGATGGAGTT
droSec2	scaffold_1:2807474-2807632 +		CACCGAAAAGGAGAACTTATCGTTGCTGTTCAAAAAGTGCGATAAGCAGGGTAAGAAA----------AGAAAATGC--------ATCCTTTAAGGC----ACTAAAATAATGCT------C----------TT-T---T---CGGT--TT--GCAATAGATATTTCGACCAGCTGCAGAACGCTTTGGCTACATAGCCGATGGAGTT
droYak3	2L:17830494-17830652 +		CACCGAAAAGGAGAACCTATCGTTGCTGTTCAAGAAGTGCGATAAGCAGGGTGAGATA----------ATTAATGC--------ATCCATTAATGG----ACTAACCTAATTAT------C----------TT-T---T---AGTT--TT--GCAACAGATATTTCGACCAGCTGCAGAACGCCTTGGGTTACATAGCCGATGGAGTA
droEre2	scaffold_4929:17482200-17482358 -		CACCGAAAAGGAGAACCTATCGTTACTGTTCAAAAAGTGTGATAAGCAGGGTAAGATA----------AGTAAATGA--------ATCCATTAAGGG----ACTAACCTAATGGT------C----------TT-T---T---TGTT--TT--GCAATAGATATCTCAGACGAGCTGCAGAACGCTTTGGGTTACATAGCCGATGGAGTA

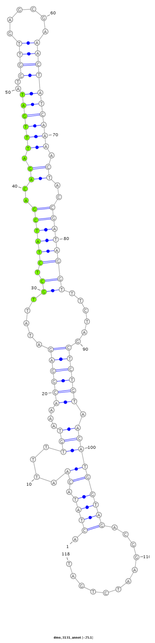
Generated: 09/08/2015 at 07:05 PM

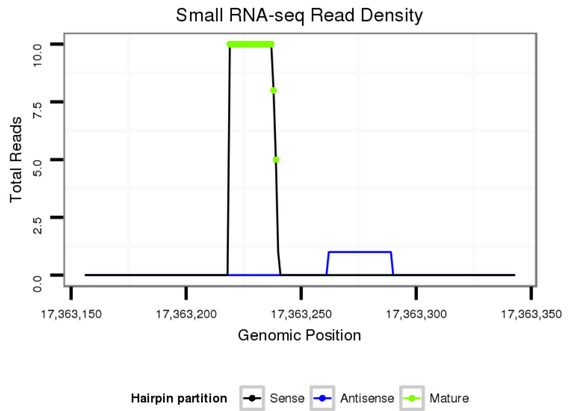
	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	0
crit.uri	1
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

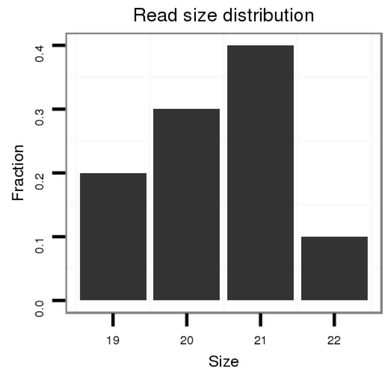
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_3131	**scaffold_6680:17363206-17363293 +**	**candidate**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

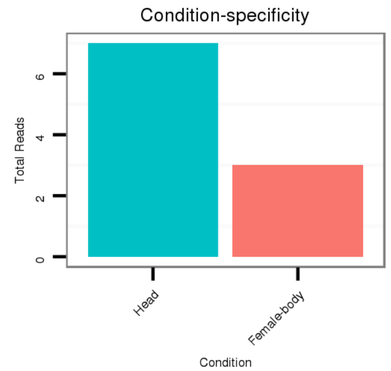
Legend: mature star mismatch in alignment mismatch in read

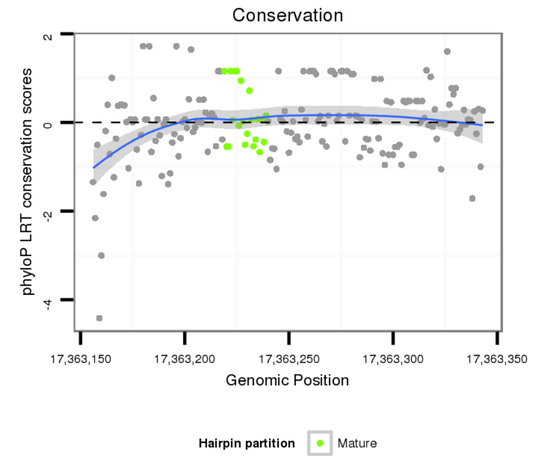
Predicted structure











Show Alternate Folds

Flybase annotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

CTTGGACTTTGGTTTTTAAAACAATTTATTTTTGAACTATACAATTTTGTAAAACGGAGATATTGCTCTATCGACAGATTTGATATGGTTGAGCGAAACTATCAAAACTACCGATAGGTTTCTAGCTCTGTAACATGGTAGACGGAATCTGATATATATATTTAAACCTATTTCACTTTCAAATTTAT **********.((((.((....(((...((((((.....((.(((((((..((.((((((..((((.....))))))))))).))..)))))))).....)))))).)))))))).....********** **Read size**	**#Mismatch**	**Hit Count**	**Total Norm**	**Total**	**M046 female body**	**V056 head**	**V110 male body**	**V049 head**	**M060 embryo**
21	0	1	4.00	4	0	3	0	1	0
20	0	1	3.00	3	1	2	0	0	0
19	0	1	2.00	2	2	0	0	0	0
22	0	1	1.00	1	0	1	0	0	0

Anti-sense strand reads

GAACCTGAAACCAAAAATTTTGTTAAATAAAAACTTGATATGTTAAAACATTTTGCCTCTATAACGAGATAGCTGTCTAAACTATACCAACTCGCTTTGATAGTTTTGATGGCTATCCAAAGATCGAGACATTGTACCATCTGCCTTAGACTATATATATAAATTTGGATAAAGTGAAAGTTTAAATA **********.((((.((....(((...((((((.....((.(((((((..((.((((((..((((.....))))))))))).))..)))))))).....)))))).)))))))).....********** **Read size**	**#Mismatch**	**Hit Count**	**Total Norm**	**Total**	**V110 male body**	**M046 female body**	**V056 head**	**V049 head**	**M060 embryo**
28	0	1	1.00	1	1	0	0	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6680:17363156-17363343 +	dmo_3131	CTTGGACTTT----------GG--TTT-----TTA-AAACAATTT----------ATTTTTGAACTATACAA-TTTTG---TAAAACGGAGATATTGCT-CTATCGACAGATTTGATATGGTTGAGCGAAA----CTATCAAAACTACCGATAGGTTTCTAGCTCTGTAACATGGTAGACGGAATCTGATATATATATTTAAACCTATTTC----------ACTTTCAAATTTAT
droVir3	scaffold_13049:22743117-22743310 +	dvi_429	CTTCTTA---------GAAAACTTCA----------GC--TTT-----TGC-ACAGTTTTT----------ATTGTCATAATACAAAAATTTTGTCATAACACCGAGTTAATATTACTATCGGTAGTATCGATAATGCTAATGTAAA----ATATCGAAACTATCGATAGTTTTTAGCTCGTGATAATCATTCAAGTTTCGTGATCGAT-TAT---ATCAACTTTC----------ACTTTCAATTTGAT
droGri2	scaffold_15110:20785665-20785909 -		GAAACTTTATATCGTAGAAATCCACTTCTGCAGATTGCTGAAAGCTTTCAATCAAATTTG--GCCAGGACTTT-ACAGTTTTTGACTTGTACTTAAAGTTATAAACAGGGC--TT--ATAAAACTGGGTTAATACTTCTA----TAGTATTAATGCGCATAGTTTGT----CATTCGAAACTATCATAGTTTTTAGCTCTGGTTAG----------TTTATTTCATTTTCCATCCTAATCAACTTCTTTTGCACTCTGCAATTTAT
droWil2	scf2_1100000004511:713301-713336 -		ATATATAT---**--**---**-----**---**--------**----------**----------**-----**---**----------**-**----------**----**----------ATATAAATCTATTTC----------ATTTTCAGCTCTA-
droPer2	scaffold_9:1867622-1867657 +		TATGTAT---**--**---**-----**---**--------**----------**----------**-----**---**----------**-**----------**----**----------GTATGTACATATTTC----------TCCTACAAATTTGT
droAna3	scaffold_12613:345788-345884 +		CTTTAAT---------AAAA-ATACT--CC---AT--ATTTTTT-----AAA-TAGCAATAT----------ATTATTTGAAGTATGA-TTTTG---TGAAA----------**-**----------G-----ATTTTA----------AGCAATTGAA----------AAATTTAGGATAAT
droFic1	scf7180000454073:2938897-2938926 -		ATATATT---------GAAAAATGCT----------**--**---**-----**---**--------**----------**----------**-----**---**----------**-**----------**----**----------TC----------AAACTAAAA---GC
droEle1	scf7180000491255:1165984-1166000 -		ATTGTCTTT---**--**---**-----**---**--------**----------**----------**-----**---**----------**-**----------**----**----------**----------**----------TAGTTTT
droRho1	scf7180000767806:17680-17730 -		GGCCTCT---GA--TTT-----ATA-AAAACATTT----------ATTTTTTAAGGGTACGA-TATTA---CAGAA----------**-**----------**----**----------**----------**----------
droBia1	scf7180000302402:2698515-2698583 -		GAATATAAAGTT---**--**---**-----**-TTGAAACAATTC----------AATTACGAAATGTACAA-ATTTT---AAATGTTTAG--------**-**----------**----**----------**----------**--AATAAAACCTAT
droTak1	scf7180000415185:52121-52165 +		GGTGGTCTT---T---**--**---**-----**-TTGGAATTATAT----------AATGTCATTTGGA---**-**----------**----**----------**----------**-----GCACTGTGT
droSim2	x:2837878-2838042 -		GTTCGAT---------GCGGTGTACGGTCTAACAATTTTG--TTT-----ATATAAGCACTTC----------AGTTTCAAGCCTACAG-AACTA---CGAAATTTATGTATTCAT-ATGCA---TGTGGCCACAATTAAGATTAGAATTCGATAAAACTTAGCGTAGTCTTATGGCCTAGTGATATAATG----------**----------**----------GTCG
droYak3	2R:15012572-15012587 -		GCTGTT----------**--**---**-----**---**--------**----------**----------**-----**---**----------**-**----------**----**----------TC----------ACCTTCAG------

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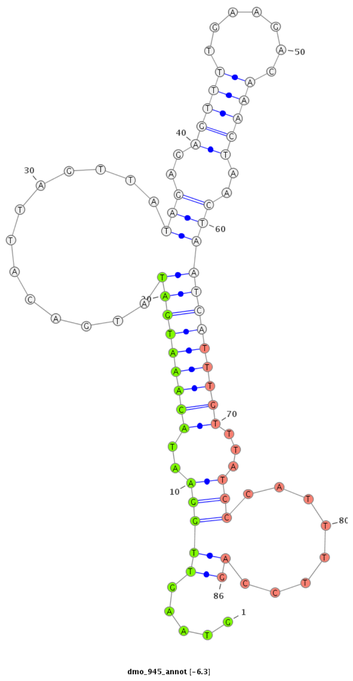
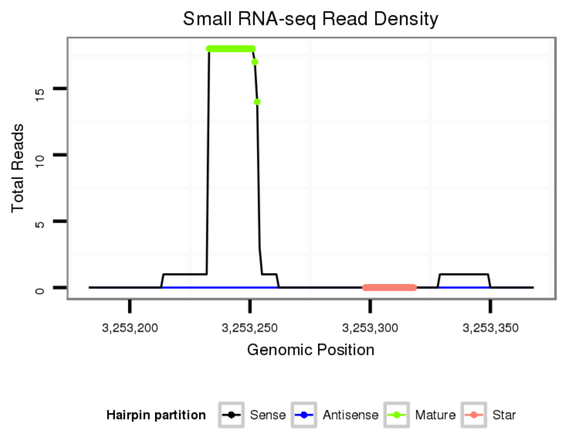
	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	0
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	2

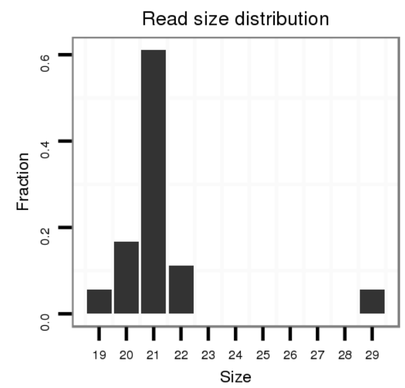
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_945	**scaffold_6496:3253233-3253318 +**	**confident-exception**	**Mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

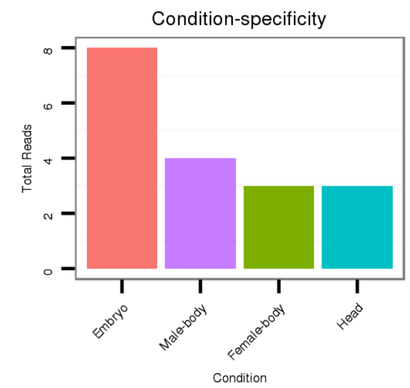
Legend: mature star mismatch in alignment mismatch in read

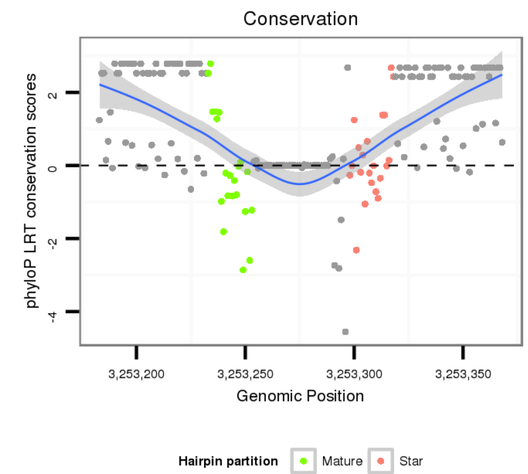
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dmoj\GI19952-in]; CDS [Dmoj\GI19952-cds]; CDS [Dmoj\GI19952-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

GGGTCTGTGGAACAATACCACGCCCGTGGCCATCAAAACTCTTAAGTCGGGTAAGTTGGAATACAAATGATATGACATTAGTTATAGAGAGTTTTGAAGACAAACTAACTAATCATTTGTTTATCCCATTTTCCAGGCACTATGGATCCCAAGGACTTTTTGGCTGAGGCACAAATAATGAAGAAG	Read size	# Mismatch	Hit Count	Total Norm	Total	M060 embryo	V110 male body	M046 female body	V056 head	V041 embryo	V049 head
**********											
.....GTAAGTTGGAATACAAATGAT.....	21	0	1	11.00	11	7	1	1	1	1	0
.....GTAAGTTGGAATACAAATGA.....	20	0	1	3.00	3	0	0	1	1	0	1
.....TTTGTTTATCCCATTTTCCAGT.....	22	1	1	2.00	2	1	1	0	0	0	0
.....GTAAGTTGGAATACAAATGATA.....	22	0	1	2.00	2	0	2	0	0	0	0
.....TCCCAAGGACTTTTTGGCTGA.....	21	0	1	1.00	1	0	0	1	0	0	0
.....GTAAGTTGGAATACAAATGATATGACATT.....	29	0	1	1.00	1	0	0	1	0	0	0
.....GTAAGTTGGAATACAAATG.....	19	0	1	1.00	1	0	1	0	0	0	0
.....ATCAAAACTCTTAAGTCGG.....	19	0	1	1.00	1	0	0	1	0	0	0

Anti-sense strand reads

CCCAGACACCTTGTTATGGTGCGGGCACCGGTAGTTTTGAGAATTCAGCCCATTCAACCTTATGTTTACTATACTGTAATCAATATCTCTCAAAACTTCTGTTTGATTGATTAGTAAACAAATAGGGTAAAGGTCCGTGATACCTAGGGTTCCTGAAAAACCGACTCCGTGTTTATTACTTCTTC	Read size	# Mismatch	Hit Count	Total Norm	Total	V056 head	V110 male body	M046 female body
**********								

Show Alignment With Reads

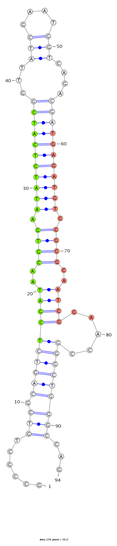
Re-alignment of all predicted orthologs

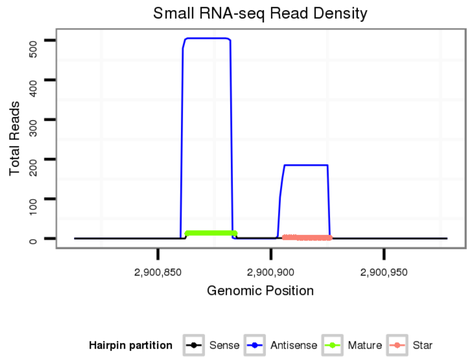
Species	Coordinate	ID	Alignment
droMoj3	scaffold_6496:3253183-3253368 +	dmo_945	GGGTCTGTGGAACAATACCACGCCCGTGGCCATCAAAACTCTTAAGTCGGGTAAGTTG--GAATA-CAAATG----------ATATGACATTAGTTATAGAGAGTTT-TGAAGACAAACTAA----CTAATCAT--TT--GTTTAT------C---------CCATTTTCCAGGCACTATGGATCCCAAGGACTTTTTGGCTGAGGCACAAATAATGAAGAAG
droVir3	scaffold_12823:735822-735887 -		GGGAGTATGGAATAATACAACGCCCGTGGCTATCAAAACCTCAAGTCGGGTAAGTCA--AATG---AGAT--

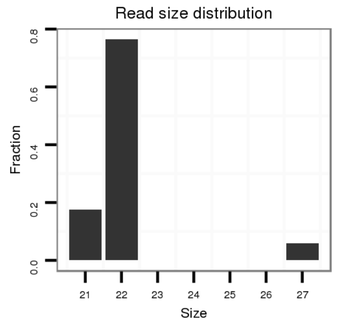
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_159	**scaffold_6328:2900863-2900928 +**	**confident-exception**	**Testes-restricted**	**intergenic**	[View on UCSC Genome Browser [Cornell Mirror]]

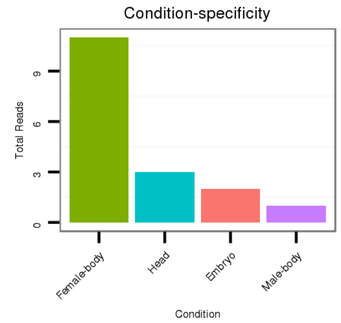
Legend: mature star mismatch in alignment mismatch in read

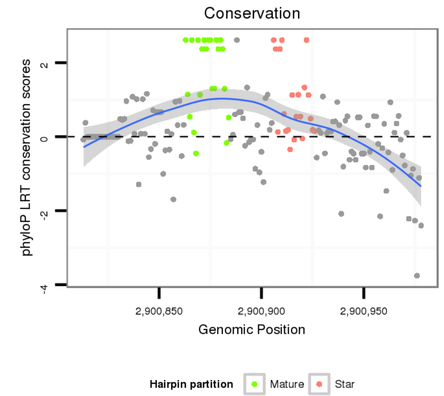
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

```
TAGTCATAGGACACATGCACAAATTTGAAGTCAGTGCCGCTGTCGCAGTCTCGATAACGTGAATATCTCATCGGTTATCGAATGGTCAGACGATGAGATGTCCGCGCAATCGGAACCGGGCTGGGCCAGAACAACGAACTGGTTCATTTCGTTTAACTCATGTTGT
**********************************......(((.((((((((((..((((.((((((((((...(((....)))....)))))))))))).))))..))))).....)))))))))...**********************************
```

Read size	# Mismatch	Hit Count	Total Norm	Total	M046 female body	M060 embryo	V056 head	V041 embryo	V110 male body
22	0	1	12.00	12	7	1	2	1	1
21	0	1	1.00	1	1	0	0	0	0
27	0	1	1.00	1	1	0	0	0	0
21	0	1	1.00	1	1	0	0	0	0
22	0	1	1.00	1	0	0	1	0	0
21	0	1	1.00	1	1	0	0	0	0

Anti-sense strand reads

```
AGAGCTATTGCACTTATAGAGTCTACTCTACAGGCGCGTTAGCCTAGAGCTATTGCACTTATAGAGTAGCCAATAGCTTACCAGTCTGCTACTCTACAGGCGCGTTAGCCTTGGCCCGACCCGGTCTTGTTGCTTGACCAAGTAAAGCAAATTGAGTACAACA
**********************************......(((.((((((((((..((((.((((((((((...(((....)))....)))))))))))).))))..))))).....)))))))))...**********************************
```

Read size	# Mismatch	Hit Count	Total Norm	Total	V110 male body	M046 female body	V056 head	V049 head	M060 embryo	V041 embryo
22	0	1	473.00	473	382	61	16	7	6	1
22	0	1	99.00	99	81	14	0	2	2	0
21	0	1	46.00	46	36	7	2	0	1	0
20	0	1	34.00	34	28	4	0	2	0	0
21	0	1	22.00	22	11	7	0	0	4	0
23	1	1	6.00	6	4	1	1	0	0	0
23	0	1	6.00	6	5	1	0	0	0	0
22	1	1	6.00	6	5	1	0	0	0	0
21	0	1	4.00	4	0	4	0	0	0	0
22	1	1	4.00	4	4	0	0	0	0	0
23	1	1	3.00	3	2	1	0	0	0	0
20	0	1	3.00	3	3	0	0	0	0	0
23	0	1	2.00	2	1	1	0	0	0	0
20	2	1	1.00	1	1	0	0	0	0	0
24	1	1	1.00	1	0	1	0	0	0	0
22	1	1	1.00	1	1	0	0	0	0	0
23	1	1	1.00	1	1	0	0	0	0	0
20	0	1	1.00	1	0	1	0	0	0	0
21	1	1	1.00	1	1	0	0	0	0	0
22	1	1	1.00	1	1	0	0	0	0	0
22	1	1	1.00	1	0	0	0	0	1	0
23	1	1	1.00	1	1	0	0	0	0	0
23	1	1	1.00	1	1	0	0	0	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6328:2900813-2900978 +	dmo_159	-TAGTCATAGGACACATGCACAAATTTGAAGTCAGTGCCGCTGTCGCAGTCTCGATAACGTGAA-TATCTCATCGGTTATCGAATGGTC-AGA---C------GAT--GA-GATGTCCGCGCAATCGGAACCGGGCTGGGCCAGAACAACGAACTGGTTCA----TTTC----------GTTT--A---ACTCA----TGTTGT----------
droVir3	scaffold_13042:906555-906728 +		-GC----------ACAATCTTGCAGTGTTGCCGACGTCTCAGTCTCGATAACGTGAA-TATCTCGTGGTTATCGAATGTTT-AGA---C------GAT--GA-GATGTCCGCGCAATCGCAACTGGGCTGGGCCAG---------G-----------GGGA----------A----------CACAATTTCTTTTCCTGTTTCTGTTCCGGTTCCTGTTTCC------GTT--G-CTATT---------CCTGT----------
droGri2	scaffold_15081:2044474-2044610 +		-GT----------GTTACCGTACGCCGCGTCGAGTGTGAA-CGTCTCATTGGTTATCAAATGGTC-AGA---C------AAT--GA-GACTTGGCAAAATCGTAACGGAATGGGCGAACTTCGTTGTACTTGA----------TTTT----------GTT--G----TTTTG----TGTTGT----------
droWil2	scf2_1100000004909:7956889-7957031 -		TCA----------GAACTTCAACAACGTGAA-TATCTCATCTCCTTATCAAATAT--GCTAAAAAAAAACGAT--GC-GATAATTATCTTATTGAATTTGTATA----------TGAA---TTTT----------GTT----------GTT----G-ATCGTCACGGTGCACACACAATACACTGCACGCACAATATA
droAna3	scaffold_13417:2467464-2467562 +		-GA----------GGGTTCGACGCACGTGAA-TATCTCATCATATGGAATGTA-ACTA---A------GAT--GC-GACGTTGCGCTCATCGAGGCCGAACTCCGCGG---------TA--CGCG----TGT--GC----------GTT----G-----CTG----------
droBip1	scf7180000395874:39829-39926 +		-GA----------GGGTTCGACGCACGTGAA-TATCTCATCATATGAAAAGGTA-ACTA---A------GAT--GC-GACGTTGCGCTCATCGAGGCCGAACTCAGCGG---------TA--TGCG----TTTG--G----------GTT----G-----CTG----GT----------
droKik1	scf7180000302517:1183782-1183942 -		-GA----------GGGACTCGACCACGTGAA-TATCTCACCAGATATCAAAGCGGT-CAA---A------GGT--GC-GATATTGCGCTAATCCAGACCCGTGCATGAGG---------TT--TGCA----TCTAGAGC--GT----------CGACTCCCAGAGG----------AGCTGAGTAGATGGGT----------AGCTGT----------TTAGCTGG----G-----G-----TTACTGGATACCGGT----------
droFic1	scf7180000454073:1734013-1734133 -		-GA----------GGGATCCACGCACGTGAA-TATCTCACCGATATCAAATGAGCGGA---A------GGGACT-GATACCCACCTGGTCGAATCGGATGTTGGAT----------TGGA----CTTGCGGGAATTAG------G----------G-----G-----CACTTAGAAAAAAA----------
droEle1	scf7180000490751:1118886-1118989 -		---TCGACGCACGTGAA-TATCTCACCGATTATCGATTGC-A-GGA---A------GGT--GC-GATACTCGCCTCATCGAGTCCATAGCTTGGAG----------GGGA----AAGGATGGA----------T----------CACGAT----------G-----G-----G-----TGTCGG----------
droRho1	scf7180000761121:189953-190093 +		-GA----------GGGCTTCGACGCACGTGAA-TATCTCACCGAATATCGATTGC-A-GGA---A------GGT--GC-GATACTCGCCTCATCGAGGCCAGACTTGGTG----------TGGA----AAGGATGATGCTGGCAA-GTGGATGGGTCGGGA----------T-----CTAAGATT----------T---G-GGGATG----TGCTGG----------
droBia1	scf7180000302069:1150857-1151026 +		-GA----------AATTCGTGCGCAA-------GGTTGGTTTCGAAGACGTGAA-TATCTCATCAGATATCAGTTGC--T----A------GAT--GC-GATACCCGCCTCATCGAGGCCAGGCTTGGTG----------TGAA----TTGGGTAGGTCTGG-------A----------CTAGTACTGGAACATAGGACCCACTGC----------GACGTTGGGGATGCCACCGTAGTGCG----------
droTak1	scf7180000415169:844668-844819 +		-AA----------ATTCGAGCGCAA-------GGATGGTTTCGAAGACGTGAA-TATCTCACCAGATATCAATTGC--T----A------GAT--GC-GATATCCGCCTCATCGAGGCCAGACTTGGGG----------TTAA----CAAGCAAGATTCAATAATTAGACAATACGATACCCATTAG----------G-----G-----ATCTCA----CCTTAT----------
droEug1	scf7180000409230:879540-879663 +		---TCGACTACGTGAA-TATCTCACCAGATATACAAAATGC-----A------AAT--GCAGATACCCGCCTCATCGAGACCAGACTTGGT----------TGGT----GGGCCTGTAGATTTCCACTGGACATGGATA--TGGATT----AT---AA----------G-----G-----G-----AGATAT----------
dm3	chrX:19453028-19453141 -		---TTTAGAGAACGTGAA-TATCTCATCAGATTTCGAACAC--TTGA---A------GAT--GT-GATATTCCATCTTATCTAAACGATACCTTCTTTG----------TGATTCGTTGT----------GTT----------G-----G-GGATTCCCGGCGCGATGT----------
droSim2	x:18342638-18342761 -		-GA----------TGTTTAGAGAACGTGAA-TATCTCATCAGATATCGAACAC--TTGA---A------AAT--GT-GATATTCCATCTTATCTAAACGATACCTTCGGA----------TGCA----TTTTCGGCACTCCGGAGTT----------G-----G-GTATTCCATTGCGCG--AA----------
droSec2	scaffold_8:1735338-1735463 -		-GA----------TGTTTAGAGAACGTGAA-TATCTCACCAGATATCGAACAC--TTGA---A------GAT--GT-GATATTCCATCTTATCTAAACGATACCTTCGGA----------TGAA----TTTTCGGCACTCCGGAGTT----------G-----G-GTATTCCATTGCGCGAAGT----------
droYak3	X:11885655-11885778 +		-GA----------TGTTTAGAGAACGTGAA-TATCTCACCAGATATCGAATGC-A-TAA---A------GAT--GT-GATACCCGTCTTATCTAGGCCATACTTGGG----------TGAA----CTCTGAGCTGTCCGCACTTTGGT----------T-T--G---ATTCGC----AATCGC----------
droEre2	scaffold_4690:9689048-9689162 -		-GA----------TGTTTAGAGAACGTGAATTATCTCACCAGATATCGAATGC-A-TAA---A------GAT--GT-GATACCCGATCTTATCTAGGCCATACTTGGT----------TGAA----TTCTG----------CT----------CGTTTGTTT--G---ACA--------AGAGTT----------

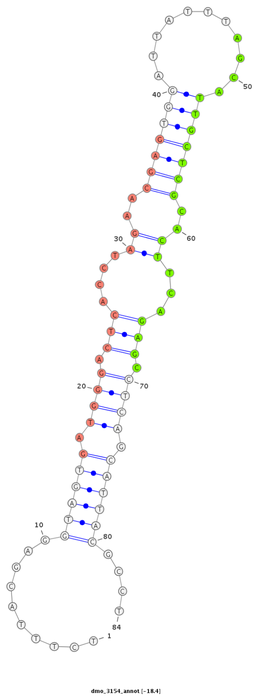
Generated: 09/08/2015 at 08:07 PM

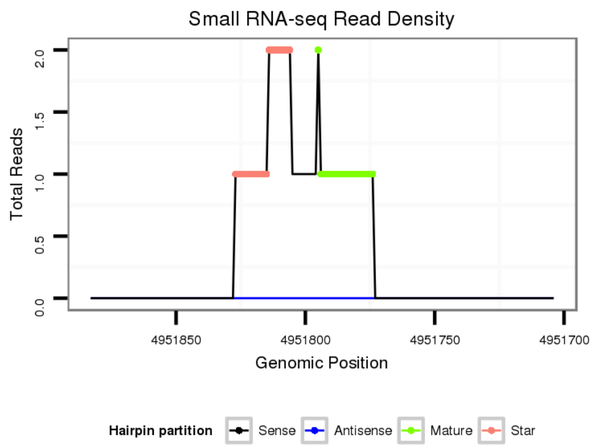
	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	1
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

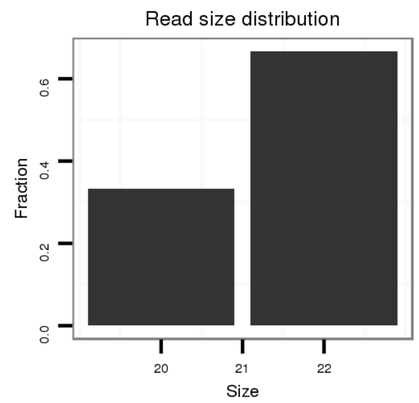
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_3154	**scaffold_6473:4951754-4951833 -**	**candidate**	**Canonical miRNA**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

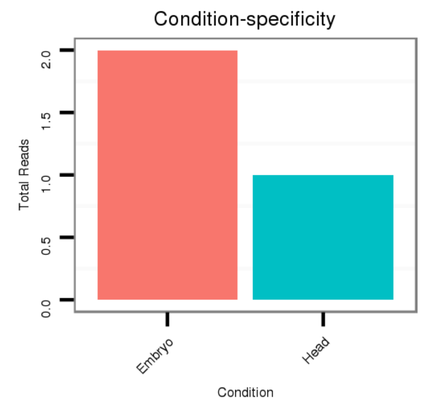
Legend: mature star mismatch in alignment mismatch in read

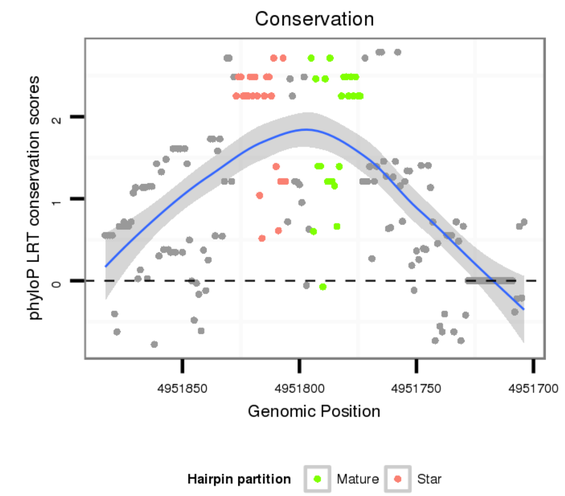
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dmoj\GI15077-in]

No Repeatable elements found

Sense Strand Reads

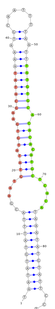
hide 3p reads show mid mismatch reads

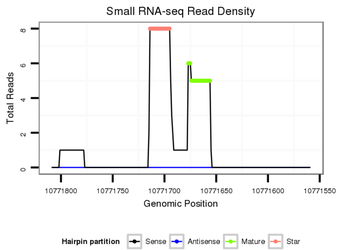
```
                                                
```

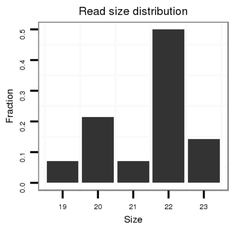
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_1085	**scaffold_6496:10771609-10771759 -**	**confident-exception**	**Canonical miRNA**	**intron**	[View on UCSC Genome Browser [Comell Mirror]]

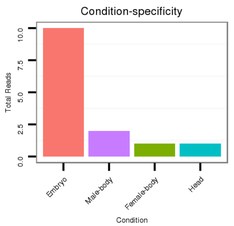
Legend: mature star mismatch in alignment mismatch in read

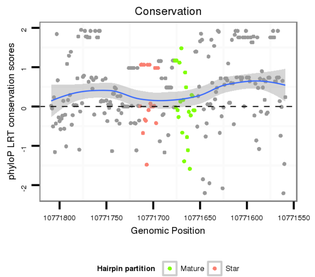
Predicted structure











Show Alternate Folds

Flybase annotation

intron [Dmo]GH19134-in]; utr5 [utr5_minus_4980]; CDS [Dmo]GH19134-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

```
AAGCTTAAGTAAATCGACTGTACTTAAAAGCAATAATGGGCCAAATCAGGGTAAGTACAATTACATAATCGTGCCTTTGTTAATATGTATTTACGAATGTATATGTGAAGCATATAAAATGCAATTTTAATTTATGTGCACACACATGCTCACATAAATATGTATTCCTTTATGTGCCTATATATTAAGCTACCTGTTATCCTTTGACAAGCTGGCAACGCTGATATATATAAAGCGTGGGAATATTTATA
**********.((((((((((.....((((.((((..(((((((((.((.....)).)))))))).)))).)))).....)))))))))))...**********
```

Read size	# Mismatch	Hit Count	Total Norm	Total	M060 embryo	M046 female body	V041 embryo	V110 male body	V049 head body
..... TATGTGCACACATGCTCACA..... 22	0	1	4.00	4	4	0	0	0	0
..... AATGTATATGTGAAGCATAT..... 20	0	1	3.00	3	0	0	0	2	1
..... GAATGTATATGTGAAGCATATA..... 22	0	1	2.00	2	2	0	0	0	0
.....GTAAATCGACTGTACTTAAAAGCA..... 24	0	1	1.00	1	0	1	0	0	0
..... AATGTATATGTGAAGCATATA..... 21	0	1	1.00	1	0	0	1	0	0
.....CAAATCAGGGTAAGTACAATTGTG..... 24	3	1	1.00	1	0	1	0	0	0
..... TATGTGCACACATGCTCACAT..... 23	0	1	1.00	1	1	0	0	0	0
..... AAATGCAATTTTAATTTAT..... 19	0	1	1.00	1	0	1	0	0	0
..... AATGTATATGTGAAGCATATAA..... 22	0	1	1.00	1	0	0	1	0	0
..... AATGTATATGTGAAGCATATAAA..... 23	0	1	1.00	1	0	0	1	0	0

Anti-sense strand reads

```
TTCGAATTCATTTAGCTGACATGAATTTTCGTTATTACCCGGTTTAGTCCCATTCATGTTAATGTATTAGCACGGAAACAATTATACATAAATGCTTACATATACACTTCGTATATTTACGTTAAAATTAATACACGTGTGTGTACGAGTGTATTTATACATAAGGAAATACACGGATATATAATTCGATGGACAATAGGAAACTGTTCGACCGTTGCGACTATATATATTTCGCACCCTTATAAATAT
**********..((((((((((.....((((.((((..(((((((((.((.....)).)))))))).)))).)))).....)))))))))))...**********
```

Read size	# Mismatch	Hit Count	Total Norm	Total	M046 female body	V110 male body

Show Alignment With Reads

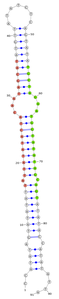
Re-alignment of all predicted orthologs

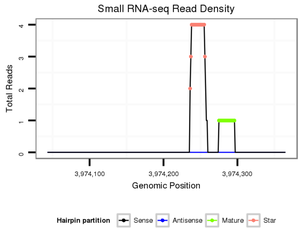
Species	Coordinate	ID	Alignment
droMoj3	scaffold_6496:10771559-10771809_-	dmo_1085	AAGCTTAAG-TAAATCGACT-GTA----------C----------TTAAA-AG----C-AATAATGGGCCAAATCAGGGTAAGTACAATTACATA---ATCGTGCCTTTGTTAATATGTATTTACGA----------ATGTATATGTGAAGCATATAAAATGCA--------ATTTTAATTTAT--------GTGCACACA--CATGC--------TCACATAAATATGT-ATTCCTTT----ATGTGCCT----ATAT--A-------T----------TAAGCTACCTGTTATCCTT-----TGACAAGCTGGCAACGCTGATA----TATAT---AAAGCGTGGGAATATTTA
droVir3	scaffold_12875:17234174-17234444_+	dvi_7433	AAGCTTAAG-TAAATCATA-- ---------GTGCA----------TTG-TAAG-----S-AATAATGGG-AAATCAGGTAAGTACA-AATACATA--AATC----------TAGTACATACA----------ATGTACGCAAG---CACAG-AATGG-ACATTTTTAATTTATAAGAAACAGCATACTCATAACATATTACCATGTGAGTGTG------TA-TCTGG----------GTGTATATATG-AATATT---ATGTATT---CT-----ATAT--T-------T----------AAGCTACCTGTTATCCTT-----TGACAAGCTGGCAACGCTGGTA---TAATT---AAGCGTGGGAATATTTA
droGri2	scaffold_15245:16754059-16754264_+		A CA-C--- ---------- ---------- -----------AA-A-AG-----S-AATATGGGCCAATCTG-AGGTAATACAATTACAA---------- ---------- ----------

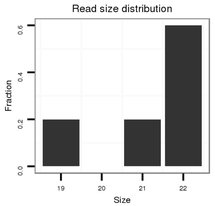
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_3122	**scaffold_6359:3974093-3974315 +**	**candidate**	**Canonical miRNA**	**intron**	[View on UCSC Genome Browser (Cornell Mirror)]

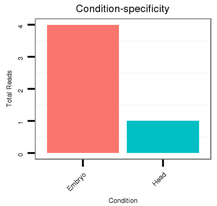
Legend: nature size mismatch in alignment mismatch in read

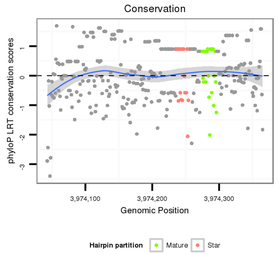
Predicted structure











Show Alternate Folds

Flybase annotation

intron [Dmel|GH21789-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

```
AGGGCCATTAGCATATATCCTATGGTATACATCAGTATATACTATAATAGCATGTATATATACTGAAATACTGCTATATATACTGATAACATATGGTATATATCAGTATATACTATGGATATATCAGTATATACTAGAATAGTATCTGCCAGTATTTACCATAAAGCATATATCATTATATATAATATTTTCCAGTATATACCATATAGTATATATTATTATAGTATTTTCCAGTATATGCTAGAATGGTATATAGCAGTATATACCATATATTAATGCACTGTGTACTATTTATGTCTATTCCATAAAGTATACCATACACAAATATAC
**********************************************************************************************************************************************************..((((.(((((((((.((((((((((.....))))))))))).))))))))).))))....**********************************************************************************
```

	Read size	# Mismatch	Hit Count	Total Norm	Total	M060 embryo	V041 embryo	V056 head	M046 female body
....TGCTAGAATGGTATATAGCAGT....	22	0	1	1.00	1	0	1	0	0
....TATTATATACTACAATAGCAT....	21	0	1	1.00	1	0	0	1	0
....TATTATATACTACAATAGCATA....	22	0	1	1.00	1	1	0	0	0
....ATTATATACTACAATAGCA....	19	0	1	1.00	1	1	0	0	0
....TTATATACTACAATAGCATATG....	22	0	1	1.00	1	1	0	0	0

Anti-sense strand reads

```
TCCCGGTAATCGTATATAGGATACCATATGTAGTCATATATGATATTATCGTACATATATATGACTTTATGACGATATATATGACTATTGTATACCATATATAGTCATATATGATCTTATCATAGAGCGGTCATAAATGGTATTTCGTATATAGTAATATATTATAAAAGGTCATATATGGTATATCATATATATATAATATATGAGTCATATACGATCTTACCATATATCGTCATATGGTATATAATTACGTGACACATGATAAATACAGATAAGTATTTCATATGGTATGTGTTTATATG
**********************************************************************************************************************************************************..((((.(((((((((.((((((((((.....))))))))))...))))))))))).))))....**********************************************************************************
```

	Read size	# Mismatch	Hit Count	Total Norm	Total	M046 female body	V056 head	V110 male body

Show Alignment With Reads

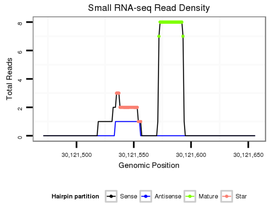
Re-alignment of all predicted orthologs

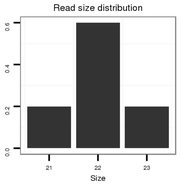
Species	Coordinate	ID	Alignment
droMoj3	scaffold_6359:3974043-3974365 +	dmo_3122	AGGGCCATTA-GCATATATCCTATGGTATACATCAGTATATACTATAAT----AGCATGTATATATACTGAAATACTGCTATATATACTGATAACATATGGTATATATCAG----------TATATACTA----------GAATAG----TATCTGCCAGT----------ATTTACCATAA-AGCATATATCATTATATAATATTTTCCAGTATA-TACCATATAGTATATATG----------ATTATATACTACAATAGCATATGTATA--------TCTCAGTATAGCTAGAATG------TATATAGCAGTATATACCATATATT--AATGCACTGTGTACTATTTATGTCTATTC-----AT------AAA----------GTATACCAT-----ACACAAATAT----------AC
droVir3	scaffold_12970:9687888-9688178 -		TAAAGTATA-A----------A-T-A-TATAG-TA-A----AATATATATATAT-A-T--ATGTATATAT----------TATATATATATATATATATA-TA-TATGTATATTTCATATATATATATATATATATATATATATATATATATAAATATATAAAGTATTT----GTCTATTTAAGCAAGCTGAAGAAGAGAAAAGAGACCCCCA-TCTG-TA----------**********----------**********----------**********----------CG-TATATT--A-TATG-T-A-TG-AGT-TT-TATATA-T-T----T-CTAAACGTAAAGTGGA----------**********----AT-----**********-------ACGAAAAACAAAAAA-T-T
droGri2	scaffold_15203:1569710-1583947 -		GTATACATA-A-TATATAAAATAT----------GTAT-----------A-T-CTATA-TATA-TA-TATATATA-TATATATATATATATATATATATATATATATATACTCTATATA-TCCC-----G-GATTTTACGAAGCGATATAGCATATATTATTT-T-TA-CATA-TA----------**********----------**********----------**********

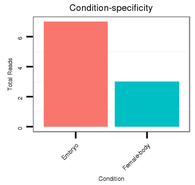
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_2862	**scaffold_6500:30121521-30121606 +**	**candidate**	**Canonical miRNA**	**intron**	[View on UCSC Genome Browser (Conell Mirror)]

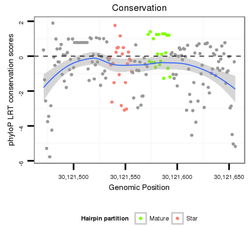
Legend: master star mismatch in alignment mismatch in read

Predicted structure









Show Alternate Folds

Flybase annotation

intron [Dmo]GE18267-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

```
AATGACAGAATTAGTAACAGACTTGCGTGTAGTATTTTGTGTGCAGTATTTTAATCATTACTCGGAAGTATTTTTAAGTATTAGCAGTATAATACTCTGGAAATATTTAAAAATACTTCCGAATAATGATAAAAAGTTTAGGTACACAACGATTTTCAACTTAACTGTATTAAAAAGTGGTT
****************************************((((((.(((((((((((((((((((((((.(((.........)))..)))))))))))))))))))).)))))).))))).. ****************************************
```

	Read size	# Mismatch	Hit Count	Total Norm	Total	M060 embryo	M046 female body	V110 male body
AAATATTTAAAAATACTTCCGA	22	0	1	4.00	4	4	0	0
ATTTTAATCATTACTCGGA	19	0	1	1.00	1	0	1	0
GAAATATTTAAAAATACTTCCGA	23	0	1	1.00	1	1	0	0
GGAAGTATTTTTAAGTATTAGC	22	0	1	1.00	1	1	0	0
AAATATTTAAAAATACTTCCGA	21	0	1	1.00	1	1	0	0
AATATTTAAAAATACTTCCGA	21	0	1	1.00	1	0	1	0
CTCGGAAGTATTTTTAAGTATT	22	0	1	1.00	1	0	1	0
AAATATTTAAAAATACTTCCGAA	23	0	1	1.00	1	0	1	0

Anti-sense strand reads

```
TTACTGTCTTAAATCATTGTCTGAACGCACATCATAAAACACACGTCATAAAATTAGTAATGAGCCTTGATAAAAATTCATAATCGTCATATTATGAGACCTTTATAAATTTTTATGAAGCTTATTACTTATTTTTTCAAATCCATGTGTTGCTAAAAAGTTGAATTGACATAATTTTTCACCAA
****************************************((((((.(((((((((((((((((((((((.(((.........)))..)))))))))))))))))))).)))))).))))).. ****************************************
```

	Read size	# Mismatch	Hit Count	Total Norm	Total	M046 female body	V110 male body	M060 embryo body
GCCTTGATAAAATTCATAATC	22	0	1	1.00	1	1	0	0
TTGCTAAAAAGTTGAATTGACAT	23	0	3	0.33	1	1	0	0
CCATGTGTTGCTAAAAAGTTGAA	23	0	3	0.33	1	0	0	1

Show Alignment With Reads

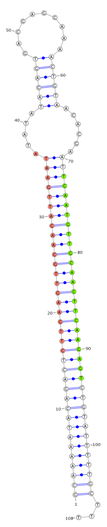
Re-alignment of all predicted orthologs

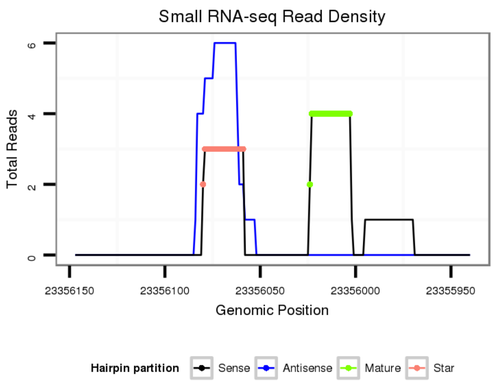
Species	Coordinate	ID	Alignment
droMel	scaffold_6500:30121514:30121611:-	dmo_2862	AATGACA-GAA-----TT--------TAGTAACAGACTTGCGTGTAGTATTTTGTGTGCAGTATTTTAATCATTACTCGGAAGTATTTTTAAGTATTAGCAGTATAATACTCTGGAAATATTTAAAAATACTTCCGAATAATG--A--AT--A--AA----A----AAGTTTAGGTACACAACGA--TTTT--C--AACCT--TAACTGTATTAAAA----AGTGTT
droVir	scaffold_12370:8036912:8037168:+		-G-TAG-GAA-----TT--G-G-G-

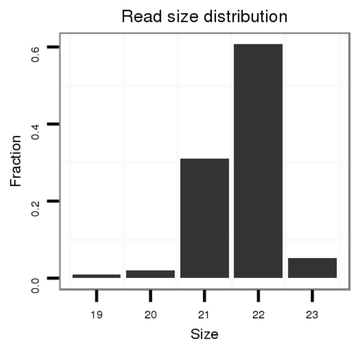
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_2899	**scaffold_6680:23355990-23356097 -**	**candidate**	**Canonical miRNA**	**antisense_to_intron**	[View on UCSC Genome Browser [Cornell Mirror]]

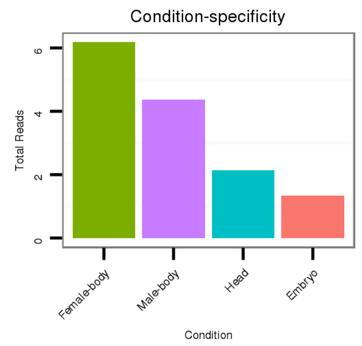
Legend: mature star mismatch in alignment mismatch in read

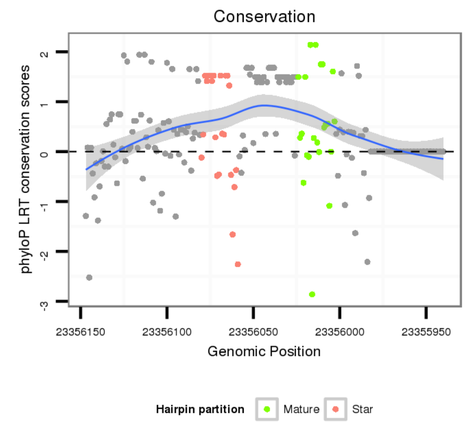
Predicted structure











Show Alternate Folds

Flybase annnotation

Antisense to intron [Dmoj\GI13950-in]

No Repeatable elements found

mature	star
1. scaffold_4010:2006-2027 - 2. scaffold_6262:35377-35398 + 3. scaffold_6262:36191-36212 - 4. scaffold_6473:12234990-12235011 + 5. scaffold_6482:2373591-2373612 - 6. scaffold_6500:31709686-31709707 + 7. scaffold_6500:31710535-31710556 - 8. scaffold_6540:6287635-6287656 - 9. scaffold_6541:653576-653597 - 10. scaffold_6541:1563824-1563845 + 11. dmo_2899 scaffold_6680:23356003-23356024 - 12. dmo_2878 scaffold_6680:23356062-23356083 + 13. scaffold_6680:23464350-23464371 -	

Sense Strand Reads

hide 3p reads show mid mismatch reads

```
AATATCATACTAACAAAATAAAATTAAGATCTTAAACATCCATAGAGTAGAAGCAAAAATACAGACTCTTGAAGTTGCAACATTGAATATATATACAGTGACGAGCAAAACTGTAACACGAATTCAATGTTGCAACTTCAAGAGTCTGTATTTTTGCTTTGGATGTCGCTACGCTGGGTCGATGATTCTGGGTTGCCTATAAGCCCAC
**************************************************((((((((((((((((((((((((((((((((((.....((((((..........))))))......)))))))))))))))))))))))))))))))))))...**************************************************
```

Read size	# Mismatch	Hit Count	Total Norm	Total	M046 female body	V110 male body	M060 embryo	V056 head	V049 head	V041 embryo
22	0	13	2.46	32	13	8	9	1	0	1
22	0	1	2.00	2	1	1	0	0	0	0
22	0	12	1.33	16	5	4	4	2	1	0
21	0	13	1.31	17	5	5	0	4	3	0
26	0	1	1.00	1	0	1	0	0	0	0
21	0	1	1.00	1	1	0	0	0	0	0
22	0	13	0.62	8	7	0	1	0	0	0
22	0	13	0.54	7	2	1	1	2	0	1
22	0	2	0.50	1	0	1	0	0	0	0
23	0	2	0.50	1	0	1	0	0	0	0
22	0	2	0.50	1	1	0	0	0	0	0
20	1	2	0.50	1	1	0	0	0	0	0
21	0	2	0.50	1	0	0	0	1	0	0
21	0	13	0.46	6	2	4	0	0	0	0
22	0	12	0.42	5	3	2	0	0	0	0
21	0	13	0.31	4	2	1	0	1	0	0
21	0	13	0.23	3	2	1	0	0	0	0
22	1	13	0.23	3	0	0	3	0	0	0
21	0	12	0.17	2	0	1	0	0	1	0
21	0	12	0.17	2	0	2	0	0	0	0
20	0	13	0.15	2	0	0	0	2	0	0
23	0	13	0.15	2	0	0	0	2	0	0
22	1	12	0.08	1	0	0	1	0	0	0
23	1	12	0.08	1	0	0	1	0	0	0
22	0	13	0.08	1	1	0	0	0	0	0
23	0	13	0.08	1	0	1	0	0	0	0
19	0	13	0.08	1	1	0	0	0	0	0
24	2	13	0.08	1	1	0	0	0	0	0
22	0	13	0.08	1	1	0	0	0	0	0
22	1	13	0.08	1	1	0	0	0	0	0
21	0	13	0.08	1	0	0	0	0	1	0
23	1	13	0.08	1	0	0	0	0	0	0
21	0	13	0.08	1	0	0	0	0	0	0
20	0	14	0.07	1	1	0	0	0	0	0
19	0	16	0.06	1	1	0	0	0	0	0
20	0	16	0.06	1	1	0	0	0	0	0
21	0	20	0.05	1	1	0	0	0	0	0

Anti-sense strand reads

```
TTATAGTATGATTGTTTTATTTTAATTCTAGAATTTGTAGGTATCTCATCTTCGTTTTTATGTCTGAGAACTTCAACGTTGTAACTTATATATATGTCACTGCTCGTTTTGACATTGTGCTTAAGTTACAACGTTGAAGTTCTCAGACATAAAAACGAAACCTACAGCGATGCGACCCAGCTACTAAGACCCAACGGATATTCGGGTG
**************************************************((((((((((((((((((((((((((((((((((.....((((((..........))))))......)))))))))))))))))))))))))))))))))))...**************************************************
```

Read size	# Mismatch	Hit Count	Total Norm	Total	M046 female body	M060 embryo	V110 male body	V056 head	V049 head	V041 embryo
22	0	13	2.46	32	13	9	8	1	0	1
22	0	12	1.33	16	5	4	4	2	1	0
21	0	13	1.31	17	5	0	5	4	3	0
21	0	1	1.00	1	0	1	0	0	0	0
22	0	1	1.00	1	0	1	0	0	0	0
22	0	13	0.62	8	7	1	0	0	0	0
22	0	13	0.54	7	2	1	1	2	0	1
22	0	13	0.54	7	5	0	1	0	1	0
22	0	2	0.50	1	1	0	0	0	0	0
21	0	2	0.50	1	0	0	0	1	0	0
23	0	2	0.50	1	0	0	1	0	0	0
20	1	2	0.50	1	1	0	0	0	0	0
22	0	2	0.50	1	0	0	1	0	0	0
21	0	13	0.46	6	2	0	4	0	0	0
22	0	12	0.42	5	3	0	2	0	0	0
21	0	13	0.31	4	2	0	1	1	0	0
22	1	13	0.23	3	0	3	0	0	0	0
21	0	13	0.23	3	2	0	1	0	0	0
21	0	12	0.17	2	0	0	1	0	1	0
21	0	12	0.17	2	0	0	2	0	0	0
20	0	13	0.15	2	0	0	0	2	0	0
23	0	13	0.15	2	0	0	0	2	0	0
21	0	20	0.10	2	0	0	2	0	0	0
23	1	12	0.08	1	0	1	0	0	0	0
22	1	12	0.08	1	0	1	0	0	0	0
24	2	13	0.08	1	1	0	0	0	0	0
19	0	13	0.08	1	1	0	0	0	0	0
22	0	13	0.08	1	1	0	0	0	0	0
23	0	13	0.08	1	0	0	1	0	0	0
21	0	13	0.08	1	0	0	0	1	0	0
23	1	13	0.08	1	1	0	0	0	0	0
22	0	13	0.08	1	1	0	0	0	0	0
21	0	13	0.08	1	0	0	0	0	1	0
22	1	13	0.08	1	1	0	0	0	0	0
20	0	14	0.07	1	1	0	0	0	0	0
19	0	16	0.06	1	1	0	0	0	0	0
20	0	16	0.06	1	1	0	0	0	0	0
21	0	17	0.06	1	1	0	0	0	0	0
22	0	17	0.06	1	1	0	0	0	0	0
21	0	20	0.05	1	1	0	0	0	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6680:23355940-23356147 -	dmo_2899	AATATCAT----------ACT-AACAAAATAAAATTAAGATCTTAAA----------CATCCATAGAGTAGAAGCAAAAATACAGACTCTTGAAGTTGCAACATTGAATATAT----------ATACAGTGACGAGCAAAACTGTAACACGAATTCAATGTTGCAACTTCAAGAGTCTGTATTTTTGCTTTGGA----------TGTCGCTACGCTGGGTCGATGATTCTGGGTTGCCTATAAGCCCAC
droVir3	scaffold_13246:1290058-1290131 +		TTTAAG-G----------TCGAATTCATGTAAAAATGTAGCCTTAAA----------CATCCACCTAGTATATACATACATATATA----------TTCTTA----------AA----------
droGri2	scaffold_15112:4085932-4086005 +		AAAATA-T----------AG-----------ATTTCTAAAATT------GATATATAAATAT----------ATACA--------AAAAA----------TGCCAAATTCAATGTGTGAA----------TTTTTGA----------
droWil2	scf2_1100000004762:6364929-6365026 +		AACATT-T----------GCG-TAAAAAACAAGACTATGATCTTCAA----------CATGCATTAAGTATAACAGACAATAT-GAGCGATGAAGTGAAAACATTGAGTCTGT----------GTTACAG----------T----------
droAna3	scaffold_13248:4556009-4556096 -		CAACTT-C----------AGGTGAAT----------ATACACTGACGAGCAAAACTGTAACACGAGTCATATGCTGCAACTTCAAAGGTCTGTAACTTTTTTTCTAA----------TG----------
droBip1	scf7180000393228:8493-8647 -		ATTATATA----------ACG-TACAAAAAAGACTAAGATCTTTAA----------AATGCGTGCCTTAGAAAAAAGTACAGAGCTTTGAAGTTGTAACATTGAATCTCGT----------GTTACGTGTTTGCTCGTCAGTGTAAATTCT---TTACCTTTTCAAGAATCAGTGATGCCAATTTGG----------
droKik1	scf7180000302707:514292-514390 +		TACACA-T----------ACG-AACAAAACAAGATTAAGATTTTAG----------AATCTATAGATTAGAACAGAAGTTATGGAGCTTTGAAGTTCGTGTATTGAATCTTGT----------GTTACA----------GT----------
droFic1	scf7180000453906:3375-3534 +		AATTCA-AGAAAAATAAAATCAATTGAAATTGTAATTT-----------------------TAATT---C----------AGGCAAATAATGCGAAATAGTGAAAATAAGACTTTGTAATATACTTACACTGACGAGCAAAACTGTAACACGATTCATTGTTTCAACTTCAAAGGTCTGTAACTTTTTTTCTAA----------TG----------
droRho1	scf7180000777770:3995-4093 +		TTGAA---------------------AATAGCTAAT---ATG----------ACACTTTC----------CTACACTGACGAACAAAACTGTAACACGATTCAATACTCTAACTTCAAAGGTCTGTATCTTCTGTTCTAA----------AT----------
droBia1	scf7180000302140:96632-96712 +		AATATA-A----------G-C-TACAAAACAAGACTAAGATCTTCAA----------AGTGCGTGCATTAGAAAAAAGTTACAGAGCTTTGAAGTTGAACAT--------**********----------
droEug1	scf7180000409464:1430694-1430806 -		AAACGA-A----------GGCAGTCTTA----------GTAT----------ATACACTGACGAGCAAAACTGTAACACGATTCATTGTTGCAACTTCAAAGGTCTGTAACTTTTTTTCTAA----------TG----------
droYak3	w2_chrUn_4652:4059-4173 -		TACAGT-G----------GA-AACAATGAAGCAC------TTTAAAACTGCCTACA---AAT----------CTGTATAG----------ATACACTGACGAGCAAAACTGTAACACGATGCATATTCTAACTTCAAGCGCGAGTATGTTCTCT-----**********----------

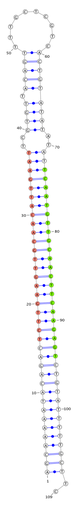
Generated: 09/08/2015 at 07:58 PM

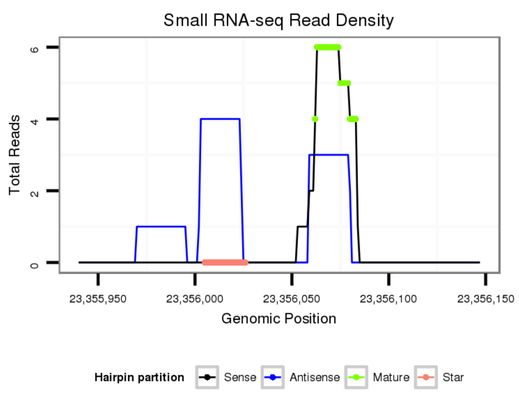
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	0
crit.tptop3	0
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

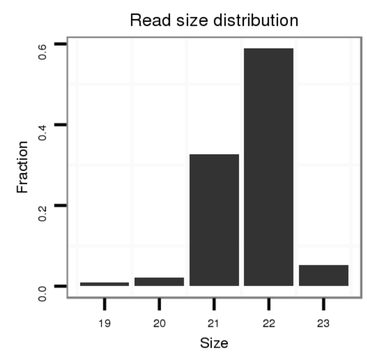
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_2878	**scaffold_6680:23355990-23356097 +**	**confident-exception**	**Canonical miRNA**	**intron**	[View on UCSC Genome Browser [Cornell Mirror]]

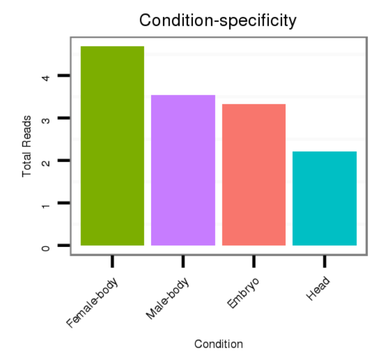
Legend: mature star mismatch in alignment mismatch in read

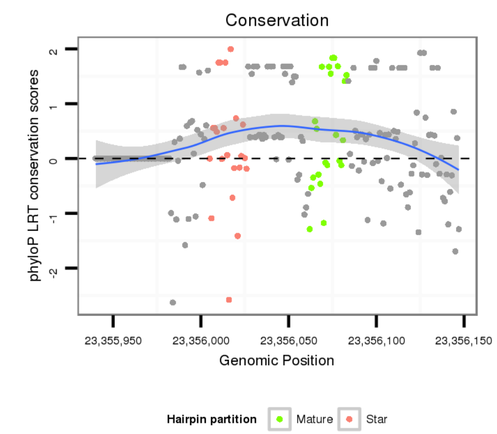
Predicted structure











Show Alternate Folds

Flybase annotation

intron [Dmoj:GI13950-in]

No Repeatable elements found

mature	star
1. scaffold_4010:2006-2027 -	1. scaffold_4010:2008-2029 +
2. scaffold_6262:35377-35398 +	2. scaffold_6262:35375-35396 -
3. scaffold_6262:36191-36212 -	3. scaffold_6262:36193-36214 +
4. scaffold_6473:12234990-12235011 +	4. scaffold_6473:12234988-12235009 -
5. scaffold_6482:2373591-2373612 -	5. scaffold_6482:2373593-2373614 +
6. scaffold_6500:31709686-31709707 +	6. scaffold_6500:31709684-31709705 -
7. scaffold_6500:31710535-31710556 -	7. scaffold_6500:31710537-31710558 +
8. scaffold_6540:6287635-6287656 -	8. scaffold_6540:6287637-6287658 +
9. scaffold_6541:653576-653597 -	9. scaffold_6541:653578-653599 +
10. scaffold_6541:1563824-1563845 +	10. scaffold_6541:1563822-1563843 -
11. dmo_2899 scaffold_6680:23356003-23356024 -	11. dmo_2878 scaffold_6680:23356005-23356026 +
12. dmo_2878 scaffold_6680:23356062-23356083 +	12. dmo_2899 scaffold_6680:23356060-23356081 -
13. scaffold_6680:23464350-23464371 -	13. scaffold_6680:23464352-23464373 +

Sense Strand Reads

hide 3p reads show mid mismatch reads

GTGGGCTTATAGGCAACCCAGAATCATCGACCCAGCGTAGCGACATCCAAAGCAAAAATACAGACTCTTGAAGTTGCAACATTGAATTCGTGTTACAGTTTTGCTCGTCACTGTATATATATTCAATGTTGCAACTTCAAGAGTCTGTATTTTTGCTTCTACTCTATGGATGTTTAAGATCTTAATTTTATTTTGTTAGTATGATATT **********(((((((((((((((((((((((((((((((((((..((((.((((.....)))))))))..))))))))))))))))))))))))))))))))))))))..**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M046 female body	M060 embryo	V110 male body	V056 head	V049 head	V041 embryo
.....TCAATGTTGCAACTTCAAGAGT.....	22	0	13	2.46	32	13	9	8	1	0	1
.....CAATGTTGCAACTTCAAGAGTC.....	22	0	12	1.33	16	5	4	4	2	1	0
.....CAATGTTGCAACTTCAAGAGT.....	21	0	13	1.31	17	5	0	5	4	3	0
.....TATTCAATGTTGCAACTTCAA.....	21	0	1	1.00	1	0	1	0	0	0	0
.....TATATATATTCAATGTTGCAAC.....	22	0	1	1.00	1	0	1	0	0	0	0
.....ATTCAATGTTGCAACTTCAAGA.....	22	0	13	0.62	8	7	1	0	0	0	0
.....TCTTGAAGTTGCAACATTGAAT.....	22	0	13	0.54	7	2	1	1	2	0	1
.....TTGAAGTTGCAACATTGAATTC.....	22	0	13	0.54	7	5	0	1	0	1	0
.....ATGTTGCAACTTCAAGAGTCTG.....	22	0	2	0.50	1	1	0	0	0	0	0
.....TGTTGCAACTTCAAGAGTCTG.....	21	0	2	0.50	1	0	0	0	1	0	0
.....AATGTTGCAACTTCAAGAGTCTG.....	23	0	2	0.50	1	0	0	1	0	0	0
.....TGCAACTTCAAGAGTCTGTC.....	20	1	2	0.50	1	1	0	0	0	0	0
.....GTTGCAACTTCAAGAGTCTGTA.....	22	0	2	0.50	1	0	0	1	0	0	0
.....CTCTTGAAGTTGCAACATTGA.....	21	0	13	0.46	6	2	0	4	0	0	0
.....AATGTTGCAACTTCAAGAGTCT.....	22	0	12	0.42	5	3	0	2	0	0	0
.....TCAATGTTGCAACTTCAAGAG.....	21	0	13	0.31	4	2	0	1	1	0	0
.....TCAATGTTGCAACTTCAAGAGC.....	22	1	13	0.23	3	0	3	0	0	0	0
.....TTCAATGTTGCAACTTCAAGA.....	21	0	13	0.23	3	2	0	1	0	0	0
.....AATGTTGCAACTTCAAGAGTC.....	21	0	12	0.17	2	0	0	1	0	1	0
.....ATGTTGCAACTTCAAGAGTCT.....	21	0	12	0.17	2	0	0	2	0	0	0
.....CAATGTTGCAACTTCAAGAG.....	20	0	13	0.15	2	0	0	0	2	0	0
.....CTCTTGAAGTTGCAACATTGAAT.....	23	0	13	0.15	2	0	0	0	2	0	0
.....TTCGTGTTACAGTTTTGCTCG.....	21	0	20	0.10	2	0	0	2	0	0	0
.....CAATGTTGCAACTTCAAGAGTCC.....	23	1	12	0.08	1	0	1	0	0	0	0
.....AATGTTGCAACTTCAAGAGTCC.....	22	1	12	0.08	1	0	1	0	0	0	0
.....ATTCAATGTTGCAACTTCAAGAAA.....	24	2	13	0.08	1	1	0	0	0	0	0
.....ACTCTTGAAGTTGCAACAT.....	19	0	13	0.08	1	1	0	0	0	0	0
.....ACTCTTGAAGTTGCAACATTGA.....	22	0	13	0.08	1	1	0	0	0	0	0
.....ATTCAATGTTGCAACTTCAAGAG.....	23	0	13	0.08	1	0	0	1	0	0	0
.....TCTTGAAGTTGCAACATTGAA.....	21	0	13	0.08	1	0	0	0	1	0	0
.....ATTCAATGTTGCAACTTCAAGAA.....	23	1	13	0.08	1	1	0	0	0	0	0
.....CTCTTGAAGTTGCAACATTGAA.....	22	0	13	0.08	1	1	0	0	0	0	0
.....ACTCTTGAAGTTGCAACATTG.....	21	0	13	0.08	1	0	0	0	0	1	0
.....TCAATGTTGCAACTTCAAGAGA.....	22	1	13	0.08	1	1	0	0	0	0	0
.....GAAGTTGCAACATTGAATTC.....	20	0	14	0.07	1	1	0	0	0	0	0
.....ATTCAATGTTGCAACTTCA.....	19	0	16	0.06	1	1	0	0	0	0	0
.....TTGAAGTTGCAACATTGAAT.....	20	0	16	0.06	1	1	0	0	0	0	0
.....TTGCAACATTGAATTCGTGTT.....	21	0	17	0.06	1	1	0	0	0	0	0
.....TTGCAACATTGAATTCGTGTTA.....	22	0	17	0.06	1	1	0	0	0	0	0
.....GTTACAGTTTTGCTCGTCACT.....	21	0	20	0.05	1	1	0	0	0	0	0

Anti-sense strand reads

CACCCGAATATCCGTTGGGTCTTAGTAGCTGGGTCGCATCGCTGTAGGTTTCGTTTTTATGTCTGAGAACTTCAACGTTGTAACTTAAGCACAATGTCAAAACGAGCAGTGACATATATATAAGTTACAACGTTGAAGTTCTCAGACATAAAAACGAAGATGAGATACCTACAAATTCTAGAATTAAAATAAAACAATCATACTATAA **********(((((((((((((((((((((((((((((((((((..((((.((((.....)))))))))..))))))))))))))))))))))))))))))))))))))..**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M046 female body	V110 male body	M060 embryo	V056 head	V049 head	V041 embryo
.....TGAGAACTTCAACGTTGTAACT.....	22	0	13	2.46	32	13	8	9	1	0	1
.....ATAAGTTACAACGTTGAAGTTC.....	22	0	1	2.00	2	1	1	0	0	0	0
.....CTGAGAACTTCAACGTTGTAAC.....	22	0	12	1.33	16	5	4	4	2	1	0
.....TGAGAACTTCAACGTTGTAAC.....	21	0	13	1.31	17	5	5	0	4	3	0
.....GGGTCGCATCGCTGTAGGTTTCGTTT.....	26	0	1	1.00	1	0	1	0	0	0	0
.....ATAAGTTACAACGTTGAAGTT.....	21	0	1	1.00	1	1	0	0	0	0	0
.....AGAACTTCAACGTTGTAACTTA.....	22	0	13	0.62	8	7	0	1	0	0	0
.....TAAGTTACAACGTTGAAGTTCT.....	22	0	13	0.54	7	2	1	1	2	0	1
.....ATGTCTGAGAACTTCAACGTTG.....	22	0	2	0.50	1	0	1	0	0	0	0
.....GTCTGAGAACTTCAACGTTGTAA.....	23	0	2	0.50	1	0	1	0	0	0	0
.....GTCTGAGAACTTCAACGTTGTA.....	22	0	2	0.50	1	1	0	0	0	0	0
.....CTGTCTGAGAACTTCAACGT.....	20	1	2	0.50	1	1	0	0	0	0	0
.....GTCTGAGAACTTCAACGTTGT.....	21	0	2	0.50	1	0	0	0	1	0	0
.....AGTTACAACGTTGAAGTTCTC.....	21	0	13	0.46	6	2	4	0	0	0	0
.....TCTGAGAACTTCAACGTTGTAA.....	22	0	12	0.42	5	3	2	0	0	0	0
.....GAGAACTTCAACGTTGTAACT.....	21	0	13	0.31	4	2	1	0	1	0	0
.....AGAACTTCAACGTTGTAACTT.....	21	0	13	0.23	3	2	1	0	0	0	0
.....CGAGAACTTCAACGTTGTAACT.....	22	1	13	0.23	3	0	0	3	0	0	0
.....CTGAGAACTTCAACGTTGTAA.....	21	0	12	0.17	2	0	1	0	0	1	0
.....TCTGAGAACTTCAACGTTGTA.....	21	0	12	0.17	2	0	2	0	0	0	0
.....GAGAACTTCAACGTTGTAAC.....	20	0	13	0.15	2	0	0	0	2	0	0
.....TAAGTTACAACGTTGAAGTTCTC.....	23	0	13	0.15	2	0	0	0	2	0	0
.....CCTGAGAACTTCAACGTTGTAA.....	22	1	12	0.08	1	0	0	1	0	0	0
.....CCTGAGAACTTCAACGTTGTAAC.....	23	1	12	0.08	1	0	0	1	0	0	0
.....AAGTTACAACGTTGAAGTTCTC.....	22	0	13	0.08	1	1	0	0	0	0	0
.....GAGAACTTCAACGTTGTAACTTA.....	23	0	13	0.08	1	0	1	0	0	0	0
.....TACAACGTTGAAGTTCTCA.....	19	0	13	0.08	1	1	0	0	0	0	0
.....AAAGAACTTCAACGTTGTAACTTA.....	24	2	13	0.08	1	1	0	0	0	0	0
.....AGTTACAACGTTGAAGTTCTCA.....	22	0	13	0.08	1	1	0	0	0	0	0
.....AGAGAACTTCAACGTTGTAACT.....	22	1	13	0.08	1	1	0	0	0	0	0
.....GTTACAACGTTGAAGTTCTCA.....	21	0	13	0.08	1	0	0	0	0	1	0
.....AGAACTTCAACGTTGTAACTTA.....	23	1	13	0.08	1	1	0	0	0	0	0
.....AAGTTACAACGTTGAAGTTCT.....	21	0	13	0.08	1	0	0	1	0	0	0
.....CTTCAACGTTGTAACTTAAG.....	20	0	14	0.07	1	1	0	0	0	0	0
.....ACTTCAACGTTGTAACTTA.....	19	0	16	0.06	1	1	0	0	0	0	0
.....TAAGTTACAACGTTGAAGTT.....	20	0	16	0.06	1	1	0	0	0	0	0
.....CACAATGTCAAAACGAGCAGT.....	21	0	20	0.05	1	1	0	0	0	0	0

Show Alignment With Reads

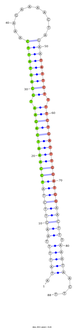
Re-alignment of all predicted orthologs

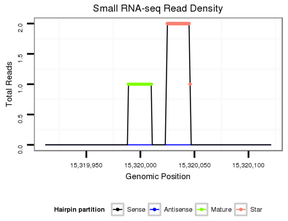
Species	Coordinate	ID	Alignment
droMoj3	scaffold_6680:23355940-23356147 +	dmo_2878	GTGGGCTTATAGGCAACCCAGAATCATCGACCCAGCGTAGCGACATCC----------AAAGCAAAAATACAGACTCTTGAAGTTGCAACATTGAATTCGTGTTACAGTTTTGCTCGTCACTGTATATAT----------ATTCAATGTTGCAACTTCAAGAGTCTGTATTTTTGCTTCTACTCTATGGATGTTTAA----------GATCTTAATTTTATTTT-GTTAGT----------ATGATATT
droVir3	scaffold_13246:1290058-1290131 -		----------TTAAA----------GAATATA----------TATGATGTATACTAGGTGGATGTTTAA----------GGCTACATTTTACATGAATTACG----------ACGATAAA
droGri2	scaffold_15112:4085932-4086005 -		----------TCAAA----------------AA---TTGAGCATTGAATTGGACATTT---TTGTATATATTTTTATATATCAAT-------TTTTG----------AAATGTATA----------
droWil2	scf2_1100000004762:6364929-6365026 -		----------ACTGT----------AACACAGACT----------CAATGTTTTCACTTCATCGTCTATTGTCTGTTATACTAATGCATGTTCAA----------GATCATATGTTTGTTTT-TTAGC----------AAATGTT
droAna3	scaffold_13248:4556009-4556096 +		----------CATTA----------GAAAAAAGTTACAGAGCTTTGAAGTTGGACCAATGAAGTCGTGTTACAGTTTTGCTCGTCAGTGTATATTC----------ACCTGAA----------TTTTTGTTTTTTTCTAGGCACGCATTTTAAA----------GATCTTAGTGTTTTTTT-GTAGGT----------TATATAAT
droBip1	scf7180000393228:8493-8647 +		----------GCAAATTGGCATCACTGATTCTTGAAAAGGTAAAG---ATTTTAGAGTGAGGAGCAAACTGTAACACGAGTT----------CAATGTTTCAACTTCAAAGGTCTGTTACTTTTTTTCTAAGGCACGCATTTTAAA----------GATCTTAGTGTTTTTTT-GTAGGT----------TATATAAT
droKik1	scf7180000302707:514292-514390 -		----------ACTGT----------AACACAAGTA----------CAATACTCGAACTTCAAAGGTCCATAACTTCTGTTCTAATGTATAGATTCTTAAA----------AATCTTAATGTTGTTTT-GTTGGT----------ATGTGTA
droFic1	scf7180000453055:1054-1213 +		----------CATTA----------GAAAAAAGTTACAGAGCTTTGAAGTTGAACAATGAAGTCGTGTTACAGTTTTGCTCGTCAGTGTAAGTATATTACAAAGTCTTATTTTCACTATTTCGCATTATTTGCCTGA----------AT----------TAAAATTACAATTTCAATTGATTTTATTTTTCTTGAATT
droRho1	scf7180000777770:3995-4093 -		----------ATTTA----------GAACAGAAGATACAGAGCTTTGAAGTTAGAGTATTGAAGTCGTGTTACAGTTTTGTTCGTCAGTGTACGAAA----------GTGTGATAT----------TAGCTAATTTCA----------A
droBia1	scf7180000302140:96632-96712 -		----------AT-------------------------

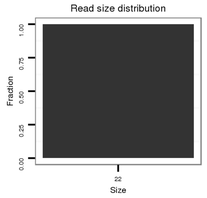
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_3032	**scaffold_6500:15319962-15320071 +**	**candidate**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser (Cornell Mirror)]

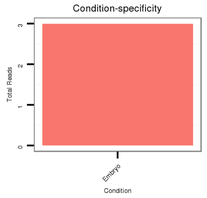
Legend: seqseq star mismatch in alignment mismatch in read

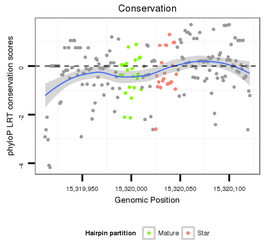
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

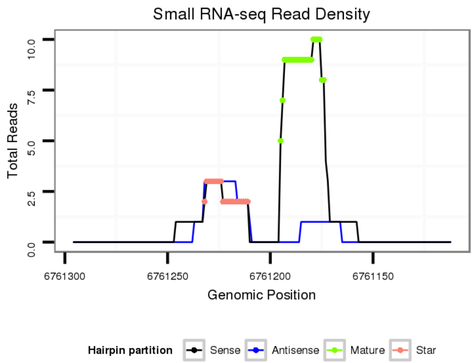
hide 3p reads show mid mismatch reads

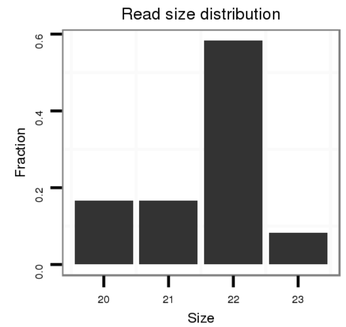
```
                                                
```

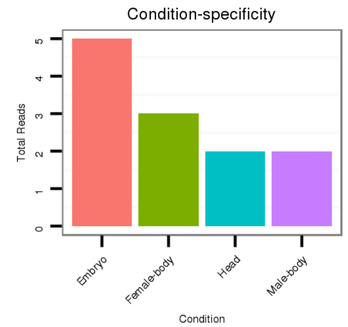
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_2891	**scaffold_6500:6761162-6761246 -**	**candidate**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser [Cornell Mirror]]

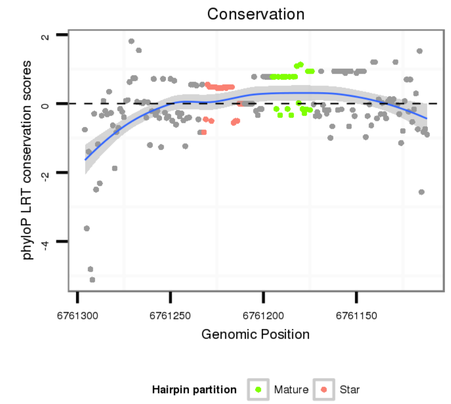
Legend: mature star mismatch in alignment mismatch in read

Predicted structure









Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

```
GGGATTGTGATTGATGAACAGAAAAATACATAAAGTAAAATGTAAAAGCCTACGCTGATTGACTCTAAAATGCCCTGTAAAATAAAAATTCATGTACATTTTTATTTTACAGGGCATTTGAGAGTCAATCAGCGTACAGACAGACTCAAAACTAAAATTAGGTAAGAATTATTTAACAATAGTTA
**********************************************.((((((((((((((((.((((((((((((((((((((((.......)))))))))))))))))))))))))).))))))))))))))..**********************************************
```

Read size	# Mismatch	Hit Count	Total Norm	Total	M060 embryo	V041 embryo	M046 female body	V110 male body	V056 head	V049 head
22	0	1	3.00	3	0	0	1	1	1	0
22	0	1	2.00	2	0	0	0	1	0	1
20	0	1	2.00	2	1	1	0	0	0	0
21	0	1	1.00	1	0	0	1	0	0	0
23	0	1	1.00	1	0	1	0	0	0	0
22	0	1	1.00	1	0	1	0	0	0	0
23	1	1	1.00	1	1	0	0	0	0	0
22	0	1	1.00	1	0	0	0	1	0	0
22	0	1	1.00	1	1	0	0	0	0	0
21	0	1	1.00	1	0	0	1	0	0	0

Anti-sense strand reads

```
CCCTAACACTAACTACTTGTCTTTTTATGTATTTCATTTTACATTTTCGGATGCGACTAACTGAGATTTTACGGGACATTTTATTTTTAAGTACATGTAAAAATAAAATGTCCCGTAAACTCTCAGTTAGTCGCATGTCTGTCTGAGTTTTGATTTTAATCCATTCTTAATAAATTGTTATCAAT
**********************************************.((((((((((((((((.((((((((((((((((((((((.......)))))))))))))))))))))))))).))))))))))))))..**********************************************
```

Read size	# Mismatch	Hit Count	Total Norm	Total	M060 embryo	V041 embryo	V110 male body
22	0	1	1.00	1	1	0	0
23	0	1	1.00	1	1	0	0
22	1	1	1.00	1	0	1	0
20	0	1	1.00	1	1	0	0
21	0	1	1.00	1	0	0	1

Show Alignment With Reads

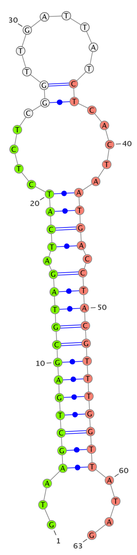
Re-alignment of all predicted orthologs

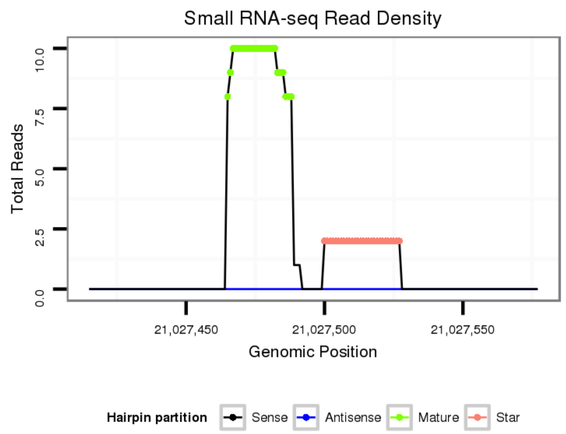
Species	Coordinate	ID	Alignment
droMoj3	scaffold_6500:6761112-6761296 -	dmo_2891	GGGATTGTGATT----------GATGAACAGAAAAATACA---TAAAGTAAAA-TGTAAAAGCCTACGCT----------GATTGACTCTA----------AAATGCCCTGTAAAATAAAAATTCATGTACATTTTTATTTTACAGGGCATTT------GAGAGTCAATCAGCGTACA-GACAGACTCAAAACTAA----------AATTAGGTAAGAATTATTTAACAATAGTTA-
droVir3	scaffold_12723:3096000-3096080 +		TCTGAT-----------GATGAGCAGGCAAATACA---GTGGCAAGATAGTTGATGAGTTGAGCGAACGTC----------AGATGCCCTGTAATGC----------GGGG

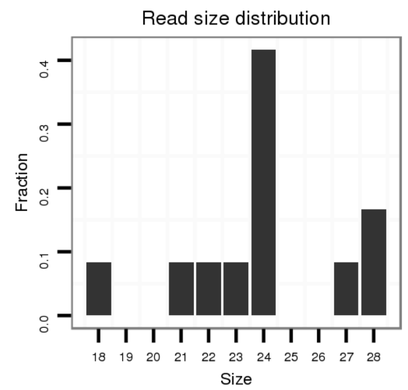
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_2013	**scaffold_6540:21027465-21027527 +**	**candidate**	**Mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

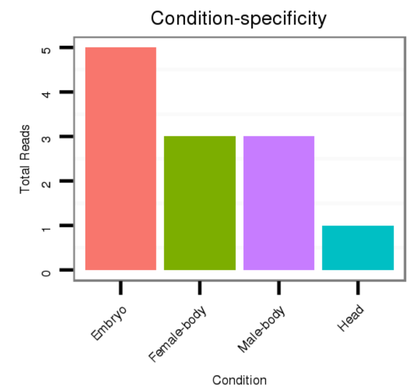
Legend: mature star mismatch in alignment mismatch in read

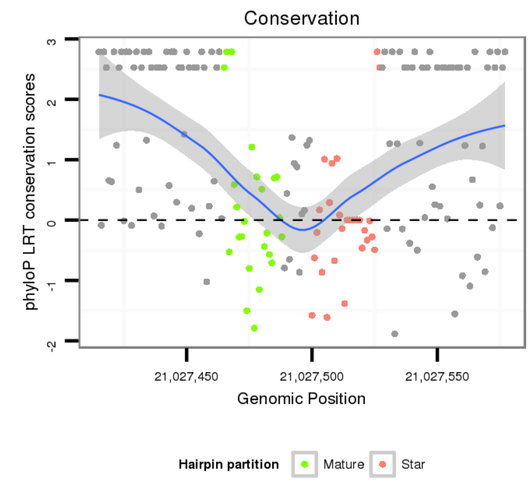
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [DmojGI10098-in]; CDS [DmojGI10098-cds]; CDS [DmojGI10098-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

```
TCAGCTTGGACTTCGATCAGACCGGTCAAATAGCATCAGCCTCTTTGCAGGTAAGCTGAGCGTAGATCATCTCTCGGTTGATTATCTCACTAATGACCTACGTTTGGTTATAGGTGCTGCTGCCGGAGCGACAACGTGCGGGTCGCAGGCTTGCGCACGAGCA
**************************************************...(((((((((((.((((.....((........)).....)))).))))))))))).....**************************************************
```

Read size	# Mismatch	Hit Count	Total Norm	Total	M060 embryo	M046 female body	V110 male body	V049 head	V056 head
....GTAAGCTGAGCGTAGATCATCTCT....	24	0	1	5.00	5	2	0	3	0	0
....CTCACTAATGACCTACGTTTGGTTATAG....	28	0	1	2.00	2	2	0	0	0	0
....TAAGCTGAGCGTAGATCATCTCT....	23	0	1	1.00	1	0	0	0	1	0
....AAGCTGAGCGTAGATCATCTCT....	22	0	1	1.00	1	0	1	0	0	0
....GTAAGCTGAGCGTAGATC....	18	0	1	1.00	1	0	1	0	0	0
....GTAAGCTGAGCGTAGATCATC....	21	0	1	1.00	1	1	0	0	0	0
....GTAAGCTGAGCGTAGATCATCTCC....	24	1	1	1.00	1	1	0	0	0	0
....GTAAGCTGAGCGTAGATCATCTCTCGG....	27	0	1	1.00	1	0	1	0	0	0

Anti-sense strand reads

```
AGTCGAACCTGAAGCTAGTCTGGCCAGTTTATCGTAGTCGGAGAAACGTCCATTCGACTCGCATCTAGTAGAGAGCCAACTAATAGAGTGATTACTGGATGCAAACCAATATCCACGACGACGGCCTCGCTGTTGCACGCCCAGCGTCCGAACGCGTGCTCGT
**************************************************...(((((((((((.((((.....((........)).....)))).))))))))))).....**************************************************
```

Read size	# Mismatch	Hit Count	Total Norm	Total	V110 male body	M046 female body

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6540:21027415-21027577 +	dmo_2013	TCAGCTTGGACTTCGATCAGACCGGTCAAATAGCATCAGCCTCTTTGCAGGTAAGCTGAGCGTA--GATC-------A----------TCT----------CT-----CGGTTGATTATCTCAC---T-AA----------TGACCTACGTTTGG----------TTATAGGTGCTGCTGCCGGAGCGACAACGTGCGGGTCGCAGGCTTGCGCACGAGCA
droVir3	scaffold_13047:4028644-4028801 +		TCAGCCTGGATTTCGATCAGACCGGGCAAATAGCATCAGCCTCGTTACAGGTAAGCCGAGT----TAAC-------\-----------ATCTC--AAACT-----AGACT-----GCAT----------TGCT-CATGCGTCAAAAT----------GG----------CTACAGGTTCTTCTGCCGGAGCGTCAACGTGCGGGACGCCGGCTGTCGCACGAGCA
droGri2	scaffold_14906:677884-678055 +		TCAGCCTGGATTTCGATCAGACCGGTCAAATAGCATCAGGTTCATTGCAGGTAACGTTGCG----\----\-------\-CACCTCATTCATAT----ACCTAGATTATATA-----TCGTTGCTTATGCTTA----\--\---------TGCTTATTG-----CT----------ACTCAGGTGCTTTGCCGGAGCGACAACGAGCGGGCCGACGGCTGGCACAGGAGCA
droWil2	scf2_1100000004943:7930928-7931102 +		TTAGCTTGGATTTTGATCAGACTGGTCAAATTGCATCCGCTTCCTGCAGGTGAGTCGAAA----\----\-------\----------\---------\--------\-----\----------\--\--\--------AAT--\----------GGTATTTCATAATTCTAAATACATTTATTTACCCTTTTCTATCTTCCTATTCTATCAATAGGTATTGCTGCCAGAACGACAACGGGCAGGACGTCGGCTAGCCATGAGCA
dp5	2:26156555-26156717 +		TGAGCCTGGACTTGATCAGACGGACAGATAGCCTCGCCTCGCTGCAGGTGAGTGTGTGGTA--AAAC-------\----------A--ACTAAA------AGACA-----GTCTTGTTATGCCAA----\--\---------TGGTAATCC-----TC----------TTTCAGGTACTCCTACCCGAGCGACACCGTGCTGGCCGACGGCTCGCGCACGAGCA
droPer2	scaffold_6:1487169-1487331 +		TGAGCCTGGACTTGATCAGACGGACAGATAGCCTCGCCTCGCTGCAGGTGAGTGTGTGCA--AAAC-------\----------A--ACTAAA------AGACA-----GTCTTGTTATGCCAA----\--\---------TGGTAATCC-----TC----------TTTCAGGTACTCCTACCCGAGCGACACGTGCTGGCCGACGGCTAGCGCACGAGCA
droAna3	scaffold_13340:21661116-21661274 +		TCAGCCTGGACTTCGACCAGACTGGCCAAATTGCATCCGCCTCCTGCAGGTTAGCAGTCT---TGTCTATTGTCCTTAT----------\---\----------\--\---AAG---------TCATAGTGATA-TATCCTT--------\--TGAT-----CC----------TTTTAGGTTCTTCTGCCAGAACGACACCGAGCTGGCCGCCGTTTCGCTCATGATCA
droBip1	scf7180000396413:877801-877961 -		TCAGCCTGGATTTCGACCAGACTGGCCAAATAGCATCCGCCTCGCTGCAGGTAAGCAATCTC--G-ACTACT----\----------C--\----------\-TCCAATGT-----GAATTATAATGCT-TATCCC-T-----T--TTAT-----CC----------TTTTAGGTCCTACTACCAGAACGTGACCGAGCTGGACGCCGTTTAGCCACCGATCA
droKik1	scf7180000302639:742721-742876 +		TGAGCCTTGACTTTGACCAGACTGGACAGATTGCATCCGCCTCGCTGCAGGTTAGTCAGAA---TCCAATTCCAGGCTTA----------\---\----------\--\---GAAT---------GC---TGCT-AATACTT--------\--TGGG------AT----------TTTAAGGTTCTGCTCCCAGAGCGACACCGAGCCGGTCGACCTTCGCCCACGAGCA
droFic1	scf7180000452523:1309357-1309514 -		TGAGCCTGGATTTTGACCAACACCGGCCAGATTGCATCTGCTTCGCTTGCAGGTGAGTTTTAA---TTAAATGCAGGCAGTC----------\---\----------\--\---GTAT---------GG---TTTT-CATACCTG-----G--TTTT-----CC----------GATTAGGTCTGCTCCCGGAGCGTCAGAGAGCTGGTCGTCGCTTGAGCCACCGAGCA
droEle1	scf7180000491080:1714396-1714554 -		TGAGCCTGGATTTTGACCAACACCGGCCAGATTGCATCTGCTTCATTGCAGGTAAGTTTTTA---TTTTCAACGGCCATTC----------\---\----------\--\---ATAT---------AG---TTTTTTTTACCCG-----G--TTTC-----TC----------GCTCAGGTTCTGCTTCCAGAGCGACACCGAGCTGGTCGTCGATTCGGACACGAGCA
droRho1	scf7180000779241:40378-40535 +		TGAGCCTGGATTTTGACCAACACCGGCCAGATTGCATCTGCTTCATTGCAGTGAGTTTTTA---TTTTAATACAGGCATTC----------\---\----------\--\---GCAT---------AG---TTTT-TTCACCTG-----G--TTTT-----TC----------ACTTAGGTTCTGCTCCCAGAACGACAGAGAGCTGGTCGTCGCTTAGGCCACGAACA
droBia1	scf7180000302136:1535716-1535873 -		TGAGCCTGGATTTCGACCAACACCGGCCAGATTGCATCGCTTCATTGCAGGTAAGTTTTCA---ATTAAGACCGACAATC----------\---\----------\--\---GTGT---------AG---TTCT-CTAACCAT-----G--TTTC-----TC----------GCCCAGGTTCTGCTCCCGGAGCGACAGAGAGCGGGTCGTCGTTTCGGCCACGAACA
droTak1	scf7180000415242:184636-184796 +		TGAGCCTGGATTTCGACCAACACCGGCCAGATTGCATCGCTTCATTGCAGGTAAGTTTTCTG--TGTAATACCCACAATT----------\---\----------\--\---GTGTGT-------AG---TTTT-ATAACAAG-----A--TTTC-----TC----------GCCTAGGTTCTGCTCCCGGAACGGCAGAGAGCTGGCCGTCGCTTCGGCCACGAACA
droEug1	scf7180000409797:1616490-1616647 +		TGAGCCTGGATTTTGATCAACACCGGCCAGATTGCATCTGCATGACTACAGGTAAATTTTCA---TTAGATACCAGCAATC----------\---\----------\--\---GTGT---------AA---TTTT-CATACCTG-----G--TTTT-----TC----------GCTTAGGTTCTACTCCCGGAACGACAGAGAGCTGGTCGTCGTTTCGGCCATGAACA
dm3	chr3R:11915268-11915425 -		TAAGCCTGGATTTCGATCAAACCGGCCAGATTGCATCTGCCTCATTGCAAGTAAGTTTTG---TTTTAATACATACAATC----------\---\----------\--\---AAGT---------GG---TTTA-AATGCCTG-----G--TTTC-----TC----------GCCTAGGTTCTCCTCCCAGAAAGACAACGAGCTGGCCGACGACTTGGTCATGATCA
droSim2	3r:9335598-9335755 +		TAAGCCTGGATTTCGATCAAACCGGCCAGATTGCATCTGCCTCGTTGCAAGTAAGTTTTG---TTTTAATACATACAATC----------\---\----------\--\---AAGT---------GG---TTTA-AATGCCTG-----G--TTTC-----TC----------GCCTAGGTTCTCCTCCCAGAAAGACAACGAGCTGGCCGACGTCTTGGCCATGATCA
droSec2	scaffold_0:10044065-10044217 +		TAAGCCTGGATTTCGATCAAACCGGCCAGATTGCATCTGCCTCATTGCAAGTAAGTTTTG---TTTTAATACATACCATC----------\---\----------\--\---AAGT---------GG---TTTA-AAT----------G--TTTC-----TC----------GCCTAGGTTCTCCTCCCAGAAAGACAACGAGCTGGCCGACGACTTGGCCATGATCA
droYak3	3R:14519255-14519412 +		TAAGCCTGGATTTCGATCAAACCGGCCAGATTGCATCTGCTTCATTGCAAGTAAGTTTTG---CTCAGTACATACAGTC----------\---\----------\--\---AAGT---------GG---TTTA-AATGCCTG-----G--TTTC-----TT----------GCATAGGTTCTCCTCCCAGAGAGACAAAAGAGCTGGCCGACGATTGAGCCATGATCA
droEre2	scaffold_4770:11438795-11438952 -		TAAGCCTGGATTTCGATCAAACCGGCCAGATTGCATCTGCTTCATTGCAGGTAAGTTTTG---TTTTAATGCATGCAATC----------\---\----------\--\---AAGT---------TG---CTTA-AATGCCTG-----G--TTTC-----TC----------GCCTAGGTTCTCTCCCAGAGAGACAAAAGAGCTGGCCGACGATTGGCCATGATCA

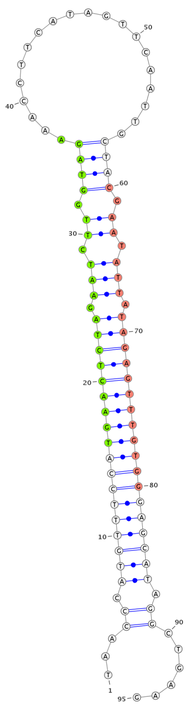
Generated: 09/08/2015 at 07:06 PM

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

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_2974	**scaffold_6540:30823371-30823495 -**	**candidate**	**Canonical miRNA**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

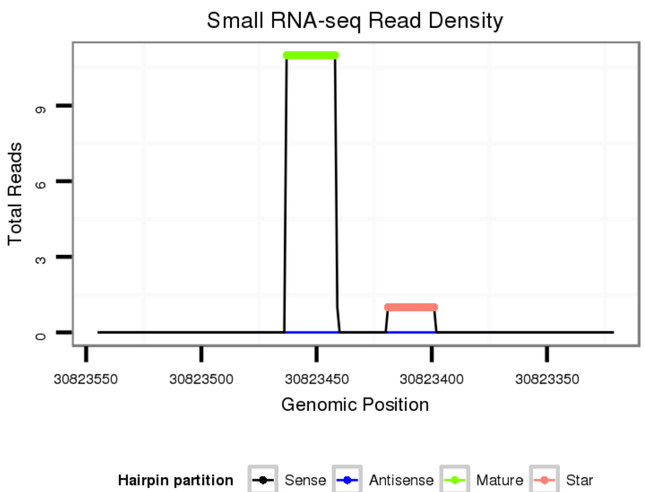
Legend: mature star **mismatch in alignment** mismatch in read

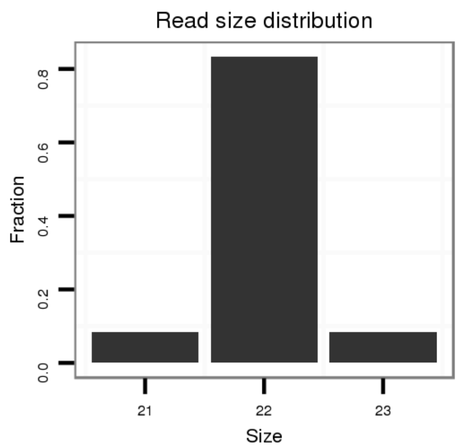
Predicted structure

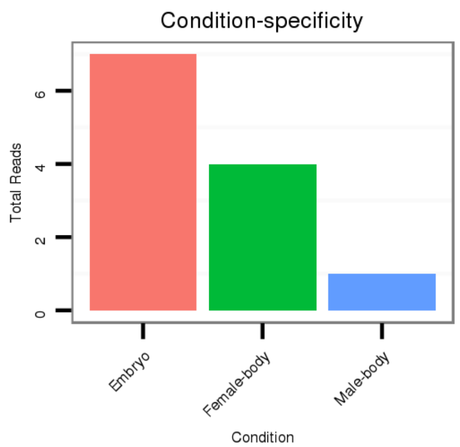


dmo_2974_secst (-33.7)

Show Alternate Folds







No conservation details.

Flybase annnotation

intron [Dmoj\GI22097-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

TTCCCAAAATAAATATATAATTAATTTTAAAATCAAGCTTGTAACGACATTAGACTTTATCTTTGTATAACCCATGTTTCCATGAACTCTAGAATCTTGGTAGAAACCTTCATAGTTCAATTGCTACGAATATTATAGAGTTTGTGGGAGCATAGGCTGAAGAAAGATAAATTCTAGAGAAAATGCTTTCAACTGAGGGAACTGCGGGTAGTTTAAACTCGATTT	Read size	# Mismatch	Hit Count	Total Norm	Total	M060 embryo	M046 female body	V049 head	V110 male body
**********...((.((((((((((((((((((.(((.((.((((.....))))).)).))).))))))))))))))))).)).....**********									
.....TGAACTCTAGAATCTTGGTAGA.....	22	0	1	10.00	10	7	3	0	0
.....CGAATATTATAGAGTTTGTGG.....	21	0	1	1.00	1	0	0	0	1
.....TGAACTCTAGAATCTTGGTAGAA.....	23	0	1	1.00	1	0	1	0	0

Anti-sense strand reads

AAGGGTTTTATTTATATATTAATTAAAATTTTAGTTCGAACATTGCTGTAATCTGAAATAGAAACATATTGGGTACAAAGGTACTTGAGATCTTAGAACCATCTTTGGAAGTATCAAGTTAACGATGCTTATAATATCTCAAACACCCTCGTATCCGACTTCTTTCTATTTAAGATCTCTTTTACGAAAGTTGACTCCCTTGACGCCCATCAAATTTGAGCTAAA	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
droMoj3	scaffold_6540:30823321-30823545 -	dmo_2974	TTCCCAAAATAAATATATAATTAATTTTAAAATCAAGCTTGTAACGACATTAGACTTTATCTTTGTATAACCCATGTTTCCATGAACTCTAGAATCTTGGTAGAAACCTTCATAGTTCAATTGCTACGAATATTATAGAGTTTGTGGGAGCATAGGCTGAAGAAAGATAAATTCTAGAGAAAATGCTTTCAACTGAGGGAACTGCGGGTAGTTTAAACTCGATTT

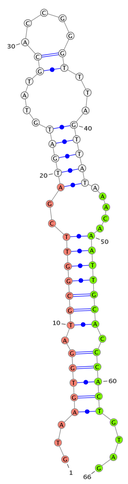
PASS/FAIL	
crit.star	0
crit.hor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

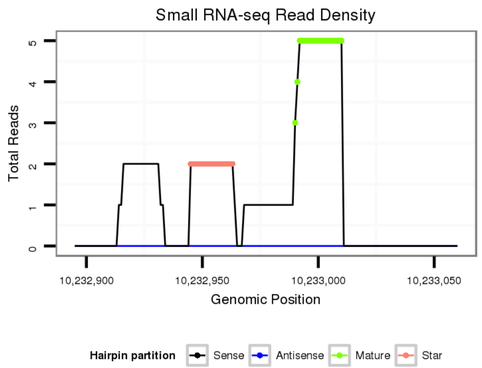
Generated: 03/10/2015 at 07:58 PM

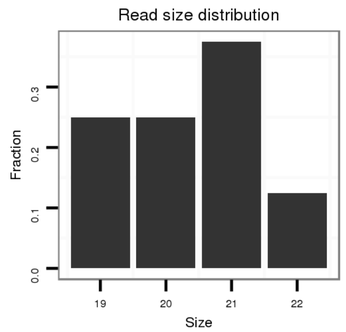
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_2431	**scaffold_6680:10232945-10233010 +**	**confident-exception**	**Mirtron**	**intron**	[View on UCSC Genome Browser [Cornell Mirror]]

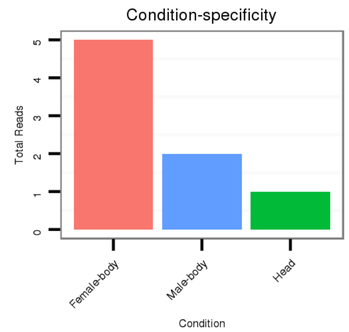
Legend: mature star **mismatch in alignment** mismatch in read

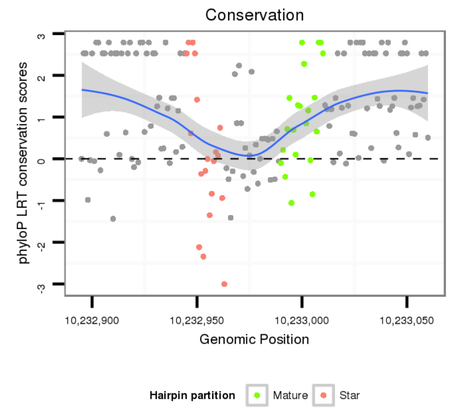
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [DmojGI13224-in]; CDS [DmojGI13224-cds]; CDS [DmojGI13224-cds]; utr3 [utr3_minus_4972]; utr3 [utr3_minus_4971]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

```
GCCGCGCATACCCACGCCGGAGGTGACGAAGGATGGCAGCACCAACACAGGTAAGTGGATGCGGTTCGATGATGTATGCACCGGGTTTAGTTATAAACAAATTGCACCCACTGTAGCCACAAGCGCCGTTATCATGGCCCCACAACAGCTGAGCACCCAAAGCACT
**********************************************...(((((.(((((((..(((((....((.....))...)))))).....)))))))..)))))....**********************************************
```

Read size	# Mismatch	Hit Count	Total Norm	Total	M046 female body	M060 embryo	V056 head	V110 male body	V041 embryo
.....AACAAATTGCACCCACTGTAGA..... 22	1	1	5.00	5	3	1	0	0	1
.....AACAAATTGCACCCACTGTAG..... 21	0	1	2.00	2	2	0	0	0	0
.....GGTGACGAAGGATGGCAG..... 18	0	1	1.00	1	1	0	0	0	0
.....GTAAGTGGATGCGGTTCGA..... 19	0	1	1.00	1	1	0	0	0	0
.....AACAAATTGCACCCACTGTAGAA..... 23	2	1	1.00	1	0	1	0	0	0
.....GTAAGTGGATGCGGTTCGAT..... 20	0	1	1.00	1	0	0	0	1	0
.....CAAATTGCACCCACTGTAG..... 19	0	1	1.00	1	1	0	0	0	0
.....ACAAATTGCACCCACTGTAGAA..... 22	2	1	1.00	1	1	0	0	0	0
.....GTATGCACCGGGTTTAGTTAT..... 21	0	1	1.00	1	0	0	1	0	0
.....AACAAATTGCACCCACTGTAGT..... 22	1	1	1.00	1	1	0	0	0	0
.....ACAAATTGCACCCACTGTAGA..... 21	1	1	1.00	1	1	0	0	0	0
.....GAGGTGACGAAGGATGGC..... 18	0	1	1.00	1	0	0	1	0	0
.....CAAATTGCACCCACTGTAGA..... 20	1	1	1.00	1	1	0	0	0	0
.....AAACAAATTGCACCCACTGTAG..... 22	0	1	1.00	1	0	0	0	1	0
.....ACAAATTGCACCCACTGTAG..... 20	0	1	1.00	1	1	0	0	0	0

Anti-sense strand reads

```
CGGCGCGTATGGGTGCGGCCTCCACTGCTTCCTACCGTCGTGGTTGTGTCCATTCACCTACGCCAAGCTACTACATACGTGGCCCAAATCAATATTTGTTTAACGTGGGTGACATCGGTGTTCGCGGCAATAGTACCGGGGTGTTGTCGACTCGTGGGTTTCGTGA
**********************************************...(((((.(((((((..(((((....((.....))...)))))).....)))))))..)))))....**********************************************
```

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
droMoj3	scaffold_6680:10232895-10233060 +	dmo_2431	GCCGCGCATACCCACGCCGGAGGTGACGAAGGATGGCAGCACCAACACAGGTAAGTGGATGCGGTTCG----------AT-----GATGTATGCAC----------CGGGTTTAGTT----------ATAAACAAATTGCACC----C----------ACTGTAGCCACAAGCGCCGTTATCATGGCCCCAC---AACAGCT--GAGCACC-----CAAAGCAC---T----------
droVir3	scaffold_13049:10545121-10545281 -	dvi_19403	GCCACGCATACCCACGCCGGAGGTGACCAAGGATGGTAGCACCAACACGGTAAGTCTCTGTTGA----------TT-----TTGCAC----------CATTTAGCTGAAACCAAT--------AC-AATTGCA--C----C----------CTGTAGCCACCAGTGCCGTTATAATGGCACCAC---AACAGCT--GAGCACC-----CAAAGCAC---T----------
droGri2	scaffold_15110:8699111-8699286 +		TCCACGCATCCCAACGCCGGAGGTAACCAAGGATGGCAGCACAATAGCGGTAAGTTTGTGCTAGAT----------CTTT----TC--CCACAAGTCA----AC----------TCAACTCA------AC-ACAAAACTTACAATAAATTGCAC----T----------CTGTAGCCAGCGCAGTGCCGTTATAATGGCCCCAC---AACAGCT--GAGCACC-----CAAAGCAC---T----------
droWil2	scf2_1100000004762:5734331-5734577 +		ACCACGCATACCCACCCTGAGGTGCCAAAAGATGGCAGCAATTTGACCGGTGAGTGTACGCAAACAAAGATTTGACATTGGTTTCGTTTTTCGTTGTTGTTCGATTTGATTTGT---------TTTGTTTT----TAATTGAGCACCATAATAATT---------TAAAAAAATTTGCACAAAATTAATATATATGTGTATATATAGCCACCGCTGCATCATATGTCACCAC---AACAGCT--AGGCACGAACACACAAAGCACTTGT----------
dp5	XR_group3a:255083-255269 -		GCCGCGCATCCCCACTCCGGAGGTGCCAAAAGACGGCAGCACCAATCCAGGTGAGCGGCATGCGTCT----------TT----CC---------CCCCCCCC----GCACCGAGCACCCCACTCATGCACCGTA------TTGTGTATC-CTT---TCC----------ACTGTAGCCTTTAGTGCCGTCATAATGGCCCACTCACAACACCAAACCGCACCAG----AGCAGCCC---C----------
droPer2	scaffold_23:257763-257976 -		GCCGCGCATCCCCACTCCGGAGGTGCCAAAAGACGGCAGCACCAATCCAGGTGAGTGGCATGCGTCT----------TT----CC---------CCCCCCTCCCCATCTCCGAGCACCCCACTCATGCACCGTA------TTGTGTATC-CTT---TCC----------ACTGTAGCCTTTAGTGCCGTCATAATGGCCCACTCACAACACCAAACCGCACCAG----AGCAGCCC---CCGCAACAGGCACAGGGAGGGGCG
droAna3	scaffold_13337:20700364-20700543 +		GCCGCGCATTCCCACCCCGAGGTGCCAAGGATGGCACACCAATCCAGGTGAGTACA-ATTCACAA----------CT----CCTGCACGAACTT---TTGCA--ACTCCTTCCTC----------ATATACGTTCGCACCACTCC----------CCCTGTAGCCACCAGTGCATCCTATATGGCACCAC---ACCAGCT--AGGCACCCC----CAGCGCAC---C----------
droBip1	scf7180000396707:720328-720503 -		GCCTAGATTCCCACTCCGAACGTGCCAAGGATGGCACACCAATCCAGGTGAGTACG-ATTCACAC----------GT----CCTGCACGAACTC---TTGCA--ACTCCTTCCTC----------ATGTTTGCTCGCACC----C----------CCTGTAGCCACCAGTGCATCCTATATGGCACCAC---ACCAGCT--GAGCACCCC----CAGCGCAC---CT----------
droKik1	scf7180000302334:757311-757477 -		GCCCAGATACCAACGCCGAGGTGACCAAGGATGGCAATACCAATCCAGGTAAGTAAAATCCCTGAA----------G-----------CAC----TTGCAAAACT----------CTTT------CT----AAATCGCACCACTTCACC----------ACCTTGTAGCCACCAGCCTGATTTTAATGGCACCC---ACCAGCT--GAGCACAAC----CAGCGCAC---C----------
droFic1	scf7180000453929:1354105-1354276 +		ACCGCGCATTCCCACCCCGAAGTCACCAAGGATGGCAGCACCAATCCAGGTGAGTGAG-ATCCACAA----------AT----CCTGCACGAAACC----CC----------GCAACTTA------CTGAACACTCGCACCACTTC----------CCTGTAGCCACCAGCTTCGTCCTATGGCACCAC---ATCAGCT--GAGCACCAG----CAGCGCAC---C----------
droEle1	scf7180000491193:1059592-1059762 -		ACCAACCATTCCCACGCCCGAGGTAGCCAAGGATGGCAACACCAACCAGGTGAGTAAC-ACCCACAA----------CA----CCCGCACGAAAC----CT----------GCAACATT------TTGTTAACTTGCACCACCTC----------CATGTAGCCACCAGTTCGTCCTCATGGCACCAC---ACCAGCT--GAGCACCAG----CAGCGCAC---C----------
droRho1	scf7180000780231:42181-42351 +		ACCAACCATTCCCACGCCCGAGGTAGCCAAGGATGGCAGCACCAATCCAGGTGAGTGAG-ACCCACAA----------CC----CATGCACGAAAC----CT----------GCAACATG------TTGTTAACCTGCACCACTCC----------CCTGTAGCCACCAGTTCGTCCTCATGGCACCAC---ACCAGCT--GAGCACCAG----CAGCACAC---C----------
droBia1	scf7180000302193:3774729-3774900 -		ACCGCGCATTCCCACCCCGAGGTAACCAAGGAAGGCAATACCAATCCAGGTGAGTGAGAACCCACAA----------AC----AACCCACCAACC----CT----------GCAACTTT------TTGAACACTCGCACCACTCC----------CCTGTAGCCACCAGCTCCGTCCTATGGCACCAC---AACAGCT--GAGCACCAG----CAGCGCAC---C----------
droTak1	scf7180000415809:144779-144959 -		ACCGCGCATTCCCACGCCCGAGGTAACCAAGGATGGCCAGACCAATCCAGGTGAGTTAGAATCCACAT----------TT----CCTGCACTGCAATCGAACT----------GCAACTTT------TTGAACAATTCGCACCAGTCC----------TTCTGTAGCCTTCAGGTTCGTCCTAATGGCACCAGCTCACCAGAT--GAGCACCAG----CAGCGCAC---C----------
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droSec2	scaffold_2:6206572-6206743		ACCGCGCATTCCCACGCCCGAGGTGCCAAGGATGGCAACACCAATCCAGGTGAGTAACAACCCACAA----------GA----CCCGCACAAAAC----CT----------GCAACTTT------TTGTACAACTCGCACCACTCC----------CACTTAGCCACCAGCTCGTCCTAATGGCACCAC---ACCAGCT--GAGCACCAG----CAGCGCAC---C----------
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droEre2	scaffold_4784:8929966-8930137 -		GCCGCGCATTCCCACCCCGAGGTGCCAAGGATGGCAACACCAATCCAGGTGAGTGACAAGCCACAA----------GT----CCCGCACAAAAC----CT----------GCAACTTT------TTGAACAACTCGCACCGCTCC----------CCTGTAGCCACCAGCTCGTCCTAATGGCACCAC---ACCAGCT--GAGCACCAG----CAGCGCAC---C----------

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crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
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crit.uri	1
crit.back	1
rescue.total	1
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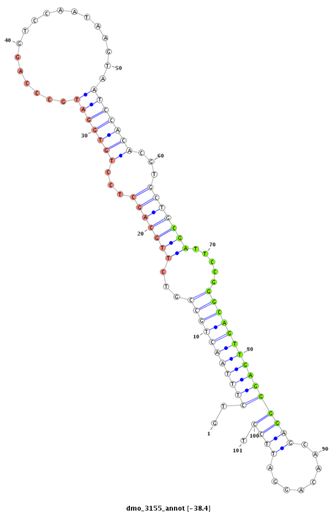
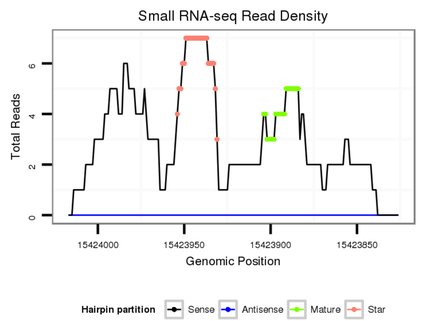
rescue.confident	0
rescue.candidate	1

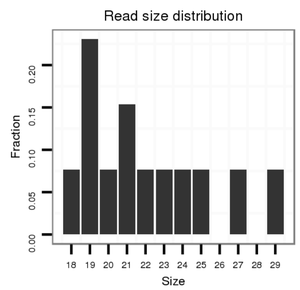
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_3155	**scaffold_6500:15423876-15423967 -**	**candidate**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

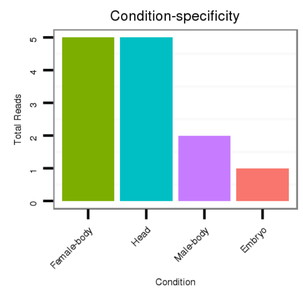
Legend: mature star mismatch in alignment mismatch in read

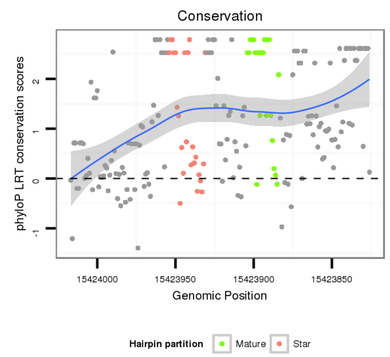
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

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..ACAGCAGCCGGCACTCGTCTT	21	0	1	2.00	2	1	0	0	1	0
CGATTCCGGGCAGTTGAGGGG	21	0	1	2.00	2	1	1	0	0	0
CTTGCAGCTCCTGTGGATGCCCAG	24	0	1	1.00	1	0	1	0	0	0
GGGCAGTTGAGGGGAGCA	18	0	1	1.00	1	0	0	1	0	0
TGCAGCTCCTGTGGATGCCCAGGTCCA	27	0	1	1.00	1	0	0	0	1	0
AGCTAGCAATAGATTCAAC	19	0	1	1.00	1	1	0	0	0	0
TAAGAACTACAGCTAGCAATAGATTC	26	0	1	1.00	1	1	0	0	0	0
TAGACAACAGCACAGCAGCCGGCAC	25	0	1	1.00	1	0	0	0	1	0
TGCCGTCTTGCAGCTCCTGTGGATGCCCA	29	0	1	1.00	1	1	0	0	0	0
TCTTGCAGCTCCTGTGGAT	19	0	1	1.00	1	1	0	0	0	0
TAAGTAATCCACACGTGCTG	20	0	1	1.00	1	1	0	0	0	0
ATTTTGGACGGTAGACAACAGCACA	25	0	1	1.00	1	0	1	0	0	0
GCAGCTCCTGTGGATGCCC	19	0	1	1.00	1	0	0	0	0	1
TTGCAGCTCCTGTGGATGCCCA	22	0	1	1.00	1	0	0	1	0	0
GCGATTCCGGGCAGTTGAGGGGAGC	25	0	1	1.00	1	0	0	1	0	0
ACTCGTCTTTAACTGCCGTCT	21	0	1	1.00	1	0	1	0	0	0
AGCTCCTGTGGATGCCCAG	19	0	1	1.00	1	0	0	1	0	0
TTGAGGGGAGCAACAGGATTC	21	0	1	1.00	1	1	0	0	0	0
GCAACAGGATTCCTTTAAGAACTACAGC	28	0	1	1.00	1	1	0	0	0	0
ACCAACGATTTTGGACGGTAGACAAC	26	0	1	1.00	1	1	0	0	0	0
ACAACAGCACAGCAGCCGGCA	21	0	1	1.00	1	1	0	0	0	0
ATAAGTAATCCACACGTGCTGCG	23	0	1	1.00	1	1	0	0	0	0
GGACGGTAGACAACAGCACAGCAG	24	0	1	1.00	1	1	0	0	0	0

Anti-sense strand reads

TGTTGGTTGCTAAAACCTGCCATCTGTTGTCGTGTCGTCGGCCGTGAGCAGAAATTGACGGCAGAACGTCGAGGACACCTACGGGTCCAGGTTATTCATTAGGTGTGCACGACGCTAAGGCCCGTCAACTCCCCTCGTTGTCCTAAGGAAATTCTTGATGTCGATCGTTATCTAAGTTGATTGGTTTATATT	Read size	# Mismatch	Hit Count	Total Norm	Total	V056 head	M046 female body	M060 embryo

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6500:15423826-15424017 -	dmo_3155	ACAACCAAC----------GATTT----TGGACGG------TA--G------AC---AACAGCAC-----AGCAGCCGG-C-------ACT-----CGTCTTTAACTGCCGTCTTGCAGCTCCT--GTGGA-TGCCCAGGTCCAATAAGT-A---ATCCACACGTGCTGCGATTCCG-GGCAGTTGAGG-GGA-GCAA-CAG-G----------ATTCCTTTAAGAACTACA--GCTAGCAAT-AGA---TTC-AACTAACCAAATATAA----------
droVir3	scaffold_12963:14467400-14467599 -	dvi_24646	C-------A----------AGAGTT----T------------G-------G-----AGCA-----------AGTCTATGTA-------A-G--TAACTGCCGTCTTGCAAGCCT--GTGGA-TAAAAGGTCCAAAAAGT-A----ATCCACACGTGCTGCGATTCGTGG-GGCAGTTGAG----------TTTTACTAAAATCTT--TATGCACATGTAAAG---ATGGGAG----------AGT--GT--C------AGCATTCCTTGGGAACTACAGCAAGCGCAAT-AGA---TGC-AAATAACCAAATATAA----------
droGri2	scaffold_15252:2029226-2029442 +	dgr_469	TT---GGATATAGAGGAATGTCATAATTTGTATATGAATCTA-T------AT------A-------ATCTTACAATTAT--TAACTGCCGTCTTGCCCGGCCT--GTGGCCACCCAGGTCCAAA-CAA-AAGTTGCCACATTGT-CGCGATTCTGAGCAGTAAA----------CTC---AGT-------TTA--ACTT--CATTCACA----------A-CT------GACATTCCTTGAGATCTACAGCTAGCGCAAT-GAACGTCGC-AACTTACCAAATATAT----------
droWil2	scf2_1100000004945:407303-407461 +	dwi_5419	CA-------------------A----------A-----------------T--G-------AG---AATTAGATAATAGTTATTGCCATGG-------ATC-----GATTA-TAATTGCCGTCTTGCAGGTGTCTTGTAATGATCGAGGAATCGAGGTCCAAA-TTA-AAA-TTGCTTTTATGATCGCGATTCTGAGCAGTAGAA----------C-CAC---C----------A-CT-GAACGTCGC-CAACTTACCAAATATAT----------
dp5	4_group3:7165323-7165560 -	dps_30	AGAAATTAACCATTT--ACGCACAGCAACAAAAGATAAACTAATC---T-----------------G-------G-----GATCGCGTGTTCCTTA-------A-------A-------C-C-GTAACTGCCGTCTTGCAGGCCCT--GTGGA-CG-AAGGTCCAAAATTTCGA---GTCGTACAGAGCGTCGATTCCG-GGCAGTTGAGTT-GGATCCCC---TTTAAATCACACTTAAAGCTAT--TGTGCACAGTA-----GTACAGT----------AGT--AG-CCGCGAAGCGACATTCCTTTGAGATCTG---G---C-CAT-AG-C---C---C-----------
droPer2	scaffold_1:8612735-8612972 -	dpe_229	AGAAATTAACCATTT--ACGCACAGCAACAAAAGATAAAACTAATC---T-----------------G-------G-----GATCGCGTGTTCCTTA-------A-------A-------C-C-GTAACTGCCGTCTTGCAGCCCT--GTGGA-CG-AAGGTCCAAAATTTCGA---GTCGTACAGAGCGTCGATTCCG-GGCAGTTGAGTT-GGATCCCC---TTTAAATCACACTTAAAGCTAT--TGTGCACAGTA-----GTACAGT----------AGT--AG-CCGCGAATCGACATTCCTTTGAGATCTG---G---C-CAT-AG-C---C---C-----------
droAna3	scaffold_12916:9588020-9588242 -	dan_4042	AG-------TTAAACGCACAGCTTTAA----------G-----G-------G---GAACCGTT-------T-------T-------ATC-------TCCCATTAACTGCCGTCTTGCAGAGTCT--GTGGA-C--G-TGGTCCAAA-TTT-T---GTCGTACAGCCATGCGATTCCG-GGCAGTTGAAAGTAA--AA-TAG-G-GACT--CCCCAAAAACACATCACATCTGCGCTTT-TGTGCACCGC-----AG----------CCAA-----GACATTCCTTTGAGAGCGA--G---GAGCGCACT-AGACGTCGC-AACTTACCAAATATAT----------
droBip1	scf7180000396580:1442842-1443065 +		AG-------TTAAACGCACAGCTTTAA----------G-----G-------G---GATCAGCA-------TT-------T-------ATC-------TCCCATTAACTGCCGTCTTGCAGGGTCT--GTGGA-C--G-TGGTCCAAA-TTT-T---GTCGTACAGCGCGTCGATTCCGGCGGCAGTTGCAAGTAAA-GAATGCG-GATT-CCTCA--AATACATCACATCTGCGCTTT-TGTGCACCGC-----AG----------C--CCA-----GACATTCCTTTGAGAGCGA--G---GAGCGCACT-AGACGTCGC-AACTTACCAAATATAT----------
droKik1	scf7180000302246:274519-274717 +		G-------G----------G-----G-------G---GA-------TGGATCGATCGCTT-----GG-------G-------ATC-------TCGC-TAACTGCCGTCTTGCAGGCCT--GTGGA-C--TGTGGTCCAAA-TTA-A---GTCGTACATGCGCTGCGATTCCG-GGCAGTTGAGT-GCCC--GA-TGCTG----------GATCGCACTTAACGCTTCGTGTGCACCGCAGAGAA--AGAGTTC----------AGTAATCCC------GACATTCCTTGAAAGCTACA--GAGGCGCGCT-AGACGTCGC-AACTTACCAAATATAT----------
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droRho1	scf7180000780028:158239-158474 +		A-------A----------A-GTCAACGGAT----GGATTG------GA--A------AG---GATCGCGT-------TG-------G-------ATC-------TCGC-TAACTGCCGTCTTGCAGGGCT--GTATTC-C--TTTGGTCCAAATTT-A----GTCGTATGTGCGCTGCGATTCTGGCAGTTGAAA-TAAAGCAA-GAG-GAGAG---GCCC---AATCCATCACACTTAACGCTT--TGTGCACCGT-------ACAGTTC----------AGT--AG-CA-------GACATTCCTTGAGAGCTAA--GAGGCGCAC-AGACGTCGC-AACTTACCAAATATATGC----------
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droTak1	scf7180000415438:753015-753231 -		AG-------TTT-GCGCACAG----------G-----G-------G---GATCGCGT-------TG-------G-------ATC-------TCGC-TAACTGCGTCTTGCAGCGCCT--GTAGA-C--TTTGGTCCAAATTT-A----GTCGTATGTGCGCTGCGATTCCG-GGCAGTTGAAA-GGATGCGA-AAG-GAGAG--ACCC---A--------ACCTAACGCTT--TGTGCACCGT-------A----------C-CC------GACATTCCTTGAGAGCTAA--GAGGCGCAT-AGACGTCGC-AACTTACCAAATATACTTTTATG----------
droEug1	scf7180000409554:3024211-3024448 +		A-------A----------A-CTCAACGGT----GGATTG------GA--G------AG---GATCGCGT-------TG-------A-------ATC-------TCGAT-TAACTGCGTCTTGCAGCGCCT--GTAGA-C--TGTGGTCCAAATTT-A----GTCGTATGTGCGCTGCGATTCTGGCAGTTGTAA-GGATAAAAAGAG-GAGAG--GCGC---AAACCATCACACTTAACGCTT--TGTGCACCGT-------ACAGATT----------AGT--AC--C------GACATTCCTTTGAGAGCTAA--GAGGCGCAT-AGACGTCGC-AACTTACCAAATATACC----------
dm3	chr2L:3067725-3067967 +	dme_436	A-------A----------A--GTTAACGAT----TGGATTT------GC--G------TC---GATCGCGT-------TG-------A-------ATC-------TCGC-TAACTGCGTCTTGCAGGGCCT--GTAGG-C--TTCGGTCCAAATTTA-A----GTCGTACAGTCGTCGCGATTCCG-GGCAGTTGAAA-TGAAGCAA-GAG-GAGAG--GCTC---AGTCCATAACACTTAACGCTT--TGTGCACCGT-------ACAATTT----------AGT--AG-CC------GACATTCCTTTGAGAGCTAA--GAGGCGCAC-AGACGTCGC-AACTTACCAAATATACTTTTATG----------
droSim2	21:2946910-2947152 +	dsi_32463	A-------A----------A--GTCAACGAT----TGGATTT------GC--G------TC---GATCGCGT-------TG-------A-------ATC-------TCGC-TAACTGCGTCTTGCAGGGCCT--GTAGG-C--TTCGGTCCAAATTTA-A----GTCGTACAGTCGTCGCGATTCCG-GGCAGTTGAAA-TGAAGCAA-GAG-GAGAG--GCCC---AGTCCATAACACTTAACGCTT--TGTGCACCGT-------ACAATTC----------AGT--AG-CC------GACATTCCTTTGAGAGCTAA--GAGGCGCAC-AGACGTCGC-AACTTACCAAATATACTTTTATG----------
droSec2	scaffold_5:1224968-1225210 +	dse_1854	A-------A----------A-GTCAACGAT----TGGATTT------GC--G------TC---GATCGCGT-------TG-------A-------ATC-------TCGC-TAACTGCGTCTTGCAGGGCCT--GTAGG-C--TTCGGTCCAAATTTA-A----GTCGTACAGTCGTCGCGATTCCG-GGCAGTTGAAA-TGAAGCAA-GAG-GAGAG--GCCC---AGTCCATAACACTTAACGCTT--TGTGCACCGT-------ACAATTC----------AGT--AG-CC------GACATTCCTTTGAGAGCTGG--GAGGCGCAC-AGACGTCGC-AACTTACCAAATATACTTTTATG----------
droYak3	2L:3063709-3063949 +	dya_1801	AC-------AGCTAGAA----------GAGAT----GGATTG------GC--G------TC---GATCGCGT-------TG-------A-------ATC-------TCGC-TAACTGCGTCTTGCAGGGCCT--GTAGG-C--TTCGGTCCAAATTTA-A----GTCGTACAGTCGTCGCGATTCCG-GGCAGTTGAAA-TGAAGCAA-GAG-GAAAGAGAGCGC---GGTCCATAACACTTAACGCTT--TGTGCACCGT-------ACAATTC----------AGT--AG-CC------GACATTCCTTGAGAGCTAA--GAGCGCACC-AGACGTCGC-AACTTACCAAATATAA----------
droEre2	scaffold_4929:3115453-3115699 +	der_1527	AC-------AGCTAGAA----------GAGAT----GGATTG------GC--G------TC---AATCGCGT-------TG-------A-------ATC-------TCGC-TAACTGCGTCTTGCAGGGCCT--GTAGG-C--TTCGGTCCAAATTTA-A----GTCGTACAGTCGTCGCGATTCCG-GGCAGTTGAAA-GGATGCAA-GAG-GAGAG--GCCC---AGTCCATGACACTTAACGCTT--TGTGCACCGT-------ACATTTT----------CAGT--AG-AC------GACATTCCTTGAGAGCTAA--GCGCGCACC-AGACGTCGC-AACTTACCAAATATACTTTTATG----------

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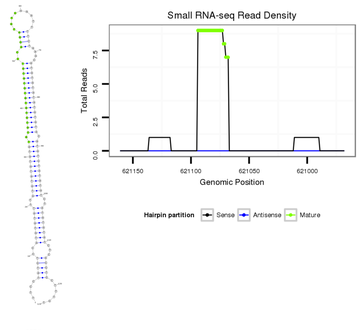
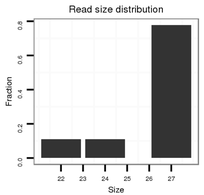
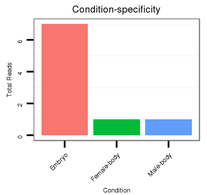
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_2656	**scaffold_6328:621018-621111 -**	**candidate**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser [Cornell Mirror]]

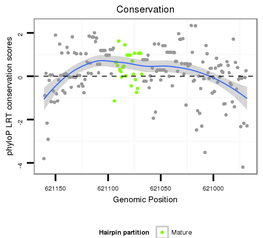
Legend: mature star sub-match in alignment mismatch in read

Predicted structure









Show Alternate Folds

Flybase annotation

intergenic

Repeatable elements

Name	Class	Family	Strand
(TA)n	Simple_repeat	Simple_repeat	+

Sense Strand Reads

hide 3p reads show mid mismatch reads

```
ATTCCGAATCCATCTACTGGACTATGAACAAACCCTTCCTATGTCCATATATATTTATATATATATATATATGTATATGTATATCCAGGATATGAAATTTTCTAAACATATATATATATACATATGTATATATCTATATATATCTCACGTGCTTTGTACTATCGTCTATTTGTTGTCATGAATTAGCTCATA
*******************************....((((((.(((((((((.(((((((((((((((.(((((((.....)))))....)))))))))))))).))))))))))..)))))))).....))))))......*******************************
```

	Read size	# Mismatch	Hit Count	Total Norm	Total	M060 embryo	M046 female body	V041 embryo	V056 male head	V110 male body
.....TATATGTATATGTATATCCAGGATATG.....	27	0	1	7.00	7	5	0	1	0	1
.....GTGCTTTGTACTATCGTCTATT.....	22	0	1	1.00	1	0	0	0	1	0
.....TATATGTATATGTATATCCAGGATATCG.....	28	2	1	1.00	1	1	0	0	0	0
.....TATATGTATATGTATATCCAGGGAT.....	24	0	1	1.00	1	0	1	0	0	0
.....GAACAAACCCTTCCTATGT.....	19	0	1	1.00	1	0	1	0	0	0
.....TATATGTATATGTATATCCAGG.....	22	0	1	1.00	1	1	0	0	0	0

Anti-sense strand reads

```
TAAGGCTTAGGTAGATGGACCTGATACTTGTTTGGGAAGGATACAGGTATATATAAATATATATATATATATATACATATACATATAGGTCCTATAGTTTAAAAGATTTGTATATATATATATGTATACATATATAGATATATATAGAGTGCACGAAACATGATAGCAGATAAACAACAGTACTTAATCGAGTAT
*******************************....((((((.(((((((((((((((((((((((((.(((((((.....)))))....)))))))))))))).))))))))))..)))))))).....))))))......*******************************
```

	Read size	# Mismatch	Hit Count	Total Norm	Total

No data available in table

Show Alignment With Reads

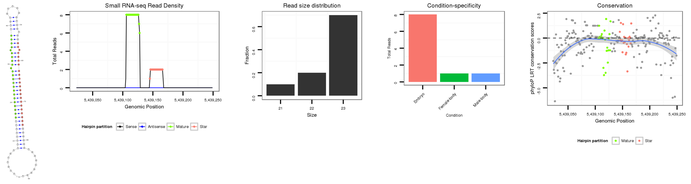
Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMo13	scaffold_6328:620968-621613 -	dmo_2656	ATT----------CCGAATCCA-T----------CTACTG----------GACTATGAACAA------ACCCTTCCTA----+----TGTCCATA---TATAT-TTATATATATATAG[redacted]ATAT--GTATATATAT[redacted]C[redacted]CAGGATATGAAATTTTCTAAA-CATATATATATATATACATATGTATATATCT--ATATATATC[redacted]TCACGTG-----C----TT-TGTACTATC[redacted]GTCTATTT---GTTGT-------CATGAATTA-GCTCATA
droVir3	scaffold_13042:2221725-2221894 -		AG-CGCAAATCATTTACAATTTACGCAAATTATATATGAA-T[redacted]A-T[redacted]-[redacted]-[redacted]-

ID	Coordinate	Confidence	Class	Genome Locale	
dmo_2951	**scaffold_6496:5439073-5439199 +**	**candidate**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser (GenomeMatters)]

Legend: Sense Antisense Mature Star Mismatch Read

Predicted structure



Show Alternate Folds

Flybase annotation

miscRNA

Repeatable elements

Name	Class	Family	Strand
rl_Arb2[Low_complexity]	Low_complexity		
rl_Arb2[Low_complexity]	Low_complexity		

Sense Strand Reads

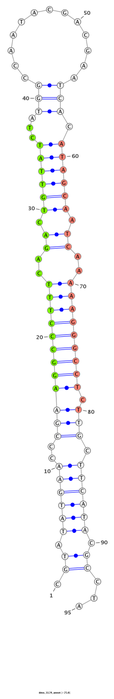
Hide 3p reads Show mid mismatch reads

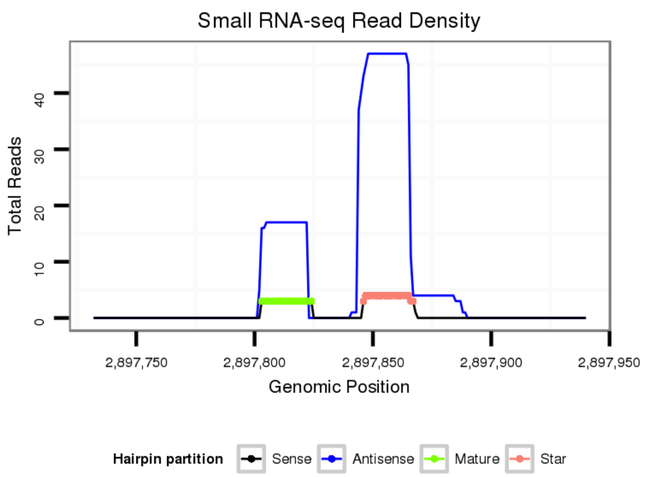
	Read #	5t1	Total	MO2	V141	MO4	5t1	V141
	Alignments	Match	Count	Total		embryos	embryos	body	male	head body
TAGCTAACTCTATCTAGAAAATTATACATATTGAAAAAAAACATCTAATTTTATCCTTTCTAGATTTATTTTTTTTCTTTCAAATTTATTTTTTTT

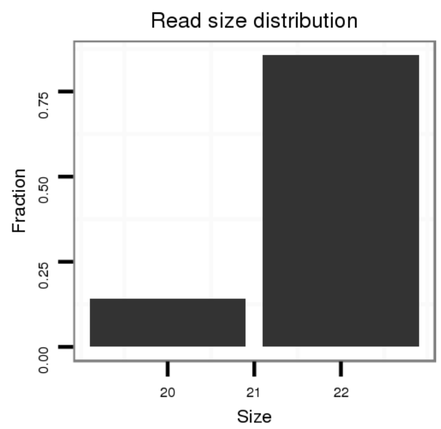
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_3129	**scaffold_6328:2897782-2897890 +**	**candidate**	**Testes-restricted**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

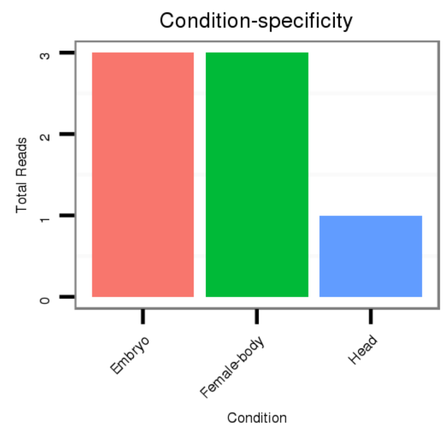
Legend: mature star mismatch in alignment mismatch in read

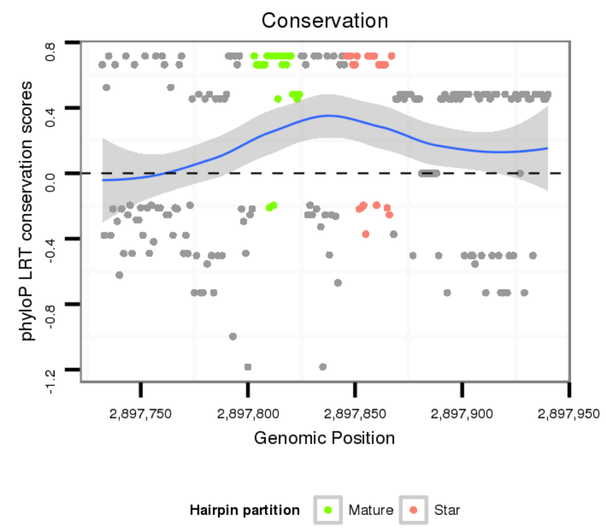
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

```
GTCTATCGATGACCGCCCAAATCGATATTGCCGATTGTGAGCGGCAGAGATGGCACCGTATATGAACCCGAAGGCCCTTTCAGACTGTTATCTATGGCCAATACGACGAATCACATAGCAATCAAAAAGGGCCTCTTGCTTCATACGCCTATCCACGGCGTTGCACTCACTTCCTAGCTGAGATTCGATGCGAACTTATCGATAATGCT
*******************************************************.((.(((((((..(((((((((((((.((.((((((...(((.............))).)))))))..))..)))))))))).))).))))))).))...*******************************************************
```

	Read size	# Mismatch	Hit Count	Total Norm	Total	M060 embryo	M046 female body	V056 head	V110 male body	V049 head
.....AGGCCCTTTCAGACTGTTATCT.....	22	0	1	3.00	3	1	2	0	0	0
.....ATAGCAATCAAAAAGGGCCTCT.....	22	0	1	2.00	2	2	0	0	0	0
.....ATAGCAATCAAAAAGGGCCT.....	20	0	1	1.00	1	0	0	1	0	0
.....TAGCAATCAAAAAGGGCCTCTT.....	22	0	1	1.00	1	0	1	0	0	0

Anti-sense strand reads

```
CAGATAGCTACTGGCGGGTTTAGCTATAACGGCTAACACTCGCCGTCTCTACCGTGGCATATACTTGGGCTTCCGGGAAAGTCTGACAATAGATACCGGTTATGCTGCTTAGTGTATCGTTAGTTTTTCCCGGAGAACGAAGTATGCGGATAGGTGCCGCAACGTGAGTGAAGGATCGACTCTAAGCTACGCTTGAATAGCTATTACGA
*******************************************************.((.(((((((..(((((((((((((.((.((((((...(((.............))).)))))))..))..)))))))))).))).))))))).))...*******************************************************
```

	Read size	# Mismatch	Hit Count	Total Norm	Total	V110 male body	M046 female body	V056 head	M060 embryo	V049 head	V041 embryo
.....TTTCCGGGAAAGTCTGACAATA.....	22	1	1	70.00	70	69	1	0	0	0	0
.....TTTTCCGGGAAAGTCTGACAATA.....	23	2	1	36.00	36	33	2	1	0	0	0
.....TGTATCGTTAGTTTTTCCCGGA.....	22	0	1	34.00	34	28	1	5	0	0	0
.....CTGTATCGTTAGTTTTTCCCGGA.....	23	1	1	21.00	21	19	2	0	0	0	0
.....CTTTTCCGGGAAAGTCTGACAATA.....	24	3	1	12.00	12	12	0	0	0	0	0
.....TCCGGGAAAGTCTGACAATA.....	20	0	1	11.00	11	9	1	0	1	0	0
.....TTCCGGGAAAGTCTGACAATA.....	21	0	1	5.00	5	3	2	0	0	0	0
.....TTTTTCCGGGAAAGTCTGACAATA.....	24	3	1	4.00	4	4	0	0	0	0	0
.....TCTTTCCGGGAAAGTCTGACAATA.....	24	3	1	4.00	4	4	0	0	0	0	0
.....GTATCGTTAGTTTTTCCCGGA.....	21	0	1	3.00	3	1	2	0	0	0	0
.....TATCGTTAGTTTTTCCCGGAG.....	21	0	1	3.00	3	2	0	0	1	0	0
.....TCGTTAGTTTTTCCCGGAG.....	19	0	1	2.00	2	1	0	0	0	1	0
.....CTTTCCGGGAAAGTCTGACAATA.....	23	2	1	2.00	2	2	0	0	0	0	0
.....ATCGTTAGTTTTCCCGGAG.....	20	0	1	2.00	2	2	0	0	0	0	0
.....GAACGAAGTATGCGGATAGGTG.....	22	0	1	2.00	2	2	0	0	0	0	0
.....TGTATCGTTAGTTTTTCCCGG.....	21	0	1	2.00	2	0	2	0	0	0	0
.....TTTTTCCGGGAAAGTCTGACAA.....	22	3	3	1.33	4	1	2	0	0	0	1
.....TCTGTATCGTTAGTTTTCCCGGA.....	24	2	1	1.00	1	1	0	0	0	0	0
.....CCTTTCCGGGAAAGTCTGACAATA.....	24	3	1	1.00	1	1	0	0	0	0	0
.....CTGTATCGTTAGTTTTTCCCGGAG.....	24	1	1	1.00	1	1	0	0	0	0	0
.....GAACGAAGTATGCGGATAG.....	19	0	1	1.00	1	1	0	0	0	0	0
.....TAGTGTATCGTTAGTTTTTCCCGGA.....	25	0	1	1.00	1	0	1	0	0	0	0
.....CCGTTAGTTTTTCCCGGAG.....	19	1	1	1.00	1	0	0	0	1	0	0
.....CCTTTCCGGGAAAGTCTGACAA.....	22	3	1	1.00	1	1	0	0	0	0	0
.....CCTCGTTAGTTTTTCCCGGAG.....	21	2	1	1.00	1	0	0	0	0	1	0
.....GAACGAAGTATGCGGATAGGTGCC.....	24	0	1	1.00	1	1	0	0	0	0	0
.....ATTTTCCGGGAAAGTCTGACAATA.....	24	3	1	1.00	1	1	0	0	0	0	0
.....CGGGAAAGTCTGACAATA.....	18	0	1	1.00	1	1	0	0	0	0	0
.....GCTGTATCGTTAGTTTTTCCCGGA.....	24	2	1	1.00	1	1	0	0	0	0	0
.....TTTTTCCGGGAAAGTCTGACAAT.....	22	2	1	1.00	1	1	0	0	0	0	0
.....ATTTTCCGGGAAAGTCTGACAA.....	22	3	2	0.50	1	1	0	0	0	0	0
.....ACTTTCCGGGAAAGTCTGACAATA.....	24	3	2	0.50	1	1	0	0	0	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6328:2897732-2897940 +	dmo_3129	GTCTATCGATGACCGCCCAA----ATCGATATTGCCGATTGTGAGCGGCAGAGATGGCACCGT------ATATGAACCCGAAGGCCCTTTCAGACTGTTATCTATGGCCAATACGACGAATCACATAGCAATCAAAAAGGGCCTCTTGCTTCATACGCCTATCCACGGCGTTGCACTC---ACTTCCTAGCTGAGATTCGATGCG-----AACTTATCGA----TAATGCT
droVir3	scaffold_13042:903124-903341 +	dvi_82	GT-TATCG-TTATCGGTTAAGTT-ATCGTTATTGTT-ATCGTTATCGTTATCGTTATCGTGTGTTTGCATCTGAGCCAAAAGGCCCTTTCAGACTGTTATCTATGAGTAGTCAAAAAATCGCACATAGCAGTCGAAAAGGGCCTTCGCTTCATATGCG--------ACGTGGCACTCTAAATTTTTAAGTTTAGCTTTTCTTTGGCATAGAG-TCTCGGTTTTTAATGCT
droGri2	scaffold_15081:2041247-2041363 +		GGCTCACTCAGATTCCCGCC---CACGAATGCTGTTGCCCGTGCGT----------CATTTGAGAGGATAGGCCCTCTTA-ACTGTT----ATGATTAGTCGAAAAATTCACATAGCAGCTAAAAAAGGGCCTTT----------Y----------Y----------Y----------Y----------Y----------Y----------

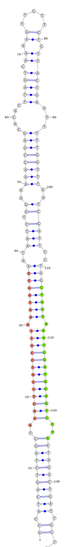
Generated: 09/08/2015 at 08:07 PM

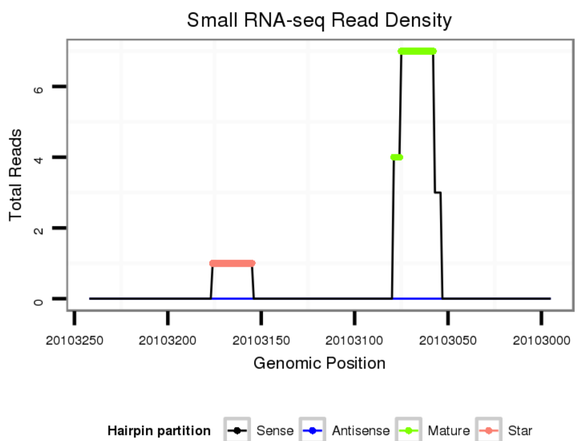
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	1

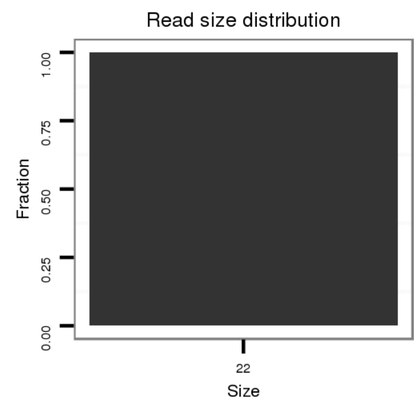
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_2682	**scaffold_6540:20103045-20103192 -**	**candidate**	**Canonical miRNA**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

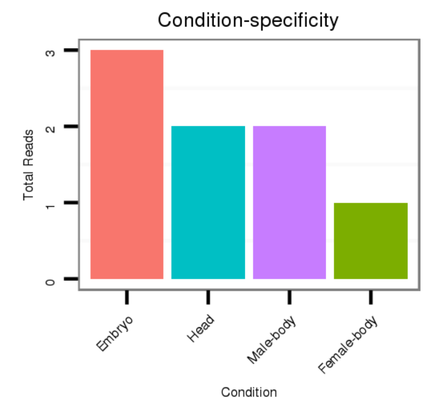
Legend: mature star mismatch in alignment mismatch in read

Predicted structure









No conservation details.

Show Alternate Folds

Flybase annnotation

intron [DmojGI22708-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

```
TTTATAAAAGTTTATTGAAATAAAATTATTTTATATAATGATAGAGCGTAAGCCATCAGTCTAGCTAGACTTCATCCATTAAATAGTTAATAATCTGGAAAAACCGAGCACACTTAGTCAAAAGTTCTTCTCTTACTGAATTTTTGGTTTGATCGATTCCTAGCTATTAAATGGATGGAGTCCTGCTAGGCTGATTGCTATCATATCCTATCTCTTTCACGATATGTGATCTATTGGGTCGTGCACTA
************************************************((.(((((((((..((((((((((((.(((((((..((((.((..(((((((((.....(((((.((.((.....)).)))))))...)))))))).))))))).))))))).))))))))).))))))))))))))..))))))))))).))..**********************************************
.......................................................................................................................................CTATTAAATGGATGGAGTCCTG.......................................................
.......................................................................................................................................TAAATGGATGGAGTCCTGCTAG.......................................................
.............................................................AGACTTCATCCATTAAATAGTT.......................................................
```

Read size	# Mismatch	Hit Count	Total Norm	Total	V049 head	V041 embryo	V110 male body	M046 female body	M060 embryo	V056 head
22	0	1	4.00	4	1	0	1	1	0	1
22	0	1	3.00	3	0	1	1	0	1	0
22	0	1	1.00	1	0	1	0	0	0	0

Anti-sense strand reads

```
AAATATTTTCAAATAACTTTATTTTAATAAAATATATTACTATCTCGCATTCGGTAGTCAGATCGATCTGAAGTAGGTAATTTATCAATTATTAGACCTTTTTGGCTCGTGTGAATCAGTTTTCAAGAAGAGAATGACTTAAAAACCAAACTAGCTAAGGATCGATAATTTACCTACCTCAGGACGATCCGACTAACGATAGTATAGGATAGAGAAAGTGCTATACACTAGATAACCCAGCACGTGAT
************************************************((.(((((((((..((((((((((((.(((((((..((((.((..(((((((((.....(((((.((.((.....)).)))))))...)))))))).))))))).))))))))).))))))))))))))..))))))))))).))..**********************************************
```

Read size	# Mismatch	Hit Count	Total Norm	Total	V110 male body	V049 head

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6540:20102995-20103244	dmo_2682	TTTATAAAAGTTTATTGAAATAAAATTATTTTATATAATGATAGAGCGTAAGCCATCAGTCTAGCTAGACTTCATCCATTAAATAGTTAATAATCTGGAAAAACCGAGCACACTTAGTCAAAAGTTCTTCTCTTACTGAATTTTTGGTTTGATCGATTCCTAGCTATTAAATGGATGGAGTCCTGCTAGGCTGATTGCTATCATATCCTATCTCTTTCACGATATGTGATCTATTGGGTCGTGCACTA

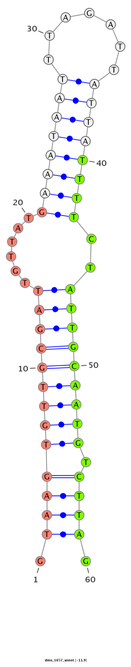
PASS/FAIL	
crit.star	0
crit.loop	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

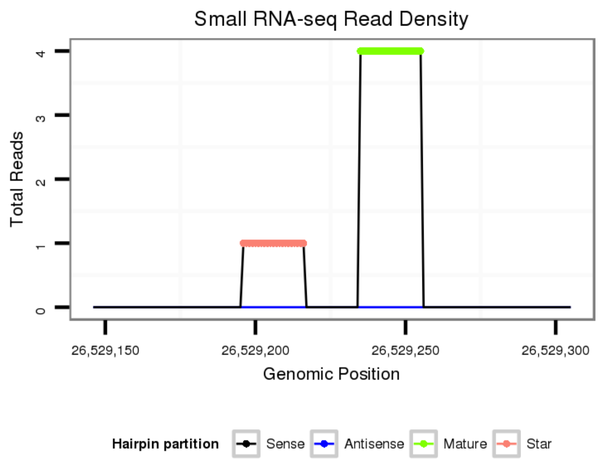
Generated: 06/06/2015 at 07:59 PM

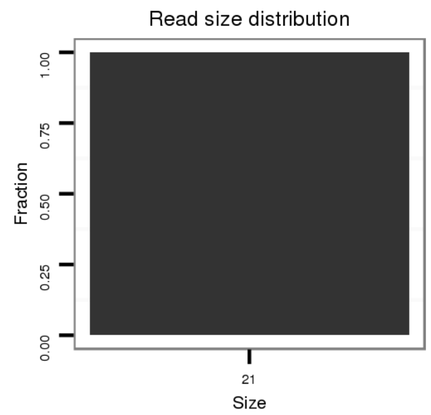
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_1657	**scaffold_6500:26529196-26529255 +**	**confident-exception**	**Mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

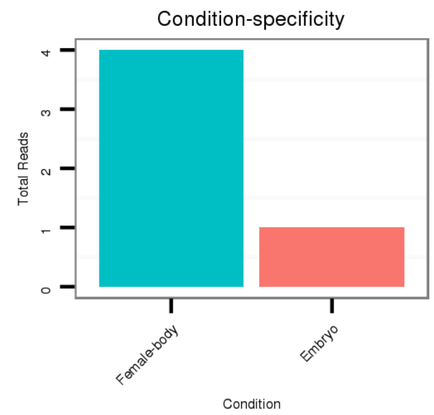
Legend: mature star mismatch in alignment mismatch in read

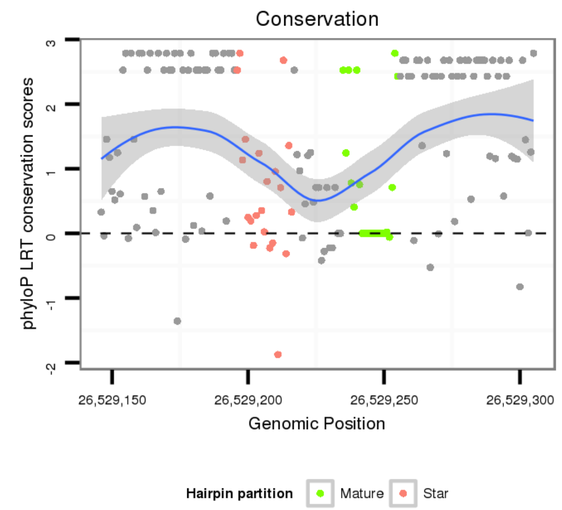
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dmoj\GI18116-in]; CDS [Dmoj\GI18116-cds]; CDS [Dmoj\GI18116-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

TCTGCAAGGATAAATATCATTTGCAGGTCTCCGAAGCAGCGATGGAGAAGGTAAGTGTTGCGATTGTTATGAAATAATTTAGATTATTATTTTCTATTGCAATGTCTTAGGAACCAAATGTAGCTCTCACTGAGATCGATATGCTGCATGTGAAAAAGGA	Read size	# Mismatch	Hit Count	Total Norm	Total	M046 female body	M060 embryo	V110 male body	V049 head	V056 head
**********.(((((((((((.....(((((((.....)))))))).))))))))).))))).***********										
.....TTTTCTATTGCAATGTCTTAG.....	21	0	1	4.00	4	3	1	0	0	0
.....TTTTCTATTGCAATGTCTTAGT.....	22	1	1	4.00	4	2	2	0	0	0
.....TTTTCTATTGCAATGTCTTAGA.....	22	1	1	2.00	2	2	0	0	0	0
.....TTTTCTATTGCAATGTCTTAGC.....	22	1	1	2.00	2	0	2	0	0	0
.....TTTTCTATTGCAATGTCTTAGTC.....	23	2	1	1.00	1	0	1	0	0	0
.....GTAAGTGTTGCGATTGTTATG.....	21	0	1	1.00	1	1	0	0	0	0
.....TTTTCTATTGCAATGTCTTAGTT.....	23	2	1	1.00	1	1	0	0	0	0

Anti-sense strand reads

AGACGTTCCTATTTATAGTAAACGTCCAGAGGCTTCGTCGCTACCTCTTCCATTCACAACGCTAACAATACTTTATTAAATCTAATAATAAAAGATAACGTTACAGAATCCTTGGTTTACATCGAGAGTGACTCTAGCTATACGACGTACACTTTTTCCT	Read size	# Mismatch	Hit Count	Total Norm	Total	M046 female body	V110 male body
**********.(((((((((((.....(((((((.....)))))))).))))))))).))))).***********							

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6500:26529146-26529305 +	dmo_1657	TCTGCAAGGATAAATATCATTTGCAGGTCTCCGAAGCAGCGATGGAGAAGGTAAGTGTTGC----------GATTGTTATGAAATAA------T---------TTAGATTATTATTTTCTATTGCAATGTCTTAGGAACCAAATGTAGCTCTCACTGAGATCGATATGCTGCATGTGAAAAAGGA
droVir3	scaffold_13246:2450609-2450676 +		TCTGCAAAGATAAATATCATTTGCAGGTCTCCGAAGCAGCCATGGAAAAGGTAAATATT--**********----------**-**---------**********A********TTAA**********GAAA
droGri2	scaffold_15252:5898314-5898504 +		TTTGTCAGGATAAATATCATTTGCAGGTCTCCGAAGCAGCCATGGAAAAGGTAACCATTCC----------CTACGTATTTTACACACTT---CTATCAATTTAATTTTGATCATTTATTATTATTAATATTTTGTGTAATTTATTAT-------**********-**---------**********T********CACAGGAACCCAATGTCGCCTCACAGAGATTGATATGCTGCATGTGAAAAAGGA
droWil2	scf2_1100000004521:9768079-9768238 +		ACTGCAAGGATAAATATCATCTGCAGGTATCTGATGCCGCCATGGAAAAGGTAAGTTTTC----------**********----ACTCCAAAATGTATGCATATAGAGTAATTTATTTCGT--TTTTCTA---------TTTAGGAACCAAATGTCGCACTCACCGAGATCGATATGCTGCATGTGAAAAAAGA
dp5	4_group3:4847726-4847892 -		TCACCAAGGACAGGTACCACTTGCAGGTTTCCGATGCCGCCATGGAAAAGGTGGTTTT--**********GTTTTC----------TTTCTTTCTTACC----------TTTA-----CCCCTTTTAATAGCATATGTAT---------T---------TTTCGTT--------TTTAGGAACCGAACGTGCTCTCACTGAGATTGATATGCTGCATGTGAAAAAGGA
droPer2	scaffold_1:6338860-6339026 -		TCACCAAGGACAGGTACCACTTGCAGGTCTCCGATGCCGCCATGGAAAAGGTGGTTTT--**********GTTTTC----------TTTCTTTCTTACC----------TTTA-----CCCCTTTTAATACATATGTAT---------T---------TTTCGTT--------TTTAGGAACCGAACGTGCTCTCACTGAGATTGATATGCTGCATGTGAAAAAGGA
droAna3	scaffold_12916:1871634-1871809 +		ACTGCCGGGACAAGTATCATCTGCAGGTTTCGGACGCCGCCATGGAGAAGGTGAACCC--A----------TCCCCATACCC----ATTT----------AGCTTTCGCTATC----------GCTTCTGTAGCTCGTTCTCAAGTCA------T---------A---------TTTCTTA--------CCTAGGAACCCAATGTCGCACTTACCGAGATCGATATGCTACACGTACGCAAGGA
droBip1	scf7180000396728:528585-528760 +		ATTGCCGGGACAAGTATCATCTGCAGGTTTCAGACGCCGCCATGGAGAAGGTGAACC--CA----------ACCCCATACCC----CTTT----------CGCTTTCGCTATC----------GCTTCTGTAGCTCGTTCTCAAGTCA------T---------A---------TTTCTTA--------CCTAGGAACCCAATGTCGCACTTACCGAGATCGATATGCTGCACGTACGCAAGGA
droKik1	scf7180000302270:648373-648533 -		TCTGCCGGGAAAAGTACCATCTGCAGGTGTCCGACGCCGCCATGGAGAAGGTGAATGCCGCCATTTTGGCACATTTAA**********CAGTCCCTTTTCAAGTCA------T---------A---------TATCTTA--------TTTAGGAACCAAATGTCGCACTTACCGAGATCGATATGCTGCATGTGCGCAAGGA
droFic1	scf7180000453904:64428-64603 +		ACTGCCGGGACAAGTACCACCTGCAGGTCTCGACGCCGCCATGGAGAAGGTGATCGATCA----------GTTTCACACAA-----CC----------CCCTTTCCGTACC----------GCTTCTGCAGCCCCTTCTCAAGTCA------T---------G---------TTTCTTA--------CCTAGGAACCCAATGTCGCTCTACCGAGATCGATATGCTGCACGTCCGCAAGGA
droEle1	scf7180000490728:648200-648387 +		ACTGCCGCGATAAGTACCATCTGCAGGTCTCGACGCCGCCATGGAGAAGGTGAACGATCA----------ATTCAATTCCGCCCAATTTCTA--G----CCCCCTTTCCGTACC----------GCTTCCGCAGCACGTTCTCAAGCCA------C---------A---------TTTCTTA--------TCTAGGAACCAAATGTCGCACTTACCGAGATCGATATGCTGCACGTCCGCAAGGA
droRho1	scf7180000777918:14604-14785 +		ACTGCCGGGACAAATACCATTTGCAGGTATCGACGCCGCCATGGAGAAGGTGAACGATCA----------ATACAATATTTCAACATTT----------CCCATTCCGTCCC----------GCTTCCGTAGCTCATTTTCAAGTCA------T---------A---------TTTCTTA--------TCTAGGAACCAAATGTCGCACTTACCGAGATCGATATGTTGCACGTCCGCAAAGGA
droBia1	scf7180000302261:2264588-2264763 +		ACTGCCGGGACAAGTACCACCTGCAGGTCTCGACGCCGCCATGGAGAAGGTGAACGATCA----------ATTCAATGC------ATTT----------CCCTTTCCGTACC----------GCTTCTGCAGCCCAATTTCAAGTCA------T---------A---------TTTCTTA--------TCTAGGAACCAAATGTCGCACTTACCGAGATCGATATGCTGCACGTCCGCAAAGA
droTak1	scf7180000415874:59293-59447 +		ATTGCCGGGATAAGTACCATCTGCAGGTCTCGACGCCGCCATGGAGAAGGTGAACGATCG----------A**********TATC----------GCTTCTGTAGCCCCTTTTCAAGTCA------T---------A---------TTTCTTA--------TCTAGGAACCAAATGTCGCACTTACCGAGATCGATATGCTGCACGTCCGCAAGGA
droEug1	scf7180000409554:2206131-2206306 -		ATTGTCCGGACAAATACCATCTGCAGGTCTCGATGCCGCCATGGAGAAGGTGAACGATCA----------ATTTAATAC------ATTT----------CCCTTTACGTACC----------GCTTCTGTAGTCCATTTTCAAGTCA------T---------A---------TTTCTTA--------TGTAGGAACCAAATGTCGCACTTACCGAGATCGATATGCTGCACGTCCGAAAGGA
dm3	chr2L:3866937-3867118 +		ATTGCCGGGACAAATACCATTTACAGGTGTCGACGCCGCCATGGAAAAGGTGAACGATCA----------ATTCAATTCAATTGAATTT----------CCCCTTCCGTACC----------GCTTCTGTAGTCCATTTTCAAGTCA------T---------A---------TTTCTTA--------TCTAGGAACCAAATGTCGCACTTACCGAGATCGATATGCTGCACGTCCGCAAAGGA
droSim2	2l:3718223-3718404 +	dsi_21127	ATTGCCGGGACAAATACCATTTGCAGGTGTCGACGCCGCTATGGAAAAGGTGAACGATCA----------ATTCAATTCAATTGAATTC----------CCCCTTCCGTACC----------GCTTCTGTAGTCCGTTTTCAAGTCA------T---------A---------TTTCTTA--------TCTAGGAACCAAATGTCGCACTTACCGAGATCGATATGCTGCACGTCCGCAAGGA
droSec2	scaffold_5:1968262-1968443		ATTGCCGGGACAAATACCATTTGCAGGTGTCGACGCCGCTATGGAAAAGGTGAACGATCA----------ATTCAATTCAATTGAATTC----------CCCCTTCCGTACC----------GCTTCTGTAGTCCGTTTTCAAGTCA------T---------A---------TTTCTTA--------TCTAGGAACCAAATGTCGCACTTACCGAGATCGATATGCTGCACGTCCGCAAAGA
droYak3	2L:3872690-3872871 +		ATTGCCGGGACAAATACCATTTACAGGTGTCGACGCCGCCATGGAAAAGGTGAACGATCA----------ATTCAATTCAATTGAATTT----------CCCCTTCCGTACC----------GCTTCTCTAGTCCATTTTCAAGTCA------T---------A---------TTTCTTA--------TCTAGGAACCAAATGTCGCACTTACCGAGATCGATATGCTGCACGTCCGCAAAGGA
droEre2	scaffold_4929:3918653-3918834 +		ATTGCCGGGACAAATACCATTTACAGGTGTCGACGCCGCCATGGAAAAGGTGAACGATCA----------ATTCAATTCAATTGAATTT----------CCCCTTCCGTACC----------GCTTCTGTAGTCCATTTTCAAGTCA------T---------A---------TTTCTTA--------TCTAGGAACCAAATGTCGCACTTACCGAGATCGATATGCTGCACGTCCGCAAAGGA

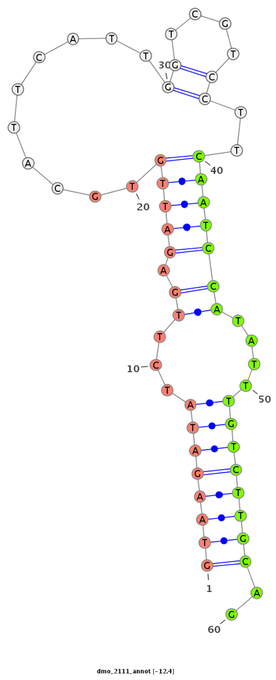
Generated: 09/08/2015 at 07:06 PM

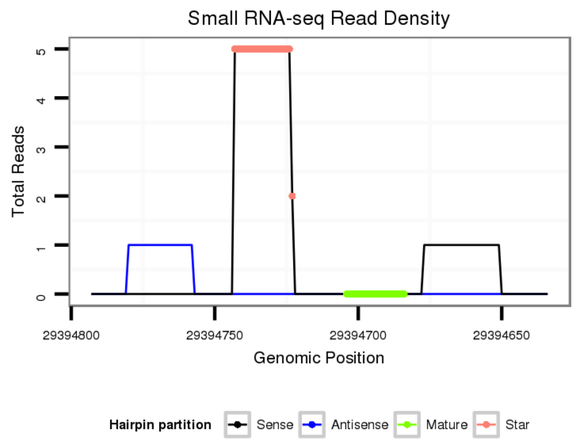
	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

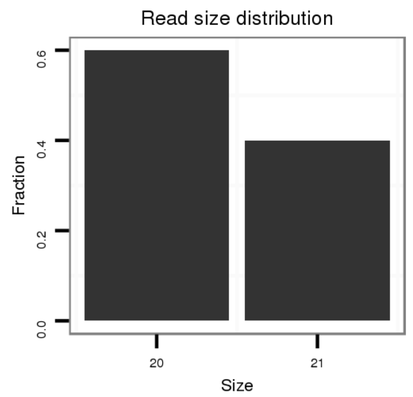
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_2111	**scaffold_6540:29394684-29394743 -**	**confident-exception**	**Mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

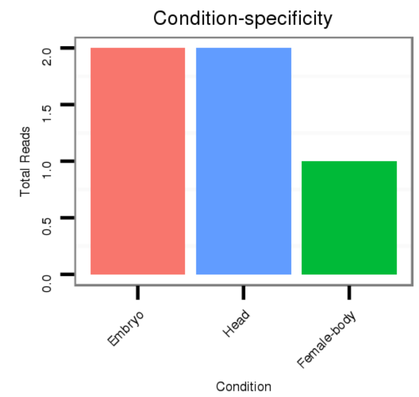
Legend: mature star **mismatch in alignment** mismatch in read

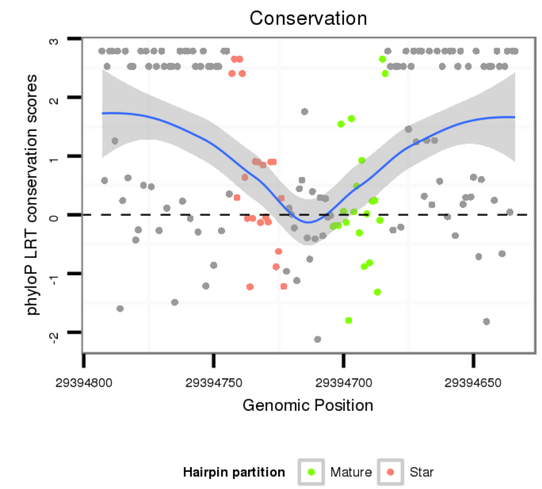
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [DmojGI22184-in]; CDS [DmojGI22184-cds]; CDS [DmojGI22184-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

TGGATCTGCTGCCGCTCTCCACCAGCGGTGACATTACCGTGGCAGGCATAGTAAGATATCTTGAGATTGTGCATTCATTGGTCGTCCTTCAATCCATATTTGTCTTGCAGACGGCGGACGAGTATCTGGTTGAGTATGATCGACTACGCGGCACAGAATA	Read size	# Mismatch	Hit Count	Total Norm	Total		M060 embryo	V049 head	M046 female body	V110 male body	V041 embryo
(((((((...((.((((.....((....)).)))))))....)))))))..	22	1	1	7.00	7	6	1	0	0	0
.....CAATCCATATTTGTCTTGCAGT.....	20	0	1	3.00	3	0	2	1	0	0
.....GTAAGATATCTTGAGATTGT.....	21	0	1	2.00	2	1	0	0	0	1
.....GTAAGATATCTTGAGATTGTG.....	27	0	1	1.00	1	0	0	0	1	0
.....GACGAGTATCTGGTTGAGTATGATCGA.....	22	1	1	1.00	1	1	0	0	0	0
.....CAATCCATATTTGTCTTGCAGC.....	26	1	1	1.00	1	1	0	0	0	0
.....CCTTCAATCCATATTTGTCTTGCAGT.....										

Anti-sense strand reads

ACCTAGACGACGGCGAGAGGTGGTCGCCACTGTAATGGCACCGTCCGTATCATTCTATAGAACTCTAACACGTAAGTAACCAGCAGGAGGTTAGGTATAAACAGAACGTCTGCCGCCTGCTCATAGACCAACTCATACTAGCTGATGCGCCGTGTCTTAT	Read size	# Mismatch	Hit Count	Total Norm	Total		M060 embryo	V110 male body
(((((((...((.((((.....((....)).)))))))....)))))))..	23	0	1	1.00	1	1		0
.....CGAGAGGTGGTCGCCACTGTAAT.....								

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6540:29394634-29394793 -	dmo_2111	TGGATCTGCTGCCGCTCTCCACCAGCGGTGACATTACCGTGGCAGGCATAGTAAGATATCTTGAGAT----------TGTGCAT-TCATTG----------G----TCGTCCTTC----------A-ATCCA---T----ATTTG-TCTTGCAGACGGCGGACGAGTATCTGGTTGAGTATGATCGACTACGCGGCACAGAATA
droVir3	scaffold_13047:12422700-12422859 +		TCGATTTGCTAGCGCTCTCAACCAGCGGAGACATAAGAGTTGCAGGCATTGTAAGATGACTCGAGATTTTGGCCAT----A-------------------TATGCAACCTCTTATGGGT--------------------------------------T----ATTTA-TTTTCAGACGGCGGATGAGTATCTGGTTGAGTATGATAGATTACGTGGCAGCGAATA
droGri2	scaffold_14830:707031-707130 -		TGGATCTGTTGCCCTGTCGACGAGTGGAGACATTAGCGTTGCCGGCATT----------TGACTCTCTTTAGTTC----------T----TTGAC----CT----------TAC-CCT---T----AAATCCCTTGCAGACGGCGGATGAGTATCTCGTCGAATATGATAGACTACGCGGCAGTGAATA
droWil2	scf2_1100000004943:11644420-11644574 -		TGGATCTTCTGCCATTGTCCACCAGTGGCGACATTAGAGTGGCAGGCATTGTAAGTAGA--------------TGACTCTCTTTAGTTC----------T----TTGAC----CT----------TAC-CCT---T----AAATCCCTTGCAGACGGCGGATGAGTATCTCGTCGAATATGATAGACTACGCGGCAGTGAATA
dp5	2:6452838-6452998 -		TGGATCTACTGCCCTTGTCCACCAGCGGCGACATCACTGTGGCAGGAATTGTAAGTGGA-TCGTTATTTCCGCCAT-----------GATA----------C----------CTATGAGTATTAATTGA-ATCCA---T----T-TTTACAGACAGCGGATGAGTACTTGGTCGAGTACGACAGCTGCGCGGCAGCGAATA
droPer2	scaffold_0:278721-278885 -		TGGATCTACTGCCCTTGTCCACCAGCGGCGACATCACTGTGGCAGGAATTGTAAGTGGA-TCGTTATTACCGCCAT---GA-------------TATGTA----------C----------CTATGAGTATTAATTGA-ATGTA---T----T-TTTACAGACAGCGGATGAGTACTTGGTCGAGTACGACAGCTGCGCGGCAGCGAATA
droAna3	scaffold_13340:8589777-8589929 -		TGGATCTACTGCCATCTGTCCACCAGCGGCGACATTAGTGTAGCCGGAATTGTAAGTAAA--------------TTA---------AATTTTCTTATC----------T----CC-AATT--G----------GGC-TTGAAATATTC-----TTGGACAGACTGGAGATGAGTACCTGGTTGAGTACGACCGTCTAGGGGCACCGAGTA
droBip1	scf7180000396708:248847-248999 +		TGGATCTATTGCCTCTGTCCACCAGTGGCGACATTAGTGGCCGGAATTGTAAGTATA--------------TAA-AAAT-----TTTA--CTATC----------T----GAAA-TTG----------GTC-TTCAAATATCG-----TTGGACAGACTGGAGATGAATACCTGGTCGAGTACGACCGTCTGAGAGGCACCGAGTA
droKik1	scf7180000302388:1485428-1485583 +		TGGATCTGCTGCCCTTGTCCACCAGTGGCGATATAGAGTAGCTGGCATTGTAAGTTAA--------------TTTAAT-ATATTT--C----------C----TTTTTATAT----------A-TTTAAAATATTT---TA-AACTATAGACAGCGGATGAGTATCTGGTCGAGTACGACAGCCTAAGAGGTACCGAGTA
droFic1	scf7180000454106:734086-734249 -		TGGATCTGCTGCCTCTTTCCACAAGTGGAGACATCACAGTGGCCGGCATTGTAAGTAGC--------------CAAAAAATTT---------AACTTCGTAAGATATCCTTTT----AATAT----------A-CTCTC---T----AATTA-TTTTTAGAGTGGAGATGAGTATCTGGTCGAATACGACAGACTGCCGGGCACTGAATA
droEle1	scf7180000491212:2023537-2023706 -		TGGATCTTCTGCCCCTGTCCACAAGTGGTGACATCAGAGTTGCTGGAATTGTAAGTAGTG--------------AAA-TTATTCAAA-A-----AACTTCTTGTAGAATTTTACT----AATA-TTC----------TAT-CTA---T----AAATT-TCTTGAAGACTGGAGATGAGTATCTGGTCGAGTACGATAGACTACGCGGCAGTGAGTA
droRho1	scf7180000779489:20087-20255 +		TGGATCTCCTGCCCCTGTCCACAAGTGGTGACATCAGAGTGGCCGGCATTGTCAGTAGC--------------AAA-ATATGCTAA-T-----AACTTCTTAAGGAATACGACT----AATA-TTT----------TTT-CTC---T----CAATT-TCTTGTAGAGTGGAGATGAGTATCTGGTCGAATATGACAGACTACGCGGTAGCGAATA
droBia1	scf7180000302402:6517089-6517256 +		TGGATCTTCTTGCCCTGTCCACCAGTGGCGATATCAGAGTCGCCGGCATTGTTAGTATC--------------TAA-ACTTTGAAA-T-----CACTTCTTAAAGAACGCTTCT----AAGA-ACA----------CAT-CTT---T----TATT-ATGTTCAGACCGGAGATGAGTACCTGGTCGAATATGACAGACTGCGCGGCAGTGAGTA
droTak1	scf7180000415711:1552230-1552394 +		TGGATCTGCTGCCCTTGTCCACCAGTGGCGATATCAGAGTGGCCGGCATAGTAAGTATC--------------TAC-ATGTACAGA-A-----CATTTTTTAA---TAGTTCT----ATCA-TGT----------CAT-CTA---T----TAA-T-TCTTGTAGAGTGGCGATGAGTATCTGGTCGAATATGACAGACTGCGAGGCACTGAATA
droEug1	scf7180000409490:894173-894341 -		TGGATCTGCTGCCCTTGTCCACCAGTGGTGATATCAGTGTGGCTGGTATAGTAAGTATC--------------AGA-ATCCTCAAT-A-----AATTTCTTAAATAATATTTTT----AATA-CCT----------ATT-TTT---T----AAATT-TCTTGTAGAGTGGAGATGAGTATCTTGTCGAATATGATAGACTTCGCGGGAAGTGAATA
dm3	chr3R:17599802-17599956 -		TGGATCTTTTGCCCTTGTCCACCAGTGGTGACATCAGAGTGGCTGGCATTGTTAGTACC--------------AGT-AAACTCTATTAAAATT----------C----TTGTAATAA----------A-TTTCA---T----AT-TTTACTAGAGTGGTGATGAGTATCTTGTCGAGTACGACAGACTGCGAGGCACTGAATA
droSim2	3r:17111718-17111872 -		TGGATCTTCTGCCCTTGTCCACCAGTGGCGACATCAGAGTAGCTGGCATTGTAAGTACC--------------AGT-GAAGTCAATTAAAATT----------C----TTGTAATAA----------A-TTTTA---T----AT-TTTACTAGAGTGGTGATGAGTATCTTGTCGAGTACGACCGACTGCGAGGCACTGAATA
droSec2	scaffold_0:17972010-17972164 -		TGGATCTTCTGCCCTTGTCCACCAGTGGCGACATCAGAGTAGCTGGCATTGTAAGTACC--------------AGT-GAAGTCAATTAAAATT----------C----TTGTAATAA----------A-TTTCA---T----AT-TTTACTAGAGTGGTGATGAGTATCTTGTCGAGTACGACCGACTGCGAGGCACTGAATA
droYak3	3R:18416158-18416315 -		TCGATCTTCTGCCCTTGTCCACCAGTGGCGACATCAGAGTGGCTGGCATTGTAAGTACC--------------TAT-TACA-----T---TTT--CTATTAAATTT----------C----TTATGATAA----------A-TTTCA---T----ATTTTTGCCAGAGTGGTGATGAGTATCTGGTCGAGTACGACAGACTGCGAGGCACTGAATA
droEre2	scaffold_3511:4541-4694 +		TGGATCTTCTGCCCTTGTCCACCAGTGGCGACATCAGAGTGGCTGGAATTGTAAGATTT--------------CGA-CTA-TTTATTACATTT----------C----CCCTAATGA----------A-TTTCA---T----AA-CTTGCTAGAGTGGCGATGAGTATCTGGTCGAGTATGACAGACTGCGAGGCACTGAATA

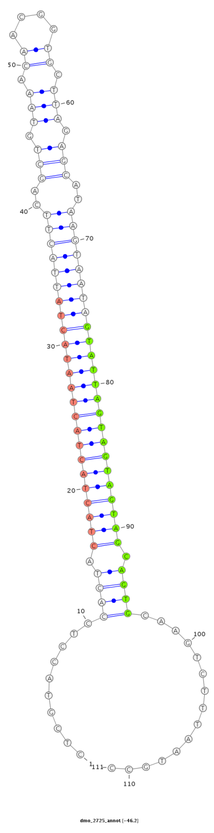
Generated: 09/08/2015 at 07:06 PM

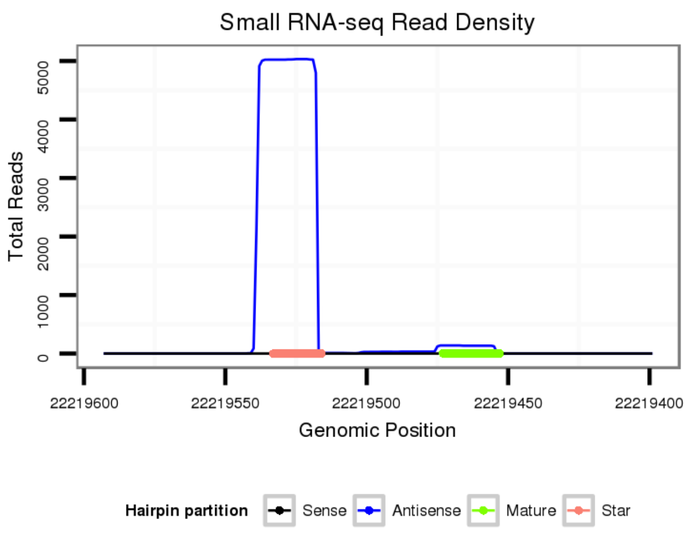
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

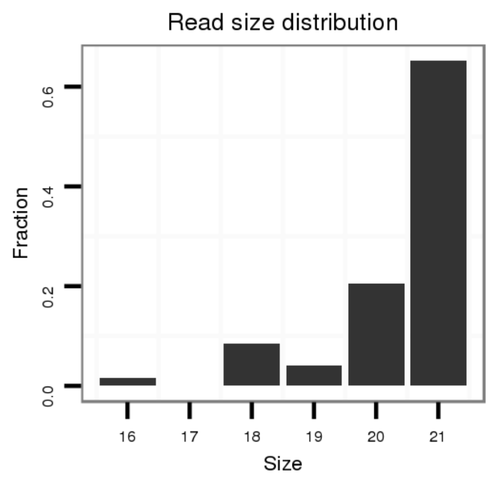
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_2725	**scaffold_6540:22219449-22219543 -**	**candidate**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

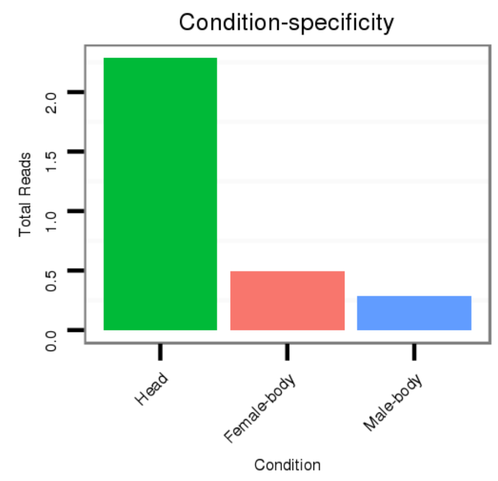
Legend: mature star **mismatch in alignment** mismatch in read

Predicted structure









No conservation details.

Show Alternate Folds

Flybase annnotation

intergenic

Repeatable elements

Name	Class	Family	Strand
(TAG)n	Simple_repeat	Simple_repeat	+

mature	star
	1. scaffold_6308:1825525-1825542 + 2. scaffold_6308:2493144-2493161 + 3. scaffold_6308:2493186-2493203 + 4. scaffold_6308:2493207-2493224 + 5. scaffold_6308:2493249-2493266 + 6. scaffold_6308:2493270-2493287 + 7. scaffold_6473:10689136-10689153 + 8. scaffold_6473:10963671-10963688 + 9. scaffold_6496:12174768-12174785 - 10. scaffold_6496:12174798-12174815 - 11. scaffold_6496:21496561-21496578 - 12. scaffold_6500:15602454-15602471 + 13. scaffold_6500:19922451-19922468 + 14. scaffold_6540:3314867-3314884 - 15. scaffold_6540:8931758-8931775 + 16. dmo_30 scaffold_6540:22219458-22219475 + 17. dmo_2725 scaffold_6540:22219516-22219533 - 18. scaffold_6680:3820134-3820151 - 19. scaffold_6680:14552076-14552093 - 20. scaffold_6680:14552130-14552147 -

Sense Strand Reads

hide 3p reads show mid mismatch reads

CAATAGCGCCATCAATCTAGTATAATATAGTTAAAGTACTAAATACTCGTACCTCCACTACTACTACTACTAATACTATTACTTCAGCTGTAAACAACGGTGCTTAGAGCATAAGTAATAGTATTAGTAGTAGTAGCAGTGCAAGTCTTTAATGCCTTTAACTACATATATTATGCTAGTAGAAGAAAACTATAT	Read size	# Mismatch	Hit Count	Total Norm	Total	V110 male body	M046 female body	V056 head	V049 head
**********									
.....GTATTAGTAGTAGTAGCAGTG.....	21	0	1	2.00	2	0	0	1	1
.....GTATTAGTAGTAGTAGCAGTGT.....	22	1	1	1.00	1	1	0	0	0
.....GTATTAGTAGTAGTAGCAGT.....	20	0	7	0.43	3	2	1	0	0
.....GTATTAGTAGTAGTAGCAGTGG.....	22	1	8	0.25	2	1	1	0	0
.....CTACTACTACTAATACTA.....	18	0	20	0.15	3	0	3	0	0
.....CTACTACTACTACTAATACT.....	20	0	8	0.13	1	0	1	0	0
.....GTATTAGTAGTAGTAGCAG.....	19	0	8	0.13	1	0	0	0	1
.....GTATTAGTAGTAGTAGCA.....	18	0	9	0.11	1	0	0	1	0
.....TACTACTACTACTAATACTA.....	20	0	13	0.08	1	0	1	0	0
.....GTATTAGTAGTAGTAG.....	16	0	20	0.05	1	0	0	1	0

Anti-sense strand reads

GTTATCGCGGTAGTTAGATCATATTATATCAATTTCATGATTTATGAGCATGGAGGTGATGATGATGATGATTATGATAATGAAGTCGACATTTGTTGCCACGAATCTCGTATTCATTATCATAATCATCATCATCGTCACGTTCAGAAATTACGGAAATTGATGTATATAATACGATCATCTTCTTTTGATATA	Read size	# Mismatch	Hit Count	Total Norm	Total	M046 female body	V110 male body	V056 head	V049 head	M060 embryo	V041 embryo
**********											
.....GTGATGATGATGATGATTATG.....	21	0	1	2712.00	2712	1600	692	227	190	1	2
.....GGTGATGATGATGATGATTATG.....	22	0	1	1955.00	1955	659	1274	19	3	0	0
.....TGTGATGATGATGATGATTATG.....	22	1	4	166.50	666	203	438	20	5	0	0
.....ATCATAATCATCATCATCGTC.....	21	0	7	96.71	677	643	23	8	3	0	0
.....TGATGATGATGATGATTATG.....	20	0	7	92.71	649	262	345	24	18	0	0
.....GGTGATGATGATGATGATTAT.....	21	0	1	79.00	79	61	17	0	1	0	0
.....GTGATGATGATGATGATTAT.....	20	0	1	79.00	79	79	0	0	0	0	0
.....AGGTGATGATGATGATGATTAT.....	22	0	1	68.00	68	30	30	7	1	0	0
.....AGTGATGATGATGATGATTATG.....	22	1	4	23.50	94	35	46	11	2	0	0
.....GATGATGATGATGATTATG.....	19	0	9	17.33	156	103	40	4	9	0	0
.....TTTGTTGCCACGAATCTCGTATTCATT.....	27	0	1	12.00	12	8	3	0	1	0	0
.....AGGTGATGATGATGATGATTATG.....	23	0	1	11.00	11	5	5	0	1	0	0
.....ATCATAATCATCATCATCGTCA.....	22	0	7	11.00	77	75	0	1	0	1	0
.....CGTGATGATGATGATGATTATG.....	22	1	4	9.50	38	7	27	3	1	0	0
.....ATCATAATCATCATCATCGT.....	20	0	8	9.13	73	73	0	0	0	0	0
.....CGGTGATGATGATGATGATTATG.....	23	1	1	8.00	8	3	3	1	1	0	0
.....CTTTGTTGCCACGAATCTCGTATTCATT.....	28	1	1	7.00	7	6	1	0	0	0	0
.....GGAGGTGATGATGATGATGATT.....	22	0	1	6.00	6	2	3	1	0	0	0
.....TCATAATCATCATCATCGTCAC.....	22	0	1	6.00	6	5	0	0	1	0	0
.....ATTTGTTGCCACGAATCTCGTATTCATT.....	28	0	1	6.00	6	2	2	1	1	0	0
.....TCATAATCATCATCATCGTC.....	20	0	7	5.86	41	41	0	0	0	0	0
.....TTGTTGCCACGAATCTCGTATTCATT.....	26	0	1	5.00	5	3	1	0	1	0	0
.....TCATAATCATCATCATCGTCA.....	21	0	7	4.57	32	32	0	0	0	0	0
.....TGGTGATGATGATGATGATTATG.....	23	1	17	4.12	70	14	49	6	1	0	0
.....CTGATGATGATGATGATTATG.....	21	1	15	3.27	49	27	18	3	1	0	0
.....TATCATAATCATCATCATCGTC.....	22	0	1	3.00	3	1	1	1	0	0	0
.....TCTCGTATTCATTATCATAATC.....	22	0	1	3.00	3	3	0	0	0	0	0
.....TGATTATGATAATGAAGTCGA.....	21	0	1	2.00	2	0	1	1	0	0	0
.....TGATTATGATAATGAAGTCGAC.....	22	0	1	2.00	2	1	1	0	0	0	0
.....CCACGAATCTCGTATTCATT.....	20	0	1	2.00	2	2	0	0	0	0	0
.....CATTTGTTGCCACGAATCTCGTATTCATT.....	29	0	1	2.00	2	2	0	0	0	0	0
.....TGATGATTATGATAATGAAGTC.....	22	0	1	2.00	2	1	1	0	0	0	0
.....CTGTGATGATGATGATGATTATG.....	23	2	4	2.00	8	2	6	0	0	0	0
.....ATGATGATGATGATTATG.....	18	0	15	1.60	24	2	2	7	13	0	0
.....TGTGATGATGATGATGATTAT.....	21	1	7	1.43	10	10	0	0	0	0	0
.....ATGATTATGATAATGAAGTCGA.....	22	0	1	1.00	1	1	0	0	0	0	0
.....CTGATTATGATAATGAAGTCGA.....	22	1	1	1.00	1	0	1	0	0	0	0
.....AGATGATTATGATAATGAAGTCG.....	23	1	1	1.00	1	0	1	0	0	0	0
.....CCTCGTATTCATTATCATAATCAT.....	24	1	1	1.00	1	1	0	0	0	0	0
.....AGGTGATGATGATGATGATTA.....	21	0	1	1.00	1	1	0	0	0	0	0
.....CTAATGAAGTCGACATTTGTTGCCA.....	25	1	1	1.00	1	1	0	0	0	0	0
.....GTTGCCACGAATCTCGTATTCATT.....	24	0	1	1.00	1	1	0	0	0	0	0
.....ATGATTATGATAATGAAGTCG.....	21	0	1	1.00	1	1	0	0	0	0	0
.....ATAATGAAGTCGACATTTGTTGCCACG.....	27	0	1	1.00	1	1	0	0	0	0	0
.....GAGGTGATGATGATGATGATTATG.....	24	0	1	1.00	1	0	1	0	0	0	0
.....CTTTGTTGCCACGAATCTCGTATTCAT.....	27	1	1	1.00	1	1	0	0	0	0	0
.....CTGATTATGATAATGAAGTCG.....	21	1	1	1.00	1	1	0	0	0	0	0
.....GACATTTGTTGCCACGAATC.....	20	0	1	1.00	1	0	1	0	0	0	0
.....TGATGATTATGATAATGAAGT.....	21	0	1	1.00	1	1	0	0	0	0	0
.....CTCGTATTCATTATCATAATCA.....	22	0	1	1.00	1	0	1	0	0	0	0
.....CTGTTGCCACGAATCTCGTATTCATT.....	26	1	1	1.00	1	0	1	0	0	0	0
.....CTGATTATGATAATGAAGTCGAC.....	23	1	1	1.00	1	0	1	0	0	0	0
.....TTGTTGCCACGAATCTCGTATTCAT.....	25	0	1	1.00	1	1	0	0	0	0	0
.....CCTTATGATAATGAAGTCGACAT.....	23	2	1	1.00	1	1	0	0	0	0	0
.....GGTGATGATGATGATGATTA.....	20	0	4	1.00	4	4	0	0	0	0	0
.....CTCATAATCATCATCATCGTC.....	21	1	10	1.00	10	10	0	0	0	0	0
.....TGATGATGATGATGATTAT.....	19	0	15	0.87	13	13	0	0	0	0	0
.....TCATAATCATCATCATCGT.....	19	0	8	0.63	5	4	1	0	0	0	0
.....AAGGTGATGATGATGATGATTAT.....	23	1	2	0.50	1	1	0	0	0	0	0
.....GTGATGATGATGATGATTA.....	19	0	4	0.50	2	2	0	0	0	0	0
.....CTCATAATCATCATCATCGTCA.....	22	1	7	0.43	3	3	0	0	0	0	0
.....GATGATGATGATGATTAT.....	18	0	17	0.41	7	7	0	0	0	0	0
.....GTGATGATGATGATTATG.....	18	1	20	0.40	8	6	0	0	2	0	0
.....CATAATCATCATCATCGTC.....	19	0	8	0.38	3	3	0	0	0	0	0
.....AGTGATGATGATGATGATTAT.....	21	1	6	0.33	2	2	0	0	0	0	0
.....AATCATAATCATCATCATCGTCA.....	23	1	9	0.33	3	3	0	0	0	0	0
.....AATCATAATCATCATCATCGTC.....	22	1	10	0.30	3	3	0	0	0	0	0
.....CGTGATGATGATGATGATTAT.....	21	1	4	0.25	1	1	0	0	0	0	0
.....ATCATAATCATCATCATCG.....	19	0	8	0.25	2	2	0	0	0	0	0
.....GGTGATGATGATGATGATT.....	19	0	5	0.20	1	1	0	0	0	0	0
.....CCGGTGATGATGATGATGATTATG.....	24	2	5	0.20	1	0	1	0	0	0	0
.....GTGATGATGATGATGATT.....	18	0	6	0.17	1	1	0	0	0	0	0
.....AATCATAATCATCATCATCGT.....	21	1	12	0.17	2	2	0	0	0	0	0
.....GGTGATGATGATGATGAT.....	18	0	20	0.15	3	3	0	0	0	0	0
.....ATCATAATCATCATCATC.....	18	0	20	0.15	3	3	0	0	0	0	0
.....CTGATGATGATGATTATG.....	18	1	20	0.15	3	2	0	1	0	0	0
.....CATAATCATCATCATCGTCA.....	20	0	7	0.14	1	0	0	0	1	0	0
.....GATCATAATCATCATCATCGTC.....	22	1	7	0.14	1	1	0	0	0	0	0
.....TTCATAATCATCATCATCGTC.....	21	1	7	0.14	1	0	1	0	0	0	0
.....TCATAATCATCATCATCG.....	18	0	9	0.11	1	1	0	0	0	0	0
.....AGCTATCATAATCATCATCATCGT.....	24	3	11	0.09	1	1	0	0	0	0	0
.....CTCGGTGATGATGATGATTATG.....	25	3	11	0.09	1	0	1	0	0	0	0
.....GGATGATGATGATGATTATG.....	20	1	20	0.05	1	0	0	1	0	0	0
.....TGATGATGATGATGATTA.....	18	0	20	0.05	1	1	0	0	0	0	0
.....CTGATGATGATGATGATTAT.....	20	1	20	0.05	1	1	0	0	0	0	0
.....TGGTGATGATGATGATGATTAT.....	22	1	20	0.05	1	0	0	1	0	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6540:22219399-22219593 -	dmo_2725	CAATAGCGCCATCAATCTAGTATAATATAGTTAAAGTACTAAATACTCGTACCTCCACTACTACTACTACTAATACTATTACTTCAGCTGTAAACAACGGTGCTTAGAGCATAAGTAATAGTATTAGTAGTAGTAGCAGTGCAAGTCTTTAATGCCTTTAACTACATATATTATGCTAGTAGAAGAAAACTATAT

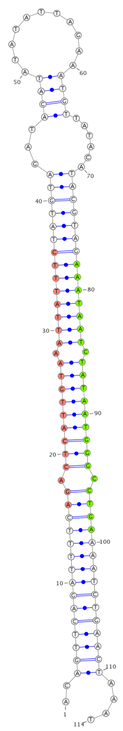
Generated: 09/08/2015 at 08:01 PM

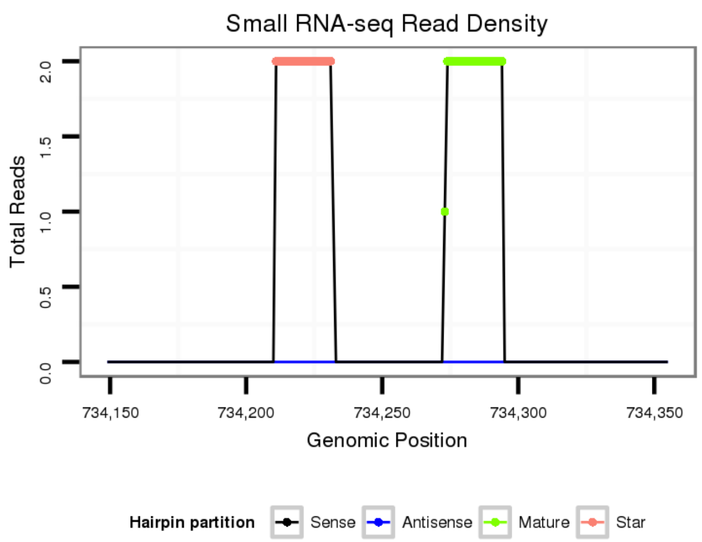
	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

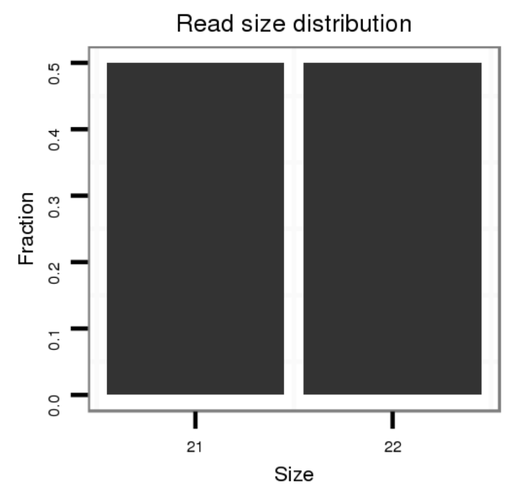
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_3073	**scaffold_6482:734199-734305 +**	**candidate**	**Canonical miRNA**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

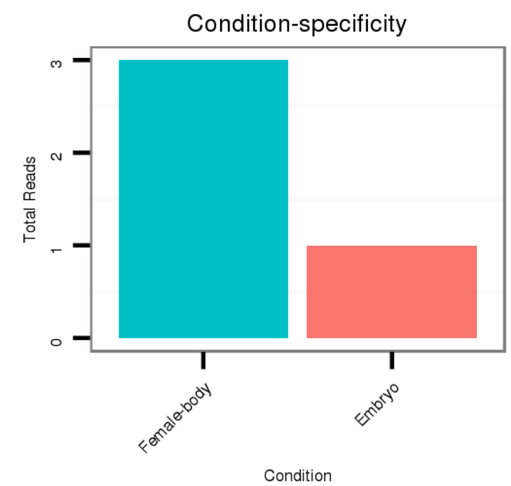
Legend: mature star **mismatch in alignment** mismatch in read

Predicted structure









No conservation details.

Show Alternate Folds

Flybase annnotation

intron [Dmoj\GI14403-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

AGAATGGACTGAATTGGATCAGTGGGATGTAGCATAAATGAGATATAACAGTTCAGATTTTCAGACTCATTGTAAATTATTTCTATGTAGATACATATATATTAGAAATGTTATACATACGTAGAAATAATCTATAATGGGCCTGAAAATCTGAACTAAATGTCAAGTATTACATTAAAGTTAATGGCGCAATGAACTGAGATGGGA	Read size	# Mismatch	Hit Count	Total Norm	Total	M046 female body	M060 embryo	V110 male body
**********..((((((((((((((.(((((((((.(((((((((((((...((((..........))))......)))))))))))))).)))))))))).))))))))))))))....**********								
.....AAATAATCTATAATGGGCCTGA.....	22	0	1	1.00	1	0	1	0
.....AGACTCATTGTAAATTATTTC.....	21	0	1	1.00	1	1	0	0
.....AGACTCATTGTAAATTATTTCT.....	22	0	1	1.00	1	1	0	0
.....AATAATCTATAATGGGCCTGA.....	21	0	1	1.00	1	1	0	0

Anti-sense strand reads

TCTTACCTGACTTAACCTAGTCACCCTACATCGTATTTACTCTATATTGTCAAGTCTAAAAGTCTGAGTAACATTTAATAAAGATACATCTATGTATATATAATCTTTACAATATGTATGCATCTTTATTAGATATTACCCGGACTTTTAGACTTGATTTACAGTTCATAATGTAATTTCAATTACCGCGTTACTTGACTCTACCCT	Read size	# Mismatch	Hit Count	Total Norm	Total	V110 male body
**********..((((((((((((((.(((((((((.(((((((((((((...((((..........))))......)))))))))))))).)))))))))).))))))))))))))....**********						

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6482:734149-734355 +	dmo_3073	AGAATGGACTGAATTGGATCAGTGGGATGTAGCATAAATGAGATATAACAGTTCAGATTTTCAGACTCATTGTAAATTATTTCTATGTAGATACATATATATTAGAAATGTTATACATACGTAGAAATAATCTATAATGGGCCTGAAAATCTGAACTAAATGTCAAGTATTACATTAAAGTTAATGGCGCAATGAACTGAGATGGGA

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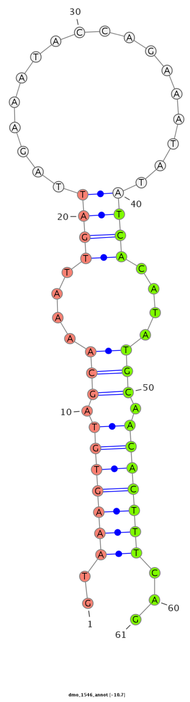
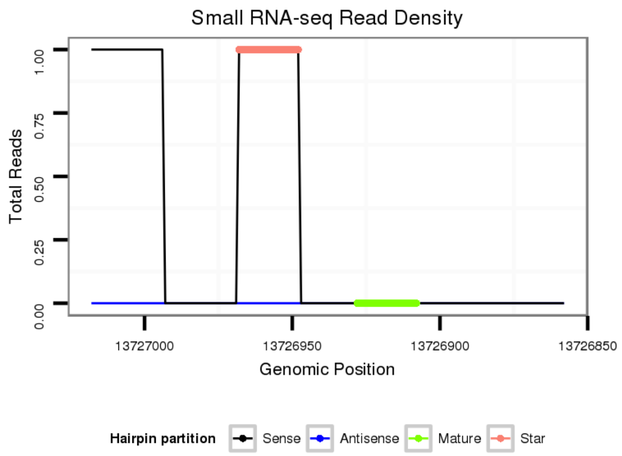
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

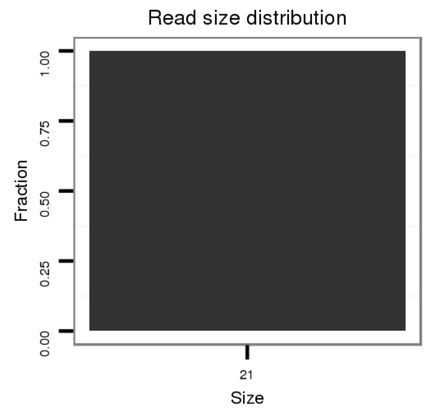
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_1546	**scaffold_6500:13726908-13726968 -**	**candidate**	**Mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

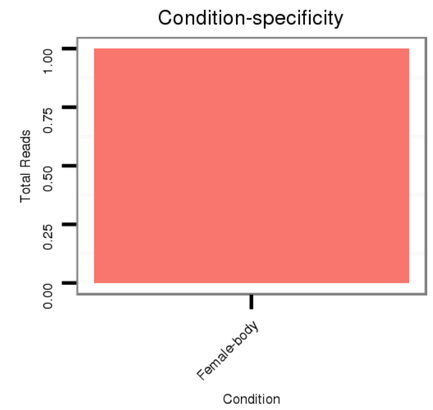
Legend: mature star mismatch in alignment mismatch in read

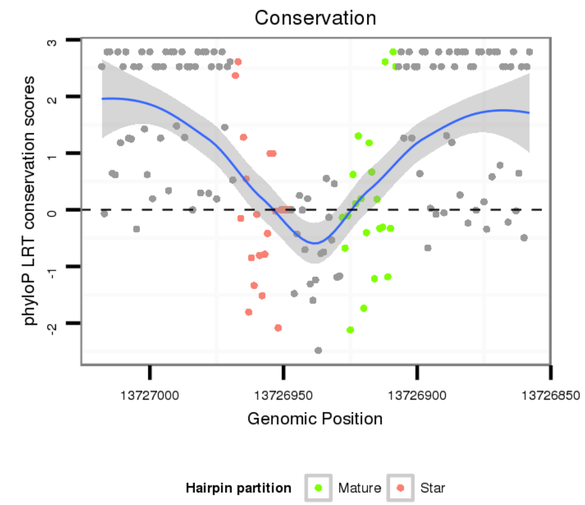
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dmoj\GI11283-in]; CDS [Dmoj\GI11283-cds]; CDS [Dmoj\GI11283-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

CGAAGCTCCAGCGAGATTTGCGCGAAAATGTGGCACAAAAGGAAGATCAGGTAAAGTGTAGCAAAATTGATTAGAAATACCAGAAATATATCACATATGCAACACTTTCAGGAGGAGCGCATAGCTACACTGGAGAAACGTTATCTCAATGCTCAACGGGA **********..(((((((.(((....((((.....))))....))).)))))))...**********						M060	M046 female embryo	body	V110 male body
Read size	**# Mismatch**	**Hit Count**	**Total Norm**	**Total**					
.....TCACATATGCAACACTTTCAGT.....	22	1	1	3.00	3	2	0	1	
.....GTAAAGTGTAGCAAAATTGAT.....	21	0	1	1.00	1	0	1	0	
CGAAGCTCCAGCGAGATTTGCGCGA.....	25	0	1	1.00	1	0	1	0	
.....GTAAAGTGTAGCAAAATTGATG.....	22	1	1	1.00	1	0	1	0	
.....CACATATGCAACACTTTCAGTG.....	22	2	1	1.00	1	0	1	0	
.....CACATATGCAACACTTTCAGA.....	21	1	1	1.00	1	1	0	0	

Anti-sense strand reads

GCTTCGAGGTCGCTCTAAACGCGCTTTTACACCGTGTTTTCCTTCTAGTCCATTTCACATCGTTTTAACTAATCTTTATGGTCTTTATATAGTGTATACGTTGTGAAAGTCCTCCTCGCGTATCGATGTGACCTCTTTGCAATAGAGTTACGAGTTGCCCT **********..(((((((.(((....((((.....))))....))).)))))))...**********					M046 female body
Read size	**# Mismatch**	**Hit Count**	**Total Norm**	**Total**	

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6500:13726858-13727018 -	dmo_1546	CGAAGCTCCAGCGAGATTTGCGCGAAAATGTGGCACAAAAGGAAGATCAGGTAAAGTG---TAGCAAA-----ATTGATTAGAA-ATACCAGA-AATATAT----------CACATATGC-AACA-CTTTCAGGAGGAGCGCATAGCTACACTGGAGAAACGTTATCTCAATGCTCAACGGGA
droVir3	scaffold_12963:3354910-3355072 -		CGAAGCTGCAGCGCGATCTGCGCGAAAATGTGGCACAAAAGGAAGATCAGGTGCGTAACCATTACA---T-TA-----ATAT-ATTTAAAG-TATATA--T----------AAAAAA---TTAT--AAAATTCA-TTTGTAGGAGGAGCGTATAATACGCGTGGAAAGCGCTATTTGAATGCTCAACGCGA
droGri2	scaffold_15252:2926591-2926752 -		CGAAGCTGCAGCGTGATCTGCGCGAAAATGTGGCACAAAAGGAGGATCAGGTAAGTAAACATAACAAA-----TT-----CAATTTGCATCAAAACTGAT----------TTTATATTTGATGA-CCTGTAGGAAGAGCGTATTACTACGCTCGAGAAGCGTTACTTGAATGCACAACGTGA
droWil2	scf2_1100000004585:7336305-7336483 +		CAAAATTGAACGTGATCTAGGTGAGAATGTGGCTCAAAAGGAAGATCAGGTAAGAGCAACTATTC----TTTT-----TTTT-TAATTAA-------GTGACATTTTAATTCGCCCGCTTTCTCTCT-A--TCTCTTCACTTTCCAGGAGGAACGCATTGCCACGCTGGAGAAGCGATATCTGAATGCTCAGCGAGA
dp5	4_group1:3826259-3826358 +		CCAAGCTGCAGCGTGATCTTGGCGAGAATGTGGCCCAAAAGGAGGACC----------GC-------C-----C-----------C-------C-------C-------C-----C-----AGGAGGAGCGCATAACCACGCTGGAGAAGCGCTATGTGAACGCGCACGCGGA
droPer2	scaffold_5:1443841-1443940 -		CCAAGCTGCAGCGTGATCTGCGCGAGAATGTGGCCCAAAAGGAGGACC----------GC-------C-----C-----------C-------C-------C-------C-----C-----AGGAGGAGCGCATAACCACGCTGGAGAAGCGCTATGTGAACGCGCACGCGGA
droAna3	scaffold_12916:8076-8233 -	dan_468	CTAAATTGCAGCGAGACCTGCGCGAAAATGTGGCCCAAAAAGAAGATCAAGTTAGTTAATGGTAGT--A--TCTG-----TTATT-TGTACGGT-ATCTAA----------TTAA--TAATTTTC-CGTTCAGGAGGAGCGCATTGCTACGCTGGAGAAACGCTATTTGAATGCTCAAAGGGA
droBip1	scf7180000392937:60476-60636 -		CCAAACTGCAGCGAGATCTGCGCGAAAATGTGGCCCAGAAAGAAGATCAGGTTAGTTGGTTATAGT--GGTTATA-----GTAT-TCTATGG-TTTCTA----------ATTTCATGTTTTCC-TCTTCAGGAGGAGCGCATTGCCACGCTGGAGAAGCGCTATTTGAATGCTCAAAGGGA
droKik1	scf7180000302468:437635-437799 -		CCAAGCTGCAGCGAGATCTGCGCGAAAATGTGGCTCAAAAGGAGGATCAGGTGAGAATATCAAGTT----TATA-----TAAT-TTTATTGG-TTTCTA-AT----------GAATTT---TTTC--TAATTTTT-CTTTTAGGAGGAGCGCATTACTACACTGGAAAAACGCTACGCTAAATGCCCAGAGAGA
droFic1	scf7180000453815:51508-51664 +		CCAAGCTGCAGAGAGATCTGCGCGAAAACGTGGCCCAAAAAGAGGATCAGGTAAAGGGATAGTTCT----CCTA-----TAACAATCTTGAA-TTTTAA----------CCTA---CTTTTGG-TTTACAGGAGGAGCGCATTGCGACTCTGGAGAAACGCTACCTGAATGCCCAGCGGGA
droEle1	scf7180000490640:397387-397545 +		CCAAGCTGCAGCGAGATTTGCGCGAAAATGTGGCCCAAAAAGAGGATCAGGTGAGTGCACTCGCAAA-----GT-----CTGTTTTCGTGGA-ACTTGTA----------TAAA--TCTTTTGA-TGTTCAGGAGGAGCGCATCAGCACGCTGGAGAAACGCTACCTGAATGCTCAGAGGGA
droRho1	scf7180000779930:2936-3093 -		CCAAGCTGCAGCGAGATTTGCGCGAAAATGTGGCCCAAAAAGAGGATCAGGTGAGAGGATAATGCA----AAGC-----ATATTGTCATAGA-TGTTTT----------TAAA--CCTGTTTA-AATTCAGGAGGAGCGCATTAGCACACTGGAGAAGCGCTACCTGAATGCTCAAAGGGA
droBia1	scf7180000302422:2485483-2485638 +		CCAAGCTGCAGCGAGATCTAGCGCAAAATGTGGCCCAGAAGGAGGATCAGGTGAGCGAAATATCTC----TTTT-----ATACT-TCATAAA-TTTTAA----------TCAA--TTTGTCGA-TTTCTAGGAGGAGCGCATCAGCACATTGGAGAAGCGCTACCTGAACGCTCAAAGGGA
droTak1	scf7180000415399:1446092-1446248 +		CAAAGCTGCAGCGAGATCTACGCGAAAATGTGGCCCAGAAAGAGGATCAGGTGAGGAAAAAACTCC----T-TT-----ATATATTCTTATA-TTTTAT----------TCAA--TCTATTGA-TTTACAGGAGGAGCGCATTAGCACATTGGAGAAGCGCTACCTGAATGCACAGAGGGA
droEug1	scf7180000409463:48290-48449 -		CCAAGCTGCAGCGAGATCTGCGCGAAAATGTGGCCCAGAAAGAGGATCAGGTGAGCTGCTAAGTCA----TAAA-----ATTCAGTCTTAAA-TTTATA----------CTTATATCTTTTGA-TTTCCAGGAGGAGCGCATAAGCACATTGGAGAAGCGCTACCTGAATGCTCAGAGGGA
dm3	chr2L:6726491-6726648 +		CCAAGCTGCAGCGCGATCTGCGCGAGAATGTGCCCAGAAAGAGGATCAGGTGAGTGAATAATACT----CACA-----GCATAGGTTTCAGT-TTTTTA----------CTTA--TAGGTTCA-TTTTTAGGAGGAGCGCATTAGCACATTGGAAAGCGATACCTGAATGCTCAGAGGGA
droSim2	2L:6499928-6500084 +		CCAAGCTGCAGCGCGATCTGCGCGAGAATGTGGCCCAGAAAGAGGATCAGGTGAGTGAATAATAAT----TACG-----GCAT-GGCTTGCG-TTTTTA----------TTCA--TAGGTTCA-TTTTCAGGAGGAGCGCATTAGCACATTGGAAAGCGATACCTGAATGCTCAGAGGGA
droSec2	scaffold_3:2265157-2265313 +		CCAAGCTGCAGCGCGATCTGCGCGAGAATGTGGCCCAGAAAGAGGATCAGGTGAGTGAATAATACT----CACG-----GCAT-GGCTTGCG-TTTTTA----------TTCA--TAGGTTCA-TTTTCAGGAGGAGCGCATTAGCACATTGGAAAGCGATACCTGAATGCTCAGAGGGA
droYak3	2L:6185259-6185415 -		CCAAGCTGCAGCGTGATCTGCGCGAAAATGTGGCCCAAAAAGAGGATCAGGTGAGTGAATAATACT----GATA-----ACAT-GTTTGCGG-TTTATA----------TTAA--CATGTTCA-TTTTCAGGAGGAGCGCATTAGCACATTGGAAAGCGATACCTGAATGCTCAGAGGGA
droEre2	scaffold_4929:15642942-15643098 +		CCAAGCTGCAGCGAGATCTGCGCGAAAATGTGGCCCAGAAAGAGGATCAGGTGAGTGAATAATAGT----TATA-----ACAT-GTTTGCGG-TTTATA----------TTAA--TATGTTCA-TTTTCAGGAGGAGCGCATTAGCACATTGGAAAGCGATACCTGAATGCTCAGAGGGA

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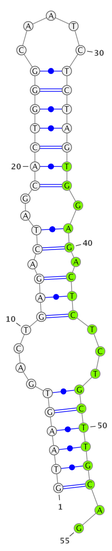
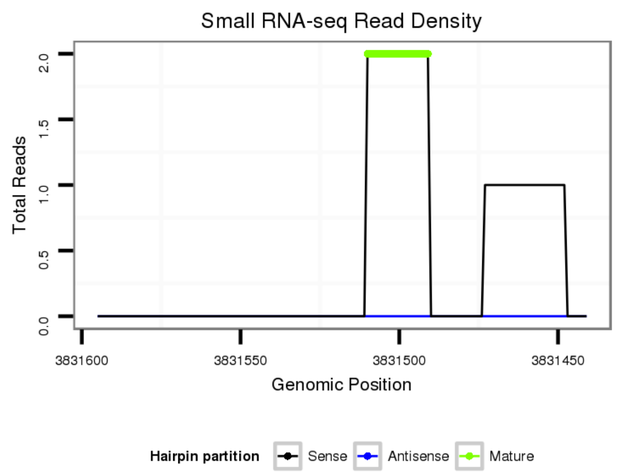
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

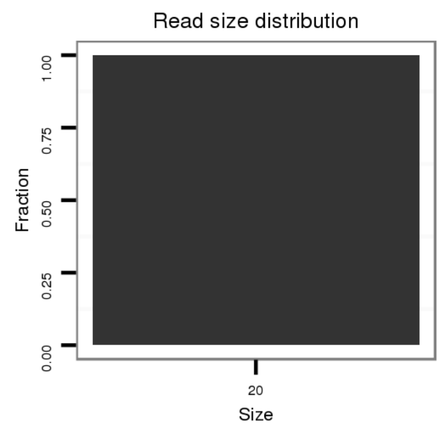
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_2337	**scaffold_6680:3831491-3831545 -**	**candidate**	**Mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

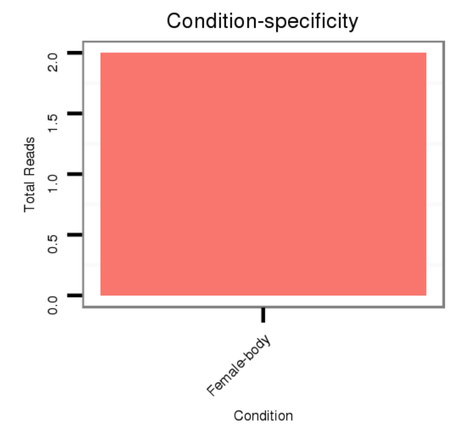
Legend: mature star mismatch in alignment mismatch in read

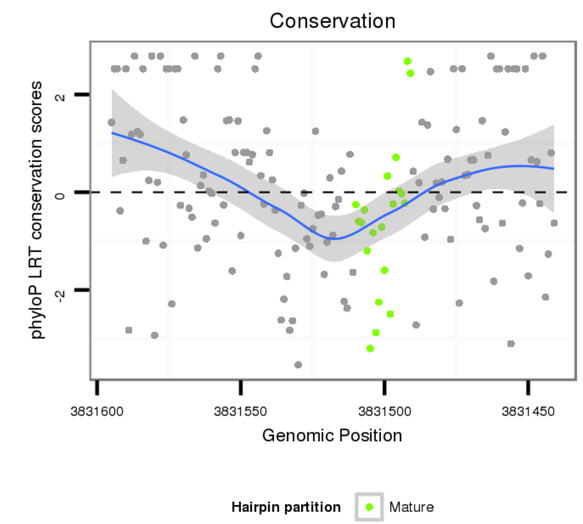
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dmoj\GI12456-in]; CDS [Dmoj\GI12456-cds]; CDS [Dmoj\GI12456-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

	Read size	# Mismatch	Hit Count	Total Norm	Total	M046 male body	M046 female body	V110 male body	V110 female body	M060 embryo	M060 male body	V056 head	V056 head	V049 head	V049 embryo
TCCGCCTCTGGCGCTCGTCGGGCGCAAGCTGCAGGCAGACTTCAGATACAGTAAGTGACTGAGACTAGCACTGGGCAATCTCTAGTGGAGACTCTCTGCTTGCAGCGCACTCCAAGTTCGGAGCAGGCGTCATTCCCTCTGGGTCGGAGATTTTC														
(((((((....(((.((..(((((((.....)))))))).)).)))...)))))))..															
.....TGGAGACTCTCTGCTTGCAGT.....	21	1	1	5.00	5	1		2		1		1		1	0
.....TGGAGACTCTCTGCTTGCAG.....	20	0	1	2.00	2	2		0		0		0		0	0
.....GCAGGCGTCATTCCCTCTGGGTCGGA.....	26	0	1	1.00	1	0		1		0		0		0	0

Anti-sense strand reads

	Read size	# Mismatch	Hit Count	Total Norm	Total	V110 male body	M046 female body	M060 embryo	V056 head	V049 head
AGGCGGAGACCGCGAGCAGCCCGCGTTCGACGTCCGTCTGAAGTCTATGTCATTCACTGACTCTGATCGTGACCCGTTAGAGATCACCTCTGAGAGACGAACGTCGCGTGAGGTTCAAGCCTCGTCCGCAGTAAGGGAGACCCAGCCTCTAAAAG										
(((((((....(((.((..(((((((.....)))))))).)).)))...)))))))..										

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6680:3831441-3831595 -	dmo_2337	TCCGCCTCTGGCGCTCGTCGGGCGCAAGCTGCAGGCAGACTTCAGATACAGTAAGTGACTGAGA---------CTAGCAC----------TGGGCAATCTCTAGTGGAGA----------CTC---TCTGCTTGCAGCGCACTCCAAGTTCGGAGCAGGCGTCATTCCCTCTGGGTCGGAGATTTTC
droVir3	scaffold_13049:5477250-5477410 -	dvi_18494	TCGCCCAGTGCCGCTAGTGGGACGCACGCTCCAAGCGGACTTTAAGTACTGTAAATGGGCGATA---------CCCAGAAC----------TGGGATGA---------CAC---CACATGCTAGAGAACA----------CCT---TTTGCTTGCAGCACATTCCAAGGTGGCCGATGGTGTTATACCCGCTGGCTCCGAGGTGATC
droGri2	scaffold_15110:13541835-13541993 +		TCCGCCAGTGCCCTGCTGGGACGCAAATTGCATTGGGACTTTAAGTACAGTAAGTGAGAAGACAAC-----TT------TAC-------TTTCT----------ACTTTCATT----------CGAACAAC---T--CTC---TCTCTCAACAGCCCACTCCAAGTGGGTGATGGTATCATTCCGCCGCGCGAGAGATCCTA
droWil2	scf2_1100000004511:6029988-6030156 -		TCCATCGGTGCCCTTGTAGGACGCAAATTGCAAACGGATTTCAAATACAGTAGGTGACAAAACATT--CTCTAATTGGTCAGA----CTTT----------TTTTT----------T------A--------AATCAT-TATTTC--TCG---ATTCTTCTAGGCCATTCAAAGTACGGTGATGGTATTTTGCCAGCTGGTACCGAGGTACTC
dp5	XR_group6:1487218-1487382 -		TCCGCCCGTGCCCTGGTGGGACGAAAGCTGCAAAGGGACTTCAAGTACAGTAGGTGTGAAGTAGTC-----TA------AAT--------AGAGT----------GCTTTCTCCAGGCTGTACTGACCC----------CCA---TCTGCTTGCAGGCCACTCCAAGTACGGCGATGGCGTTATTCCGGCCGGGTCTGAGTTTCTC
droPer2	scaffold_12:2176878-2177042 -		TCCGCCCGTGCCCTGGTCGGACGAAAGCTGCAAAGGGACTTCAAGTACAGTAGGTGTGAAGTAGTC-----TA------AAT------AGAGT----------GCTTTCTCCAGGCTCCACTGCTCC----------CCA---TCTTCTTGCAGGCCACTCCAAGTACGGCGATGGCGTTATTCCGGCCGGATCTGAGTTCCTC
droAna3	scaffold_13337:16274664-16274822 -		TCCGCCCGTGCCTATCGTGGGTCGTAAGCTGTCAATGATTTCAAGTACAGTGAGTACTCTTTA----------TGTAAACTGA----A----------TTA----------CAACCCTTAAAAAATTT----------GAA---TATTTGTTAGCCAATTCAAAGCATGGTGATGGTATTATCCCGGCTGGCTCTGAGATCATT
droBip1	scf7180000396589:166020-166178 +		CCCGCCAGTGCCTATTGTGGGTCGCAAGCTTGTCAATGACTTCAAGTATAGTAAGTACTCTTCA----------GATAATATGG----T----------TTT----------CAATCCTTAACACATTC----------CGA---TATTGGTTAGCCAATGCAAAGCATGGTGATGGAATTATTCCGGCTGGTGCTGAGATCGTT
droKik1	scf7180000301706:158265-158432 -		TCCACCCGTTCCGATTGTGGGACGCAAATTGCAAAAGGACTTTAAATACAGTAGGTGTGGTAGGG---------A-A-AATGGGG----ATTTTTAGTCTT--TCTTTT----------T------A--------TACATTTTT--TT--TTT---AATTTTTCCAGCCAACTCTACTTACGGAGATGGAGTACTACCAGCCGGCTCAGAGTTCTTA
droFic1	scf7180000453787:71380-71537 -		TCCACCTGTGCCTATCGTTGGCCGCAAAGTACAGAGTGACTTTAAATACAGTAGGTGTATCTTAA---AT----------TC---AA----------ATAATTTGTAAAG----------C-------AATCCAAC----------AAA---ATCCTTTTAGCAAACTCCAAATACGGAGATGGAGTAATCCCAGCTGGTTCAGAGATCATA
droEle1	scf7180000491193:2736071-2736237 -		TCCACCTGTGCCAATTGTGGGTCGCAAGCTACAGAGTGATTTTAAGTACAGTAGGTGTCTTACG---AA----------TT---TA----------ATAATCAATATGA---AAAAAT-T------A---AGT----TAAATGTT------TTA---CCTTCTTTCAGCGAATTCTGTGTACGGCGATGGAGTTATACCAGCGGCTCAGAGATTATA
droRho1	scf7180000779506:137145-137289 +		TCCGCCAGTGCCCATGATCGGCCGGTGTTCGCCGAGGATCTGGAAATACGTAGGTGGTGCGATTGAGAT----------CC---TA----------GTCCTCTATCTAA---TC----------AG-ACTCC----------TCT---TCTACTTTC----------AGGTGGCAAGCCGATTCCAGCCGGCAGTAACTTCACC
droBia1	scf7180000302193:6430662-6430826 -		TCCACCCGTGCCCATCGTGGGCCGCAAAGTGCAGAGTGATTTTAAGTACAGTGGGTGTGCATAGAAA-----T-----AC---TTATC-------TCATT----------ACTATCTGTAATATCTATTG---A----------CTT---TCTTCTCTCAGCGAATTGTGTGTACGGCGATGGAATAATTCCAGCGGCTCAGAGATCTTG
droTak1	scf7180000415773:147458-147613 +		TCCACCTGTGCCCATCGTGGGCCGCAAAGTGCAGAGTGACTTTAAATACAGTAGGTGTCTTATAATC--TTTT-GGTGGCA---TT----------GT-------TTCTTAT------C------A---------TG----------GA---ATATTTTTTAGCTAACTCTAAGTACGGCGATGGAGTAATTCCTGCCGGCTCAGAGATAATA
droEug1	scf7180000409215:179039-179198 +		TCCACCTGTGCCCATTGTGGGACGAAAGTTGCAGAGTGATTTTAAATACAGTAAGTGTTCCTGGG---------A-A-A-CC---TTGAC-------TTACTGAAATT----------T------A--------CCTAACGAT--T---A-T---ATCGCTTCTAGCTAATTCTGTGTATGGAGATGGAGTAATACCAGCGGTTCCGAGATTATA
dm3	chr3L:7487018-7487177 -		TCCACCAGTGCCCATCGTAGGGCGCAAATTGCAGAGCGACTTCAAATACAGTAGGATTCCTATA----------TTTAATCGCA----GTTTTCATAATC--GTAATT----------T------A--------TT----------TAA---TATTTTTCAGCCCATTCCGTGCATGGAGATGGAGTAATTCCGGCTGGCTGAGAGATTATA
droSim2	3L:7351407-7351578 -		TCCACCAGTGCCCATCGTAGGCCGAAATTGCAGAGCGACTTCAAATACAGTAAGATTCCTATA----------TTTAATCGCA----GTTTTCACAATG--TTAATT----------T------A--------TTTAATATT--TTTG--TAAAACCCTTTCAGCCCATTCCGTGCATGGAGATGGAGTAATTCCGGCTGGCTGAGAGATTATA
droSec2	scaffold_2:7417214-7417385 -		TCCACCAGTGCCCATCGTAGGGCGCAAATTGCAGAGCGACTTTAAATACAGTAGGGTTCCTATA----------TATAATCGTA----GTTTTCAAATTG--GTAATT----------T------A--------TTCAATATT--TTTG--TAAAACCCTTTCAGCCCATTCCGTGCATGGAGATGGAGTAATTCCGGCTGGCTGAGAGATTATA
droYak3	X:6270763-6270902 +		TCCGTCTGTGCCGCTCCTCGGTCGTAAGGTTCTCGAGACTGCGAGATCAGTGAGTACTGAGAGG---------GGAATCACA----CTTC----------TTCTTAACTTG----------G-----G----------CATTCTCCAATGCAGATGGAAAACTCATCCCGGCCGGCACGAATATCGGC
droEre2	scaffold_4784:3847017-3847185 +		TCCACCAGTGCCCATCGTAGGGCGCAAATTGCAGAGTGACTTTAAGTACAGTAGGTTTCGCAATT---------AATTCTAA----GTTTCCAAAATA--GCAATT----------T------A--------TTTAATGTC--CTTATTG---ACTCTTATCAGCCAACTCCGTGTATGGAGATGGAGTAATTCCAGCCGGCTCGGAGATTATA

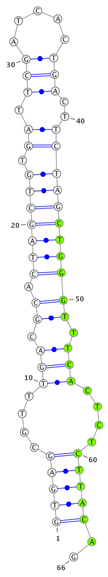
Generated: 09/08/2015 at 07:07 PM

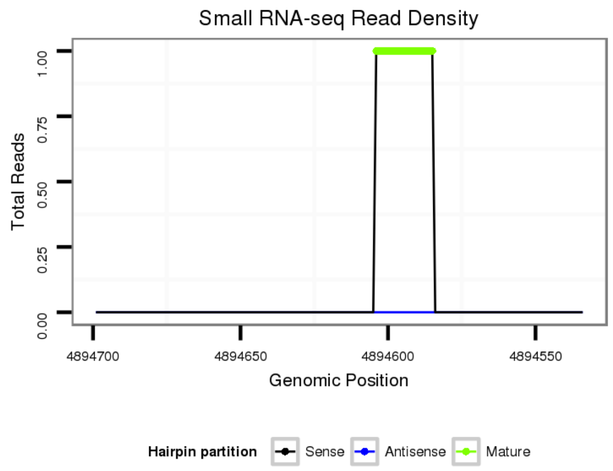
	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

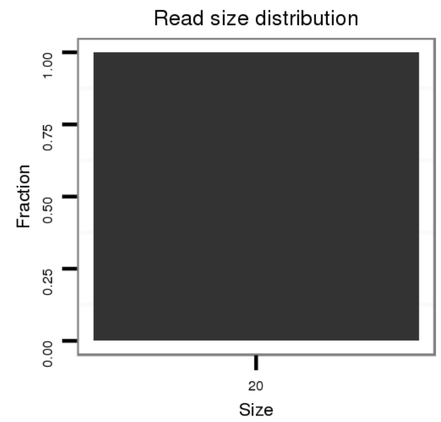
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_2353	**scaffold_6680:4894584-4894649 -**	**candidate**	**Mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

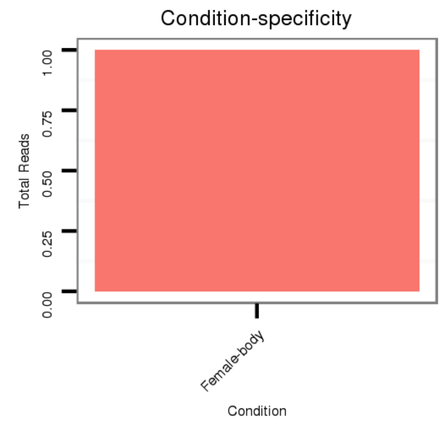
Legend: mature star mismatch in alignment mismatch in read

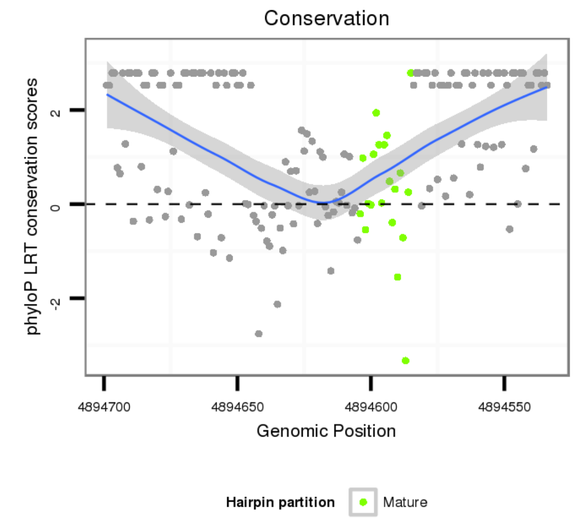
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [DmojGI12404-in]; CDS [DmojGI12404-cds]; CDS [DmojGI12404-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            
CCATACTGATCATTGCCTTTGGCCTCGCCTTCTACATCCTGCTGTCGAAGGTGAGCGTTTGACGCACTAGCTGTGATTCGATCACTGACTTCTAGCTGGGTTTCACTCTCTTACAGATCATCGATCCGCAGCCGAATCATCTGTCCTTCTCCAACATACCCATGTC   V056  M046 female  M060  V110
**********(((((....(((.((.(((((((.((.(((.....)))..)))))))))).)))....)))))..**********   Read size  #Mismatch  Hit Count  Total Norm  Total  head  body  embryo  male body
.....TGGGTTTCACTCTCTTACAGT.....   21  1  1  5.00  5  2  2  1  0
.....CTGGGTTTCACTCTCTTACAGT.....   22  1  1  4.00  4  1  1  1  1
.....CTGGGTTTCACTCTCTTACA.....   20  0  1  1.00  1  0  1  0  0
```

Anti-sense strand reads

```
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                
GGTATGACTAGTAACGGAAACCGGAGCGGAAGATGTAGGACGACAGCTTCCACTCGCAAACTGCGTGATCGACACTAAGCTAGTGACTGAAGATCGACCCAAAGTGAGAGAATGTCTAGTAGCTAGGCGTCGGCTTAGTAGACAGGAAGAGGTTGTATGGGTACAG   M046 female body  V110 male body  V056 head
**********(((((....(((.((.(((((((.((.(((.....)))..)))))))))).)))....)))))..**********   Read size  #Mismatch  Hit Count  Total Norm  Total
```

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6680:4894534-4894699 -	dmo_2353	CCATACTGATCATTGCCTTTGGCCTCGCCTTCTACATCCTGCTGTCGAAGGTGAGCGTTTGAC---GC----ACTAGCTGTGA----TTCGATC----------ACTGACTTCTAGCT-G-GGT-TTCA--------CTC----T---CTTACAGATCATCGATCCGCAGCCGAA------TCATCTGTCCTTCTCCAACATACCCATGTC
droVir3	scaffold_13049:6574813-6574973 -		CCATACTGATTATTGCTTTTGGCCTCGGATTCTACATATTGCTCTCGAAGGTGAGTGTCTGCC---TC----TGTA-------GCTTGACA----------AATAATTCTCTGAAATCT----------GGAATTTGT---------G----G----------G---T---TTTGCAGATTATTGACCCACAGCCGAA------TCACTTGTCCTTCTCGAACATACCCATGTC
droGri2	scaffold_15110:6197967-6198132 +		CCATATTGATTATTGCTTTTGGCCTGGCATTTTATATATTGCTCTCCAAGGTGAGTTTTTGCT---GA----------TGA----TTTGATT------AATCT-------TTT----------GCTT-AAGC-TTCACTTCTT---T----C---T-GCCAGATTATTGATCCACAGCCGAATCCCAATCACTTGTCCTTTTCAAATATACCCATGTC
droWil2	scf2_1100000004511:7920230-7920393 +		CCATTCTGATTATTGCTTTTGGCCTGGCCTTCTATATCCTACTCTCAAAGGTAGGTCACCACC---TTG---ATGGATGTGAGTTGTTTGATC----------AAAGA-TTCACTCTTT---T-CTCT---TCCCTAGATTATTGATCCACAACCGAA------TCACTTGTGATTCTCGAATATACCCATGTC
dp5	XR_group8:8672552-8672718 +		CCATACTGATCATTGCTTTTGGACTGGCCTTTTACATTTTGCTCTCGAAGGTGGGTTTCGTT---TGAGAGG------GTGAGTCGTTT----------GTG-GTATATATTTCC----AGAGAT-T---------TTCCTT----C---ATTCCAGATTATCGATCCACAGCCGAA------CCACTTATCCTTCTCGAACATACCGATGTC
droPer2	scaffold_50:526316-526482 -		CCATACTGATCATTGCTTTTGGACTGGCCTTTTACATTTTGCTCTCGAAGGTGGGTTTCGTT---TGAGAGG------GTGAGTCGTTT----------GTG-GTATATATTTCC----AGAGAT-T---------TTCCTT----C---ATTCCAGATTATCGATCCACAGCCGAA------CCACTTGTCCTTCTCGAACATACCGATGTC
droAna3	scaffold_13337:7761384-7761554 +		CCATACTGATTATTGCCTTTGGCCTGGCTTTCTATATACTGCTTTCAAAGGTGGGTTATT---T--C-GAAG------AT--------TAGAC-TTCTTTTCT----------TGAATCTAT--ATC---GTATAT---------G----G----------CTTCTGCCCTTTCCTTTGCAGATCATTGACCCCAGCCGAA------TCACTTGTCCTTCTCAAATATACCCATGTC
droBip1	scf7180000395543:427020-427182 +		CCATACTGATCATTGCCTTTGGCCTGGCTTTCTATATACTACTCTCAAAGGTGGGTTCTT---T--T-GAAG------AT-AGTCG----ATTTGGA----------ATCTAGAATCTAT--ATC---GTATAT---------G----G----------TT---C----T---CTTGCAGATCATTGACCCCAGCCGAA------TCACTTGTCCTTCTCAAATATTCCCATGTC
droKik1	scf7180000302486:1369989-1370146 -		CCATACTGATTATTGCCTTTGGCCTGGCTTTCTACATACTGCTGTCAAAGGTGGGTTAA----GAATGTTT--T---------G----TATTT------ATTA-------CTC----------GGTTATAAA--TTGACTTTAT---T----T---TTTGCAGATTATTGACCCCAACCGAA------CCACTTGTCCTTCTCCAACATACCCATGTC
droFic1	scf7180000451564:217236-217392 +		CCATACTGATCATTGCTTTCGGATTGGCTTTCTACATATTACTTTCGAAGGTAAGGCACCAA---ATAAAGA------T---G----------TGAGT-TTCCTAT----------T-AATT----TA-AGCATTTAT---------G----G----------T---TCCACAGATTATTGACCCGCAACCGAA------CCACTTGTCCTTCTCCAATATACCCATGTC
droEle1	scf7180000490564:117032-117185 -		CCATACTGATCATTGCCTTTGGCTTGGCTTTCTACATATTGCTCTCTAAGGTTGGCACTT--C---TA----------G----ATTGGGT-GTTTTAT----------TGCATTA--AA---AGCATTTAT---------G----G----------T---G----T---CCTGCAGATTATTGACCCCAACCGAA------CCACCTGTCCTTCTCGAACATACCCATGTC
droRho1	scf7180000766314:127204-127354 -		CCATACTGATCATTGCTTTTGGCCTGGCTTTCTATATACTACTCTCAAAGGTGGGTTGTTA--T---G----------G----TATTGGGT-TTCTTA----------ATATGT--ATT---GATTAT---------G----G----------T---G----T---CCTTCAGATTATTGACCCCAACCGAA------CCACTTGTCCTTCTCCAACATACCCATGTC
droBia1	scf7180000300910:2320463-2320621 +		CCATCCTGATCATTGCCTTCGGCCTGGCTTTCTACATACTGCTTTCAAAGGTGAGATAG----GACTTATT-T---------G----TGTA----------C-GTATATCATCCT----ATATATAT---G----ATCCTTCT--T---TCACTAGATTATTGACCCCAACCGAA------CCACTTGTCCTTCTCCAACATACCCATGTC
droTak1	scf7180000415356:322195-322347 +		CCATACTGATCATTGCCTTTGGCCTGGCTTTCTACATACTACTTTCAAAGGTCGGATATCT---G---T----------G----TA--TGGAAG-TT--TCA----------TGTATTT--AT---AGCTATTAT---------G----G----------TT---G----C---CACTAGATTATCGACCCCAACCGAA------CCACTTGTCCTTCTCCAACATCCCCATGTC
droEug1	scf7180000409467:98361-98515 -		CCATATTGATCATTGCTTTTGGCCTGGCTTTTTATATACTACTATCGAAGGTGAGCTTTTGGC---TATT--G----------G----ATTGGGA-GTT---------GA----------TATTCTT--AT---AGCTCTTAT---------G----G----------T---TCCACAGATTATTGACCCCAACCAAA------CCACTTGTCCTTCTCCAACATACCCATGTC
dm3	chr3L:8888591-8888744 -		CCATACTTATAATCGCCTTTGGTCTGGCTTTCTATATACTACTTTCAAAGGTAGGTGCTT---T--G----------G----TATTTGGATT-TT--TCGAGTG----------AGATA---------G----T---G----TTCCTACTTAT---CCCTTAGATTATTGACCCCAACCGAA------CCACTTGTCCTTCTCCAACATACCCATGTC
droSim2	3L:8672689-8672841 -	dsi_17456	CCATACTGATAATCGCCTTTGGTCTGGCATTCTATATACTACTTTCAAAGGTAGGTGCTT---T--G----------G----AATTGGTTT-TT--TCGAGTG----------AATAG---------G----T---G----TTCCTACTTTT---CCCTTAGATTATTGACCCCAACCGAA------CCACTTGTCCTTCTCCAACATACCCATGTC
droSec2	scaffold_0:1159249-1159403		CCATACTGATAATCGCCTTTGGTCTGGCTTTCTATATACTCTTTCAAAGGTAGGTGCTT---T--G----------G----AATTGGT-TTTTTTTCGAGTG----------AATAG---------G----T---G----TTCCTACTTTT---CCCTTAGATTATTGACCCCAACCGAA------TCACTTGTCCTTCTCCAACATACCCATGTC
droYak3	3L:3024971-3025124 +		CCATACTGATAATAGCCTTCGGCTTGGCTTTTTATATACTACTTTCGAAGGTAGGTGCT---T--G----------G----GCTATCGAAT-TT--TCAGAAG----------GTAA---------G----T---G----TTCCTACTTTTT---CCTTTAGATTATTGACCCCAACCGAA------CCACTTGTCCTTCTCCAACATACCCATGTC
droEre2	scaffold_4784:5154599-5154755 +		CCATACTGATAATAGCCTTCGGTCTGGCTTTTACATACTGCTTTCGAAGGTAGGTGCTT---T--G----------G----GATTTCCATT-T----------C-CATTC--AA---AGTAGTAA---------G----T---G----TTCCCACTCTT---GCCCTAGATCATTGACCCCAACCGAA------CCACTTGTCCTTCTCCAACATACCCATGTC

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